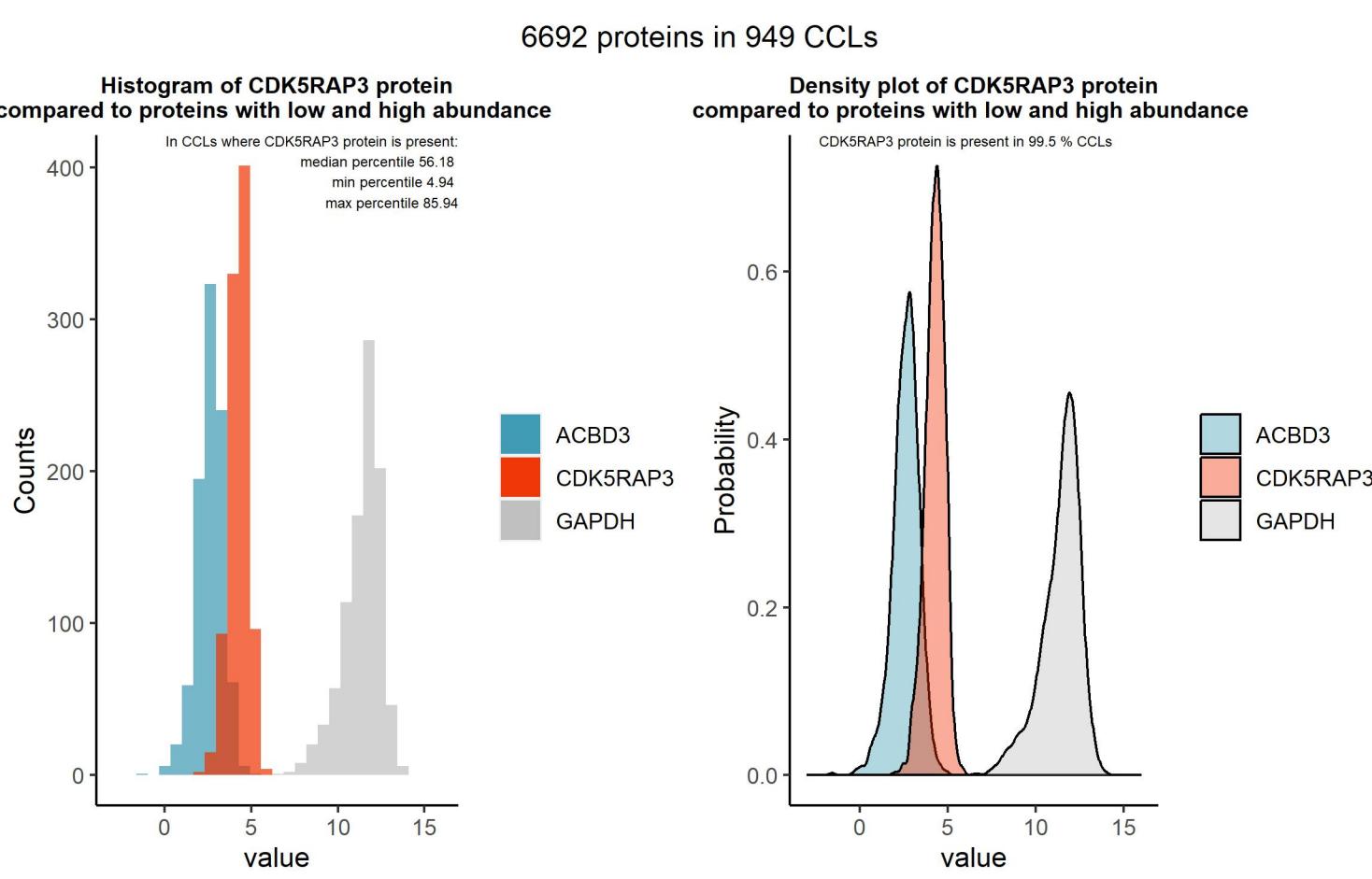


CDK5RAP3

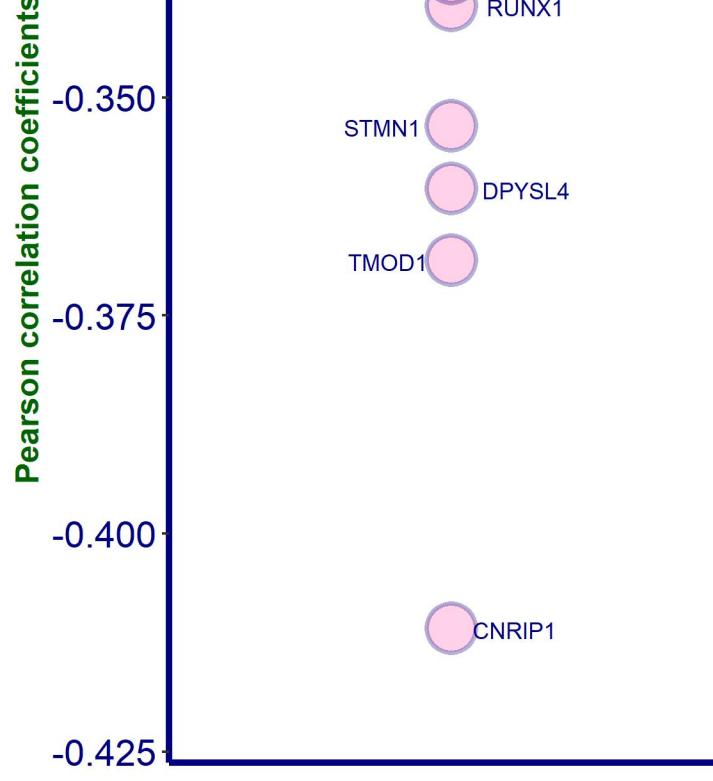
Protein name: CK5P3 ; UNIPROT: Q96JB5 ; Gene name: CDK5 regulatory subunit associated protein 3

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

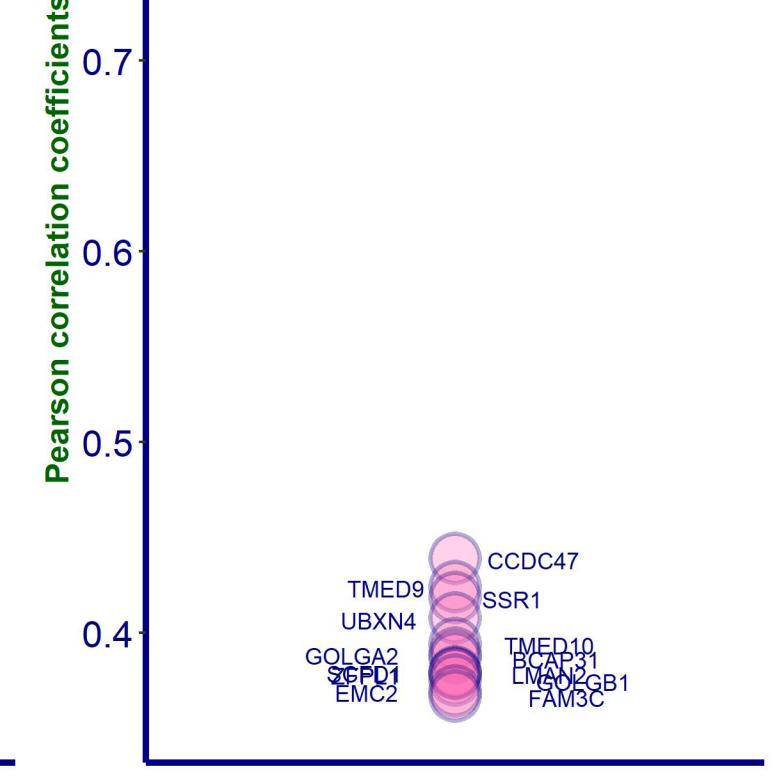
Sanger Institute Protein Database 1 (DB1), protein presence is certain



Top negative correlations of CDK5RAP3 protein, I

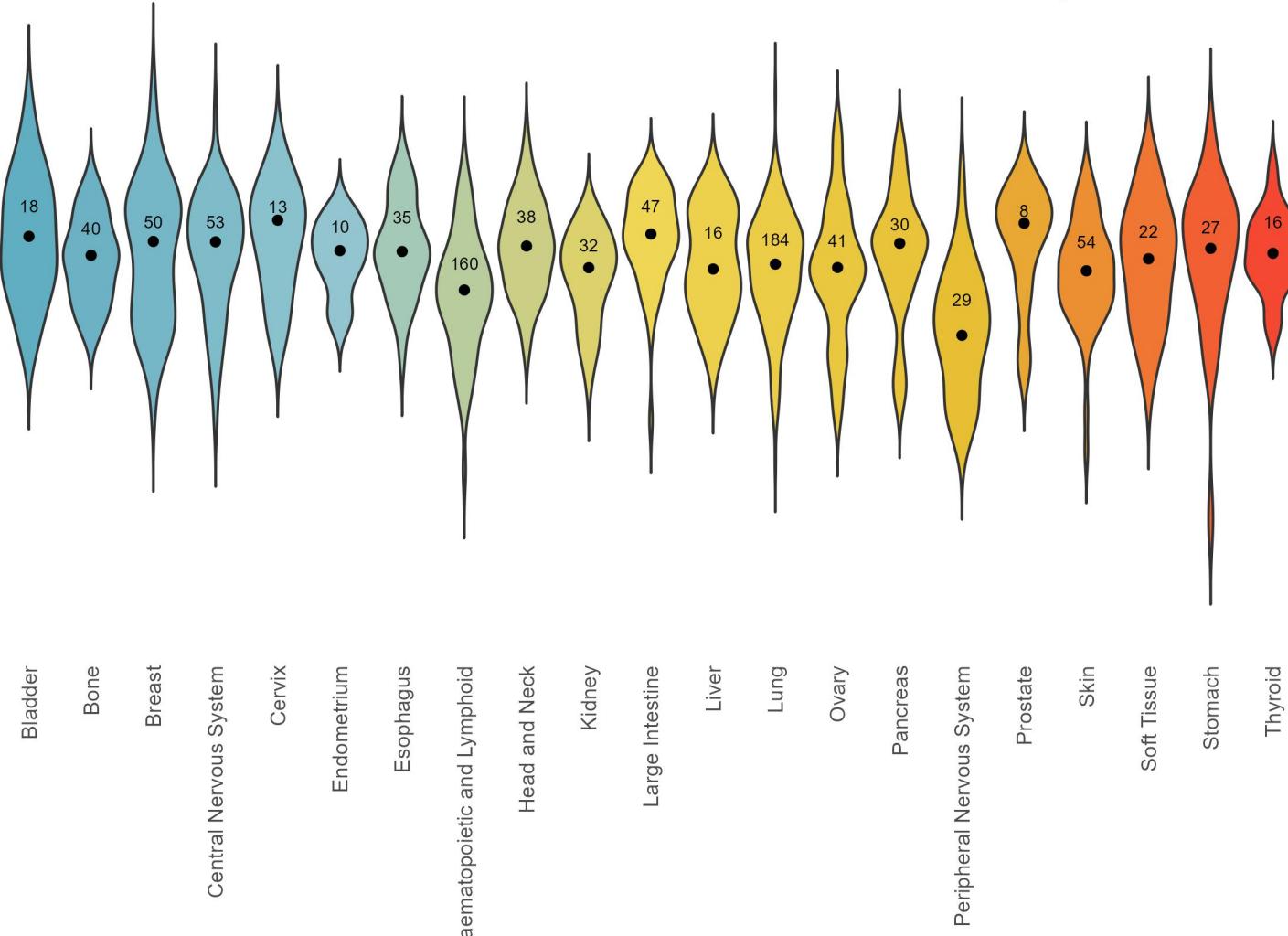


Top positive correlations of CDK5RAP3 protein, DB



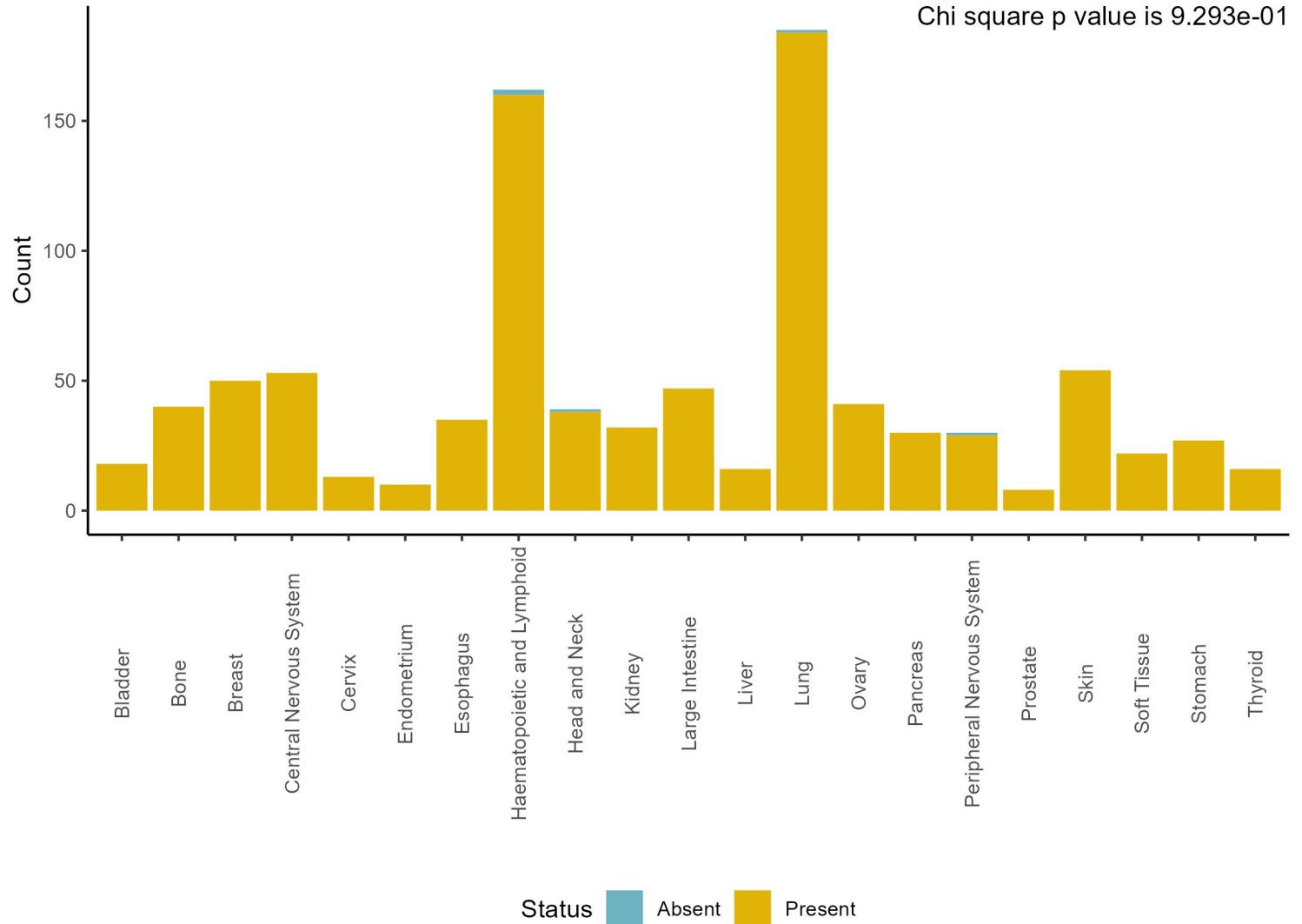
Amount of CDK5RAP3 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 4.612e-14



Present and absent CDK5RAP3 protein counts by tissue, DB1

Chi square p value is 9.293e-01

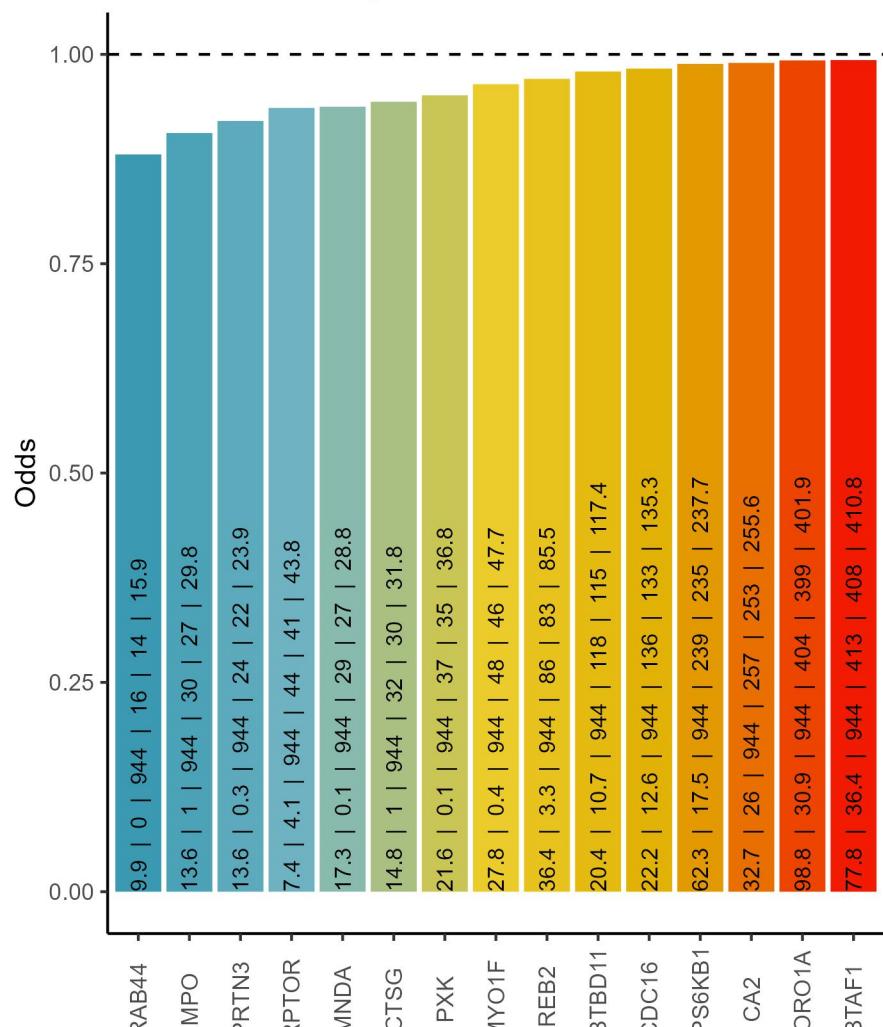


Cooccurrence with CDK5RAP3 protein, DB1

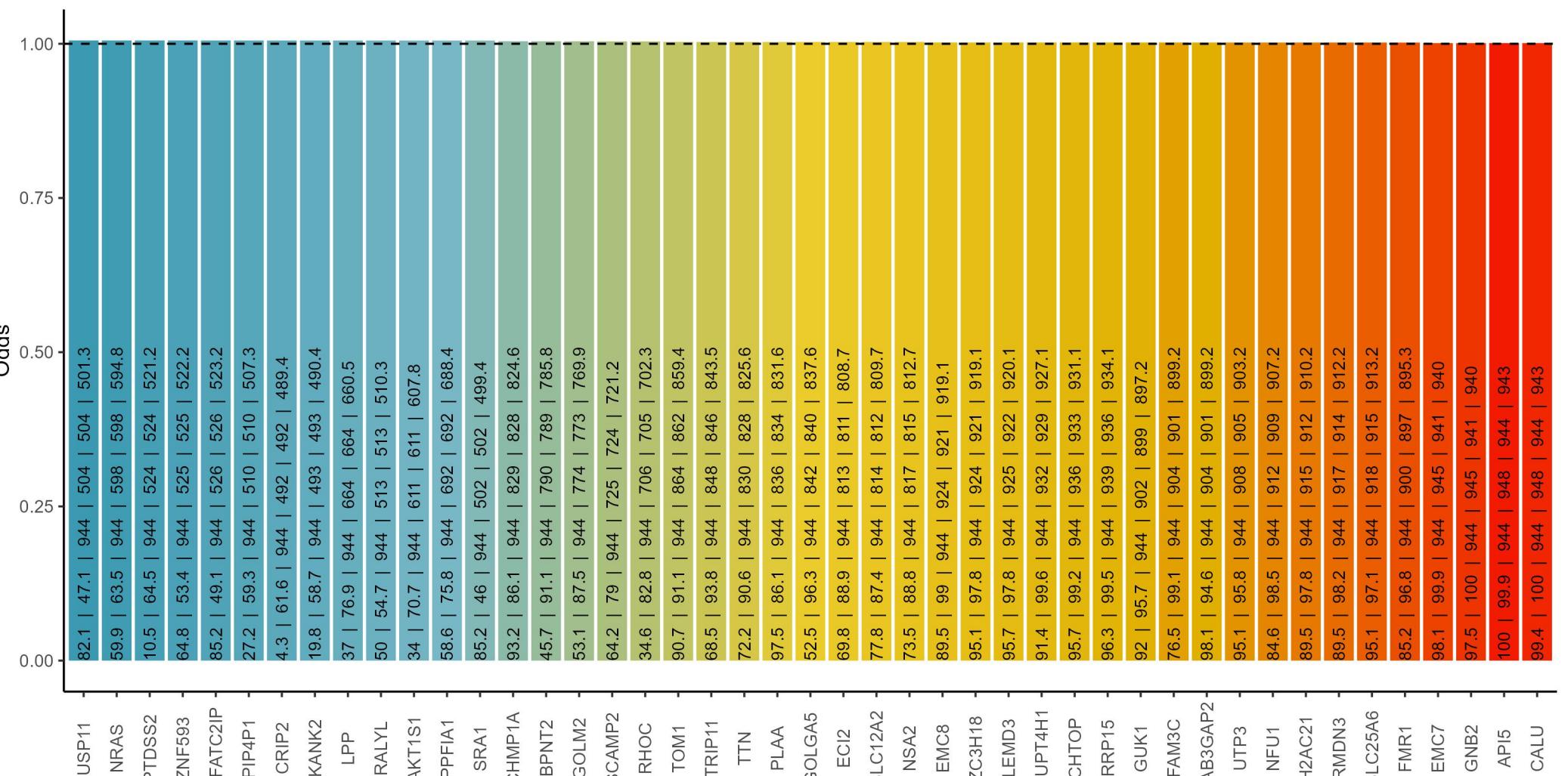
% of CDK5RAP3 in blood cancers: 98.8 ; % of CDK5RAP3 in solid cancers: 99.6

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CDK5RAP3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

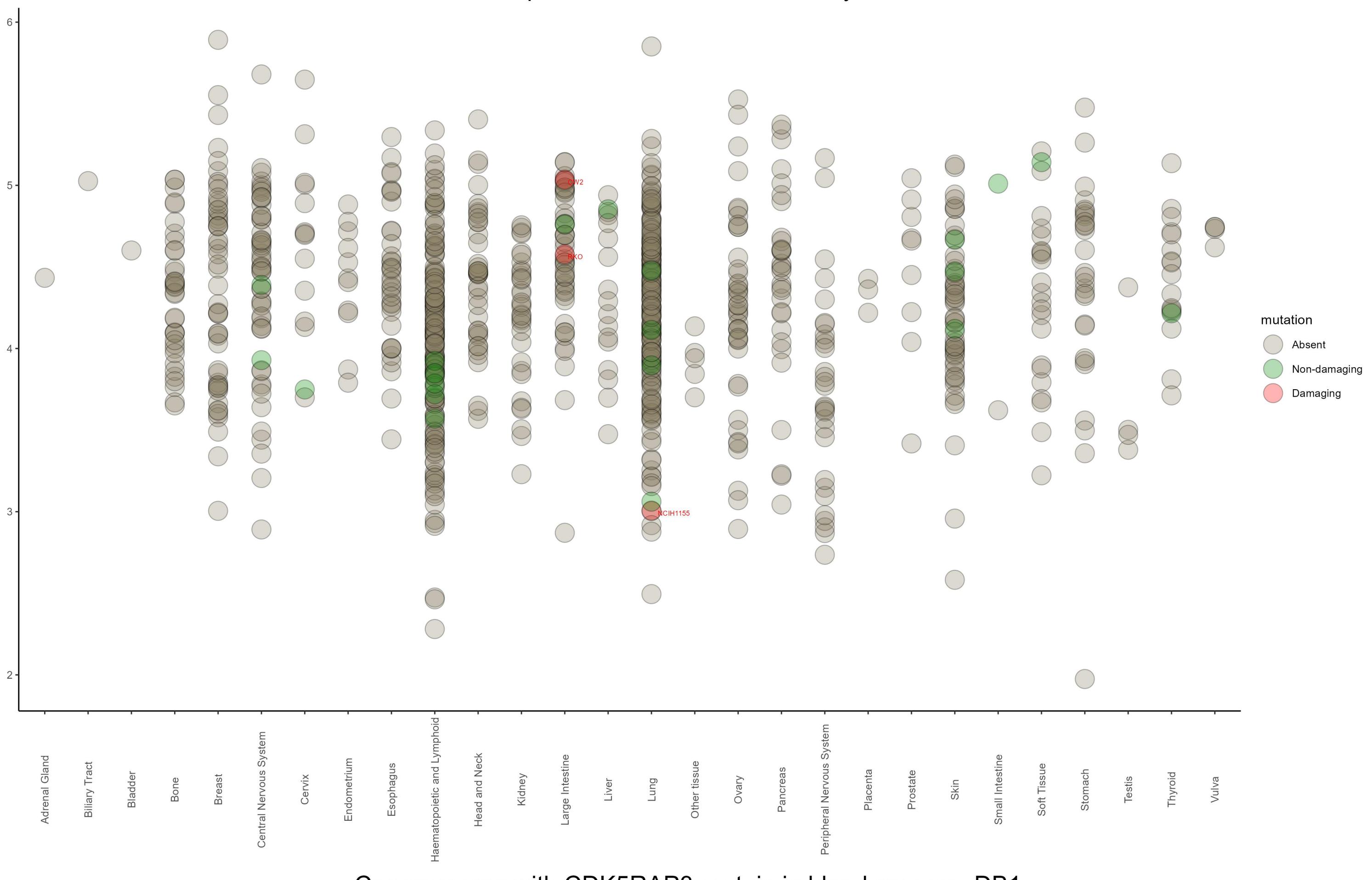
Negative cooccurrence



Positive cooccurrence

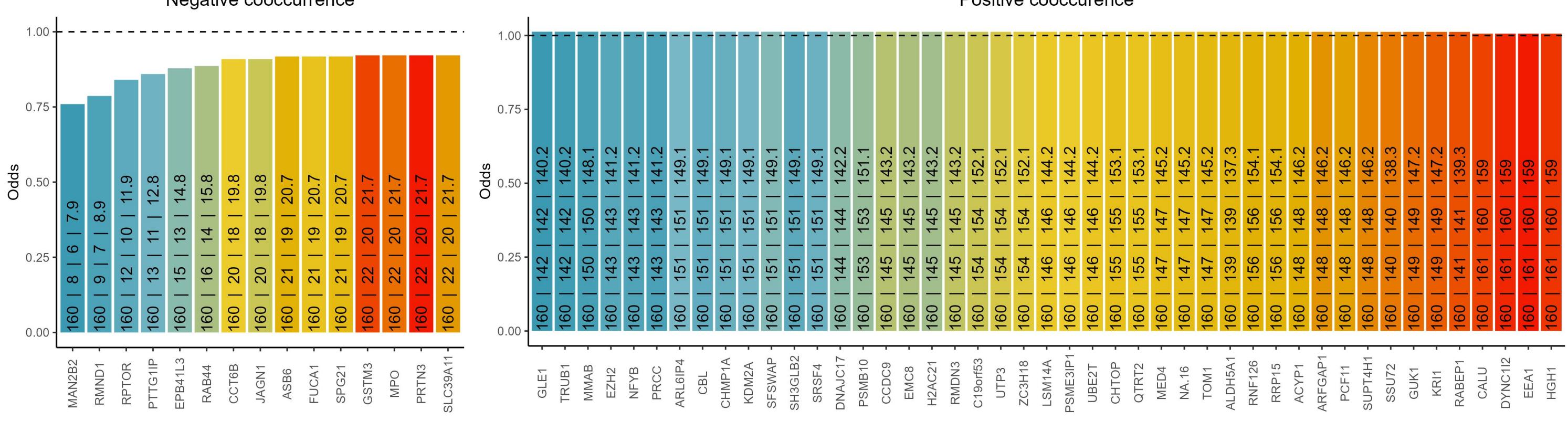


Amount of CDK5RAP3 protein and mutation status by tissue, DB1



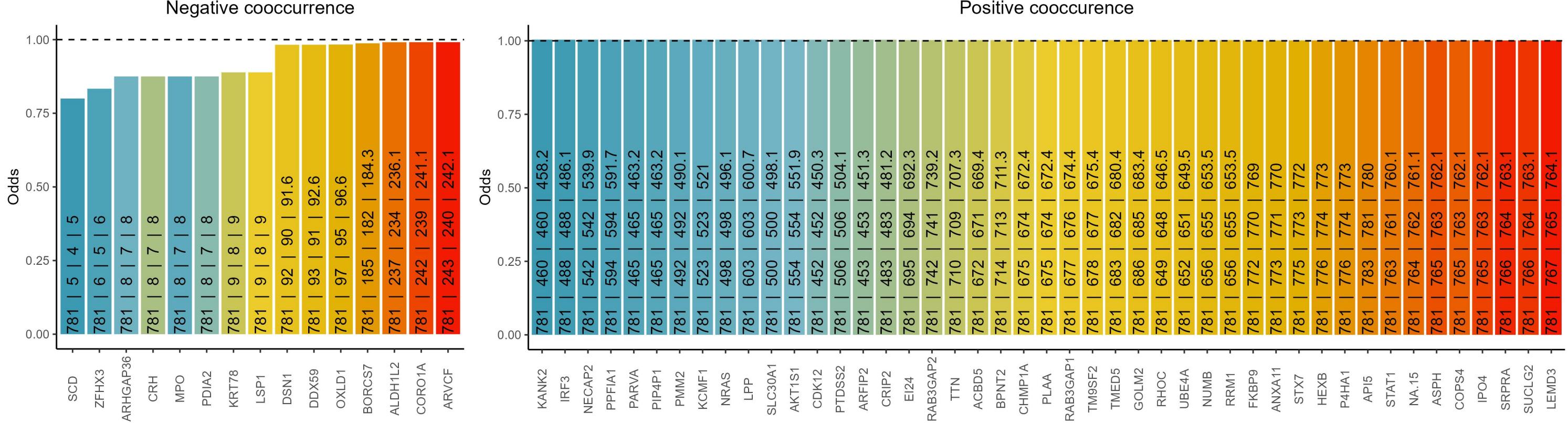
Cooccurrence with CDK5RAP3 protein in blood cancers, DB1

The text in the bars: incidence of CDK5RAP3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

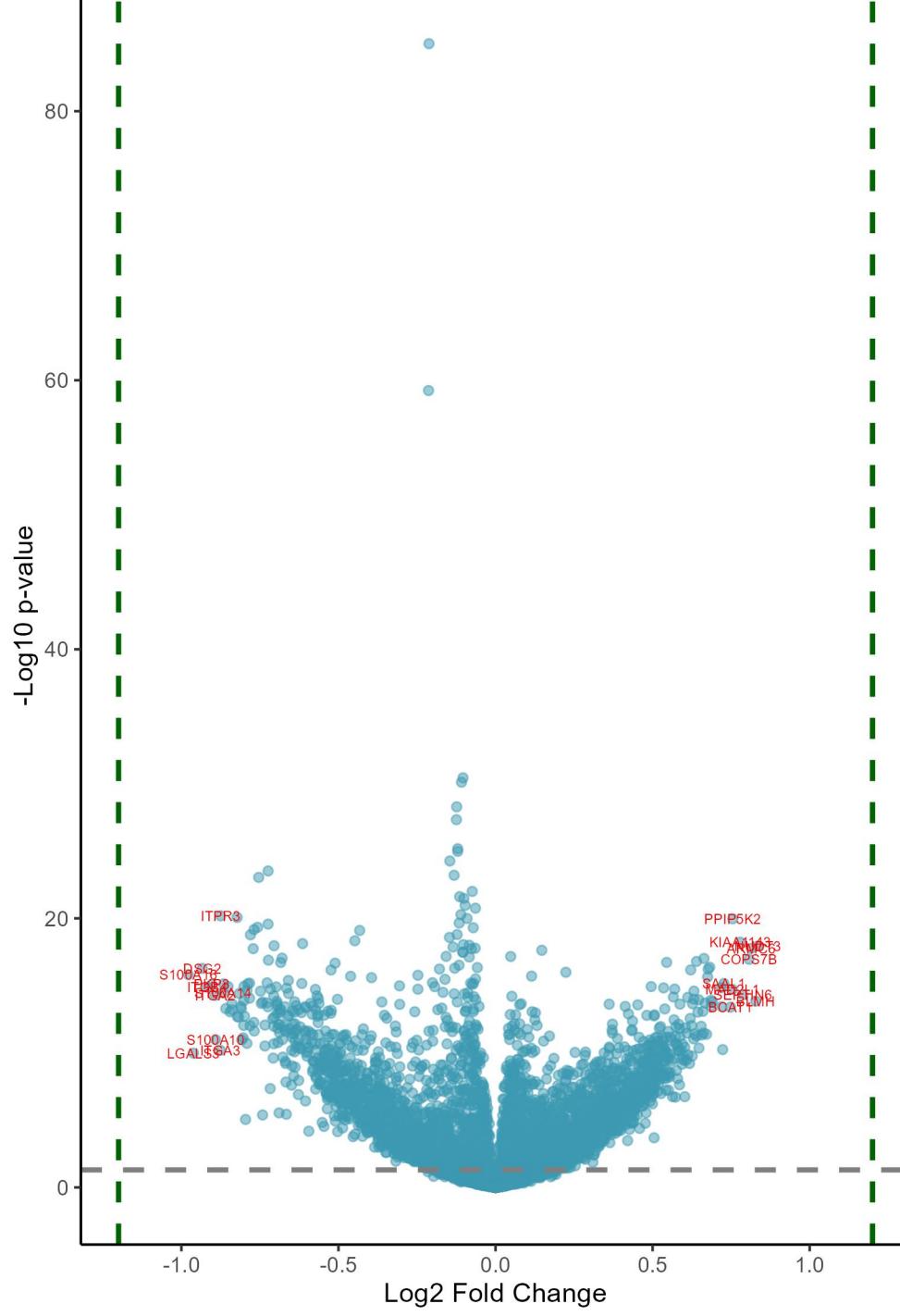


Cooccurrence with CDK5RAP3 protein in solid cancers, DB1

The text in the bars: incidence of CDK5RAP3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

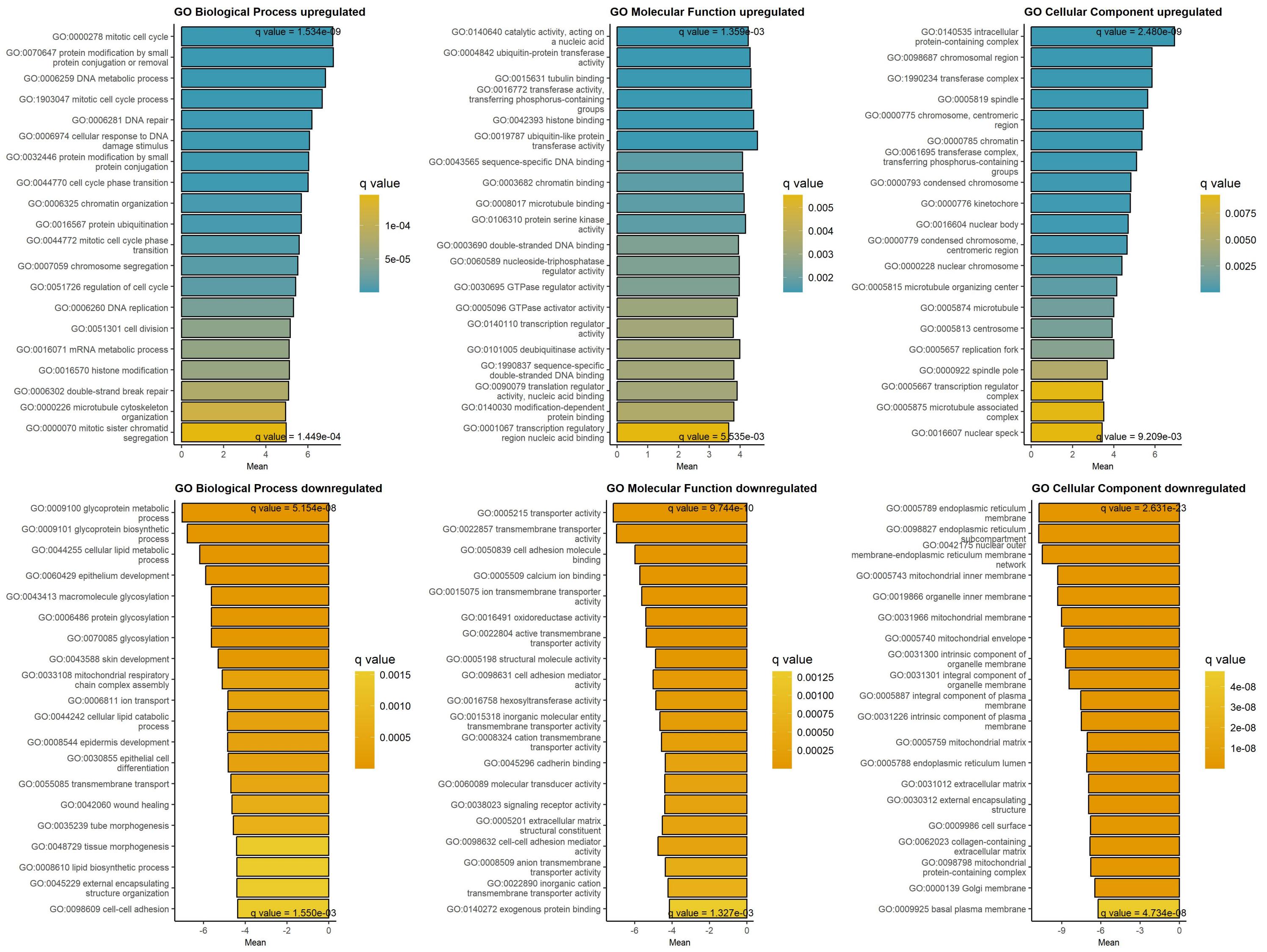


Downregulated at low/absent CDK5RAP3 Upregulated at low/absent CDK5RAP3



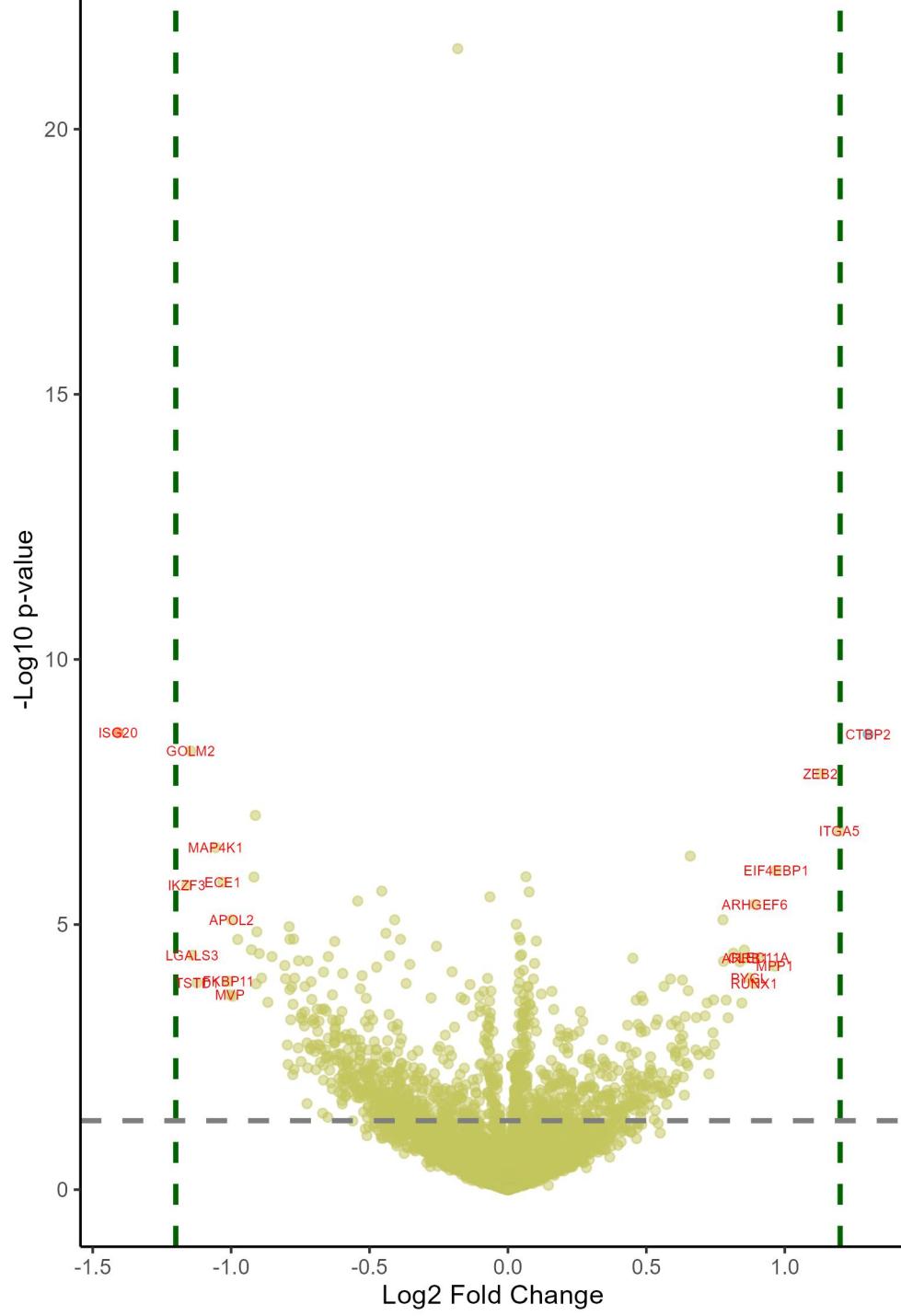
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.98	1.48e-14	S100A16	S100 calcium binding protein A16	0.84	1.90e-16	NUDT3	nudix hydrolase 3
-0.96	1.57e-09	LGALS3	galectin 3	0.83	7.17e-13	BLMH	bleomycin hydrolase
-0.93	5.57e-15	DSG2	desmoglein 2	0.81	2.70e-16	ARMC6	armadillo repeat containing 6
-0.92	9.40e-14	ITGB4	integrin subunit beta 4	0.81	1.39e-15	COPS7B	COP9 signalosome subunit 7B
-0.9	6.16e-14	PKP3	plakophilin 3	0.79	2.79e-13	SEPTIN6	septin 6
-0.89	3.07e-13	ITGA2	integrin subunit alpha 2	0.78	1.16e-16	KIAA1143	KIAA1143
-0.89	2.08e-10	S100A10	S100 calcium binding protein A10	0.76	3.13e-18	PPIP5K2	diphosphoinositol pentakisphosphate
-0.88	1.04e-09	ITGA3	integrin subunit alpha 3	0.75	1.24e-13	MAD2L1	mitotic arrest deficient 2 like 1
-0.88	2.16e-18	ITPR3	inositol 1,4,5-trisphosphate recept	0.75	1.62e-12	BCAT1	branched chain amino acid transamin
-0.87	2.09e-13	S100A14	S100 calcium binding protein A14	0.73	5.53e-14	SAAL1	serum amyloid A like 1
-0.87	5.69e-14	LAD1	ladinin 1	0.72	9.30e-10	CORO1A	coronin 1A
-0.86	2.03e-12	NT5E	5'-nucleotidase ecto	0.72	1.52e-12	PPP6R1	protein phosphatase 6 regulatory su
-0.85	8.54e-14	SPINT1	serine peptidase inhibitor, Kunitz	0.72	9.94e-14	PDXP	pyridoxal phosphatase
-0.85	3.16e-12	ANXA3	annexin A3	0.69	7.83e-13	TYMS	thymidylate synthetase
-0.84	9.89e-13	PPIC	peptidylprolyl isomerase C	0.69	1.45e-12	UBE2R2	ubiquitin conjugating enzyme E2 R2
-0.84	2.36e-12	CDH1	cadherin 1	0.69	6.31e-13	PPM1F	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe
-0.82	2.73e-18	CANT1	calcium activated nucleotidase 1	0.68	4.77e-15	CKS1B	CDC28 protein kinase regulatory sub
-0.82	6.34e-12	EGFR	epidermal growth factor receptor	0.68	6.09e-15	SMYD3	SET and MYND domain containing 3
-0.82	7.00e-12	NCEH1	neutral cholesterol ester hydrolase	0.68	2.04e-14	RWDD4	RWD domain containing 4
-0.82	2.29e-13	ADAM9	ADAM metallopeptidase domain 9	0.67	9.43e-11	PRPS1	phosphoribosyl pyrophosphate synthe
-0.81	1.48e-12	SQOR	sulfide quinone oxidoreductase	0.67	9.42e-13	CCDC43	coiled-coil domain containing 43
-0.81	2.01e-12	LSR	lipolysis stimulated lipoprotein re	0.66	1.23e-15	YJU2	YJU2 splicing factor homolog
-0.81	2.14e-10	JUP	junction plakoglobin	0.66	7.87e-11	ACYP1	acylphosphatase 1
-0.8	1.57e-10	AGR2	anterior gradient 2, protein disulp	0.66	3.02e-12	RNASEH2B	ribonuclease H2 subunit B
-0.8	2.61e-11	PKP2	plakophilin 2	0.66	1.03e-10	FKBP1A	FKBP prolyl isomerase 1A
-0.8	6.87e-13	EPCAM	epithelial cell adhesion molecule	0.65	2.89e-11	UBE2T	ubiquitin conjugating enzyme E2 T
-0.8	8.31e-14	TPBG	trophoblast glycoprotein	0.65	7.45e-10	UBE2V2	ubiquitin conjugating enzyme E2 V2
-0.8	6.09e-12	MISP	mitotic spindle positioning	0.65	5.90e-13	UCK2	uridine-cytidine kinase 2
-0.8	3.41e-05	KRT18	keratin 18	0.64	3.31e-12	ARPP19	cAMP regulated phosphoprotein 19

GAGE analysis on upregulated and downregulated proteins at low/absent CDK5RAP3 protein, DB1

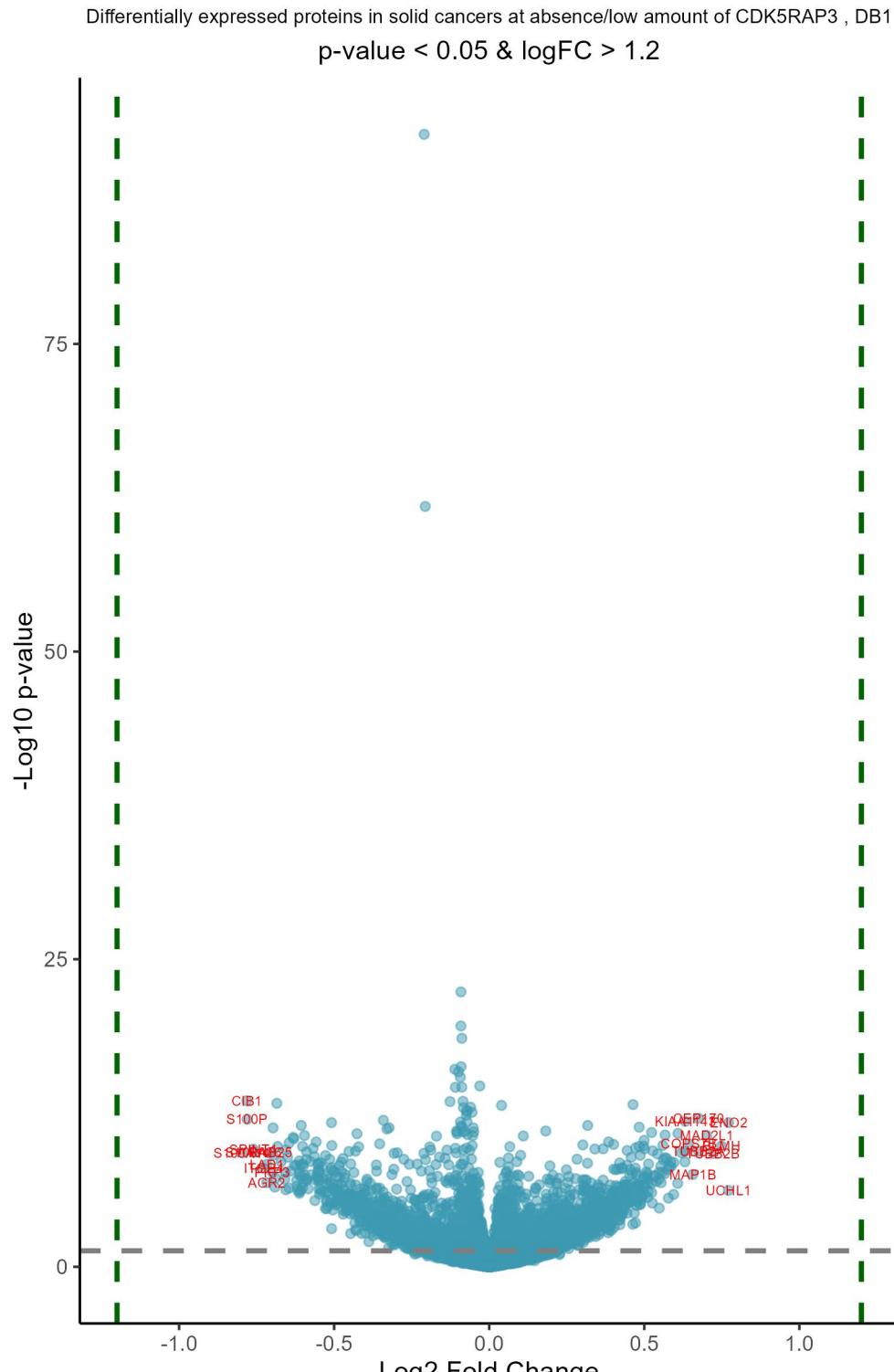


p-value < 0.05 & logFC > 1.2

Downregulated in blood cancers at low/absent CDK5RAP3 Upregulated in blood cancers at low/absent CDK5RAP3



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.41	4.26e-06	ISG20	interferon stimulated exonuclease g	1.3	4.26e-06	CTBP2	C-terminal binding protein 2
-1.16	8.10e-04	IKZF3	IKAROS family zinc finger 3	1.2	1.44e-04	ITGA5	integrin subunit alpha 5
-1.15	7.10e-06	GOLM2	golgi membrane protein 2	1.13	1.58e-05	ZEB2	zinc finger E-box binding homeobox
-1.14	5.81e-03	LGALS3	galectin 3	0.97	5.80e-04	EIF4EBP1	eukaryotic translation initiation f
-1.12	1.10e-02	TSTD1	thiosulfate sulfurtransferase like	0.96	7.12e-03	MPP1	MAGUK p55 scaffold protein 1
-1.06	2.61e-04	MAP4K1	mitogen-activated protein kinase ki	0.91	5.87e-03	CLEC11A	C-type lectin domain containing 11A
-1.03	7.57e-04	ECE1	endothelin converting enzyme 1	0.89	1.38e-03	ARHGEF6	Rac/Cdc42 guanine nucleotide exchan
-1.01	1.07e-02	FKBP11	FKBP prolyl isomerase 11	0.89	1.10e-02	RUNX1	RUNX family transcription factor 1
-1	1.47e-02	MVP	major vault protein	0.87	9.97e-03	PYGL	glycogen phosphorylase L
-1	2.36e-03	APOL2	apolipoprotein L2	0.86	5.87e-03	ARRB1	arrestin beta 1
-0.99	1.50e-02	IRF4	interferon regulatory factor 4	0.85	5.31e-03	CYFIP1	cytoplasmic FMR1 interacting protei
-0.98	3.96e-03	TYMP	thymidine phosphorylase	0.84	1.75e-02	MACROD1	mono-ADP ribosylhydrolase 1
-0.93	5.31e-03	ARID3B	AT-rich interaction domain 3B	0.84	6.32e-03	PDLIM7	PDZ and LIM domain 7
-0.92	6.49e-04	PARP4	poly(ADP-ribose) polymerase family	0.81	5.81e-03	CKS1B	CDC28 protein kinase regulatory sub
-0.91	8.29e-05	COMTD1	catechol-O-methyltransferase domain	0.8	2.56e-02	PC	pyruvate carboxylase
-0.91	1.10e-02	CD40	CD40 molecule	0.79	1.64e-02	LPCAT2	lysophosphatidylcholine acyltransfe
-0.91	3.50e-03	YIPF4	Yip1 domain family member 4	0.78	6.31e-03	MRC2	mannose receptor C type 2
-0.9	5.81e-03	STAT2	signal transducer and activator of	0.78	2.36e-03	RCOR1	REST corepressor 1
-0.89	9.97e-03	ITGB7	integrin subunit beta 7	0.75	3.43e-02	DOK3	docking protein 3
-0.87	1.72e-02	MX1	MX dynamin like GTPase 1	0.74	1.64e-02	BCR	BCR activator of RhoGEF and GTPase
-0.85	5.81e-03	TRPV2	transient receptor potential cation	0.74	3.43e-02	GLUL	glutamate-ammonia ligase
-0.81	7.03e-03	MCEE	methylmalonyl-CoA epimerase	0.73	3.43e-02	CSTA	cystatin A
-0.8	9.97e-03	GCC2	GRIP and coiled-coil domain contain	0.73	4.52e-02	IGFBP1	insulin like growth factor 2 mRNA b
-0.8	3.43e-02	ITGAL	integrin subunit alpha L	0.72	1.75e-02	PLCB3	phospholipase C beta 3
-0.79	3.43e-02	HLA-DQB1	major histocompatibility complex, c	0.71	3.43e-02	BCAT1	branched chain amino acid transamin
-0.79	2.92e-03	HLA-F	major histocompatibility complex, c	0.71	2.45e-02	GNAQ	G protein subunit alpha q
-0.79	1.27e-02	TREX1	three prime repair exonuclease 1	0.69	3.43e-02	EEF1A2	eukaryotic translation elongation f
-0.79	3.96e-03	TRADD	TNFRSF1A associated via death domai	0.68	2.56e-02	CA8	carbonic anhydrase 8
-0.78	2.68e-02	DST	dystonin	0.68	3.43e-02	SCML2	Scm polycomb group protein like 2

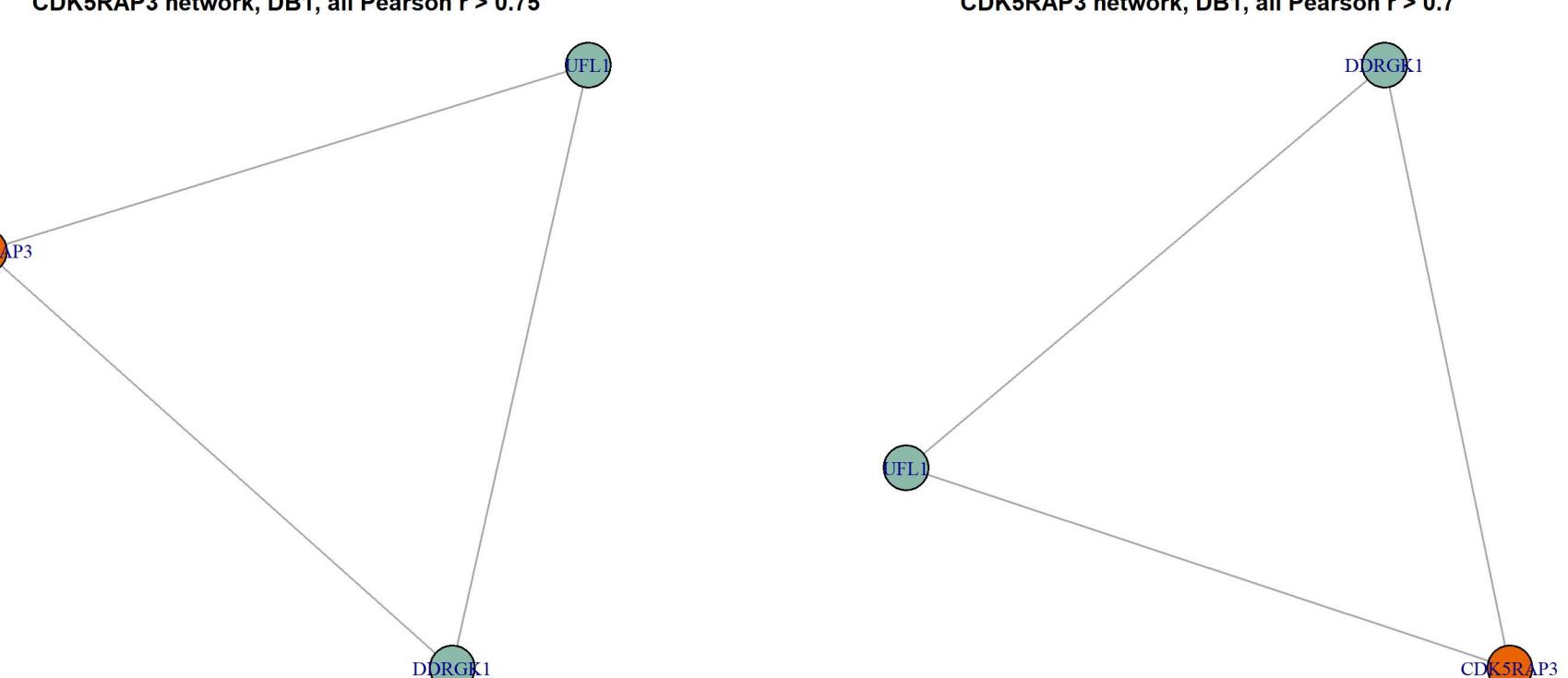


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.8	3.38e-08	S100A14	S100 calcium binding protein A14	0.77	3.88e-10	ENO2	enolase 2
-0.78	1.53e-11	CIB1	calcium and integrin binding 1	0.77	1.06e-05	UCHL1	ubiquitin C-terminal hydrolase L1
-0.78	2.49e-10	S100P	S100 calcium binding protein P	0.75	1.35e-08	BLMH	bleomycin hydrolase
-0.76	3.20e-08	S100A16	S100 calcium binding protein A16	0.72	3.65e-08	TUBB2B	tubulin beta 2B class IIb
-0.76	2.06e-08	SPINT1	serine peptidase inhibitor, Kunitz	0.7	2.53e-09	MAD2L1	mitotic arrest deficient 2 like 1
-0.73	3.68e-07	ITGB4	integrin subunit beta 4	0.67	2.80e-08	TUBB2A	tubulin beta 2A class IIa
-0.72	3.33e-06	AGR2	anterior gradient 2, protein disulp	0.67	2.15e-10	CEP170	centrosomal protein 170
-0.72	2.09e-07	LAD1	ladinin 1	0.66	9.81e-07	MAP1B	microtubule associated protein 1B
-0.71	3.30e-08	RAB25	RAB25, member RAS oncogene family	0.64	1.01e-08	COPS7B	COP9 signalosome subunit 7B
-0.7	6.87e-07	PKP3	plakophilin 3	0.63	3.49e-10	KIAA1143	KIAA1143
-0.7	8.28e-10	PATJ	PATJ crumbs cell polarity complex c	0.63	2.83e-08	NUDT3	nudix hydrolase 3
-0.7	5.06e-08	TAP2	transporter 2, ATP binding cassette	0.63	1.40e-07	FKBP1A	FKBP prolyl isomerase 1A
-0.69	6.55e-06	KRT17	keratin 17	0.62	3.38e-08	SAAL1	serum amyloid A like 1
-0.69	1.69e-06	CDH1	cadherin 1	0.61	1.91e-09	PFN2	profilin 2
-0.68	2.01e-11	CANT1	calcium activated nucleotidase 1	0.61	3.71e-06	NCAM1	neural cell adhesion molecule 1
-0.68	1.41e-08	LRP10	LDL receptor related protein 10	0.6	1.60e-07	CDK4	cyclin dependent kinase 4
-0.67	1.39e-07	SQOR	sulfide quinone oxidoreductase	0.59	1.92e-05	DPYSL3	dihydropyrimidinase like 3
-0.66	1.98e-06	MISP	mitotic spindle positioning	0.59	2.83e-07	NME4	NME/NM23 nucleoside diphosphate kin
-0.66	6.89e-07	EPCAM	epithelial cell adhesion molecule	0.59	1.40e-07	ARMC6	armadillo repeat containing 6
-0.66	2.31e-08	ST14	ST14 transmembrane serine protease	0.58	2.85e-07	PPM1A	protein phosphatase, Mg2+/Mn2+ depe
-0.66	9.75e-06	BRI3BP	BRI3 binding protein	0.58	3.37e-05	QPRT	quinolinate phosphoribosyltransf
-0.65	6.99e-08	ITGB6	integrin subunit beta 6	0.57	4.39e-07	CRMP1	collapsin response mediator protein
-0.65	8.69e-09	LLGL2	LLGL scribble cell polarity complex	0.57	8.42e-08	UBE2R2	ubiquitin conjugating enzyme E2 R2
-0.64	7.53e-06	TACSTD2	tumor associated calcium signal tra	0.57	2.42e-09	CDC34	cell division cycle 34, ubiquitin c
-0.64	5.70e-07	ZNF185	zinc finger protein 185 with LIM do	0.57	7.54e-08	USP13	ubiquitin specific peptidase 13
-0.63	3.33e-09	DHRS7B	dehydrogenase/reductase 7B	0.57	8.59e-07	PFKM	phosphofructokinase, muscle
-0.63	4.24e-09	RABAC1	Rab acceptor 1	0.56	1.01e-07	UCK2	uridine-cytidine kinase 2
-0.63	2.33e-07	EVPL	envoplakin	0.56	1.30e-08	RWDD4	RWD domain containing 4
-0.62	2.35e-07	JUNB	JunB proto-oncogene, AP-1 transcript	0.56	6.82e-07	PPM1F	protein phosphatase, Mg2+/Mn2+ depe

CDK5RAP3 network, DB1, all Pearson r > 0.8

CDK5RAP3 network, DB1, all Pearson r > 0.75

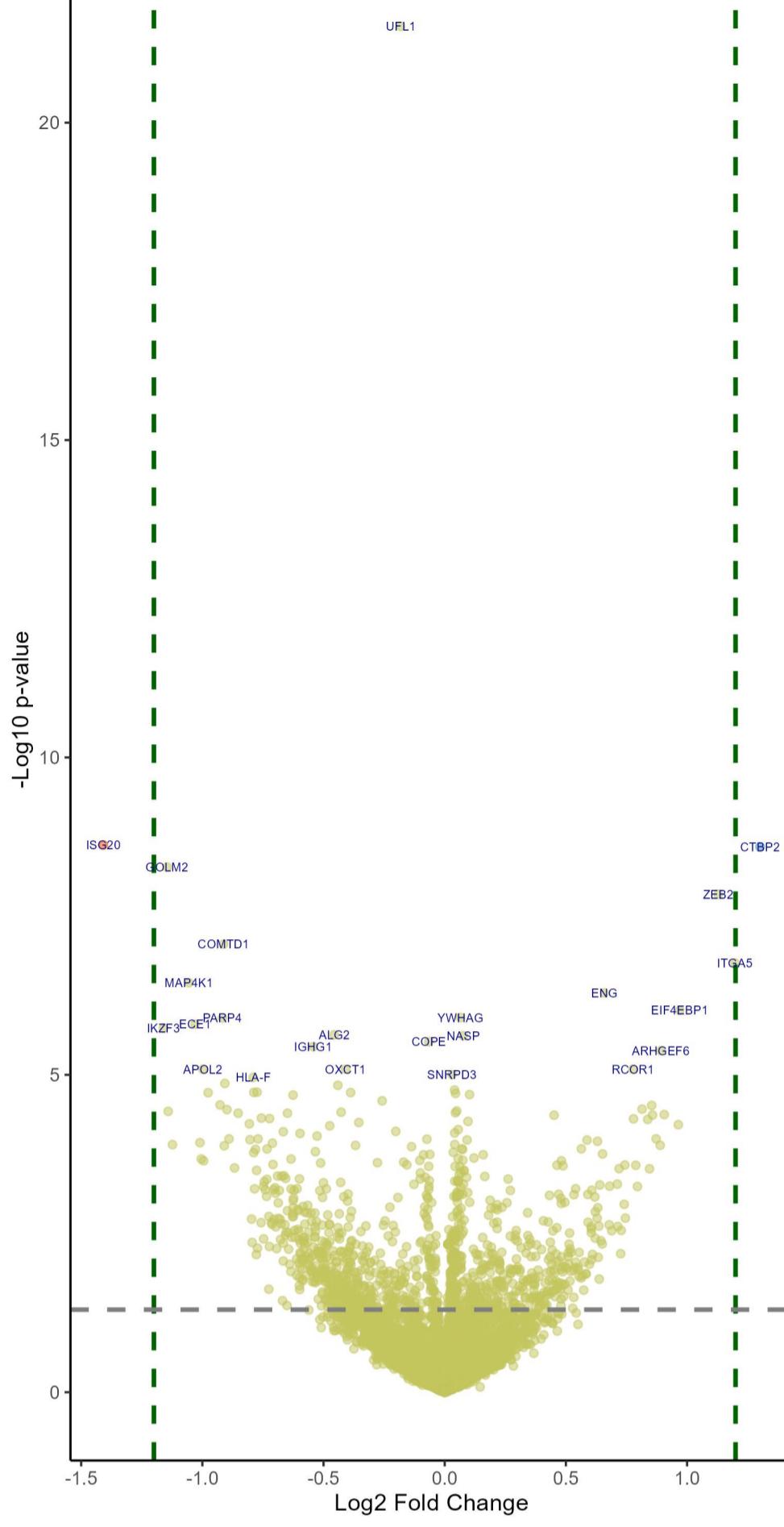
CDK5RAP3 network, DB1, all Pearson r > 0.7



Differentially expressed proteins in blood cancers at absence/low amount of CDK5RAP3 , DB1
p-value < 0.05 & logFC > 1.2

Sorted by p values!

Downregulated in blood cancers at low/absent CDK5RAP3 Upregulated in blood cancers at low/absent CDK5RAP3

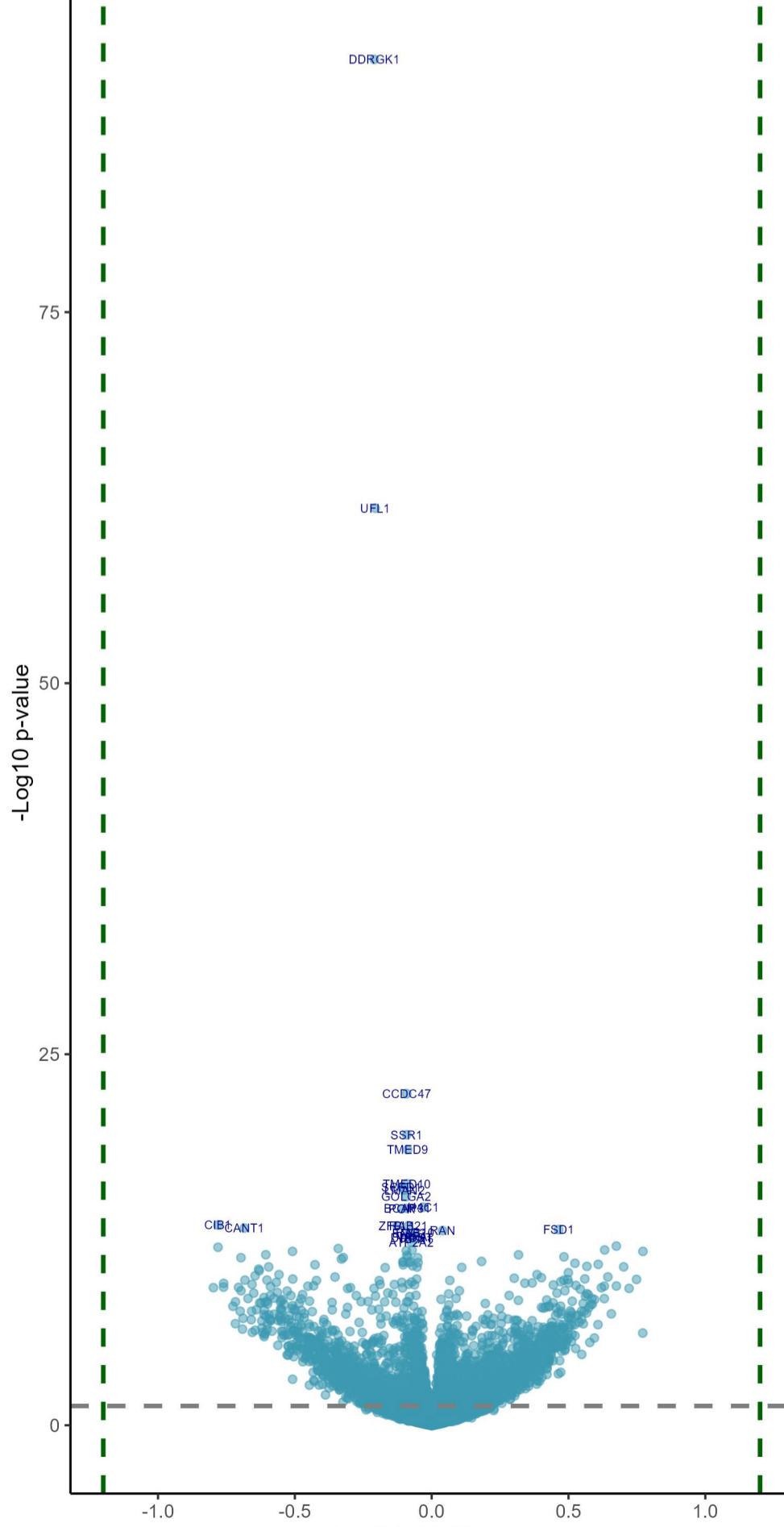


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.18	2.02e-18	UFL1	UFM1 specific ligase 1	1.3	4.26e-06	CTBP2	C-terminal binding protein 2
-1.41	4.26e-06	ISG20	interferon stimulated exonuclease g	1.13	1.58e-05	ZEB2	zinc finger E-box binding homeobox
-1.15	7.10e-06	GOLM2	golgi membrane protein 2	1.2	1.44e-04	ITGA5	integrin subunit alpha 5
-0.91	8.29e-05	COMTD1	catechol-O-methyltransferase domain	0.66	3.40e-04	ENG	endoglin
-1.06	2.61e-04	MAP4K1	mitogen-activated protein kinase ki	0.97	5.80e-04	EIF4EBP1	eukaryotic translation initiation f
-0.92	6.49e-04	PARP4	poly(ADP-ribose) polymerase family	0.07	6.49e-04	YWHAG	tyrosine 3-monoxygenase/tryptophan
-1.03	7.57e-04	ECE1	endothelin converting enzyme 1	0.08	9.49e-04	NASP	nuclear autoantigenic sperm protein
-1.16	8.10e-04	IKZF3	IKAROS family zinc finger 3	0.89	1.38e-03	ARHGEF6	Rac/Cdc42 guanine nucleotide exchan
-0.46	9.49e-04	ALG2	ALG2 alpha-1,3/1,6-mannosyltransfer	0.78	2.36e-03	RCOR1	REST corepressor 1
-0.07	1.11e-03	COPE	COPII coat complex subunit epsilon	0.03	2.75e-03	SNRPD3	small nuclear ribonucleoprotein D3
-0.54	1.26e-03	IGHG1	immunoglobulin heavy constant gamma	0.04	3.96e-03	SF3B1	splicing factor 3b subunit 1
-0.41	2.36e-03	OXCT1	3-oxoacid CoA-transferase 1	0.04	3.96e-03	SF3A1	splicing factor 3a subunit 1
-1	2.36e-03	APOL2	apolipoprotein L2	0.1	3.96e-03	PAK2	p21 (RAC1) activated kinase 2
-0.79	2.92e-03	HLA-F	major histocompatibility complex, c	0.85	5.31e-03	CYFIP1	cytoplasmic FMR1 interacting protei
-0.91	3.50e-03	YIPF4	Yip1 domain family member 4	0.81	5.81e-03	CKS1B	CDC28 protein kinase regulatory sub
-0.44	3.60e-03	ADPRH	ADP-ribosylarginine hydrolase	0.05	5.81e-03	CHD4	chromodomain helicase DNA binding p
-0.77	3.96e-03	EML2	EMAP like 2	0.04	5.81e-03	DDX46	DEAD-box helicase 46
-0.79	3.96e-03	TRADD	TNFRSF1A associated via death domai	0.91	5.87e-03	CLEC11A	C-type lectin domain containing 11A
-0.39	3.96e-03	EPS8	epidermal growth factor receptor pa	0.86	5.87e-03	ARRB1	arrestin beta 1
-0.98	3.96e-03	TYMP	thymidine phosphorylase	0.45	5.87e-03	DYSF	dysferlin
-0.63	3.96e-03	HMOX1	heme oxygenase 1	0.78	6.31e-03	MRC2	mannose receptor C type 2
-0.26	4.74e-03	CHMP4A	charged multivesicular body protein	0.84	6.32e-03	PDLIM7	PDZ and LIM domain 7
-0.93	5.31e-03	ARID3B	AT-rich interaction domain 3B	0.1	6.67e-03	STMN1	stathmin 1
-0.9	5.81e-03	STAT2	signal transducer and activator of	0.96	7.12e-03	MPP1	MAGUK p55 scaffold protein 1
-1.14	5.81e-03	LGALS3	galectin 3	0.06	8.20e-03	SSB	small RNA binding exonuclease prote
-0.43	5.81e-03	ACTL8	actin like 8	0.04	8.83e-03	PUF60	poly(U) binding splicing factor 60
-0.65	5.81e-03	IRF9	interferon regulatory factor 9	0.87	9.97e-03	PYGL	glycogen phosphorylase L
-0.85	5.81e-03	TRPV2	transient receptor potential cation	0.09	9.97e-03	ADSS2	adenylosuccinate synthase 2
-0.76	6.31e-03	MYO5A	myosin VA	0.59	9.97e-03	PTPN12	protein tyrosine phosphatase non-re
-0.72	6.31e-03	IRF5	interferon regulatory factor 5	0.63	1.03e-02	PPIP5K2	diphosphoinositol pentakisphosphate
-0.35	6.81e-03	HAAO	3-hydroxyanthranilate 3,4-dioxygena	0.04	1.10e-02	SF3A3	splicing factor 3a subunit 3
-0.81	7.03e-03	MCEE	methylmalonyl-CoA epimerase	0.89	1.10e-02	RUNX1	RUNX family transcription factor 1
-0.47	7.29e-03	RAP2C	RAP2C, member of RAS oncogene famil	0.07	1.18e-02	PPIH	peptidylprolyl isomerase H
-0.2	8.57e-03	SPCS2	signal peptidase complex subunit 2	0.56	1.18e-02	AIF1	allograft inflammatory factor 1
-0.67	8.57e-03	STX11	syntaxin 11	0.07	1.18e-02	RCC2	regulator of chromosome condensatio
-0.6	8.85e-03	THTPA	thiamine triphosphatase	0.04	1.27e-02	SAP18	Sin3A associated protein 18
-0.53	9.57e-03	SLAMF7	SLAM family member 7	0.65	1.31e-02	ERG	ETS transcription factor ERG
-0.89	9.97e-03	ITGB7	integrin subunit beta 7	0.16	1.31e-02	TOP2B	DNA topoisomerase II beta
0.77	0.97e-03	NME3	NME/NM23 nucleoside diphosphate kin	0.12	1.46e-02	GATA2A	GATA zinc finger domain containing

Differentially expressed proteins in solid cancers at absence/low amount of CDK5RAP3 , DB1
p-value < 0.05 & logFC > 1.2

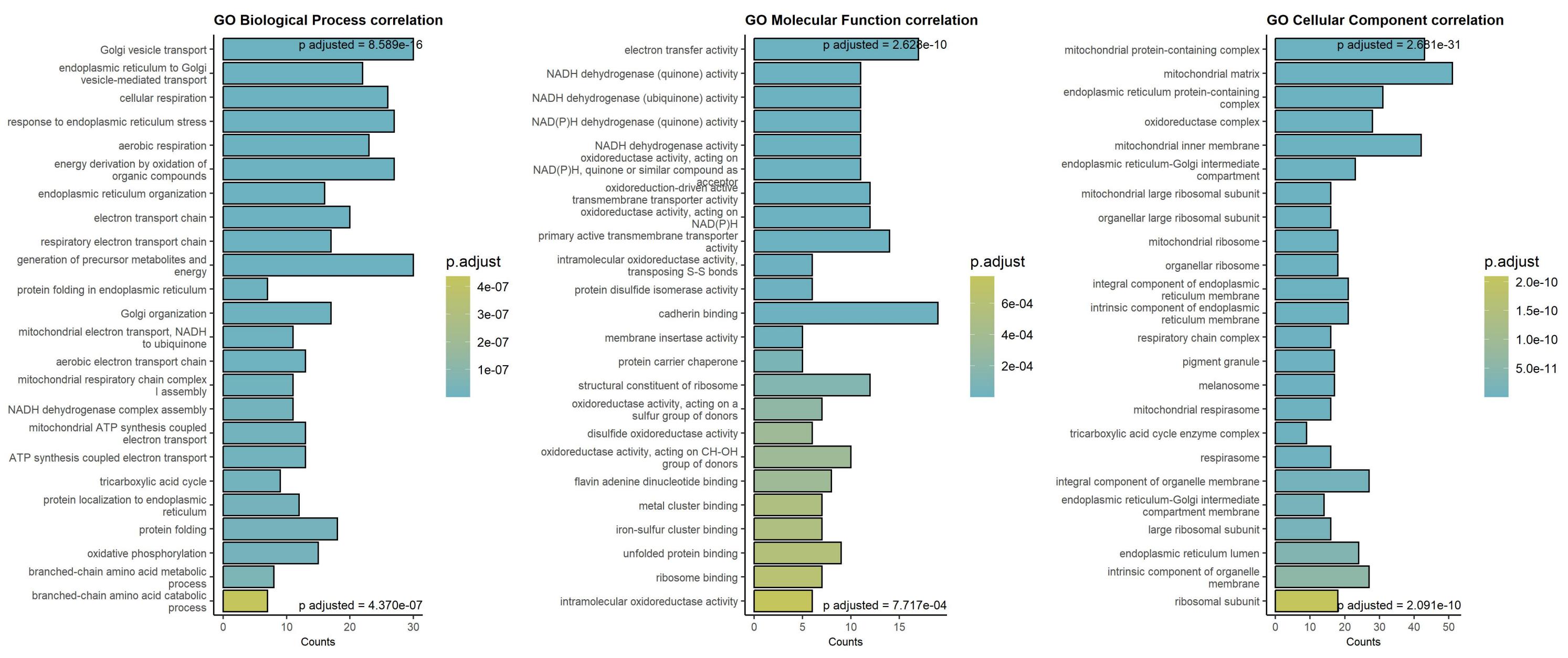
Sorted by p values!

Downregulated in solid cancers at low/absent CDK5RAP3 Upregulated in solid cancers at low/absent CDK5RAP3

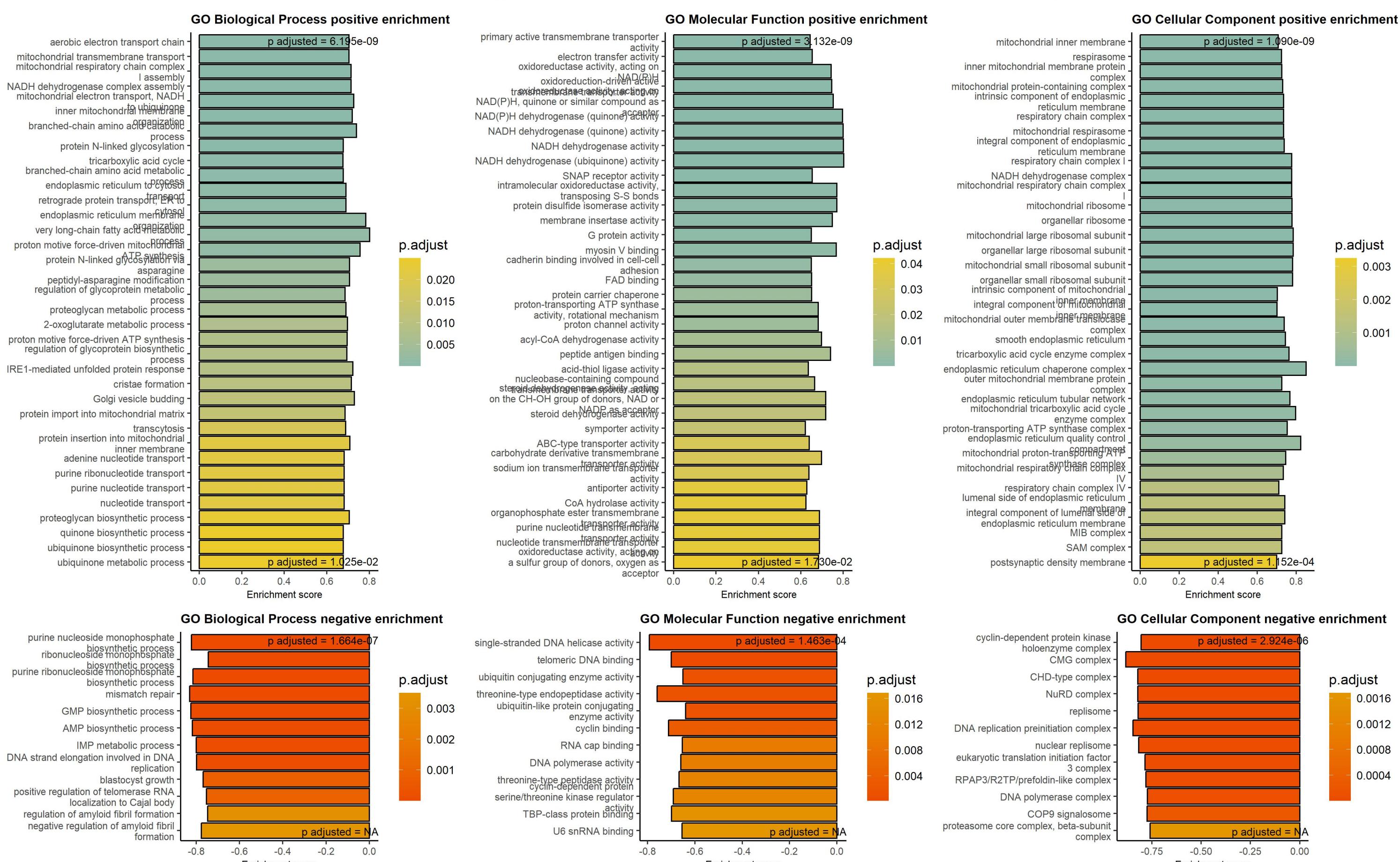


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.21	6.18e-89	DDRGK1	DDRGK domain containing 1	0.46	2.40e-11	FSD1	fibronectin type III and SPRY domai
-0.21	3.58e-59	UFL1	UFM1 specific ligase 1	0.04	2.66e-11	RAN	RAN, member RAS oncogene family
-0.09	7.56e-20	CCDC47	coiled-coil domain containing 47	0.67	2.15e-10	CEP170	centrosomal protein 170
-0.09	3.56e-17	SSR1	signal sequence receptor subunit 1	0.63	3.49e-10	KIAA1143	KIAA1143
-0.09	2.96e-16	TMED9	transmembrane p24 trafficking prote	0.77	3.88e-10	ENO2	enolase 2
-0.09	5.18e-14	TMED10	transmembrane p24 trafficking prote	0.32	6.22e-10	ELAVL4	ELAV like RNA binding protein 4
-0.11	7.34e-14	SCFD1	sec1 family domain containing 1	0.48	7.95e-10	KCTD15	potassium channel tetramerization d
-0.1	1.04e-13	LMAN2	lectin, mannose binding 2	0.18	1.41e-09	STMN1	stathmin 1
-0.09	2.60e-13	GOLGA2	golgin A2	0.52	1.65e-09	HPF1	histone PARylation factor 1
-0.03	1.21e-12	H4C1	H4 clustered histone 1	0.61	1.91e-09	PFN2	profilin 2
-0.09	1.31e-12	BCAP31	B cell receptor associated protein	0.57	2.42e-09	CDC34	cell division cycle 34, ubiquitin c
-0.11	1.31e-12	POR	cytochrome p450 oxidoreductase	0.7	2.53e-09	MAD2L1	mitotic arrest deficient 2 like 1
-0.78	1.53e-11	CIB1	calcium and integrin binding 1	0.11	2.64e-09	NASP	nuclear autoantigenic sperm protein
-0.08	1.54e-11	RAB21	RAB21, member RAS oncogene family	0.5	5.64e-09	SPAG7	sperm associated antigen 7
-0.13	1.54e-11	ZFPL1	zinc finger protein like 1	0.38	7.35e-09	ELAVL3	ELAV like RNA binding protein 3
-0.68	2.01e-11	CANT1	calcium activated nucleotidase 1	0.64	1.01e-08	COPS7B	COP9 signalosome subunit 7B
-0.06	3.53e-11	RAB10	RAB10, member RAS oncogene family	0.4	1.11e-08	MEX3A	mex-3 RNA binding family member A
-0.08	3.67e-11	EMC2	ER membrane protein complex subunit	0.3	1.19e-08	CAMK4	calcium/calmodulin dependent protei
-0.07	5.98e-11	VAPA	VAMP associated protein A	0.56	1.30e-08	RWDD4	RWD domain containing 4
-0.07	6.74e-11	DDOST	dolichyl-diphosphooligosaccharide--	0.75	1.35e-08	BLMH	bleomycin hydrolase
-0.06	7.66e-11	RPN1	ribophorin I	0.5	1.35e-08	SEPTIN3	septin 3
-0.07	1.26e-10	ATP2A2	ATPase sarcoplasmic/endoplasmic ret	0.48	1.41e-08	ELAVL2	ELAV like RNA binding protein 2
-0.78	2.49e-10	S100P	S100 calcium binding protein P	0.07	1.46e-08	HSPA4	heat shock protein family A (Hsp70)
-0.34	2.94e-10	HMGCL	3-hydroxy-3-methylglutaryl-CoA lyas	0.47	1.73e-08	ASDURF	ASNSD1 upstream open reading frame
-0.07	3.49e-10	NCLN	nicalin	0.37	1.97e-08	PCBP4	poly(rC) binding protein 4
-0.09	3.67e-10	RPN2	ribophorin II	0.5	1.97e-08	GPSM1	G protein signaling modulator 1
-0.51	3.88e-10	GOLM2	golgi membrane protein 2	0.34	2.01e-08	GLCCI1	glucocorticoid induced 1
-0.61	6.22e-10	ITPR3	inositol 1,4,5-tr				

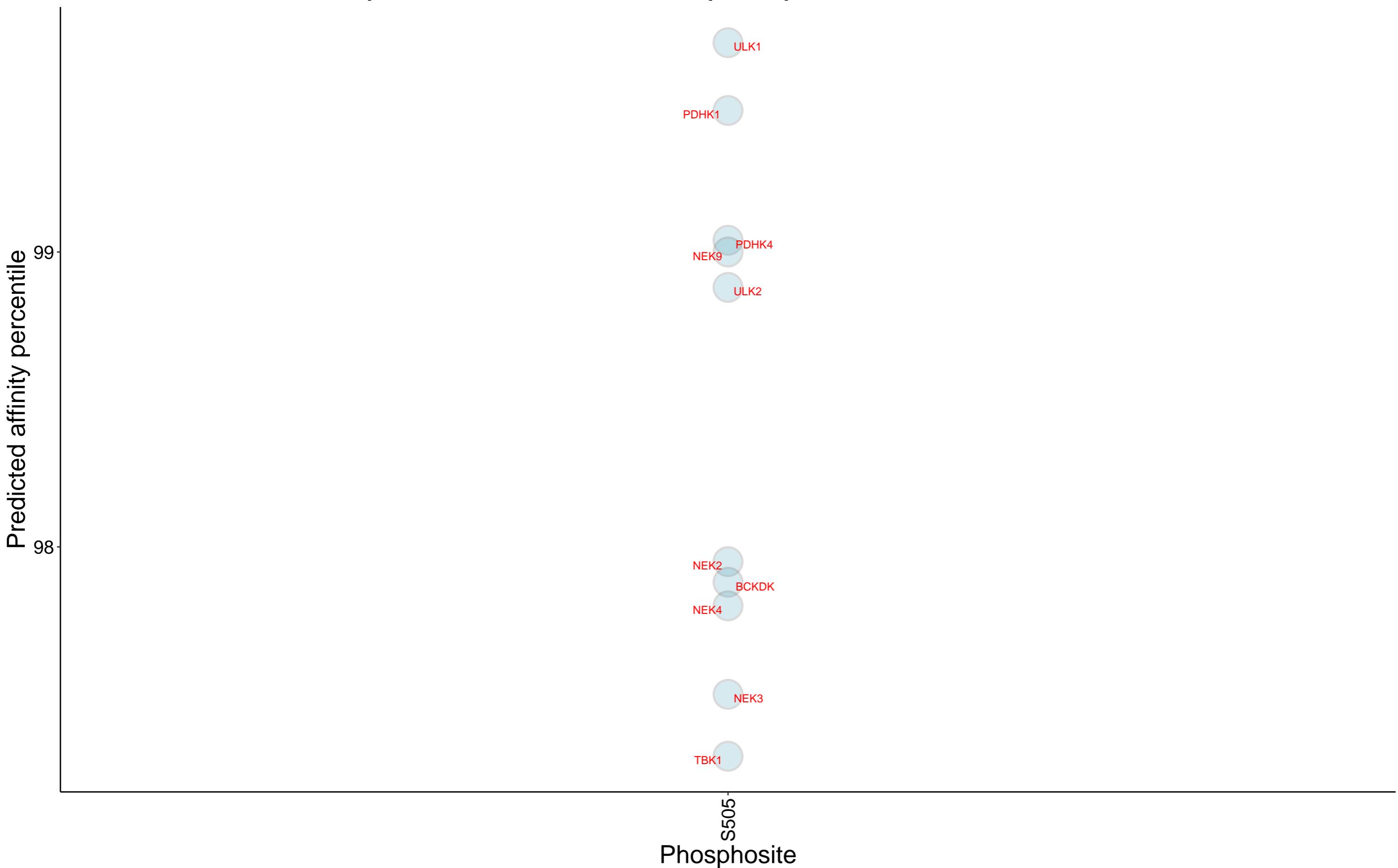
Top 250 correlation coefficients overrepresentation, CDK5RAP3 protein, DB1



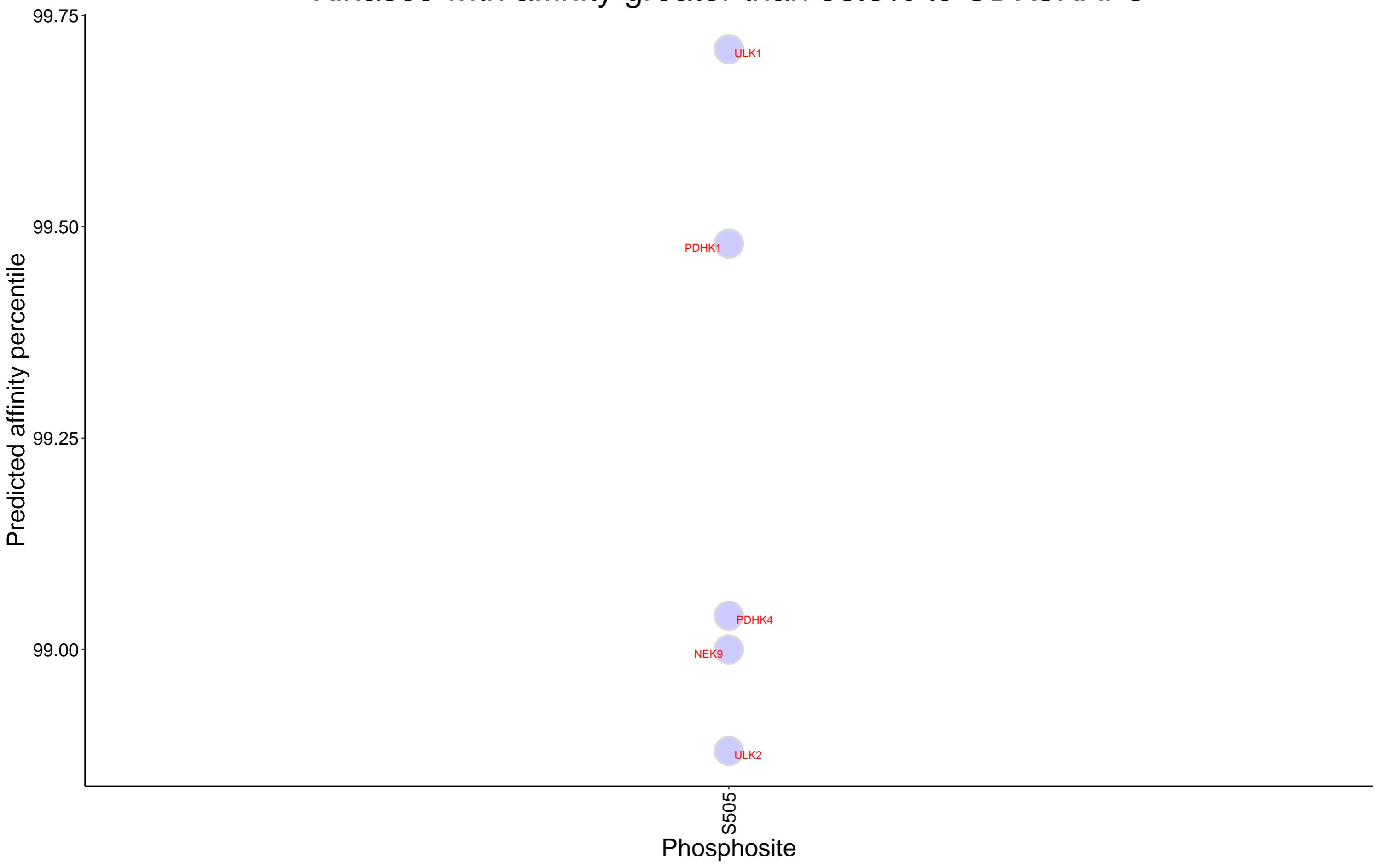
Gene Set Enrichment analysis on protein correlation coefficients, CDK5RAP3 protein, DB1



Top 10 kinases for each phosphosite in CDK5RAP3



Kinases with affinity greater than 98.5% to CDK5RAP3



Top 15 positive correlation coefficients for CDK5RAP3 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

