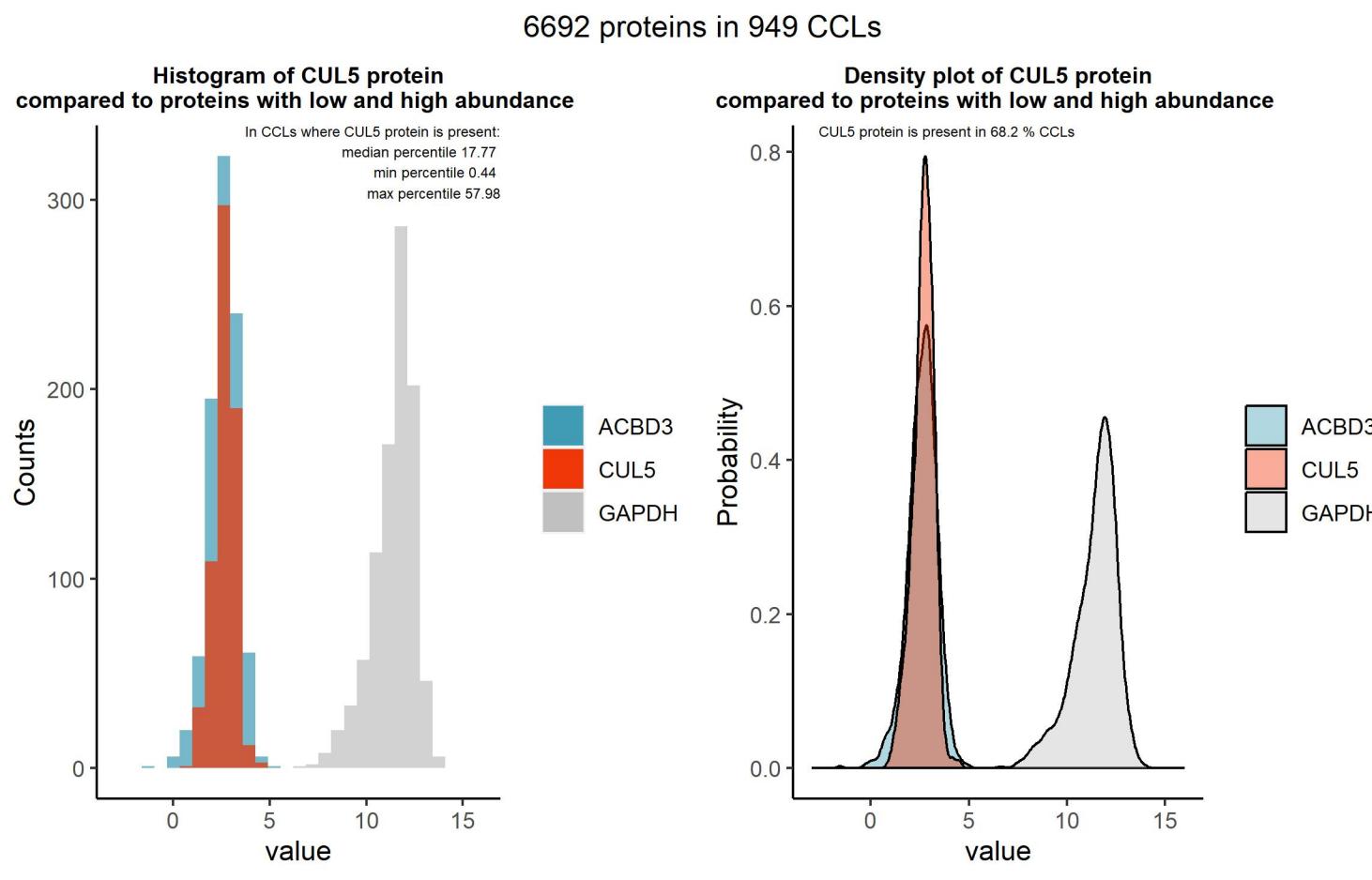


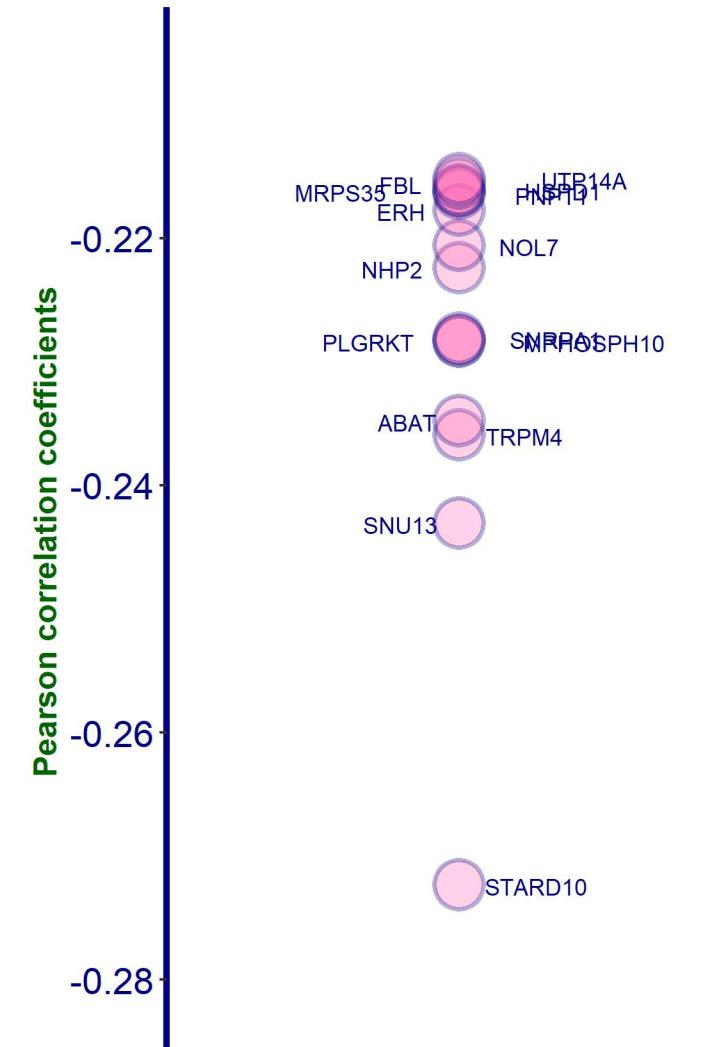
CUL5

Protein name: CUL5 ; UNIPROT: Q93034 ; Gene name: cullin 5
 Ligandable: Yes ; Ligandable_by_Chem: NA ; Is_enzyme: NA (<https://cansar.ai/>)

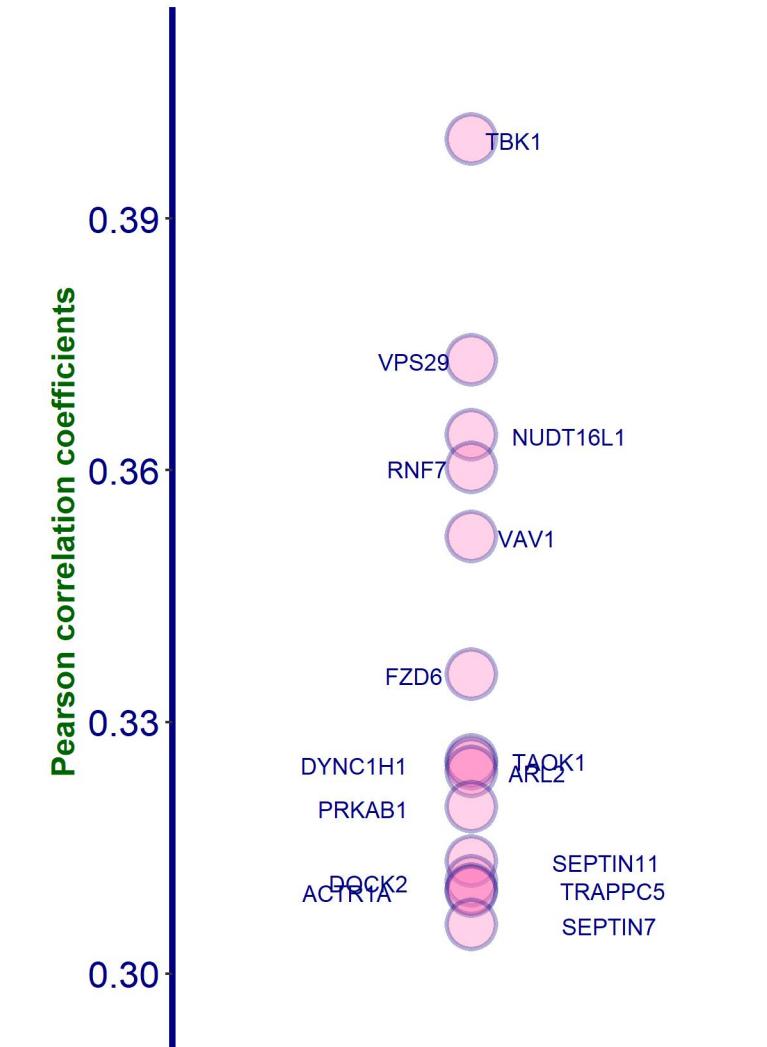
Sanger Institute Protein Database 1 (DB1), protein presence is certain



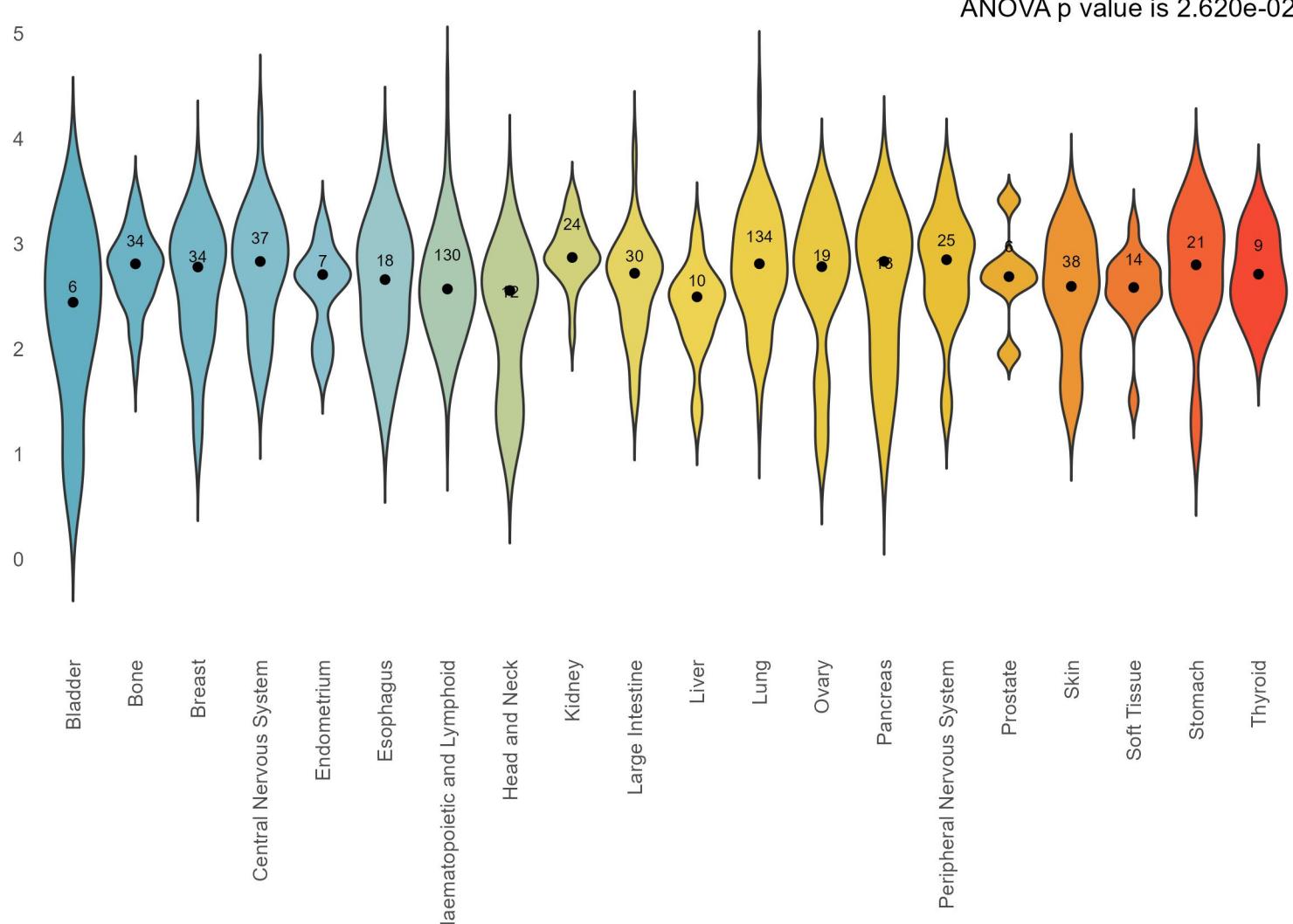
Top negative correlations of CUL5 protein, DB1



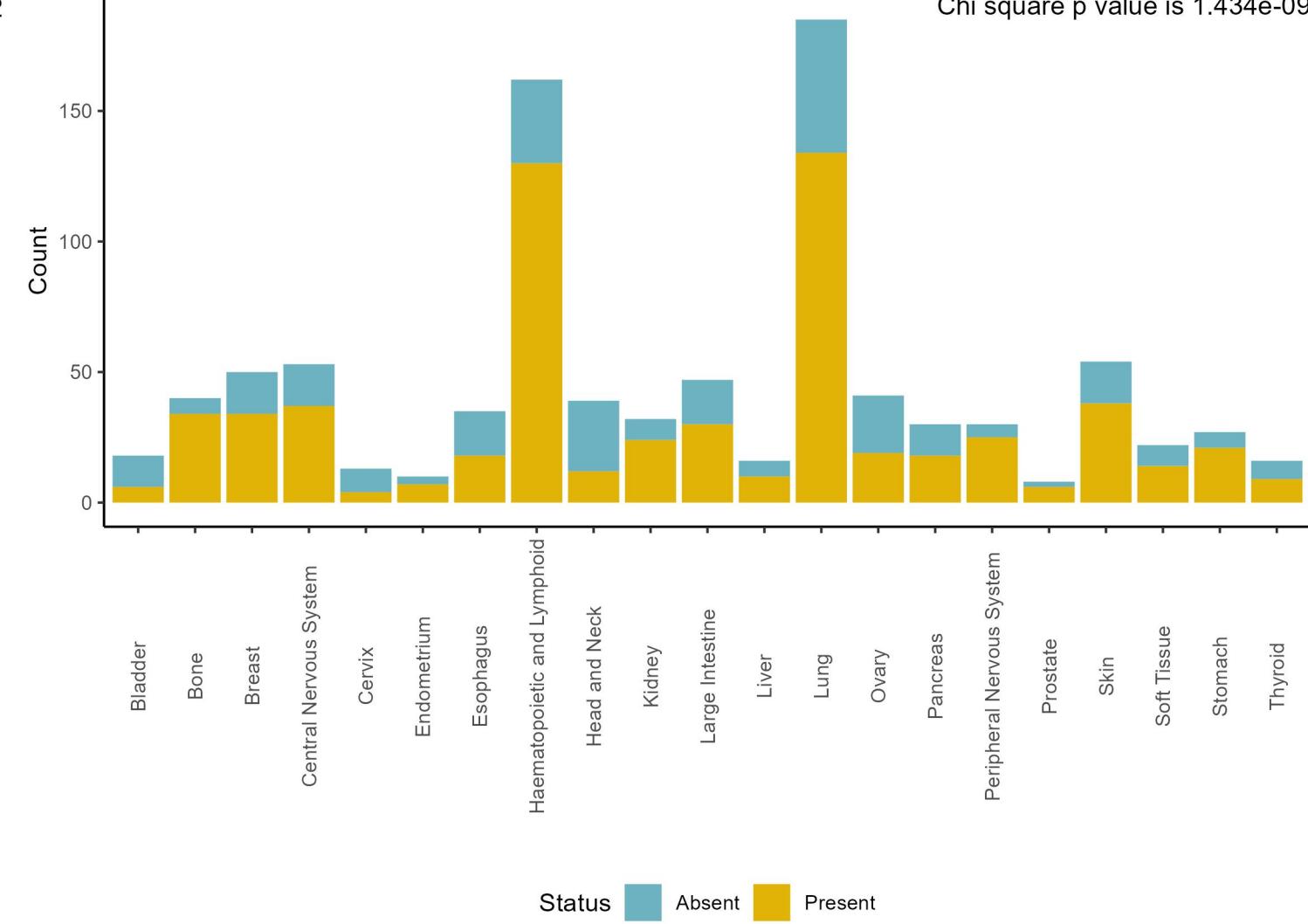
Top positive correlations of CUL5 protein, DB1



Amount of CUL5 protein, number of CCLs where it is present by tissue, DB1



Present and absent CUL5 protein counts by tissue, DB1

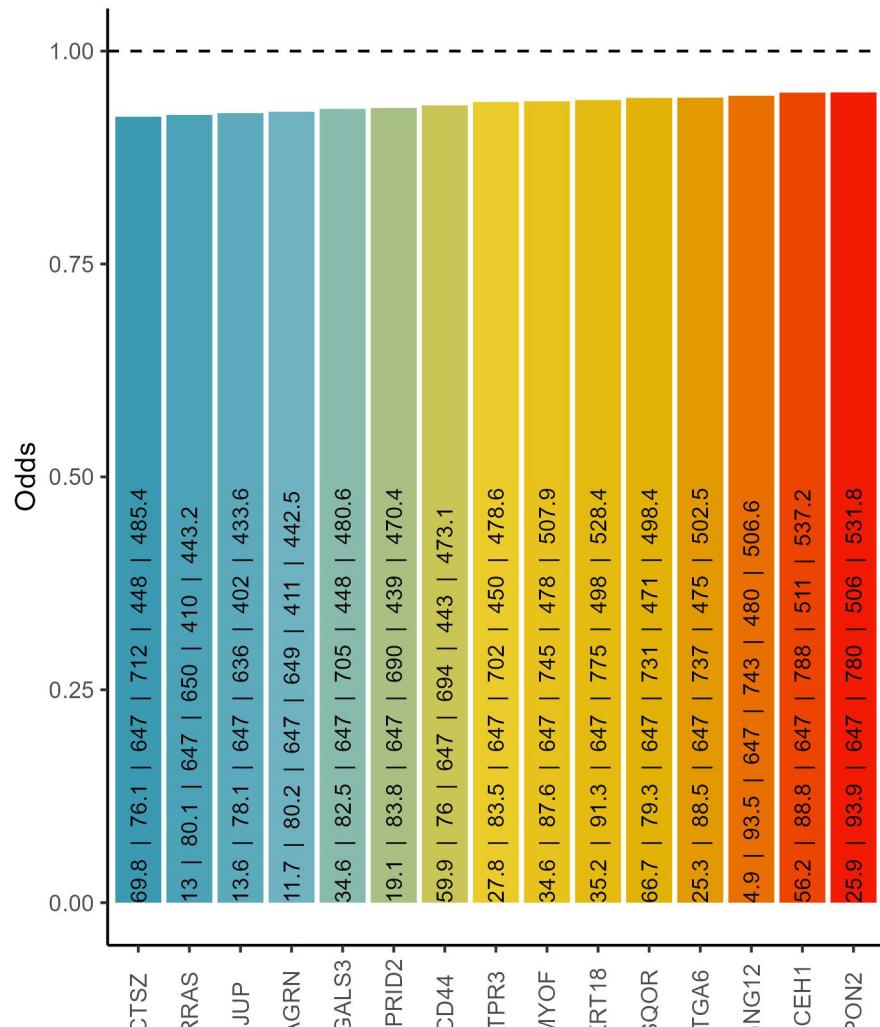


Cooccurrence with CUL5 protein, DB1

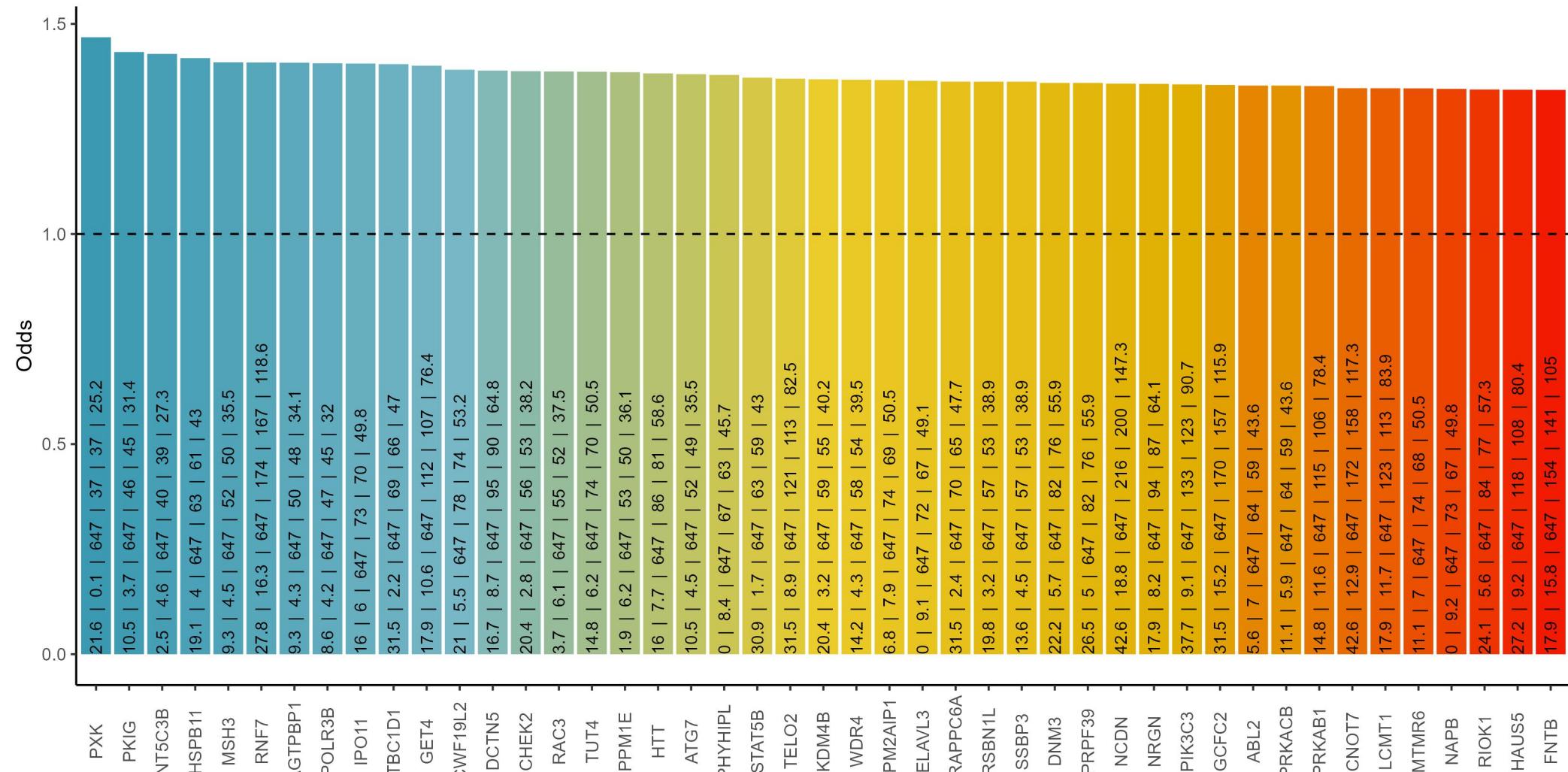
% of CUL5 in blood cancers: 80.2 ; % of CUL5 in solid cancers: 65.6

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CUL5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

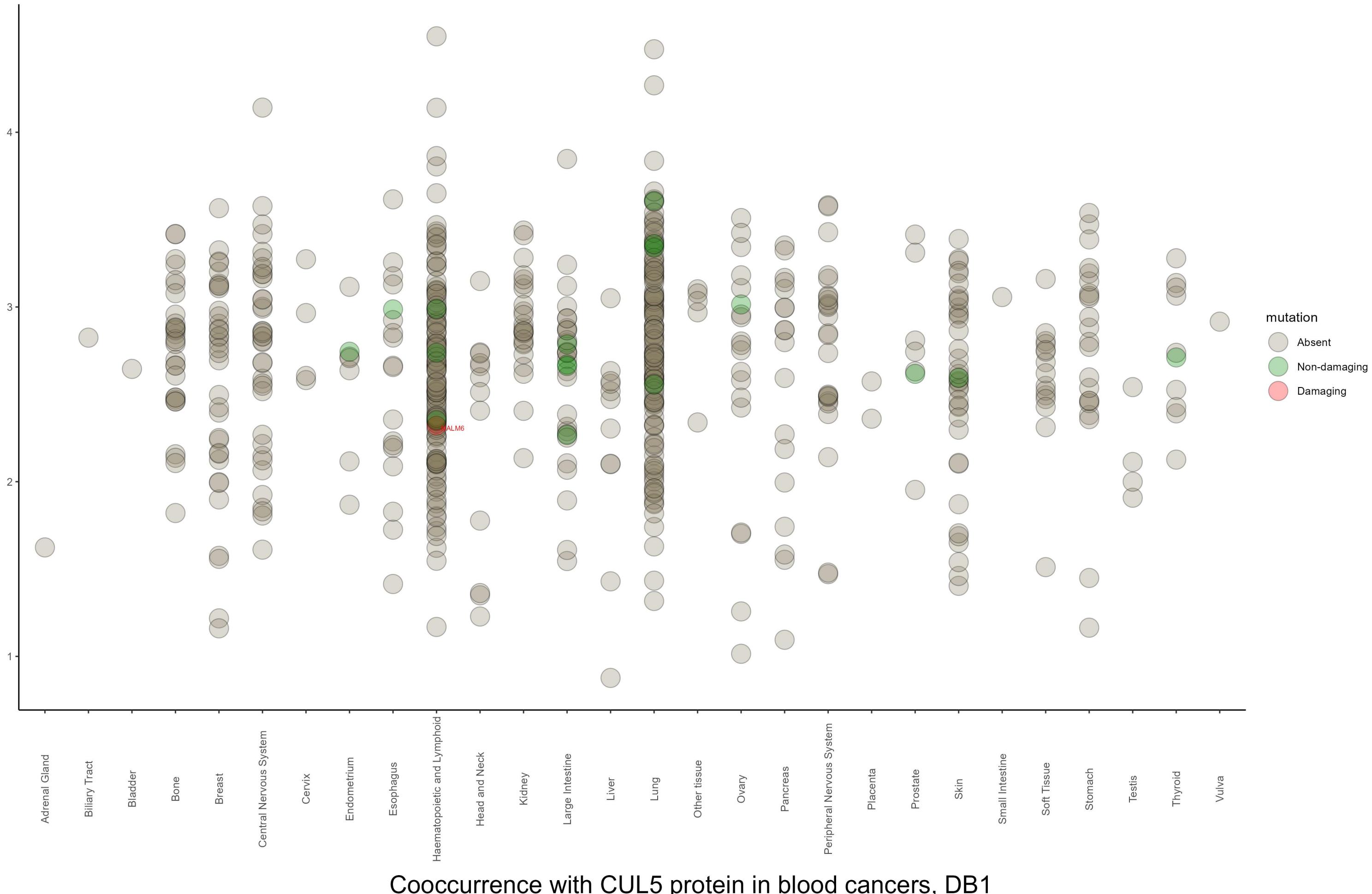
Negative cooccurrence



Positive cooccurrence

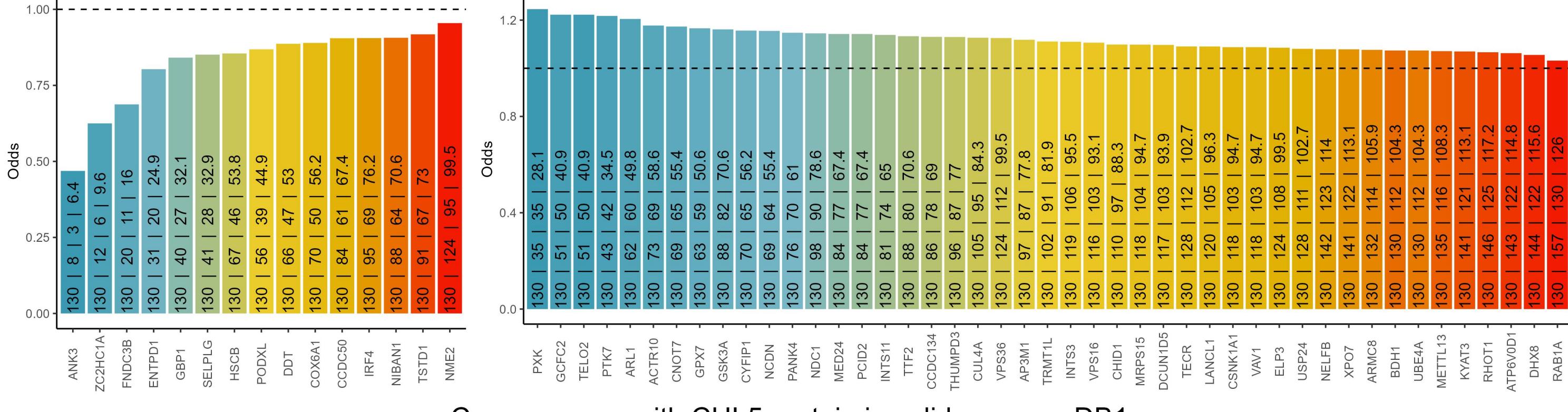


Amount of CUL5 protein and mutation status by tissue, DB1



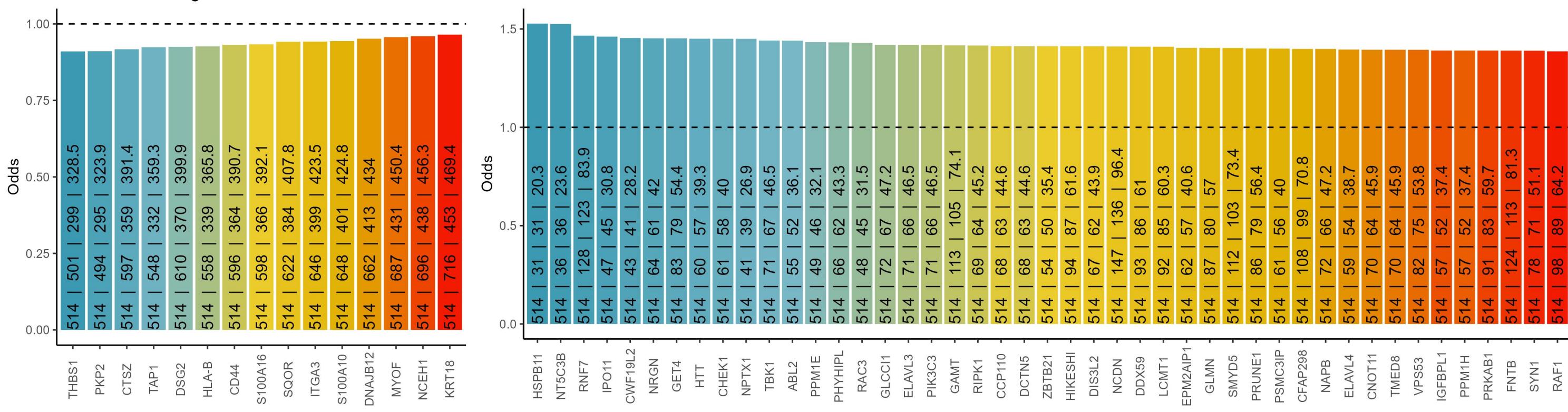
Cooccurrence with CUL5 protein in blood cancers, DB1

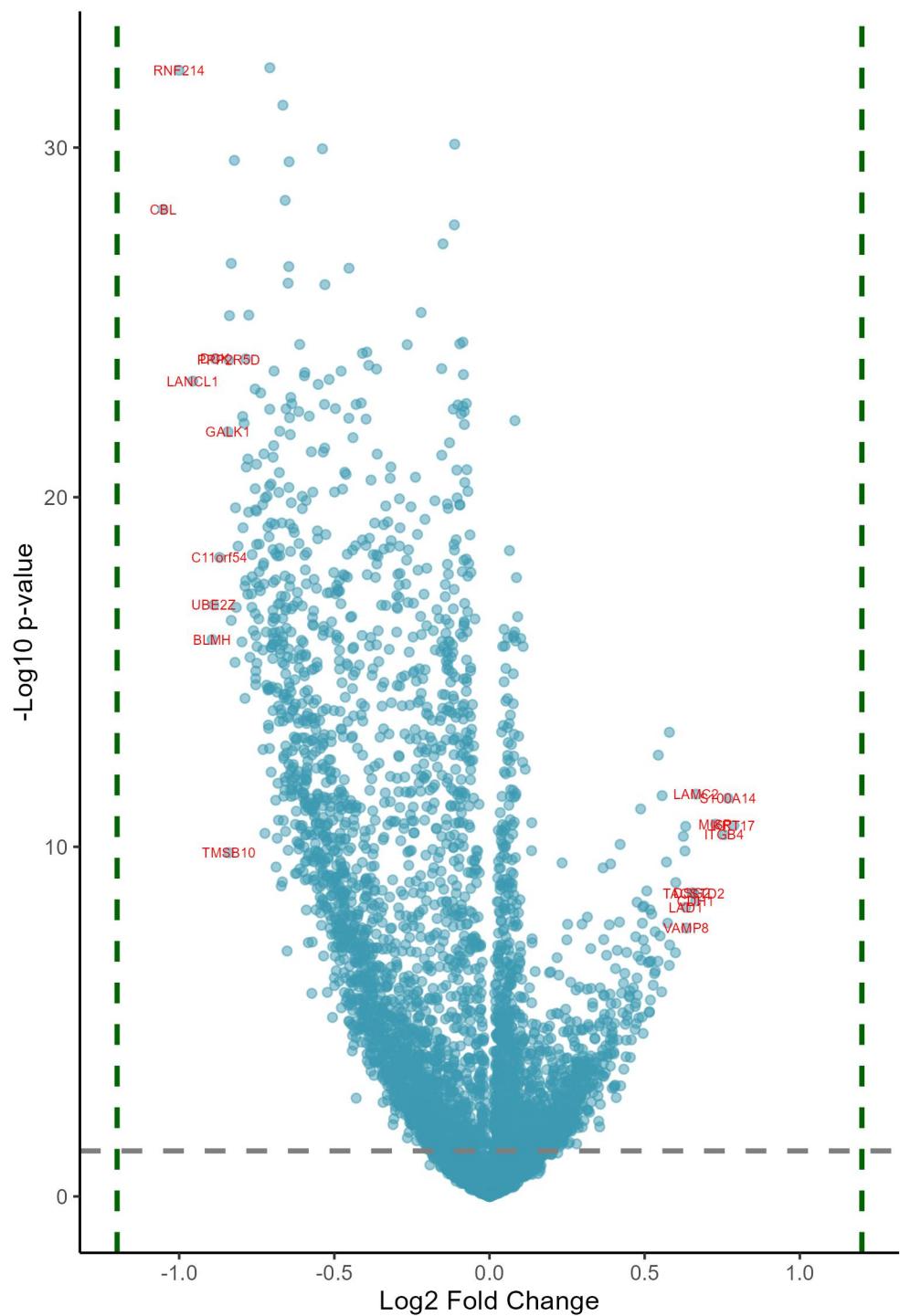
The text in the bars: incidence of CUL5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Cooccurrence with CUL5 protein in solid cancers, DB1

The text in the bars: incidence of CUL5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

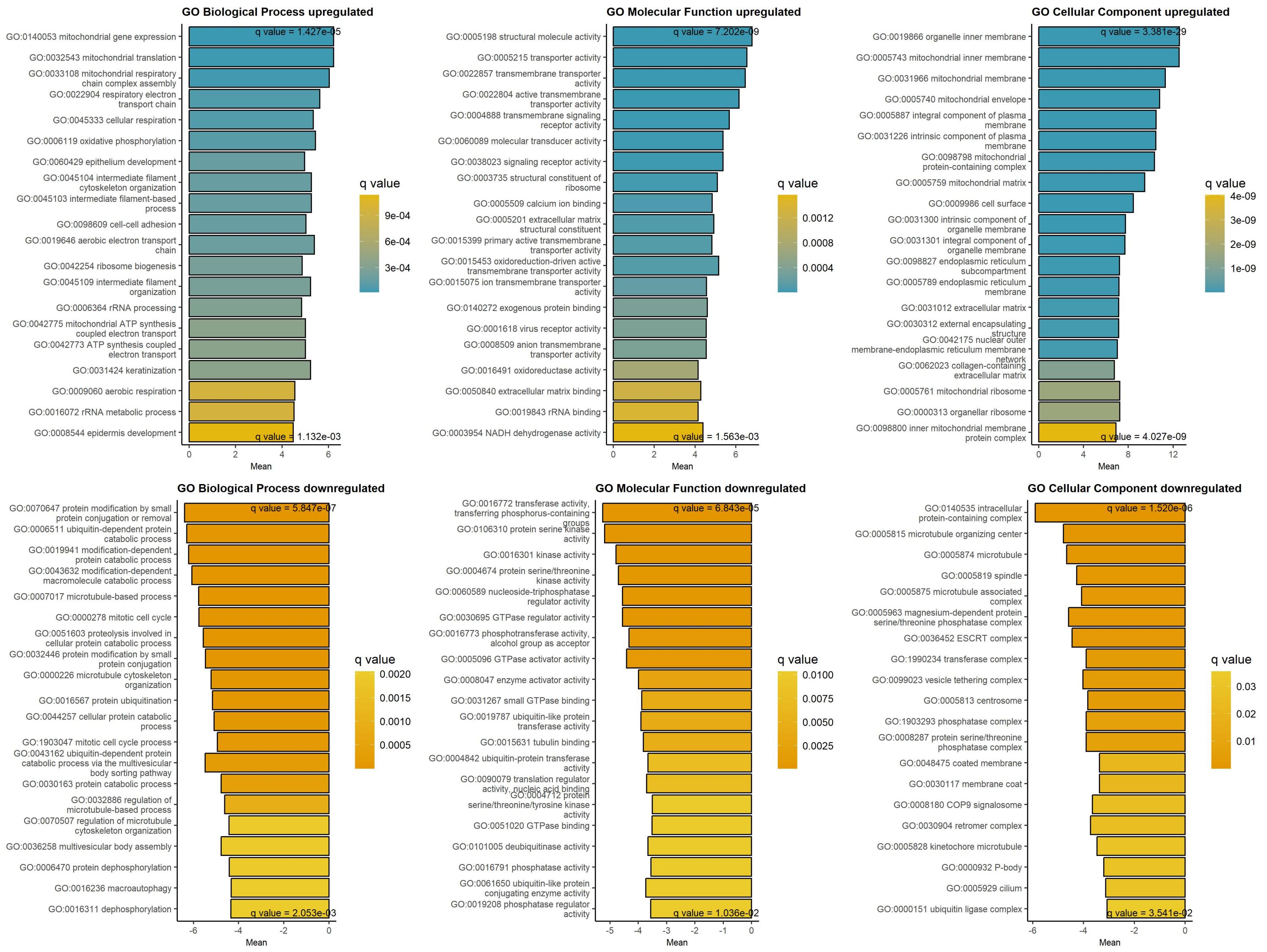


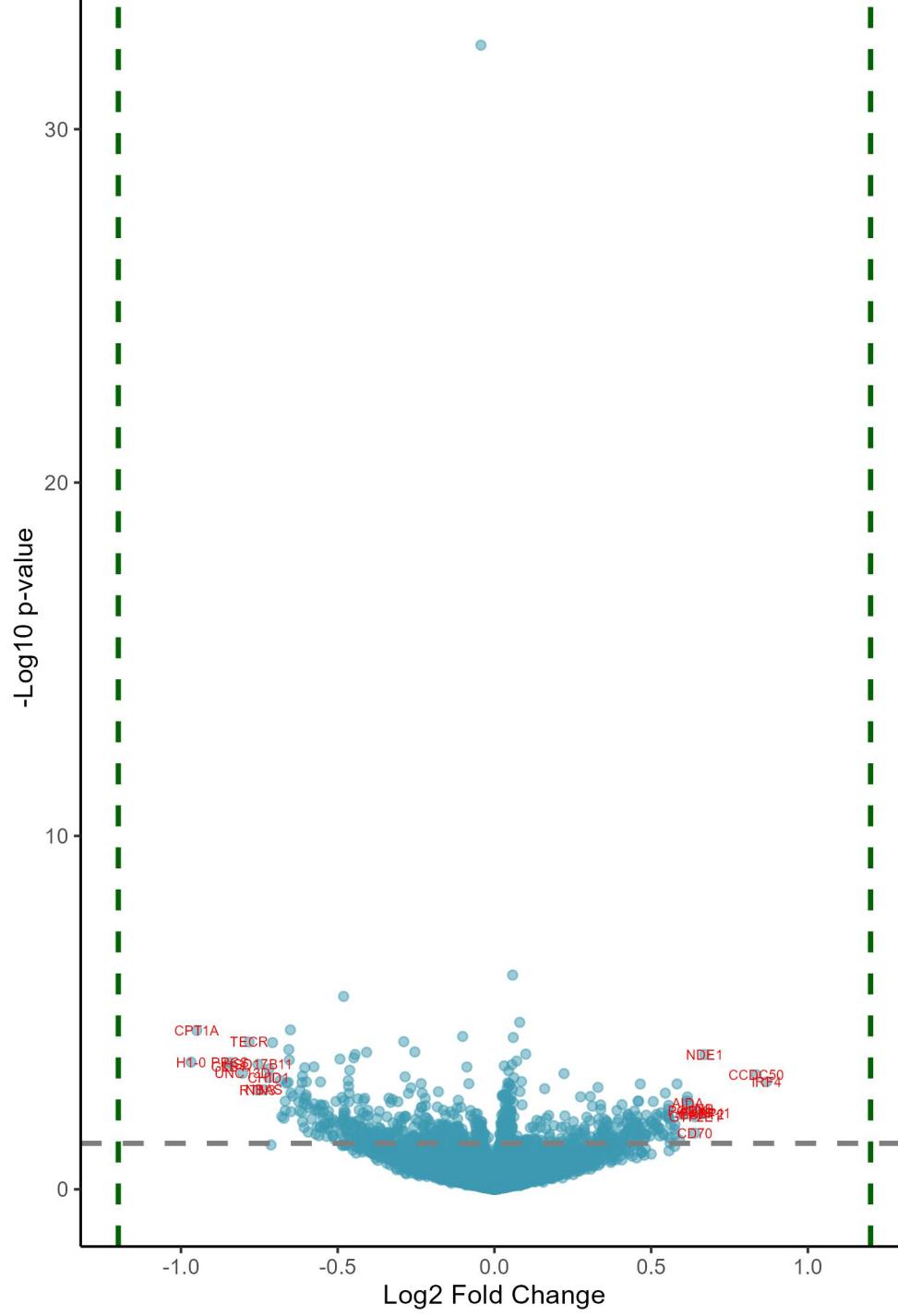


Downregulated at low/absent CUL5 Upregulated at low/absent CUL5

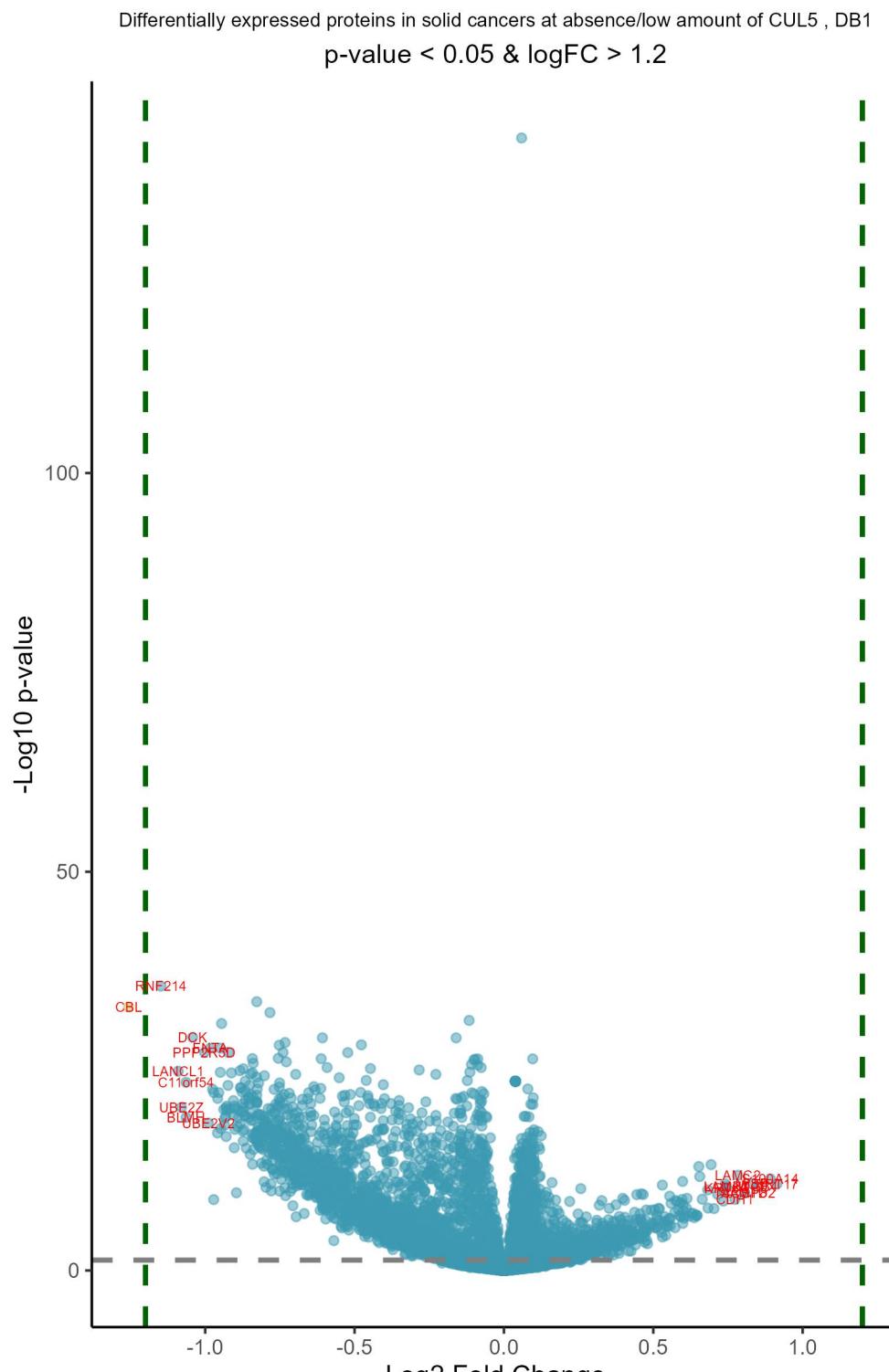
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-1.05	3.89e-26	CBL	Cbl proto-oncogene	0.79	2.00e-10	KRT17	keratin 17
-1	1.37e-29	RNF214	ring finger protein 214	0.77	3.78e-11	S100A14	S100 calcium binding protein A14
-0.96	8.16e-22	LANCL1	LanC like 1	0.76	3.56e-10	ITGB4	integrin subunit beta 4
-0.89	2.50e-15	BLMH	bleomycin hydrolase	0.73	1.87e-10	MISP	mitotic spindle positioning
-0.89	3.35e-16	UBE2Z	ubiquitin conjugating enzyme E2 Z	0.67	2.97e-11	LAMC2	laminin subunit gamma 2
-0.88	2.62e-22	DCK	deoxyctydine kinase	0.66	2.16e-08	CDH1	cadherin 1
-0.87	2.06e-17	C11orf54	chromosome 11 open reading frame 54	0.66	1.34e-08	TACSTD2	tumor associated calcium signal tra
-0.84	1.34e-20	GALK1	galactokinase 1	0.65	1.30e-08	DSG2	desmoglein 2
-0.84	1.08e-09	TMSB10	thymosin beta 10	0.63	1.16e-07	VAMP8	vesicle associated membrane protein
-0.84	2.74e-22	PPP2R5D	protein phosphatase 2 regulatory su	0.63	3.21e-08	LAD1	ladinin 1
-0.84	2.13e-23	FNTA	farnesyltransferase, CAAX box, alph	0.63	2.12e-10	CDH3	cadherin 3
-0.83	8.23e-16	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.63	9.72e-10	LAMB3	laminin subunit beta 3
-0.83	1.05e-24	TBCD	tubulin folding cofactor D	0.62	3.94e-10	KRT6A	keratin 6A
-0.82	2.12e-27	RAP1GDS1	Rap1 GTPase-GDP dissociation stimul	0.6	6.92e-09	RAB25	RAB25, member RAS oncogene family
-0.82	9.62e-15	UBLCP1	ubiquitin like domain containing CT	0.6	5.30e-07	PKP3	plakophilin 3
-0.82	1.16e-18	PPM1F	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe	0.58	3.31e-07	SPINT1	serine peptidase inhibitor, Kunitz
-0.82	3.84e-16	FKBP1A	FKBP prolyl isomerase 1A	0.58	6.73e-13	LAMA3	laminin subunit alpha 3
-0.81	1.11e-17	GNPDA1	glucosamine-6-phosphate deaminase 1	0.58	1.17e-06	PKP2	plakophilin 2
-0.8	2.85e-15	PRPS1	phosphoribosyl pyrophosphate synth	0.57	8.55e-08	FAM83H	family with sequence similarity 83
-0.8	5.54e-21	PHPT1	phosphohistidine phosphatase 1	0.57	1.93e-09	ITGB6	integrin subunit beta 6
-0.79	3.82e-18	PITHD1	PITH domain containing 1	0.56	3.25e-11	PLEKHG3	pleckstrin homology and RhoGEF doma
-0.79	8.02e-21	MAPK14	mitogen-activated protein kinase 14	0.55	6.09e-06	JUP	junction plakoglobin
-0.79	8.59e-14	TMEM263	transmembrane protein 263	0.55	1.89e-07	CGN	cingulin
-0.79	1.10e-16	PRPSAP2	phosphoribosyl pyrophosphate synth	0.54	2.70e-12	FAM83B	family with sequence similarity 83
-0.79	2.62e-22	PPP6C	protein phosphatase 6 catalytic sub	0.54	9.07e-07	EPB41L1	erythrocyte membrane protein band 4
-0.79	8.01e-17	ABI2	abl interactor 2	0.53	1.68e-06	EPCAM	epithelial cell adhesion molecule
-0.78	1.11e-19	PPP1R14B	protein phosphatase 1 regulatory in	0.53	1.46e-07	EVPL	envoplakin
-0.78	1.76e-16	PPP2CA	protein phosphatase 2 catalytic sub	0.53	1.95e-06	KRT80	keratin 80
-0.78	6.82e-20	UBXN6	UBX domain protein 6	0.53	4.02e-06	CTSZ	cathepsin Z

GAGE analysis on upregulated and downregulated proteins at low/absent CUL5 protein, DB1



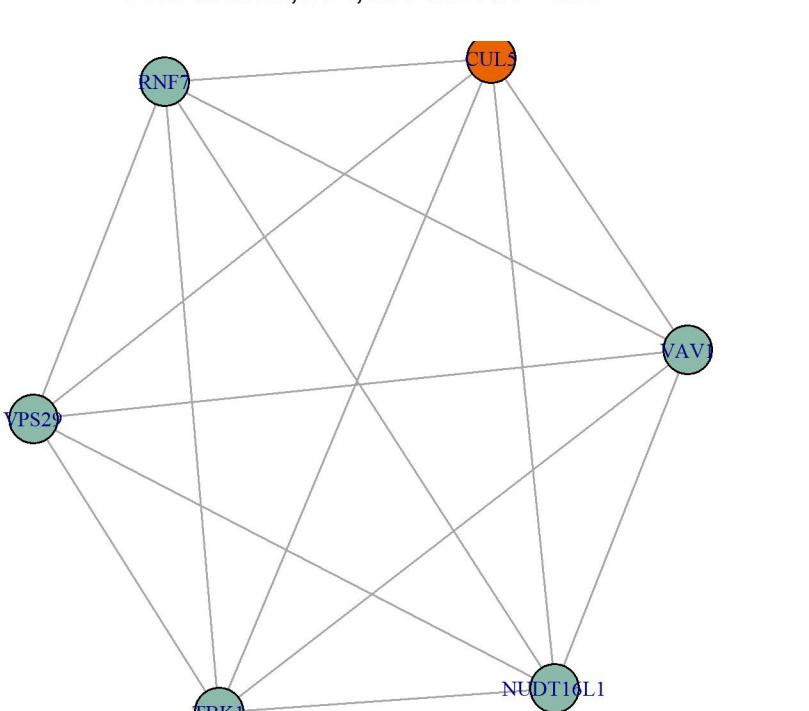


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.97	7.11e-02	H1-0	H1.0 linker histone	0.87	1.24e-01	IRF4	interferon regulatory factor 4
-0.95	3.03e-02	CPT1A	carnitine palmitoyltransferase 1A	0.84	1.03e-01	CCDC50	coiled-coil domain containing 50
-0.85	7.65e-02	GLB1	galactosidase beta 1	0.67	2.80e-01	FKBP11	FKBP prolyl isomerase 11
-0.84	7.11e-02	PPCS	phosphopantethenoylcysteine synthet	0.67	5.69e-02	NDE1	nudE neurodevelopment protein 1
-0.8	9.82e-02	UNC13D	unc-13 homolog D	0.66	2.81e-01	GSPT2	G1 to S phase transition 2
-0.78	3.91e-02	TECR	trans-2,3-enoyl-CoA reductase	0.64	2.66e-01	JUNB	JunB proto-oncogene, AP-1 transcrip
-0.76	1.58e-01	RTN3	reticulon 3	0.64	2.92e-01	GTF2E1	general transcription factor IIE su
-0.75	7.63e-02	HSD17B11	hydroxysteroid 17-beta dehydrogenas	0.64	3.89e-01	CD70	CD70 molecule
-0.74	1.57e-01	NBAS	NBAS subunit of NRZ tethering compl	0.63	2.66e-01	PODXL	podocalyxin like
-0.72	1.13e-01	CHID1	chitinase domain containing 1	0.62	2.14e-01	AIDA	axin interactor, dorsalization asso
-0.72	8.10e-02	ARL1	ADP ribosylation factor like GTPase	0.62	2.81e-01	GINS1	GINS complex subunit 1
-0.71	4.26e-01	S100A4	S100 calcium binding protein A4	0.62	1.87e-01	RAD18	RAD18 E3 ubiquitin protein ligase
-0.71	3.91e-02	IL18	interleukin 18	0.61	2.01e-01	DLG1	discs large MAGUK scaffold protein
-0.68	1.24e-01	VAV1	vav guanine nucleotide exchange fac	0.59	2.83e-01	ZMAT2	zinc finger matrin-type 2
-0.68	2.92e-01	GSN	gelsolin	0.59	4.26e-01	JCHAIN	joining chain of multimeric IgA and
-0.67	3.06e-01	STOM	stomatin	0.58	1.24e-01	ZC3H8	zinc finger CCCH-type containing 8
-0.67	2.66e-01	INTS7	integrator complex subunit 7	0.58	3.98e-01	RPL22L1	ribosomal protein L22 like 1
-0.67	2.01e-01	CRTAP	cartilage associated protein	0.58	3.37e-01	UBE2G2	ubiquitin conjugating enzyme E2 G2
-0.66	1.24e-01	TRAPP5	trafficking protein particle comple	0.57	4.26e-01	LSP1	lymphocyte specific protein 1
-0.66	1.24e-01	UBAC2	UBA domain containing 2	0.57	3.58e-01	ISG20	interferon stimulated exonuclease g
-0.66	5.66e-02	ABHD16A	abhydrolase domain containing 16A,	0.56	3.37e-01	GLCCI1	glucocorticoid induced 1
-0.65	6.93e-02	VPS16	VPS16 core subunit of CORVET and HO	0.56	4.26e-01	NME2	NME/NM23 nucleoside diphosphate kin
-0.65	3.03e-02	QDPR	quinoid dihydropteridine reductase	0.56	4.15e-01	POLR1D	RNA polymerase I and III subunit D
-0.65	1.74e-01	PECAM1	platelet and endothelial cell adhes	0.56	4.26e-01	UCHL1	ubiquitin C-terminal hydrolase L1
-0.65	2.69e-01	ATP5MF	ATP synthase membrane subunit f	0.56	3.08e-01	RPS19BP1	ribosomal protein S19 binding prote
-0.64	1.87e-01	ARRB1	arrestin beta 1	0.56	2.94e-01	USP13	ubiquitin specific peptidase 13
-0.62	2.01e-01	MYO1F	myosin IF	0.56	2.28e-01	KNOP1	lysine rich nucleolar protein 1
-0.62	2.66e-01	VAMP7	vesicle associated membrane protein	0.56	2.66e-01	SNTB2	syntrophin beta 2
-0.62	1.58e-01	BDH1	3-hydroxybutyrate dehydrogenase 1	0.55	2.89e-01	ATP2B1	ATPase plasma membrane Ca ²⁺ transpo

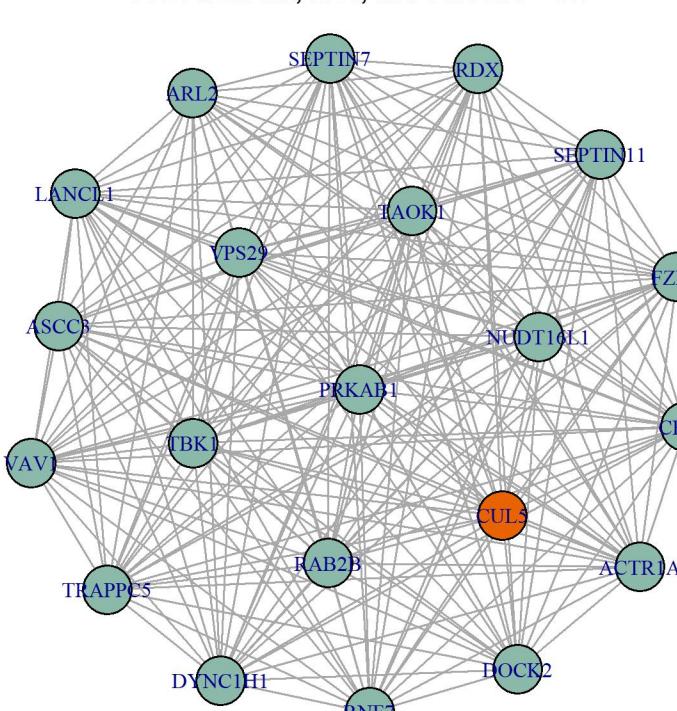


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.26	1.25e-30	CBL	Cbl proto-oncogene	0.91	9.31e-11	KRT17	keratin 17
-1.15	4.84e-33	RNF214	ring finger protein 214	0.89	2.25e-11	S100A14	S100 calcium binding protein A14
-1.09	1.78e-23	LANCL1	LanC like 1	0.85	1.84e-10	ITGB4	integrin subunit beta 4
-1.08	1.05e-19	UBE2Z	ubiquitin conjugating enzyme E2 Z	0.83	7.80e-11	MISP	mitotic spindle positioning
-1.06	1.28e-22	C11orf54	chromosome 11 open reading frame 54	0.81	1.06e-09	TACSTD2	tumor associated calcium signal tra
-1.06	1.52e-18	BLMH	bleomycin hydrolase	0.81	1.05e-09	VAMP8	vesicle associated membrane protein
-1.04	4.08e-27	DCK	deoxyctydine kinase	0.78	8.80e-12	LAMC2	laminin subunit gamma 2
-1	1.59e-25	PPP2R5D	protein phosphatase 2 regulatory su	0.77	6.25e-09	CDH1	cadherin 1
-0.99	6.94e-18	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.75	2.66e-10	KRT6A	keratin 6A
-0.98	5.60e-26	FNTA	farnesyltransferase, CAAX box, alph	0.74	1.86e-10	LAMB3	laminin subunit beta 3
-0.98	8.55e-22	GALK1	galactokinase 1	0.74	8.59e-11	CDH3	cadherin 3
-0.97	6.57e-09	TMSB10	thymosin beta 10	0.74	5.88e-10	DSG2	desmoglein 2
-0.97	2.07e-21	MVD	mevalonate diphosphate decarboxylas	0.73	9.84e-09	LAD1	ladinin 1
-0.96	1.00e-16	TMEM263	transmembrane protein 263	0.72	1.57e-09	RAB25	RAB25, member RAS oncogene family
-0.96	1.00e-20	PITHD1	PITH domain containing 1	0.7	7.66e-08	PKP3	plakophilin 3
-0.95	2.16e-21	ABI2	abl interactor 2	0.69	4.84e-13	LAMA3	laminin subunit alpha 3
-0.95	2.37e-23	PHPT1	phosphohistidine phosphatase 1	0.68	6.65e-08	SPINT1	serine peptidase inhibitor, Kunitz
-0.95	5.60e-26	TBCD	tubulin folding cofactor D	0.68	4.77e-10	ITGB6	integrin subunit beta 6
-0.95	3.04e-17	FKBP1A	FKBP prolyl isomerase 1A	0.66	6.04e-09	FAM83H	family with sequence similarity 83
-0.95	8.89e-29	RAP1GDS1	Rap1 GTPase-GDP dissociation stimul	0.66	1.21e-11	PLEKHG3	pleckstrin homology and RhoGEF doma
-0.94	1.80e-19	PRPSAP2	phosphoribosyl pyrophosphate synthe	0.65	8.19e-13	FAM83B	family with sequence similarity 83
-0.94	1.28e-17	PRPS1	phosphoribosyl pyrophosphate synthe	0.65	5.30e-07	PKP2	plakophilin 2
-0.93	1.77e-18	PPP2CA	protein phosphatase 2 catalytic sub	0.64	4.49e-07	CTSZ	cathepsin Z
-0.93	1.29e-19	CZIB	CXXC motif containing zinc binding	0.64	5.24e-07	SPINT2	serine peptidase inhibitor, Kunitz
-0.93	1.18e-18	ACYP1	acylphosphatase 1	0.64	9.01e-07	ANXA3	annexin A3
-0.93	2.61e-16	PBK	PDZ binding kinase	0.63	2.86e-07	EPCAM	epithelial cell adhesion molecule
-0.93	7.63e-20	PPM1F	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe	0.63	2.61e-07	F3	coagulation factor III, tissue fact
-0.93	2.42e-19	MCRIP1	MAPK regulated corepressor interact	0.62	6.04e-07	KRT80	keratin 80
-0.92	2.99e-22	DHPS	deoxyhypusine synthase	0.61	4.76e-09	COL17A1	collagen type XVII alpha 1 chain

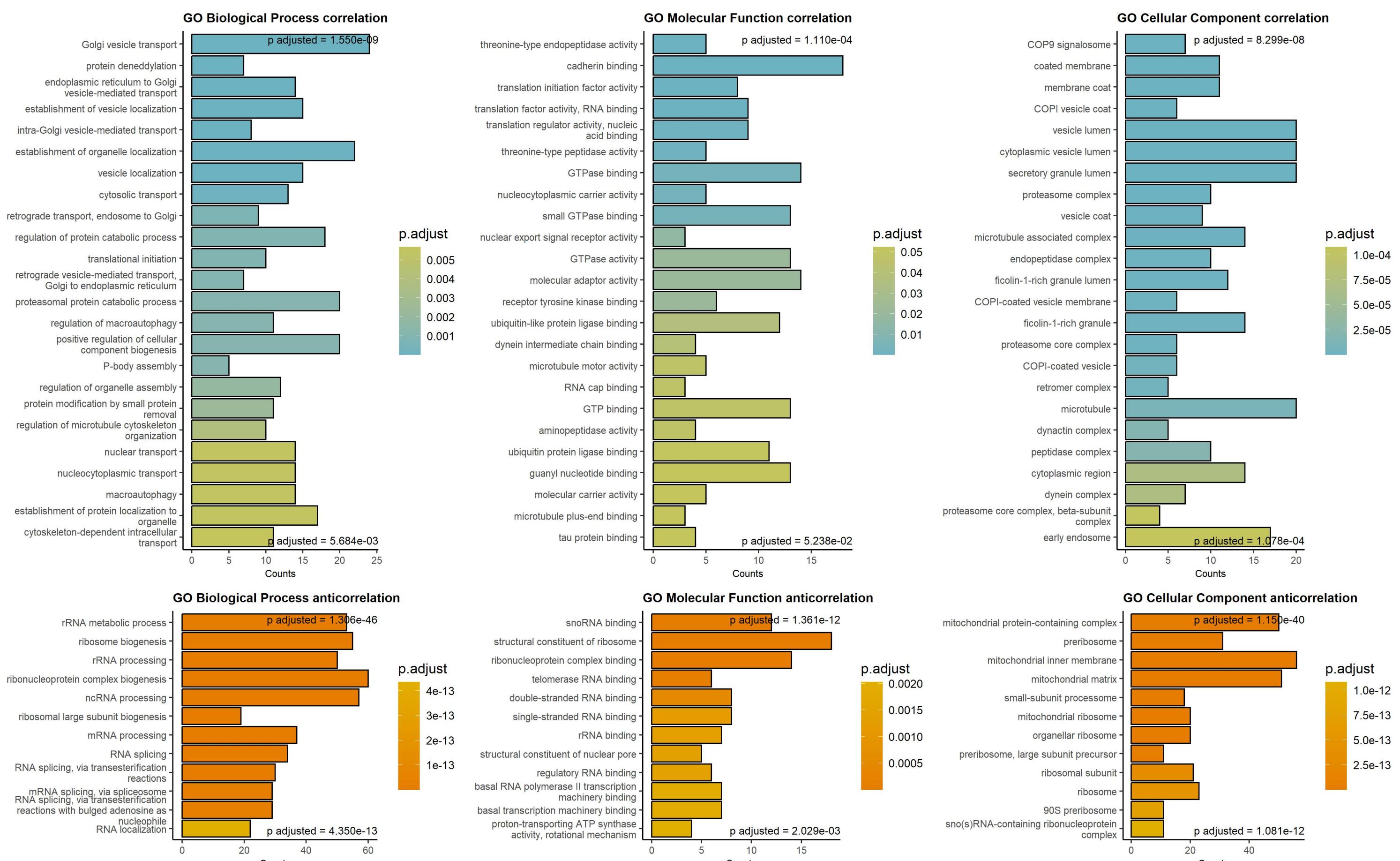
CUL5 network, DB1, all Pearson r > 0.35



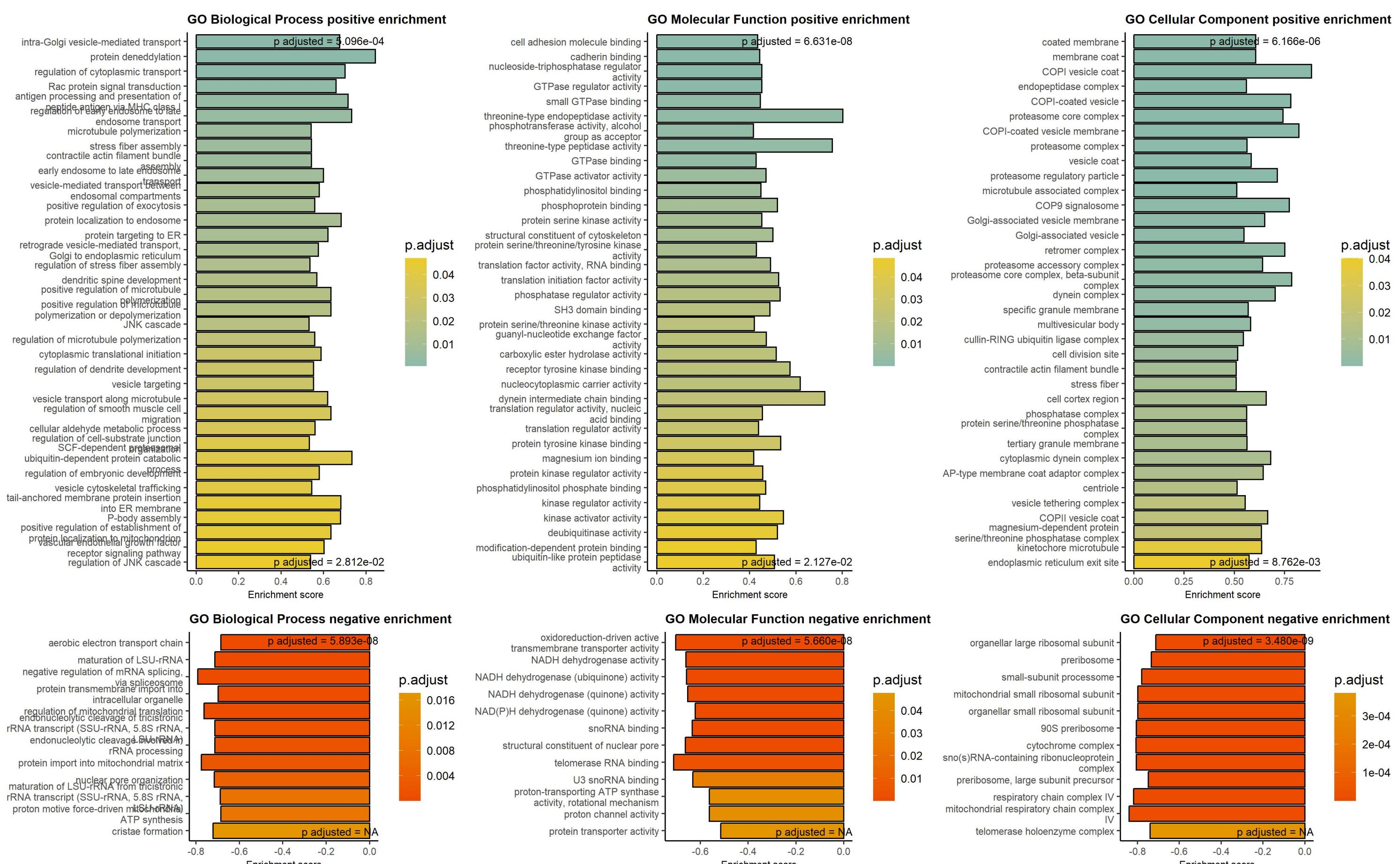
CUL5 network, DB1, all Pearson r > 0.3



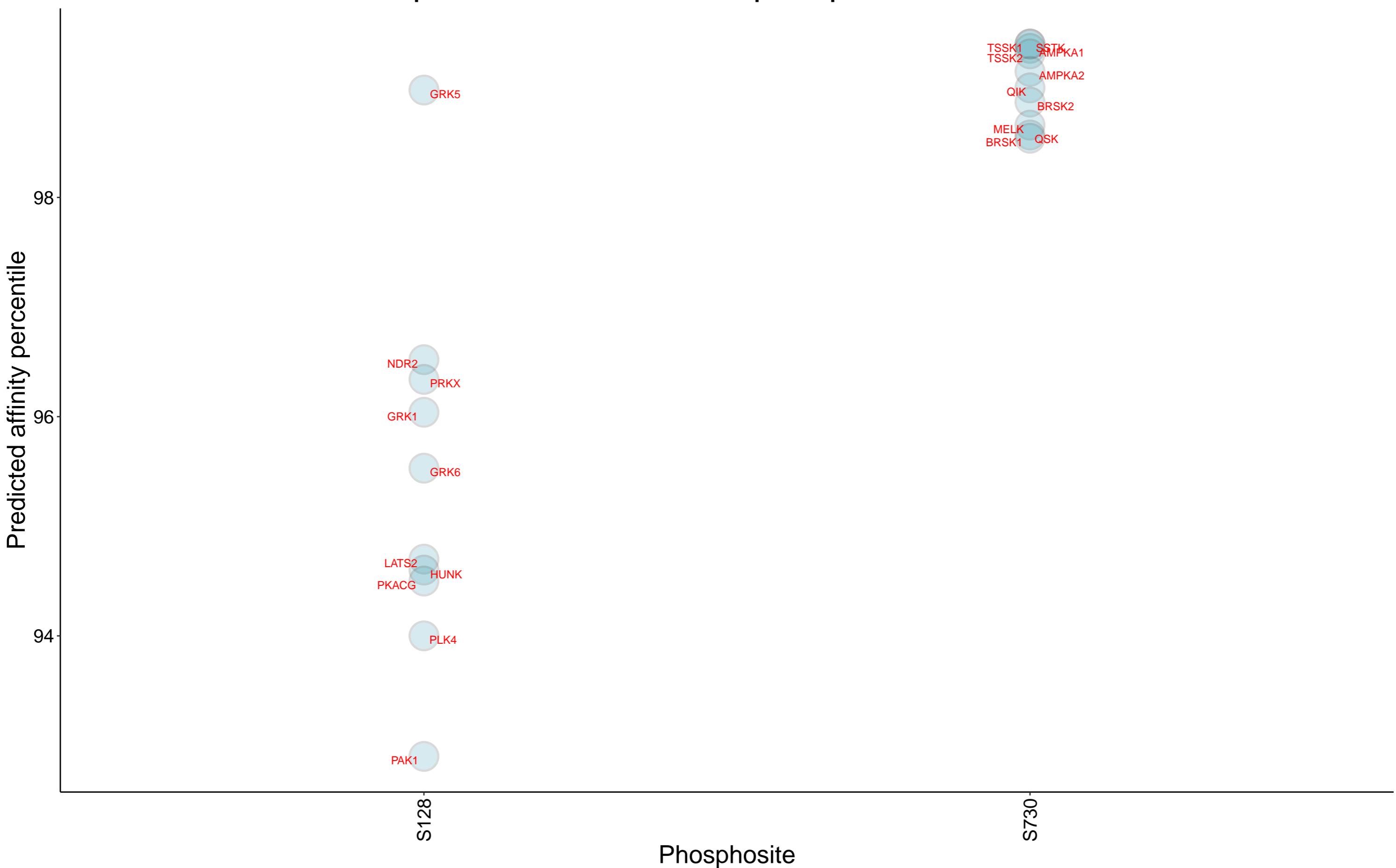
Top 250 correlation coefficients overrepresentation, CUL5 protein, DB1



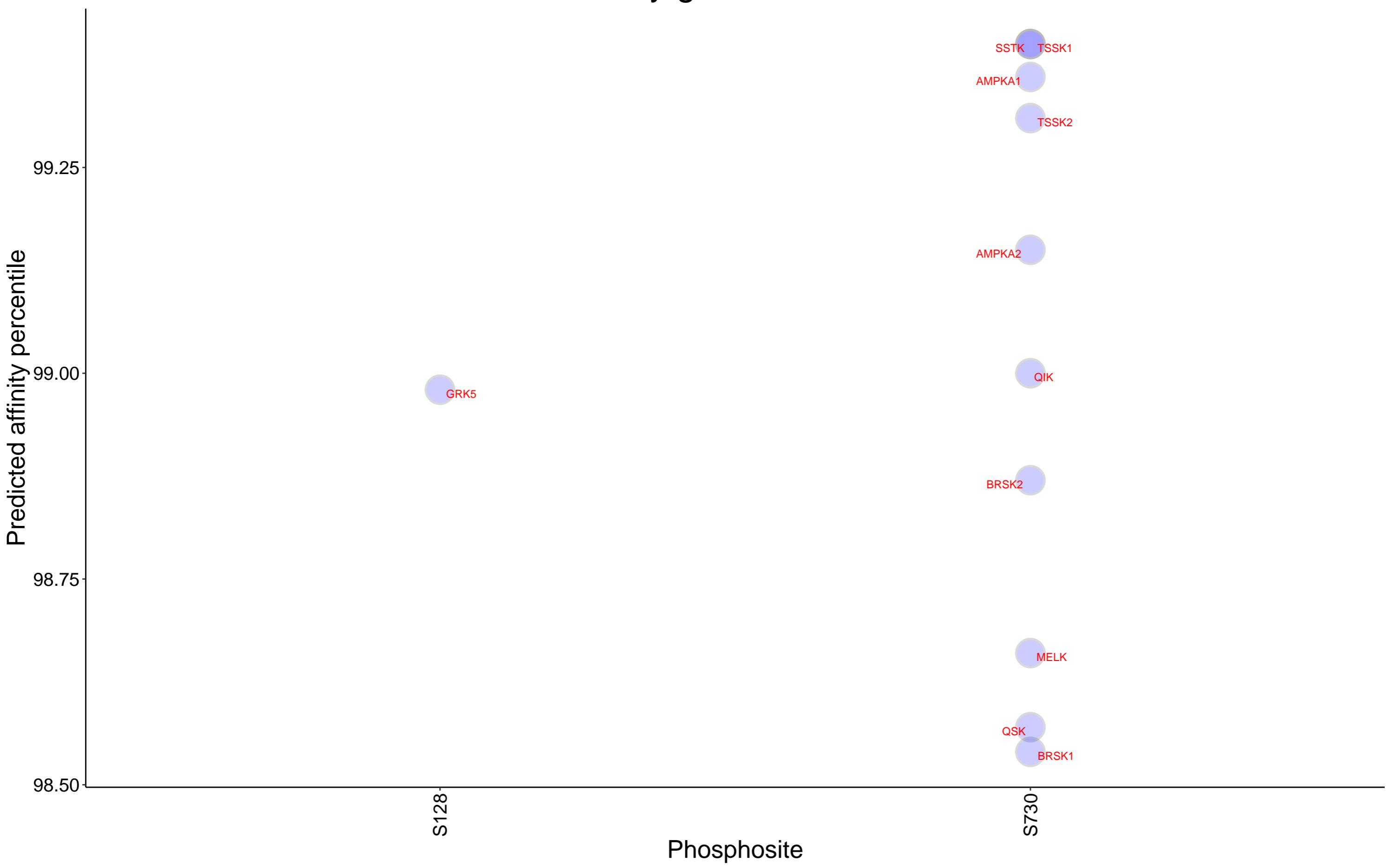
Gene Set Enrichment analysis on protein correlation coefficients, CUL5 protein, DB1



Top 10 kinases for each phosphosite in CUL5



Kinases with affinity greater than 98.5% to CUL5



Top 15 positive correlation coefficients for CUL5 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

