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A multi-omics approach to advance precision medicine and study patient heterogeneity in ALS

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A thesis submitted for the degree of

Doctor of Philosophy in Clinical Neuroscience

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Abstract

Amyotrophic lateral sclerosis (ALS) is a fatal neurodegenerative disease caused by degeneration of both upper and lower motor neurons, with death from respiratory failure typically occurring 2-3 years after onset. More than 40 genes are definitively linked to ALS with a further 125 involved in either pathogenic processes or as modifiers of phenotype. However, the complex architecture of ALS has impacted negatively on further genetic variant discovery and the interaction of known and non-canonical variants with transcriptomic factors, such as alterations in gene expression. Despite identifying a number of pertinent risk loci in recent years, genome-wide association studies (GWAS) are plagued by issues. Single nucleotide polymorphism (SNP)-based microarray genotyping approaches can only explain 8.5-20% of the estimated 60% heritability of ALS as only common variants are tagged, leaving the remaining ~40% explicable by rare and low frequency SNPs, other classes of variation such as structural variants, transposable elements, post-transcriptional and splicing alterations, and changes in gene expression. Consequently, more research groups and dedicated ALS consortia such as Project MinE and TargetALS, are opting for next-generation sequencing (NGS) technologies such as whole genome sequencing (WGS) and RNA-sequencing (RNAseq), as they are capable of detecting variation missed by microarray technologies and therefore can be used to better understand the complexity of ALS. NGS can be utilised for precision medicine approaches, which involve harnessing big data and bioinformatics or machine learning frameworks to identify biologically homogeneous groups of individuals. It is therefore important to adopt NGS-based precision medicine strategies in ALS research to define people with ALS into biologically relevant subgroups to better inform biomarker discovery or future clinical trial design.

The overall focus of this thesis was to employ several bioinformatics and machine learning techniques which can exploit the potentialities of WGS and RNAseq to delineate the complex heterogeneity of ALS and provide new molecular insights into disease for the advancement of precision medicine. Chapter 4 reports the update of a previously published NGS bioinformatics pipeline developed by our group, which demonstrates enhanced detection, annotation and prioritisation of structural variants, including transposable elements and tandem repeats. In Chapter 5, I confirm that rare missense variants and in-frame deletions in the tail domain of the neurofilament heavy

chain gene (*NEFH*) increase ALS risk, through a meta-analysis of previous reports from the literature, and variant screening and rare burden analysis of SNPs, indels and structural variants from the Project MinE WGS cohort. This is in agreement with previous reports using smaller sample sizes. Causal associations are also found for intronic SNPs and indels in the rod domain, and a protective effect is identified for a large 113 base-pair deletion in the tail domain; both identified in Project MinE with rare variant burden analysis. Despite these findings, these associations do not have large effect sizes and require more experimental follow-up studies to assess their functional impact before determining whether their inclusion in genetic screening panels is warranted. In Chapter 6, I investigate the molecular architecture of ALS by conducting a case-control differential gene expression analysis of post-mortem motor cortex RNAseq data from the KCL BrainBank (a subsidiary of Project MinE) and TargetALS, which identify genes in the neuropeptide signalling pathway as differentially expressed and enriched in both datasets. Analysis of neuropeptide-related genes and their receptors find that higher expression of *TACR1* and *NPBWR1* is associated with longer disease duration and lower age of onset, respectively, suggesting that neuropeptides could be used as diagnostic and prognostic biomarkers. Finally, in Chapter 7 I identify and characterise three molecular subtypes of ALS which reflect predominant molecular mechanisms of pathogenesis, using unsupervised hierarchical clustering of KCL BrainBank for initial discovery of the clusters, followed by linear discriminant analysis for validation in independent brain and blood datasets. I show that these molecular phenotypes are robust, with their expression signatures being able to distinguish people with ALS from controls, and the motor cortex from occipital cortex and cerebellum regions in the TargetALS cohort. Cell type analysis also reinforces the biological interpretation of the clusters. This demonstrates that these motor-cortex derived molecular phenotypes could be used to successfully stratify people with ALS into biologically relevant subgroups, although further work needs to be carried out to determine whether these subgroups are truly ALS-specific. Distinct cluster-related onset and progression measures in both motor cortex case datasets are also identified, which demonstrates the potential for future identification of subgroup-specific prognostic biomarkers.

“To my grandparents, who inspired my journey into neuroscience and provided immeasurable support and encouragement even in the face of adversity; to my late grandmother, who demonstrated great strength and courage whilst living with PSP; and to my grandfather, whose unwavering resolve and loyalty still spurs me on.”

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Chapter 1. Introduction

1.1 Introduction to ALS

Amyotrophic lateral sclerosis (ALS) is a fatal neurodegenerative disease which is caused by progressive degeneration of upper and lower motor neurons in the brainstem and spinal cord. There are two types of typical ALS, where individuals present with both upper motor neuron (UMN) and lower motor neuron (LMN) involvement at onset, usually between 50-65 years of age; spinal (70-75% of individuals), which causes limb and trunk weakness, and bulbar (25-30% of individuals), which presents as difficulty with speech, swallowing and chewing. As the disease progresses to end-stage, the majority of people with spinal-onset ALS will have some degree of bulbar involvement. Despite ALS being frequently described as a rare disease, the lifetime risk of ALS is approximately 1 in 350 for males and 1 in 400 for females (R. H. Brown & Al-Chalabi, 2017; Ryan et al., 2019), with the mean global prevalence and incidence of ALS currently estimated at 4.1-5.0 and 0.86-1.75 in 100,000 people, respectively (GBD 2016 Motor Neuron Disease Collaborators, 2018; Marin et al., 2017; L. Xu et al., 2020). Typically, ALS is diagnosed based on a combination of clinical and electrophysiological evidence based on the presence of mixed UMN and LMN signs, with several diagnostic classification guidelines, such as the revised El-Escorial, Awaji and Gold Coast criteria (Brooks et al., 2000; de Carvalho et al., 2008; Turner & UK MND Clinical Studies Group, 2022), created over the last three decades to increase diagnostic sensitivity (Costa et al., 2012; De Carvalho & Swash, 2009; Pugdahl et al., 2021) and reduce diagnostic delay, which is the time period between symptom onset and diagnosis. This is necessary as death typically occurs from respiratory failure 2 to 3 years after symptom onset, although this can vary based on site and age of onset, as well as the involvement of genetic and environmental factors.

Traditionally, ALS is defined as being either familial or sporadic. Sporadic ALS (SALS) accounts for approximately 90% of cases, where there is either no apparent family history of the disease or discernible genetic mutation attributed to its onset. The remainder of cases are classified as familial (FALS), which means that at least one first- or second-degree family member has to have previously been diagnosed with ALS, and the individual must harbour a mutation in a highly penetrant Mendelian ALS-linked gene; penetrance refers to the proportion of people carrying a genetic mutation that will go on to develop ALS. Mutations in the 4 main ALS-linked genes *C9orf72, SOD1, FUS* and *TARDBP* account for approximately 60-80% of FALS, although these mutations are also present in up to 15% of people with SALS. As the heritability of SALS, which refers to the proportion of disease explained by genetic variation, is estimated at between 40 and 60% from twin and parent-offspring studies in European populations (Al-Chalabi et al., 2010; Ryan et al., 2019), it suggests that there are other types of variation, i.e. environmental exposures, gene expression levels, epigenetic alterations, additional genetic mutations, that are unaccounted for.

Indeed, there are now upwards of 40 genes that are causally linked to ALS, with a further 130 putatively associated with ALS risk or shown to modify onset or progression (Mejzini et al., 2019). Furthermore, ALS displays a complex disease architecture, with a combination of gene variants with varying effects in addition to environmental and lifestyle factors influencing its onset.

For instance, some genetic variants demonstrate age-related and incomplete penetrance. Age-related penetrance is a phenomenon where ALS onset is dependent on the age of the individual carrying an ALS-linked genetic mutation. This is demonstrated in country and global population-based epidemiological studies, which report that the prevalence and incidence of ALS increases until the peak age of 70-79 (Fontana et al., 2021; L. Xu et al., 2020), with males displaying higher incidence and prevalence rates than females (Fontana et al., 2021; Marin et al., 2017; L. Xu et al., 2020). One example of a genetic variant which displays this phenomena is the *C9orf72* hexanucleotide repeat expansion, whereby the cumulative incidence of people carrying the pathogenic expansion repeat size increases with age, with 50% penetrance occurring at 57 years of age, which is typically the mean age of onset. Furthermore, FALS and SALS demonstrate near identical incidence estimates, with male carriers and those with spinal onset ALS displaying a 2 year reduced median age of onset, reflective of the increased penetrance in those groups (Murphy et al., 2017). In contrast, incomplete penetrance is where not all carriers of a genetic mutation will be affected by the disease. This was recently exemplified from a recent penetrance analysis of *SOD1* carriers in the European population, which found that when aggregating all 180 pathogenic variants, the penetrance estimate was 0.70, although for individual variants, the penetrance is variable: the A5V mutation, which causes rapidly-progressive ALS, has a 100% penetrance, whereas the second most common mutation, I44T, has a penetrance estimate of 0.64. The D91A mutation, which is associated with slower progression, has an estimated penetrance of 0, which is partly due to its mode of inheritance, as it can be inherited in a dominant, recessive or oligogenic fashion (Spargo et al., 2022).

Oligogenicity is another component of the complex disease genetics of ALS, which is where variants in multiple genes, with varying effects and population frequencies, contribute to the onset of ALS. The multistep model of ALS onset rationalises the oligogenic effects of ALS, whereby based on a least squares regression approach conventionally applied to cancer in 5 European ALS population registers, a strong linear relationship between log incidence and log age was found, with a slope estimate suggestive of a six-step process required for ALS onset (Al-Chalabi et al., 2014). Since then, support for the six-step multistep process has been strongly replicated in Italian, Irish, Australian, Danish and Japanese register-based population cohorts (Chiò et al., 2018; Garton et al., 2021; Vucic et al., 2019, 2020). Identification of these steps has been more challenging due to the complex nature of ALS. Indeed, for people with SALS, the impact of highly penetrant ALS risk genes on ALS onset is clear: individuals harbouring genetic variants in *TARDBP*, *C9orf72* and *SOD1* require 2-4 fewer steps for ALS to develop in Italian (Chiò et al., 2018) and South Korean populations (Choi et al., 2022), which corroborates with the finding that reduced age of onset in people with FALS is due to the presence of causal ALS gene variants (Mehta et al., 2019). However, it is clear that as there are still steps unaccounted for, and as there does not appear to be a striking difference in the number of steps needed for ALS onset between FALS and SALS, rare variants and multiple variants with medium to large effects will most likely make up most of the remainder of the steps. A multitude of molecular processes are also implicated in ALS onset and progression, including RNA metabolism, excitotoxicity, oxidative stress, axonal and vesicular transport, neuroinflammation, autophagy, mitochondrial function, nucleocytoplasmic transport and proteostasis (Mejzini et al., 2019), which means that it is hard to pinpoint the processes which induce motor neuron degeneration at a molecular level on an individual basis.

This complexity has posed many challenges pertaining to further gene and variant discovery and the characterisation of molecular processes which contribute to our understanding of pathogenesis and progression in apparently homogenous groups of people with ALS. This is in part due to the traditional genome-wide association study frameworks and microarray technologies used to identify genes and characterise the effects of their mutations and changes in expression levels on the ALS phenotype. This has a consequential effect on the development of precision medicine approaches in ALS, which concerns the identification of effective biomarkers and therapeutic treatments both readily available and accessible via clinical trials for specific groups of people with ALS, based on their biological characteristics. It is therefore necessary to adopt frameworks capable of detecting a wide range of genomic variation as well as capturing subtleties in gene expression in order to define subgroups of people with ALS more accurately to speed up the discovery of novel biomarkers and allow earlier access to clinical trials.

This chapter will highlight current efforts to integrate precision medicine strategies into translational and clinical ALS research, before discussing issues faced by the ALS genomics community in deciphering the genetic and molecular heterogeneity of ALS. Finally, approaches which could be used to resolve the genomic heterogeneity of ALS and ultimately improve precision medicine strategies will be explored, through the adoption of next-generation sequencing (NGS) in combination with bioinformatics, statistical genetics and machine learning methods.

1.2 What is Precision Medicine?

Precision medicine is described as the tailoring of treatment and symptom management to biologically homogeneous groups of individuals, identified through the analysis of omics data with artificial intelligence and machine learning methods. Various types of omics data such as genetic, transcriptomic, epigenetic, proteomic, and clinical information are utilised. The importance of this approach is that biomarkers which are indicative of differential treatment response or disease progression, which cannot be gathered from clinical assessment alone, can be identified (Ginsburg & Phillips, 2018). The creation of clinicogenetic and molecular patient stratification models can also be created for use in further genomic discovery and characterisation studies. In the last year, a large-scale precision medicine initiative, PRECISION ALS (McFarlane et al., 2023), has been established to identify genomic biomarkers and develop progression prediction models. Through a collaborative partnership with 9 academic sites and 7 industry partners throughout Europe, phenotypic and omics data will be collected from over 21,000 people with ALS via a dedicated data platform.

Longitudinal collection of multimodal data will also be achieved as the infrastructure allows the documentation of all stages of the individuals journey through the healthcare system. Although this collaboration is still in the initial data collection phase, it is hoped that this approach will be highly beneficial for ALS research. Despite this effort representing a major milestone in how cross-collaborative data infrastructure can improve patient stratification and biomarker identification, a lot remains to be explored at a more foundational level with regards to understanding the role of causal and modifier genes to molecular mechanisms of pathogenesis, as well as developing frameworks to identify biomarkers of said molecular mechanisms to use for patient stratification, biomarkers of clinical progression, and clinical trial recruitment based on the tested therapeutic’s mode of action.

1.3 Barriers to Precision Medicine in ALS

1.3.1 The genetic classification of ALS is outdated

As previously stated, the classification of ALS is heavily dependent on family history and the presence of causal gene mutations. However, this distinction is highly misleading and detrimental to both people with ALS and the ALS research community. International surveys evaluating clinical testing practices report that 27-49% of people with SALS are offered genetic testing, whereas approximately 90% of people with FALS are afforded this opportunity (De Oliveira et al., 2023; Klepek et al., 2019; Salmon, Anoja, et al., 2022; Vajda et al., 2017), despite FALS often being misdiagnosed as SALS due to small family sizes or age-dependent gene penetrance (Salmon, Kiernan, et al., 2022).

This has a consequential effect upon the identification of individuals who may be eligible for targeted clinical trials and therapies; recent genetic screening studies report that 11-14% of people with SALS carry a pathogenic or likely pathogenic variant in an ALS-linked gene (Ruf et al., 2023; Shepheard et al., 2021; Van Daele et al., 2023), with an estimated 20% of UK individuals in one study having a clinically actionable result according to Genomics England guidelines (Mehta et al., 2022). This, along with the estimation that 54% of *SOD1* and 74% of *C9orf72* incident cases are likely to be SALS (C. A. Brown et al., 2021), and that upwards of 15% of people with SALS meet the eligibility criteria to be recruited into *SOD1* and *C9orf72* gene-therapy based clinical trials (Shepheard et al., 2021), stresses the importance of making genetic testing available to the same percentage of people with SALS as with FALS, to ultimately improve access to appropriate clinical trials and therapies. Although, genetic testing in the UK is currently offered to either those with FALS or young-onset SALS (below the age of 40), which is unjust given that this policy potentially misses 98% of SALS patients with a clinically actionable result (Mehta et al., 2022), as the age of onset of ALS can range from 45 to 75 years of age.

1.3.2 Genome-wide association studies and microarray technologies are falling out of favour for genetic discovery in ALS

In the last two decades, there has been monumental progress in our understanding of how genes contribute to and modulate ALS onset and progression, largely through the application of genome-wide association studies (GWAS), which utilise genetic information from microarray technologies to identify genomic variants associated with ALS risk or phenotype.

Examples of tentative SALS susceptibility loci discovered using this approach in individuals of European ancestry include *DPP6* (rs10260404) (van Es et al., 2008), *ITPR2* (rs2306677) (van Es et al., 2007), *FGGY* (rs6690993) (Dunckley et al., 2007), a 175kb linkage disequilibrium block containing *SUNC1*, *HUS1* and *C7orf57* (rs2708909 and rs2708851) (Chiò et al., 2009), and a locus at chromosome 17q11.2 containing the tag-SNP for *KRT18P55* (rs34517613) (van Es et al., 2007). Several modulators of age of onset have also been discovered; the first being a 750kb spanning region on chromosome 1p34.1, with each copy of the minor allele of the intronic *ST3GAL3* tag-single nucleotide polymorphism (SNP) (rs3011225) conferring a 2.5 year earlier age of onset (Ahmeti et al., 2013). More recently, *CTIF* (rs2046243) and two genes containing SNPs at DNA methylation sites; a 144.7kb region tagged by rs9357140 (*C6orf10/LOC101929163*), and a 16kb region tagged by rs4970944 (*CTSS*). The presence of at least one copy of the major allele of *CTIF* reduces age of onset by approximately 1.3 years (C. Li et al., 2023), with the AA genotype of the *CTSS* SNP delaying onset by two years (M. Zhang et al., 2021). In patients harbouring *C9orf72* mutations, each A allele in *CTIF* delays onset by 1.6 years (C. Li et al., 2023), with the *C6orf10* AA genotype demonstrating a 6 year delayed age of onset (M. Zhang et al., 2018). Survival-associated SALS loci have also been reported, such as *KIFAP3* (rs1541160), where the CC genotype is associated with 14-months longer survival (Landers et al., 2009), as well as *CAMTA1* (rs2412208) and I*DE* (rs139550538), whose GG/GT and AA/AT genotypes correspond to a 4- and 8-month reduction in survival, respectively (Fogh et al., 2016). Although, the only reproducible ALS SNP locus identified thus far has been *UNC13A* (rs12608932) (van Es et al., 2009), with a 5 to 33 month shorter survival in people with ALS carrying the homozygous CC genotype (Diekstra et al., 2012)

GWAS studies can also identify structural variants (SV) and copy number variants (CNV) which are associated with ALS. Structural and copy number variants comprise various forms of genomic imbalance, including insertion, deletion, inversion, duplication and inter-chromosomal translocation (Carvalho & Lupski, 2016; McCarroll & Altshuler, 2007; Roses et al., 2016), with SVs representing a major difference between individuals in health and disease (Lupski et al., 2010; Marshall et al., 2017; Weischenfeldt et al., 2013). The most well-defined ALS SV risk locus captured by GWAS is 9p21.2 (Laaksovirta et al., 2010; Shatunov et al., 2010; van Es et al., 2009), for which the haplotype was later identified as the intronic hexanucleotide *C9orf72* repeat expansion (DeJesus-Hernandez et al., 2011; Renton et al., 2011). Due to the elusive and heterogeneous nature of CNVs, many CNV susceptibility loci discovered with GWAS have been found to be inconsequential (Morello et al., 2018) - only duplications in the survival motor neuron gene *SMN1* consistently demonstrate an association with SALS risk (Blauw, Barnes, et al., 2012; X.-B. Wang et al., 2014).

Despite the wealth of SNP and SV loci discovered by GWAS, only those in *C9orf72*, *UNC13A, CAMTA1* and *SARM1* (Chiò et al., 2023; Su et al., 2022; van Rheenen et al., 2016a, 2021; Vidal-Taboada et al., 2015; Yang et al., 2019) have been consistently associated with ALS risk and survival. Many of the aforementioned previous GWAS associations have been lost in replication studies (Ahmeti et al., 2013; Cai et al., 2014; Y. Chen et al., 2012; Czell et al., 2017; Daoud et al., 2010; Fernández-Santiago et al., 2011; Fogh et al., 2011; Koçoğlu et al., 2021; van Doormaal et al., 2014), whilst for other loci, GWAS replication studies have not been performed. Therefore, it is uncertain whether these genes modulate ALS risk or phenotype, or if their preliminary associations are an effect of the study design. Furthermore, there are several methodological and technical aspects of GWAS and microarray technologies that have hindered both the discovery and replication of causal and modifier genes and their variants in ALS. These are discussed in more detail below.

1.3.2.1 Replicable and reliable associations can only be obtained with large sample sizes and appropriate control-to-case ratios

The main reason why so many associations are refuted in independent replication studies is largely due to the effect known as the ‘winner’s curse’, which is where the estimates of variant effect sizes in discovery studies are often inflated. This means that replication studies will fail as they will be underpowered to detect such associations (Xiao & Boehnke, 2009). One of the reasons why this can occur is that there may be an inadequate case-to-control ratio in the cohorts used in these analyses. It is generally accepted that in order to improve power in genetic association studies, at least 4 controls to every case should be recruited, although this is rarely achieved in practice (Katki et al., 2023). Another reason is that the total sample size is not large enough to detect causal associations, even if they have smaller effect sizes i.e., odds ratio (OR) of 1.3-1.5 (Hong & Park, 2012). There are two recent examples of GWAS that illustrate the benefits of using large sample sizes and higher control-to-case ratios for ALS gene discovery. Using 12,577 cases and 23,475 controls, *MOBP*, *SCFD1*, and a locus fine-mapped for *C21orf2 (CFAP410)*, were discovered and validated in a replication cohort as novel ALS risk loci (van Rheenen et al., 2016a). When expanding this cohort to 27,505 cases and 110,881 controls, 15 risk loci were discovered. These included novel associations for *HLA*, *GPX-TNIP1*, *SLC9A8-SPATA2*, *ERGIC1*, *COG3* and *PTPRN2,* and replication of *SCFD1*, *TBK1*, *NEK1*, *KIF5A*, *C21orf2* (*CFAP410*), and *MOBP-RPSA* loci, alongside the well-defined associations at *C9orf72*, *UNC13A* and *SOD1* (van Rheenen et al., 2021).

1.3.2.2 The calculated genome-wide heritability of ALS is not accurate as GWAS studies and microarray technologies consider only common variation

One important application of GWAS besides the identification of causal variants, is determination of the genetic architecture of ALS through SNP-based heritability estimates. Usually, linear mixed-model approaches are employed in the GWAS framework, which consider all SNPs regardless of their association to account for polygenic effects, which are the combined effects of multiple SNP-based associations in each locus. As a result, the calculated heritability estimates are considerably lower then what is observed in twin and parent-offspring studies; ranging between 12 and 21% (Fogh et al., 2014; Keller et al., 2014). This is because estimates derived from twin and family-based studies compare phenotypic similarities between either monozygotic (identical) and dizygotic (non-identical) twins, or individuals within the family or inherited structure, therefore the genetic contribution of traits can also be influenced by indirect genetic effects from relatives, gene-environment interactions, and epistatic or non-linear effects, which are not captured in traditional SNP-based heritability estimates of unrelated individuals. Furthermore, it is assumed that identical and non-identical twins have similar environmental influences on the studied trait, and that the effects of population stratification and assortative mating are mitigated when using family-based measures of heritability, although these assumptions can be violated (Young et al., 2019; Matthews and Turkheimer, 2022).

More sophisticated methods to calculate SNP-based heritability, such as linkage disequilibrium score regression, which tangles out confounding effects such as population stratification and cryptic relatedness from polygenicity, estimate the heritability of ALS as 8.2% (McLaughlin et al., 2017), which despite replicating a previous population-based estimate of 8.5% identified with the standard GWAS approach (van Rheenen et al., 2016a), still inadequately captures the full genetic architecture of ALS. Therefore, the underestimation of SNP-based heritability ultimately lies within the inability for GWAS to consider rare variation (< 1% MAF), and the inability for microarray technologies to reliably tag low frequency (MAF 0.5-5%) and rare SNPs. In ALS, the drivers of phenotype are rare variants which have medium-to-large effects, therefore by calculating SNP-based heritability using standard GWAS approaches, estimates are constrained by the variance explained by the additive effects of common variants.

1.3.2.3 Variants other than SNPs are not reliably tagged and characterised by microarrays

Whether microarrays are used for GWAS or for the screening of variants in potential ALS risk genes, they cannot characterise more complex variation i.e., small insertions and deletions (indels), SVs and copy number alterations. The genotype of a SNP is easily deduced as the intensity levels of each probe cluster into three groups, representing each of the three possible genotypes. However, as SVs and CNVs usually span multiple probes, intensities have to be either aggregated from adjacent SNPs or across samples to make consensus calls. Microarrays also often incur hybridisation-related biases as single fragments of genomic sequences can map to more than one probe. Furthermore, highly polymorphic regions and tandem repeats are difficult to detect as a lower density of available probes map to those regions (Alkan et al., 2011). As the upper estimate for heritability explained by genetic information captured on genome-wide microarrays for SALS is approximately 20%, this implies that the remainder is in rare variants and other types of genetic variation such as copy number variation, short tandem repeats, post-transcription RNA editing, and epigenetic changes (DeJesus-Hernandez et al., 2011), that cannot be identified easily by microarrays.

1.3.3 Current ALS gene panels for use in diagnostic and research settings are not regulated

Genetic panel screening in ALS is beneficial for not only evidencing an ALS diagnosis, but to also signpost individuals to appropriate therapeutic treatments and identify those best suited for enrolment in gene-mutation specific clinical trials. Despite these advantages, many of the ALS-defined gene panels used in diagnostic and research settings contain genes whose evidence mainly originates from traditional linkage and GWAS study designs, and often contain genes which have conflicting or no evidence to support their role with ALS risk or phenotype. For instance, the Genomics England PanelApp, which curates evidence on 42 genes included in the ALS/motor neuron disease genetic testing panel, finds that only 24 (57.1%) are classified as green, which means that there is sufficient evidence for those genes to explain the disease phenotype, as their variants are pathogenic and diagnostically reportable (Martin et al., 2019). One gene, *NEFH*, is classified as amber as there is borderline supportive evidence for a causal relationship, but there are not enough reported pathogenic or likely pathogenic variants in the literature to be deemed clinically actionable. Furthermore, there is not a well-defined consensus on which genes should be included in these panels, nor is there a rigorous procedure to standardise genetic panels in healthcare and laboratory settings nationwide. A recent worldwide survey of 14 widely used ALS clinical gene panels (Dilliott et al., 2023) identified a total of 91 genes present in at least one panel, with 44% of those unique to only one panel. Furthermore, more than 90% of panels contained the causally linked ALS genes *ANG*, *FUS*, *OPTN*, *SETX*, *SOD1*, *TARDBP, UBQLN2, VAPB, and VCP,* with half of the panels offering the option to screen for the *C9orf72* repeat expansion. There was no relationship with ALS identified for 14 (15.4%) genes; *ABCD1, ABHD12, ATL1, BSCL2, GBE1, HEXA, HNRNPD, HSPD1, LMNB1, PRF1, PRPH2, PSEN1, REEP1, SPAST*.

1.4 Next-Generation Sequencing (NGS) Approaches to Advance Precision Medicine in ALS

As previously mentioned, genotyping microarrays are the most widely used method for detecting SNPs and SVs, as well as quantifiable changes in gene expression, although next-generation sequencing (NGS) approaches (short-read WGS and RNAseq) are rapidly becoming the preferred choice as they can more reliably detect complex genetic variation (Majewski et al., 2011; Spielmann & Mundlos, 2013), multiple gene transcripts and lowly expressed genes, because they do not rely on the selection of known DNA and RNA probes. Instead, the whole genome and transcriptome is randomly sampled and sequenced into 150 base-pair fragments before being mapped to a reference genome, which achieves a consistent average read depth coverage (how many fragments overlap a genomic position) of 30-40x. Consequently, NGS is more sensitive for quantifying gene expression and calling genomic variants as the confidence of the presence of a genetic variant or level of gene expression from dedicated bioinformatics tools are determined from a read-count or abundance-based approach rather than a relative measurement of probe intensity at each gene or base pair (Alkan et al., 2011). Moreover, as NGS provides better distribution of sequencing position and coverage of the non-coding region of the genome and transcriptome, a hypothesis-free experimental design can be employed. The quantification of variation and expression for thousands of genes and regions at any one time is highly beneficial when trying to characterise the genetic and molecular landscape of a complex disease such as ALS.

1.4.1 Design aspects of NGS to consider

1.4.1.1 Tissue Types

The most extensively utilised tissues to study genetic and transcriptomic alterations in people with ALS using WGS and RNAseq are the motor cortex and blood. The motor cortex is a valuable region to examine as regardless of inheritance or clinical phenotype, pyramidal cell degeneration and cytoplasmic phosphorylated TDP-43 inclusion pathology is observed in 97% of individuals (Nolan et al., 2020; Suk & Rousseaux, 2020). There is also substantial evidence that hyperexcitability of the motor cortex can precede UMN degeneration by propagating ALS pathology along the descending corticofugal axons of the corticospinal tract: the ‘dying forward’ hypothesis of ALS (Eisen, 2021; Eisen et al., 2017). Although, the collection and preparation of motor cortex tissue can only occur post-mortem, and questions still emerge over whether any quantifiable changes are a consequence of the end-stage of disease or the differential contribution of various molecular processes throughout the disease course. Nevertheless, it remains a pivotal tissue to interrogate patient heterogeneity in SALS, particularly in transcriptomic studies. Nevertheless, from a precision medicine perspective, it can be more practical to utilise blood tissue as samples can be collected relatively non-invasively and you can more easily and confidently identify genetic and molecular biomarkers of progression and differential treatment response.

1.4.1.2 ALS Sequencing Consortia

As previously elucidated, collaboration between geneticists, bioinformaticians, and clinicians, and data sharing between research centres can be an effective strategy to study the genetic and molecular heterogeneity of ALS. Besides PRECISION ALS, there are already several smaller case-control research initiatives operating both nationally and internationally which have adopted this framework, via collection of NGS data from motor cortex and blood. The largest is Project MinE, which was developed in 2018 with the aim of collecting WGS genetic profiles of 15,000 people with ALS and 7,500 controls of European ancestry from 21 countries, as well as matching RNAseq and methylation data available for a proportion of individuals (Project MinE ALS Sequencing Consortium, 2018). Another notable consortium is TargetALS, which contains WGS and RNAseq data of hundreds of post-mortem brain tissue samples from five centres across the USA (*TargetALS*, n.d.). As these consortia recruit a very high percentage of people with SALS or apparent SALS i.e., people with no family history or mutations in Mendelian or FALS-linked genes, this means that any discoveries are more likely to generalise to the entirety of the ALS population. There is also considerably higher power for detecting novel and rare genetic variants and gene expression alterations as well as confirming or disputing previously identified modulators of ALS risk or phenotype, as a product of the large sample sizes acquired.

1.4.1.3 Use of Bioinformatics Tools to Identify Genetic Variation

One of the most crucial processes in NGS variant discovery is the application of various bioinformatic tools which utilise a range of calling algorithms that perform downstream genotyping and optional variant filtering. Unlike SNPs and indels, which have dedicated best practice guidelines i.e., the Genome Analysis Toolkit (GATK) (DePristo et al., 2011) and Global Alliance for Genomics and Health (Krusche et al., 2019), structural variant calling is largely unregulated. Their intrinsic unpredictability makes it difficult for calling algorithms to distinguish between interspersed duplications and inversions, tandem duplications and insertions, and deletions and translocations (Mahmoud et al., 2019). Stringent benchmarking and evaluation studies of multi-purpose and specific SV callers on both real and simulated short-read WGS data can offer recommendations to researchers, although the general consensus is that there is no singular tool that offers a 'one size fits all' approach to the detection of SVs. For instance, Manta (X. Chen et al., 2016) performs best on non-reference insertions, small-to-medium deletion and duplication variants with micro-homology features (≥ 30bp) and insertions with varying breakpoint sizes, whereas Wham (Kronenberg et al., 2015) and the GRIDSS rearrangement detection suite (Cameron et al., 2017) are suited towards deletion and duplication events (Cameron et al., 2019; Kosugi et al., 2019). Conversely, Delly cannot handle structural variants smaller than 300 base-pairs, and consistently miscalls inversion events (Cameron et al., 2019). Fortunately, in the last 5 years, there have been a proliferation of meta-callers, which integrate several different SV tools (Collins et al., 2020; O'Donnell & Fischer, 2020; Zarate et al., 2020) as well as more specialised SV calling algorithms, such as MELT for mobile element insertions (Gardner et al., 2017), ExpansionHunter and ExpansionHunter Denovo for known and novel tandem repeat expansions (Dolzhenko et al., 2019, 2020), TARDIS for interspersed duplications (Soylev et al., 2019), and for SVs which reside in low complexity regions (Delage et al., 2020; Kosugi et al., 2019).

1.4.2 Whole Genome Sequencing (WGS) Analysis Frameworks used in ALS

1.4.2.1 Case-Control Variant Screening

This approach consists of screening for specific classes of genetic variation in people with ALS and controls using variant calling tools, before determining their pathogenicity status and comparing their frequency in both populations to determine whether they contribute to ALS susceptibility. Generally, these studies will look for variants in genes present in clinical and laboratory-based testing panels or identified from the literature, as an unbiased genome-wide approach can be computationally exhaustive and time consuming.

As GWAS is suitable for screening of SNPs, WGS is used to offer populational insights on their contribution to the complexity of ALS. One of the most recent and most notable studies was a WGS analysis of 1043 Italian people with ALS who were screened for variants in 42 ALS-linked genes, which identified that 26.9% of people with ALS, including 21.5% of people with SALS, carried a disease-causing variant. The same authors also found that 10.7% carried the *UNC13A* C/C survival modifier SNP genotype, with 24.2% more people with early onset ALS (< 50 years) carrying a causal mutation than late-onset ALS (> 75 years), consistent with the multistep model of ALS (Grassano et al., 2022). There have also been genetic screening studies of German (Krüger et al., 2016), Australian (McCann et al., 2021), and British (Morgan et al., 2017) populations which also report a significant proportion of people with ALS carrying more than one pathogenic variant in ALS-associated genes, with oligogenic SALS cases in the Australian population demonstrating earlier age of onset than those without a mutation (McCann et al., 2021).

There are a couple of instances where the advantages of using WGS to identify and genotype SVs comes into effect. Recently, two repeat expansions were associated with increased ALS susceptibility in individuals of European ancestry; a downstream tetranucleotide (TTTA) *NEK1* repeat of ≥ 11 from the largest ALS GWAS to date from Project MinE (van Rheenen et al., 2021), and a non-coding CA repeat of ≥ 19 in *STMN2*, using targeted PCR for ~390 SALS and 330 controls (Theunissen, Anderton, et al., 2021). Individuals harbouring the *STMN2* repeat were reported to have a 7.5 year earlier age of onset, with accelerated disease progression in people with bulbar-onset SALS. However, both of these associations were lost when applying ExpansionHunter to independent WGS cohorts with the same European genetic background: neurologically normal individuals also displayed *NEK1* and *STMN2* repeat lengths above their proposed pathogenic thresholds (Grima et al., 2022; Ross et al., 2022), which was likely detected as large population-based control cohorts were used.

The most encouraging result so far for the ALS community is the confirmation that the *C9orf72* repeat expansion modifies age of onset in bulbar-onset ALS, and that there are novel associations with a *VCP* inversion and *ERBB4* insertion in bulbar- and respiratory-onset ALS, respectively, for reduced age of onset and survival (Al Khleifat, Iacoangeli, van Vugt, et al., 2022). These were ultimately discovered because the large sample size used for screening (over 6,000 individuals from Project MinE) combined with the use of dedicated WGS variant calling tools and a bioinformatic validation protocol meant that the above associations had large effect sizes and the variant calls were robust. The likelihood that screening for these variants in clinical and prognostic settings would be beneficial needs to be elucidated, especially as a possible synergistic interaction for ALS risk was found in *C9orf72* expansion carriers who also harboured the *VCP* inversion, and that since the discovery of *ERBB4* as a causative ALS gene in 2013, only missense mutations have been linked to ALS pathogenesis (Scarlino et al., 2020a; Takahashi et al., 2013, p. 4, 2019, p. 4).

1.4.2.2 Meta-Analysis

Meta-analysis is a statistical framework which involves combining the findings from multiple independent genetic association studies in order to statistically determine the absolute effect of genetic variants to disease risk. The advantage of using this approach is that by pooling results from multiple smaller studies, you can more accurately estimate the effect sizes of the genetic variants being tested, therefore enhancing statistical power and making any findings highly generalisable as more appropriate sample sizes are utilised (Haidich, 2010). The benefits of meta-analysis in ALS are huge, as you can more credibly confirm or refute the association of a novel or putative ALS-linked gene, or causally linked genes whose association with ALS have long been established but no definitive evidence exists from replication studies.

Several multicentre case-control meta-analyses have been performed in recent years to validate the role of certain SVs in ALS risk. The validation of *NIPA1* polyalanine and *ATXN1/ATXN2* polyglutamine intermediate trinucleotide repeats through separate meta-analyses of the Project MinE cohort have been instrumental in further explicating their role as ALS susceptibility genes (Sproviero et al., 2017; Tazelaar et al., 2019, 2020); repeat expansions in *ATXN2* and *NIPA1* had previously been linked to ALS, albeit with conflicting results in GWAS and CNV genome-wide screens (Blauw, van Rheenen, et al., 2012a; Dekker et al., 2016; Elden et al., 2010). However, despite functional evidence indicating that these genes participate in analogous *C9orf72* processes, including defective intracellular RNA processing and endoplasmic reticulum transport (Martinez-Lage et al., 2012; Tazelaar et al., 2020), all three genes failed to show a modifying effect on age of onset or survival in both intermediate repeat-positive SALS cases and those harbouring *C9orf72* repeat expansions (Sproviero et al., 2017; Tazelaar et al., 2019, 2020). The recruitment of consanguineous European and American subjects within the Project MinE cohort could have contributed to this finding, as in Southern European, Korean, Japanese and Northern Indian populations, large normal *ATXN2* repeat alleles have been linked to increased ALS susceptibility (Gonçalves et al., 2020; Y.-E. Kim et al., 2018; Narain et al., 2017; Naruse et al., 2019; Tavares de Andrade et al., 2018).

Another WGS study which utilised 8,747 European and American samples in addition to meta-analysing 9 previously studied populations, finally confirmed that *SMN1* and *SMN2* copy number is not determinant of survival or age of onset in people with ALS, nor is their copy number distribution on ALS susceptibility (Moisse et al., 2021), in accordance with previous reports on smaller datasets (Corcia et al., 2002, 2018). A further meta-analysis, which combined European and North American datasets from four recently published studies and British Project MinE samples, found 24-30 intermediate *C9orf72* hexanucleotide repeat expansions to be an adjuvant to ALS susceptibility, contrary to the long-held belief that only expansions 100-1000 repeats in size increase ALS risk (Iacoangeli, Al Khleifat, Jones, et al., 2019). Since then, this association has also been identified in the Finnish population, for compound heterozygous carriers of two intermediate length alleles where the longer allele is larger than 17 repeats, with an additional connection to reduced survival (Kaivola et al., 2020). Further studies need to address these results in more homogeneous populations, such as Ashkenazi and North African Jews, where only 0.52% of people carry intermediate repeat alleles (Goldstein et al., 2018), and Sardinia, where 13.6% of all ALS cases carry the *C9orf72* expansion (Borghero et al., 2014), as well as in a wider context; the only other support for *C9orf72* compound heterozygosity is in a British frontotemporal dementia report of someone with a 200-repeat long allele (Cooper-Knock et al., 2013) and a Belgian ALS-frontotemporal dementia cohort with homozygous repeats ranging from 8 to 21 units (Gijselinck et al., 2016).

1.4.2.3 Rare Variant Burden Analysis

Burden analysis is a type of gene-based association test which collapses variants into gene- or regulatory region-based units. The purpose of this is to increase the power of identifying rare or low-frequency variants in case-control studies, which could be missed in a standard variant-by-variant screening approach, particularly if there are many variants which would not survive multiple testing correction (S. Lee et al., 2014). There are several types of burden methods that one can employ, with the most frequently used being the combined multivariate and collapsing (CMC) (B. Li & Leal, 2008), sequence kernel association test (SKAT) (Wu et al., 2011), the optimal unified test (SKAT-O) (S. Lee et al., 2012), and Madsen-Browning (Madsen & Browning, 2009).

Each of these methods have their advantages. For instance, the CMC method is useful if all of the rare variants are assumed to be causal and have similar effect sizes, as the means of each variant are compared in different MAF categories. The Madsen-Browning test is similar but uses a combination of a weighted-sum test and permutation of case status to adjust for the variant weights and more reliably identify an excess of variants in a gene or region which contribute to disease. However, both SKAT tests are more commonly used, as because a variance component approach is adopted to evaluate the distribution of variants, they consider that there will be a large amount of non-causal variants, and causal variants who display different directions of effect.

In recent years, exome-wide variant burden analysis has been integral for the discovery of *NEK1* (Kenna et al., 2016), *GLT8D1* (Cooper-Knock et al., 2019), *DNAJC7* (Farhan et al., 2019), and *TUBA4A* (B. Smith et al., 2014) as causal and modifier ALS genes. Burden analysis frameworks have also been used in combination with WGS to identify novel associations between gene variation in *MYH15* (H. Kim et al., 2019), *CAV1* (Cooper-Knock et al., 2021) and *IL18RAP* (Eitan et al., 2022) with ALS susceptibility. Project MinE has also been an invaluable resource for refuting associations due to the sheer scale of WGS data available. The most recent example is tumor protein p73 (*TP73*), a transcription factor belonging to the p53 tumor suppressor gene family which is responsible for regulating apoptosis in the cytoplasm and mitochondria (Melino et al., 2004). It was initially identified as a potential SALS risk gene by initial exome screening of 87 cases and 324 controls with variant prioritisation tools and subsequent sequencing in two additional cohorts. Altogether, twenty-four rare nonsynonymous pathogenic variants were identified, at a similar frequency reported in other ALS-related genes (Russell et al., 2021). Although, the association of rare non-synonymous *TP73* variants was refuted in a much larger cohort of 8,230 cases and 9,671 controls obtained from Project MinE and the ALS Knowledge Portal, as a large number of controls carried these variants, therefore diluting the previous association (Dilliott et al., 2022). Another example is *CHCHD10,* a mitochondrial gene which was initially suggested as a new ALS gene after an initial report of a mutation carrier with mitochondrial disease who also displayed ALS-like features and related phenotypes, such as myopathy and cerebellar ataxia (Bannwarth et al., 2014), and follow-up screening determining that pathogenic non-synonymous variants are present in people with FALS (Johnson et al., 2014). Although, analysis of all non-synonymous *CHCHD10* variants in 4,365 cases and 1,832 controls of Project MinE using a range of aggregate gene burden analyses methods did not find any additional evidence supporting their role in ALS, as burden analyses were insignificant and carriers of *CHCHD10* mutations did not exhibit pure ALS phenotypes (“CHCHD10 Variants in Amyotrophic Lateral Sclerosis,” 2018).

1.4.3 Bulk RNAseq Analysis Frameworks used in ALS

1.4.3.1 Differential Expression Analysis

The most common use of RNAseq data is to quantify and compare the levels of gene expression between people with ALS and controls, by performing differential expression analysis. The number of reads which map to each gene are acquired via alignment to a reference genome or transcriptome, before aggregating the counts of each transcript to produce gene counts. These are then normalised for factors such as gene transcript length, average number of reads per sample and sequencing protocol and platform specific batch effects (Conesa et al., 2016). Popular packages used to perform expression analysis include edgeR (Robinson et al., 2010) and DESeq2 (Love et al., 2014). They take normalised gene count matrices and phenotypic information containing covariates to adjust for any potential factors which may affect the accuracy of expression estimates, such as sex, age, and site of onset. Further preprocessing may be conducted, such as the removal of genes with low read counts across samples, and algorithm-specific normalisation. Both of these packages perform parametric analysis as they assume a negative binomial distribution of the data; edgeR introduces sources of bias into the design to perform normalisation and differential expression, whereas DESeq2 normalises based on size factors, which is the median ratio or geometric mean of all samples for each gene (Conesa et al., 2016). Once the list of differentially expressed genes (DEGs) are obtained, downstream analysis can be performed to elucidate the biological processes that the DEGs are involved in. Typical methods include gene enrichment, pathway and network analysis.

1.4.3.2 Molecular Subtyping

Molecular subtyping involves applying various machine learning techniques to expression data to cluster individuals into biologically homogeneous groups, which is the main method implemented in precision medicine frameworks. Unsupervised machine learning approaches, which do not require labelled data such as ALS-control status, are typically used to identify molecular phenotypes which can be used for stratification, as they can find unknown clusters of genes with similar expression profiles which would otherwise be hidden.

There have been several recent studies which have performed molecular subtyping using post-mortem brain expression data of people with SALS and controls. The earliest study, performed in 2015, used hierarchical clustering to analyse the motor cortex transcriptome of 31 people with SALS and 10 controls. They identified three clusters; one represented a control-specific signature, with two being unique to SALS. The first group, termed SALS 1, was occupied by 16 patients and exhibited increased expression of genes involved in antigen processing, glycolysis and mitochondrial energy homeostasis, whereas the remainder of people with ALS, assigned to SALS 2, displayed downregulation in expression of these pathways. In fact, the SALS 2 expression signature was enriched for several biologically relevant pathways, with the upregulation of genes involved in extrinsic apoptotic signalling, caspase activation and cytokine signalling, and the downregulation of antigen processing genes, vascular endothelial growth factors, alongside differential expression of cell adhesion genes (Aronica et al., 2015). A subsequent follow-up study focusing on the expression of 203 causal and susceptibility-linked ALS genes was performed in the same dataset using the same clustering approach, which again, identified two subgroups of SALS and a control-specific cluster. A total of 118 genes were differentially expressed between SALS and controls, with 75 of them residing in SALS 2. Functional analysis revealed that SALS1 was enriched for intracellular signal transduction, regulation of cellular communication and chemotaxis, whereas SALS2 showed enrichment for oxidative stress responses, cytoskeleton organisation and cellular localisation, confirming that these subtypes confer diverging processes of ALS pathogenesis in specific subgroups of patients (Morello et al., 2017).

Other molecular stratification studies have been able to separate people with ALS based on their dominant pathology, with hierarchical clustering analysis of 148 frontal and motor cortex transcriptomes of people with SALS revealing that samples can be assigned to one of three distinct molecular subtypes; oxidative and endoplasmic reticulum stress (61%), TDP-43 mediated transposable element activation and increased cytoplasmic aggregate formation (20%), and glial activation (19%). Further analysis also confirmed that three transposable elements were significantly upregulated in motor cortex tissue in those assigned to the transposable element subtype - long interspersed nuclear element (LINE) L1HS, and the small interspersed nuclear repeat family classes AluYk12 and AluYa5 (Tam et al., 2019). Finally, 451 samples from 208 people with ALS from a publicly available ALS RNAseq dataset (Prudencio et al., 2020) were analysed using the same approach, which yielded three subtypes: glial activation with reduced transposable element expression, oxidative stress and synaptic signalling, and dysregulation of transcription. These strengthen the support for the previous defined molecular phenotypes. Interestingly, people with ALS assigned to the glial subtype demonstrated the fastest disease progression, with a median survival of 28 months (Eshima et al., 2023).

Chapter 2. Summary of Thesis Objectives

In this thesis, I demonstrate how exploiting the potentialities of large-scale NGS data by using several bioinformatics and machine learning approaches can help us to decipher the genomic heterogeneity of ALS, in relation to the missing heritability incurred by GWAS and microarray-based technologies. These are explored in depth using two cohorts which have predominantly recruited people with SALS: Project MinE and TargetALS.

Chapter 4 explores how WGS can advance our understanding of the genetic basis of ALS, in particular through the lens of structural variation. I develop an upgraded version of a previously developed end-to-end bioinformatics pipeline, DNAscan2, through the addition of tools frequently used for WGS studies of complex neurodegenerative diseases.

Chapter 5 examines how genetic variation in the neurofilament heavy chain gene (*NEFH*) influences ALS susceptibility in a combined cohort of 11,130 people with ALS and 7,416 controls from a literature search and the Project MinE cohort. I firstly analysed the contribution of previously identified SNVs to ALS risk by performing a literature-based meta-analysis of genetic association studies which employ traditional sequencing and NGS approaches. Comprehensive screening of SNVs and SVs in the Project MinE cohort was then performed, followed by assessment of their contributions to ALS risk via logistic regression and rare variant burden analysis.

In Chapters 6 and 7, I utilise bulk RNAseq expression data of the motor cortex from TargetALS and a subset of Project MinE (KCL BrainBank), which when combined, represents the largest motor cortex expression cohort to date. Chapter 6 assesses the molecular landscape of ALS by performing independent case-control differential expression analyses of both cohorts. Differentially expressed genes underwent gene and pathway enrichment analysis, with genes common to both datasets reviewed in regard to their involvement in known mechanisms of ALS pathogenesis. Correlation analysis of genes implicated in commonly enriched pathways was also performed against clinical outcomes; namely age of onset and survival. Cell type deconvolution was performed to assess if gene enrichment results were a product of the differential contribution of cell types in both datasets. In Chapter 7, I try to test the hypothesis that molecular subgroups of people with ALS are defined by a predominant molecular mechanism of pathogenesis that reflect differences in onset, progression and survival measures. I do this by performing unsupervised hierarchical clustering of KCL BrainBank cases to generate the molecular subtypes, before determining their molecular architectures via gene enrichment, network and cell composition analysis. Subtype validation was achieved by applying linear discriminant models to the cases from TargetALS, as well as Italian and Dutch blood expression datasets. I also determine the ALS and regional specificity of the expression signatures of each subtype using KCL BrainBank, TargetALS and Dutch controls, and occipital cortex and cerebellum samples from TargetALS before constructing case-control and motor cortex-other region logistic regression classifier models. Phenotype analysis was also performed to assess subtype-specific clinical outcomes.

Chapter 3. Materials and Methods

3.1 Data Preparation

This section outlines the data preparation protocol of datasets that were used for analysis in multiple chapters. The Project MinE WGS dataset was used for Chapters 4, 5 and 7. The KCL BrainBank and Target ALS RNAseq data were used for Chapters 6 and 7.

3.1.1 Project MinE WGS Dataset

Genomic DNA from venous blood drawn from patients and controls was isolated using standard methods before DNA integrity was assessed using gel electrophoresis. Samples were sequenced using Illumina’s FastTrack Services (San Diego, CA), using PCR-free library preparation on the Illumina HiSeq2000 platform (for Chapters 4, 5 and 7) and HiSeqX platforms (for Chapter 5) to ~35× coverage with 100 bp reads and ~25× coverage with 150 bp reads, respectively.

3.1.1.1 Development of a next-generation sequencing bioinformatics analysis pipeline

Sequenced samples were aligned to the hg38 genome using BWA-mem and were provided to us in compressed reference-oriented alignment map (CRAM) format to be inputted into DNAscan and DNAscan2.

3.1.1.2 Investigating the role of *NEFH* as an ALS risk gene

Sequencing data alignment to GRCh37 (with the Issac aligner) and variant calling (SNVs and indels with Strelka; SVs with Manta) were performed using the Illumina Isaac pipeline.

3.1.1.3 Utilising hierarchical clustering to identify molecular subtypes of ALS

Sequenced data was aligned to GRCh37 using BWA-mem and binary sequence alignment/map (BAM) format files were generated for each individual.

3.1.2 RNAseq Protocol

3.1.2.1 MRC London Neurodegenerative Diseases Brain Bank (KCL BrainBank)

3.1.2.1.1 Purification, isolation, and quality control

For all individuals, postmortem delay (PMD), defined as the time between death and tissue being frozen in hours, was collected, before the 100mg frozen tissue blocks were divided; one for RNA purification and the other for DNA. The 30mg tissue block for RNA was homogenised using a Qiagen PowerLyzer 24 Homogenizer. Total RNA was purified from the homogenate using the standard protocol of the RNeasy Lipid Tissue Mini Kit (Qiagen), with on-column DNAse digestion. RNA integrity was estimated using Agilent Bioanalyzer 2100’s RNA 6000 Nano assays. RNA quantification was performed using a NanoDrop.

3.1.2.1.2 Library preparation and RNA sequencing

Library preparation was performed using the standard Illumina TruSeq Stranded Total RNA Sample Preparation Guide with Ribo-Zero Human/Mouse/Rat (October 2013 Rev E.). Fragmentation steps were tailored to degrees of degraded RNA samples using Agilent Bioanalyzer 2100’s Nano assay results from the previous section. Libraries were validated using an Agilent Bioanalyzer 2100 to assess fragment size distribution. Library concentrations were estimated using a Qubit RNA High Sensitivity Assay Kit. Nanomolar (nM) concentrations were estimated using nM = ng/ul X (1500/Average bp). Libraries were sequenced using Illumina HiSeq 4000 flow cells with 150bp paired-end reads with a target depth of 30 million clusters (60 million reads per sample).

3.1.2.2 TargetALS

Information for the library preparation and RNA extraction of the TargetALS dataset is available at http://www.targetals.org/wp-content/uploads/2020/11/README-1.zip.

3.1.3 RNAseq Data Processing Pipeline

Paired FASTQ files from KCL BrainBank and TargetALS datasets (used in Chapters 6 and 7), and the Zucca PBMC case-only dataset (used in Chapter 7) were transformed to raw transcript counts using a standard bioinformatics processing pipeline (available at https://github.com/rkabiljo/RNASeq_Genes_ERVs). Paired reads were interleaved using BBMap reformat (v38.18.0) under default options before adapters were right-clipped and low-quality reads were removed using BBMap bbduk (v38.18.0), as part of the BBTools suite (Bushnell, 2014). The interleaved reads were aligned to hg38 using STAR (v2.7.10a) under default settings (Dobin et al., 2013), using the Homo_sapiens.GRCH38.104.gtf reference assembly. Raw transcript counts for each gene were then quantified using HTSeq (Anders et al., 2015) on a sample-wide basis before merging into dataset-specific matrices.

3.2 Development of a next-generation sequencing bioinformatics analysis pipeline

The information presented below was restricted to the Supplementary Methods in the publication due to journal formatting constraints.

3.2.1 Datasets

To compare the SNV and indel calling performance of Freebayes, Strelka2 and GATK Haplotype Caller, we used the paired-end Illumina HiSeq4000 WES of NA12878 (NCBI SRA Accession: ERR1905890) and Illumina HiSeqX PCR-free WGS of HG002 (NCBI SRA Accession: SRR14724544). Samples were aligned to the hg19 genome using the `-alignment` flag of DNAscan in both fast and normal mode prior to SNV and indel calling. Alignment is performed by HISAT2 in fast and normal mode, with BWA-mem introduced in the latter for realignment of soft clipped and unaligned reads to improve the detection of small indels and structural variants in downstream calling steps. Structural variant calling performance of Manta and Delly was evaluated using the aligned HG002 reads in addition to simulated paired-end Illumina WGS reads containing the positions of haplotype-resolved deletion and inversion calls of NA12878 (Sudmant et al., 2015), generated and aligned to the hg38 genome using the VISOR package (Bolognini et al., 2020). For comparing the variant calling and computational power of the new and previous implementations of DNAscan, we utilised 10 UK control WGS samples sequenced as part of the Project MinE amyotrophic lateral sclerosis sequencing consortium (Project MinE ALS Sequencing Consortium, 2018). Sequencing information is provided in Chapters 3.1.1 and 3.1.1.1.

3.2.2 Benchmarking of variant callers for DNAscan2

It was not necessary for callers associated with every additional functionality to undergo benchmarking as they either demonstrate beneficial value for identifying novel disease relevant loci i.e., ExpansionHunter Denovo (Fazal et al., 2020; Rafehi et al., 2019), or consistently show high performance in benchmarking studies i.e., MELT for mobile element insertion detection (Kosugi et al., 2019; Vendrell-Mir et al., 2019).

3.2.2.1 SNVs and Indels

The calling performance of Freebayes and GATK HaplotypeCaller was assessed by running DNAscan with the `-variantcalling` flag in fast, normal and intensive modes for the NA12878 WES and HG002 WGS samples. Fast and normal mode uses Freebayes to call SNVs and indels from a coordinate sorted BAM file. Intensive mode employs GATK HaplotypeCaller to call indels from genomic positions (identified from HISAT2 and BWA-mem alignment) that contain at least one read that potentially harbours a deletion or insertion variant. A similar approach was adopted for Strelka2; both SNVs and indels were called from aligned reads generated by fast and normal mode of DNAscan, with the BED file of probable indel variant positions being used to separate output into SNV and indel variant files with the VCFtools `--exclude-bed` and `--bed` flags, analogous to DNAscan intensive mode. For NA12878, Strelka2 was run with the `--exome` flag. Benchmarking of variant calling performance was performed using hap.py v0.3.14 (*Haplotype Comparison Tools*, 2015/2021) with the RTG vcfeval engine. An example command is shown below, where the baseline VCF and confident regions BED file correspond to the appropriate true positive callsets used to evaluate the SNV and indel calls:

```
hap.py --false-positives {confident_regions.bed} –-reference hg19.fa –-
report-prefix {outdir} –-engine=vcfeval –-threads {4} {baseline.vcf}
{comparison.vcf}
```

The NA12878 WES calls were evaluated against the National Institute of Science and Technology (NIST) with Platinum Genomes phase transfer small variant truth set (v3.3.2). Confident call regions were defined as the hg19 exome probe locations from the Agilent SureSelect Human All Exon v5 kit (ELID:S04380110). HG002 calls were evaluated with both the truth variants and confident regions of the NIST small variant benchmarking (v4.2.1) and Genome In A Bottle Challenging Medically-Relevant Genes (GIAB CMRG v1.00) datasets.

3.2.2.2 Structural Variants

The structural variant detection power of Manta and Delly was assessed in a similar fashion to that of SNV and indel callers. The HISAT2 and/or BWA-mem aligned BAM files of HG002 and NA12878 WGS samples were processed by Manta as per the old DNAscan implementation, with the same approach adopted for Delly as to obtain a comparable dataset. Calls were then evaluated using Truvari v2.2.1 (*Spiralgenetics/Truvari*, 2018/2021) using the following command:

```
truvari bench -b {baseline.vcf} -c {comparison.vcf} -f {reference.fasta} -
o {outdir} --includebed {confident_regions.bed}
```

For HG002, the performance of Delly and Manta on detecting deletions was evaluated using the variant calls and confident regions of the GIAB CMRG deletion SV truth set (v0.6). Deletion and inversion calls of NA12878 were evaluated using calls from the 1000 Genomes structural variant map (Sudmant et al., 2015) as the comparison VCF. To further compare the obtained structural variant calls, the `--sizemin` and `--sizemax` flags were supplied to Truvari. Parameters were defined as 50-100, 101-1000, 1001-10000 and 10000-50000bp (the default `--sizemax` parameter of Truvari).

3.2.3 Comparison between DNAscan and DNAscan2

3.2.3.1 Variant Calling Performance

Both SNV/indel and structural variant calls were evaluated using precision, recall and F-measure metrics calculated by hap.py and Truvari, where precision is $\frac{True\ Positives}{(True\ Positives+False\ Positives)}$, recall is $\frac{True\ Positives}{(True\ Positives+False\ Negatives)}$ and F1 score is $\frac{True\ Positives}{True\ Positives+\frac{1}{2}(False\ Positives+False\ Negatives)}$.

Where possible, calling performance of DNAscan and DNAscan2 was assessed by averaging the number of SNV/indel, SV, repeat expansion and MEI calls and STR loci obtained for all Project MinE samples. SV and MEI calls were also separated into their respective subclasses i.e., deletions, insertions, inversions, duplications, Alu, SVA, LINE1. Additionally, the number and percentage of filtered synonymous and non-synonymous SNV variants was acquired from the classification given by refGene annotation.

3.2.3.2 Computational Performance

Computational efficiency of the SNV/indel and structural variant callers was assessed by obtaining the wall and CPU time (in hh:mm:ss format) and RAM usage (maximum resident set size in gigabytes) for HG002 and NA12878 samples from the SLURM `sacct` command `--format` `“Elapsed,CPUTime,MaxRSS”`. The same approach was applied for the comparison of DNAscan and DNAscan2, albeit with time and memory usage being averaged across the 10 samples, and estimated disk read and write usage obtained with addition of `“MaxDiskRead,MaxDiskWrite”` to the above `sacct` command.

3.2.4 Hardware

All tests were performed on an Intel Xeon E5-2670 2.6GHz processor with 4 CPUs and 16Gb RAM (in line with the standard computational requirements of DNAscan), except for processes which involved Freebayes, which ran with 4 CPUs and 64Gb RAM.

3.2.5 Data Availability

The variant call file containing haplotype-resolved deletion and inversion calls of NA12878 is available at:

http://ftp.1000genomes.ebi.ac.uk/vol1/ftp/phase3/integrated_sv_map/supporting/GRCh38_positions/ALL.wgs.integrated_sv_map_v1_GRCh38.20130502.svs.genotypes.vcf.gz

The NA12878 NIST with Platinum Genomes phase transfer small variant callset (v3.3.2) is available at:

https://ftp-trace.ncbi.nlm.nih.gov/giab/ftp/release/NA12878_HG001/latest/GRCh37/HG001_GRCh37_GIAB_highconf_CG-IllFB-IllGATKHC-Ion-10X-SOLID_CHROM1-X_v.3.3.2_highconf_PGandRTGphasetransfer.vcf.gz

Probe regions used for the whole exome sequencing of NA12878 are available from the Agilent SureDesign Dashboard (https://earray.chem.agilent.com/suredesign/). Account registration and sign-in is required to access the regions file from the Agilent catalogue (S04380110_Regions.bed).

The HG002 NIST small variant benchmarking callset containing variant calls and confident regions files (v4.2.1) are available at the following directory:

https://ftp-trace.ncbi.nlm.nih.gov/giab/ftp/release/AshkenazimTrio/HG002_NA24385_son/NIST v4.2.1/GRCh37/

The HG002 GIAB CMRG small variant calls and confident regions files (v1.00) are available at the following directory:

https://ftp-trace.ncbi.nlm.nih.gov/ReferenceSamples/giab/release/AshkenazimTrio/HG002_NA24385_son/CMRG_v1.00/GRCh37/SmallVariant/

3.3 Investigating the role of *NEFH* as an ALS risk gene

3.3.1 Quality Control of Project MinE

After sequencing data was processed (see Chapters 3.1.1 and 3.1.1.2), sites with a genotype quality <10 and variants with low quality scores (<20 for single nucleotide variants and <30 for indels) were removed. Samples with a transition-transversion ratio, total number of single nucleotide variants, indels and singletons outside the interval mean ± 6 SD from the full distribution of samples were removed. Variants with missingness >2% across all samples were excluded. Genetically inferred sex, based on the number of X and Y chromosomes, was compared to the sex reported in the phenotypic data. The full dataset consisted of 9,050 individuals: 6,603 ALS cases and 2,447 age and sex-matched controls. We then removed duplicates and individuals who did not have available matching clinical or variant information.

3.4 Differential gene expression analysis of two large ALS sequencing consortia

3.4.1 TargetALS Sample Selection

In this study, we included 234 samples from 132 subjects from the TargetALS dataset (information about sequencing available in Chapter 3.1.2.2). The region distribution is as follows: 112 samples in the medial motor cortex, 112 in the lateral motor cortex and a further 10 samples in unspecified motor cortex. Of these, 30 subjects contributed a single sample, while 102 subjects contributed two samples from two different regions of the motor cortex. Figure 3-1A shows the principal component analysis of the 234 samples, coloured by the motor cortex region, which showed that the motor cortex regions do not form distinct groups. Instead, there appears to be a strong sex effect in this cohort (Figure 3-1B). To assess if merging the three motor cortex regions was suitable, we performed separate case-control differential expression analysis of the medial and lateral motor cortices and compared the results to an analysis which pools all motor cortex regions together. We did not perform differential expression analysis for the unspecified motor cortex as there was only 10 samples available. In the medial motor cortex (93 ALS cases and 19 controls), 42 genes crossed genome wide significance (corrected p-value<0.05), with 39 of these genes (93%) also being significant in the merged dataset. In the lateral motor cortex (96 ALS cases and 16 controls), 8 genes crossed genome wide significance (corrected p-value<0.05). All these genes are significant in the merged dataset. Therefore, the merged dataset was used as it gives us more statistical power and still detects the vast majority of differentially expressed genes in the two regional subsets.

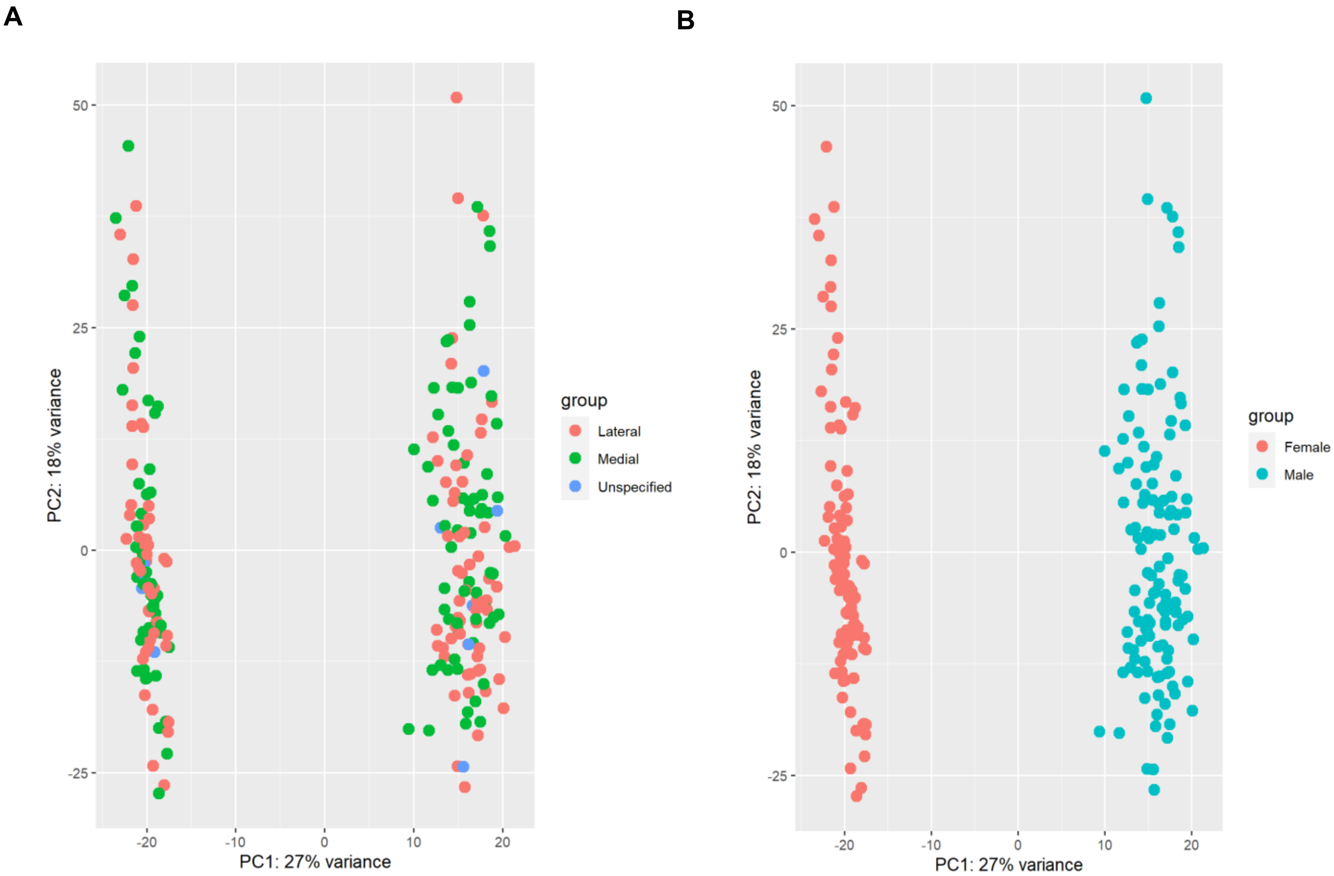

Figure 3-1. Principal component analysis of 234 samples (cases and controls) from a total of 132 individuals in the TargetALS dataset. Samples were coloured by A) motor cortex region and B) sex.

3.4.2 Gene Expression Explorer Webserver

The backend and frontend code for the webserver is publicly available at (https://github.com/guypwhunt/alsgeexplorer) and requires R v4.1.2 ≤.

3.5 Utilising hierarchical clustering to identify molecular subtypes of ALS

3.5.1 RNAseq Dataset Preparation

Information about the preparation of the KCL BrainBank and TargetALS datasets are available in Chapters 3.1.2.1 and 3.1.2.2. The library preparation and RNA extraction of the Zucca PBMC dataset is available at (Zucca et al., 2019) and the RNA sequencing and microarray normalisation protocol for the van Rheenen PBMC dataset is available at (van Rheenen et al., 2018). The Zucca dataset (RNA-seq) is available at GEO: GSE106443, GSE115259. The van Rheenen dataset (microarray) is available at GEO: GSE112681.

3.5.2 KCL BrainBank Methylation Microarray Preparation

DNA methylation was analysed using Illumina Infinium EPIC array following the standard Infinium HD array methylation protocol (Illumina).

Chapter 4. Development of a next-generation sequencing bioinformatics analysis pipeline

4.1 Publication

The work described in this chapter was published in *Bioinformatics* (Marriott, Kabiljo, Al Khleifat, et al., 2023):

DNAscan2: a versatile, scalable, and user-friendly analysis pipeline for human next-generation sequencing data

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4.2 Abstract

Summary

The current widespread adoption of next-generation sequencing (NGS) in all branches of basic research and clinical genetics fields means that users with highly variable informatics skills, computing facilities and application purposes need to process, analyse, and interpret NGS data. In this landscape, versatility, scalability, and user-friendliness are key characteristics for an NGS analysis software. We developed DNAscan2, a highly flexible, end-to-end pipeline for the analysis of NGS data, which (i) can be used for the detection of multiple variant types, including SNVs, small indels, transposable elements, short tandem repeats, and other large structural variants; (ii) covers all standard steps of NGS analysis, from quality control of raw data and genome

alignment to variant calling, annotation, and generation of reports for the interpretation and prioritization of results; (iii) is highly adaptable as it can be deployed and run via either a graphic user interface for non-bioinformaticians and a command line tool for personal computer usage; (iv) is scalable as it can be executed in parallel as a Snakemake workflow, and; (v) is computationally efficient by minimizing RAM and CPU time requirements.

Availability and implementation

DNAscan2 is implemented in Python3 and is available at https://github.com/KHP-Informatics/DNAscanv2.

4.3 Background

Thanks to its growing accessibility and affordability, next-generation sequencing (NGS) is now being adopted in all fields of clinical and biomedical genetics. As a consequence, a broad audience of users require flexible and easy-to-use bioinformatics software able to adapt to their informatics proficiency, computing infrastructure, and study objectives. Current publicly available NGS pipelines normally focus on the analysis of specific types of genetic variants, e.g., only SNVs and small indels, or only structural variants, do not cover the whole analysis process (i.e., they are not end-to-end), and are not suitable for users with limited informatics skill (Chiang et al., 2015; Collins et al., 2020; DePristo et al., 2011; Zarate et al., 2020). Although tools that focus on solving some of these factors exist, e.g., being end-to-end (Causey et al., 2018) or user-friendly (Blankenberg et al., 2010), to our knowledge, only commercial bioinformatics solutions which are not accessible to the majority of NGS users, cover all of these aspects (Miller et al., 2015). On such a basis, we developed DNAscan2.

4.4 Results and Interpretation

DNAscan2 is written in Python3 and is an open-source software tool available to download from GitHub (https://github.com/KHPInformatics/DNAscanv2). The installation of its software and database dependencies (Table A1) can be performed manually, with a bash helper script or via a GUI. An Anaconda (Anaconda Software

Distribution. (2022), n.d.) environment file of available binary dependencies is also provided for those who want to install software without package conflicts. The full list of dependencies with their installation specifics are shown in Table A2.

4.4.1 New and upgraded features

DNAscan2 presents substantial improvements with respect to DNAscan (Iacoangeli, Al Khleifat, Sproviero, Shatunov, Jones, Morgan, et al., 2019) in all phases of the analysis (see sections below). Unlike in DNAscan, where users could select one of three modes (fast, normal, and intensive) to tailor the computational requirements to their availability, DNAscan2 implements a single protocol that automatically tailors itself according to the type of variants the user is interested in by default (see Figure A1A and Table A2), and it allows the selection of a fast mode which does not perform computationally intensive steps for users with limited RAM and/or CPU time constraints. It also demonstrates improved calling power for several variant classes (Table A3). Descriptions of the benchmarking procedure is available in Chapter 3.2, and detailed results are available in Appendices I. Chapter 4 and II. Chapter 4.

4.4.1.1 SNV and indel calling

The Strelka2 small variant caller (S. Kim et al., 2018) has replaced Freebayes (Garrison & Marth, 2012) and GATK Haplotype Caller (Poplin et al., 2018) for both SNV and indel calling (Figure A1A), as it has a similar performance for SNVs and consistently demonstrates a higher precision and F-measure for indel detection on both NA12878 WES and HG002 WGS samples for both standard calls (Figures A2 and A3A) and medically relevant genetic variants in challenging regions (Figure A3B).

4.4.1.2 Structural variant calling

An enhanced structural variant calling protocol was developed via the addition of Delly (Rausch et al., 2012) to call inversion and deletion variants as well as tandem duplications and translocation events. Delly exhibits a 28–35% higher F-measure for small (50–1000 bp) and medium (1001–10 000 bp) deletions (Figure A4A) on BWA-mem and HISAT2 aligned HG002 WGS reads generated with DNAscan, in addition to a 35% increase in precision for small (101– 1000 bp) haplotype-resolved inversion calls (Sudmant et al., 2015) on simulated NA12878 WGS reads (Figure A5A). Furthermore, almost all true positive deletion and inversion calls for both datasets are exclusive to Delly or shared by both Manta and Delly (Figures A4B and A5B). This improved calling comes at the expense of increased runtime, with DNAscan2 taking 24- 30hours longer to run (Table A4). Structural variant calling with Delly is not performed in fast mode.

4.4.1.3 Transposable element and short tandem repeat discovery

The protocol for the detection of mobile element insertions (Alu, SVA and LINE1) and tandem repeats has been substantially improved with the addition of new state-of-the-art tools. Mobile elements can now be discovered and genotyped via MELT (Gardner et al., 2017) and a genome-wide non-reference short tandem repeat loci profile with details of the motif composition and estimated repeat size of each identified repeat can be generated using ExpansionHunter Denovo (Dolzhenko et al., 2020). Users also have the option to convert the repeat loci into a catalog format compatible with ExpansionHunter (using a conversion script available at https://github.com/francesca-lucas/ehdn-to-eh) to undergo repeat size estimation and genotyping (Figure A1A). Short tandem repeat genotyping is not performed in fast mode.

4.4.1.4 Variant annotation and report generation

The spectrum of variants that can now be annotated has been extended to include structural and transposable elements (Figure A1A) with the incorporation of AnnotSV (Geoffroy et al., 2018), in addition to known and novel repeat expansions using user-defined ANNOVAR databases. Additionally, an HTML report of variants annotated with AnnotSV produced with the knotAnnotSV program (Geoffroy et al., 2021), and a generalized annotation report giving type, genomic location, overlapping genes and population variant frequency of all identified variants are created for the user's convenience (Figure A6).

4.4.2 Snakemake and GUI accessibility

To expand the accessibility of DNAscan2, both a graphical user interface (Figures A1B–D) and a Snakemake workflow (available at https://github.com/KHP-Informatics/DNAscanv2_snakemake) have been developed. This renders DNAscan2 available as both an easy-to-use, end-to-end program via its GUI and as a highly scalable command line tool which can be executed on high-performance computing facilities.

4.4.3 Computational performance

DNAscan2 is optimized to minimize the computational resources necessary for its use. The average memory usage in the SNV and indel calling stage for WGS is approximately 1 Gb (Table A4, Figure A7); an improvement of 97% compared with DNAscan. DNAscan2 can complete the full protocol, including alignment, full SV calling and annotation, on WGS data in 50 hours using 4 CPUs and 15 Gb RAM (Table A4, Figures A7 and A8), which is reduced to 20 h when fast mode is implemented, generally within the hardware specifications of a midrange personal computer.

4.5 Conclusions

DNAscan2 adapts to the heterogenic needs of a wide audience that uses NGS data nowadays. It shows potential to be of great value for a broad range of users and applications, e.g., clinical geneticists focusing on disease diagnostics ((Iacoangeli, Al Khleifat, Sproviero, Shatunov, Jones, Opie-Martin, et al., 2019); Figure A9, Table A5), as well as biomedical researchers working on large-scale genomic studies.

Chapter 5. Investigating the role of *NEFH* as an ALS risk gene

5.1 Abstract

Background

Neurofilament heavy chain gene (*NEFH*) variants are associated with multiple neurodegenerative diseases, however, their relationship with ALS susceptibility has not been robustly explored. Still, *NEFH* is commonly included in genetic screening panels worldwide. We aimed to determine if genetic variants in *NEFH* modify ALS risk.

Methods

Genetic data of 11,130 ALS patients and 7,416 controls from both the literature and Project MinE, were analysed. We performed fixed and random effects model meta-analysis of published case-control studies reporting *NEFH* variants, and rare variant analysis of *NEFH* variation in the Project MinE whole-genome sequencing data.

Results

Fixed effects meta-analysis found that rare (MAF<1%) missense variants in the tail domain of *NEFH* increase ALS risk (OR 4.55, 95% CI 2.13-9.71, p<0.0001). In Project MinE *NEFH* ultra-rare variants increased ALS risk (OR 1.37 95% CI 1.14-1.63, p=0.0007). When stratifying variants by functional effect and gene domain, we showed that ultra-rare variants, mostly intronic, in the rod domain appeared to drive the association (OR 1.45 95% CI 1.18-1.77, Madsen-Browning p=0.0007, SKAT-O p=0.003). Also, ultra-rare (MAF<0.1%) pathogenic missense variants in the tail domain were associated with ALS (OR 1.94, 95% CI 0.86-4.37, Madsen-Browning p=0.039). High-frequency rare (MAF 0.1-1%) tail in-frame deletions were also found to confer disease susceptibility (OR 1.18, 95% CI 0.67-2.07, SKAT-O p=0.03).

Conclusions

This study shows that *NEFH* tail missense and in-frame deletion variants and intronic rod variants are a risk factor for ALS. However, they are not variants of large effect, and their functional impact needs to be assessed in further experimental studies before determining whether they should be included in routine genetic screening panels.

5.2 Introduction

Amyotrophic lateral sclerosis (ALS) is a fatal neurodegenerative disease resulting from upper and lower motor neuron loss. Around 40 genes have been implicated in ALS and are involved in cellular processes such as autophagy, DNA damage repair, protein degradation, mitochondrial function and cellular/axonal transport (Mejzini et al., 2019). The neurofilament heavy chain gene (*NEFH*), encodes the neurofilament heavy subunit protein (NF-H), which regulates several of these activities to maintain neuronal homeostasis.

Neurofilament protein subunits preserve neuronal architecture by using their side-arms to construct cross-bridges with cytoskeletal components such as microtubules and actin filaments, forming a stable filament-centred matrix that allows intracellular signalling, mitochondrial localisation and ER transport to occur (Yuan et al., 2017). This is predominantly orchestrated by the phosphorylation of the head and tail domains of neurofilament genes. For instance, phosphorylation of the head domain acts as a primer for matrix formation, controlling polymerisation of the NF-H subunit in the cell body before the subunits move to the axon, where the lysine-serine-proline (KSP) repeat of the tail domain is phosphorylated to construct the matrix structure and stabilise the neurofilament side arms (Didonna & Opal, 2019). As a result, *NEFH* disruption could influence selective motor neuron degeneration in the brain and spinal cord of affected individuals with ALS via dysregulation of neuronal function (Theunissen, West, et al., 2021).

Frameshift and missense mutations in *NEFH* have been convincingly linked to various neurological diseases, including Charcot-Marie-Tooth disease type 2CC (Ikenberg et al., 2019; Pipis et al., 2022), spinal muscular atrophy (Ando et al., 2022) and Alzheimer’s disease (Yemni et al., 2019).

Several lines of evidence suggest hyperphosphorylation of the KSP repeat causes axonal aggregation of phosphorylated NF-H (pNF-H), thereby compromising neuronal integrity and increasing circulating pNF-H levels in the serum and CSF (Didonna & Opal, 2019). Raised pNF-H levels have already been established as a biomarker for ALS progression, survival (Puentes et al., 2021; Z. Xu et al., 2016), patterns of motor neuron involvement, and can clinically distinguish ALS from mimics such as hereditary spastic paraplegia, spinal muscular atrophy and myasthenia gravis (Poesen et al., 2017). While pNF-H demonstrates prognostic value, there have not been robust studies examining the relationship between *NEFH* mutations and ALS susceptibility. The association between small insertions and deletions (indels) in the KSP repeat and ALS risk has been suggestively reported in a number of studies (Al-Chalabi et al., 1999; Figlewicz et al., 1994; Tomkins et al., 1998), however, it has not been widely reproduced nor does solid statistical evidence exist. Still, *NEFH* is commonly included in genetic testing panels worldwide (Dilliott et al., 2023). This study aims to fill this gap by first performing a meta-analysis of published ALS case-control studies that reported *NEFH* variants and second conducting a large-scale investigation of *NEFH* variation using genetic data from the Project MinE international ALS whole-genome sequencing consortium.

5.3 Methods

5.3.1 Systematic Review

This study was performed in accordance with the 2020 Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines (Page et al., 2021). Registration and study protocol of the review aspect of this study was not performed.

5.3.1.1 Eligibility Criteria

Primary research articles published in the English language between January 1993 and October 2021 were included if they reported individual *NEFH* variant frequencies in ALS patients via a candidate or panel gene approach (targeted panel resequencing, variant screening), whole genome sequencing, whole-exome sequencing, microarray, or PCR-based approaches. Studies were excluded if they were clinical, functional, or epidemiological, if *NEFH* variants were not identified, were identified in non-ALS cases only, or if individual frequencies of all variants were not reported.

5.3.1.2 Information Sources, Search Strategy and Screening Process

Relevant studies were identified by searching PubMed, Embase and Medline databases with the search terms “amyotrophic lateral sclerosis” OR “ALS” in combination with “neurofilament heavy chain gene”, “NEFH”, “NFH” OR “NF-H”. After removing duplicate records, title and abstract screening was performed against the eligibility criteria, which were formatted into a table checklist. Studies which advanced to full text screening were subject to backward citation screening using Web of Science to identify any articles which may have been missed. Full text screening of database and citation identified records was then performed. The search strategy was independently performed, and the results were crosschecked by two members of the team.

5.3.1.3 Data Collection Process and Data Synthesis

The following characteristics were extracted from the eligible records: author, publication year, study design, screening method and genetic technology used to detect *NEFH* variants, population (country of origin), study groups, sex and age of ALS groups and diagnostic criteria. For each variant, the following information was obtained: HGVS nomenclature, mutation type, *NEFH* domain location, rsID, and pathogenicity according to SIFT and PolyPhen. Study-specific variant information i.e., frequency in cases and controls, odds ratios (ORs) and 95% confidence intervals with p-values and other ALS-associated gene variants carried in *NEFH*-positive individuals, were also extracted. Population-specific *NEFH* variant frequencies were added to each variant record using the gnomADv2.1.1 non-neuro database (Karczewski et al., 2020). If the rsID was not supplied, dbSNP (Sherry et al., 2001) and gnomAD were searched. For variants without pathogenicity predictions, gnomAD and the Variant Effect Predictor (VEP) (McLaren et al., 2016) were used to obtain variant consequence status. All of this information was tabulated into separate study-specific and variant-specific characteristics tables.

5.3.2 Meta-Analysis

Individual missense and exonic indel variants found in two or more case-control studies were eligible for variant-level meta-analysis. Subgroup meta-analysis was also performed according to combinations of population-specific gnomAD non-neuro frequency (ultra-rare: <0.1%, high-frequency rare: 0.1-1%, rare: <1%, or common: >1%), domain (head, rod, or tail) and variant type. Studies that identified variants absent from gnomAD but present in more than one control were classified as common for the stratified analysis. Synonymous variants were excluded from the analysis. Inverse-variance weighted meta-analyses were conducted with both fixed-effect (Cochran-Mantel-Haenszel) and random-effect (DerSimonian-Laird) models. Crude ORs were calculated from the extracted data. Between-study heterogeneity was assessed using the combination of the I^2 test and Cochran-Q statistic, with significant heterogeneity indicated when I^2 >50% and Q <0.10. In this case, the result from the random-effect model is the result that we report and use. Publication bias was assessed with both Egger's and Harbord's test, with p-values <0.05 classed as displaying significant outcome heterogeneity and selective reporting. All statistical analyses were performed using the *metabin* and *metabias* functions of the meta R package (v6.5.0; (Balduzzi et al., 2019)).

5.3.3 Genetic Screening

Whole-genome sequencing samples collected as part of the Project MinE ALS sequencing consortium (Project MinE ALS Sequencing Consortium, 2018) were used to investigate *NEFH* variants in ALS and for replicating the literature based meta-analysis results. Information about recruitment and data collection is available in the Project MinE paper. After standard data preparation (see Chapter 3.3.1), the dataset comprised of 6,469 ALS cases and 2,434 controls from 13 countries (breakdown available in Table A6) for which SNV and small indel data were available. Structural variants (SVs) generated with Manta (X. Chen et al., 2016) were available for approximately two thirds of samples (4,686 ALS cases and 1,859 controls). Variants were annotated with VEP for both functional consequence/type (e.g., UTR, intronic, missense, indel, synonymous) and impact classification (high, moderate, low, modifier) before a union SV dataset was created. SVs greater than 100,000bp were excluded to reduce false positives. The remaining SVs were annotated with AnnotSV (Geoffroy et al., 2018) and CADD-SV (Kleinert & Kircher, 2022) to assess their potential pathogenicity. All results files were converted into a matrix to calculate case-control frequencies. For the review-identified variants and SVs present in Project MinE, Firth logistic regression was performed using RVTests (Zhan et al., 2016) with default settings, to assess potential associations between variants and ALS susceptibility. Results were corrected for sex and the first 10 principal components. All data was aligned to hg19.

5.3.4 Rare Variant Burden Analysis

Burden analysis of all *NEFH* variants identified in Project MinE was performed with RVTests, using Madsen-Browning and SKAT-O methods with default settings. Results were corrected for sex and the first 10 principal components. Variants were initially grouped by frequency (ultra-rare: <0.1%, high-frequency rare: 0.1-1%, rare: <1%), according to the highest value in control databases (gnomAD non-neuro non-Finnish European and Project MinE controls), before being grouped by functional domain (whole gene, head, rod, tail) with the *ensembldb* R package (v2.22.0; (Rainer et al., 2019). For each functional domain, variant burden was calculated for several variant types (missense, synonymous, insertion, deletion, 3'UTR, 5'UTR, intronic) and VEP impact classes (high, moderate, low, modifier). Also, the burden of missense variants predicted pathogenic by SIFT and/or PolyPhen was assessed.

5.3.5 Controlling for Multiplicity of Testing

In both meta-analysis and burden analyses, we report p-values <0.05 as indicators of nominal significance in addition to estimate of effects and 95% confidence intervals. In our initial discovery phase, we took multiple testing into account (Bonferroni correction) testing the association between variants and ALS risk based on four NEFH variant frequencies (MAF <0.1%, MAF 0.1–1%, MAF <1%, and MAF >1%.), that is, corrected p-values <0.0125. Any additional subgroup analyses aiming to explain which types of frequency-grouped variants contributed to the already discovered associations were considered significant if p-values <0.05 and the direction of effect was concordant with the initial association.

5.4 Results

5.4.1 Systematic Review

5.4.1.1 Study Selection

The systematic literature review process flowchart is presented in Figure 5-1. The initial search identified 29 articles which were eligible for title and abstract screening, of which 16 were the wrong study type, disease, or instances where genetic screening did not include *NEFH* or identify *NEFH* variants even if *NEFH* was present in the targeted sequencing panel. Backward citation searching of the remaining 13 articles found an additional 251 records for screening. Manual full text inspection removed a further 242 records (2 from database search and 240 from citation search) as the inclusion criteria were not met. In total, 22 studies involving a total of 10,959 individuals (6,090 ALS cases and 4,869 controls) from 14 countries were included in the present study.

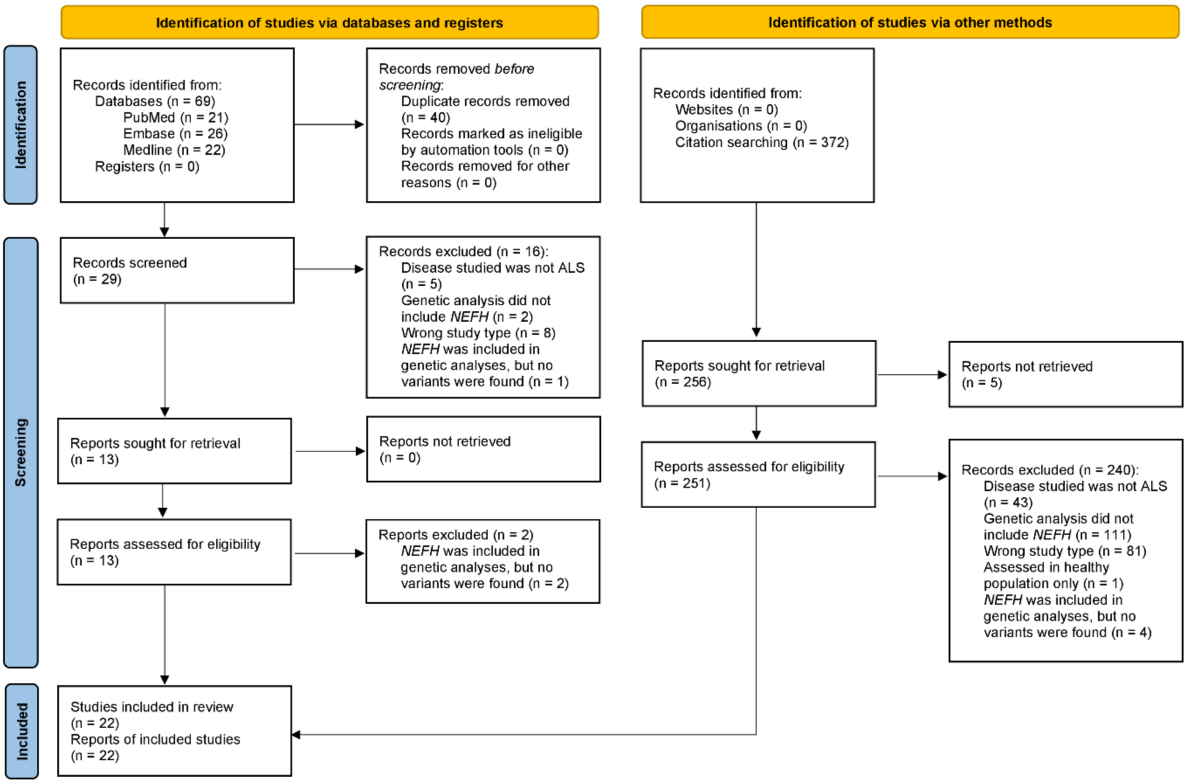

Figure 5-1. PRISMA flowchart of the systematic review process for identification of NEFH variants from the literature. The left of the figure outlines screening for articles identified via PubMed, Embase and Medline databases, whilst the right outlines the process for articles found via backwards citation screening of articles undergoing full-text screening.

5.4.1.2 Study Characteristics

An overview of the characteristics of all included studies is given in Table A7. European (N Studies = 9) and Asian (N Studies = 7) populations were the most represented, with family disease history reported in 77% of studies. Diagnostic criteria were applied to support inclusion in 15 studies (68%), with varying definitions of El Escorial criteria employed in 93% of those. A combination of El Escorial and Awaji-Shima criteria was used in one study. The average age of recruitment of the ALS patients ranged from 30.7 to 62.1 (median 58.1), with a male: female ratio ranging between 0.60 and 1.78 (median 1.38) across studies. When separating by country, Asian populations had a younger median age at recruitment and a higher median male: female ratio than European populations (Asian: age 52.01, sex ratio 1.52; European: age 60.1, sex ratio 1.22). A case-control design was adopted in 12 studies (55%), with 6 investigating *NEFH* variation in ALS via candidate gene-based methods. Gene panels including *NEFH* were used in 13 studies, with a further 2 opting for custom variant panel screening. The most popular genetic technology was whole-exome sequencing (N Studies = 6) and a combination of whole-exome sequencing with validation approaches such as PCR and Sanger sequencing (N Studies = 6).

5.4.1.3 Variant Characteristics

We extracted information for 59 *NEFH* variants from the included studies. The full synthesised variant information is represented in Table A8, with the genomic coordinates and base-pair substitutions available in Table A9. Missense variants were the most represented (67.8%), followed by inframe deletions (13.6%), synonymous variants (13.6%), inframe insertions (1.7%), frameshift deletions (1.7%) and stop-gained SNVs (1.7%). Indels ranged from 3bp to 48bp in length and exclusively occupied the tail, whilst only two missense variants were found in the head domain (Figure 5-2). Only 18 variants (30.5%) were reported in more than one study. Eleven people with *NEFH* variants also harboured variants in other ALS-associated genes, including *SOD1*, *FUS*, *OPTN*, *SETX*, *ALS2* and *CHMP2B* (Table A8). When looking at the functional impact of these variants in the gnomAD database, both *OPTN* variants (M98K and R545Q) and the *ALS2* T293I variant are predicted to be tolerated and benign according to SIFT and PolyPhen, whilst the *FUS* c.37 C>T variant is predicted as benign with CADD and SpliceAI. The remaining variants have conflicting pathogenicity results, therefore their influence on ALS risk in individuals harbouring these variants are uncertain.

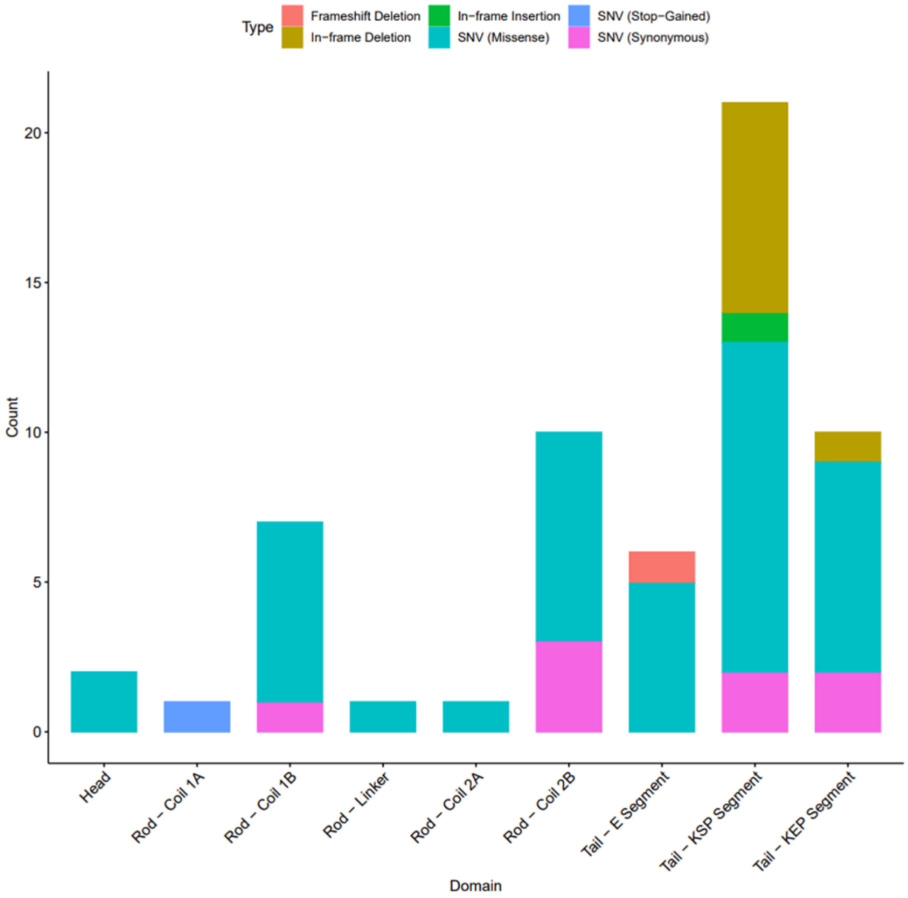

Figure 5-2. NEFH domain distribution of the 59 SNV and indel variants identified from the systematic review. Colours characterise the different variant types. KEP = lysine-glutamic acid-proline; KSP = lysine-serine-proline.

5.4.2 Meta-Analysis

The twelve case-control studies were selected for meta-analysis. In total, 34 deletion, insertion and missense variants were reported across them (top panel of Figure 5-3A) in 9,496 individuals (4,527 cases; 4,969 controls). Of these, 9 variants (3 in-frame deletions and 6 missense) were identified in two or more case-control studies and were included in the variant-level meta-analysis. No singular variant was shown to significantly alter risk for ALS (Table A10), with K790del displaying high between-study heterogeneity (Cochran's Q = 3.03 , p-value = 0.08; I^2 = 67%).

We then performed meta-analyses of *NEFH* variants based on the aggregation of variants stratified by frequency, domain, and variant type. We found that both rare missense and rare tail variants were associated with an increased risk of ALS (Table 5-1). We determined that the rare missense tail variants were driving this result as they were more significant, with a higher OR (OR 4.55, 95% CI 2.13-9.71, $p_{fixed\text{-}effect}<0.0001$, Figure 5-4), and removing them from the rare missense and rare tail meta-analyses caused these associations to be lost. There was no evidence of inter-study heterogeneity (Cochran's Q = 2.30, p=0.51; I^2 = 0%) or publication bias (Egger t=2.07, p=0.17; Harbord t=1.82, p=0.21). By further stratifying *NEFH* variants into high-frequency rare and ultra-rare categories, we identified a similar but albeit weaker significant association for the high-frequency rare missense tail variants (OR 3.91, 95% CI 1.77-8.64, $p_{fixed\text{-}effect}=0.0007$), with ultra-rare missense tail variants approaching significance for increasing ALS risk (OR 5.05, 95% CI 0.84-30.22; $p_{fixed\text{-}effect}=0.08$). Across all categories, tail deletions did not significantly increase or reduce susceptibility for ALS (Table 5-1). High between-study heterogeneity was reported for common missense and tail missense variants, and all tail missense variants, with tail ultra-rare variants displaying publication/reporting bias (Table 5-1).

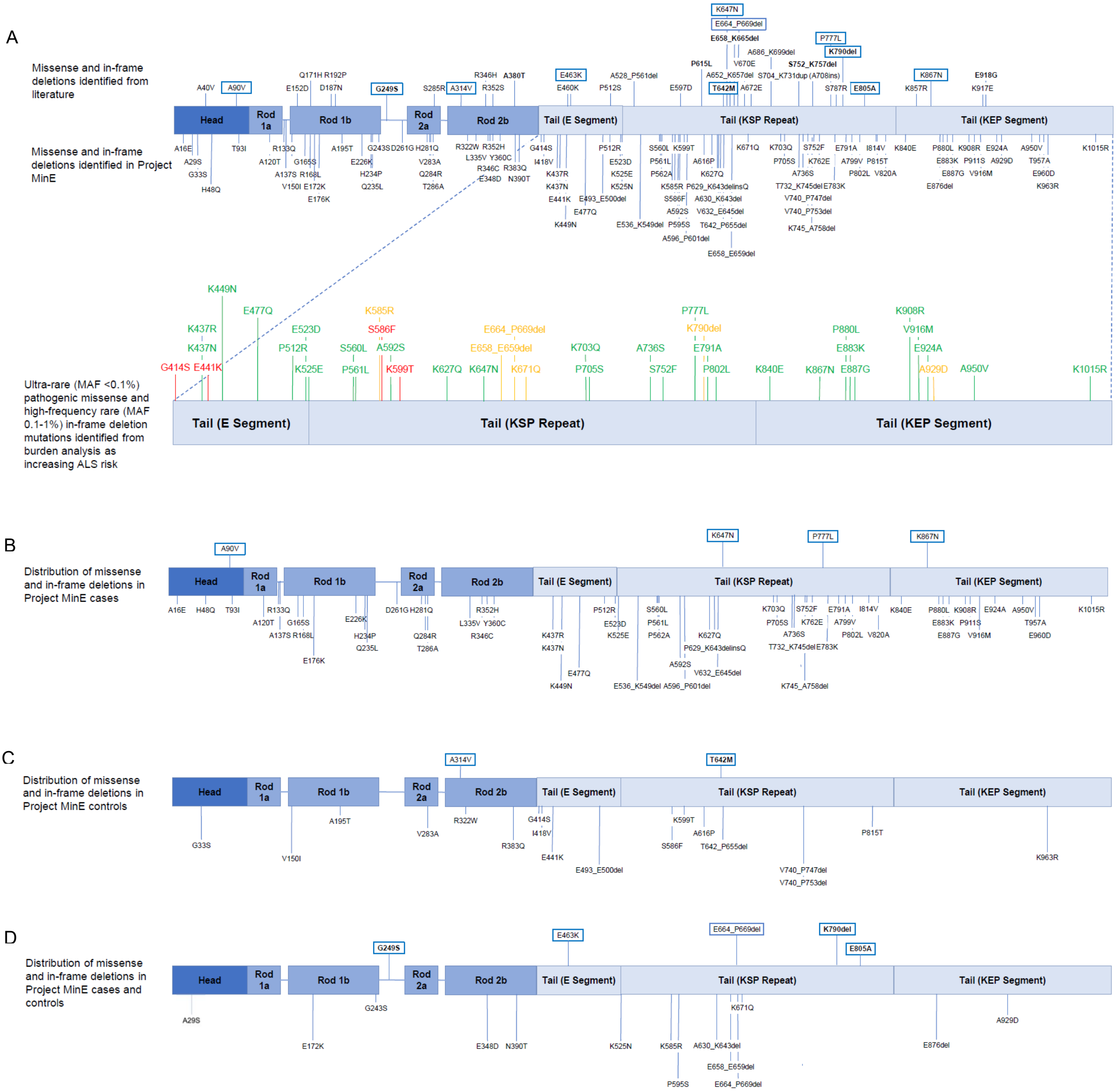

Figure 5-3. A) Schematic depicting the locations of the gene variants included in the meta-analysis and in both meta-analysis and Project MinE (top), as well as the variants that were found to increase the risk of ALS with burden analysis (bottom). Variants in bold denote those included in variant-level meta-analysis. Variants in blue bordering represent those which were also identified in the Project MinE cohort. Green = only present in cases. Amber = present in cases and controls. Red = only present in controls. B-D) Locations of missense and in-frame deletions present in Project MinE cases (B), controls (C) and both cases and controls (D).

MAF Category	**Subgroup**	**No. Studies**	**N Cases**	**N Controls**	**Fixed OR (95% CI; p-value)**	**Random OR (95% CI; p-value)**	**Heterogeneity (Q statistic; p-value)**	**Heterogeneity (I-squared)**	**Publication Bias (Egger t statistic; p-value)**	**Publication Bias (Harbord t statistic; p-value)**
Ultra-Rare (<0.1%)	All	10	2729	2483	2.64 (1.22-5.68; **0.01**)	2.27 (0.99-5.18; 0.05)	5.12 (0.82)	0%	2.17; 0.06	1.13; 0.29
	Tail	7	1918	2063	2.01 (0.80-5.05; 0.14)	1.82 (0.68-4.87; 0.24)	3.06 (0.80)	0%	4.38; **7.2E-03**	3.01; **0.03**
	Missense	6	1679	1521	4.35 (1.39-13.64; **0.01**)	4.14 (1.30-13.18; **0.02**)	1.17 (0.95)	0%	-0.29; 0.78	0.40; 0.71
	Head Missense	2	285	290	1.70 (0.22-12.95; 0.61)	1.63 (0.20-13.35; 0.65)	0.25 (0.62)	0%	N/A	N/A
	Rod Missense	5	1368	1321	3.28 (0.82-13.15; 0.09)	3.17 (0.78-12.90; 0.11)	0.77 (0.94)	0%	-0.92; 0.43	-0.76; 0.50
	Tail Missense	3	868	1101	5.05 (0.84-30.22; 0.08)	5.10 (0.87-29.98; 0.07)	0.01 (0.99)	0%	3.88; 0.16	15.36; **0.04**
	Tail Deletion	3	886	753	0.97 (0.28-3.40; 0.97)	0.94 (0.26-3.38; 0.93)	0.52 (0.77)	0%	2.25; 0.27	2.45; 0.25
High-Frequency Rare (0.1-1%)	All	7	2764	3106	2.11 (1.23-3.62; **6.5E-03**)	2.16 (0.77-6.10; 0.15)	9.92 (0.13)	40%	0.55; 0.61	0.45; 0.67
	Missense	5	1282	2187	2.23 (1.25-3.97; **6.7E-03**)	2.53 (0.82-7.85; 0.11)	6.49 (0.17)	38%	0.80; 0.48	0.79; 0.49
	Tail	5	2464	2906	3.14 (1.56-6.31; **1.3E-03**)	3.26 (0.99-10.74; 0.05)	6.64 (0.16)	40%	0.30; 0.79	0.17; 0.88
High-Frequency Rare (0.1-1%)	Rod Missense	4	982	1111	1.01 (0.42-2.44; 0.98)	0.95 (0.38-2.39, 0.91)	1.58 (0.66)	0%	1.30; 0.32	1.39; 0.30
	Tail Missense	3	982	1987	3.91 (1.77-8.64; **7.0E-04**)	4.44 (1.41-13.96; **0.01**)	2.16 (0.34)	7%	1.81; 0.32	1.93; 0.30

Rare (< 1%)	All	13	4355	4272	2.54 (1.59-4.06; **< 1.0E-04**)	2.28 (1.38-3.77; **1.3E-03**)	12.08 (0.44)	1%	0.23; 0.82	0.12; 0.90
	Tail	9	3344	3752	2.83 (1.59-5.04; **4.0E-04**)	2.57 (1.10-5.98; **0.03**)	10.80 (0.21)	26%	0.30; 0.78	0.03; 0.98
	Tail (exc. Missense)	5	2176	1575	1.37 (0.54-3.43; 0.51)	1.05 (0.37-3.01; 0.93)	4.32 (0.36)	7%	1.22; 0.31	0.16; 0.88
	Missense	8	2179	2697	2.78 (1.64-4.71; **< 1.0E-04**)	2.60 (1.34-5.10; **4.8E-03**)	7.52 (0.38)	7%	0.93; 0.39	0.89; 0.41
	Missense (exc. Tail)	7	1879	1621	1.57 (0.77-3.21; 0.22)	1.44 (0.68-3.05; 0.34)	2.71 (0.84)	0%	1.22; 0.28	1.44; 0.21
	Rod Missense	7	1879	1621	1.51 (0.72-3.15; 0.28)	1.41 (0.67-3.04; 0.38)	2.37 (0.89)	0%	1.33; 0.24	1.97; 0.11
Rare (< 1%)	Tail Missense	4	1168	2177	4.55 (2.13-9.71; **< 1.0E-04**)	4.65 (1.79-12.11; **1.6E-03**)	2.30 (0.51)	0%	2.07; 0.17	1.82; 0.21
	Tail Deletion	4	2012	1366	1.22 (0.46-3.22; 0.68)	0.90 (0.30-2.74; 0.85)	3.62 (0.31)	17%	0.75; 0.53	-0.50; 0.66
	All	6	2025	2442	1.11 (0.94-1.30; 0.21)	1.20 (0.87-1.65; 0.26)	9.30 (0.10)	46%	0.99; 0.38	1.13; 0.32
	Tail	6	2025	2442	1.11 (0.95-1.31; 0.19)	1.20 (0.88-1.63; 0.25)	8.95 (0.11)	44%	1.00; 0.37	1.14; 0.32

Common (> 1%)	Missense	5	1818	2223	1.12 (0.94-1.34; 0.20)	1.18 (0.79-1.78; 0.42)	10.12 (**0.04**)	**61%**	0.32; 0.77	0.34; 0.76
	Tail Missense	5	1818	2223	1.13 (0.95-1.36; 0.17)	1.19 (0.79-1.77; 0.40)	9.62 (**0.05**)	**58%**	0.30; 0.78	0.32; 0.77
	Tail Deletion	2	578	930	1.03 (0.78-1.35; 0.85)	1.03 (0.78-1.35; 0.86)	0.48 (0.49)	0%	N/A	N/A
All	Rod Missense	7	1879	1721	1.26 (0.67-2.37; 0.48)	1.18 (0.61-2.29; 0.62)	2.69 (0.85)	0%	1.82; 0.13	2.42; 0.06
	Tail Missense	8	2615	3689	1.24 (1.04-1.48; **0.02**)	1.45 (0.96-2.19; 0.08)	14.58 (**0.04**)	**52%**	2.20; 0.07	2.41; 0.05
	Tail Deletion	5	2383	2077	1.04 (0.80-1.35; 0.77)	1.02 (0.78-1.33; 0.89)	4.02 (0.40)	1%	0.29; 0.79	0.35; 0.75

Table 5-1. Results of the subgroup meta-analysis of variants identified from the systematic review that were supported by two or more case-control studies. N/A values represent instances where publication bias could not be calculated as the minimum number of studies required for calculation was not reached.

Study	ALS Events	ALS Total	Control Events	Control Total	Weight (Fixed)	Weight (Random)	OR	95%-CI
Daoud et al., 2011	2	186	0	190	7.2%	9.3%	5.16	[0.25; 108.26]
Zhang et al., 2018	8	311	0	200	8.7%	10.4%	11.23	[0.64; 195.66]
Lin et al., 2021	12	371	8	711	77.9%	63.5%	2.94	[1.19; 7.25]
Lin et al., 2021 (Replication)	4	300	1	1076	6.3%	16.8%	14.53	[1.62; 130.46]
Total (Fixed Effects, 95% CI)		**1168**		**2177**	**100.0%**	**--**	**4.55**	**[2.13; 9.71]**
Total (Random Effects, 95% CI)					**--**	**100.0%**	**4.65**	**[1.79; 12.11]**

Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0.1622$, $\chi^2_3 = 2.30$ ($p = 0.51$)
Total (Fixed Effects) $p < 0.0001$
Total (Random Effects) $p = 0.0016$

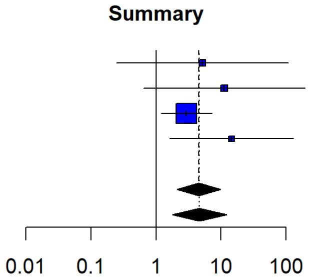

Figure 5-4. Forest plot demonstrating that rare (MAF < 1%) missense variants in the tail domain increase the risk of ALS. Breakdown of heterogeneity values are as follows: I^2 = I^2 statistic, τ^2 = Tau-squared (estimate of between-study variance in random-effects models), χ^2_3 = Cochrane's Q (chi-squared distribution).

5.4.3 Genetic Screening in Project MinE

5.4.3.1 SNVs and Indels

We screened the whole *NEFH* gene in the Project MinE dataset (6,469 ALS cases and 2,434 controls). A total of 591 SNVs and indels were identified (Figure 5-5A and Table A11). Interestingly, intronic regions contained 65% of all variants found in the cohort, with 220 (57.29%) being singletons (Figure 5-5B). 462 (78.17%) were identified only in Project MinE and not in the review or gnomAD non-neuro non-Finnish database (Figure 5-5C) and are therefore classified as 'novel' in this study.

Sixteen (27.1%) of the *NEFH* variants identified from the systematic review were found in Project MinE (Figure 5-5C). Examination of case-control frequencies of review-identified variants present in Project MinE (Table 5-2) suggested that K790del could be protective against ALS (0.14% cases, 0.37% controls; OR = 0.38, 95% 0.15-0.95). Using Project MinE as an additional study for meta-analysis of individual review-identified variants did not offer any additional insight into their role in ALS risk (Figure 5-6; Table A12).

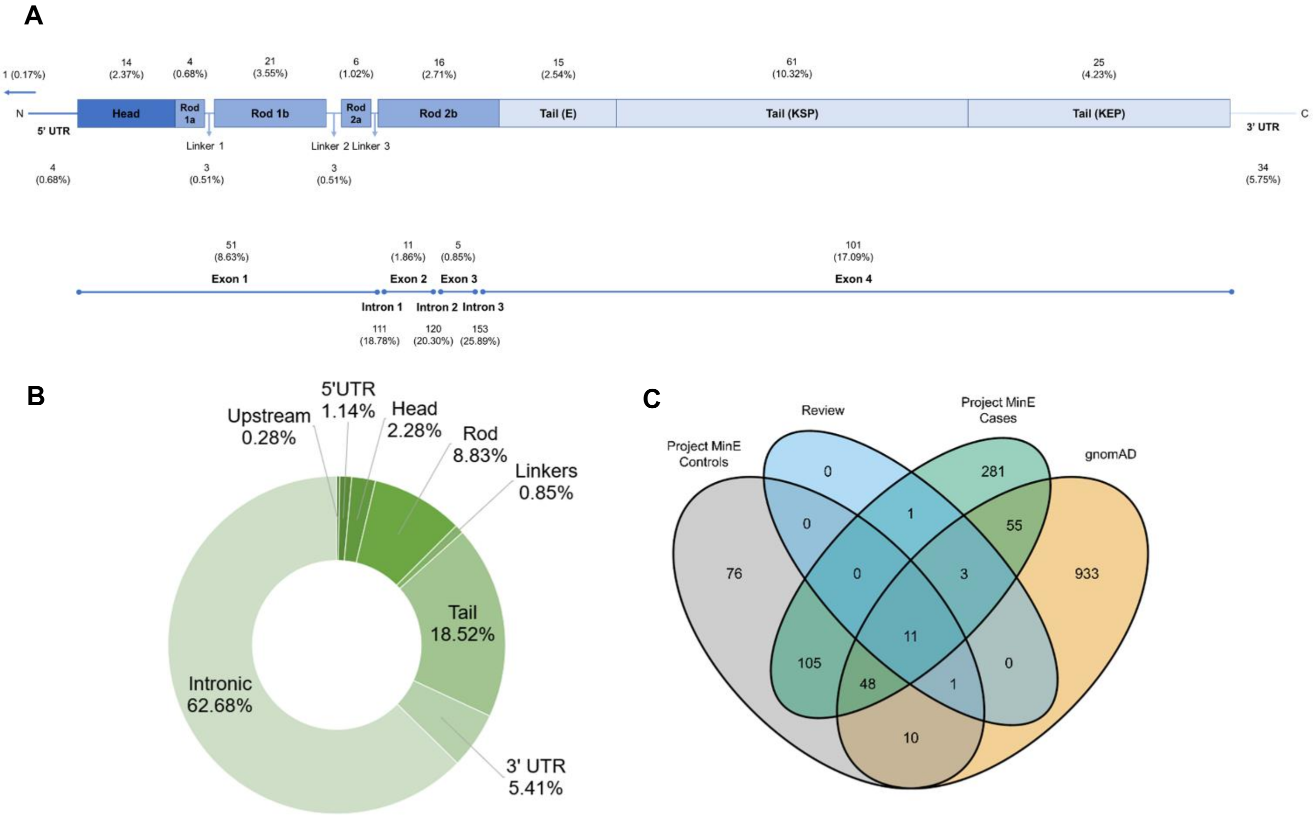

Figure 5-5. Results of the SNV/indel screening analysis in the Project MinE cohort. Additional information on all 591 variants identified are available in Table A11. a) Proportion of variants found in various gene domains and untranslated regions (top), and in exons and introns (bottom). b) Breakdown of the 351 NEFH singletons by domain. c) A Venn diagram illustrating the overlap of the NEFH variants in Project MinE cases and controls, the systematic review and the gnomAD v2.1.1 database. The value for variants that are only in gnomAD (933) refers to the remaining NEFH variants in the catalogue after accounting for variants shared with Project MinE or the review.

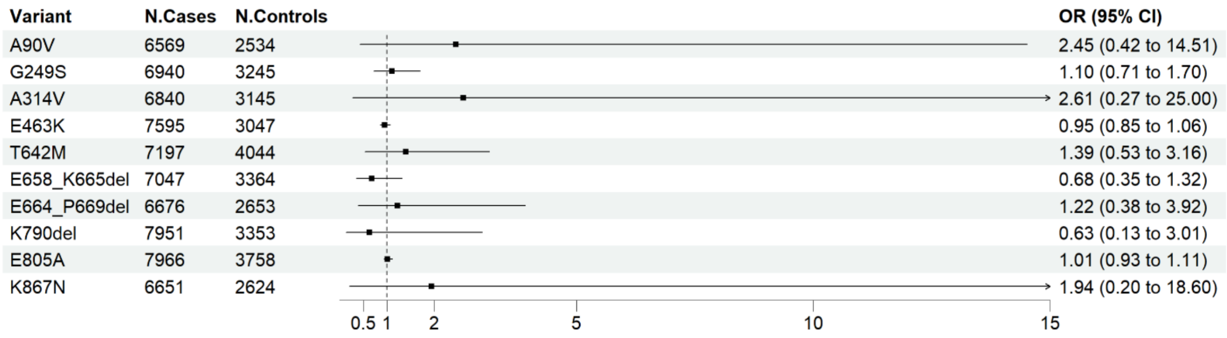

Figure 5-6. Summary forest plot demonstrating that offering Project MinE as an additional study for meta-analysis of systematic-review identified variants does not appear to reveal any further insights into their modulation on ALS risk. The full results are available in Table A12. N. Cases and N. Controls refers to the sample sizes used to evaluate each variant.

5.4.3.2 Structural Variants

Only 4 SVs were identified in Project MinE (Table 5-2). All were in the KSP and KEP segments of the tail domain, and none were pathogenic according to CADD-SV. When comparing case-control frequencies of the SVs, the 113bp KEP segment deletion was found to be strongly protective against ALS (17.95% cases vs 23.91% controls; OR 0.72, 95% CI 0.64-0.81).

Variant	**Position**	**Type**	**Pathogenicity Prediction**	**CADD-SV Score**	**Total Carriers (Case/Control)**	**Beta (SE)**	**OR (95% CI)**	**P Value**
A90V	29876520	Missense	Tolerated/Benign	N/A	7 (6/1)	0.49 (0.95)	2.26 (0.27-18.77)	0.61
G249S	29876996	Missense	Tolerated/Benign	N/A	92 (69/23)	0.03 (0.23)	1.13 (0.70-1.82)	0.91
A314V	29879421	Missense	Deleterious/ Probably Damaging	N/A	1 (1/0)	0.22 (2.11)	1.13 (0.05-27.73)	0.92
E463K	29885016	Missense	Deleterious/ Probably Damaging	N/A	1527 (1103/424)	-0.0065 (0.06)	0.97 (0.86-1.10)	0.91
T642M	29885554	Missense	Tolerated/Benign	N/A	1 (0/1)	-2.47 (2.11)	0.13 (0.005-3.08)	0.24
K647N	29885570	Missense	Deleterious/ Possibly Damaging	N/A	1 (1/0)	0.40 (2.12)	1.13 (0.05-27.73)	0.85
P777L	29885959	Missense	Deleterious/ Probably Damaging	N/A	1 (1/0)	0.14 (2.12)	1.13 (0.05-27.73)	0.95
E805A	29886043	Missense	Deleterious/ Possibly Damaging	N/A	2578 (1873/705)	-0.028 (0.05)	1.00 (0.90-1.11)	0.54
K867N	29886230	Missense	Deleterious/ Possibly Damaging	N/A	1 (1/0)	0.40 (2.12)	1.13 (0.05-27.73)	0.85
A400A	29881828	Synonymous	N/A	N/A	2569 (1867/702)	0.03 (0.05)	1.00 (0.90-1.11)	0.57
S580S	29885369	Synonymous	N/A	N/A	199 (147/52)	0.10 (0.16)	1.07 (0.77-1.47)	0.56
D919D	29886386	Synonymous	N/A	N/A	148 (105/43)	-0.05 (0.18)	0.92 (0.64-1.31)	0.77
V928V	29886413	Synonymous	N/A	N/A	8492 (6198/2324)	-0.007 (0.04)	1.08 (0.86-1.36)	0.85
K790del	29885996	Small Deletion	N/A	N/A	18 (9/9)	-1.03 (0.47)	0.38 (0.15-0.95)	**0.03**
E658_K665del	29885604	Small Deletion	N/A	N/A	29 (18/11)	0.02 (0.64)	0.61 (0.29-1.30)	0.98
E664_P669del	29885622	Small Deletion	N/A	N/A	13 (10/3)	-2.20 (2.11)	1.25 (0.35-4.56)	0.30
INS_61	29877834-29877895	Large Deletion	N/A	14.27	1 (1/0)	0.47 (2.11)	1.19 (0.049-29.24)	0.82

INS_56	29879816-29879872	Large Deletion	N/A	0.75	1 (0/1)	-2.38 (2.11)	0.13 (0.0054-3.25)	0.26
DEL_1169	29880841-29882010	Large Deletion	Likely Pathogenic	9.83	1 (1/0)	0.65 (2.11)	1.19 (0.049-29.24)	0.76
DEL_113	29885279-29885870	Large Deletion	VUS	4.85	1743 (1161/582)	-0.34 (0.061)	0.72 (0.64-0.81)	**2.60E-08**

Table 5-2 Case-control frequencies and results of logistic regression association analysis of the 16 SNV/indel variants found in the systematic review and Project MinE, and the 4 structural variants identified in a subset of Project MinE. Results were corrected for sex and 10 principal components. N/A refers to a pathogenicity prediction that could not be reached as the variant type was inappropriate for the tool (SIFT/PolyPhen for SNVs and indels; ACMG and CADD-SV for SVs).

5.4.4 Rare Variant Burden Analysis in Project MinE

All the SNV/indel variants from Project MinE were subject to burden analysis stratified by frequency and domain (Tables 5-3, 5-4, and 5-5). We found that ultra-rare variants in *NEFH* increase ALS risk (OR 1.37 95% CI 1.14-1.63, Madsen-Browning p=0.0007, SKAT-O p=0.0033). When stratifying by domain and functional effect, ultra-rare variants, mostly intronic, in the rod domain appeared to drive the association (OR 1.45 95% CI 1.18-1.77, Madsen-Browning p=0.0007, SKAT-O p=0.003). However, ultra-rare pathogenic missense tail variants were also associated with an increased risk of ALS (OR 1.94, 95% CI 0.86-4.37; Madsen-Browning p=0.039), which supported the result of the meta-analysis to a high degree, despite high-frequency rare pathogenic missense tail variants in this cohort not appearing to confer ALS risk (Table 5-4). Stratifying this by subdomain revealed that the KEP repeat drove this result (OR 5.65, 95% CI 0.75-42.83, Madsen-Browning p=0.02), and that other sub-domains showed consistent, although not significant, effects (OR >1) (Table 5-3). In line with previous reports, ultra-rare tail domain in-frame deletions had a large impact on ALS risk, but this finding was at the border of the significance testing threshold (OR 3.01, 95% CI 0.69-13.12, Madsen-Browning p=0.052). A similar but significant effect was observed for high-frequency rare in-frame deletions (Table 5-4), with an OR of 1.18 (95% CI 0.67-2.07, SKAT-O p=0.03). Ultra-rare pathogenic missense variants and high-frequency rare in-frame deletions identified and assessed in these burden analyses are detailed in Figure 5-3A (bottom panel) and Table A13. The case-control distribution of all missense and in-frame deletion variants are displayed in Figure 5-3B,C,D.

Frequency (<0.1%)	**No. of Variants**	**Madsen Browning p-value**	**SKAT-O p-value**	**Cases**	**Controls**	**Odds Ratio (95% CI)**
All (29876207-29887379)	512	**7.0E-04**	**3.3E-03**	595	168	1.37 (1.14-1.63)
Synonymous	37	0.12	0.43	47	12	1.48 (0.78-2.79)
Missense	80	0.11	0.25	85	24	1.34 (0.85-2.11)
All pathogenic missense	51	0.11	0.37	51	13	1.48 (0.80-2.73)
Inframe Deletion	11	0.051	0.35	16	2	3.01 (0.69-13.12)
Inframe Insertion	11	0.38	0.75	12	3	1.51 (0.42-5.34)
Intronic	332	**4.3E-03**	**0.01**	419	115	1.40 (1.13-1.73)
3' UTR	30	0.29	0.72	39	12	1.22 (0.64-2.34)
5' UTR	4	**4.0E-03**	**0.037**	1	3	0.13 (0.01-1.21)
VEP High	6	0.13	0.11	3	4	0.28 (0.06-1.26)
VEP Low	37	0.12	0.43	47	12	1.48 (0.78-2.79)
VEP Moderate	102	**0.032**	0.16	113	29	1.47 (0.98-2.22)
VEP Modifier	367	**4.5E-03**	**0.012**	458	130	1.35 (1.10-1.65)
Head (29876252-29876554)	13	0.76	0.26	15	9	0.63 (0.27-1.43)
Synonymous	7	0.49	0.24	8	3	1.00 (0.27-3.79)
Missense	6	0.091	0.17	7	6	0.44 (0.15-1.31)
Pathogenic missense	1	N/A	0.069	1	0	1.13 (0.05-27.73)
VEP Low	7	0.49	0.24	8	3	1.00 (0.27-3.79)
VEP Moderate	6	0.091	0.17	7	6	0.44 (0.15-1.31)
Rod (29876555-29884868)	379	**7.0E-04**	**3.0E-03**	473	126	1.45 (1.18-1.77)
Synonymous	20	0.08	0.25	28	5	2.11 (0.81-5.48)
Missense	23	0.065	0.25	29	6	1.82 (0.76-4.39)
Pathogenic missense	14	0.48	0.73	15	5	1.13 (0.41-3.11)
Inframe Insertion	1	0.26	0.53	1	0	1.13 (0.041-27.73)
Intronic	332	**4.0E-03**	**0.01**	419	115	1.40 (1.13-1.73)
VEP High	3	0.18	0.20	1	2	0.19 (0.02-2.07)
VEP Low	20	0.08	0.25	28	5	2.11 (0.81-5.48)
VEP Moderate	24	0.052	0.22	30	6	1.89 (0.78-4.54)
VEP Modifier	332	**0.004**	**0.01**	419	115	1.40 (1.13-1.73)
Tail (29884869-29886689)	85	**0.057**	0.30	89	23	1.46 (0.92-2.32)
Synonymous	10	0.65	0.71	11	4	1.03 (0.33-3.25)
Missense	51	0.084	0.21	49	12	1.54 (0.82-2.90)
Pathogenic Missense	36	**0.039**	0.19	36	7	1.94 (0.86-4.37)
E Segment	8	0.48	0.68	6	2	1.19 (0.23-5.60)
KSP Segment	17	0.34	0.73	16	4	1.51 (0.50-4.51)
KEP Segment	11	**0.02**	0.11	15	1	5.65 (0.75-42.83)
Inframe Deletion	11	0.052	0.35	16	2	3.01 (0.69-13.12)
Inframe Insertion	10	0.43	0.84	11	3	1.38 (0.38-4.95)
VEP High	3	0.36	0.35	2	2	0.38 (0.05-2.67)

VEP Low	10	0.65	0.71	11	4	1.03 (0.33-3.25)
VEP Moderate	72	**0.024**	0.15	76	17	1.69 (1.00-2.87)
All excluding tail (29876207-29884868)	392	**3.0E-03**	**7.5E-03**	478	133	1.38 (1.13-1.68)

Table 5-3. Results of the ultra-rare (MAF < 0.1%) NEFH variant burden analysis. Significant results are denoted by bold p-values. All results are corrected for sex and the first 10 principal components.

Frequency (0.1-1%)	**No. Variants**	**Madsen Browning p-value**	**SKAT-O p-value**	**Cases**	**Controls**	**Odds Ratio (95% CI)**
All (29876207-29887379)	45	0.78	0.61	735	285	0.97 (0.84-1.12)
Synonymous	4	0.97	1.00	38	13	1.10 (0.59-2.07)
Missense	7	0.26	0.58	91	34	1.01 (0.68-1.50)
All pathogenic missense	5	0.27	0.39	18	9	0.75 (0.34-1.68)
Inframe Deletion	3	0.44	**0.03**	50	16	1.18 (0.67-2.07)
Intronic	29	0.82	0.64	625	240	0.98 (0.84-1.14)
3’ UTR	2	0.82	0.80	21	9	0.88 (0.40-1.92)
VEP Low	4	0.97	1.00	38	13	1.10 (0.59-2.07)
VEP Moderate	10	0.69	0.27	141	50	1.06 (0.77-1.47)
VEP Modifier	31	0.82	0.64	644	248	0.97 (0.84-1.14)
Head (29876252-29876554)	-	-	-	-	-	-
Rod (29876555-29884868)	34	0.60	0.56	641	252	0.95 (0.82-1.11)
Missense	5	0.11	0.52	81	32	0.95 (0.63-1.44)
Intronic	29	0.82	0.64	625	240	0.98 (0.84-1.14)
VEP Moderate	5	0.11	0.52	81	32	0.95 (0.63-1.44)
VEP Modifier	29	0.82	0.64	625	240	0.98 (0.84-1.14)
Tail (29884869-29886689)	9	0.71	0.22	95	33	1.08 (0.73-1.62)
Synonymous	4	0.96	1.00	38	13	1.10 (0.59-2.07)
Missense	2	0.91	0.73	16	6	1.00 (0.39-2.57)
Inframe Deletion	3	0.45	**0.03**	50	16	1.18 (0.67-2.07)
VEP Low	4	0.96	1.00	38	13	1.10 (0.59-2.07)
VEP Moderate	5	0.58	**0.04**	66	22	1.13 (0.70-1.84)
All excluding tail (29876207-29884868)	34	0.60	0.56	641	252	0.95 (0.82-1.11)

Table 5-4. Results of the high-frequency rare (MAF 0.1-1%) NEFH variant burden analysis. Significant results are denoted by bold p-values. All results are corrected for sex and the first 10 principal components.

Frequency (<1%)	**No. Variants**	**Madsen Browning p-value**	**SKAT-O p-value**	**Cases**	**Controls**	**Odds Ratio (95% CI)**
All (29876207-29887379)	557	**0.03**	0.38	1269	438	1.11 (0.99-1.25)
Synonymous	41	0.11	0.32	47	12	1.48 (0.78-2.79)
Missense	87	0.11	0.56	85	24	1.34 (0.85-2.11)
All pathogenic missense	56	0.36	0.8	69	22	1.18 (0.73-1.91)
Inframe Deletion	15	**0.05**	0.42	16	2	3.01 (0.69-13.12)
Inframe Insertion	11	0.38	0.75	12	3	1.51 (0.42-5.34)
Intronic	361	**4.0E-03**	**0.034**	419	115	1.40 (1.13-1.73)
3’ UTR	31	0.22	0.66	39	11	1.34 (0.68-2.61)
5’ UTR	4	**4.0E-03**	**0.037**	1	3	0.13 (0.01-1.21)
VEP High	6	0.13	0.11	3	4	0.28 (0.06-1.26)
VEP Low	41	0.11	0.32	47	12	1.48 (0.78-2.79)
VEP Moderate	113	**0.029**	0.18	113	29	1.47 (0.98-2.22)
VEP Modifier	397	**3.1E-03**	**0.034**	460	127	1.39 (1.14-1.70)
Head (29876252-29876554)	13	0.76	0.26	15	9	0.63 (0.27-1.43)
Synonymous	7	0.49	0.24	8	3	1.00 (0.27-3.79)
Missense	6	0.091	0.17	7	6	0.44 (0.15-1.31)
Pathogenic missense	1	N/A	0.069	1	0	1.13 (0.05-27.73)
VEP Low	7	0.49	0.24	8	3	1.00 (0.27-3.79)
VEP Moderate	6	0.091	0.17	7	6	0.44 (0.15-1.31)
Rod (29876555-29884868)	413	**0.03**	0.32	1062	363	1.12 (0.98-1.28)
Synonymous	20	0.08	0.25	28	5	2.11 (0.81-5.48)
Missense	28	0.07	0.55	29	6	1.82 (0.76-4.39)
Pathogenic missense	17	0.85	0.46	23	12	0.72 (0.36-1.45)
Inframe Insertion	1	0.26	0.53	1	0	1.13 (0.041-27.73)
Intronic	361	**4.0E-03**	**0.034**	419	115	1.40 (1.13-1.73)
VEP High	3	0.18	0.2	1	2	0.19 (0.02-2.07)
VEP Low	20	0.08	0.25	28	5	2.11 (0.81-5.48)
VEP Moderate	29	**0.05**	0.48	30	6	1.89 (0.78-4.54)
VEP Modifier	397	**3.1E-03**	**0.034**	460	127	1.39 (1.14-1.70)
Tail (29884869-29886689)	95	0.18	0.21	193	63	1.15 (0.86-1.54)
Synonymous	14	0.65	0.89	10	4	0.94 (0.29-3.00)
Missense	53	0.08	0.41	49	12	1.54 (0.82-2.90)
Pathogenic Missense	38	0.09	0.36	52	13	1.51 (0.82-2.78)
Inframe Deletion	15	**0.05**	0.42	16	2	3.01 (0.69-13.12)
Inframe Insertion	10	0.43	0.84	11	3	1.38 (0.38-4.95)
VEP High	3	0.36	0.35	2	2	0.38 (0.05-2.67)
VEP Low	14	0.65	0.89	10	4	0.94 (0.29-3.00)
VEP Moderate	78	**0.024**	0.28	76	17	1.69 (1.00-2.87)

All excluding tail (29876207-29884868)	431	0.06	0.43	1068	372	1.10 (0.96-1.25)

Table 5-5. Results of the rare (MAF < 1%) NEFH variant burden analysis. Significant results are denoted by bold p-values. All results are corrected for sex and the first 10 principal components.

5.5 Discussion

Leveraging genetic data from 11,130 ALS patients and 7,416 controls from both the literature and Project MinE, we found that rare variants (MAF<1%) in the *NEFH* gene increase the risk of ALS (meta-analysis p<0.0001 and Project MinE burden analysis p=0.0007 when taking multiple testing into account). We report that this association may be primarily driven by missense variants in the tail domain and intronic variants in the rod domain. Our meta-analysis reported that rare missense tail *NEFH* variants in a total of 1164 ALS patients and 2177 controls yielded an OR of 4.55 (p<0.0001). This was replicated to some extent, although with a lower OR and nominal association, when performing ultra-rare variant burden analysis of pathogenic missense tail variants in the Project MinE dataset (OR 1.94, Madsen-Browning p=0.039). The difference between effect sizes is likely due to the discrepancy in sample size between the two cohorts, with smaller sample sizes often reporting a larger effect size for significant relationships in either direction (L. Lin, 2018), or also the ‘winner’s curse’ effect commonly observed in genetic association discovery studies (Xiao & Boehnke, 2009). Furthermore, as the aforementioned Project MinE association is nominal, but there was no association with rare missense variants as a whole due to the nature of how we dealt with multiple testing, we could deliberate as to whether these effects are consistent. However, as most missense variants in the meta-analysis are deleterious and possibly/probably damaging according to SIFT and PolyPhen, which are the same criteria used in the Project MinE burden analyses, we can attest that the effects we are seeing do share some consistency.

The effect of missense tail variants on *NEFH* is not clear (Theunissen, West, et al., 2021), but it is plausible to hypothesise that they could modify the effects of phosphorylation in the KSP repeat, thereby changing the conformation of the NF-H subunit in such a way that simultaneously increases the propensity of pNF-H aggregate formation in the axon and disrupts energy metabolism and protein transport. We also found that rare small in-frame deletions in the tail domain confer susceptibility to ALS within Project MinE, which agrees with previous findings in the literature (Al-

Chalabi et al., 1999; Figlewicz et al., 1994), but not in the meta-analysis. This discrepancy could again be due to the relatively small sample sizes used in the meta-analysis compared to Project MinE, or that there may be subdomain-specific effects occurring in the tail that the meta-analysis design could not account for. For instance, we identified that deletions in the KSP repeat were associated with an increased risk for ALS, and we also found a novel protective common (MAF > 1%) 113bp deletion in the KEP segment, which despite having discordance in direction of effect with the non-significant ultra-rare KEP repeat in-frame deletions from the burden analysis, is still suggestive of the fact that there is a complex genetic architecture in this domain with different classes and frequencies of variants playing different roles. This is plausible in other domains as well given that recent studies identified other protective variants in the gene (Grassano et al., 2021; Theunissen et al., 2022) and that we found ultra-rare (MAF<0.1%) intronic rod SNVs and indels were the main drivers of the association between *NEFH* variants and ALS, despite a recent study reporting a common non-coding repeat polymorphism in the same domain as being protective against ALS (Theunissen et al., 2022). Therefore, future studies should incorporate genetic evidence of missense tail mutations and the characterisation of both small and large deletions with proteomic and transcriptomic data to determine if there is an aberrant stoichiometry of NF-H that is due solely to the action of these mutations or is a product of a more complex interaction between microRNA and protein targets.

In conclusion, we demonstrate that missense variants and in-frame deletions in the tail domain, and intronic variants in the rod domain of *NEFH* are associated with an increased risk of ALS. However, they are not variants of large effect, and their functional impact needs to be assessed in further experimental studies before determining whether they should be included in routine genetic screening panels. In recent years several studies have shown that non-coding variants have a major role in ALS: for example, enhancer variants in *CAV1* and *CAV2* (Adey et al., 2023; Cooper-Knock et al., 2021) and intronic variants in *UNC13A* (A.-L. Brown et al., 2022; Ma et al., 2022). Our findings expand this by also implicating *NEFH* non-coding variants in ALS. However, understanding the functional effect of variants in non-coding regions is challenging and further research is needed to understand how non-coding neurofilament variants contribute to ALS risk.

Chapter 6. Differential gene expression analysis of two large ALS sequencing consortia

6.1 Abstract

Background

Amyotrophic lateral sclerosis (ALS) is a fatal heterogeneous neurodegenerative disease that typically leads to death from respiratory failure within two to five years. Despite the identification of several genetic risk factors, the biological processes involved in ALS pathogenesis remain poorly understood. The motor cortex is an ideal region to study dysregulated pathological processes in ALS as it is affected from the earliest stages of the disease. In this study, we investigated motor cortex gene expression of cases and controls to gain new insight into the molecular footprint of ALS.

Methods

We performed a large case-control differential expression analysis of two independent post-mortem motor cortex bulk RNAseq datasets from the King's College London BrainBank (N = 171) and TargetALS (N = 132). Differentially expressed genes from both datasets were subjected to gene and pathway enrichment analysis. Genes common to both datasets were also reviewed for their involvement with known mechanisms of ALS pathogenesis to identify potential candidate genes. Finally, we performed a correlation analysis of genes implicated in pathways enriched in both datasets with clinical outcomes such as age of onset and survival. Cell type deconvolution was performed to assess if gene enrichment results were a product of the differential contribution of cell types in both datasets.

Results

Differential expression analysis identified 2,290 and 402 differentially expressed genes in KCL BrainBank and TargetALS cases, respectively. There were 45 differentially expressed genes which were common to both datasets, which represented previously recognised mechanisms of ALS pathogenesis, such as lipid metabolism, mitochondrial energy homeostasis and neurovascular unit dysfunction. Differentially expressed genes in both datasets were significantly enriched for the neuropeptide signalling

pathway. By looking at the relationship between the expression of neuropeptides and their receptors with clinical measures, we found that *TACR1* expression positively correlated with disease duration, and *NPBWR1* expression negatively correlated with age of onset in both datasets. We provide access to gene-level expression results to the broader research community through a publicly available web application (https://alsgeexplorer.er.kcl.ac.uk).

Conclusion

This study identified motor-cortex specific genes and pathways altered in ALS patients, and a set of neuropeptides and receptors for further investigation as potential biomarkers of onset and progression.

6.2 Introduction

Amyotrophic lateral sclerosis (ALS) is a devastating, heterogeneous neurodegenerative disease that leads to death from neuromuscular respiratory failure within two to five years. Despite the heritability of ALS being largely unknown, the discovery of several genetic risk factors has driven the identification of multiple biological processes involved in the disease aetiology (Julien, 2001; Rowland & Shneider, 2001). However, the pathogenic mechanisms of ALS remain poorly understood.

The motor cortex is affected from the earliest stages of the disease and is one of the brain regions majorly affected by ALS pathology. Consequently, its disease expression signatures have been investigated to gain insight into the disease aetiology. Recent studies have reported differential expression of genes related to transcription, neurotransmission, protein synthesis and oxidative stress processes (X.-S. Wang et al., 2006), with extensive RNA expression alterations of neuroinflammatory and synaptic-related pathways identified at both gene and isoform levels (Dols-Icardo et al., 2020). Nevertheless, studies of this critical region at the whole-transcriptome level usually involve relatively small sample sizes and do not replicate their results in independent datasets.

To study functional changes occurring in the motor cortex of ALS patients, we have utilised two large independent RNAseq datasets of ALS patients and controls from the

King's College London (KCL) BrainBank (171 subjects) and TargetALS (234 samples from 132 subjects). By analysing the two datasets, our goal was to obtain profiles of altered gene expression that would identify the underlying molecular footprint of ALS and use this information to propose novel hypotheses about disease mechanisms, potential drug targets and biomarkers.

6.3 Methods

6.3.1 Datasets

The KCL BrainBank RNAseq dataset (described previously in Iacoangeli et al., 2021; Jones et al., 2021) consists of post-mortem RNAseq samples from KCL and the Medical Research Council (MRC) London Neurodegenerative Diseases Brain Bank. Frozen human post-mortem tissue was taken from the primary motor cortex. The RNAseq protocol is outlined in Chapter 3.1.2.1. In total, 112 sporadic ALS cases and 59 controls were included in this analysis.

The TargetALS RNAseq dataset comes from The TargetALS Human Postmortem Tissue Core and the New York Genome Centre (NYGC). We obtained the TargetALS dataset from https://www.targetals.org/. Details about the RNAseq protocol is available in Chapter 3.1.2.2. A list of the sample IDs of 234 samples (from 132 subjects, 112 ALS cases and 20 controls) used in this study is available in Table A14. Frozen human post-mortem tissue was taken from the motor cortex (medial, lateral, and unspecified). Samples from different motor cortex regions for the same subjects were included, where available, for differential expression analysis (see Chapter 3.4.1 for more information on the inclusion of multiple samples per subject).

To determine whether the sample characteristics for cases and controls differed in each dataset, we performed unpaired t-tests for age at death, RIN number and post-mortem delay (PMD) and the chi-square test for sex assigned at birth for both datasets. Any continuous variables that were not normally distributed were assessed with the Wilcoxon-rank test. A p-value of < 0.05 denotes significance.

6.3.2 Bioinformatics, data processing and expression analysis

Both datasets were processed using the same transcript quantification pipeline, which is detailed in Chapter 3.1.3. Normalisation and differential expression was performed using DESeq2 (Love et al., 2014). For normalisation we used the *estimateSizeFactors* function of DESeq2, before the Wald test was used for differential expression analysis, with the Benjamini-Hochberg method used for p-value adjustment. For both datasets, we included age, sex, RIN number, PMD and a surrogate variable obtained by SVA (Leek & Storey, 2007) as covariates in the DESeq2 design. The sequencing centre was also included as a covariate for the TargetALS dataset. We decided to include surrogate variables in our design as they can effectively eliminate the influence of naturally grouped variables which might unknowingly be affecting the differential expression results. For instance, principal component analysis of the TargetALS dataset reveals that there two distinct groups which are not influenced by motor cortex region (Figure 3-1), but this grouping was effectively eliminated with the application of the one surrogate variable identified during analysis (Figure A10).

The differential expression code is available at https://github.com/rkabiljo/DifferentialExpression_Genes. For MA Plots, apeglm was used for LFC shrinkage (Zhu et al., 2019). Enrichment analysis was performed using MetaCore^{TM} (available at https://portal.genego.com) for Gene Ontology (GO) Biological Processes, Pathway Maps, Process Networks and Disease by Biomarker enrichments, whilst gProfiler2 (Kolberg et al., 2020) was used for Reactome (Gillespie et al., 2022) enrichment. Due to a non-one-to-one mapping of the MetaCore algorithm of uploaded gene lists to their proprietary concept of network objects, the resulting enrichment lists consisted of 1,004 objects for KCL BrainBank and 366 for TargetALS. For background genes, we used a list of 41,709 transcripts which had at least 10 counts in at least 5 subjects, which were subsequently mapped in MetaCore to 26,484 network objects.

To test whether the number of differentially expressed genes identified in our analysis was due to chance, we performed 1,000 random permutations of case/control labels and performed differential expression analysis on each permutation. For each permutation, we counted the number of genes with false discovery rate (FDR) adjusted p-value lower than our selected cut-off of 0.05. The random permutation scripts are available here https://github.com/rkabiljo/ShufflingLabelsForDE.

To assess if gene enrichment results were a product of the contribution of different cell types, we used the MuSiC2 R package (v1.0.0; (Fan et al., 2022)) to derive cell proportions for the following cell types; astrocytes, endothelial cells, microglia, neurons, and oligodendrocytes. We performed deconvolution using the raw RNAseq count matrix of KCL BrainBank, TargetALS medial motor cortex, and TargetALS lateral motor cortex. The single-cell RNAseq reference dataset which was used to derive expression information for each cell type consisted of 8 adults and 4 embryonic samples (16-18 weeks gestational age) from the temporal lobe (Darmanis et al., 2015), which was downloaded via the scRNAseq R package (v2.14.0; (Risso D, Cole M, 2023)). Due to the relatively small sample sizes of each of our datasets, the detection of cell-type-specific differentially expressed genes and cell-type deconvolution was performed using the t-statistic approach of MuSiC2. Case-control differences in cell type proportions were assessed using one-way ANCOVA corrected for age of death and sex, with a p-value of < 0.05 denoting significance.

To assess the relationship between neuropeptide receptors and ligands with age of onset and disease duration, we performed correlation analysis of RNAseq counts normalised via the variance-stabilising transformation algorithm in DESeq2 for ALS patients in the KCL BrainBank and TargetALS medial and lateral motor cortex datasets. We derived the neuropeptide-related genes from the Hugo Gene Nomenclature Committee (HGNC) Neuropeptides and Peptide Receptors lists (available at https://www.genenames.org) before the receptors and ligands which were expressed in each dataset (102 in KCL BrainBank, 105 in TargetALS medial motor cortex and 106 in TargetALS lateral motor cortex) were analysed. Correlation analysis was performed using the *cor.test* function in the stats R package (v4.2.3) Nominal p-values were identified from the output of these tests, with adjusted p-values calculated using the false-discovery rate method, whereby the p-values were multiplied by the number of neuropeptides tested in each dataset. A p-value of < 0.05 denoted significance.

To share the results with the wider community, we developed a web application using the R “shiny” framework (v1.7.1) to allow quick visualisation of specific gene expression in ALS cases and controls, available at https://alsgeexplorer.er.kcl.ac.uk.

6.4 Results

6.4.1 Sample Characteristics

The summary characteristics of the two datasets are shown in Table 6-1. The KCL BrainBank dataset had significant differences between cases and controls in terms of age, RNA integrity number (RIN) and post-mortem delay (PMD). The TargetALS dataset showed no significant differences in age, sex, and RIN between cases and controls, but did display a significant difference in PMD (p-value = 0.0027). We accounted for these differences through our choice of covariates included in the differential expression analyses.

Dataset	**Variables**	**ALS Cases**	**Controls**	**Statistic and p-value***
KCL BrainBank	***Total (Individuals)***	112	59	
	Age (mean ± SD)	64.8 ± 12.7	76.2 ± 14.6	5.28; **3.9E-07**
	Male : Female (%)	65 (58%) : 47 (42%)	26 (44.1%) : 33 (55.9%)	3.03; 0.08
	RIN Number (mean ± SD)**	6.45 ± 1.26	5.33 ± 1.58	1847; **2.2E-06**
	PMD (mean ± SD)	26.0 ± 12.1	37.6 ± 19.3	4.17; **7.6E-05**
TargetALS	***Total (Individuals)***	112	20	
	Age (mean ± SD)	63.9 ± 10.6	62.6 ± 11.9	-0.52; 0.61
	Male : Female (%)	64 (57.1%) : 48 (42.9%)	9 (45%): 11 (55%)	1.01; 0.31
	Total (Samples)	198	36	
	RIN Number (mean ± SD)**	6.21 ± 1.15	5.91 ± 1.25	3161; 0.28
	PMD (mean ± SD)**	10.5 ± 6.92	21.2 ± 22.8	4683; **2.7E-03**

*Table 6-1. Sample characteristics of KCL BrainBank and TargetALS. Age: Age at death. PMD: Post-mortem delay. RIN: RNA integrity number. *Statistic and p-value refers to the Chi-square test for categorical variables (Sex assigned at birth – Male: Female) and unpaired T-test for continuous variables (Age, RIN Number, PMD). **Wilcoxon test was performed as data was not normally distributed.*

6.4.2 Differential expression analysis

6.4.2.1 KCL BrainBank

A total of 2,290 genes were differentially expressed with an adjusted p-value of <0.05, in the KCL BrainBank dataset. Of these, 1,507 of the genes were upregulated and 783 were downregulated in cases (Figures 6-1A and 6-1B). None of the 1000 random permutations produced more differentially expressed genes than the actual differential expression analysis, thus confirming the significance of these results. In the vast majority of the permutations, there were no differentially expressed genes (with adjusted p-value <0.05), with the number of significant genes across permutations averaging 4.5. Table A15 displays the full details of the 2,290 significant differentially expressed genes discovered using DESeq2.

6.4.2.2 TargetALS

A total of 402 genes were differentially expressed, with an adjusted p-value of <0.05, in the TargetALS dataset. Of these, 250 of these genes were downregulated and 152 were upregulated in cases (Figures 6-1C and 6-1D). When performing random permutations, 9 (0.9%) produced as many or more differentially expressed genes as the actual differential expression analysis. In most of the permutations, there were no differentially expressed genes (with adjusted p-value <0.05), with an average of 28 significantly expressed genes across permutations. Table A16 displays the full details of the 402 significant differentially expressed genes discovered using DESeq2.

6.4.2.3 Shared differentially expressed genes

We found 45 genes significant in both datasets with an adjusted p-value of <0.05. Of these, 44 of these had a concordant direction of regulation in both datasets; 29 genes were downregulated and 15 were upregulated (Figure 6-1E). To estimate the significance of this intersection between differentially expressed genes in the two datasets, we performed a hypergeometric test, using 41,709 as the number of background genes. The p-value obtained was < 1.2E-05. Genes that were significant in both datasets are listed in Table 6-2.

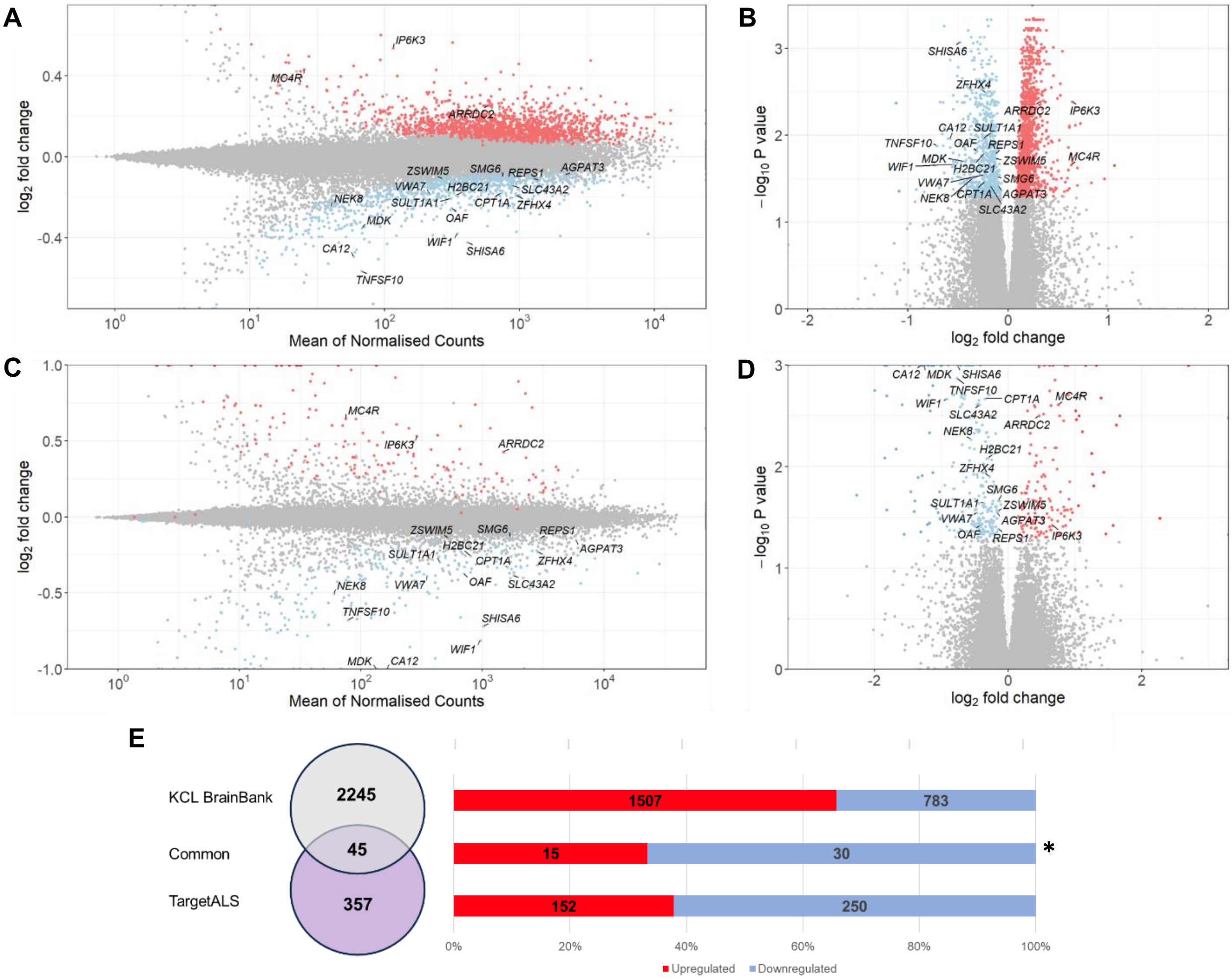

*Figure 6-1. Visualisation of the distribution of differentially expressed genes in KCL BrainBank and TargetALS. A) KCL BrainBank and C) TargetALS MA plots representing the distribution of log2 fold change (logFC) across all expression levels; B) KCL BrainBank and D) TargetALS Volcano plots. In plots A - D, genes coloured red are significantly upregulated in ALS cases and genes coloured blue are significantly downregulated in ALS cases. E) Numbers of differentially expressed genes in the two datasets. Left: Number of unique and shared differentially expressed genes. Right: Breakdown of numbers of upregulated and downregulated genes in each dataset (Total KCL BrainBank: 2,290, TargetALS: 402, Common: 45). * One gene is missing from this breakdown as it displayed a discordant direction of expression.*

Ensembl ID	**Gene Symbol**	**KCL BrainBank**			**TargetALS**			**Biological Theme**
		LogFC	**p-value**	**adj. p-value**	**LogFC**	**p-value**	**adj. p-value**	
ENSG00000121858	*TNFSF10*	-0.71	3.4E-04	0.013	-0.77	1.7E-06	1.3E-03	UPS/Autophagy
ENSG00000164309	*CMYA5*	-0.28	1.8E-04	5.8E-03	-0.29	1.9E-04	0.027	UPS/Autophagy
ENSG00000074410	*CA12*	-0.58	2.0E-04	0.011	-1.3	6.0E-15	5.2E-11	NVU Dysfunction
ENSG00000101439	*CST3*	-0.27	5.4E-03	0.042	-0.41	4.2E-04	0.039	NVU Dysfunction
ENSG00000271447	*MMP28*	-0.33	3.1E-03	0.030	-0.58	9.4E-06	3.3E-03	Neuroinflammation
ENSG00000110492	*MDK*	-0.43	5.5E-04	0.02	-1.26	2.1E-18	6.3E-14	Neuroinflammation, Neurogenesis
ENSG00000188803	*SHISA6*	-0.48	2.6E-06	8.4E-04	-0.76	4.7E-10	1.6E-06	Neuronal Signalling (AMPA/NMDA)
ENSG00000196502	*SULT1A1*	-0.25	5.8E-04	0.011	-0.36	1.7E-04	0.023	Metabolism, Neuronal Signalling (AMPA/NMDA)
ENSG00000110090	*CPT1A*	-0.23	4.1E-03	0.034	-0.35	4.2E-06	2.1E-03	Metabolism (Fatty Acid)
ENSG00000204396	*VWA7*	-0.24	2.4E-03	0.028	-0.47	2.4E-04	0.028	Extracellular Matrix
ENSG00000156076	*WIF1*	-0.55	1.5E-03	0.022	-0.92	3.8E-06	2.1E-03	WNT/β-Catenin Signalling
ENSG00000160602	*NEK8*	-0.35	1.4E-03	0.031	-0.56	1.9E-05	5.4E-03	DNA Damage Response
ENSG00000091656	*ZFHX4*	-0.22	6.5E-05	3.3E-03	-0.28	6.2E-05	0.013	Transcriptional Regulation
ENSG00000184678	*H2BC21*	-0.24	9.7E-04	0.016	-0.30	3.2E-05	8.2E-03	Nucleosome
ENSG00000237686	*SCIRT*	-0.65	2.6E-05	4.2E-03	-0.65	1.1E-05	4.7E-03	NVU Dysfunction
ENSG00000261888	*Lnc-METRNL-1*	-0.64	7.5E-04	0.027	-0.81	1.4E-06	1.9E-03	Metabolism (Glucose)
ENSG00000271646	*IRF2-DT*	-0.45	9.4E-05	6.5E-03	-0.38	5.7E-04	0.046	Neuroinflammation
ENSG00000134042	*MRO*	-0.31	5.6E-03	0.041	-0.47	4.5E-06	2.4E-03	-
ENSG00000184232	*OAF*	-0.31	8.9E-04	0.015	-0.42	4.0E-04	0.038	Molecular Chaperone
ENSG00000267904	*Lnc-MED26-2*	-0.27	7.0E-04	0.020	-0.21	4.4E-04	0.031	Transcriptional Regulation
ENSG00000135597	*REPS1*	-0.13	1.1E-03	0.016	-0.15	4.4E-04	0.041	Neuronal Signalling (Vesicular Transport and Endocytosis)
ENSG00000162415	*ZSWIM5*	-0.13	1.3E-03	0.018	-0.15	2.2E-04	0.028	Metal Ion Binding
ENSG00000070366	*SMG6*	-0.11	2.9E-03	0.030	-0.15	1.6E-04	0.022	Telomere Maintenance, Nonsense-Mediated Decay
ENSG00000145476	*CYP4V2*	-0.20	3.0E-03	0.030	-0.23	3.9E-04	0.036	Metabolism (Fatty Acid)
ENSG00000167703	*SLC43A2*	-0.18	4.3E-03	0.037	-0.43	4.5E-06	2.4E-03	Amino Acid and Ion Transport
ENSG00000160216	*AGPAT3*	-0.10	4.4E-03	0.038	-0.17	2.5E-04	0.028	Metabolism (Lipid)
ENSG00000215154	*LOC652276*	-0.26	6.9E-04	0.019	-0.28	1.1E-03	0.048	-
ENSG00000172270	*BSG*	-0.16	6.2E-04	0.044	-0.30	3.5E-04	0.035	Neuroinflammation

ENSG00000143819	*EPHX1*	-0.19	6.2E-03	0.046	-0.37	2.9E-04	0.032	Metabolism (Fatty Acid)
ENSG00000166603	*MC4R*	0.63	7.4E-04	0.022	0.75	8.2E-06	2.4E-03	Neuropeptide Signalling, Metabolism
ENSG00000105643	*ARRDC2*	0.32	9.5E-05	4.1E-03	0.46	8.4E-06	3.1E-03	Metabolism, Neuronal Signalling
ENSG00000161896	*IP6K3*	0.64	1.0E-04	4.1E-03	0.66	4.1E-04	0.038	Metabolism
ENSG00000183196	*CHST6*	0.41	1.2E-05	1.5E-03	0.62	4.2E-07	4.9E-04	Metabolism
ENSG00000176641	*RNF152*	0.29	4.2E-04	8.5E-03	0.33	1.4E-05	4.7E-03	UPS/Autophagy
ENSG00000156804	*FBXO32*	0.21	8.2E-04	0.014	0.25	1.0E-04	0.018	UPS/Autophagy
ENSG00000240583	*AQP1*	0.63	1.1E-03	0.016	0.86	2.1E-04	0.027	NVU Dysfunction
ENSG00000154188	*ANGPT1*	0.42	2.3E-03	0.042	0.67	6.2E-07	4.0E-04	NVU Dysfunction
ENSG00000134817	*APLNR*	0.56	5.7E-03	0.044	0.90	2.8E-06	2.0E-03	NVU Dysfunction, Apelin Signalling
ENSG00000168386	*FILIP1L*	0.30	5.1E-05	3.3E-03	0.25	2.6E-04	0.032	WNT/β-Catenin Signalling
ENSG00000286653	NA (novel transcript)	0.57	3.0E-04	0.034	0.61	1.4E-04	0.021	-
ENSG00000052795	*FNIP2*	0.14	1.7E-03	0.020	0.20	1.1E-04	0.018	Metabolism, Autophagy, Apoptosis
ENSG00000171451	*DSEL*	0.16	5.9E-03	0.045	0.30	1.3E-04	0.021	-
ENSG00000198740	*ZNF652*	0.19	8.6E-04	0.013	0.34	2.3E-05	6.1E-03	Transcriptional Regulation
ENSG00000138798	*EGF*	0.40	3.2E-04	0.012	0.42	3.9E-05	9.1E-03	-
ENSG00000272505	*Lnc-PRSS55-1*	-0.20	0.0011	0.018	0.21	1.9E-04	0.024	-

Table 6-2. Significantly differentially expressed genes shared in both KCL BrainBank and TargetALS (adjusted p-value < 0.05). For each gene, the fold change, p-value and adjusted p-value is displayed for both datasets, along with their major biological function. Red: Upregulated; Blue: Downregulated. White: Discordant direction of expression.' LogFC: Log2 of Fold Change.

6.4.3 Gene and Pathway Enrichment Analysis

To compensate for the different numbers of differentially expressed genes in the two datasets when using 0.05 as the corrected p-value threshold (2,290 genes in KCL BrainBank and 402 in TargetALS), we applied an additional threshold of logFC > 0.2 to the KCL BrainBank dataset. This yielded differential expression for 1,013 genes, which were uploaded to MetaCore for enrichment analysis along with the 402 differentially expressed genes in TargetALS. We performed analyses using MetaCore to obtain enrichments for Pathway Maps, Process Networks, Disease Networks and Gene Ontology (GO) Biological Processes, and gProfiler2 for Reactome enrichment. Tables A17-A26 list the top 100 results for each of the enrichment categories (50 for Process Networks), with their p-value, false discovery rate (FDR) adjusted p-value, and the genes from each dataset contributing to each enrichment within each category.

6.4.3.1 Process Networks

Among the most significant processes in KCL BrainBank (Figure 6-2A; Table A17) were several neurophysiological processes, such as transmission of nerve impulse (adjusted p-value = 0.000047) and GABAergic neurotransmission (adjusted p-value = 0.017), as well as axonal guidance (adjusted p-value = 0.0037). A related process that approached significance after adjustment was cholecystokinin signalling (adjusted p-value = 0.057). In addition, there was one significant process broadly related to muscle contraction (adjusted p-value = 0.0037); nitric oxide signalling in cardiovascular system (adjusted p-value = 0.016). In TargetALS, the most enriched networks, albeit not significant, were several processes related to inflammation; interferon signalling and natural killer (NK) cell cytotoxicity (Figure 6-2A; Table A18). There were two commonly significantly enriched processes; neuropeptide signalling pathways (KCL BrainBank adjusted p-value = 0.0025; TargetALS adjusted p-value = 1.5E-14) and blood vessel morphogenesis (KCL BrainBank adjusted p-value = 0.016; TargetALS adjusted p-value = 0.037).

6.4.3.2 Diseases by Biomarkers, GO Biological Processes and Reactome

We found that the two datasets demonstrated divergent enrichments for Diseases by Biomarkers (Tables A19 and A20), GO Biological Processes (Tables A21 and A22) and Reactome pathways (Tables A23 and A24). For instance, KCL BrainBank showed clear enrichments for nervous-system related diseases (Table A19), such as movement disorders (adjusted p-value = 1.2E-21), dyskinesias (adjusted p-value = 1.2E-20), neurodegenerative (adjusted p-value = 1.3E-19) and neuromuscular (adjusted p-value = 3.6E-12) diseases, as well as schizophrenia (adjusted p-value = 4.1E-13). The significant GO processes echoed this (Table A21), with enrichments for nervous system development (adjusted p-value = 1.2E-19) and synaptic signalling (adjusted p-value = 2.5E-15) and ion transmembrane transport (adjusted p-value = 1.5E-16) alongside chemical synaptic transmission, which related to several significant enrichments in Reactome (Figure 6-2B; Table A23).

In contrast, TargetALS was enriched for immune-system related diseases and processes, which includes several diseases connected with response to various viral infections (Table A20) including COVID-19 and pneumonia (adjusted p-value = 1.5E-22), GO processes related to immune response (Table A22), including innate immune response (adjusted p-value = 5.1E-09), negative regulation of cytokine production (adjusted p-value = 6.5E-08) and phagocytosis (adjusted p-value = 1.5E-07), and Reactome pathways pertaining to interferon signalling (Figure 6-2B).

6.4.3.3 Pathway Maps

Prominent themes in the KCL BrainBank enrichments were oxidative stress and signal transduction (Figure 6-2C; Table A25). The most significant pathways concerned *NRF2* regulation of oxidative stress (adjusted p-value = 0.0023) and excitability of cortical pyramidal neurons (adjusted p-value = 0.0025). Related neuronal excitability enrichments included activity-dependent AMPA receptor removal (adjusted p-value = 0.0074), GABA-A receptor life cycle (adjusted p-value = 0.0075), synaptic vesicle fusion and recycling at nerve terminals (adjusted p-value = 0.0075), the regulation of dopamine D1A receptor signalling by glutamic acid (adjusted p-value = 0.014) and NMDA receptor trafficking (adjusted p-value = 0.020). Other oxidative stress-specific enrichments included apoptosis signal-regulating kinase 1 (*ASK1*) function (adjusted p-value = 0.0043), BAD phosphorylation (adjusted p-value = 0.010) and activation of *NOX1*, *NOX5*, *DUOX1* and *DUOX2* (adjusted p-value = 0.010). In contrast, there were three significant TargetALS pathway maps; two related to pro-opiomelanocortin (POMC) processing and one to immune response (Figure 6-2C; Table A26). Interestingly, the most significant network in TargetALS (POMC processing in protein folding and maturation) includes several agonists of *MC4R* (Figure 6-3), a neuropeptide receptor which was found to be significantly upregulated in both datasets (see Chapter 6.4.2.3 and Table 6-2) and is present in the neuropeptide signalling process network which was significantly enriched in both datasets (see Chapter 6.4.3.1).

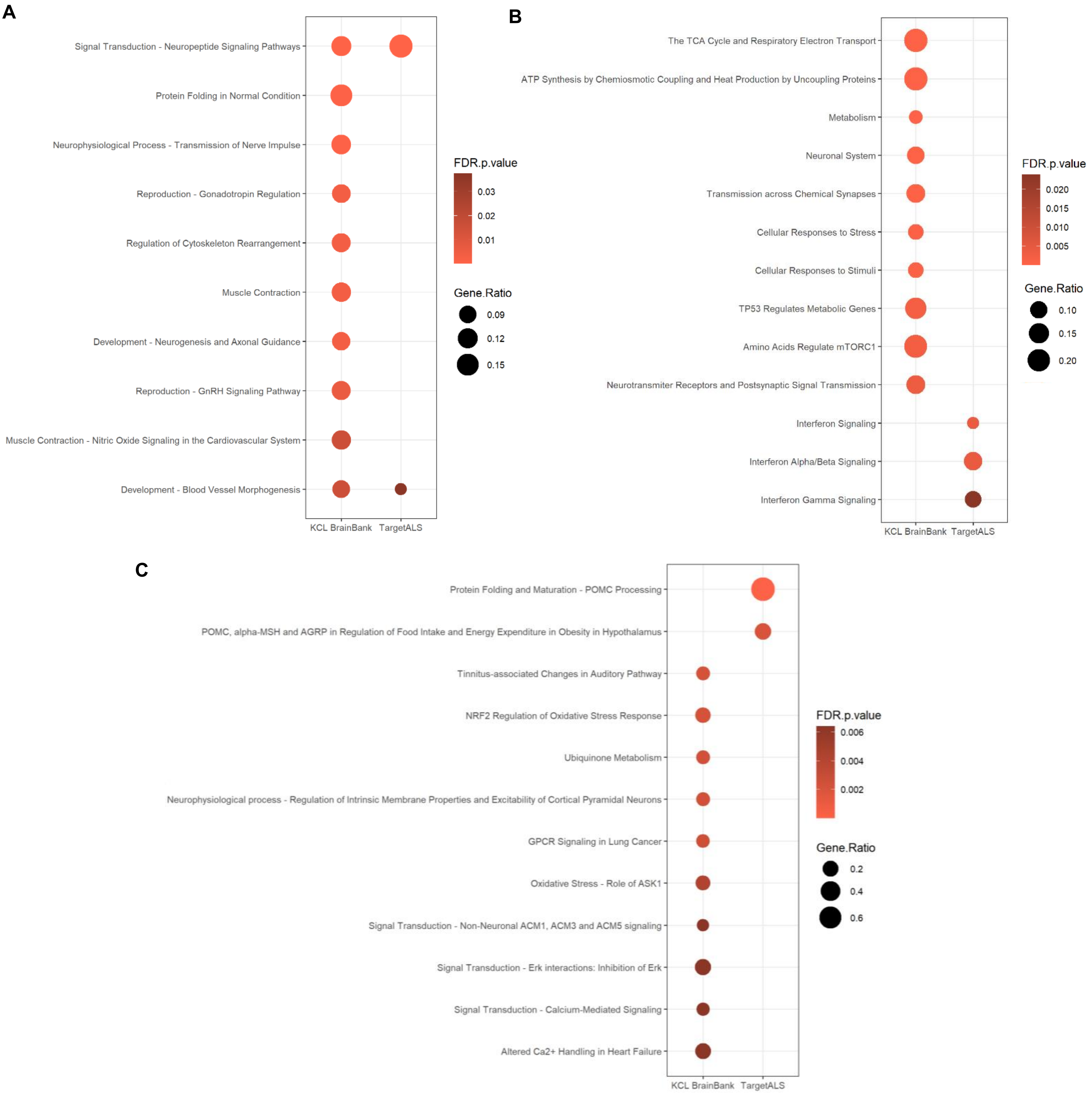

Figure 6-2. Gene and pathway enrichment results in KCL BrainBank and TargetALS for A) MetaCore Process Networks, B) Reactome and C) MetaCore Pathway Maps. The ten most significant enrichments, sorted by adjusted p-value (FDR.p.value) are shown, or fewer if less than ten were significant after multiple testing correction. Gene.Ratio refers to the number of differentially expressed genes identified in each dataset for that term, divided by the total number of genes which are included in the term definition.

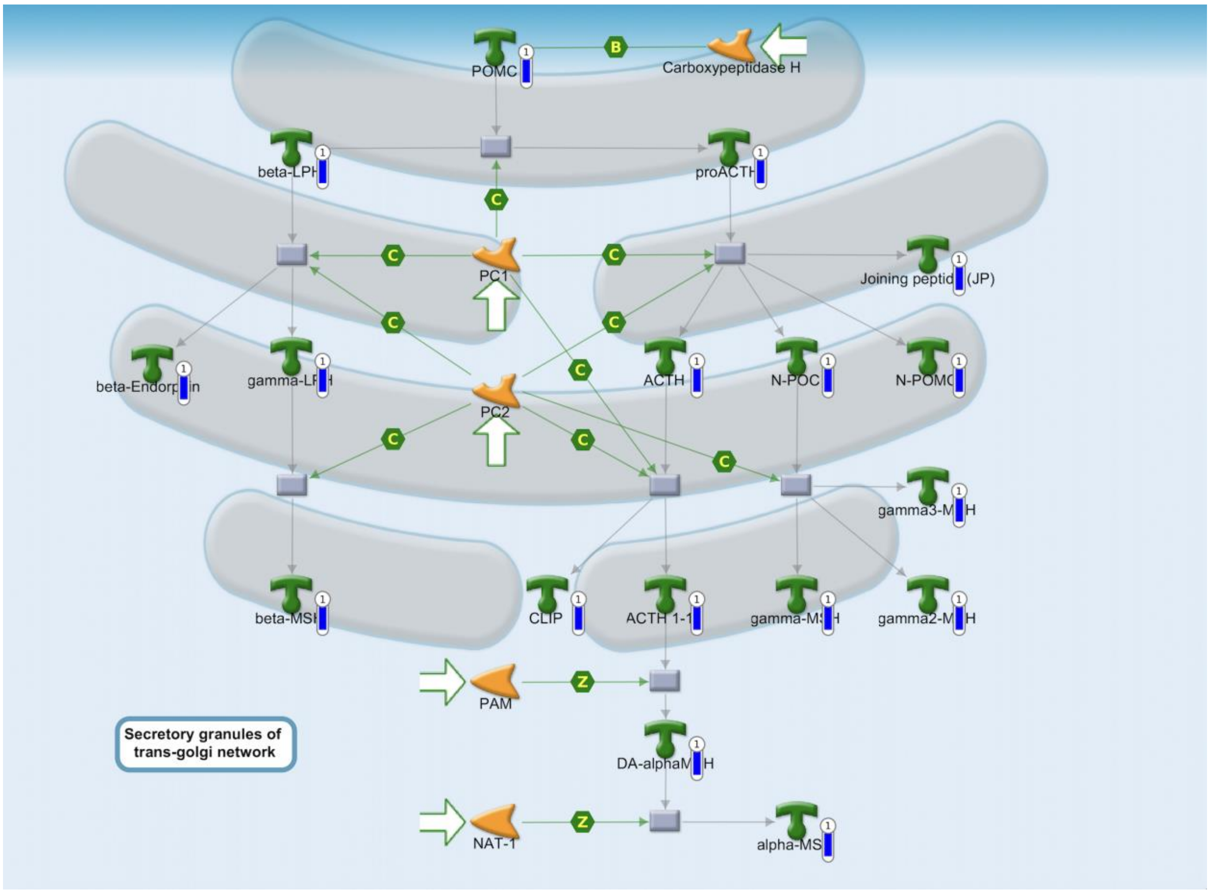

Figure 6-3. Protein folding and maturation POMC processing pathway map from MetaCore, where blue barometers represent downregulated genes from the TargetALS dataset. The descriptions of what the other symbols represent are available in Figure A11.

6.4.4 Correlation analysis of neuropeptides and neuropeptide receptors with ALS clinical phenotype

As neuropeptide signalling was the only altered biological network in both datasets, and neuropeptides have been implicated with the ALS clinical phenotype (Ahmed et al., 2019; Clark et al., 2021; Zuccaro et al., 2021), we decided to test the correlation between the expression of neuropeptides and their receptors with age at onset and disease duration of the ALS patients in the KCL BrainBank (n = 112), and the medial (n = 93) and lateral (n = 96) TargetALS motor cortex datasets. There were 102, 105 and 106 neuropeptide ligand and receptor genes in KCL BrainBank, TargetALS medial and TargetALS lateral datasets, respectively. We found that 18 neuropeptide-related genes were nominally correlated with disease duration in at least one dataset, although none of them maintained significance after multiple testing correction (Table 6-3). The only gene which was nominally significant in KCL BrainBank and at least one of the TargetALS datasets was *TACR1,* whose expression weakly positively correlated with disease duration (KCL BrainBank: r = 0.211, p-value=0.0370; TargetALS lateral: r = 0.233, p-value=0.0245). Visualisation of *TACR1* expression against disease duration is available in Figures 6-4A (KCL BrainBank) and 6-4B (TargetALS lateral motor cortex). On the contrary, 32 genes nominally correlated with age of onset in at least one dataset, with *PTHLH* and *IGF1* surviving multiple correction in KCL BrainBank (*PTHLH*: r = -0.385, adjusted p-value=0.0111; *IGF1*: r = -0.380, adjusted p-value=0.0136), and *TRH* surviving multiple correction in TargetALS lateral motor cortex (r = -0.467, adjusted p-value=0.000371). As with disease duration, the expression of only one gene, *NPBWR1*, was found to be nominally negatively correlated with age of onset in KCL BrainBank (r = -0.346, p-value=0.000565) and the TargetALS lateral motor cortex (r = -0.336, p-value=0.000991). Visualisation of *NPBWR1* expression against age of onset is available in Figure 6-4C (KCL BrainBank) and 6-4D (TargetALS lateral motor cortex). Complete correlation results can be found in Table A27.

6.4.5 Cell Type Composition Analysis

The cell type composition analysis is shown in Figure 6-5. Compared to controls, KCL BrainBank cases (shown in Figure 6-5A) contained a significantly smaller proportion of astrocytes (median ± IQR: 0.191 ± 0.0748 vs 0.279 ± 0.106, F = 18.192, p-value = 3.34E-05), whilst neuronal content was significantly higher (median ± IQR: 0.662 ± 0.118 vs 0.578 ± 0.179, F = 15.295, p-value = 1.34E-04). There were no differences in the proportion of cell types between cases and controls in both the medial and lateral TargetALS datasets (Figure 6-5B and 5C). The full breakdown is available in Table A28.

6.4.6 ALS Gene Expression Explorer

The ALS Gene Expression Explorer web application (https://alsgeexplorer.er.kcl.ac.uk) enables users to explore and compare the expression levels for specific genes in ALS cases and controls in the two datasets.

Clinical Phenotype	Ensembl ID	Gene Symbol	KCL BrainBank			TargetALS (medial)			TargetALS (lateral)		
			Pearson's r	p-value	p-value (adj)	Pearson's r	p-value	p-value (adj)	Pearson's r	p-value	p-value (adj)
Disease Duration (months)	ENSG00000126895	*AVPR2*	-0.323	**1.17E-03**	0.119	0.0397	0.710	1.0	-0.0608	0.563	1.0
	ENSG00000144891	*AGTR1*	-0.237	**0.0187**	1.0	-0.0541	0.613	1.0	-0.130	0.214	1.0
	ENSG00000115353	*TACR1*	0.211	**0.0370**	1.0	0.114	0.285	1.0	0.233	**0.0245**	1.0
	ENSG00000157005	*SST*	0.206	**0.0418**	1.0	0.139	0.193	1.0	0.129	0.217	1.0
	ENSG00000101188	*NTSR1*	0.0691	0.499	1.0	0.286	**6.37E-03**	0.669	0.0337	0.749	1.0
	ENSG00000171596	*NMUR1*	-0.079	0.440	1.0	0.266	**0.0112**	1.0	0.221	**0.0329**	1.0
	ENSG00000147437	*GNRH1*	-0.189	0.0622	1.0	-0.257	**0.0147**	1.0	-0.214	**0.0400**	1.0
	ENSG00000110680	*CALCA*	-0.0377	0.713	1.0	0.251	**0.0169**	1.0	-0.0568	0.589	1.0
	ENSG00000135744	*AGT*	0.0847	0.407	1.0	0.220	**0.0374**	1.0	0.0880	0.401	1.0
	ENSG00000166148	*AVPR1A*	-0.0991	0.332	1.0	0.218	**0.0393**	1.0	0.0951	0.365	1.0
	ENSG00000162009	*SSTR5*	NA	NA	NA	0.216	**0.0408**	1.0	0.143	0.171	1.0
	ENSG00000121764	*HCRTR1*	-0.0368	0.719	1.0	0.0450	0.674	1.0	0.241	**0.0200**	1.0
	ENSG00000288611	*NPBWR1*	0.0556	0.587	1.0	0.0200	0.852	1.0	0.239	**0.0208**	1.0
	ENSG00000170498	*KISS1*	NA	NA	NA	NA	NA	NA	0.220	**0.0342**	1.0
	ENSG00000163394	*CCKAR*	0.0179	0.861	1.0	0.0286	0.789	1.0	-0.216	**0.0380**	1.0
	ENSG00000166863	*TAC3*	0.120	0.241	1.0	0.0782	0.464	1.0	0.212	**0.0409**	1.0
	ENSG00000119973	*PRLHR*	0.140	0.169	1.0	0.0857	0.422	1.0	0.208	**0.0450**	1.0
	ENSG00000017427	*IGF1*	0.0900	0.378	1.0	0.0388	0.717	1.0	0.208	**0.0456**	1.0
Age of Onset	ENSG00000087494	*PTHLH*	-0.385	**1.09E-04**	**0.0111**	0.0196	0.855	1.0	-0.0614	0.559	1.0
	ENSG00000017427	*IGF1*	-0.380	**1.33E-04**	**0.0136**	-0.0720	0.500	1.0	-0.204	**0.0495**	1.0
	ENSG00000288611	*NPBWR1*	-0.346	**5.65E-04**	0.0576	-0.112	0.293	1.0	-0.336	**9.91E-04**	0.105
	ENSG00000168081	*PNOC*	-0.344	**6.07E-04**	0.0619	-0.143	0.179	1.0	-0.111	0.289	1.0
	ENSG00000146469	*VIP*	-0.317	**1.64E-03**	0.167	-0.0154	0.886	1.0	-0.174	0.0959	1.0
	ENSG00000139874	*SSTR1*	-0.305	**2.56E-03**	0.261	-0.146	0.170	1.0	-0.146	0.164	1.0
	ENSG00000175206	*NPPA*	-0.304	**2.56E-03**	0.262	0.0873	0.413	1.0	0.0266	0.800	1.0
	ENSG00000171388	*APLN*	0.291	**3.99E-03**	0.407	-0.0612	0.567	1.0	-0.0290	0.783	1.0
	ENSG00000157005	*SST*	-0.287	**4.51E-03**	0.460	-0.0494	0.644	1.0	-0.0444	0.672	1.0
	ENSG00000148926	*ADM*	0.284	**5.02E-03**	0.512	-0.149	0.160	1.0	-0.106	0.314	1.0
	ENSG00000134443	*GRP*	-0.282	**5.45E-03**	0.555	0.113	0.291	1.0	0.0530	0.614	1.0
	ENSG00000166863	*TAC3*	-0.282	**5.45E-03**	0.556	-0.021	0.847	1.0	-0.175	0.0941	1.0
	ENSG00000152034	*MCHR2*	-0.279	**5.84E-03**	0.595	0.0456	0.669	1.0	-0.144	0.167	1.0
	ENSG00000166573	*GALR1*	-0.266	**8.79E-03**	0.897	-0.130	0.221	1.0	-0.108	0.301	1.0

	ENSG00000049247	*UTS2*	0.253	**0.0129**	1.0	0.0690	0.518	1.0	0.0833	0.427	1.0
	ENSG00000147571	*CRH*	-0.250	**0.0140**	1.0	-0.129	0.226	1.0	-0.999	0.341	1.0
	ENSG00000180616	*SSTR2*	-0.246	**0.0157**	1.0	-0.0379	0.723	1.0	-0.0605	0.565	1.0
	ENSG00000119973	*PRLHR*	-0.246	**0.0157**	1.0	0.0165	0.877	1.0	-0.0385	0.714	1.0
	ENSG00000132911	*NMUR2*	0.228	**0.0257**	1.0	-0.0404	0.706	1.0	-0.0762	0.468	1.0
	ENSG00000147437	*GNRH1*	0.225	**0.0275**	1.0	0.109	0.306	1.0	0.0614	0.559	1.0
	ENSG00000181408	*UTS2R*	0.223	**0.0291**	1.0	0.0880	0.409	1.0	-0.00624	0.953	1.0
	ENSG00000132671	*SSTR4*	-0.211	**0.0394**	1.0	-0.0826	0.439	1.0	-0.0776	0.460	1.0
	ENSG00000139574	*NPFF*	0.207	**0.0426**	1.0	0.0377	0.724	1.0	-0.0171	0.871	1.0
	ENSG00000181195	*PENK*	-0.204	**0.0461**	1.0	-0.0747	0.484	1.0	-0.152	0.145	1.0
	ENSG00000163794	*UCN*	0.204	**0.0462**	1.0	0.0709	0.506	1.0	0.0290	0.782	1.0
	ENSG00000078401	*EDN1*	0.204	**0.0462**	1.0	-0.133	0.212	1.0	0.00845	0.936	1.0
	ENSG00000109255	*NMU*	-0.202	**0.0483**	1.0	-0.0547	0.609	1.0	-0.0979	0.350	1.0
	ENSG00000170893	*TRH*	-0.0334	0.747	1.0	-0.467	**3.53E-06**	**3.71E-04**	-0.200	0.0546	1.0
	ENSG00000166148	*AVPR1A*	-0.115	0.266	1.0	-0.319	**2.18E-03**	0.229	-0.181	0.0818	1.0
	ENSG00000145040	*UCN2*	-0.151	0.141	1.0	0.302	**3.77E-03**	0.396	0.141	0.178	1.0
	ENSG00000112038	*OPRM1*	0.0760	0.461	1.0	0.221	**0.0367**	1.0	0.0478	0.649	1.0
	ENSG00000121764	*HCRTR1*	-0.136	0.186	1.0	-0.0805	0.451	1.0	-0.233	**0.0247**	1.0

Table 6-3. Neuropeptide receptors and ligands whose gene expression is significantly correlated with either disease duration or age of onset in people with ALS from either KCL BrainBank or medial and lateral samples from TargetALS. Adjusted p-values reflect the number of neuropeptide-related genes tested in each dataset (102 in KCL BrainBank, 105 in TargetALS medial and 106 in TargetALS lateral motor cortex). A p-value of < 0.05 denotes significance.

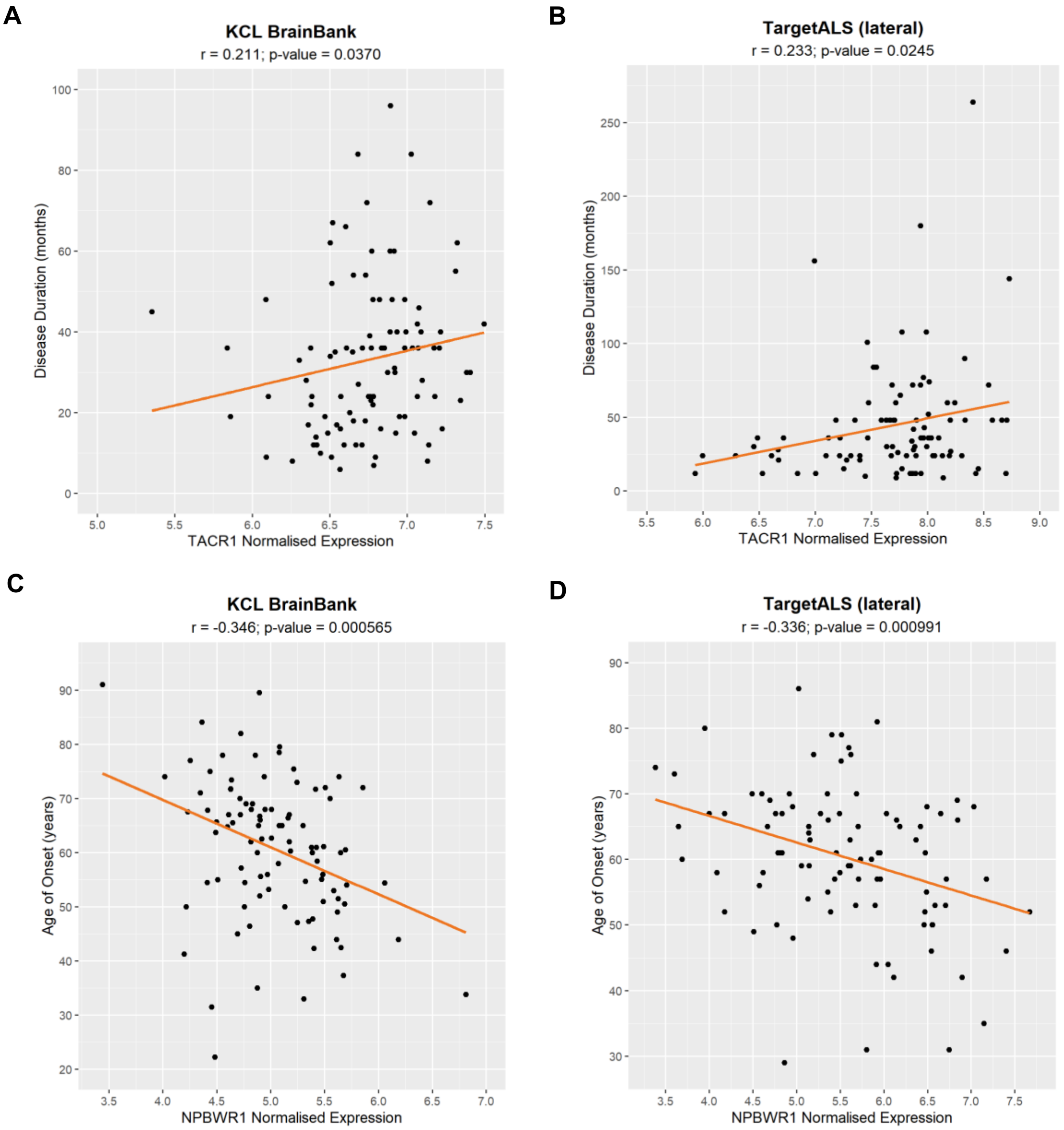

Figure 6-4. Scatterplots visualising the relationship between TACR1 and NPBWR1 normalised gene expression and clinical phenotype of ALS in both KCL BrainBank and TargetALS samples from the lateral motor cortex. A) and B) represent the absolute values for TACR1 normalised gene expression and disease duration in months. C) and D) represent the absolute values for NPBWR1 normalised gene expression and age of onset in years. Correlations with the clinical phenotype are represented visually with the orange line and numerically with the Pearson's correlation coefficient (r) and p-value.

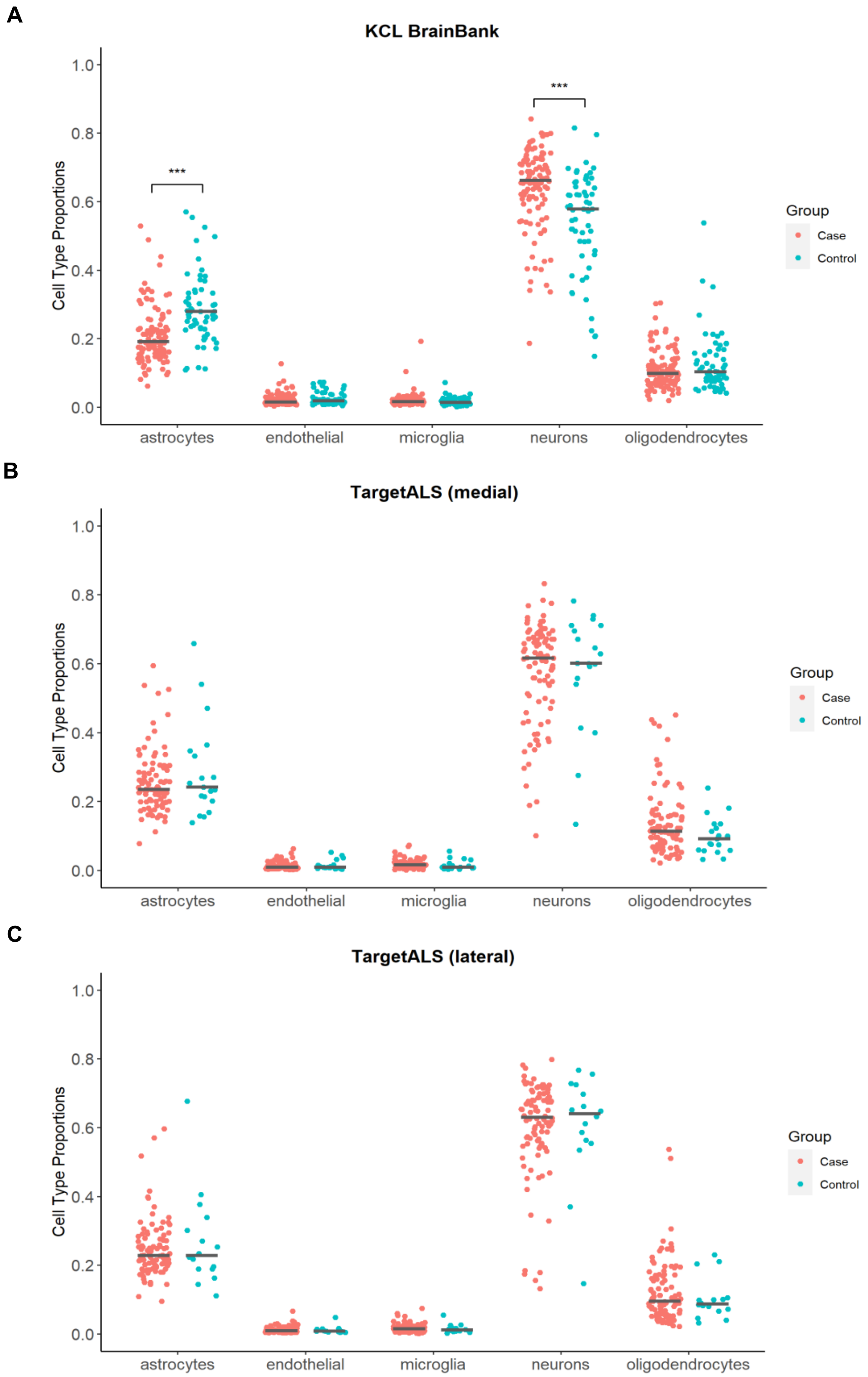

*Figure 6-5. Case-control cell deconvolution analysis in KCL BrainBank (top panel) and TargetALS (medial: middle panel, lateral: bottom panel), using MuSiC2. Significance was assessed using one-way ANCOVA corrected for age of death and sex. Case-control comparisons with asterisks denote significance in cell type proportions. *** corresponds to a p-value of < 0.001.*

6.5 Discussion

By leveraging motor cortex expression data from two independent large datasets (KCL BrainBank and TargetALS; 224 ALS cases and 79 controls) to obtain and compare ALS gene expression profiles, we identify alterations in the neuropeptide signalling pathway that indicate that this may be a key feature of ALS pathogenesis, whilst also reporting shared differentially expressed genes that represent previously recognised biological processes dysregulated in ALS.

There were several lines of evidence in this study to support the role of neuropeptide signalling in ALS pathogenesis. We found that differentially expressed genes involved in the neuropeptide signalling pathway were significantly overrepresented in both datasets via gene pathway enrichment, and whilst both datasets exhibited unique and shared differential expression of several neuropeptide ligands and receptors, the melanocortin receptor 4 gene (*MC4R*) was significantly upregulated across datasets. The role of the melanocortin system in ALS has largely been overlooked, despite *MC4R* activation inducing hypermetabolism, increased energy expenditure and cachexia; three processes associated with increased lower motor neuron weakness and poor prognosis in ALS patients (Holm et al., 2013; Jésus et al., 2018; Kasarskis et al., 2014; Kurihara et al., 2021; Steyn et al., 2018). Furthermore, *MC4R*-mediated signalling in the motor cortex also enhances the activity of sympathetic preganglionic neurons in the spinal cord, which modulates skeletal muscle contraction (Sohn et al., 2013; Ye et al., 2014), and rare (MAF < 1%) disruptive and damaging missense variants in *MC4R* might increase the risk of ALS (Beta = 2.15 SE = 1.52, p-value = 0.037, http://databrowser.projectmine.com). Therefore, we suggest further investigation on *MC4R* as a potential candidate target gene for future biomarker and screening studies.

To further investigate how neuropeptide signalling affects the ALS clinical phenotype, we also performed correlation analyses of neuropeptide-related genes (102 in KCL BrainBank, 105 in TargetALS medial and 106 in TargetALS lateral motor cortex) with age of onset and disease duration. We found that the expression levels of two genes in both KCL BrainBank and TargetALS datasets were found to nominally associate with the ALS phenotype; *TACR1* with disease duration, and *NPBWR1* with age of onset. Interestingly, both genes activate other biological processes that have been linked to ALS. For instance, one function of *TACR1* is to stimulate the production and release of arachidonic acid (Naor & Catt, 1981; Steinhoff et al., 2014), a polyunsaturated fatty acid whose levels can distinguish ALS patients from mimics and controls and positively correlates with disease progression (Lawton et al., 2014), with higher levels also found in spinal cord motor neuron cultures (H. Lee et al., 2021). Furthermore, *NPBWR1* is expressed by GABAergic interneurons and when activated, can dampen their inhibitory effects (Chottova Dvorakova, 2018) and potentially modulate their excitability patterns in the motor cortex, which has been proposed as a possible trigger for the spread of ALS pathology (Eisen et al., 2017; Scekic-Zahirovic et al., 2021). Therefore, the role of the neuropeptide signalling system on both lipid metabolism and cortical signalling in ALS and also its full impact on clinical phenotype is warranted, especially as our correlation results do not fully support and are only suggestive of a potential link between expression and modulation of phenotype.

We also linked many of the 45 differentially expressed genes common to both datasets with integral themes of ALS pathogenesis. These include carbohydrate/lipid metabolism, mitochondrial energy homeostasis (*SULT1A1, IP6K3, CPT1A*) (Dato et al., 2021; Sidharthan et al., 2013; Trabjerg et al., 2021), and neurovascular unit dysfunction (*AQP1, APLNR, CA12, AGPT1, CST3*) (Benndorf, 2018; Bonomini & Rezzani, 2010; Hosford et al., 2022; Hu et al., 2021; Siddiqui et al., 2015). Further investigations of these genes are needed to determine if they are the drivers of alterations in these pathways in ALS.

Despite the agreement in gene expression profiles, there was discrepancy between the number of differentially expressed genes; 2,290 and 402 in KCL BrainBank and TargetALS respectively. Moreover, synapse-related processes, such as GABAergic neurotransmission, calcium-mediated signalling and postsynaptic signalling were significantly enriched in KCL BrainBank, whilst TargetALS carried an immune-system related signature, with strong enrichments for interferon signalling and a related enrichment for natural killer cell neurotoxicity. While these enrichment profiles do reflect previously hypothesised mechanisms of ALS pathogenesis and so could be a product of the molecular heterogeneity which exists within each dataset, the inconsistency in pathway enrichment is most likely due to the fact that there were 5.7 times more differentially expressed genes found in the KCL BrainBank cohort. Although this might be linked to the larger number of controls in the KCL datasets (~3 times more than in TargetALS), there could also be several external factors influencing these datasets, such as the methods of library preparation and RNA extraction, and populational variability in gene expression. Another important aspect which may have affected the lack of reproducibility of results were the demographic differences that existed between cases and controls across datasets. For example, there was a strong gender effect in the TargetALS cohort (Figure 3-1B) which we cannot be certain was removed with the generation of surrogate variables. Furthermore, whilst the ages of the cases in both datasets were similar, and the ages of TargetALS control samples were not statistically different to cases, the KCL BrainBank controls were 11.4 years older than cases, and 13.6 years older than the TargetALS controls. This could explain why there was a significantly lower proportion of neurons in KCL BrainBank controls, as you would expect to see this phenomenon as a consequence of aging. Gene expression levels can also be affected by RIN number, which is a measure of RNA sample quality, and post-mortem delay, which is the time from death to sample collection; both measures were significantly different between cases and controls, with lower RIN numbers and a longer post-mortem delay in controls. The average RIN numbers for cases and controls across both datasets were sub-optimal and indicative of moderate RNA degradation, which would affect the measurement of gene expression levels, although controlling for these effects in the differential expression framework can correct almost completely for this. As for the influence of post-mortem delay, longer intervals between death and sample collection could reduce the magnitude of gene expression changes, which could have also contributed to discrepancies in the number of statistically differentially expressed genes between datasets. Our study also has some limitations which are primarily linked to the fact that we identified gene expression signatures in post-mortem tissue. Firstly, as the cells we derive expression for have survived the neurodegenerative processes of ALS, we cannot infer if the changes we are observing are causing or are a consequence of the ALS phenotype. We do not have information on the staging of ALS in these patients so cannot attribute the expression profiles to a certain point of ALS progression.

In summary, we identified shared differentially expressed genes which represent several previously reported biological themes of ALS pathogenesis as well as identifying genes in the neuropeptide signalling pathway that warrant further investigation as potential biomarkers of onset and progression.

Chapter 7. Utilising hierarchical clustering to identify molecular subtypes of ALS

7.1 Publication

The majority of the work described in this chapter was published in *Acta Neuropathologica Communications* (Marriott, Kabiljo, Hunt, et al., 2023):

Unsupervised machine learning identifies distinct ALS molecular subtypes in post-mortem motor cortex and blood expression data

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7.2 Abstract

Background

Amyotrophic lateral sclerosis (ALS) displays considerable clinical and genetic heterogeneity. Machine learning approaches have previously been utilised for patient stratification in ALS as they can disentangle complex disease landscapes. However, lack of independent validation in different populations and tissue samples have greatly limited their use in clinical and research settings.

Methods

Hierarchical clustering was performed on the 5000 most variably expressed autosomal genes from motor cortex expression data of people with sporadic ALS from the KCL BrainBank (N=112). The molecular architectures of each cluster were established from gene enrichment, network and cell composition analysis. Cluster validation was achieved by applying linear discriminant analysis models trained on KCL BrainBank to cases from TargetALS US motor cortex (N=168), as well as Italian (N=15) and Dutch (N=397) blood expression datasets. The ALS and regional specificity of the expression signatures were tested by mapping KCL BrainBank (N=59), TargetALS (N=34) and Dutch (N=645) controls, and occipital cortex (N=45) and cerebellum (N=123) samples from TargetALS to each cluster, before constructing case-control and motor cortex-other region logistic regression classifiers. Cluster stability was assessed in all datasets using bootstrapping to derive uncertainty metrics for class assignment, and dominance analysis was performed in the case datasets to identify genes which drove assignment to one cluster over the others. Cell type composition analysis was performed in KCL BrainBank and TargetALS datasets to aid in the biological interpretation of the clusters. Phenotype analysis was also performed to assess cluster-specific differences in clinical- and omics-based outcomes.

Results

Three clusters were identified: synaptic and neuropeptide signalling, oxidative stress and apoptosis, and neuroinflammation. These molecular phenotypes were validated across both motor cortex and blood independent datasets as samples were assigned to each with a high average assignment probability (80-90%), with these sample assignments being relatively stable. There was also considerable overlap in the top

15 key drivers of cluster assignment in case datasets, further demonstrating the robustness of each molecular phenotype. We found that the expression signatures of each molecular phenotype not only demonstrated were not only able to distinguish people with ALS from controls with good-to-excellent discriminative ability (ROC AUC 0.7-1.0), but also reflect the motor cortex-based disease process, as there was near perfect discrimination between motor cortex and the other brain regions. Analysis of the top 30 case-control status predictors by cluster revealed 19 genes that were shared in at least two datasets, with the schizophrenia-linked gene *CTXN3* present in all. Cell types known to be involved in the biological processes of each molecular phenotype were found in higher proportions, reinforcing their biological interpretation. Phenotype analysis revealed distinct cluster-related outcomes in both motor cortex datasets, relating to disease onset and progression related measures.

Conclusion

Our results support the hypothesis that different mechanisms underpin ALS pathogenesis in subgroups of patients and demonstrates potential for patient stratification and the development of personalised treatment approaches. Further work needs to be carried out to determine with certainty whether expression of specific genes within each molecular phenotype can accurately distinguish between people with ALS and controls. Our method is available for the scientific and clinical community at https://alsgeclustering.er.kcl.ac.uk.

7.3 Introduction

Amyotrophic lateral sclerosis (ALS) is a fatal neurodegenerative disease which displays considerable genetic heterogeneity. In approximately 90% of people with ALS, the disease is labelled as sporadic, without an apparent family history of the disease, with the remainder classed as familial (R. H. Brown & Al-Chalabi, 2017). Mutations in approximately 40 genes are known to be linked with ALS and can explain the majority of familial cases and approximately 20% of sporadic cases (SALS) (Mehta et al., 2022). However, a further 130 genes have been proposed to contribute to its risk or act as disease modifiers (Abel et al., 2012; Mejzini et al., 2019). ALS is also phenotypically variable, with differences in age and site of onset (spinal-innervated muscles vs bulbar), the balance of upper and lower motor neuron involvement, rate of disease progression, and the presence of cognitive or non-motor symptoms (Couratier et al., 2021). Furthermore, a multitude of molecular processes have been implicated in its pathogenesis, in part due to the vast number of causative and modifier genes associated with ALS that code for diverse cellular functions (Morgan & Orrell, 2016). It is therefore plausible that there is no universal approach to the treatment of people with ALS, especially given that many therapeutic strategies target specific molecular pathways. For example, the protective action of Riluzole on motor neurons is proposed to be the result of a reduction in glutamate-mediated excitotoxicity (Doble, 1996).

Machine learning approaches can be used to help us to understand the genetic and molecular complexity and heterogeneity of ALS, for example, by finding patterns in biological and clinical data that distinguish some groups of patients from the others. These subgroups can aid in identifying the best candidates for therapeutics which target specific biological processes. Machine learning methods have previously been applied to brain expression data to stratify people with SALS into molecular subgroups (Aronica et al., 2015; La Cognata et al., 2020; Morello et al., 2017; Tam et al., 2019), and has led to valuable insights into the genomic heterogeneity of ALS. However, some of these studies integrated samples from different brain regions to generate clusters and characterise their molecular architectures (Eshima et al., 2023; La Cognata et al., 2020; Tam et al., 2019). This design might present limitations in reflecting motor neuron-related ALS pathogenesis. Other studies adopted a case-control framework (Aronica et al., 2015; La Cognata et al., 2020; Morello et al., 2017), which could lead to reduced power given the potential decoupling between mechanisms underlying risk and phenotype variability (Kalia et al., 2022; Opie-Martin et al., 2022; van Rheenen et al., 2021). Furthermore, previous work has not been validated in independent datasets or in different populations and did not investigate whether molecular subtypes identified in post-mortem brains are reflected in other tissues available pre-mortem. Such factors have greatly limited the applicability and impact of these results. We therefore aimed to identify and validate molecular and phenotypic patterns across multiple independent datasets, tissue types and populations, to generate gene expression derived molecular subtypes of ALS that can be utilised for stratification in the design and interpretation of future research and clinical studies.

7.4 Methods

7.4.1 Study Cohorts

We obtained raw post-mortem motor cortex bulk RNA sequencing data in FASTQ format from two datasets. The first, which was used to generate the clusters, consisted of 112 people from the UK with SALS from King’s College London and the MRC London Neurodegenerative Diseases Brain Bank (KCL BrainBank), which has been previously described in (Iacoangeli et al., 2021). We additionally obtained matching whole-genome sequencing (WGS), methylation data and clinical data for the KCL BrainBank samples from Project MinE (Project MinE ALS Sequencing Consortium, 2018) to perform subgroup clinical and omics-based phenotype analysis. Additional information for WGS is available in Chapters 3.1.1 and 3.1.1.3, with the methylation protocol available in Chapter 3.5.2. For validation of KCL BrainBank-derived cluster expression signatures, 168 US samples from 93 people with SALS of North European ancestry, present in the Target ALS Human Post-mortem Tissue Core (TargetALS) were used. For further validation of KCL BrainBank-derived clusters, we also processed two peripheral blood mononuclear cell (PBMC) datasets; bulk RNA sequencing data in FASTQ format of 15 Italian people with SALS (Zucca) (Zucca et al., 2019), and hg18-aligned log2 transformed and quantile normalised microarray gene probe intensities of 397 Dutch people with ALS (van Rheenen) (van Rheenen et al., 2018). Accession numbers of these datasets are available in Chapter 3.5.1. To determine if the clusters could discriminate between ALS cases and controls, we also used RNA sequencing data in FASTQ format from 59 individuals from the KCL

BrainBank, and 34 samples from 19 individuals in TargetALS, as well as microarray data from 645 individuals from the van Rheenen study. We also obtained raw transcript counts for two additional TargetALS case datasets to determine if the expression signatures reflected a motor cortex-specific disease process, which included 45 samples from the occipital cortex, and 128 samples from 123 individuals from the cerebellum. The sequencing specific methods are described in more detail in Chapter 3.1.2.1. The basic demographics of each of the datasets used in this study are detailed in Table A29. We did not randomise the samples or conduct power analysis to estimate the appropriate sample size, as all available samples were used, nor were experimenters blinded to group assignment and outcome assessment.

7.4.2 Bulk RNA Sequencing Data Processing

The processing pipeline to convert paired FASTQ files from KCL BrainBank, TargetALS and Zucca datasets into raw transcript count matrices is described in Chapter 3.1.3. For the TargetALS occipital cortex and cerebellum datasets, transcripts were quantified with Salmon (Patro et al., 2017) before being converted into gene-specific expression counts with tximport (Soneson et al., 2015). For all datasets, raw counts were normalised using the *estimateSizeFactors* function of DESeq2, before lowly expressed genes and non-autosomal chromosomes were removed. Expression values were then standardized using the variance stabilising transformation *(vsd)* function in DESeq2 (Love et al., 2014).

7.4.3 Hierarchical Clustering of KCL BrainBank Samples

Our hierarchical clustering was based on a protocol that was previously used to identify cortical molecular phenotypes of ALS (Tam et al., 2019). Briefly, the 5000 most variably expressed genes, selected based on the highest median absolute deviation values, were extracted from the KCL BrainBank gene expression matrix. Unsupervised hierarchical clustering was then performed with the non-smooth negative factorisation (nsNMF) algorithm, using helper functions outlined in the SAKE package (Ho et al., 2018). The optimal number of clusters was identified by running nsNMF with 100 runs and 1000 iterations for different values of k (two to ten). Cluster estimation results are available in Figure A12. We then ran the nsNMF algorithm with k = three, 100 runs and 1000 iterations, with the resulting consensus matrix showing a clear separation of samples (Figure A13). Informative gene and sample assignment for each of the three clusters was then extracted. The list of informative genes for each cluster was then used to characterise their molecular phenotypes by performing gene enrichment analysis using the GProfiler2 R package (Kolberg et al., 2020). Genes from the whole KCL expression matrix were used as a custom gene background. The default g:SCS algorithm was used to assess significant enrichment for several process and pathway categories in the following databases: Gene Ontology (Biological Process (GO:BP), Molecular Function (GO:MF) and Cellular Component (GO:CC)), Kyoto Encyclopaedia of Genes and Genomes (KEGG), Reactome, CORUM, TRANSFAC, and miRTarBase. Additionally, MetaCore^{TM} (available at https://portal.genego.com) was used to construct cluster-specific gene pathway networks using the *'analyze network'* algorithm under default options, with the network that displayed the highest significance selected as the one that most defines the cluster.

7.4.4 Validation of KCL BrainBank-derived clusters

To determine if the informative genes which defined each cluster could be used to successfully stratify samples in other ALS datasets, we applied linear discriminant analysis (LDA) models to the TargetALS, Zucca, and van Rheenen ALS datasets, using the MASS R package (Venables & Ripley, 2002). Each dataset-specific model was trained using the intersection of dataset-specific and informative cluster genes, which yielded 470, 381, and 535 genes for TargetALS, Zucca and van Rheenen, respectively. The linear discriminants were derived from the KCL BrainBank gene and sample cluster assignments. The same approach was carried out for KCL BrainBank (787 genes), TargetALS (787 genes) and van Rheenen (535 genes) controls, as well as the occipital cortex and cerebellum of people with ALS from TargetALS, with 651 and 622 genes shared between each respective dataset and KCL BrainBank cases. Classification probability was evaluated based on the average dataset-specific posterior probabilities of cluster assignment. Cluster stability was then assessed using bootstrapping, implemented in the resample function of the scikit-learn package (Pedregosa et al., 2011). Resampling with replacement was performed with 1000 iterations. For each iteration, the median and 95% confidence intervals for accuracy and silhouette of the cluster assignment was collected, before being averaged to form the final estimate.

As linear discriminant analysis is constrained to assign every sample to one class, we performed additional analyses to confirm that controls and post-mortem expression data from different brain regions assigned to each molecular phenotype could be distinguished from cases. To determine the specificity of the cluster one signature for ALS in the KCL BrainBank dataset, we performed case-control differential expression analysis of the 131 genes which constituted its signature using DESeq2 (Love et al., 2014), applying the same standardisation and normalisation procedure that was used to pre-process the expression data for hierarchical clustering. Differentially expressed genes were identified via the independent hypothesis weighting multiple testing approach using Benjamini-Hochberg adjustment, with p-value < 0.050 denoting significance. For the KCL BrainBank cluster 1 case-control dataset, the TargetALS and van Rheenen case-control datasets and TargetALS motor-occipital and motor-cerebellum case datasets for all clusters, we bult logistic regression classifiers with ten-fold cross validation using the scikit-learn and imblearn Python libraries (Lemaître et al., 2017; Pedregosa et al., 2011), to ascertain the discriminative ability of each cluster-specific gene signature. Three scenarios were employed: 1) using all of the cluster-specific genes present in each dataset, 2) removing multicollinear features using the SelectNonCollinear function of the collinearity package with a correlation threshold of 0.4 and ANOVA F-value as the scoring parameter (Malato, n.d.), and 3) extracting the uncorrelated features present in all folds to subset the cluster-specific signatures before retraining the model. For all scenarios, the data was firstly normalised by removing the mean and scaling to unit variance using StandardScaler before oversampling was performed to address potential class imbalance using the synthetic-minority oversampling technique (SMOTE) function of *imblearn*. For each scenario, the best hyperparameters were selected using GridSearchCV with ROC_AUC as the scoring parameter, before the model was evaluated using the average ROC_AUC, precision, recall, and F1-score over all folds. Both hyperparameter tuning and cross-validation was performed using StratifiedKFold with ten splits and shuffling of the samples within each cluster.

We also performed two additional analyses to determine the robustness of our discovery and validation methods. The first analysis involved performing hierarchical clustering on the top 5000 variably expressed genes in TargetALS motor cortex samples to obtain informative-gene based cluster assignments in the same way as described for KCL BrainBank. By doing this, TargetALS was the discovery dataset, whilst KCL BrainBank served as the replication dataset. We then analysed the overlap between the original assignments and new assignments to gather the natural grouping of samples. To support the discriminative performance of the KCL BrainBank classifier, we constructed ten additional logistic regression classifier models with 10-fold cross validation using the cases and controls assigned to cluster 1. Each classifier was supplied with 131 randomly sampled genes from the transformed expression matrix. The resulting performance metrics over all ten classifiers were averaged to form the final estimate before the performance was compared to the cluster 1 expression signature specific classifier.

7.4.5 Interpretation of Predictor Genes

The top predictors explained by each of the case-control classifier models for scenarios one and two in each cluster were obtained via calculation of SHapley Additive exPlanations (SHAP) values using the SHAP python package (v0.41.0; (Lundberg & Lee, 2017)), with the final values representing averaged SHAP values over all of the ten folds. These values were calculated using the model-agnostic permutation-based explainer approach.

To obtain the genes which favour assignment of cases into one cluster over the others, we performed dominance analysis using the dominance-analysis Python package (v1.1.9; (Luo & Azen, 2013)) for the KCL BrainBank, TargetALS and van Rheenen datasets. The expression data was normalised between 0 and 1 using the MinMaxScaler scikit-learn function before executing the analysis, where a one vs rest approach was adopted i.e., cluster one vs clusters two and three. The top 15 predictors were selected for each one vs rest scenario for each cluster. For the Zucca dataset, we chose to use permutation importance to obtain the top predictors as dominance analysis cannot be used if only one case is assigned to a cluster.

7.4.6 Cell Type Deconvolution Analysis of Motor Cortex Case Datasets

To assess whether the molecular phenotypes we identified in bulk RNAseq data could also be reflective of cell composition, we used the MuSiC R package (v1.0.0; (X. Wang et al., 2019)) to derive cell proportions in the KCL BrainBank and TargetALS case datasets for the following cell types: astrocytes, endothelial cells, microglia, neurons, and oligodendrocytes. We performed deconvolution with the raw RNAseq counts. The single-cell RNAseq reference dataset which was used to derive expression information for each cell type consisted of 8 adults and 4 embryonic samples (16-18 weeks gestational age) from the temporal lobe (Darmanis et al., 2015), which was downloaded via the scRNAseq R package (v2.14.0; (Risso D, Cole M, 2023)). Differences in composition between clusters in each dataset were assessed using one-way ANCOVA corrected for sex assigned at birth and age of death, with post-hoc Tukey's test used to determine subcluster-specific trends. The normality of each variable for each dataset was assessed using the Shapiro-Wilk test, with any variables that were non-normally distributed (p-value < 0.050) being log-transformed before analysis.

7.4.7 Subgroup Phenotype Analysis

To reveal and compare the phenotypic architecture of each cluster, we extracted several clinical and omics variables from each case-specific dataset. We performed the chi-square test of independence to assess if there were differences in the proportion of *C9orf72*-positive, limb-onset, bulbar-onset, and combined limb and bulbar onset cases between each of the clusters in the KCL BrainBank and TargetALS datasets, the limb: bulbar ratio in the van Rheenen datasets, and the male:female ratio in all four case-only datasets. A p-value < 0.05 denotes significance. Due to variations in the phenotypic information collected and accessibility of other omics data, we could not extract some phenotypic variables for all datasets. A breakdown of the collected phenotypic variables for each dataset is available in Table A30. Transcriptional age acceleration was calculated by using RNAAgeCalc to obtain tissue-specific transcriptional age estimates for each dataset (Ren & Kuan, 2020), before being subtracted from the chronological age (age at death for KCL BrainBank and TargetALS, age at last blood draw for Zucca and van Rheenen). Telomere length and mitochondrial DNA copy number were obtained by applying TelSeq v0.0.2 (Ding et al., 2014) and fastMitoCalc v1.2 (Qian et al., 2017) to the whole-genome sequencing BAM files, respectively. Biological age was estimated from the methylation beta-value matrix using CorticalClock (Shireby et al., 2020), before acceleration was calculated by subtracting each value from the age at death. Differences between clusters were assessed using one-way ANCOVA corrected for sex assigned at birth, with post-hoc Tukey's test used to determine subcluster-specific trends. The normality of each variable for each dataset was assessed using the Shapiro-Wilk test, with any variables that were non-normally distributed (p-value < 0.050) being log-transformed before analysis. Additionally, we applied a Cox proportional-hazards model to assess differences in age of onset among clusters by combining samples from both KCL BrainBank and TargetALS datasets, with which p-value < 0.050 denotes significance.

7.4.8 Code Availability

The implementation of our class assignment model based on the KCL BrainBank data, can be used to assign class membership to new expression samples (both microarray and RNAseq) and is publicly available at https://alsgeclustering.er.kcl.ac.uk. The code for the analyses performed in this study is available at https://github.com/KHP-Informatics/HierarchicalClusteringALS/.

7.5 Results

The nsNMF algorithm identified 794 of the 5000 most variably expressed genes as being the most informative for defining the clusters. Each informative gene was uniquely assigned to one cluster, yielding three distinct clusters, each with a unique gene expression profile. There were 131, 291, and 372 genes which defined clusters one, two, and three, respectively (Figure 7-1A). The full list of genes which comprise each cluster are available in Table A31. The larger proportion of people with ALS (60; 53.6%) were assigned to cluster one, followed by cluster two (28; 25%) and cluster three (24; 21.4%), without substantial differences in male:female ratio in each cluster, based on sex assigned at birth (Figure 7-1B) or the proportion of males and females assigned to the clusters (X^2 = 0.43, p-value = 0.81). Almost all *C9orf72* positive cases (7; 87.5%) were assigned to cluster one (Table 7-1), with no significant difference in the proportion of these cases between clusters (X^2 = 4.24, p-value = 0.12).

Four known ALS-associated genes (*HSPB1, CAV1, CX3CR1, RNASE2*) were among the informative genes selected for the cluster signatures, with all four demonstrating significant differences in their average expression values between clusters when performing one-way ANCOVA corrected for sex assigned at birth, age at death and post-mortem delay (Figures A14A-D). When performing post-hoc analysis to assess which clusters show differential expression, only *CX3CR1*, which was assigned to cluster three, was significantly upregulated compared to cluster one (Tukey p-value = 1.2E-05) and cluster two (Tukey p-value = 7.2E-05) without difference in expression between clusters one and two (Figure A14C). The other gene's cluster assignments did not have a complete influence on their expression in cases assigned to the gene's cluster, although for the cluster three informative gene *RNASE2*, there was a trend for higher expression in cases assigned to that cluster compared to the others (Figure A14D). The full statistical results are available in Figure A14E.

7.5.1 Each cluster represents a molecularly distinct phenotype enriched for genes and pathways previously linked to ALS pathogenesis

Characterising the molecular architectures of each cluster by using gene enrichment and gene network analyses, we found that each cluster represents a distinct molecular phenotype, with genes and pathways that have been previously linked to ALS pathogenesis. Cluster one was significantly enriched for various neuronal and synaptic signalling-related processes such as neuropeptide activity, cAMP signalling, and neuroactive ligand transcription, binding, and receptor interaction (Figure 7-2A, Table A32). Network analysis revealed that a mitochondria specific signalling network is also present (Figure 7-2B). Led by *NXPH2*, *ATP12A*, *PTPRV*, *SV2C* and *C18orf42*, this network is enriched for mitochondrial ATP synthesis coupled electron transport and the aerobic electron transport chain.

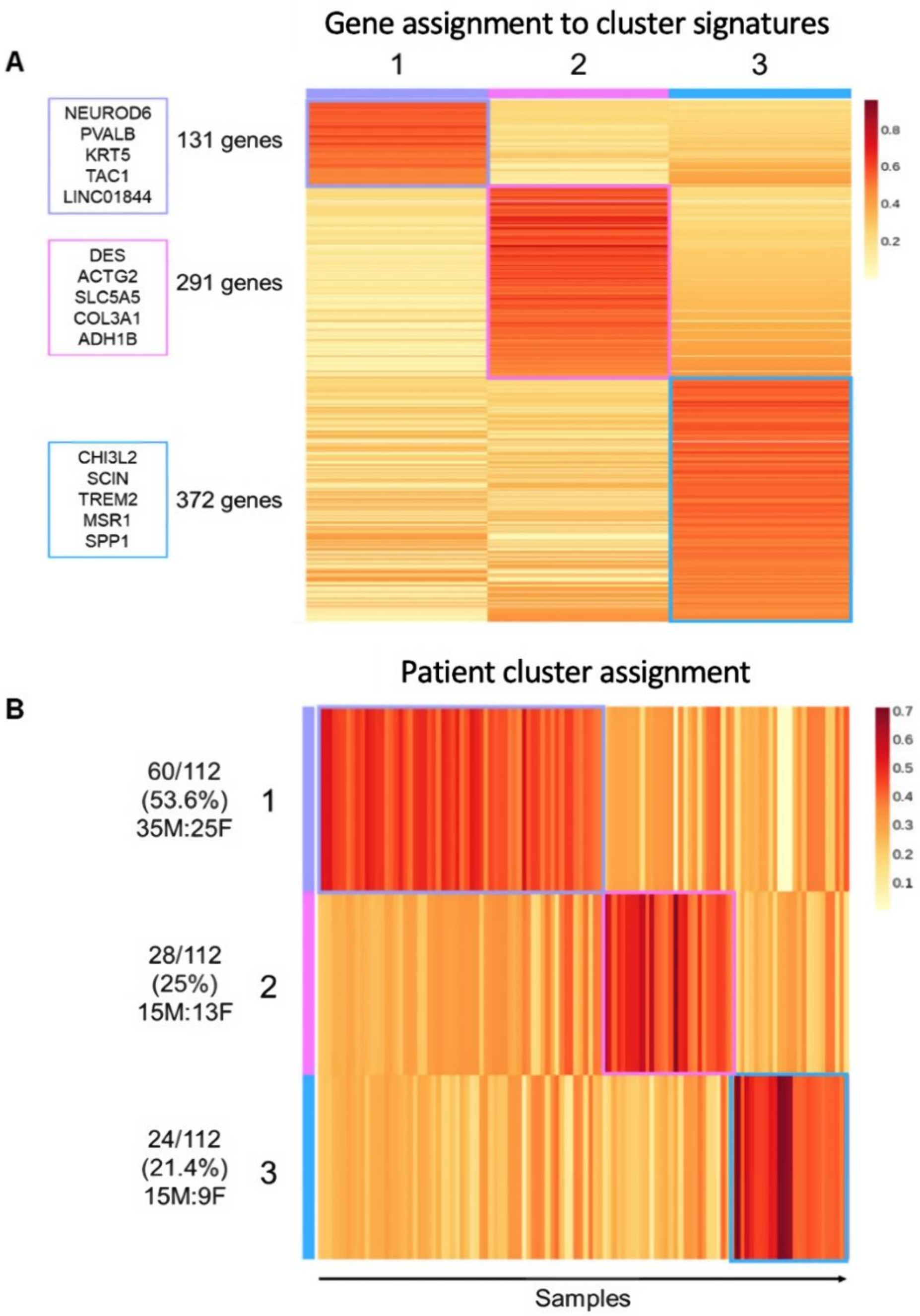


Figure 7-1. Informative gene and sample assignment for KCL BrainBank-generated clusters. A) Number of the 794 informative genes uniquely assigned to each cluster, with the top five contributing genes (defined by posterior probability) listed at the side. B) Distribution of cluster assignment of people with SALS alongside the male:female ratio, based on sex assigned at birth. The coloured scale refers to the posterior probability value.

	KCL BrainBank (motor cortex)			**TargetALS (motor cortex)**			**Zucca (blood)**			**van Rheenen (blood)**		
	1	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**
Number of Samples (%)	60 (53.57)	28 (25.00)	24 (21.43)	97 (57.7)	28 (16.6)	43 (25.6)	13 (86.70)	1 (6.65)	1 (6.65)	335 (84.4)	33 (8.31)	29 (7.31)
Number of Samples with a posterior probability ≥ 80% (%)	NA	NA	NA	88 (90.7)	22 (78.6)	31 (72.1)	9 (69.2)	1 (100)	0 (0)	275 (82.1)	31 (93.9)	11 (37.9)
N Males: N Females (Ratio)	35:25 (1.4)	15:13 (1.15)	15:9 (1.67)	60:37 (1.62)	18:10 (1.80)	21:22 (0.95)	6:7 (0.86)	0:1 (0)	1:0 (0)	205:130 (1.58)	18:15 (1.20)	16:13 (1.23)
C9 positive individuals (N)	7	1	0	11	0	4	NA	NA	NA	NA	NA	NA
Age at Symptom Onset in Years (mean ± SD)	58.8 ± 11.6	65.7 ± 12.3	61.7 ± 15.7	59.6 ± 11.1	64.9 ± 9.52	60.3 ± 11.5	63.6 ± 8.6	67.0 ± 0.0	65.0 ± 0.0	62.7 ± 11.9	57.9 ± 12.0	60.9 ± 12.3
Age at Blood Draw in Years (mean ± SD)	NA	NA	NA	NA	NA	NA	66.1 ± 9.8	69.0 ± 0.0	68.0 ± 0.0	NA	NA	NA
Age At Death in Years (mean ± SD)	62.5 ± 11.4	70.2 ± 11.4	64.2 ± 15.6	63.2 ± 10.2	69.5 ± 9.0	64.5 ± 8.9	NA	NA	NA	NA	NA	NA
Limb Onset (N)	36	10	17	65	22	17	NA	NA	NA	215	21	15
Bulbar Onset (N)	15	7	5	14	5	21	NA	NA	NA	120	12	14
Limb + Bulbar Onset (N)	1	1	0	7	0	1	NA	NA	NA	NA	NA	NA
Diagnostic Delay in Years (mean ± SD)	0.0015 ± 0.0013	0.00047 ± 0.00085	0.001 ± 0.0012	0.025 ± 0.32	0.073 ± 0.59	0.12 ± 0.35	NA	NA	NA	NA	NA	NA

Disease Duration in Years (median (IQR))	3.16 (1.96)	2.30 (1.81)	2.38 (1.75)	3.00 (2.13)	4.00 (3.48)	2.00 (2.00)	NA	NA	NA	2.41 (2.02)	2.47 (1.14)	2.37 (1.53)
Post-mortem Delay in Hours (mean ± SD)	26.1 ± 12.10	26.0 ± 10.70	25.9 ± 13.90	9.9 ± 6.10	10.0 ± 7.45	12.0 ± 8.26	NA	NA	NA	NA	NA	NA
Mitochondrial DNA Copy Number (mean ± SD)	465 ± 22.0	457 ± 22.4	459 ± 17.3	NA	NA	NA	NA	NA	NA	NA	NA	NA
Telomere Length in Kilobytes (mean ± SD)	4.04 ± 0.46	3.98 ± 0.56	3.77 ± 0.42	NA	NA	NA	NA	NA	NA	NA	NA	NA
Transcriptional Age Acceleration in Years (mean ± SD)	6.16 ± 9.24	0.45 ± 10.90	5.59 ± 10.80	10.50 ± 8.63	4.19 ± 8.08	8.54 ± 8.44	-23.50 ± 9.90	-28.60 ± 0.00	-26.93 ± 0.00	-41.21 ± 11.66	-36.68 ± 11.84	-38.62 ± 11.69
Biological Age Acceleration in Years (mean ± SD)	5.99 ± 2.92	4.06 ± 4.65	7.93 ± 4.67	NA	NA	NA	NA	NA	NA	NA	NA	NA

Table 7-1. Demographics and omics-based/clinical phenotypes for the samples assigned to each cluster, for each dataset. NA represents values that could not be collected due to omics and clinical data availability.

Cluster two was strongly linked with oxidative stress, apoptotic signalling, and vasculature related processes including angiogenesis, blood vessel development, epithelial cell differentiation and atherosclerosis (Figure 7-3A). Moreover, muscle-system and extracellular-matrix (ECM) specific enrichments (e.g., collagen synthesis and degradation, smooth muscle contraction, ECM proteoglycans and degradation), and anti-inflammatory pathways (interleukin-4 and interleukin-13 signalling, neutrophil degranulation) from Reactome were also associated with this cluster (Figure 7-3A). The muscle contraction theme was strengthened with GO:CC enrichments for banded collagen fibril, supramolecular fiber, myofibril, Z disc, I band, sarcomere, and the actin cytoskeleton (Table A33). Cluster two was also enriched for the ALS-gene related NOS3-CAV1 CORUM complex (p=0.018). Furthermore, the cluster two network (Figure 7-4B), which was driven by *MFAP4*, *FPRL1*, *TUSC5*, *MRGPRF*, and *PLAUR*, was associated with muscle contraction and actin-myosin filament sliding as well as phospholipase C-activating G protein coupled signalling. Cluster three represents an inflammatory phenotype, with biological process enrichment strongly associated with immune response in GO:BP and KEGG (Table A34), as well as links with adaptive immunity, complement cascade, and interferon gamma signalling in Reactome and immunoglobulin activity and major histocompatibility complex (MHC) class II in GO:MF (Figure 7-4A). Furthermore, C1q and TLR1-TLR2 CORUM complexes and viral diseases present in KEGG, such as Epstein-Barr disease, herpes simplex virus 1, and influenza A were among the most significant enrichments. Nine microRNAs were also significantly enriched in cluster two (including hsa-miR-335-5p, hsa-miR-146a-5p, hsa-mIR-124-3p, hsa-miR-29a-3p, and hsa-miR-204-5p), with hsa-miR-335-5p also being enriched in cluster three (Tables A33 and A34). The cluster three network (Figure 7-4B), defined by *GNLY*, *HSPA7*, *SLAMF8*, *CLEC17A,* and *Sgo1*, is MHC-class II specific and enriched for antigen processing, peptide antigen assembly, and presentation of peptides and polysaccharide antigens. Furthermore, the centre of the network, *GATA-2*, was the most significantly enriched TRANSFAC element in cluster three (*GATAD2A*, p=9.56E-17, Table A34).

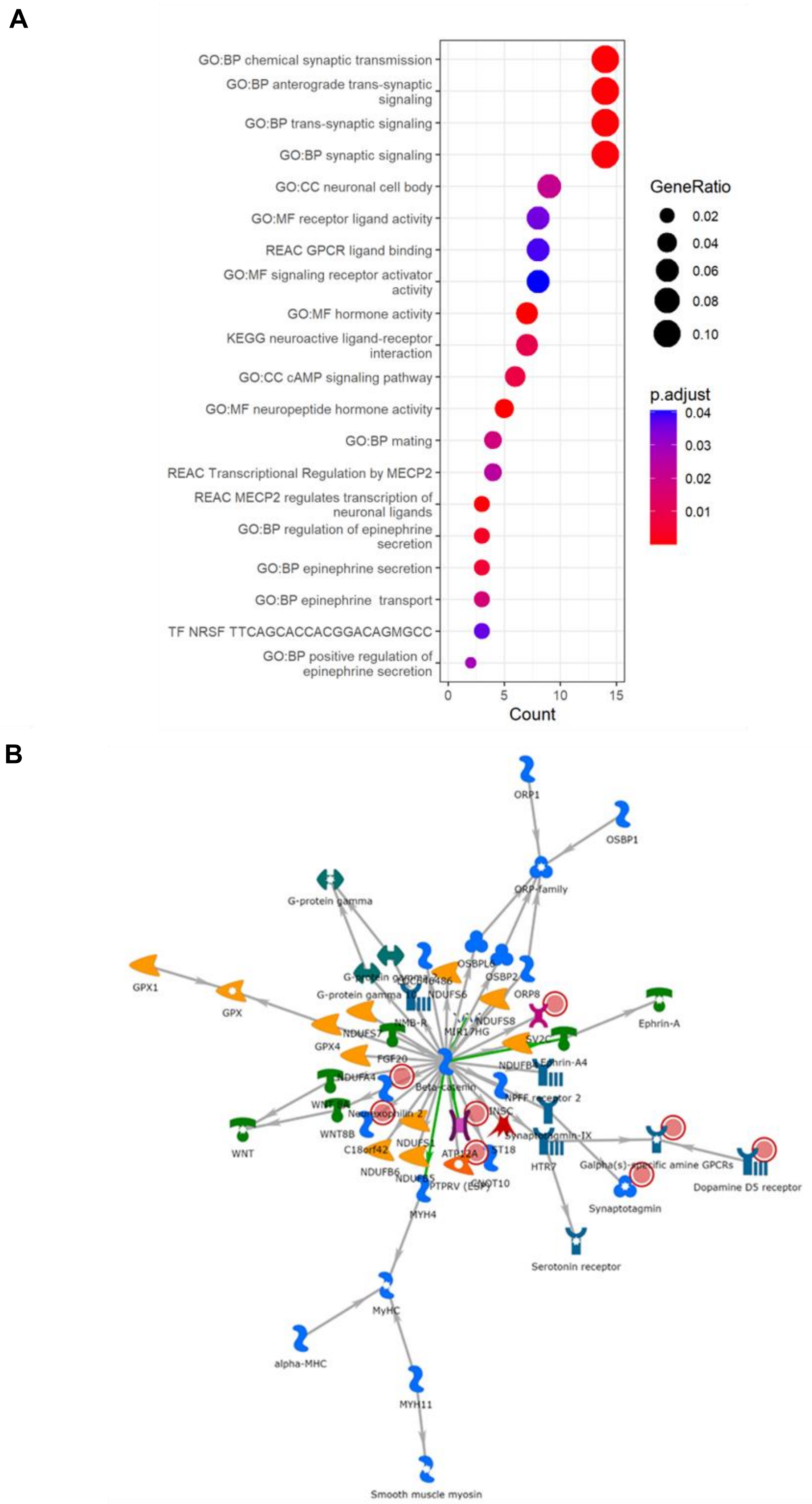


Figure 7-2. Results of gene enrichment and network analyses for Cluster 1. A) GProfiler2 reveals enrichment for various synaptic and neuropeptide signalling related processes. B) The most significant sub-cluster reveals a mitochondrial-specific and neuronal signalling network. Red circles present in each network represent informative genes identified in each cluster. The descriptions of what each symbol represents is available in Figure A11.

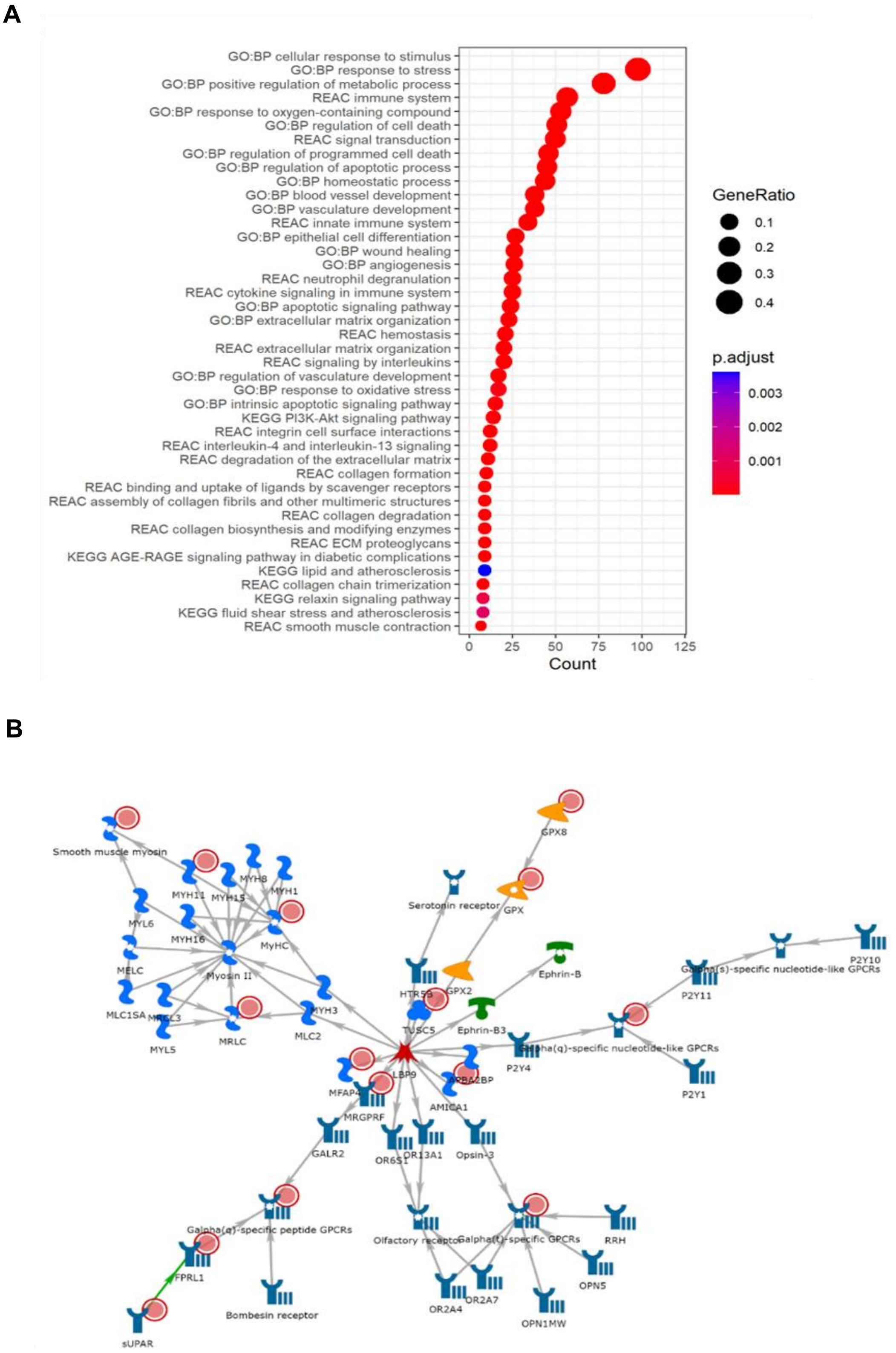


Figure 7-3. Results of gene enrichment and network analyses for Cluster 2. A) GProfiler2 reveals enrichment for oxidative stress, apoptosis, anti-inflammatory and muscle system-related processes. B) The most significant sub-cluster strengthens the support for muscle contraction processes defining the core of the cluster. Red circles present in each network represent informative genes identified in each cluster. The descriptions of what each symbol represents is available in Figure A11.

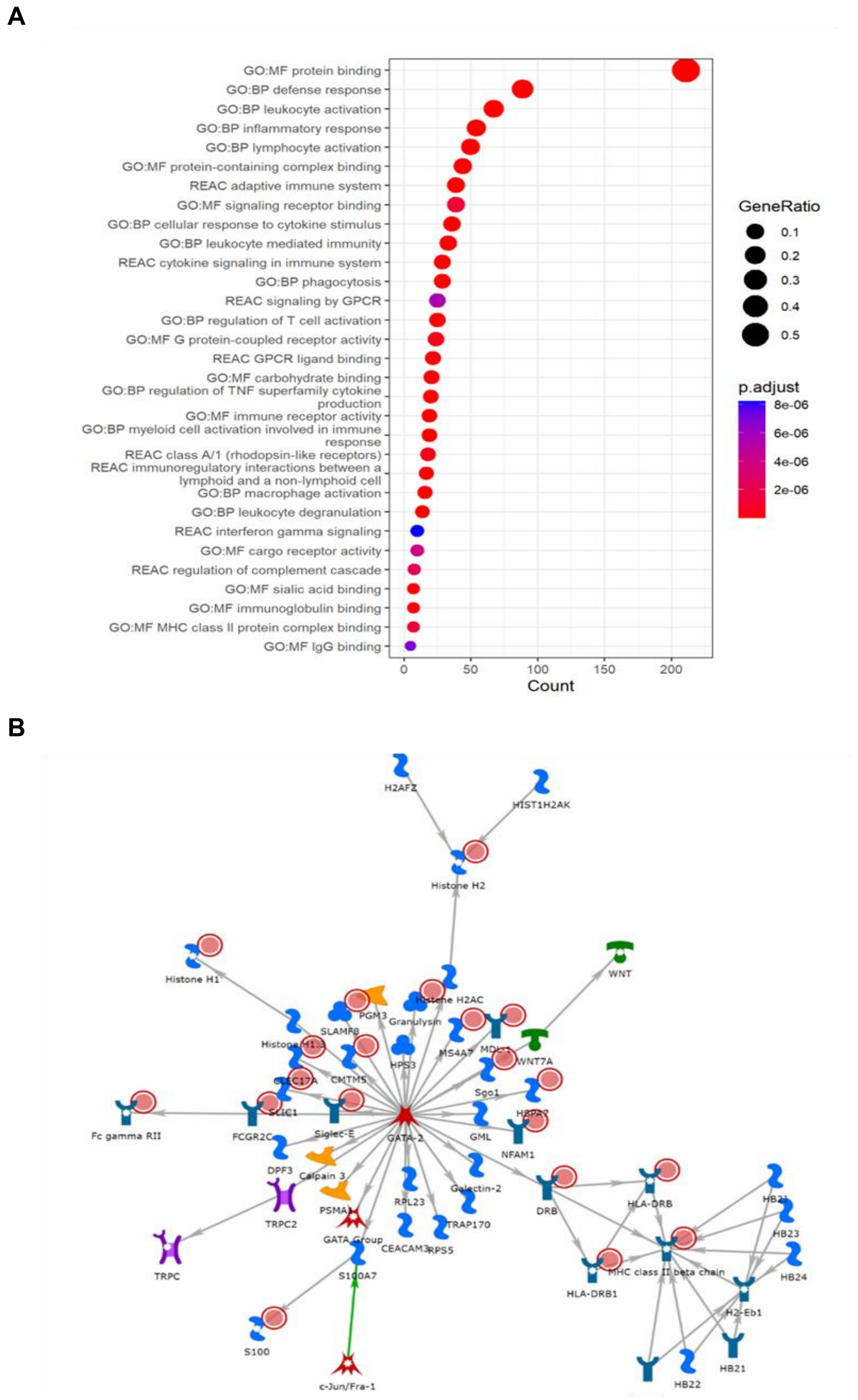


Figure 7-4. Results of gene enrichment and network analyses for Cluster 3. A) GProfiler2 reveals enrichment for pro-inflammatory processes. B) The most significant sub-cluster reinforces the link to inflammation with the identification of an MHC Class 2 specific network. Red circles present in each network represent informative genes identified in each cluster. The descriptions of what each symbol represents is available in Figure A11.

7.5.2 The molecular phenotypes are robust and validated in independent brain and blood datasets

To validate the KCL BrainBank derived clusters, we performed linear discriminant-driven cluster assignments of the TargetALS, Zucca and van Rheenen samples, using the intersection between the genes expressed in each one of them and the 794 genes that were used to define the clusters in the KCL BrainBank. Samples from each dataset were assigned to one of the three clusters with high certainty (between 80-90%) based on average posterior probability (diagonal cells in Figures 7-5A, B and C). A breakdown of the sample to cluster composition for all case datasets is available in Table 7-1. For the Zucca dataset, the posterior probability of belonging to cluster three is marginally higher than cluster 2 as only one sample was assigned to it.

To determine whether the molecular phenotypes also withheld validity in control datasets, we applied the same approach to healthy controls from the KCL BrainBank, TargetALS and van Rheenen datasets as well as TargetALS case datasets of the occipital cortex and cerebellum (demographics available in Table A29). We found that all KCL BrainBank controls were assigned to cluster one (Figure 7-5D), whereas for the other control datasets and TargetALS datasets from different tissues, cluster accuracy was not degraded as there were similar average probability estimates for cluster assignment as in the motor cortex case datasets (diagonal cells in Figures 7-5E-H).

The intersection and union of the overall and cluster-specific genes for the case and control motor cortex and blood datasets are represented in Figures A15 (cases) and A16 (controls), with a visual inspection of the sample assignments based on the calculated linear discriminants in all datasets available in Figures A17 (cases) and A18 (controls). The posterior probability of assignment to each of the three clusters for each sample in the case datasets is available in Table A35. Bootstrapping to assess cluster assignment stability for each of the eight datasets revealed that all TargetALS datasets and the Zucca dataset had a 100% median assignment accuracy, with van Rheenen controls having an accuracy of 98.9% (Table 7-2), confirming that these cluster assignments are robust. In contrast, KCL BrainBank controls and van Rheenen cases had a poor-to-average assignment accuracy, therefore their cluster stability was deemed to be unstable.

We also performed a reverse validation of the TargetALS motor cortex case dataset by performing hierarchical clustering in the replication dataset (TargetALS) as initially performed on KCL BrainBank (the discovery dataset). The purpose of this was to assess whether unsupervised clustering in both datasets leads to similar clustering assignments. Three clusters were defined by a total of 238 informative genes, with 47, 42 and 79 samples assigned to three clusters when TargetALS was utilised for the hierarchical clustering. We found that high proportions of samples assigned to these clusters (81.4%, 67% and 71.4% respectively) were the same as when the UK BrainBank was utilised for clustering.

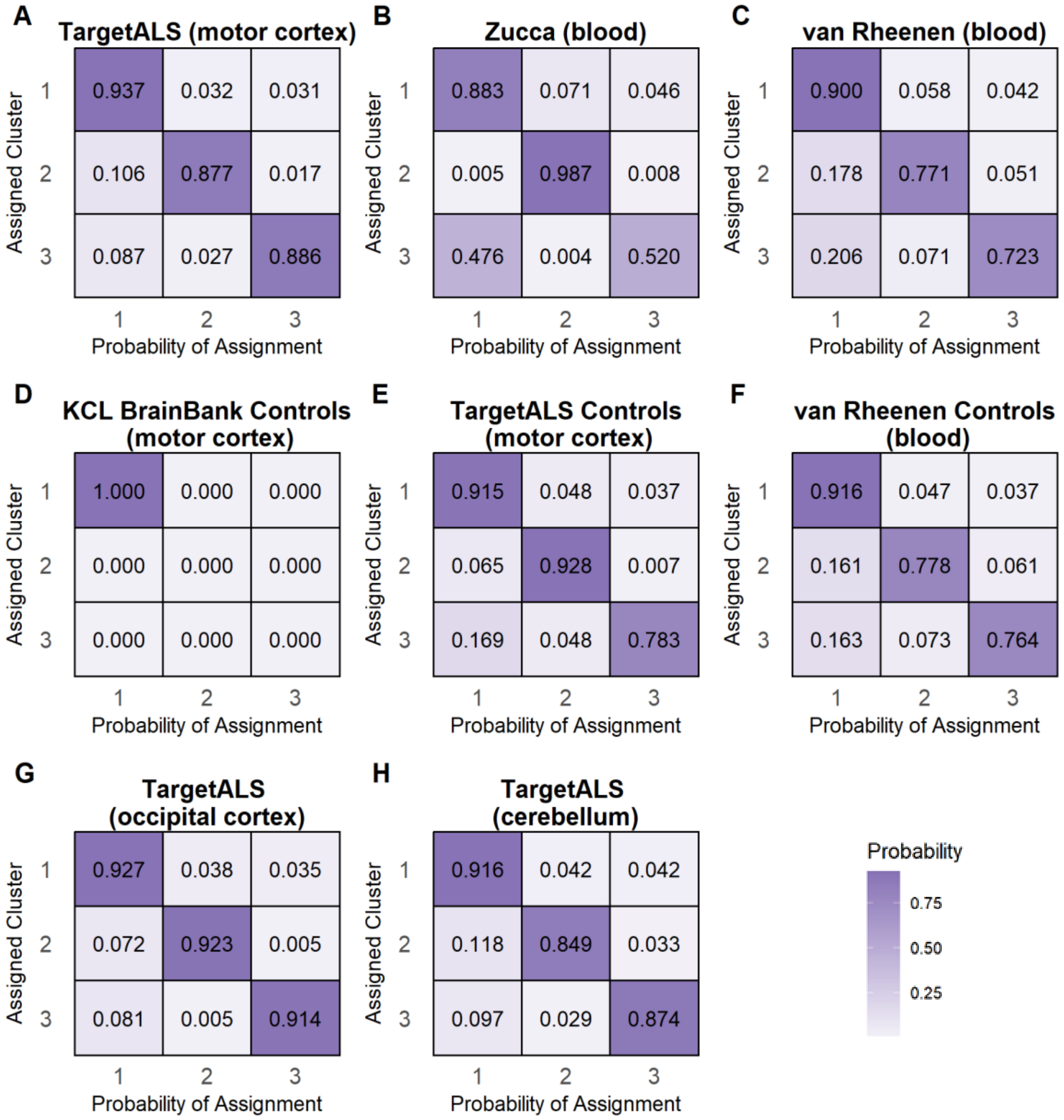


Figure 7-5. Posterior probabilities of cluster assignment for the eight independent expression datasets using linear discriminant analysis trained on the shared informative genes between each dataset and KCL BrainBank. The x-axis represents the average predicted posterior probability of being assigned to one of the three clusters, with the diagonals of the y-axis representing the average posterior probability of being assigned to the correct cluster.

Dataset	**Number of Genes**	**Accuracy**	**Silhouette**
TargetALS	470	1.000 (1.000-1.000)	0.137 (0.109-0.168)
Zucca	381	1.000 (1.000-1.000)	0.127 (0.0560-0.234)
Van Rheenen	535	0.738 (0.693, 0.778)	0.0185 (-0.0145, 0.0512)
BrainBank Controls	787	0.661 (0.543-0.780)	0.220 (0.167-0.281)
TargetALS Controls	787	1.000 (1.000-1.000)	0.210 (0.131-0.305)
Van Rheenen Controls	535	0.989 (0.981-0.997)	0.0782 (0.0539-0.103)
TargetALS (occipital cortex)	651	1.000 (1.000-1.000)	0.199 (0.132-0.283)
TargetALS (cerebellum)	622	1.000 (1.000-1.000)	0.174 (0.139-0.217)

Table 7-2. Bootstrapping results for the linear discriminant analysis-derived sample assignments for the eight independent datasets. Bootstrapping was performed with 1000 iterations, with average accuracy of correct class assignment used as the evaluation metric. Average accuracy and silhouette values are reported as median and 95% confidence intervals.

7.5.3 The expression signatures of each molecular phenotype can discriminate between cases and controls and represent specific features of motor cortex gene expression

As all KCL BrainBank controls were assigned to cluster one, and the model is constrained to assign each sample to at least one class, we sought to see if there were differences in the expression of informative genes between cases and controls belonging to cluster one. We found that 87 genes (66.4%) were differentially expressed in cases (Figure A19, Table A36), which supports that this gene-specific expression profile is altered in ALS. We then constructed a logistic regression classification model with ten-fold cross-validation to determine if this expression profile is altered in such a way that it can accurately discriminate between ALS and control status (Figure 7-6A). We supplied the model with three different gene signature scenarios (one: all shared genes in the signature, two: removing multicollinear genes from each fold, three: genes common to all folds after removing multicollinearity). We found that training the models under scenarios one and two achieved excellent discriminative ability (one: ROC AUC 0.88 ± 0.10, two: ROC AUC 0.82 ± 0.11). Notably, scenario one also achieved the highest performance based on all metrics (precision = 0.80 ± 0.13, recall = 0.82 ± 0.19, and F1 = 0.79 ± 0.14). Conversely, the discriminative power under scenario three was poor (ROC AUC 0.61 ± 0.14). The specificity of the cluster one expression signature for ALS was further supported with the finding that the average performance over ten rounds of supplying the classifier with 131 randomly sampled genes for ROC AUC and the other metrics are in line with and below what would be expected by chance, regardless of scenario (Figure 7-6B).

We adopted the same approach with the TargetALS and van Rheenen case-control datasets, and found that regardless of dataset, training the models under scenarios one and two achieved excellent discriminative ability based on ROC AUC score, whereas the discriminative power under scenario three was highly variable (Figure 7-6). For all of the cluster-specific TargetALS models, the average ROC AUC score ranged between 0.93 and 1.00 (Figures 7-6C, D and E), which is the gold standard in research settings. However, in Cluster 3, after removing collinearity (scenario two), the recall and F1 score was relatively poor (recall = 0.55 ± 0.18, F1 = 0.70 ± 0.16), despite the high ROC AUC (0.96 ± 0.063) and precision (1.00 ± 0.00) scores (Figure 7-6E). The performance of the van Rheenen cluster-specific classifiers was quite changeable, with the average ROC AUC score ranging from 0.69 to 1.00 (Figures 7-6F, G and H). For instance, the cluster one classifier (Figure 7-6F) could distinguish perfectly between cases and controls for scenarios one and two, according to ROC AUC score, but this dropped considerably in scenario three (0.69 ± 0.056). The discriminative power of cluster two under scenarios one and two (Figure 7-6G) was worse than cluster three (Figure 7-6H) based on all of the four performance metrics.

We then assessed whether these molecular phenotypes are truly representative of a motor-cortex based disease process by constructing motor cortex-occipital cortex and motor cortex-cerebellum logistic regression classifiers for each cluster and scenario. We found that each molecular phenotype did indeed reflect features of motor cortex gene expression as there was almost perfect discrimination between motor cortex and the other brain regions when supplying all of the cluster-specific informative genes to the model. The full results, including the best hyperparameters and the number of genes supplied to each model, are available in Table A37.

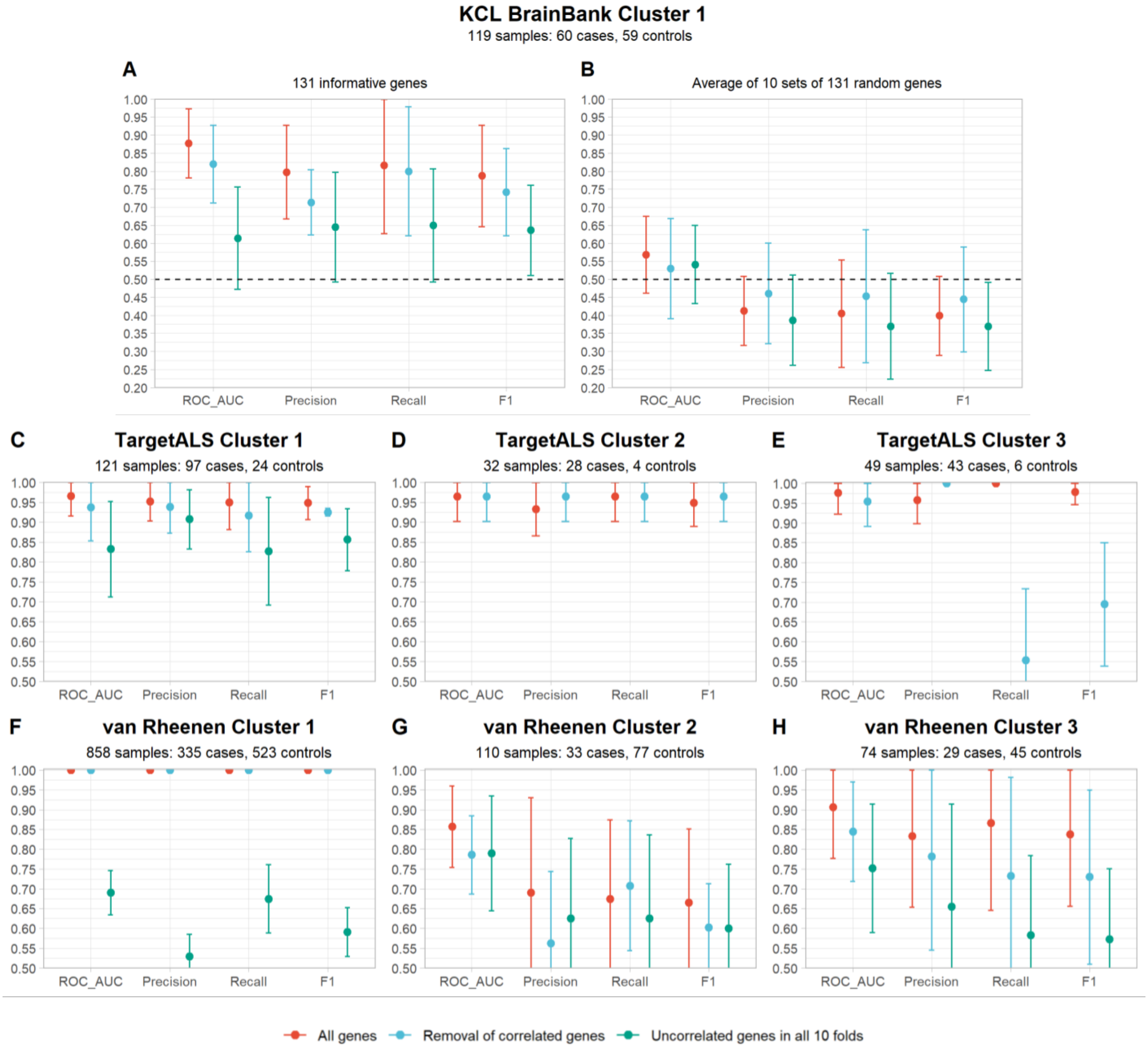


Figure 7-6. Averaged performance metrics over all ten cross-validation folds for each cluster under three scenarios in the three case-control datasets. KCL BrainBank: A) using all 131 informative gene of cluster one, B) random sets of 131 genes from the full expression matrix, TargetALS: Panels C-E, van Rheenen: Panels F-H. The x-axis represents each metric used to assess the discriminative performance of each model, with the average score of the metric represented on the y-axis. Each point represents the mean and the standard deviation. The y-axis starts from 0.5 in Panels C-H as this is the value that you would expect by chance, with the dotted line in Panels A and B representing this also.

7.5.4 There are common top predictor genes of case-control status and key driver genes of cluster assignment in case datasets

To gather the most important predictor genes in each model, SHAP importance analysis was performed, with the top 10 gene-based SHAP values being extracted for further examination and discussion (Table 7-3). The complete SHAP value results are available in Tables A38, A39 and A40 for the KCL BrainBank, TargetALS and van Rheenen datasets, respectively. As expected, when multicollinearity was removed, the relative SHAP importance values were higher as the influence of correlation with another predictor would have been removed, therefore making the importance estimate more accurate.

In the van Rheenen dataset, the 100% accuracy for scenarios 1 and 2 in cluster 1 (Figure 7-6F) is attributed to *NME1,* as its relative importance is 1462 and 1105 times larger than the next important predictor gene in scenarios 1 and 2, respectively, and when removing *NME1* from the scenario 1 model, the discriminative performance drops considerably (ROC AUC 0.69 ± 0.051; Table A37). A similar but diluted effect was also observed for the Thioesterase gene for scenario 1 in cluster 3 with TargetALS (3.25x larger), *VIP* (3.07x larger) and *SLN* (2.61x larger) for scenario 2 in cluster 1 of KCL BrainBank and TargetALS, respectively, and for *ANGPTL4* (2.14x larger) for scenario 2 in cluster 2 of TargetALS (Table 7-3).

Scenario	Cluster	Gene Symbol (or Ensembl ID if no symbol is available)	SHAP Importance	Dataset
1 (All Genes)	1	*VIP*	0.0479	KCL BrainBank
		WIF1	0.0391	KCL BrainBank
		SST	0.0355	KCL BrainBank
		LINC01007	0.0347	KCL BrainBank
		NPY2R	0.0346	KCL BrainBank
		HSD11B1	0.0342	KCL BrainBank
		LOC105374524	0.0334	KCL BrainBank
		SV2C	0.0326	KCL BrainBank
		Antisense to ADTRP	0.0324	KCL BrainBank
		LINC02055	0.0323	KCL BrainBank
		SLN	0.0600	TargetALS
		LINC02192	0.0336	TargetALS
		miR-1255	0.0321	TargetALS
		LINC01107	0.0311	TargetALS
		HSD17B12 Pseudogene	0.0290	TargetALS

		Lnc-DUSP22-2	0.0285	TargetALS
		SNORA74A	0.0251	TargetALS
		KRT17P1	0.0243	TargetALS
		GATD3	0.0230	TargetALS
		FAM8A6P	0.0224	TargetALS
		NME1	0.484	van Rheenen
		GPAT3	0.000331	van Rheenen
		LINC01844	0.000112	van Rheenen
		ADTRP	0.0000820	van Rheenen
		DNAJC22	0.0000340	van Rheenen
		CRH	0.0000190	van Rheenen
		DRD5	0.0000120	van Rheenen
		GATD3	0.0000100	van Rheenen
		CTXN3	0.00000600	van Rheenen
		OSTN	0.00000400	van Rheenen
	2	*HILPDA*	0.0106	TargetALS
		STC1	0.0104	TargetALS
		ANGPTL4	0.00760	TargetALS
		SECTM1	0.00730	TargetALS
		ADM	0.00720	TargetALS
		RRAD	0.00650	TargetALS
		ADAMTS9	0.00630	TargetALS
		FCAR	0.00540	TargetALS
		SAMD11	0.00520	TargetALS
		IGFN1	0.00440	TargetALS
		MIR3667HG	0.0377	van Rheenen
		HSPA1A	0.0332	van Rheenen
		CLEC4E	0.0276	van Rheenen
		ADGRG3	0.0261	van Rheenen
		HSPB7	0.0246	van Rheenen
		VNN2	0.0238	van Rheenen
		THBS1	0.0237	van Rheenen
		COL1A2	0.0230	van Rheenen
		VCAM1	0.0220	van Rheenen
		SOCS3	0.0215	van Rheenen
	3	*Thioesterase*	0.1406	TargetALS
		ITGAL	0.0435	TargetALS
		NAPSB	0.0312	TargetALS
		FCGR1CP	0.0301	TargetALS
		C4A	0.0285	TargetALS
		DHRS9	0.0111	TargetALS
		CLEC7A	0.0108	TargetALS
		POM121L9P	0.00900	TargetALS
		LNCAROD	0.00500	TargetALS
		LINC01299	0.00370	TargetALS
		SLA	0.0323	van Rheenen

		TMEM119	0.0310	van Rheenen
		FGD2	0.0278	van Rheenen
		MAG	0.0266	van Rheenen
		PKD1L2	0.0226	van Rheenen
		GPNMB	0.0222	van Rheenen
		FFAR1	0.0216	van Rheenen
		GPR62	0.0215	van Rheenen
		SLC31A2	0.0200	van Rheenen
		TAS2R39	0.0176	van Rheenen
2 (Removal of Correlated Genes)	1	*VIP*	0.359	KCL BrainBank
		WIF1	0.117	KCL BrainBank
		HSD11B1	0.0436	KCL BrainBank
		ENSG00000254561	0.0377	KCL BrainBank
		CR2	0.0303	KCL BrainBank
		LINC00898	0.0265	KCL BrainBank
		LINC01830	0.0214	KCL BrainBank
		Antisense to ADTRP	0.0131	KCL BrainBank
		CSN1S1	0.00670	KCL BrainBank
		ENSG00000286016	0.00660	KCL BrainBank
		SLN	0.129	TargetALS
		LINC01107	0.0494	TargetALS
		KRT17P1	0.0466	TargetALS
		Lnc-MYB-5	0.0449	TargetALS
		miR-1255	0.0445	TargetALS
		LINC02192	0.0424	TargetALS
		GATD3	0.0346	TargetALS
		Lnc-DUSP22-2	0.0304	TargetALS
		VGF	0.0293	TargetALS
		ATP12A	0.0289	TargetALS
		NME1	0.484	van Rheenen
		GPAT3	0.000488	van Rheenen
		LINC01844	0.0000820	van Rheenen
		ADTRP	0.0000440	van Rheenen
		DNAJC22	0.0000230	van Rheenen
		GATD3	0.0000160	van Rheenen
		CRH	0.0000150	van Rheenen
		CTXN3	0.00000900	van Rheenen
		DRD5	0.00000900	van Rheenen
		OSTN	0.00000600	van Rheenen
	2	*ANGPTL4*	0.116	TargetALS
		ADM	0.0540	TargetALS
		STC1	0.0462	TargetALS
		LINC02080	0.00930	TargetALS
		SNX31	0.00910	TargetALS
		Lnc-KCTD8-1	0.00470	TargetALS
		HGFAC	0.00260	TargetALS

		MUC19	0.000700	TargetALS
		SLC22A8	0.000700	TargetALS
		FOXD2	0.000500	TargetALS
		MIR3667HG	0.0433	van Rheenen
		COL1A2	0.0410	van Rheenen
		SULT1B1	0.0395	van Rheenen
		CLEC4E	0.0349	van Rheenen
		HSPB7	0.0345	van Rheenen
		TENT5C	0.0344	van Rheenen
		HSPA1A	0.0325	van Rheenen
		VCAM1	0.0304	van Rheenen
		ADH1B	0.0287	van Rheenen
		VNN2	0.0281	van Rheenen
	3	*C4A*	0.321	TargetALS
		Thioesterase	0.171	TargetALS
		RASSF9	0.00180	TargetALS
		FGD2	0.0493	van Rheenen
		SLA	0.0472	van Rheenen
		TMEM119	0.0401	van Rheenen
		PKD1L2	0.0325	van Rheenen
		TLR2	0.0311	van Rheenen
		GPR62	0.0285	van Rheenen
		SERPINA5	0.0279	van Rheenen
		RASSF9	0.0277	van Rheenen
		AQP1	0.0272	van Rheenen
		MYO1G	0.0255	van Rheenen

Table 7-3. The top 10 most important predictors for each case-control dataset obtained via calculation of SHAP values, for each cluster-based model under scenarios one and two.

Examination of the top 30 most important predictors of each of the cluster-specific models for each scenario in each dataset revealed 19 genes which were shared in at least 2 of the case-control datasets (Table 7-4). Only one gene which resided in cluster one, *CTXN3*, was important in all three case-control datasets when considering all genes in the signature. Regardless of scenario, a total of 8 genes were shared between KCL BrainBank and TargetALS datasets, with 1 present in KCL BrainBank and van Rheenen and 9 in both TargetALS and van Rheenen.

We then performed dominance analysis for the KCL BrainBank, TargetALS and van Rheenen case datasets, to determine key genes which drove assignment into one particular cluster in a one vs rest strategy. For the three strategies, the top 15 predictors (or fewer if 15 predictors were not available) were extracted from each dataset. For the Zucca dataset, permutation importance was performed (as only one sample was present in clusters two and three), with the top 45 predictors extracted and combined with the results from the dominance analysis before identifying the shared genes. There were a total of 15 genes which were shared key drivers of cluster assignment in at least two datasets (Table 7-5). Interestingly, the drivers of assignment in the cluster two vs others and cluster three vs others strategies are assigned to those clusters, but for cluster one vs others, the driver genes are from clusters two and three. This trend continues when looking at the full dominance analysis results for each dataset, available in Tables A41 (cluster one vs others), A42 (cluster two vs others) and A43 (cluster 3 vs others). This suggests that the cluster one gene signature is not distinct enough in individuals assigned to this cluster: instead, perhaps the divergence in the gene expression profiles of the other clusters is driving their assignment. This is feasible, especially given that the linear discriminant analysis model is constrained to assign samples to one of the three clusters. Regardless, the McFadden's pseudo R-squared of each dataset under each scenario (Tables A41, A42 and A43) ranged from 0.34 to 0.89, which indicates that the top predictors contribute to a good to excellent model fit. The full permutation importance results for the Zucca dataset is available in Table A44.

Scenario	**Cluster**	**Gene Symbol**	**Datasets**
1 (All Genes)	1	*CTXN3*	KCL BrainBank, TargetALS, van Rheenen
		NPY2R	KCL BrainBank, TargetALS
		AKAIN1	KCL BrainBank, TargetALS
		CR2	KCL BrainBank, TargetALS
		DUSP4	KCL BrainBank, TargetALS
		LINC02427	KCL BrainBank, TargetALS
		HSD11B1	KCL BrainBank, van Rheenen
		OSTN	TargetALS, van Rheenen
		CRH	TargetALS, van Rheenen
		GATD3	TargetALS, van Rheenen
	2	*IGFN1*	TargetALS, van Rheenen
		HILPDA/C7orf68	TargetALS, van Rheenen
		PLA1A	TargetALS, van Rheenen
		VNN1	TargetALS, van Rheenen
	3	*TNFSF14*	TargetALS, van Rheenen
2 (Removal of Correlated Genes)	1	*LERFS*	KCL BrainBank, TargetALS
		Antisense to *ADTRP*	KCL BrainBank, TargetALS
		LOC124908056/LINC01830	KCL BrainBank, TargetALS

		DUSP4	KCL BrainBank, TargetALS
		HSD11B1	KCL BrainBank, van Rheenen
		GATD3	TargetALS, van Rheenen
	3	*RASSF9*	TargetALS, van Rheenen

Table 7-4. Shared predictors for each case-control dataset obtained via calculation of SHAP values, for each cluster-based model under scenarios one and two. These were determined based on the top 30 predictors for each dataset.

Scenario (one vs (rest))	**Gene Symbol**	**Cluster**	**Datasets**
Cluster 1 vs (Cluster 2 and Cluster 3)	*CD44*	3	TargetALS, KCL BrainBank
	CP	2	TargetALS, KCL BrainBank
	COL14A1	2	KCL BrainBank, van Rheenen
	LINC01088	2	TargetALS, Zucca
	CPAMD8	2	TargetALS, Zucca
	TNFSF14	3	TargetALS, Zucca
	ADGRE1	3	KCL BrainBank, Zucca
	PDLIM1	2	van Rheenen, Zucca
Cluster 2 vs (Cluster 1 and Cluster 3)	*SLC22A2*	2	TargetALS, KCL BrainBank
	ACTG2	2	TargetALS, KCL BrainBank
	ITGA5	2	KCL BrainBank, van Rheenen
	MYL9	2	KCL BrainBank, van Rheenen
	COL14A1	2	KCL BrainBank, van Rheenen
	IHO1	2	TargetALS, Zucca
Cluster 3 vs (Cluster 1 and Cluster 2)	*HOXD3*	3	KCL BrainBank, van Rheenen
	LRRC63	3	TargetALS, KCL BrainBank
	ADGRE1	3	KCL BrainBank, Zucca
	TNFSF14	3	KCL BrainBank, Zucca
	PDLIM1	2	KCL BrainBank, Zucca

Table 7-5. Shared top predictors of the case datasets with dominance analysis (KCL BrainBank, TargetALS, van Rheenen) and permutation importance (Zucca). For each one vs rest scenario, the gene and original cluster assignment is shown, along with the datasets the respective genes are found to be highly predictive in. For the Zucca dataset, dominance analysis could not be performed as there was perfect convergence between class assignment, given only one sample resided in clusters two and three, therefore, the shared predictor genes for this dataset were taken from the top 45 genes identified with permutation importance, which was ran with 50 iterations.

7.5.5 Cell composition analysis of the ALS motor cortex reinforces the biological interpretation of each molecular subtype

When performing cell deconvolution analysis for the KCL BrainBank and TargetALS case datasets, we found that the samples that were assigned to each cluster had distinctive cell-type profiles, which were reflective of the predominant biological processes of each molecular phenotype. These profiles were almost identical in both datasets (Figure 7-7), with significant overall differences in the proportion of all five cell types. Samples residing in cluster one had a significantly higher proportion of neurons compared to clusters two and three. A higher proportion of astrocytes and endothelial cells were present in samples assigned to cluster two than in cluster one, whilst samples residing in cluster three displayed higher proportions of microglia than cluster one, and oligodendrocytes than clusters one and two. The full results are available in Tables A45 (KCL BrainBank) and A46 (TargetALS).

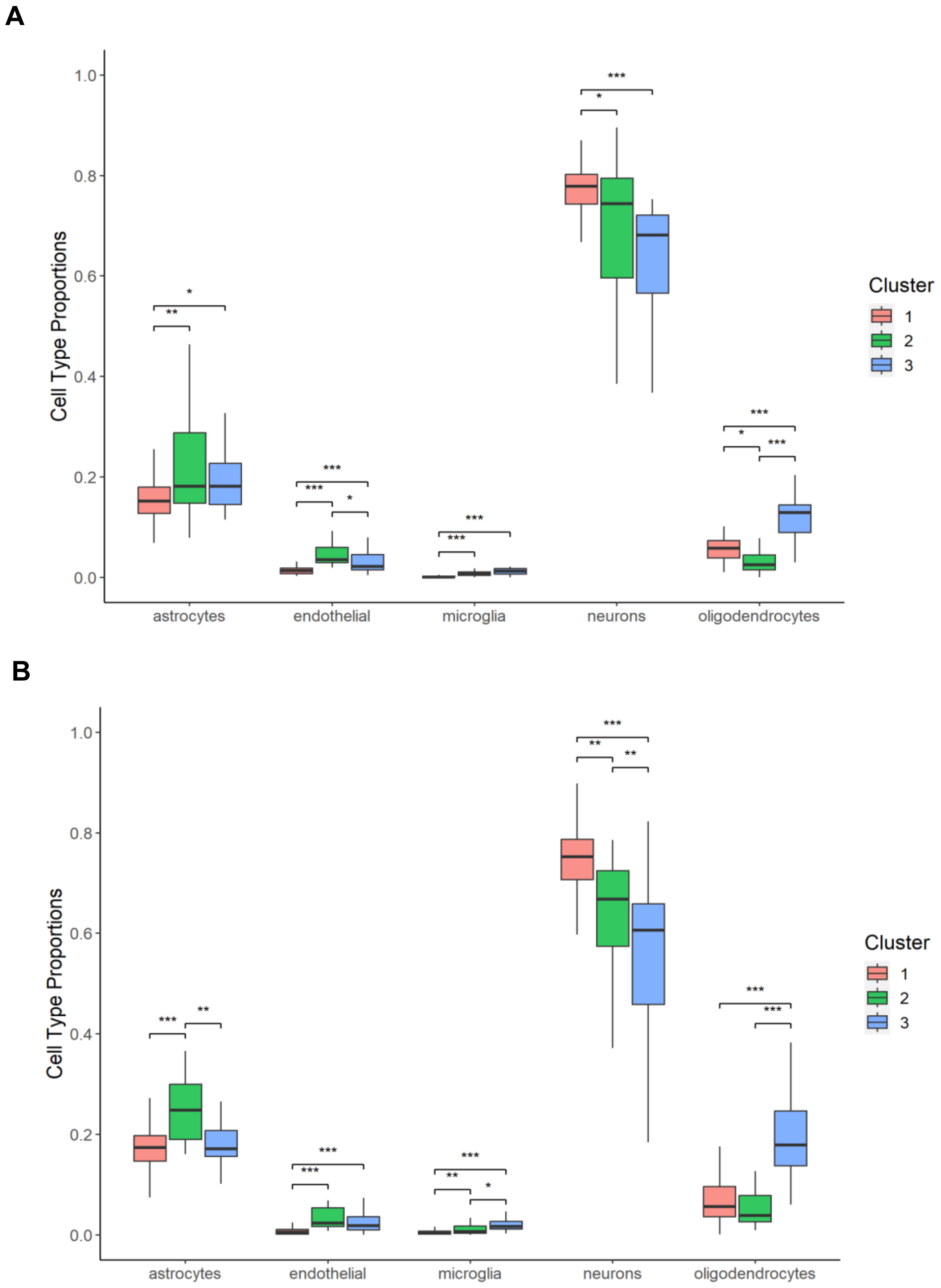


*Figure 7-7. Results of the cell type deconvolution analysis for A) KCL BrainBank cases and B) TargetALS cases. Results were corrected for age of death and sex assigned at birth. Asterisks refer to one-way ANCOVA post-hoc Tukey p-values: * < 0.05, ** < 0.01, *** < 0.001.*

7.5.6 Cluster assignment is correlated with different clinical outcomes and omics measures

In both KCL BrainBank and TargetALS, we observed that cluster two demonstrated differences in several phenotypic and omics measures (full results available in Table 7-6). For instance, cluster two compared to cluster one had a higher age of death (Figures 7-8A and 7-8B) and smaller transcriptional age acceleration (Figures 7-8C and 7-8D). This trend continues when looking at variables present in one of the two datasets, with a 3.87 year slower biological age acceleration being observed in cluster two compared to cluster three in KCL BrainBank (p=0.020), and a longer but albeit non-significant increase in disease duration in TargetALS samples assigned to cluster two. We also found trends for higher mitochondrial DNA copy number in cluster one, and shorter telomere length in cluster 3 in KCL BrainBank samples (Table 7-2). When assessing differences in age of onset based on samples combined from KCL BrainBank and TargetALS, we found that samples residing in cluster one had a lower age of onset compared to clusters two and three (Figure 7-8E; p=0.013). For the Zucca and van Rheenen datasets, there was no significant alteration in age of onset and transcriptional age acceleration between clusters, although samples assigned to the van Rheenen dataset displayed a borderline significant increase in transcriptional age acceleration and also reduced disease duration, which contradicts what was found in the motor cortex datasets.

When assessing potential differences in the site of onset between clusters, we found that in KCL BrainBank, there was a borderline significant difference in the proportion of people with limb-onset SALS assigned to the clusters (X^2 = 6.05, p-value = 0.05). Bulbar-onset and combined limb and bulbar onset SALS were not overrepresented in any of the clusters (bulbar: X^2 = 0.18, p-value = 0.91; limb and bulbar: X^2 = 0.95, p-value = 0.62). As found with the KCL BrainBank dataset, the proportion of limb-onset TargetALS cases differed significantly between clusters (X^2 = 13.49, p-value = 1.2E-03). The distribution of bulbar-onset cases also varied significantly (X^2 = 20.10, p-value = 4.3E-05). There was no difference in the proportion of *C9orf72*-positive (X^2 = 3.45, p-value = 0.18) or combined limb and bulbar onset cases (X^2 = 3.25, p-value = 0.20). In the van Rheenen dataset, there was no association between limb: bulbar ratio and cluster assignment (X^2 = 1.78, p-value = 0.41). Across the three case-only datasets, there was no difference in the male:female ratio (TargetALS: X^2 = 2.48, p-value = 0.29; Zucca: X^2 = 2.02, p-value = 0.36; van Rheenen: X^2 = 0.88, p-value = 0.64).

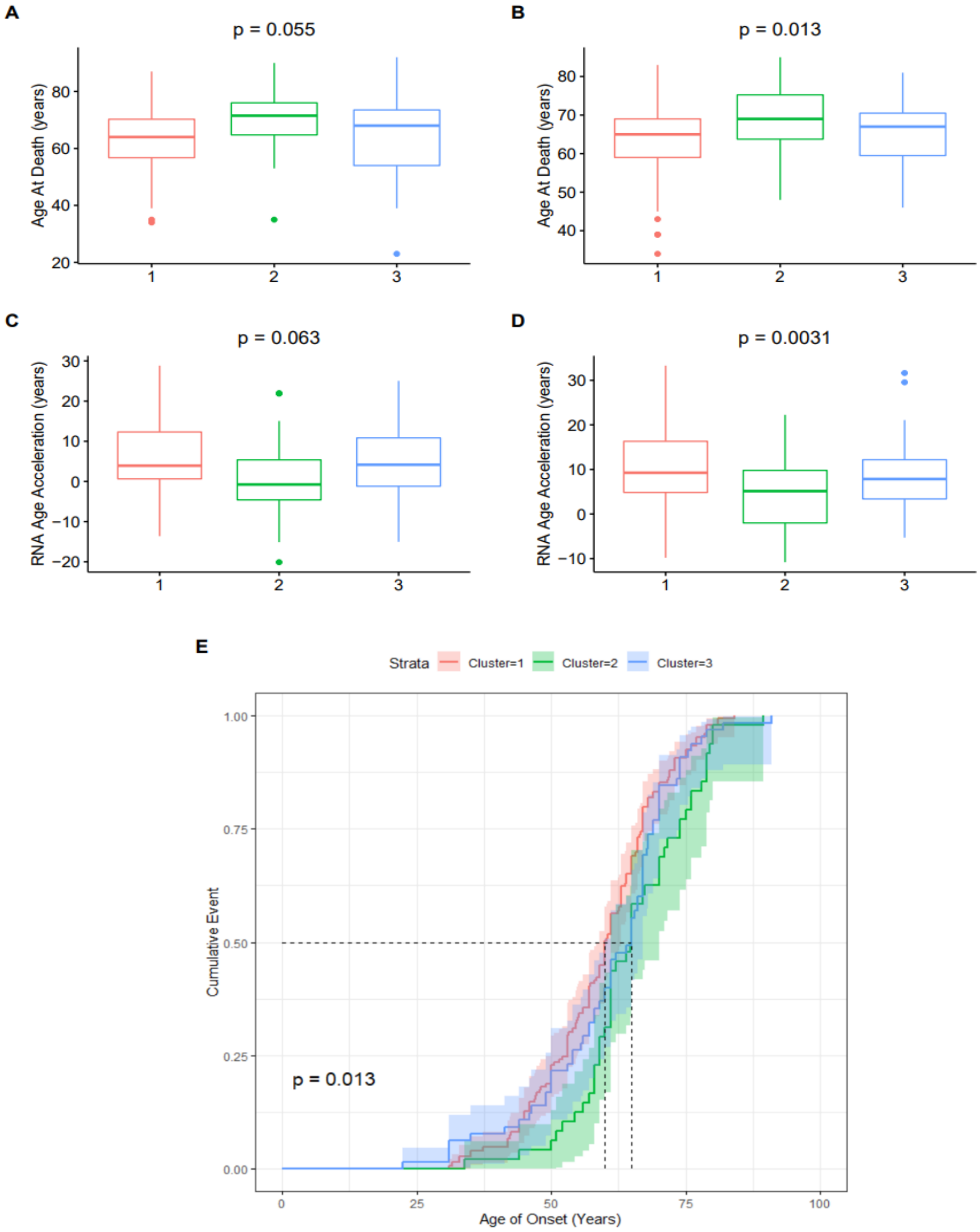


Figure 7-8. Subgroup phenotype analysis between samples residing in each cluster for KCL BrainBank and TargetALS. Variables visualised here includes the age of death for A) KCL BrainBank and B) TargetALS, and transcriptional age acceleration for C) KCL BrainBank and D) TargetALS. P-values are from performing one-way ANCOVA, corrected for sex. E) Cox proportional hazards model for the age of onset of samples from both BrainBank and TargetALS datasets, showing that samples from Cluster 1 have a significantly lower age of onset than Clusters 2 and 3.

KCL BrainBank (motor cortex)

Phenotype	***Normality (Shapiro-Wilk W, p-value)***	***One-Way ANCOVA (F-statistic, p-value)***	***Post-Hoc Analysis (Tukey p-value)***
Age at Onset	0.983, 0.22	2.160, 0.121	1 vs 2; 0.107, 1 vs 3; 0.622, 2 vs 3; 0.569
Age at Death	0.976, **0.042**	2.979, 0.055	1 vs 2; 0.051, 1 vs 3; 0.988, 2 vs 3; 0.168
Disease Duration (years)	0.943; **3.5E-04**	4.211; **0.018**	1 vs 2; **0.036,** 1 vs 3; 0.092, 2 vs 3; 0.890
Post-mortem Delay	0.951, **4.4E-04**	0.178, 0.837	1 vs 2; 0.997, 1 vs 3; 0.851, 2 vs 3; 0.855
mtDNA Coverage	0.944, **3.2E-04**	1.886, 0.157	1 vs 2; 0.988, 1 vs 3; 0.145, 2 vs 3; 0.294
mtDNA Copy Number	0.966; **9.9E-03**	1.643, 0.199	1 vs 2; 0.231, 1 vs 3; 0.458, 2 vs 3; 0.945
Telomere Length	0.972, **0.028**	2.451, 0.092	1 vs 2; 0.810, 1 vs 3; 0.074, 2 vs 3; 0.350
Biological Age Acceleration	0.971, **0.025**	3.858, **0.025**	1 vs 2; 0.110, 1 vs 3; 0.414, 2 vs 3; **0.020**
RNA Age Acceleration	0.981, 0.142	2.847, 0.063	1 vs 2; 0.055, 1 vs 3; 0.973, 2 vs 3; 0.203

TargetALS (motor cortex)

Phenotype	***Normality (Shapiro-Wilk W, p-value)***	***One-Way ANCOVA (F-statistic, p-value)***	***Post-Hoc Analysis (Tukey p-value)***
Age at Onset	0.977, **7.1E-03**	2.463, 0.088	1 vs 2; 0.075, 1 vs 3; 0.968, 2 vs 3; 0.194
Age at Death	0.984, 0.053	4.456, **0.013**	1 vs 2; **0.009**, 1 vs 3; 0.765, 2 vs 3; 0.089
Diagnostic Delay	0.776, **2.9E-14**	0.926, 0.398	1 vs 2; 0.840, 1 vs 3; 0.373, 2 vs 3; 0.867
Disease Duration (years)	0.705, **2.2E-16**	2.403, 0.094	1 vs 2; 0.114, 1 vs 3; 0.944, 2 vs 3; 0.110
Post-mortem Delay	0.883, **6.8E-10**	1.176, 0.311	1 vs 2; 0.892, 1 vs 3; 0.405, 2 vs 3; 0.349
RNA Age Acceleration	0.989, 0.292	6.004, **3.1E-03**	1 vs 2; **0.002**, 1 vs 3; 0.420, 2 vs 3; 0.092

Zucca (blood)

Phenotype	***Normality (Shapiro-Wilk W, p-value)***	***One-Way ANCOVA (F-statistic, p-value)***	***Post-Hoc Analysis (Tukey p-value)***
Age at Onset	0.926, 0.242	0.078, 0.926	1 vs 2; 0.926, 1 vs 3; 0.987, 2 vs 3; 0.986
RNA Age Acceleration	0.990, 0.999	0.178, 0.839	1 vs 2; 0.868, 1 vs 3; 0.936, 2 vs 3; 0.992

van Rheenen (blood)

Phenotype	***Normality (Shapiro-Wilk W, p-value)***	***One-Way ANCOVA (F-statistic, p-value)***	***Post-Hoc Analysis (Tukey p-value)***
Age at Onset	0.975, **2.0E-06**	2.282, 0.103	1 vs 2; 0.100, 1 vs 3; 0.738, 2 vs 3; 0.634
Disease Duration (years)*	0.815; **< 2.2E-16**	0.00950, 0.991	1 vs 2; 0.990, 1 vs 3; 1.000, 2 vs 3; 0.992
RNA Age Acceleration	0.973, **9.1E-07**	2.788, 0.063	1 vs 2; 0.082, 1 vs 3; 0.479, 2 vs 3; 0.787

Table 7-6. Statistical results of clinical and omics-based phenotype analysis. Variables that demonstrated non-normality via Shapiro Wilk were log transformed before running one-way ANCOVA (corrected for sex) and post-hoc Tukey's to assess cluster-specific trends. Disease duration was calculated using all of the data, regardless of censoring status.*

7.6 Discussion

In this study, we used KCL BrainBank motor cortex gene expression data and machine learning to identify expression signatures which constitute three biologically homogeneous subgroups of SALS: synaptic and neuropeptide signalling (cluster one), oxidative stress and apoptosis (cluster two), and neuroinflammation (cluster three). These molecular phenotypes reflect three previously hypothesised key mechanisms of ALS pathogenesis, which have recently been identified using a deep learning-based approach, albeit using expression data from human iPSC-derived *C9orf72*, *TARDBP*, *SOD1* and *FUS* mutant motor neurons (Catanese et al., 2023). The biological interpretation of each cluster is further reinforced by the fact that in KCL BrainBank and TargetALS case datasets, there are significantly higher proportions of neurons, endothelial cells, and microglia in clusters one, two and three, respectively.

Genes which constitute the three main subgroups of cortical inhibitory GABAergic interneurons (*PVALB, SST, VIP*) were identified in cluster one (Tremblay et al., 2016), which is interesting given alterations in their excitability patterns cause global hyperexcitability of corticospinal neurons (Brunet et al., 2020), of which has long been hypothesised as a trigger for the spread of ALS pathology (Eisen et al., 2017; Scekic-Zahirovic et al., 2021). There were also several informative genes related to body mass index, metabolism, and energy homeostasis (*LINC01844*, *ADCYAP1*, *CRH, CRHBP, CARTPT, VGF)*. These processes are linked with worse survival and progression outcomes in ALS (Dardiotis et al., 2018; He et al., 2022; Jésus et al., 2018; Steyn et al., 2018).

Several oxidative stress, apoptosis and muscle system related enrichments defined cluster two, as well as anti-inflammatory signalling processes. In fact, this cluster contained several neuroprotective microglial secretory markers (*IL4R, TGFB1I1, TGFBI, CD163*) (Jurga et al., 2020), as well as the *MMP9* metalloproteinase gene, whose knockdown slows disease progression in ALS mutant models (Kaplan et al., 2014; Kiaei et al., 2007; Spiller et al., 2016). With microglia contributing minimally to this cluster, based on cell deconvolution analysis of KCL BrainBank cases, and better clinical and omics-based age outcomes defining the clusters phenotypic profile in this dataset, we can postulate that a reversal of pro-inflammatory processes may be occurring in this SALS subpopulation. This is further supported by evidence that knockout of the ALS risk gene *CAV1* (Cooper-Knock et al., 2021) in endothelial cells, whose proportion in samples assigned to this cluster was significantly higher, can reduce innate immune system signalling via activation of endothelial nitric oxide synthase (*NOS3*) (Mirza et al., 2010); a complex of which was observed in our enrichment analysis. Moreover, this cluster was enriched for several potential microRNA biomarkers. The most encouraging in terms of its impact on the molecular phenotype are miR-335-5p and miR-29b-3, as they are downregulated in ALS patients (Banack et al., 2022). Additionally, their downregulation in model systems induces reactive oxygen species-mediated excitotoxicity (De Luna et al., 2020), and intrinsic apoptosis mediated motor neuron loss (Klatt et al., 2019); key processes which defined this cluster.

In cluster three, there was clear involvement of the major histocompatibility complex class II and the HLA complex (*HLA-DRA, HLA-DMB, HLA-DOA, HLA-DPA1, HLA-DRB1, HLA-DRB5, HLA-DRB6*), M1 or activated microglia (*CD14, CD86, TREM2, TYROBP, TMEM119, TMEM125)* (Jurga et al., 2020), and pro-inflammatory metalloproteinases (*MMP14*), as well as many immune related genes which were identified in other motor cortex and spinal cord SALS expression studies (Aronica et al., 2015; Dols-Icardo et al., 2020; Humphrey et al., 2023). The tentative ALS-related modifier gene *CX3CR1* (Lopez-Lopez et al., 2014)), which is thought to protect against proinflammatory processes and microglial-induced neuronal cell loss (C. Liu et al., 2019), was also present in this cluster. Several well studied serum and CSF biomarkers of ALS progression were also present, such as *SPP1* (de Luna et al., 2022), the human chitinases *CHI3L1* and *CHI3L2* (Thompson et al., 2019; Vu et al., 2020), and complement C3 (Thompson et al., 2022), in addition to prognostic and predictive CSF biomarkers such as *TREM2*, *LILRA2* and *ITGB2* (Cooper-Knock et al., 2017).

We also demonstrated that these molecular phenotypes can also define distinct subgroups of people with SALS across independent motor cortex (TargetALS) and blood (Zucca et al.; van Rheenen et al.,) datasets of European ancestry, by applying separate linear discriminant models trained on the KCL BrainBank case-derived sample assignments and gene intersections. The average probability of being assigned to the cluster that the samples from each dataset were allocated to was very high (between 0.8-0.9). Because this model is constrained to assign samples to one class, the same approach was carried out in three additional control datasets (KCL

BrainBank, TargetALS, van Rheenen et al.,), and the occipital cortex and cerebellum of TargetALS, which yielded varying results. All KCL BrainBank controls were assigned to cluster one, whereas for the TargetALS and van Rheenen control datasets, the probability estimates for cluster assignment were similar to cases, with similar average probability estimates found for the TargetALS datasets from other regions compared to the motor cortex. With the exception of KCL BrainBank controls, the cluster stability estimates were robust for the motor cortex and other region control dataset, which demonstrates that the cluster assignments are valid. When also performing reverse validation by applying hierarchical clustering to the TargetALS motor cortex dataset and comparing the grouping of samples to the linear discriminant analysis derived assignments with KCL BrainBank-derived clusters and genes, we found a 67-81% overlap in sample assignment which demonstrates that the cluster assignments, regardless of gene composition, is adequate.

Because the probability estimates for cluster assignments were comparable in cases and controls, we cannot confidently state that the entirety of the informative genes within each molecular phenotype are ALS-specific, but we can identify differential drivers of assignment within and across clusters by comparing cases and controls that fall into each. To determine if the expression signature of cluster one could distinguish between cases and controls in KCL BrainBank, we constructed a logistic regression classifier and found that the signature had excellent discriminative power, which indicates that expression of certain genes in this molecular phenotype are differentially regulated in ALS. This was also aided by the fact that when supplying the classifier with sets of random genes, the performance is the same as what would be expected by chance. Case-control logistic regression classifiers were also constructed for each cluster with TargetALS and van Rheenen motor cortex datasets. We discovered that regardless of dataset, the gene signature of each molecular phenotype had excellent power in discriminating cases from controls, indicating again that expression of certain genes in this molecular phenotype are differentially regulated in ALS. Furthermore, key driver analysis of the case-only datasets revealed that there was considerable overlap in genes which determine a sample assignment to one cluster over another, which reinforces the robustness of cluster assignments across datasets.

Analysis of the 30 most important predictors for each model revealed a total of 19 genes (13 in cluster one, 4 in cluster two, and 2 in cluster three) which were shared in at least two case-control datasets. Only one gene, *CTXN3*, which is part of cluster one, was present in all three datasets when all genes in the molecular phenotype were used to construct the model. *CTXN3*, which encodes for the highly conserved integral membrane protein cortexin 3, resides in the genomic region which has been associated with schizophrenia (5q23.2-q34) in individuals of European ancestry (Lewis et al., 2003), with the AG genotype of the rs6595788 polymorphism conferring a 1.5 fold increase in schizophrenia risk in males (Šerý et al., 2015). This is an interesting result as ALS and schizophrenia overlap in terms of their genetic correlations, heritability and polygenic risk scores (McLaughlin et al., 2017; Spargo et al., 2023). Other notable genes which were shared predictors in both motor cortex and blood tissues and therefore show potential for further investigation as potential patient stratification biomarkers includes the cluster one genes *CRH*, *HSD11B1*, and *LERFS*, and the cluster two genes *PLA1A* and *VNN1*. Both *CRH*, which encodes for corticotrophin releasing hormone, and *HSD11B1*, which encodes for the 11-beta hydroxysteroid dehydrogenase type 1 enzyme, modulate the hypothalamic-pituitary-adrenal (HPA) axis, which is primarily responsible for regulating the stress response. Dysregulation of the HPA axis can induce alterations in autonomic nervous system responses, which has been consistently reported as a main non-motor symptom in ALS (Papadopoulou et al., 2022; Pimentel et al., 2019; Shojaie et al., 2023). HPA axis dysregulation is also linked to cortical hyperexcitability and changes in metabolism, which as previously mentioned, is a predominant molecular process which defines cluster one and is linked to differential outcomes in ALS. Release of CRH has also been associated with a reduction in mitochondrial activity and accompanying modification of neuronal activity in hippocampal neurons (Battaglia et al., 2020); two other processes which define the cluster one phenotype. Furthermore, *LERFS*, a non-coding RNA gene, interacts with heterogeneous nuclear ribonucleoprotein Q, which is present in cytoplasmic and internuclear inclusions of people with FTLD-FUS (Gittings et al., 2019). With regard to cross-tissue predictors of cluster two, *VNN1* (vanin 1) plays a role in regulating the glutathione-dependent oxidative stress response (Berruyer et al., 2004). Dysregulation of glutathione metabolism is thought to be one harbinger of reactive oxygen species-mediated toxicity contributing to ALS pathogenesis (K. Kim, 2021), with reduced levels of glutathione reported in the CSF of people with ALS (Tohgi et al., 1999). Finally, *PLA1A* (phospholipase A1 member A) is responsible for regulating the phosphorylation and kinase activity of *TBK1* (X. Gao et al., 2018), which is a causative ALS gene (Cirulli et al., 2015; Freischmidt et al., 2015) whose missense mutations contribute to protein aggregation via defects in autophagy and mitophagy (Gerbino et al., 2020; Harding et al., 2021); another key element of the molecular phenotype of this cluster. We noticed that for the van Rheenen dataset, the predictor that was driving the perfect discrimination in cluster one was *NME1* (nucleoside diphosphate kinase A), as removing this from the model led to a 35% decrease in discriminative power. Not much is known about *NME1* in relation to ALS, although a recent study revealed that its overexpression can stimulate neurite outgrowth and increase mitochondrial function in cell models of Parkinson’s disease (Anantha et al., 2022).

In regard to the sample assignment to different clusters, specifically cluster one, the proportion of samples varied based on tissue type (approximately 60% for the motor cortex versus 85% for the blood datasets). A potential explanation for this is that as the motor cortex represents the end stage of disease, perhaps other biological processes explained by the remaining molecular phenotypes more strongly influence the progression of disease in samples assigned to those clusters. This may not be as apparent in the blood datasets given that the samples were collected at different stages of the disease.

We also discovered that there were distinct clinical and omics-related outcomes that correlated with cluster assignment in both motor cortex case datasets. Cluster two was associated with a higher age of death and longer disease duration, accompanied by a decrease in transcriptional age acceleration. There are several plausible explanations as to why this trend was observed; the first is that more people assigned to this cluster may have had a history of Riluzole usage than other clusters, as it modulates apoptosis, autophagy and other excitotoxicity-related processes which are prevalent biological processes in this cluster (Koh et al., 1999; Storch et al., 2000). Another possibility is that genomic variants present in inflammatory genes assigned to this cluster may diminish their effects. This theory is supported by the example of *IL18RAP*, which is an M1 secretory marker present in this cluster (Jurga et al., 2020), of whom 3’UTR variants were recently found to protect against ALS, by impeding microglial-dependent motor neuron degeneration (Eitan et al., 2022). However, this must be interpreted with caution as information on Riluzole usage was not available, and genetic data was not used in this study. In KCL BrainBank cases assigned to cluster two, there was also a significant decrease in biological age acceleration. Whether this phenomena is also apparent in TargetALS, and the blood datasets could not be analysed because biological age acceleration could only be measured in KCL BrainBank as there was matching epigenetic information available. However, this warrants further investigation in additional datasets as evidence links increased serum levels of the chronic inflammation marker suPAR, encoded by the cluster two gene *PLAUR*, with higher biological age acceleration in the normal population (Rasmussen et al., 2021). Telomere length was shorter in cluster three in KCL BrainBank, which despite being non-significant, is also an important trend to investigate as although mounting evidence supports the association between longer telomere length and worsened severity of ALS (Al Khleifat et al., 2019; Al Khleifat, Iacoangeli, Jones, et al., 2022), there is also an established link between chronic inflammatory states and telomere shortening in aging and disease (Jurk et al., 2014; Lex et al., 2020; Niveta et al., 2022). Finally, we found that samples in cluster one had a lower age of onset in a combined analysis of KCL BrainBank and TargetALS, which makes sense given that this cluster is linked to neuronal dysfunction and therefore motor neuron degeneration. The proportion of people with limb-onset ALS assigned to the clusters also differed significantly in both motor cortex datasets. Despite the association between distinct age of onset with each cluster in the motor cortex datasets, this was not replicated in the blood datasets, therefore further examination is needed to establish if clear phenotype differences exist across clusters.

There are several limitations of this study which will require further investigation in the context of our findings. First, only samples belonging to the KCL BrainBank dataset had matching multi-omics data, which meant that cluster-specific effects on omics variables could not be assessed in the other datasets. Likewise, both blood datasets had limited clinical information, which did not allow us to validate all possible clinical phenotype associations. Furthermore, the van Rheenen blood dataset did not replicate the association between disease duration and age at onset with class membership, with the opposite trends occurring for disease duration and transcriptional age with cluster two, and age of onset with cluster one. Some potential explanations are that microarray technology was used to obtain the transcriptomic profiles in this dataset, translating in a lower number of genes available that were part of the subtype signatures and lower class assignment accuracy. Indeed, clusters two and three represented approximately 25% of ALS patients each in the brain datasets, while only ~8% each in the van Rheenen blood dataset. Moreover, the Dutch population might present a more distinct structure compared to other European countries (Byrne et al., 2020). Also, as this dataset has nearly twice the number of controls than cases, the effects of the predictor genes, specifically *NME1* in cluster one, for discriminating cases and controls needs to be evaluated, despite our analysis oversampling for the minority class to address class imbalance before supplying to the classifier models. Finally, we did not integrate genomic variants into our analysis to further enhance our molecular classification, like recent studies that built upon their previous clustering analyses (La Cognata et al., 2020; Morello et al., 2019), as this would have resulted in underpowered analyses given our sample sizes, or correlated our clustering findings with neuropathological findings and co-existing pathologies in the motor cortex datasets, as this data was not available to us when the study took place. As we did not perform a comparative analysis of the cluster assignment of people with familial ALS or other neurodegenerative diseases i.e., FTD, Parkinson’s disease, we cannot be absolutely sure that the molecular phenotypes identified in this study are truly ALS-specific. Although, we can discern that the expression of genes in these phenotypes that distinguish cases from controls represent sporadic ALS subtypes as the clusters were validated in three independent ALS datasets which did not contain samples from those with familial ALS. They also represent motor-cortex specific aspects of the disease process as the expression signatures of each molecular phenotype can distinguish samples from the motor cortex from other brain regions for TargetALS cases.

In conclusion, we have demonstrated that people with ALS can be successfully stratified into molecularly distinct subgroups using gene expression data. Our results support the hypothesis that different subgroups could underly previously investigated forms of ALS pathogenesis and can be identified in patients via specific expression signatures. These molecular phenotypes discovered in a UK cohort, were validated in independent motor cortex and blood datasets and could be used to distinguish patients from controls, showing potential to be used for clinical trial stratification and the development of biomarkers for personalised treatments and diagnostics. Our analysis also revealed several known candidate gene biomarkers which could be exploited in future stratification studies to verify our findings. We have developed a publicly available web app (https://alsgeclustering.er.kcl.ac.uk) to allow the broader scientific and clinical community to use our model for the stratification of pre- and post-mortem samples in their studies.

Chapter 8. Summary of Findings and Future Directions

8.1 Chapter 4: Development of a next-generation sequencing bioinformatics analysis pipeline

The development of DNAscan2 expands the potential target audience to include both bioinformaticians and researchers in basic and translational scientific fields with limited access to computational resources and experience in NGS analysis. This application allows for the straightforward and efficient identification and characterisation of several types of genetic variation, which is particularly useful in the big-data era as the popularity of NGS exceeds that of traditional approaches.

Future revisions of the pipeline should focus on incorporating tools which can identify other types of genomic variation which can modulate disease risk and progression, particularly in relation to ALS. These include non-canonical structural variation, such as telomere length and mitochondrial DNA copy number. Telomeres are highly conserved TTAGGG hexameric non-coding DNA repeats responsible for maintaining chromosomal stability and integrity during cellular replication (Shammas, 2011), whilst mitochondrial copy number acts as a proxy for mitochondrial function (O’Hara et al., 2019), which is dysregulated in ALS due to mutations in several ALS-linked genes responsible for regulating varying mitochondrial processes (e.g. *FUS, TARDBP, SOD1, C9orf72, CHCHD10, TBK1, KIF5A, VCP, VAPB, SIGMAR1, OPTN, SQSTM1, ALS2*; (Jankovic et al., 2021)). Decreased telomere length and mitochondrial DNA (mtDNA) copy number have consistently been linked to aging and mortality in both neurologically normal people (Ghimire et al., 2019; Praveen et al., 2020; R. Zhang et al., 2017) and people with Alzheimer’s disease (Forero et al., 2016; Guo & Yu, 2019; Wei et al., 2017), however, an opposite trend is noted in ALS, through the adoption of bioinformatics tools. The quantification of telomere length from WGS using the TelSeq tool (Ding et al., 2014) in over 6,500 people with ALS and controls from Project MinE found people with ALS harboured telomere lengths which were 20% longer than controls, with shorter telomere lengths in people with ALS conferring a 10% increase in survival (Al Khleifat, Iacoangeli, Jones, et al., 2022), in accordance with a previous pilot study in the British cohort of Project MinE (Al Khleifat et al., 2019). Thus, telomere length could be incorporated as a prognostic biomarker. Why telomere lengths seem to be larger in ALS than other neurodegenerative diseases remains unclear, although a Mendelian randomisation study found that in European populations, the changes in telomere length may be driven by low density lipoprotein and overall cholesterol levels (Y. Gao et al., 2020). Likewise, a bioinformatics analysis quantifying leukocyte mtDNA copy number in the Project MinE cohort confirmed that this is increased in ALS after adjusting for mitochondrial haplotype and correlates with worse survival outcomes, albeit with small effect sizes (Harvey et al., 2022). This had previously been found in smaller SALS and FALS cohorts using qualitative PCR (Stoccoro et al., 2018, 2020). This phenomenon is likely to be representative of a compensatory mechanism against TDP-43 mislocalisation or reduction in mitochondrial energy metabolism function, as demethylation of the regulatory D-loop and mitochondrial haplotype are associated with mtDNA copy number and reduced survival (Harvey et al., 2022; Stoccoro et al., 2020).

The need for incorporating long-read WGS technology processing and analysis into this pipeline for the identification of other types of structural variation not characterisable with short-read NGS, such as variable number tandem repeats (VNTRs), is also warranted. Despite short-read WGS prevailing in genetic diagnostics and counselling practices, and the population-wide characterisation of genomic variation, complex chromosomal rearrangements, segmental duplications, VNTRs which are longer than the 150-bp read length and repeat expansions with high GC content are notoriously problematic to capture, as coverage, depth and mapping biases incurred by paired-end WGS can make approximately 480kb of protein coding exons (Barbitoff et al., 2020) and nearly 38,000 majority intronic and non-coding RNA regions (Ebbert et al., 2019) inaccessible to conventional alignment tools. Furthermore, most protein coding gene regions are also camouflaged i.e., had low mapping quality due to the presence of segmental duplications and tandem repeats creating multi-mapping reads (Ebbert et al., 2019). Furthermore, as VNTRs are longer than 20 base-pairs in length, this far exceeds the capabilities of current tools employed in this pipeline, such as ExpansionHunter and ExpansionHunterDenovo, which currently deal with tandem repeats up to 6 base-pairs in length. VNTR profiling in ALS using long-read sequencing is highly relevant as the identification and characterisation of the first SALS-linked 69 base-pair VNTR in the last intron of the vacuolar-ATPase gene *WDR7* was discovered using this technology (Course et al., 2020). As it resides within the ALS3 locus, which has yet to have a causal gene formally linked with it, WDR7 may be involved in ALS3 pathogenesis. Despite having a similar repeat unit distribution as Parkinson's disease genomes, people with SALS carry higher copy numbers of this VNTR (Course et al., 2020). Furthermore, like TDP-43 and FUS (Lim et al., 2016; Loughlin et al., 2019), this VNTR can also self-interact and form aggregable RNA stem-loop structures, increasing the prospect of its involvement in abnormal DNA repair, transcription and splicing processes.

Besides the addition of tools capable of identifying more complex variation, it is important that the current and future developments to DNAscan2 should incorporate strategies to ensure that the tool reaches the correct target user group. The two key strategies that should be adopted concern wider dissemination of the tool beyond publication (which applies to both current and future versions), and also providing the opportunity for target users to be involved with the implementation of new features. Dissemination of the tool would most likely be achieved via social media platforms such as X/Twitter and LinkedIn, in combination with the departmental and school specific media offices to ensure the tool reaches institutional and scientific audiences as well as the wider bioinformatics community. Up-to-date video walkthrough tutorials for different use cases could also be considered in order to better highlight what the tool delivers. Concerning the implementation of new features in future versions, it would be pertinent to create shareable online surveys (e.g. SurveyMonkey, Google Forms) to allow potential target users to give their opinions and suggestions on what they would like to be added to the tool to enhance their research. This could be followed by further email communication and a user meeting to keep them informed about what suggestions we will be taking forward.

8.2 Chapter 5: Investigating the role of *NEFH* as an ALS risk gene

This study illuminates how performing meta-analyses of the literature and leveraging large-scale WGS data in combination with screening and a variant effect and frequency stratified burden analysis can assist in confirming or discovering variant associations in the *NEFH* gene with ALS susceptibility. We confirmed the association of rare variants (MAF <1%) in the *NEFH* gene with ALS risk by performing meta-analysis and rare variant burden analysis of a combined cohort of 18,500 people with ALS and controls across previous reports from the literature and Project MinE. Both of these analyses were significant when taking multiple testing into account, highlighting that this result is highly reconcilable. We also revealed that missense tail domain variants likely drove this association, as our variant-based rare meta-analysis of 1164 people with ALS and 2177 controls, for which the majority of variants were pathogenic, and ultra-rare (MAF < 0.1%) burden analysis of pathogenic variants in Project MinE found these to be significantly associated with ALS. Despite the lower OR and nominal association with burden analysis, the direction and size of the effect was similar, which argues for a consistent effect of missense tail variants with ALS susceptibility.

Furthermore, we also found that rare in-frame deletions in the KSP segment of the tail domain nominally confer susceptibility to ALS in Project MinE, which agrees with previous reports using smaller sample sizes and traditional sequencing-based approaches, and that ultra-rare intronic variants in the rod domain were also nominally dominant factors of association with ALS risk in the Project MinE cohort, albeit nominal. Although our SV analysis in Project MinE identified a 113bp deletion in the KEP segment that seems to have a protective effect against ALS, and there is a report of a protective intronic rod domain repeat polymorphism that could be protective also, both of these mutations are common, which indicates that subdomain-specific effects for different classes of variants at different MAF cut-offs may play different roles for ALS susceptibility. This may also be a phenomenon occurring for other causal, modifier or predicted ALS genes, which could not have been investigated using whole exome sequencing and conventional burden analysis, as it usually considers the whole gene, or exons within a gene as the functional unit studied and would therefore dilute any region-specific effects which could span multiple exons. In light of this, I am now currently adopting a large-scale unbiased and systematic genome-wide approach using the burden test framework in the Project MinE cohort to see if mutations of different frequencies and classes that cluster in single annotated protein domains are indeed responsible for driving genetic associations with ALS risk. This is highly relevant given that for example in known ALS genes such as *FUS* and *TARDBP*, the majority of identified pathogenic missense mutations reside within the nuclear localisation signal domain (Boer et al., 2021; Shang & Huang, 2016).

As the effect of missense *NEFH* variants and the protective 113bp deletion on ALS susceptibility has not been established previously, this finding also opens new avenues for future work in our team to explore if the rare missense variants identified computationally here are not false positives, with qPCR validation. Functional characterisation of selected missense variants could also be carried out to determine their impact on phosphorylation with techniques such as Western blot or ELISA. As for the deletion mutation, it would be better suited to perform in-silico computational dynamics simulations to determine how it could alter the phosphorylation and aggregation propensity of the NF-H protein as it would be quite difficult to introduce such a mutation into a model system.

Despite these findings, the effect sizes of the associations even in this large cohort are fairly small and have nominal significance, which argues against the presence of *NEFH* in genetic screening panels and suggests that perhaps *NEFH* should either remain an amber classification in the NHS screening panel or be classified as red. Of course, further screening and in-silico / model system characterisation needs to be performed to solidify this interpretation.

8.3 Chapter 6: Differential gene expression analysis of two large ALS sequencing consortia

By performing independent differential gene expression in KCL BrainBank and TargetALS bulk RNAseq datasets, we identified ALS gene expression profiles that explicate various biological processes and modulatory themes as harbingers of ALS pathogenesis. There was strong evidence to suggest that alterations in the neuropeptide signalling pathway may be a key feature of the ALS phenotype, as in both cohorts we observed that this pathway was enriched amongst their differentially expressed genes, the melanocortin receptor 4 gene (*MC4R*) was significantly upregulated, and higher expression levels of two neuropeptide-related genes, *TACR1* and *NPBWR1*, correlated with longer disease duration and lower age of onset, respectively. There were also links between many of the 45 common differentially expressed genes with other previously studied themes of ALS pathogenesis, such as lipid metabolism and mitochondrial energy homeostasis.

Despite these findings, there was considerable divergence in the number of differentially expressed genes as well as the overall biological enrichments in the two datasets, which we attributed to the inevitability of differences in RNA collection and storage methods, sample demographics (especially the influence of a significantly older control group in the KCL BrainBank cohort, the gender effect which existed in the TargetALS cohort, and lower RIN numbers and a higher post-mortem delay in controls in both datasets), and populational variability in gene expression.

It is promising that even though these cohorts are inherently different, we managed to find an association with neuropeptide signalling at several levels, although further investigation is warranted to assess the potentiality of neuropeptide-coding genes and regulators of neuropeptide signalling as potential prognostic biomarkers as our results are only suggestive of a potential link between expression levels and modulation of phenotype. Future work therefore will exploit pre-mortem transcript expression of PBMCs and IPSC-derived motor neurons, and serum or CSF-based protein expression in publicly available datasets such as GEO and AnswerALS to confirm if the correlations between *TACR1* and *NPBWR1* remain. If these associations can be replicated, we could generate IPSCs or other cell lines or mice models with overexpression and knockdown of *TACR1* and *NPBWR1*, respectively, to determine if they can improve functional outcomes and alter the efficiency of neuropeptide signalling.

Likewise, because we only performed differential expression analysis for this study, it would be beneficial to implement other expression-based designs, like differential transcript usage and isoform expression analysis and the integration and analysis of alternative splicing variation such as intron retention, and the presence of cryptic exons to quantify splicing alterations at both a global level and for specific enrichments and shared differentially expressed genes observed in our analysis.

8.4 Chapter 7: Utilising hierarchical clustering to identify molecular subtypes of ALS

We demonstrated that the application of unsupervised machine learning to bulk motor RNAseq expression data of KCL BrainBank can identify three distinct expression signatures which constitute biologically homogeneous subgroups of SALS and contain several known candidate gene biomarkers which could be exploited for further investigation of SALS heterogeneity. When combined with supervised machine learning trained on KCL BrainBank gene and sample assignments, these molecular phenotypes (synaptic and neuropeptide signalling, oxidative stress and apoptosis, and inflammation) can be used to successfully stratify people with ALS across three independent motor cortex and blood datasets (TargetALS, Zucca, van Rheenen), can distinguish between people with ALS and controls assigned to the same subgroup with high discriminative power and reflect motor-cortex disease relevant signatures as there was near perfect discrimination between motor cortex and other brain regions from TargetALS; the occipital cortex and cerebellum. Although, one limitation of the classification of the molecular subtype expression signatures between the motor cortex and other brain regions is that despite being processed in the same manner as the motor cortex and blood datasets, a different aligner was used to gather raw gene counts for the other regions in TargetALS.

To ensure that each molecular phenotype was robust and valid across datasets, we performed several sanity checks. Firstly, higher proportions of cell types predominantly involved in the biological processes of each molecular phenotype were found in people with ALS from the KCL BrainBank and TargetALS motor cortex datasets, which reinforces their biological interpretation. Moreover, cluster stability estimates were robust for all datasets except KCL BrainBank controls, as they were all assigned to cluster one. Reverse validation by applying unsupervised machine learning to TargetALS motor cortex revealed a 67-81% overlap in sample assignment with grouping using KCL BrainBank-derived clusters, with the performance of the cluster one case-control KCL BrainBank classifier being the same as expected by chance when supplying with 10 sets of random genes instead of the 131-gene signature of the molecular phenotype. Finally, there was a high overlap in the driver genes of sample assignment in the case-only datasets.

Our analysis of the predictors of case-control status in KCL BrainBank, TargetALS and van Rheenen datasets revealed that the schizophrenia-linked gene *CTXN3* was a shared top predictor of cluster one, which offers fresh insights into the well-established similarities in genomic architecture between ALS and schizophrenia. There were also shared predictors in at least two of these datasets; the most remarkable being *CRH*, *HSD11B1* and *LERFS* for cluster one, and *PLA1A* and *VNN1* in cluster two. A logical next step in determining if these are a true predictor of molecular phenotype assignment is to perform feature ablation studies i.e. remove each gene and then see how the predictor values (feature driver proportion) and posterior probability assignment of molecular phenotype assignment changes.

Assignment to molecular phenotypes were also correlated with differential clinical and omics-based outcomes in the motor-cortex case datasets; individuals assigned to cluster two exhibited with significantly higher age of death, longer disease duration and decrease in transcriptional age acceleration. Therefore, the expression signature of cluster two needs to be investigated in more depth to identify isolated genomic biomarkers of onset and progression.

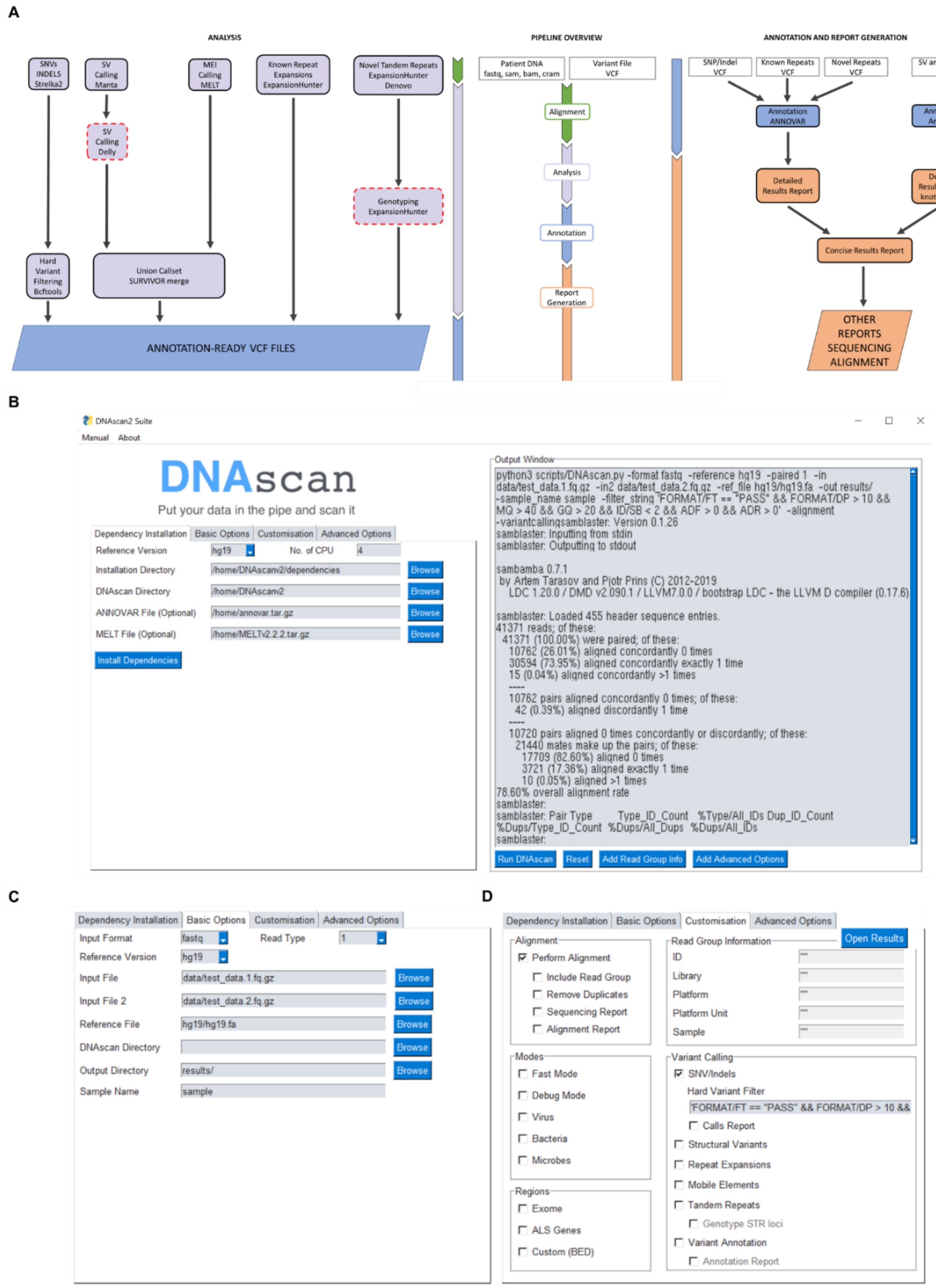
These molecular phenotypes show great potential to be used in clinical trial settings to prevent enrolment of potential non-responders or stratify people with ALS into appropriate treatment arms. Currently, the individuals’ genomic response to a therapeutic being tested in clinical trial is only carried out after the trial has ended, as the primary outcome for the effectiveness of a candidate drug in ALS is a slowing of clinically observable functional decline as assessed with progression severity scales like ALSFRS-R (Cedarbaum et al., 1999). These post-hoc analyses have uncovered important interactions between therapeutics and genetic variation, such as carriers of the C/C genotype and C allele of the *UNC13A* survival modifier-linked SNP (rs12608932). Individuals carrying the C/C genotype had a 30% increase in the probability of survival when treated with lithium carbonate (van Eijk et al., 2017), with the presence of at least one C allele conferring the opposite effect with valproic acid treatment (van Eijk et al., 2020). This result has now led to the creation of a new clinical trial of lithium carbonate specifically for people with ALS that are homozygous for the C allele (Willemse et al., 2022). Despite this, there are a paucity of clinical trial inclusion criteria frameworks or prognostic prediction models of survival and functional decline (Elamin et al., 2015; Kjældgaard et al., 2021; Xu et al., 2021; Westeneng et al., 2018) that incorporate schemes to account for molecular heterogeneity of ALS at the level of recruitment or primary outcome assessment.

We do acknowledge, like in Chapter 6, that there are several factors such as the use of post-mortem tissue, differential RNA expression protocol, and demographic and population-based variability, that could influence the likelihood of belonging to a certain molecular phenotype. Furthermore, we did not supplement this analysis with enough multi-omics data i.e methylation and genomic variants of informative genes or include data from people with known ALS mutations or other related neurodegenerative diseases, which means that we cannot definitively say that these molecular subtypes are ALS-specific or pinpoint the molecular subtypes to even further defined mechanisms of pathogenesis. This, coupled with the fact that our method did pick up several informative genes for each cluster that have already been recognised as potential candidate biomarkers for ALS stratification, means that I am currently embarking on a larger scale multi-omics stratification study as part of my post-doctoral training to verify our findings.

There are a few avenues which I am going to pursue to improve this method and then hopefully develop a more robust ALS subtype detection tool. For one, I am going to use the method here (LDA projections of molecular subtypes trained on KCL BrainBank gene and sample assignments) with additional pre-mortem datasets from the MNDA collection (static measurements) and AnswerALS (longitudinal) to ascertain if the posterior probabilities of assignment are similar as the other pre-mortem datasets used in Chapter 7. I will then use several different preprocessing, gene/marker selection and machine learning approaches for multi-omics stratification of MNDA and AnswerALS datasets. For feature selection, I will 1) use an unbiased approach like used in Chapter 7 to select the genes with the highest variability, 2) knowledge graph-based methods to refine the gene list to those predicted to be causal for ALS, and 3) use the informative genes identified as those defining the clusters from the hierarchical clustering analysis in Chapter 7. Different machine learning approaches employed depends on the nature of the temporal measurements in the datasets, but for the longitudinal datasets, I would like to use an approach like hidden Markov models, generative adversarial networks or Gaussian processes to determine if cluster assignment remains stable over the time course. For the static datasets, I hope to use latent factor and multi-set correlation based analysis in addition to hierarchical clustering to compare their performance in identification of both expression- and multi-omics-based subtype identification. Throughout this process, I will keep mindful of the limitations that we faced in Chapter 7 regarding how to handle data from different tissues and disease stages, and any possible batch and site effects that arise from utilising several cohorts which may pose issues in training and testing of the models.

Appendix I. Figures

Chapter 4



Reference Version: hg19 No. of CPU: 4
Installation Directory: /home/DNAscanv2/dependencies
DNAscan Directory: /home/DNAscanv2
ANNOVAR File (Optional): /home/annovar.tar.gz
MELT File (Optional): /home/MELTv2.2.2.tar.gz

```
python3 scripts/DNAscan.py -format fastq  -reference hg19  -paired 1  -in
data/test_data.1.fq.gz  -in2 data/test_data.2.fq.gz  -ref_file hg19/hg19.fa  -out results/
-sample_name sample  -filter_string 'FORMAT/FT == "PASS" && FORMAT/DP > 10 &&
MQ > 40 && GQ > 20 && ID/SB < 2 && ADF > 0 && ADR > 0'  -alignment
-variantcallingsamblaster: Version 0.1.26
samblaster: Inputting from stdin
samblaster: Outputting to stdout

sambamba 0.7.1
 by Artem Tarasov and Pjotr Prins (C) 2012-2019
    LDC 1.20.0 / DMD v2.090.1 / LLVM7.0.0 / bootstrap LDC - the LLVM D compiler (0.17.6)

samblaster: Loaded 455 header sequence entries.
41371 reads; of these:
  41371 (100.00%) were paired; of these:
    10762 (26.01%) aligned concordantly 0 times
    30594 (73.95%) aligned concordantly exactly 1 time
    15 (0.04%) aligned concordantly >1 times
    ----
    10762 pairs aligned concordantly 0 times; of these:
      42 (0.39%) aligned discordantly 1 time
    ----
    10720 pairs aligned 0 times concordantly or discordantly; of these:
      21440 mates make up the pairs; of these:
        17709 (82.60%) aligned 0 times
        3721 (17.36%) aligned exactly 1 time
        10 (0.05%) aligned >1 times
78.60% overall alignment rate
samblaster:
samblaster: Pair Type        Type_ID_Count    %Type/All_IDs Dup_ID_Count
%Dups/Type_ID_Count  %Dups/All_Dups  %Dups/All_IDs
samblaster:
```

Input Format: fastq Read Type: 1
Reference Version: hg19
Input File: data/test_data.1.fq.gz
Input File 2: data/test_data.2.fq.gz
Reference File: hg19/hg19.fa
DNAscan Directory:
Output Directory: results/
Sample Name: sample

Alignment
- ☑ Perform Alignment
  - ☐ Include Read Group
  - ☐ Remove Duplicates
  - ☐ Sequencing Report
  - ☐ Alignment Report

Modes
- ☐ Fast Mode
- ☐ Debug Mode
- ☐ Virus
- ☐ Bacteria
- ☐ Microbes

Regions
- ☐ Exome
- ☐ ALS Genes
- ☐ Custom (BED)

Read Group Information
ID: ""
Library: ""
Platform: ""
Platform Unit: ""
Sample: ""

Variant Calling
- ☑ SNV/Indels
  - Hard Variant Filter: 'FORMAT/FT == "PASS" && FORMAT/DP > 10 &&
  - ☐ Calls Report
- ☐ Structural Variants
- ☐ Repeat Expansions
- ☐ Mobile Elements
- ☐ Tandem Repeats
  - ☐ Genotype STR loci
- ☐ Variant Annotation
  - ☐ Annotation Report

Figure A1. Panel A: Overview of the DNAscan2 pipeline, which consists of four main stages: Alignment, Analysis, Annotation and Report Generation, following input of patient DNA in several different formats. Steps in red dotted lines are removed if the '-fast_mode' flag is set, which massively increases computational efficiency for those with limited computing resources. Panel B: Screengrab of the main DNAscan2 GUI window with an example alignment and variant calling output. Panel C: 'Basic Options' tab displaying the default settings. Panel D: 'Customisation' tab.

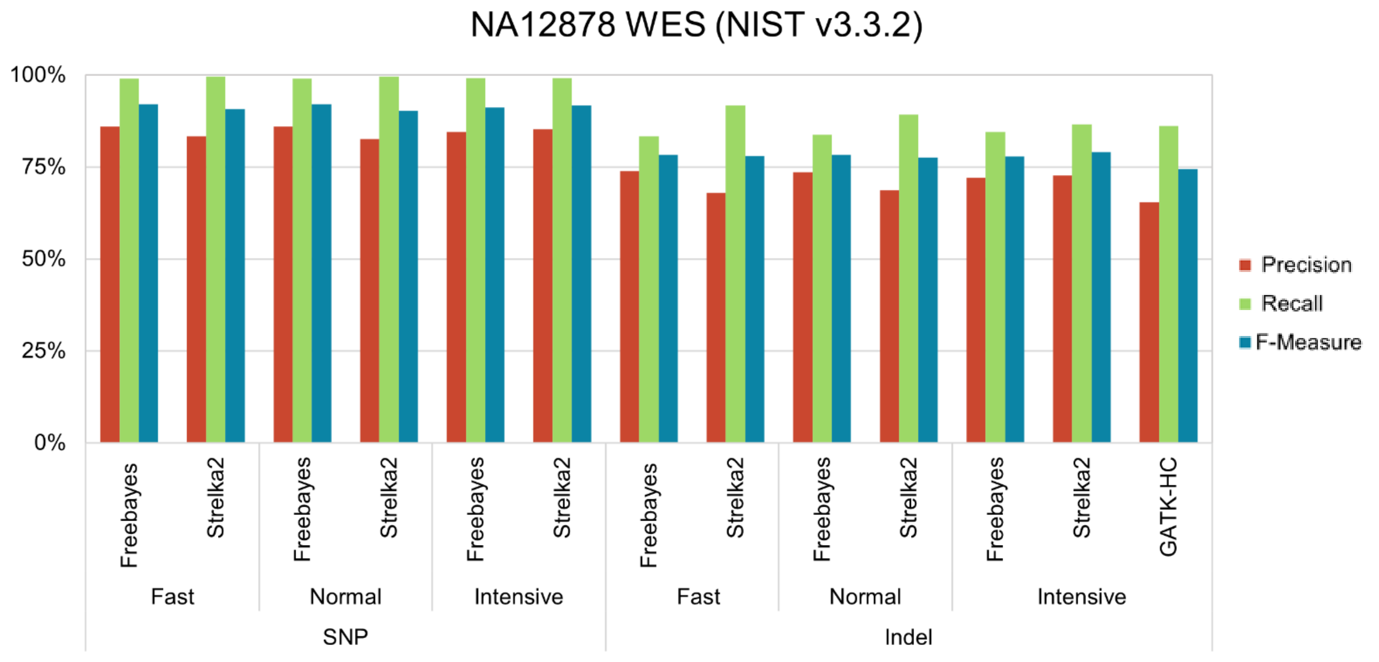


Figure A2. SNV and indel calling performance of Freebayes, Strelka2 and GATK HaplotypeCaller on the whole exome sequencing of NA12878, against the NIST small variant benchmarking callset (v3.3.2). DNAscan was run in fast, normal and intensive mode.

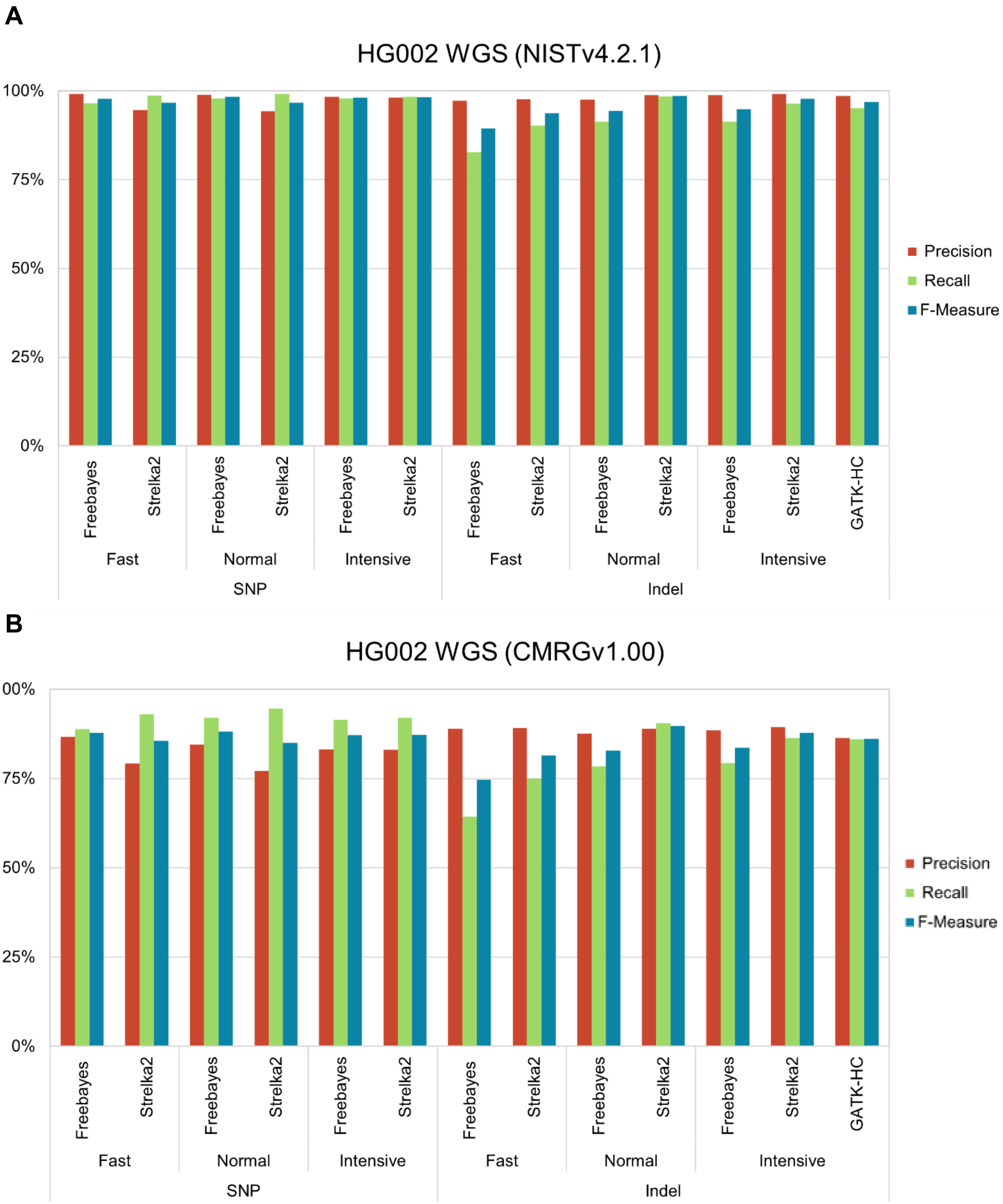


Figure A3. SNV and indel calling performance of Freebayes, Strelka2 and GATK HaplotypeCaller on the whole genome sequencing of HG002, against the A) NIST small variant benchmarking callset (v4.2.1), and the B) GIAB CMRG structural variant callset (v1.00). DNAscan was run in fast, normal and intensive mode.

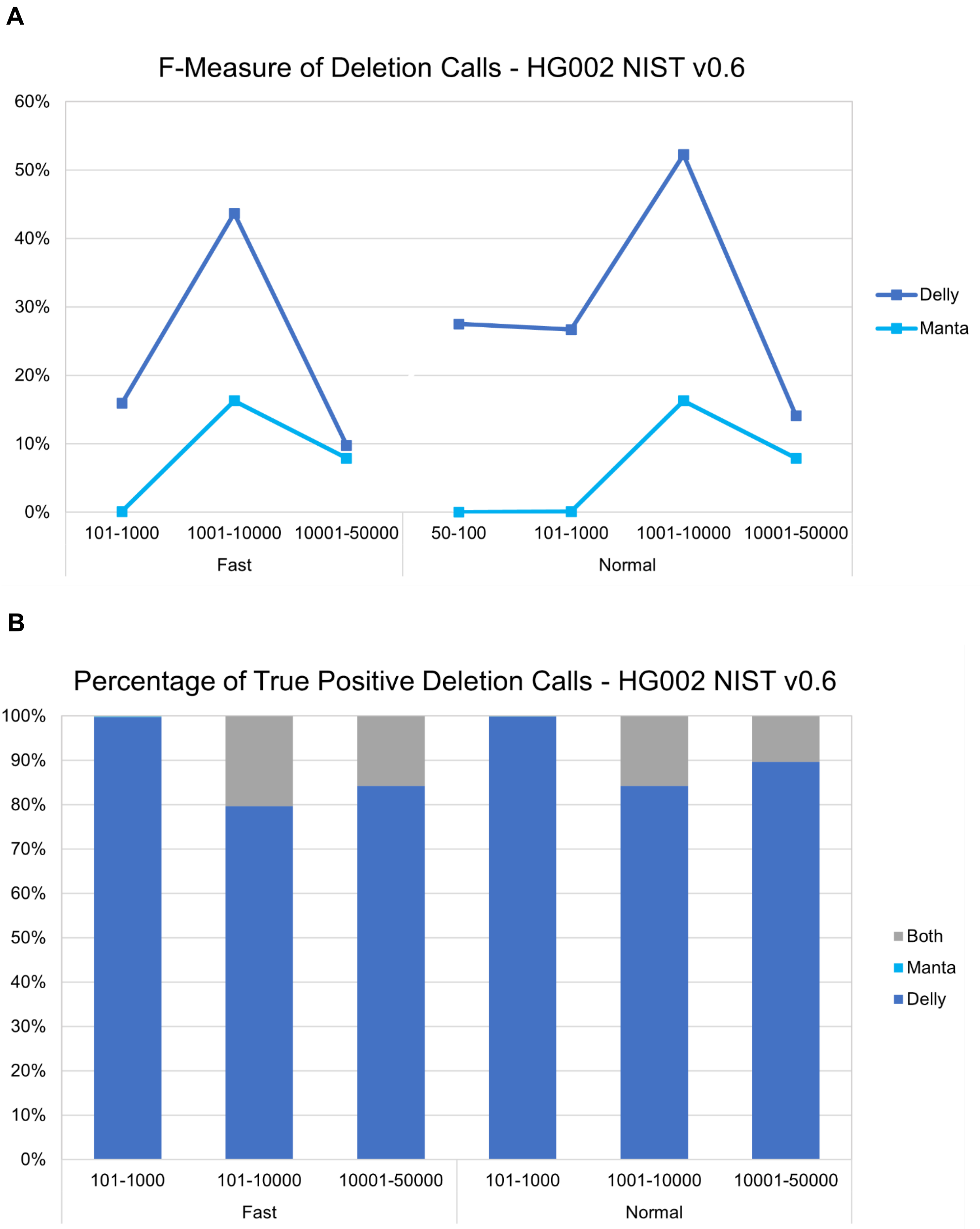
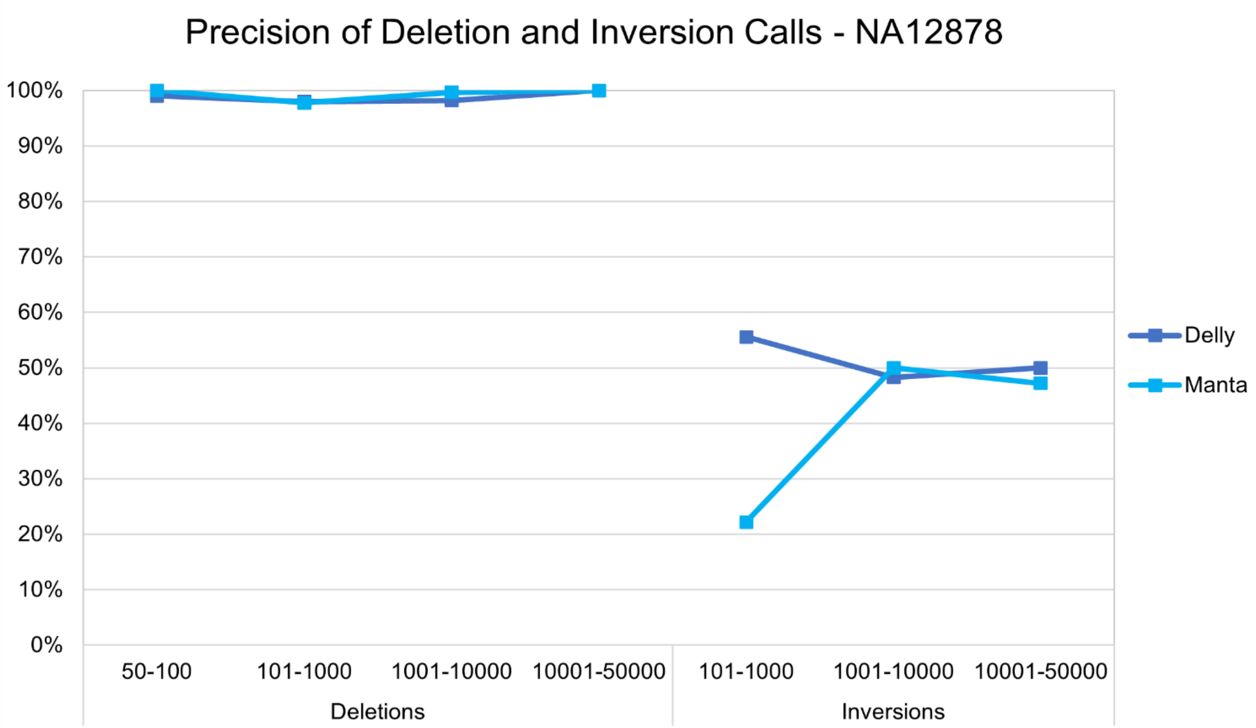


Figure A4. Deletion SV calling performance of Manta and Delly on the whole genome sequencing of HG002 against the NIST SV benchmarking callset (v0.6). Fast and normal modes refer to the alignment specifics as defined by DNAscan. Fast: HISAT2 alignment. Normal: HISAT2 alignment and BWA-mem realignment of soft-clipped and/or unaligned reads. A) F-Measure of calls, and B) Percentage of true positive calls shared by or exclusive to Manta and Delly, in fast and normal mode for multiple deletion variant sizes.

A



B

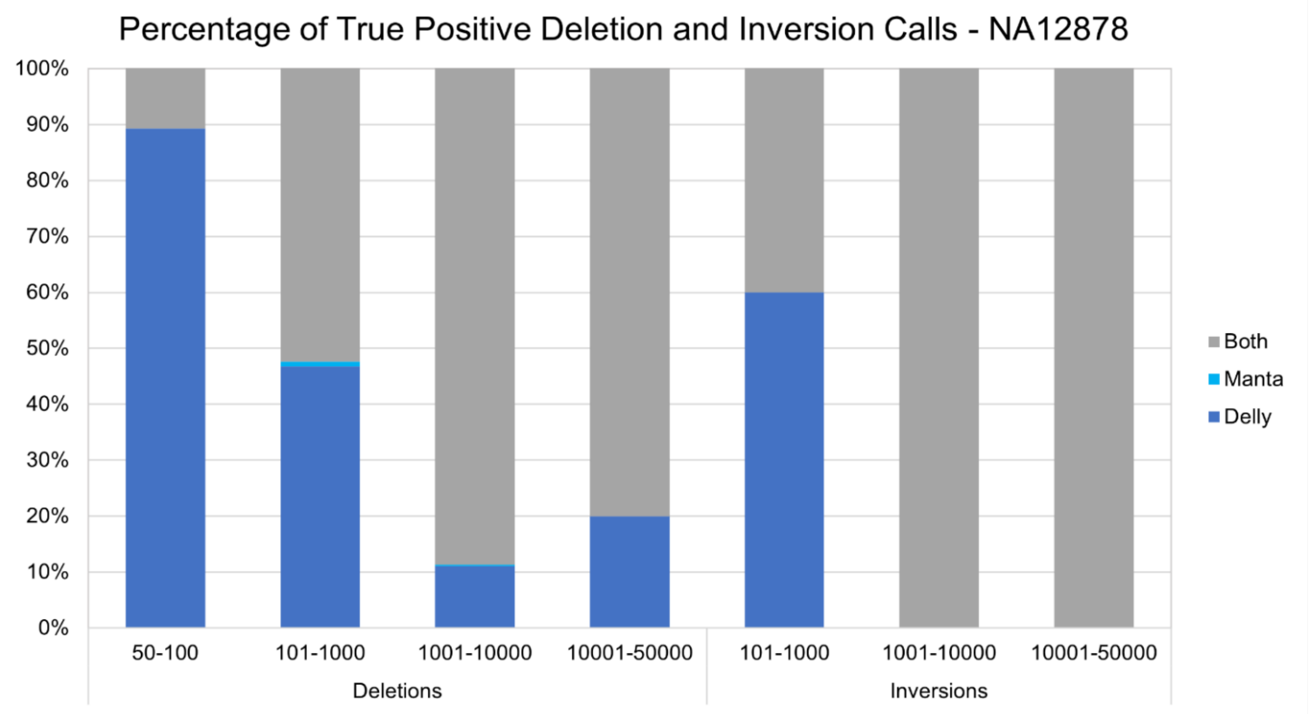
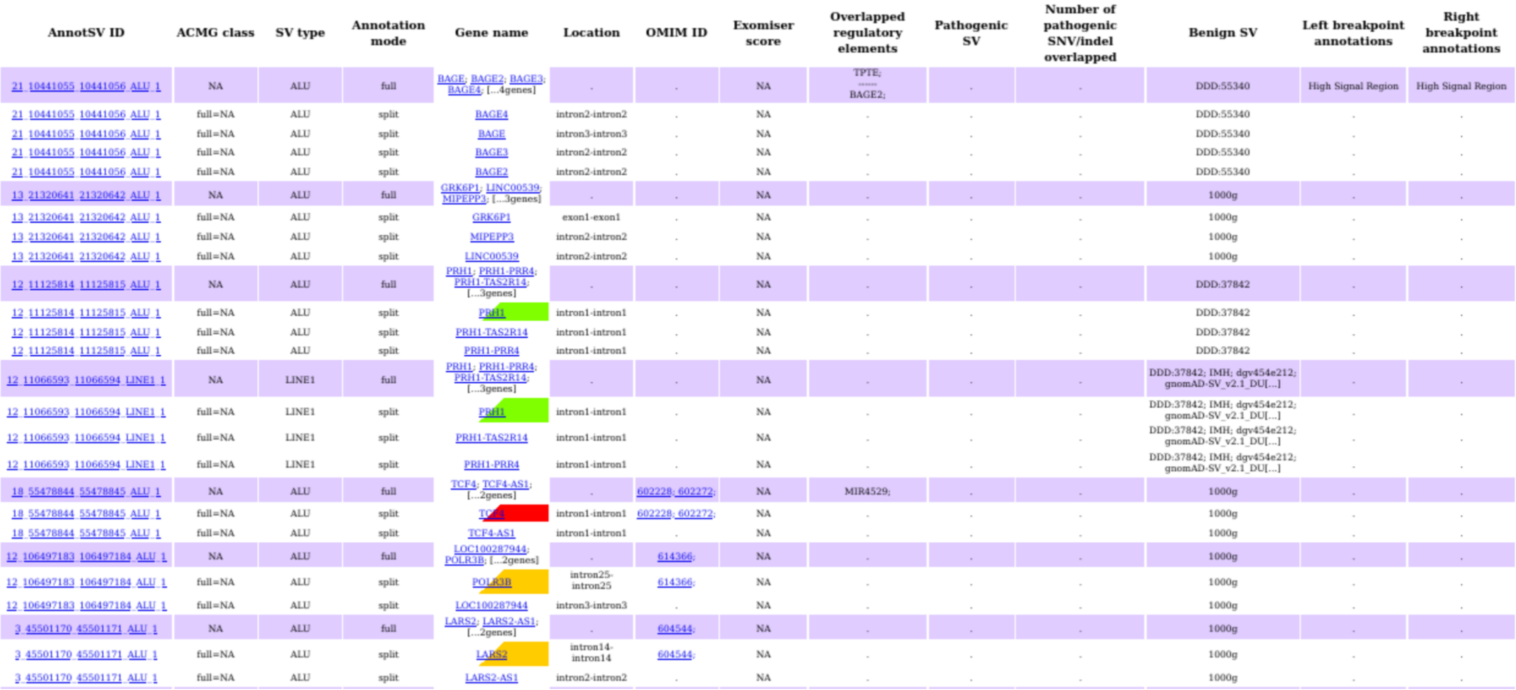


Figure A5. Deletion and inversion SV calling performance of Manta and Delly on simulated whole genome sequencing reads of NA12878 generated with VISOR. A) Precision of calls, and B) Percentage of true positive calls shared by or exclusive to Manta and Delly, for multiple deletion and inversion variant sizes.



AnnotSV ID	ACMG class	SV type	Annotation mode	Gene name	Location	OMIM ID	Exomiser score	Overlapped regulatory elements	Pathogenic SV	Number of pathogenic SNV/indel overlapped	Benign SV	Left breakpoint annotations	Right breakpoint annotations
21_10441055_10441056_ALU_1	NA	ALU	full	BAGE; BAGE2; BAGE3; BAGE4; [...4genes]	.	.	NA	TPTE; ------ BAGE2;	.	.	DDD:55340	High Signal Region	High Signal Region
21_10441055_10441056_ALU_1	full=NA	ALU	split	BAGE4	intron2-intron2	.	NA	.	.	.	DDD:55340	.	.
21_10441055_10441056_ALU_1	full=NA	ALU	split	BAGE	intron3-intron3	.	NA	.	.	.	DDD:55340	.	.
21_10441055_10441056_ALU_1	full=NA	ALU	split	BAGE3	intron2-intron2	.	NA	.	.	.	DDD:55340	.	.
21_10441055_10441056_ALU_1	full=NA	ALU	split	BAGE2	intron2-intron2	.	NA	.	.	.	DDD:55340	.	.
13_21320641_21320642_ALU_1	NA	ALU	full	GRK6P1; LINC00539; MIPEPP3; [...3genes]	.	.	NA	.	.	.	1000g	.	.
13_21320641_21320642_ALU_1	full=NA	ALU	split	GRK6P1	exon1-exon1	.	NA	.	.	.	1000g	.	.
13_21320641_21320642_ALU_1	full=NA	ALU	split	MIPEPP3	intron2-intron2	.	NA	.	.	.	1000g	.	.
13_21320641_21320642_ALU_1	full=NA	ALU	split	LINC00539	intron2-intron2	.	NA	.	.	.	1000g	.	.
12_11125814_11125815_ALU_1	NA	ALU	full	PRH1; PRH1-PRR4; PRH1-TAS2R14; [...3genes]	.	.	NA	.	.	.	DDD:37842	.	.
12_11125814_11125815_ALU_1	full=NA	ALU	split	PRH1	intron1-intron1	.	NA	.	.	.	DDD:37842	.	.
12_11125814_11125815_ALU_1	full=NA	ALU	split	PRH1-TAS2R14	intron1-intron1	.	NA	.	.	.	DDD:37842	.	.
12_11125814_11125815_ALU_1	full=NA	ALU	split	PRH1-PRR4	intron1-intron1	.	NA	.	.	.	DDD:37842	.	.
12_11066593_11066594_LINE1_1	NA	LINE1	full	PRH1; PRH1-PRR4; PRH1-TAS2R14; [...3genes]	.	.	NA	.	.	.	DDD:37842; IMH; dgv454e212; gnomAD-SV_v2.1_DU[...]	.	.
12_11066593_11066594_LINE1_1	full=NA	LINE1	split	PRH1	intron1-intron1	.	NA	.	.	.	DDD:37842; IMH; dgv454e212; gnomAD-SV_v2.1_DU[...]	.	.
12_11066593_11066594_LINE1_1	full=NA	LINE1	split	PRH1-TAS2R14	intron1-intron1	.	NA	.	.	.	DDD:37842; IMH; dgv454e212; gnomAD-SV_v2.1_DU[...]	.	.
12_11066593_11066594_LINE1_1	full=NA	LINE1	split	PRH1-PRR4	intron1-intron1	.	NA	.	.	.	DDD:37842; IMH; dgv454e212; gnomAD-SV_v2.1_DU[...]	.	.
18_55478844_55478845_ALU_1	NA	ALU	full	TCF4; TCF4-AS1; [...2genes]	.	602228; 602272;	NA	MIR4529;	.	.	1000g	.	.
18_55478844_55478845_ALU_1	full=NA	ALU	split	TCF4	intron1-intron1	602228; 602272;	NA	.	.	.	1000g	.	.
18_55478844_55478845_ALU_1	full=NA	ALU	split	TCF4-AS1	intron1-intron1	.	NA	.	.	.	1000g	.	.
12_106497183_106497184_ALU_1	NA	ALU	full	LOC100287944; POLR3B; [...2genes]	.	614366;	NA	.	.	.	1000g	.	.
12_106497183_106497184_ALU_1	full=NA	ALU	split	POLR3B	intron25-intron25	614366;	NA	.	.	.	1000g	.	.
12_106497183_106497184_ALU_1	full=NA	ALU	split	LOC100287944	intron3-intron3	.	NA	.	.	.	1000g	.	.
3_45501170_45501171_ALU_1	NA	ALU	full	LARS2; LARS2-AS1; [...2genes]	.	604544;	NA	.	.	.	1000g	.	.
3_45501170_45501171_ALU_1	full=NA	ALU	split	LARS2	intron14-intron14	604544;	NA	.	.	.	1000g	.	.
3_45501170_45501171_ALU_1	full=NA	ALU	split	LARS2-AS1	intron2-intron2	.	NA	.	.	.	1000g	.	.

Figure A6. Screengrab of the transposable element report generated by DNAscan2 using knotAnnotSV for 1 Project MinE control sample.

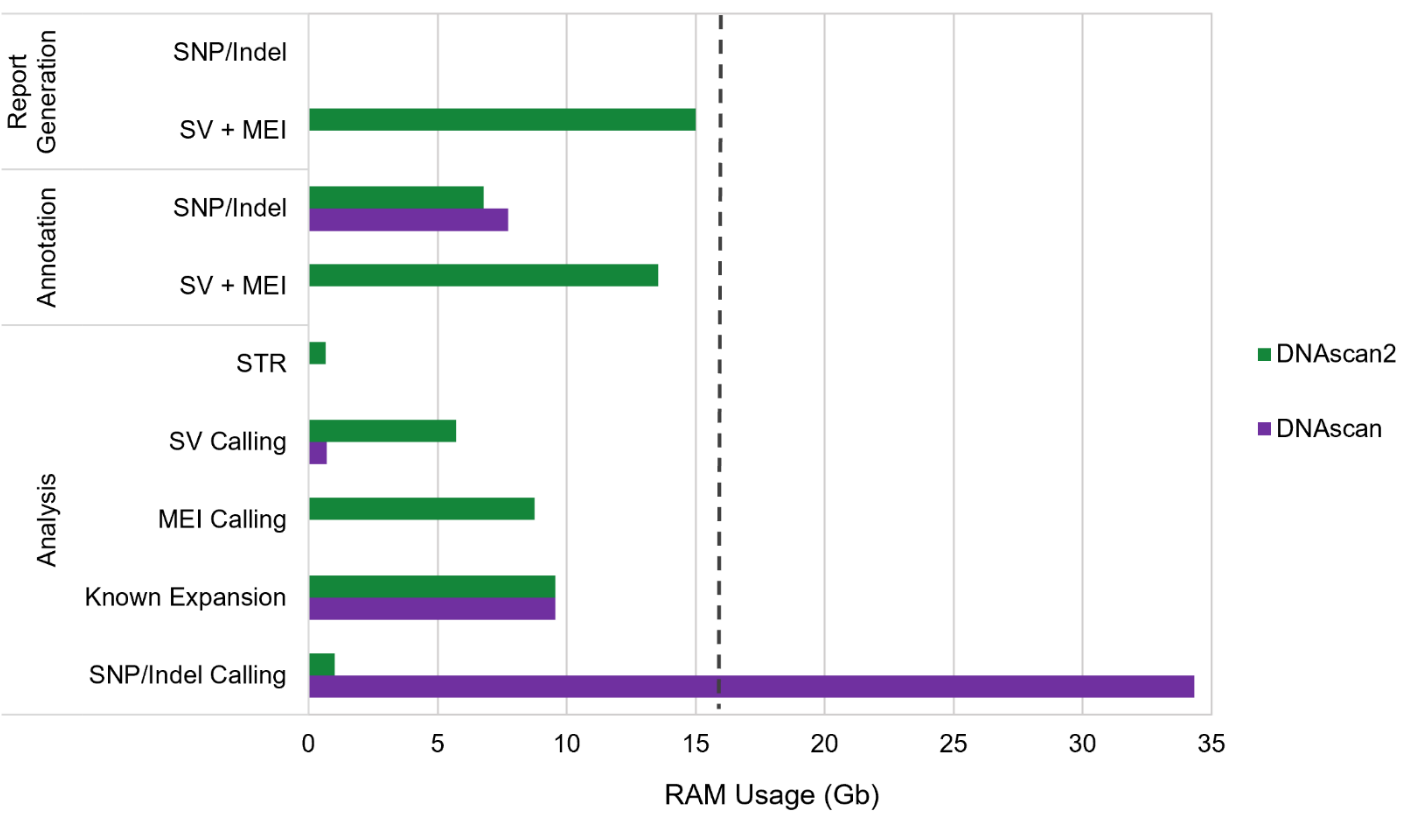


Figure A7. Comparison of average memory usage (in gigabytes) between DNAscan and DNAscan2 for each step following alignment, using whole genomes of 10 Project MinE control samples. The steps were categorised by the main stage of the workflow (Analysis, Annotation, Report Generation). The dotted line represents the average RAM of a standard midrange personal computer.

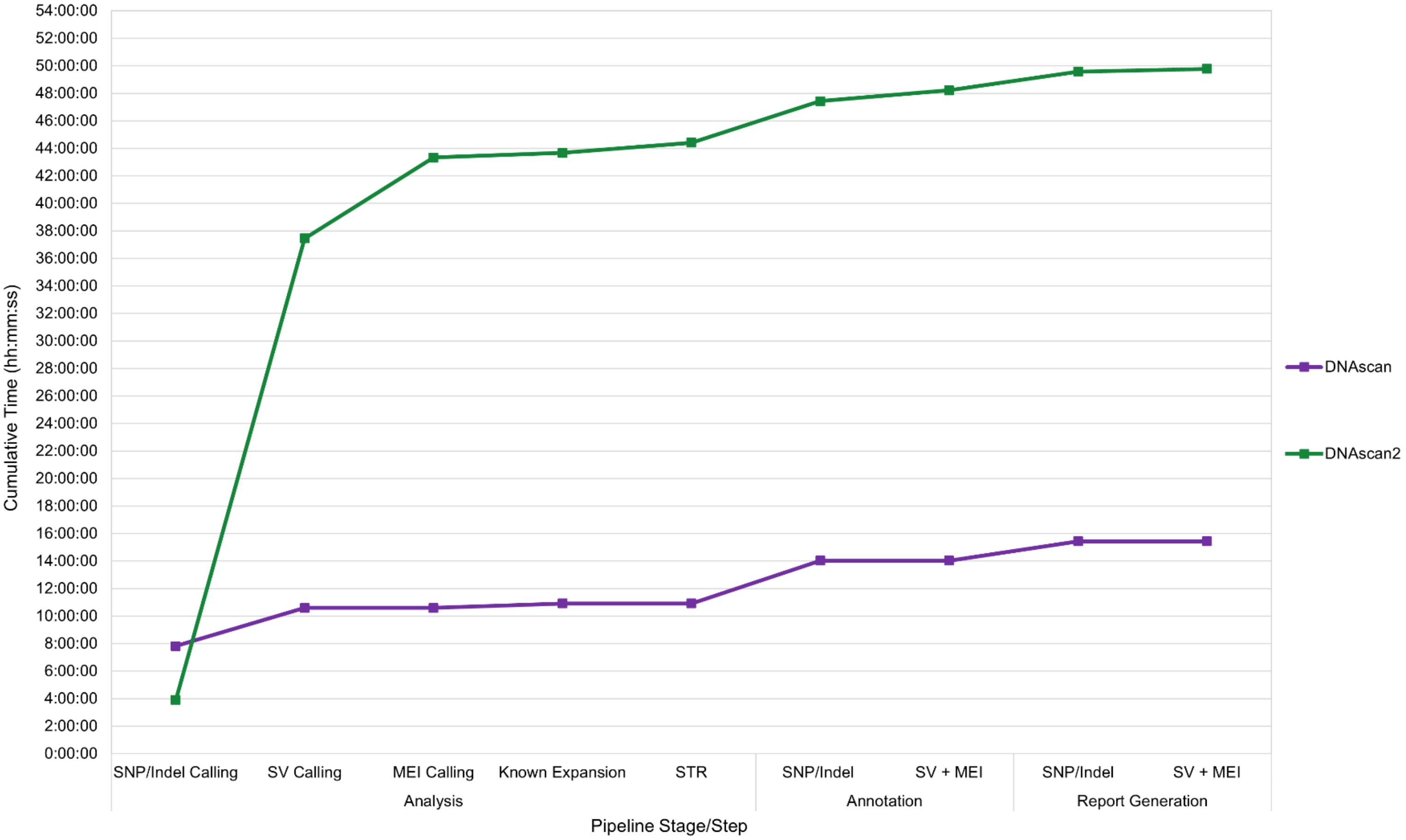
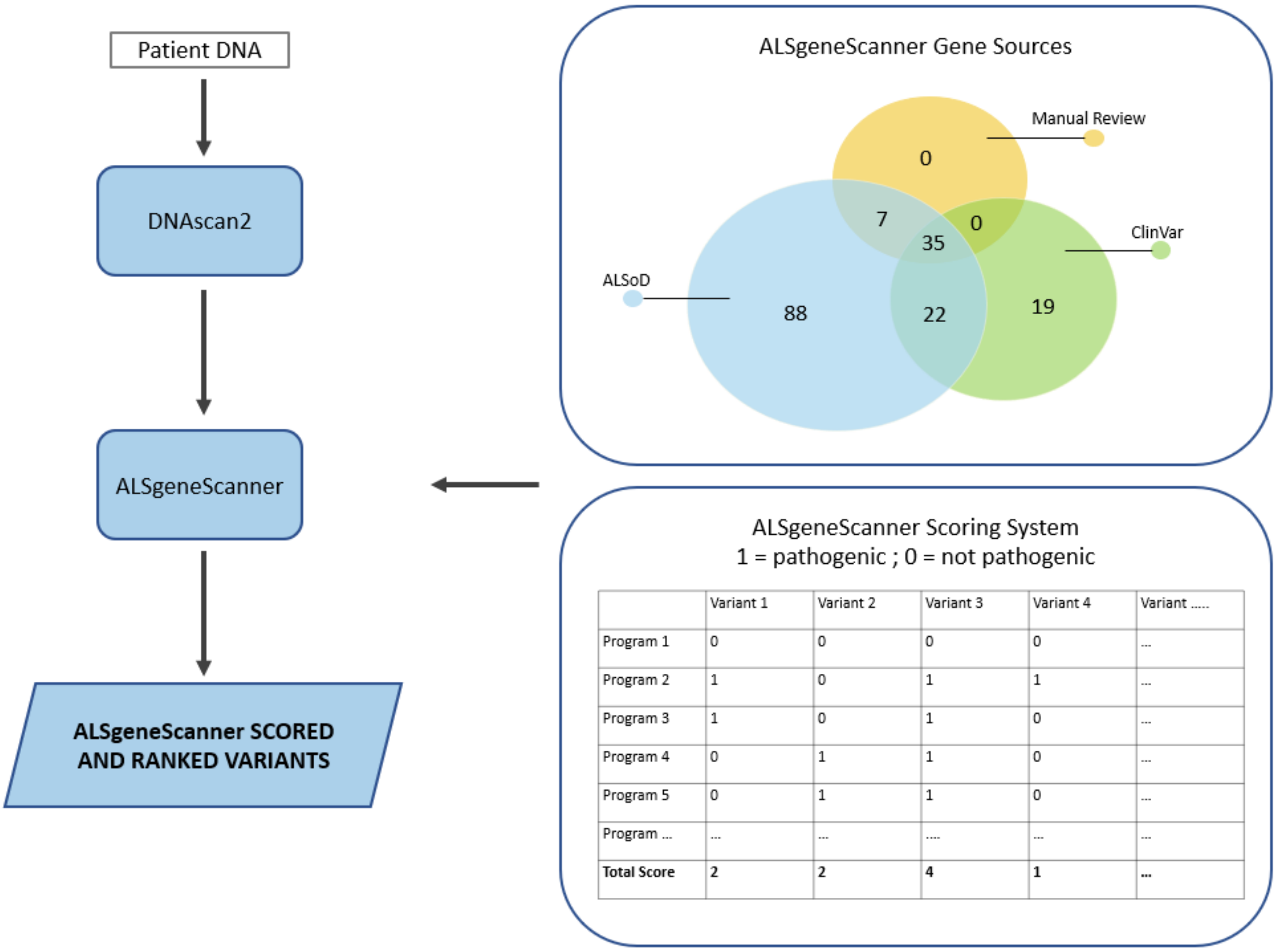


Figure A8. Average cumulative elapsed time (in hours:minutes:seconds format) between DNAscan and DNAscan2 for each step following alignment, using whole genomes of 10 Project MinE control samples. The steps were categorised by the main stage of the workflow (Analysis, Annotation, Report Generation).



	Variant 1	Variant 2	Variant 3	Variant 4	Variant .....
Program 1	0	0	0	0	...
Program 2	1	0	1	1	...
Program 3	1	0	1	0	...
Program 4	0	1	1	0	...
Program 5	0	1	1	0	...
Program ...	...	...	....	...	...
Total Score	**2**	**2**	**4**	**1**	**...**

Figure A9. The ALSgeneScanner scoring module of DNAscan2. After the main DNAscan pipeline has completed, ALSgeneScanner takes SNV and indel annotation files as input and keeps only the variants whose genes are identified to be associated with ALS (171 in total, from three different sources). Afterwards, each of these filtered variants are scored based on the pathogenicity prediction assigned by each of the 13 prediction databases (SIFT, Polyphen-2 HDIV, PolyPhen-2 HVAR, LRT, MutationTaster, MutationAssessor, FATHMM, PROVEAN, FATHMM-mkl coding, MetaSVM, CADD and Intervar) and then ranked based on the total cumulative score from all programs.

Chapter 6

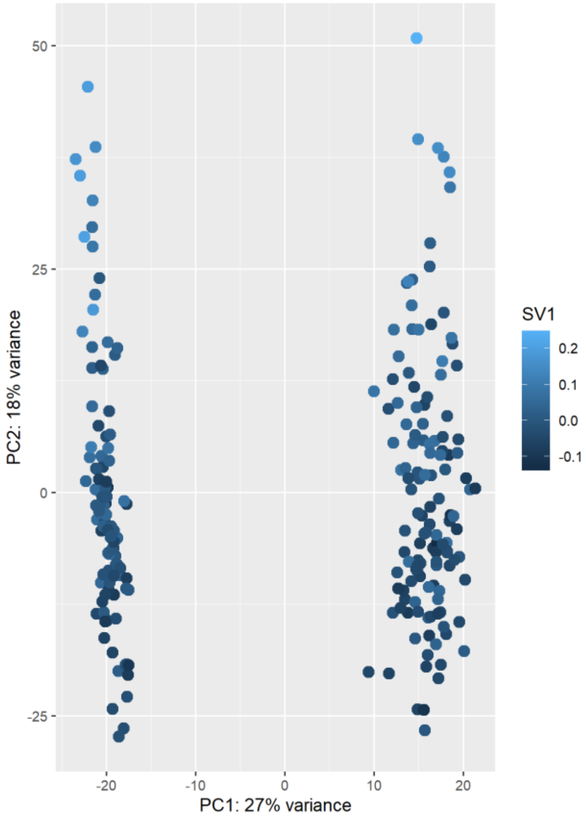


Figure A10. Principal component analysis of 234 samples from a total of 132 individuals in the TargetALS dataset (112 ALS cases and 20 controls) for the surrogate variable derived with SVA analysis. The inclusion of the surrogate variable accounted for the natural grouping of the TargetALS dataset.

Chapters 6 and 7

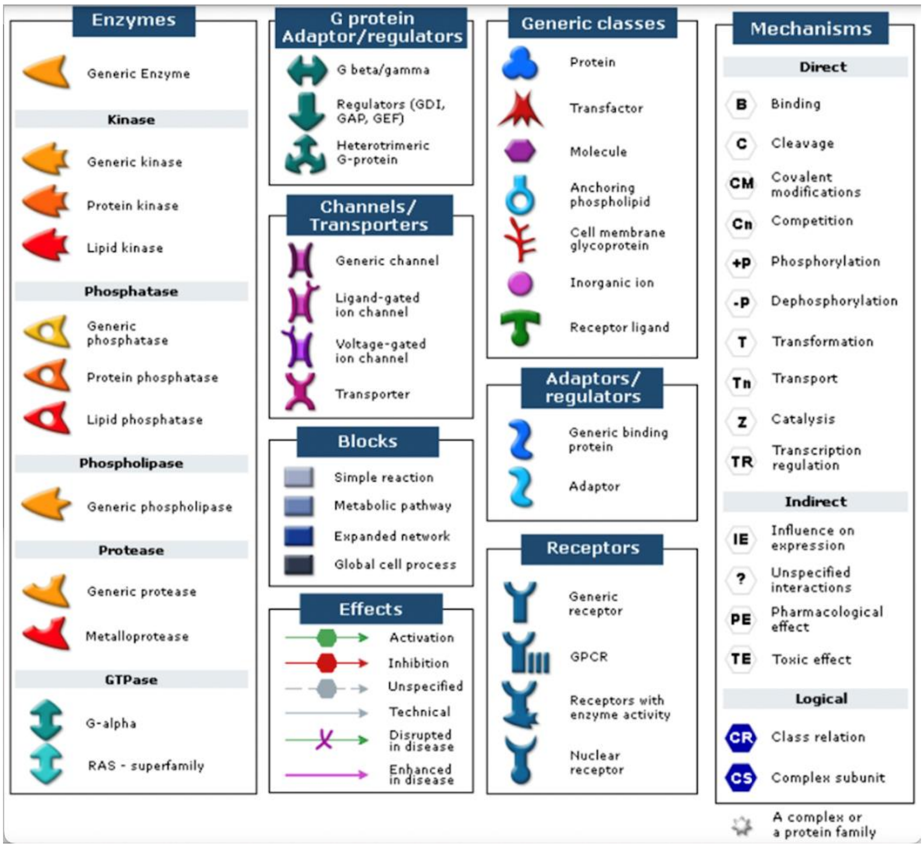


Figure A11. Key of the MetaCore pathway network symbols.

Chapter 7

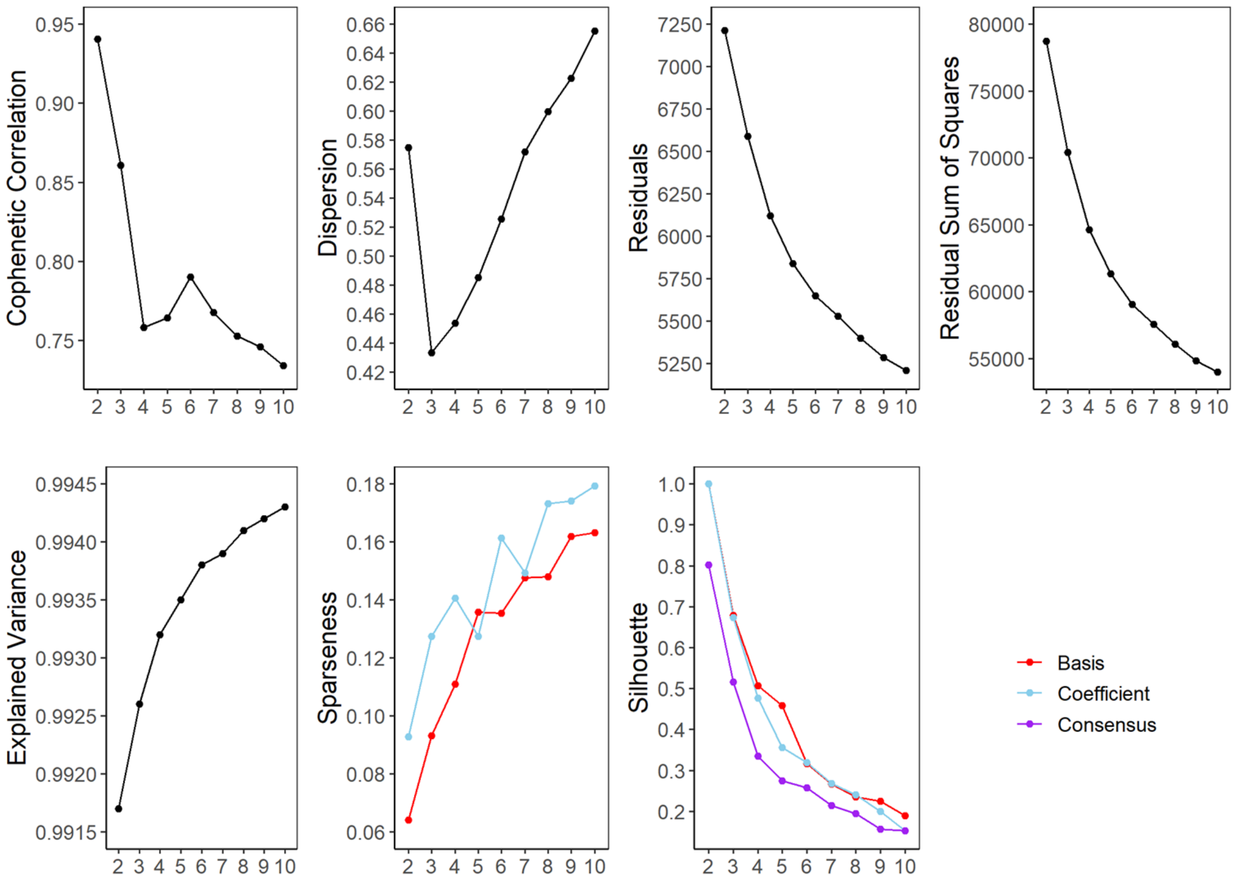


Figure A12. Cluster estimation metrics produced when running nsNMF with k = 2-10, 100 runs and 1000 iterations.

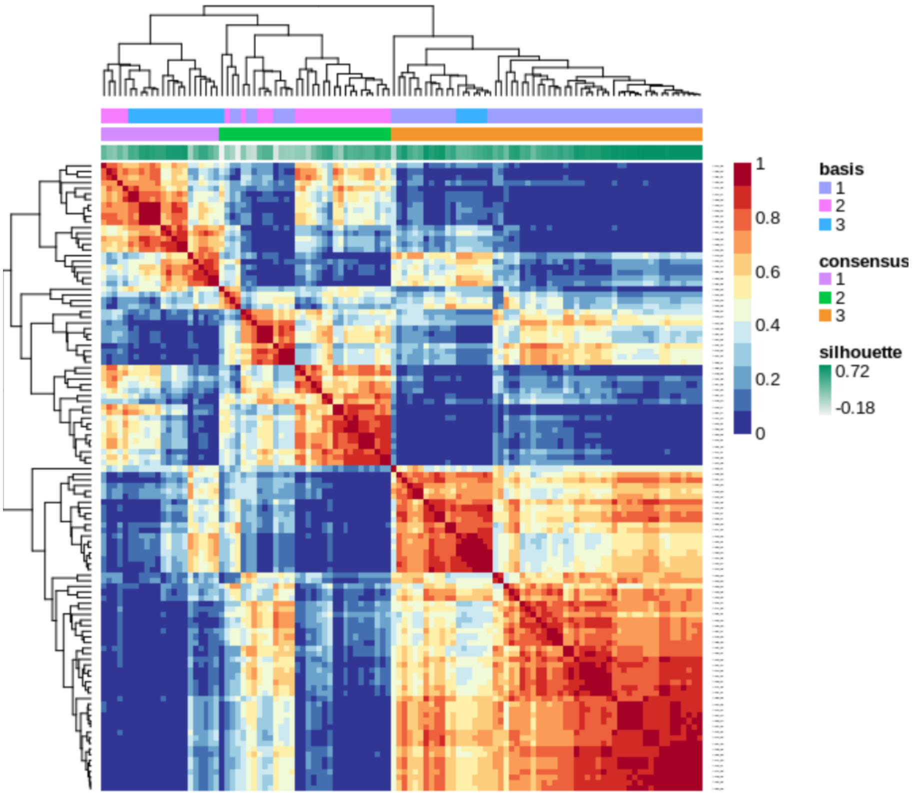
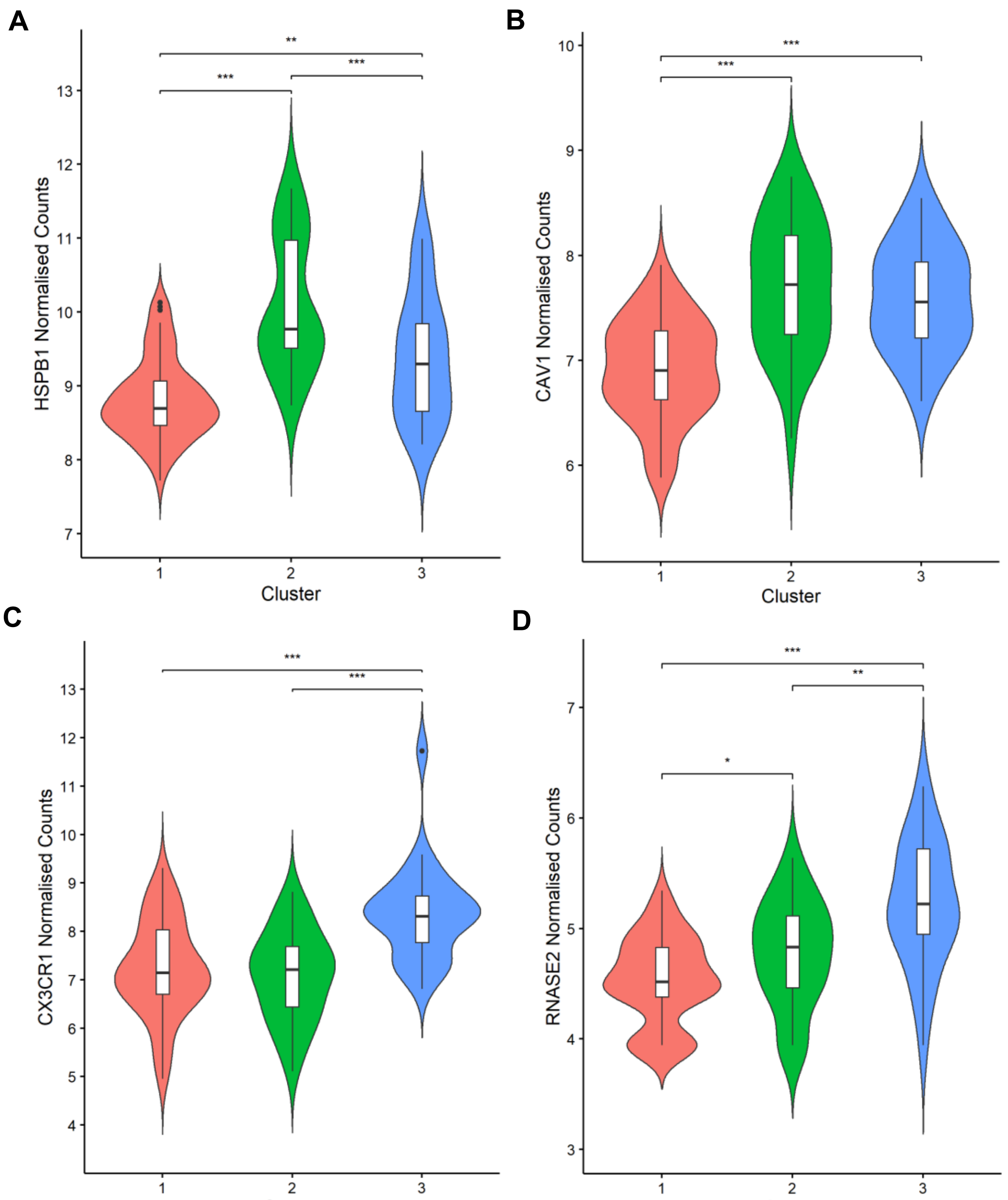


Figure A13. Cluster construction with the KCL BrainBank sample matrix, sorted by consensus, for the KCL BrainBank dataset. The nsNMF clustering algorithm was run with k = 3, 100 runs and 1000 iterations.



E

Informative ALS-linked Gene	***Cluster***	***One-Way ANOVA (F-statistic, p-value)***	***Post-Hoc Analysis (Tukey p-value)***
HSPB1	1	31.45, **1.9E-11**	1 vs 2; **<0.001**, 1 vs 3; **4.9E-03**, 2 vs 3; **<0.001**
CAV1	2	28.12, **1.6E-10**	1 vs 2; **<0.001** , 1 vs 3; **<0.001**, 2 vs 3; 0.58
CX3CR1	3	14.72; **2.3E-06**	1 vs 2; 0.94 **,** 1 vs 3; **1.2E-05**, 2 vs 3; **7.2E-05**
RNASE2	3	19.65, **5.5E-08**	1 vs 2; **0.036**, 1 vs 3; **< 0.001**, 2 vs 3; **4.5E-03**

*Figure A14. Comparison of the expression of the four identified ALS-related genes. Genes are as follows: A) HSPB1, B) CAV1, C) CX3CR1, and D) RNASE2, in each cluster. Asterisks represent significance levels of * <0.05, ** < 0.01, *** < 0.0001 with post-hoc Tukey's test after running one-way ANCOVA corrected for sex, age at death and post-mortem delay. E) Summary of the ANCOVA results assessing the differences in gene expression levels in ALS-linked genes between clusters. Bold p-values denote significance (< 0.05).*

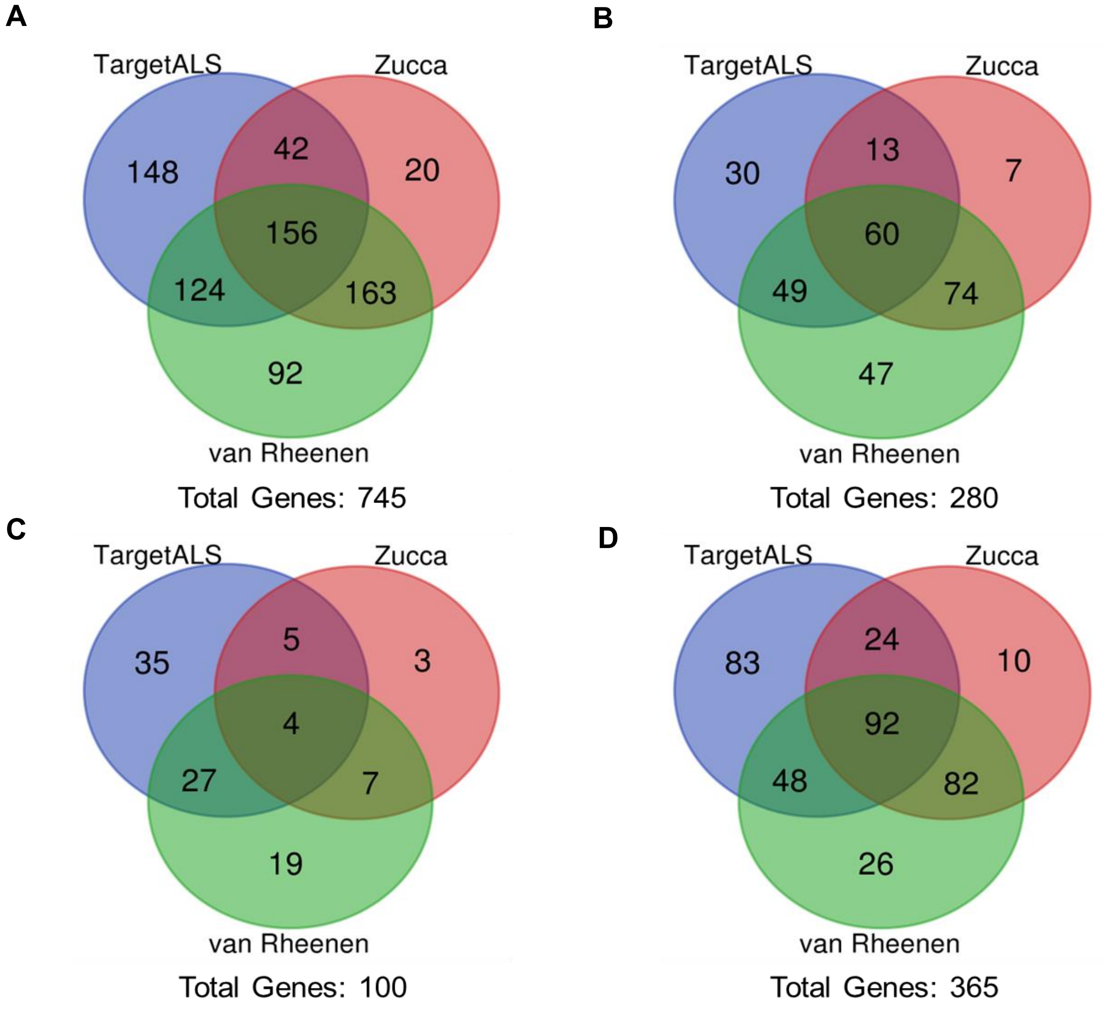


Figure A15. Union and intersection of genes for the three case datasets. A) All genes (TargetALS: 470, Zucca: 381, van Rheenen: 535), B) Cluster one genes, C) Cluster two genes and D) Cluster three genes. The 'total genes' at the bottom of each panel represents the sum of all genes in each Venn diagram.

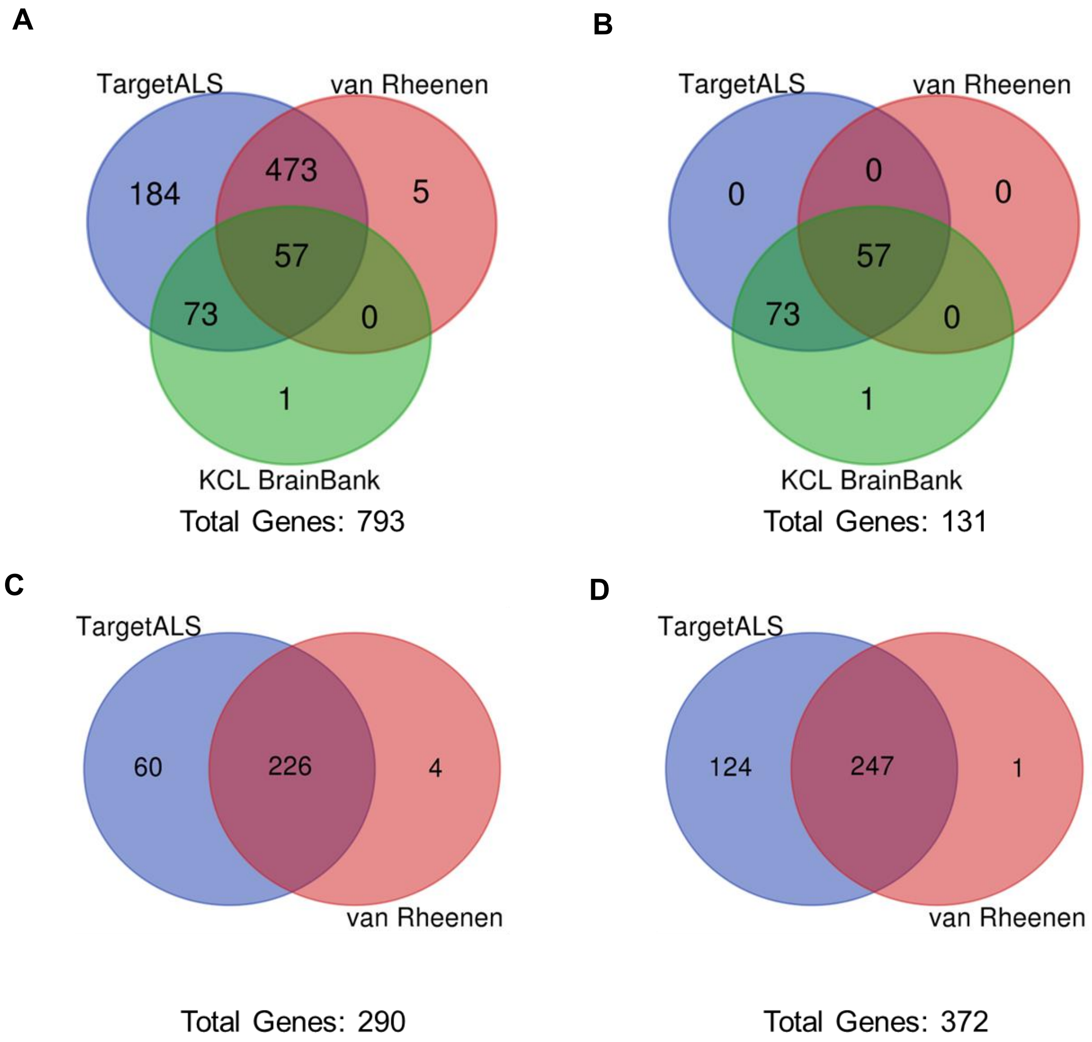


Figure A16. Union and intersection of genes for the three control datasets. A) All genes (KCL BrainBank: 787, TargetALS: 787, van Rheenen: 535), B) Cluster one genes, C) Cluster two genes and D) Cluster three genes. The 'total genes' at the bottom of each panel represents the sum of all genes in each Venn diagram.

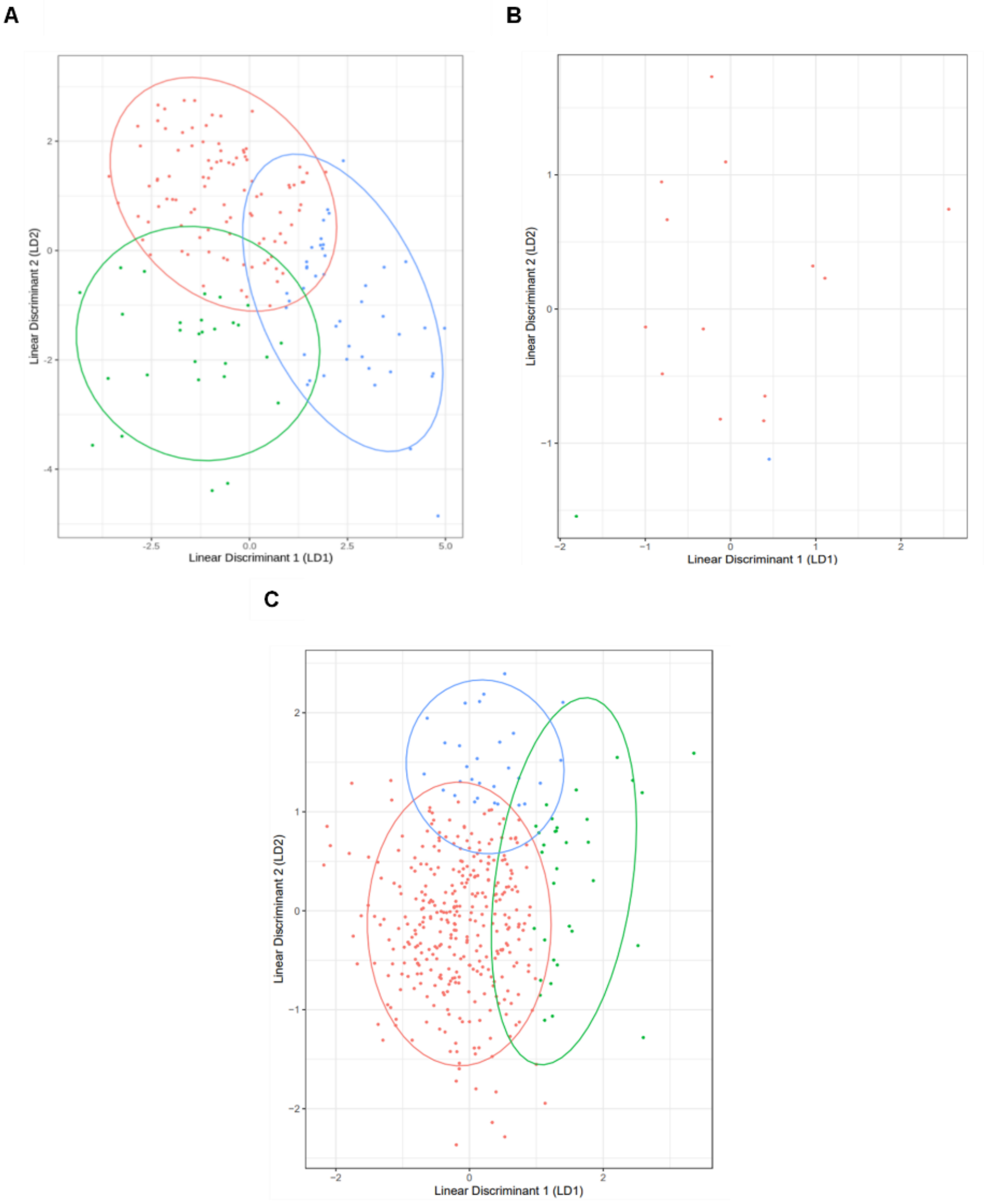


Figure A17. Sample assignment of A) TargetALS, B) Zucca, and C) van Rheenen case datasets to the KCL BrainBank case-defined clusters. Linear discriminant analysis models were trained on the KCL sample assignments and informative genes shared with each dataset. The number of genes for each dataset are as follows: A) 470, B) 381 and C) 535. Red: Cluster 1; Green: Cluster 2, Blue: Cluster 3.

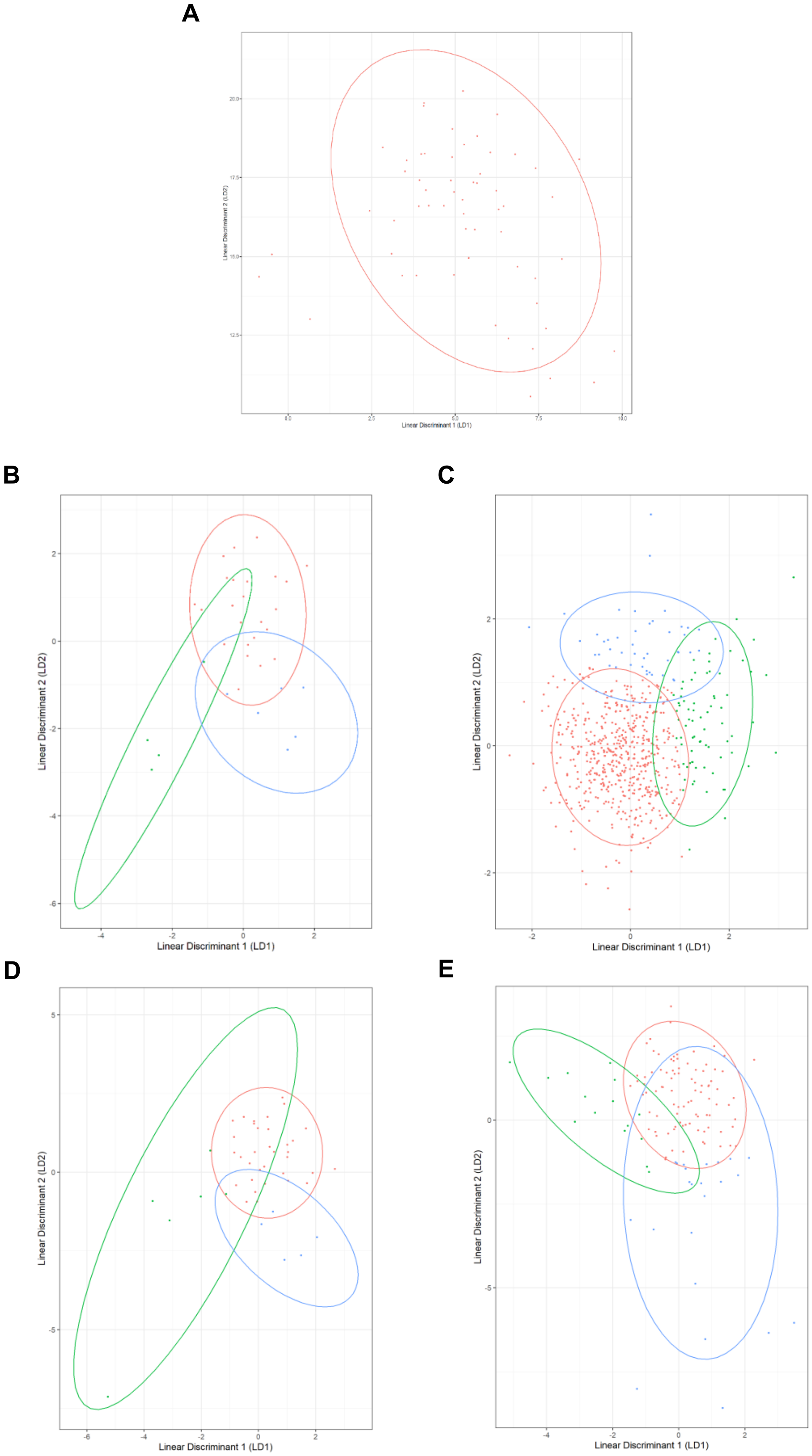


Figure A18. Sample assignment of A) KCL BrainBank controls, B) TargetALS controls, C) van Rheenen controls, D)TargetALS occipital cortex and E) TargetALS cerebellum control datasets to the KCL BrainBank case-defined clusters. Linear discriminant analysis models were trained on the KCL sample assignments and informative genes shared with each dataset. Red: Cluster 1; Green: Cluster 2, Blue: Cluster 3.

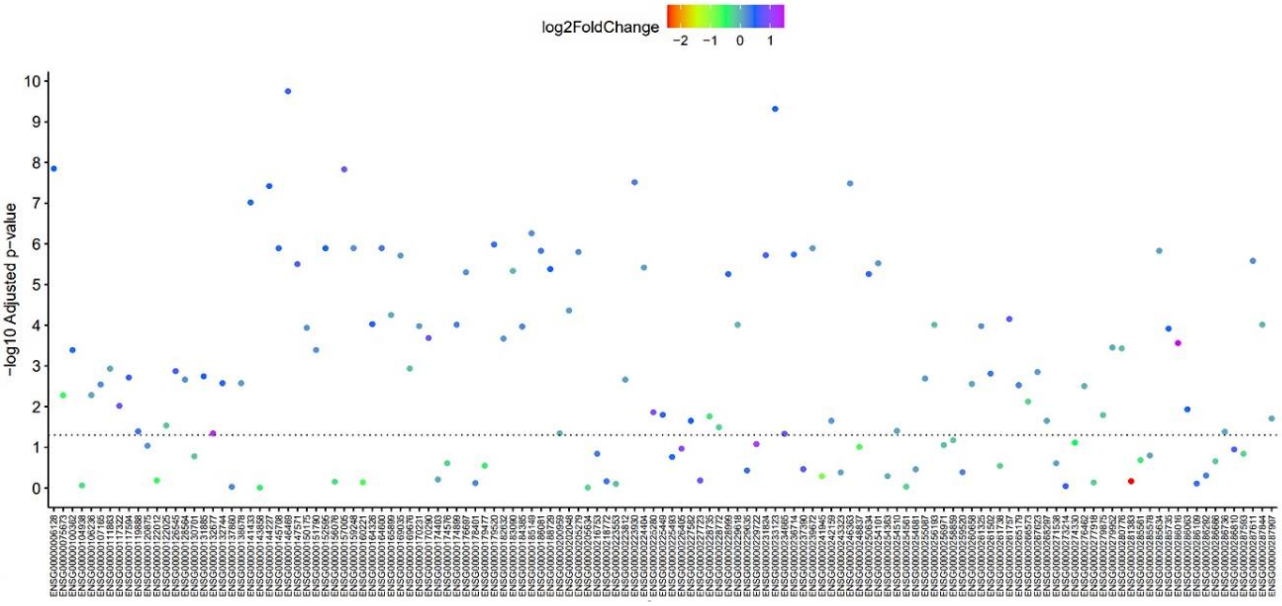


Figure A19. Dot chart demonstrating significant differences in expression of 87 of the 131 cluster one genes between KCL BrainBank cases and controls, coloured by log2 fold change. An increase in log2 fold change means the gene is upregulated in cases, and vice versa. The dotted line represents the -log10 adjusted p-value that corresponds to a Benjamini-Hochberg p-value of 0.05.

Appendix II. Tables

Chapter 4

Dependency Category	**Dependency Details**	**Required Storage (Gb)**	
		hg19	**hg38**
References	Reference Genome and Index	3.16	3.27
	BWA-mem Index	5.42	5.62
	HISAT2 Index	4.37	4.66
Databases and Catalogues	ExpansionHunter Variant Catalogue	< 0.01	< 0.01
	ANNOVAR Databases*	91.34	91.67
	AnnotSV Databases**	3.31	3.31
Tools	Conda Installation	0.10	0.10
	Conda-Installed Tools	1.50	1.50
	Manually Installed Tools	12.01	12.01
Miscellaneous	Additional Disk Space***	20.00	20.00
Total free space needed:		**141.21**	**142.14**

*Table A1. Storage requirements of all dependencies necessary to run DNAscan2, divided by reference version. *Default DNAscan2 ANNOVAR databases (refGene, dbnsfp33a, clinvar_20210501, intervar_20180118, avsnp147, exac03,1000g2015aug, gnomad211_genome) were used. **AnnotSV was only run using databases that do not require a commercial licence to download. ***This refers to the additional overhead storage space that MELT requires to temporarily hold intermediate files.*

Pipeline Stage	Tool	Tool Version	Installation Method	Reference
Alignment	BWA-mem	0.7.17	Conda	(H. Li, 2013)
	HISAT2	2.2.1	Conda	(Kim et al., 2019)
	Samblaster	0.1.26	Conda	(Faust & Hall, 2014)
	Sambamba	0.7.1	Conda	(Tarasov et al., 2015)
Analysis	Strelka2	2.9.10	Manual Download	(Kim et al., 2018)
	Manta	1.6.0	Manual Download	(X. Chen et al., 2016b)
	Delly	0.8.3	Conda	(Rausch et al., 2012)
	MELT	2.2.2	Manual Registration and Download	(Gardner et al., 2017)
	ExpansionHunter	3.2.2	Conda	(Dolzhenko et al., 2019)
	ExpansionHunter Denovo	0.9.0	Manual Download	(Dolzhenko et al., 2020)
	SURVIVOR	1.0.7	Manual Download	(Jeffares et al., 2017)
Annotation	ANNOVAR	08/06/2019	Manual Registration and Download	(K. Wang et al., 2010)
	AnnotSV	3.0.9	Manual Download	(Geoffroy et al., 2018)
Report Generation	FastQC	0.11.9	Conda	(FastQC, no date)
	MultiQC	1.10.1	Conda	(Ewels et al., 2016)
	knotAnnotSV	1.0.0	Manual Download	(Geoffroy et al., 2021)
General	Miniconda	4.10.3	Manual Download	(Anaconda Software Distribution. (2022))
	Perl	5.26.2	Conda	
	Python	3.8	Conda	
	Biopython	1.78	Conda	(Cock et al., 2009)
	Pysam	0.16.0.1	Conda	(*Pysam*, 2014/2021)
	SAMtools	1.9	Conda	(H. Li et al., 2009)
	BEDTools	2.25.0	Conda	(Quinlan & Hall, 2010)
	BCFtools	1.9	Conda	(H. Li, 2011)
	VCFtools	0.1.16	Conda	(Danecek et al., 2011)
	PySimpleGUI*	4.40.0	Conda	(*PySimpleGUI*, n.d.)
	Snakemake**	≥ 5.32.1	Conda	(Mölder et al., 2021)

*Table A2. List of tools and corresponding versions that DNAscan2 requires for each pipeline stage. 'General' refers to tools which are necessary for the basic execution of DNAscan2. The 'Installation Method' column lists the easiest way to obtain the software to avoid software version clashes. *This is only required if you want to run DNAscan2 as a standalone application and not as a command-line tool. **This is only required if you want to deploy DNAscan2 on a high performance computing facility or execute the workflow in a multi-sample parallel fashion.*

Variant Calling Metrics per Variant Type	**DNAscan**	**DNAscan2**
SNV/Indel Calling		
- Total called variants	29192123	30000110
- Total called and filtered variants	4285989	4611498
- Number of filtered non-synonymous variants	10165 (0.237%)	10727 (0.250%)
- Number of filtered synonymous variants	21304 (0.497%)	22285 (0.483%)
Structural Variant Calling		
- Total called variants	28831	56970
• Deletions	8478	16069
• Insertions	6455	6189
• Inversions	3410	7280
• Duplications	4031	9285
• Translocations	6457	18147
MEI Calling		
- Total called variants	N/A	1694
• ALU	N/A	1287
• SVA	N/A	148
• LINE1	N/A	259
Expansion/Repeat Scanning		
- Total called and genotyped expansions	37	37
- Total Identified STR loci	N/A	3043

Table A3. Comparison of the variant calling power of DNAscan and DNAscan2 for several variant classes. 'N/A' represents tasks that could not be performed in DNAscan due to lack of available software. Synonymous and non-synonymous SNV and indel variants were obtained from the corresponding refGene annotation classification. Values here denote the average number of variant types identified using whole genomes of 10 Project MinE control samples.

	Pipeline Stage	Pipeline Step	Elapsed Time (hh:mm:ss)	CPU Time (hh:mm:ss)	RAM Usage (Gb)	MaxDiskRead	MaxDiskWrite
DNAscan	Analysis	SNV/Indel	07:48:52	32:10:31	34.34	144046	71073
		SV	02:46:41	11:06:44	0.69	827571	338
		MEI	N/A	N/A	N/A	N/A	N/A
		Known Expansion	00:19:48	01:19:10	9.55	23669	1
		STR	N/A	N/A	N/A	N/A	N/A
	Annotation	SNV/Indel	03:06:26	12:25:44	7.74	402697	71254
		SV + MEI	N/A	N/A	N/A	N/A	N/A
	Report Generation	SNV/Indel	01:24:58	05:39:51	0.02	1953279	8
		SV + MEI	N/A	N/A	N/A	N/A	N/A
DNAscan2	Analysis	SNV/Indel	03:54:10	15:36:41	1.00	81794	9294
		SV	33:32:53	133:53:30	5.70	1222044	55738
		MEI	05:53:05	23:32:20	8.75	2710405	38612
		Known Expansion	00:19:48	01:19:10	9.55	23669	1
		STR	00:44:51	02:59:24	0.66	28505	30
	Annotation	SNV/Indel	03:00:48	12:03:12	6.78	353781	35076
		SV + MEI	00:47:15	03:08:58	13.54	8653	8386
	Report Generation	SNV/Indel	01:22:17	05:29:06	0.02	1840523	10
		SV + MEI	00:11:52	00:47:27	15.00	980	2331

Table A4. Comparison of the average elapsed time of DNAscan and DNAscan2 for each step following alignment, using whole genomes of 10 Project MinE control samples. The steps were categorised by the main stage of the workflow (Analysis, Annotation, Report Generation). 'N/A' represents tasks that could not be performed in DNAscan due to lack of available software.

Gene Name	Chromosome	Sources of Identification			Reference
		Manual Review	***ALSoD***	***ClinVar***	
DNAJC7	17q21.2	✓			(Farhan et al., 2019)
ERBB4	2q34	✓			(Takahashi et al., 2013)
ANXA11	10q22.3		✓		(Smith et al., 2017)
ARPP21	3p22.3		✓		(Cooper-Knock et al., 2019)
ATXN1	6p22.3		✓		(Tazelaar et al., 2020)
C21orf2	21q22.3		✓	✓	(van Rheenen et al., 2016b)
CAV1	7q31.2		✓		(Cooper-Knock et al., 2021)
CAV2	7q31.2		✓		(Cooper-Knock et al., 2021)
CCNF	16p13.3		✓	✓	(Williams et al., 2016)
DNMT3A	2p23.3		✓		(Chestnut et al., 2011)
DNMT3B	20q11.21		✓		(Chestnut et al., 2011)
ENAH	1q42.12		✓		(Cirulli et al., 2015)
EPHA3	3p11.1		✓		(Uyan et al., 2013)
ERLIN1	10q24.31		✓	✓	(Tunca et al., 2018)
GLT8D1	3p21.1		✓		(Cooper-Knock et al., 2019)
GPX3	5q33.1		✓		(Benyamin et al., 2017)
KIF5A	12q13.3		✓		(Nicolas et al., 2018)
MOBP	3p22.1		✓	✓	(van Rheenen et al., 2016b)
NEFL	8p21.2		✓	✓	(Benatar et al., 2018)
NEK1	4q33		✓		(Kenna et al., 2016)
PGRN	17q21.31		✓		(Philips et al., 2010)
PNPLA6	19p13.2		✓	✓	(Pensato et al., 2020)
RFTN1	3p24.3		✓		(Zhai et al., 2009)
SCFD1	14q12		✓	✓	(van Rheenen et al., 2016b)
TIA1	2p13.3		✓	✓	(Mackenzie et al., 2017)
UBQLN1	9q21.32		✓		(Wang, et al., 2020)
VRK1	14q32.2		✓	✓	(Nguyen et al., 2015)
CAPN14	2p23.1			✓	(Dekker et al., 2019)
CHRNA3	15q25.1			✓	(Sabatelli et al., 2009)
CHRNB4	15q25.1			✓	(Sabatelli et al., 2009)
CNTF	11q12.1			✓	(Laaksovirta et al., 2008)
CYLD	16q12.1			✓	(Dobson-Stone et al., 2020)
DDX20	1p13.2			✓	(Cacciottolo et al., 2019)
DYNC1H1	14q32.31			✓	(Scarlino et al., 2020b)
ELP3	8p21.1			✓	(Bento-Abreu et al., 2018)
EWSR1	22q12.2			✓	(Couthouis et al., 2012)
GARS1	7p14.3			✓	(Corcia et al., 2019)
GLE1	9q34.11			✓	(Kaneb et al., 2015)
MFN2	1p36.22			✓	(Wang et al., 2018)
MPZ	1q23.3			✓	(Bisogni et al., 2022)
NIPA1	15q11.2			✓	(Blauw, van Rheenen, et al., 2012b)
PLEKHG5	1p36.31			✓	(Gonzalez-Quereda et al., 2021)

PON1	7q21.3			✓	(Verde et al., 2019)
PON3	7q21.3			✓	(Saeed et al., 2006)
SCN11A	3p22.2			✓	(Castoro et al., 2018)
SLC52A3	20p13			✓	(Johnson et al., 2012)
SYNE1	6q25.2			✓	(Naruse et al., 2020)
TRPV4	12q24.11			✓	(Pensato et al., 2020)
UNC13A	19p13.11			✓	(Diekstra et al., 2012)

Table A5. New additions and/or reclassifications in the ALSgeneScanner database. Breakdown of identified gene sources are as follows: 2 manual review, 16 ALSoD, 9 ALSoD and ClinVar, and 22 ClinVar.

Chapter 5

Country	**Cases**	**Controls**	**Total**
Belgium	561	89	650
Netherlands	1854	1081	2935
France	251	40	291
Italy	55	0	55
US	435	80	515
UK	1445	453	1898
Turkey	618	150	768
Ireland	467	234	701
Israel	105	0	105
Portugal	53	19	72
Sweden	204	112	316
Switzerland	44	1	45
Spain	377	175	552
Total	**6469**	**2434**	**8903**

Table A6. Breakdown of Project MinE samples used for variant screening and burden analysis by country of sample collection.

Reference	Study Type	Discovery Method	Genetic Technology	Population (Country)	Sample Groups	Sex (M:F (Ratio))	Age (years (SD or range))	Diagnostic Criteria
(Figlewicz et al., 1994)	Case-Control	Candidate Gene/Region	PCR	France and America	Case: 356 SALS Control: 306 neurologically healthy unrelated individuals	-	-	Definite ALS (El Escorial)
(Vechio et al., 1996)	Case-Control	Candidate Gene/Region	PCR-SSCP	-	Case: 100 FALS + 75 SALS Control: 100 unrelated individuals	-	-	-
(Tomkins et al., 1998)	Case-Control	Candidate Gene/Region	PCR	UK	Case: 164 ALS Control: 207 age-matched unrelated individuals	-	-	-
(Al-Chalabi et al., 1999)	Case-Control	Candidate Gene/Region	PCR-SSCP	UK and Scandinavia (Denmark, Norway, Sweden and Finland)	Case: UK: 19 FALS + 188 SALS Scandinavia: 59 FALS + 264 SALS Control: UK: 219 age, sex and ethnicity-matched individuals Scandinavia: 228 age, sex and ethnicity-matched individuals	UK SALS: 109:79 (1.38) Scandinavian Cases: 194:129 (1.50)	UK SALS: 55.2 Scandinavian Cases: 61.5	-
(Garcia et al., 2006)	Case-Control	Candidate Gene/Region	PCR	America	Case: 100 FALS + 100 SALS Control: 100 neurologically healthy individuals	-	-	-
(Daoud et al., 2011)	Case-Control	Gene Panel	PCR	France and Canada	Case: 80 FALS + 110 SALS Control: 190 neurologically healthy individuals	104:86 (1.21)	55.4 ± 13.1	Definite or probable ALS (El Escorial)
(Couthouis et al., 2014)	Case-Control	Gene Panel	WES	America	Case: 242 SALS Control: 29 age-matched individuals	131:111 (1.18)	60 (44-82)	Definite, probable or possible ALS (El Escorial)

(Nakamura et al., 2016)	Case-Control	Gene Panel	WES + PCR	Japan	Case: 39 FALS + 469 SALS Control: 191 neurologically healthy individuals	298:210 (1.42)	62.1 (53.5-68.4)	Definite, probable, probable laboratory-supported or possible ALS (El Escorial)
(Krüger et al., 2016)	Case	Gene Panel	NGS	Germany	Case: 80 ALS	44:36 (1.22)	60.1 (29-88)	-
(Pang et al., 2017)	Case-Control	Gene Panel	WGS + WES	China (Hong-Kong)	Case: 8 FALS + 46 SALS Control: 699 volunteer individuals	FALS: 3:5 (0.60) SALS: 28:18 (1.56)	FALS: 41.4 ± 8.71 SALS: 58.1 ± 13.45	Definite, probable or probable laboratory-supported ALS (El Escorial)
(Morgan et al., 2017)	Case-Control	Gene Panel	WES + PCR	UK	Case: 131 FALS + 995 SALS Control: 613 neurologically healthy age and ethnicity-matched individuals	FALS: 67:64 (1.05) SALS: 567:428 (1.32)	FALS: 56 (24-85) SALS: 61 (25-88)	-
(Nishiyama et al., 2017)	Case	Gene Panel	WES + Sanger	Japan	51 FALS	-	-	El Escorial
(Garton et al., 2017)	Case	Variant Panel	WES	Australia	120 ALS	75:45 (1.67)	61 ± 10.1	Definite or probable ALS (revised El Escorial)
(Muller et al., 2018)	Case	Gene Panel	WES + PCR	Germany	171 FALS	-	-	El Escorial
(H. Zhang et al., 2018)	Case-Control	Gene Panel	WES + Sanger	China	Case: 311 SALS Control: 200 neurologically healthy individuals	199:112 (1.78)	51.92 ± 10.8	Definite, probable, probable laboratory-supported or possible ALS (El Escorial)

(Z.-J. Liu et al., 2019)	Case	Gene Panel	WES	China	24 FALS + 21 early-onset SALS	FALS: 13:11 (1.18) SALS: 13:8 (1.63)	FALS: 40.3 ± 14.8 SALS: 30.7 ± 11.5	El Escorial
(Tripolszki et al., 2019)	Case	Gene Panel	WES	Hungary	107 ALS	45:62 (0.73)	60 (30-79)	El Escorial + Awaji-Shima
(W. Chen et al., 2020)	Case	Gene Panel	WES + Sanger	China	268 ALS	160:108 (1.48)	52.1 ± 10.4	Definite or probable ALS (El Escorial)
(F. Lin et al., 2021)	Case-Control	Candidate Gene/Region	PCR	China	Case: 671 SALS Control: 1787 neurologically healthy individuals	410:261 (1.57)	53.45 ± 9.96	El Escorial
(Giguet-Valard et al., 2021)	Case Report	Whole Genome	WES	Martinique	5 related FALS	-	-	-
(Shepheard et al., 2021)	Case	Gene Panel	WES	UK	7 FALS + 93 SALS	54:46 (1.17)	60.4 (22-87)	Definite, probable, probable laboratory-supported or possible ALS (revised El Escorial)
(McCann et al., 2021)	Case	Variant Panel	WGS	Australia	616 SALS	346:221 (1.57)	60 ± 12	Definite or probable ALS (El Escorial)

Table A7. Summary characteristics of all included studies identified from the systematic review. All case-control studies (12) proceeded to the meta-analysis stage. FALS = familial ALS, SALS = sporadic ALS, WES = whole exome sequencing, WGS = whole genome sequencing, PCR = polymerase chain reaction, NGS = next-generation sequencing, PCR-SSCP = polymerase chain reaction-single-strand conformation polymorphism.

Variant Name (HGVS Protein Notation)	**Domain**	**rsID**	**SIFT Prediction**	**PolyPhen Prediction**	**Case Frequency**	**Control Frequency**	**gnomAD v2.1.1 non-neuro Frequency**	**Other Carried Variants**	**Statistical Analysis Results**	**References**
E459Gfs*7	Tail (E)	rs59297913	Deleterious	Benign	1/171	-	N/A	-	-	(Muller et al., 2018)
A528_P561del	Tail (KSP)	rs2063061681	-	-	1/356	0/306	N/A	-	-	(Figlewicz et al., 1994)
A652_K657del	Tail (KSP)	rs147489453	-	-	55/371	106/711	0.8726	-	OR 0.98 (95% CI 0.77-1.26); p=0.89	(F. Lin et al., 2021)
E658_K665del	Tail (KSP)	rs1183993443	-	-	1/207	0/219	0.01947	-	-	(Al-Chalabi et al., 1999)
					2/371	6/711	0.02722	-	OR 0.64 (95% CI 0.13-3.17); p=0.72	(F. Lin et al., 2021)
E664_P669del	Tail (KSP)	rs1317619836	-	-	1/207	1/219	0.0005205	-	-	(Al-Chalabi et al., 1999)
A686_K699del	Tail (KSP)	-	-	-	2/323	1/228	N/A	-	-	(Al-Chalabi et al., 1999)
S752_K757del	Tail (KSP)	rs570663492	-	-	1/323	2/228	0.0003574	-	-	(Al-Chalabi et al., 1999)
					1/616	-		OPTN M98K	-	(McCann et al., 2021)
					56/371	102/711	0.1138		OR 1.07 (95% CI 0.83-1.37); p=0.61	(F. Lin et al., 2021)
K790del	Tail (KSP)	rs59551486	-	-	4/356	0/306	0.001226	-	-	(Figlewicz et al., 1994)

					1/1126	2/613		-	-	(Morgan et al., 2017)
K857del	Tail (KEP)	rs762969612	-	-	1/171	-	0.00002324	-	-	(Muller et al., 2018)
S704_K731dup (A708ins)	Tail (KSP)	-	-	-	1/164	0/209	N/A	-	-	(Tomkins et al., 1998)
A40V	Head	rs1474351396	Tolerated	Benign	1/185	1/190	0	-	-	(Daoud et al., 2011)
A90V	Head	rs61556467	Tolerated	Benign	1/100	0/100	0.0005063	-	-	(Garcia et al., 2006)
					1/185	-		-	-	(Daoud et al., 2011)
R148P	Rod (Coil 1B)	-	Deleterious	Damaging	1/107	-	N/A	-	-	(Tripolszki et al., 2019)
E152D	Rod (Coil 1B)	rs774792100	Tolerated	Benign	3/268	-	0.003991	-	-	(W. Chen et al., 2020)
					1/371	1/711		-	OR 1.92 (95% CI 0.12-30.70); p=0.76	(F. Lin et al., 2021)
Q171H	Rod (Coil 1B)	-	-	-	1/371	0/711	N/A	-	OR Inf (95% CI Na-Inf); p=0.34	(F. Lin et al., 2021)
D187N	Rod (Coil 1B)	rs1372062630	Deleterious	Probably Damaging	1/469	0/191	0	SOD1 L39V	-	(Nakamura et al., 2016)
					1/51	-	0	-	-	(Nishiyama et al., 2017)

R192P	Rod (Coil 1B)	rs2063001424	Deleterious	-	1/242	0/129	N/A	-	-	(Couthouis et al., 2014)
A203P	Rod (Coil 1B)	-	Tolerated	Possibly Damaging	1/51	-	N/A	SETX C1554G	-	(Nishiyama et al., 2017)
G249S	Rod (linker between Coil 1B and 2A)	rs60825978	Tolerated	Benign	1/100	0/100	0.007444	-	-	(Garcia et al., 2006)
					1/268	-	0.0305	-	-	(W. Chen et al., 2020)
					3/371	8/711		-	-	(F. Lin et al., 2021)
S285R	Rod (Coil 2A)	rs1479105421	Deleterious	Benign	1/469	0/191	0.0005071	-	-	(Nakamura et al., 2016)
					1/51	-		-	-	(Nishiyama et al., 2017)
A314V	Rod (Coil 2B)	rs539511579	Deleterious	Probably Damaging	1/371	0/711	0.0002238	-	OR Inf (95% CI Na-Inf); p=0.34	(F. Lin et al., 2021)
T338I	Rod (Coil 2B)	rs774252076	Deleterious	Damaging	2/107	-	0.00003355	-	-	(Tripolszki et al., 2019)
R346H	Rod (Coil 2B)	rs1401155915	Tolerated	Possibly Damaging	1/186	0/190	0	-	-	(Daoud et al., 2011)
R352S	Rod (Coil 2B)	rs149955255	Deleterious	Possibly Damaging	2/200	2/100	0.003516	-	-	(Garcia et al., 2006)
A380T	Rod (Coil 2B)	rs201416955	Tolerated	Possibly Damaging	1/100	0/100	0.00001939	-	-	(Garcia et al., 2006)
					2/311	0/200	0.005275	OPTN R545Q	-	(H. Zhang et al., 2018)

					2/268	-		-	-	(W. Chen et al., 2020)
					3/371	8/711		-	OR 0.72 (95% CI 0.19-2.71); p=0.76	(F. Lin et al., 2021)
A400V	Rod (Coil 2B)	rs757021413	Deleterious	Probably Damaging	51/190	-	N/A	-	-	(Daoud et al., 2011)
R412Q	Rod (Coil 2B)	rs763701610	Deleterious	Possibly Damaging	1/51	-	0.00005584	ITPR2 A612T, FUS c.-37C>T, ALS2 I1373M	-	(Krüger et al., 2016)
E460K	Tail (E)	-	-	-	20/100	8/100	N/A	-	-	(Vechio et al., 1996)
E463K	Tail (E)	rs59371099	Deleterious	Probably Damaging	32/180	-	0.09682	-	-	(Daoud et al., 2011)
					173/1126	109/613		-	-	(Morgan et al., 2017)
E491K	Tail (E)	-	-	-	1/268	-	N/A	-	-	(W. Chen et al., 2020)
P505L	Tail (E)	rs1414968372	Deleterious	Benign	1/107	-	N/A	GRN C335R	-	(Tripolszki et al., 2019)
P512S	Tail (E)	-	-	-	1/371	0/711	N/A	-	OR Inf (95% CI Na-Inf); p=0.34	(F. Lin et al., 2021)
E597D	Tail (KSP)	rs753850528	Tolerated	Benign	1/311	0/200	0.0002236	-	-	(H. Zhang et al., 2018)
P615L	Tail (KSP)	rs5763269	Deleterious	Possibly Damaging	55/175	27/100	0.196	-	-	(Vechio et al., 1996)

					84/188	-	0.2131	-	-	(Daoud et al., 2011)
					414/1126	205/613		-	-	(Morgan et al., 2017)
					30/371	66/711	0.07552	-	OR 0.84 (95% CI 0.61-1.16); p=0.30	(F. Lin et al., 2021)
T642M	Tail (KSP)	rs117258406	Tolerated	Benign	1/46	18/699	0.008416	SPG11 L1982S	OR 0.78 (95% CI 0.02-5.19); p=1.00	(Pang et al., 2017)
					4/311	0/200		-	-	(H. Zhang et al., 2018)
					4/268	-		-	-	(W. Chen et al., 2020)
					4/371	5/711		-	-	(F. Lin et al., 2021)
K647N	Tail (KSP)	rs200634512	Deleterious	Possibly Damaging	1/5	-	0.000358	-	-	(Giguet-Valard et al., 2021)
V670E	Tail (KSP)	rs190692435	Tolerated	Possibly Damaging	2/371	5/711	0.02705	-	OR 0.77 (95% CI 0.15-3.96); p=1.00	(F. Lin et al., 2021)
A672E	Tail (KSP)	rs775497149	Tolerated	Benign	1/371	5/711	0.02376	-	OR 0.38 (95% CI 0.05-3.28); p=0.67	(F. Lin et al., 2021)
V726L	Tail (KSP)	rs1051285707	Tolerated	Benign	1/120	-	0.00003891	-	-	(Garton et al., 2017)
P777L	Tail (KSP)	rs199748453	Deleterious	Probably Damaging	1/100	-	0.00005831	ALS2 T293I	-	(Shepheard et al., 2021)
S787R	Tail (KSP)	rs568759161	Deleterious	Probably Damaging	2/268	-	0.002405	-	-	(W. Chen et al., 2020)

					9/671	2/1787		-	Discovery: OR 9.64 (95% CI 1.12-82.67); p=0.02 Replication: OR 14.43 (95% CI 1.61-129.40); p=0.009 Combined: OR 12.06 (95% CI 2.60-55.88); p=0.0003	(F. Lin et al., 2021)
A805E	Tail (KSP)	-	-	-	80/100	-	N/A	-	-	(Vechio et al., 1996)
E805A	Tail (KSP)	rs165602	Deleterious	Possibly Damaging	45/176	-	0.1551	-	-	(Daoud et al., 2011)
					309/1126	152/613	0.04673	-	-	(Morgan et al., 2017)
					10/371	30/711		-	-	(F. Lin et al., 2021)
P848S	Tail (KEP)	-	-	-	2/268	-	N/A	-	-	(W. Chen et al., 2020)
K857R	Tail (KEP)	rs747689406	Deleterious	Possibly Damaging	1/311	0/200	0.00007522	-	-	(H. Zhang et al., 2018)
K867N	Tail (KEP)	rs138156220	Deleterious	Probably Damaging	1/182	0/190	0	-	-	(Daoud et al., 2011)

					1/5	-	0	SOD1 G93V	-	(Giguet-Valard et al., 2021)
E868K	Tail (KEP)	rs1295979036	Tolerated	Probably Damaging	1/45	-	0	-	-	(Z.-J. Liu et al., 2019)
T905I	Tail (KEP)	rs202199780	Tolerated	Benign	2/268	-	0.001673	-	-	(W. Chen et al., 2020)
K917E	Tail (KEP)	-	Deleterious	Possibly Damaging	1/311	0/200	0	CHMP2B A138T	-	(H. Zhang et al., 2018)
E918G	Tail (KEP)	rs189881592	Deleterious	Possibly Damaging	1/186	0/190	0	-	-	(Daoud et al., 2011)
					1/311	0/200	0.003143	-	-	(H. Zhang et al., 2018)
					2/268	-		-	-	(W. Chen et al., 2020)
					2/371	2/711		-	OR 1.92 (95% CI 0.27-13.65); p=0.61	(F. Lin et al., 2021)
Q117Ter	Rod (Coil 1A)	rs1317368575	-	-	1/371	0/711	0.00009524	-	OR Inf (95% CI Na-Inf); p=0.34	(F. Lin et al., 2021)
L158L	Rod (Coil 1B)	rs1002065392	-	-	1/75	1/50	0	-	-	(Vechio et al., 1996)
L349L	Rod (Coil 2B)	rs1269206770	-	-	1/186	-	N/A	-	-	(Daoud et al., 2011)
A400A	Rod (Coil 2B)	rs165734	-	-	10/371	30/711	0.1807	-	-	(F. Lin et al., 2021)

A401A	Rod (Coil 2B)	-	-	-	2x lower than in controls	2x higher than in ALS	N/A	-	-	(Vechio et al., 1996)
S580S	Tail (KSP)	rs114263951	-	-	5/188	-	0.01183	-	-	(Daoud et al., 2011)
A744A	Tail (KSP)	rs165923	-	-	104/185	-	0.7855	-	-	(Daoud et al., 2011)
D919D	Tail (KEP)	rs56200920	-	-	1/186	-	0.005927	-	-	(Daoud et al., 2011)
					2/371	10/711	0.01124	-	-	(F. Lin et al., 2021)
V928V	Tail (KEP)	rs165625	-	-	149/186	-	0.7856	-	-	(Daoud et al., 2011)
					30/371	67/711	0.9238	-	-	(F. Lin et al., 2021)

Table A8. Variant characteristics of all included records identified from the systematic review. All variants supported by case-control studies (34) were subject to subgroup-level meta-analysis, with 8 going forward to variant-level meta-analysis as the mutation was supported by at least 2 case-control studies. N/A values represent instances where the variant was not present in the population-specific gnomAD non-neuro database.

Variant	Start	End	Ref	Alt
E459Gfs*7	29885004	29885004	GAACA	G
A528_P561del	29885211	29885211	GCTGAGGCCAAGTCCCCAGAGAAGGAGGAAGCAAAATCCCCAGCCGAAGTCAAGTCCCCTGAGAAGGCC	G
A652_K657del	29885576	29885576	TGAGAAGGCCAAGTCCCC	T
E658_K665del	29885580	29885580	AAGGCCAAGTCCCCAGAGAAGGAAG	A
E664_P669del	29885604	29885604	GAGGCCAAGTCCCCTGAGA	G
A686_K699del	29885609	29885609	CAAGTCCCCTGAGAAGGCCAAGTCCCCAGTGAAGGCAGAAGCA	C
S752_K757del	29885858	29885858	AGCTAAGTCCCCAGAGAAG	A
K790del	29885996	29885996	CAAG	C
K857del	29886192	29886192	GAGA	G
S704_K731dup (A708ins)	29885709	29885709	GCCAAGTCCCCAGTGAAGGAAGAAGCAAAGTCCCCTGAGAAGGCCAAGTCCCCAGTGAAGGAAGAAGCAAAGTCCCCTGAGAAG	G
A40V	29876370	29876370	C	T
A90V	29876520	29876520	C	T
R148P	29876694	29876694	G	C
E152D	29876707	29876707	G	C
Q171H	29876764	29876764	G	C
D187N	29876810	29876810	G	A
R192P	29876826	29876826	G	C
A203P	29876858	29876858	G	C
G249S	29876996	29876996	G	A
S285R	29877106	29877106	C	A
A314V	29879421	29879421	C	T
T338I	29879493	29879493	C	T
R346H	29879517	29879517	G	A
R352S	29879534	29879534	C	A
A380T	29881766	29881766	G	A
A400V	29881827	29881827	C	T
R412Q	29884864	29884864	G	A

E460K	-	-	-	-
E463K	29885016	29885016	G	A
E491K	29885100	29885100	G	A
P505L	29885143	29885143	C	T
P512S	29885163	29885163	C	T
E597D	29885420	29885420	G	C
P615L	29885473	29885473	C	T
T642M	29885554	29885554	C	T
K647N	29885570	29885570	G	C
V670E	29885638	29885638	T	A
A672E	29885644	29885644	C	A
V726L	29885805	29885805	G	C
P777L	29885959	29885959	C	T
S787R	29885990	29885990	C	G
A805E	29886043	29886043	C	A
E805A	29886043	29886043	A	C
P848S	29886171	29886171	C	T
K857R	29886199	29886199	A	G
K867N	29886230	29886230	G	T
E868K	29886231	29886231	G	A
T905I	29886343	29886343	C	T
K917E	29886378	29886378	A	G
E918G	29886382	29886382	A	G
Q117Ter	29876600	29876600	C	T
L158L	29876725	29876725	G	A
L349L	29879527	29879527	G	T
A400A	29881828	29881828	C	T
A401A	-	-	-	-
S580S	29885369	29885369	C	T

A744A	29885861	29885861	T	C
D919D	29886386	29886386	C	T
V928V	29886413	29886413	A	G

Table A9. Genomic coordinates and base pair substitutions (hg19) of all variants identified from the systematic review.

Variant	No. Studies	N Cases	N Controls	Fixed OR (95% CI; p-value)	Random OR (95% CI; p-value)	Heterogeneity (Q statistic; p-value)	Heterogeneity (I-squared)	Publication Bias (Egger t statistic; p-value)	Publication Bias (Harbord t statistic; p-value)
G249S	2	471	811	0.91 (0.28-2.94; 0.87)	0.89 (0.26-3.03; 0.85)	0.66 (0.42)	0%	N/A	N/A
A380T	3	782	1011	1.12 (0.39-3.21; 0.83)	1.06 (0.34-3.33; 0.92)	1.26 (0.53)	0%	12.17; **0.05**	5.01; 0.13
P615L	3	1672	1424	1.11 (0.93-1.33; 0.24)	1.11 (0.93-1.33; 0.24)	1.54 (0.46)	0%	-0.46; 0.73	-0.46; 0.73
T642M	3	728	1610	1.71 (0.66-4.42; 0.27)	1.56 (0.55-4.39; 0.40)	1.14 (0.57)	0%	0.56; 0.67	0.35; 0.79
E658_K665del	2	578	930	0.91 (0.24-3.45; 0.88)	0.88 (0.21-3.70; 0.86)	0.78 (0.38)	0%	N/A	N/A
S752_K757del	2	694	939	1.03 (0.73-1.47; 0.85)	1.04 (0.73-1.47; 0.84)	0.80 (0.37)	0%	N/A	N/A
K790del	2	1482	919	1.56 (0.37-6.64; 0.55)	1.31 (0.05-35.02; 0.87)	3.03 (0.08)	**67%**	N/A	N/A
E805A	2	1497	1324	1.08 (0.88-1.34; 0.46)	0.94 (0.54-1.64; 0.83)	2.40 (0.12)	**58%**	N/A	N/A
E918G	3	868	1101	2.16 (0.49-9.46; 0.31)	2.13 (0.48-9.40; 0.32)	0.06 (0.97)	0%	0.78; 0.58	4.18; 0.15

Table A10. Results of the variant-level meta-analysis. N/A values represent instances where publication bias could not be calculated as the minimum number of studies used for calculation was not reached.

Start	End	Ref	Alt	Variant Type	VEP Impact	Exon	Intron	HGVS.c	HGVS.p	rsID
29876227	29876227	C	G	5' UTR	Modifier	1	-	c.-25C>G	-	-
29876229	29876229	G	A	5' UTR	Modifier	1	-	c.-23G>A	-	rs1280164847
29876235	29876235	G	C	5' UTR	Modifier	1	-	c.-17G>C	-	-
29876236	29876236	C	A	5' UTR	Modifier	1	-	c.-16C>A	-	rs996402317
29876272	29876272	G	A	Synonymous	Low	1	-	c.21G>A	p.Ala7Ala	rs192350983
29876298	29876298	C	A	Missense	Moderate	1	-	c.47C>A	p.Ala16Glu	rs1468605569
29876336	29876336	G	T	Missense	Moderate	1	-	c.85G>T	p.Ala29Ser	rs752311867
29876338	29876338	C	T	Synonymous	Low	1	-	c.87C>T	p.Ala29Ala	-
29876348	29876348	G	A	Missense	Moderate	1	-	c.97G>A	p.Gly33Ser	-
29876392	29876392	C	T	Synonymous	Low	1	-	c.141C>T	p.Phe47Phe	rs780966618
29876395	29876395	C	G	Missense	Moderate	1	-	c.144C>G	p.His48Gln	rs1325065979
29876404	29876404	A	G	Synonymous	Low	1	-	c.153A>G	p.Thr51Thr	rs755886692
29876410	29876410	G	A	Synonymous	Low	1	-	c.159G>A	p.Thr53Thr	rs1205368020
29876416	29876416	G	A	Synonymous	Low	1	-	c.165G>A	p.Val55Val	rs897546803
29876473	29876473	C	T	Synonymous	Low	1	-	c.222C>T	p.Thr74Thr	rs1413495861
29876520	29876520	C	T	Missense	Moderate	1	-	c.269C>T	p.Ala90Val	rs61556467
29876529	29876529	C	T	Missense	Moderate	1	-	c.278C>T	p.Thr93Ile	rs751160327
29876552	29876552	C	T	Synonymous	Low	1	-	c.301C>T	p.Leu101Leu	rs1231899865
29876555	29876555	C	T	Stop Gained	High	1	-	c.304C>T	p.Gln102Ter	rs948554818
29876609	29876609	G	A	Missense	Moderate	1	-	c.358G>A	p.Ala120Thr	rs1386911340
29876620	29876620	C	T	Synonymous	Low	1	-	c.369C>T	p.Arg123Arg	rs768460278
29876632	29876632	C	G	Synonymous	Low	1	-	c.381C>G	p.Gly127Gly	rs760591823
29876649	29876649	G	A	Missense	Moderate	1	-	c.398G>A	p.Arg133Gln	rs997535105
29876660	29876660	G	T	Missense	Moderate	1	-	c.409G>T	p.Ala137Ser	rs754799725
29876668	29876668	C	G	Synonymous	Low	1	-	c.417C>G	p.Arg139Arg	rs912176188
29876699	29876699	G	A	Missense	Moderate	1	-	c.448G>A	p.Val150Ile	rs769162779
29876744	29876744	G	A	Missense	Moderate	1	-	c.493G>A	p.Gly165Ser	-
29876747	29876747	C	T	Stop Gained	High	1	-	c.496C>T	p.Gln166Ter	-
29876754	29876754	G	T	Missense	Moderate	1	-	c.503G>T	p.Arg168Leu	rs1009899708
29876756	29876756	C	T	Synonymous	Low	1	-	c.505C>T	p.Leu169Leu	rs1277092292
29876761	29876761	G	A	Synonymous	Low	1	-	c.510G>A	p.Glu170Glu	rs1208767813
29876765	29876765	G	A	Missense	Moderate	1	-	c.514G>A	p.Glu172Lys	rs1176398662

29876777	29876777	G	A	Missense	Moderate	1	-	c.526G>A	p.Glu176Lys	rs1422942222
29876800	29876800	G	A	Synonymous	Low	1	-	c.549G>A	p.Gln183Gln	-
29876834	29876834	G	A	Missense	Moderate	1	-	c.583G>A	p.Ala195Thr	rs1273011909
29876842	29876842	G	C	Synonymous	Low	1	-	c.591G>C	p.Ala197Ala	rs1459116357
29876845	29876845	G	A	Synonymous	Low	1	-	c.594G>A	p.Ala198Ala	rs748478910
29876857	29876857	CGCGCGCTG	-	Frameshift Deletion	High	1	-	c.606_613del	p.Ala203ArgfsTer74	-
29876866	29876866	C	T	Synonymous	Low	1	-	c.615C>T	p.Phe205Phe	rs1301849129
29876878	29876878	C	G	Synonymous	Low	1	-	c.627C>G	p.Ala209Ala	rs562497163
29876927	29876927	G	A	Missense	Moderate	1	-	c.676G>A	p.Glu226Lys	-
29876952	29876952	A	C	Missense	Moderate	1	-	c.701A>C	p.His234Pro	-
29876955	29876955	A	T	Missense	Moderate	1	-	c.704A>T	p.Gln235Leu	-
29876977	29876977	C	G	Synonymous	Low	1	-	c.726C>G	p.Leu242Leu	rs560344725
29876978	29876978	G	A	Missense	Moderate	1	-	c.727G>A	p.Gly243Ser	rs548521745
29876983	29876983	G	A	Synonymous	Low	1	-	c.732G>A	p.Gln244Gln	rs527475764
29876996	29876996	G	A	Missense	Moderate	1	-	c.745G>A	p.Gly249Ser	rs60825978
29877028	29877028	G	T	Synonymous	Low	1	-	c.777G>T	p.Thr259Thr	rs915610438
29877033	29877033	A	G	Missense	Moderate	1	-	c.782A>G	p.Asp261Gly	rs768531339
29877061	29877061	G	C	Synonymous	Low	1	-	c.810G>C	p.Ala270Ala	rs201868609
29877094	29877094	C	G	Missense	Moderate	1	-	c.843C>G	p.His281Gln	rs1267522365
29877099	29877099	T	C	Missense	Moderate	1	-	c.848T>C	p.Val283Ala	-
29877102	29877102	A	G	Missense	Moderate	1	-	c.851A>G	p.Gln284Arg	rs746595090
29877107	29877107	A	G	Missense	Moderate	1	-	c.856A>G	p.Thr286Ala	rs770443491
29877109	29877109	G	C	Synonymous	Low	1	-	c.858G>C	p.Thr286Thr	rs1477253596
29877142	29877142	G	A	Intronic	Low	-	1	c.883+8G>A	-	rs1191279791
29877150	29877150	G	A	Intronic	Modifier	-	1	c.883+16G>A	-	rs534281794
29877158	29877158	G	C	Intronic	Modifier	-	1	c.883+24G>C	-	rs1359878602
29877205	29877205	C	G	Intronic	Modifier	-	1	c.883+71C>G	-	rs1474258062
29877208	29877208	A	G	Intronic	Modifier	-	1	c.883+74A>G	-	-
29877222	29877222	G	A	Intronic	Modifier	-	1	c.883+88G>A	-	rs567088364
29877234	29877234	A	G	Intronic	Modifier	-	1	c.883+100A>G	-	-
29877239	29877239	C	T	Intronic	Modifier	-	1	c.883+105C>T	-	rs1414146401
29877256	29877256	C	T	Intronic	Modifier	-	1	c.883+122C>T	-	rs534144890
29877263	29877263	A	G	Intronic	Modifier	-	1	c.883+129A>G	-	rs138081293

29877317	29877317	C	T	Intronic	Modifier	-	1	c.883+183C>T	-	-
29877321	29877321	A	G	Intronic	Modifier	-	1	c.883+187A>G	-	rs367951665
29877324	29877324	C	T	Intronic	Modifier	-	1	c.883+190C>T	-	-
29877343	29877343	C	T	Intronic	Modifier	-	1	c.883+209C>T	-	rs1373636600
29877344	29877344	C	T	Intronic	Modifier	-	1	c.883+210C>T	-	rs573999650
29877346	29877346	C	G	Intronic	Modifier	-	1	c.883+212C>G	-	-
29877367	29877367	G	A	Intronic	Modifier	-	1	c.883+233G>A	-	rs56083406
29877370	29877370	C	T	Intronic	Modifier	-	1	c.883+236C>T	-	-
29877386	29877386	C	T	Intronic	Modifier	-	1	c.883+252C>T	-	-
29877417	29877417	C	T	Intronic	Modifier	-	1	c.883+283C>T	-	rs165607
29877432	29877432	C	T	Intronic	Modifier	-	1	c.883+298C>T	-	rs556602600
29877437	29877437	C	CGTCAAGAAAAAAACAAGTTT	Intronic	Modifier	-	1	c.883+305_883+325dup	-	rs760534140
29877441	29877441	C	G	Intronic	Modifier	-	1	c.883+307C>G	-	rs73407035
29877444	29877444	G	A	Intronic	Modifier	-	1	c.883+317dup	-	rs763994664
29877448	29877448	A	G	Intronic	Modifier	-	1	c.883+314A>G	-	-
29877475	29877475	G	A	Intronic	Modifier	-	1	c.883+341G>A	-	rs576631246
29877541	29877541	G	C	Intronic	Modifier	-	1	c.883+407G>C	-	-
29877545	29877545	A	G	Intronic	Modifier	-	1	c.883+411A>G	-	rs75956622
29877557	29877557	C	T	Intronic	Modifier	-	1	c.883+423C>T	-	rs165697
29877565	29877565	A	G	Intronic	Modifier	-	1	c.883+431A>G	-	rs165865
29877581	29877581	T	A	Intronic	Modifier	-	1	c.883+447T>A	-	rs188853358
29877587	29877587	C	T	Intronic	Modifier	-	1	c.883+453C>T	-	rs144739005
29877592	29877592	C	A	Intronic	Modifier	-	1	c.883+458C>A	-	rs1218743924
29877620	29877620	T	A	Intronic	Modifier	-	1	c.883+486T>A	-	-
29877624	29877624	C	T	Intronic	Modifier	-	1	c.883+490C>T	-	rs79658766
29877625	29877625	A	G	Intronic	Modifier	-	1	c.883+491A>G	-	rs165821
29877656	29877656	AC	-	Intronic	Modifier	-	1	c.883+522del	-	rs1168824251
29877657	29877657	G	C	Intronic	Modifier	-	1	c.883+523G>C	-	rs78580989
29877693	29877693	C	A	Intronic	Modifier	-	1	c.883+559C>A	-	-
29877699	29877699	G	A	Intronic	Modifier	-	1	c.883+565G>A	-	rs780172669
29877700	29877700	G	A	Intronic	Modifier	-	1	c.883+566G>A	-	-
29877710	29877710	C	T	Intronic	Modifier	-	1	c.883+576C>T	-	-
29877715	29877715	G	A	Intronic	Modifier	-	1	c.883+581G>A	-	-

29877716	29877716	T	G	Intronic	Modifier	-	1	c.883+582T>G	-	-
29877803	29877803	A	G	Intronic	Modifier	-	1	c.883+669A>G	-	-
29877809	29877809	G	A	Intronic	Modifier	-	1	c.883+675G>A	-	rs1187445478
29877855	29877855	G	T	Intronic	Modifier	-	1	c.883+721G>T	-	-
29877860	29877860	G	T	Intronic	Modifier	-	1	c.883+726G>T	-	rs73881537
29877874	29877874	C	G	Intronic	Modifier	-	1	c.883+740C>G	-	-
29877877	29877877	C	TGCA	Intronic	Modifier	-	1	c.883+744_883+747dup	-	rs1265330728
29877882	29877882	G	A	Intronic	Modifier	-	1	c.883+748G>A	-	rs561113494
29877893	29877893	A	G	Intronic	Modifier	-	1	c.883+759A>G	-	-
29877907	29877907	T	G	Intronic	Modifier	-	1	c.883+773T>G	-	-
29877961	29877961	G	C	Intronic	Modifier	-	1	c.883+827G>C	-	-
29877979	29877979	C	T	Intronic	Modifier	-	1	c.883+845C>T	-	-
29877999	29877999	ACTGT	-	Intronic	Modifier	-	1	c.883+866_883+869del	-	rs1359000475
29878010	29878010	CTT	-	Intronic	Modifier	-	1	c.883+876_883+877del	-	rs1341072419
29878010	29878010	T	C	Intronic	Modifier	-	1	c.883+876T>C	-	rs563803182
29878026	29878026	TGAGA	-	Intronic	Modifier	-	1	c.883+894_883+897del	-	rs918545488
29878039	29878039	G	T	Intronic	Modifier	-	1	c.883+905G>T	-	rs747959620
29878057	29878057	A	G	Intronic	Modifier	-	1	c.883+923A>G	-	-
29878068	29878068	A	T	Intronic	Modifier	-	1	c.883+934A>T	-	-
29878168	29878168	C	T	Intronic	Modifier	-	1	c.883+1034C>T	-	rs577782932
29878198	29878198	T	C	Intronic	Modifier	-	1	c.883+1068dup	-	rs543584318
29878200	29878200	C	T	Intronic	Modifier	-	1	c.883+1066C>T	-	rs1018018710
29878201	29878201	C	T	Intronic	Modifier	-	1	c.883+1067C>T	-	rs115007285
29878318	29878318	G	A	Intronic	Modifier	-	1	c.884-1046G>A	-	rs137916245
29878328	29878328	G	A	Intronic	Modifier	-	1	c.884-1036G>A	-	rs776842833
29878367	29878367	C	G	Intronic	Modifier	-	1	c.884-997C>G	-	rs980795548
29878435	29878435	AGGTTTCCTGGGAACCACGAGCG	-	Intronic	Modifier	-	1	c.884-946_884-925del	-	-
29878445	29878445	C	G	Intronic	Modifier	-	1	c.884-914dup	-	rs148457788
29878448	29878448	G	A	Intronic	Modifier	-	1	c.884-916_884-915insA	-	rs59399758

29878450	29878450	G	C	Intronic	Modifier	-	1	c.884-914G>C	-	-
29878452	29878452	C	G	Intronic	Modifier	-	1	c.884-912C>G	-	rs759563670
29878481	29878481	A	G	Intronic	Modifier	-	1	c.884-883A>G	-	rs114042882
29878483	29878483	G	A	Intronic	Modifier	-	1	c.884-881G>A	-	rs995319069
29878525	29878525	C	T	Intronic	Modifier	-	1	c.884-839C>T	-	rs982635274
29878581	29878581	G	A	Intronic	Modifier	-	1	c.884-783G>A	-	-
29878583	29878583	C	T	Intronic	Modifier	-	1	c.884-781C>T	-	-
29878629	29878629	G	A	Intronic	Modifier	-	1	c.884-735G>A	-	rs990302434
29878670	29878670	T	C	Intronic	Modifier	-	1	c.884-694T>C	-	rs114681751
29878698	29878698	A	G	Intronic	Modifier	-	1	c.884-666A>G	-	-
29878709	29878709	C	T	Intronic	Modifier	-	1	c.884-655C>T	-	rs1050867473
29878820	29878820	T	C	Intronic	Modifier	-	1	c.884-544T>C	-	-
29878865	29878865	G	A	Intronic	Modifier	-	1	c.884-499G>A	-	rs60499988
29878869	29878869	C	T	Intronic	Modifier	-	1	c.884-495C>T	-	rs1268750543
29878874	29878874	G	A	Intronic	Modifier	-	1	c.884-490G>A	-	-
29878890	29878890	C	T	Intronic	Modifier	-	1	c.884-474C>T	-	-
29878894	29878894	A	C	Intronic	Modifier	-	1	c.884-470A>C	-	-
29878930	29878930	G	T	Intronic	Modifier	-	1	c.884-434G>T	-	rs1046802224
29878947	29878947	T	C	Intronic	Modifier	-	1	c.884-417T>C	-	rs957592448
29878961	29878961	CAT	-	Intronic	Modifier	-	1	c.884-404_884-403del	-	rs1482065911
29878995	29878995	C	T	Intronic	Modifier	-	1	c.884-369C>T	-	rs762182598
29879010	29879010	C	T	Intronic	Modifier	-	1	c.884-354C>T	-	rs1012822803
29879022	29879022	C	A	Intronic	Modifier	-	1	c.884-342C>A	-	rs143372377
29879036	29879036	G	A	Intronic	Modifier	-	1	c.884-328G>A	-	rs942354319
29879044	29879044	C	T	Intronic	Modifier	-	1	c.884-320C>T	-	rs1039764937
29879072	29879072	G	A	Intronic	Modifier	-	1	c.884-292G>A	-	rs577074185
29879079	29879079	G	A	Intronic	Modifier	-	1	c.884-285G>A	-	rs949238939
29879211	29879211	C	T	Intronic	Modifier	-	1	c.884-153C>T	-	rs1249661164
29879212	29879212	G	A	Intronic	Modifier	-	1	c.884-152G>A	-	rs1456261265
29879229	29879229	C	T	Intronic	Modifier	-	1	c.884-135C>T	-	rs562037652
29879246	29879246	C	T	Intronic	Modifier	-	1	c.884-118C>T	-	-
29879247	29879247	G	A	Intronic	Modifier	-	1	c.884-117G>A	-	rs112005621
29879251	29879251	G	A	Intronic	Modifier	-	1	c.884-113G>A	-	rs1176098439

29879252	29879252	C	T	Intronic	Modifier	-	1	c.884-112C>T	-	rs1359134672
29879264	29879264	CT	-	Intronic	Modifier	-	1	c.884-100del	-	-
29879264	29879264	T	A	Intronic	Modifier	-	1	c.884-100_884-99insA	-	rs1291058402
29879281	29879281	AAG	-	Intronic	Modifier	-	1	c.884-83_884-82del	-	rs1295712746
29879281	29879281	AG	-	Intronic	Modifier	-	1	c.884-83del	-	-
29879308	29879308	C	T	Intronic	Modifier	-	1	c.884-56C>T	-	rs1019810165
29879343	29879343	C	T	Intronic	Modifier	-	1	c.884-21C>T	-	rs1482031249
29879383	29879383	G	A	Synonymous	Low	2	-	c.903G>A	p.Ser301Ser	rs781291855
29879402	29879402	A	CAGACGCTATGCGCT	In-frame Insertion	Moderate	2	-	c.926_940dup	p.Asp309_Ser313dup	rs1380569251
29879421	29879421	C	T	Missense	Moderate	2	-	c.941C>T	p.Ala314Val	rs539511579
29879444	29879444	C	T	Missense	Moderate	2	-	c.964C>T	p.Arg322Trp	rs778265423
29879483	29879483	C	G	Missense	Moderate	2	-	c.1003C>G	p.Leu335Val	-
29879516	29879516	C	T	Missense	Moderate	2	-	c.1036C>T	p.Arg346Cys	rs139219355
29879518	29879518	C	G	Synonymous	Low	2	-	c.1038C>G	p.Arg346Arg	rs377262654
29879524	29879524	G	C	Missense	Moderate	2	-	c.1044G>C	p.Glu348Asp	rs1475562664
29879535	29879535	G	A	Missense	Moderate	2	-	c.1055G>A	p.Arg352His	rs750088241
29879545	29879545	C	T	Synonymous	Low	2	-	c.1065C>T	p.Ala355Ala	rs144040465
29879559	29879559	A	G	Missense	Moderate	2	-	c.1079A>G	p.Tyr360Cys	rs768679590
29879570	29879570	CA	-	Intronic	Low	-	2	c.1083+7del	-	-
29879592	29879592	C	G	Intronic	Modifier	-	2	c.1083+29C>G	-	rs1357430644
29879601	29879601	C	T	Intronic	Modifier	-	2	c.1083+38C>T	-	rs1020522395
29879604	29879604	A	G	Intronic	Modifier	-	2	c.1083+41A>G	-	rs371191443
29879646	29879646	G	T	Intronic	Modifier	-	2	c.1083+83G>T	-	rs570932481
29879653	29879653	T	C	Intronic	Modifier	-	2	c.1083+90T>C	-	-
29879659	29879659	A	C	Intronic	Modifier	-	2	c.1083+96A>C	-	rs558830358
29879661	29879661	A	T	Intronic	Modifier	-	2	c.1083+98A>T	-	rs775797988
29879662	29879662	T	C	Intronic	Modifier	-	2	c.1083+99T>C	-	rs1004871512
29879671	29879671	T	C	Intronic	Modifier	-	2	c.1083+108T>C	-	rs747239243
29879693	29879693	CT	-	Intronic	Modifier	-	2	c.1083+132del	-	-
29879695	29879695	T	C	Intronic	Modifier	-	2	c.1083+132T>C	-	rs1403096338
29879745	29879745	C	G	Intronic	Modifier	-	2	c.1083+182C>G	-	rs77685295
29879753	29879753	C	T	Intronic	Modifier	-	2	c.1083+190C>T	-	-

29879754	29879754	C	T	Intronic	Modifier	-	2	c.1083+191C>T	-	rs114811985
29879817	29879817	GATAGACTT	-	Intronic	Modifier	-	2	c.1083+247_1083+254del	-	-
29879828	29879828	A	TTTATTTT	Intronic	Modifier	-	2	c.1083+272_1083+273insTTTTATTT	-	-
29879841	29879841	TTTATTTAT	A	Intronic	Modifier	-	2	c.1083+270_1083+278delinsA	-	-
29879844	29879844	A	TTTTTTTT	Intronic	Modifier	-	2	c.1083+284_1083+285insTTTTTTTT	-	-
29879847	29879847	T	TGAG	Intronic	Modifier	-	2	c.1083+284_1083+285insTGAG	-	-
29879853	29879853	T	TTATTTAC	Intronic	Modifier	-	2	c.1083+292_1083+293insATTTACTT	-	rs1342137926
29879888	29879888	G	T	Intronic	Modifier	-	2	c.1083+325G>T	-	-
29879914	29879914	C	T	Intronic	Modifier	-	2	c.1083+351C>T	-	-
29879917	29879917	C	A	Intronic	Modifier	-	2	c.1083+354C>A	-	rs34915139
29879923	29879923	C	T	Intronic	Modifier	-	2	c.1083+360C>T	-	-
29879943	29879943	A	G	Intronic	Modifier	-	2	c.1083+380A>G	-	rs969772763
29879946	29879946	TTC	-	Intronic	Modifier	-	2	c.1083+384_1083+385del	-	-
29879948	29879948	C	T	Intronic	Modifier	-	2	c.1083+385C>T	-	rs761560241
29879963	29879963	C	T	Intronic	Modifier	-	2	c.1083+400C>T	-	rs903216611
29879970	29879970	C	T	Intronic	Modifier	-	2	c.1083+407C>T	-	rs369540636
29879979	29879979	C	T	Intronic	Modifier	-	2	c.1083+416C>T	-	rs899973194
29879984	29879984	G	A	Intronic	Modifier	-	2	c.1083+421G>A	-	rs988563535
29880013	29880013	A	G	Intronic	Modifier	-	2	c.1083+450A>G	-	rs545472872
29880049	29880049	G	A	Intronic	Modifier	-	2	c.1083+486G>A	-	rs8136014
29880091	29880091	A	G	Intronic	Modifier	-	2	c.1083+528A>G	-	rs1003956839
29880114	29880114	C	T	Intronic	Modifier	-	2	c.1083+551C>T	-	-
29880119	29880119	G	T	Intronic	Modifier	-	2	c.1083+556G>T	-	-
29880128	29880128	C	T	Intronic	Modifier	-	2	c.1083+565C>T	-	rs148546902
29880129	29880129	G	A	Intronic	Modifier	-	2	c.1083+566G>A	-	rs868328509
29880141	29880141	A	AGAGAT	Intronic	Modifier	-	2	c.1083+580_1083+585dup	-	rs1321513053

29880155	29880155	TA	-	Intronic	Modifier	-	2	c.1083+594del	-	-
29880167	29880167	T	C	Intronic	Modifier	-	2	c.1083+604T>C	-	rs778934270
29880187	29880187	C	T	Intronic	Modifier	-	2	c.1083+624C>T	-	rs959441263
29880193	29880193	G	T	Intronic	Modifier	-	2	c.1083+630G>T	-	-
29880194	29880194	G	A	Intronic	Modifier	-	2	c.1083+631G>A	-	rs117259769
29880211	29880211	C	T	Intronic	Modifier	-	2	c.1083+648C>T	-	rs77580710
29880233	29880233	T	C	Intronic	Modifier	-	2	c.1083+670T>C	-	rs1458642140
29880260	29880260	C	T	Intronic	Modifier	-	2	c.1083+697C>T	-	rs537568541
29880261	29880261	G	A	Intronic	Modifier	-	2	c.1083+698G>A	-	rs57986874
29880277	29880277	A	G	Intronic	Modifier	-	2	c.1083+714A>G	-	rs189299986
29880346	29880346	C	T	Intronic	Modifier	-	2	c.1083+783C>T	-	rs552866413
29880382	29880382	A	C	Intronic	Modifier	-	2	c.1083+819A>C	-	-
29880386	29880386	T	C	Intronic	Modifier	-	2	c.1083+823T>C	-	rs556568863
29880400	29880400	G	A	Intronic	Modifier	-	2	c.1083+837G>A	-	rs1451269879
29880445	29880445	A	G	Intronic	Modifier	-	2	c.1083+882A>G	-	rs572804768
29880458	29880458	G	T	Intronic	Modifier	-	2	c.1083+895G>T	-	rs924730895
29880492	29880492	A	G	Intronic	Modifier	-	2	c.1083+929A>G	-	rs151051572
29880502	29880502	G	A	Intronic	Modifier	-	2	c.1083+939G>A	-	rs2240634
29880528	29880528	G	A	Intronic	Modifier	-	2	c.1083+965G>A	-	rs563717409
29880580	29880580	G	C	Intronic	Modifier	-	2	c.1083+1017G>C	-	-
29880585	29880585	G	A	Intronic	Modifier	-	2	c.1083+1022G>A	-	rs543290585
29880591	29880591	G	A	Intronic	Modifier	-	2	c.1083+1028G>A	-	rs1366926907
29880621	29880621	C	T	Intronic	Modifier	-	2	c.1083+1058C>T	-	rs534776514
29880630	29880630	G	A	Intronic	Modifier	-	2	c.1083+1067G>A	-	rs1019218040
29880652	29880652	T	A	Intronic	Modifier	-	2	c.1084-1053dup	-	rs773168247
29880653	29880653	A	T	Intronic	Modifier	-	2	c.1084-1059A>T	-	rs965488701
29880662	29880662	A	T	Intronic	Modifier	-	2	c.1084-1050A>T	-	rs180872873
29880665	29880665	TAAAA	-	Intronic	Modifier	-	2	c.1084-1047_1084-1044del	-	rs1273203992
29880692	29880692	C	T	Intronic	Modifier	-	2	c.1084-1020C>T	-	-

29880693	29880693	C	G	Intronic	Modifier	-	2	c.1084-1019C>G	-	rs567894563
29880694	29880694	T	C	Intronic	Modifier	-	2	c.1084-1018T>C	-	rs984314659
29880705	29880705	C	G	Intronic	Modifier	-	2	c.1084-1007C>G	-	rs760470586
29880759	29880759	G	A	Intronic	Modifier	-	2	c.1084-953G>A	-	-
29880765	29880765	T	C	Intronic	Modifier	-	2	c.1084-947T>C	-	rs939108695
29880766	29880766	CTG	-	Intronic	Modifier	-	2	c.1084-945_1084-944del	-	rs770692971
29880766	29880766	G	A	Intronic	Modifier	-	2	c.1084-946G>A	-	rs114456709
29880787	29880787	G	A	Intronic	Modifier	-	2	c.1084-925G>A	-	-
29880800	29880800	G	A	Intronic	Modifier	-	2	c.1084-912G>A	-	rs1010587199
29880804	29880804	G	C	Intronic	Modifier	-	2	c.1084-908G>C	-	rs573878341
29880814	29880814	C	T	Intronic	Modifier	-	2	c.1084-898C>T	-	rs868582729
29880823	29880823	T	G	Intronic	Modifier	-	2	c.1084-889T>G	-	-
29880856	29880856	C	T	Intronic	Modifier	-	2	c.1084-856C>T	-	rs1366171508
29880884	29880884	C	G	Intronic	Modifier	-	2	c.1084-828C>G	-	rs566334659
29880907	29880907	T	C	Intronic	Modifier	-	2	c.1084-805T>C	-	rs931732579
29880914	29880914	T	C	Intronic	Modifier	-	2	c.1084-798T>C	-	rs5763264
29880916	29880916	C	T	Intronic	Modifier	-	2	c.1084-796C>T	-	rs553558060
29880942	29880942	G	A	Intronic	Modifier	-	2	c.1084-770G>A	-	-
29880948	29880948	T	G	Intronic	Modifier	-	2	c.1084-764T>G	-	-
29880977	29880977	C	T	Intronic	Modifier	-	2	c.1084-735C>T	-	rs1181856343
29880990	29880990	A	C	Intronic	Modifier	-	2	c.1084-722A>C	-	-
29881010	29881010	A	G	Intronic	Modifier	-	2	c.1084-702A>G	-	rs1319767449
29881149	29881149	T	C	Intronic	Modifier	-	2	c.1084-563T>C	-	-
29881150	29881150	G	GTAT	Intronic	Modifier	-	2	c.1084-560_1084-557dup	-	rs1286429529
29881162	29881162	G	A	Intronic	Modifier	-	2	c.1084-550G>A	-	-
29881176	29881176	C	T	Intronic	Modifier	-	2	c.1084-536C>T	-	rs559654353
29881195	29881195	A	G	Intronic	Modifier	-	2	c.1084-517A>G	-	rs913417474
29881212	29881212	C	T	Intronic	Modifier	-	2	c.1084-500C>T	-	-
29881214	29881214	C	T	Intronic	Modifier	-	2	c.1084-498C>T	-	rs2240635

29881237	29881237	A	G	Intronic	Modifier	-	2	c.1084-475A>G	-	rs142119901
29881265	29881265	T	C	Intronic	Modifier	-	2	c.1084-447T>C	-	rs1040695377
29881277	29881277	A	G	Intronic	Modifier	-	2	c.1084-435A>G	-	-
29881292	29881292	A	T	Intronic	Modifier	-	2	c.1084-420A>T	-	-
29881333	29881333	C	G	Intronic	Modifier	-	2	c.1084-379C>G	-	-
29881340	29881340	C	T	Intronic	Modifier	-	2	c.1084-372C>T	-	rs1303062643
29881369	29881369	G	A	Intronic	Modifier	-	2	c.1084-343G>A	-	rs534920944
29881378	29881378	C	T	Intronic	Modifier	-	2	c.1084-334C>T	-	rs555490349
29881388	29881388	G	A	Intronic	Modifier	-	2	c.1084-324G>A	-	rs138583539
29881405	29881405	T	C	Intronic	Modifier	-	2	c.1084-307T>C	-	-
29881459	29881459	G	A	Intronic	Modifier	-	2	c.1084-253G>A	-	rs946441565
29881461	29881461	A	G	Intronic	Modifier	-	2	c.1084-251A>G	-	rs12484008
29881468	29881468	G	A	Intronic	Modifier	-	2	c.1084-244G>A	-	rs3815335
29881537	29881537	C	T	Intronic	Modifier	-	2	c.1084-175C>T	-	rs78248741
29881559	29881559	A	G	Intronic	Modifier	-	2	c.1084-153A>G	-	-
29881622	29881622	G	A	Intronic	Modifier	-	2	c.1084-90G>A	-	rs368599359
29881633	29881633	G	A	Intronic	Modifier	-	2	c.1084-79G>A	-	rs533283887
29881645	29881645	G	A	Intronic	Modifier	-	2	c.1084-67G>A	-	rs551382175
29881673	29881673	A	G	Intronic	Modifier	-	2	c.1084-39A>G	-	rs755841191
29881683	29881683	A	G	Intronic	Modifier	-	2	c.1084-29A>G	-	-
29881703	29881703	C	T	Intronic	Low	-	2	c.1084-9C>T	-	-
29881704	29881704	C	G	Intronic	Low	-	2	c.1084-8C>G	-	-
29881727	29881727	C	T	Synonymous	Low	3	-	c.1099C>T	p.Leu367Leu	-
29881776	29881776	G	A	Missense	Moderate	3	-	c.1148G>A	p.Arg383Gln	rs377149236
29881797	29881797	A	C	Missense	Moderate	3	-	c.1169A>C	p.Asn390Thr	rs148653339
29881810	29881810	T	G	Synonymous	Low	3	-	c.1182T>G	p.Ala394Ala	rs1033200120
29881828	29881828	C	T	Synonymous	Low	3	-	c.1200C>T	p.Ala400Ala	rs165734
29881854	29881854	T	C	Intronic	Modifier	-	3	c.1208+18T>C	-	-
29881868	29881868	G	A	Intronic	Modifier	-	3	c.1208+32G>A	-	-
29881884	29881884	G	A	Intronic	Modifier	-	3	c.1208+48G>A	-	rs4823040
29881885	29881885	C	T	Intronic	Modifier	-	3	c.1208+49C>T	-	rs540168753
29881890	29881890	C	T	Intronic	Modifier	-	3	c.1208+54C>T	-	rs114903253
29881907	29881907	C	G	Intronic	Modifier	-	3	c.1208+71C>G	-	rs1187543862
29881962	29881962	C	T	Intronic	Modifier	-	3	c.1208+126C>T	-	rs1031194111

29881963	29881963	G	A	Intronic	Modifier	-	3	c.1208+127G>A	-	rs937910485
29881990	29881990	C	T	Intronic	Modifier	-	3	c.1208+154C>T	-	rs1466417517
29882005	29882005	C	A	Intronic	Modifier	-	3	c.1208+169C>A	-	rs1056424058
29882071	29882071	G	A	Intronic	Modifier	-	3	c.1208+235G>A	-	rs779090983
29882082	29882082	A	G	Intronic	Modifier	-	3	c.1208+246A>G	-	-
29882092	29882092	C	T	Intronic	Modifier	-	3	c.1208+256C>T	-	rs897689341
29882110	29882110	C	T	Intronic	Modifier	-	3	c.1208+274C>T	-	rs1012266468
29882111	29882111	G	A	Intronic	Modifier	-	3	c.1208+275G>A	-	rs28525662
29882150	29882150	C	T	Intronic	Modifier	-	3	c.1208+314C>T	-	rs1177767322
29882157	29882157	G	A	Intronic	Modifier	-	3	c.1208+321G>A	-	rs147136515
29882183	29882183	T	A	Intronic	Modifier	-	3	c.1208+347_1208+348insA	-	rs111690803
29882184	29882184	T	A	Intronic	Modifier	-	3	c.1208+348T>A	-	rs190911251
29882187	29882187	T	A	Intronic	Modifier	-	3	c.1208+351T>A	-	rs375863529
29882247	29882247	C	G	Intronic	Modifier	-	3	c.1208+411C>G	-	rs143316545
29882294	29882294	G	A	Intronic	Modifier	-	3	c.1208+458G>A	-	rs5997481
29882303	29882303	C	T	Intronic	Modifier	-	3	c.1208+467C>T	-	-
29882324	29882324	A	G	Intronic	Modifier	-	3	c.1208+488A>G	-	rs6006162
29882326	29882326	G	C	Intronic	Modifier	-	3	c.1208+490G>C	-	rs903889822
29882328	29882328	T	A	Intronic	Modifier	-	3	c.1208+492T>A	-	-
29882386	29882386	G	C	Intronic	Modifier	-	3	c.1208+550G>C	-	-
29882403	29882403	T	C	Intronic	Modifier	-	3	c.1208+567T>C	-	rs1319062352
29882443	29882443	G	A	Intronic	Modifier	-	3	c.1208+607G>A	-	rs188013725
29882460	29882460	C	T	Intronic	Modifier	-	3	c.1208+624C>T	-	rs555368787
29882484	29882484	T	A	Intronic	Modifier	-	3	c.1208+648T>A	-	-
29882489	29882489	T	A	Intronic	Modifier	-	3	c.1208+653T>A	-	rs752352485
29882500	29882500	A	T	Intronic	Modifier	-	3	c.1208+664A>T	-	rs1240145238
29882506	29882506	G	T	Intronic	Modifier	-	3	c.1208+671dup	-	-
29882508	29882508	TC	-	Intronic	Modifier	-	3	c.1208+672del	-	rs527873265
29882530	29882530	TTTTG	-	Intronic	Modifier	-	3	c.1208+691_1208+694del	-	rs1198608745
29882546	29882546	C	T	Intronic	Modifier	-	3	c.1208+710C>T	-	rs757583792
29882555	29882555	A	T	Intronic	Modifier	-	3	c.1208+719A>T	-	rs193062610
29882556	29882556	G	A	Intronic	Modifier	-	3	c.1208+720G>A	-	rs963017814

29882569	29882569	C	T	Intronic	Modifier	-	3	c.1208+733C>T	-	rs1231911858
29882571	29882571	AG	-	Intronic	Modifier	-	3	c.1208+735del	-	-
29882573	29882573	A	C	Intronic	Modifier	-	3	c.1208+737A>C	-	rs780861559
29882580	29882580	C	T	Intronic	Modifier	-	3	c.1208+744C>T	-	rs1392375542
29882630	29882630	G	A	Intronic	Modifier	-	3	c.1208+794G>A	-	rs747407223
29882664	29882664	A	G	Intronic	Modifier	-	3	c.1208+828A>G	-	-
29882687	29882687	T	A	Intronic	Modifier	-	3	c.1208+851T>A	-	rs150888215
29882693	29882693	G	A	Intronic	Modifier	-	3	c.1208+857G>A	-	rs531344127
29882694	29882694	T	G	Intronic	Modifier	-	3	c.1208+858T>G	-	-
29882713	29882713	T	C	Intronic	Modifier	-	3	c.1208+877T>C	-	-
29882715	29882715	T	C	Intronic	Modifier	-	3	c.1208+879T>C	-	-
29882738	29882738	C	T	Intronic	Modifier	-	3	c.1208+902C>T	-	-
29882754	29882754	C	T	Intronic	Modifier	-	3	c.1208+918C>T	-	rs1051929078
29882755	29882755	G	A	Intronic	Modifier	-	3	c.1208+919G>A	-	rs139362410
29882760	29882760	C	T	Intronic	Modifier	-	3	c.1208+924C>T	-	rs551722146
29882791	29882791	C	A	Intronic	Modifier	-	3	c.1208+955C>A	-	rs537125677
29882794	29882794	G	A	Intronic	Modifier	-	3	c.1208+958G>A	-	rs1026424254
29882813	29882813	A	G	Intronic	Modifier	-	3	c.1208+977A>G	-	rs1299918179
29882830	29882830	C	T	Intronic	Modifier	-	3	c.1208+994C>T	-	rs556908766
29882838	29882838	C	A	Intronic	Modifier	-	3	c.1208+1002C>A	-	rs187342281
29882849	29882849	G	T	Intronic	Modifier	-	3	c.1208+1013G>T	-	rs980830606
29882850	29882850	A	C	Intronic	Modifier	-	3	c.1208+1014A>C	-	rs925373768
29882857	29882857	C	T	Intronic	Modifier	-	3	c.1208+1021C>T	-	rs936782201
29882864	29882864	A	G	Intronic	Modifier	-	3	c.1208+1028A>G	-	rs913923260
29882865	29882865	G	A	Intronic	Modifier	-	3	c.1208+1029G>A	-	rs1205303005
29882882	29882882	C	T	Intronic	Modifier	-	3	c.1208+1046C>T	-	rs764790044
29882902	29882902	C	T	Intronic	Modifier	-	3	c.1208+1066C>T	-	-
29882915	29882915	G	C	Intronic	Modifier	-	3	c.1208+1079G>C	-	rs1486110150

29882945	29882945	A	G	Intronic	Modifier	-	3	c.1208+1109A>G	-	rs150023132
29882967	29882967	T	G	Intronic	Modifier	-	3	c.1208+1131T>G	-	-
29882973	29882973	C	T	Intronic	Modifier	-	3	c.1208+1137C>T	-	rs165899
29882976	29882976	C	G	Intronic	Modifier	-	3	c.1208+1140C>G	-	rs542818912
29883007	29883007	A	T	Intronic	Modifier	-	3	c.1208+1171A>T	-	-
29883018	29883018	A	G	Intronic	Modifier	-	3	c.1208+1182A>G	-	rs573136532
29883076	29883076	C	T	Intronic	Modifier	-	3	c.1208+1240C>T	-	rs553734179
29883087	29883087	A	T	Intronic	Modifier	-	3	c.1208+1251A>T	-	rs1304338716
29883094	29883094	CA	-	Intronic	Modifier	-	3	c.1208+1258del	-	-
29883123	29883123	TAGTC	-	Intronic	Modifier	-	3	c.1208+1287_1208+1290del	-	rs362061
29883162	29883162	C	G	Intronic	Modifier	-	3	c.1208+1326C>G	-	-
29883164	29883164	G	T	Intronic	Modifier	-	3	c.1208+1328G>T	-	rs561170932
29883165	29883165	G	C	Intronic	Modifier	-	3	c.1208+1329G>C	-	-
29883208	29883208	T	C	Intronic	Modifier	-	3	c.1208+1372T>C	-	rs1201391625
29883254	29883254	G	T	Intronic	Modifier	-	3	c.1208+1418G>T	-	-
29883316	29883316	C	G	Intronic	Modifier	-	3	c.1208+1480C>G	-	-
29883346	29883346	G	A	Intronic	Modifier	-	3	c.1209-1492G>A	-	rs189670956
29883380	29883380	G	A	Intronic	Modifier	-	3	c.1209-1458G>A	-	-
29883413	29883413	G	C	Intronic	Modifier	-	3	c.1209-1425G>C	-	-
29883466	29883466	A	AAG	Intronic	Modifier	-	3	c.1209-1370_1209-1369insGAA	-	rs1285972523

29883513	29883513	C	T	Intronic	Modifier	-	3	c.1209-1325C>T	-	rs1030352345
29883524	29883524	C	T	Intronic	Modifier	-	3	c.1209-1314C>T	-	rs750190295
29883525	29883525	G	A	Intronic	Modifier	-	3	c.1209-1313G>A	-	rs950766752
29883530	29883530	A	T	Intronic	Modifier	-	3	c.1209-1308A>T	-	-
29883561	29883561	C	T	Intronic	Modifier	-	3	c.1209-1277C>T	-	-
29883568	29883568	C	T	Intronic	Modifier	-	3	c.1209-1270C>T	-	-
29883576	29883576	G	A	Intronic	Modifier	-	3	c.1209-1262G>A	-	rs373486863
29883630	29883630	TAAC	-	Intronic	Modifier	-	3	c.1209-1203_1209-1201del	-	rs916778818
29883635	29883635	A	C	Intronic	Modifier	-	3	c.1209-1203A>C	-	rs1418123505
29883636	29883636	C	A	Intronic	Modifier	-	3	c.1209-1202C>A	-	rs1164703398
29883648	29883648	A	C	Intronic	Modifier	-	3	c.1209-1190A>C	-	-
29883658	29883658	C	T	Intronic	Modifier	-	3	c.1209-1180C>T	-	rs1281070945
29883659	29883659	G	A	Intronic	Modifier	-	3	c.1209-1179G>A	-	rs143625327
29883662	29883662	C	T	Intronic	Modifier	-	3	c.1209-1176C>T	-	rs1334347932
29883710	29883710	C	G	Intronic	Modifier	-	3	c.1209-1128C>G	-	-
29883714	29883714	G	A	Intronic	Modifier	-	3	c.1209-1124G>A	-	rs998962613
29883772	29883772	CACTT	-	Intronic	Modifier	-	3	c.1209-1066_1209-1063del	-	rs362231
29883787	29883787	A	G	Intronic	Modifier	-	3	c.1209-1051A>G	-	rs901063529
29883797	29883797	G	A	Intronic	Modifier	-	3	c.1209-1041G>A	-	rs571615682
29883810	29883810	A	C	Intronic	Modifier	-	3	c.1209-1028A>C	-	-
29883836	29883836	C	T	Intronic	Modifier	-	3	c.1209-1002C>T	-	rs781731242
29883842	29883842	G	T	Intronic	Modifier	-	3	c.1209-996G>T	-	rs563602777

29883892	29883892	G	T	Intronic	Modifier	-	3	c.1209-946G>T	-	rs174650
29883923	29883923	G	A	Intronic	Modifier	-	3	c.1209-915G>A	-	-
29883942	29883942	A	T	Intronic	Modifier	-	3	c.1209-896A>T	-	-
29883945	29883945	A	C	Intronic	Modifier	-	3	c.1209-893A>C	-	-
29883958	29883958	A	C	Intronic	Modifier	-	3	c.1209-880A>C	-	rs80091782
29884011	29884011	C	T	Intronic	Modifier	-	3	c.1209-827C>T	-	rs555103444
29884027	29884027	G	A	Intronic	Modifier	-	3	c.1209-811G>A	-	rs769503095
29884037	29884037	C	T	Intronic	Modifier	-	3	c.1209-801C>T	-	-
29884047	29884047	C	T	Intronic	Modifier	-	3	c.1209-791C>T	-	-
29884073	29884073	C	T	Intronic	Modifier	-	3	c.1209-765C>T	-	rs141161567
29884123	29884123	G	A	Intronic	Modifier	-	3	c.1209-715G>A	-	rs566071826
29884131	29884131	C	T	Intronic	Modifier	-	3	c.1209-707C>T	-	rs528754360
29884181	29884181	C	T	Intronic	Modifier	-	3	c.1209-657C>T	-	rs567502217
29884182	29884182	G	A	Intronic	Modifier	-	3	c.1209-656G>A	-	rs185791469
29884208	29884208	C	T	Intronic	Modifier	-	3	c.1209-630C>T	-	rs377340059
29884226	29884226	G	A	Intronic	Modifier	-	3	c.1209-612G>A	-	rs1432228295
29884229	29884229	CGTGCGCCT	-	Intronic	Modifier	-	3	c.1209-614_1209-607del	-	-
29884231	29884231	T	C	Intronic	Modifier	-	3	c.1209-607T>C	-	rs956995883
29884235	29884235	C	T	Intronic	Modifier	-	3	c.1209-603C>T	-	rs971572887
29884278	29884278	G	A	Intronic	Modifier	-	3	c.1209-560G>A	-	rs935759554
29884285	29884285	T	G	Intronic	Modifier	-	3	c.1209-553T>G	-	rs571203555
29884367	29884367	G	A	Intronic	Modifier	-	3	c.1209-471G>A	-	rs536728781
29884432	29884432	T	C	Intronic	Modifier	-	3	c.1209-406T>C	-	-
29884485	29884485	T	C	Intronic	Modifier	-	3	c.1209-353T>C	-	rs6006163
29884509	29884509	G	T	Intronic	Modifier	-	3	c.1209-329G>T	-	rs760318118
29884520	29884520	T	C	Intronic	Modifier	-	3	c.1209-318T>C	-	rs886441058
29884567	29884567	C	T	Intronic	Modifier	-	3	c.1209-271C>T	-	rs165624
29884574	29884574	A	G	Intronic	Modifier	-	3	c.1209-264A>G	-	-
29884575	29884575	G	T	Intronic	Modifier	-	3	c.1209-263G>T	-	rs181661746
29884599	29884599	C	T	Intronic	Modifier	-	3	c.1209-239C>T	-	-
29884603	29884603	A	G	Intronic	Modifier	-	3	c.1209-235A>G	-	rs557043300
29884612	29884612	A	T	Intronic	Modifier	-	3	c.1209-226A>T	-	rs1022377385

29884639	29884639	C	T	Intronic	Modifier	-	3	c.1209-199C>T	-	rs541500423
29884640	29884640	G	A	Intronic	Modifier	-	3	c.1209-198G>A	-	rs912855297
29884643	29884643	G	T	Intronic	Modifier	-	3	c.1209-195G>T	-	rs751682286
29884650	29884650	T	C	Intronic	Modifier	-	3	c.1209-188T>C	-	rs982583256
29884712	29884712	T	G	Intronic	Modifier	-	3	c.1209-126T>G	-	rs1323270119
29884734	29884734	C	T	Intronic	Modifier	-	3	c.1209-104C>T	-	rs565596168
29884736	29884736	C	G	Intronic	Modifier	-	3	c.1209-102C>G	-	rs1039501899
29884799	29884799	C	T	Intronic	Modifier	-	3	c.1209-39C>T	-	rs376487122
29884804	29884804	GT	-	Intronic	Modifier	-	3	c.1209-32del	-	rs1427581204
29884809	29884809	A	G	Intronic	Modifier	-	3	c.1209-29A>G	-	rs746250651
29884814	29884814	T	C	Intronic	Modifier	-	3	c.1209-24T>C	-	rs770018275
29884817	29884817	G	A	Intronic	Modifier	-	3	c.1209-21G>A	-	rs201134753
29884869	29884869	G	A	Missense	Moderate	4	-	c.1240G>A	p.Gly414Ser	-
29884881	29884881	A	G	Missense	Moderate	4	-	c.1252A>G	p.Ile418Val	rs751075628
29884939	29884939	A	G	Missense	Moderate	4	-	c.1310A>G	p.Lys437Arg	rs1602971285
29884940	29884940	G	T	Missense	Moderate	4	-	c.1311G>T	p.Lys437Asn	-
29884950	29884950	G	A	Missense	Moderate	4	-	c.1321G>A	p.Glu441Lys	rs145061116
29884976	29884976	G	C	Missense	Moderate	4	-	c.1347G>C	p.Lys449Asn	rs199932977
29885016	29885016	G	A	Missense	Moderate	4	-	c.1387G>A	p.Glu463Lys	rs59371099
29885058	29885058	G	C	Missense	Moderate	4	-	c.1429G>C	p.Glu477Gln	-
29885075	29885075	G	A	Synonymous	Low	4	-	c.1446G>A	p.Glu482Glu	rs5997482
29885120	29885120	TGAAGAAGAGGAGGCAGAAGGGGGA	-	In-frame Deletion	Moderate	4	-	c.1476_1499del	p.Glu493_Glu500del	rs748774766
29885127	29885127	G	AAACAA	In-frame Insertion	Moderate	4	-	c.1500_1505dup	p.Thr501_Lys502dup	rs576586746
29885164	29885164	C	G	Missense	Moderate	4	-	c.1535C>G	p.Pro512Arg	-
29885198	29885198	G	C	Missense	Moderate	4	-	c.1569G>C	p.Glu523Asp	rs138278265
29885202	29885202	A	G	Missense	Moderate	4	-	c.1573A>G	p.Lys525Glu	rs751816018
29885204	29885204	G	C	Missense	Moderate	4	-	c.1575G>C	p.Lys525Asn	rs149183166
29885255	29885255	C	T	Synonymous	Low	4	-	c.1626C>T	p.Ala542Ala	rs747901802
29885260	29885260	CCAAGTCCCCAGAGAAGGAGGAAGCAAAATCCCCAGCCGAAGT	-	In-frame Deletion	Moderate	4	-	c.1599_1640del	p.Glu536_Lys549del	rs1353196821

29885308	29885308	C	T	Missense	Moderate	4	-	c.1679C>T	p.Ser560Leu	rs750569231
29885311	29885311	C	T	Missense	Moderate	4	-	c.1682C>T	p.Pro561Leu	rs548556825
29885313	29885313	C	G	Missense	Moderate	4	-	c.1684C>G	p.Pro562Ala	rs530872313
29885369	29885369	C	T	Synonymous	Low	4	-	c.1740C>T	p.Ser580Ser	rs114263951
29885378	29885378	G	GAA	In-frame Insertion	Moderate	4	-	c.1750_1751insAAG	p.Lys583_Ala584insGlu	-
29885383	29885383	A	G	Missense	Moderate	4	-	c.1754A>G	p.Lys585Arg	-
29885386	29885386	C	T	Missense	Moderate	4	-	c.1757C>T	p.Ser586Phe	-
29885403	29885403	G	T	Missense	Moderate	4	-	c.1774G>T	p.Ala592Ser	rs768529407
29885412	29885412	C	T	Missense	Moderate	4	-	c.1783C>T	p.Pro595Ser	rs6006165
29885423	29885423	AAAGTCACCGGCTGAGGCC	-	In-frame Deletion	Moderate	4	-	c.1782_1799del	p.Ala596_Pro601del	-
29885425	29885425	A	C	Missense	Moderate	4	-	c.1796A>C	p.Lys599Thr	rs1403224343
29885436	29885436	A	AGGCCAAGTCCCCAGCGAAGGAAGAAGCAAAGTCCCCGGCTG	In-frame Insertion	Moderate	4	-	c.1822_1823insCGAAGGAAGAAGCAAAGTCCCCGGCTGAGGCCAAGTCCCCAG	p.Pro607_Val608insAlaLysGluGluAlaLysSerProAlaGluAlaLysSerPro	-
29885438	29885438	G	GAA	In-frame Insertion	Moderate	4	-	c.1810_1811insAAG	p.Lys603_Ala604insGlu	-
29885462	29885462	A	G	Synonymous	Low	4	-	c.1833A>G	p.Glu611Glu	rs1196681707
29885475	29885475	G	C	Missense	Moderate	4	-	c.1846G>C	p.Ala616Pro	rs1398309477
29885508	29885508	A	C	Missense	Moderate	4	-	c.1879A>C	p.Lys627Gln	rs1353842666
29885554	29885554	C	T	Missense	Moderate	4	-	c.1925C>T	p.Thr642Met	rs117258406
29885556	29885556	CCAGCTGAGGTCAAGTCCCCGGAAAAGGCCAAGTCTCCAACGA	-	In-frame Deletion	Moderate	4	-	c.1886_1927del	p.Pro629_Lys643delinsGln	-
29885558	29885558	AGCTGAGGTCAAGTCCCCGGAAAAGGCCAAGTCTCCAACGAAG	-	In-frame Deletion	Moderate	4	-	c.1889_1930del	p.Ala630_Lys643del	-
29885564	29885564	GGTCAAGTCCCCGGAAAAGGCCAAGTCTCCAACGAAGGAGGAA	-	In-frame Deletion	Moderate	4	-	c.1895_1936del	p.Val632_Glu645del	-
29885564	29885564	A	GCAAAGTCCCCTGAGAAG	In-frame Insertion	Moderate	4	-	c.1938_1955dup	p.Ala652_Lys657dup	-

29885570	29885570	G	C	Missense	Moderate	4	-	c.1941G>C	p.Lys647Asn	rs200634512
29885571	29885571	T	CCCCTGAGAAGGCCAAGG	In-frame Insertion	Moderate	4	-	c.1959_1960insGCCCCTGAGAAGGCCAAG	p.Lys653_Ser654insAlaProGluLysAlaLys	-
29885576	29885576	GGAAAAGGCCAAGTCTCCAACGAAGGAGGAAGCAAAGTCCCCT	-	In-frame Deletion	Moderate	4	-	c.1908_1949del	p.Thr642_Pro655del	-
29885582	29885582	G	GCCAAGTCCCCTGAGAAC	In-frame Insertion	Moderate	4	-	c.1964_1965insTGAGAACGCCAAGTCCCC	p.Glu656_Lys657insAsnAlaLysSerProGlu	-
29885585	29885585	C	AAGGCCCCAGAGAAGGCA	In-frame Insertion	Moderate	4	-	c.1959_1960insGCCCCAGAGAAGGCAAAG	p.Lys653_Ser654insAlaProGluLysAlaLys	-
29885599	29885599	A	GGACAAGGCCCCAGCGAC	In-frame Insertion	Moderate	4	-	c.1973_1974insCAAGGCCCCAGCGACGGA	p.Lys657_Glu658insAspLysAlaProAlaThr	-
29885601	29885601	G	CC	Frameshift Insertion	High	4	-	c.1972_1973insCC	p.Glu658AlafsTer14	rs1427435154
29885604	29885604	AAGGCCAAGTCCCCAGAGAAGGAAG	-	In-frame Deletion	Moderate	4	-	c.1965_1988del	p.Glu658_Lys665del	rs267607533
29885604	29885604	AAGGAAG	-	In-frame Deletion	Moderate	4	-	c.1973_1978del	p.Glu658_Glu659del	rs149571560
29885622	29885622	GAGGCCAAGTCCCCTGAGA	-	In-frame Deletion	Moderate	4	-	c.1989_2006del	p.Glu664_Pro669del	rs267607534
29885622	29885622	A	AGGGAG	In-frame Insertion	Moderate	4	-	c.1996_1997insGAGAGG	p.Lys665_Ala666insGlyGlu	-
29885640	29885640	A	C	Missense	Moderate	4	-	c.2011A>C	p.Lys671Gln	-
29885648	29885648	A	G	Synonymous	Low	4	-	c.2019A>G	p.Glu673Glu	rs746048017
29885651	29885651	A	C	Synonymous	Low	4	-	c.2022A>C	p.Ala674Ala	rs763507482
29885711	29885711	C	T	Synonymous	Low	4	-	c.2082C>T	p.Ala694Ala	rs1452419487
29885736	29885736	A	C	Missense	Moderate	4	-	c.2107A>C	p.Lys703Gln	-
29885742	29885742	C	T	Missense	Moderate	4	-	c.2113C>T	p.Pro705Ser	rs770039871
29885783	29885783	C	T	Synonymous	Low	4	-	c.2154C>T	p.Ser718Ser	rs772385634
29885819	29885819	AAAGACCCCCGAGAAGGCCAAGTCCCCAGTGAAGGAAGAAGCT	C	In-frame Deletion	Moderate	4	-	c.2190_2232delinsC	p.Thr732_Lys745del	-
29885835	29885835	G	T	Missense	Moderate	4	-	c.2206G>T	p.Ala736Ser	-

29885861	29885861	AAAGACCCCGAGAAGGCCAAGTCCCCAGTGAAGGAAGAAGCT	C	In-frame Deletion	Moderate	4	-	c.2232_2274delinsC	p.Lys745_Ala758del	-
29885861	29885861	CAAGTCCCCAGTGAAGGAAGAAGCT	-	In-frame Deletion	Moderate	4	-	c.2219_2242del	p.Val740_Pro747del	rs778386609
29885870	29885870	CGAGAAGGCCAAGTCCCCAGTGAAGGAAGAAGCTAAGTCCCCA	-	In-frame Deletion	Moderate	4	-	c.2219_2260del	p.Val740_Pro753del	-
29885884	29885884	C	T	Missense	Moderate	4	-	c.2255C>T	p.Ser752Phe	-
29885913	29885913	A	G	Missense	Moderate	4	-	c.2284A>G	p.Lys762Glu	-
29885939	29885939	G	A	Synonymous	Low	4	-	c.2310G>A	p.Ala770Ala	rs757096652
29885959	29885959	C	T	Missense	Moderate	4	-	c.2330C>T	p.Pro777Leu	rs199748453
29885976	29885976	G	A	Missense	Moderate	4	-	c.2347G>A	p.Glu783Lys	-
29885996	29885996	CAAG	-	In-frame Deletion	Moderate	4	-	c.2368_2370del	p.Lys790del	rs59551486
29886001	29886001	A	C	Missense	Moderate	4	-	c.2372A>C	p.Glu791Ala	-
29886025	29886025	C	T	Missense	Moderate	4	-	c.2396C>T	p.Ala799Val	rs375529650
29886026	29886026	G	A	Synonymous	Low	4	-	c.2397G>A	p.Ala799Ala	rs376035598
29886034	29886034	C	T	Missense	Moderate	4	-	c.2405C>T	p.Pro802Leu	rs758520448
29886043	29886043	A	C	Missense	Moderate	4	-	c.2414A>C	p.Glu805Ala	rs165602
29886044	29886044	G	A	Synonymous	Low	4	-	c.2415G>A	p.Glu805Glu	rs940285527
29886069	29886069	A	G	Missense	Moderate	4	-	c.2440A>G	p.Ile814Val	rs748832999
29886072	29886072	C	A	Missense	Moderate	4	-	c.2443C>A	p.Pro815Thr	-
29886088	29886088	T	C	Missense	Moderate	4	-	c.2459T>C	p.Val820Ala	-
29886140	29886140	G	A	Synonymous	Low	4	-	c.2511G>A	p.Glu837Glu	rs751566708
29886147	29886147	A	G	Missense	Moderate	4	-	c.2518A>G	p.Lys840Glu	rs750908593
29886189	29886189	CAG	-	Frameshift Variant	High	4	-	c.2561_2562del	p.Glu854GlyfsTer37	rs775700827
29886200	29886200	G	A	Synonymous	Low	4	-	c.2571G>A	p.Lys857Lys	rs145669735
29886230	29886230	G	T	Missense	Moderate	4	-	c.2601G>T	p.Lys867Asn	rs138156220
29886253	29886253	TGGA	-	In-frame Deletion	Moderate	4	-	c.2626_2628del	p.Glu876del	rs768937935
29886268	29886268	C	T	Missense	Moderate	4	-	c.2639C>T	p.Pro880Leu	rs756683695
29886275	29886275	C	T	Synonymous	Low	4	-	c.2646C>T	p.Val882Val	rs528790943

29886276	29886276	G	A	Missense	Moderate	4	-	c.2647G>A	p.Glu883Lys	rs754121553
29886289	29886289	A	G	Missense	Moderate	4	-	c.2660A>G	p.Glu887Gly	-
29886352	29886352	A	G	Missense	Moderate	4	-	c.2723A>G	p.Lys908Arg	-
29886360	29886360	C	T	Missense	Moderate	4	-	c.2731C>T	p.Pro911Ser	rs376751999
29886375	29886375	G	A	Missense	Moderate	4	-	c.2746G>A	p.Val916Met	rs762057603
29886386	29886386	C	T	Synonymous	Low	4	-	c.2757C>T	p.Asp919Asp	rs56200920
29886400	29886400	A	C	Missense	Moderate	4	-	c.2771A>C	p.Glu924Ala	rs199737170
29886413	29886413	A	G	Synonymous	Low	4	-	c.2784A>G	p.Val928Val	rs165625
29886415	29886415	C	A	Missense	Moderate	4	-	c.2786C>A	p.Ala929Asp	-
29886478	29886478	C	T	Missense	Moderate	4	-	c.2849C>T	p.Ala950Val	rs553629461
29886485	29886485	G	A	Synonymous	Low	4	-	c.2856G>A	p.Pro952Pro	rs147416824
29886498	29886498	A	G	Missense	Moderate	4	-	c.2869A>G	p.Thr957Ala	rs760693353
29886509	29886509	G	T	Missense	Moderate	4	-	c.2880G>T	p.Glu960Asp	rs372070551
29886517	29886517	A	G	Missense	Moderate	4	-	c.2888A>G	p.Lys963Arg	rs1480895257
29886543	29886543	CAG	-	Frameshift Variant	High	4	-	c.2915_2916del	p.Glu972GlyfsTer7	rs1346887118
29886635	29886635	A	G	Synonymous	Low	4	-	c.3006A>G	p.Gln1002Gln	rs768522862
29886673	29886673	A	G	Missense	Moderate	4	-	c.3044A>G	p.Lys1015Arg	-
29886713	29886713	C	T	3' UTR	Modifier	4	-	c.*21C>T		rs191972471
29886714	29886714	G	A	3' UTR	Modifier	4	-	c.*22G>A		rs183499750
29886718	29886718	C	G	3' UTR	Modifier	4	-	c.*26C>G		rs374202245
29886726	29886726	G	A	3' UTR	Modifier	4	-	c.*34G>A		-
29886744	29886744	G	A	3' UTR	Modifier	4	-	c.*52G>A		rs766995345
29886758	29886758	A	G	3' UTR	Modifier	4	-	c.*66A>G		rs753770865
29886778	29886778	T	C	3' UTR	Modifier	4	-	c.*86T>C		rs1270308635
29886797	29886797	GA	-	3' UTR	Modifier	4	-	c.*106del		rs748195897
29886798	29886798	A	G	3' UTR	Modifier	4	-	c.*106A>G		rs771159816
29886815	29886815	C	T	3' UTR	Modifier	4	-	c.*123C>T		rs781167046
29886835	29886835	A	G	3' UTR	Modifier	4	-	c.*143A>G		rs1050302661
29886840	29886840	AT	-	3' UTR	Modifier	4	-	c.*150del		rs747501203
29886852	29886852	A	G	3' UTR	Modifier	4	-	c.*160A>G		-
29886893	29886893	G	T	3' UTR	Modifier	4	-	c.*201G>T		rs1061373
29886906	29886906	C	T	3' UTR	Modifier	4	-	c.*214C>T		rs533220152
29886907	29886907	G	A	3' UTR	Modifier	4	-	c.*215G>A		rs755046912

29886909	29886909	T	C	3' UTR	Modifier	4	-	c.*217T>C		rs897216138
29887012	29887012	T	C	3' UTR	Modifier	4	-	c.*320T>C		rs192696400
29887018	29887018	G	A	3' UTR	Modifier	4	-	c.*326G>A		-
29887053	29887053	G	C	3' UTR	Modifier	4	-	c.*361G>C		rs185039421
29887072	29887072	C	T	3' UTR	Modifier	4	-	c.*380C>T		rs978569780
29887112	29887112	TTC	-	3' UTR	Modifier	4	-	c.*420_*421del		rs1490643558
29887148	29887148	G	A	3' UTR	Modifier	4	-	c.*456G>A		-
29887151	29887151	C	G	3' UTR	Modifier	4	-	c.*459C>G		rs540106485
29887182	29887182	C	T	3' UTR	Modifier	4	-	c.*490C>T		rs142042497
29887186	29887186	G	C	3' UTR	Modifier	4	-	c.*494G>C		rs710195
29887211	29887211	C	T	3' UTR	Modifier	4	-	c.*519C>T		rs911785075
29887212	29887212	G	A	3' UTR	Modifier	4	-	c.*520G>A		rs944633264
29887216	29887216	T	C	3' UTR	Modifier	4	-	c.*524T>C		rs1218993302
29887227	29887227	G	T	3' UTR	Modifier	4	-	c.*535G>T		rs772755733
29887238	29887238	A	G	3' UTR	Modifier	4	-	c.*546A>G		rs561850196
29887249	29887249	G	A	3' UTR	Modifier	4	-	c.*557G>A		rs1321602381
29887271	29887271	A	T	3' UTR	Modifier	4	-	c.*579A>T		-
29887315	29887315	G	C	3' UTR	Modifier	4	-	c.*623G>C		-

Table A11. Details of all of the 591 variants (hg19) identified in the Project MinE dataset. HGVS.c notation refers to the ENST00000310624.6 transcript. HGVS.p notation refers to the ENSP00000311997.6 protein transcript.

Variant	**No. Studies**	**N Cases**	**N Controls**	**Fixed OR (95% CI; p-value)**	**Random OR (95% CI; p-value)**	**Heterogeneity (Q statistic; p-value)**	**Heterogeneity (I-squared)**	**Publication Bias (Egger t statistic; p-value)**	**Publication Bias (Harbord t statistic; p-value)**
A90V	2	6569	2534	2.45 (0.42-14.51; 0.32)	2.47 (0.42-14.47; 0.32)	0.02 (0.88)	0%	N/A	N/A
G249S	3	6940	3245	1.10 (0.71-1.70; 0.68)	1.10 (0.70-1.70; 0.69)	0.79 (0.67)	0%	0.14; 0.91	0.40; 0.76
A314V	2	6840	3145	2.61 (0.27-25.00; 0.41)	2.55 (0.26-24.53; 0.42)	0.50 (0.48)	0%	N/A	N/A
E463K	2	7595	3047	0.95 (0.85-1.06; 0.36)	0.95 (0.85-1.06; 0.36)	1.01 (0.31)	2%	N/A	N/A
T642M	4	7197	4044	1.39 (0.53-3.16; 0.56)	1.23 (0.46-3.28; 0.69)	3.29 (0.35)	9%	-0.44; 0.71	-1.21; 0.35
E658_K665del	3	7047	3364	0.68 (0.35-1.32; 0.25)	0.66 (0.34-1.29; 0.23)	0.96 (0.62)	0%	1.59; 0.36	2.58; 0.24
E664_P669del	2	6676	2653	1.22 (0.38-3.92; 0.74)	1.22 (0.38-3.93; 0.74)	0.01 (0.91)	0%	N/A	N/A
K790del	3	7951	3353	0.60 (0.28-1.29; 0.19)	0.63 (0.13-3.01; 0.57)	3.97 (0.14)	**50%**	0.81; 0.57	0.55; 0.68
E805A	3	7966	3758	1.01 (0.93-1.11; 0.76)	1.02 (0.93-1.11; 0.75)	2.89 (0.24)	31%	N/A	N/A
K867N	2	6651	2624	1.94 (0.20-18.60; 0.57)	1.88 (0.20-18.15; 0.58)	0.20 (0.66)	0%	N/A	N/A

Table A12. Results of variant-level meta-analysis when including the Project MinE cohort as an additional study. Meta-analysis was repeated for 5 variants (G249S, T642M, E658_K665del, K790del, E805A)), and new meta-analysis was performed for 5 variants (A90V, A314V, E463K, E664_P669del, K867N), who now have sufficient evidence to be included (≥2 case-control studies). N/A values represent instances where publication bias could not be calculated as the minimum number of studies used for calculation was not reached.

Variant	**Start**	**End**	**Ref**	**Alt**	**SIFT**	**PolyPhen**	**Total Frequency (Case/Control)**
G414S	29884869	29884869	G	A	Tolerated	Possibly Damaging	1 (0/1)
K437R	29884939	29884939	A	G	Deleterious	Probably Damaging	1 (1/0)
K437N	29884940	29884940	G	T	Deleterious	Probably Damaging	1 (1/0)
E441K	29884950	29884950	G	A	Deleterious	Probably Damaging	1 (0/1)
K449N	29884976	29884976	G	C	Deleterious	Probably Damaging	1 (1/0)
E477Q	29885058	29885058	G	C	Deleterious	Possibly Damaging	1 (1/0)
P512R	29885164	29885164	C	G	Deleterious	Possibly Damaging	1 (1/0)
E523D	29885198	29885198	G	C	Deleterious	Benign	1 (1/0)
K525E	29885202	29885202	A	G	Deleterious	Benign	1 (1/0)
S560L	29885308	29885308	C	T	Deleterious	Benign	1 (1/0)
P561L	29885311	29885311	C	T	Deleterious	Benign	1 (1/0)
K585R	29885383	29885383	A	G	Deleterious	Possibly Damaging	2 (1/1)
S586F	29885386	29885386	C	T	Deleterious	Benign	1 (0/1)
A592S	29885403	29885403	G	T	Deleterious	Benign	2 (2/0)
K599T	29885425	29885425	A	C	Deleterious	Probably Damaging	1 (0/1)
K627Q	29885508	29885508	A	C	Deleterious	Benign	1 (1/0)
K647N	29885570	29885570	G	C	Deleterious (Low Confidence)	Possibly Damaging	1 (1/0)
E658_E659del	29885598	29885598	AAGGAAG	A	-	-	36 (31/5)
E664_P669del	29885604	29885604	GAGGCCA	G	-	-	13 (10/3)
K671Q	29885640	29885640	A	C	Deleterious (Low Confidence)	Possibly Damaging	2 (1/1)
K703Q	29885736	29885736	A	C	Deleterious (Low Confidence)	Probably Damaging	1 (1/0)
P705S	29885742	29885742	C	T	Deleterious (Low Confidence)	Probably Damaging	1 (1/0)
A736S	29885835	29885835	G	T	Deleterious (Low Confidence)	Benign	1 (1/0)
S752F	29885884	29885884	C	T	Deleterious (Low Confidence)	Possibly Damaging	1 (1/0)
P777L	29885959	29885959	C	T	Deleterious (Low Confidence)	Probably Damaging	1 (1/0)
K790del	29885996	29885996	CAAG	C	-	-	18 (9/9)
E791A	29886001	29886001	A	C	Deleterious (Low Confidence)	Benign	1 (1/0)

P802L	29886034	29886034	C	T	Deleterious (Low Confidence)	Benign	1 (1/0)
K840E	29886147	29886147	A	G	Tolerated (Low Confidence)	Possibly Damaging	1 (1/0)
K867N	29886230	29886230	G	T	Deleterious (Low Confidence)	Probably Damaging	1 (1/0)
P880L	29886268	29886268	C	T	Deleterious (Low Confidence)	Benign	1 (1/0)
E883K	29886276	29886276	G	A	Deleterious (Low Confidence)	Probably Damaging	1 (1/0)
E887G	29886289	29886289	A	G	Deleterious (Low Confidence)	Benign	1 (1/0)
K908R	29886352	29886352	A	G	Deleterious (Low Confidence)	Benign	1 (1/0)
V916M	29886375	29886375	G	A	Deleterious (Low Confidence)	Benign	4 (4/0)
E924A	29886400	29886400	A	C	Deleterious (Low Confidence)	Benign	2 (2/0)
A929D	29886415	29886415	C	A	Deleterious (Low Confidence)	Benign	1 (0/1)
A950V	29886478	29886478	C	T	Deleterious (Low Confidence)	Probably Damaging	2 (2/0)
K1015R	29886673	29886673	A	G	Deleterious (Low Confidence)	Benign	1 (1/0)

Table A13. Genomic coordinates (hg19) and pathogenicity prediction of the ultra-rare pathogenic missense and high-frequency rare in-frame deletion variants which were found to significantly increase the risk of ALS when performing burden analysis in the Project MinE dataset.

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Gene ID	Mean	log2Fold Change (lfc)	lfcSE	stat	p-value	p-value adjusted	weight
ENSG00000084090	1721.952	0.242756	0.041782	5.810036	6.25E-09	0.000101	2.293762
ENSG00000105887	2245.828	0.252967	0.046694	5.4175	6.04E-08	0.000448	2.492774
ENSG00000143319	298.83	-0.21298	0.04011	-5.30991	1.10E-07	0.00046	1.995423
ENSG00000125868	1916.511	0.346591	0.066092	5.244052	1.57E-07	0.00046	2.514347
ENSG00000151229	1712.515	0.296613	0.057164	5.188791	2.12E-07	0.00046	2.295759
ENSG00000164116	968.0289	0.32409	0.062948	5.148558	2.62E-07	0.00046	2.514347
ENSG00000107758	2081.728	0.283809	0.055477	5.115808	3.12E-07	0.00046	2.583187
ENSG00000135624	1176.327	0.252105	0.049392	5.104126	3.32E-07	0.00046	2.583187
ENSG00000215114	785.4728	0.182654	0.035798	5.102296	3.36E-07	0.00046	2.293762
ENSG00000266412	1772.36	0.212498	0.04176	5.088504	3.61E-07	0.00046	2.295759
ENSG00000198728	1276.734	-0.1693	0.033307	-5.08293	3.72E-07	0.00046	2.295759
ENSG00000173598	1129.096	0.284701	0.056138	5.071433	3.95E-07	0.00046	2.514347
ENSG00000119801	1224.95	0.274382	0.054132	5.068781	4.00E-07	0.00046	2.514347
ENSG00000259392	25.69186	-0.63532	0.122442	-5.18875	2.12E-07	0.00055	0.947688
ENSG00000078687	1841.534	-0.1989	0.03963	-5.01895	5.20E-07	0.00055	2.456745
ENSG00000103160	590.9191	0.249458	0.049912	4.997977	5.79E-07	0.000576	2.295759
ENSG00000155096	1937.293	0.23596	0.047507	4.966812	6.81E-07	0.000576	2.295759
ENSG00000091039	1869.347	0.222329	0.044784	4.96446	6.89E-07	0.000576	2.456745
ENSG00000101558	2149.075	0.183109	0.036914	4.960451	7.03E-07	0.000576	2.456745
ENSG00000144746	1332.314	0.29681	0.059881	4.956655	7.17E-07	0.000577	2.295759
ENSG00000260230	3763.358	0.198697	0.040171	4.946289	7.56E-07	0.00058	2.295759
ENSG00000185864	275.2925	-0.40285	0.082249	-4.898	9.68E-07	0.00062	2.025126
ENSG00000155304	829.9333	0.275986	0.056347	4.897959	9.68E-07	0.00062	2.293762
ENSG00000118432	1221.16	0.383092	0.078262	4.894973	9.83E-07	0.00062	2.225762
ENSG00000100804	558.0857	0.285526	0.058359	4.892575	9.95E-07	0.00062	2.293762
ENSG00000156136	265.4173	0.293191	0.060194	4.870728	1.11E-06	0.00062	2.225762
ENSG00000100030	4643.508	0.214551	0.044133	4.861481	1.17E-06	0.00062	2.583187
ENSG00000147044	801.0537	0.162133	0.033383	4.856746	1.19E-06	0.00062	2.514347
ENSG00000140391	2222.775	0.230645	0.047496	4.856053	1.20E-06	0.00062	2.514347
ENSG00000023734	918.7745	0.227714	0.046962	4.848882	1.24E-06	0.00062	2.225762
ENSG00000169116	1622.504	0.317037	0.065421	4.84613	1.26E-06	0.00062	2.225762
ENSG00000165672	710.933	0.279459	0.057687	4.844399	1.27E-06	0.00062	2.225762
ENSG00000143612	1279.955	0.210298	0.043461	4.83883	1.31E-06	0.00062	2.514347
ENSG00000106771	2464.576	0.203686	0.042129	4.834759	1.33E-06	0.00062	2.492774
ENSG00000102753	747.1184	0.190268	0.039629	4.801229	1.58E-06	0.000726	2.293762
ENSG00000115484	856.5296	0.25676	0.053554	4.79445	1.63E-06	0.00073	2.293762
ENSG00000223599	56.31848	-0.37378	0.075877	-4.92618	8.39E-07	0.000739	1.023066
ENSG00000176834	231.258	-0.24426	0.051114	-4.77881	1.76E-06	0.000739	2.225762
ENSG00000100934	1091.095	0.257899	0.054028	4.773422	1.81E-06	0.000739	2.293762
ENSG00000214193	519.0564	-0.2849	0.059785	-4.76539	1.88E-06	0.000739	2.29693
ENSG00000061676	5108.546	0.212295	0.044697	4.749684	2.04E-06	0.000739	2.583187
ENSG00000085662	486.9222	0.219263	0.046254	4.740455	2.13E-06	0.000787	2.29693
ENSG00000132341	1591.055	0.257585	0.054514	4.725089	2.30E-06	0.000787	2.514347
ENSG00000169018	2219.018	0.218945	0.046425	4.716132	2.40E-06	0.000787	2.514347
ENSG00000067560	1859.156	0.169361	0.035957	4.710065	2.48E-06	0.000787	2.583187
ENSG00000182220	1515.18	0.278711	0.059072	4.718169	2.38E-06	0.00083	2.295759
ENSG00000232931	1204.536	-0.31348	0.066491	-4.71457	2.42E-06	0.00083	2.293762
ENSG00000188803	411.0558	-0.47584	0.101163	-4.70365	2.56E-06	0.000848	2.225762
ENSG00000078140	1452.7	0.188588	0.04013	4.699484	2.61E-06	0.000848	2.293762
ENSG00000124486	3834.897	0.179042	0.038208	4.686052	2.79E-06	0.000848	2.456745
ENSG00000083720	1440.696	0.277057	0.059097	4.688184	2.76E-06	0.00087	2.295759
ENSG00000206149	577.4827	-0.3456	0.073684	-4.69025	2.73E-06	0.000871	2.225762
ENSG00000249673	259.7063	-0.27728	0.058918	-4.70614	2.52E-06	0.000879	1.977088
ENSG00000146433	1143.316	0.187559	0.040124	4.674533	2.95E-06	0.000879	2.293762
ENSG00000120265	1260.131	0.329445	0.070501	4.672925	2.97E-06	0.000896	2.225762
ENSG00000119446	381.1576	0.216776	0.046507	4.661176	3.14E-06	0.000903	2.295759
ENSG00000082458	1344.287	0.220027	0.047407	4.641254	3.46E-06	0.000957	2.225762

ENSG00000071073	1232.949	0.248443	0.053581	4.636771	3.54E-06	0.000957	2.295759
ENSG00000108924	2666.586	0.227575	0.049168	4.628525	3.68E-06	0.000957	2.492774
ENSG00000163630	900.3796	0.451432	0.09754	4.628151	3.69E-06	0.000957	2.225762
ENSG00000102401	1089.287	0.241552	0.052307	4.618003	3.87E-06	0.000957	2.295759
ENSG00000165934	776.0951	0.154109	0.033437	4.608993	4.05E-06	0.000957	2.295759
ENSG00000050165	6409.342	0.253925	0.055153	4.603973	4.15E-06	0.000957	2.583187
ENSG00000184408	736.6054	0.231484	0.050281	4.603779	4.15E-06	0.000957	2.514347
ENSG00000132294	2570.606	0.238936	0.052007	4.59427	4.34E-06	0.000957	2.514347
ENSG00000123836	1089.718	0.361735	0.078788	4.591261	4.41E-06	0.000957	2.583187
ENSG00000119414	851.3815	0.191817	0.041779	4.591183	4.41E-06	0.000957	2.514347
ENSG00000113595	1187.221	0.239731	0.052279	4.585612	4.53E-06	0.000957	2.583187
ENSG00000164032	442.6725	0.328643	0.071014	4.627869	3.69E-06	0.000984	1.995423
ENSG00000159674	121.7896	-0.44379	0.096327	-4.60708	4.08E-06	0.000984	2.189833
ENSG00000187094	1116.395	0.351872	0.076947	4.572933	4.81E-06	0.000995	2.514347
ENSG00000090447	162.5607	-0.2996	0.065045	-4.60594	4.11E-06	0.001011	1.995423
ENSG00000072135	439.2264	-0.22441	0.048903	-4.58892	4.46E-06	0.001011	2.225762
ENSG00000072401	202.8735	0.253116	0.055218	4.583934	4.56E-06	0.001011	2.295759
ENSG00000123091	2889.178	0.192521	0.042243	4.557514	5.18E-06	0.001011	2.456745
ENSG00000205339	1937.275	0.189092	0.041519	4.554354	5.25E-06	0.001011	2.583187
ENSG00000101966	1304.978	0.127584	0.028042	4.54968	5.37E-06	0.001011	2.583187
ENSG00000113575	1663.785	0.242499	0.053335	4.546686	5.45E-06	0.001027	2.514347
ENSG00000198668	26595.52	0.196944	0.043385	4.539412	5.64E-06	0.001058	2.492774
ENSG00000047597	280.2855	0.31585	0.06916	4.566967	4.95E-06	0.001062	2.025126
ENSG00000115839	1371.386	0.169783	0.037351	4.54555	5.48E-06	0.001062	2.295759
ENSG00000115091	1250.743	0.211337	0.046522	4.542727	5.55E-06	0.001062	2.295759
ENSG00000065154	1522.94	0.300507	0.066429	4.523765	6.07E-06	0.001062	2.583187
ENSG00000006007	803.6137	0.217806	0.048171	4.521542	6.14E-06	0.001062	2.514347
ENSG00000159459	1293.831	0.14561	0.032215	4.519931	6.19E-06	0.001062	2.583187
ENSG00000237887	61.35785	-0.36966	0.078593	-4.70352	2.56E-06	0.001074	0.989117
ENSG00000164841	195.5155	0.294075	0.064865	4.533674	5.80E-06	0.001074	2.295759
ENSG00000136750	986.8132	0.536389	0.118435	4.528995	5.93E-06	0.001074	2.293762
ENSG00000162378	2402.099	0.20499	0.045417	4.51353	6.38E-06	0.001074	2.456745
ENSG00000196950	2588.512	0.321057	0.071207	4.508788	6.52E-06	0.001074	2.492774
ENSG00000165434	2862.022	0.380763	0.084462	4.508115	6.54E-06	0.001081	2.456745
ENSG00000178974	924.8954	0.210421	0.046865	4.489915	7.13E-06	0.001108	2.583187
ENSG00000102471	1659.68	0.295537	0.065494	4.512437	6.41E-06	0.001109	2.295759
ENSG00000171867	6006.938	0.238464	0.053181	4.483986	7.33E-06	0.001115	2.583187
ENSG00000168283	445.7878	0.242222	0.053692	4.511307	6.44E-06	0.00112	2.225762
ENSG00000196792	713.0654	0.140627	0.031254	4.499494	6.81E-06	0.00112	2.295759
ENSG00000243915	113.4061	-0.29369	0.065334	-4.49524	6.95E-06	0.00112	2.338927
ENSG00000142686	1415.688	0.27173	0.060679	4.478135	7.53E-06	0.00112	2.583187
ENSG00000001561	892.7404	0.290946	0.064744	4.493827	7.00E-06	0.001138	2.293762
ENSG00000182481	350.5815	0.297752	0.065927	4.516398	6.29E-06	0.001206	1.918337
ENSG00000198791	1289.091	0.211858	0.047529	4.457471	8.29E-06	0.001206	2.514347
ENSG00000163950	327.2803	0.215807	0.048098	4.486808	7.23E-06	0.001232	1.977088
ENSG00000125386	877.1625	-0.16944	0.037914	-4.46901	7.86E-06	0.001232	2.225762
ENSG00000005812	679.7816	0.182184	0.040775	4.468002	7.90E-06	0.001232	2.293762
ENSG00000197006	778.5986	0.223899	0.050184	4.461524	8.14E-06	0.001232	2.293762
ENSG00000109929	1460.464	0.224821	0.050421	4.458894	8.24E-06	0.001232	2.225762
ENSG00000064726	1213.656	0.231767	0.05204	4.453595	8.44E-06	0.001232	2.293762
ENSG00000186432	1430.525	0.179137	0.040323	4.44257	8.89E-06	0.001232	2.583187
ENSG00000113013	2771.068	0.18897	0.042551	4.440976	8.96E-06	0.001232	2.456745
ENSG00000069849	594.2952	0.3056	0.068841	4.439239	9.03E-06	0.001232	2.583187
ENSG00000134852	1624.373	0.16173	0.036482	4.43317	9.29E-06	0.001232	2.514347
ENSG00000150768	541.71	0.216098	0.048634	4.443386	8.86E-06	0.00126	2.29693
ENSG00000166546	145.2804	-0.34369	0.077408	-4.44001	9.00E-06	0.00126	2.338927
ENSG00000117153	607.4601	0.213935	0.048169	4.441335	8.94E-06	0.001302	2.225762
ENSG00000131236	1471.002	0.21652	0.048809	4.436052	9.16E-06	0.001311	2.225762
ENSG00000128989	4827.841	0.23519	0.053332	4.40994	1.03E-05	0.001311	2.514347
ENSG00000145428	237.8568	0.280781	0.063369	4.430861	9.39E-06	0.001331	2.225762

ENSG00000117410	782.5546	0.252665	0.057483	4.395482	1.11E-05	0.001339	2.583187
ENSG00000180096	87.6	-0.33522	0.073737	-4.54612	5.46E-06	0.001352	1.182918
ENSG00000240707	89.22004	-0.57742	0.127032	-4.54547	5.48E-06	0.001352	1.182918
ENSG00000165832	449.2055	0.285777	0.064484	4.431714	9.35E-06	0.001352	1.995423
ENSG00000198563	671.2974	-0.1861	0.042134	-4.41687	1.00E-05	0.001352	2.225762
ENSG00000153914	1261.815	0.138242	0.031344	4.410421	1.03E-05	0.001352	2.295759
ENSG00000230989	850.7762	0.216527	0.049252	4.396293	1.10E-05	0.001352	2.514347
ENSG00000156976	6187.731	0.305338	0.069524	4.391831	1.12E-05	0.001352	2.456745
ENSG00000104723	713.2545	0.245677	0.055995	4.387455	1.15E-05	0.001352	2.514347
ENSG00000152332	2975.992	0.252967	0.05775	4.380418	1.18E-05	0.001352	2.583187
ENSG00000177565	2658.079	0.171843	0.039265	4.376431	1.21E-05	0.001352	2.583187
ENSG00000132824	2836.276	0.203458	0.046529	4.372681	1.23E-05	0.001361	2.583187
ENSG00000185291	229.6775	-0.36118	0.081336	-4.4406	8.97E-06	0.001365	1.867169
ENSG00000186369	208.7862	0.362565	0.081955	4.423957	9.69E-06	0.001366	1.995423
ENSG00000139192	144.4407	-0.25954	0.05884	-4.41098	1.03E-05	0.001366	2.108016
ENSG00000090905	2591.282	-0.13369	0.030616	-4.36676	1.26E-05	0.001393	2.514347
ENSG00000187676	331.966	0.24811	0.056311	4.406088	1.05E-05	0.001433	2.025126
ENSG00000281649	752.8293	0.181562	0.041505	4.374504	1.22E-05	0.001451	2.295759
ENSG00000061918	1619.662	0.289209	0.066154	4.371768	1.23E-05	0.001459	2.293762
ENSG00000205133	507.4931	0.225617	0.051678	4.365827	1.27E-05	0.001472	2.29693
ENSG00000157540	2260.297	0.115259	0.026515	4.346886	1.38E-05	0.001472	2.492774
ENSG00000164091	1610.608	0.144629	0.033298	4.343422	1.40E-05	0.001472	2.514347
ENSG00000128245	5117.523	0.318034	0.073249	4.341829	1.41E-05	0.001472	2.583187
ENSG00000072315	457.7623	0.292016	0.066848	4.368372	1.25E-05	0.001473	2.225762
ENSG00000141759	476.1458	0.176428	0.040471	4.359334	1.30E-05	0.001478	2.295759
ENSG00000151465	296.0594	0.237544	0.054199	4.382808	1.17E-05	0.001489	1.977088
ENSG00000009844	539.1262	0.237336	0.054435	4.359989	1.30E-05	0.001489	2.225762
ENSG00000134294	2330.114	0.380781	0.087434	4.355078	1.33E-05	0.001489	2.295759
ENSG00000164211	601.4825	0.312503	0.071803	4.352223	1.35E-05	0.001489	2.295759
ENSG00000125755	1311.732	-0.1862	0.042792	-4.35126	1.35E-05	0.001489	2.295759

ENSG00000183196	399.6358	0.412814	0.09447	4.369787	1.24E-05	0.001495	2.025126
ENSG00000185163	592.2894	-0.21359	0.049092	-4.35076	1.36E-05	0.001495	2.225762
ENSG00000187957	1452.574	0.276327	0.063538	4.349017	1.37E-05	0.001495	2.225762
ENSG00000143155	546.6117	0.224282	0.051651	4.342258	1.41E-05	0.001495	2.293762
ENSG00000163536	2169.723	0.377276	0.087189	4.327091	1.51E-05	0.001495	2.456745
ENSG00000176155	1095.888	-0.27023	0.062279	-4.33905	1.43E-05	0.001506	2.293762
ENSG00000113638	746.248	0.207654	0.047893	4.335766	1.45E-05	0.001518	2.295759
ENSG00000091527	1100.537	0.209885	0.048402	4.336313	1.45E-05	0.001551	2.225762
ENSG00000236670	29.08773	-0.49583	0.109462	-4.52967	5.91E-06	0.001636	0.848718
ENSG00000151893	1299.275	0.13783	0.031889	4.32221	1.54E-05	0.001636	2.225762
ENSG00000151458	658.1073	0.216885	0.050216	4.319064	1.57E-05	0.001636	2.225762
ENSG00000126858	1042.219	0.175743	0.04074	4.313798	1.60E-05	0.001636	2.293762
ENSG00000135835	351.5175	-0.25833	0.059547	-4.33824	1.44E-05	0.001638	1.995423
ENSG00000178104	3886.383	0.183278	0.042736	4.288584	1.80E-05	0.001638	2.492774
ENSG00000119900	2808.354	0.24199	0.056441	4.287497	1.81E-05	0.001638	2.514347
ENSG00000117450	763.6182	0.247153	0.057662	4.286227	1.82E-05	0.001638	2.514347
ENSG00000121579	976.8994	0.172714	0.040165	4.300094	1.71E-05	0.001666	2.295759
ENSG00000162980	530.0916	0.200728	0.046681	4.300003	1.71E-05	0.001666	2.295759
ENSG00000179456	1933.673	0.200591	0.04688	4.27885	1.88E-05	0.001702	2.456745
ENSG00000091073	95.41358	-0.33966	0.077981	-4.35573	1.33E-05	0.001726	1.695647
ENSG00000134278	1499.98	0.1537	0.036013	4.267874	1.97E-05	0.001726	2.514347
ENSG00000173915	400.3349	0.34234	0.079165	4.324373	1.53E-05	0.001743	1.918337
ENSG00000012660	773.2433	0.25722	0.060396	4.258871	2.05E-05	0.001776	2.514347
ENSG00000180817	1082.016	0.277453	0.064864	4.277437	1.89E-05	0.001779	2.295759
ENSG00000068366	1187.617	0.260978	0.061449	4.247084	2.17E-05	0.00185	2.514347
ENSG00000102024	753.0453	0.269489	0.063209	4.263479	2.01E-05	0.001871	2.295759
ENSG00000005893	3113.607	0.323039	0.076262	4.235925	2.28E-05	0.001871	2.583187
ENSG00000224531	1148.43	0.208708	0.049006	4.258831	2.05E-05	0.001916	2.225762
ENSG00000143889	654.9022	0.156105	0.036696	4.254035	2.10E-05	0.001916	2.295759
ENSG00000147676	509.977	0.323532	0.076074	4.252874	2.11E-05	0.001916	2.295759

ENSG00000213639	2044.897	0.186834	0.044089	4.237668	2.26E-05	0.001916	2.456745
ENSG00000176953	387.4917	-0.16305	0.038359	-4.25063	2.13E-05	0.001957	2.225762
ENSG00000139684	523.3045	0.232384	0.054674	4.250367	2.13E-05	0.001957	2.225762
ENSG00000162368	1003.171	0.221678	0.052217	4.245361	2.18E-05	0.001957	2.293762
ENSG00000121775	135.1546	-0.23265	0.054744	-4.24975	2.14E-05	0.001979	2.189833
ENSG00000103978	399.1491	0.212212	0.049986	4.245397	2.18E-05	0.001979	2.225762
ENSG00000023330	585.2115	0.222756	0.052617	4.233529	2.30E-05	0.002014	2.293762
ENSG00000104327	232.363	0.453369	0.106545	4.255204	2.09E-05	0.002057	2.025126
ENSG00000133703	822.3711	0.159649	0.037715	4.233076	2.31E-05	0.002057	2.225762
ENSG00000175920	103.7361	-0.51173	0.116866	-4.37879	1.19E-05	0.002063	1.142898
ENSG00000116151	272.569	-0.22055	0.052243	-4.22167	2.42E-05	0.002071	2.295759
ENSG00000156642	2659.277	0.216887	0.05161	4.202399	2.64E-05	0.002071	2.492774
ENSG00000130856	1010.246	-0.11903	0.028223	-4.21737	2.47E-05	0.00209	2.295759
ENSG00000156261	754.0756	0.218627	0.051848	4.216699	2.48E-05	0.00209	2.293762
ENSG00000116106	2993.512	0.219887	0.052485	4.189515	2.80E-05	0.002158	2.492774
ENSG00000165678	2406.201	0.264126	0.063102	4.185688	2.84E-05	0.002164	2.514347
ENSG00000203930	8975.668	-0.46151	0.109782	-4.2039	2.62E-05	0.002176	2.295759
ENSG00000147133	1265.067	-0.17585	0.041842	-4.20266	2.64E-05	0.002245	2.225762
ENSG00000106459	328.3592	-0.15978	0.037802	-4.22679	2.37E-05	0.002248	1.977088
ENSG00000075415	3102.255	0.188372	0.044916	4.193866	2.74E-05	0.002248	2.295759
ENSG00000114841	1408.696	-0.32385	0.077282	-4.19055	2.78E-05	0.002263	2.293762
ENSG00000197885	529.0499	0.224446	0.053582	4.188839	2.80E-05	0.002267	2.295759
ENSG00000131730	203.7718	-0.23559	0.05617	-4.19421	2.74E-05	0.002272	2.225762
ENSG00000166987	243.2017	-0.28973	0.069113	-4.19214	2.76E-05	0.002282	2.225762
ENSG00000197062	372.0157	-0.18909	0.045123	-4.19045	2.78E-05	0.002287	2.225762
ENSG00000112992	1740.211	0.167062	0.039903	4.186646	2.83E-05	0.002312	2.225762
ENSG00000114316	832.3448	-0.12295	0.029569	-4.15802	3.21E-05	0.002312	2.514347
ENSG00000104731	518.1874	-0.22611	0.054162	-4.17477	2.98E-05	0.002343	2.293762
ENSG00000235244	460.132	-0.24489	0.058402	-4.19325	2.75E-05	0.002361	2.025126
ENSG00000147649	1557.4	0.138696	0.033232	4.173611	3.00E-05	0.002361	2.225762
ENSG00000072415	1023.596	0.168272	0.040353	4.169998	3.05E-05	0.002361	2.225762
ENSG00000141425	1813.145	0.18528	0.04445	4.168271	3.07E-05	0.002361	2.295759
ENSG00000108984	663.2154	0.199888	0.047993	4.164928	3.11E-05	0.002361	2.295759
ENSG00000266714	1253.155	-0.27318	0.06564	-4.16177	3.16E-05	0.002361	2.293762
ENSG00000101911	293.2781	0.328625	0.078968	4.161505	3.16E-05	0.002361	2.295759
ENSG00000108861	1965.722	0.193471	0.046551	4.15613	3.24E-05	0.002361	2.456745
ENSG00000164754	2053.9	0.186343	0.045009	4.140122	3.47E-05	0.002361	2.514347
ENSG00000198898	1163.712	0.279556	0.067595	4.135766	3.54E-05	0.002361	2.583187
ENSG00000172795	1236.343	0.191215	0.046243	4.135006	3.55E-05	0.002361	2.583187
ENSG00000261529	363.2345	-0.30246	0.072305	-4.18306	2.88E-05	0.002414	2.025126
ENSG00000154001	920.3386	0.155517	0.037376	4.160874	3.17E-05	0.002414	2.225762
ENSG00000101290	4205.339	0.143927	0.034816	4.133901	3.57E-05	0.002449	2.456745
ENSG00000164823	378.2155	0.249975	0.059836	4.177642	2.95E-05	0.002479	1.995423
ENSG00000145681	58.33947	0.521549	0.120678	4.32184	1.55E-05	0.002511	1.020896
ENSG00000077721	374.2756	0.190767	0.046065	4.141237	3.45E-05	0.002511	2.295759
ENSG00000163605	1082.561	0.22368	0.054391	4.112439	3.92E-05	0.002511	2.583187
ENSG00000215301	3169.293	0.15801	0.038388	4.116149	3.85E-05	0.002549	2.492774
ENSG00000111203	268.1501	-0.21938	0.052725	-4.16085	3.17E-05	0.002591	1.995423
ENSG00000071894	889.1666	-0.26552	0.064318	-4.12823	3.66E-05	0.002591	2.295759
ENSG00000117155	1876.853	0.180965	0.044115	4.102113	4.09E-05	0.002591	2.583187
ENSG00000116127	2921.057	-0.18857	0.045874	-4.11054	3.95E-05	0.002603	2.456745
ENSG00000056097	2298.68	0.160842	0.039239	4.099027	4.15E-05	0.002662	2.514347
ENSG00000255182	55.33617	-0.41345	0.096373	-4.29015	1.79E-05	0.002732	1.044965
ENSG00000156735	996.6696	0.187785	0.045893	4.091793	4.28E-05	0.002732	2.514347
ENSG00000180089	28.11927	-0.47238	0.109411	-4.31745	1.58E-05	0.002758	0.911386
ENSG00000092841	1190.496	0.26264	0.063935	4.107888	3.99E-05	0.002758	2.295759
ENSG00000204305	51.82251	-0.37591	0.087622	-4.29007	1.79E-05	0.00276	1.020896
ENSG00000147224	367.3749	0.238455	0.058088	4.105096	4.04E-05	0.00276	2.295759
ENSG00000167615	3344.154	-0.28544	0.070005	-4.07741	4.55E-05	0.00276	2.583187
ENSG00000168286	155.5578	0.250079	0.060694	4.120337	3.78E-05	0.002792	2.108016

ENSG00000147041	123.6408	0.42945	0.104608	4.105341	4.04E-05	0.002792	2.225762
ENSG00000115944	750.1011	0.230231	0.056173	4.098626	4.16E-05	0.002792	2.295759
ENSG00000105968	2827.646	0.140284	0.034376	4.080875	4.49E-05	0.002792	2.492774
ENSG00000129128	1246.725	0.177279	0.043276	4.096509	4.19E-05	0.002803	2.293762
ENSG00000131507	3960.19	0.233524	0.057454	4.064578	4.81E-05	0.002844	2.583187
ENSG00000235072	57.00977	-0.39342	0.092046	-4.27416	1.92E-05	0.002848	1.020896
ENSG00000118680	803.6069	0.25942	0.063437	4.089409	4.32E-05	0.002848	2.293762
ENSG00000133872	3588.317	0.190009	0.046785	4.061314	4.88E-05	0.002848	2.583187
ENSG00000179406	282.7007	-0.23848	0.05829	-4.09117	4.29E-05	0.002893	2.225762
ENSG00000109466	1184.258	0.211383	0.051778	4.082494	4.46E-05	0.002893	2.295759
ENSG00000108946	3857.101	0.231734	0.056986	4.066545	4.77E-05	0.002893	2.456745
ENSG00000117118	484.8721	0.215112	0.052712	4.080871	4.49E-05	0.002898	2.29693
ENSG00000143195	1261.969	0.213239	0.052268	4.079735	4.51E-05	0.002902	2.295759
ENSG00000224430	222.3238	-0.26889	0.06518	-4.12542	3.70E-05	0.002917	1.867169
ENSG00000168843	304.7167	0.368193	0.089767	4.101633	4.10E-05	0.002986	1.995423
ENSG00000155959	424.1295	0.297826	0.073097	4.07437	4.61E-05	0.002986	2.225762
ENSG00000124209	1685.085	0.14589	0.036034	4.048726	5.15E-05	0.002986	2.514347
ENSG00000111726	561.6383	0.269275	0.06664	4.040764	5.33E-05	0.002986	2.583187
ENSG00000111775	541.2527	0.290668	0.071939	4.040486	5.33E-05	0.002986	2.583187
ENSG00000141367	9459.708	0.233697	0.057859	4.039088	5.37E-05	0.002986	2.583187
ENSG00000234771	159.5865	-0.37065	0.090116	-4.11308	3.90E-05	0.002994	1.867169
ENSG00000170270	62.62337	0.34813	0.082214	4.234444	2.29E-05	0.00307	1.044965
ENSG00000169330	141.828	0.283815	0.069168	4.103299	4.07E-05	0.00307	1.867169
ENSG00000178397	250.6856	0.231668	0.056599	4.093108	4.26E-05	0.00307	1.977088
ENSG00000174013	618.6006	0.210464	0.051886	4.056305	4.99E-05	0.00307	2.295759
ENSG00000170606	2002.499	0.233589	0.05784	4.038563	5.38E-05	0.00307	2.456745
ENSG00000166913	4791.695	0.22705	0.056275	4.034647	5.47E-05	0.00307	2.492774
ENSG00000251474	324.9842	-0.20498	0.050578	-4.0528	5.06E-05	0.003073	2.295759
ENSG00000144535	586.8259	-0.1818	0.04522	-4.02025	5.81E-05	0.003125	2.583187
ENSG00000174695	1117.919	0.193439	0.047796	4.047167	5.18E-05	0.003127	2.293762
ENSG00000137040	769.413	0.243779	0.060251	4.046019	5.21E-05	0.003131	2.293762
ENSG00000197956	510.6223	0.340978	0.084149	4.05208	5.08E-05	0.003132	2.225762
ENSG00000117906	745.2869	0.195337	0.048311	4.043342	5.27E-05	0.003142	2.293762
ENSG00000104290	2313.672	0.171804	0.042501	4.042328	5.29E-05	0.003142	2.295759
ENSG00000088808	945.4137	-0.14412	0.035908	-4.01365	5.98E-05	0.003143	2.583187
ENSG00000133731	543.9388	0.22794	0.056317	4.047421	5.18E-05	0.003148	2.225762
ENSG00000169021	532.0929	0.281245	0.070176	4.007728	6.13E-05	0.00319	2.583187
ENSG00000018236	6098.323	0.251288	0.062703	4.007611	6.13E-05	0.00319	2.583187
ENSG00000196810	276.2497	-0.17382	0.042752	-4.06582	4.79E-05	0.003204	1.995423
ENSG00000145817	421.2609	0.201004	0.049865	4.030938	5.56E-05	0.003204	2.295759
ENSG00000155097	2860.051	0.209076	0.052115	4.01183	6.02E-05	0.003204	2.492774
ENSG00000138757	2986.309	0.233664	0.058358	4.00399	6.23E-05	0.003204	2.583187
ENSG00000176472	42.64008	-0.35873	0.085207	-4.2101	2.55E-05	0.003223	1.044965
ENSG00000108468	622.7843	0.14608	0.036208	4.03447	5.47E-05	0.003227	2.225762
ENSG00000146731	1012.825	0.189857	0.047147	4.026951	5.65E-05	0.003227	2.293762
ENSG00000137166	334.8341	-0.32245	0.079526	-4.05463	5.02E-05	0.003237	2.025126
ENSG00000186298	854.7299	0.216366	0.053679	4.030762	5.56E-05	0.003249	2.225762
ENSG00000168386	325.8293	0.29699	0.07334	4.049487	5.13E-05	0.003262	2.025126
ENSG00000138069	892.3629	0.157238	0.039375	3.993376	6.51E-05	0.003262	2.583187
ENSG00000091656	941.5625	-0.22339	0.055952	-3.9926	6.54E-05	0.003262	2.583187
ENSG00000128595	769.3107	0.198275	0.049341	4.018487	5.86E-05	0.003275	2.293762
ENSG00000185900	1674.778	0.139859	0.034822	4.016362	5.91E-05	0.003291	2.295759
ENSG00000136143	859.8065	0.277716	0.06907	4.020781	5.80E-05	0.003308	2.225762
ENSG00000184277	625.8636	0.206768	0.051513	4.01389	5.97E-05	0.003308	2.295759
ENSG00000125347	265.8363	-0.27128	0.067112	-4.04213	5.30E-05	0.003353	1.995423
ENSG00000163913	614.8758	-0.15622	0.039244	-3.98074	6.87E-05	0.003353	2.583187
ENSG00000260412	242.5287	0.331408	0.081992	4.041957	5.30E-05	0.003357	1.977088
ENSG00000138698	1296.506	0.268521	0.067481	3.97919	6.92E-05	0.003357	2.583187
ENSG00000116586	133.1525	0.246463	0.061255	4.023581	5.73E-05	0.003394	2.108016
ENSG00000197363	282.6219	-0.23944	0.059763	-4.00647	6.16E-05	0.003421	2.225762

ENSG00000115762	2499.432	0.199615	0.05011	3.983537	6.79E-05	0.003421	2.456745
ENSG00000101079	1936.273	0.249421	0.06266	3.980558	6.88E-05	0.003421	2.492774
ENSG00000184923	59.5848	-0.55043	0.131627	-4.18176	2.89E-05	0.003446	1.023066
ENSG00000144227	72.91984	0.523796	0.128842	4.065413	4.79E-05	0.003446	1.695647
ENSG00000120645	1605.363	-0.2804	0.070037	-4.00361	6.24E-05	0.003446	2.225762
ENSG00000114098	908.626	0.126184	0.031563	3.997807	6.39E-05	0.003446	2.225762
ENSG00000196104	1085.698	0.335226	0.083893	3.995848	6.45E-05	0.003446	2.295759
ENSG00000144827	495.149	0.216406	0.054228	3.990638	6.59E-05	0.003446	2.293762
ENSG00000137409	3497.57	0.184455	0.04645	3.971063	7.16E-05	0.003446	2.514347
ENSG00000118200	3852.292	0.144188	0.036315	3.970445	7.17E-05	0.003446	2.514347
ENSG00000253719	2027.24	0.182295	0.045932	3.968833	7.22E-05	0.003446	2.514347
ENSG00000164885	322.9828	0.269617	0.067588	3.989122	6.63E-05	0.003453	2.295759
ENSG00000183978	273.3314	0.231329	0.058011	3.987666	6.67E-05	0.003464	2.295759
ENSG00000070367	1373.586	0.136478	0.034179	3.993062	6.52E-05	0.003481	2.225762
ENSG00000245248	91.95635	-0.40626	0.098266	-4.13432	3.56E-05	0.003496	1.182918
ENSG00000050130	399.6782	0.212134	0.053283	3.981252	6.86E-05	0.003496	2.295759
ENSG00000131398	947.8308	-0.42838	0.107609	-3.98087	6.87E-05	0.003496	2.295759
ENSG00000015532	439.7108	-0.18012	0.045262	-3.97952	6.91E-05	0.003496	2.295759
ENSG00000092148	3683.522	0.13078	0.032978	3.965633	7.32E-05	0.003496	2.456745
ENSG00000112697	2870.565	0.164796	0.041579	3.963416	7.39E-05	0.003496	2.456745
ENSG00000072657	837.5739	0.24768	0.062541	3.960249	7.49E-05	0.003496	2.514347
ENSG00000113328	414.9993	0.237336	0.05916	4.011776	6.03E-05	0.003497	1.995423
ENSG00000131697	634.022	-0.21491	0.053933	-3.98478	6.75E-05	0.003503	2.225762
ENSG00000163964	340.5448	0.192558	0.04814	3.999945	6.34E-05	0.003589	2.025126
ENSG00000109572	2333.27	0.17815	0.044865	3.970803	7.16E-05	0.003589	2.295759
ENSG00000109158	1982.174	0.233386	0.059114	3.94806	7.88E-05	0.003615	2.492774
ENSG00000100916	194.2834	0.23416	0.059043	3.965901	7.31E-05	0.003618	2.295759
ENSG00000109971	13196.12	0.265413	0.067268	3.945614	7.96E-05	0.003618	2.492774
ENSG00000129473	1750.933	0.161561	0.040965	3.943872	8.02E-05	0.003618	2.514347
ENSG00000130590	92.80163	-0.28429	0.06887	-4.12786	3.66E-05	0.003629	1.136415
ENSG00000135387	2557.73	0.143646	0.036246	3.963143	7.40E-05	0.003629	2.295759
ENSG00000132463	1400.93	0.153908	0.038851	3.961485	7.45E-05	0.003642	2.295759
ENSG00000156467	1571.821	0.238937	0.060332	3.960387	7.48E-05	0.003642	2.295759
ENSG00000122550	582.6146	0.151032	0.038146	3.959323	7.52E-05	0.003642	2.29693
ENSG00000065559	2015.556	0.241482	0.061241	3.943159	8.04E-05	0.003642	2.456745
ENSG00000234841	79.54185	-0.33451	0.081399	-4.10958	3.96E-05	0.003659	1.201846
ENSG00000112996	1541.717	0.164948	0.041917	3.935077	8.32E-05	0.003659	2.514347
ENSG00000175175	758.5276	0.2265	0.05757	3.934342	8.34E-05	0.003659	2.514347
ENSG00000163541	525.3773	0.217084	0.054891	3.954824	7.66E-05	0.003671	2.293762
ENSG00000065518	451.7737	0.234056	0.058752	3.983806	6.78E-05	0.003693	1.995423
ENSG00000114999	1363.608	0.145858	0.036901	3.952693	7.73E-05	0.003693	2.293762
ENSG00000180616	619.5128	0.283617	0.071787	3.950789	7.79E-05	0.003693	2.29693
ENSG00000135002	536.4034	0.265309	0.067157	3.950595	7.80E-05	0.003693	2.295759
ENSG00000183723	2430.915	0.167948	0.042833	3.921004	8.82E-05	0.003698	2.583187
ENSG00000151135	357.9559	0.230034	0.057681	3.988055	6.66E-05	0.003701	1.918337
ENSG00000184613	3551.456	0.298815	0.075708	3.946953	7.92E-05	0.003701	2.295759
ENSG00000005249	1134.279	0.204265	0.051754	3.946886	7.92E-05	0.003701	2.293762
ENSG00000149196	224.2876	0.208874	0.052944	3.945215	7.97E-05	0.003701	2.295759
ENSG00000115419	3972.303	0.228094	0.0581	3.925904	8.64E-05	0.003701	2.492774
ENSG00000197746	11666.22	0.193709	0.049458	3.916627	8.98E-05	0.003701	2.583187
ENSG00000164983	720.4739	0.189858	0.048055	3.950837	7.79E-05	0.003711	2.225762
ENSG00000109332	2648.828	0.153831	0.039297	3.914551	9.06E-05	0.003711	2.583187
ENSG00000164603	266.8207	0.226873	0.057143	3.970242	7.18E-05	0.003724	2.025126
ENSG00000166266	940.139	0.182153	0.046145	3.947389	7.90E-05	0.003724	2.225762
ENSG00000174460	240.527	0.489478	0.12422	3.940411	8.13E-05	0.003724	2.295759
ENSG00000164172	636.3239	0.237069	0.06018	3.93935	8.17E-05	0.003724	2.295759
ENSG00000196388	50.42413	-0.32131	0.07783	-4.12836	3.65E-05	0.003727	1.023066
ENSG00000101856	1041.355	0.278135	0.070667	3.935877	8.29E-05	0.003761	2.293762
ENSG00000228274	74.06458	-0.26518	0.066188	-4.00645	6.16E-05	0.003762	1.695647
ENSG00000100554	1168.134	0.224776	0.05754	3.906404	9.37E-05	0.003762	2.583187

ENSG00000142168	1970.887	0.225799	0.057448	3.930461	8.48E-05	0.003811	2.295759
ENSG00000108176	189.6087	0.28731	0.072252	3.976524	6.99E-05	0.003811	1.867169
ENSG00000175463	141.4229	-0.38205	0.096752	-3.94879	7.85E-05	0.003811	2.108016
ENSG00000134001	653.7437	0.228751	0.058122	3.935681	8.30E-05	0.003811	2.225762
ENSG00000211456	813.9484	0.165341	0.042334	3.905623	9.40E-05	0.003811	2.514347
ENSG00000153130	1231.938	0.253529	0.065015	3.899538	9.64E-05	0.003811	2.583187
ENSG00000122873	449.8242	0.269013	0.068003	3.955916	7.62E-05	0.003864	1.995423
ENSG00000166073	407.5743	0.223847	0.057073	3.922087	8.78E-05	0.003864	2.295759
ENSG00000163527	990.2214	0.171586	0.04375	3.921983	8.78E-05	0.003864	2.293762
ENSG00000170091	1843.31	0.267062	0.068518	3.897713	9.71E-05	0.003886	2.514347
ENSG00000178971	627.4186	-0.16106	0.041398	-3.8906	1.00E-04	0.003886	2.583187
ENSG00000069345	1083.095	0.21236	0.054544	3.893379	9.89E-05	0.003936	2.514347
ENSG00000003096	96.0184	0.353702	0.086683	4.080405	4.50E-05	0.003949	1.136415
ENSG00000078668	1076.964	0.24259	0.061873	3.920757	8.83E-05	0.003949	2.225762
ENSG00000165943	2313.112	0.260694	0.067143	3.882652	0.000103	0.003972	2.583187
ENSG00000139973	2756.187	0.260805	0.066706	3.909793	9.24E-05	0.003985	2.295759
ENSG00000100505	3475.929	-0.13814	0.035502	-3.89107	9.98E-05	0.004013	2.456745
ENSG00000096384	10033.9	0.245754	0.062936	3.90484	9.43E-05	0.004044	2.295759
ENSG00000105643	593.9657	0.316329	0.081021	3.904279	9.45E-05	0.004044	2.295759
ENSG00000143222	297.2898	0.229684	0.058763	3.908639	9.28E-05	0.004086	2.225762
ENSG00000175164	45.18917	-0.51456	0.126012	-4.08343	4.44E-05	0.004091	1.044965
ENSG00000161896	115.2135	0.636817	0.163626	3.891902	9.95E-05	0.004091	2.338927
ENSG00000118058	4061.709	-0.12415	0.031995	-3.88037	0.000104	0.004091	2.456745
ENSG00000134308	2552.793	0.19357	0.049899	3.879253	0.000105	0.004091	2.492774
ENSG00000067992	2676.834	0.217089	0.056008	3.876048	0.000106	0.004091	2.514347
ENSG00000170871	2060.609	0.131071	0.033818	3.875783	0.000106	0.004091	2.514347
ENSG00000084733	1379.422	0.14749	0.038117	3.86935	0.000109	0.004091	2.583187
ENSG00000006715	1774.382	0.156428	0.040464	3.865846	0.000111	0.004112	2.583187
ENSG00000067601	81.13136	-0.31536	0.077846	-4.0511	5.10E-05	0.004114	1.182918
ENSG00000114744	325.1453	0.173901	0.044581	3.900815	9.59E-05	0.004114	2.225762
ENSG00000179082	24.78549	-0.6784	0.166461	-4.07539	4.59E-05	0.004114	1.053218
ENSG00000184675	255.2633	-0.17455	0.044461	-3.92588	8.64E-05	0.004114	1.995423
ENSG00000006071	1452.205	-0.21385	0.054971	-3.89024	0.0001	0.004114	2.293762
ENSG00000152932	3987.162	0.365307	0.09438	3.870605	0.000109	0.004114	2.492774
ENSG00000083099	475.2291	0.166297	0.043063	3.861687	0.000113	0.004114	2.583187
ENSG00000048540	3009.402	0.234877	0.060395	3.88904	0.000101	0.004121	2.295759
ENSG00000143933	9004.941	0.240492	0.062192	3.866911	0.00011	0.004146	2.492774
ENSG00000237686	21.3667	-0.64537	0.153519	-4.20382	2.62E-05	0.004171	0.583933
ENSG00000237476	24.25393	-0.45991	0.112152	-4.10082	4.12E-05	0.004171	0.911386
ENSG00000169246	51.2398	-0.43716	0.107055	-4.08348	4.44E-05	0.004171	0.989117
ENSG00000167283	247.7978	0.237672	0.060665	3.917759	8.94E-05	0.004171	1.995423
ENSG00000017260	1758.071	0.156734	0.040593	3.861091	0.000113	0.004171	2.514347
ENSG00000129351	2011.169	-0.10415	0.027026	-3.85357	0.000116	0.004171	2.583187
ENSG00000106780	1964.63	0.168352	0.0437	3.852423	0.000117	0.004171	2.583187
ENSG00000259067	5.147643	-1.11673	0.24002	-4.65268	3.28E-06	0.00419	0.071665
ENSG00000160229	183.0596	-0.28768	0.074176	-3.87829	0.000105	0.00419	2.295759
ENSG00000135636	726.819	-0.28539	0.074001	-3.85652	0.000115	0.00419	2.514347
ENSG00000129084	125.3241	0.240377	0.061676	3.897415	9.72E-05	0.004207	2.108016
ENSG00000143442	2083.397	-0.14093	0.036576	-3.85303	0.000117	0.004222	2.514347
ENSG00000174684	1865.785	0.227703	0.059108	3.8523	0.000117	0.004261	2.492774
ENSG00000141279	1491.591	0.13508	0.0349	3.870483	0.000109	0.004284	2.295759
ENSG00000226419	304.0973	-0.20648	0.053301	-3.87392	0.000107	0.004344	2.225762
ENSG00000196937	611.4421	0.259485	0.067627	3.836984	0.000125	0.004344	2.583187
ENSG00000009307	4857.41	0.156677	0.040842	3.836162	0.000125	0.004348	2.583187
ENSG00000142609	198.7433	-0.32925	0.084576	-3.89292	9.90E-05	0.004351	2.025126
ENSG00000117598	224.3327	0.231841	0.059922	3.86908	0.000109	0.004351	2.225762
ENSG00000083799	1748.068	0.139107	0.035954	3.869067	0.000109	0.004351	2.225762
ENSG00000106993	402.1971	0.193467	0.050097	3.861857	0.000113	0.004351	2.295759
ENSG00000125304	1164.129	0.210749	0.054582	3.861151	0.000113	0.004351	2.295759
ENSG00000232406	158.416	-0.26195	0.067921	-3.85674	0.000115	0.004351	2.338927

ENSG00000125848	479.482	0.241055	0.062909	3.831839	0.000127	0.004351	2.583187
ENSG00000215712	346.8737	0.175552	0.045404	3.866399	0.00011	0.004365	2.225762
ENSG00000018510	784.04	0.16677	0.043213	3.859232	0.000114	0.004365	2.295759
ENSG00000176871	2169.774	0.16159	0.042125	3.835967	0.000125	0.004365	2.514347
ENSG00000136021	769.3457	0.143687	0.03718	3.864635	0.000111	0.004374	2.225762
ENSG00000148925	1145.43	0.209454	0.054311	3.856605	0.000115	0.004374	2.295759
ENSG00000150753	663.9041	0.220884	0.057292	3.855367	0.000116	0.004385	2.295759
ENSG00000107798	700.2653	0.31676	0.082197	3.853653	0.000116	0.004389	2.295759
ENSG00000182013	2596.296	0.204331	0.053304	3.833329	0.000126	0.004389	2.492774
ENSG00000172667	2303.513	0.1723	0.044949	3.833263	0.000126	0.004389	2.492774
ENSG00000161010	463.8658	-0.18407	0.047419	-3.88168	0.000104	0.004391	2.025126
ENSG00000177879	467.3934	0.203554	0.052745	3.859191	0.000114	0.004391	2.225762
ENSG00000095139	1275.743	0.140263	0.036688	3.823106	0.000132	0.004391	2.583187
ENSG00000106537	705.7754	0.240853	0.063011	3.822404	0.000132	0.004391	2.583187
ENSG00000101190	441.5333	-0.27349	0.070901	-3.85736	0.000115	0.004403	2.225762
ENSG00000175582	2833.934	0.218442	0.057056	3.828568	0.000129	0.004411	2.492774
ENSG00000108960	623.4419	0.308017	0.07995	3.852621	0.000117	0.004446	2.225762
ENSG00000213199	163.867	-0.29957	0.077771	-3.85198	0.000117	0.004446	2.225762
ENSG00000168036	3628.186	0.165259	0.042969	3.846025	0.00012	0.004446	2.295759
ENSG00000136279	1669.716	-0.12486	0.032469	-3.84537	0.00012	0.004446	2.293762
ENSG00000167595	137.9763	-0.27964	0.072833	-3.83948	0.000123	0.004446	2.338927
ENSG00000196912	849.0807	-0.29612	0.076955	-3.84792	0.000119	0.004504	2.225762
ENSG00000177302	578.8633	-0.1381	0.03625	-3.80954	0.000139	0.004525	2.583187
ENSG00000178381	192.1313	0.219693	0.056524	3.886731	0.000102	0.004558	1.867169
ENSG00000272578	59.81894	-0.31339	0.07783	-4.02656	5.66E-05	0.004622	1.020896
ENSG00000187792	265.8979	-0.23631	0.061183	-3.86234	0.000112	0.004622	2.025126
ENSG00000070961	7225.587	0.231258	0.060824	3.802068	0.000143	0.004622	2.583187
ENSG00000132964	298.8897	0.1636	0.042413	3.857286	0.000115	0.004699	2.025126
ENSG00000169567	1081.47	0.23824	0.062265	3.826204	0.00013	0.004699	2.293762
ENSG00000246922	992.2473	-0.22425	0.058539	-3.83077	0.000128	0.004743	2.225762

ENSG00000025800	1709.22	0.128291	0.033767	3.799261	0.000145	0.004759	2.514347
ENSG00000198843	1147.15	0.199559	0.052655	3.789965	0.000151	0.004799	2.583187
ENSG00000114686	345.7839	0.282114	0.07323	3.852431	0.000117	0.004799	1.995423
ENSG00000169490	289.9024	0.212921	0.055328	3.848351	0.000119	0.004799	2.025126
ENSG00000116661	911.1405	0.272359	0.071891	3.788499	0.000152	0.004799	2.583187
ENSG00000124299	407.3335	0.191166	0.049516	3.86072	0.000113	0.0048	1.918337
ENSG00000178951	1570.711	-0.21369	0.056327	-3.7938	0.000148	0.0048	2.514347
ENSG00000186106	850.4619	0.188316	0.049644	3.793323	0.000149	0.0048	2.514347
ENSG00000135829	1618.433	0.147779	0.038751	3.81355	0.000137	0.004838	2.293762
ENSG00000271717	20.4537	-0.54898	0.132906	-4.13059	3.62E-05	0.004975	0.583933
ENSG00000137337	437.4951	-0.19218	0.050068	-3.8383	0.000124	0.004975	1.995423
ENSG00000198380	894.9733	0.144045	0.037854	3.805275	0.000142	0.004975	2.293762
ENSG00000166501	7413.639	0.226574	0.059878	3.783894	0.000154	0.004975	2.492774
ENSG00000165280	2053.263	0.121464	0.032115	3.782147	0.000155	0.004975	2.514347
ENSG00000259834	135.1272	0.343452	0.090193	3.807983	0.00014	0.005033	2.225762
ENSG00000152495	1816.412	0.256786	0.067989	3.776887	0.000159	0.005039	2.514347
ENSG00000277200	242.9088	-0.25215	0.066396	-3.79767	0.000146	0.005065	2.295759
ENSG00000135018	2471.143	0.144052	0.038112	3.779729	0.000157	0.005077	2.456745
ENSG00000153933	972.6615	0.14929	0.039401	3.788982	0.000151	0.005213	2.295759
ENSG00000178502	828.4717	0.171141	0.045522	3.759513	0.00017	0.005213	2.583187
ENSG00000197894	726.7844	0.202582	0.053532	3.784336	0.000154	0.005299	2.295759
ENSG00000188312	113.1456	-0.21593	0.057148	-3.77841	0.000158	0.005315	2.338927
ENSG00000198258	390.5741	0.240052	0.062989	3.811036	0.000138	0.005429	1.995423
ENSG00000154511	525.9508	0.238421	0.063138	3.776189	0.000159	0.005429	2.295759
ENSG00000077264	2661.34	0.221715	0.058975	3.759465	0.00017	0.005429	2.456745
ENSG00000115520	315.9918	0.191437	0.050602	3.783174	0.000155	0.005433	2.225762
ENSG00000156411	591.3382	0.261319	0.069229	3.774713	0.00016	0.005438	2.295759
ENSG00000147123	365.023	0.196964	0.052198	3.773411	0.000161	0.005455	2.295759
ENSG00000085433	2081.313	0.212284	0.056585	3.751587	0.000176	0.005471	2.492774
ENSG00000081307	775.0317	0.139289	0.036932	3.771543	0.000162	0.005473	2.295759

ENSG00000077147	1652.034	0.163474	0.043698	3.740983	0.000183	0.005484	2.583187
ENSG00000115947	725.9221	0.180813	0.047973	3.769038	0.000164	0.005501	2.293762
ENSG00000205269	1497.904	0.169792	0.04541	3.739133	0.000185	0.005501	2.583187
ENSG00000119772	1383.937	-0.17032	0.045486	-3.74451	0.000181	0.00551	2.514347
ENSG00000181852	1123.372	0.162925	0.043511	3.744463	0.000181	0.00551	2.514347
ENSG00000197713	632.5667	0.175142	0.046501	3.766386	0.000166	0.005515	2.29693
ENSG00000273611	255.5211	0.172096	0.045618	3.772565	0.000162	0.005541	2.225762
ENSG00000111237	330.6016	0.191007	0.050307	3.79681	0.000147	0.005541	1.995423
ENSG00000145907	1333.379	0.126171	0.033526	3.763359	0.000168	0.005541	2.293762
ENSG00000151806	570.8456	0.161631	0.042957	3.762657	0.000168	0.005541	2.295759
ENSG00000133059	1392.136	0.136253	0.036218	3.761984	0.000169	0.005541	2.293762
ENSG00000213585	1658.976	0.225017	0.059817	3.761746	0.000169	0.005541	2.295759
ENSG00000189241	3797.953	0.169667	0.045346	3.741574	0.000183	0.005541	2.492774
ENSG00000132694	2603.783	-0.11492	0.030745	-3.73771	0.000186	0.005557	2.514347
ENSG00000152234	4261.024	0.247415	0.066249	3.734614	0.000188	0.005614	2.514347
ENSG00000153814	409.6317	0.209513	0.055311	3.787931	0.000152	0.005621	2.025126
ENSG00000114626	687.2168	-0.22689	0.060298	-3.76275	0.000168	0.005621	2.225762
ENSG00000042753	442.7651	0.241659	0.064231	3.762358	0.000168	0.005621	2.225762
ENSG00000057608	1340.623	0.199249	0.053057	3.755382	0.000173	0.005621	2.295759
ENSG00000116161	1019.885	0.248057	0.066055	3.75531	0.000173	0.005621	2.295759
ENSG00000284707	131.354	-0.23607	0.062076	-3.80284	0.000143	0.005627	1.867169
ENSG00000162086	368.6047	-0.16877	0.044968	-3.75303	0.000175	0.005627	2.295759
ENSG00000214176	604.2358	-0.20539	0.054749	-3.75151	0.000176	0.005627	2.29693
ENSG00000198689	1817.621	0.228946	0.061309	3.734316	0.000188	0.005627	2.456745
ENSG00000168016	1976.43	-0.28063	0.07523	-3.73033	0.000191	0.005627	2.514347
ENSG00000174672	1551.782	-0.20068	0.053916	-3.72202	0.000198	0.005627	2.583187
ENSG00000196498	3173.422	-0.27789	0.074436	-3.73326	0.000189	0.005639	2.456745
ENSG00000171045	425.7856	-0.23793	0.062864	-3.7848	0.000154	0.005639	1.995423
ENSG00000167608	59.92477	-0.38231	0.096864	-3.94692	7.92E-05	0.005649	1.023066
ENSG00000144744	452.2007	0.187838	0.04952	3.793178	0.000149	0.005649	1.918337

ENSG00000134375	397.0334	0.259612	0.06875	3.776164	0.000159	0.005663	2.025126
ENSG00000139291	314.113	0.182677	0.048669	3.753493	0.000174	0.005663	2.225762
ENSG00000066923	549.3864	-0.20104	0.053566	-3.75322	0.000175	0.005663	2.225762
ENSG00000110274	836.2831	-0.17607	0.046914	-3.75297	0.000175	0.005663	2.225762
ENSG00000084623	649.3114	0.152984	0.040851	3.744886	0.00018	0.005663	2.29693
ENSG00000073921	2778.206	0.121623	0.032615	3.729093	0.000192	0.005663	2.456745
ENSG00000134779	912.2432	0.136642	0.036425	3.751364	0.000176	0.005668	2.225762
ENSG00000188419	867.2136	0.159326	0.04282	3.720838	0.000199	0.005668	2.514347
ENSG00000161021	667.9111	-0.20096	0.053727	-3.74039	0.000184	0.00573	2.295759
ENSG00000113552	385.5477	0.165726	0.043919	3.773428	0.000161	0.005744	1.995423
ENSG00000112695	586.711	0.322265	0.086201	3.73854	0.000185	0.005744	2.29693
ENSG00000090487	370.1046	0.155072	0.041482	3.738285	0.000185	0.005744	2.295759
ENSG00000143158	507.3677	0.238455	0.063797	3.737735	0.000186	0.005751	2.293762
ENSG00000127957	164.6539	-0.20222	0.053663	-3.76835	0.000164	0.005811	1.995423
ENSG00000172663	149.4264	-0.21652	0.057659	-3.75508	0.000173	0.005811	2.108016
ENSG00000164309	818.4288	-0.28265	0.075556	-3.74091	0.000183	0.005811	2.225762
ENSG00000113407	507.7434	0.201196	0.053785	3.740769	0.000183	0.005811	2.225762
ENSG00000135900	172.3078	0.18535	0.049203	3.76708	0.000165	0.005824	1.995423
ENSG00000120438	1187.455	0.213147	0.057125	3.731206	0.000191	0.00583	2.295759
ENSG00000092108	981.8342	0.149346	0.039959	3.737525	0.000186	0.005853	2.225762
ENSG00000101843	345.7449	0.204466	0.054717	3.736757	0.000186	0.00586	2.225762
ENSG00000160908	327.7955	-0.14409	0.038269	-3.76517	0.000166	0.005879	1.977088
ENSG00000177054	220.5271	0.200188	0.053261	3.758636	0.000171	0.005935	1.995423
ENSG00000163590	2568.476	0.161856	0.043471	3.723362	0.000197	0.005935	2.295759
ENSG00000072803	1903.375	0.13831	0.037352	3.702898	0.000213	0.005935	2.492774
ENSG00000158321	1286.215	-0.15757	0.042658	-3.69371	0.000221	0.005935	2.583187
ENSG00000070718	1011.776	0.191625	0.051894	3.692645	0.000222	0.005943	2.583187
ENSG00000140650	326.7273	-0.20258	0.05432	-3.72939	0.000192	0.005955	2.225762
ENSG00000143727	558.119	0.193034	0.05177	3.728668	0.000192	0.005961	2.225762
ENSG00000116406	978.9497	0.165495	0.044844	3.690431	0.000224	0.005962	2.583187

ENSG00000089289	298.3617	0.177254	0.047262	3.750456	0.000177	0.005985	2.025126
ENSG00000055483	714.7057	-0.1957	0.052529	-3.72551	0.000195	0.006002	2.225762
ENSG00000118094	132.7192	-0.40125	0.107662	-3.72692	0.000194	0.006021	2.189833
ENSG00000174453	160.5065	0.317721	0.085271	3.726031	0.000195	0.006021	2.189833
ENSG00000137575	1079.073	0.224476	0.060285	3.723567	0.000196	0.006021	2.225762
ENSG00000151729	1802.709	0.217402	0.05879	3.697959	0.000217	0.006021	2.456745
ENSG00000170017	1702.964	0.235611	0.063811	3.692323	0.000222	0.006021	2.514347
ENSG00000039123	778.6604	0.132882	0.036067	3.684317	0.000229	0.006021	2.583187
ENSG00000125863	479.8406	0.196493	0.052931	3.712278	0.000205	0.006059	2.293762
ENSG00000127616	2324.084	-0.16022	0.043465	-3.6861	0.000228	0.006116	2.514347
ENSG00000060491	1059.189	-0.18381	0.049563	-3.70853	0.000208	0.006121	2.295759
ENSG00000101972	1324.207	0.13754	0.037052	3.712065	0.000206	0.006208	2.225762
ENSG00000086061	2010.182	0.278286	0.075602	3.680926	0.000232	0.006208	2.514347
ENSG00000104643	1049.038	0.182611	0.049319	3.702652	0.000213	0.006236	2.293762
ENSG00000121989	372.2612	0.191558	0.051654	3.708495	0.000208	0.006254	2.225762
ENSG00000104897	242.1599	-0.23169	0.062481	-3.70818	0.000209	0.006254	2.225762
ENSG00000113384	545.9205	0.146302	0.03953	3.701082	0.000215	0.006254	2.293762
ENSG00000152556	2360.97	0.185345	0.050395	3.677874	0.000235	0.00628	2.492774
ENSG00000112186	1513.697	0.265457	0.07167	3.703898	0.000212	0.006326	2.225762
ENSG00000186479	1527.757	0.193584	0.05237	3.696454	0.000219	0.006326	2.293762
ENSG00000244932	40.60104	-0.34075	0.08745	-3.89657	9.76E-05	0.006327	1.020896
ENSG00000108557	1276.443	-0.24165	0.065406	-3.69453	0.00022	0.006347	2.293762
ENSG00000047932	708.0025	0.1673	0.045299	3.693261	0.000221	0.006367	2.293762
ENSG00000136156	3484.643	0.151455	0.041289	3.6682	0.000244	0.006397	2.514347
ENSG00000271646	32.15456	-0.45412	0.116262	-3.90603	9.38E-05	0.006398	0.963911
ENSG00000226746	48.7737	-0.39536	0.101854	-3.8816	0.000104	0.006493	1.044965
ENSG00000132313	749.4561	0.182971	0.049637	3.686201	0.000228	0.006493	2.293762
ENSG00000111530	3060.297	0.171419	0.046727	3.668553	0.000244	0.006493	2.456745
ENSG00000169446	427.9001	0.186246	0.05007	3.719721	0.000199	0.006496	1.995423
ENSG00000213983	397.0033	-0.32639	0.087748	-3.7197	0.000199	0.006496	1.995423

ENSG00000075239	424.2648	0.158651	0.043066	3.683894	0.00023	0.006496	2.295759
ENSG00000070831	1542.904	0.154147	0.042178	3.654708	0.000257	0.006496	2.583187
ENSG00000181350	208.4565	-0.21791	0.059171	-3.6827	0.000231	0.006513	2.295759
ENSG00000107779	508.3889	0.211098	0.057801	3.652134	0.00026	0.006513	2.583187
ENSG00000243302	156.7309	-0.24933	0.06681	-3.73198	0.00019	0.006555	1.867169
ENSG00000186660	866.2347	0.165691	0.044927	3.687995	0.000226	0.006555	2.225762
ENSG00000172239	520.7785	0.156671	0.042583	3.679209	0.000234	0.006555	2.29693
ENSG00000113387	1763.421	0.246543	0.067622	3.645901	0.000266	0.006627	2.583187
ENSG00000288612	119.6936	-0.32024	0.086728	-3.69249	0.000222	0.006733	2.108016
ENSG00000187699	296.7742	0.210023	0.057213	3.670896	0.000242	0.006733	2.295759
ENSG00000184432	1805.015	0.109926	0.030084	3.654016	0.000258	0.006733	2.456745
ENSG00000135678	302.1538	0.336939	0.090897	3.706828	0.00021	0.006749	1.977088
ENSG00000166169	327.9966	-0.15999	0.043226	-3.70113	0.000215	0.006749	2.025126
ENSG00000162704	618.9477	0.172688	0.047065	3.669127	0.000243	0.006749	2.295759
ENSG00000163902	1017.237	0.172132	0.046926	3.66817	0.000244	0.006754	2.295759
ENSG00000164024	378.3788	0.171052	0.046675	3.664757	0.000248	0.006833	2.295759
ENSG00000117360	772.5294	-0.16625	0.045668	-3.64047	0.000272	0.006846	2.514347
ENSG00000254656	147.547	-0.30971	0.084393	-3.66988	0.000243	0.006874	2.225762
ENSG00000141750	818.8945	-0.34989	0.095571	-3.66103	0.000251	0.006874	2.295759
ENSG00000124767	954.1221	0.217653	0.059828	3.638011	0.000275	0.006874	2.514347
ENSG00000131149	933.338	-0.22011	0.060508	-3.63769	0.000275	0.006874	2.514347
ENSG00000171497	207.6582	0.26162	0.071546	3.65665	0.000256	0.006981	2.295759
ENSG00000196262	3167.242	0.207736	0.057199	3.631793	0.000281	0.007009	2.514347
ENSG00000102172	608.5209	0.244137	0.067399	3.622271	0.000292	0.007066	2.583187
ENSG00000135824	125.7385	0.386759	0.1057	3.659018	0.000253	0.007098	2.225762
ENSG00000144959	1331.499	0.199404	0.05498	3.626859	0.000287	0.007108	2.514347
ENSG00000187601	506.4631	0.23902	0.065527	3.647665	0.000265	0.007169	2.295759
ENSG00000092199	3078.033	0.147402	0.040629	3.627992	0.000286	0.007218	2.456745
ENSG00000047249	1550.704	0.217514	0.059679	3.644742	0.000268	0.007226	2.295759
ENSG00000162241	105.389	-0.31808	0.083493	-3.8097	0.000139	0.007236	1.182918

ENSG00000279675	241.7603	0.255624	0.069474	3.679419	0.000234	0.007236	1.995423
ENSG00000156110	337.4285	0.154781	0.042124	3.674405	0.000238	0.007236	2.025126
ENSG00000168288	288.6983	0.249928	0.068449	3.651292	0.000261	0.007236	2.225762
ENSG00000172292	992.3256	0.200148	0.054824	3.650766	0.000261	0.007236	2.225762
ENSG00000154518	891.446	0.240121	0.065936	3.641746	0.000271	0.007238	2.295759
ENSG00000168763	436.7435	-0.17203	0.046806	-3.67542	0.000237	0.00729	1.995423
ENSG00000041982	318.4705	0.723429	0.19706	3.671116	0.000241	0.007293	2.025126
ENSG00000196419	1377.432	0.190956	0.052514	3.636308	0.000277	0.007356	2.295759
ENSG00000116209	1602.048	0.17827	0.049058	3.633854	0.000279	0.007414	2.295759
ENSG00000262877	227.0145	-0.47268	0.129838	-3.64056	0.000272	0.007426	2.225762
ENSG00000131100	2049.045	0.260985	0.072269	3.611283	0.000305	0.007426	2.492774
ENSG00000228544	53.38018	-0.32011	0.083575	-3.83018	0.000128	0.007433	1.044965
ENSG00000102032	107.6245	0.300306	0.08102	3.706549	0.00021	0.00744	1.695647
ENSG00000114573	4333.828	0.257521	0.070942	3.630039	0.000283	0.00744	2.295759
ENSG00000138459	559.8719	0.213096	0.058707	3.629819	0.000284	0.00744	2.295759
ENSG00000113761	487.1015	-0.12515	0.034484	-3.62935	0.000284	0.00744	2.293762
ENSG00000108406	390.9748	0.160884	0.044333	3.628962	0.000285	0.00744	2.295759
ENSG00000139718	581.5335	-0.25387	0.069963	-3.62859	0.000285	0.00744	2.29693
ENSG00000145016	859.4863	-0.14597	0.040461	-3.60768	0.000309	0.00744	2.514347
ENSG00000102468	807.9407	0.246261	0.067892	3.627257	0.000286	0.00747	2.295759
ENSG00000113845	384.8053	0.165123	0.045562	3.6241	0.00029	0.00755	2.295759
ENSG00000019995	514.9471	0.152205	0.04195	3.628247	0.000285	0.007615	2.225762
ENSG00000105699	206.1066	-0.22547	0.062271	-3.6208	0.000294	0.007615	2.295759
ENSG00000118785	3367.533	0.667842	0.185587	3.598541	0.00032	0.007615	2.492774
ENSG00000136193	5989.468	0.147213	0.040941	3.595764	0.000323	0.007615	2.514347
ENSG00000172757	2843.361	0.169183	0.04713	3.589716	0.000331	0.007615	2.583187
ENSG00000131943	626.745	0.131684	0.036692	3.588903	0.000332	0.007615	2.583187
ENSG00000168118	592.4193	0.159861	0.044178	3.618607	0.000296	0.007622	2.29693
ENSG00000261340	76.3569	0.342294	0.092668	3.693773	0.000221	0.007677	1.695647
ENSG00000183775	2896.752	0.211404	0.058845	3.592567	0.000327	0.007677	2.514347

ENSG00000100058	292.1556	-0.20773	0.056862	-3.6532	0.000259	0.007691	1.977088
ENSG00000148572	188.0877	0.203403	0.056149	3.622564	0.000292	0.007691	2.225762
ENSG00000198160	664.7628	0.129222	0.035756	3.614035	0.000301	0.007691	2.29693
ENSG00000080854	2137.073	-0.27944	0.077782	-3.59254	0.000327	0.007691	2.492774
ENSG00000131238	1119.988	0.207252	0.057359	3.613267	0.000302	0.007705	2.293762
ENSG00000154813	309.6463	0.201599	0.055811	3.612156	0.000304	0.007719	2.295759
ENSG00000107984	18.87642	0.61009	0.154428	3.950646	7.79E-05	0.007728	0.583933
ENSG00000282692	65.24793	-0.36987	0.096926	-3.81601	0.000136	0.007728	1.020896
ENSG00000131591	248.4382	-0.23549	0.064546	-3.6484	0.000264	0.007728	1.977088
ENSG00000198785	374.9296	0.28878	0.079282	3.642425	0.00027	0.007728	2.025126
ENSG00000112033	559.4032	-0.18787	0.052475	-3.58021	0.000343	0.007728	2.583187
ENSG00000088179	2329.103	0.164072	0.045861	3.577619	0.000347	0.00776	2.583187
ENSG00000130508	282.6473	-0.28233	0.077596	-3.63841	0.000274	0.007807	2.025126
ENSG00000165637	703.438	0.198559	0.055533	3.575501	0.00035	0.007807	2.583187
ENSG00000243660	265.0111	-0.19086	0.052479	-3.63688	0.000276	0.007815	2.025126
ENSG00000100150	386.3163	-0.16355	0.044989	-3.63531	0.000278	0.007815	2.025126
ENSG00000054116	397.7045	0.14153	0.039208	3.609732	0.000307	0.007815	2.225762
ENSG00000070047	970.2805	-0.18259	0.050694	-3.60189	0.000316	0.007815	2.293762
ENSG00000064651	2190.06	0.219608	0.06137	3.578437	0.000346	0.007815	2.514347
ENSG00000080823	519.7628	-0.15422	0.043155	-3.57363	0.000352	0.007815	2.583187
ENSG00000083312	2092.44	0.129472	0.03624	3.57262	0.000353	0.007815	2.583187
ENSG00000167193	817.6005	0.151682	0.042464	3.57198	0.000354	0.007815	2.583187
ENSG00000177311	2429.947	0.136813	0.038304	3.57173	0.000355	0.007815	2.583187
ENSG00000138018	1528.54	0.208505	0.058381	3.571428	0.000355	0.007815	2.583187
ENSG00000215458	88.25942	-0.3799	0.100581	-3.77708	0.000159	0.007829	1.142898
ENSG00000188827	423.8893	-0.20387	0.056516	-3.60723	0.000309	0.007829	2.225762
ENSG00000100325	305.4803	-0.16072	0.04464	-3.60035	0.000318	0.007829	2.295759
ENSG00000167468	1237.285	0.179407	0.049833	3.600164	0.000318	0.007829	2.293762
ENSG00000185736	898.3131	-0.28505	0.079201	-3.59906	0.000319	0.007829	2.295759
ENSG00000275023	3022.022	-0.15716	0.044047	-3.56802	0.00036	0.007829	2.583187

ENSG00000054983	606.2208	0.172961	0.048096	3.596183	0.000323	0.007881	2.29693
ENSG00000112624	888.4626	-0.13666	0.038327	-3.5657	0.000363	0.007881	2.583187
ENSG00000196591	525.9496	0.156402	0.043495	3.595888	0.000323	0.007889	2.293762
ENSG00000162817	1392.926	0.226403	0.062997	3.593874	0.000326	0.007931	2.295759
ENSG00000020181	307.4501	-0.29876	0.082311	-3.62965	0.000284	0.007937	1.995423
ENSG00000176715	462.5806	-0.14871	0.040882	-3.63739	0.000275	0.007952	1.918337
ENSG00000180998	412.226	0.286185	0.078888	3.627746	0.000286	0.007952	1.995423
ENSG00000183049	3986.114	-0.13212	0.037	-3.57085	0.000356	0.007952	2.492774
ENSG00000171862	2056.899	0.159469	0.0447	3.567528	0.00036	0.007952	2.514347
ENSG00000001497	747.9653	-0.20226	0.056812	-3.56008	0.000371	0.007952	2.583187
ENSG00000198431	834.5627	0.229252	0.063855	3.59018	0.00033	0.007955	2.293762
ENSG00000174282	2911.322	-0.12177	0.034211	-3.55927	0.000372	0.007955	2.583187
ENSG00000128656	8697.864	0.239295	0.067136	3.564327	0.000365	0.007999	2.514347
ENSG00000228315	295.483	-0.18952	0.05274	-3.59357	0.000326	0.008062	2.225762
ENSG00000162636	878.2016	0.228213	0.063512	3.593253	0.000327	0.008062	2.225762
ENSG00000156671	1880.943	0.120052	0.033658	3.566788	0.000361	0.008062	2.456745
ENSG00000006125	4527.305	0.1334	0.037438	3.563227	0.000366	0.008062	2.492774
ENSG00000168743	92.14303	0.611	0.162832	3.752335	0.000175	0.008065	1.182918
ENSG00000152484	784.5095	0.158446	0.044128	3.59059	0.00033	0.008065	2.225762
ENSG00000160613	733.2833	-0.15855	0.044242	-3.58382	0.000339	0.008065	2.293762
ENSG00000145687	1063.229	0.161101	0.045258	3.559654	0.000371	0.008065	2.514347
ENSG00000265972	2004.698	-0.46865	0.13193	-3.55222	0.000382	0.008065	2.583187
ENSG00000215717	512.2601	0.179542	0.050568	3.550505	0.000384	0.008086	2.583187
ENSG00000162852	1111.348	0.208608	0.058262	3.580547	0.000343	0.008102	2.295759
ENSG00000165973	476.6831	0.308276	0.086864	3.548953	0.000387	0.00811	2.583187
ENSG00000137947	217.2617	0.222893	0.061741	3.610122	0.000306	0.008174	2.025126
ENSG00000100216	314.3897	0.205722	0.057394	3.584385	0.000338	0.008186	2.225762
ENSG00000119397	661.7427	-0.18416	0.051495	-3.57632	0.000348	0.008186	2.29693
ENSG00000160094	436.4284	-0.14446	0.039884	-3.62209	0.000292	0.008192	1.918337
ENSG00000011566	985.3582	0.122731	0.034331	3.574976	0.00035	0.008192	2.295759
ENSG00000154917	5275.775	0.160602	0.045316	3.544011	0.000394	0.008192	2.583187
ENSG00000073464	2177.939	0.24052	0.067696	3.552934	0.000381	0.008194	2.492774
ENSG00000164112	384.4795	0.282106	0.078143	3.610145	0.000306	0.008211	1.995423
ENSG00000158014	13.12858	-0.64406	0.165886	-3.88253	0.000103	0.008242	0.670508
ENSG00000104154	469.1672	0.194716	0.054544	3.569892	0.000357	0.008304	2.295759
ENSG00000130299	174.5346	-0.22029	0.060805	-3.62289	0.000291	0.008317	1.867169
ENSG00000183155	193.7297	0.19817	0.055536	3.56834	0.000359	0.00833	2.295759
ENSG00000136367	718.7331	-0.26778	0.07558	-3.54305	0.000396	0.008361	2.514347
ENSG00000179361	88.50638	-0.25175	0.067372	-3.73668	0.000186	0.008367	1.182918
ENSG00000155961	339.9046	0.225162	0.062543	3.600144	0.000318	0.008436	1.995423
ENSG00000177337	189.1331	-0.22648	0.062984	-3.5959	0.000323	0.008436	2.025126
ENSG00000168575	1136.174	0.154355	0.043221	3.571311	0.000355	0.008436	2.225762
ENSG00000229569	21.80781	-0.56289	0.144633	-3.89185	9.95E-05	0.008451	0.616514
ENSG00000234913	94.24932	-0.3403	0.090967	-3.74087	0.000183	0.008451	1.136415
ENSG00000162627	113.4642	0.283437	0.078405	3.615027	0.0003	0.008451	1.867169
ENSG00000070501	213.6534	0.183333	0.051031	3.592596	0.000327	0.008451	2.025126
ENSG00000141424	630.4135	0.176621	0.049478	3.569676	0.000357	0.008451	2.225762
ENSG00000136485	1184.588	0.113679	0.03191	3.562454	0.000367	0.008451	2.293762
ENSG00000178741	496.7227	0.203703	0.0572	3.561255	0.000369	0.008451	2.295759
ENSG00000136783	207.0332	0.239307	0.067227	3.559674	0.000371	0.008451	2.295759
ENSG00000176641	621.4088	0.290392	0.082345	3.526544	0.000421	0.008504	2.583187
ENSG00000173113	288.8412	0.199944	0.056085	3.565039	0.000364	0.008516	2.225762
ENSG00000079385	74.07153	-0.28534	0.076352	-3.73712	0.000186	0.008522	1.136415
ENSG00000165684	564.1998	-0.20875	0.058571	-3.564	0.000365	0.008526	2.225762
ENSG00000285888	26.04961	-0.44791	0.118631	-3.77567	0.00016	0.008546	0.963911
ENSG00000286989	91.65624	-0.29597	0.079268	-3.73372	0.000189	0.008546	1.142898
ENSG00000128590	358.8732	0.216772	0.06019	3.601471	0.000316	0.008546	1.918337
ENSG00000101247	390.853	0.191724	0.053452	3.586861	0.000335	0.008546	1.995423
ENSG00000085449	431.959	0.175424	0.049282	3.559581	0.000371	0.008546	2.225762
ENSG00000166946	528.3839	0.180699	0.050769	3.559252	0.000372	0.008546	2.225762

ENSG00000129933	1100.032	-0.15199	0.042772	-3.55356	0.00038	0.008546	2.295759
ENSG00000184900	687.7854	0.212487	0.059798	3.553404	0.00038	0.008546	2.295759
ENSG00000206527	686.3985	0.189744	0.053424	3.551641	0.000383	0.008546	2.295759
ENSG00000106615	644.7548	0.203732	0.057381	3.550501	0.000384	0.008546	2.29693
ENSG00000135535	986.7453	0.15718	0.044272	3.550355	0.000385	0.008546	2.295759
ENSG00000152102	3003.506	0.118607	0.033562	3.533924	0.000409	0.008546	2.456745
ENSG00000144635	643.6945	0.180806	0.051352	3.520917	0.00043	0.008546	2.583187
ENSG00000180626	518.2192	-0.17857	0.050729	-3.52006	0.000431	0.008546	2.583187
ENSG00000129993	103.6732	-0.38758	0.106829	-3.62804	0.000286	0.00857	1.695647
ENSG00000104904	2346.825	0.158634	0.045009	3.524505	0.000424	0.008574	2.514347
ENSG00000228594	200.9685	-0.27988	0.078891	-3.5477	0.000389	0.008589	2.295759
ENSG00000168092	1986.395	0.154902	0.04368	3.54633	0.000391	0.008611	2.295759
ENSG00000056586	1876.532	0.121225	0.034392	3.524832	0.000424	0.008611	2.492774
ENSG00000086065	578.892	0.21839	0.06159	3.545899	0.000391	0.00862	2.293762
ENSG00000180440	204.9135	0.377148	0.104831	3.597677	0.000321	0.008678	1.867169
ENSG00000136522	208.8331	0.222179	0.062075	3.579223	0.000345	0.008704	1.995423
ENSG00000150054	307.8862	0.228788	0.064443	3.550207	0.000385	0.008704	2.225762
ENSG00000137876	574.7853	0.200295	0.056564	3.541011	0.000399	0.008726	2.295759
ENSG00000277142	88.34691	-0.25642	0.069181	-3.70644	0.00021	0.008743	1.201846
ENSG00000113966	336.804	0.229888	0.064352	3.57233	0.000354	0.008743	2.025126
ENSG00000184428	190.7541	-0.23381	0.065455	-3.57211	0.000354	0.008743	2.025126
ENSG00000158985	1336.211	0.185768	0.052472	3.540324	0.0004	0.008743	2.293762
ENSG00000084693	400.6168	-0.12526	0.035033	-3.57537	0.00035	0.008747	1.995423
ENSG00000162543	259.6017	-0.23923	0.067613	-3.53823	0.000403	0.008747	2.295759
ENSG00000146066	155.1312	0.185242	0.052245	3.54562	0.000392	0.008761	2.225762
ENSG00000175893	1751.042	0.138348	0.039468	3.505319	0.000456	0.008778	2.583187
ENSG00000133624	476.1662	-0.13945	0.039437	-3.53605	0.000406	0.00878	2.29693
ENSG00000137275	402.3297	-0.16965	0.047545	-3.5681	0.00036	0.008781	2.025126
ENSG00000120137	2119.593	0.143559	0.040861	3.51337	0.000442	0.008781	2.492774
ENSG00000234420	1324.519	-0.1213	0.034618	-3.50407	0.000458	0.008781	2.583187

ENSG00000081189	5883.445	0.205143	0.058429	3.510975	0.000446	0.008845	2.492774
ENSG00000171388	228.6671	0.383506	0.108579	3.532041	0.000412	0.008855	2.295759
ENSG00000104765	1995.053	0.182923	0.052058	3.513845	0.000442	0.008855	2.456745
ENSG00000186566	1602.661	-0.16027	0.045388	-3.53106	0.000414	0.008868	2.295759
ENSG00000135913	405.199	-0.12854	0.036361	-3.53518	0.000407	0.008994	2.225762
ENSG00000168216	950.1146	0.174655	0.049986	3.494059	0.000476	0.009026	2.583187
ENSG00000036257	1033.615	0.132351	0.03788	3.493973	0.000476	0.009026	2.583187
ENSG00000109189	1564.687	0.157917	0.045202	3.493556	0.000477	0.009028	2.583187
ENSG00000185947	164.5652	0.241476	0.068545	3.522879	0.000427	0.009086	2.295759
ENSG00000162521	1315.71	0.102462	0.029028	3.529823	0.000416	0.009105	2.225762
ENSG00000131966	560.6904	0.213708	0.060679	3.521946	0.000428	0.009105	2.295759
ENSG00000166226	872.5437	0.18893	0.053558	3.527586	0.000419	0.00917	2.225762
ENSG00000157680	2436.854	0.169156	0.048423	3.493309	0.000477	0.009223	2.514347
ENSG00000082701	2441.925	0.100376	0.028718	3.495183	0.000474	0.009225	2.492774
ENSG00000170919	699.2526	-0.16983	0.048316	-3.51497	0.00044	0.009295	2.293762
ENSG00000130224	245.5992	0.186235	0.052455	3.550359	0.000385	0.009421	1.977088
ENSG00000087448	1196.401	0.171654	0.048907	3.509767	0.000449	0.009454	2.293762
ENSG00000146676	1629.461	0.135377	0.038598	3.507393	0.000453	0.009527	2.293762
ENSG00000134121	5716.797	0.199159	0.056832	3.504369	0.000458	0.009614	2.295759
ENSG00000111727	606.4033	0.139196	0.039734	3.503175	0.00046	0.009653	2.293762
ENSG00000004779	392.1194	0.261377	0.073847	3.53942	0.000401	0.009654	1.995423
ENSG00000186297	736.8736	0.342593	0.097601	3.510125	0.000448	0.009654	2.225762
ENSG00000108582	1954.852	0.17511	0.050317	3.48014	0.000501	0.009654	2.492774
ENSG00000134253	121.4327	-0.2579	0.072523	-3.55618	0.000376	0.009656	1.867169
ENSG00000116906	440.4629	0.138726	0.039268	3.532821	0.000411	0.009715	2.025126
ENSG00000129562	320.075	0.190314	0.054265	3.50712	0.000453	0.009726	2.225762
ENSG00000279712	158.5772	-0.36931	0.105205	-3.5104	0.000447	0.009739	2.189833
ENSG00000165175	884.26	0.245702	0.070884	3.466235	0.000528	0.009739	2.583187
ENSG00000059758	1613.956	0.17012	0.048536	3.505012	0.000457	0.009765	2.225762
ENSG00000265125	77.20965	-0.32365	0.088206	-3.66922	0.000243	0.009766	1.182918

ENSG00000173542	764.2846	0.20688	0.059589	3.471805	0.000517	0.009766	2.514347
ENSG00000116459	1133.058	0.187098	0.053532	3.495059	0.000474	0.009786	2.293762
ENSG00000071537	1836.858	0.13215	0.038009	3.476787	0.000507	0.009786	2.456745
ENSG00000089094	589.4917	-0.1574	0.045059	-3.49319	0.000477	0.009816	2.29693
ENSG00000164830	3743.205	0.201078	0.058086	3.461701	0.000537	0.009816	2.583187
ENSG00000119013	262.8823	0.27052	0.077292	3.499982	0.000465	0.00985	2.225762
ENSG00000167005	543.8582	0.184296	0.05278	3.491763	0.00048	0.00985	2.29693
ENSG00000145675	5384.445	0.148897	0.042874	3.472908	0.000515	0.009862	2.456745
ENSG00000183283	1203.717	0.163096	0.046612	3.498978	0.000467	0.009862	2.225762
ENSG00000170632	325.8192	0.18029	0.051656	3.490228	0.000483	0.009867	2.295759
ENSG00000114346	174.9631	0.266907	0.075672	3.527177	0.00042	0.009868	1.995423
ENSG00000146151	353.4417	0.246516	0.069694	3.537134	0.000404	0.009872	1.918337
ENSG00000049130	631.5022	0.232723	0.066701	3.489032	0.000485	0.009883	2.293762
ENSG00000116199	1424.038	0.150564	0.043083	3.494763	0.000474	0.009956	2.225762
ENSG00000143363	219.4695	0.163806	0.046899	3.492732	0.000478	0.010019	2.225762
ENSG00000145715	1297.145	0.115299	0.033047	3.48897	0.000485	0.010068	2.225762
ENSG00000130177	658.1677	-0.13043	0.037457	-3.48223	0.000497	0.010068	2.295759
ENSG00000153989	282.7081	0.176377	0.05066	3.481609	0.000498	0.010068	2.295759
ENSG00000103150	597.575	-0.25207	0.07241	-3.48116	0.000499	0.010068	2.293762
ENSG00000196361	1626.587	-0.17911	0.051457	-3.4807	0.0005	0.010068	2.293762
ENSG00000117533	619.2407	0.165787	0.047631	3.48065	0.0005	0.010068	2.295759
ENSG00000079246	2875.856	0.162999	0.047235	3.450832	0.000559	0.010068	2.583187
ENSG00000137845	1475.188	0.120725	0.034994	3.449827	0.000561	0.010068	2.583187
ENSG00000119421	389.9196	0.206209	0.058654	3.515679	0.000439	0.010071	1.995423
ENSG00000136877	283.5728	-0.1941	0.055262	-3.5123	0.000444	0.010071	2.025126
ENSG00000280234	923.5117	-0.32888	0.09431	-3.48719	0.000488	0.010071	2.225762
ENSG00000130962	478.3329	0.26657	0.07664	3.478222	0.000505	0.010071	2.29693
ENSG00000109436	1170.794	0.169628	0.049115	3.45367	0.000553	0.010071	2.514347
ENSG00000115561	791.102	0.154226	0.044746	3.446689	0.000568	0.010071	2.583187
ENSG00000110321	5593.222	0.138535	0.040198	3.446292	0.000568	0.010071	2.583187

ENSG00000085231	91.45296	0.273107	0.0746	3.660947	0.000251	0.010084	1.136415
ENSG00000132388	432.3143	0.133508	0.03803	3.510616	0.000447	0.010084	2.025126
ENSG00000226696	109.2678	-0.22437	0.064378	-3.48516	0.000492	0.010084	2.225762
ENSG00000104763	1296.531	0.211742	0.060768	3.484401	0.000493	0.010094	2.225762
ENSG00000117758	1165.163	0.163594	0.047068	3.475675	0.00051	0.010098	2.295759
ENSG00000107669	1041.024	0.150884	0.043418	3.475121	0.000511	0.010106	2.295759
ENSG00000235316	81.16781	-0.31485	0.086116	-3.65612	0.000256	0.010181	1.136415
ENSG00000183648	348.1487	0.202122	0.057589	3.50976	0.000449	0.010181	1.995423
ENSG00000047621	447.6852	0.188242	0.053698	3.505558	0.000456	0.010181	2.025126
ENSG00000138663	478.2243	0.231972	0.066669	3.479486	0.000502	0.010181	2.225762
ENSG00000088812	2406.812	0.138567	0.040202	3.446722	0.000567	0.010181	2.514347
ENSG00000100664	2867.449	0.168663	0.049022	3.440543	0.000581	0.010181	2.583187
ENSG00000172466	1670.144	0.100226	0.029152	3.438034	0.000586	0.010219	2.583187
ENSG00000111897	8742.944	0.177633	0.051212	3.46857	0.000523	0.010255	2.295759
ENSG00000203761	79.92896	-0.25759	0.072653	-3.54542	0.000392	0.010339	1.695647
ENSG00000109452	530.6018	0.178763	0.051468	3.473269	0.000514	0.010339	2.225762
ENSG00000082996	857.302	0.197473	0.056981	3.465573	0.000529	0.010339	2.295759
ENSG00000177728	1624.701	-0.18458	0.053643	-3.4409	0.00058	0.010339	2.514347
ENSG00000110888	1400.629	-0.15344	0.044599	-3.44044	0.000581	0.010339	2.514347
ENSG00000106153	1317.457	0.21764	0.062696	3.47138	0.000518	0.010391	2.225762
ENSG00000041353	615.1517	0.403525	0.116262	3.470828	0.000519	0.0104	2.225762
ENSG00000081087	364.2366	0.168053	0.048111	3.493002	0.000478	0.01051	2.025126
ENSG00000244165	54.09844	-0.29599	0.080768	-3.66477	0.000248	0.010544	1.044965
ENSG00000137814	229.4043	0.193076	0.055238	3.495369	0.000473	0.010546	1.995423
ENSG00000074410	58.46098	-0.57931	0.155914	-3.71557	0.000203	0.010594	0.848718
ENSG00000164209	1348.992	0.207515	0.060046	3.455952	0.000548	0.010594	2.295759
ENSG00000118407	67.80753	0.377369	0.101639	3.712855	0.000205	0.01067	0.848718
ENSG00000110675	1163.695	0.193677	0.056083	3.453404	0.000554	0.01067	2.293762
ENSG00000104164	903.407	0.16549	0.048262	3.429007	0.000606	0.01067	2.514347
ENSG00000168615	939.1147	0.170181	0.049312	3.451083	0.000558	0.010734	2.295759

ENSG00000178449	139.9454	0.244743	0.070464	3.473318	0.000514	0.01075	2.108016
ENSG00000166128	615.0446	0.175751	0.050836	3.457192	0.000546	0.010759	2.225762
ENSG00000131263	2415.391	0.170875	0.049802	3.431121	0.000601	0.010759	2.456745
ENSG00000204116	1053.496	0.203676	0.059469	3.424917	0.000615	0.010759	2.514347
ENSG00000145349	1452.047	0.241933	0.070647	3.424511	0.000616	0.010759	2.514347
ENSG00000197872	1787.951	0.180672	0.052881	3.416548	0.000634	0.010759	2.583187
ENSG00000242797	12.30617	-0.60254	0.158932	-3.79115	0.00015	0.010814	0.60691
ENSG00000161267	948.2113	-0.22674	0.06579	-3.44646	0.000568	0.010816	2.295759
ENSG00000230358	37.93617	-0.37569	0.102684	-3.65868	0.000254	0.010844	1.020896
ENSG00000129083	685.4507	0.147123	0.04302	3.419876	0.000626	0.010867	2.514347
ENSG00000273267	16.79883	-0.57705	0.152642	-3.78042	0.000157	0.010908	0.622589
ENSG00000111647	1261.308	0.161085	0.04667	3.451576	0.000557	0.010908	2.225762
ENSG00000196502	310.5795	-0.2479	0.072012	-3.4425	0.000576	0.010908	2.295759
ENSG00000114742	877.2981	0.112834	0.032782	3.441941	0.000578	0.010908	2.295759
ENSG00000141314	796.1068	-0.22338	0.065368	-3.41734	0.000632	0.010908	2.514347
ENSG00000128683	1655.068	0.325724	0.094647	3.441459	0.000579	0.010924	2.293762
ENSG00000165194	716.9288	0.212159	0.061606	3.443812	0.000574	0.011136	2.225762
ENSG00000113712	1291.355	0.114874	0.033436	3.435621	0.000591	0.011136	2.293762
ENSG00000147416	3953.457	0.244196	0.071774	3.40228	0.000668	0.011164	2.583187
ENSG00000153561	1687.662	0.15679	0.045669	3.433182	0.000597	0.01121	2.293762
ENSG00000116731	2415.484	-0.14969	0.044023	-3.40022	0.000673	0.011222	2.583187
ENSG00000133460	426.4633	-0.1757	0.050482	-3.48042	0.000501	0.011223	1.918337
ENSG00000100473	46.6983	0.428424	0.116029	3.69237	0.000222	0.011245	0.848718
ENSG00000076344	787.2961	-0.22368	0.065826	-3.39799	0.000679	0.011275	2.583187
ENSG00000164611	26.07652	0.514337	0.140484	3.661165	0.000251	0.011347	0.947688
ENSG00000272927	32.11064	-0.4661	0.127313	-3.66103	0.000251	0.011347	0.947688
ENSG00000112335	1065.443	0.187071	0.054589	3.426885	0.000611	0.011358	2.293762
ENSG00000165629	904.2203	0.22678	0.066183	3.426567	0.000611	0.011358	2.295759
ENSG00000119844	992.9476	0.144579	0.042501	3.40179	0.000669	0.011358	2.514347
ENSG00000128191	463.494	-0.14607	0.042637	-3.42591	0.000613	0.011372	2.295759
ENSG00000181135	136.3861	-0.25548	0.074412	-3.43327	0.000596	0.011402	2.225762
ENSG00000102547	878.266	0.203587	0.059454	3.424261	0.000616	0.011402	2.295759
ENSG00000149328	521.1713	-0.22263	0.065629	-3.39221	0.000693	0.011402	2.583187
ENSG00000087502	581.1104	0.154576	0.04504	3.43197	0.000599	0.011418	2.225762
ENSG00000137075	973.9808	0.111821	0.033008	3.387652	0.000705	0.011561	2.583187
ENSG00000080546	809.553	0.183558	0.054193	3.387115	0.000706	0.01157	2.583187
ENSG00000128059	234.6509	0.196356	0.056868	3.452856	0.000555	0.011577	2.025126
ENSG00000118873	1208.769	0.153947	0.04504	3.418024	0.000631	0.0116	2.295759
ENSG00000204899	264.2663	0.207087	0.059924	3.455817	0.000549	0.011675	1.977088
ENSG00000101134	157.7878	0.231176	0.067432	3.428293	0.000607	0.011675	2.189833
ENSG00000163468	1272.152	0.172789	0.05058	3.416115	0.000635	0.011675	2.293762
ENSG00000198590	167.193	0.266499	0.077276	3.44868	0.000563	0.011677	2.025126
ENSG00000146267	1303.342	0.208703	0.061117	3.414793	0.000638	0.011677	2.295759
ENSG00000165643	475.6306	-0.29281	0.085549	-3.42273	0.00062	0.011679	2.225762
ENSG00000065989	864.6525	-0.21774	0.064389	-3.3816	0.000721	0.011685	2.583187
ENSG00000047315	1073.552	0.196583	0.057453	3.421613	0.000623	0.011701	2.225762
ENSG00000177000	713.2695	-0.13563	0.039742	-3.41269	0.000643	0.011719	2.293762
ENSG00000080189	483.7199	-0.14768	0.043286	-3.41159	0.000646	0.011753	2.293762
ENSG00000120053	1812.386	0.297787	0.087881	3.388523	0.000703	0.011753	2.492774
ENSG00000169288	175.1708	0.211569	0.061352	3.448469	0.000564	0.011753	1.995423
ENSG00000285796	157.1315	-0.23041	0.06766	-3.40545	0.000661	0.011753	2.338927
ENSG00000124172	666.5428	0.23005	0.067515	3.407407	0.000656	0.011881	2.293762
ENSG00000135324	250.9079	0.319137	0.092678	3.443501	0.000574	0.011937	1.995423
ENSG00000278259	487.448	-0.16552	0.048606	-3.40528	0.000661	0.011937	2.295759
ENSG00000132570	186.6837	-0.213	0.062575	-3.40388	0.000664	0.011984	2.295759
ENSG00000145242	642.492	0.278789	0.081913	3.403457	0.000665	0.01199	2.295759
ENSG00000121022	470.031	0.156509	0.045484	3.440955	0.00058	0.01199	1.995423
ENSG00000011426	1660.776	0.44199	0.129567	3.411299	0.000647	0.01199	2.225762
ENSG00000015475	521.7705	0.162976	0.047904	3.402138	0.000669	0.012002	2.293762
ENSG00000014641	4049.209	0.286673	0.084271	3.401812	0.000669	0.012002	2.295759

ENSG00000117600	1344.202	0.230452	0.067747	3.401653	0.00067	0.012002	2.295759
ENSG00000111077	1375.026	-0.2189	0.064357	-3.40132	0.000671	0.012013	2.293762
ENSG00000243696	68.13038	-0.31224	0.086362	-3.61549	0.0003	0.01204	1.020896
ENSG00000236408	25.2561	-0.42144	0.116817	-3.60766	0.000309	0.01204	1.053218
ENSG00000133422	505.2365	-0.11682	0.034374	-3.39851	0.000678	0.012081	2.29693
ENSG00000082153	714.1219	0.199628	0.058624	3.405246	0.000661	0.01215	2.225762
ENSG00000074696	1905.694	0.165109	0.048979	3.371008	0.000749	0.012172	2.514347
ENSG00000166181	873.0876	0.150056	0.044202	3.394788	0.000687	0.012201	2.295759
ENSG00000104231	443.5039	0.183047	0.053924	3.394518	0.000687	0.012201	2.295759
ENSG00000169499	739.7354	0.161866	0.047686	3.394413	0.000688	0.012201	2.295759
ENSG00000122335	366.6388	0.183902	0.054184	3.394063	0.000689	0.012204	2.295759
ENSG00000086300	700.5163	0.293936	0.086629	3.393047	0.000691	0.012234	2.293762
ENSG00000106299	1564.307	0.143714	0.042359	3.39279	0.000692	0.012234	2.295759
ENSG00000182253	1616.449	0.189233	0.056199	3.367218	0.000759	0.012246	2.514347
ENSG00000256443	187.8908	-0.48415	0.141152	-3.42995	0.000604	0.012254	1.995423
ENSG00000236540	71.41893	-0.3209	0.092402	-3.47287	0.000515	0.012287	1.695647
ENSG00000138798	58.87247	0.396589	0.110186	3.599275	0.000319	0.01233	1.044965
ENSG00000136448	1957.292	0.106608	0.03176	3.356646	0.000789	0.01233	2.583187
ENSG00000047578	634.3818	-0.13368	0.039351	-3.39703	0.000681	0.012332	2.225762
ENSG00000074657	2288.064	-0.12278	0.036479	-3.36584	0.000763	0.012332	2.492774
ENSG00000261971	54.93769	-0.34612	0.096091	-3.60207	0.000316	0.01239	1.023066
ENSG00000140157	301.2509	0.173668	0.050708	3.424866	0.000615	0.01239	1.995423
ENSG00000273079	7048.87	0.183297	0.054524	3.361775	0.000774	0.01239	2.514347
ENSG00000188674	211.281	0.280827	0.082036	3.42323	0.000619	0.012439	1.995423
ENSG00000279278	228.6504	-0.22478	0.065358	-3.43921	0.000583	0.012441	1.867169
ENSG00000163904	956.3412	0.108542	0.032005	3.391428	0.000695	0.012441	2.225762
ENSG00000229180	579.1741	-0.20673	0.06108	-3.38456	0.000713	0.012441	2.295759
ENSG00000088986	1392.056	0.221245	0.065391	3.383429	0.000716	0.012441	2.293762
ENSG00000119125	2210.334	0.292639	0.087092	3.360127	0.000779	0.012441	2.492774
ENSG00000120896	491.9117	-0.24579	0.073341	-3.35139	0.000804	0.012441	2.583187
ENSG00000124535	596.8058	0.116426	0.034746	3.350777	0.000806	0.012441	2.583187
ENSG00000136731	1278.092	0.09569	0.028293	3.382074	0.000719	0.012457	2.295759
ENSG00000242265	2530.556	0.251424	0.0749	3.356787	0.000789	0.012457	2.514347
ENSG00000117751	315.4274	0.148216	0.043837	3.381089	0.000722	0.012479	2.295759
ENSG00000155275	471.5826	-0.17899	0.052435	-3.41355	0.000641	0.012537	2.025126
ENSG00000163291	538.308	0.153472	0.045414	3.379371	0.000727	0.012537	2.295759
ENSG00000183011	316.708	0.215239	0.063081	3.412088	0.000645	0.012564	2.025126
ENSG00000185787	2103.533	0.126574	0.03747	3.378045	0.00073	0.012564	2.295759
ENSG00000139278	192.4338	0.281032	0.0832	3.377792	0.000731	0.012564	2.295759
ENSG00000164346	297.2553	0.254783	0.074599	3.415361	0.000637	0.012585	1.995423
ENSG00000128524	363.2868	0.190935	0.056412	3.38466	0.000713	0.012607	2.225762
ENSG00000173852	1098.299	0.243276	0.072602	3.350808	0.000806	0.012607	2.514347
ENSG00000154174	1345.755	0.195589	0.057995	3.372499	0.000745	0.012751	2.295759
ENSG00000136935	515.7854	-0.13186	0.039022	-3.37902	0.000727	0.012806	2.225762
ENSG00000145730	1688.942	0.219063	0.064991	3.370681	0.00075	0.012806	2.293762
ENSG00000122545	5596.046	0.145832	0.043593	3.345322	0.000822	0.012806	2.514347
ENSG00000123395	106.3934	0.23812	0.067185	3.544253	0.000394	0.01282	1.201846
ENSG00000184517	388.977	0.171913	0.05046	3.406907	0.000657	0.012858	1.995423
ENSG00000106723	2562.473	0.136744	0.040821	3.349854	0.000809	0.012858	2.456745
ENSG00000062725	1402.85	0.152688	0.045346	3.367151	0.000759	0.012916	2.293762
ENSG00000066583	100.1494	0.278013	0.078439	3.544316	0.000394	0.01294	1.182918
ENSG00000102003	5719.8	0.256748	0.076802	3.342979	0.000829	0.01294	2.492774
ENSG00000198740	1334.244	0.185766	0.055733	3.33316	0.000859	0.01294	2.583187
ENSG00000118242	141.9036	0.240168	0.07119	3.373609	0.000742	0.012948	2.225762
ENSG00000108561	426.6094	0.189246	0.056247	3.364561	0.000767	0.012958	2.295759
ENSG00000092140	405.4104	0.141619	0.041628	3.401962	0.000669	0.012983	1.995423
ENSG00000119574	150.8532	-0.20563	0.060898	-3.37659	0.000734	0.012983	2.189833
ENSG00000215397	37.62081	-0.64802	0.181031	-3.57963	0.000344	0.013037	1.020896
ENSG00000087053	996.5976	0.179387	0.053893	3.328599	0.000873	0.013057	2.583187
ENSG00000140015	966.4966	0.239464	0.071268	3.360068	0.000779	0.013113	2.293762

ENSG00000073969	3152.774	0.264727	0.079395	3.334304	0.000855	0.013114	2.514347
ENSG00000100425	689.1819	-0.14082	0.041921	-3.35915	0.000782	0.013118	2.295759
ENSG00000086102	913.651	-0.12865	0.038694	-3.32481	0.000885	0.01318	2.583187
ENSG00000142864	1322.589	0.118826	0.035744	3.324367	0.000886	0.013187	2.583187
ENSG00000163818	437.3077	0.178331	0.052589	3.391007	0.000696	0.013191	2.025126
ENSG00000120705	795.3251	0.146477	0.044068	3.323861	0.000888	0.013191	2.583187
ENSG00000156030	1031.347	-0.14704	0.043813	-3.35599	0.000791	0.0132	2.295759
ENSG00000198818	211.5074	0.171219	0.050177	3.41229	0.000644	0.013207	1.867169
ENSG00000178568	2320.941	0.194739	0.058438	3.332418	0.000861	0.013208	2.492774
ENSG00000121858	67.06577	-0.707	0.197452	-3.58064	0.000343	0.013211	0.989117
ENSG00000127415	250.909	-0.24764	0.073003	-3.3922	0.000693	0.013211	1.995423
ENSG00000173818	308.2285	-0.15906	0.046892	-3.39211	0.000694	0.013211	1.995423
ENSG00000050030	828.2668	0.169512	0.050421	3.361913	0.000774	0.013211	2.225762
ENSG00000188732	185.7903	0.227763	0.067751	3.361762	0.000774	0.013211	2.225762
ENSG00000233321	207.6555	-0.25344	0.075555	-3.35442	0.000795	0.013211	2.295759
ENSG00000138032	574.3534	0.160716	0.048386	3.321546	0.000895	0.013211	2.583187
ENSG00000255247	11.42048	-0.66112	0.164304	-4.02374	5.73E-05	0.01324	0.163912
ENSG00000183495	1859.696	-0.15403	0.046208	-3.33332	0.000858	0.01324	2.456745
ENSG00000250722	233.8071	0.361904	0.106759	3.389913	0.000699	0.013262	1.995423
ENSG00000170092	86.58892	-0.29037	0.084568	-3.4336	0.000596	0.013271	1.695647
ENSG00000155876	632.9064	0.172408	0.051457	3.350512	0.000807	0.013271	2.295759
ENSG00000165264	279.3237	0.205102	0.061225	3.349983	0.000808	0.013283	2.295759
ENSG00000137825	443.5249	0.273449	0.080461	3.398536	0.000677	0.013301	1.918337
ENSG00000036054	485.8977	0.13348	0.039858	3.348909	0.000811	0.013301	2.29693
ENSG00000169032	1247.47	0.198532	0.05929	3.348494	0.000813	0.013314	2.295759
ENSG00000198961	7986.767	0.192683	0.057888	3.328562	0.000873	0.013353	2.456745
ENSG00000159720	1350.991	0.148581	0.044282	3.355292	0.000793	0.013359	2.225762
ENSG00000069329	1897.914	0.190122	0.057126	3.328097	0.000874	0.013359	2.456745
ENSG00000111229	458.9719	0.180391	0.053367	3.380197	0.000724	0.013392	2.025126
ENSG00000104131	517.017	0.131888	0.03942	3.345708	0.000821	0.013392	2.293762

ENSG00000139163	1717.817	0.166114	0.050168	3.311165	0.000929	0.013448	2.583187
ENSG00000127337	96.84985	0.289504	0.084505	3.425888	0.000613	0.013495	1.695647
ENSG00000180901	1481.28	0.124569	0.037268	3.342495	0.00083	0.013495	2.295759
ENSG00000185053	108.9886	0.257703	0.075823	3.398744	0.000677	0.013515	1.867169
ENSG00000102890	100.5049	-0.28093	0.079798	-3.5205	0.000431	0.013559	1.182918
ENSG00000182264	27.50924	-0.43584	0.120851	-3.60646	0.00031	0.013596	0.848718
ENSG00000145782	688.7609	0.128419	0.038457	3.339301	0.00084	0.013596	2.295759
ENSG00000156804	965.7151	0.208164	0.062188	3.347324	0.000816	0.013599	2.225762
ENSG00000175606	198.0828	0.227277	0.067899	3.347281	0.000816	0.013599	2.225762
ENSG00000147421	1186.162	0.143988	0.043128	3.338614	0.000842	0.013601	2.293762
ENSG00000250571	156.7098	-0.23288	0.0686	-3.39476	0.000687	0.013603	1.867169
ENSG00000116030	609.6683	0.168821	0.050577	3.337877	0.000844	0.013603	2.29693
ENSG00000141577	196.2169	-0.24469	0.072481	-3.37588	0.000736	0.013622	1.995423
ENSG00000141994	140.4252	-0.24448	0.072761	-3.36002	0.000779	0.013644	2.108016
ENSG00000142230	780.7856	0.12923	0.038735	3.336225	0.000849	0.01365	2.293762
ENSG00000278845	143.2345	0.185651	0.055456	3.347751	0.000815	0.013689	2.189833
ENSG00000105819	703.3906	0.135881	0.041155	3.301713	0.000961	0.013689	2.583187
ENSG00000254561	61.38345	-0.57506	0.161509	-3.56053	0.00037	0.013716	0.989117
ENSG00000005020	432.149	0.216744	0.064072	3.382821	0.000717	0.013716	1.918337
ENSG00000152944	464.836	0.161054	0.048317	3.333284	0.000858	0.013716	2.295759
ENSG00000133606	881.9217	0.114929	0.03448	3.333208	0.000859	0.013716	2.293762
ENSG00000139287	18.99639	0.603762	0.163282	3.697675	0.000218	0.013752	0.578677
ENSG00000019505	2054.996	0.181835	0.054576	3.331748	0.000863	0.013752	2.295759
ENSG00000124496	462.1991	-0.2016	0.05963	-3.38085	0.000723	0.013762	1.918337
ENSG00000177613	546.6935	0.154797	0.046937	3.297973	0.000974	0.013762	2.583187
ENSG00000183317	527.9433	-0.19775	0.059379	-3.33024	0.000868	0.01379	2.293762
ENSG00000169282	832.5601	0.186349	0.056394	3.304421	0.000952	0.01379	2.514347
ENSG00000198556	217.3639	-0.17824	0.053428	-3.33612	0.00085	0.013892	2.225762
ENSG00000125520	167.8238	-0.26626	0.079213	-3.36136	0.000776	0.013925	2.025126
ENSG00000127824	1424.425	0.260607	0.078349	3.32622	0.00088	0.013941	2.293762

ENSG00000243156	2540.903	-0.17847	0.05408	-3.30011	0.000966	0.013948	2.514347
ENSG00000122584	270.1691	0.278282	0.082825	3.3599	0.00078	0.013953	2.025126
ENSG00000196914	6835.426	0.127693	0.038676	3.30163	0.000961	0.013953	2.492774
ENSG00000105662	1754.137	-0.24779	0.075281	-3.2916	0.000996	0.013953	2.583187
ENSG00000126214	1066.517	0.113429	0.034468	3.290829	0.000999	0.013978	2.583187
ENSG00000160949	134.6208	-0.24752	0.073956	-3.34689	0.000817	0.013989	2.108016
ENSG00000072133	314.3932	0.169365	0.050834	3.331718	0.000863	0.013989	2.225762
ENSG00000134108	1717.562	0.172854	0.051888	3.331275	0.000864	0.013998	2.225762
ENSG00000149313	991.3393	0.19572	0.059375	3.296318	0.00098	0.014028	2.514347
ENSG00000143578	37.10142	-0.3068	0.086737	-3.53715	0.000404	0.014052	1.035363
ENSG00000166233	1958.029	0.111462	0.033573	3.31995	0.0009	0.014093	2.295759
ENSG00000109118	633.845	-0.11311	0.034075	-3.31934	0.000902	0.01411	2.295759
ENSG00000141837	3262.342	-0.20844	0.063445	-3.28536	0.001019	0.014141	2.583187
ENSG00000143977	85.04806	0.261854	0.074654	3.507563	0.000452	0.014178	1.142898
ENSG00000145495	5247.899	0.141212	0.042584	3.316075	0.000913	0.014234	2.295759
ENSG00000112110	287.3382	0.187171	0.056309	3.323974	0.000887	0.014252	2.225762
ENSG00000075089	265.3189	0.203693	0.061443	3.315177	0.000916	0.014252	2.295759
ENSG00000065548	812.0264	0.179773	0.054099	3.323062	0.00089	0.014277	2.225762
ENSG00000179846	50.45896	-0.34009	0.096238	-3.53382	0.00041	0.014292	1.020896
ENSG00000205302	506.677	0.148504	0.044819	3.313444	0.000922	0.014292	2.29693
ENSG00000091164	1231.572	0.146076	0.043979	3.321535	0.000895	0.014314	2.225762
ENSG00000138660	360.9156	0.182872	0.054568	3.351282	0.000804	0.014319	1.995423
ENSG00000131171	1004.726	0.18747	0.056596	3.312451	0.000925	0.014319	2.295759
ENSG00000100811	1365.256	0.106218	0.032406	3.277752	0.001046	0.014366	2.583187
ENSG00000187391	3959.64	-0.10393	0.03171	-3.27764	0.001047	0.014366	2.583187
ENSG00000104490	2293.817	0.301	0.091669	3.283553	0.001025	0.01444	2.514347
ENSG00000104388	1609.449	0.183918	0.056148	3.275576	0.001054	0.014444	2.583187
ENSG00000259666	44.90322	-0.42579	0.120892	-3.52205	0.000428	0.014473	1.044965
ENSG00000135932	1965.106	0.158672	0.048249	3.288621	0.001007	0.014473	2.456745
ENSG00000126821	388.7051	0.154355	0.046144	3.345064	0.000823	0.014546	1.995423

ENSG00000124380	285.5455	0.140994	0.042231	3.338612	0.000842	0.014655	2.025126
ENSG00000196376	1222.633	0.198033	0.060461	3.275376	0.001055	0.014779	2.514347
ENSG00000144290	3126.407	0.19125	0.058535	3.267248	0.001086	0.014791	2.583187
ENSG00000279792	74.29747	-0.25058	0.071966	-3.48194	0.000498	0.014791	1.182918
ENSG00000280222	171.4279	-0.3229	0.096706	-3.33902	0.000841	0.014795	1.995423
ENSG00000068654	1261.468	-0.12523	0.038266	-3.27276	0.001065	0.01486	2.514347
ENSG00000110955	3936.117	0.231121	0.070591	3.274081	0.00106	0.014904	2.492774
ENSG00000145794	1251.546	0.214996	0.065734	3.27067	0.001073	0.014942	2.514347
ENSG00000147526	5341.144	0.141385	0.043257	3.268503	0.001081	0.015042	2.514347
ENSG00000176444	402.4087	-0.14831	0.044912	-3.30218	0.000959	0.015064	2.225762
ENSG00000144366	266.8848	0.235013	0.070624	3.327686	0.000876	0.015098	2.025126
ENSG00000113558	2330.465	0.156055	0.0479	3.257924	0.001122	0.015155	2.583187
ENSG00000022267	1612.371	0.155006	0.047117	3.289768	0.001003	0.015221	2.295759
ENSG00000227398	194.0466	-0.16633	0.049971	-3.32856	0.000873	0.015226	1.995423
ENSG00000076984	331.1749	-0.16488	0.049552	-3.32735	0.000877	0.015226	1.995423
ENSG00000184232	313.4588	-0.30563	0.091961	-3.32345	0.000889	0.015226	2.025126
ENSG00000072818	136.0819	-0.24933	0.075508	-3.30208	0.00096	0.015226	2.189833
ENSG00000142507	387.2648	0.184595	0.055992	3.296831	0.000978	0.015226	2.225762
ENSG00000076108	1346.86	-0.14663	0.044941	-3.26272	0.001103	0.015226	2.514347
ENSG00000140280	248.013	0.187531	0.05704	3.287719	0.00101	0.015228	2.295759
ENSG00000155846	650.8276	-0.1376	0.041855	-3.28752	0.001011	0.015228	2.295759
ENSG00000070761	231.773	0.223041	0.067151	3.321487	0.000895	0.015279	2.025126
ENSG00000106367	578.3222	0.195076	0.059211	3.294581	0.000986	0.015289	2.225762
ENSG00000269858	221.5118	-0.18117	0.054208	-3.34208	0.000832	0.015361	1.867169
ENSG00000128563	358.9753	-0.15459	0.046526	-3.32276	0.000891	0.015393	1.995423
ENSG00000134248	180.7908	0.215524	0.065483	3.291296	0.000997	0.015426	2.225762
ENSG00000172575	646.7184	0.224678	0.069164	3.248493	0.00116	0.015448	2.583187
ENSG00000114480	212.5575	0.217482	0.066128	3.288823	0.001006	0.015533	2.225762
ENSG00000041357	422.9224	0.164591	0.050189	3.279431	0.00104	0.015541	2.295759
ENSG00000163682	1731.883	0.214859	0.066192	3.245988	0.00117	0.015541	2.583187

ENSG00000134153	216.3511	0.187706	0.056606	3.316013	0.000913	0.015681	1.995423
ENSG00000126261	992.229	0.133936	0.040771	3.285108	0.001019	0.015681	2.225762
ENSG00000111269	1005.1	0.173525	0.053396	3.249785	0.001155	0.015711	2.514347
ENSG00000153936	590.3995	0.191107	0.058957	3.241449	0.001189	0.015732	2.583187
ENSG00000038532	1381.441	-0.12444	0.038401	-3.24042	0.001194	0.015775	2.583187
ENSG00000164764	50.6307	0.376641	0.107474	3.504493	0.000457	0.015776	0.989117
ENSG00000076003	211.9249	0.215366	0.065027	3.311969	0.000926	0.015822	1.995423
ENSG00000196378	197.5189	-0.21974	0.066976	-3.28091	0.001035	0.015828	2.225762
ENSG00000240024	130.4223	0.205296	0.062512	3.284097	0.001023	0.015892	2.189833
ENSG00000174405	469.836	0.182401	0.055631	3.27875	0.001043	0.01592	2.225762
ENSG00000197043	3481.224	0.198964	0.060864	3.269018	0.001079	0.015947	2.295759
ENSG00000204469	4660.031	-0.14869	0.045755	-3.24978	0.001155	0.015947	2.456745
ENSG00000280163	54.23107	-0.33377	0.095796	-3.48421	0.000494	0.015995	1.044965
ENSG00000112902	953.8934	0.223119	0.068276	3.26788	0.001084	0.015995	2.293762
ENSG00000155189	614.122	0.140971	0.043042	3.275195	0.001056	0.016019	2.225762
ENSG00000231312	471.2905	-0.1619	0.049564	-3.26646	0.001089	0.016019	2.295759
ENSG00000178980	2776.971	0.137719	0.042598	3.233016	0.001225	0.016019	2.583187
ENSG00000103342	1469.933	0.107278	0.033187	3.232522	0.001227	0.016025	2.583187
ENSG00000153339	970.5001	0.127067	0.038808	3.274238	0.001059	0.016029	2.225762
ENSG00000125826	526.5271	-0.16285	0.049865	-3.26592	0.001091	0.016029	2.293762
ENSG00000184678	338.9535	-0.23963	0.072611	-3.30026	0.000966	0.016048	2.025126
ENSG00000184863	1743.325	-0.14352	0.043972	-3.26393	0.001099	0.016077	2.295759
ENSG00000014824	1526.777	0.17722	0.054298	3.263858	0.001099	0.016077	2.295759
ENSG00000033867	1338.581	0.18308	0.055956	3.27184	0.001069	0.016107	2.225762
ENSG00000133169	1431.051	0.278352	0.086215	3.228562	0.001244	0.016145	2.583187
ENSG00000272335	286.7363	0.180464	0.055189	3.269963	0.001076	0.016185	2.225762
ENSG00000100519	713.2807	0.169258	0.052487	3.22477	0.001261	0.016331	2.583187
ENSG00000135597	1395.194	-0.13298	0.040815	-3.25821	0.001121	0.016341	2.293762
ENSG00000240583	726.7186	0.626509	0.19185	3.265621	0.001092	0.016391	2.225762
ENSG00000269044	130.1414	-0.19841	0.060787	-3.26407	0.001098	0.016436	2.225762
ENSG00000166848	1717.127	0.173551	0.053309	3.25554	0.001132	0.016436	2.295759
ENSG00000118564	1600.434	0.117021	0.036233	3.22967	0.001239	0.016436	2.514347
ENSG00000103042	321.1915	-0.16084	0.049333	-3.2604	0.001113	0.016635	2.225762
ENSG00000260022	12.03889	-0.63084	0.174741	-3.61018	0.000306	0.016682	0.60691
ENSG00000152207	89.76717	-0.42668	0.127916	-3.3356	0.000851	0.016682	1.695647
ENSG00000075303	422.3135	0.187082	0.056682	3.300539	0.000965	0.016682	1.918337
ENSG00000141429	472.6681	0.187172	0.056915	3.288645	0.001007	0.016682	1.995423
ENSG00000269069	160.4956	-0.22382	0.068608	-3.26238	0.001105	0.016682	2.189833
ENSG00000143207	610.2037	0.125956	0.038765	3.24919	0.001157	0.016682	2.293762
ENSG00000138138	1007.128	0.185178	0.056995	3.249006	0.001158	0.016682	2.293762
ENSG00000044115	2182.874	0.118891	0.036878	3.223936	0.001264	0.016682	2.514347
ENSG00000174327	19.49917	-0.49493	0.136828	-3.61721	0.000298	0.016821	0.583933
ENSG00000227500	446.4399	-0.16513	0.050257	-3.28568	0.001017	0.016821	1.995423
ENSG00000133107	165.7535	0.267433	0.082409	3.245204	0.001174	0.016847	2.295759
ENSG00000240891	662.4005	0.274171	0.084509	3.244302	0.001177	0.016877	2.29693
ENSG00000277449	69.047	-0.27132	0.078078	-3.47498	0.000511	0.016947	0.989117
ENSG00000164081	282.6209	0.139129	0.042445	3.27786	0.001046	0.016947	2.025126
ENSG00000127995	1030.243	0.179811	0.055459	3.242254	0.001186	0.016947	2.293762
ENSG00000162989	1299.006	0.181081	0.055854	3.242034	0.001187	0.016947	2.293762
ENSG00000166971	640.241	0.121031	0.037336	3.24165	0.001188	0.016947	2.29693
ENSG00000178234	967.5419	0.138879	0.043292	3.207967	0.001337	0.016947	2.583187
ENSG00000184076	238.9393	0.251018	0.076633	3.275593	0.001054	0.017036	2.025126
ENSG00000166557	268.3767	0.164479	0.050783	3.238837	0.0012	0.017076	2.295759
ENSG00000159082	2887.401	0.187386	0.05828	3.215266	0.001303	0.017076	2.492774
ENSG00000151366	312.6644	0.192993	0.058981	3.272117	0.001067	0.017192	2.025126
ENSG00000121905	955.0631	0.211567	0.065366	3.236642	0.001209	0.017192	2.293762
ENSG00000185730	264.2551	-0.17126	0.052258	-3.27728	0.001048	0.017245	1.977088
ENSG00000154822	710.1947	0.167171	0.051533	3.243945	0.001179	0.017245	2.225762
ENSG00000126698	679.0386	0.158998	0.049153	3.234758	0.001217	0.017245	2.295759
ENSG00000176903	1638.301	0.133105	0.041083	3.239941	0.001196	0.017452	2.225762

ENSG00000141905	2165.083	-0.25019	0.077908	-3.21135	0.001321	0.017456	2.456745
ENSG00000177679	1101.339	-0.21025	0.064938	-3.23771	0.001205	0.017557	2.225762
ENSG00000272505	404.3334	-0.19875	0.06091	-3.26303	0.001102	0.017612	2.025126
ENSG00000071553	1445.419	0.159112	0.049704	3.20118	0.001369	0.017612	2.514347
ENSG00000144711	5866.227	-0.14887	0.046621	-3.19329	0.001407	0.017612	2.583187
ENSG00000115568	663.1171	-0.14602	0.045731	-3.19308	0.001408	0.017612	2.583187
ENSG00000259495	182.9182	-0.18995	0.05782	-3.28522	0.001019	0.017623	1.867169
ENSG00000163444	586.0264	0.186072	0.05771	3.224249	0.001263	0.017734	2.295759
ENSG00000127022	5324.195	0.141844	0.044258	3.204953	0.001351	0.017734	2.456745
ENSG00000059145	316.8309	-0.19486	0.059791	-3.25899	0.001118	0.017774	2.025126
ENSG00000166747	1667.038	0.106151	0.032932	3.223359	0.001267	0.017774	2.293762
ENSG00000110218	333.3292	0.235623	0.073146	3.22129	0.001276	0.017872	2.295759
ENSG00000225756	35.74854	-0.39309	0.11408	-3.44576	0.000569	0.017918	1.020896
ENSG00000009950	379.038	-0.24987	0.076421	-3.26961	0.001077	0.01794	1.918337
ENSG00000180287	185.0822	0.236681	0.072713	3.255012	0.001134	0.01794	2.025126
ENSG00000103091	701.9846	-0.13058	0.040451	-3.22799	0.001247	0.01794	2.225762
ENSG00000073050	203.0472	-0.15222	0.047166	-3.22735	0.001249	0.01794	2.225762
ENSG00000108424	1958.759	0.097359	0.030424	3.200106	0.001374	0.01794	2.456745
ENSG00000169504	1506.129	0.259041	0.081136	3.192685	0.00141	0.01794	2.514347
ENSG00000102271	303.6811	0.249368	0.076554	3.257396	0.001124	0.017988	1.995423
ENSG00000136450	668.8132	0.116343	0.036164	3.21705	0.001295	0.017988	2.29693
ENSG00000028310	588.0431	-0.1326	0.04168	-3.18129	0.001466	0.018091	2.583187
ENSG00000057757	1105.845	0.19986	0.062175	3.214452	0.001307	0.018145	2.293762
ENSG00000197860	1837.076	0.176532	0.055522	3.179505	0.001475	0.018172	2.583187
ENSG00000279759	245.5191	-0.23664	0.072898	-3.2462	0.00117	0.018328	2.025126
ENSG00000162415	270.6757	-0.1261	0.039169	-3.21932	0.001285	0.018328	2.225762
ENSG00000171314	713.4036	0.210498	0.066267	3.176499	0.001491	0.018328	2.583187
ENSG00000169139	999.8571	0.174449	0.054363	3.208941	0.001332	0.018401	2.293762
ENSG00000124795	722.7205	0.146987	0.0463	3.174641	0.0015	0.018401	2.583187
ENSG00000120992	223.8563	0.2068	0.063664	3.248328	0.001161	0.018407	1.995423

ENSG00000213923	967.2384	-0.12217	0.037979	-3.21676	0.001296	0.018407	2.225762
ENSG00000115233	562.2938	0.187529	0.058457	3.207958	0.001337	0.018407	2.29693
ENSG00000163625	5514.974	0.07811	0.024351	3.207608	0.001338	0.018408	2.295759
ENSG00000241269	30.1614	-0.37392	0.108432	-3.44844	0.000564	0.018428	0.963911
ENSG00000079462	93.1246	0.260483	0.076571	3.401844	0.000669	0.018428	1.142898
ENSG00000188735	387.023	-0.16603	0.051633	-3.2155	0.001302	0.018428	2.225762
ENSG00000122565	733.2609	0.124219	0.03874	3.206457	0.001344	0.018428	2.295759
ENSG00000168291	471.9417	0.203039	0.063365	3.204272	0.001354	0.018543	2.295759
ENSG00000163328	1507.186	0.145026	0.045756	3.169536	0.001527	0.018567	2.583187
ENSG00000197724	864.7696	-0.13275	0.041891	-3.16891	0.00153	0.018591	2.583187
ENSG00000215154	87.30611	-0.25774	0.075907	-3.39545	0.000685	0.01879	1.142898
ENSG00000215440	123.9863	-0.25856	0.079358	-3.25817	0.001121	0.01879	1.867169
ENSG00000176209	167.9247	0.21213	0.066127	3.20792	0.001337	0.01879	2.225762
ENSG00000165023	4248.079	0.24541	0.07729	3.175185	0.001497	0.01879	2.492774
ENSG00000168374	559.2347	0.152205	0.047606	3.197187	0.001388	0.018892	2.295759
ENSG00000268471	78.6572	-0.22695	0.06686	-3.3944	0.000688	0.018899	1.136415
ENSG00000111843	329.0886	0.185364	0.058006	3.195578	0.001396	0.018965	2.295759
ENSG00000261649	38.33615	-0.4228	0.123925	-3.41176	0.000645	0.019003	1.053218
ENSG00000177051	142.6654	-0.19383	0.059586	-3.253	0.001142	0.019003	1.867169
ENSG00000158286	312.6318	-0.21996	0.067965	-3.23639	0.001211	0.019003	1.977088
ENSG00000152219	385.8528	0.13597	0.042449	3.203145	0.001359	0.019003	2.225762
ENSG00000113361	548.5886	0.233949	0.073239	3.194329	0.001402	0.019003	2.295759
ENSG00000119396	1361.62	0.129876	0.040669	3.193462	0.001406	0.019003	2.293762
ENSG00000154473	616.459	0.130306	0.040806	3.193316	0.001406	0.019003	2.293762
ENSG00000158458	158.2323	-0.17558	0.055059	-3.18894	0.001428	0.019003	2.338927
ENSG00000198198	1778.416	-0.15808	0.049535	-3.19134	0.001416	0.019101	2.295759
ENSG00000113262	77.79762	-0.2986	0.088514	-3.37344	0.000742	0.01911	1.201846
ENSG00000161203	3358.532	0.163783	0.051649	3.171054	0.001519	0.019112	2.456745
ENSG00000163644	2691.605	0.129792	0.041136	3.155237	0.001604	0.019175	2.583187
ENSG00000169783	1132.373	-0.22712	0.07122	-3.18896	0.001428	0.019194	2.295759

ENSG00000224616	168.0701	-0.20645	0.06404	-3.22381	0.001265	0.01922	2.025126
ENSG00000169951	156.4229	-0.18381	0.057497	-3.19688	0.001389	0.01922	2.225762
ENSG00000198860	340.3699	0.167995	0.052555	3.196547	0.001391	0.01922	2.225762
ENSG00000145864	5213.204	0.216094	0.068346	3.161765	0.001568	0.01922	2.514347
ENSG00000234911	45.43501	-0.34126	0.100196	-3.40588	0.00066	0.019244	1.053218
ENSG00000232287	77.75982	-0.31952	0.097615	-3.27331	0.001063	0.019244	1.695647
ENSG00000102967	213.4031	-0.18346	0.056927	-3.22264	0.00127	0.019244	2.025126
ENSG00000108179	419.7977	0.148653	0.046658	3.185997	0.001443	0.019263	2.295759
ENSG00000136738	535.7108	0.168382	0.052863	3.185224	0.001446	0.019289	2.29693
ENSG00000224383	36.79595	0.492965	0.144873	3.402745	0.000667	0.019386	1.053218
ENSG00000004139	259.9529	-0.16548	0.051425	-3.21792	0.001291	0.019386	2.025126
ENSG00000131508	702.5267	0.134734	0.04232	3.183693	0.001454	0.019386	2.293762
ENSG00000149218	1762.284	0.185605	0.058322	3.182441	0.00146	0.019386	2.295759
ENSG00000153902	875.0778	-0.21002	0.066003	-3.182	0.001463	0.019386	2.295759
ENSG00000275342	347.883	-0.2483	0.078033	-3.18195	0.001463	0.019386	2.295759
ENSG00000164924	5719.454	0.176005	0.055734	3.157952	0.001589	0.019386	2.492774
ENSG00000162105	1779.325	-0.15892	0.050345	-3.15667	0.001596	0.019386	2.514347
ENSG00000089737	3723.111	0.166859	0.053006	3.147942	0.001644	0.019386	2.583187
ENSG00000136463	149.9546	0.190918	0.059553	3.205876	0.001347	0.019405	2.108016
ENSG00000119401	438.5523	0.133678	0.042024	3.18101	0.001468	0.019405	2.295759
ENSG00000233436	102.0111	-0.25022	0.074316	-3.36691	0.00076	0.019442	1.182918
ENSG00000160961	472.4979	-0.16616	0.051417	-3.23156	0.001231	0.019442	1.918337
ENSG00000116791	156.1246	0.325723	0.101644	3.204551	0.001353	0.019442	2.108016
ENSG00000187109	3459.255	0.126041	0.039974	3.153076	0.001616	0.019442	2.514347
ENSG00000229020	21.65936	-0.55411	0.144144	-3.84414	0.000121	0.019529	0.187229
ENSG00000110492	67.45768	-0.42846	0.123984	-3.45576	0.000549	0.019529	0.848718
ENSG00000197362	246.5822	-0.17312	0.053781	-3.21907	0.001286	0.019632	1.977088
ENSG00000087095	1895.035	0.136077	0.042852	3.175517	0.001496	0.019647	2.295759
ENSG00000267169	113.1552	-0.26442	0.08292	-3.18889	0.001428	0.019651	2.189833
ENSG00000172465	273.3595	0.184384	0.057304	3.217635	0.001293	0.019672	1.977088

ENSG00000145348	917.1766	0.117138	0.036897	3.174687	0.0015	0.019672	2.293762
ENSG00000226237	34.20145	-0.3724	0.10958	-3.39847	0.000678	0.019673	1.035363
ENSG00000052795	1463.991	0.136923	0.043503	3.147445	0.001647	0.019674	2.514347
ENSG00000280434	88.29491	-0.34512	0.102404	-3.37018	0.000751	0.019702	1.142898
ENSG00000185728	992.8187	0.119011	0.037826	3.146314	0.001653	0.019702	2.514347
ENSG00000139364	3640.909	0.101504	0.03234	3.138611	0.001698	0.019702	2.583187
ENSG00000214331	207.9972	-0.19673	0.061315	-3.20855	0.001334	0.019707	2.025126
ENSG00000105605	593.9509	-0.16153	0.050917	-3.17252	0.001511	0.019707	2.293762
ENSG00000168096	476.6292	-0.15496	0.049391	-3.13736	0.001705	0.019724	2.583187
ENSG00000178163	637.1407	0.14837	0.046782	3.171537	0.001516	0.019725	2.295759
ENSG00000231824	18.03484	0.637618	0.179637	3.549473	0.000386	0.019725	0.583933
ENSG00000175727	1009.405	-0.17293	0.054998	-3.14424	0.001665	0.019746	2.514347
ENSG00000129460	201.5149	0.162235	0.051026	3.179442	0.001476	0.01975	2.225762
ENSG00000205482	48.25809	-0.32835	0.095223	-3.44828	0.000564	0.019787	0.848718
ENSG00000148154	580.8793	0.203302	0.06485	3.134964	0.001719	0.01979	2.583187
ENSG00000105298	287.3495	-0.16735	0.05281	-3.16887	0.00153	0.019797	2.295759
ENSG00000188612	591.4605	0.152109	0.048004	3.168658	0.001531	0.019797	2.295759
ENSG00000101266	1449.952	0.083847	0.026685	3.142073	0.001678	0.019797	2.514347
ENSG00000267904	65.26206	-0.27232	0.080357	-3.38881	0.000702	0.019917	1.044965
ENSG00000125356	466.6388	0.224203	0.069688	3.217256	0.001294	0.019986	1.918337
ENSG00000124333	380.3151	0.176424	0.055039	3.205447	0.001349	0.020004	1.995423
ENSG00000145293	730.9114	0.187587	0.059275	3.164686	0.001553	0.020018	2.293762
ENSG00000106052	1821.76	0.118272	0.037703	3.136904	0.001707	0.020068	2.514347
ENSG00000287558	67.52559	-0.53241	0.157285	-3.38501	0.000712	0.020078	1.044965
ENSG00000114735	326.5542	-0.15102	0.04711	-3.20572	0.001347	0.020078	1.977088
ENSG00000204348	167.5176	-0.15018	0.046941	-3.19924	0.001378	0.020078	2.025126
ENSG00000107679	2204.594	0.150924	0.04809	3.13836	0.001699	0.020078	2.492774
ENSG00000261678	1087.725	-0.34411	0.10977	-3.13487	0.001719	0.020127	2.514347
ENSG00000141084	387.478	-0.14899	0.046369	-3.21307	0.001313	0.020134	1.918337
ENSG00000181191	695.9917	0.185921	0.058828	3.160447	0.001575	0.020149	2.295759

ENSG00000099341	813.9379	0.167749	0.053664	3.12594	0.001772	0.020149	2.583187
ENSG00000170381	304.6037	0.451751	0.141167	3.200113	0.001374	0.0202	1.995423
ENSG00000068912	761.1392	0.175195	0.05547	3.158343	0.001587	0.020263	2.295759
ENSG00000027847	250.6515	-0.13785	0.043165	-3.19341	0.001406	0.020275	2.025126
ENSG00000116141	996.8468	0.115553	0.036488	3.166852	0.001541	0.020275	2.225762
ENSG00000171467	1002.286	-0.13134	0.041478	-3.1665	0.001543	0.020275	2.225762
ENSG00000130770	546.3529	0.1553	0.049187	3.157309	0.001592	0.020275	2.29693
ENSG00000163947	1061.133	0.164125	0.051983	3.157305	0.001592	0.020275	2.293762
ENSG00000135930	484.9359	0.115947	0.03673	3.156729	0.001595	0.020279	2.295759
ENSG00000241553	399.1282	0.144264	0.045704	3.15649	0.001597	0.020279	2.295759
ENSG00000142039	224.0259	-0.18004	0.056884	-3.16515	0.00155	0.020289	2.225762
ENSG00000234500	58.97846	-0.36668	0.106805	-3.43318	0.000597	0.020461	0.848718
ENSG00000144848	332.7627	0.174136	0.054543	3.19263	0.00141	0.020519	1.995423
ENSG00000166159	383.6066	-0.18677	0.058572	-3.18868	0.001429	0.020519	2.025126
ENSG00000169714	1848.17	0.126805	0.04054	3.127901	0.001761	0.020519	2.492774
ENSG00000286379	14.85021	-0.51135	0.145097	-3.5242	0.000425	0.020528	0.600464
ENSG00000171617	10915.51	0.224983	0.072202	3.116045	0.001833	0.020559	2.583187
ENSG00000143753	489.0084	0.139056	0.044626	3.116037	0.001833	0.020559	2.583187
ENSG00000272595	45.51798	-0.47436	0.140898	-3.36669	0.000761	0.020889	1.053218
ENSG00000170340	207.2078	0.210317	0.066099	3.181823	0.001464	0.020889	2.025126
ENSG00000022355	3698.892	0.263735	0.084774	3.111044	0.001864	0.020889	2.583187
ENSG00000123545	451.6214	0.246022	0.078228	3.144942	0.001661	0.020899	2.295759
ENSG00000004897	1328.205	0.144719	0.046422	3.117489	0.001824	0.020936	2.514347
ENSG00000105953	1898.863	0.121967	0.039041	3.124048	0.001784	0.020939	2.456745
ENSG00000109445	201.3945	0.169683	0.053997	3.142442	0.001675	0.021029	2.295759
ENSG00000116191	286.2493	0.1998	0.062775	3.182791	0.001459	0.021031	1.995423
ENSG00000145391	1630.293	0.119449	0.038342	3.115347	0.001837	0.021031	2.514347
ENSG00000122042	1745.583	0.128062	0.040764	3.141534	0.001681	0.021045	2.295759
ENSG00000164751	317.5321	0.136754	0.043537	3.141116	0.001683	0.021053	2.295759
ENSG00000160551	5108.8	0.107199	0.03413	3.140885	0.001684	0.021053	2.295759

ENSG00000114209	337.984	0.153993	0.049034	3.140555	0.001686	0.021053	2.295759
ENSG00000110880	1264.531	0.097209	0.031299	3.105801	0.001898	0.021053	2.583187
ENSG00000229894	40.15349	-0.2887	0.085826	-3.36383	0.000769	0.021065	1.044965
ENSG00000112210	210.8097	0.20213	0.063657	3.175284	0.001497	0.021134	2.025126
ENSG00000033178	999.5952	0.124588	0.039689	3.139117	0.001695	0.021134	2.293762
ENSG00000168014	974.4576	-0.09131	0.029095	-3.1382	0.0017	0.021154	2.295759
ENSG00000172824	877.8133	-0.28625	0.09097	-3.14667	0.001651	0.021181	2.225762
ENSG00000134186	391.963	0.116976	0.037178	3.146329	0.001653	0.02119	2.225762
ENSG00000164163	544.1711	0.159919	0.050979	3.136987	0.001707	0.021195	2.293762
ENSG00000116667	2411.863	0.122044	0.03921	3.112582	0.001855	0.021195	2.492774
ENSG00000136986	336.6797	0.144148	0.045442	3.172157	0.001513	0.021248	2.025126
ENSG00000261879	149.8018	-0.24073	0.07655	-3.14471	0.001662	0.021248	2.225762
ENSG00000172403	1278.835	0.28935	0.092033	3.143995	0.001667	0.021277	2.225762
ENSG00000236908	42.96966	-0.42018	0.12305	-3.41468	0.000639	0.021364	0.848718
ENSG00000163807	464.9913	0.151916	0.048373	3.140517	0.001687	0.021465	2.225762
ENSG00000011677	496.6304	0.24156	0.07713	3.131854	0.001737	0.021465	2.295759
ENSG00000139977	731.6775	0.129826	0.041454	3.131795	0.001737	0.021465	2.293762
ENSG00000163125	1221.248	-0.09353	0.029787	-3.14008	0.001689	0.021481	2.225762
ENSG00000172458	393.6317	-0.23556	0.07504	-3.13919	0.001694	0.021511	2.225762
ENSG00000114405	336.1743	0.192491	0.061324	3.138909	0.001696	0.021511	2.225762
ENSG00000132950	352.0238	-0.13793	0.043943	-3.13878	0.001697	0.021511	2.225762
ENSG00000175497	1527.632	0.179943	0.05798	3.103544	0.001912	0.021511	2.514347
ENSG00000156076	345.2835	-0.55325	0.174517	-3.17017	0.001523	0.02153	1.995423
ENSG00000161057	633.7869	0.166242	0.052995	3.136963	0.001707	0.021611	2.225762
ENSG00000169760	877.9898	0.137123	0.044222	3.100767	0.00193	0.021615	2.514347
ENSG00000253649	431.5328	-0.18024	0.057639	-3.12707	0.001766	0.021637	2.295759
ENSG00000205559	134.4269	-0.20122	0.064465	-3.12131	0.0018	0.021641	2.338927
ENSG00000121067	670.8765	0.1142	0.036528	3.126395	0.00177	0.021654	2.295759
ENSG00000105705	456.79	-0.12817	0.04089	-3.13445	0.001722	0.021715	2.225762
ENSG00000145743	1126.667	0.122282	0.039134	3.124682	0.00178	0.021748	2.295759

ENSG00000263584	8.177449	-0.73672	0.174676	-4.21764	2.47E-05	0.021781	0.031719
ENSG00000147231	105.0878	0.306715	0.092555	3.313885	0.00092	0.021781	1.182918
ENSG00000178662	3752.508	0.189105	0.061067	3.096693	0.001957	0.021781	2.514347
ENSG00000163159	266.395	0.168013	0.053651	3.131571	0.001739	0.021845	2.225762
ENSG00000166603	24.76075	0.631761	0.187251	3.373864	0.000741	0.021855	0.947688
ENSG00000164405	371.5494	0.201254	0.063648	3.161976	0.001567	0.021895	1.995423
ENSG00000134970	666.2072	0.164419	0.052523	3.130416	0.001746	0.021895	2.225762
ENSG00000138002	1399.019	-0.13784	0.044668	-3.086	0.002029	0.021895	2.583187
ENSG00000184575	1336.716	0.137301	0.044001	3.120384	0.001806	0.021937	2.293762
ENSG00000205085	218.9479	-0.23276	0.07374	-3.15647	0.001597	0.021952	2.025126
ENSG00000103769	1467.712	0.172892	0.055908	3.092457	0.001985	0.021961	2.514347
ENSG00000127870	741.6794	0.15707	0.050218	3.127792	0.001761	0.021995	2.225762
ENSG00000160883	70.08736	-0.53648	0.15974	-3.35843	0.000784	0.022011	0.989117
ENSG00000160570	285.5638	0.199788	0.063246	3.158899	0.001584	0.022027	1.995423
ENSG00000101752	2211.514	0.131019	0.042027	3.117485	0.001824	0.022035	2.295759
ENSG00000136810	339.218	0.2222	0.070457	3.153722	0.001612	0.02206	2.025126
ENSG00000120334	51.39193	0.264425	0.078775	3.356726	0.000789	0.022081	0.989117
ENSG00000123575	1855.332	0.121147	0.038881	3.115871	0.001834	0.022106	2.295759
ENSG00000169442	5.073635	1.059364	0.264492	4.005278	6.19E-05	0.022121	0.077262
ENSG00000137727	628.1987	0.156862	0.050204	3.124518	0.001781	0.022121	2.225762
ENSG00000102781	1114.921	0.139456	0.044641	3.123951	0.001784	0.022121	2.225762
ENSG00000138801	852.483	0.180934	0.058596	3.087853	0.002016	0.022121	2.514347
ENSG00000245025	95.48854	-0.26229	0.081896	-3.20267	0.001362	0.022137	1.695647
ENSG00000186462	1154.772	0.220175	0.070706	3.11393	0.001846	0.022171	2.293762
ENSG00000166847	2283.196	0.092519	0.029727	3.112291	0.001856	0.022259	2.295759
ENSG00000138443	3896.136	0.108966	0.03532	3.085122	0.002035	0.022259	2.514347
ENSG00000179832	2083.291	-0.18196	0.058853	-3.09172	0.00199	0.022264	2.456745
ENSG00000249626	26.98589	-0.43813	0.130441	-3.35882	0.000783	0.022304	0.963911
ENSG00000167447	193.1066	0.164744	0.051959	3.170658	0.001521	0.022318	1.867169
ENSG00000108064	356.6175	0.137459	0.043622	3.151153	0.001626	0.022318	1.995423

ENSG00000119705	223.2336	0.219695	0.07043	3.11933	0.001813	0.022318	2.225762
ENSG00000243147	211.3031	0.202476	0.064911	3.119271	0.001813	0.022318	2.225762
ENSG00000265678	11.08551	-0.55421	0.14511	-3.81922	0.000134	0.022331	0.163912
ENSG00000213152	27.42762	-0.35477	0.105538	-3.36154	0.000775	0.022331	0.947688
ENSG00000175662	3577.579	-0.13396	0.043458	-3.08259	0.002052	0.022331	2.514347
ENSG00000104341	516.6594	0.206048	0.06703	3.073963	0.002112	0.022331	2.583187
ENSG00000151743	225.6037	0.18461	0.058255	3.168996	0.00153	0.022339	1.867169
ENSG00000221823	1350.172	0.156888	0.050328	3.117302	0.001825	0.022339	2.225762
ENSG00000234608	146.105	0.196709	0.063397	3.102814	0.001917	0.022339	2.338927
ENSG00000034713	1089.231	0.123651	0.039795	3.107204	0.001889	0.022395	2.295759
ENSG00000116983	3333.901	0.22367	0.072627	3.079712	0.002072	0.022417	2.514347
ENSG00000125249	2684.861	0.147037	0.047337	3.106189	0.001895	0.022439	2.295759
ENSG00000179841	791.8065	0.184944	0.060067	3.078936	0.002077	0.022442	2.514347
ENSG00000115540	327.6444	0.17858	0.057346	3.114071	0.001845	0.022502	2.225762
ENSG00000108654	5464.512	0.082654	0.026858	3.07746	0.002088	0.022521	2.514347
ENSG00000158864	1053.77	0.169289	0.05453	3.104492	0.001906	0.022522	2.293762
ENSG00000213341	358.5296	0.141438	0.045435	3.112992	0.001852	0.022525	2.225762
ENSG00000103199	330.3336	-0.15288	0.04926	-3.10354	0.001912	0.022525	2.295759
ENSG00000139112	3175.902	0.190489	0.062077	3.068603	0.002151	0.022525	2.583187
ENSG00000137312	1633.727	0.133074	0.042762	3.111971	0.001858	0.022564	2.225762
ENSG00000100744	258.5723	0.204225	0.06563	3.111745	0.00186	0.022564	2.225762
ENSG00000099284	265.9958	-0.12078	0.038953	-3.10077	0.00193	0.022687	2.295759
ENSG00000109846	2724.485	0.301621	0.09728	3.100552	0.001932	0.022687	2.295759
ENSG00000080822	2386.855	0.285605	0.092934	3.073195	0.002118	0.022695	2.514347
ENSG00000089248	356.347	0.169882	0.054814	3.099234	0.00194	0.022739	2.295759
ENSG00000144895	628.1993	0.162819	0.052537	3.09914	0.001941	0.022739	2.29693
ENSG00000117983	76.58001	-0.55178	0.167706	-3.29018	0.001001	0.022745	1.182918
ENSG00000196072	411.5943	0.185455	0.059062	3.140019	0.001689	0.022745	1.995423
ENSG00000197782	435.7609	0.124505	0.039682	3.137533	0.001704	0.022906	1.995423
ENSG00000114867	2900.103	0.101317	0.033098	3.061101	0.002205	0.022906	2.583187

ENSG00000287655	17.054	-0.55521	0.160293	-3.46372	0.000533	0.022923	0.622589
ENSG00000197045	2122.512	0.169352	0.054708	3.095543	0.001965	0.022923	2.295759
ENSG00000242259	476.5597	0.119992	0.038793	3.093149	0.00198	0.02308	2.29693
ENSG00000171208	473.7807	0.203567	0.065833	3.092165	0.001987	0.023152	2.295759
ENSG00000265443	67.81285	-0.32838	0.098811	-3.32331	0.00089	0.023208	1.023066
ENSG00000279520	31.08305	-0.33976	0.102484	-3.31524	0.000916	0.023208	1.053218
ENSG00000011201	408.4104	0.317194	0.100893	3.143856	0.001667	0.023208	1.918337
ENSG00000114450	496.0081	0.246394	0.079492	3.099602	0.001938	0.023222	2.225762
ENSG00000165410	826.2693	0.19291	0.06298	3.063048	0.002191	0.023225	2.514347
ENSG00000180964	408.1709	0.172189	0.054791	3.14267	0.001674	0.023234	1.918337
ENSG00000170540	2420.288	0.187796	0.061321	3.062503	0.002195	0.023234	2.514347
ENSG00000168785	1379.11	0.133404	0.043186	3.08906	0.002008	0.023261	2.295759
ENSG00000176422	200.8693	-0.1494	0.047795	-3.12586	0.001773	0.023266	2.025126
ENSG00000205710	42.72683	-0.28462	0.085704	-3.32102	0.000897	0.023315	1.020896
ENSG00000126860	265.7412	0.373621	0.12064	3.096998	0.001955	0.023315	2.225762
ENSG00000187105	152.5488	-0.17437	0.056581	-3.08172	0.002058	0.023335	2.338927
ENSG00000146476	245.3105	0.192706	0.06155	3.130912	0.001743	0.023358	1.977088
ENSG00000164187	1999.574	0.164893	0.05378	3.066075	0.002169	0.023378	2.456745
ENSG00000183023	7099.792	0.216423	0.070754	3.058823	0.002222	0.023386	2.514347
ENSG00000133134	770.2414	0.267924	0.086827	3.085732	0.002031	0.023408	2.293762
ENSG00000249436	59.68932	0.427464	0.126853	3.369764	0.000752	0.023423	0.848718
ENSG00000182841	228.1748	-0.21878	0.070717	-3.09377	0.001976	0.023446	2.225762
ENSG00000267321	63.24987	0.237895	0.071534	3.325636	0.000882	0.023494	0.989117
ENSG00000164258	302.74	0.200177	0.064155	3.120186	0.001807	0.023494	2.025126
ENSG00000142784	1173.776	-0.12292	0.039745	-3.09271	0.001983	0.023494	2.225762
ENSG00000108829	422.287	0.130068	0.042183	3.083444	0.002046	0.023494	2.295759
ENSG00000163320	906.7381	0.15288	0.049585	3.083163	0.002048	0.023494	2.293762
ENSG00000226049	143.8166	-0.27786	0.089406	-3.10782	0.001885	0.023508	2.108016
ENSG00000167863	500.1701	0.185982	0.060339	3.082288	0.002054	0.023509	2.295759
ENSG00000122515	1482.075	-0.17714	0.057474	-3.08204	0.002056	0.02351	2.295759
ENSG00000103363	667.6225	0.14806	0.048045	3.0817	0.002058	0.02351	2.29693
ENSG00000006327	26.89991	0.694484	0.207523	3.34654	0.000818	0.023539	0.911386
ENSG00000182831	1448.52	0.087642	0.028777	3.045551	0.002323	0.023556	2.583187
ENSG00000134243	7840.968	0.15663	0.051297	3.053428	0.002262	0.023558	2.514347
ENSG00000166862	319.5079	-0.17992	0.057583	-3.12455	0.001781	0.023558	1.977088
ENSG00000124214	1280.728	0.092976	0.030095	3.089398	0.002006	0.023558	2.225762
ENSG00000187189	2634.601	0.144942	0.047606	3.044591	0.00233	0.023564	2.583187
ENSG00000180694	247.2963	0.169593	0.054342	3.120856	0.001803	0.023593	1.995423
ENSG00000128609	1405.984	0.2082	0.067612	3.079309	0.002075	0.023598	2.293762
ENSG00000196689	197.1224	-0.22107	0.07181	-3.07849	0.002081	0.023626	2.295759
ENSG00000090263	213.7441	0.167344	0.054212	3.086871	0.002023	0.023675	2.225762
ENSG00000143793	162.7219	-0.18578	0.060202	-3.08594	0.002029	0.023733	2.225762
ENSG00000242173	641.1575	0.165172	0.054313	3.041085	0.002357	0.02374	2.583187
ENSG00000228623	234.6479	-0.19385	0.062849	-3.08444	0.002039	0.023778	2.225762
ENSG00000182287	526.329	0.189651	0.061493	3.084126	0.002042	0.023778	2.225762
ENSG00000257093	1880.26	0.110917	0.036066	3.075393	0.002102	0.023778	2.295759
ENSG00000109270	558.8994	0.162984	0.053004	3.07494	0.002105	0.023778	2.29693
ENSG00000171490	868.5067	0.110461	0.036333	3.040224	0.002364	0.023778	2.583187
ENSG00000116288	895.1173	0.164472	0.053493	3.074632	0.002108	0.023803	2.293762
ENSG00000119335	1779.735	0.140083	0.046101	3.038617	0.002377	0.023818	2.583187
ENSG00000185684	368.8124	-0.18646	0.059652	-3.12572	0.001774	0.023885	1.918337
ENSG00000265354	345.4202	0.16762	0.053627	3.125666	0.001774	0.023885	1.918337
ENSG00000146776	349.6586	-0.13719	0.044522	-3.08132	0.002061	0.023885	2.225762
ENSG00000129625	2848.661	0.162401	0.053212	3.051965	0.002273	0.023885	2.456745
ENSG00000072042	738.6986	0.166183	0.054715	3.03725	0.002387	0.023885	2.583187
ENSG00000281961	32.18739	-0.40438	0.122695	-3.29583	0.000981	0.024002	1.053218
ENSG00000196323	1552.723	0.125859	0.041469	3.035029	0.002405	0.024002	2.583187
ENSG00000166200	910.1478	0.144386	0.04704	3.069448	0.002145	0.024068	2.293762
ENSG00000196990	1349.112	-0.178	0.057829	-3.078	0.002084	0.024086	2.225762
ENSG00000132952	377.1838	0.142493	0.04565	3.121386	0.0018	0.024105	1.918337

ENSG00000122406	1676.265	0.172806	0.056827	3.040933	0.002358	0.024105	2.514347
ENSG00000204685	94.7779	-0.20069	0.063584	-3.15627	0.001598	0.02416	1.695647
ENSG00000106688	617.14	0.19779	0.064494	3.066766	0.002164	0.02416	2.29693
ENSG00000085365	1855.126	0.147789	0.048507	3.046757	0.002313	0.02416	2.456745
ENSG00000150394	630.1467	0.233272	0.076089	3.065771	0.002171	0.024248	2.293762
ENSG00000120686	600.8021	0.16856	0.054828	3.074317	0.00211	0.024267	2.225762
ENSG00000182173	224.8446	-0.17271	0.05637	-3.06391	0.002185	0.024335	2.295759
ENSG00000023228	3994.637	0.128416	0.042405	3.028346	0.002459	0.024335	2.583187
ENSG00000127184	1008.129	0.197888	0.064404	3.072614	0.002122	0.024338	2.225762
ENSG00000115966	1250.992	0.108504	0.035418	3.063568	0.002187	0.024338	2.295759
ENSG00000131044	89.03149	-0.26142	0.080397	-3.25165	0.001147	0.024355	1.201846
ENSG00000137414	911.0458	0.126319	0.041128	3.071341	0.002131	0.024392	2.225762
ENSG00000126432	1328.52	0.183707	0.059993	3.062114	0.002198	0.024392	2.295759
ENSG00000132872	1971.566	0.269559	0.088107	3.059454	0.002217	0.02459	2.295759
ENSG00000229325	71.78253	0.252958	0.077521	3.26309	0.001102	0.024672	1.136415
ENSG00000175311	20.12821	-0.46509	0.135613	-3.42953	0.000605	0.024686	0.622231
ENSG00000173141	279.5646	0.160284	0.05179	3.094864	0.001969	0.024686	2.025126
ENSG00000061273	633.4927	-0.17789	0.058178	-3.05765	0.002231	0.024686	2.29693
ENSG00000174292	61.93424	-0.30129	0.091522	-3.29203	0.000995	0.02472	1.020896
ENSG00000225907	17.99097	-0.52662	0.140736	-3.7419	0.000183	0.024732	0.187229
ENSG00000100461	687.9048	0.114325	0.037854	3.02014	0.002527	0.024782	2.583187
ENSG00000231738	15.73184	0.598108	0.175588	3.406309	0.000658	0.024865	0.670508
ENSG00000186184	396.8909	0.128252	0.041275	3.107239	0.001888	0.024891	1.918337
ENSG00000163635	868.4037	-0.09072	0.029708	-3.05392	0.002259	0.024891	2.295759
ENSG00000172301	438.5311	0.195157	0.063747	3.061446	0.002203	0.025006	2.225762
ENSG00000232233	37.66362	-0.33048	0.100657	-3.28322	0.001026	0.025017	1.035363
ENSG00000047662	124.2655	-0.2357	0.075711	-3.11313	0.001851	0.025017	1.867169
ENSG00000249478	98.17735	-0.30018	0.092183	-3.25638	0.001128	0.025021	1.136415
ENSG00000116679	985.5516	0.160527	0.052449	3.060644	0.002209	0.025021	2.225762
ENSG00000168438	661.3005	0.159485	0.052281	3.050512	0.002285	0.025028	2.29693
ENSG00000165156	1202.965	0.127581	0.0422	3.023272	0.002501	0.025028	2.514347
ENSG00000165152	1161.306	0.18812	0.061698	3.049056	0.002296	0.025167	2.293762
ENSG00000153214	278.3584	0.205214	0.066418	3.089735	0.002003	0.025214	1.995423
ENSG00000163743	369.6455	0.15015	0.048597	3.089721	0.002003	0.025214	1.995423
ENSG00000164442	355.7303	0.202785	0.0654	3.100703	0.001931	0.025256	1.918337
ENSG00000170153	821.5615	0.154076	0.050582	3.04605	0.002319	0.025351	2.293762
ENSG00000224271	851.1917	-0.27518	0.090106	-3.05394	0.002259	0.025431	2.225762
ENSG00000011260	369.5901	0.153777	0.050361	3.053493	0.002262	0.025442	2.225762
ENSG00000010256	1374.748	0.18535	0.061443	3.016634	0.002556	0.025442	2.514347
ENSG00000164284	262.9679	0.172719	0.056058	3.081103	0.002062	0.025471	2.025126
ENSG00000233840	115.3876	0.26258	0.084567	3.104989	0.001903	0.025472	1.867169
ENSG00000186532	326.1885	-0.11219	0.036364	-3.08503	0.002035	0.025476	1.995423
ENSG00000169255	530.962	0.185477	0.06077	3.052098	0.002272	0.025484	2.225762
ENSG00000139211	66.06187	0.49834	0.152007	3.278395	0.001044	0.025496	1.020896
ENSG00000179010	2155.388	0.155553	0.051131	3.042239	0.002348	0.025496	2.295759
ENSG00000134910	500.8594	0.132776	0.043673	3.040238	0.002364	0.025636	2.29693
ENSG00000158683	146.2337	-0.22496	0.073668	-3.05372	0.00226	0.025676	2.189833
ENSG00000038274	604.9366	0.160887	0.052932	3.039519	0.00237	0.025676	2.295759
ENSG00000143198	1061.867	0.140646	0.04685	3.002054	0.002682	0.025807	2.583187
ENSG00000261647	132.6858	-0.23593	0.077031	-3.06273	0.002193	0.02583	2.108016
ENSG00000173744	1617.023	0.097061	0.031954	3.037491	0.002386	0.02583	2.293762
ENSG00000173660	862.3465	0.213714	0.070397	3.035838	0.002399	0.025922	2.295759
ENSG00000188517	155.3413	0.263185	0.08686	3.02999	0.002446	0.025924	2.338927
ENSG00000197223	136.7022	0.204332	0.065979	3.096917	0.001955	0.025941	1.867169
ENSG00000108799	1711.98	-0.10189	0.033573	-3.03501	0.002405	0.025941	2.295759
ENSG00000139505	846.9049	0.175331	0.057618	3.042983	0.002342	0.02604	2.225762
ENSG00000149577	863.0275	-0.17403	0.05737	-3.03349	0.002417	0.026059	2.293762
ENSG00000172432	425.5356	-0.1188	0.039053	-3.04214	0.002349	0.026061	2.225762
ENSG00000279207	207.509	0.267084	0.088061	3.032926	0.002422	0.026061	2.295759
ENSG00000259924	103.1548	-0.24331	0.077917	-3.12265	0.001792	0.026083	1.695647

ENSG00000287990	73.58792	-0.22687	0.070313	-3.2266	0.001253	0.026115	1.182918
ENSG00000144619	602.3657	0.183168	0.061144	2.995703	0.002738	0.026122	2.583187
ENSG00000108830	348.1259	0.212428	0.069886	3.03963	0.002369	0.026209	2.225762
ENSG00000120696	260.1436	0.149671	0.049257	3.038593	0.002377	0.026245	2.225762
ENSG00000132849	595.8786	-0.14704	0.048397	-3.03821	0.00238	0.026245	2.225762
ENSG00000035687	533.0236	0.204949	0.067648	3.029658	0.002448	0.026245	2.295759
ENSG00000170315	1225.493	0.185858	0.06135	3.029458	0.00245	0.026245	2.293762
ENSG00000255302	2149.519	0.183883	0.061213	3.003979	0.002665	0.026245	2.492774
ENSG00000126524	759.9406	0.158482	0.052959	2.992548	0.002767	0.026271	2.583187
ENSG00000182359	305.4076	0.19134	0.063005	3.03689	0.00239	0.026325	2.225762
ENSG00000138074	424.3259	-0.29346	0.095304	-3.07918	0.002076	0.026487	1.918337
ENSG00000140259	224.6607	0.152762	0.049804	3.067241	0.00216	0.026487	1.995423
ENSG00000177103	871.0981	-0.22984	0.076878	-2.98961	0.002793	0.026487	2.583187
ENSG00000175445	352.4809	0.341071	0.110795	3.078394	0.002081	0.026524	1.918337
ENSG00000280375	25.35797	-0.50244	0.151721	-3.31161	0.000928	0.026528	0.848718
ENSG00000234546	40.07956	-0.53532	0.161658	-3.31142	0.000928	0.026528	0.848718
ENSG00000149243	87.95917	-0.22119	0.068844	-3.21287	0.001314	0.026528	1.201846
ENSG00000250320	113.7357	-0.23285	0.076786	-3.0325	0.002425	0.026528	2.225762
ENSG00000171365	229.198	0.202621	0.066822	3.032271	0.002427	0.026528	2.225762
ENSG00000159461	1604.64	0.104148	0.034351	3.031878	0.00243	0.026528	2.225762
ENSG00000154582	325.5221	0.167166	0.055141	3.031623	0.002432	0.026528	2.225762
ENSG00000135940	1355.329	0.179585	0.059391	3.023764	0.002497	0.026528	2.293762
ENSG00000058804	229.8097	0.161683	0.053486	3.022898	0.002504	0.026528	2.295759
ENSG00000149547	507.3229	0.125119	0.041395	3.02256	0.002506	0.026528	2.29693
ENSG00000170500	5912.484	0.127878	0.042592	3.002426	0.002678	0.026528	2.456745
ENSG00000169213	764.5487	0.397698	0.132787	2.995002	0.002744	0.026528	2.514347
ENSG00000078124	1046.231	0.165099	0.055147	2.993803	0.002755	0.026562	2.514347
ENSG00000154864	583.0886	0.381816	0.126472	3.018987	0.002536	0.026747	2.29693
ENSG00000122965	748.093	-0.16546	0.054638	-3.02829	0.002459	0.026749	2.225762
ENSG00000198356	333.7394	0.175171	0.057208	3.062028	0.002198	0.026847	1.977088
ENSG00000174989	272.4308	-0.13959	0.045627	-3.0594	0.002218	0.026847	1.995423
ENSG00000139436	671.6945	-0.11909	0.039351	-3.02639	0.002475	0.026847	2.225762
ENSG00000101474	853.2447	0.169403	0.056137	3.017677	0.002547	0.026847	2.293762
ENSG00000261888	12.94593	-0.64054	0.18997	-3.37178	0.000747	0.026875	0.670508
ENSG00000144320	1093.85	0.131738	0.043681	3.015899	0.002562	0.026918	2.293762
ENSG00000196405	2177.263	-0.13237	0.044423	-2.97967	0.002886	0.026918	2.583187
ENSG00000108433	646.6904	-0.11036	0.036599	-3.0153	0.002567	0.02693	2.295759
ENSG00000184164	255.5228	-0.15757	0.051632	-3.05187	0.002274	0.027025	2.025126
ENSG00000189266	466.8881	0.191313	0.063507	3.012483	0.002591	0.027127	2.295759
ENSG00000081154	1190.873	0.12577	0.042252	2.976659	0.002914	0.027127	2.583187
ENSG00000088876	222.3975	-0.15095	0.049495	-3.04979	0.00229	0.02716	2.025126
ENSG00000103197	2083.412	-0.14234	0.047591	-2.99084	0.002782	0.027182	2.456745
ENSG00000181396	393.1876	-0.14601	0.047665	-3.0633	0.002189	0.027355	1.918337
ENSG00000112406	698.4975	0.161073	0.054022	2.981596	0.002868	0.027355	2.514347
ENSG00000109738	989.1611	0.215841	0.071771	3.00736	0.002635	0.027506	2.293762
ENSG00000108469	499.234	-0.13805	0.045907	-3.00725	0.002636	0.027506	2.295759
ENSG00000181652	40.1445	-0.27641	0.085473	-3.23387	0.001221	0.027742	1.053218
ENSG00000068796	1501.021	0.11625	0.038702	3.003705	0.002667	0.027742	2.295759
ENSG00000159433	1738.539	-0.17831	0.060085	-2.96769	0.003	0.027742	2.583187
ENSG00000174501	1790.197	-0.15074	0.050793	-2.96768	0.003001	0.027742	2.583187
ENSG00000071127	1091.662	0.165435	0.055112	3.001794	0.002684	0.027899	2.295759
ENSG00000182117	128.3638	0.248481	0.082093	3.026837	0.002471	0.027958	2.108016
ENSG00000198920	487.9898	-0.1158	0.038472	-3.00997	0.002613	0.027977	2.225762
ENSG00000275389	30.66481	-0.38035	0.11556	-3.29139	0.000997	0.027977	0.848718
ENSG00000119986	226.7139	0.210291	0.069117	3.042543	0.002346	0.027983	1.995423
ENSG00000164347	410.0795	0.156552	0.052208	2.99864	0.002712	0.028086	2.295759
ENSG00000126945	645.8023	0.155441	0.051841	2.998424	0.002714	0.028086	2.29693
ENSG00000200488	16.22895	0.43233	0.128098	3.374988	0.000738	0.028164	0.622589
ENSG00000197951	366.3536	-0.13201	0.043494	-3.03517	0.002404	0.028164	2.025126
ENSG00000089693	1353.156	0.144683	0.048862	2.961052	0.003066	0.028164	2.583187

ENSG00000019102	70.26376	-0.43948	0.135474	-3.24402	0.001179	0.02822	0.989117
ENSG00000143106	458.3097	0.211802	0.069801	3.034344	0.002411	0.02822	2.025126
ENSG00000187555	1692.376	0.09886	0.032897	3.00519	0.002654	0.02822	2.225762
ENSG00000117152	4533.03	0.27899	0.093125	2.995856	0.002737	0.02822	2.295759
ENSG00000124702	1969.969	0.15008	0.050529	2.970202	0.002976	0.028235	2.492774
ENSG00000079974	307.0809	-0.13742	0.04527	-3.03555	0.002401	0.02841	1.995423
ENSG00000204396	217.4159	-0.2369	0.078059	-3.03486	0.002407	0.02841	1.995423
ENSG00000123728	218.5139	0.147309	0.048612	3.030303	0.002443	0.02841	2.025126
ENSG00000166432	609.5009	-0.21963	0.073383	-2.99292	0.002763	0.02841	2.293762
ENSG00000181163	1357.527	0.150203	0.050194	2.992459	0.002767	0.02841	2.293762
ENSG00000096401	774.7675	0.12155	0.041005	2.964272	0.003034	0.02841	2.514347
ENSG00000147454	818.4663	-0.16833	0.05693	-2.95685	0.003108	0.02841	2.583187
ENSG00000158863	739.0757	-0.13463	0.045003	-2.99152	0.002776	0.02845	2.295759
ENSG00000264538	638.6661	-0.08905	0.029768	-2.99159	0.002775	0.02845	2.293762
ENSG00000142453	455.4977	-0.12602	0.04155	-3.03303	0.002421	0.028512	1.995423
ENSG00000126883	891.3035	-0.10842	0.036151	-2.99893	0.002709	0.028586	2.225762
ENSG00000133794	692.0097	0.128824	0.043101	2.988908	0.0028	0.028604	2.295759
ENSG00000140983	810.9186	-0.17072	0.057653	-2.9611	0.003065	0.028604	2.514347
ENSG00000126464	996.5611	-0.24272	0.080969	-2.99764	0.002721	0.028635	2.225762
ENSG00000125166	1212.591	0.193225	0.064656	2.988511	0.002803	0.028635	2.293762
ENSG00000174607	1103.741	0.429205	0.14367	2.987448	0.002813	0.028686	2.295759
ENSG00000175161	5747.081	0.147574	0.049415	2.98641	0.002823	0.028765	2.295759
ENSG00000100600	474.7917	0.185997	0.062108	2.994745	0.002747	0.028847	2.225762
ENSG00000272333	835.1068	-0.18991	0.064401	-2.94889	0.003189	0.028847	2.583187
ENSG00000007545	253.489	-0.1222	0.040333	-3.02971	0.002448	0.028893	1.977088
ENSG00000121864	361.0132	0.131186	0.043401	3.022638	0.002506	0.028893	2.025126
ENSG00000140307	182.8616	0.174493	0.057274	3.046608	0.002314	0.028907	1.867169
ENSG00000111144	399.1577	0.132979	0.044447	2.99185	0.002773	0.028981	2.225762
ENSG00000262001	241.5764	-0.15527	0.052055	-2.9828	0.002856	0.028981	2.295759
ENSG00000111911	842.381	0.112415	0.037689	2.98271	0.002857	0.028981	2.293762
ENSG00000186166	573.4546	-0.16957	0.056857	-2.98248	0.002859	0.028981	2.295759
ENSG00000165816	114.298	-0.26298	0.086388	-3.04416	0.002333	0.029052	1.867169
ENSG00000089818	1205.566	0.187198	0.063583	2.944145	0.003238	0.029127	2.583187
ENSG00000248994	371.8081	-0.22456	0.075123	-2.98922	0.002797	0.029177	2.225762
ENSG00000106105	1198.629	0.146858	0.049163	2.987185	0.002816	0.029353	2.225762
ENSG00000166006	1214.117	0.158488	0.053068	2.986508	0.002822	0.0294	2.225762
ENSG00000198169	390.4655	-0.16636	0.054881	-3.03122	0.002436	0.029425	1.918337
ENSG00000168959	1260.98	0.150187	0.051087	2.939819	0.003284	0.029444	2.583187
ENSG00000164919	782.0786	0.206336	0.069335	2.975919	0.002921	0.029451	2.295759
ENSG00000163686	527.1825	0.181726	0.061083	2.975046	0.002929	0.029478	2.29693
ENSG00000067064	807.5447	0.227997	0.077362	2.947142	0.003207	0.029478	2.514347
ENSG00000077380	1298.979	0.146659	0.049765	2.947046	0.003208	0.029478	2.514347
ENSG00000111790	1185.925	0.127315	0.042801	2.97459	0.002934	0.029531	2.293762
ENSG00000228510	33.79399	-0.5083	0.158204	-3.21294	0.001314	0.029676	1.020896
ENSG00000146376	142.0843	0.251147	0.08465	2.966897	0.003008	0.029676	2.338927
ENSG00000096092	341.8792	0.208547	0.069946	2.98155	0.002868	0.029694	2.225762
ENSG00000105983	1232.656	0.117803	0.039528	2.980224	0.00288	0.029783	2.225762
ENSG00000104714	282.3563	-0.18867	0.063311	-2.98006	0.002882	0.029783	2.225762
ENSG00000105993	973.5149	0.184505	0.062879	2.934304	0.003343	0.029783	2.583187
ENSG00000175416	983.9266	0.138125	0.046959	2.94142	0.003267	0.02987	2.514347
ENSG00000276255	45.46355	-0.34504	0.107796	-3.20088	0.00137	0.029885	1.053218
ENSG00000164031	1747.787	0.150772	0.051416	2.932383	0.003364	0.029896	2.583187
ENSG00000196230	1617.555	0.180201	0.061311	2.939151	0.003291	0.029996	2.514347
ENSG00000134030	2521.081	-0.11694	0.039898	-2.93085	0.00338	0.029996	2.583187
ENSG00000137955	485.0552	0.119985	0.040939	2.930822	0.003381	0.029996	2.583187
ENSG00000082146	319.4286	0.15156	0.050929	2.975922	0.002921	0.030025	2.225762
ENSG00000102144	3834.227	0.168443	0.05678	2.966595	0.003011	0.030025	2.295759
ENSG00000173821	3497.469	-0.12999	0.044134	-2.94545	0.003225	0.030025	2.456745
ENSG00000070366	754.9293	-0.11271	0.037877	-2.97562	0.002924	0.03003	2.225762
ENSG00000143420	2380.53	0.124807	0.042081	2.965919	0.003018	0.030031	2.295759

ENSG00000248837	47.46264	-0.48747	0.152052	-3.20595	0.001346	0.030042	1.023066
ENSG00000183337	429.9418	-0.16925	0.056894	-2.9748	0.002932	0.030047	2.225762
ENSG00000064763	483.6883	0.160051	0.053977	2.96518	0.003025	0.030047	2.295759
ENSG00000113555	180.1134	-0.17754	0.059124	-3.00283	0.002675	0.030072	2.025126
ENSG00000271447	158.6656	-0.33449	0.113065	-2.95843	0.003092	0.030072	2.338927
ENSG00000182149	1228.735	0.073548	0.025047	2.936405	0.00332	0.030072	2.514347
ENSG00000166922	1438.302	0.250957	0.085716	2.927769	0.003414	0.030072	2.583187
ENSG00000142303	685.2858	-0.20749	0.070879	-2.92739	0.003418	0.030081	2.583187
ENSG00000131797	299.9711	-0.14077	0.046779	-3.00932	0.002618	0.030088	1.977088
ENSG00000100612	290.9394	0.181376	0.061226	2.962395	0.003053	0.030171	2.295759
ENSG00000148337	1133.608	-0.1348	0.04594	-2.93438	0.003342	0.030171	2.514347
ENSG00000182827	390.677	0.136094	0.045813	2.970645	0.002972	0.030222	2.225762
ENSG00000196715	644.1548	0.122729	0.041442	2.961464	0.003062	0.030222	2.293762
ENSG00000178074	392.8562	0.136351	0.046044	2.961287	0.003064	0.030222	2.295759
ENSG00000145476	693.6833	-0.19787	0.067649	-2.92501	0.003444	0.030222	2.583187
ENSG00000138769	459.4498	0.183013	0.060697	3.015199	0.002568	0.030228	1.918337
ENSG00000170946	308.9539	0.12649	0.04218	2.998797	0.00271	0.030228	2.025126
ENSG00000179933	143.6654	0.19511	0.066035	2.954627	0.00313	0.030228	2.338927
ENSG00000094916	4609.282	0.089726	0.030572	2.934913	0.003336	0.030228	2.492774
ENSG00000100596	1503.535	0.180142	0.06086	2.959935	0.003077	0.030272	2.293762
ENSG00000164176	2742.95	0.300632	0.10235	2.937309	0.003311	0.030392	2.456745
ENSG00000115421	472.3984	0.118793	0.040041	2.966765	0.00301	0.030475	2.225762
ENSG00000073146	92.69057	-0.24273	0.07961	-3.04893	0.002297	0.030508	1.695647
ENSG00000278156	87.31068	-0.19292	0.063293	-3.0481	0.002303	0.030555	1.695647
ENSG00000185630	2512.008	0.085148	0.029012	2.934953	0.003336	0.030555	2.456745
ENSG00000240053	31.9249	-0.38392	0.119295	-3.21827	0.00129	0.030598	0.947688
ENSG00000062096	23.66396	0.590321	0.161435	3.65671	0.000255	0.030644	0.187229
ENSG00000105926	1689.731	0.168695	0.057095	2.954669	0.00313	0.030644	2.293762
ENSG00000147457	529.7226	0.095364	0.032286	2.953743	0.003139	0.030691	2.295759
ENSG00000008083	730.0775	-0.12359	0.041845	-2.95339	0.003143	0.030707	2.295759
ENSG00000171303	186.397	0.168326	0.057023	2.951869	0.003159	0.030829	2.295759
ENSG00000007168	5516.297	0.137853	0.047152	2.923593	0.00346	0.030829	2.514347
ENSG00000282978	15.57073	-0.47078	0.1408	-3.34359	0.000827	0.030836	0.600464
ENSG00000160602	39.49811	-0.34906	0.109487	-3.18811	0.001432	0.030925	1.035363
ENSG00000077279	339.7343	0.163738	0.054703	2.993245	0.00276	0.030925	1.995423
ENSG00000167904	177.8101	0.139893	0.04742	2.950082	0.003177	0.030925	2.295759
ENSG00000179388	424.4981	-0.18251	0.060982	-2.99289	0.002763	0.030931	1.995423
ENSG00000259657	12.8714	-0.43898	0.132581	-3.31101	0.00093	0.030944	0.670508
ENSG00000081148	66.94775	0.282495	0.088541	3.190567	0.00142	0.030944	1.023066
ENSG00000132912	1266.959	0.121658	0.041651	2.920926	0.00349	0.030944	2.514347
ENSG00000162630	691.3571	0.242758	0.082337	2.948356	0.003195	0.031005	2.295759
ENSG00000239521	865.4734	-0.13714	0.046386	-2.9566	0.003111	0.0311	2.225762
ENSG00000173611	1624.002	0.13562	0.046598	2.910447	0.003609	0.0311	2.583187
ENSG00000081181	112.6083	0.217319	0.07339	2.961145	0.003065	0.03111	2.189833
ENSG00000102466	799.1661	0.152695	0.05232	2.918503	0.003517	0.03111	2.514347
ENSG00000221914	902.8915	0.128671	0.043677	2.945959	0.00322	0.031152	2.295759
ENSG00000086598	826.7291	0.141406	0.047848	2.955299	0.003124	0.031154	2.225762
ENSG00000104497	169.7551	0.207297	0.070148	2.955131	0.003125	0.031154	2.225762
ENSG00000151090	1923.043	0.137267	0.046605	2.945357	0.003226	0.031156	2.295759
ENSG00000230102	18.21792	-0.56489	0.169617	-3.33037	0.000867	0.03117	0.616514
ENSG00000078401	213.0729	0.532019	0.180075	2.954421	0.003133	0.03117	2.225762
ENSG00000147592	49.47062	0.290621	0.090949	3.195448	0.001396	0.031223	0.989117
ENSG00000119787	783.4446	0.131962	0.044823	2.944076	0.003239	0.031223	2.295759
ENSG00000058091	2435.665	0.177762	0.060995	2.914387	0.003564	0.031335	2.514347
ENSG00000233705	603.6421	0.220709	0.075011	2.94237	0.003257	0.031346	2.295759
ENSG00000007923	461.3529	-0.11651	0.039601	-2.94204	0.003261	0.031361	2.295759
ENSG00000122585	138.7645	0.452415	0.150551	3.005061	0.002655	0.031382	1.867169
ENSG00000013561	774.7526	0.127092	0.043753	2.904729	0.003676	0.031382	2.583187
ENSG00000156687	882.652	0.164743	0.056578	2.911802	0.003594	0.031501	2.514347
ENSG00000287855	53.33726	-0.38507	0.121032	-3.18156	0.001465	0.031511	1.023066

ENSG00000163938	423.4965	0.147329	0.049471	2.978101	0.0029	0.031511	2.025126
ENSG00000103257	1246.06	-0.25532	0.087699	-2.91135	0.003599	0.031511	2.514347
ENSG00000184601	58.79807	-0.40642	0.127405	-3.18997	0.001423	0.031632	0.989117
ENSG00000218793	5.62421	0.964938	0.254305	3.794407	0.000148	0.031664	0.102715
ENSG00000053770	1465.716	0.134335	0.046317	2.900326	0.003728	0.031694	2.583187
ENSG00000110013	386.8311	0.159018	0.053451	2.975012	0.00293	0.031755	2.025126
ENSG00000155970	1178.313	0.164716	0.056126	2.934739	0.003338	0.031926	2.293762
ENSG00000165443	1365.069	0.151554	0.05165	2.934265	0.003343	0.031928	2.295759
ENSG00000215475	130.3721	0.200433	0.068093	2.94351	0.003245	0.031945	2.225762
ENSG00000067048	562.1811	0.479127	0.163355	2.933046	0.003357	0.031999	2.29693
ENSG00000114656	174.2146	-0.15891	0.053492	-2.97065	0.002972	0.032077	2.025126
ENSG00000135341	964.3654	0.105471	0.035974	2.931898	0.003369	0.032077	2.295759
ENSG00000119865	796.5217	0.123089	0.042513	2.895361	0.003787	0.032077	2.583187
ENSG00000100441	385.253	-0.13843	0.047084	-2.93999	0.003282	0.03219	2.225762
ENSG00000099246	1508.479	0.119133	0.040656	2.930259	0.003387	0.03219	2.295759
ENSG00000080371	1075.209	0.102369	0.035276	2.901972	0.003708	0.03219	2.514347
ENSG00000187398	308.4261	0.244459	0.082362	2.968118	0.002996	0.0322	2.025126
ENSG00000130540	1894.692	0.212842	0.072648	2.929786	0.003392	0.0322	2.295759
ENSG00000105204	273.9821	-0.16789	0.057315	-2.92924	0.003398	0.0322	2.295759
ENSG00000143157	1266.034	0.111644	0.038479	2.901442	0.003714	0.0322	2.514347
ENSG00000122068	794.0779	0.111179	0.038435	2.892683	0.00382	0.0322	2.583187
ENSG00000180773	505.4628	0.16718	0.057806	2.892108	0.003827	0.032209	2.583187
ENSG00000113615	389.9876	0.116213	0.039111	2.971378	0.002965	0.032282	1.995423
ENSG00000102878	493.1386	-0.18031	0.061578	-2.92818	0.00341	0.032282	2.293762
ENSG00000118402	462.5995	0.210886	0.071805	2.93694	0.003315	0.032323	2.225762
ENSG00000180592	106.5687	-0.18828	0.062372	-3.01872	0.002538	0.032455	1.695647
ENSG00000067704	763.3733	0.127486	0.043568	2.92612	0.003432	0.032455	2.293762
ENSG00000111711	463.2529	0.182858	0.06161	2.968002	0.002997	0.032546	1.995423
ENSG00000167619	371.2952	-0.19179	0.06559	-2.92403	0.003455	0.03259	2.295759
ENSG00000008441	3065.674	-0.17525	0.060481	-2.89762	0.00376	0.032642	2.492774

ENSG00000100023	687.5606	-0.12487	0.042613	-2.93029	0.003386	0.032907	2.225762
ENSG00000067715	13164.55	0.223027	0.077131	2.891528	0.003834	0.032958	2.514347
ENSG00000152749	572.3642	0.145504	0.049671	2.929334	0.003397	0.03297	2.225762
ENSG00000260855	130.2786	-0.24093	0.082266	-2.92861	0.003405	0.033027	2.225762
ENSG00000075223	376.4417	0.356843	0.12065	2.957674	0.0031	0.033027	2.025126
ENSG00000167548	3575.695	-0.18086	0.062771	-2.88124	0.003961	0.033068	2.583187
ENSG00000114279	2480.317	0.192597	0.066654	2.889503	0.003859	0.033074	2.514347
ENSG00000136531	6181.91	0.177756	0.061491	2.890777	0.003843	0.033206	2.492774
ENSG00000072609	739.2371	-0.14685	0.050356	-2.91622	0.003543	0.033241	2.293762
ENSG00000170185	501.2872	0.110588	0.037926	2.915863	0.003547	0.033241	2.295759
ENSG00000234409	65.396	-0.43808	0.138652	-3.15953	0.00158	0.033284	1.020896
ENSG00000235609	66.68717	0.335821	0.106653	3.148723	0.00164	0.033724	1.044965
ENSG00000253208	21.92678	-0.40589	0.123114	-3.29687	0.000978	0.033746	0.622231
ENSG00000052802	657.8856	0.297953	0.102052	2.919631	0.003504	0.033759	2.225762
ENSG00000226328	214.1898	0.160459	0.055141	2.909947	0.003615	0.033759	2.295759
ENSG00000100614	2841.908	0.116845	0.040548	2.881614	0.003956	0.033759	2.514347
ENSG00000119899	310.0715	0.12512	0.043	2.909746	0.003617	0.033761	2.295759
ENSG00000173221	260.1344	0.225413	0.076475	2.947548	0.003203	0.033871	2.025126
ENSG00000151292	630.6039	0.140593	0.048359	2.90731	0.003646	0.033949	2.29693
ENSG00000110090	736.4023	-0.23427	0.081613	-2.87045	0.004099	0.033949	2.583187
ENSG00000238113	211.153	-0.20825	0.070611	-2.94927	0.003185	0.033974	1.995423
ENSG00000170677	467.6224	0.206636	0.070167	2.944905	0.003231	0.033974	2.025126
ENSG00000106113	120.0896	-0.28507	0.09759	-2.92107	0.003488	0.033974	2.189833
ENSG00000124574	468.5118	-0.15668	0.053748	-2.91511	0.003556	0.033974	2.225762
ENSG00000132485	929.2536	0.129171	0.044429	2.907323	0.003645	0.033974	2.293762
ENSG00000146701	1180.069	0.140774	0.048435	2.906487	0.003655	0.033974	2.293762
ENSG00000163946	1786.525	0.085761	0.029511	2.906053	0.00366	0.033974	2.295759
ENSG00000198780	1205.303	0.134297	0.046214	2.905975	0.003661	0.033974	2.295759
ENSG00000140740	1670.185	0.154645	0.05322	2.905748	0.003664	0.033974	2.293762
ENSG00000146007	576.6562	0.183047	0.063001	2.905459	0.003667	0.033974	2.295759

ENSG00000278090	29.03583	-0.4149	0.131034	-3.16631	0.001544	0.034015	0.963911
ENSG00000239763	42.52796	-0.32245	0.102679	-3.14035	0.001687	0.034015	1.053218
ENSG00000198089	631.0956	-0.1536	0.053567	-2.86747	0.004138	0.034015	2.583187
ENSG00000224255	11.85866	-0.61347	0.162167	-3.78293	0.000155	0.034073	0.0964
ENSG00000255710	31.94841	-0.37201	0.118512	-3.13901	0.001695	0.034073	1.053218
ENSG00000170624	346.1648	0.172008	0.058454	2.942611	0.003255	0.034073	2.025126
ENSG00000106479	460.9522	-0.10098	0.034776	-2.9037	0.003688	0.034073	2.295759
ENSG00000198612	863.6663	0.15924	0.055563	2.865958	0.004157	0.034073	2.583187
ENSG00000008294	4954.461	0.089018	0.031067	2.865325	0.004166	0.03412	2.583187
ENSG00000157219	180.2578	0.213961	0.072642	2.945405	0.003225	0.034179	1.995423
ENSG00000103591	568.0467	0.144316	0.049576	2.911033	0.003602	0.034204	2.225762
ENSG00000286653	23.22767	0.569336	0.157624	3.611989	0.000304	0.034235	0.187229
ENSG00000153093	31.37086	-0.34714	0.110663	-3.13688	0.001708	0.034235	1.053218
ENSG00000165389	140.9282	0.16938	0.058105	2.91508	0.003556	0.034235	2.189833
ENSG00000105738	942.7606	-0.18354	0.063913	-2.87178	0.004082	0.034235	2.514347
ENSG00000144357	3158.099	0.116195	0.040464	2.87154	0.004085	0.034235	2.514347
ENSG00000132017	143.0085	-0.18319	0.063299	-2.89404	0.003803	0.034246	2.338927
ENSG00000187902	942.381	-0.20853	0.072632	-2.87106	0.004091	0.034248	2.514347
ENSG00000162188	105.9103	0.30339	0.097834	3.101082	0.001928	0.03429	1.182918
ENSG00000129559	297.7426	0.1806	0.062306	2.89858	0.003749	0.03433	2.295759
ENSG00000134077	317.4966	0.124419	0.042788	2.907795	0.00364	0.034363	2.225762
ENSG00000172209	531.1836	0.217783	0.074919	2.906911	0.00365	0.034411	2.225762
ENSG00000107295	2409.116	0.229392	0.07976	2.876039	0.004027	0.034411	2.456745
ENSG00000101367	695.0794	0.117601	0.04112	2.859926	0.004237	0.034411	2.583187
ENSG00000279568	28.38006	-0.38463	0.121153	-3.17478	0.001499	0.034475	0.911386
ENSG00000116489	751.0989	0.133332	0.046496	2.86762	0.004136	0.034475	2.514347
ENSG00000107854	1347.553	0.093904	0.032855	2.858103	0.004262	0.03455	2.583187
ENSG00000233822	83.66245	0.268992	0.090016	2.988278	0.002806	0.034629	1.695647
ENSG00000104936	475.0516	-0.17809	0.061542	-2.89383	0.003806	0.034707	2.293762
ENSG00000157388	1420.47	-0.13767	0.047434	-2.90233	0.003704	0.03479	2.225762
ENSG00000176383	92.00725	-0.21269	0.068475	-3.10611	0.001896	0.034794	1.136415
ENSG00000287677	84.77997	-0.44789	0.144264	-3.10464	0.001905	0.034794	1.142898
ENSG00000188599	88.47083	-0.23494	0.075924	-3.09436	0.001972	0.034794	1.182918
ENSG00000113441	2860.981	0.109087	0.038063	2.865927	0.004158	0.034794	2.492774
ENSG00000273108	62.59144	-0.29529	0.092538	-3.191	0.001418	0.034819	0.848718
ENSG00000095319	672.5697	-0.10334	0.035745	-2.89095	0.003841	0.034819	2.293762
ENSG00000241685	136.3505	0.156655	0.054303	2.884832	0.003916	0.034819	2.338927
ENSG00000122218	2705.049	0.115244	0.040166	2.86922	0.004115	0.034819	2.456745
ENSG00000113161	1209.451	0.210037	0.073375	2.862534	0.004203	0.034819	2.514347
ENSG00000050748	2112.013	0.141323	0.04938	2.861971	0.00421	0.034819	2.514347
ENSG00000168913	587.7424	-0.32542	0.11409	-2.85235	0.00434	0.034905	2.583187
ENSG00000246223	26.76047	-0.4613	0.145647	-3.16727	0.001539	0.034993	0.911386
ENSG00000130176	93.02917	0.833615	0.279545	2.982044	0.002863	0.034993	1.695647
ENSG00000105514	234.7363	-0.1759	0.060901	-2.88833	0.003873	0.034993	2.295759
ENSG00000198743	1510.054	0.35575	0.124398	2.859772	0.004239	0.034993	2.514347
ENSG00000130638	1342.047	0.119934	0.041946	2.859234	0.004247	0.034993	2.514347
ENSG00000141198	244.3453	0.178271	0.060817	2.931289	0.003376	0.035029	1.995423
ENSG00000224086	275.6984	-0.17727	0.061194	-2.89684	0.003769	0.035048	2.225762
ENSG00000272645	96.49982	-0.24226	0.078115	-3.10136	0.001926	0.035061	1.136415
ENSG00000126756	87.96699	0.199696	0.067004	2.980355	0.002879	0.0351	1.695647
ENSG00000152147	125.3558	0.17971	0.06094	2.948949	0.003189	0.035263	1.867169
ENSG00000174871	360.8623	0.210796	0.071694	2.940209	0.00328	0.035263	1.918337
ENSG00000126733	269.8466	0.264353	0.091663	2.883974	0.003927	0.035263	2.295759
ENSG00000164506	2722.371	0.131697	0.046007	2.862543	0.004203	0.035263	2.456745
ENSG00000099917	860.2244	-0.12955	0.045505	-2.84693	0.004414	0.035263	2.583187
ENSG00000118985	1462.273	0.156314	0.054931	2.845651	0.004432	0.035349	2.583187
ENSG00000234509	17.26794	-0.43769	0.129527	-3.37919	0.000727	0.035383	0.42288
ENSG00000259494	68.61685	0.19917	0.063673	3.12801	0.00176	0.035383	1.023066
ENSG00000164638	320.7372	0.286995	0.099238	2.891985	0.003828	0.035383	2.225762
ENSG00000135436	47.03979	-0.2806	0.089731	-3.12709	0.001765	0.035384	1.020896

ENSG00000203397	58.90623	-0.25228	0.080838	-3.12082	0.001803	0.035384	1.044965
ENSG00000221826	25.51575	-0.42399	0.135966	-3.11834	0.001819	0.035384	1.053218
ENSG00000024862	235.102	0.166219	0.056833	2.924703	0.003448	0.035384	1.995423
ENSG00000228810	126.5184	0.22398	0.077356	2.895462	0.003786	0.035384	2.189833
ENSG00000103248	190.921	-0.13932	0.048178	-2.89172	0.003831	0.035384	2.225762
ENSG00000167978	9009.592	-0.21876	0.076619	-2.85523	0.004301	0.035384	2.492774
ENSG00000099822	1298.064	-0.22371	0.078429	-2.85241	0.004339	0.035384	2.514347
ENSG00000143164	1597.875	0.162488	0.056981	2.851632	0.00435	0.035384	2.514347
ENSG00000104133	1729.486	-0.0707	0.024855	-2.84437	0.00445	0.035384	2.583187
ENSG00000162813	177.1329	0.13695	0.0474	2.889256	0.003862	0.035468	2.225762
ENSG00000240356	51.86481	0.317053	0.099706	3.179868	0.001473	0.035471	0.848718
ENSG00000144668	516.8671	0.1293	0.044916	2.878704	0.003993	0.035501	2.29693
ENSG00000145332	508.0131	0.140104	0.048668	2.878791	0.003992	0.03552	2.293762
ENSG00000105355	196.1681	0.232647	0.079613	2.92221	0.003476	0.035529	1.995423
ENSG00000125870	228.1979	0.155053	0.053705	2.887144	0.003888	0.035608	2.225762
ENSG00000009413	1896.855	-0.09784	0.034461	-2.8393	0.004521	0.035663	2.583187
ENSG00000110429	951.4273	0.103997	0.036039	2.885691	0.003906	0.035733	2.225762
ENSG00000177889	993.2696	0.166184	0.057792	2.875551	0.004033	0.035768	2.293762
ENSG00000111481	518.6756	0.123696	0.04302	2.875289	0.004037	0.035768	2.29693
ENSG00000254330	14.07231	-0.47659	0.145985	-3.26466	0.001096	0.035789	0.622589
ENSG00000286705	28.69788	0.281499	0.090452	3.112136	0.001857	0.035808	1.053218
ENSG00000153956	1937.269	0.14835	0.052136	2.845446	0.004435	0.035808	2.514347
ENSG00000158186	2292.428	0.216473	0.076082	2.845242	0.004438	0.035808	2.514347
ENSG00000152078	742.3767	0.174361	0.061282	2.84521	0.004438	0.035808	2.514347
ENSG00000107771	2458.554	0.11814	0.041526	2.844963	0.004442	0.035816	2.514347
ENSG00000102900	1302.77	-0.13533	0.047723	-2.83571	0.004572	0.035868	2.583187
ENSG00000198478	1597.69	0.126071	0.043884	2.872822	0.004068	0.035874	2.295759
ENSG00000049246	822.6059	-0.13137	0.045729	-2.87278	0.004069	0.035874	2.295759
ENSG00000115963	144.453	0.393827	0.136436	2.886525	0.003895	0.035943	2.189833
ENSG00000119242	1428.998	-0.11921	0.041373	-2.8813	0.00396	0.035943	2.225762

ENSG00000129055	267.7538	0.180696	0.062926	2.871582	0.004084	0.035943	2.295759
ENSG00000068305	1949.133	0.120383	0.042349	2.842619	0.004474	0.035943	2.514347
ENSG00000106460	1557.736	0.138511	0.048736	2.842089	0.004482	0.035983	2.514347
ENSG00000126267	823.6183	0.160569	0.055958	2.869448	0.004112	0.036167	2.293762
ENSG00000259258	26.06214	-0.3569	0.114875	-3.1068	0.001891	0.036169	1.053218
ENSG00000112981	168.2387	0.2149	0.074653	2.878647	0.003994	0.036169	2.225762
ENSG00000145494	177.3742	0.215888	0.074999	2.878534	0.003995	0.036169	2.225762
ENSG00000155749	127.8268	-0.19856	0.068994	-2.87798	0.004002	0.0362	2.225762
ENSG00000075945	2041.722	0.181921	0.063456	2.866891	0.004145	0.03633	2.295759
ENSG00000238273	45.93471	-0.29843	0.094209	-3.16775	0.001536	0.036339	0.848718
ENSG00000150540	181.9867	0.23186	0.079663	2.910531	0.003608	0.036339	1.995423
ENSG00000156011	8672.975	0.127255	0.044399	2.866189	0.004154	0.036339	2.295759
ENSG00000102038	965.1648	0.120096	0.042455	2.828765	0.004673	0.036339	2.583187
ENSG00000152778	378.9102	0.165875	0.057892	2.865265	0.004167	0.036405	2.295759
ENSG00000166974	3304.298	0.128456	0.04529	2.83628	0.004564	0.036405	2.514347
ENSG00000166908	911.9851	0.127363	0.04433	2.873036	0.004065	0.036608	2.225762
ENSG00000166479	970.8161	0.12798	0.045294	2.825514	0.00472	0.036608	2.583187
ENSG00000185800	776.9501	-0.13377	0.04735	-2.82509	0.004727	0.036637	2.583187
ENSG00000079785	1216.422	0.138863	0.048515	2.862265	0.004206	0.036648	2.295759
ENSG00000128872	11146.72	0.126795	0.044636	2.840686	0.004502	0.036648	2.456745
ENSG00000233038	51.60703	-0.41449	0.133308	-3.10928	0.001875	0.036723	1.020896
ENSG00000153310	1266.116	0.169409	0.059204	2.861437	0.004217	0.036733	2.293762
ENSG00000157833	476.9827	0.334069	0.116405	2.869897	0.004106	0.036837	2.225762
ENSG00000117500	508.956	0.186538	0.065009	2.869399	0.004113	0.036875	2.225762
ENSG00000143379	458.6732	-0.11162	0.038909	-2.86883	0.00412	0.036921	2.225762
ENSG00000162639	136.5191	0.2128	0.07421	2.867549	0.004137	0.037031	2.225762
ENSG00000113163	1157.188	0.109406	0.038284	2.857746	0.004267	0.037031	2.295759
ENSG00000243927	167.5551	0.298451	0.102852	2.901733	0.003711	0.037036	1.995423
ENSG00000139874	212.0812	0.238952	0.082365	2.901132	0.003718	0.037087	1.995423
ENSG00000286230	9.761666	0.687175	0.182255	3.770396	0.000163	0.03717	0.087091

ENSG00000213693	50.95375	-0.30519	0.098335	-3.1036	0.001912	0.03717	1.020896
ENSG00000049540	302.5654	0.326799	0.114042	2.865608	0.004162	0.03717	2.225762
ENSG00000167703	871.6301	-0.18097	0.063382	-2.85519	0.004301	0.03717	2.295759
ENSG00000162066	158.4919	-0.21008	0.073713	-2.85002	0.004372	0.03717	2.338927
ENSG00000163161	683.6368	-0.1161	0.04108	-2.82628	0.004709	0.03717	2.514347
ENSG00000197150	829.4143	-0.13998	0.049044	-2.85424	0.004314	0.037241	2.295759
ENSG00000126217	4240.755	-0.15603	0.055172	-2.82814	0.004682	0.037241	2.492774
ENSG00000137038	329.5155	0.168764	0.058244	2.897513	0.003761	0.037337	1.995423
ENSG00000197536	227.7095	-0.20145	0.069035	-2.91807	0.003522	0.037338	1.867169
ENSG00000108953	4321.971	0.128699	0.045112	2.852902	0.004332	0.037338	2.295759
ENSG00000163516	647.3384	-0.16717	0.058606	-2.85241	0.004339	0.03737	2.293762
ENSG00000079313	742.3081	-0.15904	0.056504	-2.81465	0.004883	0.03737	2.583187
ENSG00000185352	1773.134	0.183856	0.065331	2.814243	0.004889	0.03737	2.583187
ENSG00000143742	1108.817	0.152514	0.054194	2.814241	0.004889	0.03737	2.583187
ENSG00000228526	243.3922	-0.37237	0.130139	-2.86135	0.004218	0.0374	2.225762
ENSG00000184154	104.9341	-0.22997	0.074974	-3.06729	0.00216	0.037469	1.136415
ENSG00000137642	9781.591	0.146122	0.051785	2.821671	0.004777	0.037469	2.514347
ENSG00000236830	63.52558	-0.27724	0.089462	-3.09901	0.001942	0.037471	1.020896
ENSG00000167552	4463.836	0.262726	0.093127	2.821147	0.004785	0.037476	2.514347
ENSG00000103335	711.1824	-0.18677	0.065549	-2.84932	0.004381	0.037592	2.293762
ENSG00000124207	909.5797	0.158596	0.055672	2.848785	0.004389	0.037598	2.295759
ENSG00000160216	2173.4	-0.10405	0.036526	-2.84865	0.00439	0.037598	2.295759
ENSG00000198176	390.8933	-0.12226	0.042338	-2.88777	0.00388	0.037613	2.025126
ENSG00000144228	486.4083	0.11642	0.040873	2.848343	0.004395	0.037613	2.295759
ENSG00000113448	1779.015	0.106419	0.037868	2.810269	0.00495	0.037613	2.583187
ENSG00000136404	126.3655	0.211391	0.07439	2.841681	0.004488	0.037641	2.338927
ENSG00000101213	63.58819	-0.36586	0.117813	-3.10539	0.0019	0.03767	0.989117
ENSG00000268205	928.45	0.114534	0.040246	2.845814	0.00443	0.037814	2.295759
ENSG00000189339	1147.633	-0.21069	0.074036	-2.84573	0.004431	0.037837	2.293762
ENSG00000094804	68.38706	0.297754	0.096286	3.092407	0.001985	0.037991	1.023066

ENSG00000004799	913.3573	-0.3637	0.12791	-2.84337	0.004464	0.038045	2.295759
ENSG00000176920	105.5614	-0.24463	0.080255	-3.04814	0.002303	0.038067	1.182918
ENSG00000182512	251.6916	0.168752	0.05936	2.842842	0.004471	0.038068	2.295759
ENSG00000196700	869.4698	-0.13331	0.046897	-2.84256	0.004475	0.038074	2.293762
ENSG00000232354	125.1282	-0.23301	0.082149	-2.83642	0.004562	0.038074	2.338927
ENSG00000088367	6319.371	-0.13523	0.047939	-2.82085	0.00479	0.038074	2.456745
ENSG00000077454	150.1934	-0.19681	0.069396	-2.83608	0.004567	0.038085	2.338927
ENSG00000101958	72.68901	0.32763	0.111554	2.936962	0.003314	0.038094	1.695647
ENSG00000135047	483.6839	0.194468	0.069359	2.803788	0.005051	0.038094	2.583187
ENSG00000084444	1483.911	0.156036	0.054912	2.841565	0.004489	0.038113	2.293762
ENSG00000274461	128.2899	-0.20342	0.070923	-2.86818	0.004128	0.038117	2.108016
ENSG00000274220	42.06186	-0.30005	0.09543	-3.14419	0.001665	0.038173	0.848718
ENSG00000245526	1138.177	-0.13198	0.046952	-2.81102	0.004938	0.038187	2.514347
ENSG00000133958	2110.575	-0.10809	0.038065	-2.83974	0.004515	0.038218	2.295759
ENSG00000127586	161.9316	-0.23985	0.083684	-2.86613	0.004155	0.038284	2.108016
ENSG00000066084	2872.777	0.159279	0.056695	2.809374	0.004964	0.038323	2.514347
ENSG00000008952	2279.345	0.105728	0.037647	2.808385	0.004979	0.038421	2.514347
ENSG00000196353	507.3655	0.204827	0.073178	2.799034	0.005126	0.038477	2.583187
ENSG00000162931	251.6508	-0.18452	0.063987	-2.8838	0.003929	0.038517	1.977088
ENSG00000001036	144.0811	0.15478	0.054289	2.851033	0.004358	0.038549	2.189833
ENSG00000068976	327.5919	0.313036	0.108578	2.883051	0.003938	0.038558	1.977088
ENSG00000101182	586.3023	0.136454	0.048774	2.797674	0.005147	0.038558	2.583187
ENSG00000110330	665.4547	0.126127	0.044334	2.844941	0.004442	0.038586	2.225762
ENSG00000107362	532.6375	0.177117	0.062265	2.84457	0.004447	0.038586	2.225762
ENSG00000068903	1760.343	0.127642	0.045377	2.812945	0.004909	0.038586	2.456745
ENSG00000123560	19894.54	0.368889	0.131348	2.808483	0.004978	0.038586	2.492774
ENSG00000274180	232.2151	-0.19495	0.06856	-2.8435	0.004462	0.038693	2.225762
ENSG00000103227	389.8901	-0.21207	0.07381	-2.87316	0.004064	0.038695	2.025126
ENSG00000162694	482.5391	0.204884	0.072062	2.843146	0.004467	0.038695	2.225762
ENSG00000158290	1107.724	0.104896	0.037412	2.803791	0.005051	0.038708	2.514347

ENSG00000067365	259.3878	-0.14604	0.051378	-2.84244	0.004477	0.038721	2.225762
ENSG00000121769	553.2756	0.180989	0.063674	2.842435	0.004477	0.038721	2.225762
ENSG00000250329	39.13512	-0.31099	0.100927	-3.08137	0.002061	0.0388	1.020896
ENSG00000141564	1147.975	-0.11809	0.041562	-2.84129	0.004493	0.0388	2.225762
ENSG00000113319	2749.865	0.184751	0.065861	2.805163	0.005029	0.0388	2.492774
ENSG00000206418	401.8977	0.138303	0.048179	2.870636	0.004096	0.038859	2.025126
ENSG00000004961	165.804	0.172282	0.060673	2.839504	0.004518	0.03892	2.225762
ENSG00000125912	551.2229	-0.13719	0.048318	-2.83934	0.004521	0.03892	2.225762
ENSG00000099954	490.5089	-0.20128	0.07113	-2.82969	0.004659	0.03892	2.293762
ENSG00000145425	1023.092	0.171966	0.061597	2.79181	0.005241	0.03892	2.583187
ENSG00000151067	2354.944	-0.13102	0.046936	-2.79146	0.005247	0.03892	2.583187
ENSG00000170745	80.28362	0.323261	0.106505	3.035158	0.002404	0.03892	1.182918
ENSG00000198894	1352.926	0.103953	0.036746	2.828944	0.00467	0.038937	2.295759
ENSG00000163466	1136.943	0.12624	0.044625	2.828879	0.004671	0.038958	2.293762
ENSG00000116266	678.4346	0.119999	0.043016	2.789628	0.005277	0.039059	2.583187
ENSG00000128284	117.5661	-0.34005	0.117555	-2.8927	0.00382	0.039093	1.867169
ENSG00000135637	197.4955	-0.1493	0.052633	-2.83665	0.004559	0.039124	2.225762
ENSG00000146830	1409.312	-0.14116	0.050462	-2.79725	0.005154	0.039133	2.514347
ENSG00000147164	618.0612	0.106679	0.03826	2.788273	0.005299	0.039142	2.583187
ENSG00000235944	175.5485	-0.20892	0.072783	-2.87048	0.004099	0.039166	1.995423
ENSG00000157306	117.0735	-0.21671	0.075963	-2.8528	0.004334	0.039166	2.108016
ENSG00000117425	208.4538	-0.21967	0.077743	-2.82559	0.004719	0.039166	2.295759
ENSG00000250490	27.55062	-0.39494	0.1262	-3.12946	0.001751	0.03919	0.848718
ENSG00000185245	39.32373	-0.37079	0.120735	-3.07106	0.002133	0.03919	1.035363
ENSG00000280157	78.24464	-0.24094	0.079178	-3.04304	0.002342	0.03919	1.136415
ENSG00000124562	166.5828	0.180187	0.06356	2.83493	0.004584	0.03919	2.225762
ENSG00000128917	140.8701	-0.40151	0.142448	-2.81866	0.004822	0.03919	2.338927
ENSG00000139687	658.086	0.135352	0.048574	2.786494	0.005328	0.03919	2.583187
ENSG00000162591	161.5425	-0.29528	0.102197	-2.88928	0.003861	0.039256	1.867169
ENSG00000136273	263.865	-0.12802	0.044715	-2.86297	0.004197	0.039321	2.025126
ENSG00000139174	365.4681	0.127566	0.045194	2.822625	0.004763	0.039345	2.295759
ENSG00000107560	1027.994	0.107935	0.038643	2.793134	0.00522	0.03935	2.514347
ENSG00000095951	1210.522	-0.10651	0.037611	-2.8319	0.004627	0.039368	2.225762
ENSG00000188807	333.4477	-0.16441	0.058261	-2.82195	0.004773	0.039368	2.295759
ENSG00000105171	222.9151	0.142744	0.050593	2.821392	0.004782	0.039416	2.295759
ENSG00000061337	1104.233	-0.16292	0.058566	-2.78187	0.005405	0.039575	2.583187
ENSG00000286388	193.031	-0.27203	0.095027	-2.86264	0.004201	0.039784	1.995423
ENSG00000106624	712.7249	0.470795	0.167051	2.818271	0.004828	0.039784	2.293762
ENSG00000243433	16.94645	-0.40891	0.126861	-3.22329	0.001267	0.039858	0.600464
ENSG00000152402	3401.368	0.179768	0.064691	2.778894	0.005454	0.039858	2.583187
ENSG00000259660	49.7354	-0.47151	0.153716	-3.06739	0.002159	0.039907	1.020896
ENSG00000283031	66.10886	-0.41253	0.134092	-3.0765	0.002094	0.039929	0.989117
ENSG00000134508	1012.588	-0.28127	0.099554	-2.82525	0.004724	0.039983	2.225762
ENSG00000106028	361.3722	0.151602	0.053662	2.825105	0.004727	0.039983	2.225762
ENSG00000033800	996.46	0.109875	0.039561	2.777359	0.00548	0.039983	2.583187
ENSG00000267287	16.10793	-0.68514	0.212726	-3.22075	0.001279	0.040024	0.600464
ENSG00000006128	92.35826	0.481884	0.158876	3.033085	0.002421	0.040024	1.136415
ENSG00000061794	405.2961	0.162043	0.056672	2.859316	0.004246	0.040024	1.995423
ENSG00000164434	241.678	0.37388	0.130783	2.85879	0.004253	0.040024	1.995423
ENSG00000116580	1374.425	-0.11802	0.041787	-2.82426	0.004739	0.040024	2.225762
ENSG00000110011	157.5225	-0.15631	0.055387	-2.82206	0.004772	0.040241	2.225762
ENSG00000247708	496.3999	-0.13387	0.047612	-2.81165	0.004929	0.040259	2.29693
ENSG00000138834	6879.904	-0.12878	0.046161	-2.78974	0.005275	0.040263	2.456745
ENSG00000186908	1472.127	0.126978	0.045795	2.77276	0.005558	0.040328	2.583187
ENSG00000122641	45.05972	0.436966	0.140277	3.115027	0.001839	0.040372	0.848718
ENSG00000266538	35.71681	-0.30224	0.099053	-3.05132	0.002278	0.040372	1.053218
ENSG00000065833	427.4721	0.156864	0.054714	2.866952	0.004144	0.040372	1.918337
ENSG00000105053	404.7811	-0.09132	0.031864	-2.86597	0.004157	0.040372	1.918337
ENSG00000139289	452.4034	0.188954	0.06702	2.819356	0.004812	0.040372	2.225762
ENSG00000119729	701.1779	0.157601	0.056089	2.809856	0.004956	0.040372	2.293762

ENSG00000164985	1734.517	0.119043	0.042367	2.809829	0.004957	0.040372	2.293762
ENSG00000125977	546.9499	0.133169	0.047406	2.80913	0.004968	0.040372	2.295759
ENSG00000258890	637.5461	-0.11532	0.041058	-2.80881	0.004972	0.040372	2.295759
ENSG00000074842	143.1217	0.166722	0.059487	2.802673	0.005068	0.040372	2.338927
ENSG00000065923	1524.422	0.135739	0.048976	2.771538	0.005579	0.040372	2.583187
ENSG00000076928	641.2218	-0.19079	0.068859	-2.77072	0.005593	0.040372	2.583187
ENSG00000113389	36.71627	0.416562	0.136452	3.05281	0.002267	0.040396	1.044965
ENSG00000155011	36.52553	0.605377	0.19787	3.05947	0.002217	0.040399	1.020896
ENSG00000008405	209.5918	0.158013	0.05548	2.848105	0.004398	0.040399	2.025126
ENSG00000287067	145.0547	-0.19251	0.067911	-2.83475	0.004586	0.040447	2.108016
ENSG00000206432	223.089	0.181254	0.063093	2.872785	0.004069	0.040475	1.867169
ENSG00000140990	472.5097	0.160585	0.056075	2.863751	0.004187	0.040475	1.918337
ENSG00000213741	733.6902	0.172602	0.061499	2.806591	0.005007	0.040475	2.295759
ENSG00000172009	732.142	-0.12582	0.044833	-2.80635	0.005011	0.040475	2.295759
ENSG00000164076	1856.164	0.186882	0.067106	2.784901	0.005354	0.040475	2.456745
ENSG00000184786	51.96966	0.267493	0.087505	3.056901	0.002236	0.040496	1.023066
ENSG00000070444	489.9923	-0.15511	0.055277	-2.80597	0.005016	0.040496	2.293762
ENSG00000206579	1064.095	0.205676	0.073305	2.805763	0.00502	0.040496	2.295759
ENSG00000253641	354.2268	-0.15211	0.053373	-2.84999	0.004372	0.040511	1.995423
ENSG00000197121	1184.78	0.165934	0.059146	2.805473	0.005024	0.040511	2.293762
ENSG00000177707	573.4629	0.15236	0.05506	2.767175	0.005654	0.040511	2.583187
ENSG00000146729	627.0916	0.142124	0.050672	2.804753	0.005036	0.040513	2.29693
ENSG00000183576	1235.827	0.105568	0.03764	2.804627	0.005037	0.040529	2.295759
ENSG00000156026	216.5875	0.145893	0.051298	2.844015	0.004455	0.040568	2.025126
ENSG00000204217	4338.751	0.139658	0.050205	2.781745	0.005407	0.040568	2.456745
ENSG00000129353	1132.086	-0.18285	0.065901	-2.77459	0.005527	0.040568	2.514347
ENSG00000197603	2494.639	-0.09736	0.03509	-2.77452	0.005528	0.040568	2.514347
ENSG00000187741	118.1181	-0.19868	0.070492	-2.81847	0.004825	0.040599	2.189833
ENSG00000082482	126.6771	0.272947	0.097031	2.813	0.004908	0.040609	2.225762
ENSG00000255317	37.34229	-0.34674	0.113879	-3.04478	0.002328	0.040693	1.053218

ENSG00000279382	90.23316	-0.2455	0.081308	-3.01944	0.002532	0.040735	1.142898
ENSG00000165476	618.2933	0.183216	0.065389	2.801941	0.00508	0.040735	2.293762
ENSG00000138669	167.5103	0.209947	0.074948	2.801222	0.005091	0.040735	2.295759
ENSG00000134042	751.6863	-0.31373	0.11319	-2.77175	0.005576	0.040735	2.514347
ENSG00000164305	168.6585	0.147229	0.051742	2.84544	0.004435	0.040789	1.995423
ENSG00000171824	797.2749	-0.1394	0.049776	-2.80047	0.005103	0.040789	2.295759
ENSG00000155380	1010.539	-0.41172	0.147064	-2.7996	0.005117	0.040879	2.295759
ENSG00000146085	525.9324	0.142993	0.050915	2.80843	0.004978	0.041006	2.225762
ENSG00000254839	35.31735	-0.33409	0.109681	-3.04603	0.002319	0.041039	1.035363
ENSG00000249915	206.2179	-0.16445	0.058798	-2.79686	0.00516	0.041167	2.295759
ENSG00000123983	2902.884	0.147862	0.053627	2.757237	0.005829	0.041309	2.583187
ENSG00000160214	394.8107	-0.1339	0.047731	-2.80527	0.005027	0.041328	2.225762
ENSG00000154736	49.16235	0.30035	0.098278	3.056132	0.002242	0.041454	0.989117
ENSG00000134013	84.60044	-0.2618	0.087351	-2.99709	0.002726	0.041454	1.201846
ENSG00000160051	95.68122	-0.18008	0.060093	-2.99676	0.002729	0.041458	1.201846
ENSG00000280798	442.4488	0.1214	0.043299	2.803767	0.005051	0.041458	2.225762
ENSG00000132938	885.9001	-0.17661	0.063007	-2.80311	0.005061	0.041471	2.225762
ENSG00000151413	191.4218	0.156715	0.056107	2.793152	0.00522	0.041471	2.295759
ENSG00000110435	723.0004	0.136482	0.048865	2.793039	0.005222	0.041471	2.295759
ENSG00000166206	2569.932	0.151333	0.054621	2.770619	0.005595	0.041504	2.456745
ENSG00000100380	1971.772	0.12574	0.045031	2.792289	0.005234	0.041526	2.295759
ENSG00000231458	12.63738	-0.54533	0.170614	-3.19627	0.001392	0.0416	0.60691
ENSG00000154188	70.87527	0.421046	0.138322	3.043963	0.002335	0.0416	1.020896
ENSG00000287537	53.55788	-0.3359	0.11038	-3.04314	0.002341	0.0416	1.020896
ENSG00000254995	82.13551	-0.30869	0.102528	-3.01083	0.002605	0.0416	1.136415
ENSG00000243679	141.7697	-0.2217	0.077582	-2.85763	0.004268	0.0416	1.867169
ENSG00000198276	309.6021	-0.17426	0.06222	-2.80067	0.0051	0.0416	2.225762
ENSG00000124733	248.9436	0.166667	0.059729	2.790385	0.005265	0.0416	2.295759
ENSG00000170027	10013.48	0.168789	0.061125	2.761348	0.005756	0.0416	2.514347
ENSG00000116005	1273.676	0.119794	0.043529	2.752052	0.005922	0.0416	2.583187

ENSG00000223959	347.7701	-0.18651	0.066848	-2.79006	0.00527	0.041608	2.295759
ENSG00000268307	4.890967	-0.92324	0.246108	-3.75136	0.000176	0.041623	0.076553
ENSG00000162923	1625.287	0.084635	0.030339	2.78965	0.005277	0.041635	2.293762
ENSG00000160392	280.1785	-0.12953	0.046437	-2.78942	0.00528	0.041635	2.295759
ENSG00000089063	595.3755	0.129175	0.046311	2.789275	0.005283	0.041663	2.293762
ENSG00000198945	125.829	-0.16912	0.060432	-2.79849	0.005134	0.0417	2.225762
ENSG00000103174	617.834	-0.12789	0.045865	-2.78839	0.005297	0.0417	2.295759
ENSG00000148481	738.7804	0.142826	0.051223	2.788317	0.005298	0.041725	2.293762
ENSG00000252835	187.2047	0.245935	0.086879	2.830769	0.004644	0.041955	1.995423
ENSG00000213465	285.9192	0.152122	0.053826	2.826192	0.004711	0.041955	2.025126
ENSG00000170085	247.3155	-0.12897	0.045635	-2.82617	0.004711	0.041955	2.025126
ENSG00000085872	284.004	-0.17529	0.062701	-2.79567	0.005179	0.041955	2.225762
ENSG00000152595	82.2275	0.469184	0.156746	2.993284	0.00276	0.042043	1.182918
ENSG00000101439	5829.223	-0.2667	0.095792	-2.78418	0.005366	0.042091	2.295759
ENSG00000113456	370.142	0.128866	0.04629	2.783906	0.005371	0.042091	2.295759
ENSG00000126368	541.9208	-0.20753	0.074553	-2.78362	0.005376	0.042091	2.29693
ENSG00000162409	894.6202	0.128835	0.046929	2.745325	0.006045	0.042091	2.583187
ENSG00000167721	335.9179	-0.1115	0.039484	-2.82401	0.004743	0.042098	2.025126
ENSG00000227533	67.55321	-0.28659	0.094423	-3.03513	0.002404	0.042225	1.023066
ENSG00000169933	1668.538	0.151005	0.054275	2.782217	0.005399	0.042264	2.293762
ENSG00000081791	961.2561	-0.08731	0.031723	-2.75217	0.00592	0.042264	2.514347
ENSG00000099769	24.58502	-0.42013	0.13768	-3.05153	0.002277	0.042316	0.963911
ENSG00000197608	440.7752	-0.12823	0.045449	-2.8214	0.004781	0.042316	2.025126
ENSG00000083937	432.2323	0.153897	0.055141	2.790982	0.005255	0.042316	2.225762
ENSG00000189043	2339.606	0.226172	0.08133	2.780926	0.00542	0.042316	2.295759
ENSG00000205089	74.53184	-0.20286	0.067624	-2.99974	0.002702	0.042335	1.142898
ENSG00000104859	533.711	-0.18061	0.064964	-2.7801	0.005434	0.042381	2.293762
ENSG00000131459	336.5869	-0.16461	0.059213	-2.77992	0.005437	0.042381	2.295759
ENSG00000165006	678.0993	0.10187	0.036649	2.779581	0.005443	0.042392	2.295759
ENSG00000141337	191.2628	-0.18099	0.065134	-2.77868	0.005458	0.042487	2.295759

ENSG00000117461	544.4621	0.23626	0.085035	2.778377	0.005463	0.042487	2.29693
ENSG00000084234	4740.88	0.111255	0.040051	2.777802	0.005473	0.042542	2.295759
ENSG00000061938	3138.819	-0.17977	0.065236	-2.75574	0.005856	0.042542	2.456745
ENSG00000128791	264.7272	0.142599	0.051339	2.777622	0.005476	0.042545	2.295759
ENSG00000175764	822.4437	-0.14934	0.053773	-2.7773	0.005481	0.042566	2.295759
ENSG00000132510	375.9575	-0.22754	0.080281	-2.83432	0.004592	0.042582	1.918337
ENSG00000137857	251.3902	-0.20752	0.073538	-2.8219	0.004774	0.042582	1.995423
ENSG00000065970	367.8429	-0.10993	0.039444	-2.78705	0.005319	0.042582	2.225762
ENSG00000113312	796.8335	0.111672	0.040218	2.776666	0.005492	0.042582	2.295759
ENSG00000174456	562.9081	0.164016	0.059079	2.776238	0.005499	0.042582	2.29693
ENSG00000149679	240.2445	-0.13542	0.048779	-2.77617	0.0055	0.042592	2.295759
ENSG00000100568	683.1616	0.105959	0.038583	2.746228	0.006028	0.042603	2.514347
ENSG00000177947	27.94063	-0.4221	0.138557	-3.04642	0.002316	0.042669	0.963911
ENSG00000253771	244.0608	-0.18834	0.066721	-2.82285	0.00476	0.042737	1.977088
ENSG00000056291	18.30388	0.586152	0.183564	3.193167	0.001407	0.042759	0.583933
ENSG00000122705	959.8604	0.133396	0.048086	2.774126	0.005535	0.042774	2.293762
ENSG00000135749	2284.284	-0.07435	0.027066	-2.74701	0.006014	0.042774	2.492774
ENSG00000172461	3847.192	0.142414	0.051904	2.743821	0.006073	0.042793	2.514347
ENSG00000111364	287.2765	-0.14775	0.053275	-2.77328	0.005549	0.042803	2.295759
ENSG00000174437	7686.714	0.111653	0.040698	2.743427	0.00608	0.042803	2.514347
ENSG00000133103	624.5411	0.112031	0.040972	2.734351	0.00625	0.042808	2.583187
ENSG00000204392	86.55173	0.21079	0.07346	2.869438	0.004112	0.04287	1.695647
ENSG00000018189	4362.899	0.125218	0.045808	2.733559	0.006265	0.04287	2.583187
ENSG00000260790	15.35271	-0.38826	0.12326	-3.14995	0.001633	0.042987	0.670508
ENSG00000139200	465.9396	-0.23595	0.084841	-2.78103	0.005419	0.042987	2.225762
ENSG00000064419	900.2666	0.091583	0.033411	2.741076	0.006124	0.042987	2.514347
ENSG00000238230	37.19389	-0.41839	0.138646	-3.0177	0.002547	0.042999	1.044965
ENSG00000275052	1186.724	0.089031	0.032489	2.740302	0.006138	0.043047	2.514347
ENSG00000147874	369.1887	0.120912	0.043663	2.769205	0.005619	0.043139	2.295759
ENSG00000128655	40.82547	0.34239	0.11353	3.015857	0.002563	0.0432	1.044965

ENSG00000120942	194.6802	-0.1269	0.045192	-2.80804	0.004984	0.043318	2.025126
ENSG00000179818	1432.504	-0.12663	0.045756	-2.76739	0.005651	0.043318	2.295759
ENSG00000107643	1022.132	0.123093	0.044967	2.737403	0.006193	0.043325	2.514347
ENSG00000180611	137.7006	0.223868	0.080467	2.782117	0.005401	0.043358	2.189833
ENSG00000204977	519.7104	0.119516	0.043042	2.776707	0.005491	0.043358	2.225762
ENSG00000158545	511.5692	-0.13614	0.049235	-2.76502	0.005692	0.043551	2.295759
ENSG00000142599	3213.065	-0.10736	0.039382	-2.72602	0.00641	0.04357	2.583187
ENSG00000172270	3788.797	-0.16192	0.059152	-2.73731	0.006194	0.043609	2.492774
ENSG00000147162	4633.564	0.103254	0.037732	2.73647	0.00621	0.043699	2.492774
ENSG00000090020	520.588	-0.15543	0.056252	-2.76308	0.005726	0.043728	2.295759
ENSG00000138190	536.8146	0.137665	0.049648	2.772812	0.005557	0.043756	2.225762
ENSG00000167395	469.6678	-0.13647	0.048403	-2.81954	0.004809	0.04383	1.918337
ENSG00000159840	907.6068	-0.1622	0.058513	-2.77198	0.005572	0.04383	2.225762
ENSG00000100632	269.6313	0.157338	0.056764	2.771766	0.005575	0.04383	2.225762
ENSG00000134817	532.9572	0.561512	0.203289	2.762131	0.005743	0.04383	2.293762
ENSG00000132382	893.2925	-0.13021	0.047823	-2.72265	0.006476	0.04383	2.583187
ENSG00000128654	330.0993	0.176331	0.062779	2.808774	0.004973	0.043933	1.977088
ENSG00000171204	262.1815	0.170756	0.061635	2.770456	0.005598	0.043933	2.225762
ENSG00000114120	1321.02	0.13951	0.050542	2.760261	0.005776	0.043958	2.293762
ENSG00000163848	1495.627	0.101197	0.036666	2.759988	0.00578	0.043974	2.293762
ENSG00000134318	3246.416	0.102198	0.037564	2.720635	0.006516	0.043993	2.583187
ENSG00000136261	230.1664	0.163065	0.058889	2.76903	0.005622	0.044037	2.225762
ENSG00000241769	38.61223	-0.28812	0.095645	-3.01239	0.002592	0.044117	1.020896
ENSG00000230715	103.3414	-0.23032	0.077607	-2.96778	0.003	0.044117	1.182918
ENSG00000119318	1349.955	0.115937	0.042042	2.757616	0.005822	0.044117	2.295759
ENSG00000166411	593.7212	0.146162	0.053009	2.757305	0.005828	0.044117	2.295759
ENSG00000151883	689.6353	0.123662	0.045336	2.727707	0.006378	0.044117	2.514347
ENSG00000112062	910.5785	0.089452	0.032895	2.719348	0.006541	0.044117	2.583187
ENSG00000111669	3890.345	0.188451	0.069321	2.718531	0.006557	0.044117	2.583187
ENSG00000236333	335.1843	0.165344	0.059098	2.79779	0.005145	0.044117	2.025126
ENSG00000144134	252.2364	-0.1394	0.050378	-2.76706	0.005657	0.044117	2.225762
ENSG00000187446	1245.283	0.121827	0.044194	2.756636	0.00584	0.044138	2.295759
ENSG00000188848	93.48271	0.281161	0.094792	2.966081	0.003016	0.044222	1.182918
ENSG00000231211	15.20688	0.450148	0.14257	3.157383	0.001592	0.044262	0.622589
ENSG00000273218	41.53761	-0.33436	0.111421	-3.00089	0.002692	0.044262	1.053218
ENSG00000171798	3609.106	-0.14896	0.054063	-2.75529	0.005864	0.044262	2.295759
ENSG00000100263	261.1351	-0.1357	0.049252	-2.75517	0.005866	0.044262	2.295759
ENSG00000144559	273.3159	-0.14811	0.052902	-2.79973	0.005115	0.044349	1.995423
ENSG00000105357	868.2038	-0.17834	0.064759	-2.75386	0.00589	0.044368	2.295759
ENSG00000171451	477.8517	0.162338	0.058964	2.753178	0.005902	0.04444	2.295759
ENSG00000100307	1635.509	-0.11421	0.041349	-2.76204	0.005744	0.044591	2.225762
ENSG00000100813	1768.775	-0.10779	0.039499	-2.7289	0.006355	0.044671	2.456745
ENSG00000106546	191.2554	0.168391	0.060327	2.791316	0.005249	0.044725	2.025126
ENSG00000165169	679.3021	0.219637	0.079854	2.750473	0.005951	0.044725	2.295759
ENSG00000270171	32.91348	-0.32584	0.107788	-3.02295	0.002503	0.044766	0.963911
ENSG00000183662	254.332	0.189926	0.068812	2.76008	0.005779	0.044766	2.225762
ENSG00000273682	5.183653	-0.8435	0.226723	-3.72039	0.000199	0.04477	0.076553
ENSG00000105325	849.5797	-0.12888	0.046703	-2.75946	0.00579	0.044777	2.225762
ENSG00000197857	380.1597	-0.11441	0.041612	-2.74936	0.005971	0.044777	2.295759
ENSG00000118596	865.1768	0.152116	0.055341	2.74873	0.005983	0.044877	2.293762
ENSG00000093144	359.6945	0.125465	0.04491	2.793671	0.005211	0.044915	1.995423
ENSG00000171847	279.0209	-0.21244	0.07598	-2.79601	0.005174	0.044968	1.977088
ENSG00000100220	553.0729	0.129738	0.047902	2.708412	0.006761	0.044968	2.583187
ENSG00000074071	206.1492	0.147886	0.053048	2.787784	0.005307	0.045005	2.025126
ENSG00000100372	169.1693	0.159751	0.056774	2.813791	0.004896	0.045013	1.867169
ENSG00000188185	129.5196	-0.21925	0.079566	-2.7556	0.005859	0.045141	2.225762
ENSG00000139737	1865.447	0.183703	0.067872	2.706598	0.006798	0.045141	2.583187
ENSG00000196535	3289.773	-0.14025	0.051517	-2.72236	0.006482	0.045226	2.456745
ENSG00000229122	28.51836	-0.33698	0.111479	-3.02285	0.002504	0.045274	0.947688
ENSG00000277534	150.8057	0.171231	0.062076	2.758412	0.005808	0.045425	2.189833

ENSG00000178177	401.0055	0.125285	0.04474	2.800304	0.005105	0.045537	1.918337
ENSG00000159202	1073.8	0.09013	0.033235	2.711884	0.00669	0.045537	2.514347
ENSG00000247516	94.46122	0.247315	0.087111	2.839074	0.004524	0.045605	1.695647
ENSG00000198862	1148.189	0.129994	0.047248	2.751316	0.005936	0.045605	2.225762
ENSG00000187325	459.5455	0.151986	0.055452	2.740878	0.006128	0.045605	2.295759
ENSG00000150990	315.5525	-0.14927	0.053579	-2.78603	0.005336	0.045655	1.995423
ENSG00000272391	442.5816	-0.15114	0.054252	-2.78591	0.005338	0.045655	1.995423
ENSG00000230084	275.7311	0.175622	0.06315	2.781034	0.005419	0.045655	2.025126
ENSG00000165861	465.19	-0.08747	0.031461	-2.78038	0.005429	0.045704	2.025126
ENSG00000114796	2987.376	0.12637	0.046128	2.739547	0.006152	0.045704	2.295759
ENSG00000164051	100.6464	0.184479	0.06265	2.944604	0.003234	0.045719	1.201846
ENSG00000188542	122.4901	-0.15541	0.055396	-2.80544	0.005025	0.045719	1.867169
ENSG00000185532	314.4158	0.244677	0.08788	2.784231	0.005365	0.045719	1.995423
ENSG00000095209	123.6711	0.179351	0.065249	2.748717	0.005983	0.045719	2.225762
ENSG00000160685	296.7249	0.181884	0.066411	2.738745	0.006167	0.045719	2.295759
ENSG00000104946	575.6406	-0.1277	0.046641	-2.73784	0.006184	0.045719	2.29693
ENSG00000174173	151.8813	0.180612	0.066115	2.731801	0.006299	0.045719	2.338927
ENSG00000006831	1287.879	0.15923	0.058793	2.708319	0.006763	0.045719	2.514347
ENSG00000099219	838.177	0.139149	0.05139	2.707737	0.006774	0.045719	2.514347
ENSG00000198015	1339.524	0.123051	0.045578	2.69977	0.006939	0.045719	2.583187
ENSG00000279693	29.71279	-0.31048	0.1018	-3.04994	0.002289	0.045741	0.848718
ENSG00000166004	721.4014	-0.14027	0.051244	-2.73733	0.006194	0.045741	2.293762
ENSG00000177189	864.4917	0.143205	0.052324	2.736884	0.006202	0.045741	2.295759
ENSG00000143819	716.1745	-0.18904	0.069073	-2.73687	0.006203	0.045741	2.295759
ENSG00000063046	2577.837	0.144877	0.053371	2.714551	0.006637	0.045741	2.456745
ENSG00000125743	353.0934	0.163683	0.059592	2.746751	0.006019	0.045761	2.225762
ENSG00000119661	686.937	0.120164	0.043911	2.736563	0.006208	0.045782	2.293762
ENSG00000241837	216.5498	0.177777	0.064035	2.776242	0.005499	0.045909	2.025126
ENSG00000278873	88.83804	-0.27456	0.093194	-2.94612	0.003218	0.04597	1.182918
ENSG00000169057	2745.275	-0.07981	0.029485	-2.70671	0.006795	0.046046	2.492774
ENSG00000196976	157.7063	0.196853	0.070295	2.800389	0.005104	0.046153	1.867169
ENSG00000111845	143.9056	0.170145	0.062405	2.726476	0.006401	0.046188	2.338927
ENSG00000161692	294.5683	-0.18201	0.065463	-2.78028	0.005431	0.046337	1.977088
ENSG00000169718	532.9898	-0.11932	0.043692	-2.73086	0.006317	0.046348	2.29693
ENSG00000093000	765.966	0.090972	0.033681	2.700987	0.006913	0.046348	2.514347
ENSG00000173692	1730.575	0.120907	0.044919	2.691671	0.00711	0.046361	2.583187
ENSG00000117528	703.8799	0.137229	0.050081	2.740136	0.006141	0.046449	2.225762
ENSG00000104695	1225.681	0.129468	0.048116	2.690731	0.00713	0.046449	2.583187
ENSG00000154429	1611.044	0.112167	0.04157	2.698288	0.00697	0.04663	2.514347
ENSG00000184939	898.867	-0.0845	0.030975	-2.72802	0.006372	0.046666	2.295759
ENSG00000283199	48.86707	-0.35332	0.118664	-2.97746	0.002907	0.046704	1.044965
ENSG00000196428	1348.348	0.101071	0.03692	2.737566	0.00619	0.046704	2.225762
ENSG00000122484	1512.989	-0.14074	0.051602	-2.72742	0.006383	0.046704	2.295759
ENSG00000134440	1942.096	0.157238	0.058512	2.687288	0.007203	0.046803	2.583187
ENSG00000165238	2604.149	-0.18742	0.069516	-2.69606	0.007016	0.046815	2.514347
ENSG00000206077	1163.749	-0.36772	0.134936	-2.72518	0.006427	0.046941	2.295759
ENSG00000152467	82.85541	-0.23263	0.079361	-2.93129	0.003376	0.047074	1.201846
ENSG00000184867	625.9047	0.129569	0.047567	2.723945	0.006451	0.047074	2.295759
ENSG00000167962	256.646	-0.13417	0.049086	-2.73345	0.006267	0.047154	2.225762
ENSG00000184752	378.3928	0.190075	0.068786	2.763279	0.005722	0.047297	2.025126
ENSG00000152620	696.2127	0.16014	0.059494	2.691687	0.007109	0.047305	2.514347
ENSG00000100138	1033.759	0.136911	0.050124	2.731429	0.006306	0.04738	2.225762
ENSG00000233579	110.6046	-0.23501	0.085893	-2.73602	0.006219	0.047469	2.189833
ENSG00000131437	2792.491	0.139539	0.051735	2.697179	0.006993	0.047558	2.456745
ENSG00000145832	187.9567	0.329392	0.119315	2.760691	0.005768	0.047565	2.025126
ENSG00000268879	8.948407	-0.64028	0.174931	-3.66019	0.000252	0.047631	0.088325
ENSG00000169885	12.52127	-0.52892	0.168861	-3.13228	0.001735	0.047687	0.60691
ENSG00000221978	1572.712	-0.11522	0.042387	-2.71828	0.006562	0.047713	2.293762
ENSG00000171055	961.6799	0.116274	0.042782	2.717856	0.006571	0.047753	2.293762
ENSG00000063169	206.3337	-0.26101	0.09464	-2.75792	0.005817	0.047819	2.025126

ENSG00000090266	308.976	0.160687	0.058923	2.727055	0.00639	0.047819	2.225762
ENSG00000085185	226.6518	-0.17707	0.064939	-2.72675	0.006396	0.047819	2.225762
ENSG00000161791	828.4861	-0.16591	0.061063	-2.71709	0.006586	0.047819	2.293762
ENSG00000100077	2130.679	0.139525	0.051374	2.715848	0.006611	0.047893	2.295759
ENSG00000137124	153.588	0.196491	0.072083	2.725899	0.006413	0.047899	2.225762
ENSG00000161800	169.1926	0.155309	0.057198	2.715287	0.006622	0.047931	2.295759
ENSG00000091140	760.5788	0.164439	0.060563	2.715162	0.006624	0.047951	2.293762
ENSG00000120913	117.4042	-0.24242	0.089498	-2.70868	0.006755	0.047951	2.338927
ENSG00000279315	34.07536	-0.32673	0.11026	-2.96328	0.003044	0.04796	1.053218
ENSG00000158528	2932.421	0.137454	0.051167	2.686402	0.007223	0.048062	2.492774
ENSG00000124074	136.8065	-0.18335	0.06732	-2.72354	0.006459	0.048091	2.225762
ENSG00000198794	3737.129	0.103793	0.038253	2.713309	0.006662	0.048091	2.295759
ENSG00000078747	1801.846	0.106152	0.039701	2.673802	0.0075	0.048094	2.583187
ENSG00000234361	18.22198	0.381936	0.122451	3.119109	0.001814	0.048214	0.622231
ENSG00000183291	477.6339	0.148473	0.054742	2.712238	0.006683	0.048214	2.293762
ENSG00000113583	277.7214	0.148151	0.054629	2.71196	0.006689	0.048214	2.295759
ENSG00000065150	2184.367	0.111151	0.041452	2.681414	0.007331	0.048214	2.514347
ENSG00000183696	579.5305	-0.15432	0.056721	-2.72072	0.006514	0.048322	2.225762
ENSG00000213676	545.7635	-0.12658	0.046696	-2.71066	0.006715	0.048322	2.293762
ENSG00000100591	868.4526	0.212924	0.078555	2.710528	0.006718	0.048322	2.295759
ENSG00000171853	1125.621	-0.11926	0.044498	-2.68008	0.00736	0.048322	2.514347
ENSG00000197647	76.24979	-0.20551	0.070052	-2.93359	0.003351	0.048349	1.142898
ENSG00000244968	108.7516	-0.29013	0.099262	-2.92289	0.003468	0.048349	1.182918
ENSG00000275427	211.7495	-0.20138	0.074319	-2.70965	0.006735	0.048363	2.295759
ENSG00000125814	6215.799	0.241406	0.089104	2.709246	0.006744	0.048378	2.295759
ENSG00000111540	2446.007	0.077262	0.028937	2.670025	0.007585	0.048378	2.583187
ENSG00000073150	521.7799	-0.233	0.086023	-2.70854	0.006758	0.048459	2.295759
ENSG00000287168	47.78899	-0.36948	0.124128	-2.97661	0.002915	0.048486	0.989117
ENSG00000229593	19.82581	-0.4271	0.136153	-3.13693	0.001707	0.048525	0.578677
ENSG00000261292	108.8244	0.31188	0.112382	2.775178	0.005517	0.048556	1.867169

ENSG00000181315	151.4645	0.158182	0.05856	2.701178	0.006909	0.048556	2.338927
ENSG00000276975	764.426	-0.19981	0.073538	-2.71714	0.006585	0.048585	2.225762
ENSG00000156860	694.0718	-0.14098	0.052852	-2.66739	0.007644	0.048585	2.583187
ENSG00000181610	596.6427	0.121948	0.045056	2.706572	0.006798	0.048596	2.295759
ENSG00000026036	135.9406	-0.22823	0.084026	-2.71616	0.006604	0.048656	2.225762
ENSG00000111371	2769.755	0.161287	0.060218	2.678408	0.007397	0.048656	2.492774
ENSG00000119698	495.0256	0.208093	0.076912	2.705592	0.006818	0.048675	2.295759
ENSG00000184319	123.2338	0.184715	0.067577	2.7334	0.006268	0.048698	2.108016
ENSG00000197816	180.8666	-0.16355	0.060231	-2.7154	0.006619	0.048698	2.225762
ENSG00000232611	145.709	-0.1605	0.059117	-2.71496	0.006628	0.048743	2.225762
ENSG00000248394	19.57346	-0.39231	0.125283	-3.13134	0.00174	0.048752	0.583933
ENSG00000165055	368.3391	-0.12359	0.044723	-2.76341	0.00572	0.048761	1.918337
ENSG00000203666	180.1998	-0.18438	0.067941	-2.71388	0.00665	0.048815	2.225762
ENSG00000146005	1777.003	0.220517	0.082398	2.67625	0.007445	0.048815	2.492774
ENSG00000163864	269.9807	-0.15102	0.055038	-2.74393	0.006071	0.048957	2.025126
ENSG00000120805	930.8098	0.151714	0.056782	2.671863	0.007543	0.048972	2.514347
ENSG00000232928	114.0656	-0.23014	0.084682	-2.7177	0.006574	0.048981	2.189833
ENSG00000149575	2164.343	0.142542	0.05276	2.701713	0.006898	0.049007	2.295759
ENSG00000133135	89.66591	0.2807	0.09595	2.925468	0.003439	0.049059	1.142898
ENSG00000100426	438.3397	-0.121	0.044133	-2.74164	0.006113	0.049191	2.025126
ENSG00000185158	469.1116	-0.14819	0.054072	-2.74064	0.006132	0.049315	2.025126
ENSG00000164951	2922.917	0.162426	0.061073	2.659546	0.007825	0.049315	2.583187
ENSG00000175701	140.9395	0.19005	0.070581	2.692656	0.007089	0.04932	2.338927
ENSG00000156521	273.7173	-0.13623	0.049722	-2.73972	0.006149	0.049392	2.025126
ENSG00000103811	576.049	0.195123	0.072331	2.697642	0.006983	0.04946	2.293762
ENSG00000182504	955.9076	0.123382	0.046423	2.657767	0.007866	0.04946	2.583187
ENSG00000198420	859.3353	0.11657	0.043861	2.657721	0.007867	0.04946	2.583187
ENSG00000138944	1251.8	0.199056	0.074899	2.65767	0.007868	0.04946	2.583187
ENSG00000187566	48.62118	-0.26257	0.089058	-2.94828	0.003196	0.049554	1.044965
ENSG00000114982	1161.327	-0.07942	0.029347	-2.70626	0.006804	0.049554	2.225762

ENSG00000198836	2457.036	0.142547	0.052866	2.696382	0.00701	0.049554	2.295759
ENSG00000168488	1193.865	-0.14671	0.054418	-2.69595	0.007019	0.049554	2.295759
ENSG00000102780	1197.059	0.138076	0.051981	2.656285	0.007901	0.049554	2.583187
ENSG00000286998	35.62473	-0.30505	0.103586	-2.94492	0.00323	0.049646	1.053218
ENSG00000165186	498.5419	0.217647	0.080758	2.695055	0.007038	0.049646	2.293762
ENSG00000083642	2149.284	0.122382	0.045929	2.664603	0.007708	0.049646	2.514347
ENSG00000181458	15.16927	0.541463	0.175704	3.08167	0.002058	0.049653	0.670508
ENSG00000279138	58.65614	0.304809	0.102849	2.963656	0.00304	0.049689	0.989117
ENSG00000150471	3708.509	0.096855	0.036327	2.666222	0.007671	0.049727	2.492774
ENSG00000120733	1803.283	-0.07524	0.028227	-2.66543	0.007689	0.049823	2.492774
ENSG00000081870	138.9408	0.146965	0.054381	2.702519	0.006882	0.049919	2.225762
ENSG00000164651	22.83151	0.445477	0.143502	3.104325	0.001907	0.049923	0.616514
ENSG00000179144	39.87324	-0.44708	0.151465	-2.95172	0.00316	0.049933	1.020896

Table A15. Differential gene expression results of the 2,290 identified significant genes in KCL BrainBank (112 cases and 59 controls) using DESeq2.

Gene ID	Mean	log2Fold Change (lfc)	lfcSE	stat	p-value	p-value adjusted	weight
ENSG00000110492	133.5512	-1.25677	0.1436	-8.75189	2.10E-18	6.25E-14	1.351128
ENSG00000074410	162.787	-1.30137	0.166754	-7.80414	5.99E-15	5.22E-11	2.309341
ENSG00000263503	31.6298	6.539068	0.863893	7.5693	3.75E-14	4.13E-10	1.217444
ENSG00000280022	64.22935	2.697014	0.380911	7.080425	1.44E-12	6.49E-09	2.226625
ENSG00000156510	27.18357	-1.12371	0.161379	-6.96317	3.33E-12	2.49E-08	1.07387
ENSG00000225972	2196.419	-3.3143	0.491492	-6.74334	1.55E-11	8.16E-08	1.270767
ENSG00000262539	25.23384	3.854736	0.582695	6.615364	3.71E-11	3.85E-07	0.553372
ENSG00000188803	1015.372	-0.7648	0.122788	-6.22864	4.71E-10	1.61E-06	1.466075
ENSG00000253661	120.3669	-0.71605	0.119247	-6.00477	1.92E-09	4.43E-06	1.931656
ENSG00000147256	67.66208	-1.14947	0.194808	-5.90055	3.62E-09	1.08E-05	1.351128
ENSG00000260604	28.83856	1.160571	0.197831	5.866472	4.45E-09	1.52E-05	1.07387
ENSG00000133067	38.37801	-1.20298	0.208847	-5.76011	8.41E-09	2.22E-05	1.269879
ENSG00000186407	8.641325	-1.56512	0.266986	-5.8622	4.57E-09	2.27E-05	0.612254
ENSG00000162654	231.2506	-0.6389	0.111933	-5.70785	1.14E-08	2.27E-05	1.445883
ENSG00000274370	12.58547	-0.99811	0.172466	-5.78728	7.15E-09	3.25E-05	0.553372
ENSG00000118292	81.89972	-0.60244	0.106764	-5.6427	1.67E-08	3.25E-05	1.351128
ENSG00000115138	48.39594	-1.12311	0.200235	-5.60898	2.04E-08	3.56E-05	1.351128
ENSG00000206192	10.5623	-1.81807	0.318041	-5.71646	1.09E-08	3.78E-05	0.64362
ENSG00000129521	1134.879	-0.42475	0.076375	-5.56138	2.68E-08	3.92E-05	1.445883
ENSG00000262500	4.009117	3.444991	0.595785	5.782269	7.37E-09	5.48E-05	0.27027
ENSG00000266918	41.36129	0.887806	0.161954	5.48183	4.21E-08	6.29E-05	1.280812
ENSG00000179869	12.62954	-1.47936	0.275509	-5.36955	7.89E-08	0.000261	0.553372
ENSG00000074803	127.8479	-0.70928	0.137265	-5.16723	2.38E-07	0.0003	1.351128
ENSG00000144115	407.3358	-1.01487	0.203547	-4.98594	6.17E-07	0.0003	3.446452
ENSG00000279082	252.0769	-0.90238	0.17868	-5.05028	4.41E-07	0.000367	1.931656
ENSG00000185710	30.70662	-1.84991	0.351971	-5.25585	1.47E-07	0.000399	0.553372
ENSG00000084628	267.3802	0.54497	0.10711	5.087939	3.62E-07	0.000399	1.351128
ENSG00000154188	195.4752	0.66512	0.133414	4.985373	6.18E-07	0.000399	2.226625
ENSG00000183196	1153.305	0.624723	0.12347	5.059718	4.20E-07	0.000491	1.185475
ENSG00000231305	38.75656	-0.55757	0.112071	-4.97512	6.52E-07	0.000679	1.269879
ENSG00000183484	39.24346	-0.62651	0.126021	-4.97149	6.64E-07	0.000679	1.269879
ENSG00000237840	19.1028	-0.59121	0.116147	-5.09022	3.58E-07	0.000751	0.598245
ENSG00000170412	219.343	-0.53373	0.111314	-4.7948	1.63E-06	0.000891	2.226625
ENSG00000270547	19.4663	1.315129	0.260464	5.049185	4.44E-07	0.000948	0.553372
ENSG00000170927	13.05592	0.848056	0.168494	5.033151	4.82E-07	0.001002	0.553372
ENSG00000283503	268.4364	0.457918	0.095856	4.777159	1.78E-06	0.001028	1.931656
ENSG00000121858	77.60314	-0.768	0.160318	-4.79051	1.66E-06	0.001338	1.351128
ENSG00000170160	657.6304	0.696677	0.146314	4.761516	1.92E-06	0.001387	1.466075
ENSG00000132967	11.86973	-1.13069	0.225967	-5.00377	5.62E-07	0.001575	0.368099
ENSG00000211896	6.758291	-1.99604	0.400981	-4.9779	6.43E-07	0.001756	0.368099
ENSG00000185829	102.7036	0.615767	0.133811	4.601762	4.19E-06	0.001779	2.309341
ENSG00000270098	21.55012	-0.69135	0.141873	-4.87304	1.10E-06	0.001902	0.553372
ENSG00000259781	29.17013	-0.83118	0.170963	-4.86178	1.16E-06	0.001937	0.553372
ENSG00000261888	24.23126	-0.81265	0.1684	-4.82569	1.40E-06	0.001937	0.64362
ENSG00000173402	2968.423	-0.28583	0.061093	-4.67867	2.89E-06	0.001937	1.351128
ENSG00000134817	2248.8	0.901673	0.192572	4.682257	2.84E-06	0.001952	1.270767
ENSG00000100033	8.439501	-1.18645	0.243723	-4.86802	1.13E-06	0.001964	0.471379
ENSG00000259433	39.11882	1.083201	0.232	4.668964	3.03E-06	0.001964	1.280812
ENSG00000135094	186.3328	-0.64649	0.138866	-4.65547	3.23E-06	0.001964	1.351128
ENSG00000169248	6.231895	-1.81811	0.369668	-4.91821	8.73E-07	0.001993	0.351128
ENSG00000077327	74.43465	-0.6953	0.149717	-4.64411	3.42E-06	0.001993	1.351128
ENSG00000228570	32.89021	-0.70408	0.149957	-4.69521	2.66E-06	0.002064	0.998163
ENSG00000280096	3.556621	1.38743	0.281933	4.921134	8.60E-07	0.002094	0.311788
ENSG00000110090	1614.559	-0.34875	0.075808	-4.60039	4.22E-06	0.002133	1.445883
ENSG00000082175	108.7168	-0.65746	0.145695	-4.51257	6.40E-06	0.002133	2.226625
ENSG00000156076	960.124	-0.91799	0.198526	-4.62404	3.76E-06	0.00214	1.26296
ENSG00000104368	408.7614	-0.43574	0.096938	-4.49503	6.96E-06	0.002204	2.226625
ENSG00000115556	107.5359	-0.45069	0.098722	-4.56526	4.99E-06	0.002392	1.445883
ENSG00000162595	99.51092	-0.69272	0.151429	-4.57453	4.77E-06	0.002408	1.351128

ENSG00000163586	5.960733	-1.59193	0.326897	-4.86983	1.12E-06	0.002439	0.301937
ENSG00000166603	74.26673	0.75271	0.168728	4.461093	8.15E-06	0.002439	2.226625
ENSG00000134042	2461.257	-0.47493	0.103553	-4.58637	4.51E-06	0.002442	1.185475
ENSG00000167703	1800.358	-0.42574	0.09285	-4.58523	4.53E-06	0.002442	1.185475
ENSG00000131095	162600.1	0.644156	0.141639	4.547887	5.42E-06	0.002481	1.351128
ENSG00000226320	88.01614	0.387915	0.086689	4.474763	7.65E-06	0.002481	1.931656
ENSG00000181019	657.8029	-0.72136	0.15906	-4.53515	5.76E-06	0.002557	1.351128
ENSG00000061455	74.93929	0.395185	0.088616	4.459513	8.21E-06	0.002557	1.931656
ENSG00000085265	14.40145	-1.172	0.2506	-4.67678	2.91E-06	0.002799	0.598245
ENSG00000026508	1969.677	1.010434	0.223539	4.520171	6.18E-06	0.002799	1.270767
ENSG00000127328	2738.296	0.292084	0.064709	4.513833	6.37E-06	0.002799	1.315447
ENSG00000286602	135.1801	0.525448	0.117445	4.473996	7.68E-06	0.003008	1.445883
ENSG00000285668	10.5989	1.666001	0.360527	4.621016	3.82E-06	0.00314	0.64362
ENSG00000228459	41.9649	0.774618	0.172102	4.500935	6.77E-06	0.00314	1.152902
ENSG00000149480	1432.899	-0.25949	0.058012	-4.47306	7.71E-06	0.00314	1.315447
ENSG00000105643	1488.917	0.46359	0.104086	4.453917	8.43E-06	0.00314	1.466075
ENSG00000228696	190.8604	1.059703	0.242611	4.367906	1.25E-05	0.00314	2.226625
ENSG00000015133	350.929	-0.52627	0.120667	-4.36135	1.29E-05	0.003205	2.106768
ENSG00000154451	22.0554	-0.61722	0.133901	-4.60957	4.04E-06	0.003233	0.64362
ENSG00000259383	1.313792	22.19183	4.433095	5.005944	5.56E-07	0.00329	0.083834
ENSG00000249170	31.75053	-0.72108	0.161649	-4.46077	8.17E-06	0.00329	1.217444
ENSG00000143641	1496.256	-0.21772	0.048933	-4.44931	8.61E-06	0.00329	1.315447
ENSG00000271447	362.7948	-0.58346	0.131675	-4.43106	9.38E-06	0.00329	1.445883
ENSG00000239961	37.76158	1.02089	0.22997	4.439232	9.03E-06	0.003415	1.280812
ENSG00000136235	869.0736	0.827179	0.186543	4.434259	9.24E-06	0.003502	1.26296
ENSG00000273382	38.83502	-0.47881	0.107853	-4.43951	9.02E-06	0.003647	1.16988
ENSG00000273259	21.68011	1.61979	0.355889	4.551388	5.33E-06	0.003863	0.64362
ENSG00000204758	27.26221	-0.38753	0.087271	-4.44055	8.97E-06	0.003863	1.07387
ENSG00000261159	17.76737	-0.62163	0.141765	-4.38496	1.16E-05	0.004299	1.217444
ENSG00000133106	101.5349	-0.47511	0.108967	-4.36015	1.30E-05	0.004299	1.351128
ENSG00000160606	77.60832	-0.44054	0.103572	-4.2535	2.10E-05	0.004299	2.226625
ENSG00000188133	53.35818	-0.78253	0.179791	-4.35247	1.35E-05	0.004416	1.347187
ENSG00000179761	260.5534	-0.43082	0.099393	-4.33448	1.46E-05	0.004417	1.445883
ENSG00000125337	82.02922	1.109148	0.256271	4.328026	1.50E-05	0.0045	1.445883
ENSG00000153446	274.2878	-0.44856	0.103389	-4.33859	1.43E-05	0.004541	1.351128
ENSG00000186638	153.5907	-0.31581	0.07476	-4.22431	2.40E-05	0.004557	2.226625
ENSG00000157601	983.4162	-0.32967	0.076469	-4.3111	1.62E-05	0.004607	1.466075
ENSG00000164326	166.9693	-1.18004	0.280367	-4.20889	2.57E-05	0.004607	2.309341
ENSG00000237686	28.78739	-0.64995	0.148066	-4.38957	1.14E-05	0.004656	0.998163
ENSG00000176641	1306.538	0.329762	0.075838	4.348229	1.37E-05	0.004656	1.185475
ENSG00000176845	242.6388	-0.51397	0.11895	-4.32088	1.55E-05	0.004656	1.351128
ENSG00000135407	412.0547	-0.19298	0.04702	-4.10419	4.06E-05	0.004688	3.446452
ENSG00000115902	3113.24	-0.29678	0.06886	-4.30986	1.63E-05	0.005069	1.270767
ENSG00000160602	59.47598	-0.56416	0.131803	-4.2803	1.87E-05	0.005394	1.351128
ENSG00000129657	5811.898	-0.33541	0.07829	-4.28417	1.83E-05	0.005617	1.262783
ENSG00000251381	29.56053	-0.68706	0.157406	-4.36489	1.27E-05	0.006045	0.798279
ENSG00000198740	4190.632	0.339745	0.080236	4.234335	2.29E-05	0.006045	1.445883
ENSG00000288235	57.05243	0.698918	0.164415	4.250948	2.13E-05	0.006477	1.212648
ENSG00000257277	41.38851	0.547955	0.129146	4.242927	2.21E-05	0.006477	1.269879
ENSG00000187634	90.00486	0.718748	0.1733	4.147417	3.36E-05	0.006477	1.931656
ENSG00000186188	69.49396	-0.58405	0.140982	-4.14271	3.43E-05	0.006496	1.931656
ENSG00000108774	437.3061	-0.26668	0.064978	-4.10411	4.06E-05	0.006604	2.226625
ENSG00000143171	160.9837	-0.50558	0.11997	-4.21423	2.51E-05	0.006661	1.351128
ENSG00000211592	7.7389	-1.67945	0.377869	-4.44453	8.81E-06	0.006674	0.469722
ENSG00000166033	6082.421	-0.27753	0.064505	-4.30252	1.69E-05	0.007039	0.84637
ENSG00000286870	29.73585	1.248447	0.290311	4.300375	1.71E-05	0.007381	0.798279
ENSG00000159348	637.5377	-0.19755	0.047076	-4.19641	2.71E-05	0.007381	1.26296
ENSG00000286215	279.1383	0.315662	0.07571	4.169345	3.05E-05	0.007381	1.445883
ENSG00000137573	571.0085	0.419139	0.100391	4.17505	2.98E-05	0.007719	1.315447
ENSG00000173678	3.049237	-1.8528	0.413925	-4.47618	7.60E-06	0.008169	0.311788

ENSG00000184678	797.6461	-0.29649	0.071281	-4.15947	3.19E-05	0.008169	1.315447
ENSG00000162174	1101.206	-0.31854	0.077168	-4.12791	3.66E-05	0.008299	1.466075
ENSG00000196208	1709.461	-0.25425	0.061696	-4.12108	3.77E-05	0.008528	1.445883
ENSG00000188933	150.5036	0.669884	0.165196	4.055081	5.01E-05	0.008528	1.931656
ENSG00000255542	34.45218	-0.58034	0.139342	-4.16488	3.12E-05	0.008636	1.16988
ENSG00000215367	28.38202	0.494061	0.119144	4.146771	3.37E-05	0.008911	1.217444
ENSG00000280350	16.15258	-0.82054	0.193691	-4.23634	2.27E-05	0.009084	0.798279
ENSG00000138798	147.1282	0.420264	0.102145	4.114383	3.88E-05	0.009099	1.351128
ENSG00000031081	1878.174	-0.37193	0.090271	-4.12015	3.79E-05	0.009362	1.270767
ENSG00000166341	1313.541	-0.36471	0.088907	-4.10213	4.09E-05	0.009702	1.315447
ENSG00000241015	169.1738	0.402388	0.098304	4.093321	4.25E-05	0.009737	1.351128
ENSG00000286117	40.44825	-0.83557	0.20378	-4.10037	4.12E-05	0.009887	1.280812
ENSG00000010310	69.86611	0.729416	0.184509	3.95328	7.71E-05	0.010548	2.226625
ENSG00000172137	421.3868	-0.64533	0.168066	-3.83976	0.000123	0.010806	3.446452
ENSG00000183347	20.8462	-0.62634	0.147483	-4.24684	2.17E-05	0.010877	0.598245
ENSG00000012223	132.9679	1.43223	0.365193	3.92184	8.79E-05	0.011336	2.309341
ENSG00000114547	62.21449	-0.33997	0.083556	-4.06874	4.73E-05	0.01136	1.230506
ENSG00000004939	16.0025	-1.13386	0.267934	-4.23185	2.32E-05	0.011373	0.598245
ENSG00000162711	161.3007	-0.38052	0.094121	-4.04292	5.28E-05	0.011387	1.351128
ENSG00000279673	34.33318	-0.51956	0.12666	-4.10205	4.10E-05	0.011796	0.998163
ENSG00000283307	12.95121	1.260601	0.310824	4.055679	5.00E-05	0.011796	1.217444
ENSG00000080493	6421.253	-0.4725	0.117823	-4.01023	6.07E-05	0.011944	1.445883
ENSG00000158270	646.7901	0.528726	0.131993	4.005724	6.18E-05	0.011944	1.466075
ENSG00000004948	8.498729	-1.29393	0.303751	-4.25984	2.05E-05	0.012206	0.471379
ENSG00000154529	241.1537	0.549681	0.137548	3.996291	6.43E-05	0.012429	1.445883
ENSG00000091656	2839.561	-0.27895	0.069615	-4.007	6.15E-05	0.012537	1.351128
ENSG00000153993	269.4473	0.503051	0.126031	3.99148	6.57E-05	0.012537	1.445883
ENSG00000150551	163.1567	-0.46228	0.115911	-3.98825	6.66E-05	0.012595	1.445883
ENSG00000140287	11.03146	-1.34846	0.326967	-4.12414	3.72E-05	0.012654	0.798279
ENSG00000189238	29.84552	-0.63177	0.153236	-4.12284	3.74E-05	0.012654	0.798279

ENSG00000185052	529.6451	-0.37884	0.094833	-3.9948	6.47E-05	0.012849	1.351128
ENSG00000225899	6.930469	0.9193	0.214834	4.279109	1.88E-05	0.013956	0.351128
ENSG00000224805	8.979922	-0.66766	0.156281	-4.2722	1.94E-05	0.013956	0.368099
ENSG00000283491	26.10571	0.43775	0.109608	3.993758	6.50E-05	0.013956	1.217444
ENSG00000280254	127.7172	-0.32659	0.085009	-3.84183	0.000122	0.013956	2.309341
ENSG00000154040	384.0765	0.306081	0.077195	3.965023	7.34E-05	0.014024	1.351128
ENSG00000214717	1267.272	-0.21815	0.05525	-3.94846	7.87E-05	0.014024	1.445883
ENSG00000227232	5.940264	-0.94873	0.223004	-4.25433	2.10E-05	0.0152	0.351128
ENSG00000099992	216.3347	-0.40648	0.103502	-3.92722	8.59E-05	0.0152	1.445883
ENSG00000072506	309.6401	-0.21394	0.055534	-3.85245	0.000117	0.015217	1.931656
ENSG00000028277	284.2344	-0.38867	0.102038	-3.80902	0.00014	0.015217	2.309341
ENSG00000072694	19.69931	1.283341	0.309756	4.143075	3.43E-05	0.015391	0.553372
ENSG00000225265	38.16861	-0.40966	0.103812	-3.94619	7.94E-05	0.015391	1.280812
ENSG00000134202	2154.804	-0.39564	0.099975	-3.95742	7.58E-05	0.015486	1.185475
ENSG00000127993	1045.042	0.292956	0.074913	3.910632	9.21E-05	0.015486	1.445883
ENSG00000198342	148.8905	-0.37676	0.099219	-3.79724	0.000146	0.015486	2.309341
ENSG00000238083	375.3227	0.542064	0.14672	3.694539	0.00022	0.015486	3.446452
ENSG00000180644	14.27254	-0.81081	0.198454	-4.08564	4.40E-05	0.016425	0.64362
ENSG00000135114	10.08749	-0.81916	0.200618	-4.08319	4.44E-05	0.016425	0.64362
ENSG00000136870	2413.658	0.283105	0.072311	3.915109	9.04E-05	0.016425	1.315447
ENSG00000227992	9.752316	0.556297	0.135953	4.091831	4.28E-05	0.016537	0.612254
ENSG00000261770	166.2669	0.407494	0.10466	3.893486	9.88E-05	0.017201	1.351128
ENSG00000170498	4.282905	-1.45934	0.344781	-4.23267	2.31E-05	0.01764	0.301937
ENSG00000261603	3.138347	-1.02595	0.244402	-4.1978	2.70E-05	0.01764	0.351128
ENSG00000277987	22.59759	0.77975	0.191242	4.077292	4.56E-05	0.01764	0.598245
ENSG00000110063	367.4512	-0.20671	0.054966	-3.76061	0.000169	0.01764	2.226625
ENSG00000156804	3148.913	0.252824	0.065087	3.884416	0.000103	0.01815	1.262783
ENSG00000052795	3789.35	0.204287	0.052768	3.871432	0.000108	0.01815	1.351128
ENSG00000184260	638.1467	-0.37157	0.096025	-3.86956	0.000109	0.01815	1.351128
ENSG00000137959	430.302	-0.58221	0.150487	-3.86882	0.000109	0.01815	1.351128

ENSG00000106714	424.672	0.266983	0.069275	3.853971	0.000116	0.01815	1.445883
ENSG00000198892	1299.427	-0.21732	0.05575	-3.89802	9.70E-05	0.018178	1.185475
ENSG00000211895	7.302154	-2.26772	0.552409	-4.10515	4.04E-05	0.019008	0.469722
ENSG00000105251	327.6787	-0.44306	0.115114	-3.84883	0.000119	0.019304	1.351128
ENSG00000258655	122.6579	-0.35257	0.093993	-3.75101	0.000176	0.01993	1.931656
ENSG00000265218	84.61754	0.481725	0.12993	3.707577	0.000209	0.02043	2.226625
ENSG00000286653	71.04917	0.610517	0.160125	3.812744	0.000137	0.020552	1.445883
ENSG00000171451	1443.825	0.304497	0.079464	3.831861	0.000127	0.020793	1.315447
ENSG00000244921	16.11977	-0.82878	0.215454	-3.84668	0.00012	0.020825	1.217444
ENSG00000131042	23.00341	-0.77933	0.202615	-3.84635	0.00012	0.020825	1.217444
ENSG00000225178	37.15403	0.914494	0.238594	3.832842	0.000127	0.020825	1.280812
ENSG00000170667	97.1336	-0.50162	0.131193	-3.82352	0.000132	0.020825	1.351128
ENSG00000183908	522.5764	0.370554	0.096771	3.829186	0.000129	0.021324	1.26296
ENSG00000242756	1.867762	-1.39689	0.319581	-4.371	1.24E-05	0.021705	0.117166
ENSG00000141580	2095.302	-0.12917	0.033653	-3.83824	0.000124	0.021705	1.185475
ENSG00000268087	82.10616	-0.2333	0.061184	-3.81307	0.000137	0.021705	1.299739
ENSG00000103710	425.4441	0.629235	0.165476	3.802582	0.000143	0.021705	1.351128
ENSG00000276043	127.2902	0.484191	0.127948	3.784279	0.000154	0.021705	1.445883
ENSG00000070366	1687.992	-0.14964	0.039555	-3.78307	0.000155	0.021705	1.445883
ENSG00000248079	87.41768	0.388263	0.102676	3.781436	0.000156	0.021705	1.445883
ENSG00000078098	115.8441	0.407826	0.109971	3.708488	0.000209	0.021705	1.931656
ENSG00000135046	480.182	0.417268	0.117416	3.553746	0.00038	0.022049	3.446452
ENSG00000121742	1200.898	-0.65128	0.173051	-3.76351	0.000168	0.022754	1.466075
ENSG00000285825	51.76019	-0.43887	0.115369	-3.80403	0.000142	0.022863	1.230506
ENSG00000261087	1028.43	0.235676	0.062069	3.796987	0.000146	0.022863	1.26296
ENSG00000196502	444.7595	-0.36178	0.096215	-3.76019	0.00017	0.023038	1.445883
ENSG00000234177	268.2376	-0.24153	0.06621	-3.64796	0.000264	0.023177	2.226625
ENSG00000109111	4710.721	-0.11247	0.029839	-3.76935	0.000164	0.023536	1.351128
ENSG00000273706	10.65592	-1.15257	0.282607	-4.07836	4.54E-05	0.023824	0.368099
ENSG00000118257	708.2095	-0.38204	0.101066	-3.78013	0.000157	0.023882	1.26296

ENSG00000198774	49.24417	1.051707	0.279676	3.760443	0.00017	0.024112	1.347187
ENSG00000154856	1290.505	-0.36526	0.097031	-3.76437	0.000167	0.024189	1.315447
ENSG00000170989	1726.666	-0.37153	0.098726	-3.76323	0.000168	0.024189	1.315447
ENSG00000288574	61.83671	0.47351	0.125493	3.773198	0.000161	0.024417	1.230506
ENSG00000140450	2273.99	0.438904	0.117056	3.749508	0.000177	0.024417	1.351128
ENSG00000117362	854.1133	-0.18171	0.048657	-3.7344	0.000188	0.024417	1.445883
ENSG00000272505	866.2084	0.214767	0.057553	3.731649	0.00019	0.024417	1.466075
ENSG00000133121	2397.617	0.179147	0.047649	3.759694	0.00017	0.024812	1.270767
ENSG00000273407	15.74309	0.505796	0.127915	3.954146	7.68E-05	0.024921	0.553372
ENSG00000286241	18.21282	0.825528	0.213289	3.870467	0.000109	0.024921	0.798279
ENSG00000165370	20.02107	-0.91745	0.243813	-3.76294	0.000168	0.024921	1.217444
ENSG00000130287	7218.267	-0.34119	0.09088	-3.75428	0.000174	0.024921	1.262783
ENSG00000180104	2101.531	-0.19141	0.051003	-3.75291	0.000175	0.024921	1.270767
ENSG00000188064	186.2337	-0.58686	0.157823	-3.71844	0.0002	0.024921	1.445883
ENSG00000137965	184.1171	-0.36518	0.101478	-3.59856	0.00032	0.024921	2.309341
ENSG00000283378	11.04495	0.653433	0.169136	3.863351	0.000112	0.025043	0.798279
ENSG00000102445	347.4989	-0.25816	0.069187	-3.73129	0.00019	0.02509	1.351128
ENSG00000159261	4.8448	-1.07902	0.264454	-4.08018	4.50E-05	0.025572	0.311788
ENSG00000254858	130.8154	-0.28886	0.079568	-3.63033	0.000283	0.025848	1.931656
ENSG00000261575	8.796402	0.940395	0.24038	3.912113	9.15E-05	0.026098	0.612254
ENSG00000183486	104.4597	-0.47759	0.128521	-3.71603	0.000202	0.026098	1.351128
ENSG00000056998	426.0883	0.39588	0.107033	3.698664	0.000217	0.026098	1.445883
ENSG00000172965	465.6063	0.213438	0.059534	3.585129	0.000337	0.02623	2.226625
ENSG00000227243	14.37327	0.886214	0.22664	3.910234	9.22E-05	0.026604	0.598245
ENSG00000100450	1.413186	-1.81526	0.449796	-4.03575	5.44E-05	0.026614	0.351128
ENSG00000254031	17.30413	0.736052	0.187443	3.926812	8.61E-05	0.026614	0.553372
ENSG00000149357	1160.527	-0.17137	0.045859	-3.73691	0.000186	0.026614	1.185475
ENSG00000164309	1869.177	-0.29287	0.078446	-3.7334	0.000189	0.026614	1.185475
ENSG00000109501	2064.288	-0.30931	0.083476	-3.70542	0.000211	0.026614	1.351128
ENSG00000240583	2551.87	0.857319	0.231616	3.701474	0.000214	0.026614	1.351128

ENSG00000285908	115.3032	0.660109	0.17915	3.68468	0.000229	0.026614	1.445883
ENSG00000165949	300.7437	-0.4998	0.138509	-3.60843	0.000308	0.026614	1.931656
ENSG00000261465	6.933466	0.841256	0.209542	4.014738	5.95E-05	0.026869	0.368099
ENSG00000175283	199.2821	-0.24517	0.068124	-3.5988	0.00032	0.027391	1.931656
ENSG00000257408	1.334011	-1.40549	0.354746	-3.96196	7.43E-05	0.02748	0.445883
ENSG00000162415	528.6921	-0.14763	0.039962	-3.69421	0.000221	0.027525	1.315447
ENSG00000226478	7.693835	-0.68929	0.172192	-4.00301	6.25E-05	0.027665	0.368099
ENSG00000221990	99.19657	-0.30804	0.085739	-3.59271	0.000327	0.027665	1.931656
ENSG00000212371	7.486317	0.963045	0.244438	3.939831	8.15E-05	0.028151	0.469722
ENSG00000116833	8.701728	-1.05398	0.263793	-3.9955	6.46E-05	0.028214	0.368099
ENSG00000160216	5883.99	-0.1666	0.045531	-3.65913	0.000253	0.028214	1.445883
ENSG00000204396	349.1062	-0.46743	0.127242	-3.67353	0.000239	0.02837	1.351128
ENSG00000161955	174.1592	-0.39167	0.106708	-3.67046	0.000242	0.028599	1.351128
ENSG00000261839	47.65689	0.400185	0.103563	3.864157	0.000111	0.028625	0.61906
ENSG00000287907	22.74844	0.789943	0.205057	3.852315	0.000117	0.028785	0.64362
ENSG00000144182	95.58521	0.303238	0.082748	3.664593	0.000248	0.028918	1.351128
ENSG00000019991	665.3317	0.582619	0.158296	3.680558	0.000233	0.028949	1.26296
ENSG00000139410	132.718	-0.40864	0.115701	-3.53186	0.000413	0.029001	2.226625
ENSG00000196436	36.19548	0.842614	0.228813	3.682544	0.000231	0.03065	1.16988
ENSG00000267904	112.3894	-0.2138	0.060813	-3.51579	0.000438	0.03065	2.226625
ENSG00000121406	598.4298	0.153519	0.042147	3.642498	0.00027	0.030912	1.351128
ENSG00000274588	17.27518	-0.92253	0.240188	-3.84085	0.000123	0.031484	0.598245
ENSG00000168386	690.4881	0.248009	0.06789	3.653095	0.000259	0.031484	1.26296
ENSG00000127472	98.93731	-0.57163	0.157265	-3.63482	0.000278	0.031484	1.351128
ENSG00000159723	24.9255	-0.82794	0.219978	-3.76374	0.000167	0.03162	0.798279
ENSG00000164736	41.83361	-0.69283	0.186926	-3.70643	0.00021	0.03162	0.998163
ENSG00000087085	796.5464	-0.44231	0.12236	-3.61478	0.000301	0.03162	1.445883
ENSG00000206195	87.39852	0.605936	0.167759	3.611944	0.000304	0.03162	1.445883
ENSG00000164972	221.3599	-0.37826	0.104743	-3.6113	0.000305	0.03162	1.445883
ENSG00000251093	2.338633	2.266637	0.521155	4.349253	1.37E-05	0.0321	0.063389
ENSG00000143819	2330.961	-0.37165	0.102563	-3.62365	0.00029	0.0321	1.351128
ENSG00000170509	34.25606	0.511837	0.139943	3.657472	0.000255	0.032193	1.16988
ENSG00000171551	35.70253	-1.01844	0.280219	-3.63443	0.000279	0.032193	1.280812
ENSG00000117305	421.1037	-0.16998	0.050457	-3.36873	0.000755	0.032279	3.446452
ENSG00000253875	129.7744	0.329449	0.094825	3.474278	0.000512	0.032557	2.309341
ENSG00000255998	3.876123	-1.01663	0.25745	-3.94884	7.85E-05	0.032709	0.351128
ENSG00000284726	42.42487	0.331716	0.090899	3.649292	0.000263	0.032754	1.16988
ENSG00000260018	21.63167	-0.44727	0.122987	-3.63674	0.000276	0.032928	1.217444
ENSG00000239467	112.1888	-0.25414	0.070437	-3.60811	0.000308	0.033025	1.351128
ENSG00000165474	41.18608	-0.69217	0.189951	-3.64392	0.000269	0.033086	1.16988
ENSG00000255550	12.85642	0.651055	0.179321	3.630664	0.000283	0.033268	1.217444
ENSG00000259417	617.987	-0.41902	0.115722	-3.62091	0.000294	0.033268	1.26296
ENSG00000286712	8.61979	0.934669	0.245844	3.801883	0.000144	0.033352	0.614045
ENSG00000224511	14.21789	-0.75407	0.201995	-3.73309	0.000189	0.033404	0.798279
ENSG00000182492	964.3747	0.419885	0.117255	3.580952	0.000342	0.033404	1.445883
ENSG00000156218	542.9067	0.310795	0.086873	3.577602	0.000347	0.033404	1.466075
ENSG00000203808	152.144	0.393065	0.113417	3.465668	0.000529	0.033404	2.226625
ENSG00000169860	810.3534	-0.43442	0.121636	-3.5715	0.000355	0.033926	1.466075
ENSG00000144136	2000.849	-0.21687	0.060436	-3.58845	0.000333	0.034084	1.351128
ENSG00000259868	82.59178	0.36914	0.102882	3.58801	0.000333	0.034084	1.351128
ENSG00000169836	78.6486	-0.54238	0.151813	-3.5727	0.000353	0.034084	1.445883
ENSG00000172428	1081.066	-0.26521	0.074277	-3.57059	0.000356	0.034084	1.445883
ENSG00000273456	37.98449	-0.31275	0.086259	-3.62575	0.000288	0.034304	1.152902
ENSG00000262039	17.05034	0.736791	0.203985	3.61198	0.000304	0.034304	1.217444
ENSG00000224738	40.86304	0.30735	0.084816	3.623734	0.00029	0.034455	1.152902
ENSG00000134595	20.07541	-0.66657	0.176914	-3.76778	0.000165	0.034681	0.64362
ENSG00000107738	1276.307	-0.52464	0.145292	-3.61095	0.000305	0.034681	1.185475
ENSG00000172270	8410.822	-0.30184	0.084397	-3.57639	0.000348	0.034681	1.351128
ENSG00000141449	589.2182	-0.3394	0.095362	-3.55905	0.000372	0.034681	1.445883
ENSG00000184898	239.4005	-0.29045	0.084582	-3.43398	0.000595	0.034681	2.309341

ENSG00000118503	175.3402	-0.43606	0.126838	-3.43795	0.000586	0.035289	2.226625
ENSG00000013573	201.623	0.530101	0.154724	3.426096	0.000612	0.035428	2.309341
ENSG00000136872	183.9155	0.459344	0.134143	3.424278	0.000616	0.035548	2.309341
ENSG00000205609	1.776186	-1.181	0.307129	-3.84527	0.00012	0.03575	0.445883
ENSG00000170275	3135.171	0.186438	0.052084	3.579567	0.000344	0.03575	1.270767
ENSG00000145476	1590.1	-0.23147	0.065288	-3.54541	0.000392	0.03575	1.445883
ENSG00000288075	498.1664	-0.27435	0.080009	-3.42904	0.000606	0.035754	2.226625
ENSG00000235310	154.3131	0.377218	0.110075	3.426913	0.00061	0.035918	2.226625
ENSG00000196767	99.68631	-0.4495	0.126985	-3.53976	0.0004	0.036168	1.445883
ENSG00000280107	86.97176	0.361388	0.105601	3.422213	0.000621	0.036308	2.226625
ENSG00000205106	23.69501	-0.5534	0.147089	-3.76233	0.000168	0.036491	0.598245
ENSG00000204525	2054.375	-0.38554	0.109068	-3.53485	0.000408	0.036491	1.445883
ENSG00000132164	1688.176	-0.41439	0.115575	-3.58543	0.000337	0.036525	1.185475
ENSG00000109610	405.8953	-0.48964	0.138593	-3.53292	0.000411	0.036525	1.445883
ENSG00000138083	11.47923	-1.20631	0.327554	-3.68277	0.000231	0.037018	0.798279
ENSG00000243007	1.796855	1.565414	0.403757	3.877123	0.000106	0.037785	0.351128
ENSG00000281248	9.728692	0.859806	0.225795	3.807913	0.00014	0.037785	0.471379
ENSG00000150764	3291.995	0.233446	0.065822	3.546657	0.00039	0.037785	1.315447
ENSG00000167766	1438.076	0.284514	0.080295	3.54336	0.000395	0.037785	1.315447
ENSG00000184232	704.3398	-0.41993	0.118542	-3.54244	0.000396	0.037785	1.315447
ENSG00000161896	287.3565	0.655516	0.185424	3.535231	0.000407	0.037785	1.351128
ENSG00000141485	304.7288	-0.52213	0.147695	-3.5352	0.000407	0.037785	1.351128
ENSG00000186815	2558.343	-0.28108	0.079186	-3.54957	0.000386	0.037926	1.270767
ENSG00000229828	11.23487	-0.92014	0.245058	-3.75478	0.000173	0.038678	0.553372
ENSG00000250948	10.22919	0.818093	0.223402	3.661979	0.00025	0.038678	0.798279
ENSG00000101439	18894.46	-0.40958	0.116135	-3.52678	0.000421	0.038678	1.351128
ENSG00000253854	142.5921	0.198387	0.058662	3.381876	0.00072	0.038678	2.309341
ENSG00000288052	13.15503	0.618358	0.168973	3.659513	0.000253	0.038923	0.798279
ENSG00000141349	638.7688	-0.1873	0.053116	-3.52631	0.000421	0.038923	1.315447
ENSG00000134864	74.05516	-0.33815	0.096535	-3.50292	0.00046	0.038923	1.445883

ENSG00000132768	287.477	-0.19189	0.054804	-3.50142	0.000463	0.038923	1.445883
ENSG00000171169	123.1967	-0.24471	0.071474	-3.42382	0.000617	0.038923	1.931656
ENSG00000175832	78.67042	-0.4713	0.133642	-3.52659	0.000421	0.039116	1.299739
ENSG00000286330	95.64693	-0.48822	0.144362	-3.3819	0.00072	0.039116	2.226625
ENSG00000269825	279.7401	0.419812	0.124706	3.366397	0.000762	0.03971	2.309341
ENSG00000120215	108.8079	0.341788	0.097871	3.492227	0.000479	0.039773	1.445883
ENSG00000246089	88.53114	-0.25925	0.073656	-3.51967	0.000432	0.039791	1.299739
ENSG00000137285	3400.25	-0.4419	0.125904	-3.50978	0.000448	0.040567	1.315447
ENSG00000278970	93.13204	-0.23905	0.068588	-3.48523	0.000492	0.040567	1.445883
ENSG00000286300	32.62895	0.404785	0.114716	3.52858	0.000418	0.040713	1.217444
ENSG00000261451	973.9347	0.205772	0.058819	3.498402	0.000468	0.040857	1.351128
ENSG00000268996	98.60553	-0.38314	0.114276	-3.3528	0.0008	0.040857	2.309341
ENSG00000007129	16.71484	-0.71615	0.194197	-3.68774	0.000226	0.041119	0.64362
ENSG00000135597	2957.747	-0.15162	0.043153	-3.51358	0.000442	0.041119	1.262783
ENSG00000163346	4387.389	-0.37711	0.108484	-3.47623	0.000509	0.041119	1.445883
ENSG00000152049	170.46	0.633742	0.189001	3.353118	0.000799	0.041835	2.226625
ENSG00000236796	24.50437	-0.55575	0.153253	-3.62638	0.000287	0.041851	0.798279
ENSG00000158578	35.11793	-0.87797	0.250696	-3.50214	0.000462	0.042003	1.269879
ENSG00000198574	73.27962	0.635186	0.183183	3.467487	0.000525	0.042003	1.445883
ENSG00000231193	6.608506	-0.8149	0.218277	-3.7333	0.000189	0.042339	0.514262
ENSG00000115112	187.5358	-0.70128	0.201406	-3.48192	0.000498	0.042339	1.351128
ENSG00000088543	799.6962	-0.24279	0.069417	-3.49753	0.00047	0.042482	1.26296
ENSG00000003400	140.941	-0.35824	0.103485	-3.4618	0.000537	0.042482	1.445883
ENSG00000196335	79.50753	-0.42042	0.125889	-3.33959	0.000839	0.042931	2.226625
ENSG00000285549	9.012423	0.565697	0.152707	3.704462	0.000212	0.043248	0.551111
ENSG00000189431	31.64362	-0.61607	0.174383	-3.53285	0.000411	0.043248	1.07387
ENSG00000172554	63.03614	-0.52115	0.150037	-3.47346	0.000514	0.043248	1.347187
ENSG00000219607	197.9717	-0.4158	0.120482	-3.45116	0.000558	0.043248	1.445883
ENSG00000132530	240.9373	-0.34699	0.102861	-3.37335	0.000743	0.043248	1.931656
ENSG00000278291	138.3737	-0.30418	0.091254	-3.33334	0.000858	0.043248	2.226625

ENSG00000255052	665.1259	0.438941	0.127423	3.444764	0.000572	0.043553	1.466075
ENSG00000099995	2777.045	-0.16922	0.048586	-3.4829	0.000496	0.04365	1.262783
ENSG00000100342	137.2116	-0.43382	0.130416	-3.32643	0.00088	0.04365	2.226625
ENSG00000287225	120.5658	-0.39861	0.120148	-3.31763	0.000908	0.04365	2.309341
ENSG00000146374	137.1924	0.486791	0.146775	3.31658	0.000911	0.04365	2.309341
ENSG00000249119	11.70589	-1.30715	0.357513	-3.65624	0.000256	0.043724	0.64362
ENSG00000111331	492.6771	-0.34892	0.101363	-3.44232	0.000577	0.043724	1.445883
ENSG00000134321	215.8309	-0.31697	0.094249	-3.3631	0.000771	0.043724	1.931656
ENSG00000229921	26.97223	1.057625	0.303246	3.487674	0.000487	0.043739	1.217444
ENSG00000144026	1230.21	0.232783	0.06718	3.465047	0.00053	0.043925	1.315447
ENSG00000162692	82.66317	-0.74618	0.215288	-3.46594	0.000528	0.044188	1.299739
ENSG00000286695	87.23677	0.530285	0.158269	3.350538	0.000807	0.045263	1.931656
ENSG00000109794	645.0499	-0.22677	0.066205	-3.4252	0.000614	0.045304	1.466075
ENSG00000255503	19.52915	0.477414	0.133143	3.585729	0.000336	0.045402	0.798279
ENSG00000251639	6.375982	0.73175	0.196774	3.718733	0.0002	0.045484	0.469722
ENSG00000271646	72.7062	-0.38465	0.111673	-3.44443	0.000572	0.045484	1.351128
ENSG00000164104	661.6875	-0.26668	0.077855	-3.42538	0.000614	0.045484	1.445883
ENSG00000183798	198.0727	-0.39447	0.119352	-3.30512	0.000949	0.045484	2.226625
ENSG00000203435	43.86957	-0.41377	0.118767	-3.4839	0.000494	0.045604	1.152902
ENSG00000287876	5.840832	1.459035	0.382149	3.817969	0.000135	0.045795	0.311788
ENSG00000005882	1215.111	-0.2091	0.060833	-3.43725	0.000588	0.046032	1.351128
ENSG00000140545	1012.628	-0.36957	0.108151	-3.41714	0.000633	0.046157	1.445883
ENSG00000196605	685.5106	0.168638	0.049412	3.412903	0.000643	0.046157	1.466075
ENSG00000244155	1.444926	-1.561	0.412647	-3.7829	0.000155	0.046237	0.351128
ENSG00000151623	2563.873	-0.20121	0.058321	-3.44997	0.000561	0.046237	1.270767
ENSG00000233013	4.54267	0.981193	0.25959	3.779785	0.000157	0.046456	0.351128
ENSG00000244731	246.4866	0.768251	0.225191	3.411559	0.000646	0.046456	1.445883
ENSG00000271714	108.485	-0.26607	0.079848	-3.33227	0.000861	0.046456	1.931656
ENSG00000271287	2.845935	7.209205	1.730007	4.167153	3.08E-05	0.046597	0.06861
ENSG00000287347	35.65952	0.455621	0.129971	3.505567	0.000456	0.047194	0.998163
ENSG00000182141	2613.924	0.352603	0.10366	3.401533	0.00067	0.047792	1.445883
ENSG00000215154	182.7251	-0.27851	0.085222	-3.26809	0.001083	0.048227	2.309341
ENSG00000174640	143.0272	-0.44708	0.136962	-3.26428	0.001097	0.048755	2.309341
ENSG00000091986	507.2881	0.412469	0.12606	3.272011	0.001068	0.049079	2.226625
ENSG00000164694	10.20439	-0.7918	0.219679	-3.60435	0.000313	0.0492	0.64362
ENSG00000280079	24.92972	0.411046	0.115853	3.547991	0.000388	0.0492	0.798279
ENSG00000226490	19.15065	-0.66838	0.194454	-3.43719	0.000588	0.0492	1.217444
ENSG00000072210	3174.636	0.210905	0.061596	3.424017	0.000617	0.0492	1.262783
ENSG00000165959	4026.907	0.422124	0.123295	3.423682	0.000618	0.0492	1.262783
ENSG00000287593	44.44002	0.581016	0.169787	3.422034	0.000622	0.0492	1.280812
ENSG00000255020	53.56483	-0.40827	0.119867	-3.406	0.000659	0.0492	1.347187
ENSG00000270966	13.0287	-0.43829	0.121719	-3.60085	0.000317	0.049302	0.64362
ENSG00000003989	1929.228	0.557115	0.162869	3.420629	0.000625	0.049302	1.270767

Table A16. Differential gene expression results of the 402 identified significant genes in TargetALS (112 cases and 20 controls) using DESeq2.

#	Term Name	Term Size	p-value	adjusted p-value (FDR)	Intersection Size	Intersection Gene Names
1	Protein folding_Folding in normal condition	119	3.774E-06	4.667E-04	18	HSP90, Alpha crystallin B, HSP70, HSPA4, Aha1, TCP1-theta, VBP-1, PPID, TCP1-delta, HSP90 beta, TCP1-eta, Calcineurin A (catalytic), Hdj-2, DNAJA2, HSC70, Calcineurin A (beta), TCP1-alpha, TCP1-epsilon
2	Neurophysiological process_Transmission of nerve impulse	213	6.101E-06	4.667E-04	25	PRKAR2B, GABA-A receptor alpha-1 subunit, PKC-beta, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, CaMK IV, GLRA, GABA-A receptor beta-2 subunit, Galpha(i)-specific metabotropic glutamate GPCRs, GlyRA2, cPKC (conventional), Serotonin receptor, PKA-reg (cAMP-dependent), GRM6, Galpha(i)-specific amine GPCRs, GABA-A receptor alpha-5 subunit, Glycine receptor, GABA-A receptor alpha-3 subunit, Glycine receptor beta chain, Kv4.2 channel, Calmodulin, ERK1/2, HTR2A, ERK2 (MAPK1), PRKAR1A
3	Signal transduction_Neuropeptide signaling pathways	156	4.897E-05	2.497E-03	19	NPY, PAM, NPFF receptor 2, MC4R, Substance P extracellular region, GPR124, Galpha(i)-specific peptide GPCRs, CRH receptor 2, Secretogranin V, PKA-reg (cAMP-dependent), Substance P, Galpha(q)-specific peptide GPCRs, PKD1L1, Calmodulin, ERK1/2, SSTR2, ERK2 (MAPK1), SSTR1, Galpha(s)-specific peptide GPCRs
4	Cytoskeleton_Regulation of cytoskeleton rearrangement	183	1.447E-04	3.724E-03	20	Tubulin alpha 1A, MELC, 14-3-3 beta/alpha, G-protein beta/gamma, ECT2, Galpha(i)-specific amine GPCRs, Protein kinase G1, Calponin-1, Zeta-sarcoglycan, Destrin, CAPZA, Tubulin alpha, MRLC, ERK1/2, PKC, Protein kinase G, ERK2 (MAPK1), ARP3, 14-3-3, 14-3-3 eta
5	Reproduction_Gonadotropin regulation	199	1.630E-04	3.724E-03	21	GABA-A receptor alpha-1 subunit, PKC-beta, G-protein beta/gamma, GABA-A receptor beta-2 subunit, Galpha(i)-specific metabotropic glutamate GPCRs, EGF, GABA-A receptor alpha-4 subunit, PKA-reg (cAMP-dependent), Protein kinase G1, GABA-A receptor alpha-5 subunit, GABA-A receptor alpha-3 subunit, PKC-beta2, G-protein gamma 3, Protein kinase G 2, PKC-beta1, Calmodulin, ERK1/2, Guanylate Cyclase 1, soluble, Protein kinase G, MEK4(MAP2K4), PI3K reg class IA
6	Development_Neurogenesis_Axonal guidance	229	1.691E-04	3.724E-03	23	Semaphorin 3C, NckAP1, MELC, Ephrin-A receptor 5, Semaphorin 5A, Ephrin-A receptor 4, Semaphorin 3E, cPKC (conventional), PKA-reg (cAMP-dependent), PP1-cat, Ephrin-A receptors, CDK5, Selenoprotein P, Calcineurin A (catalytic), ENC1, Calmodulin, Calcyclin, Syntenin 1, ERK1/2, Mindin, Guanine deaminase, PI3K reg class IA, 14-3-3 eta

7	Muscle contraction	171	1.704E-04	3.724E-03	19	Alpha crystallin B, Smooth muscle myosin, MELC, HCN2, Galpha(i)-specific peptide GPCRs, CaMK IV, Myotrophin, cPKC (conventional), Galpha(q)-specific amine GPCRs, NCX1, Protein kinase G1, Calponin-1, Galpha(q)-specific peptide GPCRs, PP2A catalytic, MRLC, Calmodulin, PKC, Guanylate Cyclase 1, soluble, Protein kinase G
8	Reproduction_GnRH signaling pathway	166	3.416E-04	6.534E-03	18	GABA-A receptor alpha-1 subunit, PKC-beta, G-protein beta/gamma, GABA-A receptor beta-2 subunit, Galpha(i)-specific metabotropic glutamate GPCRs, EGF, GABA-A receptor alpha-4 subunit, PKA-reg (cAMP-dependent), Protein kinase G1, GABA-A receptor alpha-5 subunit, GABA-A receptor alpha-3 subunit, PKC-beta2, Protein kinase G 2, Calmodulin, ERK1/2, Guanylate Cyclase 1, soluble, Protein kinase G, PI3K reg class IA
9	Development_Blood vessel morphogenesis	227	9.665E-04	1.586E-02	21	Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, APJ, Endothelin-1, PDE, Galpha(i)-specific peptide GPCRs, Galpha(q)-specific nucleotide-like GPCRs, CRH receptor 2, EGF, DLL4, Galpha(q)-specific amine GPCRs, Galpha(i)-specific amine GPCRs, Protein kinase G1, Galpha(q)-specific peptide GPCRs, CEACAM1, Galpha(s)-specific CRF GPCRs, ERK1/2, Protein kinase G, ERK2 (MAPK1), MEK4(MAP2K4), PI3K reg class IA
10	Muscle contraction_Nitric oxide signaling in the cardiovascular system	124	1.036E-03	1.586E-02	14	HSP90, Endothelin-1, G-protein beta/gamma, PKA-reg type II (cAMP-dependent), PKA-reg (cAMP-dependent), PP1-cat, Protein kinase G1, Calcineurin A (catalytic), PP2A catalytic, PDE4A, Calmodulin, Guanylate Cyclase 1, soluble, MEF2C, PI3K reg class IA
11	Neurophysiological process_GABAergic neurotransmission	140	1.193E-03	1.660E-02	15	GLSK, GAD1, ALDR, Synaptotagmin I, GABA-A receptor alpha-1 subunit, G-protein beta/gamma, P/Q-type calcium channel alpha-1A subunit, NSF, GABA-A receptor beta-2 subunit, PP1-cat, Clathrin heavy chain, MDH1, Calmodulin, AATC, GAD2
12	Development_Melanocyte development and pigmentation	50	1.368E-03	1.744E-02	8	MGF, PKC-beta, PKA-reg (cAMP-dependent), Protein kinase G1, Guanylate cyclase (alpha-1/beta-1), ERK1/2, PI3K reg class IA, Galpha(s)-specific peptide GPCRs
13	Translation_Regulation of initiation	127	3.730E-03	4.390E-02	13	PP2A cat (alpha), PP1-cat gamma, EGF, PP1-cat, PP2A catalytic, eIF4A, eIF2S1, RHEB2, ERK1/2, PI3K reg class IA (p55-gamma), ERK2 (MAPK1), MEK4(MAP2K4), PI3K reg class IA
14	Signal transduction_Oxytocin signaling	86	4.272E-03	4.647E-02	10	PKC-beta, G-protein beta/gamma, cPKC (conventional), Protein kinase G1, PP2A catalytic, Calmodulin, ERK1/2, PKC, Guanylate Cyclase 1, soluble, MEF2C
15	Reproduction_Male sex differentiation	241	4.556E-03	4.647E-02	20	Cadherin 8, PTCH2, HSP70, PKC-beta, PAFAH gamma, EGF, BMPR1A, PKA-reg (cAMP-dependent), HMDH, Clathrin heavy chain, Histone H2, Histone H2A, Selenoprotein P, NCOA4 (ARA70), Patched, Calmodulin, ERK1/2, PKC, Ran, TCP1-alpha

16	Reproduction_Feeding and Neurohormone signaling	210	4.994E-03	4.775E-02	18	PAM, IRF1, Endothelin-1, MGF, HSP70, Substance P extracellular region, Galpha(q)-specific Class A Orphan/other GPCRs, G-protein beta/gamma, Galpha(i)-specific peptide GPCRs, PKA-reg (cAMP-dependent), Substance P, CDK5, Galpha(q)-specific peptide GPCRs, PP2A catalytic, Galpha(s)-specific CRF GPCRs, RHEB2, Calmodulin, PI3K reg class IA
17	Signal Transduction_Cholecystokinin signaling	106	6.672E-03	5.671E-02	11	PKC-beta, G-protein beta/gamma, Galpha(i)-specific peptide GPCRs, Pro-CCK, M-Ras, PKA-reg (cAMP-dependent), PKC-beta2, Galpha(q)-specific peptide GPCRs, Calmodulin, ERK1/2, ERK2 (MAPK1)
18	Cell cycle_Meiosis	106	6.672E-03	5.671E-02	11	HSP70, 14-3-3 beta/alpha, EGF, PP1-cat, Tubulin alpha, PP2A catalytic, STAG3, Securin, PI3K reg class IA, 14-3-3, 14-3-3 eta
19	Transport_Calcium transport	192	1.025E-02	8.258E-02	16	HPCA, Pannexin-1, Synaptotagmin I, TRPC5, PKC-beta, P/Q-type calcium channel alpha-1A subunit, TRPV1, cPKC (conventional), TRPC4, PMCA1, NCX1, Calcineurin A (catalytic), MPTP complex, Calmodulin, SAP102, CALB1
20	Cell cycle_G1-S Growth factor regulation	195	1.179E-02	9.021E-02	16	PP2A cat (alpha), IRF1, Activin A, PKC-beta, EGF, cPKC (conventional), Activin beta A, MEK4/7, PP2A catalytic, Activin, ERK1/2, PI3K reg class IA (p55-gamma), PKC, ERK2 (MAPK1), MEK4(MAP2K4), PI3K reg class IA
21	Protein folding_Protein folding nucleus	58	1.305E-02	9.213E-02	7	HSP90, HSP70, HSPA4, Calcineurin A (catalytic), HSC70, Calcineurin A (beta), Glutaredoxin 1
22	Protein folding_Response to unfolded proteins	72	1.325E-02	9.213E-02	8	HSP90, HSP70, HSPA4, HSP90 beta, Hdj-2, Glutaredoxin, HSC70, Glutaredoxin 1
23	Neurophysiological process_Corticoliberin signaling	49	1.964E-02	1.306E-01	6	G-protein beta/gamma, CRH receptor 2, cPKC (conventional), PKA-reg (cAMP-dependent), Calmodulin, ERK2 (MAPK1)
24	Apoptosis_Apoptotic mitochondria	79	2.220E-02	1.415E-01	8	HSP70, VDAC 1, Glutaredoxin, ERK2 (MAPK1), MAP1, 14-3-3, 14-3-3 eta, Glutaredoxin 1
25	Neurophysiological process_Long-term potentiation	82	2.711E-02	1.659E-01	8	CaMK IV, PKA-reg (cAMP-dependent), Protein kinase G 2, Calmodulin, ERK1/2, Guanylate Cyclase 1, soluble, Protein kinase G, ERK2 (MAPK1)
26	Cell cycle_G2-M	206	3.755E-02	2.210E-01	15	Cyclin G, 14-3-3 beta/alpha, TCP1-theta, EGF, TCP1-delta, TCP1-eta, Nek8, Cyclin G1, MRLC, Securin, ERK1/2, TCP1-alpha, TCP1-epsilon, 14-3-3, 14-3-3 eta
27	Reproduction_Spermatogenesis, motility and copulation	230	4.614E-02	2.615E-01	16	HSP70, Tcfl5, ODF3, PKC-beta, G-protein beta/gamma, EGF, BMPR1A, PKA-reg (cAMP-dependent), HMDH, Histone H2, Histone H2A, NCOA4 (ARA70), Hdj-2, Calmodulin, PKC, Ran

28	Neurophysiological process_Circadian rhythm	76	4.886E-02	2.670E-01	7	REV-ERBalpha, cPKC (conventional), PKA-reg (cAMP-dependent), Protein kinase G 2, Calmodulin, ERK1/2, Guanylate Cyclase 1, soluble
29	Response to hypoxia and oxidative stress	161	5.099E-02	2.690E-01	12	Peroxiredoxin, PRDX3, Thioredoxin, PRDX1, TXNRD1, HSP90 beta, Selenoprotein P, Glutaredoxin, ERK2 (MAPK1), MEK4(MAP2K4), SOD1, Glutaredoxin 1
30	Reproduction_Progesterone signaling	216	5.308E-02	2.707E-01	15	GABA-A receptor alpha-1 subunit, GABA-A receptor beta-2 subunit, EGF, GABA-A receptor alpha-4 subunit, PKA-reg (cAMP-dependent), GABA-A receptor alpha-5 subunit, GABA-A receptor alpha-3 subunit, Galpha(q)-specific peptide GPCRs, DLC1 (Dynein LC8a), Calmodulin, PGRMC1, CLIC4, ERK2 (MAPK1), TFIIB, PI3K reg class IA
31	Apoptosis_Anti-Apoptosis mediated by external signals by Estrogen	95	5.700E-02	2.813E-01	8	Thioredoxin, G-protein beta/gamma, Protein kinase G1, ERK1/2, Guanylate Cyclase 1, soluble, MEK4(MAP2K4), SOD1, PI3K reg class IA
32	Muscle contraction_Relaxin signaling	82	6.827E-02	3.264E-01	7	Endothelin-1, G-protein beta/gamma, PKA-reg (cAMP-dependent), Protein kinase G1, PDE4A, ERK1/2, Guanylate Cyclase 1, soluble
33	Signal transduction_WNT signaling	176	8.682E-02	3.795E-01	12	PP2A cat (alpha), PKC-beta, EGF, PKA-reg type II (cAMP-dependent), PKA-reg (cAMP-dependent), PKC-beta2, Calcineurin A (catalytic), PP2A catalytic, Calmodulin, CaMK II delta, Calcineurin A (beta), MEK4(MAP2K4)
34	Cell adhesion_Synaptic contact	176	8.682E-02	3.795E-01	12	Synaptotagmin I, Synaptotagmin, CNTN1 (F3), GABA-A receptor alpha-1 subunit, GABA-A receptor beta-2 subunit, GABA-A receptor alpha-4 subunit, GABA-A receptor alpha-5 subunit, GABA-A receptor alpha-3 subunit, Syntenin 1, CaMK II delta, SAP102, 14-3-3 eta
35	Cytoskeleton_Actin filaments	176	8.682E-02	3.795E-01	12	MELC, Protein kinase G1, Calponin-1, Zeta-sarcoglycan, Destrin, CAPZA, MRLC, ERK1/2, Protein kinase G, ERK2 (MAPK1), Nephrocystin-4, ARP3
36	Development_Skeletal muscle development	144	1.019E-01	3.929E-01	10	Alpha crystallin B, Smooth muscle myosin, MELC, CaMK IV, Elastin, Myotrophin, MEF2, MRLC, Calmodulin, MEF2C
37	Transport_Manganese transport	108	1.023E-01	3.929E-01	8	PP2A cat (alpha), ARG2, PPM1E, TRPC5, TRPC4, NCX1, IDI1, PRNP
38	Cell adhesion_Cadherins	182	1.047E-01	3.929E-01	12	Cadherin 8, PKC-beta, DKK2, WIF1, PP1-cat, Vinexin, PKC-beta2, PP2A catalytic, PKC-beta1, PKC, K-cadherin (CDH6), DKK1
39	Cytoskeleton_Spindle microtubules	109	1.064E-01	3.929E-01	8	Tubulin alpha 1A, Importin (karyopherin)-alpha, Karyopherin alpha 2, Tubulin alpha, DLC1 (Dynein LC8a), Securin, Ran, TCP1-alpha

40	Proliferation_Positive regulation cell proliferation	221	1.077E-01	3.929E-01	14	Endothelin-1, MGF, Galpha(i)-specific peptide GPCRs, MTG16 (CBFA2T3), EGF, Serotonin receptor, PKA-reg (cAMP-dependent), Galpha(i)-specific amine GPCRs, MRLC, ERK1/2, ERK2 (MAPK1), MEK4(MAP2K4), PRKAR1A, PI3K reg class IA
41	Development_Regulation of angiogenesis	221	1.077E-01	3.929E-01	14	Angiopoietin 1, Endothelin-1, Galpha(i)-specific peptide GPCRs, Semaphorin 5A, Ephrin-A receptor 4, HMDH, Ephrin-A receptors, Galpha(q)-specific peptide GPCRs, Patched, CEACAM1, ERK1/2, PKC, ERK2 (MAPK1), PI3K reg class IA
42	Proliferation_Negative regulation of cell proliferation	183	1.079E-01	3.929E-01	12	CNOT7, CDC18L (CDC6), Tcfl5, G-protein beta/gamma, Galpha(i)-specific peptide GPCRs, Securin, ERK1/2, SSTR2, Guanylate Cyclase 1, soluble, ERK2 (MAPK1), SSTR1, SAP102
43	Cardiac development_Wnt_beta-catenin, Notch, VEGF, IP3 and integrin signaling	151	1.280E-01	4.556E-01	10	Semaphorin 3C, G-protein beta/gamma, DLL4, Calcineurin A (catalytic), MEF2, Kv4.2 channel, Calmodulin, MEF2C, Calcineurin A (beta), DKK1
44	Protein folding_ER and cytoplasm	45	1.344E-01	4.675E-01	4	HSP90, HSP70, Glutaredoxin, HSC70
45	Signal transduction_CREM pathway	98	1.395E-01	4.696E-01	7	ODF3, CaMK IV, EGF, CREB4, PKA-reg (cAMP-dependent), ERK1/2, ERK2 (MAPK1)
46	Cell adhesion_Attractive and repulsive receptors	174	1.439E-01	4.696E-01	11	Semaphorin 3C, Ephrin-A receptor 5, Semaphorin 5A, Ephrin-A receptor 4, Semaphorin 3E, Ephrin-A receptors, CDK5, Destrin, ERK1/2, PI3K reg class IA (p55-gamma), PI3K reg class IA
47	Development_Hemopoiesis, Erythropoietin pathway	136	1.442E-01	4.696E-01	9	PAK3, MGF, G-protein beta/gamma, PKC-beta2, Calmodulin, ERK1/2, PI3K reg class IA (p55-gamma), ERK2 (MAPK1), PI3K reg class IA
48	Inflammation_Histamine signaling	215	1.519E-01	4.842E-01	13	Guanylate cyclase, Guanylate cyclase alpha, GUCY1B1, G-protein beta/gamma, PKA-reg (cAMP-dependent), GUCY1A3, Guanylate cyclase beta, Calcineurin A (catalytic), Calmodulin, ERK1/2, CaMK II delta, Guanylate Cyclase 1, soluble, ERK2 (MAPK1)
49	Development_Neurogenesis_Synaptogenesis	178	1.603E-01	5.005E-01	11	Synaptotagmin I, Synaptotagmin, TRPC5, KIS, P/Q-type calcium channel alpha-1A subunit, NSF, SYP, Calmodulin, Endophilin A1, SAP102, 14-3-3 eta
50	Inflammation_MIF signaling	141	1.679E-01	5.133E-01	9	PRDX1, G-protein beta/gamma, PKA-reg (cAMP-dependent), CDK5, PP2A catalytic, Galpha(s)-specific CRF GPCRs, ERK1/2, PKC, ERK2 (MAPK1)

Table A17. Top 50 KCL BrainBank Process Networks enrichments with MetaCore. Term size refers to the number of genes in the term, with the intersection size denoting the number of genes in the dataset found in the term.

#	Term Name	Term Size	p-value	adjusted p-value (FDR)	Intersection Size	Intersection Gene Names
1	Signal transduction_Neuropeptide signaling pathways	139	1.458E-16	1.618E-14	25	CLIP, ACTH, alpha-MSH, beta-Endorphin, Galpha(s)-specific calcitonin GPCRs, MC4R, Galpha(q)-specific peptide GPCRs, proACTH, POMC, Joining peptide (JP), N-POMC, gamma-MSH, N-POC, beta-LPH, Galpha(i)-specific peptide GPCRs, Calcitonin receptor, gamma-LPH, ACTH 1-17, DA-alphaMSH, gamma2-MSH, gamma3-MSH, Galpha(s)-specific peptide GPCRs, AGRP, beta-MSH, CART
2	Development_Blood vessel morphogenesis	208	6.720E-04	3.730E-02	13	Angiopoietin 1, APJ, Neuropilin-2, VCAM1, HIF-prolyl hydroxylase, Galpha(q)-specific peptide GPCRs, PLAT (TPA), Galpha(i)-specific peptide GPCRs, S1P1 receptor, Lactoferrin, Galpha(q)-specific nucleotide-like GPCRs, Galpha(i)-specific EDG GPCRs, EGF
3	Reproduction_Progesterone signaling	187	8.481E-03	2.490E-01	10	HGF, PLA2, Galpha(s)-specific calcitonin GPCRs, Galpha(q)-specific peptide GPCRs, PLC-delta, EGF, PR (membrane), Oct-2, WNT, PR (nuclear)
4	Inflammation_Interferon signaling	106	9.021E-03	2.490E-01	7	MxB, ILT4, IFI27, I-TAC, Apo-2L(TNFSF10), MxA, IFI44
5	Reproduction_Spermatogenesis, motility and copulation	195	1.122E-02	2.490E-01	10	Histone H2, Histone H2A, SPAG6, MFGE8, Galpha(s)-specific calcitonin GPCRs, Connexin 26, Calcitonin receptor, EGF, SOX3, Oct-2
6	Transport_Sodium transport	153	2.024E-02	3.744E-01	8	SLC6A11, ASCT1 (SLC1A4), NCKX3, SLC13A5, GLVR1, SLC4A4, Aquaporin 1, SLC12A1
7	Transport_Bile acids transport and its regulation	33	3.611E-02	5.146E-01	3	HYEP, L-FABP, LRH1
8	Inflammation_NK cell cytotoxicity	141	3.709E-02	5.146E-01	7	Caspase-10, EAT-2, Histone H2B, HMGB2, Perforin, Apo-2L(TNFSF10), HLAC
9	Inflammation_Complement system	60	4.379E-02	5.401E-01	4	C4, Ficolin, C4a, C4b
10	Development_Melanocyte development and pigmentation	39	5.498E-02	5.908E-01	3	ACTH, alpha-MSH, Galpha(s)-specific peptide GPCRs

11	Immune response_Innate immune response to RNA viral infection	66	5.855E-02	5.908E-01	4	Caspase-10, I-TAC, 2'-5'-oligoadenylate synthetase, MxA
12	Signal transduction_ESR1-nuclear pathway	204	8.375E-02	7.747E-01	8	HMG1,2, APJ, LRH1, Lactoferrin, SUPT6H, EGF, MTA2, PR (nuclear)
13	Inflammation_Histamine signaling	167	1.672E-01	9.915E-01	6	HDC, Kappa chain (Ig light chain), VCAM1, PLA2, IGHG1, PLA2G5
14	Development_Neurogenesis in general	180	2.111E-01	9.915E-01	6	LHX1, SIX3, POU class III, SOX3, WNT, Midkine
15	Transcription_Nuclear receptors transcriptional regulation	181	2.147E-01	9.915E-01	6	HMG1,2, HMGB2, EGF, RXR, RXRG, PR (nuclear)
16	Signal transduction_ESR1-membrane pathway	77	2.447E-01	9.915E-01	3	EGF, PR (membrane), PR (nuclear)
17	Apoptosis_Apoptotic nucleus	155	2.620E-01	9.915E-01	5	Caspase-10, Histone H2B, HMGB2, Perforin, Proline oxidase 1
18	Cell adhesion_Cell-matrix interactions	195	2.663E-01	9.915E-01	6	CD44, CD44 soluble, CD44 (ICD), Neurocan, Biglycan, CD44 (EXT)
19	Apoptosis_Death Domain receptors & caspases in apoptosis	118	2.675E-01	9.915E-01	4	A20, Caspase-10, Apo-2L(TNFSF10), NALP3
20	Immune response_BCR pathway	118	2.675E-01	9.915E-01	4	Kappa chain (Ig light chain), IGHG1, Fc gamma RII beta, Oct-2
21	Blood coagulation	82	2.748E-01	9.915E-01	3	PLAT (TPA), Galpha(q)-specific nucleotide-like GPCRs, P2Y1
22	Cell adhesion_Leucocyte chemotaxis	158	2.748E-01	9.915E-01	5	Tubulin beta, VCAM1, Galpha(q)-specific peptide GPCRs, Galpha(i)-specific peptide GPCRs, I-TAC
23	Transport_Iron transport	85	2.931E-01	9.915E-01	3	HIF-prolyl hydroxylase, EGLN3, Lactoferrin
24	Transcription_Chromatin modification	124	2.975E-01	9.915E-01	4	Histone H2, Histone H2A, Histone H2B, MTA2

25	Cell adhesion_Platelet-endothelium-leucocyte interactions	166	3.096E-01	9.915E-01	5	HGF, VCAM1, CD44, PLAT (TPA), EGF
26	Chemotaxis	128	3.177E-01	9.915E-01	4	CD44, Galpha(q)-specific peptide GPCRs, Galpha(i)-specific peptide GPCRs, I-TAC
27	Inflammation_Protein C signaling	93	3.421E-01	9.915E-01	3	PLAT (TPA), S1P1 receptor, Galpha(i)-specific EDG GPCRs
28	Reproduction_Male sex differentiation	220	3.646E-01	9.915E-01	6	Histone H2, HGF, Histone H2A, Connexin 26, EGF, SOX3
29	Signal transduction_Androgen receptor signaling cross-talk	61	3.951E-01	9.915E-01	2	EGF, WNT
30	Response to hypoxia and oxidative stress	105	4.150E-01	9.915E-01	3	HIF-prolyl hydroxylase, GSTM3, SOD3 (EC-SOD)
31	Reproduction_Feeding and Neurohormone signaling	194	4.340E-01	9.915E-01	5	CD44, Galpha(q)-specific peptide GPCRs, POMC, Galpha(i)-specific peptide GPCRs, PEA3
32	Cytoskeleton_Macropinocytosis and its regulation	70	4.641E-01	9.915E-01	2	HGF, EGF
33	Muscle contraction	157	4.642E-01	9.915E-01	4	Galpha(q)-specific peptide GPCRs, Galpha(i)-specific peptide GPCRs, Dystroglycan, ACES
34	Development_Regulation of angiogenesis	202	4.691E-01	9.915E-01	5	Angiopoietin 1, Galpha(q)-specific peptide GPCRs, Biglycan, Galpha(i)-specific peptide GPCRs, PLC-delta
35	Transport_Potassium transport	161	4.837E-01	9.915E-01	4	KCNE4, NCKX3, Aquaporin 1, SLC12A1
36	Cytoskeleton_Intermediate filaments	74	4.933E-01	9.915E-01	2	Tubulin beta, GFAP
37	Proteolysis_ECM remodeling	75	5.004E-01	9.915E-01	2	Cystatin C, PLAT (TPA)

38	Proteolysis_Proteolysis in cell cycle and apoptosis	120	5.022E-01	9.915E-01	3	A20, Caspase-10, APH-1A
39	Signal transduction_WNT signaling	168	5.173E-01	9.915E-01	4	CD44, WNT7B, EGF, WNT
40	Cell adhesion_Platelet aggregation	125	5.298E-01	9.915E-01	3	PLA2, SLC21A2, P2Y1
41	Development_Neurogenesis_Synaptogenesis	175	5.498E-01	9.915E-01	4	Syntrophin gamma 2, Dystroglycan, ACES, WNT
42	Development_Neuromuscular junction	131	5.618E-01	9.915E-01	3	P2Y1, Dystroglycan, ACES
43	Cardiac development_Wnt_beta-catenin, Notch, VEGF, IP3 and integrin signaling	133	5.722E-01	9.915E-01	3	Neuropilin-2, Galpha(s)-specific calcitonin GPCRs, WNT
44	Cell adhesion_Amyloid proteins	180	5.724E-01	9.915E-01	4	WNT7B, CD147, ACES, WNT
45	Signal transduction_Leptin signaling	87	5.809E-01	9.915E-01	2	POMC, CPT-1A
46	Signal transduction_CREM pathway	87	5.809E-01	9.915E-01	2	PLAT (TPA), EGF
47	Neurophysiological process_Corticoliberin signaling	39	5.852E-01	9.915E-01	1	POMC
48	Signal Transduction_BMP and GDF signaling	88	5.872E-01	9.915E-01	2	CD44, PRSS11 (HtrA1)
49	Signal Transduction_Cholecystokinin signaling	93	6.175E-01	9.915E-01	2	Galpha(q)-specific peptide GPCRs, Galpha(i)-specific peptide GPCRs
50	Inflammation_Innate inflammatory response	144	6.265E-01	9.915E-01	3	PLA2, C4, I-TAC

Table A18. Top 50 TargetALS Process Networks enrichments with MetaCore. Term size refers to the number of genes in the term, with the intersection size denoting the number of genes in the dataset found in the term.

#	Term Name	Term Size	p-value	adjusted p-value (FDR)	Intersection Size	Intersection Gene Names
1	Heredodegenerative Disorders, Nervous System	3074	5.958E-31	1.301E-27	215	PLP1, NPY, PRPS1, HSP90, PAK3, Galpha(s)-specific nucleotide-like GPCRs, Alpha crystallin B, G3BP2, ILDR2, MAL2, COX VIc, GAD1, MEGF10, THAP11, PTCH2, ELOVL5, Peroxiredoxin, Esterase D, Neuropeptide K, PSMB5, T-plastin, BRSK2, UQCRQPC, DYNLT3, G-protein beta, UQCRH, NDUFAB1, CCK8-Gly, NckAP1, NDUFA1, MGF, PDH E2 subunit N6-lipoyllysine, MELC, NDUFB4, NDUFA8, Synaptotagmin I, HSP70, Substance P extracellular region, CNR1, Synaptotagmin IV, Synaptotagmin, PRDX3, Thioredoxin, NDUFA4, PDE, Cystatin C, PPT1, SCF, SDHB, ANKRD36B, NCKP1 subunit, CCK8, TPH2, Neuropeptide gamma, RAB39B, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, Kv3.3, ORP-family, TRPC5, PKC-beta, TCP1-theta, PRDX1, G-protein beta/gamma, NDUFB6, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, UQCRB, S100, TXNRD1, ORP8, PIMT, TRPV1, PDK3, ZFHX4, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, NDUFB3, Rab-3, GRAIL, CaMK IV, CHCHD2, GABA-A receptor beta-2 subunit, SYP, Rho GTPase, PDE4, G-protein gamma, Dysferlin, Elastin, EGF, Pro-CCK, SYTC, Dynein, axonemal, heavy chains, cPKC (conventional), NDUFB1, ELOVL4, Serotonin receptor, GABA-A receptor alpha-4 subunit, TRPC, HTR5A, COX VIa, CLCN4, SMRT, NHE6, Neurokinin A, PDLIM2, UQCR10, Clathrin heavy chain, Substance P, Histone H2, CCK5, Galpha(q)-specific amine GPCRs, UQCRFS1, Histone H2A, C9orf5, Galpha(i)-specific amine GPCRs, TRPC4, HCN, RTEL1-TNFRSF6B, HLF, CAP1, MEGF6, NDUFS6, GABA-A receptor alpha-5 subunit, CDK5, PAK, SYT16, Fatty acid-binding protein, HINT, IZUMO1, GABA-A receptor alpha-3 subunit, DYNLT, SPSY, COX Va, CAPZA, PKC-beta2, Calcineurin A (catalytic), TOP1MT, Galpha(i)-specific cannabis GPSRs, sRAGE, SLC25A46, Galpha(q)-specific peptide GPCRs, NDUFA5, Tubulin alpha, Creatine kinase, DSCAML1, Azi1, Patched, TNK1, MEF2, NAPB, HNMT, APRIO, MEK4/7, ACSL4, ATF/CREB, GLGB, ODP2, G-protein gamma 3, LAMP2-C, FN14(TNFRSF12A), G-protein beta-4, Acyl-CoA synthetase, IDI1, SNAPs, LAMP2, COX VIa-1, YPEL5, Kv4.2 channel, PRNP, HSPC138, RHEB2, NKCC1, Malin, PKC-beta1, LOXL2, NME5, Calcyclin, SCOT, Octanoyl-holo-acp, ERK1/2, AATC, NFIC, CaMK II delta, HSC70, PKC, HTR2A, GS1-124K5.11, MEF2C, ERK2 (MAPK1), OAT, MEK4(MAP2K4), CCK8-GlyArgArg, IMPA1, sKITLG, PRPS, SOD1, TFIIB, SAP102, Cyclophilin A, FOXP1/2/4 proteins,

						PI3K reg class IA, Galpha(s)-specific peptide GPCRs, ATP6AP2, CALB1, TCP1-epsilon, NF-I, MRPL3, HXK3, COX VIIa-2, Midkine, 14-3-3, RAGE
2	Huntington Disease	984	8.344E-30	9.107E-27	107	NPY, Galpha(s)-specific nucleotide-like GPCRs, Alpha crystallin B, MAL2, COX VIc, GAD1, Peroxiredoxin, Neuropeptide K, UQCRQPC, UQCRH, NDUFAB1, CCK8-Gly, NDUFA1, NDUFB4, NDUFA8, Synaptotagmin I, Substance P extracellular region, CNR1, Synaptotagmin IV, Synaptotagmin, Thioredoxin, NDUFA4, PDE, SDHB, CCK8, Neuropeptide gamma, GABA-A receptor alpha-1 subunit, ORP-family, TRPC5, PKC-beta, PRDX1, G-protein beta/gamma, NDUFB6, NDUFS4, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, UQCRB, TXNRD1, ORP8, PIMT, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, NDUFB3, Rab-3, CaMK IV, GABA-A receptor beta-2 subunit, SYP, Rho GTPase, PDE4, G-protein gamma, Pro-CCK, cPKC (conventional), NDUFB1, Serotonin receptor, GABA-A receptor alpha-4 subunit, TRPC, HTR5A, COX VIa, Neurokinin A, UQCR10, Clathrin heavy chain, Substance P, Histone H2, CCK5, Galpha(q)-specific amine GPCRs, UQCRFS1, Histone H2A, Galpha(i)-specific amine GPCRs, CAP1, NDUFS6, GABA-A receptor alpha-5 subunit, CDK5, SYT16, GABA-A receptor alpha-3 subunit, COX Va, CAPZA, PKC-beta2, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, Galpha(q)-specific peptide GPCRs, NDUFA5, Tubulin alpha, Creatine kinase, NAPB, HNMT, APRIO, ATF/CREB, SNAPs, COX VIa-1, YPEL5, PRNP, NKCC1, PKC-beta1, SCOT, Octanoyl-holo-acp, CaMK II delta, PKC, HTR2A, OAT, CCK8-GlyArgArg, SOD1, Cyclophilin A, FOXP1/2/4 proteins, CALB1, COX VIIa-2, 14-3-3
3	Chorea	1029	3.633E-28	2.644E-25	107	NPY, Galpha(s)-specific nucleotide-like GPCRs, Alpha crystallin B, MAL2, COX VIc, GAD1, Peroxiredoxin, Neuropeptide K, UQCRQPC, UQCRH, NDUFAB1, CCK8-Gly, NDUFA1, NDUFB4, NDUFA8, Synaptotagmin I, Substance P extracellular region, CNR1, Synaptotagmin IV, Synaptotagmin, Thioredoxin, NDUFA4, PDE, SDHB, CCK8, Neuropeptide gamma, GABA-A receptor alpha-1 subunit, ORP-family, TRPC5, PKC-beta, PRDX1, G-protein beta/gamma, NDUFB6, NDUFS4, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, UQCRB, TXNRD1, ORP8, PIMT, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, NDUFB3, Rab-3, CaMK IV, GABA-A receptor beta-2 subunit, SYP, Rho GTPase, PDE4, G-protein gamma, Pro-CCK, cPKC (conventional), NDUFB1, Serotonin receptor, GABA-A receptor alpha-4 subunit, TRPC, HTR5A, COX VIa, Neurokinin A, UQCR10, Clathrin heavy chain, Substance P, Histone H2, CCK5,

						Galpha(q)-specific amine GPCRs, UQCRFS1, Histone H2A, Galpha(i)-specific amine GPCRs, CAP1, NDUFS6, GABA-A receptor alpha-5 subunit, CDK5, SYT16, GABA-A receptor alpha-3 subunit, COX Va, CAPZA, PKC-beta2, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, Galpha(q)-specific peptide GPCRs, NDUFA5, Tubulin alpha, Creatine kinase, NAPB, HNMT, APRIO, ATF/CREB, SNAPs, COX VIa-1, YPEL5, PRNP, NKCC1, PKC-beta1, SCOT, Octanoyl-holo-acp, CaMK II delta, PKC, HTR2A, OAT, CCK8-GlyArgArg, SOD1, Cyclophilin A, FOXP1/2/4 proteins, CALB1, COX VIIa-2, 14-3-3
4	Basal Ganglia Diseases	2881	1.223E-25	6.673E-23	194	NPY, HSP90, Galpha(s)-specific nucleotide-like GPCRs, Alpha crystallin B, ET-1, G3BP2, ILDR2, MAL2, COX VIc, GAD1, HPCA, ELOVL5, Peroxiredoxin, Esterase D, Endothelin-1, Neuropeptide K, BRSK2, UQCRQPC, ALDR, UQCRH, PSMA5, NDUFAB1, CCK8-Gly, BTBD12, NDUFA1, MGF, NDUFB4, NDUFA8, Synaptotagmin I, HSP70, Substance P extracellular region, CNR1, Synaptotagmin IV, PPM1E, DnaJB9, Synaptotagmin, CNTN1 (F3), Thioredoxin, NDUFA4, HSPA4, PDE, Cystatin C, SCF, SDHB, SLC39A10, DKK3, CCK8, TPH2, Neuropeptide gamma, RAB39B, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, ORP-family, LY6G5B, TRPC5, PKC-beta, PRDX1, G-protein beta/gamma, NDUFB6, SUR, NDUFS4, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, UQCRB, S100, TXNRD1, ORP8, AMIGO2, LASS6, PIMT, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, Aldose reductase, NDUFB3, Rab-3, IDUA, SLC2A13, Semaphorin 5A, NSF, CaMK IV, CHCHD2, GABA-A receptor beta-2 subunit, FBXO2, SYP, Rho GTPase, PDE4, G-protein gamma, Rap1GDS1, Elastin, EGF, Pro-CCK, HIST1H2BN, cPKC (conventional), NDUFB1, AP3S1, Serotonin receptor, GABA-A receptor alpha-4 subunit, TRPC, HTR5A, VDAC 1, COX VIa, Osteopontin, Big ET-1, Lingo1, Neurokinin A, UQCR10, Clathrin heavy chain, Substance P, AP-3 sigma subunits, Histone H2, CCK5, Galpha(q)-specific amine GPCRs, UQCRFS1, Ephrin-A receptors, Histone H2A, C9orf5, Galpha(i)-specific amine GPCRs, DNAJC12, RTEL1-TNFRSF6B, CAP1, NDUFS6, GABA-A receptor alpha-5 subunit, CDK5, PAK, FLJ32001, SYT16, Fatty acid-binding protein, IZUMO1, GABA-A receptor alpha-3 subunit, COX Va, CAPZA, PKC-beta2, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, sRAGE, SLC25A46, Galpha(q)-specific peptide GPCRs, H2AFZ, Histone H2B, NDUFA5, Tubulin alpha, Creatine kinase, B-FABP, MEF2, NAPB, HNMT, APRIO, ATF/CREB, RAI1, LAMP2-C, SNAPs, eIF2S1, Galpha(s)-specific CRF GPCRs, LAMP2, COX VIa-1, YPEL5, PRNP, MPTP complex, NKCC1, HIST2H2BE, PKC-beta1,

						LOXL2, Endophilin A1, Aquaporin 1, NDFIP1, Syntenin 1, SCOT, Octanoyl-holo-acp, ADHX, AATC, CaMK II delta, HSC70, PKC, SUR1, HTR2A, GS1-124K5.11, OAT, CCK8-GlyArgArg, sKITLG, SOD1, GSE1, Cyclophilin A, FOXP1/2/4 proteins, DBH-AS1, Galpha(s)-specific peptide GPCRs, CALB1, GAD2, MRPL3, COX VIIa-2, ARP3, 14-3-3, RAGE, 14-3-3 eta
5	Movement Disorders	2994	5.030E-24	2.196E-21	195	NPY, HSP90, Galpha(s)-specific nucleotide-like GPCRs, Alpha crystallin B, ET-1, G3BP2, ILDR2, MAL2, COX VIc, GAD1, HPCA, ELOVL5, Peroxiredoxin, Esterase D, Endothelin-1, Neuropeptide K, BRSK2, UQCRQPC, ALDR, UQCRH, PSMA5, NDUFAB1, CCK8-Gly, NDUFA1, MGF, NDUFB4, NDUFA8, Synaptotagmin I, HSP70, Substance P extracellular region, CNR1, Synaptotagmin IV, PPM1E, DnaJB9, Synaptotagmin, CNTN1 (F3), Thioredoxin, NDUFA4, HSPA4, Dynein, axonemal, light chains, PDE, Cystatin C, SCF, SDHB, SLC39A10, DKK3, CCK8, TPH2, Neuropeptide gamma, RAB39B, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, ORP-family, LY6G5B, TRPC5, PKC-beta, PRDX1, G-protein beta/gamma, NDUFB6, SUR, NDUFS4, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, UQCRB, S100, TXNRD1, ORP8, AMIGO2, LASS6, PIMT, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, Aldose reductase, NDUFB3, Rab-3, IDUA, SLC2A13, Semaphorin 5A, NSF, CaMK IV, CHCHD2, GABA-A receptor beta-2 subunit, FBXO2, SYP, Rho GTPase, PDE4, G-protein gamma, Elastin, EGF, Pro-CCK, Dynein, axonemal, heavy chains, HIST1H2BN, cPKC (conventional), NDUFB1, AP3S1, Serotonin receptor, GABA-A receptor alpha-4 subunit, TRPC, HTR5A, VDAC 1, COX VIa, Osteopontin, Big ET-1, NHE6, Lingo1, Neurokinin A, UQCR10, Clathrin heavy chain, Substance P, AP-3 sigma subunits, Histone H2, CCK5, Galpha(q)-specific amine GPCRs, UQCRFS1, Ephrin-A receptors, Histone H2A, C9orf5, DOC1, Galpha(i)-specific amine GPCRs, DNAJC12, RTEL1-TNFRSF6B, CAP1, NDUFS6, GABA-A receptor alpha-5 subunit, CDK5, PAK, FLJ32001, SYT16, Fatty acid-binding protein, IZUMO1, GABA-A receptor alpha-3 subunit, COX Va, CAPZA, PKC-beta2, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, sRAGE, SLC25A46, Galpha(q)-specific peptide GPCRs, H2AFZ, Histone H2B, NDUFA5, Tubulin alpha, Creatine kinase, B-FABP, MEF2, NAPB, HNMT, APRIO, ATF/CREB, RAI1, LAMP2-C, SNAPs, eIF2S1, Galpha(s)-specific CRF GPCRs, LAMP2, COX VIa-1, YPEL5, PRNP, MPTP complex, NKCC1, HIST2H2BE, PKC-beta1, LOXL2, Endophilin A1, Aquaporin 1, NDFIP1, Syntenin 1, SCOT, Octanoyl-holo-acp, ADHX, AATC, CaMK II delta, HSC70, PKC, SUR1, HTR2A, GS1-124K5.11, OAT, CCK8-GlyArgArg, sKITLG,

						SOD1, Cyclophilin A, FOXP1/2/4 proteins, DBH-AS1, Galpha(s)-specific peptide GPCRs, CALB1, GAD2, MRPL3, COX VIIa-2, ARP3, 14-3-3, RAGE, 14-3-3 eta
6	Dyskinesias	1854	3.305E-23	1.201E-20	141	NPY, Galpha(s)-specific nucleotide-like GPCRs, Alpha crystallin B, MAL2, COX VIc, GAD1, THAP11, HPCA, ELOVL5, Peroxiredoxin, Neuropeptide K, UQCRQPC, KLHL4, UQCRH, NDUFAB1, CCK8-Gly, NDUFA1, NPFF receptor 2, NDUFB4, NDUFA8, Synaptotagmin I, Substance P extracellular region, CNR1, Glycogen phosphorylase, Synaptotagmin IV, Synaptotagmin, PRDX3, Thioredoxin, NDUFA4, Dynein, axonemal, light chains, PDE, Cystatin C, SDHB, SLC39A10, ANKRD36B, CCK8, TPH2, Neuropeptide gamma, GABA-A receptor alpha-1 subunit, Kv3.3, ORP-family, TRPC5, PKC-beta, PAFAH gamma, PRDX1, G-protein beta/gamma, NDUFB6, NDUFS4, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, UQCRB, TXNRD1, ORP8, PIMT, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, NDUFB3, Rab-3, IP3KA, CaMK IV, GABA-A receptor beta-2 subunit, SYP, Rho GTPase, PDE4, G-protein gamma, Pro-CCK, Dynein, axonemal, heavy chains, cPKC (conventional), NDUFB1, ELOVL4, Serotonin receptor, GABA-A receptor alpha-4 subunit, TRPC, HTR5A, COX VIa, SMRT, NHE6, Neurokinin A, PDLIM2, UQCR10, Clathrin heavy chain, Substance P, Histone H2, CCK5, Galpha(q)-specific amine GPCRs, UQCRFS1, Histone H2A, DOC1, Galpha(i)-specific amine GPCRs, HLF, CAP1, NDUFS6, GABA-A receptor alpha-5 subunit, Zeta-sarcoglycan, CDK5, SYT16, ASAH, GABA-A receptor alpha-3 subunit, COX Va, CAPZA, PKC-beta2, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, SLC25A46, PDH beta, Galpha(q)-specific peptide GPCRs, NDUFA5, Tubulin alpha, Creatine kinase, NAPB, HNMT, APRIO, ATF/CREB, GLGB, LAMP2-C, BMI-1, SNAPs, LAMP2, COX VIa-1, YPEL5, PRNP, NKCC1, PKC-beta1, SCOT, Octanoyl-holo-acp, NFIC, CaMK II delta, PKC, HTR2A, PMM2, OAT, CCK8-GlyArgArg, SOD1, Cyclophilin A, FOXP1/2/4 proteins, CALB1, GAD2, NF-I, COX VIIa-2, 14-3-3
7	Cognition Disorders	1319	3.852E-23	1.201E-20	114	NPY, Galpha(s)-specific nucleotide-like GPCRs, Alpha crystallin B, MAL2, COX VIc, GAD1, Peroxiredoxin, Neuropeptide K, UQCRQPC, UQCRH, NDUFAB1, CCK8-Gly, NDUFA1, NDUFB4, NDUFA8, Synaptotagmin I, Substance P extracellular region, CNR1, Synaptotagmin IV, Synaptotagmin, Thioredoxin, NDUFA4, PDE, Cystatin C, SDHB, CCK8, Neuropeptide gamma, GABA-A receptor alpha-1 subunit, ORP-family, TRPC5, PKC-beta, PRDX1, G-protein beta/gamma, NDUFB6, NDUFS4, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, UQCRB,

						S100, TXNRD1, ORP8, PIMT, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, NDUFB3, Rab-3, CaMK IV, GABA-A receptor beta-2 subunit, SYP, Rho GTPase, PDE4, G-protein gamma, Pro-CCK, cPKC (conventional), NDUFB1, Serotonin receptor, GABA-A receptor alpha-4 subunit, TRPC, HTR5A, COX VIa, Neurokinin A, UQCR10, Clathrin heavy chain, Substance P, Histone H2, CCK5, Galpha(q)-specific amine GPCRs, UQCRFS1, Histone H2A, Galpha(i)-specific amine GPCRs, CAP1, NDUFS6, GABA-A receptor alpha-5 subunit, CDK5, SYT16, Fatty acid-binding protein, GABA-A receptor alpha-3 subunit, COX Va, CAPZA, PKC-beta2, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, sRAGE, Galpha(q)-specific peptide GPCRs, NDUFA5, Tubulin alpha, Creatine kinase, B-FABP, TNK1, NAPB, HNMT, APRIO, ATF/CREB, SNAPs, COX VIa-1, YPEL5, PRNP, NKCC1, PKC-beta1, SCOT, Octanoyl-holo-acp, CaMK II delta, PKC, HTR2A, OAT, CCK8-GlyArgArg, SOD1, Cyclophilin A, FOXP1/2/4 proteins, CALB1, COX VIIa-2, 14-3-3, RAGE
8	Brain Diseases	8447	7.345E-23	2.004E-20	400	PLP1, NPY, FAM3C, PP2A cat (alpha), HSP90, PAM, HMGCLL1, Cadherin 8, NPEPL1, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Alpha crystallin B, ET-1, G3BP2, IRF1, ILDR2, MAL2, GLSK, Rab-3B, COX VIc, GAD1, THAP11, PTCH2, N-chimaerin, Tubulin alpha 1A, HPCA, APJ, ELOVL5, Peroxiredoxin, Activin A, UBL5, Esterase D, Endothelin-1, Trehalase, Neuropeptide K, Nkpd1, BRSK2, UQCRQPC, G-protein beta, KLHL4, ALDR, UQCRH, Rab-6A, Mucin 5B, PSMA5, NDUFAB1, CCK8-Gly, BTBD12, NDUFA1, DNAH1, MRPL1, Lgi4, Pannexin-1, FAM90A1, MGF, PDH E2 subunit N6-lipoyllysine, PRKAR2B, NPFF receptor 2, NDUFB4, MC4R, NDUFA8, Synaptotagmin I, Guanylate cyclase, ARL6, KCNK2, HSP70, Substance P extracellular region, DDX3Y, CNR1, Glycogen phosphorylase, Synaptotagmin IV, PPM1E, DnaJB9, Synaptotagmin, PRDX3, CNTN1 (F3), Thioredoxin, NDUFA4, ATP6V1A (70kD), HSPA4, Septin 1, PDE, Cystatin C, PPT1, SCF, SDHB, SLC39A10, DKK3, LUZP2, ANKRD36B, HCN2, Guanylate cyclase alpha, CCK8, GPR124, TPH2, Neuropeptide gamma, KAL1, RAB39B, RGS4, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, TUSC3, UGT8, LINC00342, D330028D13Rik, Kv3.3, ORP-family, LY6G5B, Tenascin-C, CEACAM, TRPC5, PKC-beta, PRDX1, G-protein beta/gamma, NDUFB6, SDFR1, SUR, ABO system transferase, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, UQCRB, CPT-1A, S100, Rab-6, TXNRD1, ORP8, KCNH5, AMIGO2, LASS6, PIMT, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, Aldose

						reductase, NDUFB3, Rab-3, ATG9B, TM2D3, Ephrin-A receptor 5, LAPTM4B, IDUA, CRH receptor 2, SLC2A13, Semaphorin 5A, NSF, CaMK IV, CHCHD2, GLRA, GABA-A receptor beta-2 subunit, FBXO2, ZNF433, SYP, Carbohydrate sulfotransferases, Rho GTPase, PDE4, G-protein gamma, UBE2D1, ZNF70, Dysferlin, Rap1GDS1, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, A830006F12Rik, EGF, Pro-CCK, Dynein, axonemal, heavy chains, MMADHC, HIST1H2BN, PKA-reg type II (cAMP-dependent), cPKC (conventional), NDUFB1, ELOVL4, AP3S1, Serotonin receptor, CHMP5, Apelin, GABA-A receptor alpha-4 subunit, PPID, TRPC, SLC7A5, HTR5A, VDAC 1, C17orf76, WIF1, COX VIa, CLCN4, Osteopontin, SMRT, Big ET-1, NHE6, Rab-3C, M-Ras, PKA-reg (cAMP-dependent), RNF152, Lingo1, PP1-cat, HMDH, Neurokinin A, PDLIM2, UQCR10, GUCY1A3, Clathrin heavy chain, Substance P, AP-3 sigma subunits, StARD4, GRM6, Histone H2, LIPA, MCT1 (SLC16A1), CCK5, Galpha(q)-specific amine GPCRs, UQCRFS1, Ephrin-A receptors, Histone H2A, NPR3, C9orf5, GP-IB alpha, Galpha(i)-specific amine GPCRs, Stch, LINGO1-AS1, NCX1, DNAJC12, HCN, RTEL1-TNFRSF6B, Protein kinase G1, HLF, CAP1, HSP90 beta, TXNIP (VDUP1), Vinexin, COL25A1, NDUFS6, Activin beta A, GABA-A receptor alpha-5 subunit, Zeta-sarcoglycan, CDK5, PANX2, PAK, Guanylate cyclase (alpha-1/beta-1), FLJ32001, SYT16, Glycine receptor, Fatty acid-binding protein, Synaptoporin, MAML1, IZUMO1, MDH1, ASAH, GABA-A receptor alpha-3 subunit, COX Va, ATP5A, Glycine receptor beta chain, CAPZA, RTL1, PKC-beta2, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, sRAGE, SLC25A46, Glyoxalase I, Galpha(q)-specific peptide GPCRs, H2AFZ, Histone H2B, SNAP190, NDUFA5, Tubulin alpha, Creatine kinase, ACAP1(CENTB1), DSCAML1, B-FABP, C17orf72, Patched, TNK1, CHKB-AS1, XK, MEF2, NAPB, ADAR3, HNMT, APRIO, MEK4/7, ACSL4, ATF/CREB, GLGB, ODP2, RAI1, LAMP2-C, Acyl-CoA synthetase, PP2A catalytic, IDI1, AP-4, MRLC, BMI-1, SNAPs, eIF2S1, Galpha(s)-specific CRF GPCRs, LAMP2, COX VIa-1, YPEL5, PRNP, HSPC138, MPTP complex, ENC1, STAG3, RHEB2, NKCC1, Neurocalcin delta, Malin, HIST2H2BE, PKC-beta1, Calmodulin, LPL, DIRAS2, Apo-2L(TNFSF10), SET1B, LOXL2, HSPC125, USMG5, Endophilin A1, Activin, Aquaporin 1, NDFIP1, Calcyclin, Syntenin 1, SCOT, Octanoyl-holo-acp, KCRS, Securin, ADHX, ERK1/2, AATC, UGCG, Anks4b, NFIC, CaMK II delta, HSC70, PKC, SSTR2, SUR1, HTR2A, PMM2, MPP7, GS1-124K5.11, ARPP-19, K-cadherin (CDH6), Guanylate Cyclase 1, soluble, APEL13, MEF2C, Protein kinase G, ERK2 (MAPK1),

						DREV1, LISCH7, Ran, OAT, MEK4(MAP2K4), TMEM70, PRKAR1A, IGFALS, CCK8-GlyArgArg, UFC1, Nephrocystin-4, DKK1, sKITLG, SSTR1, Guanine deaminase, SOD1, PPP4R2, GSE1, FSTL5, CALM2, Cyclophilin A, FOXP1/2/4 proteins, PI3K reg class IA, PTCHD1, DBH-AS1, Galpha(s)-specific peptide GPCRs, ATP5L, ACTR3, OXR1, CALB1, Tubulin alpha-4A, RhoE, Pcdh19, CD166, GAD2, NF-I, MRPL3, Neuroserpin, COX VIIa-2, Midkine, ARP3, PXDN, 14-3-3, RAGE, 14-3-3 eta, SNX10
9	Neurodegenerative Diseases	6726	5.305E-22	1.287E-19	336	PLP1, NPY, FAM3C, PP2A cat (alpha), PRPS1, HSP90, PAM, Cadherin 8, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Alpha crystallin B, ET-1, G3BP2, IRF1, ILDR2, MAL2, Rab-3B, COX VIc, GAD1, MEGF10, THAP11, PTCH2, N-chimaerin, Tubulin alpha 1A, HPCA, ELOVL5, Peroxiredoxin, UBL5, Esterase D, Endothelin-1, Neuropeptide K, PSMB5, T-plastin, Nkpd1, BRSK2, UQCRQPC, DYNLT3, G-protein beta, LAS1L, ALDR, UQCRH, Rab-6A, PSMA5, NDUFAB1, CCK8-Gly, NckAP1, NDUFA1, MGF, PRKAR2B, MELC, NPFF receptor 2, NDUFB4, NDUFA8, Synaptotagmin I, HSP70, Substance P extracellular region, DDX3Y, CNR1, Synaptotagmin IV, DnaJB9, Synaptotagmin, PRDX3, CNTN1 (F3), Thioredoxin, NDUFA4, HSPA4, Septin 1, PDE, Cystatin C, PPT1, SCF, SDHB, DKK3, LUZP2, ANKRD36B, NCKP1 subunit, CCK8, TPH2, Neuropeptide gamma, RAB39B, RGS4, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, TUSC3, Kv3.3, ORP-family, LY6G5B, Tenascin-C, CEACAM, TRPC5, PKC-beta, TCP1-theta, PRDX1, G-protein beta/gamma, NDUFB6, SDFR1, SUR, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, UQCRB, S100, Rab-6, TXNRD1, ORP8, AMIGO2, LASS6, PIMT, TRPV1, PDK3, ZFHX4, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, Aldose reductase, NDUFB3, Rab-3, TM2D3, Ephrin-A receptor 5, IDUA, SLC2A13, Semaphorin 5A, RPL9, NSF, CaMK IV, CHCHD2, GABA-A receptor beta-2 subunit, FBXO2, SYP, Rho GTPase, PDE4, G-protein gamma, UBE2D1, Dysferlin, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, A830006F12Rik, EGF, Pro-CCK, SYTC, Dynein, axonemal, heavy chains, HIST1H2BN, PKA-reg type II (cAMP-dependent), NELL1, cPKC (conventional), NDUFB1, ELOVL4, AP3S1, PSMA1, Serotonin receptor, CHMP5, GABA-A receptor alpha-4 subunit, PPID, TRPC, HTR5A, PDK4, VDAC 1, C17orf76, COX VIa, Osteopontin, SMRT, Big ET-1, NHE6, Rab-3C, PKA-reg (cAMP-dependent), Lingo1, PP1-cat, HMDH, Neurokinin A, PDLIM2, UQCR10, Clathrin heavy chain, Substance P, AP-3 sigma subunits, StARD4, Histone H2, LIPA, ARHGAP18, CCK5, Galpha(q)-specific amine GPCRs, UQCRFS1, Ephrin-A receptors,

						Histone H2A, C9orf5, Galpha(i)-specific amine GPCRs, TRPC4, NCX1, DNAJC12, HCN, RTEL1-TNFRSF6B, Protein kinase G1, HLF, CAP1, HSP90 beta, Vinexin, COL25A1, MEGF6, NDUFS6, GABA-A receptor alpha-5 subunit, CDK5, PAK, FLJ32001, SYT16, Fatty acid-binding protein, HINT, Synaptoporin, IZUMO1, MDH1, ASAH, GABA-A receptor alpha-3 subunit, DYNLT, COX Va, ATP5A, CAPZA, PKC-beta2, Calcineurin A (catalytic), TOP1MT, Galpha(i)-specific cannabis GPSRs, sRAGE, SLC25A46, Galpha(q)-specific peptide GPCRs, H2AFZ, Histone H2B, MAFbx, NDUFA5, Tubulin alpha, Creatine kinase, ACAP1(CENTB1), DSCAML1, B-FABP, Azi1, Patched, TNK1, MEF2, NAPB, ADAR3, HNMT, APRIO, BTBD10, MEK4/7, Peg10, ACSL4, ATF/CREB, GLGB, RAI1, G-protein gamma 3, LAMP2-C, FN14(TNFRSF12A), G-protein beta-4, Acyl-CoA synthetase, PP2A catalytic, SNAPs, eIF2S1, Galpha(s)-specific CRF GPCRs, LAMP2, COX VIa-1, YPEL5, Kv4.2 channel, PRNP, HSPC138, MPTP complex, STAG3, RHEB2, NKCC1, Neurocalcin delta, Malin, HIST2H2BE, PKC-beta1, LPL, DIRAS2, Apo-2L(TNFSF10), LOXL2, Endophilin A1, Aquaporin 1, NDFIP1, NME5, Calcyclin, Syntenin 1, SCOT, Octanoyl-holo-acp, KCRS, ADHX, ERK1/2, AATC, UGCG, NFIC, CaMK II delta, HSC70, PKC, SSTR2, SUR1, HTR2A, MPP7, GS1-124K5.11, ARPP-19, K-cadherin (CDH6), MEF2C, Protein kinase G, ERK2 (MAPK1), DREV1, LISCH7, Ran, OAT, MEK4(MAP2K4), PRKAR1A, CCK8-GlyArgArg, IMPA1, UFC1, DKK1, sKITLG, PRPS, SOD1, TFIIB, FSTL5, Cyclophilin A, FOXP1/2/4 proteins, PI3K reg class IA, DBH-AS1, Galpha(s)-specific peptide GPCRs, ATP5L, CALB1, Tubulin alpha-4A, CD166, GAD2, TCP1-epsilon, NF-I, MRPL3, HXK3, COX VIIa-2, Midkine, SAMD10, ARP3, 14-3-3, RAGE, 14-3-3 eta, SNX10
10	Mental Disorders	7319	5.398E-21	1.178E-18	354	PLP1, NPY, FAM3C, PP2A cat (alpha), HSP90, PAK3, PAM, Cadherin 8, NPEPL1, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Alpha crystallin B, ET-1, G3BP2, ILDR2, MAL2, GLSK, Rab-3B, COX VIc, GAD1, MEGF10, PTCH2, N-chimaerin, APJ, Smooth muscle myosin, ELOVL5, Peroxiredoxin, UBL5, Endothelin-1, Neuropeptide K, AP-1 gamma subunits, Nkpd1, REV-ERBalpha, BRSK2, UQCRQPC, P2Y11, G-protein beta, LAS1L, UQCRH, Rab-6A, PSMA5, NDUFAB1, Importin (karyopherin)-alpha, CCK8-Gly, NckAP1, NDUFA1, DCMC, PRKAR2B, PLD5, NPFF receptor 2, NDUFB4, MC4R, NDUFA8, C12orf62, Synaptotagmin I, Guanylate cyclase, KCNK2, HSP70, Substance P extracellular region, DDX3Y, CNR1, Synaptotagmin IV, HDBP1, DnaJB9, Synaptotagmin, PRDX3, CNTN1 (F3), Thioredoxin, MRLC2, NDUFA4, ATP6V1A (70kD), HSPA4, Septin 1, PDE, Cystatin C, PPT1, SDHB, DKK3, LUZP2, NCKP1 subunit, HCN2, Galpha(q)-

						specific Class A Orphan/other GPCRs, CCK8, GPR124, TPH2, Neuropeptide gamma, RAB39B, Aha1, RGS4, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, TUSC3, GUCY1B1, ORP-family, Tenascin-C, CEACAM, TRPC5, PKC-beta, KIS, PAFAH gamma, PRDX1, G-protein beta/gamma, NDUFB6, SDFR1, FLJ35776, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, UQCRB, S100, FAM69A, Rab-6, TXNRD1, ORP8, AMIGO2, PIMT, TRPV1, PRR12, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, NDUFB3, Rab-3, TM2D3, Ephrin-A receptor 5, CRH receptor 2, Semaphorin 5A, NSF, CaMK IV, CHCHD2, GLRA, GABA-A receptor beta-2 subunit, CECR2, SYP, Carbohydrate sulfotransferases, Rho GTPase, PDE4, G-protein gamma, UBE2D1, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, A830006F12Rik, Secretogranin V, EGF, Pro-CCK, SYTC, Dynein, axonemal, heavy chains, BMPR1A, PKA-reg type II (cAMP-dependent), cPKC (conventional), ATP6V1B2, NDUFB1, AP3S1, Serotonin receptor, CHMP5, GABA-A receptor alpha-4 subunit, ADSS, Rab-27B, PPID, TRPC, HTR5A, VDAC 1, C17orf76, COX VIa, CLCN4, Osteopontin, ZNF238, SMRT, Big ET-1, NHE6, Rab-3C, PKA-reg (cAMP-dependent), Lingo1, PP1-cat, HMDH, Neurokinin A, UQCR10, NR3A, Cables1, Clathrin heavy chain, IL3RA, Substance P, AP-3 sigma subunits, StARD4, GRM6, Histone H2, LIPA, CCK5, Galpha(q)-specific amine GPCRs, UQCRFS1, Ephrin-A receptors, Histone H2A, NPR3, C9orf5, GP-IB alpha, Galpha(i)-specific amine GPCRs, NCX1, DNAJC12, HCN, RTEL1-TNFRSF6B, Protein kinase G1, CAP1, HSP90 beta, Vinexin, COL25A1, NDUFS6, GABA-A receptor alpha-5 subunit, CDK5, PANX2, PAK, Guanylate cyclase (alpha-1/beta-1), SYT16, Guanylate cyclase beta, Glycine receptor, Fatty acid-binding protein, HINT, Synaptoporin, SgK223, IZUMO1, MDH1, ASAH, GABA-A receptor alpha-3 subunit, SPSY, COX Va, eIF4A2, ATP5A, Glycine receptor beta chain, CAPZA, RTL1, PKC-beta2, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, sRAGE, Glyoxalase I, DDX51, Galpha(q)-specific peptide GPCRs, Histone H2B, NDUFA5, Tubulin alpha, Creatine kinase, ACAP1(CENTB1), TBC1D10C, B-FABP, Patched, TNK1, CHKB-AS1, MEF2, NAPB, HNMT, APRIO, BTBD10, ACSL4, ATF/CREB, RAI1, Hdj-2, LAMP2-C, G-protein beta-4, Acyl-CoA synthetase, PP2A catalytic, MRLC, eIF4A, SNAPs, eIF2S1, Galpha(s)-specific CRF GPCRs, LAMP2, COX VIa-1, YPEL5, ATP6V1B, Kv4.2 channel, PRNP, TMS-1, MPTP complex, STAG3, RHEB2, NKCC1, Neurocalcin delta, HIST2H2BE, PKC-beta1, PDE4A, Calmodulin, LPL, DIRAS2, Apo-2L(TNFSF10), SET1B,

						PDE11A, FLJ45455, Endophilin A1, STAC2, Activin, Aquaporin 1, C6orf27, Calcyclin, SCOT, Octanoyl-holo-acp, ADHX, ERK1/2, AATC, UGCG, CaMK II delta, HSC70, PI3K reg class IA (p55-gamma), SLC35A5, PKC, SSTR2, HTR2A, MPP7, ARPP-19, K-cadherin (CDH6), Guanylate Cyclase 1, soluble, MEF2C, SULT4A1, Protein kinase G, ERK2 (MAPK1), Calcineurin A (beta), DREV1, LISCH7, Ran, OAT, CCK8-GlyArgArg, IMPA1, UFC1, DKK1, SOD1, KIAA1024, PPP4R2, SAP102, FSTL5, CALM2, Cyclophilin A, FOXP1/2/4 proteins, PI3K reg class IA, PTCHD1, DBH-AS1, Galpha(s)-specific peptide GPCRs, TCP1-alpha, ATP5L, ATP6AP2, CALB1, Tubulin alpha-4A, Pcdh19, CD166, GAD2, NF-I, NPNT, MRPL3, HXK3, Neuroserpin, COX VIIa-2, 14-3-3, RAGE, 14-3-3 eta, ZCCHC12, SNX10
11	Psychiatry and Psychology	7410	6.351E-21	1.260E-18	357	PLP1, NPY, FAM3C, PP2A cat (alpha), HSP90, PAK3, PAM, Cadherin 8, NPEPL1, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Alpha crystallin B, ET-1, G3BP2, ILDR2, MAL2, GLSK, Rab-3B, COX VIc, GAD1, MEGF10, PTCH2, N-chimaerin, APJ, Smooth muscle myosin, ELOVL5, Peroxiredoxin, UBL5, Endothelin-1, Neuropeptide K, AP-1 gamma subunits, Nkpd1, REV-ERBalpha, BRSK2, UQCRQPC, P2Y11, G-protein beta, LAS1L, UQCRH, Rab-6A, PSMA5, NDUFAB1, Importin (karyopherin)-alpha, CCK8-Gly, NckAP1, NDUFA1, DCMC, PRKAR2B, PLD5, NPFF receptor 2, NDUFB4, MC4R, NDUFA8, C12orf62, Synaptotagmin I, Guanylate cyclase, KCNK2, HSP70, Substance P extracellular region, DDX3Y, CNR1, Glycogen phosphorylase, Synaptotagmin IV, HDBP1, DnaJB9, Synaptotagmin, PRDX3, CNTN1 (F3), Thioredoxin, MRLC2, NDUFA4, ATP6V1A (70kD), HSPA4, Septin 1, PDE, Cystatin C, PPT1, SDHB, DKK3, LUZP2, NCKP1 subunit, HCN2, Galpha(q)-specific Class A Orphan/other GPCRs, CCK8, GPR124, TPH2, Neuropeptide gamma, RAB39B, Aha1, RGS4, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, TUSC3, GUCY1B1, ORP-family, Tenascin-C, CEACAM, TRPC5, PKC-beta, KIS, PAFAH gamma, PRDX1, G-protein beta/gamma, NDUFB6, SDFR1, FLJ35776, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, UQCRB, S100, FAM69A, Rab-6, TXNRD1, ORP8, AMIGO2, PIMT, TRPV1, PRR12, ZFHX4, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, NDUFB3, Rab-3, TM2D3, Ephrin-A receptor 5, CRH receptor 2, Semaphorin 5A, NSF, CaMK IV, CHCHD2, GLRA, GABA-A receptor beta-2 subunit, CECR2, SYP, Carbohydrate sulfotransferases, Rho GTPase, PDE4, G-protein gamma, UBE2D1, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, A830006F12Rik, Secretogranin V, EGF, Pro-CCK, SYTC, Dynein,

						axonemal, heavy chains, BMPR1A, PKA-reg type II (cAMP-dependent), cPKC (conventional), ATP6V1B2, NDUFB1, DLL4, AP3S1, Serotonin receptor, CHMP5, GABA-A receptor alpha-4 subunit, ADSS, Rab-27B, PPID, TRPC, HTR5A, VDAC 1, C17orf76, COX VIa, CLCN4, Osteopontin, ZNF238, SMRT, Big ET-1, NHE6, Rab-3C, PKA-reg (cAMP-dependent), Lingo1, PP1-cat, HMDH, Neurokinin A, UQCR10, NR3A, Cables1, Clathrin heavy chain, IL3RA, Substance P, AP-3 sigma subunits, StARD4, GRM6, Histone H2, LIPA, CCK5, Galpha(q)-specific amine GPCRs, UQCRFS1, Ephrin-A receptors, Histone H2A, NPR3, C9orf5, GP-IB alpha, Galpha(i)-specific amine GPCRs, NCX1, DNAJC12, HCN, RTEL1-TNFRSF6B, Protein kinase G1, CAP1, HSP90 beta, Vinexin, COL25A1, NDUFS6, GABA-A receptor alpha-5 subunit, CDK5, PANX2, PAK, Guanylate cyclase (alpha-1/beta-1), SYT16, Guanylate cyclase beta, Glycine receptor, Fatty acid-binding protein, HINT, Synaptoporin, SgK223, IZUMO1, MDH1, ASAH, GABA-A receptor alpha-3 subunit, SPSY, COX Va, eIF4A2, ATP5A, Glycine receptor beta chain, CAPZA, RTL1, PKC-beta2, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, sRAGE, Glyoxalase I, DDX51, Galpha(q)-specific peptide GPCRs, Histone H2B, NDUFA5, Tubulin alpha, Creatine kinase, ACAP1(CENTB1), TBC1D10C, B-FABP, Patched, TNK1, CHKB-AS1, MEF2, NAPB, HNMT, APRIO, BTBD10, ACSL4, ATF/CREB, RAI1, Hdj-2, LAMP2-C, G-protein beta-4, Acyl-CoA synthetase, PP2A catalytic, MRLC, eIF4A, SNAPs, eIF2S1, Galpha(s)-specific CRF GPCRs, LAMP2, COX VIa-1, YPEL5, ATP6V1B, Kv4.2 channel, PRNP, TMS-1, MPTP complex, STAG3, RHEB2, NKCC1, Neurocalcin delta, HIST2H2BE, PKC-beta1, PDE4A, Calmodulin, LPL, DIRAS2, Apo-2L(TNFSF10), SET1B, PDE11A, FLJ45455, Endophilin A1, STAC2, Activin, Aquaporin 1, C6orf27, Calcyclin, SCOT, Octanoyl-holo-acp, ADHX, ERK1/2, AATC, UGCG, CaMK II delta, HSC70, PI3K reg class IA (p55-gamma), SLC35A5, PKC, SSTR2, HTR2A, MPP7, ARPP-19, K-cadherin (CDH6), Guanylate Cyclase 1, soluble, MEF2C, SULT4A1, Protein kinase G, ERK2 (MAPK1), Calcineurin A (beta), DREV1, LISCH7, Ran, OAT, CCK8-GlyArgArg, IMPA1, UFC1, DKK1, SOD1, KIAA1024, PPP4R2, SAP102, FSTL5, CALM2, Cyclophilin A, FOXP1/2/4 proteins, PI3K reg class IA, PTCHD1, DBH-AS1, Galpha(s)-specific peptide GPCRs, TCP1-alpha, ATP5L, ATP6AP2, CALB1, Tubulin alpha-4A, Pcdh19, CD166, GAD2, NF-I, NPNT, MRPL3, HXK3, Neuroserpin, COX VIIa-2, 14-3-3, RAGE, 14-3-3 eta, ZCCHC12, SNX10

12	Central Nervous System Diseases	9151	1.693E-20	3.079E-18	416	PLP1, NPY, FAM3C, PP2A cat (alpha), HSP90, PAM, HMGCLL1, Cadherin 8, NPEPL1, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Alpha crystallin B, ET-1, G3BP2, IRF1, ILDR2, MAL2, GLSK, Rab-3B, COX VIc, GAD1, THAP11, PTCH2, N-chimaerin, Tubulin alpha 1A, HPCA, APJ, ELOVL5, Peroxiredoxin, Activin A, UBL5, Esterase D, Endothelin-1, Trehalase, Neuropeptide K, T-plastin, Nkpd1, BRSK2, UQCRQPC, G-protein beta, KLHL4, LAS1L, ALDR, UQCRH, Rab-6A, Mucin 5B, PSMA5, NDUFAB1, CCK8-Gly, BTBD12, NDUFA1, DNAH1, MRPL1, Lgi4, Pannexin-1, FAM90A1, MGF, PDH E2 subunit N6-lipoyllysine, PRKAR2B, MELC, NPFF receptor 2, NDUFB4, MC4R, NDUFA8, Synaptotagmin I, Guanylate cyclase, ARL6, KCNK2, HSP70, Substance P extracellular region, DDX3Y, CNR1, Glycogen phosphorylase, Synaptotagmin IV, PPM1E, DnaJB9, Synaptotagmin, PRDX3, CNTN1 (F3), Thioredoxin, NDUFA4, ATP6V1A (70kD), HSPA4, Septin 1, Dynein, axonemal, light chains, PDE, Cystatin C, PPT1, SCF, SDHB, SLC39A10, DKK3, LUZP2, ANKRD36B, HCN2, Guanylate cyclase alpha, CCK8, GPR124, TPH2, Neuropeptide gamma, KAL1, RAB39B, RGS4, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, TUSC3, UGT8, LINC00342, D330028D13Rik, Kv3.3, ORP-family, LY6G5B, Tenascin-C, CEACAM, TRPC5, PKC-beta, PRDX1, G-protein beta/gamma, NDUFB6, SDFR1, SUR, ABO system transferase, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, UQCRB, CPT-1A, S100, Rab-6, TXNRD1, ORP8, KCNH5, AMIGO2, LASS6, PIMT, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, Aldose reductase, NDUFB3, Rab-3, ATG9B, TM2D3, Ephrin-A receptor 5, LAPTM4B, IDUA, CRH receptor 2, SLC2A13, Semaphorin 5A, RPL9, NSF, CaMK IV, CHCHD2, GLRA, GABA-A receptor beta-2 subunit, FBXO2, ZNF433, SYP, Carbohydrate sulfotransferases, Rho GTPase, PDE4, G-protein gamma, UBE2D1, ZNF70, Dysferlin, Rap1GDS1, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, A830006F12Rik, EGF, Pro-CCK, Dynein, axonemal, heavy chains, MMADHC, HIST1H2BN, PKA-reg type II (cAMP-dependent), NELL1, cPKC (conventional), NDUFB1, ELOVL4, AP3S1, PSMA1, Serotonin receptor, CHMP5, Apelin, GABA-A receptor alpha-4 subunit, PPID, TRPC, SLC7A5, HTR5A, VDAC 1, C17orf76, WIF1, COX VIa, CLCN4, Osteopontin, SMRT, Big ET-1, NHE6, Rab-3C, M-Ras, PKA-reg (cAMP-dependent), RNF152, Lingo1, PP1-cat, HMDH, Neurokinin A, PDLIM2, UQCR10, GUCY1A3, Clathrin heavy chain, Substance P, AP-3 sigma subunits, StARD4, GRM6, Histone H2, LIPA, MCT1 (SLC16A1),

						ARHGAP18, CCK5, Galpha(q)-specific amine GPCRs, UQCRFS1, Ephrin-A receptors, Histone H2A, NPR3, C9orf5, GP-IB alpha, DOC1, Galpha(i)-specific amine GPCRs, Stch, LINGO1-AS1, NCX1, DNAJC12, HCN, RTEL1-TNFRSF6B, Protein kinase G1, HLF, CAP1, HSP90 beta, TXNIP (VDUP1), Vinexin, COL25A1, NDUFS6, Activin beta A, GABA-A receptor alpha-5 subunit, Zeta-sarcoglycan, CDK5, PANX2, PAK, Guanylate cyclase (alpha-1/beta-1), FLJ32001, SYT16, Glycine receptor, Fatty acid-binding protein, HINT, Synaptoporin, MAML1, IZUMO1, MDH1, ASAH, GABA-A receptor alpha-3 subunit, COX Va, ATP5A, Glycine receptor beta chain, CAPZA, RTL1, PKC-beta2, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, sRAGE, SLC25A46, Glyoxalase I, Galpha(q)-specific peptide GPCRs, H2AFZ, Histone H2B, MAFbx, SNAP190, NDUFA5, Tubulin alpha, Creatine kinase, ACAP1(CENTB1), DSCAML1, B-FABP, C17orf72, Patched, TNK1, CHKB-AS1, XK, MEF2, NAPB, ADAR3, HNMT, APRIO, BTBD10, MEK4/7, Peg10, ACSL4, ATF/CREB, GLGB, ODP2, RAI1, LAMP2-C, G-protein beta-4, Acyl-CoA synthetase, PP2A catalytic, IDI1, AP-4, MRLC, BMI-1, SNAPs, eIF2S1, Galpha(s)-specific CRF GPCRs, LAMP2, COX VIa-1, YPEL5, PRNP, HSPC138, MPTP complex, ENC1, STAG3, RHEB2, NKCC1, Neurocalcin delta, Malin, HIST2H2BE, PKC-beta1, Calmodulin, LPL, DIRAS2, NELL2, Apo-2L(TNFSF10), SET1B, LOXL2, HSPC125, USMG5, Endophilin A1, Activin, Aquaporin 1, NDFIP1, Calcyclin, Syntenin 1, SCOT, Octanoyl-holo-acp, KCRS, Securin, ADHX, ERK1/2, AATC, UGCG, Anks4b, NFIC, CaMK II delta, HSC70, PKC, SSTR2, SUR1, HTR2A, PMM2, MPP7, GS1-124K5.11, ARPP-19, K-cadherin (CDH6), Guanylate Cyclase 1, soluble, APEL13, MEF2C, Protein kinase G, ERK2 (MAPK1), DREV1, LISCH7, Ran, OAT, MEK4(MAP2K4), TMEM70, PRKAR1A, IGFALS, CCK8-GlyArgArg, UFC1, Nephrocystin-4, DKK1, sKITLG, SSTR1, Guanine deaminase, SOD1, PPP4R2, GSE1, FSTL5, CALM2, Cyclophilin A, FOXP1/2/4 proteins, PI3K reg class IA, PTCHD1, DBH-AS1, Galpha(s)-specific peptide GPCRs, ATP5L, ACTR3, OXR1, CALB1, Tubulin alpha-4A, RhoE, Pcdh19, CD166, GAD2, NF-I, MRPL3, Neuroserpin, COX VIIa-2, Midkine, SAMD10, ARP3, PXDN, 14-3-3, RAGE, 14-3-3 eta, SNX10
13	Dementia	4320	8.626E-20	1.449E-17	238	PLP1, NPY, FAM3C, PP2A cat (alpha), HSP90, PAM, Cadherin 8, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Alpha crystallin B, ET-1, MAL2, Rab-3B, COX VIc, GAD1, PTCH2, N-chimaerin, Peroxiredoxin, UBL5, Endothelin-1, Neuropeptide K, Nkpd1, UQCRQPC, G-protein beta, UQCRH, Rab-6A, PSMA5, NDUFAB1, CCK8-Gly, NDUFA1, PRKAR2B, NPFF receptor 2,

						NDUFB4, NDUFA8, Synaptotagmin I, HSP70, Substance P extracellular region, DDX3Y, CNR1, Synaptotagmin IV, DnaJB9, Synaptotagmin, PRDX3, CNTN1 (F3), Thioredoxin, NDUFA4, HSPA4, Septin 1, PDE, Cystatin C, PPT1, SDHB, DKK3, LUZP2, CCK8, Neuropeptide gamma, RGS4, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, TUSC3, ORP-family, Tenascin-C, CEACAM, TRPC5, PKC-beta, PRDX1, G-protein beta/gamma, NDUFB6, SDFR1, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, UQCRB, S100, Rab-6, TXNRD1, ORP8, AMIGO2, PIMT, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, NDUFB3, Rab-3, TM2D3, Ephrin-A receptor 5, NSF, CaMK IV, CHCHD2, GABA-A receptor beta-2 subunit, SYP, Rho GTPase, PDE4, G-protein gamma, UBE2D1, Galpha(i)-specific metabotropic glutamate GPCRs, A830006F12Rik, EGF, Pro-CCK, Dynein, axonemal, heavy chains, PKA-reg type II (cAMP-dependent), cPKC (conventional), NDUFB1, Serotonin receptor, CHMP5, GABA-A receptor alpha-4 subunit, PPID, TRPC, HTR5A, VDAC 1, C17orf76, COX VIa, Osteopontin, SMRT, Big ET-1, NHE6, Rab-3C, PKA-reg (cAMP-dependent), PP1-cat, HMDH, Neurokinin A, UQCR10, Clathrin heavy chain, Substance P, StARD4, Histone H2, LIPA, CCK5, Galpha(q)-specific amine GPCRs, UQCRFS1, Ephrin-A receptors, Histone H2A, Galpha(i)-specific amine GPCRs, NCX1, DNAJC12, HCN, Protein kinase G1, CAP1, HSP90 beta, Vinexin, COL25A1, NDUFS6, GABA-A receptor alpha-5 subunit, CDK5, PAK, SYT16, Fatty acid-binding protein, Synaptoporin, MDH1, ASAH, GABA-A receptor alpha-3 subunit, COX Va, ATP5A, CAPZA, PKC-beta2, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, sRAGE, Galpha(q)-specific peptide GPCRs, Histone H2B, NDUFA5, Tubulin alpha, Creatine kinase, ACAP1(CENTB1), B-FABP, Patched, TNK1, MEF2, NAPB, HNMT, APRIO, ACSL4, ATF/CREB, LAMP2-C, Acyl-CoA synthetase, PP2A catalytic, MRLC, SNAPs, eIF2S1, Galpha(s)-specific CRF GPCRs, LAMP2, COX VIa-1, YPEL5, PRNP, MPTP complex, STAG3, RHEB2, NKCC1, Neurocalcin delta, HIST2H2BE, PKC-beta1, LPL, DIRAS2, Apo-2L(TNFSF10), Aquaporin 1, Calcyclin, SCOT, Octanoyl-holo-acp, ERK1/2, AATC, UGCG, CaMK II delta, HSC70, PKC, SSTR2, HTR2A, MPP7, ARPP-19, K-cadherin (CDH6), MEF2C, Protein kinase G, ERK2 (MAPK1), DREV1, LISCH7, Ran, OAT, CCK8-GlyArgArg, UFC1, DKK1, SOD1, FSTL5, Cyclophilin A, FOXP1/2/4 proteins, PI3K reg class IA, DBH-AS1, Galpha(s)-specific peptide GPCRs, ATP5L, CALB1, Tubulin alpha-4A, CD166, GAD2, Neuroserpin, COX VIIa-2, 14-3-3, RAGE, 14-3-3 eta, SNX10

14	Genetic Diseases, Inborn	7327	1.796E-19	2.776E-17	349	PLP1, NPY, PP2A cat (alpha), PRPS1, HSP90, PAK3, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Alpha crystallin B, ET-1, G3BP2, IRF1, ILDR2, MAL2, COX VIc, GAD1, SMVT, MEGF10, THAP11, PTCH2, N-chimaerin, SUCLG1, Smooth muscle myosin, ELOVL5, Peroxiredoxin, Activin A, Esterase D, Endothelin-1, Neuropeptide K, PSMB5, ARG2, T-plastin, REV-ERBalpha, BRSK2, UQCRQPC, DYNLT3, G-protein beta, UQCRH, Mucin 5B, PSMA5, NDUFAB1, CCK8-Gly, NckAP1, BTBD12, NDUFA1, LSMD1, DNAH1, MCM6, OGFRL1, DCMC, MGF, PDH E2 subunit N6-lipoyllysine, PRKAR2B, MELC, NDUFB4, NDUFA8, Synaptotagmin I, Guanylate cyclase, ARL6, HSP70, Substance P extracellular region, CNR1, Glycogen phosphorylase, Synaptotagmin IV, Synaptotagmin, PRDX3, Thioredoxin, NDUFA4, ATP6V1A (70kD), HSPA4, Dynein, axonemal, light chains, PDE, Cystatin C, PPT1, SCF, SDHB, IGSF9B, ANKRD36B, NCKP1 subunit, Galpha(q)-specific Class A Orphan/other GPCRs, IMPG2, CCK8, GPR124, TPH2, Neuropeptide gamma, KAL1, RAB39B, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, UGT8, Exostosin-like 2, Kv3.3, ORP-family, B3GN6, Tenascin-C, CEACAM, TRPC5, PKC-beta, TCP1-theta, PRDX1, G-protein beta/gamma, NDUFB6, SUR, ABO system transferase, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, FUT2, UQCRB, CPT-1A, S100, TXNRD1, CC188, ORP8, PIMT, TRPV1, PDK3, ZFHX4, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, NDUFB3, Rab-3, IDUA, V-ATPase E subunit, GRAIL, CaMK IV, CHCHD2, GABA-A receptor beta-2 subunit, DOK7, SYP, Carbohydrate sulfotransferases, MOCS2(small), Rho GTPase, PDE4, G-protein gamma, UBE2D1, PRPS2, Dysferlin, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, ChREBP, EGF, Pro-CCK, SYTC, Dynein, axonemal, heavy chains, BMPR1A, MMADHC, LOC283174, PKA-reg type II (cAMP-dependent), cPKC (conventional), NDUFB1, DLL4, ELOVL4, Serotonin receptor, GABA-A receptor alpha-4 subunit, TRPC, HTR5A, PYGM, Sp8, ACTR10, MOC2B, WIF1, COX VIa, CLCN4, Osteopontin, SMRT, Big ET-1, CysLT2 receptor, NHE6, PKA-reg (cAMP-dependent), ANT, HMDH, Neurokinin A, PDLIM2, UQCR10, Clathrin heavy chain, Substance P, StARD4, GRM6, Histone H2, LIPA, MCT1 (SLC16A1), CCK5, COPS4, Galpha(q)-specific amine GPCRs, UQCRFS1, Histone H2A, NPR3, C9orf5, GP-IB alpha, Galpha(i)-specific amine GPCRs, TRPC4, DNAJC12, HCN, RTEL1-TNFRSF6B, HLF, CAP1, TXNIP (VDUP1), COL25A1, MEGF6, NDUFS6, Activin beta A, GABA-A receptor alpha-5 subunit, CDK5, PAK, SYT16, Fatty acid-binding protein, HINT, MAML1, IZUMO1,

						MDH1, ASAH, GABA-A receptor alpha-3 subunit, DYNLT, SPOCK3, SPSY, COX Va, Tetraspanin-3, ATP5A, Nek8, CAPZA, PKC-beta2, Calcineurin A (catalytic), TOP1MT, Galpha(i)-specific cannabis GPSRs, sRAGE, SLC25A46, Glyoxalase I, Galpha(q)-specific peptide GPCRs, ATP6V1C, MAFbx, NDUFA5, Tubulin alpha, Creatine kinase, DSCAML1, MRAP2, B-FABP, Azi1, Patched, TNK1, XK, MEF2, NAPB, HNMT, Sec23, APRIO, SCS-A, MEK4/7, ACSL4, ATF/CREB, GLGB, ODP2, RAI1, G-protein gamma 3, Hdj-2, CQ107, LAMP2-C, FN14(TNFRSF12A), G-protein beta-4, Acyl-CoA synthetase, PP2A catalytic, IDI1, MRLC, BMI-1, SNAPs, RNF175, LAMP2, COX VIa-1, YPEL5, ATP6V1B, Kv4.2 channel, PRNP, HSPC138, MPTP complex, RHEB2, NKCC1, Malin, PKC-beta1, PDE4A, LPL, NELL2, SUMO-3, ATP6V1E, Apo-2L(TNFSF10), LOXL2, NOLA3 (NOP10), HSPC125, USMG5, Activin, Aquaporin 1, NME5, Calcyclin, SCOT, Octanoyl-holo-acp, ERK1/2, AATC, UGCG, NFIC, CaMK II delta, HSC70, PKC, HTR2A, PMM2, SLC25A4, GS1-124K5.11, K-cadherin (CDH6), MEF2C, ERK2 (MAPK1), OAT, MEK4(MAP2K4), TMEM70, IGFALS, CCK8-GlyArgArg, CLCN5, IMPA1, Nephrocystin-4, sKITLG, PRPS, SOD1, TFIIB, SAP102, SPDYE5, Cyclophilin A, FOXP1/2/4 proteins, PI3K reg class IA, PTCHD1, CLDND1, Galpha(s)-specific peptide GPCRs, TCP1-alpha, ACTR3, ATP6AP2, CALB1, SRm300, Pcdh19, CD166, TCP1-epsilon, NF-I, MRPL3, HXK3, COX VIIa-2, ACOXL, Midkine, SAMD10, ARP3, 14-3-3, RAGE, ATP1beta subunit, CHST6
15	Neurocognitive Disorders	4347	1.907E-19	2.776E-17	238	PLP1, NPY, FAM3C, PP2A cat (alpha), HSP90, PAM, Cadherin 8, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Alpha crystallin B, ET-1, MAL2, Rab-3B, COX VIc, GAD1, PTCH2, N-chimaerin, Peroxiredoxin, UBL5, Endothelin-1, Neuropeptide K, Nkpd1, UQCRQPC, G-protein beta, UQCRH, Rab-6A, PSMA5, NDUFAB1, CCK8-Gly, NDUFA1, PRKAR2B, NPFF receptor 2, NDUFB4, NDUFA8, Synaptotagmin I, HSP70, Substance P extracellular region, DDX3Y, CNR1, Synaptotagmin IV, DnaJB9, Synaptotagmin, PRDX3, CNTN1 (F3), Thioredoxin, NDUFA4, HSPA4, Septin 1, PDE, Cystatin C, PPT1, SDHB, DKK3, LUZP2, CCK8, Neuropeptide gamma, RGS4, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, TUSC3, ORP-family, Tenascin-C, CEACAM, TRPC5, PKC-beta, PRDX1, G-protein beta/gamma, NDUFB6, SDFR1, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, UQCRB, S100, Rab-6, TXNRD1, ORP8, AMIGO2, PIMT, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, NDUFB3, Rab-3, TM2D3, Ephrin-A receptor 5, NSF, CaMK IV, CHCHD2, GABA-A receptor beta-2 subunit, SYP, Rho GTPase, PDE4, G-protein

						gamma, UBE2D1, Galpha(i)-specific metabotropic glutamate GPCRs, A830006F12Rik, EGF, Pro-CCK, Dynein, axonemal, heavy chains, PKA-reg type II (cAMP-dependent), cPKC (conventional), NDUFB1, Serotonin receptor, CHMP5, GABA-A receptor alpha-4 subunit, PPID, TRPC, HTR5A, VDAC 1, C17orf76, COX VIa, Osteopontin, SMRT, Big ET-1, NHE6, Rab-3C, PKA-reg (cAMP-dependent), PP1-cat, HMDH, Neurokinin A, UQCR10, Clathrin heavy chain, Substance P, StARD4, Histone H2, LIPA, CCK5, Galpha(q)-specific amine GPCRs, UQCRFS1, Ephrin-A receptors, Histone H2A, Galpha(i)-specific amine GPCRs, NCX1, DNAJC12, HCN, Protein kinase G1, CAP1, HSP90 beta, Vinexin, COL25A1, NDUFS6, GABA-A receptor alpha-5 subunit, CDK5, PAK, SYT16, Fatty acid-binding protein, Synaptoporin, MDH1, ASAH, GABA-A receptor alpha-3 subunit, COX Va, ATP5A, CAPZA, PKC-beta2, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, sRAGE, Galpha(q)-specific peptide GPCRs, Histone H2B, NDUFA5, Tubulin alpha, Creatine kinase, ACAP1(CENTB1), B-FABP, Patched, TNK1, MEF2, NAPB, HNMT, APRIO, ACSL4, ATF/CREB, LAMP2-C, Acyl-CoA synthetase, PP2A catalytic, MRLC, SNAPs, eIF2S1, Galpha(s)-specific CRF GPCRs, LAMP2, COX VIa-1, YPEL5, PRNP, MPTP complex, STAG3, RHEB2, NKCC1, Neurocalcin delta, HIST2H2BE, PKC-beta1, LPL, DIRAS2, Apo-2L(TNFSF10), Aquaporin 1, Calcyclin, SCOT, Octanoyl-holo-acp, ERK1/2, AATC, UGCG, CaMK II delta, HSC70, PKC, SSTR2, HTR2A, MPP7, ARPP-19, K-cadherin (CDH6), MEF2C, Protein kinase G, ERK2 (MAPK1), DREV1, LISCH7, Ran, OAT, CCK8-GlyArgArg, UFC1, DKK1, SOD1, FSTL5, Cyclophilin A, FOXP1/2/4 proteins, PI3K reg class IA, DBH-AS1, Galpha(s)-specific peptide GPCRs, ATP5L, CALB1, Tubulin alpha-4A, CD166, GAD2, Neuroserpin, COX VIIa-2, 14-3-3, RAGE, 14-3-3 eta, SNX10
16	Nervous System Diseases	13323	1.685E-17	2.300E-15	540	PLP1, Cyclin G, NPY, FAM3C, PP2A cat (alpha), PRPS1, HSP90, PAK3, PAM, HMGCLL1, Cadherin 8, CPSF1, ARP6, CXorf57, NPEPL1, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Alpha crystallin B, ET-1, G3BP2, IRF1, ILDR2, MAL2, GLSK, Rab-3B, COX VIc, GAD1, MEGF10, THAP11, PTCH2, N-chimaerin, Tubulin alpha 1A, SUCLG1, HPCA, APJ, Smooth muscle myosin, ELOVL5, Peroxiredoxin, Activin A, UBL5, Esterase D, Endothelin-1, Trehalase, Neuropeptide K, PSMB5, AP-1 gamma subunits, T-plastin, Nkpd1, REV-ERBalpha, BRSK2, UQCRQPC, DYNLT3, P2Y11, G-protein beta, KLHL4, LAS1L, ALDR, CRTL1, UQCRH, Rab-6A, Mucin 5B, PSMA5, NDUFAB1, CCK8-Gly, NckAP1, KIAA1276, BTBD12, NDUFA1, DNAH1, MRPL1, Lgi4, Pannexin-1, DCMC, PSD2, FAM90A1, NIPSNAP3A, MGF, PDH E2 subunit N6-

						lipoyllysine, PRKAR2B, MELC, PLD5, NPFF receptor 2, NDUFB4, MC4R, NDUFA8, Synaptotagmin I, COCH, Guanylate cyclase, ARL6, KCNK2, HSP70, Substance P extracellular region, DDX3Y, CNR1, Glycogen phosphorylase, Synaptotagmin IV, CITED2, PPM1E, HDBP1, DnaJB9, Synaptotagmin, PRDX3, CNTN1 (F3), Thioredoxin, NDUFA4, ATP6V1A (70kD), HSPA4, Septin 1, Dynein, axonemal, light chains, PDE, Cystatin C, PPT1, SCF, SDHB, SLC39A10, IGSF9B, DKK3, LUZP2, ANKRD36B, NCKP1 subunit, HCN2, Guanylate cyclase alpha, FLJ20674, Galpha(q)-specific Class A Orphan/other GPCRs, IMPG2, CCK8, GPR124, TPH2, Neuropeptide gamma, KAL1, RAB39B, RGS4, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, TUSC3, UGT8, LINC00342, D330028D13Rik, Kv3.3, ORP-family, B3GN6, LY6G5B, Tenascin-C, HSDL1, CEACAM, TRPC5, PKC-beta, KIS, PAFAH gamma, TCP1-theta, PRDX1, G-protein beta/gamma, NET6(TSPAN13), NDUFB6, SDFR1, SUR, ABO system transferase, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, FUT2, UQCRB, CPT-1A, S100, FAM69A, Rab-6, TXNRD1, ORP8, KCNH5, AMIGO2, LASS6, PIMT, TRPV1, PRR12, PDK3, ZFHX4, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, Aldose reductase, NDUFB3, Rab-3, MTG16 (CBFA2T3), ATG9B, TM2D3, FAM38B, Ephrin-A receptor 5, LAPTM4B, IDUA, IP3KA, CRH receptor 2, SLC2A13, Semaphorin 5A, GRAIL, RPL9, NSF, Tomt, ADAM-TS10, FAM102B, CaMK IV, CHCHD2, GLRA, DKK2, GABA-A receptor beta-2 subunit, FBXO2, ZNF433, MYO15B, DOK7, SYP, Carbohydrate sulfotransferases, Rho GTPase, PDE4, GTPBP3, Lba1, G-protein gamma, UBE2D1, ZNF70, SOCS6, Dysferlin, Rap1GDS1, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, ChREBP, A830006F12Rik, Secretogranin V, EGF, ATP5B, Pro-CCK, SYTC, XKR4, Dynein, axonemal, heavy chains, Semaphorin 3E, MMADHC, LOC283174, HIST1H2BN, PKA-reg type II (cAMP-dependent), NELL1, cPKC (conventional), ATP6V1B2, NDUFB1, DLL4, ELOVL4, AP3S1, PSMA1, Serotonin receptor, CHMP5, Apelin, GABA-A receptor alpha-4 subunit, Rab-27B, PPID, TRPC, SLC7A5, HTR5A, Sp8, PDK4, VDAC 1, C17orf76, WIF1, COX VIa, CLCN4, Osteopontin, ZNF238, SMRT, Big ET-1, CysLT2 receptor, NHE6, Rab-3C, M-Ras, PKA-reg (cAMP-dependent), RNF152, Lingo1, ANT, PP1-cat, HMDH, Neurokinin A, PDLIM2, UQCR10, GUCY1A3, Clathrin heavy chain, Substance P, AP-3 sigma subunits, PSMD10 (Gankyrin), StARD4, GRM6, Histone H2, LIPA, MCT1 (SLC16A1), ARHGAP18, CCK5, COPS4, LRRC51, Galpha(q)-specific amine GPCRs, UQCRFS1, Ephrin-A receptors,

						Histone H2A, NPR3, C9orf5, GP-IB alpha, DOC1, Galpha(i)-specific amine GPCRs, Stch, TRPC4, LINGO1-AS1, SLC26A4-AS1, NCX1, DNAJC12, HCN, RTEL1-TNFRSF6B, Protein kinase G1, HLF, CAP1, HSP90 beta, TXNIP (VDUP1), Vinexin, COL25A1, MEGF6, NDUFS6, Calponin-1, Activin beta A, GABA-A receptor alpha-5 subunit, Zeta-sarcoglycan, CDK5, PANX2, PAK, Guanylate cyclase (alpha-1/beta-1), FLJ32001, SYT16, Glycine receptor, Fatty acid-binding protein, FOXP4, HINT, Synaptoporin, MAML1, IZUMO1, MDH1, ASAH, GABA-A receptor alpha-3 subunit, DYNLT, SPSY, COX Va, ATP5A, Glycine receptor beta chain, CAPZA, RTL1, PKC-beta2, Calcineurin A (catalytic), TOP1MT, Galpha(i)-specific cannabis GPSRs, Cyclin G1, sRAGE, SLC25A46, Glyoxalase I, PDH beta, Galpha(q)-specific peptide GPCRs, H2AFZ, Histone H2B, MAFbx, SNAP190, NDUFA5, Tubulin alpha, Creatine kinase, ACAP1(CENTB1), DSCAML1, TBC1D10C, MRAP2, PAP-II, B-FABP, Azi1, C17orf72, Patched, TNK1, CHKB-AS1, XK, MEF2, SLC2A1-AS1, NAPB, ADAR3, PGAM1, HNMT, APRIO, SCS-A, BTBD10, MEK4/7, Peg10, ACSL4, ATF/CREB, GLGB, ODP2, RAI1, G-protein gamma 3, Hdj-2, CQ107, DelGIP1, LAMP2-C, FN14(TNFRSF12A), G-protein beta-4, Acyl-CoA synthetase, PP2A catalytic, GAS41, IDI1, AP-4, MRLC, BMI-1, SNAPs, eIF2S1, Galpha(s)-specific CRF GPCRs, LAMP2, COX VIa-1, YPEL5, ATP6V1B, Kv4.2 channel, PRNP, HSPC138, TMS-1, MPTP complex, ENC1, STAG3, RHEB2, NKCC1, Neurocalcin delta, Malin, HIST2H2BE, ATP6V0B, PKC-beta1, WDT2, Calmodulin, CENPP, LPL, DIRAS2, NELL2, SUMO-3, Apo-2L(TNFSF10), SET1B, LOXL2, FLJ45455, HSPC125, USMG5, Endophilin A1, Activin, Aquaporin 1, NDFIP1, C6orf27, NME5, Calcyclin, Syntenin 1, SCOT, Octanoyl-holo-acp, KCRS, Securin, ADHX, ERK1/2, CDw52, AATC, UGCG, Anks4b, NFIC, CaMK II delta, HSC70, SLC35A5, PKC, SSTR2, SUR1, HTR2A, PMM2, SLC25A4, MPP7, GS1-124K5.11, ARPP-19, K-cadherin (CDH6), Guanylate Cyclase 1, soluble, APEL13, MEF2C, Protein kinase G, ERK2 (MAPK1), DREV1, LISCH7, Ran, OAT, MEK4(MAP2K4), TMEM70, PRKAR1A, IGFALS, CCK8-GlyArgArg, CLCN5, IMPA1, UFC1, Nephrocystin-4, DKK1, sKITLG, SSTR1, Guanine deaminase, PRPS, SOD1, TFIIB, KIAA1024, PPP4R2, GSE1, MMP-28, SAP102, FSTL5, SPDYE5, CALM2, Cyclophilin A, FOXP1/2/4 proteins, PI3K reg class IA, PTCHD1, DBH-AS1, Galpha(s)-specific peptide GPCRs, TCP1-alpha, ATP5L, ACTR3, ATP6AP2, OXR1, CALB1, Tubulin alpha-4A, SRm300, RhoE, Pcdh19, CD166, GAD2, TCP1-epsilon, NF-I, MRPL3, HXK3, Neuroserpin, COX VIIa-2, ACOXL, Midkine,

						SAMD10, ARP3, PXDN, 14-3-3, RAGE, 14-3-3 eta, ATP1beta subunit, ZCCHC12, SNX10, CMAS
17	Neoplasms by Site	25424	1.093E-15	1.404E-13	861	SCAP2, Cyclin G, FBXO45, NPY, C13orf36, FAM3C, PP2A cat (alpha), HSP90, PAK3, PAM, Cadherin 8, ZYG11B, CPSF1, ZNF575, ARP6, CXorf57, NPEPL1, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, ZNF34, Semaphorin 3C, Alpha crystallin B, TMEM87B, AEBP1, ET-1, G3BP2, RhoN, MBD6, IRF1, ILDR2, FILIP, ZnT-2, MAL2, GLSK, Rab-3B, MAGEH-1, SLC35E2B, COX VIc, SMVT, C1D, MEGF10, THAP11, TINP1, PTCH2, N-chimaerin, Tubulin alpha 1A, ATP5C, SUCLG1, HPCA, LOC284837, APJ, Smooth muscle myosin, EDIL3, FLJ12671, ELOVL5, GLB1B2, RNF207, Peroxiredoxin, Activin A, UBL5, D630023F18Rik, Esterase D, Endothelin-1, SULT1A1, Trehalase, Neuropeptide K, PSMB5, AP-1 gamma subunits, ARG2, T-plastin, DUOX1, Nkpd1, NETO2, GHITM, REV-ERBalpha, IL-17D, BRSK2, UQCRQPC, DYNLT3, P2Y11, UBXD3, G-protein beta, KLHL4, LAS1L, SC5D, JWA, ALDR, CRTL1, UQCRH, TMC4, Rab-6A, RGS8, Mucin 5B, SC4MOL, MRPS6, PSMA5, CNOT7, MDS028, NFKBIL2, NDUFAB1, Importin (karyopherin)-alpha, CCK8-Gly, NckAP1, KIAA1276, GLIPR, BTBD12, CDC18L (CDC6), ANKRD50, LSMD1, DNAH1, MRPL1, Lgi4, GPR137C, TTLL9, MOBKL1A, AP1G2, ZNF707, LOC153328, Pannexin-1, MCM6, OGFRL1, NKIRAS1, DCMC, HPCAL4, RHBDL3, PSD2, FAM90A1, NIPSNAP3A, MGF, PDH E2 subunit N6-lipoyllysine, TIP47, PRKAR2B, MELC, PLD5, DPY19L1, NPFF receptor 2, NDUFB4, MC4R, UNRIP, NDUFA8, KLHL12, Synaptotagmin I, COCH, Guanylate cyclase, ARL6, KCNK2, HSP70, CCDC4, SCRT2, Substance P extracellular region, DDX3Y, CNR1, MAPBPIP, MYL6, Glycogen phosphorylase, Synaptotagmin IV, Tim17, CITED2, PPM1E, SLIRP, HDBP1, NUDT4P1, GIMAP7, DnaJB9, Synaptotagmin, PRDX3, CNTN1 (F3), Thioredoxin, MRLC2, NDUFA4, ZMAT1, ATP6V1A (70kD), HSPA4, JMJD3, Septin 1, Dynein, axonemal, light chains, PDE, Cystatin C, CNIH2, Tcfl5, PPT1, SCF, SDHB, MGAT4A, SLC39A10, IGSF9B, DKK3, Karyopherin alpha 2, LUZP2, VIPR1-AS1, PNMAL1, NCKP1 subunit, TM9SF2, HCN2, D123, LOC441108, Guanylate cyclase alpha, FLJ20674, Galpha(q)-specific Class A Orphan/other GPCRs, IMPG2, LMF1, OAF, ATP5G, C6orf168, CCK8, GPR124, TPH2, Neuropeptide gamma, KAL1, RAB39B, Aha1, PTPN18, RGS4, VSIG2, VDAC 3, 14-3-3 beta/alpha, BTBD18, GABA-A receptor alpha-1 subunit, TUSC3, UGT8, D330028D13Rik, GUCY1B1, FLRT3, Exostosin-like 2, Kv3.3, SELI, C13orf37, ORP-family, B3GN6, LY6G5B, Tenascin-C, Myopodin, HSDL1, PP1-cat gamma,

						CEACAM, ODF3, TRPC5, PKC-beta, KIS, PAFAH gamma, TCP1-theta, PRDX1, ELMO3, G-protein beta/gamma, B3GN1, NET6(TSPAN13), SLC25A45, NDUFB6, SDFR1, SUR, ABO system transferase, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, VBP-1, FUT2, TORC1, KLHL13, UQCRB, ATP5E, SCRT1, CPT-1A, S100, Rab-6, TXNRD1, ORP8, KCNH5, AMIGO2, VWA2, LINC02043, FLJ38984, LASS6, TRPV1, PRR12, PDK3, ZFHX4, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, TIP41, ATP6V1C1, PRRG1, ZDH13, Aldose reductase, ATP6M, NDUFB3, Rab-3, MTG16 (CBFA2T3), ATG9B, TM2D3, DNER, FAM38B, APOL3, TMEM45A, ZFHX2, Ephrin-A receptor 5, LAPTM4B, IDUA, IP3KA, CRH receptor 2, AMDHD2, CacyBP(SIP), InsP6 kinase 3, SLC2A13, Semaphorin 5A, Adropin, V-ATPase E subunit, GRAIL, UBA1L, NSF, Tomt, ADAM-TS10, GPR176, FAM102B, CaMK IV, CHCHD2, GLRA, DKK2, ZNF499, GABA-A receptor beta-2 subunit, FBXO2, H41, ZNF433, CECR2, DOK7, SYP, Carbohydrate sulfotransferases, TIMM17, LACTB2, LPL1, Rho GTPase, PDE4, GTPBP3, Tensin 2, Lba1, G-protein gamma, UBE2D1, OSGIN2, PLCXD2, PRPS2, ZNF70, SOCS6, Dysferlin, Rap1GDS1, Ephrin-A receptor 4, TMEM86B, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, ChREBP, ZNF267, A830006F12Rik, PP4R4, Secretogranin V, EGF, GlyRA2, ATP5B, PPase (inorganic), NAP1L2, Pro-CCK, CED-6, SYTC, XKR4, Dynein, axonemal, heavy chains, B3GALTL, BMPR1A, Semaphorin 3E, MMADHC, MMD, LOC283174, HIST1H2BN, Neurexophilin 2, RBM18, PKA-reg type II (cAMP-dependent), B3GNT4, Myotrophin, NELL1, CAP2, HKR4, cPKC (conventional), SF3A2, ATP6V1B2, NDUFB1, DLL4, ELOVL4, AP3S1, PSMA1, Serotonin receptor, CHMP5, Apelin, Neurexophilin 1, AP complex 2 small (sigma) chain, TMEM39B, ADSS, Rab-27B, mADAMTS5, PPID, TRPC, SLC7A5, HTR5A, PYGM, NOP14-AS1, ACTR10, PDK4, VDAC 1, C17orf76, WIF1, NDRG3, COX VIa, SUCB1, ATP6V1H, Osteopontin, ATP5G3, Slp5, ABHD10, SLC6A1-AS1, SMRT, Big ET-1, CysLT2 receptor, NHE6, Rab-3C, M-Ras, KCY, CREB4, PC4, SMIM43_132332, CHAMP, PKA-reg (cAMP-dependent), TReP-132, RNF152, Lingo1, ANT, PP1-cat, CFA74, HMDH, Neurokinin A, PDLIM2, NR3A, KLHDC4, VTA1, Cables1, KIAA1110, ECT2, Clathrin heavy chain, IL3RA, Substance P, AP-3 sigma subunits, HBXIP, PSMD10 (Gankyrin), StARD4, GRM6, CHTF18, CalDAG-GEFII, Histone H2, LIPA, KLHL35, MCT1 (SLC16A1), ARHGAP18, CCK5, TMEM14A, LRRC51, Galpha(q)-specific amine GPCRs, UQCRFS1, Maestro, Ephrin-A receptors, MRPL47, Histone H2A, HMP19, NPR3, C9orf5, GP-IB alpha,

						DOC1, Galpha(i)-specific amine GPCRs, CCNI2, Stch, DAT1, TRPC4, PMCA1, LINGO1-AS1, Rab-23, NCX1, DNAJC12, SLBP, HCN, RTEL1-TNFRSF6B, Protein kinase G1, HLF, BDH, C1orf113, LENG8, CAP1, HSP90 beta, Anillin, TXNIP (VDUP1), Vinexin, COL25A1, C14orf142, PMS2L3, MEGF6, NDUFS6, Calponin-1, Activin beta A, BRMS1L, Zeta-sarcoglycan, CDK5, PANX2, DUS3L, PAK, Guanylate cyclase (alpha-1/beta-1), FLJ32001, SYT16, Guanylate cyclase beta, BEX1, TCP1-eta, Glycine receptor, Fatty acid-binding protein, Tmem134, PSG3, FOXP4, HINT, ENPP4, MAML1, KIAA0143, MORN1, SOHLH1, IZUMO1, FLJ37078, TOM22, GTL3, USP2-AS1, ASAH, GABA-A receptor alpha-3 subunit, GNT-IV, LPPR4, ISOC1, DYNLT, SLC16A13, Atg101, TMEM74, TM6SF1, BEX2, SPSY, COX Va, Tetraspanin-3, Copine-4, Destrin, eIF4A2, BRK, ATP5A, Glycine receptor beta chain, Nek8, Selenoprotein P, CAPZA, Carbonic anhydrase XII, Kv9.3, RTL1, PKC-beta2, Calcineurin A (catalytic), LSM2, TOP1MT, Galpha(i)-specific cannabis GPSRs, STARD7, B3GT2, Cyclin G1, sRAGE, SLC25A46, SEC23A, Glyoxalase I, DDX51, SMIT, FBI-1 (Pokemon), PDH beta, Galpha(q)-specific peptide GPCRs, H2AFZ, ATP6V1C, Histone H2B, NCOA4 (ARA70), MAFbx, SNAP190, WDR47, NDUFA5, Tubulin alpha, Creatine kinase, ACAP1(CENTB1), DSCAML1, TBC1D10C, DCK, MRAP2, PAP-II, B-FABP, VIP32, Azi1, NUDT4, DYNLL, Patched, TNK1, XK, MEF2, INCA1, SLC2A1-AS1, NAPB, ADAR3, BICRA, PGAM1, HNMT, TAPBPL, Sec23, APRIO, SCS-A, BTBD10, MEK4/7, Peg10, ACSL4, RENBP, LOC440248, F262, CEACAM1, RANBP6, ATF/CREB, GLGB, ODP2, RAI1, G-protein gamma 3, Hdj-2, LAMP2-C, FN14(TNFRSF12A), Trim45, RSL24D1, C3orf59, G-protein beta-4, FEM1B, Acyl-CoA synthetase, PP2A catalytic, SULT1A1 isoform 1, CAPZA2, GAS41, IDI1, SNX7, ARRDC2, ZFAND2A, AP-4, MRLC, eIF4A, BMI-1, C9orf106, SNAPs, OAZIN, eIF2S1, Glutaredoxin, DLC1 (Dynein LC8a), RNF175, Galpha(s)-specific CRF GPCRs, LAMP2, COX VIa-1, C1orf115, KAD6, ALAS1, TMEM87A, YPEL5, TSNARE1, ATP6V1B, Quinone oxidoreductase, Kv4.2 channel, JKAMP, PKD1L1, Protein kinase G 2, PRNP, HSPC138, Osrf, SLC16A1-AS1, FAM22A, TM2D2, DNAJA2, TMS-1, MPTP complex, ENC1, STAG3, RHEB2, CENPL, NKCC1, Neurocalcin delta, Malin, C1orf59, HIST2H2BE, ATP6V0B, PKC-beta1, PDE4A, WDT2, ZSCAN1, CAB39L, Calmodulin, CENPP, LPL, DIRAS2, NELL2, SUMO-3, FLJ31818, PGRMC1, ATP6V1E, Apo-2L(TNFSF10), SET1B, LOXL2, PDE11A, FLJ45455, NOLA3 (NOP10), HSPC125, USMG5, Endophilin A1, STAC2, Activin, SIPAR, C1orf43, Aquaporin 1, NDFIP1, KCTD16, C6orf27, NME5, CLIC4, Calcyclin, FAM186B,

						Syntenin 1, SCOT, Octanoyl-holo-acp, KCRS, Securin, ADHX, ZNF517, ERK1/2, Carboxypeptidase M, CDw52, AATC, UGCG, SLC29A4, Anks4b, TRUB1, NFIC, CaMK II delta, HSC70, PI3K reg class IA (p55-gamma), ARL5, SLC35A5, PKC, SSTR2, SUR1, ABTB1, C19orf55, HTR2A, PMM2, SLC25A4, MPP7, CCDC57, ATP1B3, ARPP-19, K-cadherin (CDH6), Guanylate Cyclase 1, soluble, APEL13, MEF2C, SULT4A1, MRPL33, Protein kinase G, RIFK, ERK2 (MAPK1), Calcineurin A (beta), DREV1, SLC25A25-AS1, LISCH7, Ran, OAT, MEK4(MAP2K4), CBR3-AS1, DACH2, C14orf2, TMEM70, Mindin, PRKAR1A, IGFALS, CCK8-GlyArgArg, CLCN5, STX16-NPEPL1, IMPA1, TRIM23, UFC1, Nephrocystin-4, DKK1, PARM-1, sKITLG, SSTR1, Guanine deaminase, PRPS, SOD1, TFIIB, YIPF5, KIAA1024, PPP4R2, GDE1, SLC38A2, MMP-28, SAP102, FSTL5, EVI2A, MAP1, RPESP, CALM2, Cyclophilin A, FOXP1/2/4 proteins, Aggrecanase-2, PI3K reg class IA, KIAA1614, PTCHD1, DCoHM, CLDND1, Galpha(s)-specific peptide GPCRs, GPR22, TSPAN19, TCP1-alpha, ATP5L, ACTR3, ATP6AP2, OXR1, CALB1, Tubulin alpha-4A, CALML6, SRm300, RhoE, Pcdh19, CD166, TIP27, GAD2, DRIL2, SIAH3, PGM2L1, TCP1-epsilon, NF-I, MRPL3, HXK3, Neuroserpin, COX VIIa-2, ACOXL, NRBF2, Midkine, FLJ37464, SAMD10, IRS6(DOK5), ARP3, PXDN, 14-3-3, ARMCX3, ACCN3 (ASIC3), COX VIIa-2L, C8orf83, AATBC, RAGE, 14-3-3 eta, ATP1beta subunit, Myospryn, Glutaredoxin 1, ZCCHC12, SNX10, CMAS, TCTE3, CHST6
18	Congenital, Hereditary, and Neonatal Diseases and Abnormalities	9068	2.913E-15	3.533E-13	393	PLP1, Cyclin G, NPY, PP2A cat (alpha), PRPS1, HSP90, PAK3, NPEPL1, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Alpha crystallin B, AEBP1, ET-1, G3BP2, IRF1, ILDR2, MAL2, COX VIc, GAD1, SMVT, MEGF10, THAP11, PTCH2, N-chimaerin, Tubulin alpha 1A, SUCLG1, Smooth muscle myosin, ELOVL5, RNF207, Peroxiredoxin, Activin A, Esterase D, Endothelin-1, Trehalase, Neuropeptide K, PSMB5, AP-1 gamma subunits, ARG2, T-plastin, REV-ERBalpha, BRSK2, UQCRQPC, DYNLT3, G-protein beta, ALDR, UQCRH, Mucin 5B, PSMA5, NFKBIL2, NDUFAB1, CCK8-Gly, NckAP1, BTBD12, NDUFA1, LSMD1, DNAH1, Lgi4, MCM6, OGFRL1, DCMC, MGF, PDH E2 subunit N6-lipoyllysine, PRKAR2B, MELC, NDUFB4, MC4R, NDUFA8, Synaptotagmin I, Guanylate cyclase, ARL6, HSP70, Substance P extracellular region, CNR1, Glycogen phosphorylase, Synaptotagmin IV, CITED2, HDBP1, Synaptotagmin, PRDX3, Thioredoxin, NDUFA4, ATP6V1A (70kD), HSPA4, Dynein, axonemal, light chains, PDE, Cystatin C, PPT1, SCF, SDHB, IGSF9B, ANKRD36B, NCKP1 subunit, Galpha(q)-specific Class A Orphan/other GPCRs, IMPG2, CCK8, GPR124, TPH2, Neuropeptide gamma, KAL1, RAB39B, 14-3-3

						beta/alpha, GABA-A receptor alpha-1 subunit, UGT8, Exostosin-like 2, Kv3.3, ORP-family, B3GN6, Tenascin-C, CEACAM, TRPC5, PKC-beta, TCP1-theta, PRDX1, ELMO3, G-protein beta/gamma, NDUFB6, SUR, ABO system transferase, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, FUT2, UQCRB, CPT-1A, S100, TXNRD1, CC188, ORP8, PIMT, TRPV1, PDK3, ZFHX4, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, Aldose reductase, NDUFB3, Rab-3, FAM38B, ZFHX2, IDUA, V-ATPase E subunit, GRAIL, GPR176, CaMK IV, CHCHD2, GABA-A receptor beta-2 subunit, DOK7, SYP, Carbohydrate sulfotransferases, MOCS2(small), Rho GTPase, PDE4, G-protein gamma, UBE2D1, PRPS2, Dysferlin, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, ChREBP, EGF, Pro-CCK, SYTC, Dynein, axonemal, heavy chains, B3GALTL, BMPR1A, MMADHC, LOC283174, PKA-reg type II (cAMP-dependent), NELL1, cPKC (conventional), NDUFB1, DLL4, ELOVL4, Serotonin receptor, GABA-A receptor alpha-4 subunit, TRPC, HTR5A, PYGM, Sp8, ACTR10, MOC2B, WIF1, COX VIa, CLCN4, Osteopontin, SMRT, Big ET-1, CysLT2 receptor, NHE6, M-Ras, PKA-reg (cAMP-dependent), ANT, HMDH, Neurokinin A, PDLIM2, UQCR10, Clathrin heavy chain, Substance P, StARD4, GRM6, Histone H2, LIPA, MCT1 (SLC16A1), CCK5, COPS4, Galpha(q)-specific amine GPCRs, UQCRFS1, Ephrin-A receptors, Histone H2A, NPR3, C9orf5, GP-IB alpha, Galpha(i)-specific amine GPCRs, TRPC4, PMCA1, DNAJC12, HCN, RTEL1-TNFRSF6B, HLF, CAP1, TXNIP (VDUP1), COL25A1, C14orf142, MEGF6, NDUFS6, Activin beta A, GABA-A receptor alpha-5 subunit, CDK5, PAK, FLJ32001, SYT16, Fatty acid-binding protein, PSG3, HINT, MAML1, IZUMO1, MDH1, ASAH, GABA-A receptor alpha-3 subunit, DYNLT, SPOCK3, SPSY, COX Va, Tetraspanin-3, ATP5A, Nek8, CAPZA, PKC-beta2, Calcineurin A (catalytic), TOP1MT, Galpha(i)-specific cannabis GPSRs, Cyclin G1, sRAGE, SLC25A46, SEC23A, Glyoxalase I, Galpha(q)-specific peptide GPCRs, ATP6V1C, Histone H2B, MAFbx, NDUFA5, Tubulin alpha, Creatine kinase, DSCAML1, MRAP2, B-FABP, Azi1, Patched, TNK1, XK, MEF2, SLC2A1-AS1, NAPB, HNMT, Sec23, APRIO, SCS-A, MEK4/7, ACSL4, ATF/CREB, GLGB, ODP2, RAI1, G-protein gamma 3, Hdj-2, CQ107, LAMP2-C, FN14(TNFRSF12A), G-protein beta-4, Acyl-CoA synthetase, PP2A catalytic, IDI1, MRLC, BMI-1, SNAPs, RNF175, Galpha(s)-specific CRF GPCRs, LAMP2, COX VIa-1, YPEL5, ATP6V1B, Kv4.2 channel, PRNP, HSPC138, SLC16A1-AS1, MPTP complex, RHEB2, NKCC1, Malin, PKC-beta1, PDE4A, LPL, NELL2, SUMO-3, ATP6V1E, Apo-2L(TNFSF10), LOXL2, PDE11A, NOLA3 (NOP10),

						HSPC125, USMG5, Activin, Aquaporin 1, NME5, Calcyclin, SCOT, Octanoyl-holo-acp, ZNF517, ERK1/2, AATC, UGCG, NFIC, CaMK II delta, HSC70, PKC, SUR1, HTR2A, PMM2, SLC25A4, GS1-124K5.11, K-cadherin (CDH6), MEF2C, ERK2 (MAPK1), OAT, MEK4(MAP2K4), DACH2, TMEM70, PRKAR1A, IGFALS, CCK8-GlyArgArg, CLCN5, IMPA1, UFC1, Nephrocystin-4, DKK1, sKITLG, PRPS, SOD1, TFIIB, SAP102, SPDYE5, Cyclophilin A, FOXP1/2/4 proteins, PI3K reg class IA, PTCHD1, CLDND1, Galpha(s)-specific peptide GPCRs, TCP1-alpha, ACTR3, ATP6AP2, CALB1, SRm300, Pcdh19, CD166, TIP27, DRIL2, TCP1-epsilon, NF-I, MRPL3, HXK3, Neuroserpin, COX VIIa-2, ACOXL, Midkine, SAMD10, ARP3, PXDN, 14-3-3, RAGE, ATP1beta subunit, CHST6
19	Schizophrenia	1615	3.534E-15	4.060E-13	111	PLP1, NPY, HSP90, Galpha(s)-specific nucleotide-like GPCRs, GLSK, GAD1, MEGF10, Peroxiredoxin, Neuropeptide K, G-protein beta, Importin (karyopherin)-alpha, CCK8-Gly, HSP70, Substance P extracellular region, CNR1, Synaptotagmin, MRLC2, ATP6V1A (70kD), PDE, PPT1, Galpha(q)-specific Class A Orphan/other GPCRs, CCK8, TPH2, Neuropeptide gamma, RGS4, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, KIS, G-protein beta/gamma, SDFR1, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, S100, FAM69A, PIMT, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, CRH receptor 2, GABA-A receptor beta-2 subunit, SYP, Carbohydrate sulfotransferases, PDE4, Galpha(i)-specific metabotropic glutamate GPCRs, EGF, Pro-CCK, cPKC (conventional), Serotonin receptor, GABA-A receptor alpha-4 subunit, ADSS, HTR5A, Neurokinin A, IL3RA, Substance P, CCK5, Galpha(q)-specific amine GPCRs, Galpha(i)-specific amine GPCRs, Protein kinase G1, NDUFS6, GABA-A receptor alpha-5 subunit, PANX2, Fatty acid-binding protein, MDH1, eIF4A2, ATP5A, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, Glyoxalase I, Galpha(q)-specific peptide GPCRs, Tubulin alpha, Creatine kinase, B-FABP, HNMT, APRIO, ACSL4, ATF/CREB, Acyl-CoA synthetase, MRLC, eIF4A, Galpha(s)-specific CRF GPCRs, PRNP, PDE4A, Calmodulin, PDE11A, Endophilin A1, Aquaporin 1, ADHX, ERK1/2, HSC70, PI3K reg class IA (p55-gamma), PKC, HTR2A, SULT4A1, Protein kinase G, ERK2 (MAPK1), OAT, CCK8-GlyArgArg, SOD1, SAP102, CALM2, Cyclophilin A, FOXP1/2/4 proteins, PI3K reg class IA, DBH-AS1, Galpha(s)-specific peptide GPCRs, TCP1-alpha, CALB1, GAD2, COX VIIa-2, 14-3-3, 14-3-3 eta
20	Schizophrenia Spectrum and Other Psychotic Disorders	1675	6.978E-15	7.616E-13	113	PLP1, NPY, HSP90, Galpha(s)-specific nucleotide-like GPCRs, GLSK, GAD1, MEGF10, Smooth muscle myosin, Peroxiredoxin, Neuropeptide K, G-protein beta, Importin (karyopherin)-alpha,

						CCK8-Gly, HSP70, Substance P extracellular region, CNR1, Synaptotagmin, MRLC2, ATP6V1A (70kD), PDE, PPT1, Galpha(q)-specific Class A Orphan/other GPCRs, CCK8, TPH2, Neuropeptide gamma, RGS4, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, KIS, G-protein beta/gamma, SDFR1, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, S100, FAM69A, PIMT, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, CRH receptor 2, GABA-A receptor beta-2 subunit, SYP, Carbohydrate sulfotransferases, PDE4, Galpha(i)-specific metabotropic glutamate GPCRs, EGF, Pro-CCK, cPKC (conventional), Serotonin receptor, GABA-A receptor alpha-4 subunit, ADSS, HTR5A, Neurokinin A, IL3RA, Substance P, CCK5, Galpha(q)-specific amine GPCRs, Galpha(i)-specific amine GPCRs, Protein kinase G1, NDUFS6, GABA-A receptor alpha-5 subunit, PANX2, Fatty acid-binding protein, MDH1, GABA-A receptor alpha-3 subunit, eIF4A2, ATP5A, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, Glyoxalase I, Galpha(q)-specific peptide GPCRs, Tubulin alpha, Creatine kinase, B-FABP, HNMT, APRIO, ACSL4, ATF/CREB, Acyl-CoA synthetase, MRLC, eIF4A, Galpha(s)-specific CRF GPCRs, PRNP, PDE4A, Calmodulin, PDE11A, Endophilin A1, Aquaporin 1, ADHX, ERK1/2, HSC70, PI3K reg class IA (p55-gamma), PKC, HTR2A, SULT4A1, Protein kinase G, ERK2 (MAPK1), OAT, CCK8-GlyArgArg, SOD1, SAP102, CALM2, Cyclophilin A, FOXP1/2/4 proteins, PI3K reg class IA, DBH-AS1, Galpha(s)-specific peptide GPCRs, TCP1-alpha, CALB1, GAD2, COX VIIa-2, 14-3-3, 14-3-3 eta
21	Thoracic Neoplasms	20326	9.992E-15	1.039E-12	733	SCAP2, Cyclin G, FBXO45, C13orf36, FAM3C, PP2A cat (alpha), HSP90, PAK3, PAM, Cadherin 8, ZYG11B, CPSF1, ZNF575, ARP6, CXorf57, NPEPL1, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, ZNF34, Semaphorin 3C, TMEM87B, AEBP1, ET-1, G3BP2, MBD6, IRF1, ILDR2, FILIP, ZnT-2, MAL2, Rab-3B, MAGEH-1, COX VIc, SMVT, C1D, MEGF10, THAP11, PTCH2, N-chimaerin, Tubulin alpha 1A, ATP5C, SUCLG1, HPCA, APJ, Smooth muscle myosin, EDIL3, FLJ12671, ELOVL5, GLB1B2, RNF207, Peroxiredoxin, Activin A, UBL5, D630023F18Rik, Esterase D, Endothelin-1, SULT1A1, Trehalase, Neuropeptide K, AP-1 gamma subunits, ARG2, DUOX1, Nkpd1, NETO2, GHITM, REV-ERBalpha, BRSK2, UQCRQPC, DYNLT3, UBXD3, G-protein beta, KLHL4, LAS1L, SC5D, ALDR, CRTL1, UQCRH, Rab-6A, RGS8, Mucin 5B, MRPS6, PSMA5, CNOT7, MDS028, NFKBIL2, NDUFAB1, Importin (karyopherin)-alpha, CCK8-Gly, NckAP1, GLIPR, BTBD12, CDC18L (CDC6), ANKRD50, LSMD1, DNAH1, MRPL1, Lgi4, GPR137C, TTLL9, MOBKL1A, AP1G2, ZNF707, LOC153328, Pannexin-1,

						MCM6, NKIRAS1, HPCAL4, RHBDL3, PSD2, FAM90A1, NIPSNAP3A, MGF, PDH E2 subunit N6-lipoyllysine, TIP47, PRKAR2B, MELC, PLD5, DPY19L1, NPFF receptor 2, NDUFB4, MC4R, UNRIP, NDUFA8, KLHL12, Synaptotagmin I, COCH, Guanylate cyclase, ARL6, KCNK2, HSP70, CCDC4, Substance P extracellular region, DDX3Y, MAPBPIP, MYL6, Glycogen phosphorylase, Synaptotagmin IV, Tim17, PPM1E, HDBP1, GIMAP7, DnaJB9, Synaptotagmin, PRDX3, CNTN1 (F3), Thioredoxin, MRLC2, NDUFA4, ZMAT1, ATP6V1A (70kD), HSPA4, JMJD3, Septin 1, Dynein, axonemal, light chains, PDE, CNIH2, Tcfl5, PPT1, SCF, SDHB, SLC39A10, IGSF9B, DKK3, Karyopherin alpha 2, LUZP2, PNMAL1, NCKP1 subunit, TM9SF2, HCN2, D123, LOC441108, FLJ20674, Galpha(q)-specific Class A Orphan/other GPCRs, IMPG2, LMF1, OAF, ATP5G, C6orf168, CCK8, GPR124, TPH2, Neuropeptide gamma, KAL1, RAB39B, RGS4, VSIG2, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, TUSC3, UGT8, D330028D13Rik, GUCY1B1, FLRT3, Exostosin-like 2, Kv3.3, SELI, ORP-family, B3GN6, LY6G5B, Tenascin-C, CEACAM, TRPC5, PKC-beta, KIS, PRDX1, G-protein beta/gamma, B3GN1, SLC25A45, NDUFB6, SDFR1, SUR, ABO system transferase, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, VBP-1, FUT2, TORC1, KLHL13, UQCRB, CPT-1A, S100, Rab-6, TXNRD1, ORP8, KCNH5, AMIGO2, VWA2, FLJ38984, LASS6, TRPV1, PRR12, PDK3, ZFHX4, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, ATP6V1C1, PRRG1, ZDH13, Aldose reductase, ATP6M, NDUFB3, Rab-3, MTG16 (CBFA2T3), TM2D3, DNER, FAM38B, APOL3, TMEM45A, Ephrin-A receptor 5, LAPTM4B, IDUA, IP3KA, CRH receptor 2, AMDHD2, CacyBP(SIP), InsP6 kinase 3, SLC2A13, Semaphorin 5A, V-ATPase E subunit, GRAIL, NSF, Tomt, ADAM-TS10, GPR176, FAM102B, CaMK IV, CHCHD2, GLRA, DKK2, ZNF499, GABA-A receptor beta-2 subunit, FBXO2, ZNF433, CECR2, SYP, Carbohydrate sulfotransferases, TIMM17, LACTB2, LPL1, Rho GTPase, PDE4, GTPBP3, Tensin 2, Lba1, G-protein gamma, UBE2D1, OSGIN2, PLCXD2, PRPS2, ZNF70, SOCS6, Dysferlin, Rap1GDS1, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, ChREBP, ZNF267, A830006F12Rik, PP4R4, Secretogranin V, EGF, GlyRA2, ATP5B, PPase (inorganic), NAP1L2, Pro-CCK, CED-6, SYTC, XKR4, Dynein, axonemal, heavy chains, B3GALTL, BMPR1A, Semaphorin 3E, MMADHC, MMD, LOC283174, HIST1H2BN, Neurexophilin 2, RBM18, PKA-reg type II (cAMP-dependent), B3GNT4, Myotrophin, NELL1, CAP2, HKR4, cPKC (conventional), SF3A2, ATP6V1B2, NDUFB1, DLL4, ELOVL4,

						Serotonin receptor, CHMP5, Neurexophilin 1, TMEM39B, ADSS, Rab-27B, mADAMTS5, TRPC, SLC7A5, HTR5A, ACTR10, PDK4, VDAC 1, WIF1, COX VIa, SUCB1, ATP6V1H, Osteopontin, ATP5G3, Slp5, ABHD10, SMRT, Big ET-1, CysLT2 receptor, NHE6, Rab-3C, KCY, CREB4, PC4, SMIM43_132332, CHAMP, PKA-reg (cAMP-dependent), TReP-132, RNF152, Lingo1, ANT, PP1-cat, CFA74, Neurokinin A, PDLIM2, NR3A, KLHDC4, VTA1, Cables1, KIAA1110, ECT2, Clathrin heavy chain, IL3RA, Substance P, AP-3 sigma subunits, HBXIP, PSMD10 (Gankyrin), StARD4, GRM6, CHTF18, CalDAG-GEFII, Histone H2, LIPA, KLHL35, MCT1 (SLC16A1), ARHGAP18, CCK5, TMEM14A, LRRC51, Galpha(q)-specific amine GPCRs, UQCRFS1, Maestro, Ephrin-A receptors, MRPL47, Histone H2A, HMP19, NPR3, GP-IB alpha, DOC1, Galpha(i)-specific amine GPCRs, Stch, TRPC4, PMCA1, NCX1, DNAJC12, SLBP, HCN, Protein kinase G1, HLF, BDH, C1orf113, LENG8, CAP1, HSP90 beta, Anillin, TXNIP (VDUP1), Vinexin, COL25A1, MEGF6, NDUFS6, Calponin-1, Activin beta A, BRMS1L, Zeta-sarcoglycan, CDK5, PANX2, DUS3L, PAK, Guanylate cyclase (alpha-1/beta-1), FLJ32001, SYT16, Guanylate cyclase beta, BEX1, TCP1-eta, Glycine receptor, Fatty acid-binding protein, Tmem134, PSG3, FOXP4, HINT, ENPP4, MAML1, KIAA0143, MORN1, SOHLH1, IZUMO1, FLJ37078, TOM22, GABA-A receptor alpha-3 subunit, GNT-IV, LPPR4, ISOC1, DYNLT, SLC16A13, Atg101, TMEM74, TM6SF1, Tetraspanin-3, Copine-4, Destrin, eIF4A2, ATP5A, Glycine receptor beta chain, Nek8, Selenoprotein P, CAPZA, Carbonic anhydrase XII, Kv9.3, RTL1, PKC-beta2, Calcineurin A (catalytic), LSM2, TOP1MT, Galpha(i)-specific cannabis GPSRs, STARD7, B3GT2, Cyclin G1, sRAGE, SEC23A, Glyoxalase I, DDX51, SMIT, FBI-1 (Pokemon), Galpha(q)-specific peptide GPCRs, H2AFZ, ATP6V1C, Histone H2B, SNAP190, WDR47, Tubulin alpha, Creatine kinase, ACAP1(CENTB1), DSCAML1, TBC1D10C, DCK, MRAP2, PAP-II, B-FABP, Azi1, DYNLL, Patched, TNK1, XK, MEF2, NAPB, ADAR3, BICRA, HNMT, Sec23, APRIO, SCS-A, BTBD10, MEK4/7, Peg10, ACSL4, RENBP, LOC440248, CEACAM1, RANBP6, ATF/CREB, GLGB, ODP2, RAI1, G-protein gamma 3, LAMP2-C, FN14(TNFRSF12A), Trim45, RSL24D1, C3orf59, G-protein beta-4, FEM1B, Acyl-CoA synthetase, PP2A catalytic, SULT1A1 isoform 1, CAPZA2, IDI1, SNX7, ARRDC2, ZFAND2A, AP-4, MRLC, eIF4A, BMI-1, C9orf106, SNAPs, eIF2S1, Glutaredoxin, RNF175, Galpha(s)-specific CRF GPCRs, LAMP2, C1orf115, KAD6, TMEM87A, YPEL5, TSNARE1, ATP6V1B, Kv4.2 channel, JKAMP, PKD1L1, Protein kinase G 2, PRNP, Osrf, FAM22A, DNAJA2, TMS-1, MPTP complex, ENC1,

						STAG3, RHEB2, CENPL, NKCC1, Malin, C1orf59, HIST2H2BE, ATP6V0B, PKC-beta1, PDE4A, WDT2, ZSCAN1, CAB39L, Calmodulin, CENPP, LPL, DIRAS2, NELL2, FLJ31818, PGRMC1, ATP6V1E, Apo-2L(TNFSF10), LOXL2, PDE11A, NOLA3 (NOP10), HSPC125, Endophilin A1, STAC2, Activin, SIPAR, C1orf43, Aquaporin 1, NDFIP1, KCTD16, C6orf27, Calcyclin, FAM186B, Syntenin 1, SCOT, Octanoyl-holo-acp, KCRS, Securin, ADHX, ZNF517, ERK1/2, Carboxypeptidase M, AATC, UGCG, SLC29A4, Anks4b, TRUB1, NFIC, HSC70, PI3K reg class IA (p55-gamma), SLC35A5, PKC, SSTR2, SUR1, ABTB1, C19orf55, HTR2A, SLC25A4, MPP7, CCDC57, ATP1B3, K-cadherin (CDH6), Guanylate Cyclase 1, soluble, MEF2C, SULT4A1, MRPL33, Protein kinase G, ERK2 (MAPK1), Calcineurin A (beta), LISCH7, Ran, OAT, MEK4(MAP2K4), DACH2, PRKAR1A, CCK8-GlyArgArg, CLCN5, STX16-NPEPL1, IMPA1, TRIM23, UFC1, Nephrocystin-4, DKK1, PARM-1, sKITLG, SSTR1, Guanine deaminase, PRPS, SOD1, TFIIB, YIPF5, KIAA1024, PPP4R2, GDE1, SLC38A2, MMP-28, SAP102, FSTL5, EVI2A, MAP1, RPESP, CALM2, Cyclophilin A, FOXP1/2/4 proteins, Aggrecanase-2, PI3K reg class IA, KIAA1614, PTCHD1, Galpha(s)-specific peptide GPCRs, GPR22, TSPAN19, TCP1-alpha, ATP5L, ACTR3, ATP6AP2, OXR1, CALB1, Tubulin alpha-4A, CALML6, SRm300, RhoE, CD166, TIP27, GAD2, DRIL2, SIAH3, PGM2L1, TCP1-epsilon, NF-I, MRPL3, HXK3, COX VIIa-2, ACOXL, NRBF2, Midkine, FLJ37464, SAMD10, IRS6(DOK5), ARP3, PXDN, 14-3-3, ARMCX3, ACCN3 (ASIC3), COX VIIa-2L, RAGE, 14-3-3 eta, ATP1beta subunit, Myospryn, Glutaredoxin 1, ZCCHC12, CMAS, CHST6
22	Respiratory Tract Neoplasms	20404	1.071E-14	1.062E-12	735	SCAP2, Cyclin G, FBXO45, C13orf36, FAM3C, PP2A cat (alpha), HSP90, PAK3, PAM, Cadherin 8, ZYG11B, CPSF1, ZNF575, ARP6, CXorf57, NPEPL1, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, ZNF34, Semaphorin 3C, TMEM87B, AEBP1, ET-1, G3BP2, MBD6, IRF1, ILDR2, FILIP, ZnT-2, MAL2, Rab-3B, MAGEH-1, COX VIc, SMVT, C1D, MEGF10, THAP11, PTCH2, N-chimaerin, Tubulin alpha 1A, ATP5C, SUCLG1, HPCA, APJ, Smooth muscle myosin, EDIL3, FLJ12671, ELOVL5, GLB1B2, RNF207, Peroxiredoxin, Activin A, UBL5, D630023F18Rik, Esterase D, Endothelin-1, SULT1A1, Trehalase, Neuropeptide K, AP-1 gamma subunits, ARG2, DUOX1, Nkpd1, NETO2, GHITM, REV-ERBalpha, BRSK2, UQCRQPC, DYNLT3, UBXD3, G-protein beta, KLHL4, LAS1L, SC5D, ALDR, CRTL1, UQCRH, Rab-6A, RGS8, Mucin 5B, MRPS6, PSMA5, CNOT7, MDS028, NFKBIL2, NDUFAB1, Importin (karyopherin)-alpha, CCK8-Gly, NckAP1, GLIPR, BTBD12, CDC18L (CDC6), ANKRD50, LSMD1, DNAH1, MRPL1, Lgi4, GPR137C,

						TTLL9, MOBKL1A, AP1G2, ZNF707, LOC153328, Pannexin-1, MCM6, OGFRL1, NKIRAS1, HPCAL4, RHBDL3, PSD2, FAM90A1, NIPSNAP3A, MGF, PDH E2 subunit N6-lipoyllysine, TIP47, PRKAR2B, MELC, PLD5, DPY19L1, NPFF receptor 2, NDUFB4, MC4R, UNRIP, NDUFA8, KLHL12, Synaptotagmin I, COCH, Guanylate cyclase, ARL6, KCNK2, HSP70, CCDC4, Substance P extracellular region, DDX3Y, MAPBPIP, MYL6, Glycogen phosphorylase, Synaptotagmin IV, Tim17, PPM1E, HDBP1, GIMAP7, DnaJB9, Synaptotagmin, PRDX3, CNTN1 (F3), Thioredoxin, MRLC2, NDUFA4, ZMAT1, ATP6V1A (70kD), HSPA4, JMJD3, Septin 1, Dynein, axonemal, light chains, PDE, CNIH2, Tcfl5, PPT1, SCF, SDHB, SLC39A10, IGSF9B, DKK3, Karyopherin alpha 2, LUZP2, PNMAL1, NCKP1 subunit, TM9SF2, HCN2, D123, LOC441108, FLJ20674, Galpha(q)-specific Class A Orphan/other GPCRs, IMPG2, LMF1, OAF, ATP5G, C6orf168, CCK8, GPR124, TPH2, Neuropeptide gamma, KAL1, RAB39B, RGS4, VSIG2, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, TUSC3, UGT8, D330028D13Rik, GUCY1B1, FLRT3, Exostosin-like 2, Kv3.3, SELI, ORP-family, B3GN6, LY6G5B, Tenascin-C, CEACAM, TRPC5, PKC-beta, KIS, PRDX1, G-protein beta/gamma, B3GN1, SLC25A45, NDUFB6, SDFR1, SUR, ABO system transferase, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, VBP-1, FUT2, TORC1, KLHL13, UQCRB, CPT-1A, S100, Rab-6, TXNRD1, ORP8, KCNH5, AMIGO2, VWA2, FLJ38984, LASS6, TRPV1, PRR12, PDK3, ZFHX4, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, ATP6V1C1, PRRG1, ZDH13, Aldose reductase, ATP6M, NDUFB3, Rab-3, MTG16 (CBFA2T3), TM2D3, DNER, FAM38B, APOL3, TMEM45A, Ephrin-A receptor 5, LAPTM4B, IDUA, IP3KA, CRH receptor 2, AMDHD2, CacyBP(SIP), InsP6 kinase 3, SLC2A13, Semaphorin 5A, V-ATPase E subunit, GRAIL, NSF, Tomt, ADAM-TS10, GPR176, FAM102B, CaMK IV, CHCHD2, GLRA, DKK2, ZNF499, GABA-A receptor beta-2 subunit, FBXO2, ZNF433, CECR2, DOK7, SYP, Carbohydrate sulfotransferases, TIMM17, LACTB2, LPL1, Rho GTPase, PDE4, GTPBP3, Tensin 2, Lba1, G-protein gamma, UBE2D1, OSGIN2, PLCXD2, PRPS2, ZNF70, SOCS6, Dysferlin, Rap1GDS1, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, ChREBP, ZNF267, A830006F12Rik, PP4R4, Secretogranin V, EGF, GlyRA2, ATP5B, PPase (inorganic), NAP1L2, Pro-CCK, CED-6, SYTC, XKR4, Dynein, axonemal, heavy chains, B3GALTL, BMPR1A, Semaphorin 3E, MMADHC, MMD, LOC283174, HIST1H2BN, Neurexophilin 2, RBM18, PKA-reg type II (cAMP-dependent), B3GNT4, Myotrophin, NELL1, CAP2, HKR4, cPKC

						(conventional), SF3A2, ATP6V1B2, NDUFB1, DLL4, ELOVL4, Serotonin receptor, CHMP5, Neurexophilin 1, TMEM39B, ADSS, Rab-27B, mADAMTS5, TRPC, SLC7A5, HTR5A, ACTR10, PDK4, VDAC 1, WIF1, COX VIa, SUCB1, ATP6V1H, Osteopontin, ATP5G3, Slp5, ABHD10, SMRT, Big ET-1, CysLT2 receptor, NHE6, Rab-3C, KCY, CREB4, PC4, SMIM43_132332, CHAMP, PKA-reg (cAMP-dependent), TReP-132, RNF152, Lingo1, ANT, PP1-cat, CFA74, Neurokinin A, PDLIM2, NR3A, KLHDC4, VTA1, Cables1, KIAA1110, ECT2, Clathrin heavy chain, IL3RA, Substance P, AP-3 sigma subunits, HBXIP, PSMD10 (Gankyrin), StARD4, GRM6, CHTF18, CalDAG-GEFII, Histone H2, LIPA, KLHL35, MCT1 (SLC16A1), ARHGAP18, CCK5, TMEM14A, LRRC51, Galpha(q)-specific amine GPCRs, UQCRFS1, Maestro, Ephrin-A receptors, MRPL47, Histone H2A, HMP19, NPR3, GP-IB alpha, DOC1, Galpha(i)-specific amine GPCRs, Stch, TRPC4, PMCA1, NCX1, DNAJC12, SLBP, HCN, Protein kinase G1, HLF, BDH, C1orf113, LENG8, CAP1, HSP90 beta, Anillin, TXNIP (VDUP1), Vinexin, COL25A1, MEGF6, NDUFS6, Calponin-1, Activin beta A, BRMS1L, Zeta-sarcoglycan, CDK5, PANX2, DUS3L, PAK, Guanylate cyclase (alpha-1/beta-1), FLJ32001, SYT16, Guanylate cyclase beta, BEX1, TCP1-eta, Glycine receptor, Fatty acid-binding protein, Tmem134, PSG3, FOXP4, HINT, ENPP4, MAML1, KIAA0143, MORN1, SOHLH1, IZUMO1, FLJ37078, TOM22, GABA-A receptor alpha-3 subunit, GNT-IV, LPPR4, ISOC1, DYNLT, SLC16A13, Atg101, TMEM74, TM6SF1, Tetraspanin-3, Copine-4, Destrin, eIF4A2, ATP5A, Glycine receptor beta chain, Nek8, Selenoprotein P, CAPZA, Carbonic anhydrase XII, Kv9.3, RTL1, PKC-beta2, Calcineurin A (catalytic), LSM2, TOP1MT, Galpha(i)-specific cannabis GPSRs, STARD7, B3GT2, Cyclin G1, sRAGE, SEC23A, Glyoxalase I, DDX51, SMIT, FBI-1 (Pokemon), Galpha(q)-specific peptide GPCRs, H2AFZ, ATP6V1C, Histone H2B, SNAP190, WDR47, Tubulin alpha, Creatine kinase, ACAP1(CENTB1), DSCAML1, TBC1D10C, DCK, MRAP2, PAP-II, B-FABP, Azi1, DYNLL, Patched, TNK1, XK, MEF2, INCA1, NAPB, ADAR3, BICRA, HNMT, Sec23, APRIO, SCS-A, BTBD10, MEK4/7, Peg10, ACSL4, RENBP, LOC440248, CEACAM1, RANBP6, ATF/CREB, GLGB, ODP2, RAI1, G-protein gamma 3, LAMP2-C, FN14(TNFRSF12A), Trim45, RSL24D1, C3orf59, G-protein beta-4, FEM1B, Acyl-CoA synthetase, PP2A catalytic, SULT1A1 isoform 1, CAPZA2, IDI1, SNX7, ARRDC2, ZFAND2A, AP-4, MRLC, eIF4A, BMI-1, C9orf106, SNAPs, eIF2S1, Glutaredoxin, RNF175, Galpha(s)-specific CRF GPCRs, LAMP2, C1orf115, KAD6, TMEM87A, YPEL5, TSNARE1, ATP6V1B, Kv4.2 channel, JKAMP, PKD1L1, Protein kinase G 2,

						PRNP, Osrf, FAM22A, DNAJA2, TMS-1, MPTP complex, ENC1, STAG3, RHEB2, CENPL, NKCC1, Malin, C1orf59, HIST2H2BE, ATP6V0B, PKC-beta1, PDE4A, WDT2, ZSCAN1, CAB39L, Calmodulin, CENPP, LPL, DIRAS2, NELL2, FLJ31818, PGRMC1, ATP6V1E, Apo-2L(TNFSF10), LOXL2, PDE11A, NOLA3 (NOP10), HSPC125, Endophilin A1, STAC2, Activin, SIPAR, C1orf43, Aquaporin 1, NDFIP1, KCTD16, C6orf27, Calcyclin, FAM186B, Syntenin 1, SCOT, Octanoyl-holo-acp, KCRS, Securin, ADHX, ZNF517, ERK1/2, Carboxypeptidase M, AATC, UGCG, SLC29A4, Anks4b, TRUB1, NFIC, HSC70, PI3K reg class IA (p55-gamma), SLC35A5, PKC, SSTR2, SUR1, ABTB1, C19orf55, HTR2A, SLC25A4, MPP7, CCDC57, ATP1B3, K-cadherin (CDH6), Guanylate Cyclase 1, soluble, MEF2C, SULT4A1, MRPL33, Protein kinase G, ERK2 (MAPK1), Calcineurin A (beta), LISCH7, Ran, OAT, MEK4(MAP2K4), DACH2, CCK8-GlyArgArg, CLCN5, STX16-NPEPL1, IMPA1, TRIM23, UFC1, Nephrocystin-4, DKK1, PARM-1, sKITLG, SSTR1, Guanine deaminase, PRPS, SOD1, TFIIB, YIPF5, KIAA1024, PPP4R2, GDE1, SLC38A2, MMP-28, SAP102, FSTL5, EVI2A, MAP1, RPESP, CALM2, Cyclophilin A, FOXP1/2/4 proteins, Aggrecanase-2, PI3K reg class IA, KIAA1614, PTCHD1, Galpha(s)-specific peptide GPCRs, GPR22, TSPAN19, TCP1-alpha, ATP5L, ACTR3, ATP6AP2, OXR1, CALB1, Tubulin alpha-4A, CALML6, SRm300, RhoE, CD166, TIP27, GAD2, DRIL2, SIAH3, PGM2L1, TCP1-epsilon, NF-I, MRPL3, HXK3, COX VIIa-2, ACOXL, NRBF2, Midkine, FLJ37464, SAMD10, IRS6(DOK5), ARP3, PXDN, 14-3-3, ARMCX3, ACCN3 (ASIC3), COX VIIa-2L, RAGE, 14-3-3 eta, ATP1beta subunit, Myospryn, Glutaredoxin 1, ZCCHC12, CMAS, CHST6
23	Lung Neoplasms	20304	1.289E-14	1.224E-12	732	SCAP2, Cyclin G, FBXO45, C13orf36, FAM3C, PP2A cat (alpha), HSP90, PAK3, PAM, Cadherin 8, ZYG11B, CPSF1, ZNF575, ARP6, CXorf57, NPEPL1, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, ZNF34, Semaphorin 3C, TMEM87B, AEBP1, ET-1, G3BP2, MBD6, IRF1, ILDR2, FILIP, ZnT-2, MAL2, Rab-3B, MAGEH-1, COX VIc, SMVT, C1D, MEGF10, THAP11, PTCH2, N-chimaerin, Tubulin alpha 1A, ATP5C, SUCLG1, HPCA, APJ, Smooth muscle myosin, EDIL3, FLJ12671, ELOVL5, GLB1B2, RNF207, Peroxiredoxin, Activin A, UBL5, D630023F18Rik, Esterase D, Endothelin-1, SULT1A1, Trehalase, Neuropeptide K, AP-1 gamma subunits, ARG2, DUOX1, Nkpd1, NETO2, GHITM, REV-ERBalpha, BRSK2, UQCRQPC, DYNLT3, UBXD3, G-protein beta, KLHL4, LAS1L, SC5D, ALDR, CRTL1, UQCRH, Rab-6A, RGS8, Mucin 5B, MRPS6, PSMA5, CNOT7, MDS028, NFKBIL2, NDUFAB1, Importin (karyopherin)-alpha, CCK8-Gly, NckAP1, GLIPR, BTBD12, CDC18L

						(CDC6), ANKRD50, LSMD1, DNAH1, MRPL1, Lgi4, GPR137C, TTLL9, MOBKL1A, AP1G2, ZNF707, LOC153328, Pannexin-1, MCM6, NKIRAS1, HPCAL4, RHBDL3, PSD2, FAM90A1, NIPSNAP3A, MGF, PDH E2 subunit N6-lipoyllysine, TIP47, PRKAR2B, MELC, PLD5, DPY19L1, NPFF receptor 2, NDUFB4, MC4R, UNRIP, NDUFA8, KLHL12, Synaptotagmin I, COCH, Guanylate cyclase, ARL6, KCNK2, HSP70, CCDC4, Substance P extracellular region, DDX3Y, MAPBPIP, MYL6, Glycogen phosphorylase, Synaptotagmin IV, Tim17, PPM1E, HDBP1, GIMAP7, DnaJB9, Synaptotagmin, PRDX3, CNTN1 (F3), Thioredoxin, MRLC2, NDUFA4, ZMAT1, ATP6V1A (70kD), HSPA4, JMJD3, Septin 1, Dynein, axonemal, light chains, PDE, CNIH2, Tcfl5, PPT1, SCF, SDHB, SLC39A10, IGSF9B, DKK3, Karyopherin alpha 2, LUZP2, PNMAL1, NCKP1 subunit, TM9SF2, HCN2, D123, LOC441108, FLJ20674, Galpha(q)-specific Class A Orphan/other GPCRs, IMPG2, LMF1, OAF, ATP5G, C6orf168, CCK8, GPR124, TPH2, Neuropeptide gamma, KAL1, RAB39B, RGS4, VSIG2, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, TUSC3, UGT8, D330028D13Rik, GUCY1B1, FLRT3, Exostosin-like 2, Kv3.3, SELI, ORP-family, B3GN6, LY6G5B, Tenascin-C, CEACAM, TRPC5, PKC-beta, KIS, PRDX1, G-protein beta/gamma, B3GN1, SLC25A45, NDUFB6, SDFR1, SUR, ABO system transferase, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, VBP-1, FUT2, TORC1, KLHL13, UQCRB, CPT-1A, S100, Rab-6, TXNRD1, ORP8, KCNH5, AMIGO2, VWA2, FLJ38984, LASS6, TRPV1, PRR12, PDK3, ZFHX4, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, ATP6V1C1, PRRG1, ZDH13, Aldose reductase, ATP6M, NDUFB3, Rab-3, MTG16 (CBFA2T3), TM2D3, DNER, FAM38B, APOL3, TMEM45A, Ephrin-A receptor 5, LAPTM4B, IDUA, IP3KA, CRH receptor 2, AMDHD2, CacyBP(SIP), InsP6 kinase 3, SLC2A13, Semaphorin 5A, V-ATPase E subunit, GRAIL, NSF, Tomt, ADAM-TS10, GPR176, FAM102B, CaMK IV, CHCHD2, GLRA, DKK2, ZNF499, GABA-A receptor beta-2 subunit, FBXO2, ZNF433, CECR2, SYP, Carbohydrate sulfotransferases, TIMM17, LACTB2, LPL1, Rho GTPase, PDE4, GTPBP3, Tensin 2, Lba1, G-protein gamma, UBE2D1, OSGIN2, PLCXD2, PRPS2, ZNF70, SOCS6, Dysferlin, Rap1GDS1, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, ChREBP, ZNF267, A830006F12Rik, PP4R4, Secretogranin V, EGF, GlyRA2, ATP5B, PPase (inorganic), NAP1L2, Pro-CCK, CED-6, SYTC, XKR4, Dynein, axonemal, heavy chains, B3GALTL, BMPR1A, Semaphorin 3E, MMADHC, MMD, LOC283174, HIST1H2BN, Neurexophilin 2, RBM18, PKA-reg type II (cAMP-

						dependent), B3GNT4, Myotrophin, NELL1, CAP2, HKR4, cPKC (conventional), SF3A2, ATP6V1B2, NDUFB1, DLL4, ELOVL4, Serotonin receptor, CHMP5, Neurexophilin 1, TMEM39B, ADSS, Rab-27B, mADAMTS5, TRPC, SLC7A5, HTR5A, ACTR10, PDK4, VDAC 1, WIF1, COX VIa, SUCB1, ATP6V1H, Osteopontin, ATP5G3, Slp5, ABHD10, SMRT, Big ET-1, CysLT2 receptor, NHE6, Rab-3C, KCY, CREB4, PC4, SMIM43_132332, CHAMP, PKA-reg (cAMP-dependent), TReP-132, RNF152, Lingo1, ANT, PP1-cat, CFA74, Neurokinin A, PDLIM2, NR3A, KLHDC4, VTA1, Cables1, KIAA1110, ECT2, Clathrin heavy chain, IL3RA, Substance P, AP-3 sigma subunits, HBXIP, PSMD10 (Gankyrin), StARD4, GRM6, CHTF18, CalDAG-GEFII, Histone H2, LIPA, KLHL35, MCT1 (SLC16A1), ARHGAP18, CCK5, TMEM14A, LRRC51, Galpha(q)-specific amine GPCRs, UQCRFS1, Maestro, Ephrin-A receptors, MRPL47, Histone H2A, HMP19, NPR3, GP-IB alpha, DOC1, Galpha(i)-specific amine GPCRs, Stch, TRPC4, PMCA1, NCX1, DNAJC12, SLBP, HCN, Protein kinase G1, HLF, BDH, C1orf113, LENG8, CAP1, HSP90 beta, Anillin, TXNIP (VDUP1), Vinexin, COL25A1, MEGF6, NDUFS6, Calponin-1, Activin beta A, BRMS1L, Zeta-sarcoglycan, CDK5, PANX2, DUS3L, PAK, Guanylate cyclase (alpha-1/beta-1), FLJ32001, SYT16, Guanylate cyclase beta, BEX1, TCP1-eta, Glycine receptor, Fatty acid-binding protein, Tmem134, PSG3, FOXP4, HINT, ENPP4, MAML1, KIAA0143, MORN1, SOHLH1, IZUMO1, FLJ37078, TOM22, GABA-A receptor alpha-3 subunit, GNT-IV, LPPR4, ISOC1, DYNLT, SLC16A13, Atg101, TMEM74, TM6SF1, Tetraspanin-3, Copine-4, Destrin, eIF4A2, ATP5A, Glycine receptor beta chain, Nek8, Selenoprotein P, CAPZA, Carbonic anhydrase XII, Kv9.3, RTL1, PKC-beta2, Calcineurin A (catalytic), LSM2, TOP1MT, Galpha(i)-specific cannabis GPSRs, STARD7, B3GT2, Cyclin G1, sRAGE, SEC23A, Glyoxalase I, DDX51, SMIT, FBI-1 (Pokemon), Galpha(q)-specific peptide GPCRs, H2AFZ, ATP6V1C, Histone H2B, SNAP190, WDR47, Tubulin alpha, Creatine kinase, ACAP1(CENTB1), DSCAML1, TBC1D10C, DCK, MRAP2, PAP-II, B-FABP, Azi1, DYNLL, Patched, TNK1, XK, MEF2, NAPB, ADAR3, BICRA, HNMT, Sec23, APRIO, SCS-A, BTBD10, MEK4/7, Peg10, ACSL4, RENBP, LOC440248, CEACAM1, RANBP6, ATF/CREB, GLGB, ODP2, RAI1, G-protein gamma 3, LAMP2-C, FN14(TNFRSF12A), Trim45, RSL24D1, C3orf59, G-protein beta-4, FEM1B, Acyl-CoA synthetase, PP2A catalytic, SULT1A1 isoform 1, CAPZA2, IDI1, SNX7, ARRDC2, ZFAND2A, AP-4, MRLC, eIF4A, BMI-1, C9orf106, SNAPs, eIF2S1, Glutaredoxin, RNF175, Galpha(s)-specific CRF GPCRs, LAMP2, C1orf115, KAD6, TMEM87A, YPEL5, TSNARE1,

						ATP6V1B, Kv4.2 channel, JKAMP, PKD1L1, Protein kinase G 2, PRNP, Osrf, FAM22A, DNAJA2, TMS-1, MPTP complex, ENC1, STAG3, RHEB2, CENPL, NKCC1, Malin, C1orf59, HIST2H2BE, ATP6V0B, PKC-beta1, PDE4A, WDT2, ZSCAN1, CAB39L, Calmodulin, CENPP, LPL, DIRAS2, NELL2, FLJ31818, PGRMC1, ATP6V1E, Apo-2L(TNFSF10), LOXL2, PDE11A, NOLA3 (NOP10), HSPC125, Endophilin A1, STAC2, Activin, SIPAR, C1orf43, Aquaporin 1, NDFIP1, KCTD16, C6orf27, Calcyclin, FAM186B, Syntenin 1, SCOT, Octanoyl-holo-acp, KCRS, Securin, ADHX, ZNF517, ERK1/2, Carboxypeptidase M, AATC, UGCG, SLC29A4, Anks4b, TRUB1, NFIC, HSC70, PI3K reg class IA (p55-gamma), SLC35A5, PKC, SSTR2, SUR1, ABTB1, C19orf55, HTR2A, SLC25A4, MPP7, CCDC57, ATP1B3, K-cadherin (CDH6), Guanylate Cyclase 1, soluble, MEF2C, SULT4A1, MRPL33, Protein kinase G, ERK2 (MAPK1), Calcineurin A (beta), LISCH7, Ran, OAT, MEK4(MAP2K4), DACH2, CCK8-GlyArgArg, CLCN5, STX16-NPEPL1, IMPA1, TRIM23, UFC1, Nephrocystin-4, DKK1, PARM-1, sKITLG, SSTR1, Guanine deaminase, PRPS, SOD1, TFIIB, YIPF5, KIAA1024, PPP4R2, GDE1, SLC38A2, MMP-28, SAP102, FSTL5, EVI2A, MAP1, RPESP, CALM2, Cyclophilin A, FOXP1/2/4 proteins, Aggrecanase-2, PI3K reg class IA, KIAA1614, PTCHD1, Galpha(s)-specific peptide GPCRs, GPR22, TSPAN19, TCP1-alpha, ATP5L, ACTR3, ATP6AP2, OXR1, CALB1, Tubulin alpha-4A, CALML6, SRm300, RhoE, CD166, TIP27, GAD2, DRIL2, SIAH3, PGM2L1, TCP1-epsilon, NF-I, MRPL3, HXK3, COX VIIa-2, ACOXL, NRBF2, Midkine, FLJ37464, SAMD10, IRS6(DOK5), ARP3, PXDN, 14-3-3, ARMCX3, ACCN3 (ASIC3), COX VIIa-2L, RAGE, 14-3-3 eta, ATP1beta subunit, Myospryn, Glutaredoxin 1, ZCCHC12, CMAS, CHST6
24	Panic Disorder	127	1.912E-14	1.739E-12	26	NPY, Galpha(s)-specific nucleotide-like GPCRs, GAD1, G-protein beta, CCK8-Gly, PDE, CCK8, TPH2, G-protein beta/gamma, Galpha(i)-specific peptide GPCRs, Galpha(q)-specific nucleotide-like GPCRs, CRH receptor 2, PDE4, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, Pro-CCK, Serotonin receptor, CCK5, Galpha(q)-specific amine GPCRs, Galpha(i)-specific amine GPCRs, Glyoxalase I, Galpha(q)-specific peptide GPCRs, ATF/CREB, Galpha(s)-specific CRF GPCRs, HTR2A, CCK8-GlyArgArg
25	Neuromuscular Diseases	4369	4.173E-14	3.644E-12	221	PLP1, NPY, PP2A cat (alpha), PRPS1, HSP90, PAM, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Alpha crystallin B, ET-1, IRF1, ILDR2, COX VIc, GAD1, MEGF10, PTCH2, Tubulin alpha 1A, SUCLG1, ELOVL5, Peroxiredoxin, Activin A, Endothelin-1, Neuropeptide K, T-plastin, DYNLT3, G-protein beta, LAS1L, ALDR, PSMA5, NDUFAB1, NckAP1, NDUFA1, MGF, MELC, NDUFB4,

						NDUFA8, Synaptotagmin I, COCH, HSP70, Substance P extracellular region, DnaJB9, Synaptotagmin, CNTN1 (F3), Thioredoxin, NDUFA4, HSPA4, PDE, Cystatin C, SCF, SDHB, IGSF9B, DKK3, NCKP1 subunit, GPR124, TPH2, Neuropeptide gamma, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, ORP-family, Tenascin-C, PKC-beta, KIS, TCP1-theta, PRDX1, G-protein beta/gamma, NDUFB6, SUR, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, S100, TXNRD1, TRPV1, PDK3, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, Aldose reductase, NDUFB3, FAM38B, IDUA, RPL9, CHCHD2, GLRA, DKK2, GABA-A receptor beta-2 subunit, DOK7, Rho GTPase, PDE4, G-protein gamma, Dysferlin, Galpha(i)-specific metabotropic glutamate GPCRs, EGF, ATP5B, SYTC, Dynein, axonemal, heavy chains, LOC283174, NELL1, cPKC (conventional), NDUFB1, PSMA1, Serotonin receptor, PDK4, WIF1, COX VIa, Osteopontin, SMRT, Big ET-1, PKA-reg (cAMP-dependent), ANT, Neurokinin A, Substance P, Histone H2, MCT1 (SLC16A1), ARHGAP18, Galpha(q)-specific amine GPCRs, Ephrin-A receptors, Histone H2A, Galpha(i)-specific amine GPCRs, NCX1, HSP90 beta, MEGF6, NDUFS6, Activin beta A, CDK5, Glycine receptor, Fatty acid-binding protein, HINT, MDH1, ASAH, DYNLT, COX Va, Glycine receptor beta chain, CAPZA, PKC-beta2, Calcineurin A (catalytic), TOP1MT, sRAGE, SLC25A46, Galpha(q)-specific peptide GPCRs, MAFbx, NDUFA5, Tubulin alpha, Creatine kinase, DSCAML1, B-FABP, Azi1, Patched, MEF2, ADAR3, HNMT, APRIO, SCS-A, BTBD10, MEK4/7, Peg10, ACSL4, ATF/CREB, GLGB, RAI1, G-protein gamma 3, Hdj-2, CQ107, LAMP2-C, FN14(TNFRSF12A), G-protein beta-4, Acyl-CoA synthetase, PP2A catalytic, MRLC, Galpha(s)-specific CRF GPCRs, LAMP2, COX VIa-1, PRNP, MPTP complex, PKC-beta1, Calmodulin, Apo-2L(TNFSF10), HSPC125, Activin, Aquaporin 1, NME5, Calcyclin, Octanoyl-holo-acp, KCRS, ERK1/2, AATC, UGCG, HSC70, PKC, SUR1, HTR2A, SLC25A4, MEF2C, ERK2 (MAPK1), MEK4(MAP2K4), TMEM70, PRKAR1A, IGFALS, IMPA1, DKK1, sKITLG, PRPS, SOD1, TFIIB, CALM2, PI3K reg class IA, CALB1, Tubulin alpha-4A, GAD2, TCP1-epsilon, NF-I, HXK3, COX VIIa-2, Midkine, SAMD10, PXDN, 14-3-3, RAGE, ATP1beta subunit, SNX10
26	Urogenital Neoplasms	20725	1.062E-13	8.914E-12	740	Cyclin G, FBXO45, NPY, PP2A cat (alpha), HSP90, PAK3, PAM, Cadherin 8, ZYG11B, CPSF1, ZNF575, ARP6, CXorf57, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Semaphorin 3C, Alpha crystallin B, AEBP1, ET-1, G3BP2, RhoN, MBD6, IRF1, ILDR2, FILIP, ZnT-2, MAL2, GLSK, Rab-3B, MAGEH-1, SLC35E2B, COX VIc, SMVT, C1D, MEGF10, THAP11, TINP1, PTCH2, N-

						chimaerin, Tubulin alpha 1A, ATP5C, SUCLG1, HPCA, LOC284837, APJ, Smooth muscle myosin, EDIL3, FLJ12671, ELOVL5, GLB1B2, RNF207, Peroxiredoxin, Activin A, UBL5, D630023F18Rik, Esterase D, Endothelin-1, SULT1A1, Trehalase, Neuropeptide K, PSMB5, AP-1 gamma subunits, ARG2, DUOX1, Nkpd1, NETO2, GHITM, IL-17D, BRSK2, DYNLT3, P2Y11, UBXD3, G-protein beta, KLHL4, LAS1L, JWA, ALDR, CRTL1, TMC4, Mucin 5B, SC4MOL, PSMA5, NFKBIL2, NDUFAB1, Importin (karyopherin)-alpha, NckAP1, KIAA1276, GLIPR, BTBD12, CDC18L (CDC6), ANKRD50, DNAH1, MRPL1, Lgi4, GPR137C, MOBKL1A, AP1G2, ZNF707, LOC153328, Pannexin-1, MCM6, OGFRL1, NKIRAS1, DCMC, RHBDL3, PSD2, FAM90A1, NIPSNAP3A, MGF, PDH E2 subunit N6-lipoyllysine, TIP47, PRKAR2B, MELC, PLD5, DPY19L1, NPFF receptor 2, NDUFB4, UNRIP, NDUFA8, Synaptotagmin I, COCH, Guanylate cyclase, KCNK2, HSP70, CCDC4, SCRT2, Substance P extracellular region, DDX3Y, CNR1, MAPBPIP, MYL6, Glycogen phosphorylase, Synaptotagmin IV, Tim17, PPM1E, SLIRP, HDBP1, NUDT4P1, GIMAP7, DnaJB9, Synaptotagmin, PRDX3, CNTN1 (F3), Thioredoxin, ZMAT1, ATP6V1A (70kD), HSPA4, JMJD3, Septin 1, Dynein, axonemal, light chains, PDE, Cystatin C, CNIH2, Tcfl5, PPT1, SCF, SDHB, SLC39A10, IGSF9B, DKK3, Karyopherin alpha 2, LUZP2, PNMAL1, NCKP1 subunit, TM9SF2, HCN2, D123, FLJ20674, Galpha(q)-specific Class A Orphan/other GPCRs, IMPG2, LMF1, OAF, ATP5G, C6orf168, GPR124, TPH2, Neuropeptide gamma, KAL1, RAB39B, Aha1, PTPN18, RGS4, VSIG2, 14-3-3 beta/alpha, BTBD18, GABA-A receptor alpha-1 subunit, TUSC3, UGT8, D330028D13Rik, GUCY1B1, FLRT3, Exostosin-like 2, SELI, C13orf37, ORP-family, B3GN6, Tenascin-C, Myopodin, HSDL1, CEACAM, ODF3, TRPC5, PKC-beta, KIS, TCP1-theta, PRDX1, ELMO3, G-protein beta/gamma, B3GN1, NET6(TSPAN13), SLC25A45, NDUFB6, SDFR1, SUR, ABO system transferase, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, VBP-1, TORC1, KLHL13, UQCRB, CPT-1A, S100, Rab-6, TXNRD1, ORP8, KCNH5, AMIGO2, VWA2, FLJ38984, LASS6, TRPV1, PRR12, PDK3, ZFHX4, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, TIP41, ATP6V1C1, PRRG1, Aldose reductase, NDUFB3, Rab-3, MTG16 (CBFA2T3), ATG9B, TM2D3, DNER, FAM38B, APOL3, TMEM45A, Ephrin-A receptor 5, LAPTM4B, IDUA, IP3KA, CRH receptor 2, AMDHD2, CacyBP(SIP), InsP6 kinase 3, SLC2A13, Semaphorin 5A, Adropin, V-ATPase E subunit, GRAIL, UBA1L, NSF, Tomt, ADAM-TS10, GPR176, FAM102B, CaMK IV, GLRA, DKK2, ZNF499, GABA-A receptor beta-2 subunit, FBXO2, H41, ZNF433,

						CECR2, DOK7, SYP, Carbohydrate sulfotransferases, TIMM17, LACTB2, LPL1, Rho GTPase, PDE4, GTPBP3, Tensin 2, Lba1, G-protein gamma, UBE2D1, OSGIN2, PLCXD2, PRPS2, ZNF70, SOCS6, Dysferlin, Rap1GDS1, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, ChREBP, ZNF267, A830006F12Rik, Secretogranin V, EGF, GlyRA2, ATP5B, PPase (inorganic), NAP1L2, CED-6, SYTC, XKR4, Dynein, axonemal, heavy chains, B3GALTL, BMPR1A, Semaphorin 3E, MMADHC, MMD, LOC283174, HIST1H2BN, Neurexophilin 2, PKA-reg type II (cAMP-dependent), B3GNT4, Myotrophin, NELL1, CAP2, cPKC (conventional), ATP6V1B2, DLL4, ELOVL4, AP3S1, PSMA1, Serotonin receptor, Apelin, Neurexophilin 1, TMEM39B, ADSS, mADAMTS5, TRPC, SLC7A5, HTR5A, NOP14-AS1, ACTR10, PDK4, VDAC 1, C17orf76, WIF1, NDRG3, SUCB1, ATP6V1H, Osteopontin, Slp5, SLC6A1-AS1, SMRT, Big ET-1, CysLT2 receptor, NHE6, Rab-3C, KCY, CREB4, PC4, CHAMP, PKA-reg (cAMP-dependent), TReP-132, RNF152, Lingo1, ANT, PP1-cat, CFA74, Neurokinin A, PDLIM2, NR3A, KLHDC4, VTA1, Cables1, KIAA1110, ECT2, Clathrin heavy chain, IL3RA, Substance P, AP-3 sigma subunits, PSMD10 (Gankyrin), StARD4, GRM6, CHTF18, CalDAG-GEFII, Histone H2, KLHL35, MCT1 (SLC16A1), ARHGAP18, LRRC51, Galpha(q)-specific amine GPCRs, UQCRFS1, Maestro, Ephrin-A receptors, MRPL47, Histone H2A, HMP19, NPR3, C9orf5, GP-IB alpha, DOC1, Galpha(i)-specific amine GPCRs, CCNI2, Stch, TRPC4, PMCA1, NCX1, DNAJC12, SLBP, HCN, Protein kinase G1, HLF, BDH, C1orf113, LENG8, CAP1, HSP90 beta, Anillin, TXNIP (VDUP1), Vinexin, COL25A1, C14orf142, MEGF6, NDUFS6, Calponin-1, Activin beta A, BRMS1L, Zeta-sarcoglycan, CDK5, PANX2, DUS3L, PAK, Guanylate cyclase (alpha-1/beta-1), FLJ32001, SYT16, Guanylate cyclase beta, BEX1, TCP1-eta, Glycine receptor, Fatty acid-binding protein, PSG3, HINT, ENPP4, MAML1, KIAA0143, SOHLH1, IZUMO1, FLJ37078, GTL3, ASAH, GABA-A receptor alpha-3 subunit, GNT-IV, LPPR4, ISOC1, DYNLT, TMEM74, TM6SF1, SPSY, COX Va, Tetraspanin-3, Copine-4, eIF4A2, ATP5A, Glycine receptor beta chain, Nek8, Selenoprotein P, CAPZA, Carbonic anhydrase XII, Kv9.3, RTL1, PKC-beta2, Calcineurin A (catalytic), TOP1MT, Galpha(i)-specific cannabis GPSRs, STARD7, B3GT2, Cyclin G1, sRAGE, SLC25A46, SEC23A, Glyoxalase I, DDX51, SMIT, FBI-1 (Pokemon), PDH beta, Galpha(q)-specific peptide GPCRs, H2AFZ, ATP6V1C, Histone H2B, NCOA4 (ARA70), SNAP190, WDR47, NDUFA5, Tubulin alpha, Creatine kinase, ACAP1(CENTB1), DSCAML1, TBC1D10C, DCK, PAP-II, B-FABP, VIP32, Azi1, NUDT4, DYNLL, Patched,

						TNK1, XK, MEF2, SLC2A1-AS1, NAPB, ADAR3, BICRA, PGAM1, TAPBPL, Sec23, APRIO, SCS-A, BTBD10, MEK4/7, Peg10, ACSL4, RENBP, CEACAM1, RANBP6, ATF/CREB, GLGB, ODP2, RAI1, G-protein gamma 3, Hdj-2, LAMP2-C, FN14(TNFRSF12A), Trim45, C3orf59, G-protein beta-4, FEM1B, Acyl-CoA synthetase, PP2A catalytic, SULT1A1 isoform 1, CAPZA2, GAS41, IDI1, ARRDC2, AP-4, MRLC, eIF4A, BMI-1, SNAPs, eIF2S1, Glutaredoxin, DLC1 (Dynein LC8a), RNF175, Galpha(s)-specific CRF GPCRs, LAMP2, KAD6, ALAS1, TMEM87A, YPEL5, TSNARE1, ATP6V1B, Kv4.2 channel, JKAMP, PKD1L1, Protein kinase G 2, PRNP, HSPC138, Osrf, FAM22A, TM2D2, DNAJA2, TMS-1, MPTP complex, ENC1, STAG3, RHEB2, CENPL, NKCC1, Neurocalcin delta, Malin, C1orf59, PKC-beta1, PDE4A, ZSCAN1, CAB39L, Calmodulin, CENPP, LPL, DIRAS2, NELL2, SUMO-3, FLJ31818, PGRMC1, ATP6V1E, Apo-2L(TNFSF10), SET1B, LOXL2, PDE11A, FLJ45455, NOLA3 (NOP10), Endophilin A1, STAC2, Activin, C1orf43, Aquaporin 1, NDFIP1, KCTD16, C6orf27, NME5, Calcyclin, FAM186B, Syntenin 1, SCOT, Octanoyl-holo-acp, KCRS, Securin, ADHX, ZNF517, ERK1/2, Carboxypeptidase M, AATC, UGCG, SLC29A4, Anks4b, TRUB1, NFIC, HSC70, PI3K reg class IA (p55-gamma), SLC35A5, PKC, SSTR2, SUR1, ABTB1, C19orf55, HTR2A, PMM2, SLC25A4, MPP7, CCDC57, ATP1B3, ARPP-19, K-cadherin (CDH6), Guanylate Cyclase 1, soluble, APEL13, MEF2C, SULT4A1, Protein kinase G, RIFK, ERK2 (MAPK1), Calcineurin A (beta), DREV1, SLC25A25-AS1, LISCH7, Ran, OAT, MEK4(MAP2K4), CBR3-AS1, DACH2, C14orf2, TMEM70, PRKAR1A, IGFALS, CLCN5, IMPA1, TRIM23, UFC1, Nephrocystin-4, DKK1, PARM-1, sKITLG, SSTR1, Guanine deaminase, PRPS, SOD1, TFIIB, KIAA1024, PPP4R2, GDE1, SLC38A2, MMP-28, SAP102, FSTL5, EVI2A, MAP1, RPESP, CALM2, Cyclophilin A, FOXP1/2/4 proteins, Aggrecanase-2, PI3K reg class IA, KIAA1614, PTCHD1, DCoHM, Galpha(s)-specific peptide GPCRs, TSPAN19, TCP1-alpha, ACTR3, OXR1, CALB1, Tubulin alpha-4A, CALML6, SRm300, RhoE, Pcdh19, CD166, TIP27, GAD2, DRIL2, SIAH3, PGM2L1, TCP1-epsilon, NF-I, MRPL3, HXK3, Neuroserpin, COX VIIa-2, ACOXL, Midkine, SAMD10, IRS6(DOK5), ARP3, PXDN, 14-3-3, ARMCX3, ACCN3 (ASIC3), C8orf83, AATBC, RAGE, 14-3-3 eta, ATP1beta subunit, Myospryn, Glutaredoxin 1, ZCCHC12, TCTE3, CHST6
27	Neoplasms	26016	1.234E-13	9.978E-12	869	SCAP2, PLP1, Cyclin G, FBXO45, NPY, C13orf36, FAM3C, PP2A cat (alpha), HSP90, PAK3, PAM, Cadherin 8, ZYG11B, CPSF1, ZNF575, ARP6, CXorf57, NPEPL1, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, ZNF34, LINC01410, Semaphorin 3C,

						Alpha crystallin B, TMEM87B, AEBP1, ET-1, G3BP2, RhoN, MBD6, IRF1, ILDR2, FILIP, ZnT-2, MAL2, GLSK, Rab-3B, MAGEH-1, SLC35E2B, COX VIc, GAD1, SMVT, C1D, MEGF10, THAP11, TINP1, PTCH2, N-chimaerin, Tubulin alpha 1A, ATP5C, SUCLG1, HPCA, LOC284837, APJ, Smooth muscle myosin, EDIL3, FLJ12671, ELOVL5, GLB1B2, RNF207, Peroxiredoxin, Activin A, UBL5, D630023F18Rik, Esterase D, Endothelin-1, SULT1A1, Trehalase, Neuropeptide K, PSMB5, AP-1 gamma subunits, ARG2, T-plastin, DUOX1, Nkpd1, NETO2, GHITM, REV-ERBalpha, IL-17D, BRSK2, UQCRQPC, DYNLT3, P2Y11, UBXD3, G-protein beta, KLHL4, LAS1L, SC5D, JWA, ALDR, CRTL1, UQCRH, TMC4, Rab-6A, RGS8, Mucin 5B, SC4MOL, MRPS6, PSMA5, CNOT7, MDS028, NFKBIL2, NDUFAB1, Importin (karyopherin)-alpha, CCK8-Gly, NckAP1, KIAA1276, GLIPR, BTBD12, NDUFA1, CDC18L (CDC6), ANKRD50, LSMD1, DNAH1, MRPL1, Lgi4, GPR137C, TTLL9, MOBKL1A, AP1G2, ZNF707, LOC153328, Pannexin-1, MCM6, OGFRL1, NKIRAS1, DCMC, HPCAL4, RHBDL3, PSD2, FAM90A1, NIPSNAP3A, MGF, PDH E2 subunit N6-lipoyllysine, TIP47, PRKAR2B, MELC, PLD5, DPY19L1, NPFF receptor 2, NDUFB4, MC4R, UNRIP, NDUFA8, KLHL12, Synaptotagmin I, COCH, Guanylate cyclase, ARL6, KCNK2, HSP70, CCDC4, SCRT2, Substance P extracellular region, DDX3Y, CNR1, MAPBPIP, MYL6, Glycogen phosphorylase, Synaptotagmin IV, Tim17, CITED2, PPM1E, SLIRP, HDBP1, NUDT4P1, GIMAP7, DnaJB9, Synaptotagmin, PRDX3, CNTN1 (F3), Thioredoxin, MRLC2, NDUFA4, ZMAT1, ATP6V1A (70kD), HSPA4, JMJD3, Septin 1, Dynein, axonemal, light chains, PDE, Cystatin C, CNIH2, Tcfl5, PPT1, SCF, SDHB, MGAT4A, SLC39A10, IGSF9B, DKK3, Karyopherin alpha 2, LUZP2, VIPR1-AS1, PNMAL1, NCKP1 subunit, TM9SF2, HCN2, D123, LOC441108, Guanylate cyclase alpha, FLJ20674, Galpha(q)-specific Class A Orphan/other GPCRs, IMPG2, LMF1, OAF, ATP5G, C6orf168, CCK8, GPR124, TPH2, Neuropeptide gamma, KAL1, RAB39B, Aha1, PTPN18, RGS4, VSIG2, VDAC 3, 14-3-3 beta/alpha, BTBD18, GABA-A receptor alpha-1 subunit, TUSC3, UGT8, D330028D13Rik, GUCY1B1, FLRT3, Exostosin-like 2, Kv3.3, SELI, C13orf37, ORP-family, B3GN6, LY6G5B, Tenascin-C, Myopodin, HSDL1, PP1-cat gamma, CEACAM, ODF3, TRPC5, PKC-beta, KIS, PAFAH gamma, TCP1-theta, PRDX1, ELMO3, G-protein beta/gamma, B3GN1, NET6(TSPAN13), SLC25A45, NDUFB6, SDFR1, SUR, ABO system transferase, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, VBP-1, FUT2, TORC1, KLHL13, UQCRB, ATP5E, SCRT1, CPT-1A, S100, Rab-6,

						TXNRD1, ORP8, KCNH5, AMIGO2, VWA2, LINC02043, FLJ38984, LASS6, PIMT, TRPV1, PRR12, PDK3, ZFHX4, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, TIP41, ATP6V1C1, PRRG1, ZDH13, Aldose reductase, ATP6M, NDUFB3, Rab-3, MTG16 (CBFA2T3), ATG9B, TM2D3, DNER, FAM38B, APOL3, TMEM45A, ZFHX2, Ephrin-A receptor 5, LAPTM4B, IDUA, IP3KA, CRH receptor 2, AMDHD2, CacyBP(SIP), InsP6 kinase 3, SLC2A13, Semaphorin 5A, Adropin, V-ATPase E subunit, GRAIL, UBA1L, NSF, Tomt, ADAM-TS10, GPR176, FAM102B, CaMK IV, CHCHD2, GLRA, DKK2, ZNF499, GABA-A receptor beta-2 subunit, FBXO2, H41, ZNF433, CECR2, DOK7, SYP, Carbohydrate sulfotransferases, TIMM17, LACTB2, LPL1, Rho GTPase, PDE4, GTPBP3, Tensin 2, Lba1, G-protein gamma, UBE2D1, OSGIN2, PLCXD2, PRPS2, ZNF70, SOCS6, Dysferlin, Rap1GDS1, Ephrin-A receptor 4, TMEM86B, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, ChREBP, ZNF267, A830006F12Rik, PP4R4, Secretogranin V, EGF, GlyRA2, ATP5B, PPase (inorganic), NAP1L2, Pro-CCK, CED-6, SYTC, XKR4, Dynein, axonemal, heavy chains, B3GALTL, BMPR1A, Semaphorin 3E, MMADHC, MMD, LOC283174, HIST1H2BN, Neurexophilin 2, RBM18, PKA-reg type II (cAMP-dependent), B3GNT4, Myotrophin, NELL1, CAP2, HKR4, cPKC (conventional), SF3A2, ATP6V1B2, NDUFB1, DLL4, ELOVL4, AP3S1, PSMA1, Serotonin receptor, CHMP5, Apelin, Neurexophilin 1, AP complex 2 small (sigma) chain, TMEM39B, ADSS, Rab-27B, mADAMTS5, PPID, TRPC, SLC7A5, HTR5A, PYGM, NOP14-AS1, ACTR10, PDK4, VDAC 1, C17orf76, WIF1, NDRG3, COX VIa, SUCB1, ATP6V1H, Osteopontin, ATP5G3, Slp5, ABHD10, SLC6A1-AS1, SMRT, Big ET-1, CysLT2 receptor, NHE6, Rab-3C, M-Ras, KCY, CREB4, PC4, SMIM43_132332, CHAMP, PKA-reg (cAMP-dependent), TReP-132, RNF152, Lingo1, ANT, PP1-cat, CFA74, HMDH, Neurokinin A, PDLIM2, NR3A, GUCY1A3, KLHDC4, VTA1, Cables1, KIAA1110, ECT2, Clathrin heavy chain, IL3RA, Substance P, AP-3 sigma subunits, HBXIP, PSMD10 (Gankyrin), StARD4, GRM6, CHTF18, CalDAG-GEFII, Histone H2, LIPA, KLHL35, MCT1 (SLC16A1), ARHGAP18, CCK5, TMEM14A, LRRC51, Galpha(q)-specific amine GPCRs, UQCRFS1, Maestro, Ephrin-A receptors, MRPL47, Histone H2A, HMP19, NPR3, C9orf5, GP-IB alpha, DOC1, Galpha(i)-specific amine GPCRs, CCNI2, Stch, DAT1, TRPC4, PMCA1, LINGO1-AS1, Rab-23, NCX1, DNAJC12, SLBP, HCN, RTEL1-TNFRSF6B, Protein kinase G1, HLF, BDH, C1orf113, LENG8, CAP1, HSP90 beta, Anillin, TXNIP (VDUP1), Vinexin, COL25A1, C14orf142, PMS2L3, MEGF6, NDUFS6, Calponin-1, Activin beta A, BRMS1L, Zeta-sarcoglycan, CDK5, PANX2, DUS3L,

						PAK, Guanylate cyclase (alpha-1/beta-1), FLJ32001, SYT16, Guanylate cyclase beta, BEX1, TCP1-eta, Glycine receptor, Fatty acid-binding protein, Tmem134, PSG3, FOXP4, HINT, ENPP4, MAML1, KIAA0143, SgK223, MORN1, SOHLH1, IZUMO1, FLJ37078, TOM22, GTL3, USP2-AS1, ASAH, GABA-A receptor alpha-3 subunit, GNT-IV, LPPR4, ISOC1, DYNLT, SLC16A13, Atg101, TMEM74, TM6SF1, BEX2, SPSY, COX Va, Tetraspanin-3, Copine-4, Destrin, eIF4A2, BRK, ATP5A, Glycine receptor beta chain, Nek8, Selenoprotein P, CAPZA, Carbonic anhydrase XII, Kv9.3, RTL1, PKC-beta2, Calcineurin A (catalytic), LSM2, TOP1MT, Galpha(i)-specific cannabis GPSRs, STARD7, B3GT2, Cyclin G1, sRAGE, SLC25A46, SEC23A, Glyoxalase I, DDX51, SMIT, FBI-1 (Pokemon), PDH beta, Galpha(q)-specific peptide GPCRs, H2AFZ, ATP6V1C, Histone H2B, NCOA4 (ARA70), MAFbx, SNAP190, WDR47, NDUFA5, Tubulin alpha, Creatine kinase, ACAP1(CENTB1), DSCAML1, TBC1D10C, DCK, MRAP2, PAP-II, B-FABP, VIP32, Azi1, NUDT4, DYNLL, Patched, TNK1, XK, MEF2, INCA1, SLC2A1-AS1, NAPB, ADAR3, BICRA, PGAM1, HNMT, TAPBPL, Sec23, APRIO, SCS-A, BTBD10, MEK4/7, Peg10, ACSL4, RENBP, LOC440248, F262, CEACAM1, RANBP6, ATF/CREB, GLGB, ODP2, RAI1, G-protein gamma 3, Hdj-2, LAMP2-C, FN14(TNFRSF12A), Trim45, RSL24D1, C3orf59, G-protein beta-4, FEM1B, Acyl-CoA synthetase, PP2A catalytic, SULT1A1 isoform 1, CAPZA2, GAS41, IDI1, SNX7, ARRDC2, ZFAND2A, AP-4, MRLC, eIF4A, BMI-1, C9orf106, SNAPs, OAZIN, eIF2S1, Glutaredoxin, DLC1 (Dynein LC8a), RNF175, Galpha(s)-specific CRF GPCRs, LAMP2, COX VIa-1, C1orf115, KAD6, ALAS1, TMEM87A, YPEL5, TSNARE1, ATP6V1B, Quinone oxidoreductase, Kv4.2 channel, JKAMP, PKD1L1, Protein kinase G 2, PRNP, HSPC138, Osrf, SLC16A1-AS1, FAM22A, TM2D2, DNAJA2, TMS-1, MPTP complex, ENC1, STAG3, RHEB2, CENPL, NKCC1, Neurocalcin delta, Malin, C1orf59, HIST2H2BE, ATP6V0B, PKC-beta1, PDE4A, WDT2, ZSCAN1, CAB39L, Calmodulin, CENPP, LPL, DIRAS2, NELL2, SUMO-3, FLJ31818, PGRMC1, ATP6V1E, Apo-2L(TNFSF10), SET1B, LOXL2, PDE11A, FLJ45455, KLHL2, NOLA3 (NOP10), HSPC125, USMG5, Endophilin A1, STAC2, Activin, SIPAR, C1orf43, Aquaporin 1, NDFIP1, KCTD16, C6orf27, NME5, CLIC4, Calcyclin, FAM186B, Syntenin 1, SCOT, Octanoyl-holo-acp, KCRS, Securin, ADHX, ZNF517, ERK1/2, Carboxypeptidase M, CDw52, AATC, UGCG, SLC29A4, Anks4b, TRUB1, NFIC, CaMK II delta, HSC70, PI3K reg class IA (p55-gamma), ARL5, SLC35A5, PKC, SSTR2, SUR1, ABTB1, C19orf55, HTR2A, PMM2, SLC25A4, MPP7, CCDC57, ATP1B3, ARPP-19, K-cadherin (CDH6), Guanylate

						Cyclase 1, soluble, APEL13, MEF2C, SULT4A1, MRPL33, Protein kinase G, RIFK, ERK2 (MAPK1), Calcineurin A (beta), DREV1, SLC25A25-AS1, LISCH7, Ran, OAT, MEK4(MAP2K4), CBR3-AS1, DACH2, C14orf2, TMEM70, Mindin, PRKAR1A, IGFALS, CCK8-GlyArgArg, CLCN5, STX16-NPEPL1, IMPA1, TRIM23, UFC1, Nephrocystin-4, DKK1, PARM-1, sKITLG, SSTR1, Guanine deaminase, PRPS, SOD1, TFIIB, YIPF5, KIAA1024, PPP4R2, GDE1, SLC38A2, MMP-28, SAP102, FSTL5, EVI2A, MAP1, RPESP, CALM2, Cyclophilin A, FOXP1/2/4 proteins, Aggrecanase-2, PI3K reg class IA, KIAA1614, PTCHD1, DCoHM, CLDND1, Galpha(s)-specific peptide GPCRs, GPR22, TSPAN19, TCP1-alpha, ATP5L, ACTR3, ATP6AP2, OXR1, CALB1, Tubulin alpha-4A, CALML6, SRm300, RhoE, Pcdh19, CD166, TIP27, GAD2, DRIL2, SIAH3, PGM2L1, TCP1-epsilon, NF-I, MRPL3, HXK3, Neuroserpin, COX VIIa-2, ACOXL, NRBF2, Midkine, FLJ37464, SAMD10, IRS6(DOK5), ARP3, PXDN, 14-3-3, ARMCX3, ACCN3 (ASIC3), COX VIIa-2L, C8orf83, AATBC, RAGE, 14-3-3 eta, ATP1beta subunit, Myospryn, Glutaredoxin 1, ZCCHC12, SNX10, CMAS, TCTE3, CHST6
28	Lung Diseases	20966	4.896E-13	3.817E-11	744	SCAP2, Cyclin G, FBXO45, NPY, C13orf36, FAM3C, PP2A cat (alpha), HSP90, PAK3, PAM, Cadherin 8, ZYG11B, CPSF1, ZNF575, ARP6, CXorf57, NPEPL1, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, ZNF34, Semaphorin 3C, TMEM87B, AEBP1, ET-1, G3BP2, MBD6, IRF1, ILDR2, FILIP, ZnT-2, MAL2, Rab-3B, MAGEH-1, COX VIc, SMVT, C1D, MEGF10, THAP11, PTCH2, N-chimaerin, Tubulin alpha 1A, ATP5C, SUCLG1, HPCA, APJ, Smooth muscle myosin, EDIL3, FLJ12671, ELOVL5, GLB1B2, RNF207, Peroxiredoxin, Activin A, UBL5, D630023F18Rik, Esterase D, Endothelin-1, SULT1A1, Trehalase, Neuropeptide K, AP-1 gamma subunits, ARG2, DUOX1, Nkpd1, NETO2, GHITM, REV-ERBalpha, IL-17D, BRSK2, UQCRQPC, DYNLT3, UBXD3, G-protein beta, KLHL4, LAS1L, SC5D, ALDR, CRTL1, UQCRH, Rab-6A, RGS8, Mucin 5B, MRPS6, PSMA5, CNOT7, MDS028, NFKBIL2, NDUFAB1, Importin (karyopherin)-alpha, CCK8-Gly, NckAP1, GLIPR, BTBD12, CDC18L (CDC6), ANKRD50, LSMD1, DNAH1, MRPL1, Lgi4, GPR137C, TTLL9, MOBKL1A, AP1G2, ZNF707, LOC153328, Pannexin-1, MCM6, NKIRAS1, HPCAL4, RHBDL3, PSD2, FAM90A1, NIPSNAP3A, MGF, PDH E2 subunit N6-lipoyllysine, TIP47, PRKAR2B, MELC, PLD5, DPY19L1, NPFF receptor 2, NDUFB4, MC4R, UNRIP, NDUFA8, KLHL12, Synaptotagmin I, COCH, Guanylate cyclase, ARL6, KCNK2, HSP70, CCDC4, Substance P extracellular region, DDX3Y, MAPBPIP, MYL6, Glycogen phosphorylase, Synaptotagmin IV,

						Tim17, PPM1E, HDBP1, GIMAP7, DnaJB9, Synaptotagmin, PRDX3, CNTN1 (F3), Thioredoxin, MRLC2, NDUFA4, ZMAT1, ATP6V1A (70kD), HSPA4, JMJD3, Septin 1, Dynein, axonemal, light chains, PDE, Cystatin C, CNIH2, Tcfl5, PPT1, SCF, SDHB, SLC39A10, IGSF9B, DKK3, Karyopherin alpha 2, LUZP2, PNMAL1, NCKP1 subunit, TM9SF2, HCN2, D123, LOC441108, FLJ20674, Galpha(q)-specific Class A Orphan/other GPCRs, IMPG2, LMF1, OAF, ATP5G, C6orf168, CCK8, GPR124, TPH2, Neuropeptide gamma, KAL1, RAB39B, RGS4, VSIG2, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, TUSC3, UGT8, D330028D13Rik, GUCY1B1, FLRT3, Exostosin-like 2, Kv3.3, SELI, ORP-family, B3GN6, LY6G5B, Tenascin-C, PP1-cat gamma, CEACAM, TRPC5, PKC-beta, KIS, PRDX1, G-protein beta/gamma, B3GN1, SLC25A45, NDUFB6, SDFR1, SUR, ABO system transferase, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, VBP-1, FUT2, TORC1, KLHL13, UQCRB, CPT-1A, S100, Rab-6, TXNRD1, ORP8, KCNH5, AMIGO2, VWA2, FLJ38984, LASS6, TRPV1, PRR12, PDK3, ZFHX4, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, TIP41, ATP6V1C1, PRRG1, ZDH13, Aldose reductase, ATP6M, NDUFB3, Rab-3, MTG16 (CBFA2T3), TM2D3, DNER, FAM38B, APOL3, TMEM45A, Ephrin-A receptor 5, LAPTM4B, IDUA, IP3KA, CRH receptor 2, AMDHD2, CacyBP(SIP), InsP6 kinase 3, SLC2A13, Semaphorin 5A, V-ATPase E subunit, GRAIL, NSF, Tomt, ADAM-TS10, GPR176, FAM102B, CaMK IV, CHCHD2, GLRA, DKK2, ZNF499, GABA-A receptor beta-2 subunit, FBXO2, ZNF433, CECR2, SYP, Carbohydrate sulfotransferases, TIMM17, LACTB2, LPL1, Rho GTPase, PDE4, GTPBP3, Tensin 2, Lba1, G-protein gamma, UBE2D1, OSGIN2, PLCXD2, PRPS2, ZNF70, SOCS6, Dysferlin, Rap1GDS1, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, ChREBP, ZNF267, A830006F12Rik, PP4R4, Secretogranin V, EGF, GlyRA2, ATP5B, PPase (inorganic), NAP1L2, Pro-CCK, CED-6, SYTC, XKR4, Dynein, axonemal, heavy chains, B3GALTL, BMPR1A, Semaphorin 3E, MMADHC, MMD, LOC283174, HIST1H2BN, Neurexophilin 2, RBM18, PKA-reg type II (cAMP-dependent), B3GNT4, Myotrophin, NELL1, CAP2, HKR4, cPKC (conventional), SF3A2, ATP6V1B2, NDUFB1, DLL4, ELOVL4, Serotonin receptor, CHMP5, Neurexophilin 1, TMEM39B, ADSS, Rab-27B, mADAMTS5, TRPC, SLC7A5, HTR5A, ACTR10, PDK4, VDAC 1, WIF1, COX VIa, SUCB1, ATP6V1H, Osteopontin, ATP5G3, Slp5, ABHD10, SMRT, Big ET-1, CysLT2 receptor, NHE6, Rab-3C, KCY, CREB4, PC4, SMIM43_132332, CHAMP, PKA-reg (cAMP-dependent), TReP-132,

						RNF152, Lingo1, ANT, PP1-cat, CFA74, Neurokinin A, PDLIM2, NR3A, KLHDC4, VTA1, Cables1, KIAA1110, ECT2, Clathrin heavy chain, IL3RA, Substance P, AP-3 sigma subunits, HBXIP, PSMD10 (Gankyrin), StARD4, GRM6, CHTF18, CalDAG-GEFII, Histone H2, LIPA, KLHL35, MCT1 (SLC16A1), ARHGAP18, CCK5, TMEM14A, LRRC51, Galpha(q)-specific amine GPCRs, UQCRFS1, Maestro, Ephrin-A receptors, MRPL47, Histone H2A, HMP19, NPR3, GP-IB alpha, DOC1, Galpha(i)-specific amine GPCRs, Stch, TRPC4, PMCA1, NCX1, DNAJC12, SLBP, HCN, RTEL1-TNFRSF6B, Protein kinase G1, HLF, BDH, C1orf113, LENG8, CAP1, HSP90 beta, Anillin, TXNIP (VDUP1), Vinexin, COL25A1, MEGF6, NDUFS6, Calponin-1, Activin beta A, BRMS1L, Zeta-sarcoglycan, CDK5, PANX2, DUS3L, PAK, Guanylate cyclase (alpha-1/beta-1), FLJ32001, SYT16, Guanylate cyclase beta, BEX1, TCP1-eta, Glycine receptor, Fatty acid-binding protein, Tmem134, PSG3, FOXP4, HINT, ENPP4, MAML1, KIAA0143, MORN1, SOHLH1, IZUMO1, FLJ37078, TOM22, GABA-A receptor alpha-3 subunit, GNT-IV, LPPR4, ISOC1, DYNLT, SLC16A13, Atg101, TMEM74, TM6SF1, COX Va, Tetraspanin-3, Copine-4, Destrin, eIF4A2, ATP5A, Glycine receptor beta chain, Nek8, Selenoprotein P, CAPZA, Carbonic anhydrase XII, Kv9.3, RTL1, PKC-beta2, Calcineurin A (catalytic), LSM2, TOP1MT, Galpha(i)-specific cannabis GPSRs, STARD7, B3GT2, Cyclin G1, sRAGE, SEC23A, Glyoxalase I, DDX51, SMIT, FBI-1 (Pokemon), Galpha(q)-specific peptide GPCRs, H2AFZ, ATP6V1C, Histone H2B, MAFbx, SNAP190, WDR47, Tubulin alpha, Creatine kinase, ACAP1(CENTB1), DSCAML1, TBC1D10C, DCK, MRAP2, PAP-II, B-FABP, Azi1, DYNLL, Patched, TNK1, XK, MEF2, NAPB, ADAR3, BICRA, HNMT, Sec23, APRIO, SCS-A, BTBD10, MEK4/7, Peg10, ACSL4, RENBP, LOC440248, CEACAM1, RANBP6, ATF/CREB, GLGB, ODP2, RAI1, G-protein gamma 3, LAMP2-C, FN14(TNFRSF12A), Trim45, RSL24D1, C3orf59, G-protein beta-4, FEM1B, Acyl-CoA synthetase, PP2A catalytic, SULT1A1 isoform 1, CAPZA2, IDI1, SNX7, ARRDC2, ZFAND2A, AP-4, MRLC, eIF4A, BMI-1, C9orf106, SNAPs, OAZIN, eIF2S1, Glutaredoxin, RNF175, Galpha(s)-specific CRF GPCRs, LAMP2, COX VIa-1, C1orf115, KAD6, ALAS1, TMEM87A, YPEL5, TSNARE1, ATP6V1B, Kv4.2 channel, JKAMP, PKD1L1, Protein kinase G 2, PRNP, Osrf, FAM22A, DNAJA2, TMS-1, MPTP complex, ENC1, STAG3, RHEB2, CENPL, NKCC1, Malin, C1orf59, HIST2H2BE, ATP6V0B, PKC-beta1, PDE4A, WDT2, ZSCAN1, CAB39L, Calmodulin, CENPP, LPL, DIRAS2, NELL2, FLJ31818, PGRMC1, ATP6V1E, Apo-2L(TNFSF10), LOXL2, PDE11A, NOLA3 (NOP10), HSPC125,

						Endophilin A1, STAC2, Activin, SIPAR, C1orf43, Aquaporin 1, NDFIP1, KCTD16, C6orf27, Calcyclin, FAM186B, Syntenin 1, SCOT, Octanoyl-holo-acp, KCRS, Securin, ADHX, ZNF517, ERK1/2, Carboxypeptidase M, AATC, UGCG, SLC29A4, Anks4b, TRUB1, NFIC, HSC70, PI3K reg class IA (p55-gamma), SLC35A5, PKC, SSTR2, SUR1, ABTB1, C19orf55, HTR2A, SLC25A4, MPP7, CCDC57, ATP1B3, K-cadherin (CDH6), Guanylate Cyclase 1, soluble, MEF2C, SULT4A1, MRPL33, Protein kinase G, ERK2 (MAPK1), Calcineurin A (beta), LISCH7, Ran, OAT, MEK4(MAP2K4), DACH2, PRKAR1A, CCK8-GlyArgArg, CLCN5, STX16-NPEPL1, IMPA1, TRIM23, UFC1, Nephrocystin-4, DKK1, PARM-1, sKITLG, SSTR1, Guanine deaminase, PRPS, SOD1, TFIIB, YIPF5, KIAA1024, PPP4R2, GDE1, SLC38A2, MMP-28, SAP102, FSTL5, EVI2A, MAP1, RPESP, CALM2, Cyclophilin A, FOXP1/2/4 proteins, Aggrecanase-2, PI3K reg class IA, KIAA1614, PTCHD1, Galpha(s)-specific peptide GPCRs, GPR22, TSPAN19, TCP1-alpha, ATP5L, ACTR3, ATP6AP2, OXR1, CALB1, Tubulin alpha-4A, CALML6, SRm300, RhoE, CD166, TIP27, GAD2, DRIL2, SIAH3, PGM2L1, TCP1-epsilon, NF-I, MRPL3, HXK3, COX VIIa-2, ACOXL, NRBF2, Midkine, FLJ37464, SAMD10, IRS6(DOK5), ARP3, PXDN, 14-3-3, ARMCX3, ACCN3 (ASIC3), COX VIIa-2L, RAGE, 14-3-3 eta, ATP1beta subunit, Myospryn, Glutaredoxin 1, ZCCHC12, CMAS, CHST6
29	Respiratory Tract Diseases	21141	7.524E-13	5.664E-11	748	SCAP2, Cyclin G, FBXO45, NPY, C13orf36, FAM3C, PP2A cat (alpha), HSP90, PAK3, PAM, Cadherin 8, ZYG11B, CPSF1, ZNF575, ARP6, CXorf57, NPEPL1, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, ZNF34, Semaphorin 3C, TMEM87B, AEBP1, ET-1, G3BP2, MBD6, IRF1, ILDR2, FILIP, ZnT-2, MAL2, Rab-3B, MAGEH-1, COX VIc, SMVT, C1D, MEGF10, THAP11, PTCH2, N-chimaerin, Tubulin alpha 1A, ATP5C, SUCLG1, HPCA, APJ, Smooth muscle myosin, EDIL3, FLJ12671, ELOVL5, GLB1B2, RNF207, Peroxiredoxin, Activin A, UBL5, D630023F18Rik, Esterase D, Endothelin-1, SULT1A1, Trehalase, Neuropeptide K, AP-1 gamma subunits, ARG2, DUOX1, Nkpd1, NETO2, GHITM, REV-ERBalpha, IL-17D, BRSK2, UQCRQPC, DYNLT3, UBXD3, G-protein beta, KLHL4, LAS1L, SC5D, ALDR, CRTL1, UQCRH, Rab-6A, RGS8, Mucin 5B, MRPS6, PSMA5, CNOT7, MDS028, NFKBIL2, NDUFAB1, Importin (karyopherin)-alpha, CCK8-Gly, NckAP1, GLIPR, BTBD12, CDC18L (CDC6), ANKRD50, LSMD1, DNAH1, MRPL1, Lgi4, GPR137C, TTLL9, MOBKL1A, AP1G2, ZNF707, LOC153328, Pannexin-1, MCM6, OGFRL1, NKIRAS1, HPCAL4, RHBDL3, PSD2, FAM90A1, NIPSNAP3A, MGF, PDH E2 subunit N6-lipoyllysine, TIP47, PRKAR2B, MELC, PLD5, DPY19L1,

						NPFF receptor 2, NDUFB4, MC4R, UNRIP, NDUFA8, KLHL12, Synaptotagmin I, COCH, Guanylate cyclase, ARL6, KCNK2, HSP70, CCDC4, Substance P extracellular region, DDX3Y, CNR1, MAPBPIP, MYL6, Glycogen phosphorylase, Synaptotagmin IV, Tim17, PPM1E, HDBP1, GIMAP7, DnaJB9, Synaptotagmin, PRDX3, CNTN1 (F3), Thioredoxin, MRLC2, NDUFA4, ZMAT1, ATP6V1A (70kD), HSPA4, JMJD3, Septin 1, Dynein, axonemal, light chains, PDE, Cystatin C, CNIH2, Tcfl5, PPT1, SCF, SDHB, SLC39A10, IGSF9B, DKK3, Karyopherin alpha 2, LUZP2, PNMAL1, NCKP1 subunit, TM9SF2, HCN2, D123, LOC441108, FLJ20674, Galpha(q)-specific Class A Orphan/other GPCRs, IMPG2, LMF1, OAF, ATP5G, C6orf168, CCK8, GPR124, TPH2, Neuropeptide gamma, KAL1, RAB39B, RGS4, VSIG2, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, TUSC3, UGT8, D330028D13Rik, GUCY1B1, FLRT3, Exostosin-like 2, Kv3.3, SELI, ORP-family, B3GN6, LY6G5B, Tenascin-C, PP1-cat gamma, CEACAM, TRPC5, PKC-beta, KIS, PRDX1, G-protein beta/gamma, B3GN1, SLC25A45, NDUFB6, SDFR1, SUR, ABO system transferase, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, VBP-1, FUT2, TORC1, KLHL13, UQCRB, CPT-1A, S100, Rab-6, TXNRD1, ORP8, KCNH5, AMIGO2, VWA2, FLJ38984, LASS6, TRPV1, PRR12, PDK3, ZFHX4, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, TIP41, ATP6V1C1, PRRG1, ZDH13, Aldose reductase, ATP6M, NDUFB3, Rab-3, MTG16 (CBFA2T3), TM2D3, DNER, FAM38B, APOL3, TMEM45A, Ephrin-A receptor 5, LAPTM4B, IDUA, IP3KA, CRH receptor 2, AMDHD2, CacyBP(SIP), InsP6 kinase 3, SLC2A13, Semaphorin 5A, V-ATPase E subunit, GRAIL, NSF, Tomt, ADAM-TS10, GPR176, FAM102B, CaMK IV, CHCHD2, GLRA, DKK2, ZNF499, GABA-A receptor beta-2 subunit, FBXO2, ZNF433, CECR2, DOK7, SYP, Carbohydrate sulfotransferases, TIMM17, LACTB2, LPL1, Rho GTPase, PDE4, GTPBP3, Tensin 2, Lba1, G-protein gamma, UBE2D1, OSGIN2, PLCXD2, PRPS2, ZNF70, SOCS6, Dysferlin, Rap1GDS1, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, ChREBP, ZNF267, A830006F12Rik, PP4R4, Secretogranin V, EGF, GlyRA2, ATP5B, PPase (inorganic), NAP1L2, Pro-CCK, CED-6, SYTC, XKR4, Dynein, axonemal, heavy chains, B3GALTL, BMPR1A, Semaphorin 3E, MMADHC, MMD, LOC283174, HIST1H2BN, Neurexophilin 2, RBM18, PKA-reg type II (cAMP-dependent), B3GNT4, Myotrophin, NELL1, CAP2, HKR4, cPKC (conventional), SF3A2, ATP6V1B2, NDUFB1, DLL4, ELOVL4, Serotonin receptor, CHMP5, Neurexophilin 1, TMEM39B, ADSS, Rab-27B, mADAMTS5, TRPC,

						SLC7A5, HTR5A, ACTR10, PDK4, VDAC 1, WIF1, COX VIa, SUCB1, ATP6V1H, Osteopontin, ATP5G3, Slp5, ABHD10, SMRT, Big ET-1, CysLT2 receptor, NHE6, Rab-3C, KCY, CREB4, PC4, SMIM43_132332, CHAMP, PKA-reg (cAMP-dependent), TReP-132, RNF152, Lingo1, ANT, PP1-cat, CFA74, Neurokinin A, PDLIM2, NR3A, KLHDC4, VTA1, Cables1, KIAA1110, ECT2, Clathrin heavy chain, IL3RA, Substance P, AP-3 sigma subunits, HBXIP, PSMD10 (Gankyrin), StARD4, GRM6, CHTF18, CalDAG-GEFII, Histone H2, LIPA, KLHL35, MCT1 (SLC16A1), ARHGAP18, CCK5, TMEM14A, LRRC51, Galpha(q)-specific amine GPCRs, UQCRFS1, Maestro, Ephrin-A receptors, MRPL47, Histone H2A, HMP19, NPR3, GP-IB alpha, DOC1, Galpha(i)-specific amine GPCRs, Stch, TRPC4, PMCA1, NCX1, DNAJC12, SLBP, HCN, RTEL1-TNFRSF6B, Protein kinase G1, HLF, BDH, C1orf113, LENG8, CAP1, HSP90 beta, Anillin, TXNIP (VDUP1), Vinexin, COL25A1, MEGF6, NDUFS6, Calponin-1, Activin beta A, BRMS1L, Zeta-sarcoglycan, CDK5, PANX2, DUS3L, PAK, Guanylate cyclase (alpha-1/beta-1), FLJ32001, SYT16, Guanylate cyclase beta, BEX1, TCP1-eta, Glycine receptor, Fatty acid-binding protein, Tmem134, PSG3, FOXP4, HINT, ENPP4, MAML1, KIAA0143, MORN1, SOHLH1, IZUMO1, FLJ37078, TOM22, GABA-A receptor alpha-3 subunit, GNT-IV, LPPR4, ISOC1, DYNLT, SLC16A13, Atg101, TMEM74, TM6SF1, COX Va, Tetraspanin-3, Copine-4, Destrin, eIF4A2, ATP5A, Glycine receptor beta chain, Nek8, Selenoprotein P, CAPZA, Carbonic anhydrase XII, Kv9.3, RTL1, PKC-beta2, Calcineurin A (catalytic), LSM2, TOP1MT, Galpha(i)-specific cannabis GPSRs, STARD7, B3GT2, Cyclin G1, sRAGE, SEC23A, Glyoxalase I, DDX51, SMIT, FBI-1 (Pokemon), Galpha(q)-specific peptide GPCRs, H2AFZ, ATP6V1C, Histone H2B, MAFbx, SNAP190, WDR47, Tubulin alpha, Creatine kinase, ACAP1(CENTB1), DSCAML1, TBC1D10C, DCK, MRAP2, PAP-II, B-FABP, Azi1, DYNLL, Patched, TNK1, XK, MEF2, INCA1, NAPB, ADAR3, BICRA, HNMT, Sec23, APRIO, SCS-A, BTBD10, MEK4/7, Peg10, ACSL4, RENBP, LOC440248, CEACAM1, RANBP6, ATF/CREB, GLGB, ODP2, RAI1, G-protein gamma 3, LAMP2-C, FN14(TNFRSF12A), Trim45, RSL24D1, C3orf59, G-protein beta-4, FEM1B, Acyl-CoA synthetase, PP2A catalytic, SULT1A1 isoform 1, CAPZA2, IDI1, SNX7, ARRDC2, ZFAND2A, AP-4, MRLC, eIF4A, BMI-1, C9orf106, SNAPs, OAZIN, eIF2S1, Glutaredoxin, RNF175, Galpha(s)-specific CRF GPCRs, LAMP2, COX VIa-1, C1orf115, KAD6, ALAS1, TMEM87A, YPEL5, TSNARE1, ATP6V1B, Kv4.2 channel, JKAMP, PKD1L1, Protein kinase G 2, PRNP, Osrf, FAM22A, DNAJA2, TMS-1, MPTP complex, ENC1, STAG3, RHEB2,

						CENPL, NKCC1, Malin, C1orf59, HIST2H2BE, ATP6V0B, PKC-beta1, PDE4A, WDT2, ZSCAN1, CAB39L, Calmodulin, CENPP, LPL, DIRAS2, NELL2, FLJ31818, PGRMC1, ATP6V1E, Apo-2L(TNFSF10), LOXL2, PDE11A, NOLA3 (NOP10), HSPC125, Endophilin A1, STAC2, Activin, SIPAR, C1orf43, Aquaporin 1, NDFIP1, KCTD16, C6orf27, Calcyclin, FAM186B, Syntenin 1, SCOT, Octanoyl-holo-acp, KCRS, Securin, ADHX, ZNF517, ERK1/2, Carboxypeptidase M, AATC, UGCG, SLC29A4, Anks4b, TRUB1, NFIC, HSC70, PI3K reg class IA (p55-gamma), SLC35A5, PKC, SSTR2, SUR1, ABTB1, C19orf55, HTR2A, SLC25A4, MPP7, CCDC57, ATP1B3, K-cadherin (CDH6), Guanylate Cyclase 1, soluble, MEF2C, SULT4A1, MRPL33, Protein kinase G, ERK2 (MAPK1), Calcineurin A (beta), LISCH7, Ran, OAT, MEK4(MAP2K4), DACH2, PRKAR1A, CCK8-GlyArgArg, CLCN5, STX16-NPEPL1, IMPA1, TRIM23, UFC1, Nephrocystin-4, DKK1, PARM-1, sKITLG, SSTR1, Guanine deaminase, PRPS, SOD1, TFIIB, YIPF5, KIAA1024, PPP4R2, GDE1, SLC38A2, MMP-28, SAP102, FSTL5, EVI2A, MAP1, RPESP, CALM2, Cyclophilin A, FOXP1/2/4 proteins, Aggrecanase-2, PI3K reg class IA, KIAA1614, PTCHD1, Galpha(s)-specific peptide GPCRs, GPR22, TSPAN19, TCP1-alpha, ATP5L, ACTR3, ATP6AP2, OXR1, CALB1, Tubulin alpha-4A, CALML6, SRm300, RhoE, CD166, TIP27, GAD2, DRIL2, SIAH3, PGM2L1, TCP1-epsilon, NF-I, MRPL3, HXK3, COX VIIa-2, ACOXL, NRBF2, Midkine, FLJ37464, SAMD10, IRS6(DOK5), ARP3, PXDN, 14-3-3, ARMCX3, ACCN3 (ASIC3), COX VIIa-2L, RAGE, 14-3-3 eta, ATP1beta subunit, Myospryn, Glutaredoxin 1, ZCCHC12, CMAS, CHST6
30	Female Urogenital Diseases	19660	1.715E-12	1.248E-10	706	Cyclin G, FBXO45, NPY, PP2A cat (alpha), HSP90, PAK3, PAM, Cadherin 8, ZYG11B, CPSF1, ZNF575, ARP6, CXorf57, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, LINC01410, Semaphorin 3C, Alpha crystallin B, AEBP1, ET-1, G3BP2, RhoN, MBD6, IRF1, ILDR2, FILIP, ZnT-2, MAL2, GLSK, MAGEH-1, SLC35E2B, SMVT, C1D, MEGF10, THAP11, TINP1, PTCH2, N-chimaerin, Tubulin alpha 1A, ATP5C, SUCLG1, HPCA, LOC284837, APJ, Smooth muscle myosin, EDIL3, FLJ12671, ELOVL5, GLB1B2, RNF207, Peroxiredoxin, Activin A, UBL5, D630023F18Rik, Esterase D, Endothelin-1, SULT1A1, Trehalase, Neuropeptide K, PSMB5, AP-1 gamma subunits, ARG2, DUOX1, Nkpd1, NETO2, GHITM, IL-17D, BRSK2, DYNLT3, P2Y11, UBXD3, G-protein beta, KLHL4, LAS1L, JWA, ALDR, CRTL1, TMC4, Mucin 5B, SC4MOL, PSMA5, NFKBIL2, NDUFAB1, Importin (karyopherin)-alpha, CCK8-Gly, NckAP1, GLIPR, BTBD12, CDC18L (CDC6), ANKRD50, DNAH1, MRPL1, MOBKL1A, AP1G2, ZNF707, LOC153328, Pannexin-1,

						OGFRL1, NKIRAS1, DCMC, PSD2, NIPSNAP3A, MGF, PDH E2 subunit N6-lipoyllysine, TIP47, PRKAR2B, MELC, PLD5, DPY19L1, NPFF receptor 2, NDUFB4, MC4R, UNRIP, NDUFA8, Synaptotagmin I, COCH, Guanylate cyclase, KCNK2, HSP70, CCDC4, SCRT2, Substance P extracellular region, DDX3Y, CNR1, MAPBPIP, Glycogen phosphorylase, Synaptotagmin IV, Tim17, CITED2, PPM1E, SLIRP, NUDT4P1, DnaJB9, Synaptotagmin, PRDX3, CNTN1 (F3), Thioredoxin, ZMAT1, ATP6V1A (70kD), HSPA4, JMJD3, Septin 1, Dynein, axonemal, light chains, PDE, Cystatin C, Tcfl5, PPT1, SCF, SDHB, SLC39A10, IGSF9B, DKK3, Karyopherin alpha 2, LUZP2, PNMAL1, NCKP1 subunit, TM9SF2, HCN2, D123, FLJ20674, Galpha(q)-specific Class A Orphan/other GPCRs, IMPG2, LMF1, OAF, ATP5G, C6orf168, CCK8, GPR124, TPH2, Neuropeptide gamma, KAL1, RAB39B, Aha1, PTPN18, RGS4, VSIG2, 14-3-3 beta/alpha, BTBD18, GABA-A receptor alpha-1 subunit, TUSC3, UGT8, D330028D13Rik, GUCY1B1, FLRT3, Exostosin-like 2, SELI, C13orf37, ORP-family, B3GN6, Tenascin-C, Myopodin, HSDL1, CEACAM, TRPC5, PKC-beta, KIS, TCP1-theta, PRDX1, ELMO3, G-protein beta/gamma, B3GN1, SLC25A45, NDUFB6, SDFR1, SUR, ABO system transferase, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, VBP-1, TORC1, KLHL13, UQCRB, CPT-1A, S100, Rab-6, TXNRD1, ORP8, KCNH5, AMIGO2, VWA2, FLJ38984, TRPV1, PRR12, PDK3, ZFHX4, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, TIP41, ATP6V1C1, PRRG1, Aldose reductase, NDUFB3, Rab-3, MTG16 (CBFA2T3), ATG9B, TM2D3, DNER, FAM38B, APOL3, TMEM45A, Ephrin-A receptor 5, LAPTM4B, IDUA, IP3KA, CRH receptor 2, AMDHD2, CacyBP(SIP), InsP6 kinase 3, SLC2A13, Semaphorin 5A, Adropin, V-ATPase E subunit, GRAIL, UBA1L, NSF, Tomt, ADAM-TS10, GPR176, FAM102B, CaMK IV, GLRA, DKK2, ZNF499, GABA-A receptor beta-2 subunit, FBXO2, H41, ZNF433, CECR2, DOK7, SYP, Carbohydrate sulfotransferases, TIMM17, LACTB2, LPL1, Rho GTPase, PDE4, GTPBP3, Tensin 2, Lba1, G-protein gamma, UBE2D1, OSGIN2, PRPS2, ZNF70, SOCS6, Dysferlin, Rap1GDS1, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, ChREBP, ZNF267, A830006F12Rik, Secretogranin V, EGF, GlyRA2, ATP5B, NAP1L2, Pro-CCK, CED-6, SYTC, XKR4, Dynein, axonemal, heavy chains, B3GALTL, BMPR1A, Semaphorin 3E, MMADHC, LOC283174, HIST1H2BN, Neurexophilin 2, PKA-reg type II (cAMP-dependent), B3GNT4, Myotrophin, NELL1, CAP2, cPKC (conventional), ATP6V1B2, DLL4, ELOVL4, AP3S1, PSMA1, Serotonin receptor, Neurexophilin 1, TMEM39B, ADSS,

						mADAMTS5, TRPC, SLC7A5, HTR5A, NOP14-AS1, ACTR10, PDK4, VDAC 1, WIF1, SUCB1, ATP6V1H, Osteopontin, Slp5, SMRT, Big ET-1, CysLT2 receptor, NHE6, Rab-3C, KCY, CREB4, PC4, CHAMP, PKA-reg (cAMP-dependent), TReP-132, RNF152, Lingo1, ANT, PP1-cat, CFA74, HMDH, Neurokinin A, PDLIM2, NR3A, KLHDC4, VTA1, Cables1, KIAA1110, ECT2, Clathrin heavy chain, IL3RA, Substance P, AP-3 sigma subunits, PSMD10 (Gankyrin), StARD4, GRM6, CHTF18, CalDAG-GEFII, Histone H2, KLHL35, MCT1 (SLC16A1), ARHGAP18, CCK5, LRRC51, Galpha(q)-specific amine GPCRs, UQCRFS1, Maestro, Ephrin-A receptors, MRPL47, Histone H2A, HMP19, NPR3, C9orf5, GP-IB alpha, DOC1, Galpha(i)-specific amine GPCRs, CCNI2, Stch, TRPC4, PMCA1, NCX1, DNAJC12, SLBP, HCN, Protein kinase G1, HLF, BDH, C1orf113, LENG8, CAP1, HSP90 beta, Anillin, TXNIP (VDUP1), Vinexin, COL25A1, C14orf142, MEGF6, Calponin-1, Activin beta A, BRMS1L, Zeta-sarcoglycan, PANX2, DUS3L, PAK, Guanylate cyclase (alpha-1/beta-1), FLJ32001, SYT16, Guanylate cyclase beta, BEX1, TCP1-eta, Glycine receptor, Fatty acid-binding protein, PSG3, HINT, MAML1, KIAA0143, SOHLH1, IZUMO1, FLJ37078, ASAH, GABA-A receptor alpha-3 subunit, GNT-IV, LPPR4, ISOC1, DYNLT, TMEM74, TM6SF1, SPSY, COX Va, Tetraspanin-3, Copine-4, eIF4A2, ATP5A, Glycine receptor beta chain, Nek8, Selenoprotein P, CAPZA, Carbonic anhydrase XII, Kv9.3, RTL1, PKC-beta2, Calcineurin A (catalytic), TOP1MT, Galpha(i)-specific cannabis GPSRs, STARD7, B3GT2, Cyclin G1, sRAGE, SLC25A46, SEC23A, Glyoxalase I, DDX51, SMIT, FBI-1 (Pokemon), PDH beta, Galpha(q)-specific peptide GPCRs, H2AFZ, ATP6V1C, Histone H2B, NCOA4 (ARA70), SNAP190, WDR47, NDUFA5, Tubulin alpha, Creatine kinase, ACAP1(CENTB1), DSCAML1, TBC1D10C, DCK, PAP-II, B-FABP, VIP32, Azi1, NUDT4, Patched, TNK1, XK, MEF2, SLC2A1-AS1, NAPB, ADAR3, BICRA, PGAM1, TAPBPL, Sec23, APRIO, SCS-A, BTBD10, MEK4/7, Peg10, ACSL4, RENBP, CEACAM1, RANBP6, ATF/CREB, GLGB, ODP2, RAI1, G-protein gamma 3, Hdj-2, LAMP2-C, FN14(TNFRSF12A), Trim45, C3orf59, G-protein beta-4, FEM1B, Acyl-CoA synthetase, PP2A catalytic, SULT1A1 isoform 1, CAPZA2, GAS41, IDI1, ARRDC2, MRLC, eIF4A, BMI-1, SNAPs, eIF2S1, Glutaredoxin, Galpha(s)-specific CRF GPCRs, LAMP2, KAD6, ALAS1, TMEM87A, YPEL5, TSNARE1, ATP6V1B, Kv4.2 channel, JKAMP, PKD1L1, Protein kinase G 2, PRNP, HSPC138, Osrf, FAM22A, TM2D2, TMS-1, MPTP complex, ENC1, STAG3, RHEB2, CENPL, NKCC1, Neurocalcin delta, Malin, C1orf59, PKC-beta1, PDE4A, ZSCAN1, CAB39L, Calmodulin, CENPP, LPL, DIRAS2,

						NELL2, FLJ31818, PGRMC1, ATP6V1E, Apo-2L(TNFSF10), SET1B, LOXL2, PDE11A, FLJ45455, NOLA3 (NOP10), Endophilin A1, STAC2, Activin, C1orf43, Aquaporin 1, NDFIP1, KCTD16, C6orf27, NME5, Calcyclin, FAM186B, Syntenin 1, SCOT, Octanoyl-holo-acp, KCRS, Securin, ADHX, ZNF517, ERK1/2, AATC, UGCG, SLC29A4, Anks4b, TRUB1, NFIC, HSC70, SLC35A5, PKC, SSTR2, SUR1, ABTB1, C19orf55, HTR2A, PMM2, SLC25A4, MPP7, CCDC57, ATP1B3, ARPP-19, K-cadherin (CDH6), Guanylate Cyclase 1, soluble, MEF2C, SULT4A1, Protein kinase G, RIFK, ERK2 (MAPK1), Calcineurin A (beta), DREV1, LISCH7, Ran, OAT, MEK4(MAP2K4), DACH2, C14orf2, TMEM70, CCK8-GlyArgArg, CLCN5, IMPA1, TRIM23, UFC1, Nephrocystin-4, DKK1, PARM-1, sKITLG, SSTR1, Guanine deaminase, PRPS, SOD1, TFIIB, KIAA1024, PPP4R2, GDE1, SLC38A2, MMP-28, SAP102, FSTL5, EVI2A, MAP1, RPESP, CALM2, Cyclophilin A, FOXP1/2/4 proteins, Aggrecanase-2, PI3K reg class IA, KIAA1614, PTCHD1, DCoHM, Galpha(s)-specific peptide GPCRs, TSPAN19, TCP1-alpha, ACTR3, OXR1, CALB1, Tubulin alpha-4A, CALML6, SRm300, RhoE, Pcdh19, CD166, TIP27, GAD2, PGM2L1, NF-I, MRPL3, HXK3, Neuroserpin, COX VIIa-2, ACOXL, Midkine, SAMD10, IRS6(DOK5), ARP3, PXDN, 14-3-3, ARMCX3, ACCN3 (ASIC3), C8orf83, AATBC, RAGE, 14-3-3 eta, ATP1beta subunit, Myospryn, Glutaredoxin 1, ZCCHC12, CHST6
31	Female Urogenital Diseases and Pregnancy Complications	19809	1.865E-12	1.314E-10	710	Cyclin G, FBXO45, NPY, PP2A cat (alpha), HSP90, PAK3, PAM, Cadherin 8, ZYG11B, CPSF1, ZNF575, ARP6, CXorf57, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, LINC01410, Semaphorin 3C, Alpha crystallin B, AEBP1, ET-1, G3BP2, RhoN, MBD6, IRF1, ILDR2, FILIP, ZnT-2, MAL2, GLSK, MAGEH-1, SLC35E2B, SMVT, C1D, MEGF10, THAP11, TINP1, PTCH2, N-chimaerin, Tubulin alpha 1A, ATP5C, SUCLG1, HPCA, LOC284837, APJ, Smooth muscle myosin, EDIL3, FLJ12671, ELOVL5, GLB1B2, RNF207, Peroxiredoxin, Activin A, UBL5, D630023F18Rik, Esterase D, Endothelin-1, SULT1A1, Trehalase, Neuropeptide K, PSMB5, AP-1 gamma subunits, ARG2, DUOX1, Nkpd1, NETO2, GHITM, IL-17D, BRSK2, DYNLT3, P2Y11, UBXD3, G-protein beta, KLHL4, LAS1L, JWA, ALDR, CRTL1, TMC4, Mucin 5B, SC4MOL, PSMA5, NFKBIL2, NDUFAB1, Importin (karyopherin)-alpha, CCK8-Gly, NckAP1, GLIPR, BTBD12, CDC18L (CDC6), ANKRD50, DNAH1, MRPL1, MOBKL1A, AP1G2, ZNF707, LOC153328, Pannexin-1, OGFRL1, NKIRAS1, DCMC, PSD2, NIPSNAP3A, MGF, PDH E2 subunit N6-lipoyllysine, TIP47, PRKAR2B, MELC, PLD5, DPY19L1, NPFF receptor 2, NDUFB4, MC4R, UNRIP, NDUFA8, Synaptotagmin I, COCH, Guanylate cyclase, KCNK2, HSP70,

						CCDC4, SCRT2, Substance P extracellular region, DDX3Y, CNR1, MAPBPIP, Glycogen phosphorylase, Synaptotagmin IV, Tim17, CITED2, PPM1E, SLIRP, NUDT4P1, DnaJB9, Synaptotagmin, PRDX3, CNTN1 (F3), Thioredoxin, ZMAT1, ATP6V1A (70kD), HSPA4, JMJD3, Septin 1, Dynein, axonemal, light chains, PDE, Cystatin C, Tcfl5, PPT1, SCF, SDHB, SLC39A10, IGSF9B, DKK3, Karyopherin alpha 2, LUZP2, PNMAL1, NCKP1 subunit, TM9SF2, HCN2, D123, FLJ20674, Galpha(q)-specific Class A Orphan/other GPCRs, IMPG2, LMF1, OAF, ATP5G, C6orf168, CCK8, GPR124, TPH2, Neuropeptide gamma, KAL1, RAB39B, Aha1, PTPN18, RGS4, VSIG2, 14-3-3 beta/alpha, BTBD18, GABA-A receptor alpha-1 subunit, TUSC3, UGT8, D330028D13Rik, GUCY1B1, FLRT3, Exostosin-like 2, SELI, C13orf37, ORP-family, B3GN6, Tenascin-C, Myopodin, HSDL1, CEACAM, TRPC5, PKC-beta, KIS, TCP1-theta, PRDX1, ELMO3, G-protein beta/gamma, B3GN1, SLC25A45, NDUFB6, SDFR1, SUR, ABO system transferase, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, VBP-1, TORC1, KLHL13, UQCRB, CPT-1A, S100, Rab-6, TXNRD1, ORP8, KCNH5, AMIGO2, VWA2, FLJ38984, TRPV1, PRR12, PDK3, ZFHX4, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, TIP41, ATP6V1C1, PRRG1, Aldose reductase, NDUFB3, Rab-3, MTG16 (CBFA2T3), ATG9B, TM2D3, DNER, FAM38B, APOL3, TMEM45A, Ephrin-A receptor 5, LAPTM4B, IDUA, IP3KA, CRH receptor 2, AMDHD2, CacyBP(SIP), InsP6 kinase 3, SLC2A13, Semaphorin 5A, Adropin, V-ATPase E subunit, GRAIL, UBA1L, NSF, Tomt, ADAM-TS10, GPR176, FAM102B, CaMK IV, GLRA, DKK2, ZNF499, GABA-A receptor beta-2 subunit, FBXO2, H41, ZNF433, CECR2, DOK7, SYP, Carbohydrate sulfotransferases, TIMM17, LACTB2, LPL1, Rho GTPase, PDE4, GTPBP3, Tensin 2, Lba1, G-protein gamma, UBE2D1, OSGIN2, PRPS2, ZNF70, SOCS6, Dysferlin, Rap1GDS1, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, ChREBP, ZNF267, A830006F12Rik, Secretogranin V, EGF, GlyRA2, ATP5B, NAP1L2, Pro-CCK, CED-6, SYTC, XKR4, Dynein, axonemal, heavy chains, B3GALTL, BMPR1A, Semaphorin 3E, MMADHC, LOC283174, HIST1H2BN, Neurexophilin 2, PKA-reg type II (cAMP-dependent), B3GNT4, Myotrophin, NELL1, CAP2, cPKC (conventional), ATP6V1B2, DLL4, ELOVL4, AP3S1, PSMA1, Serotonin receptor, Apelin, Neurexophilin 1, TMEM39B, ADSS, mADAMTS5, TRPC, SLC7A5, HTR5A, PYGM, NOP14-AS1, ACTR10, PDK4, VDAC 1, WIF1, SUCB1, ATP6V1H, Osteopontin, Slp5, SMRT, Big ET-1, CysLT2 receptor, NHE6, Rab-3C, KCY, CREB4, PC4, CHAMP, PKA-reg (cAMP-dependent), TReP-132,

						RNF152, Lingo1, ANT, PP1-cat, CFA74, HMDH, Neurokinin A, PDLIM2, NR3A, KLHDC4, VTA1, Cables1, KIAA1110, ECT2, Clathrin heavy chain, IL3RA, Substance P, AP-3 sigma subunits, PSMD10 (Gankyrin), StARD4, GRM6, CHTF18, CalDAG-GEFII, Histone H2, KLHL35, MCT1 (SLC16A1), ARHGAP18, CCK5, LRRC51, Galpha(q)-specific amine GPCRs, UQCRFS1, Maestro, Ephrin-A receptors, MRPL47, Histone H2A, HMP19, NPR3, C9orf5, GP-IB alpha, DOC1, Galpha(i)-specific amine GPCRs, CCNI2, Stch, TRPC4, PMCA1, NCX1, DNAJC12, SLBP, HCN, Protein kinase G1, HLF, BDH, C1orf113, LENG8, CAP1, HSP90 beta, Anillin, TXNIP (VDUP1), Vinexin, COL25A1, C14orf142, MEGF6, Calponin-1, Activin beta A, BRMS1L, Zeta-sarcoglycan, PANX2, DUS3L, PAK, Guanylate cyclase (alpha-1/beta-1), FLJ32001, SYT16, Guanylate cyclase beta, BEX1, TCP1-eta, Glycine receptor, Fatty acid-binding protein, PSG3, HINT, MAML1, KIAA0143, SOHLH1, IZUMO1, FLJ37078, ASAH, GABA-A receptor alpha-3 subunit, GNT-IV, LPPR4, ISOC1, DYNLT, TMEM74, TM6SF1, SPSY, COX Va, Tetraspanin-3, Copine-4, eIF4A2, ATP5A, Glycine receptor beta chain, Nek8, Selenoprotein P, CAPZA, Carbonic anhydrase XII, Kv9.3, RTL1, PKC-beta2, Calcineurin A (catalytic), TOP1MT, Galpha(i)-specific cannabis GPSRs, STARD7, B3GT2, Cyclin G1, sRAGE, SLC25A46, SEC23A, Glyoxalase I, DDX51, SMIT, FBI-1 (Pokemon), PDH beta, Galpha(q)-specific peptide GPCRs, H2AFZ, ATP6V1C, Histone H2B, NCOA4 (ARA70), SNAP190, WDR47, NDUFA5, Tubulin alpha, Creatine kinase, ACAP1(CENTB1), DSCAML1, TBC1D10C, DCK, PAP-II, B-FABP, VIP32, Azi1, NUDT4, Patched, TNK1, XK, MEF2, SLC2A1-AS1, NAPB, ADAR3, BICRA, PGAM1, TAPBPL, Sec23, APRIO, SCS-A, BTBD10, MEK4/7, Peg10, ACSL4, RENBP, CEACAM1, RANBP6, ATF/CREB, GLGB, ODP2, RAI1, G-protein gamma 3, Hdj-2, LAMP2-C, FN14(TNFRSF12A), Trim45, C3orf59, G-protein beta-4, FEM1B, Acyl-CoA synthetase, PP2A catalytic, SULT1A1 isoform 1, CAPZA2, GAS41, IDI1, ARRDC2, MRLC, eIF4A, BMI-1, SNAPs, eIF2S1, Glutaredoxin, Galpha(s)-specific CRF GPCRs, LAMP2, KAD6, ALAS1, TMEM87A, YPEL5, TSNARE1, ATP6V1B, Kv4.2 channel, JKAMP, PKD1L1, Protein kinase G 2, PRNP, HSPC138, Osrf, FAM22A, TM2D2, TMS-1, MPTP complex, ENC1, STAG3, RHEB2, CENPL, NKCC1, Neurocalcin delta, Malin, C1orf59, PKC-beta1, PDE4A, ZSCAN1, CAB39L, Calmodulin, CENPP, LPL, DIRAS2, NELL2, FLJ31818, PGRMC1, ATP6V1E, Apo-2L(TNFSF10), SET1B, LOXL2, PDE11A, FLJ45455, NOLA3 (NOP10), Endophilin A1, STAC2, Activin, C1orf43, Aquaporin 1, NDFIP1, KCTD16, C6orf27, NME5, Calcyclin, FAM186B, Syntenin 1, SCOT, Octanoyl-

						holo-acp, KCRS, Securin, ADHX, ZNF517, ERK1/2, AATC, UGCG, SLC29A4, Anks4b, TRUB1, NFIC, HSC70, SLC35A5, PKC, SSTR2, SUR1, ABTB1, C19orf55, HTR2A, PMM2, SLC25A4, MPP7, CCDC57, ATP1B3, ARPP-19, K-cadherin (CDH6), Guanylate Cyclase 1, soluble, APEL13, MEF2C, SULT4A1, Protein kinase G, RIFK, ERK2 (MAPK1), Calcineurin A (beta), DREV1, LISCH7, Ran, OAT, MEK4(MAP2K4), DACH2, C14orf2, TMEM70, CCK8-GlyArgArg, CLCN5, IMPA1, TRIM23, UFC1, Nephrocystin-4, DKK1, PARM-1, sKITLG, SSTR1, Guanine deaminase, PRPS, SOD1, TFIIB, KIAA1024, PPP4R2, GDE1, SLC38A2, MMP-28, SAP102, FSTL5, EVI2A, MAP1, RPESP, CALM2, Cyclophilin A, FOXP1/2/4 proteins, Aggrecanase-2, PI3K reg class IA, KIAA1614, PTCHD1, DCoHM, Galpha(s)-specific peptide GPCRs, TSPAN19, TCP1-alpha, ACTR3, OXR1, CALB1, Tubulin alpha-4A, CALML6, SRm300, RhoE, Pcdh19, CD166, TIP27, GAD2, DRIL2, PGM2L1, NF-I, MRPL3, HXK3, Neuroserpin, COX VIIa-2, ACOXL, Midkine, SAMD10, IRS6(DOK5), ARP3, PXDN, 14-3-3, ARMCX3, ACCN3 (ASIC3), C8orf83, AATBC, RAGE, 14-3-3 eta, ATP1beta subunit, Myospryn, Glutaredoxin 1, ZCCHC12, CHST6
32	Parkinsonian Disorders	2001	6.878E-12	4.692E-10	119	NPY, Galpha(s)-specific nucleotide-like GPCRs, Alpha crystallin B, ET-1, GAD1, HPCA, Endothelin-1, Neuropeptide K, ALDR, PSMA5, NDUFAB1, CCK8-Gly, NDUFA1, MGF, NDUFB4, NDUFA8, HSP70, Substance P extracellular region, CNR1, PPM1E, DnaJB9, Synaptotagmin, CNTN1 (F3), NDUFA4, HSPA4, Cystatin C, SCF, SDHB, SLC39A10, DKK3, CCK8, Neuropeptide gamma, RAB39B, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, LY6G5B, NDUFB6, SUR, NDUFS4, Galpha(i)-specific peptide GPCRs, S100, AMIGO2, LASS6, Galpha(q)-specific nucleotide-like GPCRs, Aldose reductase, NDUFB3, IDUA, SLC2A13, Semaphorin 5A, CHCHD2, FBXO2, SYP, EGF, Pro-CCK, HIST1H2BN, NDUFB1, AP3S1, Serotonin receptor, TRPC, VDAC 1, Osteopontin, Big ET-1, Lingo1, Neurokinin A, Substance P, AP-3 sigma subunits, Histone H2, CCK5, Galpha(q)-specific amine GPCRs, Histone H2A, Galpha(i)-specific amine GPCRs, DNAJC12, NDUFS6, CDK5, PAK, FLJ32001, Fatty acid-binding protein, CAPZA, Galpha(i)-specific cannabis GPSRs, sRAGE, SLC25A46, Galpha(q)-specific peptide GPCRs, H2AFZ, Histone H2B, NDUFA5, B-FABP, MEF2, HNMT, APRIO, ATF/CREB, RAI1, LAMP2-C, Galpha(s)-specific CRF GPCRs, LAMP2, YPEL5, PRNP, MPTP complex, HIST2H2BE, Endophilin A1, Aquaporin 1, NDFIP1, Syntenin 1, Octanoyl-holo-acp, ADHX, HSC70, SUR1, HTR2A, CCK8-GlyArgArg, sKITLG, SOD1, FOXP1/2/4 proteins, DBH-AS1, Galpha(s)-specific peptide GPCRs, CALB1, GAD2, ARP3, 14-3-3, RAGE, 14-3-3 eta

33	Neurologic Manifestations	4790	1.390E-11	9.196E-10	227	PLP1, NPY, PRPS1, PAK3, PAM, NPEPL1, Galpha(s)-specific nucleotide-like GPCRs, TMEM87B, ET-1, ILDR2, GAD1, THAP11, Tubulin alpha 1A, HPCA, APJ, Smooth muscle myosin, ELOVL5, Peroxiredoxin, Endothelin-1, Neuropeptide K, PSMB5, BRSK2, G-protein beta, KLHL4, LAS1L, PSMA5, CCK8-Gly, NDUFA1, DCMC, PSD2, MGF, PDH E2 subunit N6-lipoyllysine, PRKAR2B, NPFF receptor 2, Synaptotagmin I, COCH, Guanylate cyclase, HSP70, Substance P extracellular region, CNR1, Glycogen phosphorylase, HDBP1, Synaptotagmin, PRDX3, ATP6V1A (70kD), HSPA4, Dynein, axonemal, light chains, PDE, Cystatin C, SCF, SDHB, SLC39A10, ANKRD36B, HCN2, CCK8, TPH2, Neuropeptide gamma, RAB39B, GABA-A receptor alpha-1 subunit, TUSC3, Kv3.3, ORP-family, Tenascin-C, CEACAM, TRPC5, PAFAH gamma, PRDX1, G-protein beta/gamma, SUR, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, S100, TRPV1, PRR12, ZFHX4, Galpha(q)-specific nucleotide-like GPCRs, Aldose reductase, Rab-3, FAM38B, IP3KA, GRAIL, NSF, Tomt, GLRA, GABA-A receptor beta-2 subunit, DOK7, SYP, Rho GTPase, PDE4, GTPBP3, G-protein gamma, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, ChREBP, EGF, Pro-CCK, Dynein, axonemal, heavy chains, Semaphorin 3E, PKA-reg type II (cAMP-dependent), cPKC (conventional), ATP6V1B2, DLL4, ELOVL4, PSMA1, Serotonin receptor, Apelin, Rab-27B, TRPC, CLCN4, ZNF238, SMRT, Big ET-1, NHE6, PKA-reg (cAMP-dependent), Lingo1, ANT, Neurokinin A, PDLIM2, Clathrin heavy chain, Substance P, PSMD10 (Gankyrin), StARD4, Histone H2, CCK5, COPS4, LRRC51, Galpha(q)-specific amine GPCRs, Ephrin-A receptors, Histone H2A, GP-IB alpha, DOC1, Galpha(i)-specific amine GPCRs, SLC26A4-AS1, HCN, HLF, GABA-A receptor alpha-5 subunit, Zeta-sarcoglycan, CDK5, PAK, Glycine receptor, Fatty acid-binding protein, HINT, MAML1, ASAH, SPSY, Glycine receptor beta chain, RTL1, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, SLC25A46, PDH beta, Galpha(q)-specific peptide GPCRs, MAFbx, Tubulin alpha, DSCAML1, TBC1D10C, MRAP2, B-FABP, Patched, MEF2, PGAM1, HNMT, APRIO, ACSL4, ATF/CREB, GLGB, ODP2, RAI1, Hdj-2, DelGIP1, LAMP2-C, Acyl-CoA synthetase, IDI1, BMI-1, eIF2S1, Galpha(s)-specific CRF GPCRs, LAMP2, ATP6V1B, PRNP, TMS-1, MPTP complex, RHEB2, NKCC1, SUMO-3, SET1B, FLJ45455, Aquaporin 1, C6orf27, ERK1/2, AATC, NFIC, SLC35A5, PKC, SUR1, HTR2A, PMM2, SLC25A4, APEL13, MEF2C, ERK2 (MAPK1), Ran, IGFALS, CCK8-GlyArgArg, CLCN5, sKITLG, PRPS, SOD1, KIAA1024, MMP-28, SAP102, SPDYE5, FOXP1/2/4 proteins, PTCHD1, DBH-AS1, TCP1-alpha, ATP6AP2, Tubulin

						alpha-4A, SRm300, Pcdh19, GAD2, TCP1-epsilon, NF-I, Neuroserpin, ACOXL, 14-3-3, ACCN3 (ASIC3), ZCCHC12
34	Anxiety Disorders	254	2.261E-11	1.452E-09	32	NPY, Galpha(s)-specific nucleotide-like GPCRs, GAD1, G-protein beta, CCK8-Gly, CNR1, PDE, CCK8, TPH2, G-protein beta/gamma, FLJ35776, Galpha(i)-specific peptide GPCRs, Galpha(q)-specific nucleotide-like GPCRs, CRH receptor 2, PDE4, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, Pro-CCK, Serotonin receptor, CCK5, Galpha(q)-specific amine GPCRs, Galpha(i)-specific amine GPCRs, Glycine receptor, GABA-A receptor alpha-3 subunit, Glycine receptor beta chain, Galpha(i)-specific cannabis GPSRs, Glyoxalase I, Galpha(q)-specific peptide GPCRs, ATF/CREB, Galpha(s)-specific CRF GPCRs, HTR2A, CCK8-GlyArgArg
35	Synucleinopathies	2054	3.643E-11	2.272E-09	119	NPY, Galpha(s)-specific nucleotide-like GPCRs, Alpha crystallin B, ET-1, GAD1, HPCA, Endothelin-1, Neuropeptide K, BRSK2, ALDR, PSMA5, NDUFAB1, CCK8-Gly, NDUFA1, MGF, NDUFB4, NDUFA8, HSP70, Substance P extracellular region, CNR1, DnaJB9, Synaptotagmin, CNTN1 (F3), NDUFA4, HSPA4, Cystatin C, SCF, SDHB, DKK3, CCK8, Neuropeptide gamma, RAB39B, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, LY6G5B, NDUFB6, SUR, NDUFS4, Galpha(i)-specific peptide GPCRs, S100, AMIGO2, LASS6, Galpha(q)-specific nucleotide-like GPCRs, Aldose reductase, NDUFB3, IDUA, SLC2A13, Semaphorin 5A, CHCHD2, FBXO2, SYP, EGF, Pro-CCK, HIST1H2BN, NDUFB1, AP3S1, Serotonin receptor, TRPC, VDAC 1, Osteopontin, Big ET-1, Lingo1, Neurokinin A, Substance P, AP-3 sigma subunits, Histone H2, CCK5, Galpha(q)-specific amine GPCRs, Ephrin-A receptors, Histone H2A, Galpha(i)-specific amine GPCRs, DNAJC12, NDUFS6, CDK5, FLJ32001, Fatty acid-binding protein, CAPZA, Galpha(i)-specific cannabis GPSRs, sRAGE, SLC25A46, Galpha(q)-specific peptide GPCRs, H2AFZ, Histone H2B, NDUFA5, B-FABP, MEF2, HNMT, APRIO, ATF/CREB, RAI1, LAMP2-C, Galpha(s)-specific CRF GPCRs, LAMP2, YPEL5, PRNP, MPTP complex, HIST2H2BE, Endophilin A1, Aquaporin 1, NDFIP1, Syntenin 1, Octanoyl-holo-acp, ADHX, HSC70, SUR1, HTR2A, GS1-124K5.11, CCK8-GlyArgArg, sKITLG, SOD1, FOXP1/2/4 proteins, DBH-AS1, Galpha(s)-specific peptide GPCRs, CALB1, GAD2, ARP3, 14-3-3, RAGE, 14-3-3 eta
36	Mood Disorders	1270	1.750E-10	1.061E-08	83	NPY, HSP90, PAM, Galpha(s)-specific nucleotide-like GPCRs, GLSK, GAD1, ELOVL5, Neuropeptide K, REV-ERBalpha, G-protein beta, Importin (karyopherin)-alpha, CCK8-Gly, KCNK2, HSP70, Substance P extracellular region, CNR1, Synaptotagmin IV,

						Synaptotagmin, PDE, CCK8, TPH2, Neuropeptide gamma, RGS4, GABA-A receptor alpha-1 subunit, PKC-beta, G-protein beta/gamma, Galpha(i)-specific peptide GPCRs, S100, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, CRH receptor 2, SYP, PDE4, Galpha(i)-specific metabotropic glutamate GPCRs, EGF, Pro-CCK, Dynein, axonemal, heavy chains, cPKC (conventional), Serotonin receptor, Rab-27B, TRPC, Neurokinin A, NR3A, Substance P, Histone H2, CCK5, Galpha(q)-specific amine GPCRs, Histone H2A, NPR3, Galpha(i)-specific amine GPCRs, Protein kinase G1, GABA-A receptor alpha-5 subunit, GABA-A receptor alpha-3 subunit, PKC-beta2, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, Glyoxalase I, Galpha(q)-specific peptide GPCRs, BTBD10, ACSL4, ATF/CREB, G-protein beta-4, Acyl-CoA synthetase, Galpha(s)-specific CRF GPCRs, PKC-beta1, PDE4A, Apo-2L(TNFSF10), PDE11A, ERK1/2, CaMK II delta, PKC, HTR2A, Protein kinase G, ERK2 (MAPK1), CCK8-GlyArgArg, SOD1, SAP102, PI3K reg class IA, DBH-AS1, Galpha(s)-specific peptide GPCRs, CALB1, GAD2, COX VIIa-2
37	Epilepsy	1751	1.849E-10	1.091E-08	104	HSP90, Galpha(s)-specific nucleotide-like GPCRs, GAD1, Neuropeptide K, G-protein beta, Mucin 5B, NDUFA1, Lgi4, Pannexin-1, MC4R, Synaptotagmin I, HSP70, Substance P extracellular region, Synaptotagmin, ATP6V1A (70kD), HSPA4, Cystatin C, PPT1, SDHB, HCN2, Neuropeptide gamma, KAL1, GABA-A receptor alpha-1 subunit, ORP-family, Tenascin-C, PKC-beta, G-protein beta/gamma, NCX, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, S100, TXNRD1, KCNH5, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, CRH receptor 2, NSF, GLRA, GABA-A receptor beta-2 subunit, SYP, Rho GTPase, Galpha(i)-specific metabotropic glutamate GPCRs, cPKC (conventional), Serotonin receptor, Apelin, GABA-A receptor alpha-4 subunit, CLCN4, NHE6, Neurokinin A, Substance P, Histone H2, MCT1 (SLC16A1), Galpha(q)-specific amine GPCRs, Histone H2A, Galpha(i)-specific amine GPCRs, Stch, NCX1, HCN, GABA-A receptor alpha-5 subunit, PANX2, Glycine receptor, Fatty acid-binding protein, Glycine receptor beta chain, PKC-beta2, Calcineurin A (catalytic), sRAGE, Galpha(q)-specific peptide GPCRs, SNAP190, CHKB-AS1, MEF2, NAPB, APRIO, ATF/CREB, SNAPs, eIF2S1, Galpha(s)-specific CRF GPCRs, PRNP, RHEB2, NKCC1, Malin, PKC-beta1, SET1B, Aquaporin 1, ERK1/2, HSC70, PKC, SSTR2, HTR2A, APEL13, MEF2C, ERK2 (MAPK1), SSTR1, SOD1, PPP4R2, PI3K reg class IA, PTCHD1, Galpha(s)-specific peptide GPCRs, ACTR3, Pcdh19, GAD2, Neuroserpin, ARP3, 14-3-3, RAGE

38	Parkinson Disease	1876	2.298E-10	1.320E-08	109	Galpha(s)-specific nucleotide-like GPCRs, Alpha crystallin B, GAD1, HPCA, Neuropeptide K, ALDR, PSMA5, NDUFAB1, CCK8-Gly, NDUFA1, MGF, NDUFB4, NDUFA8, HSP70, Substance P extracellular region, CNR1, DnaJB9, Synaptotagmin, NDUFA4, HSPA4, Cystatin C, SCF, SDHB, CCK8, Neuropeptide gamma, RAB39B, 14-3-3 beta/alpha, LY6G5B, NDUFB6, SUR, NDUFS4, Galpha(i)-specific peptide GPCRs, S100, AMIGO2, LASS6, Galpha(q)-specific nucleotide-like GPCRs, Aldose reductase, NDUFB3, IDUA, SLC2A13, Semaphorin 5A, CHCHD2, FBXO2, SYP, EGF, Pro-CCK, HIST1H2BN, NDUFB1, AP3S1, Serotonin receptor, TRPC, VDAC 1, Osteopontin, Lingo1, Neurokinin A, Substance P, AP-3 sigma subunits, Histone H2, CCK5, Galpha(q)-specific amine GPCRs, Histone H2A, Galpha(i)-specific amine GPCRs, DNAJC12, NDUFS6, CDK5, FLJ32001, Fatty acid-binding protein, CAPZA, Galpha(i)-specific cannabis GPSRs, sRAGE, SLC25A46, Galpha(q)-specific peptide GPCRs, H2AFZ, Histone H2B, NDUFA5, B-FABP, MEF2, HNMT, APRIO, ATF/CREB, RAI1, LAMP2-C, Galpha(s)-specific CRF GPCRs, LAMP2, YPEL5, PRNP, MPTP complex, HIST2H2BE, Endophilin A1, Aquaporin 1, NDFIP1, Syntenin 1, Octanoyl-holo-acp, ADHX, HSC70, SUR1, HTR2A, CCK8-GlyArgArg, sKITLG, SOD1, FOXP1/2/4 proteins, DBH-AS1, Galpha(s)-specific peptide GPCRs, CALB1, GAD2, ARP3, 14-3-3, RAGE, 14-3-3 eta
39	Depressive Disorder	1214	2.595E-10	1.453E-08	80	NPY, HSP90, PAM, GLSK, GAD1, ELOVL5, Neuropeptide K, REV-ERBalpha, G-protein beta, Importin (karyopherin)-alpha, CCK8-Gly, KCNK2, HSP70, Substance P extracellular region, CNR1, Synaptotagmin IV, Synaptotagmin, PDE, CCK8, TPH2, Neuropeptide gamma, RGS4, GABA-A receptor alpha-1 subunit, PKC-beta, G-protein beta/gamma, Galpha(i)-specific peptide GPCRs, S100, COX VIIa, CRH receptor 2, SYP, PDE4, Galpha(i)-specific metabotropic glutamate GPCRs, EGF, Pro-CCK, Dynein, axonemal, heavy chains, cPKC (conventional), Serotonin receptor, Rab-27B, TRPC, Neurokinin A, NR3A, Substance P, Histone H2, CCK5, Galpha(q)-specific amine GPCRs, Histone H2A, NPR3, Galpha(i)-specific amine GPCRs, Protein kinase G1, GABA-A receptor alpha-5 subunit, GABA-A receptor alpha-3 subunit, PKC-beta2, Galpha(i)-specific cannabis GPSRs, Glyoxalase I, Galpha(q)-specific peptide GPCRs, BTBD10, ACSL4, ATF/CREB, G-protein beta-4, Acyl-CoA synthetase, Galpha(s)-specific CRF GPCRs, PKC-beta1, PDE4A, Apo-2L(TNFSF10), PDE11A, ERK1/2, CaMK II delta, PKC, HTR2A, Protein kinase G, ERK2 (MAPK1), CCK8-GlyArgArg, SOD1, SAP102, PI3K reg class IA, DBH-AS1, Galpha(s)-specific peptide GPCRs, CALB1, GAD2, COX VIIa-2

40	Spinal Cord Diseases	2384	8.295E-10	4.527E-08	128	PP2A cat (alpha), HSP90, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Alpha crystallin B, IRF1, COX VIc, GAD1, THAP11, Tubulin alpha 1A, ELOVL5, Peroxiredoxin, T-plastin, BRSK2, G-protein beta, LAS1L, PSMA5, NDUFAB1, NDUFA1, MELC, NDUFB4, NDUFA8, Synaptotagmin I, HSP70, DnaJB9, Synaptotagmin, NDUFA4, HSPA4, Cystatin C, SDHB, ANKRD36B, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, Kv3.3, PKC-beta, G-protein beta/gamma, NDUFB6, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, S100, TXNRD1, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, NDUFB3, IDUA, RPL9, CHCHD2, GABA-A receptor beta-2 subunit, Dysferlin, Galpha(i)-specific metabotropic glutamate GPCRs, NELL1, cPKC (conventional), NDUFB1, ELOVL4, PSMA1, Serotonin receptor, TRPC, COX VIa, Osteopontin, SMRT, PKA-reg (cAMP-dependent), PDLIM2, Histone H2, ARHGAP18, Galpha(q)-specific amine GPCRs, Ephrin-A receptors, Histone H2A, Galpha(i)-specific amine GPCRs, NCX1, HLF, NDUFS6, CDK5, Glycine receptor, Fatty acid-binding protein, HINT, COX Va, Glycine receptor beta chain, CAPZA, PKC-beta2, Calcineurin A (catalytic), sRAGE, SLC25A46, Galpha(q)-specific peptide GPCRs, MAFbx, NDUFA5, Tubulin alpha, Creatine kinase, MEF2, ADAR3, HNMT, APRIO, BTBD10, Peg10, ATF/CREB, RAI1, LAMP2-C, G-protein beta-4, Acyl-CoA synthetase, PP2A catalytic, LAMP2, COX VIa-1, PRNP, PKC-beta1, Apo-2L(TNFSF10), Aquaporin 1, Calcyclin, Octanoyl-holo-acp, KCRS, UGCG, NFIC, HSC70, PKC, GS1-124K5.11, MEF2C, PRKAR1A, DKK1, SOD1, Tubulin alpha-4A, GAD2, NF-I, COX VIIa-2, Midkine, SAMD10, 14-3-3, RAGE, SNX10
41	Epileptic Syndromes	1187	1.163E-09	6.194E-08	77	HSP90, Galpha(s)-specific nucleotide-like GPCRs, GAD1, Neuropeptide K, G-protein beta, Mucin 5B, NDUFA1, Lgi4, Pannexin-1, MC4R, Synaptotagmin I, HSP70, Substance P extracellular region, Synaptotagmin, ATP6V1A (70kD), HSPA4, PPT1, SDHB, Neuropeptide gamma, GABA-A receptor alpha-1 subunit, ORP-family, Tenascin-C, PKC-beta, G-protein beta/gamma, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, S100, TXNRD1, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, CRH receptor 2, NSF, GABA-A receptor beta-2 subunit, SYP, Rho GTPase, Galpha(i)-specific metabotropic glutamate GPCRs, cPKC (conventional), Serotonin receptor, Apelin, Neurokinin A, Substance P, MCT1 (SLC16A1), Galpha(q)-specific amine GPCRs, Galpha(i)-specific amine GPCRs, HCN, GABA-A receptor alpha-5 subunit, PANX2, PKC-beta2, Calcineurin A (catalytic), Galpha(q)-specific peptide GPCRs, SNAP190, CHKB-AS1, MEF2, NAPB, APRIO, ATF/CREB, SNAPs, eIF2S1, Galpha(s)-

						specific CRF GPCRs, PRNP, NKCC1, Malin, PKC-beta1, Aquaporin 1, HSC70, PKC, SSTR2, HTR2A, APEL13, MEF2C, SOD1, PPP4R2, PI3K reg class IA, PTCHD1, Galpha(s)-specific peptide GPCRs, Pcdh19, Neuroserpin
42	Metabolic Diseases	6085	1.779E-09	8.899E-08	264	SCAP2, PLP1, NPY, PP2A cat (alpha), PRPS1, HSP90, PAM, Cadherin 8, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Alpha crystallin B, ET-1, IRF1, ILDR2, GLSK, COX VIc, GAD1, SMVT, Tubulin alpha 1A, ELOVL5, RNF207, Peroxiredoxin, UBL5, Esterase D, Endothelin-1, Neuropeptide K, T-plastin, G-protein beta, ALDR, PSMA5, NDUFAB1, NDUFA1, MCM6, DCMC, MGF, PDH E2 subunit N6-lipoyllysine, PRKAR2B, MELC, NDUFB4, MC4R, NDUFA8, Synaptotagmin I, HSP70, Substance P extracellular region, DDX3Y, CNR1, Glycogen phosphorylase, DnaJB9, Synaptotagmin, Thioredoxin, NDUFA4, HSPA4, PDE, Cystatin C, PPT1, SCF, SDHB, DKK3, Galpha(q)-specific Class A Orphan/other GPCRs, TPH2, Neuropeptide gamma, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, UGT8, ORP-family, CEACAM, PKC-beta, TCP1-theta, PRDX1, G-protein beta/gamma, NDUFB6, SUR, ABO system transferase, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, FUT2, UQCRB, CPT-1A, S100, TXNRD1, VWA2, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, Aldose reductase, NDUFB3, ATG9B, FAM38B, IDUA, CRH receptor 2, CaMK IV, CHCHD2, GABA-A receptor beta-2 subunit, SYP, MOCS2(small), Rho GTPase, PDE4, GTPBP3, G-protein gamma, UBE2D1, PRPS2, Dysferlin, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, ChREBP, A830006F12Rik, EGF, Dynein, axonemal, heavy chains, BMPR1A, MMADHC, PKA-reg type II (cAMP-dependent), NELL1, cPKC (conventional), NDUFB1, AP3S1, PSMA1, Serotonin receptor, CHMP5, Apelin, Neurexophilin 1, AP complex 2 small (sigma) chain, GABA-A receptor alpha-4 subunit, TRPC, HTR5A, PYGM, MOC2B, PDK4, COX VIa, CLCN4, ATP6V1H, Osteopontin, Big ET-1, PKA-reg (cAMP-dependent), ANT, HMDH, Neurokinin A, TCP1-delta, Substance P, AP-3 sigma subunits, CalDAG-GEFII, Histone H2, LIPA, MCT1 (SLC16A1), ARHGAP18, Galpha(q)-specific amine GPCRs, Ephrin-A receptors, Histone H2A, GP-IB alpha, Galpha(i)-specific amine GPCRs, TRPC4, NCX1, DNAJC12, HLF, TXNIP (VDUP1), NDUFS6, GABA-A receptor alpha-5 subunit, CDK5, PAK, Fatty acid-binding protein, ASAH, GABA-A receptor alpha-3 subunit, COX Va, ATP5A, Selenoprotein P, CAPZA, PKC-beta2, Calcineurin A (catalytic), TOP1MT, Galpha(i)-specific cannabis GPSRs, sRAGE, SLC25A46, Glyoxalase I, Galpha(q)-specific peptide GPCRs, ATP6V1C, MAFbx,

						NDUFA5, Tubulin alpha, Creatine kinase, Patched, MEF2, SLC2A1-AS1, ADAR3, HNMT, APRIO, BTBD10, Peg10, ACSL4, CEACAM1, ATF/CREB, GLGB, ODP2, RAI1, LAMP2-C, FEM1B, Acyl-CoA synthetase, PP2A catalytic, IDI1, MRLC, BMI-1, Galpha(s)-specific CRF GPCRs, LAMP2, COX VIa-1, ATP6V1B, Protein kinase G 2, PRNP, HSPC138, SLC16A1-AS1, MPTP complex, RHEB2, PKC-beta1, LPL, SUMO-3, Apo-2L(TNFSF10), LOXL2, HSPC125, USMG5, Activin, Aquaporin 1, Calcyclin, SCOT, Octanoyl-holo-acp, KCRS, ERK1/2, AATC, UGCG, HSC70, PKC, SUR1, HTR2A, PMM2, SLC25A4, APEL13, MEF2C, Protein kinase G, ERK2 (MAPK1), SLC25A25-AS1, CBR3-AS1, TMEM70, PRKAR1A, CLCN5, DKK1, sKITLG, PRPS, SOD1, MAP1, RPESP, FOXP1/2/4 proteins, PI3K reg class IA, Galpha(s)-specific peptide GPCRs, CALB1, Tubulin alpha-4A, TIP27, GAD2, COX VIIa-2, Midkine, SAMD10, IRS6(DOK5), PXDN, 14-3-3, RAGE, ATP1beta subunit, SNX10
43	Craniomandibular Disorders	32	1.794E-09	8.899E-08	11	Neuropeptide K, Substance P extracellular region, Neuropeptide gamma, Serotonin receptor, Neurokinin A, Substance P, Galpha(q)-specific amine GPCRs, Galpha(i)-specific amine GPCRs, ERK1/2, HTR2A, ERK2 (MAPK1)
44	Temporomandibular Joint Disorders	32	1.794E-09	8.899E-08	11	Neuropeptide K, Substance P extracellular region, Neuropeptide gamma, Serotonin receptor, Neurokinin A, Substance P, Galpha(q)-specific amine GPCRs, Galpha(i)-specific amine GPCRs, ERK1/2, HTR2A, ERK2 (MAPK1)
45	Borderline Personality Disorder	19	1.857E-09	9.009E-08	9	PKC-beta, cPKC (conventional), Serotonin receptor, Galpha(q)-specific amine GPCRs, PKC-beta2, Galpha(q)-specific peptide GPCRs, PKC-beta1, PKC, HTR2A
46	Behavior and Behavior Mechanisms	1741	2.526E-09	1.169E-07	100	PAK3, NPEPL1, Galpha(s)-specific nucleotide-like GPCRs, ILDR2, GLSK, BRSK2, G-protein beta, LAS1L, CCK8-Gly, DCMC, PRKAR2B, Synaptotagmin I, HSP70, CNR1, Glycogen phosphorylase, Synaptotagmin IV, HDBP1, Synaptotagmin, ATP6V1A (70kD), PDE, HCN2, CCK8, TPH2, RAB39B, GABA-A receptor alpha-1 subunit, TUSC3, TRPC5, PAFAH gamma, G-protein beta/gamma, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, S100, PRR12, ZFHX4, Galpha(q)-specific nucleotide-like GPCRs, Rab-3, GABA-A receptor beta-2 subunit, SYP, Rho GTPase, PDE4, Galpha(i)-specific metabotropic glutamate GPCRs, Pro-CCK, PKA-reg type II (cAMP-dependent), cPKC (conventional), ATP6V1B2, DLL4, Serotonin receptor, Rab-27B, TRPC, CLCN4, ZNF238, NHE6, PKA-reg (cAMP-dependent), Lingo1, Clathrin heavy chain, CCK5, Galpha(q)-specific amine GPCRs, Ephrin-A receptors, GP-IB alpha, Galpha(i)-

						specific amine GPCRs, HCN, GABA-A receptor alpha-5 subunit, CDK5, PAK, Glycine receptor, SPSY, Glycine receptor beta chain, RTL1, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, Galpha(q)-specific peptide GPCRs, TBC1D10C, Patched, MEF2, HNMT, ACSL4, ATF/CREB, Hdj-2, Acyl-CoA synthetase, Galpha(s)-specific CRF GPCRs, ATP6V1B, TMS-1, RHEB2, SET1B, FLJ45455, C6orf27, AATC, SLC35A5, PKC, HTR2A, MEF2C, CCK8-GlyArgArg, KIAA1024, SAP102, FOXP1/2/4 proteins, ATP6AP2, Pcdh19, NF-I, 14-3-3, ZCCHC12
47	Personality Disorders	33	2.615E-09	1.169E-07	11	TPH2, PKC-beta, cPKC (conventional), Serotonin receptor, Galpha(q)-specific amine GPCRs, Galpha(i)-specific amine GPCRs, PKC-beta2, Galpha(q)-specific peptide GPCRs, PKC-beta1, PKC, HTR2A
48	Bipolar and Related Disorders	903	2.624E-09	1.169E-07	63	NPY, HSP90, Galpha(s)-specific nucleotide-like GPCRs, GAD1, REV-ERBalpha, G-protein beta, Synaptotagmin I, HSP70, CNR1, Synaptotagmin, PDE, TPH2, RGS4, GABA-A receptor alpha-1 subunit, PKC-beta, G-protein beta/gamma, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, S100, FAM69A, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, CRH receptor 2, GLRA, SYP, PDE4, Galpha(i)-specific metabotropic glutamate GPCRs, cPKC (conventional), Serotonin receptor, TRPC, SMRT, Galpha(q)-specific amine GPCRs, Galpha(i)-specific amine GPCRs, Protein kinase G1, GABA-A receptor alpha-5 subunit, Glycine receptor, GABA-A receptor alpha-3 subunit, PKC-beta2, Galpha(i)-specific cannabis GPSRs, Glyoxalase I, Galpha(q)-specific peptide GPCRs, APRIO, ATF/CREB, SNAPs, Galpha(s)-specific CRF GPCRs, PRNP, PKC-beta1, PDE4A, Apo-2L(TNFSF10), PDE11A, ERK1/2, PKC, HTR2A, Protein kinase G, ERK2 (MAPK1), IMPA1, SOD1, SAP102, PI3K reg class IA, Galpha(s)-specific peptide GPCRs, CALB1, GAD2, COX VIIa-2
49	Bipolar Disorder	903	2.624E-09	1.169E-07	63	NPY, HSP90, Galpha(s)-specific nucleotide-like GPCRs, GAD1, REV-ERBalpha, G-protein beta, Synaptotagmin I, HSP70, CNR1, Synaptotagmin, PDE, TPH2, RGS4, GABA-A receptor alpha-1 subunit, PKC-beta, G-protein beta/gamma, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, S100, FAM69A, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, CRH receptor 2, GLRA, SYP, PDE4, Galpha(i)-specific metabotropic glutamate GPCRs, cPKC (conventional), Serotonin receptor, TRPC, SMRT, Galpha(q)-specific amine GPCRs, Galpha(i)-specific amine GPCRs, Protein kinase G1, GABA-A receptor alpha-5 subunit, Glycine receptor, GABA-A receptor alpha-3 subunit, PKC-beta2, Galpha(i)-specific cannabis GPSRs, Glyoxalase I, Galpha(q)-specific peptide GPCRs, APRIO, ATF/CREB, SNAPs, Galpha(s)-

						specific CRF GPCRs, PRNP, PKC-beta1, PDE4A, Apo-2L(TNFSF10), PDE11A, ERK1/2, PKC, HTR2A, Protein kinase G, ERK2 (MAPK1), IMPA1, SOD1, SAP102, PI3K reg class IA, Galpha(s)-specific peptide GPCRs, CALB1, GAD2, COX VIIa-2
50	Genital Diseases, Female	15572	2.767E-09	1.208E-07	571	Cyclin G, FBXO45, PP2A cat (alpha), HSP90, PAK3, PAM, Cadherin 8, CPSF1, ARP6, CXorf57, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, LINC01410, Semaphorin 3C, Alpha crystallin B, AEBP1, G3BP2, RhoN, MBD6, IRF1, FILIP, ZnT-2, MAGEH-1, SMVT, MEGF10, THAP11, TINP1, PTCH2, Tubulin alpha 1A, HPCA, APJ, Smooth muscle myosin, EDIL3, FLJ12671, ELOVL5, GLB1B2, RNF207, Peroxiredoxin, Activin A, D630023F18Rik, Esterase D, SULT1A1, PSMB5, AP-1 gamma subunits, ARG2, DUOX1, NETO2, GHITM, IL-17D, BRSK2, DYNLT3, P2Y11, UBXD3, G-protein beta, KLHL4, LAS1L, JWA, CRTL1, Mucin 5B, SC4MOL, PSMA5, NFKBIL2, NDUFAB1, Importin (karyopherin)-alpha, CCK8-Gly, NckAP1, GLIPR, BTBD12, CDC18L (CDC6), ANKRD50, DNAH1, MOBKL1A, AP1G2, ZNF707, Pannexin-1, OGFRL1, NKIRAS1, PSD2, NIPSNAP3A, MGF, TIP47, PRKAR2B, MELC, NPFF receptor 2, NDUFB4, UNRIP, NDUFA8, Synaptotagmin I, COCH, Guanylate cyclase, KCNK2, HSP70, CCDC4, DDX3Y, MAPBPIP, Glycogen phosphorylase, CITED2, PPM1E, NUDT4P1, DnaJB9, Synaptotagmin, CNTN1 (F3), Thioredoxin, ZMAT1, ATP6V1A (70kD), HSPA4, JMJD3, Septin 1, PDE, Cystatin C, Tcfl5, PPT1, SCF, SDHB, IGSF9B, DKK3, Karyopherin alpha 2, LUZP2, PNMAL1, NCKP1 subunit, TM9SF2, HCN2, D123, FLJ20674, Galpha(q)-specific Class A Orphan/other GPCRs, IMPG2, LMF1, C6orf168, CCK8, GPR124, TPH2, KAL1, RAB39B, PTPN18, RGS4, VSIG2, TUSC3, UGT8, GUCY1B1, SELI, C13orf37, ORP-family, Tenascin-C, HSDL1, CEACAM, TRPC5, PKC-beta, KIS, TCP1-theta, PRDX1, ELMO3, G-protein beta/gamma, SLC25A45, NDUFB6, SDFR1, SUR, ABO system transferase, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, VBP-1, TORC1, KLHL13, CPT-1A, S100, TXNRD1, ORP8, KCNH5, AMIGO2, VWA2, TRPV1, PRR12, PDK3, ZFHX4, Galpha(q)-specific nucleotide-like GPCRs, ATP6V1C1, PRRG1, Aldose reductase, Rab-3, MTG16 (CBFA2T3), ATG9B, TM2D3, DNER, FAM38B, APOL3, Ephrin-A receptor 5, LAPTM4B, IDUA, AMDHD2, CacyBP(SIP), InsP6 kinase 3, SLC2A13, Semaphorin 5A, Adropin, V-ATPase E subunit, GRAIL, NSF, Tomt, ADAM-TS10, GPR176, CaMK IV, GLRA, DKK2, ZNF499, GABA-A receptor beta-2 subunit, ZNF433, CECR2, SYP, Carbohydrate sulfotransferases, LACTB2, Rho GTPase, PDE4, Lba1, G-protein gamma, OSGIN2, PRPS2, ZNF70, SOCS6, Dysferlin, Rap1GDS1, Ephrin-A receptor

						4, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, ChREBP, ZNF267, A830006F12Rik, Secretogranin V, EGF, GlyRA2, ATP5B, Pro-CCK, CED-6, SYTC, XKR4, Dynein, axonemal, heavy chains, B3GALTL, BMPR1A, Semaphorin 3E, MMADHC, LOC283174, HIST1H2BN, Neurexophilin 2, PKA-reg type II (cAMP-dependent), B3GNT4, Myotrophin, NELL1, CAP2, cPKC (conventional), ATP6V1B2, DLL4, ELOVL4, AP3S1, PSMA1, Serotonin receptor, Neurexophilin 1, TMEM39B, ADSS, mADAMTS5, TRPC, SLC7A5, HTR5A, NOP14-AS1, ACTR10, PDK4, VDAC 1, WIF1, SUCB1, ATP6V1H, Osteopontin, Slp5, SMRT, CysLT2 receptor, NHE6, Rab-3C, KCY, CREB4, PC4, CHAMP, PKA-reg (cAMP-dependent), TReP-132, RNF152, ANT, CFA74, HMDH, PDLIM2, NR3A, KLHDC4, VTA1, Cables1, KIAA1110, ECT2, Clathrin heavy chain, IL3RA, AP-3 sigma subunits, PSMD10 (Gankyrin), StARD4, GRM6, CalDAG-GEFII, Histone H2, MCT1 (SLC16A1), ARHGAP18, CCK5, LRRC51, Galpha(q)-specific amine GPCRs, UQCRFS1, Maestro, Ephrin-A receptors, MRPL47, Histone H2A, HMP19, NPR3, GP-IB alpha, DOC1, Galpha(i)-specific amine GPCRs, Stch, TRPC4, PMCA1, NCX1, SLBP, HCN, BDH, C1orf113, CAP1, HSP90 beta, Anillin, TXNIP (VDUP1), Vinexin, COL25A1, C14orf142, MEGF6, Calponin-1, Activin beta A, BRMS1L, PANX2, DUS3L, PAK, Guanylate cyclase (alpha-1/beta-1), FLJ32001, SYT16, Guanylate cyclase beta, BEX1, TCP1-eta, Glycine receptor, Fatty acid-binding protein, PSG3, HINT, MAML1, KIAA0143, SOHLH1, IZUMO1, FLJ37078, ASAH, GABA-A receptor alpha-3 subunit, GNT-IV, LPPR4, DYNLT, TMEM74, TM6SF1, SPSY, COX Va, Copine-4, eIF4A2, Glycine receptor beta chain, Nek8, CAPZA, Carbonic anhydrase XII, Kv9.3, RTL1, PKC-beta2, Calcineurin A (catalytic), TOP1MT, Galpha(i)-specific cannabis GPSRs, STARD7, B3GT2, Cyclin G1, sRAGE, SLC25A46, DDX51, SMIT, FBI-1 (Pokemon), Galpha(q)-specific peptide GPCRs, H2AFZ, ATP6V1C, Histone H2B, NCOA4 (ARA70), SNAP190, WDR47, Tubulin alpha, Creatine kinase, ACAP1(CENTB1), DSCAML1, TBC1D10C, DCK, PAP-II, VIP32, Azi1, NUDT4, Patched, TNK1, XK, MEF2, NAPB, ADAR3, PGAM1, TAPBPL, SCS-A, BTBD10, MEK4/7, Peg10, ACSL4, RENBP, CEACAM1, RANBP6, ATF/CREB, GLGB, RAI1, Hdj-2, LAMP2-C, FN14(TNFRSF12A), Trim45, C3orf59, G-protein beta-4, FEM1B, Acyl-CoA synthetase, PP2A catalytic, SULT1A1 isoform 1, CAPZA2, IDI1, ARRDC2, MRLC, eIF4A, BMI-1, SNAPs, eIF2S1, Glutaredoxin, LAMP2, KAD6, TMEM87A, TSNARE1, ATP6V1B, Kv4.2 channel, PKD1L1, Protein kinase G 2, FAM22A, TM2D2, TMS-1, MPTP complex, STAG3, RHEB2, NKCC1, C1orf59, PKC-

						beta1, PDE4A, ZSCAN1, CAB39L, Calmodulin, CENPP, LPL, NELL2, FLJ31818, PGRMC1, ATP6V1E, Apo-2L(TNFSF10), SET1B, LOXL2, PDE11A, FLJ45455, NOLA3 (NOP10), Endophilin A1, STAC2, Activin, C1orf43, Aquaporin 1, NDFIP1, FAM186B, Syntenin 1, SCOT, Octanoyl-holo-acp, KCRS, Securin, ADHX, ZNF517, ERK1/2, AATC, UGCG, SLC29A4, Anks4b, NFIC, HSC70, PKC, SSTR2, SUR1, ABTB1, C19orf55, HTR2A, PMM2, SLC25A4, MPP7, ATP1B3, K-cadherin (CDH6), Guanylate Cyclase 1, soluble, Protein kinase G, ERK2 (MAPK1), Calcineurin A (beta), DREV1, LISCH7, Ran, OAT, MEK4(MAP2K4), DACH2, CCK8-GlyArgArg, CLCN5, IMPA1, TRIM23, UFC1, Nephrocystin-4, DKK1, PARM-1, sKITLG, SSTR1, PRPS, SOD1, TFIIB, KIAA1024, PPP4R2, GDE1, SLC38A2, MMP-28, SAP102, FSTL5, EVI2A, MAP1, RPESP, CALM2, Cyclophilin A, FOXP1/2/4 proteins, Aggrecanase-2, PI3K reg class IA, KIAA1614, PTCHD1, Galpha(s)-specific peptide GPCRs, TSPAN19, TCP1-alpha, ACTR3, OXR1, Tubulin alpha-4A, CALML6, SRm300, Pcdh19, CD166, TIP27, GAD2, PGM2L1, NF-I, MRPL3, HXK3, Neuroserpin, Midkine, IRS6(DOK5), ARP3, PXDN, 14-3-3, ARMCX3, ACCN3 (ASIC3), C8orf83, RAGE, ATP1beta subunit, Myospryn, Glutaredoxin 1, CHST6

Table A14. Top 50 KCL BrainBank Diseases by Biomarkers enrichments with MetaCore. Term size refers to the number of genes in the term, with the intersection size denoting the number of genes in the dataset found in the term.

#	Term Name	Term Size	p-value	adjusted p-value (FDR)	Intersection Size	Intersection Gene Names
1	COVID-19	882	1.599E-25	1.491E-22	65	HMG1,2, Angiopoietin 1, Kappa chain (Ig light chain), HGF, KV139, C4Ab, C4A protein, CLIP, VCAM1, IGHA1, PLA2, C4, ACTH, MHC Class I alpha chain, RSAD2, alpha-MSH, IGKC, beta-Endorphin, IGHG1, Galpha(q)-specific peptide GPCRs, ALDOB, proACTH, POMC, Cystatin C, sVCAM1, PLAT (TPA), Fc gamma RII beta, APOL1, Joining peptide (JP), Perforin, Beta-MSH / Beta-Endorphin, Fc gamma RII, IFI27, CD147, N-POMC, CEACAM, gamma-MSH, N-POC, beta-LPH, Galpha(i)-specific peptide GPCRs, I-TAC, Apo-2L(TNFSF10), 2'-5'-oligoadenylate synthetase, gamma-LPH, H28, MxA, CEACAM21, ACTH 1-17, DA-alphaMSH, SLC12A1, Ig light chain, C4Aa, OAS3, EGF, gamma2-MSH, APRIL(TNFSF13), GFAP, gamma3-MSH, C4a, IFI44, C4b, WNT, beta-MSH, KVD16, HLAC
2	Pneumonia, Viral	882	1.599E-25	1.491E-22	65	HMG1,2, Angiopoietin 1, Kappa chain (Ig light chain), HGF, KV139, C4Ab, C4A protein, CLIP, VCAM1, IGHA1, PLA2, C4, ACTH, MHC Class I alpha chain, RSAD2, alpha-MSH, IGKC, beta-Endorphin, IGHG1, Galpha(q)-specific peptide GPCRs, ALDOB, proACTH, POMC, Cystatin C, sVCAM1, PLAT (TPA), Fc gamma RII beta, APOL1, Joining peptide (JP), Perforin, Beta-MSH / Beta-Endorphin, Fc gamma RII, IFI27, CD147, N-POMC, CEACAM, gamma-MSH, N-POC, beta-LPH, Galpha(i)-specific peptide GPCRs, I-TAC, Apo-2L(TNFSF10), 2'-5'-oligoadenylate synthetase, gamma-LPH, H28, MxA, CEACAM21, ACTH 1-17, DA-alphaMSH, SLC12A1, Ig light chain, C4Aa, OAS3, EGF, gamma2-MSH, APRIL(TNFSF13), GFAP, gamma3-MSH, C4a, IFI44, C4b, WNT, beta-MSH, KVD16, HLAC
3	Coronaviridae Infections	903	5.926E-25	2.209E-22	65	HMG1,2, Angiopoietin 1, Kappa chain (Ig light chain), HGF, KV139, C4Ab, C4A protein, CLIP, VCAM1, IGHA1, PLA2, C4, ACTH, MHC Class I alpha chain, RSAD2, alpha-MSH, IGKC, beta-Endorphin, IGHG1, Galpha(q)-specific peptide GPCRs, ALDOB, proACTH, POMC, Cystatin C, sVCAM1, PLAT (TPA), Fc gamma RII beta, APOL1, Joining peptide (JP), Perforin, Beta-MSH / Beta-Endorphin, Fc gamma RII, IFI27, CD147, N-POMC, CEACAM, gamma-MSH, N-POC, beta-LPH, Galpha(i)-specific peptide GPCRs, I-TAC, Apo-2L(TNFSF10), 2'-5'-oligoadenylate synthetase, gamma-LPH, H28, MxA, CEACAM21, ACTH 1-17, DA-alphaMSH, SLC12A1, Ig light chain, C4Aa, OAS3, EGF, gamma2-MSH, APRIL(TNFSF13), GFAP, gamma3-MSH, C4a, IFI44, C4b, WNT, beta-MSH, KVD16, HLAC

4	Coronavirus Infections	903	5.926E-25	2.209E-22	65	HMG1,2, Angiopoietin 1, Kappa chain (Ig light chain), HGF, KV139, C4Ab, C4A protein, CLIP, VCAM1, IGHA1, PLA2, C4, ACTH, MHC Class I alpha chain, RSAD2, alpha-MSH, IGKC, beta-Endorphin, IGHG1, Galpha(q)-specific peptide GPCRs, ALDOB, proACTH, POMC, Cystatin C, sVCAM1, PLAT (TPA), Fc gamma RII beta, APOL1, Joining peptide (JP), Perforin, Beta-MSH / Beta-Endorphin, Fc gamma RII, IFI27, CD147, N-POMC, CEACAM, gamma-MSH, N-POC, beta-LPH, Galpha(i)-specific peptide GPCRs, I-TAC, Apo-2L(TNFSF10), 2'-5'-oligoadenylate synthetase, gamma-LPH, H28, MxA, CEACAM21, ACTH 1-17, DA-alphaMSH, SLC12A1, Ig light chain, C4Aa, OAS3, EGF, gamma2-MSH, APRIL(TNFSF13), GFAP, gamma3-MSH, C4a, IFI44, C4b, WNT, beta-MSH, KVD16, HLAC
5	Nidovirales Infections	903	5.926E-25	2.209E-22	65	HMG1,2, Angiopoietin 1, Kappa chain (Ig light chain), HGF, KV139, C4Ab, C4A protein, CLIP, VCAM1, IGHA1, PLA2, C4, ACTH, MHC Class I alpha chain, RSAD2, alpha-MSH, IGKC, beta-Endorphin, IGHG1, Galpha(q)-specific peptide GPCRs, ALDOB, proACTH, POMC, Cystatin C, sVCAM1, PLAT (TPA), Fc gamma RII beta, APOL1, Joining peptide (JP), Perforin, Beta-MSH / Beta-Endorphin, Fc gamma RII, IFI27, CD147, N-POMC, CEACAM, gamma-MSH, N-POC, beta-LPH, Galpha(i)-specific peptide GPCRs, I-TAC, Apo-2L(TNFSF10), 2'-5'-oligoadenylate synthetase, gamma-LPH, H28, MxA, CEACAM21, ACTH 1-17, DA-alphaMSH, SLC12A1, Ig light chain, C4Aa, OAS3, EGF, gamma2-MSH, APRIL(TNFSF13), GFAP, gamma3-MSH, C4a, IFI44, C4b, WNT, beta-MSH, KVD16, HLAC
6	Pneumonia	950	9.705E-24	3.015E-21	65	HMG1,2, Angiopoietin 1, Kappa chain (Ig light chain), HGF, KV139, C4Ab, C4A protein, CLIP, VCAM1, IGHA1, PLA2, C4, ACTH, MHC Class I alpha chain, RSAD2, alpha-MSH, IGKC, beta-Endorphin, IGHG1, Galpha(q)-specific peptide GPCRs, ALDOB, proACTH, POMC, Cystatin C, sVCAM1, PLAT (TPA), Fc gamma RII beta, APOL1, Joining peptide (JP), Perforin, Beta-MSH / Beta-Endorphin, Fc gamma RII, IFI27, CD147, N-POMC, CEACAM, gamma-MSH, N-POC, beta-LPH, Galpha(i)-specific peptide GPCRs, I-TAC, Apo-2L(TNFSF10), 2'-5'-oligoadenylate synthetase, gamma-LPH, H28, MxA, CEACAM21, ACTH 1-17, DA-alphaMSH, SLC12A1, Ig light chain, C4Aa, OAS3, EGF, gamma2-MSH, APRIL(TNFSF13), GFAP, gamma3-MSH, C4a, IFI44, C4b, WNT, beta-MSH, KVD16, HLAC

7	Respiratory Tract Infections	1482	1.143E-22	3.043E-20	80	HMG1,2, Angiopoietin 1, Kappa chain (Ig light chain), HGF, MxB, KV139, GSTs, C4Ab, C4A protein, CLIP, VCAM1, IGHA1, PLA2, CD44, C4, ACTH, MHC Class I alpha chain, Ficolin, RSAD2, CD44 soluble, alpha-MSH, IGKC, DCPS, beta-Endorphin, IGHG1, Galpha(q)-specific peptide GPCRs, CD44 (ICD), ALDOB, proACTH, SOD3 (EC-SOD), POMC, Cystatin C, sVCAM1, PLAT (TPA), Fc gamma RII beta, APOL1, Joining peptide (JP), Perforin, Beta-MSH / Beta-Endorphin, Fc gamma RII, IFI27, CD147, N-POMC, CEACAM, gamma-MSH, N-POC, beta-LPH, Galpha(i)-specific peptide GPCRs, I-TAC, Ficolin-1, Apo-2L(TNFSF10), Lactoferrin, 2'-5'-oligoadenylate synthetase, gamma-LPH, H28, MxA, CEACAM21, ACTH 1-17, DA-alphaMSH, SLC12A1, Ig light chain, C4Aa, OAS3, NALP3, EGF, gamma2-MSH, APRIL(TNFSF13), GFAP, gamma3-MSH, C4a, RXR, IFI44, CD44 (EXT), Galpha(s)-specific peptide GPCRs, C4b, WNT, beta-MSH, KVD16, HLAC, LIRB
8	Alstrom Syndrome	40	2.427E-22	5.395E-20	18	CLIP, ACTH, alpha-MSH, beta-Endorphin, proACTH, POMC, Joining peptide (JP), Beta-MSH / Beta-Endorphin, N-POMC, gamma-MSH, N-POC, beta-LPH, gamma-LPH, ACTH 1-17, DA-alphaMSH, gamma2-MSH, gamma3-MSH, beta-MSH
9	Sensation	74	2.605E-22	5.395E-20	22	CLIP, ACTH, alpha-MSH, beta-Endorphin, Galpha(q)-specific peptide GPCRs, proACTH, POMC, Cystatin C, Joining peptide (JP), Beta-MSH / Beta-Endorphin, N-POMC, gamma-MSH, N-POC, beta-LPH, Galpha(i)-specific peptide GPCRs, gamma-LPH, ACTH 1-17, DA-alphaMSH, gamma2-MSH, gamma3-MSH, ACES, beta-MSH
10	Musculoskeletal and Neural Physiological Phenomena	177	3.215E-22	5.992E-20	30	CLIP, ACTH, alpha-MSH, Carbonic anhydrase XII, beta-Endorphin, Galpha(s)-specific calcitonin GPCRs, MC4R, Galpha(q)-specific peptide GPCRs, proACTH, POMC, Cystatin C, Joining peptide (JP), Beta-MSH / Beta-Endorphin, N-POMC, gamma-MSH, N-POC, beta-LPH, Galpha(i)-specific peptide GPCRs, Calcitonin receptor, Galpha(q)-specific nucleotide-like GPCRs, gamma-LPH, ACTH 1-17, P2Y1, DA-alphaMSH, gamma2-MSH, gamma3-MSH, Galpha(s)-specific peptide GPCRs, ACES, beta-MSH, CART
11	Nervous System Physiological Phenomena	77	6.956E-22	1.143E-19	22	CLIP, ACTH, alpha-MSH, beta-Endorphin, Galpha(q)-specific peptide GPCRs, proACTH, POMC, Cystatin C, Joining peptide (JP), Beta-MSH / Beta-Endorphin, N-POMC, gamma-MSH, N-POC, beta-LPH, Galpha(i)-specific peptide GPCRs, gamma-LPH, ACTH 1-17, DA-alphaMSH, gamma2-MSH, gamma3-MSH, ACES, beta-MSH
12	Pediatric Obesity	42	7.357E-22	1.143E-19	18	CLIP, ACTH, alpha-MSH, beta-Endorphin, proACTH, POMC, Joining peptide (JP), Beta-MSH / Beta-Endorphin, N-POMC, gamma-MSH, N-POC, beta-LPH, gamma-LPH, ACTH 1-17, DA-alphaMSH, gamma2-MSH, gamma3-MSH, beta-MSH

13	Hepatitis, Autoimmune	112	8.626E-22	1.237E-19	25	GSTs, CLIP, ACTH, MHC Class I alpha chain, alpha-MSH, beta-Endorphin, Galpha(q)-specific peptide GPCRs, proACTH, POMC, Fc gamma RII beta, Joining peptide (JP), Beta-MSH / Beta-Endorphin, Fc gamma RII, N-POMC, gamma-MSH, N-POC, beta-LPH, Galpha(i)-specific peptide GPCRs, gamma-LPH, ACTH 1-17, DA-alphaMSH, gamma2-MSH, gamma3-MSH, beta-MSH, HLAC
14	Vitiligo	102	1.497E-21	1.993E-19	24	GSTs, CLIP, ACTH, MHC Class I alpha chain, alpha-MSH, beta-Endorphin, proACTH, POMC, Joining peptide (JP), Beta-MSH / Beta-Endorphin, N-POMC, gamma-MSH, N-POC, beta-LPH, gamma-LPH, ACTH 1-17, DA-alphaMSH, gamma2-MSH, gamma3-MSH, MLANA, Galpha(s)-specific peptide GPCRs, ACES, beta-MSH, HLAC
15	Lupus Nephritis	550	4.096E-21	5.089E-19	47	HMG1,2, Kappa chain (Ig light chain), A20, KV139, C4Ab, C4A protein, CLIP, VCAM1, C4, ACTH, MHC Class I alpha chain, Ficolin, alpha-MSH, IGKC, beta-Endorphin, IGHG1, Galpha(q)-specific peptide GPCRs, proACTH, POMC, sVCAM1, Fc gamma RII beta, APOL1, Joining peptide (JP), Beta-MSH / Beta-Endorphin, Fc gamma RII, N-POMC, gamma-MSH, N-POC, beta-LPH, Galpha(i)-specific peptide GPCRs, Ficolin-1, gamma-LPH, ACTH 1-17, DA-alphaMSH, Ig light chain, C4Aa, NALP3, EGF, gamma2-MSH, NQO1, APRIL(TNFSF13), gamma3-MSH, C4a, C4b, beta-MSH, KVD16, HLAC
16	Alopecia Areata	75	9.734E-21	1.134E-18	21	CLIP, ACTH, MHC Class I alpha chain, alpha-MSH, beta-Endorphin, proACTH, POMC, Joining peptide (JP), Beta-MSH / Beta-Endorphin, N-POMC, gamma-MSH, N-POC, beta-LPH, gamma-LPH, ACTH 1-17, DA-alphaMSH, gamma2-MSH, APRIL(TNFSF13), gamma3-MSH, beta-MSH, HLAC
17	Spinal Fractures	49	2.172E-20	2.131E-18	18	CLIP, ACTH, alpha-MSH, beta-Endorphin, proACTH, POMC, Joining peptide (JP), Beta-MSH / Beta-Endorphin, N-POMC, gamma-MSH, N-POC, beta-LPH, gamma-LPH, ACTH 1-17, DA-alphaMSH, gamma2-MSH, gamma3-MSH, beta-MSH
18	Spinal Injuries	49	2.172E-20	2.131E-18	18	CLIP, ACTH, alpha-MSH, beta-Endorphin, proACTH, POMC, Joining peptide (JP), Beta-MSH / Beta-Endorphin, N-POMC, gamma-MSH, N-POC, beta-LPH, gamma-LPH, ACTH 1-17, DA-alphaMSH, gamma2-MSH, gamma3-MSH, beta-MSH
19	Back Injuries	49	2.172E-20	2.131E-18	18	CLIP, ACTH, alpha-MSH, beta-Endorphin, proACTH, POMC, Joining peptide (JP), Beta-MSH / Beta-Endorphin, N-POMC, gamma-MSH, N-POC, beta-LPH, gamma-LPH, ACTH 1-17, DA-alphaMSH, gamma2-MSH, gamma3-MSH, beta-MSH

20	Eclampsia	80	4.349E-20	4.054E-18	21	CLIP, ACTH, MHC Class I alpha chain, alpha-MSH, HYEP, beta-Endorphin, Galpha(q)-specific peptide GPCRs, proACTH, POMC, Joining peptide (JP), Beta-MSH / Beta-Endorphin, N-POMC, gamma-MSH, N-POC, beta-LPH, gamma-LPH, ACTH 1-17, DA-alphaMSH, gamma2-MSH, gamma3-MSH, beta-MSH
21	Mesothelioma	265	5.198E-20	4.404E-18	33	Calretinin, GSTs, CLIP, CD44, ACTH, CD44 soluble, alpha-MSH, HYEP, GSTM3, beta-Endorphin, CD44 (ICD), proACTH, POMC, Joining peptide (JP), Beta-MSH / Beta-Endorphin, N-POMC, CEACAM, gamma-MSH, N-POC, PRSS11 (HtrA1), beta-LPH, gamma-LPH, CEACAM21, ACTH 1-17, DA-alphaMSH, gamma2-MSH, PR (membrane), gamma3-MSH, CD44 (EXT), WNT, beta-MSH, WIF1, PR (nuclear)
22	Neoplasms, Mesothelial	265	5.198E-20	4.404E-18	33	Calretinin, GSTs, CLIP, CD44, ACTH, CD44 soluble, alpha-MSH, HYEP, GSTM3, beta-Endorphin, CD44 (ICD), proACTH, POMC, Joining peptide (JP), Beta-MSH / Beta-Endorphin, N-POMC, CEACAM, gamma-MSH, N-POC, PRSS11 (HtrA1), beta-LPH, gamma-LPH, CEACAM21, ACTH 1-17, DA-alphaMSH, gamma2-MSH, PR (membrane), gamma3-MSH, CD44 (EXT), WNT, beta-MSH, WIF1, PR (nuclear)
23	Arthritis, Rheumatoid	2207	1.503E-19	1.218E-17	94	HDC, HMG1,2, Angiopoietin 1, Kappa chain (Ig light chain), Histone H2, HGF, A20, Histone H2A, KV139, GSTs, C4Ab, C4A protein, CLIP, Annexin I, VCAM1, PLA2, CD44, C4, Fatty acid-binding protein, ACTH, MHC Class I alpha chain, Ficolin, UHRF1, CD44 soluble, alpha-MSH, HYEP, IGKC, Carbonic anhydrase XII, beta-Endorphin, Galpha(s)-specific calcitonin GPCRs, IGHG1, Galpha(q)-specific peptide GPCRs, CD44 (ICD), Histone H2B, proACTH, SOD3 (EC-SOD), POMC, XAF1, Cystatin C, sVCAM1, PLAT (TPA), Fc gamma RII beta, Seprase, ILT4, Joining peptide (JP), Perforin, Beta-MSH / Beta-Endorphin, Fc gamma RII, IFI27, CD147, N-POMC, CEACAM, gamma-MSH, N-POC, PRSS11 (HtrA1), beta-LPH, Galpha(i)-specific peptide GPCRs, S1P1 receptor, I-TAC, Ficolin-1, Apo-2L(TNFSF10), Lactoferrin, Galpha(q)-specific nucleotide-like GPCRs, 2'-5'-oligoadenylate synthetase, gamma-LPH, Aquaporin 1, H28, MxA, Galpha(i)-specific EDG GPCRs, CEACAM21, ACTH 1-17, DA-alphaMSH, Ig light chain, C4Aa, NALP3, EGF, gamma2-MSH, APRIL(TNFSF13), PR (membrane), gamma3-MSH, C4a, IFI44, MMP-28, CD44 (EXT), PLA2G5, C4b, ACES, WNT, beta-MSH, KVD16, PR (nuclear), Midkine, HLAC, LIRB
24	Pituitary ACTH Hypersecretion	54	1.695E-19	1.317E-17	18	CLIP, ACTH, alpha-MSH, beta-Endorphin, proACTH, POMC, Joining peptide (JP), Beta-MSH / Beta-Endorphin, N-POMC, gamma-MSH,

						N-POC, beta-LPH, gamma-LPH, ACTH 1-17, DA-alphaMSH, gamma2-MSH, gamma3-MSH, beta-MSH
25	Eye Diseases	2865	3.273E-19	2.440E-17	109	HDC, HMG1,2, Angiopoietin 1, R-spondins, Kappa chain (Ig light chain), Histone H2, HGF, A20, KV139, GSTs, C4Ab, C4A protein, CLIP, KiSS-1, Tubulin beta, VCAM1, PLA2, CD44, C4, MFGE8, SAMD11, SIX3, Fatty acid-binding protein, ACTH, MHC Class I alpha chain, Ficolin, Beta dystroglycan, UHRF1, CD44 soluble, alpha-MSH, HYEP, IGKC, GSTM3, Carbonic anhydrase XII, beta-Endorphin, Galpha(s)-specific calcitonin GPCRs, IGHG1, Galpha(q)-specific peptide GPCRs, CD44 (ICD), Histone H2B, proACTH, SOD3 (EC-SOD), POMC, WFS1, XAF1, Cystatin C, sVCAM1, PLAT (TPA), Fc gamma RII beta, ABCA13, ILT4, Joining peptide (JP), Perforin, Beta-MSH / Beta-Endorphin, Fc gamma RII, IFI27, Connexin 26, N-POMC, CEACAM, gamma-MSH, N-POC, PRSS11 (HtrA1), beta-LPH, HKDC1, HIST2H2BE, Galpha(i)-specific peptide GPCRs, I-TAC, Ficolin-1, Apo-2L(TNFSF10), Lactoferrin, 2'-5'-oligoadenylate synthetase, SLC4A4, gamma-LPH, Aquaporin 1, H28, Tubulin beta 2B, MxA, ACTH 1-17, DA-alphaMSH, Carbohydrate sulfotransferases, Ig light chain, C4Aa, OAS3, NALP3, EGF, gamma2-MSH, NQO1, APRIL(TNFSF13), GFAP, PR (membrane), gamma3-MSH, C4a, POU class III, IFI44, MLANA, Dystroglycan, CD44 (EXT), SOX3, Galpha(s)-specific peptide GPCRs, CYP4V2, C4b, WNT, beta-MSH, KVD16, PR (nuclear), HLAC, LIRB, Alpha dystroglycan, CHST6
26	Adrenocortical Hyperfunction	143	4.856E-19	3.481E-17	25	CLIP, ACTH, alpha-MSH, beta-Endorphin, Galpha(q)-specific peptide GPCRs, proACTH, POMC, Joining peptide (JP), Beta-MSH / Beta-Endorphin, GIPR, Connexin 26, N-POMC, gamma-MSH, N-POC, beta-LPH, gamma-LPH, ACTH 1-17, DA-alphaMSH, SLC12A1, gamma2-MSH, PR (membrane), gamma3-MSH, Galpha(s)-specific peptide GPCRs, beta-MSH, PR (nuclear)
27	Hypopigmentation	147	9.746E-19	6.729E-17	25	GSTs, CLIP, Tubulin beta, ACTH, MHC Class I alpha chain, alpha-MSH, beta-Endorphin, proACTH, POMC, Joining peptide (JP), Beta-MSH / Beta-Endorphin, N-POMC, gamma-MSH, N-POC, beta-LPH, gamma-LPH, ACTH 1-17, DA-alphaMSH, gamma2-MSH, gamma3-MSH, MLANA, Galpha(s)-specific peptide GPCRs, ACES, beta-MSH, HLAC
28	Alopecia	107	1.719E-18	1.145E-16	22	MCR, CLIP, ACTH, MHC Class I alpha chain, alpha-MSH, beta-Endorphin, proACTH, POMC, Joining peptide (JP), Beta-MSH / Beta-Endorphin, N-POMC, gamma-MSH, N-POC, beta-LPH, gamma-LPH, ACTH 1-17, DA-alphaMSH, gamma2-MSH, APRIL(TNFSF13), gamma3-MSH, beta-MSH, HLAC

29	Carcinoma, Basal Cell	283	3.598E-18	2.313E-16	32	GSTs, CLIP, Tubulin beta, CD44, Fatty acid-binding protein, ACTH, Beta dystroglycan, CD44 soluble, alpha-MSH, beta-Endorphin, CD44 (ICD), proACTH, POMC, Seprase, Joining peptide (JP), Beta-MSH / Beta-Endorphin, N-POMC, CEACAM, gamma-MSH, N-POC, beta-LPH, gamma-LPH, ACTH 1-17, DA-alphaMSH, gamma2-MSH, gamma3-MSH, Dystroglycan, CD44 (EXT), Galpha(s)-specific peptide GPCRs, WNT, beta-MSH, Alpha dystroglycan
30	Rheumatic Diseases	2611	3.858E-18	2.322E-16	101	HDC, HMG1,2, Angiopoietin 1, Kappa chain (Ig light chain), Histone H2, HGF, A20, Histone H2A, KV139, GSTs, C4Ab, C4A protein, APJ, MCR, CLIP, Annexin I, VCAM1, PLA2, CD44, C4, Fatty acid-binding protein, ACTH, MHC Class I alpha chain, Ficolin, UHRF1, CD44 soluble, alpha-MSH, SULF1, HYEP, IGKC, Carbonic anhydrase XII, beta-Endorphin, Galpha(s)-specific calcitonin GPCRs, IGHG1, Galpha(q)-specific peptide GPCRs, CD44 (ICD), Histone H2B, proACTH, SOD3 (EC-SOD), POMC, XAF1, Cystatin C, sVCAM1, PLAT (TPA), Fc gamma RII beta, Seprase, ILT4, Joining peptide (JP), Perforin, Beta-MSH / Beta-Endorphin, Fc gamma RII, IFI27, CD147, N-POMC, CEACAM, gamma-MSH, N-POC, PRSS11 (HtrA1), beta-LPH, Galpha(i)-specific peptide GPCRs, GLVR1, S1P1 receptor, I-TAC, Ficolin-1, Apo-2L(TNFSF10), Lactoferrin, Calcitonin receptor, Galpha(q)-specific nucleotide-like GPCRs, 2'-5'-oligoadenylate synthetase, gamma-LPH, Aquaporin 1, H28, MxA, Galpha(i)-specific EDG GPCRs, CEACAM21, ACTH 1-17, DA-alphaMSH, Ig light chain, C4Aa, NALP3, EGF, gamma2-MSH, NQO1, APRIL(TNFSF13), PR (membrane), gamma3-MSH, C4a, RXR, IFI44, MMP-28, CD44 (EXT), PLA2G5, C4b, ACES, WNT, beta-MSH, KVD16, PR (nuclear), Midkine, HLAC, LIRB
31	Glomerulonephritis	766	3.861E-18	2.322E-16	51	HMG1,2, Kappa chain (Ig light chain), A20, KV139, C4Ab, C4A protein, CLIP, VCAM1, IGHA1, C4, ACTH, MHC Class I alpha chain, Ficolin, alpha-MSH, IGKC, beta-Endorphin, IGHG1, Galpha(q)-specific peptide GPCRs, proACTH, POMC, sVCAM1, PLAT (TPA), Fc gamma RII beta, APOL1, Joining peptide (JP), Beta-MSH / Beta-Endorphin, Fc gamma RII, N-POMC, gamma-MSH, N-POC, beta-LPH, Galpha(i)-specific peptide GPCRs, Ficolin-1, Lactoferrin, gamma-LPH, Aquaporin 1, ACTH 1-17, DA-alphaMSH, Ig light chain, C4Aa, NALP3, EGF, gamma2-MSH, NQO1, APRIL(TNFSF13), gamma3-MSH, C4a, C4b, beta-MSH, KVD16, HLAC

32	Neoplasms, Basal Cell	286	4.929E-18	2.871E-16	32	GSTs, CLIP, Tubulin beta, CD44, Fatty acid-binding protein, ACTH, Beta dystroglycan, CD44 soluble, alpha-MSH, beta-Endorphin, CD44 (ICD), proACTH, POMC, Seprase, Joining peptide (JP), Beta-MSH / Beta-Endorphin, N-POMC, CEACAM, gamma-MSH, N-POC, beta-LPH, gamma-LPH, ACTH 1-17, DA-alphaMSH, gamma2-MSH, gamma3-MSH, Dystroglycan, CD44 (EXT), Galpha(s)-specific peptide GPCRs, WNT, beta-MSH, Alpha dystroglycan
33	Arthritis	2622	5.184E-18	2.928E-16	101	HDC, HMG1,2, Angiopoietin 1, Kappa chain (Ig light chain), Histone H2, HGF, A20, Histone H2A, KV139, GSTs, C4Ab, C4A protein, APJ, CLIP, Annexin I, VCAM1, IGHA1, PLA2, CD44, C4, Fatty acid-binding protein, ACTH, MHC Class I alpha chain, Ficolin, UHRF1, CD44 soluble, alpha-MSH, SULF1, HYEP, IGKC, Carbonic anhydrase XII, beta-Endorphin, Galpha(s)-specific calcitonin GPCRs, IGHG1, Galpha(q)-specific peptide GPCRs, CD44 (ICD), Histone H2B, proACTH, SOD3 (EC-SOD), POMC, XAF1, Cystatin C, sVCAM1, PLAT (TPA), Fc gamma RII beta, Seprase, ILT4, Joining peptide (JP), Perforin, Beta-MSH / Beta-Endorphin, Fc gamma RII, IFI27, CD147, N-POMC, CEACAM, gamma-MSH, N-POC, PRSS11 (HtrA1), beta-LPH, Galpha(i)-specific peptide GPCRs, GLVR1, S1P1 receptor, I-TAC, Ficolin-1, Apo-2L(TNFSF10), Lactoferrin, Calcitonin receptor, Galpha(q)-specific nucleotide-like GPCRs, 2'-5'-oligoadenylate synthetase, gamma-LPH, Aquaporin 1, H28, MxA, Galpha(i)-specific EDG GPCRs, CEACAM21, ACTH 1-17, DA-alphaMSH, Ig light chain, C4Aa, NALP3, EGF, gamma2-MSH, NQO1, APRIL(TNFSF13), PR (membrane), gamma3-MSH, C4a, RXR, IFI44, MMP-28, CD44 (EXT), PLA2G5, C4b, ACES, WNT, beta-MSH, KVD16, PR (nuclear), Midkine, HLAC, LIRB
34	Cushing Syndrome	114	7.301E-18	4.003E-16	22	CLIP, ACTH, alpha-MSH, beta-Endorphin, proACTH, POMC, Joining peptide (JP), Beta-MSH / Beta-Endorphin, GIPR, N-POMC, gamma-MSH, N-POC, beta-LPH, gamma-LPH, ACTH 1-17, DA-alphaMSH, gamma2-MSH, PR (membrane), gamma3-MSH, Galpha(s)-specific peptide GPCRs, beta-MSH, PR (nuclear)

35	Joint Diseases	2683	8.318E-18	4.430E-16	102	HDC, HMG1,2, Angiopoietin 1, Kappa chain (Ig light chain), Histone H2, HGF, A20, Histone H2A, KV139, GSTs, C4Ab, C4A protein, APJ, CLIP, Annexin I, VCAM1, IGHA1, PLA2, CD44, C4, Fatty acid-binding protein, ACTH, MHC Class I alpha chain, Ficolin, UHRF1, CD44 soluble, alpha-MSH, SULF1, HYEP, IGKC, Carbonic anhydrase XII, beta-Endorphin, Galpha(s)-specific calcitonin GPCRs, IGHG1, Galpha(q)-specific peptide GPCRs, CD44 (ICD), Histone H2B, proACTH, SOD3 (EC-SOD), POMC, XAF1, Cystatin C, sVCAM1, PLAT (TPA), Fc gamma RII beta, Seprase, ILT4, Joining peptide (JP), Perforin, Beta-MSH / Beta-Endorphin, Fc gamma RII, IFI27, CD147, N-POMC, CEACAM, gamma-MSH, N-POC, PRSS11 (HtrA1), beta-LPH, Galpha(i)-specific peptide GPCRs, GLVR1, S1P1 receptor, I-TAC, Ficolin-1, Apo-2L(TNFSF10), Lactoferrin, Calcitonin receptor, Galpha(q)-specific nucleotide-like GPCRs, 2'-5'-oligoadenylate synthetase, gamma-LPH, Aquaporin 1, H28, MxA, Galpha(i)-specific EDG GPCRs, CEACAM21, ACTH 1-17, DA-alphaMSH, Carbohydrate sulfotransferases, Ig light chain, C4Aa, NALP3, EGF, gamma2-MSH, NQO1, APRIL(TNFSF13), PR (membrane), gamma3-MSH, C4a, RXR, IFI44, MMP-28, CD44 (EXT), PLA2G5, C4b, ACES, WNT, beta-MSH, KVD16, PR (nuclear), Midkine, HLAC, LIRB
36	Hypotrichosis	116	1.082E-17	5.605E-16	22	MCR, CLIP, ACTH, MHC Class I alpha chain, alpha-MSH, beta-Endorphin, proACTH, POMC, Joining peptide (JP), Beta-MSH / Beta-Endorphin, N-POMC, gamma-MSH, N-POC, beta-LPH, gamma-LPH, ACTH 1-17, DA-alphaMSH, gamma2-MSH, APRIL(TNFSF13), gamma3-MSH, beta-MSH, HLAC
37	Brain Infarction	385	1.338E-17	6.743E-16	36	HGF, Biglycan proteoglycan, APJ, CLIP, VCAM1, PLA2, Fatty acid-binding protein, ACTH, alpha-MSH, beta-Endorphin, Galpha(q)-specific peptide GPCRs, proACTH, POMC, Cystatin C, sVCAM1, PLAT (TPA), Biglycan, Joining peptide (JP), Beta-MSH / Beta-Endorphin, CD147, N-POMC, gamma-MSH, N-POC, PRSS11 (HtrA1), beta-LPH, L-FABP, Galpha(i)-specific peptide GPCRs, gamma-LPH, Galpha(i)-specific EDG GPCRs, ACTH 1-17, DA-alphaMSH, gamma2-MSH, GFAP, gamma3-MSH, beta-MSH, Midkine
38	Pigmentation Disorders	217	1.499E-17	7.353E-16	28	GSTs, CLIP, Tubulin beta, ACTH, MHC Class I alpha chain, RSAD2, alpha-MSH, beta-Endorphin, proACTH, POMC, Joining peptide (JP), Beta-MSH / Beta-Endorphin, IFI27, N-POMC, gamma-MSH, N-POC, beta-LPH, gamma-LPH, H28, ACTH 1-17, DA-alphaMSH, gamma2-MSH, gamma3-MSH, MLANA, Galpha(s)-specific peptide GPCRs, ACES, beta-MSH, HLAC

39	Nephritis	792	1.568E-17	7.496E-16	51	HMG1,2, Kappa chain (Ig light chain), A20, KV139, C4Ab, C4A protein, CLIP, VCAM1, IGHA1, C4, ACTH, MHC Class I alpha chain, Ficolin, alpha-MSH, IGKC, beta-Endorphin, IGHG1, Galpha(q)-specific peptide GPCRs, proACTH, POMC, sVCAM1, PLAT (TPA), Fc gamma RII beta, APOL1, Joining peptide (JP), Beta-MSH / Beta-Endorphin, Fc gamma RII, N-POMC, gamma-MSH, N-POC, beta-LPH, Galpha(i)-specific peptide GPCRs, Ficolin-1, Lactoferrin, gamma-LPH, Aquaporin 1, ACTH 1-17, DA-alphaMSH, Ig light chain, C4Aa, NALP3, EGF, gamma2-MSH, NQO1, APRIL(TNFSF13), gamma3-MSH, C4a, C4b, beta-MSH, KVD16, HLAC
40	RNA Virus Infections	1920	1.691E-17	7.878E-16	83	HMG1,2, Angiopoietin 1, Kappa chain (Ig light chain), Histone H2, HGF, OASL, MxB, Histone H2A, KV139, GZMH, GSTs, C4Ab, C4A protein, APJ, CLIP, VCAM1, IGHA1, PLA2, C4, ACTH, MHC Class I alpha chain, Ficolin, RSAD2, Beta dystroglycan, alpha-MSH, HYEP, IGKC, beta-Endorphin, GPNMB (Osteoactivin), IGHG1, Galpha(q)-specific peptide GPCRs, ALDOB, proACTH, POMC, Cystatin C, sVCAM1, PLAT (TPA), Fc gamma RII beta, Seprase, APOL1, Joining peptide (JP), Perforin, Beta-MSH / Beta-Endorphin, Fc gamma RII, IFI27, CD147, N-POMC, CEACAM, gamma-MSH, N-POC, beta-LPH, Galpha(i)-specific peptide GPCRs, CPT-1A, I-TAC, Apo-2L(TNFSF10), Lactoferrin, 2'-5'-oligoadenylate synthetase, gamma-LPH, H28, MxA, CEACAM21, ACTH 1-17, DA-alphaMSH, SLC12A1, Ig light chain, C4Aa, OAS3, EGF, gamma2-MSH, APRIL(TNFSF13), GFAP, gamma3-MSH, C4a, IFI44, Dystroglycan, C4b, WNT, beta-MSH, KVD16, Midkine, HLAC, LIRB, Alpha dystroglycan
41	Lupus Erythematosus, Systemic	1768	1.933E-17	8.790E-16	79	HMG1,2, Angiopoietin 1, Kappa chain (Ig light chain), HGF, A20, OASL, MxB, KV139, GSTs, C4Ab, C4A protein, CLIP, EPSTI1, VCAM1, PLA2, CD44, C4, MFGE8, ACTH, MHC Class I alpha chain, Ficolin, RSAD2, CD44 soluble, alpha-MSH, IGKC, beta-Endorphin, IGHG1, Galpha(q)-specific peptide GPCRs, CD44 (ICD), proACTH, SOD3 (EC-SOD), POMC, XAF1, Cystatin C, sVCAM1, PLAT (TPA), Fc gamma RII beta, Seprase, APOL1, ILT4, Joining peptide (JP), Perforin, Beta-MSH / Beta-Endorphin, Fc gamma RII, IFI27, CD147, N-POMC, gamma-MSH, N-POC, beta-LPH, Galpha(i)-specific peptide GPCRs, S1P1 receptor, Ficolin-1, Apo-2L(TNFSF10), Lactoferrin, 2'-5'-oligoadenylate synthetase, gamma-LPH, H28, MxA, Galpha(i)-specific EDG GPCRs, ACTH 1-17, DA-alphaMSH, Ig light chain, C4Aa, OAS3, NALP3, EGF, gamma2-MSH, NQO1, APRIL(TNFSF13), gamma3-MSH, C4a, IFI44, CD44 (EXT), C4b, beta-MSH, KVD16, HLAC, LIRB

42	Osteoporosis	322	2.100E-17	9.321E-16	33	HGF, GSTs, CLIP, ACTH, MHC Class I alpha chain, alpha-MSH, beta-Endorphin, Galpha(s)-specific calcitonin GPCRs, Galpha(q)-specific peptide GPCRs, proACTH, POMC, Joining peptide (JP), Beta-MSH / Beta-Endorphin, N-POMC, CEACAM, gamma-MSH, N-POC, beta-LPH, Galpha(i)-specific peptide GPCRs, I-TAC, Lactoferrin, Calcitonin receptor, gamma-LPH, ACTH 1-17, DA-alphaMSH, gamma2-MSH, NQO1, PR (membrane), gamma3-MSH, WNT, beta-MSH, PR (nuclear), HLAC
43	Adrenal Insufficiency	154	3.989E-17	1.699E-15	24	HGF, MCR, CLIP, PLA2, ACTH, alpha-MSH, beta-Endorphin, Galpha(q)-specific peptide GPCRs, proACTH, POMC, Seprase, Joining peptide (JP), Beta-MSH / Beta-Endorphin, Fc gamma RII, N-POMC, gamma-MSH, N-POC, beta-LPH, gamma-LPH, ACTH 1-17, DA-alphaMSH, gamma2-MSH, gamma3-MSH, beta-MSH
44	Cerebral Infarction	307	4.010E-17	1.699E-15	32	HGF, Biglycan proteoglycan, CLIP, PLA2, Fatty acid-binding protein, ACTH, alpha-MSH, beta-Endorphin, Galpha(q)-specific peptide GPCRs, proACTH, POMC, Cystatin C, PLAT (TPA), Biglycan, Joining peptide (JP), Beta-MSH / Beta-Endorphin, CD147, N-POMC, gamma-MSH, N-POC, PRSS11 (HtrA1), beta-LPH, L-FABP, gamma-LPH, Galpha(i)-specific EDG GPCRs, ACTH 1-17, DA-alphaMSH, gamma2-MSH, GFAP, gamma3-MSH, beta-MSH, Midkine
45	Brain Ischemia	448	4.234E-17	1.754E-15	38	HGF, Biglycan proteoglycan, APJ, CLIP, VCAM1, PLA2, HIF-prolyl hydroxylase, Fatty acid-binding protein, ACTH, alpha-MSH, beta-Endorphin, Galpha(q)-specific peptide GPCRs, proACTH, POMC, Cystatin C, sVCAM1, PLAT (TPA), Biglycan, Joining peptide (JP), Beta-MSH / Beta-Endorphin, CD147, N-POMC, gamma-MSH, N-POC, PRSS11 (HtrA1), beta-LPH, L-FABP, Galpha(i)-specific peptide GPCRs, gamma-LPH, Galpha(i)-specific EDG GPCRs, ACTH 1-17, DA-alphaMSH, NALP3, gamma2-MSH, GFAP, gamma3-MSH, beta-MSH, Midkine

46	Wounds and Injuries	1314	5.280E-17	2.139E-15	66	DCHS1, HMG1,2, HGF, GSTs, Connexin 30, Biglycan proteoglycan, CLIP, Annexin I, PLA2, CD44, C4, Fatty acid-binding protein, ACTH, MHC Class I alpha chain, Ficolin, CD44 soluble, alpha-MSH, beta-Endorphin, GPNMB (Osteoactivin), Galpha(q)-specific peptide GPCRs, CD44 (ICD), MAFbx, proACTH, POMC, Neurocan, Cystatin C, Biglycan, Seprase, Joining peptide (JP), Perforin, Beta-MSH / Beta-Endorphin, Connexin 26, CD147, N-POMC, CEACAM, gamma-MSH, N-POC, beta-LPH, L-FABP, Galpha(i)-specific peptide GPCRs, I-TAC, Ficolin-1, Apo-2L(TNFSF10), Lactoferrin, Galpha(q)-specific nucleotide-like GPCRs, gamma-LPH, Galpha(i)-specific EDG GPCRs, ACTH 1-17, P2Y1, DA-alphaMSH, Carbohydrate sulfotransferases, EGF, gamma2-MSH, NQO1, GFAP, PR (membrane), gamma3-MSH, C4a, MMP-28, CD44 (EXT), ECEL1, C4b, WNT, beta-MSH, PR (nuclear), DPH2
47	Hepatitis, Chronic	848	5.733E-17	2.274E-15	52	Kappa chain (Ig light chain), Histone H2, HGF, Histone H2A, KV139, GSTs, CLIP, PLA2, ACTH, MHC Class I alpha chain, Ficolin, alpha-MSH, HYEP, IGKC, beta-Endorphin, GPNMB (Osteoactivin), EAT-2, Galpha(q)-specific peptide GPCRs, Histone H2B, proACTH, POMC, Fc gamma RII beta, Joining peptide (JP), Perforin, Beta-MSH / Beta-Endorphin, Fc gamma RII, IFI27, N-POMC, CEACAM, gamma-MSH, N-POC, beta-LPH, Galpha(i)-specific peptide GPCRs, CPT-1A, I-TAC, Apo-2L(TNFSF10), 2'-5'-oligoadenylate synthetase, gamma-LPH, MxA, ACTH 1-17, DA-alphaMSH, Ig light chain, OAS3, gamma2-MSH, gamma3-MSH, IFI44, ACES, WNT, beta-MSH, KVD16, Midkine, HLAC
48	Hypersensitivity, Immediate	1858	9.752E-17	3.787E-15	80	HDC, HMG1,2, Angiopoietin 1, Kappa chain (Ig light chain), A20, Nk3R, KV139, GSTs, CAT-2, Biglycan proteoglycan, C4Ab, C4A protein, CLIP, SMG6, Tubulin beta, SULT1A1, VCAM1, PLA2, CD44, C4, Fatty acid-binding protein, ACTH, MHC Class I alpha chain, CD44 soluble, alpha-MSH, HYEP, IGKC, ASCT1 (SLC1A4), GSTM3, beta-Endorphin, Galpha(q)-specific peptide GPCRs, CD44 (ICD), proACTH, SOD3 (EC-SOD), POMC, Cystatin C, sVCAM1, Biglycan, Joining peptide (JP), Perforin, Beta-MSH / Beta-Endorphin, SULT1A1 isoform 1, Fc gamma RII, N-POMC, gamma-MSH, N-POC, beta-LPH, L-FABP, Galpha(i)-specific peptide GPCRs, CPT-1A, S1P1 receptor, I-TAC, Apo-2L(TNFSF10), Lactoferrin, Galpha(q)-specific nucleotide-like GPCRs, 2'-5'-oligoadenylate synthetase, gamma-LPH, Galpha(i)-specific EDG GPCRs, ACTH 1-17, DA-alphaMSH, Carbohydrate sulfotransferases, Ig light chain, C4Aa, NALP3, EGF, gamma2-MSH, NQO1, APRIL(TNFSF13), gamma3-MSH, C4a, RXR, MMP-

						28, CD44 (EXT), PLA2G5, Galpha(s)-specific peptide GPCRs, C4b, beta-MSH, KVD16, HLAC, LIRB
49	Cardiovascular Diseases	4762	1.469E-16	5.504E-15	143	HMG1,2, Angiopoietin 1, Kappa chain (Ig light chain), Histone H2, HGF, A20, Histone H2A, KV139, KCNE4, GSTs, Biglycan proteoglycan, C4Ab, C4A protein, APJ, MCR, CLIP, Caspase-10, Tubulin beta, APH-1, SLC4A1, Annexin I, VCAM1, PLA2, HIF-prolyl hydroxylase, CD44, C4, SIX3, Fatty acid-binding protein, ARHI, ACTH, MHC Class I alpha chain, Ficolin, RSAD2, Claudin-14, Beta dystroglycan, CD44 soluble, alpha-MSH, HYEP, IGKC, GSTM3, Nek8, beta-Endorphin, Galpha(s)-specific calcitonin GPCRs, MC4R, IGHG1, Galpha(q)-specific peptide GPCRs, CD44 (ICD), Histone H2B, MAFbx, proACTH, SOD3 (EC-SOD), POMC, Neurocan, Cystatin C, sVCAM1, PLAT (TPA), Biglycan, GBP6, Fc gamma RII beta, ABCA13, SOX17, APOL1, Joining peptide (JP), Perforin, Beta-MSH / Beta-Endorphin, BC028528, Fc gamma RII, GIPR, CD147, N-POMC, CEACAM, gamma-MSH, N-POC, PRSS11 (HtrA1), beta-LPH, L-FABP, NQO3A2, Galpha(i)-specific peptide GPCRs, GLVR1, CPT-1A, I-TAC, Ficolin-1, Apo-2L(TNFSF10), Lactoferrin, Calcitonin receptor, STARD13, Galpha(q)-specific nucleotide-like GPCRs, AGS8, gamma-LPH, Aquaporin 1, C6orf27, MxA, Galpha(i)-specific EDG GPCRs, ACTH 1-17, P2Y1, RAB3IP, PKHD1, DA-alphaMSH, Carbohydrate sulfotransferases, MYEOV2, SLC12A1, Syntrophin gamma 2, Ig light chain, C4Aa, PLC-delta, NALP3, EGF, gamma2-MSH, NQO1, APRIL(TNFSF13), GFAP, PR (membrane), gamma3-MSH, C4a, RXR, FAM149A, Dystroglycan, CD44 (EXT), PLA2G5, LRRC55, GALNT2, SOX3, Galpha(s)-specific peptide GPCRs, Oct-2, CYP4V2, C4b, ACES, HMGCL, WNT, SPE2B, beta-MSH, Proline oxidase 1, WIF1, RXRG, CART, KVD16, PR (nuclear), Midkine, GREB1, HLAC, Myospryn, RNF152, Alpha dystroglycan
50	Pain	321	1.476E-16	5.504E-15	32	HMG1,2, C4Ab, C4A protein, CLIP, C4, Fatty acid-binding protein, ACTH, MHC Class I alpha chain, alpha-MSH, beta-Endorphin, Galpha(q)-specific peptide GPCRs, proACTH, POMC, Cystatin C, Joining peptide (JP), Beta-MSH / Beta-Endorphin, N-POMC, gamma-MSH, N-POC, beta-LPH, Galpha(i)-specific peptide GPCRs, gamma-LPH, ACTH 1-17, DA-alphaMSH, C4Aa, NALP3, gamma2-MSH, gamma3-MSH, C4a, C4b, ACES, beta-MSH

Table A15. Top 50 TargetALS Diseases by Biomarkers enrichments with MetaCore. Term size refers to the number of genes in the term, with the intersection size denoting the number of genes in the dataset found in the term.

#	Term Name	Term Size	p-value	adjusted p-value (FDR)	Intersection Size	Intersection Gene Names
1	regulation of transport	2767	2.288E-23	1.198E-19	185	PLP1, NPY, PP2A cat (alpha), HSP90, PAM, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Alpha crystallin B, Rab-3B, HPCA, APJ, RNF207, Activin A, UBL5, Endothelin-1, AP-1 gamma subunits, ARG2, T-plastin, NETO2, REV-ERBalpha, BRSK2, G-protein beta, JWA, Synaptotagmin I, Guanylate cyclase, HSP70, CNR1, Synaptotagmin IV, Synaptotagmin, CNTN1 (F3), Thioredoxin, NDUFA4, Septin 1, PDE, CNIH2, PPT1, NCKP1 subunit, HCN2, Galpha(q)-specific Class A Orphan/other GPCRs, SHISA7, RGS4, Kv3.3, ORP-family, PP1-cat gamma, CEACAM, PKC-beta, KIS, G-protein beta/gamma, NET6(TSPAN13), SUR, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, CPT-1A, S100, ORP8, KCNH5, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, Rab-3, Ephrin-A receptor 5, IDUA, CRH receptor 2, NSF, Tomt, CaMK IV, GLRA, SYP, LPL1, Rho GTPase, PDE4, Dysferlin, Rap1GDS1, Galpha(i)-specific metabotropic glutamate GPCRs, Secretogranin V, EGF, Pro-CCK, cPKC (conventional), Serotonin receptor, Apelin, AP complex 2 small (sigma) chain, Rab-27B, PPID, TRPC, VDAC 1, Osteopontin, Rab-3C, PKA-reg (cAMP-dependent), ANT, PP1-cat, HMDH, NDFIP2, NR3A, ECT2, Substance P, GRM6, MCT1 (SLC16A1), TMEM14A, LRRC51, Galpha(q)-specific amine GPCRs, Ephrin-A receptors, Galpha(i)-specific amine GPCRs, TRPC4, PMCA1, Rab-23, NCX1, HCN, Protein kinase G1, HSP90 beta, Activin beta A, CDK5, PAK, FLJ32001, Glycine receptor, Fatty acid-binding protein, Kv9.3, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, Galpha(q)-specific peptide GPCRs, Azi1, DYNLL, Patched, MEF2, NAPB, APRIO, ACSL4, F262, CEACAM1, ATF/CREB, Hdj-2, DelGIP1, Acyl-CoA synthetase, PP2A catalytic, SNAPs, OAZIN, Glutaredoxin, DLC1 (Dynein LC8a), Galpha(s)-specific CRF GPCRs, Kv4.2 channel, Protein kinase G 2, PRNP, MPTP complex, NKCC1, Calmodulin, NELL2, FLJ45455, Endophilin A1, STAC2, Activin, Aquaporin 1, NDFIP1, CLIC4, Syntenin 1, SCOT, ERK1/2, CaMK II delta, HSC70, PKC, SUR1, HTR2A, SLC25A4, ATP1B3, ARPP-19, MEF2C, Protein kinase G, ERK2 (MAPK1), Calcineurin A (beta), Ran, DKK1, MPC2, SOD1, YIPF5, CALM2, Cyclophilin A, PI3K reg class IA, Galpha(s)-specific peptide GPCRs, ACTR3, SIAH3, ARP3, 14-3-3, RAGE, 14-3-3 eta, ATP1beta subunit, Glutaredoxin 1

2	nervous system development	3420	3.074E-23	1.198E-19	213	PLP1, Cyclin G, FBXO45, NPY, PRPS1, HSP90, PAK3, PAM, Galpha(s)-specific nucleotide-like GPCRs, Semaphorin 3C, RhoN, MAL2, MEGF10, N-chimaerin, HPCA, Activin A, Endothelin-1, T-plastin, REV-ERBalpha, BRSK2, UQCRQPC, G-protein beta, CRTL1, RGS8, NckAP1, Lgi4, HPCAL4, PSD2, UNRIP, Synaptotagmin I, ARL6, HSP70, CNR1, Synaptotagmin IV, CITED2, Synaptotagmin, CNTN1 (F3), JMJD3, Dynein, axonemal, light chains, PDE, Cystatin C, PPT1, IGSF9B, NCKP1 subunit, HCN2, Galpha(q)-specific Class A Orphan/other GPCRs, ATP5G, GPR124, KAL1, RGS4, GABA-A receptor alpha-1 subunit, UGT8, FLRT3, B3GN6, Tenascin-C, PP1-cat gamma, TRPC5, KIS, PAFAH gamma, G-protein beta/gamma, B3GN1, SDFR1, SUR, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, S100, AMIGO2, Galpha(q)-specific nucleotide-like GPCRs, Rab-3, DNER, ZFHX2, Ephrin-A receptor 5, IP3KA, CRH receptor 2, Semaphorin 5A, Tomt, GLRA, ZNF499, GABA-A receptor beta-2 subunit, CECR2, Carbohydrate sulfotransferases, Rho GTPase, G-protein gamma, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, GlyRA2, Pro-CCK, Dynein, axonemal, heavy chains, BMPR1A, Semaphorin 3E, LOC283174, Myotrophin, NELL1, cPKC (conventional), DLL4, Serotonin receptor, GABA-A receptor alpha-4 subunit, TRPC, HTR5A, Osteopontin, ZNF238, SMRT, NHE6, Lingo1, PP1-cat, NR3A, Cables1, ECT2, Histone H2, LRRC51, Galpha(q)-specific amine GPCRs, Ephrin-A receptors, Histone H2A, Galpha(i)-specific amine GPCRs, TRPC4, PMCA1, Rab-23, NCX1, HCN, Protein kinase G1, BDH, HSP90 beta, COL25A1, Activin beta A, GABA-A receptor alpha-5 subunit, CDK5, PAK, BEX1, Glycine receptor, Fatty acid-binding protein, LPPR4, DYNLT, Glycine receptor beta chain, Selenoprotein P, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, Cyclin G1, SLC25A46, SMIT, Galpha(q)-specific peptide GPCRs, Histone H2B, Creatine kinase, DSCAML1, B-FABP, DYNLL, Patched, XK, MEF2, HNMT, ACSL4, ATF/CREB, FN14(TNFRSF12A), G-protein beta-4, Acyl-CoA synthetase, BMI-1, SNAPs, DLC1 (Dynein LC8a), Galpha(s)-specific CRF GPCRs, ENC1, RHEB2, Calmodulin, PGRMC1, Endophilin A1, BTBD1, Activin, Aquaporin 1, NME5, Calcyclin, Syntenin 1, SCOT, ERK1/2, UGCG, HSC70, PKC, SSTR2, SUR1, MEF2C, SULT4A1, Protein kinase G, ERK2 (MAPK1), Calcineurin A (beta), LISCH7, Ran, IGFALS, UFC1, Nephrocystin-4, DKK1, SSTR1, Guanine deaminase, PRPS, SOD1, SLC38A2, CALM2, Cyclophilin A, FOXP1/2/4 proteins, PTCHD1, Galpha(s)-specific peptide GPCRs,

						ACTR3, ATP6AP2, Pcdh19, CD166, NF-I, Neuroserpin, Midkine, IRS6(DOK5), ARP3, 14-3-3, RAGE, 14-3-3 eta, ATP1beta subunit
3	central nervous system development	1772	1.251E-22	3.251E-19	137	PLP1, Cyclin G, FBXO45, NPY, HSP90, PAM, Galpha(s)-specific nucleotide-like GPCRs, HPCA, Activin A, UQCRQPC, G-protein beta, CRTL1, RGS8, NckAP1, HPCAL4, Synaptotagmin I, ARL6, HSP70, Synaptotagmin IV, CITED2, Synaptotagmin, CNTN1 (F3), JMJD3, Cystatin C, PPT1, NCKP1 subunit, HCN2, Galpha(q)-specific Class A Orphan/other GPCRs, GPR124, RGS4, UGT8, PAFAH gamma, G-protein beta/gamma, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, S100, AMIGO2, Galpha(q)-specific nucleotide-like GPCRs, DNER, ZFHX2, Ephrin-A receptor 5, CRH receptor 2, Semaphorin 5A, GLRA, Carbohydrate sulfotransferases, Rho GTPase, G-protein gamma, Ephrin-A receptor 4, GlyRA2, Dynein, axonemal, heavy chains, BMPR1A, Myotrophin, cPKC (conventional), DLL4, Serotonin receptor, GABA-A receptor alpha-4 subunit, TRPC, HTR5A, ZNF238, SMRT, Lingo1, Histone H2, Ephrin-A receptors, Histone H2A, Galpha(i)-specific amine GPCRs, TRPC4, PMCA1, Rab-23, NCX1, HCN, Protein kinase G1, BDH, HSP90 beta, Activin beta A, GABA-A receptor alpha-5 subunit, CDK5, PAK, Glycine receptor, Fatty acid-binding protein, Selenoprotein P, Calcineurin A (catalytic), Cyclin G1, SLC25A46, Galpha(q)-specific peptide GPCRs, Histone H2B, Creatine kinase, DSCAML1, B-FABP, DYNLL, Patched, MEF2, HNMT, ATF/CREB, G-protein beta-4, Acyl-CoA synthetase, BMI-1, SNAPs, DLC1 (Dynein LC8a), Galpha(s)-specific CRF GPCRs, Calmodulin, Endophilin A1, Activin, Aquaporin 1, NME5, SCOT, ERK1/2, HSC70, PKC, SSTR2, MEF2C, Protein kinase G, ERK2 (MAPK1), Calcineurin A (beta), LISCH7, Ran, UFC1, DKK1, SSTR1, SLC38A2, CALM2, FOXP1/2/4 proteins, PTCHD1, Galpha(s)-specific peptide GPCRs, ACTR3, ATP6AP2, Pcdh19, NF-I, Neuroserpin, Midkine, ARP3, 14-3-3, RAGE, 14-3-3 eta, ATP1beta subunit
4	cellular process	20764	5.944E-22	1.158E-18	758	SCAP2, PLP1, Cyclin G, FBXO45, NPY, FAM3C, PP2A cat (alpha), PRPS1, HSP90, PAK3, PAM, HMGCLL1, Cadherin 8, ZYG11B, CPSF1, ARP6, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Semaphorin 3C, Alpha crystallin B, TMEM87B, AEBP1, G3BP2, RhoN, IRF1, ILDR2, FILIP, ZnT-2, MAL2, GLSK, Rab-3B, MAGEH-1, SLC35E2B, COX VIc, GAD1, SMVT, C1D, MEGF10, TINP1, PTCH2, ZH11B, N-chimaerin, Tubulin alpha 1A, ATP5C, SUCLG1, HPCA, APJ, Smooth muscle myosin, EDIL3, FLJ12671, ELOVL5, RNF207, Peroxiredoxin, Activin A, UBL5,

						Esterase D, Endothelin-1, SULT1A1, Trehalase, PSMB5, AP-1 gamma subunits, ARG2, T-plastin, DUOX1, GSKIP, GHITM, REV-ERBalpha, IL-17D, BRSK2, UQCRQPC, DYNLT3, P2Y11, UBXD3, G-protein beta, LAS1L, SC5D, JWA, ALDR, CRTL1, UQCRH, TMC4, Rab-6A, RGS8, SC4MOL, MRPS6, PSMA5, CNOT7, MDS028, NFKBIL2, NDUFAB1, Importin (karyopherin)-alpha, NckAP1, BTBD12, NDUFA1, CDC18L (CDC6), ANKRD50, DNAH1, MRPL1, Lgi4, TTLL9, MOBKL1A, AP1G2, DTX2, LOC153328, Pannexin-1, MCM6, NKIRAS1, DCMC, HPCAL4, PSD2, MGF, PDH E2 subunit N6-lipoyllysine, TIP47, PRKAR2B, MELC, DPY19L1, NPFF receptor 2, NDUFB4, MC4R, UNRIP, NDUFA8, KLHL12, C12orf62, Synaptotagmin I, Guanylate cyclase, ARL6, KCNK2, HSP70, DDX3Y, CNR1, MAPBPIP, MYL6, Glycogen phosphorylase, Synaptotagmin IV, Tim17, CITED2, PPM1E, SLIRP, NUDT4P1, GIMAP7, DnaJB9, Synaptotagmin, PRDX3, CNTN1 (F3), Thioredoxin, MRLC2, NDUFA4, ATP6V1A (70kD), HSPA4, JMJD3, Septin 1, Dynein, axonemal, light chains, PDE, Cystatin C, CNIH2, Tcfl5, PPT1, SDHB, MGAT4A, SLC39A10, IGSF9B, DKK3, Karyopherin alpha 2, NCKP1 subunit, TM9SF2, HCN2, D123, Guanylate cyclase alpha, FLJ20674, Galpha(q)-specific Class A Orphan/other GPCRs, IMPG2, LMF1, ATP5G, GPR124, TPH2, SHISA7, KAL1, RAB39B, Aha1, PTPN18, RGS4, VDAC 3, 14-3-3 beta/alpha, BTBD18, GABA-A receptor alpha-1 subunit, TUSC3, UGT8, GUCY1B1, FLRT3, Exostosin-like 2, Kv3.3, SELI, C13orf37, ORP-family, B3GN6, Tenascin-C, Myopodin, PP1-cat gamma, CEACAM, ODF3, TRPC5, PKC-beta, KIS, TCP1-theta, PRDX1, ELMO3, G-protein beta/gamma, B3GN1, SLC25A45, NDUFB6, SDFR1, SUR, ABO system transferase, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, VBP-1, FUT2, TORC1, KLHL13, UQCRB, ATP5E, CPT-1A, S100, Rab-6, TXNRD1, ORP8, KCNH5, AMIGO2, VWA2, LASS6, PIMT, TRPV1, PDK3, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, TIP41, ATP6V1C1, ZDH13, Aldose reductase, ATP6M, NDUFB3, Rab-3, MTG16 (CBFA2T3), ATG9B, TM2D3, DNER, FAM38B, Ephrin-A receptor 5, LAPTM4B, IDUA, IP3KA, CRH receptor 2, AMDHD2, CacyBP(SIP), InsP6 kinase 3, SLC2A13, Semaphorin 5A, Adropin, V-ATPase E subunit, GRAIL, UBA1L, RPL9, NSF, Tomt, ADAM-TS10, GPR176, CaMK IV, CHCHD2, GLRA, DKK2, GABA-A receptor beta-2 subunit, FBXO2, CECR2, DOK7, SYP, Carbohydrate sulfotransferases, TIMM17, LACTB2, LPL1, MOCS2(small), Rho GTPase, PDE4, GTPBP3, Tensin 2, G-protein gamma, UBE2D1, OSGIN2, PLCXD2, PRPS2, SOCS6, Dysferlin, Rap1GDS1, Ephrin-A receptor 4, TMEM86B,

						Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, ChREBP, Secretogranin V, EGF, GlyRA2, ATP5B, PPase (inorganic), NAP1L2, Pro-CCK, CED-6, SYTC, XKR4, Dynein, axonemal, heavy chains, B3GALTL, BMPR1A, Semaphorin 3E, MMADHC, MMD, LOC283174, HIST1H2BN, Neurexophilin 2, PKA-reg type II (cAMP-dependent), B3GNT4, Myotrophin, NELL1, CAP2, cPKC (conventional), SF3A2, ATP6V1B2, NDUFB1, DLL4, ELOVL4, AP3S1, PSMA1, Serotonin receptor, CHMP5, Apelin, AP complex 2 small (sigma) chain, GABA-A receptor alpha-4 subunit, ADSS, Rab-27B, PPID, TRPC, SLC7A5, HTR5A, PYGM, ACTR10, MOC2B, PDK4, VDAC 1, WIF1, NDRG3, COX VIa, SUCB1, CLCN4, ATP6V1H, Osteopontin, ATP5G3, ZNF238, Slp5, ABHD10, SMRT, CysLT2 receptor, NHE6, Rab-3C, RGS11, M-Ras, KCY, CREB4, PC4, CHAMP, PKA-reg (cAMP-dependent), TReP-132, RNF152, Lingo1, ANT, PP1-cat, CFA74, HMDH, PDLIM2, TCP1-delta, UQCR10, NDFIP2, NR3A, GUCY1A3, HSBP1, VTA1, Cables1, KIAA1110, ECT2, Clathrin heavy chain, IL3RA, Substance P, AP-3 sigma subunits, HBXIP, PSMD10 (Gankyrin), StARD4, MID1IP1, GRM6, CHTF18, CalDAG-GEFII, Histone H2, LIPA, KLHL35, MCT1 (SLC16A1), ARHGAP18, COPS4, TMEM14A, LRRC51, Galpha(q)-specific amine GPCRs, UQCRFS1, Ephrin-A receptors, MRPL47, Histone H2A, HMP19, NPR3, GP-IB alpha, Galpha(i)-specific amine GPCRs, CCNI2, Stch, TRPC4, PMCA1, Rab-23, NCX1, SLBP, HCN, Protein kinase G1, HLF, C1orf113, CAP1, HSP90 beta, Anillin, TXNIP (VDUP1), Vinexin, COL25A1, PMS2L3, NDUFS6, Calponin-1, Activin beta A, GABA-A receptor alpha-5 subunit, BRMS1L, Zeta-sarcoglycan, CDK5, PANX2, DUS3L, PAK, Guanylate cyclase (alpha-1/beta-1), SYT16, Guanylate cyclase beta, BEX1, TCP1-eta, Glycine receptor, Fatty acid-binding protein, PSG3, FOXP4, HINT, ENPP4, MAML1, KIAA0143, SgK223, SOHLH1, IZUMO1, TOM22, MDH1, GTL3, ASAH, GABA-A receptor alpha-3 subunit, GNT-IV, LPPR4, DYNLT, SLC16A13, Atg101, TMEM74, SPOCK3, BEX2, SPSY, COX Va, Copine-4, Destrin, eIF4A2, BRK, ATP5A, Glycine receptor beta chain, Nek8, Selenoprotein P, CAPZA, Carbonic anhydrase XII, Kv9.3, RTL1, Calcineurin A (catalytic), LSM2, TOP1MT, Galpha(i)-specific cannabis GPSRs, STARD7, 4833424O15Rik, B3GT2, Cyclin G1, SLC25A46, SEC23A, Glyoxalase I, DDX51, SMIT, FBI-1 (Pokemon), PDH beta, Galpha(q)-specific peptide GPCRs, H2AFZ, ATP6V1C, Histone H2B, NCOA4 (ARA70), MAFbx, SNAP190, NDUFA5, Tubulin alpha, Creatine kinase, ACAP1(CENTB1), DSCAML1, TBC1D10C, DCK, MRAP2, PAP-II, B-FABP, VIP32, Azi1, NUDT4, DYNLL, Patched, TNK1, XK, MEF2, INCA1, NAPB, ADAR3, PGAM1, HNMT, TAPBPL,

						Sec23, APRIO, SCS-A, BTBD10, MEK4/7, Peg10, ACSL4, RENBP, F262, CEACAM1, RANBP6, ATF/CREB, GLGB, ODP2, G-protein gamma 3, Hdj-2, DelGIP1, FN14(TNFRSF12A), Trim45, RSL24D1, G-protein beta-4, Ccdc56, FEM1B, Acyl-CoA synthetase, PP2A catalytic, CAPZA2, GAS41, IDI1, SNX7, ARRDC2, ZFAND2A, AP-4, MRLC, eIF4A, BMI-1, SNAPs, OAZIN, eIF2S1, Glutaredoxin, DLC1 (Dynein LC8a), RNF175, Galpha(s)-specific CRF GPCRs, LAMP2, COX VIa-1, KAD6, ALAS1, TMEM87A, YPEL5, TSNARE1, ATP6V1B, Quinone oxidoreductase, Kv4.2 channel, JKAMP, PKD1L1, Protein kinase G 2, PRNP, HSPC138, SNX16, DNAJA2, TMS-1, GKP3, MPTP complex, ENC1, STAG3, RHEB2, NKCC1, Neurocalcin delta, Malin, C1orf59, HIST2H2BE, ATP6V0B, PDE4A, WDT2, CAB39L, Calmodulin, CENPP, LPL, DIRAS2, NELL2, SUMO-3, FLJ31818, PGRMC1, ATP6V1E, Apo-2L(TNFSF10), SET1B, LOXL2, PDE11A, FLJ45455, KLHL2, NOLA3 (NOP10), HSPC125, Endophilin A1, BTBD1, STAC2, Activin, SIPAR, Aquaporin 1, NDFIP1, KCTD16, NME5, CLIC4, Calcyclin, Syntenin 1, SCOT, Octanoyl-holo-acp, KCRS, Securin, ADHX, ERK1/2, Carboxypeptidase M, snRNP-G, CDw52, AATC, UGCG, SLC29A4, Anks4b, TRUB1, NFIC, CaMK II delta, HSC70, PI3K reg class IA (p55-gamma), ARL5, SLC35A5, PKC, SSTR2, SUR1, ABTB1, HTR2A, PMM2, SLC25A4, MPP7, CCDC57, ATP1B3, ARPP-19, K-cadherin (CDH6), Guanylate Cyclase 1, soluble, MEF2C, SULT4A1, MRPL33, Protein kinase G, RIFK, ERK2 (MAPK1), Calcineurin A (beta), DREV1, LISCH7, Ran, OAT, MEK4(MAP2K4), TMEM70, Mindin, PRKAR1A, IGFALS, CLCN5, IMPA1, TRIM23, UFC1, Nephrocystin-4, DKK1, PARM-1, MPC2, SSTR1, Guanine deaminase, PRPS, SOD1, TFIIB, YIPF5, dJ222E13.2, PPP4R2, GDE1, SLC38A2, MMP-28, SAP102, FSTL5, MAP1, CALM2, Cyclophilin A, FOXP1/2/4 proteins, Aggrecanase-2, PI3K reg class IA, KIAA1614, PTCHD1, DCoHM, Galpha(s)-specific peptide GPCRs, GPR22, TCP1-alpha, ATP5L, ACTR3, ATP6AP2, OXR1, CALB1, Tubulin alpha-4A, SRm300, RhoE, Pcdh19, CD166, GAD2, SIAH3, PGM2L1, TCP1-epsilon, NF-I, NPNT, MRPL3, B930041F14Rik, HXK3, COX VIIa-2, ACOXL, NRBF2, Midkine, SAMD10, IRS6(DOK5), ARP3, PXDN, 14-3-3, ARMCX3, ACCN3 (ASIC3), COX VIIa-2L, RAGE, 14-3-3 eta, ATP1beta subunit, Glutaredoxin 1, ZCCHC12, SNX10, CMAS, TCTE3, CHST6
5	regulation of biological quality	5537	5.166E-21	7.309E-18	291	NPY, PP2A cat (alpha), HSP90, PAK3, PAM, Cadherin 8, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Semaphorin 3C, Alpha crystallin B, RhoN, ILDR2, ZnT-2, GLSK, Rab-3B, GAD1, Tubulin alpha 1A, HPCA, APJ, Smooth muscle myosin, RNF207, Peroxiredoxin, Activin A, Endothelin-1, SULT1A1, DUOX1, NETO2,

						REV-ERBalpha, BRSK2, G-protein beta, JWA, ALDR, CNOT7, NckAP1, NKIRAS1, MELC, MC4R, UNRIP, Synaptotagmin I, COCH, Guanylate cyclase, KCNK2, HSP70, DDX3Y, CNR1, Glycogen phosphorylase, Synaptotagmin IV, CITED2, Synaptotagmin, PRDX3, Thioredoxin, MRLC2, ATP6V1A (70kD), JMJD3, Dynein, axonemal, light chains, PDE, CNIH2, PPT1, SLC39A10, IGSF9B, DKK3, NCKP1 subunit, HCN2, Guanylate cyclase alpha, Galpha(q)-specific Class A Orphan/other GPCRs, ATP5G, SHISA7, RGS4, GABA-A receptor alpha-1 subunit, TUSC3, FLRT3, Kv3.3, ORP-family, CEACAM, TRPC5, PKC-beta, TCP1-theta, PRDX1, G-protein beta/gamma, SDFR1, SUR, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, TORC1, CPT-1A, S100, TXNRD1, KCNH5, AMIGO2, TRPV1, PDK3, Galpha(q)-specific nucleotide-like GPCRs, Aldose reductase, Rab-3, ATG9B, FAM38B, Ephrin-A receptor 5, LAPTM4B, IDUA, IP3KA, CRH receptor 2, Semaphorin 5A, GRAIL, Tomt, GLRA, GABA-A receptor beta-2 subunit, SYP, Carbohydrate sulfotransferases, Rho GTPase, PDE4, Tensin 2, G-protein gamma, SOCS6, Rap1GDS1, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, ChREBP, Secretogranin V, GlyRA2, ATP5B, Pro-CCK, XKR4, Semaphorin 3E, LOC283174, Myotrophin, cPKC (conventional), ATP6V1B2, Serotonin receptor, Apelin, GABA-A receptor alpha-4 subunit, PPID, TRPC, SLC7A5, PYGM, PDK4, ATP6V1H, Osteopontin, ZNF238, SMRT, NHE6, PKA-reg (cAMP-dependent), ANT, PP1-cat, HMDH, TCP1-delta, NR3A, GUCY1A3, Substance P, HBXIP, LIPA, MCT1 (SLC16A1), ARHGAP18, TMEM14A, LRRC51, Galpha(q)-specific amine GPCRs, Ephrin-A receptors, NPR3, GP-IB alpha, Galpha(i)-specific amine GPCRs, TRPC4, PMCA1, NCX1, HCN, Protein kinase G1, HSP90 beta, Activin beta A, GABA-A receptor alpha-5 subunit, Zeta-sarcoglycan, CDK5, PAK, Guanylate cyclase (alpha-1/beta-1), TCP1-eta, Glycine receptor, Fatty acid-binding protein, ENPP4, SgK223, IZUMO1, GTL3, GABA-A receptor alpha-3 subunit, DYNLT, Destrin, Glycine receptor beta chain, CAPZA, Carbonic anhydrase XII, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, STARD7, FBI-1 (Pokemon), Galpha(q)-specific peptide GPCRs, NCOA4 (ARA70), Tubulin alpha, Creatine kinase, MRAP2, PAP-II, DYNLL, Patched, XK, MEF2, HNMT, APRIO, ACSL4, RENBP, F262, CEACAM1, ATF/CREB, G-protein gamma 3, FN14(TNFRSF12A), Acyl-CoA synthetase, PP2A catalytic, CAPZA2, MRLC, BMI-1, SNAPs, Glutaredoxin, DLC1 (Dynein LC8a), Galpha(s)-specific CRF GPCRs, LAMP2, ALAS1, ATP6V1B, Kv4.2 channel, Protein kinase G 2, PRNP, MPTP complex, RHEB2, NKCC1, Neurocalcin delta,

						Calmodulin, LPL, NELL2, PGRMC1, FLJ45455, Endophilin A1, Activin, Aquaporin 1, NDFIP1, SCOCO, CLIC4, SCOT, ADHX, ERK1/2, CDw52, AATC, UGCG, SLC29A4, CaMK II delta, HSC70, PKC, SUR1, HTR2A, SLC25A4, ATP1B3, Guanylate Cyclase 1, soluble, MEF2C, Protein kinase G, ERK2 (MAPK1), Calcineurin A (beta), LISCH7, Nephrocystin-4, DKK1, MPC2, SOD1, YIPF5, SAP102, MAP1, CALM2, Cyclophilin A, FOXP1/2/4 proteins, Aggrecanase-2, PI3K reg class IA, Galpha(s)-specific peptide GPCRs, TCP1-alpha, ACTR3, ATP6AP2, CALB1, RhoE, GAD2, SIAH3, TCP1-epsilon, HXK3, ACOXL, ARP3, 14-3-3, RAGE, 14-3-3 eta, ATP1beta subunit, Glutaredoxin 1, SNX10
6	regulation of localization	4055	5.626E-21	7.309E-18	233	PLP1, NPY, PP2A cat (alpha), HSP90, PAK3, PAM, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Semaphorin 3C, Alpha crystallin B, ZnT-2, Rab-3B, HPCA, APJ, RNF207, Activin A, UBL5, Endothelin-1, AP-1 gamma subunits, ARG2, T-plastin, DUOX1, NETO2, REV-ERBalpha, BRSK2, G-protein beta, JWA, NckAP1, MGF, TIP47, Synaptotagmin I, Guanylate cyclase, HSP70, SCRT2, CNR1, Synaptotagmin IV, CITED2, Synaptotagmin, CNTN1 (F3), Thioredoxin, NDUFA4, Septin 1, PDE, CNIH2, PPT1, NCKP1 subunit, HCN2, Galpha(q)-specific Class A Orphan/other GPCRs, GPR124, SHISA7, RGS4, Kv3.3, ORP-family, Myopodin, PP1-cat gamma, CEACAM, PKC-beta, KIS, TCP1-theta, G-protein beta/gamma, NET6(TSPAN13), SDFR1, SUR, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, SCRT1, CPT-1A, S100, ORP8, KCNH5, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, Rab-3, Ephrin-A receptor 5, IDUA, CRH receptor 2, Semaphorin 5A, NSF, Tomt, CaMK IV, GLRA, SYP, Carbohydrate sulfotransferases, LPL1, Rho GTPase, PDE4, G-protein gamma, Dysferlin, Rap1GDS1, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, Secretogranin V, EGF, ATP5B, Pro-CCK, Dynein, axonemal, heavy chains, BMPR1A, Semaphorin 3E, MMD, cPKC (conventional), DLL4, Serotonin receptor, Apelin, AP complex 2 small (sigma) chain, Rab-27B, PPID, TRPC, VDAC 1, Osteopontin, Rab-3C, PKA-reg (cAMP-dependent), ANT, PP1-cat, HMDH, TCP1-delta, NDFIP2, NR3A, ECT2, Clathrin heavy chain, Substance P, HBXIP, GRM6, MCT1 (SLC16A1), ARHGAP18, TMEM14A, LRRC51, Galpha(q)-specific amine GPCRs, Ephrin-A receptors, GP-IB alpha, Galpha(i)-specific amine GPCRs, TRPC4, PMCA1, Rab-23, NCX1, HCN, Protein kinase G1, HSP90 beta, Activin beta A, CDK5, PAK, FLJ32001, TCP1-eta, Glycine receptor, Fatty acid-binding protein, SgK223, GTL3, SPOCK3, ATP5A, Kv9.3, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, SMIT, Galpha(q)-specific peptide GPCRs,

						MRAP2, Azi1, DYNLL, Patched, MEF2, NAPB, APRIO, ACSL4, F262, CEACAM1, ATF/CREB, Hdj-2, DelGIP1, Acyl-CoA synthetase, PP2A catalytic, SNAPs, OAZIN, Glutaredoxin, DLC1 (Dynein LC8a), Galpha(s)-specific CRF GPCRs, Kv4.2 channel, Protein kinase G 2, PRNP, MPTP complex, NKCC1, Malin, Calmodulin, LPL, NELL2, SUMO-3, PGRMC1, FLJ45455, NOLA3 (NOP10), Endophilin A1, STAC2, Activin, Aquaporin 1, NDFIP1, CLIC4, Syntenin 1, SCOT, ERK1/2, CaMK II delta, HSC70, PI3K reg class IA (p55-gamma), PKC, SUR1, HTR2A, SLC25A4, ATP1B3, ARPP-19, MEF2C, Protein kinase G, ERK2 (MAPK1), Calcineurin A (beta), Ran, DKK1, MPC2, SOD1, YIPF5, MMP-28, CALM2, Cyclophilin A, FOXP1/2/4 proteins, PI3K reg class IA, KIAA1614, Galpha(s)-specific peptide GPCRs, TCP1-alpha, ACTR3, SIAH3, TCP1-epsilon, Midkine, ARP3, 14-3-3, RAGE, 14-3-3 eta, ATP1beta subunit, Glutaredoxin 1
7	inorganic ion transmembrane transport	904	9.046E-20	1.007E-16	86	ZnT-2, SMVT, ATP5C, Endothelin-1, UQCRQPC, UQCRH, Pannexin-1, KCNK2, NDUFA4, ATP6V1A (70kD), SLC39A10, HCN2, ATP5G, GABA-A receptor alpha-1 subunit, TUSC3, Kv3.3, TRPC5, SUR, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, ATP5E, KCNH5, TRPV1, COX VIIa, ATP6V1C1, ZDH13, ATP6M, V-ATPase E subunit, GLRA, GABA-A receptor beta-2 subunit, Galpha(i)-specific metabotropic glutamate GPCRs, GlyRA2, ATP5B, Dynein, axonemal, heavy chains, ATP6V1B2, Serotonin receptor, GABA-A receptor alpha-4 subunit, TRPC, VDAC 1, COX VIa, CLCN4, ATP6V1H, ATP5G3, NHE6, ANT, UQCR10, NR3A, Galpha(q)-specific amine GPCRs, UQCRFS1, GP-IB alpha, Galpha(i)-specific amine GPCRs, TRPC4, PMCA1, NCX1, HCN, GABA-A receptor alpha-5 subunit, Glycine receptor, GABA-A receptor alpha-3 subunit, COX Va, ATP5A, Glycine receptor beta chain, Kv9.3, Galpha(q)-specific peptide GPCRs, ATP6V1C, COX VIa-1, ATP6V1B, Kv4.2 channel, PKD1L1, MPTP complex, NKCC1, ATP6V0B, Calmodulin, ATP6V1E, Aquaporin 1, SUR1, HTR2A, SLC25A4, ATP1B3, CLCN5, CALM2, ATP5L, ACCN3 (ASIC3), COX VIIa-2L, ATP1beta subunit
8	localization	6993	1.333E-19	1.299E-16	340	FBXO45, HSP90, PAM, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Semaphorin 3C, TMEM87B, G3BP2, RhoN, ILDR2, ZnT-2, MAL2, Rab-3B, SLC35E2B, SMVT, MEGF10, ZH11B, Tubulin alpha 1A, ATP5C, Activin A, Endothelin-1, AP-1 gamma subunits, C18orf42, BRSK2, UQCRQPC, JWA, UQCRH, TMC4, Rab-6A, Importin (karyopherin)-alpha, NckAP1, ANKRD50, DNAH1, TTLL9, AP1G2, LOC153328, Pannexin-1, PSD2, MGF, TIP47, MC4R, KLHL12, Synaptotagmin I, Guanylate cyclase, ARL6,

						KCNK2, HSP70, DDX3Y, MAPBPIP, Synaptotagmin IV, Tim17, SLIRP, Synaptotagmin, Thioredoxin, MRLC2, NDUFA4, ATP6V1A (70kD), HSPA4, Septin 1, Dynein, axonemal, light chains, PDE, CNIH2, PPT1, SLC39A10, Karyopherin alpha 2, NCKP1 subunit, TM9SF2, HCN2, Galpha(q)-specific Class A Orphan/other GPCRs, IMPG2, LMF1, ATP5G, GPR124, SHISA7, RAB39B, VDAC 3, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, TUSC3, UGT8, FLRT3, Kv3.3, C13orf37, ORP-family, CEACAM, TRPC5, PKC-beta, TCP1-theta, ELMO3, G-protein beta/gamma, SLC25A45, SUR, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, ATP5E, CPT-1A, S100, Rab-6, ORP8, KCNH5, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, ATP6V1C1, ZDH13, ATP6M, Rab-3, ATG9B, DNER, FAM38B, APOL3, LAPTM4B, SLC2A13, Semaphorin 5A, V-ATPase E subunit, GRAIL, NSF, CaMK IV, GLRA, GABA-A receptor beta-2 subunit, CECR2, DOK7, SYP, Carbohydrate sulfotransferases, TIMM17, Rho GTPase, PDE4, G-protein gamma, Dysferlin, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, Secretogranin V, GlyRA2, ATP5B, Pro-CCK, CED-6, XKR4, Dynein, axonemal, heavy chains, Semaphorin 3E, cPKC (conventional), ATP6V1B2, AP3S1, Serotonin receptor, CHMP5, Apelin, AP complex 2 small (sigma) chain, GABA-A receptor alpha-4 subunit, Rab-27B, PPID, TRPC, SLC7A5, ACTR10, VDAC 1, COX VIa, CLCN4, ATP6V1H, Osteopontin, ATP5G3, Slp5, SMRT, NHE6, Rab-3C, ANT, TCP1-delta, UQCR10, NDFIP2, NR3A, HSBP1, VTA1, ECT2, Clathrin heavy chain, AP-3 sigma subunits, HBXIP, PSMD10 (Gankyrin), StARD4, CalDAG-GEFII, MCT1 (SLC16A1), TMEM14A, Galpha(q)-specific amine GPCRs, UQCRFS1, Ephrin-A receptors, HMP19, NPR3, GP-IB alpha, Galpha(i)-specific amine GPCRs, TRPC4, PMCA1, Rab-23, NCX1, SLBP, HCN, Protein kinase G1, C1orf113, CAP1, Anillin, TXNIP (VDUP1), Activin beta A, GABA-A receptor alpha-5 subunit, CDK5, PANX2, PAK, SYT16, TCP1-eta, Glycine receptor, Fatty acid-binding protein, HINT, KIAA0143, SgK223, TOM22, GABA-A receptor alpha-3 subunit, LPPR4, DYNLT, SLC16A13, COX Va, Destrin, BRK, ATP5A, Glycine receptor beta chain, Carbonic anhydrase XII, Kv9.3, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, STARD7, SLC25A46, SEC23A, SMIT, FBI-1 (Pokemon), Galpha(q)-specific peptide GPCRs, ATP6V1C, NCOA4 (ARA70), Tubulin alpha, ACAP1(CENTB1), TBC1D10C, MRAP2, B-FABP, Azi1, DYNLL, Patched, XK, MEF2, NAPB, Sec23, Peg10, ACSL4, CEACAM1, RANBP6, ATF/CREB, Hdj-2, FN14(TNFRSF12A), Acyl-CoA synthetase, SNX7, ARRDC2, ZFAND2A, MRLC, SNAPs, DLC1

						(Dynein LC8a), Galpha(s)-specific CRF GPCRs, LAMP2, COX VIa-1, TMEM87A, TSNARE1, ATP6V1B, Kv4.2 channel, PKD1L1, Protein kinase G 2, HSPC138, SNX16, TMS-1, MPTP complex, STAG3, NKCC1, Neurocalcin delta, ATP6V0B, WDT2, Calmodulin, SUMO-3, ATP6V1E, LOXL2, FLJ45455, Endophilin A1, Activin, C1orf43, Aquaporin 1, NDFIP1, NME5, CLIC4, Calcyclin, Syntenin 1, ERK1/2, UGCG, SLC29A4, Anks4b, CaMK II delta, HSC70, PI3K reg class IA (p55-gamma), ARL5, SLC35A5, PKC, SUR1, HTR2A, SLC25A4, MPP7, ATP1B3, MEF2C, Protein kinase G, ERK2 (MAPK1), Calcineurin A (beta), LISCH7, Ran, CLCN5, TRIM23, Nephrocystin-4, MPC2, SOD1, YIPF5, SLC38A2, SAP102, MAP1, CALM2, Cyclophilin A, PI3K reg class IA, Galpha(s)-specific peptide GPCRs, TCP1-alpha, ATP5L, ACTR3, RhoE, TCP1-epsilon, NPNT, Midkine, ARP3, 14-3-3, ARMCX3, ACCN3 (ASIC3), COX VIIa-2L, RAGE, 14-3-3 eta, ATP1beta subunit, SNX10
9	regulation of establishment of protein localization	913	1.698E-19	1.448E-16	86	PP2A cat (alpha), HSP90, PAM, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, HPCA, UBL5, REV-ERBalpha, BRSK2, HSP70, CNR1, Synaptotagmin IV, Synaptotagmin, Thioredoxin, PDE, Galpha(q)-specific Class A Orphan/other GPCRs, ORP-family, KIS, TCP1-theta, SUR, Galpha(i)-specific peptide GPCRs, CPT-1A, Galpha(q)-specific nucleotide-like GPCRs, Ephrin-A receptor 5, IDUA, CRH receptor 2, Tomt, CaMK IV, LPL1, Rho GTPase, PDE4, Rap1GDS1, EGF, PPID, HMDH, TCP1-delta, NDFIP2, ECT2, MCT1 (SLC16A1), LRRC51, Galpha(q)-specific amine GPCRs, Ephrin-A receptors, Galpha(i)-specific amine GPCRs, Rab-23, HSP90 beta, CDK5, PAK, FLJ32001, TCP1-eta, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, Galpha(q)-specific peptide GPCRs, Azi1, DYNLL, APRIO, ACSL4, F262, Hdj-2, DelGIP1, Acyl-CoA synthetase, PP2A catalytic, Glutaredoxin, DLC1 (Dynein LC8a), Galpha(s)-specific CRF GPCRs, PRNP, NKCC1, Activin, NDFIP1, SCOT, ERK1/2, HSC70, PKC, SUR1, ERK2 (MAPK1), Calcineurin A (beta), Ran, MPC2, Cyclophilin A, PI3K reg class IA, TCP1-alpha, ACTR3, SIAH3, TCP1-epsilon, ARP3, 14-3-3, Glutaredoxin 1
10	ion transmembrane transport	1192	1.858E-19	1.448E-16	101	ZnT-2, SMVT, ATP5C, Endothelin-1, UQCRQPC, JWA, UQCRH, TMC4, LOC153328, Pannexin-1, KCNK2, NDUFA4, ATP6V1A (70kD), SLC39A10, HCN2, ATP5G, VDAC 3, GABA-A receptor alpha-1 subunit, TUSC3, Kv3.3, TRPC5, SLC25A45, SUR, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, ATP5E, S100, KCNH5, TRPV1, COX VIIa, ATP6V1C1, ZDH13, ATP6M, FAM38B, V-ATPase E subunit, GLRA, GABA-A receptor beta-2 subunit, Galpha(i)-specific metabotropic glutamate GPCRs, GlyRA2, ATP5B, Dynein, axonemal, heavy chains, ATP6V1B2, Serotonin receptor, GABA-A

						receptor alpha-4 subunit, TRPC, SLC7A5, VDAC 1, COX VIa, CLCN4, ATP6V1H, ATP5G3, NHE6, ANT, UQCR10, NR3A, MCT1 (SLC16A1), Galpha(q)-specific amine GPCRs, UQCRFS1, GP-IB alpha, Galpha(i)-specific amine GPCRs, TRPC4, PMCA1, NCX1, HCN, GABA-A receptor alpha-5 subunit, Glycine receptor, GABA-A receptor alpha-3 subunit, COX Va, ATP5A, Glycine receptor beta chain, Kv9.3, Galpha(q)-specific peptide GPCRs, ATP6V1C, COX VIa-1, ATP6V1B, Kv4.2 channel, PKD1L1, MPTP complex, NKCC1, ATP6V0B, Calmodulin, ATP6V1E, Aquaporin 1, CLIC4, Calcyclin, SLC29A4, PKC, SUR1, HTR2A, SLC25A4, ATP1B3, CLCN5, MPC2, CALM2, ATP5L, 14-3-3, ACCN3 (ASIC3), COX VIIa-2L, ATP1beta subunit
11	transport	5211	6.052E-19	4.257E-16	272	HSP90, PAM, Galpha(s)-specific nucleotide-like GPCRs, TMEM87B, G3BP2, ILDR2, ZnT-2, MAL2, Rab-3B, SLC35E2B, SMVT, MEGF10, ZH11B, Tubulin alpha 1A, ATP5C, Activin A, Endothelin-1, AP-1 gamma subunits, BRSK2, UQCRQPC, JWA, UQCRH, TMC4, Rab-6A, Importin (karyopherin)-alpha, ANKRD50, DNAH1, AP1G2, LOC153328, Pannexin-1, PSD2, TIP47, MC4R, KLHL12, Synaptotagmin I, Guanylate cyclase, ARL6, KCNK2, HSP70, Synaptotagmin IV, Tim17, Synaptotagmin, NDUFA4, ATP6V1A (70kD), HSPA4, Dynein, axonemal, light chains, CNIH2, PPT1, SLC39A10, Karyopherin alpha 2, HCN2, Galpha(q)-specific Class A Orphan/other GPCRs, LMF1, ATP5G, RAB39B, VDAC 3, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, TUSC3, Kv3.3, ORP-family, CEACAM, TRPC5, PKC-beta, TCP1-theta, ELMO3, SLC25A45, SUR, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, ATP5E, CPT-1A, S100, Rab-6, ORP8, KCNH5, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, ATP6V1C1, ZDH13, ATP6M, Rab-3, ATG9B, DNER, FAM38B, APOL3, LAPTM4B, SLC2A13, V-ATPase E subunit, NSF, CaMK IV, GLRA, GABA-A receptor beta-2 subunit, CECR2, SYP, TIMM17, Rho GTPase, Dysferlin, Galpha(i)-specific metabotropic glutamate GPCRs, Secretogranin V, GlyRA2, ATP5B, CED-6, XKR4, Dynein, axonemal, heavy chains, cPKC (conventional), ATP6V1B2, AP3S1, Serotonin receptor, CHMP5, Apelin, AP complex 2 small (sigma) chain, GABA-A receptor alpha-4 subunit, Rab-27B, PPID, TRPC, SLC7A5, ACTR10, VDAC 1, COX VIa, CLCN4, ATP6V1H, ATP5G3, Slp5, SMRT, NHE6, Rab-3C, ANT, TCP1-delta, UQCR10, NDFIP2, NR3A, HSBP1, VTA1, ECT2, Clathrin heavy chain, AP-3 sigma subunits, StARD4, CalDAG-GEFII, MCT1 (SLC16A1), TMEM14A, Galpha(q)-specific amine GPCRs, UQCRFS1, HMP19, NPR3, GP-IB alpha, Galpha(i)-specific amine GPCRs, TRPC4, PMCA1, Rab-23, NCX1, SLBP, HCN,

						CAP1, TXNIP (VDUP1), Activin beta A, GABA-A receptor alpha-5 subunit, CDK5, PANX2, PAK, SYT16, TCP1-eta, Glycine receptor, Fatty acid-binding protein, HINT, TOM22, GABA-A receptor alpha-3 subunit, LPPR4, DYNLT, SLC16A13, COX Va, ATP5A, Glycine receptor beta chain, Carbonic anhydrase XII, Kv9.3, Calcineurin A (catalytic), STARD7, SLC25A46, SEC23A, SMIT, Galpha(q)-specific peptide GPCRs, ATP6V1C, NCOA4 (ARA70), Tubulin alpha, ACAP1(CENTB1), TBC1D10C, B-FABP, Azi1, DYNLL, XK, NAPB, Sec23, Peg10, ACSL4, CEACAM1, RANBP6, ATF/CREB, Hdj-2, Acyl-CoA synthetase, SNX7, ARRDC2, ZFAND2A, SNAPs, DLC1 (Dynein LC8a), Galpha(s)-specific CRF GPCRs, LAMP2, COX VIa-1, TMEM87A, TSNARE1, ATP6V1B, Kv4.2 channel, PKD1L1, HSPC138, SNX16, TMS-1, MPTP complex, NKCC1, Neurocalcin delta, ATP6V0B, WDT2, Calmodulin, ATP6V1E, LOXL2, Endophilin A1, Activin, C1orf43, Aquaporin 1, NDFIP1, NME5, CLIC4, Calcyclin, Syntenin 1, ERK1/2, UGCG, SLC29A4, CaMK II delta, HSC70, ARL5, SLC35A5, PKC, SUR1, HTR2A, SLC25A4, ATP1B3, ERK2 (MAPK1), Calcineurin A (beta), LISCH7, Ran, CLCN5, TRIM23, MPC2, SOD1, YIPF5, SLC38A2, MAP1, CALM2, PI3K reg class IA, Galpha(s)-specific peptide GPCRs, TCP1-alpha, ATP5L, TCP1-epsilon, 14-3-3, ARMCX3, ACCN3 (ASIC3), COX VIIa-2L, RAGE, 14-3-3 eta, ATP1beta subunit, SNX10
12	generation of precursor metabolites and energy	559	6.553E-19	4.257E-16	64	HMGCLL1, COX VIc, ATP5C, SUCLG1, REV-ERBalpha, UQCRQPC, ALDR, UQCRH, NDUFAB1, NDUFA1, PDH E2 subunit N6-lipoyllysine, NDUFB4, MC4R, NDUFA8, Glycogen phosphorylase, NDUFA4, SDHB, Galpha(q)-specific Class A Orphan/other GPCRs, PP1-cat gamma, NDUFB6, NDUFS4, UQCRB, ATP5E, S100, COX VIIa, Aldose reductase, NDUFB3, ATP5B, NDUFB1, PYGM, COX VIa, SUCB1, ANT, PP1-cat, UQCR10, UQCRFS1, Galpha(i)-specific amine GPCRs, NDUFS6, MDH1, COX Va, ATP5A, PDH beta, Galpha(q)-specific peptide GPCRs, NDUFA5, MRAP2, PGAM1, SCS-A, F262, GLGB, ODP2, Glutaredoxin, COX VIa-1, MPTP complex, Malin, LOXL2, SCOT, Octanoyl-holo-acp, ADHX, SLC25A4, Galpha(s)-specific peptide GPCRs, ATP5L, HXK3, COX VIIa-2, COX VIIa-2L
13	cation transport	1181	9.256E-19	5.551E-16	99	ZnT-2, SMVT, ATP5C, Endothelin-1, UQCRQPC, UQCRH, LOC153328, Pannexin-1, KCNK2, NDUFA4, ATP6V1A (70kD), SLC39A10, HCN2, Galpha(q)-specific Class A Orphan/other GPCRs, ATP5G, TUSC3, Kv3.3, TRPC5, PKC-beta, SLC25A45, SUR, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, ATP5E, KCNH5, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, ATP6V1C1, ZDH13, ATP6M, FAM38B, V-ATPase E subunit, NSF, Galpha(i)-

						specific metabotropic glutamate GPCRs, ATP5B, Dynein, axonemal, heavy chains, cPKC (conventional), ATP6V1B2, Serotonin receptor, TRPC, SLC7A5, VDAC 1, COX VIa, CLCN4, ATP6V1H, ATP5G3, NHE6, ANT, UQCR10, NDFIP2, NR3A, Clathrin heavy chain, Galpha(q)-specific amine GPCRs, UQCRFS1, GP-IB alpha, Galpha(i)-specific amine GPCRs, TRPC4, PMCA1, NCX1, HCN, CDK5, PANX2, COX Va, ATP5A, Kv9.3, Calcineurin A (catalytic), SMIT, Galpha(q)-specific peptide GPCRs, ATP6V1C, COX VIa-1, ATP6V1B, Kv4.2 channel, PKD1L1, TMS-1, MPTP complex, NKCC1, ATP6V0B, Calmodulin, ATP6V1E, Aquaporin 1, NDFIP1, SLC29A4, CaMK II delta, PKC, SUR1, HTR2A, SLC25A4, ATP1B3, CLCN5, SLC38A2, CALM2, ATP5L, 14-3-3, ACCN3 (ASIC3), COX VIIa-2L, ATP1beta subunit
14	behavior	1125	1.001E-18	5.572E-16	96	NPY, Galpha(s)-specific nucleotide-like GPCRs, GLSK, GAD1, JWA, Lgi4, PRKAR2B, MC4R, KCNK2, CNR1, Synaptotagmin IV, Synaptotagmin, CNTN1 (F3), PDE, Cystatin C, PPT1, Galpha(q)-specific Class A Orphan/other GPCRs, SHISA7, VDAC 3, G-protein beta/gamma, SDFR1, SUR, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, TORC1, CPT-1A, S100, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, ZFHX2, IDUA, CRH receptor 2, GPR176, CaMK IV, GLRA, PDE4, G-protein gamma, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, Pro-CCK, Dynein, axonemal, heavy chains, PKA-reg type II (cAMP-dependent), cPKC (conventional), Serotonin receptor, Apelin, TRPC, VDAC 1, PKA-reg (cAMP-dependent), HMDH, Substance P, GRM6, MCT1 (SLC16A1), Galpha(q)-specific amine GPCRs, Ephrin-A receptors, Galpha(i)-specific amine GPCRs, HCN, GABA-A receptor alpha-5 subunit, CDK5, PAK, Glycine receptor, Glycine receptor beta chain, Selenoprotein P, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, SLC25A46, Galpha(q)-specific peptide GPCRs, MRAP2, MEF2, APRIO, ATF/CREB, Galpha(s)-specific CRF GPCRs, ATP6V1B, Kv4.2 channel, PRNP, MPTP complex, PGRMC1, ERK1/2, PKC, SUR1, HTR2A, MEF2C, ERK2 (MAPK1), Calcineurin A (beta), Nephrocystin-4, DKK1, SOD1, FOXP1/2/4 proteins, PTCHD1, Galpha(s)-specific peptide GPCRs, OXR1, CALB1, Midkine, RAGE, ATP1beta subunit
15	regulation of muscle system process	434	2.192E-18	1.139E-15	55	HSP90, Galpha(s)-specific nucleotide-like GPCRs, Smooth muscle myosin, RNF207, Endothelin-1, ARG2, MELC, Guanylate cyclase, PDE, Guanylate cyclase alpha, RGS4, SUR, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, Galpha(q)-specific nucleotide-like GPCRs, Rho GTPase, PDE4, Myotrophin, cPKC (conventional), Serotonin receptor, TRPC, ANT, GUCY1A3,

						Galpha(q)-specific amine GPCRs, Galpha(i)-specific amine GPCRs, PMCA1, NCX1, HCN, Protein kinase G1, Calponin-1, PAK, Guanylate cyclase (alpha-1/beta-1), Calcineurin A (catalytic), Galpha(q)-specific peptide GPCRs, MAFbx, MEF2, MRLC, MPTP complex, Calmodulin, CaMK II delta, PKC, SSTR2, SUR1, SLC25A4, Guanylate Cyclase 1, soluble, MEF2C, Protein kinase G, SOD1, CALM2, FOXP1/2/4 proteins, NPNT, ATP1beta subunit, Myospryn
16	system development	6559	2.400E-18	1.169E-15	320	PLP1, Cyclin G, FBXO45, NPY, PP2A cat (alpha), PRPS1, HSP90, PAK3, PAM, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Semaphorin 3C, Alpha crystallin B, RhoN, IRF1, ILDR2, MAL2, MEGF10, PTCH2, N-chimaerin, HPCA, APJ, Smooth muscle myosin, Peroxiredoxin, Activin A, Endothelin-1, Trehalase, ARG2, T-plastin, REV-ERBalpha, BRSK2, UQCRQPC, G-protein beta, ALDR, CRTL1, RGS8, MDS028, NckAP1, Lgi4, NKIRAS1, HPCAL4, PSD2, MGF, MEPE, MELC, UNRIP, KLHL12, Synaptotagmin I, Guanylate cyclase, ARL6, KCNK2, HSP70, CNR1, MYL6, Synaptotagmin IV, CITED2, DnaJB9, Synaptotagmin, PRDX3, CNTN1 (F3), HSPA4, JMJD3, Dynein, axonemal, light chains, PDE, Cystatin C, PPT1, IGSF9B, DKK3, NCKP1 subunit, HCN2, Galpha(q)-specific Class A Orphan/other GPCRs, IMPG2, ATP5G, GPR124, KAL1, RGS4, GABA-A receptor alpha-1 subunit, UGT8, FLRT3, B3GN6, Tenascin-C, PP1-cat gamma, CEACAM, TRPC5, KIS, PAFAH gamma, PRDX1, G-protein beta/gamma, B3GN1, SDFR1, SUR, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, CPT-1A, S100, TXNRD1, AMIGO2, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, Aldose reductase, Rab-3, MTG16 (CBFA2T3), ATG9B, DNER, ZFHX2, Ephrin-A receptor 5, IDUA, IP3KA, CRH receptor 2, CacyBP(SIP), Semaphorin 5A, Tomt, CaMK IV, GLRA, ZNF499, GABA-A receptor beta-2 subunit, CECR2, Carbohydrate sulfotransferases, Rho GTPase, PDE4, Tensin 2, G-protein gamma, PRPS2, Dysferlin, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, EGF, GlyRA2, ATP5B, Pro-CCK, Dynein, axonemal, heavy chains, BMPR1A, Semaphorin 3E, LOC283174, Myotrophin, NELL1, cPKC (conventional), DLL4, Serotonin receptor, Apelin, GABA-A receptor alpha-4 subunit, TRPC, HTR5A, Osteopontin, ZNF238, SMRT, NHE6, M-Ras, CHAMP, PKA-reg (cAMP-dependent), Lingo1, ANT, PP1-cat, PDLIM2, NR3A, Cables1, ECT2, IL3RA, GRM6, Histone H2, LIPA, LRRC51, Galpha(q)-specific amine GPCRs, Ephrin-A receptors, Histone H2A, NPR3, GP-IB alpha, Galpha(i)-specific amine GPCRs, TRPC4, PMCA1, Rab-23, NCX1, HCN, Protein kinase G1, HLF, BDH,

						HSP90 beta, Anillin, TXNIP (VDUP1), COL25A1, NDUFS6, Activin beta A, GABA-A receptor alpha-5 subunit, Zeta-sarcoglycan, CDK5, PAK, BEX1, Glycine receptor, Fatty acid-binding protein, FOXP4, MAML1, SOHLH1, IZUMO1, ASAH, LPPR4, DYNLT, BRK, Glycine receptor beta chain, Nek8, Selenoprotein P, RTL1, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, STARD7, Cyclin G1, SLC25A46, Glyoxalase I, SMIT, FBI-1 (Pokemon), Galpha(q)-specific peptide GPCRs, Histone H2B, NCOA4 (ARA70), Creatine kinase, DSCAML1, B-FABP, DYNLL, Patched, XK, MEF2, HNMT, MEK4/7, Peg10, ACSL4, CEACAM1, ATF/CREB, RAI1, FN14(TNFRSF12A), Trim45, G-protein beta-4, FEM1B, Acyl-CoA synthetase, PP2A catalytic, MRLC, eIF4A, BMI-1, SNAPs, DLC1 (Dynein LC8a), Galpha(s)-specific CRF GPCRs, ALAS1, ATP6V1B, PKD1L1, HSPC138, MPTP complex, ENC1, RHEB2, NKCC1, WDT2, Calmodulin, PGRMC1, Apo-2L(TNFSF10), LOXL2, Endophilin A1, BTBD1, Activin, Aquaporin 1, NME5, CLIC4, Calcyclin, Syntenin 1, SCOT, KCRS, ERK1/2, UGCG, NFIC, CaMK II delta, HSC70, PI3K reg class IA (p55-gamma), PKC, SSTR2, SUR1, SLC25A4, K-cadherin (CDH6), MEF2C, SULT4A1, Protein kinase G, ERK2 (MAPK1), Calcineurin A (beta), LISCH7, Ran, MEK4(MAP2K4), PRKAR1A, IGFALS, UFC1, Nephrocystin-4, DKK1, SSTR1, Guanine deaminase, PRPS, SOD1, KIAA1024, PPP4R2, SLC38A2, FSTL5, CALM2, Cyclophilin A, FOXP1/2/4 proteins, Aggrecanase-2, PI3K reg class IA, PTCHD1, Galpha(s)-specific peptide GPCRs, ACTR3, ATP6AP2, CALB1, Pcdh19, CD166, NF-I, NPNT, Neuroserpin, Midkine, IRS6(DOK5), ARP3, 14-3-3, RAGE, 14-3-3 eta, ATP1beta subunit, SNX10
17	regulation of protein transport	873	5.115E-18	2.346E-15	81	PP2A cat (alpha), HSP90, PAM, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, HPCA, UBL5, REV-ERBalpha, BRSK2, HSP70, CNR1, Synaptotagmin IV, Synaptotagmin, Thioredoxin, PDE, Galpha(q)-specific Class A Orphan/other GPCRs, ORP-family, KIS, SUR, Galpha(i)-specific peptide GPCRs, CPT-1A, Galpha(q)-specific nucleotide-like GPCRs, Ephrin-A receptor 5, IDUA, CRH receptor 2, Tomt, CaMK IV, LPL1, Rho GTPase, PDE4, Rap1GDS1, EGF, PPID, HMDH, NDFIP2, ECT2, MCT1 (SLC16A1), LRRC51, Galpha(q)-specific amine GPCRs, Ephrin-A receptors, Galpha(i)-specific amine GPCRs, Rab-23, HSP90 beta, CDK5, PAK, FLJ32001, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, Galpha(q)-specific peptide GPCRs, Azi1, DYNLL, APRIO, ACSL4, F262, Hdj-2, DelGIP1, Acyl-CoA synthetase, PP2A catalytic, Glutaredoxin, DLC1 (Dynein LC8a), Galpha(s)-specific CRF GPCRs, PRNP, NKCC1, Activin, NDFIP1, SCOT, ERK1/2, HSC70, PKC, SUR1, ERK2 (MAPK1), Calcineurin A (beta), Ran, MPC2,

						Cyclophilin A, PI3K reg class IA, ACTR3, SIAH3, ARP3, 14-3-3, Glutaredoxin 1
18	synaptic signaling	769	6.011E-18	2.512E-15	75	PLP1, NPY, Cadherin 8, Galpha(s)-specific nucleotide-like GPCRs, GLSK, GAD1, G-protein beta, RGS8, Importin (karyopherin)-alpha, Synaptotagmin I, Guanylate cyclase, CNR1, Synaptotagmin IV, Synaptotagmin, PDE, CNIH2, PPT1, Karyopherin alpha 2, Guanylate cyclase alpha, VDAC 3, GABA-A receptor alpha-1 subunit, GUCY1B1, G-protein beta/gamma, SDFR1, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, TORC1, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, Rab-3, GPR176, CaMK IV, GLRA, GABA-A receptor beta-2 subunit, SYP, Rho GTPase, Galpha(i)-specific metabotropic glutamate GPCRs, GlyRA2, cPKC (conventional), Serotonin receptor, GABA-A receptor alpha-4 subunit, HTR5A, VDAC 1, GUCY1A3, Substance P, GRM6, Galpha(q)-specific amine GPCRs, Galpha(i)-specific amine GPCRs, GABA-A receptor alpha-5 subunit, CDK5, PAK, Guanylate cyclase (alpha-1/beta-1), Guanylate cyclase beta, Glycine receptor, GABA-A receptor alpha-3 subunit, Glycine receptor beta chain, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, Galpha(q)-specific peptide GPCRs, MEF2, NAPB, SNAPs, Kv4.2 channel, MPTP complex, FLJ45455, Syntenin 1, ERK1/2, PKC, HTR2A, Guanylate Cyclase 1, soluble, MEF2C, ERK2 (MAPK1), PTCHD1, Galpha(s)-specific peptide GPCRs, GAD2
19	establishment of localization	5405	6.123E-18	2.512E-15	276	HSP90, PAM, Galpha(s)-specific nucleotide-like GPCRs, TMEM87B, G3BP2, ILDR2, ZnT-2, MAL2, Rab-3B, SLC35E2B, SMVT, MEGF10, ZH11B, Tubulin alpha 1A, ATP5C, Activin A, Endothelin-1, AP-1 gamma subunits, BRSK2, UQCRQPC, JWA, UQCRH, TMC4, Rab-6A, Importin (karyopherin)-alpha, ANKRD50, DNAH1, AP1G2, LOC153328, Pannexin-1, PSD2, TIP47, MC4R, KLHL12, Synaptotagmin I, Guanylate cyclase, ARL6, KCNK2, HSP70, Synaptotagmin IV, Tim17, Synaptotagmin, NDUFA4, ATP6V1A (70kD), HSPA4, Septin 1, Dynein, axonemal, light chains, CNIH2, PPT1, SLC39A10, Karyopherin alpha 2, HCN2, Galpha(q)-specific Class A Orphan/other GPCRs, LMF1, ATP5G, RAB39B, VDAC 3, 14-3-3 beta/alpha, GABA-A receptor alpha-1 subunit, TUSC3, Kv3.3, ORP-family, CEACAM, TRPC5, PKC-beta, TCP1-theta, ELMO3, SLC25A45, SUR, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, ATP5E, CPT-1A, S100, Rab-6, ORP8, KCNH5, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, ATP6V1C1, ZDH13, ATP6M, Rab-3, ATG9B, DNER, FAM38B, APOL3, LAPTM4B,

						SLC2A13, V-ATPase E subunit, NSF, CaMK IV, GLRA, GABA-A receptor beta-2 subunit, CECR2, SYP, TIMM17, Rho GTPase, Dysferlin, Galpha(i)-specific metabotropic glutamate GPCRs, Secretogranin V, GlyRA2, ATP5B, CED-6, XKR4, Dynein, axonemal, heavy chains, cPKC (conventional), ATP6V1B2, AP3S1, Serotonin receptor, CHMP5, Apelin, AP complex 2 small (sigma) chain, GABA-A receptor alpha-4 subunit, Rab-27B, PPID, TRPC, SLC7A5, ACTR10, VDAC 1, COX VIa, CLCN4, ATP6V1H, ATP5G3, Slp5, SMRT, NHE6, Rab-3C, ANT, TCP1-delta, UQCR10, NDFIP2, NR3A, HSBP1, VTA1, ECT2, Clathrin heavy chain, AP-3 sigma subunits, StARD4, CalDAG-GEFII, MCT1 (SLC16A1), TMEM14A, Galpha(q)-specific amine GPCRs, UQCRFS1, HMP19, NPR3, GP-IB alpha, Galpha(i)-specific amine GPCRs, TRPC4, PMCA1, Rab-23, NCX1, SLBP, HCN, CAP1, TXNIP (VDUP1), Activin beta A, GABA-A receptor alpha-5 subunit, CDK5, PANX2, PAK, SYT16, TCP1-eta, Glycine receptor, Fatty acid-binding protein, HINT, TOM22, GABA-A receptor alpha-3 subunit, LPPR4, DYNLT, SLC16A13, COX Va, ATP5A, Glycine receptor beta chain, Carbonic anhydrase XII, Kv9.3, Calcineurin A (catalytic), STARD7, SLC25A46, SEC23A, SMIT, Galpha(q)-specific peptide GPCRs, ATP6V1C, NCOA4 (ARA70), Tubulin alpha, ACAP1(CENTB1), TBC1D10C, B-FABP, Azi1, DYNLL, XK, NAPB, Sec23, Peg10, ACSL4, CEACAM1, RANBP6, ATF/CREB, Hdj-2, Acyl-CoA synthetase, SNX7, ARRDC2, ZFAND2A, SNAPs, DLC1 (Dynein LC8a), Galpha(s)-specific CRF GPCRs, LAMP2, COX VIa-1, TMEM87A, TSNARE1, ATP6V1B, Kv4.2 channel, PKD1L1, HSPC138, SNX16, TMS-1, MPTP complex, NKCC1, Neurocalcin delta, ATP6V0B, WDT2, Calmodulin, ATP6V1E, LOXL2, Endophilin A1, Activin, C1orf43, Aquaporin 1, NDFIP1, NME5, CLIC4, Calcyclin, Syntenin 1, ERK1/2, UGCG, SLC29A4, CaMK II delta, HSC70, ARL5, SLC35A5, PKC, SUR1, HTR2A, SLC25A4, ATP1B3, ERK2 (MAPK1), Calcineurin A (beta), LISCH7, Ran, CLCN5, TRIM23, MPC2, SOD1, YIPF5, SLC38A2, MAP1, CALM2, PI3K reg class IA, Galpha(s)-specific peptide GPCRs, TCP1-alpha, ATP5L, ACTR3, TCP1-epsilon, NPNT, ARP3, 14-3-3, ARMCX3, ACCN3 (ASIC3), COX VIIa-2L, RAGE, 14-3-3 eta, ATP1beta subunit, SNX10
20	inorganic cation transmembrane transport	791	8.307E-18	3.238E-15	76	ZnT-2, ATP5C, Endothelin-1, UQCRQPC, UQCRH, Pannexin-1, KCNK2, NDUFA4, ATP6V1A (70kD), SLC39A10, HCN2, ATP5G, TUSC3, Kv3.3, TRPC5, SUR, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, ATP5E, KCNH5, TRPV1, COX VIIa, ATP6V1C1, ZDH13, ATP6M, V-ATPase E subunit, Galpha(i)-specific metabotropic glutamate GPCRs, ATP5B, Dynein, axonemal, heavy chains, ATP6V1B2,

						Serotonin receptor, TRPC, VDAC 1, COX VIa, CLCN4, ATP6V1H, ATP5G3, NHE6, ANT, UQCR10, NR3A, Galpha(q)-specific amine GPCRs, UQCRFS1, GP-IB alpha, Galpha(i)-specific amine GPCRs, TRPC4, PMCA1, NCX1, HCN, COX Va, ATP5A, Kv9.3, Galpha(q)-specific peptide GPCRs, ATP6V1C, COX VIa-1, ATP6V1B, Kv4.2 channel, PKD1L1, MPTP complex, NKCC1, ATP6V0B, Calmodulin, ATP6V1E, Aquaporin 1, SUR1, HTR2A, SLC25A4, ATP1B3, CLCN5, CALM2, ATP5L, ACCN3 (ASIC3), COX VIIa-2L, ATP1beta subunit
21	small molecule metabolic process	2145	9.364E-18	3.319E-15	143	PLP1, PRPS1, PAM, HMGCLL1, GLSK, GAD1, ATP5C, SUCLG1, ELOVL5, Esterase D, Endothelin-1, SULT1A1, ARG2, SC5D, ALDR, SC4MOL, NDUFAB1, DCMC, PDH E2 subunit N6-lipoyllysine, PRKAR2B, Guanylate cyclase, NUDT4P1, GIMAP7, Thioredoxin, ATP6V1A (70kD), PDE, PPT1, SDHB, Guanylate cyclase alpha, ATP5G, TPH2, GUCY1B1, Exostosin-like 2, ORP-family, PKC-beta, Galpha(i)-specific peptide GPCRs, FUT2, ATP5E, CPT-1A, TXNRD1, PIMT, PDK3, Aldose reductase, IP3KA, AMDHD2, InsP6 kinase 3, Carbohydrate sulfotransferases, LPL1, Rho GTPase, PDE4, PRPS2, Dysferlin, TMEM86B, ATP5B, SYTC, B3GALTL, MMADHC, PKA-reg type II (cAMP-dependent), cPKC (conventional), ELOVL4, Serotonin receptor, ADSS, PDK4, VDAC 1, SUCB1, Osteopontin, ATP5G3, ABHD10, KCY, PKA-reg (cAMP-dependent), HMDH, GUCY1A3, LIPA, Galpha(q)-specific amine GPCRs, Ephrin-A receptors, Rab-23, NDUFS6, Guanylate cyclase (alpha-1/beta-1), Guanylate cyclase beta, Fatty acid-binding protein, HINT, ENPP4, MDH1, ASAH, SPSY, ATP5A, Carbonic anhydrase XII, Glyoxalase I, SMIT, PDH beta, Galpha(q)-specific peptide GPCRs, Tubulin alpha, DCK, NUDT4, PGAM1, HNMT, SCS-A, ACSL4, RENBP, F262, ATF/CREB, ODP2, Acyl-CoA synthetase, IDI1, OAZIN, Glutaredoxin, KAD6, ATP6V1B, Protein kinase G 2, TMS-1, GKP3, MPTP complex, PDE4A, LPL, NME5, SCOT, Octanoyl-holo-acp, ADHX, ERK1/2, AATC, PKC, PMM2, Guanylate Cyclase 1, soluble, Protein kinase G, RIFK, ERK2 (MAPK1), Ran, OAT, IMPA1, MPC2, Guanine deaminase, PRPS, GDE1, PI3K reg class IA, DCoHM, ATP5L, CALB1, GAD2, PGM2L1, HXK3, ACOXL, Glutaredoxin 1, CMAS
22	cation transmembrane transport	882	9.367E-18	3.319E-15	81	ZnT-2, ATP5C, Endothelin-1, UQCRQPC, UQCRH, LOC153328, Pannexin-1, KCNK2, NDUFA4, ATP6V1A (70kD), SLC39A10, HCN2, ATP5G, TUSC3, Kv3.3, TRPC5, SLC25A45, SUR, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, ATP5E, KCNH5, TRPV1, COX VIIa, ATP6V1C1, ZDH13, ATP6M, FAM38B, V-ATPase E subunit, Galpha(i)-specific metabotropic glutamate GPCRs, ATP5B, Dynein,

						axonemal, heavy chains, ATP6V1B2, Serotonin receptor, TRPC, SLC7A5, VDAC 1, COX VIa, CLCN4, ATP6V1H, ATP5G3, NHE6, ANT, UQCR10, NR3A, Galpha(q)-specific amine GPCRs, UQCRFS1, GP-IB alpha, Galpha(i)-specific amine GPCRs, TRPC4, PMCA1, NCX1, HCN, COX Va, ATP5A, Kv9.3, Galpha(q)-specific peptide GPCRs, ATP6V1C, COX VIa-1, ATP6V1B, Kv4.2 channel, PKD1L1, MPTP complex, NKCC1, ATP6V0B, Calmodulin, ATP6V1E, Aquaporin 1, SLC29A4, SUR1, HTR2A, SLC25A4, ATP1B3, CLCN5, CALM2, ATP5L, ACCN3 (ASIC3), COX VIIa-2L, ATP1beta subunit
23	regulation of ion transport	1107	1.016E-17	3.442E-15	93	PLP1, PP2A cat (alpha), Galpha(s)-specific nucleotide-like GPCRs, Rab-3B, HPCA, APJ, RNF207, Endothelin-1, ARG2, NETO2, G-protein beta, JWA, Synaptotagmin I, HSP70, CNR1, Synaptotagmin IV, Synaptotagmin, CNTN1 (F3), NDUFA4, PDE, CNIH2, HCN2, Galpha(q)-specific Class A Orphan/other GPCRs, SHISA7, RGS4, Kv3.3, PKC-beta, G-protein beta/gamma, NET6(TSPAN13), SUR, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, S100, KCNH5, Galpha(q)-specific nucleotide-like GPCRs, Rab-3, CRH receptor 2, Rho GTPase, PDE4, Dysferlin, Galpha(i)-specific metabotropic glutamate GPCRs, EGF, Pro-CCK, cPKC (conventional), Serotonin receptor, TRPC, VDAC 1, ANT, GRM6, Galpha(q)-specific amine GPCRs, Galpha(i)-specific amine GPCRs, TRPC4, PMCA1, NCX1, HCN, Protein kinase G1, CDK5, Kv9.3, Galpha(i)-specific cannabis GPSRs, Galpha(q)-specific peptide GPCRs, MEF2, APRIO, ACSL4, ATF/CREB, Acyl-CoA synthetase, PP2A catalytic, Glutaredoxin, Galpha(s)-specific CRF GPCRs, Kv4.2 channel, Protein kinase G 2, PRNP, MPTP complex, NKCC1, Calmodulin, FLJ45455, STAC2, CLIC4, CaMK II delta, PKC, SUR1, HTR2A, SLC25A4, ATP1B3, MEF2C, Protein kinase G, CALM2, 14-3-3, RAGE, 14-3-3 eta, ATP1beta subunit, Glutaredoxin 1
24	energy derivation by oxidation of organic compounds	363	1.221E-17	3.966E-15	49	COX VIc, ATP5C, SUCLG1, REV-ERBalpha, UQCRQPC, UQCRH, NDUFAB1, NDUFA1, PDH E2 subunit N6-lipoyllysine, NDUFB4, MC4R, NDUFA8, Glycogen phosphorylase, NDUFA4, SDHB, PP1-cat gamma, NDUFB6, NDUFS4, UQCRB, ATP5E, S100, COX VIIa, NDUFB3, ATP5B, NDUFB1, PYGM, COX VIa, SUCB1, PP1-cat, UQCR10, UQCRFS1, Galpha(i)-specific amine GPCRs, NDUFS6, MDH1, COX Va, ATP5A, PDH beta, NDUFA5, MRAP2, SCS-A, GLGB, ODP2, COX VIa-1, Malin, Octanoyl-holo-acp, Galpha(s)-specific peptide GPCRs, ATP5L, COX VIIa-2, COX VIIa-2L
25	ion transport	1658	1.468E-17	4.578E-15	120	ZnT-2, SMVT, ATP5C, Endothelin-1, UQCRQPC, JWA, UQCRH, TMC4, LOC153328, Pannexin-1, KCNK2, NDUFA4, ATP6V1A (70kD), SLC39A10, HCN2, Galpha(q)-specific Class A Orphan/other

						GPCRs, ATP5G, VDAC 3, GABA-A receptor alpha-1 subunit, TUSC3, Kv3.3, CEACAM, TRPC5, PKC-beta, SLC25A45, SUR, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, ATP5E, S100, KCNH5, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, COX VIIa, ATP6V1C1, ZDH13, ATP6M, FAM38B, V-ATPase E subunit, NSF, GLRA, GABA-A receptor beta-2 subunit, Galpha(i)-specific metabotropic glutamate GPCRs, GlyRA2, ATP5B, Dynein, axonemal, heavy chains, cPKC (conventional), ATP6V1B2, Serotonin receptor, GABA-A receptor alpha-4 subunit, TRPC, SLC7A5, VDAC 1, COX VIa, CLCN4, ATP6V1H, ATP5G3, NHE6, ANT, UQCR10, NDFIP2, NR3A, Clathrin heavy chain, MCT1 (SLC16A1), Galpha(q)-specific amine GPCRs, UQCRFS1, GP-IB alpha, Galpha(i)-specific amine GPCRs, TRPC4, PMCA1, NCX1, HCN, GABA-A receptor alpha-5 subunit, CDK5, PANX2, PAK, Glycine receptor, GABA-A receptor alpha-3 subunit, SLC16A13, COX Va, ATP5A, Glycine receptor beta chain, Kv9.3, Calcineurin A (catalytic), SMIT, Galpha(q)-specific peptide GPCRs, ATP6V1C, CEACAM1, COX VIa-1, ATP6V1B, Kv4.2 channel, PKD1L1, TMS-1, MPTP complex, NKCC1, ATP6V0B, Calmodulin, ATP6V1E, Aquaporin 1, NDFIP1, CLIC4, Calcyclin, SLC29A4, CaMK II delta, PKC, SUR1, HTR2A, SLC25A4, ATP1B3, CLCN5, MPC2, SLC38A2, CALM2, ATP5L, 14-3-3, ACCN3 (ASIC3), COX VIIa-2L, ATP1beta subunit
26	response to organic cyclic compound	1988	2.065E-17	6.110E-15	135	PP2A cat (alpha), HSP90, PAK3, PAM, Galpha(s)-specific nucleotide-like GPCRs, Alpha crystallin B, IRF1, HPCA, Activin A, Endothelin-1, SULT1A1, ARG2, DUOX1, REV-ERBalpha, P2Y11, G-protein beta, JWA, Pannexin-1, TIP47, PRKAR2B, Guanylate cyclase, HSP70, CNR1, Glycogen phosphorylase, Thioredoxin, PDE, Cystatin C, HCN2, Guanylate cyclase alpha, Galpha(q)-specific Class A Orphan/other GPCRs, ATP5G, TPH2, RGS4, GABA-A receptor alpha-1 subunit, ORP-family, Tenascin-C, PKC-beta, G-protein beta/gamma, SUR, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, CPT-1A, S100, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, Ephrin-A receptor 5, CRH receptor 2, GABA-A receptor beta-2 subunit, Rho GTPase, PDE4, G-protein gamma, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, ATP5B, PKA-reg type II (cAMP-dependent), cPKC (conventional), Serotonin receptor, ADSS, TRPC, HTR5A, PYGM, Osteopontin, SMRT, PKA-reg (cAMP-dependent), TReP-132, HMDH, GUCY1A3, Substance P, Histone H2, MCT1 (SLC16A1), Galpha(q)-specific amine GPCRs, Ephrin-A receptors, Histone H2A, HMP19, Galpha(i)-specific amine GPCRs, PMCA1, NCX1, HCN, BDH, HSP90 beta, TXNIP (VDUP1), Activin beta A, CDK5, PAK,

						Guanylate cyclase (alpha-1/beta-1), Fatty acid-binding protein, ATP5A, Galpha(i)-specific cannabis GPSRs, Galpha(q)-specific peptide GPCRs, H2AFZ, NCOA4 (ARA70), MAFbx, Patched, MEF2, HNMT, ATF/CREB, Hdj-2, Acyl-CoA synthetase, PP2A catalytic, IDI1, AP-4, BMI-1, Glutaredoxin, Galpha(s)-specific CRF GPCRs, ALAS1, Calmodulin, Activin, Aquaporin 1, ERK1/2, AATC, HSC70, PKC, SSTR2, HTR2A, ARPP-19, Guanylate Cyclase 1, soluble, MEF2C, ERK2 (MAPK1), Ran, IGFALS, SSTR1, SOD1, CALM2, FOXP1/2/4 proteins, PI3K reg class IA, ACTR3, NF-I, Midkine, ARP3, 14-3-3, RAGE, 14-3-3 eta, Glutaredoxin 1
27	multicellular organism development	7381	2.138E-17	6.110E-15	346	PLP1, Cyclin G, FBXO45, NPY, FAM3C, PP2A cat (alpha), PRPS1, HSP90, PAK3, PAM, Cadherin 8, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Semaphorin 3C, Alpha crystallin B, RhoN, IRF1, ILDR2, MAL2, SLC35E2B, MEGF10, PTCH2, N-chimaerin, HPCA, APJ, Smooth muscle myosin, EDIL3, Peroxiredoxin, Activin A, Endothelin-1, Trehalase, ARG2, T-plastin, DUOX1, REV-ERBalpha, BRSK2, UQCRQPC, G-protein beta, ALDR, CRTL1, RGS8, MDS028, NckAP1, Lgi4, NKIRAS1, HPCAL4, PSD2, MGF, MEPE, MELC, UNRIP, KLHL12, Synaptotagmin I, Guanylate cyclase, ARL6, KCNK2, HSP70, DDX3Y, CNR1, MYL6, Synaptotagmin IV, CITED2, DnaJB9, Synaptotagmin, PRDX3, CNTN1 (F3), HSPA4, JMJD3, Dynein, axonemal, light chains, PDE, Cystatin C, PPT1, IGSF9B, DKK3, NCKP1 subunit, HCN2, Galpha(q)-specific Class A Orphan/other GPCRs, IMPG2, ATP5G, GPR124, KAL1, PTPN18, RGS4, GABA-A receptor alpha-1 subunit, UGT8, FLRT3, B3GN6, Tenascin-C, PP1-cat gamma, CEACAM, ODF3, TRPC5, KIS, PAFAH gamma, PRDX1, G-protein beta/gamma, B3GN1, SDFR1, SUR, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, CPT-1A, S100, TXNRD1, AMIGO2, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, Aldose reductase, Rab-3, MTG16 (CBFA2T3), ATG9B, DNER, ZFHX2, Ephrin-A receptor 5, IDUA, IP3KA, CRH receptor 2, CacyBP(SIP), Semaphorin 5A, Tomt, CaMK IV, GLRA, DKK2, ZNF499, GABA-A receptor beta-2 subunit, CECR2, Carbohydrate sulfotransferases, Rho GTPase, PDE4, Tensin 2, G-protein gamma, PRPS2, Dysferlin, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, ZNF267, A830006F12Rik, PP4R4, EGF, GlyRA2, ATP5B, Pro-CCK, Dynein, axonemal, heavy chains, BMPR1A, Semaphorin 3E, LOC283174, Myotrophin, NELL1, cPKC (conventional), DLL4, Serotonin receptor, Apelin, GABA-A receptor alpha-4 subunit, TRPC, HTR5A, Sp8, WIF1, Osteopontin, ZNF238, SMRT, NHE6, M-Ras, CREB4, CHAMP, PKA-reg (cAMP-dependent), Lingo1, ANT, PP1-cat,

						HMDH, PDLIM2, NR3A, HSBP1, Cables1, ECT2, IL3RA, GRM6, Histone H2, LIPA, LRRC51, Galpha(q)-specific amine GPCRs, Ephrin-A receptors, Histone H2A, NPR3, GP-IB alpha, Galpha(i)-specific amine GPCRs, TRPC4, PMCA1, Rab-23, NCX1, HCN, Protein kinase G1, HLF, BDH, HSP90 beta, Anillin, TXNIP (VDUP1), COL25A1, NDUFS6, Activin beta A, GABA-A receptor alpha-5 subunit, Zeta-sarcoglycan, CDK5, PAK, BEX1, Glycine receptor, Fatty acid-binding protein, FOXP4, MAML1, SOHLH1, IZUMO1, GTL3, ASAH, LPPR4, DYNLT, BRK, ATP5A, Glycine receptor beta chain, Nek8, Selenoprotein P, RTL1, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, STARD7, Cyclin G1, SLC25A46, Glyoxalase I, SMIT, FBI-1 (Pokemon), Galpha(q)-specific peptide GPCRs, H2AFZ, Histone H2B, NCOA4 (ARA70), WDR47, Creatine kinase, DSCAML1, B-FABP, Azi1, DYNLL, Patched, XK, MEF2, HNMT, MEK4/7, Peg10, ACSL4, CEACAM1, ATF/CREB, RAI1, FN14(TNFRSF12A), Trim45, G-protein beta-4, FEM1B, Acyl-CoA synthetase, PP2A catalytic, MRLC, eIF4A, BMI-1, SNAPs, DLC1 (Dynein LC8a), Galpha(s)-specific CRF GPCRs, ALAS1, ATP6V1B, PKD1L1, HSPC138, MPTP complex, ENC1, RHEB2, NKCC1, WDT2, Calmodulin, PGRMC1, Apo-2L(TNFSF10), LOXL2, Endophilin A1, BTBD1, Activin, C1orf43, Aquaporin 1, NME5, CLIC4, Calcyclin, Syntenin 1, SCOT, KCRS, ERK1/2, UGCG, NFIC, CaMK II delta, HSC70, PI3K reg class IA (p55-gamma), PKC, SSTR2, SUR1, SLC25A4, K-cadherin (CDH6), MEF2C, SULT4A1, Protein kinase G, ERK2 (MAPK1), Calcineurin A (beta), LISCH7, Ran, MEK4(MAP2K4), DACH2, PRKAR1A, IGFALS, UFC1, Nephrocystin-4, DKK1, SSTR1, Guanine deaminase, PRPS, SOD1, KIAA1024, PPP4R2, SLC38A2, SAP102, FSTL5, CALM2, Cyclophilin A, FOXP1/2/4 proteins, Aggrecanase-2, PI3K reg class IA, PTCHD1, Galpha(s)-specific peptide GPCRs, ACTR3, ATP6AP2, CALB1, Pcdh19, CD166, DRIL2, NF-I, NPNT, Neuroserpin, Midkine, IRS6(DOK5), ARP3, 14-3-3, RAGE, 14-3-3 eta, ATP1beta subunit, SNX10
28	regulation of molecular function	4409	2.230E-17	6.110E-15	236	Cyclin G, PP2A cat (alpha), HSP90, PAK3, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Alpha crystallin B, G3BP2, N-chimaerin, HPCA, RNF207, Peroxiredoxin, Endothelin-1, ARG2, GSKIP, NETO2, BRSK2, P2Y11, G-protein beta, JWA, Rab-6A, RGS8, BTBD12, CDC18L (CDC6), MOBKL1A, PSD2, MGF, PRKAR2B, MELC, NPFF receptor 2, UNRIP, HSP70, DDX3Y, CNR1, MAPBPIP, PPM1E, PRDX3, Thioredoxin, NDUFA4, HSPA4, Dynein, axonemal, light chains, PDE, Cystatin C, CNIH2, PPT1, SLC39A10, DKK3, NCKP1 subunit, Galpha(q)-specific Class A Orphan/other GPCRs, LMF1, SHISA7, KAL1, Aha1, RGS4, 14-3-3

						beta/alpha, ORP-family, Myopodin, CEACAM, PKC-beta, G-protein beta/gamma, SUR, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, TORC1, S100, Rab-6, ORP8, Galpha(q)-specific nucleotide-like GPCRs, TIP41, Rab-3, Ephrin-A receptor 5, CRH receptor 2, DKK2, DOK7, Rho GTPase, PDE4, G-protein gamma, SOCS6, Dysferlin, Rap1GDS1, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, PP4R4, Secretogranin V, EGF, Pro-CCK, BMPR1A, MMD, PKA-reg type II (cAMP-dependent), Myotrophin, CAP2, cPKC (conventional), Serotonin receptor, TRPC, COX VIa, ATP6V1H, SMRT, CysLT2 receptor, RGS11, PKA-reg (cAMP-dependent), ANT, PP1-cat, HMDH, TCP1-delta, NDFIP2, KIAA1110, ECT2, HBXIP, PSMD10 (Gankyrin), MID1IP1, CHTF18, CalDAG-GEFII, ARHGAP18, Galpha(q)-specific amine GPCRs, Ephrin-A receptors, NPR3, Galpha(i)-specific amine GPCRs, CCNI2, NCX1, HCN, Protein kinase G1, CAP1, HSP90 beta, TXNIP (VDUP1), CDK5, PAK, FLJ32001, BEX1, Fatty acid-binding protein, FOXP4, IZUMO1, DYNLT, SPOCK3, BEX2, eIF4A2, BRK, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, Cyclin G1, SEC23A, SMIT, FBI-1 (Pokemon), Galpha(q)-specific peptide GPCRs, Creatine kinase, ACAP1(CENTB1), TBC1D10C, DYNLL, Patched, MEF2, INCA1, NAPB, Sec23, APRIO, MEK4/7, RENBP, F262, CEACAM1, ATF/CREB, Hdj-2, DelGIP1, FEM1B, Acyl-CoA synthetase, PP2A catalytic, AP-4, eIF4A, BMI-1, SNAPs, OAZIN, eIF2S1, Glutaredoxin, DLC1 (Dynein LC8a), Galpha(s)-specific CRF GPCRs, COX VIa-1, PRNP, DNAJA2, TMS-1, MPTP complex, Malin, CAB39L, Calmodulin, DIRAS2, SUMO-3, Apo-2L(TNFSF10), FLJ45455, BTBD1, STAC2, SIPAR, Aquaporin 1, NDFIP1, Securin, ERK1/2, CaMK II delta, HSC70, PI3K reg class IA (p55-gamma), PKC, SUR1, HTR2A, SLC25A4, ATP1B3, ARPP-19, MEF2C, Protein kinase G, RIFK, ERK2 (MAPK1), Ran, MEK4(MAP2K4), PRKAR1A, TRIM23, DKK1, PARM-1, SOD1, TFIIB, PPP4R2, SAP102, MAP1, CALM2, Cyclophilin A, FOXP1/2/4 proteins, PI3K reg class IA, Galpha(s)-specific peptide GPCRs, TCP1-alpha, ACTR3, CALML6, NF-I, NPNT, Neuroserpin, NRBF2, ARP3, 14-3-3, RAGE, 14-3-3 eta, ATP1beta subunit, Myospryn, Glutaredoxin 1
29	aerobic respiration	211	2.285E-17	6.110E-15	37	COX VIc, ATP5C, SUCLG1, UQCRQPC, UQCRH, NDUFAB1, NDUFA1, PDH E2 subunit N6-lipoyllysine, NDUFB4, NDUFA8, NDUFA4, SDHB, NDUFB6, NDUFS4, UQCRB, ATP5E, COX VIIa, NDUFB3, ATP5B, NDUFB1, COX VIa, SUCB1, UQCR10, UQCRFS1, NDUFS6, MDH1, COX Va, ATP5A, PDH beta, NDUFA5, SCS-A, ODP2, COX VIa-1, Octanoyl-holo-acp, ATP5L, COX VIIa-2, COX VIIa-2L

30	regulation of secretion by cell	1045	2.351E-17	6.110E-15	89	NPY, PAM, Galpha(s)-specific nucleotide-like GPCRs, Rab-3B, Activin A, Endothelin-1, AP-1 gamma subunits, REV-ERBalpha, BRSK2, Synaptotagmin I, CNR1, Synaptotagmin IV, Synaptotagmin, Septin 1, PDE, NCKP1 subunit, Galpha(q)-specific Class A Orphan/other GPCRs, Kv3.3, ORP-family, CEACAM, PKC-beta, SUR, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, CPT-1A, Galpha(q)-specific nucleotide-like GPCRs, Rab-3, Ephrin-A receptor 5, IDUA, CRH receptor 2, NSF, GLRA, SYP, Rho GTPase, PDE4, Rap1GDS1, Galpha(i)-specific metabotropic glutamate GPCRs, Secretogranin V, EGF, Pro-CCK, cPKC (conventional), Serotonin receptor, Apelin, Rab-27B, PPID, Osteopontin, Rab-3C, HMDH, NR3A, Substance P, MCT1 (SLC16A1), Galpha(q)-specific amine GPCRs, Ephrin-A receptors, Galpha(i)-specific amine GPCRs, Protein kinase G1, Activin beta A, CDK5, Glycine receptor, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, Galpha(q)-specific peptide GPCRs, DYNLL, MEF2, ACSL4, F262, CEACAM1, ATF/CREB, DelGIP1, Acyl-CoA synthetase, Glutaredoxin, DLC1 (Dynein LC8a), Galpha(s)-specific CRF GPCRs, NKCC1, Calmodulin, NELL2, Activin, Syntenin 1, SCOT, PKC, SUR1, HTR2A, MEF2C, Protein kinase G, Calcineurin A (beta), MPC2, CALM2, Cyclophilin A, Glutaredoxin 1
31	regulation of system process	1019	4.781E-17	1.202E-14	87	HSP90, Galpha(s)-specific nucleotide-like GPCRs, GLSK, Smooth muscle myosin, RNF207, Activin A, Endothelin-1, ARG2, NETO2, MELC, Guanylate cyclase, HSP70, PDE, CNIH2, IGSF9B, Guanylate cyclase alpha, Galpha(q)-specific Class A Orphan/other GPCRs, SHISA7, RGS4, SUR, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, S100, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, ZFHX2, CRH receptor 2, GLRA, Rho GTPase, PDE4, Galpha(i)-specific metabotropic glutamate GPCRs, Pro-CCK, LOC283174, Myotrophin, cPKC (conventional), Serotonin receptor, Apelin, TRPC, PKA-reg (cAMP-dependent), ANT, HMDH, GUCY1A3, Substance P, Galpha(q)-specific amine GPCRs, Galpha(i)-specific amine GPCRs, PMCA1, NCX1, HCN, Protein kinase G1, Calponin-1, Activin beta A, PAK, Guanylate cyclase (alpha-1/beta-1), Glycine receptor, Fatty acid-binding protein, Calcineurin A (catalytic), Galpha(q)-specific peptide GPCRs, MAFbx, MEF2, MRLC, Galpha(s)-specific CRF GPCRs, MPTP complex, Calmodulin, FLJ45455, Activin, Aquaporin 1, CaMK II delta, PKC, SSTR2, SUR1, HTR2A, SLC25A4, Guanylate Cyclase 1, soluble, MEF2C, Protein kinase G, SOD1, CALM2, FOXP1/2/4 proteins, PI3K reg class IA, Galpha(s)-specific peptide GPCRs, NPNT, 14-3-3, RAGE, ATP1beta subunit, Myospryn

32	regulation of secretion	1159	6.467E-17	1.576E-14	94	NPY, PAM, Galpha(s)-specific nucleotide-like GPCRs, Rab-3B, Activin A, Endothelin-1, AP-1 gamma subunits, REV-ERBalpha, BRSK2, Synaptotagmin I, Guanylate cyclase, CNR1, Synaptotagmin IV, Synaptotagmin, Septin 1, PDE, NCKP1 subunit, Galpha(q)-specific Class A Orphan/other GPCRs, Kv3.3, ORP-family, CEACAM, PKC-beta, SUR, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, CPT-1A, S100, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, Rab-3, Ephrin-A receptor 5, IDUA, CRH receptor 2, NSF, GLRA, SYP, Rho GTPase, PDE4, Rap1GDS1, Galpha(i)-specific metabotropic glutamate GPCRs, Secretogranin V, EGF, Pro-CCK, cPKC (conventional), Serotonin receptor, Apelin, Rab-27B, PPID, Osteopontin, Rab-3C, HMDH, NR3A, Substance P, MCT1 (SLC16A1), Galpha(q)-specific amine GPCRs, Ephrin-A receptors, Galpha(i)-specific amine GPCRs, Protein kinase G1, Activin beta A, CDK5, Glycine receptor, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, Galpha(q)-specific peptide GPCRs, DYNLL, MEF2, ACSL4, F262, CEACAM1, ATF/CREB, DelGIP1, Acyl-CoA synthetase, Glutaredoxin, DLC1 (Dynein LC8a), Galpha(s)-specific CRF GPCRs, NKCC1, Calmodulin, NELL2, Activin, Aquaporin 1, Syntenin 1, SCOT, PKC, SUR1, HTR2A, MEF2C, Protein kinase G, Calcineurin A (beta), MPC2, CALM2, Cyclophilin A, Galpha(s)-specific peptide GPCRs, Glutaredoxin 1
33	regulation of transporter activity	485	7.543E-17	1.782E-14	56	PP2A cat (alpha), HPCA, RNF207, Endothelin-1, NETO2, G-protein beta, HSP70, NDUFA4, PDE, CNIH2, SHISA7, G-protein beta/gamma, SUR, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, S100, Galpha(q)-specific nucleotide-like GPCRs, PDE4, Dysferlin, cPKC (conventional), Serotonin receptor, TRPC, ANT, NDFIP2, Galpha(q)-specific amine GPCRs, Galpha(i)-specific amine GPCRs, HCN, Protein kinase G1, CDK5, SMIT, Galpha(q)-specific peptide GPCRs, MEF2, APRIO, PP2A catalytic, Glutaredoxin, Galpha(s)-specific CRF GPCRs, PRNP, MPTP complex, Calmodulin, FLJ45455, STAC2, NDFIP1, CaMK II delta, PKC, SUR1, SLC25A4, ATP1B3, MEF2C, Protein kinase G, CALM2, 14-3-3, RAGE, 14-3-3 eta, ATP1beta subunit, Glutaredoxin 1
34	trans-synaptic signaling	702	9.199E-17	2.109E-14	69	PLP1, NPY, Cadherin 8, Galpha(s)-specific nucleotide-like GPCRs, GLSK, GAD1, Synaptotagmin I, Guanylate cyclase, CNR1, Synaptotagmin IV, Synaptotagmin, PDE, CNIH2, PPT1, Guanylate cyclase alpha, VDAC 3, GABA-A receptor alpha-1 subunit, GUCY1B1, SDFR1, Galpha(i)-specific peptide GPCRs, P/Q-type calcium channel alpha-1A subunit, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, Rab-3, GPR176, CaMK IV, GLRA, GABA-A

						receptor beta-2 subunit, SYP, Rho GTPase, Galpha(i)-specific metabotropic glutamate GPCRs, GlyRA2, cPKC (conventional), Serotonin receptor, GABA-A receptor alpha-4 subunit, HTR5A, VDAC 1, GUCY1A3, Substance P, GRM6, Galpha(q)-specific amine GPCRs, Galpha(i)-specific amine GPCRs, GABA-A receptor alpha-5 subunit, CDK5, PAK, Guanylate cyclase (alpha-1/beta-1), Guanylate cyclase beta, Glycine receptor, GABA-A receptor alpha-3 subunit, Glycine receptor beta chain, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, Galpha(q)-specific peptide GPCRs, MEF2, NAPB, SNAPs, Kv4.2 channel, MPTP complex, FLJ45455, Syntenin 1, ERK1/2, PKC, HTR2A, Guanylate Cyclase 1, soluble, MEF2C, ERK2 (MAPK1), PTCHD1, Galpha(s)-specific peptide GPCRs, GAD2
35	regulation of transmembrane transporter activity	443	1.140E-16	2.539E-14	53	PP2A cat (alpha), HPCA, RNF207, Endothelin-1, NETO2, G-protein beta, HSP70, NDUFA4, PDE, CNIH2, SHISA7, G-protein beta/gamma, SUR, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, S100, Galpha(q)-specific nucleotide-like GPCRs, PDE4, Dysferlin, cPKC (conventional), Serotonin receptor, TRPC, ANT, Galpha(q)-specific amine GPCRs, Galpha(i)-specific amine GPCRs, HCN, Protein kinase G1, CDK5, Galpha(q)-specific peptide GPCRs, MEF2, APRIO, PP2A catalytic, Glutaredoxin, Galpha(s)-specific CRF GPCRs, PRNP, MPTP complex, Calmodulin, FLJ45455, STAC2, CaMK II delta, PKC, SUR1, SLC25A4, ATP1B3, MEF2C, Protein kinase G, CALM2, 14-3-3, RAGE, 14-3-3 eta, ATP1beta subunit, Glutaredoxin 1
36	regulation of signaling	4708	1.321E-16	2.862E-14	245	NPY, PP2A cat (alpha), HSP90, PAK3, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, IRF1, PTCH2, N-chimaerin, APJ, Peroxiredoxin, Activin A, Endothelin-1, GSKIP, NETO2, GHITM, REV-ERBalpha, BRSK2, JWA, ALDR, RGS8, CNOT7, MDS028, Importin (karyopherin)-alpha, GPR137C, NKIRAS1, PSD2, MGF, TIP47, PRKAR2B, NPFF receptor 2, UNRIP, Synaptotagmin I, Guanylate cyclase, ARL6, HSP70, SCRT2, DDX3Y, CNR1, MAPBPIP, Synaptotagmin IV, CITED2, DnaJB9, Synaptotagmin, Thioredoxin, Dynein, axonemal, light chains, PDE, CNIH2, PPT1, SLC39A10, IGSF9B, DKK3, NCKP1 subunit, Guanylate cyclase alpha, Galpha(q)-specific Class A Orphan/other GPCRs, GPR124, SHISA7, PTPN18, RGS4, 14-3-3 beta/alpha, Kv3.3, ORP-family, CEACAM, PKC-beta, PRDX1, G-protein beta/gamma, SDFR1, SUR, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, TORC1, CPT-1A, S100, ORP8, VWA2, Galpha(q)-specific nucleotide-like GPCRs, ZDH13, Aldose reductase, Rab-3, TM2D3, APOL3, Ephrin-A receptor 5, IP3KA, CRH receptor 2, Semaphorin

						5A, Adropin, NSF, GLRA, DKK2, SYP, Rho GTPase, PDE4, Tensin 2, G-protein gamma, UBE2D1, SOCS6, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, A830006F12Rik, Secretogranin V, EGF, BMPR1A, LOC283174, PKA-reg type II (cAMP-dependent), cPKC (conventional), DLL4, Serotonin receptor, CHMP5, Apelin, TRPC, WIF1, Osteopontin, SMRT, CysLT2 receptor, NHE6, RGS11, PKA-reg (cAMP-dependent), RNF152, ANT, PP1-cat, HMDH, NDFIP2, NR3A, GUCY1A3, KIAA1110, ECT2, Substance P, HBXIP, PSMD10 (Gankyrin), GRM6, CalDAG-GEFII, Histone H2, MCT1 (SLC16A1), ARHGAP18, TMEM14A, Galpha(q)-specific amine GPCRs, Ephrin-A receptors, Galpha(i)-specific amine GPCRs, DAT1, PMCA1, Rab-23, NCX1, HCN, HSP90 beta, Vinexin, Activin beta A, CDK5, PAK, Guanylate cyclase (alpha-1/beta-1), Glycine receptor, Fatty acid-binding protein, HINT, SgK223, IZUMO1, LPPR4, DYNLT, BRK, Nek8, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, FBI-1 (Pokemon), Galpha(q)-specific peptide GPCRs, ATP6V1C, Histone H2B, TBC1D10C, MRAP2, VIP32, DYNLL, Patched, TNK1, MEF2, INCA1, APRIO, MEK4/7, Peg10, ACSL4, F262, CEACAM1, ATF/CREB, Hdj-2, FN14(TNFRSF12A), FEM1B, Acyl-CoA synthetase, PP2A catalytic, BMI-1, Glutaredoxin, DLC1 (Dynein LC8a), Galpha(s)-specific CRF GPCRs, PRNP, TMS-1, MPTP complex, RHEB2, NKCC1, PDE4A, Calmodulin, DIRAS2, NELL2, FLJ31818, Apo-2L(TNFSF10), PDE11A, FLJ45455, Activin, NDFIP1, KCTD16, NME5, Syntenin 1, SCOT, ERK1/2, AATC, UGCG, CaMK II delta, PKC, SUR1, HTR2A, SLC25A4, ARPP-19, Guanylate Cyclase 1, soluble, MEF2C, ERK2 (MAPK1), Calcineurin A (beta), MEK4(MAP2K4), PRKAR1A, Nephrocystin-4, DKK1, MPC2, SOD1, KIAA1024, CALM2, Cyclophilin A, FOXP1/2/4 proteins, PI3K reg class IA, Galpha(s)-specific peptide GPCRs, ATP6AP2, CALB1, NPNT, Midkine, IRS6(DOK5), PXDN, 14-3-3, RAGE, 14-3-3 eta, Myospryn, Glutaredoxin 1
37	cellular metabolic process	9304	1.494E-16	3.147E-14	409	PLP1, FBXO45, PP2A cat (alpha), PRPS1, HSP90, PAK3, PAM, HMGCLL1, ZYG11B, CPSF1, Angiopoietin 1, AEBP1, GLSK, Rab-3B, COX VIc, GAD1, C1D, TINP1, ZH11B, ATP5C, SUCLG1, FLJ12671, ELOVL5, Peroxiredoxin, Activin A, UBL5, Esterase D, Endothelin-1, SULT1A1, Trehalase, PSMB5, ARG2, DUOX1, REV-ERBalpha, BRSK2, UQCRQPC, UBXD3, LAS1L, SC5D, JWA, ALDR, UQCRH, Rab-6A, SC4MOL, MRPS6, PSMA5, CNOT7, NFKBIL2, NDUFAB1, Importin (karyopherin)-alpha, BTBD12, NDUFA1, CDC18L (CDC6), MRPL1, TTLL9, MOBKL1A, DTX2, MCM6, DCMC, PDH E2 subunit N6-lipoyllysine, PRKAR2B, DPY19L1, NDUFB4, MC4R, UNRIP, NDUFA8, KLHL12, Guanylate

						cyclase, ARL6, HSP70, DDX3Y, Glycogen phosphorylase, PPM1E, NUDT4P1, GIMAP7, DnaJB9, Synaptotagmin, PRDX3, NDUFA4, ATP6V1A (70kD), JMJD3, PDE, Tcfl5, PPT1, SDHB, MGAT4A, Karyopherin alpha 2, TM9SF2, Guanylate cyclase alpha, Galpha(q)-specific Class A Orphan/other GPCRs, LMF1, ATP5G, TPH2, RAB39B, PTPN18, BTBD18, TUSC3, UGT8, GUCY1B1, Exostosin-like 2, SELI, ORP-family, B3GN6, Myopodin, PP1-cat gamma, PKC-beta, KIS, PRDX1, B3GN1, NDUFB6, ABO system transferase, NDUFS4, Galpha(i)-specific peptide GPCRs, CALM3, FUT2, KLHL13, UQCRB, ATP5E, CPT-1A, S100, Rab-6, TXNRD1, ORP8, LASS6, PIMT, PDK3, COX VIIa, ZDH13, Aldose reductase, NDUFB3, Rab-3, MTG16 (CBFA2T3), ATG9B, DNER, Ephrin-A receptor 5, IDUA, IP3KA, CRH receptor 2, AMDHD2, InsP6 kinase 3, GRAIL, UBA1L, RPL9, Tomt, CaMK IV, FBXO2, CECR2, Carbohydrate sulfotransferases, LACTB2, LPL1, MOCS2(small), Rho GTPase, PDE4, GTPBP3, Tensin 2, UBE2D1, PRPS2, SOCS6, Dysferlin, Ephrin-A receptor 4, TMEM86B, Secretogranin V, EGF, ATP5B, PPase (inorganic), SYTC, Dynein, axonemal, heavy chains, B3GALTL, BMPR1A, MMADHC, MMD, PKA-reg type II (cAMP-dependent), B3GNT4, Myotrophin, cPKC (conventional), SF3A2, NDUFB1, ELOVL4, PSMA1, Serotonin receptor, CHMP5, ADSS, PPID, TRPC, PYGM, MOC2B, PDK4, VDAC 1, COX VIa, SUCB1, Osteopontin, ATP5G3, ABHD10, KCY, PC4, CHAMP, PKA-reg (cAMP-dependent), TReP-132, RNF152, ANT, PP1-cat, HMDH, UQCR10, NDFIP2, GUCY1A3, VTA1, Clathrin heavy chain, StARD4, CHTF18, Histone H2, LIPA, KLHL35, COPS4, LRRC51, Galpha(q)-specific amine GPCRs, UQCRFS1, Ephrin-A receptors, MRPL47, Histone H2A, Galpha(i)-specific amine GPCRs, Rab-23, SLBP, Protein kinase G1, HSP90 beta, PMS2L3, NDUFS6, Activin beta A, BRMS1L, CDK5, DUS3L, PAK, Guanylate cyclase (alpha-1/beta-1), Guanylate cyclase beta, Fatty acid-binding protein, HINT, ENPP4, MAML1, KIAA0143, SgK223, MDH1, GTL3, ASAH, GNT-IV, LPPR4, Atg101, TMEM74, SPOCK3, SPSY, COX Va, eIF4A2, BRK, ATP5A, Nek8, Selenoprotein P, Carbonic anhydrase XII, Calcineurin A (catalytic), LSM2, TOP1MT, 4833424O15Rik, B3GT2, SLC25A46, Glyoxalase I, DDX51, SMIT, FBI-1 (Pokemon), PDH beta, Galpha(q)-specific peptide GPCRs, MAFbx, SNAP190, NDUFA5, Tubulin alpha, Creatine kinase, DCK, MRAP2, PAP-II, NUDT4, DYNLL, TNK1, MEF2, ADAR3, PGAM1, HNMT, APRIO, SCS-A, MEK4/7, ACSL4, RENBP, F262, ATF/CREB, GLGB, ODP2, DelGIP1, Trim45, RSL24D1, FEM1B, Acyl-CoA synthetase, PP2A catalytic, GAS41, IDI1, ZFAND2A, eIF4A, BMI-1, OAZIN, eIF2S1, Glutaredoxin, DLC1 (Dynein LC8a), RNF175, Galpha(s)-specific

						CRF GPCRs, LAMP2, COX VIa-1, KAD6, ALAS1, ATP6V1B, Quinone oxidoreductase, JKAMP, Protein kinase G 2, PRNP, DNAJA2, TMS-1, GKP3, MPTP complex, ENC1, Malin, C1orf59, PDE4A, Calmodulin, LPL, SUMO-3, PGRMC1, SET1B, LOXL2, KLHL2, NOLA3 (NOP10), BTBD1, Activin, SIPAR, NDFIP1, NME5, SCOT, Octanoyl-holo-acp, KCRS, Securin, ADHX, ERK1/2, Carboxypeptidase M, snRNP-G, AATC, UGCG, SLC29A4, TRUB1, NFIC, CaMK II delta, HSC70, PI3K reg class IA (p55-gamma), PKC, ABTB1, PMM2, SLC25A4, Guanylate Cyclase 1, soluble, SULT4A1, MRPL33, Protein kinase G, RIFK, ERK2 (MAPK1), Calcineurin A (beta), DREV1, Ran, OAT, MEK4(MAP2K4), PRKAR1A, IMPA1, TRIM23, UFC1, MPC2, Guanine deaminase, PRPS, SOD1, TFIIB, YIPF5, dJ222E13.2, PPP4R2, GDE1, CALM2, Cyclophilin A, FOXP1/2/4 proteins, PI3K reg class IA, DCoHM, Galpha(s)-specific peptide GPCRs, ATP5L, ATP6AP2, SRm300, GAD2, SIAH3, PGM2L1, NF-I, MRPL3, B930041F14Rik, HXK3, COX VIIa-2, ACOXL, NRBF2, IRS6(DOK5), PXDN, 14-3-3, COX VIIa-2L, RAGE, Glutaredoxin 1, CMAS, CHST6
38	ribose phosphate metabolic process	479	1.838E-16	3.770E-14	55	PRPS1, ATP5C, SUCLG1, ELOVL5, SULT1A1, DCMC, PDH E2 subunit N6-lipoyllysine, Guanylate cyclase, Glycogen phosphorylase, NUDT4P1, GIMAP7, ATP6V1A (70kD), PDE, PPT1, Guanylate cyclase alpha, ATP5G, GUCY1B1, ATP5E, Rho GTPase, PDE4, PRPS2, ATP5B, ELOVL4, ADSS, PDK4, SUCB1, ATP5G3, KCY, HMDH, GUCY1A3, Ephrin-A receptors, Rab-23, Guanylate cyclase (alpha-1/beta-1), Guanylate cyclase beta, HINT, ATP5A, PDH beta, NUDT4, PGAM1, SCS-A, ACSL4, F262, ODP2, Acyl-CoA synthetase, KAD6, PDE4A, NME5, Guanylate Cyclase 1, soluble, RIFK, Ran, MPC2, Guanine deaminase, PRPS, ATP5L, HXK3
39	regulation of trans-synaptic signaling	783	1.943E-16	3.884E-14	73	Galpha(s)-specific nucleotide-like GPCRs, Endothelin-1, NETO2, PRKAR2B, Synaptotagmin I, CNR1, Synaptotagmin IV, Synaptotagmin, PDE, CNIH2, PPT1, SHISA7, RGS4, Kv3.3, PKC-beta, SDFR1, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, TORC1, S100, Galpha(q)-specific nucleotide-like GPCRs, Rab-3, IP3KA, CRH receptor 2, GLRA, SYP, Rho GTPase, PDE4, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, PKA-reg type II (cAMP-dependent), cPKC (conventional), Serotonin receptor, PKA-reg (cAMP-dependent), NR3A, Substance P, GRM6, Galpha(q)-specific amine GPCRs, Ephrin-A receptors, Galpha(i)-specific amine GPCRs, HCN, CDK5, PAK, Glycine receptor, Fatty acid-binding protein, LPPR4, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, Galpha(q)-specific peptide GPCRs, MEF2, APRIO, ATF/CREB, Galpha(s)-specific CRF GPCRs, PRNP,

						RHEB2, NKCC1, PDE4A, Calmodulin, FLJ45455, ERK1/2, PKC, HTR2A, MEF2C, ERK2 (MAPK1), Calcineurin A (beta), DKK1, CALM2, CALB1, 14-3-3, RAGE, 14-3-3 eta
40	ribonucleotide metabolic process	468	2.821E-16	5.498E-14	54	PRPS1, ATP5C, SUCLG1, ELOVL5, SULT1A1, DCMC, PDH E2 subunit N6-lipoyllysine, Guanylate cyclase, NUDT4P1, GIMAP7, ATP6V1A (70kD), PDE, PPT1, Guanylate cyclase alpha, ATP5G, GUCY1B1, ATP5E, Rho GTPase, PDE4, PRPS2, ATP5B, ELOVL4, ADSS, PDK4, SUCB1, ATP5G3, KCY, HMDH, GUCY1A3, Ephrin-A receptors, Rab-23, Guanylate cyclase (alpha-1/beta-1), Guanylate cyclase beta, HINT, ATP5A, PDH beta, NUDT4, PGAM1, SCS-A, ACSL4, F262, ODP2, Acyl-CoA synthetase, KAD6, PDE4A, NME5, Guanylate Cyclase 1, soluble, RIFK, Ran, MPC2, Guanine deaminase, PRPS, ATP5L, HXK3
41	proton transmembrane transport	192	3.347E-16	6.364E-14	34	ATP5C, UQCRQPC, UQCRH, NDUFA4, ATP6V1A (70kD), ATP5G, ATP5E, COX VIIa, ATP6V1C1, ATP6M, V-ATPase E subunit, ATP5B, Dynein, axonemal, heavy chains, ATP6V1B2, COX VIa, CLCN4, ATP6V1H, ATP5G3, NHE6, ANT, UQCR10, UQCRFS1, COX Va, ATP5A, ATP6V1C, COX VIa-1, ATP6V1B, MPTP complex, ATP6V0B, ATP6V1E, SLC25A4, CLCN5, ATP5L, COX VIIa-2L
42	developmental process	8639	3.590E-16	6.663E-14	385	PLP1, Cyclin G, FBXO45, NPY, FAM3C, PP2A cat (alpha), PRPS1, HSP90, PAK3, PAM, Cadherin 8, Galpha(s)-specific nucleotide-like GPCRs, Angiopoietin 1, Semaphorin 3C, Alpha crystallin B, RhoN, IRF1, ILDR2, MAL2, SLC35E2B, MEGF10, PTCH2, N-chimaerin, HPCA, APJ, Smooth muscle myosin, EDIL3, Peroxiredoxin, Activin A, Endothelin-1, Trehalase, AP-1 gamma subunits, ARG2, T-plastin, DUOX1, REV-ERBalpha, BRSK2, UQCRQPC, G-protein beta, ALDR, CRTL1, RGS8, MDS028, Importin (karyopherin)-alpha, NckAP1, DNAH1, Lgi4, Pannexin-1, NKIRAS1, HPCAL4, PSD2, MGF, MEPE, MELC, UNRIP, KLHL12, Synaptotagmin I, Guanylate cyclase, ARL6, KCNK2, HSP70, DDX3Y, CNR1, MYL6, Synaptotagmin IV, CITED2, SLIRP, DnaJB9, Synaptotagmin, PRDX3, CNTN1 (F3), HSPA4, JMJD3, Dynein, axonemal, light chains, PDE, Cystatin C, Tcfl5, PPT1, IGSF9B, DKK3, NCKP1 subunit, HCN2, Galpha(q)-specific Class A Orphan/other GPCRs, IMPG2, ATP5G, GPR124, KAL1, PTPN18, RGS4, BTBD18, GABA-A receptor alpha-1 subunit, UGT8, FLRT3, ORP-family, B3GN6, Tenascin-C, PP1-cat gamma, CEACAM, ODF3, TRPC5, KIS, PAFAH gamma, PRDX1, G-protein beta/gamma, B3GN1, SDFR1, SUR, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, CPT-1A, S100, TXNRD1, ORP8, AMIGO2, PIMT, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, Aldose reductase, Rab-3, MTG16 (CBFA2T3), ATG9B, TM2D3, DNER, ZFHX2, Ephrin-A receptor 5,

						IDUA, IP3KA, CRH receptor 2, CacyBP(SIP), Semaphorin 5A, Tomt, CaMK IV, GLRA, DKK2, ZNF499, GABA-A receptor beta-2 subunit, CECR2, SYP, Carbohydrate sulfotransferases, Rho GTPase, PDE4, Tensin 2, G-protein gamma, PRPS2, Dysferlin, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, Elastin, ChREBP, ZNF267, A830006F12Rik, PP4R4, EGF, GlyRA2, ATP5B, Pro-CCK, XKR4, Dynein, axonemal, heavy chains, BMPR1A, Semaphorin 3E, LOC283174, Myotrophin, NELL1, CAP2, cPKC (conventional), DLL4, Serotonin receptor, Apelin, GABA-A receptor alpha-4 subunit, TRPC, HTR5A, Sp8, VDAC 1, WIF1, NDRG3, Osteopontin, ATP5G3, ZNF238, SMRT, NHE6, M-Ras, CREB4, CHAMP, PKA-reg (cAMP-dependent), Lingo1, ANT, PP1-cat, HMDH, PDLIM2, NR3A, HSBP1, Cables1, ECT2, Clathrin heavy chain, IL3RA, GRM6, CHTF18, CalDAG-GEFII, Histone H2, LIPA, LRRC51, Galpha(q)-specific amine GPCRs, Ephrin-A receptors, Histone H2A, NPR3, GP-IB alpha, Galpha(i)-specific amine GPCRs, TRPC4, PMCA1, Rab-23, NCX1, HCN, Protein kinase G1, HLF, BDH, CAP1, HSP90 beta, Anillin, TXNIP (VDUP1), COL25A1, NDUFS6, Activin beta A, GABA-A receptor alpha-5 subunit, Zeta-sarcoglycan, CDK5, PAK, BEX1, Glycine receptor, Fatty acid-binding protein, FOXP4, MAML1, SOHLH1, IZUMO1, GTL3, ASAH, LPPR4, DYNLT, BRK, ATP5A, Glycine receptor beta chain, Nek8, Selenoprotein P, CAPZA, RTL1, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, STARD7, Cyclin G1, SLC25A46, Glyoxalase I, SMIT, FBI-1 (Pokemon), Galpha(q)-specific peptide GPCRs, H2AFZ, Histone H2B, NCOA4 (ARA70), WDR47, Creatine kinase, DSCAML1, B-FABP, Azi1, DYNLL, Patched, TNK1, XK, MEF2, HNMT, APRIO, MEK4/7, Peg10, ACSL4, CEACAM1, ATF/CREB, RAI1, Hdj-2, FN14(TNFRSF12A), Trim45, G-protein beta-4, FEM1B, Acyl-CoA synthetase, PP2A catalytic, MRLC, eIF4A, BMI-1, SNAPs, eIF2S1, Glutaredoxin, DLC1 (Dynein LC8a), Galpha(s)-specific CRF GPCRs, ALAS1, ATP6V1B, PKD1L1, PRNP, HSPC138, MPTP complex, ENC1, RHEB2, NKCC1, WDT2, Calmodulin, NELL2, PGRMC1, Apo-2L(TNFSF10), LOXL2, FLJ45455, Endophilin A1, BTBD1, Activin, C1orf43, Aquaporin 1, NME5, CLIC4, Calcyclin, Syntenin 1, SCOT, KCRS, Securin, ADHX, ERK1/2, Carboxypeptidase M, AATC, UGCG, Anks4b, NFIC, CaMK II delta, HSC70, PI3K reg class IA (p55-gamma), PKC, SSTR2, SUR1, HTR2A, SLC25A4, K-cadherin (CDH6), MEF2C, SULT4A1, Protein kinase G, ERK2 (MAPK1), Calcineurin A (beta), LISCH7, Ran, MEK4(MAP2K4), DACH2, PRKAR1A, IGFALS, UFC1, Nephrocystin-4, DKK1, SSTR1, Guanine deaminase, PRPS, SOD1, KIAA1024, PPP4R2, SLC38A2, SAP102, FSTL5, CALM2,

						Cyclophilin A, FOXP1/2/4 proteins, Aggrecanase-2, PI3K reg class IA, PTCHD1, Galpha(s)-specific peptide GPCRs, TCP1-alpha, ACTR3, ATP6AP2, CALB1, Pcdh19, CD166, DRIL2, NF-I, NPNT, Neuroserpin, Midkine, IRS6(DOK5), ARP3, 14-3-3, RAGE, 14-3-3 eta, ATP1beta subunit, Glutaredoxin 1, SNX10
43	head development	1457	3.957E-16	7.174E-14	107	PLP1, Cyclin G, FBXO45, NPY, HPCA, Activin A, UQCRQPC, G-protein beta, RGS8, Synaptotagmin I, ARL6, HSP70, Synaptotagmin IV, Synaptotagmin, CNTN1 (F3), JMJD3, Cystatin C, PPT1, HCN2, Galpha(q)-specific Class A Orphan/other GPCRs, RGS4, FLRT3, PAFAH gamma, G-protein beta/gamma, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, S100, AMIGO2, ZFHX2, Ephrin-A receptor 5, CRH receptor 2, Semaphorin 5A, Rho GTPase, G-protein gamma, Dynein, axonemal, heavy chains, BMPR1A, Myotrophin, Serotonin receptor, HTR5A, ZNF238, SMRT, Histone H2, Ephrin-A receptors, Histone H2A, Galpha(i)-specific amine GPCRs, PMCA1, NCX1, HCN, Protein kinase G1, BDH, Activin beta A, GABA-A receptor alpha-5 subunit, CDK5, PAK, Fatty acid-binding protein, Selenoprotein P, Calcineurin A (catalytic), Cyclin G1, SLC25A46, Galpha(q)-specific peptide GPCRs, Histone H2B, Creatine kinase, DSCAML1, B-FABP, DYNLL, Patched, MEF2, HNMT, ATF/CREB, G-protein beta-4, Acyl-CoA synthetase, BMI-1, SNAPs, DLC1 (Dynein LC8a), Galpha(s)-specific CRF GPCRs, Calmodulin, Activin, Aquaporin 1, NME5, SCOT, ERK1/2, HSC70, SSTR2, MEF2C, Protein kinase G, ERK2 (MAPK1), Calcineurin A (beta), Ran, UFC1, DKK1, SSTR1, SLC38A2, CALM2, FOXP1/2/4 proteins, PTCHD1, Galpha(s)-specific peptide GPCRs, ATP6AP2, Pcdh19, NF-I, Midkine, 14-3-3, RAGE, 14-3-3 eta, ATP1beta subunit
44	transmembrane transport	1628	4.478E-16	7.934E-14	115	ZnT-2, SLC35E2B, SMVT, ATP5C, Endothelin-1, UQCRQPC, JWA, UQCRH, TMC4, LOC153328, Pannexin-1, KCNK2, HSP70, Tim17, NDUFA4, ATP6V1A (70kD), SLC39A10, HCN2, ATP5G, VDAC 3, GABA-A receptor alpha-1 subunit, TUSC3, Kv3.3, TRPC5, SLC25A45, SUR, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, ATP5E, CPT-1A, S100, KCNH5, TRPV1, COX VIIa, ATP6V1C1, ZDH13, ATP6M, FAM38B, SLC2A13, V-ATPase E subunit, GLRA, GABA-A receptor beta-2 subunit, TIMM17, Galpha(i)-specific metabotropic glutamate GPCRs, GlyRA2, ATP5B, Dynein, axonemal, heavy chains, ATP6V1B2, Serotonin receptor, GABA-A receptor alpha-4 subunit, TRPC, SLC7A5, VDAC 1, COX VIa, CLCN4, ATP6V1H, ATP5G3, NHE6, ANT, UQCR10, NR3A, MCT1 (SLC16A1), Galpha(q)-specific amine GPCRs, UQCRFS1, GP-IB alpha, Galpha(i)-specific amine GPCRs, TRPC4, PMCA1, NCX1, HCN, GABA-A receptor alpha-5

						subunit, PANX2, Glycine receptor, Fatty acid-binding protein, TOM22, GABA-A receptor alpha-3 subunit, SLC16A13, COX Va, ATP5A, Glycine receptor beta chain, Kv9.3, SMIT, Galpha(q)-specific peptide GPCRs, ATP6V1C, COX VIa-1, ATP6V1B, Kv4.2 channel, PKD1L1, MPTP complex, NKCC1, ATP6V0B, Calmodulin, ATP6V1E, Aquaporin 1, CLIC4, Calcyclin, SLC29A4, HSC70, SLC35A5, PKC, SUR1, HTR2A, SLC25A4, ATP1B3, CLCN5, MPC2, SLC38A2, CALM2, ATP5L, 14-3-3, ACCN3 (ASIC3), COX VIIa-2L, ATP1beta subunit
45	modulation of chemical synaptic transmission	781	5.703E-16	9.880E-14	72	Galpha(s)-specific nucleotide-like GPCRs, Endothelin-1, NETO2, PRKAR2B, Synaptotagmin I, CNR1, Synaptotagmin IV, Synaptotagmin, PDE, CNIH2, PPT1, SHISA7, RGS4, Kv3.3, PKC-beta, SDFR1, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, TORC1, S100, Galpha(q)-specific nucleotide-like GPCRs, Rab-3, IP3KA, CRH receptor 2, GLRA, SYP, Rho GTPase, PDE4, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, PKA-reg type II (cAMP-dependent), cPKC (conventional), Serotonin receptor, PKA-reg (cAMP-dependent), NR3A, Substance P, GRM6, Galpha(q)-specific amine GPCRs, Ephrin-A receptors, Galpha(i)-specific amine GPCRs, HCN, CDK5, PAK, Glycine receptor, LPPR4, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, Galpha(q)-specific peptide GPCRs, MEF2, APRIO, ATF/CREB, Galpha(s)-specific CRF GPCRs, PRNP, RHEB2, NKCC1, PDE4A, Calmodulin, FLJ45455, ERK1/2, PKC, HTR2A, MEF2C, ERK2 (MAPK1), Calcineurin A (beta), DKK1, CALM2, CALB1, 14-3-3, RAGE, 14-3-3 eta
46	brain development	1385	6.591E-16	1.117E-13	103	PLP1, Cyclin G, FBXO45, NPY, HPCA, Activin A, UQCRQPC, G-protein beta, RGS8, Synaptotagmin I, ARL6, HSP70, Synaptotagmin IV, Synaptotagmin, CNTN1 (F3), JMJD3, Cystatin C, PPT1, HCN2, Galpha(q)-specific Class A Orphan/other GPCRs, RGS4, PAFAH gamma, G-protein beta/gamma, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, S100, AMIGO2, ZFHX2, Ephrin-A receptor 5, CRH receptor 2, Semaphorin 5A, Rho GTPase, G-protein gamma, Dynein, axonemal, heavy chains, BMPR1A, Myotrophin, Serotonin receptor, HTR5A, ZNF238, SMRT, Histone H2, Ephrin-A receptors, Histone H2A, Galpha(i)-specific amine GPCRs, PMCA1, NCX1, HCN, Protein kinase G1, BDH, Activin beta A, GABA-A receptor alpha-5 subunit, CDK5, PAK, Fatty acid-binding protein, Selenoprotein P, Calcineurin A (catalytic), Cyclin G1, SLC25A46, Galpha(q)-specific peptide GPCRs, Histone H2B, Creatine kinase, DSCAML1, B-FABP, DYNLL, Patched, MEF2, HNMT, ATF/CREB, G-protein beta-4, Acyl-CoA synthetase, BMI-1, SNAPs, DLC1 (Dynein LC8a), Galpha(s)-

						specific CRF GPCRs, Calmodulin, Activin, Aquaporin 1, NME5, SCOT, HSC70, SSTR2, MEF2C, Protein kinase G, Calcineurin A (beta), Ran, UFC1, DKK1, SSTR1, SLC38A2, CALM2, FOXP1/2/4 proteins, PTCHD1, Galpha(s)-specific peptide GPCRs, Pcdh19, NF-I, Midkine, 14-3-3, RAGE, 14-3-3 eta, ATP1beta subunit
47	cellular homeostasis	1389	7.981E-16	1.324E-13	103	PP2A cat (alpha), HSP90, Galpha(s)-specific nucleotide-like GPCRs, APJ, Peroxiredoxin, Endothelin-1, REV-ERBalpha, G-protein beta, CNR1, Glycogen phosphorylase, PRDX3, Thioredoxin, ATP6V1A (70kD), PDE, PPT1, SLC39A10, Galpha(q)-specific Class A Orphan/other GPCRs, TUSC3, TRPC5, PKC-beta, PRDX1, G-protein beta/gamma, SDFR1, SUR, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, S100, TXNRD1, TRPV1, PDK3, Galpha(q)-specific nucleotide-like GPCRs, Tensin 2, G-protein gamma, SOCS6, Rap1GDS1, ChREBP, ATP5B, cPKC (conventional), ATP6V1B2, Serotonin receptor, TRPC, PYGM, ATP6V1H, Osteopontin, NHE6, Substance P, Galpha(q)-specific amine GPCRs, GP-IB alpha, Galpha(i)-specific amine GPCRs, TRPC4, PMCA1, NCX1, Protein kinase G1, Zeta-sarcoglycan, CDK5, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, Galpha(q)-specific peptide GPCRs, NCOA4 (ARA70), Creatine kinase, XK, MEF2, APRIO, ATF/CREB, G-protein gamma 3, PP2A catalytic, Glutaredoxin, Galpha(s)-specific CRF GPCRs, LAMP2, ATP6V1B, Protein kinase G 2, PRNP, NKCC1, Calmodulin, NELL2, Aquaporin 1, NDFIP1, CLIC4, ERK1/2, CDw52, AATC, CaMK II delta, PKC, SUR1, HTR2A, ATP1B3, MEF2C, Protein kinase G, ERK2 (MAPK1), Calcineurin A (beta), SOD1, CALM2, PI3K reg class IA, Galpha(s)-specific peptide GPCRs, ATP6AP2, CALB1, HXK3, 14-3-3, RAGE, ATP1beta subunit, Glutaredoxin 1
48	response to nitrogen compound	2149	8.504E-16	1.381E-13	138	Cyclin G, PP2A cat (alpha), HSP90, Galpha(s)-specific nucleotide-like GPCRs, IRF1, ATP5C, HPCA, Endothelin-1, ARG2, DUOX1, BRSK2, P2Y11, UBXD3, G-protein beta, ALDR, RGS8, CDC18L (CDC6), Pannexin-1, TIP47, PRKAR2B, MC4R, Guanylate cyclase, HSP70, CNR1, MAPBPIP, Glycogen phosphorylase, DnaJB9, Thioredoxin, PDE, HCN2, Galpha(q)-specific Class A Orphan/other GPCRs, ATP5G, RGS4, GABA-A receptor alpha-1 subunit, GUCY1B1, CEACAM, G-protein beta/gamma, SUR, NDUFS4, NCX, Galpha(i)-specific peptide GPCRs, CALM3, P/Q-type calcium channel alpha-1A subunit, CPT-1A, TRPV1, Galpha(q)-specific nucleotide-like GPCRs, Aldose reductase, CRH receptor 2, CacyBP(SIP), GLRA, GABA-A receptor beta-2 subunit, FBXO2, SYP, Rho GTPase, PDE4, G-protein gamma, Rap1GDS1, Ephrin-A receptor 4, Galpha(i)-specific metabotropic glutamate GPCRs, GlyRA2, ATP5B, PKA-reg type II (cAMP-dependent), cPKC

						(conventional), AP3S1, Serotonin receptor, CHMP5, ADSS, TRPC, HTR5A, PYGM, PDK4, ATP5G3, SMRT, CysLT2 receptor, PKA-reg (cAMP-dependent), Substance P, AP-3 sigma subunits, HBXIP, Histone H2, Galpha(q)-specific amine GPCRs, Ephrin-A receptors, Histone H2A, HMP19, Galpha(i)-specific amine GPCRs, NCX1, HCN, BDH, HSP90 beta, CDK5, PAK, Guanylate cyclase (alpha-1/beta-1), Guanylate cyclase beta, Glycine receptor, Fatty acid-binding protein, ATP5A, Glycine receptor beta chain, Calcineurin A (catalytic), Galpha(i)-specific cannabis GPSRs, Cyclin G1, Galpha(q)-specific peptide GPCRs, H2AFZ, MEF2, HNMT, APRIO, CEACAM1, ATF/CREB, Acyl-CoA synthetase, PP2A catalytic, RNF175, Galpha(s)-specific CRF GPCRs, ALAS1, JKAMP, PRNP, Calmodulin, LPL, Apo-2L(TNFSF10), Activin, Aquaporin 1, ERK1/2, AATC, PI3K reg class IA (p55-gamma), PKC, SUR1, HTR2A, ARPP-19, Guanylate Cyclase 1, soluble, MEF2C, ERK2 (MAPK1), Calcineurin A (beta), IGFALS, SOD1, CALM2, PI3K reg class IA, Galpha(s)-specific peptide GPCRs, ACTR3, ARP3, 14-3-3, RAGE
49	purine ribonucleotide metabolic process	449	8.745E-16	1.391E-13	52	PRPS1, ATP5C, SUCLG1, ELOVL5, SULT1A1, DCMC, PDH E2 subunit N6-lipoyllysine, Guanylate cyclase, NUDT4P1, GIMAP7, ATP6V1A (70kD), PDE, PPT1, Guanylate cyclase alpha, ATP5G, GUCY1B1, ATP5E, Rho GTPase, PDE4, PRPS2, ATP5B, ELOVL4, ADSS, PDK4, SUCB1, ATP5G3, HMDH, GUCY1A3, Ephrin-A receptors, Rab-23, Guanylate cyclase (alpha-1/beta-1), Guanylate cyclase beta, HINT, ATP5A, PDH beta, NUDT4, PGAM1, SCS-A, ACSL4, F262, ODP2, Acyl-CoA synthetase, KAD6, PDE4A, NME5, Guanylate Cyclase 1, soluble, Ran, MPC2, Guanine deaminase, PRPS, ATP5L, HXK3
50	purine nucleotide metabolic process	465	9.024E-16	1.407E-13	53	PRPS1, ATP5C, SUCLG1, ELOVL5, SULT1A1, DCMC, PDH E2 subunit N6-lipoyllysine, Guanylate cyclase, NUDT4P1, GIMAP7, ATP6V1A (70kD), PDE, PPT1, Guanylate cyclase alpha, ATP5G, GUCY1B1, ATP5E, Rho GTPase, PDE4, PRPS2, ATP5B, ELOVL4, ADSS, PDK4, SUCB1, ATP5G3, HMDH, GUCY1A3, Ephrin-A receptors, Rab-23, Guanylate cyclase (alpha-1/beta-1), Guanylate cyclase beta, HINT, ATP5A, PDH beta, DCK, NUDT4, PGAM1, SCS-A, ACSL4, F262, ODP2, Acyl-CoA synthetase, KAD6, PDE4A, NME5, Guanylate Cyclase 1, soluble, Ran, MPC2, Guanine deaminase, PRPS, ATP5L, HXK3

Table A16. Top 50 KCL BrainBank Gene Ontology (GO) Biological Processes enrichments with MetaCore. Term size refers to the number of genes in the term, with the intersection size denoting the number of genes in the dataset found in the term.

#	Term Name	Term Size	p-value	adjusted p-value (FDR)	Intersection Size	Intersection Gene Names
1	phagocytosis, recognition	43	1.653E-12	5.115E-09	12	Kappa chain (Ig light chain), KV139, COLEC12, IGHA1, MFGE8, Ficolin, IGKC, IGHG1, Fc gamma RII, Ficolin-1, Ig light chain, KVD16
2	immune response	1463	2.644E-12	5.115E-09	60	HMG1,2, Kappa chain (Ig light chain), Histone H2, A20, OASL, MxB, KV139, GZMH, COLEC12, C4A protein, Tubulin beta, Annexin I, IGHA1, PLA2, C4, MHC Class I alpha chain, Ficolin, RSAD2, IGKC, EAT-2, IGHG1, Galpha(q)-specific peptide GPCRs, Histone H2B, POMC, HMGB2, GBP6, Fc gamma RII beta, APOL1, ILT4, Perforin, Fc gamma RII, IFI27, CEACAM, HIST2H2BE, Galpha(i)-specific peptide GPCRs, I-TAC, Ficolin-1, Apo-2L(TNFSF10), Lactoferrin, Galpha(q)-specific nucleotide-like GPCRs, 2'-5'-oligoadenylate synthetase, H28, MxA, Galpha(i)-specific EDG GPCRs, Carbohydrate sulfotransferases, Ig light chain, OAS3, NALP3, GBP5, APRIL(TNFSF13), GBP4, IFI44, Oct-2, WNT, KVD16, Midkine, SEC14L1, HLAC, LIRB, ILT7
3	defense response to bacterium	311	3.489E-12	5.115E-09	26	HMG1,2, Kappa chain (Ig light chain), Histone H2, KV139, COLEC12, IGHA1, PLA2, MHC Class I alpha chain, Ficolin, IGKC, IGHG1, Galpha(q)-specific peptide GPCRs, Histone H2B, HMGB2, GBP6, HIST2H2BE, Galpha(i)-specific peptide GPCRs, Lactoferrin, 2'-5'-oligoadenylate synthetase, Aquaporin 1, Ig light chain, OAS3, NALP3, GBP4, KVD16, HLAC
4	defense response	1641	3.780E-12	5.115E-09	64	HMG1,2, Kappa chain (Ig light chain), Histone H2, PBXIP1, A20, OASL, MxB, KV139, GZMH, COLEC12, CAT-2, C4A protein, Tubulin beta, Annexin I, VCAM1, IGHA1, PLA2, CD44, C4, MHC Class I alpha chain, Ficolin, RSAD2, GPR120, IGKC, LYPD1, EAT-2, IGHG1, Galpha(q)-specific peptide GPCRs, Histone H2B, HMGB2, Cystatin C, GBP6, Fc gamma RII beta, APOL1, ILT4, Perforin, Fc gamma RII, IFI27, HIST2H2BE, Galpha(i)-specific peptide GPCRs, I-TAC, Ficolin-1, Lactoferrin, Galpha(q)-specific nucleotide-like GPCRs, 2'-5'-oligoadenylate synthetase, Aquaporin 1, H28, MxA, Galpha(i)-specific EDG GPCRs, P2Y1, Carbohydrate sulfotransferases, Ig light chain, OAS3, NALP3, GBP5, GBP4, RXR, WNT, KVD16, Midkine, SEC14L1, HLAC, LIRB, ILT7

5	innate immune response	799	4.298E-12	5.115E-09	42	HMG1,2, Kappa chain (Ig light chain), Histone H2, OASL, MxB, KV139, GZMH, COLEC12, C4A protein, Tubulin beta, Annexin I, IGHA1, PLA2, C4, MHC Class I alpha chain, Ficolin, RSAD2, IGKC, EAT-2, IGHG1, Galpha(q)-specific peptide GPCRs, Histone H2B, HMGB2, GBP6, APOL1, IFI27, HIST2H2BE, Galpha(i)-specific peptide GPCRs, Ficolin-1, Lactoferrin, 2'-5'-oligoadenylate synthetase, MxA, Ig light chain, OAS3, NALP3, GBP5, GBP4, WNT, KVD16, SEC14L1, HLAC, ILT7
6	response to bacterium	970	1.263E-11	1.253E-08	46	HMG1,2, Kappa chain (Ig light chain), Histone H2, A20, KV139, COLEC12, GSTs, Connexin 30, C4A protein, VCAM1, IGHA1, PLA2, C4, Fatty acid-binding protein, MHC Class I alpha chain, Ficolin, IGKC, IGHG1, Galpha(q)-specific peptide GPCRs, Histone H2B, HMGB2, GBP6, Fc gamma RII beta, ILT4, Fc gamma RII, Connexin 26, CEACAM, HIST2H2BE, Galpha(i)-specific peptide GPCRs, I-TAC, Lactoferrin, Galpha(q)-specific nucleotide-like GPCRs, 2'-5'-oligoadenylate synthetase, Aquaporin 1, MxA, Ig light chain, OAS3, NALP3, GBP5, GBP4, IFI44, WNT, KVD16, HLAC, LIRB, CCDC80
7	response to external stimulus	3141	1.711E-11	1.455E-08	95	HMG1,2, Angiopoietin 1, Kappa chain (Ig light chain), LHX1, Histone H2, HGF, A20, OASL, MxB, KV139, GZMH, COLEC12, GSTs, Connexin 30, C4A protein, Tubulin beta, APH-1, SLC4A1, Neuropilin-2, Annexin I, VCAM1, IGHA1, PLA2, CD44, C4, WNT7B, PDK2, Fatty acid-binding protein, MHC Class I alpha chain, Ficolin, RSAD2, SDHL, LGR6, IGKC, DCPS, GPNMB (Osteoactivin), MC4R, EAT-2, IGHG1, Galpha(q)-specific peptide GPCRs, ALDOB, Histone H2B, POMC, HMGB2, Cystatin C, GBP6, Fc gamma RII beta, APOL1, ILT4, Perforin, Fc gamma RII, IFI27, GIPR, Connexin 26, CD147, CEACAM, HIST2H2BE, Galpha(i)-specific peptide GPCRs, Semaphorin 3D, CPT-1A, S1P1 receptor, I-TAC, Ficolin-1, Lactoferrin, Galpha(q)-specific nucleotide-like GPCRs, 2'-5'-oligoadenylate synthetase, Aquaporin 1, H28, MxA, PEA3, Galpha(i)-specific EDG GPCRs, P2Y1, Ig light chain, OAS3, NALP3, GBP5, WDR45L, NQO1, GBP4, RXR, IFI44, Dystroglycan, Galpha(s)-specific peptide GPCRs, Oct-2, HMGCL, WNT, CART, KVD16, Midkine, SEC14L1, HLAC, LIRB, RNF152, ILT7, CCDC80

8	negative regulation of response to external stimulus	540	2.159E-11	1.606E-08	33	METRNL, HGF, A20, GSTs, APH-1, PLA2, CD44, Fatty acid-binding protein, MHC Class I alpha chain, GPR120, Galpha(s)-specific calcitonin GPCRs, EAT-2, Galpha(q)-specific peptide GPCRs, PLAT (TPA), Fc gamma RII beta, Fc gamma RII, CEACAM, PRSS11 (HtrA1), Galpha(i)-specific peptide GPCRs, Semaphorin 3D, Lactoferrin, Galpha(q)-specific nucleotide-like GPCRs, 2'-5'-oligoadenylate synthetase, OAS3, NALP3, MMP-28, PLA2G5, WNT, CART, Midkine, SEC14L1, HLAC, LIRB
9	response to biotic stimulus	1742	5.004E-11	3.309E-08	64	HMG1,2, Kappa chain (Ig light chain), Histone H2, A20, OASL, MxB, KV139, GZMH, COLEC12, GSTs, Connexin 30, C4A protein, Tubulin beta, Annexin I, VCAM1, IGHA1, PLA2, C4, Fatty acid-binding protein, MHC Class I alpha chain, Ficolin, RSAD2, IGKC, EAT-2, IGHG1, Galpha(q)-specific peptide GPCRs, Histone H2B, POMC, WFS1, HMGB2, GBP6, Fc gamma RII beta, Seprase, APOL1, ILT4, Perforin, Fc gamma RII, IFI27, Connexin 26, CEACAM, HIST2H2BE, Galpha(i)-specific peptide GPCRs, I-TAC, Ficolin-1, Lactoferrin, Galpha(q)-specific nucleotide-like GPCRs, 2'-5'-oligoadenylate synthetase, Aquaporin 1, H28, MxA, Ig light chain, OAS3, NALP3, GBP5, GBP4, IFI44, Oct-2, WNT, KVD16, SEC14L1, HLAC, LIRB, ILT7, CCDC80
10	negative regulation of defense response	327	6.436E-11	3.830E-08	25	METRNL, HGF, A20, GSTs, PLA2, CD44, MHC Class I alpha chain, GPR120, Galpha(s)-specific calcitonin GPCRs, EAT-2, Galpha(q)-specific peptide GPCRs, Fc gamma RII beta, Fc gamma RII, CEACAM, PRSS11 (HtrA1), Galpha(i)-specific peptide GPCRs, Galpha(q)-specific nucleotide-like GPCRs, 2'-5'-oligoadenylate synthetase, OAS3, NALP3, PLA2G5, Midkine, SEC14L1, HLAC, LIRB

11	response to other organism	1681	9.331E-11	4.885E-08	62	HMG1,2, Kappa chain (Ig light chain), Histone H2, A20, OASL, MxB, KV139, GZMH, COLEC12, GSTs, Connexin 30, C4A protein, Tubulin beta, Annexin I, VCAM1, IGHA1, PLA2, C4, Fatty acid-binding protein, MHC Class I alpha chain, Ficolin, RSAD2, IGKC, EAT-2, IGHG1, Galpha(q)-specific peptide GPCRs, Histone H2B, POMC, HMGB2, GBP6, Fc gamma RII beta, APOL1, ILT4, Perforin, Fc gamma RII, IFI27, Connexin 26, CEACAM, HIST2H2BE, Galpha(i)-specific peptide GPCRs, I-TAC, Ficolin-1, Lactoferrin, Galpha(q)-specific nucleotide-like GPCRs, 2'-5'-oligoadenylate synthetase, Aquaporin 1, H28, MxA, Ig light chain, OAS3, NALP3, GBP5, GBP4, IFI44, Oct-2, WNT, KVD16, SEC14L1, HLAC, LIRB, ILT7, CCDC80
12	response to external biotic stimulus	1685	1.029E-10	4.885E-08	62	HMG1,2, Kappa chain (Ig light chain), Histone H2, A20, OASL, MxB, KV139, GZMH, COLEC12, GSTs, Connexin 30, C4A protein, Tubulin beta, Annexin I, VCAM1, IGHA1, PLA2, C4, Fatty acid-binding protein, MHC Class I alpha chain, Ficolin, RSAD2, IGKC, EAT-2, IGHG1, Galpha(q)-specific peptide GPCRs, Histone H2B, POMC, HMGB2, GBP6, Fc gamma RII beta, APOL1, ILT4, Perforin, Fc gamma RII, IFI27, Connexin 26, CEACAM, HIST2H2BE, Galpha(i)-specific peptide GPCRs, I-TAC, Ficolin-1, Lactoferrin, Galpha(q)-specific nucleotide-like GPCRs, 2'-5'-oligoadenylate synthetase, Aquaporin 1, H28, MxA, Ig light chain, OAS3, NALP3, GBP5, GBP4, IFI44, Oct-2, WNT, KVD16, SEC14L1, HLAC, LIRB, ILT7, CCDC80
13	biological process involved in interspecies interaction between organisms	1906	1.067E-10	4.885E-08	67	HMG1,2, Kappa chain (Ig light chain), Histone H2, A20, OASL, MxB, KV139, GZMH, COLEC12, GSTs, Connexin 30, C4A protein, Tubulin beta, Annexin I, VCAM1, IGHA1, PLA2, C4, Fatty acid-binding protein, MHC Class I alpha chain, Ficolin, RSAD2, TPCN1, IGKC, EAT-2, IGHG1, Galpha(q)-specific peptide GPCRs, Histone H2B, POMC, HMGB2, GBP6, Fc gamma RII beta, APOL1, ILT4, Perforin, Fc gamma RII, IFI27, Connexin 26, CD147, CEACAM, HIST2H2BE, Galpha(i)-specific peptide GPCRs, I-TAC, Ficolin-1, Lactoferrin, Galpha(q)-specific nucleotide-like GPCRs, 2'-5'-oligoadenylate synthetase, Aquaporin 1, H28, MxA, Ig light chain, OAS3, NALP3, GBP5, ZBED1, GBP4, RXR, IFI44, Dystroglycan, Oct-2, WNT, KVD16, SEC14L1, HLAC, LIRB, ILT7, CCDC80

14	negative regulation of cytokine production	398	1.619E-10	6.521E-08	27	HMG1,2, Angiopoietin 1, HGF, A20, GSTs, Annexin I, PLA2, MHC Class I alpha chain, GPR120, GPNMB (Osteoactivin), EAT-2, Galpha(q)-specific peptide GPCRs, POMC, PP2135, GBP6, Fc gamma RII beta, Fc gamma RII, CEACAM, Galpha(i)-specific peptide GPCRs, Lactoferrin, 2'-5'-oligoadenylate synthetase, OAS3, NALP3, Galpha(s)-specific peptide GPCRs, WNT, LIRB, ILT7
15	defense response to other organism	1048	1.684E-10	6.521E-08	46	HMG1,2, Kappa chain (Ig light chain), Histone H2, OASL, MxB, KV139, GZMH, COLEC12, C4A protein, Tubulin beta, Annexin I, IGHA1, PLA2, C4, MHC Class I alpha chain, Ficolin, RSAD2, IGKC, EAT-2, IGHG1, Galpha(q)-specific peptide GPCRs, Histone H2B, HMGB2, GBP6, APOL1, Perforin, IFI27, HIST2H2BE, Galpha(i)-specific peptide GPCRs, Ficolin-1, Lactoferrin, 2'-5'-oligoadenylate synthetase, Aquaporin 1, H28, MxA, Ig light chain, OAS3, NALP3, GBP5, GBP4, WNT, KVD16, SEC14L1, HLAC, LIRB, ILT7
16	regulation of response to external stimulus	1246	1.753E-10	6.521E-08	51	METRNL, HMG1,2, HGF, A20, OASL, GSTs, CAT-2, Tubulin beta, APH-1, Annexin I, PLA2, CD44, Fatty acid-binding protein, MHC Class I alpha chain, Ficolin, GPR120, Galpha(s)-specific calcitonin GPCRs, EAT-2, IGHG1, Galpha(q)-specific peptide GPCRs, POMC, HMGB2, PLAT (TPA), GBP6, Fc gamma RII beta, Seprase, Fc gamma RII, CEACAM, PRSS11 (HtrA1), ZSWIM5, Galpha(i)-specific peptide GPCRs, Semaphorin 3D, S1P1 receptor, Ficolin-1, Lactoferrin, Galpha(q)-specific nucleotide-like GPCRs, 2'-5'-oligoadenylate synthetase, Tubulin beta 2B, Galpha(i)-specific EDG GPCRs, OAS3, NALP3, GBP5, RXR, MMP-28, PLA2G5, WNT, CART, Midkine, SEC14L1, HLAC, LIRB
17	humoral immune response	272	3.249E-10	1.137E-07	22	Kappa chain (Ig light chain), Histone H2, KV139, C4A protein, IGHA1, PLA2, C4, MHC Class I alpha chain, Ficolin, IGKC, IGHG1, Galpha(q)-specific peptide GPCRs, Histone H2B, POMC, HIST2H2BE, Galpha(i)-specific peptide GPCRs, I-TAC, Ficolin-1, Lactoferrin, Ig light chain, Oct-2, KVD16
18	regulation of immune complex clearance by monocytes and macrophages	8	3.752E-10	1.240E-07	6	PLA2, Galpha(q)-specific peptide GPCRs, Fc gamma RII beta, Fc gamma RII, Galpha(i)-specific peptide GPCRs, PLA2G5

19	phagocytosis	252	4.822E-10	1.510E-07	21	HMG1,2, Kappa chain (Ig light chain), KV139, COLEC12, Annexin I, IGHA1, PLA2, MFGE8, Ficolin, IGKC, IGHG1, Galpha(q)-specific peptide GPCRs, Fc gamma RII beta, Fc gamma RII, CEACAM, Galpha(i)-specific peptide GPCRs, Ficolin-1, Galpha(q)-specific nucleotide-like GPCRs, Ig light chain, PLA2G5, KVD16
20	cell recognition	193	1.445E-09	4.301E-07	18	Kappa chain (Ig light chain), KV139, COLEC12, IGHA1, MFGE8, Ficolin, IGKC, IGHG1, Galpha(q)-specific peptide GPCRs, Perforin, Fc gamma RII, CD147, Galpha(i)-specific peptide GPCRs, Ficolin-1, Ig light chain, CNTNAP3, WNT, KVD16
21	defense response to Gram-positive bacterium	123	7.797E-09	2.209E-06	14	HMG1,2, Histone H2, PLA2, MHC Class I alpha chain, Ficolin, Galpha(q)-specific peptide GPCRs, Histone H2B, HMGB2, GBP6, HIST2H2BE, Galpha(i)-specific peptide GPCRs, Lactoferrin, NALP3, GBP4
22	regulation of immune response	1068	9.712E-09	2.537E-06	43	HMG1,2, Kappa chain (Ig light chain), A20, OASL, KV139, COLEC12, C4A protein, Annexin I, IGHA1, PLA2, CD44, C4, MHC Class I alpha chain, Ficolin, RSAD2, IGKC, EAT-2, IGHG1, Galpha(q)-specific peptide GPCRs, HMGB2, PP2135, Fc gamma RII beta, ILT4, Fc gamma RII, CEACAM, Galpha(i)-specific peptide GPCRs, Ficolin-1, Lactoferrin, SUPT6H, Galpha(q)-specific nucleotide-like GPCRs, 2'-5'-oligoadenylate synthetase, Ig light chain, OAS3, NALP3, GBP5, APRIL(TNFSF13), PLA2G5, WNT, KVD16, SEC14L1, HLAC, LIRB, ILT7
23	regulation of defense response	834	9.805E-09	2.537E-06	37	METRNL, HMG1,2, HGF, A20, GSTs, CAT-2, Annexin I, PLA2, CD44, Fatty acid-binding protein, MHC Class I alpha chain, Ficolin, GPR120, Galpha(s)-specific calcitonin GPCRs, EAT-2, IGHG1, Galpha(q)-specific peptide GPCRs, POMC, HMGB2, GBP6, Fc gamma RII beta, Fc gamma RII, CEACAM, PRSS11 (HtrA1), Galpha(i)-specific peptide GPCRs, Ficolin-1, Galpha(q)-specific nucleotide-like GPCRs, 2'-5'-oligoadenylate synthetase, OAS3, NALP3, GBP5, PLA2G5, WNT, Midkine, SEC14L1, HLAC, LIRB

24	immune effector process	521	1.343E-08	3.330E-06	28	HMG1,2, Kappa chain (Ig light chain), A20, KV139, GZMH, C4A protein, Tubulin beta, IGHA1, PLA2, C4, MHC Class I alpha chain, Ficolin, IGKC, EAT-2, IGHG1, Galpha(q)-specific peptide GPCRs, Fc gamma RII beta, Perforin, Fc gamma RII, Galpha(i)-specific peptide GPCRs, Ficolin-1, Galpha(q)-specific nucleotide-like GPCRs, Ig light chain, APRIL(TNFSF13), Oct-2, KVD16, Midkine, LIRB
25	B cell mediated immunity	174	1.478E-08	3.517E-06	16	Kappa chain (Ig light chain), KV139, C4A protein, IGHA1, C4, MHC Class I alpha chain, IGKC, IGHG1, Galpha(q)-specific peptide GPCRs, Fc gamma RII beta, Fc gamma RII, Ig light chain, APRIL(TNFSF13), Oct-2, KVD16, LIRB
26	immune response-regulating signaling pathway	398	1.771E-08	4.053E-06	24	HMG1,2, Kappa chain (Ig light chain), A20, KV139, COLEC12, IGHA1, PLA2, MHC Class I alpha chain, Ficolin, IGKC, EAT-2, IGHG1, Galpha(q)-specific peptide GPCRs, Fc gamma RII beta, ILT4, Fc gamma RII, Galpha(i)-specific peptide GPCRs, Ficolin-1, 2'-5'-oligoadenylate synthetase, Ig light chain, OAS3, KVD16, LIRB, ILT7
27	complement activation	74	1.933E-08	4.261E-06	11	Kappa chain (Ig light chain), KV139, C4A protein, IGHA1, C4, Ficolin, IGKC, IGHG1, Ficolin-1, Ig light chain, KVD16
28	regulation of cytokine production	977	2.168E-08	4.608E-06	40	HMG1,2, Angiopoietin 1, HGF, A20, GSTs, Annexin I, PLA2, MHC Class I alpha chain, Ficolin, RSAD2, GPR120, SULF1, GPNMB (Osteoactivin), EAT-2, Galpha(q)-specific peptide GPCRs, POMC, HMGB2, PP2135, GBP6, Fc gamma RII beta, ILT4, Fc gamma RII, CD147, CEACAM, Galpha(i)-specific peptide GPCRs, Ficolin-1, Lactoferrin, Galpha(q)-specific nucleotide-like GPCRs, 2'-5'-oligoadenylate synthetase, Galpha(i)-specific EDG GPCRs, OAS3, NALP3, GBP5, Galpha(s)-specific peptide GPCRs, Oct-2, WNT, Midkine, HLAC, LIRB, ILT7

29	immune system process	2517	2.655E-08	5.448E-06	74	HMG1,2, Angiopoietin 1, Kappa chain (Ig light chain), Histone H2, PBXIP1, A20, OASL, MxB, KV139, GZMH, COLEC12, CAT-2, C4A protein, Tubulin beta, SLC4A1, Annexin I, VCAM1, IGHA1, PLA2, CD44, C4, MHC Class I alpha chain, Ficolin, RSAD2, IGKC, Galpha(s)-specific calcitonin GPCRs, EAT-2, IGHG1, Galpha(q)-specific peptide GPCRs, Histone H2B, POMC, HMGB2, GBP6, Fc gamma RII beta, APOL1, ILT4, Perforin, Fc gamma RII, IFI27, CD147, ALAS2, CD300E, CEACAM, HIST2H2BE, Galpha(i)-specific peptide GPCRs, S1P1 receptor, I-TAC, Ficolin-1, Apo-2L(TNFSF10), Lactoferrin, Calcitonin receptor, Galpha(q)-specific nucleotide-like GPCRs, 2'-5'-oligoadenylate synthetase, H28, MxA, Galpha(i)-specific EDG GPCRs, P2Y1, Carbohydrate sulfotransferases, Ig light chain, OAS3, NALP3, GBP5, APRIL(TNFSF13), GBP4, IFI44, GALNT2, Oct-2, WNT, KVD16, Midkine, SEC14L1, HLAC, LIRB, ILT7
30	lymphocyte mediated immunity	260	2.841E-08	5.635E-06	19	Kappa chain (Ig light chain), KV139, GZMH, C4A protein, Tubulin beta, IGHA1, C4, MHC Class I alpha chain, IGKC, IGHG1, Galpha(q)-specific peptide GPCRs, Fc gamma RII beta, Perforin, Fc gamma RII, Ig light chain, APRIL(TNFSF13), Oct-2, KVD16, LIRB
31	regulation of cell population proliferation	2297	4.019E-08	7.715E-06	69	HMG1,2, Angiopoietin 1, R-spondins, LHX1, Histone H2, PBXIP1, HGF, A20, Histone H2A, GSTs, FNIP2, Connexin 30, APJ, MCR, KiSS-1, SLC4A1, Neuropilin-2, Annexin I, VCAM1, PLA2, HIF-prolyl hydroxylase, CD44, MFGE8, WNT7B, SIX3, Fatty acid-binding protein, MHC Class I alpha chain, EGLN3, UHRF1, SULF1, Galpha(s)-specific calcitonin GPCRs, GPNMB (Osteoactivin), Galpha(q)-specific peptide GPCRs, HMGB2, Cystatin C, PP2135, Fc gamma RII beta, SOX17, Seprase, Clmn, ILT4, Fc gamma RII, CEACAM, PRSS11 (HtrA1), LRH1, Galpha(i)-specific peptide GPCRs, S1P1 receptor, I-TAC, Apo-2L(TNFSF10), Lactoferrin, Galpha(q)-specific nucleotide-like GPCRs, RASSF10, Aquaporin 1, PEA3, Galpha(i)-specific EDG GPCRs, PKHD1, MYEOV2, PLC-delta, EGF, APRIL(TNFSF13), GFAP, PR (membrane), POU class III, RXR, Galpha(s)-specific peptide GPCRs, WNT, PR (nuclear), Midkine, LIRB

32	leukocyte mediated immunity	327	4.922E-08	9.075E-06	21	Kappa chain (Ig light chain), KV139, GZMH, C4A protein, Tubulin beta, IGHA1, PLA2, C4, MHC Class I alpha chain, IGKC, IGHG1, Galpha(q)-specific peptide GPCRs, Fc gamma RII beta, Perforin, Fc gamma RII, Galpha(q)-specific nucleotide-like GPCRs, Ig light chain, APRIL(TNFSF13), Oct-2, KVD16, LIRB
33	regulation of tumor necrosis factor production	242	5.074E-08	9.075E-06	18	HMG1,2, Angiopoietin 1, A20, GSTs, MHC Class I alpha chain, GPNMB (Osteoactivin), Galpha(q)-specific peptide GPCRs, POMC, PP2135, Fc gamma RII, Galpha(i)-specific peptide GPCRs, Lactoferrin, 2'-5'-oligoadenylate synthetase, OAS3, Galpha(s)-specific peptide GPCRs, WNT, LIRB, ILT7
34	positive regulation of immune response	662	5.185E-08	9.075E-06	31	HMG1,2, Kappa chain (Ig light chain), KV139, C4A protein, Annexin I, IGHA1, PLA2, CD44, C4, MHC Class I alpha chain, Ficolin, RSAD2, IGKC, EAT-2, IGHG1, Galpha(q)-specific peptide GPCRs, HMGB2, Fc gamma RII beta, Fc gamma RII, Galpha(i)-specific peptide GPCRs, Ficolin-1, Galpha(q)-specific nucleotide-like GPCRs, Ig light chain, NALP3, GBP5, APRIL(TNFSF13), PLA2G5, WNT, KVD16, HLAC, LIRB
35	regulation of dendritic cell differentiation	24	5.795E-08	9.853E-06	7	HMG1,2, MHC Class I alpha chain, Fc gamma RII beta, ILT4, Fc gamma RII, HLAC, LIRB
36	regulation of neutrophil apoptotic process	15	6.116E-08	1.011E-05	6	Annexin I, CD44, Galpha(q)-specific peptide GPCRs, Fc gamma RII beta, Fc gamma RII, Galpha(i)-specific peptide GPCRs
37	response to peptide	857	6.319E-08	1.016E-05	36	HMG1,2, Histone H2, A20, Histone H2A, GSTs, Annexin I, VCAM1, PLA2, PDK2, Fatty acid-binding protein, UHRF1, Galpha(s)-specific calcitonin GPCRs, MC4R, Galpha(q)-specific peptide GPCRs, ALDOB, POMC, PLAT (TPA), Fc gamma RII beta, Fc gamma RII, Connexin 26, CD147, CEACAM, Galpha(i)-specific peptide GPCRs, Apo-2L(TNFSF10), Calcitonin receptor, Galpha(q)-specific nucleotide-like GPCRs, DDX11, PLC-delta, PR (membrane), RXR, Dystroglycan, Galpha(s)-specific peptide GPCRs, AGRP, ACES, WNT, PR (nuclear)

38	regulation of immune effector process	494	6.918E-08	1.083E-05	26	HMG1,2, Angiopoietin 1, A20, Annexin I, PLA2, MHC Class I alpha chain, Ficolin, RSAD2, EAT-2, IGHG1, Galpha(q)-specific peptide GPCRs, POMC, PP2135, Fc gamma RII beta, Fc gamma RII, CEACAM, Galpha(i)-specific peptide GPCRs, Ficolin-1, SUPT6H, Galpha(q)-specific nucleotide-like GPCRs, NALP3, APRIL(TNFSF13), PLA2G5, WNT, HLAC, LIRB
39	regulation of tumor necrosis factor superfamily cytokine production	249	7.833E-08	1.190E-05	18	HMG1,2, Angiopoietin 1, A20, GSTs, MHC Class I alpha chain, GPNMB (Osteoactivin), Galpha(q)-specific peptide GPCRs, POMC, PP2135, Fc gamma RII, Galpha(i)-specific peptide GPCRs, Lactoferrin, 2'-5'-oligoadenylate synthetase, OAS3, Galpha(s)-specific peptide GPCRs, WNT, LIRB, ILT7
40	regulation of response to biotic stimulus	464	8.001E-08	1.190E-05	25	HMG1,2, A20, OASL, PLA2, MHC Class I alpha chain, Ficolin, EAT-2, Galpha(q)-specific peptide GPCRs, POMC, HMGB2, GBP6, Fc gamma RII beta, Fc gamma RII, CEACAM, PRSS11 (HtrA1), Ficolin-1, Lactoferrin, 2'-5'-oligoadenylate synthetase, OAS3, GBP5, PLA2G5, WNT, SEC14L1, HLAC, LIRB
41	response to stress	4173	9.203E-08	1.336E-05	104	METRNL, HMG1,2, Angiopoietin 1, Kappa chain (Ig light chain), Histone H2, PBXIP1, A20, OASL, Nk3R, MxB, Histone H2A, KV139, GZMH, COLEC12, GSTs, FNIP2, CAT-2, C4A protein, Tubulin beta, SLC4A1, Annexin I, VCAM1, IGHA1, PLA2, HIF-prolyl hydroxylase, CD44, C4, PDK2, Fatty acid-binding protein, MHC Class I alpha chain, Ficolin, RSAD2, GPR120, EGLN3, UHRF1, IGKC, GSTM3, LYPD1, EAT-2, IGHG1, Galpha(q)-specific peptide GPCRs, ALDOB, Histone H2B, SOD3 (EC-SOD), POMC, WFS1, HMGB2, Cystatin C, PLAT (TPA), GBP6, Fc gamma RII beta, APOL1, ILT4, Perforin, Fc gamma RII, IFI27, GIPR, Connexin 26, ALAS2, CEACAM, L-FABP, HIST2H2BE, Galpha(i)-specific peptide GPCRs, DGK-kappa, I-TAC, Ficolin-1, Lactoferrin, STARD13, Galpha(q)-specific nucleotide-like GPCRs, 2'-5'-oligoadenylate synthetase, AGS8, Aquaporin 1, H28, MxA, Galpha(i)-specific EDG GPCRs, P2Y1, DDX11, Carbohydrate sulfotransferases, SLC12A1, Ig light chain, OAS3, PLC-delta, NALP3, GBP5, WDR45L, NQO1, CCDC88C, GBP4, AL3A2, GFAP, RXR, Dystroglycan, Galpha(s)-specific peptide GPCRs, HMGCL, WNT, Proline oxidase 1, CART, KVD16, Midkine, SEC14L1, HLAC, LIRB, RNF152, ILT7

42	regulation of lymphocyte activation	652	1.268E-07	1.781E-05	30	HMG1,2, Kappa chain (Ig light chain), A20, KV139, SLC4A1, Annexin I, VCAM1, IGHA1, PLA2, CD44, MHC Class I alpha chain, IGKC, GPNMB (Osteoactivin), IGHG1, Galpha(q)-specific peptide GPCRs, PP2135, Fc gamma RII beta, ILT4, Fc gamma RII, CEACAM, Galpha(i)-specific peptide GPCRs, SUPT6H, Galpha(q)-specific nucleotide-like GPCRs, Ig light chain, NALP3, APRIL(TNFSF13), WNT, KVD16, Midkine, LIRB
43	regulation of adaptive immune response	286	1.287E-07	1.781E-05	19	HMG1,2, A20, Annexin I, PLA2, CD44, MHC Class I alpha chain, RSAD2, IGHG1, Galpha(q)-specific peptide GPCRs, PP2135, Fc gamma RII beta, Fc gamma RII, CEACAM, Galpha(i)-specific peptide GPCRs, SUPT6H, NALP3, APRIL(TNFSF13), HLAC, LIRB
44	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	288	1.434E-07	1.940E-05	19	HMG1,2, Kappa chain (Ig light chain), KV139, C4A protein, IGHA1, C4, MHC Class I alpha chain, IGKC, IGHG1, Galpha(q)-specific peptide GPCRs, Fc gamma RII beta, Perforin, Fc gamma RII, Galpha(i)-specific peptide GPCRs, Ig light chain, APRIL(TNFSF13), Oct-2, KVD16, LIRB
45	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	261	1.592E-07	2.105E-05	18	HMG1,2, A20, Annexin I, PLA2, MHC Class I alpha chain, RSAD2, IGHG1, Galpha(q)-specific peptide GPCRs, PP2135, Fc gamma RII beta, Fc gamma RII, CEACAM, Galpha(i)-specific peptide GPCRs, SUPT6H, NALP3, APRIL(TNFSF13), HLAC, LIRB
46	regulation of innate immune response	293	1.875E-07	2.395E-05	19	HMG1,2, A20, PLA2, MHC Class I alpha chain, Ficolin, EAT-2, Galpha(q)-specific peptide GPCRs, HMGB2, Fc gamma RII beta, Fc gamma RII, CEACAM, Ficolin-1, 2'-5'-oligoadenylate synthetase, OAS3, GBP5, PLA2G5, WNT, HLAC, LIRB

47	response to stimulus	8783	1.892E-07	2.395E-05	179	METRNL, DCHS1, HMG1,2, Angiopoietin 1, R-spondins, Kappa chain (Ig light chain), SLC6A11, LHX1, Histone H2, PBXIP1, HGF, A20, OASL, Nk3R, MxB, Histone H2A, KV139, GZMH, COLEC12, GSTs, FNIP2, CAT-2, Connexin 30, C4A protein, APJ, MCR, Caspase-10, R-spondin 3, KiSS-1, Tubulin beta, SULT1A1, APH-1, SLC4A1, Neuropilin-2, Annexin I, VCAM1, IGHA1, PLA2, Rab-5C, HIF-prolyl hydroxylase, CD44, C4, MFGE8, CDGAP, WNT7B, PDK2, Fatty acid-binding protein, ARHI, MHC Class I alpha chain, Ficolin, RSAD2, G2A, SDHL, LGR6, GPR120, GPRC5C, EGLN3, UHRF1, SULF1, PAMCI, HYEP, IGKC, DCPS, GSTM3, LYPD1, Galpha(s)-specific calcitonin GPCRs, GPNMB (Osteoactivin), MC4R, EAT-2, IGHG1, Galpha(q)-specific peptide GPCRs, RP13-102H20.1, ALDOB, Histone H2B, MAFbx, FLJ20625, Ccd1, SOD3 (EC-SOD), POMC, WFS1, HMGB2, XAF1, Cystatin C, RIS, PLAT (TPA), PP2135, GPR101, GBP6, Fc gamma RII beta, SOX17, Seprase, APOL1, ILT4, SLC13A5, Perforin, Fc gamma RII, ARRDC2, IFI27, GIPR, Connexin 26, CD147, ALAS2, CEACAM, L-FABP, LRH1, HIST2H2BE, Galpha(i)-specific peptide GPCRs, DGK-kappa, Semaphorin 3D, CPT-1A, S1P1 receptor, I-TAC, Ficolin-1, Apo-2L(TNFSF10), Lactoferrin, FLJ45455, Calcitonin receptor, STARD13, Galpha(q)-specific nucleotide-like GPCRs, 2'-5'-oligoadenylate synthetase, AGS8, RASSF10, Aquaporin 1, H28, MxA, PEA3, Galpha(i)-specific EDG GPCRs, P2Y1, THNSL2, DDX11, Carbohydrate sulfotransferases, MYEOV2, SLC12A1, Ig light chain, APH-1A, OAS3, PLC-delta, NALP3, EGF, GBP5, WDR45L, NQO1, CCDC88C, RAS4B, APRIL(TNFSF13), GBP4, AL3A2, GFAP, PR (membrane), POU class III, RXR, IFI44, Dystroglycan, ROPN1B, ECEL1, PLA2G5, CABYR, PLCD4, Galpha(s)-specific peptide GPCRs, Oct-2, CYP4V2, AGRP, ACES, HMGCL, WNT, Proline oxidase 1, WIF1, RXRG, CART, KVD16, PR (nuclear), Midkine, SEC14L1, HLAC, LIRB, RNF152, ILT7, CCDC80, APCDD1
48	complement activation, classical pathway	56	1.935E-07	2.399E-05	9	Kappa chain (Ig light chain), KV139, C4A protein, IGHA1, C4, IGKC, IGHG1, Ig light chain, KVD16

49	immune response-regulating cell surface receptor signaling pathway	299	2.566E-07	3.116E-05	19	Kappa chain (Ig light chain), KV139, IGHA1, PLA2, MHC Class I alpha chain, Ficolin, IGKC, EAT-2, IGHG1, Galpha(q)-specific peptide GPCRs, Fc gamma RII beta, ILT4, Fc gamma RII, Galpha(i)-specific peptide GPCRs, Ficolin-1, Ig light chain, KVD16, LIRB, ILT7
50	negative regulation of leukocyte cell-cell adhesion	190	3.140E-07	3.738E-05	15	HMG1,2, GSTs, Annexin I, PLA2, CD44, MHC Class I alpha chain, GPNMB (Osteoactivin), PP2135, Fc gamma RII beta, ILT4, Fc gamma RII, CEACAM, Galpha(q)-specific nucleotide-like GPCRs, Midkine, LIRB

Table A17. Top 50 TargetALS Gene Ontology (GO) Biological Processes enrichments with MetaCore. Term size refers to the number of genes in the term, with the intersection size denoting the number of genes in the dataset found in the term.

#	Term Name	Term ID	Term Size	adjusted p-value (FDR)	Intersection Size	Intersection Gene Names
1	The citric acid (TCA) cycle and respiratory electron transport	REAC:R-HSA-1428517	177	2.05E-14	39	ENSG00000155380,ENSG00000004799,ENSG00000164258,ENSG00000164405,ENSG00000183648,ENSG00000168291,ENSG00000178741,ENSG00000165264,ENSG00000119421,ENSG00000164919,ENSG00000128609,ENSG00000173660,ENSG00000117118,ENSG00000145494,ENSG00000150768,ENSG00000163541,ENSG00000067992,ENSG00000124767,ENSG00000125356,ENSG00000213585,ENSG00000189043,ENSG00000165629,ENSG00000124172,ENSG00000115944,ENSG00000110955,ENSG00000065518,ENSG00000167283,ENSG00000143158,ENSG00000156467,ENSG00000154518,ENSG00000178449,ENSG00000123545,ENSG00000152234,ENSG00000184076,ENSG00000004779,ENSG00000119013,ENSG00000136143,ENSG00000169021,ENSG00000111775
2	Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	REAC:R-HSA-163200	127	9.56E-11	29	ENSG00000164258,ENSG00000164405,ENSG00000183648,ENSG00000178741,ENSG00000165264,ENSG00000119421,ENSG00000164919,ENSG00000128609,ENSG00000173660,ENSG00000117118,ENSG00000145494,ENSG00000125356,ENSG00000189043,ENSG00000165629,ENSG00000124172,ENSG00000115944,ENSG00000110955,ENSG00000065518,ENSG00000167283,ENSG00000156467,ENSG00000154518,ENSG00000178449,ENSG00000123545,ENSG00000152234,ENSG00000184076,ENSG00000004779,ENSG00000119013,ENSG00000169021,ENSG00000111775
3	Respiratory electron transport	REAC:R-HSA-611105	103	5.17E-08	23	ENSG00000164258,ENSG00000164405,ENSG00000183648,ENSG00000178741,ENSG00000165264,ENSG00000119421,ENSG00000164919,ENSG00000128609,ENSG00000173660,ENSG00000117118,ENSG00000145494,ENSG00000125356,ENSG00000189043,ENSG00000115944,ENSG00000065518,ENSG00000156467,ENSG00000178449,ENSG00000123545,ENSG00000184076,ENSG00000004779,ENSG00000119013,ENSG00000169021,ENSG00000111775

4	Metabolism	REAC:R-HSA-1430728	2075	7.41E-07	146	ENSG00000074410,ENSG00000160883,ENSG00000180089,ENSG00000152207,ENSG00000155380,ENSG00000004799,ENSG00000153093,ENSG00000138074,ENSG00000229894,ENSG00000196498,ENSG00000187566,ENSG00000103257,ENSG00000009950,ENSG00000196502,ENSG00000127415,ENSG00000176920,ENSG00000131730,ENSG00000110090,ENSG00000161267,ENSG00000006071,ENSG00000176383,ENSG00000141837,ENSG00000126368,ENSG00000137857,ENSG00000172292,ENSG00000164258,ENSG00000164405,ENSG00000183648,ENSG00000197894,ENSG00000168291,ENSG00000148154,ENSG00000132824,ENSG00000178741,ENSG00000005249,ENSG00000101843,ENSG00000035687,ENSG00000165264,ENSG00000119421,ENSG00000164919,ENSG00000120992,ENSG00000131238,ENSG00000128609,ENSG00000138018,ENSG00000138669,ENSG00000170340,ENSG00000171314,ENSG00000118402,ENSG00000104763,ENSG00000143106,ENSG00000130540,ENSG00000173660,ENSG00000163682,ENSG00000117118,ENSG00000145494,ENSG00000150768,ENSG00000186298,ENSG00000144827,ENSG00000163541,ENSG00000067992,ENSG00000081181,ENSG00000114480,ENSG00000124767,ENSG00000006007,ENSG00000085662,ENSG00000162368,ENSG00000136810,ENSG00000091039,ENSG00000023330,ENSG00000125356,ENSG00000109929,ENSG00000213585,ENSG00000173221,ENSG00000189043,ENSG00000165629,ENSG00000174684,ENSG00000133731,ENSG00000067064,ENSG00000115419,ENSG00000198431,ENSG00000124172,ENSG00000115944,ENSG00000110955,ENSG00000108946,ENSG00000150540,ENSG00000139684,ENSG00000105355,ENSG00000065518,ENSG00000155096,ENSG00000117461,ENSG00000164172,ENSG00000167283,ENSG00000143158,ENSG00000147224,ENSG00000156467,ENSG00000154518,ENSG00000129084,ENSG00000113575,ENSG00000084090,ENSG00000162630,ENSG00000102172,ENSG00000178449,ENSG00000165175,ENSG00000096384,ENSG00000123545,ENSG00000114450,ENSG00000146151,ENSG00000152234,ENSG00000168288,ENSG00000184076,ENSG00000012660,ENSG00000132341,ENSG00000100934,ENSG00000068366,ENSG00000004779,ENSG00000135002,ENSG00000119013,ENSG00000085231,ENSG00000137825,ENSG00000083720,ENSG00000180817,ENSG00000136143,ENSG00000139278,ENSG00000169021,ENSG00000173598,ENSG00000100804,ENSG00000014641,ENSG0000011

						1775,ENSG00000119125,ENSG00000156136,ENSG00000120053,ENSG00000052802,ENSG00000065154,ENSG00000162188,ENSG00000164211,ENSG00000068976,ENSG00000170745,ENSG00000101911,ENSG00000175445,ENSG00000123836,ENSG00000164434,ENSG00000165434,ENSG00000183196,ENSG00000174607,ENSG00000062096,ENSG00000139287,ENSG00000161896

5	Transmission across Chemical Synapses	REAC:R-HSA-112315	259	7.99E-05	32	ENSG00000141837,ENSG00000005249,ENSG00000100030,ENSG00000109738,ENSG00000145864,ENSG00000156642,ENSG00000082458,ENSG00000067715,ENSG00000175175,ENSG00000166501,ENSG00000115419,ENSG00000108946,ENSG00000109158,ENSG00000011677,ENSG00000145349,ENSG00000114450,ENSG00000152495,ENSG00000127824,ENSG00000167552,ENSG00000022355,ENSG00000073969,ENSG00000109971,ENSG00000198785,ENSG00000144746,ENSG00000182481,ENSG00000104490,ENSG00000162188,ENSG00000128683,ENSG00000101958,ENSG00000186297,ENSG00000134294,ENSG00000136750
6	Neuronal System	REAC:R-HSA-112316	400	0.000261829	41	ENSG00000131398,ENSG00000073150,ENSG00000099822,ENSG00000006071,ENSG00000141837,ENSG00000005249,ENSG00000100030,ENSG00000109738,ENSG00000145864,ENSG00000156642,ENSG00000082458,ENSG00000067715,ENSG00000175175,ENSG00000166501,ENSG00000115419,ENSG00000184408,ENSG00000108946,ENSG00000109158,ENSG00000110218,ENSG00000140015,ENSG00000011677,ENSG00000145349,ENSG00000114450,ENSG00000152495,ENSG00000127824,ENSG00000167552,ENSG00000022355,ENSG00000073969,ENSG00000109971,ENSG00000082482,ENSG00000198785,ENSG00000144746,ENSG00000182481,ENSG00000104490,ENSG00000162188,ENSG00000170745,ENSG00000128683,ENSG00000101958,ENSG00000186297,ENSG00000134294,ENSG00000136750

7	Cellular responses to stress	REAC:R-HSA-2262752	751	0.000347886	63	ENSG00000265972,ENSG00000101213,ENSG00000143578,ENSG00000196498,ENSG00000105662,ENSG00000108557,ENSG00000184678,ENSG00000132510,ENSG00000111203,ENSG00000126368,ENSG00000164442,ENSG00000178741,ENSG00000106615,ENSG00000101843,ENSG00000162694,ENSG00000081189,ENSG00000164919,ENSG00000149196,ENSG00000155097,ENSG00000143106,ENSG00000069345,ENSG00000131966,ENSG00000100030,ENSG00000163682,ENSG00000134248,ENSG00000230989,ENSG00000128590,ENSG00000047249,ENSG00000088986,ENSG00000136810,ENSG00000100554,ENSG00000142168,ENSG00000189043,ENSG00000164603,ENSG00000134001,ENSG00000198431,ENSG00000115944,ENSG00000170606,ENSG00000129084,ENSG00000065559,ENSG00000145349,ENSG00000168283,ENSG00000147416,ENSG00000178449,ENSG00000096384,ENSG00000116586,ENSG00000117450,ENSG00000117410,ENSG00000072401,ENSG00000114573,ENSG00000127824,ENSG00000131100,ENSG00000167552,ENSG00000109971,ENSG00000233822,ENSG00000155304,ENSG00000086061,ENSG00000165672,ENSG00000198898,ENSG00000100804,ENSG00000111775,ENSG00000109846,ENSG00000164032

8	Cellular responses to stimuli	REAC:R-HSA-8953897	765	0.000657571	63	ENSG00000265972,ENSG00000101213,ENSG00000143578,ENSG00000196498,ENSG00000105662,ENSG00000108557,ENSG00000184678,ENSG00000132510,ENSG00000111203,ENSG00000126368,ENSG00000164442,ENSG00000178741,ENSG00000106615,ENSG00000101843,ENSG00000162694,ENSG00000081189,ENSG00000164919,ENSG00000149196,ENSG00000155097,ENSG00000143106,ENSG00000069345,ENSG00000131966,ENSG00000100030,ENSG00000163682,ENSG00000134248,ENSG00000230989,ENSG00000128590,ENSG00000047249,ENSG00000088986,ENSG00000136810,ENSG00000100554,ENSG00000142168,ENSG00000189043,ENSG00000164603,ENSG00000134001,ENSG00000198431,ENSG00000115944,ENSG00000170606,ENSG00000129084,ENSG00000065559,ENSG00000145349,ENSG00000168283,ENSG00000147416,ENSG00000178449,ENSG00000096384,ENSG00000116586,ENSG00000117450,ENSG00000117410,ENSG00000072401,ENSG00000114573,ENSG00000127824,ENSG00000131100,ENSG00000167552,ENSG00000109971,ENSG00000233822,ENSG00000155304,ENSG00000086061,ENSG00000165672,ENSG00000198898,ENSG00000100804,ENSG00000111775,ENSG00000109846,ENSG00000164032
9	TP53 Regulates Metabolic Genes	REAC:R-HSA-5628897	84	0.002015317	15	ENSG00000178741,ENSG00000106615,ENSG00000164919,ENSG00000134248,ENSG00000136810,ENSG00000189043,ENSG00000166913,ENSG00000115419,ENSG00000198431,ENSG00000115944,ENSG00000178449,ENSG00000116586,ENSG00000117450,ENSG00000111775,ENSG00000128245
10	Amino acids regulate mTORC1	REAC:R-HSA-9639288	55	0.002169899	12	ENSG00000111203,ENSG00000106615,ENSG00000155097,ENSG00000134248,ENSG00000047249,ENSG00000100554,ENSG00000164603,ENSG00000147416,ENSG00000116586,ENSG00000117410,ENSG00000114573,ENSG00000131100

11	Neurotransmitter receptors and postsynaptic signal transmission	REAC:R-HSA-112314	196	0.003430639	24	ENSG00000005249,ENSG00000100030,ENSG00000109738,ENSG00000145864,ENSG00000156642,ENSG00000082458,ENSG00000175175,ENSG00000166501,ENSG00000108946,ENSG00000109158,ENSG00000011677,ENSG00000145349,ENSG00000114450,ENSG00000152495,ENSG00000127824,ENSG00000167552,ENSG00000022355,ENSG00000073969,ENSG00000198785,ENSG00000182481,ENSG00000104490,ENSG00000162188,ENSG00000101958,ENSG00000186297
12	Pyruvate metabolism and Citric Acid (TCA) cycle	REAC:R-HSA-71406	54	0.010976225	11	ENSG00000155380,ENSG00000004799,ENSG00000168291,ENSG00000117118,ENSG00000150768,ENSG00000163541,ENSG00000067992,ENSG00000124767,ENSG00000213585,ENSG00000143158,ENSG00000136143
13	Prefoldin mediated transfer of substrate to CCT/TriC	REAC:R-HSA-389957	28	0.011022993	8	ENSG00000120438,ENSG00000156261,ENSG00000150753,ENSG00000135624,ENSG00000115484,ENSG00000127824,ENSG00000167552,ENSG00000155959
14	Complex I biogenesis	REAC:R-HSA-6799198	57	0.018746131	11	ENSG00000164258,ENSG00000183648,ENSG00000165264,ENSG00000119421,ENSG00000128609,ENSG00000145494,ENSG00000125356,ENSG00000065518,ENSG00000123545,ENSG00000004779,ENSG00000119013
15	Folding of actin by CCT/TriC	REAC:R-HSA-390450	10	0.019165304	5	ENSG00000120438,ENSG00000156261,ENSG00000150753,ENSG00000135624,ENSG00000115484
16	Pyruvate metabolism	REAC:R-HSA-70268	30	0.019185317	8	ENSG00000155380,ENSG00000004799,ENSG00000168291,ENSG00000150768,ENSG00000067992,ENSG00000124767,ENSG00000213585,ENSG00000143158
17	Cooperation of Prefoldin and TriC/CCT in actin and tubulin folding	REAC:R-HSA-389958	33	0.040445511	8	ENSG00000120438,ENSG00000156261,ENSG00000150753,ENSG00000135624,ENSG00000115484,ENSG00000127824,ENSG00000167552,ENSG00000155959
18	Formation of ATP by chemiosmotic coupling	REAC:R-HSA-163210	18	0.047422293	6	ENSG00000165629,ENSG00000124172,ENSG00000110955,ENSG00000167283,ENSG00000154518,ENSG00000152234

Table A18. Significant KCL BrainBank Reactome enrichments (adjusted p-value (FDR) < 0.05) with gProfiler2. Term size refers to the number of genes in the term, with the intersection size denoting the number of genes in the dataset found in the term.

#	Term Name	Term ID	Term Size	adjusted p-value (FDR)	Intersection Size	Intersection Gene Names
1	Interferon Signaling	REAC:R-HSA-913531	193	0.00376404	13	ENSG00000162654,ENSG00000026508,ENSG00000154451,ENSG00000157601,ENSG00000183347,ENSG00000135114,ENSG00000183486,ENSG00000165949,ENSG00000204525,ENSG00000132530,ENSG00000111331,ENSG00000134321,ENSG00000162692
2	Interferon alpha/beta signaling	REAC:R-HSA-909733	68	0.00388184	8	ENSG00000157601,ENSG00000135114,ENSG00000183486,ENSG00000165949,ENSG00000204525,ENSG00000132530,ENSG00000111331,ENSG00000134321
3	Interferon gamma signaling	REAC:R-HSA-877300	87	0.02391092	8	ENSG00000162654,ENSG00000026508,ENSG00000154451,ENSG00000183347,ENSG00000135114,ENSG00000204525,ENSG00000111331,ENSG00000162692

Table A19. Significant TargetALS Reactome enrichments (adjusted p-value (FDR) < 0.05) with gProfiler2. Term size refers to the number of genes in the term, with the intersection size denoting the number of genes in the dataset found in the term.

#	Term Name	Term Size	p-value	adjusted p-value (FDR)	Intersection Size	Intersection Gene Names
1	NRF2 regulation of oxidative stress response	54	2.681E-06	2.257E-03	10	Thioredoxin, PRDX1, TXNRD1, SMRT, ENC1, PKC, ERK2 (MAPK1), MEK4(MAP2K4), SOD1, PI3K reg class IA
2	Tinnitus-associated changes in auditory pathway	82	3.658E-06	2.257E-03	12	GAD1, HCN2, GABA-A receptor alpha-1 subunit, GLRA, GABA-A receptor beta-2 subunit, GABA-A receptor alpha-4 subunit, GRM6, GABA-A receptor alpha-5 subunit, Glycine receptor, GABA-A receptor alpha-3 subunit, Glycine receptor beta chain, GAD2
3	Neurophysiological process_Regulation of intrinsic membrane properties and excitability of cortical pyramidal neurons	74	7.984E-06	2.463E-03	11	HPCA, TRPC5, G-protein beta/gamma, cPKC (conventional), PKA-reg (cAMP-dependent), TRPC4, Calcineurin A (catalytic), Neurocalcin delta, Calmodulin, PKC, HTR2A
4	Ubiquinone metabolism	74	7.984E-06	2.463E-03	11	NDUFAB1, NDUFA1, NDUFB4, NDUFA8, NDUFA4, NDUFB6, NDUFS4, NDUFB3, NDUFB1, NDUFS6, NDUFA5
5	G protein-coupled receptors signaling in lung cancer	76	1.039E-05	2.564E-03	11	Endothelin-1, CNR1, G-protein beta/gamma, Galpha(i)-specific peptide GPCRs, EGF, PKA-reg (cAMP-dependent), Galpha(i)-specific cannabis GPSRs, Galpha(q)-specific peptide GPCRs, Calmodulin, ERK1/2, SSTR2
6	Oxidative stress_Role of ASK1 under oxidative stress	54	2.087E-05	4.292E-03	9	UNRIP, Thioredoxin, PRDX1, TXNIP (VDUP1), PP2A catalytic, Glutaredoxin, MEK4(MAP2K4), SOD1, 14-3-3
7	Signal transduction_Calcium-mediated signaling	72	3.791E-05	6.412E-03	10	PKC-beta, CaMK IV, cPKC (conventional), Calcineurin A (catalytic), MEF2, Calmodulin, ERK1/2, PKC, MEK4(MAP2K4), 14-3-3
8	Signal transduction_Erk Interactions: Inhibition of Erk	34	4.261E-05	6.412E-03	7	PKA-reg (cAMP-dependent), Calcineurin A (catalytic), PP2A catalytic, Calmodulin, ERK1/2, PKC, ERK2 (MAPK1)
9	Signal transduction_Non-neuronal ACM1, ACM3 and ACM5 signaling	74	4.826E-05	6.412E-03	10	MRLC2, PKA-reg (cAMP-dependent), MRLC, Calmodulin, ERK1/2, PKC, Guanylate Cyclase 1, soluble, MEF2C, Protein kinase G, PI3K reg class IA
10	Altered Ca2+ handling in heart failure	35	5.196E-05	6.412E-03	7	G-protein beta/gamma, PP1-cat, NCX1, Calcineurin A (catalytic), PP2A catalytic, Calmodulin, CaMK II delta
11	Bipolar Disorder	76	6.094E-05	6.674E-03	10	Synaptotagmin I, PKC-beta, G-protein beta/gamma, cPKC (conventional), Serotonin receptor, PKA-reg (cAMP-dependent), Calcineurin A (catalytic), Calmodulin, ERK1/2, PKC
12	Development_Melanocyte development and pigmentation	49	7.031E-05	6.674E-03	8	MGF, PKC-beta, PKA-reg (cAMP-dependent), Protein kinase G1, Guanylate cyclase (alpha-1/beta-1), ERK1/2, PI3K reg class IA, Galpha(s)-specific peptide GPCRs

13	Transcription_CREB signaling pathway	49	7.031E-05	6.674E-03	8	CaMK IV, cPKC (conventional), PKA-reg (cAMP-dependent), PP1-cat, PP2A catalytic, Calmodulin, ERK1/2, PI3K reg class IA
14	Neurophysiological process_Activity-dependent synaptic AMPA receptor removal	64	8.388E-05	7.371E-03	9	HPCA, NSF, cPKC (conventional), PP1-cat, Calcineurin A (catalytic), NAPB, PP2A catalytic, Calmodulin, PKC
15	LRRK2 in neuronal apoptosis in Parkinson's disease	17	8.960E-05	7.371E-03	5	PRDX3, Thioredoxin, VDAC 1, ANT, MPTP complex
16	Neurophysiological process_GABA-A receptor life cycle	27	9.701E-05	7.461E-03	6	GABA-A receptor alpha-1 subunit, NSF, GABA-A receptor beta-2 subunit, PP1-cat, Clathrin heavy chain, Tubulin alpha
17	Regulation of degradation of deltaF508-CFTR in CF	39	1.076E-04	7.461E-03	7	HSP90, HSP70, Aha1, UBE2D1, Hdj-2, SUMO-3, HSC70
18	Neurophysiological process_Synaptic vesicle fusion and recycling in nerve terminals	52	1.088E-04	7.461E-03	8	Synaptotagmin I, P/Q-type calcium channel alpha-1A subunit, NSF, SYP, Calcineurin A (catalytic), Calmodulin, Endophilin A1, HSC70
19	Development_Role of HDAC and calcium/calmodulin-dependent kinase (CaMK) in control of skeletal myogenesis	53	1.250E-04	8.119E-03	8	CaMK IV, Calcineurin A (catalytic), MEF2, RHEB2, Calmodulin, MEF2C, PI3K reg class IA, 14-3-3
20	Apoptosis and survival_BAD phosphorylation	42	1.753E-04	1.030E-02	7	G-protein beta/gamma, PKA-reg (cAMP-dependent), Calcineurin A (catalytic), PP2A catalytic, ERK1/2, PI3K reg class IA, 14-3-3
21	Oxidative stress_Activation of NOX1, NOX5, DUOX1 and DUOX2 NADPH Oxidases	42	1.753E-04	1.030E-02	7	DUOX1, PKC-beta, cPKC (conventional), PKA-reg (cAMP-dependent), Calmodulin, PKC, ERK2 (MAPK1)
22	Ca(2+)-dependent NF-AT signaling in cardiac hypertrophy	57	2.109E-04	1.089E-02	8	PKC-beta, G-protein beta/gamma, PKA-reg (cAMP-dependent), NCX1, Calcineurin A (catalytic), MEF2, Calmodulin, MEF2C
23	Regulation of intrinsic membrane properties and excitability of striatopallidal medium spiny neurons in Huntington's disease	57	2.109E-04	1.089E-02	8	G-protein beta/gamma, P/Q-type calcium channel alpha-1A subunit, cPKC (conventional), Calcineurin A (catalytic), Kv4.2 channel, Calmodulin, PKC, Guanylate Cyclase 1, soluble
24	Angiotensin II Signaling in Cardiac Hypertrophy	72	2.118E-04	1.089E-02	9	Thioredoxin, G-protein beta/gamma, CaMK IV, NCX1, Calcineurin A (catalytic), Calmodulin, ERK1/2, MEK4(MAP2K4), SOD1
25	Neurophysiological process_Glutamic acid regulation of Dopamine D1A receptor signaling	45	2.738E-04	1.351E-02	7	GABA-A receptor beta-2 subunit, PKA-reg (cAMP-dependent), PP1-cat, CDK5, Calcineurin A (catalytic), PP2A catalytic, Calmodulin
26	A shift from oxidative to glycolytic muscle fiber phenotype in quadriceps muscles in COPD	60	3.029E-04	1.438E-02	8	DCMC, CPT-1A, ATP5B, PDK4, Fatty acid-binding protein, MEF2, ALAS1, ERK2 (MAPK1)

27	Regulation of intrinsic membrane properties and excitability of striatonigral medium spiny neurons in Huntington's disease	62	3.808E-04	1.740E-02	8	P/Q-type calcium channel alpha-1A subunit, cPKC (conventional), PKA-reg (cAMP-dependent), PP1-cat, Kv4.2 channel, Calmodulin, PKC, Guanylate Cyclase 1, soluble
28	Transcription_ChREBP regulation pathway	23	4.225E-04	1.862E-02	5	G-protein beta/gamma, ChREBP, PKA-reg (cAMP-dependent), Acyl-CoA synthetase, PP2A catalytic
29	Neurophysiological process_Constitutive and regulated NMDA receptor trafficking	65	5.274E-04	2.014E-02	8	cPKC (conventional), PKA-reg (cAMP-dependent), PP1-cat, CDK5, Calcineurin A (catalytic), Calmodulin, PKC, SAP102
30	NF-AT signaling in cardiac hypertrophy	65	5.274E-04	2.014E-02	8	Endothelin-1, G-protein beta/gamma, CaMK IV, NCX1, Calcineurin A (catalytic), Calmodulin, MEF2C, PI3K reg class IA
31	Transport_The role of AVP in regulation of Aquaporin 2 and renal water reabsorption	50	5.328E-04	2.014E-02	7	PRKAR2B, MRLC2, PKA-reg type II (cAMP-dependent), PKA-reg (cAMP-dependent), MRLC, Calmodulin, ERK1/2
32	Immune response_Function of MEF2 in T lymphocytes	50	5.328E-04	2.014E-02	7	CaMK IV, Calcineurin A (catalytic), MEF2, Calmodulin, MEF2C, Calcineurin A (beta), 14-3-3
33	Transport_RAB3 regulation pathway	14	5.385E-04	2.014E-02	4	Rab-3B, Rab-3, NSF, Slp5
34	Immune response_Reactive oxygen species (ROS) in IL-4 signaling	66	5.854E-04	2.125E-02	8	DUOX1, cPKC (conventional), PKA-reg (cAMP-dependent), Protein kinase G1, Guanylate cyclase (alpha-1/beta-1), PP2A catalytic, Calmodulin, PKC
35	Muscle contraction_GPCRs in the regulation of smooth muscle tone	83	6.197E-04	2.142E-02	9	Endothelin-1, MELC, TRPC5, PKA-reg (cAMP-dependent), TRPC4, NCX1, MRLC, Calmodulin, HTR2A
36	HSP70 and HSP40-dependent folding in Huntington's disease	25	6.363E-04	2.142E-02	5	HSP90, HSP70, HSP90 beta, Hdj-2, HSC70
37	Signal transduction_Activation of PKC via G-Protein coupled receptor	52	6.793E-04	2.142E-02	7	MELC, PKC-beta, G-protein beta/gamma, Calcineurin A (catalytic), MEF2, Calmodulin, ERK1/2
38	Nicotine signaling in cholinergic neurons	52	6.793E-04	2.142E-02	7	G-protein beta/gamma, P/Q-type calcium channel alpha-1A subunit, Protein kinase G1, Calmodulin, Guanylate Cyclase 1, soluble, ERK2 (MAPK1), PI3K reg class IA
39	Signal transduction_Cyclic AMP signaling	38	6.927E-04	2.142E-02	6	G-protein beta/gamma, CaMK IV, PKA-reg (cAMP-dependent), Calcineurin A (catalytic), Calmodulin, PKC
40	Epigenetic regulation of neuronal hyperexcitability in neuropathic pain	102	7.020E-04	2.142E-02	10	PP2A cat (alpha), JMJD3, 14-3-3 beta/alpha, SYP, CDK5, Histone H2B, PP2A catalytic, Kv4.2 channel, Calmodulin, GAD2

41	Calcium-dependent regulation of normal and asthmatic smooth muscle contraction	68	7.168E-04	2.142E-02	8	Endothelin-1, Substance P extracellular region, G-protein beta/gamma, Neurokinin A, TRPC4, NCX1, MRLC, Calmodulin
42	ENaC regulation in normal and CF airways	53	7.636E-04	2.142E-02	7	Endothelin-1, G-protein beta/gamma, cPKC (conventional), PKA-reg (cAMP-dependent), ERK1/2, Protein kinase G, PI3K reg class IA
43	Neurophysiological process_Long-term depression in cerebellum	53	7.636E-04	2.142E-02	7	G-protein beta/gamma, P/Q-type calcium channel alpha-1A subunit, PP2A catalytic, Galpha(s)-specific CRF GPCRs, ERK1/2, Guanylate Cyclase 1, soluble, Protein kinase G
44	Translation_Regulation of EIF4F activity	53	7.636E-04	2.142E-02	7	EGF, PP2A catalytic, eIF4A, RHEB2, ERK1/2, MEK4(MAP2K4), PI3K reg class IA
45	Transcription_Negative regulation of HIF1A function	69	7.908E-04	2.169E-02	8	HSP90, HSP70, CITED2, HSPA4, MTG16 (CBFA2T3), HSP90 beta, LAMP2, HSC70
46	HCV-dependent cytoplasmic signaling leading to HCC	27	9.223E-04	2.474E-02	5	14-3-3 beta/alpha, eIF2S1, ERK1/2, PKC, ERK2 (MAPK1)
47	Development_Oxytocin receptor signaling	41	1.049E-03	2.755E-02	6	G-protein beta/gamma, cPKC (conventional), Protein kinase G1, Calmodulin, Guanylate Cyclase 1, soluble, MEF2C
48	Signal transduction_NO synthesis	90	1.117E-03	2.840E-02	9	HSP90, IRF1, Endothelin-1, G-protein beta/gamma, TRPC, PKA-reg (cAMP-dependent), Calmodulin, ERK1/2, MEF2C
49	CHDI_Correlations from Discovery data_Causal network	73	1.151E-03	2.840E-02	8	Substance P extracellular region, G-protein beta/gamma, CaMK IV, CDK5, MEF2, RHEB2, Calmodulin, ERK1/2
50	Neurophysiological process_Thyroliberin signaling	73	1.151E-03	2.840E-02	8	Endothelin-1, PKC-beta, G-protein beta/gamma, cPKC (conventional), PKA-reg (cAMP-dependent), Calmodulin, ERK1/2, PKC

Table A25. Top 50 KCL BrainBank Pathway Maps enrichments with MetaCore. Term size refers to the number of genes in the term, with the intersection size denoting the number of genes in the dataset found in the term.

#	Term Name	Term Size	p-value	adjusted p-value (FDR)	Intersection Size	Intersection Gene Names
1	Protein folding and maturation_POMC processing	22	3.761E-24	2.223E-21	17	CLIP, ACTH, alpha-MSH, beta-Endorphin, proACTH, POMC, Joining peptide (JP), N-POMC, gamma-MSH, N-POC, beta-LPH, gamma-LPH, ACTH 1-17, DA-alphaMSH, gamma2-MSH, gamma3-MSH, beta-MSH
2	POMC, alpha-MSH and AGRP in regulation of food intake and energy expenditure in obesity in hypothalamus	31	7.127E-06	2.106E-03	7	alpha-MSH, MC4R, proACTH, POMC, Beta-MSH / Beta-Endorphin, beta-LPH, AGRP
3	Immune response_IFN-alpha/beta signaling via JAK/STAT	59	5.218E-04	1.028E-01	7	MxB, RSAD2, XAF1, IFI27, I-TAC, Apo-2L(TNFSF10), GBP4
4	Development_Positive regulation of WNT/Beta-catenin signaling at the receptor level	64	8.582E-04	1.268E-01	7	R-spondins, CD44, WNT7B, LGR6, Biglycan, RAB3IP, WNT
5	Role of metalloproteases and heparanase in progression of pancreatic cancer	29	4.986E-03	5.787E-01	4	CD44, CD44 soluble, CD147, CD44 (EXT)
6	Dysregulation of germinal center response in SLE	51	7.630E-03	5.787E-01	5	VCAM1, MFGE8, Fc gamma RII beta, APRIL(TNFSF13), Oct-2
7	Gamma-secretase regulation of osteogenesis	33	7.967E-03	5.787E-01	4	CD44, CD44 soluble, CD44 (ICD), CD44 (EXT)
8	Role of osteoblasts in bone lesions formation in multiple myeloma	33	7.967E-03	5.787E-01	4	HGF, VCAM1, Apo-2L(TNFSF10), WNT
9	Role of Nicotine-induced Leptin resistance in hypothalamus in development of obesity	18	8.812E-03	5.787E-01	3	POMC, AGRP, CART
10	L-Threonine metabolism	20	1.188E-02	5.890E-01	3	SDHL, ASCT1 (SLC1A4), SDSL
11	Role of Leptin in regulation of eating behavior in obesity	20	1.188E-02	5.890E-01	3	POMC, AGRP, CART
12	Renal secretion of inorganic electrolytes	21	1.362E-02	5.890E-01	3	SLC4A4, Aquaporin 1, SLC12A1
13	Neurophysiological process_Glucose-excited neurons of arcuate nucleus (rodent model)	21	1.362E-02	5.890E-01	3	HIF-prolyl hydroxylase, POMC, CART

14	Type 2 diabetes (general schema)	8	1.495E-02	5.890E-01	2	POMC, AGRP
15	Cell adhesion_Gap junctions	22	1.549E-02	5.890E-01	3	Connexin 30, Tubulin beta, Connexin 26
16	Inhibition of apoptosis in gastric cancer	41	1.698E-02	5.890E-01	4	HGF, Caspase-10, XAF1, Apo-2L(TNFSF10)
17	Stem cells_Aberrant Wnt signaling in medulloblastoma stem cells	23	1.750E-02	5.890E-01	3	CD44, WNT, WIF1
18	Transcription_Hypoxia- and receptor-mediated HIF-1 activation	42	1.842E-02	5.890E-01	4	HGF, HIF-prolyl hydroxylase, GPNMB (Osteoactivin), EGF
19	Putative pathways of activation of classical complement system in major depressive disorder	24	1.965E-02	5.890E-01	3	C4A protein, C4, C4b
20	Glycine and L-Serine metabolism	43	1.993E-02	5.890E-01	4	PIPOX, SDHL, ASCT1 (SLC1A4), SDSL
21	Development_Astrocyte differentiation (general schema)	25	2.194E-02	6.176E-01	3	SLC6A11, CD44, GFAP
22	Development_Signaling pathways in embryonic hepatocyte maturation	45	2.318E-02	6.228E-01	4	HGF, ALDOB, L-FABP, LRH1
23	Role of tumor-infiltrating B cells in anti-tumor immunity	69	2.579E-02	6.628E-01	5	Kappa chain (Ig light chain), Perforin, I-TAC, Apo-2L(TNFSF10), MLANA
24	Inter-cellular relations in COPD (general schema)	27	2.694E-02	6.634E-01	3	Perforin, I-TAC, EGF
25	Colorectal cancer (general schema)	28	2.965E-02	7.009E-01	3	HGF, EGF, WNT
26	Glomerular filtration and renal reabsorption of bile acids / Rodent version	12	3.307E-02	7.517E-01	2	HYEP, L-FABP
27	WNT signaling in invasive-type melanoma cells	30	3.548E-02	7.766E-01	3	KiSS-1, CD44, MLANA
28	Gamma-secretase proteolytic targets	52	3.700E-02	7.810E-01	4	CD44, CD44 soluble, CD44 (ICD), CD44 (EXT)
29	Disruption of epithelial layer restitution in asthma	31	3.860E-02	7.866E-01	3	HGF, EGF, RXRG

30	Role of red blood cell adhesion to endothelium in vaso-occlusion in Sickle cell disease	32	4.185E-02	7.895E-01	3	VCAM1, CD44, CD147
31	Cholehepatic circulation of bile acids / Rodent version	14	4.418E-02	7.895E-01	2	HYEP, L-FABP
32	Beta-catenin-dependent transcription regulation in colorectal cancer	33	4.524E-02	7.895E-01	3	CD44, CD44 soluble, CD44 (EXT)
33	Immune response_Antiviral actions of Interferons	33	4.524E-02	7.895E-01	3	2'-5'-oligoadenylate synthetase, MxA, OAS3
34	E-cadherin signaling and its regulation in gastric cancer	34	4.876E-02	7.895E-01	3	HGF, EGF, WNT
35	PR action in breast cancer: stimulation of metastasis	15	5.018E-02	7.895E-01	2	PR (membrane), PR (nuclear)
36	Anandamide biosynthesis and metabolism	15	5.018E-02	7.895E-01	2	PLC-delta, PLA2G5
37	L-Lysine metabolism	35	5.241E-02	7.895E-01	3	PIPOX, CAT-2, HCD2
38	HGF signaling in melanoma	36	5.619E-02	7.895E-01	3	HGF, CD44, alpha-MSH
39	Development_Role of proteases in hematopoietic stem cell mobilization	16	5.645E-02	7.895E-01	2	VCAM1, CD44
40	Enterohepatic circulation of bile acids / Rodent version	16	5.645E-02	7.895E-01	2	HYEP, L-FABP
41	Mitochondrial beta-oxidation of long-chain saturated fatty acids	37	6.010E-02	7.895E-01	3	L-FABP, CPT-1A, HCD2
42	Influence of bone marrow cell environment on progression of multiple myeloma	37	6.010E-02	7.895E-01	3	HGF, VCAM1, CD44
43	Multiple sclerosis (general schema)	17	6.298E-02	7.895E-01	2	VCAM1, Apo-2L(TNFSF10)
44	Development_Melanocyte development and pigmentation	38	6.413E-02	7.895E-01	3	ACTH, alpha-MSH, Galpha(s)-specific peptide GPCRs
45	Signal transduction_Leptin signaling via JAK/STAT and MAPK cascade	38	6.413E-02	7.895E-01	3	POMC, AGRP, CART

46	WNT signaling in proliferative-type melanoma cells	38	6.413E-02	7.895E-01	3	WNT7B, WNT, WIF1
47	Apoptosis and survival_Granzyme A signaling	38	6.413E-02	7.895E-01	3	Histone H2B, HMGB2, Perforin
48	Development_WNT/Beta-catenin signaling in embryogenesis	38	6.413E-02	7.895E-01	3	SOX17, LRH1, WNT
49	Breast cancer (general schema)	39	6.828E-02	7.927E-01	3	EGF, PR (membrane), PR (nuclear)
50	Immune response_Lectin induced complement pathway	39	6.828E-02	7.927E-01	3	C4, C4a, C4b

Table A26. Top 50 TargetALS Pathway Maps enrichments with MetaCore. Term size refers to the number of genes in the term, with the intersection size denoting the number of genes in the dataset found in the term.

Clinical Phenotype	**Ensembl ID**	**Gene Symbol**	**KCL BrainBank**			**TargetALS (medial)**			**TargetALS (lateral)**		
			Pearson's r	p-value	p-value (adj)	Pearson's r	p-value	p-value (adj)	Pearson's r	p-value	p-value (adj)
Disease Duration (months)	ENSG00000006128	*TAC1*	0.1815	0.0737	1.0	0.0384	0.7192	1.0	0.1036	0.3229	1.0
	ENSG00000017427	*IGF1*	0.0900	0.3783	1.0	0.0388	0.7166	1.0	0.2078	**0.0456**	1.0
	ENSG00000049247	*UTS2*	-0.1975	0.0513	1.0	-0.1057	0.3215	1.0	-0.1596	0.1264	1.0
	ENSG00000056291	*NPFFR2*	-0.1236	0.2255	1.0	0.0271	0.8000	1.0	-0.1015	0.3329	1.0
	ENSG00000069482	*GAL*	0.1076	0.2917	1.0	-0.0451	0.6727	1.0	0.1017	0.3320	1.0
	ENSG00000070031	*SCT*	-0.0149	0.8841	1.0	0.1510	0.1554	1.0	0.0956	0.3619	1.0
	ENSG00000075073	*TACR2*	0.0318	0.7561	1.0	0.1199	0.2605	1.0	0.0609	0.5622	1.0
	ENSG00000078401	*EDN1*	0.0073	0.9428	1.0	0.0756	0.4788	1.0	-0.0616	0.5575	1.0
	ENSG00000082556	*OPRK1*	-0.0529	0.6050	1.0	-0.0561	0.5994	1.0	0.0510	0.6276	1.0
	ENSG00000087494	*PTHLH*	0.1521	0.1348	1.0	0.1445	0.1743	1.0	0.1739	0.0954	1.0
	ENSG00000096395	*MLN*	-0.0067	0.9474	1.0	0.1168	0.2730	1.0	-0.1418	0.1752	1.0
	ENSG00000100604	*CHGA*	0.0101	0.9211	1.0	0.0181	0.8653	1.0	0.0058	0.9561	1.0
	ENSG00000100739	*BDKRB1*	-0.0304	0.7666	1.0	-0.1843	0.0821	1.0	0.1753	0.0928	1.0
	ENSG00000101188	*NTSR1*	0.0691	0.4990	1.0	0.2855	**0.0064**	0.6720	0.0337	0.7485	1.0
	ENSG00000101200	*AVP*	NA	NA	NA	0.0928	0.3841	1.0	0.0653	0.5343	1.0
	ENSG00000101327	*PDYN*	-0.0009	0.9933	1.0	0.1611	0.1294	1.0	0.0651	0.5350	1.0
	ENSG00000102539	*MLNR*	-0.1471	0.1484	1.0	0.0488	0.6480	1.0	-0.0344	0.7431	1.0
	ENSG00000107014	*RLN2*	-0.0005	0.9965	1.0	-0.0660	0.5363	1.0	0.0198	0.8505	1.0
	ENSG00000107018	*RLN1*	0.0989	0.3326	1.0	-0.0701	0.5114	1.0	-0.0024	0.9814	1.0
	ENSG00000109163	*GNRHR*	0.0356	0.7280	1.0	-0.1190	0.2639	1.0	-0.0563	0.5922	1.0
	ENSG00000109255	*NMU*	0.1481	0.1455	1.0	-0.0484	0.6504	1.0	0.0588	0.5754	1.0
	ENSG00000110148	*CCKBR*	0.1223	0.2302	1.0	0.0809	0.4486	1.0	0.1342	0.1996	1.0
	ENSG00000110680	*CALCA*	-0.0377	0.7127	1.0	0.2513	**0.0169**	1.0	-0.0568	0.5887	1.0
	ENSG00000112038	*OPRM1*	0.1160	0.2552	1.0	-0.0459	0.6676	1.0	-0.0303	0.7728	1.0
	ENSG00000113889	*KNG1*	-0.0556	0.5863	1.0	-0.1042	0.3285	1.0	0.0214	0.8384	1.0
	ENSG00000115138	*POMC*	-0.1024	0.3157	1.0	0.0342	0.7486	1.0	-0.1015	0.3329	1.0
	ENSG00000115353	*TACR1*	0.2110	**0.0370**	1.0	0.1140	0.2848	1.0	0.2331	**0.0245**	1.0
	ENSG00000116014	*KISS1R*	0.1325	0.1936	1.0	0.0840	0.4312	1.0	-0.0502	0.6326	1.0
	ENSG00000116329	*OPRD1*	-0.1212	0.2346	1.0	0.0173	0.8714	1.0	0.0147	0.8886	1.0
	ENSG00000119973	*PRLHR*	0.1400	0.1690	1.0	0.0857	0.4219	1.0	0.2083	**0.0451**	1.0
	ENSG00000120937	*NPPB*	0.0934	0.3605	1.0	NA	NA	NA	NA	NA	NA
	ENSG00000121764	*HCRTR1*	-0.0368	0.7187	1.0	0.0450	0.6735	1.0	0.2409	**0.0200**	1.0

	ENSG00000122585	*NPY*	0.0448	0.6616	1.0	0.1185	0.2661	1.0	-0.0445	0.6718	1.0
	ENSG00000124089	*MC3R*	NA	NA	NA	0.0514	0.6301	1.0	0.1424	0.1733	1.0
	ENSG00000124205	*EDN3*	-0.0173	0.8659	1.0	0.0197	0.8537	1.0	-0.1067	0.3087	1.0
	ENSG00000125510	*OPRL1*	0.0612	0.5495	1.0	0.1287	0.2267	1.0	0.0272	0.7959	1.0
	ENSG00000125522	*NPBWR2*	0.1138	0.2646	1.0	0.0049	0.9636	1.0	-0.0196	0.8522	1.0
	ENSG00000125787	*GNRH2*	-0.1234	0.2260	1.0	0.1036	0.3314	1.0	-0.0928	0.3762	1.0
	ENSG00000126895	*AVPR2*	-0.3233	**0.0012**	0.1224	0.0397	0.7099	1.0	-0.0608	0.5626	1.0
	ENSG00000128165	*ADM2*	-0.1500	0.1404	1.0	0.0627	0.5569	1.0	0.0008	0.9942	1.0
	ENSG00000128285	*MCHR1*	0.1154	0.2579	1.0	-0.0195	0.8553	1.0	0.0193	0.8545	1.0
	ENSG00000128310	*GALR3*	-0.0094	0.9269	1.0	0.0028	0.9790	1.0	0.0048	0.9635	1.0
	ENSG00000131096	*PYY*	0.0847	0.4071	1.0	0.0215	0.8404	1.0	0.0636	0.5445	1.0
	ENSG00000132671	*SSTR4*	0.1646	0.1054	1.0	0.1120	0.2933	1.0	0.1557	0.1361	1.0
	ENSG00000132911	*NMUR2*	-0.0494	0.6289	1.0	-0.0782	0.4637	1.0	-0.1404	0.1796	1.0
	ENSG00000133636	*NTS*	NA	NA	NA	-0.0727	0.4957	1.0	0.0832	0.4278	1.0
	ENSG00000134443	*GRP*	0.0054	0.9577	1.0	0.0464	0.6639	1.0	-0.1242	0.2357	1.0
	ENSG00000135744	*AGT*	0.0847	0.4072	1.0	0.2198	**0.0374**	1.0	0.0880	0.4014	1.0
	ENSG00000136160	*EDNRB*	0.0497	0.6269	1.0	0.0136	0.8991	1.0	-0.0649	0.5364	1.0
	ENSG00000137252	*HCRTR2*	0.0853	0.4035	1.0	0.0403	0.7060	1.0	0.1035	0.3237	1.0
	ENSG00000139574	*NPFF*	-0.0754	0.4606	1.0	-0.0697	0.5138	1.0	-0.1424	0.1732	1.0
	ENSG00000139874	*SSTR1*	0.0541	0.5965	1.0	0.1074	0.3135	1.0	0.0419	0.6899	1.0
	ENSG00000141433	*ADCYAP1*	0.1210	0.2351	1.0	0.1118	0.2942	1.0	0.1684	0.1067	1.0
	ENSG00000144891	*AGTR1*	-0.2372	**0.0187**	1.0	-0.0541	0.6127	1.0	-0.1301	0.2138	1.0
	ENSG00000145040	*UCN2*	0.0169	0.8685	1.0	-0.0236	0.8250	1.0	-0.1320	0.2072	1.0
	ENSG00000146469	*VIP*	0.1764	0.0824	1.0	0.0727	0.4962	1.0	0.1854	0.0753	1.0
	ENSG00000147437	*GNRH1*	-0.1891	0.0622	1.0	-0.2565	**0.0147**	1.0	-0.2138	**0.0396**	1.0
	ENSG00000147571	*CRH*	0.1047	0.3048	1.0	0.1427	0.1796	1.0	0.1438	0.1691	1.0
	ENSG00000148734	*NPFFR1*	0.0256	0.8021	1.0	-0.1112	0.2967	1.0	-0.1638	0.1166	1.0
	ENSG00000148926	*ADM*	-0.0558	0.5851	1.0	0.0401	0.7077	1.0	0.0673	0.5215	1.0
	ENSG00000151617	*EDNRA*	-0.1943	0.0552	1.0	0.0612	0.5667	1.0	0.1770	0.0897	1.0
	ENSG00000152034	*MCHR2*	0.1232	0.2269	1.0	-0.0395	0.7117	1.0	0.0376	0.7205	1.0
	ENSG00000157005	*SST*	0.2060	**0.0418**	1.0	0.1386	0.1927	1.0	0.1291	0.2173	1.0
	ENSG00000157017	*GHRL*	-0.1210	0.2353	1.0	0.0463	0.6650	1.0	-0.0624	0.5524	1.0
	ENSG00000159723	*AGRP*	-0.1807	0.0749	1.0	-0.0014	0.9896	1.0	-0.0762	0.4677	1.0
	ENSG00000161610	*HCRT*	-0.0527	0.6062	1.0	NA	NA	NA	NA	NA	NA

	ENSG00000162009	*SSTR5*	NA	NA	NA	0.2161	**0.0408**	1.0	0.1433	0.1707	1.0
	ENSG00000163273	*NPPC*	0.0876	0.3909	1.0	0.0587	0.5826	1.0	0.0660	0.5295	1.0
	ENSG00000163394	*CCKAR*	0.0179	0.8608	1.0	0.0286	0.7893	1.0	-0.2155	**0.0380**	1.0
	ENSG00000163794	*UCN*	-0.0228	0.8239	1.0	0.0410	0.7015	1.0	0.0102	0.9226	1.0
	ENSG00000164128	*NPY1R*	-0.1165	0.2531	1.0	0.0008	0.9943	1.0	0.0176	0.8667	1.0
	ENSG00000164129	*NPY5R*	0.0968	0.3429	1.0	0.0166	0.8766	1.0	0.0064	0.9512	1.0
	ENSG00000166148	*AVPR1A*	-0.0991	0.3316	1.0	0.2177	**0.0393**	1.0	0.0951	0.3646	1.0
	ENSG00000166573	*GALR1*	0.0037	0.9713	1.0	0.1054	0.3229	1.0	0.1167	0.2653	1.0
	ENSG00000166603	*MC4R*	0.1065	0.2965	1.0	-0.1098	0.3028	1.0	-0.0531	0.6133	1.0
	ENSG00000166863	*TAC3*	0.1196	0.2408	1.0	0.0782	0.4639	1.0	0.2125	**0.0409**	1.0
	ENSG00000167244	*IGF2*	-0.0464	0.6502	1.0	0.0044	0.9671	1.0	0.0396	0.7062	1.0
	ENSG00000168081	*PNOC*	0.0691	0.4991	1.0	0.2000	0.0587	1.0	0.2315	**0.0256**	1.0
	ENSG00000168398	*BDKRB2*	0.1000	0.3273	1.0	-0.0307	0.7736	1.0	0.0200	0.8494	1.0
	ENSG00000169006	*NTSR2*	0.1501	0.1400	1.0	0.0667	0.5321	1.0	0.0282	0.7888	1.0
	ENSG00000169836	*TACR3*	0.0013	0.9899	1.0	-0.1422	0.1811	1.0	0.0974	0.3529	1.0
	ENSG00000170498	*KISS1*	NA	NA	NA	NA	NA	NA	0.2198	**0.0342**	1.0
	ENSG00000170893	*TRH*	0.1858	0.0670	1.0	0.1824	0.0852	1.0	0.0973	0.3536	1.0
	ENSG00000171388	*APLN*	-0.0811	0.4273	1.0	-0.0556	0.6028	1.0	-0.0076	0.9426	1.0
	ENSG00000171596	*NMUR1*	-0.0789	0.4402	1.0	0.2664	**0.0112**	1.0	0.2215	**0.0329**	1.0
	ENSG00000174417	*TRHR*	-0.0020	0.9844	1.0	-0.0412	0.6996	1.0	-0.0264	0.8018	1.0
	ENSG00000174697	*LEP*	-0.0942	0.3561	1.0	0.0821	0.4419	1.0	-0.0350	0.7391	1.0
	ENSG00000175206	*NPPA*	-0.1106	0.2785	1.0	-0.1117	0.2946	1.0	0.0937	0.3718	1.0
	ENSG00000175868	*CALCB*	-0.1456	0.1526	1.0	0.0478	0.6548	1.0	-0.0209	0.8421	1.0
	ENSG00000176136	*MC5R*	0.0629	0.5385	1.0	0.0690	0.5181	1.0	0.1699	0.1034	1.0
	ENSG00000176358	*TAC4*	-0.0249	0.8075	1.0	0.0160	0.8811	1.0	0.0395	0.7067	1.0
	ENSG00000180616	*SSTR2*	0.0732	0.4741	1.0	0.0264	0.8047	1.0	-0.0563	0.5919	1.0
	ENSG00000180914	*OXTR*	-0.1290	0.2056	1.0	-0.1326	0.2129	1.0	-0.1716	0.1000	1.0
	ENSG00000181195	*PENK*	0.1098	0.2819	1.0	0.0599	0.5746	1.0	0.1415	0.1761	1.0
	ENSG00000181408	*UTS2R*	-0.1650	0.1045	1.0	0.0794	0.4567	1.0	0.1567	0.1336	1.0
	ENSG00000182687	*GALR2*	-0.0956	0.3492	1.0	0.1189	0.2642	1.0	-0.0959	0.3602	1.0
	ENSG00000183971	*NPW*	0.0450	0.6601	1.0	-0.1178	0.2687	1.0	0.1524	0.1448	1.0
	ENSG00000184502	*GAST*	NA	NA	NA	-0.1530	0.1500	1.0	0.1348	0.1976	1.0
	ENSG00000185149	*NPY2R*	0.0213	0.8353	1.0	0.0230	0.8297	1.0	0.0034	0.9742	1.0
	ENSG00000186867	*QRFPR*	-0.0483	0.6369	1.0	-0.0657	0.5381	1.0	-0.0248	0.8134	1.0

	ENSG00000187094	*CCK*	0.0498	0.6264	1.0	0.0019	0.9861	1.0	0.0725	0.4900	1.0
	ENSG00000187258	*NPSR1*	0.0818	0.4233	1.0	0.0802	0.4523	1.0	-0.0401	0.7027	1.0
	ENSG00000198049	*AVPR1B*	0.0141	0.8905	1.0	0.1396	0.1895	1.0	0.0462	0.6601	1.0
	ENSG00000211451	*GNRHR2*	0.1613	0.1125	1.0	-0.0754	0.4798	1.0	0.0129	0.9025	1.0
	ENSG00000226306	*NPY6R*	0.1497	0.1412	1.0	-0.0120	0.9108	1.0	-0.0553	0.5985	1.0
	ENSG00000258839	*MC1R*	-0.1272	0.2118	1.0	0.1826	0.0850	1.0	0.0568	0.5885	1.0
	ENSG00000278195	*SSTR3*	-0.0127	0.9016	1.0	0.0651	0.5423	1.0	0.0980	0.3498	1.0
	ENSG00000288611	*NPBWR1*	0.0556	0.5866	1.0	0.0200	0.8515	1.0	0.2394	**0.0208**	1.0
Age of Onset	ENSG00000006128	*TAC1*	-0.1357	0.1873	1.0	-0.0021	0.9841	1.0	-0.0373	0.7227	1.0
	ENSG00000017427	*IGF1*	-0.3803	**0.000129**	**0.01357**	-0.0720	0.5003	1.0	-0.2043	**0.0495**	1.0
	ENSG00000049247	*UTS2*	0.2531	**0.0129**	1.0	0.0690	0.5181	1.0	0.0833	0.4272	1.0
	ENSG00000056291	*NPFFR2*	0.0702	0.4967	1.0	-0.0616	0.5640	1.0	-0.0736	0.4831	1.0
	ENSG00000069482	*GAL*	-0.0817	0.4286	1.0	0.0033	0.9752	1.0	-0.0418	0.6907	1.0
	ENSG00000070031	*SCT*	0.0657	0.5247	1.0	-0.0827	0.4383	1.0	0.0230	0.8267	1.0
	ENSG00000075073	*TACR2*	-0.1129	0.2736	1.0	0.0280	0.7932	1.0	-0.0236	0.8221	1.0
	ENSG00000078401	*EDN1*	0.2040	**0.0462**	1.0	-0.1328	0.2122	1.0	0.0085	0.9359	1.0
	ENSG00000082556	*OPRK1*	-0.0024	0.9812	1.0	0.1525	0.1513	1.0	-0.0298	0.7769	1.0
	ENSG00000087494	*PTHLH*	-0.3846	**0.000109**	**0.0111**	0.0196	0.8548	1.0	-0.0614	0.5590	1.0
	ENSG00000096395	*MLN*	-0.0312	0.7628	1.0	0.0910	0.3938	1.0	0.0489	0.6419	1.0
	ENSG00000100604	*CHGA*	0.1952	0.0566	1.0	0.1180	0.2681	1.0	0.0254	0.8088	1.0
	ENSG00000100739	*BDKRB1*	-0.0276	0.7899	1.0	-0.0703	0.5101	1.0	-0.0350	0.7388	1.0
	ENSG00000101188	*NTSR1*	-0.0907	0.3796	1.0	-0.0495	0.6430	1.0	-0.1129	0.2813	1.0
	ENSG00000101200	*AVP*	NA	NA	NA	0.0236	0.8251	1.0	0.1641	0.1160	1.0
	ENSG00000101327	*PDYN*	-0.0955	0.3546	1.0	-0.0339	0.7514	1.0	-0.0569	0.5883	1.0
	ENSG00000102539	*MLNR*	-0.0148	0.8864	1.0	-0.0057	0.9573	1.0	-0.0721	0.4919	1.0
	ENSG00000107014	*RLN2*	-0.0843	0.4142	1.0	0.0459	0.6676	1.0	0.0931	0.3747	1.0
	ENSG00000107018	*RLN1*	-0.0444	0.6674	1.0	-0.0440	0.6804	1.0	-0.0158	0.8802	1.0
	ENSG00000109163	*GNRHR*	-0.1990	0.0520	1.0	0.1309	0.2189	1.0	-0.0710	0.4988	1.0
	ENSG00000109255	*NMU*	-0.2021	**0.0483**	1.0	-0.0547	0.6085	1.0	-0.0979	0.3505	1.0
	ENSG00000110148	*CCKBR*	-0.1890	0.0652	1.0	-0.0347	0.7453	1.0	-0.1088	0.2991	1.0
	ENSG00000110680	*CALCA*	0.0907	0.3796	1.0	-0.0398	0.7093	1.0	0.1060	0.3120	1.0
	ENSG00000112038	*OPRM1*	0.0760	0.4615	1.0	0.2205	**0.03674**	1.0	0.0478	0.6490	1.0
	ENSG00000113889	*KNG1*	0.1441	0.1612	1.0	0.0356	0.7392	1.0	-0.0674	0.5211	1.0
	ENSG00000115138	*POMC*	-0.1645	0.1093	1.0	-0.2047	0.0529	1.0	-0.0315	0.7645	1.0

	ENSG00000115353	*TACR1*	-0.1094	0.2886	1.0	-0.0115	0.9143	1.0	-0.0955	0.3626	1.0
	ENSG00000116014	*KISS1R*	-0.1644	0.1094	1.0	0.0917	0.3899	1.0	0.1150	0.2726	1.0
	ENSG00000116329	*OPRD1*	0.1236	0.2300	1.0	0.1277	0.2303	1.0	-0.0459	0.6622	1.0
	ENSG00000119973	*PRLHR*	-0.2459	**0.0157**	1.0	0.0165	0.8774	1.0	-0.0385	0.7142	1.0
	ENSG00000120937	*NPPB*	0.1641	0.1102	1.0	NA	NA	NA	NA	NA	NA
	ENSG00000121764	*HCRTR1*	-0.1361	0.1861	1.0	-0.0805	0.4507	1.0	-0.2328	**0.0247**	1.0
	ENSG00000121853	*GHSR*	NA	NA	NA	NA	NA	NA	-0.0806	0.4422	1.0
	ENSG00000122585	*NPY*	-0.1055	0.3062	1.0	-0.1413	0.1840	1.0	-0.0287	0.7847	1.0
	ENSG00000124089	*MC3R*	NA	NA	NA	-0.0312	0.7707	1.0	NA	NA	NA
	ENSG00000124205	*EDN3*	-0.1654	0.1073	1.0	-0.1443	0.1749	1.0	-0.0592	0.5729	1.0
	ENSG00000125510	*OPRL1*	-0.1626	0.1134	1.0	-0.1360	0.2012	1.0	-0.0740	0.4807	1.0
	ENSG00000125522	*NPBWR2*	0.0645	0.5323	1.0	0.1264	0.2350	1.0	0.0042	0.9682	1.0
	ENSG00000125787	*GNRH2*	0.0027	0.9795	1.0	0.0153	0.8860	1.0	0.0504	0.6312	1.0
	ENSG00000126895	*AVPR2*	-0.0442	0.6690	1.0	-0.0175	0.8699	1.0	0.0211	0.8411	1.0
	ENSG00000128165	*ADM2*	-0.0277	0.7884	1.0	-0.0637	0.5510	1.0	0.0534	0.6110	1.0
	ENSG00000128285	*MCHR1*	-0.1521	0.1390	1.0	0.0221	0.8362	1.0	-0.0815	0.4375	1.0
	ENSG00000128310	*GALR3*	0.0454	0.6608	1.0	-0.0116	0.9134	1.0	0.0144	0.8908	1.0
	ENSG00000131096	*PYY*	0.1272	0.2169	1.0	-0.0766	0.4728	1.0	0.1272	0.2244	1.0
	ENSG00000132671	*SSTR4*	-0.2106	**0.0394**	1.0	-0.0826	0.4392	1.0	-0.0776	0.4598	1.0
	ENSG00000132911	*NMUR2*	0.2277	**0.0257**	1.0	-0.0404	0.7055	1.0	-0.0762	0.4681	1.0
	ENSG00000133636	*NTS*	NA	NA	NA	0.1286	0.2271	1.0	-0.1354	0.1957	1.0
	ENSG00000134443	*GRP*	-0.2816	**0.0054**	0.5555	0.1126	0.2908	1.0	0.0530	0.6142	1.0
	ENSG00000135744	*AGT*	-0.1429	0.1647	1.0	-0.0721	0.4997	1.0	0.0264	0.8017	1.0
	ENSG00000136160	*EDNRB*	-0.1339	0.1934	1.0	-0.1359	0.2016	1.0	-0.0864	0.4100	1.0
	ENSG00000137252	*HCRTR2*	-0.0949	0.3580	1.0	0.1082	0.3099	1.0	0.0451	0.6676	1.0
	ENSG00000139574	*NPFF*	0.2074	**0.0426**	1.0	0.0377	0.7242	1.0	-0.0171	0.8707	1.0
	ENSG00000139874	*SSTR1*	-0.3046	**0.0026**	0.2605	-0.1458	0.1703	1.0	-0.1456	0.1636	1.0
	ENSG00000141433	*ADCYAP1*	-0.1075	0.2972	1.0	0.0470	0.6598	1.0	-0.0334	0.7505	1.0
	ENSG00000144891	*AGTR1*	0.0487	0.6376	1.0	0.0631	0.5548	1.0	0.0785	0.4547	1.0
	ENSG00000145040	*UCN2*	-0.1512	0.1413	1.0	0.3024	**0.003771**	0.3960	0.1408	0.1781	1.0
	ENSG00000146469	*VIP*	-0.3173	**0.0016**	0.1669	-0.0154	0.8856	1.0	-0.1737	0.0959	1.0
	ENSG00000147437	*GNRH1*	0.2251	**0.0275**	1.0	0.1091	0.3060	1.0	0.0614	0.5588	1.0
	ENSG00000147571	*CRH*	-0.2499	**0.0140**	1.0	-0.1290	0.2256	1.0	-0.0999	0.3406	1.0
	ENSG00000148734	*NPFFR1*	0.1346	0.1911	1.0	0.0676	0.5266	1.0	-0.0276	0.7932	1.0

	ENSG00000148926	*ADM*	0.2841	**0.0050**	0.5121	-0.1494	0.1598	1.0	-0.1056	0.3137	1.0
	ENSG00000151617	*EDNRA*	-0.0844	0.4134	1.0	-0.1591	0.1342	1.0	-0.1037	0.3226	1.0
	ENSG00000152034	*MCHR2*	-0.2794	0.0058	0.5952	0.0456	0.6693	1.0	-0.1445	0.1671	1.0
	ENSG00000157005	*SST*	-0.2875	**0.0045**	0.4599	-0.0494	0.6439	1.0	-0.0444	0.6724	1.0
	ENSG00000157017	*GHRL*	-0.0143	0.8898	1.0	-0.0259	0.8085	1.0	-0.0326	0.7566	1.0
	ENSG00000159723	*AGRP*	-0.0404	0.6960	1.0	-0.0130	0.9029	1.0	0.0536	0.6097	1.0
	ENSG00000161610	*HCRT*	-0.1026	0.3201	1.0	NA	NA	NA	NA	NA	NA
	ENSG00000162009	*SSTR5*	NA	NA	NA	-0.1674	0.1149	1.0	-0.1395	0.1822	1.0
	ENSG00000163273	*NPPC*	0.0447	0.6653	1.0	0.0346	0.7459	1.0	0.0535	0.6104	1.0
	ENSG00000163394	*CCKAR*	-0.0489	0.6362	1.0	-0.0582	0.5860	1.0	-0.0224	0.8313	1.0
	ENSG00000163794	*UCN*	0.2040	**0.0462**	1.0	0.0709	0.5064	1.0	0.0290	0.7823	1.0
	ENSG00000164128	*NPY1R*	-0.1644	0.1095	1.0	0.0482	0.6517	1.0	-0.0779	0.4578	1.0
	ENSG00000164129	*NPY5R*	-0.1523	0.1385	1.0	-0.0662	0.5355	1.0	-0.0716	0.4953	1.0
	ENSG00000166148	*AVPR1A*	-0.1146	0.2661	1.0	-0.3190	**0.002182**	0.2291	-0.1814	0.0818	1.0
	ENSG00000166573	*GALR1*	-0.2661	**0.0088**	0.8967	-0.1302	0.2213	1.0	-0.1084	0.3010	1.0
	ENSG00000166603	*MC4R*	-0.0408	0.6929	1.0	0.0390	0.7150	1.0	0.0224	0.8312	1.0
	ENSG00000166863	*TAC3*	-0.2816	**0.0054**	0.5556	-0.0206	0.8473	1.0	-0.1746	0.0941	1.0
	ENSG00000167244	*IGF2*	0.0924	0.3704	1.0	-0.0037	0.9721	1.0	0.0150	0.8864	1.0
	ENSG00000168081	*PNOC*	-0.3437	**0.0006**	0.06191	-0.1428	0.1793	1.0	-0.1111	0.2891	1.0
	ENSG00000168398	*BDKRB2*	-0.0239	0.8172	1.0	-0.0383	0.7203	1.0	-0.1111	0.2892	1.0
	ENSG00000169006	*NTSR2*	-0.1129	0.2735	1.0	-0.0912	0.3924	1.0	0.0436	0.6783	1.0
	ENSG00000169836	*TACR3*	0.0696	0.5006	1.0	0.0198	0.8530	1.0	-0.0876	0.4036	1.0
	ENSG00000170498	*KISS1*	NA	NA	NA	NA	NA	NA	0.1204	0.2504	1.0
	ENSG00000170893	*TRH*	-0.0334	0.7467	1.0	-0.4667	**0.000003534**	**0.000371**	-0.2000	0.0546	1.0
	ENSG00000171388	*APLN*	0.2912	**0.0040**	0.4074	-0.0612	0.5667	1.0	-0.0290	0.7829	1.0
	ENSG00000171596	*NMUR1*	-0.1836	0.0733	1.0	-0.1833	0.0837	1.0	-0.0874	0.4049	1.0
	ENSG00000174417	*TRHR*	0.1381	0.1798	1.0	0.0152	0.8867	1.0	-0.0738	0.4823	1.0
	ENSG00000174697	*LEP*	0.0503	0.6262	1.0	0.1129	0.2893	1.0	0.0916	0.3827	1.0
	ENSG00000175206	*NPPA*	-0.3044	**0.0026**	0.2615	0.0873	0.4133	1.0	0.0266	0.8000	1.0
	ENSG00000175868	*CALCB*	0.0423	0.6824	1.0	0.0450	0.6734	1.0	0.0303	0.7732	1.0
	ENSG00000176136	*MC5R*	-0.1545	0.1329	1.0	-0.1071	0.3150	1.0	-0.0580	0.5805	1.0
	ENSG00000176358	*TAC4*	0.1046	0.3107	1.0	0.0601	0.5738	1.0	0.0500	0.6338	1.0
	ENSG00000180616	*SSTR2*	-0.2460	**0.0157**	1.0	-0.0379	0.7231	1.0	-0.0605	0.5648	1.0

	ENSG00000180914	*OXTR*	0.1973	0.0540	1.0	-0.0058	0.9569	1.0	0.0219	0.8349	1.0
	ENSG00000181195	*PENK*	-0.2041	**0.0461**	1.0	-0.0747	0.4840	1.0	-0.1524	0.1447	1.0
	ENSG00000181408	*UTS2R*	0.2228	**0.0291**	1.0	0.0880	0.4094	1.0	-0.0062	0.9526	1.0
	ENSG00000182687	*GALR2*	0.0792	0.4431	1.0	-0.0837	0.4327	1.0	0.1472	0.1591	1.0
	ENSG00000183971	*NPW*	-0.1160	0.2605	1.0	-0.0233	0.8276	1.0	-0.0137	0.8963	1.0
	ENSG00000184502	*GAST*	NA	NA	NA	0.0023	0.9828	1.0	-0.0216	0.8373	1.0
	ENSG00000185149	*NPY2R*	-0.1678	0.1022	1.0	-0.0911	0.3931	1.0	-0.1469	0.1599	1.0
	ENSG00000186867	*QRFPR*	-0.1669	0.1041	1.0	0.0539	0.6136	1.0	0.0069	0.9477	1.0
	ENSG00000187094	*CCK*	-0.1280	0.2141	1.0	0.0091	0.9318	1.0	-0.0403	0.7010	1.0
	ENSG00000187258	*NPSR1*	-0.0828	0.4227	1.0	0.0357	0.7384	1.0	0.0712	0.4975	1.0
	ENSG00000198049	*AVPR1B*	-0.0800	0.4385	1.0	0.1615	0.1282	1.0	-0.0206	0.8449	1.0
	ENSG00000211451	*GNRHR2*	-0.1188	0.2491	1.0	0.0011	0.9917	1.0	-0.0935	0.3729	1.0
	ENSG00000226306	*NPY6R*	0.0943	0.3606	1.0	-0.0575	0.5906	1.0	-0.0845	0.4206	1.0
	ENSG00000258839	*MC1R*	0.1264	0.2196	1.0	-0.0351	0.7426	1.0	0.0469	0.6556	1.0
	ENSG00000278195	*SSTR3*	0.1343	0.1920	1.0	0.1144	0.2830	1.0	-0.0486	0.6433	1.0
	ENSG00000288611	*NPBWR1*	-0.3455	**0.0006**	0.05763	-0.1121	0.2927	1.0	-0.3360	**0.0009912**	0.1050

Table A27. Results of the correlation analysis of neuropeptide receptors and ligand expression with disease duration or age of onset in people with ALS from either KCL BrainBank or medial and lateral samples from TargetALS. Adjusted p-values reflect the number of neuropeptide-related genes tested in each dataset (102 in KCL BrainBank, 105 in TargetALS medial and 106 in TargetALS lateral motor cortex). A p-value of < 0.05 denotes significance.

Dataset	Cell Type	Median ± IQR (case)	Median ± IQR (control)	Levene's Test (F statistic; p-value)	ANCOVA (F statistic; p-value)
KCL BrainBank	Neurons	0.662 ± 0.118	0.578 ± 0.179	4.213; **0.0417**	15.295; **1.34E-04**
	Astrocytes	0.191 ± 0.0748	0.279 ± 0.106	2.525; 0.114	18.192; **3.34E-05**
	Microglia	0.0159 ± 0.00972	0.0139 ± 0.0151	0.0275; 0.869	0.0369; 0.848
	Endothelial	0.0146 ± 0.0128	0.0182 ± 0.0204	1.851; 0.175	0.666; 0.416
	Oligodendrocytes	0.0987 ± 0.0556	0.103 ± 0.0836	3.306; 0.0708	2.688; 0.103
TargetALS (medial)	Neurons	0.616 ± 0.187	0.602 ± 0.154	0.0278; 0.868	0.0173; 0.896
	Astrocytes	0.235 ± 0.0936	0.242 ± 0.131	2.590; 0.110	1.885; 0.173
	Microglia	0.0165 ± 0.0129	0.00976 ± 0.0103	0.0140; 0.906	1.164; 0.283
	Endothelial	0.000924 ± 0.0101	0.00900 ± 0.00850	0.459; 0.499	0.667; 0.416
	Oligodendrocytes	0.114 ± 0.0934	0.0916 ± 0.0700	2.035; 0.157	2.907; 0.091
TargetALS (lateral)	Neurons	0.630 ± 0.128	0.640 ± 0.143	0.131; 0.719	0.0102; 0.920
	Astrocytes	0.227 ± 0.0808	0.228 ± 0.121	2.996; 0.086	0.840; 0.361
	Microglia	0.0152 ± 0.0137	0.0121 ± 0.00775	0.322; 0.571	0.968; 0.327
	Endothelial	0.00897 ± 0.00739	0.00838 ± 0.00712	0.0236; 0.878	0.00180; 0.966
	Oligodendrocytes	0.0955 ± 0.110	0.0872 ± 0.0317	1.409; 0.238	0.00770; 0.310

Table A28. Results of the case-control cell type deconvolution analysis with MuSiC2. Case and control median values represent the relative proportion of each cell type. Equality of variance was assessed using Levene's test, with significance in the proportions of cell types between disease status in each dataset assessed using ANCOVA corrected for age of death and sex. A p-value of < 0.05, highlighted in bold, denotes significance.

Chapter 7

	KCL BrainBank (Cases)	**TargetALS**	**Zucca**	**van Rheenen**	**KCL BrainBank (Controls)**	**van Rheenen (Controls)**	**TargetALS (Controls)**	**TargetALS (occipital cortex)**	**TargetALS (cerebellum)**
Number of Individuals	112	93 (168 samples)	15	397	59	645	19 (34 samples)	45	123 (128 samples)
Male (%)	65 (58.0%)	55 (59.1%)	7 (46.7%)	239 (60.2%)	26 (44.1%)	360 (55.8%)	9 (47.4%)	22 (48.89%)	71 (57.72%)
Age (mean ± SD)	68.8 ± 12.7	64.2 ± 10.2	66.4 ± 9.12	62.2 ± 12.0	76.2 ± 14.6	NA	62.2 ± 12.0	64.40 ± 10.53	63.66 ± 9.34
PMD (mean ± SD)	26.1 ± 12.1	10.5 ± 6.96	NA	NA	37.6 ± 19.3	NA	21.8 ± 23.4	10.00 ± 7.12	10.12 ± 6.90

Table A29. Basic demographics of each of the nine datasets used in this study. PMD: postmortem delay, measured in hours. Age refers to age of death in KCL BrainBank and TargetALS, and age at last blood draw in Zucca and van Rheenen.

	KCL BrainBank	**TargetALS**	**Zucca**	**van Rheenen**
Clinical				
Age at Symptom Onset	✓	✓	✓	✓
Age at Death	✓	✓	·	·
Disease Duration	✓	✓	·	✓
Diagnostic Delay	✓	✓	·	·
Postmortem Delay	✓	✓	·	·
Omics				
Telomere Length	✓	·	·	·
Mitochondrial DNA Copy Number	✓	·	·	·
Transcriptional Age Acceleration	✓	✓	✓	✓
Biological Age Acceleration	✓	·	·	·

Table A30. Breakdown of the phenotypic variables available for each of the 4 ALS datasets used in this study.

Cluster	Gene ID	Gene Symbol	Feature Score	Probability
1	ENSG00000164600	NEUROD6	0.2928	0.7002
1	ENSG00000100362	PVALB	0.2442	0.6736
1	ENSG00000186081	KRT5	0.2344	0.6725
1	ENSG00000006128	TAC1	0.2378	0.6502
1	ENSG00000236714	LINC01844	0.2060	0.6443
1	ENSG00000141433	ADCYAP1	0.1663	0.6258
1	ENSG00000128564	VGF	0.1616	0.6254
1	ENSG00000147571	CRH	0.1534	0.6083
1	ENSG00000280776	LINC01202	0.1441	0.6068
1	ENSG00000205279	CTXN3	0.1418	0.6043
1	ENSG00000246363	LINC02458	0.1693	0.6036
1	ENSG00000164326	CARTPT	0.2121	0.6029
1	ENSG00000233123	LINC01007	0.1434	0.5992
1	ENSG00000157005	SST	0.2557	0.5984
1	ENSG00000223812	PYDC2-AS1	0.1476	0.5963
1	ENSG00000205634	LINC00898	0.1320	0.5941
1	ENSG00000224404	Lnc-LARGE1-1	0.1353	0.5926
1	ENSG00000151790	TDO2	0.1494	0.5917
1	ENSG00000122012	SV2C	0.1272	0.5900
1	ENSG00000144227	NXPH2	0.1520	0.5897
1	ENSG00000261757	miR-1255	0.1283	0.5827
1	ENSG00000254363	LOC101929719	0.1810	0.5804
1	ENSG00000183090	FREM3	0.1174	0.5758
1	ENSG00000188729	OSTN	0.1506	0.5757
1	ENSG00000159248	GJD2	0.1175	0.5743
1	ENSG00000285561	None	0.1102	0.5732
1	ENSG00000261738	MIR3976HG	0.1128	0.5712
1	ENSG00000131885	KRT17P1	0.1079	0.5698
1	ENSG00000261325	LINC02192	0.1131	0.5683
1	ENSG00000254561	None	0.1068	0.5679
1	ENSG00000237390	Lnc-RHBG-1	0.1131	0.5645
1	ENSG00000242159	ABCF2P1	0.1116	0.5637
1	ENSG00000256193	LINC00507	0.1380	0.5636
1	ENSG00000130701	RBBP8NL	0.1008	0.5625
1	ENSG00000265179	Lnc-YES1-8	0.1087	0.5602
1	ENSG00000169035	KLK7	0.0983	0.5602
1	ENSG00000150175	FRMPD2B	0.0995	0.5592
1	ENSG00000271538	LINC02427	0.1744	0.5588
1	ENSG00000104938	CLEC4M	0.1060	0.5573
1	ENSG00000228735	LOC124901635	0.0935	0.5545
1	ENSG00000170290	SLN	0.1750	0.5544
1	ENSG00000281383	Lnc-KCNE1B-157	0.0933	0.5532
1	ENSG00000143858	SYT2	0.0924	0.5522
1	ENSG00000228999	LINC01830	0.1127	0.5497
1	ENSG00000254101	LINC02055	0.0925	0.5489
1	ENSG00000285735	LINC02717	0.0886	0.5486
1	ENSG00000276462	LINC03025	0.0907	0.5477
1	ENSG00000286736	None	0.0923	0.5462
1	ENSG00000075673	ATP12A	0.0913	0.5442
1	ENSG00000174403	MIR1-1HG-AS1	0.0865	0.5438
1	ENSG00000287844	None	0.0860	0.5438
1	ENSG00000286063	None	0.0889	0.5432
1	ENSG00000111863	ADTRP	0.1065	0.5421
1	ENSG00000176697	BDNF	0.0847	0.5415
1	ENSG00000287611	Lnc-HRH4-2	0.0847	0.5403
1	ENSG00000279875	None	0.0948	0.5391
1	ENSG00000223930	Lnc-ZMAT3-3	0.0928	0.5381
1	ENSG00000160221	GATD3A	0.0864	0.5375

1	ENSG00000225493	LINC01107	0.0903	0.5375
1	ENSG00000279952	None	0.0826	0.5373
1	ENSG00000185149	NPY2R	0.1257	0.5354
1	ENSG00000248837	LOC105374524	0.0860	0.5341
1	ENSG00000202048	SNORD114-20	0.0838	0.5338
1	ENSG00000250634	LINC01182	0.0784	0.5329
1	ENSG00000169676	DRD5	0.1015	0.5324
1	ENSG00000268297	CLEC4GP1	0.0753	0.5315
1	ENSG00000120875	DUSP4	0.0753	0.5310
1	ENSG00000122025	FLT3	0.0920	0.5308
1	ENSG00000231824	AKAIN1	0.0803	0.5303
1	ENSG00000145708	CRHBP	0.1696	0.5296
1	ENSG00000182632	CCNYL2	0.0952	0.5295
1	ENSG00000174576	NPAS4	0.0765	0.5284
1	ENSG00000241945	PWP2	0.0735	0.5259
1	ENSG00000285578	Lnc-DUSP22-2	0.0837	0.5259
1	ENSG00000165899	OTOGL	0.0717	0.5256
1	ENSG00000267623	Cyclin Y-Like Pseudogene	0.0717	0.5248
1	ENSG00000152595	MEPE	0.1049	0.5242
1	ENSG00000138678	GPAT3	0.0725	0.5235
1	ENSG00000239672	NME1	0.0979	0.5225
1	ENSG00000179477	ALOX12B	0.0699	0.5218
1	ENSG00000254510	Lnc-NPAS4-1	0.0688	0.5217
1	ENSG00000286292	None	0.1351	0.5215
1	ENSG00000274330	ADAM20 Pseudogene	0.0686	0.5209
1	ENSG00000106236	NPTX2	0.0749	0.5204
1	ENSG00000285634	LOC105376121	0.0825	0.5184
1	ENSG00000170231	FABP6	0.1070	0.5184
1	ENSG00000146469	VIP	0.0681	0.5180

1	ENSG00000117594	HSD11B1	0.2147	0.5167
1	ENSG00000254681	PKD1P5	0.1017	0.5151
1	ENSG00000258859	LINC02296	0.0909	0.5148
1	ENSG00000260658	Lnc-CDH8-10	0.1106	0.5143
1	ENSG00000286016	None	0.0947	0.5108
1	ENSG00000229618	Lnc-ARL4A-54	0.0836	0.5104
1	ENSG00000132677	RHBG	0.0677	0.5103
1	ENSG00000287593	Antisense to ADTRP	0.0751	0.5091
1	ENSG00000229722	Lnc-SGK1-3	0.1479	0.5090
1	ENSG00000225280	LOC105372558	0.0998	0.5087
1	ENSG00000227582	ADGRF5P1	0.1094	0.5078
1	ENSG00000119888	EPCAM	0.0706	0.5069
1	ENSG00000156076	WIF1	0.0761	0.5035
1	ENSG00000174899	SLC66A1L	0.0722	0.5015
1	ENSG00000229635	Pseudogene Similar to Part of FBXW1B	0.0740	0.5011
1	ENSG00000226405	HSD17B12 Pseudogene	0.1263	0.5006
1	ENSG00000286109	Lnc-KCNK1-1	0.0681	0.5001
1	ENSG00000287907	None	0.0696	0.4981
1	ENSG00000228772	Lnc-PRL-3	0.0822	0.4979
1	ENSG00000255087	LOC101929473	0.0713	0.4973
1	ENSG00000107165	TYRP1	0.1184	0.4971
1	ENSG00000126545	CSN1S1	0.0804	0.4955
1	ENSG00000184385	UMODL1-AS1	0.0734	0.4942
1	ENSG00000261502	Lnc-CDH8-10	0.1012	0.4918
1	ENSG00000225449	RAB6C-AS1	0.1405	0.4911
1	ENSG00000137860	SLC28A2	0.1007	0.4906
1	ENSG00000259520	SLC28A2-AS1	0.1289	0.4866
1	ENSG00000266573	Lnc-HRH4-7	0.0936	0.4845
1	ENSG00000132744	ACY3	0.0824	0.4835

1	ENSG00000234665	LERFS	0.0886	0.4825
1	ENSG00000227723	Lnc-MYB-5	0.1588	0.4812
1	ENSG00000273214	Lnc-POLR2F-1	0.1015	0.4796
1	ENSG00000218772	FAM8A6P	0.1215	0.4786
1	ENSG00000286666	None	0.0834	0.4784
1	ENSG00000179520	SLC17A8	0.0938	0.4775
1	ENSG00000277918	RNVU1-28	0.1078	0.4766
1	ENSG00000216753	HMGA1P7	0.1011	0.4670
1	ENSG00000117322	CR2	0.0698	0.4657
1	ENSG00000256971	LINC00508	0.0889	0.4610
1	ENSG00000286810	None	0.0805	0.4581
1	ENSG00000178401	DNAJC22	0.0983	0.4531
1	ENSG00000223553	SMPD4P1	0.0675	0.4308
1	ENSG00000200959	SNORA74A	0.0681	0.4273
1	ENSG00000243323	PTPRVP	0.0713	0.4221
2	ENSG00000175084	DES	0.8407	0.9591
2	ENSG00000163017	ACTG2	0.5157	0.8158
2	ENSG00000105641	SLC5A5	0.4185	0.7857
2	ENSG00000168542	COL3A1	0.4631	0.7699
2	ENSG00000196616	ADH1B	0.4705	0.7698
2	ENSG00000108821	COL1A1	0.4247	0.7545
2	ENSG00000118271	TTR	0.3322	0.7462
2	ENSG00000096696	DSP	0.3321	0.7450
2	ENSG00000144810	COL8A1	0.3937	0.7423
2	ENSG00000111341	MGP	0.3728	0.7233
2	ENSG00000133392	MYH11	0.3091	0.7219
2	ENSG00000149596	JPH2	0.2880	0.7045
2	ENSG00000101335	MYL9	0.2608	0.6917
2	ENSG00000112214	FHL5	0.2641	0.6903
2	ENSG00000130176	CNN1	0.2413	0.6892
2	ENSG00000198467	TPM2	0.2413	0.6876
2	ENSG00000187955	COL14A1	0.2812	0.6777
2	ENSG00000124253	PCK1	0.3288	0.6772
2	ENSG00000141052	MYOCD	0.2321	0.6735
2	ENSG00000013588	GPRC5A	0.3677	0.6732
2	ENSG00000163817	SLC6A20	0.2255	0.6732
2	ENSG00000143867	OSR1	0.2179	0.6726
2	ENSG00000115602	IL1RL1	0.2727	0.6724
2	ENSG00000054598	FOXC1	0.2789	0.6712
2	ENSG00000287338	Lnc-TLR5-1	0.3582	0.6663
2	ENSG00000107796	ACTA2	0.2111	0.6644
2	ENSG00000115590	IL1R2	0.3469	0.6638
2	ENSG00000115648	MLPH	0.2497	0.6630
2	ENSG00000112499	SLC22A2	0.2091	0.6619
2	ENSG00000205038	PKHD1L1	0.2324	0.6579
2	ENSG00000164692	COL1A2	0.2609	0.6567
2	ENSG00000162458	FBLIM1	0.2227	0.6525
2	ENSG00000269113	TRABD2B	0.2354	0.6522
2	ENSG00000112837	TBX18	0.2049	0.6503
2	ENSG00000152779	SLC16A12	0.1988	0.6485
2	ENSG00000131471	AOC3	0.2022	0.6476
2	ENSG00000241644	INMT	0.1894	0.6471
2	ENSG00000186564	FOXD2	0.2019	0.6410
2	ENSG00000107438	PDLIM1	0.2306	0.6385
2	ENSG00000161638	ITGA5	0.2232	0.6385
2	ENSG00000149257	SERPINH1	0.3113	0.6370
2	ENSG00000177575	CD163	0.4013	0.6367
2	ENSG00000164707	SLC13A4	0.1768	0.6366
2	ENSG00000149591	TAGLN	0.1862	0.6346
2	ENSG00000149573	MPZL2	0.2436	0.6342

2	ENSG00000112936	C7	0.3239	0.6312
2	ENSG00000237424	FOXD2-AS1	0.1845	0.6312
2	ENSG00000226390	KCNQ2-AS1	0.1684	0.6311
2	ENSG00000124107	SLPI	0.1963	0.6308
2	ENSG00000185585	OLFML2A	0.1824	0.6269
2	ENSG00000176692	FOXC2	0.1617	0.6250
2	ENSG00000152049	KCNE4	0.2716	0.6242
2	ENSG00000000971	CFH	0.2495	0.6231
2	ENSG00000173597	SULT1B1	0.2169	0.6223
2	ENSG00000144837	PLA1A	0.2179	0.6212
2	ENSG00000115604	IL18R1	0.1820	0.6208
2	ENSG00000279821	None	0.1868	0.6201
2	ENSG00000112175	BMP5	0.1541	0.6177
2	ENSG00000173530	TNFRSF10D	0.2506	0.6163
2	ENSG00000015520	NPC1L1	0.1809	0.6157
2	ENSG00000142173	COL6A2	0.1894	0.6138
2	ENSG00000027644	INSRR	0.1484	0.6127
2	ENSG00000102802	MEDAG	0.1481	0.6126
2	ENSG00000099994	SUSD2	0.1962	0.6125
2	ENSG00000198848	CES1	0.1597	0.6098
2	ENSG00000198959	TGM2	0.1946	0.6095
2	ENSG00000143546	S100A8	0.3517	0.6077
2	ENSG00000184811	TRARG1	0.1404	0.6053
2	ENSG00000130635	COL5A1	0.1363	0.6012
2	ENSG00000163736	PPBP	0.1520	0.6009
2	ENSG00000163220	S100A9	0.3857	0.6009
2	ENSG00000172935	MRGPRF	0.1409	0.5978
2	ENSG00000166523	CLEC4E	0.1432	0.5978
2	ENSG00000118729	CASQ2	0.1389	0.5977
2	ENSG00000265107	GJA5	0.1532	0.5977

2	ENSG00000115594	IL1R1	0.2082	0.5974
2	ENSG00000124212	PTGIS	0.1438	0.5956
2	ENSG00000165474	GJB2	0.1371	0.5954
2	ENSG00000196154	S100A4	0.2512	0.5943
2	ENSG00000128274	A4GALT	0.2053	0.5942
2	ENSG00000173110	HSPA6	0.3594	0.5917
2	ENSG00000164761	TNFRSF11B	0.2011	0.5914
2	ENSG00000163431	LMOD1	0.1365	0.5912
2	ENSG00000135842	NIBAN1	0.2978	0.5905
2	ENSG00000167244	IGF2	0.1261	0.5904
2	ENSG00000106366	SERPINE1	0.1559	0.5904
2	ENSG00000174348	PODN	0.1846	0.5897
2	ENSG00000206538	VGLL3	0.1305	0.5883
2	ENSG00000122176	FMOD	0.1288	0.5881
2	ENSG00000088882	CPXM1	0.1336	0.5870
2	ENSG00000221869	CEBPD	0.1630	0.5867
2	ENSG00000074219	TEAD2	0.1467	0.5861
2	ENSG00000153404	PLEKHG4B	0.1228	0.5853
2	ENSG00000120708	TGFBI	0.2404	0.5845
2	ENSG00000047617	ANO2	0.1433	0.5842
2	ENSG00000142973	CYP4B1	0.1186	0.5828
2	ENSG00000260337	Lnc-FAM174B-1	0.1209	0.5816
2	ENSG00000125733	TRIP10	0.1981	0.5798
2	ENSG00000244734	HBB	0.1650	0.5781
2	ENSG00000138722	MMRN1	0.1785	0.5778
2	ENSG00000110852	CLEC2B	0.2295	0.5774
2	ENSG00000166482	MFAP4	0.1255	0.5773
2	ENSG00000101187	SLCO4A1	0.1270	0.5771
2	ENSG00000106211	HSPB1	0.1555	0.5770
2	ENSG00000137834	SMAD6	0.1622	0.5762

2	ENSG00000073792	IGF2BP2	0.1389	0.5754
2	ENSG00000164294	GPX8	0.1488	0.5753
2	ENSG00000142798	HSPG2	0.1443	0.5747
2	ENSG00000137507	LRRC32	0.1669	0.5745
2	ENSG00000140682	TGFB1I1	0.1366	0.5739
2	ENSG00000187498	COL4A1	0.1411	0.5727
2	ENSG00000188536	HBA2	0.1400	0.5720
2	ENSG00000279142	None	0.1117	0.5718
2	ENSG00000125810	CD93	0.3224	0.5718
2	ENSG00000184058	TBX1	0.1091	0.5717
2	ENSG00000281732	LOC284933	0.1097	0.5715
2	ENSG00000287652	Antisense to DGCR8 and CDC45	0.1736	0.5709
2	ENSG00000173641	HSPB7	0.1194	0.5700
2	ENSG00000159403	C1R	0.2205	0.5690
2	ENSG00000206172	HBA1	0.1478	0.5680
2	ENSG00000159212	CLIC6	0.1114	0.5659
2	ENSG00000100985	MMP9	0.1078	0.5650
2	ENSG00000250863	Lnc-KCTD8-1	0.2379	0.5643
2	ENSG00000169429	CXCL8	0.1011	0.5636
2	ENSG00000177464	GPR4	0.1500	0.5636
2	ENSG00000162998	FRZB	0.1011	0.5635
2	ENSG00000160183	TMPRSS3	0.1281	0.5617
2	ENSG00000109758	HGFAC	0.0997	0.5615
2	ENSG00000233117	LINC00702	0.1065	0.5614
2	ENSG00000183508	TENT5C	0.1446	0.5602
2	ENSG00000258647	LINC00930	0.0996	0.5592
2	ENSG00000173421	IHO1	0.1189	0.5576
2	ENSG00000111057	KRT18	0.1250	0.5570
2	ENSG00000060138	YBX3	0.1784	0.5568
2	ENSG00000128917	DLL4	0.1135	0.5567
2	ENSG00000124762	CDKN1A	0.1752	0.5554
2	ENSG00000239677	PDZRN3-AS1	0.0937	0.5545
2	ENSG00000243620	Lnc-ZIC4-3	0.1434	0.5534
2	ENSG00000249307	LINC01088	0.1275	0.5529
2	ENSG00000115607	IL18RAP	0.1272	0.5526
2	ENSG00000261170	LOC107984827	0.1218	0.5520
2	ENSG00000138061	CYP1B1	0.1214	0.5517
2	ENSG00000106624	AEBP1	0.1317	0.5514
2	ENSG00000117595	IRF6	0.0949	0.5510
2	ENSG00000187479	C11orf96	0.0954	0.5504
2	ENSG00000179023	KLHDC7A	0.0897	0.5499
2	ENSG00000168427	KLHL30	0.0902	0.5498
2	ENSG00000250033	SLC7A11-AS1	0.1174	0.5488
2	ENSG00000183888	SRARP	0.0986	0.5487
2	ENSG00000162383	SLC1A7	0.2594	0.5470
2	ENSG00000185201	IFITM2	0.2451	0.5458
2	ENSG00000125430	HS3ST3B1	0.1002	0.5457
2	ENSG00000182718	ANXA2	0.2208	0.5457
2	ENSG00000253123	LOC100507403	0.0915	0.5454
2	ENSG00000094963	FMO2	0.1120	0.5448
2	ENSG00000229380	PRKAR1B-AS2	0.0871	0.5447
2	ENSG00000285938	BCL6-AS1	0.1633	0.5444
2	ENSG00000149452	SLC22A8	0.1339	0.5427
2	ENSG00000163739	CXCL1	0.0862	0.5420
2	ENSG00000196954	CASP4	0.2211	0.5413
2	ENSG00000173068	BNC2	0.2439	0.5410
2	ENSG00000003436	TFPI	0.1344	0.5407
2	ENSG00000171345	KRT19	0.0834	0.5407
2	ENSG00000253686	LINC01484	0.1257	0.5405

2	ENSG00000004939	SLC4A1	0.1226	0.5398
2	ENSG00000112303	VNN2	0.1302	0.5396
2	ENSG00000106034	CPED1	0.1185	0.5393
2	ENSG00000204389	HSPA1A	0.1690	0.5393
2	ENSG00000262152	GREP1	0.0831	0.5389
2	ENSG00000148604	RGR	0.0865	0.5387
2	ENSG00000187922	LCN10	0.0839	0.5387
2	ENSG00000126778	SIX1	0.1048	0.5384
2	ENSG00000174226	SNX31	0.0937	0.5383
2	ENSG00000164867	NOS3	0.1047	0.5379
2	ENSG00000187513	GJA4	0.0914	0.5377
2	ENSG00000229926	IL9RP1	0.0889	0.5374
2	ENSG00000276317	Lnc-GATA5-10	0.0815	0.5371
2	ENSG00000173918	C1QTNF1	0.1052	0.5369
2	ENSG00000256955	Lnc-MMP17-1	0.0837	0.5357
2	ENSG00000163638	ADAMTS9	0.1670	0.5355
2	ENSG00000077238	IL4R	0.1918	0.5351
2	ENSG00000100336	APOL4	0.3160	0.5349
2	ENSG00000047457	CP	0.3633	0.5349
2	ENSG00000162747	FCGR3B	0.1056	0.5344
2	ENSG00000278130	FAM166A Pseudogene	0.0809	0.5335
2	ENSG00000151929	BAG3	0.1593	0.5334
2	ENSG00000272512	Lnc-HES4-2	0.0765	0.5332
2	ENSG00000165507	DEPP1	0.1676	0.5330
2	ENSG00000186150	UBL4B	0.0873	0.5326
2	ENSG00000129654	FOXJ1	0.1860	0.5320
2	ENSG00000168079	SCARA5	0.0786	0.5318
2	ENSG00000230122	ECEL1P3	0.0777	0.5313
2	ENSG00000241158	ADAMTS9-AS1	0.1303	0.5305

2	ENSG00000122862	SRGN	0.1557	0.5294
2	ENSG00000135245	HILPDA	0.1222	0.5294
2	ENSG00000050327	ARHGEF5	0.0878	0.5292
2	ENSG00000233588	CYP51A1P2	0.1109	0.5285
2	ENSG00000232803	SLCO4A1-AS1	0.0783	0.5282
2	ENSG00000184557	SOCS3	0.3501	0.5275
2	ENSG00000287656	Antisense to SLC22A3	0.0726	0.5271
2	ENSG00000170577	SIX2	0.0784	0.5270
2	ENSG00000137801	THBS1	0.0703	0.5243
2	ENSG00000185561	TLCD2	0.1310	0.5236
2	ENSG00000197405	C5AR1	0.2152	0.5233
2	ENSG00000249669	CARMN	0.0902	0.5231
2	ENSG00000182885	ADGRG3	0.0785	0.5222
2	ENSG00000163623	NKX6-1	0.0762	0.5212
2	ENSG00000163464	CXCR1	0.0771	0.5210
2	ENSG00000267304	Lnc-TJP3-2	0.0679	0.5210
2	ENSG00000267065	LINC02080	0.0687	0.5208
2	ENSG00000258676	Lnc-ST8SIA2-1	0.0683	0.5202
2	ENSG00000130600	H19	0.0842	0.5194
2	ENSG00000160593	JAML	0.0916	0.5190
2	ENSG00000141574	SECTM1	0.1016	0.5185
2	ENSG00000251493	FOXD1	0.0706	0.5185
2	ENSG00000228133	LOC105371485	0.0710	0.5178
2	ENSG00000074047	GLI2	0.0794	0.5177
2	ENSG00000262003	LOC101927727	0.0716	0.5171
2	ENSG00000254362	Lnc-PPP2R2A-2	0.0734	0.5165
2	ENSG00000198542	ITGBL1	0.0744	0.5158
2	ENSG00000150048	CLEC1A	0.1016	0.5149
2	ENSG00000197901	SLC22A6	0.1006	0.5148

2	ENSG00000188511	MIR3667HG	0.0821	0.5145
2	ENSG00000145623	OSMR	0.1585	0.5141
2	ENSG00000163395	IGFN1	0.1503	0.5121
2	ENSG00000117318	ID3	0.1579	0.5119
2	ENSG00000270640	Lnc-BABAM2-2	0.0681	0.5117
2	ENSG00000140839	CLEC18B	0.0926	0.5105
2	ENSG00000168404	MLKL	0.1351	0.5098
2	ENSG00000125144	MT1G	0.0702	0.5098
2	ENSG00000169894	MUC3A	0.0727	0.5086
2	ENSG00000170801	HTRA3	0.0950	0.5082
2	ENSG00000171049	FPR2	0.0841	0.5080
2	ENSG00000148926	ADM	0.1033	0.5077
2	ENSG00000000938	FGR	0.1132	0.5075
2	ENSG00000279320	None	0.0784	0.5070
2	ENSG00000213719	CLIC1	0.1690	0.5068
2	ENSG00000169908	TM4SF1	0.1260	0.5067
2	ENSG00000108823	SGCA	0.0927	0.5051
2	ENSG00000205592	MUC19	0.0809	0.5050
2	ENSG00000112299	VNN1	0.1115	0.5050
2	ENSG00000134531	EMP1	0.1952	0.5048
2	ENSG00000136732	GYPC	0.1909	0.5046
2	ENSG00000256443	Lnc-CPSF7-3	0.0683	0.5023
2	ENSG00000162692	VCAM1	0.1084	0.5019
2	ENSG00000123374	CDK2	0.1392	0.4990
2	ENSG00000187634	SAMD11	0.1889	0.4974
2	ENSG00000205364	MT1M	0.0792	0.4971
2	ENSG00000142089	IFITM3	0.1127	0.4960
2	ENSG00000205358	MT1H	0.0677	0.4953
2	ENSG00000280109	PLAC4	0.0771	0.4950
2	ENSG00000125731	SH2D3A	0.0905	0.4942
2	ENSG00000235750	KIAA0040	0.1544	0.4933
2	ENSG00000268388	FENDRR	0.0698	0.4933
2	ENSG00000115165	CYTIP	0.1310	0.4923
2	ENSG00000152977	ZIC1	0.0967	0.4917
2	ENSG00000159167	STC1	0.2229	0.4904
2	ENSG00000185885	IFITM1	0.1422	0.4897
2	ENSG00000100060	MFNG	0.1947	0.4889
2	ENSG00000132357	CARD6	0.1124	0.4887
2	ENSG00000145779	TNFAIP8	0.1175	0.4887
2	ENSG00000183615	FAM167B	0.1053	0.4886
2	ENSG00000124549	BTN2A3P	0.1080	0.4876
2	ENSG00000110719	TCIRG1	0.1600	0.4860
2	ENSG00000276412	Lnc-CNTNAP3B-13	0.0763	0.4851
2	ENSG00000028137	TNFRSF1B	0.2047	0.4815
2	ENSG00000281327	LINC01338	0.1457	0.4808
2	ENSG00000185499	MUC1	0.0847	0.4793
2	ENSG00000186431	FCAR	0.0737	0.4782
2	ENSG00000105559	PLEKHA4	0.1353	0.4772
2	ENSG00000118503	TNFAIP3	0.0913	0.4767
2	ENSG00000231246	LINC02884	0.0746	0.4754
2	ENSG00000160111	CPAMD8	0.1501	0.4751
2	ENSG00000070729	CNGB1	0.1294	0.4748
2	ENSG00000011422	PLAUR	0.1129	0.4747
2	ENSG00000236908	LINC02827	0.0676	0.4702
2	ENSG00000176046	NUPR1	0.1310	0.4701
2	ENSG00000090339	ICAM1	0.1558	0.4689
2	ENSG00000105974	CAV1	0.0781	0.4680
2	ENSG00000100504	PYGL	0.0952	0.4621
2	ENSG00000166592	RRAD	0.0733	0.4614
2	ENSG00000103710	RASL12	0.1499	0.4578

2	ENSG00000128016	ZFP36	0.1257	0.4530
2	ENSG00000170345	FOS	0.0876	0.4526
2	ENSG00000167772	ANGPTL4	0.1161	0.4514
2	ENSG00000142102	PGGHG	0.0681	0.4497
2	ENSG00000175591	P2RY2	0.0895	0.4371
2	ENSG00000020633	RUNX3	0.0743	0.4361
2	ENSG00000156463	SH3RF2	0.0891	0.4310
2	ENSG00000287689	None	0.0712	0.4284
2	ENSG00000154188	ANGPT1	0.0687	0.4277
3	ENSG00000064886	CHI3L2	0.4444	0.7458
3	ENSG00000006747	SCIN	0.4155	0.6644
3	ENSG00000095970	TREM2	0.2306	0.6507
3	ENSG00000038945	MSR1	0.3232	0.6468
3	ENSG00000118785	SPP1	0.1842	0.6451
3	ENSG00000224189	HAGLR	0.2821	0.6409
3	ENSG00000012223	LTF	0.1864	0.6378
3	ENSG00000163823	CCR1	0.2533	0.6327
3	ENSG00000196136	SERPINA3	0.3858	0.6323
3	ENSG00000173391	OLR1	0.1675	0.6306
3	ENSG00000026508	CD44	0.3408	0.6300
3	ENSG00000203747	FCGR3A	0.2844	0.6260
3	ENSG00000150337	FCGR1A	0.1995	0.6243
3	ENSG00000066294	CD84	0.1908	0.6191
3	ENSG00000168329	CX3CR1	0.1554	0.6083
3	ENSG00000173369	C1QB	0.3041	0.6062
3	ENSG00000005844	ITGAL	0.2456	0.6054
3	ENSG00000155307	SAMSN1	0.2182	0.6042
3	ENSG00000108691	CCL2	0.2850	0.6042
3	ENSG00000240583	AQP1	0.2052	0.6041
3	ENSG00000166927	MS4A7	0.2270	0.6031
3	ENSG00000185811	IKZF1	0.2204	0.6021
3	ENSG00000148773	MKI67	0.3404	0.6020
3	ENSG00000077420	APBB1IP	0.1666	0.5975
3	ENSG00000158869	FCER1G	0.2290	0.5966
3	ENSG00000204287	HLA-DRA	0.1752	0.5957
3	ENSG00000011600	TYROBP	0.1881	0.5945
3	ENSG00000082074	FYB1	0.2092	0.5931
3	ENSG00000167613	LAIR1	0.2646	0.5931
3	ENSG00000105697	HAMP	0.1858	0.5916
3	ENSG00000258342	LINC00609	0.2780	0.5912
3	ENSG00000239961	LILRA4	0.1370	0.5882
3	ENSG00000160255	ITGB2	0.2669	0.5882
3	ENSG00000104972	LILRB1	0.2167	0.5874
3	ENSG00000125730	C3	0.1568	0.5841
3	ENSG00000159189	C1QC	0.2604	0.5840
3	ENSG00000162511	LAPTM5	0.1968	0.5834
3	ENSG00000134061	CD180	0.2625	0.5832
3	ENSG00000140968	IRF8	0.1710	0.5831
3	ENSG00000018280	SLC11A1	0.2388	0.5819
3	ENSG00000271605	MILR1	0.1310	0.5815
3	ENSG00000204472	AIF1	0.1678	0.5814
3	ENSG00000129450	SIGLEC9	0.2089	0.5802
3	ENSG00000239998	LILRA2	0.1916	0.5801
3	ENSG00000242574	HLA-DMB	0.1448	0.5797
3	ENSG00000184574	LPAR5	0.1204	0.5796
3	ENSG00000173988	LRRC63	0.1636	0.5787
3	ENSG00000226496	LINC00323	0.2143	0.5778
3	ENSG00000257585	LINC00609	0.1563	0.5776
3	ENSG00000257826	Lnc-MBIP-3	0.2340	0.5772
3	ENSG00000276980	Lnc-GPR108-3	0.1544	0.5759

3	ENSG00000132965	ALOX5AP	0.2384	0.5757
3	ENSG00000165025	SYK	0.1635	0.5747
3	ENSG00000121933	TMIGD3	0.1161	0.5733
3	ENSG00000131747	TOP2A	0.2065	0.5730
3	ENSG00000233670	PIRT	0.1656	0.5724
3	ENSG00000250771	TLR2 Pseudogene	0.1736	0.5723
3	ENSG00000115956	PLEK	0.1586	0.5708
3	ENSG00000100292	HMOX1	0.2271	0.5693
3	ENSG00000167755	KLK6	0.3529	0.5686
3	ENSG00000173372	C1QA	0.2941	0.5682
3	ENSG00000158715	SLC45A3	0.1833	0.5679
3	ENSG00000155629	PIK3AP1	0.2317	0.5677
3	ENSG00000086205	FOLH1	0.3113	0.5675
3	ENSG00000261795	Lnc-PDGFA-4	0.1338	0.5672
3	ENSG00000204252	HLA-DOA	0.1157	0.5669
3	ENSG00000175567	UCP2	0.1424	0.5666
3	ENSG00000204161	TMEM273	0.1158	0.5659
3	ENSG00000175785	PRIMA1	0.1161	0.5650
3	ENSG00000265531	FCGR1CP	0.1028	0.5650
3	ENSG00000253924	Lnc-NPBWR1-8	0.2240	0.5648
3	ENSG00000167851	CD300A	0.2093	0.5647
3	ENSG00000228392	None	0.2104	0.5645
3	ENSG00000169403	PTAFR	0.1752	0.5639
3	ENSG00000105366	SIGLEC8	0.1177	0.5639
3	ENSG00000269553	Lnc-MAG-2	0.1194	0.5636
3	ENSG00000016602	CLCA4	0.1681	0.5630
3	ENSG00000013297	CLDN11	0.1882	0.5627
3	ENSG00000186417	GLDN	0.2349	0.5612
3	ENSG00000259104	PTCSC3	0.1650	0.5609
3	ENSG00000105967	TFEC	0.1231	0.5609
3	ENSG00000110077	MS4A6A	0.3586	0.5605
3	ENSG00000232310	LINC03002	0.1724	0.5599
3	ENSG00000158865	SLC5A11	0.2242	0.5596
3	ENSG00000101336	HCK	0.1635	0.5594
3	ENSG00000090104	RGS1	0.1631	0.5578
3	ENSG00000041982	TNC	0.0966	0.5564
3	ENSG00000255216	Lnc-TRIM29-2	0.2158	0.5560
3	ENSG00000138964	PARVG	0.1641	0.5553
3	ENSG00000171860	C3AR1	0.1675	0.5548
3	ENSG00000275395	FCGBP	0.3690	0.5546
3	ENSG00000204655	MOG	0.2646	0.5546
3	ENSG00000197249	SERPINA1	0.3593	0.5541
3	ENSG00000187908	DMBT1	0.2145	0.5540
3	ENSG00000254314	Lnc-NPBWR1-9	0.1663	0.5539
3	ENSG00000081237	PTPRC	0.1697	0.5526
3	ENSG00000231389	HLA-DPA1	0.1207	0.5513
3	ENSG00000250072	SH3TC2-DT	0.2859	0.5506
3	ENSG00000154864	PIEZO2	0.1379	0.5501
3	ENSG00000134817	APLNR	0.1656	0.5494
3	ENSG00000139292	LGR5	0.1987	0.5487
3	ENSG00000183160	TMEM119	0.0974	0.5479
3	ENSG00000225781	OR6V1	0.1580	0.5472
3	ENSG00000152689	RASGRP3	0.1192	0.5470
3	ENSG00000251138	LINC02882	0.3034	0.5470
3	ENSG00000174607	UGT8	0.2070	0.5466
3	ENSG00000197471	SPN	0.1518	0.5465
3	ENSG00000267432	DNAH17-AS1	0.2638	0.5465
3	ENSG00000213186	TRIM59	0.2357	0.5465
3	ENSG00000071991	CDH19	0.1692	0.5465
3	ENSG00000171051	FPR1	0.1661	0.5464

3	ENSG00000136167	LCP1	0.2126	0.5462
3	ENSG00000228789	HCG22	0.1308	0.5458
3	ENSG00000142583	SLC2A5	0.1205	0.5456
3	ENSG00000277494	GPIHBP1	0.1423	0.5446
3	ENSG00000286558	None	0.2273	0.5445
3	ENSG00000114013	CD86	0.1466	0.5440
3	ENSG00000081479	LRP2	0.1365	0.5439
3	ENSG00000148908	RGS10	0.0901	0.5436
3	ENSG00000042493	CAPG	0.1489	0.5434
3	ENSG00000105383	CD33	0.1443	0.5428
3	ENSG00000204482	LST1	0.0920	0.5425
3	ENSG00000205116	TMEM88B	0.1989	0.5423
3	ENSG00000161896	IP6K3	0.1400	0.5423
3	ENSG00000231131	LNCAROD	0.1219	0.5419
3	ENSG00000134516	DOCK2	0.1101	0.5418
3	ENSG00000104974	LILRA1	0.0889	0.5414
3	ENSG00000207955	MIR219A2HG	0.3251	0.5414
3	ENSG00000126860	EVI2A	0.1890	0.5402
3	ENSG00000268758	ADGRE4P	0.0917	0.5401
3	ENSG00000279419	None	0.2489	0.5400
3	ENSG00000244062	ACSL3 Pseudogene	0.2810	0.5397
3	ENSG00000261121	LINC02473	0.1756	0.5397
3	ENSG00000143226	FCGR2A	0.2433	0.5395
3	ENSG00000172243	CLEC7A	0.0942	0.5394
3	ENSG00000080031	PTPRH	0.1945	0.5393
3	ENSG00000019582	CD74	0.1044	0.5391
3	ENSG00000103089	FA2H	0.2255	0.5390
3	ENSG00000166091	CMTM5	0.2567	0.5389
3	ENSG00000198502	HLA-DRB5	0.1264	0.5383
3	ENSG00000170458	CD14	0.2002	0.5383
3	ENSG00000127412	TRPV5	0.1333	0.5382
3	ENSG00000148826	NKX6-2	0.0973	0.5366
3	ENSG00000105695	MAG	0.2540	0.5362
3	ENSG00000188488	SERPINA5	0.1245	0.5360
3	ENSG00000112799	LY86	0.1109	0.5355
3	ENSG00000142512	SIGLEC10	0.0913	0.5349
3	ENSG00000160791	CCR5	0.1243	0.5345
3	ENSG00000261997	None	0.0881	0.5342
3	ENSG00000270547	LINC01235	0.0773	0.5341
3	ENSG00000197993	KEL	0.1067	0.5334
3	ENSG00000179178	TMEM125	0.3213	0.5328
3	ENSG00000204644	ZFP57	0.1625	0.5326
3	ENSG00000139629	GALNT6	0.1594	0.5326
3	ENSG00000286279	Lnc-SLC16A7-4	0.2188	0.5319
3	ENSG00000251429	AIDAP2	0.1537	0.5318
3	ENSG00000012124	CD22	0.1227	0.5311
3	ENSG00000140030	GPR65	0.1490	0.5307
3	ENSG00000180739	S1PR5	0.1704	0.5297
3	ENSG00000163694	RBM47	0.2062	0.5297
3	ENSG00000228058	LINC01736	0.0948	0.5295
3	ENSG00000204278	TMEM235	0.1819	0.5292
3	ENSG00000198019	FCGR1B	0.0741	0.5287
3	ENSG00000172578	KLHL6	0.2254	0.5286
3	ENSG00000282608	ADORA3	0.1216	0.5285
3	ENSG00000233828	MIR4280HG	0.2797	0.5284
3	ENSG00000116774	OLFML3	0.0919	0.5284
3	ENSG00000250198	LINC02199	0.1212	0.5280
3	ENSG00000169896	ITGAM	0.1538	0.5278
3	ENSG00000268170	Lnc-FAM131B-2	0.1720	0.5275
3	ENSG00000127507	ADGRE2	0.0830	0.5275

3	ENSG00000187912	CLEC17A	0.0857	0.5272
3	ENSG00000287372	None	0.0722	0.5271
3	ENSG00000286749	Antisense to NMUR2	0.1255	0.5271
3	ENSG00000158859	ADAMTS4	0.1169	0.5270
3	ENSG00000174125	TLR1	0.1138	0.5270
3	ENSG00000171840	NINJ2	0.1958	0.5261
3	ENSG00000272808	GCAWKR	0.2691	0.5258
3	ENSG00000064300	NGFR	0.0736	0.5257
3	ENSG00000126266	FFAR1	0.1173	0.5257
3	ENSG00000236398	TAS2R39	0.0990	0.5254
3	ENSG00000228408	Lnc-TAB2-1	0.3106	0.5246
3	ENSG00000130300	PLVAP	0.0702	0.5246
3	ENSG00000086730	LAT2	0.1724	0.5242
3	ENSG00000167641	PPP1R14A	0.1141	0.5234
3	ENSG00000184357	H1-5	0.2146	0.5231
3	ENSG00000133321	PLAAT4	0.1197	0.5230
3	ENSG00000231427	LINC01445	0.1206	0.5228
3	ENSG00000162444	RBP7	0.2111	0.5224
3	ENSG00000159216	RUNX1	0.1434	0.5221
3	ENSG00000110934	BIN2	0.1052	0.5219
3	ENSG00000174123	TLR10	0.0753	0.5211
3	ENSG00000136960	ENPP2	0.2141	0.5210
3	ENSG00000254415	SIGLEC14	0.0754	0.5208
3	ENSG00000011426	ANLN	0.1141	0.5207
3	ENSG00000287939	None	0.0793	0.5203
3	ENSG00000241345	LOC105375483	0.1202	0.5200
3	ENSG00000169413	RNASE6	0.0759	0.5195
3	ENSG00000178082	TWF1P1	0.1148	0.5192
3	ENSG00000124915	MYRF-AS1	0.0889	0.5184
3	ENSG00000256618	MTRNR2L1	0.1613	0.5184
3	ENSG00000162949	CAPN13	0.1591	0.5183
3	ENSG00000249484	LINC01470	0.1220	0.5183
3	ENSG00000073737	DHRS9	0.0817	0.5182
3	ENSG00000146192	FGD2	0.0924	0.5179
3	ENSG00000244682	FCGR2C	0.1287	0.5177
3	ENSG00000286403	None	0.1016	0.5177
3	ENSG00000179468	OR9A2	0.1493	0.5176
3	ENSG00000101049	SGK2	0.1796	0.5174
3	ENSG00000051523	CYBA	0.1548	0.5162
3	ENSG00000225217	HSPA7	0.2140	0.5161
3	ENSG00000183196	CHST6	0.0768	0.5160
3	ENSG00000180353	HCLS1	0.1249	0.5154
3	ENSG00000138316	ADAMTS14	0.1382	0.5153
3	ENSG00000175489	LRRC25	0.1485	0.5151
3	ENSG00000070190	DAPP1	0.0724	0.5148
3	ENSG00000107099	DOCK8	0.0916	0.5146
3	ENSG00000108798	ABI3	0.0964	0.5144
3	ENSG00000136867	SLC31A2	0.1023	0.5144
3	ENSG00000163191	S100A11	0.3018	0.5140
3	ENSG00000283608	Lnc-SUMO4-6	0.1398	0.5131
3	ENSG00000240534	RPL34P17	0.2349	0.5130
3	ENSG00000229391	HLA-DRB6	0.0948	0.5126
3	ENSG00000224389	C4B	0.2260	0.5119
3	ENSG00000154642	C21orf91	0.1296	0.5118
3	ENSG00000180929	GPR62	0.1292	0.5116
3	ENSG00000125735	TNFSF14	0.1245	0.5113
3	ENSG00000167588	GPD1	0.3039	0.5112
3	ENSG00000137462	TLR2	0.1196	0.5096
3	ENSG00000262188	LINC01978	0.1429	0.5092
3	ENSG00000196126	HLA-DRB1	0.0822	0.5089

3	ENSG00000226448	RPL7AP51	0.1549	0.5088
3	ENSG00000184730	APOBR	0.1201	0.5084
3	ENSG00000237166	LINC01792	0.1283	0.5082
3	ENSG00000227544	LINC03013	0.1727	0.5080
3	ENSG00000183760	ACP7	0.1075	0.5079
3	ENSG00000006042	TMEM98	0.0994	0.5073
3	ENSG00000235568	NFAM1	0.1035	0.5073
3	ENSG00000228793	LOC100507336	0.0786	0.5072
3	ENSG00000286522	H3C2	0.1474	0.5070
3	ENSG00000158714	SLAMF8	0.2027	0.5063
3	ENSG00000225924	TAB2-AS1	0.0742	0.5062
3	ENSG00000248208	WDR45P1	0.0856	0.5059
3	ENSG00000131401	NAPSB	0.1100	0.5053
3	ENSG00000226994	Lnc-RASGRP3-5	0.2097	0.5051
3	ENSG00000159399	HK2	0.1393	0.5048
3	ENSG00000231840	TMEM139-AS1	0.0943	0.5047
3	ENSG00000166923	GREM1	0.2348	0.5042
3	ENSG00000128283	CDC42EP1	0.0740	0.5041
3	ENSG00000105122	RASAL3	0.0911	0.5039
3	ENSG00000167208	SNX20	0.1051	0.5034
3	ENSG00000150656	CNDP1	0.2512	0.5034
3	ENSG00000287609	None	0.0942	0.5025
3	ENSG00000113396	SLC27A6	0.1071	0.5021
3	ENSG00000140379	BCL2A1	0.1602	0.5020
3	ENSG00000129757	CDKN1C	0.0953	0.5013
3	ENSG00000283462	LOC101930276	0.1841	0.5010
3	ENSG00000169385	RNASE2	0.0788	0.5005
3	ENSG00000236700	LINC01010	0.0749	0.5005
3	ENSG00000136286	MYO1G	0.0689	0.5000
3	ENSG00000221937	TAS2R40	0.0786	0.4998
3	ENSG00000176381	PRR18	0.1319	0.4988
3	ENSG00000137869	CYP19A1	0.0816	0.4979
3	ENSG00000173253	DMRT2	0.1261	0.4975
3	ENSG00000172005	MAL	0.1617	0.4968
3	ENSG00000197430	OPALIN	0.2467	0.4965
3	ENSG00000100365	NCF4	0.1516	0.4964
3	ENSG00000171631	P2RY6	0.1131	0.4951
3	ENSG00000119535	CSF3R	0.1157	0.4950
3	ENSG00000232560	LINC01549	0.0799	0.4948
3	ENSG00000014257	ACP3	0.0803	0.4948
3	ENSG00000244301	AOX3P	0.1489	0.4939
3	ENSG00000140873	ADAMTS18	0.1981	0.4934
3	ENSG00000129667	RHBDF2	0.1048	0.4932
3	ENSG00000253877	LINC01608	0.1697	0.4931
3	ENSG00000172548	NIPAL4	0.1423	0.4930
3	ENSG00000128645	HOXD1	0.1054	0.4924
3	ENSG00000163565	IFI16	0.1153	0.4920
3	ENSG00000286625	None	0.1128	0.4916
3	ENSG00000250215	CIR1P2	0.2653	0.4913
3	ENSG00000170775	GPR37	0.1659	0.4912
3	ENSG00000130592	LSP1	0.1076	0.4910
3	ENSG00000251442	LINC01094	0.1477	0.4909
3	ENSG00000110079	MS4A4A	0.2060	0.4905
3	ENSG00000232474	NCKAP5-IT1	0.0993	0.4901
3	ENSG00000254081	LINC01299	0.2365	0.4899
3	ENSG00000152766	ANKRD22	0.1144	0.4899
3	ENSG00000221887	HMSD	0.1194	0.4898
3	ENSG00000277117	LOC102723996	0.0830	0.4898
3	ENSG00000237082	COX5BP6	0.1287	0.4893
3	ENSG00000025708	TYMP	0.1410	0.4891

3	ENSG00000012779	ALOX5	0.1019	0.4890
3	ENSG00000275713	H2BC9	0.1015	0.4889
3	ENSG00000122367	LDB3	0.1561	0.4886
3	ENSG00000165131	LLCFC1	0.0803	0.4877
3	ENSG00000285269	SLC35D2-HSD17B3 readthrough	0.0822	0.4877
3	ENSG00000227088	Lnc-LRRTM4-1	0.1546	0.4877
3	ENSG00000252312	RN7SKP21	0.0857	0.4874
3	ENSG00000179420	OR6W1P	0.1194	0.4869
3	ENSG00000258948	KRT8P1	0.0795	0.4866
3	ENSG00000198774	RASSF9	0.1114	0.4862
3	ENSG00000288533	Antisense to TYMS and CLUL1	0.1653	0.4860
3	ENSG00000127324	TSPAN8	0.0709	0.4858
3	ENSG00000254863	LINC02744	0.1007	0.4851
3	ENSG00000279223	None	0.0911	0.4846
3	ENSG00000285712	None	0.1039	0.4836
3	ENSG00000128652	HOXD3	0.0765	0.4825
3	ENSG00000231171	LINC01098	0.1112	0.4816
3	ENSG00000229140	CCDC26	0.0901	0.4812
3	ENSG00000155926	SLA	0.1026	0.4811
3	ENSG00000133048	CHI3L1	0.1678	0.4809
3	ENSG00000164342	TLR3	0.0717	0.4808
3	ENSG00000273259	Thioesterase	0.1471	0.4808
3	ENSG00000286569	None	0.0794	0.4806
3	ENSG00000157227	MMP14	0.2251	0.4805
3	ENSG00000257720	ILF2P2	0.1511	0.4801
3	ENSG00000100368	CSF2RB	0.1802	0.4799
3	ENSG00000174837	ADGRE1	0.0964	0.4799
3	ENSG00000259764	PCSK6-AS1	0.1262	0.4791
3	ENSG00000244738	Lnc-CLDN11-2	0.0942	0.4785
3	ENSG00000160223	ICOSLG	0.0727	0.4773
3	ENSG00000115523	GNLY	0.0901	0.4770
3	ENSG00000244731	C4A	0.1582	0.4768
3	ENSG00000118640	VAMP8	0.1102	0.4767
3	ENSG00000105281	SLC1A5	0.1965	0.4765
3	ENSG00000066336	SPI1	0.1143	0.4761
3	ENSG00000248529	LOC101928651	0.1135	0.4756
3	ENSG00000166928	MS4A14	0.1456	0.4753
3	ENSG00000166473	PKD1L2	0.0930	0.4750
3	ENSG00000163563	MNDA	0.1076	0.4747
3	ENSG00000010327	STAB1	0.2132	0.4740
3	ENSG00000277775	H3C7	0.0732	0.4734
3	ENSG00000187554	TLR5	0.0922	0.4718
3	ENSG00000232504	ST3GAL5-AS1	0.1183	0.4707
3	ENSG00000132702	HAPLN2	0.1061	0.4696
3	ENSG00000129465	RIPK3	0.0762	0.4676
3	ENSG00000287538	None	0.1149	0.4666
3	ENSG00000153551	CMTM7	0.0872	0.4662
3	ENSG00000205403	CFI	0.1287	0.4656
3	ENSG00000207736	MIR657	0.0843	0.4652
3	ENSG00000137752	CASP1	0.1240	0.4649
3	ENSG00000128340	RAC2	0.0997	0.4643
3	ENSG00000287736	PTCSC1	0.0953	0.4643
3	ENSG00000145287	PLAC8	0.1238	0.4637
3	ENSG00000263154	Lnc-BAHCC1-1	0.0776	0.4619
3	ENSG00000203710	CR1	0.0840	0.4616
3	ENSG00000198835	GJC2	0.0819	0.4607
3	ENSG00000258227	CLEC5A	0.0896	0.4606
3	ENSG00000090382	LYZ	0.1161	0.4600

3	ENSG00000260922	Antisense to ADAMTS18	0.0977	0.4583
3	ENSG00000285885	Antisense to MOBP	0.0999	0.4581
3	ENSG00000214688	C10orf105	0.0833	0.4551
3	ENSG00000286048	Antisense to ITGA2	0.0949	0.4543
3	ENSG00000229494	LOC101927948	0.1134	0.4542
3	ENSG00000197747	S100A10	0.1026	0.4542
3	ENSG00000136235	GPNMB	0.0836	0.4536
3	ENSG00000267287	Lnc-NFATC1-1	0.0916	0.4532
3	ENSG00000185905	C16orf54	0.0831	0.4531
3	ENSG00000257183	Lnc-KCNC2-2	0.1148	0.4526
3	ENSG00000152804	HHEX	0.0788	0.4524
3	ENSG00000129810	SGO1	0.0700	0.4517
3	ENSG00000132854	KANK4	0.0883	0.4501
3	ENSG00000286541	None	0.0795	0.4495
3	ENSG00000283431	Novel Zinc Finger Protein Pseudogene	0.0805	0.4477
3	ENSG00000117228	GBP1	0.0698	0.4451
3	ENSG00000122585	NPY	0.0969	0.4421
3	ENSG00000101670	LIPG	0.0778	0.4418
3	ENSG00000224397	PELATON	0.0792	0.4413
3	ENSG00000261710	Lnc-ADGRB1-3	0.0753	0.4369
3	ENSG00000141526	SLC16A3	0.0949	0.4368
3	ENSG00000128262	POM121L9P	0.0709	0.4355
3	ENSG00000283787	PRR33	0.0741	0.4291

Table A31. Genetic Composition of KCL BrainBank case-derived clusters. Feature score refers to the basis components which contribute the most to the samples mapped to each cluster, whilst probability refers to the probability that the gene belongs to that cluster, where the baseline probability is 0.3333.

Source	Term Name	Term ID	Term Size	p adjusted	Intersection Size
GO:MF	neuropeptide hormone activity	GO:0005184	22	9.90E-06	5
GO:MF	hormone activity	GO:0005179	78	1.10E-05	7
GO:BP	chemical synaptic transmission	GO:0007268	663	4.00E-04	14
GO:BP	anterograde trans-synaptic signaling	GO:0098916	663	4.00E-04	14
GO:BP	trans-synaptic signaling	GO:0099537	671	4.60E-04	14
REAC	MECP2 regulates transcription of neuronal ligands	REAC:R-HSA-9022702	7	6.30E-04	3
GO:BP	synaptic signaling	GO:0099536	694	6.90E-04	14
GO:BP	regulation of epinephrine secretion	GO:0014060	7	3.60E-03	3
GO:BP	epinephrine secretion	GO:0048242	8	5.70E-03	3
KEGG	cAMP signaling pathway	KEGG:04024	203	8.00E-03	6
KEGG	neuroactive ligand-receptor interaction	KEGG:04080	301	9.60E-03	7
GO:BP	epinephrine transport	GO:0048241	11	1.70E-02	3
GO:BP	mating	GO:0007618	35	1.80E-02	4
GO:CC	neuronal cell body	GO:0043025	471	2.10E-02	9
REAC	Transcriptional Regulation by MECP2	REAC:R-HSA-8986944	58	2.40E-02	4
GO:BP	positive regulation of epinephrine secretion	GO:0032812	2	2.80E-02	2
GO:MF	receptor ligand activity	GO:0048018	356	3.50E-02	8
TF	NRSF TTCAGCACCACGGACAGMGCC	TF:M00256_1	13	3.70E-02	3
REAC	GPCR ligand binding	REAC:R-HSA-500792	388	3.90E-02	8
GO:MF	signaling receptor activator activity	GO:0030546	363	4.10E-02	8
GO:BP	neuropeptide signaling pathway	GO:0007218	89	4.40E-02	5

Table A32. KCL BrainBank enrichment for Cluster 1 with gProfiler2. Term size refers to the number of genes in the term, with the intersection size denoting the number of genes in the dataset found in the term. GO:BP – Gene Ontology Biological Process, GO:CC – Gene Ontology Cellular Components, GO:MF – Gene Ontology Molecular Function, KEGG: Kyoto Encyclopaedia of Genes and Genomes, REAC: Reactome, TF: Transfac.

Source	Term Name	Term ID	Term Size	p adjusted	Intersection Size
GO:CC	cell periphery	GO:0071944	5188	1.70E-39	140
GO:BP	response to stimulus	GO:0050896	7482	7.30E-37	165
GO:CC	extracellular region	GO:0005576	3516	7.40E-34	109
GO:BP	biological regulation	GO:0065007	10837	1.60E-33	194
TF	Factor: Kid3; motif: CCACN	TF:M01160	17056	3.70E-31	241
TF	Factor: Spi-B; motif: TTCYBC	TF:M03851	17110	6.80E-31	241
TF	Transfac	TF:M00000	17114	7.10E-31	241
GO:BP	response to chemical	GO:0042221	3698	2.30E-30	108
TF	Factor: Spi-B; motif: TTCYBC; match class: 1	TF:M03851_1	17095	2.90E-30	240
GO:BP	cellular response to chemical stimulus	GO:0070887	2745	4.70E-30	93
GO:CC	extracellular space	GO:0005615	2749	4.70E-30	92
TF	Factor: CPBP; motif: SNCCCNN	TF:M01822	16885	6.80E-30	238
TF	Factor: Kid3; motif: CCACN; match class: 1	TF:M01160_1	16941	1.30E-29	238
TF	Factor: PU.1; motif: AGGAAG	TF:M02031	15486	2.10E-29	227
TF	Factor: Elf-1; motif: AGGAAG	TF:M01266	15486	2.10E-29	227
GO:BP	regulation of biological process	GO:0050789	10213	5.60E-29	181
TF	Factor: ZNF35; motif: SSAAKA	TF:M07479	16059	1.50E-28	230
GO:MF	molecular_function	GO:0003674	16562	5.10E-28	232
TF	Factor: GKLF; motif: CCTCCYN	TF:M01835	13756	6.60E-28	211
GO:CC	cellular anatomical entity	GO:0110165	16869	1.30E-27	233
GO:BP	biological_process	GO:0008150	16323	1.80E-27	230
GO:CC	cellular_component	GO:0005575	16974	4.00E-27	233
GO:BP	response to stress	GO:0006950	3345	6.10E-27	98
GO:BP	response to organic substance	GO:0010033	2758	6.40E-27	89
GO:BP	cellular response to stimulus	GO:0051716	6392	5.00E-26	136
GO:MF	binding	GO:0005488	15390	5.10E-26	220
GO:BP	multicellular organismal process	GO:0032501	6431	9.30E-26	136
GO:BP	tissue development	GO:0009888	1688	1.10E-25	69
TF	Factor: CPBP; motif: SNCCCNN; match class: 1	TF:M01822_1	16464	2.50E-25	228
TF	Factor: ZNF684; motif: MAAGGGGTGGACTGT	TF:M10550	13426	2.50E-25	204
GO:MF	protein binding	GO:0005515	13368	4.80E-25	202
GO:CC	plasma membrane	GO:0005886	4761	7.20E-25	113
TF	Factor: Lyl-1; motif: NCAKCTGYTNYCNN	TF:M09977	11924	9.50E-25	190
TF	Factor: HSF4; motif: CTGCMRN	TF:M07322	14568	1.60E-24	212
GO:BP	cellular response to organic substance	GO:0071310	2188	3.30E-24	76
TF	Factor: TR4; motif: ACCCCGS	TF:M04934	15997	8.10E-24	222
MIRNA	MIRNA root	MIRNA:000000	13878	8.10E-24	204
GO:BP	cellular process	GO:0009987	15441	1.30E-23	217
TF	Factor: Smad2; motif: AGACAN	TF:M03580	13070	1.30E-23	198
TF	Factor: Elf-1; motif: AGGAAG; match class: 1	TF:M01266_1	11933	1.40E-23	188
TF	Factor: PU.1; motif: AGGAAG; match class: 1	TF:M02031_1	11933	1.40E-23	188
TF	Factor: Pax-4; motif: DTTTTCCACCN	TF:M04624	13570	1.80E-23	202
GO:BP	regulation of cellular process	GO:0050794	9657	2.30E-23	166
TF	Factor: Pax-4; motif: NNNNNYCACCCB	TF:M00378	15748	3.60E-23	219
GO:BP	anatomical structure development	GO:0048856	5153	6.80E-23	116
TF	Factor: GKLF; motif: NNRRGRRNGNSNNN	TF:M07040	11567	1.30E-22	183
GO:BP	animal organ development	GO:0048513	3102	1.50E-22	88
TF	Factor: THAP1; motif: YTGCCCNNA	TF:M07407	9580	1.80E-22	164
TF	Factor: myogenin; motif: CAGCTG	TF:M02101	11284	2.20E-22	180
TF	Factor: myogenin; motif: CAGCTG; match class: 1	TF:M02101_1	11284	2.20E-22	180
TF	Factor: Sox-18; motif: CAAWGBB	TF:M03848	15043	2.50E-22	212

TF	Factor: Sox-17; motif: TTGTYY	TF:M03803	13366	3.30E-22	198
GO:BP	positive regulation of biological process	GO:0048518	5512	4.40E-22	119
TF	Factor: ER71:E2A; motif: CASSTGNACCGGAWRYN	TF:M08568	15994	4.40E-22	219
GO:BP	circulatory system development	GO:0072359	1015	5.20E-22	51
GO:BP	signaling	GO:0023052	5550	8.00E-22	119
GO:BP	developmental process	GO:0032502	5648	1.00E-21	120
TF	Factor: ZBTB39; motif: CNCTGY	TF:M12689	13477	1.10E-21	198
GO:BP	cell communication	GO:0007154	5601	6.70E-21	118
TF	Factor: Zbtb44; motif: CKGTGA	TF:M05405	11777	1.60E-20	181
GO:BP	signal transduction	GO:0007165	5094	2.20E-20	111
GO:CC	vesicle	GO:0031982	3591	3.20E-20	90
TF	Factor: Erg; motif: NRRSAGGAAGNGG	TF:M09907	10225	3.30E-20	166
GO:BP	system development	GO:0048731	4335	4.10E-20	101
TF	Factor: T3R-beta; motif: NTGACCTYRNYRAGGTCAN	TF:M11818	10182	6.60E-20	165
GO:CC	external encapsulating structure	GO:0030312	498	1.10E-19	35
GO:BP	multicellular organism development	GO:0007275	4634	1.20E-19	104
GO:BP	regulation of multicellular organismal process	GO:0051239	2403	1.40E-19	73
TF	Factor: sin3A; motif: TGTCCNNGGTGCTG	TF:M04756	12573	1.80E-19	186
TF	Factor: ING4; motif: CCACCA	TF:M01743	13898	2.80E-19	197
TF	Factor: CTF/NF1; motif: TTGGCN	TF:M02050	9395	3.30E-19	156
GO:BP	anatomical structure morphogenesis	GO:0009653	2447	3.90E-19	73
GO:BP	cell adhesion	GO:0007155	1388	4.60E-19	55
GO:CC	collagen-containing extracellular matrix	GO:0062023	383	4.70E-19	31
GO:BP	cell surface receptor signaling pathway	GO:0007166	2456	4.80E-19	73
GO:BP	negative regulation of biological process	GO:0048519	4967	5.30E-19	107
GO:BP	biological adhesion	GO:0022610	1393	5.40E-19	55
TF	Factor: Zic3; motif: NGGGKGGTC	TF:M00450	12380	8.40E-19	183
GO:CC	extracellular matrix	GO:0031012	497	1.00E-18	34
REAC	REACTOME root term	REAC:0000000	9607	1.60E-18	155
GO:BP	anatomical structure formation involved in morphogenesis	GO:0048646	1026	2.20E-18	47
TF	Factor: T3R-beta; motif: NTGACCTYRNYRAGGTCAN; match class: 1	TF:M11818_1	9678	2.60E-18	157
TF	Factor: GEMIN3; motif: NCWGGRARRGRGNGNG	TF:M09727	7710	2.90E-18	137
GO:BP	blood vessel development	GO:0001568	641	3.90E-18	38
GO:BP	immune system process	GO:0002376	2161	4.10E-18	67
TF	Factor: ZNF644; motif: TCCWGCCTCTSN	TF:M09737	6371	4.90E-18	122
TF	Factor: ZNF35; motif: SSAAKA; match class: 1	TF:M07479_1	13256	5.40E-18	189
TF	Factor: PUR1; motif: GGGNCAGNN	TF:M01721	8254	6.30E-18	142
TF	Factor: SALL2; motif: GGGTGGG	TF:M04595	11697	7.40E-18	175
TF	Factor: LF-A1; motif: GGGSTCWR	TF:M00646	11261	7.70E-18	171
GO:BP	positive regulation of cellular process	GO:0048522	5061	8.10E-18	106
TF	Factor: NF1C; motif: WGCCARR	TF:M09763	9428	1.50E-17	153
TF	Factor: ETV4; motif: NCAGGAAGNN	TF:M12556	9336	1.70E-17	152
GO:BP	vasculature development	GO:0001944	671	1.90E-17	38
TF	Factor: Pax-4; motif: NNNNNYCACCCB; match class: 1	TF:M00378_1	13163	2.10E-17	187
KEGG	KEGG root term	KEGG:00000	7044	2.30E-17	125
TF	Factor: ETF; motif: CCCCGCCCCYN	TF:M07039	14877	3.20E-17	201
TF	Factor: BEN; motif: CAGCGRNV	TF:M01240	15004	3.30E-17	202
TF	Factor: TR4; motif: ACCCCGS; match class: 1	TF:M04934_1	13946	4.40E-17	193
TF	Factor: Erg; motif: NACCGGATATCCGGTN	TF:M11393	12672	4.80E-17	182
TF	Factor: LRH-1; motif: TGACCTTGRNYCAAGGTCA	TF:M11830	6126	7.20E-17	117
TF	Factor: GKLF; motif: NNNRGGNGNGGSN	TF:M07289	13294	7.40E-17	187
TF	Factor: E2F-1:HES-7; motif: GGCRCGTGSYNNWNGGCGCSM	TF:M08525	15473	7.90E-17	205

TF	Factor: CSX; motif: NKRAGWGS	TF:M10008	9182	9.00E-17	149
GO:BP	animal organ morphogenesis	GO:0009887	931	1.00E-16	43
TF	Factor: RREB-1; motif: CCCCAAACMMCCCC	TF:M00257	9419	1.30E-16	151
GO:BP	response to external stimulus	GO:0009605	2310	1.40E-16	67
TF	Factor: NMYC; motif: CAYCTG	TF:M01808	10951	2.50E-16	165
GO:BP	response to oxygen-containing compound	GO:1901700	1480	2.60E-16	53
TF	Factor: PEA3; motif: NNCAGGAARNN	TF:M09915	10849	2.60E-16	164
REAC	Immune System	REAC:R-HSA-168256	1770	2.80E-16	57
TF	Factor: p300; motif: ACNTCCG	TF:M04826	15885	3.30E-16	207
TF	Factor: FOXO1A:ETV7; motif: NWMAACAGGAMNNNCTTCCNN	TF:M08304	12194	3.40E-16	176
TF	Factor: RXRA; motif: RRGGTCATGACCYY	TF:M04490	6522	3.80E-16	120
TF	Factor: egr-3; motif: GTGGGY	TF:M03818	11653	4.00E-16	171
TF	Factor: IRF-4; motif: AAGTTTC	TF:M04855	6624	4.40E-16	121
TF	Factor: LUMAN; motif: CYCAGCYYCY	TF:M09729	9533	4.40E-16	151
TF	Factor: ZBTB39; motif: CNCTGY; match class: 1	TF:M12689_1	8347	5.40E-16	139
TF	Factor: E2F4; motif: YCCCGCCNCNNSSNNSNN	TF:M12599	15611	8.30E-16	204
TF	Factor: HSF4; motif: CTGCMRN; match class: 1	TF:M07322_1	10436	8.90E-16	159
TF	Factor: IRF-4; motif: RGGAASWGR	TF:M04818	8202	9.60E-16	137
TF	Factor: c-Ets-2; motif: CTTCCTG	TF:M01207	8932	1.40E-15	144
TF	Factor: Elk-1; motif: CTTCCKG	TF:M07252	8932	1.40E-15	144
GO:BP	regulation of developmental process	GO:0050793	2221	1.60E-15	64
TF	Factor: NFATc2; motif: GGAAAA	TF:M03555	13979	1.60E-15	190
TF	Factor: NFATc3; motif: GGAAAA	TF:M01886	13979	1.60E-15	190
TF	Factor: NFATc2; motif: GGAAAA	TF:M01281	13979	1.60E-15	190
TF	Factor: LRH-1; motif: TCAAGGTCRYGACCTTGR	TF:M11828	9272	2.10E-15	147
GO:BP	regulation of cell death	GO:0010941	1440	2.30E-15	51
TF	Factor: Sox-10; motif: CWTTGT	TF:M03138	11286	2.30E-15	166
TF	Factor: TCF-1; motif: CTTTGW	TF:M03857	11286	2.30E-15	166
TF	Factor: GKLF; motif: CCTCCYN; match class: 1	TF:M01835_1	9081	2.40E-15	145
TF	Factor: Smad2; motif: AGACAN; match class: 1	TF:M03580_1	7607	2.40E-15	130
TF	Factor: GATAD2A; motif: CCTKTG	TF:M09726	13089	2.50E-15	182
TF	Factor: Pax-5; motif: RRNGRNGCAN	TF:M03577	7727	3.20E-15	131
TF	Factor: ZXDA; motif: NAGGGTG	TF:M06203	6420	3.20E-15	117
TF	Factor: ZXDB; motif: NAGGGTG	TF:M06202	6420	3.20E-15	117
TF	Factor: ZNF273; motif: GAGAGGAGCTAC	TF:M10460	11221	3.60E-15	165
TF	Factor: Kaiso; motif: GCMGGGRGCRGS	TF:M03876	12564	3.80E-15	177
TF	Factor: NF1B; motif: CYTGGCNYNCWGCCAN	TF:M09762	4967	4.90E-15	100
TF	Factor: GR; motif: RGNACANKNTGTNCY	TF:M09625	7867	5.20E-15	132
TF	Factor: NR1B1; motif: NRGGNCRTGACCTN	TF:M11796	9466	5.50E-15	148
TF	Factor: ZNFPT1; motif: YCNNCNCWGCCNY	TF:M12721	8164	5.60E-15	135
TF	Factor: Elk-1; motif: GGAAGN	TF:M03819	12382	5.80E-15	175
TF	Factor: Erg; motif: NACCGGATATCCGGTN; match class: 1	TF:M11393_1	12292	7.10E-15	174
GO:CC	membrane	GO:0016020	8518	8.50E-15	136
GO:BP	cellular developmental process	GO:0048869	3759	1.10E-14	84
GO:CC	organelle	GO:0043226	13412	1.20E-14	181
TF	Factor: MAZ; motif: GGGMGGGGSSGGGGGGGGGGGG	TF:M09636	14816	1.30E-14	195
TF	Factor: LRH-1; motif: TGACCTTGRNYCAAGGTCA; match class: 1	TF:M11830_1	5296	1.40E-14	103
TF	Factor: CDP:SRF; motif: NCCWTAYAAGGTMNKRATCRATN	TF:M08520	8843	1.40E-14	141
TF	Factor: PRDM16; motif: KGGTCATRACCM	TF:M05946	6003	1.50E-14	111
TF	Factor: Sox-9; motif: NNNNNACAAARGNNSMN	TF:M07269	8565	1.70E-14	138
GO:BP	cell death	GO:0008219	1881	2.00E-14	57
TF	Factor: PARP; motif: TTTCYN	TF:M02027	14025	2.00E-14	188

GO:CC	extracellular exosome	GO:0070062	1901	2.20E-14	56
TF	Factor: AP-2gamma:Elk-1; motif: NGCCKNRGGSGRCGGAAGTG	TF:M08441	14756	2.20E-14	194
TF	Factor: FOXO1A:PDEF; motif: WNCCGGATGTTDN	TF:M08486	9927	2.50E-14	151
GO:BP	response to cytokine	GO:0034097	833	2.70E-14	38
GO:BP	inflammatory response	GO:0006954	651	2.70E-14	34
TF	Factor: LBP-1; motif: CAGCTGS	TF:M00644	7824	2.80E-14	130
GO:BP	cellular response to cytokine stimulus	GO:0071345	744	3.20E-14	36
GO:BP	positive regulation of metabolic process	GO:0009893	3369	3.50E-14	78
GO:CC	extracellular vesicle	GO:1903561	1921	3.50E-14	56
GO:CC	extracellular membrane-bounded organelle	GO:0065010	1922	3.50E-14	56
GO:CC	extracellular organelle	GO:0043230	1922	3.50E-14	56
GO:CC	cytoplasm	GO:0005737	11064	3.70E-14	159
GO:BP	cell differentiation	GO:0030154	3683	4.00E-14	82
TF	Factor: TFII-I; motif: NAGGAAGTGN	TF:M04636	11048	4.30E-14	161
GO:BP	negative regulation of cellular process	GO:0048523	4412	4.70E-14	91
TF	Factor: RORA; motif: CCYTGNCCTN	TF:M12659	6920	4.70E-14	120
TF	Factor: NF-1C; motif: NYTGGCNNYNNGCCARN	TF:M10002	5930	5.60E-14	109
GO:BP	response to endogenous stimulus	GO:0009719	1439	5.70E-14	49
GO:BP	localization	GO:0051179	5792	5.80E-14	107
TF	Factor: ZNF586; motif: CAGGCCYRGAGG	TF:M10491	12307	6.30E-14	172
TF	Factor: PURBETA; motif: NCWGRGGCTGGGG	TF:M12726	6869	7.70E-14	119
TF	Factor: Zic1; motif: KGGGTGGTC	TF:M00448	9729	7.70E-14	148
GO:BP	epithelium development	GO:0060429	1015	9.10E-14	41
GO:BP	cell activation	GO:0001775	914	9.20E-14	39
GO:BP	defense response	GO:0006952	1343	9.70E-14	47
TF	Factor: GTF2IRD1-isoform2; motif: GGGATTRNR	TF:M01229	13062	1.20E-13	178
TF	Factor: VDR; motif: RRGGTCANNGRGKTCA	TF:M09671	7096	1.20E-13	121
TF	Factor: NURR1:RXR-ALPHA; motif: NRGGTCRTTGACCYN	TF:M08957	9681	1.30E-13	147
TF	Factor: Ikaros; motif: TGGGAGN	TF:M07260	11832	1.40E-13	167
TF	Factor: T3R-beta; motif: NRGGTCAAAGGTCRN	TF:M11814	12177	1.50E-13	170
TF	Factor: MafB; motif: GNTGAC	TF:M01227	10227	1.60E-13	152
GO:BP	regulation of biological quality	GO:0065008	3465	1.70E-13	78
GO:BP	positive regulation of macromolecule metabolic process	GO:0010604	3089	1.70E-13	73
GO:BP	regulation of programmed cell death	GO:0043067	1308	1.80E-13	46
TF	Factor: MAFB; motif: NTCAGCN	TF:M08888	8591	1.80E-13	136
TF	Factor: MAZ; motif: GGGMGGGGSSGGGGGGGGGGGG; match class: 1	TF:M09636_1	13118	1.90E-13	178
GO:BP	tube morphogenesis	GO:0035239	788	2.00E-13	36
TF	Factor: Sox-18; motif: CAAWGBB; match class: 1	TF:M03848_1	10894	2.10E-13	158
TF	Factor: T3R-beta; motif: NRGGTCAAAGGTCAN	TF:M11816	10084	3.10E-13	150
TF	Factor: IRX-1; motif: NACRYNNNNNNNNRYGNN	TF:M11018	15325	3.30E-13	196
TF	Factor: E2F-3:TBR2; motif: ANGTGYKANGGCGCSTTNNCRNNT	TF:M08207	15326	3.30E-13	196
GO:BP	regulation of response to stimulus	GO:0048583	3512	3.60E-13	78
TF	Factor: PHB; motif: NCCCAGCCCCY	TF:M12725	8966	3.80E-13	139
TF	Factor: ZGPAT; motif: GRGGCWGNGGNG	TF:M09739	7490	4.00E-13	124
GO:BP	regulation of apoptotic process	GO:0042981	1281	4.20E-13	45
GO:CC	membrane-bounded organelle	GO:0043227	12679	4.20E-13	171
GO:BP	cellular response to oxygen-containing compound	GO:1901701	1062	4.30E-13	41
GO:BP	cell migration	GO:0016477	1339	4.30E-13	46
GO:CC	secretory granule	GO:0030141	760	4.40E-13	34
GO:BP	wound healing	GO:0042060	384	4.60E-13	26
TF	Factor: MEL1; motif: GATGAG	TF:M08793	10128	4.70E-13	150
TF	Factor: NKX2-2; motif: NNNCCACTCAANNN	TF:M12456	8199	5.30E-13	131

TF	Factor: HLTF; motif: AGSCARAAAGYRGSTGS	TF:M04613	6765	5.70E-13	116
TF	Factor: MZF-1; motif: TGGGGAR	TF:M01733	10043	5.70E-13	149
GO:BP	tube development	GO:0035295	967	6.00E-13	39
TF	Factor: REST; motif: AAGGTGCT	TF:M04926	5504	6.20E-13	102
GO:BP	response to wounding	GO:0009611	505	6.40E-13	29
TF	Factor: DREF; motif: CTYYCWCTTCCY	TF:M09725	6415	7.10E-13	112
GO:CC	intracellular anatomical structure	GO:0005622	14269	7.90E-13	184
GO:MF	extracellular matrix structural constituent	GO:0005201	156	8.10E-13	18
TF	Factor: Pax-5; motif: BCNNNRNGCANBGNTGNRTAGCSGCHNB	TF:M00143	10199	9.20E-13	150
TF	Factor: GR; motif: NNNNNNCNNTNTGTNCTNN	TF:M00192	6349	9.60E-13	111
TF	Factor: PAX5; motif: RNGCGTGACCNN	TF:M09817	11285	1.00E-12	160
TF	Factor: BRN1; motif: HAATGCN	TF:M03813	11080	1.10E-12	158
TF	Factor: TWIST; motif: CACCTGG	TF:M03582	7309	1.20E-12	121
TF	Factor: CP2; motif: NNNNCCAGNCNN	TF:M07602	9815	1.30E-12	146
GO:BP	blood vessel morphogenesis	GO:0048514	563	1.40E-12	30
TF	Factor: KLF; motif: GGGNGGGG	TF:M07461	7906	1.50E-12	127
TF	Factor: GABP-alpha; motif: AACCGGAAR	TF:M04748	14181	1.50E-12	185
GO:BP	positive regulation of response to stimulus	GO:0048584	1882	1.60E-12	54
TF	Factor: Fli-1; motif: NNRGGMAGGAAGGRRRGR	TF:M09920	8216	1.70E-12	130
TF	Factor: E2F-3:Prrxl1; motif: SGCGCTAATTNN	TF:M08206	10480	1.70E-12	152
GO:BP	extracellular matrix organization	GO:0030198	300	1.80E-12	23
GO:BP	extracellular structure organization	GO:0043062	301	1.90E-12	23
TF	Factor: ZNF684; motif: MAAGGGGTGGACTGT; match class: 1	TF:M10550_1	8324	1.90E-12	131
GO:BP	external encapsulating structure organization	GO:0045229	302	2.10E-12	23
TF	Factor: RUNX2; motif: NRACCGCAAACCGCAN	TF:M04106	12597	2.10E-12	171
TF	Factor: PEA3; motif: NNCAGGAARNN; match class: 1	TF:M09915_1	4914	2.30E-12	94
TF	Factor: MRF4; motif: CASCTGC	TF:M03831	7565	2.40E-12	123
TF	Factor: HTF4; motif: CASCTGB	TF:M02018	7565	2.40E-12	123
TF	Factor: TCF-7; motif: TCAAAG	TF:M00805	10201	2.50E-12	149
TF	Factor: TCF-3; motif: CTTTGA	TF:M03858	10201	2.50E-12	149
TF	Factor: AR; motif: ARGAACANNNTGTNC	TF:M07204	4006	2.60E-12	83
TF	Factor: ERG; motif: ACCGGAWATCCGGT	TF:M03976	11502	2.60E-12	161
TF	Factor: ZNF37A; motif: CCYYGGCTCCNTSCCMN	TF:M12354	10103	2.70E-12	148
TF	Factor: KLF15; motif: RCCMCRCCCMCN	TF:M12160	11726	2.70E-12	163
TF	Factor: ER71:E2A; motif: CASSTGNACCGGAWRYN; match class: 1	TF:M08568_1	13552	2.80E-12	179
TF	Factor: NF-KAPPAB1; motif: NGGKRNTTYCCCN	TF:M08952	7005	2.80E-12	117
TF	Factor: Erg; motif: MCAGGAAA	TF:M07284	9694	2.90E-12	144
TF	Factor: Pax-4; motif: DTTTTCCACCN; match class: 1	TF:M04624_1	8077	3.10E-12	128
TF	Factor: GEMIN3; motif: NCWGGRARRGRGNGNG; match class: 1	TF:M09727_1	2934	3.10E-12	69
TF	Factor: SMAD5; motif: GSGGCAGM	TF:M03846	7589	3.10E-12	123
GO:BP	positive regulation of developmental process	GO:0051094	1182	3.20E-12	42
TF	Factor: E2F-4; motif: SNGGGCGGGAANN	TF:M09894	14891	3.60E-12	190
TF	Factor: Erm; motif: NRRSAGGAARNGRN	TF:M09916	5923	3.90E-12	105
TF	Factor: T3R-beta; motif: NTGACCTNRNYNAGGTCAN	TF:M11820	4448	4.00E-12	88
TF	Factor: EHF; motif: BTTCCTGC	TF:M07251	5394	4.10E-12	99
GO:BP	programmed cell death	GO:0012501	1737	4.70E-12	51
TF	Factor: AP-2gamma; motif: GCCYNNGGS	TF:M00470	8826	5.00E-12	135
TF	Factor: Churchill; motif: CGGGNN	TF:M00986	13164	5.20E-12	175
TF	Factor: LUMAN; motif: CYCAGCYYCY; match class: 1	TF:M09729_1	4222	5.40E-12	85
TF	Factor: RelA-p65; motif: AAASTCCC	TF:M04849	5419	5.60E-12	99
TF	Factor: E2F-3:HES-7; motif: NNNSGCGCSNNNNNCRCGYGNN	TF:M08526	15314	5.70E-12	193

GO:CC	endomembrane system	GO:0012505	4326	6.60E-12	84
TF	Factor: Sox-17; motif: TTGTYY; match class: 1	TF:M03803_1	7955	6.60E-12	126
TF	Factor: ZNF300; motif: SWGGGGGSN	TF:M07486	11503	6.80E-12	160
TF	Factor: NF-E4; motif: GTGAGGS	TF:M08826	10022	8.70E-12	146
TF	Factor: GCMa:PEA3; motif: ATRCGGGCGGAAGTR	TF:M08313	13815	9.20E-12	180
GO:BP	cellular response to endogenous stimulus	GO:0071495	1220	9.40E-12	42
TF	Factor: ZNF777; motif: GTCCGYCCCGTCSAACAAT	TF:M08993	9617	9.80E-12	142
GO:BP	biological process involved in interspecies interaction between organisms	GO:0044419	1282	1.10E-11	43
GO:CC	intrinsic component of membrane	GO:0031224	5051	1.10E-11	92
TF	Factor: Lyl-1; motif: NCAKCTGYTNYCNN; match class: 1	TF:M09977_1	6570	1.10E-11	111
TF	Factor: ZNF436; motif: TCCTCCAGGAAGCCY	TF:M10477	12825	1.40E-11	171
TF	Factor: TCF-1; motif: ACATCGRGRCGCTGW	TF:M11603	14822	1.40E-11	188
TF	Factor: ZFP14; motif: SCNNYCCNGNNSCTSCNC	TF:M12694	9765	1.50E-11	143
TF	Factor: ZNF592; motif: NSARNATGGAGKN	TF:M09766	6223	1.50E-11	107
GO:BP	positive regulation of multicellular organismal process	GO:0051240	1298	1.60E-11	43
TF	Factor: HDAC1; motif: KGCARGGTC	TF:M07041	11165	1.60E-11	156
TF	Factor: c-Fos; motif: ACTCACCA	TF:M04802	6417	1.60E-11	109
GO:BP	negative regulation of multicellular organismal process	GO:0051241	913	1.80E-11	36
GO:BP	locomotion	GO:0040011	1669	1.80E-11	49
GO:BP	immune response	GO:0006955	1363	1.90E-11	44
TF	Factor: SRY; motif: TTGTTT	TF:M03854	12068	1.90E-11	164
TF	Factor: FOXO1A; motif: AAACAA	TF:M03823	12068	1.90E-11	164
TF	Factor: TORC2; motif: TGGGCTKKD	TF:M07341	4235	2.00E-11	84
TF	Factor: NR3C1; motif: NRGWACAYNRTGTWCYN	TF:M04476	6162	2.10E-11	106
GO:BP	heart development	GO:0007507	535	2.20E-11	28
TF	Factor: Kaiso; motif: TCTCGCGAG	TF:M04691	13571	2.20E-11	177
TF	Factor: Zic3; motif: NGGGKGGTC; match class: 1	TF:M00450_1	7106	2.20E-11	116
TF	Factor: AP-2rep; motif: CAGTGGG	TF:M00468	6084	2.40E-11	105
MIRNA	hsa-miR-335-5p	MIRNA:hsa-miR-335-5p	2271	2.50E-11	57
GO:BP	response to other organism	GO:0051707	1142	2.60E-11	40
GO:BP	response to external biotic stimulus	GO:0043207	1145	2.80E-11	40
TF	Factor: E2F-3; motif: NNTTTTGGCGCCAAAACT	TF:M03962	9734	2.80E-11	142
TF	Factor: VDR:RXR-ALPHA; motif: NRGGTCANNNGGTTCNN	TF:M08980	9219	2.90E-11	137
REAC	Neutrophil degranulation	REAC:R-HSA-6798695	446	3.00E-11	25
GO:BP	apoptotic process	GO:0006915	1692	3.10E-11	49
GO:BP	cell motility	GO:0048870	1504	3.10E-11	46
GO:BP	localization of cell	GO:0051674	1504	3.10E-11	46
TF	Factor: Fli-1:Max; motif: NCCGGAAACACGTGN	TF:M08289	8814	3.10E-11	133
TF	Factor: E2F2; motif: AAAATGGCGCCATTTT	TF:M04517	8014	3.10E-11	125
TF	Factor: Fli-1:FIGLA; motif: NCCGGAARCASSTGN	TF:M08284	6950	3.20E-11	114
TF	Factor: HDAC1; motif: KGCARGGTC; match class: 1	TF:M07041_1	5751	3.40E-11	101
TF	Factor: GKLF; motif: NNNRGGNGNGGSN; match class: 1	TF:M07289_1	9758	3.50E-11	142
TF	Factor: myogenin; motif: CRSCTGTTBNNTTTGGCACGSNGCCARCH	TF:M00056	9551	3.60E-11	140
TF	Factor: GATAD2A; motif: CCTKTG; match class: 1	TF:M09726_1	7641	3.80E-11	121
TF	Factor: ZNF462; motif: YYYYCTSCWG	TF:M12707	8440	4.10E-11	129
TF	Factor: ZF5; motif: GGSGCGCGS	TF:M10438	14973	4.50E-11	188
TF	Factor: Elk-1:PDEF; motif: NCMGGAMGGANATCCGGN	TF:M08227	7470	4.80E-11	119
GO:CC	integral component of membrane	GO:0016021	4917	5.00E-11	89
GO:BP	system process	GO:0003008	1781	5.20E-11	50
TF	Factor: GCMa; motif: RTGCGGGTN	TF:M11595	10870	5.30E-11	152
TF	Factor: Erg; motif: NRRSAGGAAGNGG; match class: 1	TF:M09907_1	4480	5.50E-11	86

TF	Factor: T3R-beta; motif: NTGACCTNRNYNAGGTCAN; match class: 1	TF:M11820_1	4065	5.70E-11	81
GO:BP	movement of cell or subcellular component	GO:0006928	1918	5.80E-11	52
GO:CC	intracellular organelle	GO:0043229	12728	6.00E-11	166
TF	Factor: AR; motif: RGGWACAYNGTGTWCYN	TF:M04453	6079	6.30E-11	104
TF	Factor: PUR1; motif: GGGNCAGNN; match class: 1	TF:M01721_1	3127	7.20E-11	69
GO:BP	angiogenesis	GO:0001525	477	7.80E-11	26
GO:BP	response to biotic stimulus	GO:0009607	1182	7.80E-11	40
TF	Factor: RELA; motif: GGGRMTKYCCC	TF:M12657	5734	7.80E-11	100
TF	Factor: PU.1; motif: WGAGGAAG	TF:M00658	3851	8.70E-11	78
REAC	Extracellular matrix organization	REAC:R-HSA-1474244	276	9.10E-11	20
TF	Factor: ZXDL; motif: NGGGGWS	TF:M05775	6205	9.10E-11	105
GO:CC	secretory vesicle	GO:0099503	920	1.00E-10	34
GO:BP	cell population proliferation	GO:0008283	1750	1.10E-10	49
TF	Factor: MLLT10; motif: CYNNCCNNGGNGCTG	TF:M12636	8543	1.10E-10	129
TF	Factor: HOXA3; motif: NNNNRNTAATTARY	TF:M01337	13550	1.10E-10	175
REAC	Innate Immune System	REAC:R-HSA-168249	914	1.20E-10	34
TF	Factor: Sox-10; motif: NACAAWG	TF:M02116	12073	1.20E-10	162
TF	Factor: SRY; motif: AACAATNR	TF:M08976	11740	1.20E-10	159
TF	Factor: HNRPUL1; motif: NCNCAGN	TF:M09746	12084	1.30E-10	162
TF	Factor: GATA-5; motif: TATCTN	TF:M02006	7582	1.50E-10	119
TF	Factor: GCMa:FOXO1A; motif: GTMAATAMGGGTRN	TF:M08318	10029	1.50E-10	143
GO:CC	integral component of plasma membrane	GO:0005887	1466	1.60E-10	43
TF	Factor: NR3C1; motif: NRGWACAYNRTGTWCYN; match class: 1	TF:M04476_1	4480	1.60E-10	85
TF	Factor: ING4; motif: CCACCA; match class: 1	TF:M01743_1	8903	1.80E-10	132
TF	Factor: Elk-1:OC-2; motif: RCCGGAASCGATCGATNN	TF:M08223	11348	1.80E-10	155
TF	Factor: SREBP-1; motif: CACSCCA	TF:M00749	7520	2.00E-10	118
GO:BP	regulation of multicellular organismal development	GO:2000026	1218	2.10E-10	40
GO:BP	negative regulation of cell death	GO:0060548	884	2.10E-10	34
GO:CC	intrinsic component of plasma membrane	GO:0031226	1541	2.10E-10	44
TF	Factor: Pet-1; motif: GCNGGAAGYG	TF:M09918	12251	2.10E-10	163
TF	Factor: TF3C-beta; motif: CCNGGAGGGCTTCCTGGAGGAG	TF:M04863	12366	2.10E-10	164
TF	Factor: Sox-10; motif: CWTTGTN	TF:M01131	7621	2.10E-10	119
GO:BP	negative regulation of apoptotic process	GO:0043066	783	2.30E-10	32
TF	Factor: ZNF614; motif: NCYCWGCCYYNNN	TF:M09862	8627	2.30E-10	129
TF	Factor: ZF5; motif: GSGCGCGR	TF:M00716	14856	2.90E-10	185
TF	Factor: YB-1; motif: CCAMTCNGMR	TF:M03805	8857	2.90E-10	131
TF	Factor: NF-kappaB; motif: NGGGACTTTCCA	TF:M00208	3300	3.00E-10	70
TF	Factor: AP-4; motif: RNCAGCTGC	TF:M00927	5587	3.10E-10	97
GO:BP	regulation of metabolic process	GO:0019222	6103	3.70E-10	102
GO:BP	epithelial cell differentiation	GO:0030855	555	3.70E-10	27
GO:BP	negative regulation of programmed cell death	GO:0043069	799	4.00E-10	32
TF	Factor: sin3A; motif: TGTCCNNGGTGCTG; match class: 1	TF:M04756_1	6912	4.00E-10	111
TF	Factor: CTF1; motif: TGGCASCNNGCCAA	TF:M01196	4131	4.10E-10	80
TF	Factor: ESE-1; motif: NTGTGCGGATGCN	TF:M11385	10801	4.40E-10	149
TF	Factor: NF-1B; motif: CTGGCASGV	TF:M07051	3030	5.60E-10	66
TF	Factor: E2F-3; motif: NTTTTGGCGCCAAAAN	TF:M11526	6287	5.80E-10	104
TF	Factor: ZNF333; motif: ATAAT	TF:M01230	13185	5.90E-10	170
TF	Factor: RXR-alpha; motif: NNGNNRNNNARAGGTCANNG	TF:M10055	5021	6.00E-10	90
TF	Factor: AP-4:Fli-1; motif: RSCGGAWRCAGSTGN	TF:M08445	8339	6.60E-10	125
TF	Factor: CP2; motif: GCHCDAMCCAG	TF:M00072	7846	7.00E-10	120
REAC	Integrin cell surface interactions	REAC:R-HSA-216083	77	7.40E-10	12

TF	Factor: PR; motif: NNNNNNGGNACRNNNTGTTCTNNNNNN	TF:M00954	4519	7.50E-10	84
TF	Factor: LKLF; motif: GGGGTGGKSN	TF:M07261	8865	7.70E-10	130
TF	Factor: MAZ; motif: GGGGAGGG	TF:M00649	8569	8.40E-10	127
GO:BP	cell-cell adhesion	GO:0098609	828	1.00E-09	32
GO:BP	tissue morphogenesis	GO:0048729	581	1.10E-09	27
TF	Factor: nerf; motif: YRNCAGGAAGYRGSTBDS	TF:M00531	6635	1.10E-09	107
GO:MF	signaling receptor binding	GO:0005102	1265	1.20E-09	39
GO:BP	collagen fibril organization	GO:0030199	71	1.20E-09	12
TF	Factor: c-Maf; motif: NWNNNTGCTGACKNNNNNN	TF:M01070	5525	1.20E-09	95
TF	Factor: NFE2L1; motif: NNNATGACTCAGCANW	TF:M12499	8308	1.20E-09	124
TF	Factor: TEF-1; motif: GRRATG	TF:M00704	10603	1.20E-09	146
TF	Factor: SALL2; motif: GGGTGGG; match class: 1	TF:M04595_1	6741	1.30E-09	108
TF	Factor: IRF-7; motif: AAGWGAA	TF:M01884	9133	1.30E-09	132
TF	Factor: AP-2gamma; motif: NTGSCCTGRGGSNN	TF:M09591	7528	1.40E-09	116
GO:BP	response to lipid	GO:0033993	787	1.50E-09	31
TF	Factor: CSX; motif: NKRAGWGS; match class: 1	TF:M10008_1	3652	1.50E-09	73
TF	Factor: E2F3; motif: NNRGMKGGAR	TF:M12598	11508	1.60E-09	154
TF	Factor: ZNF342; motif: TRSTGGACRNT	TF:M12075	5465	1.60E-09	94
TF	Factor: LRF; motif: RCGACCACCNN	TF:M12230	7744	1.70E-09	118
GO:CC	cytoplasmic vesicle	GO:0031410	2275	1.80E-09	53
TF	Factor: SMAD4; motif: GKSRKKCAGMCANCY	TF:M00733	7655	1.80E-09	117
GO:CC	intracellular vesicle	GO:0097708	2277	1.90E-09	53
TF	Factor: HNF-4alpha; motif: AGTCCAAR	TF:M04903	5939	1.90E-09	99
GO:BP	leukocyte activation	GO:0045321	795	2.00E-09	31
GO:BP	response to bacterium	GO:0009617	504	2.00E-09	25
TF	Factor: GLI; motif: NGACCMCCCAN	TF:M07290	6316	2.00E-09	103
TF	Factor: GKLF; motif: NNRRGRRNGNSNNN; match class: 1	TF:M07040_1	7566	2.00E-09	116
TF	Factor: AP-4:Max; motif: NCAGCTGNNNNNNNCACGTGN	TF:M08674	10025	2.10E-09	140
TF	Factor: GCMa:Erg; motif: ATGCGGGCGGAARKG	TF:M08487	12781	2.10E-09	165
GO:BP	regulation of macromolecule metabolic process	GO:0060255	5629	2.20E-09	95
TF	Factor: FXR:RXR-ALPHA; motif: NAGKTCATTGACCYN	TF:M08954	5497	2.30E-09	94
TF	Factor: NMYC; motif: CAYCTG; match class: 1	TF:M01808_1	5049	2.30E-09	89
TF	Factor: LRF; motif: GGGGKYNNB	TF:M01100	6997	2.30E-09	110
TF	Factor: FOXO1A:Elk-1; motif: RWMAACAGGAAGTN	TF:M08299	6145	2.40E-09	101
TF	Factor: C-Jun; motif: TGACTC	TF:M03541	9625	2.50E-09	136
GO:BP	negative regulation of developmental process	GO:0051093	804	2.60E-09	31
TF	Factor: Zbtb44; motif: CKGTGA; match class: 1	TF:M05405_1	5881	2.70E-09	98
TF	Factor: E2F-2; motif: GCGCGCGCNCS	TF:M11529	14928	2.80E-09	183
TF	Factor: E2F-3; motif: NTTTTGGCGCCAAAAN; match class: 1	TF:M11526_1	5975	2.80E-09	99
TF	Factor: LRF; motif: NCGACCACCGN	TF:M12231	10281	2.90E-09	142
TF	Factor: E2F-3; motif: NNTTTTGGCGCCAAAACT; match class: 1	TF:M03962_1	5799	3.00E-09	97
TF	Factor: PPARgamma:RXRalpha, motif: AAGTAGGTCACNGTGACCYACTT	TF:M00515	6738	3.10E-09	107
TF	Factor: SMAD3; motif: CAGACAS	TF:M07429	5352	3.30E-09	92
GO:BP	positive regulation of signal transduction	GO:0009967	1394	3.40E-09	41
TF	Factor: TFII-I; motif: RGAGGKAGG	TF:M00706	5174	3.40E-09	90
TF	Factor: p300; motif: NNNGGGAGTNNNNS	TF:M00033	7624	3.40E-09	116
TF	Factor: AP-2alpha; motif: NNNGSCCTGRGGSN	TF:M04896	5266	3.50E-09	91
GO:BP	cytokine-mediated signaling pathway	GO:0019221	430	3.60E-09	23
GO:BP	regulation of cell communication	GO:0010646	3111	3.60E-09	65
TF	Factor: RelA-p65; motif: BCWGGGRANNK	TF:M04811	6469	3.60E-09	104
TF	Factor: ER-beta; motif: RGGTCASCNTGMCCY	TF:M09910	8635	3.70E-09	126
TF	Factor: BTEB3; motif: BNRNGGGAGGNGT	TF:M01865	9056	4.00E-09	130

TF	Factor: p54NRB; motif: GRNNNMGGATGRMNNCGGA	TF:M07611	6106	4.10E-09	100
TF	Factor: SATB1; motif: NTTTAT	TF:M03564	13565	4.20E-09	171
TF	Factor: c-Ets-2; motif: NACCGGAAGYRCTTCCGGTN	TF:M11417	12989	4.20E-09	166
GO:BP	regulation of signaling	GO:0023051	3125	4.40E-09	65
TF	Factor: GR; motif: RGNACANMNTGTNCY	TF:M09941	4931	4.40E-09	87
TF	Factor: KLF4; motif: NNCCCCACCCNN	TF:M12489	5471	4.50E-09	93
TF	Factor: GLI4; motif: RGGCCTTGAATGCCANGCYMA	TF:M10514	11095	4.60E-09	149
TF	Factor: SP2; motif: NNRRCCAATSRGNRNSNGSN	TF:M12668	10569	5.30E-09	144
TF	Factor: Sox-4; motif: AACAAA	TF:M03849	12223	5.30E-09	159
TF	Factor: VDR; motif: GGGKNARNRRGGWSA	TF:M00444	9297	5.30E-09	132
GO:BP	regulation of signal transduction	GO:0009966	2751	5.50E-09	60
TF	Factor: TBX2; motif: NNNGTGTSNN	TF:M12026	6418	5.50E-09	103
GO:BP	regulation of cell population proliferation	GO:0042127	1482	5.80E-09	42
TF	Factor: TFAP2A; motif: NGCCCYNNGGGCN	TF:M04148	9313	6.00E-09	132
TF	Factor: Fli-1; motif: NACCGGAWWTCCGGTY	TF:M11399	11690	6.40E-09	154
TF	Factor: ZNF586; motif: CAGGCCYRGAGG; match class: 1	TF:M10491_1	6912	6.50E-09	108
GO:CC	intracellular membrane-bounded organelle	GO:0043231	11785	6.60E-09	152
TF	Factor: NFATc3; motif: GGAAAA; match class: 1	TF:M01886_1	9439	7.20E-09	133
TF	Factor: NFATc2; motif: GGAAAA; match class: 1	TF:M03555_1	9439	7.20E-09	133
TF	Factor: NFATc2; motif: GGAAAA; match class: 1	TF:M01281_1	9439	7.20E-09	133
TF	Factor: NR1B2; motif: NTGACCY	TF:M02111	8513	7.40E-09	124
TF	Factor: ZF5; motif: NRNGNGCGCGCWN	TF:M00333	13999	7.60E-09	174
TF	Factor: VDR, motif: RRTGNMCYTNNTGAMCCNYNT	TF:M00966	8419	7.90E-09	123
TF	Factor: AP-2gamma; motif: GCCYNCRGSN	TF:M03811	8219	8.00E-09	121
GO:BP	regulation of gene expression	GO:0010468	4415	8.20E-09	80
TF	Factor: ESE-1; motif: SATKGCGGATGCN	TF:M11381	13896	8.40E-09	173
TF	Factor: RORbeta; motif: TGACCYA	TF:M01722	5168	8.40E-09	89
TF	Factor: ETF; motif: CCCCGCCCCYN; match class: 1	TF:M07039_1	12626	8.40E-09	162
GO:BP	circulatory system process	GO:0003013	539	8.50E-09	25
GO:BP	homeostatic process	GO:0042592	1631	8.60E-09	44
GO:BP	positive regulation of cell communication	GO:0010647	1569	9.30E-09	43
GO:BP	positive regulation of signaling	GO:0023056	1573	1.00E-08	43
TF	Factor: CRX; motif: YTAATC	TF:M01712	9480	1.00E-08	133
TF	Factor: E2F-3:TBR2; motif: ANGTGYKANGGCGCSTTNNCRNNT; match class: 1	TF:M08207_1	14160	1.00E-08	175
GO:BP	response to molecule of bacterial origin	GO:0002237	292	1.10E-08	19
TF	Factor: PPARalpha:RXRalpha; motif: NNRGGTCATWGGGGTSANG	TF:M00518	8354	1.10E-08	122
TF	Factor: ETV4; motif: NCAGGAAGNN; match class: 1	TF:M12556_1	3399	1.10E-08	68
REAC	Interleukin-4 and Interleukin-13 signaling	REAC:R-HSA-6785807	97	1.20E-08	12
TF	Factor: CP2/LBP-1c/LSF; motif: GCTGGNTNGNNCYNG	TF:M00947	7463	1.20E-08	113
TF	Factor: Erg; motif: NACCGGATATCCGGTN	TF:M11397	10892	1.20E-08	146
TF	Factor: GATA-3; motif: AGATAA	TF:M01878	8472	1.20E-08	123
TF	Factor: ZNF273; motif: GAGAGGAGCTAC; match class: 1	TF:M10460_1	5118	1.30E-08	88
TF	Factor: HOXA13; motif: ATAAMA	TF:M01292	11353	1.40E-08	150
TF	Factor: ZFP14; motif: SCNNYCCNGNNSCTSCNC; match class: 1	TF:M12694_1	4775	1.50E-08	84
TF	Factor: Elk-1; motif: GGAAGN; match class: 1	TF:M03819_1	6527	1.60E-08	103
TF	Factor: BEN; motif: CAGCGRNV; match class: 1	TF:M01240_1	12381	1.70E-08	159
GO:BP	regulation of immune system process	GO:0002682	1217	1.80E-08	37
REAC	Binding and Uptake of Ligands by Scavenger Receptors	REAC:R-HSA-2173782	41	1.80E-08	9
TF	Factor: c-Ets-2; motif: NACCGGAAGYRCTTCCGGTN; match class: 1	TF:M11417_1	12734	1.80E-08	162
TF	Factor: Cdx-1; motif: TTTATK	TF:M02086	12282	1.90E-08	158

TF	Factor: c-Myb; motif: NNWGRCAGTTRN	TF:M09990	9243	1.90E-08	130
TF	Factor: PMX1; motif: TAATHA	TF:M03560	11838	1.90E-08	154
TF	Factor: CP2; motif: NNNNCCAGNCNN; match class: 1	TF:M07602_1	4106	2.00E-08	76
TF	Factor: AREB6; motif: NNYNYACCTGWVT	TF:M00412	3939	2.00E-08	74
TF	Factor: REST; motif: GGACAGCKC	TF:M04726	5256	2.10E-08	89
TF	Factor: myogenin; motif: RGCAGSTG	TF:M00712	6086	2.10E-08	98
TF	Factor: Tal-1; motif: CAGATGG	TF:M03804	4459	2.20E-08	80
TF	Factor: SZF1-1; motif: CCAGGGTAWCAGCNG	TF:M01109	3781	2.30E-08	72
TF	Factor: LF-A1; motif: GGGSTCWR; match class: 1	TF:M00646_1	5629	2.30E-08	93
GO:BP	negative regulation of nitrogen compound metabolic process	GO:0051172	2106	2.60E-08	50
GO:BP	ossification	GO:0001503	388	2.70E-08	21
KEGG	Cytokine-cytokine receptor interaction	KEGG:04060	213	2.80E-08	15
TF	Factor: GR; motif: RGWACATWAYGTWCY	TF:M11846	5101	2.80E-08	87
GO:BP	transport	GO:0006810	4269	3.00E-08	77
TF	Factor: NF-1C; motif: NTTGGCNNNNTGCCARN	TF:M11728	2233	3.00E-08	52
TF	Factor: SMAD; motif: TGTCTGNNN	TF:M08897	3891	3.10E-08	73
TF	Factor: AP-2; motif: SNNNCCNCAGGCN	TF:M00915	8995	3.10E-08	127
TF	Factor: VDR; motif: NRGGTCANNGRGKTCA	TF:M10106	6125	3.10E-08	98
GO:BP	positive regulation of gene expression	GO:0010628	1001	3.20E-08	33
TF	Factor: Elk-1; motif: CTTCCKG; match class: 1	TF:M07252_1	3080	3.40E-08	63
TF	Factor: c-Ets-2; motif: CTTCCTG; match class: 1	TF:M01207_1	3080	3.40E-08	63
TF	Factor: NF-E2; motif: TGCTGAGTCAY	TF:M00037	5577	3.50E-08	92
TF	Factor: AR; motif: NGNACANNNTGTTCYNN	TF:M09589	4327	3.50E-08	78
TF	Factor: E2F1; motif: GSGCGGGAAN	TF:M12597	13064	3.80E-08	164
TF	Factor: E2F4; motif: YCCCGCCNCNNSSNNSNN; match class: 1	TF:M12599_1	14589	3.90E-08	177
GO:BP	response to lipopolysaccharide	GO:0032496	277	4.10E-08	18
GO:BP	negative regulation of response to stimulus	GO:0048585	1510	4.10E-08	41
TF	Factor: FOXO1A:Net; motif: RWMAACAGGAAGTN	TF:M08302	7909	4.20E-08	116
TF	Factor: PPARALPHA:RXR-ALPHA; motif: AWNTRGGTNAAAGGTCAN	TF:M08960	10094	4.50E-08	137
TF	Factor: MIF-1; motif: NNGTTGCWWGGYAACNGS	TF:M00279	9883	4.60E-08	135
TF	Factor: Erm:E2A; motif: CASGTGNNNCGGAAGNN	TF:M08571	9890	4.80E-08	135
GO:BP	muscle tissue development	GO:0060537	359	5.00E-08	20
TF	Factor: c-Rel; motif: NRNRGGGRAATKCCA	TF:M10046	4101	5.00E-08	75
TF	Factor: GR; motif: NNNNNNNGKACNNNNTGTTCTNNNNNN	TF:M00955	4102	5.10E-08	75
TF	Factor: E2F-1:HES-7; motif: GGCRCGTGSYNNWNGGCGCSM; match class: 1	TF:M08525_1	14157	5.10E-08	173
TF	Factor: LRH-1; motif: TCAAGGTCRYGACCTTGR; match class: 1	TF:M11828_1	6856	5.60E-08	105
TF	Factor: ZNF692; motif: SYNGGSCCCASCCNC	TF:M09734	10664	5.70E-08	142
TF	Factor: Tbx5; motif: TNAGGTGTKV	TF:M01020	9490	5.80E-08	131
GO:BP	response to growth factor	GO:0070848	640	5.90E-08	26
GO:BP	establishment of localization	GO:0051234	4416	6.00E-08	78
REAC	Cytokine Signaling in Immune system	REAC:R-HSA-1280215	634	6.00E-08	25
GO:BP	regulation of cell differentiation	GO:0045595	1400	6.30E-08	39
TF	Factor: FXR:RXR-ALPHA; motif: NRGGTCANRGGKN	TF:M08955	8470	6.60E-08	121
TF	Factor: GR; motif: RGWACATWATGTWCY	TF:M11847	4559	6.60E-08	80
TF	Factor: ESRRA; motif: CAAGGTCANNYSAAGGTCA	TF:M04458	9722	6.80E-08	133
TF	Factor: AP-2alpha; motif: NGCCYSNNGSN	TF:M01857	8679	6.80E-08	123
TF	Factor: AP-4:ER81; motif: RSCGGAAGCAGSTGNN	TF:M08443	9517	7.10E-08	131
TF	Factor: ZNF432; motif: NCAGNRCCNSRGRCAGC	TF:M12704	9203	7.10E-08	128
GO:BP	embryo development	GO:0009790	976	7.50E-08	32
TF	Factor: AML1; motif: TGTGGT	TF:M00751	10268	7.50E-08	138
TF	Factor: AML1a; motif: TGTGGT	TF:M00271	10268	7.50E-08	138

TF	Factor: AML1; motif: TGTGGT	TF:M02084	10268	7.50E-08	138
GO:BP	positive regulation of cellular metabolic process	GO:0031325	2936	7.80E-08	60
TF	Factor: GR; motif: RGRACATTNTGTYC	TF:M04750	4487	7.90E-08	79
GO:BP	regulation of localization	GO:0032879	2549	8.00E-08	55
TF	Factor: Elk-1:Pax-5; motif: ACCGGAACYACGCWTSANYG	TF:M08225	12715	8.00E-08	160
TF	Factor: DATF1; motif: SNGGRRGCWGNGGG	TF:M09724	7588	8.20E-08	112
GO:BP	skeletal system development	GO:0001501	457	8.40E-08	22
GO:BP	regulation of cellular metabolic process	GO:0031323	5347	8.60E-08	88
TF	Factor: THAP1; motif: YTGCCCNNA; match class: 1	TF:M07407_1	3639	8.60E-08	69
TF	Factor: GR; motif: RGWACATWATGTWCY; match class: 1	TF:M11847_1	3311	8.70E-08	65
TF	Factor: STAT5A; motif: TTCCNRGAANNNNNNTTCCNNGRR	TF:M00460	6618	8.90E-08	102
GO:BP	negative regulation of cellular metabolic process	GO:0031324	2256	9.10E-08	51
TF	Factor: TFAP2A; motif: NGCCCYNNGGGCN; match class: 1	TF:M04148_1	8927	9.50E-08	125
TF	Factor: Smad4; motif: NCAGACAN	TF:M07368	3322	1.00E-07	65
GO:BP	regulation of angiogenesis	GO:0045765	256	1.10E-07	17
GO:CC	blood microparticle	GO:0072562	94	1.10E-07	11
TF	Factor: Sohlh2; motif: NNCACGTGNN	TF:M11075	10531	1.10E-07	140
TF	Factor: Fli-1; motif: NACCGGATATCCGGTN	TF:M11401	10861	1.10E-07	143
TF	Factor: DPF2; motif: NYCACYTCCYCNYYCY	TF:M09760	7424	1.10E-07	110
TF	Factor: PEA3; motif: ACWTCCK	TF:M00655	8027	1.10E-07	116
TF	Factor: pax-6; motif: NYACGCNYSANYGMNCN	TF:M11882	14157	1.10E-07	172
GO:BP	negative regulation of molecular function	GO:0044092	935	1.20E-07	31
GO:BP	response to organonitrogen compound	GO:0010243	937	1.20E-07	31
REAC	Signaling by Interleukins	REAC:R-HSA-449147	411	1.20E-07	20
TF	Factor: rfx3:SREBP-2; motif: ATGGYAACRTCACGTGAY	TF:M08412	9163	1.20E-07	127
GO:BP	regulation of vasculature development	GO:1901342	260	1.30E-07	17

KEGG	Staphylococcus aureus infection	KEGG:05150	60	1.30E-07	9
TF	Factor: CTCF; motif: ACCAGGKGGC	TF:M04727	5802	1.30E-07	93
TF	Factor: C/EBP; motif: NTTRCNNAANNN	TF:M00912	4188	1.40E-07	75
GO:BP	apoptotic signaling pathway	GO:0097190	566	1.50E-07	24
GO:BP	cellular response to growth factor stimulus	GO:0071363	616	1.50E-07	25
TF	Factor: CDX-2; motif: TTTATN	TF:M02087	8261	1.50E-07	118
TF	Factor: TFAP2C; motif: NGCCCNNRGGCA	TF:M04152	7062	1.50E-07	106
TF	Factor: HES-5; motif: NCACACKY	TF:M11069	9505	1.50E-07	130
TF	Factor: DEC1; motif: NCNCACRTGNSC	TF:M08870	6965	1.50E-07	105
TF	Factor: Spic; motif: NGNGGAASTN	TF:M02077	7359	1.50E-07	109
TF	Factor: E2F-1; motif: NGGGCGGGARV	TF:M07206	13501	1.50E-07	166
GO:BP	mesenchyme development	GO:0060485	263	1.60E-07	17
TF	Factor: TIEG1; motif: GGSGGKGNNN	TF:M08905	4638	1.60E-07	80
TF	Factor: GLI; motif: NTGGGTGGTN	TF:M07292	5098	1.80E-07	85
TF	Factor: NRL; motif: NNNNTGCTGAC	TF:M04224	3869	1.80E-07	71
TF	Factor: CPBP; motif: GNNRGGGHGGGGNNGGGRN	TF:M09973	10173	1.80E-07	136
GO:BP	muscle structure development	GO:0061061	573	1.90E-07	24
GO:BP	regulation of body fluid levels	GO:0050878	345	1.90E-07	19
TF	Factor: ZNF549; motif: NTGCTKYCMW	TF:M12355	5656	1.90E-07	91
TF	Factor: AP2; motif: GCCYGSGGSN	TF:M08867	9433	1.90E-07	129
TF	Factor: Spz1; motif: DNNGGRGGGWWNNNN	TF:M00446	7790	1.90E-07	113
TF	Factor: Fli-1; motif: NACCGGATATCCGGTN; match class: 1	TF:M11401_1	10722	1.90E-07	141
GO:BP	response to nitrogen compound	GO:1901698	1015	2.00E-07	32
TF	Factor: ER-alpha; motif: AGGTCASMNTGACCY	TF:M09909	5943	2.00E-07	94
TF	Factor: E2F-3:FOXO6; motif: NAATGACACGCGCCCMC	TF:M08209	12393	2.00E-07	156
GO:MF	structural molecule activity	GO:0005198	657	2.20E-07	25

GO:BP	negative regulation of metabolic process	GO:0009892	2853	2.20E-07	58
TF	Factor: ZABC1; motif: ATTCCNAC	TF:M01306	8006	2.20E-07	115
TF	Factor: Hey2; motif: NNCACGYGNN	TF:M11052	11397	2.20E-07	147
TF	Factor: Zic1; motif: KGGGTGGTC; match class: 1	TF:M00448_1	3888	2.20E-07	71
TF	Factor: HSF2; motif: NGAANNWTCK	TF:M00147	4941	2.20E-07	83
TF	Factor: E2F2; motif: NNTTTTGGCGCCAAAAWN	TF:M03959	7017	2.30E-07	105
GO:BP	regulation of cell migration	GO:0030334	847	2.40E-07	29
TF	Factor: HNRPUL1; motif: NCNCAGN; match class: 1	TF:M09746_1	6727	2.40E-07	102
TF	Factor: Six-2; motif: NNGTAWCRNN	TF:M11032	9253	2.40E-07	127
TF	Factor: CTCF; motif: CANNWRRTGGCAG	TF:M04745	7022	2.40E-07	105
TF	Factor: Erg; motif: NACCGGATATCCGGTN; match class: 1	TF:M11397_1	10645	2.40E-07	140
GO:BP	cellular response to organonitrogen compound	GO:0071417	582	2.60E-07	24
TF	Factor: DLX2; motif: AMSMCTGACKG	TF:M08873	6450	2.60E-07	99
GO:BP	regulation of cell adhesion	GO:0030155	687	2.70E-07	26
GO:CC	contractile fiber	GO:0043292	229	2.80E-07	15
GO:BP	cellular response to nitrogen compound	GO:1901699	636	2.90E-07	25
GO:BP	connective tissue development	GO:0061448	236	2.90E-07	16
TF	Factor: AP-2; motif: MKCCCSCNGGCG	TF:M00189	10020	2.90E-07	134
TF	Factor: MAZ; motif: GGGGGAGGGGGNGRGRRGNRG	TF:M09984	8861	2.90E-07	123
GO:BP	regulation of cellular component movement	GO:0051270	972	3.00E-07	31
TF	Factor: C/EBPbeta; motif: TKNNGCAANN	TF:M01896	3827	3.00E-07	70
TF	Factor: DB1; motif: GGRRRRGRRGGAGGGGGNGRRR	TF:M10107	5428	3.00E-07	88
TF	Factor: Sox-4; motif: NYCTTTGTYYYN	TF:M10069	6179	3.10E-07	96
TF	Factor: NR1H4; motif: NNAATGACCNN	TF:M09777	3246	3.10E-07	63
REAC	Signal Transduction	REAC:R-HSA-162582	2365	3.20E-07	50
TF	Factor: STAT1; motif: NTTCCNGGA	TF:M04721	6860	3.20E-07	103

TF	Factor: JUNB:C-JUN; motif: KRTGACGTCATN	TF:M08945	8056	3.30E-07	115
TF	Factor: Tax/CREB; motif: RTGACGCATAYCCCC	TF:M00115	8263	3.40E-07	117
REAC	Assembly of collagen fibrils and other multimeric structures	REAC:R-HSA-2022090	56	3.50E-07	9
TF	Factor: Sall1; motif: NGGTCCKRGKRA	TF:M05467	3757	3.50E-07	69
TF	Factor: AR; motif: AGAACANNNTGTTCT; match class: 1	TF:M08907_1	1804	3.50E-07	44
TF	Factor: ZNF511; motif: GGRRGRGGCWGNG	TF:M09738	9835	3.50E-07	132
GO:BP	regulation of primary metabolic process	GO:0080090	5129	3.70E-07	84
GO:BP	blood coagulation	GO:0007596	205	3.70E-07	15
TF	Factor: Sox-2; motif: NNCCTTTGTNYYN	TF:M10067	5172	3.70E-07	85
TF	Factor: AP-2gamma; motif: GCCYNNGGS; match class: 1	TF:M00470_1	5364	4.00E-07	87
TF	Factor: IRF-2; motif: NAANYGAAASYR	TF:M08775	7180	4.00E-07	106
REAC	Collagen degradation	REAC:R-HSA-1442490	57	4.10E-07	9
TF	Factor: VDR; motif: GRGTTCATYGRGTTCA	TF:M04498	4463	4.10E-07	77
TF	Factor: NF-kappaB; motif: GGGGATYCCC	TF:M00051	5840	4.40E-07	92
TF	Factor: AP-2gamma:Max; motif: NNSCCYNRGGSNNNNCACGTGN	TF:M08664	2105	4.40E-07	48
TF	Factor: ER71:Pax-5; motif: ACCGGAACYACGCWTSANTG	TF:M08266	13080	4.40E-07	161
KEGG	Malaria	KEGG:05144	48	4.50E-07	8
GO:BP	coagulation	GO:0050817	208	4.60E-07	15
TF	Factor: NURR1; motif: YRRCCTT	TF:M01269	5012	4.60E-07	83
TF	Factor: c-Rel; motif: NGGGAATYTCCN	TF:M03545	4836	4.80E-07	81
GO:BP	regulation of nitrogen compound metabolic process	GO:0051171	4981	5.20E-07	82
TF	Factor: FOXM1; motif: TRTTTATNN	TF:M08883	5673	5.30E-07	90
TF	Factor: ZBRK1; motif: NGNNNGGTNAWAAAARRGCNG	TF:M10468	9361	5.30E-07	127
GO:BP	positive regulation of immune system process	GO:0002684	764	5.40E-07	27
GO:BP	hemostasis	GO:0007599	211	5.60E-07	15

TF	Factor: DBP; motif: TTRCATAANN	TF:M07038	4582	5.60E-07	78
TF	Factor: BTEB2; motif: WGGGTGKGGCNGGN	TF:M09972	8433	5.70E-07	118
TF	Factor: RUNX3; motif: NRACCGCAAACCGCAN	TF:M04109	8951	5.70E-07	123
TF	Factor: NF-1; motif: NNTTGGCNNNNNNCCNNN	TF:M00193	4407	5.70E-07	76
TF	Factor: MTF-1; motif: NTTTTGCACACGGCNYN	TF:M12279	5776	5.80E-07	91
TF	Factor: NF-kappaB; motif: AGGGGAWTCCCCT	TF:M04054	2656	5.90E-07	55
TF	Factor: AP-2alphaA; motif: ANMGCCTNAGGCKNT	TF:M01047	7728	6.00E-07	111
TF	Factor: AP-2alphaA; motif: ANMGCCTNAGGCKNT; match class: 1	TF:M01047_1	7728	6.00E-07	111
TF	Factor: PURBETA; motif: NCWGRGGCTGGGG; match class: 1	TF:M12726_1	2201	6.20E-07	49
TF	Factor: SREBP-1; motif: CACSCCA; match class: 1	TF:M00749_1	2428	6.20E-07	52
TF	Factor: HSF2; motif: NGAANNWTCK; match class: 1	TF:M00147_1	3725	6.50E-07	68
TF	Factor: AP-4; motif: AWCAGCTGWT	TF:M11206	6263	6.50E-07	96
TF	Factor: AP-4; motif: AWCAGCTGWT; match class: 1	TF:M11206_1	6263	6.50E-07	96
GO:BP	leukocyte migration	GO:0050900	329	6.70E-07	18
GO:BP	cellular response to lipid	GO:0071396	511	7.00E-07	22
TF	Factor: TEF-3:Elk-1; motif: RMATWCCGGAWGT	TF:M08418	10468	7.00E-07	137
TF	Factor: c-Ets-1; motif: RCAGGAAGTGNNTNS	TF:M00339	5893	7.10E-07	92
TF	Factor: Elf5; motif: CSMGGAARNN	TF:M02057	9296	7.20E-07	126
GO:BP	enzyme linked receptor protein signaling pathway	GO:0007167	889	7.30E-07	29
TF	Factor: RelA-p65; motif: GGGANTTTCCNN	TF:M03563	4079	7.30E-07	72
GO:BP	renal system development	GO:0072001	291	7.70E-07	17
TF	Factor: Fli-1; motif: RCAGGAAGTGR	TF:M07089	4264	8.20E-07	74
GO:BP	response to toxic substance	GO:0009636	217	8.30E-07	15
GO:CC	collagen trimer	GO:0005581	87	8.30E-07	10
TF	Factor: CP2; motif: NTGNCTGGNN	TF:M03868	4006	8.50E-07	71
TF	Factor: HSF1; motif: TCYAGAANNTTC	TF:M07259	4006	8.50E-07	71
TF	Factor: AP-4:Max; motif: NCAGCTGNNNNNNNNCACGTGN; match class: 1	TF:M08674_1	4802	8.50E-07	80
GO:MF	extracellular matrix structural constituent conferring tensile strength	GO:0030020	40	8.70E-07	8
TF	Factor: CP2; motif: NRRRCCGGCYNRARCCGGNN	TF:M12590	10284	8.90E-07	135
GO:BP	positive regulation of cell differentiation	GO:0045597	782	9.00E-07	27
TF	Factor: NR1B1; motif: NRGGTCANNRGGTCAN	TF:M11795	6883	9.00E-07	102
REAC	Collagen chain trimerization	REAC:R-HSA-8948216	43	9.10E-07	8
TF	Factor: ZNF300; motif: SWGGGGGSN; match class: 1	TF:M07486_1	6786	9.10E-07	101
GO:BP	regulation of cell motility	GO:2000145	898	9.20E-07	29
TF	Factor: ZNF436; motif: TCCTCCAGGAAGCCY; match class: 1	TF:M10477_1	7782	9.20E-07	111
REAC	Collagen formation	REAC:R-HSA-1474290	85	9.30E-07	10
MIRNA	hsa-miR-26b-5p	MIRNA:hsa-miR-26b-5p	1739	9.60E-07	41
TF	Factor: AR; motif: AGAACANNNTGTTCT	TF:M08907	1863	9.70E-07	44
TF	Factor: GR; motif: AGAACAN	TF:M07355	4913	1.00E-06	81
GO:BP	striated muscle tissue development	GO:0014706	340	1.10E-06	18
TF	Factor: FOXO1A:ETV7; motif: NWMAACAGGAMNNNCTTCCNN; match class: 1	TF:M08304_1	6512	1.10E-06	98
TF	Factor: E2F-4; motif: GCGGGAAANA	TF:M02090	11183	1.10E-06	143
TF	Factor: Nrf2; motif: NNTGACTCAGCAN	TF:M07265	4114	1.10E-06	72
GO:BP	sensory organ development	GO:0007423	525	1.20E-06	22
TF	Factor: E2F-3:T-bet; motif: AGGTGTNANGGCGCST	TF:M08529	10334	1.30E-06	135
TF	Factor: HNF4A; motif: NNCAAAGTCCANN	TF:M12503	2555	1.30E-06	53
TF	Factor: ER-beta; motif: NRGGTCANKSTGACCTNN	TF:M09610	5122	1.30E-06	83
GO:MF	protein-containing complex binding	GO:0044877	1204	1.40E-06	33
GO:BP	muscle organ development	GO:0007517	303	1.40E-06	17
TF	Factor: SRY; motif: TTGTTT; match class: 1	TF:M03854_1	7628	1.40E-06	109
TF	Factor: FOXO1A; motif: AAACAA; match class: 1	TF:M03823_1	7628	1.40E-06	109

TF	Factor: NR1B1; motif: NRGGNCRTGACCTN; match class: 1	TF:M11796_1	4315	1.40E-06	74
TF	Factor: c-ets-1; motif: GGAGTTG	TF:M04822	4763	1.40E-06	79
TF	Factor: ERF:FOXO1A; motif: RTMAACAGGAARNS	TF:M08241	6745	1.50E-06	100
TF	Factor: LHX3; motif: ATTAAW	TF:M02097	10034	1.50E-06	132
TF	Factor: MAZ; motif: NKGGGAGGGGRGGR	TF:M02023	6650	1.50E-06	99
TF	Factor: c-Ets-2; motif: NNNRGGAARNRRR	TF:M09912	4412	1.50E-06	75
TF	Factor: FLI1; motif: ACCGGAAATCCGGT	TF:M03989	9505	1.50E-06	127
GO:BP	chronic inflammatory response	GO:0002544	14	1.60E-06	6
REAC	Collagen biosynthesis and modifying enzymes	REAC:R-HSA-1650814	66	1.60E-06	9
TF	Factor: C/EBPalpha; motif: NGWVTKNKGYAAKNSAYA	TF:M00201	3296	1.60E-06	62
TF	Factor: HMGIY; motif: NNKKNAWTTTNYTNN	TF:M01010	6852	1.60E-06	101
TF	Factor: MOVO-B; motif: GNGGGGG	TF:M01104	9727	1.60E-06	129
GO:BP	metabolic process	GO:0008152	11098	1.70E-06	141
TF	Factor: Ik-3; motif: TNYTGGGAATACC	TF:M00088	5052	1.70E-06	82
TF	Factor: ER-alpha; motif: NAGGTCACSGYGACCTN	TF:M11844	4779	1.70E-06	79
TF	Factor: MAZ; motif: CCCTCCCYCYN	TF:M07297	2734	1.70E-06	55
TF	Factor: JunB; motif: GATGACGTCAYC	TF:M11273	7663	1.80E-06	109
TF	Factor: ZBTB44; motif: MACWGCAGS	TF:M12352	5619	1.80E-06	88
KEGG	TNF signaling pathway	KEGG:04668	108	1.90E-06	10
TF	Factor: TWIST1; motif: NNNCCAGATGTNN	TF:M09790	2428	1.90E-06	51
TF	Factor: AR; motif: RGGWACAYNGTGTWCYN; match class: 1	TF:M04453_1	3232	2.00E-06	61
GO:MF	collagen binding	GO:0005518	64	2.10E-06	9
TF	Factor: Elk-1:HOXA3; motif: ACCGGWAATKRNNTNWCNNATTAN	TF:M08220	10624	2.10E-06	137
TF	Factor: FOXO1A:Elf-1; motif: NAGAAAACCGAANM	TF:M08295	10193	2.10E-06	133
GO:BP	regulation of inflammatory response	GO:0050727	313	2.30E-06	17
GO:CC	Z disc	GO:0030018	125	2.30E-06	11
TF	Factor: AP2; motif: GCCYGSGGSN; match class: 1	TF:M08867_1	4993	2.30E-06	81
GO:BP	regulation of molecular function	GO:0065009	2797	2.40E-06	55
GO:BP	regulation of locomotion	GO:0040012	937	2.40E-06	29
TF	Factor: SP1; motif: GGGGYGGGGNS	TF:M01303	7502	2.40E-06	107
TF	Factor: MTF-1; motif: NTTTTGCACACGGCNNN	TF:M12280	6032	2.50E-06	92
TF	Factor: rfx3:SRF; motif: TRGCAACNNNNNCCNWATANGGN	TF:M08623	12775	2.50E-06	156
TF	Factor: AP-2gamma:Elk-1; motif: NGCCKNRGGSGRCGGAAGTG; match class: 1	TF:M08441_1	11870	2.50E-06	148
TF	Factor: VDR; motif: GGGKNARNRRGGWSA; match class: 1	TF:M00444_1	4198	2.60E-06	72
TF	Factor: Sp3; motif: ASMCTTGGGSRGGG	TF:M00665	7012	2.60E-06	102
TF	Factor: AP-4; motif: WGARYCAGCTGYGGNCNK	TF:M00005	4645	2.60E-06	77
REAC	ECM proteoglycans	REAC:R-HSA-3000178	70	2.70E-06	9
TF	Factor: c-Rel; motif: SGGRNTTTCC	TF:M00053	3259	2.70E-06	61
TF	Factor: BTEB3; motif: CCNNSCCNSCCCCKCCCCC	TF:M09826	10774	2.80E-06	138
TF	Factor: TIEG1; motif: NCCCNSNCCCCGCCCCC	TF:M12351	11551	2.80E-06	145
TF	Factor: MEL1; motif: GARGAT	TF:M08794	9275	2.90E-06	124
TF	Factor: NF-1A; motif: NGCCARN	TF:M03554	4210	2.90E-06	72
GO:BP	response to inorganic substance	GO:0010035	502	3.00E-06	21
KEGG	Amoebiasis	KEGG:05146	85	3.00E-06	9
GO:BP	intracellular signal transduction	GO:0035556	2497	3.10E-06	51
GO:BP	blood circulation	GO:0008015	455	3.20E-06	20
GO:BP	negative regulation of cell population proliferation	GO:0008285	660	3.20E-06	24
TF	Factor: CKROX; motif: SCCCTCCCC	TF:M01175	6740	3.20E-06	99
TF	Factor: AR; motif: GGAACGGWACATGTTCT	TF:M08190	6740	3.20E-06	99
TF	Factor: TEF-1; motif: ACATTCCWSNN	TF:M07340	3273	3.20E-06	61

TF	Factor: IRF-4; motif: NAANGRGGAASTGAAASN	TF:M09959	2865	3.30E-06	56
TF	Factor: KLF15; motif: NCCMCGCCCMCN	TF:M12158	9935	3.30E-06	130
TF	Factor: Elk-1:SREBP-2; motif: RTCACGTGACCGGAAGN	TF:M08229	8564	3.30E-06	117
GO:BP	negative regulation of macromolecule metabolic process	GO:0010605	2662	3.40E-06	53
GO:BP	odontogenesis	GO:0042476	109	3.40E-06	11
TF	Factor: six-4; motif: ANNNATGACACCNNNNN	TF:M01374	5406	3.40E-06	85
TF	Factor: MAFA; motif: TCAGCAN	TF:M01709	5314	3.40E-06	84
GO:BP	positive regulation of nitrogen compound metabolic process	GO:0051173	2747	3.60E-06	54
TF	Factor: ZNFPT1; motif: YCNNCNCWGCCNY; match class: 1	TF:M12721_1	2874	3.70E-06	56
TF	Factor: NFATc1; motif: TTTCCWN	TF:M01718	5045	3.70E-06	81
TF	Factor: IRX-1; motif: NACRYNNNNNNNNRYGNN; match class: 1	TF:M11018_1	14591	3.90E-06	171
TF	Factor: TEF; motif: YACATTCCWSNG	TF:M01305	3207	3.90E-06	60
GO:BP	urogenital system development	GO:0001655	325	4.10E-06	17
KEGG	Viral protein interaction with cytokine and cytokine receptor	KEGG:04061	63	4.10E-06	8
TF	Factor: NF-1C; motif: NYYTGGCWNNNNKCCMN	TF:M09640	2406	4.10E-06	50
TF	Factor: KLF; motif: GGGNGGGG; match class: 1	TF:M07461_1	3129	4.10E-06	59
REAC	Degradation of the extracellular matrix	REAC:R-HSA-1474228	128	4.20E-06	11
GO:CC	complex of collagen trimers	GO:0098644	21	4.30E-06	6
GO:CC	sarcomere	GO:0030017	201	4.30E-06	13
TF	Factor: AP-4:Dlx-3; motif: NCAGCTGNNNNNNGTAATKR	TF:M08671	3638	4.40E-06	65
TF	Factor: ROX; motif: GNNNCASGTGGS	TF:M09764	5157	4.40E-06	82
GO:MF	immune receptor activity	GO:0140375	122	4.50E-06	11
TF	Factor: YB-1; motif: NNNNCCAATNN	TF:M03862	7885	4.50E-06	110
TF	Factor: ZNF37A; motif: CCYYGGCTCCNTSCCMN; match class: 1	TF:M12354_1	5347	4.60E-06	84
TF	Factor: ERF:SREBP-2; motif: NSCGGAARTCACGTGAT	TF:M08453	8820	4.70E-06	119
TF	Factor: GR; motif: CNNNNTGTYCTNN	TF:M01836	4890	4.80E-06	79
GO:BP	vascular process in circulatory system	GO:0003018	247	4.90E-06	15
TF	Factor: SMAD4; motif: GKSRKKCAGMCANCY; match class: 1	TF:M00733_1	2421	5.00E-06	50
TF	Factor: Thap1; motif: SCGCCATSTTKGNTNMGGGCARNN	TF:M04723	10537	5.10E-06	135
TF	Factor: Sox-9; motif: RNACAAAGGVN	TF:M01284	5079	5.10E-06	81
TF	Factor: SMAD3; motif: CAGACAS; match class: 1	TF:M07429_1	1137	5.30E-06	32
TF	Factor: MaFA; motif: TCTGCTGASCNN	TF:M07325	4356	5.30E-06	73
GO:BP	organic substance metabolic process	GO:0071704	10615	5.40E-06	135
TF	Factor: P50; motif: GGRRANTCCCNN	TF:M03557	4359	5.40E-06	73
TF	Factor: SREBP-2; motif: NNGYCACNNSMN	TF:M01177	7910	5.40E-06	110
TF	Factor: Oct-2; motif: ATTTGCA	TF:M04715	5273	5.50E-06	83
TF	Factor: TWIST1; motif: NNNCCAGATGTNN	TF:M12577	2350	5.50E-06	49
TF	Factor: TEF-1; motif: CRCATWCCN	TF:M12041	4007	5.50E-06	69
TF	Factor: MTF-1; motif: GTGTGCANMACTTTGCGCAC	TF:M01242	3492	5.70E-06	63
TF	Factor: ATF-1; motif: CYYTGACGTCA	TF:M00691	4277	5.80E-06	72
TF	Factor: Pax-6; motif: CTGACCTGGAACTM	TF:M00979	8330	5.90E-06	114
TF	Factor: NF-1; motif: TTGGCNN	TF:M07364	4189	5.90E-06	71
TF	Factor: Sox-4; motif: AACAAA; match class: 1	TF:M03849_1	7618	6.00E-06	107
GO:BP	cellular response to tumor necrosis factor	GO:0071356	213	6.10E-06	14
REAC	Hemostasis	REAC:R-HSA-109582	570	6.10E-06	21
TF	Factor: Erg; motif: NACCGGATATCCGGTN	TF:M11391	9170	6.10E-06	122
MIRNA	hsa-miR-146a-5p	MIRNA:hsa-miR-146a-5p	194	6.10E-06	13
GO:CC	secretory granule lumen	GO:0034774	289	6.50E-06	15
TF	Factor: LKLF; motif: CNCCACCCS	TF:M08819	5105	6.50E-06	81
TF	Factor: E2F-2; motif: GCGCGCGCNCS; match class: 1	TF:M11529_1	13618	6.50E-06	162
GO:CC	I band	GO:0031674	138	6.60E-06	11

TF	Factor: Fli-1; motif: NACCGGAWWTCCGGTY; match class: 1	TF:M11399_1	10467	6.60E-06	134
TF	Factor: ZXDL; motif: GSGSCNNGGGMRGCNCCGGGS	TF:M12722	9932	6.80E-06	129
GO:CC	endoplasmic reticulum lumen	GO:0005788	291	7.10E-06	15
GO:CC	cytoplasmic vesicle lumen	GO:0060205	291	7.10E-06	15
TF	Factor: T-bet; motif: NNGNRGGTGTGRN	TF:M10089	5395	7.10E-06	84
TF	Factor: E2F-4; motif: NTTTCSCGCC	TF:M07380	12143	7.10E-06	149
TF	Factor: MAZ; motif: GGGMGGGGS	TF:M10432	8669	7.20E-06	117
TF	Factor: Pax-3; motif: TCGTCACRCTTHM	TF:M00360	10921	7.30E-06	138
TF	Factor: SRY; motif: AAACWAM	TF:M00148	7951	7.40E-06	110
TF	Factor: Miz-1; motif: NNRGGWGGGGGAGGGGMRR	TF:M10112	8054	7.40E-06	111
GO:BP	embryonic morphogenesis	GO:0048598	530	7.70E-06	21
GO:CC	vesicle lumen	GO:0031983	293	7.70E-06	15
GO:BP	positive regulation of angiogenesis	GO:0045766	148	7.80E-06	12
GO:BP	positive regulation of vasculature development	GO:1904018	148	7.80E-06	12
GO:BP	artery morphogenesis	GO:0048844	67	8.10E-06	9
TF	Factor: PR; motif: RGNACATTYTGTNCTN	TF:M10042	2695	8.20E-06	53
TF	Factor: NFATc2; motif: NTTTCCRTNNAYGGAAAN	TF:M11984	9531	8.20E-06	125
REAC	Smooth Muscle Contraction	REAC:R-HSA-445355	37	8.30E-06	7
TF	Factor: FOXP1; motif: TNTGTTTMY	TF:M09933	4223	8.30E-06	71
TF	Factor: TEF-3:E2A; motif: NCAGSTGNGWATGYN	TF:M08438	4948	8.30E-06	79
TF	Factor: AP-2; motif: GSCCSCRGGCNRNRNN	TF:M00800	8588	8.50E-06	116
TF	Factor: PARP; motif: TTTCYN; match class: 1	TF:M02027_1	10180	8.50E-06	131
GO:BP	embryonic organ development	GO:0048568	387	8.70E-06	18
GO:MF	growth factor binding	GO:0019838	130	8.80E-06	11
TF	Factor: Hey1; motif: NGCRCGYGYN	TF:M11058	12064	8.80E-06	148
TF	Factor: E2F-3:FOXI1; motif: NGACACCGCGCCCAC	TF:M08208	11509	9.10E-06	143
TF	Factor: C-JUN:FRA-2; motif: NRTGACGTMAT	TF:M08941	5804	9.30E-06	88
TF	Factor: Pasx-5; motif: GTCACGSTT	TF:M04765	9656	9.30E-06	126
GO:BP	regulation of apoptotic signaling pathway	GO:2001233	344	9.60E-06	17
TF	Factor: pax-6; motif: NYACGCNTSRNYGCNYN	TF:M11883	12304	9.60E-06	150
GO:BP	artery development	GO:0060840	93	1.00E-05	10
GO:BP	regulation of response to stress	GO:0080134	1192	1.00E-05	32
GO:CC	supramolecular polymer	GO:0099081	834	1.00E-05	25
GO:BP	regulation of anatomical structure morphogenesis	GO:0022603	878	1.10E-05	27
GO:BP	myeloid leukocyte migration	GO:0097529	186	1.10E-05	13
REAC	Non-integrin membrane-ECM interactions	REAC:R-HSA-3000171	58	1.10E-05	8
GO:MF	platelet-derived growth factor binding	GO:0048407	11	1.20E-05	5
KEGG	AGE-RAGE signaling pathway in diabetic complications	KEGG:04933	100	1.20E-05	9
TF	Factor: SMAD3; motif: TGTCTGTCT	TF:M00701	3555	1.20E-05	63
TF	Factor: pax-6; motif: NYACGCNTSANYGCNYN	TF:M11881	11996	1.20E-05	147
TF	Factor: NFATc2; motif: NTTTCCRTNNAYGGAAAN; match class: 1	TF:M11984_1	9477	1.20E-05	124
TF	Factor: NF1C; motif: WGCCARR; match class: 1	TF:M09763_1	3644	1.20E-05	64
TF	Factor: C/EBPdelta; motif: TTGCNNMAN	TF:M03571	3137	1.20E-05	58
MIRNA	hsa-miR-124-3p	MIRNA:hsa-miR-124-3p	1393	1.20E-05	34
GO:CC	myofibril	GO:0030016	220	1.30E-05	13
TF	Factor: AP4; motif: NMNCAGCTGGN	TF:M12580	5085	1.30E-05	80
TF	Factor: DRRS; motif: GNNGGGWGGG	TF:M10056	4356	1.30E-05	72
TF	Factor: C/EBPalpha; motif: NRTTGTGCAAYNN	TF:M09596	4356	1.30E-05	72
TF	Factor: MafB; motif: GNTGAC; match class: 1	TF:M01227_1	4179	1.30E-05	70
TF	Factor: Sp1; motif: GGGGCGGGGT	TF:M00008	9493	1.30E-05	124
TF	Factor: rax; motif: NNCRTTAN	TF:M10948	10354	1.30E-05	132

GO:BP	cellular homeostasis	GO:0019725	828	1.40E-05	26
TF	Factor: SREBP-1; motif: RTCRCGTGAY	TF:M11081	9930	1.40E-05	128
TF	Factor: STAT3; motif: NNTTCCRGGAANNNNN	TF:M01595	6729	1.40E-05	97
TF	Factor: Smad3; motif: NGNCAGACASNNN	TF:M01888	3489	1.40E-05	62
TF	Factor: GR; motif: GGTACAANNTGTYCTK	TF:M00205	5664	1.40E-05	86
GO:BP	response to hormone	GO:0009725	774	1.50E-05	25
TF	Factor: IRF-7; motif: AAGWGAA; match class: 1	TF:M01884_1	3752	1.50E-05	65
TF	Factor: SATB2; motif: GSCGCTGTCCNNGGTGCTGN	TF:M12660	5015	1.50E-05	79
TF	Factor: BCL-11A; motif: NAAAGAGGAAGTGARAN	TF:M09595	3159	1.60E-05	58
TF	Factor: Egr-1; motif: NGCGTGCGY	TF:M04950	10165	1.60E-05	130
TF	Factor: E2F-3:HES-7; motif: NNNSGCGCSNNNNNCRCGYGNN; match class: 1	TF:M08526_1	14003	1.60E-05	164
TF	Factor: Lhx2; motif: WATTAN	TF:M07047	9102	1.60E-05	120
GO:BP	cellular ion homeostasis	GO:0006873	609	1.70E-05	22
TF	Factor: Fli-1; motif: NNRGGMAGGAAGGRRRGR; match class: 1	TF:M09920_1	2997	1.70E-05	56
TF	Factor: c-Myc; motif: CACGTGGC	TF:M03867	6456	1.70E-05	94
TF	Factor: RELB; motif: NNATTCCCCNN	TF:M09784	4657	1.70E-05	75
TF	Factor: p300; motif: CTGNCTYMAN	TF:M07266	6955	1.70E-05	99
GO:BP	regulation of response to external stimulus	GO:0032101	839	1.80E-05	26
GO:BP	regulation of cellular protein metabolic process	GO:0032268	2160	1.80E-05	45
TF	Factor: p300; motif: ACNTCCG; match class: 1	TF:M04826_1	14020	1.80E-05	164
TF	Factor: C/EBP; motif: NNATTGCNNAANNN	TF:M00190	4665	1.80E-05	75
TF	Factor: NF-1C; motif: NTTGGCNNNNTGCCARN	TF:M11729	1469	1.80E-05	36
TF	Factor: ZNF460; motif: NNACNCCCCCCNN	TF:M12313	5505	1.90E-05	84
TF	Factor: E2F-3; motif: NNGGCGGGAAA	TF:M09893	5600	1.90E-05	85
TF	Factor: ZNF614; motif: NCYCWGCCYYNNN; match class: 1	TF:M09862_1	3950	1.90E-05	67

TF	Factor: AR; motif: GGNACRNNRTGTWCT	TF:M01201	5602	1.90E-05	85
TF	Factor: CHD2; motif: TCTCGCGAG	TF:M04710	12870	1.90E-05	154
TF	Factor: E2F-3; motif: GGCGGGN	TF:M02089	12418	2.00E-05	150
TF	Factor: ZF5; motif: GSGCGCGR; match class: 1	TF:M00716_1	13336	2.00E-05	158
TF	Factor: SUHW1; motif: TCTCTCCAGTRTGAATTCTCTGAT	TF:M10541	6086	2.00E-05	90
GO:BP	response to tumor necrosis factor	GO:0034612	235	2.10E-05	14
TF	Factor: LTF; motif: GKVACTTNC	TF:M01692	3701	2.20E-05	64
TF	Factor: egr-3; motif: GTGGGY; match class: 1	TF:M03818_1	5816	2.30E-05	87
TF	Factor: TFAP2A; motif: YGCCCNNRGGCN	TF:M04146	6009	2.30E-05	89
TF	Factor: Smad2; motif: TGTCTGNCWCCT	TF:M10059	5342	2.30E-05	82
TF	Factor: E2A; motif: CACCTGNY	TF:M00973	4692	2.30E-05	75
TF	Factor: RAR-gamma; motif: RGGTCANNNTGNCCNNNN	TF:M10045	6400	2.30E-05	93
TF	Factor: Kaiso; motif: GCMGGGRGCRGS; match class: 1	TF:M03876_1	8628	2.30E-05	115
TF	Factor: PBX2; motif: TGANTGACAGN	TF:M09736	4240	2.40E-05	70
GO:BP	response to transforming growth factor beta	GO:0071559	238	2.50E-05	14
TF	Factor: ZNF462; motif: YYYYCTSCWG; match class: 1	TF:M12707_1	3033	2.50E-05	56
TF	Factor: RUNX2; motif: WRACCGCANWAACCGCAN	TF:M04107	11232	2.60E-05	139
TF	Factor: ZXDL; motif: NGGGGWS; match class: 1	TF:M05775_1	1561	2.60E-05	37
GO:CC	anchoring junction	GO:0070161	815	2.70E-05	24
TF	Factor: RBPJK; motif: NSNSTGGGAAN	TF:M10085	3038	2.70E-05	56
TF	Factor: ZNF592; motif: NSARNATGGAGKN; match class: 1	TF:M09766_1	1421	2.70E-05	35
TF	Factor: Sp1; motif: GGNDGGRGGCGGGG	TF:M04953	8128	2.70E-05	110
TF	Factor: E2F-1; motif: NTTTTGGCGCCAWWWN	TF:M11533	12131	2.70E-05	147
TF	Factor: ITF-2; motif: NGCAGSTGKS	TF:M09962	4254	2.70E-05	70
TF	Factor: HEB; motif: RCCWGCTG	TF:M00698	2470	2.70E-05	49
TF	Factor: SRY; motif: AACAATANCATTGTT	TF:M04555	5745	2.80E-05	86

GO:BP	cellular chemical homeostasis	GO:0055082	741	2.90E-05	24
GO:BP	epithelial cell proliferation	GO:0050673	371	2.90E-05	17
TF	Factor: ZNF148; motif: NNCCCCTCCCCC	TF:M12464	6431	3.00E-05	93
GO:BP	intrinsic apoptotic signaling pathway	GO:0097193	283	3.10E-05	15
TF	Factor: SATB1; motif: NTTTAT; match class: 1	TF:M03564_1	10054	3.10E-05	128
TF	Factor: Gscl; motif: NTAATCCN	TF:M10924	5762	3.20E-05	86
TF	Factor: BRCA1:USF2; motif: KTNNGTTG	TF:M01082	6054	3.30E-05	89
TF	Factor: TEF-3:C/EBPbeta; motif: RTTGCGYAAYNNNNNGGAATGY	TF:M08626	5958	3.30E-05	88
TF	Factor: GATA-1; motif: SNNGATNNNN	TF:M00075	6252	3.40E-05	91
TF	Factor: ZIC4; motif: NNCCNCCCRYNGYGN	TF:M12227	10284	3.40E-05	130
TF	Factor: ipf1; motif: TGATTGATK	TF:M10031	7448	3.50E-05	103
TF	Factor: HES-7; motif: GNCACGYGNN	TF:M11066	10511	3.60E-05	132
TF	Factor: C/EBPbeta; motif: RTTGCGCAA	TF:M04690	3752	3.70E-05	64
TF	Factor: Erg; motif: MCAGGAAA; match class: 1	TF:M07284_1	3752	3.70E-05	64
TF	Factor: Egr-2; motif: CCCMCNCN	TF:M02092	4289	3.80E-05	70
TF	Factor: Erm:C/EBPdelta; motif: RSCGGAWRTTGCGYAAY	TF:M08458	8491	3.80E-05	113
TF	Factor: BTEB4; motif: NCCACGCCCM	TF:M12186	8491	3.80E-05	113
GO:CC	secretory granule membrane	GO:0030667	287	4.10E-05	14
KEGG	PI3K-Akt signaling pathway	KEGG:04151	319	4.10E-05	14
TF	Factor: PLAG1; motif: CCCCCKWNNNGGSCCC	TF:M01973	5790	4.10E-05	86
TF	Factor: HOXA3; motif: NNNNRNTAATTARY; match class: 1	TF:M01337_1	10095	4.10E-05	128
TF	Factor: AP-2beta; motif: NSCCNNNGGSN	TF:M11478	9237	4.10E-05	120
GO:BP	cellular metal ion homeostasis	GO:0006875	531	4.20E-05	20
TF	Factor: C/EBPalpha; motif: NNNTTNNGCAANN	TF:M01866	4299	4.20E-05	70
TF	Factor: ZEB1; motif: CAGGTGN	TF:M04831	6971	4.20E-05	98
TF	Factor: TFIIB; motif: YTNTMTGMSN	TF:M08904	5698	4.20E-05	85
TF	Factor: AP-4; motif: YCAGCTGNKN	TF:M10097	5226	4.30E-05	80
TF	Factor: MZF-1; motif: TGGGGAR; match class: 1	TF:M01733_1	4394	4.30E-05	71
TF	Factor: Sp1; motif: NGGGGCGGGGN	TF:M07395	10215	4.40E-05	129
TF	Factor: TEAD1; motif: NNACATTCCAGNN	TF:M12500	5045	4.60E-05	78
GO:BP	regulation of cellular biosynthetic process	GO:0031326	3648	4.70E-05	62
TF	Factor: XBP-1; motif: WNNGMCACGTC	TF:M01770	9900	4.70E-05	126
TF	Factor: AP-2; motif: NNGCCTK	TF:M01859	6687	4.70E-05	95
TF	Factor: NFATc1; motif: TTTTCCATGGAAAN	TF:M04053	7187	4.70E-05	100
TF	Factor: RARG; motif: RAGGTCAASYARAGGTCA	TF:M04485	4222	4.70E-05	69
GO:BP	negative regulation of apoptotic signaling pathway	GO:2001234	211	4.80E-05	13
GO:BP	regulation of cytokine production	GO:0001817	646	4.90E-05	22
TF	Factor: Nfe2l1; motif: TGYNNAGTCATT	TF:M07390	5626	5.10E-05	84
GO:BP	negative regulation of cellular protein metabolic process	GO:0032269	885	5.20E-05	26
TF	Factor: Tbx3; motif: NRAGGTGNNAR	TF:M10090	4322	5.20E-05	70
GO:BP	chemical homeostasis	GO:0048878	1078	5.30E-05	29
GO:BP	positive regulation of cell death	GO:0010942	539	5.40E-05	20
TF	Factor: Fli-1:E2A; motif: NCCGGAWRCASCTGN	TF:M08472	7411	5.50E-05	102
TF	Factor: ZNF383; motif: SSNGGGMGGNGSNGGS	TF:M12703	8544	5.50E-05	113
TF	Factor: E2F-4; motif: SNGGGCGGGAANN; match class: 1	TF:M09894_1	13166	5.50E-05	155
TF	Factor: RXRALPHA; motif: CNNTGRCCTYTNN	TF:M09833	4604	5.60E-05	73
TF	Factor: MLR1; motif: NTGNMCYYTGNNCYN	TF:M12637	3795	5.70E-05	64
TF	Factor: ZF5; motif: GGSGCGCGS; match class: 1	TF:M10438_1	13986	5.70E-05	162
GO:BP	lymphocyte activation	GO:0046649	652	5.80E-05	22
GO:BP	cytokine production	GO:0001816	652	5.80E-05	22
GO:BP	cellular cation homeostasis	GO:0030003	596	5.80E-05	21
GO:BP	chordate embryonic development	GO:0043009	596	5.80E-05	21

TF	Factor: Erm; motif: NRRSAGGAARNGRN; match class: 1	TF:M09916_1	1466	5.80E-05	35
GO:BP	cell chemotaxis	GO:0060326	255	6.00E-05	14
GO:BP	morphogenesis of an epithelium	GO:0002009	490	6.00E-05	19
TF	Factor: CREB1; motif: NNNNSSGGCGCSSNNNNRTGACGTCAC	TF:M12591	12377	6.00E-05	148
TF	Factor: Pax-6; motif: TTTCACGCWTGANTGMNYN	TF:M04065	9085	6.10E-05	118
TF	Factor: BTEB2; motif: RGGGNGKGGN	TF:M07277	8145	6.20E-05	109
TF	Factor: Nrf-2; motif: NTGCTGAGTCAKN	TF:M00821	3984	6.30E-05	66
TF	Factor: KLF15; motif: RCCMCRCCCMCN; match class: 1	TF:M12160_1	7532	6.30E-05	103
GO:MF	cytokine binding	GO:0019955	124	6.50E-05	10
TF	Factor: IRF-8; motif: NYGAAACYGAAACTN	TF:M11684	3986	6.50E-05	66
TF	Factor: E2F-2; motif: NWTTTGGCGCCAWWNN	TF:M11530	13542	6.50E-05	158
TF	Factor: IRF-8; motif: AGTTTCW	TF:M01665	3988	6.60E-05	66
TF	Factor: LRF; motif: NRGGGKCKY	TF:M10115	6932	6.60E-05	97
TF	Factor: SPI1; motif: AGGAAGT	TF:M02278	5850	6.60E-05	86
TF	Factor: Fli-1; motif: MGGAAGT	TF:M07382	5850	6.60E-05	86
TF	Factor: PEA3; motif: AGGAAGT	TF:M03579	5850	6.60E-05	86
TF	Factor: C-ets-1; motif: AGGAAGN	TF:M01870	5850	6.60E-05	86
GO:BP	response to peptide	GO:1901652	442	6.70E-05	18
TF	Factor: Six-2; motif: NCGTATCRNN	TF:M11031	7846	6.70E-05	106
GO:MF	molecular transducer activity	GO:0060089	1139	6.80E-05	29
GO:MF	signaling receptor activity	GO:0038023	1139	6.80E-05	29
TF	Factor: SRY; motif: TCAATAMCATTGA	TF:M04557	8365	6.80E-05	111
TF	Factor: SREBP-2; motif: NTCACCYNNNN	TF:M03852	7238	6.80E-05	100
TF	Factor: Ikaros; motif: TGGGAGN; match class: 1	TF:M07260_1	6245	6.90E-05	90
GO:BP	muscle system process	GO:0003012	394	7.00E-05	17
GO:BP	immune system development	GO:0002520	899	7.00E-05	26

TF	Factor: AP-2beta; motif: GCNNNGGSCNGVGGGN	TF:M01858	7042	7.10E-05	98
TF	Factor: MafA; motif: GGTCAGCAGH	TF:M03796	2710	7.20E-05	51
GO:BP	positive regulation of cell migration	GO:0030335	496	7.30E-05	19
TF	Factor: E2F-1; motif: NNNNGGCGGGAARN	TF:M09892	12641	7.40E-05	150
TF	Factor: E2F-3; motif: NTTTTGGCGCCAAAAN	TF:M11527	6161	7.70E-05	89
TF	Factor: ZNF333; motif: ATAAT; match class: 1	TF:M01230_1	9656	7.80E-05	123
TF	Factor: RXR:RAR; motif: RGKTCANNNRGAGGTCA	TF:M02272	5486	7.80E-05	82
GO:BP	negative regulation of catalytic activity	GO:0043086	607	7.90E-05	21
KEGG	Protein digestion and absorption	KEGG:04974	92	8.00E-05	8
TF	Factor: Spz1; motif: DNNGGRGGGWWNNNN; match class: 1	TF:M00446_1	2638	8.10E-05	50
GO:BP	ion homeostasis	GO:0050801	723	8.20E-05	23
GO:BP	transforming growth factor beta receptor signaling pathway	GO:0007179	183	8.40E-05	12
TF	Factor: c-Jun; motif: NATGACGTCAYN	TF:M11266	7368	8.40E-05	101
TF	Factor: CEBPD; motif: NNTTGCACAAYNN	TF:M12567	1780	8.40E-05	39
GO:BP	regulation of biosynthetic process	GO:0009889	3706	8.50E-05	62
GO:BP	hematopoietic or lymphoid organ development	GO:0048534	846	8.60E-05	25
TF	Factor: BRN1; motif: HAATGCN; match class: 1	TF:M03813_1	5787	8.70E-05	85
TF	Factor: Erm; motif: RSAGGAAGGAAGTN	TF:M11423	4288	8.80E-05	69
TF	Factor: HELIOS; motif: RNARRRGGAASTGARAN	TF:M09745	2894	9.00E-05	53
TF	Factor: IRF-4; motif: NYGAAASYGAAACYN	TF:M11686	2895	9.10E-05	53
GO:BP	negative regulation of signal transduction	GO:0009968	1173	9.20E-05	30
TF	Factor: pax-6; motif: NYACGCWTSANYGMNCN	TF:M11880	11884	9.20E-05	143
TF	Factor: p53; motif: RGRCWWGYCYNGRCWWGYYY	TF:M01652	7281	9.30E-05	100
TF	Factor: ARP-1; motif: TGARCCYTTGAMCCCW	TF:M00155	4662	9.40E-05	73
TF	Factor: MIBP1; motif: WNWCCCCAGCTR	TF:M03878	2488	9.40E-05	48
TF	Factor: Oct-1; motif: MKVATTTGCATATT	TF:M00161	2408	9.50E-05	47

TF	Factor: Sox-10; motif: NACAAWG; match class: 1	TF:M02116_1	6582	9.50E-05	93
GO:BP	embryo development ending in birth or egg hatching	GO:0009792	614	9.60E-05	21
TF	Factor: CTF/NF1; motif: TTGGCN; match class: 1	TF:M02050_1	3413	9.90E-05	59
TF	Factor: FOXP3; motif: NNNVAAACANWD	TF:M07419	5230	9.90E-05	79
TF	Factor: HMX2; motif: SCACTTANC	TF:M10646	6195	1.00E-04	89
GO:MF	interleukin-1 receptor activity	GO:0004908	7	1.10E-04	4
TF	Factor: E2F; motif: TTTSGCGS	TF:M00426	11014	1.10E-04	135
TF	Factor: TCF-1; motif: ACATCGRGRCGCTGW	TF:M11601	13629	1.10E-04	158
TF	Factor: E2F-1; motif: WWTGGCGCCAAA	TF:M04515	12480	1.10E-04	148
GO:BP	response to oxidative stress	GO:0006979	409	1.20E-04	17
GO:BP	mesangial cell development	GO:0072143	6	1.20E-04	4
REAC	Scavenging by Class A Receptors	REAC:R-HSA-3000480	18	1.20E-04	5
TF	Factor: Pax-8; motif: NCNNTNNTGCRTGANNNN	TF:M00328	8029	1.20E-04	107
TF	Factor: FXR; motif: NRGGKCANTGRCCNNNNGG	TF:M10014	5159	1.20E-04	78
TF	Factor: Oct-2; motif: NYATGCAAATN	TF:M10034	5065	1.20E-04	77
TF	Factor: ZBTB49; motif: NGSCGCTGTCCNNGGTGCTGAN	TF:M12692	1957	1.20E-04	41
REAC	Erythrocytes take up oxygen and release carbon dioxide	REAC:R-HSA-1247673	8	1.30E-04	4
TF	Factor: E2F-1:Elk-1; motif: SGCGCSNNAMCGGAAGT	TF:M08205	13426	1.30E-04	156
TF	Factor: Pax-5; motif: BCNNNRNGCANBGNTGNRTAGCSGCHNB; match class: 1	TF:M00143_1	4608	1.30E-04	72
TF	Factor: PPARGAMMA; motif: NWNTRGGTYANN	TF:M08961	4518	1.30E-04	71
GO:BP	positive regulation of cell motility	GO:2000147	516	1.40E-04	19
GO:BP	muscle contraction	GO:0006936	317	1.40E-04	15
GO:BP	regulation of protein metabolic process	GO:0051246	2316	1.40E-04	45
GO:CC	supramolecular fiber	GO:0099512	826	1.40E-04	23
TF	Factor: NF-1B; motif: KCCAGANWN	TF:M08825	4990	1.40E-04	76
TF	Factor: RelB:p50; motif: RGAAANTCCCYNNHGC	TF:M03882	3891	1.40E-04	64
TF	Factor: E2F-2; motif: NTTTTGGCGCCAWWWN	TF:M11528	9539	1.40E-04	121
GO:BP	cellular response to transforming growth factor beta stimulus	GO:0071560	232	1.50E-04	13
GO:BP	leukocyte chemotaxis	GO:0030595	193	1.50E-04	12
GO:BP	granulocyte migration	GO:0097530	123	1.50E-04	10
GO:BP	epithelial cell differentiation involved in kidney development	GO:0035850	45	1.50E-04	7
KEGG	Complement and coagulation cascades	KEGG:04610	70	1.50E-04	7
TF	Factor: Sp2; motif: GGGGCGGGG	TF:M10435	7447	1.50E-04	101
TF	Factor: TF3C-beta; motif: CCNGGAGGGCTTCCTGGAGGAG; match class: 1	TF:M04863_1	7966	1.50E-04	106
TF	Factor: Fli-1:HOXB13; motif: NNCGGAARYNRTWAA	TF:M08471	4441	1.50E-04	70
TF	Factor: NF-1; motif: NTGGNNNNNNGCCAANN	TF:M00806	3720	1.50E-04	62
TF	Factor: PU.1; motif: NRAAAGAGGAAGTGARA	TF:M09659	2208	1.50E-04	44
TF	Factor: AP-2gamma; motif: NSCCYNNRGSN	TF:M11482	6252	1.50E-04	89
TF	Factor: ehf; motif: NRANNAGGAARNRRNNN	TF:M09604	1976	1.60E-04	41
TF	Factor: HOXB5; motif: GTCATTAN	TF:M10701	4817	1.60E-04	74
TF	Factor: PEA3; motif: NTCGTAAATGCA	TF:M11431	9024	1.60E-04	116
TF	Factor: AR; motif: NNNGNRRGNACANNGTGTTCTNNNNNN	TF:M00953	1978	1.60E-04	41
TF	Factor: Olf-1; motif: NNCDABTCCCYAGRGARBNKGN	TF:M00261	3203	1.60E-04	56
TF	Factor: MAZ; motif: GGGGAGGG; match class: 1	TF:M00649_1	3905	1.60E-04	64
TF	Factor: SREBP-1; motif: KATCACCCCAC	TF:M00221	6557	1.60E-04	92
MIRNA	hsa-miR-29a-3p	MIRNA:hsa-miR-29a-3p	256	1.60E-04	13
TF	Factor: C/EBPgamma:Elf-1; motif: TKRCGHAATWSCGGAAGT	TF:M08676	7465	1.70E-04	101
TF	Factor: NF-KAPPAB1; motif: NGGKRNTTYCCCN; match class: 1	TF:M08952_1	3120	1.70E-04	55
TF	Factor: TFII-I; motif: RGAGGKAGG; match class: 1	TF:M00706_1	1461	1.70E-04	34
TF	Factor: ESR1; motif: NNNNMAGGTCACCCTGACCY	TF:M02261	4090	1.70E-04	66

TF	Factor: AP-2gamma; motif: GCCYNCRGSN; match class: 1	TF:M03811_1	3646	1.80E-04	61
TF	Factor: POU2F1; motif: ATTTGCATN	TF:M07058	2707	1.80E-04	50
GO:MF	integrin binding	GO:0005178	139	1.90E-04	10
GO:BP	regulation of intrinsic apoptotic signaling pathway	GO:2001242	160	1.90E-04	11
GO:BP	negative regulation of protein metabolic process	GO:0051248	947	1.90E-04	26
TF	Factor: CTF1; motif: TGGCASCNNGCCAA; match class: 1	TF:M01196_1	1324	1.90E-04	32
TF	Factor: ER-beta; motif: RGGTCASCNTGMCCY; match class: 1	TF:M09910_1	3740	1.90E-04	62
TF	Factor: C/EBPbeta; motif: RTTGCGCAA; match class: 1	TF:M04690_1	3216	1.90E-04	56
TF	Factor: Gli2; motif: GACCACCCANG	TF:M01703	3303	1.90E-04	57
TF	Factor: Sp1; motif: NGGGGGCGGGGCCNGGGGGGGG	TF:M10071	8206	1.90E-04	108
TF	Factor: znf136; motif: CAAGAATWCTATAYCCAG	TF:M10535	6878	1.90E-04	95
GO:BP	epithelial cell apoptotic process	GO:1904019	96	2.00E-04	9
GO:BP	positive regulation of cellular component movement	GO:0051272	529	2.00E-04	19
GO:BP	positive regulation of locomotion	GO:0040017	530	2.00E-04	19
REAC	Signaling by Receptor Tyrosine Kinases	REAC:R-HSA-9006934	472	2.00E-04	17
TF	Factor: TEF-1; motif: GRRATG; match class: 1	TF:M00704_1	4564	2.00E-04	71
GO:BP	kidney development	GO:0001822	282	2.10E-04	14
GO:BP	pattern specification process	GO:0007389	376	2.10E-04	16
TF	Factor: Lhx8; motif: TGATTG	TF:M07476	7600	2.10E-04	102
TF	Factor: Freac-7; motif: WNNANATAAAYANNNN	TF:M00293	3753	2.10E-04	62
TF	Factor: C/EBPalpha; motif: NRTTGTGCAAYN	TF:M09880	2890	2.20E-04	52
TF	Factor: Dlx-5; motif: AATTAN	TF:M03546	9177	2.20E-04	117
TF	Factor: DRI1; motif: AATTAA	TF:M01654	9177	2.20E-04	117
TF	Factor: AP-2; motif: SNNNCCNCAGGCN; match class: 1	TF:M00915_1	4390	2.20E-04	69
TF	Factor: AHR; motif: CACGCN	TF:M01855	7712	2.20E-04	103

TF	Factor: nerf; motif: YRNCAGGAAGYRGSTBDS; match class: 1	TF:M00531_1	1624	2.30E-04	36
TF	Factor: CRX; motif: YTAATC; match class: 1	TF:M01712_1	4120	2.30E-04	66
TF	Factor: AR; motif: AGWACATNWTGTTCT	TF:M00447	3496	2.30E-04	59
TF	Factor: C-FOS; motif: NNNKATGACGTCATNNN	TF:M08947	5921	2.50E-04	85
TF	Factor: HOXA7; motif: GYMATTAN	TF:M10690	8983	2.50E-04	115
TF	Factor: TCF-1; motif: ACATCGRGRCGCTGW; match class: 1	TF:M11603_1	12396	2.50E-04	146
TF	Factor: HOXD4; motif: NNYMATTANN	TF:M08774	3332	2.50E-04	57
GO:BP	neutrophil migration	GO:1990266	99	2.60E-04	9
TF	Factor: Sox-10; motif: CWTTGT; match class: 1	TF:M03138_1	5442	2.60E-04	80
TF	Factor: TCF-1; motif: CTTTGW; match class: 1	TF:M03857_1	5442	2.60E-04	80
TF	Factor: C/EBPgamma; motif: YTBATTTCARAAW	TF:M00622	5635	2.60E-04	82
TF	Factor: Elf-1; motif: RNWMBAGGAART	TF:M00746	2905	2.60E-04	52
TF	Factor: E2F-1; motif: TTTGGCGCCAAA	TF:M04516	10723	2.60E-04	131
TF	Factor: LRF; motif: NGNAGNGGGTYN	TF:M04617	5639	2.60E-04	82
GO:CC	non-membrane-bounded organelle	GO:0043228	4977	2.70E-04	72
GO:CC	intracellular non-membrane-bounded organelle	GO:0043232	4977	2.70E-04	72
TF	Factor: MAF; motif: GCTGAGTCAN	TF:M07296	4877	2.70E-04	74
TF	Factor: BTEB1; motif: GGGGGCGGGGCNGSGGGNGS	TF:M09723	9530	2.70E-04	120
TF	Factor: FOXM1; motif: NAGASTGATTA	TF:M04611	7843	2.70E-04	104
TF	Factor: AR; motif: GNNCNNNNTGTTCTN	TF:M01996	2495	2.70E-04	47
GO:BP	regulation of cell activation	GO:0050865	541	2.80E-04	19
GO:BP	granulocyte chemotaxis	GO:0071621	100	2.80E-04	9
TF	Factor: RBPJK; motif: SYGTGRGAANN	TF:M09665	3871	2.80E-04	63
TF	Factor: B-ATF; motif: NNATGACACN	TF:M11300	7440	2.80E-04	100
TF	Factor: Rarb; motif: AGGTCANNYARAGGTCA	TF:M08035	4979	2.80E-04	75
GO:BP	mesangial cell differentiation	GO:0072007	7	2.90E-04	4

KEGG	IL-17 signaling pathway	KEGG:04657	77	2.90E-04	7
TF	Factor: NKX25; motif: NNANCCACTTRAAWTT	TF:M01414	8271	2.90E-04	108
TF	Factor: RREB-1; motif: CCCCAAACMMCCCC; match class: 1	TF:M00257_1	4057	2.90E-04	65
TF	Factor: NF-kappaB; motif: GGGAMTTYCC	TF:M00054	2179	2.90E-04	43
GO:BP	regulation of epithelial cell apoptotic process	GO:1904035	73	3.00E-04	8
TF	Factor: LBX2; motif: CTNRANSTAATTA	TF:M04383	6738	3.00E-04	93
TF	Factor: AR; motif: NGNACANNNTGTTCYNN; match class: 1	TF:M09589_1	945	3.00E-04	26
GO:BP	metal ion homeostasis	GO:0055065	601	3.10E-04	20
GO:BP	defense response to other organism	GO:0098542	842	3.10E-04	24
TF	Factor: E2F-3; motif: NTTTTGGCGCCAAAAN; match class: 1	TF:M11527_1	5953	3.10E-04	85
GO:BP	organonitrogen compound metabolic process	GO:1901564	5820	3.20E-04	83
GO:BP	nephron development	GO:0072006	133	3.20E-04	10
TF	Factor: Tbx3; motif: NAGGTGTSAN	TF:M12024	3800	3.30E-04	62
TF	Factor: NKX2-2; motif: NNNCCACTCAANNN; match class: 1	TF:M12456_1	2512	3.30E-04	47
GO:BP	supramolecular fiber organization	GO:0097435	722	3.40E-04	22
TF	Factor: GKLF; motif: GCCMCRCCCNNN	TF:M01588	8294	3.40E-04	108
TF	Factor: RXRA; motif: RRGGTCATGACCYY; match class: 1	TF:M04490_1	3016	3.40E-04	53
TF	Factor: E2F-2; motif: NWTTTGGCGCCAWWNN; match class: 1	TF:M11530_1	12570	3.50E-04	147
TF	Factor: TGIF; motif: TGACAGS	TF:M10101	4444	3.50E-04	69
TF	Factor: ZNF394; motif: NRARWRGAANNNAMWGNAAK	TF:M10147	4537	3.50E-04	70
TF	Factor: GLI; motif: NGACCMCCCAN; match class: 1	TF:M07290_1	1730	3.60E-04	37
TF	Factor: EGR3; motif: NCMCRCCCACTNMN	TF:M08877	5486	3.60E-04	80
TF	Factor: WT1; motif: NNGGGNGGGSGN	TF:M07436	6072	3.70E-04	86
TF	Factor: CTCF; motif: NNYGCCCYCTRSTGGN	TF:M09744	3458	3.70E-04	58
TF	Factor: AP-4; motif: NCAGCTGYNGNCN	TF:M01860	5298	3.70E-04	78
TF	Factor: PPARalpha; motif: NWSTRGGNSAAAGGTCA	TF:M10037	5298	3.70E-04	78
GO:BP	mesenchyme morphogenesis	GO:0072132	51	3.80E-04	7
TF	Factor: EVX1; motif: NTCATTAN	TF:M10864	4360	3.80E-04	68
TF	Factor: SNA; motif: NNRGCAGGTGCNNNN	TF:M10528	3905	3.80E-04	63
TF	Factor: T3R-beta; motif: NRGGTCAAAGGTCRN; match class: 1	TF:M11814_1	6374	3.80E-04	89
TF	Factor: Pax-3; motif: NNNNNNCGTCACGSTYNNNNN	TF:M00327	11907	3.80E-04	141
GO:MF	cytokine receptor activity	GO:0004896	85	3.90E-04	8
GO:BP	cellular divalent inorganic cation homeostasis	GO:0072503	444	3.90E-04	17
TF	Factor: ZXDA; motif: NGGGGTC	TF:M06190	5303	3.90E-04	78
TF	Factor: ZXDB; motif: NGGGGTC	TF:M06191	5303	3.90E-04	78
KEGG	ECM-receptor interaction	KEGG:04512	81	4.00E-04	7
TF	Factor: ER-beta; motif: NRGGTCANKSTGACCTNN; match class: 1	TF:M09610_1	1369	4.00E-04	32
TF	Factor: NF-E4; motif: GTGAGGS; match class: 1	TF:M08826_1	4182	4.00E-04	66
TF	Factor: Oct-1; motif: TATGCAAATN	TF:M00342	2446	4.00E-04	46
TF	Factor: ZNF563; motif: NGNNTCMTNNCNGGCAGCTGY	TF:M10158	5212	4.00E-04	77
TF	Factor: HEY1; motif: NYYYYATCTNN	TF:M12614	4742	4.10E-04	72
TF	Factor: EAR2; motif: YGNNCTTTGNCCTK	TF:M01728	5407	4.10E-04	79
GO:BP	cation homeostasis	GO:0055080	671	4.20E-04	21
TF	Factor: C/EBPbeta; motif: NNTTKCNNMAN	TF:M07315	2449	4.20E-04	46
TF	Factor: Elk-1:ETV7; motif: ANSCGGACGGATDTCCGGNT	TF:M08214	7191	4.20E-04	97
GO:BP	macromolecule metabolic process	GO:0043170	9254	4.30E-04	116
GO:BP	positive regulation of cellular biosynthetic process	GO:0031328	1776	4.30E-04	37
KEGG	African trypanosomiasis	KEGG:05143	31	4.30E-04	5
TF	Factor: C/EBPalpha; motif: NNNNNTTKCNNAAN	TF:M07037	2783	4.30E-04	50
GO:MF	cell adhesion molecule binding	GO:0050839	535	4.40E-04	18
GO:MF	molecular function regulator	GO:0098772	1692	4.40E-04	35

GO:BP	T cell activation	GO:0042110	448	4.40E-04	17
GO:BP	response to abiotic stimulus	GO:0009628	1055	4.40E-04	27
REAC	Interleukin-10 signaling	REAC:R-HSA-6783783	41	4.40E-04	6
TF	Factor: Pax-2; motif: NNNNGTCANGNRTKANNNN	TF:M00098	6494	4.40E-04	90
TF	Factor: LXR; motif: NTGACCKNNAGTRACCYNN	TF:M03795	5609	4.40E-04	81
TF	Factor: SF-1; motif: NYYCAAGGYCA	TF:M10084	3390	4.50E-04	57
TF	Factor: MAFB; motif: NTCAGCN; match class: 1	TF:M08888_1	2789	4.60E-04	50
TF	Factor: AP-2beta; motif: NSCCYNRGGSN	TF:M11477	7511	4.60E-04	100
TF	Factor: NF1B; motif: CYTGGCNYNCWGCCAN; match class: 1	TF:M09762_1	1309	4.70E-04	31
TF	Factor: P53; motif: NNNGRCATGCCCAGRCATGYCY	TF:M12647	5044	4.80E-04	75
TF	Factor: PPARgamma:RXRalpha, motif: AAGTAGGTCACNGTGACCYACTT; match class: 1	TF:M00515_1	3841	4.80E-04	62
TF	Factor: Sp1; motif: RGGGMGGRGSNGGGG	TF:M10529	6507	4.80E-04	90
TF	Factor: Octamer; motif: TNATTTGCATN	TF:M00795	3752	4.90E-04	61
TF	Factor: Fra-1; motif: NATGAWTCAYN	TF:M11286	2546	4.90E-04	47
TF	Factor: MafG; motif: CMATGACTCAGCAGA	TF:M07048	5916	4.90E-04	84
KEGG	Proteoglycans in cancer	KEGG:05205	197	5.00E-04	10
TF	Factor: E2F3; motif: NNRGMKGGAR; match class: 1	TF:M12598_1	6610	5.00E-04	91
TF	Factor: c-MAF; motif: CNNNCTCAGCA	TF:M03816	4956	5.10E-04	74
TF	Factor: WT1; motif: NGCGGGGGGGTSMMCYN	TF:M05327	5338	5.10E-04	78
TF	Factor: RelA-p65; motif: GGGRNTTTCCM	TF:M09668	3228	5.10E-04	55
TF	Factor: Sp1; motif: NGGGGGCGGGGYN	TF:M00196	9855	5.20E-04	122
TF	Factor: SAP-1a; motif: CWTCCKGT	TF:M03844	2306	5.20E-04	44
TF	Factor: ER71; motif: CWTCCTGT	TF:M07282	2306	5.20E-04	44
GO:BP	regulation of immune response	GO:0050776	741	5.30E-04	22
GO:BP	negative regulation of cell communication	GO:0010648	1273	5.30E-04	30
TF	Factor: IRF-4; motif: AAGTTTC; match class: 1	TF:M04855_1	1681	5.30E-04	36
TF	Factor: Six-1; motif: CTCARRTTWCN	TF:M07466	2887	5.30E-04	51
TF	Factor: JunD; motif: NRTGACGTCATS	TF:M11270	7948	5.30E-04	104
TF	Factor: GCMa:C/EBPbeta; motif: ATGCGGGTNNRTTGCGCAAY	TF:M08575	5928	5.40E-04	84
GO:BP	inorganic ion homeostasis	GO:0098771	682	5.50E-04	21
GO:BP	negative regulation of signaling	GO:0023057	1275	5.50E-04	30
GO:BP	neutrophil chemotaxis	GO:0030593	79	5.60E-04	8
GO:BP	cell differentiation involved in kidney development	GO:0061005	54	5.60E-04	7
TF	Factor: ER-beta; motif: ANNSTGACCYRGNN	TF:M03821	5542	5.60E-04	80
TF	Factor: HFH8; motif: NNNTGTTTATNTR	TF:M00294	2978	5.60E-04	52
TF	Factor: AP-2alpha; motif: NSCCNCRGGSN	TF:M07348	7543	5.60E-04	100
TF	Factor: RARA; motif: AGGTCANNYAAAGGTCA	TF:M08019	4689	5.80E-04	71
TF	Factor: Sp1; motif: GGGGCGGGGC	TF:M00931	9875	5.80E-04	122
GO:MF	identical protein binding	GO:0042802	1948	5.90E-04	38
GO:BP	cartilage development	GO:0051216	179	5.90E-04	11
GO:BP	regulation of DNA-binding transcription factor activity	GO:0051090	406	6.00E-04	16
GO:BP	immune effector process	GO:0002252	513	6.10E-04	18
GO:CC	fibrillar collagen trimer	GO:0005583	12	6.20E-04	4
GO:CC	banded collagen fibril	GO:0098643	12	6.20E-04	4
TF	Factor: COUP-TF1; motif: RAGGTCANTGACCTY	TF:M11745	5556	6.20E-04	80
GO:CC	ficolin-1-rich granule	GO:0101002	175	6.30E-04	10
TF	Factor: Nkx2-3; motif: NNCGTTRWS	TF:M10638	9672	6.30E-04	120
TF	Factor: IRF-8; motif: NYGAAASYGAAACYN	TF:M11682	3251	6.50E-04	55
GO:BP	positive regulation of biosynthetic process	GO:0009891	1807	6.60E-04	37
TF	Factor: En-2; motif: NTCRTTARN	TF:M10858	7670	6.60E-04	101
GO:BP	divalent inorganic cation homeostasis	GO:0072507	462	6.70E-04	17

GO:BP	hemopoiesis	GO:0030097	815	6.80E-04	23
TF	Factor: POU3F2; motif: NTATGCWAATKAG	TF:M11909	4151	6.80E-04	65
TF	Factor: SMAD; motif: TNGNCAGACWN	TF:M00974	3788	6.80E-04	61
TF	Factor: AP-2gamma; motif: NNNNWGCCYNCRGSCN	TF:M07349	2998	6.90E-04	52
TF	Factor: TR4; motif: NCCCTGACCYB	TF:M08906	3971	6.90E-04	63
TF	Factor: TWIST; motif: CACCTGG; match class: 1	TF:M03582_1	2249	7.00E-04	43
TF	Factor: GR; motif: RGNACANMNTGTNCY; match class: 1	TF:M09941_1	1701	7.00E-04	36
KEGG	Relaxin signaling pathway	KEGG:04926	123	7.10E-04	8
TF	Factor: Churchill; motif: CGGGNN; match class: 1	TF:M00986_1	9909	7.10E-04	122
TF	Factor: SMAD5; motif: GSGGCAGM; match class: 1	TF:M03846_1	2251	7.20E-04	43
TF	Factor: HES-5; motif: NCACACKY; match class: 1	TF:M11069_1	3616	7.30E-04	59
TF	Factor: NFATc1; motif: NTTTCCRTNNAYGGAAAN	TF:M11979	7686	7.30E-04	101
GO:BP	regulation of epithelial cell proliferation	GO:0050678	313	7.40E-04	14
TF	Factor: NF-1C; motif: NYTGGCNNYNNGCCARN; match class: 1	TF:M10002_1	1481	7.40E-04	33
TF	Factor: RUNX3; motif: NRACCGCANWAACCRCAN	TF:M04110	8526	7.50E-04	109
TF	Factor: STAT3; motif: NNYTTCCMRGAA	TF:M10081	3093	7.60E-04	53
GO:BP	cellular response to chemical stress	GO:0062197	314	7.70E-04	14
TF	Factor: PR; motif: NNNNNNRGNACNNKNTGTTCTNNNNNN	TF:M00957	3356	7.70E-04	56
TF	Factor: NF-kappaB; motif: NGGGANTTYCCMNNNN	TF:M00774	1632	7.70E-04	35
GO:BP	muscle cell proliferation	GO:0033002	184	7.80E-04	11
TF	Factor: TBP; motif: NGNNTATAAAA	TF:M03581	5782	7.80E-04	82
TF	Factor: E2F-1; motif: NTTSGCGG	TF:M00430	7491	7.90E-04	99
TF	Factor: RelA-p65; motif: AAATCCCCT	TF:M04814	3986	7.90E-04	63
TF	Factor: TCF-3; motif: CTTTGA; match class: 1	TF:M03858_1	4541	8.00E-04	69
TF	Factor: TCF-7; motif: TCAAAG; match class: 1	TF:M00805_1	4541	8.00E-04	69
TF	Factor: Egr; motif: GTGGGSGCRRS	TF:M00807	4079	8.00E-04	64
TF	Factor: Sp1; motif: CCCCGCCCCN	TF:M00933	9282	8.10E-04	116
TF	Factor: Erm:E2A; motif: CASGTGNNNCGGAAGNN; match class: 1	TF:M08571_1	3898	8.10E-04	62
GO:BP	regulation of heart contraction	GO:0008016	185	8.20E-04	11
TF	Factor: C/EBP; motif: NNNTKNNGNAAN	TF:M00770	4639	8.30E-04	70
TF	Factor: NF-kappaB; motif: NGGGGAMTTTCCNN	TF:M00194	2103	8.30E-04	41
TF	Factor: E2F-4; motif: NNTTCCCGCCNN	TF:M04823	11934	8.30E-04	140
REAC	Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	REAC:R-HSA-198933	101	8.40E-04	8
TF	Factor: AP-2beta; motif: NSCCNNNGGSN; match class: 1	TF:M11478_1	7500	8.40E-04	99
TF	Factor: Sox-6; motif: NARACAAAARN	TF:M03888	2932	8.50E-04	51
TF	Factor: ctcf; motif: YGGCCACCAGRKGGCRSYN	TF:M09890	7814	8.60E-04	102
GO:MF	anion transmembrane transporter activity	GO:0008509	294	8.70E-04	13
GO:BP	regulation of wound healing	GO:0061041	114	8.70E-04	9
REAC	Syndecan interactions	REAC:R-HSA-3000170	26	8.70E-04	5
TF	Factor: GCMa; motif: RTGCGGGTN; match class: 1	TF:M11595_1	5310	8.70E-04	77
TF	Factor: ATF3; motif: CBCTGACGTCANCS	TF:M00513	5504	8.70E-04	79
REAC	Erythrocytes take up carbon dioxide and release oxygen	REAC:R-HSA-1237044	12	8.80E-04	4
REAC	O2/CO2 exchange in erythrocytes	REAC:R-HSA-1480926	12	8.80E-04	4
TF	Factor: MEF-2C; motif: TATTTWT	TF:M02025	10824	8.80E-04	130
TF	Factor: ZNF692; motif: SYNGGSCCCASCCNC; match class: 1	TF:M09734_1	5798	8.80E-04	82
TF	Factor: Sp3; motif: GGGGCGGGGSNN	TF:M07615	6593	8.90E-04	90
TF	Factor: SP1; motif: GGCCCCGCCCCCN	TF:M12666	8342	8.90E-04	107
GO:BP	regulation of macromolecule biosynthetic process	GO:0010556	3510	9.00E-04	57
TF	Factor: Pbx; motif: NKTGATTGACRKSN	TF:M01967	4369	9.00E-04	67

TF	Factor: CDP:SRF; motif: NCCWTAYAAGGTMNKRATCRATN; match class: 1	TF:M08520_1	3199	9.10E-04	54
GO:BP	negative regulation of cell differentiation	GO:0045596	585	9.20E-04	19
TF	Factor: E2F-4; motif: TTTGGCGCCAAA	TF:M04519	4279	9.20E-04	66
TF	Factor: SP2; motif: GNNGGGGGCGGGGSN	TF:M03807	8142	9.50E-04	105
TF	Factor: STAT3; motif: TTCYGGGAAN	TF:M07065	4283	9.50E-04	66
TF	Factor: NR1B1:RXR-ALPHA; motif: RRGGTCANNNNNRGGTCA	TF:M08964	6106	9.60E-04	85
TF	Factor: RELA; motif: GGGRMTKYCCC; match class: 1	TF:M12657_1	1353	9.70E-04	31
GO:MF	transmembrane signaling receptor activity	GO:0004888	947	1.00E-03	24
GO:BP	cellular response to organic cyclic compound	GO:0071407	531	1.00E-03	18
GO:BP	heart morphogenesis	GO:0003007	230	1.00E-03	12
GO:BP	skeletal system morphogenesis	GO:0048705	189	1.00E-03	11
GO:BP	pericyte cell differentiation	GO:1904238	9	1.00E-03	4
GO:BP	glomerulus development	GO:0032835	59	1.00E-03	7
TF	Factor: COUP-TF1; motif: GRGGKSARAGGTCAGNG	TF:M09886	4855	1.00E-03	72
TF	Factor: E2F-1; motif: NNNNGGCGGGAARN; match class: 1	TF:M09892_1	8790	1.00E-03	111
TF	Factor: NURR1:RXR-ALPHA; motif: NRGGTCRTTGACCYN; match class: 1	TF:M08957_1	4480	1.00E-03	68
TF	Factor: AP-2alpha; motif: NGCCYSNNGSN; match class: 1	TF:M01857_1	4480	1.00E-03	68
TF	Factor: Sp1; motif: NNGGGGCGGGGNN	TF:M00932	9977	1.10E-03	122
TF	Factor: CTCF; motif: ACCAGGKGGC; match class: 1	TF:M04727_1	1359	1.10E-03	31
TF	Factor: C/EBPbeta; motif: NKNTTGCNYAAYNN	TF:M00117	3480	1.10E-03	57
TF	Factor: NFATc1; motif: NTTTCCRTNNAYGGAAAN; match class: 1	TF:M11979_1	7539	1.10E-03	99
TF	Factor: CPBP; motif: GNNRGGGHGGGGNNGGGRN; match class: 1	TF:M09973_1	6323	1.10E-03	87
TF	Factor: POU2F1; motif: ATGCAAATN	TF:M07059	1361	1.10E-03	31
TF	Factor: GATA-1; motif: NTGNNNNNNNSAGATAAGR	TF:M09621	4581	1.10E-03	69
TF	Factor: Pax-6; motif: NNNNTTCACGCWTGANTKNNN	TF:M00097	9552	1.10E-03	118
TF	Factor: Erg; motif: NACCGGATATCCGGTN; match class: 1	TF:M11391_1	8275	1.10E-03	106
GO:BP	cardiac chamber development	GO:0003205	153	1.20E-03	10
GO:BP	chemotaxis	GO:0006935	538	1.20E-03	18
GO:BP	cochlea morphogenesis	GO:0090103	21	1.20E-03	5
GO:CC	cell surface	GO:0009986	741	1.20E-03	20
KEGG	Fluid shear stress and atherosclerosis	KEGG:05418	132	1.20E-03	8
TF	Factor: CP2/LBP-1c/LSF; motif: GCTGGNTNGNNCYNG; match class: 1	TF:M00947_1	2373	1.20E-03	44
TF	Factor: HIC1; motif: NNNGGKTGCCCSNNNNNN	TF:M01073	3847	1.20E-03	61
TF	Factor: Pax-5; motif: NGTCACGCWTSANTGMNY	TF:M04064	9027	1.20E-03	113
TF	Factor: E2F; motif: TTTCGCGC	TF:M00425	10329	1.20E-03	125
TF	Factor: CLOCK; motif: NNCAYGYGYN	TF:M11046	2134	1.20E-03	41
TF	Factor: IRF-4; motif: GAAARTA	TF:M01883	6944	1.20E-03	93
TF	Factor: Dlx-5; motif: NTCRTTAN	TF:M10612	6843	1.20E-03	92
TF	Factor: Dlx-7; motif: NTCRTTAN	TF:M10603	6843	1.20E-03	92
TF	Factor: TIEG1; motif: NCCCNSNCCCCGCCCCC; match class: 1	TF:M12351_1	7871	1.20E-03	102
GO:BP	ureteric bud development	GO:0001657	88	1.30E-03	8
GO:BP	cellular response to peptide	GO:1901653	329	1.30E-03	14
GO:BP	taxis	GO:0042330	542	1.30E-03	18
GO:BP	regulation of RNA biosynthetic process	GO:2001141	3024	1.30E-03	51
GO:CC	supramolecular complex	GO:0099080	1157	1.30E-03	26
REAC	Muscle contraction	REAC:R-HSA-397014	183	1.30E-03	10
TF	Factor: ETS1; motif: GCCGGAWGTACTTCCGGN	TF:M03978	11000	1.30E-03	131
TF	Factor: pax-2; motif: NCGTCACGCNYSRNYGCNYN	TF:M11877	10450	1.30E-03	126
TF	Factor: KLF3; motif: NNNNNNGGGCGGGGCNNGN	TF:M09970	7465	1.30E-03	98
GO:BP	cardiac muscle tissue development	GO:0048738	195	1.40E-03	11
GO:BP	mesonephric tubule development	GO:0072164	89	1.40E-03	8

GO:BP	mesonephric epithelium development	GO:0072163	89	1.40E-03	8
GO:BP	regulation of proteolysis	GO:0030162	662	1.40E-03	20
GO:CC	endoplasmic reticulum	GO:0005783	1854	1.40E-03	35
GO:CC	tertiary granule	GO:0070820	151	1.40E-03	9
TF	Factor: CEBPD; motif: RTTRCGCAAY	TF:M04202	4325	1.40E-03	66
TF	Factor: IRF-2; motif: NGAAASYGAAAS	TF:M11665	2063	1.40E-03	40
TF	Factor: Ik-2; motif: NNNTGGGAWNNC	TF:M00087	3067	1.40E-03	52
GO:BP	transmembrane receptor protein serine/threonine kinase signaling pathway	GO:0007178	333	1.50E-03	14
TF	Factor: CTCF; motif: WGCGCCMYCTAGYGGYN	TF:M03895	8633	1.50E-03	109
TF	Factor: STAT3; motif: NTTCCYGGAAN	TF:M09664	4899	1.50E-03	72
TF	Factor: AP-2alpha; motif: NGCCTSAGGCN; match class: 1	TF:M11480_1	5380	1.50E-03	77
TF	Factor: BCL-6; motif: NYGCTTTCKAGGAANN	TF:M12341	5187	1.50E-03	75
TF	Factor: RUNX2; motif: NRACCGCAAACCGCAN; match class: 1	TF:M04106_1	7901	1.50E-03	102
TF	Factor: C/EBPdelta; motif: TKNNGCAATN	TF:M07316	2731	1.50E-03	48
TF	Factor: Smad2; motif: TGTCTGNCWCCT; match class: 1	TF:M10059_1	1029	1.50E-03	26
TF	Factor: TEF-1; motif: NRCATWCCN	TF:M12042	4433	1.50E-03	67
TF	Factor: ZNF432; motif: NCAGNRCCNSRGRCAGC; match class: 1	TF:M12704_1	4435	1.60E-03	67
TF	Factor: PEBP2beta; motif: TGTGGTY	TF:M03841	6476	1.60E-03	88
TF	Factor: PEA3; motif: ACAGGAAGGAAGTN	TF:M11429	4815	1.60E-03	71
TF	Factor: GR; motif: RGNACANKNTGTNCY; match class: 1	TF:M09625_1	3523	1.60E-03	57
TF	Factor: ctcf; motif: CCNCNAGRKGGCRSTN	TF:M07249	6280	1.60E-03	86
TF	Factor: DBP; motif: TTWTGYAA	TF:M01872	2158	1.60E-03	41
TF	Factor: TEF-3:Elf-1; motif: RGAATGCGGAAGTN	TF:M08415	8231	1.60E-03	105
TF	Factor: Smad4; motif: NCAGACAN; match class: 1	TF:M07368_1	423	1.60E-03	16
GO:BP	detoxification	GO:0098754	123	1.70E-03	9

GO:BP	ion transport	GO:0006811	1420	1.70E-03	31
GO:BP	regulation of defense response	GO:0031347	551	1.70E-03	18
GO:BP	reproductive structure development	GO:0048608	387	1.70E-03	15
TF	Factor: C/EBPbeta; motif: ATTGCGYAAT	TF:M07413	2826	1.70E-03	49
TF	Factor: TFAP2C; motif: NGCCCNNRGGCA; match class: 1	TF:M04152_1	5107	1.70E-03	74
TF	Factor: GKLF; motif: NNCCMCRCCCN	TF:M12173	9407	1.70E-03	116
TF	Factor: HSF1; motif: GAANNTTCTRGNAN	TF:M02017	3440	1.70E-03	56
TF	Factor: E2F-3; motif: GGCGGGN; match class: 1	TF:M02089_1	9086	1.70E-03	113
TF	Factor: AP-2alpha; motif: NGCCTSAGGCN	TF:M11480	5694	1.70E-03	80
TF	Factor: Oct-2; motif: NTATGCWAATN	TF:M11896	4354	1.70E-03	66
TF	Factor: ER-alpha; motif: AGGTCANMNTGACC	TF:M04738	3712	1.70E-03	59
TF	Factor: TGIF; motif: TGACAGS; match class: 1	TF:M10101_1	712	1.70E-03	21
GO:BP	gene expression	GO:0010467	6162	1.80E-03	84
GO:BP	leukocyte cell-cell adhesion	GO:0007159	338	1.80E-03	14
GO:BP	proteolysis	GO:0006508	1576	1.80E-03	33
REAC	Scavenging of heme from plasma	REAC:R-HSA-2168880	14	1.80E-03	4
TF	Factor: POU2F1; motif: NNATTTGCATNN	TF:M03561	1770	1.80E-03	36
TF	Factor: BTEB3; motif: CCNNSCCNSCCCCKCCCCC; match class: 1	TF:M09826_1	7207	1.80E-03	95
TF	Factor: GR; motif: RGWACATWAYGTWCY; match class: 1	TF:M11846_1	3358	1.80E-03	55
GO:BP	ear development	GO:0043583	201	1.90E-03	11
GO:BP	reproductive system development	GO:0061458	390	1.90E-03	15
GO:BP	negative regulation of epithelial cell apoptotic process	GO:1904036	41	1.90E-03	6
TF	Factor: PLAGL2; motif: AAGGACC	TF:M05548	3631	1.90E-03	58
TF	Factor: Pax-5; motif: GTYAYGCTTSRCTGVNYN	TF:M04754	4648	1.90E-03	69
TF	Factor: TBP; motif: MTATAAAARS	TF:M10088	3905	1.90E-03	61

GO:BP	mesonephros development	GO:0001823	93	2.00E-03	8
GO:BP	regulation of system process	GO:0044057	500	2.00E-03	17
GO:BP	glomerulus vasculature development	GO:0072012	23	2.00E-03	5
TF	Factor: Elk-1:Pax-9; motif: ACCGGAACYACGCWYSANTG	TF:M08226	10969	2.00E-03	130
TF	Factor: Sp1; motif: NGGGGGCGGGGYN; match class: 1	TF:M00196_1	5813	2.00E-03	81
TF	Factor: SREBP-1; motif: RTCACCCCAY	TF:M07405	5912	2.00E-03	82
TF	Factor: ZXDB; motif: NAGGGTG; match class: 1	TF:M06202_1	1701	2.00E-03	35
TF	Factor: ZXDA; motif: NAGGGTG; match class: 1	TF:M06203_1	1701	2.00E-03	35
TF	Factor: C/EBPbeta; motif: NATTGCRYAAYN	TF:M09597	2506	2.00E-03	45
TF	Factor: NR1B2; motif: RAGGTCATGACCTN	TF:M11803	2760	2.00E-03	48
GO:BP	regulation of catalytic activity	GO:0050790	2138	2.10E-03	40
TF	Factor: TTF-1; motif: NTKGAGTGSN	TF:M10007	3916	2.10E-03	61
TF	Factor: c-Jun; motif: NATGACGTCAYN; match class: 1	TF:M11266_1	5332	2.10E-03	76
GO:BP	RNA biosynthetic process	GO:0032774	3164	2.20E-03	52
TF	Factor: NR1B2; motif: NTGACCY; match class: 1	TF:M02111_1	2939	2.20E-03	50
TF	Factor: rfx3:SRF; motif: TRGCAACNNNNNCCNWATANGGN; match class: 1	TF:M08623_1	7240	2.20E-03	95
GO:BP	regulation of nucleobase-containing compound metabolic process	GO:0019219	3523	2.30E-03	56
GO:BP	myeloid leukocyte activation	GO:0002274	205	2.30E-03	11
TF	Factor: CTCF; motif: NNNGCCASCAGRKGGCRSNN	TF:M01200	3651	2.30E-03	58
TF	Factor: HMGIY; motif: NGWWATTN	TF:M01653	5150	2.30E-03	74
TF	Factor: Oct-2; motif: NNNATTATGCAW	TF:M11894	2946	2.30E-03	50
GO:BP	leukocyte differentiation	GO:0002521	507	2.40E-03	17
TF	Factor: MEL1; motif: GATGAG; match class: 1	TF:M08793_1	4116	2.40E-03	63
TF	Factor: FEZF1; motif: NYTGYYCTTTTN	TF:M09919	2030	2.40E-03	39
GO:BP	morphogenesis of a branching epithelium	GO:0061138	166	2.50E-03	10
TF	Factor: GATA-5; motif: TATCTN; match class: 1	TF:M02006_1	2441	2.50E-03	44
TF	Factor: E2F-1; motif: TTTGGCGCCAAA; match class: 1	TF:M04516_1	9692	2.50E-03	118
TF	Factor: PU.1; motif: NNNNYYYACTTCCTCTTTY	TF:M01172	3663	2.50E-03	58
GO:BP	regulation of muscle system process	GO:0090257	208	2.60E-03	11
TF	Factor: KLF8; motif: NGGGGTGYGG	TF:M08818	1417	2.60E-03	31
TF	Factor: Foxc1; motif: TTVYTTTNW	TF:M07254	6449	2.60E-03	87
TF	Factor: ATF-3; motif: GATGAYGTCATN	TF:M11288	4312	2.60E-03	65
TF	Factor: PHB; motif: NCCCAGCCCCY; match class: 1	TF:M12725_1	4127	2.60E-03	63
GO:CC	platelet alpha granule lumen	GO:0031093	59	2.70E-03	6
TF	Factor: NFATc1; motif: TTTCCAYWRTGGAAA	TF:M04052	5658	2.70E-03	79
TF	Factor: Fra-1; motif: GRTGACGTCATC	TF:M11285	6557	2.70E-03	88
TF	Factor: T3R-beta; motif: NRRGGTCRTGACCYYN	TF:M11817	4694	2.70E-03	69
TF	Factor: ER-alpha; motif: NAGGTCANSNTGACCYN	TF:M11845	3225	2.70E-03	53
GO:BP	regulation of epithelial cell differentiation	GO:0030856	131	2.80E-03	9
TF	Factor: AP-2gamma:Dlx-3; motif: NSCCYNNRGGCANNNNYAATTA	TF:M08660	3138	2.80E-03	52
TF	Factor: Sox-10; motif: MAANRRNNNCWTTGTT	TF:M10065	5861	2.80E-03	81
TF	Factor: ZGPAT; motif: GRGGCWGNGGNG; match class: 1	TF:M09739_1	2537	2.80E-03	45
TF	Factor: NF-kappaB; motif: GGGRATTTCC	TF:M00052	1650	2.80E-03	34
GO:CC	focal adhesion	GO:0005925	413	2.90E-03	14
TF	Factor: MZF-1; motif: KNGNKAGGGGNAA	TF:M00084	5964	2.90E-03	82
TF	Factor: ER71:C/EBPdelta; motif: NNCGGAWRTTRCGYAAN	TF:M08246	7178	2.90E-03	94
TF	Factor: BRN1; motif: NANNTATGCATAATNNA	TF:M01324	4046	2.90E-03	62
TF	Factor: CDX-2; motif: TTTATN; match class: 1	TF:M02087_1	3954	2.90E-03	61
GO:BP	regulation of transcription, DNA-templated	GO:0006355	3018	3.00E-03	50
GO:BP	regulation of nucleic acid-templated transcription	GO:1903506	3019	3.00E-03	50
TF	Factor: IRF-8; motif: NCGAAACCGAAACYN	TF:M11683	4049	3.00E-03	62
TF	Factor: Smad1; motif: NGGCAGACN	TF:M03845	3958	3.00E-03	61

TF	Factor: c-Myc; motif: NCCACGTGCNN	TF:M09992	4899	3.00E-03	71
GO:BP	cell adhesion mediated by integrin	GO:0033627	69	3.10E-03	7
GO:BP	regulation of RNA metabolic process	GO:0051252	3290	3.10E-03	53
TF	Factor: Fli-1:C/EBPdelta; motif: NNCGGAWATTGCGCAAT	TF:M08469	5776	3.10E-03	80
TF	Factor: IRF-1; motif: TTCACTT	TF:M00747	4332	3.10E-03	65
TF	Factor: CDP:T-bet; motif: NTCACACNYYRATCRATM	TF:M08203	5093	3.10E-03	73
TF	Factor: Cdx-2; motif: NRTCGTAANNNN	TF:M10849	9841	3.10E-03	119
TF	Factor: Oct-2; motif: NNNATTTGCATRT	TF:M07120	3962	3.10E-03	61
GO:BP	kidney vasculature development	GO:0061440	25	3.20E-03	5
GO:BP	renal system vasculature development	GO:0061437	25	3.20E-03	5
GO:BP	response to steroid hormone	GO:0048545	304	3.20E-03	13
GO:BP	humoral immune response	GO:0006959	171	3.20E-03	10
TF	Factor: TEAD4; motif: NRCATTCCWN	TF:M04145	1213	3.20E-03	28
GO:BP	response to organic cyclic compound	GO:0014070	828	3.30E-03	22
GO:BP	extrinsic apoptotic signaling pathway	GO:0097191	213	3.30E-03	11
TF	Factor: C/EBPdelta; motif: NRTTGCGYAAYN	TF:M11321	4812	3.30E-03	70
TF	Factor: Sox-9; motif: NNNNNACAAARGNNSMN; match class: 1	TF:M07269_1	2893	3.30E-03	49
TF	Factor: sp4; motif: NNGNARGRGGCGGRGCNNRR	TF:M10072	10068	3.30E-03	121
TF	Factor: Erg; motif: NACCGGAWWTCCGGTN	TF:M11395	7927	3.30E-03	101
GO:BP	regulation of endothelial cell apoptotic process	GO:2000351	45	3.40E-03	6
GO:BP	regulation of extrinsic apoptotic signaling pathway via death domain receptors	GO:1902041	45	3.40E-03	6
TF	Factor: SP2; motif: GGGCGGGAC	TF:M01783	8669	3.40E-03	108
TF	Factor: LBP9; motif: ACYRGTNNNNACYRGT	TF:M11492	6898	3.40E-03	91
TF	Factor: LHX4; motif: NNCRTTAN	TF:M11005	9424	3.40E-03	115
TF	Factor: MEF-2D; motif: WAAATAR	TF:M02026	6393	3.50E-03	86
TF	Factor: Pitx1; motif: NNNNRGGGATTAAMNNN	TF:M01484	2900	3.50E-03	49
GO:BP	cellular response to stress	GO:0033554	1782	3.60E-03	35
GO:CC	cell-substrate junction	GO:0030055	421	3.60E-03	14
KEGG	Lipid and atherosclerosis	KEGG:05417	199	3.60E-03	9
REAC	Cell surface interactions at the vascular wall	REAC:R-HSA-202733	123	3.60E-03	8
TF	Factor: TFAP2A; motif: YGCCCNNRGGCN; match class: 1	TF:M04146_1	3522	3.60E-03	56
TF	Factor: GR; motif: GGTACAANNTGTYCTK; match class: 1	TF:M00205_1	1220	3.60E-03	28
TF	Factor: FXR; motif: NAGGTCAWNKN	TF:M08953	4074	3.70E-03	62
TF	Factor: MEIS1A:HOXA9; motif: TGACAGKTTTAYGA	TF:M00420	4639	3.70E-03	68
TF	Factor: SREBP-1; motif: RTCRCGTGAY; match class: 1	TF:M11081_1	7116	3.70E-03	93
GO:BP	negative regulation of cell adhesion	GO:0007162	261	3.80E-03	12
GO:BP	positive regulation of intracellular signal transduction	GO:1902533	902	3.80E-03	23
KEGG	Rheumatoid arthritis	KEGG:05323	78	3.80E-03	6
TF	Factor: AML3; motif: NWAACCACRAAAACCACRAN	TF:M11999	5905	3.80E-03	81
GO:BP	negative regulation of endothelial cell apoptotic process	GO:2000352	26	3.90E-03	5
GO:BP	negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	GO:1902042	26	3.90E-03	5
GO:BP	mesenchymal cell differentiation	GO:0048762	217	4.00E-03	11
TF	Factor: SP3; motif: NCCACGCCCMC	TF:M03921	3536	4.00E-03	56
GO:BP	heart contraction	GO:0060047	218	4.10E-03	11
GO:CC	cytoskeleton	GO:0005856	2118	4.10E-03	37
GO:CC	actin cytoskeleton	GO:0015629	484	4.10E-03	15
TF	Factor: PARP; motif: YDRGAAAWAS	TF:M01211	2156	4.10E-03	40
TF	Factor: Tbx20; motif: SGAGGTGTGAGGSGR	TF:M07474	3181	4.10E-03	52
TF	Factor: C-JUN:FRA-2; motif: NNRTGAGTCAYN	TF:M08940	3007	4.20E-03	50
TF	Factor: ESRRA; motif: AAGGTCATNCAAGGTCA	TF:M04457	3008	4.30E-03	50
TF	Factor: TFII-I; motif: NAGGAAGTGN; match class: 1	TF:M04636_1	4849	4.30E-03	70
GO:BP	transcription, DNA-templated	GO:0006351	3149	4.40E-03	51

GO:BP	nucleic acid-templated transcription	GO:0097659	3150	4.40E-03	51
TF	Factor: ER-alpha; motif: TGACCYN	TF:M03547	4003	4.40E-03	61
GO:BP	odontogenesis of dentin-containing tooth	GO:0042475	73	4.50E-03	7
KEGG	Estrogen signaling pathway	KEGG:04915	117	4.50E-03	7
REAC	Phase I - Functionalization of compounds	REAC:R-HSA-211945	91	4.50E-03	7
TF	Factor: Pet-1; motif: GCNGGAAGYG; match class: 1	TF:M09918_1	6634	4.50E-03	88
TF	Factor: HOXA7; motif: YCAATCT	TF:M01108	2497	4.50E-03	44
GO:BP	cellular component organization	GO:0016043	6205	4.60E-03	83
TF	Factor: HOXA10; motif: NGTCGTAAAAN	TF:M10795	5936	4.70E-03	81
TF	Factor: NF-kappaB; motif: GGGGATYCCC; match class: 1	TF:M00051_1	2586	4.70E-03	45
TF	Factor: SREBP-2; motif: RTGGGGTGAY	TF:M07406	5054	4.70E-03	72
GO:BP	cellular response to oxidative stress	GO:0034599	267	4.80E-03	12
GO:BP	morphogenesis of a branching structure	GO:0001763	179	4.80E-03	10
TF	Factor: ZF5; motif: NRNGNGCGCGCWN; match class: 1	TF:M00333_1	11811	4.80E-03	136
TF	Factor: Smad4; motif: TGTCTGN	TF:M01889	4482	4.80E-03	66
TF	Factor: E2F-1; motif: WWTGGCGCCAAA; match class: 1	TF:M04515_1	11473	4.80E-03	133
TF	Factor: FLI-1; motif: CMGGAWGTSAN	TF:M01208	5544	4.80E-03	77
TF	Factor: POU6F1; motif: NNNNATAATGAGSTNNN	TF:M01462	4868	5.00E-03	70
TF	Factor: POU3F1; motif: RNYBCATTTGCATTWCAA	TF:M03842	4299	5.00E-03	64
TF	Factor: AP-4; motif: AWCAGCTGWT	TF:M11208	3562	5.10E-03	56
MIRNA	hsa-miR-29b-3p	MIRNA:hsa-miR-29b-3p	249	5.10E-03	11
TF	Factor: NeuroD; motif: NNSCWGCTGNSY	TF:M01288	4210	5.20E-03	63
TF	Factor: MafB; motif: TGCTGASTNNN	TF:M09978	2768	5.20E-03	47
GO:BP	positive regulation of RNA metabolic process	GO:0051254	1577	5.30E-03	32
GO:BP	cellular response to hormone stimulus	GO:0032870	538	5.30E-03	17
TF	Factor: ER-alpha; motif: GNCNNNNTGACCYN	TF:M07283	2597	5.30E-03	45
TF	Factor: JunD; motif: NRTGAGTCAYN	TF:M09964	4213	5.30E-03	63
TF	Factor: SP1; motif: NCCCCKCCCCC	TF:M07226	7901	5.30E-03	100
GO:MF	ion binding	GO:0043167	5669	5.40E-03	76
GO:BP	positive regulation of nucleobase-containing compound metabolic process	GO:0045935	1735	5.40E-03	34
GO:BP	transmembrane transport	GO:0055085	1426	5.40E-03	30
GO:BP	positive regulation of programmed cell death	GO:0043068	481	5.50E-03	16
GO:MF	NAD+ nucleotidase, cyclic ADP-ribose generating	GO:0061809	16	5.60E-03	4
GO:MF	NAD(P)+ nucleosidase activity	GO:0050135	16	5.60E-03	4
GO:CC	hemoglobin complex	GO:0005833	7	5.60E-03	3
GO:CC	haptoglobin-hemoglobin complex	GO:0031838	7	5.60E-03	3
TF	Factor: NF-1C; motif: TTGGCNN	TF:M07300	5371	5.60E-03	75
TF	Factor: LRF; motif: NGKGGGTSNCN	TF:M07387	4792	5.70E-03	69
TF	Factor: Oct3; motif: WTATGCGCATAW; match class: 1	TF:M11934_1	7810	5.80E-03	99
TF	Factor: LBP-1; motif: CAGCTGS; match class: 1	TF:M00644_1	3578	5.80E-03	56
TF	Factor: HoxA5; motif: RTCATTAN	TF:M10704	4413	5.80E-03	65
TF	Factor: Pax-5; motif: RRMSWGANWYCTNRAGCGKRACSRYNSM	TF:M00144	12083	6.00E-03	138
GO:BP	heart process	GO:0003015	227	6.10E-03	11
TF	Factor: CTCF; motif: NNRSYGCCMCCTGSTGGCCN	TF:M12593	8029	6.10E-03	101
TF	Factor: LKLF; motif: GGGGTGGKSN; match class: 1	TF:M07261_1	3767	6.10E-03	58
TF	Factor: Oct-2; motif: NNNTATGCAAATNNNN	TF:M01368	1947	6.10E-03	37
GO:BP	regulation of response to wounding	GO:1903034	144	6.20E-03	9
GO:BP	ear morphogenesis	GO:0042471	108	6.20E-03	8
GO:BP	innate immune response	GO:0045087	667	6.30E-03	19
TF	Factor: STAT2; motif: NRGAAANNGAAACTNA	TF:M09733	2444	6.30E-03	43
GO:BP	regulation of blood circulation	GO:1903522	228	6.40E-03	11
GO:BP	organic cyclic compound biosynthetic process	GO:1901362	3736	6.40E-03	57

GO:BP	endothelial cell apoptotic process	GO:0072577	50	6.40E-03	6
TF	Factor: OCT-x; motif: CTNATTTGCATAY	TF:M00210	3408	6.40E-03	54
TF	Factor: Pax-4; motif: SWAATWAN	TF:M04063	3957	6.40E-03	60
GO:CC	cytoplasmic vesicle membrane	GO:0030659	1119	6.50E-03	24
TF	Factor: GTF2IRD1-isoform2; motif: GGGATTRNR; match class: 1	TF:M01229_1	7936	6.50E-03	100
GO:BP	regulation of intracellular signal transduction	GO:1902531	1594	6.60E-03	32
TF	Factor: Sp1; motif: GGGGCGGGGC; match class: 1	TF:M00931_1	5788	6.60E-03	79
TF	Factor: AP-1; motif: NTGASTCAG	TF:M00199	4054	6.60E-03	61
TF	Factor: FOSB:JUND; motif: NNTNACTNATN	TF:M08928	5006	6.70E-03	71
TF	Factor: FRA-2; motif: RTGANTCA	TF:M08914	3234	6.70E-03	52
REAC	Transport of small molecules	REAC:R-HSA-382551	679	6.80E-03	18
TF	Factor: P50; motif: GGRRANTCCCNN; match class: 1	TF:M03557_1	1188	6.80E-03	27
TF	Factor: Sox-9; motif: MACARWGNNNYCNTTNW	TF:M08838	3505	6.80E-03	55
TF	Factor: ATF-2; motif: RRTGANGTCAY	TF:M09867	3596	6.80E-03	56
GO:MF	cation binding	GO:0043169	4050	6.90E-03	59
TF	Factor: ESE-1; motif: NTGTGCGGATGCN; match class: 1	TF:M11385_1	4913	6.90E-03	70
TF	Factor: AR; motif: GGTACANNRTGTTCT; match class: 1	TF:M00481_1	1957	6.90E-03	37
TF	Factor: WT1; motif: RGGNGGGGGAGGRGGNGGRG	TF:M10108	6095	6.90E-03	82
TF	Factor: E2F2; motif: AAAAATGGCGCCAAAAWG	TF:M03958	9442	6.90E-03	114
GO:BP	regulation of peptidase activity	GO:0052547	379	7.00E-03	14
TF	Factor: TAFII250; motif: RARRWGGCGGMGGNGR	TF:M10086	8689	7.00E-03	107
GO:MF	calcium ion binding	GO:0005509	653	7.10E-03	18
GO:BP	metanephros development	GO:0001656	78	7.10E-03	7
TF	Factor: AP-2beta; motif: GCNNNGGSCNGVGGGN; match class: 1	TF:M01858_1	3063	7.10E-03	50
GO:BP	negative regulation of endopeptidase activity	GO:0010951	187	7.20E-03	10
TF	Factor: FAC1; motif: NNNCAMAACACRNA	TF:M00456	6812	7.30E-03	89
TF	Factor: PATZ; motif: GGGGNGGGGGMKGGRRNGGNRN	TF:M10026	7954	7.30E-03	100
TF	Factor: AR; motif: NNNNNNRGNACRNNGTGTTCTNNNNNN	TF:M00956	2207	7.30E-03	40
TF	Factor: AP-2beta; motif: NSCCYNRGGSN; match class: 1	TF:M11477_1	6305	7.30E-03	84
TF	Factor: LXR-alpha; motif: NNRRGGTYACTNNAGGNCA	TF:M10013	2716	7.30E-03	46
GO:BP	positive regulation of macromolecule biosynthetic process	GO:0010557	1682	7.40E-03	33
TF	Factor: RORA; motif: CCYTGNCCTN; match class: 1	TF:M12659_1	1963	7.40E-03	37
TF	Factor: GATA-1; motif: NTGNNNNNNNNAGATAAGN	TF:M09936	3607	7.40E-03	56
TF	Factor: ipf1; motif: CATTAR	TF:M01275	7333	7.50E-03	94
TF	Factor: p53; motif: GGACATGCCCGGGCATGTCY	TF:M00034	3977	7.50E-03	60
TF	Factor: FXR:RXR-ALPHA; motif: NAGKTCATTGACCYN; match class: 1	TF:M08954_1	1884	7.50E-03	36
MIRNA	hsa-miR-1238-3p	MIRNA:hsa-miR-1238-3p	128	7.50E-03	8
GO:MF	metal ion binding	GO:0046872	3968	7.60E-03	58
GO:BP	cardiac chamber morphogenesis	GO:0003206	111	7.60E-03	8
GO:BP	biomineral tissue development	GO:0031214	148	7.70E-03	9
GO:BP	extrinsic apoptotic signaling pathway via death domain receptors	GO:0008625	79	7.70E-03	7
GO:BP	regionalization	GO:0003002	280	7.80E-03	12
GO:BP	positive regulation of cell activation	GO:0050867	330	7.80E-03	13
TF	Factor: AP-2gamma; motif: NTGSCCTGRGGSNN; match class: 1	TF:M09591_1	2550	7.80E-03	44
TF	Factor: Sp2; motif: TGGGCGCGCCCA	TF:M06948	8390	7.80E-03	104
GO:BP	response to reactive oxygen species	GO:0000302	189	7.90E-03	10
TF	Factor: TFAP4; motif: AWCAGCTGWT	TF:M04192	4548	7.90E-03	66
TF	Factor: A-Myb:Elf-1; motif: NMCCGGAACCGTTA	TF:M08390	10013	7.90E-03	119
GO:MF	haptoglobin binding	GO:0031720	6	8.00E-03	3
TF	Factor: SP1; motif: GGGGYGGGGNS; match class: 1	TF:M01303_1	3433	8.00E-03	54
TF	Factor: TCF-1; motif: NNNSWWCAAAGN	TF:M07433	4743	8.10E-03	68
GO:BP	biomineralization	GO:0110148	149	8.20E-03	9

TF	Factor: Sp2; motif: NYSGCCCCGCCCCCY	TF:M03567	7451	8.20E-03	95
TF	Factor: HOXA13; motif: ATAAMA; match class: 1	TF:M01292_1	6832	8.20E-03	89
TF	Factor: HSF1; motif: GAANNTTCTNGN	TF:M07459	2902	8.20E-03	48
TF	Factor: FPM315; motif: SRGGGAGGAGGN	TF:M01587	2990	8.20E-03	49
TF	Factor: AP-3; motif: TKGAAAKN	TF:M04609	3528	8.30E-03	55
TF	Factor: VDR:RXR-ALPHA; motif: NRGGTCANNNGGTTCNN; match class: 1	TF:M08980_1	3529	8.30E-03	55
GO:CC	vesicle membrane	GO:0012506	1138	8.50E-03	24
GO:CC	specific granule	GO:0042581	145	8.50E-03	8
TF	Factor: ZNF511; motif: GGRRGRGGCWGNG; match class: 1	TF:M09738_1	4367	8.50E-03	64
GO:BP	cardiac ventricle development	GO:0003231	113	8.60E-03	8
TF	Factor: CTCF; motif: NNNNANASYGCCMYCTAGTGG	TF:M04689	4847	8.60E-03	69
GO:BP	positive regulation of cell population proliferation	GO:0008284	813	8.80E-03	21
TF	Factor: DEC1; motif: NGCACGTGAS	TF:M09876	7777	8.80E-03	98
TF	Factor: Sox-15; motif: ACAAWGGG	TF:M03847	1353	8.90E-03	29
TF	Factor: ER-beta; motif: GTCANASTGRCCYNR	TF:M01875	5536	8.90E-03	76
GO:BP	regulation of leukocyte activation	GO:0002694	500	9.00E-03	16
TF	Factor: IRF; motif: NNGAAANTGAAANN	TF:M08887	1063	9.00E-03	25
TF	Factor: PPARgamma; motif: NWSTRGGKSARAGGKCA	TF:M10038	5836	9.10E-03	79
TF	Factor: AP-1; motif: NNNTGAGTCAKCN	TF:M00517	4189	9.20E-03	62
TF	Factor: STAT; motif: NNNNNTTCTKGGA	TF:M00777	4378	9.20E-03	64
GO:BP	regulation of transport	GO:0051049	1622	9.40E-03	32
REAC	SLC-mediated transmembrane transport	REAC:R-HSA-425407	229	9.40E-03	10
TF	Factor: AR; motif: GGTACANNRTGTTCT	TF:M00481	4286	9.40E-03	63
TF	Factor: CPBP; motif: NGGGCGG	TF:M05444	8104	9.40E-03	101
TF	Factor: Sp6; motif: WGGGCGG	TF:M05361	8104	9.40E-03	101
TF	Factor: Sp2; motif: WGGGCGG	TF:M05332	8104	9.40E-03	101
TF	Factor: NR3C1; motif: RRGAACATWMYGTYCTRN	TF:M02219	5643	9.40E-03	77
TF	Factor: TFAP2C; motif: NGCCTNAGGCN	TF:M04154	3363	9.50E-03	53
TF	Factor: GLI2; motif: TGGGTGGTCNS	TF:M07291	2656	9.50E-03	45
GO:BP	aorta morphogenesis	GO:0035909	31	9.70E-03	5
TF	Factor: Tbx5; motif: NNAGGTGTNANN	TF:M01019	4960	9.70E-03	70
TF	Factor: Msx-1; motif: CNGTAWNTG	TF:M00394	7584	9.70E-03	96
TF	Factor: Oct3; motif: NNWTATGYWAATKANN	TF:M11935	2402	9.70E-03	42
TF	Factor: NFATc1; motif: TTTTCCATGGAAAN; match class: 1	TF:M04053_1	4962	9.80E-03	70
GO:BP	negative regulation of peptidase activity	GO:0010466	194	9.90E-03	10
GO:CC	membrane-enclosed lumen	GO:0031974	5613	9.90E-03	73
GO:CC	intracellular organelle lumen	GO:0070013	5613	9.90E-03	73
GO:CC	organelle lumen	GO:0043233	5613	9.90E-03	73
GO:CC	external side of plasma membrane	GO:0009897	291	9.90E-03	11
TF	Factor: c-Ets; motif: KRCAGGAARTRNKT	TF:M00340	4483	9.90E-03	65
GO:BP	homotypic cell-cell adhesion	GO:0034109	82	1.00E-02	7
GO:BP	tissue migration	GO:0090130	287	1.00E-02	12
GO:BP	glomerular mesangial cell development	GO:0072144	5	1.00E-02	3
TF	Factor: SNA; motif: NRCAGGTGCA	TF:M12258	2236	1.00E-02	40
TF	Factor: B-ATF; motif: NNAYGACACN; match class: 1	TF:M11301_1	1669	1.00E-02	33
TF	Factor: TEF-3; motif: GNTATTTTT	TF:M07270	8541	1.00E-02	105
TF	Factor: Oct-1; motif: NNNNATGCAAATNAN	TF:M00195	3014	1.00E-02	49
TF	Factor: HFH2; motif: NNWAYRTAAACW	TF:M11555	3923	1.00E-02	59
GO:MF	transition metal ion binding	GO:0046914	1017	1.10E-02	23
GO:BP	nucleobase-containing compound biosynthetic process	GO:0034654	3527	1.10E-02	54
GO:BP	cellular response to cadmium ion	GO:0071276	32	1.10E-02	5
TF	Factor: Sp1; motif: GGGGCGGGGC	TF:M07063	6059	1.10E-02	81

TF	Factor: AP-4; motif: AWCAGCTGWT; match class: 1	TF:M11208_1	3285	1.10E-02	52
TF	Factor: NFATc2; motif: TTTTCCA	TF:M02265	6464	1.10E-02	85
TF	Factor: NFATc1; motif: NTTTCCRTNNAYGGAAAN	TF:M11981	5462	1.10E-02	75
TF	Factor: TFAP2A; motif: NNNNGCCYSAGGGCA	TF:M07231	4780	1.10E-02	68
TF	Factor: NKX2-5; motif: NNCACTCAANN	TF:M12495	1914	1.10E-02	36
TF	Factor: HOXD4; motif: NYMATTAN	TF:M10712	3380	1.10E-02	53
TF	Factor: SMAD; motif: AGACNBCNN	TF:M00792	3290	1.10E-02	52
TF	Factor: ESE-1; motif: NWTRCGGAWGCN	TF:M11382	9421	1.10E-02	113
TF	Factor: AR; motif: ARGAACANNNTGTNC; match class: 1	TF:M07204_1	736	1.10E-02	20
TF	Factor: gli3; motif: GACCACCCANG	TF:M01704	3113	1.10E-02	50
TF	Factor: POU2F1:PEA3; motif: ACCGGATATGCAN	TF:M08402	6988	1.10E-02	90
TF	Factor: TFEA; motif: RGTCACGTGA	TF:M10100	5277	1.10E-02	73
TF	Factor: HOXD1; motif: NATYCAKCAN	TF:M12625	4694	1.10E-02	67
TF	Factor: SMAD3; motif: YGTCTAGACA	TF:M04026	5872	1.10E-02	79
GO:BP	mononuclear cell differentiation	GO:1903131	397	1.20E-02	14
GO:BP	negative regulation of hydrolase activity	GO:0051346	293	1.20E-02	12
TF	Factor: Pbx; motif: GATTGATKGNNS	TF:M00998	4313	1.20E-02	63
TF	Factor: NF-kappaB2; motif: NGGGGAANYACCN	TF:M11997	328	1.20E-02	13
TF	Factor: MLLT10; motif: CYNNCCNNGGNGCTG; match class: 1	TF:M12636_1	3206	1.20E-02	51
TF	Factor: Sp1; motif: GGGGCGGGGT; match class: 1	TF:M00008_1	4794	1.20E-02	68
TF	Factor: MIF-1; motif: NNGTTGCWWGGYAACNGS; match class: 1	TF:M00279_1	4699	1.20E-02	67
TF	Factor: NFATc1; motif: TTTCCAYWRTGGAAA; match class: 1	TF:M04052_1	3299	1.20E-02	52
TF	Factor: AREB6; motif: VNRCACCTGKNC	TF:M00414	1527	1.20E-02	31
TF	Factor: FOSL1; motif: NNATGACTCATNN; match class: 1	TF:M12518_1	1608	1.20E-02	32
GO:BP	aorta development	GO:0035904	56	1.30E-02	6
GO:BP	ion transmembrane transport	GO:0034220	1045	1.30E-02	24
TF	Factor: ZNF775; motif: RGRGAGAAGN	TF:M12720	3038	1.30E-02	49
TF	Factor: MYB; motif: NAACNGNCN	TF:M00913	4422	1.30E-02	64
TF	Factor: COUP-TF1; motif: RRGGTCRNTGACCYY	TF:M11741	3398	1.30E-02	53
TF	Factor: JunD; motif: NRTGASTCATN	TF:M07104	2177	1.30E-02	39
TF	Factor: JUNB:C-JUN; motif: KRTGACGTCATN; match class: 1	TF:M08945_1	4907	1.30E-02	69
TF	Factor: CLOCK; motif: CNGNCACGTGNNNM	TF:M09884	7117	1.30E-02	91
TF	Factor: IRF-4; motif: RGGAASWGR; match class: 1	TF:M04818_1	2691	1.30E-02	45
TF	Factor: AP-4; motif: YCAGCTGNKN; match class: 1	TF:M10097_1	1307	1.30E-02	28
TF	Factor: AP-4; motif: AWCAGCTGWT	TF:M11210	3956	1.30E-02	59
TF	Factor: AP-4; motif: AWCAGCTGWT; match class: 1	TF:M11210_1	3956	1.30E-02	59
TF	Factor: IRF-4; motif: NCGAAACCGAAACYN	TF:M11687	3133	1.30E-02	50
GO:MF	serine-type endopeptidase inhibitor activity	GO:0004867	67	1.40E-02	6
GO:BP	negative regulation of nucleobase-containing compound metabolic process	GO:0045934	1341	1.40E-02	28
GO:BP	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	GO:0002460	247	1.40E-02	11
GO:BP	nitrogen compound metabolic process	GO:0006807	9442	1.40E-02	112
GO:BP	transmembrane receptor protein tyrosine kinase signaling pathway	GO:0007169	579	1.40E-02	17
KEGG	NF-kappa B signaling pathway	KEGG:04064	99	1.40E-02	6
TF	Factor: OVOL; motif: ANRTAACGG	TF:M08894	7120	1.40E-02	91
TF	Factor: Isl2; motif: CTAATKR	TF:M02079	4718	1.40E-02	67
TF	Factor: FOXO1A; motif: NNNYTGTTTNCN	TF:M09931	5699	1.40E-02	77
TF	Factor: JunB; motif: GATGACGTCAYC; match class: 1	TF:M11273_1	5600	1.40E-02	76
TF	Factor: FPM315; motif: GGAGGAGGRRGRGGRGGRRGR	TF:M07141	2017	1.40E-02	37
TF	Factor: ATF-3; motif: NATGATGTCATN	TF:M11290	5304	1.40E-02	73
TF	Factor: LRF; motif: GGGGKYNNB; match class: 1	TF:M01100_1	2609	1.40E-02	44
TF	Factor: Oct-2; motif: NTGCATATGCAN	TF:M11899	4532	1.40E-02	65

GO:MF	enzyme inhibitor activity	GO:0004857	327	1.50E-02	12
GO:MF	inorganic anion transmembrane transporter activity	GO:0015103	138	1.50E-02	8
GO:BP	sensory organ morphogenesis	GO:0090596	250	1.50E-02	11
GO:BP	negative regulation of cellular biosynthetic process	GO:0031327	1427	1.50E-02	29
REAC	Transport of bile salts and organic acids, metal ions and amine compounds	REAC:R-HSA-425366	75	1.50E-02	6
TF	Factor: Oct3; motif: WTATGCGCATAW	TF:M11934	8394	1.50E-02	103
TF	Factor: NF-kappaB1; motif: KGGRNTTTCCM	TF:M07221	2105	1.50E-02	38
TF	Factor: Sox-9; motif: NNNNAACAATRGNN	TF:M00410	3323	1.50E-02	52
TF	Factor: ZABC1; motif: NNTGNMCTTTGNNCYNNN	TF:M12683	3689	1.50E-02	56
TF	Factor: TEF-3:C/EBPdelta; motif: RGWATGYNRTTRCGYAAY	TF:M08413	5118	1.50E-02	71
TF	Factor: c-Ets-2; motif: NNCTTCCTNNN	TF:M07379	2966	1.50E-02	48
TF	Factor: Oct-1; motif: NNNNNNNWATGCAAATNNNWNNA	TF:M00138	2024	1.50E-02	37
TF	Factor: CEBPA; motif: NNATTGCACAATNN	TF:M12502	2530	1.50E-02	43
TF	Factor: Fra-2; motif: TGASTCANCN	TF:M03870	3056	1.50E-02	49
TF	Factor: oct-2; motif: NNWNATGCAAATNN	TF:M03836	3147	1.50E-02	50
GO:BP	regulation of blood coagulation	GO:0030193	58	1.60E-02	6
GO:BP	muscle tissue morphogenesis	GO:0060415	58	1.60E-02	6
GO:BP	cellular component organization or biogenesis	GO:0071840	6398	1.60E-02	83
GO:BP	lymphocyte differentiation	GO:0030098	353	1.60E-02	13
GO:BP	anion transport	GO:0006820	465	1.60E-02	15
TF	Factor: c-Fos; motif: NNTGASTCATN	TF:M07090	3604	1.60E-02	55
TF	Factor: E2F-1:TBR2; motif: NGGTGNNANGGCGCNNTNNCRNNN	TF:M08523	11259	1.60E-02	129
TF	Factor: JUND; motif: NNATGACTCATNN	TF:M12524	3514	1.60E-02	54
TF	Factor: MAF; motif: NGCTGAGTCAN	TF:M00983	5128	1.60E-02	71
TF	Factor: ctcf; motif: NNNCCASYAGRKGGCRSYNN	TF:M09602	6837	1.60E-02	88
TF	Factor: NF-1A; motif: NGCCARN; match class: 1	TF:M03554_1	626	1.60E-02	18

TF	Factor: BTEB2; motif: GNAGGGGGNGGGSSNN	TF:M03814	4838	1.60E-02	68
TF	Factor: VDR; motif: RRGGTCANNGRGKTCA; match class: 1	TF:M09671_1	2116	1.60E-02	38
GO:BP	regulation of endopeptidase activity	GO:0052548	354	1.70E-02	13
GO:BP	positive regulation of cell adhesion	GO:0045785	409	1.70E-02	14
GO:BP	heart valve development	GO:0003170	59	1.70E-02	6
TF	Factor: Tbx3; motif: AGGTGTNR	TF:M08786	3157	1.70E-02	50
TF	Factor: Tax/CREB; motif: RTGACGCATAYCCCC; match class: 1	TF:M00115_1	2627	1.70E-02	44
TF	Factor: c-Fos; motif: RTGASTCAY	TF:M04693	2202	1.70E-02	39
TF	Factor: AhR:Arnt; motif: GRGKATYGCGTGMCWNSCC	TF:M00237	5832	1.70E-02	78
TF	Factor: E2F-7; motif: GRGGCGGGAANNN	TF:M09896	9398	1.70E-02	112
MIRNA	hsa-miR-670-3p	MIRNA:hsa-miR-670-3p	186	1.70E-02	9
GO:BP	positive regulation of cellular protein metabolic process	GO:0032270	1284	1.80E-02	27
GO:BP	positive regulation of apoptotic process	GO:0043065	469	1.80E-02	15
GO:BP	cellular zinc ion homeostasis	GO:0006882	35	1.80E-02	5
GO:BP	middle ear morphogenesis	GO:0042474	17	1.80E-02	4
GO:BP	kidney mesenchyme development	GO:0072074	17	1.80E-02	4
GO:BP	negative regulation of cell migration	GO:0030336	255	1.80E-02	11
GO:CC	platelet alpha granule	GO:0031091	82	1.80E-02	6
TF	Factor: DATF1; motif: SNGGRRGCWGNGGG; match class: 1	TF:M09724_1	2633	1.80E-02	44
TF	Factor: AP-2alpha; motif: GCCNNNRGS	TF:M00469	4949	1.80E-02	69
TF	Factor: p53; motif: RGRCWWGYCYNGRCWWGYYY; match class: 1	TF:M01652_1	4757	1.80E-02	67
TF	Factor: C-JUN:FOSB; motif: NATGACTCAY	TF:M08936	2723	1.80E-02	45
TF	Factor: Sox-3; motif: SNNACAATRK	TF:M11617	3258	1.80E-02	51
CORUM	Calprotectin heterotetramer	CORUM:6826	2	1.80E-02	2
CORUM	NOS3-CAV1 complex	CORUM:5714	2	1.80E-02	2
GO:BP	mononuclear cell migration	GO:0071674	165	1.90E-02	9

GO:BP	regulation of hemostasis	GO:1900046	60	1.90E-02	6
GO:BP	heterocycle biosynthetic process	GO:0018130	3595	1.90E-02	54
GO:BP	regulation of tube diameter	GO:0035296	126	1.90E-02	8
GO:BP	blood vessel diameter maintenance	GO:0097746	126	1.90E-02	8
GO:CC	membrane raft	GO:0045121	312	1.90E-02	11
GO:CC	membrane microdomain	GO:0098857	313	1.90E-02	11
KEGG	Focal adhesion	KEGG:04510	195	1.90E-02	8
REAC	Metallothioneins bind metals	REAC:R-HSA-5661231	9	1.90E-02	3
TF	Factor: alpha-CP1; motif: CAGCCAATGAG	TF:M00687	2044	1.90E-02	37
TF	Factor: YY1; motif: NGCCATYTTKGRCNWWNNGTGCK	TF:M12276	8868	1.90E-02	107
TF	Factor: NF-1C; motif: NTTGGCNNNNTGCCARN; match class: 1	TF:M11728_1	967	1.90E-02	23
TF	Factor: C/EBPbeta; motif: RNRTKDNGMAAKNN	TF:M00109	2642	1.90E-02	44
TF	Factor: Oct3; motif: NNTTATGYWAATKARN	TF:M11932	2470	1.90E-02	42
TF	Factor: GATA-1; motif: NNCWGATARNNNN	TF:M00128	2048	1.90E-02	37
TF	Factor: PBX3; motif: TGANTGRCRGS	TF:M10030	1884	1.90E-02	35
GO:BP	regulation of lymphocyte activation	GO:0051249	415	2.00E-02	14
GO:BP	negative regulation of extrinsic apoptotic signaling pathway	GO:2001237	91	2.00E-02	7
GO:BP	autocrine signaling	GO:0035425	6	2.00E-02	3
GO:BP	glomerular mesangial cell differentiation	GO:0072008	6	2.00E-02	3
GO:BP	regulation of tube size	GO:0035150	127	2.00E-02	8
GO:CC	side of membrane	GO:0098552	492	2.00E-02	14
GO:CC	collagen type I trimer	GO:0005584	2	2.00E-02	2
GO:CC	interleukin-18 receptor complex	GO:0045092	2	2.00E-02	2
TF	Factor: Kaiso; motif: NTCCTGCNAN	TF:M01119	3633	2.00E-02	55
TF	Factor: PPARGAMMA:RXR-ALPHA; motif: NNRGGTCAAWAGGTCAN	TF:M08962	4100	2.00E-02	60
TF	Factor: SNA; motif: GCCACCTGNCNGYN	TF:M03566	1969	2.00E-02	36
TF	Factor: PMX1; motif: TAATHA; match class: 1	TF:M03560_1	8561	2.00E-02	104
TF	Factor: MAZ; motif: GGGMGGGGS; match class: 1	TF:M10432_1	4198	2.00E-02	61
TF	Factor: ESR1; motif: NNNNMAGGTCACCCTGACCY; match class: 1	TF:M02261_1	2053	2.00E-02	37
GO:BP	aromatic compound biosynthetic process	GO:0019438	3605	2.10E-02	54
GO:BP	response to progesterone	GO:0032570	36	2.10E-02	5
GO:BP	semi-lunar valve development	GO:1905314	36	2.10E-02	5
GO:BP	protein metabolic process	GO:0019538	4947	2.10E-02	68
TF	Factor: p73; motif: NNRCAWGYCCARRCWTGYC	TF:M10025	5463	2.10E-02	74
TF	Factor: beta-catenin; motif: CTTTGATN; match class: 1	TF:M07599_1	1809	2.10E-02	34
TF	Factor: ZNF394; motif: NRARWRGAANNNAMWGNAAK; match class: 1	TF:M10147_1	1493	2.10E-02	30
TF	Factor: TFAP2A; motif: NGCCYSAGGCN	TF:M04147	4684	2.10E-02	66
GO:BP	cellular response to lipopolysaccharide	GO:0071222	168	2.20E-02	9
GO:BP	negative regulation of biosynthetic process	GO:0009890	1454	2.20E-02	29
GO:BP	positive regulation of nucleic acid-templated transcription	GO:1903508	1456	2.20E-02	29
GO:BP	positive regulation of transcription, DNA-templated	GO:0045893	1456	2.20E-02	29
TF	Factor: C/EBPbeta; motif: NRTTRYGCAATN	TF:M09881	2226	2.20E-02	39
TF	Factor: AP4; motif: NMNCAGCTGGN; match class: 1	TF:M12580_1	1119	2.20E-02	25
TF	Factor: SOX10; motif: NNAACAAAGNN; match class: 1	TF:M09819_1	906	2.20E-02	22
TF	Factor: AR; motif: NNNGNRRGNACANNGTGTTCTNNNNNN; match class: 1	TF:M00953_1	159	2.20E-02	9
TF	Factor: WT1; motif: SMCNCCNSC	TF:M01118	6380	2.20E-02	83
TF	Factor: SF1; motif: NTGRCCTTGAMCT	TF:M12661	1979	2.20E-02	36
GO:BP	kidney epithelium development	GO:0072073	129	2.30E-02	8
GO:BP	positive regulation of RNA biosynthetic process	GO:1902680	1458	2.30E-02	29
TF	Factor: E2F1; motif: GSGCGGGAAN; match class: 1	TF:M12597_1	9447	2.30E-02	112

TF	Factor: KLF15; motif: GAGNNGGGGNGTDG	TF:M01714	1981	2.30E-02	36
TF	Factor: STAT5A; motif: NAWTTCYNGGAANYN	TF:M00457	3468	2.30E-02	53
TF	Factor: DEC1; motif: CNCACRTGASC	TF:M03572	5982	2.30E-02	79
TF	Factor: ER-alpha; motif: ARGSTGACC	TF:M04881	3378	2.30E-02	52
TF	Factor: NKX2B; motif: CACTTNA	TF:M02109	8588	2.30E-02	104
GO:BP	zinc ion homeostasis	GO:0055069	37	2.40E-02	5
GO:BP	response to purine-containing compound	GO:0014074	130	2.40E-02	8
GO:BP	regulation of hydrolase activity	GO:0051336	870	2.40E-02	21
GO:CC	specific granule membrane	GO:0035579	86	2.40E-02	6
KEGG	Bladder cancer	KEGG:05219	39	2.40E-02	4
TF	Factor: CEBPA; motif: ATTGCAYAAYN	TF:M07205	2066	2.40E-02	37
TF	Factor: HIF-1alpha; motif: NCACGT	TF:M02012	5985	2.40E-02	79
TF	Factor: ZBTB37; motif: TGGCTTTGGY	TF:M12688	3380	2.40E-02	52
TF	Factor: Six-2; motif: NNGTATCRNN	TF:M11030	5986	2.40E-02	79
TF	Factor: NR1B1; motif: NRGGTCANRRGGTCAN	TF:M11792	4126	2.40E-02	60
TF	Factor: Pax-5; motif: RRNGRNGCAN; match class: 1	TF:M03577_1	2236	2.40E-02	39
GO:BP	regulation of phosphorylation	GO:0042325	1159	2.50E-02	25
GO:BP	regulation of coagulation	GO:0050818	63	2.50E-02	6
KEGG	Human papillomavirus infection	KEGG:05165	314	2.50E-02	10
TF	Factor: NFATc1; motif: NATGGAAANWNANTTTYCMN	TF:M04051	4704	2.50E-02	66
TF	Factor: NFATc2; motif: NTTTCCATNNATGGAAAN	TF:M11986	5194	2.50E-02	71
TF	Factor: GR; motif: RGRACATTNTGTYC; match class: 1	TF:M04750_1	1428	2.50E-02	29
TF	Factor: POU3F2; motif: WTATGCWAATKAG	TF:M11904	2582	2.50E-02	43
TF	Factor: DPRX; motif: NNGGATTANN	TF:M04306	4131	2.50E-02	60
TF	Factor: POU4F3; motif: CTAATYW	TF:M07061	5993	2.50E-02	79
TF	Factor: p63; motif: NNRCAWGYCTGGRCWTGYN	TF:M09643	3386	2.50E-02	52
TF	Factor: Fli-1:ETV7; motif: NSMGGAMGGATNTCCGNN	TF:M08283	2670	2.50E-02	44
TF	Factor: ER71:SREBP-2; motif: NTSACGTGACGGAARY	TF:M08457	10905	2.50E-02	125
TF	Factor: TTF-1; motif: NNNCNCTTGASNNN	TF:M02034	3206	2.50E-02	50
GO:BP	negative regulation of ion transport	GO:0043271	131	2.60E-02	8
GO:BP	negative regulation of intrinsic apoptotic signaling pathway	GO:2001243	95	2.60E-02	7
TF	Factor: SREBP; motif: NNNNYCACNCCANNN	TF:M01168	5699	2.60E-02	76
TF	Factor: ATF2; motif: NTGACRTCAYC	TF:M12581	3762	2.60E-02	56
TF	Factor: Fli-1:C/EBPbeta; motif: RNCGGAWRTTGCGCAAY	TF:M08281	6613	2.60E-02	85
TF	Factor: DEC; motif: SCCCAMGTGAAGN	TF:M00997	7759	2.60E-02	96
TF	Factor: Gli2; motif: NTGGGTGGTCNN	TF:M07455	2502	2.60E-02	42
GO:BP	regulation of actin filament-based movement	GO:1903115	38	2.70E-02	5
GO:BP	positive regulation of molecular function	GO:0044093	1394	2.70E-02	28
GO:CC	ficolin-1-rich granule membrane	GO:0101003	55	2.70E-02	5
TF	Factor: POU2F2; motif: NTATGCWAATN	TF:M04072	1912	2.70E-02	35
TF	Factor: c-Jun; motif: NNNNRRTGASTCAN	TF:M07102	4236	2.70E-02	61
TF	Factor: TATA; motif: STATAAAWRNNNNNN	TF:M00252	3672	2.70E-02	55
TF	Factor: DB1; motif: GGRRRRGRRGGAGGGGGNGRRR; match class: 1	TF:M10107_1	2504	2.70E-02	42
TF	Factor: beta-catenin; motif: CTTTGATN	TF:M07599	6721	2.70E-02	86
TF	Factor: p73; motif: NGRCATGYYTGNRCWTGYYN	TF:M09644	3034	2.70E-02	48
GO:BP	muscle organ morphogenesis	GO:0048644	64	2.80E-02	6
GO:BP	negative regulation of ion transmembrane transporter activity	GO:0032413	64	2.80E-02	6
GO:BP	negative regulation of cell motility	GO:2000146	267	2.80E-02	11
TF	Factor: GABP-alpha; motif: AACCGGAAR; match class: 1	TF:M04748_1	9377	2.80E-02	111
TF	Factor: Sp1; motif: NNGGGGCGGGGNN; match class: 1	TF:M00932_1	5909	2.80E-02	78
TF	Factor: C/EBPepsilon; motif: HAANMTTKCNWMAC	TF:M01868	2507	2.80E-02	42
TF	Factor: Sox-18; motif: NACAAYGS	TF:M11623	4529	2.80E-02	64

TF	Factor: ATF3; motif: GRTGACKCA	TF:M12582	6319	2.80E-02	82
GO:MF	SMAD binding	GO:0046332	76	2.90E-02	6
GO:BP	positive regulation of leukocyte activation	GO:0002696	319	2.90E-02	12
TF	Factor: GATA-2; motif: NTGNNNNNNNNAGATAAGN	TF:M09937	2338	2.90E-02	40
TF	Factor: ESR1; motif: STGACCTN	TF:M12602	2862	2.90E-02	46
TF	Factor: NFATc2; motif: NTTTCCGCGGAAAN	TF:M11983	7146	2.90E-02	90
TF	Factor: E2A; motif: NRMCASCTGCNNN	TF:M02088	2511	2.90E-02	42
TF	Factor: Helios; motif: NNTWGGGANNN	TF:M01003	3131	2.90E-02	49
TF	Factor: Dlx-7; motif: NTCRTTAN	TF:M10600	6220	2.90E-02	81
TF	Factor: RFX1; motif: NNGTNRCNWRGYAACNN	TF:M00280	5716	2.90E-02	76
TF	Factor: LRH-1; motif: TCAAGGTCRTGACCTTGA	TF:M11831	3042	2.90E-02	48
TF	Factor: Prep-1; motif: GRBTGANAGATN	TF:M07464	3683	2.90E-02	55
TF	Factor: TEAD3; motif: RCATTCCW	TF:M04144	994	2.90E-02	23
TF	Factor: Oct-2; motif: NTGCATATGCAN; match class: 1	TF:M11899_1	3591	2.90E-02	54
TF	Factor: Msx-1; motif: WNGNAATTANV	TF:M08822	5618	2.90E-02	75
GO:BP	leukocyte mediated immunity	GO:0002443	320	3.00E-02	12
TF	Factor: T-box; motif: NASGTGTNAN	TF:M12021	3685	3.00E-02	55
TF	Factor: JUNB:FRA-2; motif: NRTGASTCAT	TF:M08923	2428	3.00E-02	41
TF	Factor: STAT1; motif: TTCNRGGAAN	TF:M07064	2258	3.00E-02	39
GO:BP	negative regulation of cation channel activity	GO:2001258	39	3.10E-02	5
GO:BP	programmed necrotic cell death	GO:0097300	39	3.10E-02	5
GO:BP	cellular response to molecule of bacterial origin	GO:0071219	176	3.10E-02	9
TF	Factor: GLI; motif: MCVNNGACCACCCAV	TF:M03871	3048	3.10E-02	48
TF	Factor: LRF; motif: RCGACCACCNN; match class: 1	TF:M12230_1	2432	3.10E-02	41
TF	Factor: ERR1; motif: NTGACCTTGRNN	TF:M04873	2694	3.10E-02	44
TF	Factor: Oct3; motif: NATGCAANNN	TF:M01307	3322	3.10E-02	51

GO:CC	apical part of cell	GO:0045177	391	3.20E-02	12
REAC	Signaling by PDGF	REAC:R-HSA-186797	53	3.20E-02	5
TF	Factor: RARA; motif: AGGTCAANNARAGGTCA	TF:M04483	3600	3.20E-02	54
TF	Factor: C/EBPgamma; motif: NRTKRSRMAAKN	TF:M01869	2608	3.20E-02	43
TF	Factor: AP-1; motif: RGTGACTMANN	TF:M00188	2609	3.20E-02	43
TF	Factor: MR; motif: NGNACRNNNYGTNCN	TF:M11849	3788	3.20E-02	56
GO:MF	RAGE receptor binding	GO:0050786	9	3.30E-02	3
TF	Factor: foxm1; motif: TGTTTRCTYWNN	TF:M09930	5734	3.30E-02	76
TF	Factor: RAR-gamma; motif: TGACCTBYNKN	TF:M03562	3697	3.30E-02	55
TF	Factor: HES-1; motif: GNCACGTGNC; match class: 1	TF:M08767_1	6962	3.30E-02	88
TF	Factor: RUNX2; motif: WRACCGCANWAACCGCAN; match class: 1	TF:M04107_1	6039	3.30E-02	79
TF	Factor: STAT6; motif: NNYTTCCY	TF:M00500	4076	3.30E-02	59
TF	Factor: HAIRYLIKE; motif: NNNNCANGTG	TF:M08885	5339	3.40E-02	72
TF	Factor: Brachyury; motif: NTNNCANNNNRGTGTGAANN	TF:M09878	3240	3.40E-02	50
TF	Factor: Fra-1; motif: NATGASTCAYM	TF:M11284	2615	3.40E-02	43
TF	Factor: NF-1C; motif: NTTGGCNNNNTGCCARN; match class: 1	TF:M11729_1	794	3.40E-02	20
TF	Factor: Fra-2; motif: NNRTGAGTCAYN	TF:M09923	3611	3.40E-02	54
GO:BP	response to oxygen levels	GO:0070482	325	3.50E-02	12
TF	Factor: HOXB5; motif: RTCRTTAN	TF:M10698	3800	3.50E-02	56
TF	Factor: Dlx-3; motif: NTCRTTAN	TF:M10609	3800	3.50E-02	56
TF	Factor: E2F-4; motif: NGGCGGGAARN	TF:M07084	10196	3.50E-02	118
GO:BP	growth	GO:0040007	893	3.60E-02	21
GO:BP	pulmonary valve development	GO:0003177	20	3.60E-02	4
REAC	Biological oxidations	REAC:R-HSA-211859	169	3.60E-02	8
REAC	Dissolution of Fibrin Clot	REAC:R-HSA-75205	11	3.60E-02	3

TF	Factor: NFATc2; motif: TTTTCCATGGAAAA; match class: 1	TF:M11985_1	3803	3.60E-02	56
TF	Factor: C/EBPalpha; motif: ATTGCGYAAY	TF:M07412	2888	3.60E-02	46
GO:BP	cellular nitrogen compound biosynthetic process	GO:0044271	4249	3.70E-02	60
GO:BP	negative regulation of cellular component movement	GO:0051271	275	3.70E-02	11
TF	Factor: ZNF342; motif: NRGTGGWCANT	TF:M12076	1229	3.70E-02	26
TF	Factor: Fra-1; motif: NNNTGAGTCAYN	TF:M09922	3807	3.70E-02	56
TF	Factor: T3R-beta; motif: NNRGGTCRTGACCYNN	TF:M11815	4668	3.70E-02	65
GO:BP	in utero embryonic development	GO:0001701	383	3.80E-02	13
GO:BP	response to metal ion	GO:0010038	328	3.80E-02	12
GO:CC	plasma membrane region	GO:0098590	1176	3.80E-02	23
TF	Factor: DPF2; motif: NYCACYTCCYCNYYCY; match class: 1	TF:M09760_1	2803	3.80E-02	45
TF	Factor: GCMa:Erg; motif: ATGCGGGCGGAARKG; match class: 1	TF:M08487_1	8249	3.80E-02	100
TF	Factor: POU5F1; motif: NNATGCAAANN	TF:M09782	2982	3.80E-02	47
TF	Factor: PDEF; motif: MCCGGATNTN	TF:M02075	2453	3.80E-02	41
TF	Factor: SPI1; motif: NGRGGAAGTN	TF:M02078	3073	3.80E-02	48
TF	Factor: MSANTD3; motif: SNNCACTCAC	TF:M12406	3999	3.80E-02	58
TF	Factor: FOXO1A:Net; motif: RWMAACAGGAAGTN; match class: 1	TF:M08302_1	2282	3.80E-02	39
GO:BP	nephron epithelium development	GO:0072009	101	3.90E-02	7
TF	Factor: DMBX1; motif: NNGGATTANN	TF:M04305	4383	3.90E-02	62
TF	Factor: BRCA2; motif: TGMCYCWGN	TF:M12723	3259	3.90E-02	50
GO:BP	negative regulation of blood coagulation	GO:0030195	41	4.00E-02	5
TF	Factor: IRF; motif: RAAANTGAAAN	TF:M00972	1623	4.00E-02	31
TF	Factor: AML2; motif: CCRCACCAYDN	TF:M01854	2372	4.00E-02	40
TF	Factor: CDP:HOXA13; motif: ATCGATYAYSYCRTAAA	TF:M08201	6582	4.00E-02	84
GO:CC	basement membrane	GO:0005604	95	4.10E-02	6
TF	Factor: REST; motif: NNNNGGNGCTGTCCATGGTGCT	TF:M01256	2374	4.10E-02	40
TF	Factor: ER-alpha; motif: NAGGTCACSGTGACCTN	TF:M11843	3172	4.10E-02	49
TF	Factor: HOXA6; motif: NYMATTAN	TF:M08772	6482	4.10E-02	83
TF	Factor: TEF-1; motif: NRCATWCCN; match class: 1	TF:M12042_1	672	4.20E-02	18
TF	Factor: Cdx-2; motif: NRTYRTAAAN	TF:M10851	1953	4.20E-02	35
TF	Factor: STAT3; motif: NGNNATTTCCSGGAARTGNNN	TF:M00225	2815	4.20E-02	45
TF	Factor: E2A; motif: CAGNTGNN	TF:M07353	2292	4.20E-02	39
GO:BP	defense response to bacterium	GO:0042742	183	4.30E-02	9
TF	Factor: MR; motif: NGNACRNNNYGTNCN; match class: 1	TF:M11849_1	3732	4.30E-02	55
TF	Factor: Sox-4; motif: BCWTTGT	TF:M07268	4591	4.30E-02	64
TF	Factor: E2F-4; motif: NNTTCCCGCCNN; match class: 1	TF:M04823_1	7533	4.30E-02	93
GO:BP	negative regulation of proteolysis	GO:0045861	280	4.40E-02	11
GO:BP	entry into host	GO:0044409	141	4.40E-02	8
GO:BP	cell development	GO:0048468	1919	4.40E-02	34
REAC	MET activates PTK2 signaling	REAC:R-HSA-8874081	30	4.40E-02	4
TF	Factor: FOXJ2; motif: NNTGTTGTAAAYAN	TF:M11584	3923	4.40E-02	57
TF	Factor: REST; motif: CCNNGGTGCTGAA	TF:M03883	3090	4.40E-02	48
TF	Factor: Spic; motif: NGNGGAASTN; match class: 1	TF:M02077_1	2042	4.40E-02	36
MIRNA	hsa-miR-204-5p	MIRNA:hsa-miR-204-5p	372	4.40E-02	12
GO:BP	response to interferon-alpha	GO:0035455	21	4.50E-02	4
GO:BP	negative regulation of hemostasis	GO:1900047	42	4.50E-02	5
GO:BP	anion transmembrane transport	GO:0098656	231	4.50E-02	10
GO:CC	aggresome	GO:0016235	33	4.50E-02	4
TF	Factor: AP-2alpha; motif: NTNSCCTGRGGSNAN	TF:M09590	4694	4.50E-02	65
TF	Factor: NF-E4; motif: CHCCCTCKCCWG	TF:M02105	2471	4.50E-02	41
TF	Factor: Hey2; motif: NNCACGYGNN; match class: 1	TF:M11052_1	8713	4.50E-02	104
TF	Factor: Nkx3-2; motif: TRAGTG	TF:M01181	8070	4.50E-02	98

TF	Factor: NFATc2; motif: NTTTCCATNNATGGAAAN; match class: 1	TF:M11986_1	4990	4.50E-02	68
GO:BP	positive regulation of response to external stimulus	GO:0032103	390	4.60E-02	13
TF	Factor: B-ATF; motif: NNAYGACACN	TF:M11301	6607	4.60E-02	84
TF	Factor: isx; motif: NTCRTTAA	TF:M10956	8396	4.60E-02	101
GO:MF	oxygen carrier activity	GO:0005344	10	4.70E-02	3
GO:BP	negative regulation of transcription by RNA polymerase II	GO:0000122	841	4.80E-02	20
REAC	Response to metal ions	REAC:R-HSA-5660526	12	4.80E-02	3
TF	Factor: ERF:C/EBPdelta; motif: NNCGGAWRTTGCGCAAY	TF:M08233	4997	4.80E-02	68
TF	Factor: myogenin; motif: CRSCTGTTBNNTTTGGCACGSNGCCARCH; match class: 1	TF:M00056_1	3842	4.80E-02	56
TF	Factor: Sox-9; motif: MACARWGNNNYCNTTNW; match class: 1	TF:M08838_1	552	4.80E-02	16
GO:BP	response to corticosteroid	GO:0031960	143	4.90E-02	8
GO:BP	lymphocyte mediated immunity	GO:0002449	233	4.90E-02	10
TF	Factor: E2F-4; motif: AATGGCGCCAAA	TF:M04518	4902	4.90E-02	67
TF	Factor: BEN; motif: CWGCGAYA	TF:M01241	6926	4.90E-02	87
TF	Factor: HSF1; motif: RGAANRTTCYRGAAN	TF:M11656	1721	4.90E-02	32
GO:MF	interleukin-18 receptor activity	GO:0042008	2	5.00E-02	2
GO:MF	heme binding	GO:0020037	121	5.00E-02	7

Table A33. KCL BrainBank enrichment for Cluster 2 with gProfiler2. Term size refers to the number of genes in the term, with the intersection size denoting the number of genes in the dataset found in the term. GO:BP – Gene Ontology Biological Process, GO:CC – Gene Ontology Cellular Components, GO:MF – Gene Ontology Molecular Function, KEGG: Kyoto Encyclopaedia of Genes and Genomes, REAC: Reactome, TF: Transfac.

Source	Term Name	Term ID	Term Size	p adjusted	Intersection Size
GO:BP	immune response	GO:0006955	1363	6.00E-58	106
GO:BP	immune system process	GO:0002376	2161	5.50E-57	127
GO:BP	regulation of immune system process	GO:0002682	1217	2.60E-47	91
GO:CC	cell periphery	GO:0071944	5188	2.20E-46	173
GO:BP	defense response	GO:0006952	1343	7.40E-42	89
GO:CC	plasma membrane	GO:0005886	4761	7.20E-41	158
REAC	Immune System	REAC:R-HSA-168256	1770	1.60E-40	98
GO:BP	regulation of immune response	GO:0050776	741	8.30E-40	68
GO:CC	integral component of membrane	GO:0016021	4917	4.20E-37	155
GO:BP	leukocyte activation	GO:0045321	795	8.10E-37	67
GO:CC	intrinsic component of membrane	GO:0031224	5051	2.50E-36	156
GO:BP	cell activation	GO:0001775	914	5.80E-35	69
GO:BP	positive regulation of immune system process	GO:0002684	764	7.70E-35	64
GO:CC	membrane	GO:0016020	8518	3.60E-34	203
REAC	Innate Immune System	REAC:R-HSA-168249	914	8.80E-33	66
GO:BP	response to external stimulus	GO:0009605	2310	2.40E-32	101
GO:BP	response to stimulus	GO:0050896	7482	1.60E-30	184
GO:BP	inflammatory response	GO:0006954	651	1.20E-28	54
GO:BP	immune effector process	GO:0002252	513	1.50E-28	49
GO:BP	regulation of cell activation	GO:0050865	541	1.60E-28	50
GO:MF	signaling receptor activity	GO:0038023	1139	5.80E-28	67
GO:MF	molecular transducer activity	GO:0060089	1139	5.80E-28	67
GO:MF	transmembrane signaling receptor activity	GO:0004888	947	2.40E-27	61
GO:BP	response to biotic stimulus	GO:0009607	1182	3.60E-27	68
GO:BP	defense response to other organism	GO:0098542	842	1.10E-26	58
GO:BP	positive regulation of response to stimulus	GO:0048584	1882	1.30E-26	84
KEGG	Staphylococcus aureus infection	KEGG:05150	60	1.40E-26	22
GO:BP	response to other organism	GO:0051707	1142	2.20E-26	66
GO:BP	response to external biotic stimulus	GO:0043207	1145	2.60E-26	66
GO:BP	regulation of response to stimulus	GO:0048583	3512	4.20E-26	115
GO:BP	regulation of leukocyte activation	GO:0002694	500	6.40E-26	46
GO:BP	leukocyte activation involved in immune response	GO:0002366	253	3.60E-25	35
GO:BP	biological process involved in interspecies interaction between organisms	GO:0044419	1282	4.40E-25	68
GO:BP	cell activation involved in immune response	GO:0002263	257	6.20E-25	35
GO:BP	lymphocyte activation	GO:0046649	652	1.00E-24	50
GO:BP	biological adhesion	GO:0022610	1393	1.60E-24	70
GO:BP	positive regulation of immune response	GO:0050778	464	3.50E-24	43
GO:CC	intrinsic component of plasma membrane	GO:0031226	1541	3.60E-24	72
GO:CC	integral component of plasma membrane	GO:0005887	1466	5.70E-24	70
GO:BP	cell adhesion	GO:0007155	1388	7.60E-24	69
GO:BP	regulation of multicellular organismal process	GO:0051239	2403	2.70E-23	90
GO:BP	regulation of cytokine production	GO:0001817	646	5.10E-23	48
GO:BP	cytokine production	GO:0001816	652	7.70E-23	48
REAC	Neutrophil degranulation	REAC:R-HSA-6798695	446	1.80E-22	40
GO:BP	innate immune response	GO:0045087	667	2.10E-22	48
GO:BP	signaling	GO:0023052	5550	3.40E-22	141
GO:BP	myeloid leukocyte activation	GO:0002274	205	5.50E-22	30
GO:BP	response to stress	GO:0006950	3345	7.90E-22	105
GO:BP	cell communication	GO:0007154	5601	8.50E-22	141
GO:BP	positive regulation of biological process	GO:0048518	5512	1.90E-21	139

GO:BP	biological regulation	GO:0065007	10837	2.70E-21	209
GO:BP	signal transduction	GO:0007165	5094	4.50E-21	132
GO:BP	regulation of biological process	GO:0050789	10213	4.60E-21	201
GO:CC	extracellular region	GO:0005576	3516	6.80E-21	105
GO:BP	adaptive immune response	GO:0002250	390	8.10E-21	37
GO:CC	vesicle	GO:0031982	3591	9.60E-21	106
GO:BP	activation of immune response	GO:0002253	298	1.90E-20	33
GO:BP	negative regulation of immune system process	GO:0002683	375	2.30E-20	36
GO:BP	multicellular organismal process	GO:0032501	6431	2.80E-20	150
GO:BP	cellular response to stimulus	GO:0051716	6392	4.60E-20	149
GO:CC	cytoplasmic vesicle	GO:0031410	2275	6.90E-20	81
GO:CC	intracellular vesicle	GO:0097708	2277	7.20E-20	81
GO:BP	response to bacterium	GO:0009617	504	8.50E-20	40
GO:BP	regulation of cellular process	GO:0050794	9657	1.40E-19	191
GO:BP	immune response-regulating signaling pathway	GO:0002764	396	1.50E-19	36
GO:CC	cell surface	GO:0009986	741	1.80E-19	46
GO:BP	leukocyte mediated immunity	GO:0002443	320	1.90E-19	33
GO:BP	phagocytosis	GO:0006909	229	2.40E-19	29
GO:BP	positive regulation of multicellular organismal process	GO:0051240	1298	1.10E-18	60
TF	Factor: GATAD2A; motif: CCTKTG; match class: 1	TF:M09726_1	7641	2.00E-18	163
TF	Factor: PEA3; motif: ACWTCCK	TF:M00655	8027	2.20E-18	168
TF	Factor: AML1; motif: TGTGGT	TF:M02084	10268	7.00E-18	195
TF	Factor: AML1; motif: TGTGGT	TF:M00751	10268	7.00E-18	195
TF	Factor: AML1a; motif: TGTGGT	TF:M00271	10268	7.00E-18	195
GO:BP	T cell activation	GO:0042110	448	9.30E-18	36
TF	Factor: Smad2; motif: AGACAN; match class: 1	TF:M03580_1	7607	1.00E-17	161
REAC	REACTOME root term	REAC:0000000	9607	1.90E-17	184
GO:CC	secretory granule	GO:0030141	760	2.20E-17	44
GO:CC	secretory granule membrane	GO:0030667	287	2.40E-17	29
TF	Factor: SRY; motif: AACAATNR	TF:M08976	11740	2.70E-17	211
TF	Factor: ZBTB39; motif: CNCTGY	TF:M12689	13477	4.60E-17	230
TF	Factor: PEA3; motif: NNCAGGAARNN	TF:M09915	10849	4.90E-17	200
GO:BP	leukocyte migration	GO:0050900	329	5.60E-17	31
TF	Factor: NMYC; motif: CAYCTG	TF:M01808	10951	5.90E-17	201
GO:BP	regulation of lymphocyte activation	GO:0051249	415	6.60E-17	34
GO:BP	positive regulation of cytokine production	GO:0001819	416	7.10E-17	34
TF	Factor: GATAD2A; motif: CCTKTG	TF:M09726	13089	9.30E-17	225
TF	Factor: Spi-B; motif: TTCYBC; match class: 1	TF:M03851_1	17095	9.60E-17	267
TF	Factor: Spi-B; motif: TTCYBC	TF:M03851	17110	1.10E-16	267
GO:BP	leukocyte cell-cell adhesion	GO:0007159	338	1.20E-16	31
TF	Transfac	TF:M00000	17114	1.20E-16	267
GO:BP	leukocyte proliferation	GO:0070661	286	1.30E-16	29
GO:BP	myeloid cell activation involved in immune response	GO:0002275	87	1.30E-16	19
GO:CC	extracellular space	GO:0005615	2749	1.50E-16	84
GO:BP	cell surface receptor signaling pathway	GO:0007166	2456	1.70E-16	80
KEGG	Systemic lupus erythematosus	KEGG:05322	104	1.90E-16	19
GO:CC	vesicle membrane	GO:0012506	1138	2.30E-16	52
GO:CC	cellular anatomical entity	GO:0110165	16869	4.70E-16	261
TF	Factor: PU.1; motif: AGGAAG	TF:M02031	15486	5.00E-16	249
TF	Factor: Elf-1; motif: AGGAAG	TF:M01266	15486	5.00E-16	249
GO:BP	cell-cell adhesion	GO:0098609	828	5.40E-16	45
GO:CC	cytoplasmic vesicle membrane	GO:0030659	1119	5.80E-16	51

GO:BP	positive regulation of cell activation	GO:0050867	330	6.40E-16	30
TF	Factor: Sox-18; motif: CAAWGBB	TF:M03848	15043	7.10E-16	244
TF	Factor: ZBTB39; motif: CNCTGY; match class: 1	TF:M12689_1	8347	1.10E-15	166
TF	Factor: ZNF35; motif: SSAAKA	TF:M07479	16059	1.20E-15	254
GO:CC	cellular_component	GO:0005575	16974	1.30E-15	261
TF	Factor: Kid3; motif: CCACN	TF:M01160	17056	1.30E-15	264
KEGG	KEGG root term	KEGG:00000	7044	1.40E-15	145
KEGG	Leishmaniasis	KEGG:05140	71	2.70E-15	16
TF	Factor: Smad2; motif: AGACAN	TF:M03580	13070	3.40E-15	221
KEGG	Tuberculosis	KEGG:05152	162	4.80E-15	21
GO:BP	cell population proliferation	GO:0008283	1750	6.00E-15	64
GO:BP	regulation of developmental process	GO:0050793	2221	6.10E-15	73
GO:BP	regulation of immune effector process	GO:0002697	302	6.10E-15	28
TF	Factor: NMYC; motif: CAYCTG; match class: 1	TF:M01808_1	5049	7.70E-15	119
GO:MF	molecular_function	GO:0003674	16562	8.40E-15	255
TF	Factor: ING4; motif: CCACCA	TF:M01743	13898	9.40E-15	229
GO:BP	lymphocyte proliferation	GO:0046651	261	1.70E-14	26
GO:CC	side of membrane	GO:0098552	492	1.70E-14	33
REAC	Adaptive Immune System	REAC:R-HSA-1280218	709	2.20E-14	39
GO:BP	mononuclear cell proliferation	GO:0032943	264	2.30E-14	26
GO:MF	immune receptor activity	GO:0140375	122	2.30E-14	19
TF	Factor: Sox-18; motif: CAAWGBB; match class: 1	TF:M03848_1	10894	2.40E-14	194
GO:BP	positive regulation of leukocyte activation	GO:0002696	319	2.60E-14	28
GO:CC	secretory vesicle	GO:0099503	920	2.80E-14	44
TF	Factor: ETV4; motif: NCAGGAAGNN	TF:M12556	9336	2.80E-14	175
GO:BP	regulation of response to external stimulus	GO:0032101	839	3.10E-14	43

KEGG	Neutrophil extracellular trap formation	KEGG:04613	159	4.90E-14	20
TF	Factor: Kid3; motif: CCACN; match class: 1	TF:M01160_1	16941	5.00E-14	259
TF	Factor: PU.1; motif: NNNNYYYACTTCCTCTTTY	TF:M01172	3663	5.80E-14	96
GO:BP	regulation of leukocyte cell-cell adhesion	GO:1903037	302	6.30E-14	27
GO:BP	immune response-regulating cell surface receptor signaling pathway	GO:0002768	251	7.50E-14	25
TF	Factor: Zbtb44; motif: CKGTGA	TF:M05405	11777	7.50E-14	203
TF	Factor: PARP; motif: TTTCYN	TF:M02027	14025	8.10E-14	228
KEGG	Phagosome	KEGG:04145	143	9.40E-14	19
TF	Factor: BRN1; motif: HAATGCN	TF:M03813	11080	1.70E-13	194
GO:BP	positive regulation of immune effector process	GO:0002699	211	1.90E-13	23
GO:BP	regulation of tumor necrosis factor superfamily cytokine production	GO:1903555	145	2.00E-13	20
GO:BP	tumor necrosis factor superfamily cytokine production	GO:0071706	145	2.00E-13	20
GO:BP	response to chemical	GO:0042221	3698	2.30E-13	95
GO:BP	regulation of cell population proliferation	GO:0042127	1482	2.50E-13	56
REAC	Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	REAC:R-HSA-198933	101	2.70E-13	17
TF	Factor: ZNF35; motif: SSAAKA; match class: 1	TF:M07479_1	13256	3.30E-13	218
TF	Factor: Lyl-1; motif: NCAKCTGYTNYCNN	TF:M09977	11924	3.30E-13	203
GO:BP	cellular process	GO:0009987	15441	3.60E-13	241
GO:CC	external side of plasma membrane	GO:0009897	291	4.30E-13	25
GO:BP	regulation of leukocyte proliferation	GO:0070663	219	4.40E-13	23
GO:BP	anatomical structure development	GO:0048856	5153	5.60E-13	116
TF	Factor: IRF-4; motif: GAAARTA	TF:M01883	6944	6.30E-13	141
GO:CC	endomembrane system	GO:0012505	4326	6.50E-13	102
GO:BP	positive regulation of leukocyte cell-cell adhesion	GO:1903039	223	6.60E-13	23
GO:BP	negative regulation of biological process	GO:0048519	4967	7.60E-13	113
TF	Factor: FOXO1A:Elk-1; motif: RWMAACAGGAAGTN	TF:M08299	6145	7.60E-13	130

GO:BP	immune response-activating cell surface receptor signaling pathway	GO:0002429	226	8.80E-13	23
GO:BP	immune response-activating signal transduction	GO:0002757	226	8.80E-13	23
GO:BP	biological_process	GO:0008150	16323	9.90E-13	249
GO:BP	cellular response to biotic stimulus	GO:0071216	203	1.00E-12	22
GO:BP	regulation of cell-cell adhesion	GO:0022407	400	1.10E-12	29
TF	Factor: SRY; motif: AACAATANCATTGTT	TF:M04555	5745	1.20E-12	124
GO:BP	regulation of leukocyte mediated immunity	GO:0002703	205	1.30E-12	22
GO:BP	chemotaxis	GO:0006935	538	1.30E-12	33
TF	Factor: c-Ets-1; motif: RCAGGAAGTGNNTNS	TF:M00339	5893	1.30E-12	126
TF	Factor: FOXO1A:PDEF; motif: WNCCGGATGTTDN	TF:M08486	9927	1.30E-12	178
TF	Factor: PARP; motif: TTTCYN; match class: 1	TF:M02027_1	10180	1.30E-12	181
GO:BP	developmental process	GO:0032502	5648	1.50E-12	122
GO:BP	taxis	GO:0042330	542	1.70E-12	33
GO:BP	regulation of myeloid leukocyte mediated immunity	GO:0002886	57	1.80E-12	14
GO:BP	regulation of tumor necrosis factor production	GO:0032680	141	1.80E-12	19
GO:BP	tumor necrosis factor production	GO:0032640	141	1.80E-12	19
TF	Factor: PU.1; motif: AGGAAG; match class: 1	TF:M02031_1	11933	2.00E-12	201
TF	Factor: Elf-1; motif: AGGAAG; match class: 1	TF:M01266_1	11933	2.00E-12	201
TF	Factor: ZNF333; motif: ATAAT	TF:M01230	13185	2.20E-12	215
TF	Factor: Sox-17; motif: TTGTYY	TF:M03803	13366	2.20E-12	217
GO:BP	regulation of multicellular organismal development	GO:2000026	1218	2.30E-12	49
TF	Factor: SMAD3; motif: TGTCTGTCT	TF:M00701	3555	2.30E-12	91
TF	Factor: sin3A; motif: TGTCCNNGGTGCTG	TF:M04756	12573	2.50E-12	208
GO:BP	regulation of localization	GO:0032879	2549	2.70E-12	74
GO:BP	positive regulation of cellular process	GO:0048522	5061	2.90E-12	113
GO:BP	negative regulation of cell activation	GO:0050866	190	3.20E-12	21

TF	Factor: Cdx-1; motif: TTTATK	TF:M02086	12282	4.60E-12	204
TF	Factor: Sox-17; motif: TTGTYY; match class: 1	TF:M03803_1	7955	4.70E-12	152
TF	Factor: SMAD3; motif: CAGACAS	TF:M07429	5352	4.90E-12	117
GO:BP	negative regulation of cellular process	GO:0048523	4412	5.00E-12	103
TF	Factor: SATB1; motif: NTTTAT	TF:M03564	13565	6.00E-12	218
TF	Factor: CPBP; motif: SNCCCNN	TF:M01822	16885	6.40E-12	253
GO:BP	regulation of leukocyte migration	GO:0002685	197	6.70E-12	21
GO:BP	regulation of T cell activation	GO:0050863	304	6.80E-12	25
TF	Factor: myogenin; motif: CAGCTG	TF:M02101	11284	7.30E-12	192
TF	Factor: myogenin; motif: CAGCTG; match class: 1	TF:M02101_1	11284	7.30E-12	192
GO:MF	binding	GO:0005488	15390	7.60E-12	235
KEGG	Hematopoietic cell lineage	KEGG:04640	78	7.80E-12	14
GO:BP	macrophage activation	GO:0042116	94	7.90E-12	16
TF	Factor: PEBP2beta; motif: TGTGGTY	TF:M03841	6476	7.90E-12	132
GO:BP	regulation of cell adhesion	GO:0030155	687	8.00E-12	36
GO:BP	cellular response to molecule of bacterial origin	GO:0071219	176	9.00E-12	20
TF	Factor: C-Jun; motif: TGACTC	TF:M03541	9625	9.40E-12	172
TF	Factor: GR; motif: AGAACAN	TF:M07355	4913	9.90E-12	110
TF	Factor: MEL1; motif: GATGAG	TF:M08793	10128	9.90E-12	178
GO:BP	hemopoiesis	GO:0030097	815	1.00E-11	39
GO:BP	myeloid leukocyte mediated immunity	GO:0002444	96	1.10E-11	16
GO:BP	vesicle-mediated transport	GO:0016192	1466	1.10E-11	53
GO:BP	leukocyte differentiation	GO:0002521	507	1.20E-11	31
GO:BP	regulation of lymphocyte proliferation	GO:0050670	203	1.20E-11	21
KEGG	Cell adhesion molecules	KEGG:04514	139	1.20E-11	17
TF	Factor: c-Ets-2; motif: CTTCCTG	TF:M01207	8932	1.40E-11	163

TF	Factor: Elk-1; motif: CTTCCKG	TF:M07252	8932	1.40E-11	163
GO:BP	regulation of mononuclear cell proliferation	GO:0032944	205	1.50E-11	21
TF	Factor: Pax-4; motif: DTTTTCCACCN	TF:M04624	13570	1.50E-11	217
GO:BP	cellular developmental process	GO:0048869	3759	1.60E-11	92
GO:BP	positive regulation of cell-cell adhesion	GO:0022409	259	1.70E-11	23
TF	Factor: Smad2; motif: TGTCTGNCACCT	TF:M09656	5444	1.70E-11	117
GO:BP	defense response to bacterium	GO:0042742	183	1.90E-11	20
TF	Factor: Smad3; motif: NGNCAGACASNNN	TF:M01888	3489	1.90E-11	88
TF	Factor: Pax-4; motif: NNNNNYCACCCB	TF:M00378	15748	1.90E-11	240
TF	Factor: AP-4; motif: AWCAGCTGWT	TF:M11206	6263	2.20E-11	128
TF	Factor: AP-4; motif: AWCAGCTGWT; match class: 1	TF:M11206_1	6263	2.20E-11	128
GO:BP	response to molecule of bacterial origin	GO:0002237	292	2.50E-11	24
TF	Factor: p300; motif: CTGNCTYMAN	TF:M07266	6955	2.80E-11	137
GO:BP	system development	GO:0048731	4335	3.20E-11	100
GO:BP	hematopoietic or lymphoid organ development	GO:0048534	846	3.40E-11	39
TF	Factor: GKLF; motif: CCTCCYN	TF:M01835	13756	3.40E-11	218
TF	Factor: ETV4; motif: NCAGGAAGNN; match class: 1	TF:M12556_1	3399	3.50E-11	86
GO:BP	cell differentiation	GO:0030154	3683	3.80E-11	90
KEGG	Complement and coagulation cascades	KEGG:04610	70	3.80E-11	13
TF	Factor: Oct3; motif: NYWTTSWTATGCAAAT	TF:M09646	4663	3.80E-11	105
GO:MF	protein binding	GO:0005515	13368	4.40E-11	211
TF	Factor: Zbtb44; motif: CKGTGA; match class: 1	TF:M05405_1	5881	4.60E-11	122
TF	Factor: PEA3; motif: ACWTCCK; match class: 1	TF:M00655_1	2384	5.00E-11	69
GO:MF	carbohydrate binding	GO:0030246	236	5.20E-11	21
GO:BP	negative regulation of leukocyte activation	GO:0002695	169	5.40E-11	19
TF	Factor: nerf; motif: YRNCAGGAAGYRGSTBDS	TF:M00531	6635	5.40E-11	132
GO:BP	regulation of phagocytosis	GO:0050764	88	5.60E-11	15
TF	Factor: SPI1; motif: NNNAAAGAGGAAGTGANNNN	TF:M12497	1992	5.60E-11	62
TF	Factor: Elk-1; motif: GGAAGN	TF:M03819	12382	6.10E-11	202
TF	Factor: MAFB; motif: NTCAGCN	TF:M08888	8591	6.40E-11	157
GO:BP	humoral immune response	GO:0006959	171	6.70E-11	19
TF	Factor: PEA3; motif: NNCAGGAARNN; match class: 1	TF:M09915_1	4914	6.90E-11	108
GO:BP	leukocyte degranulation	GO:0043299	73	7.40E-11	14
TF	Factor: NF1C; motif: WGCCARR	TF:M09763	9428	8.30E-11	167
TF	Factor: STAT; motif: NNNNNTTCTKGGA	TF:M00777	4378	8.60E-11	100
GO:BP	cellular response to cytokine stimulus	GO:0071345	744	8.80E-11	36
TF	Factor: FOXO1A:Net; motif: RWMAACAGGAAGTN	TF:M08302	7909	9.00E-11	148
TF	Factor: JUNB:C-JUN; motif: NATGACKCAT	TF:M08944	4454	9.60E-11	101
GO:BP	response to cytokine	GO:0034097	833	1.00E-10	38
GO:CC	tertiary granule membrane	GO:0070821	68	1.10E-10	13
TF	Factor: NFATc2; motif: GGAAAA	TF:M01281	13979	1.10E-10	219
TF	Factor: NFATc3; motif: GGAAAA	TF:M01886	13979	1.10E-10	219
TF	Factor: NFATc2; motif: GGAAAA	TF:M03555	13979	1.10E-10	219
TF	Factor: Sox-9; motif: NNNACAATRG	TF:M11626	5446	1.10E-10	115
GO:BP	multicellular organism development	GO:0007275	4634	1.20E-10	103
TF	Factor: IRF-7; motif: AAGWGAA	TF:M01884	9133	1.20E-10	163
TF	Factor: PMX1; motif: TAATHA	TF:M03560	11838	1.20E-10	195
TF	Factor: PU.1; motif: NRAAAGAGGAAGTGRNN	TF:M10073	2088	1.40E-10	63
TF	Factor: AML1; motif: TGTGGT; match class: 1	TF:M00751_1	4420	1.60E-10	100
TF	Factor: AML1; motif: TGTGGT; match class: 1	TF:M02084_1	4420	1.60E-10	100
TF	Factor: AML1a; motif: TGTGGT; match class: 1	TF:M00271_1	4420	1.60E-10	100
GO:BP	positive regulation of cell communication	GO:0010647	1569	1.70E-10	53

GO:BP	positive regulation of signaling	GO:0023056	1573	1.90E-10	53
GO:CC	extracellular vesicle	GO:1903561	1921	1.90E-10	58
GO:CC	extracellular organelle	GO:0043230	1922	1.90E-10	58
GO:CC	extracellular membrane-bounded organelle	GO:0065010	1922	1.90E-10	58
TF	Factor: SPI1; motif: AGGAAGT	TF:M02278	5850	1.90E-10	120
TF	Factor: PEA3; motif: AGGAAGT	TF:M03579	5850	1.90E-10	120
TF	Factor: C-ets-1; motif: AGGAAGN	TF:M01870	5850	1.90E-10	120
TF	Factor: Fli-1; motif: MGGAAGT	TF:M07382	5850	1.90E-10	120
GO:CC	bounding membrane of organelle	GO:0098588	2037	2.00E-10	60
TF	Factor: T3R-beta; motif: NTGACCTYRNYRAGGTCAN	TF:M11818	10182	2.00E-10	175
GO:CC	tertiary granule	GO:0070820	151	2.10E-10	17
TF	Factor: AP-4; motif: ANCATATGNT	TF:M11207	2574	2.10E-10	71
TF	Factor: YY1; motif: NGCCATYTTKGRCNWWNNGTGCK	TF:M12276	8868	2.10E-10	159
TF	Factor: GTF2IRD1-isoform2; motif: GGGATTRNR	TF:M01229	13062	2.20E-10	208
GO:BP	T cell proliferation	GO:0042098	183	2.30E-10	19
GO:BP	immune system development	GO:0002520	899	2.30E-10	39
TF	Factor: FOSB:JUND; motif: NNTNACTNATN	TF:M08928	5006	2.40E-10	108
TF	Factor: MEL1; motif: GATGAG; match class: 1	TF:M08793_1	4116	2.60E-10	95
GO:BP	positive regulation of response to external stimulus	GO:0032103	390	2.70E-10	26
TF	Factor: Pax-6; motif: CTGACCTGGAACTM	TF:M00979	8330	2.70E-10	152
TF	Factor: HOXA3; motif: NNNNRNTAATTARY	TF:M01337	13550	3.00E-10	213
GO:BP	myeloid leukocyte migration	GO:0097529	186	3.10E-10	19
TF	Factor: SPI1; motif: AAAAAGCGGAAGTW	TF:M03994	1851	3.40E-10	58
TF	Factor: ZNF462; motif: YYYYCTSCWG	TF:M12707	8440	3.70E-10	153
GO:BP	negative regulation of multicellular organismal process	GO:0051241	913	3.80E-10	39
GO:CC	extracellular exosome	GO:0070062	1901	4.10E-10	57
GO:MF	protein-containing complex binding	GO:0044877	1204	4.20E-10	44
TF	Factor: AP-4; motif: AHCATRTGKT	TF:M11213	3359	4.20E-10	83
TF	Factor: SRY; motif: TTGTTT	TF:M03854	12068	4.20E-10	196
TF	Factor: FOXO1A; motif: AAACAA	TF:M03823	12068	4.20E-10	196
GO:BP	locomotion	GO:0040011	1669	5.30E-10	54
GO:BP	cellular response to lipopolysaccharide	GO:0071222	168	6.00E-10	18
GO:BP	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	GO:0002460	247	6.10E-10	21
GO:BP	B cell activation	GO:0042113	247	6.10E-10	21
GO:BP	leukocyte chemotaxis	GO:0030595	193	6.10E-10	19
GO:BP	regulation of transport	GO:0051049	1622	6.20E-10	53
GO:BP	positive regulation of lymphocyte activation	GO:0051251	277	6.50E-10	22
GO:CC	endocytic vesicle membrane	GO:0030666	187	6.70E-10	18
TF	Factor: SMAD; motif: TNGNCAGACWN	TF:M00974	3788	7.60E-10	89
TF	Factor: DREF; motif: CTYYCWCTTCCY	TF:M09725	6415	7.90E-10	126
GO:BP	positive regulation of cell adhesion	GO:0045785	409	8.00E-10	26
TF	Factor: c-Ets-2; motif: CTTCCTG; match class: 1	TF:M01207_1	3080	8.00E-10	78
TF	Factor: Elk-1; motif: CTTCCKG; match class: 1	TF:M07252_1	3080	8.00E-10	78
TF	Factor: HES-5; motif: NCACACKY	TF:M11069	9505	8.90E-10	165
GO:BP	localization	GO:0051179	5792	9.40E-10	117
TF	Factor: T3R-beta; motif: NTGACCTYRNYRAGGTCAN; match class: 1	TF:M11818_1	9678	9.50E-10	167
TF	Factor: GATA-5; motif: TATCTN	TF:M02006	7582	9.50E-10	141
TF	Factor: MafG; motif: CMATGACTCAGCAGA	TF:M07048	5916	1.00E-09	119
GO:BP	cellular response to chemical stimulus	GO:0070887	2745	1.10E-09	72
GO:BP	positive regulation of developmental process	GO:0051094	1182	1.10E-09	44
TF	Factor: egr-3; motif: GTGGGY	TF:M03818	11653	1.10E-09	190

TF	Factor: TFII-I; motif: NAGGAAGTGN	TF:M04636	11048	1.10E-09	183
TF	Factor: C/EBP; motif: NNNTKNNGNAAN	TF:M00770	4639	1.20E-09	101
GO:BP	positive regulation of T cell activation	GO:0050870	202	1.40E-09	19
GO:BP	positive regulation of signal transduction	GO:0009967	1394	1.50E-09	48
GO:BP	positive regulation of gene expression	GO:0010628	1001	1.50E-09	40
TF	Factor: HSF4; motif: CTGCMRN	TF:M07322	14568	1.50E-09	222
GO:BP	transport	GO:0006810	4269	1.60E-09	95
TF	Factor: SRY; motif: TTGTTT; match class: 1	TF:M03854_1	7628	1.60E-09	141
TF	Factor: FOXO1A; motif: AAACAA; match class: 1	TF:M03823_1	7628	1.60E-09	141
TF	Factor: SRY; motif: AACAATNR; match class: 1	TF:M08976_1	6555	1.60E-09	127
TF	Factor: Sox-4; motif: AACAAA	TF:M03849	12223	1.70E-09	196
GO:BP	establishment of localization	GO:0051234	4416	1.80E-09	97
GO:BP	positive regulation of tumor necrosis factor superfamily cytokine production	GO:1903557	91	1.80E-09	14
TF	Factor: THAP1; motif: YTGCCCNNA	TF:M07407	9580	1.80E-09	165
TF	Factor: Erg; motif: MCAGGAAA	TF:M07284	9694	2.40E-09	166
GO:BP	regulation of molecular function	GO:0065009	2797	2.60E-09	72
TF	Factor: SREBP-1; motif: CACSCCA	TF:M00749	7520	2.60E-09	139
TF	Factor: Six-6; motif: NNSTATCRNN	TF:M11037	4351	2.70E-09	96
GO:CC	endocytic vesicle	GO:0030139	325	2.80E-09	22
TF	Factor: FOXM1; motif: NAGASTGATTA	TF:M04611	7843	2.80E-09	143
GO:BP	positive regulation of transport	GO:0051050	838	2.90E-09	36
TF	Factor: BCL-11A; motif: NAAAGAGGAAGTGARAN	TF:M09595	3159	2.90E-09	78
TF	Factor: RARG; motif: RAGGTCAASYARAGGTCA	TF:M04485	4222	3.00E-09	94
TF	Factor: POU2F1:Gscl; motif: NNGATTANNTATKCANNNN	TF:M08404	5279	3.10E-09	109
TF	Factor: HLTF; motif: AGSCARAAAGYRGSTGS	TF:M04613	6765	3.10E-09	129
TF	Factor: Erg; motif: NRRSAGGAAGNGG	TF:M09907	10225	3.20E-09	172

TF	Factor: MEF-2C; motif: TATTTWT	TF:M02025	10824	3.30E-09	179
TF	Factor: Sox-10; motif: NACAAWG	TF:M02116	12073	4.40E-09	193
TF	Factor: ZXDA; motif: NAGGGTG	TF:M06203	6420	4.50E-09	124
TF	Factor: ZXDB; motif: NAGGGTG	TF:M06202	6420	4.50E-09	124
TF	Factor: ZBRK1; motif: NGNNNGGTNAWAAAARRGCNG	TF:M10468	9361	5.20E-09	161
TF	Factor: SREBP; motif: VNNVTCACCCYA	TF:M00776	5467	5.20E-09	111
GO:BP	response to lipopolysaccharide	GO:0032496	277	5.60E-09	21
GO:BP	regulation of cell differentiation	GO:0045595	1400	6.30E-09	47
GO:BP	neutrophil activation involved in immune response	GO:0002283	17	6.80E-09	8
TF	Factor: RelA-p65; motif: AAASTCCC	TF:M04849	5419	7.00E-09	110
TF	Factor: myogenin; motif: RGCAGSTG	TF:M00712	6086	7.20E-09	119
TF	Factor: JUND; motif: NATGAGTCAT	TF:M08934	3610	7.30E-09	84
GO:BP	regulation of hydrolase activity	GO:0051336	870	8.50E-09	36
GO:BP	regulation of leukocyte degranulation	GO:0043300	50	8.60E-09	11
GO:BP	regulation of catalytic activity	GO:0050790	2138	8.70E-09	60
GO:BP	synapse pruning	GO:0098883	11	9.40E-09	7
TF	Factor: SRY; motif: TCAATAMCATTGA	TF:M04557	8365	9.50E-09	148
GO:BP	cell chemotaxis	GO:0060326	255	1.00E-08	20
TF	Factor: SPI1; motif: NNAAWGNGGAASTNNNN	TF:M01203	2304	1.00E-08	63
TF	Factor: AP-4; motif: ANCATATGNT	TF:M11209	2930	1.20E-08	73
TF	Factor: PU.1; motif: WGAGGAAG	TF:M00658	3851	1.30E-08	87
GO:BP	lymphocyte activation involved in immune response	GO:0002285	175	1.40E-08	17
TF	Factor: Erg; motif: NRRSAGGAAGNGG; match class: 1	TF:M09907_1	4480	1.50E-08	96
TF	Factor: NFATc2; motif: NTTTCCRTNNAYGGAAAN; match class: 1	TF:M11984_1	9477	1.50E-08	161
TF	Factor: DREF; motif: CTYYCWCTTCCY; match class: 1	TF:M09725_1	1747	1.50E-08	53
TF	Factor: ING4; motif: CCACCA; match class: 1	TF:M01743_1	8903	1.50E-08	154

TF	Factor: NFATc1; motif: NTTTCCRTNNAYGGAAAN; match class: 1	TF:M11979_1	7539	1.50E-08	137
GO:BP	cell killing	GO:0001906	128	1.60E-08	15
GO:BP	animal organ development	GO:0048513	3102	1.70E-08	75
GO:CC	specific granule	GO:0042581	145	1.70E-08	15
TF	Factor: MEIS1B:HOXA9; motif: TGACASTTTWAYRR	TF:M00421	5493	1.70E-08	110
TF	Factor: STAT5A; motif: TTCCNRGAANNNNNNTTCCNNGRR	TF:M00460	6618	1.70E-08	125
GO:BP	cell migration	GO:0016477	1339	1.80E-08	45
GO:BP	mononuclear cell differentiation	GO:1903131	397	1.90E-08	24
GO:BP	regulation of vesicle-mediated transport	GO:0060627	509	1.90E-08	27
GO:BP	positive regulation of tumor necrosis factor production	GO:0032760	88	2.00E-08	13
KEGG	Intestinal immune network for IgA production	KEGG:04672	39	2.00E-08	9
GO:BP	regulation of defense response	GO:0031347	551	2.10E-08	28
KEGG	Pertussis	KEGG:05133	72	2.20E-08	11
TF	Factor: GR; motif: GGTACAANNTGTYCTK	TF:M00205	5664	2.20E-08	112
REAC	Cytokine Signaling in Immune system	REAC:R-HSA-1280215	634	2.30E-08	29
TF	Factor: SPDEF; motif: NASATCCKGNW	TF:M12650	1491	2.30E-08	48
TF	Factor: NFATc2; motif: NTTTCCRTNNAYGGAAAN	TF:M11984	9531	2.40E-08	161
TF	Factor: NFE2L1; motif: NNNATGACTCAGCANW	TF:M12499	8308	2.60E-08	146
TF	Factor: Spic; motif: NGNGGAASTN	TF:M02077	7359	2.70E-08	134
KEGG	Viral myocarditis	KEGG:05416	56	3.00E-08	10
TF	Factor: Tbx5; motif: TNAGGTGTKV; match class: 1	TF:M01020_1	3443	3.00E-08	80
GO:BP	response to organic substance	GO:0010033	2758	3.10E-08	69
GO:CC	MHC class II protein complex	GO:0042613	15	3.10E-08	7
TF	Factor: GATA-3; motif: AGATAAGATCT	TF:M12193	5254	3.10E-08	106
TF	Factor: Nfe2l1; motif: TGYNNAGTCATT	TF:M07390	5626	3.30E-08	111
TF	Factor: six-4; motif: ANNNATGACACCNNNNN	TF:M01374	5406	3.30E-08	108
GO:BP	regulation of hemopoiesis	GO:1903706	338	3.40E-08	22
TF	Factor: Sox-4; motif: AACAAA; match class: 1	TF:M03849_1	7618	3.40E-08	137
GO:BP	interleukin-8 production	GO:0032637	73	3.50E-08	12
GO:BP	regulation of interleukin-8 production	GO:0032677	73	3.50E-08	12
TF	Factor: Tbx5; motif: TNAGGTGTKV	TF:M01020	9490	3.60E-08	160
TF	Factor: c-Ets; motif: KRCAGGAARTRNKT	TF:M00340	4483	3.70E-08	95
TF	Factor: BRN1; motif: HAATGCN; match class: 1	TF:M03813_1	5787	3.80E-08	113
TF	Factor: NKX2-2; motif: NNNCCACTCAANNN	TF:M12456	8199	4.20E-08	144
TF	Factor: Spi-B; motif: NRAAAGAGGAAGTGARA	TF:M10074	1415	4.60E-08	46
TF	Factor: PU.1; motif: NRAAAGAGGAAGTGARA	TF:M09659	2208	4.70E-08	60
TF	Factor: ZNF273; motif: GAGAGGAGCTAC	TF:M10460	11221	4.70E-08	180
TF	Factor: GCMa:FOXO1A; motif: GTMAATAMGGGTRN	TF:M08318	10029	4.90E-08	166
TF	Factor: AP-4; motif: ANCATATGNT	TF:M11211	2515	5.00E-08	65
TF	Factor: c-Jun; motif: NATGACKCATN	TF:M11267	2641	5.10E-08	67
GO:BP	antigen processing and presentation of peptide antigen via MHC class II	GO:0002495	31	5.20E-08	9
TF	Factor: NR1B1; motif: NRGGTCANNRGGTCAN	TF:M11795	6883	5.40E-08	127
KEGG	Rheumatoid arthritis	KEGG:05323	78	5.50E-08	11
TF	Factor: FOXP1; motif: CTGTTTNYTYTKN	TF:M09855	6424	5.50E-08	121
TF	Factor: SMAD; motif: TGTCTGNNN	TF:M08897	3891	5.60E-08	86
TF	Factor: NFATc4; motif: NGGAAAAN	TF:M07301	3354	5.70E-08	78
GO:BP	mononuclear cell migration	GO:0071674	165	5.90E-08	16
TF	Factor: C/EBPbeta; motif: TKNNGCAANN	TF:M01896	3827	6.00E-08	85
TF	Factor: Elf-1; motif: RNWMBAGGAART	TF:M00746	2905	6.20E-08	71
GO:BP	negative regulation of response to external stimulus	GO:0032102	349	6.40E-08	22
GO:MF	sialic acid binding	GO:0033691	16	6.50E-08	7

TF	Factor: NFATc1; motif: NTTTCCRTNNAYGGAAAN	TF:M11979	7686	6.50E-08	137
KEGG	Osteoclast differentiation	KEGG:04380	124	6.60E-08	13
GO:BP	secretion	GO:0046903	843	6.90E-08	34
TF	Factor: Spi-B; motif: NAWGRGGAAGTR	TF:M11374	2170	6.90E-08	59
TF	Factor: VDR, motif: RRTGNMCYTNNTGAMCCNYNT	TF:M00966	8419	7.20E-08	146
GO:BP	microglial cell activation	GO:0001774	45	7.40E-08	10
GO:BP	humoral immune response mediated by circulating immunoglobulin	GO:0002455	45	7.40E-08	10
TF	Factor: p53; motif: NGRCWTGYCY	TF:M00272	3572	7.40E-08	81
TF	Factor: Erm; motif: NRRSAGGAARNGRN	TF:M09916	5923	7.40E-08	114
GO:BP	lymphocyte differentiation	GO:0030098	353	7.90E-08	22
TF	Factor: NKX25; motif: NNANCCACTTRAAWTT	TF:M01414	8271	8.20E-08	144
TF	Factor: NFATc2; motif: TTTTCCA	TF:M02265	6464	8.30E-08	121
TF	Factor: TEF-1; motif: GRRATG	TF:M00704	10603	8.50E-08	172
TF	Factor: HMGIY; motif: NNKKNAWTTTNYTNN	TF:M01010	6852	8.60E-08	126
GO:BP	positive regulation of phagocytosis	GO:0050766	61	8.70E-08	11
TF	Factor: Sox-9; motif: NNNNAACAATRGNN	TF:M00410	3323	9.40E-08	77
GO:BP	neutrophil activation	GO:0042119	33	9.70E-08	9
GO:BP	complement activation, classical pathway	GO:0006958	33	9.70E-08	9
REAC	GPCR ligand binding	REAC:R-HSA-500792	388	1.00E-07	22
TF	Factor: IRF-2; motif: NAANYGAAASYR	TF:M08775	7180	1.00E-07	130
TF	Factor: FOXO1A:ETV7; motif: NWMAACAGGAMNNNCTTCCNN	TF:M08304	12194	1.00E-07	190
GO:BP	regulation of leukocyte differentiation	GO:1902105	259	1.10E-07	19
GO:MF	immunoglobulin binding	GO:0019865	17	1.10E-07	7
TF	Factor: T3R-beta; motif: RTGACCTYACRTGACCTYA	TF:M11819	5885	1.10E-07	113
TF	Factor: ZNF436; motif: TCCTCCAGGAAGCCY	TF:M10477	12825	1.10E-07	197
GO:BP	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	GO:0002504	34	1.30E-07	9

TF	Factor: AP-4; motif: AHCATRTGKT; match class: 1	TF:M11213_1	2446	1.30E-07	63
TF	Factor: ER71:E2A; motif: CASSTGNACCGGAWRYN	TF:M08568	15994	1.30E-07	231
TF	Factor: ZABC1; motif: ATTCCNAC	TF:M01306	8006	1.40E-07	140
TF	Factor: CRX; motif: YTAATC	TF:M01712	9480	1.40E-07	158
TF	Factor: GLI4; motif: RGGCCTTGAATGCCANGCYMA	TF:M10514	11095	1.40E-07	177
TF	Factor: ZNF644; motif: TCCWGCCTCTSN	TF:M09737	6371	1.50E-07	119
GO:BP	regulation of metabolic process	GO:0019222	6103	1.60E-07	115
TF	Factor: rfx3:SREBP-2; motif: ATGGYAACRTCACGTGAY	TF:M08412	9163	1.60E-07	154
TF	Factor: C/EBPgamma:Elf-1; motif: TKRCGHAATWSCGGAAGT	TF:M08676	7465	1.60E-07	133
TF	Factor: GR; motif: CNNNNTGTYCTNN	TF:M01836	4890	1.60E-07	99
TF	Factor: Cdx-1; motif: TTTATK; match class: 1	TF:M02086_1	8108	1.70E-07	141
KEGG	Asthma	KEGG:05310	22	1.80E-07	7
GO:BP	regulation of T cell proliferation	GO:0042129	152	1.90E-07	15
TF	Factor: Smad2; motif: TGTCTGNCWCCT	TF:M10059	5342	1.90E-07	105
GO:BP	cellular response to organic substance	GO:0071310	2188	2.00E-07	58
TF	Factor: TFAP4; motif: AWCAGCTGWT	TF:M04192	4548	2.00E-07	94
TF	Factor: NFATc2; motif: GGAAAA; match class: 1	TF:M03555_1	9439	2.00E-07	157
TF	Factor: NFATc3; motif: GGAAAA; match class: 1	TF:M01886_1	9439	2.00E-07	157
TF	Factor: NFATc2; motif: GGAAAA; match class: 1	TF:M01281_1	9439	2.00E-07	157
GO:BP	positive regulation of leukocyte migration	GO:0002687	128	2.10E-07	14
TF	Factor: c-Jun; motif: NATGACTCATN	TF:M11265	3855	2.10E-07	84
GO:BP	positive regulation of molecular function	GO:0044093	1394	2.40E-07	44
TF	Factor: LBP-1; motif: CAGCTGS	TF:M00644	7824	2.40E-07	137
TF	Factor: Smad4; motif: NCAGACAN	TF:M07368	3322	2.40E-07	76
GO:BP	positive regulation of catalytic activity	GO:0043085	1031	2.50E-07	37
TF	Factor: TTF1; motif: ASTCAAGTRK	TF:M00432	4425	2.50E-07	92

TF	Factor: CPBP; motif: SNCCCNN; match class: 1	TF:M01822_1	16464	2.50E-07	235
TF	Factor: C/EBPalpha; motif: NRTTGTGCAAYNN	TF:M09596	4356	2.50E-07	91
TF	Factor: Tbx3; motif: NAGGTGTSAN	TF:M12024	3800	2.60E-07	83
TF	Factor: ITF-2; motif: NNCACCTGNN	TF:M04191	4572	2.60E-07	94
TF	Factor: B-ATF; motif: NNATGACACN	TF:M11300	7440	2.70E-07	132
GO:BP	negative regulation of response to stimulus	GO:0048585	1510	2.80E-07	46
TF	Factor: PPARgamma:RXRalpha, motif: AAGTAGGTCACNGTGACCYACTT	TF:M00515	6738	2.80E-07	123
TF	Factor: HOXA13; motif: ATAAMA	TF:M01292	11353	2.80E-07	179
TF	Factor: SPI1; motif: NGRGGAAGTN	TF:M02078	3073	2.90E-07	72
GO:BP	positive regulation of metabolic process	GO:0009893	3369	3.20E-07	76
TF	Factor: ZNF342; motif: TRSTGGACRNT	TF:M12075	5465	3.30E-07	106
TF	Factor: Elk-1; motif: GGAAGN; match class: 1	TF:M03819_1	6527	3.40E-07	120
GO:BP	regulation of cell communication	GO:0010646	3111	3.50E-07	72
GO:MF	G protein-coupled receptor activity	GO:0004930	495	3.50E-07	24
TF	Factor: ZNF684; motif: MAAGGGGTGGACTGT	TF:M10550	13426	3.50E-07	202
REAC	Class A/1 (Rhodopsin-like receptors)	REAC:R-HSA-373076	272	3.90E-07	18
TF	Factor: Ikaros; motif: TGGGAGN	TF:M07260	11832	3.90E-07	184
GO:BP	regulation of inflammatory response	GO:0050727	313	4.00E-07	20
TF	Factor: AP-4:Max; motif: NCAGCTGNNNNNNNCACGTGN	TF:M08674	10025	4.00E-07	163
TF	Factor: SMAD3; motif: CAGACAS; match class: 1	TF:M07429_1	1137	4.00E-07	39
TF	Factor: NR3C1; motif: NRGWACAYNRTGTWCYN	TF:M04476	6162	4.10E-07	115
TF	Factor: RXR:RAR; motif: RGKTCANNNRGAGGTCA	TF:M02272	5486	4.10E-07	106
GO:BP	regulation of signaling	GO:0023051	3125	4.30E-07	72
TF	Factor: Ets; motif: ACTTCCTS	TF:M00971	2036	4.60E-07	55
TF	Factor: MZF-1; motif: TGGGGAR	TF:M01733	10043	4.70E-07	163
GO:BP	cell death	GO:0008219	1881	4.90E-07	52
GO:BP	granulocyte activation	GO:0036230	39	5.10E-07	9
GO:BP	toll-like receptor signaling pathway	GO:0002224	113	5.10E-07	13
TF	Factor: NFATc1; motif: TTTCCAYWRTGGAAA	TF:M04052	5658	5.30E-07	108
TF	Factor: gsh-1; motif: NTMATNRN	TF:M10750	6650	5.30E-07	121
TF	Factor: TR4; motif: ACCCCGS	TF:M04934	15997	5.40E-07	229
TF	Factor: AP-4; motif: RNCAGCTGC	TF:M00927	5587	5.50E-07	107
GO:BP	antigen processing and presentation of exogenous peptide antigen via MHC class II	GO:0019886	27	5.70E-07	8
TF	Factor: Oct-2; motif: NTGCATATGCAN; match class: 1	TF:M11899_1	3591	5.90E-07	79
TF	Factor: SRY; motif: AACAATANCATTGTT; match class: 1	TF:M04555_1	2669	6.00E-07	65
TF	Factor: AR; motif: GGAACGGWACATGTTCT	TF:M08190	6740	6.00E-07	122
TF	Factor: ipf1; motif: TGATTGATK	TF:M10031	7448	6.10E-07	131
GO:BP	negative regulation of immune response	GO:0050777	165	6.20E-07	15
GO:BP	positive regulation of interleukin-8 production	GO:0032757	55	6.20E-07	10
GO:BP	lipopolysaccharide-mediated signaling pathway	GO:0031663	55	6.20E-07	10
GO:BP	secretion by cell	GO:0032940	728	6.30E-07	30
TF	Factor: c-Maf; motif: NWNNNTGCTGACKNNNNNN	TF:M01070	5525	6.30E-07	106
TF	Factor: ERF:FOXO1A; motif: RTMAACAGGAARNS	TF:M08241	6745	6.30E-07	122
TF	Factor: GTF2IRD1-isoform2; motif: GGGATTRNR; match class: 1	TF:M01229_1	7936	6.60E-07	137
GO:CC	specific granule membrane	GO:0035579	86	7.00E-07	11
TF	Factor: T3R-beta; motif: NRGGTCAAAGGTCRN	TF:M11814	12177	7.20E-07	187
TF	Factor: AP-4; motif: ANCATATGNT; match class: 1	TF:M11209_1	2183	7.40E-07	57
KEGG	B cell receptor signaling pathway	KEGG:04662	77	7.50E-07	10
TF	Factor: ARP-1; motif: TGARCCYTTGAMCCCW	TF:M00155	4662	7.50E-07	94
GO:BP	negative regulation of lymphocyte activation	GO:0051250	141	7.60E-07	14
GO:CC	MHC protein complex	GO:0042611	22	7.70E-07	7
GO:BP	cell motility	GO:0048870	1504	7.90E-07	45

GO:BP	localization of cell	GO:0051674	1504	7.90E-07	45
TF	Factor: Sox-18; motif: NACAAYGS	TF:M11623	4529	8.50E-07	92
TF	Factor: c-Ets-1; motif: RCAGGAAGTGNNTNS; match class: 1	TF:M00339_1	1273	8.60E-07	41
GO:BP	regulation of secretion	GO:0051046	562	9.00E-07	26
GO:BP	interferon-gamma production	GO:0032609	96	9.60E-07	12
TF	Factor: NFATc2; motif: NTTTCCATNNATGGAAAN	TF:M11986	5194	9.60E-07	101
GO:BP	G protein-coupled receptor signaling pathway	GO:0007186	836	9.90E-07	32
TF	Factor: Nkx3-2; motif: TRAGTG	TF:M01181	8070	1.10E-06	138
TF	Factor: c-Ets-2; motif: NNCTTCCTNNN	TF:M07379	2966	1.10E-06	69
TF	Factor: STAT3; motif: NNTTCCRGGAANNNNN	TF:M01595	6729	1.10E-06	121
GO:BP	T cell activation involved in immune response	GO:0002286	98	1.20E-06	12
GO:CC	organelle membrane	GO:0031090	3469	1.20E-06	74
GO:MF	signaling receptor binding	GO:0005102	1265	1.20E-06	39
TF	Factor: TFII-I; motif: NAGGAAGTGN; match class: 1	TF:M04636_1	4849	1.20E-06	96
TF	Factor: FOXJ2; motif: NNTGTTGTAAAYAN	TF:M11584	3923	1.20E-06	83
TF	Factor: ZNF333; motif: ATAAT; match class: 1	TF:M01230_1	9656	1.20E-06	157
GO:BP	phagocytosis, engulfment	GO:0006911	59	1.30E-06	10
GO:MF	MHC class II protein complex binding	GO:0023026	23	1.30E-06	7
TF	Factor: c-Myb; motif: NNWGRCAGTTRN	TF:M09990	9243	1.30E-06	152
TF	Factor: MYB; motif: NAACNGNCN	TF:M00913	4422	1.30E-06	90
TF	Factor: Sox-10; motif: MAANRRNNNCWTTGTT; match class: 1	TF:M10065_1	1512	1.30E-06	45
GO:BP	regulation of B cell activation	GO:0050864	122	1.40E-06	13
TF	Factor: JunD; motif: NATGASTCATS	TF:M11268	2342	1.40E-06	59
TF	Factor: HNRPUL1; motif: NCNCAGN	TF:M09746	12084	1.40E-06	185
TF	Factor: NR1B2; motif: NTGACCY	TF:M02111	8513	1.40E-06	143
TF	Factor: sin3A; motif: TGTCCNNGGTGCTG; match class: 1	TF:M04756_1	6912	1.50E-06	123
GO:BP	negative regulation of leukocyte proliferation	GO:0070664	79	1.60E-06	11
GO:BP	positive regulation of intracellular signal transduction	GO:1902533	902	1.60E-06	33
TF	Factor: NFATc1; motif: NTTTCCRTNNAYGGAAAN	TF:M11981	5462	1.60E-06	104
TF	Factor: NFATc1; motif: NTTTCCRTNNAYGGAAAN; match class: 1	TF:M11981_1	4945	1.60E-06	97
TF	Factor: RORbeta; motif: TGACCYA	TF:M01722	5168	1.60E-06	100
TF	Factor: Six-3; motif: NNGTATCRNN	TF:M11034	3061	1.60E-06	70
TF	Factor: Oct3; motif: CYWTTSWNATGCAAAT	TF:M10036	3465	1.70E-06	76
TF	Factor: T-bet; motif: NNGNRGGTGTGRN	TF:M10089	5395	1.70E-06	103
TF	Factor: c-MAF; motif: CNNNCTCAGCA	TF:M03816	4956	1.80E-06	97
TF	Factor: MyoD; motif: CGNCAGCTGTYN	TF:M11187	1698	1.80E-06	48
KEGG	Graft-versus-host disease	KEGG:05332	30	1.90E-06	7
GO:BP	detection of external biotic stimulus	GO:0098581	20	2.00E-06	7
TF	Factor: Sox-10; motif: AACAATRGNCYATTGTT	TF:M11632	4174	2.00E-06	86
TF	Factor: CART1; motif: NGNNYTAATTARTNNNN	TF:M01362	3756	2.00E-06	80
GO:BP	positive regulation of cell population proliferation	GO:0008284	813	2.10E-06	31
TF	Factor: p53; motif: RGRCAWGNCY	TF:M00761	2560	2.10E-06	62
TF	Factor: PMX1; motif: TAATHA; match class: 1	TF:M03560_1	8561	2.20E-06	143
TF	Factor: SMAD5; motif: GSGGCAGM	TF:M03846	7589	2.20E-06	131
TF	Factor: C/EBPbeta; motif: RTTGCGCAA; match class: 1	TF:M04690_1	3216	2.20E-06	72
TF	Factor: beta-catenin; motif: GDMATCAAAGM	TF:M03539	3217	2.20E-06	72
TF	Factor: six4; motif: NCGTATCRTN	TF:M11024	4469	2.20E-06	90
TF	Factor: Rarb; motif: AGGTCANNYARAGGTCA	TF:M08035	4979	2.30E-06	97
TF	Factor: AP-4; motif: ANCATATGNT; match class: 1	TF:M11207_1	1827	2.30E-06	50
REAC	Regulation of Complement cascade	REAC:R-HSA-977606	38	2.40E-06	8
GO:BP	regulation of neutrophil activation	GO:1902563	12	2.50E-06	6
GO:CC	lysosome	GO:0005764	688	2.50E-06	27

GO:CC	lytic vacuole	GO:0000323	688	2.50E-06	27
KEGG	Allograft rejection	KEGG:05330	31	2.50E-06	7
TF	Factor: Sox-10; motif: CWTTGT	TF:M03138	11286	2.50E-06	175
TF	Factor: TCF-1; motif: CTTTGW	TF:M03857	11286	2.50E-06	175
TF	Factor: Fli-1; motif: RCAGGAAGTGR	TF:M07089	4264	2.50E-06	87
GO:BP	respiratory burst	GO:0045730	32	2.60E-06	8
TF	Factor: GR; motif: NNNNNNCNNTNTGTNCTNN	TF:M00192	6349	2.60E-06	115
TF	Factor: CDP:HOXA13; motif: ATCGATYAYSYCRTAAA	TF:M08201	6582	2.60E-06	118
TF	Factor: egr-3; motif: GTGGGY; match class: 1	TF:M03818_1	5816	2.70E-06	108
GO:BP	regulation of mononuclear cell migration	GO:0071675	105	2.80E-06	12
GO:CC	membrane raft	GO:0045121	312	2.90E-06	18
GO:BP	cell junction disassembly	GO:0150146	21	3.00E-06	7
GO:CC	membrane microdomain	GO:0098857	313	3.00E-06	18
TF	Factor: GR; motif: RGNACANKNTGTNCY	TF:M09625	7867	3.00E-06	134
TF	Factor: Oct-2; motif: NTATGCWAATN	TF:M11896	4354	3.10E-06	88
TF	Factor: SRY; motif: AAACWAM	TF:M00148	7951	3.10E-06	135
TF	Factor: ETSLIKE; motif: NACTTCCTNN	TF:M08881	2714	3.10E-06	64
GO:BP	export from cell	GO:0140352	780	3.20E-06	30
TF	Factor: CSX; motif: TSYCACTTSM	TF:M01043	5382	3.20E-06	102
GO:BP	regulation of anatomical structure morphogenesis	GO:0022603	878	3.30E-06	32
TF	Factor: IRF-4; motif: RGGAASWGR	TF:M04818	8202	3.30E-06	138
TF	Factor: MEL1; motif: GARGAT	TF:M08794	9275	3.30E-06	151
TF	Factor: ER-beta; motif: GTCANASTGRCCYNR	TF:M01875	5536	3.30E-06	104
GO:BP	positive regulation of cell differentiation	GO:0045597	782	3.40E-06	30
GO:BP	endocytosis	GO:0006897	555	3.40E-06	25
TF	Factor: SRY; motif: AACAATNNNCATTGTT	TF:M04556	6458	3.50E-06	116
GO:BP	mast cell degranulation	GO:0043303	48	3.70E-06	9
GO:BP	regulation of signal transduction	GO:0009966	2751	3.70E-06	64
GO:BP	intracellular signal transduction	GO:0035556	2497	3.90E-06	60
GO:MF	cargo receptor activity	GO:0038024	77	3.90E-06	10
TF	Factor: TEF; motif: ATGTTWAYATAA	TF:M00672	4809	3.90E-06	94
TF	Factor: BRCA2; motif: TGMCYCWGN	TF:M12723	3259	3.90E-06	72
TF	Factor: Msx-2; motif: NNNGACYAATTAGYNNT; match class: 1	TF:M01393_1	3193	3.90E-06	71
GO:BP	regulation of interleukin-6 production	GO:0032675	133	4.00E-06	13
GO:BP	interleukin-6 production	GO:0032635	133	4.00E-06	13
GO:BP	regulation of toll-like receptor signaling pathway	GO:0034121	66	4.00E-06	10
TF	Factor: ESRRA; motif: CAAGGTCANNYSAAGGTCA	TF:M04458	9722	4.10E-06	156
TF	Factor: CDP; motif: NATYGATSSS	TF:M00106	5335	4.20E-06	101
TF	Factor: rfx3:SRF; motif: TRGCAACNNNNNCCNWATANGGN	TF:M08623	12775	4.20E-06	191
GO:BP	regulation of protein metabolic process	GO:0051246	2316	4.50E-06	57
GO:BP	positive regulation of interleukin-6 production	GO:0032755	87	4.50E-06	11
TF	Factor: IRX5; motif: NWACAYRACAWN	TF:M04378	3270	4.50E-06	72
GO:BP	MHC class II protein complex assembly	GO:0002399	13	4.60E-06	6
GO:BP	peptide antigen assembly with MHC class II protein complex	GO:0002503	13	4.60E-06	6
TF	Factor: TEAD1; motif: NNACATTCCAGNN	TF:M12500	5045	4.60E-06	97
TF	Factor: HOXD4; motif: RTCRTTAN	TF:M10710	2741	4.60E-06	64
TF	Factor: c-Myc; motif: NCCACGTGCNN	TF:M09992	4899	4.60E-06	95
GO:BP	plasma membrane invagination	GO:0099024	67	4.70E-06	10
GO:BP	immunoglobulin mediated immune response	GO:0016064	110	4.70E-06	12
GO:BP	regulation of leukocyte chemotaxis	GO:0002688	110	4.70E-06	12
TF	Factor: Lyl-1; motif: NCAKCTGYTNYCNN; match class: 1	TF:M09977_1	6570	4.80E-06	117
TF	Factor: C/EBPbeta; motif: NKNTTGCNYAAYNN	TF:M00117	3480	4.80E-06	75

TF	Factor: SREBP-2; motif: RTGGGGTGAY	TF:M07406	5054	5.00E-06	97
TF	Factor: C/EBP; motif: NTTRCNNAANNN	TF:M00912	4188	5.30E-06	85
GO:BP	mast cell activation involved in immune response	GO:0002279	50	5.40E-06	9
GO:BP	complement activation	GO:0006956	50	5.40E-06	9
GO:BP	mast cell mediated immunity	GO:0002448	50	5.40E-06	9
GO:BP	regulation of cell migration	GO:0030334	847	5.40E-06	31
REAC	Signaling by GPCR	REAC:R-HSA-372790	615	5.50E-06	25
TF	Factor: GSX2; motif: NNYMATTANN	TF:M04328	5063	5.50E-06	97
TF	Factor: C-Jun; motif: TGACTC; match class: 1	TF:M03541_1	3560	5.50E-06	76
TF	Factor: NFATc2; motif: NTTTCCATNNATGGAAAN; match class: 1	TF:M11986_1	4990	5.60E-06	96
TF	Factor: SAP-1a; motif: CWTCCKGT	TF:M03844	2306	5.60E-06	57
TF	Factor: ER71; motif: CWTCCTGT	TF:M07282	2306	5.60E-06	57
TF	Factor: Oct-2; motif: NYATGCAAATN	TF:M10034	5065	5.60E-06	97
TF	Factor: CDP:SRF; motif: NCCWTAYAAGGTMNKRATCRATN	TF:M08520	8843	5.70E-06	145
TF	Factor: PPARgamma:RXRalpha, motif: AAGTAGGTCACNGTGACCYACTT; match class: 1	TF:M00515_1	3841	5.70E-06	80
GO:BP	B cell mediated immunity	GO:0019724	112	5.80E-06	12
TF	Factor: Spi-B; motif: NAWGCGGAAGTN	TF:M11375	2309	5.80E-06	57
TF	Factor: Sox-10; motif: AACAATGGNCCATTGTT	TF:M11633	3089	5.90E-06	69
TF	Factor: Thap1; motif: SCGCCATSTTKGNTNMGGGCARNN	TF:M04723	10537	5.90E-06	165
KEGG	Inflammatory bowel disease	KEGG:05321	52	6.10E-06	8
KEGG	Type I diabetes mellitus	KEGG:04940	35	6.10E-06	7
GO:BP	regulation of cell death	GO:0010941	1440	6.80E-06	42
TF	Factor: FOXO1A:PDEF; motif: WNCCGGATGTTDN; match class: 1	TF:M08486_1	3785	6.80E-06	79
GO:MF	IgG binding	GO:0019864	9	6.90E-06	5
TF	Factor: Oct-2; motif: NTATGCGCATAN	TF:M11895	3303	6.90E-06	72
TF	Factor: CSX; motif: NNCACTTGNRN	TF:M02108	5994	7.10E-06	109
TF	Factor: Pax-5; motif: RRNGRNGCAN	TF:M03577	7727	7.20E-06	131
TF	Factor: SATB1; motif: NTTTAT; match class: 1	TF:M03564_1	10054	7.40E-06	159
TF	Factor: Oct-4; motif: ATTGWSWTGCWAAWN	TF:M01124	4945	7.50E-06	95
TF	Factor: MEF-2C; motif: TATTTWT; match class: 1	TF:M02025_1	6386	7.50E-06	114
TF	Factor: ZBTB44; motif: MACWGCAGS	TF:M12352	5619	7.60E-06	104
GO:BP	programmed cell death	GO:0012501	1737	7.80E-06	47
TF	Factor: GATA-3; motif: AGATAA	TF:M01878	8472	7.90E-06	140
TF	Factor: Spi-B; motif: RAAWGRGGAAGTN	TF:M11376	613	8.00E-06	26
TF	Factor: CTCF; motif: CANNWRRTGGCAG	TF:M04745	7022	8.10E-06	122
REAC	Interferon gamma signaling	REAC:R-HSA-877300	83	8.20E-06	10
TF	Factor: Bcl-6; motif: NTTYCTAGRA	TF:M02085	4154	8.20E-06	84
TF	Factor: C/EBPalpha; motif: NNNTTNNGCAANN	TF:M01866	4299	8.30E-06	86
GO:BP	regulated exocytosis	GO:0045055	231	8.60E-06	16
TF	Factor: Tbx5; motif: NNAGGTGTNANN	TF:M01019	4960	8.80E-06	95
GO:BP	positive regulation of phosphate metabolic process	GO:0045937	817	9.20E-06	30
GO:BP	positive regulation of phosphorus metabolic process	GO:0010562	817	9.20E-06	30
GO:CC	cytoplasm	GO:0005737	11064	9.20E-06	167
TF	Factor: Spi-B; motif: AAAAWGMGGAAGTWNSN	TF:M01204	663	9.30E-06	27
TF	Factor: HOXD4; motif: RTCRTTAN	TF:M10713	3124	9.40E-06	69
KEGG	Legionellosis	KEGG:05134	55	9.60E-06	8
TF	Factor: C-FOS; motif: NATGAGTCATN	TF:M08946	2153	9.60E-06	54
GO:BP	lymphocyte mediated immunity	GO:0002449	233	9.70E-06	16
TF	Factor: SRY; motif: TCAATAMCATTGA; match class: 1	TF:M04557_1	3956	9.70E-06	81
TF	Factor: PPARGAMMA:RXR-ALPHA; motif: NNRGGTCAAWAGGTCAN	TF:M08962	4100	9.90E-06	83
REAC	Antimicrobial peptides	REAC:R-HSA-6803157	30	1.00E-05	7

TF	Factor: Oct-2; motif: NTGCATATGCAN	TF:M11899	4532	1.00E-05	89
TF	Factor: SMAD3; motif: TGTCTGTCT; match class: 1	TF:M00701_1	575	1.00E-05	25
TF	Factor: TBX2; motif: NNNGTGTSNN	TF:M12026	6418	1.00E-05	114
TF	Factor: FOXO1A:Net; motif: RWMAACAGGAAGTN; match class: 1	TF:M08302_1	2282	1.00E-05	56
TF	Factor: Fra-1; motif: ACTCATG	TF:M04897	2096	1.00E-05	53
TF	Factor: IRF-4; motif: NAANGRGGAASTGAAASN	TF:M09959	2865	1.00E-05	65
TF	Factor: C/EBPbeta; motif: RTTGCGCAA	TF:M04690	3752	1.10E-05	78
TF	Factor: ZNF549; motif: NTGCTKYCMW	TF:M12355	5656	1.10E-05	104
TF	Factor: NF-E4; motif: GTGAGGS	TF:M08826	10022	1.10E-05	158
GO:BP	regulation of interferon-gamma production	GO:0032649	95	1.20E-05	11
GO:BP	positive regulation of leukocyte differentiation	GO:1902107	146	1.20E-05	13
GO:BP	positive regulation of hemopoiesis	GO:1903708	146	1.20E-05	13
GO:CC	clathrin-coated endocytic vesicle membrane	GO:0030669	66	1.20E-05	9
MIRNA	hsa-miR-335-5p	MIRNA:hsa-miR-335-5p	2271	1.20E-05	54
REAC	Complement cascade	REAC:R-HSA-166658	46	1.20E-05	8
TF	Factor: TCF-7; motif: TCAAAG	TF:M00805	10201	1.20E-05	160
TF	Factor: TCF-3; motif: CTTTGA	TF:M03858	10201	1.20E-05	160
TF	Factor: OLIG2; motif: CCAKCTGYTYNYNNNNNN	TF:M10019	3416	1.20E-05	73
TF	Factor: Erg; motif: NACAGGAARTN	TF:M11390	2358	1.20E-05	57
GO:BP	response to wounding	GO:0009611	505	1.30E-05	23
GO:BP	negative regulation of lymphocyte proliferation	GO:0050672	74	1.30E-05	10
GO:BP	membrane invagination	GO:0010324	74	1.30E-05	10
GO:BP	negative regulation of mononuclear cell proliferation	GO:0032945	74	1.30E-05	10
GO:BP	peptide antigen assembly with MHC protein complex	GO:0002501	15	1.30E-05	6
GO:MF	MHC protein complex binding	GO:0023023	31	1.30E-05	7
TF	Factor: RXRA; motif: RRGGTCATGACCYY	TF:M04490	6522	1.30E-05	115
KEGG	Autoimmune thyroid disease	KEGG:05320	39	1.40E-05	7
TF	Factor: MRF4; motif: CASCTGC	TF:M03831	7565	1.40E-05	128
TF	Factor: HTF4; motif: CASCTGB	TF:M02018	7565	1.40E-05	128
TF	Factor: MafB; motif: GNTGAC	TF:M01227	10227	1.40E-05	160
GO:BP	regulation of neutrophil degranulation	GO:0043313	8	1.50E-05	5
GO:BP	positive regulation of apoptotic cell clearance	GO:2000427	8	1.50E-05	5
TF	Factor: POU2F1:Gscl; motif: NNGATTANNTATKCANNNN; match class: 1	TF:M08404_1	1404	1.50E-05	41
TF	Factor: myogenin; motif: CRSCTGTTBNNTTTGGCACGSNGCCARCH	TF:M00056	9551	1.50E-05	152
GO:BP	response to lipid	GO:0033993	787	1.60E-05	29
TF	Factor: JunD; motif: NRTGAGTCAYN	TF:M09964	4213	1.60E-05	84
TF	Factor: RelA-p65; motif: BCWGGGRANNK	TF:M04811	6469	1.60E-05	114
GO:BP	antigen processing and presentation of peptide antigen	GO:0048002	76	1.70E-05	10
GO:BP	antigen receptor-mediated signaling pathway	GO:0050851	179	1.70E-05	14
TF	Factor: DBP; motif: TTRCATAANN	TF:M07038	4582	1.70E-05	89
TF	Factor: Sox-8; motif: NGAACAATRN	TF:M11629	1030	1.70E-05	34
TF	Factor: TBP; motif: NGNNTATAAAA	TF:M03581	5782	1.70E-05	105
GO:BP	cytokine-mediated signaling pathway	GO:0019221	430	1.80E-05	21
TF	Factor: T3R-beta; motif: NRGGTCAAAGGTCAN	TF:M11816	10084	1.80E-05	158
TF	Factor: msc; motif: NRMCATATGNYN	TF:M11146	2641	1.80E-05	61
TF	Factor: Pax-4; motif: NNNNNYCACCCB; match class: 1	TF:M00378_1	13163	1.80E-05	193
TF	Factor: Sox-30; motif: NAACAATN	TF:M11641	1945	1.80E-05	50
TF	Factor: KLF4; motif: MCACACCCTNN	TF:M09808	3175	1.80E-05	69
TF	Factor: C/EBPgamma; motif: YTBATTTCARAAW	TF:M00622	5635	1.80E-05	103
TF	Factor: znf136; motif: CAAGAATWCTATAYCCAG	TF:M10535	6878	1.80E-05	119
KEGG	Transcriptional misregulation in cancer	KEGG:05202	166	1.90E-05	12

TF	Factor: HSF4; motif: CTGCMRN; match class: 1	TF:M07322_1	10436	1.90E-05	162
TF	Factor: JunD; motif: SATGACTCATN	TF:M11269	3179	1.90E-05	69
TF	Factor: CLOCK; motif: NNCAYGYGYN	TF:M11046	2134	1.90E-05	53
TF	Factor: HOXA3; motif: NNNNRNTAATTARY; match class: 1	TF:M01337_1	10095	1.90E-05	158
GO:BP	regulation of cellular protein metabolic process	GO:0032268	2160	2.00E-05	53
TF	Factor: B-ATF; motif: NNATGACACN; match class: 1	TF:M11300_1	2135	2.00E-05	53
GO:BP	MHC protein complex assembly	GO:0002396	16	2.10E-05	6
GO:BP	regulation of cell motility	GO:2000145	898	2.10E-05	31
TF	Factor: FOXO1A:Elf-1; motif: NAGAAAACCGAANM	TF:M08295	10193	2.10E-05	159
TF	Factor: DRI1; motif: AATTAA	TF:M01654	9177	2.10E-05	147
TF	Factor: Dlx-5; motif: AATTAN	TF:M03546	9177	2.10E-05	147
REAC	G alpha (i) signalling events	REAC:R-HSA-418594	276	2.20E-05	16
TF	Factor: Pit-1; motif: NMTTCATAAWTATWNMNA	TF:M00802	3743	2.20E-05	77
TF	Factor: HMX2; motif: SCACTTANC	TF:M10646	6195	2.30E-05	110
TF	Factor: foxm1; motif: TGTTTRCTYWNN	TF:M09930	5734	2.30E-05	104
TF	Factor: LHX3; motif: ATTAAW	TF:M02097	10034	2.30E-05	157
TF	Factor: GR; motif: NNTGTYCT	TF:M00921	1600	2.30E-05	44
GO:BP	negative regulation of cytokine production	GO:0001818	248	2.40E-05	16
GO:BP	positive regulation of macromolecule metabolic process	GO:0010604	3089	2.40E-05	67
GO:BP	regulation of cell killing	GO:0031341	79	2.40E-05	10
REAC	Hemostasis	REAC:R-HSA-109582	570	2.40E-05	23
TF	Factor: Octamer; motif: TNATTTGCATN	TF:M00795	3752	2.40E-05	77
TF	Factor: Oct-1; motif: NNNNNNNWATGCAAATNNNWNNA	TF:M00138	2024	2.40E-05	51
GO:BP	regulation of macromolecule metabolic process	GO:0060255	5629	2.50E-05	102
TF	Factor: HES-5; motif: NCACACKY; match class: 1	TF:M11069_1	3616	2.50E-05	75
GO:BP	complement-mediated synapse pruning	GO:0150062	4	2.60E-05	4
TF	Factor: ELF3; motif: NNCCACTTCCTGNN	TF:M12544	3272	2.60E-05	70
GO:BP	myeloid cell differentiation	GO:0030099	360	2.70E-05	19
TF	Factor: C/EBPdelta; motif: TTGCNNMAN	TF:M03571	3137	2.70E-05	68
TF	Factor: TEF-3; motif: GNTATTTTT	TF:M07270	8541	2.70E-05	139
TF	Factor: Foxc1; motif: TTVYTTTNW	TF:M07254	6449	2.70E-05	113
TF	Factor: B-ATF; motif: NNAYGACACN	TF:M11301	6607	2.70E-05	115
TF	Factor: AP-2; motif: NNGCCTK	TF:M01859	6687	2.80E-05	116
TF	Factor: Fli-1; motif: NNRGGMAGGAAGGRRRGR	TF:M09920	8216	2.80E-05	135
TF	Factor: Six-2; motif: NNGTATCRNN	TF:M11030	5986	2.80E-05	107
TF	Factor: NR1B1; motif: NRGGNCRTGACCTN	TF:M11796	9466	2.80E-05	150
GO:MF	peptide binding	GO:0042277	282	2.90E-05	16
KEGG	Coronavirus disease - COVID-19	KEGG:05171	206	2.90E-05	13
TF	Factor: FXR:RXR-ALPHA; motif: NRGGTCANRGGKN	TF:M08955	8470	2.90E-05	138
TF	Factor: LXR; motif: NTGACCKNNAGTRACCYNN	TF:M03795	5609	3.00E-05	102
TF	Factor: ipf1; motif: CATTAR	TF:M01275	7333	3.00E-05	124
GO:BP	regulation of phosphate metabolic process	GO:0019220	1289	3.10E-05	38
TF	Factor: Oct-1; motif: NNNNATGCAAATNAN	TF:M00195	3014	3.10E-05	66
GO:BP	regulation of phosphorus metabolic process	GO:0051174	1291	3.20E-05	38
GO:BP	positive regulation of superoxide anion generation	GO:0032930	17	3.20E-05	6
GO:BP	cellular defense response	GO:0006968	43	3.20E-05	8
GO:BP	regulation of mast cell activation	GO:0033003	43	3.20E-05	8
TF	Factor: IRF-4; motif: AAGTTTC	TF:M04855	6624	3.20E-05	115
TF	Factor: Six-1; motif: NCGTATCRNN	TF:M11029	1980	3.20E-05	50
TF	Factor: AR; motif: RGGWACAYNGTGTWCYN	TF:M04453	6079	3.20E-05	108
TF	Factor: HOXB2; motif: RTCATTAN	TF:M10739	3153	3.20E-05	68
GO:CC	vacuole	GO:0005773	781	3.30E-05	27

TF	Factor: MGA; motif: AGGTGTGA	TF:M04117	1738	3.30E-05	46
TF	Factor: TBX1; motif: AGGTGTGA	TF:M04126	1738	3.30E-05	46
TF	Factor: Tbx5; motif: AGGTGTKA	TF:M04137	1738	3.30E-05	46
TF	Factor: TBX15; motif: AGGTGTGA	TF:M04122	1738	3.30E-05	46
TF	Factor: TBX4; motif: AGGTGTGA	TF:M04135	1738	3.30E-05	46
TF	Factor: MEF-2D; motif: WAAATAR	TF:M02026	6393	3.30E-05	112
TF	Factor: GCMa:C/EBPbeta; motif: ATGCGGGTNNRTTGCGCAAY	TF:M08575	5928	3.30E-05	106
GO:BP	mast cell activation	GO:0045576	61	3.40E-05	9
TF	Factor: Pax-4; motif: DTTTTCCACCN; match class: 1	TF:M04624_1	8077	3.40E-05	133
TF	Factor: NF-1C; motif: NYTGGCNNYNNGCCARN	TF:M10002	5930	3.40E-05	106
GO:BP	regulation of biological quality	GO:0065008	3465	3.50E-05	72
TF	Factor: SREBP-1; motif: CACSCCA; match class: 1	TF:M00749_1	2428	3.50E-05	57
TF	Factor: Ikaros; motif: TGGGAGN; match class: 1	TF:M07260_1	6245	3.50E-05	110
TF	Factor: C/EBPalpha; motif: NRTTGTGCAAYN	TF:M09880	2890	3.60E-05	64
GO:BP	regulation of angiogenesis	GO:0045765	256	3.70E-05	16
REAC	Cell surface interactions at the vascular wall	REAC:R-HSA-202733	123	3.70E-05	11
TF	Factor: HELIOS; motif: RNARRRGGAASTGARAN	TF:M09745	2894	3.80E-05	64
TF	Factor: TCF11:MafG; motif: NNNNNATGACTCAGCANTTNNG	TF:M00284	3651	3.80E-05	75
TF	Factor: FOXO1A:HOXA10; motif: RWMAACANCRTWAA	TF:M08482	3442	3.80E-05	72
GO:BP	positive regulation of defense response	GO:0031349	257	3.90E-05	16
TF	Factor: Six-1; motif: NNGTATCRNN	TF:M11026	5183	3.90E-05	96
TF	Factor: Zic3; motif: NGGGKGGTC	TF:M00450	12380	3.90E-05	183
TF	Factor: LBX2; motif: CTNRANSTAATTA; match class: 1	TF:M04383_1	1933	4.10E-05	49
TF	Factor: FAC1; motif: NNNCAMAACACRNA	TF:M00456	6812	4.10E-05	117
TF	Factor: msc; motif: NRMCATATGNYN; match class: 1	TF:M11146_1	2505	4.20E-05	58
TF	Factor: Dlx-3; motif: NTCRTTAN	TF:M10609	3800	4.20E-05	77

TF	Factor: HOXB5; motif: RTCRTTAN	TF:M10698	3800	4.20E-05	77
TF	Factor: nanog; motif: NYWTTGWNATGCAAATN	TF:M09639	1458	4.30E-05	41
TF	Factor: Sox-10; motif: NACAAWG; match class: 1	TF:M02116_1	6582	4.30E-05	114
TF	Factor: POU2F1; motif: ATTTGCATN	TF:M07058	2707	4.50E-05	61
TF	Factor: NFATC3; motif: WNTTTCCRNN	TF:M08001	1404	4.50E-05	40
GO:BP	regulation of vasculature development	GO:1901342	260	4.60E-05	16
GO:BP	pattern recognition receptor signaling pathway	GO:0002221	163	4.70E-05	13
TF	Factor: c-Jun; motif: NATGASTCATN; match class: 1	TF:M11264_1	3183	4.70E-05	68
TF	Factor: SALL2; motif: GGGTGGG	TF:M04595	11697	4.70E-05	175
TF	Factor: MAF; motif: NGCTGAGTCAN	TF:M00983	5128	4.70E-05	95
TF	Factor: Six-3; motif: NNRTATCRNN	TF:M11035	1522	4.80E-05	42
TF	Factor: AP-4; motif: AWCAGCTGWT	TF:M11210	3956	4.80E-05	79
TF	Factor: AP-4; motif: AWCAGCTGWT; match class: 1	TF:M11210_1	3956	4.80E-05	79
GO:BP	negative regulation of inflammatory response	GO:0050728	135	4.90E-05	12
TF	Factor: FOXJ2; motif: AYMATAATATTTKN	TF:M00423	5662	4.90E-05	102
TF	Factor: Ngn-2; motif: RACATATGTY	TF:M11132	673	5.40E-05	26
TF	Factor: Erg; motif: MCAGGAAA; match class: 1	TF:M07284_1	3752	5.40E-05	76
TF	Factor: ZBTB2; motif: TCCKCCTSR	TF:M07437	3263	5.40E-05	69
GO:BP	regulation of locomotion	GO:0040012	937	5.60E-05	31
TF	Factor: CTCF; motif: NNNNANASYGCCMYCTAGTGG	TF:M04689	4847	5.70E-05	91
TF	Factor: SMAD4; motif: GKSRKKCAGMCANCY	TF:M00733	7655	5.70E-05	127
TF	Factor: Tbx1; motif: NNAGGTGTGAAN	TF:M12035	2399	5.80E-05	56
TF	Factor: OCT-x; motif: CTNATTTGCATAY	TF:M00210	3408	5.90E-05	71
TF	Factor: Oct3; motif: NNTTATGYWAATKARN	TF:M11932	2470	6.40E-05	57
TF	Factor: GATA-1; motif: NNNNNGATANKGGN	TF:M00126	3277	6.40E-05	69
TF	Factor: TEF-1; motif: GRRATG; match class: 1	TF:M00704_1	4564	6.50E-05	87

TF	Factor: IRF-4; motif: GAAARTA; match class: 1	TF:M01883_1	2342	6.50E-05	55
TF	Factor: PRDM16; motif: KGGTCATRACCM	TF:M05946	6003	6.50E-05	106
GO:BP	regulation of apoptotic cell clearance	GO:2000425	10	6.60E-05	5
TF	Factor: Nrf-2; motif: NTGCTGAGTCAKN	TF:M00821	3984	6.60E-05	79
GO:BP	exocytosis	GO:0006887	342	6.70E-05	18
TF	Factor: FOXJ2; motif: NNTGTTGTAAAYAN	TF:M11585	4568	6.70E-05	87
REAC	FCGR activation	REAC:R-HSA-2029481	13	6.80E-05	5
GO:BP	positive regulation of myeloid leukocyte mediated immunity	GO:0002888	19	6.90E-05	6
TF	Factor: AP-4; motif: AWCAGCTGWT	TF:M11208	3562	6.90E-05	73
TF	Factor: TBX15; motif: NAGGTGTGAN	TF:M12040	2218	6.90E-05	53
TF	Factor: GSX1; motif: NNYMATTANN; match class: 1	TF:M04327_1	4571	6.90E-05	87
GO:BP	regulation of interleukin-1 beta production	GO:0032651	88	7.00E-05	10
GO:BP	interleukin-1 beta production	GO:0032611	88	7.00E-05	10
TF	Factor: FOXO1A:Elk-1; motif: RWMAACAGGAAGTN; match class: 1	TF:M08299_1	1312	7.00E-05	38
TF	Factor: Blimp-1; motif: NACTTTCAC	TF:M04731	3425	7.10E-05	71
TF	Factor: Msx-2; motif: TWWTTGGDGABN	TF:M03797	4137	7.20E-05	81
TF	Factor: NeuroD-2; motif: RMCATATGKY	TF:M01287	2032	7.30E-05	50
TF	Factor: Oct-2; motif: NNNATTATGCAW	TF:M11894	2946	7.30E-05	64
GO:BP	positive regulation of hydrolase activity	GO:0051345	511	7.40E-05	22
GO:BP	regulation of secretion by cell	GO:1903530	511	7.40E-05	22
GO:BP	cellular response to lipid	GO:0071396	511	7.40E-05	22
TF	Factor: SPIB; motif: NNTCACTTCCTCTTTN	TF:M12498	1908	7.40E-05	48
TF	Factor: ATF-4; motif: GGATGATGTCATCC	TF:M11334	5176	7.50E-05	95
TF	Factor: EVX1; motif: NTCATTAN	TF:M10864	4360	7.60E-05	84
TF	Factor: GATA-3; motif: AGATAA; match class: 1	TF:M01878_1	3293	7.80E-05	69
GO:BP	regulation of mast cell degranulation	GO:0043304	32	7.90E-05	7
GO:BP	detection of biotic stimulus	GO:0009595	32	7.90E-05	7
TF	Factor: NF1C; motif: WGCCARR; match class: 1	TF:M09763_1	3644	7.90E-05	74
TF	Factor: Pax-2; motif: NNNNGTCANGNRTKANNNN	TF:M00098	6494	7.90E-05	112
GO:BP	apoptotic process	GO:0006915	1692	8.20E-05	44
TF	Factor: PU.1; motif: ACTTCCTCT	TF:M04711	1495	8.50E-05	41
TF	Factor: Spic; motif: NGNGGAASTN; match class: 1	TF:M02077_1	2042	8.50E-05	50
GO:BP	cellular response to oxygen-containing compound	GO:1901701	1062	8.60E-05	33
GO:CC	phagocytic vesicle	GO:0045335	136	8.70E-05	11
TF	Factor: POU3F2; motif: WTATGCWAATKA	TF:M04079	2624	8.70E-05	59
TF	Factor: GSX2; motif: NNYMATTANN; match class: 1	TF:M04328_1	3165	8.80E-05	67
GO:BP	positive regulation of leukocyte mediated immunity	GO:0002705	115	8.90E-05	11
GO:CC	clathrin-coated endocytic vesicle	GO:0045334	83	9.10E-05	9
TF	Factor: FOXO1A:ETV7; motif: NWMAACAGGAMNNNCTTCCNN; match class: 1	TF:M08304_1	6512	9.20E-05	112
GO:BP	blood vessel morphogenesis	GO:0048514	563	9.30E-05	23
TF	Factor: ZNF462; motif: YYYYCTSCWG; match class: 1	TF:M12707_1	3033	9.30E-05	65
GO:CC	clathrin-coated vesicle membrane	GO:0030665	109	9.50E-05	10
TF	Factor: TORC2; motif: TGGGCTKKD	TF:M07341	4235	9.50E-05	82
TF	Factor: Oct-1; motif: NNNRTAATNANNN	TF:M00137	5582	9.50E-05	100
TF	Factor: c-Jun; motif: NNNNRRTGASTCAN	TF:M07102	4236	9.60E-05	82
GO:BP	regulation of superoxide anion generation	GO:0032928	20	9.80E-05	6
TF	Factor: Pax-6; motif: NNNNTTCACGCWTGANTKNNN	TF:M00097	9552	9.80E-05	149
TF	Factor: GATA-1; motif: NCWGATAACA	TF:M00346	3594	9.90E-05	73
GO:BP	negative regulation of cell population proliferation	GO:0008285	660	1.00E-04	25
GO:BP	angiogenesis	GO:0001525	477	1.00E-04	21
TF	Factor: CDP; motif: ATCGATNNNNNATCRAT	TF:M03950	3384	1.00E-04	70
TF	Factor: TBR2; motif: AGGTGTGAA	TF:M01774	743	1.00E-04	27

TF	Factor: SATB1; motif: AKWAWTAAHGRYMNWW	TF:M01723	2569	1.00E-04	58
TF	Factor: GATA-3; motif: AGATAAGATCT; match class: 1	TF:M12193_1	1274	1.00E-04	37
GO:BP	positive regulation of cell killing	GO:0031343	50	1.10E-04	8
GO:BP	regulation of endopeptidase activity	GO:0052548	354	1.10E-04	18
MIRNA	MIRNA root	MIRNA:000000	13878	1.10E-04	195
TF	Factor: E2F-3; motif: NNTTTTGGCGCCAAAACT	TF:M03962	9734	1.10E-04	151
TF	Factor: CTF/NF1; motif: TTGGCN	TF:M02050	9395	1.10E-04	147
TF	Factor: COUP-TF1; motif: TGACCTY	TF:M03542	4395	1.10E-04	84
TF	Factor: NR1B1; motif: RAGGTCA	TF:M08963	4395	1.10E-04	84
TF	Factor: RXR-ALPHA; motif: RAGGTCA	TF:M08968	4395	1.10E-04	84
TF	Factor: ESE-1; motif: SATKGCGGATGCN	TF:M11381	13896	1.10E-04	198
TF	Factor: ZNF592; motif: NSARNATGGAGKN	TF:M09766	6223	1.10E-04	108
TF	Factor: MAF; motif: NGCTGAGTCAN; match class: 1	TF:M00983_1	952	1.10E-04	31
GO:BP	regulation of intracellular signal transduction	GO:1902531	1594	1.20E-04	42
GO:BP	detection of molecule of bacterial origin	GO:0032490	11	1.20E-04	5
GO:BP	positive regulation of protein phosphorylation	GO:0001934	666	1.20E-04	25
GO:BP	negative regulation of defense response	GO:0031348	209	1.20E-04	14
GO:BP	regulation of mast cell activation involved in immune response	GO:0033006	34	1.20E-04	7
GO:CC	plasma membrane protein complex	GO:0098797	534	1.20E-04	21
GO:MF	lipid binding	GO:0008289	723	1.20E-04	25
GO:MF	amide binding	GO:0033218	354	1.20E-04	17
TF	Factor: ITF-2; motif: NGCAGSTGKS	TF:M09962	4254	1.20E-04	82
TF	Factor: AP-4; motif: NCAGCTGYNGNCN	TF:M01860	5298	1.20E-04	96
TF	Factor: E2F2; motif: NNTTTTGGCGCCAAAAWN	TF:M03959	7017	1.20E-04	118
TF	Factor: STAT1; motif: NTTCCNGGA	TF:M04721	6860	1.20E-04	116
TF	Factor: TEF5; motif: NNWGGWATKTTT	TF:M08903	1515	1.20E-04	41
TF	Factor: HLTF; motif: AGSCARAAAGYRGSTGS; match class: 1	TF:M04613_1	1635	1.20E-04	43
TF	Factor: T-box; motif: NASGTGTNAN	TF:M12021	3685	1.20E-04	74
TF	Factor: AP-1; motif: NNNTGAGTCAKCN	TF:M00517	4189	1.20E-04	81
GO:BP	regulation of cellular component movement	GO:0051270	972	1.30E-04	31
GO:BP	anatomical structure formation involved in morphogenesis	GO:0048646	1026	1.30E-04	32
GO:BP	regulation of response to stress	GO:0080134	1192	1.30E-04	35
GO:BP	regulation of microglial cell mediated cytotoxicity	GO:1904149	5	1.30E-04	4
GO:BP	microglial cell mediated cytotoxicity	GO:0090634	5	1.30E-04	4
GO:BP	regulation of hippocampal neuron apoptotic process	GO:0110089	5	1.30E-04	4
GO:BP	hippocampal neuron apoptotic process	GO:0110088	5	1.30E-04	4
GO:CC	primary lysosome	GO:0005766	141	1.30E-04	11
GO:CC	azurophil granule	GO:0042582	141	1.30E-04	11
TF	Factor: HOXB5; motif: NNYMATTANN	TF:M04349	4707	1.30E-04	88
TF	Factor: Six-2; motif: NNGTAWCRNN	TF:M11032	9253	1.30E-04	145
TF	Factor: DEC; motif: SCCCAMGTGAAGN	TF:M00997	7759	1.30E-04	127
TF	Factor: AP-2rep; motif: CAGTGGG	TF:M00468	6084	1.30E-04	106
TF	Factor: GSX1; motif: NNYMATTANN	TF:M04327	4712	1.30E-04	88
TF	Factor: SUHW1; motif: TCTCTCCAGTRTGAATTCTCTGAT	TF:M10541	6086	1.30E-04	106
GO:BP	T cell differentiation	GO:0030217	245	1.40E-04	15
GO:BP	regulation of programmed cell death	GO:0043067	1308	1.40E-04	37
GO:CC	endosome	GO:0005768	949	1.40E-04	29
TF	Factor: Msx-1; motif: NNNNANTAATTANTNN	TF:M01412	2525	1.40E-04	57
TF	Factor: AP-1; motif: NTGASTCAG	TF:M00199	4054	1.40E-04	79
TF	Factor: Six-1; motif: NCGTATCRNN	TF:M11028	1949	1.40E-04	48
GO:BP	regulation of pattern recognition receptor signaling pathway	GO:0062207	95	1.50E-04	10
TF	Factor: Sox-10; motif: MAANRRNNNCWTTGTT	TF:M10065	5861	1.50E-04	103

TF	Factor: Ngn-2; motif: RACATATGTY	TF:M11131	708	1.50E-04	26
TF	Factor: IRF-8; motif: AGTTTCW	TF:M01665	3988	1.50E-04	78
TF	Factor: T-bet; motif: NNGNRGGTGTGRN; match class: 1	TF:M10089_1	1126	1.50E-04	34
TF	Factor: TEF-3:E2A; motif: NCAGSTGNGWATGYN	TF:M08438	4948	1.50E-04	91
TF	Factor: Sox-4; motif: NYCTTTGTYYYN	TF:M10069	6179	1.50E-04	107
TF	Factor: EAR2; motif: YGNNCTTTGNCCTK	TF:M01728	5407	1.60E-04	97
TF	Factor: AP-1; motif: NTGACTCAN	TF:M00925	2147	1.60E-04	51
TF	Factor: AP-4; motif: AWCAGCTGWT; match class: 1	TF:M11208_1	3285	1.60E-04	68
TF	Factor: NR1B1:RXR-ALPHA; motif: RRGGTCANNNNNRGGTCA	TF:M08964	6106	1.60E-04	106
TF	Factor: NR3C1; motif: RRGAACATWMYGTYCTRN	TF:M02219	5643	1.60E-04	100
TF	Factor: Ngn-2; motif: RACATATGTY; match class: 1	TF:M11132_1	664	1.70E-04	25
TF	Factor: Smad2; motif: TGTCTGNCACCT; match class: 1	TF:M09656_1	1022	1.70E-04	32
TF	Factor: HOXC11; motif: NGYMATWAANN	TF:M10816	4292	1.70E-04	82
TF	Factor: Msx-2; motif: NNNGACYAATTAGYNNT	TF:M01393	7307	1.70E-04	121
GO:BP	granulocyte migration	GO:0097530	123	1.80E-04	11
GO:MF	NAD+ nucleosidase activity	GO:0003953	28	1.80E-04	6
REAC	Diseases associated with the TLR signaling cascade	REAC:R-HSA-5602358	28	1.80E-04	6
REAC	Diseases of Immune System	REAC:R-HSA-5260271	28	1.80E-04	6
TF	Factor: SREBP-1; motif: NNNGTGGGGTGAN	TF:M04632	4149	1.80E-04	80
TF	Factor: C/EBP; motif: NNATTGCNNAANNN	TF:M00190	4665	1.80E-04	87
TF	Factor: PEA3; motif: ACAGGAAGGAAGTN	TF:M11429	4815	1.80E-04	89
TF	Factor: POU3F2; motif: NTATGCWAATKAG	TF:M11909	4151	1.80E-04	80
TF	Factor: TFAP4; motif: AWCAGCTGWT; match class: 1	TF:M04192_1	3506	1.80E-04	71
TF	Factor: POU3F1; motif: RNYBCATTTGCATTWCAA	TF:M03842	4299	1.80E-04	82
GO:BP	superoxide anion generation	GO:0042554	36	1.90E-04	7
REAC	Signal Transduction	REAC:R-HSA-162582	2365	1.90E-04	52
TF	Factor: LRH-1; motif: TGACCTTGRNYCAAGGTCA	TF:M11830	6126	1.90E-04	106
TF	Factor: PU.1; motif: NNNNYYYACTTCCTCTTTY; match class: 1	TF:M01172_1	484	1.90E-04	21
TF	Factor: DLX6; motif: NWRNGYAAWYA	TF:M12595	3231	1.90E-04	67
TF	Factor: RORA; motif: CCYTGNCCTN	TF:M12659	6920	1.90E-04	116
TF	Factor: HOXC-8; motif: NNNNNGTAATTANNNT; match class: 1	TF:M01321_1	3583	1.90E-04	72
TF	Factor: ESRRA; motif: CAAGGTCANNYSAAGGTCA; match class: 1	TF:M04458_1	3797	1.90E-04	75
TF	Factor: POU3F2; motif: TAATKAGNNNNTAATKA; match class: 1	TF:M11908_1	975	1.90E-04	31
TF	Factor: AML1; motif: TGTGGTK	TF:M01658	3726	1.90E-04	74
GO:BP	positive regulation of cell migration	GO:0030335	496	2.00E-04	21
GO:BP	negative regulation of myeloid leukocyte mediated immunity	GO:0002887	12	2.00E-04	5
GO:BP	neutrophil degranulation	GO:0043312	12	2.00E-04	5
KEGG	Toxoplasmosis	KEGG:05145	108	2.00E-04	9
TF	Factor: C-JUN:FRA-1; motif: NNATGACTCATNN	TF:M08938	3094	2.00E-04	65
TF	Factor: C/EBPdelta; motif: NTTGCNCMAYN	TF:M09882	1725	2.00E-04	44
GO:BP	regulation of phosphorylation	GO:0042325	1159	2.10E-04	34
REAC	Signaling by Interleukins	REAC:R-HSA-449147	411	2.10E-04	18
TF	Factor: DLX2; motif: AMSMCTGACKG	TF:M08873	6450	2.10E-04	110
TF	Factor: NeuroD-2; motif: RMCATATGKY; match class: 1	TF:M01287_1	1666	2.10E-04	43
GO:BP	homeostatic process	GO:0042592	1631	2.20E-04	42
REAC	GPCR downstream signalling	REAC:R-HSA-388396	549	2.20E-04	21
TF	Factor: VDR; motif: RRGGTCANNGRGKTCA	TF:M09671	7096	2.20E-04	118
TF	Factor: RARA; motif: AGGTCANNYAAAGGTCA	TF:M08019	4689	2.20E-04	87
TF	Factor: ZNF684; motif: MAAGGGGTGGACTGT; match class: 1	TF:M10550_1	8324	2.20E-04	133
REAC	Phosphorylation of CD3 and TCR zeta chains	REAC:R-HSA-202427	16	2.30E-04	5

TF	Factor: SREBP-1; motif: RTCACCCCAY	TF:M07405	5912	2.30E-04	103
TF	Factor: E2A; motif: CACCTGNY	TF:M00973	4692	2.30E-04	87
TF	Factor: Sohlh2; motif: NNCACGTGNN	TF:M11075	10531	2.30E-04	159
GO:BP	regulation of myeloid cell differentiation	GO:0045637	187	2.40E-04	13
GO:BP	negative regulation of endopeptidase activity	GO:0010951	187	2.40E-04	13
GO:BP	antigen processing and presentation of exogenous peptide antigen	GO:0002478	55	2.40E-04	8
GO:BP	B cell receptor signaling pathway	GO:0050853	55	2.40E-04	8
REAC	Toll-like Receptor Cascades	REAC:R-HSA-168898	148	2.40E-04	11
GO:BP	killing of cells of another organism	GO:0031640	23	2.50E-04	6
TF	Factor: VDR; motif: NRRGTTCA	TF:M08979	3966	2.50E-04	77
TF	Factor: PMX2B; motif: NNNAATTAATTAANNNG	TF:M01356	2639	2.50E-04	58
GO:BP	positive regulation of cellular protein metabolic process	GO:0032270	1284	2.60E-04	36
TF	Factor: NFATc1; motif: NATGGAAANWNANTTTYCMN	TF:M04051	4704	2.60E-04	87
TF	Factor: POU2F1; motif: NWTATGCWAATN	TF:M04070	2180	2.60E-04	51
TF	Factor: IRF-7; motif: AAGWGAA; match class: 1	TF:M01884_1	3752	2.60E-04	74
TF	Factor: Ets; motif: ANNCACTTCCTG	TF:M00771	3397	2.60E-04	69
GO:BP	lysosome localization	GO:0032418	77	2.70E-04	9
GO:BP	vacuolar localization	GO:1990849	77	2.70E-04	9
TF	Factor: TFIIB; motif: YTNTMTGMSN	TF:M08904	5698	2.70E-04	100
TF	Factor: GR; motif: RGWACATWATGTWCY	TF:M11847	4559	2.70E-04	85
TF	Factor: BRN1; motif: NANNTATGCATAATNNA	TF:M01324	4046	2.70E-04	78
TF	Factor: HoxA5; motif: RTCATTAN	TF:M10704	4413	2.70E-04	83
TF	Factor: Sox-10; motif: AACAATRGNCYATTGTT; match class: 1	TF:M11632_1	3758	2.70E-04	74
GO:BP	T cell migration	GO:0072678	56	2.80E-04	8
GO:BP	positive regulation of phosphorylation	GO:0042327	746	2.80E-04	26
TF	Factor: MafG; motif: CMATGACTCAGCAGA; match class: 1	TF:M07048_1	1269	2.80E-04	36

TF	Factor: HOXB2; motif: NNTMATTANN	TF:M04347	2782	2.80E-04	60
TF	Factor: Fra-2; motif: TGASTCANCN	TF:M03870	3056	2.80E-04	64
TF	Factor: Sox-10; motif: AACAATGGNCCATTGTT; match class: 1	TF:M11633_1	2648	2.80E-04	58
TF	Factor: HoxA5; motif: RTCATTAN	TF:M10707	2383	2.90E-04	54
TF	Factor: NR1B1; motif: NRGGTCANRRGGTCAN	TF:M11792	4126	2.90E-04	79
TF	Factor: Ngn-2; motif: RACATATGTY	TF:M11134	1215	3.00E-04	35
TF	Factor: c-Fos; motif: ACTCACCA	TF:M04802	6417	3.00E-04	109
TF	Factor: LKLF; motif: GGGGTGGKSN	TF:M07261	8865	3.00E-04	139
TF	Factor: Foxm1; motif: NTGTTTRT	TF:M07255	4796	3.00E-04	88
TF	Factor: TBX2; motif: TCACACCWN	TF:M08831	1049	3.00E-04	32
GO:BP	negative regulation of cell adhesion	GO:0007162	261	3.10E-04	15
GO:BP	regulation of peptidase activity	GO:0052547	379	3.10E-04	18
TF	Factor: Oct-4; motif: YWTTSTNATGCAAAT	TF:M01125	1629	3.10E-04	42
GO:BP	response to interferon-gamma	GO:0034341	130	3.20E-04	11
GO:MF	complement binding	GO:0001848	17	3.20E-04	5
TF	Factor: Erm:E2A; motif: CASGTGNNNCGGAAGNN	TF:M08571	9890	3.20E-04	151
TF	Factor: CART1; motif: NGNNYTAATTARTNNNN; match class: 1	TF:M01362_1	2860	3.20E-04	61
GO:MF	identical protein binding	GO:0042802	1948	3.30E-04	45
TF	Factor: POU2F1:PEA3; motif: ACCGGATATGCAN	TF:M08402	6988	3.30E-04	116
GO:BP	regulation of protein phosphorylation	GO:0001932	1017	3.40E-04	31
GO:BP	myeloid leukocyte differentiation	GO:0002573	193	3.40E-04	13
TF	Factor: Zic1; motif: KGGGTGGTC	TF:M00448	9729	3.40E-04	149
GO:BP	interleukin-1 production	GO:0032612	104	3.50E-04	10
GO:BP	regulation of interleukin-1 production	GO:0032652	104	3.50E-04	10
KEGG	Antigen processing and presentation	KEGG:04612	62	3.50E-04	7

TF	Factor: C/EBPdelta; motif: NRTTGCGYAAYN	TF:M11321	4812	3.50E-04	88
TF	Factor: JUND:C-FOS; motif: NNATGAGTCATNN	TF:M08933	3998	3.50E-04	77
TF	Factor: SMAD; motif: TNGNCAGACWN; match class: 1	TF:M00974_1	594	3.50E-04	23
TF	Factor: NF-E2; motif: TGCTGAGTCAY	TF:M00037	5577	3.60E-04	98
TF	Factor: Sox-4; motif: NNNNNAATTGTTNNNNN	TF:M02909	3641	3.60E-04	72
TF	Factor: VDR; motif: NRGGTCANNGRGKTCA	TF:M10106	6125	3.60E-04	105
GO:BP	negative regulation of peptidase activity	GO:0010466	194	3.70E-04	13
GO:BP	response to oxygen-containing compound	GO:1901700	1480	3.70E-04	39
GO:MF	MHC class II receptor activity	GO:0032395	8	3.70E-04	4
TF	Factor: Oct3; motif: NNWTATGYWAATKANN	TF:M11935	2402	3.70E-04	54
TF	Factor: Ngn-2; motif: RMCATATGYY	TF:M11133	1170	3.70E-04	34
GO:BP	regulation of myeloid leukocyte differentiation	GO:0002761	105	3.80E-04	10
REAC	Peptide ligand-binding receptors	REAC:R-HSA-375276	155	3.80E-04	11
TF	Factor: Sox-30; motif: NRACAATG	TF:M11640	794	3.80E-04	27
GO:BP	positive regulation of cell motility	GO:2000147	516	3.90E-04	21
TF	Factor: TBX15; motif: NAGGTGTGAN	TF:M12039	2145	3.90E-04	50
TF	Factor: Smad4; motif: NWGTCTGNCACCT	TF:M10061	3223	3.90E-04	66
GO:BP	regulation of gene expression	GO:0010468	4415	4.00E-04	82
TF	Factor: Oct-1; motif: MKVATTTGCATATT	TF:M00161	2408	4.00E-04	54
GO:BP	positive regulation of protein metabolic process	GO:0051247	1367	4.10E-04	37
GO:BP	response to fungus	GO:0009620	40	4.10E-04	7
TF	Factor: JUN; motif: NRTGACTCA	TF:M12589	3227	4.10E-04	66
TF	Factor: Oct3; motif: NYWTTSWTATGCAAAT; match class: 1	TF:M09646_1	1119	4.10E-04	33
TF	Factor: GKLF; motif: CCTCCYN; match class: 1	TF:M01835_1	9081	4.20E-04	141
GO:BP	positive regulation of toll-like receptor signaling pathway	GO:0034123	25	4.30E-04	6
GO:BP	alpha-beta T cell activation	GO:0046631	134	4.30E-04	11

TF	Factor: POU2F1; motif: ANKNRWATGSAAWYAW	TF:M10033	3948	4.40E-04	76
TF	Factor: NF-1C; motif: TTGGCNN	TF:M07300	5371	4.40E-04	95
TF	Factor: MYB; motif: NNCAACTGNN	TF:M09813	4688	4.50E-04	86
TF	Factor: TCF-3; motif: CTTTGA; match class: 1	TF:M03858_1	4541	4.60E-04	84
TF	Factor: TCF-7; motif: TCAAAG; match class: 1	TF:M00805_1	4541	4.60E-04	84
TF	Factor: Fra-1; motif: NNNTGAGTCAYN	TF:M09922	3807	4.60E-04	74
TF	Factor: POU2F1:HOXB13; motif: NGMATATACCAATAAA	TF:M08405	3168	4.60E-04	65
TF	Factor: Lhx8; motif: TGATTG	TF:M07476	7600	4.70E-04	123
TF	Factor: HOXD1; motif: NATYCAKCAN	TF:M12625	4694	4.70E-04	86
TF	Factor: MIBP1; motif: WNWCCCCAGCTR	TF:M03878	2488	4.80E-04	55
TF	Factor: AP-4; motif: YCAGCTGNKN	TF:M10097	5226	4.80E-04	93
GO:BP	cellular component organization	GO:0016043	6205	4.90E-04	105
TF	Factor: SREBP-1; motif: KATCACCCCAC	TF:M00221	6557	4.90E-04	110
TF	Factor: E2F2; motif: AAAAATGGCGCCAAAAWG	TF:M03958	9442	4.90E-04	145
TF	Factor: ATF3; motif: GRTGACKCA	TF:M12582	6319	4.90E-04	107
GO:BP	positive regulation of response to biotic stimulus	GO:0002833	167	5.10E-04	12
GO:BP	regulation of chemotaxis	GO:0050920	200	5.20E-04	13
TF	Factor: MAFA; motif: TCAGCAN	TF:M01709	5314	5.30E-04	94
TF	Factor: HNF3alpha; motif: TRTTTGYTYWN	TF:M00724	2167	5.30E-04	50
TF	Factor: AP4; motif: NMNCAGCTGGN	TF:M12580	5085	5.30E-04	91
TF	Factor: Sox-10; motif: NACAATRNNNNYATTGTN	TF:M11635	5086	5.40E-04	91
GO:BP	regulation of lymphocyte differentiation	GO:0045619	168	5.50E-04	12
GO:BP	positive regulation of chemokine production	GO:0032722	61	5.50E-04	8
TF	Factor: TIF2; motif: ANANAGAWAAGN	TF:M09849	2975	5.50E-04	62
TF	Factor: STAT5A; motif: NAWTTCYNGGAANYN	TF:M00457	3468	5.70E-04	69
TF	Factor: ER-alpha; motif: AGGTCASMNTGACCY	TF:M09909	5943	5.70E-04	102

GO:BP	chemokine production	GO:0032602	84	5.80E-04	9
GO:BP	regulation of chemokine production	GO:0032642	84	5.80E-04	9
GO:BP	positive regulation of cellular component movement	GO:0051272	529	5.80E-04	21
TF	Factor: NR1B2; motif: RAGGTCRTGACCTY	TF:M11800	3188	5.80E-04	65
TF	Factor: Sox-17; motif: NCCATTGTNNN	TF:M10066	2239	5.80E-04	51
GO:BP	negative regulation of T cell activation	GO:0050868	110	6.00E-04	10
GO:BP	positive regulation of locomotion	GO:0040017	530	6.00E-04	21
TF	Factor: Sox-8; motif: NNAACAATRN	TF:M11628	1082	6.00E-04	32
TF	Factor: Hoxa9; motif: NTTAAWTAMA	TF:M07457	3906	6.00E-04	75
TF	Factor: GR; motif: AGAACAN; match class: 1	TF:M07355_1	813	6.10E-04	27
TF	Factor: VDR:RXR-ALPHA; motif: NRGGTCANNNGGTTCNN	TF:M08980	9219	6.10E-04	142
TF	Factor: C/EBPepsilon; motif: HAANMTTKCNWMAC	TF:M01868	2507	6.10E-04	55
GO:BP	negative regulation of cell-cell adhesion	GO:0022408	170	6.20E-04	12
GO:BP	antigen processing and presentation of exogenous antigen	GO:0019884	62	6.30E-04	8
TF	Factor: MRF4; motif: CASCTGC; match class: 1	TF:M03831_1	2377	6.40E-04	53
TF	Factor: HTF4; motif: CASCTGB; match class: 1	TF:M02018_1	2377	6.40E-04	53
TF	Factor: JunB; motif: TGACTCAN	TF:M03551	3551	6.40E-04	70
TF	Factor: AP1; motif: TGACTCA	TF:M02280	3553	6.50E-04	70
KEGG	Fc gamma R-mediated phagocytosis	KEGG:04666	95	6.60E-04	8
GO:BP	axon ensheathment	GO:0008366	140	6.70E-04	11
GO:BP	ensheathment of neurons	GO:0007272	140	6.70E-04	11
GO:CC	ficolin-1-rich granule membrane	GO:0101003	55	6.80E-04	7
TF	Factor: Pitx3; motif: GATTANA	TF:M07057	1864	6.80E-04	45
TF	Factor: POU3F2; motif: TAATKAGNNNNTAATKA	TF:M11908	2993	6.80E-04	62
GO:BP	regulation of inflammatory response to antigenic stimulus	GO:0002861	43	6.90E-04	7
TF	Factor: Dlx-5; motif: NNRGYAATTRNYKNNN; match class: 1	TF:M01388_1	4735	6.90E-04	86
TF	Factor: Tst-1; motif: NNKGAATTAVAVTDN	TF:M00133	4735	6.90E-04	86
GO:BP	positive regulation of secretion	GO:0051047	278	7.00E-04	15
TF	Factor: Erm; motif: RSAGGAAGGAAGTN	TF:M11423	4288	7.00E-04	80
TF	Factor: AP-1; motif: NTGASTCAG; match class: 1	TF:M00199_1	3560	7.10E-04	70
GO:BP	NIK/NF-kappaB signaling	GO:0038061	141	7.20E-04	11
GO:BP	regulation of response to biotic stimulus	GO:0002831	318	7.20E-04	16
TF	Factor: MTF-1; motif: GTGTGCANMACTTTGCGCAC	TF:M01242	3492	7.30E-04	69
TF	Factor: AP-4:Dlx-3; motif: NCAGCTGNNNNNNGTAATKR	TF:M08671	3638	7.50E-04	71
TF	Factor: ZNFPT1; motif: YCNNCNCWGCCNY	TF:M12721	8164	7.80E-04	129
TF	Factor: ZNF586; motif: CAGGCCYRGAGG	TF:M10491	12307	7.80E-04	177
TF	Factor: AML3; motif: NWAACCACRAAAACCACRAN	TF:M11999	5905	7.90E-04	101
GO:BP	positive regulation of NIK/NF-kappaB signaling	GO:1901224	64	8.10E-04	8
TF	Factor: HOXA4; motif: RTMATTAN	TF:M10716	3290	8.30E-04	66
TF	Factor: HDAC1; motif: KGCARGGTC	TF:M07041	11165	8.30E-04	164
TF	Factor: Ngn-2; motif: RACATATGTY; match class: 1	TF:M11131_1	624	8.40E-04	23
TF	Factor: gsh-1; motif: NTMATNRN; match class: 1	TF:M10750_1	3221	8.40E-04	65
GO:CC	plasma membrane raft	GO:0044853	108	8.60E-04	9
TF	Factor: Lhx2; motif: WATTAN	TF:M07047	9102	8.70E-04	140
GO:BP	regulation of superoxide metabolic process	GO:0090322	28	8.80E-04	6
TF	Factor: Fra-1; motif: NRTGACTCATN	TF:M09615	3439	8.90E-04	68
TF	Factor: Tbx3; motif: AGGTGTNR	TF:M08786	3157	9.00E-04	64
GO:BP	regulation of leukocyte mediated cytotoxicity	GO:0001910	65	9.10E-04	8
GO:BP	second-messenger-mediated signaling	GO:0019932	284	9.10E-04	15
TF	Factor: PEA3; motif: NTCGTAAATGCA	TF:M11431	9024	9.10E-04	139
TF	Factor: LCOR; motif: CMAAGKNCANN	TF:M12628	2949	9.10E-04	61
TF	Factor: FOSL1; motif: NNATGACTCATNN	TF:M12518	3875	9.20E-04	74

TF	Factor: SP2; motif: NNRRCCAATSRGNRNSNGSN	TF:M12668	10569	9.20E-04	157
GO:BP	blood vessel development	GO:0001568	641	9.30E-04	23
TF	Factor: POU3F1; motif: NTAATKWATGCNN	TF:M11929	5613	9.40E-04	97
TF	Factor: NFATc3; motif: NTTTCCRYGGAAAN	TF:M11988	6242	9.40E-04	105
GO:BP	positive regulation of T cell proliferation	GO:0042102	89	9.50E-04	9
GO:BP	regulation of regulated secretory pathway	GO:1903305	145	9.50E-04	11
TF	Factor: Oct-2; motif: NTATGCWAATN; match class: 1	TF:M11896_1	993	9.50E-04	30
TF	Factor: Fra-2; motif: RTGACTCANNN	TF:M09616	3952	9.60E-04	75
TF	Factor: SREBP-1; motif: NSNNTCACNCCANNN	TF:M01173	4099	9.60E-04	77
TF	Factor: six4; motif: NCGTATCRNN	TF:M11025	5538	9.60E-04	96
TF	Factor: Spi-B; motif: NAAWGNGGAAGTN	TF:M11377	399	9.60E-04	18
GO:BP	antigen processing and presentation	GO:0019882	116	9.80E-04	10
TF	Factor: Tal-1; motif: CTTCCTTMTCTSY	TF:M01591	1889	9.80E-04	45
TF	Factor: Sox-9; motif: AANGGNNNCWTTGTTY	TF:M10070	2212	9.80E-04	50
GO:BP	movement of cell or subcellular component	GO:0006928	1918	1.00E-03	45
GO:MF	pattern recognition receptor activity	GO:0038187	21	1.00E-03	5
GO:MF	amyloid-beta binding	GO:0001540	81	1.00E-03	8
REAC	Initial triggering of complement	REAC:R-HSA-166663	21	1.00E-03	5
TF	Factor: MTF-1; motif: NTTTTGCACACGGCNYN	TF:M12279	5776	1.00E-03	99
TF	Factor: Sox-10; motif: CWTTGTN	TF:M01131	7621	1.00E-03	122
TF	Factor: Smad1; motif: NGGCAGACN	TF:M03845	3958	1.00E-03	75
TF	Factor: POU3F2; motif: ATGMATWWATTCAT	TF:M00463	2550	1.00E-03	55
GO:BP	positive regulation of protein modification process	GO:0031401	906	1.10E-03	28
GO:BP	anatomical structure morphogenesis	GO:0009653	2447	1.10E-03	53
GO:BP	toll-like receptor 2 signaling pathway	GO:0034134	16	1.10E-03	5
GO:BP	detection of other organism	GO:0098543	16	1.10E-03	5
GO:CC	ficolin-1-rich granule	GO:0101002	175	1.10E-03	11
GO:CC	receptor complex	GO:0043235	376	1.10E-03	16
TF	Factor: NFE2L1; motif: NNNATGACTCAGCANW; match class: 1	TF:M12499_1	2824	1.10E-03	59
TF	Factor: Smad4; motif: TGTCTGN	TF:M01889	4482	1.10E-03	82
TF	Factor: POU1F1; motif: AWTATGCWAATKAG	TF:M04069	2623	1.10E-03	56
GO:BP	positive regulation of vasculature development	GO:1904018	148	1.20E-03	11
GO:BP	positive regulation of angiogenesis	GO:0045766	148	1.20E-03	11
GO:BP	positive regulation of cellular metabolic process	GO:0031325	2936	1.20E-03	60
GO:MF	peptidase regulator activity	GO:0061134	174	1.20E-03	11
TF	Factor: OC-2; motif: TCAATA	TF:M02112	6190	1.20E-03	104
TF	Factor: CRX; motif: YTAATC; match class: 1	TF:M01712_1	4120	1.20E-03	77
TF	Factor: ER-alpha; motif: AGGTCACNGTGACCT	TF:M01801	2834	1.20E-03	59
TF	Factor: GR; motif: RGWACATWAYGTWCY	TF:M11846	5101	1.20E-03	90
TF	Factor: Fra-2; motif: NNRTGAGTCAYN	TF:M09923	3611	1.20E-03	70
TF	Factor: Oct3; motif: WTATGCGCATAW	TF:M11934	8394	1.20E-03	131
TF	Factor: TEF-3:C/EBPbeta; motif: RTTGCGYAAYNNNNNGGAATGY	TF:M08626	5958	1.20E-03	101
TF	Factor: STAT3; motif: NTTCYKGGAAN	TF:M07229	3185	1.20E-03	64
TF	Factor: PPARALPHA:RXR-ALPHA; motif: AWNTRGGTNAAAGGTCAN	TF:M08960	10094	1.20E-03	151
TF	Factor: AP-4; motif: ANCATATGNT; match class: 1	TF:M11211_1	1841	1.20E-03	44
TF	Factor: Sox-9; motif: NAACAATRN	TF:M04004	897	1.20E-03	28
GO:BP	defense response to Gram-negative bacterium	GO:0050829	47	1.30E-03	7
GO:BP	negative regulation of leukocyte cell-cell adhesion	GO:1903038	120	1.30E-03	10
TF	Factor: CEBPD; motif: NNTTGCACAAYNN	TF:M12567	1780	1.30E-03	43
TF	Factor: BCL-6; motif: NYGCTTTCKAGGAANN	TF:M12341	5187	1.30E-03	91
TF	Factor: CDP:HOXA13; motif: ATCGATYAYSYCRTAAA; match class: 1	TF:M08201_1	2433	1.30E-03	53
TF	Factor: Pax-2; motif: CAYSCCTSAGT	TF:M03839	4355	1.30E-03	80

TF	Factor: Dlx-5; motif: NNRGYAATTRNYKNNN	TF:M01388	6366	1.30E-03	106
GO:BP	defense response to fungus	GO:0050832	30	1.40E-03	6
TF	Factor: TCF-3; motif: NCTTTGWTNTKYW	TF:M01594	3987	1.40E-03	75
TF	Factor: VDR, motif: RRTGNMCYTNNTGAMCCNYNT; match class: 1	TF:M00966_1	2778	1.40E-03	58
TF	Factor: TR4; motif: ACCCCGS; match class: 1	TF:M04934_1	13946	1.40E-03	194
TF	Factor: POU2F1:HOXB13; motif: NGMATATACCAATAAA; match class: 1	TF:M08405_1	744	1.40E-03	25
TF	Factor: Oct-2; motif: NNNATTATGCAN	TF:M11897	3920	1.40E-03	74
GO:BP	positive regulation of myeloid leukocyte differentiation	GO:0002763	48	1.50E-03	7
TF	Factor: HEY1; motif: NYYYYATCTNN	TF:M12614	4742	1.50E-03	85
TF	Factor: NFATc1; motif: TTTTCCATGGAAAN	TF:M04053	7187	1.50E-03	116
TF	Factor: TGIF; motif: TGACAGS	TF:M10101	4444	1.50E-03	81
TF	Factor: LF-A1; motif: GGGSTCWR	TF:M00646	11261	1.50E-03	164
TF	Factor: Six-2; motif: NCGTATCRNN	TF:M11031	7846	1.50E-03	124
GO:CC	lytic vacuole membrane	GO:0098852	387	1.60E-03	16
GO:CC	lysosomal membrane	GO:0005765	387	1.60E-03	16
TF	Factor: MITF; motif: CATGTGM	TF:M02099	2582	1.60E-03	55
TF	Factor: Fli-1; motif: NNRGGMAGGAAGGRRRGR; match class: 1	TF:M09920_1	2997	1.60E-03	61
TF	Factor: ER-alpha; motif: TGACCYN	TF:M03547	4003	1.60E-03	75
TF	Factor: SPIC; motif: NAAAAGMGGAAGTA	TF:M03996	550	1.60E-03	21
TF	Factor: SOX13; motif: NNACAATGGNN	TF:M09787	550	1.60E-03	21
TF	Factor: Pax-3; motif: TCGTCACRCTTHM	TF:M00360	10921	1.60E-03	160
GO:BP	regulation of NIK/NF-kappaB signaling	GO:1901222	95	1.70E-03	9
GO:BP	negative regulation of inflammatory response to antigenic stimulus	GO:0002862	31	1.70E-03	6
TF	Factor: Gscl; motif: NTAATCCN	TF:M10924	5762	1.70E-03	98
TF	Factor: Msx-2; motif: TAATTAN	TF:M07425	3073	1.70E-03	62

TF	Factor: AP-2gamma; motif: NNNNSCCYCAGGSCN	TF:M07137	1078	1.70E-03	31
TF	Factor: oct-2; motif: NNWNATGCAAATNN	TF:M03836	3147	1.70E-03	63
GO:BP	response to bacterial lipoprotein	GO:0032493	8	1.80E-03	4
GO:BP	positive regulation of lymphocyte proliferation	GO:0050671	124	1.80E-03	10
TF	Factor: C-JUN:FRA-2; motif: NNRTGAGTCAYN	TF:M08940	3007	1.80E-03	61
TF	Factor: DEC1; motif: NCNCACRTGNSC	TF:M08870	6965	1.80E-03	113
TF	Factor: ZNF394; motif: NRARWRGAANNNAMWGNAAK	TF:M10147	4537	1.80E-03	82
TF	Factor: HSF1; motif: GAANNTTCTRGNAN; match class: 1	TF:M02017_1	462	1.80E-03	19
REAC	Interleukin-10 signaling	REAC:R-HSA-6783783	41	1.90E-03	6
TF	Factor: Ngn-2; motif: RACATATGTY; match class: 1	TF:M11134_1	970	1.90E-03	29
TF	Factor: CP2; motif: NNNNCCAGNCNN	TF:M07602	9815	1.90E-03	147
TF	Factor: ipf1; motif: RTCATTAN	TF:M10745	2599	1.90E-03	55
TF	Factor: HB9; motif: NTCRTTAN	TF:M10569	2599	1.90E-03	55
GO:BP	macrophage migration	GO:1905517	50	2.00E-03	7
GO:BP	vasculature development	GO:0001944	671	2.00E-03	23
GO:BP	cellular response to mechanical stimulus	GO:0071260	72	2.00E-03	8
GO:BP	regulation of apoptotic process	GO:0042981	1281	2.00E-03	34
GO:BP	dendritic cell migration	GO:0036336	32	2.00E-03	6
GO:MF	lipopolysaccharide binding	GO:0001530	24	2.00E-03	5
TF	Factor: HNF-4alpha; motif: AGTCCAAR	TF:M04903	5939	2.00E-03	100
TF	Factor: LBX2; motif: CTNRANSTAATTA	TF:M04383	6738	2.00E-03	110
TF	Factor: ELF3; motif: NNCCACTTCCTGNN; match class: 1	TF:M12544_1	334	2.00E-03	16
TF	Factor: GR; motif: RGNACANMNTGTNCY	TF:M09941	4931	2.00E-03	87
TF	Factor: TWIST; motif: CACCTGG	TF:M03582	7309	2.00E-03	117
TF	Factor: HOXB4; motif: NTMATTAN	TF:M10720	1500	2.00E-03	38
TF	Factor: c-Ets-2; motif: NNCTTCCTNNN; match class: 1	TF:M07379_1	294	2.00E-03	15

GO:BP	positive regulation of mononuclear cell proliferation	GO:0032946	126	2.10E-03	10
GO:BP	negative regulation of cell death	GO:0060548	884	2.10E-03	27
GO:CC	lumenal side of endoplasmic reticulum membrane	GO:0098553	25	2.10E-03	5
GO:CC	integral component of lumenal side of endoplasmic reticulum membrane	GO:0071556	25	2.10E-03	5
TF	Factor: nerf; motif: YRNCAGGAAGYRGSTBDS; match class: 1	TF:M00531_1	1624	2.10E-03	40
TF	Factor: JUNB:C-FOS; motif: NATGAGTCATNN	TF:M08925	2882	2.10E-03	59
TF	Factor: c-Jun; motif: NRTGAGTCAYN	TF:M09965	3738	2.10E-03	71
TF	Factor: c-Jun; motif: NATGASTCATN	TF:M11264	3593	2.10E-03	69
TF	Factor: ipf1; motif: RNWCATTAANWN	TF:M01255	3449	2.10E-03	67
TF	Factor: SRY; motif: AACAATNNNCATTGTT; match class: 1	TF:M04556_1	5013	2.10E-03	88
TF	Factor: ERF:pitx1; motif: NNCGGAWGNNNRGNTTA	TF:M08692	4709	2.10E-03	84
TF	Factor: HOXA7; motif: GYMATTAN	TF:M10690	8983	2.10E-03	137
GO:BP	cellular component organization or biogenesis	GO:0071840	6398	2.20E-03	105
TF	Factor: CDP:T-bet; motif: NTCACACNYYRATCRATM	TF:M08203	5093	2.20E-03	89
TF	Factor: JunB; motif: NRRTGASTCAK	TF:M07103	2010	2.20E-03	46
TF	Factor: RelB:p50; motif: RGAAANTCCCYNNHGC	TF:M03882	3891	2.20E-03	73
TF	Factor: NFATc3; motif: NTTTCCRYGGAAAN; match class: 1	TF:M11988_1	5797	2.20E-03	98
TF	Factor: HOXC-8; motif: NNNNNGTAATTANNNT	TF:M01321	4639	2.20E-03	83
GO:BP	apoptotic cell clearance	GO:0043277	51	2.30E-03	7
GO:BP	positive regulation of MAPK cascade	GO:0043410	435	2.30E-03	18
GO:BP	neutrophil migration	GO:1990266	99	2.40E-03	9
TF	Factor: NR1H4; motif: NNAATGACCNN	TF:M09777	3246	2.40E-03	64
TF	Factor: Pax-5; motif: BCNNNRNGCANBGNTGNRTAGCSGCHNB	TF:M00143	10199	2.40E-03	151
TF	Factor: C/EBPbeta; motif: ATTGCGYAAT	TF:M07413	2826	2.40E-03	58
TF	Factor: NFATc2; motif: TTTTCCATGGAAAA	TF:M11985	4876	2.40E-03	86
TF	Factor: ZXDL; motif: NGGGGWS	TF:M05775	6205	2.40E-03	103
GO:BP	negative regulation of B cell activation	GO:0050869	33	2.50E-03	6
GO:BP	vertebrate eye-specific patterning	GO:0150064	3	2.50E-03	3
GO:BP	response to triacyl bacterial lipopeptide	GO:0071725	3	2.50E-03	3
GO:BP	cellular response to triacyl bacterial lipopeptide	GO:0071727	3	2.50E-03	3
GO:BP	regulation of peptidyl-tyrosine phosphorylation	GO:0050730	230	2.50E-03	13
TF	Factor: Msx-1; motif: CNGTAWNTG	TF:M00394	7584	2.50E-03	120
TF	Factor: MATH1; motif: NCASCTGGYN	TF:M01716	665	2.50E-03	23
TF	Factor: ER71:C/EBPdelta; motif: NNCGGAWRTTRCGYAAN	TF:M08246	7178	2.50E-03	115
GO:BP	granulocyte chemotaxis	GO:0071621	100	2.60E-03	9
GO:BP	negative regulation of immune effector process	GO:0002698	100	2.60E-03	9
TF	Factor: NKX2B; motif: CACTTNA	TF:M02109	8588	2.60E-03	132
TF	Factor: BRCA1:USF2; motif: KTNNGTTG	TF:M01082	6054	2.60E-03	101
TF	Factor: YY1; motif: NGCCATYTTKGRCNWWNNGTGCK; match class: 1	TF:M12276_1	2903	2.60E-03	59
TF	Factor: JunD; motif: NATGASTCATS; match class: 1	TF:M11268_1	1455	2.60E-03	37
TF	Factor: Oct-4; motif: ATTGWSWTGCWAAWN; match class: 1	TF:M01124_1	1335	2.70E-03	35
TF	Factor: C/EBPalpha; motif: NNNTTNNGCAANN; match class: 1	TF:M01866_1	771	2.70E-03	25
TF	Factor: ipf1; motif: NNRNTAATTAGYNCAN	TF:M01438	2697	2.70E-03	56
TF	Factor: c-Fos; motif: RTGAGTCAYNN	TF:M09617	2224	2.70E-03	49
GO:BP	ion transport	GO:0006811	1420	2.80E-03	36
TF	Factor: HOXB5; motif: NNYMATTANN; match class: 1	TF:M04349_1	3333	2.80E-03	65
TF	Factor: RARA; motif: GAGGTCAAAAGGTCAAKK	TF:M08018	3915	2.80E-03	73
TF	Factor: AR; motif: GNNCNNNNTGTTCTN	TF:M01996	2495	2.80E-03	53
TF	Factor: HOXB5; motif: GTCATTAN	TF:M10701	4817	2.80E-03	85
TF	Factor: znf136; motif: CAAGAATWCTATAYCCAG; match class: 1	TF:M10535_1	2029	2.80E-03	46

KEGG	Epstein-Barr virus infection	KEGG:05169	188	2.90E-03	10
GO:BP	B cell differentiation	GO:0030183	131	3.00E-03	10
GO:BP	positive regulation of lymphocyte differentiation	GO:0045621	102	3.00E-03	9
TF	Factor: CLOCK; motif: CNGNCACGTGNNNM	TF:M09884	7117	3.00E-03	114
TF	Factor: HFH2; motif: NNWAYRTAAACW	TF:M11555	3923	3.00E-03	73
TF	Factor: ZNF436; motif: TCCTCCAGGAAGCCY; match class: 1	TF:M10477_1	7782	3.10E-03	122
GO:BP	cellular chemical homeostasis	GO:0055082	741	3.20E-03	24
TF	Factor: HOXD12:Elk-1; motif: NRNCGGAAGTCGTAAAN	TF:M08359	5293	3.20E-03	91
TF	Factor: GABP-alpha; motif: AACCGGAAR	TF:M04748	14181	3.20E-03	195
TF	Factor: RAR-gamma; motif: RGGTCANNNTGNCCNNNN	TF:M10045	6400	3.20E-03	105
TF	Factor: LRH-1; motif: TGACCTTGRNYCAAGGTCA; match class: 1	TF:M11830_1	5296	3.20E-03	91
TF	Factor: Blimp-1; motif: RRGNGAAAGNRANNN	TF:M10526	1974	3.20E-03	45
KEGG	Influenza A	KEGG:05164	153	3.30E-03	9
TF	Factor: HSF1; motif: TCYAGAANNTTC	TF:M07259	4006	3.30E-03	74
TF	Factor: HOXC4; motif: RTCRTTAN	TF:M10718	2239	3.30E-03	49
TF	Factor: AR; motif: AGWACATNWTGTTCT	TF:M00447	3496	3.40E-03	67
TF	Factor: RORbeta; motif: TGACCYA; match class: 1	TF:M01722_1	944	3.40E-03	28
TF	Factor: VSX1; motif: NGCYAATTRNN	TF:M04450	5852	3.40E-03	98
TF	Factor: HOXA10; motif: TTATNNYWN	TF:M07257	2998	3.50E-03	60
TF	Factor: POU3F1; motif: NTAATKWATGCNN; match class: 1	TF:M11929_1	1472	3.50E-03	37
TF	Factor: NFATc4; motif: NRYGGAAANW	TF:M11995	578	3.50E-03	21
TF	Factor: p73; motif: NNRCAWGYCCARRCWTGYC	TF:M10025	5463	3.50E-03	93
TF	Factor: Pbx; motif: GATTGATKGNNS	TF:M00998	4313	3.50E-03	78
GO:MF	opsonin binding	GO:0001846	13	3.60E-03	4
REAC	Translocation of ZAP-70 to Immunological synapse	REAC:R-HSA-202430	13	3.60E-03	4
TF	Factor: SREBP; motif: NNNNYCACNCCANNN	TF:M01168	5699	3.60E-03	96

TF	Factor: C-JUN:FOSB; motif: NATGACTCAY	TF:M08936	2723	3.60E-03	56
TF	Factor: AP-4; motif: NNCAGCTGNN	TF:M11212	2517	3.60E-03	53
TF	Factor: Isl2; motif: YTAAGTG	TF:M02082	6418	3.70E-03	105
TF	Factor: Sox-9; motif: MACARWGNNNYCNTTNW	TF:M08838	3505	3.70E-03	67
TF	Factor: Pax-2; motif: NNNNGTCANGNRTKANNNN; match class: 1	TF:M00098_1	1663	3.70E-03	40
TF	Factor: Freac-3; motif: NNNNNGTAAATAAACA	TF:M00291	4394	3.70E-03	79
TF	Factor: GATA-3; motif: AGATAACGATCW	TF:M12192	3947	3.80E-03	73
TF	Factor: Fli-1; motif: MGGAAGT; match class: 1	TF:M07382_1	1237	3.80E-03	33
TF	Factor: C-ets-1; motif: AGGAAGN; match class: 1	TF:M01870_1	1237	3.80E-03	33
TF	Factor: SPI1; motif: AGGAAGT; match class: 1	TF:M02278_1	1237	3.80E-03	33
TF	Factor: PEA3; motif: AGGAAGT; match class: 1	TF:M03579_1	1237	3.80E-03	33
GO:MF	endopeptidase inhibitor activity	GO:0004866	127	3.90E-03	9
TF	Factor: Nkx2-3; motif: NNCGTTRWS	TF:M10638	9672	3.90E-03	144
TF	Factor: COUP-TF1; motif: GRGGKSARAGGTCAGNG	TF:M09886	4855	3.90E-03	85
TF	Factor: HMGIY; motif: NNKKNAWTTTNYTNN; match class: 1	TF:M01010_1	2523	3.90E-03	53
TF	Factor: c-Myb; motif: NNNNCMGTTNNN	TF:M07299	3223	3.90E-03	63
TF	Factor: HOXA13; motif: ATAAMA; match class: 1	TF:M01292_1	6832	3.90E-03	110
GO:BP	positive regulation of leukocyte proliferation	GO:0070665	135	4.00E-03	10
GO:BP	regulation of reactive oxygen species metabolic process	GO:2000377	135	4.00E-03	10
GO:BP	viral entry into host cell	GO:0046718	135	4.00E-03	10
TF	Factor: HSF1; motif: GAANNTTCTRGNAN	TF:M02017	3440	4.00E-03	66
TF	Factor: Sox-2; motif: NNCCTTTGTNYYN; match class: 1	TF:M10067_1	1065	4.00E-03	30
TF	Factor: GATA-1; motif: MNAGATAANR	TF:M00347	3733	4.00E-03	70
TF	Factor: DMRT5; motif: NNNNGWTACANT	TF:M11513	1733	4.10E-03	41
TF	Factor: Sox-9; motif: NNNACAATRG; match class: 1	TF:M11626_1	1241	4.10E-03	33
TF	Factor: SPIB; motif: NAAAAGMGGAAGTN	TF:M03995	634	4.10E-03	22

GO:BP	neutrophil chemotaxis	GO:0030593	79	4.20E-03	8
GO:BP	negative regulation of proteolysis	GO:0045861	280	4.20E-03	14
GO:BP	positive regulation of interleukin-12 production	GO:0032735	36	4.20E-03	6
TF	Factor: ERF:FOXO1A; motif: RTMAACAGGAARNS; match class: 1	TF:M08241_1	1671	4.20E-03	40
TF	Factor: RXRA; motif: RRGGTCATGACCYY; match class: 1	TF:M04490_1	3016	4.20E-03	60
GO:BP	cation transport	GO:0006812	1088	4.30E-03	30
TF	Factor: elf5; motif: AANRAGGAAGTR	TF:M11388	537	4.30E-03	20
TF	Factor: Oct-2; motif: NNNATTTGCATRT	TF:M07120	3962	4.30E-03	73
TF	Factor: Sox-10; motif: NACAATRNNNNYATTGTN; match class: 1	TF:M11635_1	4716	4.40E-03	83
TF	Factor: MZF-1; motif: KNGNKAGGGGNAA	TF:M00084	5964	4.40E-03	99
TF	Factor: Brn-3c; motif: NNTTATTAATKANKNC	TF:M01408	3964	4.40E-03	73
GO:MF	glycosaminoglycan binding	GO:0005539	200	4.50E-03	11
REAC	Disease	REAC:R-HSA-1643685	1493	4.50E-03	35
TF	Factor: Hoxa9; motif: NTTAAWTAMA; match class: 1	TF:M07457_1	1366	4.50E-03	35
TF	Factor: ipf1; motif: CATTAR; match class: 1	TF:M01275_1	2742	4.50E-03	56
TF	Factor: DPF2; motif: NYCACYTCCYCNYYCY	TF:M09760	7424	4.50E-03	117
REAC	Generation of second messenger molecules	REAC:R-HSA-202433	28	4.60E-03	5
TF	Factor: RARA; motif: AGGTCAANNARAGGTCA	TF:M04483	3600	4.60E-03	68
TF	Factor: LRH-1; motif: TCAAGGTCRYGACCTTGR	TF:M11828	9272	4.60E-03	139
TF	Factor: AP-4:Max; motif: NCAGCTGNNNNNNNCACGTGN; match class: 1	TF:M08674_1	4802	4.70E-03	84
GO:BP	myelination	GO:0042552	138	4.80E-03	10
KEGG	Toll-like receptor signaling pathway	KEGG:04620	92	4.80E-03	7
KEGG	Th17 cell differentiation	KEGG:04659	92	4.80E-03	7
TF	Factor: ALX3; motif: NNYAATTANN	TF:M04279	3243	4.80E-03	63
GO:BP	negative regulation of metabolic process	GO:0009892	2853	4.90E-03	57
TF	Factor: E2F2; motif: AAAATGGCGCCATTTT	TF:M04517	8014	4.90E-03	124
TF	Factor: FOX; motif: KWTTGTTTRTTTW	TF:M00809	3102	4.90E-03	61
TF	Factor: YB-1; motif: CCAMTCNGMR	TF:M03805	8857	4.90E-03	134
GO:BP	gliogenesis	GO:0042063	284	5.00E-03	14
GO:BP	amyloid-beta clearance	GO:0097242	37	5.00E-03	6
TF	Factor: FOXM1; motif: NAGASTGATTA; match class: 1	TF:M04611_1	2751	5.00E-03	56
GO:BP	protein phosphorylation	GO:0006468	1459	5.10E-03	36
GO:MF	lipopeptide binding	GO:0071723	5	5.10E-03	3
GO:MF	complement component C3b binding	GO:0001851	5	5.10E-03	3
KEGG	Acute myeloid leukemia	KEGG:05221	64	5.10E-03	6
KEGG	Rap1 signaling pathway	KEGG:04015	201	5.10E-03	10
TF	Factor: CDP; motif: TRATCRATAN	TF:M03952	3537	5.10E-03	67
TF	Factor: islet1; motif: SCAMTTAN	TF:M11012	5352	5.10E-03	91
TF	Factor: GATA-3; motif: MGATAASATCT	TF:M12195	3177	5.10E-03	62
TF	Factor: ER-beta; motif: GTCANASTGRCCYNR; match class: 1	TF:M01875_1	1196	5.20E-03	32
GO:CC	secretory granule lumen	GO:0034774	289	5.30E-03	13
GO:MF	peptidase inhibitor activity	GO:0030414	132	5.30E-03	9
TF	Factor: HOXA4; motif: RYCATTRN	TF:M08771	2345	5.30E-03	50
REAC	Antigen processing-Cross presentation	REAC:R-HSA-1236975	101	5.50E-03	8
TF	Factor: Fra-2; motif: NRRTGASTCAB	TF:M07092	2621	5.50E-03	54
TF	Factor: CEBPD; motif: NRTTGCNCAAYN	TF:M12587	2484	5.50E-03	52
GO:BP	positive regulation of mononuclear cell migration	GO:0071677	58	5.60E-03	7
GO:MF	antigen binding	GO:0003823	49	5.60E-03	6
TF	Factor: Sox-3; motif: SNNACAATRK	TF:M11617	3258	5.60E-03	63
TF	Factor: OSR2; motif: NGCTACTGNN	TF:M12051	2148	5.60E-03	47
GO:BP	regulation of protein modification process	GO:0031399	1404	5.70E-03	35

GO:CC	cytoplasmic vesicle lumen	GO:0060205	291	5.70E-03	13
TF	Factor: SUHW1; motif: TCTCTCCAGTRTGAATTCTCTGAT; match class: 1	TF:M10541_1	1442	5.70E-03	36
GO:BP	positive regulation of ERK1 and ERK2 cascade	GO:0070374	174	5.80E-03	11
GO:BP	regulation of proteolysis	GO:0030162	662	5.80E-03	22
KEGG	Alcoholic liver disease	KEGG:04936	128	5.80E-03	8
TF	Factor: HOXA7; motif: GYMATTAN; match class: 1	TF:M10690_1	4980	5.80E-03	86
GO:BP	entry into host	GO:0044409	141	5.90E-03	10
GO:BP	regulation of macrophage migration	GO:1905521	38	5.90E-03	6
TF	Factor: ESE-1; motif: NNANVAGGAAGTNN	TF:M09902	2697	5.90E-03	55
GO:CC	coated vesicle membrane	GO:0030662	172	6.00E-03	10
GO:CC	phagocytic vesicle membrane	GO:0030670	76	6.00E-03	7
TF	Factor: T3R-beta; motif: NTGACCTNRNYNAGGTCAN	TF:M11820	4448	6.00E-03	79
TF	Factor: TCF-1; motif: ASATCAAAG	TF:M11602	5688	6.00E-03	95
GO:CC	vesicle lumen	GO:0031983	293	6.10E-03	13
TF	Factor: p300; motif: ACNTCCG	TF:M04826	15885	6.10E-03	212
TF	Factor: SPI1; motif: NGRGGAAGTN; match class: 1	TF:M02078_1	321	6.10E-03	15
TF	Factor: MOX1; motif: NTCRTTAN	TF:M10761	2561	6.10E-03	53
GO:BP	cellular response to interferon-gamma	GO:0071346	111	6.20E-03	9
GO:BP	MyD88-dependent toll-like receptor signaling pathway	GO:0002755	22	6.20E-03	5
TF	Factor: GABPA; motif: NNCACTTCCTGTNN	TF:M12494	1762	6.20E-03	41
TF	Factor: GATA-3; motif: ANAGATMWWA	TF:M00351	2155	6.20E-03	47
TF	Factor: POU5F1; motif: NNATGCAAANN	TF:M09782	2982	6.20E-03	59
TF	Factor: p53; motif: NGRCWTGYCY; match class: 1	TF:M00272_1	974	6.20E-03	28
TF	Factor: CTF/NF1; motif: TTGGCN; match class: 1	TF:M02050_1	3413	6.20E-03	65
GO:BP	negative regulation of leukocyte mediated immunity	GO:0002704	59	6.30E-03	7
GO:BP	regulation of interleukin-2 production	GO:0032663	59	6.30E-03	7

GO:BP	interleukin-2 production	GO:0032623	59	6.30E-03	7
GO:MF	hydrolase activity, hydrolyzing N-glycosyl compounds	GO:0016799	50	6.30E-03	6
TF	Factor: YB-1; motif: NNNNCCAATNN	TF:M03862	7885	6.30E-03	122
TF	Factor: RARA; motif: AGGTCAANNARAGGTCA; match class: 1	TF:M04483_1	502	6.30E-03	19
TF	Factor: Pit-1; motif: NTAATGAKATGCRN	TF:M11950	4913	6.30E-03	85
TF	Factor: Sox-4; motif: NYCTTTGTYYYN; match class: 1	TF:M10069_1	1449	6.30E-03	36
TF	Factor: CDP:SRF; motif: NCCWTAYAAGGTMNKRATCRATN; match class: 1	TF:M08520_1	3199	6.40E-03	62
GO:CC	lumenal side of membrane	GO:0098576	31	6.50E-03	5
GO:BP	cellular homeostasis	GO:0019725	828	6.60E-03	25
GO:BP	positive regulation of leukocyte chemotaxis	GO:0002690	84	6.60E-03	8
TF	Factor: ESE-1; motif: NTGTGCGGATGCN	TF:M11385	10801	6.60E-03	156
TF	Factor: STAT1; motif: NNTTTCYNGGAARNNNNNNNNN	TF:M01260	1832	6.70E-03	42
TF	Factor: THAP1; motif: YTGCCCNNA; match class: 1	TF:M07407_1	3639	6.70E-03	68
TF	Factor: RAR-gamma; motif: NRGGTCAAAAGGTCAN	TF:M11804	2639	6.70E-03	54
TF	Factor: CSX; motif: NCCACTTRAN	TF:M10640	5466	6.70E-03	92
GO:BP	response to abiotic stimulus	GO:0009628	1055	6.80E-03	29
TF	Factor: Nkx2-3; motif: NSCACTTNNC	TF:M10634	1641	6.80E-03	39
GO:BP	viral life cycle	GO:0019058	292	6.90E-03	14
TF	Factor: AP-2alpha; motif: NTNSCCTGRGGSNAN	TF:M09590	4694	6.90E-03	82
TF	Factor: T3R-beta; motif: NRRGGTCRTGACCYYN	TF:M11817	4694	6.90E-03	82
TF	Factor: RUSH-1alpha; motif: NNMCWTNKNN	TF:M01107	2573	7.00E-03	53
GO:BP	superoxide metabolic process	GO:0006801	60	7.10E-03	7
GO:BP	inflammatory response to antigenic stimulus	GO:0002437	60	7.10E-03	7
GO:CC	vacuolar membrane	GO:0005774	436	7.10E-03	16
TF	Factor: PBX2; motif: TGANTGACAGN	TF:M09736	4240	7.10E-03	76

TF	Factor: MZF-1; motif: TGGGGAR; match class: 1	TF:M01733_1	4394	7.20E-03	78
TF	Factor: SOX2; motif: NNACAATGGNN	TF:M12505	1396	7.20E-03	35
TF	Factor: Dlx-5; motif: AATTAN; match class: 1	TF:M03546_1	4779	7.40E-03	83
TF	Factor: DRI1; motif: AATTAA; match class: 1	TF:M01654_1	4779	7.40E-03	83
TF	Factor: hoxa9; motif: NCGGYCATWAAAWTANW	TF:M01351	1712	7.50E-03	40
TF	Factor: E2A; motif: NRMCASCTGCNNN	TF:M02088	2511	7.60E-03	52
TF	Factor: POU6F1; motif: NTAATGAKATGNNN	TF:M11958	2239	7.60E-03	48
GO:BP	regulation of cellular localization	GO:0060341	781	7.80E-03	24
TF	Factor: GATA-4; motif: NNGATAASNN	TF:M12207	2377	7.80E-03	50
GO:BP	membrane raft organization	GO:0031579	23	7.90E-03	5
TF	Factor: Pax-4; motif: WNNNYTAATTARYNSNN	TF:M01385	2724	8.00E-03	55
TF	Factor: ESE-1; motif: ACCAGGAAGTANNNNNNNAAWAA	TF:M11383	3150	8.10E-03	61
TF	Factor: GATA-6; motif: NGATAACGATCN	TF:M12209	1717	8.10E-03	40
TF	Factor: POU2F2; motif: NTATGCWAATN	TF:M04072	1912	8.10E-03	43
TF	Factor: IRF-1; motif: TTCACTT	TF:M00747	4332	8.10E-03	77
GO:BP	phosphorylation	GO:0016310	1744	8.20E-03	40
TF	Factor: AP-4; motif: NNCAGCTGNN; match class: 1	TF:M11212_1	2449	8.20E-03	51
TF	Factor: JUND; motif: NNATGACTCATNN	TF:M12524	3514	8.20E-03	66
TF	Factor: CDX-2; motif: TTTATN	TF:M02087	8261	8.20E-03	126
GO:MF	cell adhesion molecule binding	GO:0050839	535	8.30E-03	18
TF	Factor: Ngn-2; motif: RACATATGTC	TF:M04183	822	8.40E-03	25
TF	Factor: Prx2; motif: TYAWAKTAA	TF:M02115	2870	8.50E-03	57
TF	Factor: POU3F3; motif: WTNAATAWKNAW	TF:M04082	2941	8.50E-03	58
TF	Factor: GR; motif: NNNNNNCNNTNTGTNCTNN; match class: 1	TF:M00192_1	1531	8.60E-03	37
GO:BP	MAPK cascade	GO:0000165	732	8.70E-03	23
GO:BP	positive regulation of alpha-beta T cell activation	GO:0046635	62	8.80E-03	7

GO:BP	regulation of ERK1 and ERK2 cascade	GO:0070372	258	9.00E-03	13
GO:BP	tube morphogenesis	GO:0035239	788	9.00E-03	24
GO:CC	plasma membrane region	GO:0098590	1176	9.00E-03	29
GO:MF	endopeptidase regulator activity	GO:0061135	141	9.00E-03	9
TF	Factor: Dlx-7; motif: NTCRTTAN	TF:M10600	6220	9.00E-03	101
REAC	DAP12 interactions	REAC:R-HSA-2172127	32	9.10E-03	5
TF	Factor: FRA-2; motif: RTGANTCA	TF:M08914	3234	9.10E-03	62
TF	Factor: Pit-1; motif: NTAATTTATKCGY	TF:M11949	4653	9.30E-03	81
GO:BP	positive regulation of pattern recognition receptor signaling pathway	GO:0062208	41	9.40E-03	6
GO:BP	positive regulation of myeloid cell differentiation	GO:0045639	88	9.40E-03	8
GO:BP	positive regulation of T cell differentiation	GO:0045582	88	9.40E-03	8
TF	Factor: Oct-2; motif: ATTTGCA	TF:M04715	5273	9.40E-03	89
TF	Factor: NFATc1; motif: TTTTCCATGGAAAN; match class: 1	TF:M04053_1	4962	9.40E-03	85
TF	Factor: TEF-3:C/EBPdelta; motif: RGWATGYNRTTRCGYAAY	TF:M08413	5118	9.40E-03	87
GO:CC	extracellular matrix	GO:0031012	497	9.60E-03	17
TF	Factor: GATA-3; motif: MGATAACGATCT	TF:M12194	2811	9.60E-03	56
TF	Factor: BCL-6; motif: WRCTTTCKAGGRAT	TF:M01185	5120	9.60E-03	87
TF	Factor: c-Fos; motif: NNTGASTCATN	TF:M07090	3604	9.60E-03	67
TF	Factor: HOXD12:Elk-1; motif: NRNCGGAAGTCGTAAAN; match class: 1	TF:M08359_1	997	9.70E-03	28
TF	Factor: MyoD; motif: YGNCAGSTGTYN	TF:M11185	997	9.70E-03	28
TF	Factor: GATA-1; motif: NTGNNNNNNNSAGATAAGR	TF:M09621	4581	9.70E-03	80
GO:BP	positive regulation of interferon-gamma production	GO:0032729	63	9.80E-03	7
TF	Factor: GATA-4; motif: AGATAAN	TF:M03549	3977	9.80E-03	72
TF	Factor: SOX; motif: CTCTTTGTTANGA	TF:M01014	4278	9.80E-03	76
TF	Factor: c-Myb; motif: NNNAACKGNNN	TF:M01821	3242	9.80E-03	62

GO:BP	regulation of monocyte chemotaxis	GO:0090025	24	9.90E-03	5
GO:CC	external encapsulating structure	GO:0030312	498	9.90E-03	17
GO:BP	positive regulation of microglial cell mediated cytotoxicity	GO:1904151	4	1.00E-02	3
GO:BP	positive regulation of neutrophil degranulation	GO:0043315	4	1.00E-02	3
GO:BP	interleukin-3-mediated signaling pathway	GO:0038156	4	1.00E-02	3
GO:BP	chemical homeostasis	GO:0048878	1078	1.00E-02	29
GO:BP	regulation of alpha-beta T cell activation	GO:0046634	89	1.00E-02	8
TF	Factor: RARA; motif: ARGGTCAAAAGGTCA	TF:M04481	2675	1.00E-02	54
TF	Factor: FOXJ2; motif: NNTGTTGTAAAYAN; match class: 1	TF:M11585_1	1057	1.00E-02	29
TF	Factor: ipf1; motif: NVSTAATTAC; match class: 1	TF:M01235_1	1295	1.00E-02	33
TF	Factor: NKX3A; motif: NTNAAGTGNTTN	TF:M10009	3102	1.00E-02	60
TF	Factor: FAC1; motif: NNNCAMAACACRNA; match class: 1	TF:M00456_1	2264	1.00E-02	48
GO:BP	negative regulation of programmed cell death	GO:0043069	799	1.10E-02	24
GO:BP	regulation of cellular metabolic process	GO:0031323	5347	1.10E-02	89
GO:MF	molecular function regulator	GO:0098772	1692	1.10E-02	37
KEGG	Natural killer cell mediated cytotoxicity	KEGG:04650	105	1.10E-02	7
TF	Factor: AR; motif: GGTACANNRTGTTCT	TF:M00481	4286	1.10E-02	76
TF	Factor: HNRPUL1; motif: NCNCAGN; match class: 1	TF:M09746_1	6727	1.10E-02	107
TF	Factor: HOXC4; motif: NTMATTAN	TF:M10717	2962	1.10E-02	58
TF	Factor: Oct3; motif: NATGCAANNN	TF:M01307	3322	1.10E-02	63
TF	Factor: ZNF775; motif: RGRGAGAAGN	TF:M12720	3038	1.10E-02	59
TF	Factor: Oct3; motif: WTATGCGCATAW; match class: 1	TF:M11934_1	7810	1.10E-02	120
GO:BP	movement in host environment	GO:0052126	152	1.20E-02	10
GO:BP	lymphocyte migration	GO:0072676	91	1.20E-02	8
GO:BP	dendritic cell antigen processing and presentation	GO:0002468	12	1.20E-02	4
GO:BP	negative regulation of leukocyte migration	GO:0002686	43	1.20E-02	6
GO:CC	endosome membrane	GO:0010008	507	1.20E-02	17
REAC	Interferon Signaling	REAC:R-HSA-913531	182	1.20E-02	10
REAC	PD-1 signaling	REAC:R-HSA-389948	17	1.20E-02	4
REAC	Leishmania infection	REAC:R-HSA-9658195	223	1.20E-02	11
TF	Factor: ZABC1; motif: ATTCCNAC; match class: 1	TF:M01306_1	2342	1.20E-02	49
TF	Factor: NF-1B; motif: KCCAGANWN	TF:M08825	4990	1.20E-02	85
TF	Factor: Msx-1; motif: WNGNAATTANV	TF:M08822	5618	1.20E-02	93
TF	Factor: FOXO1A; motif: NNNYTGTTTNCN	TF:M09931	5699	1.20E-02	94
TF	Factor: STAT6; motif: NNYTTCCY	TF:M00500	4076	1.20E-02	73
TF	Factor: RAR-gamma; motif: RAGGTCATGACCTY	TF:M11807	1747	1.20E-02	40
TF	Factor: ZNF586; motif: CAGGCCYRGAGG; match class: 1	TF:M10491_1	6912	1.20E-02	109
GO:BP	central nervous system development	GO:0007417	974	1.30E-02	27
GO:BP	positive regulation of reactive oxygen species metabolic process	GO:2000379	66	1.30E-02	7
GO:CC	clathrin-coated vesicle	GO:0030136	188	1.30E-02	10
GO:MF	carboxylic acid binding	GO:0031406	147	1.30E-02	9
KEGG	Malaria	KEGG:05144	48	1.30E-02	5
KEGG	Leukocyte transendothelial migration	KEGG:04670	108	1.30E-02	7
TF	Factor: DMBX1; motif: NNGGATTANN	TF:M04305	4383	1.30E-02	77
TF	Factor: Cdx-2; motif: BNNATAAANRN	TF:M01659	1188	1.30E-02	31
TF	Factor: MafB; motif: TGCTGASTNNN	TF:M09978	2768	1.30E-02	55
TF	Factor: Oct-2; motif: NNNTATGCAAATNNNN	TF:M01368	1947	1.30E-02	43
TF	Factor: Spi-B; motif: NGNGGAAGYN	TF:M02076	258	1.30E-02	13
TF	Factor: Smad2:Smad3:Smad4; motif: NTGTCTGNCACCT	TF:M07126	3639	1.30E-02	67
TF	Factor: UNCX; motif: NYAATTAN	TF:M04443	2702	1.30E-02	54
GO:BP	calcium-mediated signaling	GO:0019722	191	1.40E-02	11
GO:BP	positive regulation of leukocyte mediated cytotoxicity	GO:0001912	44	1.40E-02	6

GO:BP	monocyte chemotaxis	GO:0002548	44	1.40E-02	6
TF	Factor: ESR1; motif: NNNNMAGGTCACCCTGACCY	TF:M02261	4090	1.40E-02	73
TF	Factor: STAT5B; motif: NAWTTCYNGGAAWTN	TF:M00459	2634	1.40E-02	53
TF	Factor: Oct-1; motif: NNNNWTATGCAAATNTNNN	TF:M00135	1692	1.40E-02	39
TF	Factor: MLR1; motif: NTGNMCYYTGNNCYN	TF:M12637	3795	1.40E-02	69
TF	Factor: VDR:RXR; motif: GGGTCAWNGRGTTCA	TF:M01202	3426	1.40E-02	64
TF	Factor: HNF-3alpha; motif: CNYTAAGTAAACAAAN	TF:M11570	3064	1.40E-02	59
TF	Factor: CP2; motif: GCHCDAMCCAG	TF:M00072	7846	1.40E-02	120
TF	Factor: T-bet; motif: NAGGTGTGAA	TF:M12019	483	1.40E-02	18
GO:BP	positive regulation of leukocyte degranulation	GO:0043302	26	1.50E-02	5
GO:BP	metal ion transport	GO:0030001	813	1.50E-02	24
GO:MF	lipoprotein particle receptor activity	GO:0030228	18	1.50E-02	4
GO:MF	cytokine receptor activity	GO:0004896	85	1.50E-02	7
TF	Factor: POU3F1; motif: WTGMATAAWTNA	TF:M04077	2294	1.50E-02	48
TF	Factor: Fli-1:C/EBPbeta; motif: RNCGGAWRTTGCGCAAY	TF:M08281	6613	1.50E-02	105
TF	Factor: FOXL2; motif: TWAKACWAMTTT	TF:M03548	3875	1.50E-02	70
TF	Factor: C-FOS:C-JUN; motif: ATGAGTCAYN	TF:M08942	2715	1.50E-02	54
GO:BP	regulation of tissue remodeling	GO:0034103	68	1.60E-02	7
TF	Factor: FXR:RXR-ALPHA; motif: NAGKTCATTGACCYN	TF:M08954	5497	1.60E-02	91
TF	Factor: POU3F2; motif: TTATGYTAAT	TF:M00464	2716	1.60E-02	54
TF	Factor: C/EBPalpha; motif: NRTTGTGCAAYNN; match class: 1	TF:M09596_1	852	1.60E-02	25
TF	Factor: MEIS1A:HOXA9; motif: TGACAGKTTTAYGA	TF:M00420	4639	1.60E-02	80
TF	Factor: nanog; motif: NYYWTTGWNATGCAAAT	TF:M09996	1141	1.60E-02	30
TF	Factor: Ncx; motif: NAATNAATTAATAANWW; match class: 1	TF:M01420_1	1701	1.60E-02	39
TF	Factor: MAFB; motif: NTCAGCN; match class: 1	TF:M08888_1	2789	1.60E-02	55
TF	Factor: c-Ets-2; motif: NNNRGGAARNRRR	TF:M09912	4412	1.60E-02	77
TF	Factor: JunD; motif: NRTGACGTCATS	TF:M11270	7948	1.60E-02	121
TF	Factor: Sox-3; motif: NNAACAATRN	TF:M11616	393	1.60E-02	16
TF	Factor: RARA; motif: ARRGGTCANSNGAGGTCA	TF:M04482	3221	1.60E-02	61
TF	Factor: HPX42B; motif: NNYNATTANN	TF:M10681	2033	1.60E-02	44
TF	Factor: AP-4; motif: WGARYCAGCTGYGGNCNK	TF:M00005	4645	1.60E-02	80
GO:BP	regulation of DNA-binding transcription factor activity	GO:0051090	406	1.70E-02	16
GO:BP	negative regulation of mast cell activation	GO:0033004	13	1.70E-02	4
REAC	Costimulation by the CD28 family	REAC:R-HSA-388841	59	1.70E-02	6
TF	Factor: POU3F2; motif: WTATGCWAATKAG	TF:M11904	2582	1.70E-02	52
TF	Factor: ZNF644; motif: TCCWGCCTCTSN; match class: 1	TF:M09737_1	1577	1.70E-02	37
TF	Factor: Tal-1; motif: TCCAKCTGNY	TF:M00993	1642	1.70E-02	38
TF	Factor: OC-2; motif: TCAATA; match class: 1	TF:M02112_1	1837	1.70E-02	41
TF	Factor: NFATc1; motif: TTTCCAYWRTGGAAA; match class: 1	TF:M04052_1	3299	1.70E-02	62
TF	Factor: PRDM16; motif: KGGTCATRACCM; match class: 1	TF:M05946_1	1838	1.70E-02	41
TF	Factor: COUP-TF, motif: TGAMCTTTGMMCYT	TF:M00158	1904	1.70E-02	42
TF	Factor: Oct-1; motif: TATGCAAATN	TF:M00342	2446	1.70E-02	50
TF	Factor: NR1B2; motif: NTGACCY; match class: 1	TF:M02111_1	2939	1.70E-02	57
GO:BP	cellular extravasation	GO:0045123	69	1.80E-02	7
KEGG	Th1 and Th2 cell differentiation	KEGG:04658	80	1.80E-02	6
REAC	Activation of C3 and C5	REAC:R-HSA-174577	7	1.80E-02	3
TF	Factor: GEMIN3; motif: NCWGGRARRGRGNGNG	TF:M09727	7710	1.80E-02	118
TF	Factor: Fra-1; motif: RRTGASTCAKN	TF:M07091	1454	1.80E-02	35
TF	Factor: TTF-1; motif: CTTGASN	TF:M03891	3013	1.80E-02	58
TF	Factor: PPARgamma; motif: NWSTRGGKSARAGGKCA; match class: 1	TF:M10038_1	1269	1.80E-02	32
TF	Factor: CP2/LBP-1c/LSF; motif: GCTGGNTNGNNCYNG	TF:M00947	7463	1.80E-02	115

TF	Factor: CIZ; motif: TTTTNNNNNNNNNNNNNAAAAA; match class: 1	TF:M12070_1	2108	1.80E-02	45
TF	Factor: HOXA2; motif: RTCRTTAR	TF:M10736	1583	1.80E-02	37
TF	Factor: Oct3; motif: CYWTTSWNATGCAAAT; match class: 1	TF:M10036_1	696	1.80E-02	22
GO:BP	positive regulation of chemotaxis	GO:0050921	127	1.90E-02	9
GO:BP	response to mechanical stimulus	GO:0009612	197	1.90E-02	11
GO:BP	ERK1 and ERK2 cascade	GO:0070371	277	1.90E-02	13
TF	Factor: HNF-3beta; motif: NTRTTTRYT	TF:M02014	2179	1.90E-02	46
TF	Factor: HOXA6; motif: NGYMATTANN	TF:M10696	4053	1.90E-02	72
GO:BP	activation of innate immune response	GO:0002218	70	2.00E-02	7
GO:CC	apical plasma membrane	GO:0016324	328	2.00E-02	13
TF	Factor: STAT3; motif: NTTCCYGGAAN	TF:M09664	4899	2.00E-02	83
TF	Factor: NURR1:RXR-ALPHA; motif: NRGGTCRTTGACCYN	TF:M08957	9681	2.00E-02	141
TF	Factor: CDP; motif: NNNNWGWYMAATR	TF:M04610	3683	2.00E-02	67
TF	Factor: Pit-1; motif: NNWWATTCAT	TF:M03559	4362	2.00E-02	76
TF	Factor: PPARGAMMA; motif: NWNTRGGTYANN	TF:M08961	4518	2.00E-02	78
REAC	FCGR3A-mediated IL10 synthesis	REAC:R-HSA-9664323	38	2.10E-02	5
TF	Factor: SPIB; motif: NNTCACTTCCTCTTTN; match class: 1	TF:M12498_1	123	2.10E-02	9
TF	Factor: PMX2B; motif: NNNAATTAATTAANNNG; match class: 1	TF:M01356_1	1722	2.10E-02	39
TF	Factor: Erm; motif: NRRSAGGAARNGRN; match class: 1	TF:M09916_1	1466	2.10E-02	35
TF	Factor: Pbx; motif: NKTGATTGACRKSN	TF:M01967	4369	2.10E-02	76
TF	Factor: Prop-1; motif: TAATTNNRTTA	TF:M10928	1404	2.10E-02	34
GO:BP	regulation of MAPK cascade	GO:0043408	613	2.20E-02	20
GO:BP	Fc receptor signaling pathway	GO:0038093	71	2.20E-02	7
GO:BP	regulation of B cell differentiation	GO:0045577	28	2.20E-02	5
TF	Factor: HNF-3alpha; motif: YTRWGTMAATATTTRCWYWN	TF:M11571	3470	2.20E-02	64

TF	Factor: c-MYB; motif: NNNGNCAGTTN	TF:M00773	2962	2.20E-02	57
TF	Factor: COUPTF; motif: NNNNNTGACCYTTGNMCNYNGMN	TF:M01036	3252	2.20E-02	61
TF	Factor: JunD; motif: RTGACGTCA	TF:M04681	4994	2.20E-02	84
TF	Factor: HOXB2:Sox-20; motif: ACAATRSNNNNNNNATYA	TF:M08719	1470	2.20E-02	35
TF	Factor: FOXP3; motif: NNNVAAACANWD	TF:M07419	5230	2.20E-02	87
TF	Factor: Sox-14; motif: NNNACAATGN	TF:M11618	927	2.20E-02	26
GO:BP	regulation of adaptive immune response	GO:0002819	164	2.30E-02	10
GO:BP	leukocyte mediated cytotoxicity	GO:0001909	99	2.30E-02	8
TF	Factor: JUNB:FOSB; motif: NRTGASTCAT	TF:M08920	2610	2.30E-02	52
TF	Factor: LUMAN; motif: CYCAGCYYCY	TF:M09729	9533	2.30E-02	139
TF	Factor: PLZF; motif: ACTKTANNTN	TF:M04625	5075	2.30E-02	85
TF	Factor: TBR2; motif: NAGGTGTGAN	TF:M12017	1044	2.30E-02	28
TF	Factor: AP-2rep; motif: CAGTGGG; match class: 1	TF:M00468_1	1409	2.30E-02	34
TF	Factor: TEF-3; motif: GNTATTTTT; match class: 1	TF:M07270_1	3552	2.30E-02	65
TF	Factor: LHX2; motif: NNYTAATTRNNN	TF:M09976	1928	2.30E-02	42
TF	Factor: HTF4; motif: NCACCTGN	TF:M11157	1601	2.30E-02	37
GO:BP	production of molecular mediator involved in inflammatory response	GO:0002532	72	2.40E-02	7
GO:BP	detection of bacterium	GO:0016045	14	2.40E-02	4
GO:BP	negative regulation of leukocyte degranulation	GO:0043301	14	2.40E-02	4
TF	Factor: Tal-1; motif: CAGATGG	TF:M03804	4459	2.40E-02	77
TF	Factor: C/EBP; motif: NNATTGCNNAANNN; match class: 1	TF:M00190_1	1046	2.40E-02	28
TF	Factor: BCL-6; motif: NNCTTTCYAGGAA	TF:M09874	2405	2.40E-02	49
TF	Factor: Fra-1; motif: NATGASTCAYM	TF:M11284	2615	2.40E-02	52
TF	Factor: TTF-1; motif: NNNNCAAGNRNN	TF:M00794	4005	2.40E-02	71
TF	Factor: C/EBPgamma:Elf-1; motif: TKRCGHAATWSCGGAAGT; match class: 1	TF:M08676_1	2065	2.40E-02	44
TF	Factor: CP2; motif: NTGNCTGGNN	TF:M03868	4006	2.40E-02	71

GO:BP	positive regulation of complement activation	GO:0045917	5	2.50E-02	3
GO:BP	detection of bacterial lipoprotein	GO:0042494	5	2.50E-02	3
GO:BP	microglial cell activation involved in immune response	GO:0002282	5	2.50E-02	3
GO:BP	positive regulation of neutrophil activation	GO:1902565	5	2.50E-02	3
GO:BP	positive regulation of peptidyl-tyrosine phosphorylation	GO:0050731	166	2.50E-02	10
GO:CC	actin cytoskeleton	GO:0015629	484	2.50E-02	16
TF	Factor: HSF1; motif: GAANNTTCTNGN	TF:M07459	2902	2.50E-02	56
TF	Factor: T3R-beta; motif: NTGACCTNACGTGACCTYA	TF:M11821	2134	2.50E-02	45
TF	Factor: NR1B2; motif: NAAAGGTCAN	TF:M11798	2760	2.50E-02	54
TF	Factor: JUND:FRA-1; motif: NRTGACTCAN	TF:M08929	1290	2.50E-02	32
TF	Factor: c-Ets-2; motif: NACCGGAAGYRCTTCCGGTN; match class: 1	TF:M11417_1	12734	2.50E-02	175
TF	Factor: LHX3; motif: ATTAAW; match class: 1	TF:M02097_1	5323	2.50E-02	88
TF	Factor: IRF-4; motif: RGGAASWGR; match class: 1	TF:M04818_1	2691	2.50E-02	53
TF	Factor: MyoD; motif: CGNCAGSTGTTN	TF:M11183	3049	2.50E-02	58
GO:BP	negative regulation of apoptotic process	GO:0043066	783	2.60E-02	23
GO:BP	membrane organization	GO:0061024	728	2.60E-02	22
GO:BP	regulation of exocytosis	GO:0017157	204	2.60E-02	11
GO:BP	regulation of glial cell differentiation	GO:0045685	73	2.60E-02	7
GO:CC	intracellular anatomical structure	GO:0005622	14269	2.60E-02	187
TF	Factor: Pbx-1; motif: ATCAATCAW	TF:M00096	2137	2.60E-02	45
TF	Factor: Oct-1; motif: NNGAATATKCANNNN	TF:M00136	3417	2.60E-02	63
TF	Factor: AREB6; motif: NNYNYACCTGWVT	TF:M00412	3939	2.60E-02	70
GO:BP	biological process involved in symbiotic interaction	GO:0044403	244	2.70E-02	12
GO:BP	negative regulation of macromolecule metabolic process	GO:0010605	2662	2.70E-02	52
TF	Factor: TEF-1; motif: ACATTCCWSNN	TF:M07340	3273	2.70E-02	61
TF	Factor: GATA-3; motif: WGATAASN	TF:M08918	3568	2.70E-02	65
TF	Factor: GATA3; motif: NGATAANN	TF:M03997	3568	2.70E-02	65
TF	Factor: HNF4alpha; motif: VTGAACTTTGMMB	TF:M00638	2348	2.70E-02	48
TF	Factor: ipf1; motif: TSNGYCATTANNNNC	TF:M01013	2348	2.70E-02	48
TF	Factor: NRL; motif: NNNNTGCTGAC	TF:M04224	3869	2.70E-02	69
TF	Factor: SREBP-2; motif: ATCACMCCAY	TF:M11084	2770	2.70E-02	54
GO:BP	biological process involved in interaction with host	GO:0051701	168	2.80E-02	10
GO:MF	CD4 receptor binding	GO:0042609	8	2.80E-02	3
GO:MF	inhibitory MHC class I receptor activity	GO:0032396	8	2.80E-02	3
TF	Factor: NR3C1; motif: NRGWACAYNRTGTWCYN; match class: 1	TF:M04476_1	4480	2.80E-02	77
TF	Factor: AR; motif: NGNACANNNTGTTCYNN	TF:M09589	4327	2.80E-02	75
TF	Factor: HSF1; motif: NTTCTRGAANNTTCY	TF:M07100	2844	2.80E-02	55
TF	Factor: CIZ; motif: TTTTNNNNNNNNNNNNAAAAA	TF:M12070	2146	2.80E-02	45
GO:BP	actin cytoskeleton organization	GO:0030036	680	2.90E-02	21
REAC	Toll Like Receptor 4 (TLR4) Cascade	REAC:R-HSA-166016	127	2.90E-02	8
TF	Factor: POU2F1:Elk-1; motif: ACCGGAWATGCAW	TF:M08398	7041	2.90E-02	109
TF	Factor: TAL1:GATA1; motif: NTTATCWNNNNNNNNCAG	TF:M07230	2991	2.90E-02	57
TF	Factor: ETF; motif: CCCCGCCCCYN	TF:M07039	14877	2.90E-02	198
GO:BP	reactive oxygen species metabolic process	GO:0072593	207	3.00E-02	11
TF	Factor: NFATc2; motif: TTTTCCATGGAAAA; match class: 1	TF:M11985_1	3803	3.00E-02	68
TF	Factor: c-Ets; motif: KRCAGGAARTRNKT; match class: 1	TF:M00340_1	718	3.00E-02	22
TF	Factor: CP2; motif: NNNNCCAGNCNN; match class: 1	TF:M07602_1	4106	3.00E-02	72
TF	Factor: BCL-11A; motif: NAAAGAGGAAGTGARAN; match class: 1	TF:M09595_1	413	3.00E-02	16
TF	Factor: CDP; motif: NNATYGATYN	TF:M11508	3068	3.00E-02	58
GO:BP	positive regulation of nitrogen compound metabolic process	GO:0051173	2747	3.10E-02	53
GO:BP	mature B cell differentiation	GO:0002335	30	3.10E-02	5

GO:CC	apical part of cell	GO:0045177	391	3.10E-02	14
TF	Factor: FXR:RXR-alpha; motif: CAAGGTSAWTAACC	TF:M00631	2924	3.10E-02	56
TF	Factor: beta-catenin; motif: CTTTGATN	TF:M07599	6721	3.10E-02	105
TF	Factor: Cdx-2; motif: NYMATAANN	TF:M10850	2154	3.10E-02	45
TF	Factor: POU4F3; motif: CTAATYW	TF:M07061	5993	3.10E-02	96
TF	Factor: TFF-1; motif: NNANCCACTTGAMNTT	TF:M01312	4653	3.20E-02	79
TF	Factor: SRY; motif: AAACWAM; match class: 1	TF:M00148_1	3665	3.30E-02	66
TF	Factor: C/EBPbeta; motif: NATTGCRYAAYN	TF:M09597	2506	3.30E-02	50
KEGG	Human T-cell leukemia virus 1 infection	KEGG:05166	208	3.40E-02	9
TF	Factor: ESR1; motif: STGACCTN	TF:M12602	2862	3.40E-02	55
TF	Factor: JunB; motif: NNNTGAGTCAY	TF:M09631	1628	3.40E-02	37
TF	Factor: HOXA5; motif: ANGNTAATTANCNNAN	TF:M01452	3008	3.40E-02	57
GO:BP	detection of stimulus	GO:0051606	337	3.50E-02	14
GO:BP	negative regulation of hydrolase activity	GO:0051346	293	3.50E-02	13
TF	Factor: Oct-1; motif: CWNAWTKWSATRYN	TF:M00162	2937	3.50E-02	56
TF	Factor: GATA-6; motif: WGATAACGATCW	TF:M12208	3449	3.50E-02	63
TF	Factor: AML2; motif: CCRCACCAYDN	TF:M01854	2372	3.50E-02	48
TF	Factor: NKX2-2; motif: NNNCCACTCAANNN; match class: 1	TF:M12456_1	2512	3.50E-02	50
TF	Factor: ZNF7; motif: NCYYTGYCWNCWCTTR	TF:M12716	2166	3.60E-02	45
GO:BP	cellular component disassembly	GO:0022411	432	3.70E-02	16
GO:BP	Fc-gamma receptor signaling pathway	GO:0038094	31	3.70E-02	5
TF	Factor: HOXD4; motif: NYMATTAN	TF:M10712	3380	3.70E-02	62
TF	Factor: c-Ets-2; motif: NACCGGAAGYRCTTCCGGTN	TF:M11417	12989	3.70E-02	177
GO:BP	regeneration	GO:0031099	174	3.80E-02	10
TF	Factor: NeuroD; motif: NNSCWGCTGNSY	TF:M01288	4210	3.80E-02	73
TF	Factor: PUR1; motif: GGGNCAGNN	TF:M01721	8254	3.80E-02	123
TF	Factor: NF-kappaB; motif: NGGGGAMTTTCCNN	TF:M00194	2103	3.80E-02	44
TF	Factor: AP-4:Fli-1; motif: RSCGGAWRCAGSTGN	TF:M08445	8339	3.80E-02	124
TF	Factor: Sall1; motif: NGGTCCKRGKRA	TF:M05467	3757	3.80E-02	67
TF	Factor: GR; motif: RGWACATWATGTWCY; match class: 1	TF:M11847_1	3311	3.80E-02	61
GO:BP	regulation of interleukin-10 production	GO:0032653	52	3.90E-02	6
GO:BP	interleukin-10 production	GO:0032613	52	3.90E-02	6
GO:BP	negative regulation of developmental process	GO:0051093	804	3.90E-02	23
TF	Factor: Brachyury; motif: NTNNCANNNNRGTGTGAANN	TF:M09878	3240	3.90E-02	60
TF	Factor: HPX42B; motif: NNYAATTANN	TF:M10679	1770	3.90E-02	39
TF	Factor: Smad3; motif: NGNCAGACASNNN; match class: 1	TF:M01888_1	571	3.90E-02	19
TF	Factor: OCT-2; motif: ATGMATATGCWAAT	TF:M08836	2950	3.90E-02	56
TF	Factor: ipf1; motif: NVSTAATTAC	TF:M01235	2878	3.90E-02	55
GO:BP	positive regulation of secretion by cell	GO:1903532	254	4.00E-02	12
TF	Factor: Brn-4; motif: NATTATGCAWGN	TF:M11921	1076	4.00E-02	28
TF	Factor: SF-1; motif: NYYCAAGGYCA	TF:M10084	3390	4.00E-02	62
TF	Factor: GSC2; motif: NNTAATCCNN	TF:M04325	3097	4.00E-02	58
GO:MF	peptide antigen binding	GO:0042605	23	4.10E-02	4
GO:MF	polysaccharide binding	GO:0030247	23	4.10E-02	4
GO:BP	negative regulation of cell migration	GO:0030336	255	4.20E-02	12
GO:CC	Fc-epsilon receptor I complex	GO:0032998	2	4.20E-02	2
GO:CC	Fc receptor complex	GO:0032997	2	4.20E-02	2
GO:CC	integrin alphaL-beta2 complex	GO:0034687	2	4.20E-02	2
GO:CC	integrin alphaM-beta2 complex	GO:0034688	2	4.20E-02	2
GO:CC	Toll-like receptor 1-Toll-like receptor 2 protein complex	GO:0035354	2	4.20E-02	2
GO:CC	macrophage migration inhibitory factor receptor complex	GO:0035692	2	4.20E-02	2
GO:MF	complement receptor activity	GO:0004875	9	4.20E-02	3

GO:MF	T cell receptor binding	GO:0042608	9	4.20E-02	3
TF	Factor: SPI1; motif: NNNAAAGAGGAAGTGANNNN; match class: 1	TF:M12497_1	134	4.20E-02	9
TF	Factor: FOXP1; motif: TNTGTTTMY	TF:M09933	4223	4.20E-02	73
TF	Factor: NF-1B; motif: KCCAGANWN; match class: 1	TF:M08825_1	903	4.20E-02	25
TF	Factor: VDR; motif: GGGKNARNRRGGWSA	TF:M00444	9297	4.20E-02	135
GO:BP	positive regulation of humoral immune response	GO:0002922	16	4.30E-02	4
GO:BP	regulation of T cell differentiation	GO:0045580	141	4.30E-02	9
KEGG	Fc epsilon RI signaling pathway	KEGG:04664	62	4.30E-02	5
TF	Factor: HNF3; motif: NNNNNTRTTTRYTYWNKN	TF:M01012	1910	4.30E-02	41
TF	Factor: Six-1; motif: CTCARRTTWCN	TF:M07466	2887	4.30E-02	55
GO:BP	neutrophil mediated immunity	GO:0002446	32	4.40E-02	5
GO:BP	positive regulation of cell death	GO:0010942	539	4.40E-02	18
GO:MF	scavenger receptor activity	GO:0005044	44	4.40E-02	5
TF	Factor: HOXA5; motif: ANGNTAATTANCNNAN; match class: 1	TF:M01452_1	1143	4.40E-02	29
TF	Factor: HNF-3alpha; motif: NNYTAWGTAAACAAAN; match class: 1	TF:M11568_1	170	4.40E-02	10
TF	Factor: CTCF; motif: ACCAGGKGGC	TF:M04727	5802	4.40E-02	93
GO:BP	cellular response to external stimulus	GO:0071496	300	4.50E-02	13
GO:BP	peptidyl-tyrosine phosphorylation	GO:0018108	345	4.50E-02	14
KEGG	Chagas disease	KEGG:05142	95	4.50E-02	6
TF	Factor: Tbx20; motif: SGAGGTGTGAGGSGR	TF:M07474	3181	4.50E-02	59
TF	Factor: CDP; motif: ATCGATNNNNNNATCRAT	TF:M03951	3255	4.50E-02	60
TF	Factor: msc; motif: NRACAGCTGTYN	TF:M11145	1024	4.50E-02	27
TF	Factor: HOXB6; motif: NTAATKRC	TF:M10691	4386	4.50E-02	75
TF	Factor: NFATc2; motif: TTTTCCA; match class: 1	TF:M02265_1	1650	4.50E-02	37
TF	Factor: MZF1; motif: NNAATCCCCANNN	TF:M12493	1330	4.50E-02	32
GO:BP	integrin-mediated signaling pathway	GO:0007229	109	4.60E-02	8
KEGG	Herpes simplex virus 1 infection	KEGG:05168	471	4.60E-02	14
KEGG	Viral protein interaction with cytokine and cytokine receptor	KEGG:04061	63	4.60E-02	5
TF	Factor: IRF-3; motif: GCNGTTTCCWGGAAACNGAAAC	TF:M11674	3929	4.60E-02	69
TF	Factor: POU2F1; motif: ANKNRWATGSAAWYAW; match class: 1	TF:M10033_1	794	4.60E-02	23
TF	Factor: AR; motif: ARGAACANNNTGTNC	TF:M07204	4006	4.60E-02	70
GO:BP	phosphate-containing compound metabolic process	GO:0006796	2574	4.70E-02	50
GO:MF	virus receptor activity	GO:0001618	71	4.70E-02	6
TF	Factor: CDX2; motif: NNGCAATAAANN	TF:M12513	2609	4.70E-02	51
TF	Factor: POU2F3; motif: NNAYGCTNATS	TF:M11903	1395	4.70E-02	33
TF	Factor: ZBRK1; motif: NGNNNGGTNAWAWAAARRGCNG; match class: 1	TF:M10468_1	3933	4.70E-02	69
GO:BP	interleukin-12 production	GO:0032615	54	4.80E-02	6
GO:BP	regulation of interleukin-12 production	GO:0032655	54	4.80E-02	6
TF	Factor: Kaiso; motif: NTCCTGCNAN	TF:M01119	3633	4.80E-02	65
TF	Factor: POU3F2; motif: NWTGCATAAWTTA	TF:M04078	3189	4.80E-02	59
TF	Factor: EMX1; motif: NNTAATKANN	TF:M07988	2898	4.80E-02	55
GO:BP	regulation of innate immune response	GO:0045088	218	4.90E-02	11
GO:BP	positive regulation of lipoprotein particle clearance	GO:0010986	6	4.90E-02	3
GO:BP	membrane raft distribution	GO:0031580	6	4.90E-02	3
GO:BP	cellular response to bacterial lipoprotein	GO:0071220	6	4.90E-02	3
GO:BP	response to bacterial lipopeptide	GO:0070339	6	4.90E-02	3
GO:BP	cellular response to bacterial lipopeptide	GO:0071221	6	4.90E-02	3
TF	Factor: Blimp-1; motif: NAGKGAAAGTGN	TF:M12243	1721	4.90E-02	38
TF	Factor: Pit-1; motif: NMTTCATAAWTATWNMNA; match class: 1	TF:M00802_1	797	4.90E-02	23
TF	Factor: HSF2; motif: NGAANNWTCK	TF:M00147	4941	4.90E-02	82
CORUM	C1q complex	CORUM:6418	2	5.00E-02	2

CORUM	TLR1-TLR2 complex	CORUM:7048	2	5.00E-02	2
CORUM	TLR1-TLR2-lipoprotein complex	CORUM:7049	2	5.00E-02	2
GO:BP	peptidyl-tyrosine modification	GO:0018212	348	5.00E-02	14
GO:MF	arachidonate 5-lipoxygenase activity	GO:0004051	2	5.00E-02	2
GO:MF	chemokine (C-C motif) ligand 5 binding	GO:0071791	2	5.00E-02	2
GO:MF	IgM binding	GO:0001791	2	5.00E-02	2

Table A34. KCL BrainBank enrichment for Cluster 3 with gProfiler2. Term size refers to the number of genes in the term, with the intersection size denoting the number of genes in the dataset found in the term. GO:BP – Gene Ontology Biological Process, GO:CC – Gene Ontology Cellular Components, GO:MF – Gene Ontology Molecular Function, KEGG: Kyoto Encyclopaedia of Genes and Genomes, REAC: Reactome.

Dataset	Sample ID	Cluster One	Cluster Two	Cluster Three
TargetALS (case)	CGND.HRA.00217	0.0000	0.0000	1.0000
TargetALS (case)	CGND.HRA.00359	0.0000	0.0000	1.0000
TargetALS (case)	CGND.HRA.02228	0.0000	0.0000	1.0000
TargetALS (case)	CGND.HRA.02233	0.0000	0.0000	1.0000
TargetALS (case)	CGND.HRA.00223	0.0000	0.0000	1.0000
TargetALS (case)	CGND.HRA.00366	0.0000	0.0000	1.0000
TargetALS (case)	CGND.HRA.00587	0.0000	0.0000	1.0000
TargetALS (case)	CGND.HRA.00615	0.0000	0.0000	1.0000
TargetALS (case)	CGND.HRA.00089.2	0.0000	0.0000	1.0000
TargetALS (case)	CGND.HRA.01517	0.0000	0.0000	1.0000
TargetALS (case)	CGND.HRA.00604	0.0000	0.0002	0.9998
TargetALS (case)	CGND.HRA.01574	0.0002	0.0000	0.9998
TargetALS (case)	CGND.HRA.02239	0.0000	0.0002	0.9998
TargetALS (case)	CGND.HRA.01403	0.0001	0.0003	0.9996
TargetALS (case)	CGND.HRA.02227	0.0005	0.0001	0.9995
TargetALS (case)	CGND.HRA.00225	0.0006	0.0000	0.9994
TargetALS (case)	CGND.HRA.00083	0.0003	0.0010	0.9987
TargetALS (case)	CGND.HRA.01586.2	0.0002	0.0020	0.9978
TargetALS (case)	CGND.HRA.00334	0.0018	0.0012	0.9970
TargetALS (case)	CGND.HRA.00603	0.0021	0.0022	0.9957
TargetALS (case)	CGND.HRA.02427	0.0416	0.0015	0.9569
TargetALS (case)	CGND.HRA.01511	0.0011	0.0436	0.9553
TargetALS (case)	CGND.HRA.00215	0.0719	0.0007	0.9275
TargetALS (case)	CGND.HRA.01635	0.0811	0.0038	0.9151
TargetALS (case)	CGND.HRA.02252	0.1130	0.0007	0.8863
TargetALS (case)	CGND.HRA.00394	0.1197	0.0005	0.8797
TargetALS (case)	CGND.HRA.00733	0.1476	0.0007	0.8516
TargetALS (case)	CGND.HRA.01424	0.1467	0.0203	0.8330
TargetALS (case)	CGND.HRA.00664	0.1718	0.0005	0.8276
TargetALS (case)	CGND.HRA.00312	0.0120	0.1679	0.8201
TargetALS (case)	CGND.HRA.00393	0.1993	0.0001	0.8006
TargetALS (case)	CGND.HRA.00222	0.0027	0.2104	0.7869
TargetALS (case)	CGND.HRA.00561	0.2119	0.0067	0.7814
TargetALS (case)	CGND.HRA.00663	0.2177	0.0063	0.7760
TargetALS (case)	CGND.HRA.02428	0.2436	0.0001	0.7563
TargetALS (case)	CGND.HRA.00631	0.2443	0.0002	0.7555
TargetALS (case)	CGND.HRA.01568	0.2543	0.0052	0.7405
TargetALS (case)	CGND.HRA.01575	0.2639	0.0018	0.7343
TargetALS (case)	CGND.HRA.00599	0.0026	0.2822	0.7152
TargetALS (case)	CGND.HRA.01500	0.3084	0.0000	0.6916
TargetALS (case)	CGND.HRA.00586	0.2600	0.1167	0.6233

TargetALS (case)	CGND.HRA.01407	0.2472	0.1868	0.5661
TargetALS (case)	CGND.HRA.00624	0.3666	0.1009	0.5325
TargetALS (case)	CGND.HRA.00582	0.6016	0.0000	0.3984
TargetALS (case)	CGND.HRA.00313	0.0619	0.6137	0.3245
TargetALS (case)	CGND.HRA.00462	0.6421	0.0475	0.3104
TargetALS (case)	CGND.HRA.00748	0.6507	0.0950	0.2543
TargetALS (case)	CGND.HRA.02240	0.4191	0.3825	0.1984
TargetALS (case)	CGND.HRA.00430	0.8144	0.0005	0.1851
TargetALS (case)	CGND.HRA.00374	0.8247	0.0004	0.1749
TargetALS (case)	CGND.HRA.01320	0.7792	0.0472	0.1736
TargetALS (case)	CGND.HRA.00424	0.8274	0.0068	0.1659
TargetALS (case)	CGND.HRA.01398	0.8417	0.0018	0.1565
TargetALS (case)	CGND.HRA.00435	0.8915	0.0001	0.1084
TargetALS (case)	CGND.HRA.00488	0.8930	0.0000	0.1069
TargetALS (case)	CGND.HRA.00095	0.9025	0.0001	0.0974
TargetALS (case)	CGND.HRA.00461	0.9128	0.0044	0.0827
TargetALS (case)	CGND.HRA.01174	0.8919	0.0260	0.0821
TargetALS (case)	CGND.HRA.00226	0.9246	0.0086	0.0669
TargetALS (case)	CGND.HRA.01482	0.8987	0.0351	0.0662
TargetALS (case)	CGND.HRA.00250	0.0262	0.9138	0.0600
TargetALS (case)	CGND.HRA.00429	0.8988	0.0464	0.0548
TargetALS (case)	CGND.HRA.01518	0.9474	0.0001	0.0525
TargetALS (case)	CGND.HRA.00563	0.0014	0.9507	0.0480
TargetALS (case)	CGND.HRA.01415	0.9531	0.0000	0.0469
TargetALS (case)	CGND.HRA.00423	0.9591	0.0011	0.0399
TargetALS (case)	CGND.HRA.01394	0.9610	0.0002	0.0388
TargetALS (case)	CGND.HRA.02489	0.9662	0.0001	0.0336
TargetALS (case)	CGND.HRA.00285	0.4111	0.5641	0.0248
TargetALS (case)	CGND.HRA.01636	0.9683	0.0093	0.0224
TargetALS (case)	CGND.HRA.00065	0.5498	0.4288	0.0215
TargetALS (case)	CGND.HRA.01428	0.9009	0.0795	0.0196
TargetALS (case)	CGND.HRA.00358	0.9682	0.0141	0.0177
TargetALS (case)	CGND.HRA.00747	0.6360	0.3518	0.0122
TargetALS (case)	CGND.HRA.01175	0.9114	0.0801	0.0085
TargetALS (case)	CGND.HRA.02526	0.1310	0.8624	0.0066
TargetALS (case)	CGND.HRA.00342	0.1379	0.8581	0.0040
TargetALS (case)	CGND.HRA.01569	0.9959	0.0004	0.0036
TargetALS (case)	CGND.HRA.00220	0.9943	0.0024	0.0033
TargetALS (case)	CGND.HRA.00732	0.9952	0.0021	0.0026
TargetALS (case)	CGND.HRA.01493	0.9968	0.0006	0.0026
TargetALS (case)	CGND.HRA.00335	0.9191	0.0794	0.0015
TargetALS (case)	CGND.HRA.00367	0.4251	0.5735	0.0014

TargetALS (case)	CGND.HRA.00574	0.9234	0.0756	0.0010
TargetALS (case)	CGND.HRA.02905	0.9988	0.0002	0.0010
TargetALS (case)	CGND.HRA.00061	0.9860	0.0131	0.0008
TargetALS (case)	CGND.HRA.02904	0.9989	0.0005	0.0007
TargetALS (case)	CGND.HRA.00343	0.0080	0.9915	0.0005
TargetALS (case)	CGND.HRA.01321	0.9953	0.0042	0.0005
TargetALS (case)	CGND.HRA.01512	0.0669	0.9327	0.0004
TargetALS (case)	CGND.HRA.00351	0.9935	0.0061	0.0004
TargetALS (case)	CGND.HRA.00087	0.4071	0.5927	0.0003
TargetALS (case)	CGND.HRA.02170	0.0031	0.9966	0.0003
TargetALS (case)	CGND.HRA.02739	0.9997	0.0001	0.0003
TargetALS (case)	CGND.HRA.00600	0.5374	0.4624	0.0003
TargetALS (case)	CGND.HRA.02251	0.9327	0.0671	0.0002
TargetALS (case)	CGND.HRA.00350	0.9997	0.0000	0.0002
TargetALS (case)	CGND.HRA.01429	0.9998	0.0000	0.0002
TargetALS (case)	CGND.HRA.00436	0.9979	0.0020	0.0002
TargetALS (case)	CGND.HRA.00373	0.9998	0.0000	0.0002
TargetALS (case)	CGND.HRA.01557	0.9998	0.0000	0.0001
TargetALS (case)	CGND.HRA.00616	0.0934	0.9064	0.0001
TargetALS (case)	CGND.HRA.01481	0.0434	0.9565	0.0001
TargetALS (case)	CGND.HRA.00581	0.9998	0.0001	0.0001
TargetALS (case)	CGND.HRA.00638	0.9845	0.0154	0.0001
TargetALS (case)	CGND.HRA.01280	0.9998	0.0001	0.0001
TargetALS (case)	CGND.HRA.00147	0.9999	0.0000	0.0001
TargetALS (case)	CGND.HRA.00678	0.0362	0.9638	0.0001
TargetALS (case)	CGND.HRA.00219	0.9998	0.0001	0.0001
TargetALS (case)	CGND.HRA.01587	0.9694	0.0305	0.0001
TargetALS (case)	CGND.HRA.00556	0.8843	0.1157	0.0000
TargetALS (case)	CGND.HRA.01414	0.9999	0.0001	0.0000
TargetALS (case)	CGND.HRA.02221	0.9999	0.0001	0.0000
TargetALS (case)	CGND.HRA.00059	0.0050	0.9950	0.0000
TargetALS (case)	CGND.HRA.02234	0.9999	0.0000	0.0000
TargetALS (case)	CGND.HRA.00252	0.8953	0.1047	0.0000
TargetALS (case)	CGND.HRA.00575	0.9996	0.0004	0.0000
TargetALS (case)	CGND.HRA.02171	0.0015	0.9985	0.0000
TargetALS (case)	CGND.HRA.01629	0.9992	0.0008	0.0000
TargetALS (case)	CGND.HRA.01279	0.9998	0.0002	0.0000
TargetALS (case)	CGND.HRA.00134	0.9952	0.0048	0.0000
TargetALS (case)	CGND.HRA.00055	0.0000	1.0000	0.0000
TargetALS (case)	CGND.HRA.00677	0.0533	0.9467	0.0000
TargetALS (case)	CGND.HRA.00489	1.0000	0.0000	0.0000
TargetALS (case)	CGND.HRA.00562	0.9936	0.0064	0.0000

TargetALS (case)	CGND.HRA.00284	0.0321	0.9678	0.0000
TargetALS (case)	CGND.HRA.02222	0.9996	0.0004	0.0000
TargetALS (case)	CGND.HRA.02490	0.9999	0.0001	0.0000
TargetALS (case)	CGND.HRA.01399	0.9806	0.0194	0.0000
TargetALS (case)	CGND.HRA.02246	1.0000	0.0000	0.0000
TargetALS (case)	CGND.HRA.00564	0.0000	1.0000	0.0000
TargetALS (case)	CGND.HRA.02914	0.9964	0.0036	0.0000
TargetALS (case)	CGND.HRA.01532	1.0000	0.0000	0.0000
TargetALS (case)	CGND.HRA.01528	1.0000	0.0000	0.0000
TargetALS (case)	CGND.HRA.01531	1.0000	0.0000	0.0000
TargetALS (case)	CGND.HRA.00193	0.4984	0.5016	0.0000
TargetALS (case)	CGND.HRA.00093	0.7809	0.2191	0.0000
TargetALS (case)	CGND.HRA.00557	0.9959	0.0041	0.0000
TargetALS (case)	CGND.HRA.02520	0.9962	0.0038	0.0000
TargetALS (case)	CGND.HRA.02150	0.9999	0.0001	0.0000
TargetALS (case)	CGND.HRA.00321	1.0000	0.0000	0.0000
TargetALS (case)	CGND.HRA.00066	0.0000	1.0000	0.0000
TargetALS (case)	CGND.HRA.01505	0.0000	1.0000	0.0000
TargetALS (case)	CGND.HRA.01628	0.0003	0.9997	0.0000
TargetALS (case)	CGND.HRA.00249	0.0008	0.9992	0.0000
TargetALS (case)	CGND.HRA.00216	0.0313	0.9687	0.0000

TargetALS (case)	CGND.HRA.01384	0.0592	0.9408	0.0000
TargetALS (case)	CGND.HRA.01506	0.4441	0.5559	0.0000
TargetALS (case)	CGND.HRA.02644	0.8966	0.1034	0.0000
TargetALS (case)	CGND.HRA.00633	0.9712	0.0288	0.0000
TargetALS (case)	CGND.HRA.00068	0.9762	0.0238	0.0000
TargetALS (case)	CGND.HRA.00096	0.9858	0.0142	0.0000
TargetALS (case)	CGND.HRA.02915	0.9919	0.0081	0.0000
TargetALS (case)	CGND.HRA.01425	0.9973	0.0027	0.0000
TargetALS (case)	CGND.HRA.00637	0.9976	0.0024	0.0000
TargetALS (case)	CGND.HRA.01499	0.9986	0.0014	0.0000
TargetALS (case)	CGND.HRA.01494	0.9988	0.0012	0.0000
TargetALS (case)	CGND.HRA.01540	0.9992	0.0008	0.0000
TargetALS (case)	CGND.HRA.02151	0.9998	0.0002	0.0000
TargetALS (case)	CGND.HRA.00221	0.9999	0.0001	0.0000
TargetALS (case)	CGND.HRA.01539	1.0000	0.0000	0.0000
TargetALS (case)	CGND.HRA.01387	1.0000	0.0000	0.0000
TargetALS (case)	CGND.HRA.02740	1.0000	0.0000	0.0000
TargetALS (case)	CGND.HRA.01524	1.0000	0.0000	0.0000
TargetALS (case)	CGND.HRA.01527	1.0000	0.0000	0.0000
TargetALS (case)	CGND.HRA.00320	1.0000	0.0000	0.0000
TargetALS (case)	CGND.HRA.02245	1.0000	0.0000	0.0000

TargetALS (case)	CGND.HRA.01386	1.0000	0.0000	0.0000
TargetALS (control)	CGND.HRA.00063	0.0000	0.9944	0.0056
TargetALS (control)	CGND.HRA.00091	0.9079	0.0280	0.0641
TargetALS (control)	CGND.HRA.00218	0.2764	0.0001	0.7235
TargetALS (control)	CGND.HRA.00224	0.0069	0.0000	0.9930
TargetALS (control)	CGND.HRA.00467	0.2592	0.7275	0.0132
TargetALS (control)	CGND.HRA.00477	0.9947	0.0048	0.0006
TargetALS (control)	CGND.HRA.00478	0.8574	0.0023	0.1403
TargetALS (control)	CGND.HRA.00590	0.9981	0.0018	0.0001
TargetALS (control)	CGND.HRA.00594	0.4474	0.1307	0.4218
TargetALS (control)	CGND.HRA.00595	0.8086	0.1777	0.0137
TargetALS (control)	CGND.HRA.00596	0.9981	0.0019	0.0000
TargetALS (control)	CGND.HRA.00644	0.3218	0.2746	0.4037
TargetALS (control)	CGND.HRA.00646	0.0001	0.9987	0.0012
TargetALS (control)	CGND.HRA.00647	0.0001	0.9923	0.0075
TargetALS (control)	CGND.HRA.00658	0.9899	0.0100	0.0001
TargetALS (control)	CGND.HRA.00659	0.9729	0.0263	0.0008
TargetALS (control)	CGND.HRA.00660	0.9860	0.0022	0.0118
TargetALS (control)	CGND.HRA.00661	0.9743	0.0216	0.0041
TargetALS (control)	CGND.HRA.01180	0.9971	0.0003	0.0026
TargetALS (control)	CGND.HRA.01181	0.9997	0.0001	0.0002
TargetALS (control)	CGND.HRA.01186	0.7127	0.2868	0.0005
TargetALS (control)	CGND.HRA.01187	0.5971	0.4027	0.0002
TargetALS (control)	CGND.HRA.01312	0.9721	0.0097	0.0183
TargetALS (control)	CGND.HRA.01313	0.0024	0.0001	0.9975
TargetALS (control)	CGND.HRA.01380	0.9882	0.0118	0.0001
TargetALS (control)	CGND.HRA.01381	0.9931	0.0069	0.0000
TargetALS (control)	CGND.HRA.01977	0.9998	0.0002	0.0000
TargetALS (control)	CGND.HRA.01978	0.9919	0.0026	0.0055
TargetALS (control)	CGND.HRA.02176	0.9999	0.0000	0.0001
TargetALS (control)	CGND.HRA.02177	0.9996	0.0001	0.0003
TargetALS (control)	CGND.HRA.02496	0.8171	0.0112	0.1717
TargetALS (control)	CGND.HRA.02497	0.3176	0.0015	0.6809
TargetALS (control)	CGND.HRA.02792	0.0886	0.0099	0.9015
TargetALS (control)	CGND.HRA.02793	0.9527	0.0211	0.0262
van Rheenen (case)	GSM3077801	0.0037	0.0024	0.9939
van Rheenen (case)	GSM3078181	0.0107	0.0018	0.9876
van Rheenen (case)	GSM3078009	0.0150	0.0018	0.9831
van Rheenen (case)	GSM3078360	0.0188	0.0010	0.9803
van Rheenen (case)	GSM3078171	0.0511	0.0002	0.9487
van Rheenen (case)	GSM3077825	0.0360	0.0288	0.9352
van Rheenen (case)	GSM3077701	0.0591	0.0198	0.9211

van Rheenen (case)	GSM3077063	0.1036	0.0030	0.8934
van Rheenen (case)	GSM3078169	0.1080	0.0013	0.8907
van Rheenen (case)	GSM3077787	0.0056	0.1042	0.8902
van Rheenen (case)	GSM3078387	0.1374	0.0108	0.8518
van Rheenen (case)	GSM3078247	0.1339	0.0664	0.7997
van Rheenen (case)	GSM3076775	0.1991	0.0080	0.7928
van Rheenen (case)	GSM3078232	0.2814	0.0144	0.7042
van Rheenen (case)	GSM3077663	0.1590	0.1394	0.7016
van Rheenen (case)	GSM3076586	0.2931	0.0233	0.6836
van Rheenen (case)	GSM3077792	0.2797	0.0523	0.6680
van Rheenen (case)	GSM3078154	0.3290	0.0082	0.6628
van Rheenen (case)	GSM3080153	0.3518	0.0010	0.6472
van Rheenen (case)	GSM3080115	0.4577	0.0039	0.5384
van Rheenen (case)	GSM3078258	0.4350	0.0283	0.5368
van Rheenen (case)	GSM3079919	0.0362	0.4376	0.5263
van Rheenen (case)	GSM3080127	0.1154	0.3588	0.5259
van Rheenen (case)	GSM3080144	0.4786	0.0081	0.5134
van Rheenen (case)	GSM3078304	0.4159	0.0740	0.5101
van Rheenen (case)	GSM3079992	0.4114	0.0884	0.5002
van Rheenen (case)	GSM3077141	0.5054	0.0002	0.4944
van Rheenen (case)	GSM3078166	0.4804	0.0259	0.4938

van Rheenen (case)	GSM3080102	0.5332	0.0107	0.4561
van Rheenen (case)	GSM3077843	0.3086	0.2372	0.4542
van Rheenen (case)	GSM3080108	0.4893	0.0700	0.4408
van Rheenen (case)	GSM3078230	0.2677	0.2919	0.4404
van Rheenen (case)	GSM3080109	0.5049	0.0624	0.4327
van Rheenen (case)	GSM3076867	0.5569	0.0507	0.3924
van Rheenen (case)	GSM3078011	0.6374	0.0000	0.3626
van Rheenen (case)	GSM3080135	0.5016	0.1420	0.3565
van Rheenen (case)	GSM3078242	0.6667	0.0023	0.3310
van Rheenen (case)	GSM3079864	0.3975	0.2825	0.3200
van Rheenen (case)	GSM3078176	0.5652	0.1214	0.3134
van Rheenen (case)	GSM3078139	0.6918	0.0003	0.3080
van Rheenen (case)	GSM3077827	0.6977	0.0024	0.3000
van Rheenen (case)	GSM3080180	0.7062	0.0028	0.2910
van Rheenen (case)	GSM3078335	0.1420	0.5710	0.2870
van Rheenen (case)	GSM3077807	0.7227	0.0079	0.2694
van Rheenen (case)	GSM3077061	0.7338	0.0186	0.2477
van Rheenen (case)	GSM3078250	0.7408	0.0188	0.2404
van Rheenen (case)	GSM3076821	0.7602	0.0032	0.2366
van Rheenen (case)	GSM3076602	0.7629	0.0289	0.2082
van Rheenen (case)	GSM3079763	0.6445	0.1476	0.2079

van Rheenen (case)	GSM3080105	0.7899	0.0029	0.2073
van Rheenen (case)	GSM3080141	0.2733	0.5210	0.2057
van Rheenen (case)	GSM3077366	0.5752	0.2264	0.1984
van Rheenen (case)	GSM3080130	0.5239	0.2788	0.1974
van Rheenen (case)	GSM3079849	0.7195	0.0884	0.1922
van Rheenen (case)	GSM3076702	0.5332	0.2762	0.1906
van Rheenen (case)	GSM3077804	0.8160	0.0133	0.1707
van Rheenen (case)	GSM3080113	0.8291	0.0046	0.1663
van Rheenen (case)	GSM3077426	0.5327	0.3012	0.1661
van Rheenen (case)	GSM3079859	0.7555	0.0785	0.1660
van Rheenen (case)	GSM3079993	0.7902	0.0457	0.1642
van Rheenen (case)	GSM3079876	0.1340	0.7032	0.1628
van Rheenen (case)	GSM3077975	0.0310	0.8099	0.1592
van Rheenen (case)	GSM3076893	0.8184	0.0228	0.1587
van Rheenen (case)	GSM3076994	0.8415	0.0023	0.1563
van Rheenen (case)	GSM3078188	0.2632	0.5806	0.1562
van Rheenen (case)	GSM3077704	0.8419	0.0067	0.1514
van Rheenen (case)	GSM3078499	0.8579	0.0045	0.1376
van Rheenen (case)	GSM3079913	0.4348	0.4279	0.1373
van Rheenen (case)	GSM3077098	0.8612	0.0106	0.1282
van Rheenen (case)	GSM3076832	0.8278	0.0469	0.1253
van Rheenen (case)	GSM3077227	0.8487	0.0262	0.1251
van Rheenen (case)	GSM3076704	0.8709	0.0045	0.1245
van Rheenen (case)	GSM3078234	0.8703	0.0156	0.1141
van Rheenen (case)	GSM3079758	0.7136	0.1724	0.1140
van Rheenen (case)	GSM3076647	0.8495	0.0412	0.1092
van Rheenen (case)	GSM3080160	0.8175	0.0779	0.1047
van Rheenen (case)	GSM3079841	0.1158	0.7811	0.1031
van Rheenen (case)	GSM3078503	0.8965	0.0005	0.1029
van Rheenen (case)	GSM3079890	0.7220	0.1789	0.0991
van Rheenen (case)	GSM3078425	0.1305	0.7716	0.0979
van Rheenen (case)	GSM3079851	0.9000	0.0034	0.0966
van Rheenen (case)	GSM3078237	0.7455	0.1584	0.0961
van Rheenen (case)	GSM3077112	0.8704	0.0337	0.0959
van Rheenen (case)	GSM3078444	0.1233	0.7815	0.0952
van Rheenen (case)	GSM3079891	0.8039	0.1015	0.0946
van Rheenen (case)	GSM3080168	0.2405	0.6682	0.0914
van Rheenen (case)	GSM3076842	0.9093	0.0044	0.0862
van Rheenen (case)	GSM3076622	0.9121	0.0017	0.0862
van Rheenen (case)	GSM3078497	0.8650	0.0496	0.0855
van Rheenen (case)	GSM3077625	0.7189	0.1976	0.0835
van Rheenen (case)	GSM3077364	0.8432	0.0746	0.0822

van Rheenen (case)	GSM3079996	0.8422	0.0765	0.0813
van Rheenen (case)	GSM3078038	0.0025	0.9208	0.0767
van Rheenen (case)	GSM3077934	0.2723	0.6522	0.0755
van Rheenen (case)	GSM3077114	0.9118	0.0156	0.0726
van Rheenen (case)	GSM3077441	0.9111	0.0170	0.0719
van Rheenen (case)	GSM3076729	0.9306	0.0000	0.0694
van Rheenen (case)	GSM3079961	0.6985	0.2361	0.0654
van Rheenen (case)	GSM3080134	0.8637	0.0712	0.0651
van Rheenen (case)	GSM3076681	0.4997	0.4375	0.0629
van Rheenen (case)	GSM3079920	0.9151	0.0224	0.0625
van Rheenen (case)	GSM3078252	0.6968	0.2450	0.0582
van Rheenen (case)	GSM3076901	0.9417	0.0004	0.0579
van Rheenen (case)	GSM3077266	0.9111	0.0323	0.0566
van Rheenen (case)	GSM3079870	0.9272	0.0178	0.0550
van Rheenen (case)	GSM3078227	0.9474	0.0010	0.0516
van Rheenen (case)	GSM3080028	0.7241	0.2272	0.0487
van Rheenen (case)	GSM3076955	0.9415	0.0099	0.0486
van Rheenen (case)	GSM3080149	0.9115	0.0404	0.0481
van Rheenen (case)	GSM3076865	0.9390	0.0138	0.0472
van Rheenen (case)	GSM3079823	0.9274	0.0265	0.0461
van Rheenen (case)	GSM3079772	0.9194	0.0347	0.0458

van Rheenen (case)	GSM3077724	0.9526	0.0020	0.0454
van Rheenen (case)	GSM3078178	0.9510	0.0041	0.0450
van Rheenen (case)	GSM3080111	0.8830	0.0728	0.0443
van Rheenen (case)	GSM3079960	0.9224	0.0335	0.0441
van Rheenen (case)	GSM3080003	0.0805	0.8763	0.0432
van Rheenen (case)	GSM3078068	0.8844	0.0724	0.0432
van Rheenen (case)	GSM3078502	0.9554	0.0015	0.0431
van Rheenen (case)	GSM3079834	0.9415	0.0167	0.0418
van Rheenen (case)	GSM3076916	0.8389	0.1200	0.0411
van Rheenen (case)	GSM3076843	0.9582	0.0026	0.0392
van Rheenen (case)	GSM3077641	0.0219	0.9400	0.0382
van Rheenen (case)	GSM3077721	0.9399	0.0223	0.0378
van Rheenen (case)	GSM3076607	0.8571	0.1065	0.0364
van Rheenen (case)	GSM3080006	0.7604	0.2039	0.0357
van Rheenen (case)	GSM3078036	0.7817	0.1831	0.0352
van Rheenen (case)	GSM3077246	0.6869	0.2782	0.0349
van Rheenen (case)	GSM3076662	0.9660	0.0000	0.0340
van Rheenen (case)	GSM3076798	0.9655	0.0008	0.0337
van Rheenen (case)	GSM3080148	0.9636	0.0032	0.0332
van Rheenen (case)	GSM3079989	0.9468	0.0204	0.0328
van Rheenen (case)	GSM3077165	0.9674	0.0001	0.0325

van Rheenen (case)	GSM3080023	0.7293	0.2391	0.0316
van Rheenen (case)	GSM3078510	0.9536	0.0155	0.0309
van Rheenen (case)	GSM3077079	0.9684	0.0010	0.0306
van Rheenen (case)	GSM3076794	0.9694	0.0000	0.0306
van Rheenen (case)	GSM3077008	0.9706	0.0001	0.0293
van Rheenen (case)	GSM3079925	0.8076	0.1635	0.0289
van Rheenen (case)	GSM3076929	0.6708	0.3007	0.0286
van Rheenen (case)	GSM3080034	0.9547	0.0181	0.0272
van Rheenen (case)	GSM3079812	0.8256	0.1477	0.0267
van Rheenen (case)	GSM3079945	0.8680	0.1057	0.0262
van Rheenen (case)	GSM3079779	0.9657	0.0087	0.0256
van Rheenen (case)	GSM3078190	0.1535	0.8209	0.0256
van Rheenen (case)	GSM3080119	0.9248	0.0499	0.0253
van Rheenen (case)	GSM3078013	0.8779	0.0969	0.0252
van Rheenen (case)	GSM3076753	0.9385	0.0375	0.0240
van Rheenen (case)	GSM3077172	0.9503	0.0276	0.0222
van Rheenen (case)	GSM3076767	0.9206	0.0574	0.0220
van Rheenen (case)	GSM3079832	0.8527	0.1259	0.0215
van Rheenen (case)	GSM3080124	0.9691	0.0099	0.0211
van Rheenen (case)	GSM3077623	0.9462	0.0328	0.0210
van Rheenen (case)	GSM3079985	0.8774	0.1027	0.0199
van Rheenen (case)	GSM3080099	0.9792	0.0018	0.0190
van Rheenen (case)	GSM3079803	0.9728	0.0086	0.0186
van Rheenen (case)	GSM3076974	0.9761	0.0057	0.0182
van Rheenen (case)	GSM3077679	0.1911	0.7919	0.0170
van Rheenen (case)	GSM3077822	0.0012	0.9820	0.0168
van Rheenen (case)	GSM3077919	0.0234	0.9604	0.0163
van Rheenen (case)	GSM3077276	0.9838	0.0001	0.0161
van Rheenen (case)	GSM3079740	0.9261	0.0588	0.0152
van Rheenen (case)	GSM3076997	0.9846	0.0003	0.0151
van Rheenen (case)	GSM3077303	0.9854	0.0000	0.0146
van Rheenen (case)	GSM3079957	0.9843	0.0014	0.0143
van Rheenen (case)	GSM3077076	0.7126	0.2732	0.0142
van Rheenen (case)	GSM3077930	0.9758	0.0101	0.0141
van Rheenen (case)	GSM3079982	0.9856	0.0004	0.0140
van Rheenen (case)	GSM3079988	0.5253	0.4610	0.0137
van Rheenen (case)	GSM3080120	0.9850	0.0017	0.0134
van Rheenen (case)	GSM3080077	0.9606	0.0261	0.0133
van Rheenen (case)	GSM3079824	0.9755	0.0125	0.0121
van Rheenen (case)	GSM3079770	0.8340	0.1541	0.0120
van Rheenen (case)	GSM3080019	0.8969	0.0912	0.0119
van Rheenen (case)	GSM3077224	0.9780	0.0104	0.0117

van Rheenen (case)	GSM3076972	0.9833	0.0050	0.0117
van Rheenen (case)	GSM3077170	0.9864	0.0023	0.0113
van Rheenen (case)	GSM3077568	0.9799	0.0089	0.0112
van Rheenen (case)	GSM3080125	0.9866	0.0025	0.0109
van Rheenen (case)	GSM3079783	0.9450	0.0443	0.0107
van Rheenen (case)	GSM3079857	0.9804	0.0088	0.0107
van Rheenen (case)	GSM3080027	0.8016	0.1877	0.0107
van Rheenen (case)	GSM3076877	0.9890	0.0004	0.0107
van Rheenen (case)	GSM3080020	0.9659	0.0237	0.0104
van Rheenen (case)	GSM3078505	0.9883	0.0014	0.0103
van Rheenen (case)	GSM3076911	0.9878	0.0021	0.0102
van Rheenen (case)	GSM3076661	0.9889	0.0009	0.0102
van Rheenen (case)	GSM3078192	0.5481	0.4417	0.0101
van Rheenen (case)	GSM3078495	0.9876	0.0028	0.0096
van Rheenen (case)	GSM3078507	0.9804	0.0101	0.0095
van Rheenen (case)	GSM3079863	0.9845	0.0068	0.0087
van Rheenen (case)	GSM3079885	0.8337	0.1582	0.0081
van Rheenen (case)	GSM3077473	0.9803	0.0116	0.0081
van Rheenen (case)	GSM3079843	0.9864	0.0055	0.0081
van Rheenen (case)	GSM3079881	0.9879	0.0040	0.0081
van Rheenen (case)	GSM3079975	0.7033	0.2887	0.0081
van Rheenen (case)	GSM3079896	0.9147	0.0773	0.0080
van Rheenen (case)	GSM3076813	0.9832	0.0088	0.0080
van Rheenen (case)	GSM3079926	0.7025	0.2896	0.0080
van Rheenen (case)	GSM3080002	0.9875	0.0046	0.0080
van Rheenen (case)	GSM3077650	0.6291	0.3631	0.0078
van Rheenen (case)	GSM3077383	0.9706	0.0216	0.0077
van Rheenen (case)	GSM3077344	0.9633	0.0290	0.0077
van Rheenen (case)	GSM3077579	0.9910	0.0014	0.0076
van Rheenen (case)	GSM3077582	0.9895	0.0031	0.0074
van Rheenen (case)	GSM3078041	0.8119	0.1808	0.0073
van Rheenen (case)	GSM3080059	0.7123	0.2805	0.0072
van Rheenen (case)	GSM3076693	0.9916	0.0013	0.0071
van Rheenen (case)	GSM3078390	0.0007	0.9924	0.0069
van Rheenen (case)	GSM3080103	0.9474	0.0457	0.0069
van Rheenen (case)	GSM3079785	0.8231	0.1700	0.0068
van Rheenen (case)	GSM3079978	0.6573	0.3366	0.0061
van Rheenen (case)	GSM3079908	0.9885	0.0054	0.0060
van Rheenen (case)	GSM3079964	0.9001	0.0938	0.0060
van Rheenen (case)	GSM3079897	0.9902	0.0039	0.0059
van Rheenen (case)	GSM3076619	0.9921	0.0021	0.0058
van Rheenen (case)	GSM3080074	0.9860	0.0083	0.0057

van Rheenen (case)	GSM3079931	0.4950	0.4994	0.0056
van Rheenen (case)	GSM3077269	0.9887	0.0057	0.0056
van Rheenen (case)	GSM3076927	0.9859	0.0086	0.0055
van Rheenen (case)	GSM3076951	0.9925	0.0021	0.0054
van Rheenen (case)	GSM3076669	0.9934	0.0014	0.0052
van Rheenen (case)	GSM3079829	0.9953	0.0001	0.0047
van Rheenen (case)	GSM3079871	0.9642	0.0314	0.0044
van Rheenen (case)	GSM3079974	0.7226	0.2730	0.0044
van Rheenen (case)	GSM3076845	0.9868	0.0089	0.0044
van Rheenen (case)	GSM3079756	0.9952	0.0005	0.0044
van Rheenen (case)	GSM3077492	0.9877	0.0080	0.0043
van Rheenen (case)	GSM3080012	0.9945	0.0013	0.0043
van Rheenen (case)	GSM3080041	0.8487	0.1474	0.0039
van Rheenen (case)	GSM3079953	0.9797	0.0165	0.0038
van Rheenen (case)	GSM3080009	0.9952	0.0010	0.0037
van Rheenen (case)	GSM3077428	0.8404	0.1560	0.0036
van Rheenen (case)	GSM3079965	0.9931	0.0034	0.0035
van Rheenen (case)	GSM3079765	0.9952	0.0013	0.0035
van Rheenen (case)	GSM3080022	0.9901	0.0064	0.0035
van Rheenen (case)	GSM3077203	0.9962	0.0005	0.0034
van Rheenen (case)	GSM3078244	0.0215	0.9752	0.0033
van Rheenen (case)	GSM3080056	0.9804	0.0163	0.0033
van Rheenen (case)	GSM3076718	0.9967	0.0001	0.0032
van Rheenen (case)	GSM3080054	0.9885	0.0084	0.0031
van Rheenen (case)	GSM3076812	0.9967	0.0001	0.0031
van Rheenen (case)	GSM3080072	0.9907	0.0063	0.0030
van Rheenen (case)	GSM3079995	0.9811	0.0159	0.0030
van Rheenen (case)	GSM3077539	0.8783	0.1188	0.0030
van Rheenen (case)	GSM3077330	0.9623	0.0348	0.0030
van Rheenen (case)	GSM3077469	0.8905	0.1066	0.0029
van Rheenen (case)	GSM3080044	0.8822	0.1150	0.0029
van Rheenen (case)	GSM3080067	0.3584	0.6388	0.0029
van Rheenen (case)	GSM3077143	0.9972	0.0000	0.0028
van Rheenen (case)	GSM3077030	0.9964	0.0008	0.0028
van Rheenen (case)	GSM3080084	0.9105	0.0868	0.0027
van Rheenen (case)	GSM3080029	0.8285	0.1688	0.0027
van Rheenen (case)	GSM3079930	0.5759	0.4214	0.0027
van Rheenen (case)	GSM3079877	0.9972	0.0003	0.0025
van Rheenen (case)	GSM3079902	0.9071	0.0904	0.0025
van Rheenen (case)	GSM3076679	0.9968	0.0008	0.0024
van Rheenen (case)	GSM3077300	0.9975	0.0001	0.0024
van Rheenen (case)	GSM3076584	0.9707	0.0270	0.0023

van Rheenen (case)	GSM3078255	0.0000	0.9978	0.0022
van Rheenen (case)	GSM3076598	0.9945	0.0034	0.0021
van Rheenen (case)	GSM3076683	0.9924	0.0055	0.0021
van Rheenen (case)	GSM3077352	0.9973	0.0006	0.0021
van Rheenen (case)	GSM3077325	0.9224	0.0756	0.0020
van Rheenen (case)	GSM3077682	0.9516	0.0464	0.0020
van Rheenen (case)	GSM3076708	0.9950	0.0031	0.0020
van Rheenen (case)	GSM3080080	0.1054	0.8927	0.0019
van Rheenen (case)	GSM3080087	0.9959	0.0023	0.0018
van Rheenen (case)	GSM3079950	0.7720	0.2262	0.0018
van Rheenen (case)	GSM3079794	0.9973	0.0010	0.0018
van Rheenen (case)	GSM3076854	0.9957	0.0026	0.0017
van Rheenen (case)	GSM3079742	0.9861	0.0123	0.0016
van Rheenen (case)	GSM3076847	0.9979	0.0005	0.0016
van Rheenen (case)	GSM3076956	0.9913	0.0071	0.0016
van Rheenen (case)	GSM3076849	0.9680	0.0304	0.0016
van Rheenen (case)	GSM3079958	0.8023	0.1962	0.0016
van Rheenen (case)	GSM3076991	0.9976	0.0008	0.0016
van Rheenen (case)	GSM3076823	0.9969	0.0016	0.0015
van Rheenen (case)	GSM3077380	0.9980	0.0005	0.0015
van Rheenen (case)	GSM3080098	0.6251	0.3734	0.0015
van Rheenen (case)	GSM3079838	0.9884	0.0101	0.0015
van Rheenen (case)	GSM3080000	0.0936	0.9050	0.0014
van Rheenen (case)	GSM3076933	0.9984	0.0002	0.0014
van Rheenen (case)	GSM3076899	0.9979	0.0007	0.0014
van Rheenen (case)	GSM3080013	0.9631	0.0356	0.0013
van Rheenen (case)	GSM3079751	0.9968	0.0020	0.0013
van Rheenen (case)	GSM3076597	0.9984	0.0004	0.0013
van Rheenen (case)	GSM3078174	0.9500	0.0488	0.0012
van Rheenen (case)	GSM3077684	0.9818	0.0170	0.0012
van Rheenen (case)	GSM3077251	0.9824	0.0164	0.0012
van Rheenen (case)	GSM3076600	0.9978	0.0010	0.0012
van Rheenen (case)	GSM3079914	0.6374	0.3615	0.0012
van Rheenen (case)	GSM3077084	0.9989	0.0000	0.0011
van Rheenen (case)	GSM3079807	0.9965	0.0024	0.0011
van Rheenen (case)	GSM3079944	0.9788	0.0202	0.0011
van Rheenen (case)	GSM3079867	0.2654	0.7336	0.0010
van Rheenen (case)	GSM3077332	0.9737	0.0253	0.0010
van Rheenen (case)	GSM3077408	0.9988	0.0002	0.0010
van Rheenen (case)	GSM3077201	0.8979	0.1011	0.0010
van Rheenen (case)	GSM3077386	0.9977	0.0013	0.0010
van Rheenen (case)	GSM3077253	0.9681	0.0310	0.0009

van Rheenen (case)	GSM3076895	0.9438	0.0553	0.0009
van Rheenen (case)	GSM3077281	0.9985	0.0007	0.0009
van Rheenen (case)	GSM3077295	0.9944	0.0047	0.0009
van Rheenen (case)	GSM3080075	0.5460	0.4532	0.0008
van Rheenen (case)	GSM3080060	0.9918	0.0074	0.0008
van Rheenen (case)	GSM3076891	0.9349	0.0644	0.0008
van Rheenen (case)	GSM3077599	0.2301	0.7692	0.0008
van Rheenen (case)	GSM3079776	0.9985	0.0007	0.0008
van Rheenen (case)	GSM3077248	0.9985	0.0008	0.0007
van Rheenen (case)	GSM3077790	0.9985	0.0008	0.0007
van Rheenen (case)	GSM3077991	0.4690	0.5303	0.0007
van Rheenen (case)	GSM3076880	0.9909	0.0084	0.0007
van Rheenen (case)	GSM3077117	0.9977	0.0016	0.0007
van Rheenen (case)	GSM3077278	0.9990	0.0003	0.0007
van Rheenen (case)	GSM3077350	0.9403	0.0591	0.0007
van Rheenen (case)	GSM3079749	0.9930	0.0064	0.0006
van Rheenen (case)	GSM3080093	0.9938	0.0056	0.0006
van Rheenen (case)	GSM3077368	0.9966	0.0028	0.0006
van Rheenen (case)	GSM3077081	0.8706	0.1288	0.0006
van Rheenen (case)	GSM3076617	0.9993	0.0002	0.0006
van Rheenen (case)	GSM3079967	0.9969	0.0026	0.0005

van Rheenen (case)	GSM3079827	0.9915	0.0080	0.0005
van Rheenen (case)	GSM3079968	0.9929	0.0066	0.0005
van Rheenen (case)	GSM3080039	0.9946	0.0049	0.0005
van Rheenen (case)	GSM3077430	0.9967	0.0028	0.0005
van Rheenen (case)	GSM3080139	0.9986	0.0009	0.0005
van Rheenen (case)	GSM3080065	0.7843	0.2152	0.0005
van Rheenen (case)	GSM3079979	0.9988	0.0007	0.0005
van Rheenen (case)	GSM3077272	0.3263	0.6733	0.0005
van Rheenen (case)	GSM3077027	0.9995	0.0001	0.0005
van Rheenen (case)	GSM3079972	0.9951	0.0044	0.0005
van Rheenen (case)	GSM3080086	0.9652	0.0344	0.0004
van Rheenen (case)	GSM3079868	0.9322	0.0673	0.0004
van Rheenen (case)	GSM3079954	0.9858	0.0138	0.0004
van Rheenen (case)	GSM3076768	0.9993	0.0003	0.0004
van Rheenen (case)	GSM3080015	0.8961	0.1035	0.0004
van Rheenen (case)	GSM3076788	0.9992	0.0004	0.0004
van Rheenen (case)	GSM3079907	0.4956	0.5040	0.0004
van Rheenen (case)	GSM3076706	0.9996	0.0000	0.0004
van Rheenen (case)	GSM3077274	0.9977	0.0019	0.0004
van Rheenen (case)	GSM3076882	0.8545	0.1452	0.0004
van Rheenen (case)	GSM3077643	0.9989	0.0008	0.0003

van Rheenen (case)	GSM3079986	0.9253	0.0744	0.0003
van Rheenen (case)	GSM3077611	0.9958	0.0039	0.0003
van Rheenen (case)	GSM3077563	0.9996	0.0001	0.0003
van Rheenen (case)	GSM3080122	0.9967	0.0030	0.0003
van Rheenen (case)	GSM3077994	0.9808	0.0189	0.0003
van Rheenen (case)	GSM3076851	0.9966	0.0031	0.0003
van Rheenen (case)	GSM3077542	0.9992	0.0005	0.0003
van Rheenen (case)	GSM3077199	0.6307	0.3691	0.0003
van Rheenen (case)	GSM3080064	0.9556	0.0442	0.0002
van Rheenen (case)	GSM3077561	0.8935	0.1063	0.0002
van Rheenen (case)	GSM3077707	0.9987	0.0011	0.0002
van Rheenen (case)	GSM3077293	0.9996	0.0002	0.0002
van Rheenen (case)	GSM3077566	0.7984	0.2015	0.0002
van Rheenen (case)	GSM3079999	0.9963	0.0036	0.0002
van Rheenen (case)	GSM3079971	0.9983	0.0016	0.0002
van Rheenen (case)	GSM3077741	0.8315	0.1684	0.0002
van Rheenen (case)	GSM3079789	0.4606	0.5393	0.0001
van Rheenen (case)	GSM3080047	0.9770	0.0229	0.0001
van Rheenen (case)	GSM3077647	0.3438	0.6561	0.0001
van Rheenen (case)	GSM3080050	0.9928	0.0071	0.0001
van Rheenen (case)	GSM3080069	0.9961	0.0038	0.0001

van Rheenen (case)	GSM3080038	0.9875	0.0124	0.0001
van Rheenen (case)	GSM3080043	0.9918	0.0081	0.0001
van Rheenen (case)	GSM3076604	0.9998	0.0001	0.0001
van Rheenen (case)	GSM3080061	0.8817	0.1182	0.0001
van Rheenen (case)	GSM3077508	0.9998	0.0001	0.0001
van Rheenen (case)	GSM3077971	0.9611	0.0389	0.0001
van Rheenen (case)	GSM3079801	0.9990	0.0009	0.0001
van Rheenen (case)	GSM3079981	0.9980	0.0020	0.0001
van Rheenen (case)	GSM3076913	0.9972	0.0027	0.0001
van Rheenen (case)	GSM3076897	0.9998	0.0002	0.0001
van Rheenen (case)	GSM3079937	0.9810	0.0190	0.0001
van Rheenen (case)	GSM3076796	0.9998	0.0001	0.0001
van Rheenen (case)	GSM3077977	0.0021	0.9979	0.0000
van Rheenen (case)	GSM3077476	0.9607	0.0393	0.0000
van Rheenen (case)	GSM3076595	0.9856	0.0143	0.0000
van Rheenen (case)	GSM3079875	0.9951	0.0049	0.0000
van Rheenen (case)	GSM3079837	0.9999	0.0001	0.0000
van Rheenen (case)	GSM3079936	0.6413	0.3587	0.0000
van Rheenen (case)	GSM3076931	0.9852	0.0148	0.0000
van Rheenen (case)	GSM3077101	0.9950	0.0050	0.0000
van Rheenen (case)	GSM3080008	0.9966	0.0034	0.0000

van Rheenen (case)	GSM3077627	0.9996	0.0004	0.0000
van Rheenen (case)	GSM3080070	0.9945	0.0054	0.0000
van Rheenen (case)	GSM3077916	0.9947	0.0053	0.0000
van Rheenen (case)	GSM3076863	0.9999	0.0001	0.0000
van Rheenen (case)	GSM3076582	0.5628	0.4372	0.0000
van Rheenen (case)	GSM3077334	0.9589	0.0411	0.0000
van Rheenen (case)	GSM3077032	0.9872	0.0128	0.0000
van Rheenen (case)	GSM3080057	0.9959	0.0041	0.0000
van Rheenen (case)	GSM3078342	0.0025	0.9976	0.0000
van Rheenen (case)	GSM3077841	0.9456	0.0544	0.0000
van Rheenen (case)	GSM3077665	0.9717	0.0283	0.0000
van Rheenen (case)	GSM3077096	0.9970	0.0030	0.0000
van Rheenen (control)	GSM3076588	0.9557	0.0441	0.0002
van Rheenen (control)	GSM3076590	0.9900	0.0099	0.0002
van Rheenen (control)	GSM3076592	0.9106	0.0893	0.0001
van Rheenen (control)	GSM3076593	0.9996	0.0003	0.0001
van Rheenen (control)	GSM3076608	0.9955	0.0001	0.0045
van Rheenen (control)	GSM3076611	0.9963	0.0003	0.0034
van Rheenen (control)	GSM3076613	0.9967	0.0019	0.0015
van Rheenen (control)	GSM3076615	0.9226	0.0076	0.0698
van Rheenen (control)	GSM3076624	0.9785	0.0214	0.0001
van Rheenen (control)	GSM3076627	0.9959	0.0038	0.0003
van Rheenen (control)	GSM3076629	0.9923	0.0064	0.0014
van Rheenen (control)	GSM3076631	0.9980	0.0011	0.0009
van Rheenen (control)	GSM3076633	0.9972	0.0028	0.0001
van Rheenen (control)	GSM3076635	0.9197	0.0796	0.0006
van Rheenen (control)	GSM3076637	0.9990	0.0009	0.0001
van Rheenen (control)	GSM3076640	0.9968	0.0027	0.0005
van Rheenen (control)	GSM3076642	0.6360	0.3635	0.0005
van Rheenen (control)	GSM3076644	0.9286	0.0675	0.0039
van Rheenen (control)	GSM3076649	0.9891	0.0092	0.0017
van Rheenen (control)	GSM3076651	0.9847	0.0146	0.0007
van Rheenen (control)	GSM3076653	0.8794	0.1182	0.0025
van Rheenen (control)	GSM3076655	0.9958	0.0003	0.0038
van Rheenen (control)	GSM3076657	0.9705	0.0280	0.0014
van Rheenen (control)	GSM3076659	0.9996	0.0003	0.0001
van Rheenen (control)	GSM3076665	0.6860	0.0006	0.3134
van Rheenen (control)	GSM3076667	0.9308	0.0648	0.0044
van Rheenen (control)	GSM3076671	0.9999	0.0000	0.0000
van Rheenen (control)	GSM3076673	0.9978	0.0002	0.0021
van Rheenen (control)	GSM3076675	0.9916	0.0010	0.0074
van Rheenen (control)	GSM3076677	0.9496	0.0487	0.0017

van Rheenen (control)	GSM3076686	0.9960	0.0014	0.0026
van Rheenen (control)	GSM3076688	0.9806	0.0003	0.0191
van Rheenen (control)	GSM3076690	0.9895	0.0038	0.0067
van Rheenen (control)	GSM3076692	0.7856	0.0041	0.2103
van Rheenen (control)	GSM3076695	0.9639	0.0001	0.0359
van Rheenen (control)	GSM3076697	0.7674	0.0001	0.2325
van Rheenen (control)	GSM3076699	0.9874	0.0088	0.0038
van Rheenen (control)	GSM3076701	0.8780	0.0042	0.1178
van Rheenen (control)	GSM3076710	0.9986	0.0000	0.0013
van Rheenen (control)	GSM3076712	0.9980	0.0007	0.0013
van Rheenen (control)	GSM3076714	0.9024	0.0053	0.0923
van Rheenen (control)	GSM3076716	0.8524	0.0213	0.1263
van Rheenen (control)	GSM3076720	0.9552	0.0413	0.0035
van Rheenen (control)	GSM3076722	0.2036	0.7864	0.0100
van Rheenen (control)	GSM3076725	0.9870	0.0011	0.0119
van Rheenen (control)	GSM3076727	0.9979	0.0011	0.0010
van Rheenen (control)	GSM3076731	0.9957	0.0015	0.0028
van Rheenen (control)	GSM3076733	0.9994	0.0002	0.0004
van Rheenen (control)	GSM3076735	0.9837	0.0105	0.0058
van Rheenen (control)	GSM3076737	0.9775	0.0122	0.0103
van Rheenen (control)	GSM3076739	0.8713	0.0143	0.1143

van Rheenen (control)	GSM3076741	0.9959	0.0010	0.0032
van Rheenen (control)	GSM3076743	0.9821	0.0036	0.0144
van Rheenen (control)	GSM3076746	0.9995	0.0001	0.0004
van Rheenen (control)	GSM3076749	0.9921	0.0077	0.0002
van Rheenen (control)	GSM3076751	0.9453	0.0271	0.0276
van Rheenen (control)	GSM3076755	0.8916	0.0887	0.0198
van Rheenen (control)	GSM3076757	0.8439	0.0000	0.1561
van Rheenen (control)	GSM3076758	0.9709	0.0007	0.0284
van Rheenen (control)	GSM3076760	0.9665	0.0019	0.0316
van Rheenen (control)	GSM3076762	0.9332	0.0664	0.0004
van Rheenen (control)	GSM3076763	0.9700	0.0027	0.0273
van Rheenen (control)	GSM3076765	0.9901	0.0051	0.0049
van Rheenen (control)	GSM3076770	0.9908	0.0002	0.0090
van Rheenen (control)	GSM3076771	0.9972	0.0019	0.0010
van Rheenen (control)	GSM3076772	0.9869	0.0023	0.0108
van Rheenen (control)	GSM3076774	0.6542	0.0004	0.3454
van Rheenen (control)	GSM3076777	0.9998	0.0001	0.0000
van Rheenen (control)	GSM3076779	0.9890	0.0021	0.0089
van Rheenen (control)	GSM3076780	0.9193	0.0389	0.0418
van Rheenen (control)	GSM3076782	0.5238	0.4727	0.0034
van Rheenen (control)	GSM3076784	0.8358	0.1506	0.0136

van Rheenen (control)	GSM3076786	0.1951	0.0121	0.7927
van Rheenen (control)	GSM3076789	0.9603	0.0375	0.0022
van Rheenen (control)	GSM3076793	0.9013	0.0660	0.0328
van Rheenen (control)	GSM3076800	0.9932	0.0040	0.0028
van Rheenen (control)	GSM3076806	0.9925	0.0071	0.0003
van Rheenen (control)	GSM3076808	0.9890	0.0050	0.0061
van Rheenen (control)	GSM3076810	0.6699	0.0178	0.3123
van Rheenen (control)	GSM3076815	0.9991	0.0001	0.0007
van Rheenen (control)	GSM3076817	0.9810	0.0178	0.0012
van Rheenen (control)	GSM3076818	0.9743	0.0240	0.0017
van Rheenen (control)	GSM3076820	0.8194	0.0976	0.0830
van Rheenen (control)	GSM3076824	0.9974	0.0013	0.0013
van Rheenen (control)	GSM3076826	0.9723	0.0003	0.0274
van Rheenen (control)	GSM3076828	0.9875	0.0082	0.0043
van Rheenen (control)	GSM3076830	0.9596	0.0257	0.0146
van Rheenen (control)	GSM3076834	0.9658	0.0007	0.0334
van Rheenen (control)	GSM3076836	0.9987	0.0010	0.0003
van Rheenen (control)	GSM3076837	0.9889	0.0008	0.0103
van Rheenen (control)	GSM3076839	0.9958	0.0033	0.0009
van Rheenen (control)	GSM3076856	0.9965	0.0033	0.0002
van Rheenen (control)	GSM3076858	0.9816	0.0031	0.0153
van Rheenen (control)	GSM3076860	0.9982	0.0006	0.0012
van Rheenen (control)	GSM3076862	0.9516	0.0003	0.0482
van Rheenen (control)	GSM3076869	0.9875	0.0002	0.0123
van Rheenen (control)	GSM3076871	0.9752	0.0007	0.0241
van Rheenen (control)	GSM3076873	0.9199	0.0756	0.0045
van Rheenen (control)	GSM3076875	0.9725	0.0028	0.0247
van Rheenen (control)	GSM3076879	0.7857	0.1520	0.0623
van Rheenen (control)	GSM3076884	0.9276	0.0720	0.0004
van Rheenen (control)	GSM3076886	0.7048	0.2948	0.0004
van Rheenen (control)	GSM3076888	0.9479	0.0515	0.0006
van Rheenen (control)	GSM3076889	0.6252	0.3693	0.0055
van Rheenen (control)	GSM3076903	0.8890	0.1103	0.0007
van Rheenen (control)	GSM3076905	0.9694	0.0292	0.0015
van Rheenen (control)	GSM3076907	0.9968	0.0026	0.0006
van Rheenen (control)	GSM3076910	0.9977	0.0023	0.0000
van Rheenen (control)	GSM3076918	0.9950	0.0003	0.0048
van Rheenen (control)	GSM3076920	0.9925	0.0049	0.0026
van Rheenen (control)	GSM3076923	0.9777	0.0207	0.0016
van Rheenen (control)	GSM3076925	0.8678	0.1321	0.0002
van Rheenen (control)	GSM3076935	0.9692	0.0255	0.0053
van Rheenen (control)	GSM3076937	0.9998	0.0002	0.0000

van Rheenen (control)	GSM3076939	0.9996	0.0002	0.0002
van Rheenen (control)	GSM3076941	0.9988	0.0006	0.0006
van Rheenen (control)	GSM3076943	0.9525	0.0448	0.0027
van Rheenen (control)	GSM3076945	0.9971	0.0007	0.0022
van Rheenen (control)	GSM3076947	0.9646	0.0169	0.0185
van Rheenen (control)	GSM3076949	0.9118	0.0658	0.0224
van Rheenen (control)	GSM3076958	0.9901	0.0095	0.0004
van Rheenen (control)	GSM3076959	0.9979	0.0016	0.0005
van Rheenen (control)	GSM3076961	0.8322	0.0335	0.1343
van Rheenen (control)	GSM3076963	0.9234	0.0760	0.0007
van Rheenen (control)	GSM3076964	0.9717	0.0000	0.0283
van Rheenen (control)	GSM3076966	0.7570	0.1424	0.1006
van Rheenen (control)	GSM3076969	0.9890	0.0017	0.0093
van Rheenen (control)	GSM3076971	0.8500	0.1497	0.0003
van Rheenen (control)	GSM3076976	0.6441	0.0165	0.3394
van Rheenen (control)	GSM3076978	0.9063	0.0920	0.0017
van Rheenen (control)	GSM3076980	0.9999	0.0001	0.0000
van Rheenen (control)	GSM3076982	0.8810	0.1178	0.0012
van Rheenen (control)	GSM3076984	0.9885	0.0054	0.0061
van Rheenen (control)	GSM3076985	0.9492	0.0009	0.0499
van Rheenen (control)	GSM3076986	0.9650	0.0009	0.0341

van Rheenen (control)	GSM3076989	0.9758	0.0003	0.0239
van Rheenen (control)	GSM3076999	0.5247	0.0008	0.4745
van Rheenen (control)	GSM3077002	0.9991	0.0000	0.0009
van Rheenen (control)	GSM3077004	0.9974	0.0014	0.0011
van Rheenen (control)	GSM3077006	0.7489	0.0215	0.2296
van Rheenen (control)	GSM3077015	0.9866	0.0113	0.0020
van Rheenen (control)	GSM3077018	0.9901	0.0013	0.0086
van Rheenen (control)	GSM3077022	0.9997	0.0001	0.0002
van Rheenen (control)	GSM3077024	0.9989	0.0002	0.0009
van Rheenen (control)	GSM3077035	0.9977	0.0016	0.0007
van Rheenen (control)	GSM3077037	0.9150	0.0007	0.0843
van Rheenen (control)	GSM3077039	0.9969	0.0006	0.0024
van Rheenen (control)	GSM3077042	0.9923	0.0011	0.0066
van Rheenen (control)	GSM3077044	0.9685	0.0003	0.0312
van Rheenen (control)	GSM3077047	0.9552	0.0120	0.0328
van Rheenen (control)	GSM3077050	0.8606	0.0001	0.1393
van Rheenen (control)	GSM3077052	0.9986	0.0007	0.0007
van Rheenen (control)	GSM3077055	0.9998	0.0000	0.0002
van Rheenen (control)	GSM3077059	0.9349	0.0516	0.0135
van Rheenen (control)	GSM3077066	0.9717	0.0074	0.0209
van Rheenen (control)	GSM3077068	0.9949	0.0011	0.0040

van Rheenen (control)	GSM3077071	0.4049	0.5113	0.0839
van Rheenen (control)	GSM3077073	0.7810	0.0343	0.1846
van Rheenen (control)	GSM3077086	0.9878	0.0121	0.0000
van Rheenen (control)	GSM3077088	0.9996	0.0003	0.0001
van Rheenen (control)	GSM3077090	0.9992	0.0002	0.0006
van Rheenen (control)	GSM3077093	0.9208	0.0789	0.0003
van Rheenen (control)	GSM3077103	0.9871	0.0001	0.0128
van Rheenen (control)	GSM3077105	0.9538	0.0000	0.0462
van Rheenen (control)	GSM3077107	0.9915	0.0001	0.0084
van Rheenen (control)	GSM3077110	0.9804	0.0001	0.0195
van Rheenen (control)	GSM3077119	0.7047	0.0006	0.2947
van Rheenen (control)	GSM3077122	0.5172	0.0009	0.4819
van Rheenen (control)	GSM3077124	0.9925	0.0024	0.0051
van Rheenen (control)	GSM3077129	0.9991	0.0006	0.0003
van Rheenen (control)	GSM3077133	0.9843	0.0155	0.0002
van Rheenen (control)	GSM3077134	0.9837	0.0010	0.0153
van Rheenen (control)	GSM3077136	0.9955	0.0038	0.0008
van Rheenen (control)	GSM3077138	0.9720	0.0101	0.0179
van Rheenen (control)	GSM3077146	0.9998	0.0001	0.0001
van Rheenen (control)	GSM3077148	0.9976	0.0022	0.0002
van Rheenen (control)	GSM3077150	0.9947	0.0002	0.0051

van Rheenen (control)	GSM3077153	0.9764	0.0167	0.0069
van Rheenen (control)	GSM3077156	0.9944	0.0014	0.0041
van Rheenen (control)	GSM3077158	0.8224	0.0032	0.1743
van Rheenen (control)	GSM3077160	0.9997	0.0000	0.0003
van Rheenen (control)	GSM3077162	0.9946	0.0004	0.0050
van Rheenen (control)	GSM3077174	0.9964	0.0013	0.0023
van Rheenen (control)	GSM3077177	0.9859	0.0007	0.0135
van Rheenen (control)	GSM3077179	0.9908	0.0001	0.0091
van Rheenen (control)	GSM3077189	0.9980	0.0001	0.0019
van Rheenen (control)	GSM3077192	0.9433	0.0529	0.0038
van Rheenen (control)	GSM3077194	0.9908	0.0084	0.0008
van Rheenen (control)	GSM3077196	0.0134	0.0015	0.9851
van Rheenen (control)	GSM3077205	0.9987	0.0013	0.0000
van Rheenen (control)	GSM3077209	0.5748	0.3857	0.0395
van Rheenen (control)	GSM3077211	0.9625	0.0034	0.0341
van Rheenen (control)	GSM3077213	0.4431	0.5379	0.0190
van Rheenen (control)	GSM3077215	0.9888	0.0106	0.0007
van Rheenen (control)	GSM3077217	0.9862	0.0114	0.0024
van Rheenen (control)	GSM3077219	0.9841	0.0152	0.0007
van Rheenen (control)	GSM3077221	0.9837	0.0162	0.0001
van Rheenen (control)	GSM3077229	0.6156	0.3616	0.0228

van Rheenen (control)	GSM3077231	0.9494	0.0452	0.0053
van Rheenen (control)	GSM3077240	0.9719	0.0138	0.0143
van Rheenen (control)	GSM3077244	0.9887	0.0080	0.0033
van Rheenen (control)	GSM3077254	0.7748	0.2188	0.0064
van Rheenen (control)	GSM3077256	0.4815	0.5184	0.0000
van Rheenen (control)	GSM3077259	0.9959	0.0041	0.0000
van Rheenen (control)	GSM3077261	0.9960	0.0027	0.0013
van Rheenen (control)	GSM3077283	0.9984	0.0002	0.0014
van Rheenen (control)	GSM3077285	0.9975	0.0018	0.0007
van Rheenen (control)	GSM3077287	0.9243	0.0000	0.0757
van Rheenen (control)	GSM3077290	0.9899	0.0002	0.0099
van Rheenen (control)	GSM3077305	0.9817	0.0001	0.0181
van Rheenen (control)	GSM3077307	0.9988	0.0009	0.0003
van Rheenen (control)	GSM3077311	0.9983	0.0006	0.0011
van Rheenen (control)	GSM3077313	0.0494	0.0000	0.9506
van Rheenen (control)	GSM3077315	0.9776	0.0223	0.0001
van Rheenen (control)	GSM3077318	0.9991	0.0005	0.0004
van Rheenen (control)	GSM3077321	0.9887	0.0046	0.0067
van Rheenen (control)	GSM3077323	0.9907	0.0076	0.0017
van Rheenen (control)	GSM3077336	0.9891	0.0109	0.0000
van Rheenen (control)	GSM3077338	0.5075	0.4917	0.0008
van Rheenen (control)	GSM3077340	0.9941	0.0042	0.0018
van Rheenen (control)	GSM3077342	0.9751	0.0111	0.0139
van Rheenen (control)	GSM3077355	0.9917	0.0030	0.0053
van Rheenen (control)	GSM3077357	0.1932	0.8043	0.0025
van Rheenen (control)	GSM3077359	0.9477	0.0514	0.0009
van Rheenen (control)	GSM3077361	0.7966	0.0508	0.1526
van Rheenen (control)	GSM3077370	0.9998	0.0000	0.0001
van Rheenen (control)	GSM3077372	0.6931	0.2892	0.0177
van Rheenen (control)	GSM3077374	0.6701	0.0009	0.3290
van Rheenen (control)	GSM3077377	0.6990	0.1886	0.1124
van Rheenen (control)	GSM3077388	0.8165	0.0180	0.1656
van Rheenen (control)	GSM3077391	0.7282	0.2716	0.0002
van Rheenen (control)	GSM3077393	0.8744	0.1248	0.0008
van Rheenen (control)	GSM3077396	0.0584	0.5037	0.4378
van Rheenen (control)	GSM3077398	0.9963	0.0034	0.0003
van Rheenen (control)	GSM3077401	0.9415	0.0037	0.0548
van Rheenen (control)	GSM3077404	0.9367	0.0289	0.0345
van Rheenen (control)	GSM3077406	0.1610	0.0002	0.8388
van Rheenen (control)	GSM3077410	0.9813	0.0078	0.0110
van Rheenen (control)	GSM3077412	0.9963	0.0019	0.0018
van Rheenen (control)	GSM3077414	0.9975	0.0019	0.0006

van Rheenen (control)	GSM3077416	0.9672	0.0320	0.0008
van Rheenen (control)	GSM3077419	0.9981	0.0015	0.0005
van Rheenen (control)	GSM3077422	0.9885	0.0114	0.0001
van Rheenen (control)	GSM3077424	0.8683	0.0085	0.1232
van Rheenen (control)	GSM3077425	0.1070	0.8921	0.0010
van Rheenen (control)	GSM3077449	0.9633	0.0203	0.0164
van Rheenen (control)	GSM3077452	0.0988	0.9009	0.0002
van Rheenen (control)	GSM3077454	0.5607	0.4346	0.0047
van Rheenen (control)	GSM3077456	0.9778	0.0115	0.0108
van Rheenen (control)	GSM3077459	0.7200	0.2787	0.0013
van Rheenen (control)	GSM3077461	0.7288	0.0605	0.2106
van Rheenen (control)	GSM3077464	0.9740	0.0057	0.0203
van Rheenen (control)	GSM3077467	0.9725	0.0273	0.0001
van Rheenen (control)	GSM3077483	0.5580	0.2189	0.2231
van Rheenen (control)	GSM3077485	0.2182	0.3735	0.4083
van Rheenen (control)	GSM3077487	0.8029	0.1969	0.0002
van Rheenen (control)	GSM3077489	0.9933	0.0012	0.0056
van Rheenen (control)	GSM3077495	0.9622	0.0372	0.0005
van Rheenen (control)	GSM3077497	0.9911	0.0011	0.0079
van Rheenen (control)	GSM3077500	0.9942	0.0056	0.0002
van Rheenen (control)	GSM3077505	0.9933	0.0066	0.0002
van Rheenen (control)	GSM3077510	0.9998	0.0001	0.0000
van Rheenen (control)	GSM3077512	0.9922	0.0024	0.0054
van Rheenen (control)	GSM3077514	0.9909	0.0022	0.0068
van Rheenen (control)	GSM3077517	0.9944	0.0001	0.0055
van Rheenen (control)	GSM3077520	0.9955	0.0006	0.0039
van Rheenen (control)	GSM3077522	0.9233	0.0311	0.0456
van Rheenen (control)	GSM3077533	0.9978	0.0000	0.0021
van Rheenen (control)	GSM3077536	0.9979	0.0002	0.0019
van Rheenen (control)	GSM3077544	0.9385	0.0606	0.0008
van Rheenen (control)	GSM3077551	0.7879	0.2119	0.0002
van Rheenen (control)	GSM3077556	0.9808	0.0190	0.0002
van Rheenen (control)	GSM3077559	0.1252	0.8694	0.0054
van Rheenen (control)	GSM3077571	0.9956	0.0022	0.0022
van Rheenen (control)	GSM3077573	0.4012	0.3994	0.1995
van Rheenen (control)	GSM3077575	0.9129	0.0334	0.0537
van Rheenen (control)	GSM3077577	0.9847	0.0001	0.0152
van Rheenen (control)	GSM3077589	0.9889	0.0038	0.0073
van Rheenen (control)	GSM3077591	0.1010	0.8789	0.0201
van Rheenen (control)	GSM3077594	0.7424	0.1510	0.1066
van Rheenen (control)	GSM3077597	0.9779	0.0068	0.0153
van Rheenen (control)	GSM3077601	0.9973	0.0022	0.0005

van Rheenen (control)	GSM3077604	0.9991	0.0005	0.0004
van Rheenen (control)	GSM3077607	0.9973	0.0021	0.0007
van Rheenen (control)	GSM3077609	0.9904	0.0092	0.0005
van Rheenen (control)	GSM3077614	0.9553	0.0030	0.0418
van Rheenen (control)	GSM3077616	0.9995	0.0005	0.0001
van Rheenen (control)	GSM3077619	0.9963	0.0005	0.0031
van Rheenen (control)	GSM3077621	0.9787	0.0098	0.0116
van Rheenen (control)	GSM3077630	0.9964	0.0036	0.0000
van Rheenen (control)	GSM3077633	0.9196	0.0735	0.0069
van Rheenen (control)	GSM3077636	0.9436	0.0564	0.0000
van Rheenen (control)	GSM3077638	0.9146	0.0846	0.0008
van Rheenen (control)	GSM3077652	0.6224	0.3776	0.0000
van Rheenen (control)	GSM3077655	0.1347	0.8032	0.0621
van Rheenen (control)	GSM3077658	0.0108	0.5914	0.3978
van Rheenen (control)	GSM3077660	0.9823	0.0002	0.0175
van Rheenen (control)	GSM3077668	0.9989	0.0000	0.0011
van Rheenen (control)	GSM3077670	0.9872	0.0126	0.0001
van Rheenen (control)	GSM3077673	0.9994	0.0002	0.0004
van Rheenen (control)	GSM3077675	0.3913	0.3166	0.2921
van Rheenen (control)	GSM3077677	0.8111	0.0018	0.1871
van Rheenen (control)	GSM3077689	0.0286	0.9713	0.0001

van Rheenen (control)	GSM3077692	0.9672	0.0127	0.0201
van Rheenen (control)	GSM3077694	0.0209	0.9791	0.0001
van Rheenen (control)	GSM3077696	0.9877	0.0022	0.0101
van Rheenen (control)	GSM3077698	0.7118	0.2554	0.0328
van Rheenen (control)	GSM3077710	0.9649	0.0134	0.0218
van Rheenen (control)	GSM3077712	0.0499	0.9478	0.0023
van Rheenen (control)	GSM3077714	0.9390	0.0575	0.0035
van Rheenen (control)	GSM3077716	0.9368	0.0300	0.0333
van Rheenen (control)	GSM3077719	0.5019	0.3169	0.1812
van Rheenen (control)	GSM3077727	0.9705	0.0293	0.0003
van Rheenen (control)	GSM3077729	0.8701	0.1286	0.0013
van Rheenen (control)	GSM3077732	0.9859	0.0096	0.0044
van Rheenen (control)	GSM3077734	0.9854	0.0067	0.0079
van Rheenen (control)	GSM3077736	0.0052	0.8829	0.1119
van Rheenen (control)	GSM3077739	0.5538	0.4459	0.0003
van Rheenen (control)	GSM3077748	0.9177	0.0639	0.0183
van Rheenen (control)	GSM3077750	0.9981	0.0017	0.0002
van Rheenen (control)	GSM3077753	0.3102	0.5850	0.1048
van Rheenen (control)	GSM3077757	0.9616	0.0279	0.0105
van Rheenen (control)	GSM3077760	0.1978	0.8007	0.0015
van Rheenen (control)	GSM3077767	0.8824	0.0050	0.1126

van Rheenen (control)	GSM3077770	0.2721	0.7009	0.0270
van Rheenen (control)	GSM3077773	0.8541	0.1451	0.0008
van Rheenen (control)	GSM3077776	0.2402	0.7572	0.0026
van Rheenen (control)	GSM3077778	0.0035	0.9964	0.0001
van Rheenen (control)	GSM3077780	0.0701	0.9217	0.0082
van Rheenen (control)	GSM3077794	0.0149	0.9179	0.0672
van Rheenen (control)	GSM3077796	0.9960	0.0011	0.0030
van Rheenen (control)	GSM3077799	0.7436	0.2554	0.0010
van Rheenen (control)	GSM3077810	0.0179	0.9783	0.0038
van Rheenen (control)	GSM3077813	0.6217	0.0080	0.3703
van Rheenen (control)	GSM3077816	0.0377	0.8175	0.1448
van Rheenen (control)	GSM3077818	0.0698	0.1941	0.7361
van Rheenen (control)	GSM3077820	0.1644	0.7768	0.0588
van Rheenen (control)	GSM3077830	0.8698	0.0100	0.1201
van Rheenen (control)	GSM3077833	0.8890	0.1003	0.0106
van Rheenen (control)	GSM3077836	0.0165	0.9825	0.0010
van Rheenen (control)	GSM3077838	0.4667	0.5326	0.0007
van Rheenen (control)	GSM3077846	0.9672	0.0160	0.0168
van Rheenen (control)	GSM3077849	0.9346	0.0626	0.0028
van Rheenen (control)	GSM3077851	0.0448	0.9349	0.0204
van Rheenen (control)	GSM3077853	0.0104	0.9892	0.0004

van Rheenen (control)	GSM3077856	0.9729	0.0271	0.0000
van Rheenen (control)	GSM3077859	0.9998	0.0001	0.0001
van Rheenen (control)	GSM3077863	0.0800	0.9168	0.0031
van Rheenen (control)	GSM3077867	0.2225	0.5559	0.2216
van Rheenen (control)	GSM3077871	0.9854	0.0145	0.0001
van Rheenen (control)	GSM3077874	0.9959	0.0023	0.0018
van Rheenen (control)	GSM3077878	0.9772	0.0217	0.0011
van Rheenen (control)	GSM3077881	0.9946	0.0010	0.0044
van Rheenen (control)	GSM3077884	0.6903	0.3093	0.0004
van Rheenen (control)	GSM3077886	0.9929	0.0070	0.0001
van Rheenen (control)	GSM3077889	0.9674	0.0325	0.0000
van Rheenen (control)	GSM3077894	0.4178	0.5810	0.0012
van Rheenen (control)	GSM3077896	0.9740	0.0252	0.0008
van Rheenen (control)	GSM3077899	0.8441	0.1397	0.0162
van Rheenen (control)	GSM3077901	0.4718	0.5261	0.0020
van Rheenen (control)	GSM3077904	0.0301	0.9410	0.0289
van Rheenen (control)	GSM3077906	0.0282	0.9712	0.0006
van Rheenen (control)	GSM3077909	0.9798	0.0112	0.0090
van Rheenen (control)	GSM3077911	0.9793	0.0206	0.0001
van Rheenen (control)	GSM3077914	0.9684	0.0315	0.0001
van Rheenen (control)	GSM3077921	0.9950	0.0048	0.0001

van Rheenen (control)	GSM3077923	0.7664	0.0061	0.2275
van Rheenen (control)	GSM3077925	0.9741	0.0224	0.0034
van Rheenen (control)	GSM3077928	0.9320	0.0580	0.0100
van Rheenen (control)	GSM3077936	0.9874	0.0081	0.0045
van Rheenen (control)	GSM3077939	0.8776	0.1176	0.0049
van Rheenen (control)	GSM3077942	0.9291	0.0339	0.0370
van Rheenen (control)	GSM3077944	0.2484	0.6408	0.1108
van Rheenen (control)	GSM3077947	0.0011	0.9892	0.0097
van Rheenen (control)	GSM3077950	0.9903	0.0097	0.0000
van Rheenen (control)	GSM3077952	0.9640	0.0004	0.0356
van Rheenen (control)	GSM3077954	0.9693	0.0001	0.0306
van Rheenen (control)	GSM3077957	0.0867	0.0019	0.9114
van Rheenen (control)	GSM3077963	0.9974	0.0026	0.0000
van Rheenen (control)	GSM3077966	0.6035	0.2959	0.1006
van Rheenen (control)	GSM3077969	0.9741	0.0203	0.0057
van Rheenen (control)	GSM3077979	0.0310	0.9690	0.0000
van Rheenen (control)	GSM3077982	0.2474	0.7519	0.0007
van Rheenen (control)	GSM3077984	0.9948	0.0052	0.0000
van Rheenen (control)	GSM3077986	0.8003	0.1784	0.0213
van Rheenen (control)	GSM3077989	0.8682	0.0549	0.0769
van Rheenen (control)	GSM3077997	0.5631	0.4364	0.0005
van Rheenen (control)	GSM3077999	0.3242	0.0008	0.6750
van Rheenen (control)	GSM3078002	0.0987	0.0004	0.9009
van Rheenen (control)	GSM3078004	0.8039	0.0007	0.1954
van Rheenen (control)	GSM3078006	0.9729	0.0109	0.0161
van Rheenen (control)	GSM3078014	0.7677	0.0001	0.2322
van Rheenen (control)	GSM3078017	0.1208	0.0011	0.8781
van Rheenen (control)	GSM3078021	0.9489	0.0027	0.0484
van Rheenen (control)	GSM3078024	0.3349	0.0145	0.6506
van Rheenen (control)	GSM3078026	0.9144	0.0083	0.0773
van Rheenen (control)	GSM3078029	0.2228	0.7439	0.0333
van Rheenen (control)	GSM3078031	0.9584	0.0000	0.0416
van Rheenen (control)	GSM3078033	0.1481	0.1483	0.7037
van Rheenen (control)	GSM3078045	0.9672	0.0274	0.0053
van Rheenen (control)	GSM3078047	0.9913	0.0026	0.0061
van Rheenen (control)	GSM3078049	0.6684	0.1082	0.2235
van Rheenen (control)	GSM3078056	0.6405	0.3280	0.0315
van Rheenen (control)	GSM3078064	0.0204	0.0083	0.9712
van Rheenen (control)	GSM3078066	0.5554	0.2246	0.2200
van Rheenen (control)	GSM3078071	0.8510	0.0158	0.1332
van Rheenen (control)	GSM3078077	0.8963	0.0401	0.0635
van Rheenen (control)	GSM3078079	0.4855	0.0012	0.5133

van Rheenen (control)	GSM3078082	0.9438	0.0343	0.0219
van Rheenen (control)	GSM3078084	0.3620	0.0666	0.5715
van Rheenen (control)	GSM3078087	0.9837	0.0154	0.0009
van Rheenen (control)	GSM3078090	0.8664	0.0087	0.1249
van Rheenen (control)	GSM3078095	0.9882	0.0000	0.0118
van Rheenen (control)	GSM3078097	0.5458	0.0894	0.3648
van Rheenen (control)	GSM3078099	0.9908	0.0001	0.0091
van Rheenen (control)	GSM3078101	0.7764	0.0375	0.1861
van Rheenen (control)	GSM3078103	0.0759	0.1986	0.7256
van Rheenen (control)	GSM3078105	0.5722	0.4177	0.0100
van Rheenen (control)	GSM3078111	0.4811	0.5105	0.0084
van Rheenen (control)	GSM3078113	0.3954	0.0035	0.6011
van Rheenen (control)	GSM3078116	0.1977	0.0050	0.7973
van Rheenen (control)	GSM3078118	0.8298	0.0057	0.1645
van Rheenen (control)	GSM3078121	0.0334	0.0438	0.9228
van Rheenen (control)	GSM3078123	0.4994	0.0519	0.4487
van Rheenen (control)	GSM3078126	0.0573	0.9249	0.0178
van Rheenen (control)	GSM3078128	0.1198	0.0071	0.8731
van Rheenen (control)	GSM3078137	0.1761	0.0020	0.8219
van Rheenen (control)	GSM3078141	0.9074	0.0055	0.0872
van Rheenen (control)	GSM3078144	0.1083	0.6711	0.2206
van Rheenen (control)	GSM3078147	0.9378	0.0562	0.0060
van Rheenen (control)	GSM3078149	0.9975	0.0012	0.0014
van Rheenen (control)	GSM3078152	0.9449	0.0230	0.0321
van Rheenen (control)	GSM3078156	0.0000	0.0000	1.0000
van Rheenen (control)	GSM3078159	0.9013	0.0913	0.0075
van Rheenen (control)	GSM3078161	0.7480	0.1521	0.0999
van Rheenen (control)	GSM3078195	0.7386	0.1207	0.1407
van Rheenen (control)	GSM3078198	0.4374	0.0051	0.5575
van Rheenen (control)	GSM3078200	0.0454	0.0047	0.9499
van Rheenen (control)	GSM3078201	0.0174	0.0005	0.9822
van Rheenen (control)	GSM3078210	0.0795	0.6607	0.2599
van Rheenen (control)	GSM3078212	0.0545	0.3518	0.5937
van Rheenen (control)	GSM3078216	0.9129	0.0704	0.0167
van Rheenen (control)	GSM3078218	0.1721	0.0000	0.8279
van Rheenen (control)	GSM3078221	0.2076	0.0282	0.7642
van Rheenen (control)	GSM3078225	0.2842	0.0011	0.7147
van Rheenen (control)	GSM3078239	0.1876	0.5293	0.2831
van Rheenen (control)	GSM3078261	0.0643	0.9352	0.0004
van Rheenen (control)	GSM3078263	0.0391	0.4630	0.4979
van Rheenen (control)	GSM3078266	0.3157	0.1720	0.5123
van Rheenen (control)	GSM3078268	0.3334	0.6642	0.0024

van Rheenen (control)	GSM3078271	0.0003	0.9997	0.0000
van Rheenen (control)	GSM3078279	0.0076	0.9915	0.0009
van Rheenen (control)	GSM3078281	0.6171	0.2726	0.1103
van Rheenen (control)	GSM3078285	0.0209	0.6804	0.2987
van Rheenen (control)	GSM3078287	0.2769	0.5983	0.1248
van Rheenen (control)	GSM3078290	0.1544	0.8017	0.0439
van Rheenen (control)	GSM3078292	0.0098	0.9773	0.0129
van Rheenen (control)	GSM3078294	0.5721	0.3986	0.0293
van Rheenen (control)	GSM3078297	0.0136	0.9775	0.0089
van Rheenen (control)	GSM3078299	0.2688	0.5744	0.1568
van Rheenen (control)	GSM3078306	0.4880	0.1430	0.3690
van Rheenen (control)	GSM3078314	0.1563	0.8179	0.0258
van Rheenen (control)	GSM3078316	0.6786	0.0964	0.2250
van Rheenen (control)	GSM3078326	0.0004	0.9966	0.0030
van Rheenen (control)	GSM3078329	0.5766	0.2635	0.1599
van Rheenen (control)	GSM3078331	0.0130	0.2330	0.7540
van Rheenen (control)	GSM3078345	0.0304	0.9445	0.0251
van Rheenen (control)	GSM3078348	0.0023	0.9662	0.0316
van Rheenen (control)	GSM3078351	0.8485	0.0042	0.1473
van Rheenen (control)	GSM3078353	0.2695	0.0395	0.6910
van Rheenen (control)	GSM3078355	0.7697	0.2170	0.0133

van Rheenen (control)	GSM3078357	0.0017	0.6759	0.3224
van Rheenen (control)	GSM3078362	0.8847	0.0350	0.0803
van Rheenen (control)	GSM3078364	0.8740	0.0236	0.1025
van Rheenen (control)	GSM3078366	0.8975	0.1019	0.0006
van Rheenen (control)	GSM3078368	0.0000	0.9003	0.0996
van Rheenen (control)	GSM3078370	0.7700	0.0059	0.2241
van Rheenen (control)	GSM3078372	0.1228	0.8718	0.0054
van Rheenen (control)	GSM3078374	0.9425	0.0565	0.0010
van Rheenen (control)	GSM3078378	0.9364	0.0425	0.0211
van Rheenen (control)	GSM3078380	0.0193	0.0716	0.9090
van Rheenen (control)	GSM3078383	0.3724	0.3843	0.2433
van Rheenen (control)	GSM3078385	0.0090	0.0108	0.9803
van Rheenen (control)	GSM3078399	0.0260	0.0077	0.9662
van Rheenen (control)	GSM3078407	0.0262	0.8432	0.1306
van Rheenen (control)	GSM3078417	0.2404	0.7546	0.0050
van Rheenen (control)	GSM3078419	0.9546	0.0063	0.0391
van Rheenen (control)	GSM3078422	0.0019	0.9976	0.0005
van Rheenen (control)	GSM3078429	0.1317	0.0324	0.8360
van Rheenen (control)	GSM3078432	0.0175	0.1116	0.8709
van Rheenen (control)	GSM3078439	0.9815	0.0161	0.0024
van Rheenen (control)	GSM3078441	0.0284	0.1278	0.8438

van Rheenen (control)	GSM3078447	0.6279	0.1022	0.2699
van Rheenen (control)	GSM3078457	0.0006	0.9547	0.0447
van Rheenen (control)	GSM3078459	0.9381	0.0196	0.0423
van Rheenen (control)	GSM3078461	0.0004	0.0002	0.9995
van Rheenen (control)	GSM3078468	0.3954	0.0599	0.5447
van Rheenen (control)	GSM3078471	0.7794	0.1080	0.1126
van Rheenen (control)	GSM3078473	0.0261	0.7582	0.2157
van Rheenen (control)	GSM3078476	0.8792	0.0416	0.0792
van Rheenen (control)	GSM3078478	0.3391	0.0546	0.6063
van Rheenen (control)	GSM3078481	0.3577	0.0897	0.5527
van Rheenen (control)	GSM3078483	0.8682	0.1109	0.0209
van Rheenen (control)	GSM3078485	0.7851	0.0003	0.2146
van Rheenen (control)	GSM3078487	0.7449	0.0298	0.2254
van Rheenen (control)	GSM3078489	0.1367	0.0009	0.8624
van Rheenen (control)	GSM3078491	0.3481	0.6352	0.0168
van Rheenen (control)	GSM3078494	0.4524	0.2246	0.3230
van Rheenen (control)	GSM3079744	0.9893	0.0107	0.0000
van Rheenen (control)	GSM3079760	0.9380	0.0324	0.0296
van Rheenen (control)	GSM3079787	0.9722	0.0274	0.0004
van Rheenen (control)	GSM3079796	0.1818	0.8084	0.0098
van Rheenen (control)	GSM3079819	0.8061	0.1687	0.0252
van Rheenen (control)	GSM3079831	0.8525	0.1389	0.0087
van Rheenen (control)	GSM3079840	0.9773	0.0164	0.0063
van Rheenen (control)	GSM3079853	0.9996	0.0000	0.0003
van Rheenen (control)	GSM3079865	0.9388	0.0223	0.0388
van Rheenen (control)	GSM3079872	0.4577	0.1739	0.3684
van Rheenen (control)	GSM3079873	0.9666	0.0326	0.0008
van Rheenen (control)	GSM3079878	0.9315	0.0151	0.0534
van Rheenen (control)	GSM3079879	0.9978	0.0008	0.0015
van Rheenen (control)	GSM3079880	0.9845	0.0128	0.0027
van Rheenen (control)	GSM3079882	0.9952	0.0010	0.0038
van Rheenen (control)	GSM3079883	0.8325	0.1644	0.0031
van Rheenen (control)	GSM3079886	0.7447	0.2532	0.0021
van Rheenen (control)	GSM3079888	0.8416	0.0870	0.0714
van Rheenen (control)	GSM3079892	0.9693	0.0173	0.0134
van Rheenen (control)	GSM3079894	0.3823	0.6144	0.0033
van Rheenen (control)	GSM3079898	0.4660	0.5308	0.0031
van Rheenen (control)	GSM3079900	0.8340	0.1649	0.0010
van Rheenen (control)	GSM3079903	0.9733	0.0241	0.0026
van Rheenen (control)	GSM3079905	0.9612	0.0248	0.0141
van Rheenen (control)	GSM3079909	0.9190	0.0743	0.0067
van Rheenen (control)	GSM3079911	0.9737	0.0178	0.0085

van Rheenen (control)	GSM3079915	0.9918	0.0070	0.0011
van Rheenen (control)	GSM3079917	0.9988	0.0006	0.0006
van Rheenen (control)	GSM3079921	0.6514	0.3299	0.0187
van Rheenen (control)	GSM3079923	0.9333	0.0525	0.0142
van Rheenen (control)	GSM3079927	0.9950	0.0040	0.0011
van Rheenen (control)	GSM3079929	0.7693	0.2275	0.0032
van Rheenen (control)	GSM3079932	0.9599	0.0336	0.0066
van Rheenen (control)	GSM3079934	0.9974	0.0021	0.0005
van Rheenen (control)	GSM3079938	0.9137	0.0857	0.0007
van Rheenen (control)	GSM3079941	0.9737	0.0231	0.0031
van Rheenen (control)	GSM3079942	0.8891	0.1107	0.0001
van Rheenen (control)	GSM3079946	0.9953	0.0025	0.0022
van Rheenen (control)	GSM3079947	0.9995	0.0002	0.0002
van Rheenen (control)	GSM3079948	0.9715	0.0284	0.0000
van Rheenen (control)	GSM3079949	0.9192	0.0565	0.0243
van Rheenen (control)	GSM3079951	0.9881	0.0115	0.0004
van Rheenen (control)	GSM3079952	0.9868	0.0128	0.0004
van Rheenen (control)	GSM3079955	0.9974	0.0015	0.0011
van Rheenen (control)	GSM3079959	0.9960	0.0026	0.0014
van Rheenen (control)	GSM3079962	0.9635	0.0256	0.0108
van Rheenen (control)	GSM3079966	0.9601	0.0398	0.0001

van Rheenen (control)	GSM3079969	0.9741	0.0205	0.0054
van Rheenen (control)	GSM3079973	0.9946	0.0037	0.0017
van Rheenen (control)	GSM3079976	0.8612	0.1313	0.0075
van Rheenen (control)	GSM3079980	0.4580	0.4956	0.0464
van Rheenen (control)	GSM3079983	0.9472	0.0477	0.0051
van Rheenen (control)	GSM3079987	0.8349	0.1645	0.0006
van Rheenen (control)	GSM3079990	0.9586	0.0413	0.0001
van Rheenen (control)	GSM3079994	0.9923	0.0042	0.0036
van Rheenen (control)	GSM3079997	0.9771	0.0204	0.0024
van Rheenen (control)	GSM3080001	0.7697	0.2007	0.0296
van Rheenen (control)	GSM3080004	0.9985	0.0013	0.0002
van Rheenen (control)	GSM3080007	0.7834	0.0911	0.1255
van Rheenen (control)	GSM3080010	0.9783	0.0206	0.0011
van Rheenen (control)	GSM3080014	0.8935	0.0982	0.0083
van Rheenen (control)	GSM3080016	0.3579	0.6395	0.0025
van Rheenen (control)	GSM3080017	0.9979	0.0015	0.0006
van Rheenen (control)	GSM3080021	0.8874	0.0085	0.1042
van Rheenen (control)	GSM3080024	0.8486	0.1401	0.0113
van Rheenen (control)	GSM3080025	0.9534	0.0460	0.0006
van Rheenen (control)	GSM3080026	0.9255	0.0705	0.0040
van Rheenen (control)	GSM3080030	0.9278	0.0519	0.0204

van Rheenen (control)	GSM3080031	0.5984	0.2435	0.1581
van Rheenen (control)	GSM3080032	0.7154	0.2838	0.0008
van Rheenen (control)	GSM3080033	0.9892	0.0102	0.0006
van Rheenen (control)	GSM3080035	0.4893	0.5007	0.0101
van Rheenen (control)	GSM3080036	0.9890	0.0092	0.0018
van Rheenen (control)	GSM3080045	0.9561	0.0432	0.0008
van Rheenen (control)	GSM3080052	0.9992	0.0008	0.0000
van Rheenen (control)	GSM3080058	0.6768	0.3202	0.0030
van Rheenen (control)	GSM3080062	0.9959	0.0015	0.0026
van Rheenen (control)	GSM3080071	0.9909	0.0088	0.0003
van Rheenen (control)	GSM3080078	0.8601	0.1399	0.0001
van Rheenen (control)	GSM3080081	0.9590	0.0403	0.0007
van Rheenen (control)	GSM3080082	0.9785	0.0090	0.0125
van Rheenen (control)	GSM3080085	0.9917	0.0083	0.0000
van Rheenen (control)	GSM3080088	0.9402	0.0596	0.0002
van Rheenen (control)	GSM3080089	0.9996	0.0003	0.0002
van Rheenen (control)	GSM3080090	0.9999	0.0001	0.0000
van Rheenen (control)	GSM3080091	0.8950	0.1033	0.0017
van Rheenen (control)	GSM3080092	0.9093	0.0784	0.0123
van Rheenen (control)	GSM3080094	0.9099	0.0879	0.0022
van Rheenen (control)	GSM3080095	0.9732	0.0176	0.0093
van Rheenen (control)	GSM3080096	0.7561	0.0142	0.2298
van Rheenen (control)	GSM3080097	0.9995	0.0003	0.0001
van Rheenen (control)	GSM3080100	0.9117	0.0030	0.0852
van Rheenen (control)	GSM3080104	0.9994	0.0001	0.0005
van Rheenen (control)	GSM3080106	0.9084	0.0371	0.0544
van Rheenen (control)	GSM3080110	0.9918	0.0021	0.0061
van Rheenen (control)	GSM3080112	0.9627	0.0152	0.0222
van Rheenen (control)	GSM3080116	0.9926	0.0029	0.0045
van Rheenen (control)	GSM3080117	0.9920	0.0041	0.0039
van Rheenen (control)	GSM3080121	0.8306	0.0212	0.1482
van Rheenen (control)	GSM3080123	0.3190	0.6803	0.0007
van Rheenen (control)	GSM3080126	0.3185	0.3222	0.3593
van Rheenen (control)	GSM3080128	0.9862	0.0106	0.0032
van Rheenen (control)	GSM3080131	0.9999	0.0000	0.0001
van Rheenen (control)	GSM3080132	0.9776	0.0001	0.0222
van Rheenen (control)	GSM3080136	0.9706	0.0093	0.0201
van Rheenen (control)	GSM3080137	0.9971	0.0002	0.0027
van Rheenen (control)	GSM3080140	0.9012	0.0139	0.0849
van Rheenen (control)	GSM3080142	0.9781	0.0051	0.0168
van Rheenen (control)	GSM3080145	0.9279	0.0408	0.0313
van Rheenen (control)	GSM3080146	0.9963	0.0002	0.0035

van Rheenen (control)	GSM3080150	0.9998	0.0000	0.0001
van Rheenen (control)	GSM3080151	0.9915	0.0012	0.0073
van Rheenen (control)	GSM3080152	0.9928	0.0026	0.0045
van Rheenen (control)	GSM3080154	0.7544	0.0429	0.2027
van Rheenen (control)	GSM3080155	0.9892	0.0049	0.0059
van Rheenen (control)	GSM3080156	0.9066	0.0161	0.0773
van Rheenen (control)	GSM3080157	0.9895	0.0036	0.0069
van Rheenen (control)	GSM3080158	0.9989	0.0004	0.0007
van Rheenen (control)	GSM3080159	0.9931	0.0005	0.0064
van Rheenen (control)	GSM3080161	0.9114	0.0472	0.0414
van Rheenen (control)	GSM3080162	0.9980	0.0011	0.0009
van Rheenen (control)	GSM3080163	0.9926	0.0066	0.0008
van Rheenen (control)	GSM3080164	0.9911	0.0069	0.0021
van Rheenen (control)	GSM3080165	0.9965	0.0024	0.0011
van Rheenen (control)	GSM3080166	0.9948	0.0029	0.0023
van Rheenen (control)	GSM3080167	0.9762	0.0230	0.0008
van Rheenen (control)	GSM3080169	0.9931	0.0060	0.0010
van Rheenen (control)	GSM3080170	0.9276	0.0084	0.0640
van Rheenen (control)	GSM3080171	0.9667	0.0056	0.0277
van Rheenen (control)	GSM3080172	0.7020	0.2801	0.0179
van Rheenen (control)	GSM3080173	0.9962	0.0032	0.0006
van Rheenen (control)	GSM3080174	0.9994	0.0002	0.0004
van Rheenen (control)	GSM3080175	0.9943	0.0031	0.0026
van Rheenen (control)	GSM3080176	0.9727	0.0101	0.0173
van Rheenen (control)	GSM3080177	0.9887	0.0104	0.0010
van Rheenen (control)	GSM3080178	0.9953	0.0017	0.0030
van Rheenen (control)	GSM3080179	0.6958	0.0204	0.2838
Zucca	SLA3014	0.4762	0.0042	0.5196
Zucca	SLA0110	0.7524	0.0053	0.2423
Zucca	SLA0514	0.7832	0.0438	0.1731
Zucca	SLA1213	0.8645	0.0042	0.1313
Zucca	SLA615	0.6436	0.3336	0.0229
Zucca	SLA2411	0.9495	0.0389	0.0116
Zucca	SLA715	0.0051	0.9873	0.0076
Zucca	SLA0210	0.9936	0.0001	0.0063
Zucca	SLA1812	0.6049	0.3906	0.0045
Zucca	SLA0109	0.9959	0.0001	0.0040
Zucca	SLA2311	0.9981	0.0000	0.0019
Zucca	SLA3315	0.9434	0.0563	0.0003
Zucca	SLA2014	0.9536	0.0463	0.0001
Zucca	SLA3311	0.9982	0.0017	0.0001
Zucca	SLA2710	0.9988	0.0012	0.0000

Table A35. Posterior probabilities of being assigned to the KCL BrainBank-defined clusters for the TargetALS and van Rheenen case and control datasets and the Zucca case-only dataset.

Gene	log2FoldChange (lfc)	lfc SE	Statistic	Degrees of Freedom	p-value	Adjusted p-value
ENSG00000146469	0.5826	0.1822	7.9985	110.28	1.40E-12	1.80E-10
ENSG00000233123	0.4996	0.2028	7.7631	99.88	7.40E-12	4.80E-10
ENSG00000006128	0.4815	0.1777	7.0345	93.67	3.20E-10	1.40E-08
ENSG00000157005	0.8417	0.2725	6.9332	97.40	4.50E-10	1.50E-08
ENSG00000223930	0.2921	0.2232	6.6654	107.58	1.20E-09	3.10E-08
ENSG00000246363	0.1792	0.1803	6.6720	98.31	1.50E-09	3.30E-08
ENSG00000144227	0.4924	0.1627	6.6168	96.80	2.00E-09	3.80E-08
ENSG00000141433	0.4349	0.1888	6.4265	91.06	5.90E-09	9.60E-08
ENSG00000185149	0.2026	0.3090	5.9753	97.17	3.80E-08	5.50E-07
ENSG00000179520	0.3825	0.2334	5.7730	105.26	8.00E-08	1.00E-06
ENSG00000239672	0.1115	0.1238	5.7050	89.95	1.50E-07	1.30E-06
ENSG00000159248	0.1933	0.1515	5.7757	86.79	1.20E-07	1.30E-06
ENSG00000164600	0.3274	0.2167	5.7873	86.19	1.10E-07	1.30E-06
ENSG00000145708	0.4307	0.1846	5.6454	107.32	1.40E-07	1.30E-06
ENSG00000152595	0.4981	0.1935	5.7258	87.90	1.40E-07	1.30E-06
ENSG00000285634	0.1003	0.1638	5.6423	89.85	1.90E-07	1.50E-06
ENSG00000186081	0.3526	0.3386	5.5727	108.11	1.90E-07	1.50E-06
ENSG00000205279	0.2187	0.2709	5.6046	91.71	2.20E-07	1.60E-06
ENSG00000236714	0.4243	0.2311	5.6003	83.80	2.70E-07	1.80E-06
ENSG00000169035	0.1416	0.2054	5.5062	94.98	3.10E-07	1.90E-06
ENSG00000231824	0.6064	0.2400	5.5160	96.62	2.90E-07	1.90E-06
ENSG00000287611	0.2132	0.1720	5.4080	99.44	4.40E-07	2.60E-06
ENSG00000254101	0.1455	0.2118	5.3584	101.32	5.30E-07	3.00E-06
ENSG00000147571	0.6703	0.3016	5.3224	105.90	5.80E-07	3.10E-06
ENSG00000224404	0.1092	0.1903	5.3469	85.69	7.30E-07	3.80E-06
ENSG00000188729	0.4901	0.2948	5.2314	108.18	8.30E-07	4.20E-06
ENSG00000183090	-0.0761	0.2179	5.2296	98.52	9.60E-07	4.60E-06
ENSG00000176697	0.1810	0.1423	5.2128	95.55	1.10E-06	5.00E-06
ENSG00000228999	0.5340	0.4209	5.1440	104.41	1.30E-06	5.50E-06
ENSG00000250634	0.5519	0.2149	5.1427	107.88	1.20E-06	5.50E-06
ENSG00000202048	0.1086	0.2250	4.6348	105.08	1.00E-05	4.40E-05
ENSG00000165899	0.0392	0.1702	4.5758	99.95	1.40E-05	5.60E-05
ENSG00000261757	0.6922	0.3229	4.5259	92.56	1.80E-05	7.10E-05
ENSG00000164326	0.5162	0.3652	4.4130	106.96	2.40E-05	9.40E-05
ENSG00000287844	-0.0424	0.2224	4.4095	98.41	2.70E-05	9.70E-05
ENSG00000174899	0.3241	0.3399	4.4019	100.95	2.70E-05	9.70E-05
ENSG00000256193	-0.0790	0.1865	4.4520	77.26	2.80E-05	9.80E-05
ENSG00000229618	-0.0465	0.1608	4.4306	83.26	2.80E-05	9.80E-05
ENSG00000170231	0.1262	0.2016	4.3718	95.84	3.10E-05	1.10E-04
ENSG00000261325	0.1944	0.3365	4.3363	110.45	3.20E-05	1.10E-04
ENSG00000184385	0.2499	0.1928	4.3667	89.47	3.40E-05	1.10E-04
ENSG00000150175	0.1795	0.2367	4.3001	109.86	3.70E-05	1.20E-04
ENSG00000285735	0.4971	0.3623	4.2899	104.89	4.00E-05	1.20E-04
ENSG00000182632	0.1653	0.2239	4.1510	92.55	7.40E-05	2.10E-04

ENSG00000170290	0.7859	0.5126	4.1357	110.66	6.90E-05	2.10E-04
ENSG00000286016	1.4401	0.5520	4.0463	110.88	9.70E-05	2.80E-04
ENSG00000279952	0.0247	0.2134	4.0202	83.73	1.30E-04	3.50E-04
ENSG00000280776	-0.1193	0.1695	3.9769	95.67	1.40E-04	3.70E-04
ENSG00000151790	0.1886	0.2028	3.9349	102.33	1.50E-04	4.10E-04
ENSG00000100362	0.4285	0.2576	3.9480	90.51	1.60E-04	4.10E-04
ENSG00000169676	-0.0942	0.2181	3.6289	98.54	4.50E-04	1.20E-03
ENSG00000111863	0.0218	0.2133	3.6337	90.24	4.60E-04	1.20E-03
ENSG00000126545	0.5930	0.8212	3.5656	107.03	5.40E-04	1.30E-03
ENSG00000267623	0.1263	0.2689	3.5508	101.28	5.80E-04	1.40E-03
ENSG00000261502	0.3522	0.2578	3.5138	106.26	6.50E-04	1.50E-03
ENSG00000131885	0.4960	0.2605	3.5129	71.93	7.70E-04	1.80E-03
ENSG00000117594	0.5609	0.2504	3.4351	109.06	8.40E-04	1.90E-03
ENSG00000255087	0.1233	0.2625	3.4343	88.40	9.10E-04	2.00E-03
ENSG00000223812	0.0953	0.1904	3.4123	82.97	1.00E-03	2.20E-03
ENSG00000128564	0.1898	0.2351	3.4000	91.14	1.00E-03	2.20E-03
ENSG00000138678	0.1171	0.1920	3.3294	92.63	1.30E-03	2.70E-03
ENSG00000132744	0.5304	0.4546	3.3102	109.93	1.30E-03	2.70E-03
ENSG00000260658	0.0460	0.2875	3.3007	100.62	1.30E-03	2.80E-03
ENSG00000107165	0.2340	0.2287	3.2995	87.58	1.40E-03	2.90E-03
ENSG00000265179	0.2833	0.2576	3.2782	91.89	1.50E-03	3.00E-03
ENSG00000276462	-0.0214	0.2670	3.2630	85.77	1.60E-03	3.10E-03
ENSG00000106236	0.0239	0.2223	3.0808	99.51	2.70E-03	5.20E-03
ENSG00000075673	-0.5552	0.3807	3.0720	100.40	2.70E-03	5.30E-03
ENSG00000266573	-0.2465	0.2537	2.9543	91.92	4.00E-03	7.60E-03
ENSG00000117322	0.7721	0.4437	2.8580	108.69	5.10E-03	9.60E-03
ENSG00000286063	0.4493	0.3273	2.7852	105.59	6.30E-03	1.20E-02
ENSG00000225280	0.8616	0.6064	2.7201	110.87	7.60E-03	1.40E-02
ENSG00000279875	-0.1172	0.2996	2.6537	107.89	9.20E-03	1.60E-02
ENSG00000225449	0.5431	0.2423	2.6718	94.90	8.90E-03	1.60E-02
ENSG00000228735	-0.3704	0.2249	2.6427	76.21	1.00E-02	1.70E-02
ENSG00000287907	0.0617	0.2912	2.5788	99.67	1.10E-02	2.00E-02
ENSG00000268297	0.0661	0.2207	2.5171	95.54	1.40E-02	2.20E-02
ENSG00000242159	0.1469	0.2523	2.5271	93.97	1.30E-02	2.20E-02
ENSG00000227582	0.4623	0.3679	2.5140	107.52	1.30E-02	2.20E-02
ENSG00000122025	-0.1181	0.2100	2.4134	91.72	1.80E-02	2.90E-02
ENSG00000228772	-0.2214	0.2469	2.3699	91.70	2.00E-02	3.20E-02
ENSG00000254510	0.0482	0.3211	2.2773	102.91	2.50E-02	4.00E-02
ENSG00000286736	0.0391	0.2594	2.2500	100.80	2.70E-02	4.10E-02
ENSG00000119888	0.3776	0.3102	2.2609	110.98	2.60E-02	4.10E-02
ENSG00000200959	-0.0129	0.3323	2.2040	109.26	3.00E-02	4.60E-02
ENSG00000132677	1.2614	0.4052	2.1997	110.85	3.00E-02	4.60E-02
ENSG00000234665	0.7950	0.4356	2.1870	105.92	3.10E-02	4.70E-02
ENSG00000258859	-0.1401	0.2806	2.0334	91.50	4.50E-02	6.70E-02
ENSG00000274330	-0.4950	0.2849	1.9645	93.30	5.30E-02	7.70E-02
ENSG00000229722	1.1299	0.5798	1.9214	104.17	5.70E-02	8.40E-02

ENSG00000256971	-0.1039	0.2652	1.8975	81.77	6.10E-02	8.80E-02
ENSG00000120875	0.1897	0.2462	1.8693	105.01	6.40E-02	9.20E-02
ENSG00000248837	-0.6334	0.2125	1.8386	87.80	6.90E-02	9.80E-02
ENSG00000286810	0.6573	0.2933	1.7586	101.23	8.20E-02	1.10E-01
ENSG00000226405	0.9211	0.4922	1.7836	104.05	7.70E-02	1.10E-01
ENSG00000287593	-0.2611	0.2325	1.6326	81.24	1.10E-01	1.40E-01
ENSG00000216753	0.3224	0.3742	1.6290	97.69	1.10E-01	1.40E-01
ENSG00000285578	0.0606	0.4793	1.5717	109.58	1.20E-01	1.60E-01
ENSG00000130701	-0.1332	0.5085	1.5452	98.58	1.30E-01	1.70E-01
ENSG00000225493	0.4354	0.2641	1.5214	89.51	1.30E-01	1.70E-01
ENSG00000285561	-0.3713	0.2248	1.4150	96.51	1.60E-01	2.10E-01
ENSG00000286666	-0.1954	0.2788	1.3761	102.42	1.70E-01	2.20E-01
ENSG00000174576	-0.2569	0.5316	1.3091	94.96	1.90E-01	2.50E-01
ENSG00000271538	0.0750	0.2435	1.3033	97.58	2.00E-01	2.50E-01
ENSG00000179477	-0.3787	0.2521	1.2159	98.79	2.30E-01	2.80E-01
ENSG00000261738	-0.2143	0.2554	1.2061	90.70	2.30E-01	2.90E-01
ENSG00000254681	0.0922	0.5426	1.0700	109.17	2.90E-01	3.50E-01
ENSG00000237390	0.7004	0.2926	1.0810	110.92	2.80E-01	3.50E-01
ENSG00000229635	0.3925	0.3115	1.0206	104.37	3.10E-01	3.70E-01
ENSG00000243323	0.0630	0.2761	-0.9369	90.09	3.50E-01	4.10E-01
ENSG00000259520	0.2809	0.3394	0.9513	108.52	3.40E-01	4.10E-01
ENSG00000286292	0.3259	0.3065	0.8013	103.08	4.30E-01	5.00E-01
ENSG00000241945	-0.8688	0.6353	0.7611	107.48	4.50E-01	5.10E-01
ENSG00000254363	0.0074	0.3298	0.7739	107.73	4.40E-01	5.10E-01
ENSG00000174403	0.0308	0.2412	0.6103	105.19	5.40E-01	6.20E-01
ENSG00000122012	-0.5557	0.2640	0.5481	94.68	5.90E-01	6.60E-01
ENSG00000227723	0.7703	0.4205	0.5483	107.04	5.90E-01	6.60E-01
ENSG00000281383	-2.4226	0.8698	0.5042	104.89	6.20E-01	6.80E-01
ENSG00000218772	0.3719	0.5009	0.4929	101.58	6.20E-01	6.90E-01
ENSG00000156076	-0.3244	0.2400	-0.4618	98.76	6.50E-01	7.00E-01
ENSG00000160221	-0.6366	0.6024	0.4285	109.55	6.70E-01	7.20E-01
ENSG00000277918	-0.2268	0.5116	0.4067	106.86	6.90E-01	7.40E-01
ENSG00000178401	0.2587	0.2269	0.3703	106.51	7.10E-01	7.60E-01
ENSG00000286109	0.3874	0.3940	0.3355	101.58	7.40E-01	7.80E-01
ENSG00000223553	-0.1307	0.2817	0.3057	109.90	7.60E-01	8.00E-01
ENSG00000104938	-0.2947	0.4624	0.2051	107.45	8.40E-01	8.70E-01
ENSG00000273214	0.5610	0.3931	-0.1563	88.01	8.80E-01	9.00E-01
ENSG00000254561	-0.2467	0.1987	0.1129	108.58	9.10E-01	9.30E-01
ENSG00000137860	0.2537	0.3138	-0.0929	110.33	9.30E-01	9.40E-01
ENSG00000143858	-0.3986	0.2703	0.0217	105.86	9.80E-01	9.80E-01
ENSG00000205634	-0.2825	0.2264	-0.0349	103.13	9.70E-01	9.80E-01

Table A36. Results of the differential expression of KCL BrainBank Cluster 1 with DESeq2, comparing people with ALS to controls. A positive log2FoldChange refers to upregulation in gene expression in cases and vice versa. The independent hypothesis weighting method was used for p-value correction.

Scenario	**Dataset**	**Cluster**	**Number of Samples**	**Number of Genes**	**Best Hyperparameter**	**ROC AUC (mean ± SD)**	**Precision (mean ± SD)**	**Recall (mean ± SD)**	**F1-Score (mean ± SD)**
1 (All Genes)	KCL BrainBank (case-control)	1 (informative genes)	119	131	C=0.01, penalty=’l1’, solver=’liblinear’	0.832 ± 0.139	0.864 ± 0.125	0.739 ± 0.173	0.789 ± 0.137
		1 (random genes)	119	131	NA	0.569 ± 0.106	0.413 ± 0.0954	0.405 ± 0.149	0.399 ± 0.110
	TargetALS (case-control)	1	121	71	C=1.0, penalty=’l2’, solver=’lbfgs’	0.965 ± 0.0498	0.952 ± 0.0487	0.949 ± 0.0680	0.948 ± 0.0418
		2	32	148	C=1.0, penalty=’l2’, solver=’lbfgs’	0.964 ± 0.0619	0.933 ± 0.0673	0.964 ± 0.0619	0.948 ± 0.0589
		3	49	247	C=1.0, penalty=’l1’, solver=’liblinear’	0.976 ± 0.0532	0.958 ± 0.0589	1.00 ± 0.000	0.978 ± 0.0314
	Van Rheenen (case-control)	1	858	57	C=1.0, penalty=’l1’, solver=’liblinear’	1.00 ± 0.000	1.00 ± 0.000	1.00 ± 0.000	1.00 ± 0.000
		1 (after removing *NME1*)	858	56	C=0.1, penalty=’l1’, solver=’liblinear’	0.685 ± 0.0505	0.532 ± 0.0467	0.657 ± 0.0818	0.584 ± 0.0440
		2	110	230	C=0.1, penalty=’l2’, solver=’liblinear’	0.857 ± 0.103	0.690 ± 0.241	0.675 ± 0.199	0.665 ± 0.187
		3	74	247	C=1.0, penalty=none, solver=’newton-cg’	0.907 ± 0.130	0.833 ± 0.179	0.867 ± 0.221	0.838 ± 0.182
	TargetALS (motor cortex-occipital cortex)	1	131	53	C=1.0, penalty=’l1’, solver=’liblinear’	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000
		2	34	106	C=1.0, penalty=’l1’, solver=’liblinear’	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000
		3	48	195	C=1.0, penalty=’l1’, solver=’liblinear’	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000
	TargetALS (motor cortex-cerebellum)	1	187	40	C=1.0, penalty=’l1’, solver=’liblinear’	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000
		2	43	110	C=1.0, penalty=’l1’, solver=’liblinear’	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000
		3	66	197	C=1.0, penalty=’l1’, solver=’liblinear’	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000
2 (Removal of Correlated Genes)	KCL BrainBank (case-control)	1	119	31	C=0.1, penalty=’l1’, solver=’liblinear’	0.812 ± 0.110	0.877 ± 0.093	0.756 ± 0.154	0.805 ± 0.113
	TargetALS (case-control)	1	121	21	C=1.0, penalty=’l2’, solver=’liblinear’	0.937 ± 0.0837	0.938 ± 0.0657	0.917 ± 0.0907	0.925 ± 0.00928
		2	32	9	C=1.0, penalty=’l1’, solver=’liblinear’	0.964 ± 0.0619	0.964 ± 0.0619	0.964 ± 0.0619	0.964 ± 0.0619
		3	49	15	C=0.1, penalty=’l1’, solver=’liblinear’	0.955 ± 0.0633	1.00 ± 0.000	0.554 ± 0.180	0.695 ± 0.156
	Van Rheenen (case-control)	1	858	48	C=1.0, penalty=’l1’, solver=’liblinear’	1.00 ± 0.000	1.00 ± 0.000	1.00 ± 0.000	1.00 ± 0.000
		2	110	131	C=0.01, penalty=’l2’, solver=’liblinear’	0.786 ± 0.0984	0.563 ± 0.181	0.708 ± 0.164	0.603 ± 0.110
		3	74	79	C=0.1, penalty=’l2’, solver=’lbfgs’	0.845 ± 0.126	0.782 ± 0.236	0.733 ± 0.249	0.730 ± 0.220

	TargetALS (motor cortex-occipital cortex)	1	131	8	C=1.0, penalty=’l1’, solver=’liblinear’	0.997 ± 0.00990	0.974 ± 0.0542	0.979 ± 0.0423	0.975 ± 0.0324
		2	34	10	C=1.0, penalty=’l1’, solver=’liblinear’	1.000 ± 0.000	1.000 ± 0.000	0.933 ± 0.0943	0.963 ± 0.0524
		3	48	14	C=1.0, penalty=’l1’, solver=’liblinear’	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000
	TargetALS (motor cortex-cerebellum)	1	187	9	C=1.0, penalty=’l1’, solver=’liblinear’	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000
		2	43	110	C=1.0, penalty=’l1’, solver=’liblinear’	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000
		3	66	13	C=1.0, penalty=’l1’, solver=’liblinear’	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000
3 (Genes Common to All Folds)	KCL BrainBank (case-control)	1	119	7	C=0.1, penalty=’l1’, solver=’liblinear’	0.833 ± 0.114	0.893 ± 0.0930	0.767 ± 0.137	0.817 ± 0.100
	TargetALS (case-control)	1	121	2	C=0.1, penalty=’l2’, solver=’lbfgs’	0.832 ± 0.120	0.907 ± 0.0741	0.827 ± 0.135	0.856 ± 0.0781
	Van Rheenen (case-control)	1	858	38	C=0.1, penalty=’l1’, solver=’liblinear’	0.691 ± 0.0559	0.530 ± 0.0560	0.675 ± 0.0861	0.591 ± 0.0613
		2	110	54	C=0.01, penalty=’l2’, solver=’lbfgs’	0.790 ± 0.145	0.625 ± 0.203	0.625 ± 0.212	0.600 ± 0.162
		3	74	19	C=0.01, penalty=’l2’, solver=’lbfgs’	0.752 ± 0.162	0.655 ± 0.260	0.583 ± 0.201	0.573 ± 0.178
	TargetALS (motor cortex-occipital cortex)	1	131	3	C=0.0001, penalty=”l2”, solver=”lbfgs”	0.790 ± 0.150	0.906 ± 0.111	0.638 ± 0.139	0.735 ± 0.111
	TargetALS(motor cortex-cerebellum)	1	187	6	C=1.0, penalty=’l1’, solver=’liblinear’	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000
		2	43	1	C=1.0, penalty=’l1’, solver=’liblinear’	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000
		3	66	2	C=1.0, penalty=’l1’, solver=’liblinear’	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000

Table A37. Performance metrics of the cluster-specific logistic regression classifier models with ten-fold cross validation for the three case-control datasets, and two motor cortex-other brain region datasets in TargetALS under each scenario. The number of genes in scenario 1 refers to the genes shared by cases and controls in each dataset of the KCL BrainBank case-defined informative genes which constitute that cluster. The number of genes in scenario 2 refers to the average number of genes over all folds after removal of correlated genes. For scenario 3, the genes common to all folds refers to genes present in all ten folds after the effects of multicollinearity was removed. The ‘best hyperparameter’ column details the parameters which were supplied to train each logistic regression model, selected after performing hyperparameter tuning using GridSearchCV. ROC AUC: Area under the Receiver Operating Characteristic Curve.

Scenario	Cluster	Ensembl ID	Gene Symbol	SHAP Importance
1	1	ENSG00000146469	VIP	0.0479
1	1	ENSG00000156076	WIF1	0.0391
1	1	ENSG00000157005	SST	0.0355
1	1	ENSG00000233123	LINC01007	0.0347
1	1	ENSG00000185149	NPY2R	0.0346
1	1	ENSG00000117594	HSD11B1	0.0342
1	1	ENSG00000248837	LOC105374524	0.0334
1	1	ENSG00000122012	SV2C	0.0326
1	1	ENSG00000287593	Antisense to ADTRP	0.0324
1	1	ENSG00000254101	LINC02055	0.0323
1	1	ENSG00000287611	Lnc-HRH4-2	0.0314
1	1	ENSG00000254561	None	0.0313
1	1	ENSG00000231824	AKAIN1	0.0312
1	1	ENSG00000179520	SLC17A8	0.0296
1	1	ENSG00000117322	CR2	0.0274
1	1	ENSG00000285561	None	0.0273
1	1	ENSG00000205634	LINC00898	0.0268
1	1	ENSG00000261738	MIR3976HG	0.0246
1	1	ENSG00000174403	CRMA	0.0245
1	1	ENSG00000144227	NXPH2	0.0236
1	1	ENSG00000141433	ADCYAP1	0.0235
1	1	ENSG00000205279	CTXN3	0.0231
1	1	ENSG00000120875	DUSP4	0.0214
1	1	ENSG00000006128	TAC1	0.0213
1	1	ENSG00000286109	Lnc-KCNK1-1	0.0212
1	1	ENSG00000223930	Lnc-ZMAT3-3	0.0209
1	1	ENSG00000286292	None	0.0207
1	1	ENSG00000271538	LINC02427	0.0206
1	1	ENSG00000286810	None	0.0205
1	1	ENSG00000143858	SYT2	0.0200
1	1	ENSG00000126545	CSN1S1	0.0196
1	1	ENSG00000132677	RHBG	0.0196
1	1	ENSG00000228999	LINC01830	0.0195
1	1	ENSG00000152595	MEPE	0.0191
1	1	ENSG00000128564	VGF	0.0180
1	1	ENSG00000274330	ADAM20 Pseudogene	0.0179
1	1	ENSG00000159248	GJD2	0.0177
1	1	ENSG00000280776	LINC01202	0.0174
1	1	ENSG00000250634	LINC01182	0.0169
1	1	ENSG00000255087	LOC101929473	0.0157
1	1	ENSG00000234665	LERFS	0.0156
1	1	ENSG00000182632	CCNYL2	0.0154
1	1	ENSG00000229722	Lnc-SGK1-3	0.0153
1	1	ENSG00000145708	CRHBP	0.0153
1	1	ENSG00000285634	LOC105376121	0.0153
1	1	ENSG00000147571	CRH	0.0144
1	1	ENSG00000100362	PVALB	0.0142
1	1	ENSG00000164326	CARTPT	0.0141
1	1	ENSG00000227723	Lnc-MYB-5	0.0136
1	1	ENSG00000243323	PTPRVP	0.0134
1	1	ENSG00000160221	GATD3	0.0127
1	1	ENSG00000179477	ALOX12B	0.0126
1	1	ENSG00000138678	GPAT3	0.0126
1	1	ENSG00000286063	None	0.0123
1	1	ENSG00000277918	RNVU1-28	0.0119
1	1	ENSG00000256193	LINC00507	0.0117
1	1	ENSG00000227582	ADGRF5P1	0.0107

1	1	ENSG00000239672	NME1	0.0106
1	1	ENSG00000254681	PKD1P5	0.0106
1	1	ENSG00000225280	LOC105372558	0.0105
1	1	ENSG00000200959	SNORA74A	0.0104
1	1	ENSG00000229635	Pseudogene Similar to Part of FBXW1B	0.0104
1	1	ENSG00000225493	LINC01107	0.0104
1	1	ENSG00000246363	LINC02458	0.0101
1	1	ENSG00000218772	FAM8A6P	0.0100
1	1	ENSG00000224404	Lnc-LARGE1-1	0.0099
1	1	ENSG00000107165	TYRP1	0.0096
1	1	ENSG00000254363	LOC101929719	0.0096
1	1	ENSG00000286016	None	0.0095
1	1	ENSG00000228772	Lnc-PRL-3	0.0095
1	1	ENSG00000216753	HMGA1P7	0.0093
1	1	ENSG00000186081	KRT5	0.0092
1	1	ENSG00000174899	SLC66A1L	0.0090
1	1	ENSG00000254510	Lnc-NPAS4-1	0.0089
1	1	ENSG00000268297	CLEC4GP1	0.0088
1	1	ENSG00000104938	CLEC4M	0.0088
1	1	ENSG00000184385	UMODL1-AS1	0.0087
1	1	ENSG00000236714	LINC01844	0.0086
1	1	ENSG00000169676	DRD5	0.0086
1	1	ENSG00000225449	RAB6C-AS1	0.0085
1	1	ENSG00000229618	Lnc-ARL4A-54	0.0080
1	1	ENSG00000075673	ATP12A	0.0080
1	1	ENSG00000241945	PWP2	0.0078
1	1	ENSG00000151790	TDO2	0.0077
1	1	ENSG00000137860	SLC28A2	0.0075
1	1	ENSG00000286666	None	0.0075
1	1	ENSG00000266573	Lnc-HRH4-7	0.0071
1	1	ENSG00000130701	RBBP8NL	0.0071
1	1	ENSG00000261502	Lnc-CDH8-10	0.0067
1	1	ENSG00000267623	Cyclin Y-Like Pseudogene	0.0066
1	1	ENSG00000228735	LOC124901635	0.0065
1	1	ENSG00000106236	NPTX2	0.0063
1	1	ENSG00000281383	Lnc-KCNE1B-157	0.0063
1	1	ENSG00000188729	OSTN	0.0062
1	1	ENSG00000287907	None	0.0061
1	1	ENSG00000256971	LINC00508	0.0060
1	1	ENSG00000286736	None	0.0058
1	1	ENSG00000131885	KRT17P1	0.0058
1	1	ENSG00000122025	FLT3	0.0056
1	1	ENSG00000165899	OTOGL	0.0055
1	1	ENSG00000202048	SNORD114-20	0.0054
1	1	ENSG00000150175	FRMPD2B	0.0054
1	1	ENSG00000169035	KLK7	0.0053
1	1	ENSG00000287844	None	0.0053
1	1	ENSG00000226405	HSD17B12 Pseudogene	0.0051
1	1	ENSG00000285578	Lnc-DUSP22-2	0.0051
1	1	ENSG00000285735	LINC02717	0.0050
1	1	ENSG00000279875	None	0.0050
1	1	ENSG00000170290	SLN	0.0048
1	1	ENSG00000237390	Lnc-RHBG-1	0.0048
1	1	ENSG00000111863	ADTRP	0.0048
1	1	ENSG00000261325	LINC02192	0.0047
1	1	ENSG00000223812	PYDC2-AS1	0.0044

1	1	ENSG00000261757	miR-1255	0.0043
1	1	ENSG00000132744	ACY3	0.0041
1	1	ENSG00000164600	NEUROD6	0.0041
1	1	ENSG00000259520	SLC28A2-AS1	0.0040
1	1	ENSG00000119888	EPCAM	0.0040
1	1	ENSG00000276462	LINC03025	0.0040
1	1	ENSG00000170231	FABP6	0.0039
1	1	ENSG00000178401	DNAJC22	0.0039
1	1	ENSG00000265179	Lnc-YES1-8	0.0038
1	1	ENSG00000258859	LINC02296	0.0038
1	1	ENSG00000242159	ABCF2P1	0.0037
1	1	ENSG00000260658	Lnc-CDH8-10	0.0036
1	1	ENSG00000174576	NPAS4	0.0035
1	1	ENSG00000279952	None	0.0034
1	1	ENSG00000223553	SMPD4P1	0.0032
1	1	ENSG00000273214	Lnc-POLR2F-1	0.0028
1	1	ENSG00000183090	FREM3	0.0024
1	1	ENSG00000176697	BDNF	0.0023
2	1	ENSG00000146469	VIP	0.3590
2	1	ENSG00000156076	WIF1	0.1171
2	1	ENSG00000117594	HSD11B1	0.0436
2	1	ENSG00000254561	None	0.0377
2	1	ENSG00000117322	CR2	0.0303
2	1	ENSG00000205634	LINC00898	0.0265
2	1	ENSG00000228999	LINC01830	0.0214
2	1	ENSG00000287593	Antisense to ADTRP	0.0131
2	1	ENSG00000126545	CSN1S1	0.0067
2	1	ENSG00000286016	None	0.0066
2	1	ENSG00000227582	ADGRF5P1	0.0064
2	1	ENSG00000286810	None	0.0062
2	1	ENSG00000285561	None	0.0049
2	1	ENSG00000107165	TYRP1	0.0036
2	1	ENSG00000122012	SV2C	0.0022
2	1	ENSG00000286109	Lnc-KCNK1-1	0.0019
2	1	ENSG00000250634	LINC01182	0.0017
2	1	ENSG00000120875	DUSP4	0.0015
2	1	ENSG00000271538	LINC02427	0.0006
2	1	ENSG00000243323	PTPRVP	0.0004
2	1	ENSG00000234665	LERFS	0.0002

Table A38. KCL BrainBank Case-Control SHAP values under each scenario, for each cluster. Scenario 1 refers to all shared genes in the KCL BrainBank case-derived signatures. Scenario 2 removes multicollinearity from the gene signatures.

Scenario	Cluster	Ensembl ID	Gene Symbol	SHAP Importance
1	1	ENSG00000170290	SLN	0.0600
1	1	ENSG00000261325	LINC02192	0.0336
1	1	ENSG00000261757	miR-1255	0.0321
1	1	ENSG00000225493	LINC01107	0.0311
1	1	ENSG00000226405	HSD17B12 Pseudogene	0.0290
1	1	ENSG00000285578	Lnc-DUSP22-2	0.0285
1	1	ENSG00000200959	SNORA74A	0.0251
1	1	ENSG00000131885	KRT17P1	0.0243
1	1	ENSG00000160221	GATD3	0.0230
1	1	ENSG00000218772	FAM8A6P	0.0224
1	1	ENSG00000277918	RNVU1-28	0.0213
1	1	ENSG00000227723	Lnc-MYB-5	0.0206
1	1	ENSG00000100362	PVALB	0.0191
1	1	ENSG00000254363	LOC101929719	0.0191
1	1	ENSG00000152595	MEPE	0.0190
1	1	ENSG00000225280	LOC105372558	0.0186
1	1	ENSG00000285735	LINC02717	0.0183
1	1	ENSG00000128564	VGF	0.0178
1	1	ENSG00000185149	NPY2R	0.0158
1	1	ENSG00000132744	ACY3	0.0155
1	1	ENSG00000231824	AKAIN1	0.0151
1	1	ENSG00000120875	DUSP4	0.0146
1	1	ENSG00000117322	CR2	0.0146
1	1	ENSG00000188729	OSTN	0.0141
1	1	ENSG00000286292	None	0.0137
1	1	ENSG00000260658	Lnc-CDH8-10	0.0117
1	1	ENSG00000202048	SNORD114-20	0.0117
1	1	ENSG00000147571	CRH	0.0116
1	1	ENSG00000237390	Lnc-RHBG-1	0.0115
1	1	ENSG00000205279	CTXN3	0.0112
1	1	ENSG00000265179	Lnc-YES1-8	0.0106
1	1	ENSG00000174576	NPAS4	0.0100
1	1	ENSG00000174899	SLC66A1L	0.0097
1	1	ENSG00000157005	SST	0.0097
1	1	ENSG00000132677	RHBG	0.0097
1	1	ENSG00000183090	FREM3	0.0093
1	1	ENSG00000179477	ALOX12B	0.0091
1	1	ENSG00000256971	LINC00508	0.0088
1	1	ENSG00000223930	Lnc-ZMAT3-3	0.0083
1	1	ENSG00000268297	CLEC4GP1	0.0083
1	1	ENSG00000126545	CSN1S1	0.0081
1	1	ENSG00000146469	VIP	0.0079
1	1	ENSG00000075673	ATP12A	0.0079
1	1	ENSG00000216753	HMGA1P7	0.0076
1	1	ENSG00000273214	Lnc-POLR2F-1	0.0068
1	1	ENSG00000254510	Lnc-NPAS4-1	0.0065
1	1	ENSG00000287593	Antisense to ADTRP	0.0065
1	1	ENSG00000130701	RBBP8NL	0.0063
1	1	ENSG00000286063	None	0.0057
1	1	ENSG00000229722	Lnc-SGK1-3	0.0056
1	1	ENSG00000287907	None	0.0053
1	1	ENSG00000254681	PKD1P5	0.0051
1	1	ENSG00000236714	LINC01844	0.0048
1	1	ENSG00000234665	LERFS	0.0045
1	1	ENSG00000255087	LOC101929473	0.0042

1	1	ENSG00000276462	LINC03025	0.0042
1	1	ENSG00000279875	None	0.0041
1	1	ENSG00000287844	None	0.0040
1	1	ENSG00000241945	PWP2	0.0039
1	1	ENSG00000243323	PTPRVP	0.0038
1	1	ENSG00000274330	ADAM20 Pseudogene	0.0037
1	1	ENSG00000104938	CLEC4M	0.0035
1	1	ENSG00000164326	CARTPT	0.0033
1	1	ENSG00000186081	KRT5	0.0033
1	1	ENSG00000233123	LINC01007	0.0032
1	1	ENSG00000228772	Lnc-PRL-3	0.0031
1	1	ENSG00000006128	TAC1	0.0031
1	1	ENSG00000227582	ADGRF5P1	0.0026
1	1	ENSG00000141433	ADCYAP1	0.0020
1	1	ENSG00000150175	FRMPD2B	0.0017
1	1	ENSG00000228999	LINC01830	0.0011
2	1	ENSG00000170290	SLN	0.1289
2	1	ENSG00000225493	LINC01107	0.0494
2	1	ENSG00000131885	KRT17P1	0.0466
2	1	ENSG00000227723	Lnc-MYB-5	0.0449
2	1	ENSG00000261757	miR-1255	0.0445
2	1	ENSG00000261325	LINC02192	0.0424
2	1	ENSG00000160221	GATD3	0.0346
2	1	ENSG00000285578	Lnc-DUSP22-2	0.0304
2	1	ENSG00000128564	VGF	0.0293
2	1	ENSG00000075673	ATP12A	0.0289
2	1	ENSG00000200959	SNORA74A	0.0263
2	1	ENSG00000277918	RNVU1-28	0.0242
2	1	ENSG00000231824	AKAIN1	0.0213
2	1	ENSG00000185149	NPY2R	0.0209
2	1	ENSG00000164326	CARTPT	0.0190
2	1	ENSG00000276462	LINC03025	0.0179
2	1	ENSG00000256971	LINC00508	0.0152
2	1	ENSG00000179477	ALOX12B	0.0147
2	1	ENSG00000132744	ACY3	0.0142
2	1	ENSG00000287593	Antisense to ADTRP	0.0138
2	1	ENSG00000268297	CLEC4GP1	0.0133
2	1	ENSG00000216753	HMGA1P7	0.0128
2	1	ENSG00000228999	LINC01830	0.0119
2	1	ENSG00000228772	Lnc-PRL-3	0.0107
2	1	ENSG00000254681	PKD1P5	0.0104
2	1	ENSG00000234665	LERFS	0.0101
2	1	ENSG00000254363	LOC101929719	0.0096
2	1	ENSG00000104938	CLEC4M	0.0091
2	1	ENSG00000120875	DUSP4	0.0077
2	1	ENSG00000286292	None	0.0076
2	1	ENSG00000130701	RBBP8NL	0.0074
2	1	ENSG00000225280	LOC105372558	0.0073
2	1	ENSG00000202048	SNORD114-20	0.0068
2	1	ENSG00000279875	None	0.0064
2	1	ENSG00000287907	None	0.0061
2	1	ENSG00000183090	FREM3	0.0050
2	1	ENSG00000174576	NPAS4	0.0049
2	1	ENSG00000273214	Lnc-POLR2F-1	0.0047
2	1	ENSG00000241945	PWP2	0.0045
2	1	ENSG00000286063	None	0.0038
2	1	ENSG00000152595	MEPE	0.0035
2	1	ENSG00000227582	ADGRF5P1	0.0034

2	1	ENSG00000265179	Lnc-YES1-8	0.0029
2	1	ENSG00000260658	Lnc-CDH8-10	0.0017
2	1	ENSG00000285735	LINC02717	0.0016
2	1	ENSG00000132677	RHBG	0.0014
2	1	ENSG00000223930	Lnc-ZMAT3-3	0.0010
1	2	ENSG00000135245	HILPDA	0.0106
1	2	ENSG00000159167	STC1	0.0104
1	2	ENSG00000167772	ANGPTL4	0.0076
1	2	ENSG00000141574	SECTM1	0.0073
1	2	ENSG00000148926	ADM	0.0072
1	2	ENSG00000166592	RRAD	0.0065
1	2	ENSG00000163638	ADAMTS9	0.0063
1	2	ENSG00000186431	FCAR	0.0054
1	2	ENSG00000187634	SAMD11	0.0052
1	2	ENSG00000163395	IGFN1	0.0044
1	2	ENSG00000285938	BCL6-AS1	0.0044
1	2	ENSG00000253686	LINC01484	0.0039
1	2	ENSG00000103710	RASL12	0.0039
1	2	ENSG00000112299	VNN1	0.0039
1	2	ENSG00000077238	IL4R	0.0037
1	2	ENSG00000250863	Lnc-KCTD8-1	0.0036
1	2	ENSG00000258647	LINC00930	0.0036
1	2	ENSG00000144837	PLA1A	0.0034
1	2	ENSG00000100060	MFNG	0.0034
1	2	ENSG00000169894	MUC3A	0.0034
1	2	ENSG00000235750	KIAA0040	0.0034
1	2	ENSG00000260337	Lnc-FAM174B-1	0.0034
1	2	ENSG00000120708	TGFBI	0.0034
1	2	ENSG00000160111	CPAMD8	0.0034
1	2	ENSG00000124762	CDKN1A	0.0034
1	2	ENSG00000125810	CD93	0.0033
1	2	ENSG00000020633	RUNX3	0.0033
1	2	ENSG00000115607	IL18RAP	0.0033
1	2	ENSG00000143546	S100A8	0.0031
1	2	ENSG00000118729	CASQ2	0.0031
1	2	ENSG00000258676	Lnc-ST8SIA2-1	0.0031
1	2	ENSG00000185201	IFITM2	0.0031
1	2	ENSG00000196154	S100A4	0.0031
1	2	ENSG00000175591	P2RY2	0.0031
1	2	ENSG00000125731	SH2D3A	0.0029
1	2	ENSG00000115604	IL18R1	0.0029
1	2	ENSG00000229926	IL9RP1	0.0029
1	2	ENSG00000232803	SLCO4A1-AS1	0.0028
1	2	ENSG00000138722	MMRN1	0.0026
1	2	ENSG00000060138	YBX3	0.0026
1	2	ENSG00000115590	IL1R2	0.0024
1	2	ENSG00000177464	GPR4	0.0024
1	2	ENSG00000281327	LINC01338	0.0024
1	2	ENSG00000241158	ADAMTS9-AS1	0.0024
1	2	ENSG00000196616	ADH1B	0.0024
1	2	ENSG00000205592	MUC19	0.0024
1	2	ENSG00000163736	PPBP	0.0023
1	2	ENSG00000163220	S100A9	0.0023
1	2	ENSG00000262003	LOC101927727	0.0023
1	2	ENSG00000124253	PCK1	0.0023
1	2	ENSG00000173597	SULT1B1	0.0023
1	2	ENSG00000236908	LINC02827	0.0021
1	2	ENSG00000105641	SLC5A5	0.0021
1	2	ENSG00000267065	LINC02080	0.0021
1	2	ENSG00000112303	VNN2	0.0021

1	2	ENSG00000090339	ICAM1	0.0021
1	2	ENSG00000100985	MMP9	0.0020
1	2	ENSG00000152049	KCNE4	0.0020
1	2	ENSG00000182885	ADGRG3	0.0020
1	2	ENSG00000251493	FOXD1	0.0020
1	2	ENSG00000148604	RGR	0.0020
1	2	ENSG00000174226	SNX31	0.0020
1	2	ENSG00000070729	CNGB1	0.0018
1	2	ENSG00000112175	BMP5	0.0018
1	2	ENSG00000128016	ZFP36	0.0018
1	2	ENSG00000100336	APOL4	0.0018
1	2	ENSG00000205358	MT1H	0.0018
1	2	ENSG00000099994	SUSD2	0.0018
1	2	ENSG00000272512	Lnc-HES4-2	0.0018
1	2	ENSG00000013588	GPRC5A	0.0016
1	2	ENSG00000159212	CLIC6	0.0016
1	2	ENSG00000149596	JPH2	0.0016
1	2	ENSG00000166523	CLEC4E	0.0016
1	2	ENSG00000184557	SOCS3	0.0016
1	2	ENSG00000179023	KLHDC7A	0.0016
1	2	ENSG00000162383	SLC1A7	0.0016
1	2	ENSG00000270640	Lnc-BABAM2-2	0.0016
1	2	ENSG00000106366	SERPINE1	0.0016
1	2	ENSG00000169429	CXCL8	0.0015
1	2	ENSG00000230122	ECEL1P3	0.0015
1	2	ENSG00000184058	TBX1	0.0015
1	2	ENSG00000112936	C7	0.0015
1	2	ENSG00000249307	LINC01088	0.0015
1	2	ENSG00000128274	A4GALT	0.0015
1	2	ENSG00000162747	FCGR3B	0.0015
1	2	ENSG00000108823	SGCA	0.0013
1	2	ENSG00000129654	FOXJ1	0.0013
1	2	ENSG00000171049	FPR2	0.0013
1	2	ENSG00000278130	FAM166A Pseudogene	0.0013
1	2	ENSG00000167244	IGF2	0.0013
1	2	ENSG00000173110	HSPA6	0.0013
1	2	ENSG00000160183	TMPRSS3	0.0013
1	2	ENSG00000004939	SLC4A1	0.0013
1	2	ENSG00000256955	Lnc-MMP17-1	0.0013
1	2	ENSG00000015520	NPC1L1	0.0013
1	2	ENSG00000142973	CYP4B1	0.0013
1	2	ENSG00000229380	PRKAR1B-AS2	0.0013
1	2	ENSG00000125430	HS3ST3B1	0.0011
1	2	ENSG00000124107	SLPI	0.0011
1	2	ENSG00000287652	Antisense to DGCR8 and CDC45	0.0011
1	2	ENSG00000110852	CLEC2B	0.0011
1	2	ENSG00000261170	LOC107984827	0.0011
1	2	ENSG00000118271	TTR	0.0010
1	2	ENSG00000111057	KRT18	0.0010
1	2	ENSG00000115648	MLPH	0.0010
1	2	ENSG00000170345	FOS	0.0010
1	2	ENSG00000163464	CXCR1	0.0010
1	2	ENSG00000196954	CASP4	0.0010
1	2	ENSG00000188536	HBA2	0.0010
1	2	ENSG00000198848	CES1	0.0010
1	2	ENSG00000287338	Lnc-TLR5-1	0.0008
1	2	ENSG00000281732	LOC284933	0.0008
1	2	ENSG00000115602	IL1RL1	0.0008

1	2	ENSG00000074219	TEAD2	0.0008
1	2	ENSG00000163623	NKX6-1	0.0008
1	2	ENSG00000108821	COL1A1	0.0008
1	2	ENSG00000109758	HGFAC	0.0008
1	2	ENSG00000267304	Lnc-TJP3-2	0.0008
1	2	ENSG00000047457	CP	0.0008
1	2	ENSG00000149573	MPZL2	0.0008
1	2	ENSG00000163739	CXCL1	0.0007
1	2	ENSG00000162692	VCAM1	0.0007
1	2	ENSG00000050327	ARHGEF5	0.0007
1	2	ENSG00000228133	LOC105371485	0.0007
1	2	ENSG00000175084	DES	0.0007
1	2	ENSG00000088882	CPXM1	0.0007
1	2	ENSG00000226390	KCNQ2-AS1	0.0005
1	2	ENSG00000176692	FOXC2	0.0005
1	2	ENSG00000279821	None	0.0005
1	2	ENSG00000237424	FOXD2-AS1	0.0005
1	2	ENSG00000254362	Lnc-PPP2R2A-2	0.0005
1	2	ENSG00000143867	OSR1	0.0005
1	2	ENSG00000140839	CLEC18B	0.0005
1	2	ENSG00000177575	CD163	0.0005
1	2	ENSG00000249669	CARMN	0.0003
1	2	ENSG00000276317	Lnc-GATA5-10	0.0003
1	2	ENSG00000186564	FOXD2	0.0003
1	2	ENSG00000276412	Lnc-CNTNAP3B-13	0.0003
1	2	ENSG00000149452	SLC22A8	0.0003
1	2	ENSG00000287689	None	0.0003
1	2	ENSG00000171345	KRT19	0.0003
1	2	ENSG00000262152	GREP1	0.0002
1	2	ENSG00000168079	SCARA5	0.0002
1	2	ENSG00000115594	IL1R1	0.0002
1	2	ENSG00000173530	TNFRSF10D	0.0002
1	2	ENSG00000173421	IHO1	0.0002
2	2	ENSG00000167772	ANGPTL4	0.1156
2	2	ENSG00000148926	ADM	0.0540
2	2	ENSG00000159167	STC1	0.0462
2	2	ENSG00000267065	LINC02080	0.0093
2	2	ENSG00000174226	SNX31	0.0091
2	2	ENSG00000250863	Lnc-KCTD8-1	0.0047
2	2	ENSG00000109758	HGFAC	0.0026
2	2	ENSG00000205592	MUC19	0.0007
2	2	ENSG00000149452	SLC22A8	0.0007
2	2	ENSG00000186564	FOXD2	0.0005
2	2	ENSG00000099994	SUSD2	0.0002
1	3	ENSG00000273259	Thioesterase	0.1406
1	3	ENSG00000005844	ITGAL	0.0435
1	3	ENSG00000131401	NAPSB	0.0312
1	3	ENSG00000265531	FCGR1CP	0.0301
1	3	ENSG00000244731	C4A	0.0285
1	3	ENSG00000073737	DHRS9	0.0111
1	3	ENSG00000172243	CLEC7A	0.0108
1	3	ENSG00000128262	POM121L9P	0.0090
1	3	ENSG00000231131	LNCAROD	0.0050
1	3	ENSG00000254081	LINC01299	0.0037
1	3	ENSG00000115523	GNLY	0.0034
1	3	ENSG00000070190	DAPP1	0.0030
1	3	ENSG00000125735	TNFSF14	0.0027
1	3	ENSG00000261795	Lnc-PDGFA-4	0.0025
1	3	ENSG00000198774	RASSF9	0.0023

1	3	ENSG00000179420	OR6W1P	0.0023
1	3	ENSG00000287939	None	0.0020
1	3	ENSG00000254415	SIGLEC14	0.0020
1	3	ENSG00000270547	LINC01235	0.0019
1	3	ENSG00000283787	PRR33	0.0017
1	3	ENSG00000122585	NPY	0.0017
1	3	ENSG00000229391	HLA-DRB6	0.0017
1	3	ENSG00000236700	LINC01010	0.0011
1	3	ENSG00000128652	HOXD3	0.0010
1	3	ENSG00000272808	GCAWKR	0.0010
1	3	ENSG00000250215	CIR1P2	0.0007
1	3	ENSG00000260922	Antisense to ADAMTS18	0.0006
1	3	ENSG00000187908	DMBT1	0.0005
1	3	ENSG00000267287	Lnc-NFATC1-1	0.0004
1	3	ENSG00000124915	MYRF-AS1	0.0003
1	3	ENSG00000261997	None	0.0001
2	3	ENSG00000244731	C4A	0.3211
2	3	ENSG00000273259	Thioesterase	0.1712
2	3	ENSG00000198774	RASSF9	0.0018

Table A39. TargetALS Case-Control SHAP values under each scenario, for each cluster. Scenario 1 refers to all shared genes in the KCL BrainBank case-derived signatures. Scenario 2 removes multicollinearity from the gene signatures.

Scenario	Cluster	Ensembl ID	Gene Symbol	SHAP Importance
1	1	ENSG00000239672	NME1	0.484219
1	1	ENSG00000138678	GPAT3	0.000331
1	1	ENSG00000236714	LINC01844	0.000112
1	1	ENSG00000111863	ADTRP	0.000082
1	1	ENSG00000178401	DNAJC22	0.000034
1	1	ENSG00000147571	CRH	0.000019
1	1	ENSG00000169676	DRD5	0.000012
1	1	ENSG00000160221	GATD3	0.000010
1	1	ENSG00000205279	CTXN3	0.000006
1	1	ENSG00000188729	OSTN	0.000004
1	1	ENSG00000117594	HSD11B1	0.000003
1	1	ENSG00000176697	BDNF	0.000003
1	1	ENSG00000132677	RHBG	0.000001
1	1	ENSG00000174576	NPAS4	0.000001
2	1	ENSG00000239672	NME1	0.484133
2	1	ENSG00000138678	GPAT3	0.000488
2	1	ENSG00000236714	LINC01844	0.000082
2	1	ENSG00000111863	ADTRP	0.000044
2	1	ENSG00000178401	DNAJC22	0.000023
2	1	ENSG00000160221	GATD3	0.000016
2	1	ENSG00000147571	CRH	0.000015
2	1	ENSG00000205279	CTXN3	0.000009
2	1	ENSG00000169676	DRD5	0.000009
2	1	ENSG00000188729	OSTN	0.000006
2	1	ENSG00000132677	RHBG	0.000003
2	1	ENSG00000117594	HSD11B1	0.000001
1	2	ENSG00000188511	MIR3667HG	0.037730
1	2	ENSG00000204389	HSPA1A	0.033230
1	2	ENSG00000166523	CLEC4E	0.027560
1	2	ENSG00000182885	ADGRG3	0.026113
1	2	ENSG00000173641	HSPB7	0.024598
1	2	ENSG00000112303	VNN2	0.023829
1	2	ENSG00000137801	THBS1	0.023749
1	2	ENSG00000164692	COL1A2	0.023026
1	2	ENSG00000162692	VCAM1	0.022004
1	2	ENSG00000184557	SOCS3	0.021545
1	2	ENSG00000133392	MYH11	0.020179
1	2	ENSG00000173597	SULT1B1	0.020133
1	2	ENSG00000280109	PLAC4	0.019823
1	2	ENSG00000205364	MT1M	0.019318
1	2	ENSG00000100985	MMP9	0.019249
1	2	ENSG00000124253	PCK1	0.017700
1	2	ENSG00000112299	VNN1	0.017642
1	2	ENSG00000143867	OSR1	0.017573
1	2	ENSG00000144837	PLA1A	0.017206
1	2	ENSG00000196616	ADH1B	0.017160
1	2	ENSG00000142173	COL6A2	0.017068
1	2	ENSG00000163395	IGFN1	0.016816
1	2	ENSG00000135245	HILPDA	0.016793
1	2	ENSG00000183508	TENT5C	0.016368
1	2	ENSG00000110719	TCIRG1	0.016288
1	2	ENSG00000108823	SGCA	0.016058
1	2	ENSG00000112499	SLC22A2	0.015955
1	2	ENSG00000241644	INMT	0.015783
1	2	ENSG00000125144	MT1G	0.015576
1	2	ENSG00000162458	FBLIM1	0.015496
1	2	ENSG00000102802	MEDAG	0.015393

1	2	ENSG00000015520	NPC1L1	0.014681
1	2	ENSG00000205038	PKHD1L1	0.014566
1	2	ENSG00000213719	CLIC1	0.014279
1	2	ENSG00000183888	SRARP	0.014130
1	2	ENSG00000175591	P2RY2	0.013912
1	2	ENSG00000112936	C7	0.013797
1	2	ENSG00000105641	SLC5A5	0.013751
1	2	ENSG00000130635	COL5A1	0.013717
1	2	ENSG00000144810	COL8A1	0.013717
1	2	ENSG00000107438	PDLIM1	0.013108
1	2	ENSG00000103710	RASL12	0.013017
1	2	ENSG00000000971	CFH	0.012798
1	2	ENSG00000182718	ANXA2	0.012730
1	2	ENSG00000112214	FHL5	0.012684
1	2	ENSG00000141052	MYOCD	0.012580
1	2	ENSG00000187513	GJA4	0.012569
1	2	ENSG00000174226	SNX31	0.012523
1	2	ENSG00000177464	GPR4	0.012466
1	2	ENSG00000166482	MFAP4	0.012454
1	2	ENSG00000186431	FCAR	0.012339
1	2	ENSG00000105974	CAV1	0.012305
1	2	ENSG00000163736	PPBP	0.012236
1	2	ENSG00000128016	ZFP36	0.012029
1	2	ENSG00000265107	GJA5	0.011961
1	2	ENSG00000185585	OLFML2A	0.011892
1	2	ENSG00000100060	MFNG	0.011880
1	2	ENSG00000003436	TFPI	0.011846
1	2	ENSG00000160593	JAML	0.011628
1	2	ENSG00000118729	CASQ2	0.011455
1	2	ENSG00000134531	EMP1	0.011203
1	2	ENSG00000167772	ANGPTL4	0.011180
1	2	ENSG00000125810	CD93	0.011008
1	2	ENSG00000115607	IL18RAP	0.010847
1	2	ENSG00000163017	ACTG2	0.010824
1	2	ENSG00000000938	FGR	0.010778
1	2	ENSG00000115594	IL1R1	0.010698
1	2	ENSG00000004939	SLC4A1	0.010686
1	2	ENSG00000117595	IRF6	0.010618
1	2	ENSG00000060138	YBX3	0.010572
1	2	ENSG00000120708	TGFBI	0.010537
1	2	ENSG00000173068	BNC2	0.010491
1	2	ENSG00000130176	CNN1	0.010399
1	2	ENSG00000148604	RGR	0.010308
1	2	ENSG00000122862	SRGN	0.010273
1	2	ENSG00000149257	SERPINH1	0.010262
1	2	ENSG00000145623	OSMR	0.010227
1	2	ENSG00000187498	COL4A1	0.010135
1	2	ENSG00000140682	TGFB1I1	0.009940
1	2	ENSG00000162998	FRZB	0.009929
1	2	ENSG00000169894	MUC3A	0.009871
1	2	ENSG00000163638	ADAMTS9	0.009688
1	2	ENSG00000090339	ICAM1	0.009688
1	2	ENSG00000145779	TNFAIP8	0.009596
1	2	ENSG00000135842	NIBAN1	0.009504
1	2	ENSG00000020633	RUNX3	0.009493
1	2	ENSG00000162383	SLC1A7	0.009298
1	2	ENSG00000125733	TRIP10	0.009240
1	2	ENSG00000088882	CPXM1	0.008999
1	2	ENSG00000176692	FOXC2	0.008953
1	2	ENSG00000156463	SH3RF2	0.008930

1	2	ENSG00000101187	SLCO4A1	0.008781
1	2	ENSG00000168079	SCARA5	0.008747
1	2	ENSG00000101335	MYL9	0.008747
1	2	ENSG00000126778	SIX1	0.008735
1	2	ENSG00000196154	S100A4	0.008678
1	2	ENSG00000174348	PODN	0.008414
1	2	ENSG00000251493	FOXD1	0.008391
1	2	ENSG00000169908	TM4SF1	0.008333
1	2	ENSG00000124212	PTGIS	0.008299
1	2	ENSG00000163464	CXCR1	0.008287
1	2	ENSG00000099994	SUSD2	0.008242
1	2	ENSG00000125731	SH2D3A	0.008184
1	2	ENSG00000106624	AEBP1	0.008173
1	2	ENSG00000154188	ANGPT1	0.008058
1	2	ENSG00000149596	JPH2	0.007955
1	2	ENSG00000159167	STC1	0.007943
1	2	ENSG00000173530	TNFRSF10D	0.007909
1	2	ENSG00000137834	SMAD6	0.007886
1	2	ENSG00000106034	CPED1	0.007805
1	2	ENSG00000176046	NUPR1	0.007782
1	2	ENSG00000128917	DLL4	0.007656
1	2	ENSG00000185885	IFITM1	0.007656
1	2	ENSG00000163739	CXCL1	0.007587
1	2	ENSG00000198959	TGM2	0.007576
1	2	ENSG00000173918	C1QTNF1	0.007541
1	2	ENSG00000165474	GJB2	0.007438
1	2	ENSG00000142973	CYP4B1	0.007369
1	2	ENSG00000185499	MUC1	0.007346
1	2	ENSG00000074047	GLI2	0.007105
1	2	ENSG00000187922	LCN10	0.007048

1	2	ENSG00000197901	SLC22A6	0.007025
1	2	ENSG00000112837	TBX18	0.006910
1	2	ENSG00000124762	CDKN1A	0.006864
1	2	ENSG00000142089	IFITM3	0.006864
1	2	ENSG00000221869	CEBPD	0.006853
1	2	ENSG00000184811	TRARG1	0.006830
1	2	ENSG00000130600	H19	0.006784
1	2	ENSG00000132357	CARD6	0.006589
1	2	ENSG00000244734	HBB	0.006520
1	2	ENSG00000096696	DSP	0.006508
1	2	ENSG00000169429	CXCL8	0.006474
1	2	ENSG00000184058	TBX1	0.006428
1	2	ENSG00000143546	S100A8	0.006428
1	2	ENSG00000170577	SIX2	0.006359
1	2	ENSG00000149573	MPZL2	0.006313
1	2	ENSG00000168542	COL3A1	0.006302
1	2	ENSG00000111057	KRT18	0.006256
1	2	ENSG00000198542	ITGBL1	0.006221
1	2	ENSG00000142102	PGGHG	0.006015
1	2	ENSG00000094963	FMO2	0.005911
1	2	ENSG00000187634	SAMD11	0.005900
1	2	ENSG00000115604	IL18R1	0.005762
1	2	ENSG00000153404	PLEKHG4B	0.005693
1	2	ENSG00000159403	C1R	0.005693
1	2	ENSG00000115648	MLPH	0.005682
1	2	ENSG00000124549	BTN2A3P	0.005406
1	2	ENSG00000128274	A4GALT	0.005406
1	2	ENSG00000110852	CLEC2B	0.005395
1	2	ENSG00000152049	KCNE4	0.005372
1	2	ENSG00000142798	HSPG2	0.005372

1	2	ENSG00000196954	CASP4	0.005337
1	2	ENSG00000129654	FOXJ1	0.005315
1	2	ENSG00000011422	PLAUR	0.005269
1	2	ENSG00000107796	ACTA2	0.005211
1	2	ENSG00000141574	SECTM1	0.005154
1	2	ENSG00000124107	SLPI	0.005096
1	2	ENSG00000050327	ARHGEF5	0.005051
1	2	ENSG00000186150	UBL4B	0.005039
1	2	ENSG00000150048	CLEC1A	0.004901
1	2	ENSG00000047457	CP	0.004832
1	2	ENSG00000136732	GYPC	0.004809
1	2	ENSG00000074219	TEAD2	0.004775
1	2	ENSG00000125430	HS3ST3B1	0.004752
1	2	ENSG00000047617	ANO2	0.004660
1	2	ENSG00000118503	TNFAIP3	0.004637
1	2	ENSG00000108821	COL1A1	0.004637
1	2	ENSG00000117318	ID3	0.004626
1	2	ENSG00000115590	IL1R2	0.004511
1	2	ENSG00000166592	RRAD	0.004442
1	2	ENSG00000161638	ITGA5	0.004350
1	2	ENSG00000109758	HGFAC	0.004281
1	2	ENSG00000013588	GPRC5A	0.004258
1	2	ENSG00000187955	COL14A1	0.004224
1	2	ENSG00000197405	C5AR1	0.004144
1	2	ENSG00000186564	FOXD2	0.004098
1	2	ENSG00000206538	VGLL3	0.004098
1	2	ENSG00000179023	KLHDC7A	0.004029
1	2	ENSG00000175084	DES	0.003994
1	2	ENSG00000122176	FMOD	0.003994
1	2	ENSG00000115602	IL1RL1	0.003983
1	2	ENSG00000177575	CD163	0.003983
1	2	ENSG00000172935	MRGPRF	0.003972
1	2	ENSG00000111341	MGP	0.003949
1	2	ENSG00000185201	IFITM2	0.003822
1	2	ENSG00000027644	INSRR	0.003776
1	2	ENSG00000269113	TRABD2B	0.003765
1	2	ENSG00000149452	SLC22A8	0.003753
1	2	ENSG00000115165	CYTIP	0.003730
1	2	ENSG00000198467	TPM2	0.003719
1	2	ENSG00000137507	LRRC32	0.003696
1	2	ENSG00000171345	KRT19	0.003639
1	2	ENSG00000152779	SLC16A12	0.003627
1	2	ENSG00000163817	SLC6A20	0.003604
1	2	ENSG00000187479	C11orf96	0.003581
1	2	ENSG00000205592	MUC19	0.003478
1	2	ENSG00000164867	NOS3	0.003375
1	2	ENSG00000205358	MT1H	0.003352
1	2	ENSG00000160183	TMPRSS3	0.003202
1	2	ENSG00000100336	APOL4	0.003134
1	2	ENSG00000159212	CLIC6	0.003122
1	2	ENSG00000149591	TAGLN	0.003088
1	2	ENSG00000164707	SLC13A4	0.003042
1	2	ENSG00000077238	IL4R	0.003007
1	2	ENSG00000173421	IHO1	0.002938
1	2	ENSG00000138722	MMRN1	0.002904
1	2	ENSG00000118271	TTR	0.002893
1	2	ENSG00000163220	S100A9	0.002870
1	2	ENSG00000165507	DEPP1	0.002812
1	2	ENSG00000235750	KIAA0040	0.002789
1	2	ENSG00000138061	CYP1B1	0.002755

1	2	ENSG00000151929	BAG3	0.002606
1	2	ENSG00000106366	SERPINE1	0.002537
1	2	ENSG00000152977	ZIC1	0.002502
1	2	ENSG00000160111	CPAMD8	0.002479
1	2	ENSG00000170345	FOS	0.002479
1	2	ENSG00000123374	CDK2	0.002376
1	2	ENSG00000054598	FOXC1	0.002365
1	2	ENSG00000163431	LMOD1	0.002353
1	2	ENSG00000164294	GPX8	0.002238
1	2	ENSG00000171049	FPR2	0.002112
1	2	ENSG00000112175	BMP5	0.001986
1	2	ENSG00000183615	FAM167B	0.001917
1	2	ENSG00000100504	PYGL	0.001825
1	2	ENSG00000028137	TNFRSF1B	0.001814
1	2	ENSG00000168427	KLHL30	0.001756
1	2	ENSG00000131471	AOC3	0.001630
1	2	ENSG00000164761	TNFRSF11B	0.001607
1	2	ENSG00000148926	ADM	0.001423
1	2	ENSG00000168404	MLKL	0.001102
2	2	ENSG00000188511	MIR3667HG	0.043320
2	2	ENSG00000164692	COL1A2	0.041047
2	2	ENSG00000173597	SULT1B1	0.039486
2	2	ENSG00000166523	CLEC4E	0.034929
2	2	ENSG00000173641	HSPB7	0.034504
2	2	ENSG00000183508	TENT5C	0.034412
2	2	ENSG00000204389	HSPA1A	0.032472
2	2	ENSG00000162692	VCAM1	0.030406
2	2	ENSG00000196616	ADH1B	0.028696
2	2	ENSG00000112303	VNN2	0.028099
2	2	ENSG00000162458	FBLIM1	0.027835
2	2	ENSG00000133392	MYH11	0.026515
2	2	ENSG00000124253	PCK1	0.026171
2	2	ENSG00000213719	CLIC1	0.024392
2	2	ENSG00000103710	RASL12	0.022819
2	2	ENSG00000183888	SRARP	0.022371
2	2	ENSG00000144837	PLA1A	0.022348
2	2	ENSG00000125144	MT1G	0.021901
2	2	ENSG00000144810	COL8A1	0.021591
2	2	ENSG00000015520	NPC1L1	0.021247
2	2	ENSG00000163395	IGFN1	0.021097
2	2	ENSG00000105974	CAV1	0.020478
2	2	ENSG00000241644	INMT	0.020328
2	2	ENSG00000169429	CXCL8	0.019984
2	2	ENSG00000134531	EMP1	0.019410
2	2	ENSG00000020633	RUNX3	0.018411
2	2	ENSG00000130635	COL5A1	0.018297
2	2	ENSG00000126778	SIX1	0.018090
2	2	ENSG00000105641	SLC5A5	0.017872
2	2	ENSG00000205038	PKHD1L1	0.017711
2	2	ENSG00000000971	CFH	0.017562
2	2	ENSG00000142173	COL6A2	0.017114
2	2	ENSG00000140682	TGFB1I1	0.017103
2	2	ENSG00000130176	CNN1	0.016977
2	2	ENSG00000141052	MYOCD	0.016942
2	2	ENSG00000145623	OSMR	0.016736
2	2	ENSG00000175591	P2RY2	0.016690
2	2	ENSG00000074047	GLI2	0.016632
2	2	ENSG00000163638	ADAMTS9	0.016403
2	2	ENSG00000177464	GPR4	0.015840
2	2	ENSG00000280109	PLAC4	0.015278

2	2	ENSG00000150048	CLEC1A	0.015197
2	2	ENSG00000149596	JPH2	0.014842
2	2	ENSG00000112936	C7	0.014738
2	2	ENSG00000117595	IRF6	0.014348
2	2	ENSG00000265107	GJA5	0.014291
2	2	ENSG00000197405	C5AR1	0.013900
2	2	ENSG00000162383	SLC1A7	0.013682
2	2	ENSG00000251493	FOXD1	0.013671
2	2	ENSG00000162998	FRZB	0.013476
2	2	ENSG00000159403	C1R	0.013441
2	2	ENSG00000148604	RGR	0.013349
2	2	ENSG00000205364	MT1M	0.013326
2	2	ENSG00000130600	H19	0.013166
2	2	ENSG00000159167	STC1	0.012959
2	2	ENSG00000187513	GJA4	0.012821
2	2	ENSG00000163017	ACTG2	0.012661
2	2	ENSG00000149257	SERPINH1	0.012580
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2	3	ENSG00000236398	TAS2R39	0.018060
2	3	ENSG00000142583	SLC2A5	0.016963
2	3	ENSG00000139629	GALNT6	0.016861
2	3	ENSG00000183196	CHST6	0.016081
2	3	ENSG00000129450	SIGLEC9	0.015321
2	3	ENSG00000073737	DHRS9	0.015017
2	3	ENSG00000172005	MAL	0.014901
2	3	ENSG00000173369	C1QB	0.014786
2	3	ENSG00000166091	CMTM5	0.014603
2	3	ENSG00000196136	SERPINA3	0.014592
2	3	ENSG00000129757	CDKN1C	0.014577
2	3	ENSG00000110079	MS4A4A	0.014229
2	3	ENSG00000183760	ACP7	0.013745
2	3	ENSG00000134817	APLNR	0.013617
2	3	ENSG00000126266	FFAR1	0.013343
2	3	ENSG00000127412	TRPV5	0.013316

2	3	ENSG00000064886	CHI3L2	0.013099
2	3	ENSG00000172243	CLEC7A	0.013094
2	3	ENSG00000185905	C16orf54	0.012916
2	3	ENSG00000179420	OR6W1P	0.012738
2	3	ENSG00000171631	P2RY6	0.012193
2	3	ENSG00000131747	TOP2A	0.011871
2	3	ENSG00000132854	KANK4	0.011831
2	3	ENSG00000204655	MOG	0.011796
2	3	ENSG00000140968	IRF8	0.011456
2	3	ENSG00000176381	PRR18	0.011431
2	3	ENSG00000108691	CCL2	0.011160
2	3	ENSG00000221887	HMSD	0.010678
2	3	ENSG00000090382	LYZ	0.010667
2	3	ENSG00000158865	SLC5A11	0.010517
2	3	ENSG00000128645	HOXD1	0.010463
2	3	ENSG00000025708	TYMP	0.010398
2	3	ENSG00000185811	IKZF1	0.010100
2	3	ENSG00000130300	PLVAP	0.009862
2	3	ENSG00000105967	TFEC	0.009819
2	3	ENSG00000010327	STAB1	0.009764
2	3	ENSG00000251429	AIDAP2	0.008936
2	3	ENSG00000125735	TNFSF14	0.008839
2	3	ENSG00000197430	OPALIN	0.008822
2	3	ENSG00000166927	MS4A7	0.008767
2	3	ENSG00000225781	OR6V1	0.008634
2	3	ENSG00000140873	ADAMTS18	0.008371
2	3	ENSG00000179468	OR9A2	0.008351
2	3	ENSG00000180739	S1PR5	0.007086
2	3	ENSG00000150656	CNDP1	0.007024
2	3	ENSG00000173372	C1QA	0.006814
2	3	ENSG00000101049	SGK2	0.006754
2	3	ENSG00000038945	MSR1	0.006727
2	3	ENSG00000174837	ADGRE1	0.006726
2	3	ENSG00000197249	SERPINA1	0.006623
2	3	ENSG00000187908	DMBT1	0.006608
2	3	ENSG00000006747	SCIN	0.006294
2	3	ENSG00000157227	MMP14	0.006226
2	3	ENSG00000105122	RASAL3	0.006202
2	3	ENSG00000148773	MKI67	0.006193
2	3	ENSG00000026508	CD44	0.006003
2	3	ENSG00000090104	RGS1	0.005966
2	3	ENSG00000101670	LIPG	0.005717
2	3	ENSG00000137752	CASP1	0.005704
2	3	ENSG00000160223	ICOSLG	0.005695
2	3	ENSG00000175785	PRIMA1	0.005673
2	3	ENSG00000108798	ABI3	0.005503
2	3	ENSG00000103089	FA2H	0.005374
2	3	ENSG00000213186	TRIM59	0.005181
2	3	ENSG00000162511	LAPTM5	0.005143
2	3	ENSG00000126860	EVI2A	0.005017
2	3	ENSG00000018280	SLC11A1	0.004972
2	3	ENSG00000041982	TNC	0.004963
2	3	ENSG00000275713	H2BC9	0.004927
2	3	ENSG00000268758	ADGRE4P	0.004900
2	3	ENSG00000171860	C3AR1	0.004898
2	3	ENSG00000233828	MIR4280HG	0.004877
2	3	ENSG00000133321	PLAAT4	0.004837
2	3	ENSG00000169413	RNASE6	0.004812
2	3	ENSG00000158715	SLC45A3	0.004710
2	3	ENSG00000104972	LILRB1	0.004657

2	3	ENSG00000154864	PIEZO2	0.004563
2	3	ENSG00000197471	SPN	0.004538
2	3	ENSG00000221937	TAS2R40	0.004536
2	3	ENSG00000186417	GLDN	0.004518
2	3	ENSG00000081479	LRP2	0.004229
2	3	ENSG00000139292	LGR5	0.003801
2	3	ENSG00000164342	TLR3	0.003656
2	3	ENSG00000170775	GPR37	0.003562
2	3	ENSG00000286522	H3C2	0.003537
2	3	ENSG00000134061	CD180	0.003520
2	3	ENSG00000175489	LRRC25	0.003509
2	3	ENSG00000128283	CDC42EP1	0.003484
2	3	ENSG00000105697	HAMP	0.003393
2	3	ENSG00000104974	LILRA1	0.003388
2	3	ENSG00000159216	RUNX1	0.003207
2	3	ENSG00000282608	ADORA3	0.003077
2	3	ENSG00000204472	AIF1	0.003051
2	3	ENSG00000167208	SNX20	0.002941
2	3	ENSG00000275395	FCGBP	0.002849
2	3	ENSG00000095970	TREM2	0.002546
2	3	ENSG00000166928	MS4A14	0.002540
2	3	ENSG00000114013	CD86	0.002510
2	3	ENSG00000167588	GPD1	0.002439
2	3	ENSG00000277494	GPIHBP1	0.002355
2	3	ENSG00000118785	SPP1	0.002335
2	3	ENSG00000013297	CLDN11	0.002240
2	3	ENSG00000117228	GBP1	0.002201
2	3	ENSG00000066294	CD84	0.002201
2	3	ENSG00000159189	C1QC	0.002175
2	3	ENSG00000172548	NIPAL4	0.002071
2	3	ENSG00000271605	MILR1	0.002017
2	3	ENSG00000162949	CAPN13	0.001996
2	3	ENSG00000116774	OLFML3	0.001866
2	3	ENSG00000173253	DMRT2	0.001824
2	3	ENSG00000127507	ADGRE2	0.001815
2	3	ENSG00000163823	CCR1	0.001778
2	3	ENSG00000136867	SLC31A2	0.001714
2	3	ENSG00000110934	BIN2	0.001664
2	3	ENSG00000131401	NAPSB	0.001614
2	3	ENSG00000184574	LPAR5	0.001588
2	3	ENSG00000129810	SGO1	0.001543
2	3	ENSG00000142512	SIGLEC10	0.001487
2	3	ENSG00000158869	FCER1G	0.001305
2	3	ENSG00000165025	SYK	0.001250
2	3	ENSG00000100368	CSF2RB	0.001160
2	3	ENSG00000129465	RIPK3	0.001084
2	3	ENSG00000122367	LDB3	0.001075
2	3	ENSG00000132702	HAPLN2	0.000947
2	3	ENSG00000137869	CYP19A1	0.000921
2	3	ENSG00000270547	LINC01235	0.000807
2	3	ENSG00000100292	HMOX1	0.000792
2	3	ENSG00000197993	KEL	0.000731
2	3	ENSG00000229140	CCDC26	0.000731
2	3	ENSG00000012223	LTF	0.000630
2	3	ENSG00000179178	TMEM125	0.000611
2	3	ENSG00000011426	ANLN	0.000605
2	3	ENSG00000006042	TMEM98	0.000563
2	3	ENSG00000158714	SLAMF8	0.000537
2	3	ENSG00000228789	HCG22	0.000407
2	3	ENSG00000168329	CX3CR1	0.000256

2	3	ENSG00000167641	PPP1R14A	0.000256

Table A40. van Rheenen Case-Control SHAP values under each scenario, for each cluster. Scenario 1 refers to all shared genes in the KCL BrainBank case-derived signatures. Scenario 2 removes multicollinearity from the gene signatures.

Dataset (McFadden Pseudo R^2)	**Ensembl ID**	**Gene Symbol**	**Cluster**	**Total Dominance**	**Percentage Relative Importance**
KCL BrainBank (R^2 : 0.788)	ENSG00000117318	*ID3*	2	0.0906	11.495
	ENSG00000026508	*CD44*	3	0.0895	11.362
	ENSG00000010327	*STAB1*	3	0.0711	9.018
	ENSG00000135842	*NIBAN1*	2	0.0674	8.552
	ENSG00000047457	*CP*	2	0.0645	8.181
	ENSG00000187955	*COL14A1*	2	0.0586	7.438
	ENSG00000161638	*ITGA5*	2	0.0541	6.864
	ENSG00000151929	*BAG3*	2	0.0477	6.059
	ENSG00000028137	*TNFRSF1B*	2	0.0438	5.556
	ENSG00000125810	*CD93*	2	0.0411	5.217
	ENSG00000105281	*SLC1A5*	3	0.0385	4.881
	ENSG00000177575	*CD163*	2	0.0358	4.545
	ENSG00000164692	*COL1A2*	2	0.0342	4.344
	ENSG00000158714	*SLAMF8*	3	0.0280	3.557
	ENSG00000174837	*ADGRE1*	3	0.0231	2.931
TargetALS (R^2 : 0.642)	ENSG00000249307	*LINC01088*	2	0.1142	17.783
	ENSG00000152049	*KCNE4*	2	0.0583	9.088
	ENSG00000026508	*CD44*	3	0.0560	8.716
	ENSG00000187634	*SAMD11*	2	0.0542	8.442
	ENSG00000160111	*CPAMD8*	2	0.0481	7.493
	ENSG00000188488	*SERPINA5*	3	0.0435	6.769
	ENSG00000244682	*FCGR2C*	3	0.0412	6.411
	ENSG00000047457	*CP*	2	0.0375	5.845
	ENSG00000149596	*JPH2*	2	0.0336	5.231
	ENSG00000240583	*AQP1*	3	0.0319	4.974
	ENSG00000115590	*IL1R2*	2	0.0291	4.533
	ENSG00000196136	*SERPINA3*	3	0.0285	4.436
	ENSG00000273259	*Thioesterase*	3	0.0240	3.741
	ENSG00000064886	*CHI3L2*	3	0.0221	3.437
	ENSG00000125735	*TNFSF14*	3	0.0199	3.102
van Rheenen (R^2 : 0.339)	ENSG00000074219	*TEAD2*	2	0.0848	24.995
	ENSG00000110719	*TCIRG1*	2	0.0500	14.738
	ENSG00000174125	*TLR1*	3	0.0321	9.455
	ENSG00000105122	*RASAL3*	3	0.0285	8.400
	ENSG00000101187	*SLCO4A1*	2	0.0233	6.885
	ENSG00000100504	*PYGL*	2	0.0193	5.701
	ENSG00000170345	*FOS*	2	0.0163	4.798
	ENSG00000185885	*IFITM1*	2	0.0159	4.679
	ENSG00000012124	*CD22*	3	0.0122	3.600
	ENSG00000225217	*HSPA7*	3	0.0102	3.002
	ENSG00000112799	*LY86*	3	0.0102	3.001
	ENSG00000107438	*PDLIM1*	2	0.0102	3.001
	ENSG00000118503	*TNFAIP3*	2	0.0098	2.878
	ENSG00000118271	*TTR*	2	0.0092	2.713

	ENSG00000187955	*COL14A1*	2	0.0073	2.153

Table A41. Results of dominance analysis for Cluster 1 vs Clusters 2 and 3. The top 15 predictors were obtained from each dataset, or fewer if there were not at least 15 dominant genes identified. For each dataset, the McFadden's Pseudo R^2 is shown, which is the proportion of variance in the model explained by these predictor genes, with a value of 0.2-0.4 indicating good model fit, and values beyond indicating excellent model fit. For each gene identified as a key predictor, their original cluster assignment is shown, along with their total dominance, which summarises the contributions of each predictor to all of the combinatory models, and percentage relative dominance, which describes the relative importance of each predictor.

Dataset (McFadden Pseudo R^2)	**Ensembl ID**	**Gene Symbol**	**Cluster**	**Total Dominance**	**Percentage Relative Importance**
KCL BrainBank (R^2 : 0.888)	ENSG00000161638	*ITGA5*	2	0.1395	16.623
	ENSG00000107796	*ACTA2*	2	0.0815	9.717
	ENSG00000206538	*VGLL3*	2	0.0793	9.456
	ENSG00000112499	*SLC22A2*	2	0.0774	9.222
	ENSG00000168542	*COL3A1*	2	0.0625	7.447
	ENSG00000175084	*DES*	2	0.0575	6.858
	ENSG00000149591	*TAGLN*	2	0.0506	6.031
	ENSG00000108821	*COL1A1*	2	0.0504	6.008
	ENSG00000163017	*ACTG2*	2	0.0427	5.086
	ENSG00000101335	*MYL9*	2	0.0419	4.993
	ENSG00000187955	*COL14A1*	2	0.0408	4.862
	ENSG00000131471	*AOC3*	2	0.0391	4.660
	ENSG00000133392	*MYH11*	2	0.0382	4.551
	ENSG00000164692	*COL1A2*	2	0.0376	4.486
TargetALS (R^2 : 0.693)	ENSG00000166523	*CLEC4E*	2	0.0867	12.505
	ENSG00000112499	*SLC22A2*	2	0.0829	11.950
	ENSG00000163017	*ACTG2*	2	0.0782	11.283
	ENSG00000184058	*TBX1*	2	0.0777	11.201
	ENSG00000229926	*IL9RP1*	2	0.0462	6.670
	ENSG00000109758	*HGFAC*	2	0.0396	5.706
	ENSG00000115590	*IL1R2*	2	0.0391	5.643
	ENSG00000278130	*FAM166A Pseudogene*	2	0.0365	5.268
	ENSG00000170577	*SIX2*	2	0.0338	4.878
	ENSG00000258676	*Lnc-ST8SIA2-1*	2	0.0332	4.792
	ENSG00000226390	*KCNQ2-AS1*	2	0.0329	4.743
	ENSG00000173421	*IHO1*	2	0.0317	4.573
	ENSG00000279821	None	2	0.0304	4.389
	ENSG00000015520	*NPC1L1*	2	0.0266	3.837
	ENSG00000187922	*LCN10*	2	0.0178	2.561
van Rheenen (R^2 : 0.375)	ENSG00000133321	*PLAAT4*	3	0.0632	16.868
	ENSG00000166927	*MS4A7*	3	0.0410	10.957
	ENSG00000101335	*MYL9*	2	0.0365	9.746
	ENSG00000187955	*COL14A1*	2	0.0327	8.726
	ENSG00000163565	*IFI16*	3	0.0286	7.647
	ENSG00000096696	*DSP*	2	0.0268	7.142
	ENSG00000166923	*GREM1*	3	0.0234	6.237
	ENSG00000118271	*TTR*	2	0.0209	5.581
	ENSG00000128652	*HOXD3*	3	0.0181	4.825
	ENSG00000160221	*GATD3A*	1	0.0172	4.583
	ENSG00000101187	*SLCO4A1*	2	0.0171	4.572
	ENSG00000161638	*ITGA5*	2	0.0166	4.426
	ENSG00000225217	*HSPA7*	3	0.0158	4.213

	ENSG00000108823	*SGCA*	2	0.0108	2.875
	ENSG00000074219	*TEAD2*	2	0.0060	1.598

Table A42. Results of dominance analysis for Cluster 2 vs Clusters 1 and 3. The top 15 predictors were obtained from each dataset, or fewer if there were not at least 15 dominant genes identified. For each dataset, the McFadden's Pseudo R^2 is shown, which is the proportion of variance in the model explained by these predictor genes, with a value of 0.2-0.4 indicating good model fit, and values beyond indicating excellent model fit. For each gene identified as a key predictor, their original cluster assignment is shown, along with their total dominance, which summarises the contributions of each predictor to all of the combinatory models, and percentage relative dominance, which describes the relative importance of each predictor.

Dataset (McFadden Pseudo R^2)	**Ensembl ID**	**Gene Symbol**	**Cluster**	**Total Dominance**	**Percentage Relative Importance**
KCL BrainBank (R^2 : 0.822)	ENSG00000152689	*RASGRP3*	3	0.1380	16.796
	ENSG00000131401	*NAPSB*	3	0.1205	14.663
	ENSG00000283431	*Novel Zinc Finger Protein Pseudogene*	3	0.1002	12.199
	ENSG00000042493	*CAPG*	3	0.0985	11.984
	ENSG00000173988	*LRRC63*	3	0.0860	10.469
	ENSG00000175785	*PRIMA1*	3	0.0629	7.655
	ENSG00000279223	None	3	0.0473	5.761
	ENSG00000128652	*HOXD3*	3	0.0446	5.434
	ENSG00000174837	*ADGRE1*	3	0.0422	5.134
	ENSG00000188488	*SERPINA5*	3	0.0410	4.990
	ENSG00000125735	*TNFSF14*	3	0.0404	4.916
TargetALS (R^2 : 0.803)	ENSG00000064886	*CHI3L2*	3	0.1756	21.857
	ENSG00000080031	*PTPRH*	3	0.0607	7.556
	ENSG00000173988	*LRRC63*	3	0.0586	7.297
	ENSG00000172548	*NIPAL4*	3	0.0586	7.288
	ENSG00000231840	*TMEM139-AS1*	3	0.0494	6.148
	ENSG00000101049	*SGK2*	3	0.0468	5.820
	ENSG00000187908	*DMBT1*	3	0.0454	5.650
	ENSG00000139292	*LGR5*	3	0.0449	5.595
	ENSG00000127412	*TRPV5*	3	0.0441	5.483
	ENSG00000250072	*SH3TC2-DT*	3	0.0436	5.426
	ENSG00000287538	None	3	0.0416	5.183
	ENSG00000259104	*PTCSC3*	3	0.0367	4.564
	ENSG00000258342	*LINC00609*	3	0.0362	4.502
	ENSG00000231427	*LINC01445*	3	0.0326	4.054
	ENSG00000286569	None	3	0.0287	3.575
van Rheenen (R^2 : 0.408)	ENSG00000074219	*TEAD2*	2	0.0643	15.748
	ENSG00000166927	*MS4A7*	3	0.0599	14.671
	ENSG00000101187	*SLCO4A1*	2	0.0425	10.402
	ENSG00000187955	*COL14A1*	2	0.0386	9.463
	ENSG00000166923	*GREM1*	3	0.0345	8.456
	ENSG00000161638	*ITGA5*	2	0.0252	6.161
	ENSG00000232560	*LINC01549*	3	0.0210	5.143
	ENSG00000225217	*HSPA7*	3	0.0188	4.601
	ENSG00000101335	*MYL9*	2	0.0188	4.595
	ENSG00000128652	*HOXD3*	3	0.0164	4.024
	ENSG00000118271	*TTR*	2	0.0162	3.956
	ENSG00000012124	*CD22*	3	0.0155	3.797
	ENSG00000107438	*PDLIM1*	2	0.0154	3.779
	ENSG00000138964	*PARVG*	3	0.0107	2.622

	ENSG00000185885	*IFITM1*	2	0.0105	2.582

Table A43. Results of dominance analysis for Cluster 3 vs Clusters 1 and 2. The top 15 predictors were obtained from each dataset, or fewer if there were not at least 15 dominant genes identified. For each dataset, the McFadden's Pseudo R^2 is shown, which is the proportion of variance in the model explained by these predictor genes, with a value of 0.2-0.4 indicating good model fit, and values beyond indicating excellent model fit. For each gene identified as a key predictor, their original cluster assignment is shown, along with their total dominance, which summarises the contributions of each predictor to all of the combinatory models, and percentage relative dominance, which describes the relative importance of each predictor.

Ensembl ID	**Gene Symbol**	**Cluster**	**Importance**
ENSG00000138316	*ADAMTS14*	3	0.1293
ENSG00000106366	*SERPINE1*	2	0.1093
ENSG00000129465	*RIPK3*	3	0.1080
ENSG00000106624	*AEBP1*	2	0.1067
ENSG00000099994	*SUSD2*	2	0.1040
ENSG00000107438	*PDLIM1*	2	0.0973
ENSG00000249307	*LINC01088*	2	0.0933
ENSG00000106211	*HSPB1*	2	0.0893
ENSG00000160111	*CPAMD8*	2	0.0893
ENSG00000011426	*ANLN*	3	0.0867
ENSG00000167851	*CD300A*	3	0.0867
ENSG00000051523	*CYBA*	3	0.0827
ENSG00000110852	*CLEC2B*	2	0.0827
ENSG00000173597	*SULT1B1*	2	0.0813
ENSG00000171860	*C3AR1*	3	0.0813
ENSG00000111057	*KRT18*	2	0.0800
ENSG00000163739	*CXCL1*	2	0.0800
ENSG00000174837	*ADGRE1*	3	0.0747
ENSG00000270640	*Lnc-BABAM2-2*	2	0.0747
ENSG00000086730	*LAT2*	3	0.0720
ENSG00000261997	None	3	0.0720
ENSG00000120708	*TGFBI*	2	0.0707
ENSG00000162444	*RBP7*	3	0.0707
ENSG00000131747	*TOP2A*	3	0.0693
ENSG00000166482	*MFAP4*	2	0.0693
ENSG00000173421	*IHO1*	2	0.0693
ENSG00000152766	*ANKRD22*	3	0.0680
ENSG00000256618	*MTRNR2L1*	3	0.0680
ENSG00000286810	None	1	0.0667
ENSG00000286558	None	3	0.0667
ENSG00000145708	*CRHBP*	1	0.0653
ENSG00000204389	*HSPA1A*	2	0.0640
ENSG00000287593	Antisense to *ADTRP*	1	0.0640
ENSG00000129757	*CDKN1C*	3	0.0627
ENSG00000139629	*GALNT6*	3	0.0627
ENSG00000204482	*LST1*	3	0.0627
ENSG00000073792	*IGF2BP2*	2	0.0587
ENSG00000125735	*TNFSF14*	3	0.0587
ENSG00000129667	*RHBDF2*	3	0.0587
ENSG00000136235	*GPNMB*	3	0.0587
ENSG00000140379	*BCL2A1*	3	0.0587
ENSG00000160183	*TMPRSS3*	2	0.0587
ENSG00000276317	*Lnc-GATA5-10*	2	0.0573
ENSG00000277918	*RNVU1-28*	1	0.0573
ENSG00000155629	*PIK3AP1*	3	0.0573
ENSG00000163823	*CCR1*	3	0.0573
ENSG00000167641	*PPP1R14A*	3	0.0560
ENSG00000174123	*TLR10*	3	0.0560
ENSG00000254362	*Lnc-PPP2R2A-2*	2	0.0560
ENSG00000000971	*CFH*	2	0.0547
ENSG00000011422	*PLAUR*	2	0.0547
ENSG00000042493	*CAPG*	3	0.0547
ENSG00000101335	*MYL9*	2	0.0547
ENSG00000143546	*S100A8*	2	0.0547
ENSG00000152804	*HHEX*	3	0.0547
ENSG00000173068	*BNC2*	2	0.0547
ENSG00000185201	*IFITM2*	2	0.0547
ENSG00000253924	*Lnc-NPBWR1-8*	3	0.0547

ENSG00000279821	None	2	0.0547
ENSG00000268758	*ADGRE4P*	3	0.0533
ENSG00000108798	*ABI3*	3	0.0533
ENSG00000019582	*CD74*	3	0.0520
ENSG00000105383	*CD33*	3	0.0520
ENSG00000117228	*GBP1*	3	0.0520
ENSG00000197747	*S100A10*	3	0.0520
ENSG00000129810	*SGO1*	3	0.0507
ENSG00000277117	*LOC102723996*	3	0.0507
ENSG00000106034	*CPED1*	2	0.0493
ENSG00000125731	*SH2D3A*	2	0.0493
ENSG00000156463	*SH3RF2*	2	0.0493
ENSG00000174607	*UGT8*	3	0.0493
ENSG00000180353	*HCLS1*	3	0.0493
ENSG00000244682	*FCGR2C*	3	0.0493
ENSG00000134531	*EMP1*	2	0.0480
ENSG00000138678	*GPAT3*	1	0.0480
ENSG00000164867	*NOS3*	2	0.0480
ENSG00000172005	*MAL*	3	0.0467
ENSG00000172548	*NIPAL4*	3	0.0467
ENSG00000110077	*MS4A6A*	3	0.0453
ENSG00000145287	*PLAC8*	3	0.0453
ENSG00000112303	*VNN2*	2	0.0440
ENSG00000115956	*PLEK*	3	0.0440
ENSG00000130635	*COL5A1*	2	0.0440
ENSG00000149573	*MPZL2*	2	0.0440
ENSG00000025708	*TYMP*	3	0.0427
ENSG00000131401	*NAPSB*	3	0.0427
ENSG00000133392	*MYH11*	2	0.0427
ENSG00000169403	*PTAFR*	3	0.0427
ENSG00000185885	*IFITM1*	2	0.0427
ENSG00000196954	*CASP4*	2	0.0427
ENSG00000237424	*FOXD2-AS1*	2	0.0427
ENSG00000275713	*H2BC9*	3	0.0427
ENSG00000128340	*RAC2*	3	0.0413
ENSG00000169896	*ITGAM*	3	0.0413
ENSG00000171840	*NINJ2*	3	0.0413
ENSG00000185499	*MUC1*	2	0.0413
ENSG00000250771	*TLR2 Pseudogene*	3	0.0413
ENSG00000000938	*FGR*	2	0.0400
ENSG00000012779	*ALOX5*	3	0.0400
ENSG00000105641	*SLC5A5*	2	0.0400
ENSG00000117322	*CR2*	1	0.0400
ENSG00000125430	*HS3ST3B1*	2	0.0400
ENSG00000159216	*RUNX1*	3	0.0400
ENSG00000258227	*CLEC5A*	3	0.0400
ENSG00000100292	*HMOX1*	3	0.0387
ENSG00000127507	*ADGRE2*	3	0.0387
ENSG00000280109	*PLAC4*	2	0.0387
ENSG00000112299	*VNN1*	2	0.0373
ENSG00000163191	*S100A11*	3	0.0373
ENSG00000254415	*SIGLEC14*	3	0.0373
ENSG00000281383	*Lnc-KCNE1B-157*	1	0.0373
ENSG00000285938	*BCL6-AS1*	2	0.0373
ENSG00000286522	*H3C2*	3	0.0373
ENSG00000105122	*RASAL3*	3	0.0360
ENSG00000154188	*ANGPT1*	2	0.0360
ENSG00000155926	*SLA*	3	0.0360
ENSG00000173530	*TNFRSF10D*	2	0.0360
ENSG00000004939	*SLC4A1*	2	0.0347

ENSG00000054598	*FOXC1*	2	0.0347
ENSG00000137801	*THBS1*	2	0.0347
ENSG00000187554	*TLR5*	3	0.0347
ENSG00000198467	*TPM2*	2	0.0347
ENSG00000066336	*SPI1*	3	0.0333
ENSG00000105281	*SLC1A5*	3	0.0333
ENSG00000140682	*TGFB1I1*	2	0.0333
ENSG00000163736	*PPBP*	2	0.0333
ENSG00000188536	*HBA2*	2	0.0333
ENSG00000198019	*FCGR1BP*	3	0.0333
ENSG00000129450	*SIGLEC9*	3	0.0320
ENSG00000173988	*LRRC63*	3	0.0320
ENSG00000182885	*ADGRG3*	2	0.0320
ENSG00000196154	*S100A4*	2	0.0320
ENSG00000204252	*HLA-DOA*	3	0.0320
ENSG00000012124	*CD22*	3	0.0307
ENSG00000111341	*MGP*	2	0.0307
ENSG00000161638	*ITGA5*	2	0.0307
ENSG00000185561	*TLCD2*	2	0.0307
ENSG00000197405	*C5AR1*	2	0.0307
ENSG00000224397	*PELATON*	3	0.0307
ENSG00000081237	*PTPRC*	3	0.0293
ENSG00000100368	*CSF2RB*	3	0.0293
ENSG00000115604	*IL18R1*	2	0.0293
ENSG00000130592	*LSP1*	3	0.0293
ENSG00000184730	*APOBR*	3	0.0293
ENSG00000239672	*NME1*	1	0.0293
ENSG00000100060	*MFNG*	2	0.0280
ENSG00000170458	*CD14*	3	0.0280
ENSG00000041982	*TNC*	3	0.0267
ENSG00000150337	*FCGR1A*	3	0.0267
ENSG00000159403	*C1R*	2	0.0267
ENSG00000167772	*ANGPTL4*	2	0.0267
ENSG00000171631	*P2RY6*	3	0.0267
ENSG00000187912	*CLEC17A*	3	0.0267
ENSG00000237082	*COX5BP6*	3	0.0267
ENSG00000077420	*APBB1IP*	3	0.0253
ENSG00000136286	*MYO1G*	3	0.0253
ENSG00000148908	*RGS10*	3	0.0253
ENSG00000149591	*TAGLN*	2	0.0253
ENSG00000173391	*OLR1*	3	0.0253
ENSG00000175567	*UCP2*	3	0.0253
ENSG00000198848	*CES1*	2	0.0253
ENSG00000074219	*TEAD2*	2	0.0240
ENSG00000090339	*ICAM1*	2	0.0240
ENSG00000104974	*LILRA1*	3	0.0240
ENSG00000117595	*IRF6*	2	0.0240
ENSG00000126860	*EVI2A*	3	0.0240
ENSG00000137462	*TLR2*	3	0.0240
ENSG00000182718	*ANXA2*	2	0.0240
ENSG00000229140	*CCDC26*	3	0.0240
ENSG00000244734	*HBB*	2	0.0240
ENSG00000166927	*MS4A7*	3	0.0227
ENSG00000173110	*HSPA6*	2	0.0227
ENSG00000176046	*NUPR1*	2	0.0227
ENSG00000200959	*SNORA74A*	1	0.0227
ENSG00000251429	*AIDAP2*	3	0.0227
ENSG00000128016	*ZFP36*	2	0.0213
ENSG00000158865	*SLC5A11*	3	0.0213
ENSG00000158869	*FCER1G*	3	0.0213

ENSG00000160791	*CCR5*	3	0.0213
ENSG00000162747	*FCGR3B*	2	0.0213
ENSG00000197471	*SPN*	3	0.0213
ENSG00000163220	*S100A9*	2	0.0200
ENSG00000180739	*S1PR5*	3	0.0200
ENSG00000186081	*KRT5*	1	0.0200
ENSG00000221869	*CEBPD*	2	0.0200
ENSG00000011600	*TYROBP*	3	0.0187
ENSG00000026508	*CD44*	3	0.0187
ENSG00000122025	*FLT3*	1	0.0187
ENSG00000170345	*FOS*	2	0.0187
ENSG00000171051	*FPR1*	3	0.0187
ENSG00000235750	*KIAA0040*	2	0.0187
ENSG00000090104	*RGS1*	3	0.0173
ENSG00000101049	*SGK2*	3	0.0173
ENSG00000101336	*HCK*	3	0.0173
ENSG00000149257	*SERPINH1*	2	0.0173
ENSG00000279320	None	2	0.0173
ENSG00000115602	*IL1RL1*	2	0.0160
ENSG00000143858	*SYT2*	1	0.0160
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ENSG00000082074	*FYB1*	3	0.0147
ENSG00000107099	*DOCK8*	3	0.0147
ENSG00000138061	*CYP1B1*	2	0.0147
ENSG00000169429	*CXCL8*	2	0.0147
ENSG00000171049	*FPR2*	2	0.0147
ENSG00000204287	*HLA-DRA*	3	0.0147
ENSG00000225217	*HSPA7*	3	0.0147
ENSG00000006747	*SCIN*	3	0.0133
ENSG00000014257	*ACP3*	3	0.0133
ENSG00000114013	*CD86*	3	0.0133
ENSG00000125733	*TRIP10*	2	0.0133
ENSG00000145779	*TNFAIP8*	2	0.0133
ENSG00000152689	*RASGRP3*	3	0.0133
ENSG00000165025	*SYK*	3	0.0133
ENSG00000169894	*MUC3A*	2	0.0133
ENSG00000174348	*PODN*	2	0.0133
ENSG00000185585	*OLFML2A*	2	0.0133
ENSG00000185905	*C16orf54*	3	0.0133
ENSG00000188511	*MIR3667HG*	2	0.0133
ENSG00000155307	*SAMSN1*	3	0.0120
ENSG00000229391	*HLA-DRB6*	3	0.0120
ENSG00000096696	*DSP*	2	0.0107
ENSG00000105967	*TFEC*	3	0.0107
ENSG00000122012	*SV2C*	1	0.0107
ENSG00000142102	*PGGHG*	2	0.0107
ENSG00000158715	*SLC45A3*	3	0.0107
ENSG00000003436	*TFPI*	2	0.0093
ENSG00000101187	*SLCO4A1*	2	0.0093
ENSG00000118640	*VAMP8*	3	0.0093
ENSG00000160255	*ITGB2*	3	0.0093
ENSG00000186431	*FCAR*	2	0.0093
ENSG00000235568	*NFAM1*	3	0.0093
ENSG00000047457	*CP*	2	0.0080
ENSG00000070190	*DAPP1*	3	0.0080
ENSG00000135842	*NIBAN1*	2	0.0080
ENSG00000143226	*FCGR2A*	3	0.0080
ENSG00000163563	*MNDA*	3	0.0080
ENSG00000172243	*CLEC7A*	3	0.0080
ENSG00000231246	*LINC02884*	2	0.0080

ENSG00000243323	*PTPRVP*	1	0.0080
ENSG00000271605	*MILR1*	3	0.0080
ENSG00000275395	*FCGBP*	3	0.0080
ENSG00000277775	*H3C7*	3	0.0080
ENSG00000010327	*STAB1*	3	0.0067
ENSG00000117318	*ID3*	2	0.0067
ENSG00000120875	*DUSP4*	1	0.0067
ENSG00000150048	*CLEC1A*	2	0.0067
ENSG00000160593	*JAML*	2	0.0067
ENSG00000164342	*TLR3*	3	0.0067
ENSG00000183508	*TENT5C*	2	0.0067
ENSG00000261170	*LOC107984827*	2	0.0067
ENSG00000066294	*CD84*	3	0.0053
ENSG00000137752	*CASP1*	3	0.0053
ENSG00000146192	*FGD2*	3	0.0053
ENSG00000148773	*MKI67*	3	0.0053
ENSG00000158859	*ADAMTS4*	3	0.0053
ENSG00000163565	*IFI16*	3	0.0053
ENSG00000165507	*DEPP1*	2	0.0053
ENSG00000172578	*KLHL6*	3	0.0053
ENSG00000173372	*C1QA*	3	0.0053
ENSG00000177575	*CD163*	2	0.0053
ENSG00000246363	*LINC02458*	1	0.0053
ENSG00000100336	*APOL4*	2	0.0040
ENSG00000107796	*ACTA2*	2	0.0040
ENSG00000110934	*BIN2*	3	0.0040
ENSG00000118503	*TNFAIP3*	2	0.0040
ENSG00000148926	*ADM*	2	0.0040
ENSG00000153551	*CMTM7*	3	0.0040
ENSG00000162511	*LAPTM5*	3	0.0040
ENSG00000169385	*RNASE2*	3	0.0040
ENSG00000242574	*HLA-DMB*	3	0.0040
ENSG00000060138	*YBX3*	2	0.0027
ENSG00000090382	*LYZ*	3	0.0027
ENSG00000134061	*CD180*	3	0.0027
ENSG00000167613	*LAIR1*	3	0.0027
ENSG00000175489	*LRRC25*	3	0.0027
ENSG00000203710	*CR1*	3	0.0027
ENSG00000028137	*TNFRSF1B*	2	0.0013
ENSG00000157227	*MMP14*	3	0.0013

Table A44. Results of permutation importance of the Zucca dataset. The analysis was performed with 50 iterations.

Cell Type	Statistics	Cluster 1	Cluster 2	Cluster 3	Shapiro-Wilk (W, p-value)	ANCOVA (F statistic, p-value)	Tukey p-value
Neurons	Mean	0.767	0.686	0.629	0.878, 3.82E-08	9.87, 1.161E-04	1 vs 2 0.0136 1 vs 3 < 0.001 2 vs 3 0.507
	Median	0.779	0.744	0.681			
	SD	0.0574	0.167	0.121			
	IQR	0.0591	0.199	0.155			
Astrocytes	Mean	0.155	0.223	0.192	0.912, 1.83E-06	6.05, 3.241E-03	1 vs 2 6.37E-03 1 vs 3 0.0471 2 vs 3 0.836
	Median	0.152	0.181	0.181			
	SD	0.0498	0.12	0.0653			
	IQR	0.0521	0.14	0.0815			
Microglia	Mean	0.00149	0.00755	0.0245	0.542, < 2.2E-16	33.0, 3.37E-11	1 vs 2 < 0.001 1 vs 3 < 0.001 2 vs 3 0.135
	Median	0.000579	0.0062	0.0121			
	SD	0.00215	0.00568	0.0436			
	IQR	0.00192	0.00662	0.0112			
Endothelial	Mean	0.0139	0.0518	0.0306	0.747, 1.32E-12	36.8, 7.006E-13	1 vs 2 < 0.001 1 vs 3 < 0.001 2 vs 3 0.0147
	Median	0.013	0.0347	0.0212			
	SD	0.00887	0.0408	0.0212			
	IQR	0.0103	0.0301	0.0304			
Oligodendrocytes	Mean	0.0627	0.0317	0.124	0.935, 3.64E-05	28.8, 3.67E-10	1 vs 2 < 0.001 2 vs 3 < 0.001 1 vs 3 0.0162
	Median	0.058	0.0252	0.129			
	SD	0.0371	0.0255	0.0497			
	IQR	0.0348	0.0292	0.055			

Table A45. Cell deconvolution results of KCL BrainBank cases using MuSiC. Overall differences in cell type composition between the three clusters were assessed using ANCOVA corrected for age of death and sex assigned at birth, with Tukey's test used for post-hoc comparison of cell composition between clusters. A p-value of < 0.05 denotes significance. Any cell types that were not normally distributed, as assessed with the Shapiro-Wilk test was log transformed before running ANCOVA.

Cell Type	Statistics	Cluster 1	Cluster 2	Cluster 3	Shapiro-Wilk (W, p-value)	ANCOVA (F statistic, p-value)	Tukey p-value
Neurons	Mean	0.742	0.629	0.545	0.932, 5.51E-07	34.0, 5.24E-13	1 vs 2 6.74E-03 1 vs 3 < 0.001 2 vs 3 2.52E-03
	Median	0.753	0.668	0.606			
	SD	0.0704	0.137	0.165			
	IQR	0.0802	0.151	0.2			
Astrocytes	Mean	0.177	0.264	0.2	0.872, 1.27E-10	12.6, 8.21E-06	1 vs 2 < 0.0001 1 vs 3 0.404 2 vs 3 1.45E-03
	Median	0.174	0.248	0.171			
	SD	0.0453	0.0917	0.0958			
	IQR	0.0511	0.11	0.0511			
Microglia	Mean	0.00468	0.0103	0.0227	0.817, 4.82E-13	28.7, 3.67E-11	1 vs 2 9.59E-03 1 vs 3 < 0.001 2 vs 3 0.0125
	Median	0.00384	0.00673	0.0165			
	SD	0.00478	0.0088	0.0171			
	IQR	0.00603	0.0139	0.0153			
Endothelial	Mean	0.00763	0.0441	0.024	0.797, 8.38E-14	30.3, 1.15E-11	1 vs 2 < 0.0001 1 vs 3 < 0.001 2 vs 3 0.105
	Median	0.00554	0.0232	0.0179			
	SD	0.00873	0.0431	0.0208			
	IQR	0.0089	0.0369	0.0264			
Oligodendrocytes	Mean	0.068	0.0526	0.208	0.888, 8.12E-10	49.7, < 2.2E-16	1 vs 2 0.288 1 vs 3 < 0.0001 2 vs 3 < 0.0001
	Median	0.0566	0.0384	0.179			
	SD	0.0453	0.0362	0.107			
	IQR	0.0603	0.0524	0.109			

Table A46. Cell deconvolution results of TargetALS cases using MuSiC. Overall differences in cell type composition between the three clusters were assessed using ANCOVA corrected for age of death and sex assigned at birth, with Tukey's test used for post-hoc comparison of cell composition between clusters. A p-value of < 0.05 denotes significance. Any cell types that were not normally distributed, as assessed with the Shapiro-Wilk test was log transformed before running ANCOVA

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