

Appendix for:

PLK1 inhibition delays mitotic entry revealing changes to the phosphoproteome of mammalian cells early in division

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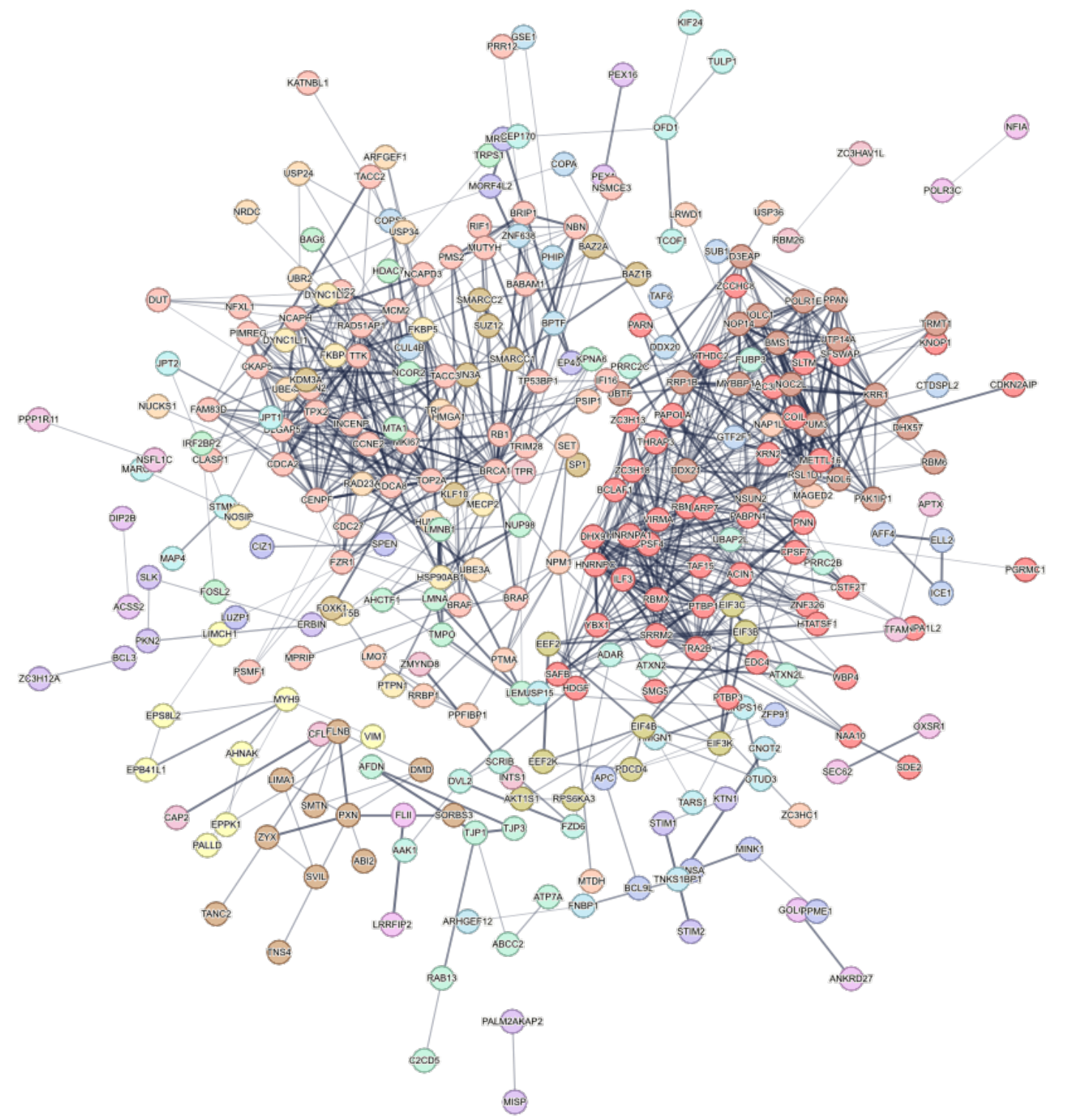
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Appendix Figure S1.



Appendix Figure S1:

Network generated by STRING database analysis depicting differentially phosphorylated proteins specific to prolonged prophase after applying linear modeling. The gene names of the corresponding proteins are shown.

Appendix Table S1.

Gene name	Protein name	Position	Sequence window	Log2 Fold Change	Adjusted p value
BABAM1	BRISC and BRCA1-A complex member 1	29	EPRPRTSRNPEGAED	-0.13564	0.452216
		65	ADDGSLNTSGAGPKS	3.204965	0.016133
BRAF	Serine/threonine-protein kinase B-raf	429	PQRERKSSSSSEDRN	0.020957	0.950661
		732	HRSASEPSLNRAFGQ	-0.46754	0.021532
BRAP	BRCA1-associated protein	97	ERKSSEASPTAQRSK	0.758572	0.036624
		571	IAMASASSPASSGGS	1.233362	0.15329
BRCA1	Breast cancer type 1 susceptibility protein	1524	LQNRNYPQQEELIKV	-1.30686	0.007531
		967	GNETGLITPNKHGLL	-0.17774	0.826994
BRIP1	Fanconi anemia group J protein	1032	SSENSASSPPRFKTE	0.035918	0.946208
		226	CSTKQGNSEQSSNTI	-1.83983	0.001085
CCNE2	G1/S-specific cyclin-E2	990	IVISRSTPTFNKQT	-0.23038	0.223636
		21	PQPSQTESPQEAQII	-2.4767	0.000111
CDC27	Cell division cycle protein 27 homolog	220	NRLNLESSNKSYSLN	-1.35576	0.004893
CDC42	Cell division cycle-associated protein 2	710	EPKAGTDSVPVCASV	1.182501	0.000399
CDCA8	Borealin	219	YNISGNGSPPLADSKE	1.338073	0.001152
		154	PSKKRTQSIQKGKGG	0.468087	0.752849
CENPF	Centromere protein F	821	CRLEADQSPKNSAIL	0.501219	0.225936
		2922	SVTEKRLSSGQNKAS	0.573635	0.094435
		1121	MTDNQNNKSKEAGGL	3.917572	0.001717
		3079	VNNLPERSPPTDSPRE	2.153058	0.000459
		3054	KVKVAQRSPVDSGTI	0.114245	0.720904
CKAP5	Cytoskeleton-associated protein 5	144	VSLNPCNTPQKIFTT	0.911767	0.011247
		816	FEKMQGQSPAPATRG	1.182614	0.044594
CLASP1	CLIP-associating protein 1	1223	SRDGGAAAPATEGRG	0.340762	0.124086
		1091	SSNTSVGSPSNTIGR	1.696642	0.040077
DLGAP5	Disks large-associated protein 5	646	RIRTRRQSSGSATNV	0.307958	0.44256
		656	SATNVASTPDNRRGS	1.075414	0.101246
		662	GIPQQTITSPENAGPQ	2.025834	0.000199
DUT	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial	777	KNTASQNSILEEGET	0.407237	0.715857
		248	RGSGGFGSTGKN	1.260963	0.002084
FAM64A	Protein FAM64A	106	RIQESQSGTKWLV	1.82903	0.009454
		16	GTSVRRRLQHQEQL	0.592557	0.057232
FAM83D	Protein FAM83D	462	GTQSTEGSPVSKMSV	1.241782	0.001824
FZR1	Fizzy-related protein homolog	70	RINENEKSPSQNRKA	0.825274	0.00045
GINS2	DNA replication complex GINS protein PSF2	182	QPLESTQSQDF	-1.61545	0.001327
		106	KKEVDATSPAPSTSS	0.976518	0.002982
IFI16	Gamma-interferon-inducible protein 16	153	EEQTQPPSPAGAGMS	-0.22222	0.496304
		123	KTEGAEATPGAQKRK	-0.25215	0.559768
		446	GPREPPQSAARRKSY	-0.0091	0.988528
INCENP	Inner centromere protein	263	KLRIAQVSPGPRDSP	0.986793	0.150242
		421	NPKPAASSPETPSAG	1.649486	0.031907
		481	PRSKTPSPSPCASKV	0.066519	0.826603
		135	SGSSQTESPSSKYSG	0.816669	0.007063
KATNBL1	KATNB1-like protein 1	13	ESFTMASSPAQRRRG	-0.20928	0.503571
MCM2	DNA replication licensing factor MCM2	139	RRLGLYDSDEEDEER	-0.19919	0.461216
		27	GNDPLTSSPGRSSRR	-1.03073	0.026971
MKI67	Antigen KI-67	584	VISPPAPSPRKTPVA	0.204023	0.909901
		2783	PAASVTGSRRRPRAP	1.784411	0.031297
		1253	TTKIPCDSPQSDPVD	1.950414	0.00924
		1329	LTENLTGSKRRPQTP	0.812784	0.592089
		1815	QPGNLPGSNRRLQTR	-0.13797	0.787722
		2022	VGKLTQTSGKTTQTH	1.108794	0.020309
		357	QYSQQQNSPQKHKNK	-0.04028	0.939795
		1376	TKMPCESSPPESADT	1.319096	0.005691
		374	YTTGRRESVNLGKSE	-0.17389	0.739664
		648	MICSKRRSGASEANL	1.680698	0.24483
		621	PKRGGGRKSGNLPSKR	1.771414	0.027648
		1628	DPDKNPASSKRRLKT	0.515792	0.524267
		328	RDVESVQTPSKAVGA	0.014021	0.984762
		2773	LKESAKQTPAPAAVS	0.50022	0.7761
		1327	LDLTENLTGSKRRPQ	0.454921	0.213038
		1503	SQDPDVPDTPTSKPKQ	0.396177	0.455166
MPRIIP	Myosin phosphatase Rho-interacting protein	891	GGGEATGSLAQGKD	1.011246	0.001912
MUTYH	A/G-specific adenine DNA glycosylase	512	SKRSQVSSPCKSRKP	0.420998	0.023535
NBN	Nibrin	343	TTPGPSLSQGVSVDE	-1.53502	0.000459
NCAPD3	Condensin-2 complex subunit D3	517	FSYQRQTSNRSEPSG	-1.86704	0.02044
		15	LPATMNNSSSETRGH	2.490922	0.032082
NCAPH	Condensin complex subunit 2	459	KQDAPSQSENKKKST	0.078348	0.943523
		87	DSPRLLASPSSRSID	0.861254	0.38164
NDNL2	Melanoma-associated antigen G1	304	PSGPAAPS	1.001316	0.008161
		64	SQGSQGPSPPQGARRA	1.064173	0.029366
NFXL1	NF-X1-type zinc finger protein NFXL1	50	GAVPSGTSPGCVATT	1.595657	0.033303
PMS2;PMS2CL	Mismatch repair endonuclease PMS2;Protein PMS2CL	403	MVEKQDQSPSLRTGE	1.193663	0.00045
PRR12	Proline-rich protein 12	917	AGAYRSPQQTGKAP	-1.10341	0.015456
PSMF1	Proteasome inhibitor P131 subunit	153	WEKANVSSPHREFPP	1.074455	0.003203
RAD51AP1	RAD51-associated protein 1	120	VTTNVQNSQDKSIEK	-1.65658	0.004118
		327	LVVSVKSPNQSLRL	0.582974	0.183504
RB1	Retinoblastoma-associated protein	249	AVIPINGSPTPRRG	0.77095	0.007063
		356	DSFETQRTPRKSNLD	0.240314	0.15906
RIF1	Telomere-associated protein RIF1	2161	SLVSANDSPSGMQTR	0.736809	0.003275
		1579	WKNKSNEVDIQDQE	0.03069	0.925885
		1688	KRLHKRDSFDNCSLG	-0.41527	0.187504
		2195	RSQEDEISSPVNKKVR	0.319566	0.418184
SLAIN2	SLAIN motif-containing protein 2	2196	SQEDEISSPVNKVRR	0.215008	0.539879
		63	IPSSGAASPRGFPLG	1.578614	0.000635
TACC2	Transforming acidic coiled-coil-containing protein 2	48	AGSLGPGSPVRAGAS	0.000119	0.999812
		1635	PRSTCAPSPQREVLT	1.402082	0.008431
TACC3	Transforming acidic coiled-coil-containing protein 3	2256	DSSGQEDSPAKGLSV	0.519993	0.036132
		2226	GGGRVQNSPPVGRKT	-0.17854	0.215832
TOP2A	DNA topoisomerase 2-alpha	317	AGRAMTILSPQEEVAA	0.369546	0.423235
		434	SEAQPPESPETRLGQ	0.822245	0.001201
TP53BP1	Tumor suppressor p53-binding protein 1	1106	DEEENEESDNEKETE	-0.05939	0.862834
		1247	KNENTEGSPQEDGVE	0.102269	0.858992
		4	MEVSPLOQPVNE	0.940392	0.003275
		1213	QMAEVLPSPRGQRVI	1.924142	7.36E-05
TPX2	Targeting protein for Xklp2	862	TQEKTSNLTEDSKM	1.845217	0.104161
		552	IEDTEPMSPVLSNKF	-2.26502	0.003153
		1028	AVAESVASPQKTMVS	-0.50497	0.007574
		831	EPVEQDSSQPSLPLV	-0.28053	0.416727
TRIM28	Transcription intermediary factor 1-beta	380	TPFIVPSSPTEQEGR	-0.57136	0.008651
		186	TAEKNASSPEKAKGR	0.140839	0.41381
TTK	Dual specificity protein kinase TTK	738	QPLTVVPVSFKFSTRF	1.107704	0.000479
		369	KICRDPQTPTVLQTKH	0.074426	0.84967
		19	AASAASGSPGPGEGS	-0.29259	0.514772
		697	TGVVAKLSPANQRKC	0.771591	0.088797
		473	SGVKRSRSGEGEVSG	-0.38443	0.018897
		436	VFSVSKQSPPISTSK	0.464797	0.018196

Appendix Table S1:

Table showing all proteins depicted in Fig. 6A, with the corresponding gene names, position of phosphosites detected, sequence window around the phosphosites and the results of enrichment in prolonged prophase after applying linear modeling for analysis.