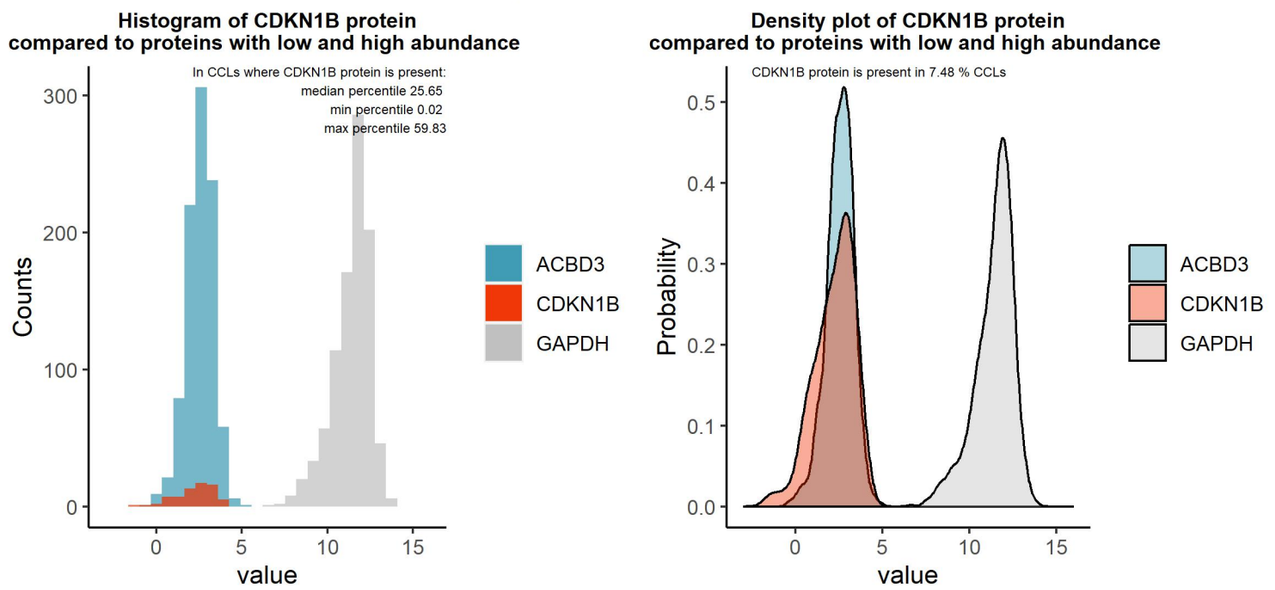
CDKN1B

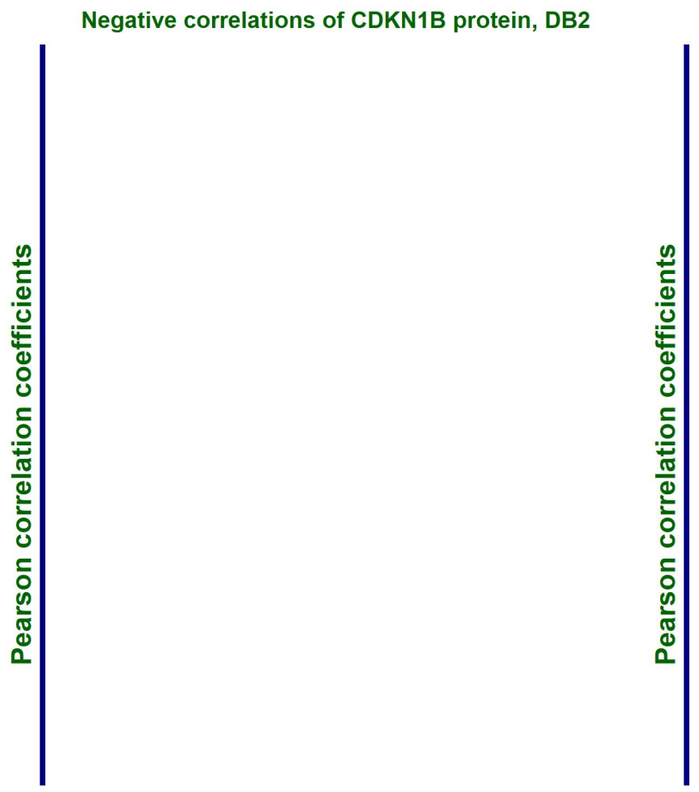
Protein name: CDN1B ; UNIPROT: P46527 ; Gene name: cyclin dependent kinase inhibitor 1B

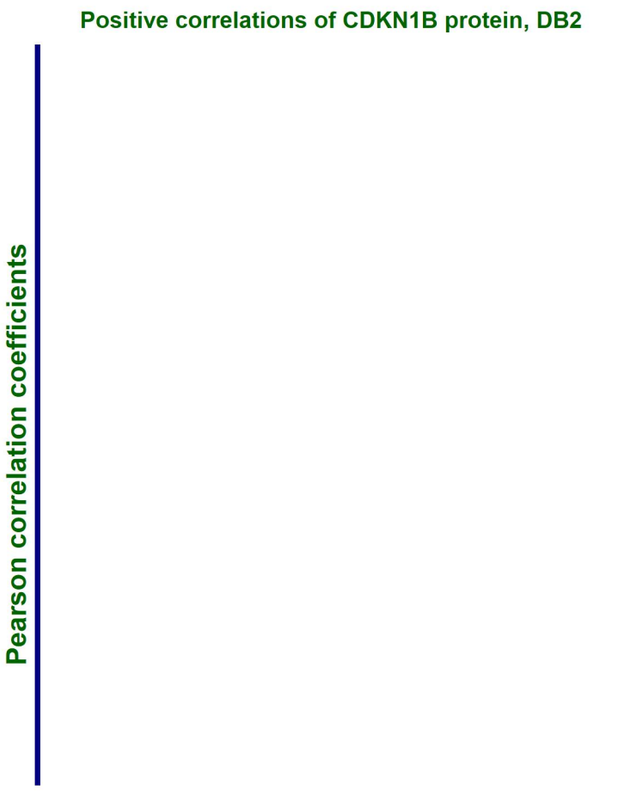
Ligandable: NA ; Ligandable_by_Chem: NA ; Is_enzyme: NA (https://cansar.ai/)

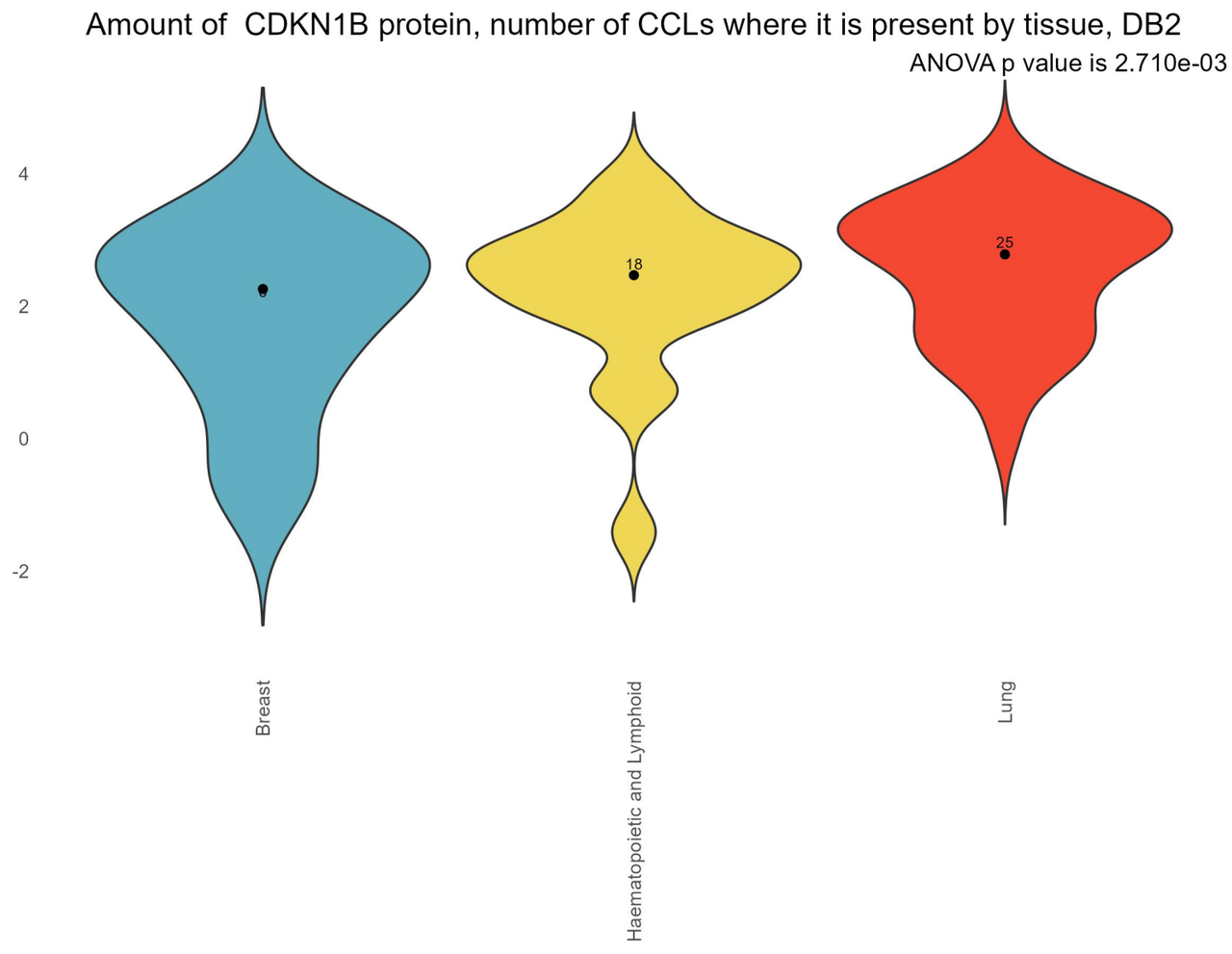
Sanger Institute Protein Database 2 (DB2), protein presence is less certain

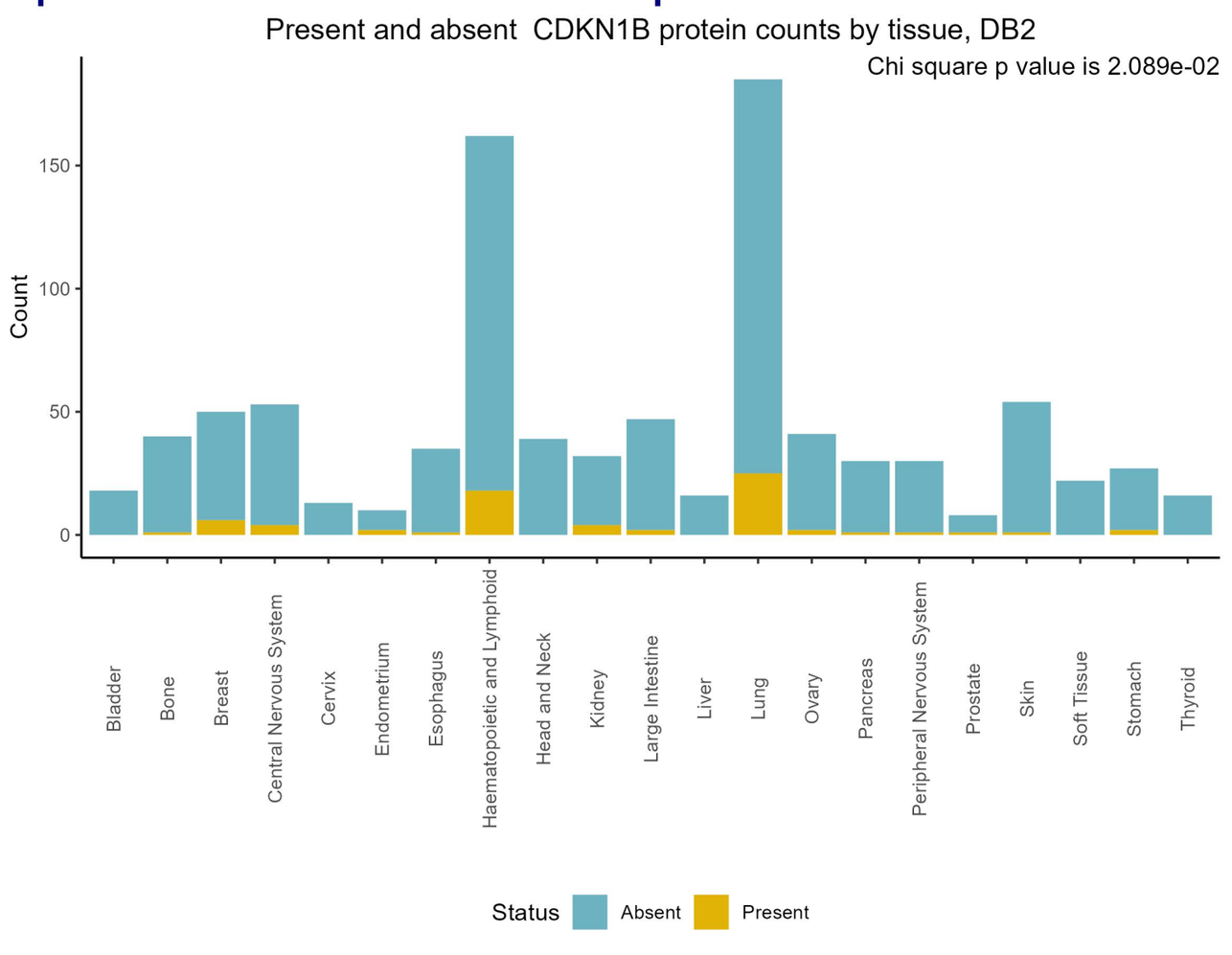
8498 proteins in same 949 CCLs







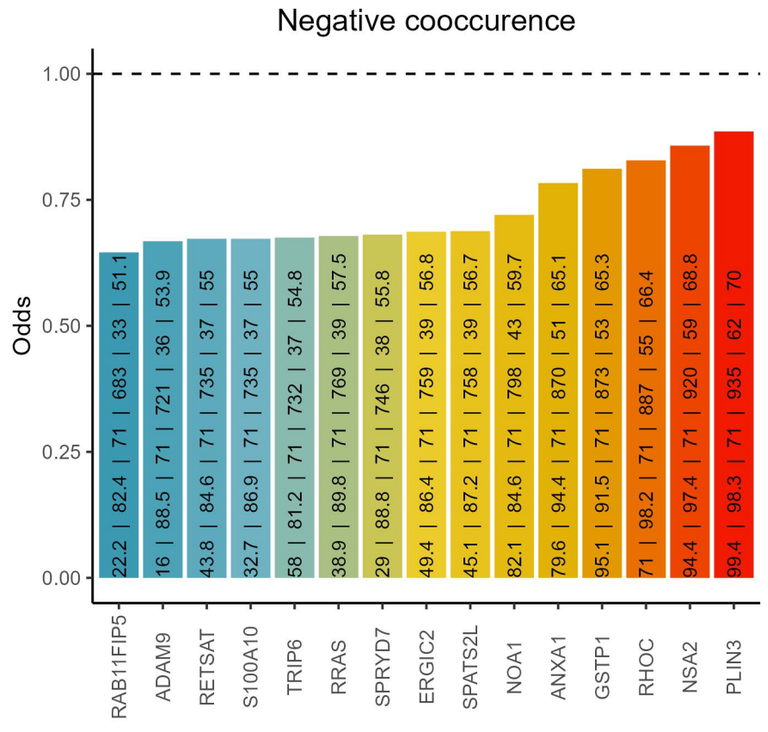


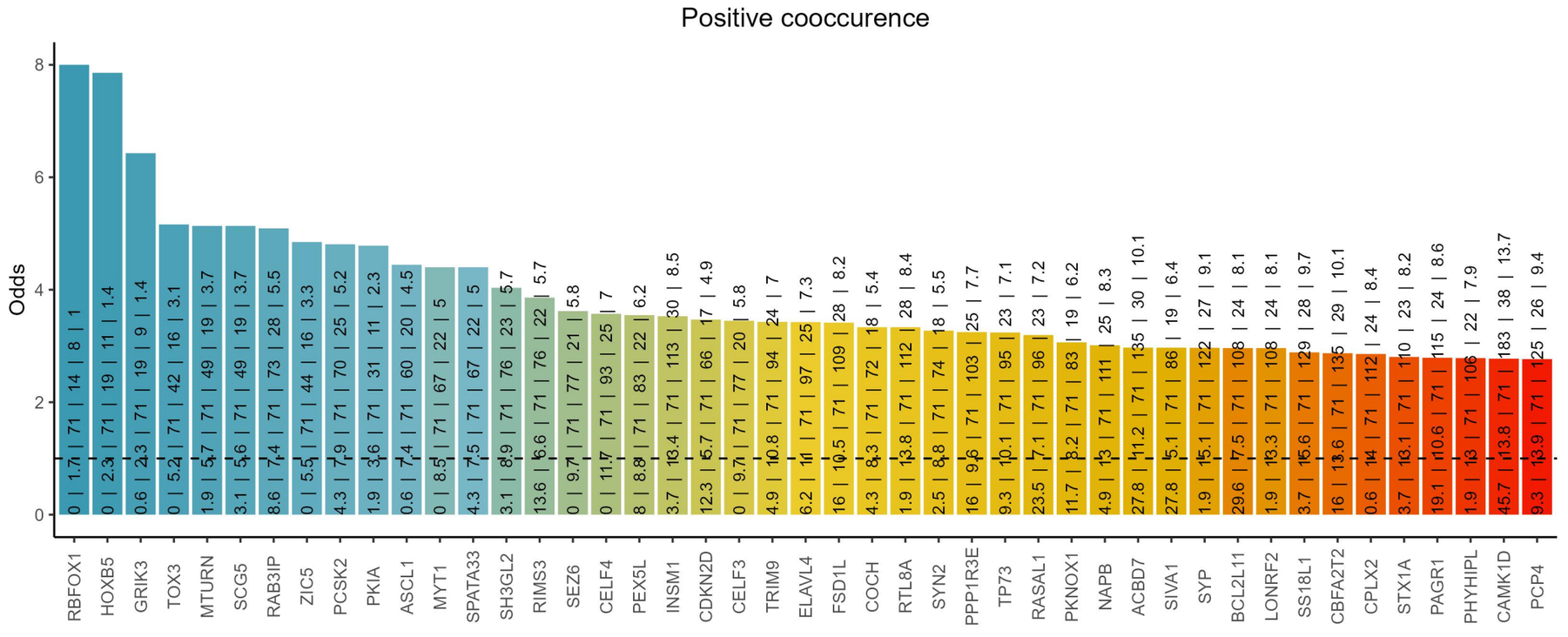


Cooccurrence with CDKN1B protein, DB2

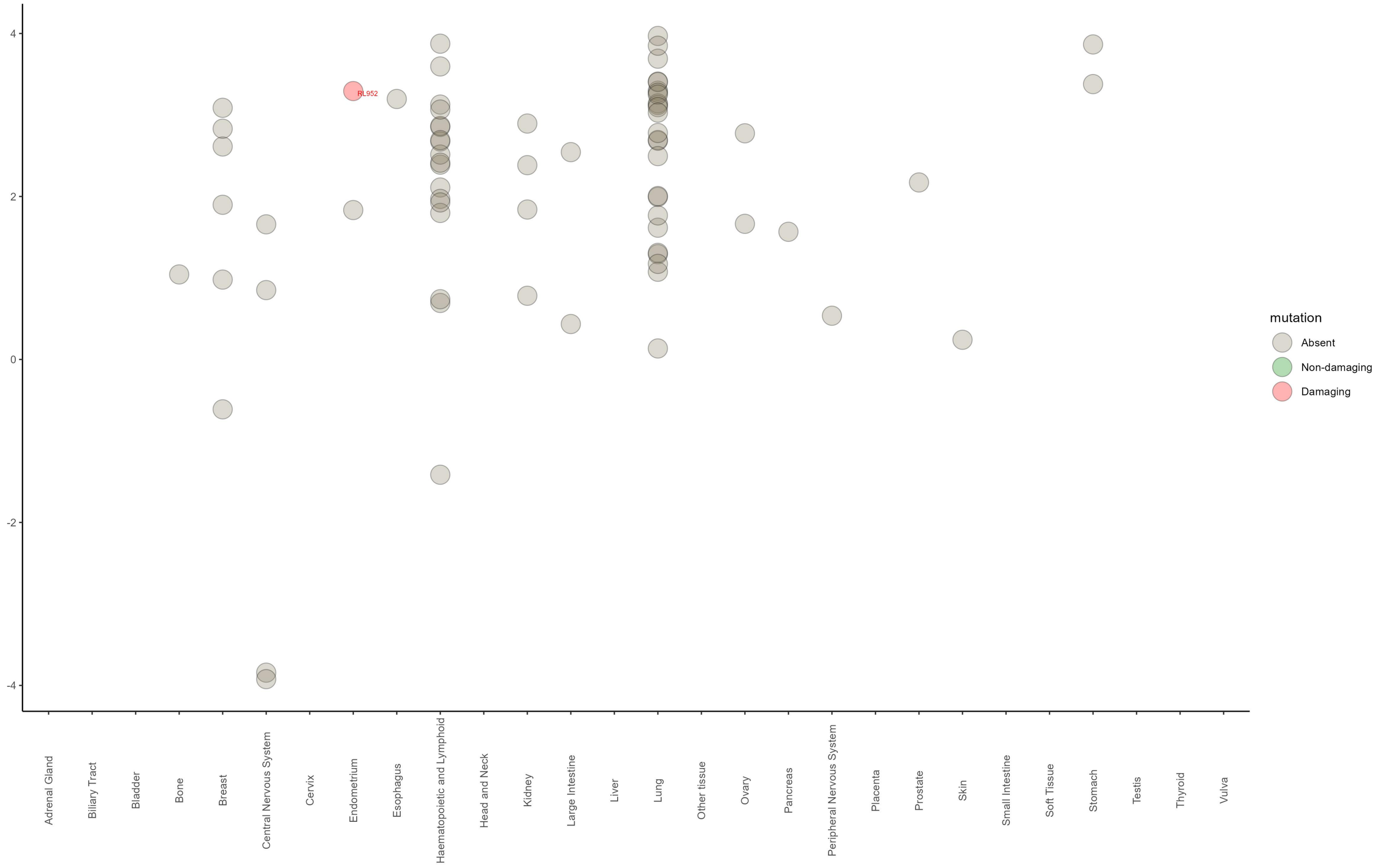
% of CDKN1B in blood cancers: 11.1 ; % of CDKN1B in solid cancers: 6.8

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CDKN1B | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



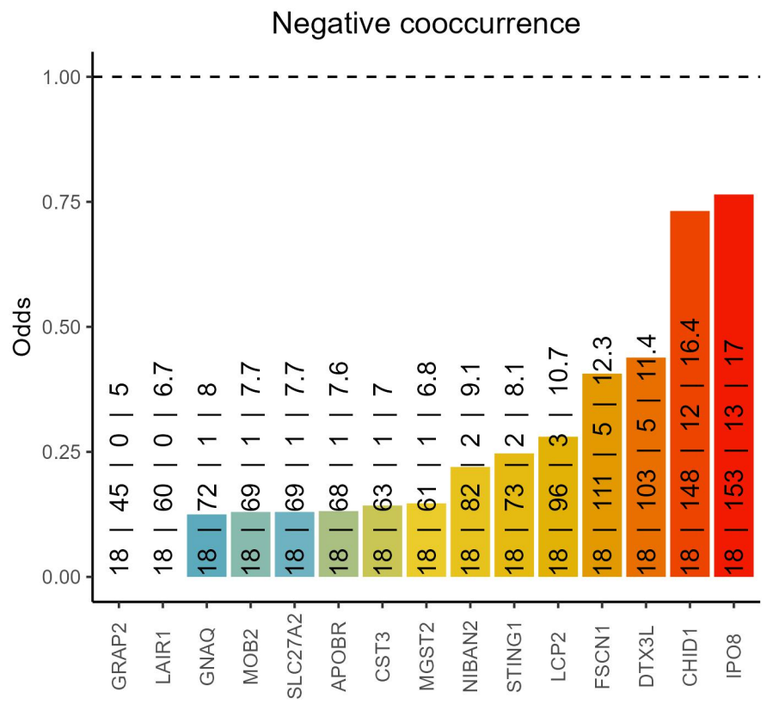


Amount of CDKN1B protein and mutation status by tissue, DB2



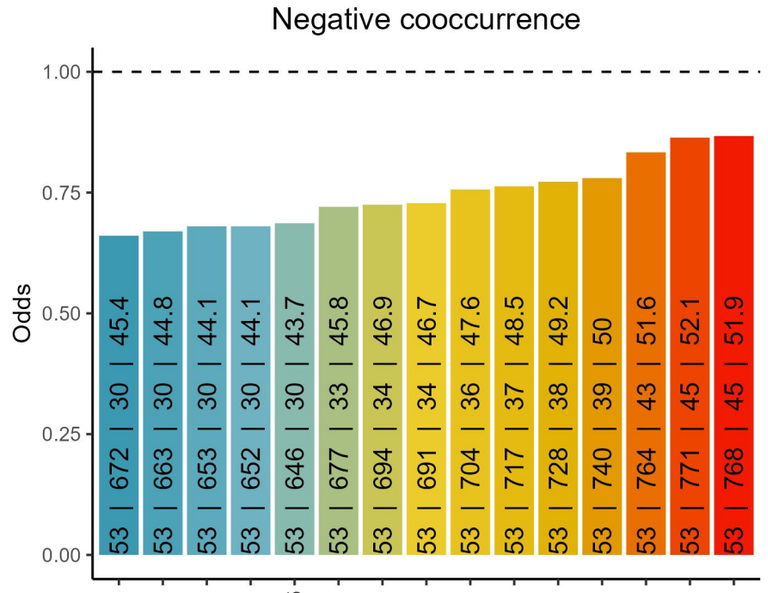
Cooccurrence with CDKN1B protein in blood cancers, DB2

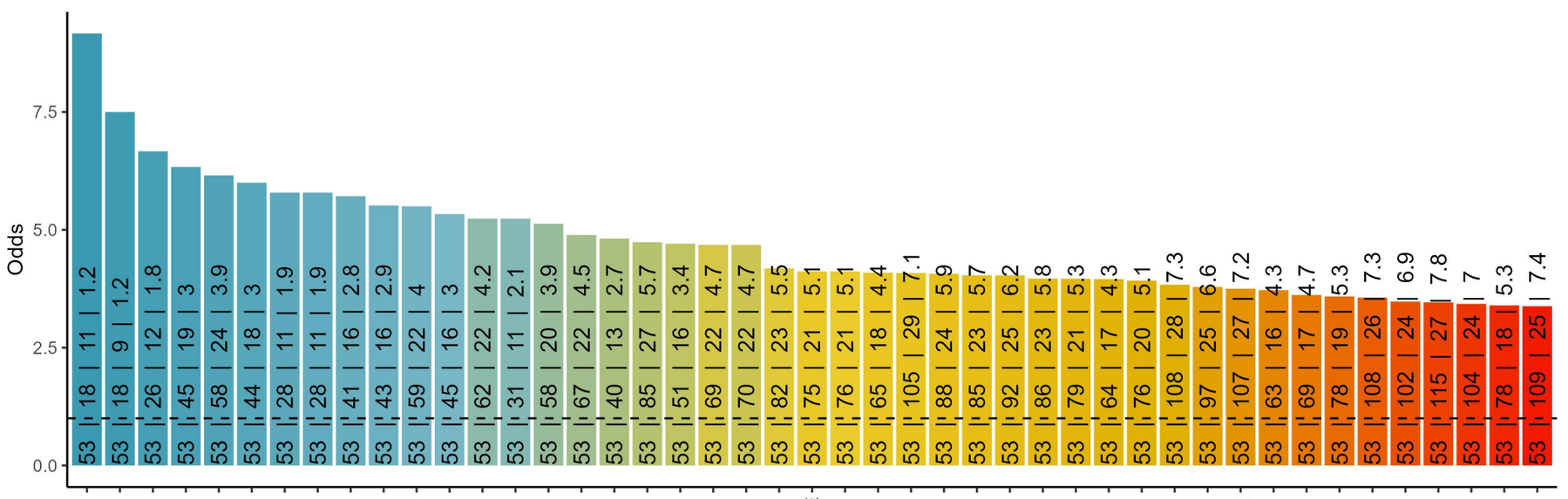
The text in the bars: incidence of CDKN1B | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

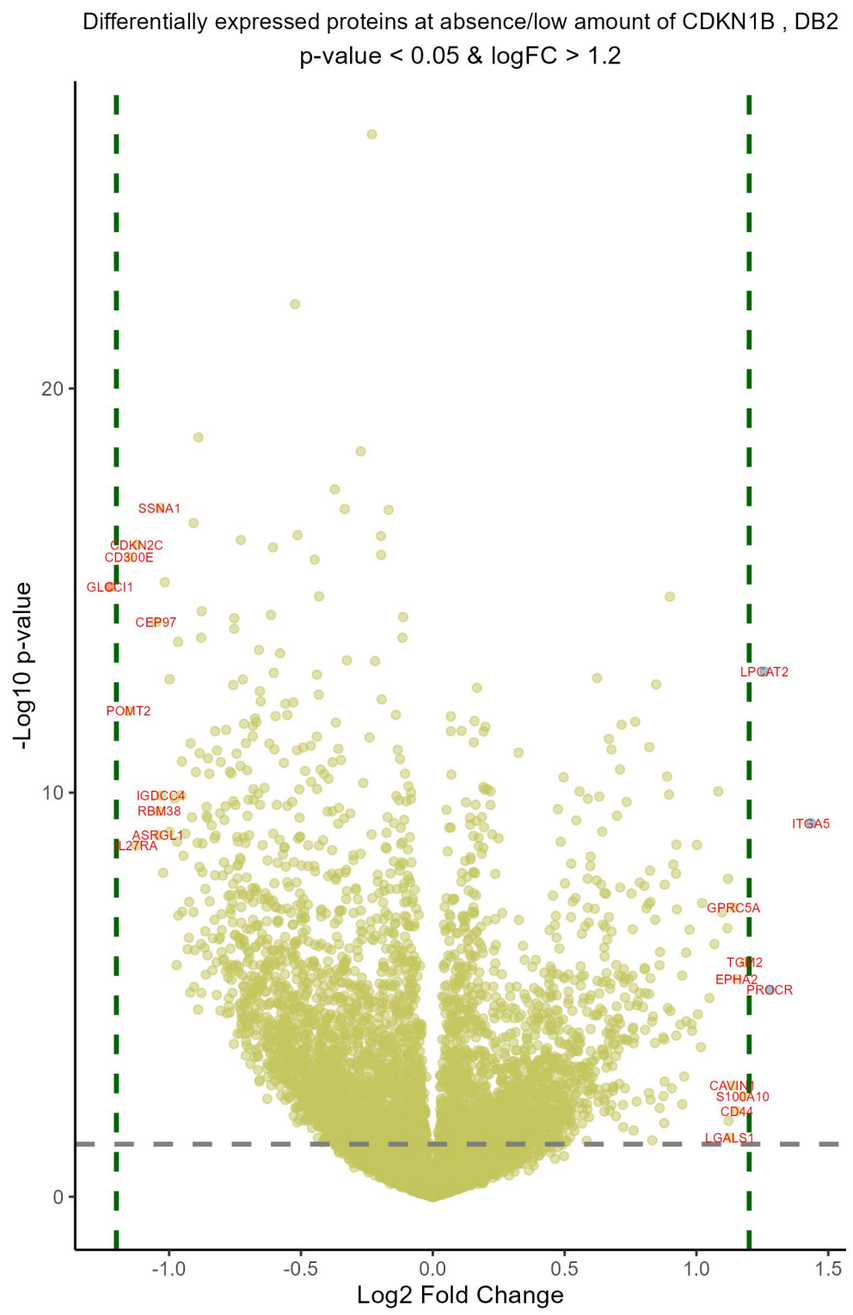


Cooccurrence with CDKN1B protein in solid cancers, DB2

The text in the bars: incidence of CDKN1B | incidence of Protein 2 | observed cooccurrence | expected cooccurrence







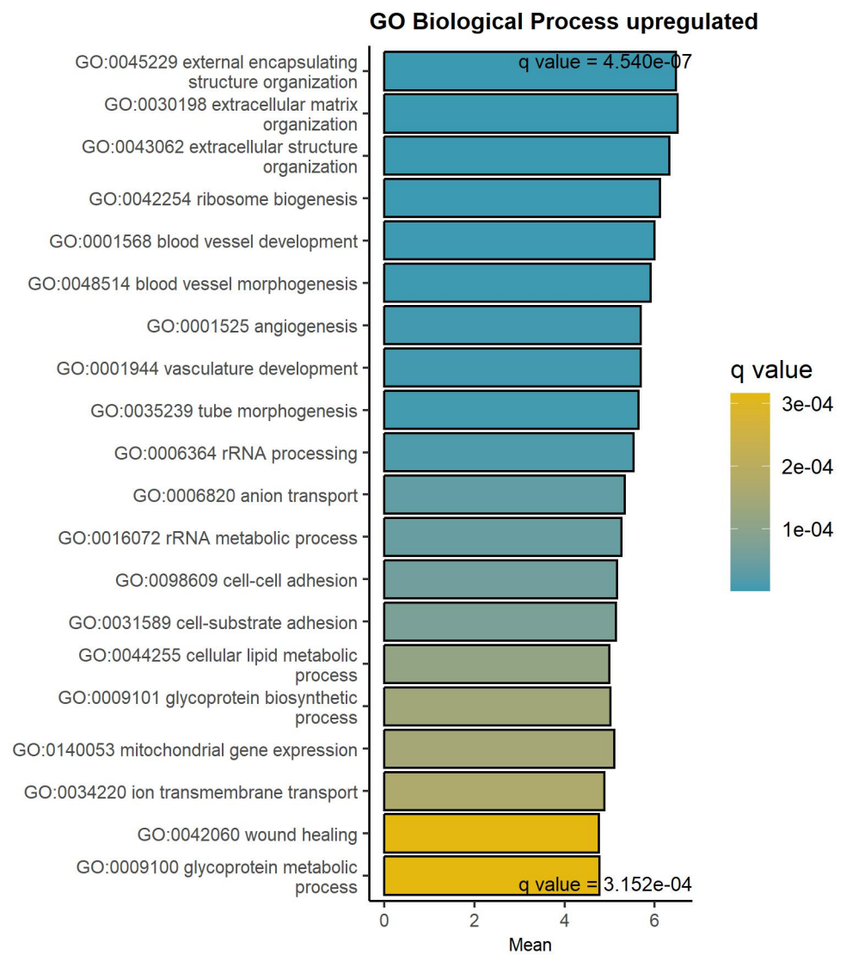
Downregulated at low/absent CDKN1B

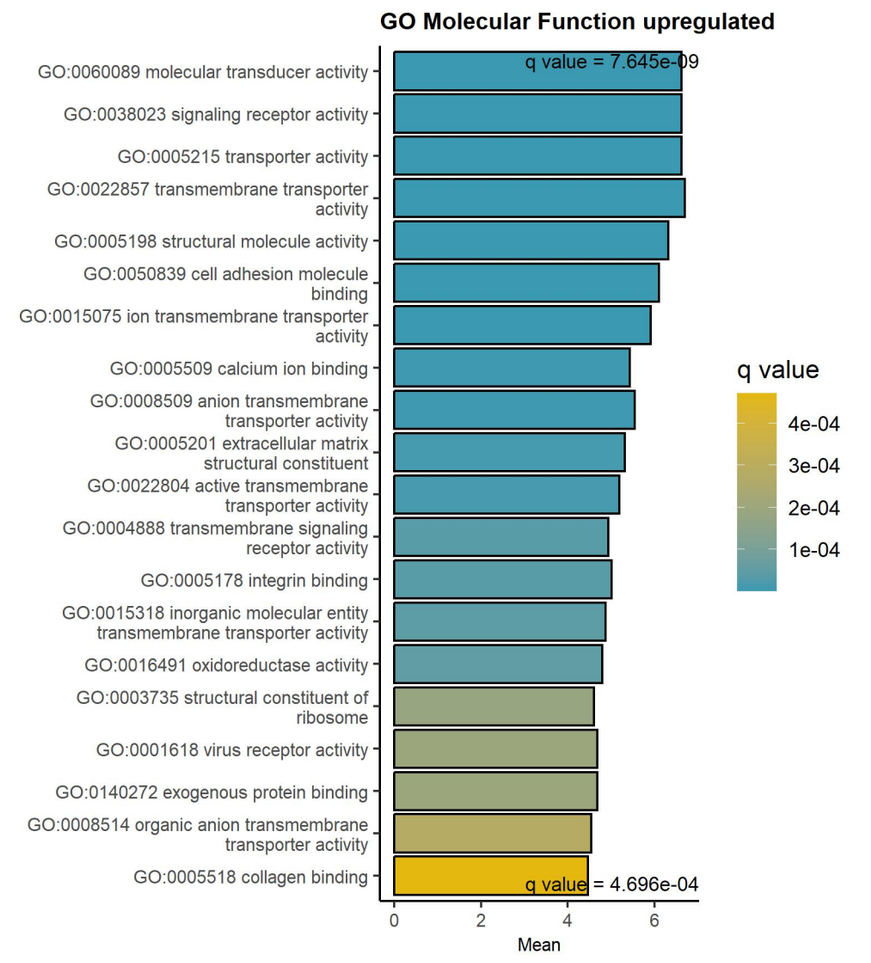
logFC	adj.P.Val	symbol	name
-1.22	3.41e-13	GLCCI1	glucocorticoid induced 1
-1.15	1.57e-10	POMT2	protein O-mannosyltransferase 2
-1.15	7.27e-14	CD300E	CD300e molecule
-1.12	7.85e-08	IL27RA	interleukin 27 receptor subunit alp
-1.12	4.41e-14	CDKN2C	cyclin dependent kinase inhibitor 2
-1.05	1.89e-12	CEP97	centrosomal protein 97
-1.04	4.99e-08	ASRGL1	asparaginase and isoaspartyl peptid
-1.04	1.56e-08	RBM38	RNA binding motif protein 38
-1.04	9.40e-15	SSNA1	SS nuclear autoantigen 1
-1.03	7.71e-09	IGDCC4	immunoglobulin superfamily DCC subc
-1.02	3.04e-07	INSM1	INSM transcriptional repressor 1
-1.02	2.74e-13	PPP1R2	protein phosphatase 1 regulatory in
-1	4.21e-08	HDAC6	histone deacetylase 6
-1	3.23e-11	UNK	unk zinc finger
-0.98	8.81e-09	TMED8	transmembrane p24 trafficking prote
-0.97	2.41e-05	SCG3	secretogranin III
-0.97	6.68e-08	MAPKAPK2	MAPK activated protein kinase 2
-0.97	5.03e-12	WDR37	WD repeat domain 37
-0.96	2.26e-06	RPAIN	RPA interacting protein
-0.95	7.59e-09	CRTC1	CREB regulated transcription coacti
-0.95	1.52e-09	CAMSAP3	calmodulin regulated spectrin assoc
-0.95	1.91e-06	CAMK1D	calcium/calmodulin dependent protei
-0.95	1.32e-07	KDM4A	lysine demethylase 4A
-0.94	4.66e-08	SYNRG	synergin gamma
-0.93	1.13e-05	SYT1	synaptotagmin 1
-0.93	6.55e-06	LVRN	laeverin
-0.92	1.20e-06	SEPTIN3	septin 3
-0.92	8.67e-05	SCGN	secretagogin, EF-hand calcium bindi
-0.92	6.62e-10	BCL7A	BAF chromatin remodeling complex su

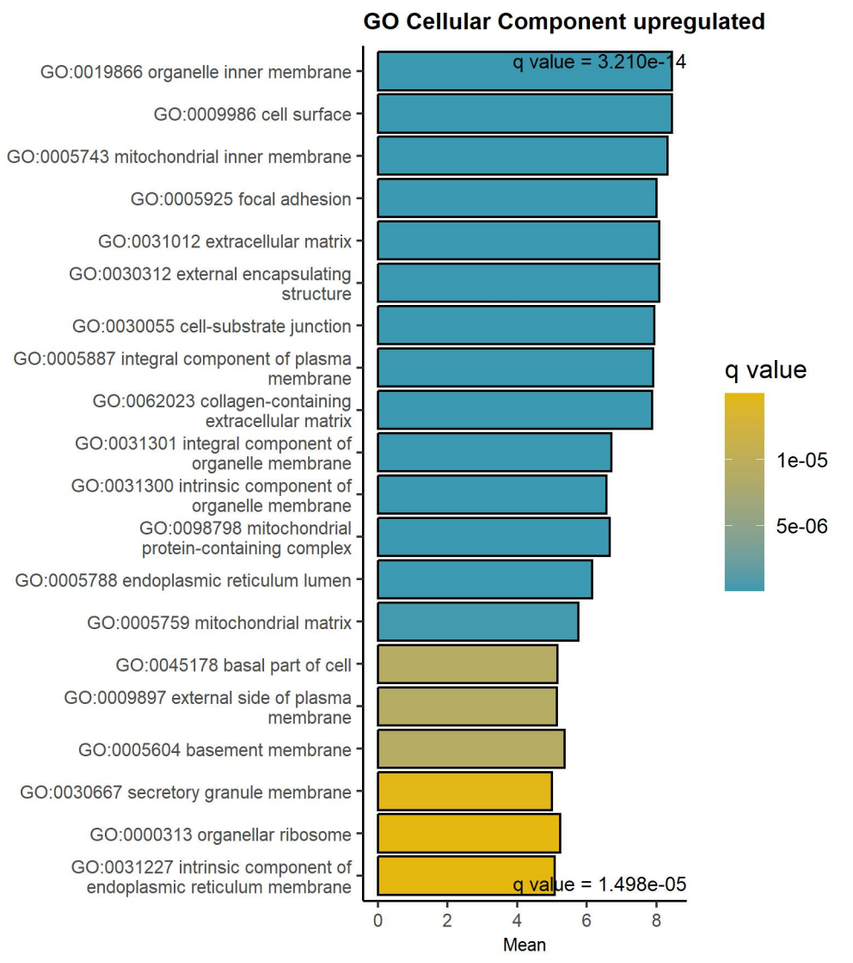
Upregulated at low/absent CDKN1B

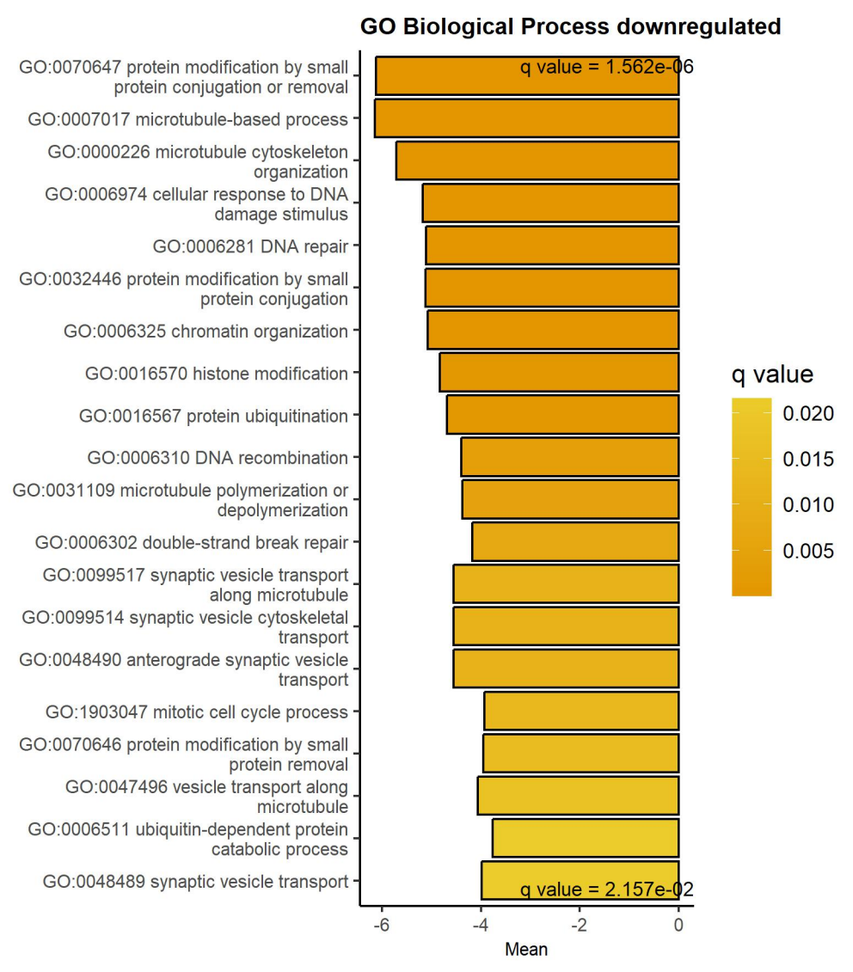
logFC	adj.P.Val	symbol	name
1.43	2.76e-08	ITGA5	integrin subunit alpha 5
1.28	7.60e-05	PROCR	protein C receptor
1.26	2.36e-11	LPCAT2	lysophosphatidylcholine acyltransfe
1.18	2.12e-05	TGM2	transglutaminase 2
1.18	1.15e-02	S100A10	S100 calcium binding protein A10
1.15	2.33e-02	CD44	CD44 molecule (Indian blood group)
1.15	4.64e-05	EPHA2	EPH receptor A2
1.14	1.57e-06	GPRC5A	G protein-coupled receptor class C
1.14	7.03e-03	CAVIN1	caveolae associated protein 1
1.13	7.70e-02	LGALS1	galectin 1
1.12	3.58e-02	ANXA1	annexin A1
1.12	4.01e-07	HMGA2	high mobility group AT-hook 2
1.12	4.09e-06	ADGRE5	adhesion G protein-coupled receptor
1.1	1.96e-06	PRNP	prion protein
1.08	6.34e-09	CAVIN3	caveolae associated protein 3
1.07	8.81e-06	SPESP1	sperm equatorial segment protein 1
1.05	1.11e-04	ZNF671	zinc finger protein 671
1.02	1.25e-06	RAB32	RAB32, member RAS oncogene family
1.02	1.13e-03	RHOC	ras homolog family member C
1.01	2.38e-04	GPX8	glutathione peroxidase 8 (putative)
1	7.72e-08	RETSAT	retinol saturase
0.98	5.16e-04	ADAM9	ADAM metallopeptidase domain 9
0.98	3.78e-04	RRAS	RAS related
0.97	4.38e-06	YAP1	Yes1 associated transcriptional reg
0.96	3.31e-04	MMP14	matrix metallopeptidase 14
0.96	1.32e-05	CTSL	cathepsin L
0.95	4.56e-03	EGFR	epidermal growth factor receptor
0.95	1.68e-02	BTNL8	butyrophilin like 8
0.95	3.88e-05	CABP7	calcium binding protein 7

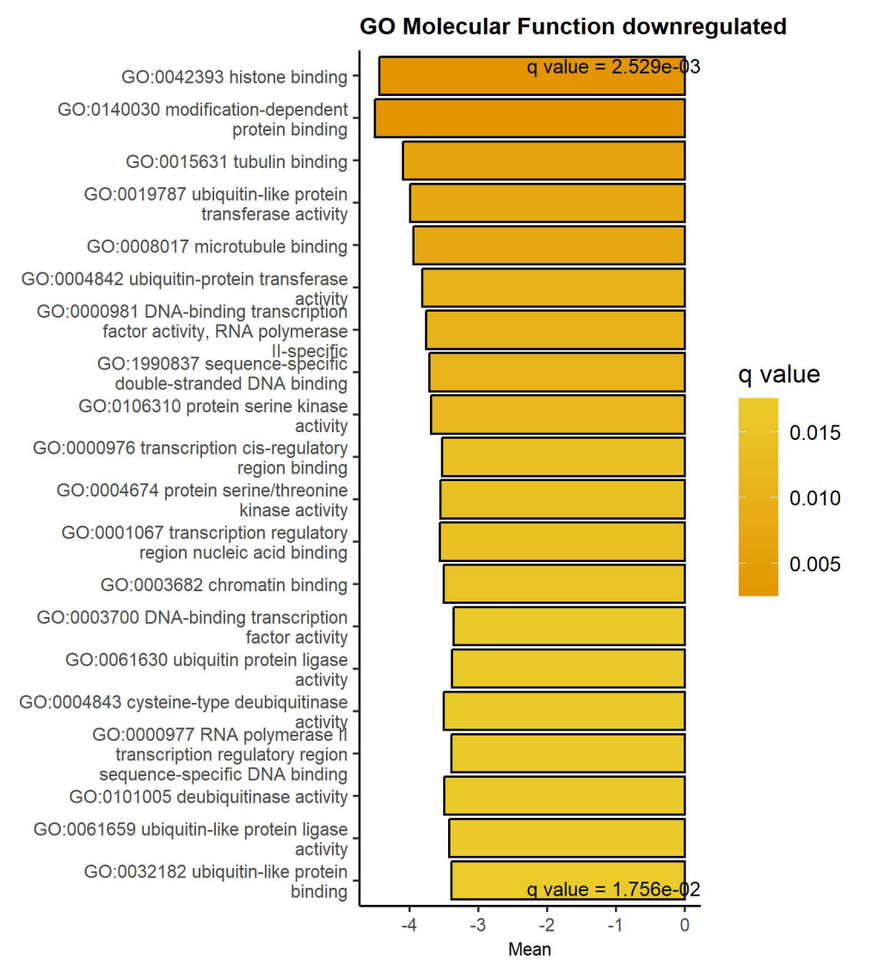
GAGE analysis on upregulated and downregulated proteins at low/absent CDKN1B protein, DB2

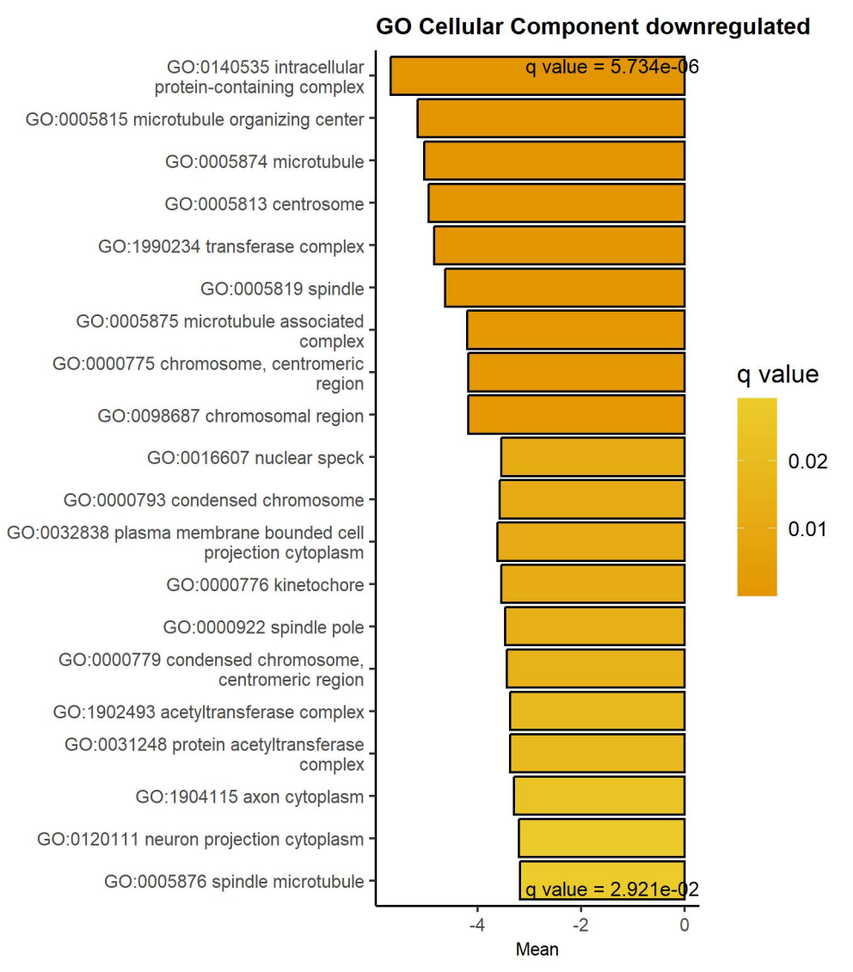


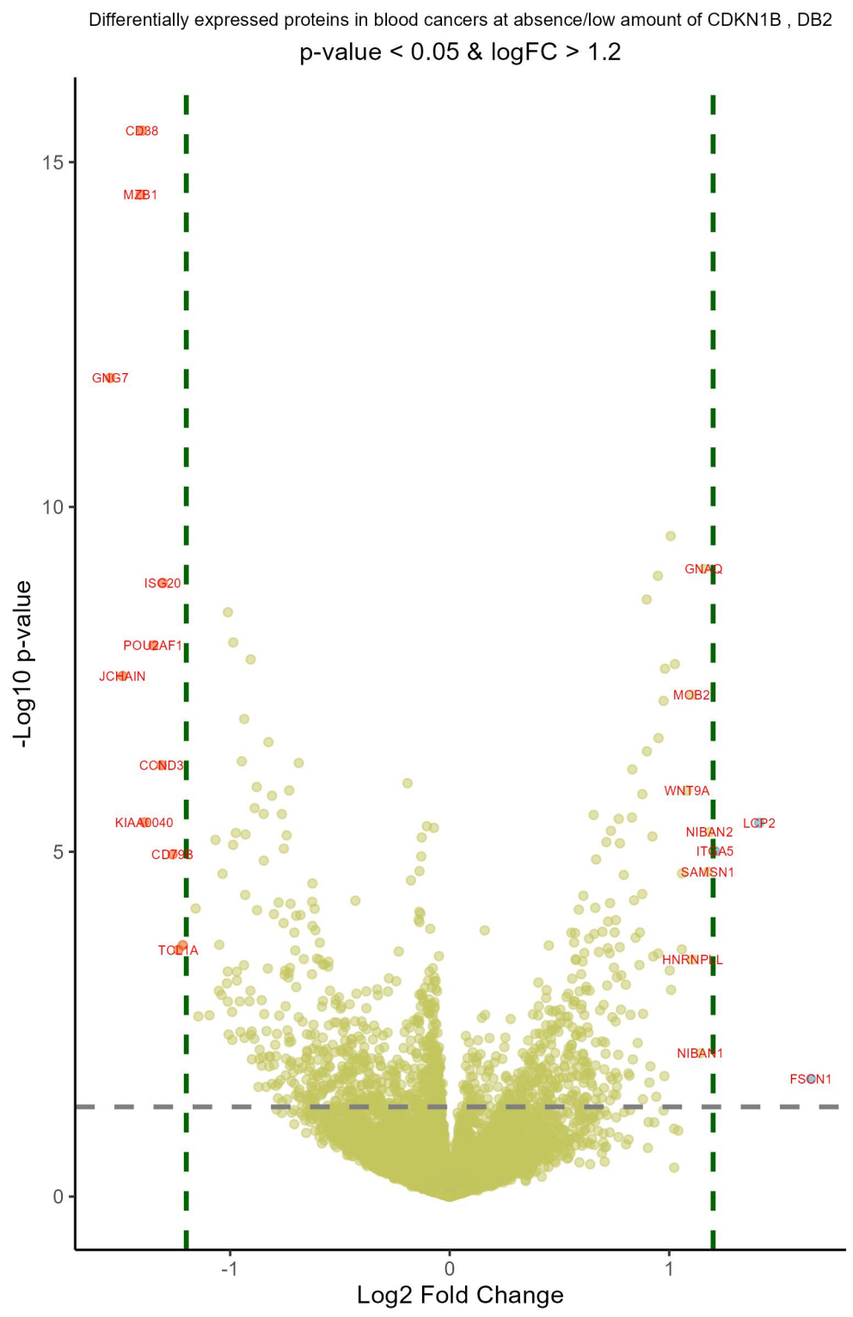


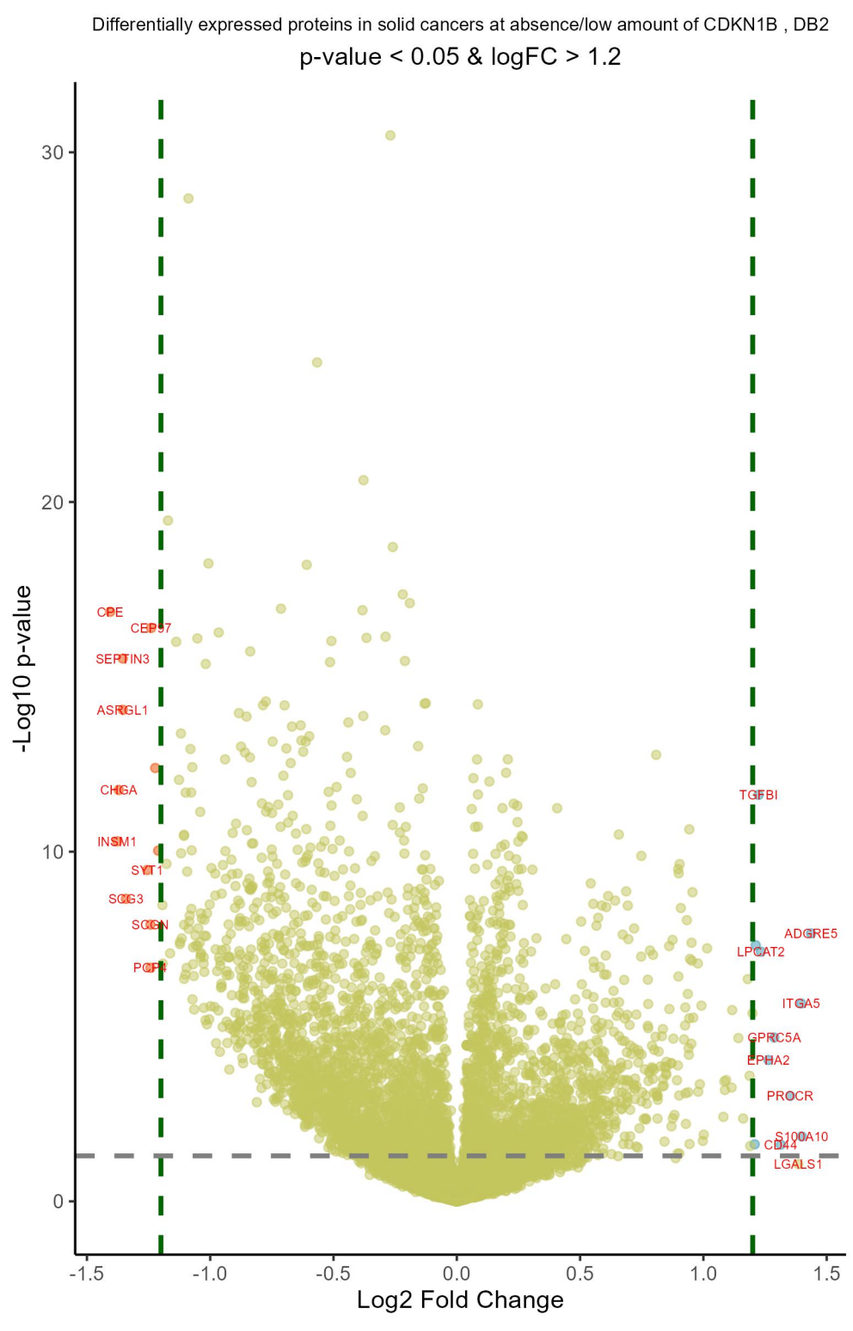












CDKN1B network, DB2, no Pearson r > 0.3

Downregulated in blood cancers at low/absent CDKN1B

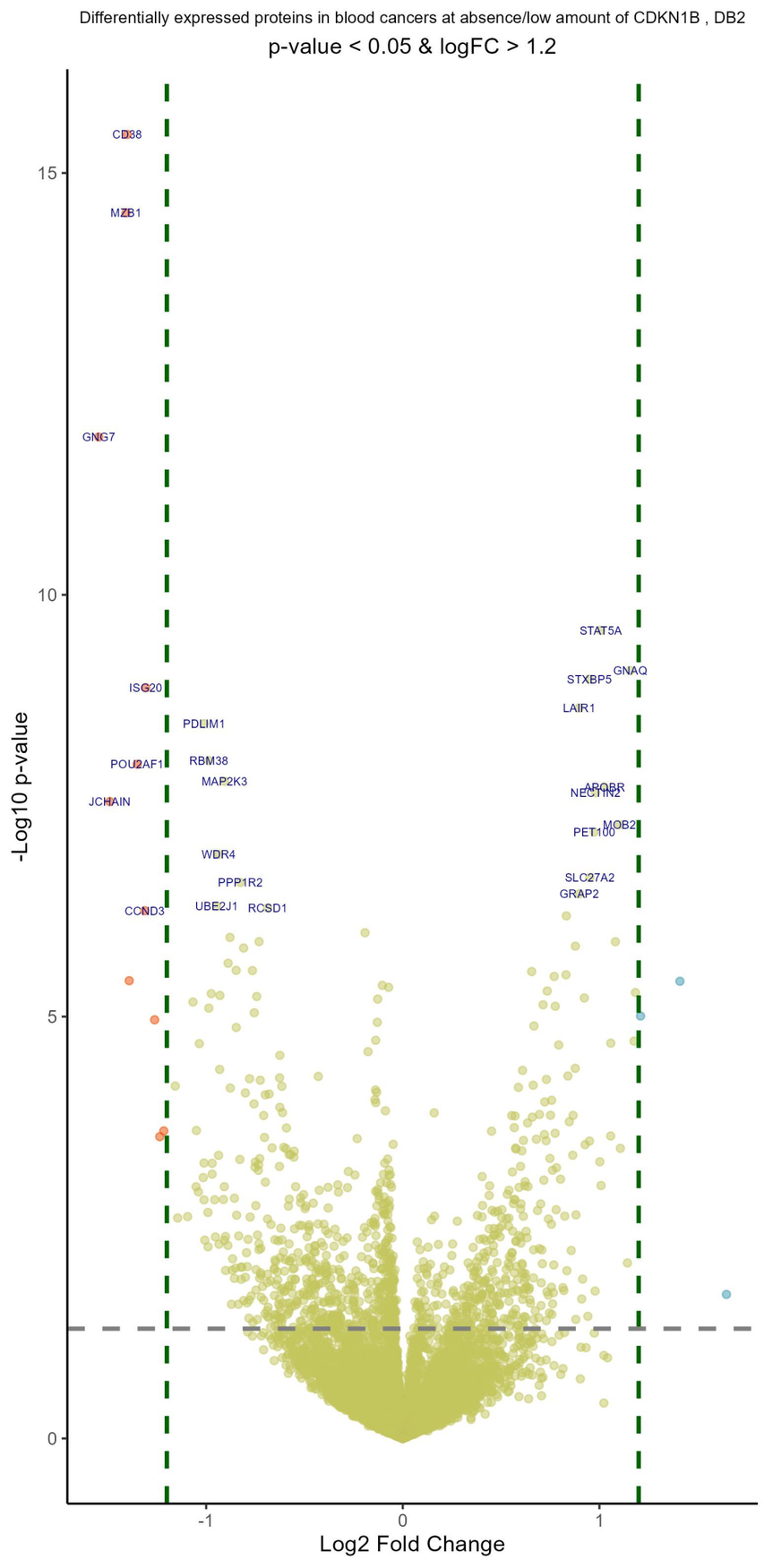
Upregulated in blood cancers at low/absent CDKN1B

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.55	2.82e-09	GNG7	G protein subunit gamma 7	1.65	2.59e-01	FSCN1	fascin actin-bundling protein 1
-1.49	1.48e-05	JCHAIN	joining chain of multimeric IgA and	1.41	7.96e-04	LCP2	lymphocyte cytosolic protein 2
-1.41	8.26e-12	MZB1	marginal zone B and B1 cell specifi	1.21	1.50e-03	ITGA5	integrin subunit alpha 5
-1.4	1.46e-12	CD38	CD38 molecule	1.18	9.85e-04	NIBAN2	niban apoptosis regulator 2
-1.39	7.96e-04	KIAA0040	KIAA0040	1.18	2.67e-03	SAMSN1	SAM domain, SH3 domain and nuclear
-1.35	7.10e-06	POU2AF1	POU class 2 homeobox associating fa	1.16	1.11e-06	GNAQ	G protein subunit alpha q
-1.31	1.86e-04	CCND3	cyclin D3	1.14	1.74e-01	NIBAN1	niban apoptosis regulator 1
-1.31	1.32e-06	ISG20	interferon stimulated exonuclease g	1.11	2.46e-02	HNRNPLL	heterogeneous nuclear ribonucleopro
-1.26	1.63e-03	CD79B	CD79b molecule	1.1	2.62e-05	MOB2	MOB kinase activator 2
-1.24	1.98e-02	TCL1A	TCL1 family AKT coactivator A	1.08	3.61e-04	WNT9A	Wnt family member 9A
-1.22	1.77e-02	ELAPOR1	endosome-lysosome associated apopto	1.06	2.77e-03	STING1	stimulator of interferon response c
-1.16	7.18e-03	CD19	CD19 molecule	1.06	1.96e-02	ANPEP	alanyl aminopeptidase, membrane
-1.15	8.42e-02	NIBAN3	niban apoptosis regulator 3	1.04	5.65e-01	S100A6	S100 calcium binding protein A6
-1.09	8.25e-02	IL27RA	interleukin 27 receptor subunit alp	1.03	1.14e-05	APOBR	apolipoprotein B receptor
-1.07	1.12e-03	GPT2	glutamic--pyruvic transaminase 2	1.02	7.81e-01	ENO3	enolase 3
-1.05	4.99e-02	UCHL1	ubiquitin C-terminal hydrolase L1	1.02	5.51e-01	ACTN1	actinin alpha 1
-1.05	1.76e-02	PAX5	paired box 5	1.01	4.99e-02	EPDR1	ependymin related 1
-1.04	5.45e-02	HLA-DRB3	major histocompatibility complex, c	1.01	4.42e-07	STAT5A	signal transducer and activator of
-1.03	2.77e-03	MCL1	MCL1 apoptosis regulator, BCL2 fami	1	3.19e-02	MYO1F	myosin IF
-1.01	4.26e-02	AP1AR	adaptor related protein complex 1 a	0.98	1.23e-05	NECTIN2	nectin cell adhesion molecule 2
-1.01	3.22e-02	PLCL2	phospholipase C like 2	0.98	2.47e-01	BIN2	bridging integrator 2
-1.01	6.26e-02	BLNK	B cell linker	0.97	3.01e-05	PET100	PET100 cytochrome c oxidase chapero
-1.01	2.82e-06	PDLIM1	PDZ and LIM domain 1	0.97	4.36e-01	CPT1A	carnitine palmitoyltransferase 1A
-1.01	1.21e-01	ST14	ST14 transmembrane serine protease	0.95	9.39e-05	SLC27A2	solute carrier family 27 member 2
-0.99	7.72e-02	MAN1A1	mannosidase alpha class 1A member 1	0.95	2.12e-02	CTSG	cathepsin G
-0.99	1.35e-01	BACH2	BTB domain and CNC homolog 2	0.95	1.19e-06	STXBP5	syntaxin binding protein 5
-0.99	1.25e-03	PIP5K1C	phosphatidylinositol-4-phosphate 5-	0.94	3.52e-01	GPHN	gephyrin
-0.99	7.01e-06	RBM38	RNA binding motif protein 38	0.93	5.10e-01	SH3RF1	SH3 domain containing ring finger 1
-0.97	9.93e-04	RWDD3	RWD domain containing 3	0.93	2.30e-02	FAM20B	FAM20B glycosaminoglycan xylosylkin

Downregulated in solid cancers at low/absent CDKN1B

Upregulated in solid cancers at low/absent CDKN1B

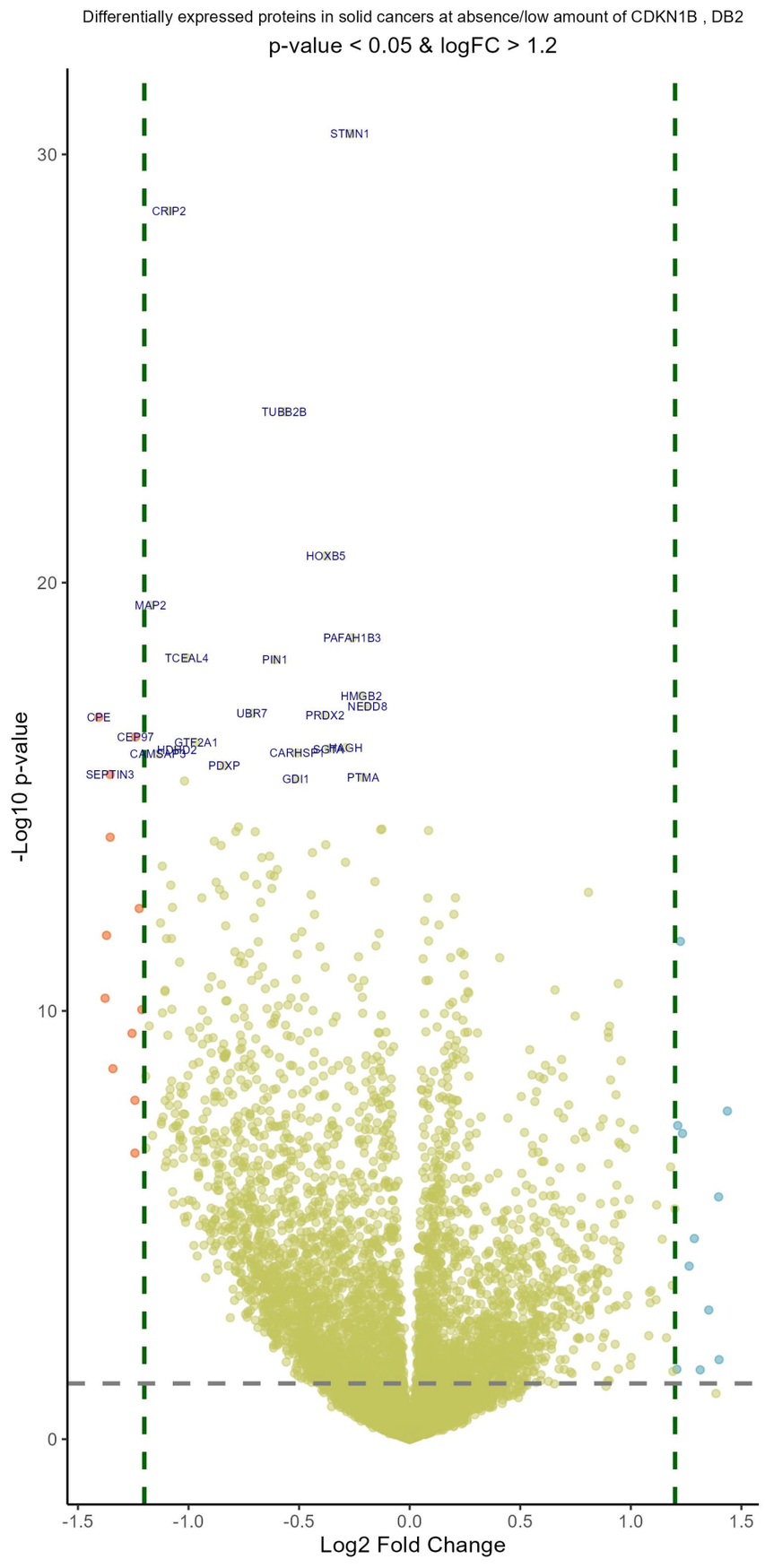
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.41	8.25e-15	CPE	carboxypeptidase E	1.44	5.23e-07	ADGRE5	adhesion G protein-coupled receptor
-1.38	3.62e-09	INSM1	INSM transcriptional repressor 1	1.4	3.71e-02	S100A10	S100 calcium binding protein A10
-1.37	2.06e-10	CHGA	chromogranin A	1.4	2.55e-05	ITGA5	integrin subunit alpha 5
-1.35	1.09e-13	SEPTIN3	septin 3	1.39	1.55e-01	LGALS1	galectin 1
-1.35	2.23e-12	ASRGL1	asparaginase and isoaspartyl peptid	1.35	4.01e-03	PROCR	protein C receptor
-1.34	7.98e-08	SCG3	secretogranin III	1.31	5.71e-02	CD44	CD44 molecule (Indian blood group)
-1.26	1.69e-08	SYT1	synaptotagmin 1	1.29	1.67e-04	GPRC5A	G protein-coupled receptor class C
-1.24	3.35e-06	PCP4	Purkinje cell protein 4	1.26	5.64e-04	EPHA2	EPH receptor A2
-1.24	3.17e-07	SCGN	secretagogin, EF-hand calcium bindi	1.23	1.39e-06	LPCAT2	lysophosphatidylcholine acyltransfe
-1.24	2.24e-14	CEP97	centrosomal protein 97	1.22	2.65e-10	TGFBI	transforming growth factor beta ind
-1.22	5.65e-11	CD300E	CD300e molecule	1.21	9.87e-07	SPESP1	sperm equatorial segment protein 1
-1.21	6.05e-09	POMT2	protein O-mannosyltransferase 2	1.21	5.60e-02	CAVIN1	caveolae associated protein 1
-1.19	1.11e-07	GLCCI1	glucocorticoid induced 1	1.2	4.37e-05	HMGA2	high mobility group AT-hook 2
-1.19	2.63e-06	CELF4	CUGBP Elav-like family member 4	1.19	6.09e-02	ANXA1	annexin A1
-1.18	1.24e-08	CDKN2A	cyclin dependent kinase inhibitor 2	1.19	1.33e-03	TGM2	transglutaminase 2
-1.17	4.72e-17	MAP2	microtubule associated protein 2	1.18	6.32e-06	CAVIN3	caveolae associated protein 3
-1.16	1.52e-06	GNG4	G protein subunit gamma 4	1.16	1.41e-02	BTNL8	butyrophilin like 8
-1.14	3.97e-14	CAMSAP3	calmodulin regulated spectrin assoc	1.14	1.72e-04	PRNP	prion protein
-1.13	1.14e-10	PRR36	proline rich 36	1.12	3.65e-05	SP100	SP100 nuclear antigen
-1.12	9.30e-07	SYN1	synapsin I	1.11	2.52e-03	ZNF671	zinc finger protein 671
-1.12	8.30e-07	MAD2L2	mitotic arrest deficient 2 like 2	1.09	1.69e-03	MMP14	matrix metallopeptidase 14
-1.12	8.51e-12	SSNA1	SS nuclear autoantigen 1	1.09	2.90e-03	ICAM1	intercellular adhesion molecule 1
-1.12	7.04e-09	RUFY3	RUN and FYVE domain containing 3	1.09	1.82e-03	GPX8	glutathione peroxidase 8 (putative)
-1.12	6.85e-07	CBFA2T2	CBFA2/RUNX1 partner transcriptional	1.08	1.29e-02	EGFR	epidermal growth factor receptor
-1.11	2.65e-09	LCMT1	leucine carboxyl methyltransferase	1.01	1.17e-06	GGCX	gamma-glutamyl carboxylase
-1.11	2.49e-09	CDKN2C	cyclin dependent kinase inhibitor 2	1	3.37e-02	CAV1	caveolin 1
-1.11	6.26e-06	IL27RA	interleukin 27 receptor subunit alp	1	4.70e-02	CTSZ	cathepsin Z
-1.11	3.20e-07	DCLK1	doublecortin like kinase 1	0.99	2.86e-05	YAP1	Yes1 associated transcriptional reg
-1.1	4.91e-06	AP3B2	adaptor related protein complex 3 s	0.99	2.11e-03	CABP7	calcium binding protein 7



Sorted by p values!

Downregulated in blood cancers at low/absent CDKN1B Upregulated in blood cancers at low/absent CDKN1B

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.4	1.46e-12	CD38	CD38 molecule	1.01	4.42e-07	STAT5A	signal transducer and activator of
-1.41	8.26e-12	MZB1	marginal zone B and B1 cell specifi	1.16	1.11e-06	GNAQ	G protein subunit alpha q
-1.55	2.82e-09	GNG7	G protein subunit gamma 7	0.95	1.19e-06	STXBP5	syntaxin binding protein 5
-1.31	1.32e-06	ISG20	interferon stimulated exonuclease g	0.9	2.04e-06	LAIR1	leukocyte associated immunoglobulin
-1.01	2.82e-06	PDLIM1	PDZ and LIM domain 1	1.03	1.14e-05	APOBR	apolipoprotein B receptor
-0.99	7.01e-06	RBM38	RNA binding motif protein 38	0.98	1.23e-05	NECTIN2	nectin cell adhesion molecule 2
-1.35	7.10e-06	POU2AF1	POU class 2 homeobox associating fa	1.1	2.62e-05	MOB2	MOB kinase activator 2
-0.91	1.05e-05	MAP2K3	mitogen-activated protein kinase ki	0.97	3.01e-05	PET100	PET100 cytochrome c oxidase chapero
-1.49	1.48e-05	JCHAIN	joining chain of multimeric IgA and	0.95	9.39e-05	SLC27A2	solute carrier family 27 member 2
-0.94	5.23e-05	WDR4	WD repeat domain 4	0.9	1.33e-04	GRAP2	GRB2 related adaptor protein 2
-0.83	1.02e-04	PPP1R2	protein phosphatase 1 regulatory in	0.83	2.06e-04	MGST2	microsomal glutathione S-transferas
-0.95	1.77e-04	UBE2J1	ubiquitin conjugating enzyme E2 J1	1.08	3.61e-04	WNT9A	Wnt family member 9A
-0.69	1.80e-04	RCSD1	RCSD domain containing 1	0.88	3.94e-04	LPCAT2	lysophosphatidylcholine acyltransfe
-1.31	1.86e-04	CCND3	cyclin D3	0.66	6.79e-04	PLCB2	phospholipase C beta 2
-0.19	3.14e-04	EIF5A	eukaryotic translation initiation f	0.83	7.21e-04	CST3	cystatin C
-0.88	3.44e-04	RPGRIP1L	RPGRIP1 like	0.77	7.34e-04	PSTPIP2	proline-serine-threonine phosphatas
-0.73	3.61e-04	IRAG2	inositol 1,4,5-triphosphate recepto	1.41	7.96e-04	LCP2	lymphocyte cytosolic protein 2
-0.81	4.02e-04	FKBP11	FKBP prolyl isomerase 11	0.73	9.66e-04	SHKBP1	SH3KBP1 binding protein 1
-0.89	5.90e-04	IRF4	interferon regulatory factor 4	1.18	9.85e-04	NIBAN2	niban apoptosis regulator 2
-0.85	6.79e-04	GLCCI1	glucocorticoid induced 1	0.92	1.05e-03	POGLUT3	protein O-glucosyltransferase 3
-0.76	6.79e-04	HIP1R	huntingtin interacting protein 1 re	0.71	1.19e-03	RAB32	RAB32, member RAS oncogene family
-1.39	7.96e-04	KIAA0040	KIAA0040	0.78	1.21e-03	S100A8	S100 calcium binding protein A8
-0.1	8.69e-04	ANP32A	acidic nuclear phosphoprotein 32 fa	1.21	1.50e-03	ITGA5	integrin subunit alpha 5
-0.07	8.95e-04	HSPD1	heat shock protein family D (Hsp60)	0.67	1.86e-03	ANKRD52	ankyrin repeat domain 52
-0.97	9.93e-04	RWDD3	RWD domain containing 3	1.18	2.67e-03	SAMSN1	SAM domain, SH3 domain and nuclear
-0.93	1.02e-03	IL16	interleukin 16	1.06	2.77e-03	STING1	stimulator of interferon response c
-0.74	1.03e-03	CDK4	cyclin dependent kinase 4	0.79	2.83e-03	STEAP3	STEAP3 metalloreductase
-0.13	1.06e-03	ANP32E	acidic nuclear phosphoprotein 32 fa	0.88	5.12e-03	ARRB1	arrestin beta 1
-1.07	1.12e-03	GPT2	glutamic--pyruvic transaminase 2	0.61	5.26e-03	FYB1	FYN binding protein 1
-0.99	1.25e-03	PIP5K1C	phosphatidylinositol-4-phosphate 5-	0.84	6.03e-03	CLEC11A	C-type lectin domain containing 11A
-0.76	1.39e-03	GLYCTK	glycerate kinase	0.73	6.28e-03	NNMT	nicotinamide N-methyltransferase
-1.26	1.63e-03	CD79B	CD79b molecule	0.66	7.15e-03	CASP4	caspase 4
-0.13	1.71e-03	CAMKV	CaM kinase like vesicle associated	0.59	7.30e-03	COX14	cytochrome c oxidase assembly facto
-0.85	1.91e-03	CDKN2C	cyclin dependent kinase inhibitor 2	0.76	9.44e-03	C9orf64	chromosome 9 open reading frame 64
-0.14	2.66e-03	SET	SET nuclear proto-oncogene	0.72	9.76e-03	ATP2B3	ATPase plasma membrane Ca2+ transpo
-1.03	2.77e-03	MCL1	MCL1 apoptosis regulator, BCL2 fami	0.16	1.23e-02	AP2B1	adaptor related protein complex 2 s
-0.18	3.34e-03	PYM1	PYM homolog 1, exon junction comple	0.7	1.26e-02	EHHADH	enoyl-CoA hydratase and 3-hydroxyac
-0.63	3.65e-03	GPD1L	glycerol-3-phosphate dehydrogenase	0.75	1.26e-02	RETSAT	retinol saturase
-0.93	5.19e-03	ISG20L2	interferon stimulated exonuclease g	0.87	1.26e-02	PARVB	parvin beta



Sorted by p values!

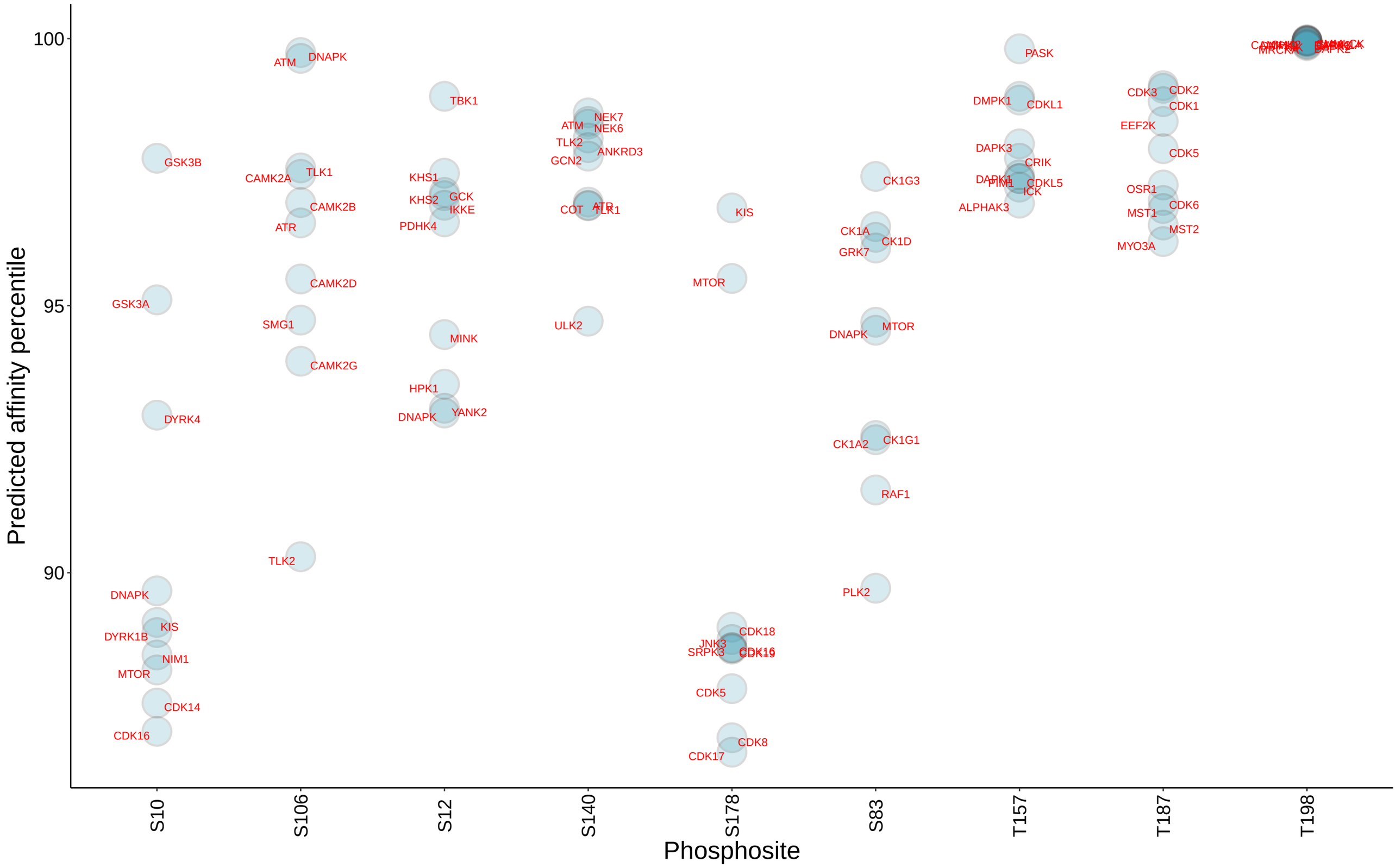
Downregulated in solid cancers at low/absent CDKN1B Upregulated in solid cancers at low/absent CDKN1B

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.27	1.37e-27	STMN1	stathmin 1	0.09	1.71e-12	RPL10A	ribosomal protein L10a
-1.09	5.84e-26	CRIP2	cysteine rich protein 2	0.81	2.74e-11	RAB43	RAB43, member RAS oncogene family
-0.57	2.14e-21	TUBB2B	tubulin beta 2B class IIb	0.21	3.39e-11	NOP16	NOP16 nucleolar protein
-0.38	3.97e-18	HOXB5	homeobox B5	0.08	3.39e-11	RPL6	ribosomal protein L6
-1.17	4.72e-17	MAP2	microtubule associated protein 2	0.2	7.57e-11	PES1	pescadillo ribosomal biogenesis fac
-0.26	2.32e-16	PAFAH1B3	platelet activating factor acetylhy	0.07	1.03e-10	RPL13	ribosomal protein L13
-1.01	5.82e-16	TCEAL4	transcription elongation factor A l	0.13	1.25e-10	RPL27	ribosomal protein L27
-0.61	5.82e-16	PIN1	peptidylprolyl cis/trans isomerase,	0.09	2.63e-10	RPL7A	ribosomal protein L7a
-0.22	3.68e-15	HMGB2	high mobility group box 2	1.22	2.65e-10	TGFBI	transforming growth factor beta ind
-0.19	5.92e-15	NEDD8	NEDD8 ubiquitin like modifier	0.23	4.46e-10	BOP1	BOP1 ribosomal biogenesis factor
-0.71	7.84e-15	UBR7	ubiquitin protein ligase E3 compone	0.25	4.93e-10	WDR36	WD repeat domain 36
-0.38	8.03e-15	PRDX2	peroxiredoxin 2	0.19	5.50e-10	GTPBP4	GTP binding protein 4
-1.41	8.25e-15	CPE	carboxypeptidase E	0.41	5.50e-10	NOL6	nucleolar protein 6
-1.24	2.24e-14	CEP97	centrosomal protein 97	0.06	5.73e-10	RPL31	ribosomal protein L31
-0.97	2.82e-14	GTF2A1	general transcription factor IIA su	0.25	1.27e-09	MYBBP1A	MYB binding protein 1a
-0.29	3.49e-14	HAGH	hydroxyacylglutathione hydrolase	0.09	1.61e-09	RPL7	ribosomal protein L7
-0.37	3.51e-14	SGTA	small glutamine rich tetratricopept	0.07	1.61e-09	RPL27A	ribosomal protein L27a
-1.05	3.51e-14	HDHD2	haloacid dehalogenase like hydrolas	0.94	1.85e-09	CCNYL1	cyclin Y like 1
-0.51	3.96e-14	CARHSP1	calcium regulated heat stable prote	0.66	2.49e-09	PKMYT1	protein kinase, membrane associated
-1.14	3.97e-14	CAMSAP3	calmodulin regulated spectrin assoc	0.26	2.65e-09	IMP3	IMP U3 small nucleolar ribonucleopr
-0.84	7.12e-14	PDXP	pyridoxal phosphatase	0.27	2.83e-09	PDCD11	programmed cell death 11
-1.35	1.09e-13	SEPTIN3	septin 3	0.25	3.64e-09	NAT10	N-acetyltransferase 10
-0.21	1.23e-13	PTMA	prothymosin alpha	0.19	4.32e-09	RRS1	ribosome biogenesis regulator 1 hom
-0.51	1.27e-13	GDI1	GDP dissociation inhibitor 1	0.18	4.92e-09	RRP1	ribosomal RNA processing 1
-1.02	1.38e-13	AAMDC	adipogenesis associated Mth938 doma	0.07	7.14e-09	RPL23A	ribosomal protein L23a
-0.77	1.57e-12	CKB	creatine kinase B	0.16	7.14e-09	RSL1D1	ribosomal L1 domain containing 1
-0.13	1.69e-12	TUBB4B	tubulin beta 4B class IVb	0.21	7.93e-09	RRP9	ribosomal RNA processing 9, U3 smal
-0.13	1.69e-12	CUTA	cutA divalent cation tolerance homo	0.75	7.93e-09	NSA2	NSA2 ribosome biogenesis factor
-0.79	1.71e-12	ZNF428	zinc finger protein 428	0.24	9.56e-09	WDR43	WD repeat domain 43
-0.7	1.71e-12	PPM1A	protein phosphatase, Mg2+/Mn2+ depe	0.9	1.25e-08	PLSCR1	phospholipid scramblase 1
-1.35	2.23e-12	ASRGL1	asparaginase and isoaspartyl peptid	0.12	1.29e-08	LRRC59	leucine rich repeat containing 59
-0.88	2.69e-12	GCA	grancalcin	0.07	1.64e-08	RPL30	ribosomal protein L30
-0.38	3.16e-12	RANBP3	RAN binding protein 3	0.26	1.64e-08	UTP4	UTP4 small subunit processome compo
-0.85	3.18e-12	TUBB2A	tubulin beta 2A class IIa	0.9	1.65e-08	CGAS	cyclic GMP-AMP synthase
-0.44	4.56e-12	IRGQ	immunity related GTPase Q	0.25	1.66e-08	SURF6	surfeit 6
-0.63	5.37e-12	PHPT1	phosphohistidine phosphatase 1	0.31	1.66e-08	RPL7L1	ribosomal protein L7 like 1
-0.67	5.65e-12	SCOC	short coiled-coil protein	0.18	1.80e-08	MRPS22	mitochondrial ribosomal protein S22
-0.29	7.07e-12	AKR1A1	aldo-keto reductase family 1 member	0.9	2.02e-08	SERPINE1	serpin family E member 1
-1.12	8.51e-12	SSNA1	SS nuclear autoantigen 1	0.21	2.31e-08	NOP2	NOP2 nucleolar protein

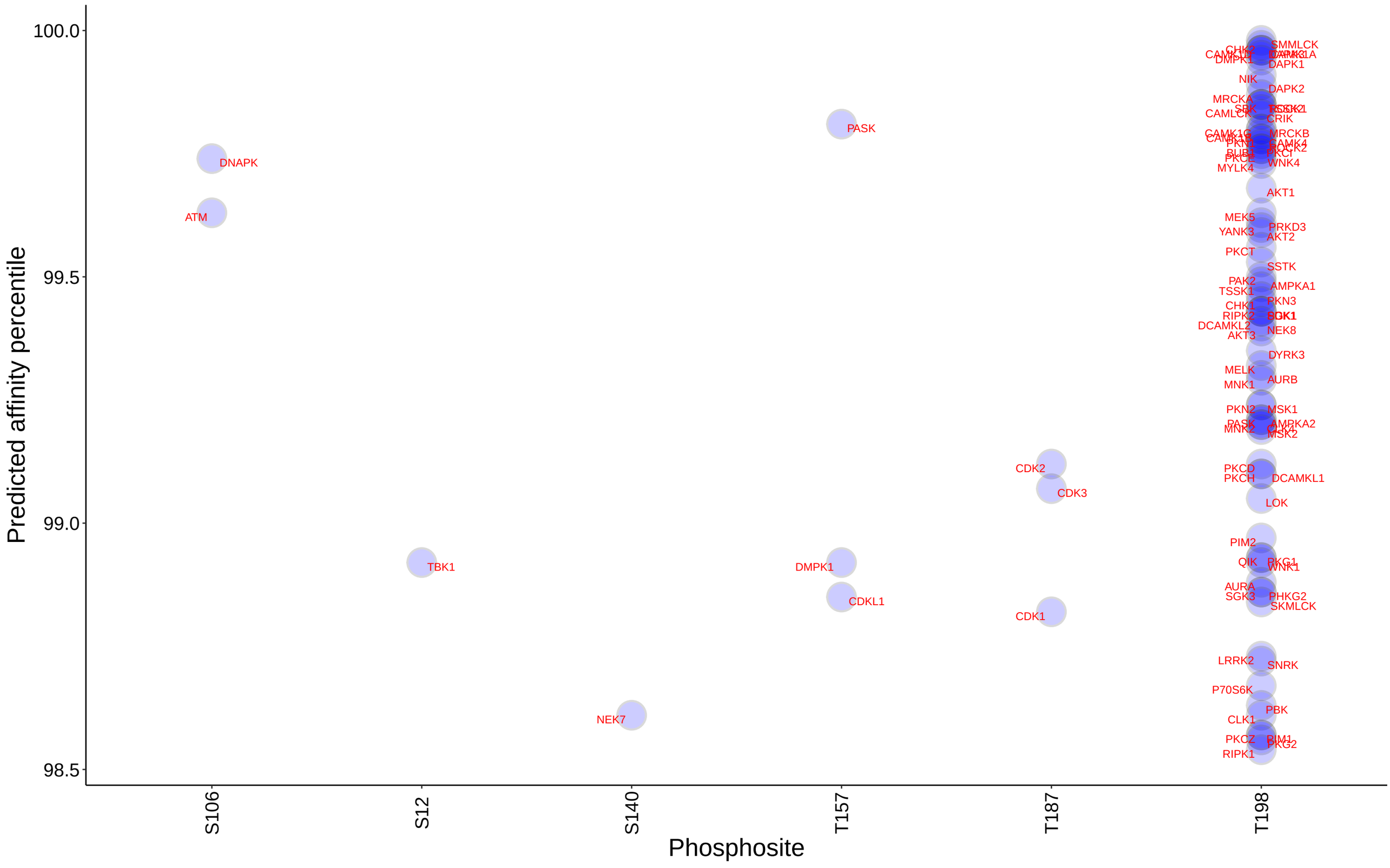
Insufficient number of paired observations in DB2 for CDKN1B

Insufficient number of paired observations in DB2 for CDKN1B

Top 10 kinases for each phosphosite in CDKN1B



Kinases with affinity greater than 98.5% to CDKN1B



No sufficient number of paired observations in DB2 for CDKN1B