

# CDK2

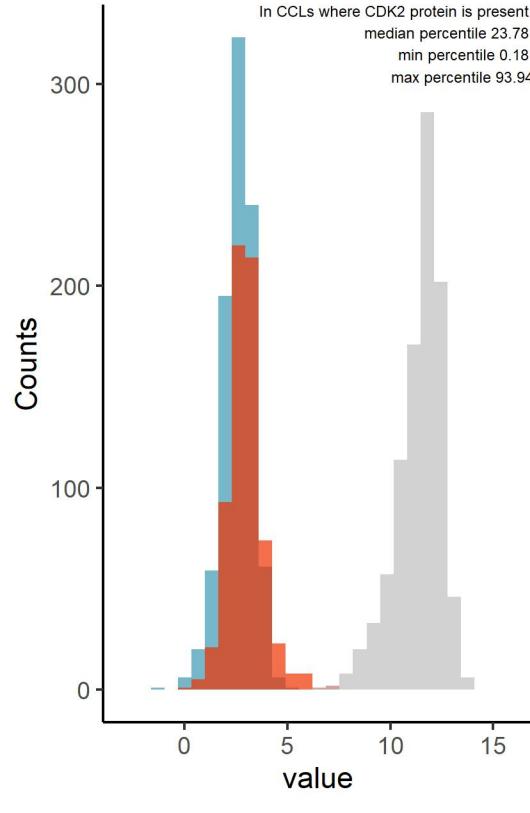
Protein name: CDK2 ; UNIPROT: P24941 ; Gene name: cyclin dependent kinase 2

Ligandable: Yes ; Ligandable\_by\_Chem: Yes ; Is\_enzyme: Yes (<https://cansar.ai/>)

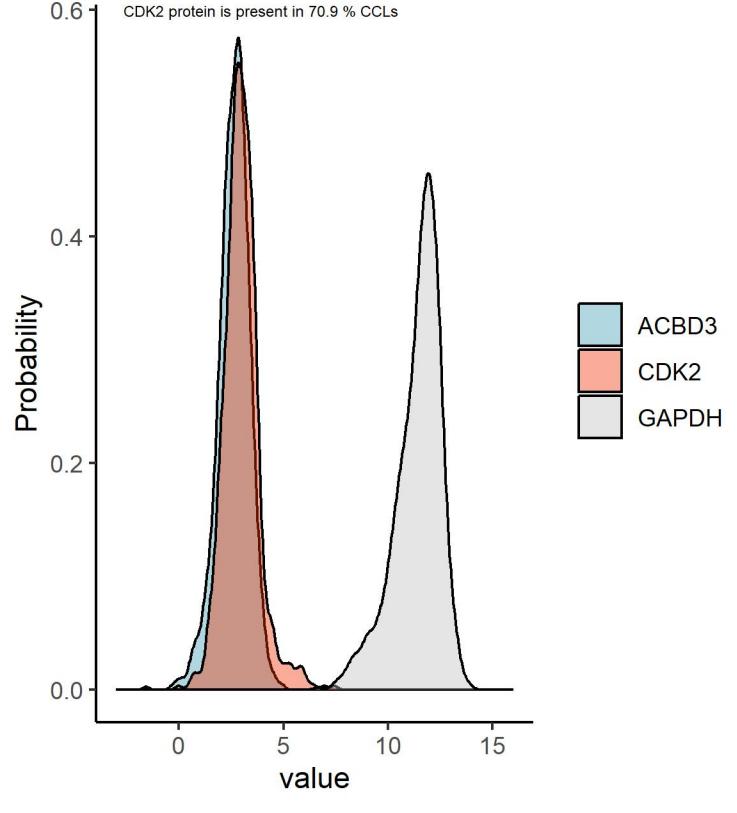
## Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

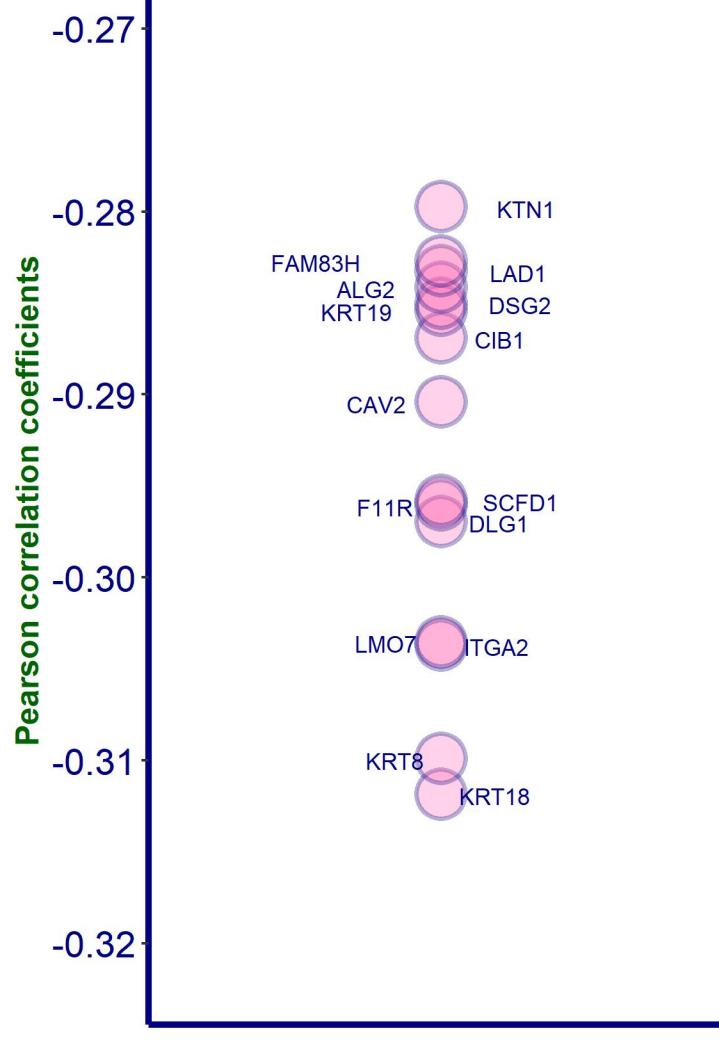
### Histogram of CDK2 protein compared to proteins with low and high abundance



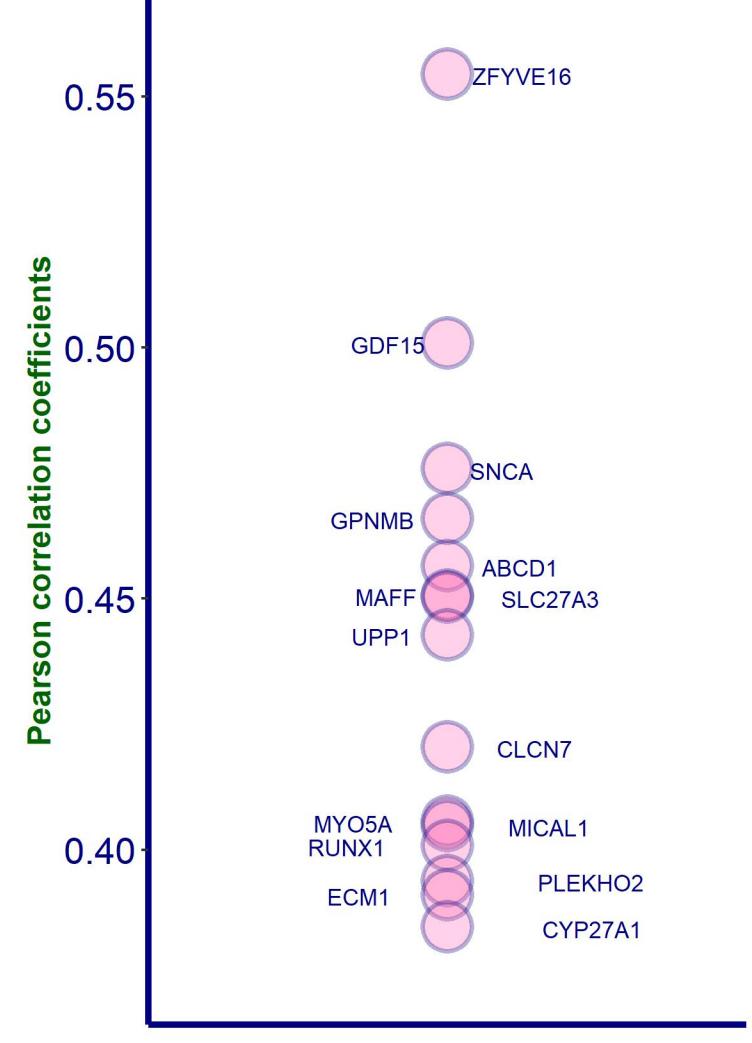
### Density plot of CDK2 protein compared to proteins with low and high abundance



### Top negative correlations of CDK2 protein, DB1

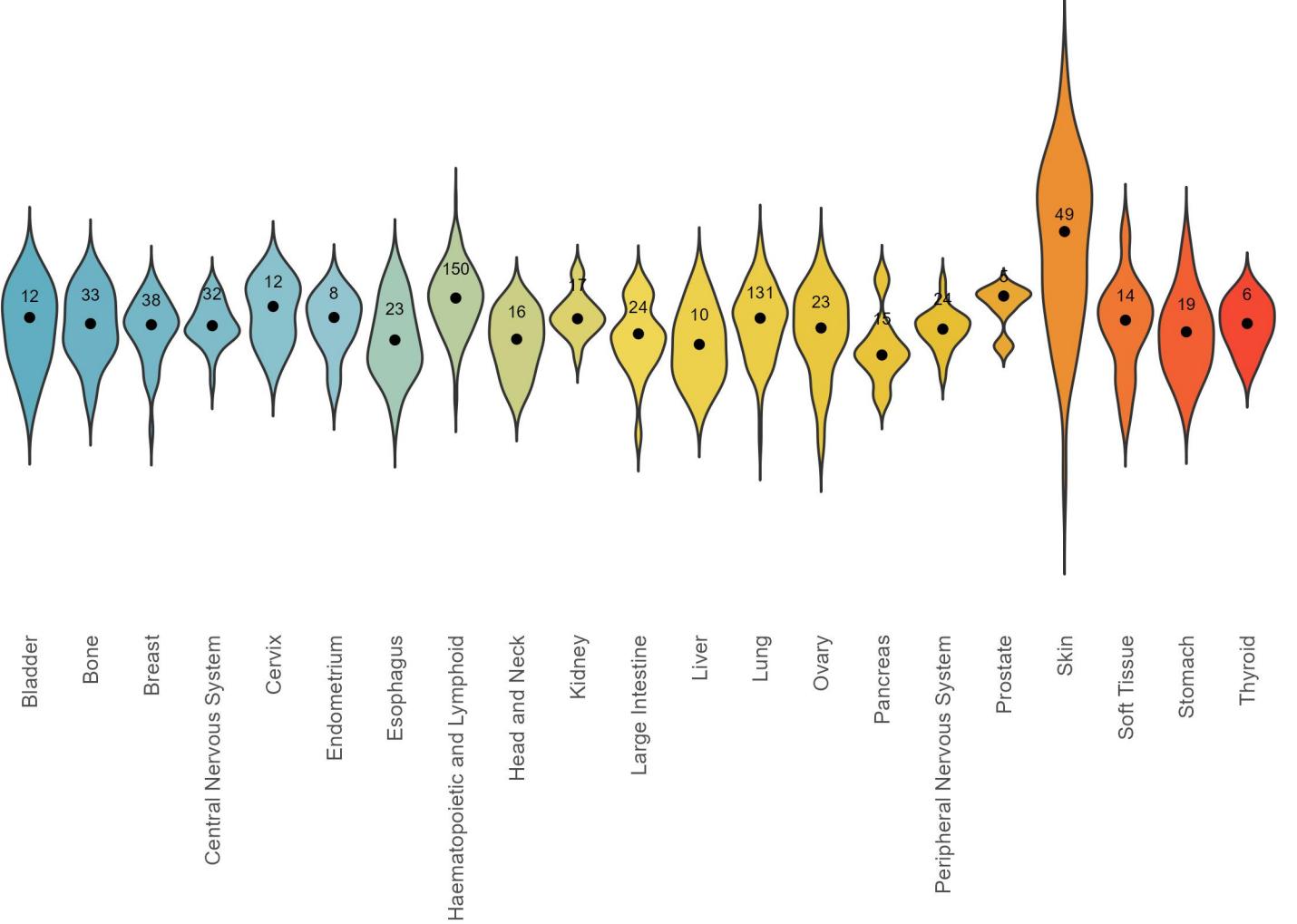


### Top positive correlations of CDK2 protein, DB1



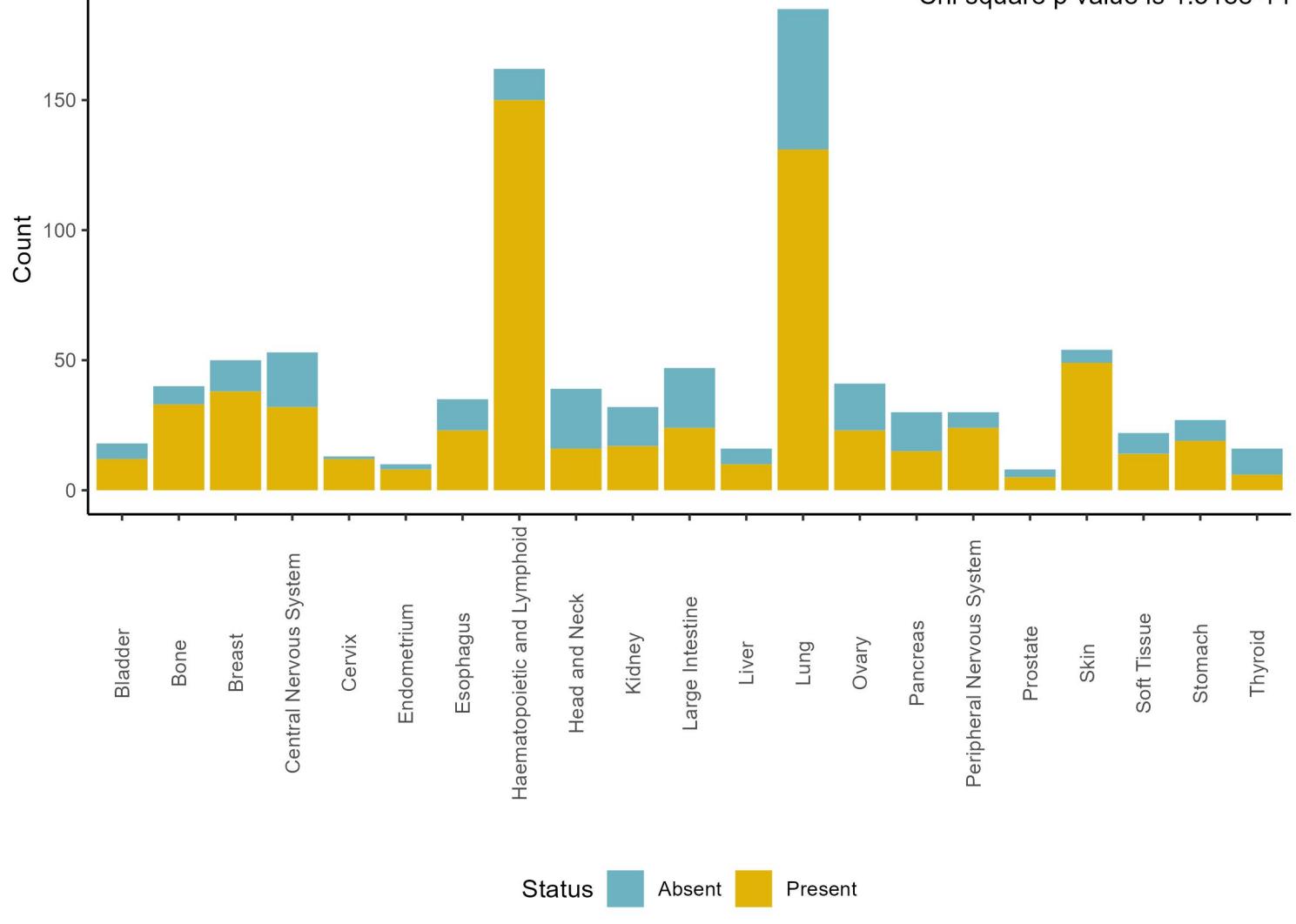
## Amount of CDK2 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 2.480e-34



## Present and absent CDK2 protein counts by tissue, DB1

Chi square p value is 1.518e-14

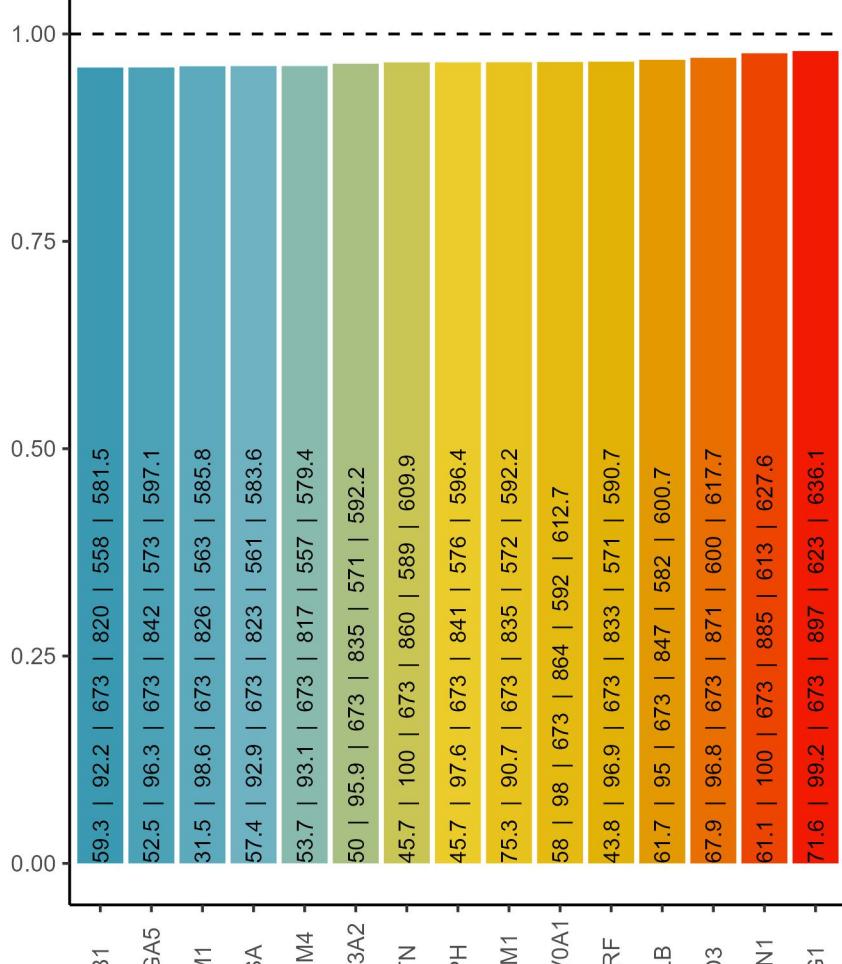


## Cooccurrence with CDK2 protein, DB1

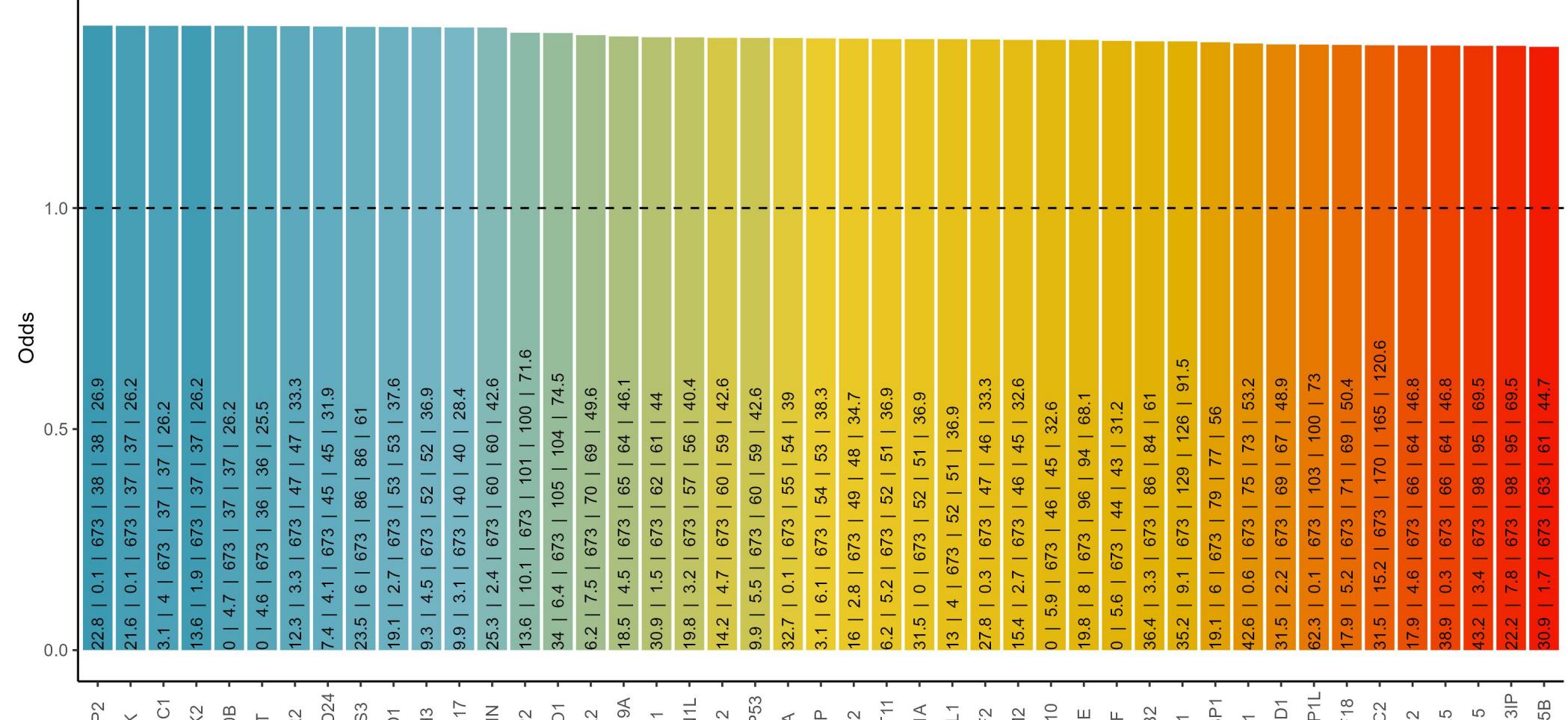
% of CDK2 in blood cancers: 92.6 ; % of CDK2 in solid cancers: 66.3

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CDK2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

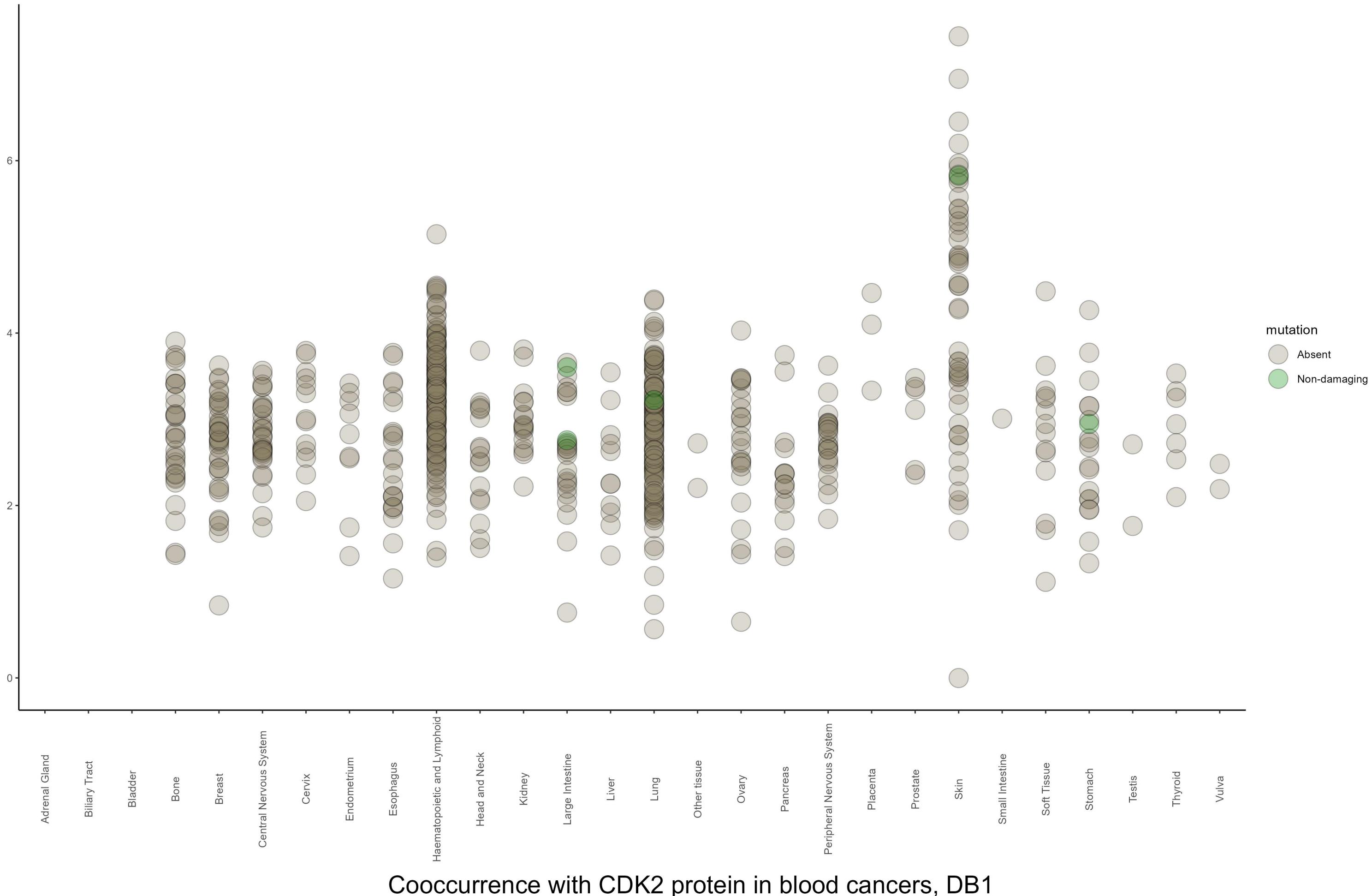
### Negative cooccurrence



### Positive cooccurrence

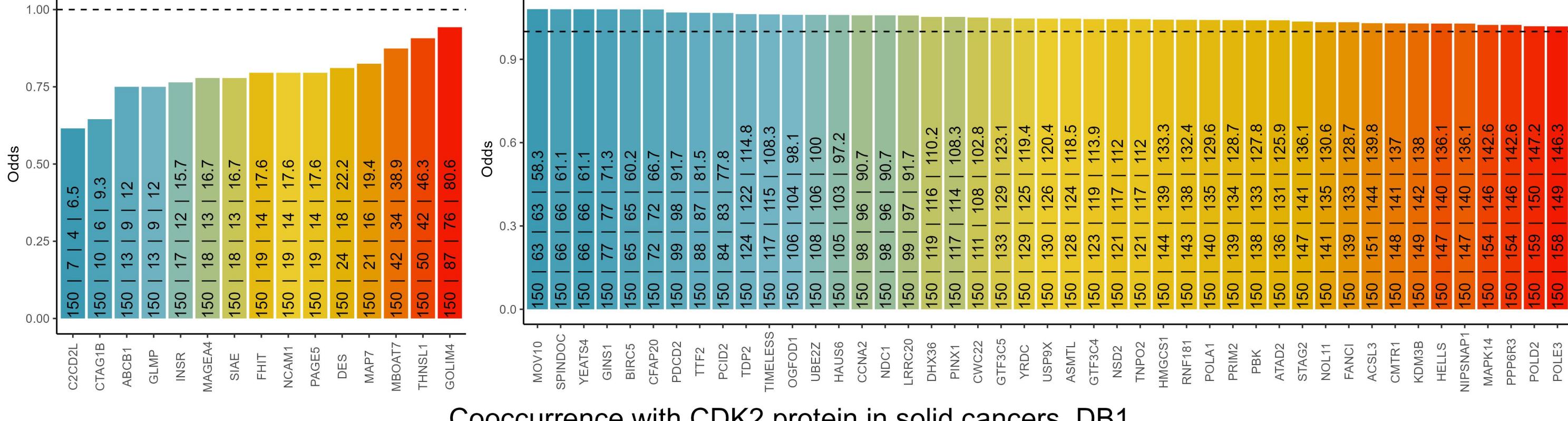


# Amount of CDK2 protein and mutation status by tissue, DB1



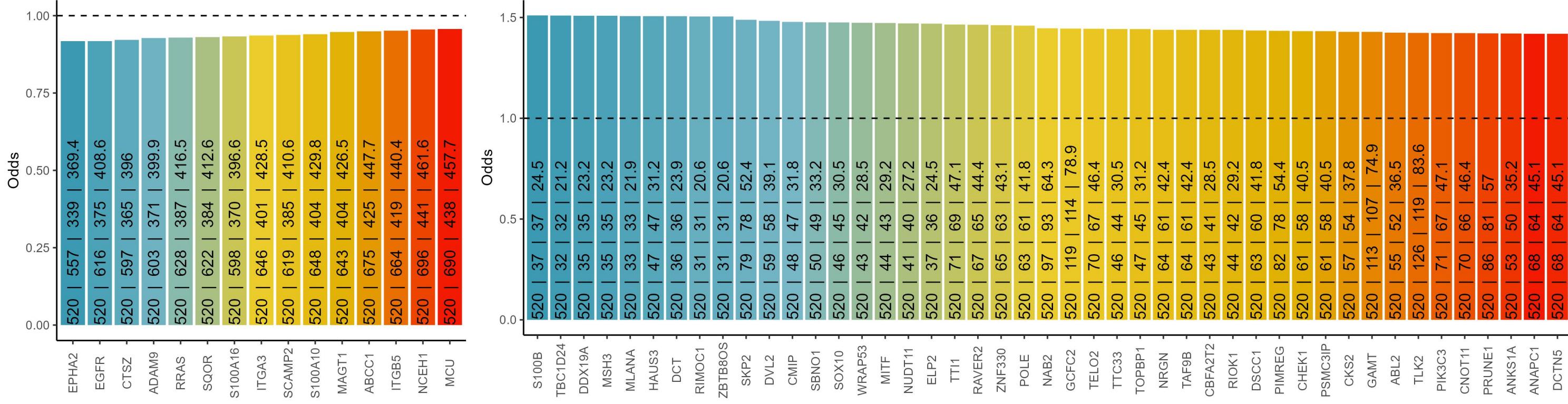
## Cooccurrence with CDK2 protein in blood cancers, DB1

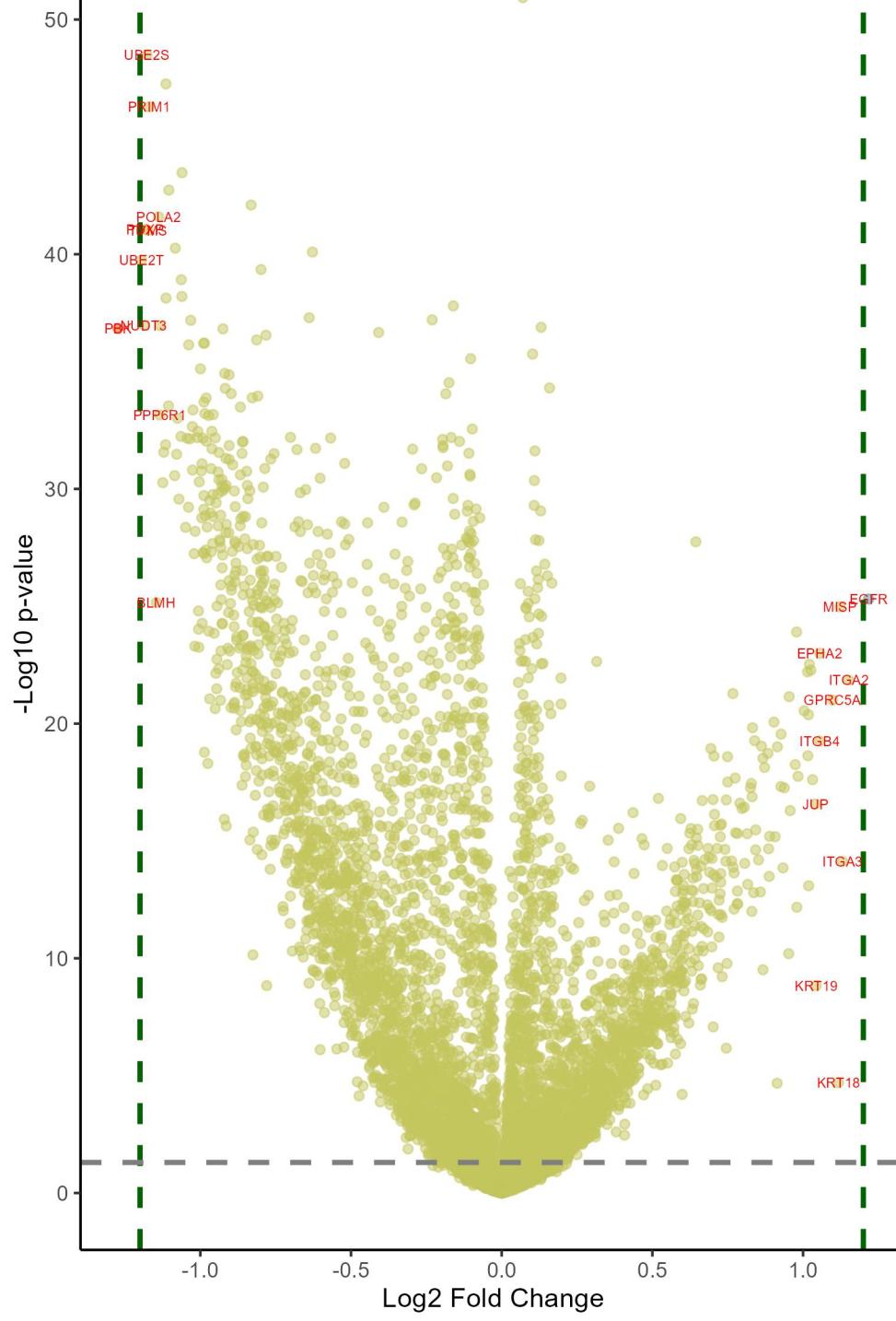
The text in the bars: incidence of CDK2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



## Cooccurrence with CDK2 protein in solid cancers, DB1

The text in the bars: incidence of CDK2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

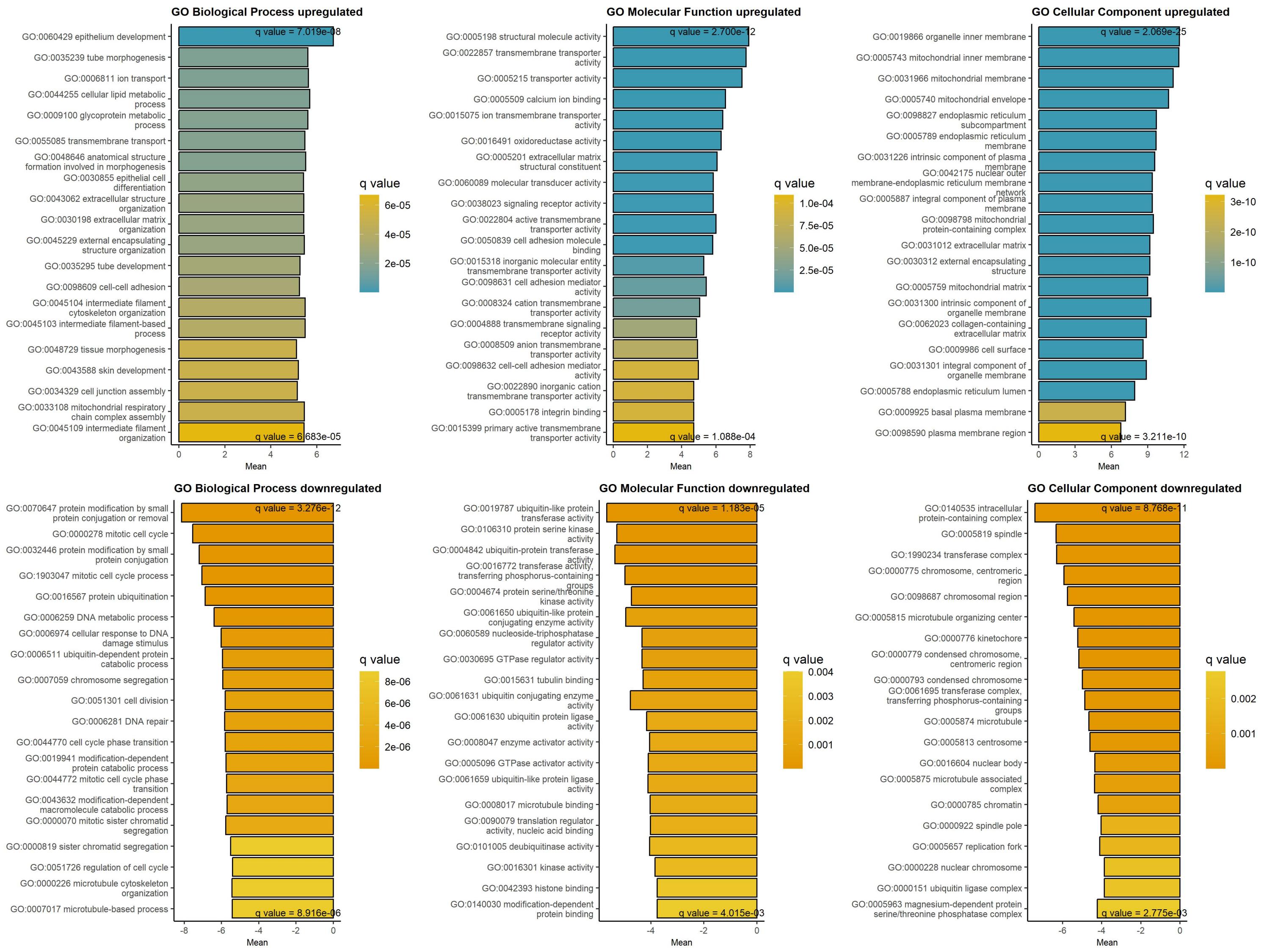




## Downregulated at low/absent CDK2

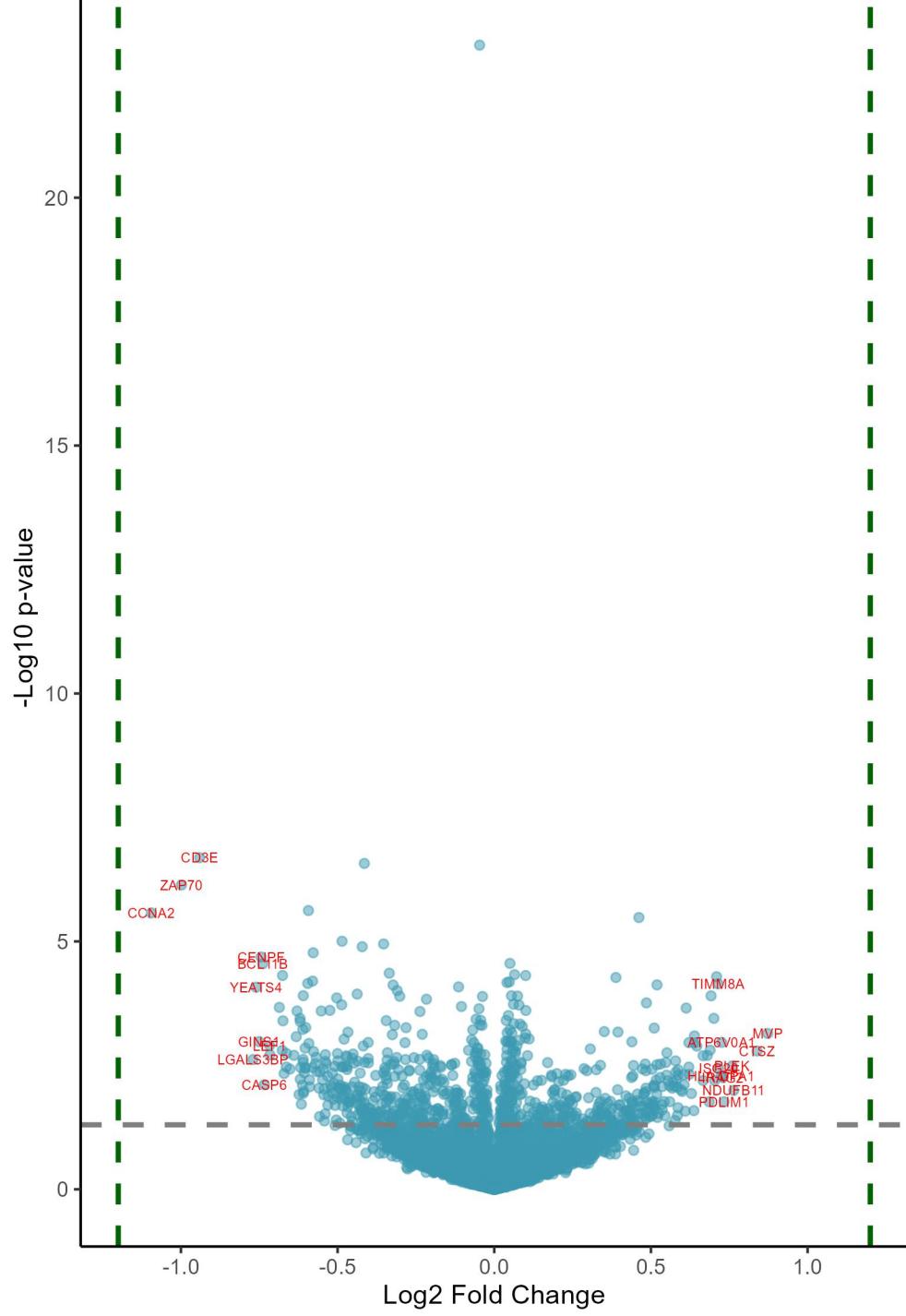
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.27	3.73e-35	PBK	PDZ binding kinase	1.22	1.11e-24	EGFR	epidermal growth factor receptor
-1.19	8.45e-38	UBE2T	ubiquitin conjugating enzyme E2 T	1.15	1.93e-21	ITGA2	integrin subunit alpha 2
-1.19	3.07e-35	NUDT3	nudix hydrolase 3	1.13	4.24e-14	ITGA3	integrin subunit alpha 3
-1.18	5.77e-39	PDXP	pyridoxal phosphatase	1.12	2.26e-24	MISP	mitotic spindle positioning
-1.18	6.87e-46	UBE2S	ubiquitin conjugating enzyme E2 S	1.12	4.16e-05	KRT18	keratin 18
-1.17	5.89e-39	TYMS	thymidylate synthetase	1.1	1.23e-20	GPRC5A	G protein-coupled receptor class C
-1.17	6.96e-44	PRIM1	DNA primase subunit 1	1.06	5.54e-19	ITGB4	integrin subunit beta 4
-1.15	1.53e-24	BLMH	bleomycin hydrolase	1.06	1.60e-22	EPHA2	EPH receptor A2
-1.14	1.87e-39	POLA2	DNA polymerase alpha 2, accessory s	1.04	4.71e-09	KRT19	keratin 19
-1.13	8.84e-32	PPP6R1	protein phosphatase 6 regulatory su	1.04	1.99e-16	JUP	junction plakoglobin
-1.13	3.07e-35	SAAL1	serum amyloid A like 1	1.03	2.01e-17	S100A16	S100 calcium binding protein A16
-1.12	3.18e-29	AK6	adenylate kinase 6	1.03	7.68e-22	ADAM9	ADAM metallopeptidase domain 9
-1.12	2.19e-30	DHFR	dihydrofolate reductase	1.02	4.42e-22	EPB41L1	erythrocyte membrane protein band 4
-1.12	1.18e-30	MAD2L1	mitotic arrest deficient 2 like 1	1.02	4.03e-13	S100A10	S100 calcium binding protein A10
-1.11	9.19e-45	RRM2	ribonucleotide reductase regulatory	1.02	4.76e-20	PPL	periplakin
-1.11	2.73e-36	KIAA1143	KIAA1143	1.02	2.17e-18	DSG2	desmoglein 2
-1.11	4.03e-32	PPP2CA	protein phosphatase 2 catalytic sub	1.01	9.06e-22	KRT80	keratin 80
-1.1	1.77e-40	HAT1	histone acetyltransferase 1	1	3.32e-20	EPS8L2	EPS8 like 2
-1.09	1.72e-29	ACYP1	acylphosphatase 1	0.98	1.48e-17	PKP3	plakophilin 3
-1.08	3.07e-38	POLA1	DNA polymerase alpha 1, catalytic s	0.98	3.05e-12	CAVIN1	caveolae associated protein 1
-1.08	2.52e-30	ARMC6	armadillo repeat containing 6	0.98	2.28e-23	NECTIN2	nectin cell adhesion molecule 2
-1.08	1.18e-31	DCK	deoxyctydine kinase	0.97	4.97e-18	S100A14	S100 calcium binding protein A14
-1.07	1.40e-28	PCLAF	PCNA clamp associated factor	0.96	3.66e-16	NT5E	5'-nucleotidase ecto
-1.06	6.43e-31	SMAP2	small ArfGAP2	0.95	9.03e-21	CDCP1	CUB domain containing protein 1
-1.06	5.06e-37	RNF114	ring finger protein 114	0.95	2.39e-10	GNG12	G protein subunit gamma 12
-1.06	2.46e-36	APPL1	adaptor protein, phosphotyrosine in	0.94	4.34e-17	TACSTD2	tumor associated calcium signal tra
-1.06	3.72e-41	DOHH	deoxyhypusine hydroxylase	0.93	7.64e-14	CAV1	caveolin 1
-1.05	1.72e-27	UBR7	ubiquitin protein ligase E3 compone	0.93	2.88e-19	FAM83H	family with sequence similarity 83
-1.04	6.90e-31	TP53RK	TP53 regulating kinase	0.93	3.83e-17	LAD1	ladinin 1

## GAGE analysis on upregulated and downregulated proteins at low/absent CDK2 protein, DB1

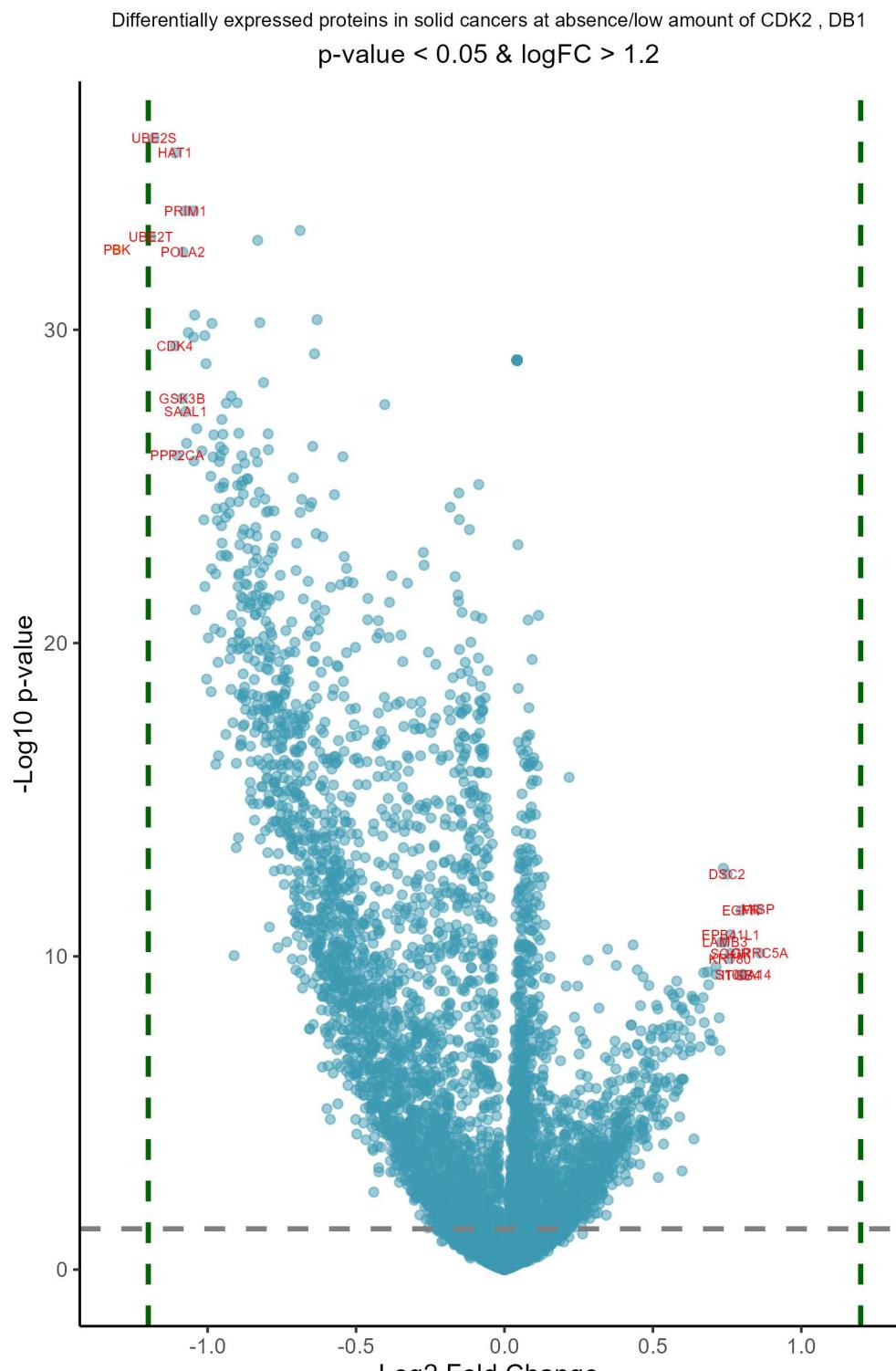


Differentially expressed proteins in blood cancers at absence/low amount of CDK2 , DB1  
p-value < 0.05 & logFC > 1.2

Downregulated in blood cancers at low/absent CDK2 Upregulated in blood cancers at low/absent CDK2



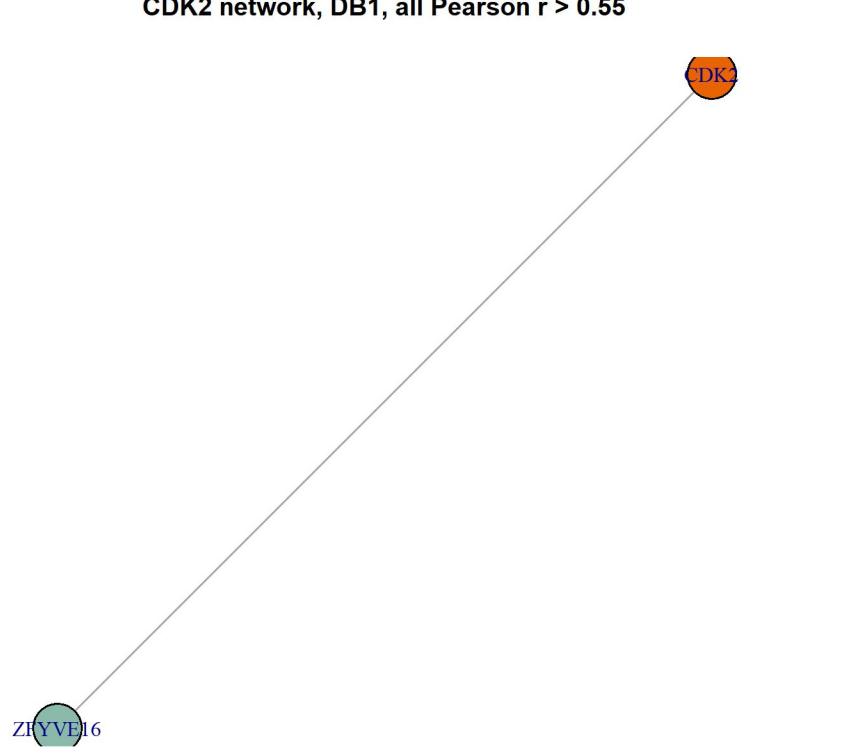
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.09	2.53e-03	CCNA2	cyclin A2	0.87	5.98e-02	MVP	major vault protein
-1	9.67e-04	ZAP70	zeta chain of T cell receptor assoc	0.84	9.06e-02	CTSZ	cathepsin Z
-0.94	4.45e-04	CD3E	CD3 epsilon subunit of T-cell recep	0.76	1.83e-01	NDUFB11	NADH:ubiquinone oxidoreductase subu
-0.77	1.05e-01	LGALS3BP	galectin 3 binding protein	0.76	1.11e-01	PLEK	pleckstrin
-0.76	1.86e-02	YEATS4	YEATS domain containing 4	0.73	2.34e-01	PDLIM1	PDZ and LIM domain 1
-0.75	7.16e-02	GINS1	GINS complex subunit 1	0.73	1.31e-01	IRAG2	inositol 1,4,5-triphosphate recepto
-0.74	1.06e-02	CENPF	centromere protein F	0.73	7.16e-02	ATP6V0A1	ATPase H <sup>+</sup> transporting V0 subunit a
-0.74	1.25e-02	BCL11B	BAF chromatin remodeling complex su	0.72	1.26e-01	HLA-DPA1	major histocompatibility complex, c
-0.73	1.60e-01	CASP6	caspase 6	0.72	1.15e-01	ISG20	interferon stimulated exonuclease g
-0.72	7.90e-02	LEF1	lymphoid enhancer binding factor 1	0.71	1.80e-02	TIMM8A	translocase of inner mitochondrial
-0.72	9.54e-02	MAGED2	MAGE family member D2	0.71	1.69e-02	AVL9	AVL9 cell migration associated
-0.69	3.10e-02	KIF20A	kinesin family member 20A	0.7	1.41e-01	NDUFB2	NADH:ubiquinone oxidoreductase subu
-0.68	8.89e-02	LANCL1	LanC like 1	0.7	4.24e-02	CTSS	cathepsin S
-0.68	1.69e-02	CD5	CD5 molecule	0.69	2.26e-02	FDX2	ferredoxin 2
-0.67	4.35e-02	DBR1	debranching RNA lariats 1	0.69	8.89e-02	PLEKHF2	pleckstrin homology and FYVE domain
-0.67	1.23e-01	GALM	galactose mutarotase	0.69	2.34e-01	JCHAIN	joining chain of multimeric IgA and
-0.66	1.12e-01	MAGT1	magnesium transporter 1	0.68	9.54e-02	COA4	cytochrome c oxidase assembly facto
-0.66	9.45e-02	ARL6IP1	ADP ribosylation factor like GTPase	0.67	9.54e-02	RPS19BP1	ribosomal protein S19 binding prote
-0.65	1.16e-01	BRD3	bromodomain containing 3	0.67	1.41e-01	IKZF3	IKAROS family zinc finger 3
-0.64	9.54e-02	STAG1	stromal antigen 1	0.65	7.90e-02	HSCB	HscB mitochondrial iron-sulfur clus
-0.63	6.52e-02	LDLR	low density lipoprotein receptor	0.64	6.39e-02	YTHDF3	YTH N6-methyladenosine RNA binding
-0.63	3.24e-02	ARF5	ADP ribosylation factor 5	0.64	7.16e-02	LYN	LYN proto-oncogene, Src family tyro
-0.62	1.96e-01	CD99	CD99 molecule (Xg blood group)	0.64	2.84e-01	SERPINB9	serpin family B member 9
-0.62	4.24e-02	SYF2	SYF2 pre-mRNA splicing factor	0.63	1.93e-01	MTAP	methylthioadenosine phosphorylase
-0.62	4.43e-02	SLFN5	schlafen family member 5	0.62	1.25e-01	PLBD2	phospholipase B domain containing 2
-0.62	1.38e-01	CFAP20	cilia and flagella associated prote	0.62	7.16e-02	RAB30	RAB30, member RAS oncogene family
-0.62	1.12e-01	HIRIP3	HIRA interacting protein 3	0.62	1.12e-01	RDH13	retinol dehydrogenase 13
-0.62	2.44e-01	ITGB2	integrin subunit beta 2	0.61	3.13e-02	ATG9A	autophagy related 9A
-0.61	1.61e-01	KIF15	kinesin family member 15	0.61	2.86e-01	CD74	CD74 molecule



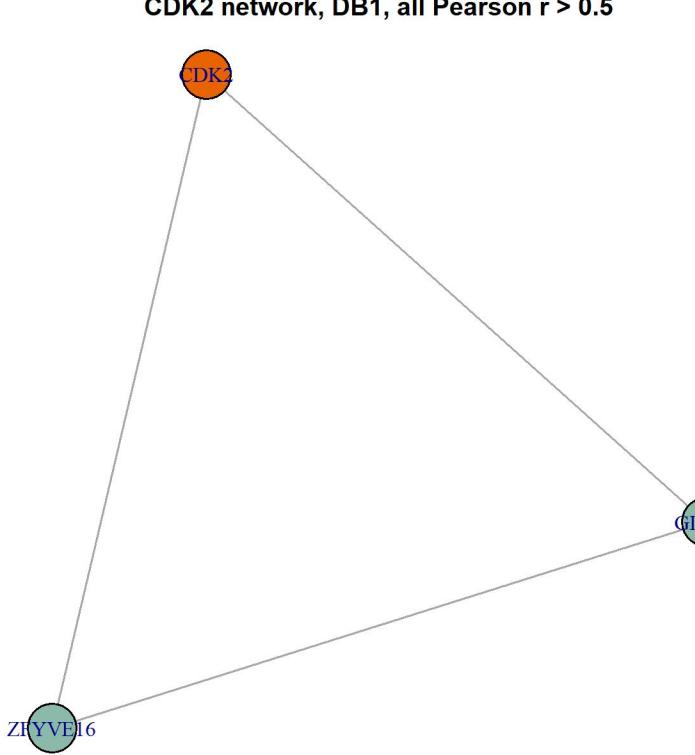
Downregulated in solid cancers at low/absent CDK2 Upregulated in solid cancers at low/absent CDK2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.31	2.05e-30	PBK	PDZ binding kinase	0.86	4.30e-10	GPRC5A	G protein-coupled receptor class C
-1.19	1.02e-30	UBE2T	ubiquitin conjugating enzyme E2 T	0.85	2.06e-11	MISP	mitotic spindle positioning
-1.18	2.49e-33	UBE2S	ubiquitin conjugating enzyme E2 S	0.8	1.87e-09	S100A14	S100 calcium binding protein A14
-1.11	4.99e-33	HAT1	histone acetyltransferase 1	0.8	1.98e-09	ITGB4	integrin subunit beta 4
-1.11	6.27e-28	CDK4	cyclin dependent kinase 4	0.8	2.27e-11	EGFR	epidermal growth factor receptor
-1.1	5.64e-25	PPP2CA	protein phosphatase 2 catalytic sub	0.76	1.21e-10	EPB41L1	erythrocyte membrane protein band 4
-1.09	1.01e-26	GSK3B	glycogen synthase kinase 3 beta	0.76	4.41e-10	SQOR	sulfide quinone oxidoreductase
-1.08	2.19e-30	POLA2	DNA polymerase alpha 2, accessory s	0.76	6.29e-10	KRT80	keratin 80
-1.07	2.13e-31	PRIM1	DNA primase subunit 1	0.75	1.83e-12	DSC2	desmocollin 2
-1.07	2.53e-26	SAAL1	serum amyloid A like 1	0.74	2.02e-10	LAMB3	laminin subunit beta 3
-1.07	2.45e-25	ENSA	endosulfine alpha	0.74	1.22e-12	COL17A1	collagen type XVII alpha 1 chain
-1.07	5.46e-28	UBE2C	ubiquitin conjugating enzyme E2 C	0.73	2.05e-10	LAMC2	laminin subunit gamma 2
-1.05	6.27e-28	UCK2	uridine-cytidine kinase 2	0.73	3.67e-07	AGR2	anterior gradient 2, protein disul
-1.05	2.13e-31	RRM2	ribonucleotide reductase regulatory	0.72	3.86e-08	VAMP8	vesicle associated membrane protein
-1.05	8.15e-25	NUDT3	nudix hydrolase 3	0.71	1.89e-09	EPS8L2	EPS8 like 2
-1.04	2.05e-28	RNF114	ring finger protein 114	0.71	1.09e-09	C15orf48	chromosome 15 open reading frame 48
-1.04	2.44e-20	NTMT1	N-terminal Xaa-Pro-Lys N-methyltran	0.7	1.90e-07	ITGA3	integrin subunit alpha 3
-1.04	8.72e-26	CNOT2	CCR4-NOT transcription complex subu	0.69	1.79e-07	TACSTD2	tumor associated calcium signal tra
-1.02	4.13e-25	PDXP	pyridoxal phosphatase	0.69	1.18e-07	PKP3	plakophilin 3
-1.01	4.74e-23	PDCL3	phosducin like 3	0.69	3.84e-09	PPL	periplakin
-1.01	6.27e-28	ELP1	elongator acetyltransferase complex	0.68	1.58e-09	CDCP1	CUB domain containing protein 1
-1.01	4.91e-21	MAD2L1	mitotic arrest deficient 2 like 1	0.67	5.38e-08	S100A16	S100 calcium binding protein A16
-1.01	8.02e-28	GINS4	GINS complex subunit 4	0.67	1.67e-09	LRP10	LDL receptor related protein 10
-1	2.89e-18	TMEM263	transmembrane protein 263	0.67	9.33e-09	ITGA2	integrin subunit alpha 2
-1	1.68e-19	AK6	adenylate kinase 6	0.66	2.87e-07	LAD1	ladin 1
-0.99	2.40e-24	SMAD4	SMAD family member 4	0.66	1.99e-08	DSG2	desmoglein 2
-0.99	6.97e-18	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.64	1.13e-08	RAB27B	RAB27B, member RAS oncogene family
-0.99	1.47e-21	PRPSAP2	phosphoribosyl pyrophosphate synth	0.64	1.68e-04	KRT19	keratin 19
-0.99	2.97e-28	TBCD	tubulin folding cofactor D	0.64	1.03e-08	MET	MET proto-oncogene, receptor tyrosi

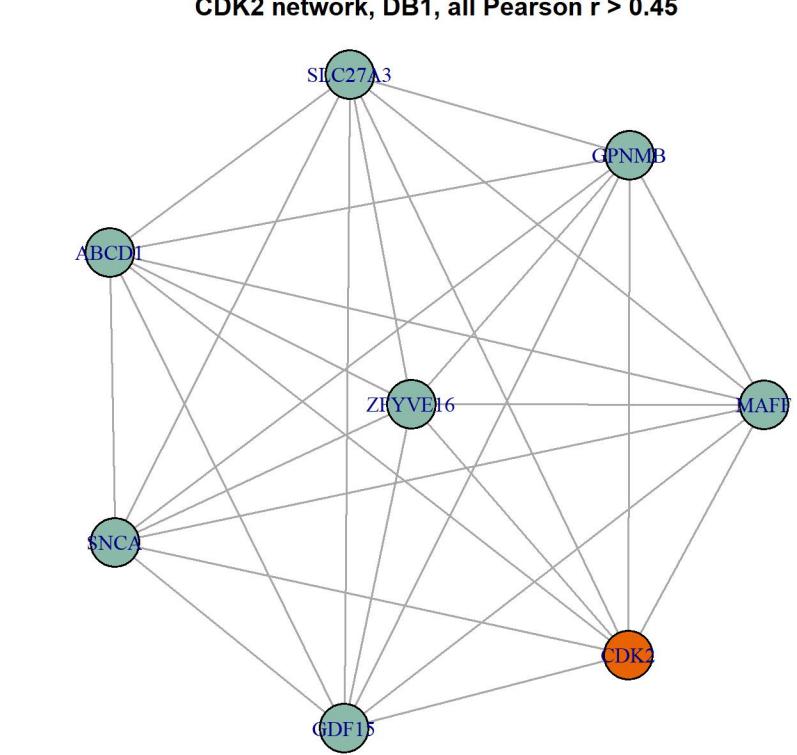
CDK2 network, DB1, all Pearson r > 0.55

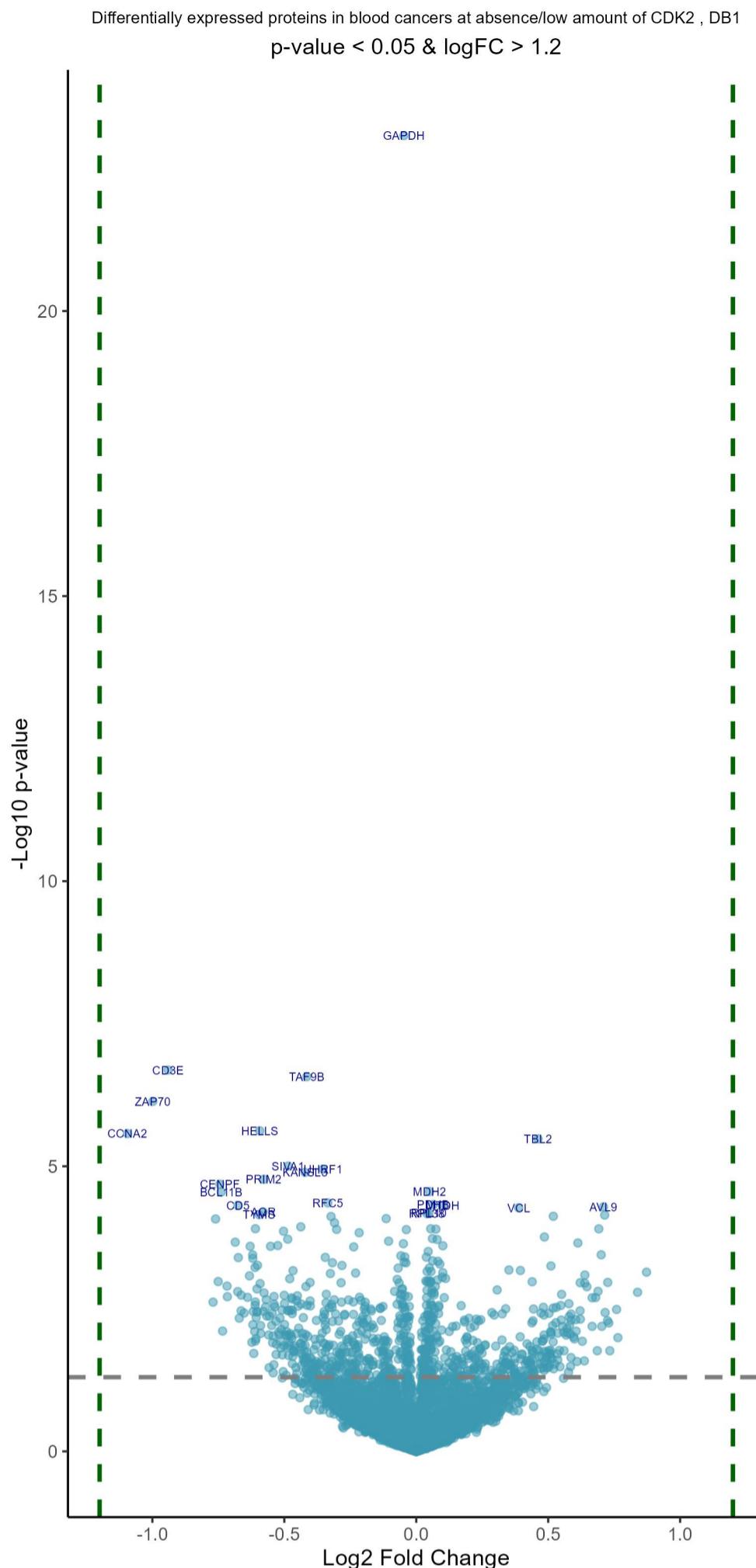


CDK2 network, DB1, all Pearson r > 0.5

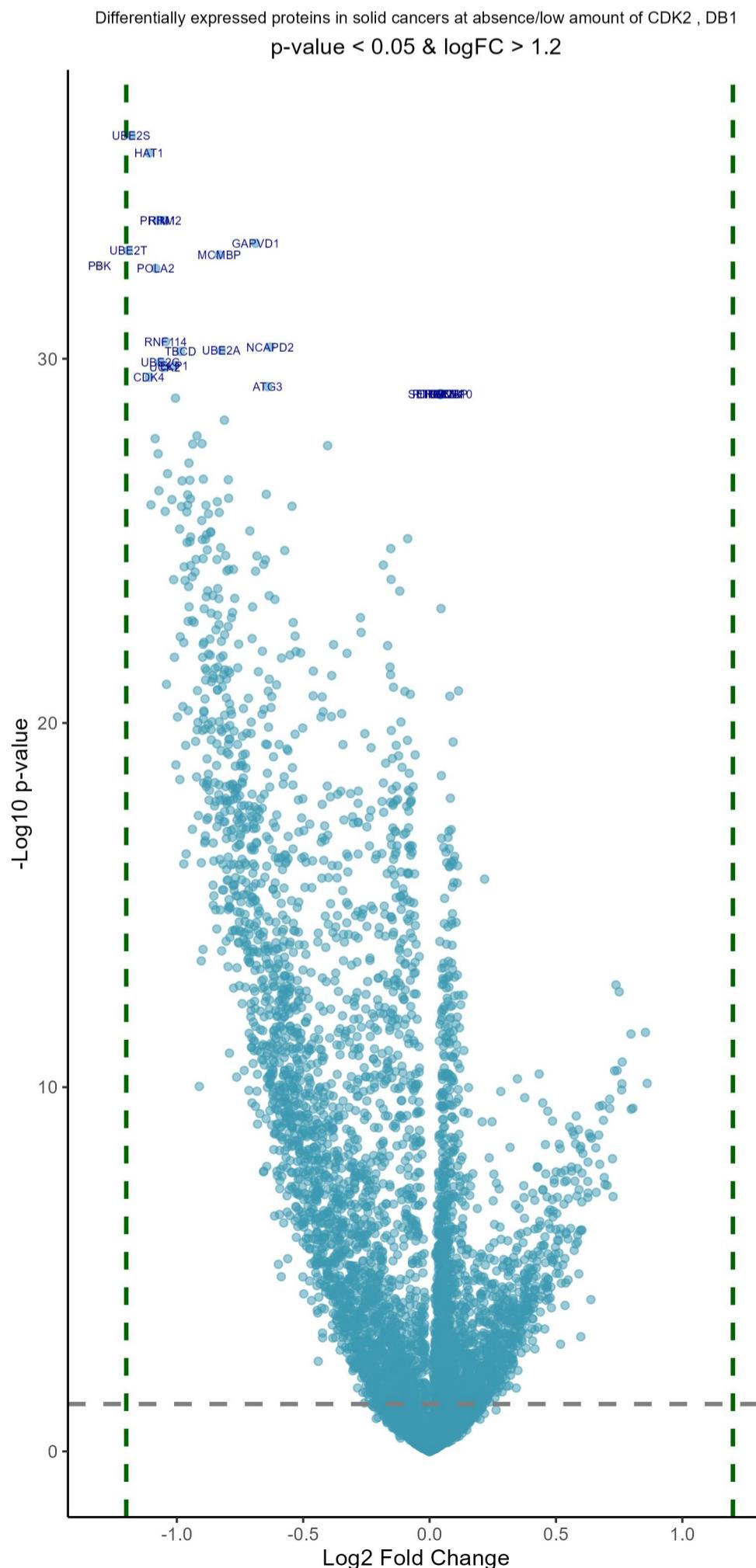


CDK2 network, DB1, all Pearson r > 0.45



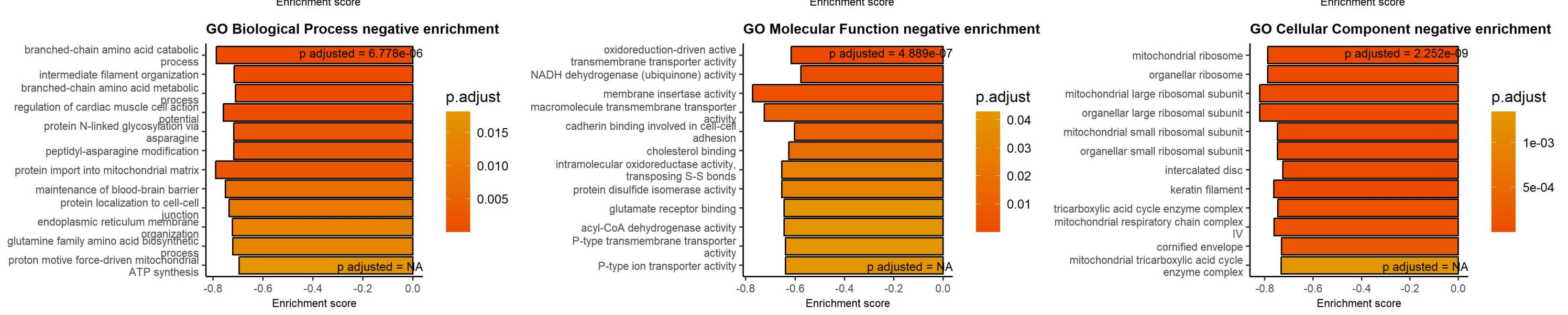
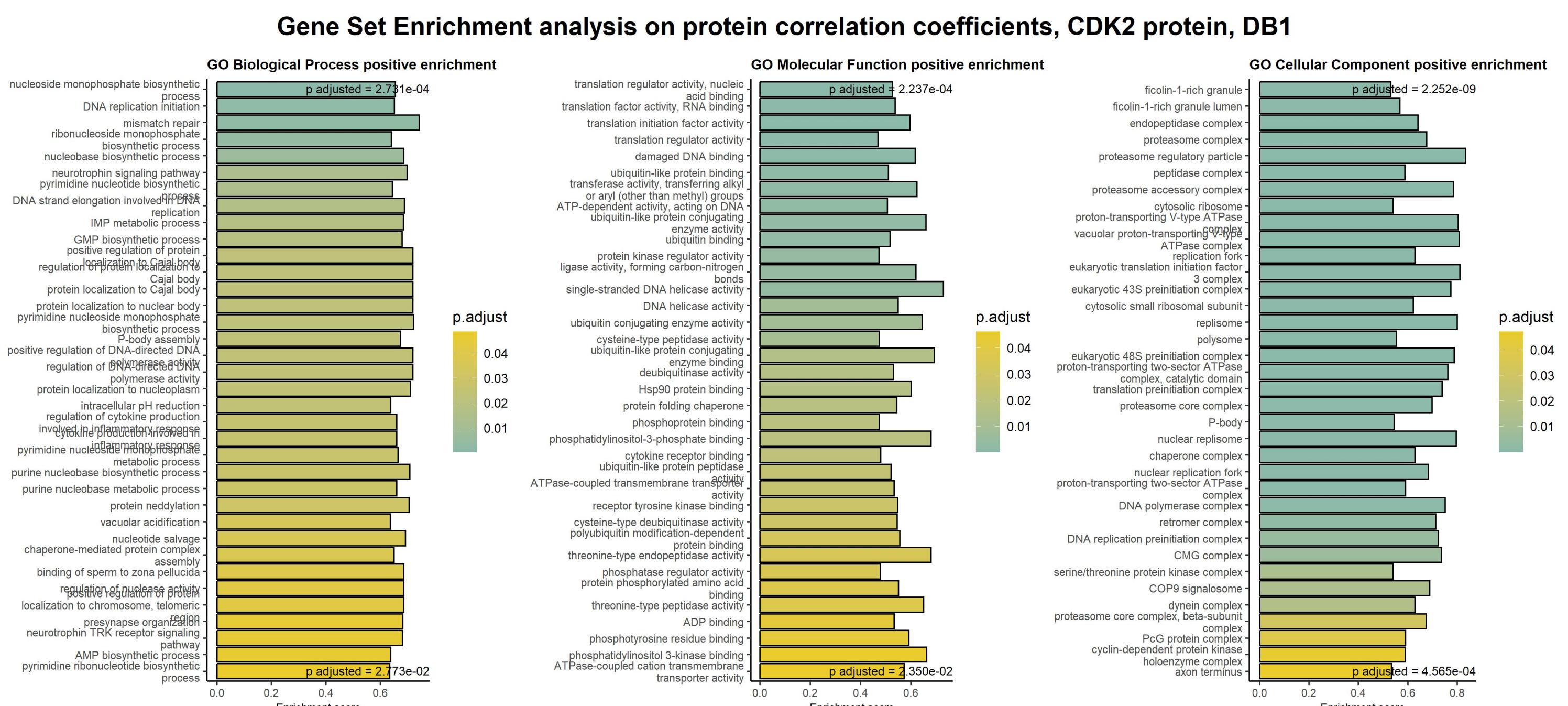
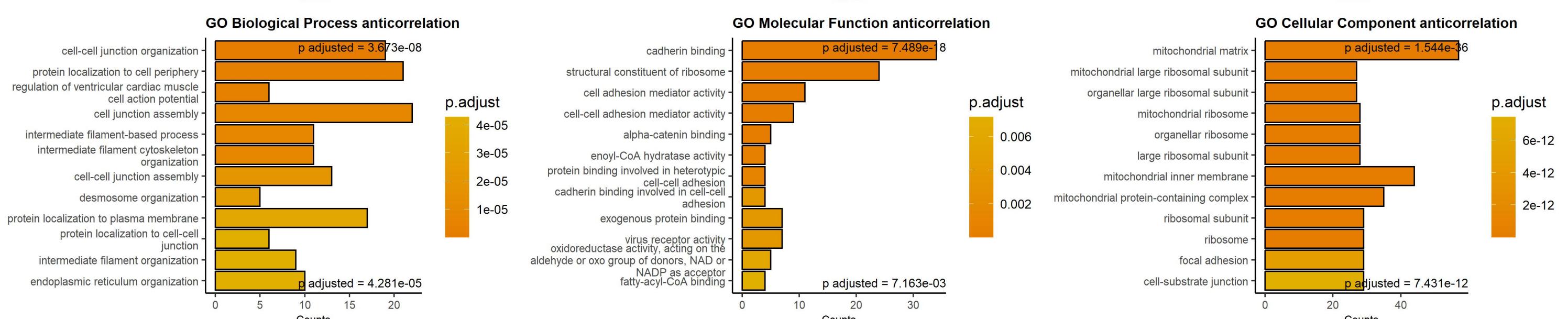
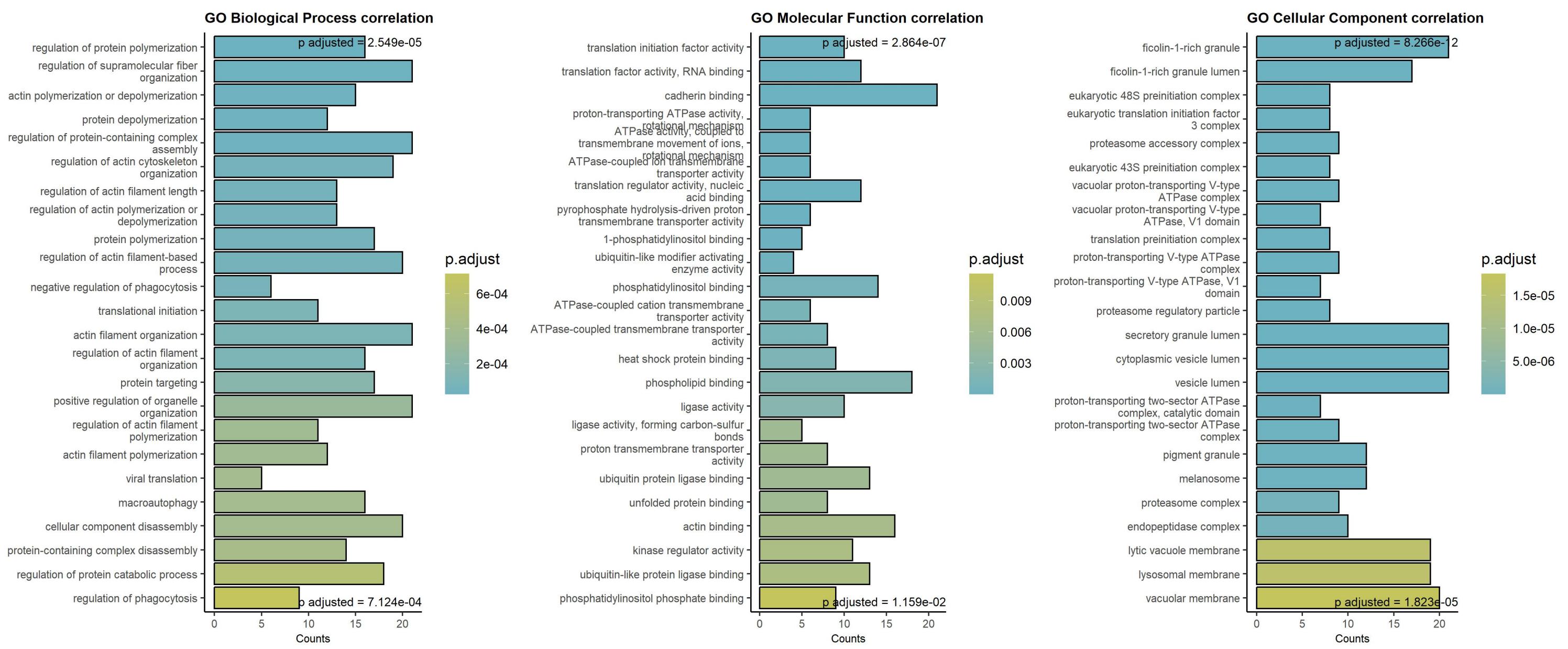


Sorted by p values!							
Downregulated in blood cancers at low/absent CDK2				Upregulated in blood cancers at low/absent CDK2			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.05	5.58e-20	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	0.46	2.75e-03	TBL2	transducin beta like 2
-0.94	4.45e-04	CD3E	CD3 epsilon subunit of T-cell receptor	0.05	1.25e-02	MDH2	malate dehydrogenase 2
-0.41	4.45e-04	TAF9B	TATA-box binding protein associated	0.06	1.69e-02	PDHB	pyruvate dehydrogenase E1 subunit b
-1	9.67e-04	ZAP70	zeta chain of T cell receptor associated	0.1	1.69e-02	MTDH	metadherin
-0.59	2.53e-03	HELLS	helicase, lymphoid specific	0.71	1.69e-02	AVL9	AVL9 cell migration associated
-1.09	2.53e-03	CCNA2	cyclin A2	0.39	1.69e-02	VCL	vinculin
-0.49	7.33e-03	SIVA1	SIVA1 apoptosis inducing factor	0.05	1.80e-02	RPL10	ribosomal protein L10
-0.35	7.49e-03	UHRF1	ubiquitin like with PHD and ring finger	0.04	1.80e-02	RPL38	ribosomal protein L38
-0.42	7.73e-03	KANSL3	KAT8 regulatory NSL complex subunit	0.71	1.80e-02	TIMM8A	translocase of inner mitochondrial membrane
-0.58	9.38e-03	PRIM2	DNA primase subunit 2	0.52	1.80e-02	GM2A	GM2 ganglioside activator
-0.74	1.06e-02	CENPF	centromere protein F	0.05	2.26e-02	SSB	small RNA binding exonuclease protein
-0.74	1.25e-02	BCL11B	BAF chromatin remodeling complex subunit	0.69	2.26e-02	FDX2	ferredoxin 2
-0.34	1.69e-02	RFC5	replication factor C subunit 5	0.07	2.26e-02	RRS1	ribosome biogenesis regulator 1 homolog
-0.68	1.69e-02	CD5	CD5 molecule	0.49	2.82e-02	ECI1	enoyl-CoA delta isomerase 1
-0.58	1.80e-02	AQR	aquarius intron-binding spliceosoma	0.06	2.91e-02	MRPS28	mitochondrial ribosomal protein S28
-0.6	1.80e-02	TYMS	thymidylate synthetase	0.08	2.91e-02	MRPS23	mitochondrial ribosomal protein S23
-0.32	1.80e-02	PGM2L1	phosphoglucomutase 2 like 1	0.61	3.13e-02	ATG9A	autophagy related 9A
-0.11	1.86e-02	TOP2A	DNA topoisomerase II alpha	0.1	3.24e-02	ACAT1	acetyl-CoA acetyltransferase 1
-0.76	1.86e-02	YEATS4	YEATS domain containing 4	0.05	3.84e-02	TUFM	Tu translation elongation factor, m
-0.31	2.10e-02	GIMAP6	GTPase, IMAP family member 6	0.7	4.24e-02	CTSS	cathepsin S
-0.44	2.26e-02	CTDSPL2	CTD small phosphatase like 2	0.04	4.35e-02	RPL19	ribosomal protein L19
-0.61	2.26e-02	SH2D1A	SH2 domain containing 1A	0.06	4.80e-02	AFG3L2	AFG3 like matrix AAA peptidase subunit
-0.3	2.26e-02	TAF5	TATA-box binding protein associated	0.08	4.82e-02	NDUFS1	NADH:ubiquinone oxidoreductase core
-0.04	2.26e-02	SNRNP200	small nuclear ribonucleoprotein U5	0.09	5.07e-02	UQCRCB	ubiquinol-cytochrome c reductase bi
-0.5	2.35e-02	NELFB	negative elongation factor complex	0.51	5.25e-02	DHRS11	dehydrogenase/reductase 11
-0.22	2.43e-02	CHAF1B	chromatin assembly factor 1 subunit	0.05	5.48e-02	DLD	dihydrolipoamide dehydrogenase
-0.49	2.91e-02	PSMC3IP	PSMC3 interacting protein	0.35	5.84e-02	HSPG2	heparan sulfate proteoglycan 2
-0.1	3.04e-02	CDK1	cyclin dependent kinase 1	0.39	5.84e-02	ATP13A1	ATPase 13A1
-0.69	3.10e-02	KIF20A	kinesin family member 20A	0.04	5.89e-02	ARCN1	archain 1
-0.05	3.16e-02	POLR2B	RNA polymerase II subunit B	0.06	5.89e-02	SRM	spermidine synthase
-0.52	3.24e-02	CDCA7	cell division cycle associated 7	0.87	5.98e-02	MVP	major vault protein
-0.55	3.24e-02	GTF3C5	general transcription factor IIIC subunit	0.1	6.03e-02	ARHGEF2	Rho/Rac guanine nucleotide exchange
-0.63	3.24e-02	ARF5	ADP ribosylation factor 5	0.64	6.39e-02	YTHDF3	YTH N6-methyladenosine RNA binding protein
-0.24	3.25e-02	TPX2	TPX2 microtubule nucleation factor	0.1	6.84e-02	FIS1	fission, mitochondrial 1
-0.62	4.24e-02	SYF2	SYF2 pre-mRNA splicing factor	0.11	7.08e-02	NDUFS6	NADH:ubiquinone oxidoreductase subunit
-0.06	4.33e-02	RFC4	replication factor C subunit 4	0.08	7.16e-02	SEC62	SEC62 homolog, preprotein transloca
-0.04	4.35e-02	CHD4	chromodomain helicase DNA binding protein 4	0.05	7.16e-02	ATP5PO	ATP synthase peripheral stalk subunit
-0.34	4.35e-02	RNF2	ring finger protein 2	0.04	7.16e-02	EPRS1	glutamyl-prolyl-tRNA synthetase 1
-0.67	4.35e-02	DRP1	debranching RNA lariate 1	0.05	7.16e-02	SUCCLC1	succinate CoA ligase GDP/ADP form

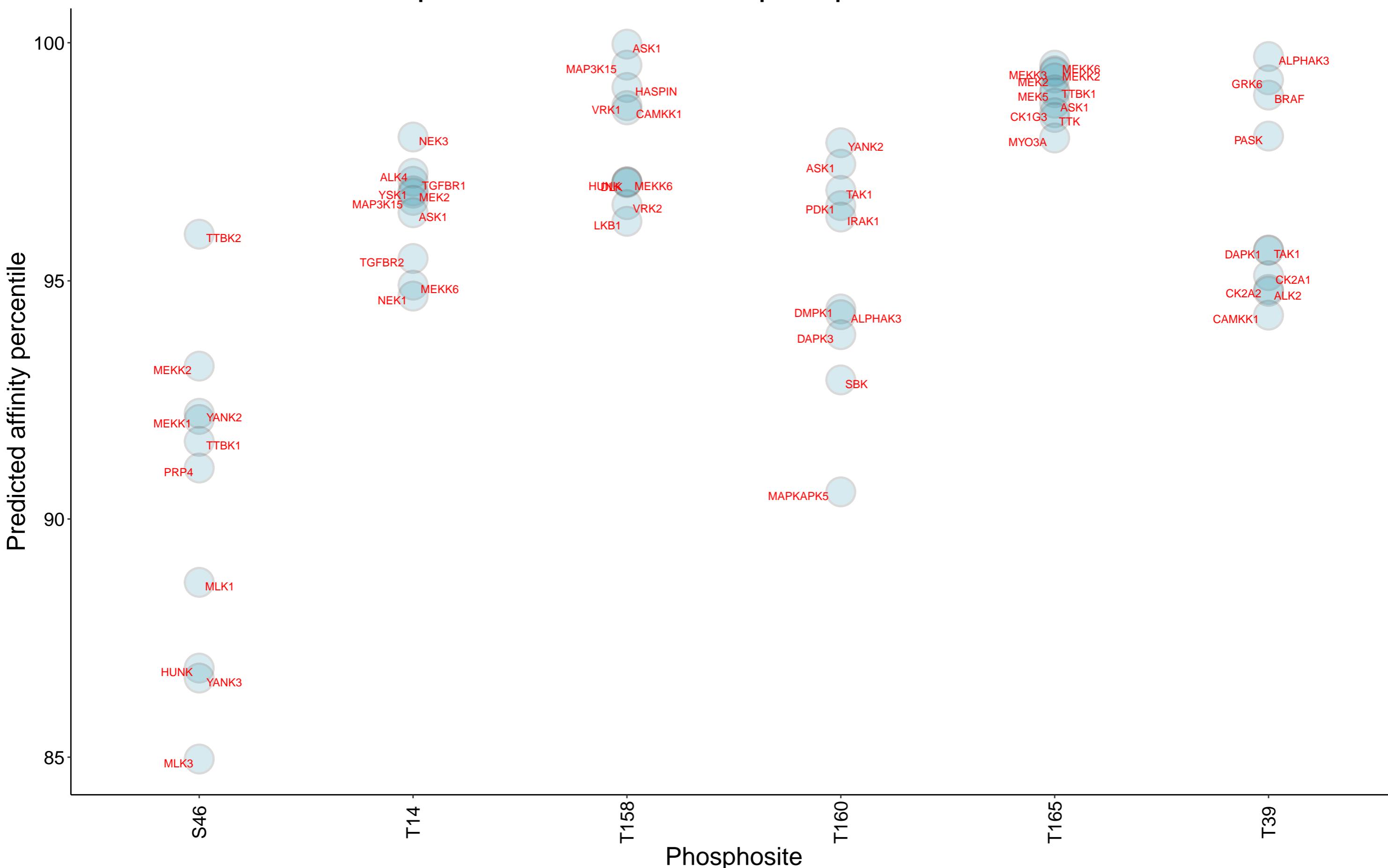


Sorted by p values!							
Downregulated in solid cancers at low/absent CDK2				Upregulated in solid cancers at low/absent CDK2			
FC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
18	2.49e-33	UBE2S	ubiquitin conjugating enzyme E2 S	0.04	6.27e-28	PTPRCAP	protein tyrosine phosphatase recept
11	4.99e-33	HAT1	histone acetyltransferase 1	0.04	6.27e-28	HBE1	hemoglobin subunit epsilon 1
07	2.13e-31	PRIM1	DNA primase subunit 1	0.04	6.27e-28	SERPINB10	serpin family B member 10
05	2.13e-31	RRM2	ribonucleotide reductase regulatory	0.04	6.27e-28	IGLL1	immunoglobulin lambda like polypept
69	7.50e-31	GAPVD1	GTPase activating protein and VPS9	0.04	6.27e-28	CRYBB1	crystallin beta B1
19	1.02e-30	UBE2T	ubiquitin conjugating enzyme E2 T	0.04	6.27e-28	ITGA2B	integrin subunit alpha 2b
83	1.16e-30	MCMBP	minichromosome maintenance complex	0.04	6.27e-28	ACAP1	ArfGAP with coiled-coil, ankyrin re
31	2.05e-30	PBK	PDZ binding kinase	0.04	6.27e-28	NCF4	neutrophil cytosolic factor 4
08	2.19e-30	POLA2	DNA polymerase alpha 2, accessory s	0.04	6.27e-28	SP140	SP140 nuclear body protein
04	2.05e-28	RNF114	ring finger protein 114	0.04	6.27e-28	PSTPIP1	proline-serine-threonine phosphatas
63	2.65e-28	NCAPD2	non-SMC condensin I complex subunit	0.04	6.27e-28	STAB1	stabilin 1
82	2.97e-28	UBE2A	ubiquitin conjugating enzyme E2 A	0.04	6.27e-28	SELPLG	selectin P ligand
99	2.97e-28	TBCD	tubulin folding cofactor D	0.04	6.27e-28	RCSD1	RCSD domain containing 1
07	5.46e-28	UBE2C	ubiquitin conjugating enzyme E2 C	0.04	6.27e-28	STAT5A	signal transducer and activator of
01	6.27e-28	ELP1	elongator acetyltransferase complex	0.04	6.27e-28	CTSW	cathepsin W
05	6.27e-28	UCK2	uridine-cytidine kinase 2	0.04	6.27e-28	GIMAP6	GTPase, IMAP family member 6
11	6.27e-28	CDK4	cyclin dependent kinase 4	0.04	6.27e-28	GZMB	granzyme B
64	6.27e-28	ATG3	autophagy related 3	0.04	6.27e-28	HK3	hexokinase 3
01	8.02e-28	GINS4	GINS complex subunit 4	0.04	6.27e-28	TUBA8	tubulin alpha 8
81	3.19e-27	UBA3	ubiquitin like modifier activating	0.04	6.27e-28	CR2	complement C3d receptor 2
92	8.52e-27	YTHDF2	YTH N6-methyladenosine RNA binding	0.04	6.27e-28	POU2F2	POU class 2 homeobox 2
09	1.01e-26	GSK3B	glycogen synthase kinase 3 beta	0.04	6.27e-28	AZU1	azurocidin 1
19	1.37e-26	RTF2	replication termination factor 2	0.04	6.27e-28	CD48	CD48 molecule
94	1.39e-26	HYPK	huntingtin interacting protein K	0.04	6.27e-28	SKAP2	src kinase associated phosphoprotei
04	1.52e-26	CDK1	cyclin dependent kinase 1	0.04	6.27e-28	CCL17	C-C motif chemokine ligand 17
07	2.53e-26	SAAL1	serum amyloid A like 1	0.04	6.27e-28	ADA2	adenosine deaminase 2
95	4.50e-26	DOHH	deoxyhypusine hydroxylase	0.04	6.27e-28	CD3E	CD3 epsilon subunit of T-cell recep
04	8.72e-26	CNOT2	CCR4-NOT transcription complex subu	0.04	6.27e-28	RNASE2	ribonuclease A family member 2
89	1.22e-25	IPO9	importin 9	0.04	6.27e-28	TEX11	testis expressed 11
08	1.25e-25	ILKAP	ILK associated serine/threonine pho	0.04	6.27e-28	PLEK	pleckstrin
95	1.29e-25	KIF11	kinesin family member 11	0.04	6.27e-28	CD300A	CD300a molecule
98	1.32e-25	APPL1	adaptor protein, phosphotyrosine in	0.04	6.27e-28	GZMA	granzyme A
07	2.45e-25	ENSA	endosulfine alpha	0.04	6.27e-28	SIGLEC12	sialic acid binding Ig like lectin
65	3.04e-25	NAE1	NEDD8 activating enzyme E1 subunit	0.04	6.27e-28	SMIM24	small integral membrane protein 24
96	3.12e-25	PAAF1	proteasomal ATPase associated facto	0.04	6.27e-28	ALOX15	arachidonate 15-lipoxygenase
08	3.84e-25	POLD2	DNA polymerase delta 2, accessory s	0.04	6.27e-28	GZMM	granzyme M
95	3.94e-25	SPC24	SPC24 component of NDC80 kinetochor	0.04	6.27e-28	ARHGAP9	Rho GTPase activating protein 9
02	4.13e-25	PDXP	pyridoxal phosphatase	0.04	6.27e-28	NINJ2	ninjurin 2

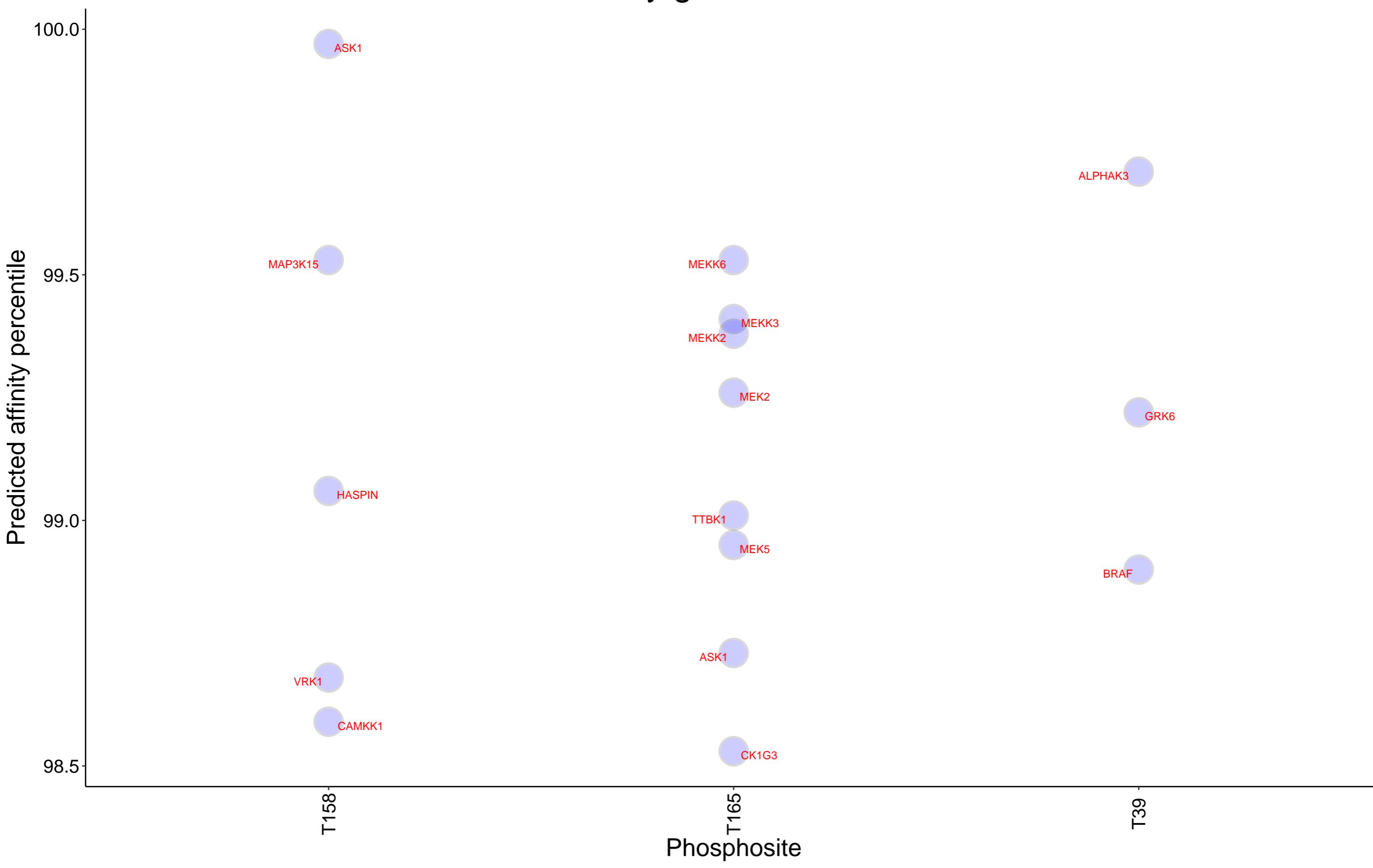
# Top 250 correlation coefficients overrepresentation, CDK2 protein, DB1



# Top 10 kinases for each phosphosite in CDK2



## Kinases with affinity greater than 98.5% to CDK2



## Top 15 positive correlation coefficients for CDK2 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

