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SKIP controls lysosome positioning using a composite kinesin-1 heavy and light chain binding domain

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ABSTRACT

The molecular interplay between cargo recognition and regulation of the activity of the kinesin-1 microtubule motor is not well understood. Using the lysosome adaptor SKIP as model cargo, we show that the heavy chains (KHCs), in addition to the light chains (KLCs), can recognize tryptophan-acidic binding determinants on the cargo when presented in the context of an extended KHC interacting domain. Mutational separation of KHC and KLC binding shows that both interactions are important for SKIP-kinesin-1 interaction *in vitro* and that KHC binding is important for lysosome transport *in vivo*. However, in the absence of KLCs, SKIP can only bind to KHC when autoinhibition is relieved, suggesting that the KLCs gate access to the KHCs. We propose a model whereby tryptophan-acidic cargo are first recognized by KLCs, resulting in destabilization of KHC autoinhibition. This primary event then makes accessible a second SKIP binding site on the KHC C-terminal tail that is adjacent to the autoinhibitory IAK region. Thus, cargo recognition and concurrent activation of kinesin-1 proceed in hierarchical stepwise fashion driven by a dynamic network of inter- and intra-molecular interactions.

INTRODUCTION

Kinesin-1 (also known as conventional kinesin) is a heterotetrameric microtubule (MT) motor that has diverse roles in both neuronal and non-neuronal cells, where it contributes to control the spatial and temporal organization of many cellular components by virtue of its ability to interact with different cargoes and drive their translocation towards the (+)-end of MTs (Fu and Holzbaur, 2014; Vale, 2003; Vale et al., 1985; Verhey and Hammond, 2009b). Kinesin-1 is hijacked by pathogens including vaccinia virus, herpes viruses and HIV-1 during infection, as well as bacteria that replicate inside the cell such as *Salmonella* (Boucrot et al., 2005; Dodding and Way, 2011; Dumont et al., 2010). It also plays a role in several neurological conditions including Alzheimer's disease and Hereditary Spastic Paraplegia (Bayrakli et al., 2015; Morihara et al., 2014). Understanding how kinesin-1 interacts with its cargoes and how it is regulated is important for determining its role in both normal cell function and pathological conditions.

Heterotetrameric kinesin-1 is comprised of two heavy chains (KHCs - *Kif5A*, *Kif5B* or *Kif5C*), which at their amino terminus, contain a motor domain which possesses MT stimulated ATPase activity, and two light chains (KLCs - *KLC1-4*), which play an important role in regulation and cargo recognition. An extended series of coiled coils mediate dimerization of the KHCs (Hackney, 2007). The carboxy-terminal region of KHC is largely unstructured. In the absence of cargo binding, kinesin-1 is autoinhibited. This folded, compact state prevents unnecessary cycles of ATP hydrolysis. A C-terminal isoleucine-alanine-lysine (IAK) from a single KHC tail binds at the interface between the two motor domains. This acts to cross-link the motor domains, preventing movement of the neck linker region that is required for ADP release (Dietrich et al., 2008; Friedman and Vale, 1999; Hackney and Stock, 2000; Hackney et al., 2009; Kaan et al., 2011; Wong et al., 2009). Cargo binding relieves autoinhibition and results in a more elongated structure that is able to hydrolyze ATP and move along MTs (Blasius et al., 2007; Cai et al., 2007; Friedman and Vale, 1999; Hackney et al., 1992; Kawano et al., 2012).

The KLCs interact with the KHC through a series of heptad repeats (Diefenbach et al., 1998). A highly charged unstructured linker region connects this KHC-binding region to a tetratricopeptide repeat (TPR) domain which is followed by a variable C-terminal domain that differs between KLC isoforms. As well as binding to cargoes, the KLCs are thought to regulate KHC autoinhibition (Cai et al., 2007; Friedman and Vale, 1999; Fu and Holzbaur, 2014; Verhey et al., 1998; Wong and Rice, 2010). We recently described how a leucine-phenylalanine-proline (LFP) motif in the unstructured KLC linker region engages in a second autoinhibitory interaction, *in cis*, with the adjacent TPR domain, to control its interaction with a subset of cargoes. This motif acts as a molecular switch to control the conformational state of the light chains and the activity of the motor (Yip et al., 2016).

Vesicular cargoes interact with kinesin-1 via adaptor proteins that can bind to several sites on both KHCs and KLCs (Gindhart, 2006; Hammond et al., 2008; Sun et al., 2011; Watt et al., 2015; Woźniak and Allan, 2006). Cargo recognition by KLCs is accomplished, in part, through interaction of their TPR domains with short linear peptide ‘W-acidic’ peptide motifs that are found in many cargo adaptors including calsynenin-1/Alcadein (CSTN1), SKIP (SifA-kinesin interacting protein), nesprin-2, gadkin, vaccinia virus A36R, cayman ataxia protein (BNIP-H) and dynein intermediate chain (Aoyama et al., 2009; Araki et al., 2007; Dodding et al., 2011; Kawano et al., 2012; Konecna et al., 2006; Pernigo et al., 2013; Rosa-Ferreira and Munro, 2011; Schmidt et al., 2009; Twelvetrees et al., 2016; Verhey et al., 2001; Wilson and Holzbaur, 2015; Zhu et al., 2012). W-acidic motifs are characterized by a central tryptophan (W) residue that is typically flanked by aspartate (D) or glutamate (E) residues and often preceded by a leucine/methionine (L/M) residue at the W (-2) position.

Fusion of these W-acidic motifs to otherwise non-kinesin-1 binding proteins is sufficient to promote kinesin-1 dependent transport/dispersion of specific cellular compartments, such as lysosomes (Dodding et al., 2011; Kawano et al., 2012; Pu et al., 2015). This has also become a useful tool to target cargoes, in a kinesin-1 dependent manner, through the pre axonal exclusion zone (Farías et al., 2015). Together these studies indicate that KLC binding to W-acidic motifs results in sufficient recruitment and relief of kinesin-1 autoinhibition to allow transport. However, other reports have clearly demonstrated that multiple contacts between cargo and both KHCs and KLCs are important for full motor activity (Blasius et al., 2007; Fu and Holzbaur, 2013; Fu and Holzbaur, 2014; Verhey and Hammond, 2009a). We therefore sought to examine whether KHC-cargo binding contributes to the capacity of W-acidic motif containing proteins to recruit kinesin-1 and drive cargo transport.

Here, we use the lysosome, melanosome and lytic granule cargo adaptor SifA-Kinesin-1 Interacting Protein (SKIP or PLEKHM2), that is mutated in hereditary cardiovascular disease, as a model cargo (Ishida et al., 2015; Muhammad et al., 2015; Rosa-Ferreira and Munro, 2011; Tuli et al., 2013). We show that KHCs, in addition to KLCs, can recognize W-acidic motifs on cargo when presented in the context of an extended interacting domain. In SKIP, both KHC and KLC binding sequences are integrated into a kinesin-1 binding cassette. Mutational separation of KHC and KLC binding shows that both interactions are important for SKIP-kinesin-1 interaction *in vitro* and that KHC binding is important for lysosome transport *in vivo*. We propose a model where KLCs first recognize the W-acidic motif on cargo, resulting in destabilization of KHC autoinhibition (Kawano et al., 2012; Pernigo et al., 2013; Yip et al., 2016). This makes accessible a second binding site in the C-terminal tail of KHC adjacent to the autoinhibitory IAK region, which then acts to reinforce the motor-cargo interaction and promote efficient transport.

RESULTS

The W-acidic motif containing kinesin-1 adaptor protein SKIP, but not CSTN1, interacts directly with the C-terminal cargo binding tail of KHC.

Several studies have indicated that cargo binding to both KHC and KLC may be important to fully activate kinesin-1 and drive efficient (+)-end directed transport (Blasius et al., 2007; Fu and Holzbaur, 2013; Sun et al., 2011; Watt et al., 2015). We tested whether the W-acidic cargo proteins SKIP and calsyntenin-1 (CSTN1), which bind to the TPR domain of KLC, could also interact with the cargo-binding C-terminal tail region of KHC. We found that the C-terminal tail of KHC (Kif5C, amino acids 815-955) fused to GST pulled down the N-terminal region of GFP-SKIP(1-310) (that includes its tandem W-acidic motifs) from 293T cell extracts, but not the equivalent cytoplasmic domain of CSTN1(879-971) (Figure 1A,B). GFP-SKIP was also pulled down by the equivalent region of Kif5B (Figure S1A).

To test whether SKIP and interact with KHC directly, SKIP(1-310) was expressed and purified from *E-coli* as a GST fusion protein. The GST moiety was subsequently separated from SKIP(1-310) by cleavage with 3C protease followed by incubation with glutathione beads (Figure S1B). GST-KHC(815-955) (0.5nmol) bound to glutathione beads was incubated with increasing concentrations of SKIP(1-310) in solution. GST alone was used as a control at the highest concentration of SKIP(1-310) tested (3.5 μ M). Complexes were analysed by SDS-PAGE and Coomassie staining (Figure 1C, top). Densitometry analysis from three independent experiments suggested that binding approached saturation at the highest concentration of SKIP(1-310) employed, with an apparent 1:1 stoichiometry. Comparison of band density at 3.5 μ M SKIP(1-310) from the same experiments showed that significantly more SKIP was retained by GST-KHC(815-955) than GST alone (Figure 1C, bottom left). Curve fitting by non-linear regression indicated a dissociation constant (K_d) of approximately 1.5 ± 0.24 μ M (Figure 1C, bottom right), although this value should be interpreted with caution given the non-equilibrium nature of the experiment, potential for avidity effects and relatively high concentration of the GST-KHC(815-955) receptor. Nonetheless, these data clearly demonstrate that SKIP(1-310) interacts directly with the C-terminal tail of KHC.

KHC binds SKIP using residues located between amino acids 876 and 917.

Consistent with the studies of Hackney (Hackney, 2007) and Rice (Seeger and Rice, 2013), analysis of the KHC C-terminal region using Pcoils (Lupas et al., 1991) indicated that most of the KHC tail construct is comprised of a coiled coil or series of coils, which terminate between amino acids 900 and 910. Further analysis using Disopred3 (Jones and Cozzetto, 2015) suggests that the

most C-terminal region is unstructured (Figure 2A). We performed GST-pull down experiments using a series of N- and C-terminal truncations of GST-KHC(815-955) (Figure 2B) to determine where SKIP binds on KHC. Removal of the C-terminal unstructured region (amino acids 918-955), that includes the autoinhibitory IAK motif, did not affect binding to SKIP(1-310) when compared to the longest KHC construct (Figure 2C, compare lanes 2 and 3). Amino acids 815-875 are also dispensable because a construct comprising residues 876-917 bound SKIP(1-310) to a similar extent as the longest construct (Figure 2C, compare lanes 2 and 6), whereas further N-terminal truncation to 891 dramatically reduced binding (Figure 2C, compare lanes 6 and 7).

In a separate experiment, C-terminal truncation of an 815-917 construct to 815-907 also resulted in a reduction in binding (Figure 2D, compare lanes 2 and 3 and graph columns 2 and 3). Taken together, these data show that the key binding determinants for the KHC-SKIP(1-310) interaction reside within the predominantly coiled coil region between amino acids 876 and 917 on KHC. This segment has previously been implicated in the binding of a number of kinesin-1 cargoes including TRAK2, the Kv3 (Shaw) voltage gated K⁺ channel, Fez1 and HAP1 (Barry et al., 2013; Blasius et al., 2007; Randall et al., 2013; Twelvetrees et al., 2010).

The KHC binding site on SKIP overlaps the W-acidic light chain binding site

To determine the KHC binding site on SKIP, SKIP(1-310) and a series of C-terminal truncations (1-276, 1-260, 1-243, 1-216 and 1-202) (Figure 3A) were expressed in *E. coli* as N-terminally His₆-tagged proteins and were purified by Ni²⁺-affinity chromatography (Figure 3B). Pull-down assays were used to assess the KHC-SKIP interaction and analysed by western blot using an anti-His₆-tag antibody. Consistent with our previous experiments indicating a direct interaction between KHC and SKIP, His₆-SKIP(1-310) was bound by GST-KHC(815-955) but not GST alone (Figure 3C, compare lanes 1 and 7). We also observed that C-terminal truncation of SKIP to amino acid 276 appeared to enhance binding (Figure 3C, lane 8). However, this was dramatically reduced when this construct was further truncated to residue 216 (lane 11) which removes the second W-acidic motif of SKIP (WE). Binding was further reduced by truncation to residue 202, which removes the first W-acidic motif (WD) (lane 12). These data suggest that an extended region of SKIP, encompassing, but not limited to, its W-acidic motifs, contributes to KHC binding. To confirm these findings, the assay was repeated using the same GFP-tagged SKIP proteins expressed in HEK293T cells. GST-KHC(815-955) did not pull down GFP alone but did efficiently pull down GFP-SKIP(1-310) (Figure 3D, lanes 2 and 3). Supporting the conclusions from the direct binding experiments, C-terminal truncation of GFP-SKIP(1-310) to residue 260 (lane 5) enhanced the interaction, whereas further truncation from residue 243 (lane 6) to 216 (lane 7) eliminated any detectable interaction in this assay.

The above data imply that the KHC and KLC binding sites on SKIP overlap. To test this, we performed a competition experiment where increasing concentrations of purified recombinant

KLC2 TPR domain (218-480, KLC2^{TPR}) were added to 293T cell extracts where GFP-SKIP(1-310) was overexpressed. Binding to KHC was then examined by GST-pulldown (Figure 3E). Addition of KLC2^{TPR} reduced binding to GST-KHC(815-955) in a concentration dependent manner (Figure 3E, left). This required a direct interaction between KLC2^{TPR} and SKIP(1-310) because the N287L variant that disrupts the W-acidic SKIP binding site on KLC2^{TPR} (Pernigo et al., 2013) did not inhibit the SKIP-KHC interaction (Figure 3E, right).

The data described above demonstrate a crucial role for an extended region of SKIP that includes the two W-acidic motifs. We used a fluorescence polarisation (FP) binding assay to test this directly. Using a TAMRA conjugated peptide comprising the two W-acidic motifs of SKIP (Pernigo et al., 2013), titration of a KHC construct comprising amino acids 866-917 revealed a concentration dependent and saturable increase in FP (Figure 4A). The resultant data fit best to a specific binding model with Hill slope (h), with an equilibrium dissociation constant of 7.8 μ M and a h value of 4, indicating positive cooperativity. Together these data clearly demonstrate a role for the W-acidic motif containing KLC binding segment of SKIP in KHC-SKIP interaction, but also suggest that residues outside of this region may also play a role in the interaction. The fact that binding is enhanced by truncation of SKIP(1-310) to residues 276 and 260 may also suggest the presence of a negative regulatory element within this region of the protein.

SKIP W-acidic motifs are an important determinant for KHC binding

As both W-acidic motifs of SKIP (WD and WE) are present in a minimal KHC interacting region on SKIP (Figure 4A), we assessed their contribution to binding directly. Pull-down of GFP-SKIP(1-310) and SKIP mutants (WD/AA, WE/AA, and WDWE/AAAA) from 293T cell lysates using GST-KHC(815-955) showed that binding is dramatically reduced upon making alanine substitutions in either or both of the SKIP W-acidic motifs (Figure 4B). It is possible that this interpretation may be confounded by endogenous KLC in the cell lysates, although unlikely given the typically low expression of KLCs in non-neuronal cells when compared to overexpressed protein. To verify that what we observed is a direct effect, we performed equivalent experiments where both proteins were produced in *E.coli*. GST-pulldown experiments using His-SKIP(1-310) and SKIP variants (WD/AA, WE/AA, and WDWE/AAAA) with GST-KHC(815-955) or GST alone again showed that binding is reduced upon making alanine substitutions in the SKIP W-acidic motifs (Figure 4C). The fact that there is no additive effect from making both substitutions may suggest that both motifs act together in the same binding mechanism.

Interaction between SKIP and KHC requires relief of KHC autoinhibition

Having established some key binding determinants on both KHC and SKIP, we next examined the interaction of SKIP with the full length KHC and the kinesin-1 complex. To confirm that overexpressed KHC and KLC form a complex, 293T cells were transfected with N-

terminally citrulline (mCit, a GFP derivative) tagged KHC (Cai et al., 2007) and HA-KLC2, or as a control GFP and HA-KLC2. Co-transfection of mCit-KHC with HA-KLC2 resulted in an increase in HA-KLC2 expression compared to co-transfection with GFP (Figure 5A, compare lanes 1,2). Cit-KHC was bound (lane 4) and efficiently depleted from cell extracts (compare lanes 2 and 6) using GFP-TRAP beads. HA-KLC2 co-immunoprecipitated with Cit-KHC, but not GFP (lanes 3,4), resulting in its total depletion from the cell extracts (compare lanes 2 and 6). Together, these data show that essentially all of Cit-KHC and HA-KLC2 are in complex. Next, GST-tagged SKIP(1-310) was purified from *E.coli* and bound to glutathione beads. GST-SKIP(1-310) beads (or control GST beads) were incubated with 293T cell extracts expressing N-terminally citrulline (Cit, a GFP derivative) tagged KHC (Blasius et al., 2007) alone or Cit-KHC coexpressed with either wild-type or the N287L/R251D mutants of HA-KLC2 that disrupt binding to SKIP (Pernigo et al., 2013). As expected, when co-expressed, both HA-KLC2 and Cit-KHC were pulled down efficiently by GST-SKIP(1-310) (Figure 5B, lane 6), but not by GST alone (lane 2), from extracts expressing wild-type KLC2. Consistent with Figure 5A, co-expression of KLC with KHC also results in an increase in KHC expression (lanes 5 and 6). Disruption of the W-acidic binding site on KLC using the N287L/R251D mutations dramatically reduced binding of the kinesin-1 complex KLCs, confirming that KLC interactions are important for SKIP-kinesin-1 interaction. (lanes 7 and 8). Surprisingly, however, we were unable to detect an interaction between GST-SKIP(1-310) and KHC in the absence of KLC (lane 5). We reasoned that this may be caused by KHC autoinhibition limiting access to the SKIP binding site that lies adjacent to the KHC IAK motif. To test this hypothesis, nine residues of the autoinhibitory IAK sequence were mutated to alanine (QIAKPIRPG/AAAAAAAA) to disrupt the binding of the C-terminal tail to the motor domain of KHC and prevent autoinhibition (Dietrich et al., 2008; Hackney and Stock, 2000). HA-KHC constructs were expressed in 293T cells and binding to SKIP(1-310) analyzed by GST-pulldown (Figure 5B). When the IAK sequence is disrupted, GST-SKIP(1-310) bound to full length KHC, suggesting that interaction with SKIP requires relief of KHC autoinhibition.

Specific disruption of SKIP-KHC binding reduces its capacity to associate with the kinesin-1 tetramer.

The data described above show that amino acid residues 202-241 of SKIP contains both KLC and KHC binding sites, although they also suggest additional role in KHC binding for sequences outside of this region. Moreover, KLC and KHC interactions share some determinants because mutation of the first W-acidic motif (WD/AA) in SKIP not only disrupts KLC binding but also inhibits SKIP binding to KHC. However, mutation of the second, WE, motif in SKIP (WE/AA) has no effect on KLC binding (Pernigo et al., 2013) but does disrupt interaction with KHC. This suggests that other residues within this region may also be differentially required for KLC and KHC binding. Interestingly, a naturally occurring splice variant of SKIP, where exon 7 is deleted,

results in removal of residues 219-238 (highlighted in green in Figure 6A) (Rosa-Ferreira and Munro, 2011). This splice variant has a reduced capacity induce lysosome dispersion (Rosa-Ferreira and Munro, 2011) suggesting that this could, in part, be due to its reduced KHC binding capacity. We therefore sought to identify mutations in SKIP that reduced KHC but not KLC binding using an alanine scanning approach targeting 3/4 amino acid clusters within exon 7 of SKIP. 293T cells were transfected with plasmids designed to express green fluorescent protein (GFP)-tagged SKIP, or SKIP alanine mutants (WD (control for KHC and KLC), EDY, DFG, DVF, PAV, PSV, PSTD, WE, DGD, LTD) or the splice variant with exon 7 deleted (Δ Ex7). The results from this screen showing relative binding to GST-KHC are summarized in Figure 6B and indicated a particularly important role for the EDY(217-219) (Figure 6C, lane 5), DFG(220-222) (lane 6) and DGD(238-240) (lane 8) triplets in addition to the WD and WE motifs (lane 4 and lane 7). Removal of the whole of exon 7 also reduced binding (Figure 6C, lane 9).

To determine whether the amino acid replacements that disrupt SKIP binding to KHC were also important in KLC binding, we performed a GFP-TRAP immunoprecipitation experiment. 293T cells were co-transfected with plasmids designed to express HA-tagged KLC2 and GFP-SKIP(1-310) (either wild type, or carrying alanine substitution at WD, EDY, DFG, WE and DGD or with exon 7 deleted). GFP-SKIP(1-310) was immunoprecipitated with GFP-TRAP beads and the amount of co-immunoprecipitated HA-KLC2 was analysed by Western blot. Co-expression of GFP-SKIP(1-310) with HA-KLC2 (in the absence of KHC) results in stabilization of HA-KLC2 and an increase in relative expression compared to GFP/HA-KLC2 transfected cells (Pernigo et al., 2013). As expected, the WD/AA replacement eliminated binding and suppressed this increase in expression, whereas the WE mutation had no effect (Pernigo et al., 2013) (Figure 6D, lanes 3 and 6). Deletion of exon 7, which encompasses the WE motif and surrounding residues also slightly reduced binding, suggesting that these residues do make some additional contribution to KLC2 binding (Figure 6D, lane 8). However, AAA replacement of EDY, DFG, or DGD triplets (Figure 5D, lanes 4-6) had no effect on expression or the interaction between SKIP and KLC2, confirming that KLC and KHC binding capacity in SKIP is separable.

To determine the effect of independently disrupting SKIP:KHC binding on association of SKIP with the kinesin-1 tetramer, 293T cells were co-transfected with plasmids to express HA-KLC2 and HA-KHC. Pull-down of HA-KLC and HA-KHC from 293T cell lysates using GST-SKIP(1-310) or GST-SKIP(1-310) carrying alanine substitutions in KHC binding residues (EDY, DFG, WE, DGD) confirmed a key role for the EDY or DFG residues (Figure 6E, lanes 3 and 4), although the mutation the WE or DGD residues had little obvious effect on binding in this assay.

To determine whether mutations in SKIP that disrupt interactions with the kinesin-1 tetramer also affect its ability to promote the association of kinesin-1 with MTs, HeLa cells were transfected with GFP, GFP-SKIP (1-310) or GFP-SKIP(1-310) carrying alanine substitutions in WD, WE, EDY or DFG residues. Cells were lysed in a MT stabilizing buffer and subjected to

ultracentrifugation to pellet intact MTs. Consistent with a capacity to promote kinesin-1-MT association, expression of GFP-SKIP promoted an increase in the amount of KHC and KLC in the MT fraction (Figure S2) (compare left blot lanes 2 and 4 and right blot lanes 10 and 12). KHC and KLC in the pellet was reduced by the WD/AA, WE/AA, EDY/AAA and DFG/AAA mutations in SKIP (lanes 6, 8, 14, 16).

Collectively, these experiments show that the capacity for SKIP to interact specifically with KHC is important for maintaining a stable interaction with kinesin-1 tetramer under conditions where KLC binding is not perturbed.

Addition of SKIP-KHC specific binding determinants to the C-terminus of CSTN1 promotes KHC binding in a CSTN WD motif dependent manner

Next we sought to test directly whether the KHC binding determinants we had identified in SKIP that follow its WD motif, were sufficient to impart KHC binding capacity on CSTN1, which does not bind KHC. Taking advantage of the fact that the second WD motif of CSTN1 is positioned close to its C-terminus, a series of CSTN1-SKIP chimeras were engineered which incorporate the cytoplasmic domain of CSTN1 fused N-terminally to GFP, followed by KHC binding region of SKIP beginning at S215 (thus excluding the SKIP WD motif)(Figure S3). This places the second WD motif of CSTN1 in a similar relative sequence position. The chimeras terminated at either residue 241 in SKIP (named GFP-CSTN1-SKIP(short)) or residue 260 in SKIP (named GFP-CSTN1-SKIP(long)). The GFP fusion proteins were expressed in 293T cells and their ability to bind to GST-KHC(815-955) was assessed by pull down and western blot. As expected, GFP-SKIP (lane 2) but neither GFP (lane 1) or GFP-CSTN1 (lane 3) bound to GST-KHC, however, inclusion of amino acids 215-241 of SKIP resulted in the retention of GFP-CSTN1-SKIP(short) (lane 4) and, (consistent with our truncation experiments (Figure 3D)) binding was further enhanced by extension of the SKIP component of the chimera to residue 260 (lane 5). As expected, mutation of the KHC binding EDYDFG cluster in SKIP prevented the interaction (lane 6). In addition, the interaction was also disrupted by mutation of the second WD motif of CSTN1 (lane 7). Thus, the second WD motif of CSTN1 is functionalized as a KHC binding determinant by being placed in the context of additional SKIP-KHC specific binding determinants.

Specific disruption of SKIP-KHC binding capacity reduces its ability to promote the dispersion of lysosomes

Identification of the residues that specifically disrupted SKIP binding to KHC offered an opportunity to determine their functional role in kinesin-1 dependent transport. Expression of full-length SKIP in HeLa promotes kinesin-1 recruitment to lysosomes and their translocation to the cell periphery (Figure 7A) (Rosa-Ferreira and Munro, 2011). This provides a useful assay to assess kinesin-1 dependent SKIP function. As the intracellular distribution of lysosomes does vary

from cell to cell, we used an unbiased quantitative approach to assess the extent of this effect. The cell is segmented into scaled percentile regions and cumulative LAMP1 distribution from the inner to peripheral regions is measured. A shift of the curve to the right indicates relative dispersion. Curve fitting and analysis using the extra sum of F-squares test allows statistical comparison of the datasets (Figure 7B)(Starling et al., 2016). As expected, mutation of the SKIP WD motif (which reduces both KHC and KLC binding), or mutation of the WD and WE motif together, essentially eliminated the capacity of SKIP to promote the dispersion of lysosomes (Figure 7A) (Rosa-Ferreira and Munro, 2011). Representative confocal fluorescence images of the lysosomal distribution are shown in Figure 7A. To determine the effect of SKIP mutations shown to disrupt KHC, but not KLC, binding to SKIP on the distribution of lysosomes, HeLa were transfected with myc-SKIP, SKIP triplet AAA variants (EDY, DFG, WE, DGD), or the Δ Ex7 splice variant. Transfection with the KHC specific EDY, DFG or DGD AAA-mutations significantly reduced their capacity to promote lysosomal dispersion in a manner that correlated well with their capacity to interact with the kinesin-1 tetramer (Figure 7A,B and Figure 6E) demonstrating a key role for KHC binding in SKIP-induced late endosome/lysosome dispersion.

DISCUSSION

Despite its key role in wide range of cellular processes and human diseases, the molecular mechanisms that allow kinesin-1 to recognize its cargoes, and how cargo binding then subsequently regulates kinesin-1 activity are not well understood. Here, using SKIP as a model cargo adaptor, we have further explored these mechanisms and examined how they are coupled to drive efficient MT transport. We have shown that KHCs, in addition to KLCs, can recognize W-acidic based determinants on cargo, but only when presented in the context of an extended interacting sequence. In SKIP, both KHC and KLC binding determinants are integrated into a kinesin-1 binding cassette. Mutational separation of KHC and KLC binding shows that both interactions are important for SKIP-kinesin-1 interaction *in vitro* and KHC binding contributes to lysosome transport *in vivo*. Interaction between full length KHC and SKIP does not occur without the relief of KHC autoinhibition. Taking this analysis with our previous work and that of others, we propose that the KLCs first recognize W-acidic cargo, causing a conformational change in KLC (Yip et al., 2016) that results in destabilisation of KHC autoinhibition (Kawano et al., 2012; Yip et al., 2016). This makes accessible the second SKIP binding site in the C-terminal tail of KHC that is adjacent to the autoinhibitory IAK region. Binding of SKIP to this secondary KHC site then acts to reinforce the motor-cargo interaction, maintain KHC in its active state, and so promote efficient transport (Figure S4).

Although the cargo binding tail of KHC and the TPR domains of KLC share no sequence similarity or structural homology, they can both recognize the same determinants on cargo. Our previous work demonstrated that the KLC^{TPR} interaction with W-acidic motifs is driven by sequence specific interactions with hydrophobic leucine and aromatic tryptophan residues combined with a large electrostatic component, where negatively charged aspartate and glutamate residues within W-acidic motif make a network of hydrogen bond and salt bridge contacts with arginine and lysine residues on the concave groove of the TPR domain (Pernigo et al., 2013). In this context, it is interesting to note that a minimal SKIP-KHC/KLC interacting cassette lacks any predicted secondary structure is also highly negatively charged with a predicted isoelectric point (pI) of 3. A similar analysis of the minimal SKIP binding region of KHC(876-917) reveals it to be highly positively charged with a predicted isoelectric point higher than 10. Thus, it seems likely that electrostatic interactions will also play an important role in KHC-cargo recognition. Consistent with this notion, the minimally-defined KHC binding regions of three other cargoes that interact with this region of KHC: TRAK2, Kv3.1T1, and HAP1 (Barry et al., 2013; Randall et al., 2013; Twelvetrees et al., 2010), also have a low predicted isoelectric points of approximately 4.3, 4.5 and 4.2 respectively and in the case of Kv3.1 T1, a basic RKR triplet in KHC(892-894) was essential for binding. It is interesting to note that Kv3.1 T1, but not the equivalent domains of related ion channels that do not bind to KHC (Xu et al., 2010), contains a highly electronegative, unstructured (as predicted by Disopred3) region (sequence

DSFGGAPLDNSADDADADGPGDSDGDELEMTKRLALSDS, pI 3.25). Similarly, HAP1 contains a negatively charged unstructured region (sequence DSDDDDDEEDEDEEEEGEEEEEREGQRDQDQQHDHPYGAPK, pI 3.72) that resides between the first and second coiled coils within its minimal KHC binding domain (Twelvetrees et al., 2010). Moreover, kinesin-1 can bind and transport negatively charged beads in the squid giant axon (Seamster et al., 2012; Terasaki et al., 1995). However, amino acid sequence, in addition to charge, can also make a contribution in this system because beads coated with a C-terminal peptide from amyloid precursor protein (SEQ: GYENPTYKFFEQMQN, pI 4.5) were transported more efficiently than beads coated with the same sequence scrambled (Seamster et al., 2012)

The data presented here show that whilst SKIP interacts with KHC, another W-acidic motif containing protein, CSTN1 does not. Neither does CSTN1 possess a motif resembling the EDYDFG cluster found in SKIP that is important for KHC binding. Thus, KHC binding is not a universal feature of W-acidic motif containing proteins, but instead depends upon the sequence context in which W-acidic motifs are presented. This notion is supported by the fact that the second CSTN1 WD motif becomes a determinant for KHC interaction, when fused to SKIP (Figure S3). Our competition experiments strongly suggest that SKIP cannot bind both KHC and KLC simultaneously (Figure 3E). Two possible models present themselves. In both, SKIP first interacts with the TPR domain of KLC, which results in a conformational change within the light chains that destabilises KHC autoinhibition (Kawano et al., 2012; Yip et al., 2016). This makes accessible the second SKIP binding site on KHC. KLC essentially gates access to KHC. One could then envisage a transfer of cargo from KLC to KHC as both binding affinities are in the low micromolar range or perhaps dynamic exchange of SKIP between the two sites. Alternatively, additional SKIP molecules associated with the surface of the lysosome via Arl8b may bind the newly exposed site. Multiple contacts with the tetramer, would enhance avidity and thus would be predicted to result in a highly stable motor-cargo interaction such as those found on PrPC containing vesicles (Encalada et al., 2011). In the context of CSTN1, a secondary set of KHC contacts could be provided by another adaptor associated with the same vesicles. Alternatively, the presence of two relatively high affinity KLC binding WD motifs in CSTN1 (Araki et al., 2007; Konecna et al., 2006; Pernigo et al., 2013) may act to circumvent the requirement for KHC binding. Indeed, fusion of multiple, sequential WD motifs to Nipah Virus F glycoprotein (NiV-F) resulted in a greater capacity to transport into axons when compared to single motifs (Farías et al., 2015).

Within the context of SKIP function in the transport of lysosomes, melanosomes and lytic granules (Ishida et al., 2015; Rosa-Ferreira and Munro, 2011; Tuli et al., 2013), it is interesting to note that some important KHC binding determinants reside within Exon 7. Whilst full length and Δ Exon7 forms of SKIP are expressed in a wide variety of tissues, their relative expression varies considerably (Rosa-Ferreira and Munro, 2011). Therefore, it may be that the transport activity of

SKIP is controlled by altering its capacity to interact with KHC and that the quite heterogeneous steady state distribution of lysosomes found when comparing different cell types may in part be regulated by this. This would allow cells to tightly control this aspect of SKIP function presumably without perturbing other interactions, for example, with the HOPS complex (Khatter et al., 2015). It would also seem worth investigating whether the relative proportion of these two splice variants is regulated more acutely by signaling pathways that control lysosome and lysosome related organelle transport. W-acidic motifs are also found in neuronal specific splice variants of dynein intermediate chain, where kinesin-1 binding is required for its slow transport down the axon (Twelvetrees et al., 2016) suggesting that alternative splicing of key binding kinesin-1 binding determinants, has a more general application for regulation of cargo attachment. It is tempting to speculate that this inherently modular kinesin-1 binding capacity (Dodding et al., 2011) in the form of an unstructured protein region defined may have evolutionary implications for the acquisition of the capacity of organelles to move on MTs. Alternatively, it also seems possible that such sequences could be generated by mutations that generate aromatic and hydrophobic amino acids in preexisting, negatively charged unstructured regions of proteins.

In summary, we have shown that both KLC and KHC can recognize very closely related determinants on cargo, that in the case of SKIP, are incorporated into a KLC/KHC binding cassette. Both interactions contribute to efficient motor recruitment. These data suggest some shared general principles for both heavy and light chain cargo recognition that both incorporate a significant electrostatic component combined with shared sequence specific elements and indicate that motor-cargo attachment is a dynamic, multi-step process.

METHODS

Plasmids and Cells

Rat kinesin-1 heavy chain (KHC, Kif5C) was obtained as an N-terminally Citruline tagged clone (Cai et al., 2007). The full length of Kif5C was amplified by PCR and subcloned into CB6-HA to express with an N-terminal HA epitope tag. Shorter C-terminal tail fragments were amplified by PCR and subcloned into pMW-GST for expression in *E. coli*. GST vectors contained a 3C protease cleavage site between GST and target protein to allow removal of the affinity tag when required. Myc-SKIP full length and delta Exon 7 constructs were a gift from S. Munro, MRC-LMB, Cambridge. SKIP(1-310) and the indicated truncated variants were amplified from those plasmids and subcloned into pMW-GST, His₆-(pET28-His) or CB6-GFP as required for expression in bacterial (His and GST) and mammalian (GFP) systems. GFP-CSTN(879–971) and HA-KLC2 constructs have been described previously (Pernigo et al., 2013). His-KLC2^{TPR} (218–480) and His-KLC2^{TPR} (218–480) with N287L mutation were described previously (Pernigo et al., 2013). Human Kif5B was obtained from Addgene (15284) and the C-terminal tail fragment (814-963) was amplified by PCR and subcloned into pMW-GST. For expression of SKIP-CSTN chimeric proteins, DNAs encoding the indicated protein sequences were synthesised by Genscript (NJ, USA) and subcloned into CB6-GFP. All mutations were introduced by site-directed mutagenesis and all plasmids were verified by DNA sequencing. HeLa and 293T used in this study were from a verified source and were regularly tested for contamination.

Protein Expression and Purification.

Proteins were expressed in *Escherichia coli* BL21(DE3) cells. Briefly, single colonies were picked and grown at 37 °C overnight. Small-scale overnight bacterial cultures were used to inoculate 4 × 1-L cultures that were incubated at 37 °C until they reached an OD₆₀₀ of 0.5. The temperature was then lowered to 16 °C, and protein synthesis was induced by the addition of 300 μM isopropyl β-D-1-thiogalactopyranoside for 16 h. Cells were harvested by centrifugation at 5,000 × g for 15 minutes at 4 °C. For GST-tagged proteins, cells were resuspended in lysis buffer (25 mM HEPES, pH 7.5, 500 mM NaCl, 5 mM β-mercaptoethanol) supplemented with protease inhibitor mixture (Roche). Lysis buffer containing 20 mM imidazole was used to purify His-tagged proteins. Cell lysis was accomplished by sonication. Insoluble material was sedimented by centrifugation at 16,500 × g for 30 minutes at 4 °C. GST-tagged proteins were obtained via batch purification using Glutathione Sepharose beads (GE Life Sciences), and His-tagged proteins were purified using His-trap FF columns (GE Life Sciences). Purified proteins from both methods were dialyzed overnight against glutathione or imidazole-free lysis buffer, respectively. His-tagged protein samples were further purified by size-exclusion chromatography (SEC) on a 16/60 HiLoad Superdex 75 column (GE Healthcare). As indicated, the GST tag on fusion proteins was removed

by incubating overnight at 4 °C using 3C Protease (GE Healthcare), according to the manufacturers protocol. This was followed by a second, 4 hours incubation with glutathione beads to remove free GST, 3C protease and any residual uncleaved protein.

Immunoprecipitation and GST pull-downs from cell extracts.

Cells were harvested in 1mL lysis buffer (25 mM HEPES pH 7.5, 150 mM NaCl, 0.1% NP-40, 0.1X Triton-X 100 containing a protease inhibitor cocktail (Roche)). Lysates were incubated on ice for 10 minutes prior to centrifugation at 13000 x g for 10 min at 4°C. The resulting supernatant was incubated for 1 ½ hours with the indicated GST-fusion protein (0.25 nmol of protein per reaction, unless otherwise indicated) bound to 20µl Glutathione Sepharose beads or with 15µl of prewashed GFP-Trap beads (ChromoTek). 50µl of supernatant was retained for analysis of cell lysate. 10µl 6x loading buffer was added. Beads were washed four times and boiled in 60µl SDS-loading buffer. 20µl samples were separated on SDS-PAGE gels, transferred onto PVDF membrane, blocked in 5% milk in TBS-T (20mM Tris, 0.25M NaCl, 0.1% Tween-20, pH 7.5 with HCl), and probed with the indicated primary antibodies followed by detection HRP conjugated secondary antibodies. Blots were developed with an ECL kit (Biorad) and chemiluminescent signal detected and quantified using a Bio-Rad XR system and ImageLab software. Antibodies used for western blot: Anti-GFP, Roche, 11814460001, 1:1000; Anti-His, Millipore, 71840; 1:1000, Anti HA, Sigma, HA-7, 1:1000)

Direct binding experiments

GST, GST-KHC⁸¹⁵⁻⁹⁵⁵ or variants (0.5 nmol of protein per reaction) bound to Glutathione Sepharose beads was incubated with 300 µL of 1.2 µM SKIP(1-310) or variants for 2 h at 4 °C. Beads were washed four times with 1mL assay buffer (25 mM Hepes, pH 7.5, 150 mM NaCl, 5 mM β-mercaptoethanol) or assay buffer containing 20 mM imidazole when using His-tagged proteins. Beads were resuspended in 50 µL of buffer and 10 µL of 6x SDS-loading buffer before boiling. Twenty microliters of each sample were loaded, and the SDS/PAGE gel was stained with InstantBlue Protein Stain (Expedeon) or analysed by western blot as described above.

Immunofluorescence

Hela cells were plated at a density of 1 x 10⁵ per well on fibronectin-coated glass cover slips in a 6 well plate 6 hours prior to transfection. Cells were transfected with 0.8µg SKIP DNA (CB6 expression vectors) using Effectene transfection reagent (Qiagen). The cells were then incubated at 37°C for 16 hours. Cells were fixed at -20°C with 100% methanol for 10 minutes. This was followed by blocking with 1% BSA in PBS for 20 minutes. Cells were washed three times with PBS. Cells were then probed with the appropriate antibody (LAMP1, Cell Signaling, D2D11, 1:200) (anti-Myc, Sigma, 9E10, 1:400) diluted in blocking solution (1% BSA in PBS). After 2

hours at room temperature, cells were washed three times for 5 minutes each with PBS followed by incubation with a secondary fluorescent conjugated antibody (in blocking solution) for 30 minutes. Coverslips were washed 3 more times with PBS, placed cell side down in fluor save reagent (Calbiochem). Widefield fluorescence images were collected using a Zeiss Olympus IX-81 microscope with a 40x objective running Metamorph. Confocal images were collected using a Nikon A1 system with a 100x objective running NIS Elements.

Quantification of lysosome distribution.

To quantify lysosome distribution, widefield images were acquired at a 40x magnification. The cell perimeter was defined by thresholding equivalent saturated images and the area was scaled at 10% decrements using ImageJ. The image was binarised and the cumulative LAMP-1 distribution (relative to the whole cell) was then plotted for increasing incremental deciles. Data points are from a minimum of 45 cells in 3 replicates and are representative of at least 3 independent experiments. For analysis of the resulting data, the non-linear regression function in Graphpad Prism was used to fit a centered 6th order polynomial. To compare models and assess the statistical significance of differences in distribution profiles, the extra sum of F-squares test was applied. P values for particular comparisons are indicated on the graphs.

Fluorescence polarisation.

N-terminal carboxytetramethylrhodamine (TAMRA) conjugated peptide used for fluorescence polarization measurements

(TAMRA-SKIPWDWE: STNLEWDDSAIAPSSDYDFGDVFPVPSVPSTDWEDGDL

was supplied by BioSynthesis (Lewisville, TX, USA). Measurements were performed on a Horiba Fluoromax-4 spectrofluorometer as described previously (Yip et al., 2016).

Cellular kinesin-1/MT pelleting assay

To determine the capacity of SKIP promote association of the kinesin-1 tetramer with MTs, 0.5 X 10⁶ HeLa cells were plated onto a 10 cm dish and co-transfected the next day with HA-KHC and HA-KLC as well as a GFP, or GFP-SKIP 1-310 (WT, WD/AA, WE/AA, EDY/AAA or DFG/AAA). Cells were lysed 24 hours post-transfection in 3 ml of MT stabilization buffer (100 mM PIPES pH 6.9, 5 mM MgCl₂, 1 mM EGTA, 30% (v/v) glycerol, 0.1% (v/v) Nonidet P40, 0.1% (v/v) Triton X-100, 0.1% (v/v) Tween-20, 0.1% (v/v) β-mercaptoethanol, 100 μM GTP and 20 μM taxol) supplemented with protease inhibitors. 1 ml of lysate was subjected to ultracentrifugation to pellet intact MTs (100 000 xg, 30 minutes, 37 °C). Supernatant containing the soluble tubulin fraction was removed into a microfuge tube with 5X SDS sample buffer. 5X Sample buffer was also added to the pellet fraction followed by dilution with 1 ml of MT stabilisation buffer. 20 μL of each fraction were separated by SDS-PAGE electrophoresis,

immunoblotted and subjected to densitometric quantitation. Data presented are the mean of 3 independent experiments.

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Author Contributions

A.S., Y.Y.Y., S.P. and M.P.D. performed experiments. A.S., R.A.S., and M.P.D. designed and interpreted experiments, M.P.D. wrote the paper.

Competing Interests

No competing interests declared.

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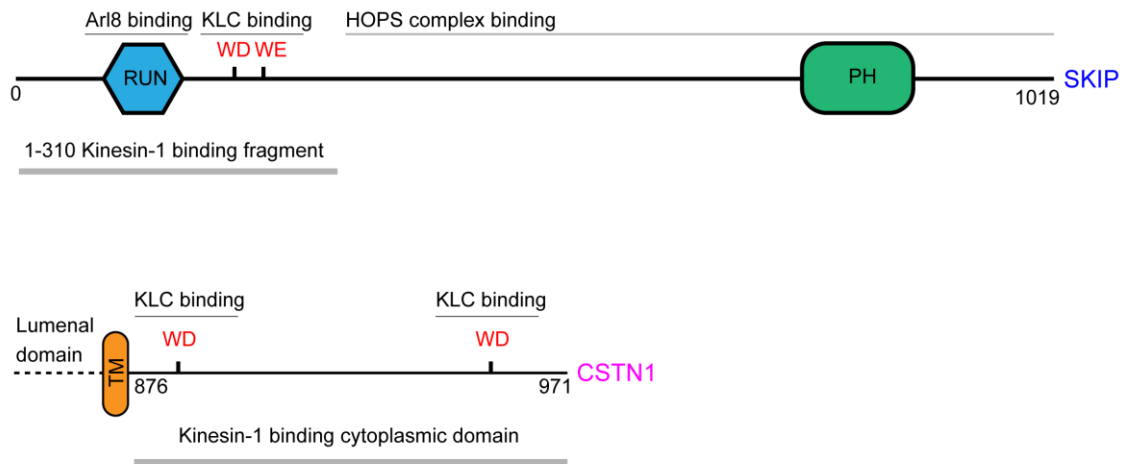
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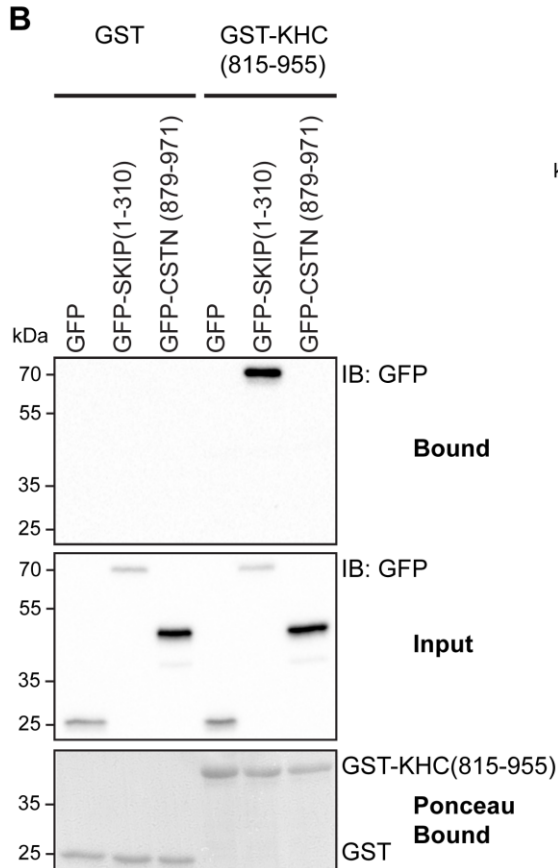
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Figures

A



B



C

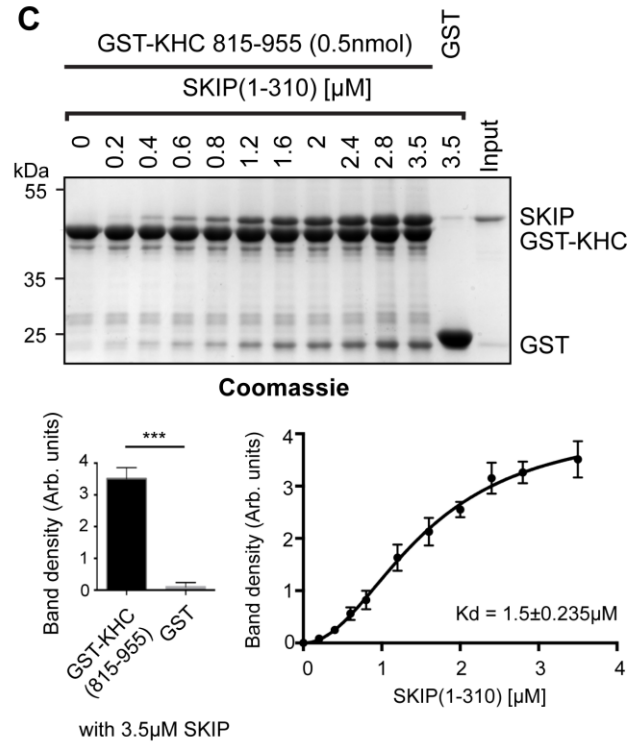


Figure 1. SKIP interacts directly with KHC

(a) Schematic showing domain organisation of SKIP and CSTN1

(b) Western blot showing that GST-KHC(815-955) retains GFP-SKIP(1-310) from 293T cell extracts but not the cytoplasmic domain of CSTN1(879-971). Data are representative of 3 independent experiments.

(c) (top) Coomassie stained SDS-PAGE gel showing from a GST-pull down experiment showing a direct interaction between GST-KHC(815-955) and SKIP(1-310). (bottom left) Graph showing relative binding of SKIP(1-310) to GST or GST-KHC(815-955) at the 3.5 μ M concentration from (top). Data is mean of independent experiments and error bars show \pm S.E.M. *** = $p < 0.001$ using a 2-tailed t-test. (bottom right) Graph showing quantification of SKIP(1-310) band density from (top) from 3 independent experiments, error bars show \pm S.E.M., fitted to a one site specific binding model with hill slope (EQ $Y=B_{max} * X^h / (K_d^h + X^h)$ where $B_{max} = 4.23$, $K_d = 1.53$, $h = 2.04$, $R^2 = 0.98$).

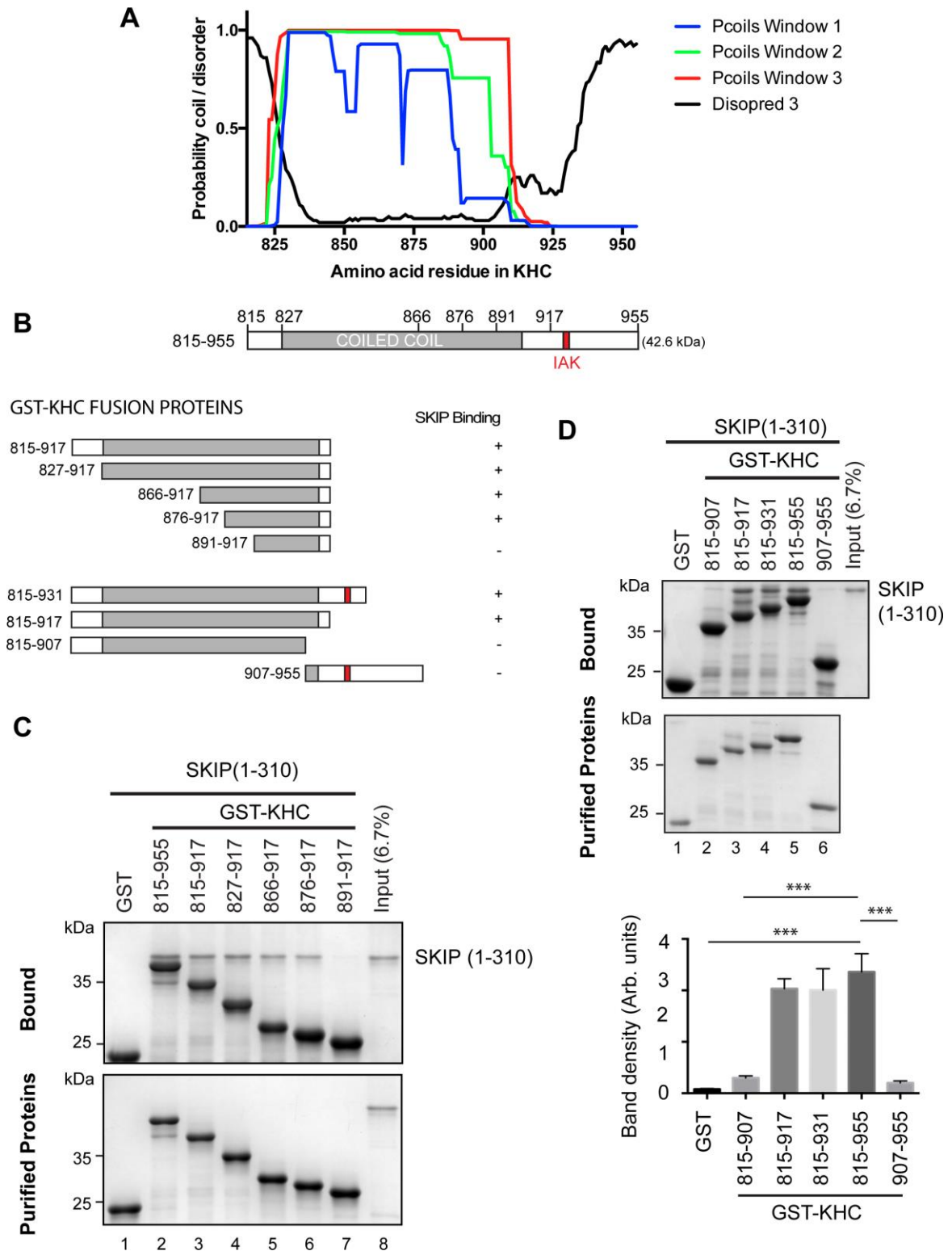


Figure 2. SKIP-KHC interaction requires amino acids 876-917 of KHC

(a) Graph and schematic showing structure predictions from Pcoils and Disopred3 for the C-terminal region of KHC. The location of the autoinhibitory IAK motif is highlighted.

(b) Schematic of constructs used in this figure with summary of SKIP(1-310) binding capacity.

*** indicates minimally defined SKIP binding segment of KHC.

(c) Coomassie stained SDS-PAGE gels from a GST-pull down experiment using a series of truncations of KHC showing that amino acids 876-917 are sufficient for SKIP¹⁻³¹⁰ binding. Data are representative of 3 independent experiments.

(d) Coomassie stained SDS-PAGE gels from a GST-pull down experiment using a series of truncations of KHC showing that amino acids 908-917 are required for SKIP¹⁻³¹⁰ binding. Graph shows quantification of relative binding from 3 independent experiments. Error bars show \pm S.E.M. ** = $p < 0.01$, *** = $p < 0.001$ using one-way ANOVA and Dunnett's multiple comparison test for comparison to 815-955.

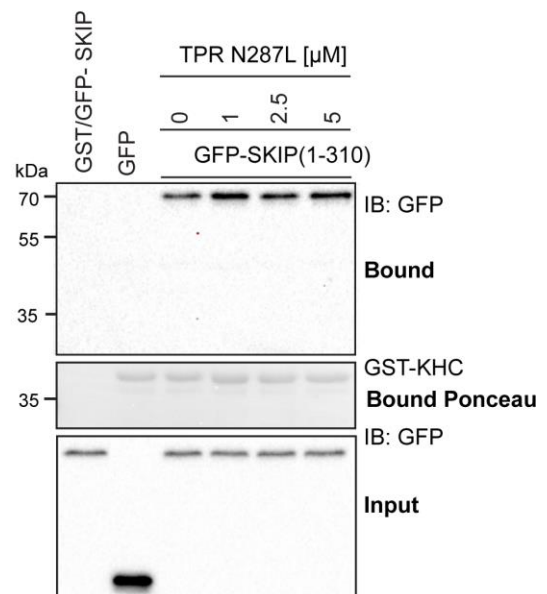
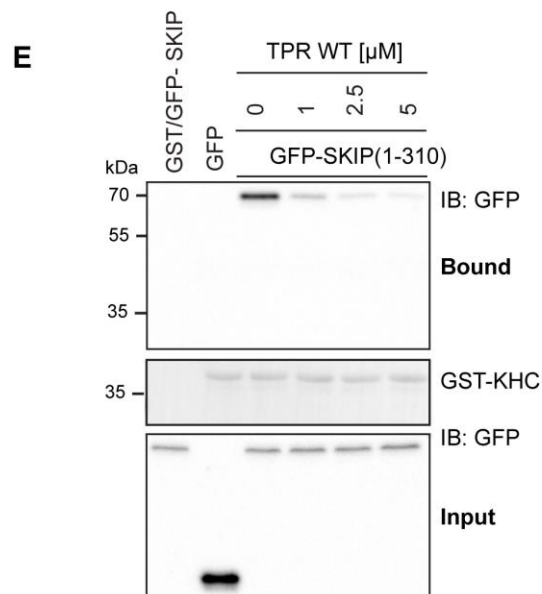
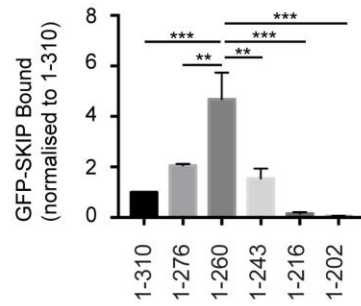
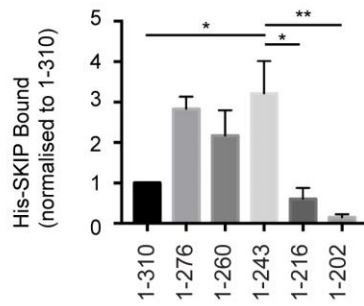
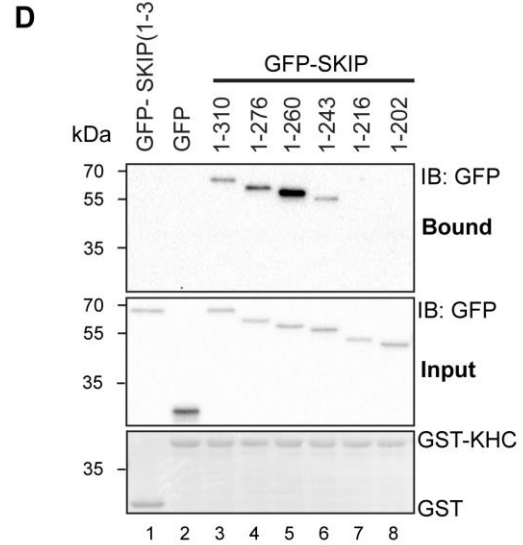
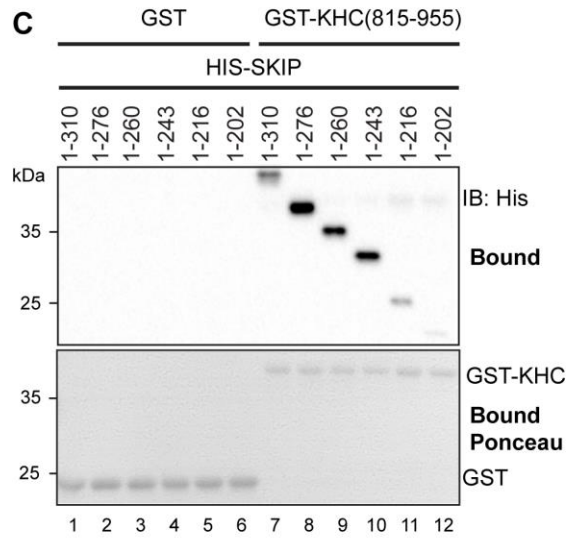
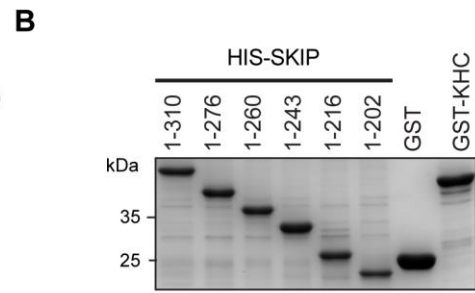
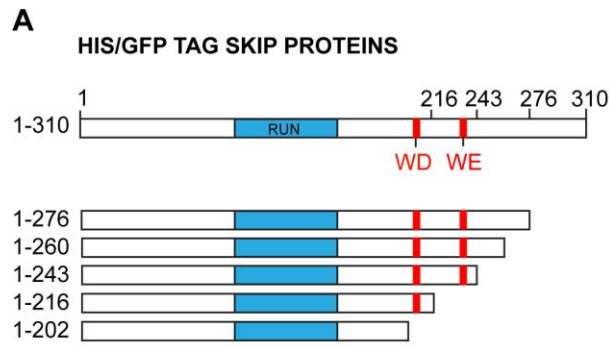
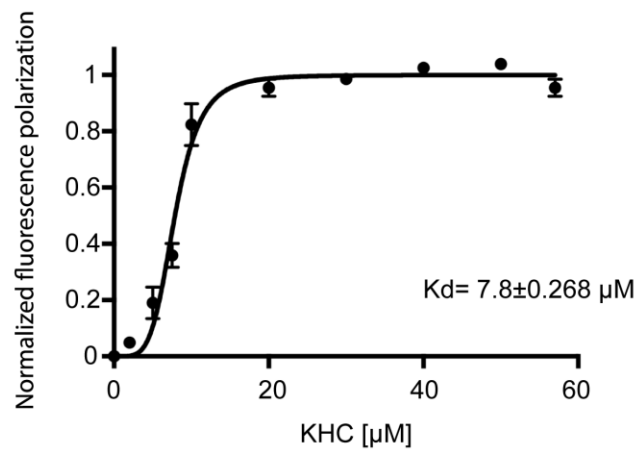


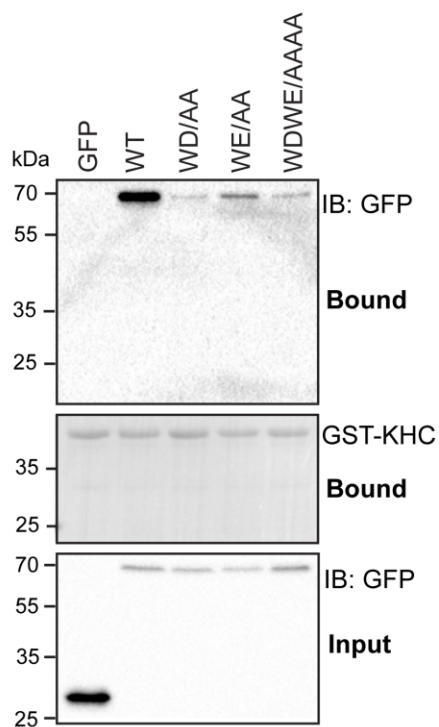
Figure 3. The KHC binding site on SKIP overlaps the KLC binding W-acidic motifs

- (a) Schematic of SKIP constructs used in this figure highlighting location of RUN domain and W-acidic motifs.
- (b) Coomassie stained SDS-PAGE gel showing samples of His-tagged SKIP proteins used in (c). 20µl loaded.
- (c) Western blot showing GST-pull down experiment using GST-KHC(815-955) and various C-terminal SKIP truncations produced in *E.coli*. Binding is reduced when W-acidic motifs are removed. Graphs show quantification from 3 independent experiments. Data was analysed using one-way ANOVA with Dunnett's multiple comparison test for comparison to 1-243, *= $p < 0.05$, ** = $p < 0.01$, *** = $p < 0.001$.
- (d) Western blot showing GST-pull down experiment using GST- KHC(815-955) and various C-terminal SKIP truncations produced 293T cells. Binding is reduced when W-acidic motifs are removed. Graphs show quantification from 3 independent experiment. Data was analysed using one-way ANOVA with Dunnett's multiple comparison test for comparison to 1-260, ** = $p < 0.01$, *** = $p < 0.001$.
- (e) Western blot showing competition experiment where purified recombinant KLC2^{TPR} is added at increasing concentration to 293T cell extracts expressing GFP-SKIP. Binding to GST-KHC(815-955) is reduced in a concentration dependent manner by wild type KLC2^{TPR} (left) but not KLC2^{TPR} carrying the W-acidic N287L (right) cargo binding mutation. Data are representative of 3 independent experiments

A SKIP(202-241): TAMRA-STNLEWDDSAIAPSSDYDFGDVFPVPSVPSTDWEDGDL
 KHC (866-917): KRLRATAERVKALESALKEAKENAMRDRKRYQQEVDRIKEAVRAKNMARRAH



B GFP-SKIP(1-310)



C

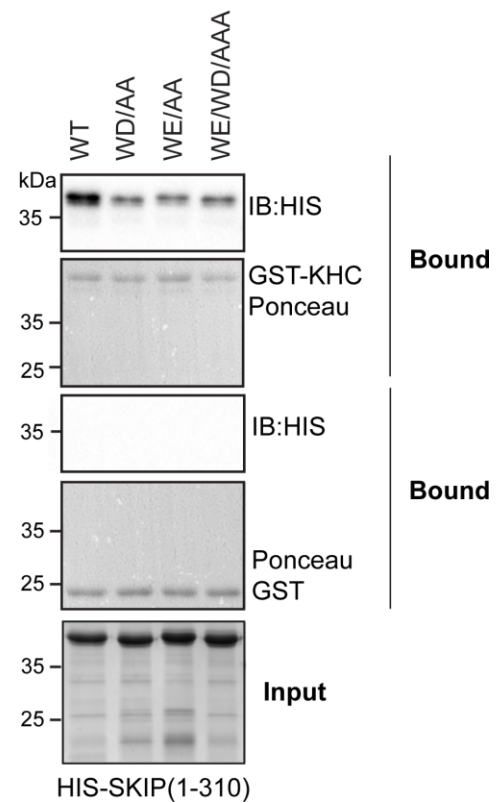


Figure 4. Interaction between KHC and SKIP requires both W-acidic motifs.

(a) Fluorescence polarisation binding assay using a TAMRA conjugated peptide from SKIP containing both W-acidic motifs. KHC(866-917) was prepared by cleavage of purified GST-KHC(866-917) and removal of free GST or uncleaved protein by incubation with glutathione beads. KHC(866-917) is added at increasing concentration. Error bars show S.E.M. from 3 replicates and curve shows fit of data to a one site specific binding model with hill slope using

Prism software (EQ $Y=B_{max} * X^h / (K_d^h + X^h)$ where $B_{max} = 180.7$, $K_d = 7.878$, $h = 4.703$. $R^2 = 0.98$).

(b) Western blot showing GST-pull down experiment from 293T extracts expressing wild type GFP-SKIP(1-310) or WD/AA, WE/AA or WDWE/AAAA mutants. Binding is reduced by disruption of either motif. Data are representative of 3 independent experiments.

(c) Western blot showing GST-pull down experiment using purified His-SKIP (1-310) produced in *E.coli*. Binding is reduced by disruption of either W-acidic motif. Data are representative of 3 independent experiments.

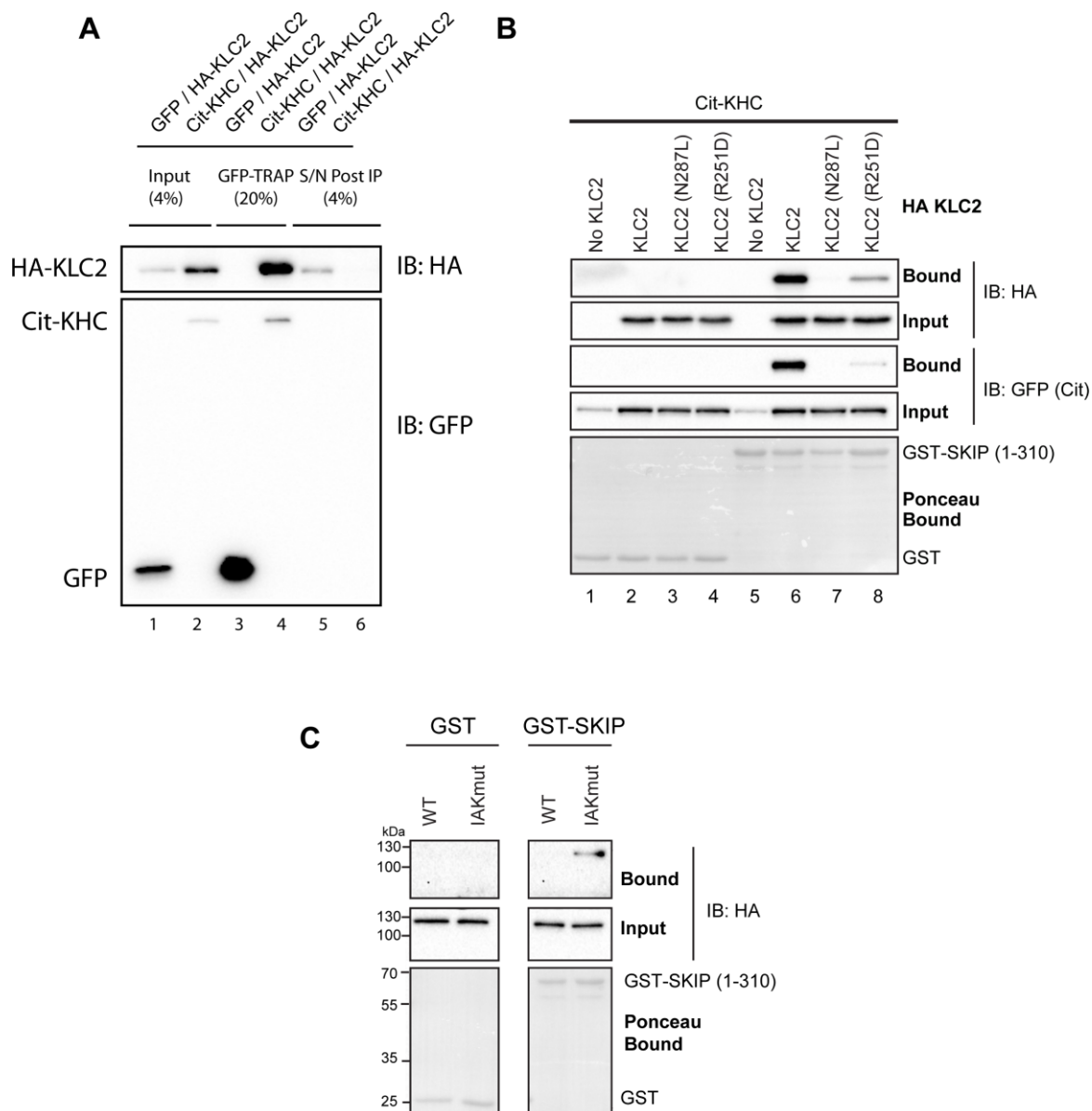


Figure 5. Interaction between SKIP and full length KHC requires relief of KHC autoinhibition.

(a) Western of GFP-TRAP immunoprecipitation experiments blot showing that Cit-KHC and HA-KLC2 form a complex when overexpressed in 293T cells. Immunoprecipitation of Cit-KHC results in co-depletion of HA-KLC2 from cell extracts.

(b) Western blot showing results GST-SKIP(1-310) pull down from transfected 293T cells expressing Citruline-tagged KHC with or without KLC2 (Wild type or W-acidic cargo binding mutants N287L and R251D). Capacity to pull down the kinesin-1 tetramer is disrupted by W-acidic binding mutations in KLC2. KHC expressed alone is not retained by GST-SKIP(1-310). Data are representative of 3 independent experiments.

(c) Western blot showing results GST-SKIP(1-310) pull down from transfected 293T cells expressing HA-tagged KHC, either wild type or with the autoinhibitory IAK sequence mutated

(IAKmut, QIAKPIRPG/AAAAAAAAA). Binding to GST-SKIP(1-310) is only detected when autoinhibition is relieved. Data are representative of 3 independent experiments.

A**SKIP 1-310 PROTEIN SEQUENCE**

MEPGEVKDRILENISLSVKKLQSYFAACEDEIPAIRNHDKVLQRLCEHLDHALLYGLQDLSSGYWLVVHFTRREAIKQIEVLQHVATNL
 ————— RUN Domain —————
 GRSRAWLYLALNENSLESYLRLFQENLGLLHKYYVKNALVCSHDHLTLFLTLVSGLEFIRFELDLDPYLDLAPYMPDYKPYLLDFED
 RLPSSVHGSDLSLNSFNSTNLEWDDSAIAPSS **EDYDFGDFVFAVPSVPS** **TDWE** **DGLT** **TVSGRSTASDLTSSKASTRSPTQRQN**
 207 215 243 260
 PFNEEPAETVSSSDTTPVHTTSQEKEEAQALDPPDACTEL-310

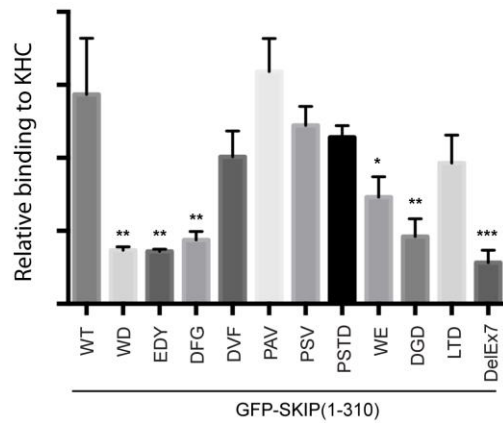
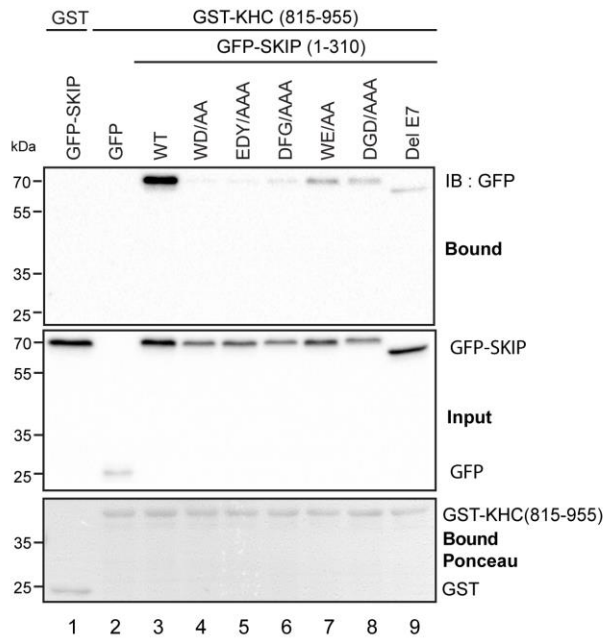
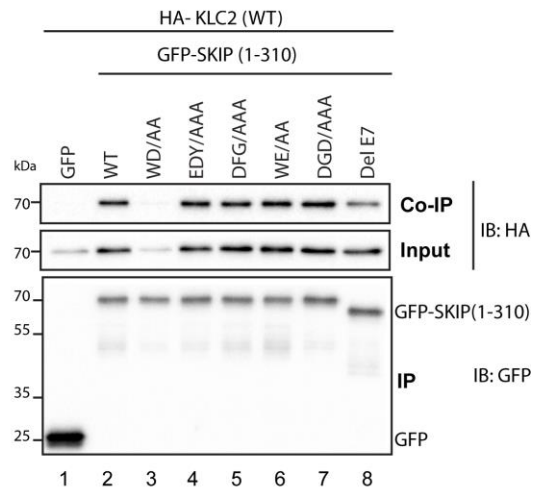
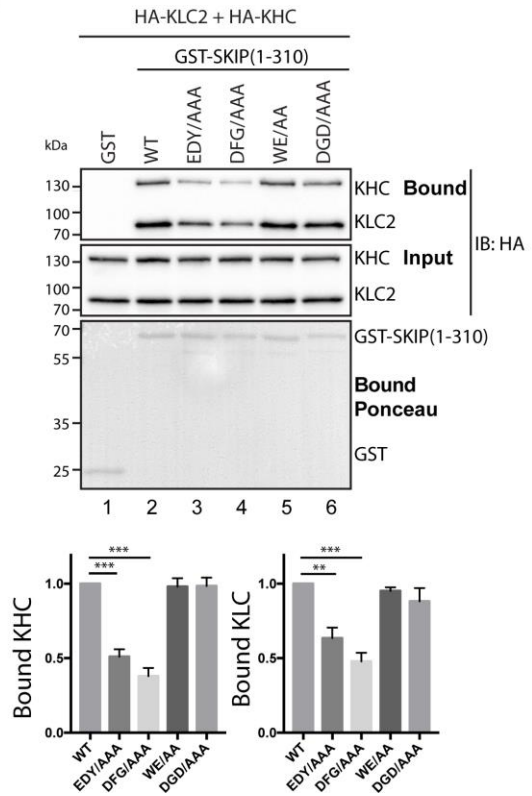
B**C****D****E**

Figure 6. Specific mutations in SKIP can separate KLC and KHC binding capacity

(a) Amino acid sequence of SKIP(1-310). The RUN domain as predicted by EMBL S.M.A.R.T. is highlighted in blue. Exon 7 is shown in green. WD and WE motifs are in red. Clusters of amino acid mutations in Exon7 are highlighted by | symbol.

(b) Graph showing quantification of relative binding to GST-KHC(815-955) by wild type GFP-SKIP(1-310) expressed in 293T cell extracts and the indicated alanine mutants. Data are from 3 independent experiments, and were normalised to input levels of GFP-SKIP proteins. Error bars show \pm S.E.M. Statistical analysis was performed using one-way ANOVA and statistical significance of comparisons to WT using Dunnett's multiple comparison test is shown as * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

(c) GST-KHC(815-955) pull down experiment with GFP-SKIP(1-310) showing effect of the indicated mutations on the SKIP-KHC interaction.

(d) GFP-TRAP immunoprecipitation experiment from 293T cells transfected with GFP-SKIP(1-310) carrying the indicated mutations and HA-KLC2. KLC binding is not perturbed by EDY, DFG, WE and DFG mutations. Data are representative of 3 independent experiments.

(e) GST-SKIP(1-310) pull down using wild type and KHC binding mutants from transfected 293T cells expressing HA-tagged KHC and HA-KLC2. Binding to the tetramer is reduced by EDY/AAA and DFG/AAA mutations. Graph shows quantification of binding from 3 independent experiments and error bars show \pm S.E.M. ***= $p < 0.001$, **= $p < 0.01$ determined using one-way ANOVA and Dunnett's multiple comparison test for comparison to WT.

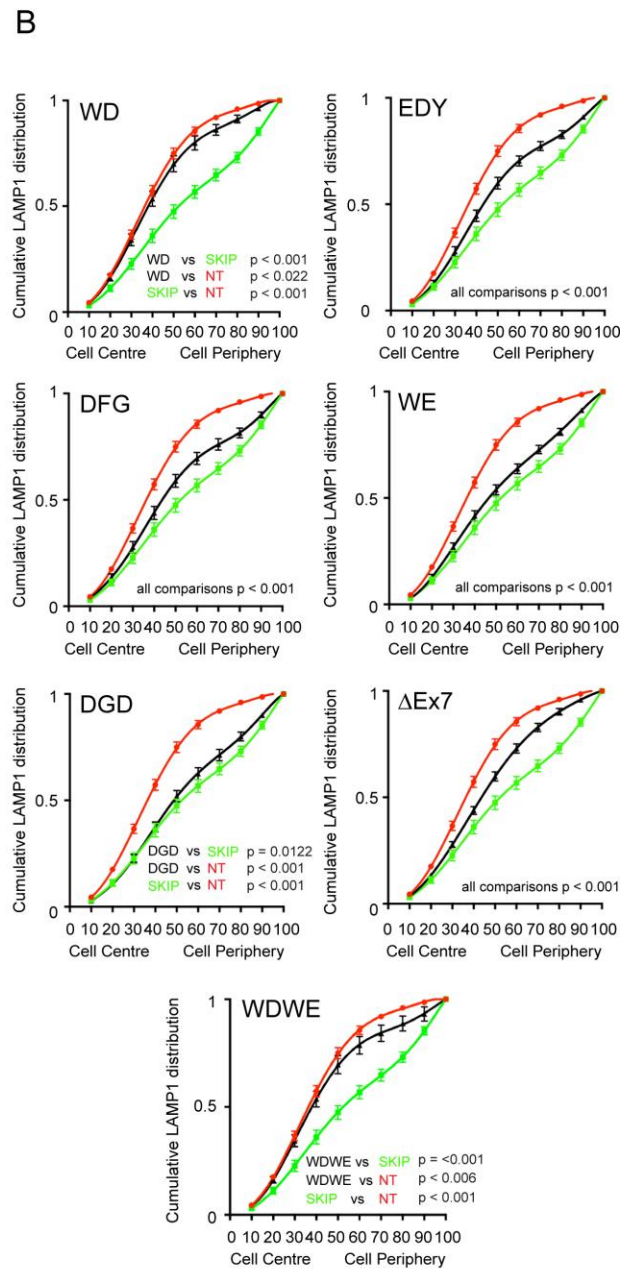
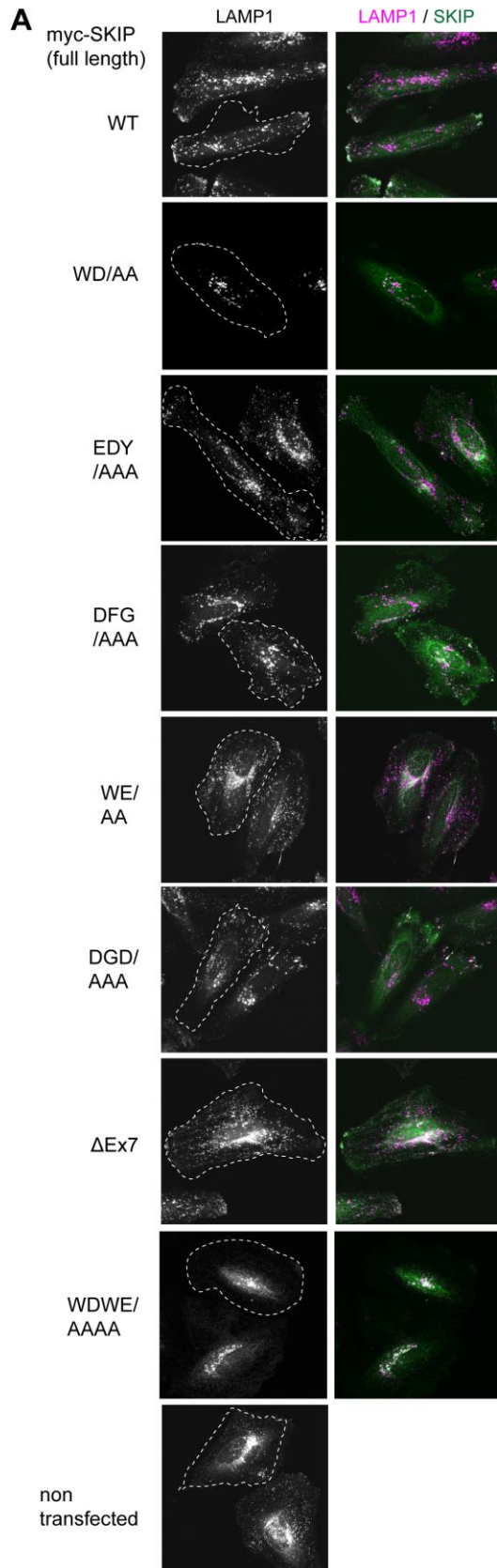
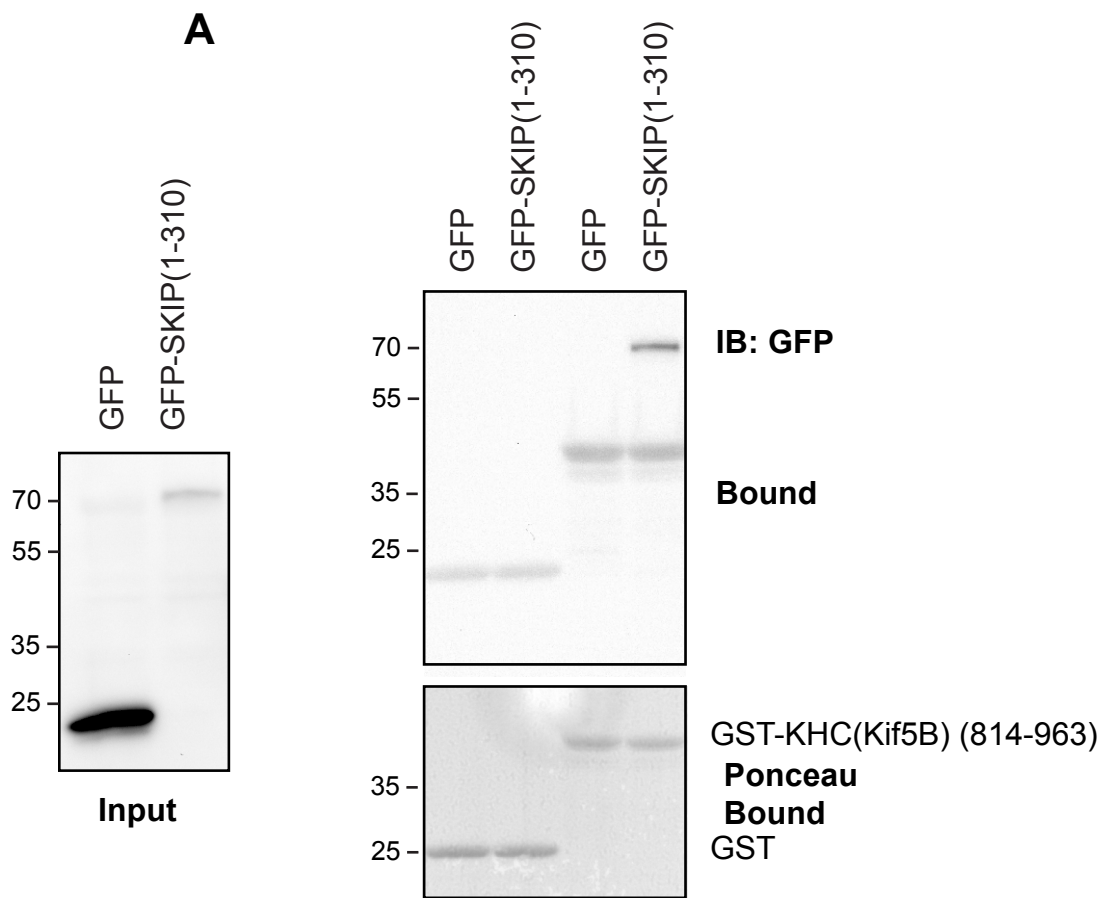


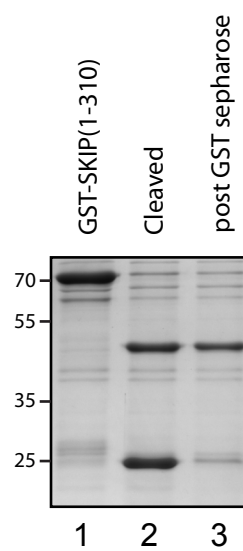
Figure 7. Specific disruption of SKIP-KHC binding capability limits its capacity to promote the peripheral dispersion of lysosomes.

(a) Immunofluorescence images showing late endosomes and lysosomes (LAMP1, magenta) in HeLa cells transfected with full length myc-SKIP (green) and the indicated heavy chain binding mutants.

(b) Graphs showing quantification of lysosome distribution from 45 cells in 3 replicates. Error bars show \pm S.E.M. Non-transfected (red) and wild type myc-SKIP transfected (green) curves are reproduced across all graphs. Black line indicates the distribution of lysosomes in cells transfected with the indicated mutant. Statistical analysis of pairwise comparison of curves was carried out as described in *Materials and Methods*.



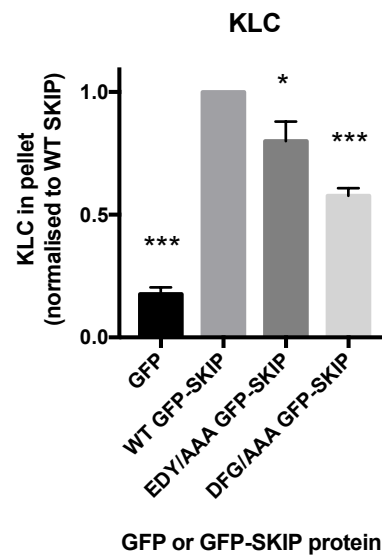
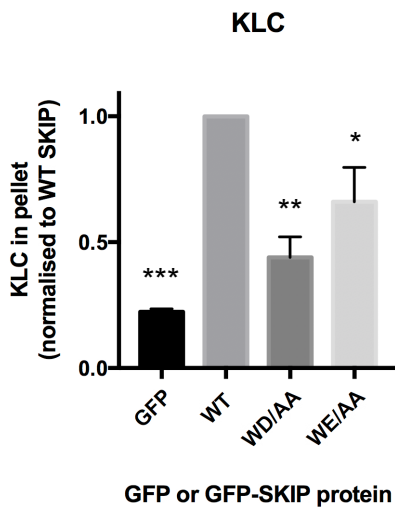
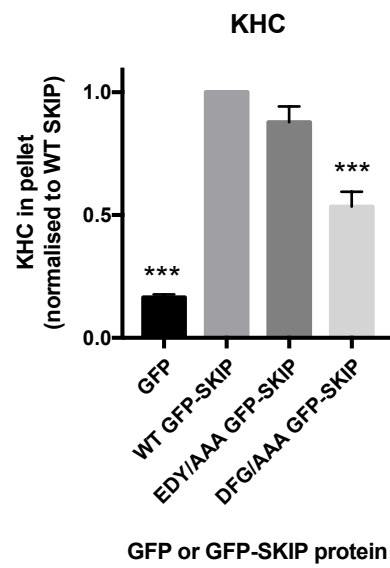
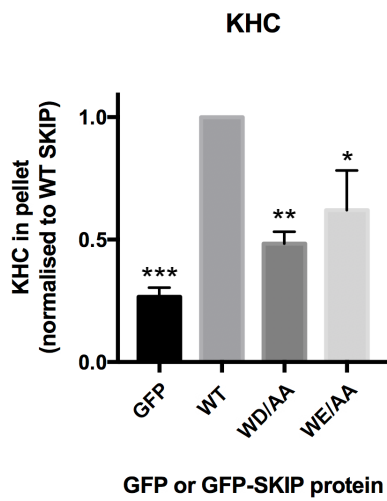
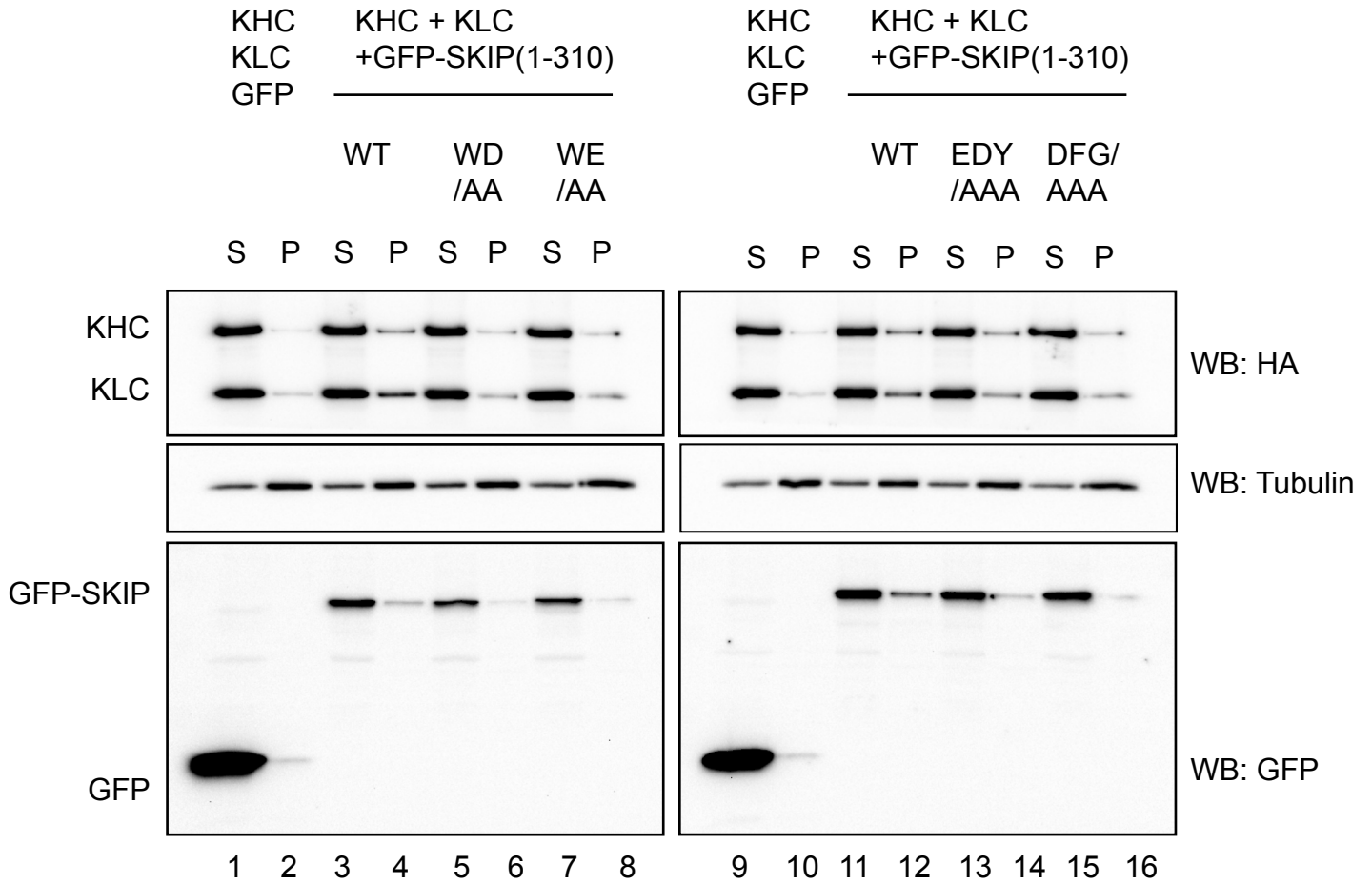
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1. purified GST-SKIP after elution and dialysis
2. (1) after incubation with 3C protease
3. (2) after incubation with glutathione resin

Supplementary Figure 1.

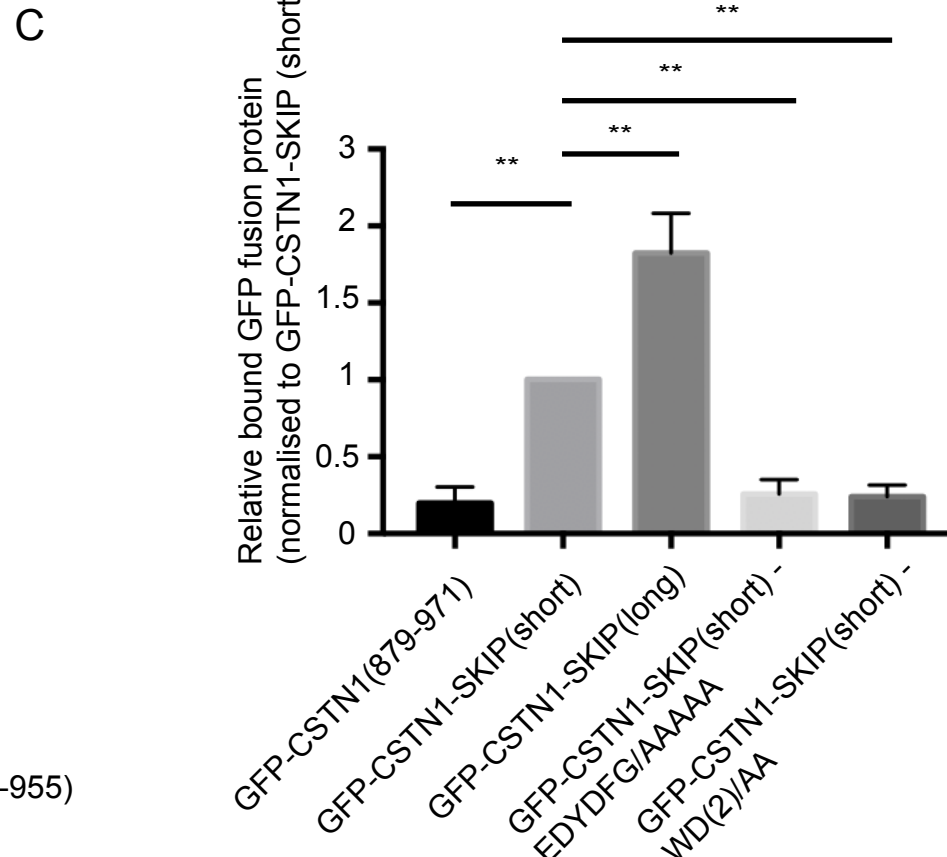
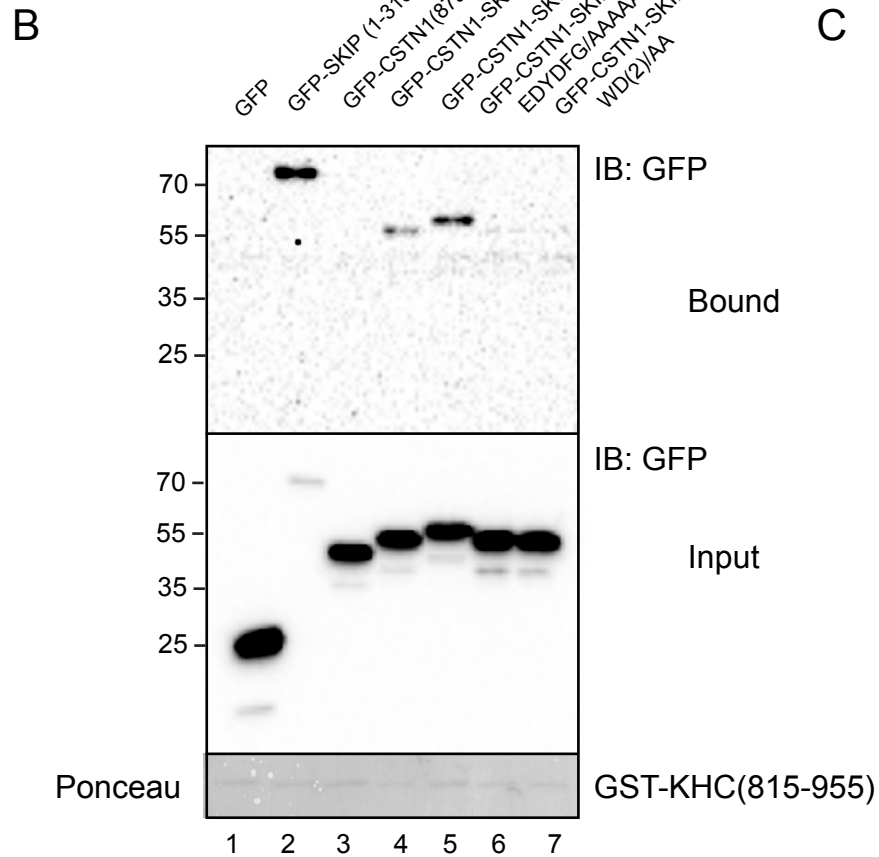
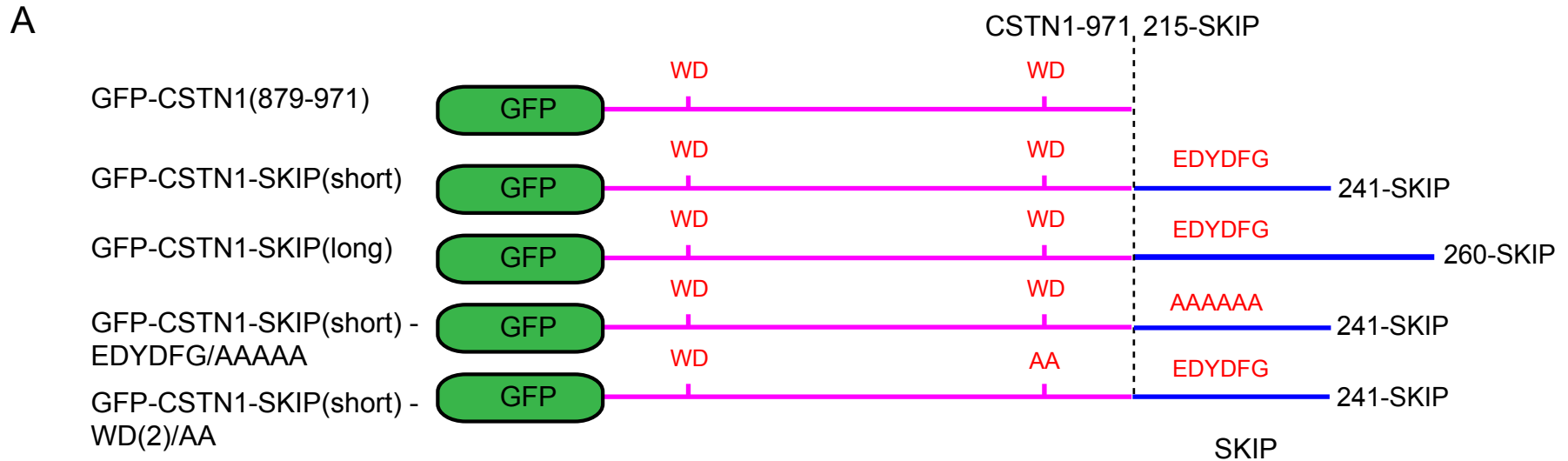
(a) Western blot showing that GST-KHC (Kif5B) (814-963) retains GFP-SKIP(1-310) from 293T cell extracts. (b) Representative coomassie stained gel showing typical proteolytic processing of GST-SKIP (1-310) to remove GST. Lane 1 shows GST-SKIP following elution from glutathione coated beads and dialysis into glutathione free buffer. Lane 2 shows the same sample after processing with 3C protease. Lane 3 shows the same sample following a second incubation with glutathione beads to remove any uncleaved GST-SKIP, free GST and 3C protease.



Supplementary Figure 2.

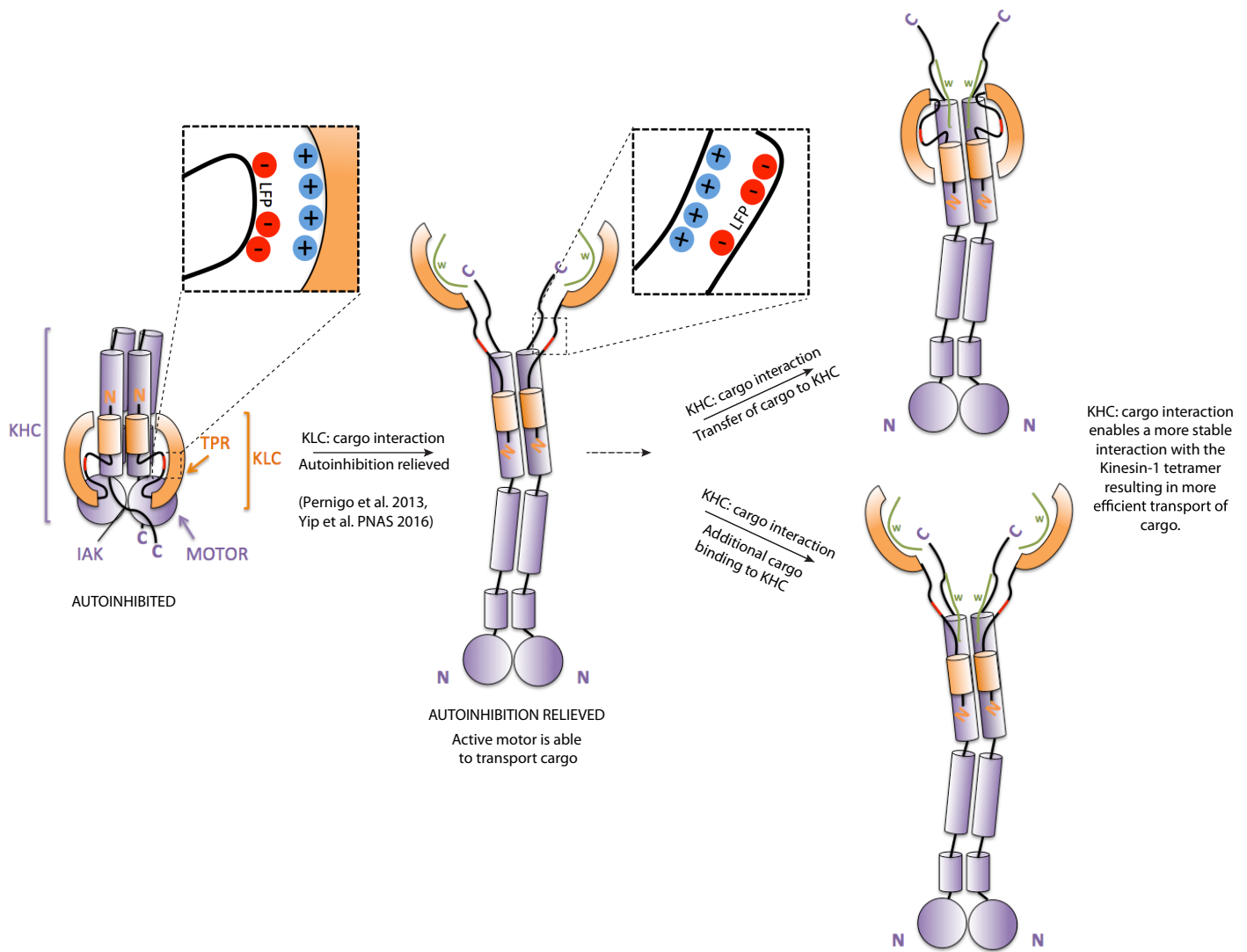
Western blots showing results of cellular MT co-sedimentation assay. HeLa cells were transfected with the indicated GFP or GFP-SKIP expression plasmid, lysed in a MT stabilizing buffer and subjected to ultracentrifugation to pellet intact MTs. Supernatant and pellet fractions were analysed by western blot. Graphs show quantification from 3 independent experiments of KHC or KLC in pellet, normalised to that observed for WT SKIP. Data was analysed using one way ANOVA and Dunnett's multiple comparison test for comparison to WT.

***= $p < 0.01$, **= $p < 0.05$, *= $p < 0.01$.



Supplementary Figure 3.

(a) Schematic showing design of CSTN1-SKIP chimeric proteins. SKIP (from S215) was fused to the C-terminus of CSTN1 (Y971). These constructs terminated at either L241 (GFP-CSTN1-SKIP(short)) or A260 (GFP-CSTN1-SKIP(long)) in SKIP. Mutations to disrupt either the EDYDFG motif in SKIP (GFP-CSTN1-SKIP(short) - EDYDFG/AAAAA) or the second WD motif of CSTN1 (GFP-CSTN1-SKIP(short) - WD(2)/AA) were also tested. All constructs were generated as synthetic DNAs (supplied by Genscript, NJ, USA), subcloned into CB6-GFP and verified by DNA sequencing. (b) Western blot showing results of GST-pull down experiment using GST-KHC(815-955, 0.1nmol), produced in *E.coli*, and indicated SKIP/CSTN proteins expressed in 293T cells. (c) Graph shows quantification of binding of CSTN and CSTN-SKIP chimeras from 3 independent experiments. Data was analysed using one way ANOVA and Dunnett's multiple comparison test for comparison to GFP-CSTN1-SKIP(short), **= $p < 0.01$.



Supplementary Figure 4

Diagram showing proposed model of binding and activation of kinesin-1 by SKIP