

Supplemental Table 4. List of high confidence preys of PLK4, post SAINTexpress (v 3.3) analysis after filtering by BFDR less than or equal to 0.02. Prey Gene is as per NCBI Entrez Gene, Prey Accession is the NCBI protein accession number; Average Spectra is the average of spectra identified for the prey in both replicates; Average Control Spectra is the average spectra found across the 8 controls for a prey; AvgP (average probability across replicates); Fold Change (sum total of counts in the purification divided by counts in the controls; If necessary, fold change column will have a value of 0.1 added to cell to prevent divisions by 0.); and Bayesian FDR are listed for each bait-prey relationship. Note that PLK4 wildtype and PLK4 S286A/T290A replicates were merged for SAINT analysis. * in Actin and Centrosome Functional Annotation columns indicates previously reported interactor based on BioGRID (PMID: 26729913) and IntAct (PMID: 22121220); annotations were selected from GO Biological Process terms and, if necessary, GO Molecular Function terms and left empty if no annotations were present in UniProt.

Prey Gene	Prey Accession	Average Spectra	Average Control Spectra	AvgP	Fold Change	BFDR	Actin Functional Annotation	Centrosome Functional Annotation
ARPC1A	22907052	9	0	1	90	0	Arp2/3 complex-mediated actin nucleation	
ARPC1B	5031601	9	0	1	90	0	Arp2/3 complex-mediated actin nucleation	
ARPC2	23238211	20	1.13	1	4.44	0	Arp2/3 complex-mediated actin nucleation	
ARPC5L	13569956	6	0	1	60	0	Arp2/3 complex-mediated actin nucleation	
CDC42BPA	30089962	22.5	0	1	225	0	actin cytoskeleton reorganization	
CENPJ	130980075	11	0	1	110	0	*	*centriole replication
CEP152	303304991	60.5	0	1	605	0	*	*centriole replication
CEP192	255003833	142.5	0	1	1425	0	*	*centrosome duplication
CEP350	171184451	47	0.5	1	23.5	0	*	*microtubule anchoring
CEP63	109255226	11	0	1	110	0	*	*centriole replication
FAM190B	80861486	13.5	0	1	135	0		microtubule bundle formation
FGFR1OP	36287110	29.5	1	1	7.38	0		microtubule anchoring to centrosome
FRMPD1	239582741	4.5	0	1	45	0		
GAS2L3	28372563	11	0	1	110	0	actin cytoskeleton reorganization	
GJA1	4504001	16	0	1	160	0		
GNG12	51036603	7	0	1	70	0		
GSN	189083772	11	0	1	110	0	actin filament reorganization	
H2AFZ	4504255	8	0	1	80	0		
HIST1H2AA	25092737	12	0	1	120	0		
MPRIP	50980301	18.5	0.63	1	7.4	0	actin binding	
NEDD1	206597465	31	0.38	1	20.67	0	*	*protein localization to centrosome
POTE1	88953571	7	0	1	70	0		
SASS6	35038601	31	0	1	310	0	*	*centriole replication
SDCCAG3	89353278	41.5	0.25	1	41.5	0	*	*
SH3BGRL2	13899317	8	0	1	80	0		
STIL	115298661	41.5	0	1	415	0	*	*centrosome duplication
TMOD2	7657647	55	2.63	1	5.24	0	actin filament reorganization	
ACTA1	4501881	85	1.75	0.99	12.14	0		
CAPZA2	5453599	31	4.88	0.99	3.26	0	barbed-end actin filament capping	
CGN	16262452	16.5	0.38	0.99	11	0		
GNAI2	261878575	3.5	0	0.99	35	0		
LSR	386781455	3.5	0	0.99	35	0		
NME7	37574614	3.5	0	0.99	35	0		microtubule nucleation
AIF1L	13899241	25	1.63	0.97	3.85	0	actin filament binding	
TXNL1	4759274	23	1.63	0.97	3.54	0		
ARPC5	394025704	3.5	0	0.95	35	0	Arp2/3 complex-mediated actin nucleation	
CAMK2D	212549753	3.5	0	0.95	35	0		
ACTR2	5031571	14.5	1.25	0.95	4.14	0.01	Arp2/3 complex-mediated actin nucleation	
ALMS1	110349786	34	0.75	0.95	11.33	0.01	*	*
CEP85	40538794	2.5	0	0.95	25	0.01	*	*
FLII	372266127	8.5	0.25	0.94	8.5	0.01		
WDR1	9257257	74	3.75	0.93	4.93	0.01	positive regulation of actin filament depolymerization	
ACTBL2	63055057	31	1	0.92	7.75	0.01		
TWF1	334724463	30.5	2.38	0.9	4.07	0.01	barbed-end actin filament capping	
ACTR3	5031573	26	1	0.9	6.5	0.02	Arp2/3 complex-mediated actin nucleation	
LRRFIP2	197276647	17.5	0.63	0.9	7	0.02		
NEXN	148839339	23.5	1	0.86	5.88	0.02	regulation of cytoskeletal reorganization	
APC	189011566	13.5	0.5	0.81	6.75	0.02		