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- 1 Article
- 2 **Dysregulated antibody, natural killer cell and**
- 3 immune mediator profiles in autoimmune thyroid
- 4 diseases
- 5 Tiphaine C. Martin 1,2,3,4,*, Kristina M. Illieva 5,6, Alessia Visconti 1, Michelle Beaumont 1, Steven J. 6 Kiddle 7,8, Richard J.B. Dobson 7,9, Massimo Mangino 1,10, Ee Mun Lim 11,12,13, Marija Pezer 14,15, Claire 7 J. Steves ¹, Jordana T. Bell ¹, Scott G. Wilson ^{1,2,11}, Gordan Lauc ^{14,15}, Mario Roederer ¹⁶, John P. Walsh 8 ^{11,12}, Tim D. Spector ^{1,a}, Sophia N. Karagiannis ^{5,6,a} 9 ¹ Department of Twin Research and Genetic Epidemiology, King's College, London, United Kingdom; 10 alessia.visconti@kcl.ac.uk, chelle_mb@hotmail.com, massimo.mangino@kcl.ac.uk, claire.j.steves@kcl.ac.uk, 11 jordana.bell@kcl.ac.uk, tim.spector@kcl.ac.uk 12 2 School of Biomedical Sciences, University of Western Australia, Crawley, Western Australia, Australia; 13 scott.wilson@uwa.edu.au 14 ³ Present address: Department of Oncological Sciences, Icahn School of Medicine at Mount Sinai, New York 15 City, NY 10029, USA; tiphaine.martin@mssm.edu 16 ⁴ Present address: Tisch Cancer Institute, Icahn School of Medicine at Mount Sinai, New York City, NY 17 10029, USA; 18 ⁵ St John's Institute of Dermatology, School of Basic & Medical Biosciences, King's College, London, Guy's 19 Hospital, London, United Kingdom; kristina.ilieva@kcl.ac.uk, sophia.karagiannis@kcl.ac.uk 20 Breast Cancer Now Research Unit, School of Cancer & Pharmaceutical Sciences, King's College London, 21 Guy's Cancer Centre, London, United Kingdom; 22 Department of Biostatistics and Health Informatics, Institute of Psychiatry, Psychology and Neuroscience, 23 King's College, London, United Kingdom; richard.j.dobson@kcl.ac.uk 24 ⁸ Present address: MRC Biostatistics Unit, University of Cambridge, Cambridge, CB2 0SR, UK; 25 steven.kiddle@mrc-bsu.cam.ac.uk 26 ⁹ Health Data Research UK (HDR UK), London Institute of Health Informatics, University College London, 27 London, United Kingdom; 28 ¹⁰ NIHR Biomedical Research Centre at Guy's and St. Thomas's NHS Foundation Trust, London, United 29 Kingdom; 30 ¹¹ Department of Endocrinology and Diabetes, Sir Charles Gairdner Hospital, Nedlands, Western Australia, 31 Australia; eemun.lim@health.wa.gov.au 32 ¹² Medical School, The University of Western Australia, Crawley, Western Australia, Australia; 33 john.walsh@health.wa.gov.au 34 ¹³ PathWest Laboratory Medicine, QEII Medical Centre, Nedlands, Western Australia; 35 ¹⁴ Faculty of Pharmacy and Biochemistry, University of Zagreb, Zagreb, Croatia; glauc@genos.hr 36 ¹⁵ Genos, Glycoscience Research Laboratory, Zagreb, Croatia; mpezer@genos.hr 37 ¹⁶ ImmunoTechnology Section, Vaccine Research Center, NIAID, NIH, Bethesda, MD 20892, USA; 38 roederer@nih.gov 39 * Correspondence: tiphaine.martin@mssm.edu; Tel.: +1-212-824-9633 (T.C.M.) 40 ^a Equal contribution as joint senior authors 41 Received: date; Accepted: date; Published: date 42 Abstract: The pathogenesis of autoimmune thyroid diseases (AITD) is poorly understood and the association 43 between different immune features and the germline variants involved in AITD are yet unclear. We previously
- 44 observed systemic depletion of IgG core fucosylation and antennary $\alpha 1,2$ fucosylation in peripheral blood
- 45 mononuclear cells in AITD, correlated with anti-thyroid peroxidase antibody (TPOAb) levels. Fucose depletion
- 46 is known to potentiate strong antibody-mediated NK cell activation and enhanced target antigen-expressing cell
- 47 killing. In autoimmunity, this may translate to autoantibody-mediated immune cell recruitment and attack of

- 48 self-antigen expressing normal tissues. Hence, we investigated the crosstalk between immune cell traits, secreted
- 49 proteins, genetic variants and the glycosylation patterns of serum IgG, in a multi-omic and cross-sectional study
- 50 of 622 individuals from the TwinsUK cohort, 172 of whom were diagnosed with AITD. We observed associations
- 51 between two genetic variants (rs505922 and rs687621), AITD status, the secretion of Desmoglein-2 protein, and 52
- the profile of two IgG N-glycan traits in AITD, but further studies need to be performed to better understand 53 their crosstalk in AITD. On the other side, enhanced afucosylated IgG was positively associated with activatory
- 54 CD335-CD314+CD158b+ NK cell subsets. Increased levels of the apoptosis and inflammation markers Caspase-
- 55 2 and Interleukin-1 α positively associated with AITD. Two genetic variants associated with AITD, rs1521 and
- 56 rs3094228, were also associated with altered expression of the thyrocyte-expressed ligands known to recognize
- 57 the NK cell immunoreceptors CD314 and CD158b. Our analyses reveal a combination of heightened Fc-active
- 58 IgG antibodies, effector cells, cytokines and apoptotic signals in AITD, and AITD genetic variants associated
- 59 with altered expression of thyrocyte-expressed ligands to NK cell immunoreceptors. Together, TPOAb
- 60 responses, dysregulated immune features, germline variants associated with immunoactivity profiles, are
- 61 consistent with a positive autoreactive antibody-dependent NK cell-mediated immune response likely drawn to
- 62 the thyroid gland in AITD.
- 63 Keywords: Multi-omic; autoimmune thyroid diseases (AITD); genetic variants; apoptosis; antibody-64
- 65

dependent cell-mediated cytotoxicity (ADCC); anti-thyroid peroxidase antibody (TPOAb)

66 1. Introduction

67 Autoimmune thyroid diseases (AITD) are a class of chronic, organ-specific disorders of the 68 thyroid gland with a high genetic heritability (55-75%) [1-4] affecting approximately 5% of the 69 population and with a gender disparity (i.e., women: 5-15%; men: 1-5%) [5-7]. Pathologically, AITD 70 are characterized by autoantibodies against three main thyroid proteins (thyroid peroxidase (TPO), 71 thyroglobulin (Tg), and the thyroid-stimulating hormone (TSH) receptor (TSH-R)), infiltration of the 72 thyroid gland by immune cells (e.g. lymphocytes, NK cells, monocytes, and macrophages), the 73 formation of germinal centers in the thyroid gland [8] and dysregulated TSH levels [9,10]. However, 74 some studies have failed to observe a significant difference in peripheral blood immune cell 75 composition between AITD patients and healthy individuals [11], while others report significant 76 differences in particular cell types or in immune marker expression [12]. Immune cells, thyroid 77 autoantibodies, and secreted proteins including cytokines may play critical roles in AITD 78 development [13] and in immune responses, including in antibody-dependent cell-mediated 79 cytotoxicity (ADCC) pathways [14,15]. However, the underlying autoimmune signatures associated 80 with AITD remain unclear.

81 ADCC is triggered via antigen/antibody/Fc receptor complex formation, bringing the effector 82 cell (macrophages, NK cells) and the target cell (expressing the antigen) in close contact. The 83 formation and function of antigen/antibody complexes are modulated by various factors including 84 post-translational modifications of glycans decorating antibodies [16,17]. One example is lack of 85 fucose on the N-linked core glycan of IgG. Afucosylated antibodies have a higher affinity (~100-fold) 86 for the immunoglobulin Fc receptor Fc γ RIIIa (CD16a), expressed on NK cells, macrophages and $\gamma\delta$ T cells, and are shown to confer enhanced ADCC potential in vitro and anti-tumor activity in vivo [18-87 88 21]. This could result in antibodies with more potent Fc-mediated effector functions able to more 89 effectively recruit and activate immune effector cells such as NK cells to kill target antigen-expressing 90 cells [22,23]. IgG core fucose, observed in approximately 95% of IgG in healthy individuals, is 91 considered a "safe switch" that can attenuate potentially harmful antibody-dependent damage 92 against self-antigen-expressing normal tissues [18-21,24]. However, it is possible that these processes

93 may be altered in autoimmune diseases.

94 We previously studied the glycosylation profiles of total immunoglobulin G (IgG) and of 95 peripheral blood mononuclear cells (PBMC) in patients with AITD [4], as well as the glycosylation of 96 IgG-depleted serum proteins in Hashimoto's thyroiditis (HT) patients [25]. In peripheral blood, we 97 identified both depleted core fucosylation of IgG antibodies and decreased antennary α 1,2 98 fucosylation of PBMC to be associated with autoantibodies to thyroid peroxidase (TPOAb) and AITD 99 status [4]. We also identified a network of genes, including FUT8 and IKZF1 that regulate 100 fucosylation, to be implicated in the development of AITD [4,26]. Based on these findings, we 101 speculated that IgG core fucose deficiencies together with elevated levels of autoantibodies may 102 participate in autoimmune responses in AITD by enhancing effector cell activation and heightened 103 immune and inflammatory signals.

104 Therefore, here we investigated immune features that may signify dysregulated, and likely 105 heightened immune effector cells, antibodies, and immune mediators in AITD. In this in silico study 106 in the blood of 622 subjects from the TwinsUK cohort, of whom 172 have AITD features, we aimed 107 to investigate: 1) the association of different components of antigen/antibody/Fc receptor complexes 108 with AITD; 2) the associations between these different immune components in a cohort of samples 109 from volunteers regardless of disease status, and 3) potential genetic drivers on these components 110 (study design summarized in Fig. 1). Specifically, we examined the association of total serum IgG 111 glycosylation, immune traits, such as immune cell subpopulation frequencies (CSFs; i.e. relative 112 frequencies of circulating immune cell subsets), immune cell surface protein expression levels (SPELs; 113 i.e. the measurement of the cell-surface expression of critical proteins) and secreted proteins, in the 114 peripheral blood of patients with AITD compared with those of healthy volunteers (sample sizes of 115 each study performed are summarized in Table S1).





117Figure 1. Multi-omics computational analyses were used to study the components of118antigen/antibody/effector cell complex structure in AITD. 1) We previously performed glycome-wide119association studies of AITD and TPOAb levels using 3,146 individuals from three European cohorts,120including the TwinsUK cohort. We identified 17 AITD-IgG N-glycan traits in the discovery TwinsUK121cohort, and seven of these 17 have been then replicated in two other cohorts [4]. 2) In the present

122 study, we studied the association of total IgG N-glycan traits with 23,485 immune cell traits in 383 123 individuals from the TwinsUK cohort (regardless of disease status). We showed that 6 out of the 17 124 AITD-IgG glycan traits were correlated with 51 immune cell traits featuring the CD335, CD134, and 125 CD158b receptors. 3) None of these 51 immune cell traits appeared to be associated with AITD in 374 126 individuals (34 with AITD). 4) The heritability of AITD, TPOAb level and several -omic features (IgG 127 N-glycan traits and immune cell traits) were performed in previous studies of the TwinsUK cohort 128 [4,27–29]. Here we estimated the heritability of secreted proteins, but we could not determine shared 129 additive genetic variance between different phenotypes studied (AITD status, TPOAb level, level of 130 IgG N-glycan traits, of immune cell traits and of circulating proteins in the bloodstream). 5) We 131 identified genetic variants that alter the expression of genes, proteins and cell-bound immune 132 receptors (highlighted in this study) using the previous GWASs performed in the TwinsUK cohort or 133 from GWAS catalog, eQTLs from GTEx project and pQTLs from INTERVAL project [27,28,30-35]. 6) 134 We previously performed transcriptome-wide association studies of AITD, TPOAb level, and N-135 glycan structures in the whole blood of approximately 300 individuals and we found no significant 136 associations [4]. 7) We observed 3 out of 1,113 circulating proteins tested in plasma of almost 300 137 individuals shown to be associated with AITD status (TSH, Caspase-2, and Interleukin- 1α). 8) Several 138 secreted proteins were correlated with the level of plasma IgG glycan traits in 164 individuals, but 139 none of them were also associated with AITD. The sample sizes of these different studies are described 140 in Table S1. GlcNAc = N-acetylglucosamine. The numbers in black depict analyses performed 141 previously [4,27-29] while the numbers in red depict analyses presented for the first time in the 142 present study.

143 2. Materials and Methods

144 2.1. Study Sample

145 The study was conducted using immune cell traits, glycosylation, proteomics, genotyping, 146 and phenotypes in samples from research volunteers from the UK Adult Twin Registry (TwinsUK 147 cohort). The TwinsUK cohort is comprised of approximately 14,000 monozygotic and dizygotic same-148 sex adult twins from the UK, unselected for any particular disease or trait (Table S1). The cohort is 149 of Northern European/UK ancestry and has been shown to be representative of singleton populations 150 and the UK population in general [36,37]. Ethical approval was granted by the National Research 151 Ethics Service London-Westminster, the St Thomas' Hospital Research Ethics Committee (EC04/015 152 and 07/H0802/84). Informed consent was obtained from all study participants.

153 2.2. Data Statement

154 Multi-omic data were derived from samples in the TwinsUK cohort. Individual-level 155 TwinsUK data, including phenotypes and genotypes, are not permitted to be shared or deposited 156 due to the original consent given at the time of data collection. Access data can be applied for through 157 the TwinsUK data access committee (<u>http://twinsuk.ac.uk/resources-for-researchers/access-our-</u> 158 <u>data/</u>).

159 2.3. Definition of AITD and detection of TSH and TPOAb

160 The study was performed using a clinical AITD definition and TPOAb as a threshold trait; it 161 was not possible for AITD (Hashimoto's disease and Graves' disease) clinical diagnosis to be 162 confirmed by a clinician. However, approximately 90% of individuals with Hashimoto's disease, 163 about 75% with Graves' disease, <20% with other thyroid diseases, and <10% of normal individuals 164 are known to have TPOAb-positivity [38-40]. Therefore, individuals were considered to have AITD 165 if they either showed significantly higher than normal TPOAb serum titers (set at 3-fold higher than 166 the threshold set by the manufacturer [18 IU/mL for the Abbott assay and 100 IU/mL for the Roche 167 assay]) or had TSH serum levels >10 mIU/L. We considered individuals as controls if they had normal 168 levels of TSH and a negative TPOAb titer, with no previous clinical diagnosis of thyroid disease and 169 who were not treated with thyroid medications or steroids. Individuals with a history of thyroid 170 cancer or thyroid surgery were excluded. Among the 622 individuals studied, 172 (27.65%) were identified with AITD, 236 (37.94%) considered normal controls, and 214 (34.41%) have TPOAb or
 TSH serum levels outside the normal range, but do not reach the 3-fold cutoff for inclusion in the

172 TSH serum levels outside the normal range, but do not reach the 3-fold cutoff for inclusion in the 173 AITD cohort. Evaluations of sera to measure TPOAb and TSH levels are described in **Appendix A**.

174 2.4. Detection of IgG glycosylation profiling for discovery

Plasma specimens for analysis of IgG glycosylation was collected between 1997 and 2013 in
2,279 individuals from the TwinsUK cohort. IgG glycosylation profiling was performed on total
plasma IgGs glycome (combined Fc and Fab glycans and all IgG subclasses) in Genos Glycoscience
Research Laboratory, Croatia using UPLC analysis of 2AB-labelled glycans. Protocol, data pre-

179 processing and normalization in the TwinsUK cohort were previously described [4] (**Appendix A**).

180 2.5. Detection of immune cell traits

181 Plasma samples for assessment of 78,000 immune traits were collected between 2010 and 2012 182 in 669 female participants from the TwinsUK cohort using high-resolution deep 183 immunophenotyping flow cytometry analysis as previously described [28]. 78,000 different cell 184 surface marker combinations captured by 7 distinct 14-color immunophenotyping panels were 185 detected and described immune cell subset frequencies (CSF) and immune cell-surface protein 186 expression levels (SPELs). After quality control to remove immune cell traits that appeared as poor 187 reproducibility or out of range, 23,485 immune cell traits from 497 individuals of the TwinsUK cohort 188 were analyzed. For this analysis, only 374 twins had immune cell traits data and TPOAb level 189 detected by Roche immunoassay and 245 individuals in a case-control study by combining Roche 190 and Abbott assays (204 controls and 41 AITD). Immune traits were quantile normalized residuals of 191 a linear mixed effect model where age was included as fixed effects, and the batches were considered 192 as random effects.

193 2.6. Detection of protein profiling in plasma

With an aptamer-based multiplex protein assay (SOMAscan v2, SomaLogic Inc, Boulder, CO)
[41,42], 1,129 proteins were measured (2013) on plasma samples collected between 2004 and 2011
from 211 female twins of the TwinsUK cohort (Appendix A).

197 2.7. Statistical analyses

All statistical analyses were run using R version 3.2.3. Linear mixed effect models were conducted using the R lme of package lme4 [43], and linear models were done in using R function lm of package stat. Custom R scripts developed for this study are available at this URL: <u>https://github.com/TiphaineCMartin/multiomic_AITD.git</u>.

For determination of effective number of independent tests for different *-omic* data, association studies between *-omics* features and thyroid phenotypes and heritability analysis for proteins (Appendix A).

205 2.8. Genome-wide Association Analysis on IgG N-glycan traits

206 To define genetic variants (i.e., single nucleotide polymorphisms (SNP), short insertions and 207 deletions (indels)) associated with glycosylation profiles regardless of specific phenotypes in the 208 TwinsUK cohort, we ran analyses with the GenABEL software package [44] designed for genome-209 wide association study (GWAS) analysis of family-based data by incorporating pairwise kinship 210 matrix calculated using genotyping data in the polygenic model to correct relatedness and hidden 211 population stratification. Data were recently published with other datasets [26,45]. We selected 212 genetic variants for each IgG N-glycan traits with a P-value under the GWAS threshold (P-value < 213 5x10-8) and added the list of previously-defined genetic variants [29,45] (Appendix A).

214 2.9. Determination of shared genetic variants and genes between IgG N-glycan traits, immune cell traits,

215 protein abundance, and thyroid functions and diseases

To examine whether IgG N-glycan, immune cell traits, proteins, thyroid functions and diseases shared genetic variants or genes, we compared the genetic variants from GWASs on TwinsUK data (NHGRI GWAS catalog and other projects). As genetic variants detected by GWASs could be lead genetic variants but not necessarily causal genetic variants [46], we extended the list of genetic variants to other variants in linkage disequilibrium (LD) with an r² threshold of 0.8 from 1000G Phase 1 European population. Using HaploReg V4.1 [47] and GTeX data [32,33], we extracted tissue-specific expression quantitative traits (eQTLs) associated with these genetic variants.

223 2.10. Visualization

Heatmaps were created in using R package ComplexHeatmap. Correlation plots were created with R package corrplot. Boxplots and scatter plot were created in using R package ggplot2.

226 **3. Results**

3.1. Depletion of IgG core fucose is positively associated with increased CD158b+CD314+CD335- NK cell subset counts

IgG N-glycosylation is considered indispensable for the effector functions of IgG and inflammation control [48–52] and plays an essential role in the recognition and binding to Fc receptors of immune cells [51]. Using high-resolution deep immunophenotyping flow cytometry analysis in 669 twins from the TwinsUK cohort and IgG N-Glycan traits in 2,297 twins from the same cohort [4,27,28], we identified 383 samples with measurements of 23,485 immune cell and 17 AITD-IgG Nglycan traits (IGP2, IGP7, IGP8, IGP15, IGP21, IGP33, IGP36, IGP42, IGP45, IGP46, IGP48, IGP56, IGP58, IGP59, IGP60, IGP62 and IGP63) and searched for any associations between them (**Table S1**).

236 In our cohort, we identified 1,357 independent immune cell traits among 23,485 potential 237 tested immune cell traits, where the partial correlation between immune cell traits is highlighted in 238 Fig. S1a, 20 independent IgG N-glycan traits among 75 potential tested IgG N-glycan traits, and 6 239 independent AITD-IgG N-glycan traits among 17 potential tested AITD-IgG N-glycan traits [53]. 240 Association studies of total IgG N-glycan traits with immune cell traits showed that 6 of the 17 241 identified significant IgG N-glycan traits (IGP2, IGP42, IGP46, IGP58, IGP59, IGP60) previously 242 associated with TPOAb level and AITD status in the TwinsUK cohort, were also associated with 51 243 immune cell traits, which are all NK cells (CD16+CD56) featuring different combinations of 6 244 immunoreceptors (CD2, CD158a, CD158b, CD314, CD335, R7) (Table S2, Fig. 2). Three IgG N-glycan 245 traits without core fucose (IGP2, IGP42, IGP46) were negatively associated with the level of the 246 activating subpopulation of CD16+CD56+CD158b-CD335+ NK cells and positively associated with the 247 level of the CD16+CD56+CD335 effector NK cell subpopulation and with the activating subpopulation 248 CD16+CD56+CD158b+CD314+CD335- NK cells [54–59]. In contrast, three other significant IgG N-249 glycan traits with core fucose (IGP58, IGP59, and IGP60) had the opposite effect associations with the 250 same subpopulations of NK cells (Fig. 2a). In agreement with our previous report, there are therefore 251 negative correlations between the set of IgG N-glycan traits without core fucose (IGP2, IGP42, IGP46) 252 and the set of IgG N-glycan traits describing IgG core fucose (IGP58, IGP59, and IGP60) [4] 253 (highlighted in Fig. 2b). Moreover, we observed strong correlations between these 51 immune cell 254 traits (Fig. 2c). The presence of correlation patterns between the 17 AITD-IgG N-glycan traits (Fig. 255 **2b**) as well as between the 51 immune cell traits (Fig. 2c) is consistent with our observation of 256 correlations between the 6 AITD-IgG N-glycan traits and the 51 immune cell traits (Fig. 2a). When 257 we extended our analysis to the 58 remaining IgG N-glycan traits also identified in our samples, but 258 not associated with AITD, we observed no significant association between them and the 23,485 259 immune cell traits. Moreover, for 23,485 peripheral blood immune cell traits (Table S1), no significant 260 association with AITD or TPOAb level could be identified (Fig. S1b).

We conclude that a subpopulation of NK cells (CD16+CD56) and specifically the activating subpopulation CD16+CD56+CD158b+CD314+CD335- NK cells is associated with fucose-depleted IgG in individuals with AITD.



Figure 2. AITD-IgG N-glycan traits associated with a subpopulation of NK cells. (a) Heatmap of immune cell traits associated with AITD-IgG N-glycan traits. The 51 NK cell types were significantly associated with 6 out of 17 AITD-IgG N-glycan traits previously identified [4]. Below the heatmap, there are one representative of IgG core afucose (IGP2) and one representative of IgG core fucose (IGP7), that were both associated with AITD and TPOAb levels [4]. (b) Co-expressions between only 17 IgG N-glycan traits previously associated significantly with AITD status and TPOAb level [4]. (c) 270 Correlations between the profile of 51 immune cell traits that were associated significantly with at
271 least one of 17 AITD-IgG N-glycan traits. The order of immune cell traits is the same as that in Fig 2a.

3.2. The AITD-associated genetic variants, rs1521 and rs3094228, alter thyroid cell expression of ligands for CD314 and CD158b immunoreceptors

The NK cell receptors, CD335 (NKp46), CD314 (NKG2D) and the killer cell immunoglobulinlike receptors (KIRs) including CD158b, are normally associated with activated NK cell states, T cell co-stimulation, and mediating tumor cell lysis [55,57]. To determine whether genetic factors could contribute to AITD, related immune features, or their pathways, we inspected genetic variants associated with AITD, TPOAb levels, and immune cell traits from previous GWAS [27,28,30]. We then compared these with recent large-scale studies on tissue-specific expression quantitative traits (eQTLs) [35], mainly from the GTEx project [32–34] in blood and thyroid tissue.

281 No genetic variants previously associated with AITD or other thyroid phenotypes appeared 282 to be associated with the expression of CD335 or its known ligands in blood and thyroid cells. 283 However, we observed that two genetic variants, rs1521 and rs3094228, associated with Graves' 284 disease and TPOAb-positivity, respectively, fall in the gene regulatory regions of MIC-A and MIC-B 285 genes, two ligands of CD314 (NKG2D), and alter their gene expressions in thyroid cells [32–34,60–62] 286 (Fig. 3, Table S4, Fig. S2). These two AITD-genetic variants, rs1521 and rs3094228, also alter the 287 expression of the HLA-C gene, ligand of CD158b, in thyroid cells. The Graves' disease (GD) risk allele 288 of rs1521 variant is primary associated with a reduced expression of HLA-C gene, ligand of CD158b, 289 in thyroid cells. Furthermore, the TPOAb-positivity risk allele of rs3094228 variant is primary 290 associated with an increased expression of MIC-B gene, ligand of CD314 (NKG2D), in thyroid cells. 291 As about 75% of patients with Graves' disease have TPOAb-positivity and rs3094228 that has been 292 associated with TPOAb-positivity and Graves' disease [61,63], it is possible that the association of 293 rs1521 with Graves' disease could be also driven by TPOAb-positivity and, so, associated with its 294 phenotypes. Downregulation of HLA-C gene expression and upregulation of MIC-A and MIC-B gene 295 expression in thyrocytes could activate NK cell functions and the cytokine production against 296 thyrocytes when NK cells and thyrocytes are in contact.

Furthermore, three genetic variants, rs2596460, rs2596457 and rs2523691, previously associated with higher levels of the subpopulation of NK cells featuring CD16⁺CD56/CD2⁻ CD314⁺CD335⁻CD337⁻CD158a⁺CD158b⁺ [28], are in the same haplotype as the rs3094228 genetic variant, but with a low linkage disequilibrium (LD, $r^2 < 0.8$) (**Table S5**). Potentially, one of the genetic variants in this locus are the causal genetic variant of higher abundance of CD158b⁺CD314⁺CD335⁻ NK cells. All of the three genetic variants could also alter the expression of the *HLA-C* gene, ligand of CD158b, and *MIC-A*, ligand of CD314 (NKG2D), in immune cells [32–34,64] (**Fig. 3, Table S4**).

Overall, two genetic variants, rs1521 and rs3094228, associated with, respectively, Graves' disease and TPOAb-positivity, appear to alter thyrocyte expression of ligands of two immunoreceptors of NK cells, CD314 and CD158b; both of which have the capacity to enhance cytotoxicity of NK cells after binding with target cells. Additionally, three genetic variants in the same haplotype than rs3094228 could increase the abundance of the immune active CD158b*CD314*CD335-NK cell subpopulation.



311Figure 3. Association of immune cell traits with AITD status. Annotation tracks around *MIC-A, MIC-*312B and *HLA-C* genes visualize significant GWAS hits for immune cell traits, the ligands of certain313immunoreceptors (such as NK), and thyroid phenotypes previously identified in the TwinsUK cohort314as well as chromatin states identified using chromHMM from whole blood from ENCODE [65] and315thyroid cells from CEMT [66] and eQTLs from GTEx project [32,33]. The plot was produced using316functions from R packages Gviz and coMET [67].

317 3.3. AITD is associated with increased serum Caspase-2 and IL-1 α

318 We next evaluated whether the abundance of 1,113 free soluble proteins, which are partially 319 correlated between each other (Fig. 4a), in peripheral blood may be associated with AITD status (27 320 AITD patients versus 130 healthy controls) and TPOAb levels (155 individuals of whom 25 have 321 AITD) in the TwinsUK cohort (Table S1) using aptamer-based multiplex protein assay (SOMAscan) 322 [68]. Firstly, we observed significant moderate correlations of the TSH levels measured by two 323 clinical-certificated assays (Abbott and Roche) with the TSH levels measured by the SOMAscan assay 324 (Fig. 4b). This indicated that the SOMAscan assay could reproduce with good accuracy the estimation 325 of TSH levels and probably also for other proteins. Levels of three proteins were positively associated 326 with AITD status (Bonferroni multiple testing correction, P-value<1.9x10⁻⁴): TSH (P-value=8.67x10⁻⁵; 327 Beta=0.67; SE=0.16), Caspase-2 (CASP-2; P-value= 2.72×10^{-7} ; Beta=1.10; SE=0.20) and Interleukin-1 α 328 (IL-1 α ; P-value=7.46x10⁻⁵; Beta=0.41; SE=0.09). We also observed higher mean levels of TSH in patients 329 with AITD (meansomascan=1443.9, sdsomascan=1238.5; meanclinical=7.1 IU/mL, sdclinical=10.47) or TPOAb-330 positivity (meansomascan=1389.9, sdsomascan=1018.3; meanclinical=5.7 IU/mL, sdclinical=7.55) compared with 331 controls (euthyroidism with TPOAb-negative) (meansomascan=851.1, sdsomascan=368.6; meanclinical=1.64 332 IU/mL, sdclinical=0.79). Although Caspase-2 and IL-1 α levels were associated with AITD status, 333 Caspase-2 and IL-1 α levels were not associated with TPOAb or TSH levels as continuous variables 334 (P-value>1.9x10⁻⁴). However, when participants were divided into 4 categories according to TSH and 335 TPOAb levels (Fig. 4c), reflecting different clinical categories (hyperthyroidism, 336 euthyroidism/TPOAb-negative, hypothyroidism and euthyroidism/TPOAb-positive), Caspase-2 337 showed significantly higher mean and variance in two groups: hypothyroidism and 338 euthyroidism/TPOAb-positive (Fig. 4d). The hypothyroidism and euthyroidism/TPOAb-positivity in

- this cohort potentially indicate underlying Hashimoto's thyroiditis (HT). This is because HT is the
- 340 most common cause of hypothyroidism, spontaneous hypothyroidism (i.e. no previous history of
- thyroid ablation) is almost always caused by HT, and euthyroid individuals with TPOAb-positivity
- 342 almost always have HT when studied by cytology and histopathology [69–71]. On the other hand, 343 the variance of IL-1 α was significantly larger in groups with euthyroidism/TPOAb-positive and
- 343 the variance of IL-1 α was significantly larger in groups with euthyroidism/TPOAb-positive and 344 hyperthyroidism (**Fig. 4e**), but there was no significant difference for their mean values. Hence,
- 345 individuals from 4 categories have the same levels of IL-1 α , but there are more inter-individual
- 346 variabilities in euthyroidism/TPOAb-positive and hyperthyroidism than euthyroidism/TPOAb-
- 347 negative and hypothyroidism.
- 348 In summary, we confirmed the association of the plasma TSH levels with AITD status, and
- 349 we found two novel associations of plasma Caspase-2 and IL-1 α with AITD status, but their secretion
- 350 (mean and variance) seems to also depend on other factors associated with thyroid diseases such as
- 351 the levels of TSH and TPOAb.



353 Figure 4. Association of circulating protein abundances with thyroid diseases and with AITD-IgG N-354 glycan structures. (a) 1,113 circulating proteins were arranged in two dimensions based on the 355 similarity of their secretion profiles in the serum by the dimensionality reduction technique UMAP 356 [72] using R package umapr [73]. (b) Correlation of log10-transformed TSH measurements between 357 two clinical FDA approved clinical immunoassays (Roche and Abbott) and SOMAscan assay in 217 358 individuals (122 using Roche immunoassay and 95 using Abbott immunoassay). (c) Box plot of the 359 level of circulating TSH measured by SOMAscan assay in the serum according to the group of thyroid 360 status. (d) Box plot of the level of circulating Caspase-2 measured by SOMAscan assay in the serum 361 according to the group of TSH. (e) Box plot of the level of circulating IL-1 α measured by SOMAscan

Cells 2020, 9, x FOR PEER REVIEW

362 assay. An extreme outlier sample in the group 4 with an IL-1 α of 250,000mg/ml was discarded for 363 the analysis. (f) Heatmap of circulating protein abundances associated with AITD-IgG N-glycan 364 structures. In fig.2c-e, participants were assigned to 4 categories according to TSH level and TPOAb 365 status: 1=hyperthyroidism (TSH<=0.1 mIU/L; 13 individuals), 2=euthyroidism/TPOAb-negative 366 (0.4<TSH>4 mIU/L & TPOAb < 6 IU/mL (Abbott) or TPOAb < 34 IU/mL (Roche); 196 healthy 367 individuals), 3=hypothyroidism (TSH>=4 mIU/L; 21 individuals), and 4=euthyroidism/TPOAb-368 positive (0.4<TSH>4 mIU/L & TPOAb >= 6 IU/mL (Abbott) or TPOAb >= 34 IU/mL (Roche); 28 369 individuals). Wilcoxon-Mann-Whitney's test has been performed between groups to estimate 370 whether there are mean differences whereas Levene's test has been performed between groups to 371 estimate whether there are variance differences.

372 3.4. Afucosylated IgG is associated with serum levels of several circulating proteins

373 When we studied the correlation between the level of secreted TSH, Caspase-2 and IL-1 α 374 proteins and IgG N-glycan trait levels in 164 individuals of whom 27 have AITD, we found no 375 significant associations (P-value>8.3x10⁴, Bonferroni test considering 3 independent proteins and 20 376 independent IgG N-glycan traits) (Table S6, Fig. 4f). However, several AITD-IgG N-glycan traits 377 appeared to be associated with 7 other circulating proteins (AMHR2, BCMA, β 2-microglobulin, 378 ERBB1, Desmoglein-2, TRAILR4, and FCGR3B) (P-value<3.67x10-5, Bonferroni test in considering 379 only 227 independent proteins and 6 independent IgG N-glycan traits) (Table S6, Fig. 4f). For 380 example, three AITD-IgG N-glycan traits (IGP2, IGP42, and IGP46) were positively associated with 381 circulating FCGR3B (FcyRIIIb or CD16b), an Fc receptor expressed by polymorphonuclear 382 neutrophils (PMN), whereas three AITD-IgG N-glycan traits (IGP58, IGP59, and IGP60) were 383 negatively associated with the antibody Fc receptor FCGR3B. Also, IGP56 and IGP48 were negatively 384 associated with β 2-microglobulin, involved in the presentation of intracellular antigens through the 385 MHC class I complex; and IGP48 was positively associated with ERBB1, the epidermal growth factor 386 receptor (EGFR), a checkpoint molecule associated with cellular proliferation and differentiation.

387 Overall, 12 AITD-IgG N-glycan traits (IGP2, IGP8, IGP42, IGP46, IGP48, IGP56, IGP57, IGP58,
 388 IGP59, IGP60, IGP62, and IGP63) were associated with serum levels of 7 circulating proteins
 389 (AMHR2, BCMA, β2-microglobulin, ERBB1, Desmoglein-2, TRAILR4, and FCGR3B) in the TwinsUK
 390 cohort.

391 3.5. Free-soluble plasma Desmoglein-2 protein is associated with AITD genetic variants and two AITD-IgG 392 N-glycan traits

393 We evaluated several GWAS on secreted proteins (protein quantification locus traits, pQTL) 394 [31], to determine whether the secretion of proteins associated with AITD or with AITD-IgG N-glycan 395 traits are driven by AITD genetic variants. We found no genetic variants associated with any of 17 396 AITD-IgG N-glycan structures that are also pQTL. However, four genetic variants associated with 397 thyroid phenotypes published in the GWAS catalog (rs3761959, rs7528684, rs505922, and rs3184504) 398 were also associated in *cis* and *trans* with nine circulating protein abundances (BGAT, CHSTB, DC-399 SIGN, Desmoglein-2, DYR, FCRL3, GP1BA, MBL, and VCAM-1) (Table S7). None of these proteins 400 were associated directly with AITD or TPOAb levels in our study. However, we found that 401 Desmoglein-2 was associated with two AITD-IgG N-glycan traits, IGP8, and IGP63 [4] (Fig. S3). 402 Desmoglein-2 is highly expressed in epithelial cells including thyrocytes and cardiomyocytes and 403 plays a role in the cell-cell junctions between epithelial, myocardial, and certain other cell types and 404 is thought to be a regulator of apoptosis [74].

Therefore, four genetic variants associated with thyroid phenotypes are also associated with nine
secreted protein abundances, including the apoptosis regulator Desmoglein-2 in blood. Desmoglein2 was also associated with two AITD-IgG N-glycan traits.

408 4. Discussion

409 The dysregulation of the immune system may affect several biological structures and 410 processes in AITD, such as antigen/antibody/Fc receptor complex formation, possibly driven by 411 genetic and environmental factors [75]. Little is known about the key players and the genetic variants 412 identified in previous GWASs of patients with AITD. Targeting of self-antigen expressing tissues by 413 immune cells may depend on the formation of antigen/antibody/Fc receptor complexes featuring 414 substantial affinity or avidity properties. In the peripheral blood of individuals with AITD, we 415 previously detected depletion in IgG core fucose that is known to enhance such interactions and may 416 influence immune effector cell engagement of target cells by antibodies. We proposed that this 417 signature is associated with TPOAb levels and with immune effector cell activation in patients with 418 AITD [4]. Here, we reveal immune and genetic features pointing to activated NK cell subsets, thyroid 419 cell-derived ligands for immunoreceptors on NK cells, alongside secreted mediators of apoptosis and 420 immune activation, all signals of heightened antibody and innate effector cell responses in AITD.

421 We applied an *in silico* multi-omic approach on peripheral blood specimens from individuals 422 from the TwinsUK cohort to investigate any association between immune features and genetic 423 variants in AITD. In AITD patient samples, we observed increased levels of three circulating proteins 424 (TSH, Caspase-2, and Interleukin-1 α) and a decreased level of IgG core fucosylation associated with 425 an activated subpopulation of NK cells defined primarily by the expression of CD335, CD134, and 426 CD158b receptors. Our data confirms the previously reported association of plasma TSH level with 427 AITD status and also reveals previously unknown potential biomarkers for AITD, which are highly 428 associated with immunological activation functions, such as ADCC, apoptosis and pro-inflammatory 429 pathways. Furthermore, several genetic variants previously associated with AITD appear to alter 430 thyrocyte gene expression of several ligands of NK immunoreceptors and abundance of plasma 431 circulating proteins. This suggest that the genetic background may also play potential roles in NK 432 cell activation likely focused on thyroid cells in individuals with AITD.

433 To our knowledge, no other cohorts have large datasets that are available to interrogate and 434 feature the same diversity of *-omics* data with AITD phenotype or TPOAb levels. In our studies, we 435 note an imbalance in the sample sizes between control individual groups and AITD groups. This is 436 because the dataset comes from unselected twins and reflects the general European population [37], 437 where approximately 5% of the population, but 5-15% for women, present individuals with AITD [5-438 7]. To overcome such imbalances in our sample sizes and low samples sizes with large *-omics* data, 439 we applied machine learning and non-parametric methods with correction for multiple testing. 440 Another limitation in our present study is the absence of AITD clinical diagnosis confirmed by 441 clinicians for all individuals. We consequently applied more stringent criteria to define patients with 442 AITD versus control individuals, by using TSH and TPOAb levels (see Section 2.3 of our Materials & 443 Methods). We also performed analysis on TPOAb levels, as this is considered the main clinical 444 quantitative biomarker of AITD status [38-40]. Replication and meta-analysis studies on larger -omic 445 datasets incorporating clinical features will help to confirm our present findings.

446 Two secreted proteins (Caspase-2 and IL-1 α), which play roles in apoptosis and the 447 inflammatory response, were positively associated with AITD. TPOAb have been proposed to target 448 thyroid cells by engaging effector cells via their Fc receptors [4,14,15,76,77], and the apoptosis protein 449 Caspase-2 may represent a marker potentially signifying antibody-mediated destruction of thyroid 450 cells [78]. In concordance, IL-1 α , produced by activated immune, epithelial and endothelial cells in 451 response to cell injury and apoptosis, is considered an apoptosis index of the target cell [79] and 452 proportional to the degree of lymphoid infiltration in thyroid disorders [80]. IL-1 α seems to reduce 453 the thyroid epithelial barrier, even in the absence of any other signs of cytotoxicity [81]. In 454 concordance, in our study we found higher levels of secreted IL-1 α in AITD blood compared with 455 levels in healthy individuals, and its variance was greater in euthyroidism/TPOAb-positive blood 456 and in hyperthyroidism. This may signify dysregulation in cellular structures in the thyroid gland. 457 Overall, Caspase-2 and IL-1 α may reflect the degree of thyroid cell death or apoptosis and of 458 lymphoid infiltration towards the thyroid gland.

A subpopulation of NK cells expressing combinations of immunoreceptors (CD2, CD158a,
CD158b, CD314, CD335, R7) was associated with the depletion of IgG core fucose in individuals with
AITD. These included an activating NK receptor (CD314) and a differentiation receptor (CD335);
whilst, fucose-depleted IgG was also positively associated with a subpopulation of NK cells with an

463 inhibitory NK receptor (CD158b) [54–59,82]. The combination of potentially autoreactive antibodies 464 with enhanced Fc domains and activated effector cells such as NK cells may signal increased 465 inflammation and susceptibility to autoimmune disease [83]. Previous studies showed that 466 afucosylated antibodies have a much higher affinity (100-fold) for FcyRIIIa (CD16a) and may thus 467 have enhanced ADCC [84]. Moreover, ADCC via FcyRIIIa may require NK cells, but not monocytes 468 or polymorphonuclear cells, and activity levels of the antigen/antibody/effector cell complexes have 469 been correlated only with the NK cell numbers present in the PBMC [20]. Our associations between 470 the levels of IgG core fucose and of a subpopulation of NK cells reinforce the notion that there is a 471 complementarity between IgG core fucose levels and NK cells, that could influence effector cell 472 potency, potentially against a range of antigens including self-antigens.

473 It has been previously estimated that AITD are highly heritable (55-75%) and that most of 474 IgG N-glycan traits and the immune cell traits associated with AITD are moderately heritable (Table 475 **S8** [4,27]. By estimating the proportion of genetic and environmental variance of 1,129 proteins in 476 our study using the Structural Equation Modeling and twin structures present in the TwinsUK cohort 477 (Table S9), we found a small proportion of proteins having additive genetic variances in their 478 heritability, in concordance with previous findings on a smaller dataset [85]. As the best model of 479 heritability in AITD is only with dominant genetic variance, the shared genetic variance between 480 AITD and proteins as well as with IgG N-glycan traits and immune cell traits could not be estimated 481 with accuracy. However, in our study, we identified several genetic variants previously associated 482 with thyroid phenotypes to be also associated with the secretion of proteins and gene expression of 483 ligands of two NK cell immunoreceptors. Specifically, genetic variants, rs1521 and rs3094228, 484 associated with Graves' disease and TPOAb-positivity, alter the expression of thyroid cell-expressed 485 ligands, MIC-A, MIC-B, and HLA-C, known to recognize CD314 and CD158b immunoreceptors 486 expressed on NK cells. Moreover, rs3094228 falls in the same European haplotype as three genetic 487 variants associated with higher abundance of the activated CD158b+CD314+CD335- NK cell subset. 488 Thus, individuals having the AITD-risk allele of rs1521 variant have reduced expression of HLA-C 489 gene and, at a lesser extent, expression of MIC-A in thyrocytes, whereas the carriers of AITD-risk 490 allele of rs3094228 genetic variant associated with TPOAb-positivity showed increased expression of 491 MIC-B gene in thyrocytes and potentially higher abundance of the highly active 492 CD158b⁺CD314⁺CD335⁻ NK cells. Consequently, if the thyrocytes in carriers of AITD-risk alleles for 493 CD158b and CD314 ligands crosstalk with the subpopulation of NK cells with CD158b and CD314 494 immunoreceptors with the help of the antibodies, they could trigger the production of cytokines and 495 cytotoxicity against thyrocytes by these NK cells.

496 Our findings thus highlight different immune features (glycan structures on antibodies, a 497 subpopulation of immunoactive NK cells, the secretion of Caspase-2 and IL-1 α) as potential signals 498 of AITD status detectable in the bloodstream in addition to TSH and TPOAb levels. Moreover, if one 499 speculates that active antibodies with low core-fucose might be thyroid autoantibodies (e.g., TPOAb) 500 [86] and target cells are thyroid cells, it is conceivable (Fig. 5) that that immune cell-antibody-target 501 cell interactions may lead to cytotoxicity functions targeting thyroid tissues [76,86,87]. Together, these 502 may form part of a dysregulated autoimmune response in AITD. Further replication studies and 503 validation studies of real-time functional evaluations associated with these immune features and 504 genetic analyses are needed to confirm this model. These features could also be tested in the context 505 of thyroid cancer immunotherapy [77] in future studies.



506 507 Figure 5. Model of different potential contributing players and their pathways activated in proposed 508 antibody-dependent NK cell-mediated cytotoxicity in the thyroid gland of AITD patients. 1) The 509 depletion of IgG core fucose was associated with TPOAb level and AITD status [4]. 2) The IgG N-510 glycan traits associated with AITD were also associated with a subpopulation of NK cells in our 511 current study; for example, the depletion of IgG core fucose is associated positively with NK cells 512 with the patterns of co-receptors CD335- or CD335-CD158b+CD314+. 3) Previous studies showed that 513 afucosylated antibodies had increased affinity for binding to CD16 (FcγRIIIa), cell receptors of NK 514 cells, and to enhance ADCC [18-21] via 4) protein tyrosine kinase-dependent pathways, through 515 crosstalk with 5) NKG2D receptor (CD314) [88,89]. 6) Two SNPs, rs3094228 and rs1521, were 516 associated with GD and TPOAb-positivity [60-62] and fall in gene regulatory regions of the MIC-A 517 and MIC-B genes and increase their expression in thyroid cells [32]. These two genes encode heavily 518 glycosylated proteins that are ligands for the NKG2D type II receptor (CD314). 7) The KIR2DL 519 (CD158b) receptor is known to regulate the cytotoxicity of NK cells by unknown pathways, whereas 520 8) the NCR1 (CD335) receptor can contribute to the increased potency of activated NK cells to mediate 521 cell lysis by unknown pathway [54,55]. 9) The SNP, rs1521 associated with GD[60], is also shown to 522 reduce the expression of HLA-C gene, producing the ligand of CD158b, in thyroid cells [32,33,58,59]. 523 10) All together (the binding of NK cells with target cells through antibodies and their ligands), these 524 lead to the activation of NK cells, which release cytotoxic granules containing perforin and 525 granzymes. This release mediates ADCC of target cells (3), which are thyrocytes in AITD. Also, 11) a 526 positive association between the circulation abundance of Caspase-2 protein and AITD were found 527 in this study that could be associated with the destruction of thyrocytes. 12) A positive correlation of 528 circulating abundance of IL-1 α with AITD was also found in the bloodstream that could be a marker 529 of lymphocyte infiltration in the thyroid gland of individuals with AITD, and thus of inflammation 530 [80,81].

531 **Supplementary Materials:** The following are available online at www.mdpi.com/xxx/s1,



Figure S1: Immune cell traits and AITD status. (a) Immune cell traits were arranged in two dimensions based on
 the similarity of their quantification profiles by the dimensionality reduction technique UMAP [72] using R
 package umapr [73]. Some clusters that emerge spontaneously can be associated with specific immune cell types

(colors). (b) Overview of associations observed between IgG core-fucose, a subpopulation of NK cells and AITD
 status in the TwinsUK cohort. *Glycome-wide association studies of AITD and TPOAb levels were previously

538 performed [4].



Figure S2. Overview of associations between AITD-SNP and eQTL in thyroid and blood cells. *Genome-wide
association studies of AITD and TPOAb-positivity were previously performed, and the findings are available
via GWAS catalog [30] whereas **eQTLs come from GTEx project [34] and Westra and al. [35]. (a) Associations
between AITD-SNP and eQTL in thyroid and blood cells for the genetic variant rs3094228. (b) Associations
between AITD-SNP and eQTL in thyroid and blood cells for the genetic variant rs1521.



546 Figure S3. Overview of multi-omic findings associated with Desmoglein-2 in individuals with AITD status and 547 general population. We highlighted a locus with high LD having SNPs and two IgG glycan traits that are both 548 associated with GD and the abundance of secreted plasma Desmoglein-2 in plasma. However, no direct 549 association of AITD status with the abundance of secreted plasma Desmoglein-2. We previously performed 550 glycome-wide association studies of AITD and TPOAb levels [4]. Genome-wide association studies of AITD and 551 TPOAb-positivity were previously performed, and the findings are available via GWAS catalog [30] whereas 552 pQTLs come from INTERVAL project[31]. IGP8 = the percentage of FA2[3]G1 glycan in total IgG glycans. IGP63 553 = The percentage of fucosylation (without bisecting GlcNAc) of agalactosylated structures.

= The percentage of fucosylation (without bisecting GICNAC) of agalactosylated structures

- 554 Table S1: Description of TwinsUK cohort used for different analysis performed here
- 555 Table S2: Significant glycome associations with immune cell traits in the TwinsUK cohort

556 Table S3: Associations of 51 immune cell traits with AITD and TPOAb level in the TwinsUK cohort

- Table S4: Hits from selected eQTL studies for two SNPs, rs1521 and rs3094228 in the thyroid cells and wholeblood
- 559 Table S5: Genes reported for genetic variants associated with thyroid phenotypes and immune cell traits

- 560 Table S6: Glycome-wide associations studies of 17 AITD-IgG N-glycan traits with 1,113 circulating proteins. 561 Only significant ones were put here.
- 562 Table S7: Genetic variants associated with thyroid phenotypes and AITD-IgG N-glycan traits overlapping pQTL 563 identified in INTERVAL project (LD r²>0.8)
- 564 Table S8: Heritability of AITD, 17 IgG N-glycan traits and 51 immune cell traits in the TwinsUK cohort
- 565 Table S9: Heritability of 1,113 proteins in the TwinsUK cohort

566 Abbreviations. ADCC (Antibody-Dependent Cell-mediated Cytotoxicity), AITD (AutoImmune Thyroid 567 Diseases), CDC (Complement-Dependent Cytotoxicity), CD158b (KIR2DL2/L3 - Killer Cell Immunoglobulin 568 Like Receptor, Two Ig Domains And Long Cytoplasmic Tail 2 or 3 - or NKAT6 - Natural Killer-Associated 569 Transcript 6), CD314 (NKG2D or KLRK1 - Killer Cell Lectin Like Receptor K1), eQTL (gene Expression 570 Quantitative Trait Loci), $Fc\gamma R$ (Fc gamma Receptor), GD (Graves' Diseases), GlcNAc (N-acetylglucosamine), 571 GWAS (Genome-wide Association Study), HT (Hashimoto's thyroiditis), IgG (Immunoglobulin G), MIC-A 572 (MHC Class I Polypeptide-Related Sequence A), MIC-B (MHC Class I Polypeptide-Related Sequence B), NK 573 (Natural Killer cell), PBMC (Peripheral Blood Mononuclear Cells), pQTL (Protein expression Quantitative Trait 574 Loci), Tg (Thyroglobulin), TSH (Thyroid-Stimulating Hormone), TSH-R (Thyroid-Stimulating Hormone 575 Receptor), TPO (Thyroid PerOxidase), TPOAb (TPO Antibody).

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- 603 in high-throughput glycomic analysis and has several patents in this field. M.P. is an employee of Genos Ltd.
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- 605 writing of the manuscript, or in the decision to publish the results.

606 Appendix A

607 A.1. Detection of TSH and TPOAb in human sera 608 Sera to assess TPOAb and TSH levels were collected by a trained nurse or phlebotomist using 609 venepuncture and a SafetyLokTM Blood Collection Kit (21G3/4 Needles) and plain 10 ml serum-610 separating tube vacutainer (no additives) between February 1994 and May 2007. After collection from 611 the study subject, whole blood was held at 22°C for 50 min at room temperature for a clot to form 612 and serum separated within 60 minutes of collection. Processing of blood was performed using a 613 refrigerated (4°C) clinical centrifuge at 3000xg for 10 minutes with the serum supernatant 614 subsequently collected, transferred to a 2ml screw capped Nunc Cryotubes and immediately frozen 615 at -80°C and kept frozen in 2ml screw capped Nunc Cryotube at -80°C until use. Quantitative 616 determination of TSH and TPOAb (only IgG class) levels was performed on the sera either by a 617 chemiluminescent microparticle immunoassay (CMIA) [ARCHITECT® Anti-TPO or TSH (ABBOTT 618 Diagnostics Division, Wiesbaden, Germany, 2005)] (TPOAb titer>6 mIU/L considered positive; 619 reference range for TSH level 0.4-4.0 mIU/L) or by an electrochemiluminescence immunoassay 620 "ECLIA" [Elecsys and Cobas e analyzers, (Roche Diagnostics, Indianapolis, IN, USA, 2010)] (TPOAb 621 titer>34 IU/mL considered positive; reference range for TSH 0.4-4.0 mIU/L).

622 A.2. Detection of IgG glycosylation profiling

623 For IgG glycosylation analysis, using UPLC analysis of 2AB-labelled glycans, 624 chromatograms were separated in the same manner into 24 peaks, and the amount of glycans in each 625 peak was expressed as a percentage of the total integrated area. One glycan was excluded before any 626 transformation and standardization of data because of its co-elution with a contaminant that 627 significantly affected its values in some samples whereas two glycan peaks (GP) GP20 and GP21 628 (Zagreb code) were combined into a single trait called GP2021 (Zagreb code) because of difficulty in 629 distinguishing between these peaks in some samples. A global normalization and natural logarithm 630 transformation were applied to 22 directly measured glycan structures. As many of these structures 631 share the same structural features (galactose, sialic acid, core-fucose, bisecting N-acetylglucosamine 632 (GlcNAc)), 55 additional derived traits were calculated that average these features across multiple 633 glycans from the 22 normalized and non-transformed directly measured glycans. Technical 634 confounders (batch and run-day effects) were addressed using R package ComBat. The 22 directly 635 measured glycans and 55 derived glycan traits were centered and scaled to have a mean of 0 and 636 standard deviation (SD) of 1. Samples being more than 6 SD from the mean were considered as 637 outliers and excluded from the analysis.

638 A.3. Detection of protein profiling in plasma

639 Plasma protein profiling was conducted using SOMAscan v2 (SomaLogic Inc, Boulder, CO) 640 as previously described [29,30]. Briefly, hemolyzed samples were first excluded. Proteins were then 641 measured using a SOMAmer-based capture array called "SOMAscan." Quality control was 642 performed at the sample and SOMAmer level and involves the use of control SOMAmers on the 643 microarray and calibration samples. At the sample level, hybridization controls on the microarray 644 are used to monitor sample-by-sample variability in hybridization, while the median signal over all 645 SOMAmers is used to monitor overall technical variability. The resulting hybridization scale factor 646 and median scale factor are used to normalize data across samples. The acceptance criteria for these 647 values are 0.4-2.5, based on historical trends in these values. Somamer-by-somamer calibration 648 occurs through the repeated measurement of calibration samples; these samples are of the same

(2)

649 matrix as the study samples and are used to monitor repeatability and batch to batch variability.

650 Historical values for these calibrator samples for each SOMAmer are used to generate a calibration

- scale factor. The acceptance criteria for calibrator scale factors is that 95% of SOMAmers must have a
- calibration scale factor within ±0.4 of the median. For the current analysis, only 1,113 proteins were
- 653 then studied.

654 A.4. Selection of SNPs associated with immune cell traits

655 To define the list of SNPs associated with immune cell traits regardless to any specific phenotypes in 656 the TwinsUK cohort, we extracted SNPs for each immune cell traits that have a P-value under GWAS 657 P-value threshold (P-value $< 5x10^{-8}$) from previous published GWASs on these immune cell traits 658 [27,28]. To define the list of SNPs associated with protein abundance found in this study, we extracted 659 the significant SNPs reported in INTERVAL project [31]. To define the list of SNPs associated with 660 gene expression (eQTL), we extracted the eQTLs reported significant by GTEx and previous papers 661 present in HaploReg V4.1 [47]. To define the list of SNPs associated with AITD and thyroid functions, 662 we selected to SNPs listed in the NHGRI GWAS catalog [52] with words "thyroid" or "Graves" or

663 "Hashimoto."

664 A.5. Determination of effective number of independent tests for different -omic data

665 Due to high and partial correlations within glycans, proteins and immune cell traits, we 666 decided to use the equation 5 proposed by Li & Ji ((2005) [45] to define an effective number (Meff) of 667 independent tests. We then used this number to define the effective Bonferroni P-value threshold 668 such as 0.05/Meff instead of 0.05/M, with M the actual number of tests. 20 independent tests were 669 estimated for 76 glycans. Consequently, to account for multiple testing in the discovery cohort, we 670 present results surpassing a conservative Bonferroni correction assuming 20 independent tests, thus 671 giving a significant threshold of (P-value <2.5x10⁻³=0.05/20). 1,357 independent tests were estimated 672 for 23,485 immune cell traits, thus giving a significant threshold of 3.68x10⁻⁵ (0.05/1,357). 227 673 independent tests were estimated among 1,113 proteins (P<0.05/227=1.9x10-4).

- 674 A.6. Association studies between -omics features and thyroid phenotypes
- To examine whether one of the 17 AITD-IgG N-glycan traits was significantly associated with one of the 23,485 immune cell traits, we compared the fitted model in equation (2) with a model that did not include the residual of glycan in equation (1):
- 678

679

Model null: $Y_i \sim a + h$ (fixe intercepts) + g (random intercepts) + ε_{ij} (1)

Model 1: Y_i ~ a + **bG**_{ij} + h (fixe intercepts) + g (random intercepts) + ε_{ij}

680 Where Y_i represents the quantification of immune cell traits for individual *i* and Gij is glycan structure

of type *j* among 75 *N*-glycans for the same individual i. If biological covariates (age, sex) have not
been adjusted before association analysis, they have been added in the model. A random intercept
was added only in the discovery cohort in order to model the family-relatedness.

To examine whether an immune cell trait was significantly associated with TPOAb level and AITD status, we compared the fitted model in equation (2) with a model that did not include the immune cell traits in equation (1) where Gij become the immune cell trait of type j among 23,485 in discovery cohort for the same individual i. For the discovery and replication cohorts in TwinsUK, we added a random intercept in order to model the family-relatedness.

Cells 2020, 9, x FOR PEER REVIEW

689 To examine whether one of the 1,113 protein was significantly associated with TPOAb level 690 and AITD status, we compared the fitted model in equation (2) with a model that did not include the 691 protein in equation (1): where Gij become the protein of type j among 1,129 in discovery cohort for 692 the same individual i. We added a random intercept in order to model the family-relatedness. To 693 examine whether one of 1,113 proteins was significantly associated with one of 17 significant glycans, 694 we compared the fitted model in equation (2) with a model that did not include the protein in 695 equation (1): where Gij become the protein of type j among 1,129 in discovery cohort for the same 696 individual i. We added a random intercept in order to model the family-relatedness.

697 11.7. Heritability analysis for proteins

698 Using twin data and ADCE models (additive genetics (A), dominante genetics (D), shared 699 environment (C) and non-shared environment (E)), heritability of glycosylation structures, immune 700 cell traits and AITD were estimated using the R package called mets that allows us to run the analysis 701 with monozygotic and dizygotic twins as well as unrelated individuals. The significance of variance 702 components A, D, and C was assessed by dropping each component sequentially from the full model 703 (ADCE) and comparing the sub-model fit to the full model. Sub-models were compared to full 704 models by hierarchical χ^2 tests. The difference between log-likelihood values between sub-model and 705 full model is asymptotically distributed as χ^2 with degrees of freedom (df) equal to the difference in 706 df of sub-model and the full model. A statistical indicator of goodness-of-fit is the Akaike information 707 criterion (AIC), computed as χ^2 - 2df; sub-models are accepted as the best-fitting model if there is no 708 significant loss of fit when a latent variable (A, C, D, or E) is fixed to equal zero. When two sub-709 models have the same AIC compared to the full model, we decide to keep the model the most likely 710 (with additive genetic variance) or with the lowest P-value for different components.

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946



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947



Table S1: Description of TwinsUK cohort used for different analysis performed here
* Roederer, M et al., Cell, 2015, doi: 10.1016/j.cell.2015.02.046 and Mangino et al, Nature Communications, 2017, https://doi.org/10.1038/ncomms13850

Analysis	GWAS on immune cell traits*	Immune-wide association studies with thyroid phenotypes association studies with IgG N- glycan traits									Glycome-wide association studies with proteins		
Phenotype		TPOAb			AITD			TPOAb			AITD		
Group		continuous	con	trol	ca	ise		continuous	con	trol	ca	se	
TPOAb immunoassay	NA	Roche	Abbott	Roche	Abbott	Roche	NA	Roche	Abbott	Roche	Abbott	Roche	NA
threshold of TPOAb- positivity (UI/mL)	NA	34	6	34	6	34	NA	34	6	34	6	34	NA
Number of individuals	497	374	77	127	19	22	383	155	25	105	9	18	164
Age (mean/sd)	60 (8.2)	55.8 (8.4)	52.59 (7.20)	55.41 (8.4)	51.58 (7.49)	53.40 (8.02)	60 (8.2)	61.19 (6.96)	56.59 (8.10)	61.64 (7.8)	55.20 (4.65)	60.66 (6.73)	64.20 (7.27)
Sex (F/M)	497/0	374/0	77/0	127/0	19/0	22/0	383/0	155/0	25/0	105/0	9/0	18/0	164/0
TPOAb (mean/sd)	NA	50.5 (108.4)	1.42 (8.49)	10.50 (5.37)	463.86 (568.45)	312.68 (146.01)	NA	66.65 (36.19)	0.14 (0.37)	9.33 (5.05)	585.66 (1156.48)	324.81 (147.69)	NA

Table S2: Significant glycome associations with immune cell traits in the TwinsUK cohort $\ensuremath{\mathsf{SE}}\xspace$ standart error

ľ	Glycan ID	Description	immuneTrait ID Trait ID Canonical Lineage			Subset name	Pvalue	Beta	SE	Zscore	
10	GP2	The percentage of A2 glycan in total IgG glycans	immuno_64161	P4:2970	NK Activating 1	16+56	16+56/314+335-337-158b+R7-	9.22E-08	0.285	0.052	5.445
10	GP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64161	P4:2970	NK Activating 1	16+56	16+56/314+335-337-158b+R7-	5.10E-08	0.277	0.050	5.555
10	GP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64161	P4:2970	NK Activating 1	16+56	16+56/314+335-337-158b+R7-	9.29E-08	0.237	0.044	5.443
10	GP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64161	P4:2970	NK Activating 1	16+56	16+56/314+335-337-158b+R7-	7.88E-08	-0.228	0.042	-5.477
10	GP59	The percentage of fucosylation of agalactosylated structures	immuno_64161	P4:2970	NK Activating 1	16+56	16+56/314+335-337-158b+R7-	8.11E-08	-0.234	0.043	-5.468
10	GP60	The percentage of fucosylation of monogalactosylated structures	immuno_64161	P4:2970	NK Activating 1	16+56	16+56/314+335-337-158b+R7-	2.14E-08	-0.242	0.042	-5.718
10	GP2	The percentage of A2 glycan in total IgG glycans	immuno 64190	P4:2997	NK Activating 1	16+56	16+56/314+335-158b+R7-	8.47E-08	0.286	0.052	5.461
10	GP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64190	P4:2997	NK Activating 1	16+56	16+56/314+335-158b+R7-	4.69E-08	0.278	0.050	5.571
10	GP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64190	P4:2997	NK Activating 1	16+56	16+56/314+335-158b+R7-	8.94E-08	0.237	0.044	5.451
10	GP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno 64190	P4:2997	NK Activating 1	16+56	16+56/314+335-158b+R7-	7.49E-08	-0.228	0.042	-5.487
10	GP59	The percentage of fucosylation of agalactosylated structures	immuno_64190	P4:2997	NK Activating 1	16+56	16+56/314+335-158b+R7-	7.62E-08	-0.234	0.043	-5.480
10	GP60	The percentage of fucosylation of monogalactosylated structures	immuno_64190	P4:2997	NK Activating 1	16+56	16+56/314+335-158b+R7-	2.03E-08	-0.243	0.042	-5.728
10	GP2	The percentage of A2 glycan in total IgG glycans	immuno_64953	P4:3683	NK Activating 1	16+56	16+56/314+335-337-158b+	9.58E-08	0.285	0.052	5.437
10	GP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64953	P4:3683	NK Activating 1	16+56	16+56/314+335-337-158b+	5.24E-08	0.277	0.050	5.550
10	GP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64953	P4:3683	NK Activating 1	16+56	16+56/314+335-337-158b+	9.70E-08	0.237	0.044	5.435
10	GP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64953	P4:3683	NK Activating 1	16+56	16+56/314+335-337-158b+	8.37E-08	-0.227	0.042	-5.466
10	GP59	The percentage of fucosylation of agalactosylated structures	immuno_64953	P4:3683	NK Activating 1	16+56	16+56/314+335-337-158b+	8.77E-08	-0.233	0.043	-5.454
10	GP60	The percentage of fucosylation of monogalactosylated structures	immuno_64953	P4:3683	NK Activating 1	16+56	16+56/314+335-337-158b+	2.28E-08	-0.242	0.042	-5.706
10	GP2	The percentage of A2 glycan in total IgG glycans	immuno_64984	P4:3710	NK Activating 1	16+56	16+56/314+335-158b+	8.51E-08	0.286	0.052	5.460
10	GP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64984	P4:3710	NK Activating 1	16+56	16+56/314+335-158b+	4.64E-08	0.278	0.050	5.573
10	GP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64984	P4:3710	NK Activating 1	16+56	16+56/314+335-158b+	8.68E-08	0.238	0.044	5.456
10	GP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64984	P4:3710	NK Activating 1	16+56	16+56/314+335-158b+	7.57E-08	-0.228	0.042	-5.485
10	GP59	The percentage of fucosylation of agalactosylated structures	immuno_64984	P4:3710	NK Activating 1	16+56	16+56/314+335-158b+	7.85E-08	-0.234	0.043	-5.475
10	GP60	The percentage of fucosylation of monogalactosylated structures	immuno_64984	P4:3710	NK Activating 1	16+56	16+56/314+335-158b+	2.06E-08	-0.243	0.042	-5.726
10	GP2	The percentage of A2 glycan in total IgG glycans	immuno_62860	P4:18	NK Activating 2	16+56	16+56/CD2+314+335+337-158a-158b-R	8.79E-07	-0.250	0.050	-4.999
10	GP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_62860	P4:18	NK Activating 2	16+56	16+56/CD2+314+335+337-158a-158b-R	8.06E-07	-0.240	0.048	-5.025
10	GP60	The percentage of fucosylation of monogalactosylated structures	immuno_62860	P4:18	NK Activating 2	16+56	16+56/CD2+314+335+337-158a-158b-R	5.26E-07	0.208	0.040	5.154
10	GP2	The percentage of A2 glycan in total IgG glycans	immuno_63595	P4:2460	NK Activating 2	16+56	16+56/335+337-158a-158b-R7-	1.77E-08	-0.284	0.049	-5.752
10	GP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63595	P4:2460	NK Activating 2	16+56	16+56/335+337-158a-158b-R7-	9.79E-09	-0.275	0.047	-5.863
10	GP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_63595	P4:2460	NK Activating 2	16+56	16+56/335+337-158a-158b-R7-	4.86E-07	-0.211	0.041	-5.131
10	GP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_63595	P4:2460	NK Activating 2	16+56	16+56/335+337-158a-158b-R7-	3.67E-07	0.202	0.039	5.183
10	GP59	The percentage of fucosylation of agalactosylated structures	immuno_63595	P4:2460	NK Activating 2	16+56	16+56/335+337-158a-158b-R7-	7.23E-07	0.204	0.040	5.044
10	GP60	The percentage of fucosylation of monogalactosylated structures	immuno_63595	P4:2460	NK Activating 2	16+56	16+56/335+337-158a-158b-R7-	6.14E-08	0.221	0.040	5.540
10	GP2	The percentage of A2 glycan in total IgG glycans	immuno_63596	P4:2461	NK Activating 2	16+56	16+56/CD2+335+337-158a-158b-R7-	4.61E-07	-0.256	0.050	-5.134
10	GP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63596	P4:2461	NK Activating 2	16+56	16+56/CD2+335+337-158a-158b-R7-	3.39E-07	-0.248	0.048	-5.206
10	GP60	The percentage of fucosylation of monogalactosylated structures	immuno_63596	P4:2461	NK Activating 2	16+56	16+56/CD2+335+337-158a-158b-R7-	4.44E-07	0.210	0.040	5.189
10	GP2	The percentage of A2 glycan in total IgG glycans	immuno_63597	P4:2462	NK Activating 2	16+56	16+56/314+335+337-158a-158b-R7-	5.91E-08	-0.276	0.050	-5.527
10	GP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63597	P4:2462	NK Activating 2	16+56	16+56/314+335+337-158a-158b-R7-	4.89E-08	-0.264	0.047	-5.565
10	GP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_63597	P4:2462	NK Activating 2	16+56	16+56/314+335+337-158a-158b-R7-	1.61E-06	-0.203	0.042	-4.891
10	GP60	The percentage of fucosylation of monogalactosylated structures	immuno_63597	P4:2462	NK Activating 2	16+56	16+56/314+335+337-158a-158b-R7-	2.99E-07	0.212	0.040	5.239
10	GP2	The percentage of A2 glycan in total IgG glycans	immuno_63622	P4:2485	NK Activating 2	16+56	16+56/335+158a-158b-R7-	4.19E-08	-0.278	0.050	-5.594
10	GP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63622	P4:2485	NK Activating 2	16+56	16+56/335+158a-158b-R7-	2.47E-08	-0.269	0.047	-5.697
10	3P46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_63622	P4:2485	NK Activating 2	16+56	16+56/335+158a-158b-R7-	1.23E-06	-0.205	0.041	-4.945
10	JP58	The percentage of all fucosylated (+/- bisecting GicNAc) structures in total neutral IgG glycans	immuno_63622	P4:2485	NK Activating 2	16+56	16+56/335+158a-158b-R7-	1.19E-06	0.195	0.039	4.948
10	3P60	The percentage of fucosylation of monogalactosylated structures	immuno_63622	P4:2485	NK Activating 2	16+56	16+56/335+1588-158D-R7-	2.07E-07	0.214	0.040	5.312
10	3P2	The percentage of A2 glycan in total IgG glycans	immuno_63623	P4:2486	NK Activating 2	16+56	16+56/CD2+335+158a-158b-R7-	8.58E-07	-0.250	0.050	-5.010
10	3P42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63623	P4:2486	NK Activating 2	16+56	16+56/CD2+335+158a-158b-R7-	6.33E-07	-0.242	0.048	-5.082
10	3P60	The percentage of fucosylation of monogalactosylated structures	Immuno_63623	P4:2486	NK Activating 2	10+50	16+56/CD2+335+1588-158D-R7-	7.60E-07	0.206	0.040	5.082
		The percentage of A2 givcan in total igG givcans	ininuno_63625	P4:2400	NK Activating 2	10+50	10+50/314+335+1508-150D-R7-	9.03E-06	-0.272	0.050	-5.447
	3P42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63625	P4:2488	NK Activating 2	10+50	16+56/314+335+1588-1580-R7-	7.32E-08	-0.261	0.048	-5.490
10		The percentage of A2 glucop in total IgC glucopa	immuno_63625	F'4:2400	NK Activating 2	16+56	10+30/314+333+1308-1300-K/-	4.19E-07	0.210	0.041	J.1/J
	3P2	The percentage of A2 givean in total ligg giveans	immuno_03020	P4:2469	NK Activating 2	10+00	10+50/CD2+314+335+1508-150D-R7-	1.34E-06	-0.245	0.050	-4.000
10	2060	The percentage of Az grycan in total ineutial igo grycans (GPII)	immuno_63626	P4:2409	NK Activating 2	16+50	10+30/0D2+314+333+1308-1380-R/-	1.340-00	-0.230	0.048	-4.921
		The percentage of the state in total lac shares	immuno_03020	P4:2469	NK Activating 2	10+30	10+50/CD2+314+335+1508-150D-R7-	0.03E-07	0.200	0.041	5.070
	2042	The percentage of A2 glycan in total inputral laC glycans (CPn)	immuno_63674	P4:2001	NK Activating 2	16+56	10+30/333+337-1300-K7- 16+56/335+337-1585 P7	4.02E-09	-0.202	0.047	-5.994
	2046	The percentage of A2C1 glycan in total ineutial igo glycans (GPn)	immuno_030/4	F4.2001	NK Activating 2	16+56	10-30/3307337-1000-K/-	2.00E-09	-0.272	0.040	-0.079
10	2052	The percentage of all fucesulated (+/ bisecting CleNAs) structures in total neutrol to chusers	immuno_63674	P4:2001	NK Activating 2	16+50	10+30/333+337-1300-K7- 16+56/335+337-1585 P7	2.20E-07	-0.207	0.039	-5.276
	2050	The percentage of fucesylation of analactosylated structures	immuno_63674	P4.2001	NK Activating 2	16+56	16+56/335+337-158h-R7-	1.73E-07	0.190	0.037	5 121
10	3P60	The percentage of fucesylation of monogalactosylated structures	immuno 63674	P4·2531	NK Activating 2	16+56	16+56/335+337-158b-R7-	3 49F-08	0.135	0.038	5 638
					······································				0.2.10	0.000	0.000

GR: Dr. Beschlage of A.2 given (DM). mmm. EA17 PA2220 (M Activating 2 16-51	IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63675	P4:2532 NK Activating 2 16+56	16+56/CD2+335+337-158b-R7-	2.26E-07	-0.251	0.048	-5.270
Offent Description of all subsysted (-1) esteering GMA) structures in teal reaching (-1) esteering (-1) esteer	IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63675	P4:2532 NK Activating 2 16+56	16+56/CD2+335+337-158b-R7-	1.72E-07	-0.241	0.045	-5.333
Bits Immuno (007) PA220 Microbial Science Instruction of the second of the seco	IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_63675	P4:2532 NK Activating 2 16+56	16+56/CD2+335+337-158b-R7-	1.62E-06	0.184	0.038	4.902
GPD The encretained of Z_{1} prioring of Z_{1} prioring Z_{2}	IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_63675	P4:2532 NK Activating 2 16+56	16+56/CD2+335+337-158b-R7-	4.20E-07	0.200	0.038	5.190
Gene The presenting of Ad genes (LP) Particle (LP) <td< td=""><td>IGP2</td><td>The percentage of A2 glycan in total IgG glycans</td><td>immuno_63677</td><td>P4:2534 NK Activating 2 16+56</td><td>16+56/314+335+337-158b-R7-</td><td>1.42E-08</td><td>-0.275</td><td>0.048</td><td>-5.793</td></td<>	IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63677	P4:2534 NK Activating 2 16+56	16+56/314+335+337-158b-R7-	1.42E-08	-0.275	0.048	-5.793
Geffer means and any of a second	IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63677	P4:2534 NK Activating 2 16+56	16+56/314+335+337-158b-R7-	1.37E-08	-0.262	0.045	-5.798
GFS3 The precentage of all incorpted in (all-backing includes in order log dynamics) mmmme. Sign 7 L2354 KK Advalants 11-56 8-005-77 0.80 5-00 The precentage of all incorpted in control log dynamics mmmme. Sign 7 L2354 KK Advalants 11-56 11-56 2-24 0.24 11-57 REP mmme. Sign 7 L2364 KK Advalants 11-56 11-56 2-24 0.24 11-57 REP MEA The precentage of Ad gynamic field inductation mmme. Sign 7 L2364 KK Advalants 11-56 11-56 2-24 0.24 11-57 REP The precentage of Ad gynamic field inductation mmmme. Sign 7 L2364 KK Advalants 11-56 11-	IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_63677	P4:2534 NK Activating 2 16+56	16+56/314+335+337-158b-R7-	7.02E-07	-0.200	0.040	-5.052
GRD The accentage of Jacobian d'incorpation of plane intermed and plane intermed plane intermed and plane intermed plane intermed and plane inte	IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_63677	P4:2534 NK Activating 2 16+56	16+56/314+335+337-158b-R7-	8.60E-07	0.189	0.038	5.008
GPC The presentage of A given in total [6 Given: mmm. 0587 PL255 NK Advance 2 16-65 (CC 2144-355-337-168-Pr.7) 0.846 / 0.207 0.208 <td>IGP60</td> <td>The percentage of fucosylation of monogalactosylated structures</td> <td>immuno_63677</td> <td>P4:2534 NK Activating 2 16+56</td> <td>16+56/314+335+337-158b-R7-</td> <td>1.39E-07</td> <td>0.207</td> <td>0.039</td> <td>5.377</td>	IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_63677	P4:2534 NK Activating 2 16+56	16+56/314+335+337-158b-R7-	1.39E-07	0.207	0.039	5.377
GH2 Immuno.3878 P4.255 NK.Advala 11-59 GH2 NK.Advala 11-59 Importantings of Adjournant total module (Gaptess (GPA) mmuno.3878 P4.255 NK.Advala 11-59 GH2 12-59 11-59	IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63678	P4:2535 NK Activating 2 16+56	16+56/CD2+314+335+337-158b-R7-	3.64E-07	-0.248	0.048	-5.174
Offen The presentage of sognation of concepted optical and opt	IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63678	P4:2535 NK Activating 2 16+56	16+56/CD2+314+335+337-158b-R7-	3.79E-07	-0.236	0.046	-5.172
GPC The percentage of A plyon in the light glyons. 0.216 10-226	IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_63678	P4:2535 NK Activating 2 16+56	16+56/CD2+314+335+337-158b-R7-	5.68E-07	0.199	0.039	5.129
GH2 The percentage of A2 plycen in ball excluding dynamic (GPin) mmmon. 5733 PL288 ML Advantup 2 Feb 1 Feb 258	IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63703	P4:2558 NK Activating 2 16+56	16+56/335+158b-R7-	6.83E-09	-0.280	0.047	-5.924
GR48 The percentage of Accel system (table) accel by System (GPn) mmm.ac. 3373 P.2388 MK-Advantog. 21-864 B-3654-1588-R7. 2.976-0 0.058 0.0	IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63703	P4:2558 NK Activating 2 16+56	16+56/335+158b-R7-	4.04E-09	-0.270	0.045	-6.017
GPB The percentage of all location (C+ bitech) (C+	IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_63703	P4:2558 NK Activating 2 16+56	16+56/335+158b-R7-	2.97E-07	-0.205	0.039	-5.224
GFB9 The percentage of Longslate of agalescoplate of structures mmune, 23701 P4 2558 N Activating of Lengslate Bit 2003 First of Lengslate First o	IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_63703	P4:2558 NK Activating 2 16+56	16+56/335+158b-R7-	2.41E-07	0.197	0.037	5.262
Bits Initiage Carlos PL2558 Area (2012) PL2588 Area (2012) Area (2012) Area (2012)	IGP59	The percentage of fucosylation of agalactosylated structures	immuno_63703	P4:2558 NK Activating 2 16+56	16+56/335+158b-R7-	6.17E-07	0.196	0.039	5.071
GPC Immune, S2734 PA2569 Nuckersbage of Agripsen in Bale AF7 1,182 or 2,248 0.448 2,329 The percentage of Agripsen in bale indexing discussions mmune, S2737 PA2559 Nuckersbage of Agripsen in bale indexing discussions 1,182 or 2,248 0.448 2,329 1,133 1,138 or 2,248 0.448 2,329 1,133 1,138 or 2,248 0.448 2,329 1,138 1,138 or 2,248 0.448 2,329 1,138 1,138 or 2,248 0.448 2,329 1,138 1,138 or 2,248 0.448 4,292 0.448 4,292 0.448 4,292 0.448 4,292 0.448 4,868 4,272 0.458 0.448 4,389 1,388 1	IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_63703	P4:2558 NK Activating 2 16+56	16+56/335+158b-R7-	4.67E-08	0.214	0.038	5.585
Units Immuno 0374 P4259 NickArsburg 2 16-56 16-56 238 271 238 271 The processing of Acy system total neutral (§ system (GPn) mmuno 03707 P4258 NickArsburg 2 16-56 16-56 238 138 16-56 152 0.15 0.1	IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63704	P4:2559 NK Activating 2 16+56	16+56/CD2+335+158b-R7-	3.13E-07	-0.248	0.048	-5.206
Junce Interpretainage or Language in the processing of Approximation in the ling of Approximatin approximation in the ling Approximation in the ling A	IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63704	P4:2559 NK Activating 2 16+56	16+56/CD2+335+158b-R7-	2.36E-07	-0.239	0.045	-5.271
Lat. Imperiedinge of AD2 grant ball agrants Imperiedinge of AD2 grant ball agrants Imperiedinge of AD2 grants <	IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_63704	P4:2559 NK Activating 2 16+56	10+56/CD2+335+158b-R/-	5.59E-07	0.198	0.039	5.133
meters/set imp processing of and system (set) 1448-50 1428-50 0.428 0.428 0.428 0.438 0.428 0.448 0.448 0.448 0.438 0.318 0.348 0.318 0.348 0.318 0.348 0.318 0.348 0.318 0.348 0.348 0.348 0.348 0.348 0.348 0.348 </td <td>IGP2</td> <td>The percentage of A2 glycan in total IgG glycans</td> <td>immuno_63707</td> <td>P4:2561 NK Activating 2 16+56</td> <td>16+56/314+335+158b-R/-</td> <td>1.98E-08</td> <td>-0.272</td> <td>0.048</td> <td>-5.731</td>	IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63707	P4:2561 NK Activating 2 16+56	16+56/314+335+158b-R/-	1.98E-08	-0.272	0.048	-5.731
Hares Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts grann hold industry (gray data (gray) Implementage in Acts gra	IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63707	P4:2561 NK Activating 2 16+56	10+56/314+335+158b-R/-	1.94E-08	-0.259	0.045	-5.734
Larder im perioritage of Layout (1) 110000 (1)	IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_63707	P4:2561 NK Activating 2 16+56	16+56/314+335+158b-R7-	1.06E-06	-0.197	0.040	-4.969
Largest Implicite	IGP58	The percentage of all fucosylated (+/- bisecting GicNAc) structures in total neutral IgG glycans	immuno_63707	P4:2561 NK Activating 2 16+56	16+56/314+335+158D-R7-	1.29E-06	0.185	0.038	4.925
Lad. Imple percentage of Aug dynam ford up gynams Imple percentage of Aug dynam ford up gynams Imple percentage of Aug dynams Imple	IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_63707	P4:2561 NK Activating 2 16+56	16+56/314+335+158D-R7-	2.06E-07	0.204	0.039	5.303
Construction minute performance of Act given in balan larger by dynamic (Ser) minute performance of Act given in balan larger by dynamic (Ser) 4.385.0 0.346 5.387 Circle minute performance of Act given in balan larger by dynamic (Ser) minute (Size) 16.586 16.586 16.586 16.586 4.385 4.385 Circle minute (Size) minute (Size) 16.586 16.586 16.586 16.586 16.586 16.586 16.586 4.316	IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63708	P4:2562 NK Activating 2 16+56	16+56/CD2+314+335+1580-R7-	4.66E-07	-0.246	0.048	-5.125
Understäge för Aggivan in bälan indelige Systami (CPr) mmmund, Edstär Prisson (CPr) Bisson (CPr) <t< td=""><td>IGP42</td><td>The percentage of A2 givcan in total neutral igG givcans (GPn)</td><td>immuno_63708</td><td>P4:2562 NK Activating 2 16+56</td><td>16+56/CD2+314+335+158D-R7-</td><td>4.49E-07</td><td>-0.235</td><td>0.046</td><td>-5.138</td></t<>	IGP42	The percentage of A2 givcan in total neutral igG givcans (GPn)	immuno_63708	P4:2562 NK Activating 2 16+56	16+56/CD2+314+335+158D-R7-	4.49E-07	-0.235	0.046	-5.138
Image interface Image interface Processing of A2 gives (PP) Image interface Processing of A2 gives Processing OA gives <td></td> <td>The percentage of fucosylation of monogalactosylated structures</td> <td>immuno_63708</td> <td>P4:2562 NK Activating 2 16+56</td> <td>16+56/CD2+314+335+158D-R7-</td> <td>6.39E-07</td> <td>0.198</td> <td>0.039</td> <td>5.105</td>		The percentage of fucosylation of monogalactosylated structures	immuno_63708	P4:2562 NK Activating 2 16+56	16+56/CD2+314+335+158D-R7-	6.39E-07	0.198	0.039	5.105
Unspective Interferentage of A2 (process) (a) (b) (b) (b) (b) (b) (b) (b) (b) (b) (b		The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63835	P4:26/7 NK Activating 2 16+56	16+56/335+337-1588-R7-	1.01E-06	-0.222	0.045	-4.881
Interpretentage of A2 given in bala (by givens) Interpre	IGP42	The percentage of A2 glycan in total ineutral IgG glycans (GPH)	immuno_63925	P4.2756 NK Activating 2 16+56	10+50/335+337-R7-	1.32E-00	-0.210	0.043	-4.916
Interprotecting of A22 gives in total neural log gives in total neural lo		The percentage of A2 glycan in total ingo glycans	immuno_64341	P4:3131 NK Activating 2 16+56	10+30/333+337-130d-130D- 16+56/225+227 159a 159b	1.57E-00	-0.200	0.050	-5.775
Interprotectage of ALD Caylacan Intella Inductang Surgeria Interprotectage of ALD Caylacan Intella Inductang Surgeria Output Surgeria Outpu Surgeria Output Surgeria		The percentage of A2C1 glucon in total Incutral IgO glucons (OPn)	immuno_64341	P4:3131 NK Activating 2 16+56	10+50/335+337-150d-150D- 16+56/325+327 159a 159b	5.00E-09	-0.277	0.047	-5.885
Interprenentage of funcosylation of an extension black backards Interprenentage of funcosylation of monogalactosylated structures 7.38E-07 0.206 0.041 6.509 IPPD The percentage of funcosylation of monogalactosylated structures mmuno. 64342 P4.3131 NK Advaining 2 16-55 18-56(027-337-158-158b- 7.28E-07 0.256 0.600 5.509 IGP2 The percentage of A2 glycan in total metral [JG glycans mmuno. 64342 P4.3131 NK Advaining 2 16-55 18-56(027+337-158-158b- 7.28E-07 0.256 0.500 5.199 IGP2 The percentage of A2 glycan in total metral [JG glycans mmuno. 64342 P4.3132 NK Advaining 2 16-56 18-56(027+333-137.158-158b- 4.48E-07 0.210 0.404 5.682 IGP2 The percentage of A2 glycan in total metral [JG glycans (GPn) mmuno. 64344 P4.3134 NK Advaining 2 16-56 16+56 <t< td=""><td></td><td>The percentage of all fucesylated (+/, bisecting GleNAc) structures in total poutral laG glycans</td><td>immuno_64341</td><td>P4:3131 NK Activating 2 16+56</td><td>16+56/335+337 1585 1585</td><td>1 26E 07</td><td>-0.210</td><td>0.041</td><td>-5.094</td></t<>		The percentage of all fucesylated (+/, bisecting GleNAc) structures in total poutral laG glycans	immuno_64341	P4:3131 NK Activating 2 16+56	16+56/335+337 1585 1585	1 26E 07	-0.210	0.041	-5.094
UPPO The parcentage of fucosylation of monogalactosylated structures mmuno 6431 P43131 NK Activating 2 116-563 6-66027-335-337-158a-158b- 72.8E-08 0.221 0.040 5.508 UPPO percentage of A2 givan in total led gi givans (GPn) immuno 6432 P4312 NK Activating 2 116-56 6-660D22335-337-158a-158b- 445E-07 0.221 0.040 5.508 UPPO percentage of A2 givan in total neutral lgG givans (GPn) immuno 6434 P4312 NK Activating 2 115-56 6-650D2335-337-158a-158b- 441E-08 0.267 0.026 5.528 UPPO the percentage of A2 givan in total led gi givans (GPn) immuno 6434 P43134 NK Activating 2 115-56 61-65014-3354-371-158a-158b- 359E-08 0.267 0.040 5.582 UPPO the percentage of A2 givan in total neutral lgG givans immuno 6434 P43134 NK Activating 2 115-56 116-56014-3354-371-158a-158b- 159E-06 0.047 5.282 UPPO the percentage of A2 givan in total neutral lgG givans immuno 6434 P431	IGP50	The percentage of fucosylation of agalactosylated structures	immuno_64341	P4:3131 NK Activating 2 16+56	16+56/335+337-158a-158b-	7 39E-07	0.202	0.035	5.040
Construction Implementagio (A.2.9/action) Construction <		The percentage of fuces viation of menegalactory viated structures	immuno_64341	P4:3131 NK Activating 2 16+56	16+56/335+337 1585 158b	7.392-07	0.203	0.041	5.509
Gr42 The percentage of A2 glycan in bala regult all gG glycans (GPn) Immuno_6432 P4.3132 NK Actualing 2 16+56 16+56/CD2+338+337-168a-158b- 4.66-07 0.048 5.186 GP60 The percentage of A2 glycan in btal neutral IgG glycans (GPn) Immuno_64342 P4.3132 NK Actualing 2 16+56 16+56/CD2+338+337-158a-158b- 4.66-07 0.048 5.186 GP42 The percentage of A2 glycan in btal neutral IgG glycans (GPn) Immuno_64342 P4.3134 NK Actualing 2 16+56 16+56/CID4-333+337-158a-158b- 3.85-06 -0.207 0.044 5.652 GP42 The percentage of A2 glycan in btal neutral IgG glycans (GPn) Immuno_64344 P4.3134 NK Actualing 2 16+56 16+56/CID4-3337-158a-158b- 1.59E-06 0.207 0.044 4.887 GP50 The percentage of A2 glycan in btal neutral IgG glycans (GPn) Immuno_6434 P4.3135 NK Actualing 2 16+56 16+56/CID4-333-37-158a-158b- 2.220-07 0.222 0.046 5.216 GP20 The percentage of A2 glycan in btal neutral IgG glycans (GPn) Immuno_6437 P4.3155 NK Actualing 2 16+56 16+56/C	IGP2	The percentage of A2 glycan in total InG glycans	immuno_64342	P4:3132 NK Activating 2 16+56	16+56/CD2+335+337-1582-158b-	4 75E-07	-0.221	0.040	-5 128
IDPE0 The percentage of fucosylation of monogalaciosylated structures immuno 64342 P43132 IXK Activating 2 16+65 16+56 14+36 0 0 </td <td></td> <td>The percentage of A2 glycan in total neutral IgG glycans (GPn)</td> <td>immuno_64342</td> <td>P4:3132 NK Activating 2 16+56</td> <td>16+56/CD2+335+337-1582-158b-</td> <td>3.55E-07</td> <td>-0.230</td> <td>0.030</td> <td>-5.120</td>		The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64342	P4:3132 NK Activating 2 16+56	16+56/CD2+335+337-1582-158b-	3.55E-07	-0.230	0.030	-5.120
GP2 The percentage of A2 glycan in bial lgG glycans (GPn) Immuno_6434 P43134 NK Activating 2 16-66 16+66014+336+337+158a-158b- 3.56E-08 -0.276 0.050 -5.682 IGP42 The percentage of A2 glycan in bial neutral lgG glycans (GPn) Immuno_64344 P43134 NK Activating 2 16+66 16+66014+335+337+158a-158b- 3.56E-08 -0.276 0.050 -5.682 IGP50 The percentage of A2 glycan in bial neutral lgG glycans (GPn) Immuno_64344 P4.3134 NK Activating 2 16+56 16+66014+335+337+158a-158b- 1.58E-06 0.194 0.040 4.821 IGP50 The percentage of A2 glycan in bial lgG glycans (GPn) Immuno_64344 P4.3134 NK Activating 2 16+56 16+66014+335+337+158a-158b- 1.58E-06 0.194 0.040 4.827 IGP2 The percentage of A2 glycan in bial neutral lgG glycans (GPn) Immuno_64345 P4.3135 NK Activating 2 16+56 16+56022+314+335+337+158a-158b- 2.22E-07 -0.222 0.040 5.211 IGP42 The percentage of A2 glycan in total neutral lgG glycans (GPn) Immuno_64370 P4.3158 NK Activating 2 16+56 16+56035+158a-158b- 2.27E-08 -	IGP60	The percentage of Az grycari in total neutral igo grycaris (of in)	immuno_64342	P4:3132 NK Activating 2 16+56	16+56/CD2+335+337-158a-158b-	4 46F-07	0.247	0.040	5 186
GP42 The percentage of A2 glycan in total neutral IgG glycans (GPn) Immuno_64344 P4:3134 NK Activating 2 16*56 16*56/314*335*37:158a-158b- 3.59E-08 -0.267 0.047 -5.823 IGP46 The percentage of A2G1 glycan in total neutral IgG glycans (GPn) immuno_64344 P4:3134 NK Activating 2 16*56 16*56/314*335*37:158a-158b- 1.358-06 -0.205 0.042 4.231 IGP60 The percentage of all tocosylated / tocosylated structures immuno_64344 P4:3134 NK Activating 2 16*56 16*56/314*335*37:158a-158b- 2.362 0.047 5.823 IGP60 The percentage of A2 glycan in total log Glycans (GPn) immuno_64345 P4:3135 NK Activating 2 16*56 16*56/314*335*37:158a-158b- 2.362-07 0.244 -5.048 IGP60 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64370 P4:3158 NK Activating 2 16*56 16*56/35*158a-158b- 2.28E-08 0.287 0.069 -5.046 IGP42 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64370 P4:3158 NK Activating 2 16*56 16*56/3	IGP2	The percentage of A2 glycan in total InG glycans	immuno_64344	P4:3134 NK Activating 2 16+56	16+56/314+335+337-158a-158b-	4 41E-08	-0.278	0.050	-5.582
GP46 The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn) Immuno_64344 P4:3134 NK Activating 2 16+56 16+56/314+335+337-158a-158b- 1.38E-06 0.205 0.042 4.921 GP50 The percentage of all lucosylated (+- bisecting GlcNAc) structures in total neutral IgG glycans Immuno_64344 P4:3134 NK Activating 2 16+56 16+56/314+335+337-158a-158b- 2.30E-07 0.214 0.040 5.200 GP20 The percentage of A2 glycan in total locuylated (structures) Immuno_64345 P4:3135 NK Activating 2 16+56 16+56/CD2+314+335+337-158a-158b- 5.22E-07 0.224 0.040 5.200 GP20 The percentage of A2 glycan in total neutral IgG glycans (GPn) Immuno_64345 P4:3155 NK Activating 2 16+56 16+56/CD2+314+335+337-158a-158b- 5.22E-07 0.242 0.048 5.048 GP42 The percentage of A2 glycan in total locuylated (+-bisecting GlcNAc) structures Immuno_64370 P4:3155 NK Activating 2 16+56 16+56/33+158a-158b- 1.27E-08 0.274 0.040 5.211 GP42 The percentage of A2 glycan in total locuylated (+-bisectring GlcNAc) structures in to	IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno 64344	P4:3134 NK Activating 2 16+56	16+56/314+335+337-158a-158b-	3 59E-08	-0.267	0.047	-5.623
GPS8 The percentage of all fucosylated (+/- bisecting GicNAc) structures in total neutral IgG glycans Immuno_64344 P4:3134 NK Activating 2 16+56 16+56/314+335+337-158a-158b- 1.59E-06 0.194 0.040 4.887 GPS0 The percentage of lucosylation of monogalactosylated structures immuno_64344 P4:3134 NK Activating 2 16+56 16+56/314+335+337-158a-158b- 2.30E-07 0.214 0.040 4.887 GPS0 The percentage of A2 glycan in total IgG glycans (GPn) immuno_64345 P4:3135 NK Activating 2 16+56 16+56/314+335+337-158a-158b- 6.22E-07 0.242 0.040 4.887 GPS0 The percentage of A2 glycan in total IgG glycans (GPn) immuno_64370 P4:3158 NK Activating 2 16+56 16+56/35+158a-158b- 2.22E-07 -0.242 0.040 4.887 GPS0 The percentage of A2 glycan in total Ineutral IgG glycans (GPn) immuno_64370 P4:3158 NK Activating 2 16+56 16+56/35+158a-158b- 16:750/35+158a-158b- 16:750/35+158a-158b- 10:7E-06 0.020 0.041 -5.018 GPS0 The percentage of A2 glycan in total Ineutral IgG glycan	IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno 64344	P4:3134 NK Activating 2 16+56	16+56/314+335+337-158a-158b-	1.38E-06	-0.205	0.042	-4 921
Impunce End percentage of fucosylation of monogalactosylated structures immunce 64344 P4:3134 NK Activating 2 16+56 16+56/314+335+337-158a-158b- 2.30E-07 0.214 0.040 5.290 IGP2 The percentage of A2 glycan in total neutral lgG glycans (GPn) immunce 64345 P4:3135 NK Activating 2 16+56 16+56/CD2+314+335+337-158a-158b- 5.22E-07 -0.224 0.048 -5.040 IGP2 The percentage of fucosylation of monogalactosylated structures immunce 64345 P4:3135 NK Activating 2 16+56 16+56/CD2+314+335+337-158a-158b- 3.24E-07 0.214 0.040 5.290 IGP2 The percentage of A2 glycan in total neutral lgG glycans (GPn) immunce 164370 P4:3158 NK Activating 2 16+56 16+56/354+158a-158b- 2.28E-08 -0.287 0.040 -5.817 IGP4 The percentage of A2 glycan in total neutral lgG glycans (GPn) immunce/4370 P4:3158 NK Activating 2 16+56 16+56/35+158a-158b- 8.07E-07 -0.202 0.041 +5.018 IGP4 The percentage of A2 glycan in total neutral lgG glycans (GPn	IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral InG glycans	immuno 64344	P4:3134 NK Activating 2 16+56	16+56/314+335+337-158a-158b-	1.59E-06	0 194	0.040	4 887
GP2 The percentage of A2 glycan in total lgG glycans immuno_64345 P4:3135 NK Activating 2 16+56 16+56/CD2+314+335+337-158a-158b- 6.22E-07 -0.225 0.050 -6.040 GP42 The percentage of A2 glycan in total neutral lgG glycans (GPn) immuno_64345 P4:3135 NK Activating 2 16+56 16+56/CD2+314+335+337-158a-158b- 3.94E-07 0.212 0.040 5.040 GP42 The percentage of A2 glycan in total log glycans (GPn) immuno_64370 P4:3158 NK Activating 2 16+56 16+56/CD2+314+335+337-158a-158b- 2.28E-08 -0.283 0.050 5.706 GP42 The percentage of A2 glycan in total neutral lgG glycans (GPn) immuno_64370 P4:3158 NK Activating 2 16+56 16+56/335+158a-158b- 1.27E-08 -0.274 0.047 -5.018 GP50 The percentage of all (uosylated ft/-b bisecting GlcNAc) structures in total neutral lgG glycans immuno_64370 P4:3158 NK Activating 2 16+56 16+56/35+158a-158b- 1.07E-06 0.202 0.041 -5.018 GP60 The percentage of Lossylation of monogalactosylated structures immuno_64371 P4:3158	IGP60	The percentage of fucosylation of monogalactosylated structures	immuno 64344	P4:3134 NK Activating 2 16+56	16+56/314+335+337-158a-158b-	2.30E-07	0.214	0.040	5.290
IGP42 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64345 P4:3135 NK Activating 2 16+56 16+56/CD2+314+335+337-158a-158b- 6.52E-07 0.242 0.048 -5.068 IGP20 The percentage of A2 glycan in total IgG glycans immuno_64345 P4:3135 NK Activating 2 16+56 16+56/CD2+314+335+337-158a-158b- 2.24E-08 0.221 0.040 5.211 IGP42 The percentage of A2 glycan in total Incutral IgG glycans (GPn) immuno_64370 P4:3158 NK Activating 2 16+56 16+56/C35+158a-158b- 2.24E-08 0.223 0.050 -5.706 IGP42 The percentage of A2 glycan in total Incutral IgG glycans (GPn) immuno_64370 P4:3158 NK Activating 2 16+56 16+56/35+158a-158b- 8.59E-07 0.208 0.041 -5.018 IGP45 The percentage of fucosylation of agalactosylated structures immuno_64370 P4:3158 NK Activating 2 16+56 16+56/35+158a-158b- 1.07E-06 0.202 0.041 4.965 IGP42 The percentage of fucosylation of agalactosylated structures immuno_64371 P4:3158 NK Activating 2 16+56 16+56/35+158a-158b- 1.07E-06 0.202 0.041 4.965 IGP42	IGP2	The percentage of A2 glycan in total IgG glycans	immuno 64345	P4:3135 NK Activating 2 16+56	16+56/CD2+314+335+337-158a-158b-	7.22E-07	-0.252	0.050	-5.040
IGP60 The percentage of Locaylation of monogalactosylated structures immuno_64345 P4:3135 NK Activating 2 16+56 16+56/CD2+314+335+337-158a-158b- 3.94E-07 0.211 0.040 5.211 IGP2 The percentage of A2 glycan in total lug glycans (GPn) immuno_64370 P4:3158 NK Activating 2 16+56 16+56/335+158a-158b- 2.28E-08 -0.228 0.047 -5.817 IGP4 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64370 P4:3158 NK Activating 2 16+56 16+56/335+158a-158b- 8.59E-07 -0.208 0.041 -5.018 IGP50 The percentage of Locaylated (+/- bisecting GICNAc) structures in total neutral IgG glycans immuno_64370 P4:3158 NK Activating 2 16+56 16+56/335+158a-158b- 1.07E-06 0.202 0.041 -5.018 IGP60 The percentage of Locaylation of monogalactosylated structures immuno_64370 P4:3158 NK Activating 2 16+56 16+56/335+158a-158b- 1.07E-06 0.202 0.041 -5.444 IGP2 The percentage of Locaylation of monogalactosylated structures immuno_64371 P4:3158 <td< td=""><td>IGP42</td><td>The percentage of A2 glycan in total neutral lgG glycans (GPn)</td><td>immuno 64345</td><td>P4:3135 NK Activating 2 16+56</td><td>16+56/CD2+314+335+337-158a-158b-</td><td>6.52E-07</td><td>-0.242</td><td>0.048</td><td>-5.068</td></td<>	IGP42	The percentage of A2 glycan in total neutral lgG glycans (GPn)	immuno 64345	P4:3135 NK Activating 2 16+56	16+56/CD2+314+335+337-158a-158b-	6.52E-07	-0.242	0.048	-5.068
IGP2 The percentage of A2 glycan in total lgG glycans immuno_64370 P4:3158 NK Activating 2 16+56/335+158a-158b- 2.28E-08 -0.283 0.050 -5.706 IGP42 The percentage of A2 glycan in total neutral lgG glycans (GPn) immuno_64370 P4:3158 NK Activating 2 16+56 16+56/335+158a-158b- 1.27E-08 -0.274 0.047 -5.817 IGP58 The percentage of A2 glycan in total neutral lgG glycans (GPn) immuno_64370 P4:3158 NK Activating 2 16+56 16+56/335+158a-158b- 8.07E-07 0.208 0.041 -5.018 IGP59 The percentage of fucosylation of agalactosylated structures immuno_64370 P4:3158 NK Activating 2 16+56 16+56/35+158a-158b- 1.07E-07 0.200 0.039 5.084 IGP2 The percentage of fucosylation of agalactosylated structures immuno_64371 P4:3158 NK Activating 2 16+56 16+56/CD2+335+158a-158b- 1.07E-07 0.208 0.040 5.144 IGP42 The percentage of A2 glycan in total log Glycans immuno_64371 P4:3159 NK Activating 2 16+56 16+56/CD2+335+158a-158b- <td>IGP60</td> <td>The percentage of fucosylation of monogalactosylated structures</td> <td>immuno 64345</td> <td>P4:3135 NK Activating 2 16+56</td> <td>16+56/CD2+314+335+337-158a-158b-</td> <td>3.94E-07</td> <td>0.211</td> <td>0.040</td> <td>5.211</td>	IGP60	The percentage of fucosylation of monogalactosylated structures	immuno 64345	P4:3135 NK Activating 2 16+56	16+56/CD2+314+335+337-158a-158b-	3.94E-07	0.211	0.040	5.211
IGP42 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64370 P4:3158 NK Activating 2 16+56 16+56/335+158a-158b- 1.27E-08 -0.274 0.047 -5.817 IGP46 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64370 P4:3158 NK Activating 2 16+56 16+56/335+158a-158b- 8.59E-07 -0.208 0.041 -5.018 IGP59 The percentage of all tocsylated (+-bickids)strictures in total neutral IgG glycans immuno_64370 P4:3158 NK Activating 2 16+56 16+56/335+158a-158b- 1.07E-06 0.202 0.041 4.965 IGP20 The percentage of A2 glycan in total glog glycans immuno_64371 P4:3158 NK Activating 2 16+56 16+56/335+158a-158b- 1.07E-06 0.202 0.041 4.965 IGP20 The percentage of A2 glycan in total glog glycans immuno_64371 P4:3159 NK Activating 2 16+56 16+56/022+335+158a-158b- 1.08E-07 0.228 0.040 5.135 IGP20 The percentage of A2 glycan in total glog glycans immuno_64371 P4:3159 NK Activating 2 16+56 16+56/022+335+158a-158b- 5.05E-07 -0.248 0.048	IGP2	The percentage of A2 glycan in total IgG glycans	immuno 64370	P4:3158 NK Activating 2 16+56	16+56/335+158a-158b-	2.28E-08	-0.283	0.050	-5.706
IGP46 The percentage of A2G1 glycan in total lneutral IgG glycans (GPn) immuno_64370 P4:3158 NK Activating 2 16+56 16+56/335+158a-158b- 8.59E-07 -0.208 0.041 -5.018 IGP58 The percentage of ILcosylation of agalactosylated structures in total neutral IgG glycans immuno_64370 P4:3158 NK Activating 2 16+56 16+56/35+158a-158b- 6.07E-07 0.200 0.039 5.048 IGP59 The percentage of ILcosylation of agalactosylated structures immuno_64370 P4:3158 NK Activating 2 16+56 16+56/35+158a-158b- 1.07E-06 0.202 0.041 4.965 IGP2 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64371 P4:3159 NK Activating 2 16+56 16+56/02+335+158a-158b- 7.27E-07 -0.228 0.040 5.135 IGP42 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64371 P4:3159 NK Activating 2 16+56 16+56/02+335+158a-158b- 5.96E-07 -0.208 0.040 5.135 IGP42 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64374 P4:3161 NK Activating 2 16+56 16+56/314+335+158a-158b- 5.23E-08	IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64370	P4:3158 NK Activating 2 16+56	16+56/335+158a-158b-	1.27E-08	-0.274	0.047	-5.817
IGP58 The percentage of all fucosylated (+/- bisecting GicNAc) structures in total neutral IgG glycans immuno_64370 P4:3158 NK Activating 2 16+56 16+56/335+158a-158b- 1.07E-06 0.202 0.041 4.965 IGP59 The percentage of fucosylation of agalactosylated structures immuno_64370 P4:3158 NK Activating 2 16+56 16+56/335+158a-158b- 1.07E-06 0.202 0.041 4.965 IGP60 The percentage of A2 glycan in total log Glycans (GPn) immuno_64371 P4:3158 NK Activating 2 16+56 16+56/0235+158a-158b- 7.27E-07 -0.224 0.040 5.444 IGP2 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64371 P4:3159 NK Activating 2 16+56 16+56/CD2+335+158a-158b- 5.35E-07 -0.244 0.048 -5.115 IGP42 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64371 P4:3159 NK Activating 2 16+56 16+56/CD2+335+158a-158b- 5.36E-07 -0.208 0.040 5.130 IGP42 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64374 P4:3161 NK Activating 2 16+56 16+56/CD2+335+158a-158b- 5.23E-07 0.218 <td>IGP46</td> <td>The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)</td> <td>immuno_64370</td> <td>P4:3158 NK Activating 2 16+56</td> <td>16+56/335+158a-158b-</td> <td>8.59E-07</td> <td>-0.208</td> <td>0.041</td> <td>-5.018</td>	IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64370	P4:3158 NK Activating 2 16+56	16+56/335+158a-158b-	8.59E-07	-0.208	0.041	-5.018
IGP59 The percentage of fucosylation of agalactosylated structures immuno_64370 P4:3158 NK Activating 2 16+56 16+56/335+158a-158b- 1.07E-06 0.202 0.041 4.965 IGP60 The percentage of fucosylation of monogalactosylated structures immuno_64370 P4:3158 NK Activating 2 16+56 16+56/335+158a-158b- 1.03E-07 0.219 0.040 5.444 IGP2 The percentage of A2 glycan in total log glycans immuno_64371 P4:3159 NK Activating 2 16+56 16+56/CD2+335+158a-158b- 5.35E-07 -0.244 0.048 -5.115 IGP60 The percentage of A2 glycan in total log glycans immuno_64371 P4:3159 NK Activating 2 16+56 16+56/CD2+335+158a-158b- 5.96E-07 0.208 0.040 5.130 IGP2 The percentage of A2 glycan in total log glycans immuno_64374 P4:3161 NK Activating 2 16+56 16+56/CD2+335+158a-158b- 5.96E-07 0.208 0.040 5.130 IGP42 The percentage of A2 glycan in total log glycans (GPn) immuno_64374 P4:3161 NK Activating 2 16+56 16+56/314+335+158a-158b- 5.23E-08 -0.275 0.050 -5.088 IGP60 The percentage of A2 glycan in total log glycans (GPn	IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64370	P4:3158 NK Activating 2 16+56	16+56/335+158a-158b-	6.07E-07	0.200	0.039	5.084
IGP60 The percentage of fucosylation of monogalactosylated structures immuno_64370 P4:3158 NK Activating 2 16+56 16+56/35+158a-158b- 1.03E-07 0.219 0.040 5.444 IGP2 The percentage of A2 glycan in total IgG glycans immuno_64371 P4:3159 NK Activating 2 16+56 16+56/02D+335+158a-158b- 7.27E-07 -0.252 0.050 -5.043 IGP42 The percentage of A2 glycan in total IgG glycans (GPn) immuno_64371 P4:3159 NK Activating 2 16+56 16+56/02D+335+158a-158b- 5.35E-07 -0.244 0.448 -5.115 IGP42 The percentage of A2 glycan in total IgG glycans immuno_64371 P4:3159 NK Activating 2 16+56 16+56/02D+335+158a-158b- 5.96E-07 0.208 0.040 5.130 IGP42 The percentage of A2 glycan in total IgG glycans (GPn) immuno_64374 P4:3161 NK Activating 2 16+56 16+56/314+335+158a-158b- 5.23E-08 -0.245 0.050 -5.508 IGP42 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64374 P4:3161 NK Activating 2 16+56 16	IGP59	The percentage of fucosylation of agalactosylated structures	immuno_64370	P4:3158 NK Activating 2 16+56	16+56/335+158a-158b-	1.07E-06	0.202	0.041	4.965
IGP2 The percentage of A2 glycan in total lgG glycans immuno_64371 P4:3159 NK Activating 2 16+56 16+56/CD2+335+158a-158b- 7.27E-07 -0.252 0.050 -5.043 IGP42 The percentage of A2 glycan in total neutral lgG glycans (GPn) immuno_64371 P4:3159 NK Activating 2 16+56 16+56/CD2+335+158a-158b- 5.35E-07 -0.244 0.048 -5.115 IGP42 The percentage of A2 glycan in total neutral lgG glycans immuno_64371 P4:3159 NK Activating 2 16+56 16+56/CD2+335+158a-158b- 5.96E-07 0.248 0.040 -5.103 IGP42 The percentage of A2 glycan in total neutral lgG glycans immuno_64374 P4:3161 NK Activating 2 16+56 16+56/CD2+335+158a-158b- 5.23E-08 -0.264 0.048 -5.553 IGP42 The percentage of A2 glycan in total neutral lgG glycans (GPn) immuno_64374 P4:3161 NK Activating 2 16+56 16+56/CD2+314+335+158a-158b- 5.23E-08 -0.244 0.041 5.243 IGP42 The percentage of A2 glycan in total neutral lgG glycans immuno_64374 P4:3161 NK Activating 2 16+56 16+56/CD2+314+335+158a-158b- 5.23E-08 -0.244 0.041 5.243 IGP42 The percentage of A2 glycan in total lgG glycans immuno_64375 P4:3162 NK	IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64370	P4:3158 NK Activating 2 16+56	16+56/335+158a-158b-	1.03E-07	0.219	0.040	5.444
IGP42 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64371 P4:3159 NK Activating 2 16+56 16+56/CD2+335+158a-158b- 5.35E-07 -0.244 0.048 -5.115 IGP60 The percentage of fucosylation of monogalactosylated structures immuno_64371 P4:3159 NK Activating 2 16+56 16+56/CD2+335+158a-158b- 5.96E-07 0.208 0.040 5.130 IGP2 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64374 P4:3161 NK Activating 2 16+56 16+56/J14+335+158a-158b- 5.23E-07 0.248 0.048 -5.553 IGP42 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64374 P4:3161 NK Activating 2 16+56 16+56/J14+335+158a-158b- 5.23E-08 -0.244 0.048 -5.553 IGP60 The percentage of A2 glycan in total neutral IgG glycans immuno_64374 P4:3161 NK Activating 2 16+56 16+56/J14+335+158a-158b- 2.93E-07 0.241 0.048 -5.553 IGP62 The percentage of A2 glycan in total neutral IgG glycans immuno_64375 P4:3162 NK Activating 2 16+56 16+56/CD2+314+335+158a-158b- 1.52E-06 -0.245	IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64371	P4:3159 NK Activating 2 16+56	16+56/CD2+335+158a-158b-	7.27E-07	-0.252	0.050	-5.043
IGP60 The percentage of fucosylation of monogalactosylated structures immuno_64371 P4:3159 NK Activating 2 16+56 16+56/CD2+335+158a-158b- 5.96E-07 0.208 0.040 5.130 IGP60 The percentage of A2 glycan in total IgG glycans immuno_64374 P4:3161 NK Activating 2 16+56 16+56/CD2+335+158a-158b- 6.54E-08 -0.275 0.040 5.130 IGP62 The percentage of A2 glycan in total IgG glycans (GPn) immuno_64374 P4:3161 NK Activating 2 16+56 16+56/CD2+335+158a-158b- 5.22.08 -0.248 0.404 -5.553 IGP60 The percentage of A2 glycan in total IgG glycans immuno_64374 P4:3161 NK Activating 2 16+56 16+56/CD2+314+335+158a-158b- 2.93E-07 0.248 0.404 -5.553 IGP60 The percentage of A2 glycan in total IgG glycans immuno_64375 P4:3161 NK Activating 2 16+56 16+56/CD2+314+335+158a-158b- 2.93E-07 0.248 0.404 -5.243 IGP42 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64375 P4:3162 NK Activating 2 16+56	IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64371	P4:3159 NK Activating 2 16+56	16+56/CD2+335+158a-158b-	5.35E-07	-0.244	0.048	-5.115
IGP2 The percentage of A2 glycan in total lgG glycans immuno_64374 P4:3161 NK Activating 2 16+56 16+56/314+335+158a-158b- 6.54E-08 -0.275 0.050 -5.508 IGP42 The percentage of A2 glycan in total neutral lgG glycans (GPn) immuno_64374 P4:3161 NK Activating 2 16+56 16+56/314+335+158a-158b- 5.23E-08 -0.264 0.048 -5.553 IGP60 The percentage of A2 glycan in total neutral lgG glycans immuno_64374 P4:3161 NK Activating 2 16+56 16+56/314+335+158a-158b- 2.93E-07 0.213 0.041 -5.538 IGP62 The percentage of A2 glycan in total neutral lgG glycans immuno_64375 P4:3161 NK Activating 2 16+56 16+56/02+314+335+158a-158b- 1.52E-06 -0.245 0.041 -5.424 IGP62 The percentage of A2 glycan in total neutral lgG glycans immuno_64375 P4:3162 NK Activating 2 16+56 16+56/02+314+335+158a-158b- 1.52E-06 -0.245 0.048 -4.918 IGP42 The percentage of A2 glycan in total neutral lgG glycans immuno_64375 P4:3162 NK Activating 2 16+56 16+56/02+314+335+158a-158b- 1.52E-06 -0.245 0.041 <td>IGP60</td> <td>The percentage of fucosylation of monogalactosylated structures</td> <td>immuno_64371</td> <td>P4:3159 NK Activating 2 16+56</td> <td>16+56/CD2+335+158a-158b-</td> <td>5.96E-07</td> <td>0.208</td> <td>0.040</td> <td>5.130</td>	IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64371	P4:3159 NK Activating 2 16+56	16+56/CD2+335+158a-158b-	5.96E-07	0.208	0.040	5.130
IGP42 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64374 P4:3161 NK Activating 2 16+56 16+56/314+335+158a-158b- 5.23E-08 -0.264 0.048 -5.553 IGP60 The percentage of fucosylation of monogalactosylated structures immuno_64374 P4:3161 NK Activating 2 16+56 16+56/314+335+158a-158b- 2.93E-07 0.213 0.041 5.243 IGP20 The percentage of A2 glycan in total IgG glycans immuno_64375 P4:3162 NK Activating 2 16+56 16+56/ICD2+314+335+158a-158b- 1.52E-06 -0.245 0.048 -5.243 IGP42 The percentage of A2 glycan in total IgG glycans (GPn) immuno_64375 P4:3162 NK Activating 2 16+56 16+56/ICD2+314+335+158a-158b- 1.52E-06 -0.245 0.048 -4.887 IGP60 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64375 P4:3162 NK Activating 2 16+56 16+56/ICD2+314+335+158a-158b- 1.36E-06 -0.245 0.044 -4.987 IGP60 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64375 P4:3162 NK Activating 2 16+56 16+56/ICD2+314+335+158a-158b- 8.44E-07 0.	IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64374	P4:3161 NK Activating 2 16+56	16+56/314+335+158a-158b-	6.54E-08	-0.275	0.050	-5.508
IGP60 The percentage of fucosylation of monogalactosylated structures immuno_64374 P4:3161 NK Activating 2 16:56 16:56/314:335+158a-158b- 2.93E-07 0.213 0.041 5.243 IGP2 The percentage of A2 glycan in total IgG glycans immuno_64375 P4:3162 NK Activating 2 16:56 16:56/CD2+314:335+158a-158b- 1.52E-06 -0.245 0.050 -4.887 IGP42 The percentage of A2 glycan in total IgG glycans (GPn) immuno_64375 P4:3162 NK Activating 2 16:56 16:56/CD2+314:335+158a-158b- 1.36E-06 -0.235 0.041 5.060 IGP60 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64375 P4:3162 NK Activating 2 16:56 16:56/CD2+314:335+158a-158b- 1.36E-06 -0.235 0.041 5.060 IGP60 The percentage of A2 glycan in total neutral IgG glycans immuno_64375 P4:3162 NK Activating 2 16:56/CD2+314:335+158a-158b- 8.44:07 0.025 0.041 5.060 IGP2 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64431 P4:3212 NK Activating 2 16:56/335+337-158b- 4.09E-09 -0.244 0.047 -6.015 1	IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64374	P4:3161 NK Activating 2 16+56	16+56/314+335+158a-158b-	5.23E-08	-0.264	0.048	-5.553
IGP2 The percentage of A2 glycan in total IgG glycans immuno_64375 P4:3162 NK Activating 2 16:56 16:56/CD2+314+335+158a-158b- 1.52E-06 -0.245 0.050 -4.887 IGP42 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64375 P4:3162 NK Activating 2 16:56 16:56/CD2+314+335+158a-158b- 1.36E-06 -0.245 0.050 -4.887 IGP40 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64375 P4:3162 NK Activating 2 16:56 16:56/CD2+314+335+158a-158b- 1.36E-06 -0.245 0.048 -4.918 IGP42 The percentage of A2 glycan in total neutral IgG glycans immuno_64375 P4:3162 NK Activating 2 16:56 16:56/CD2+314+335+158a-158b- 8.44E-07 0.205 0.041 -5.069 IGP42 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64431 P4:3212 NK Activating 2 16:56 16:56/35+337-158b- 4.09E-09 -0.244 0.047 -6.015 IGP42 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64431 P4:3212 NK Activating 2 16:56/35+337-158b- 2.54E-09 -0.274 0.045	IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64374	P4:3161 NK Activating 2 16+56	16+56/314+335+158a-158b-	2.93E-07	0.213	0.041	5.243
IGP42 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64375 P4:3162 NK Activating 2 16+56 16+56/CD2+314+335+158a-158b- 1.36E-06 -0.235 0.048 -4.918 IGP60 The percentage of fucosylation of monogalactosylated structures immuno_64375 P4:3162 NK Activating 2 16+56 16+56/CD2+314+335+158a-158b- 8.44E-07 0.205 0.041 5.060 IGP2 The percentage of A2 glycan in total IgG glycans immuno_64431 P4:3212 NK Activating 2 16+56 16+56/335+337-158b- 4.09E-09 -0.248 0.047 -6.015 IGP42 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64431 P4:3212 NK Activating 2 16+56 16+56/335+337-158b- 4.09E-09 -0.248 0.047 -6.015 IGP42 The percentage of A2 glycan in total neutral IgG glycans (GPn) immuno_64431 P4:3212 NK Activating 2 16+56 16+56/335+337-158b- 2.54E-09 -0.274 0.045 -6.099	IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64375	P4:3162 NK Activating 2 16+56	16+56/CD2+314+335+158a-158b-	1.52E-06	-0.245	0.050	-4.887
IGP60 The percentage of fucosylation of monogalactosylated structures immuno_64375 P4:3162 NK Activating 2 16+56 16+56/CD2+314+335+158a-158b- 8.44E-07 0.205 0.041 5.060 IGP2 The percentage of A2 glycan in total lgG glycans immuno_64431 P4:3212 NK Activating 2 16+56 16+56/335+337-158b- 4.09E-09 -0.284 0.047 -6.015 IGP42 The percentage of A2 glycan in total neutral lgG glycans (GPn) immuno_64431 P4:3212 NK Activating 2 16+56 16+56/335+337-158b- 2.54E-09 -0.274 0.045 -6.099	IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64375	P4:3162 NK Activating 2 16+56	16+56/CD2+314+335+158a-158b-	1.36E-06	-0.235	0.048	-4.918
IGP2 The percentage of A2 glycan in total lgG glycans 4.09E-09 -0.284 0.047 -6.015 IGP42 The percentage of A2 glycan in total neutral lgG glycans immuno_64431 P4:3212 NK Activating 2 16+56 16+56/335+337-158b- 4.09E-09 -0.284 0.047 -6.015 IGP42 The percentage of A2 glycan in total neutral lgG glycans (GPn) immuno_64431 P4:3212 NK Activating 2 16+56 16+56/335+337-158b- 2.54E-09 -0.274 0.045 -6.099	IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64375	P4:3162 NK Activating 2 16+56	16+56/CD2+314+335+158a-158b-	8.44E-07	0.205	0.041	5.060
Immuno_64431 P4:3212 NK Activating 2 16+56 16+56/335+337-158b- 2.54E-09 -0.274 0.045 -6.099	IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64431	P4:3212 NK Activating 2 16+56	16+56/335+337-158b-	4.09E-09	-0.284	0.047	-6.015
	IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	Immuno_64431	P4:3212 NK Activating 2 16+56	16+56/335+337-158b-	2.54E-09	-0.274	0.045	-6.099

IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64431	P4:3212 NK Activating 2	16+56	16+56/335+337-158b-	2.24E-07	-0.207	0.039	-5.277
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64431	P4:3212 NK Activating 2	16+56	16+56/335+337-158b-	1.80E-07	0.199	0.037	5.319
IGP59	The percentage of fucosylation of agalactosylated structures	immuno_64431	P4:3212 NK Activating 2	16+56	16+56/335+337-158b-	4.14E-07	0.199	0.039	5.151
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64431	P4:3212 NK Activating 2	16+56	16+56/335+337-158b-	3.60E-08	0.215	0.038	5.632
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64432	P4:3213 NK Activating 2	16+56	16+56/CD2+335+337-158b-	1.89E-07	-0.253	0.048	-5.305
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64432	P4:3213 NK Activating 2	16+56	16+56/CD2+335+337-158b-	1.46E-07	-0.243	0.045	-5.363
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64432	P4:3213 NK Activating 2	16+56	16+56/CD2+335+337-158b-	1.46E-06	0.185	0.038	4.922
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64432	P4:3213 NK Activating 2	16+56	16+56/CD2+335+337-158b-	3.89E-07	0.201	0.039	5.204
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64434	P4:3215 NK Activating 2	16+56	16+56/314+335+337-158b-	1.37E-08	-0.275	0.047	-5.799
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64434	P4:3215 NK Activating 2	16+56	16+56/314+335+337-158b-	1.40E-08	-0.262	0.045	-5.794
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64434	P4:3215 NK Activating 2	16+56	16+56/314+335+337-158b-	7.93E-07	-0.199	0.040	-5.027
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64434	P4:3215 NK Activating 2	16+56	16+56/314+335+337-158b-	9.69E-07	0.188	0.038	4.984
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64434	P4:3215 NK Activating 2	16+56	16+56/314+335+337-158b-	1.61E-07	0.206	0.039	5.348
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64435	P4:3216 NK Activating 2	16+56	16+56/CD2+314+335+337-158b-	3.63E-07	-0.248	0.048	-5.175
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64435	P4:3216 NK Activating 2	16+56	16+56/CD2+314+335+337-158b-	3.74E-07	-0.236	0.046	-5.174
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64435	P4:3216 NK Activating 2	16+56	16+56/CD2+314+335+337-158b-	5.36E-07	0.199	0.039	5.140
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64460	P4:3239 NK Activating 2	16+56	16+56/335+158b-	4.94E-09	-0.283	0.047	-5.982
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64460	P4:3239 NK Activating 2	16+56	16+56/335+158b-	2.97E-09	-0.273	0.045	-6.072
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64460	P4:3239 NK Activating 2	16+56	16+56/335+158b-	2.69E-07	-0.206	0.039	-5.243
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64460	P4:3239 NK Activating 2	16+56	16+56/335+158b-	2.31E-07	0.197	0.037	5.271
IGP59	The percentage of fucosylation of agalactosylated structures	immuno_64460	P4:3239 NK Activating 2	16+56	16+56/335+158b-	4.83E-07	0.198	0.039	5.120
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64460	P4:3239 NK Activating 2	16+56	16+56/335+158b-	4.55E-08	0.214	0.038	5.589
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64462	P4:3240 NK Activating 2	16+56	16+56/CD2+335+158b-	2.95E-07	-0.249	0.048	-5.218
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64462	P4:3240 NK Activating 2	16+56	16+56/CD2+335+158b-	2.28E-07	-0.240	0.045	-5.277
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64462	P4:3240 NK Activating 2	16+56	16+56/CD2+335+158b-	5.76E-07	0.198	0.039	5.126
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64464	P4:3242 NK Activating 2	16+56	16+56/314+335+158b-	2.02E-08	-0.272	0.048	-5.727
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64464	P4:3242 NK Activating 2	16+56	16+56/314+335+158b-	2.01E-08	-0.259	0.045	-5.728
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64464	P4:3242 NK Activating 2	16+56	16+56/314+335+158b-	1.16E-06	-0.196	0.040	-4.951
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64464	P4:3242 NK Activating 2	16+56	16+56/314+335+158b-	1.41E-06	0.185	0.038	4.908
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64464	P4:3242 NK Activating 2	16+56	16+56/314+335+158b-	2.28E-07	0.204	0.039	5.282
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64465	P4:3243 NK Activating 2	16+56	16+56/CD2+314+335+158b-	4.83E-07	-0.246	0.048	-5.118
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64465	P4:3243 NK Activating 2	16+56	16+56/CD2+314+335+158b-	4.53E-07	-0.235	0.046	-5.136
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64465	P4:3243 NK Activating 2	16+56	16+56/CD2+314+335+158b-	6.49E-07	0.199	0.039	5.102
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64610	P4:3374 NK Activating 2	16+56	16+56/335+337-158a-	1.18E-06	-0.225	0.045	-4.944
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64641	P4:3401 NK Activating 2	16+56	16+56/335+158a-	1.61E-06	-0.222	0.046	-4.880
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64700	P4:3455 NK Activating 2	16+56	16+56/335+337-	1.14E-06	-0.211	0.043	-4.945
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64730	P4:3482 NK Activating 2	16+56	16+56/335+	1.56E-06	-0.208	0.043	-4.881
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63906	P4:2740 NK Effector	16+56	16+56/335-337-R7-	1.83E-06	0.224	0.046	4.852
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63906	P4:2740 NK Effector	16+56	16+56/335-337-R7-	1.19E-06	0.217	0.044	4.943
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63935	P4:2767 NK Effector	16+56	16+56/335-R7-	1.60E-06	0.225	0.046	4.880
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63935	P4:2707 INK Ellector	10+30	10+30/333-R7-	1.05E-06	0.210	0.044	4.969
IGP42	The percentage of A2 glycan in total ineutral igG glycans (GPn)	immuno_64064	P4:2900 INK Ellector	10+30	10+50/335-337-1508-150D+R7-	1.07E-00	0.240	0.051	4.002
IGP40	The percentage of A2GT grycan in total ineutral igG grycans (GPH)	immuno_64064	P4.2900 INK Ellector	10+30	10+50/335-337-1508-150D+R7-	9.02E-07	0.219	0.044	4.902
IGP00	The percentage of lucosylation of monogalaciosylated structures	immuno_64064	P4:2900 INK Ellector	10+30	10+50/335-337-1508-150D+R7-	0.00E-07	-0.219	0.044	-5.017
	The percentage of A2 glycan in total ligg glycans	immuno_64157	P4:2967 INK Ellector	16+56	10+30/333-337-130D+R7-	1.01E-07	0.200	0.054	5.340
ICP42	The percentage of A2C1 glucon in total incutral igO glycans (OPn)	immuno_64157	P4:2067 NK Effector	16+56	10+50/355-357-1500+R7-	1.00E-07	0.274	0.051	5.320
	The percentage of A2GT grycan in total ineutral igG grycans (GFT)	immuno_64157	P4:2067 NK Effector	16+56	10+50/335-337-1500+R7-	1.00E-07	0.240	0.045	5.339
ICP50	The percentage of an accessible (17-bisecung Gictarc) structures in total neutral igo grycans	immuno_64157	P4:2067 NK Effector	16+56	16+56/335-337-1500+107-	5.30L-07	-0.225	0.044	-5.104
IGP59	The percentage of fucesylation of agalactosylated structures	immuno_64157	P4:2967 NK Effector	16+56	10+50/335-337-1580+R7-	9.31E-07	-0.227	0.045	-5.100
IGP2	The percentage of A2 glycan in total lgG glycans	immuno_64187	P4:2907 NK Effector	16+56	16+56/335-158b+R7-	1.52E-00	0.244	0.043	5 351
IGP42	The percentage of A2 glycan in total neutral InG glycans (GPn)	immuno_64187	P4:2004 NK Effector	16+56	16+56/335-158b+R7-	1.52E-07	0.207	0.054	5 3 3 9
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno 64187	P4-2994 NK Effector	16+56	16+56/335-158b+R7-	1.52E-07	0.240	0.045	5 349
IGP58	The percentage of all fucosylated (+/- bisecting GloNAc) structures in total neutral InG divcans	immuno 64187	P4·2994 NK Effector	16+56	16+56/335-158b+R7-	5 15E-07	-0 225	0.044	-5 110
IGP59	The percentage of fucosylation of analactosylated structures	immuno 64187	P4·2994 NK Effector	16+56	16+56/335-158b+R7-	5 10E-07	-0 227	0.045	-5 108
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno 64187	P4:2994 NK Effector	16+56	16+56/335-158b+R7-	8.11E-08	-0.244	0.045	-5.470
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno 64680	P4:3437 NK Effector	16+56	16+56/335-337-	1.80F-06	0.207	0.043	4,851
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno 64710	P4:3464 NK Effector	16+56	16+56/335-	1.68E-06	0.207	0.043	4,866
IGP2	The percentage of A2 glycan in total IoG glycans	immuno 64950	P4:3680 NK Effector	16+56	16+56/335-337-158b+	1.54F-07	0.286	0.054	5.349
IGP42	The percentage of A2 glycan in total neutral log glycans (GPn)	immuno 64950	P4:3680 NK Effector	16+56	16+56/335-337-158b+	1.58E-07	0.274	0.051	5.340
IGP46	The percentage of A2G1 glycan in total Ineutral log glycans (GPn)	immuno 64950	P4:3680 NK Effector	16+56	16+56/335-337-158b+	1.47E-07	0.240	0.045	5,356
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral lnG divcans	immuno 64950	P4:3680 NK Effector	16+56	16+56/335-337-158b+	4.96E-07	-0.226	0.044	-5,118
IGP59	The percentage of fucosylation of agalactosylated structures	immuno 64950	P4:3680 NK Effector	16+56	16+56/335-337-158b+	4.98E-07	-0.228	0.045	-5,112
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno 64950	P4:3680 NK Effector	16+56	16+56/335-337-158b+	7.72E-08	-0.244	0.045	-5.479
IGP2	The percentage of A2 glycan in total loG glycans	immuno 64980	P4:3707 NK Effector	16+56	16+56/335-158b+	1.51E-07	0.287	0.054	5 353

IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64980	P4:3707 NK Effector	16+56	16+56/335-158b+	1.54E-07	0.275	0.051	5.345
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64980	P4:3707 NK Effector	16+56	16+56/335-158b+	1.42E-07	0.240	0.045	5.362
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64980	P4:3707 NK Effector	16+56	16+56/335-158b+	4.85E-07	-0.226	0.044	-5.122
IGP59	The percentage of fucosylation of agalactosylated structures	immuno_64980	P4:3707 NK Effector	16+56	16+56/335-158b+	4.90E-07	-0.228	0.045	-5.116
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64980	P4:3707 NK Effector	16+56	16+56/335-158b+	7.54E-08	-0.244	0.045	-5.483

Table S3: Associations of 51 immune cell traits with AITD and TPOAb level in the TwinsUK cohort

						AITD				TPOAb level				
immuneTrait ID	Trait ID	Canonical name	Lineage	Subset name	Pvalue	Beta	SE	Zscore	Pvalue	Beta	SE	Zscore		
immuno_64464	P4:3242	NK Activating 2	16+56	16+56/314+335+158b-	0.043	-0.049	0.024	-2.060	0.768	0.000	0.001	-0.297		
immuno_63707	P4:2561	NK Activating 2	16+56	16+56/314+335+158b-R7-	0.045	-0.049	0.024	-2.041	0.769	0.000	0.001	-0.296		
immuno_64374	P4:3161	NK Activating 2	16+56	16+56/314+335+158a-158b-	0.049	-0.046	0.023	-1.998	0.709	0.000	0.001	-0.377		
immuno_63625	P4:2488	NK Activating 2	16+56	16+56/314+335+158a-158b-R7-	0.050	-0.046	0.023	-1.990	0.723	0.000	0.001	-0.357		
immuno_64434	P4:3215	NK Activating 2	16+56	16+56/314+335+337-158b-	0.051	-0.047	0.024	-1.986	0.850	0.000	0.001	-0.191		
immuno_63677	P4:2534	NK Activating 2	16+56	16+56/314+335+337-158b-R7-	0.051	-0.047	0.024	-1.985	0.817	0.000	0.001	-0.233		
immuno_63703	P4:2558	NK Activating 2	16+56	16+56/335+158b-R7-	0.051	-0.048	0.024	-1.980	0.949	0.000	0.001	-0.065		
immuno_64460	P4:3239	NK Activating 2	16+56	16+56/335+158b-	0.052	-0.047	0.024	-1.969	0.951	0.000	0.001	-0.062		
immuno_64344	P4:3134	NK Activating 2	16+56	16+56/314+335+337-158a-158b-	0.055	-0.045	0.023	-1.951	0.756	0.000	0.001	-0.314		
immuno_63597	P4:2462	NK Activating 2	16+56	16+56/314+335+337-158a-158b-R7-	0.056	-0.045	0.023	-1.945	0.753	0.000	0.001	-0.317		
immuno_63674	P4:2531	NK Activating 2	16+56	16+56/335+337-158b-R7-	0.057	-0.047	0.024	-1.930	0.994	0.000	0.001	-0.008		
immuno_64431	P4:3212	NK Activating 2	16+56	16+56/335+337-158b-	0.059	-0.046	0.024	-1.914	0.984	0.000	0.001	0.021		
immuno_64370	P4:3158	NK Activating 2	16+56	16+56/335+158a-158b-	0.065	-0.044	0.023	-1.870	0.851	0.000	0.001	-0.190		
immuno_63595	P4:2460	NK Activating 2	16+56	16+56/335+337-158a-158b-R7-	0.066	-0.044	0.023	-1.867	0.925	0.000	0.001	-0.095		
immuno_63622	P4:2485	NK Activating 2	16+56	16+56/335+158a-158b-R7-	0.066	-0.044	0.023	-1.865	0.844	0.000	0.001	-0.198		
immuno_64341	P4:3131	NK Activating 2	16+56	16+56/335+337-158a-158b-	0.072	-0.043	0.023	-1.826	0.945	0.000	0.001	-0.070		
immuno_64641	P4:3401	NK Activating 2	16+56	16+56/335+158a-	0.086	-0.041	0.024	-1.729	0.750	0.000	0.001	0.324		
immuno 63906	P4:2740	NK Effector	16+56	16+56/335-337-R7-	0.086	0.043	0.025	1.726	0.351	0.000	0.001	-0.954		
immuno 64680	P4:3437	NK Effector	16+56	16+56/335-337-	0.087	0.043	0.025	1.727	0.365	0.000	0.001	-0.926		
immuno 63935	P4:2767	NK Effector	16+56	16+56/335-R7-	0.087	0.043	0.025	1.720	0.335	-0.001	0.001	-0.987		
immuno 64730	P4:3482	NK Activating 2	16+56	16+56/335+	0.088	-0.043	0.025	-1.719	0.358	0.000	0.001	0.941		
immuno_64710	P4:3464	NK Effector	16+56	16+56/335-	0.088	0.043	0.025	1.718	0.355	0.000	0.001	-0.947		
immuno 64610	P4:3374	NK Activating 2	16+56	16+56/335+337-158a-	0.094	-0.040	0.024	-1.688	0.701	0.000	0.001	0.389		
immuno 63835	P4:2677	NK Activating 2	16+56	16+56/335+337-158a-R7-	0.096	-0.040	0.024	-1.675	0.710	0.000	0.001	0.378		
immuno_64700	P4:3455	NK Activating 2	16+56	16+56/335+337-	0.104	-0.041	0.025	-1.637	0.313	0.001	0.001	1.035		
immuno 63925	P4:2758	NK Activating 2	16+56	16+56/335+337-R7-	0.104	-0.041	0.025	-1.636	0.322	0.001	0.001	1.016		
immuno 64465	P4:3243	NK Activating 2	16+56	16+56/CD2+314+335+158b-	0.153	-0.033	0.023	-1.443	0.988	0.000	0.001	-0.016		
immuno_63708	P4:2562	NK Activating 2	16+56	16+56/CD2+314+335+158b-R7-	0.155	-0.033	0.023	-1.434	0.995	0.000	0.001	0.006		
immuno 64375	P4:3162	NK Activating 2	16+56	16+56/CD2+314+335+158a-158b-	0.161	-0.032	0.023	-1.414	0.838	0.000	0.001	-0.211		
immuno_63626	P4:2489	NK Activating 2	16+56	16+56/CD2+314+335+158a-158b-R7-	0.162	-0.032	0.023	-1.410	0.855	0.000	0.001	-0.188		
immuno 64435	P4:3216	NK Activating 2	16+56	16+56/CD2+314+335+337-158b-	0.164	-0.033	0.023	-1.404	0.916	0.000	0.001	0.109		
immuno_63678	P4:2535	NK Activating 2	16+56	16+56/CD2+314+335+337-158b-R7-	0.165	-0.033	0.023	-1.400	0.896	0.000	0.001	0.135		
immuno 62860	P4:18	NK Activating 2	16+56	16+56/CD2+314+335+337-158a-158b-R7-	0.175	-0.031	0.023	-1.368	0.963	0.000	0.001	-0.048		
immuno 63623	P4:2486	NK Activating 2	16+56	16+56/CD2+335+158a-158b-R7-	0.178	-0.031	0.023	-1.358	0.875	0.000	0.001	-0.162		
immuno_63704	P4:2559	NK Activating 2	16+56	16+56/CD2+335+158b-R7-	0.179	-0.032	0.024	-1.354	0.939	0.000	0.001	0.079		
immuno 64371	P4:3159	NK Activating 2	16+56	16+56/CD2+335+158a-158b-	0.179	-0.031	0.023	-1.356	0.856	0.000	0.001	-0.187		
immuno 64462	P4:3240	NK Activating 2	16+56	16+56/CD2+335+158b-	0.180	-0.032	0.024	-1.354	0.940	0.000	0.001	0.078		
immuno 64345	P4:3135	NK Activating 2	16+56	16+56/CD2+314+335+337-158a-158b-	0.180	-0.031	0.023	-1.351	0.923	0.000	0.001	-0.100		
immuno_63675	P4:2532	NK Activating 2	16+56	16+56/CD2+335+337-158b-R7-	0.189	-0.031	0.024	-1.323	0.864	0.000	0.001	0.177		
immuno 64432	P4:3213	NK Activating 2	16+56	16+56/CD2+335+337-158b-	0.189	-0.031	0.024	-1.326	0.896	0.000	0.001	0.135		
immuno 64342	P4:3132	NK Activating 2	16+56	16+56/CD2+335+337-158a-158b-	0.197	-0.030	0.023	-1.300	0.981	0.000	0.001	-0.024		
immuno_63596	P4:2461	NK Activating 2	16+56	16+56/CD2+335+337-158a-158b-R7-	0.202	-0.030	0.023	-1.286	0.978	0.000	0.001	-0.028		
immuno 64157	P4:2967	NK Effector	16+56	16+56/335-337-158b+R7-	0.805	0.006	0.023	0.248	0.464	-0.001	0.001	-0.758		
immuno_64187	P4:2994	NK Effector	16+56	16+56/335-158b+R7-	0.808	0.006	0.023	0.244	0.466	-0.001	0.001	-0.754		
immuno 64980	P4:3707	NK Effector	16+56	16+56/335-158b+	0.816	0.005	0.023	0.233	0.459	-0.001	0.001	-0.765		
immuno_64950	P4:3680	NK Effector	16+56	16+56/335-337-158b+	0.816	0.005	0.023	0.233	0.457	-0.001	0.001	-0.769		
immuno_64161	P4:2970	NK Activating 1	16+56	16+56/314+335-337-158b+R7-	0.893	0.003	0.023	0.135	0.454	-0.001	0.001	-0.778		
immuno 64953	P4:3683	NK Activating 1	16+56	16+56/314+335-337-158b+	0.896	0.003	0.023	0.130	0.453	-0.001	0.001	-0.778		
immuno 64190	P4:2997	NK Activating 1	16+56	16+56/314+335-158b+R7-	0.904	0.003	0.023	0.121	0.453	-0.001	0.001	-0.780		
immuno 64984	P4:3710	NK Activating 1	16+56	16+56/314+335-158b+	0.905	0.003	0.023	0.120	0.453	-0.001	0.001	-0.778		
immuno_64084	P4:2900	NK Effector	16+56	16+56/335-337-158a-158b+R7-	0.970	0.001	0.024	0.038	0.528	-0.001	0.001	-0.648		

Table 54: Hits from selected eQTL studies for two SNPs, rs1521 and rs3094228 in the thyroid cells and whole blood * GVIAS catalog for the genetic variants associated with thyroid phenotypes(Data downloaded from GNUAS Catalog on 17/06/2015) * eQTLs from Haploreg 4.1 (https://bubs.broadinstlub.org/mammalis/haploreg/haploreg.php) and GTEx v6v7, v8 (https://www.giaxportal.org/home/)

Lead SNP-	Thyroid	phenotypes	(from GWA	AS catalog)*	Study ID	Danas Titla	eQTL**	rof allala	Tionuo	Correlated game		NEC	n value
risk allele	nromosom(si	art (ngso)en	a (ngso)	Phenotype	Study ID	Paper Inte	PMID	reraliele	Thyroid	VARS2	ENSG00000137411.16	0.29	5.00E-12
									Thyroid	MIR6891	ENSG00000277402.1	0.35	6.20E-11
									Thyroid	HCG27	ENSG00000206344.7	0.21	1.40E-09
									Thyroid	HLA-C PSORS1C3	ENSG00000204525.16 ENSG00000204528.3	-0.24	8.20E-08 7.50E-08
									Thyroid	XXbac-BPG181B23.7	ENSG00000272221.1	-0.25	1.40E-06
									Thyroid	MICA	ENSG00000204520.12	-0.18	2.50E-05
									Thyroid	PRRT1 FLOT1	ENSG00000204314.10 ENSG00000137312.14	0.12	4.20E-05
					GTEx2019_v8	The CTEX Concertium attac of concise regulatory offers correct human ticques	i.om/10.1101	<u> </u>	Whole Blood	XXbac-BPG181B23.7	ENSG00000272221.1	-0.34	2.20E-17
					phs000424.v8.p2)	1.01g/10.110	C	Whole_Blood	MIR6891	ENSG00000277402.1	0.28	1.40E-09
						, ,			Whole_Blood	PSORS1C3	ENSG00000204528.3	0.21	2.30E-08
									Whole Blood	HCG27	ENSG00000206344.7	0.088	1.20E-07
									Whole_Blood	VARS2	ENSG00000137411.16	0.1	2.20E-05
									Whole_Blood	DDR1 7BTB12	ENSG00000204580.13 ENSG00000204366.3	0.17	2.80E-05 3.20E-05
									Whole_Blood	HLA-C	ENSG00000204525.16	-0.12	5.70E-05
rs1521-T	6 3	1382927 3	1382927	Graves' disease					Whole_Blood	C4A	ENSG00000244731.7	-0.2	1.30E-04
									Whole_Blood	VARS2	ENSG00000137312.14 ENSG00000137411.12	0.045	1.70E-04 3.40E-09
					GTEx2017_v7				Thyroid	HCG27	ENSG00000206344.6	0.23	6.90E-08
					(dbGaP Accessio	n le Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in huma	a <u>29022597</u>	С	Thyroid	HLA-C	ENSG00000204525.10	-0.25	8.30E-06
					phs000424.v7.p2)			Thyroid Whole Blood	PSORS1C3 XXbac-BPG181B23 7	ENSG00000204528.3 ENSG00000272221.1	0.31	2.00E-05 7.00E-08
									Thyroid	HLA-C	ENSG00000204525.10	NA	1.28E-08
					GTEx2015 v6	e Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in huma	25954001	с	Thyroid	XXbac-BPG248L24.12		NA	1.03E-08
									Whole_Blood	HLA-C	ENSG00000204525.10	NA	2.98E-08
									Whole Blood	XXbac-BPG248L24.12	EN300000272221.1	NA	2.80E-07 8.29E-09
									Whole Blood	-		NA	1.11E-35
									Whole Blood	- AIF1	ENSG00000204472	NA	0.04E-30 2.51E-06
					Westra2013	Systematic identification of trans eQTLs as putative drivers of known disease associations	s <u>24013639</u>		Whole_Blood	ATP6V1G2 BAT1	ENSG00000213760	NA	9.31E-16
									Whole_Blood Whole_Blood	HCP5	ENSG00000206337.6 ENSG00000226979	NA NA	4.62E-06 8.46E-10
									Whole_Blood	MICB	ENSG00000204516.5	NA	5.24E-04
									Thyroid	C4A	ENSG00000244731.7	-0.39	2.00E-16
									Thyroid	MICB	ENSG00000204338.8 ENSG00000204516.9	-0.37	2.80E-14 3.70E-09
									Thyroid	HCP5	ENSG00000206337.10	-0.24	3.00E-08
									Thyroid	FLOT1	ENSG00000137312.14	0.17	5.00E-08
									Thyroid	PSORS1C1	ENSG00000204540.10 ENSG00000204536.13	-0.37	7.00E-08 2.00E-07
					CTEv2010 v8				Thyroid	HLA-C	ENSG00000204525.16	0.25	9.30E-07
					(dbGaP Accessio	The GTEx Consortium atlas of genetic regulatory effects across human tissues	i.org/10.1101	т	Thyroid	HLA-S	ENSG00000225851.1	-0.31	3.80E-06
					phs000424.v8.p2)			Thyroid Whole Blood	RNF5	ENSG00000204308.7 ENSG00000244731.7	-0.14	2.70E-05 1.50E-16
									Whole_Blood	C4B	ENSG00000224389.8	0.48	2.60E-13
				Thyroid					Whole_Blood	CYP21A1P	ENSG00000204338.8	-0.4	1.10E-12
rs3094228.C	6 3	1462150 3	1462150	peroxidase					Whole_Blood	CYP21A2 FLOT1	ENSG00000231852.6	0.4	3.20E-10 2.20E-05
135054220-0	0 0	1402150 5	1402130	antibody positivity					Whole Blood	HLA-S	ENSG00000225851.1	-0.27	3.70E-05
				(TPOAD-positivity)					Whole_Blood	CCHCR1	ENSG00000204536.13	0.13	8.10E-05
									Whole_Blood	XXbac-BPG248L24.12	ENSG00000271581.1 ENSG00000244731.3	-0.24	1.50E-04 3.40E-13
									Thyroid	CYP21A1P	ENSG00000204338.4	-0.37	1.10E-09
									Thyroid	HCP5	ENSG00000206337.6	-0.32	1.30E-09
					GTEx2017 v7				Thyroid	PSORS1C1	ENSG00000204540.6	-0.4	4.00E-06
					(dbGaP Accessio	n le Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in huma	a <u>29022597</u>	т	Thyroid	MICB	ENSG00000204516.5	0.26	5.10E-06
					phs000424.v7.p2)			Thyroid	CCHCR1	ENSG00000204536.9	0.21	1.70E-05
									Whole_Blood	C4A	ENSG00000244731.3	-0.48	4.00E-09
									Whole Blood	C4B	ENSG00000224389.4	0.41	9.90E-06
									Whole_Blood	CYP21A2	ENSG00000231852.2	0.38	2.90E-05
					GTEx2019 v8		https://doi.or		Thyroid	ATP6V1G2 SKIV2I	ENSG00000213760.10 ENSG00000204351.11	0.28	1.10E-05 2.20E-05
				16+56/CD2-	(dbGaP Accessio	n The GTEx Consortium atlas of genetic regulatory effects across human tissues	g/10.1101/78	А	Thyroid	CCHCR1	ENSG00000204536.13	-0.22	1.30E-04
rs2596460	6 3	1449483 3	1449483	314+335-337-	phs000424.v8.p2)	7903		Thyroid	VARS2	ENSG00000137411.16	-0.27	2.00E-04
				158a+158b+	GTEx2017 v7				Whole_Blood	MICA	ENSG00000204520.12 ENSG00000204525.10	0.22	3.40E-04
					(dbGaP Accessio	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans	29022597		Thyroid	000000	ENSG0000204525.10	-0.5	2.40E-05
					phs000424 v7.p2)			Thyroid	ATP6V1G2	ENSG00000213760.10	0.3	2.10E-06
									Thyroid	SKIV2L	ENSG00000204351.11	0.24	8.70E-06
					GTEx2019_v8 (dbGaP Accessio	The GTEx Consortium atlas of genetic regulatory effects across human figures	https://doi.or	A	Thyroid	VARS2	ENSG00000137411.16	-0.28	1.70E-04
		4440005 -	4440005	16+56/CD2-	phs000424.v8.p2)	7903	~	Thyroid	CCHCR1	ENSG00000204536.13	-0.21	2.70E-04
rs2596457	6 3	1449995 3	1449995	314+335-337- 158a+158b+		•			Thyroid	DDR1	ENSG00000204580.13	-0.18	4.60E-04
				.304 1300+	GTEx2017 v7				whole blood	MICA	ENSG00000204520.12	0.22	2.40E-04
					(dbGaP Accessio	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in	29022597		Thyroid	ATP6V1G2	ENSG00000213760.6	0.31	3.60E-05
					phs000424.v7.p2) numans			Thyroid	CCHCR1	ENSG00000204536.9	-0.28	4.80E-05
					GTEx2019 VR		https://doi.c-		Thyroid	ATP6V1G2 SKIV2	ENSG00000213760.10 ENSG00000204351.11	0.28	1.10E-05 2.20E-05
				16+56/000	(dbGaP Accessio	n The GTEx Consortium atlas of genetic regulatory effects across human tissues	g/10.1101/78	G	Thyroid	CCHCR1	ENSG00000204536.13	-0.22	1.30E-04
rs2523691	6 3	1452660 3	1452660	314+335-337-	phs000424.v8.p2)	7903		Thyroid	VARS2	ENSG00000137411.16	-0.27	2.00E-04
		452660 314		158a+158b+	GTEx2017 v7				Whole_Blood	MICA	ENSG00000204520.12	0.22	3.40E-04
					(dbGaP Accessio	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in	29022597		whole_Blood	HLA-C	ENSG00000204525.10	-0.3	5.50E-05
					phs000424.v7.p2) numans			Thyroid	CCHCR1	ENSG00000204536.9	-0.29	1.90E-05

Table S5 : Genes reported for genetic variants associated with thyroid phenotypes and immune cell traits
* the closest genes reported in GWAS catalog for the genetic variants associated with thyroid phenotypes and immune cell traits (Data downloaded from GWAS Catalog on 17/06/2015)
** Roederer, M et al., Cell, 2015, doi: 10.1016/j.cell.2015.02.046 and Mangino et al, Nature Communications, 2017, https://doi.org/10.1038/ncomms13850

		Thyr	oid phenoty	pes (from GV	VAS catalog)*		Immune cell traits**										
Name of gene reported in GWAS catalog* and Roederer's paper **	Lead SNP	Chromosome	start (hg38)	end (hg38)	Phenotype	AITD status or biomarkers associated with AITD	LD (r2)	distance lead SNP(thryoid)- lead SNP(immune cell traits)	Lead SNP	Chromosome	start (hg38)	end (hg38)	start (hg19)	end (hg19)	Immune Name in TwinsUK		Phenotypes
HCP5	re3094228	6	31/62150	31462150	Thyroid peroxidase	Ves	<0.2	12667	rs2596460	6	31449483	31449483	31449733	31449733	P4:3763	NK Activating 1	16+56/CD2-314+335-337-158a+158b+
1101 0	133034220	0	01402100	01402100	antibody positivity	103	<0.2	9490	rs2523691	6	31452660	31452660	31452910	31452910	P4:3763	NK Activating 1	16+56/CD2-314+335-337-158a+158b+
MICA	rs1521	6	31382927	31382927	Graves' disease	Yes	<0.2	-66556	rs2596460	6	31449483	31449483	31449733	31449733	P4:3763	NK Activating 1	16+56/CD2-314+335-337-158a+158b+
ACCNI	TR 00017E6	17	24127125	24127125	Live other and discon	Ne	<0.2	365816	rs12603968	17	33771319	33771319	33771319	33771319	P4:3551	NK Effector	16+56/314-158a+
ACCINT	189901756	17	34137135	34137135	Hypouryroldisin	INU	<0.2	366131	rs12602135	17	33771004	33771004	33771004	33771004	P4:3551	NK Effector	16+56/314-158a+
DIRC3	rs6759952 rs966423	2 2	217406996 217445617	217406996 217445617	Thyroid cancer	No	<0.2 <0.2	-317240 -278619	rs744564	2	217724236	217724236	217724236	217724236	P4:3551	NK Effector	16+56/314-158a+
GLIS3	rs1571583	9	4267209	4267209	Thyroid hormone levels	No	<0.2	492850	rs10973456	9	3774359	3774359	3774359	3774359	P7:110	DC mDC imDC	11c+ (nodim)/1c-/16+/32+
HACE1	rs9322817	6	104784358	104784358	Thyroid stimulating hormone level	No	<0.2	378569	rs156205	6	104405789	104405789	104405789	104405789	P4:3763	NK Activating 1	16+56/CD2-314+335-337-158a+158b+
L3MBTL4	rs948426	18	6567183	6567183	Hypothyroidism	No	<0.2	438743	rs17486103	18	6128440	6128440	6128440	6128440	P7:110	DC mDC imDC	11c+ (nodim)/1c-/16+/32+
NFIA	rs334699	1	61154824	61154824	Thyroid hormone levels	No	<0.2	-240528	rs11581697	1	61395352	61395352	61395352	61395352	P4:3551	NK Effector	16+56/314-158a+
NED			44470005	44470005	Li	N.	< 0.2	-240632	rs12072379	1	61395456	61395456	61395456	61395456	P4:3551	NK Effector	16+56/314-158a+
NFIB	rs10961534	9	14470835	14470835	Hypothyroidism Thyroid stimulating	NO	<0.2	31760	rs11/8/815	9	14439075	14439075	14439075	14439075	P4:3551	INK Effector	16+56/314-1588+
NR3C2	rs10028213	4	148731458	148731458	hormone level	No	<0.2	441933	rs3910047	4	148289525	148289525	148289525	148289525	P4:3551	NK Effector	16+56/314-158a+
							<0.2	5271541	rs4279551	8	27287215	27287215	27287215	27287215	P7:110	DC mDC imDC	11c+ (nodim)/1c-/16+/32+
	rs7825175	8	32558756	32558756	Thyroid hormone levels	No	<0.2	510838	rs2881470	8	32047918	32047918	32047918	32047918	P7:110	DC mDC imDC	11c+ (nodim)/1c-/16+/32+
							<0.2	400034	re1381871	0 8	32070122	32070122	32070122	32070122	P7.110	DC mDC imDC	11c+ (nodim)/1c-/16+/32+
NRG1							<0.2	496755	rs1471387	8	32078096	32078096	32078096	32078096	P7:110	DC mDC imDC	11c+ (nodim)/1c-/16+/32+
							<0.2	494464	rs1947734	8	32080387	32080387	32080387	32080387	P7:110	DC mDC imDC	11c+ (nodim)/1c-/16+/32+
	rs2439302	8	32574851	32574851	Thyroid cancer	No	<0.2	488995	rs7818326	8	32085856	32085856	32085856	32085856	P7:110	DC mDC imDC	11c+ (nodim)/1c-/16+/32+
							<0.2	488541	rs16878780	8	32086310	32086310	32086310	32086310	P7:110	DC mDC imDC	11c+ (nodim)/1c-/16+/32+
-							<0.2	488339	rs9297185	8	32086512	32086512	32086512	32086512	P7:110	DC mDC imDC	11c+ (nodim)/1c-/16+/32+
DDE404	750700	0	40500005	40500005	The second state of the se	N	<0.2	152041	rs551901	6	165480954	165480954	165480954	165480954	P4:3763	NK Activating 1	16+56/CD2-314+335-337-158a+158b+
PDEIUA	15/53/60	6	165632995	165632995	Inyrola normone levels	NO	<0.2	151764	rs684847	6	165481231	165481231	165481231	165481231	P4:3763	NK Activating 1	16+56/CD2-314+335-337-158a+158b+
SOX9	rs9915657	17	72131395	72131395	Thyroid hormone levels	No	<0.2	691727	rs9302936	17	71439668	71439668	71439668	71439668	P4:3763	NK Activating 1	16+56/CD2-314+335-337-158a+158b+
					_		<0.2	686259	rs1990222	17	71445136	71445136	71445136	71445136	P4:3763	NK Activating 1	16+56/CD2-314+335-337-158a+158b+
	rs12126655	1	107814198	107814198	Plasma thyroid- stimulating hormone	No	<0.2	-121433	rs10494086	1	107935631	107935631	107935631	107935631	P4:3551	NK Effector	16+56/314-158a+
VAV3					levels		<0.2	-127812	rs1020812	1	107942010	107942010	107942010	107942010	P4:3551	NK Effector	16+56/314-158a+
	rs4915077	1	107823394	107823394	Hypothyroidism	No	<0.2	-123692	rs6696531	1	107947086	107947086	107947086	107947086	P4:3551	NK Effector	16+56/314-158a+

Table S6: Glycome-wide associations studies of 17 AITD-IgG N-glycan traits with 1,113 circulating proteins. Only significant ones were put here.

Glycan ID	Description	Soma ID	Target	Uniprot	P-value	Beta	SE
IGP2	The percentage of A2 glycan in total IgG glycans	SL008609	FCG3B	O75015	1.46E-06	0.051	0.010
IGP8	The percentage of FA2[3]G1 glycan in total IgG glycans	SL007464	AMHR2	Q16671	1.50E-07	0.029	0.005
IGP8	The percentage of FA2[3]G1 glycan in total IgG glycans	SL004857	Desmoglein-2	Q14126	2.15E-06	0.032	0.007
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	SL008609	FCG3B	O75015	2.63E-06	0.050	0.010
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	SL008609	FCG3B	O75015	3.88E-06	0.045	0.009
IGP48	The percentage of FA2[3]G1 glycan in total neutral IgG glycans (GPn)	SL002644	ERBB1	P00533	3.04E-06	0.023	0.005
IGP48	The percentage of FA2[3]G1 glycan in total neutral IgG glycans (GPn)	SL000283	b2-Microglobulin	P61769	4.16E-06	-0.034	0.007
IGP56	The percentage of monogalactosylated structures in total neutral IgG glycans	SL000283	b2-Microglobulin	P61769	5.10E-07	-0.037	0.007
IGP57	The percentage of digalactosylated structures in total neutral IgG glycans	SL004159	TRAIL R4	Q9UBN6	2.95E-06	-0.041	0.008
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	SL008609	FCG3B	O75015	5.21E-06	-0.044	0.009
IGP59	The percentage of fucosylation of agalactosylated structures	SL008609	FCG3B	O75015	9.33E-06	-0.044	0.010
IGP60	The percentage of fucosylation of monogalactosylated structures	SL008609	FCG3B	O75015	4.06E-07	-0.048	0.009
IGP62	The percentage of fucosylated (without bisecting GlcNAc) structures in total neutral IgG glycans	SL004672	BCMA	Q02223	5.44E-08	0.041	0.007
IGP63	The percentage of fucosylation (without bisecting GlcNAc) of agalactosylated structures	SL004672	BCMA	Q02223	1.47E-07	0.041	0.007
IGP63	The percentage of fucosylation (without bisecting GlcNAc) of agalactosylated structures	SL004857	Desmoglein-2	Q14126	8.02E-06	0.032	0.007

Table S7: Genetic variants associated with thyroid phenotypes and AITD-IgG N-glycan traits overlapping pQTL identified in INTERVAL project (LD r2>0.8) *Sun et al, Nature, 2018, doi: 10.1038/s41586-018-0175-2

			GWAS C	Catalog (Data c	downloaded from GWAS Catalo	g on 17/06/2	2015)								DQTL*				
chr	Start (hg38)	Stop (hg38)	Strongest SNPs	SNPs	Disease traits	Region	Reported Genes	Mapped Genes	Context	Extra Information about GWAS findings	SOMAmer ID (version 2) used here	SOMAmer ID (version 4)	Target	Target fullname	UniProt	cis/ trans	Mapped gene	Sentinel variant	LD with sentinel variant (r2)
1	157699488	157699488	rs3761959-A, rs3761959-G	rs3761959	Graves disease, Multiple sclerosis	1q23.1	FCRL3	FCRL3	intron										
1	157701026	157701026	rs7528684-T	rs7528684	Type 1 diabetes autoantibodies, Rheumatoid arthritis, Graves disease	1q23.1	FCRL3	FCRL3	nearGene-5	I-A2A	SL014088	FCRL3.4440.15.2	FCRL3	protein 3	Q96P31	cis	FCRL3	rs7528684	1
											No detected	DHFR.9823.2.3	DYR	Dihydrofolate reductase	P00374	trans	ABO	rs676457	0.99
9 133273813 13										SL004516	MBL2.3000.66.1	MBL	Mannose-binding protein C	P11226	trans	ABO	rs139840563	0.98	
	133273813	rs505922-C, rs505922-T,	rs505922	Protein quantitative trait loci, Venous thromboembolism, End-stage coagulation,	9q34.2	ABO	ABO	intron	Recessive, TNFA, vWF	No detected	ABO.9253.52.3	BGAT	Histo-blood group ABO system transferase	P16442	cis	ABO	rs505922	1	
		15000922-?		disease, Duodenal ulcer						SL004857	DSG2.9484.75.3	Desmoglein-2	Desmoglein-2	Q14126	trans	ABO	rs687621	0.97	
9 133273813 13											SL005157	CD209.3029.52.2	DC-SIGN	CD209 antigen	Q9NNX6	trans	ABO	rs505922	1
											No detected	CHST11.7779.86.3	CHSTB	Carbohydrate sulfotransferase 11	Q9NPF2	trans	ABO	rs687621	0.97
12	111446804	111446804	rs3184504-C,	re3184504	Type 1 diabetes, Platelet counts, Blood metabolite levels, Beta-2 microglubulin plasma levels, Diastolic blood pressure, Coronary artery disease, Eosinophil counts, Systelic blood pressure	12024 12	SH2B3, NAA25, C12orf51, ATXN2,	SH283	missansa	T1D,	51.006460	GP1BA.4990.87.1	GP1BA	Platelet glycoprotein lb alpha chain	P07359	trans	BRAP	rs11065979	0.81
			rs3184504-T		Autoimmune hepatitis type-1, Red blood cell traits, Rheumatoid arthritis, Type 1 diabetes autoantibodies, Hypothyroidism , Coronary heart disease		BRAP, LOC100101 246, PTPN11	0.1200		Hgb, EA	02030400	VCAM1.2967.8.1	VCAM-1	Vascular cell adhesion protein 1	P19320	trans	SH2B3	rs3184504	1

Table S8: Heritability of AITD, 17 IgG N-glycan traits and 51 immune cell traits in the TwinsUK cohort * Martin et al, 2018 *** Mangino et al, Nature Communications, 2017, https://doi.org/10.1038/ncomms13850

type	features	general info	best model	H2 [95%CI]	A [95%CI]	D [95%CI]	C [95%CI]	E [95%Cl]
thyroid	AITD TPOAb-positivity		DE DE	0.63 [0.59-0.67]	NS NS	0.63 [0.59-0.67]	NS NS	0.36 [0.32-0.40]
phonotype	IGP2	The percentage of A2 glycan in total IgG glycans	AF	0 731 [0 747:0 716]	0 731 [0 697:0 764]	NS	NS	0 269 [0 236:0 303]
	IGP7	The percentage of FA2[6]G1 glycan in total IgG glycans	AF	0.557 [0.563:0.552]	0.557 [0.509:0.605]	NS	NS	0.443 [0.395:0.491]
	IGP8	The percentage of FA2[3]G1 glycan in total loG glycans	AF	0.662 [0.676:0.65]	0.662 [0.621:0.702]	NS	NS	0.338 [0.298:0.379]
	IGP15	The percentage of FA2G1S1 glycan in total IgG glycane	AF	0 704 [0 72:0 691]	0 704 [0 669:0 739]	NS	NS	0 296 [0 261:0 331]
	IGP21	The percentage of A2BG2S2 glycan in total IgG glycans	AF	0.347 [0.327:0.363]	0 347 [0 288:0 406]	NS	NS	0.653 [0.594:0.712]
	101 21	Ratio of all fucosylated (+/- bisecting GlyNAc) monosialylated and	7.2	0.011 [0.021,0.000]	0.017 [0.200,01100]	0.241	0.246	0.000 [0.00 1,0.1 12]
	IGP33	disialylated structures in total IgG glycans	DCE	0.241 [0.183;0.277]	NS	[0.142;0.34]	[0.175;0.316]	0.513 [0.457;0.57]
	IGP36	GicNAc	AE	0.704 [0.72;0.691]	0.704 [0.669;0.739]	NS	NS	0.296 [0.261;0.331]
	IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	AE	0.739 [0.755;0.724]	0.739 [0.706;0.771]	NS	NS	0.261 [0.229;0.294]
	IGP45	The percentage of FA2B glycan in total neutral IgG glycans (GP ⁿ)	DCE	0.41 [0.407;0.413]	NS	0.41 [0.346;0.475]	0.361	0.229 [0.199;0.259]
IgG N-	IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GP ⁿ)	AE	0.725 [0.742;0.711]	0.725 [0.691;0.76]	NS	NS	0.275 [0.24;0.309]
giycan traits*	IGP48	The percentage of FA2[3]G1 glycan in total neutral IgG glycans (GPn)	AE	0.776 [0.793;0.761]	0.776 [0.747;0.805]	NS	NS	0.224 [0.195;0.253]
	IGP56	The percentage of monogalactosylated structures in total neutral IgG glycans	ADE	0.678 [0.492;0.749]	0.475 [0.277;0.674]	0.203 [0;0.411]	NS	0.322 [0.281;0.363]
	IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	DCE	0.57 [0.599;0.55]	NS	0.57 [0.494;0.646]	0.162 [0.098;0.226]	0.268 [0.232;0.303]
	IGP59	The percentage of fucosylation of agalactosylated structures	ADE	0.735 [0.591;0.791]	0.333 [0.136;0.531]	0.401 IO 107-0 6051	NS	0.265 [0.231;0.3]
	IGP60	The percentage of fucosylation of monogalactosylated structures	AE	0.714 [0.731;0.7]	0.714 [0.677;0.751]	NS	NS	0.286 [0.249;0.323]
	IGP62	The percentage of fucosylated (without bisecting GlcNAc) structures in total neutral IgG glycans	AE	0.76 [0.777;0.745]	0.76 [0.729;0.79]	NS	NS	0.24 [0.21;0.271]
	IGP63	The percentage of fucosylation (without bisecting GlcNAc) of agalactosylated structures	AE	0.737 [0.754;0.722]	0.737 [0.703;0.771]	NS	NS	0.263 [0.229;0.297]
	P4:3242	16+56/314+335+158b-	ACE	0.427 [0.20;0.66]	0.427 [0.20;0.66]	NS	0.356[0.14;0.54]	0.217 [0.16;0.31]
	P4:2561	16+56/314+335+158b-R7-	ACE	0.424 [0.19;0.66]	0.424 [0.19;0.66]	NS	0.358 [0.14;0.54]	0.218 [0.16;0.31]
	P4:3161	16+56/314+335+158a-158b-	AE	0.792 [0.71;0.81]	0.792 [0.71;0.81]	NS	NS	0.208 [015;0.29]
	P4:2488	16+56/314+335+158a-158b-R7-	AE	0.792 [0.71;0.81]	0.792 [0.71;0.81]	NS	NS	0.208 [015;0.29]
	P4:3215	16+56/314+335+337-158b-	ACE	0.422 [0.19;0.66]	0.422 [0.19;0.66]	NS	0.358 [0.14;0.54]	0.22[0.16;0.31]
	P4:2534	16+56/314+335+337-158b-R7-	ACE	0.423 [0.19;0.66]	0.423 [0.19;0.66]	NS	0.356 [0.14;0.54]	0.221[0.16;0.31]
	P4:2558	16+56/335+158b-R7-	ACE	0.439 [0.21;0.68]	0.439 [0.21;0.68]	NS	0.344 [0.12;0.53]	0.217[0.16;0.31]
	P4:3239	16+56/335+158b-	ACE	0.437 [0.20:0.68]	0.437 [0.20:0.68]	NS	0.344 [0.12:0.53]	0.22[0.16:0.31]
	P4:3134	16+56/314+335+337-158a-158b-	AF	0.791 [0.71:0.85]	0.792 [0.71:0.85]	NS	NS	0.209 [015:0.29]
	P4:2462	16+56/314+335+337-158a-158b-R7-	AE	0.783 [0.70:0.84]	0.783 [0.70:0.84]	NS	NS	0.217 [016:0.30]
	P4:2531	16+56/335+337-158b-R7-	ACE	0.433 [0.20:0.67]	0.433 [0.20:0.67]	NS	0.347 [0.13:0.53]	0.217[0.16:0.31]
	P4:3212	16+56/335+337-158b-	ACE	0.428 [0.19:0.67]	0.428 [0.19:0.67]	NS	0.347[0.12:0.53]	0.225 [0.16:0.32]
	P4:3158	16+56/335+158a-158b-	AF	0,792 [0,71:0,81]	0.792 [0.71:0.81]	NS	NS	0.208 [015:0.29]
	P4:2460	16+56/335+337-158a-158b-R7-	AF	0.782 [0.70:0.84]	0.782 [0.70:0.84]	NS	NS	0.218 [016:0.30]
	P4:2485	16+56/335+158a-158b-R7-	AF	0.783 [0.70:0.84]	0.783 [0.70:0.84]	NS	NS	0.217 [016:0.30]
	P4:3131	16+56/335+337-158a-158b-	AF	0.781 [0.70:0.84]	0.781 [0.70:0.84]	NS	NS	0.219 [016:0.30]
	P4:3401	16+56/335+158a-	ACE	0 475 [0 26:0 70]	0 475 [0 26:0 70]	NS	0 337 [0 12:0 51]	0 1880 130 271
	P4:2740	16+56/335_337_P7_	ACE	0.349 [0.15:0.55]	0 349 [0 15:0 55]	NS	0.461 [0.27:0.62]	0 10 [0 14:0 27]
	P4:3/37	16+56/335-337-	ACE	0.303 [0.11:0.50]	0.303 [0.11:0.50]	NS	0.509 [0.33:0.66]	0.188 [0.13:0.27]
	P4:2767	16+56/335-B7-	ACE	0.352 [0.15:0.56]	0.352 [0.15:0.56]	NS	0.46 [0.27.0.62]	0.188 [0.13:0.27]
	P4:3/82	16+56/335+	ACE	0.303 [0.11:0.50]	0.302 [0.13,0.50]	NS	0.51 [0.33:0.66]	0.187[0.13:0.27]
	P4:3464	16+56/335-	ACE	0.305 [0.11;0.50]	0.305 [0.11;0.50]	NS	0.508 (0.33-0.66)	0.187[0.13:0.27]
	D4-2274	16+56/225+227 1590	ACE	0.475 [0.26:0.70]	0.305 [0.11,0.30]	NG	0.226 [0.12:0.51]	0.109[0.13,0.27]
	P4.3374	16+56/225+227 150a-	ACE	0.473[0.20,0.70]	0.473 [0.20,0.70]	NS	0.330 [0.12,0.31]	0.100[0.14,0.27]
	P4:2077	16+56/335+337-	ACE	0.472 [0.20,0.70]	0.472[0.20,0.70]	NS	0.505 [0.13,0.51]	0.186 [0.14,0.27]
immnune	P4:3433	16+56/335+337-P7-	ACE	0.306 [0.12,0.30]	0.309 [0.12,0.30]	NS	0.505 [0.33,0.05]	0.187 [0.13;0.27]
cell traits**	P4:3243	16+56/CD2+314+335+158b-	ACE	0.461 [0.23:0.71]	0.461 [0.23:0.71]	NS	0.322 [0.10:0.51]	0.217 [0.16:0.31]
	P4:0240	16+56/CD2+314+335+1585-R7-	ACE	0.465 [0.23:0.71]	0.465 [0.23:0.71]	NS	0.32[0.10;0.51]	0.215 [0.15:0.30]
	P4-2302	16+56/CD2+314+335+158a-158b-	ACL	0.403 [0.23,0.71]	0.403[0.23,0.71]	NS	0.32 [0.03,0.31] NS	0.212 [0.15,0.30]
	P4.3102	16+56/CD2+214+335+1502=150b=		0.700 [0.71,0.04]	0.700 [0.71,0.04]	NS	NG	0.212 [010,0.29]
	P4.2403	16+56/CD2+314+335+1368=1360=177=	ACE	0.75 [0.71,0.03]	0.79 [0.71,0.03]	NS	0 222 [0 10:0 51]	0.21 [013,0.23]
	P4.3210	16+56/CD2+314+335+337=1300=	ACE	0.46[0.22,0.70]	0.46[0.22,0.70]	NS	0.323 [0.10,0.31]	0.216 [0.10,0.31]
	P4.2000	18+30/CD2+314+333+337-1360-R7-	ACE	0.46[0.23,0.70]	0.46 [0.23,0.70]	IN S	0.324 [0.10,0.51]	0.210 [0.10,0.31]
	P4:18	16+56/CD2+314+335+337-1588-1580-R7-	AE	0.788 [0.71;0.84]	0.788 [0.71;0.84]	NS NS	NS NS	0.212 [016;0.29]
	P4:2486	16+56/CD2+335+158a-158b-R7-	AE	0.782 [0.70;0.84]	0.782 [0.70;0.84]	NS	NS	0.218 [016;0.30]
	P4:2559	16+56/CD2+335+158b-R7-	ACE	0.471[0.24;0.72]	0.471[0.24;0.72]	NS	0.312 [0.08;0.50]	0.217 [0.16;0.31]
	P4:3159	16+56/CD2+335+158a-158b-	AE	0.78 [0.70;0.84]	0.78 [0.70;0.84]	NS	NS	0.22 [016;0.30]
1	P4:3240	10+50/GU2+335+158D-	ACE	0.400 [0.23;0.71]	0.400 [0.23;0.71]	NS NS	0.314 [0.09;0.51]	0.219 [0.15;0.30]
	P4:3135	16+56/CD2+314+335+337-158a-158b-	AE	0.786 [0.71;0.84]	0.786 [0.71;0.84]	NS	NS	0.214 [016;0.29]
1	P4:2532	16+56/CD2+335+337-1580-R/-	ACE	0.47 [0.24;0.72]	0.47 [0.24;0.72]	NS	0.313 [0.08;0.50]	0.217 [0.16;0.31]
1	P4:3213	10+00/UD2+335+337-158D-	ACE	0.467 [0.23;0.71]	0.467 [0.23;0.71]	NS NC	0.314 [0.08;0.51]	0.22 [0.16;0.31]
1	P4:3132	10+50/CD2+335+337-1588-1580-	AE	0.78 [0.70;0.84]	0.78 [0.70;0.84]	NS NC	NS NO	0.22 [0.16;0.30]
1	P4:2461	16+56/CD2+335+337-1588-1580-K7-	AE	0.781 [0.70;0.84]	0.781 [0.70;0.84]	NS	NS	0.219 [0.16;0.30]
1	P4:2967	16+56/335-337-158b+R7-	AE	0.772 [0.68;0.84]	0.772 [0.68;0.84]	NS	NS	0.228 [0.16;0.32]
1	P4:2994	16+56/335-158b+R7-	AE	0.772 [0.68;0.84]	0.772 [0.68;0.84]	NS	NS	0.228 [0.16;0.32]
1	P4:3707	16+56/335-158b+	AE	0.775 [0.68;0.84]	0.775 [0.68;0.84]	NS	NS	0.225 [0.16;0.32]
1	P4:3680	16+56/335-337-158b+	AE	0.775 [0.68;0.84]	0.775 [0.68;0.84]	NS	NS	0.225 [0.16;0.32]
1	P4:2970	16+56/314+335-337-158b+R7-	AE	0.775 [0.68;0.84]	0.775 [0.68;0.84]	NS	NS	0.225 [0.16;0.32]
1	P4:3683	16+56/314+335-337-158b+	AE	0.776 [0.68;0.84]	0.776 [0.68;0.84]	NS	NS	0.224 [0.16;0.31]
1	P4:2997	16+56/314+335-158b+R7-	AE	0.775 [0.68;0.84]	0.775 [0.68;0.84]	NS	NS	0.225 [0.16;0.32]
1	P4:3710	16+56/314+335-158b+	AE	0.777 [0.69;0.84]	0.777 [0.69;0.84]	NS	NS	0.223 [0.16;0.31]
1	P4:2900	16+56/335-337-158a-158b+R7-	AE	0.756 [0.66;0.82]	0.756 [0.66;0.82]	NS	NS	0.244 [018;0.34]

SomalD	Target	UniProt	Entrez Gene ID	Entrez Gene Symbol	Units	SomaQC	Associated with AITD	Associated with one ot 17 AITD- IgG N-glycan	best model	h2 estimated	h2 CI_2.50	h2 CI_97.50	A estimation	A CI_2.50	A CI_97.50	D estimation	D CI_2.50	D CI_97.50	C estimation	C CI_2.50	C CI_97.50	E estimation	E CI_2.50	E CI_97.50
SL000125	IL-1a	P01583	3552	IL1A	RFU		Yes	structures No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000589	TSH	P01215 P0	11081 123	72 CGA TSHB	RFU		Yes	No	DE	0.356	0.229	0.402	0	0	0	0.356	0.122	0.591	0	0	0	0.644	0.409	0.878
SL003710 SL000283	b2-Microglobulin	P42575 P61769	567	B2M	RFU		No	Yes	CE	0.470	0.443	0.479	0	0	0	0.470	0.238	0.701	0.509	0.356	0.662	0.530	0.299	0.762
SL002644	ERBB1	P00533	1956	EGFR	RFU		No	Yes	CE	0	0	0	0	0	0	0	0	0	0.389	0.208	0.569	0.611	0.431	0.792
SL008609 SL000002	VEGF	P15692	7422	VEGFA	RFU		No	Yes No	DE	0.479	0.468	0.485	0.479	0.303	0.655	0.500	0.302	0.697	0	0	0	0.521	0.345	0.697
SL000003	Angiogenin	P03950	283	ANG	RFU		No	No	AE	0.718	0.782	0.677	0.718	0.603	0.832	0	0	0	0	0	0	0.282	0.168	0.397
SL000004 SL000006	PAI-1	P09038 P05121	2247 5054	FGF2 SERPINE1	RFU		No No	No No	CE	0	0	0	0	0	0	0	0	0	0.497	0.343	0.650	1 0.503	1 0.350	1 0.657
SL000007	ER	P03372	2099	ESR1	RFU		No	No	DE	0.742	0.827	0.692	0	0	0	0.742	0.613	0.872	0	0	0	0.258	0.128	0.387
SL000009 SL000017	ERBB2 vWF	P04626 P04275	2064 7450	ERBB2 VWF	RFU RFU		No No	No No	E AF	0.700	0.776	0.657	0.700	0.563	0.838	0	0	0	0	0	0	0.300	1	1 0.437
SL000019	Apo A-I	P02647	335	APOA1	RFU	Calibration Scale	No	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SL000020 SL000021	Apo B Insulin	P04114 P01308	338 3630	APOB INS	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.617	0.491	0.744	0.383	0.256	0.509
SL000022	D-dimer	P02671 P0	22243 224	4 FGA FGB FGG	RFU		No	No	CE	Ő	0	0	Ő	0	0	0	Ő	ő	0.279	0.086	0.471	0.721	0.529	0.914
SL000024	TF COX-2	P13726	2152	F3 PTGS2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.383	0.208	0.558	0.617	0.442	0.792
SL000038	MCP-1	P13500	6347	CCL2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.220	0.026	0.414	0.780	0.586	0.974
SL000039	IL-8	P10145	3576	IL8	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000045 SL000047	IGF-I	P05019	3466	IGFBP3	RFU		No	No	DE	0.296	0.114	0.361	0	0	0	0.296	0.060	0.532	0.423	0.255	0.594	0.577	0.408	0.940
SL000048	Protein C	P04070	5624	PROC	RFU		No	No	AE	0.444	0.405	0.460	0.444	0.238	0.650	0	0	0	0	0	0	0.556	0.350	0.762
SL000049 SL000051	CRP	P07225 P02741	1401	CRP	RFU		No	No	AE	0.296	0.145	0.357	0.296	0.083	0.606	0	0	0	0	0	0	0.704	0.491	0.781
SL000053	tPA	P00750	5327	PLAT	RFU		No	No	AE	0.531	0.550	0.522	0.531	0.342	0.720	0	0	0	0	0	0	0.469	0.280	0.658
SL000055 SL000057	Thymidine kise	P12830 P04183	999 7083	TK1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.452	0.284	0.621	0.548	0.379	0.716
SL000062	PSA	P07288	354	KLK3	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000064 SL000070	Kallikrein / Glypican 3	P49862 P51654	5650 2719	KLK7 GPC3	RFU		No	No	DE	0	0	0	0	0	0	0.581	0.411	0.752	0.573	0.435	0.711	0.427	0.289	0.565
SL000076	p27Kip1	P46527	1027	CDKN1B	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000087 SL000088	IL-6 TGF-b2	P05231 P61812	3569 7042	IL6 TGFB2	RFU		No	No	DE	0 437	0.364	0.459	0	0	0	0.437	0.168	0.706	0.270	0.081	0.460	0.730	0.540	0.919
SL000089	TGF-b3	P10600	7043	TGFB3	RFU		No	No	DE	0.250	-0.083	0.341	ō	0	0	0.250	-0.036	0.536	ō	ō	Ō	0.750	0.464	1.036
SL000091 SL000104	PSA-ACT Bcl-2	P07288 P0 P10415	0'354 12 596	KLK3 SERPI3 BCI 2	RFU		No	No	CE	0	0 -0 116	0 293	0	0	0 439	0	0	0	0.323	0.135	0.510	0.677	0.490	0.865
SL000124	MMP-2	P08253	4313	MMP2	RFU		No	No	AE	0.593	0.640	0.570	0.593	0.425	0.762	0	ō	ő	0	ō	ō	0.407	0.238	0.575
SL000130	Cyclin B1	P14635 P12004	891 5111	CCNB1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000133	MIP-3a	P78556	6364	CCL20	RFU		No	No	E	õ	0	0	Ő	0	0	0	0	õ	0	õ	õ	1	1	1
SL000134	Met	P08581	4233	MET	RFU		No	No	AE	0.563	0.596	0.547	0.563	0.395	0.732	0	0	0	0 713	0	0	0.437	0.268	0.605
SL000138	HB-EGF	Q99075	1839	HBEGF	RFU		No	No	AE	0.587	0.632	0.565	0.587	0.416	0.758	0	0	ō	0	0.012	0.010	0.413	0.242	0.584
SL000139	EPI	O14944	2069	EREG	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000142	PSMA	Q04609	2346	FOLH1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000164	Myoglobin	P02144	4151	MB	RFU		No	No	AE	0.542	0.564	0.531	0.542	0.370	0.714	0	0	0	0	0	0	0.458	0.286	0.630
SL000247 SL000248	a1-Antichymotrypsin	P01011	12	SERPI3	RFU		No	No	CE	0.817	0.878	0.773	0.817	0.737	0.696	0	0	0	0.278	0.083	0.473	0.183	0.102	0.263
SL000249	a1-Antitrypsin	P01009	5265	SERPI1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.346	0.165	0.527	0.654	0.473	0.835
SL000250 SL000251	a2-HS-Glycoprotein	P08697 P02765	5345 197	AHSG	RFU		No	No	AE	0.679	0.795	0.628	0.442	0.235	0.649	0.879	0.462	0.876	0	0	0	0.558	0.124	0.518
SL000252	a2-Macroglobulin	P01023	2	A2M	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.602	0.471	0.733	0.398	0.267	0.529
SL000254 SL000268	Angiostatin	P02768 P00747	213 5340	PLG	RFU		No	NO	AE	0.733	0.795	0.693	0.733	0.628	0.838	0	0	0	0.562	0.419	0.704	0.438	0.296	0.581
SL000271	Angiotensinogen	P01019	183	AGT	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.395	0.220	0.571	0.605	0.429	0.780
SL000272 SL000276	Antithrombin III Apo E	P01008 P02649	462 348	APOE	RFU	Calibration Scale	No	NO	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.350 NA	0.149 NA	0.552 NA	0.650 NA	0.448 NA	0.851 NA
SL000277	Apo E2	P02649	348	APOE	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.675	0.564	0.787	0.325	0.213	0.436
SL000280 SL000299	GOT1 b-ECGF	P1/1/4 P05230	2805 2246	GOT1 FGF1	RFU		No No	No No	E	0	0	0	0	0	0	0.588	0.412	0.763	0	0	0	0.412	0.237	0.588
SL000300	b-Endorphin	P01189	5443	POMC	RFU		No	No	AE	0.524	0.537	0.518	0.524	0.354	0.694	0	0	0	0	0	0	0.476	0.306	0.646
SL000305 SL000306	b-NGF BNP-32	P01138 P16860	4803 4879	NGF NPPB	RFU RFU		No No	No No	E	0	0	0	0	0	0	0	0	0	0	0	0		1	1
SL000308	C1-Esterase Inhibitor	P05155	710	SERPING1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.621	0.494	0.747	0.379	0.253	0.506
SL000309 SL000310	C1q C1r	P02745 P0 P00736	715 713 7	1 C1QA C1QB C C1R	RFU		No No	No No	AE	0.440	0.400	0.457	0.440	0.240	0.640	0	0	0	0	0	0	1 0.560	1 0.360	1 0.760
SL000311	C1s	P09871	716	C1S	RFU		No	No	AE	0.423	0.368	0.446	0.423	0.214	0.633	0	0	0	0	0	0	0.577	0.367	0.786
SL000312 SL000313	C3 C3a	P01024 P01024	718	C3 C3	RFU	Calibration Scale	No	No	NA DE	NA 0.631	NA 0.697	NA 0.598	NA 0	NA 0	NA 0	NA 0.631	NA 0.463	NA 0.798	NA 0	NA 0	NA 0	NA 0.369	NA 0.202	NA 0.537
SL000314	C3b	P01024	718	C3	RFU	Calibration Scale	No	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SL000316 SL000318	C4 C4b	POCOL4 P	0 720 721	C4A C4B C4A C4B	RFU		No	No	DE	0.748	0.816	0.704	0	0	0	0.748	0.641	0.855	0	0 284	0 761	0.252	0.145	0.359
SL000319	C5	P01031	727	C5	RFU		No	No	CE	0	0	0	ŏ	Ő	Ő	0	0	0	0.390	0.209	0.570	0.610	0.430	0.791
SL000320	C5a C5b 6 Complex	P01031	727	C5	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.529	0.383	0.676	0.471	0.324	0.617
SL000322	C6	P13671	729	C6	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.308	0.122	0.495	0.692	0.505	0.878
SL000323	C7	P10643	730	C7	RFU		No	No	AE	0.448	0.410	0.463	0.448	0.240	0.655	0	0	0	0	0	0	0.552	0.345	0.760
SL000324 SL000325	C9	P02748	735	C9	RFU		No	No	AE	0.535	0.500	0.525	0.502	0.306	0.698	0.555	0.330	0.741	0	0	0	0.405	0.259	0.694
SL000337	Calpain I	P07384 P0	4823 826	CAPN1 CAPNS	1 RFU		No	No	AE	0.727	0.792	0.686	0.727	0.616	0.838	0	0	0	0	0	0	0.273	0.162	0.384
SL000338 SL000339	carbonic anhydrase II	P20810	760	CAST CA2	RFU		No	No	E	0.081	0.017	0.562	0.581	0.427	0.736	0	0	0	0	0	0	0.419	0.∠04 1	0.573
SL000342	Catalase	P04040	847	CAT	RFU		No	No	AE	0.487	0.477	0.490	0.487	0.285	0.688	0	0	0	0	0	0	0.513	0.312	0.715

Table S9: Heritability of 1,113 proteins in the TwinsUK cohort h2= heritability; Cl_2.5=confidence interval at 2.5; Cl_97.5=confidence interval at 97.5; A=additive genetic variance; D= dominance genetic variance; C= common environmental variance; E= unique environmental variance

SL000343	Cathepsin B	P07858	1508	CTSB	RFU	No	No	AE	0.494	0.491	0.496	0.494	0.321	0.668	0	0	0	0	0	0	0.506	0.332	0.679
SL000345	Cathepsin G	P08311	1511	CTSG	RFU	No	No	DE	0.415	0.139	0.452	0	0	0	0.415	0.033	0.797	0	0	0	0.585	0.203	0.967
SL000346 SL000347	Cathepsin H CBG	P09668 P08185	1512 866	CTSH SERPI6	RFU RFU	No	No No	CE F	0	0	0	0	0	0	0	0	0	0.557	0.414	0.701	0.443	0.299	0.586
SL000357	Coagulation Factor IX	P00740	2158	F9	RFU	No	No	AE	0.515	0.524	0.511	0.515	0.327	0.704	0	0	0	0	0	0	0.485	0.296	0.673
SL000358 SL000360	Coagulation Factor V Coagulation Factor X	P08709 P00742	2155 2159	F7 F10	RFU	No	No No	CE	0.730	0.803	0.686	0	0	0	0.730	0.610	0.850	0.396	0.218	0.573	0.270 0.604	0.150 0.427	0.390 0.782
SL000377	CK-BB	P12277	1152	CKB	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000382 SL000383	CK-MM	P06732	1158	CKM	RFU	No	No	AE	0.550	0.573	0.534	0.550	0.376	0.725	0	0	0	0	0	0	0.450	0.275	0.624
SL000384	CTLA-4 Cytochrome c	P16410	1493 54205	CTLA4 CYCS	RFU	No	No	DE	0.463	0.377	0.478	0	0	0	0.463	0.114	0.812	0	0	0	0.537	0.188	0.886
SL000398	Cytochrome P450 3A	4 P08684	1576	CYP3A4	RFU	No	No	AE	0.721	0.789	0.679	0.721	0.604	0.839	0	o	0	ō	0	0	0.279	0.161	0.396
SL000401 SL000403	Elastase Endostatin	P08246 P39060	1991 80781	ELANE COL18A1	RFU RFU	No	No No	E CE	0	0	0	0	0	0	0	0	0	0 0.687	0 0.578	0 0.797	1 0.313	1 0.203	1 0.422
SL000406	Eotaxin	P51671	6356	CCL11	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.275	0.085	0.465	0.725	0.535	0.915
SL000408 SL000409	ERK-1	P01566 P27361	2056 5595	MAPK3	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.513	0.363	0.663	0.487	0.337	0.637
SL000414	Factor B Factor H	P00751	629 3075	CFB	RFU	No	No	DE	0.405	0.325	0.435	0	0	0	0.405	0.177	0.633	0	0	0	0.595	0.367	0.823
SL000420	Ferritin	P02794 P0	22495 2512	FTH1 FTL	RFU	No	No	AE	0.623	0.673	0.595	0.623	0.479	0.768	0	0	0	Ő	0	0	0.377	0.232	0.521
SL000424 SL000426	Fibrinogen Fibronectin	P02671 P0 P02751	22243 2244 2335	FGA FGB FGG FN1	RFU RFU	No	No No	CE AE	0	0 0.683	0 0.598	0	0 0.476	0 0.779	0	0	0	0.226	0.024	0.428	0.774 0.373	0.572 0.221	0.976 0.524
SL000427	Fractalkine/CX3CL-1	P78423	6376	CX3CL1	RFU	No	No	AE	0.405	0.349	0.430	0.405	0.220	0.589	0	0	0	0	0	0	0.595	0.411	0.780
SL000428 SL000433	Glucagon	P01215 P P01275	2641	GCG	RFU	No	No	CE	0.298	0.157	0.357	0	0	0	0.298	0.157	0.357	0.539	0.394	0.683	0.702	0.497	0.908
SL000437	Haptoglobin Mixed T	y P00738	3240	HP HPY	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.370	0.195	0.546	0.630	0.454	0.805
SL000441	HGF	P14210	3082	HGF	RFU	No	No	E	0.505	0	0	0	0.000	0	0	ō	0	ō	ō	ō	1	1	1
SL000445 SL000449	HIV-2 Rev HSP 40	P18093 P25685	1724716 3337	Human-virus DJB1	RFU RFU	No No	No No	E CE	0	0	0	0	0	0	0	0	0	0 0.211	0 0.013	0 0.408	1 0.789	1 0.592	1 0.987
SL000450	HSP 60	P10809	3329	HSPD1	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.546	0.403	0.689	0.454	0.311	0.597
SL000451 SL000456	iC3b	P08107 P01024	3303 718	C3	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.345	0.163	0.653	0.655	0.473	0.837
SL000458	IFN-g R1	P15260	3459	IFNGR1	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000461	lgE	P01854	3497 5080	IGHE IGK@ IGL@	RFU	No	No	AE	0.557	0.586	0.542	0.557	0.384	0.729	0.454	0	0	ō	ō	ō	0.443	0.271	0.616
SL000462 SL000466	IGFBP-1 IGFBP-2	P08833 P18065	3484 3485	IGFBP1 IGFBP2	RFU RFU	No No	No No	CE AE	0 0.527	0 0.541	0 0.520	0	0 0.352	0 0.701	0	0	0	0.567	0.429	0.705 0	0.433 0.473	0.295 0.299	0.571 0.648
SL000467	lgG	P01857	3500 3501	IGHG1 IGHG2 IG	RFU	No	No	DE	0.502	0.503	0.501	0	0	0	0.502	0.316	0.688	0	0	0	0.498	0.312	0.684
SL000468 SL000470	IL-11	P01871 P20809	3507 3512 3589	IL11	RFU	No	No	DE	0.432	0.392	0.395	0.432	0.247	0.617	0.344	0.101	0.587	0	0	0	0.568	0.383	0.753
SL000474	L-16	Q14005 P60568	3603	IL16	RFU	No	No	AE	0.658	0.723	0.622	0.658	0.512	0.804	0	0	0	0	0	0	0.342	0.196	0.488
SL000479	IL-2	P08700	3562	IL3	RFU	No	No	E	0	0	0	0	0	0	0	o	0	0.504	0.445	0	1	1	1
SL000480 SL000481	IL-4 IL-5	P05112 P05113	3565 3567	IL4 IL5	RFU RFU	No No	No No	E CE	0	0	0	0	0	0	0	0	0	0 0.416	0 0.245	0 0.587	1 0.584	1 0.413	1 0.755
SL000483	IL-7	P13232	3574	IL7	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000493 SL000496	LDH-H 1 Lactoferrin	P07195 P02788	3945 4057	LDHB	RFU	No	No	DE	0.709	0.772	0.581	0.709	0.593	0.824	0.605	0.455	0.755	0	0	0	0.291	0.176	0.407
SL000497	Laminin	P25391 P0	3952	LAMA1 LAMB1 L	RFU	No	No	AE	0.616	0.668	0.589	0.616	0.461	0.771	0	0	0	0	0	0	0.384	0.229	0.539
SL000498	Luteinizing hormone	P01215 P0	1081 3972	CGA LHB	RFU	No	No	CE	0.022	0.080	0.595	0.022	0.402	0.785	0	0	0	0.305	0.119	0.490	0.695	0.510	0.881
SL000507 SL000508	Lymphotoxin a1/b2 Lymphotoxin a2/b1	P01374 Q0 P01374 Q0	04049 4050 04049 4050	LTA LTB	RFU RFU	No	No No	DE	0.538	0.568	0.526	0	0	0	0.538	0.317	0.759	0.296	0	0 489	0.462	0.241	0.683
SL000509	Lymphotoxin b R	P36941	4055	LTBR	RFU	No	No	CE	0	0	Ō	0	0	0	0	0	0	0.274	0.080	0.468	0.726	0.532	0.920
SL000510 SL000515	Lysozyme MCP-2	P61626 P80075	4069 6355	CCL8	RFU	No	No No	DE	0.388	0.300	0.422	0	0	0	0.388	0.168	0.608	0.682	0.570	0.795	0.318	0.205	0.430
SL000516	MCP-3	P80098	6354	CCL7	RFU	No	No	DE	0.760	0.833	0.713	0	0	0	0.760	0.650	0.870	0	0	0	0.240	0.130	0.350
SL000519	MIP-1a	P10147	6348	CCL3	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.154	-0.045	0.354	0.846	0.646	1.045
SL000521 SL000522	MMP-1 MMP-12	P03956 P39900	4312 4321	MMP1 MMP12	RFU RFU	No No	No No	CE AF	0	0 0.639	0 0.572	0	0 0.435	0 0.755	0	0	0	0.367 0	0.191 0	0.543	0.633	0.457 0.245	0.809
SL000523	MMP-13	P45452	4322	MMP13	RFU	No	No	E	0	0	0	0	0	0	ō	Ő	ő	õ	õ	Ő	1	1	1
SL000524 SL000525	MMP-3 MMP-7	P08254 P09237	4314 4316	MMP3 MMP7	RFU	No No	No No	AE CE	0.203	-0.032	0.294	0.203	-0.018 0	0.424	0	0	0	0 0.570	0 0.431	0 0.708	0.797 0.430	0.576	1.018 0.569
SL000526	MMP-8	P22894	4317	MMP8	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.477	0.319	0.636	0.523	0.364	0.681
SL000528	DPH-P450 Oxidoredu	cP16435	5447	POR	RFU	No	No	AE	0.332	0.207	0.382	0.332	0.118	0.545	0	0	0	õ	õ	0	0.668	0.455	0.882
SL000530 SL000532	OSM ON	P13725 P09486	5008 6678	OSM SPARC	RFU RFU	No No	No No	CE CE	0	0	0	0	0	0	0	0	0	0.278 0.409	0.085 0.240	0.472 0.579	0.722 0.591	0.528 0.421	0.915 0.760
SL000535	PDGF-AA	P04085	5154	PDGFA	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.397	0.226	0.569	0.603	0.431	0.774
SL000537 SL000539	PHI PHI	P01127 P06744	2821	GPI	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.460	0.300	0.655	0.540	0.379	0.700
SL000540	Plasmin	P00747	5340 5340	PLG	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000542	gpilbilla	P08514 P0	53674 3690	ITGA2B ITGB3	RFU	No	No	AE	0.695	0.762	0.655	0.695	0.566	0.824	0.001	0.417	0	ō	ō	ō	0.305	0.176	0.434
SL000545 SL000546	Prekallikrein PRL	P03952 P01236	3818 5617	KLKB1 PRL	RFU RFU	No No	No No	AE DE	0.544 0.541	0.569 0.578	0.532 0.528	0.544	0.362	0.726	0 0.541	0 0.304	0 0.778	0	0	0	0.456 0.459	0.274 0.222	0.638
SL000550	PCI	P05154	5104	SERPI5	RFU	No	No	AE	0.689	0.750	0.651	0.689	0.566	0.811	0	0	0	0	0	0	0.311	0.189	0.434
SL000551 SL000553	PKC-A PKC-B-II	P05771	5579	PRKCB	RFU	No	No	AE	0.745	0.810	0.703	0.745	0.641	0.849	0	0	0	0.562	0.423	0.702	0.438	0.298	0.359
SL000554	PKC-D PKC-G	Q05655	5580 5582	PRKCD	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000557	PKC-Z	Q05513	5590	PRKCZ	RFU	No	No	DE	0.271	0.059	0.345	0	0	0	0.271	0.031	0.511	0	0	0	0.729	0.489	0.969
SL000558 SL000560	Prothrombin P-Selectin	P00734 P16109	2147 6403	F2 SELP	RFU RFU	No No	No No	CE AF	0	0 0.798	0 0.690	0	0 0.622	0 0.843	0	0	0	0.181 0	-0.025 0	0.388 0	0.819	0.612	1.025 0.378
SL000563	RANTES	P13501	6352	CCL5	RFU	No	No	AE	0.487	0.478	0.490	0.487	0.292	0.682	0	0	0	0	0	0	0.513	0.318	0.708
SL000565 SL000566	Renin RBP	P00797 P02753	5972 5950	REN RBP4	RFU RFU	No No	No No	DE E	0.467	0.445 0	0.477 0	0	0	0	0.467 0	0.265 0	0.670 0	0	0	0	0.533 1	0.330 1	0.735 1
SL000570	Secretin	P09683	6343	SCT	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
31000572	SAA	μητης	0200	GAAT	NEU	iNO	ONI	AE	0.903	0.943	U.0/1	0.903	0.659	0.948	U	U	U	U	U	U	0.097	0.052	U.141

SL000573	SAP	P02743 P00441	325 6647	APCS SOD1	RFU		No No	No No	AE	0.475	0.459	0.482	0.475	0.284	0.666	0	0	0	0	0	0	0.525	0.334	0.716
SL000582	Survivin	O15392	332	BIRC5	RFU		No	No	DE	0.759	0.852	0.705	Ő	ŏ	ŏ	0.759	0.627	0.891	0	0	0	0.241	0.109	0.373
SL000586	Thrombin	P00734	2147	F2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.227	0.465	0.423	0.404	0.272	0.535
SL000587 SL000588	Thyroglobulin TMA	P01266 P07202	7038 7173	TG TPO	RFU RFU		No No	No No	E DE	0 0.513	0 0.537	0 0.508	0	0	0	0 0.513	0 0.180	0 0.845	0	0	0	1 0.487	1 0.155	1 0.820
SL000590	Thyroxine-Binding G	lo P05543 P01033	6906 7076	SERPI7 TIMP1	RFU		No	No	DE	0.556	0.585	0.542	0	0	0	0.556	0.388	0.725	0 261	0	0 457	0.444	0.275	0.612
SL000592	TIMP-2	P16035	7077	TIMP2	RFU		No	No	AE	0.472	0.453	0.480	0.472	0.273	0.671	Ő	Ő	Ő	0	0	0	0.528	0.329	0.727
SL000597 SL000601	Transferrin	P01374 P02787	4049 7018	TF	RFU		No No	No No	CE	0	0	0	0	0	0	0	0	0	0.260	0.062	0.457	1 0.740	1 0.543	1 0.938
SL000603 SL000605	Trypsin Ubiquitin+1	P07477 P62979	5644 6233	PRSS1 RPS27A	RFU RFU		No No	No No	AE CE	0.600 0	0.649 0	0.575 0	0.600 0	0.434 0	0.765 0	0	0	0	0 0.449	0 0.284	0 0.614	0.400 0.551	0.235 0.386	0.566 0.716
SL000613	uPA	P00749	5328	PLAU	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.478	0.319	0.637	0.522	0.363	0.681
SL000617	ALT	P24298	2875	GPT	RFU		No	No	CE	0.540	0.575	0.555	0	0	0	0.540	0.349	0.743	0.340	0.158	0.522	0.660	0.478	0.842
SL000622 SL000633	Fas ligand soluble	P12259 P48023	2153 356	F5 FASLG	RFU		No No	No No	AE DE	0.701 0.394	0.764 0.320	0.662	0.701	0.581	0.821	0.394	0 0.189	0.599	0	0	0	0.299	0.179 0.401	0.419
SL000638	Cadherin-2 Nidogen	P19022 P14543	1000 4811	CDH2 NID1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000645	MMP-10	P09238	4319	MMP10	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000655	GAS1	P05783 P54826	2619	GAS1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000668 SL000670	CD36 ANTIGEN GSTA3	P16671 Q16772	948 2940	CD36 GSTA3	RFU RFU		No No	No No	DE E	0.584	0.629 0	0.562 0	0	0	0	0.584	0.408 0	0.759 0	0	0	0	0.416	0.241 1	0.592 1
SL000674 SL000678	FST Granulysin	P19883 P22749	10468 10578	FST GNI Y	RFU		No No	No No	AE	0.213	-0.141 0.740	0.315	0.213	-0.063	0.488	0	0	0	0	0	0	0.787	0.512	1.063 0.448
SL000695	Lipocalin 2	P80188	3934	LCN2	RFU	Calibration Scale	No	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SL000836 SL001691	FGF7	P69905 P P21781	2252	FGF7	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.397	0.225	0.569	0.603	0.431	0.775
SL001713 SL001716	IL-17 IL-12	Q16552 P29459 F	3605 P2 3592 3593	IL17A 3 IL12A IL12B	RFU RFU		No No	No No	CE E	0	0	0	0	0	0	0	0	0	0.241	0.044 0	0.437 0	0.759	0.563 1	0.956 1
SL001717	IL-10	P22301 P35225	3586 3596	IL10 II 13	RFU		No No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL001720	VCAM-1	P19320	7412	VCAM1	RFU		No	No	CE	0	Ő	Ő	0	ŏ	Ő	0	0	0	0.388	0.212	0.564	0.612	0.436	0.788
SL001721 SL001726	GM-CSF	P16284 P04141	1437	CSF2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL001729 SL001737	G-CSF STRATIFIN	P09919 P31947	1440 2810	CSF3 SFN	RFU RFU		No No	No No	CE CE	0	0	0	0	0	0	0	0	0	0.223 0.475	0.029 0.317	0.416 0.634	0.777 0.525	0.584 0.366	0.971 0.683
SL001753	Sialoadhesin HCG	Q9BZZ2 P01215 P0	6614 011081 1083	SIGLEC1	RFU		No No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL001774	FABP	P05413	2170	FABP3	RFU		No	No	CE	0	0	0	0	Ö	Ö	0	0	0	0.422	0.253	0.591	0.578	0.409	0.747
SL001777 SL001795	L-1b	P01034 P01584	1471 3553	IL1B	RFU		No No	No No	CE	0.593	0.635	0.571	0	0	0	0.593	0.439	0.747	0.169	-0.029	0.367	0.407 0.831	0.253	0.561
SL001796 SL001797	Myeloperoxidase Kallikrein 6	P05164 Q92876	4353 5653	MPO KLK6	RFU RFU		No No	No No	AE CE	0.600 0	0.644 0	0.576 0	0.600 0	0.447 0	0.753 0	0	0	0	0 0.202	0 0.002	0 0.402	0.400 0.798	0.247 0.598	0.553 0.998
SL001800	TNF sR-II	P20333 P01579	7133 3458	TNFRSF1B	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.493	0.337	0.650	0.507	0.350	0.663
SL001815	Mn SOD	P04179	6648	SOD2	RFU		No	No	CE	Ő	ŏ	Ő	Ő	ŏ	ŏ	Ő	Ő	Ő	0.488	0.330	0.646	0.512	0.354	0.670
SL001888	SLPI	P03973	6590	SLPI	RFU		No	No	AE	0.529	0.543	0.521	0.529	0.362	0.695	0	0	0	0	0	0	0.471	0.305	0.638
SL001890 SL001896	GA733-1 protein Clusterin	P09758 P10909	4070 1191	TACSTD2 CLU	RFU RFU		No No	No No	E CE	0	0	0	0	0	0	0	0	0	0 0.363	0 0.184	0 0.542	1 0.637	1 0.458	1 0.816
SL001897	SPINT2 BCAM	O43291 P50895	10653 4059	SPINT2 BCAM	RFU		No	No	AE	0.685	0.751	0.646	0.685	0.553	0.816	0	0	0	0	0	0	0.315	0.184	0.447
SL001905	Mesothelin	Q13421	10232	MSLN	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL001938	IL-6 sRa	P08887	3570	IL6R	RFU		No	No	AE	0.845	0.899	0.804	0.845	0.777	0.913	0	0	0	0	0.134	0.501	0.082	0.087	0.223
SL001945 SL001947	sE-Selectin MIA	P16581 Q16674	6401 8190	SELE MIA	RFU RFU		No No	No No	AE DE	0.723 0.669	0.792 0.730	0.680 0.634	0.723	0.605 0	0.841 0	0 0.669	0 0.538	0 0.801	0	0	0	0.277 0.331	0.159 0.199	0.395 0.462
SL001973 SL001992	Mammaglobin 2 TNF sR-I	O75556 P19438	4246 7132	SCGB2A1 TNFRSF1A	RFU RFU		No No	No No	E AE	0 0.502	0 0.504	0 0.502	0	0 0.313	0 0.692	0	0	0	0	0	0	1 0.498	1 0.308	1 0.687
SL001995	Angiopoietin-1	Q15389	284	ANGPT1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.293	0.107	0.480	0.707	0.520	0.893
SL001997	IL-1 sRI	P14778	3554	L1R1	RFU		No	No	AE	0.539	0.560	0.529	0.539	0.362	0.715	0	0	0	0	0	0	0.461	0.285	0.638
SL001998 SL001999	MDM2	Q00987	7035 4193	MDM2	RFU		No No	No No	CE	0	0	0	0	0	0	0	0	0	0.540	0.392	0.687	0.460 0.780	0.313 0.585	0.608
SL002036 SL002075	FGFR4 IFN-aA	P22455 P01563	2264 3440	FGFR4 IF2	RFU RFU		No No	No No	E CE	0	0	0	0	0	0	0	0	0	0 0.836	0 0.774	0 0.898	1 0.164	1 0.102	1 0.226
SL002077	Alkaline phosphatas	e P05186	249 7048	ALPL	RFU		No	No	AE	0.592	0.635	0.570	0.592	0.435	0.749	0	0	0	0	0	0	0.408	0.251	0.565
SL002081	Cadherin-5	P33151	1003	CDH5	RFU		No	No	DE	0.645	0.706	0.611	0	Ö	Ö	0.645	0.495	0.794	0	0	0	0.355	0.206	0.505
SL002086 SL002093	Ficolin-3 Histone H2A.z	075636 P0C0S5	8547 3015	FCN3 H2AFZ	RFU RFU		No No	No No	CE DE	0 0.695	0 0.781	0 0.649	0	0	0	0 0.695	0 0.542	0 0.848	0.655 0	0.538 0	0.772	0.345 0.305	0.228 0.152	0.462 0.458
SL002506 SL002508	suPAR IL-18 BPa	Q03405 O95998	5329 10068	PLAUR IL18BP	RFU RFU		No No	No No	AE DE	0.538 0.296	0.560 0.135	0.528 0.358	0.538 0	0.357 0	0.719 0	0 0.296	0 0.075	0 0.516	0	0	0	0.462 0.704	0.281 0.484	0.643 0.925
SL002517	TNF-a	P01375	7124	TNF	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL002519	Rb	P06400	5925	RB1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0.482	0	1	1	1
SL002524 SL002525	sCD4 C2	P01730 P06681	920 717	CD4 C2	RFU RFU		No No	No No	DE AE	0.844 0.508	0.908 0.513	0.798 0.506	0 0.508	0 0.312	0 0.704	0.844	0.766 0	0.923 0	0	0	0	0.156 0.492	0.077 0.296	0.234 0.688
SL002528 SL002539	NPS-PLA2 OPG	P14555 000300	5320 4982	PLA2G2A TNFRSF11B	RFU RFU		No No	No No	CE CF	0	0	0	0	0	0	0	0	0	0.650	0.531 0.176	0.768	0.350	0.232	0.469
SL002541	sRANKL	O14788	8600	TNFSF11	RFU		No	No	CE	0	0 718	0	0	ō	ō	0	0	0 802	0.269	0.075	0.462	0.731	0.538	0.925
SL002542	PTHrP	P12272	5744	PTHLH	RFU	0.11	No	No	CE	0.052	0	0	0	0	0	0	0	0	0.327	0.144	0.510	0.673	0.490	0.856
SL002621 SL002640	Midkine PIGF	P21741 P49763	4192 5228	MDK PGF	RFU RFU	Calibration Scale	No No	No No	NA E	NA 0	NA 0	NA 0	NA 0	NA 0	NA 0	NA 0	NA 0	NA 0	NA 0	NA 0	NA 0	NA 1	NA 1	NA 1
SL002646	MMP-14 M2-PK	P50281 P14618	4323 5315	MMP14 PKM2	RFU RFU		No	No No	DE	0.372	0.077	0.425	0.731	0	0	0.372	0.023 0	0.721	0	0	0	0.628	0.279	0.977
SL002654	Epithelial cell kise	P29317	1969	EPHA2	RFU		No	No	DE	0.443	0.404	0.460	0	0 210	0	0.443	0.239	0.648	0 0	ő	0	0.557	0.352	0.761
32002033	UTOP .	F23213	1450	ordr	NFU		INU	UNI	AE	0.309	0.314	0.300	0.309	0.319	0.099	U	U	U	1 0	U	U	0.491	0.301	0.001

SL002662	Coagulation Factor XI P03951	2160	F11	RFU		No	No	AE	0.514	0.523	0.511	0.514	0.334	0.695	0	0	0	0	0	0	0.486	0.305	0.666
SL002695	Glutamate carboxypep Q96KP4	55748	CNDP2	RFU		No	No	DE	0.534	0.566	0.523	0	0	0	0.534	0.291	0.777	0	0	0	0.466	0.223	0.709
SL002702 SL002704	PIM1 P11309 PTN P21246	5292 5764	PIM1 PTN	RFU RFU		No No	No No	E	0	0	0	0	0	0	0	0	0	0	0	0	1 0.664	1 0.424	1 0.904
SL002705	Thrombospondin-1 P07996	7057	THBS1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.369	0.193	0.545	0.631	0.455	0.807
SL002706 SL002755	CD23 P06734 PAPP-A Q13219	2208 5069	FCER2 PAPPA	RFU		No	No No	AE DE	0.521 0.724	0.533	0.516	0.521	0.346	0.696	0.724	0.607	0.841	0	0	0	0.479 0.276	0.304 0.159	0.654
SL002756	hnRNPK P61978	3190	HNRNPK	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL002763 SL002783	Cardiotrophin-1 Q90BX7	11012	CTF1	RFU		No	No	DE	0.366	0.194	0.414	0	0	0	0.366	0.085	0.647	0.595	0.462	0.728	0.405	0.272	0.538
SL002792	BARK1 P25098	156	ADRBK1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.595	0.463	0.727	0.405	0.273	0.537
SL002803	sL-Selectin P14151	6402	SELL	RFU		No	No	DE	0.301	0.136	0.363	0.742	0.023	0.001	0.301	0.074	0.528	0	0	0	0.699	0.472	0.926
SL002922	sICAM-1 P05362	3383	ICAM1	RFU	Calibration Scale	No	No	CE	0	0	0	0	0	0	0	0	0	0.573 NA	0.435 NA	0.710 NA	0.427 NA	0.290	0.565 NA
SL003043	TIMP-3 P35625	7078	ТІМРЗ	RFU	Calibration Scale	No	No	AE	0.569	0.603	0.552	0.569	0.407	0.732	0	0	0	0	0	0	0.431	0.268	0.593
SL003060 SL003080	bFGF-R P11362 MIF P14174	2260 4282	FGFR1 MIF	RFU RFU		No No	No No	DE AF	0.524	0.538	0.518	0	0	0	0.524	0.342	0.707	0	0	0	0.476	0.293	0.658
SL003104	Eotaxin-2 000175	6369	CCL24	RFU		No	No	E	0	0	0	0	0	0	0	0	ő	ŏ	ŏ	Ő	1	1	1
SL003166 SL003167	ALCAM Q13740 BLC 043927	214 10563	ALCAM CXCL13	RFU RFU		No No	No No	CE AE	0 0.380	0 0.291	0 0.416	0	0 0.166	0 0.595	0	0	0	0.446 0	0.274	0.618 0	0.554 0.620	0.382	0.726
SL003168	CTACK Q9Y4X3	10850	CCL27	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.170	-0.035	0.376	0.830	0.624	1.035
SL003169 SL003171	FGF-4 P08620	2249	FGF4	RFU		No	No	DE	0.540	0.579	0.527	0	0	0	0.540	0.295	0.785	0.266	0.071	0.461	0.734	0.539	0.929
SL003172	GCP-2 P80162	6372	CXCL6	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.417	0.249	0.586	0.583	0.414	0.751
SL003175 SL003176	I-309 P22362	6346	CCL1	RFU		No	No	CE	0.566	0.000	0.550	0.566	0.366	0.748	0	0	0	0.279	0.087	0.472	0.432	0.252	0.913
SL003177 SL003178	sICAM-2 P13598 sICAM-3 P32942	3384 3385	ICAM2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.162	-0.045	0.368	0.838	0.632	1.045
SL003179	Integrin a1b1 P56199 F	P0:3672 368	8 ITGA1 ITGB1	RFU		No	No	CE	Ő	0	õ	0	0	ō	0	0	0 0	0.529	0.383	0.676	0.471	0.324	0.617
SL003182 SL003183	Integrin aVb5 P06756 F IP-10 P02778	P183685 369 3627	3 ITGAV ITGB5 CXCL10	RFU RFU		No No	No No	DE AE	0.510 0.528	0.517 0.541	0.507 0.521	0 0.528	0 0.366	0 0.690	0.510 0	0.300	0.719	0	0	0	0.490 0.472	0.281 0.310	0.700 0.634
SL003184	sLeptin R P48357	3953	LEPR	RFU		No	No	AE	0.958	0.976	0.941	0.958	0.939	0.977	0	0	0	0	0	0	0.042	0.023	0.061
SL003186 SL003187	MDC 000626	6367	CCL22	RFU		No	No	DE	0.661	0.692	0.625	0	0	0	0.661	0.519	0.803	0	0	0	0.339	0.172	0.613
SL003189 SL003190	MIP-3b Q99731 MIP-5 016663	6363 6359	CCL19 CCL15	RFU		No	No	E	0	0	0	0	0	0	0	0	0 782	0	0	0	1	1	1
SL003191	P-2 P02775	5473	PPBP	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.345	0.165	0.524	0.655	0.476	0.835
SL003192 SL003193	Properdin P27918 6Ckine 000585	5199 6366	CFP CCI 21	RFU RFU		No No	No No	CE AF	0	0	0	0	0	0	0	0	0	0.420	0.249	0.590	0.580	0.410	0.751
SL003196	TARC Q92583	6361	CCL17	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.412	0.242	0.582	0.588	0.418	0.758
SL003197 SL003198	TECK 015444 Tescin P24821	6370 3371	TNC	RFU		No	No No	AE	0.806	0.869	0.762	0.806	0.721	0 0.891	0	0	0	0.632	0.510	0.755	0.368	0.245	0.490
SL003199	sTie-1 P35590	7075	TIE1	RFU		No	No	DE	0.764	0.843	0.715	0	0	0	0.764	0.650	0.879	0	0	0	0.236	0.121	0.350
SL003200 SL003201	VEGF sR2 P35968	3791	KDR	RFU		No	No	CE	0.538	0.556	0.526	0.538	0.361	0.714	0	0	0	0.560	0.415	0.704	0.462	0.286	0.585
SL003220	C3adesArg P01024 HMC-1 P09429	718	C3 HMGB1	RFU	Calibration Scale	No	No	NA	NA 0.750	NA 0.833	NA 0.700	NA	NA	NA	NA 0.750	NA 0.624	NA 0.875	NA	NA	NA	NA 0.250	NA 0.125	NA 0.376
SL003300	HCC-4 015467	6360	CCL16	RFU		No	No	DCE	0.165	-0.077	0.249	0	0	ō	0.165	-0.040	0.370	0.646	0.451	0.841	0.189	0.104	0.273
SL003301 SL003302	Ck-b-8-1 P55773 MPIF-1 P55773	6368 6368	CCL23 CCL23	RFU RFU		No No	No No	CE AE	0 0.749	0 0.822	0 0.703	0 0.749	0 0.636	0 0.862	0	0	0	0.303	0.116 0	0.490 0	0.697 0.251	0.510 0.138	0.884 0.364
SL003303	CCL28 Q9NRJ3	56477	CCL28	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.360	0.182	0.538	0.640	0.462	0.818
SL003304 SL003305	IGF-I sR P08069 IL-2 sRa P01589	3480 3559	IGF1R IL2RA	RFU		No No	No No	E	0.529	0.546	0.521	0	0	0	0.529	0.342	0.716	0	0	0	0.471	0.284	0.658
SL003307	IL-2 sRg P31785	3561	IL2RG	RFU		No	No	ACE	0.423	0.209	0.438	0.423	0.028	0.819	0	0	0	0.371	-0.011	0.752	0.206	0.116	0.297
SL003308 SL003309	LBP P18428	3929	LBP	RFU		No	No	AE	0.603	0.647	0.579	0.603	0.451	0.755	0	0	0	0	0	0	0.397	0.245	0.549
SL003310	VEGF121 P15692	7422	VEGFA	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.156	-0.044	0.355	0.844	0.645	1.044
SL003323	PARC P55774	6362	CCL18	RFU		No	No	CE	0	0	0	0	0	0	0	0	0.010	0.641	0.521	0.762	0.359	0.238	0.479
SL003324 SL003326	Coagulation Factor Xa P00742 I-TAC 014625	2159 6373	F10 CXCL11	RFU RFU		No No	No No	DE DE	0.623 0.525	0.685 0.537	0.592 0.519	0	0	0	0.623 0.525	0.455 0.358	0.791 0.691	0	0	0	0.377 0.475	0.209 0.309	0.545 0.642
SL003327	Factor D P00746	1675	CFD	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003328 SL003329	HCC-1 Q16627	5420 6358	CCL14	RFU		No	No	AE	0.461	0.437	0.472	0.461	0.272	0.848	0	0	0	0	0	0	0.539	0.350	0.728
SL003331 SL003332	MMP-16 P51512 MMP-17 09111 79	4325 4326	MMP16 MMP17	RFU RFU		No No	No No	E	0	0	0	0	0	0	0	0	0	0	0	0	1 1	1 1	1
SL003334	EMAP-2 Q12904	9255	AIMP1	RFU		No	No	DE	0.868	0.924	0.824	0	0	0	0.868	0.801	0.934	0	0	0	0.132	0.066	0.199
SL003341 SL003362	C3d P01024	2266 718	FGG C3	RFU RFU		No No	No No	AE E	0.364 0	0.244 0	0.408 0	0.364 0	0.129 0	0.599 0	0	0	U 0	U 0	U 0	0 0	0.636 1	0.401 1	0.871 1
SL003440	PAFAH Q13093	7941	PLA2G7	RFU		No	No	DE	0.518	0.530	0.513	0	0	0	0.518	0.316	0.720	0	0	0	0.482	0.280	0.684
SL003401	calreticulin P27797	811	CALR	RFU		No	No	E	0.410	0.113	0.400	0	0	0	0.410	0.025	0.007	0	0	0	1	1	1
SL003522 SL003524	ERP29 P30040 Protein disulfide isome P30101	10961 2923	ERP29 PDIA3	RFU RFU		No No	No No	CE CF	0	0	0	0	0	0	0	0	0	0.436	0.269	0.604	0.564	0.396	0.731
SL003542	NG36 Q96KQ7	10919	EHMT2	RFU		No	No	CE	Ő	Ő	õ	Ő	Ő	õ	Ő	Ő	ő	0.421	0.249	0.594	0.579	0.406	0.751
SL003643 SL003647	annexin VI P08133	2950 309	GSTP1 ANXA6	RFU RFU	Calibration Scale	No No	No No	CE NA	U NA	0 NA	U NA	U NA	U NA	U NA	NA	0 NA	U NA	0.491 NA	0.335 NA	0.647 NA	0.509 NA	0.353 NA	0.665 NA
SL003648	Rab GDP dissociation P50395	2665	GDI2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.605	0.475	0.735	0.395	0.265	0.525
SL003653 SL003655	Transketolase P29401	5230 7086	TKT	RFU		NO NO	NO	CE	0	0	0	0	0	0	0	0	0	0.390	0.216	0.564 0.750	0.610 0.374	0.436	0.784
SL003657	Calcineurin Q08209 F	P6:5530 553	4 PPP3CA PPP3F	RFU		No	No	AE	0.718	0.784	0.677	0.718	0.602	0.834	0	0	0	0	0	0	0.282	0.166	0.398
SL003674	BCL2-like 1 protein Q07817	598	BCL2L1	RFU		No	No	DE	0.240	0.396	0.469	0	0	õ	0.452	0.182	0.470	0.546	0.525	0.771	0.212	0.277	0.818
SL003679 SL003680	IGF-II receptor P11717 sRAGE 015109	3482 177	IGF2R AGER	RFU RFU		No No	No No	DE AF	0.671 0.810	0.735 0.868	0.635	0 0.810	0 0.730	0	0.671 0	0.536 0	0.807	0	0	0	0.329	0.193 0.111	0.464
SL003685	PBEF P43490	10135	MPT	RFU		No	No	CE	0	0	0	0	0	0	Ő	Ő	õ	0.396	0.224	0.569	0.604	0.431	0.776
SL003687 SL003690	Nucleoside diphospha P15531 RANK Q9Y6Q6	4830 8792	NME1 TNFRSF11A	RFU RFU		No No	No No	E	0	0	0	0	0	0	0	0	0	0	0	0	1 1	1 1	1 1
SL003703	BFL1 Q16548	597	BCL2A1	RFU		No	No	DE	0.752	0.834	0.702	0	0	0	0.752	0.629	0.875	0	0	0	0.248	0.125	0.371
SL003711 SL003717	Caspase-3 P42574 Caspase-10 Q92851	836 843	CASP3 CASP10	RFU		NO NO	NO	CE	0	0	0	0	0	0	0	0	0	0.546	0.403	0.689	0.454	0.311	0.597
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SL003726	Chk2 clAP-2	O96017	11200	CHEK2 BIRC3	RFU		No	No No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003733	SMAC	Q9NR28	56616	DIABLO	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003738	B7	P33681	941	CD80	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.475	0.318	0.633	0.525	0.367	0.682
SL003739 SL003744	DcR3 Galectin-3	O95407 P17931	8771 3958	TNFRSF6B LGALS3	RFU RFU		No No	No No	E CE	0	0	0	0	0	0	0	0	0	0 0.615	0 0.485	0 0.744	1 0.385	1 0.256	1 0.515
SL003753	DLC8 pTEN	P63167 P60484	8655 5728	DYNLL1 PTEN	RFU		No	No No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003764	NCAM-120	P13591	4684	NCAM1	RFU		No	No	AE	0.700	0.768	0.660	0.700	0.573	0.827	0	0	Ö	0	0	0	0.300	0.173	0.427
SL003770 SL003785	GAPDH liver	Q8N474 P04406	6422 2597	GAPDH	RFU		No No	No No	AE	0.713	0.779	0.673	0.713	0.596	0.831	0	0	0	0.490	0.334	0.645	0.510 0.287	0.355 0.169	0.666
SL003793 SL003800	MEK1 Kallikrein 4	Q02750 Q9Y5K2	5604 9622	MAP2K1 KI K4	RFU RFU		No No	No No	CE F	0	0	0	0	0	0	0	0	0	0.172	-0.027	0.372	0.828	0.628	1.027 1
SL003803	ERBB4	Q15303	2066	ERBB4	RFU		No	No	DE	0.736	0.846	0.679	0	0	0	0.736	0.577	0.895	0	0	0	0.264	0.105	0.423
SL003862	CD40 ligand soluble	P29965	2254 959	CD40LG	RFU		No	No	E	0.466	0.445	0.495	0	0	0	0.466	0.100	0.875	0	0	0	1	1	1
SL003863 SL003872	kallikrein 5 op130 soluble	Q9Y337 P40189	25818 3572	KLK5 IL6ST	RFU RFU		No No	No No	CE	0	0	0	0	0	0	0	0	0	0.314 0.525	0.126	0.502 0.678	0.686 0.475	0.498	0.874 0.628
SL003915	kallikrein 8 kallikrein 12	060259	11202	KLK8 KLK12	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.528	0.379	0.677	0.472	0.323	0.621
SL003918	kallikrein 13	Q9UKR3	26085	KLK13	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003919 SL003930	HPG-	Q9P0G3 P15428	43847 3248	HPGD	RFU		No	No No	DE	0.777	0.868	0.722	0	0	0	0.777	0.653	0.901	0	0	0	0.223	0.099	0.347
SL003951 SL003970	BDNF PTH	P23560 P01270	627 5741	BDNF PTH	RFU RFU	Calibration Scale	No No	No No	NA F	NA 0	NA 0	NA 0	NA 0	NA 0	NA 0	NA 0	NA 0	NA 0	NA 0	NA 0	NA 0	NA 1	NA 1	NA 1
SL003974	Activated Protein C	P04070	5624	PROC	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003990	BMP-6	P22004	654	BMP6	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003994 SL004008	BMP-1 Proteise-3	P13497 P24158	649 5657	BMP1 PRTN3	RFU RFU		No No	No No	CE DE	0 0.534	0 0.552	0 0.525	0	0	0	0 0.534	0 0.360	0 0.708	0.505	0.350 0	0.660 0	0.495 0.466	0.340 0.292	0.650 0.640
SL004009	RAC1 SCE sR	P63000 P10721	5879 3815	RAC1	RFU		No	No No	DCE	0.242	-0.072	0.314	0	0	0	0.242	-0.027	0.512	0.508	0.258	0.758	0.250	0.140	0.359
SL004015	TAFI	Q96IY4	1361	CPB2	RFU		No	No	AE	0.631	0.688	0.601	0.631	0.480	0.783	0	0	0	0	0	0	0.369	0.217	0.520
SL004016 SL004060	Endothelin-converting	g P42892	1889	ECE1	RFU		No	No No	AE	0.676	0.738	0.640	0.676	0.546	0.806	0	0	0	0.500	0.343	0.657	0.500	0.343	0.657
SL004063 SL004064	FGFR-3 GIB	P22607 P04054	2261 5319	FGFR3 PLA2G1B	RFU RFU		No No	No No	E AE	0 0.353	0 0.232	0 0.398	0 0.353	0 0.127	0 0.578	0	0	0	0	0	0	1 0.647	1 0.422	1 0.873
SL004066	GIE	Q9NZK7	30814	PLA2G2E PLA2G10	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004068	Granzyme B	P10144	3002	GZMB	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004070 SL004078	BMP-7	P62979 P18075	6233 655	BMP7	RFU		No No	No No	AE	0.233	-0.096 0.673	0.328	0.620	0 0.467	0.773	0.233	-0.043 0	0.509	0	0	0	0.767	0.491 0.227	1.043 0.533
SL004080 SL004081	BMPR1A Bone proteoglycan II	P36894 P07585	657 1634	BMPR1A DCN	RFU RFU		No No	No No	DE	0.395	0.289	0.430	0	0	0	0.395	0.144	0.646	0	0	0	0.605	0.354	0.856
SL004118	TrATPase	P13686	54	ACP5	RFU		No	No	AE	0.698	0.771	0.655	0.698	0.561	0.834	0	0	0	0	0	0	0.302	0.166	0.439
SL004110	Discoidin domain rec	xe Q16832	4921	DDR2	RFU		No	No	CE	0	0	0	0	0	0	0	0	Ö	0.146	-0.056	0.348	0.854	0.652	1.056
SL004125 SL004126	4-1BB	Q07011	3643	INSR TNFRSF9	RFU		No	No No	E	0	0	0	0	0	0	0	0	0	0.346	0.165	0.527	0.654	0.473	0.835
SL004128 SL004131	Activin RIB B7-2	P36896 P42081	91 942	ACVR1B CD86	RFU RFU		No No	No No	E DE	0 0.190	0 -0.119	0 0.294	0	0	0	0 0.190	0 -0.060	0 0.440	0	0	0 0	1 0.810	1 0.560	1 1.060
SL004133	BMP RII	Q13873	659 939	BMPR2	RFU	Calibration Scale	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1 NA	1 NA	1 NA
SL004136	Dtk	Q06418	7301	TYRO3	RFU	Calibraton Scale	No	No	DE	0.586	0.649	0.561	0	0	0	0.586	0.377	0.796	0	0	0	0.414	0.204	0.623
SL004137 SL004140	EphA1 Ephrin-A4	P21709 P52798	2041 1945	EPHA1 EF4	RFU		No No	No No	CE	0	0	0	0	0	0	0	0	0	0.351 0.438	0.173	0.530	0.649	0.470 0.393	0.827
SL004141 SL004142	Ephrin-A5 Ephrin-B3	P52803 Q15768	1946 1949	EF5 EFNB3	RFU RFU		No No	No No	CE E	0	0	0	0	0	0	0	0	0	0.347	0.166 0	0.529	0.653 1	0.471 1	0.834 1
SL004143	GFRa-2	000451	2675	GFRA2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.633	0.510	0.757	0.367	0.243	0.490
SL004145	HVEM	Q92956	8764	TNFRSF14	RFU		No	No	Ē	0	0	0	0	0	0	0	0	Ő	0	0	0	1	1	1
SL004146 SL004147	IL-1 R4 IL-10 Rb	Q01638 Q08334	9173 3588	IL1RL1 IL10RB	RFU		No No	No No	E	0.763	0.836	0.715	0.763	0.653	0.872	0	0	0	0	0	0	0.237	0.128	0.347
SL004148 SL004149	IL-12 Rb1 IL-13 Ra1	P42701 P78552	3594 3597	IL12RB1 IL13RA1	RFU RFU		No No	No No	E CE	0	0	0	0	0	0	0	0	0	0 0.198	0 0.001	0 0.395	1 0.802	1 0.605	1 0.999
SL004151	IL-15 Ra	Q13261	3601	IL15RA	RFU		No	No	DE	0.746	0.847	0.691	0	0	0	0.746	0.601	0.891	0	0	0	0.254	0.109	0.399
SL004152	M-CSF R	P07333	1436	CSF1R	RFU		No	No	AE	0.577	0.612	0.558	0.577	0.418	0.736	0	0	0	0.598	0.400	0.750	0.402	0.264	0.582
SL004154 SL004155	NCAM-L1 PDGF Rb	P32004 P09619	3897 5159	L1CAM PDGFRB	RFU RFU		No No	No No	AE	0.578 0.725	0.615 0.791	0.560 0.683	0.578 0.725	0.420 0.610	0.737 0.839	0	0	0	0	0	0	0.422 0.275	0.263 0.161	0.580 0.390
SL004156 SL004159	TRAIL R1 TRAIL R4	000220 09UBN6	8797 8793	TNFRSF10A TNFRSF10D	RFU RFU		No No	No No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1 0.348	1 0.664
SL004160	TrkB	Q16620	4915	NTRK2	RFU		No	No	AE	0.466	0.445	0.476	0.466	0.273	0.660	0	0	0	0	0	0	0.534	0.340	0.727
SL004180 SL004182	GV	P28908 P39877	943 5322	PLA2G5	RFU		No	No	DE	0.837	0.732	0.723	0	0	0	0.837	0.433	0.842	0	0	0	0.363	0.095	0.346
SL004183 SL004208	P-Cadherin annexin I	P22223 P04083	1001 301	CDH3 ANXA1	RFU RFU		No No	No No	E AE	0 0.263	0 -0.064	0 0.350	0 0.263	0 -0.027	0 0.554	0	0	0	0	0	0	1 0.737	1 0.446	1 1.027
SL004209	annexin II	P07355	302	ANXA2	RFU		No	No	AE	0.425	0.377	0.446	0.425	0.229	0.622	0	0	0	0	0	0	0.575	0.378	0.771
SL004253	17-beta-HSD 1	P14061	3292	HSD17B1	RFU		No	No	E	0	0	ō	0	0	ō	0	0	0	o	0	0	1	1	1
SL004258 SL004260	Aaiponectin resistin	Q15848 Q9HD89	9370 56729	RETN	RFU		No No	No No	AE	0.720	0.793 0.594	0.676	0.720	0.595	0.845	0	0	0	0	0	0	0.280	0.155	0.405
SL004271 SL004296	GFAP Mvokise human	P14136 P00568	2670 203	GFAP AK1	RFU RFU		No No	No No	E AE	0 0.552	0 0.579	0 0.539	0 0.552	0 0.380	0 0.724	0	0	0	0	0	0	1 0.448	1 0.276	1 0.620
SL004297	NEUREGULIN-1	Q02297	3084	NRG1	RFU		No	No	CE	0	0	0	0	0	0	0	0 C	0	0.372	0.193	0.551	0.628	0.449	0.807
SL004298 SL004299	Livin B	Q96CA5	3001 79444	BIRC7	RFU		No	NO NO	E	0	0	0	0	0	0	0	0	0	0.161	-0.040	0.361	0.839	0.639	1.040
SL004301 SL004304	Ku70 STX1a	P12956 Q16623	2547 6804	XRCC6 STX1A	RFU RFU		No No	No No	DE E	0.353 0	0.192 0	0.404 0	0	0	0	0.353 0	0.092 0	0.615 0	0	0	0	0.647 1	0.385 1	0.908 1
SL004305	Topoisomerase I	P11387	7150	TOP1	RFU		No	No No	DE	0.716	0.804	0.668	0	0	0	0.716	0.571	0.861	0	0	0	0.284	0.139	0.429
SL004326	TNFSF18	Q9UNG2	8995	TNFSF18	RFU		No	No	E	0	0	0	0	0	0	õ	0	Ő	ő	õ	ő	1	1	1

SL004327	BAFF	Q9Y275	10673	TNFSF13B	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.299	0.110	0.487	0.701	0.513	0.890
SL004329	BMP-14 CD22	P43026 P20273	8200	GDF5 CD22	RFU	No	No	DE	0.445	0.370	0.465	0	0	0	0.445	0.158	0.731	0	0	0	0.555	0.269	0.842
SL004330	CNTE	P26441	1270	CNTE	RFU	No	No	DE	0.499	0.498	0.500	0	0	0	0.499	0.182	0.816	0	0	0	0.501	0.184	0.818
SL004332	EG-VEGF	P58294	84432	PROK1	RFU	No	No	E	0	0	0	Ō	0	ō	0	0	0	ō	0	ō	1	1	1
SL004333	FGF-10	O15520	2255	FGF10	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004334	FGF-16	043320	8823	FGF16	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.585	0.450	0.719	0.415	0.281	0.550
SL004335	FGF-17	076093	8817	FGF17 FGF18	REU	No	No	F	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004337	FGF-19	095750	9965	FGF19	RFU	No	No	AE	0.554	0.583	0.540	0.554	0.381	0.727	0	õ	0	ő	õ	Ő	0.446	0.273	0.619
SL004338	FGF-20	Q9NP95	26281	FGF20	RFU	No	No	AE	0.707	0.789	0.661	0.707	0.565	0.849	0	0	0	0	0	0	0.293	0.151	0.435
SL004339	FGF-5	P12034	2250	FGF5	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004340	FGF-6	P10/6/	2251	FGF6	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.401	0.228	0.573	0.599	0.427	0.772
SL004342	Flt3 ligand	P49771	2323	FLT3LG	RFU	No	No	Ē	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004345	GDF-11	O95390	10220	GDF11	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004346	IL-20	Q9NYY1	50604	IL20	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004347	IL-22	Q9GZX6	50616	IL22	RFU	No	No	DE	0.474	0.451	0.482	0	0	0	0.474	0.239	0.708	0	0	0	0.526	0.292	0.761
SL004348	IFN-lambda 1	0817.10	282616	129	RFU	No	No	F	0	0	0	0	0	0	0	0	0	0.529	0.361	0.677	0.471	0.323	0.019
SL004350	IL-17B	Q9UHF5	27190	IL17B	RFU	No	No	E	0	ō	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004351	IL-17E	Q9H293	64806	IL25	RFU	No	No	DE	0.434	0.348	0.458	0	0	0	0.434	0.150	0.719	0	0	0	0.566	0.281	0.850
SL004352	IL-17F	Q96PD4	112744	IL17F	RFU	No	No	DE	0.628	0.726	0.589	0	0	0	0.628	0.410	0.845	0	0	0	0.372	0.155	0.590
SL004353	IL-17D		200/0	IL17D	RFU	NO	NO	CE CE	0	0	0	0	0	0	0	0	0	0.543	0 396	0 690	0.457	1	1 0.604
SL004355	LD78-beta	P16619	414062	CCL3L1	RFU	No	No	DE	0.595	0.679	0.565	0 0	ő	0	0.595	0.360	0.830	0.040	0.000	0.050	0.405	0.170	0.640
SL004356	LAG-1	Q8NHW4	388372	CCL4L1	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.188	-0.009	0.384	0.812	0.616	1.009
SL004359	Neurotrophin-3	P20783	4908	NTF3	RFU	No	No	DE	0.640	0.725	0.602	0	0	0	0.640	0.451	0.829	0	0	0	0.360	0.171	0.549
SL004360	Neurotrophin-5	P34130	4909	NIF4	RFU	No	No	E AE	0612	0 661	0 597	0 612	0 464	0 762	0	0	0	0	0	0	1	1	1
SL004362	SCGF-alnha	Q9Y240	6320	CLEC11A	RFU	No	No	AE	0.737	0.805	0.693	0.737	0,625	0.849	0	0	0	0	0	0	0.263	0.257	0.375
SL004364	TACI	O14836	23495	TNFRSF13B	RFU	No	No	CE	0	0	0	0	0	0	Ő	õ	õ	0.246	0.047	0.445	0.754	0.555	0.953
SL004365	TWEAK	O43508	8742	TNFSF12	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004366	TWEAKR	Q9NP84	51330	TNFRSF12A	RFU	No	No No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004367	Coagulation Eactor	U94907	22943	EQ	REU	No	No	CE	0.547	0.577	0.534	0.547	0.355	0.739	0	0	0	0.438	0.267	0 000 0	0.453	0.201	0.045
SL004415	ACE2	Q9BYF1	59272	ACE2	RFU	No	No	E	ő	ő	õ	ŏ	õ	õ	Ő	õ	Ő	0	0	0	1	1	1
SL004438	Cystatin M	Q15828	1474	CST6	RFU	No	No	AE	0.755	0.825	0.710	0.755	0.647	0.862	0	0	0	0	0	0	0.245	0.138	0.353
SL004457	Protease nexin I	P07093	5270	SERPINE2	RFU	No	No	DE	0.325	0.171	0.381	0	0	0	0.325	0.091	0.559	0	0	0	0.675	0.441	0.909
SL004458	Elatin Hoporin cofector II	P19957	2052	PI3 SEPDIND1	RFU	No	No	AE	0.476	0.460	0.482	0.476	0.280	0.671	0	0	0	0 459	0 202	0 622	0.524	0.329	0.720
SL004469	amyloid precursor p	rot P05067	351	APP	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.388	0.233	0.561	0.612	0.439	0.786
SL004477	calgranulin B	P06702	6280	S100A9	RFU	No	No	DE	0.463	0.440	0.474	0	0	0	0.463	0.267	0.660	0	0	0	0.537	0.340	0.733
SL004482	Endoglin	P17813	2022	ENG	RFU	No	No	AE	0.485	0.476	0.489	0.485	0.294	0.676	0	0	0	0	0	0	0.515	0.324	0.706
SL004484	SP-D	P35247	6441	SFTPD	RFU	No	No	DE	0.597	0.669	0.568	0	0	0	0.597	0.384	0.810	0	0	0	0.403	0.190	0.616
SL004486	TLR2	P49767 060603	7424	TLR2	REU	NO	NO	CE	0	0	0	0	0	0	0	0	0	0.229	0.032	0.425	0.668	0.575	0.968
SL004511	BPI	P17213	671	BPI	RFU	No	No	DE	0.612	0.663	0.585	Ő	õ	Ő	0.612	0.456	0.768	0	0	0	0.388	0.232	0.544
SL004515	PGRP-S	075594	8993	PGLYRP1	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.313	0.130	0.497	0.687	0.503	0.870
SL004516	MBL	P11226	4153	MBL2	RFU	No	No	AE	0.813	0.873	0.770	0.813	0.733	0.893	0	0	0	0	0	0	0.187	0.107	0.267
SL004536	LEAP-1	P81172 P08174	5/81/	CD55	RFU	No	No	DE	0.224	-0.004	0.310	0 590	0 441	0 739	0.224	-0.002	0.450	0	0	0	0.776	0.550	1.002
SL004579	Macrophage manno	oseP22897	4360	MRC1	RFU	No	No	AE	0.784	0.852	0.738	0.784	0.687	0.881	0	ŏ	0	Ő	Ő	0	0.216	0.119	0.313
SL004580	Macrophage scaver	ngeP21757	4481	MSR1	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004588	IL-1 R AcP	Q9NPH3	3556	IL1RAP	RFU	No	No	AE	0.806	0.866	0.762	0.806	0.723	0.888	0	0	0	0	0	0	0.194	0.112	0.277
SL004589	Azurocidin G-CSE-R	P20160	566	AZU1 CSE3R	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.542	0.397	0.687	0.458	0.313	0.603
SL004605	40S ribosomal prote	ein P08865	3921	RPSA	RFU	No	No	E	0	0	Ő	0	ő	0	0	ŏ	0	0	0.027	0.505	1	1	1
SL004610	LRP8	Q14114	7804	LRP8	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.414	0.243	0.586	0.586	0.414	0.757
SL004625	ADAMTS-4	075173	9507	ADAMTS4	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.351	0.166	0.535	0.649	0.465	0.834
SL004626	ADAMIS-5 CD30 Ligand	Q9U0 P32071	11096 944	ADAM1S5 TNESE8	REU	NO	No		0.832	0.901	0.783	0 690	0 555	0 825	0.832	0.746	0.918 n	0	0	0	0.168	0.082	0.254
SL004636	Flt-3	P36888	2322	FLT3	RFU	No	No	CE	0.030	0	0.043	0.030	0.000	0.020	ŏ	ŏ	ŏ	0.625	0.500	0.750	0.375	0.250	0.500
SL004637	MSP R	Q04912	4486	MST1R	RFU	No	No	DE	0.482	0.443	0.490	0	0	0	0.482	0.138	0.827	0	0	0	0.518	0.173	0.862
SL004639	TrkC	Q16288	4916	NTRK3	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.498	0.343	0.653	0.502	0.347	0.657
SL004642	ADAM 9 Angiopolietin-4	Q13443	8754 51378	ADAM9	KFU REU	No	No	E	0	0	0	0	0	0	0	0	0	0 361	0	0	1	1	1
SL004644	EDA	Q92838	1896	EDA	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0.301	0.102	0.040	1	1	1
SL004645	HAI-1	O43278	6692	SPINT1	RFU	No	No	DE	0.539	0.564	0.529	0	0	0	0.539	0.350	0.729	0	0	0	0.461	0.271	0.650
SL004646	Layilin	Q6UX15	143903	LAYN	RFU	No	No	AE	0.337	0.168	0.392	0.337	0.083	0.591	0	0	0	0	0	0	0.663	0.409	0.917
SL004648	LIQUIT	1147557	8740	INFSF14	REU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
	LIGHT OX40 Licond	D22510	7202	A 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		INU INU	19()	- C		U	U	U	U	U	U	U	U		U	U	1 1		0 931
SL004649	LIGHT OX40 Ligand sFRP-3	P23510 Q92765	7292 2487	FRZB	RFU	No	No	DE	0.326	0.141	0.385	0	0	0	0.326	0.069	0.583	0	0	0	0.674	0.417	0.001
SL004650 SL004652	LIGHT OX40 Ligand sFRP-3 WIF-1	043557 P23510 Q92765 Q9Y5W5	7292 2487 11197	FRZB WIF1	RFU RFU	No No	No No	DE DE	0.326 0.231	0.141 0.019	0.385 0.313	0	0	0	0.326 0.231	0.069 0.011	0.583 0.451	0	0 0	0	0.674 0.769	0.417 0.549	0.989
SL004649 SL004650 SL004652 SL004654	LIGHT OX40 Ligand sFRP-3 WIF-1 Granzyme H	Q92765 Q9Y5W5 P20718	7292 2487 11197 2999	FRZB WIF1 GZMH	RFU RFU RFU	No No No	No No No	DE DE DE	0.326 0.231 0.251	0.141 0.019 -0.009	0.385 0.313 0.335	0	0	0 0	0.326 0.231 0.251	0.069 0.011 -0.005	0.583 0.451 0.506	0 0 0	0 0 0	0 0 0	0.674 0.769 0.749	0.417 0.549 0.494	0.989
SL004649 SL004650 SL004654 SL004654 SL004664	LIGHT OX40 Ligand sFRP-3 WIF-1 Granzyme H BSP	P23510 Q92765 Q9Y5W5 P20718 P21815 P16112	7292 2487 11197 2999 3381	FRZB WIF1 GZMH IBSP	RFU RFU RFU RFU	No No No	No No No No	DE DE CE	0.326 0.231 0.251 0	0.141 0.019 -0.009 0	0.385 0.313 0.335 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0	0 0 0 0.621	0.326 0.231 0.251 0	0.069 0.011 -0.005 0	0.583 0.451 0.506 0	0 0 0.387	0 0 0.214	0 0 0.561	0.674 0.769 0.749 0.613	0.417 0.549 0.494 0.439	0.989 1.005 0.786
SL004649 SL004650 SL004652 SL004654 SL004660 SL004661 SL004668	LIGHT OX40 Ligand sFRP-3 WIF-1 Granzyme H BSP Aggrecan Apo E3	P23510 Q92765 Q9Y5W5 P20718 P21815 P16112 P02649	7292 2487 11197 2999 3381 176 348	FRZB WIF1 GZMH IBSP ACAN APOE	RFU RFU RFU RFU RFU RFU	No No No No No	No No No No No	DE DE CE AE CF	0.326 0.231 0.251 0 0.384 0	0.141 0.019 -0.009 0 0.278 0	0.385 0.313 0.335 0 0.421 0	0 0 0 0.384 0	0 0 0 0.146 0	0 0 0 0.621 0	0.326 0.231 0.251 0 0 0	0.069 0.011 -0.005 0 0 0	0.583 0.451 0.506 0 0 0	0 0 0.387 0 0.640	0 0 0.214 0 0.520	0 0 0.561 0 0.761	0.674 0.769 0.749 0.613 0.616 0.360	0.417 0.549 0.494 0.439 0.379 0.239	0.989 1.005 0.786 0.854 0.480
SL004649 SL004650 SL004652 SL004654 SL004660 SL004661 SL004668 SL004669	LIGHT OX40 Ligand sFRP-3 WIF-1 Granzyme H BSP Aggrecan Apo E3 Apo E4	P23510 Q92765 Q9Y5W5 P20718 P21815 P16112 P02649 P02649	7292 2487 11197 2999 3381 176 348 348	FRZB WIF1 GZMH IBSP ACAN APOE APOE	RFU RFU RFU RFU RFU RFU RFU	No No No No No No	No No No No No No	DE DE CE AE CE CE	0.326 0.231 0.251 0 0.384 0 0	0.141 0.019 -0.009 0 0.278 0 0	0.385 0.313 0.335 0 0.421 0 0	0 0 0 0.384 0 0	0 0 0 0.146 0 0	0 0 0 0.621 0 0	0.326 0.231 0.251 0 0 0 0 0	0.069 0.011 -0.005 0 0 0 0	0.583 0.451 0.506 0 0 0 0	0 0 0.387 0 0.640 0.710	0 0 0.214 0 0.520 0.609	0 0 0.561 0 0.761 0.811	0.674 0.769 0.613 0.616 0.360 0.290	0.417 0.549 0.494 0.439 0.379 0.239 0.239	0.989 1.005 0.786 0.854 0.480 0.391
SL004649 SL004650 SL004654 SL004664 SL004661 SL004668 SL004669 SL004669	LIGHT OX40 Ligand sFRP-3 WIF-1 Granzyme H BSP Aggrecan Apo E3 Apo E4 Artemin	P23510 Q92765 Q975W5 P20718 P21815 P16112 P02649 Q5T4W7	7292 2487 11197 2999 3381 176 348 348 9048	FRZB WIF1 GZMH IBSP ACAN APOE APOE ARTN	RFU RFU RFU RFU RFU RFU RFU RFU	No No No No No No No	No No No No No No No	DE DE DE CE AE CE CE E	0.326 0.231 0.251 0 0.384 0 0 0	0.141 0.019 -0.009 0 0.278 0 0 0	0.385 0.313 0.335 0 0.421 0 0 0	0 0 0 0.384 0 0 0	0 0 0 0.146 0 0 0	0 0 0 0.621 0 0 0	0.326 0.231 0.251 0 0 0 0 0 0	0.069 0.011 -0.005 0 0 0 0 0 0	0.583 0.451 0.506 0 0 0 0 0 0	0 0 0.387 0 0.640 0.710 0	0 0 0.214 0 0.520 0.609 0	0 0 0.561 0 0.761 0.811 0	0.674 0.769 0.749 0.613 0.616 0.360 0.290 1	0.417 0.549 0.494 0.439 0.379 0.239 0.239 0.189 1	0.989 1.005 0.786 0.854 0.480 0.391 1
SL004649 SL004650 SL004652 SL004654 SL004660 SL004661 SL004668 SL004669 SL004670 SL004671	LIGHT OX40 Ligand sFRP-3 WIF-1 Granzyme H BSP Aggrecan Apo E3 Apo E4 Artemin BAFF Receptor	P23510 Q92765 Q9Y5W5 P20718 P21815 P16112 P02649 Q5T4W7 Q96RJ3	7292 2487 11197 2999 3381 176 348 348 9048 115650	FRZB WIF1 GZMH IBSP ACAN APOE APOE ARTN TNFRSF13C	RFU RFU RFU RFU RFU RFU RFU RFU RFU RFU	No No No No No No No	No No No No No No No	DE DE DE CE AE CE E CE	0.326 0.231 0.251 0 0.384 0 0 0 0 0	0.141 0.019 -0.009 0 0.278 0 0 0 0	0.385 0.313 0.335 0 0.421 0 0 0 0 0	0 0 0.384 0 0 0 0	0 0 0.146 0 0 0 0	0 0 0.621 0 0 0 0	0.326 0.231 0.251 0 0 0 0 0 0	0.069 0.011 -0.005 0 0 0 0 0 0	0.583 0.451 0.506 0 0 0 0 0 0 0	0 0 0.387 0 0.640 0.710 0 0.400	0 0 0.214 0 0.520 0.609 0 0.228	0 0 0.561 0.761 0.811 0 0.573	0.674 0.769 0.749 0.613 0.616 0.360 0.290 1 0.600	0.417 0.549 0.494 0.439 0.379 0.239 0.239 0.189 1 0.427	0.989 1.005 0.786 0.854 0.480 0.391 1 0.772
SL004649 SL004650 SL004654 SL004664 SL0046661 SL004669 SL004669 SL004670 SL004671 SL004673	LiGHT OX40 Ligand sFRP-3 WIF-1 BSP Aggrecan Apo E3 Apo E4 Artemin BAFF Receptor BCMA Cathensin S	P23510 Q92765 Q9Y5W5 P20718 P21815 P16112 P02649 Q5T4W7 Q96RJ3 Q02223 Q02223	7292 2487 11197 2999 3381 176 348 348 9048 115650 608 1520	FRZB WIF1 GZMH IBSP ACAN APOE APOE ARTN TNFRSF13C TNFRSF13C TNFRSF13C TNFRSF13C	RFU RFU RFU RFU RFU RFU RFU RFU RFU RFU	No No No No No No No No	No No No No No No No No	DE DE CE CE CE CE CE CE CE	0.326 0.231 0.251 0 0.384 0 0 0 0 0 0 0.706 0.521	0.141 0.019 -0.009 0 0.278 0 0 0 0 0 0 0 0.767 0.534	0.385 0.313 0.335 0 0.421 0 0 0 0 0 0 0 0.668 0.515	0 0 0.384 0 0 0 0 0 0.706 0	0 0 0.146 0 0 0 0.594 0	0 0 0 0.621 0 0 0 0 0.819 0	0.326 0.231 0.251 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.069 0.011 -0.005 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.583 0.451 0.506 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0.387 0 0.640 0.710 0 0.400 0	0 0 0.214 0.520 0.609 0 0.228 0 0	0 0 0.561 0.761 0.811 0 0.573 0	0.674 0.769 0.749 0.613 0.616 0.360 0.290 1 0.600 0.294 0.479	0.417 0.549 0.494 0.439 0.379 0.239 0.189 1 0.427 0.181 0.288	0.989 1.005 0.786 0.854 0.480 0.391 1 0.772 0.406 0.669
SL044649 SL004652 SL004654 SL004661 SL004668 SL004668 SL004669 SL004670 SL004672 SL004673 SL004673	LIGHT OX40 Ligand sFRP-3 WIF-1 Granzyme H BSP Aggrecan Apo E3 Apo E3 Artemin BAFF Receptor BCMA Cathepsin S Cathepsin S	P23510 Q92765 Q9Y5W5 P20718 P21815 P16112 P02649 Q5T4W7 Q96RJ3 Q02223 P25774 P24593	7292 2487 11197 2999 3381 176 348 348 9048 115650 608 1520 3488	FRZB FRZB WIF1 GZMH IBSP ACAN APOE APOE ARTN TNFRSF13C TNFRSF17 CTSS IGFBP5	RFU RFU RFU RFU RFU RFU RFU RFU RFU RFU	No No No No No No No No No	No No No No No No No No No No	DE DE DE CE CE CE E CE AE AE	0.326 0.231 0.251 0 0.384 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.141 0.019 -0.009 0 0.278 0 0 0 0 0 0.767 0.534 0.019	0.385 0.313 0.335 0 0.421 0 0 0 0 0 0.668 0.515 0.321	0 0 0.384 0 0 0 0 0 0.706 0 0.239	0 0 0.146 0 0 0 0.594 0 0.010	0 0 0 0.621 0 0 0 0 0.819 0 0.467	0.326 0.231 0.251 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.069 0.011 -0.005 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.583 0.451 0.506 0 0 0 0 0 0 0 0 0 0 0 0 0.712 0	0 0 0.387 0 0.640 0.710 0 0.400 0 0 0	0 0 0.214 0 0.520 0.609 0 0.228 0 0 0 0 0 0	0 0 0.561 0.761 0.811 0 0.573 0 0 0	0.674 0.769 0.749 0.613 0.616 0.360 0.290 1 0.600 0.294 0.479 0.761	0.417 0.549 0.494 0.439 0.379 0.239 0.189 1 0.427 0.181 0.288 0.533	0.331 0.989 1.005 0.786 0.854 0.480 0.391 1 0.772 0.406 0.669 0.990
SL004650 SL004650 SL004650 SL004660 SL004661 SL004661 SL004670 SL004671 SL004672 SL004673 SL004673	LIGHT OX40 Ligand sFRP-3 WIF-1 Granzyme H BSP Aggrecan Apo E3 Apo E4 Atornia Apo E4 Atornia BAFF Receptor BCMA Cathepsin S IGFBP-5 Noggin	043557 P23510 Q92765 Q9Y5W5 P20718 P21815 P16112 P02649 P02649 Q5T4W7 Q96RJ3 Q02223 P25774 P24593 Q13253	7292 2487 11197 2999 3381 176 348 348 9048 115650 608 1520 3488 9241	FRZB FRZB WIF1 GZMH IBSP ACAN APOE ARTN TNFRSF13C TNFRSF13C TNFRSF17 CTSS IGFBP5 NOG	REU REU REU RFU RFU RFU RFU RFU RFU RFU RFU RFU RF	No No No No No No No No No	No No No No No No No No No No	DE DE DE CE CE CE CE CE CE E DE E	0.326 0.231 0.251 0 0.384 0 0 0 0.706 0.706 0.521 0.239 0	0.141 0.019 -0.009 0 0.278 0 0 0 0 0.767 0.534 0.019 0	0.385 0.313 0.335 0 0.421 0 0 0 0 0 0.668 0.515 0.321 0	0 0 0.384 0 0 0 0.706 0 0.239 0	0 0 0.146 0 0 0.594 0 0.010 0	0 0 0 0.621 0 0 0 0.819 0 0.467 0	0.326 0.231 0.251 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.069 0.011 -0.005 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.583 0.451 0.506 0 0 0 0 0 0 0 0 0.712 0 0	0 0 0.387 0 0.640 0.710 0 0.400 0 0 0 0 0 0 0	0 0 0.214 0 0.520 0.609 0 0.228 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0.561 0.761 0.811 0 0.573 0 0 0 0 0	0.674 0.769 0.749 0.613 0.616 0.360 0.290 1 0.600 0.294 0.479 0.761	0.417 0.549 0.494 0.379 0.239 0.189 1 0.427 0.181 0.288 0.533 1	0.989 1.005 0.786 0.854 0.480 0.391 1 0.772 0.406 0.669 0.990 1
SL004650 SL004650 SL004650 SL004661 SL004661 SL004661 SL004670 SL004671 SL004673 SL004673 SL004673 SL004685	LIGHT OX40 Ligand sFRP-3 WIF-1 BSP Aggrecan Apo E3 Apo E4 Artemin BAFF Receptor BCMA Cathepsin S IGFBP-5 Noggin Persephin	P23510 Q92765 Q9Y5W5 P20718 P21815 P16112 P02649 P02649 Q5T4W7 Q96RJ3 Q02223 P25774 P24593 Q13253 Q60542	7292 2487 11197 2999 3381 176 348 348 9048 115650 608 1520 3488 9241 5623	FRZB FRZB WIF1 GZMH IBSP ACAN APOE ARTN TNFRSF13C TNFRSF17 CTSS IGFBP5 NOG PSPN	REU RFU RFU RFU RFU RFU RFU RFU RFU RFU RF	No No No No No No No No No No No	No No No No No No No No No No No	DE DE CE CE CE CE CE AE CE CE	0.326 0.231 0.251 0 0.384 0 0 0 0.384 0 0 0 0.706 0.521 0.239 0 0	0.141 0.019 -0.009 0 0.278 0 0 0 0 0.278 0 0 0 0 0.5767 0.534 0.019 0 0	0.385 0.313 0.335 0 0.421 0 0 0 0 0 0.668 0.515 0.321 0 0	0 0 0.384 0 0 0 0.706 0 0.239 0 0	0 0 0.146 0 0 0 0.594 0 0.010 0 0	0 0 0 0.621 0 0 0 0.819 0 0.467 0 0	0.326 0.231 0.251 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.069 0.011 -0.005 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.583 0.451 0.506 0 0 0 0 0 0 0 0 0 0 0.712 0 0 0 0 0	0 0 0.387 0 0.640 0.710 0 0.400 0 0 0 0 0 0 0 0 0 0 0.152	0 0 0.214 0 0.520 0.609 0 0.228 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0.561 0.761 0.811 0 0.573 0 0 0 0 0 0 0 0 0 0 0 0 0 354	0.674 0.769 0.749 0.613 0.616 0.360 0.290 1 0.600 0.294 0.479 0.761 1 0.848	0.417 0.549 0.494 0.439 0.379 0.239 0.189 1 0.427 0.181 0.288 0.533 1 0.646	0.989 1.005 0.786 0.854 0.480 0.391 1 0.772 0.406 0.669 0.990 1 1.051
SL004650 SL004650 SL004654 SL004660 SL004660 SL004668 SL004669 SL004670 SL004673 SL004673 SL004673 SL004675 SL004685 SL004685	LIGHT OX40 Ligand SFRP-3 WIF-1 Granzyme H BSP Aggrecan Apo E3 Apo E4 Apo E4 AfF Receptor BGMA Cathopsin S IGFBP-5 Noggin Perseptin TNYSF15	043557 P23510 Q92765 Q975W5 P20718 P21815 P16112 P02649 Q5T4W7 Q96RJ3 Q02223 P25774 P24593 Q13253 Q60542 Q95150 Q25050	7292 2487 11197 2999 3381 176 348 348 9048 115650 608 1520 3488 9241 5623 9966 9560	FR2B FR2B WIF1 GZMH IBSP ACAN APOE APOE APOE APOE ARTN TNFRSF13C TNFRSF13C TNFRSF13C TSS IGFBP5 NOG PSPN TNFSF15	REU RFU RFU RFU RFU RFU RFU RFU RFU RFU RF	No No No No No No No No No No No	No No No No No No No No No No No	DE DE DE CE E CE E CE E CE E E E E E E E	0.326 0.231 0.251 0 0.384 0 0 0 0.384 0 0 0 0.521 0.239 0 0.524	0.141 0.019 -0.009 0 0.278 0 0 0 0 0 0 0 0 0 0 0 0 0 767 0.534 0.019 0 0 0.570	0.385 0.313 0.335 0 0.421 0 0 0 0.668 0.515 0.321 0 0 0.532	0 0 0.384 0 0 0.706 0 0.239 0 0.239 0 0.544	0 0 0 0.146 0 0 0 0.594 0 0.010 0 0.353	0 0 0 0.621 0 0 0 0 0.819 0 0.467 0 0 0.734	0.326 0.231 0.251 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.069 0.011 -0.005 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.583 0.451 0.506 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0.387 0 0.640 0.710 0 0.400 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0.214 0 0.520 0.609 0 0.228 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0.561 0.761 0.7761 0.811 0 0.573 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.674 0.769 0.749 0.613 0.616 0.360 0.290 1 0.600 0.294 0.479 0.761 1 0.848 0.456	0.417 0.549 0.494 0.379 0.379 0.239 0.189 1 0.427 0.181 0.288 0.533 1 0.646 0.266	0.989 1.005 0.786 0.854 0.480 0.391 1 0.772 0.406 0.669 0.990 1 1.051 0.647
SL044659 SL044550 SL04454 SL004654 SL004669 SL004669 SL004672 SL004671 SL004672 SL004673 SL004675 SL004675 SL004685 SL004685 SL004685	LIGHT OX40 Ligand sFRP-3 WIF-1 Granzyme H BSP BSP Aggrecan Apo E3 Apo E4 Atemin BAFF Receptor BCMA Cathepsin S IGFBP-5 Noggin Persephin TNFSF15 TSLP WISP-1	043357 P23510 Q92765 Q975W5 P20718 P21815 P16112 P02649 P02649 Q574W7 Q96RJ3 Q02223 P25774 P24593 Q13253 Q13253 Q6542 Q965150 Q968D9 Q96329	7292 2487 11197 2999 3381 176 348 348 9048 115650 608 1520 3488 9241 5623 9966 85480 8840	FRZB FRZB WIF1 GZMH IBSP ACAN APOE APOE APOE APOE APOE APOE APOE TNFRSF13C TNFRSF13C TNFRSF17 CTSS IGFBP5 NOG PSPN TNFSF15 TSLP WISP1	REU REU	No No No No No No No No No No No No	Νο Νο Νο Νο Νο Νο Νο Νο Νο Νο Νο Νο Νο	DE DE DE CE E CE E CE E CE E CE E CE E	0.326 0.231 0.251 0 0.384 0 0 0 0.384 0 0 0 0.521 0.239 0 0.521 0.239 0 0.544 0 0.5544	0.141 0.019 -0.009 0 0.278 0 0 0 0 0 0 0 0 0 0 0 0 7 67 0 57 0 0 0 57	0.385 0.313 0.335 0 0.421 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0.384 0 0 0.706 0 0.239 0 0.544 0 0	0 0 0.146 0 0 0.594 0.010 0 0.353 0 0	0 0 0 0.621 0 0 0 0 0.819 0 0.467 0 0 0.734 0 0 0.734 0	0.326 0.231 0.251 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.069 0.011 -0.005 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.583 0.451 0.506 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0.387 0 0.640 0.710 0 0.400 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0.214 0 0.520 0.609 0 0 0.228 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0.561 0.761 0.811 0 0.573 0 0 0 0 0.354 0 0	0.674 0.769 0.749 0.613 0.616 0.360 0.290 1 0.600 0.294 0.479 0.761 1 0.848 0.456 1 0.725	0.417 0.549 0.494 0.379 0.239 0.189 1 0.427 0.181 0.288 0.533 1 0.646 0.266 1 0.478	0.989 1.005 0.786 0.854 0.480 0.391 1 0.772 0.406 0.669 0.990 1 1.051 0.647 1 0.971
SL044650 SL044550 SL004654 SL004660 SL004660 SL004660 SL004670 SL004672 SL004673 SL004673 SL004673 SL004683 SL004683 SL004686 SL004689 SL004689 SL004689	LIGHT OX40 Ligand sFRP-3 WIF-1 BSP Aggrecan Apo E3 Apo E4 Artemin BAFF Receptor BCMA Cathepsin S IGFBP-5 Noggin Persephin TNFSF15 TSLP WISP-1 CLF-1/CLC Comple	Q43357 P23510 Q92765 Q975W5 P20718 P21818 P21818 P02649 P02649 P02649 P02649 P02649 P02649 P02649 Q02223 Q02223 Q02223 Q1325 Q1325 Q1355 Q135	7292 2487 11197 2999 3381 176 348 9048 115650 608 1520 3488 9241 5623 3488 9241 5623 8480 8966 85480 8840	TREPART FRZB WIF1 GZMH IBSP ACAN APOE APOE APOE APTOE ARTN TNFRSF13C TNFRSF13C TNFRSF17 CTSS IGFBP5 NOG PSPN TNFSF15 TSLP WISP1 2C CRLF1 CLCF1	REU RFU RFU RFU RFU RFU RFU RFU RFU RFU RF	No No No No No No No No No No No No No N	No No No No No No No No No No No No No N	DE DE DE DE CE E CE E CE E CE E CE E E CE E E E	0.326 0.231 0.251 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.141 0.019 -0.009 0 0.278 0 0 0 0 0 0.767 0.534 0.019 0 0 0.570 0 0 0.057 0 0	0.385 0.313 0.335 0 0.421 0 0 0 0 0 0 668 0.515 0.321 0 0.532 0 0.532 0 0.532 0 0.532	0 0 0.384 0 0 0.706 0.706 0.239 0 0.544 0 0.544 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0.146 0 0 0.594 0 0.0594 0 0.010 0 0.353 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0.621 0 0 0 0.819 0 0.467 0 0.467 0 0.734 0 0.734 0 0 0.734	0.326 0.231 0.251 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.069 0.011 -0.005 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.583 0.451 0.506 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0.387 0.640 0.710 0 0.400 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0.214 0 0.609 0 0.228 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0.561 0.761 0.811 0.573 0 0.573 0 0 0 0.354 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.674 0.769 0.749 0.613 0.616 0.360 0.290 1 0.600 0.294 0.479 0.761 1 0.848 0.456 1 0.725 1	0.417 0.549 0.494 0.439 0.379 0.239 0.189 1 0.427 0.181 0.427 0.181 0.288 0.533 1 0.646 0.266 1 0.478 1	0.989 1.005 0.786 0.854 0.480 0.391 1 0.772 0.406 0.669 0.990 1 1.051 0.647 1 0.971 1
SL04659 SL04650 SL04654 SL04660 SL04668 SL04669 SL004670 SL004673 SL004673 SL004673 SL004673 SL004673 SL004675 SL004689 SL004689 SL004697	LIGHT OX40 Ligand SFRP-3 WIF-1 Granzyme H BSP Aggrecan Apo E3 Apo E4 Artemin BAFF Receptor BCMA Cathepsin S IGFBP-5 Noggin Perseptin TNFSF15 TSLP WISP-1 SLP WISP-15	04353/ P23510 Q92765 Q9Y58V5 P20718 P21815 P16112 P02649 Q574W7 Q96RJ3 Q02223 Q02223 Q02223 Q02223 Q0525774 P24593 Q02223 Q050542 Q955150 Q95848 X 075422 P03129 Q05388 X 075422 P03129	7292 2487 11197 2999 3381 176 348 9048 1520 3488 1520 3488 1520 3488 9562 3488 9562 85480 85480 85480 85480 85480	FRZB FRZB WIF1 GZMH IBSP ACAN APOE ARTN TNFRSF13C TNFRSF13C TNFRSF13C TNFRSF15 NOG PSPN TNFRSF15 TSLP WISP1 22 CRLF1 CLCF1 Human-virus	REU REU	No No No No No No No No No No No No No N	No No No No No No No No No No No No No N	DE DE DE CE ACE E CE E CA E CA E E E E E E E E	0.326 0.231 0.251 0 0.384 0 0 0 0.706 0.521 0.239 0 0.521 0.239 0 0.5544 0 0.275 0 0	0.141 0.019 -0.009 0 0.278 0 0 0 0.767 0.534 0.057 0 0 0.057 0 0 0 0.057 0 0	0.385 0.313 0.335 0 0.421 0 0 0 0 0.668 0.515 0.321 0 0 0.532 0 0.350 0 0	0 0 0.384 0 0 0.706 0 0.239 0 0.239 0 0.544 0 0 0.544 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0,04 0 0 0 0 0,0594 0 0,0594 0 0,0594 0 0,0594 0 0,050 0 0,050 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0.621 0 0 0.819 0 0.467 0 0 0.734 0 0 0.734 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.326 0.231 0.251 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.069 0.011 -0.005 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.583 0.451 0.506 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0.387 0.640 0.710 0 0.00 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0.214 0.520 0.609 0 0.28 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0.561 0.761 0.811 0 0.573 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.674 0.769 0.749 0.613 0.616 0.360 0.290 1 0.294 0.294 0.294 0.294 0.294 0.294 0.294 0.294 0.479 0.761 1 0.848 0.456 1 0.725 1	0.417 0.494 0.439 0.239 0.239 0.239 0.189 1 0.427 0.181 0.288 0.533 1 0.646 0.266 1 0.478 1	0.989 1.005 0.786 0.854 0.480 0.391 1.0772 0.406 0.690 1 1.0571 0.647 1 0.971 1 1
SL004650 SL004652 SL004652 SL004654 SL004665 SL004665 SL004665 SL004665 SL004665 SL004672 SL004672 SL004675 SL004655 SL004655 SL004655 SL004655 SL004657 SL004677 SL00477 SL04	LIGHT OX40 Ligand sFRP-3 WIF-1 Granzyme H BSP Aggrecan Apo E3 Apo E4 Artemin BAFF Receptor BCMA Cathepsin S IGFBP-5 Noggin Persephin TNFSF15 TSLP WISP-1 CLF-1/CLC Comple HPV E7 Type 18	Q45557 P23510 Q92765 Q975W5 P20718 P21815 P16112 P02649 P02649 Q574W7 Q96713 Q02223 Q02223 Q02223 Q13253 Q13557 Q13577 Q13577 Q13577 Q13577 Q13577 Q13577 Q13577 Q1357777 Q1357777 Q1357777 Q1357777 Q1357777 Q1357777 Q1357777 Q13577777 Q135777777777777777777777777777777777777	7292 2487 11197 2999 3381 176 348 348 348 1520 3488 9048 1520 3488 9241 5623 9966 85480 85480 8640 8840 919,9244 235 1499079	FRZB WIF1 GZMH IBSP ACAN APOE APOE APOE APOE APOE APOE APOE APOE APOE APOE APOE APOE APOE APOE APOE APOE APOE APOE ARTN TMFRSF13C TMFRSF15 TSLP WISP1 22 CRLF1 CLCF1 Human-virus Human-virus	REU REU REU REU REU REU REU REU REU REU	No No No No No No No No No No No No No N	. No No No No No No No No No No No No No N	DE DE CE CE CE CE CE CE CE CE CE CE CE CE CE	0.326 0.231 0.251 0 0 0.384 0 0 0.521 0.239 0 0.521 0.239 0 0.544 0 0.275 0 0.275 0 0.2511	0.141 0.019 -0.009 0 0.278 0 0 0 0.070 0.534 0.019 0 0.570 0 0.557 0 0 0.557	0.385 0.313 0.335 0.421 0 0 0.668 0.515 0.321 0 0.352 0 0.350 0 0.558	0 0 0 0.384 0 0 0.706 0 0.239 0 0.544 0 0 0 0.5511	0 0 0 0.146 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0.621 0 0 0.467 0 0.467 0 0.734 0 0 0.734 0 0 0.734 0 0 0.695	0.326 0.231 0.251 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.069 0.011 -0.005 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.583 0.451 0.506 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0.387 0 0.640 0.710 0 0.400 0 0 0.400 0 0 0 0 0 0 0 0 0 0	0 0 0.214 0 0.520 0.520 0.228 0 0 0 0.228 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0.561 0.761 0.573 0 0 0.573 0 0 0 0.554 0 0 0 0 0.354 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.674 0.769 0.749 0.613 0.616 0.360 0.290 1 0.600 0.294 0.479 0.761 1 0.848 0.456 1 0.725 1 1 0.725	0.417 0.549 0.494 0.439 0.239 0.239 0.189 1 0.427 0.181 0.288 0.533 1 0.646 0.266 1 0.646 0.478 1 0.478 1 0.478	0.989 1.005 0.786 0.854 0.480 0.391 1 0.772 0.466 0.990 1.051 0.669 0.990 1.051 0.671 1 0.971 1 0.971 1 0.6722
SL04650 SL04652 SL04652 SL04654 SL04661 SL04666 SL04667 SL04673 SL04673 SL04675 SL04675 SL04675 SL04675 SL04685 SL04652 SL04655 SL045555 SL055555 SL055555555555555555555555	LIGHT OX40 Ligand sFRP-3 WIF-1 Granzyme H BSP Aggrecan Apo E3 Apo E4 Artemin BAFF Receptor BCMA Cathepsin S IGFBP-5 Noggin Persephin TNFSF15 TSLP WISP-1 CLF-1/CLC Comple HPV E7 Type 18 COMMD7	04353/ P23510 Q92765 Q975W5 P20718 P21815 P16112 P02649 P02649 Q02223 Q02223 Q1325 Q1325 Q135	7292 2487 11197 2999 3381 176 348 9048 115650 608 1520 3488 9241 5623 9966 85480 8840 8840 1489079 1489079 1489051	FRZB FRZB WIF1 GZMH IBSP ACAN APOE ARTN TMFRSF13C TMFRSF13C TMFRSF13C TMFRSF13C TMFRSF15 TSLP WISP1 2C CRLF1 CLCF1 Human-virus COMMD7	REU RFU RFU	No No No No No No No No No No No No No N	No No No No No No No No No No No No No N	DE DE CE CE CE CE CE CE CE CE CE CE CE CE CE	0.326 0.251 0.251 0.384 0 0.706 0.521 0.239 0 0.521 0.239 0 0.544 0 0.255 0 0 0.544 0 0.2551 0 0.5511 0	0.141 0.019 0.009 0.278 0 0.767 0.534 0.019 0 0.570 0 0.5570 0 0.0577 0 0 0.5517 0	0.385 0.313 0.335 0 0.421 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0.384 0 0 0 0 0.706 0 0.7706 0 0.239 0 0 0.544 0 0 0 0 0 0 0 0 0.5511 0	0 0 0.146 0 0 0 0.594 0 0.554 0 0 0.353 0 0 0 0.353 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0.621 0 0 0 0.819 0 0.819 0 0 0.819 0 0 0.734 0 0 0.734 0 0 0.734 0 0 0 0.734 0 0 0 0.734 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.326 0.231 0.251 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.069 0.011 -0.005 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.583 0.451 0.506 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0.387 0.640 0.710 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0.214 0.520 0.520 0.228 0 0 0.228 0 0 0 0.228 0 0 0 0.251 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0.561 0.761 0.811 0 0.573 0 0 0.573 0 0 0.573 0 0 0 0.354 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.674 0.769 0.749 0.613 0.616 0.360 0.290 1 0.600 0.294 0.479 0.761 1 0.848 0.456 1 0.456 1 0.459 0.489 0.489 0.489 0.489	0.417 0.549 0.494 0.439 0.239 0.239 0.239 1 0.427 1 0.427 1 0.428 0.533 1 0.428 0.533 1 0.426 1 0.426 1 0.426 1 0.426 1 0.426 1 0.426 1 0.424 0.439 0.239 0.540	0.989 1.005 0.786 0.854 0.484 0.391 1 0.772 0.406 0.699 1 1.051 0.647 1 0.651 0.647 1 0.672 0.923

SL004708 SL004712	CTAP-III SDF-1	P02775 P48061	5473 6387	PPBP CXCL12	RFU RFU		No No	No No	CE CE	0	0	0	0	0	0	0	0	0	0.367	0.191 0.233	0.543 0.584	0.633 0.591	0.457 0.416	0.809 0.767
SL004714	LIF sR	P42702	3977	LIFR	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004716 SL004718	JNK2 Karyopherin-a2	P45984 P52292	3838	KP2	RFU		No	No	AE	0.696	-0.009	0.650	0.251	-0.005	0.506	0.696	0.541	0.851	0	0	0	0.304 0.749	0.149	1.005
SL004720	Calcineurin B a	P63098	5534 55869	PPP3R1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004724	MOZ	Q92794	7994	KAT6A	RFU		No	No	E	0	0	0.010	0	0	0	0	0	0	0	0	ō	1	1	1
SL004725 SL004726	Hat1 CD97	O14929 P48960	8520 976	HAT1 CD97	RFU RFU		No No	No No	E DE	0 0.245	0 -0.121	0 0.340	0	0	0	0 0.245	0 -0.050	0 0.540	0	0	0	1 0.755	1 0.460	1 1.050
SL004737	Tropomyosin 1 alpha	cP09493	7168	TPM1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004739 SL004742	Afamin	Q14624 P43652	3700 173	AFM	RFU		No	No No	AE	0.779 0.463	0.844 0.437	0.735 0.474	0.779 0.463	0.685	0.873 0.667	0	0	0	0	0	0	0.221 0.537	0.127 0.333	0.315 0.741
SL004750	DEAD-box protein 19	EQ9UMR2	11269	DDX19B	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004751	DRR1	O95990	11170	FAM107A	RFU		No	No	E	0	0	0	0	ō	0	0	0	0	0	0	0	1	1	1
SL004757 SL004759	DRG-1 eIE-5	Q9NP79 P55010	51534 1983	VTA1 FIE5	RFU RFU		No No	No No	CE DF	0 822	0	0	0	0	0	0	0	0	0.569	0.431	0.707	0.431	0.293	0.569
SL004760	PAFAH beta subunit	P68402	5049	PAFAH1B2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.642	0.521	0.763	0.358	0.237	0.479
SL004765 SL004768	MAPKAPK3 AIF1	Q16644 P55008	7867 199	MAPKAPK3 AIF1	RFU		No	No No	AE	0.734 0.387	0.806	0.690	0.734 0.387	0.618	0.851 0.602	0	0	0	0	0	0	0.266	0.149 0.398	0.382
SL004771	Aurora kise A	O14965	6790	AURKA	RFU		No	No	DE	0.500	0.500	0.500	0	0	0	0.500	0.260	0.739	0	0	0	0.500	0.261	0.740
SL004781	TSG-6	P98066	7130	TNFAIP6	RFU		No	No	AE	0.656	0.714	0.623	0.656	0.522	0.791	0	0	0	0	0	0	0.344	0.209	0.349
SL004791 SL004795	DR3 FRAB	Q93038	8718 3028	TNFRSF25 HSD17B10	RFU		No	No No	DE	0.880	0.927	0.843	0	0	0	0.880	0.826	0.935	0	0	0	0.120	0.065	0.174
SL004804	Nectin-like protein 1	Q8N126	57863	CADM3	RFU		No	No	E	0	0	0	Ő	ŏ	ŏ	0	0	0	0	0	0	1	1	1
SL004805 SL004812	Nectin-like protein 2 Triosephosphate isom	Q9BY67 P60174	23705 7167	CADM1 TPI1	RFU RFU		No No	No No	DE ACE	0.383 0.374	0.278	0.421 0.412	0 0.374	0 -0.039	0 0.787	0.383	0.146 0	0.620	0	0 -0.014	0 0.756	0.617 0.256	0.380 0.144	0.854 0.368
SL004814	Coactosin-like protein	Q14019	23406	COTL1	RFU	0.17	No	No	DE	0.545	0.587	0.530	0	0	0	0.545	0.304	0.787	0	0	0	0.455	0.213	0.696
SL004820 SL004823	Cyclophilin A	P62937	5223 5478	PGAM1	RFU	Calibration Scale	No	No	CE	0	0	0	0	0	0	0	0	0	0.601	0.470	0.732	0.399	0.268	0.530
SL004837	Activin AB	P08476 P0	93624 3625	EPHA5	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.389	0.215	0.563	0.611	0.437	0.785
SL004845	EphB4	P54760	2050	EPHB4	RFU		No	No	DE	0.289	0.146	0.350	0	ō	0	0.289	0.087	0.492	0	ō	0	0.711	0.508	0.913
SL004849 SL004850	IL-1 sR9 IL-17 sR	Q9NP60 Q96F46	26280 23765	IL1RAPL2 IL17RA	RFU RFU		No No	No No	E DE	0 0.936	0 0.962	0 0.912	0	0	0	0 0.936	0 0.907	0 0.965	0	0	0	1 0.064	1 0.035	1 0.093
SL004851	ALK-1	P37023	94	ACVRL1	RFU		No	No	DE	0.563	0.668	0.539	0	0	0	0.563	0.252	0.875	0	0	0	0.437	0.125	0.748
SL004852 SL004853	B7-H1 B7-H2	Q9NZQ7 075144	23308	ICOSLG	RFU		No	No	AE	0.472	0.455	0.480	0.472	0.279	0.665	0	0	0	0.152	-0.047	0.351	0.848	0.849	0.721
SL004855	contactin-1	Q12860	1272	CNTN1 DSG1	RFU		No	No	AE	0.464	0.439	0.475	0.464	0.256	0.672	0	0	0	0	0	0	0.536	0.328	0.744
SL004857	Desmoglein-2	Q14126	1829	DSG2	RFU		No	No	DE	0.618	0.673	0.590	0	0.004	0	0.618	0.461	0.776	0	0	ō	0.382	0.224	0.539
SL004858 SL004859	GFRa-1 GITR	P56159 Q9Y5U5	2674 8784	GFRA1 TNFRSF18	RFU RFU	Calibration Scale	No No	No No	NA E	NA 0	NA 0	NA 0	NA 0	NA 0	NA 0	NA 0	NA 0	NA 0	NA 0	NA 0	NA 0	NA 1	NA 1	NA 1
SL004860	HTRA2	043464	27429	HTRA2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.371	0.194	0.548	0.629	0.452	0.806
SL004861 SL004862	PD-L2	Q9BQ51	80380	PDCD1LG2	RFU		No	No	DE	0.794	0.639	0.740	0	0	0	0.794	0.885	0.908	0	0	0	0.206	0.092	0.615
SL004863 SL004864	TAJ Cadherin-12	Q9NS68 P55289	55504 1010	TNFRSF19 CDH12	RFU		No	No No	E	0	0 =0.176	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004865	Cadherin-6	P55285	1004	CDH6	RFU		No	No	E	0	0	0	Ő	õ	Ő	0	0	0	0	ō	0	1	1	1
SL004866 SL004867	Carbonic anhydrase I Carbonic anhydrase I	P00915	759 761	CA1 CA3	RFU RFU		No No	No No	AE AE	0.551 0.591	0.578 0.633	0.538 0.569	0.551 0.591	0.379 0.433	0.723 0.748	0	0	0	0	0	0	0.449 0.409	0.277 0.252	0.621 0.567
SL004868	Carbonic anhydrase	/P43166	766	CA7	RFU		No	No	DE	0.389	0.111	0.435	0	0	0	0.389	0.032	0.746	0	0	0	0.611	0.254	0.968
SL004809	DR6	075509	27242	TNFRSF21	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.538	0.390	0.686	0.462	0.349	0.610
SL004872 SL004875	EDAR II -1Rm2	Q9UNE0 Q9HB29	10913 8808	EDAR	RFU RFU		No No	No No	AE CE	0.765	0.829	0.722	0.765	0.668	0.862	0	0	0	0.286	0	0 0.478	0.235	0.138	0.332
SL004876	Kallistatin	P29622	5267	SERPI4	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.487	0.325	0.650	0.513	0.350	0.675
SL004891 SL004899	hnRNP A2/B1 HSP70 protein 8	P22626 P11142	3181 3312	HNRNPA2B1 HSPA8	RFU		No	No No	DE	0.723	0.809	0.674	0	0	0	0.723	0.583	0.862	0	0	0	0.277 0.452	0.138	0.417 0.739
SL004901	Protein disulfide-isom	eP07237	5034 7169	P4HB TPM2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004914	PPase	Q15181	5464	PPA1	RFU		No	No	E	0	0	0	0	ō	0	0	0	0	0	0	0	1	1	1
SL004915 SL004919	NCC27 Peroxiredoxin-1	O00299 Q06830	1192 5052	CLIC1 PRDX1	RFU RFU		No No	No No	AE CE	0.745 0	0.809 0	0.702	0.745	0.640 0	0.849 0	0	0	0	0	0 0.367	0 0.667	0.255	0.151 0.333	0.360 0.633
SL004920	Cofilin-1	P23528	1072	CFL1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.624	0.499	0.750	0.376	0.250	0.501
SL004921 SL004925	AGR2	r-22392 095994	4031 10551	AGR2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0.560	0.420	0.700	0.440	0.300	0.580
SL004932	Peroxiredoxin-5	P30044	25824	PRDX5	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004939	PTP-1B	P18031	5770	PTPN1	RFU		No	No	E	0	0	0	Ő	Ő	Ő	0	0	0	0	Ő	0	1	1	1
SL004940 SL005034	RAN	P29350 P62826	5777 5901	PTPN6 RAN	RFU		No No	No No	ACE AE	0.275 0.616	-0.378 0.667	0.353 0.589	0.275	-0.080 0.463	0.631 0.769	0	0	0 0	0.498 0	0.166 0	0.830 0	0.227	0.127 0.231	0.327 0.537
SL005059	TGF-b R III	Q03167	7049	TGFBR3	RFU		No	No	AE	0.544	0.568	0.533	0.544	0.372	0.717	0	0	0	0	0	0	0.456	0.283	0.628
SL005084	IGFBP-7	Q16270	3490	IGFBP7	RFU		No	No	AE	0.446	0.405	0.463	0.446	0.229	0.664	0.390	0.174	0.017	0	0	0	0.554	0.336	0.771
SL005102 SL005115	SHBG Spondin-1	P04278 Q9HCB6	6462 10418	SHBG SPON1	RFU RFU		No No	No No	CE DE	0 0.514	0 0.522	0 0.510	0	0	0	0 0.514	0 0.334	0 0.695	0.370	0.194 0	0.547 0	0.630 0.486	0.453 0.305	0.806
SL005152	TIG2	Q99969	5919	RARRES2	RFU		No	No	DE	0.615	0.681	0.584	0	0	0	0.615	0.431	0.799	Ő	õ	Ő	0.385	0.201	0.569
SL005153 SL005155	CNTER alpha Cripto	P26992 P13385	1271 6997	TDGF1	RFU		No No	No No	AE DE	0.551 0.538	0.580 0.588	0.538	0.551	0.374 0	0.729 0	0 0.538	0 0.252	0 0.823	0	0	0	0.449 0.462	0.271 0.177	0.626 0.748
SL005156	DAN	P41271	4681	NBL1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.539	0.393	0.685	0.461	0.315	0.607
SL005157	DC-SIGNR	Q9H2X3	10332	CLEC4M	RFU		No	No	CE	0.559	0.569	0.544	0.559	0.300	0.729	0	0	0	0.348	0.161	0.535	0.652	0.465	0.839
SL005159 SL005160	EPO-R ESAM	P19235 096AP7	2057 90952	EPOR ESAM	RFU RFU		No No	No No	DE	0.843	0.909	0.795	0	0	0	0.843	0.762	0.923	0	0	0	0.157	0.077	0.238
SL005161	FGF-12	P61328	2257	FGF12	RFU		No	No	E	0	0	0	0	0	0	0	Ö	0	0	õ	0	1	1	1
SL005164 SL005165	Galectin-2 Galectin-4	P05162 P56470	3957 3960	LGALS2 LGALS4	RFU RFU		No No	No No	E CE	0	0	0	0	0	0	0	0	0	0 0.147	0 -0.056	0 0.349	1 0.853	1 0.651	1 1.056
SL005167	Galectin-8	O00214	3964	LGALS8	RFU		No	No	DE	0.695	0.809	0.643	0	0	0	0.695	0.511	0.879	0	0	0	0.305	0.121	0.489
SL005168	sICAM-5	Q9UMF0	7087	ICAM5	RFU		No	No	AE	0.766	0.830	0.722	0.766	0.668	0.864	0	0	0	0.009	0.479	0.736	0.391	0.262	0.332

SL005170 SL005171	ICOS IGEBP-4	Q9Y6W8 P22692	29851 3487	ICOS IGEBP4	RFU RFU	No No	No No	E AF	0	0	0	0	0 0.462	0	0	0	0	0	0	0	1	1 0.231	1 0.538
SL005172	IGFBP-6	P24592	3489	IGFBP6	RFU	No	No	AE	0.393	0.318	0.424	0.393	0.186	0.600	0	0	0	0	ō	Ō	0.607	0.400	0.814
SL005174 SL005178	IL-178 R IL-1F7	Q9NRM6 Q9NZH6	27178	IL17RB IL1F7	RFU	No	No	E	0.356	0.244	0.399	0.356	0.138	0.574	0	0	0	0	0	0	0.644	0.426	0.862
SL005181	IL-20 Ra	Q9UHF4	53832	IL20RA	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005184	IL-23	P29460 Q	913593 5156	S1IL12B IL23A	RFU	No	No	E	0.001	0	0	0	0.047	0	0	0	0	Ö	0	ō	1	1	1
SL005185 SL005187	IL-23 R IL-3 Ra	Q5VWK5 P26951	149233 3563	IL23R IL3RA	RFU RFU	No No	No No	AE CE	0.660	0.739 0	0.620	0.660	0.495 0	0.826	0	0	0	0	0 0.255	0 0.592	0.340 0.576	0.174 0.408	0.505 0.745
SL005188	IL-5 Ra	Q01344	3568	IL5RA	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.519	0.369	0.669	0.481	0.331	0.631
SL005189 SL005190	IL-7 Ra ILT-2	Q8NHL6	3575 10859	LILRB1	RFU	No	No	AE	0.830	0.887	0.788	0.830	0.756	0.904	0	0	0	0	0	0	0.170	0.096	0.244
SL005191 SL005193	ILT-4 JAM-B	Q8N423 P57087	10288 58494	LILRB2	RFU	No	No No	AE	0.797	0.862	0.752	0.797	0.707	0.887	0	0	0	0	0	0	0.203	0.113	0.293
SL005194	JAM-C	Q9BX67	83700	JAM3	RFU	No	No	DCE	0.232	-0.034	0.304	Ő	Ő	Ő	0.232	-0.014	0.478	0.556	0.321	0.790	0.212	0.119	0.306
SL005195 SL005196	LAG-3 LSAMP	P18627 Q13449	3902 4045	LAG3 LSAMP	RFU RFU	No No	No No	AE AE	0.637 0.594	0.696 0.638	0.605 0.572	0.637 0.594	0.485 0.437	0.789 0.752	0	0	0	0	0	0	0.363	0.211 0.248	0.515 0.563
SL005197	LIMP II	Q14108	950	SCARB2	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005199 SL005200	MICA	Q29983 Q29980	4276	MICA	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.366	0.352	0.543	0.496	0.343	0.848
SL005201 SL005202	MIS	P03971 P26927	268 4485	AMH MST1	RFU RFU	No No	No No	CE AF	0	0	0 0.914	0	0	0	0	0	0	0.313	0.120	0.506	0.687	0.494	0.880
SL005204	NKG2D	P26718	22914	KLRK1	RFU	No	No	AE	0.579	0.637	0.555	0.579	0.365	0.792	Ő	0	0	0	0	0	0.421	0.208	0.635
SL005205 SL005206	NKp30 NKp44	O14931 O95944	259197 9436	NCR3 NCR2	RFU	No No	No No	E	0.865	0.924	0.821	0	0	0	0.865	0.797	0.934	0	0	0	0.135	0.066	0.203
SL005207	NKp46	076036	9437	NCR1	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005209	Notch-3	Q9UM47	4854	NOTCH3	RFU	No	No	AE	0.374	0.275	0.412	0.374	0.154	0.593	õ	0	0	0	0	0	0.626	0.407	0.846
SL005210 SL005212	Nr-CAM Prolactin Receptor	Q92823 P16471	4897 5618	NRCAM PRLR	RFU RFU	No No	No No	AE E	0.502	0.504 0	0.502 0	0.502	0.308 0	0.696 0	0	0	0	0	0	0	0.498	0.304 1	0.692 1
SL005213	RELT	Q969Z4	84957	RELT	RFU	No	No	AE	0.679	0.761	0.636	0.679	0.521	0.837	0	0	Ō	0	0	0	0.321	0.163	0.479
SL005214	Siglec-3	P20138	945	CD33	RFU	No	No	DE	0.902	0.941	0.870	0	0	0	0.902	0.858	0.946	0.452	0.200	0.015	0.048	0.054	0.142
SL005217 SL005218	Siglec-6 Siglec-7	O43699 Q9Y286	946 27036	SIGLEC6 SIGLEC7	RFU RFU	No No	No No	CE AF	0	0	0	0	0 0,401	0 0.739	0	0	0	0.287	0.100	0.475	0.713	0.525	0.900
SL005219	Siglec-9	Q9Y336	27180	SIGLEC9	RFU	No	No	AE	0.996	0.998	0.994	0.996	0.994	0.998	ŏ	õ	ō	0	0	0	0.004	0.002	0.006
SL005220 SL005221	Sonic Hedgehog SREC-I	Q15465 Q14162	6469 8578	SHH SCARF1	RFU	No No	No No	AE	0.559	0 0.591	0 0.544	0.559	0.384	0.734	0	0	0	0.422	0.253	0.592	0.578	0.408	0.747 0.616
SL005222	SREC-II	Q96GP6	91179	SCARF2	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0 250	1	1	1
SL005223	Thrombopoietin Rece	¢P40238	4352	MPL	RFU	No	No	DE	0.630	0.720	0.592	0	0	0	0.630	0.426	0.835	0.148	-0.034	0.350	0.370	0.165	0.574
SL005225 SL005226	TrkA TSLP R	P04629 09HC73	4914 64109	NTRK1 CRI F2	RFU RFU	No No	No No	AE DE	0.186	-0.095 -0.028	0.286	0.186	-0.050 0	0.422	0	0	0	0	0	0	0.814	0.578	1.050
SL005227	ULBP-1	Q9BZM6	80329	ULBP1	RFU	No	No	E	0	0	0	0	Ō	0	0	0	0	0	ō	Ō	1	1	1
SL005228 SL005229	ULBP-2 ULBP-3	Q9BZM5 Q9BZM4	80328 79465	ULBP2 ULBP3	RFU	No	No	AE	0.763	0.828	0.719	0.763	0.664	0.862	0	0	0	0	0	0	0.237	0.138	0.336
SL005230 SL005231	UNC5H3 UNC5H4	O95185 O6UX74	8633 137970	UNC5C UNC5D	RFU RFU	No No	No No	AE DE	0.473	0.458 0.488	0.480	0.473	0.294	0.651	0	0	0	0	0	0	0.527	0.349	0.706
SL005233	XEDAR	Q9HAV5	60401	EDA2R	RFU	No	No	E	0	0	0	0	Ō	0	0	0	0	0	Ō	Ō	1	1	1
SL005234 SL005235	GDF-9 NOG	Q9H9S0	2661 79923	GDF9 NOG	RFU	No No	No No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005236	NovH	P48745	4856	NOV CMA1	RFU	No	No	DE	0.235	-0.014	0.321	0	0	0	0.235	-0.007	0.477	0	0	0	0.765	0.523	1.007
SL005256	Histone H1.2	P16403	3006	HIST1H1C	RFU	No	No	DE	0.663	0.735	0.624	0	ō	ō	0.663	0.509	0.817	Ö	0	ō	0.337	0.183	0.491
SL005258 SL005261	PLK-1 TCPTP	P53350 P17706	5347 5771	PLK1 PTPN2	RFU RFU	No No	No No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005263	RAP DSME2	P30533	4043	LRPAP1	RFU	No	No	DE	0.848	0.900	0.809	0	0	0	0.848	0.785	0.912	0	0	0	0.152	0.088	0.215
SL005352	FABPE	Q01469	2171	FABP5	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005358 SL005361	prostatic binding prote Apo D	P30086 P05090	5037 347	PEBP1 APOD	RFU RFU	No No	No No	AE E	0.727	0.794 0	0.685 0	0.727	0.614 0	0.840 0	0	0	0	0	0	0	0.273	0.160 1	0.386 1
SL005372	Sorting nexin 4	095219	8723	SNX4	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.653	0.537	0.770	0.347	0.230	0.463
SL005392 SL005437	MEPE	Q9NQ76	410 56955	MEPE	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005488	SPARCL1 OBCAM	Q14515 014982	8404 4978	SPARCL1 OPCMI	RFU	No	No No	AE	0.761	0.829	0.716	0.761	0.657	0.865	0	0	0	0	0	0	0.239	0.135	0.343
SL005493	paraoxose 1	P27169	5444	PON1	RFU	No	No	E	0	0	ō	0	Ō	0	0	0	ō	0	0	Ō	1	1	1
SL005508 SL005572	Gelsolin	P06396	768 2934	GSN GSN	RFU	No No	No No	E	0	0	0	0	0	0	0	0	0	0.297	0.111	0.483	0.703	0.517	0.889
SL005574	Aminoacylase-1	Q03154	95 2525	ACY1 FUT3	RFU	No	No	DE	0.333	0.159	0.390	0	0	0	0.333	0.078	0.589	0	0	0	0.667	0.411	0.922
SL005588	FER	P16591	2241	FER	RFU	No	No	CE	0	õ	0	0	0	0	ō	0	0	0.610	0.482	0.738	0.390	0.262	0.518
SL005629 SL005630	GK PSA6	Q9UJ70 P60900	55577 5687	GK PSMA6	RFU RFU	No No	No No	AE CE	0.625	0.678 0	0.596 0	0.625	0.477 0	0.773	0	0	0	0 0.530	0 0.382	0 0.677	0.375 0.470	0.227 0.323	0.523 0.618
SL005675	ATP synthase beta ch	eP06576	506	ATP5B	RFU	No	No	E	0 795	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005685	EF-1-beta	P13693 P24534	1933	EEF1B2	RFU	No	No	CE	0.785	0.847	0.741	0.765	0.695	0.874	0	0	0	0.435	0.269	0.600	0.215	0.126	0.305
SL005687 SL005694	elF-5A-1 Peroxiredoxin-6	P63241 P30041	1984 9588	EIF5A PRDX6	RFU RFU	No No	No No	CE CF	0	0	0	0	0	0	0	0	0	0.596	0.464 0.557	0.728	0.404	0.272	0.536
SL005703	Notch 1	P46531	4851	NOTCH1	RFU	No	No	AE	0.513	0.521	0.510	0.513	0.327	0.700	0	0	0	0	0	0	0.487	0.300	0.673
SL005725 SL005730	cGMP-stimulated PDE	E O00408	9402 5138	GRAP2 PDE2A	RFU RFU	No No	No No	DE	0.265	0 -0.014	0 0.348	0	0	0	0 0.265	0 -0.007	0 0.536	0	0	0	1 0.735	1 0.464	1 1.007
SL005764	sCD163 Stanpiocoloin 1	Q86VB7	9332	CD163	RFU	No	No	AE	0.723	0.786	0.683	0.723	0.613	0.833	0	0	0	0	0	0	0.277	0.167	0.387
SL005793	Cyclophilin F	P30405	10105	PPIF	RFU	No	No	CE	0	0	0	0	0	0	õ	0	0	0.584	0.450	0.718	0.416	0.282	0.550
SL005797 SL005846	PIGR Moesin	P01833 P26038	5284 4478	PIGR MSN	RFU RFU	No No	No No	AE E	0.608 0	0.655 0	0.583 0	0.608 0	0.457 0	0.759 0	0	0	0	0	0	0	0.392	0.241 1	0.543 1
SL006029	Chitotriosidase-1	Q13231	1118	CHIT1	RFU	No	No	ACE	0.557	0.904	0.518	0.557	0.182	0.931	0	0	0	0.339	-0.038	0.716	0.104	0.057	0.151
SL006088 SL006091	Spningosine kise 1 NCK1	Q9NYA1 P16333	8877 4690	NCK1	RFU RFU	No	NO NO	E	0	0	0	0	0	0	0	0	0	0.699	0.594 0	0.803	0.301	0.197 1	0.406 1
SL006108 SL006114	CD5L ROR1	O43866 Q01973	922 4919	CD5L ROR1	RFU RFU	No No	No No	CE F	0	0	0	0	0	0	0	0	0	0.424	0.257	0.592	0.576	0.408 1	0.743 1
										-	-		-	-	-	-	-	-	-	-			

SL006119	TFF3	Q07654	7033	TFF3	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.184	-0.015	0.383	0.816	0.617	1.015
SL006189	KIF23	Q02241	9493	KIF23	RFU	No	No	DE	0.362	0.171	0.413	ō	ō	ō	0.362	0.071	0.654	Ö	0	ō	0.638	0.346	0.929
SL006197 SL006268	DJ homolog NSF1C	Q96DA6 Q9UN72	131118 55968	DJC19 NSFL1C	RFU RFU	No No	No No	E	0	0	0	0	0	0	0	0	0	0 479	0.321	0	1	1 0.364	1 0.679
SL006372	YES	P07947	7525	YES1	RFU	No	No	AE	0.704	0.770	0.664	0.704	0.581	0.826	0	0	0	0	0	0	0.296	0.174	0.419
SL006374 SL006378	BMX Esterase D	P51813 P10768	660 2098	BMX ESD	RFU RFU	No No	No No	E	0	0	0	0	0	0	0	0	0	0.337	0	0	1	1 0.481	1 0.845
SL006397	NRP1	O14786	8829	NRP1	RFU	No	No	AE	0.335	0.217	0.383	0.335	0.127	0.543	0	0	0	0	0	0	0.665	0.457	0.873
SL006406	PLXC1 HRG	O60486 P04196	10154 3273	PLXNC1 HRG	RFU	No	No	AE	0.692	0.759	0.653	0.692	0.564	0.821	0	0	0	0 467	0	0	0.308	0.179	0.436
SL006460	GP1BA	P07359	2811	GP1BA	RFU	No	No	E	0	Ö	õ	ŏ	õ	õ	0	Ö	0	0	0	0	1	1	1
SL006476 SL006480	NMT1 TRY3	P30419 P35030	4836 5646	NMT1 PRSS3	RFU	No No	No No	CE F	0	0	0	0	0	0	0	0	0	0.540	0.396	0.685	0.460	0.315	0.604 1
SL006512	HGFA	Q04756	3083	HGFAC	RFU	No	No	AE	0.826	0.881	0.785	0.826	0.755	0.898	0	0	0	0	0	Ō	0.174	0.102	0.245
SL006522 SL006523	LG3BP MFGM	Q08380 Q08431	3959 4240	LGALS3BP MFGE8	RFU RFU	No No	No No	CE CE	0	0	0	0	0	0	0	0	0	0.739 0.494	0.646 0.340	0.832	0.261 0.506	0.168 0.351	0.354 0.660
SL006528	SEPR	Q12884	2191	FAP	RFU	No	No	CE	0	0	0	0	0	Ō	0	0	Ō	0.255	0.061	0.450	0.745	0.550	0.939
SL006542 SL006544	FCN2 BGH3	Q15485 Q15582	2220 7045	FCN2 TGFBI	RFU RFU	No No	No No	DE CE	0.707	0.788	0.662	0	0	0	0.707	0.567	0.848	0.385	0	0 0.563	0.293	0.152 0.437	0.433 0.792
SL006550	ECM1	Q16610	1893	ECM1	RFU	No	No	AE	0.493	0.487	0.495	0.493	0.285	0.700	0	0	0	0	0	0	0.507	0.300	0.715
SL006610 SL006629	SIRT2	Q76LX8 Q8IXJ6	22933	SIRT2	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.600	0.468	0.732	0.400	0.268	0.532
SL006675	CKAP2	Q8WWK9	26586	CKAP2	RFU	No	No	AE	0.286	0.110	0.353	0.286	0.060	0.512	0	0	0	0	0	0	0.714	0.488	0.940
SL006694 SL006698	transcription factor M	LIQ8N3X6	254251	LCORL	RFU	No	No	E	0.870	0.730	0.635	0.870	0.540	0.801	0	0	0	0	0	0	1	1	0.460
SL006705	PFD5	Q99471	5204	PFDN5	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.341	0.154	0.528	0.659	0.472	0.846
SL006777	FETUB	Q9UGM5	26998	FETUB	RFU	No	No	AE	0.638	0.690	0.609	0.638	0.502	0.765	0	0	0	0	0	0	0.379	0.225	0.324
SL006803	ANGL3	Q9Y5C1	27329	ANGPTL3	RFU	No	No	DE	0.919	0.955	0.887	0	0	0	0.919	0.878	0.959	0	0	0	0.081	0.041	0.122
SL006830	complement factor H-	-riQ9BXR6	81494	CFHR5	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.385	0.210	0.560	0.615	0.440	0.790
SL006892 SL006910	ABL1 Cathensin V	P00519 060911	25 1515	ABL1 CTSI 2	RFU RFU	No	No No	E AF	0.361	0.269	0	0.361	0	0	0	0	0	0	0	0	1	1 0.441	1
SL006911	СНК1	014757	1111	CHEK1	RFU	No	No	E	0	0	0	0	0	0	0	Ő	0	Ő	Ő	õ	1	1	1
SL006912 SL006913	FGR FYN	P09769 P06241	2268 2534	FGR FYN	RFU RFU	No No	No No	E AF	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1 0.452
SL006914	Glucocorticoid recept	to P04150	2908	NR3C1	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.363	0.185	0.540	0.637	0.460	0.815
SL006915 SL006916	IL-27 LCK	Q8NEV9 0 P06239	21246778 1 3932	01IL27 EBI3 LCK	RFU RFU	No No	No No	AE E	0.264	-0.018 0	0.347	0.264	-0.008 0	0.536 0	0	0	0	0	0	0	0.736	0.464 1	1.008 1
SL006917	LYN	P07948	4067	LYN	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.587	0.454	0.720	0.413	0.280	0.546
SL006918 SL006919	RSK-like protein kise	P28482 075582	5594 9252	MAPK1 RPS6KA5	RFU	No No	No No	CE	0.426	0.230	0.440	0.426	0.030	0.821	0	0	0	0.364 0.543	-0.016 0.398	0.744 0.687	0.210 0.457	0.118 0.313	0.302
SL006920	MAPK14	Q16539	1432	MAPK14	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.569	0.431	0.707	0.431	0.293	0.569
SL006921 SL006922	RAD51	Q15118 Q06609	5163	RAD51	RFU	No	No	AE	0.264	-0.014	0.347	0.438	0.255	0.621	0.264	-0.007	0.534	0	0	0	0.736	0.466	0.745
SL006923	TBP	P20226	6908	TBP	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL006924 SL006970	DLL1	O00253 O00548	28514	DLL1	RFU	No	No	AE	0.505	0.054	0.333	0.257	0.030	0.485	0.505	0.308	0.702	0	0	0	0.495	0.298	0.892
SL006992	MATN3	015232	4148	MATN3	RFU	No	No	DE	0.553	0.613	0.535	0	0	0	0.553	0.287	0.819	0	0	0	0.447	0.181	0.713
SL006998	PDPK1	015530	5170	PDPK1	RFU	No	No	AE	0.730	0.794	0.689	0.730	0.622	0.838	0	0	0	0	0	0	0.270	0.162	0.378
SL007003	DHH	O43323	50846	DHH	RFU	No	No	AE	0.604	0.649	0.579	0.604	0.452	0.756	0	0	0	0 259	0	0	0.396	0.244	0.548
SL007024	GREM1	O60565	26585	GREM1	RFU	No	No	AE	0.628	0.700	0.594	0.628	0.448	0.808	0	õ	0	0	0	0	0.372	0.192	0.552
SL007025 SL007049	JAK2 CYTE	O60674 O76096	3717 8530	JAK2 CST7	RFU RFU	No No	No No	AE DE	0.779	0.841	0.736	0.779	0.687	0.870	0	0	0	0	0	0	0.221	0.130	0.313
SL007056	BMP10	O95393	27302	BMP10	RFU	No	No	CE	0	0	0	Ō	Ō	Ō	0	0	0	0.240	0.046	0.434	0.760	0.566	0.954
SL007059 SL007100	LY86 LKHA4	O95711 P09960	9450 4048	LY86 LTA4H	RFU	No No	No No	CE	0	0	0	0	0	0	0	0	0	0.211 0.506	0.010	0.411 0.658	0.789 0.494	0.589 0.342	0.990
SL007121	CATE	P14091	1510	CTSE	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL007122 SL007145	NR1D1	P14735 P20393	9572	NR1D1	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0.182	-0.016	0.379	1	1	1.016
SL007153	PERL	P22079	4025	LPO	RFU	No	No	AE	0.550	0.579	0.537	0.550	0.366	0.734	0	0	0	0	0	0	0.450	0.266	0.634
SL007179	EPHB2	P29323	2048	EPHB2	RFU	No	No	AE	0.533	0.549	0.525	0.533	0.371	0.695	0	0.000	0	0	0	0	0.467	0.305	0.629
SL007181 SL007195	TYK2 CD70	P29597 P32970	7297 970	TYK2 CD70	RFU RFU	No No	No No	AE F	0.246	0.021	0.327	0.246	0.011	0.481	0	0	0	0	0	0	0.754	0.519	0.989
SL007206	TSP2	P35442	7058	THBS2	RFU	No	No	AE	0.496	0.493	0.497	0.496	0.306	0.686	0	0	0	0	0	0	0.504	0.314	0.694
SL007207 SL007228	TSP4 KPCI	P35443 P41743	7060 5584	THBS4 PRKCI	RFU	No No	No No	AE AE	0.350	0.239	0.395	0.350	0.137	0.564	0	0	0	0	0	0	0.650	0.436	0.863
SL007237	MP2K4	P45985	6416	MAP2K4	RFU	No	No	ACE	0.365	-0.420	0.407	0.365	-0.042	0.772	0	0	0	0.375	-0.001	0.750	0.261	0.145	0.376
SL007250 SL007261	AMPM2	P48736 P50579	5294 10988	METAP2	RFU	No	No	AE	0.795	0.858	0.750	0.795	0.706	0.883	0	0	0	0	0	0	0.205	0.117	0.294
SL007266	PSD7	P51665	5713	PSMD7	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL007280 SL007281	MK12	P53634 P53778	6300	MAPK12	RFU	No	No	DE	0.678	0.759	0.635	0	0	0	0.678	0.521	0.834	0	0	0	0.322	0.166	0.479
SL007284	CRIS3	P54108	10321	CRISP3	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL007233	CSK21	P68400	1457	CSNK2A1	RFU	No	No	DE	0.479	0.452	0.487	0	0	0	0.479	0.193	0.766	0	0	0	0.521	0.234	0.807
SL007327	OLR1	P78380	4973 182	OLR1	RFU	No	No	AE	0.403	0.329	0.432	0.403	0.187	0.618	0	0	0	0	0	0	0.597	0.382	0.813
SL007336	SET	Q01105	6418	SET	RFU	No	No	CE	0	0	0	0	0	0	0	0	0.750	0.169	-0.040	0.378	0.831	0.622	1.040
SL007356 SL007358	NOTC2 KPCT	Q04721 Q04759	4853 5588	NOTCH2 PRKCO	RFU RFU	No No	No No	E	0 243	0	0	0	0	0	0.243	0	0	0	0	0	1	1 0.443	1
SL007373	PPID	Q08752	5481	PPID	RFU	No	No	AE	0.747	0.812	0.704	0.747	0.643	0.852	0	0	0	ő	õ	0	0.253	0.148	0.357
SL007385 SL007403	IL24 DMP1	Q13007 Q13316	11009 1758	IL24 DMP1	RFU RFU	No No	No No	DE DF	0.200	-0.093 -0.017	0.299	0	0	0	0.200	-0.047 -0.009	0.448 0.480	0	0	0	0.800	0.552	1.047 1.009
SL007423	IL-11 RA	Q14626	3590	IL11RA	RFU	No	No	AE	0.211	-0.008	0.298	0.211	-0.005	0.427	0	0	0	ő	õ	0	0.789	0.573	1.005
SL007429 SL007453	GPNMB MK11	Q14956 Q15759	10457 5600	GPNMB MAPK11	RFU RFU	No	No No	AE AF	0.678	0.737	0.642	0.678	0.552	0.803	0	0	0	0	0	0	0.322	0.197	0.448
SL007464	AMHR2	Q16671	269	AMHR2	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.366	0.184	0.547	0.634	0.453	0.816
SL007471	COLEC12	Q5KU26	81035	COLEC12	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1

SL007502	ST4S6	Q7LFX5	51363	CHST15	RFU	I	No	No	AE	0.617	0.674	0.588	0.617	0.452	0.782	0	0	0	0	0	0	0.383	0.218	0.548
SL007531	BMPER	Q8N8U9	168667	BMPER	RFU		No	No	E	0 422	0 271	0	0 422	0 226	0	0	0	0	0	0	0	1	1	1
SL007560	STAR2	O8WWO8	55576	STAR2	REU		No	No	F	0.422	0.371	0.444	0.422	0.220	0.018	0	0	0	0	0	0	0.576	0.362	1
SL007620	IL-12 RB2	Q99665	3595	IL12RB2	RFU		No	No	DE	0.315	0.136	0.376	0	õ	õ	0.315	0.069	0.560	Ő	ő	õ	0.685	0.440	0.931
SL007640	CLC7A	Q9BXN2	64581	CLEC7A	RFU		No	No	AE	0.707	0.786	0.663	0.707	0.570	0.845	0	0	0	0	0	0	0.293	0.155	0.430
SL007642	ANGL4	Q9BY76	51129	ANGPTL4	RFU		No	No	DE	0.335	0.098	0.396	0	0	0	0.335	0.040	0.629	0	0	0	0.665	0.371	0.960
SL007651	FGF23	Q9GZV9	8074 59277	FGF23	REU		NO	NO	DE	0.440	0 390	0 459	0	0	0	0 4 4 0	0 213	0 667	0	0	0	0.560	1	1
SL007674	LY9	Q9HBG7	4063	LY9	RFU		No	No	CE	0.440	0.000	0.455	ő	ő	ő	0.440	0.210	0.007	0.541	0.397	0.686	0.459	0.314	0.603
SL007680	ROBO2	Q9HCK4	6092	ROBO2	RFU		No	No	AE	0.505	0.508	0.504	0.505	0.314	0.696	0	0	0	0	0	0	0.495	0.304	0.686
SL007729	ARTS1	Q9NZ08	51752	ERAP1	RFU		No	No	AE	0.724	0.796	0.681	0.724	0.603	0.846	0	0	0	0	0	0	0.276	0.154	0.397
SL007747	IBK1	Q9UHD2	29110	IBK1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.294	0.106	0.482	0.706	0.518	0.894
SL007756	GDF2	Q9UK05	2658	GDF2	RFU		No	No	DE	0.675	0.740	0.638	0	0	0	0.675	0.539	0.811	0	0	0	0.325	0.189	0.461
SL007774	JAG2	Q9Y219	3714	JAG2	RFU		No	No	DE	0.718	0.825	0.664	0	0	0	0.718	0.553	0.883	0	0	0	0.282	0.117	0.447
SL007804	BGN	P21810	633	BGN	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.500	0.347	0.654	0.500	0.346	0.653
SL007806	IL22RA1	Q8N6P7	58985	IL22RA1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL007869	Cytidylate kise	P23204 P30085	5479	CMPK1	REU		No	No		0 503	0 505	0 502	0.503	0 325	0.681	0	0	0	0	0	0	0.497	0.319	0.675
SL007888	Cystatin-S	P01036	1472	CST4	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008008	ARGI1	P05089	383	ARG1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008023	HPLN1	P10915	1404	HAPLN1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008039	AK1A1 RS3	P14550 P23396	10327	RPS3	REU		NO	NO	AE F	0.829	0.884	0.787	0.829	0.756	0.901	0	0	0	0	0	0	0.171	0.099	0.244
SL008063	PPAC	P24666	52	ACP1	RFU		No	No	AE	0.824	0.882	0.781	0.824	0.748	0.900	0	0	ő	ő	ő	õ	0.176	0.100	0.252
SL008072	CO8A1	P27658	1295	COL8A1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008085	3HIDH	P31937	11112	HIBADH	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008099	MDHC	P40121 P40925	822	MDH1	REU		NO	NO	AE DE	0.759	0.820	0.718	0.759	0.665	0.854	0 784	0 682	0 886	0	0	0	0.241	0.146	0.335
SL008122	DUS3	P51452	1845	DUSP3	RFU		No	No	CE	0	0	0	ő	ő	ő	0	0	0	0.551	0.409	0.693	0.449	0.307	0.591
SL008143	UBE2N	P61088	7334	UBE2N	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.622	0.497	0.747	0.378	0.253	0.503
SL008157	UB2L3	P68036	7332	UBE2L3	RFU		No	No	AE	0.756	0.823	0.712	0.756	0.653	0.859	0	0	0	0	0	0	0.244	0.141	0.347
SL008176	C10BP	Q06323	5720	C10BP	REU		No	No	CE	0 360	0 251	0 403	0	0	0	0 360	0 1/1	0 579	0.467	0.307	0.628	0.533	0.372	0.693
SL008178	DERM	Q07507	1805	DPT	RFU		No	No	CE	0.000	0.201	0.405	0	ő	0 0	0.500	0.141	0.575	0.437	0.269	0.604	0.563	0.396	0.731
SL008190	SPTA2	Q13813	6709	SPTAN1	RFU		No	No	DE	0.479	0.434	0.488	0	0	0	0.479	0.137	0.822	0	0	0	0.521	0.178	0.863
SL008193	NID2	Q14112	22795	NID2	RFU		No	No	AE	0.249	0.016	0.331	0.249	0.008	0.490	0	0	0	0	0	0	0.751	0.510	0.992
SL008309 SL008331	RIN4 PA2G4	Q9NQC3	57142	RIN4 PA2G4	REU		NO	NO	AF	0.572	0.607	0.555	0 7 1 9	0 605	0.832	0.572	0.410	0.735	0	0	0	0.428	0.265	0.590
SL008378	4EBP2	Q13542	1979	EIF4EBP2	RFU		No	No	E	0.713	0.705	0.070	0.713	0.000	0.002	0	0 0	0	0	ő	ō	1	1	1
SL008380	CATZ	Q9UBR2	1522	CTSZ	RFU		No	No	AE	0.797	0.863	0.752	0.797	0.707	0.888	0	0	0	0	0	0	0.203	0.112	0.293
SL008382	CYTD	P28325	1473	CST5	RFU		No	No	AE	0.605	0.649	0.581	0.605	0.458	0.753	0	0	0	0	0	0	0.395	0.247	0.542
SL008414 SL008416	EpnB6 MRC2	015197 09UBG0	2051	MRC2	REU		NO	NO	DE	0.516	0 523	0 512	0	0	0	0 516	0 349	0 682	0.205	0.003	0.406	0.795	0.594	0.997
SL008421	ATS1	Q9UHI8	9510	ADAMTS1	RFU		No	No	E	0	0	0	0	Ő	ő	0	0	0	ő	ő	õ	1	1	1
SL008504	GNS	P15586	2799	GNS	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.163	-0.036	0.362	0.837	0.638	1.036
SL008516	CYTT	P09228	1470	CST2	RFU		No	No	AE	0.639	0.698	0.607	0.639	0.491	0.787	0	0	0	0	0	0	0.361	0.213	0.509
SL008574	SI AE5	Q99983 Q9UIB8	4958 8832	CD84	REU		NO	NO	CE	0.594	0.638	0.572	0	0	0	0.594	0.437	0.752	0 409	0 235	0.583	0.406	0.248	0.563
SL008590	Olfactomedin-4	Q6UX06	10562	OLFM4	RFU		No	No	E	ő	ŏ	0	0	Ő	ő	0	0	ő	0	0	0	1	1	1
SL008611	ASAHL	Q02083	27163	AA	RFU		No	No	DE	0.654	0.719	0.619	0	0	0	0.654	0.506	0.802	0	0	0	0.346	0.198	0.494
SL008623	CNTN2	Q02246	6900	CNTN2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.520	0.371	0.670	0.480	0.330	0.629
SL008639	IDS BST1	P22304 010588	3423 683	IDS BST1	REU		NO	NO	AF	0.887	0 931	0 852	0.887	0.837	0 938	0	0	0	0.440	0.275	0.605	0.560	0.395	0.725
SL008703	CBPE	P16870	1363	CPE	RFU		No	No	CE	0	0	0	0	0	0	0	0	ő	0.340	0.158	0.522	0.660	0.478	0.842
SL008709	DSC3	Q14574	1825	DSC3	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008728	NRX3B	Q9HDB5	9369	NRXN3	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.543	0.397	0.689	0.457	0.311	0.603
SL008759 SL008773	CD109	Q9HCN6 O6YHK3	135228	GP6 CD109	REU		NO	NO	AF	0.271	-0.030	0.334	0 4 4 1	0 240	0 642	0.271	-0.010	0.552	0.467	0.209	0.725	0.262	0.358	0.377
SL008808	SKP1	P63208	6500	SKP1	RFU		No	No	CE	0	0	0	0	0	0	0	0	ő	0.624	0.499	0.749	0.376	0.251	0.501
SL008822	EMR2	Q9UHX3	30817	EMR2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.385	0.211	0.559	0.615	0.441	0.789
SL008835	ASGR1	P07306	432	ASGR1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008804	LYVE1	09Y5Y7	10894	L YVF1	REU		No	No	DE	0.493	0.466	0.495	0	0	0	0.493	0.291	0.733	0	0	0	0.507	0.305	0.640
SL008909	LGMN	Q99538	5641	LGMN	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008916	DPP2	Q9UHL4	29952	DPP7	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008933	PARK/	Q99497	11315	PARK/	RFU		No	No	E AE	0 556	0 694	0 542	0 556	0 297	0 725	0	0	0	0	0	0	1	1	1
SL008945	TGM3	Q08188	7053	TGM3	RFU		No	No	DE	0.498	0.496	0.498	0.000	0	0.725	0.498	0.319	0.676	0	ő	õ	0.502	0.324	0.681
SL008956	ARSB	P15848	411	ARSB	RFU		No	No	DE	0.717	0.810	0.667	0	0	0	0.717	0.568	0.867	0	0	0	0.283	0.133	0.432
SL009045	ENPP7	Q6UWV6	339221	ENPP7	RFU		No	No	DE	0.737	0.806	0.694	0	0	0	0.737	0.625	0.850	0	0	0	0.263	0.150	0.375
SL009054	PGCB	P56400 096GW7	9370 63827	BCAN	REU		No	No	DE	0.652	0 713	0.618	0	0	0	0 652	0 508	0 796	0	0	0	0.348	0 204	0.492
SL009202	JAML1	Q86YT9	120425	AMICA1	RFU		No	No	E	0	0	0	0	õ	õ	0	0	0	Ő	ő	õ	1	1	1
SL009207	Dyctin subunit 2	Q13561	10540	DCTN2	RFU		No	No	AE	0.272	0.076	0.344	0.272	0.041	0.504	0	0	0	0	0	0	0.728	0.496	0.959
SL009213	Cathepsin A	P10619	5476 1644	CTSA	RFU		No	No	DE	0.460	0.430	0.472	0	0	0	0.460	0.245	0.675	0	0	0	0.540	0.325	0.755
SL009216	ESTL3	095633	10272	ESTI 3	REU		No	No	CE	0	0	0	0	0	0	0	0	0	0.603	0.471	0.735	0.397	0.265	0.529
SL009341	BASI	P35613	682	BSG	RFU		No	No	DE	0.293	0.000	0.370	Ő	õ	ō	0.293	0.000	0.586	0	0	0	0.707	0.414	1.000
SL009400	CRDL1	Q9BU40	91851	CHRDL1	RFU		No	No	AE	0.367	0.270	0.406	0.367	0.156	0.578	0	0	0	0	0	0	0.633	0.422	0.844
SL009412 SL009431	DKK3 HINT1	Q9UBP4 P49773	27122	DKK3 HINT1	RFU		No	No	CE F	0	0	0	0	0	U	0	0	0	0.280	0.087	0.474 0	0.720	0.526	0.913
SL009628	ING1	Q9UK53	3621	ING1	RFU		No	No	ACE	0.374	0.085	0.409	0.374	0.019	0.729	ō	0	0	0.438	0.095	0.781	0.188	0.105	0.272
SL009629	MBD4	O95243	8930	MBD4	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL009768	CBX5	P45973	23468	CBX5	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL009790 SL009791	hnRNP A/R	P62306 099729	0636 3182	SNRPF HNRNPAR	RFU		No No	No	AE DE	0.542	0.568	0.530	0.542 0	0.350	0.734	0.665	0.513	0.817	0	U O	U O	0.335	0.266	0.650
SL009792	PUR8	P30566	158	ADSL	RFU	Calibration Scale	No	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SL009868	SSRP1	Q08945	6749	SSRP1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL009951	WNT7A	O00755	7476	WNT7A	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010250	Stress-induced-phose	pIP31948	10963	STIP1	RFU		No	No	AE	0.684	0.750	0.646	0.684	0.553	0.816	0	0	0	0	0	0	0.316	0.184	0.447
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SL010288	Carbonic anhydrase	6 P23280	765	CA6	RFU	Calibration Scale	No	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SL010328 SL010348	FN1.4	P02751	2335	FN1	RFU		No	No	DE	0.557	0.586	0.542	0	0	0	0.557	0.385	0.728	0	0	0	0.443	0.272	0.615
SL010349	FN1.3	P02751	2335	FN1	RFU		No	No	DE	0.734	0.804	0.691	0	0	0	0.734	0.619	0.849	0	0	0	0.266	0.151	0.381
SL010368 SL010369	Carbonic Anhydrase	NP22748	3425 762	CA4	RFU		No	No	CE	0.722	0.793	0.078	0	0	0	0.722	0.599	0.844	0.189	-0.010	0.387	0.278	0.613	1.010
SL010371	CD39	P49961	953	ENTPD1	RFU		No	No	DE	0.536	0.582	0.523	0	0	0	0.536	0.256	0.816	0	0	0	0.464	0.184	0.744
SL010372 SL010373	Enterokise	P98073 P24071	5651 2204	PRSS7 FCAR	RFU		No	No No	F	0.714	0.836	0.657	0	0	0	0.714	0.532	0.896	0	0	0	0.286	0.104	0.468
SL010374	METAP1	P53582	23173	METAP1	RFU		No	No	AE	0.742	0.816	0.696	0.742	0.625	0.860	Ō	ō	0	Ō	0	Ō	0.258	0.140	0.375
SL010375 SL010376	ASAH2 MMFL2	Q9NR71 Q495T6	56624 79258	ASAH2 MMFL1	RFU		No	No No	DE F	0.697	0.763	0.658	0	0	0	0.697	0.572	0.822	0	0	0	0.303	0.178	0.428
SL010378	RET	P07949	5979	RET	RFU		No	No	AE	0.571	0.606	0.553	0.571	0.407	0.735	Ō	ō	0	Ō	0	Ō	0.429	0.265	0.593
SL010379 SL010381	Semaphorin 3A Soggy-1	Q14563 Q9UK85	10371 27120	SEMA3A DKKI 1	RFU		No	No No	E	0	0	0	0	0	0	0	0	0	0 407	0.235	0	1 0.593	1 0.421	1
SL010384	Testican-1	Q08629	6695	SPOCK1	RFU		No	No	AE	0.709	0.780	0.667	0.709	0.584	0.835	0	0	0	0	0	0	0.291	0.165	0.416
SL010388 SL010390	Trypsin 2 URB	P07478 Q76M96	5645 151887	PRSS2 CCDC80	RFU		No	No No	AE DE	0.562	0.598	0.546	0.562	0.379	0.746	0.505	0.327	0.683	0	0	0	0.438	0.254	0.621
SL010391	WFKN2	Q8TEU8	124857	WFIKKN2	RFU		No	No	AE	0.595	0.638	0.573	0.595	0.441	0.749	0	0	0	0	0	0	0.405	0.251	0.559
SL010392 SL010393	GASP-2 KREM2	Q96D09 08NCW0	114928 79412	GPRASP2 KREMEN2	RFU		No	No	CE F	0	0	0	0	0	0	0	0	0	0.222	0.028	0.417	0.778	0.583	0.972
SL010449	Carbonic Anhydrase	XQ9NS85	56934	CA10	RFU		No	No	E	0	0	0	0	Ō	0	0	Ō	0	0	0	0	1	1	1
SL010450 SL010451	CD48 CFC1	P09326 P0CG37	962 55997	CD48 CFC1	RFU		No	No No	DE	0.342	0.221	0.390	0	0	0	0.342	0.125	0.560	0.296	0.105	0.486	0.704	0.514	0.895
SL010454	Contactin-4	Q8IWV2	152330	CNTN4	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.544	0.396	0.693	0.456	0.307	0.604
SL010455 SL010456	Contactin-5 CYTN	O94779 P01037	53942 1469	CN1N5 CST1	RFU		No	No No	CE	0	0	0	0	0	0	0	0	0	0.283	0.096	0.471	1 0.717	1 0.529	1 0.904
SL010457	DLL4	Q9NR61	54567	DLL4	RFU		No	No	DE	0.338	-0.031	0.405	0	0	0	0.338	-0.010	0.686	0	0	0	0.662	0.314	1.010
SL010458 SL010461	Endocan FCGR1	Q9NQ30 P12314	11082 2209	ESM1 FCGR1A	RFU		No	No No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010462	FCN1	O00602	2219	FCN1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010463 SL010464	GPC2 LRIG3	Q8N158 Q6UXM1	221914 121227	GPC2 LRIG3	RFU		No No	No No	AE	0.514	0.522	0.510	0 0.514	0.330	0.698	0	0	0	0.261	0.070	0.451	0.739	0.549 0.302	0.930 0.670
SL010465	MATN2	O00339	4147	MATN2	RFU		No	No	AE	0.470	0.452	0.479	0.470	0.278	0.663	0	0	0	0	0	0	0.530	0.337	0.722
SL010466 SL010467	RGMA	Q96B86	83552 56963	RGMA	RFU		NO	NO	AE	0.440	0.396	0.458	0.440	0.227	0.653	0	0	0	0.255	0.064	0.446	0.745	0.554	0.936
SL010468	RGMB	Q6NW40	285704	RGMB	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.275	0.076	0.474	0.725	0.526	0.924
SL010469 SL010470	Semaphorin 3E	Q62VN8 015041	148738 9723	SEMA3E	RFU		No	No	AE	0.455	0.424	0.468	0.455	0.249	0.662	0	0	0	0	0	0	0.545	0.338	0.751
SL010471	Testican-2	Q92563	9806	SPOCK2	RFU		No	No	AE	0.699	0.761	0.661	0.699	0.581	0.817	0	0	0	0	0	0	0.301	0.183	0.419
SL010488 SL010489	CAMK1	Q14012	27 8536	CAMK1	RFU	Calibration Scale	NO	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1 NA
SL010490	CAMK1D	Q8IU85	57118	CAMK1D	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.214	0.016	0.412	0.786	0.588	0.984
SL010491 SL010492	CAMK2A CAMK2B	Q13554	815	CAMK2A CAMK2B	RFU		No	No	DE	0.899	0.763	0.660	0.699	0.577	0.821	0.368	0.124	0.612	0	0	0	0.301	0.179	0.423
SL010493	CAMK2D	Q13557	817	CAMK2D	RFU		No	No	AE	0.769	0.835	0.725	0.769	0.671	0.867	0	0	0	0	0	0	0.231	0.133	0.329
SL010494 SL010495	CDK1/cyclin B CDK2/cyclin A	P06493 P P24941 P2	201017 890	CDK2 CC1	RFU		No	No	DE	0.267	0.926	0.348	0	0	0	0.267	0.000	0.534	0	0	0	0.733	0.466	1.000
SL010496	CDK5/p35	Q00535 Q	151020 8851	CDK5 CDK5R1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010498	HCK	P08631	3055	HCK	RFU		No	No	CE	0.004	0.007	0.575	0.004	0.414	0.794	0	0	0	0.216	0.019	0.414	0.784	0.586	0.981
SL010500	LYNB	P07948	4067	LYN MAR2K2	RFU		No	No	CE	0 796	0	0 742	0	0	0	0	0	0	0.515	0.366	0.665	0.485	0.335	0.634
SL010502	MK08	P45983	5599	MAPK8	RFU		No	No	DE	0.621	0.689	0.589	0	ō	0	0.621	0.443	0.800	0	0	ō	0.379	0.200	0.557
SL010503	MAPK2 MAPK5	P49137	9261 8550	MAPKAPK2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.471	0.313	0.630	0.529	0.370	0.687
SL010505	MATK	P42679	4145	MATK	RFU		No	No	DE	0.283	-0.133	0.369	0	ō	0	0.283	-0.045	0.612	ő	ō	ō	0.717	0.388	1.045
SL010508	PAK3 PAK6	075914 09NOU5	5063 56924	PAK3 PAK6	RFU		No	No No	CE	0	0	0 717	0 760	0	0	0	0	0	0.168	-0.033	0.369	0.832	0.631	1.033
SL010510	PAK7	Q9P286	57144	PAK7	RFU		No	No	AE	0.449	0.418	0.463	0.449	0.263	0.634	ő	Ő	0	ŏ	Ő	õ	0.551	0.366	0.737
SL010512 SL010513	PIK3CA/PIK3R1 PRKACA	P42336 P2 P17612	27 5290 5295 5566	FIK3CA PIK3R1 PRKACA	RFU		No	No No	E	0	0	0	0	0	0	0	0	0	0.553	0 4 1 2	0	1 0.447	1	1 0.588
SL010514	PTK6	Q13882	5753	PTK6	RFU		No	No	DE	0.381	0.241	0.422	0	Ō	0	0.381	0.111	0.650	0	0	0	0.619	0.350	0.889
SL010515 SL010516	RPS6KA3 SRCN1	P51812 P12931	6197 6714	RPS6KA3 SRC	RFU RFU		No No	No No	DE AE	0.670	0.745 0.782	0.630 0.677	0 0.718	0 0.604	0 0.832	0.670 0	0.517	0.823	0	0	0	0.330	0.177 0.168	0.483 0.396
SL010517	STK16	075716	8576	STK16	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010518 SL010519	ZAP70	P42680 P43403	7535	ZAP70	RFU		No	No	CE	0.546	0.573	0.533	0	0	0	0.540 0	0.356 0	0.735	0.426	0.256	0.595	0.454	0.265	0.644
SL010520	AURKB	Q96GD4	9212 695	AURKB	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.180	-0.023	0.383	0.820	0.617	1.023
SL010521 SL010522	CDK8/cyclin C	P49336 P2	24 1024 892	CDK8 CCNC	RFU		No	No	CE	0.394	-0.508	0.424	0.394	-0.032	0.820	0	0	0	0.349	0.220	0.748	0.257	0.146	0.369
SL010523	HIPK3	Q9H422	10114	HIPK3	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.206	0.010	0.401	0.794	0.599	0.990
SL010529	UFC1	Q9Y3C8	51506	UFC1	RFU		No	No	CE	ō	0	0	0	ō	0	0	0	0	0.490	0.334	0.645	0.510	0.355	0.666
SL010530	OCAD1	Q9NX40	54940	OCIAD1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010612	Dkk-4	Q9UBT3	27121	DKK4	RFU		No	No	AE	0.540	0.564	0.530	0.540	0.357	0.724	0	0	0	0	0	0	0.460	0.276	0.643
SL010613	IL-17 RD SHP-2	Q8NFM7 006124	54756 5781	IL17RD PTPN11	RFU		No	No	DE	0.364	0.249	0.407	0	0	0	0.364	0.135	0.593	0	0	0	0.636	0.407	0.865
SL010617	TPSB2	P20231	64499	TPSB2	RFU		No	No	ACE	0.635	1.021	0.569	0.635	0.294	0.975	õ	0	õ	0.304	-0.039	0.647	0.062	0.033	0.090
SL010619 SL010830	TPSG1	Q9NRR2 1 P11171	25823 2035	TPSG1 FPB41	RFU		No	No No	E	0	0	0	0	0	0	0	0	0	0 479	0	0	1	1	1
SL010927	IMB1	Q14974	3837	KPNB1	RFU		No	No	CE	ō	õ	ō	Ő	ŏ	õ	õ	0	õ	0.496	0.342	0.650	0.504	0.350	0.658
SL010928 SL010973	IMDH2 PSA1	P12268 P25786	3615 5682	IMPDH2 PSMA1	RFU RFU		No No	No No	DE	0.622 0	0.683 0	0.592 n	0	0	0	0.622	0.456 0	0.789	0	0.085	0	0.378	0.211	0.544
SL011049	MASP3	P48740	5648	MASP1	RFU		No	No	DE	0.564	0.597	0.548	0	õ	0	0.564	0.397	0.732	0	0	0	0.436	0.268	0.603
SL011068	IL-17 RC Marapsin	Q8C3 Q9BOR3	84818 83886	IL17RC PRSS27	RFU RFU		No No	No No	CE	0	0	0	0	0	0	0	0	0	0.193	-0.004 0.242	0.389	0.807	0.611	1.004
SL011071	PDGF-CC	Q9NRA1	56034	PDGFC	RFU		No	No	E	Ő	ő	õ	0	õ	0	õ	0	õ	0	0	0	1	1	1
SL011073	XPNPEP1 CD226	Q9NQW7 Q15762	7511 10666	XPNPEP1 CD226	RFU		No	No No	CE F	0	0	0	0	0	0	0	0	0	0.479	0.322	0.636 0	0.521	0.364 1	0.678
SL011202	SA	P54920	8775	PA	RFU		No	No	ACE	0.362	-0.133	0.404	0.362	-0.021	0.746	õ	0	0	0.409	0.048	0.769	0.229	0.128	0.330
SL011211	IF4G2	P78344	1982	EIF4G2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.572	0.435	0.709	0.428	0.291	0.565

SL011232	CDC37	Q16543	11140	CDC37	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL011404 SL011405	PDE4D PDE5A	Q08499 O76074	5144 8654	PDE4D PDE5A	RFU	NO	No	CE	0	0	0	0	0	0	0	0	0	0.578	0.442	0.714	0.422	0.286	0.558
SL011406	PDE7A	Q13946	5150	PDE7A	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL011448	TNR4 PACAP-38	P43489 P18509	7293	TNFRSF4	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL011499	PH	P01298	5539	PPY	RFU	No	No	CE	0	ő	Ő	Ő	Ő	ő	ő	õ	ő	0.398	0.227	0.570	0.602	0.430	0.773
SL011508	PACAP-27	P18509	116	ADCYAP1	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL011510	Somatostatin-28	P61278	6750	SST	RFU	No	No	E	0.039	0.700	0.000	0.039	0.400	0.792	0	0	0	0	0	0	1	1	1
SL011528	RS7	P62081	6201	RPS7	RFU	No	No	DE	0.522	0.537	0.516	0	0	0	0.522	0.320	0.725	0	0	0	0.478	0.275	0.680
SL011529 SL011530	DLRB1	Q9Y3A5 Q9NP97	51119 83658	SBDS DYNLRB1	RFU	No	No No	AE AE	0.730	0.792	0.689	0.730	0.623	0.837	0	0	0	0	0	0	0.270	0.163	0.377
SL011532	ETHE1	O95571	23474	ETHE1	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.389	0.216	0.563	0.611	0.437	0.784
SL011533	SGTA RBM30	O43765	6449 9584	SGTA RBM30	RFU	No	No	CE	0 592	0	0	0	0	0	0	0	0	0.423	0.255	0.591	0.577	0.409	0.745
SL011549	ARI3A	Q99856	1820	ARID3A	RFU	No	No	CE	0.002	0	0	0	0	0	0.002	0.002	0	0.261	0.070	0.451	0.739	0.549	0.930
SL011616	IF4A3	P38919	9775	EIF4A3	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL011628 SL011629	AIP	Q90J06 O00170	28988 9049	AIP	RFU	NO	No	CE	0	0	0	0	0	0	0	0	0	0.159	-0.040	0.359	0.841	0.641	0.520
SL011630	SE6L2	Q6UXD5	26470	SEZ6L2	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.409	0.238	0.579	0.591	0.421	0.762
SL011631 SL011708	CA ARP19	Q13765 P56211	4666 10776	CA ARPP19	RFU	No	No No	CE	0	0	0	0	0	0	0	0	0	0.451 0.502	0.289	0.614	0.549	0.386	0.711 0.650
SL011709	PLPP	Q96GD0	57026	PDXP	RFU	No	No	AE	0.756	0.820	0.713	0.756	0.655	0.856	0	0	0	0	0	0	0.244	0.144	0.345
SL011768	NUDC3 ANI32B	Q8IVD9	23386	NUDCD3	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.374	0.197	0.552	0.626	0.448	0.803
SL011770	LCMT1	Q9UIC8	51451	LCMT1	RFU	No	No	AE	0.484	0.470	0.489	0.484	0.261	0.707	0	Ö	ō	0	0.200	0.000	0.516	0.293	0.739
SL011772	PESC	000541	23481	PES1	RFU	No	No	E	0	0	0 782	0	0	0	0	0	0	0	0	0	1	1	1
SL011809	XTP3A	Q99629 Q9H773	79077	DCTPP1	RFU	No	No	AE	0.366	0.005	0.406	0.366	0.149	0.903	0	0	0	0	0	0	0.634	0.425	0.251
SL012108	PLCG1	P19174	5335	PLCG1	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL012168 SL012188	EP15R	Q9HAP6 Q9UBC2	64130 58513	EPS15L1	RFU	No No	NO	AE	0.397	0 0.315	0 0.429	0.397	0 0.176	U 0.618	0	0	0	0	0	0	0.603	0.382	1 0.824
SL012248	FAK1	Q05397	5747	PTK2	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL012457 SL012469	NXPH1 GPC5	P58417 P78333	30010 2262	NXPH1 GPC5	RFU RFU	No	No No	CE	0 472	0 453	0	0 472	0 276	0	0	0	0	0.732	0.637 0	0.827 0	0.268	0.173	0.363
SL012538	ARMEL	Q49AH0	441549	CDNF	RFU	No	No	AE	0.319	0.178	0.374	0.319	0.100	0.538	Ő	ō	0	Ő	0	ō	0.681	0.462	0.900
SL012698	KI2L4	Q99706	3805	KIR2DL4	RFU	No	No	DE	0.218	-0.045	0.310	0	0	0	0.218	-0.023	0.459	0	0	0	0.782	0.541	1.023
SL012707 SL012740	ATS15	Q8TE58	170689	ADAMTS15	RFU	No	No	DE	0.558	0.594	0.542	0	0	0	0.558	0.369	0.746	0	0	0	0.442	0.252	0.816
SL012754	ASM3A	Q92484	10924	SMPDL3A	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.209	0.013	0.406	0.791	0.594	0.987
SL012822 SL013240	CRK	Q9GZN4 P46108	64063 1398	CRK	RFU	No	No No	CE	0	0	0	0	0	0	0	0	0	0.539	0.392	0.686	0.461	0.314	0.608
SL013488	CLC1B	Q9P126	51266	CLEC1B	RFU	No	No	AE	0.726	0.794	0.684	0.726	0.611	0.842	0	0	0	0	0	0	0.274	0.158	0.389
SL013489	AMNLS	Q9BXJ7	81693	AMN	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.277	0.087	0.467	0.723	0.533	0.913
SL013548	IL-34	Q6ZMJ4	146433	IL34	RFU	No	No	E	0	0	0	0	0	0	Ő	ō	0	0	0	0.570	1	1	1
SL013570	DYRK3	O43781	8444	DYRK3	RFU	No	No	DE	0.298	-0.061	0.377	0	0	0	0.298	-0.022	0.618	0	0	0	0.702	0.382	1.022
SL013754 SL013928	PPIE	Q9UNP9	10450	PPIE	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.149	0.423	0.353	0.651	0.847	0.577
SL013969	KYNU	Q16719	8942	KYNU	RFU	No	No	DE	0.525	0.540	0.518	0	0	0	0.525	0.331	0.718	0	0	0	0.475	0.282	0.669
SL013988 SL013989	RSP02	Q6UXX9	9435 340419	RSP02	RFU	NO	No	E	0	0	0	0	0	0	0	0	0	0.380	0.205	0.555	0.620	0.445	0.795
SL014008	FUT5	Q11128	2527	FUT5	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.542	0.398	0.687	0.458	0.313	0.602
SL014009 SL014028	HDGR2 ENTP5	Q724V5 Q75356	84717 957	HDGFRP2 ENTPD5	RFU	No	No	AF	0.663	0.721	0.629	0.663	0.532	0.795	0	0	0	0	0	0	1 0.337	1	1 0.468
SL014029	SPHK2	Q9NRA0	56848	SPHK2	RFU	No	No	E	0	0	0	0	0	0	ő	õ	ő	ő	Ő	õ	1	1	1
SL014048	CO1 PCSK7	Q86Y22	91522	COL23A1	RFU	No	No	DCE	0.274	0.041	0.333	0	0	0	0.274	0.017	0.532	0.512	0.266	0.757	0.214	0.120	0.309
SL014070	SLIK5	O94991	26050	SLITRK5	RFU	No	No	CE	0	0	0	0	0	0	Ő	ō	0	0.374	0.198	0.550	0.626	0.450	0.802
SL014071	FLRT1	Q9NZU1	23769	FLRT1	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.392	0.218	0.566	0.608	0.434	0.782
SL014088	SORC2	Q96PQ0	57537	SORCS2	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0.228	0.033	0.422	1	0.576	0.967
SL014092	CDON	Q4KMG0	50937	CDON	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.468	0.306	0.630	0.532	0.370	0.694
SL014093	GP114	Q8IZF4	221188	GPR114	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL014096	LRRT1	Q86UE6	347730	LRRTM1	RFU	No	No	DE	0.158	-0.104	0.262	0	0	0	0.158	-0.059	0.375	0	0	0	0.842	0.625	1.059
SL014108 SL014111	KIRR3	Q86VH5 Q8IZU9	347731 84623	KIRREL3	RFU	NO	NO	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL014113	NLGNX	Q8N0W4	57502	NLGN4X	RFU	No	No	CE	0	ō	ō	0	ō	ō	0	0	ō	0.215	0.019	0.411	0.785	0.589	0.981
SL014129 SL014130	H6ST1 CHST6	O60243 Q9G7X3	9394 4166	HS6ST1 CHST6	RFU RFU	No No	No No	F	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL014148	ROB03	Q96MS0	64221	ROB03	RFU	No	No	DE	0.699	0.809	0.647	ŏ	õ	õ	0.699	0.521	0.877	ő	õ	õ	0.301	0.123	0.479
SL014208 SL014209	CRTAM KLRF1	095727 09N7S2	56253 51348	CRTAM KLRE1	RFU RFU	No	No	EF	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL014228	SLAF6	Q96DU3	114836	SLAMF6	RFU	No	No	DE	0.332	0.185	0.386	0	0	õ	0.332	0.098	0.566	ō	0	ō	0.668	0.434	0.902
SL014268	OX2G	P41217	4345	CD200	RFU	No	No	CE	0	0	0	0	0	0	0 270	0	0	0.308	0.122	0.494	0.692	0.506	0.878
SL014209	CLM6	Q08708	10871	CD300C	RFU	No	No	AE	0.345	0.230	0.391	0.345	0.133	0.556	0.270	0.023	0.010	0	0	0	0.655	0.444	0.867
SL014288	MO2R1	Q8TD46	131450	CD200R1	RFU	No	No	DE	0.367	0.257	0.408	0	0	0	0.367	0.141	0.593	0	0	0	0.633	0.407	0.859
SL014289 SL014292	SIG14	Q14943 Q08ET2	3813 1E+08	KIR3DS1 SIGLEC14	RFU	No No	No No	DE	0.974	U 0.986	0 0.963	0	0	0	0.974	0 0.962	U 0.986	0	0	0	1 0.026	1 0.014	1 0.038
SL014294	EPHAA	Q5JZY3	284656	EPHA10	RFU	No	No	E	0	0	0	0	0	ō	0	0	0	0	Ö	ō	1	1	1
SL014308 SL014468	FGF-8A SH21A	P55075 060880	2253 4068	FGF8 SH2D1A	RFU RFU	No	No No	CE	0	0	0	0	0	0	0	0	0	0.167	-0.032	0.366	0.833	0.634	1.032
SL014469	SHC1	P29353	6464	SHC1	RFU	No	No	AE	0.684	0.746	0.647	0.684	0.557	0.811	ő	õ	õ	0	0	0	0.316	0.189	0.443
SL014470	BCAR3	075815 P20830	8412 3614	BCAR3	RFU RFU	No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL015728	GCKR	Q14397	2646	GCKR	RFU	No	No	E	0.007	0.724	0.021	0.007	0.307	0	0	0	0	0	0	0	1	1	1
SL016128	TXD12	095881	51060	TXNDC12	RFU	No	No N-	AE	0.869	0.918	0.830	0.869	0.810	0.928	0	0	0	0	0	0	0.131	0.072	0.190
SL016129 SL016130	BRF-1	Q92994	2972	BRF1	RFU	No	No	E	0	0	0	0	0	0	0	0	0	0.186	-0.012	0.384	0.614	0.016	1.012
SL016148	C34 gp41 HIV Frag	me Q70626	None	Human-virus	RFU	No	No	DE	0.331	0.122	0.391	0	0	0	0.331	0.054	0.608	0	0	0	0.669	0.392	0.946

| L016548 | AMPK a1b1g1 | Q13131 Q915562 5564 PRKAA1 PRKABR | FU | No

 | No | E

 | 0 | 0 | 0
 | 0
 | 0 | 0 | 0
 | 0 | 0 | 0 | 0 | 0 | 1
 | 1 | 1 |
|---------|---|---|--
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--|
| L016549 | AMPK a2b2g1 | P54646 0435563 5565 PRKAA2 PRKABR | FU | No

 | No | CE

 | 0 | 0 | 0
 | 0
 | 0 | 0 | 0
 | 0 | 0 | 0.181 | -0.017 | 0.378 | 0.819
 | 0.622 | 1.017 |
| L016550 | CK2-A1:B | P68400 P671457 1460 CSNK2A1 CSNKR | FU | No

 | No | CE

 | 0 | 0 | 0
 | 0
 | 0 | 0 | 0
 | 0 | 0 | 0.680 | 0.571 | 0.790 | 0.320
 | 0.210 | 0.429 |
| L016551 | CK2-A2:B | P19784 P671459 1460 CSNK2A2 CSNKR | FU | No

 | No | AE

 | 0.208 | -0.114 | 0.308
 | 0.208
 | -0.054 | 0.470 | 0
 | 0 | 0 | 0 | 0 | 0 | 0.792
 | 0.530 | 1.054 |
| L016553 | PDE3A | Q14432 5139 PDE3A R | FU | No

 | No | DE

 | 0.501 | 0.502 | 0.501
 | 0
 | 0 | 0 | 0.501
 | 0.289 | 0.713 | 0 | 0 | 0 | 0.499
 | 0.287 | 0.711 |
| L016554 | PDE9A | 076083 5152 PDE9A R | FU | No

 | No | E

 | 0 | 0 | 0
 | 0
 | 0 | 0 | 0
 | 0 | 0 | 0 | 0 | 0 | 1
 | 1 | 1 |
| L016555 | PDE11 | Q9HCR9 50940 PDE11A R | FU | No

 | No | DE

 | 0.655 | 0.727 | 0.618
 | 0
 | 0 | 0 | 0.655
 | 0.497 | 0.813 | 0 | 0 | 0 | 0.345
 | 0.187 | 0.503 |
| L016557 | HMGR | P04035 3156 HMGCR R | FU | No

 | No | E

 | 0 | 0 | 0
 | 0
 | 0 | 0 | 0
 | 0 | 0 | 0 | 0 | 0 | 1
 | 1 | 1 |
| L016563 | GHC2 | Q9H1K4 83733 SLC25A18 R | FU | No

 | No | E

 | 0 | 0 | 0
 | 0
 | 0 | 0 | 0
 | 0 | 0 | 0 | 0 | 0 | 1
 | 1 | 1 |
| L016566 | DRAK2 | O94768 9262 STK17B R | FU | No

 | No | DE

 | 0.710 | 0.788 | 0.665
 | 0
 | 0 | 0 | 0.710
 | 0.575 | 0.845 | 0 | 0 | 0 | 0.290
 | 0.155 | 0.425 |
| L016567 | TAK1-TAB1 | O43318 Q156885 10454 MAP3K7 TAB1 R | FU | No

 | No | F

 | 0 | 0 | 0
 | 0
 | 0 | 0 | 0
 | 0 | 0 | 0 | 0 | 0 | 1
 | 1 | 1 |
| L016928 | SLAF7 | Q9NQ25 57823 SLAMF7 R | FU | No

 | No | AE

 | 0.902 | 0.939 | 0.871
 | 0.902
 | 0.860 | 0.944 | ō
 | ō | ō | ō | ō | ō | 0.098
 | 0.056 | 0.140 |
| L017188 | GSK-3 alpha/beta | P49840 P492931 2932 GSK3A GSK3B R | FU | No

 | No | CE

 | 0 | 0 | 0
 | 0
 | 0 | 0 | 0
 | 0 | 0 | 0.649 | 0.531 | 0.767 | 0.351
 | 0.233 | 0.469 |
| L017189 | Kininogen HMW | P01042 3827 KNG1 R | FU | No

 | No | AF

 | 0.596 | 0.644 | 0.572
 | 0.596
 | 0.429 | 0.763 | 0
 | 0 | 0 | 0 | 0 | 0 | 0.404
 | 0.237 | 0.571 |
| L017610 | Gro-b/a | P19876 P19None CXCL3 CXCL2 R | FU | No

 | No | CE

 | 0 | 0 | 0
 | 0
 | 0 | 0 | ō
 | ō | ō | 0.432 | 0.267 | 0.598 | 0.568
 | 0.402 | 0.733 |
| L017611 | 14/03/2003 | P31946 P6:7529 7531 YWHAB YWHAF R | FU | No

 | No | CE

 | 0 | 0 | 0
 | 0
 | 0 | 0 | 0
 | 0 | 0 | 0.626 | 0.502 | 0.750 | 0.374
 | 0.250 | 0.498 |
| L017612 | HSP 90a/b | P07900 P08None HSP90AA1 HSPIR | FU | No

 | No | DCF

 | 0.253 | -0.049 | 0.321
 | ō
 | ō | ō | 0.253
 | -0.018 | 0.524 | 0.496 | 0.246 | 0.747 | 0.250
 | 0.140 | 0.361 |
| L017613 | FCG2A/B | P12318 P31 None FCGR2A FCGR2R | FU | No

 | No | DF

 | 0.940 | 0.965 | 0.917
 | ō
 | ō | ō | 0.940
 | 0.913 | 0.967 | 0 | 0 | 0 | 0.060
 | 0.033 | 0.087 |
| L017614 | PKB a/b/g | Family None None R | FU | No

 | No | CE

 | 0 | 0 | 0
 | 0
 | 0 | 0 | 0
 | 0 | 0 | 0.639 | 0.519 | 0.760 | 0.361
 | 0.240 | 0.481 |
| L018625 | TLR4:MD-2 complex | 000206 Q9 7099 2364; TLR4 LY96 R | FU | No

 | No | CE

 | ő | õ | õ
 | ŏ
 | ŏ | ő | ő
 | õ | õ | 0.593 | 0.459 | 0.727 | 0.407
 | 0.273 | 0.541 |
| | L016548
L016549
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L016567
L017682
L017188
L017761
L017611
L017611
L017613
L017613
L017614 | L016548 AMPK atb 1g1 L016549 AMPK atb 1g1 L016550 CK2-A1:8 L016551 CK2-A1:8 L016552 PDE3A L016553 PDE3A L016554 PDE9A L016555 GK2-A1:8 L016557 HMGR L016556 GHC2 L016556 GRA2 L016556 GRA2 L016566 GRA2 L016567 HMGR L016568 GRA2 L016568 GRA3 L016584 GSA-3 alphabeta L017189 Kininogen HMW L017610 Gro-big L017611 L40/32003 L017612 HS90ab L017614 PK6 alpig L017614 PK6 alpig | L016548 AMPK atb1g1 C01311 C9/5562 5564 PRKAAP RRKABP L016550 CK2-A1:B P56460 C9/5563 5565 PRKAAP RRKABP L016550 CK2-A1:B P56460 D75/1457 1460 CSNK2A1 CSNKR L016550 CK2-A1:B P56470 C97/1457 1460 CSNK2A1 CSNKR L016550 CK2-A1:B P19764 P671457 1460 CSNK2A1 CSNKR L016551 CK2-A2:B P19764 P671457 1460 CSNK2A2 CSNKR L016554 PDE9A C14432 5139 PDE9A R L016555 FDE9A C94035 5152 PDE9A R L016557 HMGR P04035 3156 HMGCR R L016556 DRAK2 O94768 9262 STK17B R L016565 DRAK2 O94768 9262 STK17B R L017686 GKA3 alphabet P4940 P42931 2932 GSKAG GSKB R L017618 GKniggen HMW P01042 3827 KNG1 R L017610 Gro-big P1976 P19None CXC13 CXC12 R | L016548 AMPK atblg1 O13131 Q915562 25544 PRKAA1 PRKAB RFU L016550 CK2-A18 P56466 045563 5565 PKRAA2 PRKAA2 RFKAB RFU L016550 CK2-A18 P56460 07671457 1460 CSNK2A1 CSNKRFU L016550 CK2-A18 P56460 07671457 1460 CSNK2A1 CSNKRFU L016551 CK2-A2B P19784 P671459 1460 CSNK2A2 CSNK RFU L016555 DESA Q14432 5139 PDE3A RFU L016555 PDE9A Q14432 5139 PDE3A RFU L016555 PDE9A Q14432 5139 PDE3A RFU L0165557 HMGR Q4035 3156 HMGCR RFU L016556 DRAK2 Q84768 9262 STK17B RFU L016566 DRAK2 Q84768 9262 STK17B RFU L016566 DRAK2 Q94768 9262 STK17B RFU L016581 L045700 GR-3 alpha/bere P49804 P42231 2932 SK3A GSK3B RFU L017618 KKinirogen HMW <th>L016548 AMPK atb1g1 C01311 09/5562 5564 PRKAAT PRKAB RFU No L016569 AMPK atb1g1 P5464 00/5563 5565 PMKAA2 PRKAB RFU No L016550 CK2-A1:B P66400 P671457 1460 CSNK2A1 CSNK RFU No L016550 CK2-A1:B P66400 P671457 1460 CSNK2A1 CSNK RFU No L016550 CK2-A1:B P063A0 CSNK2A1 CSNK RFU No L016551 CK2-A2:B P19784 P671459 1460 CSNK2A1 CSNK RFU No L016554 PDE3A C14432 S139 PDE3A RFU No L016555 PDE5A C70603 S152 PDE9A RFU No L016557 HMGR P04035 3156 HMGCR RFU No L016565 FRAK2 C9414K3 83733 SLC25A18 RFU No L016565 DFAK2 C94768 9262 STK17B RFU No L016565 DFAK4 C94768 9262 SK476K RFU No L016585</th> <th>L016548 AMPK atb1g1 C013131 C95562 2564 PRKAAP RRKAB RFU No No L016550 CK2-A1B P68460 025563 2565 PKRAAP RRKAB RFU No No No L016550 CK2-A1B P68460 025563 2565 PKRAAP RRKAB RFU No No No L016550 CK2-A1B P68400 P671457 1460 CSNK2A2 CSNKRFU No No No L016551 CK2-A2B P19784 P671459 1460 CSNK2A2 CSNKRFU No No No L016555 PDESA C14432 5139 PDESA RFU No No L016555 PDESA Q14432 5139 PDESA RFU No No L016555 PDESA Q94769 S040 PDE11A RFU No No L0165557 HMGR P04035 3156 HMMCR RFU No No L016565 DRAK2 O94768 9262 STK17B RFU No No L016565 DRAK2 O94768 9262 STK17B RFU<th>L016548 AMPK atb1g1 Q1311 Q9:5562 5564 PRKAA1 PRKAB RFU No No E L016549 AMPK atb1g1 Q1311 Q9:5562 5564 PRKA2 PRKAB RFU No No No CE L016550 CK2-A1:B P66460 Q75:1457 1460 CSNK2A1 CSNK RFU No No No CE L016550 CK2-A1:B P6974 P67 1457 1460 CSNK2A1 CSNK RFU No No No AE L016551 CK2-A2:B P19784 P67 1459 1460 CSNK2A1 CSNK RFU No No No AE L016555 PDE3A Q14432 S139 PDE3A RFU No No No DE L016557 HMGR P04035 3156 HMGCR RFU No No No E L016557 HMGR P04035 3156 HMGCR RFU No No No E L016565 DFAK2 O94768 9262 STK17B RFU No No No E</th><th>L016548 AMPK atblg1 O13131 Q915662 2564 PRKAA2 PRKAABRFU No No No E 0 L016548 AMPK atblg1 P54646 Q425563 5565 MFKAA2 PRKAABRFU No No No CE 0 L016550 CK2-A1B P58480 Q51457 1460 CSNK2A2 CSNKRFU No No No AE 0.208 L016550 CK2-A2B P19784 P671457 1460 CSNK2A2 CSNKRFU No No No AE 0.208 L016555 DFE3A C14432 5139 PDE3A RFU No No No E 0.208 L016555 PDE9A C14432 5139 PDE3A RFU No No No E 0 L0165557 HMGR P04035 3156 HMCCR RFU No No No E 0 L016556 GR422 O94768 9262 STK17B RFU No No No E 0 L016565 DRAK2 O94768 9262</th><th>Lüfteste
Lüfteste
MMPK abzlg Nothom E 0 0 Lüfteste
MMPK abzlg P5466 0.025563 5565 MKA2 PRKAA2 PRKAA2 PRKAA PFU No No CE 0 0 Lüfteste
MMPK abzlg P5466 0.025563 5565 MKA2 PRKAA2 PRKAA2 PRKAA PRFU No No No CE 0 0 Lüfteste
MMS P19784 P671457 1460 CSNK2A2 CSNKRFU No No No AE 0.208 -0.114 Lüfteste
MI6555 PDE3A P19784 P671459 1460 CSNK2A2 CSNKRFU No No No AE 0.208 -0.114 Lüfteste
MI6555 PDE3A Q14432<5 139 PDE3A RFU No No No E 0 0 0.502 Lüfteste
MI6555 PDE3A Q14432 5139 PDE3A RFU No No DE 0.501 0.502 Lüfteste
MI6555 PDE3A Q94768 S155 PDE3A RFU No No DE 0.707 0.727 Lüfteste
MI6556 DRAK2 O94768 9262 <td< th=""><th>L016548 AMPK atb1g1 Q1311 Q9:5562 5564 PRKA1 PRKAB RFU No No E 0 0 0 L016549 AMPK atb1g1 Q1311 Q9:5562 5563 5565 PRKA2 PRKAB RFU No No No CE 0 0 0 L016550 CK2-A1:B P68460 Q751 457 1460 C5NK2A1 C5NK RFU No No No AE 0.208 -0.114 0.308 L016550 CK2-A1:B P19784 P67 1459 1460 C5NK2A1 C5NK RFU No No No AE 0.208 -0.114
0.308 L016555 PDE3A Q14432 S139 PDE3A RFU No No No No DE 0.501 0.502 0.501 L016557 PDE3A Q14432 S139 PDE3A RFU No No No DE 0.501 0.502 0.501 0.502 0.501 0.502 0.501 0.501 0.502 0.501 0.502 0.501 0.502 0.501 0.502 0.501 0.550 7.277</th><th>Lüfteste
Lüfteste
MMFk abzg1 Oli St562 5564 PRKAA2 PRKAAB RFL No No E 0 0 0 Lüfteste
MMFk abzg1 P56456 OK5563 5565 HKAA2 PRKAAB RFL No No No CE 0 0 0 Lüfteste
MMFk abzg1 P56456 OK5563 5565 HKAA2 PRKAAB RFL No No No CE 0 0 0 0 Lüfteste
MK1555 CK2-A1B P58400 P671457 1460 CSNK2A2 CSNKRFU No No No AE 0.208 -0.114 0.308 0.208 Lüfteste
MK1555 PDESA Q14432 5139 PDESA RFU No No No E 0 0 0 0 Lüfteste
MK1555 PDESA Q94768 9040 PDE11A RFU No No No E 0</th><th>Lüfesse AMPK altbig1 O1311 QP/SE62 S564 PRKAA1 PRKABRFU No No E 0 <</th><th>Lüftesta AMPK atblig1 Oli 5562 SEG4 PRKAA2 PRKAAB RPL No No No E 0 <t< th=""><th>Lüfesse AMPK albig1 Olisses Stepse PRKAAP RRKABRFU No No E 0 0 0 0 0 0 0 0 Lüfesse AMPK albig1 D5466 0 CK2A1B P68400 P671457 1440 CSNKZAP CSNKARFU No No No CE 0</th><th>Lüfese AMPR altbig1 Olisses Stefa Prikkal PRKAB RFU No No E 0</th><th>Lüfese AMPK albig1 Oli 5562 5564 PRKAA2 PRKAA8 RFU No No E 0</th><th>Linesse AMPR at big 1 O1311 OPISSES 2564 PRKAA1 PRKABRFU No No E 0 0</th><th>Linesse AMPR at big 1 Original Opissez 5864 PRKAAT PRKAB RFU No No E 0</th><th>Linesse AMPK at big 1 Olision 2015626 SEG4 PRKAAP PRKAAB FLU No No E 0
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MMS P19784 P671457 1460 CSNK2A2 CSNKRFU No No No AE 0.208 -0.114 Lüfteste
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