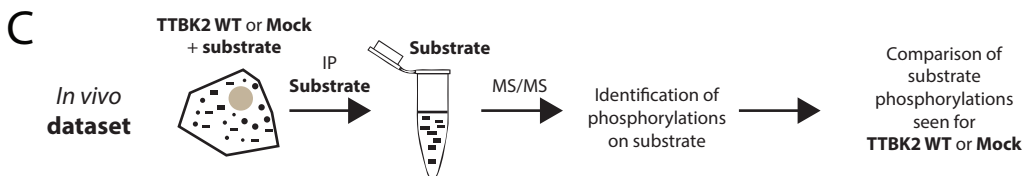
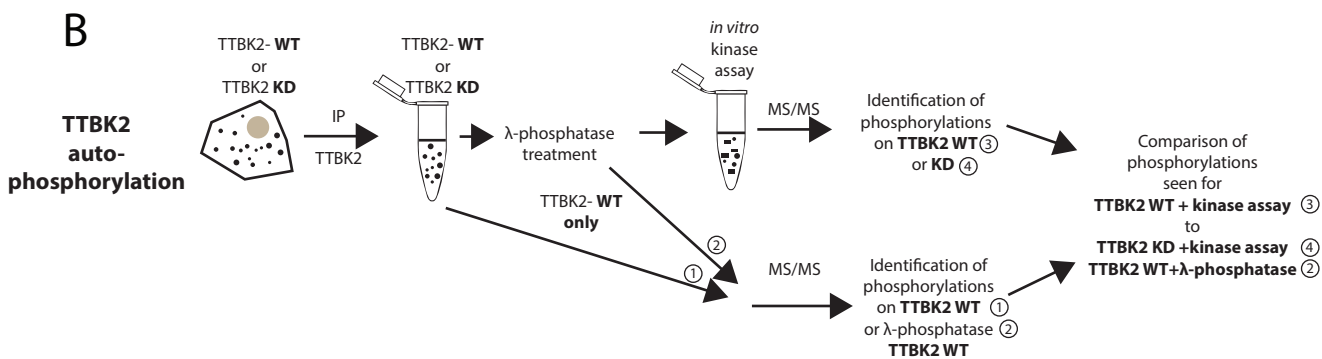
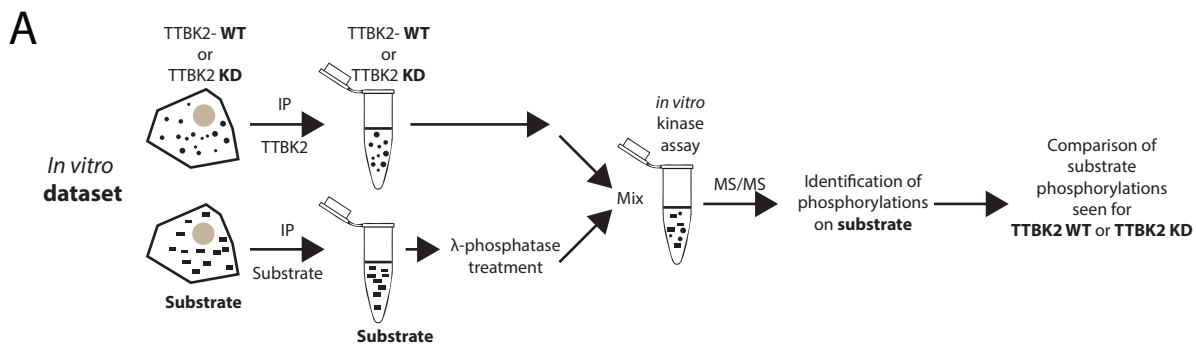


Supplemental Materials

Molecular Biology of the Cell

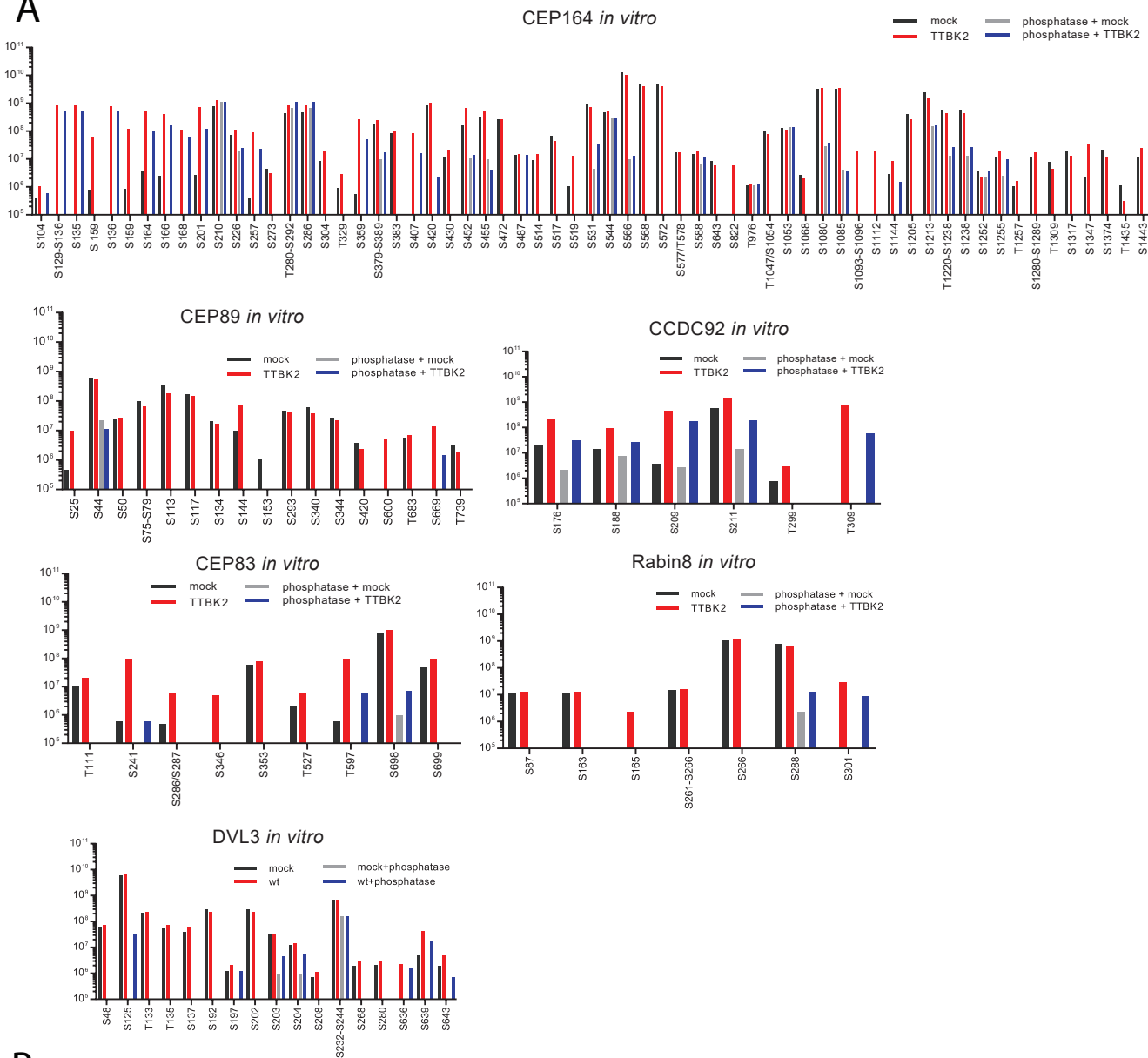
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Supplementary figure 1

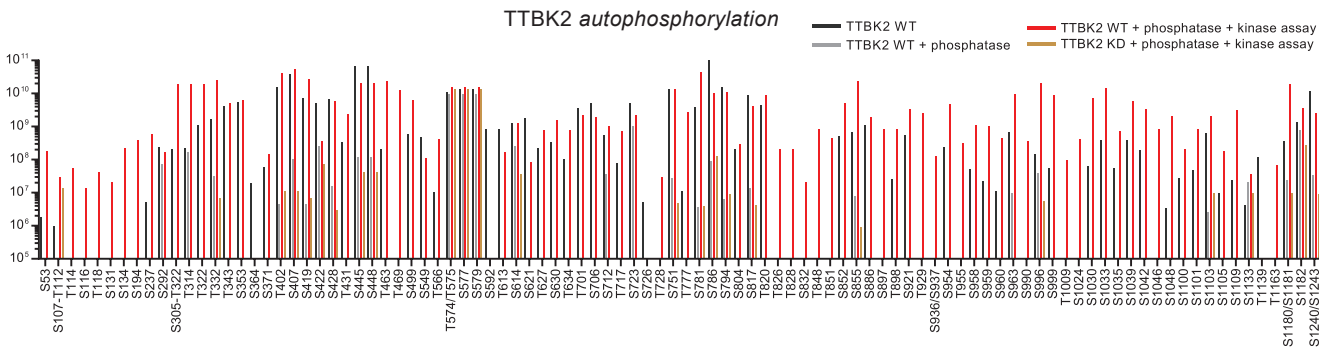


Supplementary figure 2

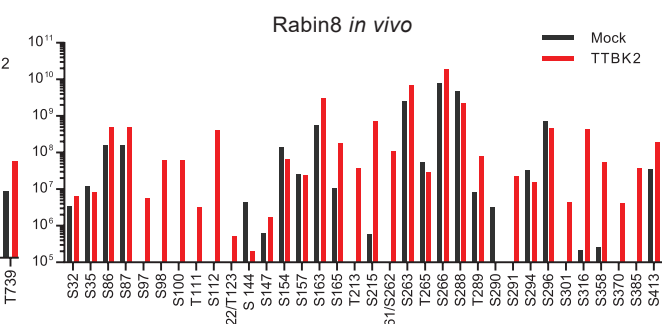
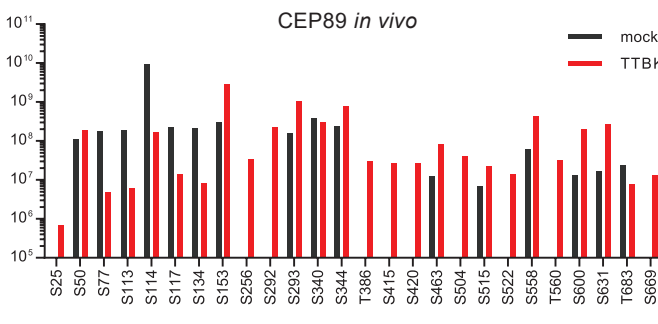
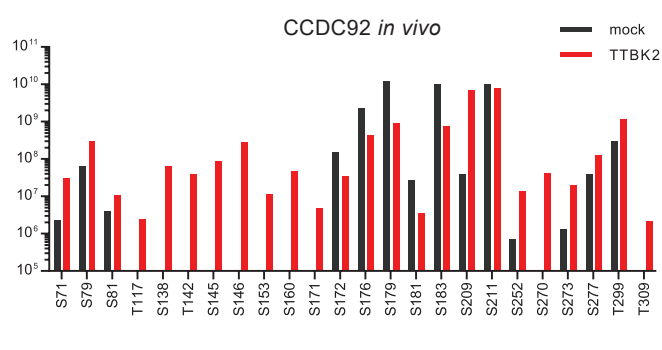
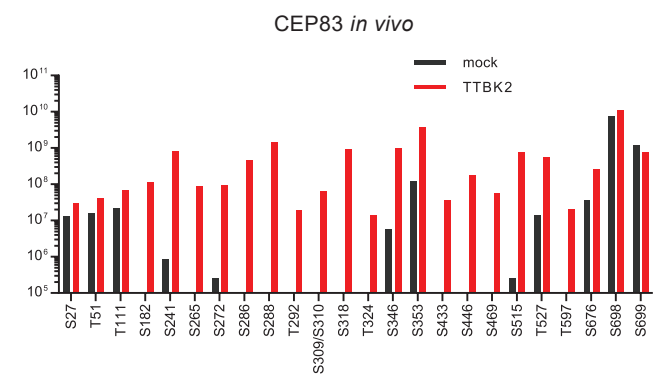
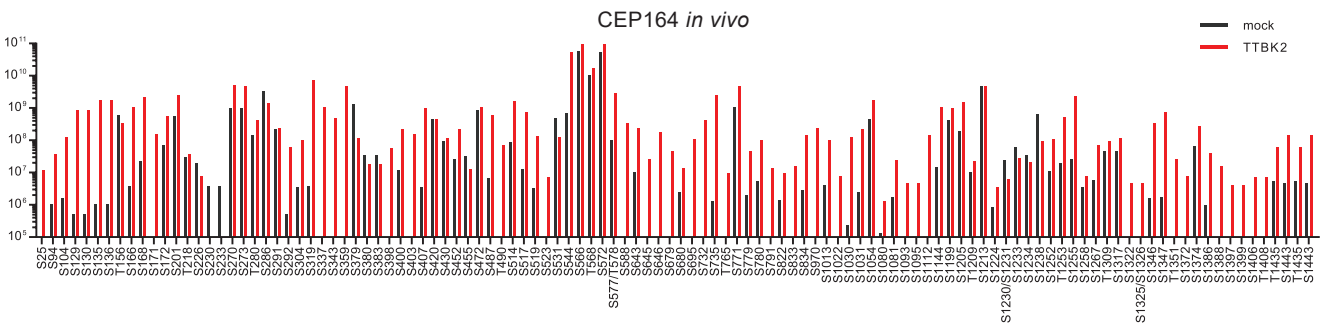
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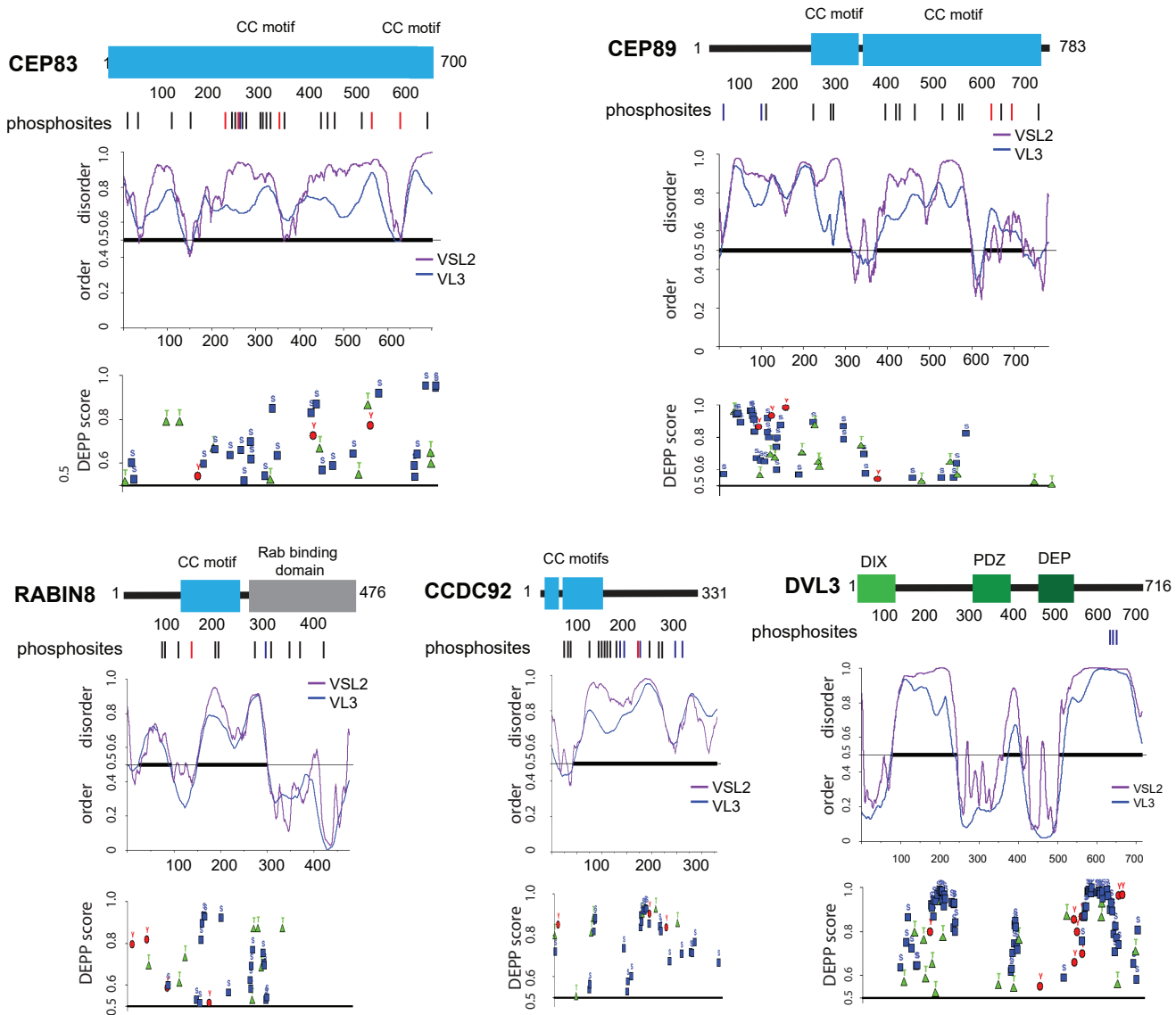
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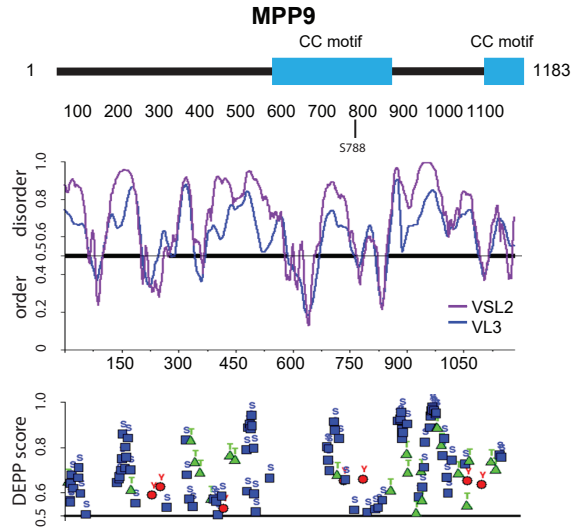
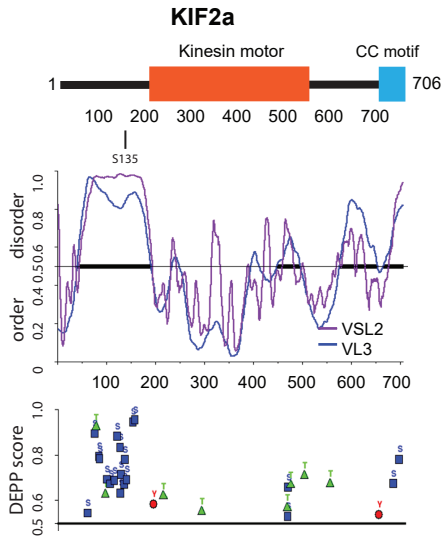
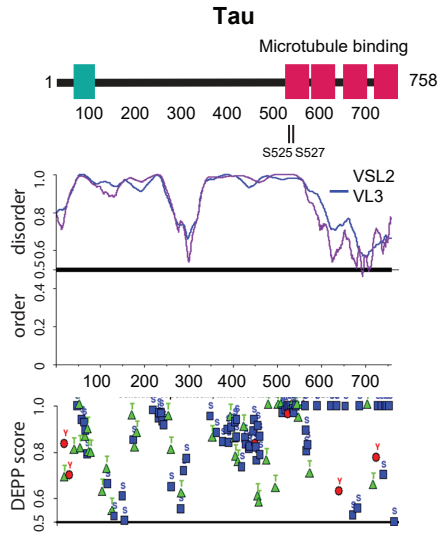
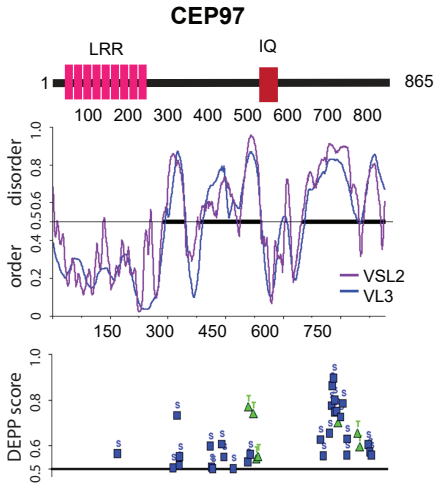
Supplementary figure 3



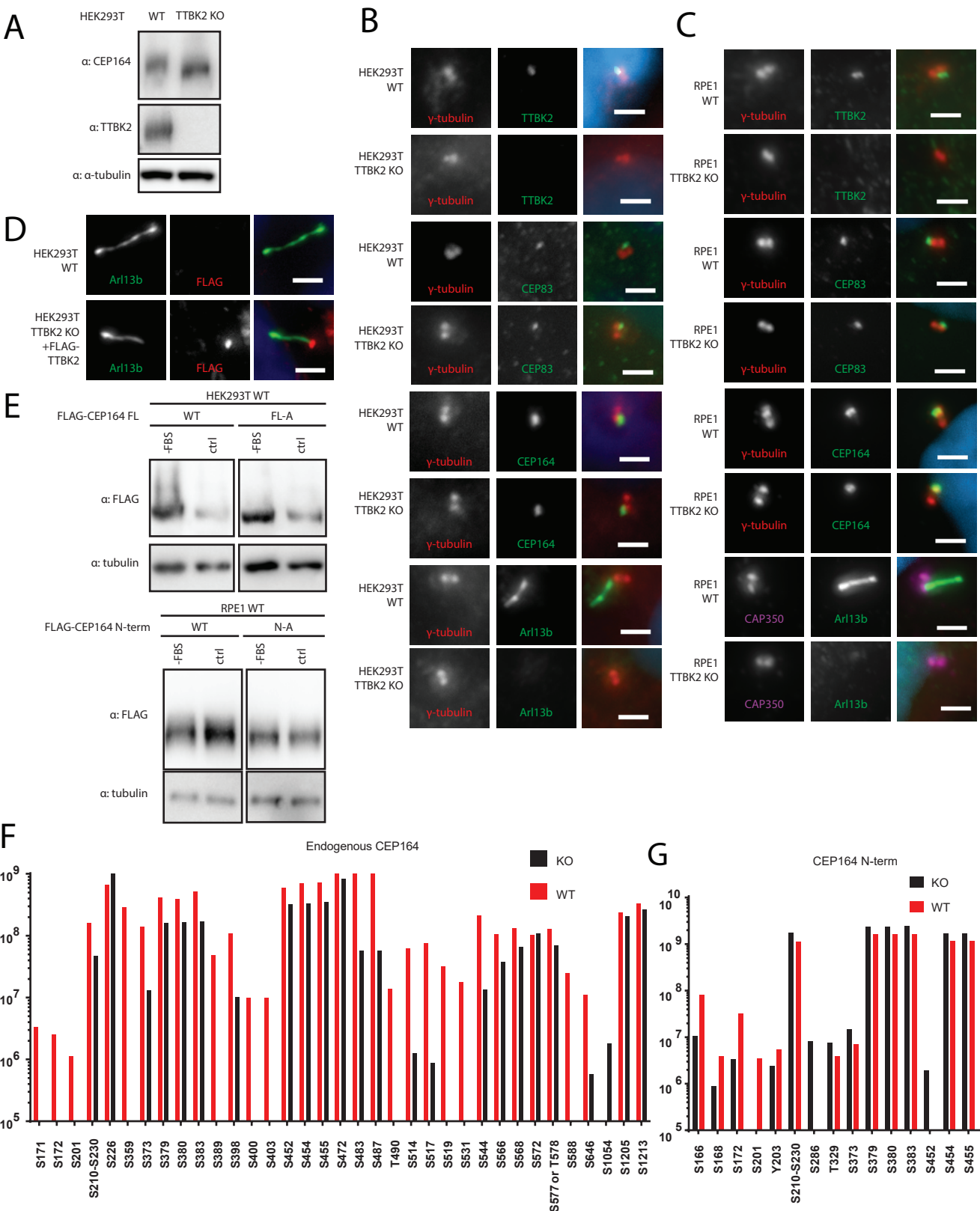
Supplementary figure 4



Supplementary figure 5



Supplementary figure 6



Supplementary figure 1. Schematized workflow of MS/MS experiments

A: HEK293T cells were transfected by tested substrate or TTBK2 WT/KD. Proteins of interest were purified by immunoprecipitation. Additional treatment with λ phosphatase was performed in second experimental repeat. Tested substrates proteins were subjected to *in vitro* kinase assay with TTBK2 WT or KD (control). Following SDS-PAGE separation samples were analyzed by MS/MS to identify phosphorylations. **B:** Transfected TTBK2 WT or TTBK2 KD were isolated from HEK293T cells by immunoprecipitation. In total, four conditions were prepared, as indicated - ① TTBK2 WT, ② TTBK2 WT treated with λ -phosphatase, ③ TTBK2 WT treated with λ -phosphatase subsequently subjected to *in vitro* kinase assay, and ④ phosphatase-treated TTBK2 KD subjected to *in vitro* kinase assay. Following SDS-PAGE separation samples were analyzed by MS/MS to identify phosphorylations. Condition ③ was compared to conditions ② and ④, respectively based on criteria described in M&M section. Sample ① was used as reference to monitor phosphatase treatment effectivity. **C:** Tested substrate transiently expressed in HEK293T cells together with exogenous TTBK2 WT or empty plasmid (mock) was purified by immunoprecipitation and following SDS-PAGE separation analyzed by MS/MS. Identified phosphorylations found in condition with TTBK2 WT were compared to those found in mock condition, based on criteria described in the M&M section.

Supplementary figure 2. Summary of phosphorylations identified for depicted substrates *in vitro*.

For each S/T site on x axis, average phosphorylation intensity is shown in y axis (log₁₀ scale) for indicated conditions. Cases where the exact position could not be assigned are indicated as (/) for two possible positions or (-) for clusters. **A:** Graphical summary of phosphorylations detected *in vitro* in following conditions. Black – Substrate + TTBK2 KD (Mock), Red – Substrate + TTBK2 WT, Grey – Substrate + λ phosphatase treatment + TTBK2 KD (Mock), Blue – Substrate + λ phosphatase treatment + TTBK2 WT. **B:** Graphical summary of phosphorylations detected in TTBK2 autophosphorylation dataset in following conditions : ① Black –TTBK2 WT, ② Grey – TTBK2 WT+ λ phosphatase treatment (Ctrl#1), ③ Red – TTBK2 WT + λ phosphatase treatment + kinase assay, ④ Brown – TTBK2 KD + phosphatase treatment + kinase assay (Ctrl#2).

Supplementary figure 3. Summary of phosphorylations identified for depicted substrates *in vivo*.

For each S/T site on x axis, average phosphorylation intensity is shown in y axis (log₁₀ scale) for indicated conditions. Cases where the exact position could not be assigned are indicated as (/). Graphical summary of phosphorylations detected *in vivo* in following conditions: Black – Substrate + Mock, Red – Substrate + TTBK2.

Supplementary figure 4. Disorder predictions of CEP89, CEP83, CCDC92, Rabin8 and DVL3 indicate long IDRs with multiple phosphorylation sites.

Protein disorder and phosphorylation prediction for CEP89, CEP83, CCDC92, Rabin8 and DVL3. Structure of all proteins is schematized, rectangles indicate presence of a domain or motif, the numbers indicate length of given protein in amino acids. Lines below the schematic protein structure indicate positions of each phosphorylation induced by TTBK2. The first graph below the schematized protein shows prediction of order/disorder (with cut-off 0.5) determined by PONDR using VSL2 (Violet line) and VL3-BA (Blue line) algorithms. The second graph plots Disorder Enhanced Phosphorylation

Predictor (DEPP) score (with cut-off score 0.5) and individual phosphosites thereby predicted (phosphoS as blue rectangle, phosphoT as green triangle, and phosphoY as red circle).

Supplementary figure 5. Disorder predictions of CEP97, KIF2a, Tau and MPP9 indicate long IDRs with multiple phosphorylation sites.

Protein disorder and phosphorylation prediction for CEP97, KIF2a, MPP9 and Tau proteins. Structure of all proteins is schematized, rectangles indicate presence of a domain or motif, the numbers indicate length of given protein in amino acids. Lines and numbers respectively, below protein structure indicate published TTBK2 phosphorylated residues (24, 29, 38, 40). The first graph below the schematized protein shows prediction of order/disorder (with cut-off 0.5) determined by PONDR using VSL2 (Violet line) and VL3-BA (Blue line) algorithms. The second graph plots Disorder Enhanced Phosphorylation Predictor (DEPP) score (with cut-off score 0.5) and individual phosphosites thereby predicted (phosphoS as blue rectangle, phosphoT as green triangle, and phosphoY as red circle).

Suppl. Fig.6. Validation of HEK293T and RPE1 TTBK2 KO cells, MSMS analysis of CEP164 phosphorylation in HEK293T WT and TTBK2 KO cells

A: WB analysis of HEK293T WT and TTBK2 KO cells. TTBK2 protein is missing in HEK293T TTBK2 KO cells, CEP164 is migrating faster in TTBK2 KO HEK293T. **B:** IC comparison of HEK293T WT and TTBK2 KO cells. γ -tubulin staining was used to visualize centrioles (red), in green are tested DA markers or ARL13b. Note that TTBK2 signal is missing in the HEK293T TTBK2 KO cells on MCs, while signal of DA proteins CEP83 and CEP164 is not changed. HEK293T TTBK2 KO cells do not form ARL13b+ PCs. **C:** IC comparison of RPE-1 WT and TTBK2 KO cells. γ -tubulin or CAP350 staining was used to visualize centrioles (red, violet), in green are tested DA markers or ARL13b. Note that TTBK2 signal is missing in the RPE1 TTBK2 KO cells on MCs, while signal of DA proteins CEP83 and CEP164 is not changed. RPE1 TTBK2 KO cells do not form ARL13b+ PCs. **D:** Transient transfection of FLAG-TTBK2 WT to HEK293T TTBK2 KO cells rescues ciliogenesis. ARL13b (green) staining was used to detect PCs respectively, expression of exogenous TTBK2 variants was detected by FLAG antibody (red). Note that FLAG-TTBK2 WT localizes to the base of PCs. **E:** WB analysis of indicated variants of CEP164. HEK293T WT and RPE1 WT cells were transfected by indicated constructs (FLAG-tagged FL CEP164 WT or FL-A mutants or CEP164 N-term WT or N-A term mutant), treated by doxycycline (FL constructs) and 12h after transfection were starved for additional 24h where indicated (-FBS). Slower migrating forms of FL CEP164 WT and CEP164 N-term WT occur upon starvation while mobility of the FL-A and N-A mutants in not changed. n=3. **F, G:** Summary of MS/MS analysis of phosphorylation of CEP164. **F:** endogenous CEP164 was immunoprecipitated from HEK293T WT and TTBK2 KO cells. **G:** FLAG-tagged CEP164 N-term was transfected to HEK293T WT and TTBK2 KO and 48h after transfection was immunoprecipitated using anti-FLAG antibody. For each S/T site on x axis, average phosphorylation intensity is shown in y axis (log₁₀ scale) for the indicated conditions. Cases where the exact position could not be assigned are indicated as (/). Conditions: Black – CEP164 in HEK293T TTBK2 KO, Red – CEP164 in HEK293T WT.

1: Name of the sheet refers to dataset (*in vitro*, *in vivo*, HEK293 wt and TTBK2 KO)

2: Number of repeats phosphorylation identified in/ total number of repeats performed

3: S/T followed by number specifies phosphoresidue

4: Number in column specifies average intensity of phosphorylation (sum of intensity/number of experiments for individual phosphosite or cluster)

5: clusters refer to phosphosites with uncertain position, "or" specifies two possible positions, "-" specifies more possible phosphorylation positions

6: Mock for *in vitro* dataset indicates use of TTBK2 KD

7: Mock for *in vivo* dataset indicates empty vector

8: Homology TTBK2 mus musculus (T2m), TTBK1 homo sapiens (T1h), mus musculus (T1m) states whether the residue in TTBK2 in homo sapiens has corresponding homologous residue in these proteins. If residue is replaced by phosphorylable residue (T/S) the swich is indicated

In vitro	CEP164 induced	average intensity of phosphorylation				PhosphoS itePlus
		CEP164+mock	CEP164+TTBK2	CEP164+ phosphatase + mock	CEP164+ phosphatase + TTBK2	
1/2	S104	4.E+05	1.E+06	0.E+00	6.E+05	
2/2	S135	0.E+00	8.E+08	0.E+00	5.E+08	
1/2	S 159	8.E+05	6.E+07	0.E+00	0.E+00	
2/2	S164	4.E+06	5.E+08	0.E+00	9.E+07	
2/2	S166	2.E+06	4.E+08	0.E+00	2.E+08	
1/2	S168	6.E+04	1.E+08	0.E+00	6.E+07	
2/2	S201	3.E+06	7.E+08	0.E+00	1.E+08	*
2/2	S257	4.E+05	9.E+07	0.E+00	2.E+07	
1/2	S304	8.E+06	2.E+07	0.E+00	0.E+00	
1/2	T329	9.E+05	3.E+06	0.E+00	0.E+00	
2/2	S359	5.E+05	3.E+08	0.E+00	5.E+07	*
2/2	S407	0.E+00	8.E+07	0.E+00	2.E+07	*
1/2	S822	0.E+00	6.E+06	0.E+00	0.E+00	
1/2	S1112	0.E+00	2.E+07	0.E+00	0.E+00	
1/2	S1144	3.E+06	8.E+06	0.E+00	3.E+06	
2/2	S1347	2.E+06	4.E+07	0.E+00	0.E+00	
2/2	S1443	1.E+07	2.E+07	0.E+00	0.E+00	*
	clusters					
2/2	S129-S136	0.E+00	8.E+08	0.E+00	5.E+08	
2/2	S1093-S1096	0.E+00	2.E+07	0.E+00	0.E+00	

In vitro	Cep164 non- induced	average intensity of phosphorylation				PhosphoS itePlus
		CEP164+mock	CEP164+TTBK2	CEP164+ phosphatase + mock	CEP164+ phosphatase + TTBK2	
1/2	S210	8.E+08	1.E+09	1.E+09	1.E+09	
2/2	S226	7.E+07	1.E+08	2.E+07	2.E+07	
1/2	S273	4.E+06	3.E+06	0.E+00	0.E+00	*
2/2	S286	4.E+08	8.E+08	7.E+08	1.E+09	*
2/2	S383	8.E+07	1.E+08	0.E+00	0.E+00	
2/2	S420	8.E+08	1.E+09	0.E+00	2.E+06	
2/2	S430	1.E+07	2.E+07	0.E+00	0.E+00	*
2/2	S452	2.E+08	6.E+08	1.E+07	1.E+07	
2/2	S455	3.E+08	5.E+08	1.E+07	4.E+06	*
2/2	S472	3.E+08	3.E+08	0.E+00	0.E+00	*
1/2	S487	1.E+07	1.E+07	0.E+00	1.E+07	
2/2	S514	9.E+06	2.E+07	0.E+00	0.E+00	
2/2	S517	7.E+07	4.E+07	0.E+00	0.E+00	
1/2	S519	1.E+06	1.E+07	0.E+00	0.E+00	
2/2	S531	9.E+08	7.E+08	4.E+06	4.E+07	
2/2	S544	5.E+08	5.E+08	3.E+08	3.E+08	
2/2	S566	1.E+10	1.E+10	9.E+06	1.E+07	*
1/2	S568	5.E+09	4.E+09	0.E+00	0.E+00	*
1/2	S572	5.E+09	4.E+09	0.E+00	0.E+00	*
1/2	S588	2.E+07	2.E+07	6.E+06	1.E+07	*
1/2	S643	8.E+06	6.E+06	0.E+00	0.E+00	
1/2	T976	1.E+06	1.E+06	1.E+06	1.E+06	
1/2	S1053	1.E+08	1.E+08	1.E+08	1.E+08	
1/2	S1068	3.E+06	2.E+06	0.E+00	0.E+00	
2/2	S1080	3.E+09	3.E+09	3.E+07	4.E+07	
2/2	S1085	3.E+09	3.E+09	4.E+06	3.E+06	*
1/2	S1205	4.E+08	3.E+08	0.E+00	0.E+00	*
2/2	S1213	2.E+09	1.E+09	1.E+08	2.E+08	
2/2	S1238	5.E+08	4.E+08	1.E+07	3.E+07	
1/2	S1252	4.E+06	2.E+06	2.E+06	4.E+06	
2/2	S1255	1.E+07	2.E+07	2.E+06	1.E+07	
1/2	T1257	1.E+06	2.E+06	0.E+00	0.E+00	
2/2	T1309	8.E+06	4.E+06	0.E+00	0.E+00	
2/2	S1317	2.E+07	1.E+07	0.E+00	0.E+00	
1/2	S1374	2.E+07	1.E+07	0.E+00	0.E+00	
1/2	T1435	1.E+06	3.E+05	0.E+00	0.E+00	*
	clusters					
2/2	T280 - S292	4.E+08	8.E+08	7.E+08	1.E+09	*
2/2	S379 - S389	2.E+08	2.E+08	1.E+07	2.E+07	*
2/2	S577 or T578	2.E+07	2.E+07	0.E+00	0.E+00	*
1/2	T1047 or S1054	9.E+07	8.E+07	0.E+00	0.E+00	*
2/2	T1220 - S1238	5.E+08	4.E+08	1.E+07	3.E+07	
1/2	S1280 - S1289	1.E+07	2.E+07	0.E+00	0.E+00	*

In vitro	CEP83 induced	average intensity of phosphorylation				PhosphoS itePlus
		phosphoresidue	CEP83+mock	CEP83+TTBK2	CEP83+ phosphatase + mock	
2/2	S241	6.E+05	1.E+08	0.E+00	6.E+05	
1/2	S346	0.E+00	5.E+06	0.E+00	0.E+00	
2/2	T527	2.E+06	6.E+06	0.E+00	0.E+00	
2/2	T597	6.E+05	1.E+08	0.E+00	6.E+06	
	clusters					
1/2	S286 or S287	5.E+05	6.E+06	0.E+00	0.E+00	

In vitro	Cep83 non-induced	average intensity of phosphorylation				PhosphoS itePlus
		phosphoresidue	CEP83+mock	CEP83+TTBK2	CEP83+ phosphatase+ mock	
1/2	T111	1.E+07	2.E+07	0.E+00	0.E+00	*
1/2	S353	6.E+07	8.E+07	0.E+00	0.E+00	
2/2	S698	8.E+08	1.E+09	1.E+06	7.E+06	*
2/2	S699	5.E+07	1.E+08	0.E+00	0.E+00	

In vitro	CEP89 induced	average intensity of phosphorylation				PhosphoS itePlus
		phosphoresidue	CEP89+mock	CEP89+TTBK2	CEP89+ phosphatase+ mock	
1/2	S25	5.E+05	1.E+07	0.E+00	0.E+00	
2/2	S144	1.E+07	7.E+07	0.E+00	0.E+00	*
1/2	S600	0.E+00	5.E+06	0.E+00	0.E+00	
2/2	S669	0.E+00	1.E+07	0.E+00	1.E+06	

In vitro	CEP89 non-induced	average intensity of phosphorylation				PhosphoS itePlus
		phosphoresidue	CEP89+mock	CEP89+TTBK2	CEP89+ phosphatase+ mock	
2/2	S44	6.E+08	5.E+08	2.E+07	1.E+07	*
2/2	S50	2.E+07	3.E+07	0.E+00	0.E+00	*
1/2	S113	3.E+08	2.E+08	0.E+00	0.E+00	*
1/2	S117	2.E+08	2.E+08	0.E+00	0.E+00	
1/2	S134	2.E+07	2.E+07	0.E+00	0.E+00	
2/2	S153	1.E+06	0.E+00	0.E+00	0.E+00	*
1/2	S293	5.E+07	4.E+07	0.E+00	0.E+00	
1/2	S340	6.E+07	4.E+07	0.E+00	0.E+00	
1/2	S344	3.E+07	2.E+07	0.E+00	0.E+00	
1/2	S420	4.E+06	2.E+06	0.E+00	0.E+00	
1/2	T683	6.E+06	7.E+06	0.E+00	0.E+00	
1/2	T739	3.E+06	2.E+06	0.E+00	0.E+00	*
	clusters					
2/2	S75 - S79	1.E+08	6.E+07	0.E+00	0.E+00	*

In vitro	CCDC92 induced	average intensity of phosphorylation				PhosphoS itePlus
		phosphoresidue	CCDC92+mock	CCDC92+TTBK2	CCDC92+ phosphatase+ mock	
1/1	S176	2.E+07	2.E+08	2.E+06	3.E+07	
1/1	S188	1.E+07	9.E+07	7.E+06	3.E+07	
1/1	S209	4.E+06	5.E+08	3.E+06	2.E+08	*
1/1	S211	5.E+08	1.E+09	1.E+07	2.E+08	*
1/1	T299	7.E+05	3.E+06	0.E+00	0.E+00	*
1/1	T309	0.E+00	7.E+08	0.E+00	6.E+07	

CCDC92 non-induced	average intensity of phosphorylation				PhosphoS itePlus
	phosphoresidue	CCDC92+mock	CCDC92+TTBK2	CCDC92+ phosphatase+ mock	

In vitro	Rabin8 induced	average intensity of phosphorylation				PhosphoS itePlus
		phosphoresidue	Rabin8+mock	Rabin8+TTBK2	Rabin8+ phosphatase+ mock	
1/1	S165	0.E+00	2.E+06	0.E+00	0.E+00	*
1/1	S301	0.E+00	3.E+07	0.E+00	9.E+06	*

In vitro	Rabin8 non-induced	average intensity of phosphorylation				PhosphoS itePlus
		phosphoresidue	Rabin8+mock	Rabin8+TTBK2	Rabin8+ phosphatase+ mock	
1/1	S87	1.E+07	1.E+07	0.E+00	0.E+00	*
1/1	S163	1.E+07	1.E+07	0.E+00	0.E+00	*
1/1	S266	1.E+09	1.E+09	0.E+00	0.E+00	*
1/1	S288	8.E+08	7.E+08	2.E+06	1.E+07	*
	clusters					
1/1	S261 - S266	2.E+07	2.E+07	0.E+00	0.E+00	*

2/2	S817	9.E+09	1.E+07	4.E+09	4.E+06	*	-
2/2	T820	4.E+09	0.E+00	9.E+09	0.E+00		T2m
2/2	T826	0.E+00	0.E+00	2.E+08	0.E+00		T1h-S, T1m-S, T2m-S
2/2	T828	0.E+00	0.E+00	2.E+08	0.E+00	*	T2m
2/2	S832	0.E+00	0.E+00	2.E+07	0.E+00		T1h, T1m, T2m
2/2	T848	0.E+00	0.E+00	8.E+08	0.E+00		T1h-S, T1m-S
2/2	T851	0.E+00	0.E+00	4.E+08	0.E+00		T2m
2/2	S852	5.E+08	0.E+00	5.E+09	0.E+00		T2m
2/2	S855	7.E+08	8.E+06	2.E+10	9.E+05		T2m
2/2	S886	1.E+09	0.E+00	2.E+09	0.E+00		T2m
2/2	S897	0.E+00	0.E+00	8.E+08	0.E+00		T2m
2/2	T898	2.E+07	0.E+00	8.E+08	0.E+00		-
2/2	S921	5.E+08	0.E+00	3.E+09	0.E+00		T1h, T1m, T2m
2/2	T929	0.E+00	0.E+00	2.E+09	0.E+00		T2m, T1m-S
2/2	S954	2.E+08	0.E+00	5.E+09	0.E+00		T2m, T1h-T, T1m-T
2/2	T955	0.E+00	0.E+00	3.E+08	0.E+00		T2m
2/2	S958	5.E+07	0.E+00	1.E+09	0.E+00		T2m
2/2	S959	2.E+07	0.E+00	1.E+09	0.E+00		T1h, T1m, T2m
2/2	S960	1.E+07	0.E+00	5.E+08	0.E+00	*	T2m
2/2	S963	7.E+08	9.E+06	9.E+09	0.E+00	*	T1h, T1m, T2m
2/2	S990	0.E+00	0.E+00	3.E+08	0.E+00		T2m
2/2	S996	1.E+08	4.E+07	2.E+10	5.E+06		T1h, T1m, T2m
2/2	S999	5.E+07	0.E+00	9.E+09	0.E+00		T1h, T1m, T2m
2/2	T1009	0.E+00	0.E+00	9.E+07	0.E+00		-
2/2	S1024	0.E+00	0.E+00	4.E+08	0.E+00		T1h, T1m, T2m
2/2	S1030	6.E+07	0.E+00	7.E+09	0.E+00		T2m, T1m-T
2/2	S1033	4.E+08	0.E+00	1.E+10	0.E+00		T2m
2/2	S1035	5.E+07	0.E+00	7.E+08	0.E+00		T2m
2/2	S1039	4.E+08	0.E+00	6.E+09	0.E+00	*	T2m
2/2	S1042	2.E+08	0.E+00	3.E+09	0.E+00	*	T2m
2/2	S1046	0.E+00	0.E+00	8.E+08	0.E+00		T2m
2/2	S1048	3.E+06	0.E+00	2.E+09	0.E+00		T1m-T
2/2	S1100	3.E+07	0.E+00	2.E+08	0.E+00		T2m, T1h
2/2	S1101	5.E+07	0.E+00	8.E+08	0.E+00		T2m
2/2	S1103	6.E+08	3.E+06	2.E+09	9.E+06	*	T2m
2/2	S1105	1.E+07	0.E+00	2.E+08	0.E+00		T2m
2/2	S1109	2.E+07	0.E+00	3.E+09	0.E+00		T2m
2/2	T1163	0.E+00	0.E+00	7.E+07	0.E+00		T2m
2/2	S1182	1.E+09	8.E+08	4.E+09	3.E+08		T2m
	clusters						
2/2	S936 or S937	0.E+00	0.E+00	1.E+08	0.E+00		T2m
2/2	S1180 or S1181	3.E+08	2.E+07	2.E+10	9.E+06		T2m
2/2	S1240 or S1243	1.E+10	3.E+07	2.E+09	9.E+06		T2m

In vivo	CEP164 induced	average intensity of phosphorylation		PhosphoSitePlus
	phosphoresidue	CEP164+mock	CEP164+TTBK2	
no.identified/no .repeats				
1/1	S94	1.E+06	4.E+07	
1/1	S104	2.E+06	1.E+08	
1/1	S129	5.E+05	8.E+08	
1/1	S130	5.E+05	8.E+08	
1/1	S135	1.E+06	2.E+09	
1/1	S136	1.E+06	2.E+09	
1/1	S166	4.E+06	1.E+09	
1/1	S168	2.E+07	2.E+09	
1/1	S171	0.E+00	1.E+08	
1/1	S172	7.E+07	5.E+08	
1/1	S201	5.E+08	2.E+09	*
1/1	S270	1.E+09	5.E+09	*
1/1	S273	1.E+09	5.E+09	*

In vivo	CEP164 non-induced	average intensity of phosphorylation		PhosphoSitePlus
	phosphoresidue	CEP164+mock	CEP164+TTBK2	
no.identified/no .repeats				
1/1	S25	0.E+00	1.E+07	
1/1	T156	6.E+08	3.E+08	
1/1	T218	3.E+07	4.E+07	
1/1	S226	2.E+07	8.E+06	
1/1	S230	4.E+06	0.E+00	
1/1	S233	4.E+06	0.E+00	
1/1	S286	3.E+09	1.E+09	*
1/1	S291	2.E+08	2.E+08	
1/1	S292	5.E+05	6.E+07	
1/1	S379	1.E+09	1.E+08	
1/1	S380	3.E+07	2.E+07	
1/1	S383	3.E+07	2.E+07	
1/1	S420	4.E+08	4.E+08	

1/1	T280	1.E+08	4.E+08	
1/1	S304	4.E+06	1.E+08	
1/1	S319	4.E+06	7.E+09	*
1/1	S337	0.E+00	1.E+09	
1/1	S343	0.E+00	5.E+08	
1/1	S359	0.E+00	5.E+09	*
1/1	S398	0.E+00	6.E+07	
1/1	S400	1.E+07	2.E+08	
1/1	S403	0.E+00	2.E+08	
1/1	S407	3.E+06	1.E+09	*
1/1	S452	3.E+07	2.E+08	
1/2	S487	7.E+06	6.E+08	
1/2	T490	0.E+00	7.E+07	
1/2	S514	9.E+07	2.E+09	
1/2	S517	1.E+07	7.E+08	
1/2	S519	3.E+06	1.E+08	
2/2	S588	0.E+00	3.E+08	*
1/2	S643	1.E+07	2.E+08	
1/2	S645	0.E+00	3.E+07	
1/2	S646	0.E+00	2.E+08	*
1/2	S679	0.E+00	4.E+07	
1/2	S680	2.E+06	1.E+07	
1/2	S695	0.E+00	1.E+08	
2/2	S732	0.E+00	4.E+08	
2/2	S735	1.E+06	2.E+09	*
1/2	T765	0.E+00	1.E+07	
2/2	S771	1.E+09	5.E+09	
1/2	S779	2.E+06	4.E+07	
1/2	S780	5.E+06	1.E+08	
1/2	S791	0.E+00	1.E+07	
1/2	S822	1.E+06	9.E+06	
1/2	S833	0.E+00	2.E+07	
1/2	S834	3.E+06	1.E+08	
3/3	S970	0.E+00	2.E+08	
2/3	S1013	4.E+06	1.E+08	*
2/3	S1022	0.E+00	7.E+06	*
3/3	S1030	2.E+05	1.E+08	
2/3	S1031	2.E+06	2.E+08	
2/3	S1054	4.E+08	2.E+09	*
1/3	S1081	2.E+06	2.E+07	
2/3	S1093	0.E+00	5.E+06	
2/3	S1095	0.E+00	5.E+06	
3/3	S1112	0.E+00	1.E+08	
2/3	S1144	1.E+07	1.E+09	
1/3	S1199	4.E+08	1.E+09	
2/3	S1255	3.E+07	2.E+09	
2/3	S1267	6.E+06	7.E+07	*
2/3	S1317	5.E+07	1.E+08	
3/3	S1346	2.E+06	3.E+08	
3/3	S1347	2.E+06	7.E+08	
1/3	T1351	0.E+00	3.E+07	
2/3	S1386	1.E+06	4.E+07	*
1/3	S1388	0.E+00	1.E+07	*
3/3	T1435	5.E+06	6.E+07	*
2/3	S1443	5.E+06	1.E+08	*
	clusters			
1/2	S577 or T578	1.E+08	3.E+09	*

In vivo	CEP83 induced	average intensity of phosphorylation	
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1/1	S430	9.E+07	1.E+08	*
1/1	S455	3.E+07	1.E+07	*
1/1	S472	9.E+08	1.E+09	*
1/2	S523	0.E+00	7.E+06	
2/2	S531	5.E+08	1.E+08	
2/2	S544	7.E+08	5.E+10	
2/2	S566	6.E+10	1.E+11	*
2/2	T568	1.E+10	2.E+10	*
2/2	S572	5.E+10	9.E+10	*
1/3	S1080	1.E+05	1.E+06	*
2/3	S1205	2.E+08	1.E+09	
2/3	T1209	1.E+07	2.E+07	
3/3	S1213	5.E+09	5.E+09	
2/3	S1224	8.E+05	4.E+06	
1/3	S1233	6.E+07	3.E+07	
1/3	S1234	3.E+07	2.E+07	
1/3	S1238	6.E+08	1.E+08	
2/3	S1252	1.E+07	1.E+08	*
2/3	T1253	2.E+07	5.E+08	
1/3	S1258	4.E+06	7.E+06	
2/3	T1309	5.E+07	9.E+07	
1/3	S1322	0.E+00	4.E+06	*
1/3	S1372	0.E+00	7.E+06	
3/3	S1374	6.E+07	3.E+08	
1/3	S1397	0.E+00	4.E+06	
1/3	S1399	0.E+00	4.E+06	
1/3	S1406	0.E+00	7.E+06	
1/3	T1408	0.E+00	7.E+06	
	clusters			
1/3	S1230 or S1231	2.E+07	6.E+06	
1/3	S1325 or S1326	0.E+00	4.E+06	

In vivo	CEP83 non-induced	average intensity of phosphorylation	PhosphoSitePlus
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no.identified/no .repeats	phosphoresidue	CEP83+mock	CEP83+TTBK2	PhosphoSitePlus
1/2	S27	1.E+07	3.E+07	
1/2	T51	2.E+07	4.E+07	
2/2	T111	2.E+07	7.E+07	*
2/2	S182	0.E+00	1.E+08	
2/2	S241	9.E+05	8.E+08	
2/2	S265	0.E+00	9.E+07	
1/2	S272	3.E+05	9.E+07	
2/2	S286	0.E+00	5.E+08	
2/2	S288	0.E+00	1.E+09	*
1/2	T292	0.E+00	2.E+07	
2/2	S318	7.E+04	9.E+08	
1/2	T324	0.E+00	1.E+07	
2/2	S346	6.E+06	1.E+09	
2/2	S353	1.E+08	4.E+09	
1/2	S433	0.E+00	4.E+07	
2/2	S446	0.E+00	2.E+08	
1/2	S469	0.E+00	6.E+07	
2/2	S515	3.E+05	7.E+08	
2/2	T527	1.E+07	6.E+08	
1/2	T597	0.E+00	2.E+07	
2/2	S676	4.E+07	3.E+08	*
	clusters			
2/2	S309 or S310	0.E+00	6.E+07	

no.identified/no .repeats	phosphoresidue	CEP83+mock	CEP83+TTBK2	*
2/2	S698	7.E+09	1.E+10	
2/2	S699	1.E+09	8.E+08	

In vivo	CEP89 induced	average intensity of phosphorylation		
no.identified/no .repeats	phosphoresidue	CEP89+mock	CEP89+TTBK2	PhosphoSitePlus
2/2	S153	3.E+08	3.E+09	*
1/2	S256	0.E+00	3.E+07	
1/2	S292	0.E+00	2.E+08	
2/2	S293	2.E+08	1.E+09	
1/2	T386	0.E+00	3.E+07	
1/2	S415	0.E+00	3.E+07	
1/2	S420	0.E+00	3.E+07	
2/2	S463	1.E+07	8.E+07	
1/2	S504	0.E+00	4.E+07	
2/2	S558	6.E+07	4.E+08	
1/2	T560	0.E+00	3.E+07	*
2/2	S600	1.E+07	2.E+08	
2/2	S631	2.E+07	3.E+08	
2/2	S669	0.E+00	1.E+07	
2/2	T739	5.E+06	3.E+07	*

In vivo	CEP89 non-induced	average intensity of phosphorylation		
no.identified/no .repeats	phosphoresidue	CEP89+mock	CEP89+TTBK2	PhosphoSitePlus
1/2	S25	0.E+00	7.E+05	*
2/2	S50	1.E+08	2.E+08	*
1/2	S77	2.E+08	5.E+06	*
1/2	S113	2.E+08	6.E+06	*
2/2	S114	9.E+09	2.E+08	
1/2	S117	2.E+08	1.E+07	
1/2	S134	2.E+08	8.E+06	
2/2	S340	4.E+08	3.E+08	
2/2	S344	2.E+08	8.E+08	
1/2	S515	7.E+06	2.E+07	
1/2	S522	0.E+00	1.E+07	
1/2	T683	2.E+07	8.E+06	

In vivo	CCDC92 induced	average intensity of phosphorylation		
no.identified/no .repeats	phosphoresidue	CCDC92+mock	CCDC92+TTBK2	PhosphoSitePlus
1/3	S71	2.E+06	3.E+07	
1/3	S79	6.E+07	3.E+08	
1/3	S81	4.E+06	1.E+07	
2/3	T117	0.E+00	2.E+06	
1/3	S138	0.E+00	6.E+07	
1/3	T142	0.E+00	4.E+07	
3/3	S145	0.E+00	9.E+07	
2/3	S146	0.E+00	3.E+08	
1/3	S153	0.E+00	1.E+07	
3/3	S160	6.E+04	5.E+07	

In vivo	CCDC92 non-induced	average intensity of phosphorylation		PhosphoSitePlus
no.identified/no .repeats	phosphoresidue	CCDC92+mock	CCDC92+TTBK2	
1/3	S171	0.E+00	5.E+06	
1/3	S172	2.E+08	3.E+07	
1/3	S176	2.E+09	4.E+08	*
2/3	S179	1.E+10	9.E+08	
1/3	S181	3.E+07	3.E+06	*
2/3	S183	1.E+10	7.E+08	*
3/3	S211	1.E+10	8.E+09	
2/3	S277	4.E+07	1.E+08	*
3/3	T299	3.E+08	1.E+09	
1/3	T309	0.E+00	2.E+06	

2/3	S209	4.E+07	7.E+09	*
2/3	S252	7.E+05	1.E+07	
2/3	S270	0.E+00	4.E+07	
2/3	S273	1.E+06	2.E+07	

In vivo no.identified/no. .repeats	Rabin8 induced phosphoresidue	average intensity of phosphorylation		PhosphoSitePlus
		Rabin8+ mock	Rabin8+ TTBK2	
1/3	S98	0.E+00	6.E+07	
1/3	S100	0.E+00	6.E+07	
1/3	S112	0.E+00	4.E+08	
2/3	S165	1.E+07	2.E+08	*
1/3	T213	0.E+00	4.E+07	
3/3	S215	6.E+05	7.E+08	
1/3	T289	9.E+06	8.E+07	*
3/3	S316	2.E+05	4.E+08	
1/3	S358	3.E+05	5.E+07	
1/3	S385	0.E+00	4.E+07	
2/3	S413	4.E+07	2.E+08	

In vivo no.identified/no. .repeats	Rabin8 non- induced phosphoresidue	average intensity of phosphorylation		PhosphoSitePlus
		Rabin8+ mock	Rabin8+ TTBK2	
1/3	S32	3.E+06	7.E+06	
1/3	S35	1.E+07	8.E+06	
3/3	S86	2.E+08	5.E+08	*
3/3	S87	2.E+08	5.E+08	
1/3	S97	0.E+00	6.E+06	
3/3	T111	0.E+00	3.E+06	
1/3	S144	4.E+06	2.E+05	
1/3	S147	6.E+05	2.E+06	*
2/3	S154	1.E+08	7.E+07	
1/3	S157	3.E+07	2.E+07	*
3/3	S163	6.E+08	3.E+09	*
3/3	S263	3.E+09	7.E+09	*
2/3	T265	6.E+07	3.E+07	*
3/3	S266	8.E+09	2.E+10	*
2/3	S288	5.E+09	2.E+09	
1/3	S290	3.E+06	0.E+00	
1/3	S291	0.E+00	2.E+07	
2/3	S294	3.E+07	2.E+07	*
2/3	S296	7.E+08	5.E+08	*
1/3	S301	0.E+00	4.E+06	
1/3	S370	0.E+00	4.E+06	
	Clusters			
1/3	T122 or T123	0.E+00	5.E+05	*
1/3	S261 or S262	0.E+00	1.E+08	

no. identified/no. repeats	HEK293 TTBK2	endogenous CEP164	
		WT	KO
2/4	S171	3.26E+06	0.00E+00
4/4	S172	2.50E+06	0.00E+00
1/4	S201	1.11E+06	0.00E+00
2/4	S226	6.67E+08	1.85E+09
3/4	S359	2.84E+08	0.00E+00
2/4	S373	1.40E+08	1.29E+07
4/4	S379	4.09E+08	1.61E+08
4/4	S380	3.93E+08	1.63E+08
4/4	S383	5.09E+08	1.69E+08
3/4	S389	4.83E+07	0.00E+00
4/4	S398	1.09E+08	1.01E+07
1/4	S400	9.97E+06	0.00E+00
1/4	S403	9.97E+06	0.00E+00
4/4	S452	5.95E+08	3.20E+08
4/4	S454	7.01E+08	3.28E+08
4/4	S455	7.25E+08	3.48E+08
4/4	S472	1.16E+09	8.21E+08
2/4	S483	1.28E+09	5.67E+07
2/4	S487	1.36E+09	5.67E+07
2/4	T490	1.37E+07	0.00E+00
4/4	S514	6.18E+07	1.26E+06

no. identified/no. repeats	HEK293 TTBK2	FLAG-CEP164 N-term	
		WT	KO
2/2	S166	7.89E+07	1.05E+07
2/2	S168	3.86E+06	8.80E+05
2/2	S172	3.23E+07	3.29E+06
1/2	S201	3.43E+06	0.00E+00
2/2	Y203	5.31E+06	2.41E+06
2/2	S210-S230	1.10E+09	1.77E+09
2/2	S286	0.00E+00	8.01E+06
2/2	T329	3.90E+06	7.61E+06
2/2	S373	7.09E+06	1.48E+07
2/2	S379	1.61E+09	2.36E+09
2/2	S380	1.62E+09	2.37E+09
2/2	S383	1.63E+09	2.39E+09
1/2	S452	0.00E+00	1.92E+06
2/2	S454	1.16E+09	1.68E+09
2/2	S455	1.16E+09	1.69E+09

4/4	S517	7.49E+07	8.60E+05
4/4	S519	3.13E+07	0.00E+00
1/4	S531	1.77E+07	0.00E+00
3/4	S544	2.08E+08	1.33E+07
4/4	S566	1.05E+08	3.74E+07
4/4	S568	1.31E+08	6.47E+07
4/4	S572	1.03E+08	1.08E+08
3/4	S588	2.49E+07	0.00E+00
2/4	S646	1.11E+07	5.65E+05
1/4	S1054	0.00E+00	1.82E+06
4/4	S1205	2.36E+08	2.05E+08
4/4	S1213	3.27E+08	2.62E+08
2/4	S210-S230	1.57E+08	4.63E+07
2/4	S577 or T578	1.29E+08	6.96E+07

>CEP164		Peptides that contain said motif as identified by algorithm are indicated by 1		
		Motif-X motif xxxxxxS/TxxExxx	MODL motif xxxxxxS/TxxExxx	MODL motif xxxxxxS/TLxxxxx
S94	CDEHYRSLVIQER			1
S104	QERAKLSTSGAIK			
S129	DRDPPKSSLALGS			
S130	RDPPKSSLALGSS			1
S135	SSLALGSSLAPVH			
S136	SLALGSSLAPVHV			1
S159	LVDTPPSALRGSQ			
S164	PSALRGSQSVSLG			
S166	ALRGSQSVSLGSS			
S168	RGSQSVSLGSSVE			1
S171	QSVSLGSSVESGR	1	1	
S172	SVSLGSSVESGRQ			
S201	TKGLLSIYEDKT	1	1	
S257	DFEYEESLRTSQP			1
S270	EKKDVLSDSDAA			1
S304	GKGRQGSGARPGL			
S319	KEENEKSEPKICR			
T329	ICRNLVTPKADPT			
S337	KADPTGSEPAKAS			
S343	SEPAKASEKEAPE	1	1	
S359	DAGEEGSRREEAA	1	1	
S398	MKEPQLSDSIASD			
S400	EPQLSDSIASDPK			
S403	LSDSIASDPKSFH			
S407	IASDPKSFHGLDF			
S452	IEDKDDSQSSQDE			
T490	PPRSLATEEPPQ		1	
S645	QKEQSLSLRERL			
S646	KEQSLSLRERLQ	1	1	
S679	LRAQVQSSTQADE			
S680	RAQVQSSTQADED			
S695	RAEQEASLQKLRE			1
S732	KEEIEASEKSEQA			
S735	IEASEKSEQAALN			
T765	RKEAVATLEKEHS			1
S771	TLEKEHSAELERL			
S779	ELERLCSSLEAKH	1	1	
S780	LERLCSSLEAKHR			1
S791	HREVVSSLQKKIQ			1
S822	HRVHQKSYHVAGY			
S833	GYEHELSSLLREK			
S834	YEHELSSLLREKR			1
S970	RQVALKSEEATAT			
S1013	RKLKLESQVDLLQ			
S1022	DLLQAQSQQLQKH			
S1030	QLQKHFSLEAEA	1	1	
S1031	LQKHFSLEAEAQ			1
S1081	TKEVSSLSQSKE			1
S1093	EDLYLDSLSSHNV			1
S1095	LYLDSLSSHNVWH			
S1096	YLDSLSSHNVWHL			
S1112	EGVALRSAKEFLV	1	1	
S1144	WRHELASAQEVAK	1	1	
S1199	LNQLESSLWEEAS	1	1	
S1267	IHGLSHSLRQISS			1
S1346	QGPRLPSSVAQTV			
S1347	GPRLPSSVAQTVD			
T1351	PSSVAQTVDDFLL			
S1386	SRLGYMSASEQLR	1	1	
S1388	LGYMSASEQLRLL			
S1443	KPKATLSLLQLGL			1

>CEP83				
S27	DSGLTGSQSEFQK	1	1	
T51	HKANYQTLKAEHT			1
S182	GKIKYESEIARLE			
S241	KAEKENSEAQVEN			
S265	MQATVRSLEAEKQ			1
S272	LEAEKQSANLRAE			
S286	LEKELQSSSEQNT	1	1	
S287	EKELQSSSEQNTF			
S288	KELQSSSEQNTFL			
T292	SSSEQNTFLINKL			
S309	REINTLSSKVKEL			
S310	EINTLSSKVKELK			
S318	VKELKHSNKLEIT			
T324	SNKLEITDIKLET			
S346	ERNKIQSELDGLQ			
S433	EEKLRASQMAEEI			
S446	TRKELQSVRLKLQ			
S469	KEKNENSDLKQQI			
S515	ECRNFRSQAEGAQ	1	1	
T527	QLEAEKTLLEEKQI		1	
T597	KKEELETENQVLN			
S676	QHORELSLLRKRL			1

>CEP89				
S25	GLLPAASVAPKAA			
S144	KELGDVSAREDRG	1	1	
S256	LNNMNQSLTLELN			1
S292	KEAEKASSQEVAA	1	1	
T386	KDELNATLKEEMR		1	
S415	HQELNKSSAVTSE			
S463	ERLQEVSKLTKQL			
S504	QELKTHSDGKIAV			
S558	LLLEKNSLTEQNK	1	1	
T560	LEKNSLTEQNKAL			
S600	AMGNEMSAHQYLA			
S631	LAKCLESEKDGVL			
S669	LKLGDISHRLLEQ			

>CCDC92				
S71	ELTVKSSEQTGDG			
S79	QTGDGTSKSELK			
S81	GDGTSKSELKKR			
T117	QKNAMITVLENTI		1	
S138	EELKAKSHKLTL			
T142	AKSHKLTLLSSEL			1
S145	HKLTLLSSELEQR			
S146	KLTLLSSELEQRA	1	1	
S153	ELEQRASTIAYLT			
S160	TIAYLTSQLHAAK			
S188	GSPVLASYKPAPP			
S209	RRRMKKSLSAPLH			1
S252	FLLARESAEVHLI			
S270	VIPPIASDRSGEQ			
S273	PIASDRSGEQHSP			
S299	HRIHHATPPQAQP			
S309	AQPEVKTLAVDQV			1

>Rabin8				
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S98	NCAEISSISFHVT			
S100	AEISSISFHVTD			
S112	PAPCSTSGVTAGL			
S165	SRLRSPSVLEVRE	1	1	
T213	QELEELTASLFEE			
S215	LEELTASLFEEAH	1	1	
T289	HTRNKSTSSAMSG			
S301	GSHQDLSVIQPIV			
S316	CKEADLSLYNEFR			1
S358	SKSELASAVLEAV			
S385	IRFVKASAVECGG	1	1	
S413	RIKLGSSNYYYI			

>DVL3				
S636	SEHSRSHHSLAS			
S639	SHRSHHSLASSLR			1
S643	HHSLASSLRSHHT			1

>TTBK2				
S53	VALKVESAQQPKQ			
T114	QSRGFTTISTTLR			
S116	RGFTTISTTLRLG			
T118	TFTTISTTLRLGRQ			1
S131	ILESIESIHSVGF			
S134	SIESIHSVGFHLR			
S194	GTVRYASINAHNR			
S237	DKEQVGSIKERYD	1	1	
S332	IGIANATPIPGDL			
S371	PDKLPGSLGHPRP			1
S428	SPIRVRSEITQPD			
T431	RVRSEITQPDRDI			
S445	LVRKLRSIHSFEL			
S448	KLRSIHSFELEKR			
T463	LEPKPDTDKFLET			
T469	TDKFLETCKEKMQ		1	
S499	PCVPAVSRTDHIW			
S549	CKQEIDSKWVIV			
T566	DLQDFRTNEAVGH			
T613	DHLKKETSGVVLAL			
S614	HLKKETSGVVLAL			
S621	GVVLALSAEGPPT			
T627	SAEGPPTAASEQY			
S630	GPPTAASEQYTDR			
T634	AASEQYTDRELELQ			
T701	LQPMPTVELYSP			
S706	PTVELYSPRENFS	1	1	
T728	PSGGSRDGLGLQI			
S751	IRESNKSQDLGPK			
T777	ENLPGETEESIL			
S781	GETEESILLES			
S786	KSILLESNEDEK	1	1	
S794	NEDEKLSRGQHCI			
S804	HCIEISSLPGLDV			1
S817	IVEKDHSATTEPL			
T820	KDHSATTEPLDVT			
T826	TEPLDVTKTQTF			
T828	PLDVTKTQTFV			
S832	TKTQTFVVPNQD			
T848	EIMKLLTVGTSEI			
T851	KLLTVGTSEISSR			

S852	LLTVGTSEISSRD			
S855	VTSEISSRDIDP			
S886	KDDDIMSEDLPGH			
S897	GHQGDSTFLHQE			
T898	HQGDSTFLHQEG			
S921	ELFHCVSENEHGA	1	1	
T929	NEHGAPTRKDMVR			
S936	RKDMVRSSFVTRH			
S937	KDMVRSSFVTRHS			
S954	LAQEIDSTLESSS	1	1	
T955	AQEIDSTLESSSP			1
S958	IDSTLESSSPVSA			
S959	DSTLESSSPVSAK			
S960	STLESSSPVSAKE			
S963	ESSPPVSAKEKLL	1	1	
S990	EKRQFKSFLGDLS			
S996	SFLGDLSASDKL			
S999	GDLSSASDKLLEE			
T1009	LEEKLATVPAPFC			
S1024	EVLTPFSRLTVDS			
S1030	SRLTVDSHLRSA			
S1033	TVDSHLRSAEDS			
S1035	DSHLRSAEDSFL			
S1039	SRSAEDSFLSPII			
S1042	AEDSFLSPIISQS			
S1046	FLSPIISQSRKSK			
S1048	SPIISQSRKSKIP			
S1100	RYKVLGSSNSDSD			
S1101	YKVLGSSNSDSDL			
S1103	VLGSSNSDSDLFS			
S1105	GSSNSDSDLFSRL			
S1109	SDSDLFSRLAQIL			
T1163	SSSLPRTSSSSPS			
S1080	PHHDQRSSSPHLG			
S1081	HHDQRSSSPHLGR			
S1182	HDQRSSSPHLGRS			
S1240	GKSKPASKLSRAA			
S1243	KPASKLSRAAAAA			

Motif-X motif xxxxxxS/TxxExxx
QSVSLGSSVESGR
TKGLLSIYEDKT
SEPAKASEKEAPE
DAGEEGSRREEAA
KEQSLSLRERLQ
ELERLCSSLEAKH
QLQKHFSLEAEA
EGVALRSAKEFLV
WRHELASAQEVAK
LNQLESSLWEEAS
SRLGYMSASEQLR
DSGLTGSQSEFQK
LEKELQSSSEQNT
ECRNFRSQAIEKAQ
KELGDVSAREDRG
KEAEKASSQEVAA
LLLEKNSLTEQNK
KLTLSSSELEQRA
SRLRSPSVLEVRE
LEELTASLFEEAH
IRFVKASAVECGG
DKEQVGSIKERYD

PTVELYSPRENFS
KSILLESDNEDEK
ELFHCVSENEHGA
LAQEIDSTLESSS
ESSSPVSAKEKLL

MODL motif xxxxxxS/TxxExxx
QSVSLGSSVESGR
TKGLLGSIYEDKT
SEPAKASEKEAPE
DAGEEGSRREEAA
PPRSLATEEPPQ
KEQSLSSLRERLQ
ELERLCSSLEAKH
QLQKHFSLEAEA
EGVALRSAKEFLV
WRHELASAQEVAK
LNQLESSLWEEAS
SRLGYMSASEQLR
DSGLTGSQSEFQK
LEKELQSSSEQNT
ECRNFRSQAEKAQ
QLEAEKTLEEKQI
KELGDVSAREDRG
KEAEKASSQEVAA
KDELNATLKEEMR
LLLEKNSLTEQNK
QKNAMITVLENTI
KLTLSSSELEQRA
SRLRSPSVLEVRE
LEELTASLFEEAH
IRFVKASAVECGG
DKEQVGSIKERYD
TDKFLETCLKMQ
PTVELYSPRENFS
KSILLESDNEDEK
ELFHCVSENEHGA
LAQEIDSTLESSS
ESSSPVSAKEKLL

MODL motif xxxxxxS/TLxxxxx
CDEHYRSLVIQER
RDPPKSSLALGSS
SLALGSSLAPVHV
RGSQSVSLGSSVE
DFEYEESLRTSQP
EEKKDVSLSDAA
RAEQEASLQKLRE
RKEAVATLEKEHS
LERLCSSLEAKHR
HREVVSSLQKKIQ
YEHELSSLLREKR
LQKHFSLEAEAQ
TKEVSSLSQSKE
EDLYLDSLSSHNV
IHGLSHSLRQISS
KPKATLSLLQLGL
HKANYQTLKAEHT
MQATVRSLEAEKQ
QHQRSLLRKRL
LNNMNQSLTLELN

AKSHKLTLSEL
RRRMKKSLSAPLH
AQPEVKTAVDQV
CKEADLSLYNEFR
SHRSHSLASSLR
HHSASSLRSHHT
TFTISTTLRGRQ
PDKLPGSLGHPRP
HCIEISSLPGLV
AQEIDSTLESSP

List of plasmids	
Plasmid	source
Myc-CEP164	Cajane et al., 2014
GFP-CEP164	Cajane et al., 2014
FLAG CEP164 N-term	Cajane et al., 2014
FLAG-CEP164-M part	Cajane et al., 2014
FLAG-CEP164-C-term	Cajane et al., 2014
FLAG-CEP164 N term	Cajane et al., 2014
FLAG-CEP164 N-A term	Site directed mutagenesis of FLAG-CEP164 N term
Myc-CEP83	cDNA from Kim Joon (Joo et al, 2013, PNAS), cloned using gateway system into pDEST-MYC
FLAG-CEP83	cDNA from Kim Joon (Joo et al, 2013, PNAS), cloned using gateway system into pDEST-FLAG
GFP-CEP83	cDNA from Kim Joon (Joo et al, 2013, PNAS), cloned using gateway system into pGLAP1
Myc-CEP89	Cajane et al., 2014
FLAG-CEP89	Cajane et al., 2014
GFP-CEP89	Cajane et al., 2014
HA-CP110	CCSB human ORFeome collection, http://horfdb.dfci.harvard.edu/hv5/index.php?page=getresults&by=detail&qury=1945
GFP-Rab8a	gift from G. Pereira (Schmidt et al, JBC, 2012)
GFP-Rabin8	gift from G. Pereira (Schmidt et al, JBC, 2012)
FLAG-Rabin8	cDNA from G. Pereira, cloned into pDEST-FLAG
GFP-CCDC92	cDNA from RPE-1 cells, cloned using gateway into pglap1

FLAG-CCDC92	cDNA from RPE-1 cells, cloned using gateway into pDEST-FLAG
GFP-DVL2	Gift from R. Lefkowitz (Chen et al., Science 2003), additional reference (2)
FLAG-DVL3	Gift from S.Angers (Angers et al., Nat Cell Biol. 2006), additional reference (3)
FLAG-TTBK2 WT	Cajanek et al., 2014
FLAG-TTBK2 KD	Cajanek et al., 2014
GFP-TTBK2 WT	Cajanek et al., 2014
Myc-TTBK2	Cajanek et al., 2014
pDEST-MYC	gift from E. Nigg (Arquint et al, JCS, 2012), additional reference (4)
pDEST-FLAG	gift from E. Nigg (Arquint et al, JCS, 2012), additional reference (4)
pgLAP1	pgLAP1 was a gift from Peter Jackson, addgene plasmid #19702
pgLAP2 NEO	Cloned from pgLAP2, hygromycin resistance replaced by G418 resistance cassette
pgLAP2 NEO TTBK2 WT	cloned using gateway cloning system
pgLAP2 NEO TTBK2 KD	cloned using gateway cloning system
pOG44	V6005-20, Thermo Fisher Scientific
pSPCas9 BB GFP	https://www.addgene.org/48138/
pgLAP2 NEO CEP164 FL WT	cloned using gateway cloning system
pgLAP2 NEO CEP164 FL-A	Site directed mutagenesis of CEP164 WT

List of antibodies					
Name	Cat.no	Manufacturer	WB	IF	IP
FLAG M2	F1804, A2220	Sigma-Aldrich, Merck	1:1000 (F1804)	1:1000 (F1804)	20 µl (slurry) of adsorbed beads/dish (A2220)
Myc 9E10	M4439	Sigma-Aldrich, Merck	1:500		
GFP	ab290	Abcam	1:500		
TTBK2	HPA018113	Sigma-Aldrich, Merck	1:500	1:500	
Arl13b	17711	Proteintech		1:1000	
CAP350		Gift of Erich A. Nigg (Yan et al.,2006 MboC) Additional reference (1)		1:1000	
HA	66006-1-Ig	Proteintech		1:1000	
CEP164	22227-1-ap	Proteintech	1:1000	1:1000	2ul/ 15 cm dish
IFT88	13967-1-AP	Proteintech		1:500	
CEP83	HPA038161	Sigma-Aldrich, Merck	1:1000	1:1000	
CEP89	HPA 040056	Sigma-Aldrich, Merck	1:1000		
CEP97	22050-1-ap	Proteintech	1:1000		
γ-tubulin	T6557	Sigma-Aldrich, Merck		1:1000	
α-tubulin	11224-1-ap	Proteintech	1:1000		

HRP-anti mouse	4416	Sigma-Aldrich, Merck	1:4000		
HRP-anti rabbit	7074	CST	1:4000		

Donkey anti-mouse Alexa fluor 488	A21202	Invitrogene, ThermoFisher scientific		1:2000	
Donkey anti-rabbit Alexa fluor 488	A21206	Invitrogene, ThermoFisher scientific		1:2000	
Donkey anti-mouse Alexa fluor 568	A10037	Invitrogene, ThermoFisher scientific		1:2000	
Donkey anti-rabbit Alexa fluor 568	A10042	Invitrogene, ThermoFisher scientific		1:2000	
Donkey anti-goat Alexa fluor 647	A32849	Invitrogene, ThermoFisher scientific		1:2000	