

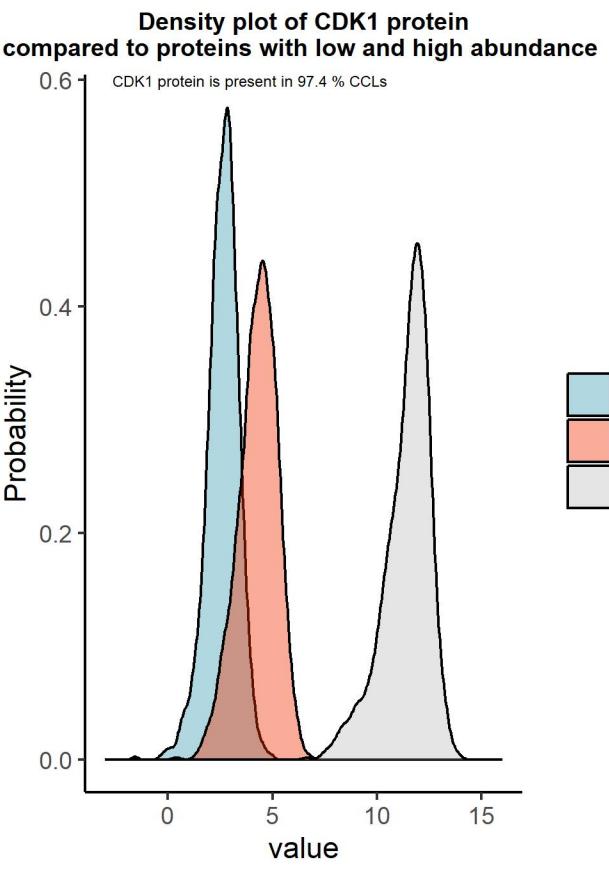
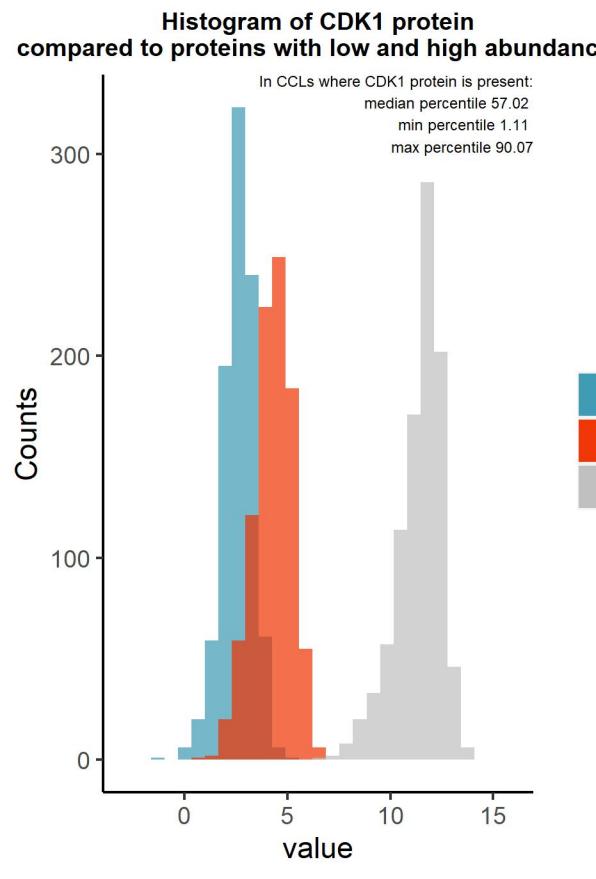
CDK1

Protein name: CDK1 ; UNIPROT: P06493 ; Gene name: cyclin dependent kinase 1

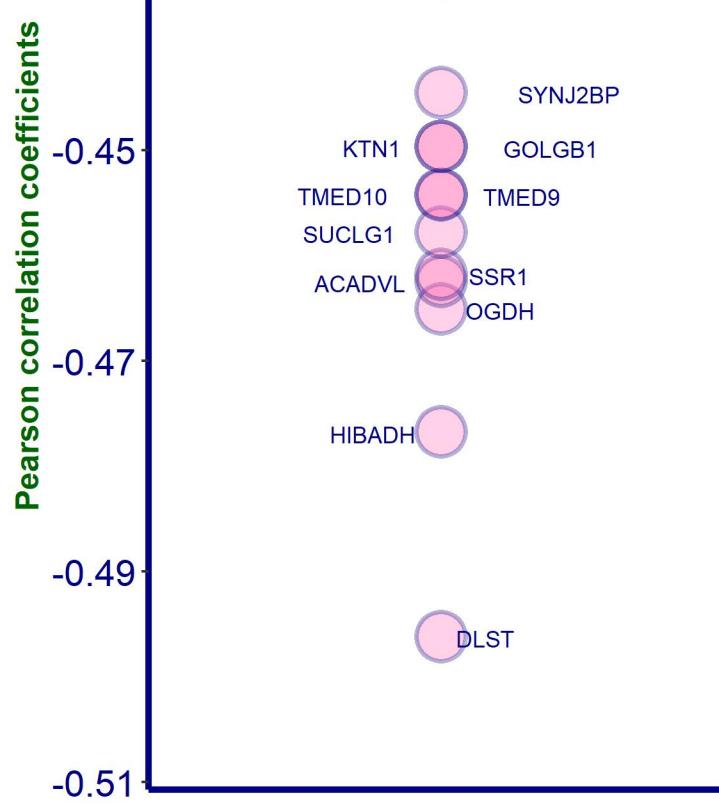
Ligandable: Yes ; Ligandable_by_Chem: Yes ; Is_enzyme: Yes (<https://cansar.ai/>)

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

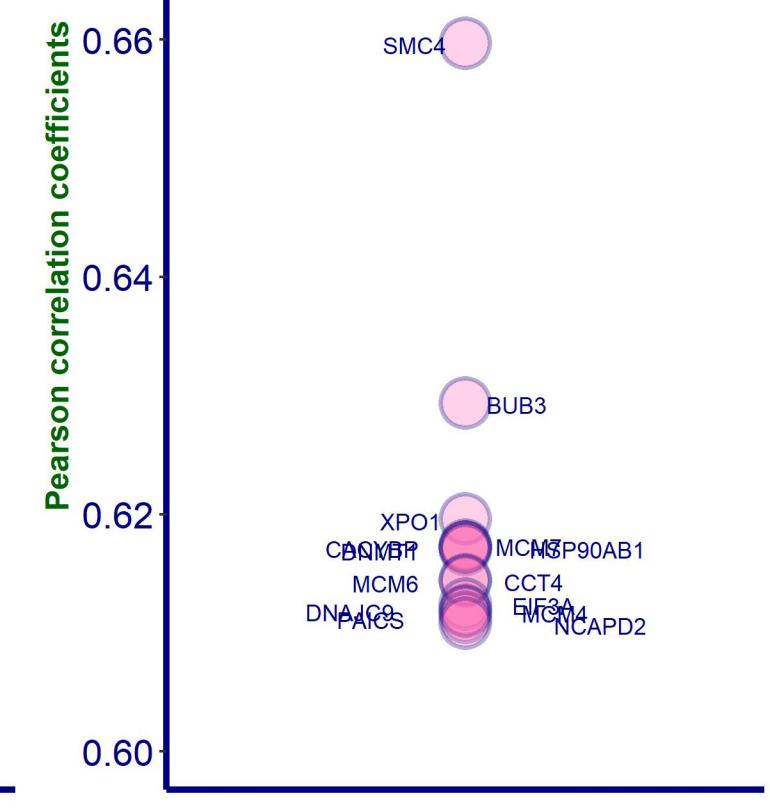
6692 proteins in 949 CCLs



Top negative correlations of CDK1 protein, DB1

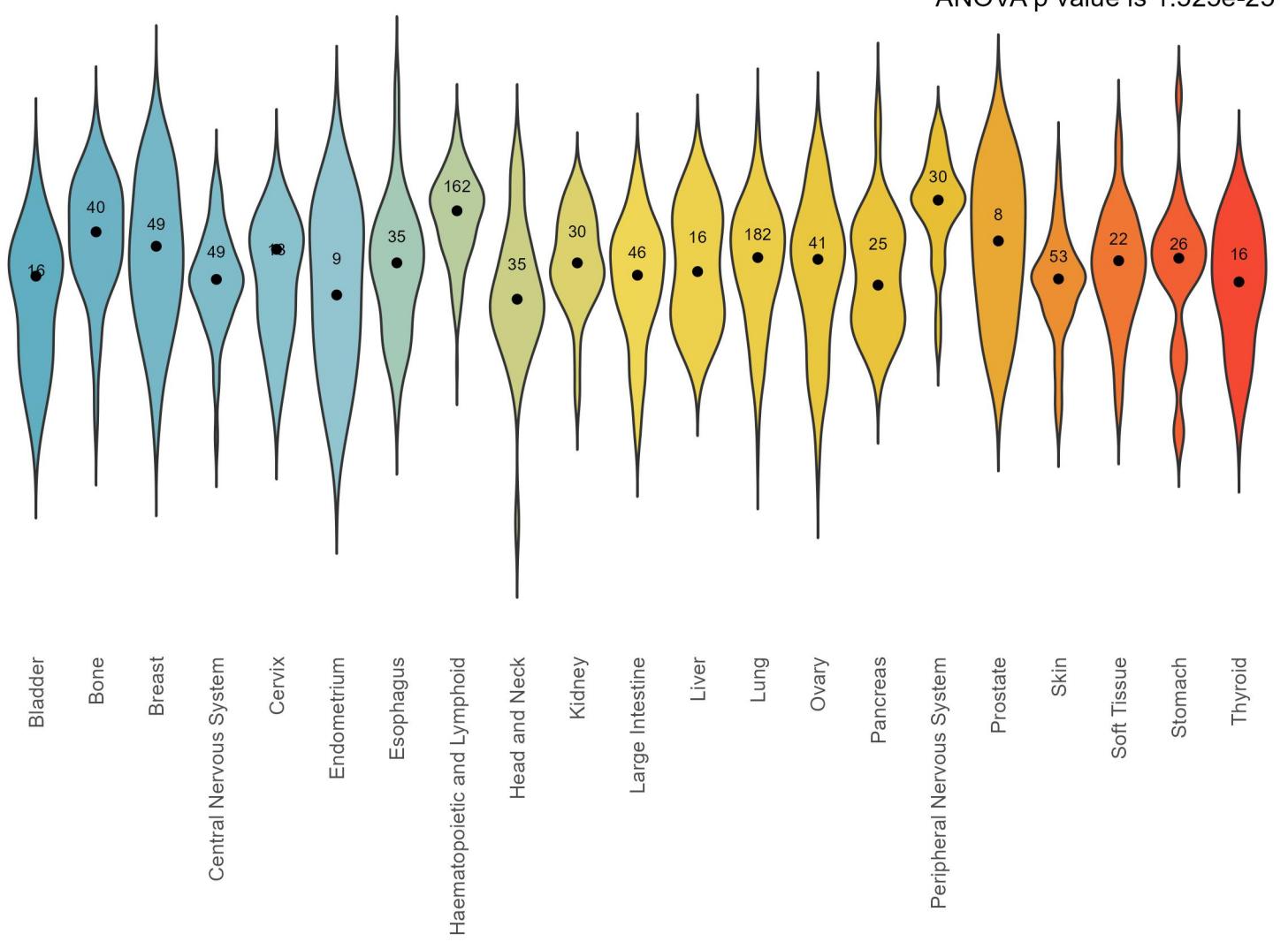


Top positive correlations of CDK1 protein, DB1



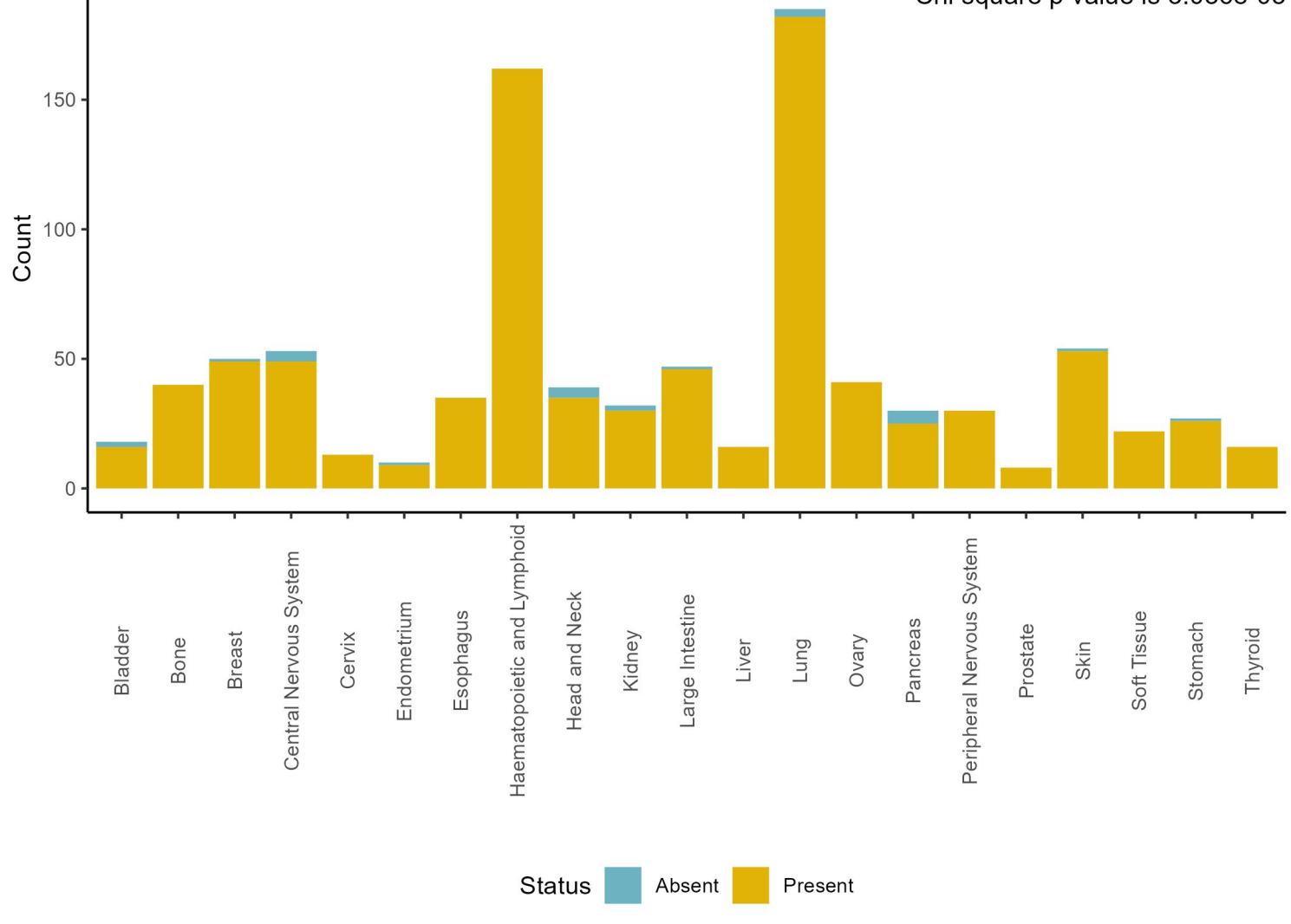
Amount of CDK1 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 1.525e-25



Present and absent CDK1 protein counts by tissue, DB1

Chi square p value is 3.036e-05

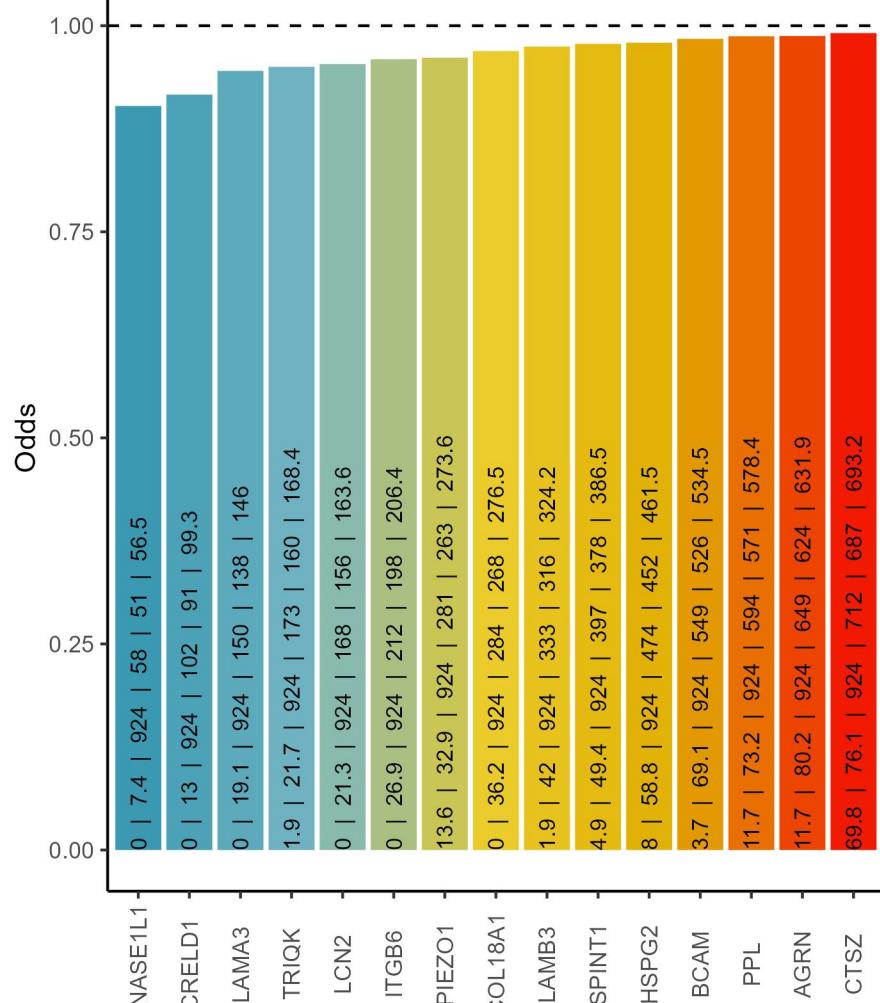


Cooccurrence with CDK1 protein, DB1

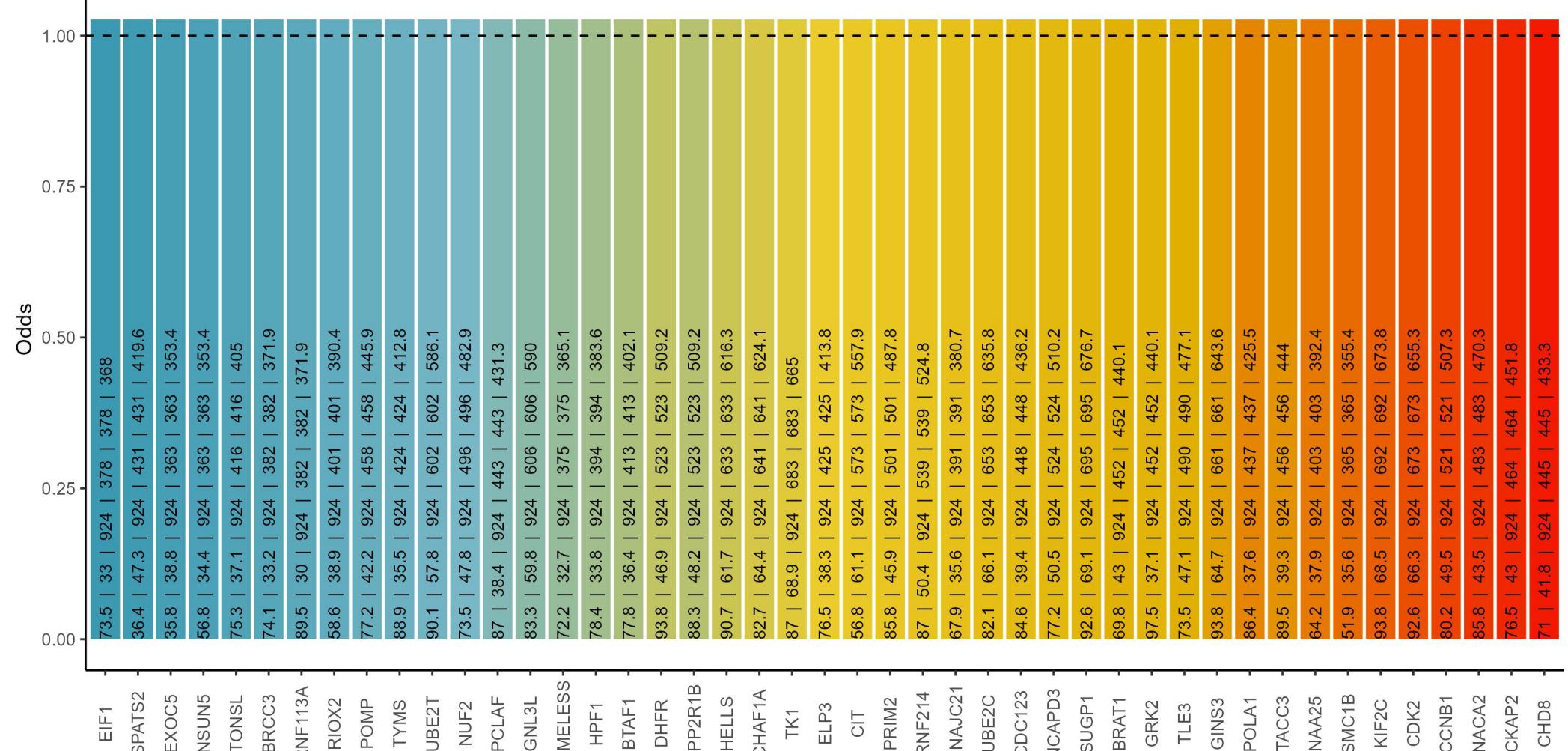
% of CDK1 in blood cancers: 100 ; % of CDK1 in solid cancers: 96.8

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CDK1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

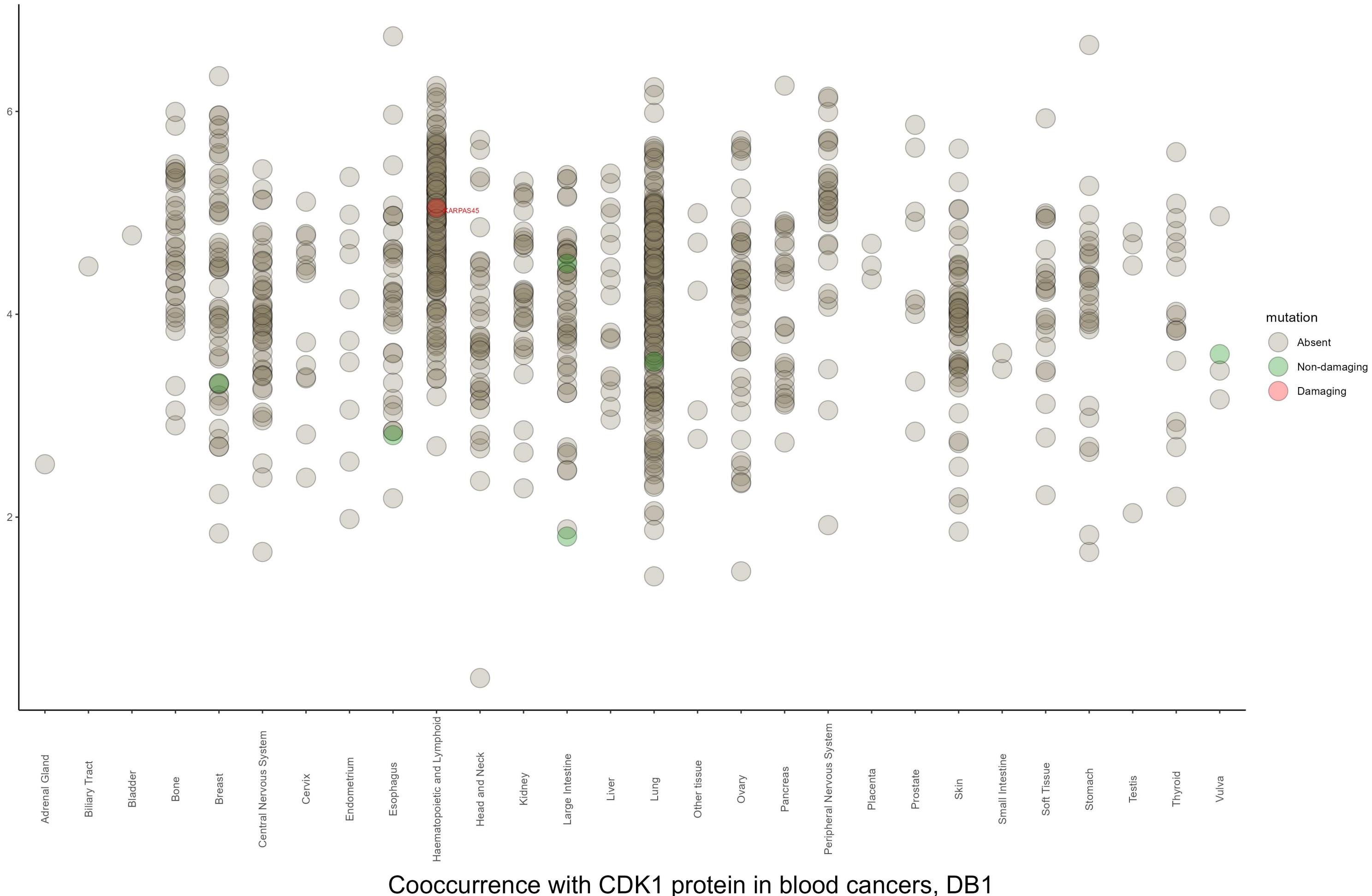
Negative cooccurrence



Positive cooccurrence



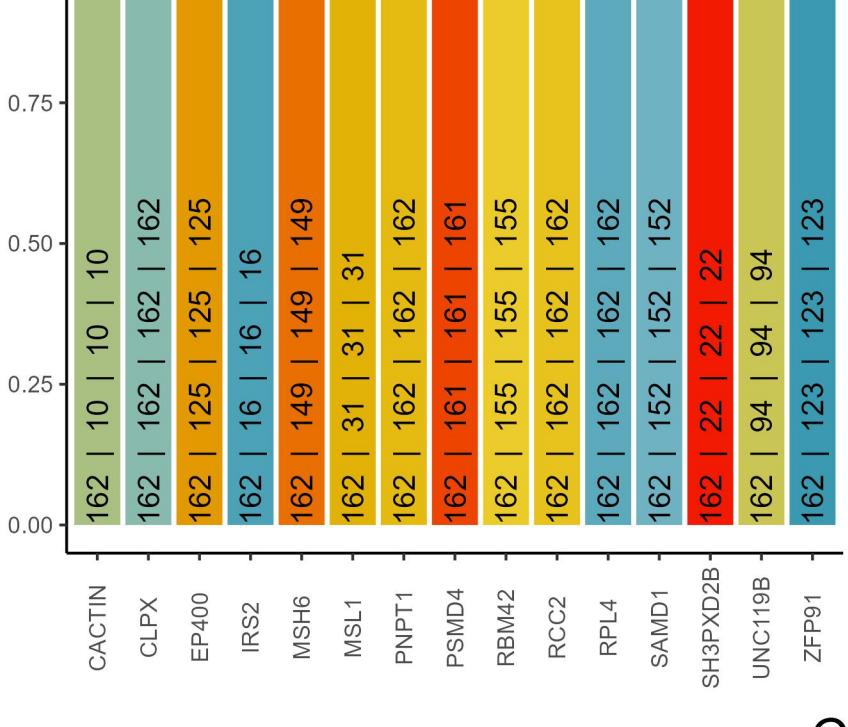
Amount of CDK1 protein and mutation status by tissue, DB1



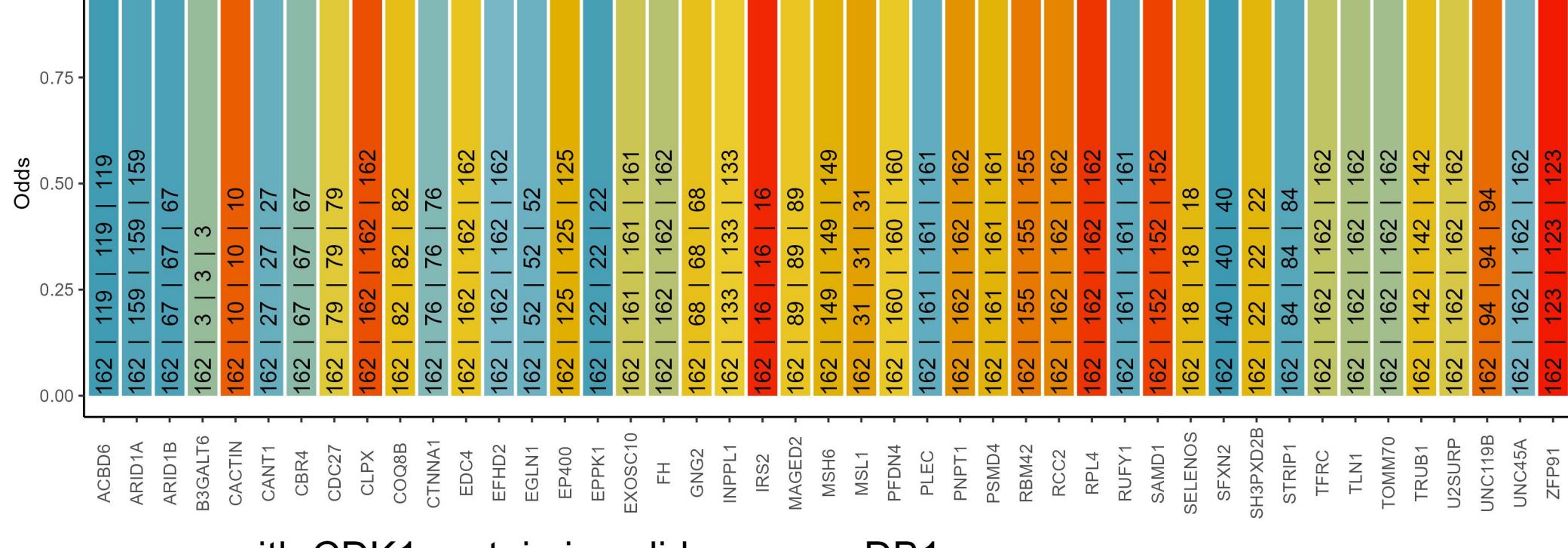
Cooccurrence with CDK1 protein in blood cancers, DB1

The text in the bars: incidence of CDK1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



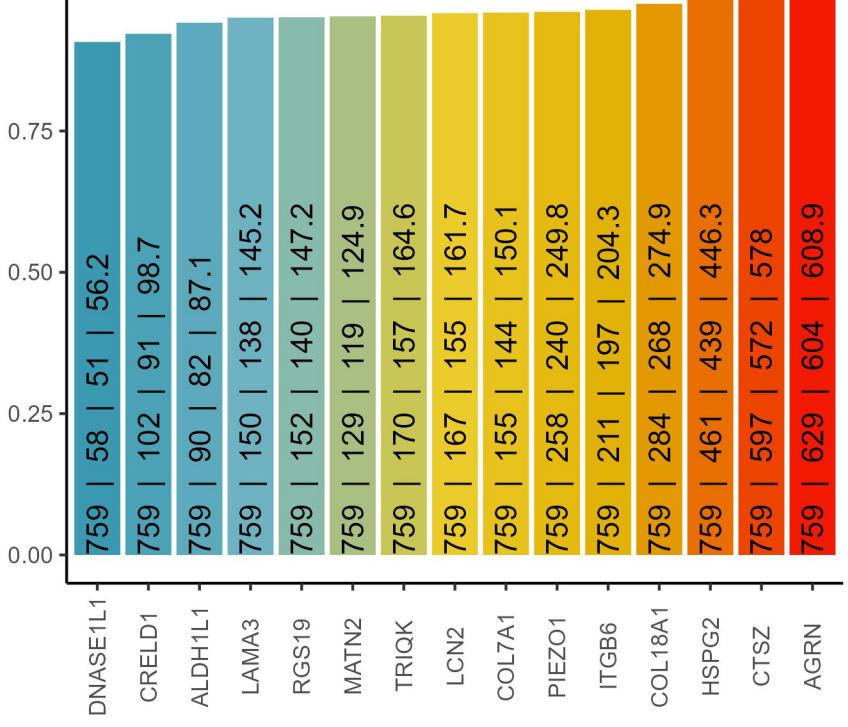
Positive cooccurrence



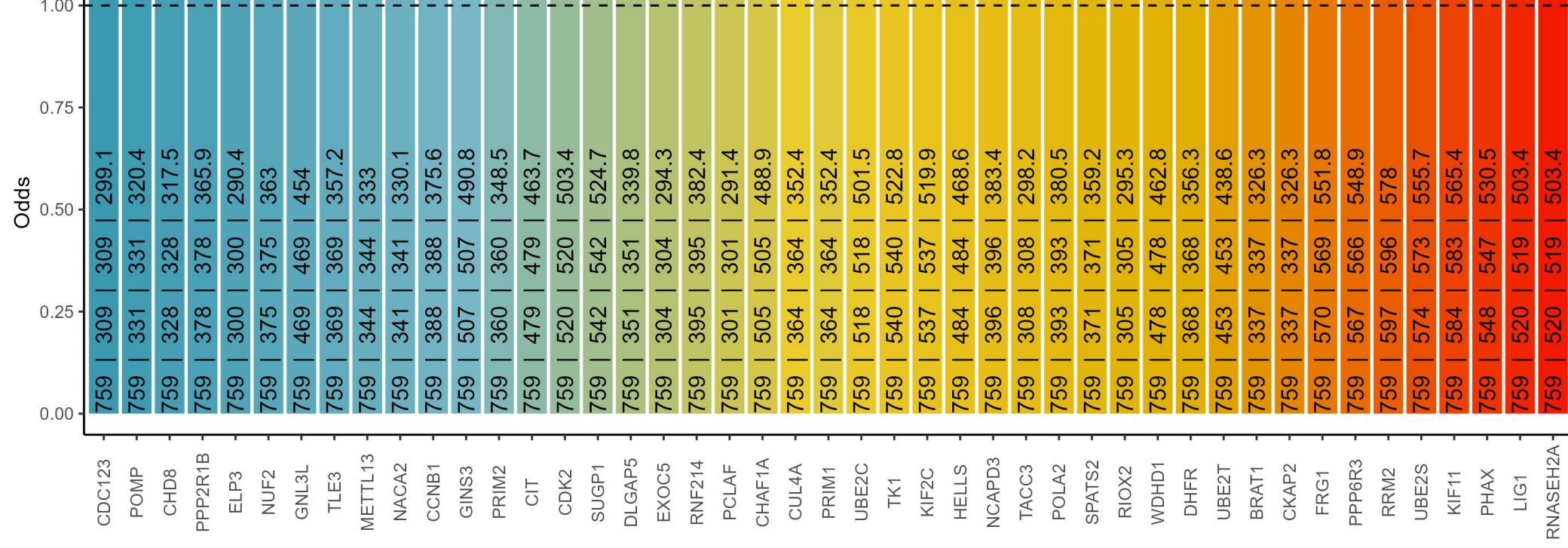
Cooccurrence with CDK1 protein in solid cancers, DB1

The text in the bars: incidence of CDK1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

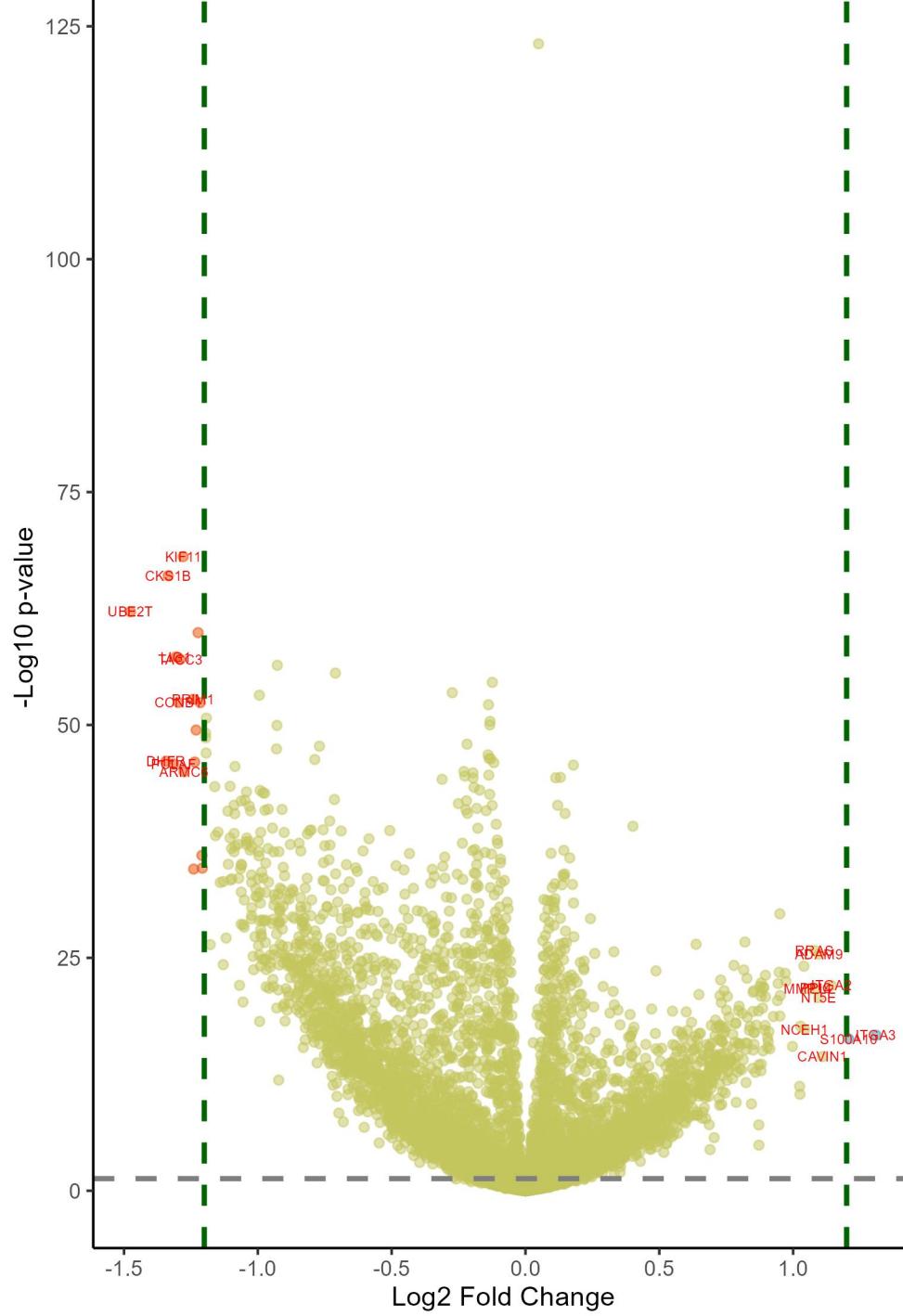
Negative cooccurrence



Positive cooccurrence

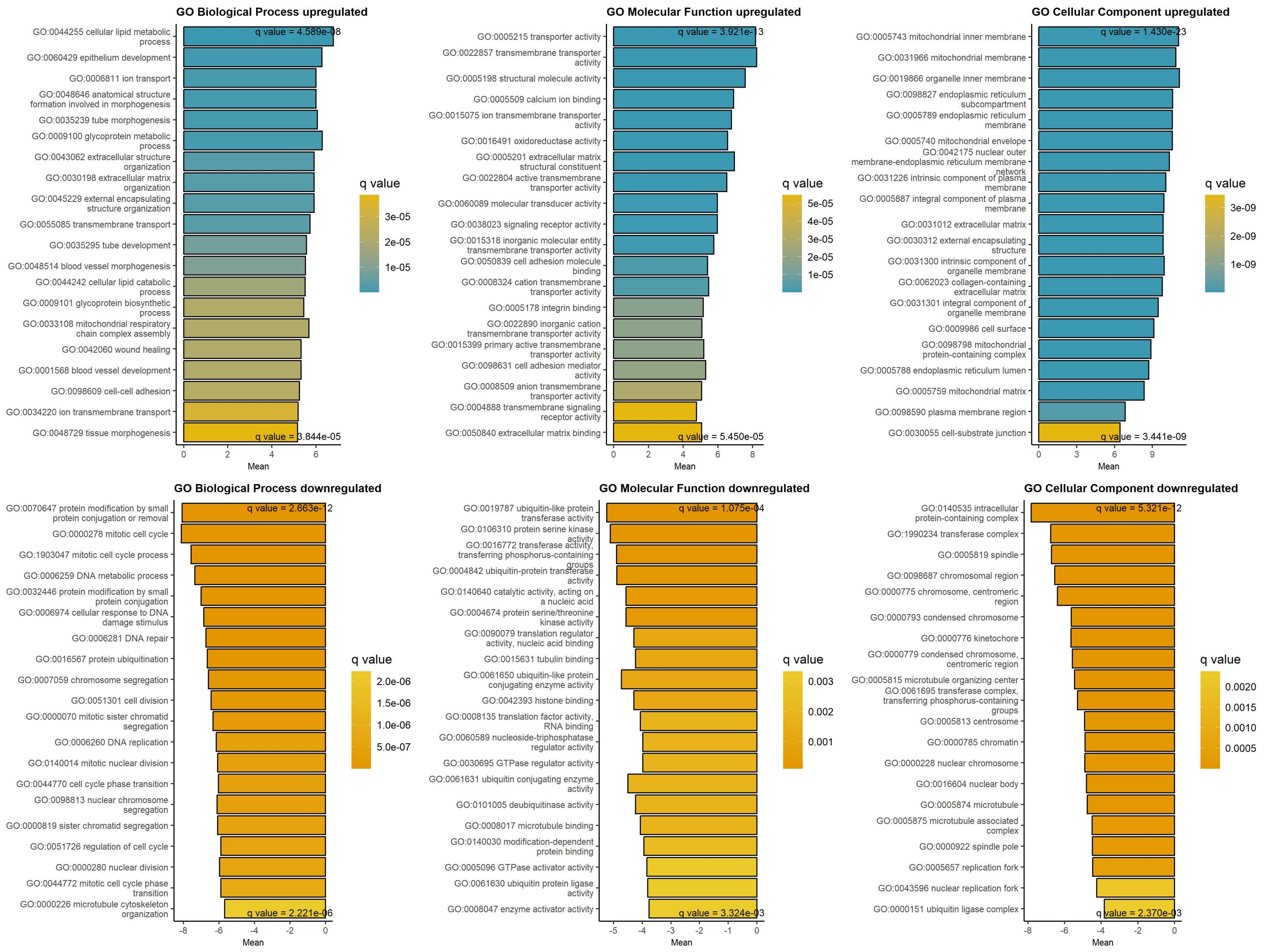


Downregulated at low/absent CDK1 Upregulated at low/absent CDK1



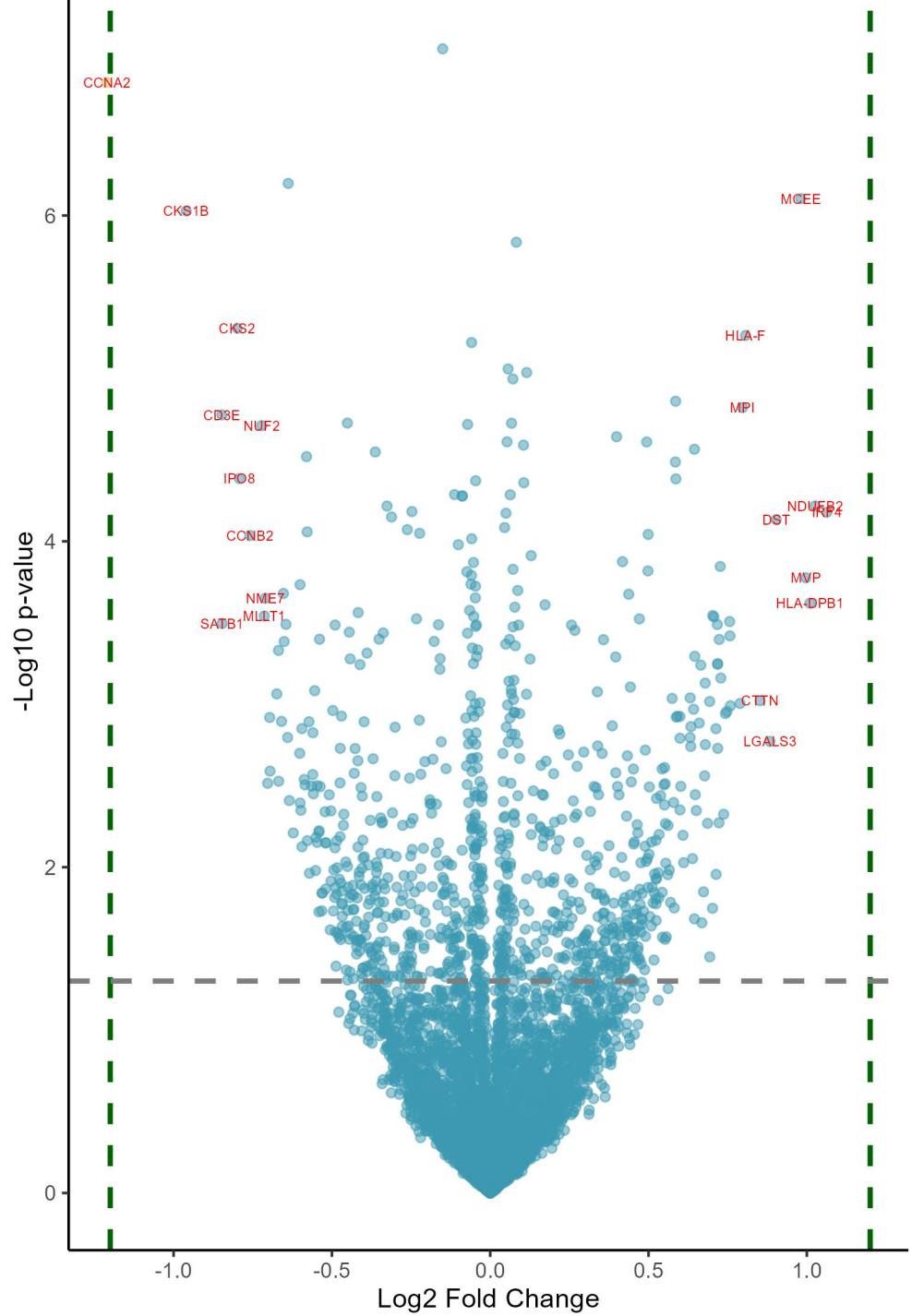
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.48	9.26e-60	UBE2T	ubiquitin conjugating enzyme E2 T	1.31	1.23e-16	ITGA3	integrin subunit alpha 3
-1.34	1.59e-44	DHFR	dihydrofolate reductase	1.21	2.92e-16	S100A10	S100 calcium binding protein A10
-1.34	1.58e-63	CKS1B	CDC28 protein kinase regulatory sub	1.14	9.23e-22	ITGA2	integrin subunit alpha 2
-1.31	2.78e-44	PCLAF	PCNA clamp associated factor	1.11	1.93e-14	CAVIN1	caveolae associated protein 1
-1.31	4.68e-55	LIG1	DNA ligase 1	1.1	6.15e-25	ADAM9	ADAM metallopeptidase domain 9
-1.3	1.66e-50	CCNB1	cyclin B1	1.1	1.67e-20	NT5E	5'-nucleotidase ecto
-1.29	7.45e-55	TACC3	transforming acidic coiled-coil con	1.09	1.85e-21	PPIC	peptidylprolyl isomerase C
-1.28	1.88e-65	KIF11	kinesin family member 11	1.08	2.55e-25	RRAS	RAS related
-1.28	1.70e-43	ARMC6	armadillo repeat containing 6	1.06	2.04e-21	MMP14	matrix metallopeptidase 14
-1.24	8.52e-51	PRIM1	DNA primase subunit 1	1.04	3.29e-17	NCEH1	neutral cholesterol ester hydrolase
-1.24	1.34e-33	PBK	PDZ binding kinase	1.04	1.00e-23	CD109	CD109 molecule
-1.24	1.86e-44	TYMS	thymidylate synthetase	1.03	1.44e-17	S100A16	S100 calcium binding protein A16
-1.23	1.05e-47	UBE2C	ubiquitin conjugating enzyme E2 C	1.03	1.49e-10	GNG12	G protein subunit gamma 12
-1.22	1.36e-57	RRM2	ribonucleotide reductase regulatory	1.02	2.25e-11	LGALS3	galectin 3
-1.22	1.66e-50	HAT1	histone acetyltransferase 1	1	1.76e-15	CAV1	caveolin 1
-1.21	5.27e-35	PSME3IP1	proteasome activator subunit 3 inte	0.97	3.51e-22	NPC1	NPC intracellular cholesterol trans
-1.21	1.07e-33	AK6	adenylate kinase 6	0.97	5.26e-23	ITGAV	integrin subunit alpha V
-1.19	2.21e-47	GINS3	GINS complex subunit 3	0.95	1.04e-20	PON2	paraoxonase 2
-1.19	6.63e-47	UCK2	uridine-cytidine kinase 2	0.95	1.34e-18	EPHA2	EPH receptor A2
-1.19	2.47e-45	UBE2S	ubiquitin conjugating enzyme E2 S	0.95	4.70e-29	MYO1C	myosin IC
-1.19	6.69e-49	GINS4	GINS complex subunit 4	0.95	4.18e-23	ITPR3	inositol 1,4,5-trisphosphate recept
-1.18	6.60e-26	NACA2	nascent polypeptide associated comp	0.94	5.97e-22	MBOAT7	membrane bound O-acyltransferase do
-1.16	5.59e-42	POLA2	DNA polymerase alpha 2, accessory s	0.94	3.38e-20	SLC12A9	solute carrier family 12 member 9
-1.16	5.53e-37	DCK	deoxycytidine kinase	0.93	1.47e-18	P4HA2	prolyl 4-hydroxylase subunit alpha
-1.15	2.40e-37	PDXP	pyridoxal phosphatase	0.91	3.09e-15	EGFR	epidermal growth factor receptor
-1.14	3.01e-32	MAD2L1	mitotic arrest deficient 2 like 1	0.91	5.25e-17	GPX8	glutathione peroxidase 8 (putative)
-1.13	7.02e-24	BLMH	bleomycin hydrolase	0.91	5.60e-16	SQOR	sulfide quinone oxidoreductase
-1.13	2.43e-32	NUDT3	nudix hydrolase 3	0.9	2.23e-16	PPL	periplakin
-1.12	1.37e-26	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.9	2.22e-15	DSG2	desmoglein 2
-1.12	1.37e-26	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.9	2.22e-15	DSG2	desmoglein 2

GAGE analysis on upregulated and downregulated proteins at low/absent CDK1 protein, DB1

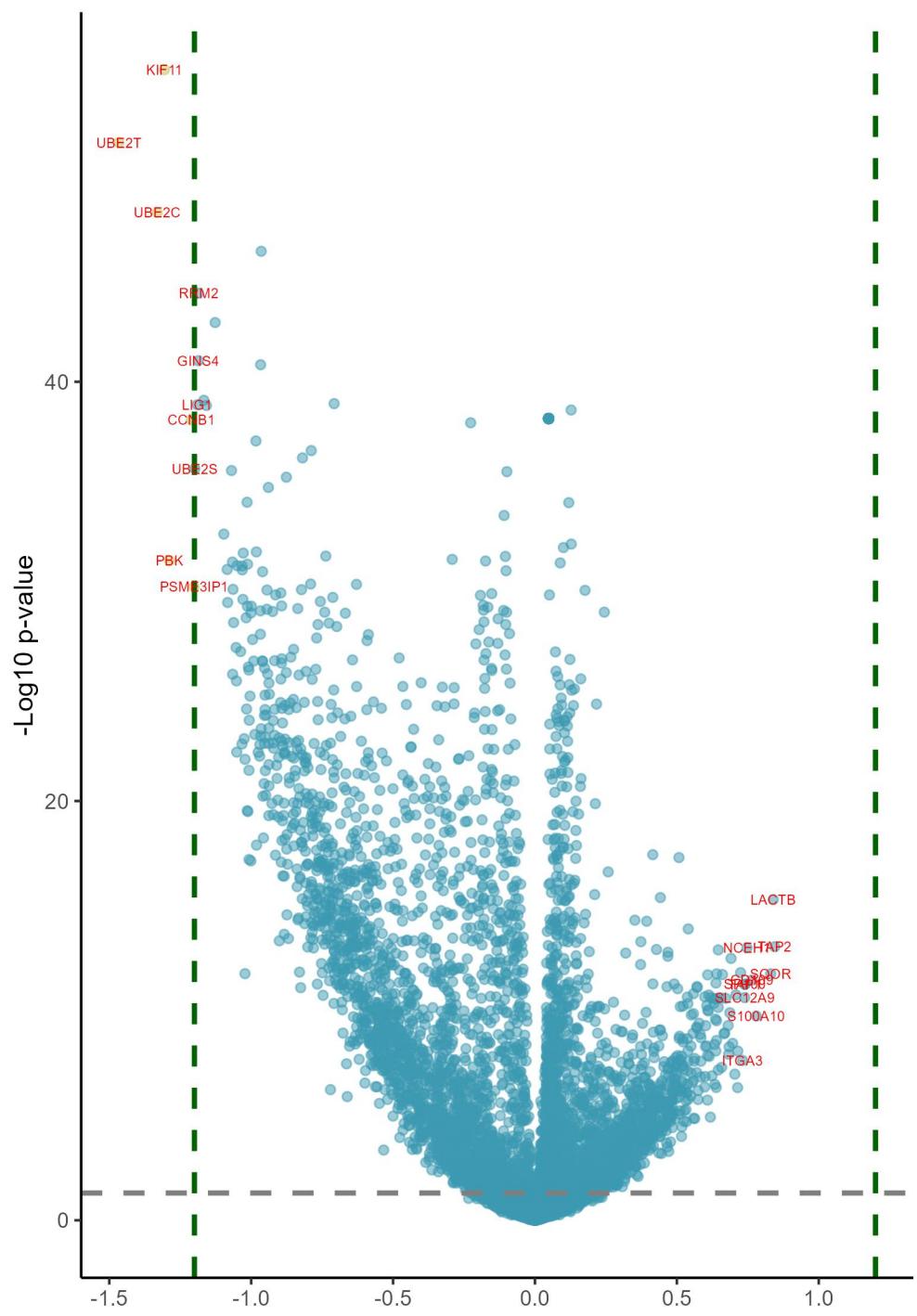


p-value < 0.05 & logFC > 1.2

Downregulated in blood cancers at low/absent CDK1 Upregulated in blood cancers at low/absent CDK1

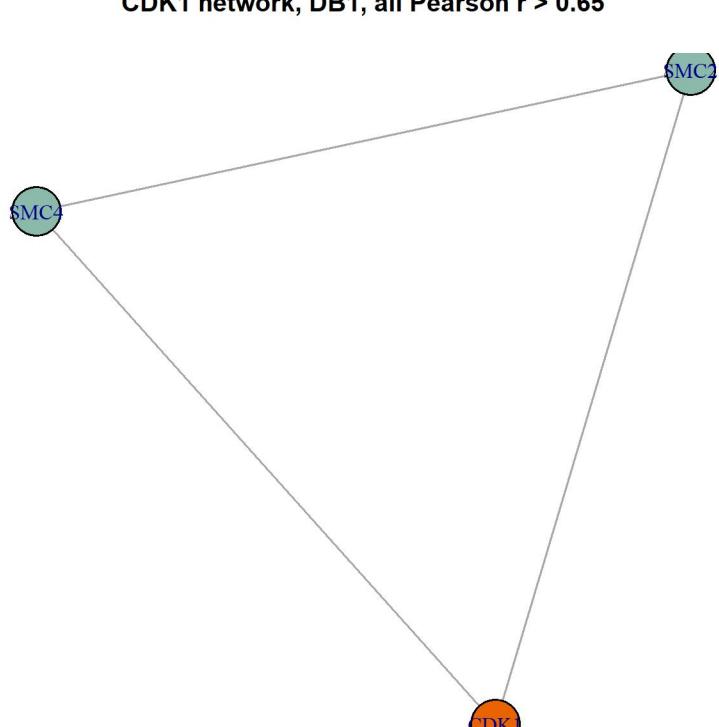


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.21	3.38e-04	CCNA2	cyclin A2	1.06	1.09e-02	IRF4	interferon regulatory factor 4
-0.96	1.04e-03	CKS1B	CDC28 protein kinase regulatory sub	1.03	1.06e-02	NDUFB2	NADH:ubiquinone oxidoreductase subu
-0.85	6.48e-03	CD3E	CD3 epsilon subunit of T-cell recep	1.01	2.31e-02	HLA-DPB1	major histocompatibility complex, c
-0.85	2.47e-02	SATB1	SATB homeobox 1	1	1.86e-02	MVP	major vault protein
-0.8	4.01e-03	CKS2	CDC28 protein kinase regulatory sub	0.98	1.04e-03	MCEE	methylmalonyl-CoA epimerase
-0.79	9.08e-03	IPO8	importin 8	0.9	1.14e-02	DST	dystonin
-0.76	1.25e-02	CCNB2	cyclin B2	0.88	6.15e-02	LGALS3	galectin 3
-0.72	6.48e-03	NUF2	NUF2 component of NDC80 kinetochore	0.85	4.64e-02	CTTN	cortactin
-0.71	2.47e-02	MLLT1	MLLT1 super elongation complex subu	0.81	4.01e-03	HLA-F	major histocompatibility complex, c
-0.71	2.18e-02	NME7	NME/NM23 family member 7	0.8	6.48e-03	MPI	mannose phosphate isomerase
-0.7	8.64e-02	MPP1	MAGUK p55 scaffold protein 1	0.79	4.72e-02	CD40	CD40 molecule
-0.7	5.08e-02	MAP1A	microtubule associated protein 1A	0.76	4.78e-02	TNFRSF8	TNF receptor superfamily member 8
-0.7	7.85e-02	MGMT	O-6-methylguanine-DNA methyltransfe	0.76	2.66e-02	PDK1	pyruvate dehydrogenase kinase 1
-0.67	4.41e-02	SUDS3	SDS3 homolog, SIN3A corepressor com	0.76	2.47e-02	LSR	lipolysis stimulated lipoprotein re
-0.67	2.90e-02	CASP2	caspase 2	0.75	5.01e-02	CD58	CD58 molecule
-0.67	8.58e-02	CFAP20	cilia and flagella associated prote	0.74	5.02e-02	MAP2K3	mitogen-activated protein kinase ki
-0.66	5.22e-02	CHEK1	checkpoint kinase 1	0.74	1.08e-01	CTSZ	cathepsin Z
-0.65	2.13e-02	FANCD2	FA complementation group D2	0.73	3.79e-02	DTD1	D-aminoacyl-tRNA deacylase 1
-0.65	2.69e-02	BCL11B	BAF chromatin remodeling complex su	0.73	1.72e-02	NDUFB8	NADH:ubiquinone oxidoreductase subu
-0.65	2.47e-02	PCLAF	PCNA clamp associated factor	0.72	2.67e-02	SIL1	SIL1 nucleotide exchange factor
-0.64	5.94e-02	RAD18	RAD18 E3 ubiquitin protein ligase	0.72	1.15e-01	HLA-DPA1	major histocompatibility complex, c
-0.64	1.04e-03	TACC3	transforming acidic coiled-coil con	0.72	3.21e-02	NUDT19	nudix hydrolase 19
-0.63	9.64e-02	HDGFL3	HDGF like 3	0.72	6.45e-02	JUNB	JunB proto-oncogene, AP-1 transcrip
-0.62	1.23e-01	STK39	serine/threonine kinase 39	0.72	3.21e-02	TRPV2	transient receptor potential cation
-0.6	6.73e-02	YEATS4	YEATS domain containing 4	0.72	2.47e-02	AVEN	apoptosis and caspase activation in
-0.6	1.98e-02	SH2D1A	SH2 domain containing 1A	0.71	1.70e-01	CD74	CD74 molecule
-0.6	9.76e-02	NUB1	negative regulator of ubiquitin lik	0.71	5.53e-02	PLXNB2	plexin B2
-0.6	1.06e-01	CFAP298	cilia and flagella associated prote	0.71	2.47e-02	MIOS	meiosis regulator for oocyte develo
-0.59	5.53e-02	KIF20A	kinesin family member 20A	0.7	2.47e-02	CTSS	cathepsin S

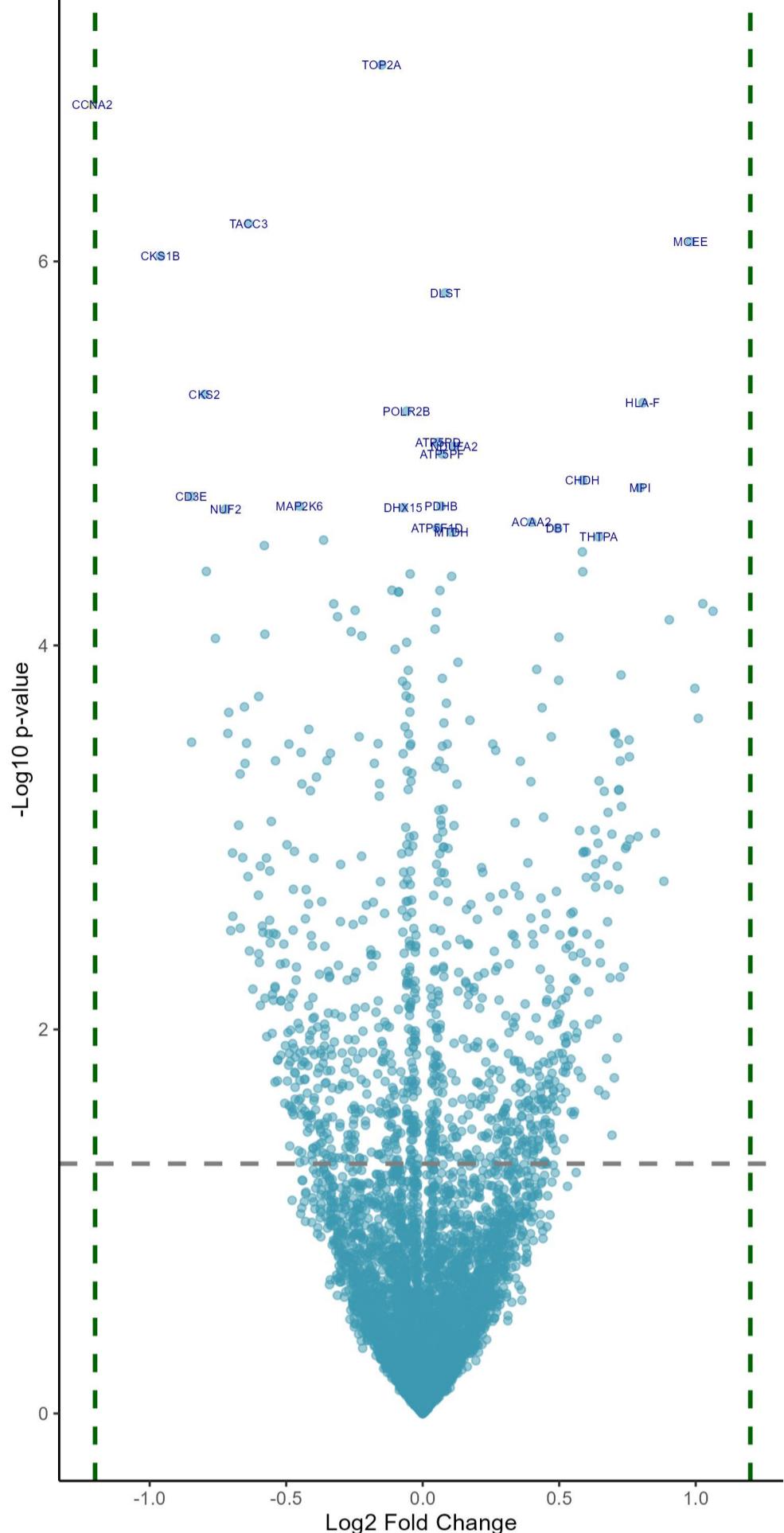
Differentially expressed proteins in solid cancers at absence/low amount of CDK1 , DB1
p-value < 0.05 & logFC > 1.2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.47	8.62e-49	UBE2T	ubiquitin conjugating enzyme E2 T	0.84	5.88e-13	TAP2	transporter 2, ATP binding cassette
-1.33	1.38e-45	UBE2C	ubiquitin conjugating enzyme E2 C	0.84	4.40e-15	LACTB	lactamase beta
-1.31	4.32e-52	KIF11	kinesin family member 11	0.83	1.01e-11	SQOR	sulfide quinone oxidoreductase
-1.29	1.95e-30	PBK	PDZ binding kinase	0.78	8.38e-10	S100A10	S100 calcium binding protein A10
-1.21	4.55e-37	CCNB1	cyclin B1	0.76	1.96e-11	CD109	CD109 molecule
-1.2	3.11e-29	PSME3IP1	proteasome activator subunit 3 inte	0.75	6.56e-13	NCEH1	neutral cholesterol ester hydrolase
-1.2	9.32e-35	UBE2S	ubiquitin conjugating enzyme E2 S	0.74	2.99e-11	SP100	SP100 nuclear antigen
-1.19	4.02e-37	LIG1	DNA ligase 1	0.74	3.07e-11	TAP1	transporter 1, ATP binding cassette
-1.19	8.22e-39	GINS4	GINS complex subunit 4	0.74	1.22e-10	SLC12A9	solute carrier family 12 member 9
-1.19	6.60e-42	RRM2	ribonucleotide reductase regulatory	0.73	8.43e-08	ITGA3	integrin subunit alpha 3
-1.17	4.02e-37	GINS3	GINS complex subunit 3	0.72	9.06e-12	ARSA	arylsulfatase A
-1.16	4.02e-37	HAT1	histone acetyltransferase 1	0.71	3.20e-08	NT5E	5'-nucleotidase ecto
-1.13	1.42e-40	CKS1B	CDC28 protein kinase regulatory sub	0.71	1.42e-06	CD44	CD44 molecule (Indian blood group)
-1.1	1.14e-31	UCK2	uridine-cytidine kinase 2	0.71	9.30e-11	NPC1	NPC intracellular cholesterol trans
-1.08	4.88e-30	DCK	deoxycytidine kinase	0.7	3.52e-07	AP2S1	adaptor related protein complex 2 s
-1.08	1.59e-28	KIF2C	kinesin family member 2C	0.7	1.45e-08	MMP14	matrix metallopeptidase 14
-1.07	1.13e-34	TACC3	transforming acidic coiled-coil con	0.69	2.03e-12	DHRS7B	dehydrogenase/reductase 7B
-1.07	2.25e-30	POLA2	DNA polymerase alpha 2, accessory s	0.69	5.96e-10	LRP10	LDL receptor related protein 10
-1.07	2.92e-25	DHFR	dihydrofolate reductase	0.68	2.08e-08	HLA-B	major histocompatibility complex, c
-1.06	4.09e-29	DLGAP5	DLG associated protein 5	0.68	4.46e-08	GPNMB	glycoprotein nmb
-1.06	1.26e-27	PCLAF	PCNA clamp associated factor	0.68	2.27e-09	PPIC	peptidylprolyl isomerase C
-1.05	1.79e-26	KIFBP	kinesin family binding protein	0.67	1.32e-10	HSPG2	heparan sulfate proteoglycan 2
-1.05	5.82e-25	PDCL3	phosducin like 3	0.67	4.92e-09	ITGA2	integrin subunit alpha 2
-1.05	9.60e-22	AK6	adenylate kinase 6	0.67	5.32e-09	RAB32	RAB32, member RAS oncogene family
-1.05	3.26e-30	CDK2	cyclin dependent kinase 2	0.66	1.09e-11	TM9SF1	transmembrane 9 superfamily member
-1.04	2.76e-26	TXNDC9	thioredoxin domain containing 9	0.66	1.74e-07	IGFBP7	insulin like growth factor binding
-1.03	4.16e-22	MAD2L1	mitotic arrest deficient 2 like 1	0.66	1.26e-10	RRAS	RAS related
-1.03	3.34e-30	SPC24	SPC24 component of NDC80 kinetochor	0.65	2.27e-07	UQCR10	ubiquinol-cytochrome c reductase, c
-1.03	5.07e-30	PRIM1	DNA primase subunit 1	0.65	8.23e-13	MAGT1	magnesium transporter 1

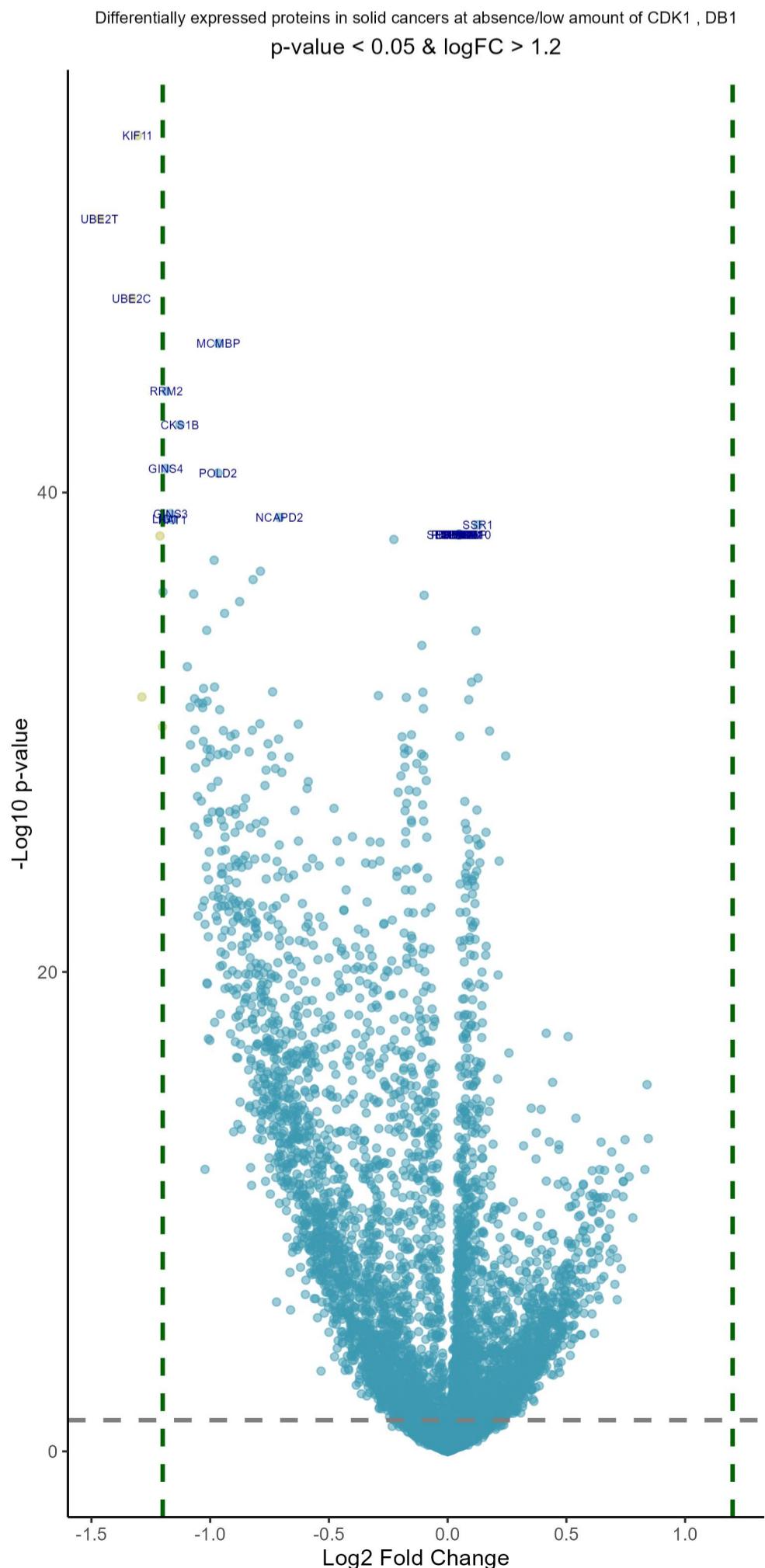
CDK1 network, DB1, all Pearson r > 0.65



Sorted by p values!
 Downregulated in blood cancers at low/absent CDK1 Upregulated in blood cancers at low/absent CDK1

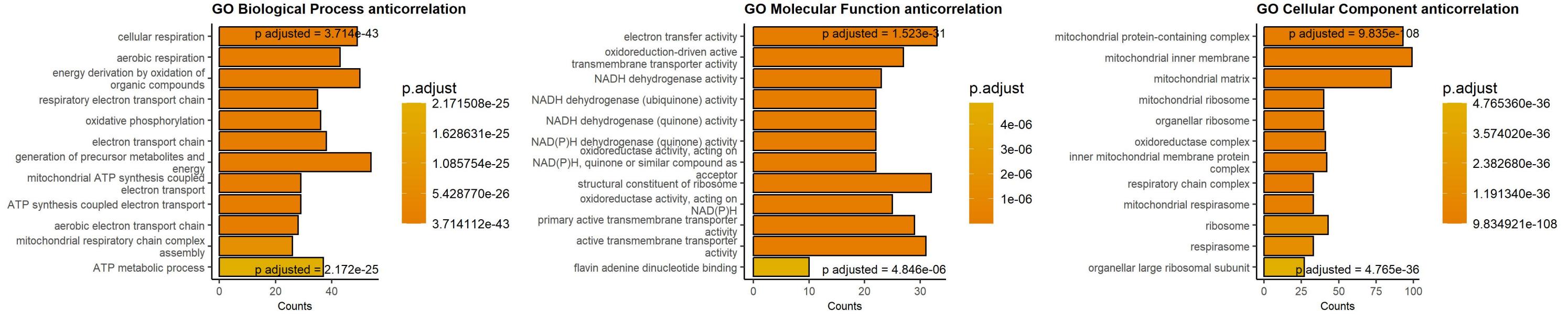
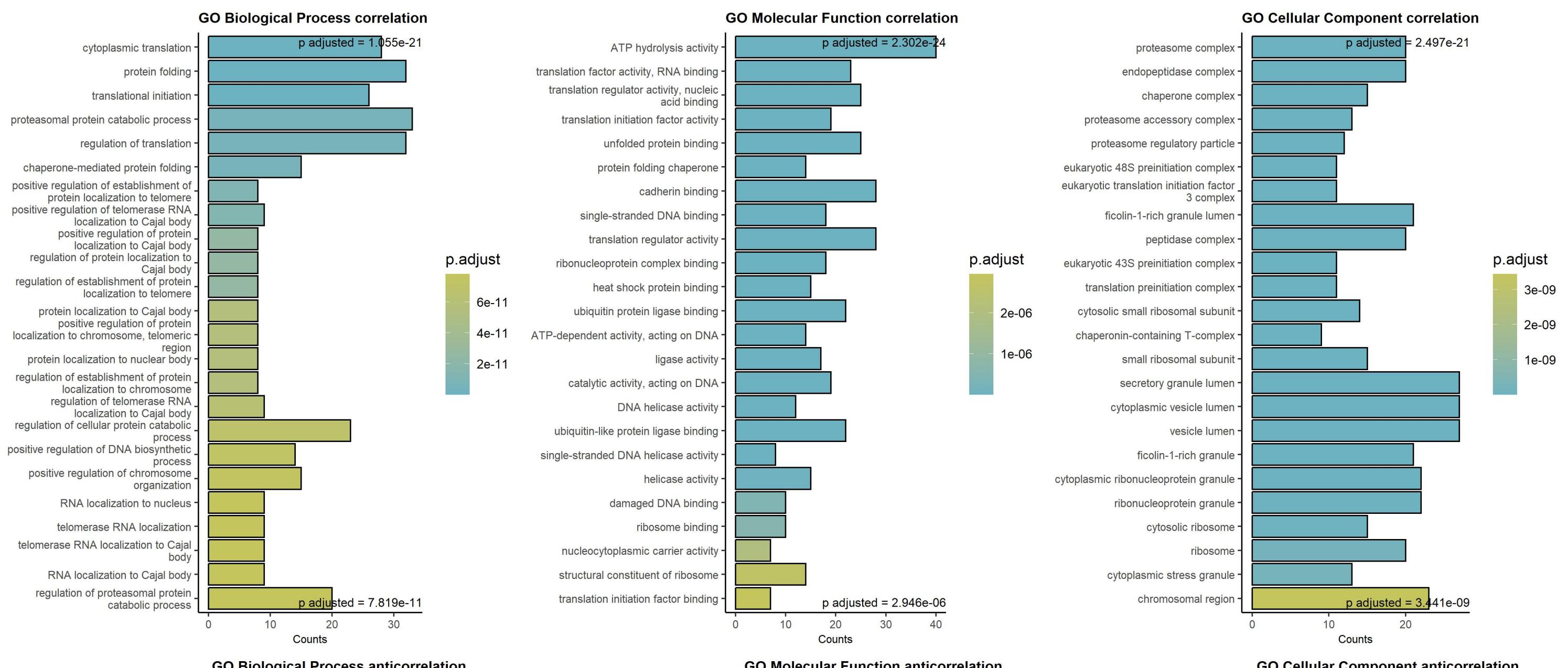


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.15	3.15e-04	TOP2A	DNA topoisomerase II alpha	0.98	1.04e-03	MCEE	methylmalonyl-CoA epimerase
-1.21	3.38e-04	CCNA2	cyclin A2	0.08	1.39e-03	DLST	dihydrolipoamide S-succinyltransfer
-0.64	1.04e-03	TACC3	transforming acidic coiled-coil con	0.81	4.01e-03	HLA-F	major histocompatibility complex, c
-0.96	1.04e-03	CKS1B	CDC28 protein kinase regulatory sub	0.06	5.10e-03	ATP5PD	ATP synthase peripheral stalk subun
-0.8	4.01e-03	CKS2	CDC28 protein kinase regulatory sub	0.12	5.10e-03	NDUFA2	NADH:ubiquinone oxidoreductase subu
-0.06	4.01e-03	POLR2B	RNA polymerase II subunit B	0.07	5.15e-03	ATP5PF	ATP synthase peripheral stalk subun
-0.85	6.48e-03	CD3E	CD3 epsilon subunit of T-cell recep	0.59	6.48e-03	CHDH	choline dehydrogenase
-0.45	6.48e-03	MAP2K6	mitogen-activated protein kinase ki	0.8	6.48e-03	MPI	mannose phosphate isomerase
-0.07	6.48e-03	DHX15	DEAH-box helicase 15	0.07	6.48e-03	PDHB	pyruvate dehydrogenase E1 subunit b
-0.72	6.48e-03	NUF2	NUF2 component of NDC80 kinetochore	0.4	7.10e-03	ACAA2	acetyl-CoA acyltransferase 2
-0.36	7.23e-03	UBE2S	ubiquitin conjugating enzyme E2 S	0.05	7.10e-03	ATP5F1D	ATP synthase F1 subunit delta
-0.58	7.44e-03	POLA1	DNA polymerase alpha 1, catalytic s	0.49	7.10e-03	DBT	dihydrolipoamide branched chain tra
-0.79	9.08e-03	IPO8	importin 8	0.11	7.11e-03	MTDH	metadherin
-0.05	9.08e-03	SF3B6	splicing factor 3b subunit 6	0.64	7.23e-03	THTPA	thiamine triphosphatase
-0.11	9.74e-03	KPNA2	karyopherin subunit alpha 2	0.58	7.74e-03	CARMIL1	capping protein regulator and myosi
-0.09	9.74e-03	SMC4	structural maintenance of chromosom	0.59	9.08e-03	EBI3	Epstein-Barr virus induced 3
-0.09	9.74e-03	BAZ1B	bromodomain adjacent to zinc finger	0.11	9.08e-03	UQCRCB	ubiquinol-cytochrome c reductase bi
-0.33	1.06e-02	PGM2L1	phosphoglucomutase 2 like 1	0.06	9.74e-03	TPI1	triosephosphate isomerase 1
-0.25	1.09e-02	KIF11	kinesin family member 11	1.03	1.06e-02	NDUFB2	NADH:ubiquinone oxidoreductase subu
-0.31	1.12e-02	UHRF1	ubiquitin like with PHD and ring fi	1.06	1.09e-02	IRF4	interferon regulatory factor 4
-0.26	1.25e-02	KIF22	kinesin family member 22	0.05	1.09e-02	TUFM	Tu translation elongation factor, m
-0.58	1.25e-02	CDC123	cell division cycle 123	0.9	1.14e-02	DST	dystonin
-0.22	1.25e-02	CHAF1B	chromatin assembly factor 1 subunit	0.05	1.24e-02	ENO1	enolase 1
-0.76	1.25e-02	CCNB2	cyclin B2	0.5	1.25e-02	GSDME	gasdermin E
-0.06	1.28e-02	SMU1	SMU1 DNA replication regulator and	0.13	1.56e-02	NDUFS6	NADH:ubiquinone oxidoreductase subu
-0.1	1.37e-02	DNMT1	DNA methyltransferase 1	0.42	1.66e-02	ROBO1	roundabout guidance receptor 1
-0.05	1.66e-02	EIF4A3	eukaryotic translation initiation f	0.73	1.72e-02	NDUFB8	NADH:ubiquinone oxidoreductase subu
-0.07	1.76e-02	DNAJA1	DnaJ heat shock protein family (Hsp	0.07	1.76e-02	NDUFS3	NADH:ubiquinone oxidoreductase core
-0.06	1.83e-02	MTA2	metastasis associated 1 family memb	0.5	1.76e-02	GM2A	GM2 ganglioside activator
-0.06	1.98e-02	RFC4	replication factor C subunit 4	1	1.86e-02	MVP	major vault protein
-0.6	1.98e-02	SH2D1A	SH2 domain containing 1A	0.09	2.08e-02	NDUFS1	NADH:ubiquinone oxidoreductase core
-0.05	1.99e-02	BUB3	BUB3 mitotic checkpoint protein	0.44	2.13e-02	ATP13A1	ATPase 13A1
-0.65	2.13e-02	FANCD2	FA complementation group D2	1.01	2.31e-02	HLA-DPB1	major histocompatibility complex, c
-0.05	2.18e-02	DDX5	DEAD-box helicase 5	0.17	2.33e-02	MRPL49	mitochondrial ribosomal protein L49
-0.71	2.18e-02	NME7	NME/NM23 family member 7	0.08	2.37e-02	MRPL58	mitochondrial ribosomal protein L58
-0.06	2.45e-02	MCM5	minichromosome maintenance complex	0.7	2.47e-02	CTSS	cathepsin S
-0.42	2.47e-02	SIVA1	SIVA1 apoptosis inducing factor	0.71	2.47e-02	MIOS	meiosis regulator for oocyte develo
-0.71	2.47e-02	MLLT1	MLLT1 super elongation complex subu	0.47	2.47e-02	ECI1	enoyl-CoA delta isomerase 1
0.05	2.47e-02	SMARDCA5	SWI/SNF related matrix associated	0.76	2.47e-02	LSBP	linoleic acid stimulated lipoprotein re

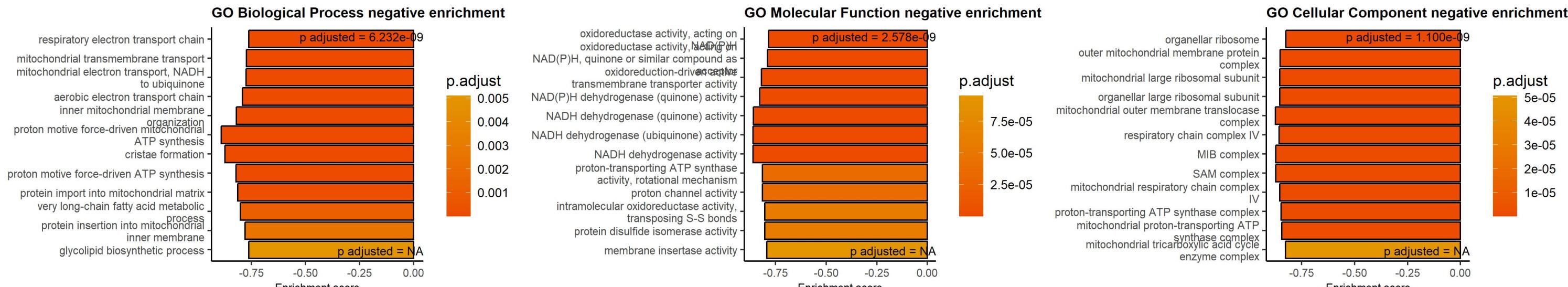
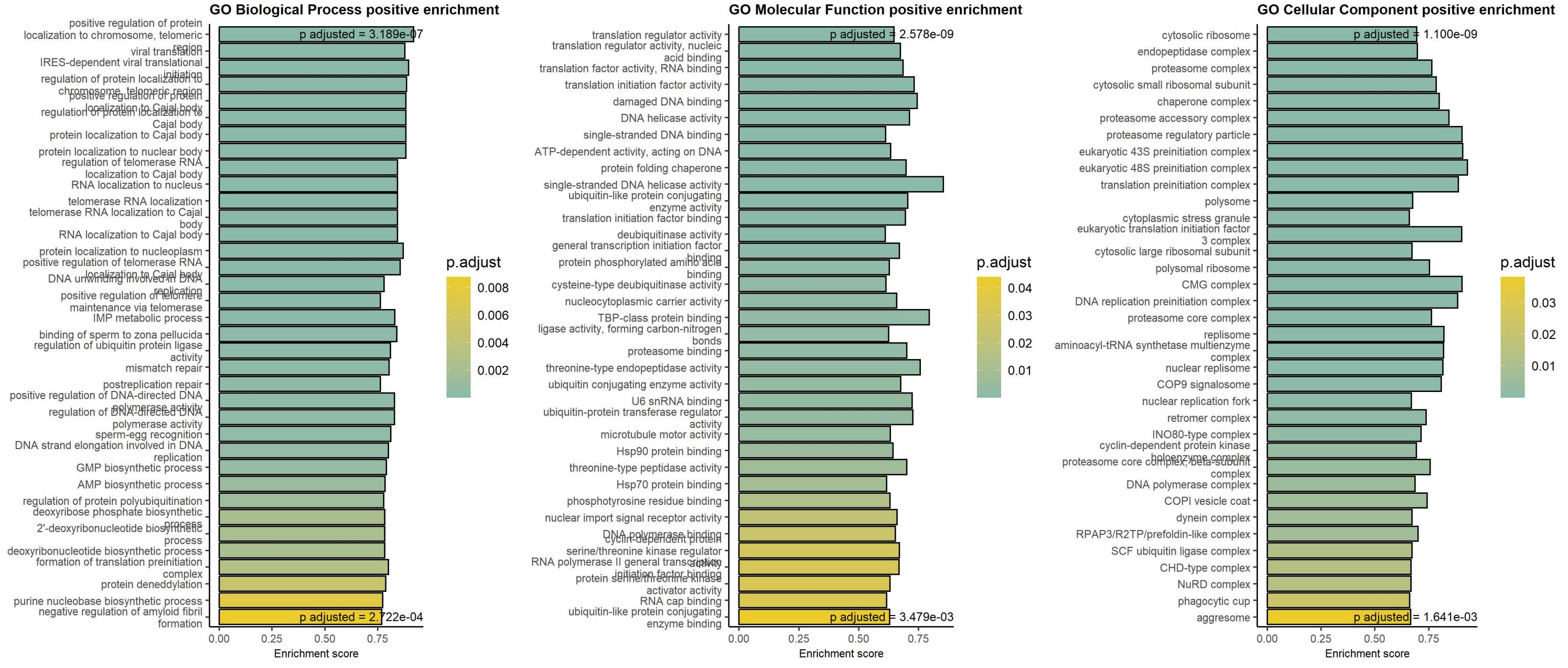


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.31	4.32e-52	KIF11	kinesin family member 11	0.13	4.02e-37	SSR1	signal sequence receptor subunit 1
-1.47	8.62e-49	UBE2T	ubiquitin conjugating enzyme E2 T	0.05	4.02e-37	PTPRCAP	protein tyrosine phosphatase recept
-1.33	1.38e-45	UBE2C	ubiquitin conjugating enzyme E2 C	0.05	4.02e-37	HBE1	hemoglobin subunit epsilon 1
-0.96	7.96e-44	MCMBP	minichromosome maintenance complex	0.05	4.02e-37	SERPINB10	serpin family B member 10
-1.19	6.60e-42	RRM2	ribonucleotide reductase regulatory	0.05	4.02e-37	IGLL1	immunoglobulin lambda like polypept
-1.13	1.42e-40	CKS1B	CDC28 protein kinase regulatory sub	0.05	4.02e-37	CRYBB1	crystallin beta B1
-1.19	8.22e-39	GINS4	GINS complex subunit 4	0.05	4.02e-37	ITGA2B	integrin subunit alpha 2b
-0.97	1.14e-38	POLD2	DNA polymerase delta 2, accessory s	0.05	4.02e-37	ACAP1	ArfGAP with coiled-coil, ankyrin re
-1.17	4.02e-37	GINS3	GINS complex subunit 3	0.05	4.02e-37	NCF4	neutrophil cytosolic factor 4
-0.71	4.02e-37	NCAPD2	non-SMC condensin I complex subunit	0.05	4.02e-37	SP140	SP140 nuclear body protein
-1.19	4.02e-37	LIG1	DNA ligase 1	0.05	4.02e-37	PSTPIP1	proline-serine-threonine phosphatas
-1.16	4.02e-37	HAT1	histone acetyltransferase 1	0.05	4.02e-37	STAB1	stabilin 1
-1.21	4.55e-37	CCNB1	cyclin B1	0.05	4.02e-37	SELPLG	selectin P ligand
-0.23	6.29e-37	MCM6	minichromosome maintenance complex	0.05	4.02e-37	RCSD1	RCSD domain containing 1
-0.98	4.58e-36	NCAPG	non-SMC condensin I complex subunit	0.05	4.02e-37	STAT5A	signal transducer and activator of
-0.79	1.31e-35	NCAPH	non-SMC condensin I complex subunit	0.05	4.02e-37	CTSW	cathepsin W
-0.82	2.88e-35	PPP5C	protein phosphatase 5 catalytic sub	0.05	4.02e-37	GIMAP6	GTPase, IMAP family member 6
-1.2	9.32e-35	UBE2S	ubiquitin conjugating enzyme E2 S	0.05	4.02e-37	GZMB	granzyme B
-1.07	1.13e-34	TACC3	transforming acidic coiled-coil con	0.05	4.02e-37	HK3	hexokinase 3
-0.1	1.27e-34	BUB3	BUB3 mitotic checkpoint protein	0.05	4.02e-37	TUBA8	tubulin alpha 8
-0.88	2.31e-34	ILKAP	ILK associated serine/threonine pho	0.05	4.02e-37	CR2	complement C3d receptor 2
-0.94	7.06e-34	HSPA14	heat shock protein family A (Hsp70)	0.05	4.02e-37	POU2F2	POU class 2 homeobox 2
-1.01	3.55e-33	UBAP2	ubiquitin associated protein 2	0.05	4.02e-37	AZU1	azurocidin 1
-0.11	1.49e-32	CCT4	chaperonin containing TCP1 subunit	0.05	4.02e-37	CD48	CD48 molecule
-1.1	1.14e-31	UCK2	uridine-cytidine kinase 2	0.05	4.02e-37	SKAP2	src kinase associated phosphoprotei
-0.98	7.82e-31	NUF2	NUF2 component of NDC80 kinetochore	0.05	4.02e-37	CCL17	C-C motif chemokine ligand 17
-1.03	8.84e-31	DOHH	deoxyhypusine hydroxylase	0.05	4.02e-37	ADA2	adenosine deaminase 2
-0.74	1.22e-30	CLUH	clustered mitochondria homolog	0.05	4.02e-37	CD3E	CD3 epsilon subunit of T-cell recep
-0.1	1.25e-30	CCT7	chaperonin containing TCP1 subunit	0.05	4.02e-37	RNASE2	ribonuclease A family member 2
-0.29	1.72e-30	SMC2	structural maintenance of chromosom	0.05	4.02e-37	TEX11	testis expressed 11
-1.29	1.95e-30	PBK	PDZ binding kinase	0.05	4.02e-37	PLEK	pleckstrin
-0.17	2.02e-30	MCM7	minichromosome maintenance complex	0.05	4.02e-37	CD300A	CD300a molecule
-1.07	2.25e-30	POLA2	DNA polymerase alpha 2, accessory s</				

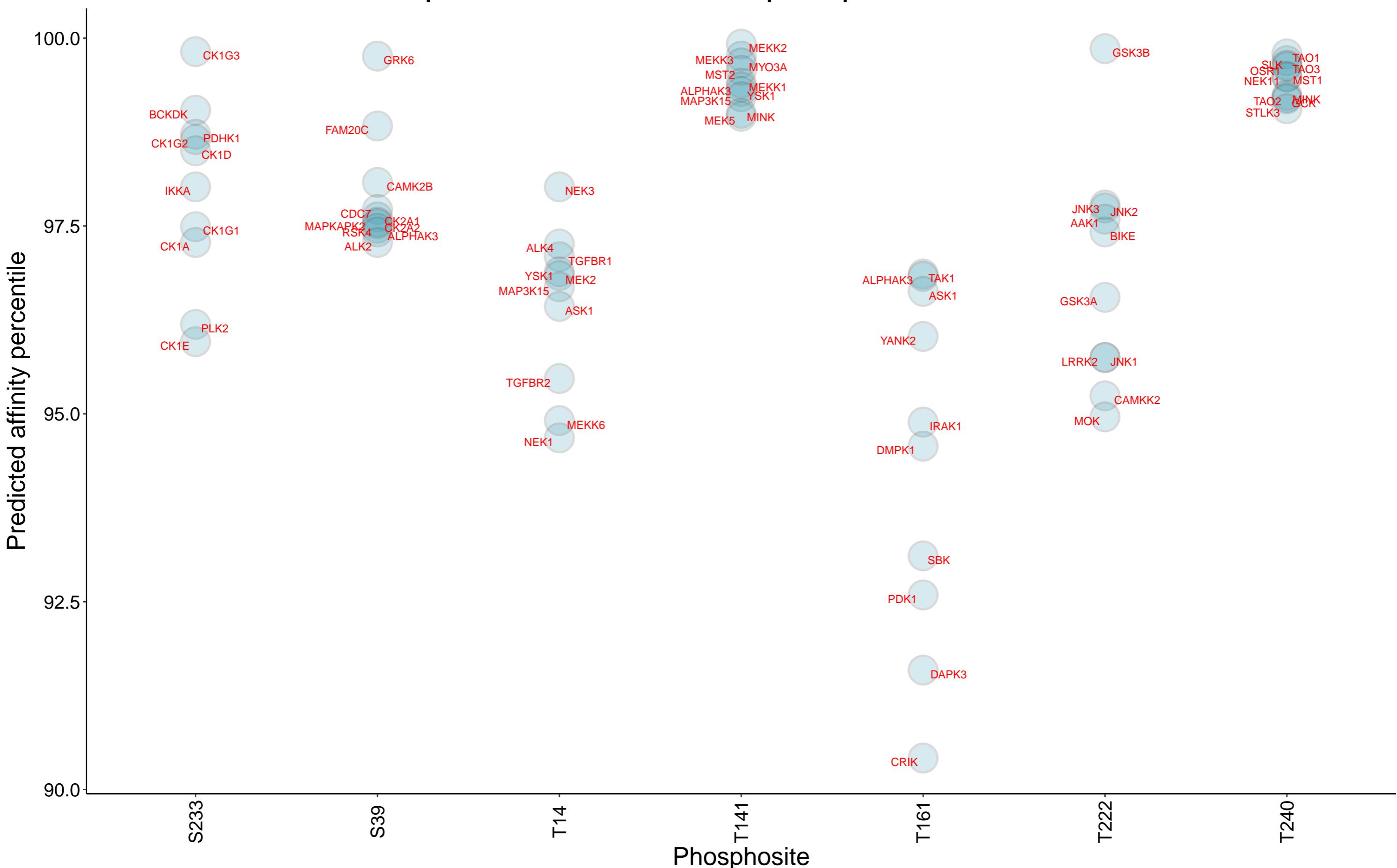
Top 250 correlation coefficients overrepresentation, CDK1 protein, DB1



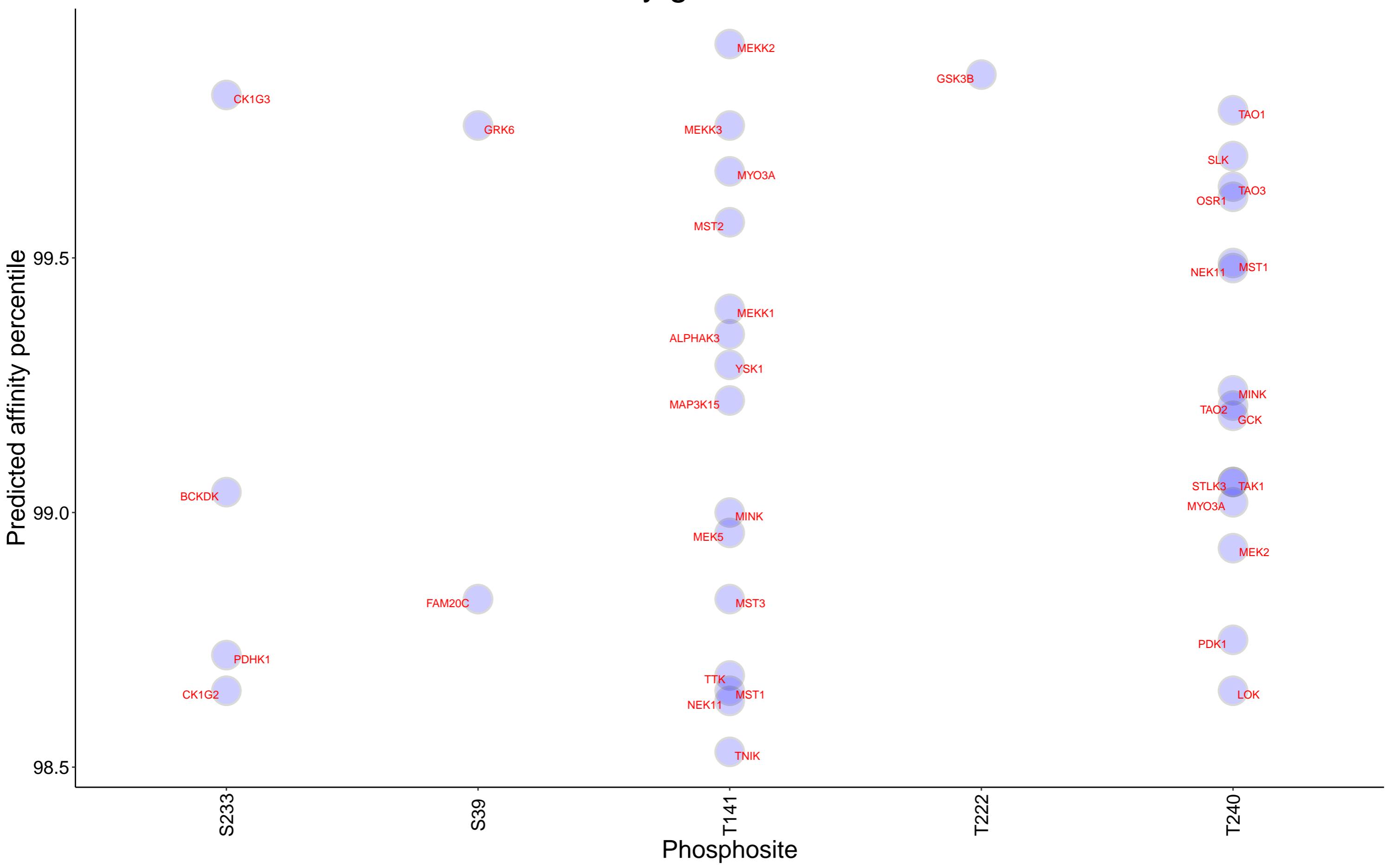
Gene Set Enrichment analysis on protein correlation coefficients, CDK1 protein, DB1



Top 10 kinases for each phosphosite in CDK1



Kinases with affinity greater than 98.5% to CDK1



Top 15 positive correlation coefficients for CDK1 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

