

CDKN1A

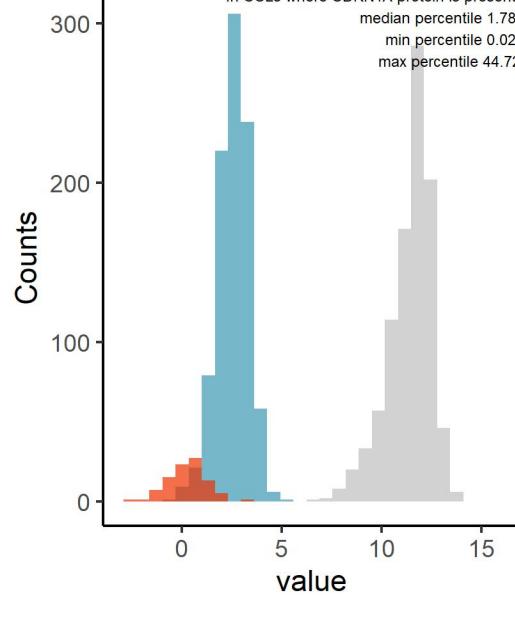
Protein name: CDKN1A ; UNIPROT: P38936 ; Gene name: cyclin dependent kinase inhibitor 1A

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

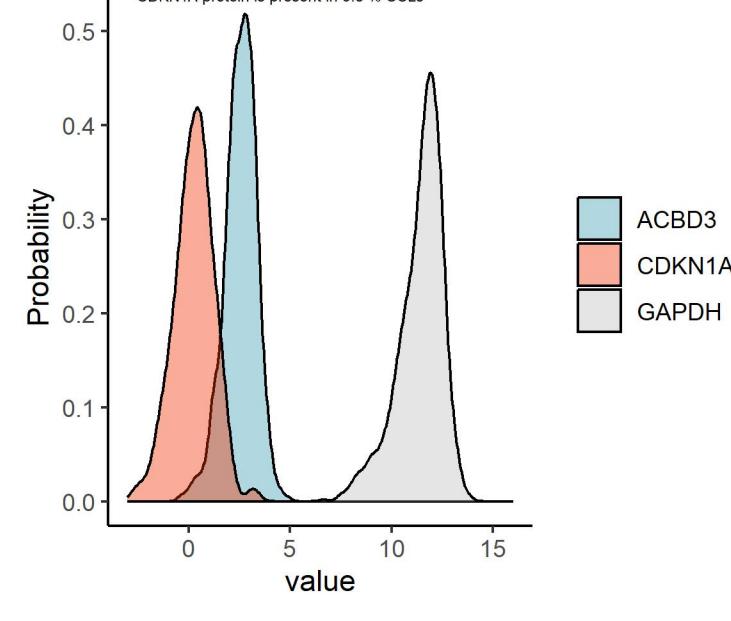
Sanger Institute Protein Database 2 (DB2), protein presence is less certain

8498 proteins in same 949 CCLs

Histogram of CDKN1A protein compared to proteins with low and high abundance



Density plot of CDKN1A protein compared to proteins with low and high abundance



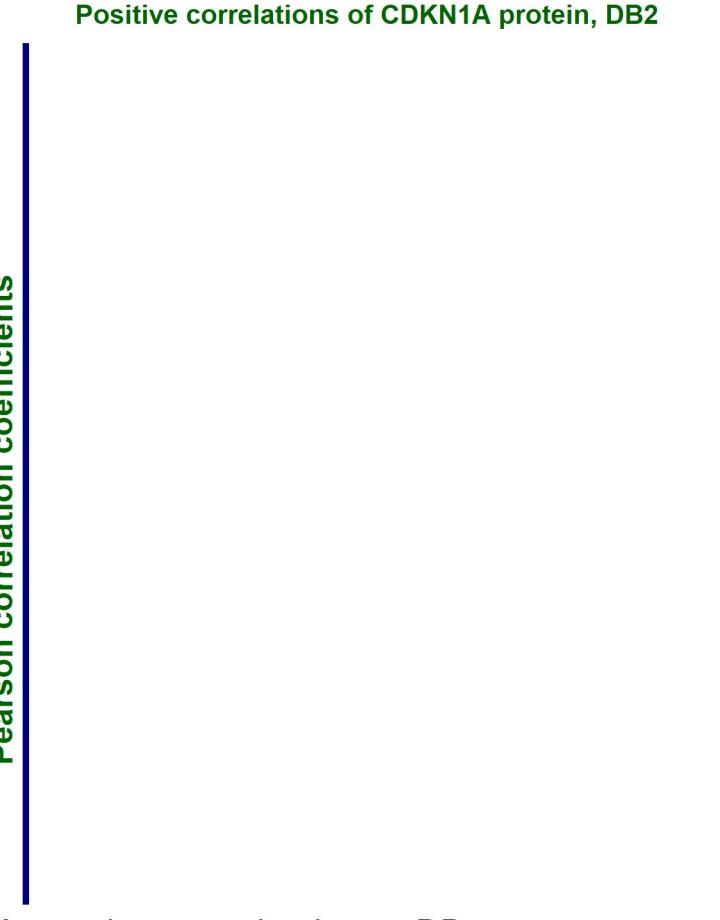
Negative correlations of CDKN1A protein, DB2

Pearson correlation coefficients



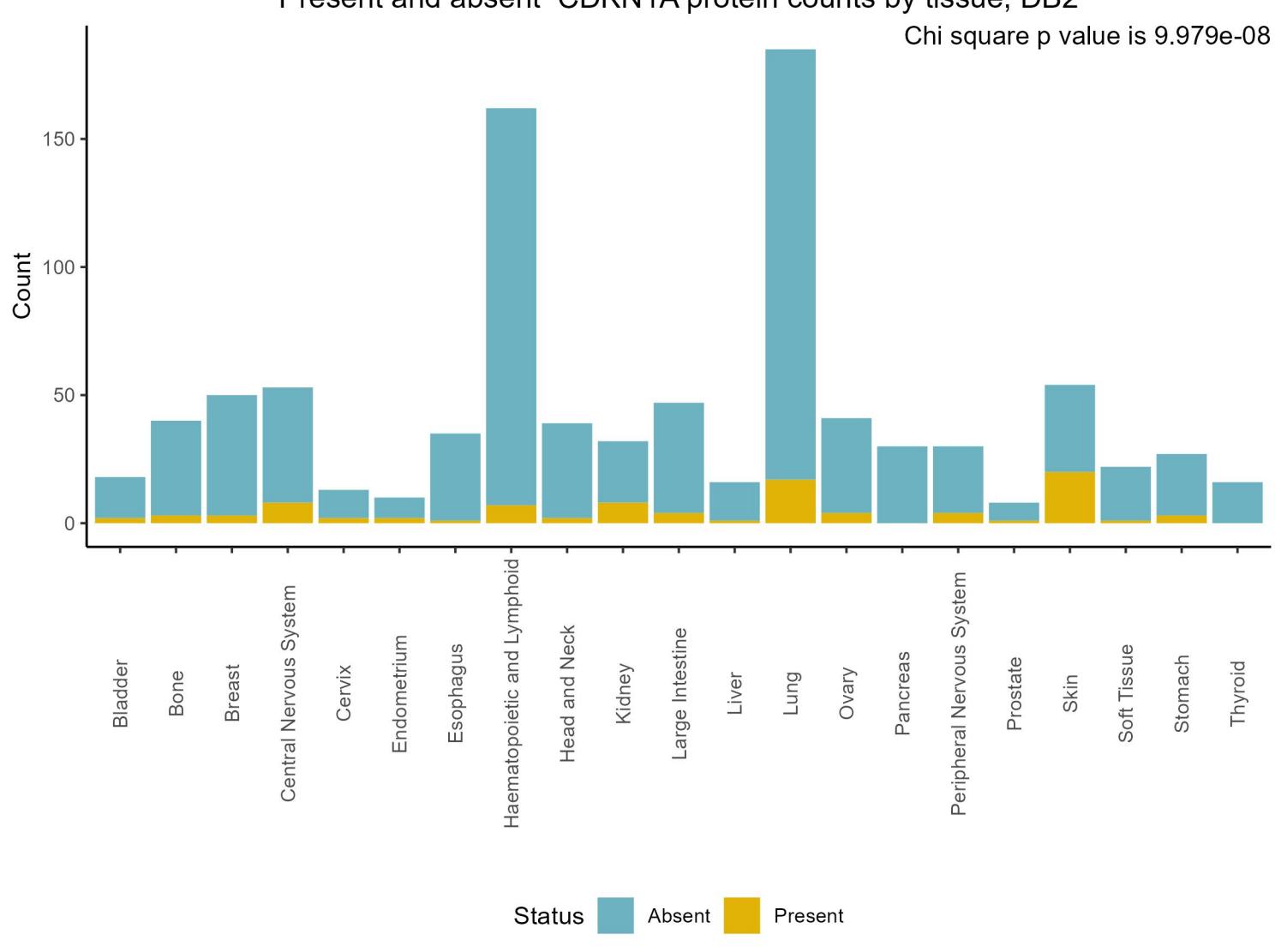
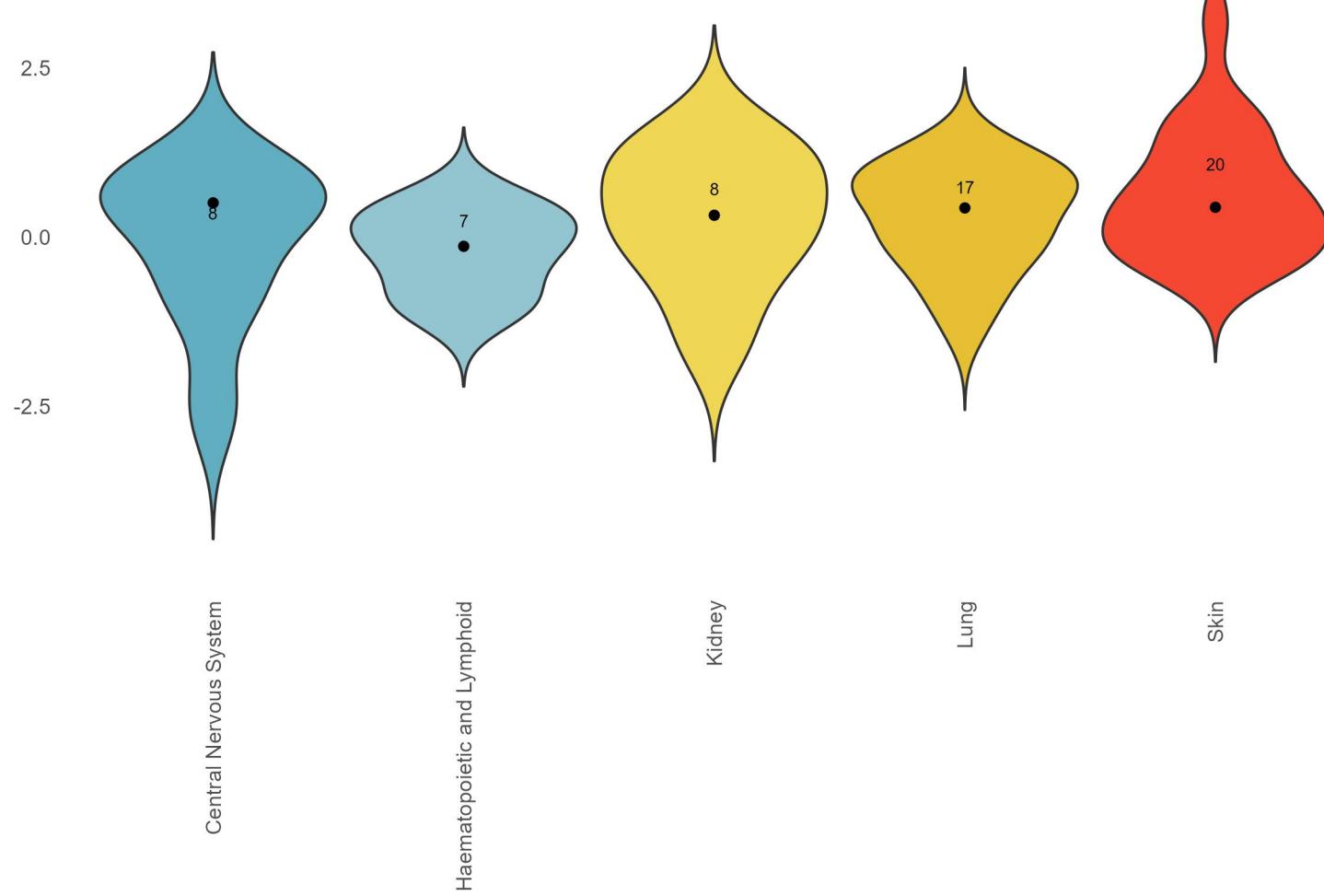
Positive correlations of CDKN1A protein, DB2

Pearson correlation coefficients



Amount of CDKN1A protein, number of CCLs where it is present by tissue, DB2

ANOVA p value is 2.146e-02

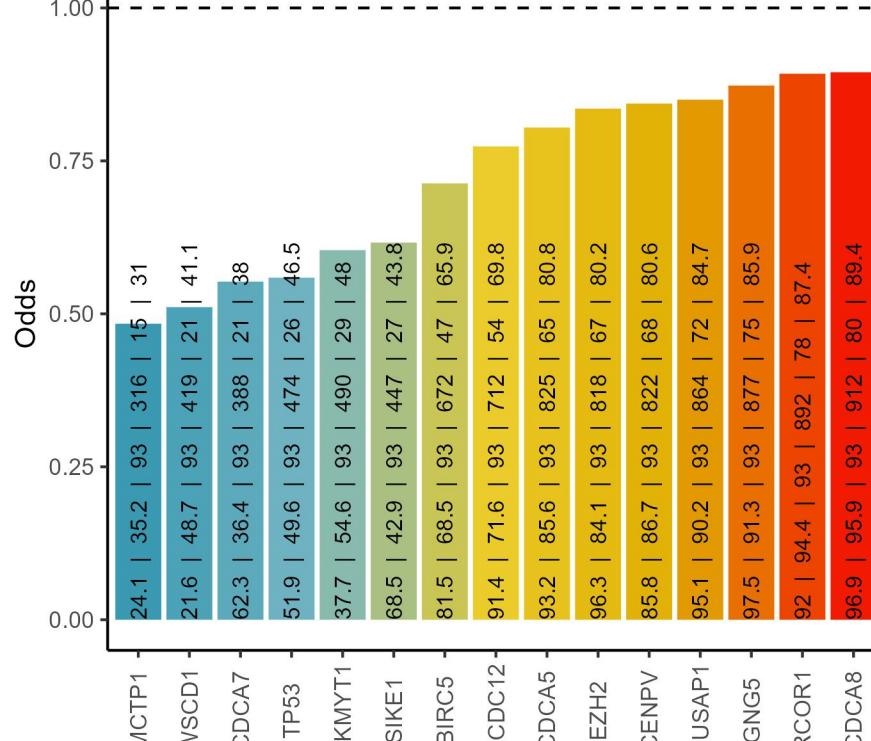


Cooccurrence with CDKN1A protein, DB2

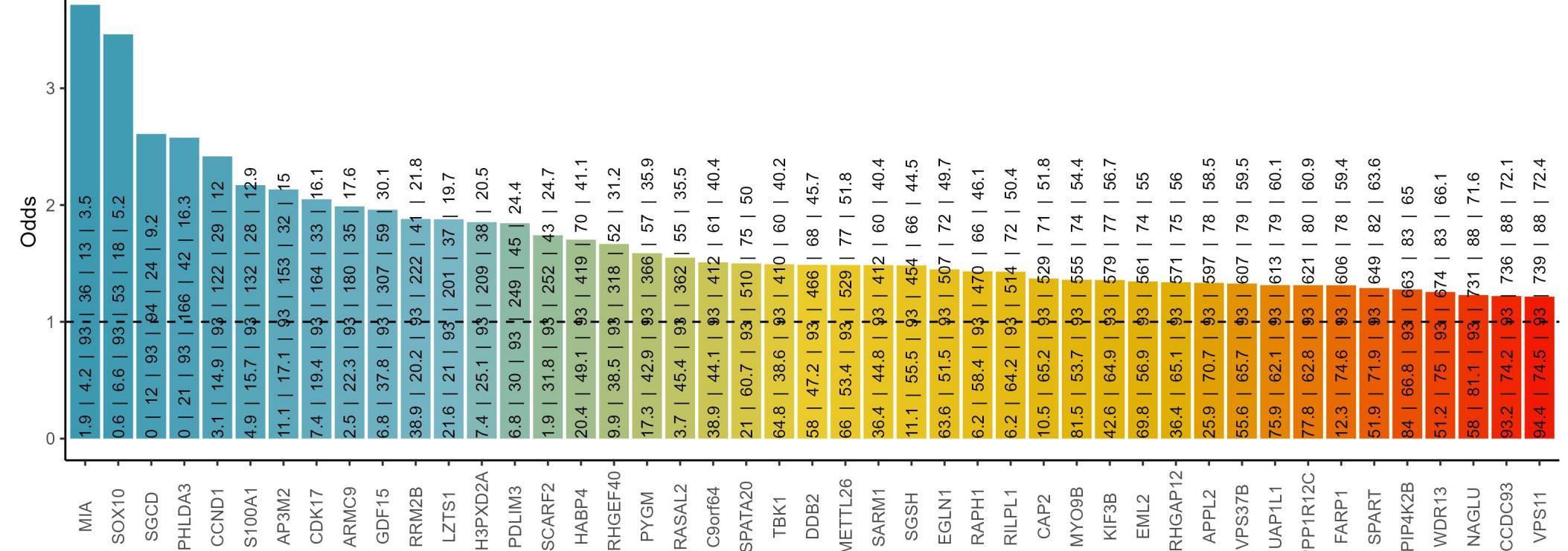
% of CDKN1A in blood cancers: 4.3 ; % of CDKN1A in solid cancers: 11

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CDKN1A | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

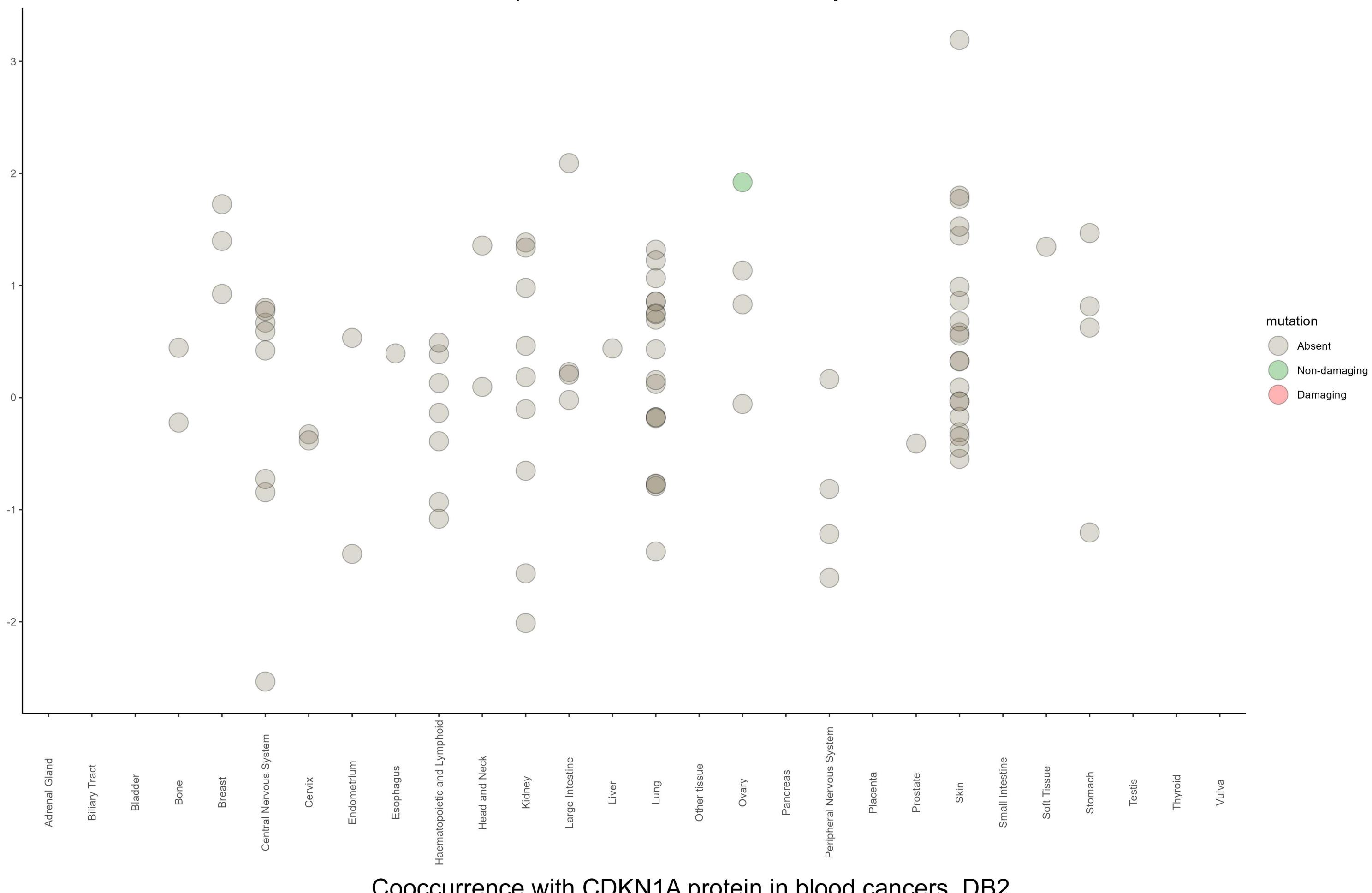
Negative cooccurrence



Positive cooccurrence

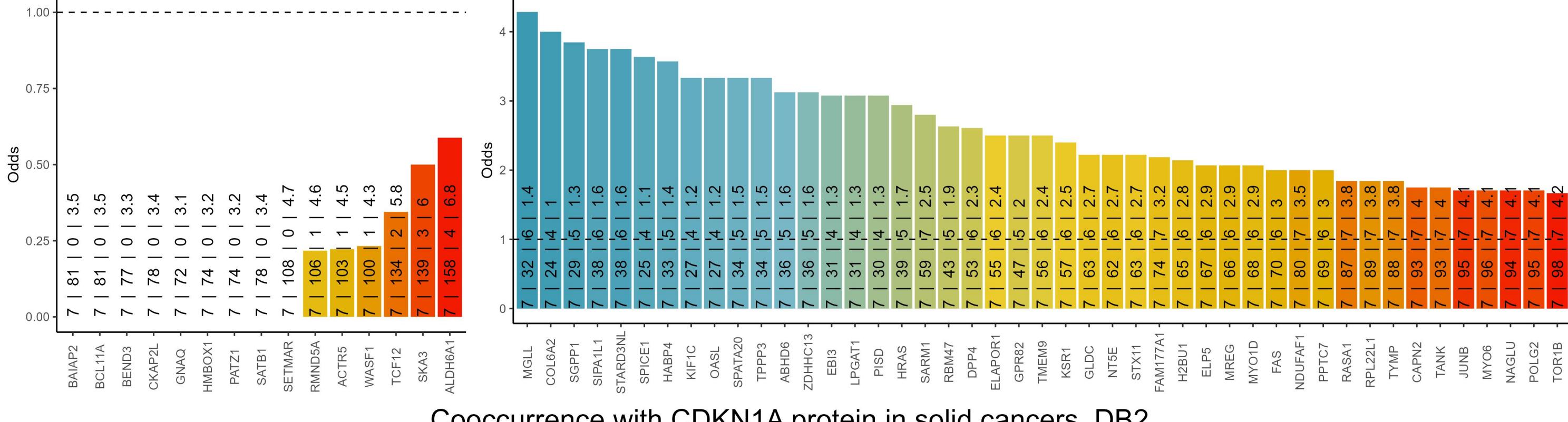


Amount of CDKN1A protein and mutation status by tissue, DB2



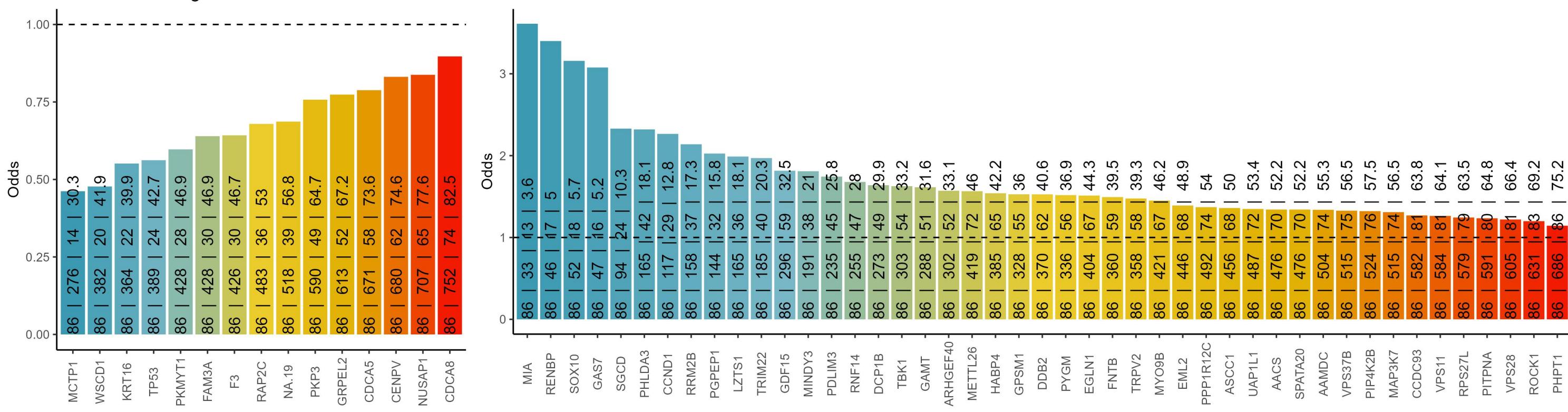
Cooccurrence with CDKN1A protein in blood cancers, DB2

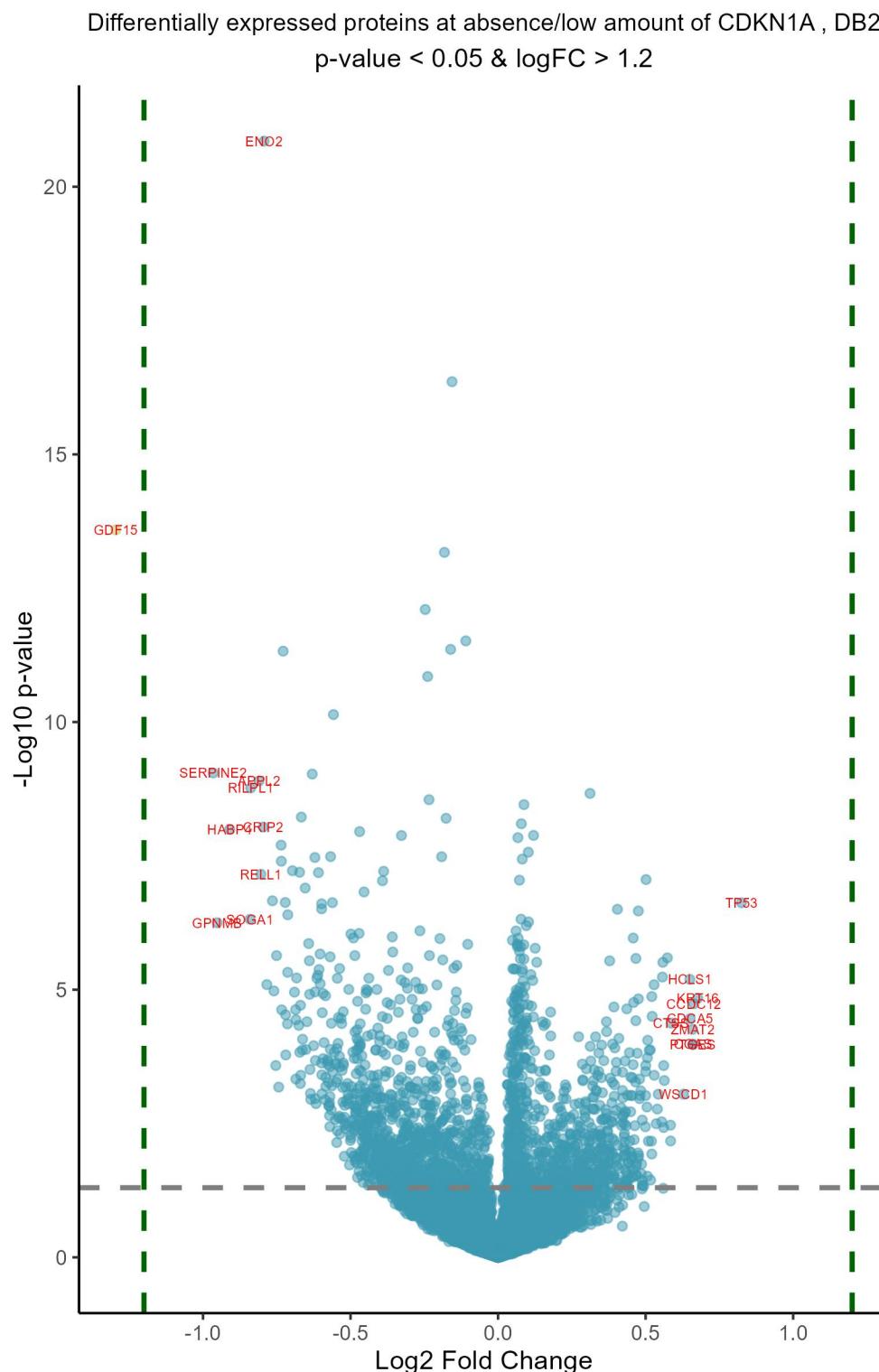
The text in the bars: incidence of CDKN1A | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Cooccurrence with CDKN1A protein in solid cancers, DB2

The text in the bars: incidence of CDKN1A | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

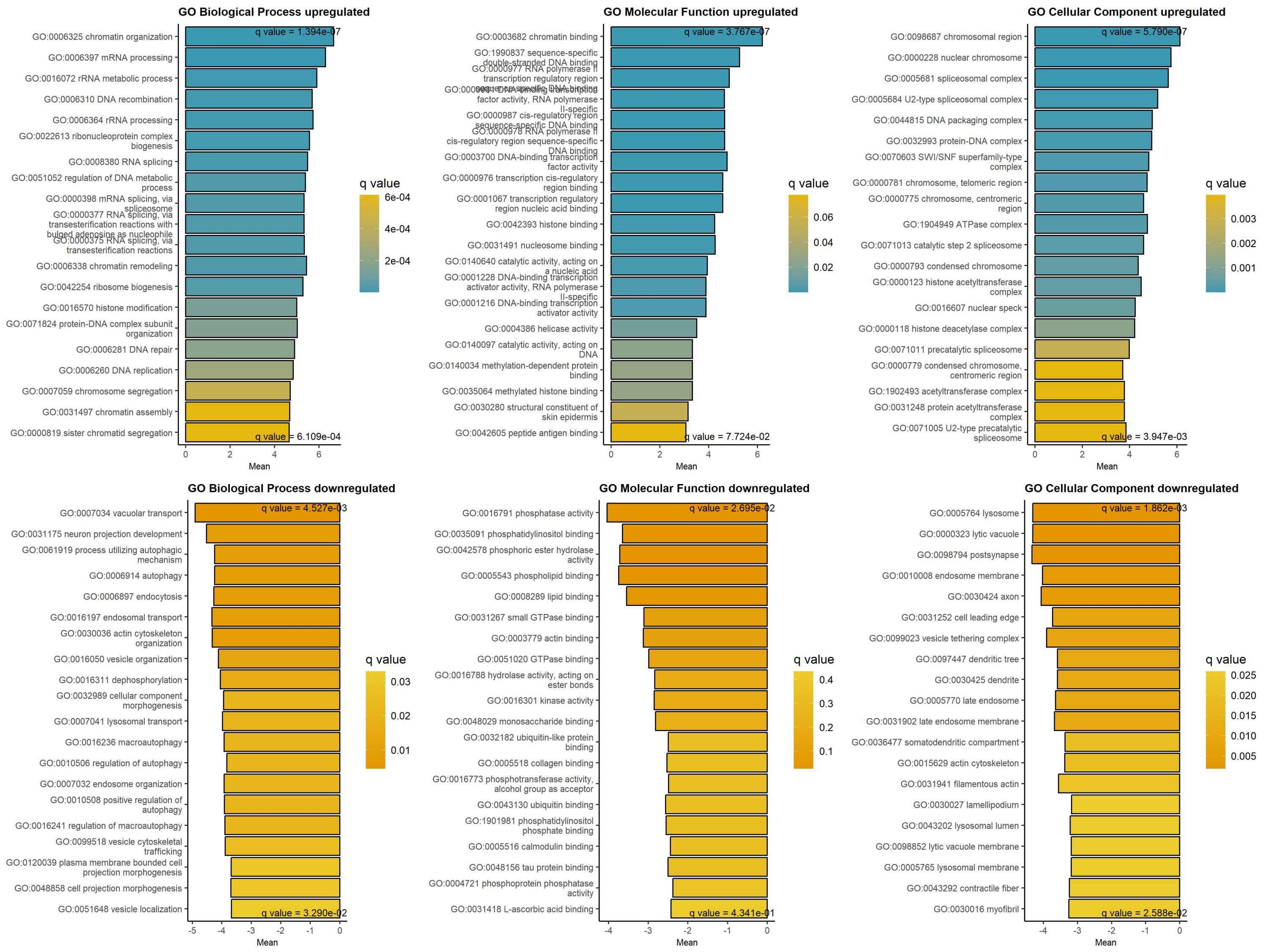




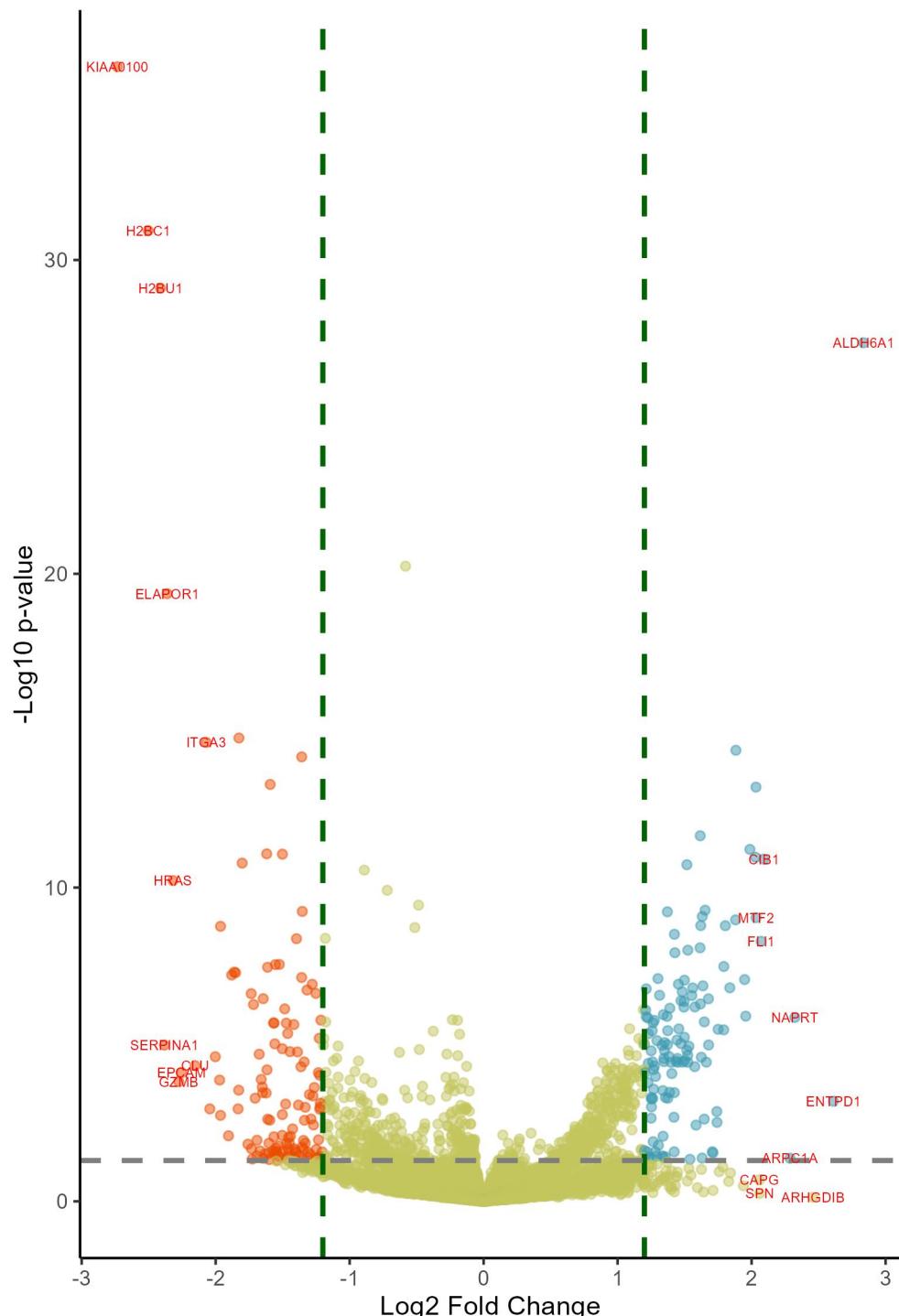
Downregulated at low/absent CDKN1A Upregulated at low/absent CDKN1A

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.3	5.38e-11	GDF15	growth differentiation factor 15	0.83	4.15e-05	TP53	tumor protein p53
-0.97	6.02e-07	SERPINE2	serpin family E member 2	0.68	8.15e-04	KRT16	keratin 16
-0.95	8.26e-05	GPNMB	glycoprotein nmb	0.66	9.63e-04	CCDC12	coiled-coil domain containing 12
-0.91	3.67e-06	HABP4	hyaluronan binding protein 4	0.66	3.21e-03	CGAS	cyclic GMP-AMP synthase
-0.84	7.36e-05	SOGA1	suppressor of glucose, autophagy as	0.66	2.04e-03	ZMAT2	zinc finger matrin-type 2
-0.84	9.52e-07	RILPL1	Rab interacting lysosomal protein I	0.66	3.27e-03	PTGES	prostaglandin E synthase
-0.81	7.54e-07	APPL2	adaptor protein, phosphotyrosine in	0.65	1.47e-03	CDCA5	cell division cycle associated 5
-0.8	1.50e-05	RELL1	RELT like 1	0.65	4.79e-04	HCLS1	hematopoietic cell-specific Lyn sub
-0.8	3.49e-06	CRIP2	cysteine rich protein 2	0.63	1.47e-02	WSCD1	WSC domain containing 1
-0.79	5.87e-18	ENO2	enolase 2	0.59	1.68e-03	CTSS	cathepsin S
-0.78	5.63e-04	IGFBP7	insulin like growth factor binding	0.58	5.76e-02	CENPV	centromere protein V
-0.76	4.06e-05	EGLN1	egl-9 family hypoxia inducible fact	0.58	3.66e-02	KRT85	keratin 85
-0.76	6.75e-04	PYGM	glycogen phosphorylase, muscle asso	0.57	2.53e-04	AURKB	aurora kinase B
-0.75	6.13e-03	TTC3	tetratricopeptide repeat domain 3	0.56	9.82e-03	RAD18	RAD18 E3 ubiquitin protein ligase
-0.75	2.36e-04	DDB2	damage specific DNA binding protein	0.56	3.94e-02	CIB1	calcium and integrin binding 1
-0.74	1.19e-02	S100A1	S100 calcium binding protein A1	0.56	6.13e-03	EZH2	enhancer of zeste 2 polycomb repres
-0.74	5.96e-06	TUBB2A	tubulin beta 2A class IIa	0.56	2.04e-01	VAMP8	vesicle associated membrane protein
-0.73	9.81e-06	UAP1L1	UDP-N-acetylglucosamine pyrophospho	0.56	2.80e-04	SIKE1	suppressor of IKBKE 1
-0.73	1.12e-03	SIRPA	signal regulatory protein alpha	0.56	4.55e-04	CD55	CD55 molecule (Cromer blood group)
-0.73	4.40e-09	RPS27L	ribosomal protein S27 like	0.55	3.31e-02	HLA-F	major histocompatibility complex, c
-0.72	4.15e-05	NYAP1	neuronal tyrosine phosphorylated ph	0.54	1.47e-02	GATM	glycine amidinotransferase
-0.72	1.32e-03	DAB2	DAB adaptor protein 2	0.54	2.26e-02	C1orf131	chromosome 1 open reading frame 131
-0.72	4.40e-03	CYP27A1	cytochrome P450 family 27 subfamily	0.54	3.51e-02	SMIM8	small integral membrane protein 8
-0.71	1.69e-03	BRCA1	BRCA1 DNA repair associated	0.53	8.25e-03	DNTTIP1	deoxynucleotidyltransferase termina
-0.71	3.81e-04	KHDRBS3	KH RNA binding domain containing, s	0.53	5.63e-04	BIRC5	baculoviral IAP repeat containing 5
-0.71	6.30e-05	DPYSL3	dihydropyrimidinase like 3	0.52	1.40e-03	MEN1	menin 1
-0.7	1.43e-05	PPP1R12C	protein phosphatase 1 regulatory su	0.52	7.65e-04	MCTP1	multiple C2 and transmembrane domai
-0.69	6.80e-04	P3H3	prolyl 3-hydroxylase 3	0.52	8.38e-02	DENND2A	DENN domain containing 2A
-0.69	1.12e-03	SGSH	N-sulfoglucosamine sulfohydrolase	0.52	5.77e-02	DSC2	desmocollin 2

GAGE analysis on upregulated and downregulated proteins at low/absent CDKN1A protein, DB2

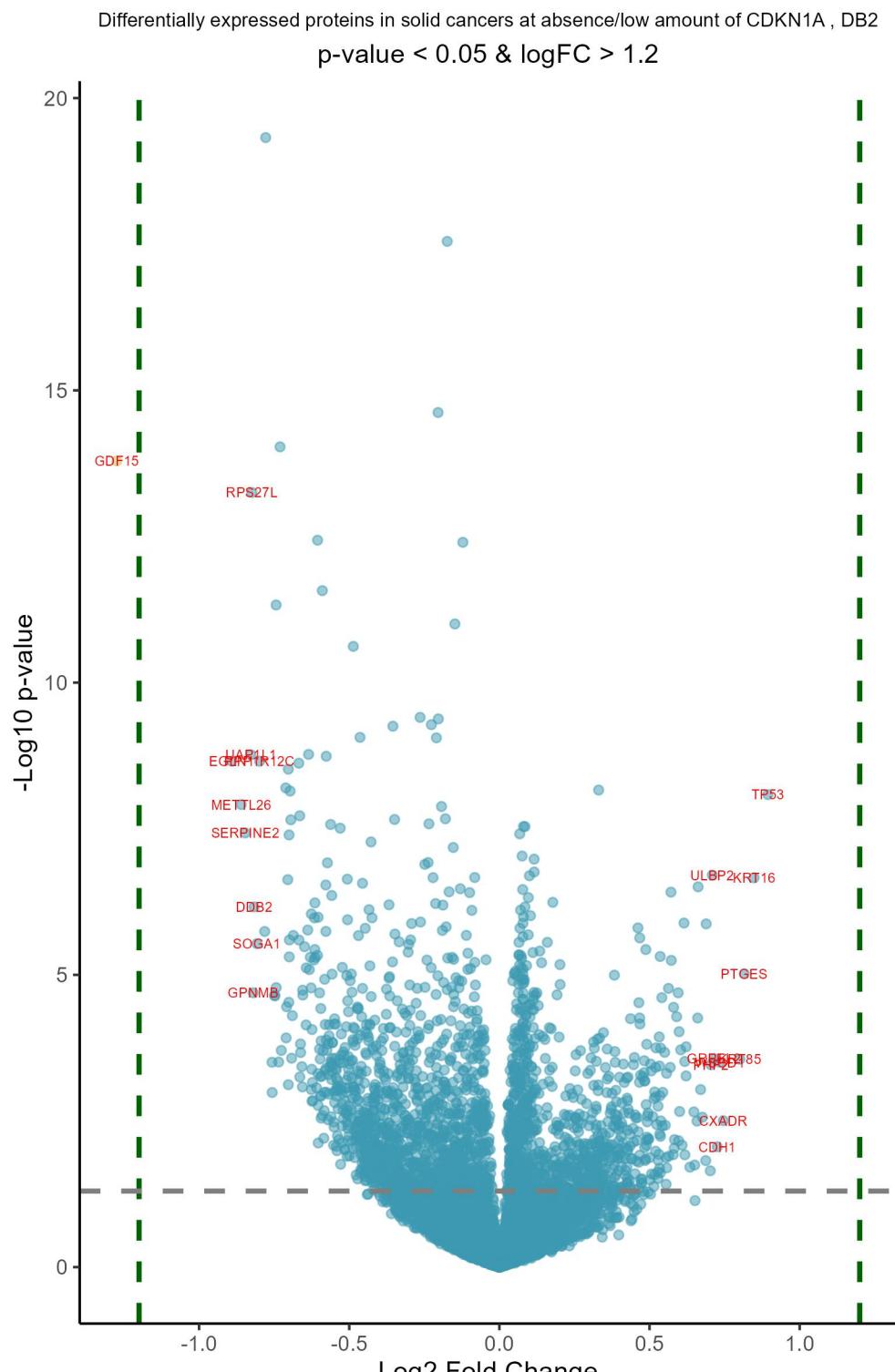


p-value < 0.05 & logFC > 1.2



Downregulated in blood cancers at low/absent CDKN1A Upregulated in blood cancers at low/absent CDKN1A

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.73	5.79e-33	KIAA0100	KIAA0100	2.84	9.09e-25	ALDH6A1	aldehyde dehydrogenase 6 family mem
-2.5	4.84e-28	H2BC1	H2B clustered histone 1	2.61	1.88e-02	ENTPD1	ectonucleoside triphosphate diphosp
-2.41	2.19e-26	H2BU1	H2B.U histone 1	2.46	9.84e-01	ARHGDI1	Rho GDP dissociation inhibitor beta
-2.38	7.35e-04	SERPINA1	serpin family A member 1	2.32	1.41e-04	NAPRT	nicotinate phosphoribosyltransferas
-2.36	6.02e-17	ELAPOR1	endosome-lysosome associated apopto	2.29	3.94e-01	ARPC1A	actin related protein 2/3 complex s
-2.32	2.18e-08	HRAS	HRas proto-oncogene, GTPase	2.09	5.47e-09	CIB1	calcium and integrin binding 1
-2.28	6.21e-03	GZMB	granzyme B	2.07	1.11e-06	FLI1	Fli-1 proto-oncogene, ETS transcri
-2.25	3.62e-03	EPCAM	epithelial cell adhesion molecule	2.06	9.84e-01	SPN	sialophorin
-2.15	2.48e-03	CLU	clusterin	2.06	8.01e-01	CAPG	capping actin protein, gelsolin lik
-2.07	2.20e-12	ITGA3	integrin subunit alpha 3	2.03	2.53e-07	MTF2	metal response element binding tran
-2.04	2.87e-02	CTSL	cathepsin L	2.03	4.05e-11	AAMDC	adipogenesis associated Mth938 doma
-2	1.47e-03	SCIN	scinderin	2.03	5.00e-09	TCF12	transcription factor 12
-1.97	5.65e-03	DCD	dermcidin	1.99	3.39e-09	URM1	ubiquitin related modifier 1
-1.96	4.23e-02	RCN3	reticulocalbin 3	1.96	1.33e-04	GRAMD1C	GRAM domain containing 1C
-1.96	4.23e-07	MAP7	microtubule associated protein 7	1.95	1.37e-05	STAG2	stromal antigen 2
-1.9	1.38e-01	APOM	apolipoprotein M	1.94	9.02e-01	RCSD1	RCSD domain containing 1
-1.88	1.05e-05	IL1RAP	interleukin 1 receptor accessory pr	1.88	3.52e-12	SCLY	seleocysteine lyase
-1.86	8.83e-06	ITIH2	inter-alpha-trypsin inhibitor heavy	1.88	2.88e-07	NT5C	5', 3'-nucleotidase, cytosolic
-1.85	9.02e-06	MYO1D	myosin ID	1.84	6.55e-01	SLC1A4	solute carrier family 1 member 4
-1.83	2.87e-02	ASCL3	achaete-scute family bHLH transcrip	1.84	2.28e-05	ELMO2	engulfment and cell motility 2
-1.83	1.02e-02	TMEM9	transmembrane protein 9	1.83	8.24e-01	AKAP12	A-kinase anchoring protein 12
-1.83	1.79e-12	JUNB	JunB proto-oncogene, AP-1 transcrip	1.8	4.16e-07	BCR	BCR activator of RhoGEF and GTPase
-1.8	6.95e-09	UVRAG	UV radiation resistance associated	1.79	6.10e-06	ASL	argininosuccinate lyase
-1.76	2.07e-01	CD274	CD274 molecule	1.79	2.92e-04	TPM2	tropomyosin 2
-1.73	3.19e-05	ELP5	elongator acetyltransferase complex	1.78	5.33e-01	ASF1A	anti-silencing function 1A histone
-1.73	2.64e-01	GALNT3	polypeptide N-acetylgalactosaminylt	1.76	6.28e-01	MSI2	musashi RNA binding protein 2
-1.73	4.05e-01	SERPINA4	serpin family B member 4	1.75	2.84e-04	LCP2	lymphocyte cytosolic protein 2
-1.72	6.27e-05	NDUFA11	NADH:ubiquinone oxidoreductase comp	1.74	6.46e-02	CACNA1B	calcium voltage-gated channel subun
-1.71	1.58e-02	APOC3	apolipoprotein C3	1.74	3.36e-02	ALAD	aminolevulinate dehydratase

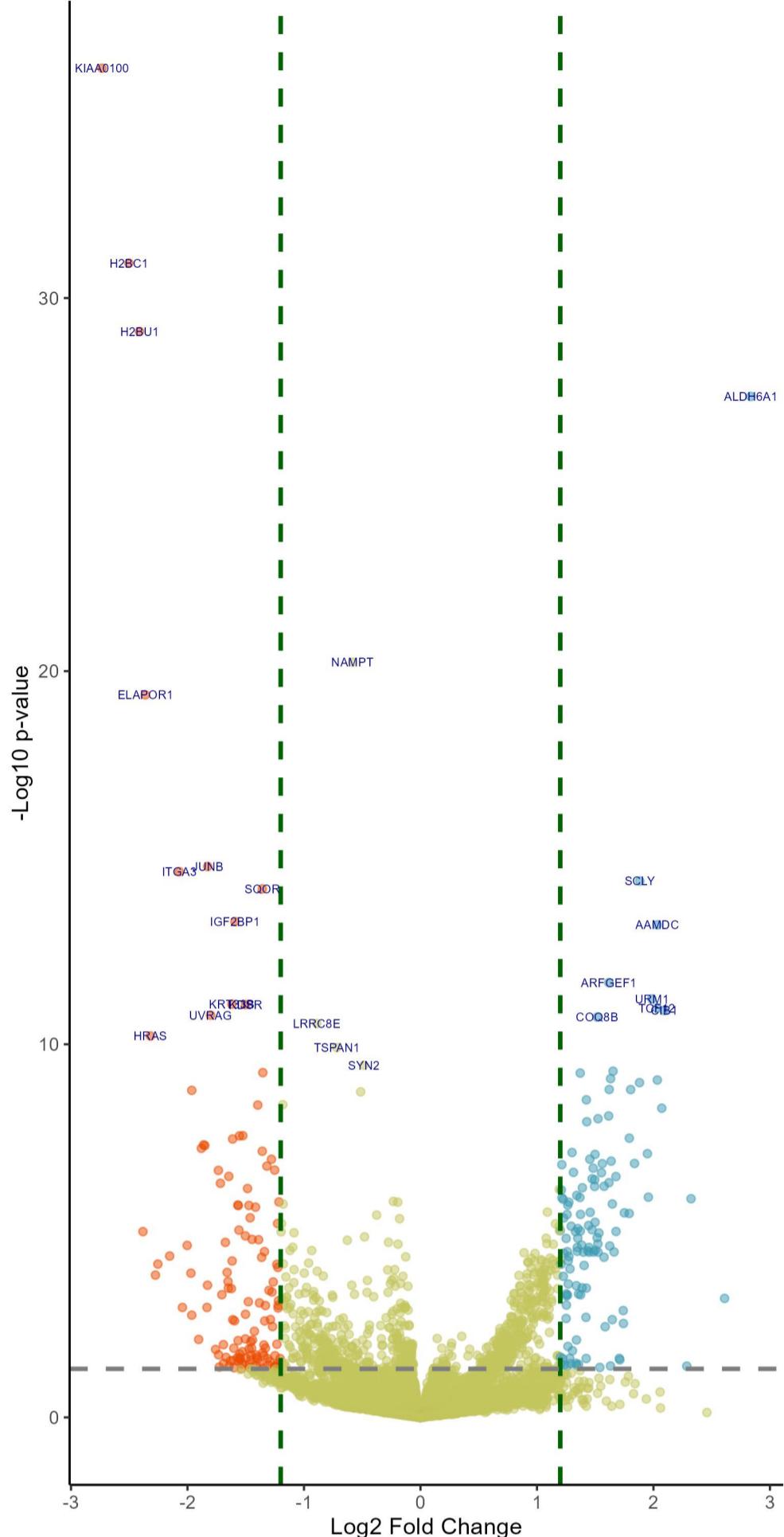


Downregulated in solid cancers at low/absent CDKN1A Upregulated in solid cancers at low/absent CDKN1A

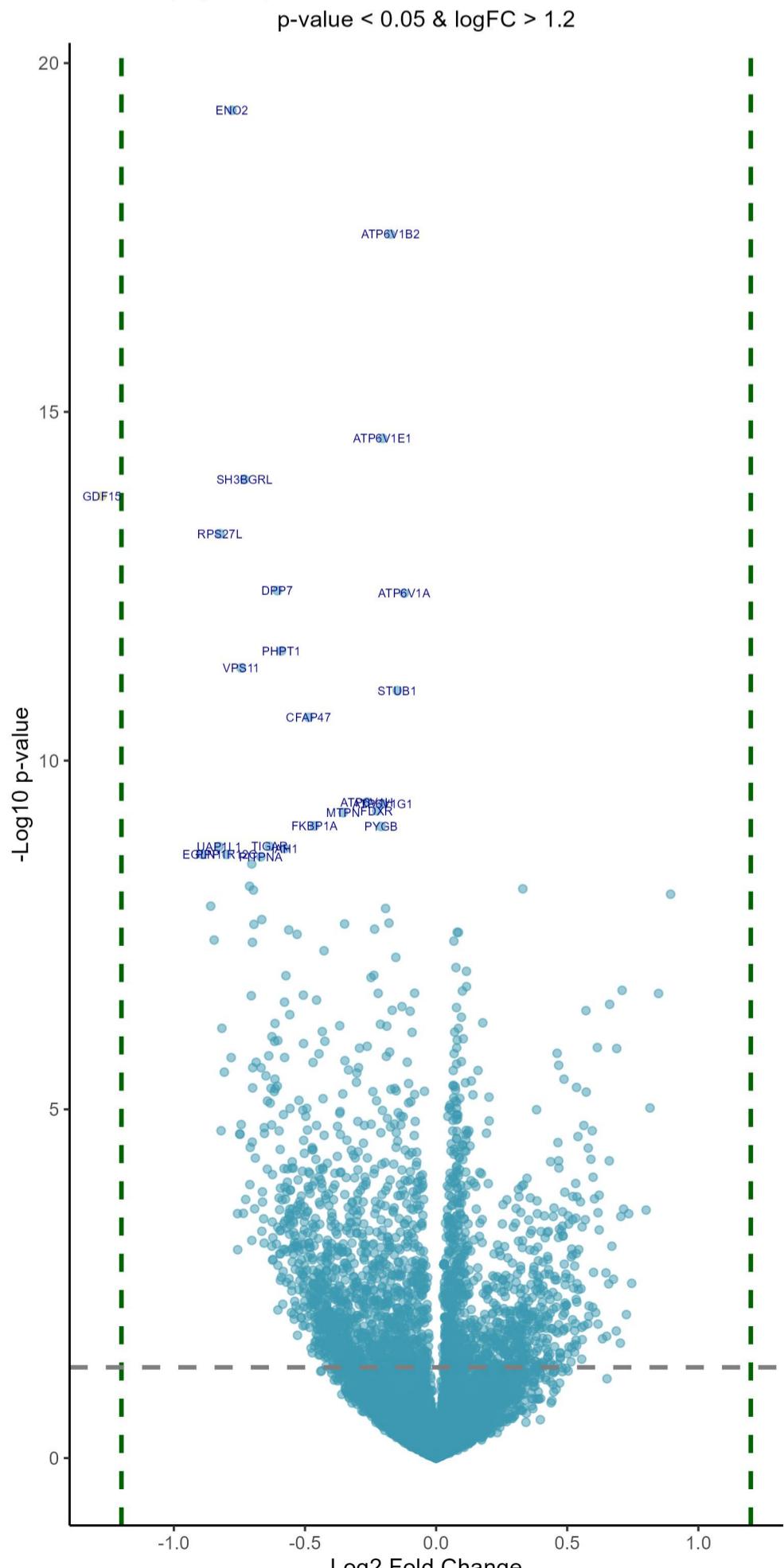
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.27	2.25e-11	GDF15	growth differentiation factor 15	0.89	2.30e-06	TP53	tumor protein p53
-0.89	7.72e-07	EGLN1	egl-9 family hypoxia inducible fact	0.85	3.20e-05	KRT16	keratin 16
-0.86	3.29e-06	METTL26	methyltransferase like 26	0.82	5.11e-04	PTGES	prostaglandin E synthase
-0.85	7.44e-06	SERPINE2	serpin family E member 2	0.8	5.26e-03	KRT85	keratin 85
-0.83	6.81e-07	UAP1L1	UDP-N-acetylglucosamine pyrophospho	0.75	2.74e-02	CXADR	CXADR Ig-like cell adhesion molecul
-0.82	6.68e-11	RPS27L	ribosomal protein S27 like	0.73	5.71e-03	WSCD1	WSC domain containing 1
-0.82	8.56e-04	GPNMB	glycoprotein nmb	0.73	5.56e-02	CDH1	cadherin 1
-0.82	7.59e-05	DDB2	damage specific DNA binding protein	0.71	5.16e-03	GRPEL2	GrpE like 2, mitochondrial
-0.81	2.17e-04	SOGA1	suppressor of glucose, autophagy as	0.71	3.11e-05	ULBP2	UL16 binding protein 2
-0.8	7.72e-07	PPP1R12C	protein phosphatase 1 regulatory su	0.7	6.08e-03	PHF2	PHD finger protein 2
-0.78	1.53e-04	HABP4	hyaluronan binding protein 4	0.7	1.06e-01	PKP3	plakophilin 3
-0.78	1.99e-16	ENO2	enolase 2	0.69	1.23e-04	KRT79	keratin 79
-0.76	5.71e-03	TTC3	tetratricopeptide repeat domain 3	0.69	8.02e-02	PODXL	podocalyxin like
-0.76	1.28e-02	S100A1	S100 calcium binding protein A1	0.68	2.48e-02	SDC4	syndecan 4
-0.75	9.12e-04	IGFBP7	insulin like growth factor binding	0.67	1.19e-02	DSC2	desmocollin 2
-0.75	9.20e-04	RNF14	ring finger protein 14	0.66	4.21e-05	CD55	CD55 molecule (Cromer blood group)
-0.74	3.57e-09	VPS11	VPS11 core subunit of CORVET and HO	0.66	1.78e-03	CDCA5	cell division cycle associated 5
-0.74	7.51e-04	PYGM	glycogen phosphorylase, muscle asso	0.66	2.77e-02	NFIC	nuclear factor I C
-0.73	5.69e-03	RPL22L1	ribosomal protein L22 like 1	0.65	2.21e-01	KRT17	keratin 17
-0.73	1.55e-11	SH3BGRL	SH3 domain binding glutamate rich p	0.65	9.10e-02	S100A14	S100 calcium binding protein A14
-0.73	4.16e-03	TRPV2	transient receptor potential cation	0.65	2.17e-02	GNG10	G protein subunit gamma 10
-0.71	1.96e-06	TUBB2A	tubulin beta 2A class IIa	0.63	9.64e-02	SPINT2	serine peptidase inhibitor, Kunitz
-0.71	3.04e-03	BRCA1	BRCA1 DNA repair associated	0.62	3.80e-03	CGAS	cyclic GMP-AMP synthase
-0.71	1.29e-03	SIRPA	signal regulatory protein alpha	0.62	8.20e-03	ASB2	ankyrin repeat and SOCS box contain
-0.7	3.33e-05	RILPL1	Rab interacting lysosomal protein I	0.62	6.89e-02	EPCAM	epithelial cell adhesion molecule
-0.7	9.75e-07	AMDHD2	amidohydrolase domain containing 2	0.62	5.61e-03	ZMAT2	zinc finger matrin-type 2
-0.7	1.05e-02	ACP5	acid phosphatase 5, tartrate resist	0.61	1.23e-04	AURKB	aurora kinase B
-0.7	1.13e-03	NUDT4	nudix hydrolase 4	0.61	5.33e-02	CENPV	centromere protein V
-0.7	7.67e-06	APPL2	adaptor protein, phosphotyrosine in	0.6	4.12e-03	C1orf116	chromosome 1 open reading frame 116

CDKN1A network, DB2, no Pearson r > 0.3

p-value < 0.05 & logFC > 1.2

Sorted by p values!
Downregulated in blood cancers at low/absent CDKN1A Upregulated in blood cancers at low/absent CDKN1A

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.73	5.79e-33	KIAA0100	KIAA0100	2.84	9.09e-25	ALDH6A1	aldehyde dehydrogenase 6 family mem
-2.5	4.84e-28	H2BC1	H2B clustered histone 1	1.88	3.52e-12	SCLY	seleocysteine lyase
-2.41	2.19e-26	H2BU1	H2B.U histone 1	2.03	4.05e-11	AAMDC	adipogenesis associated Mth938 doma
-0.58	9.58e-18	NAMPT	nicotinamide phosphoribosyltransfer	1.62	1.34e-09	ARFGEF1	ADP ribosylation factor guanine nuc
-2.36	6.02e-17	ELAPOR1	endosome-lysosome associated apopto	1.99	3.39e-09	URM1	ubiquitin related modifier 1
-1.83	1.79e-12	JUNB	JunB proto-oncogene, AP-1 transcr	2.03	5.00e-09	TCF12	transcription factor 12
-2.07	2.20e-12	ITGA3	integrin subunit alpha 3	2.09	5.47e-09	CIB1	calcium and integrin binding 1
-1.36	5.21e-12	SQOR	sulfide quinone oxidoreductase	1.52	7.44e-09	COQ8B	coenzyme Q8B
-1.59	3.60e-11	IGF2BP1	insulin like growth factor 2 mRNA b	1.65	1.69e-07	ATF2	activating transcription factor 2
-1.62	4.25e-09	KRT33B	keratin 33B	1.37	1.77e-07	F8A1	coagulation factor VIII associated
-1.5	4.25e-09	KDSR	3-ketodihydrophingosine reductase	1.63	2.40e-07	TRAF2	TNF receptor associated factor 2
-1.8	6.95e-09	UVRAG	UV radiation resistance associated	2.03	2.53e-07	MTF2	metal response element binding tran
-0.89	1.06e-08	LRRC8E	leucine rich repeat containing 8 VR	1.88	2.88e-07	NT5C	5', 3'-nucleotidase, cytosolic
-2.32	2.18e-08	HRAS	HRas proto-oncogene, GTPase	1.62	4.16e-07	ACTR6	actin related protein 6
-0.72	4.26e-08	TSPAN1	tetraspanin 1	1.8	4.16e-07	BCR	BCR activator of RhoGEF and GTPase
-0.49	1.22e-07	SYN2	synapsin II	1.42	7.16e-07	PCID2	PCI domain containing 2
-1.35	1.77e-07	IQCA1	IQ motif containing with AAA domain	2.07	1.11e-06	FLI1	Fli-1 proto-oncogene, ETS transcrip
-1.96	4.23e-07	MAP7	microtubule associated protein 7	1.62	1.74e-06	AP1S2	adaptor related protein complex 1 s
-0.51	4.50e-07	CES2	carboxylesterase 2	1.52	2.02e-06	DIS3L2	DIS3 like 3'-5' exoribonuclease 2
-1.18	9.37e-07	SERPINB1	serpin family B member 1	1.43	2.37e-06	KNTC1	kinetochore associated 1
-1.4	9.37e-07	MPRIP	myosin phosphatase Rho interacting	1.79	6.10e-06	ASL	argininosuccinate lyase
-1.52	5.43e-06	COL1A2	collagen type I alpha 2 chain	1.3	1.31e-05	BRMS1	BRMS1 transcriptional repressor and
-1.55	5.43e-06	RPL22L1	ribosomal protein L22 like 1	1.95	1.37e-05	STAG2	stromal antigen 2
-1.61	6.29e-06	PARD3B	par-3 family cell polarity regulato	1.5	1.41e-05	ASAP1	ArfGAP with SH3 domain, ankyrin rep
-1.86	8.83e-06	ITIH2	inter-alpha-trypsin inhibitor heavy	1.45	1.84e-05	SETMAR	SET domain and mariner transposase
-1.85	9.02e-06	MYO1D	myosin ID	1.64	2.02e-05	SINHCAF	SIN3-HDAC complex associated factor
-1.88	1.05e-05	IL1RAP	interleukin 1 receptor accessory pr	1.84	2.28e-05	ELMO2	engulfment and cell motility 2
-1.36	1.23e-05	MORC4	MORC family CW-type zinc finger 4	1.56	2.28e-05	SSBP3	single stranded DNA binding protein
-1.28	1.84e-05	ATP2B4	ATPase plasma membrane Ca2+ transpo	1.21	2.39e-05	ZMYM2	zinc finger MYM-type containing 2
-1.32	2.56e-05	NIBAN1	niban apoptosis regulator 1	1.48	2.87e-05	DYNLL2	dynein light chain LC8-type 2
-1.25	3.18e-05	AFF2	AF4/FMR2 family member 2	1.31	3.54e-05	SUPT7L	SPT7 like, STAGA complex subunit ga
-1.73	3.19e-05	ELP5	elongator acetyltransferase complex	1.55	3.56e-05	SYTL1	synaptotagmin like 1
-1.65	4.38e-05	CD109	CD109 molecule	1.68	4.38e-05	PAK1	p21 (RAC1) activated kinase 1
-1.72	6.27e-05	NDUFAF1	NADH:ubiquinone oxidoreductase comp	1.47	4.96e-05	ARRB2	arrestin beta 2
-1.48	8.19e-05	SARDH	sarcosine dehydrogenase	1.5	5.17e-05	METTL26	methyltransferase like 26
-0.23	1.62e-04	GLUD1	glutamate dehydrogenase 1	1.62	6.12e-05	KDM5B	lysine demethylase 5B
-1.21	1.64e-04	CFAP251	cilia and flagella associated prote	1.58	7.40e-05	SRR	serine racemase
-0.19	1.64e-04	PSMD2	proteasome 26S subunit ubiquitin re	1.5	7.40e-05	WDFY1	WD repeat and FYVE domain containin
1.19	1.80e-04	KRT19	keratin 19	1.39	7.92e-05	SSBP2	single stranded DNA binding protein

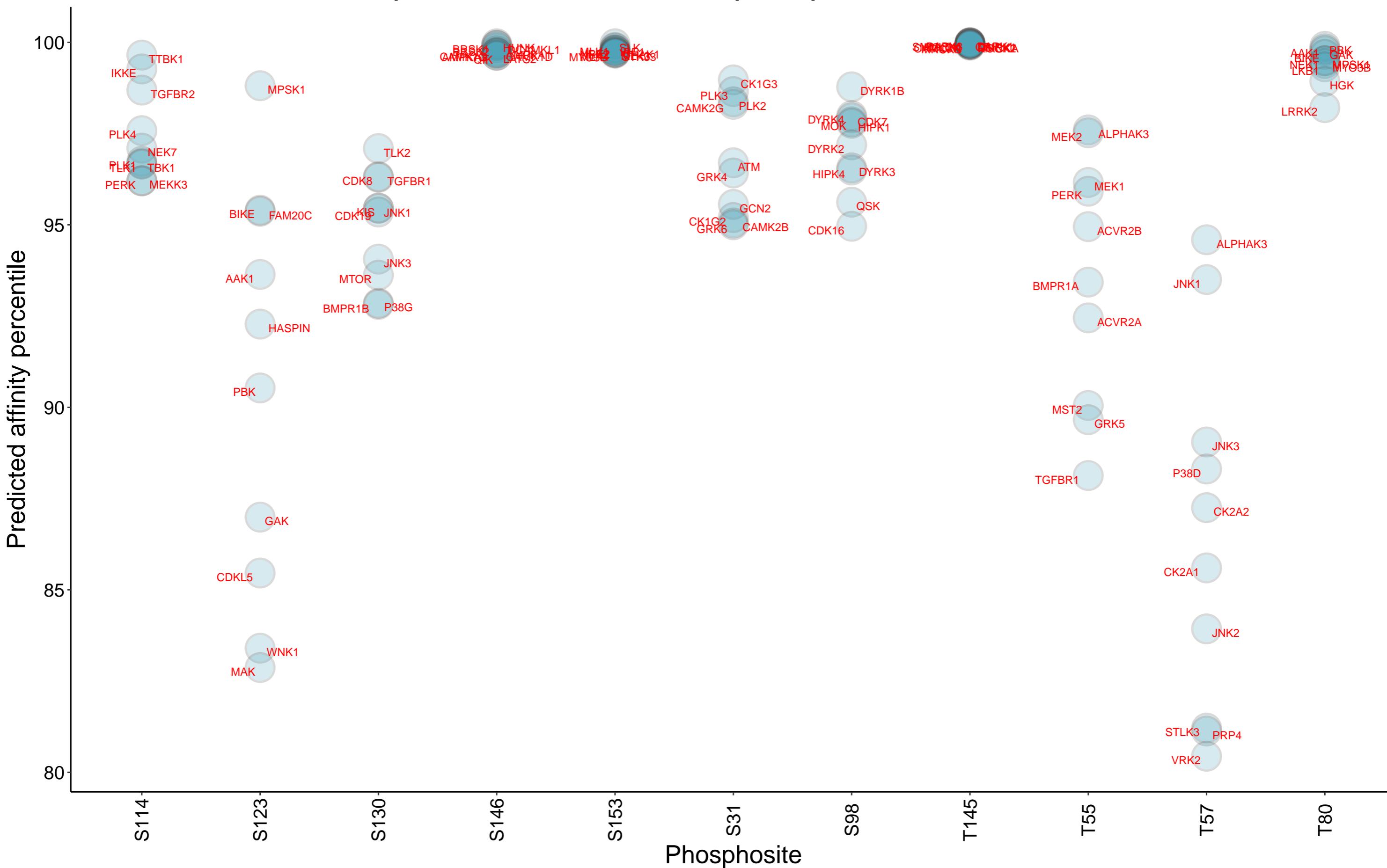
Sorted by p values!
Downregulated in solid cancers at low/absent CDKN1A Upregulated in solid cancers at low/absent CDKN1A

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.78	1.99e-16	ENO2	enolase 2	0.33	2.06e-06	TOP2A	DNA topoisomerase II alpha
-0.17	7.89e-15	ATP6V1B2	ATPase H+ transporting V1 subunit B	0.89	2.30e-06	TP53	tumor protein p53
-0.2	5.00e-12	ATP6V1E1	ATPase H+ transporting V1 subunit E	0.08	6.07e-06	U2SURP	U2 snRNP associated SURP domain con
-0.73	1.55e-11	SH3BGRL	SH3 domain binding glutamate rich p	0.09	6.07e-06	SNRPA1	small nuclear ribonucleoprotein pol
-1.27	2.25e-11	GDF15	growth differentiation factor 15	0.07	7.52e-06	SF3B1	splicing factor 3b subunit 1
-0.82	6.68e-11	RPS27L	ribosomal protein S27 like	0.08	1.65e-05	SF3B6	splicing factor 3b subunit 6
-0.61	3.70e-10	DPP7	dipeptidyl peptidase 7	0.12	1.83e-05	RBM17	RNA binding motif protein 17
-0.12	3.70e-10	ATP6V1A	ATPase H+ transporting V1 subunit A	0.12	2.80e-05	NUP133	nucleoporin 133
-0.59	2.23e-09	PHPT1	phosphohistidine phosphatase 1	0.71	3.11e-05	ULBP2	UL16 binding protein 2
-0.74	3.57e-09	VPS11	VPS11 core subunit of CORVET and HO	0.1	3.12e-05	CHERP	calcium homeostasis endoplasmic ret
-0.15	6.91e-09	STUB1	STIP1 homology and U-box containing	0.85	3.20e-05	KRT16	keratin 16
-0.49	1.55e-08	CFAP47	cilia and flagella associated prote	0.66	4.21e-05	CD55	CD55 molecule (Cromer blood group)
-0.26	2.33e-07	ATP6V1H	ATPase H+ transporting V1 subunit H	0.08	4.54e-05	RBM8A	RNA binding motif protein 8A
-0.2	2.33e-07	ATP6V1G1	ATPase H+ transporting V1 subunit G	0.57	4.87e-05	SIKE1	suppressor of IKBKE 1
-0.23	2.74e-07	FDXR	ferredoxin reductase	0.1	5.78e-05	NUP107	nucleoporin 107
-0.35	2.74e-07	MTPN	myotrophin	0.18	6.87e-05	DDX50	DExD-box helicase 50
-0.46	3.87e-07	FKBP1A	FKBP prolyl isomerase 1A	0.09	7.59e-05	PRPF40A	pre-mRNA processing factor 40 homol
-0.21	3.87e-07	PYGB	glycogen phosphorylase B	0.07	8.34e-05	CDC5L	cell division cycle 5 like
-0.64	6.81e-07	TIGAR	TP53 induced glycolysis regulatory	0.1	1.00e-04	HNRNPH3	heterogeneous nuclear ribonucleopro
-0.83	6.81e-07	UAP1L1	UDP-N-acetylglicosamine pyrophospho	0.08	1.04e-04	SNW1	SNW domain containing 1
-0.58	6.92e-07	IAH1	isoamyl acetate hydrolyzing esteras	0.61	1.23e-04	AURKB	aurora kinase B
-0.89	7.72e-07	EGLN1	egl-9 family hypoxia inducible fact	0.08	1.23e-04	ACIN1	apoptotic chromatin condensation in
-0.8	7.72e-07	PPP1R12C	protein phosphatase 1 regulatory su	0.69	1.23e-04	KRT79	keratin 79
-0.67	8.00e-07	PITPNA	phosphatidylinositol transfer prote	0.46	1.41e-04	SLC9A6	solute carrier family 9 member A6
-0.7	9.75e-07	AMDHD2	amidohydrolase domain containing 2	0.07	1.41e-04	PRPF19	pre-mRNA processing factor 19
-0.71	1.96e-06	TUBB2A	tubulin beta 2A class IIa	0.1	1.71e-04	RBM22	RNA binding motif protein 22
-0.7	2.07e-06	TPMT	thiopurine S-methyltransferase	0.08	1.78e-04	RBM14	RNA binding motif protein 14
-0.86	3.29e-06	METTL26	methyltransferase like 26	0.47	1.84e-04	CWC25	CWC25 spliceosome associated protei
-0.19	3.44e-06						

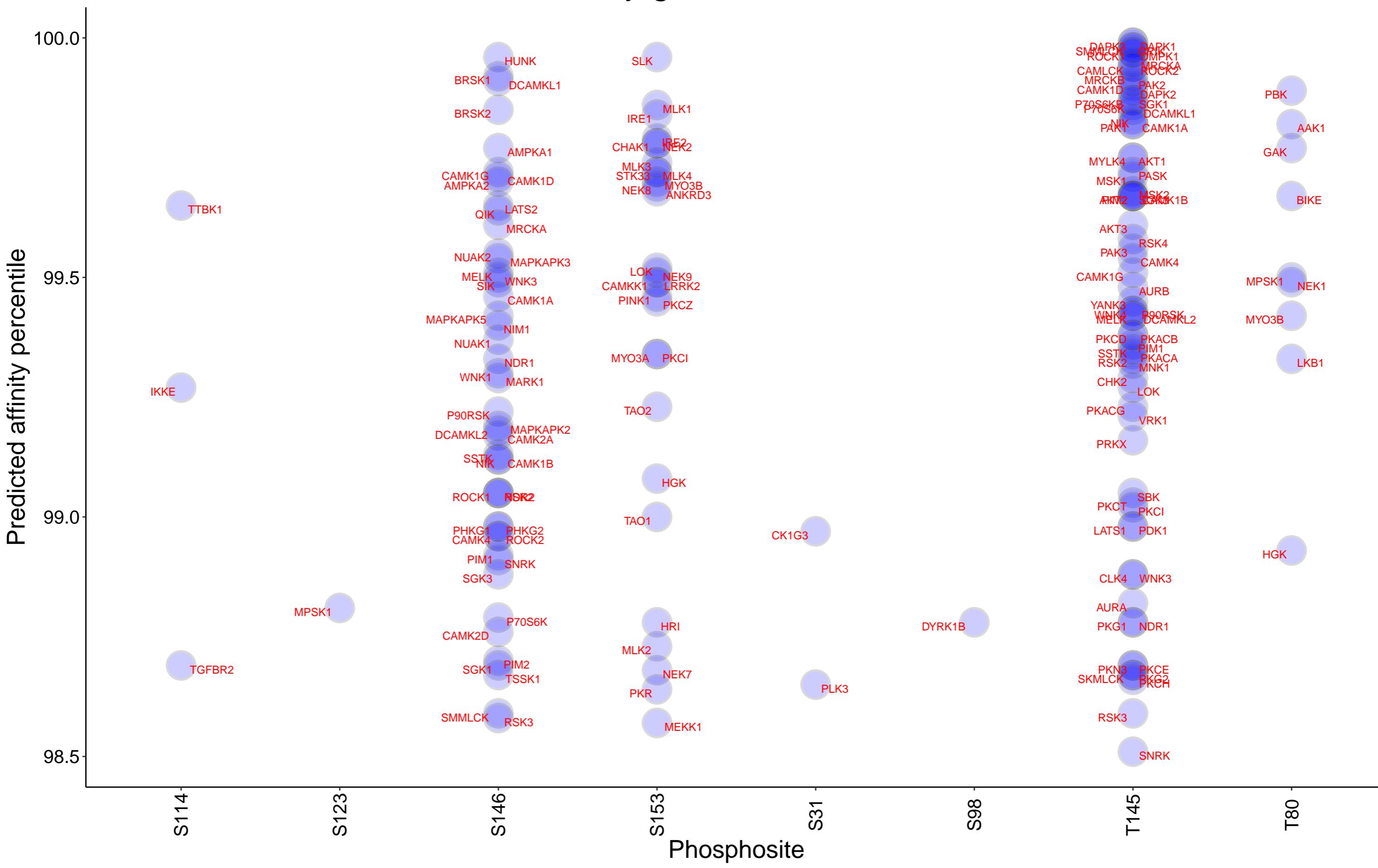
Insufficient number of paired observations in DB2 for CDKN1A

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Top 10 kinases for each phosphosite in CDKN1A



Kinases with affinity greater than 98.5% to CDKN1A



No sufficient number of paired observations in DB2 for CDKN1A