

CDK9

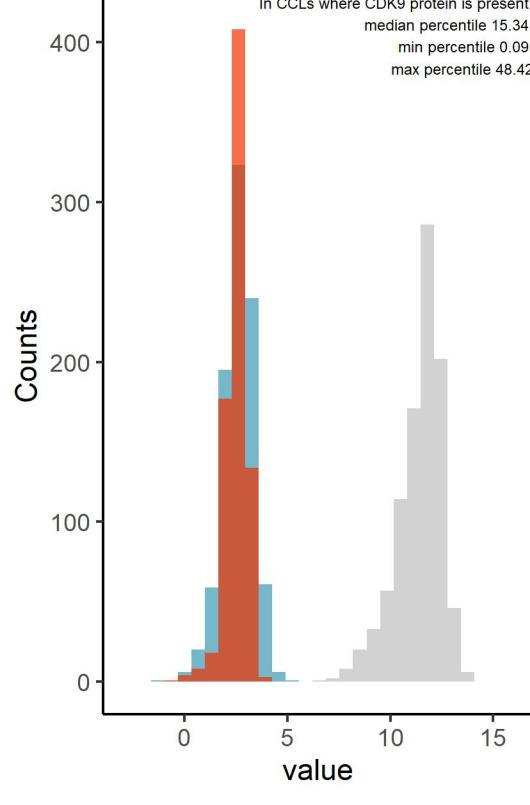
Protein name: CDK9 ; UNIPROT: P50750 ; Gene name: cyclin dependent kinase 9

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

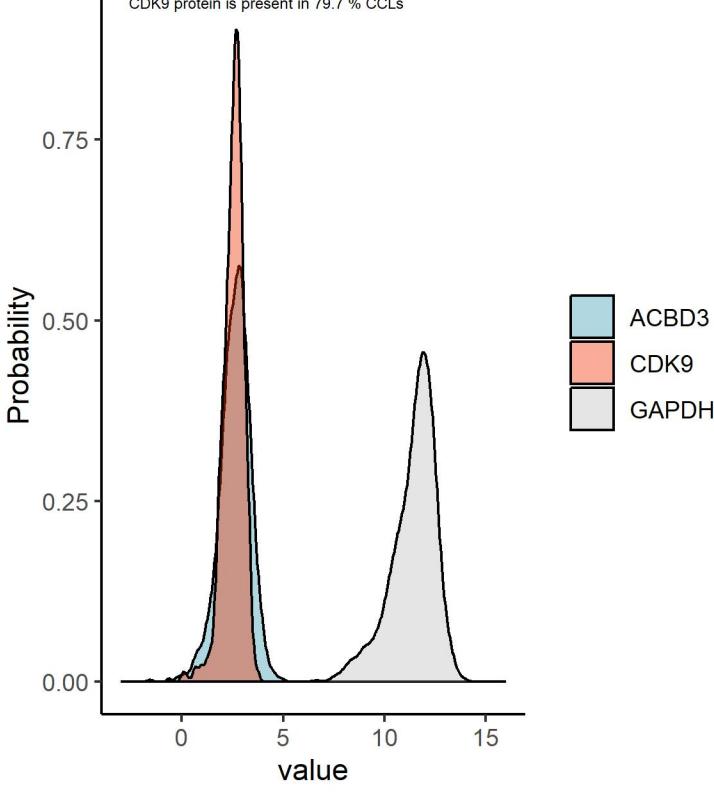
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

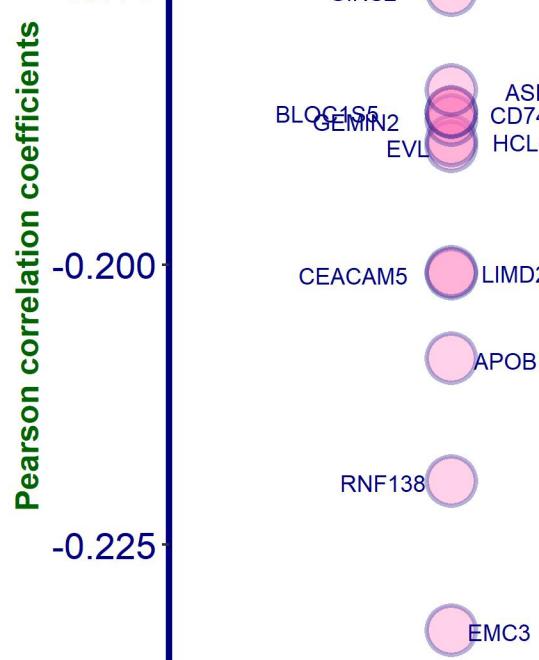
Histogram of CDK9 protein compared to proteins with low and high abundance



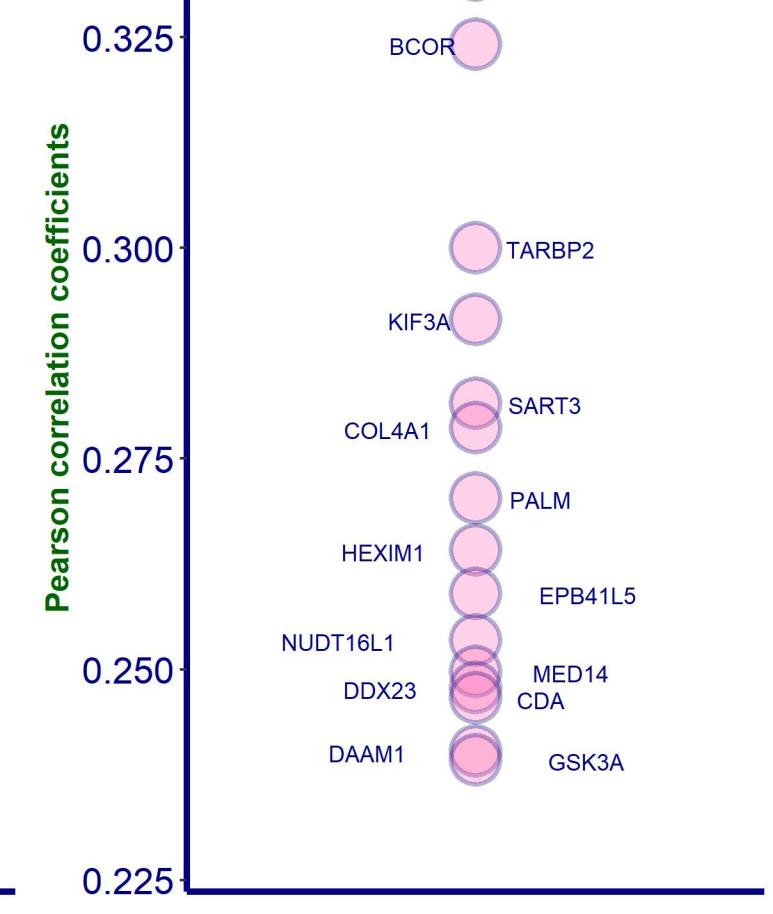
Density plot of CDK9 protein compared to proteins with low and high abundance



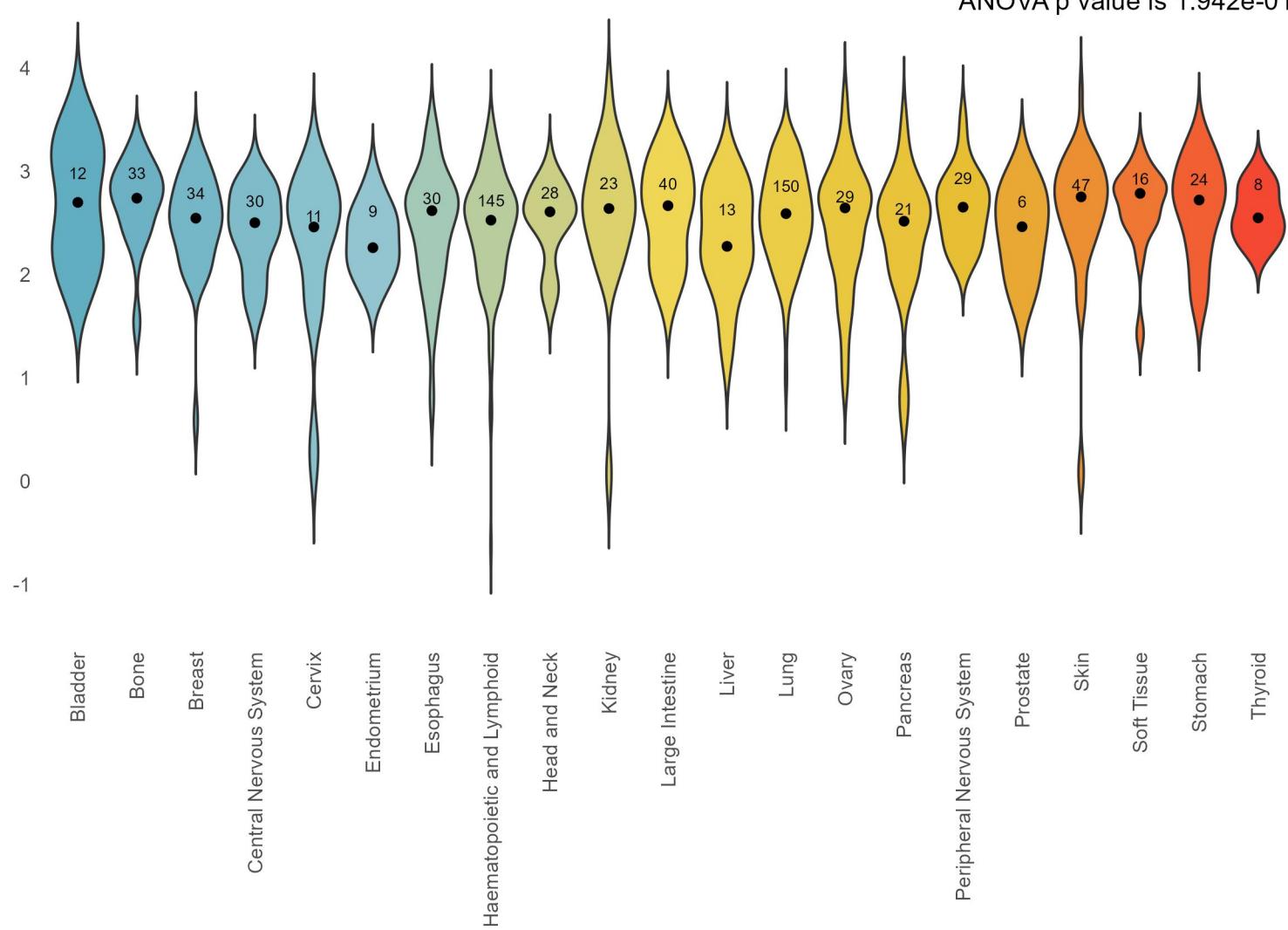
Top negative correlations of CDK9 protein, DB1



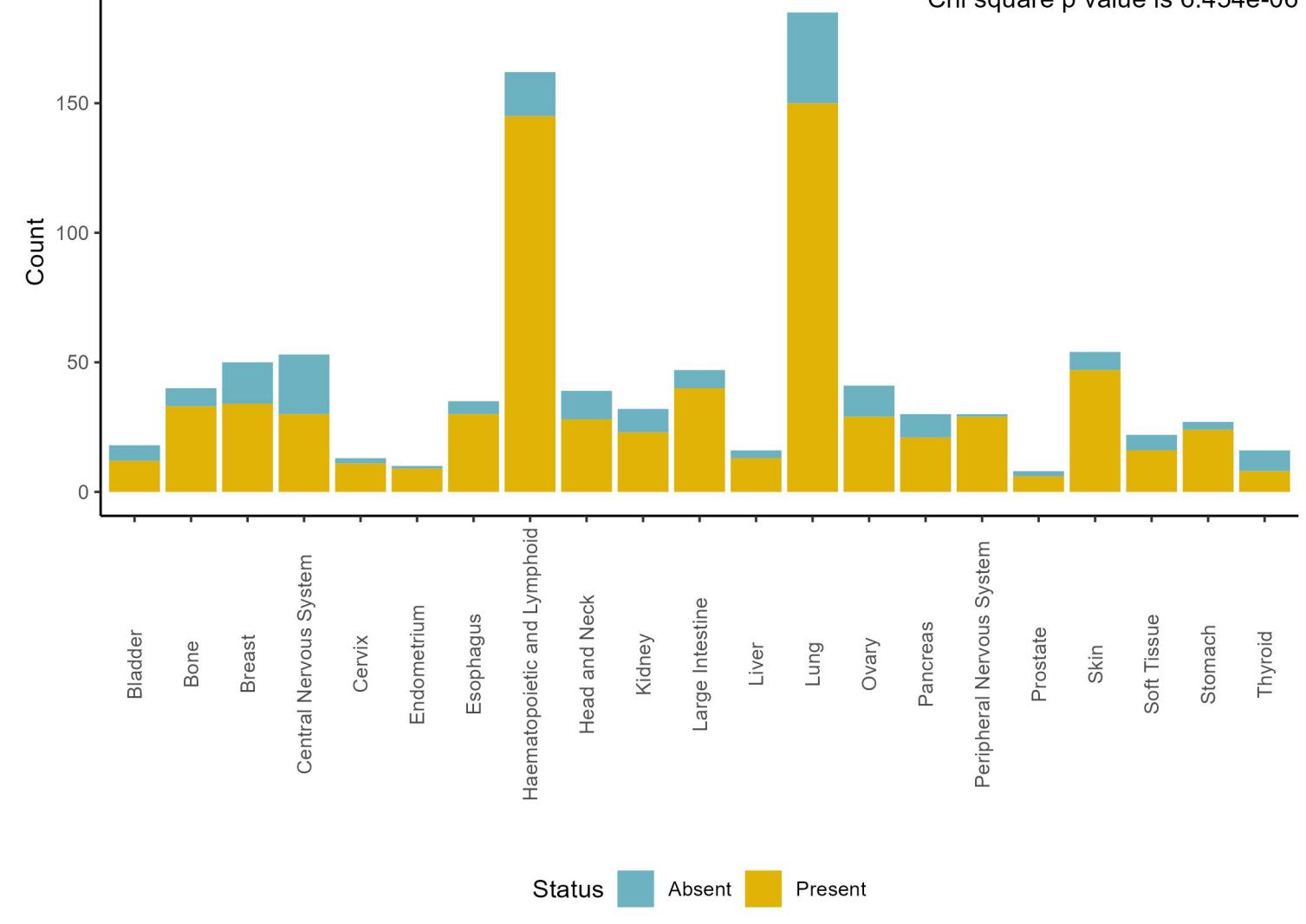
Top positive correlations of CDK9 protein, DB1



Amount of CDK9 protein, number of CCLs where it is present by tissue, DB1



Present and absent CDK9 protein counts by tissue, DB1

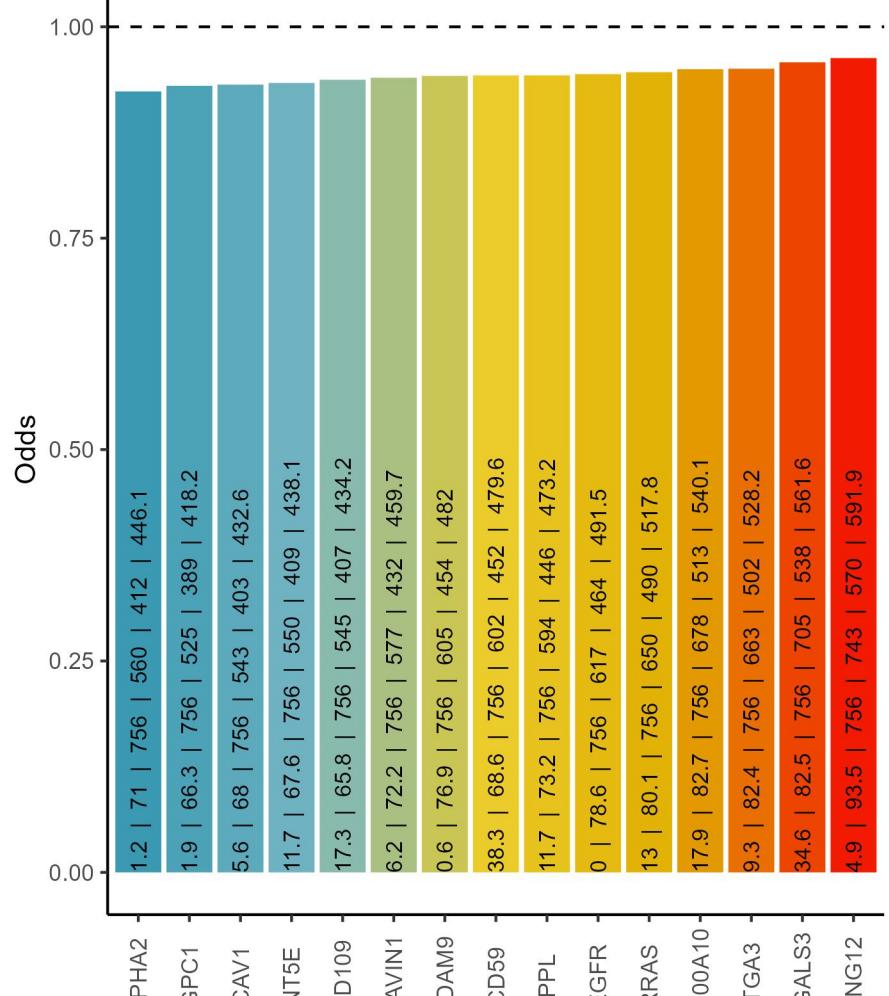


Cooccurrence with CDK9 protein, DB1

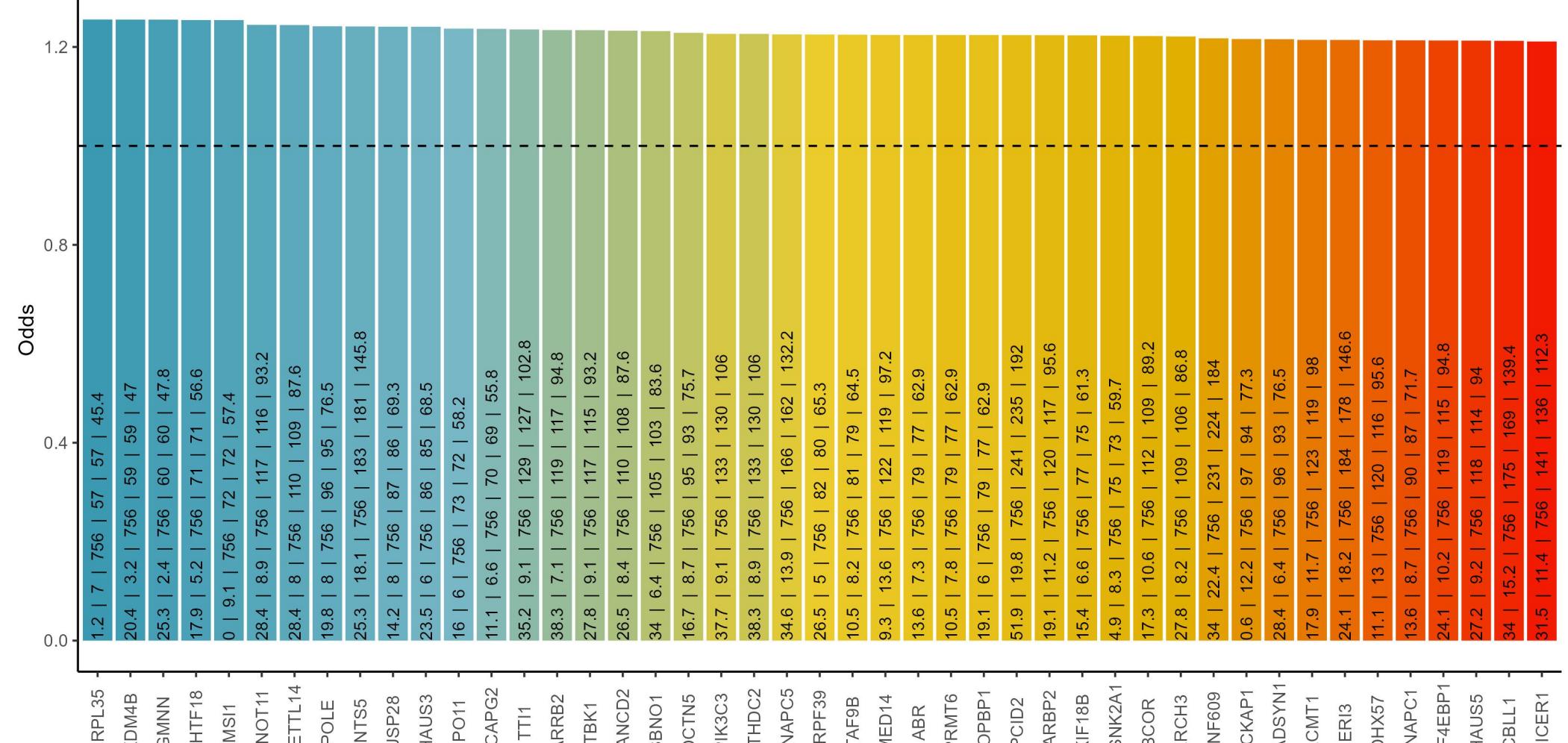
% of CDK9 in blood cancers: 89.5 ; % of CDK9 in solid cancers: 77.6

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CDK9 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

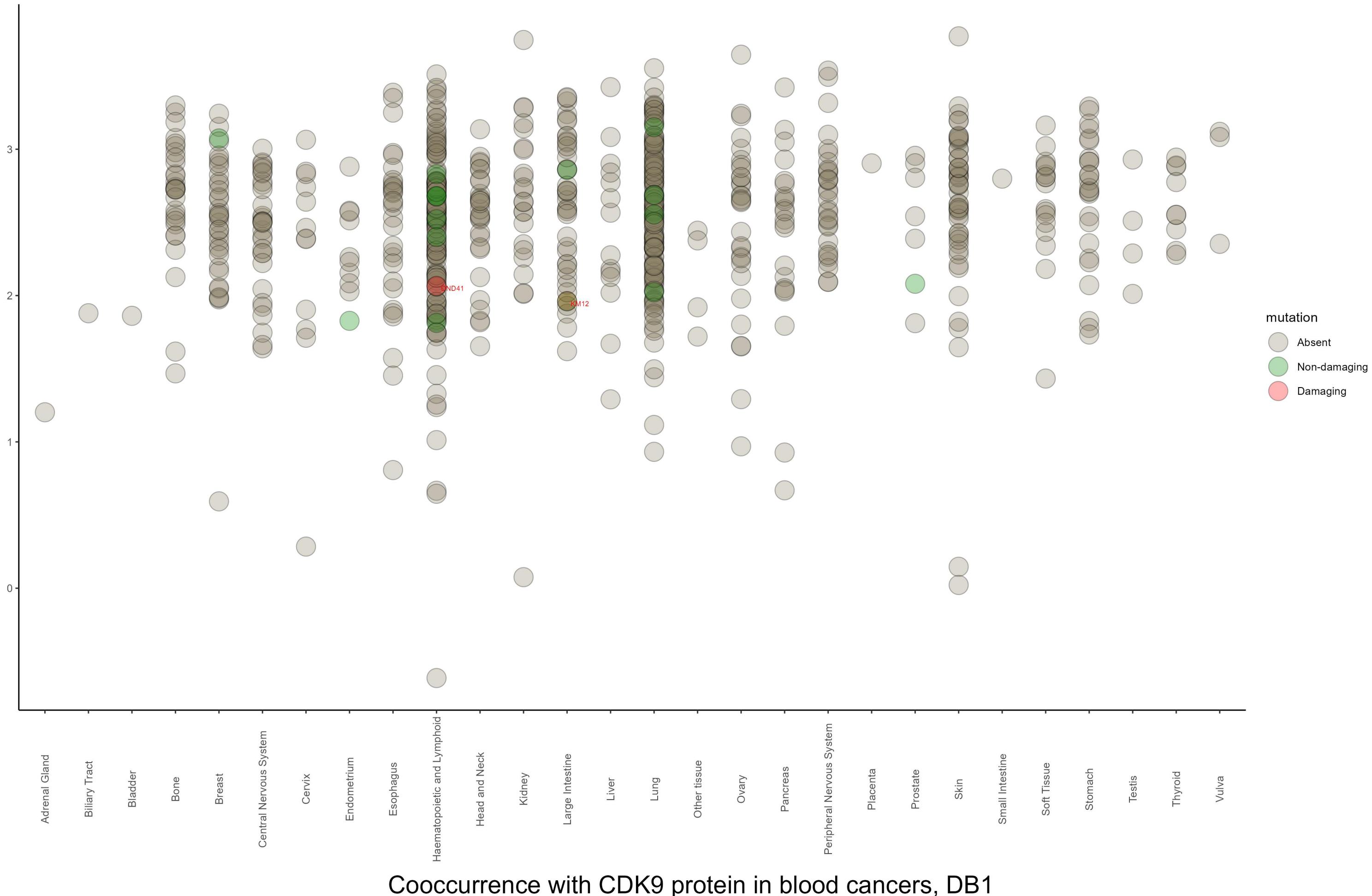
Negative cooccurrence



Positive cooccurrence

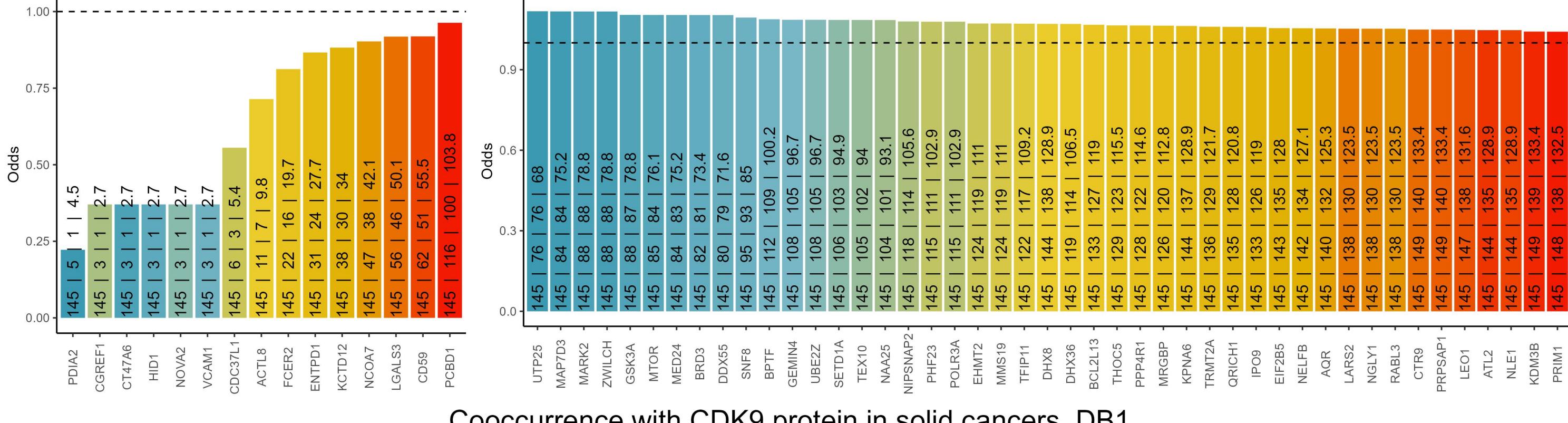


Amount of CDK9 protein and mutation status by tissue, DB1



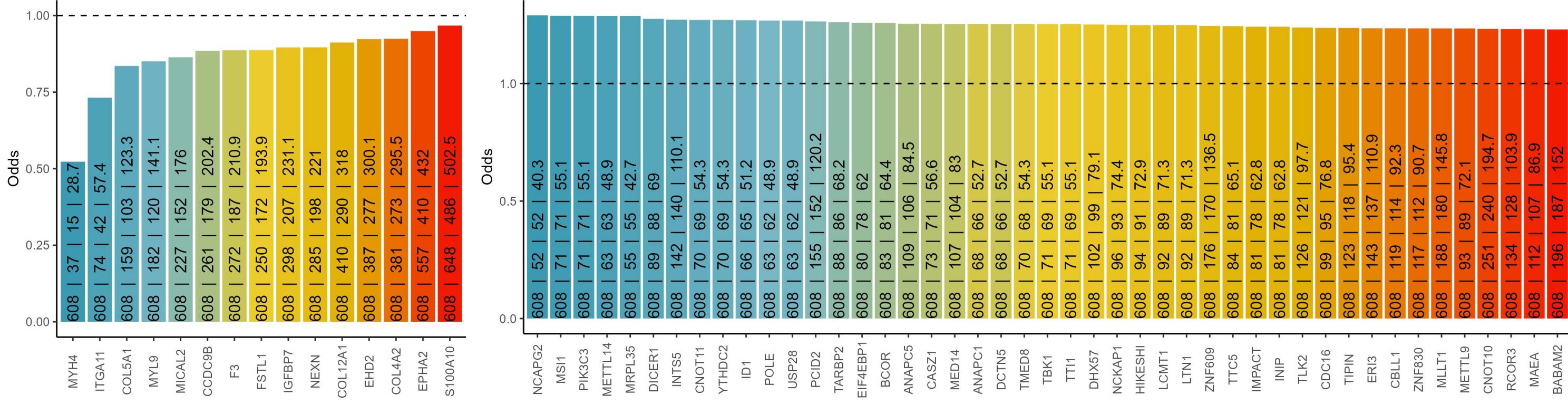
Cooccurrence with CDK9 protein in blood cancers, DB1

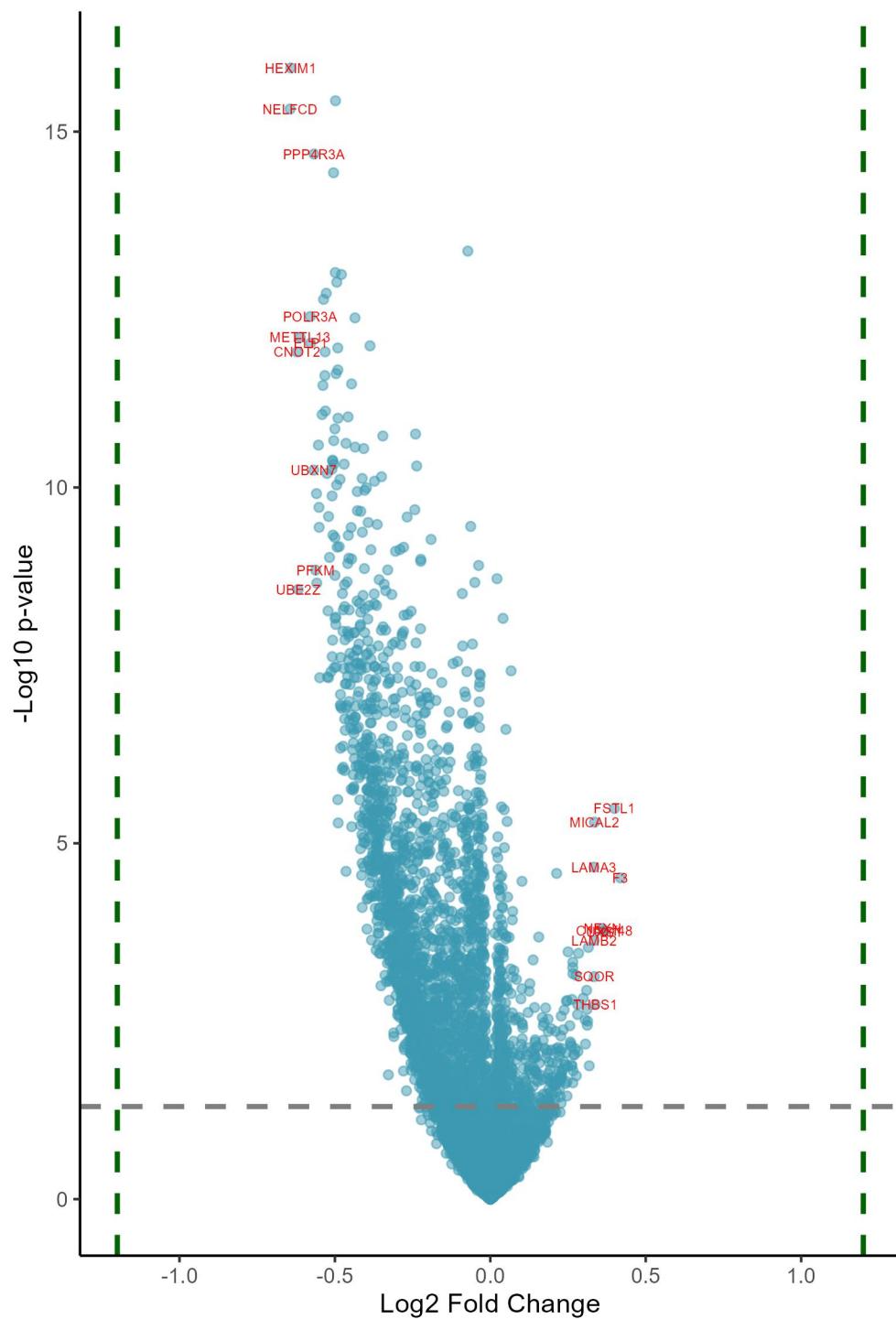
The text in the bars: incidence of CDK9 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Cooccurrence with CDK9 protein in solid cancers, DB1

The text in the bars: incidence of CDK9 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



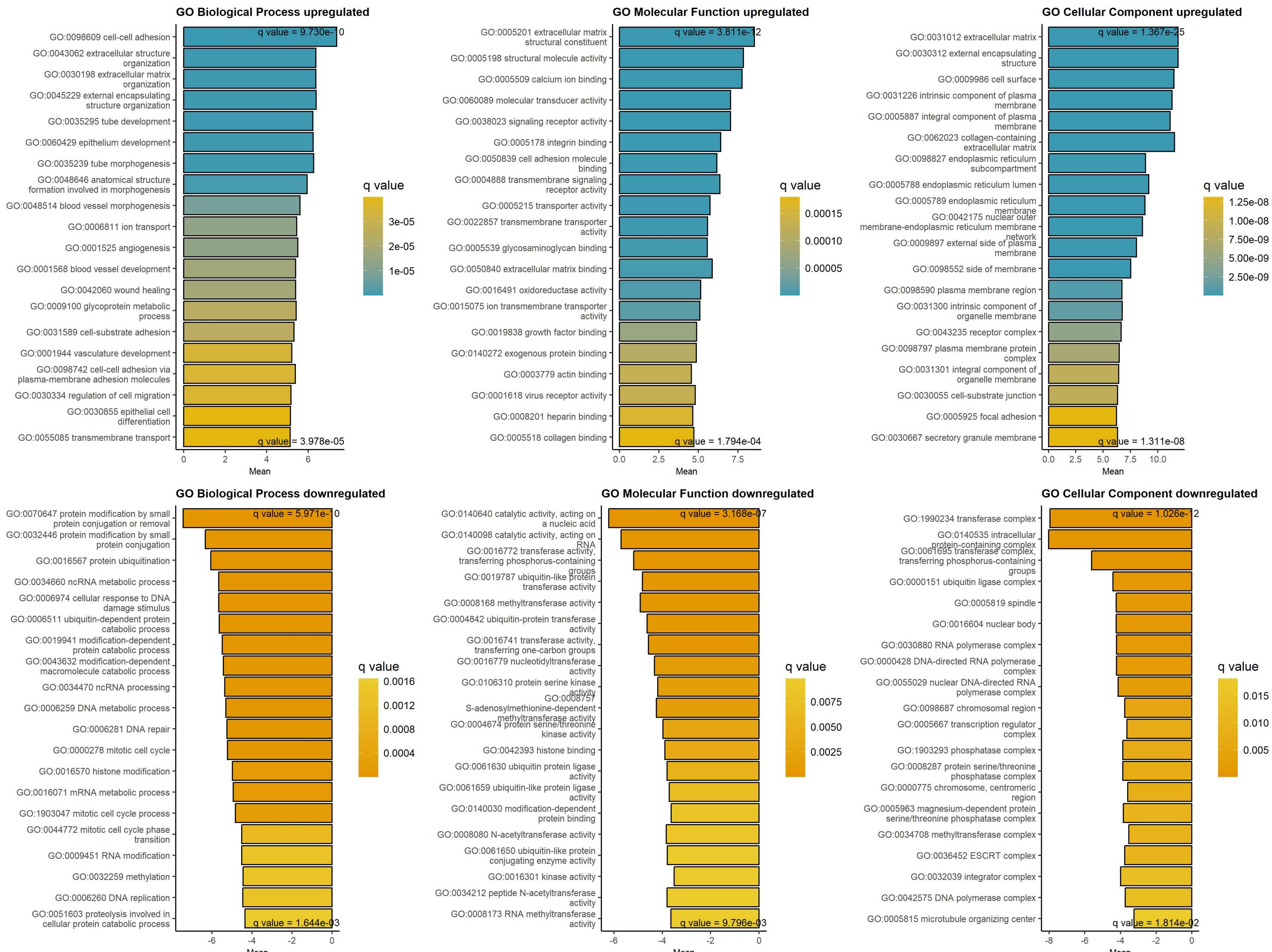


Downregulated at low/absent CDK9

Upregulated at low/absent CDK9

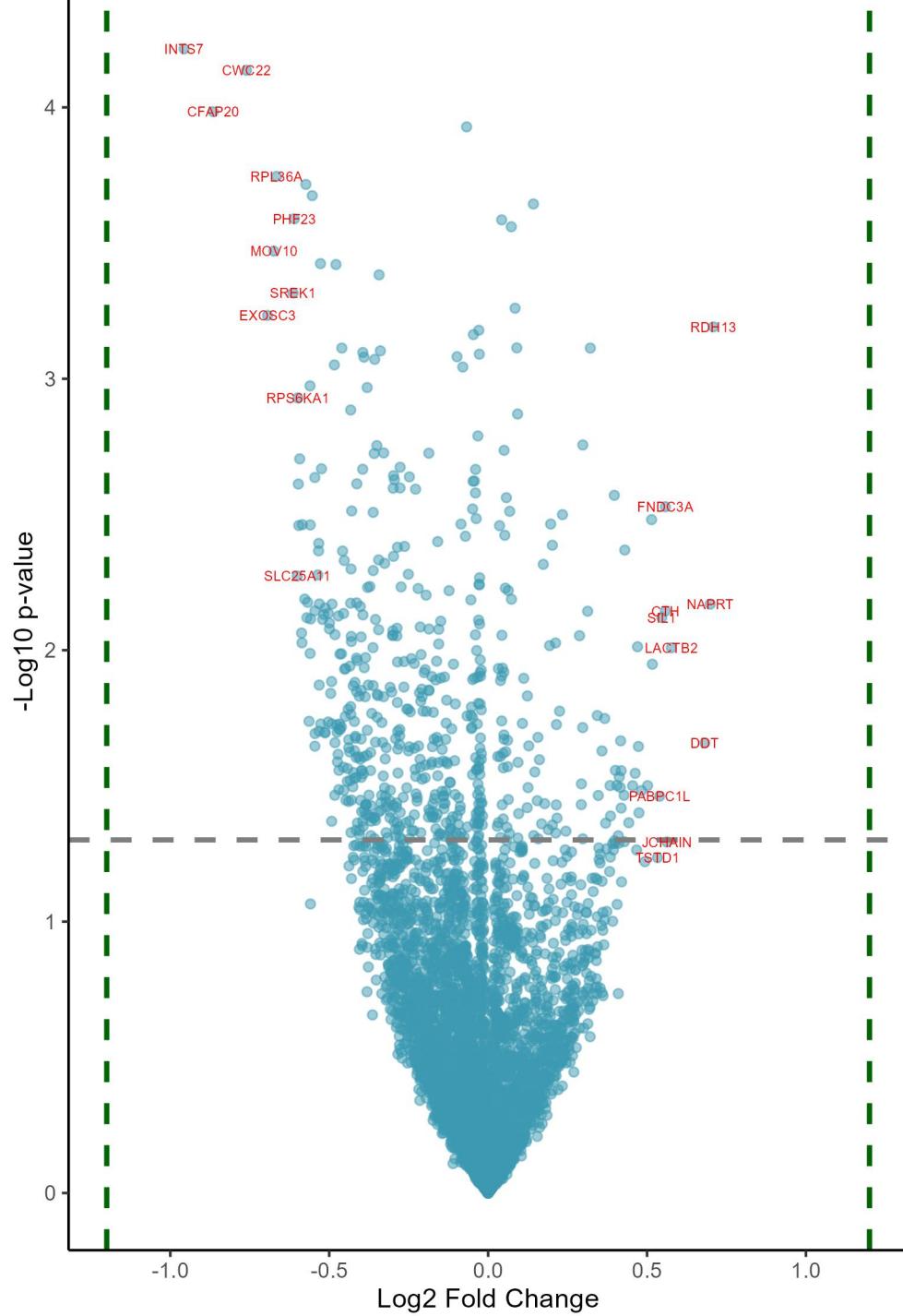
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.64	7.99e-13	NELFCD	negative elongation factor complex	0.42	2.73e-04	F3	coagulation factor III, tissue fact
-0.64	4.23e-13	HEXIM1	HEXIM P-TEFb complex subunit 1	0.4	4.62e-05	FSTL1	follistatin like 1
-0.62	4.14e-10	CNOT2	CCR4-NOT transcription complex subu	0.37	1.14e-03	C15orf48	chromosome 15 open reading frame 48
-0.62	1.88e-07	UBE2Z	ubiquitin conjugating enzyme E2 Z	0.37	1.16e-03	UXS1	UDP-glucuronate decarboxylase 1
-0.61	3.43e-10	METTL13	methyltransferase 13, eEF1A lysine	0.36	1.06e-03	NEXN	nexilin F-actin binding protein
-0.58	1.97e-10	POLR3A	RNA polymerase III subunit A	0.34	7.99e-03	THBS1	thrombospondin 1
-0.58	3.90e-10	ELP1	elongator acetyltransferase complex	0.34	6.60e-05	MICAL2	microtubule associated monooxygenases
-0.57	8.63e-09	UBXN7	UBX domain protein 7	0.33	3.74e-03	SQOR	sulfide quinone oxidoreductase
-0.57	2.75e-12	PPP4R3A	protein phosphatase 4 regulatory su	0.33	1.45e-03	LAMB2	laminin subunit beta 2
-0.56	1.11e-07	PFKM	phosphofructokinase, muscle	0.33	2.06e-04	LAMA3	laminin subunit alpha 3
-0.56	1.50e-08	DUS3L	dihydrouridine synthase 3 like	0.32	4.10e-02	RALYL	RALY RNA binding protein like
-0.56	1.58e-07	TRMT2A	tRNA methyltransferase 2 homolog A	0.32	1.75e-03	SSR3	signal sequence receptor subunit 3
-0.55	4.82e-09	PPP4R2	protein phosphatase 4 regulatory su	0.31	1.25e-02	PPL	periplakin
-0.55	2.26e-08	SSU72	SSU72 homolog, RNA polymerase II CT	0.31	1.38e-02	PPIC	peptidylprolyl isomerase C
-0.55	3.68e-08	HDDC2	HD domain containing 2	0.31	9.15e-03	COL4A2	collagen type IV alpha 2 chain
-0.55	1.61e-06	ZNF622	zinc finger protein 622	0.31	5.43e-03	COL12A1	collagen type XII alpha 1 chain
-0.54	2.33e-09	PPP2R2A	protein phosphatase 2 regulatory su	0.31	2.31e-02	NT5E	5'-nucleotidase ecto
-0.54	9.79e-10	ANAPC7	anaphase promoting complex subunit	0.31	1.21e-02	PLOD2	procollagen-lysine,2-oxoglutarate 5
-0.54	1.26e-10	INTS3	integrator complex subunit 3	0.3	6.78e-03	TGFB1	transforming growth factor beta ind
-0.53	7.73e-10	METTL16	methyltransferase 16, N6-methyladen	0.28	2.05e-03	POFUT2	protein O-fucosyltransferase 2
-0.53	4.14e-10	DCAF7	DDB1 and CUL4 associated factor 7	0.28	2.78e-02	IGFBP7	insulin like growth factor binding
-0.53	2.16e-09	NAA25	N-alpha-acetyltransferase 25, NatB	0.28	8.02e-03	LMO7	LIM domain 7
-0.53	1.13e-10	TRIM33	tripartite motif containing 33	0.28	1.05e-02	NEU1	neuraminidase 1
-0.53	9.38e-09	MEPCE	methylphosphate capping enzyme	0.28	5.32e-02	KRT18	keratin 18
-0.52	1.60e-06	NUDT3	nudix hydrolase 3	0.28	3.62e-03	EPHB2	EPH receptor B2
-0.52	3.22e-07	WDHD1	WD repeat and HMG-box DNA binding p	0.27	2.59e-02	EHD2	EH domain containing 2
-0.52	1.61e-06	COPS7B	COP9 signalosome subunit 7B	0.27	3.04e-02	CTSZ	cathepsin Z
-0.52	2.83e-08	CDK2	cyclin dependent kinase 2	0.27	3.04e-02	ADAM9	ADAM metallopeptidase domain 9
-0.52	8.19e-08	NMD3	NMD3 ribosome export adaptor	0.27	4.68e-02	KRT8	keratin 8

GAGE analysis on upregulated and downregulated proteins at low/absent CDK9 protein, DB1

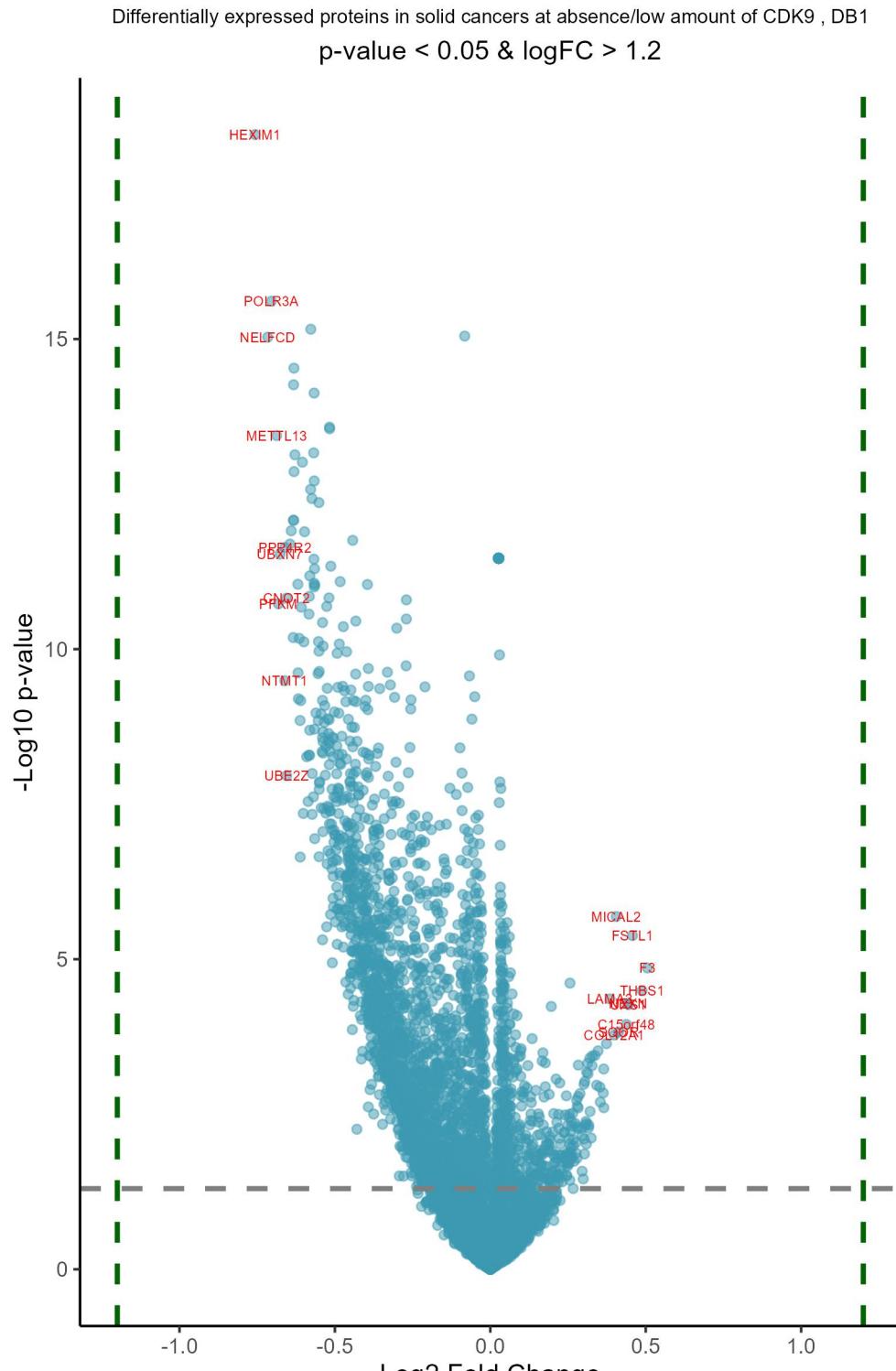


p-value < 0.05 & logFC > 1.2

Downregulated in blood cancers at low/absent CDK9 Upregulated in blood cancers at low/absent CDK9

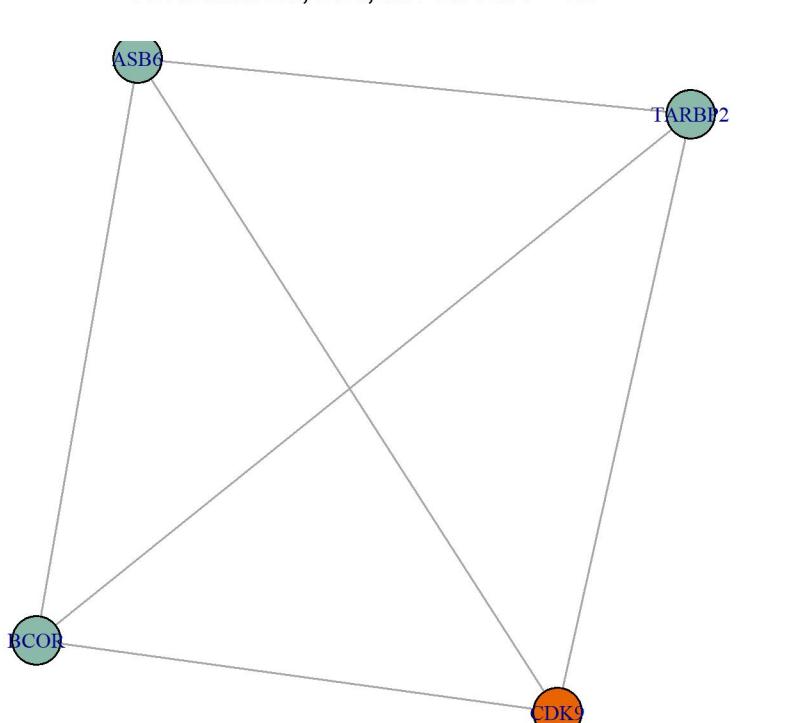


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.96	1.53e-01	INTS7	integrator complex subunit 7	0.71	1.82e-01	RDH13	retinol dehydrogenase 13
-0.86	1.53e-01	CFAP20	cilia and flagella associated prote	0.7	3.81e-01	NAPRT	nicotinate phosphoribosyltransf erase
-0.76	1.53e-01	CWC22	CWC22 spliceosome associated protei	0.68	4.92e-01	DDT	D-dopachrome tautomerase
-0.69	1.82e-01	EXOSC3	exosome component 3	0.58	4.02e-01	LACTB2	lactamase beta 2
-0.67	1.68e-01	MOV10	Mov10 RISC complex RNA helicase	0.56	6.05e-01	JCHAIN	joining chain of multimeric IgA and
-0.67	1.53e-01	RPL36A	ribosomal protein L36a	0.56	3.84e-01	CTH	cystathione gamma-lyase
-0.61	1.82e-01	SREK1	splicing regulatory glutamic acid a	0.56	2.96e-01	FNDC3A	fibronectin type III domain contain
-0.61	1.53e-01	PHF23	PHD finger protein 23	0.55	3.84e-01	SIL1	SIL1 nucleotide exchange factor
-0.6	3.62e-01	SLC25A11	solute carrier family 25 member 11	0.54	5.61e-01	PABPC1L	poly(A) binding protein cytoplasmic
-0.6	2.17e-01	RPS6KA1	ribosomal protein S6 kinase A1	0.53	6.18e-01	TSTD1	thiosulfate sulfurtransferase like
-0.6	2.78e-01	STK38	serine/threonine kinase 38	0.52	4.21e-01	DPP7	dipeptidyl peptidase 7
-0.6	2.96e-01	CHD3	chromodomain helicase DNA binding p	0.51	2.96e-01	SH2B2	SH2B adaptor protein 2
-0.59	2.78e-01	CDC27	cell division cycle 27	0.5	5.47e-01	ITGB7	integrin subunit beta 7
-0.59	3.86e-01	SCML2	Scm polycomb group protein like 2	0.49	6.18e-01	LMNA	lamin A/C
-0.59	3.98e-01	BRD3	bromodomain containing 3	0.48	5.56e-01	NUDT2	nudix hydrolase 2
-0.58	2.96e-01	MAP7D3	MAP7 domain containing 3	0.47	5.74e-01	DHRS7	dehydrogenase/reductase 7
-0.58	3.81e-01	IGLL1	immunoglobulin lambda like polypept	0.47	4.96e-01	PUDP	pseudouridine 5'-phosphatase
-0.57	1.53e-01	ANKFY1	ankyrin repeat and FYVE domain cont	0.47	4.02e-01	GSKIP	GSK3B interacting protein
-0.57	3.84e-01	LANCL1	LanC like 1	0.47	6.06e-01	HSPA2	heat shock protein family A (Hsp70)
-0.57	3.81e-01	NUB1	negative regulator of ubiquitin lik	0.46	5.22e-01	DUSP23	dual specificity phosphatase 23
-0.56	4.78e-01	MRPS2	mitochondrial ribosomal protein S2	0.45	5.47e-01	CFAP298	cilia and flagella associated prote
-0.56	2.05e-01	DERPC	DERPC proline and glycine rich nucl	0.44	5.79e-01	ALDH3A2	aldehyde dehydrogenase 3 family mem
-0.56	4.13e-01	TRAPPc4	trafficking protein particle comple	0.43	3.26e-01	COPS7A	COP9 signalosome subunit 7A
-0.56	2.96e-01	BCL2L13	BCL2 like 13	0.43	6.05e-01	BPNT2	3'(2'), 5'-bisphosphate nucleotidas
-0.56	6.66e-01	SPN	sialophorin	0.43	5.61e-01	HM13	histocompatibility minor 13
-0.56	3.84e-01	STX6	syntaxin 6	0.42	6.37e-01	HTATIP2	HIV-1 Tat interactive protein 2
-0.55	1.53e-01	GTF3C5	general transcription factor IIIC s	0.42	5.17e-01	COX20	cytochrome c oxidase assembly facto
-0.55	2.78e-01	POLR2G	RNA polymerase II subunit G	0.42	5.70e-01	ASL	argininosuccinate lyase
-0.55	4.96e-01	UBE2Z	ubiquitin conjugating enzyme E2 Z	0.42	4.91e-01	ARSA	arylsulfatase A



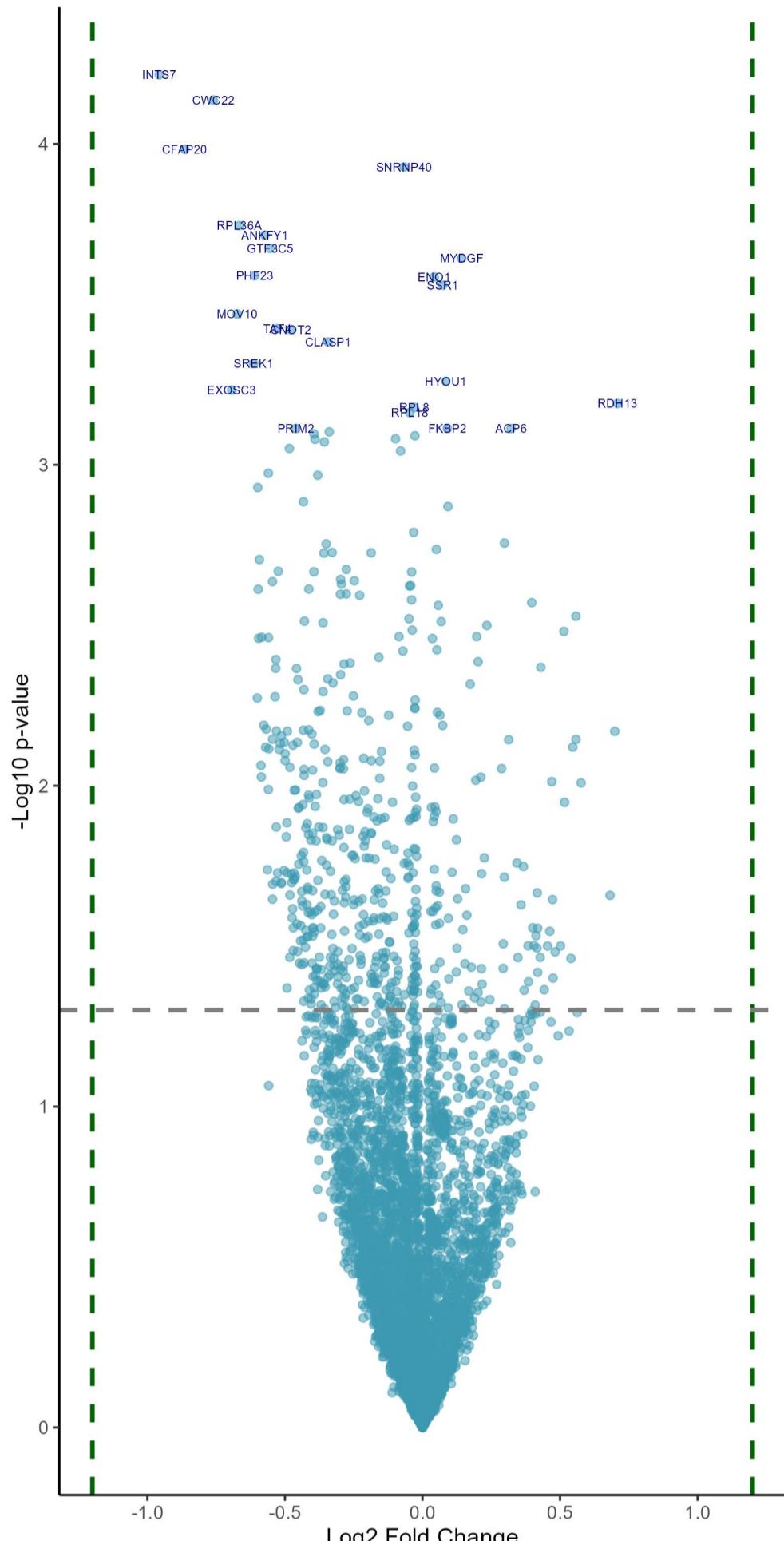
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.76	1.68e-15	HEXIM1	HEXIM P-TEFb complex subunit 1	0.51	1.20e-04	F3	coagulation factor III, tissue fact
-0.72	1.03e-12	NELFCD	negative elongation factor complex	0.49	2.42e-04	THBS1	thrombospondin 1
-0.7	5.44e-13	POLR3A	RNA polymerase III subunit A	0.46	4.42e-05	FSTL1	follistatin like 1
-0.69	2.00e-11	METTL13	methyltransferase 13, eEF1A lysine	0.44	3.71e-04	UXS1	UDP-glucuronate decarboxylase 1
-0.68	1.01e-09	PFKM	phosphofructokinase, muscle	0.44	3.57e-04	NEXN	nexilin F-actin binding protein
-0.68	2.11e-10	UBXN7	UBX domain protein 7	0.44	6.83e-04	C15orf48	chromosome 15 open reading frame 48
-0.66	1.43e-08	NTMT1	N-terminal Xaa-Pro-Lys N-methyltran	0.41	8.72e-04	SQOR	sulfide quinone oxidoreductase
-0.66	2.11e-10	PPP4R2	protein phosphatase 4 regulatory su	0.41	2.46e-05	MICAL2	microtubule associated monoxygenas
-0.66	8.27e-10	CNOT2	CCR4-NOT transcription complex subu	0.4	9.56e-04	COL12A1	collagen type XII alpha 1 chain
-0.66	3.08e-07	UBE2Z	ubiquitin conjugating enzyme E2 Z	0.38	3.13e-04	LAMA3	laminin subunit alpha 3
-0.64	2.11e-10	DUS3L	dihydrouridine synthase 3 like	0.37	1.25e-03	LAMB2	laminin subunit beta 2
-0.64	2.11e-10	ELP1	elongator acetyltransferase complex	0.37	9.23e-03	NT5E	5'-nucleotidase ecto
-0.63	3.28e-09	HDDC2	HD domain containing 2	0.36	2.77e-03	PPIC	peptidylprolyl isomerase C
-0.63	2.11e-10	USP15	ubiquitin specific peptidase 15	0.36	5.87e-03	COL4A2	collagen type IV alpha 2 chain
-0.63	4.53e-12	TRIM33	tripartite motif containing 33	0.35	7.76e-03	EHD2	EH domain containing 2
-0.63	2.11e-10	PPP2R2A	protein phosphatase 2 regulatory su	0.35	4.86e-03	TGFB1	transforming growth factor beta ind
-0.63	2.80e-12	PPP4R3A	protein phosphatase 4 regulatory su	0.35	1.57e-03	NEU1	neuraminidase 1
-0.63	5.71e-11	METTL3	methyltransferase 3, N6-adenosine-m	0.34	4.57e-03	PLOD2	procollagen-lysine,2-oxoglutarate 5
-0.63	3.49e-11	METTL16	methyltransferase 16, N6-methyladen	0.34	1.80e-03	EPHB2	EPH receptor B2
-0.62	5.20e-10	MEPCE	methylphosphate capping enzyme	0.33	1.83e-03	SSR3	signal sequence receptor subunit 3
-0.62	1.10e-08	BUD23	BUD23 rRNA methyltransferase and ri	0.33	2.48e-03	GLT8D1	glycosyltransferase 8 domain contai
-0.62	2.59e-08	WDHD1	WD repeat and HMG-box DNA binding p	0.32	2.37e-02	IGFBP7	insulin like growth factor binding
-0.61	3.35e-09	SSU72	SSU72 homolog, RNA polymerase II CT	0.32	1.04e-02	CDC42EP1	CDC42 effector protein 1
-0.61	5.14e-08	PDCD4	programmed cell death 4	0.32	1.96e-03	PLEKHA7	pleckstrin homology domain containi
-0.61	3.98e-06	ZNF706	zinc finger protein 706	0.32	1.58e-02	LAMC2	laminin subunit gamma 2
-0.61	2.69e-08	TRMT2A	tRNA methyltransferase 2 homolog A	0.32	1.72e-02	H1-1	H1.1 linker histone, cluster member
-0.61	1.12e-09	FNTA	farnesyltransferase, CAAX box, alph	0.31	3.20e-03	QSOX1	quiescin sulfhydryl oxidase 1
-0.6	4.28e-11	INTS3	integrator complex subunit 3	0.31	2.31e-03	TGFB2	transforming growth factor beta 2
-0.6	1.03e-06	ZNF622	zinc finger protein 622	0.31	3.06e-03	POFUT2	protein O-fucosyltransferase 2

CDK9 network, DB1, all Pearson r > 0.3

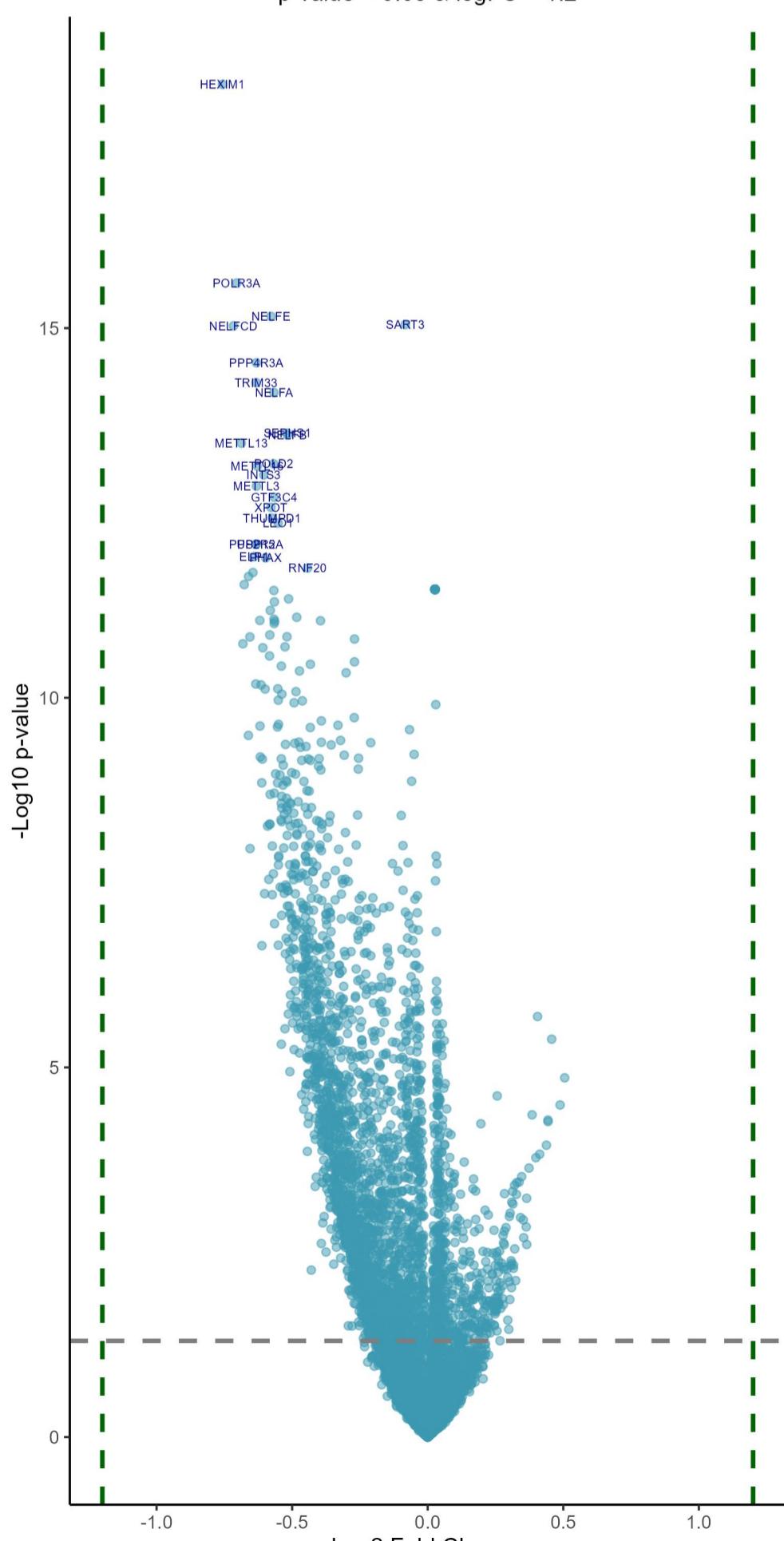


Differentially expressed proteins in blood cancers at absence/low amount of CDK9 , DB1

p-value < 0.05 & logFC > 1.2

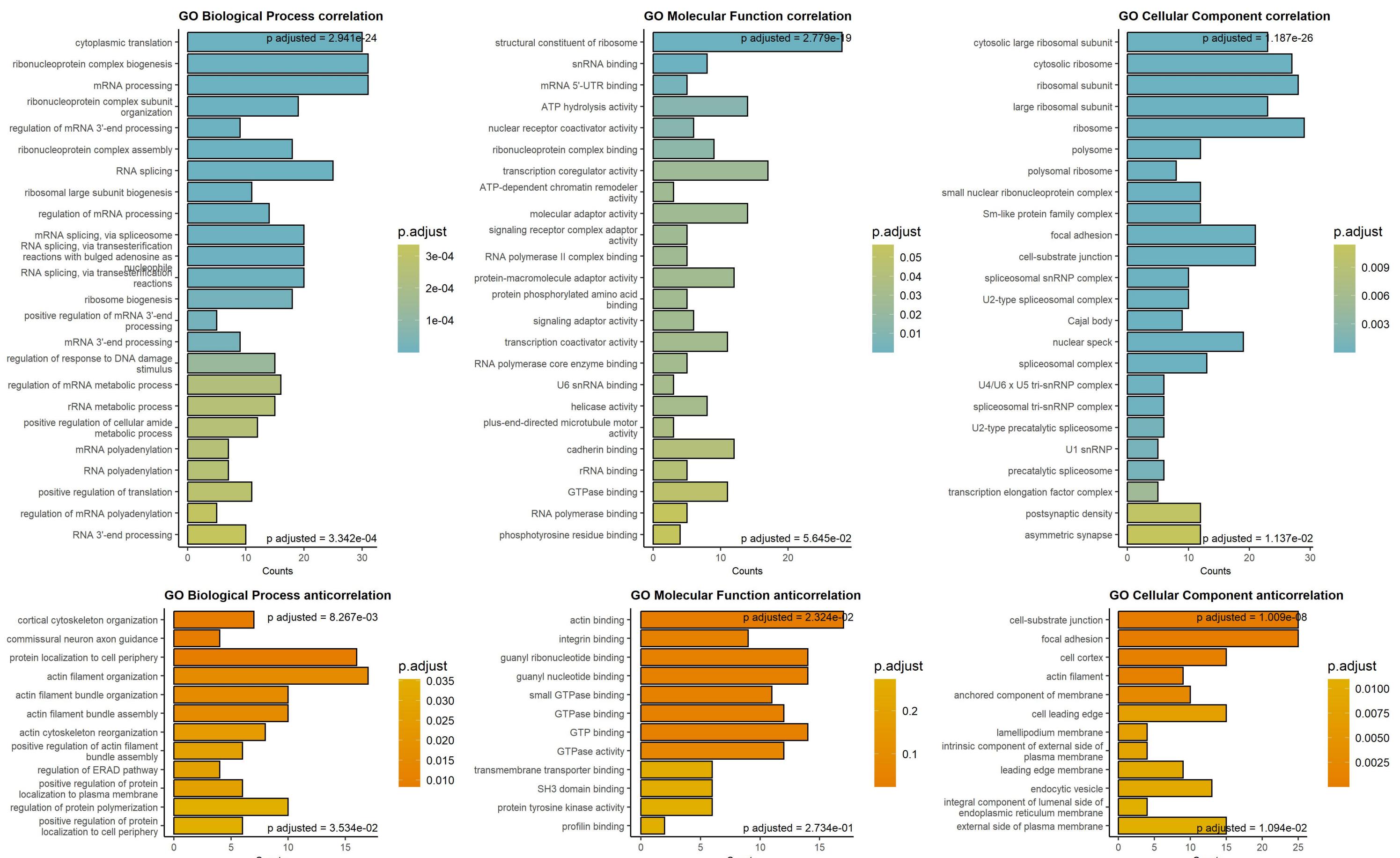
Sorted by p values!
Downregulated in blood cancers at low/absent CDK9 Upregulated in blood cancers at low/absent CDK9

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.96	1.53e-01	INTS7	integrator complex subunit 7	0.14	1.53e-01	MYDGF	myeloid derived growth factor
-0.76	1.53e-01	CWC22	CWC22 spliceosome associated protein	0.04	1.53e-01	ENO1	enolase 1
-0.86	1.53e-01	CFAP20	cilia and flagella associated protein	0.07	1.53e-01	SSR1	signal sequence receptor subunit 1
-0.07	1.53e-01	SNRNP40	small nuclear ribonucleoprotein U5	0.08	1.82e-01	HYOU1	hypoxia up-regulated 1
-0.67	1.53e-01	RPL36A	ribosomal protein L36a	0.71	1.82e-01	RDH13	retinol dehydrogenase 13
-0.57	1.53e-01	ANKFY1	ankyrin repeat and FYVE domain containing	0.09	1.82e-01	FKBP2	FKBP prolyl isomerase 2
-0.55	1.53e-01	GTF3C5	general transcription factor IIIC 5	0.32	1.82e-01	ACP6	acid phosphatase 6, lysophosphatidic acid
-0.61	1.53e-01	PHF23	PHD finger protein 23	0.09	2.36e-01	OTUD6B	OTU deubiquitinase 6B
-0.67	1.68e-01	MOV10	Mov10 RISC complex RNA helicase	0.3	2.78e-01	DEPTOR	DEP domain containing MTOR interact
-0.53	1.68e-01	TAF4	TATA-box binding protein associated	0.05	2.78e-01	TIMM44	translocase of inner mitochondrial membrane
-0.48	1.68e-01	CNOT2	CCR4-NOT transcription complex subunit 2	0.4	2.84e-01	ZBTB8OS	zinc finger and BTB domain containing 8
-0.34	1.72e-01	CLASP1	cytoplasmic linker associated protein	0.06	2.85e-01	PRKCSH	protein kinase C substrate 80K-H
-0.61	1.82e-01	SREK1	splicing regulatory glutamic acid rich	0.56	2.96e-01	FNDC3A	fibronectin type III domain containing 3
-0.69	1.82e-01	EXOSC3	exosome component 3	0.07	2.96e-01	PPIB	peptidylprolyl isomerase B
-0.03	1.82e-01	RPL18	ribosomal protein L18	0.23	2.96e-01	PEPD	peptidase D
-0.05	1.82e-01	RPL18	ribosomal protein L18	0.51	2.96e-01	SH2B2	SH2B adaptor protein 2
-0.46	1.82e-01	PRIM2	DNA primase subunit 2	0.2	2.96e-01	TXNDC5	thioredoxin domain containing 5
-0.34	1.82e-01	HACD3	3-hydroxyacyl-CoA dehydratase 3	0.04	2.96e-01	ARCN1	archain 1
-0.39	1.82e-01	MORF4L1	mortality factor 4 like 1	0.05	3.16e-01	TMED9	transmembrane p24 trafficking protein
-0.03	1.82e-01	SNRNP70	small nuclear ribonucleoprotein U1	0.2	3.26e-01	RRBP1	ribosome binding protein 1
-0.1	1.82e-01	RPL13A	ribosomal protein L13a	0.43	3.26e-01	COPS7A	COP9 signalosome subunit 7A
-0.39	1.82e-01	GIMAP4	GTPase, IMAP family member 4	0.17	3.45e-01	C2CD2L	C2CD2 like
-0.36	1.82e-01	EHMT1	euchromatic histone lysine methyltransferase 1	0.05	3.71e-01	TXNL1	thioredoxin like 1
-0.48	1.82e-01	CDCA7	cell division cycle associated 7	0.06	3.71e-01	PRDX5	peroxiredoxin 5
-0.08	1.82e-01	DDX39B	DEExD-box helicase 39B	0.07	3.81e-01	MESD	mesoderm development LRP chaperone
-0.56	2.05e-01	DERPC	DERPC proline and glycine rich nucleic acid	0.7	3.81e-01	NAPRT	nicotinate phosphoribosyltransferase
-0.38	2.05e-01	CDK2	cyclin dependent kinase 2	0.56	3.84e-01	CTH	cystathione gamma-lyase
-0.6	2.17e-01	RPS6KA1	ribosomal protein S6 kinase A1	0.31	3.84e-01	PGM3	phosphoglucomutase 3
-0.43	2.34e-01	XPO7	exportin 7	0.55	3.84e-01	SIL1	SIL1 nucleotide exchange factor
-0.03	2.77e-01	RPL34	ribosomal protein L34	0.04	3.86e-01	SRM	spermidine synthase
-0.35	2.78e-01	NAB2	NGFI-A binding protein 2	0.29	3.86e-01	SEC11C	SEC11 homolog C, signal peptidase c
-0.33	2.78e-01	VPS25	vacuolar protein sorting 25 homolog	0.21	3.98e-01	NDUFAF2	NADH:ubiquinone oxidoreductase complex I
-0.19	2.78e-01	PDS5B	PDS5 cohesin associated factor B	0.19	4.02e-01	PDIA2	protein disulfide isomerase family
-0.36	2.78e-01	CTR9	CTR9 homolog, Paf1/RNA polymerase I	0.47	4.02e-01	GSKIP	GSK3B interacting protein
-0.59	2.78e-01	CDC27	cell division cycle 27	0.58	4.02e-01	LACTB2	lactamase beta 2
-0.28	2.78e-01	SLC25A5	solute carrier family 25 member 5	0.52	4.21e-01	DPP7	dipeptidyl peptidase 7
-0.52	2.78e-01	DNAJC21	DnaJ heat shock protein family (Hsp40)	0.05	4.23e-01	MYCBP	MYC binding protein
-0.39	2.78e-01	NOC4L	nucleolar complex associated 4 homo	0.03	4.23e-01	FARSA	phenylalanyl-tRNA synthetase subunit
0.04	2.78e-01	RPL35	ribosomal protein L35	0.05	4.26e-01	HSPD15	heat shock protein family A (Hsp70)

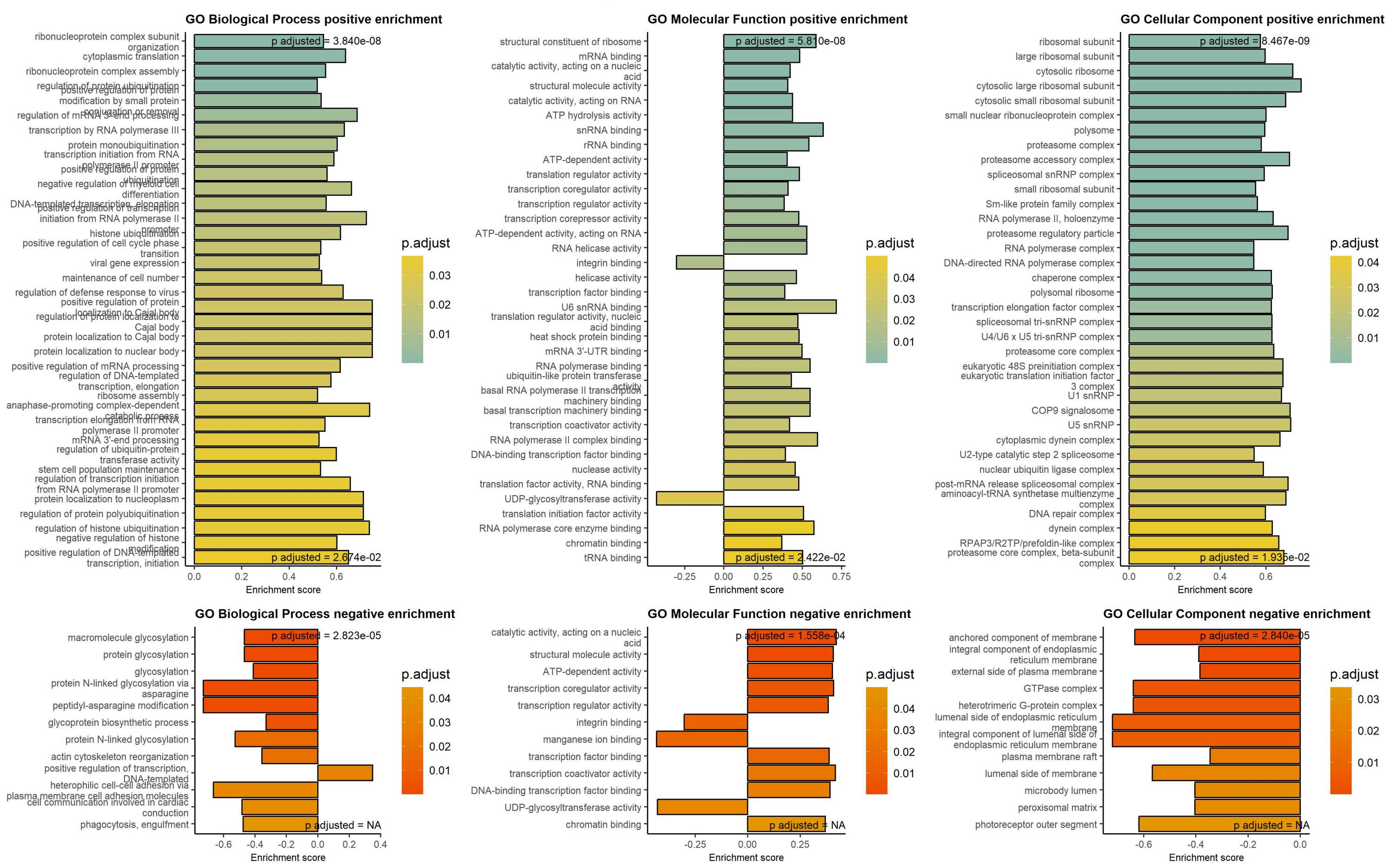
Differentially expressed proteins in solid cancers at absence/low amount of CDK9 , DB1
p-value < 0.05 & logFC > 1.2Sorted by p values!
Downregulated in solid cancers at low/absent CDK9 Upregulated in solid cancers at low/absent CDK9

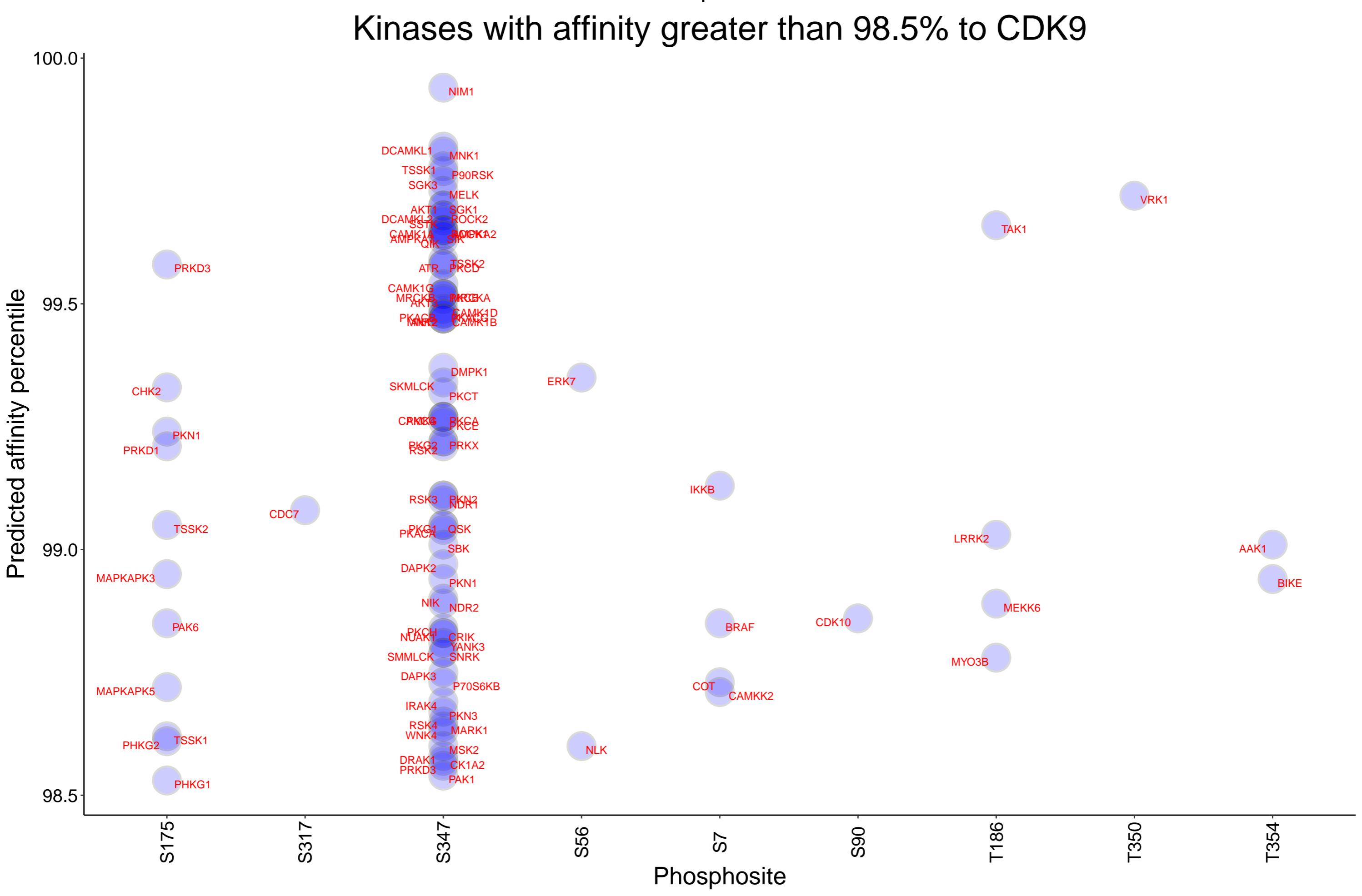
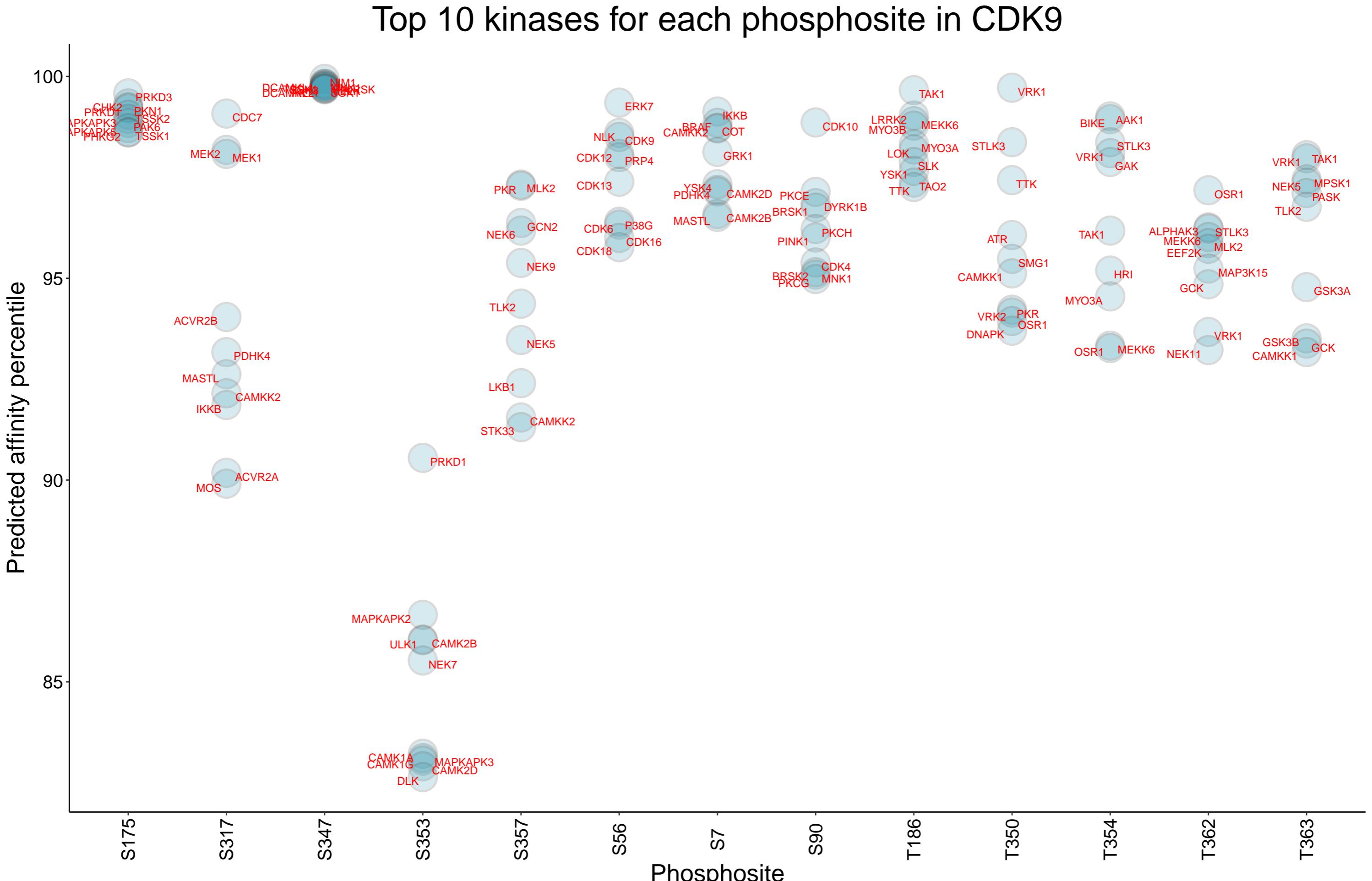
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.76	1.68e-15	HEXIM1	HEXIM P-TEFb complex subunit 1	0.03	2.11e-10	PTPRCAP	protein tyrosine phosphatase receptor
-0.7	5.44e-13	POLR3A	RNA polymerase III subunit A	0.03	2.11e-10	HBE1	hemoglobin subunit epsilon 1
-0.58	1.03e-12	NELFE	negative elongation factor complex	0.03	2.11e-10	SERPINB10	serpin family B member 10
-0.08	1.03e-12	SART3	spliceosome associated factor 3, U4	0.03	2.11e-10	IGLL1	immunoglobulin lambda like polypeptide
-0.72	1.03e-12	NELFCD	negative elongation factor complex	0.03	2.11e-10	CRYBB1	crystallin beta B1
-0.63	2.80e-12	PPP4R3A	protein phosphatase 4 regulatory subunit	0.03	2.11e-10	ITGA2B	integrin subunit alpha 2b
-0.63	4.53e-12	TRIM33	tripartite motif containing 33	0.03	2.11e-10	ACAP1	ArfGAP with coiled-coil, ankyrin repeat and PDZ-binding domains
-0.57	5.49e-12	NELFA	negative elongation factor complex	0.03	2.11e-10	NCF4	neutrophil cytosolic factor 4
-0.52	1.69e-11	SEPHS1	selenophosphate synthetase 1	0.03	2.11e-10	SP140	SP140 nuclear body protein
-0.52	1.69e-11	NELFB	negative elongation factor complex	0.03	2.11e-10	PSTPIP1	proline-serine-threonine phosphatases with dual-specificity
-0.69	2.00e-11	METTL13	methyltransferase 13, eEF1A lysine 4-methyltransferase	0.03	2.11e-10	STAB1	stabilin 1
-0.57	3.49e-11	POLD2	DNA polymerase delta 2, accessory subunit	0.03	2.11e-10	SELPLG	selectin P ligand
-0.63	3.49e-11	METTL16	methyltransferase 16, N6-methyladenosine	0.03	2.11e-10	RCSD1	RCSD domain containing 1
-0.6	4.28e-11	INTS3	integrator complex subunit 3	0.03	2.11e-10	STAT5A	signal transducer and activator of transcription 5
-0.63	5.71e-11	METTL3	methyltransferase 3, N6-adenosine-methyltransferase	0.03	2.11e-10	CTSW	cathepsin W
-0.57	7.59e-11	GTF3C4	general transcription factor IIIC 4	0.03	2.11e-10	GIMAP6	GTPase, IMAP family member 6
-0.58	9.82e-11	XPOT	exportin for tRNA	0.03	2.11e-10	GZMB	granzyme B
-0.57	1.30e-10	THUMPD1	THUMP domain containing 1	0.03	2.11e-10	HK3	hexokinase 3
-0.55	1.44e-10	LEO1	LEO1 homolog, Parf1/RNA polymerase I	0.03	2.11e-10	TUBA8	tubulin alpha 8
-0.63	2.11e-10	USP15	ubiquitin specific peptidase 15	0.03	2.11e-10	CR2	complement C3d receptor 2
-0.63	2.11e-10	PPP2R2A	protein phosphatase 2 regulatory subunit	0.03	2.11e-10	POU2F2	POU class 2 homeobox 2
-0.64	2.11e-10	ELP1	elongator acetyltransferase complex	0.03	2.11e-10	AZU1	azurocidin 1
-0.6	2.11e-10	PHAX	phosphorylated adaptor for RNA export	0.03	2.11e-10	CD48	CD48 molecule
-0.44	2.11e-10	RNF20	ring finger protein 20	0.03	2.11e-10	SKAP2	src kinase associated phosphoprotein
-0.64	2.11e-10	DUS3L	dihydrouridine synthase 3 like	0.03	2.11e-10	CCL17	C-C motif chemokine ligand 17
-0.66	2.11e-10	PPP4R2	protein phosphatase 4 regulatory subunit	0.03	2.11e-10	ADA2	adenosine deaminase 2
-0.68	2.11e-10	UBXN7	UBX domain protein 7	0.03	2.11e-10	CD3E	CD3 epsilon subunit of T-cell receptor
-0.57	2.16e-10	MED24	mediator complex subunit 24	0.03	2.11e-10	RNASE2	ribonuclease A family member 2
-0.51	2.78e-10	UBE2A	ubiquitin conjugating enzyme E2 A	0.03	2.11e-10	TEX11	testis expressed 11
-0.57	3.02e-10	INTS1	integrator complex subunit 1	0.03	2.11e-10	PLEK	pleckstrin homology domain containing EEF1B2
-0.58	3.91e-10	DCAF7	DDB1 and CUL4 associated factor 7	0.03	2.11e-10	CD300A	CD300a molecule
-0.48	4.80e-10	PRMT5	protein arginine methyltransferase 5	0.03	2.11e-10	GZMA	granzyme

Top 250 correlation coefficients overrepresentation, CDK9 protein, DB1



Gene Set Enrichment analysis on protein correlation coefficients, CDK9 protein, DB1





Top 15 positive correlation coefficients for CDK9 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

