

CUL4B

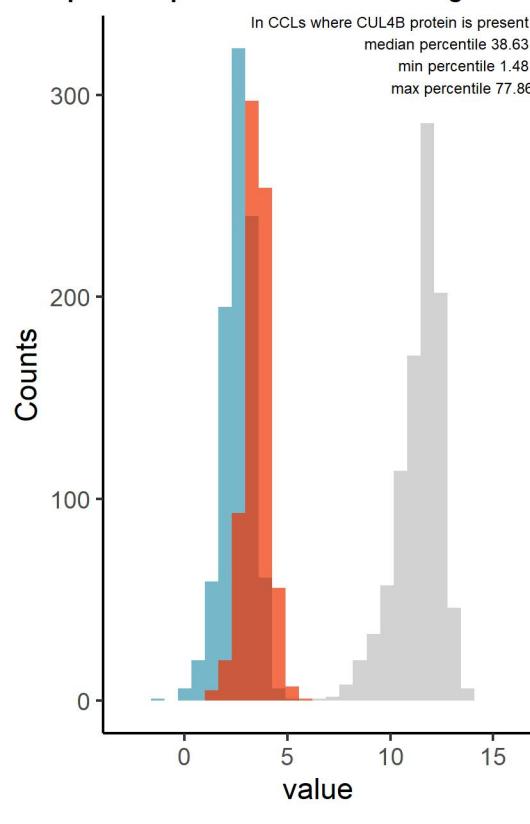
Protein name: CUL4B ; UNIPROT: Q13620 ; Gene name: cullin 4B

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

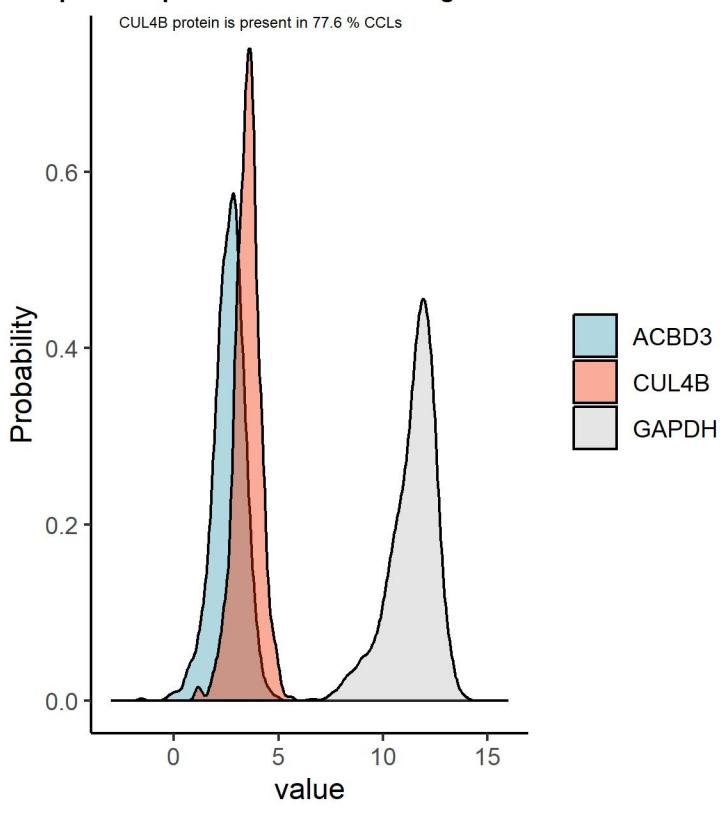
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

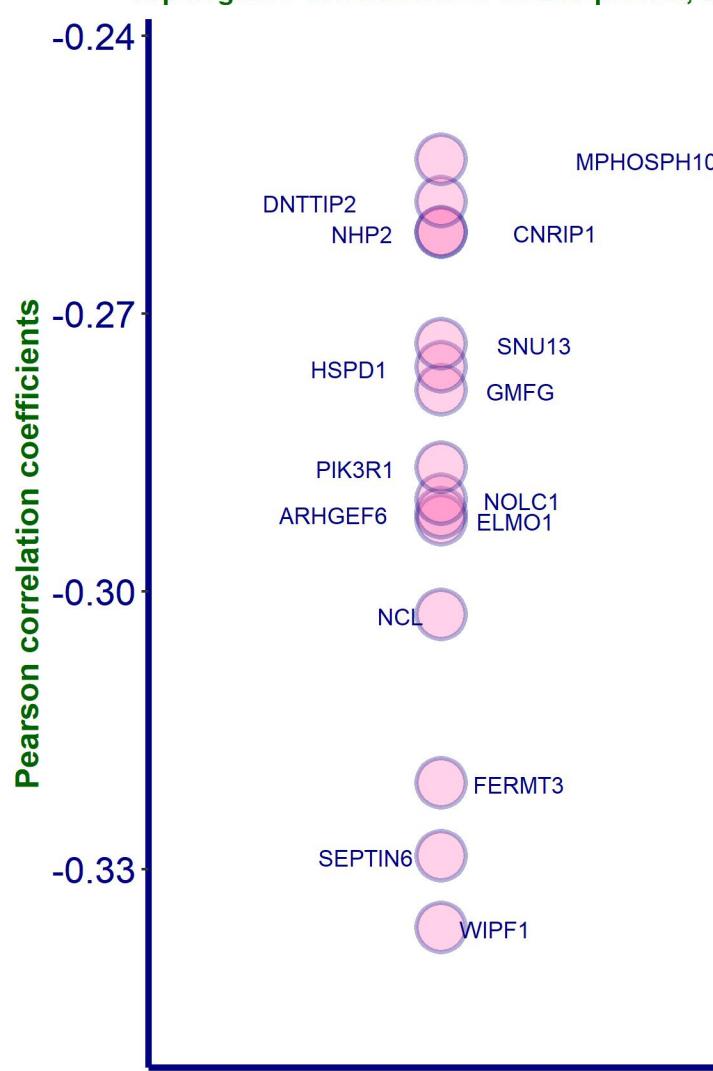
Histogram of CUL4B protein compared to proteins with low and high abundance



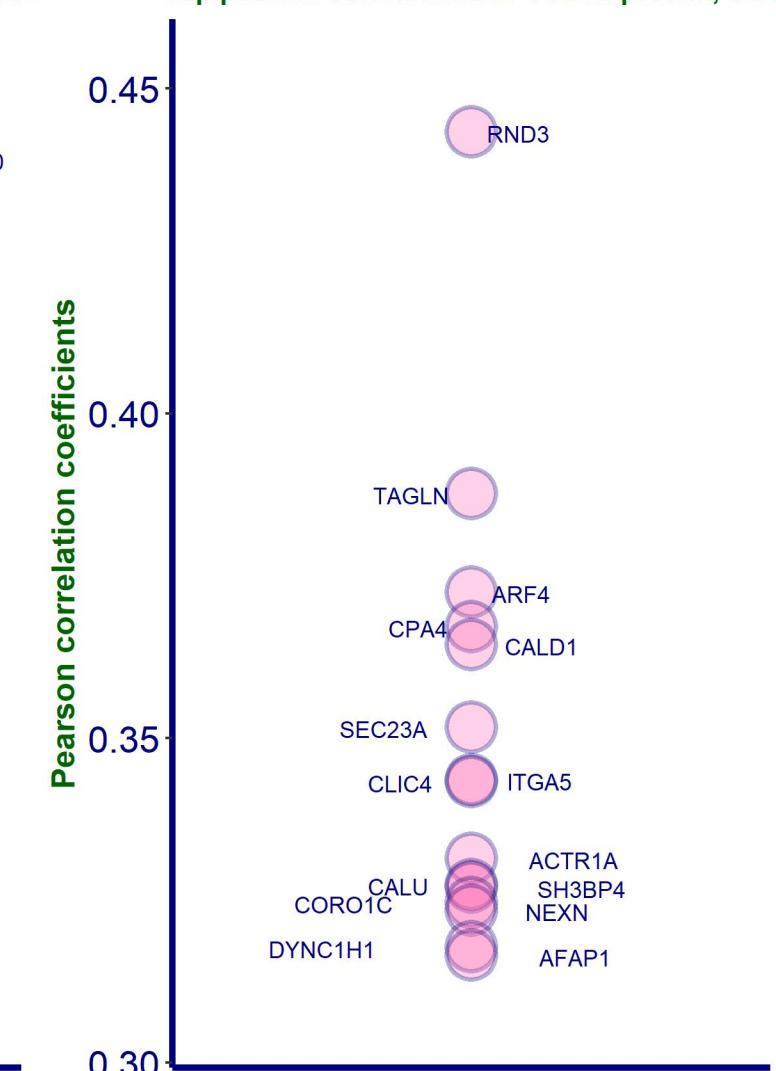
Density plot of CUL4B protein compared to proteins with low and high abundance



Top negative correlations of CUL4B protein, DB1

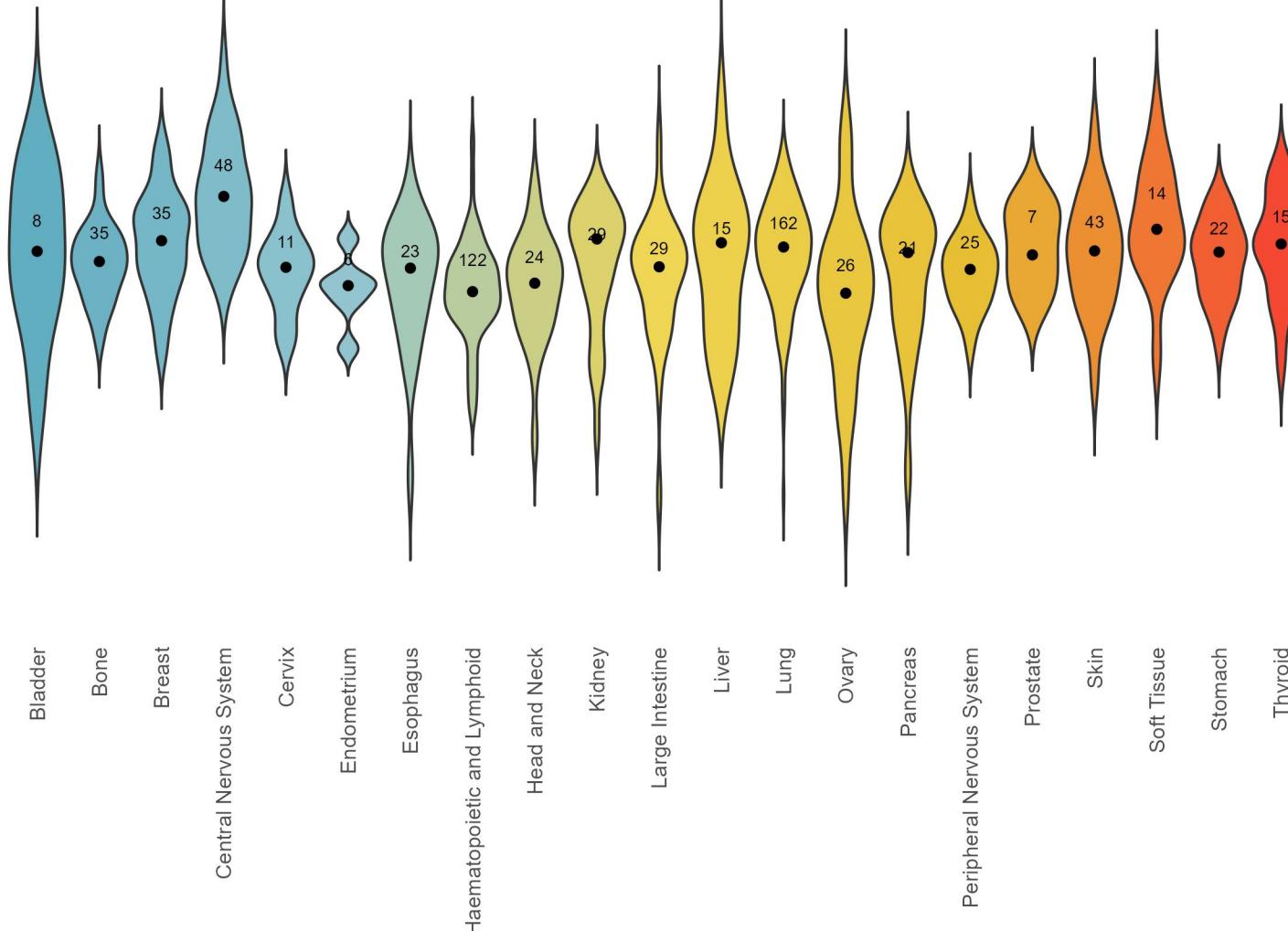


Top positive correlations of CUL4B protein, DB1



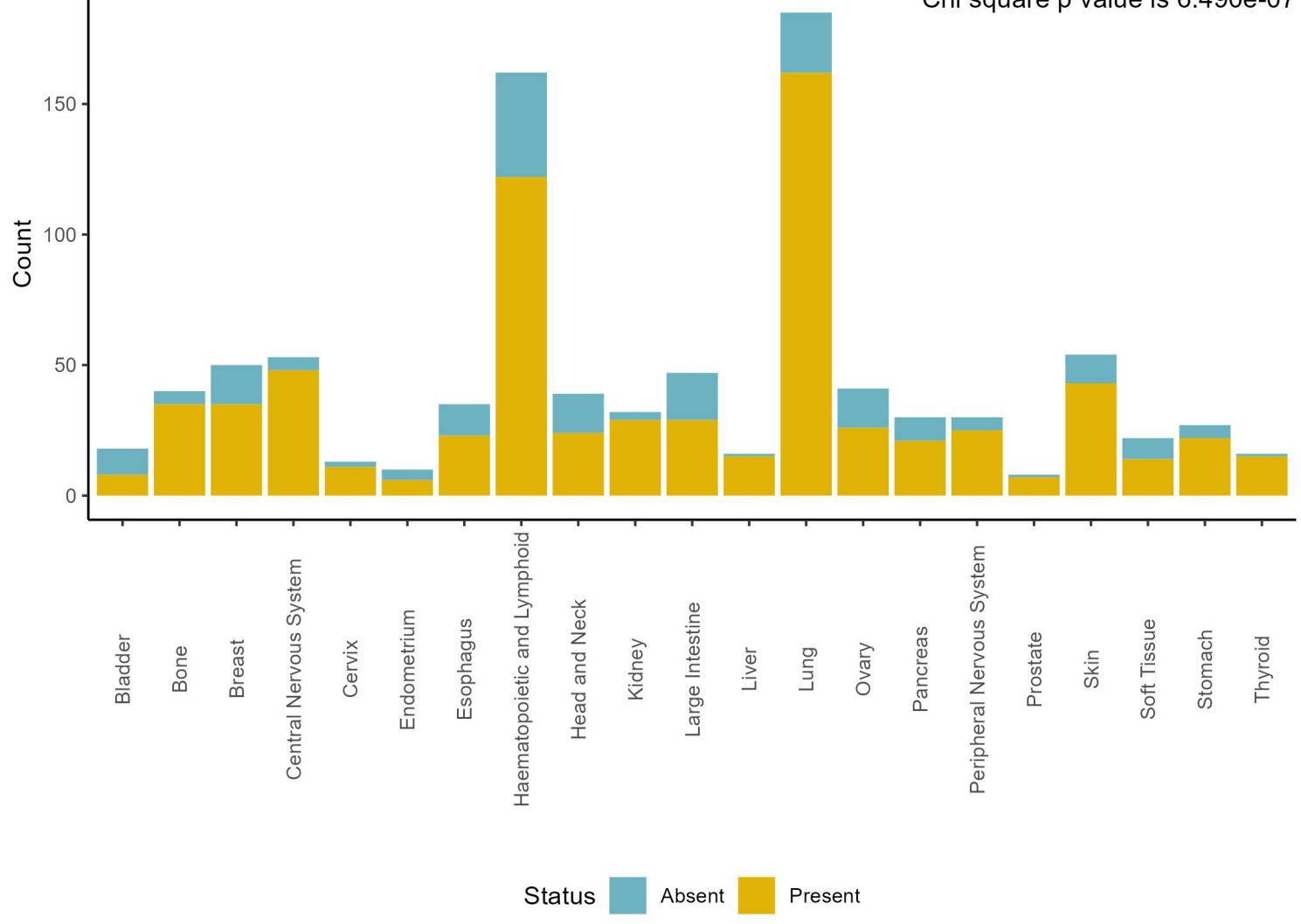
Amount of CUL4B protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 5.850e-19



Present and absent CUL4B protein counts by tissue, DB1

Chi square p value is 6.490e-07

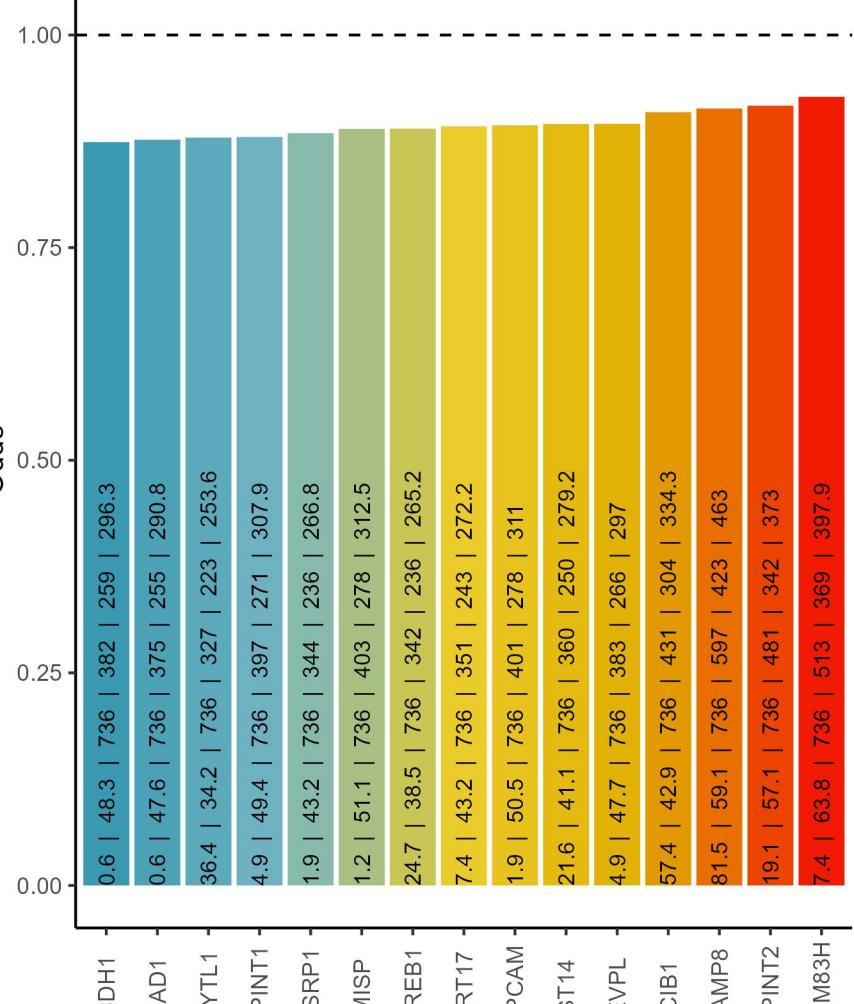


Cooccurrence with CUL4B protein, DB1

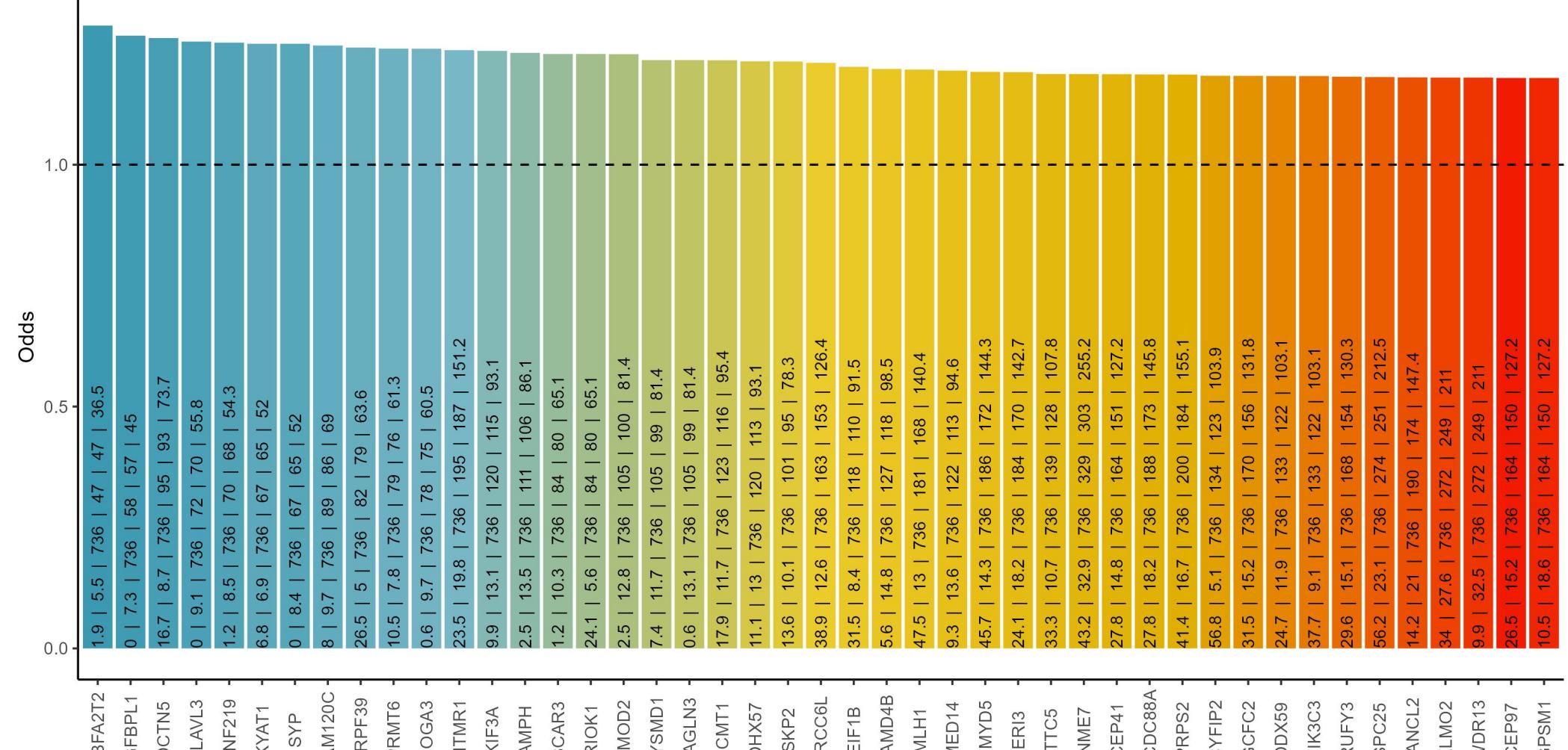
% of CUL4B in blood cancers: 75.3 ; % of CUL4B in solid cancers: 77.9

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CUL4B | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

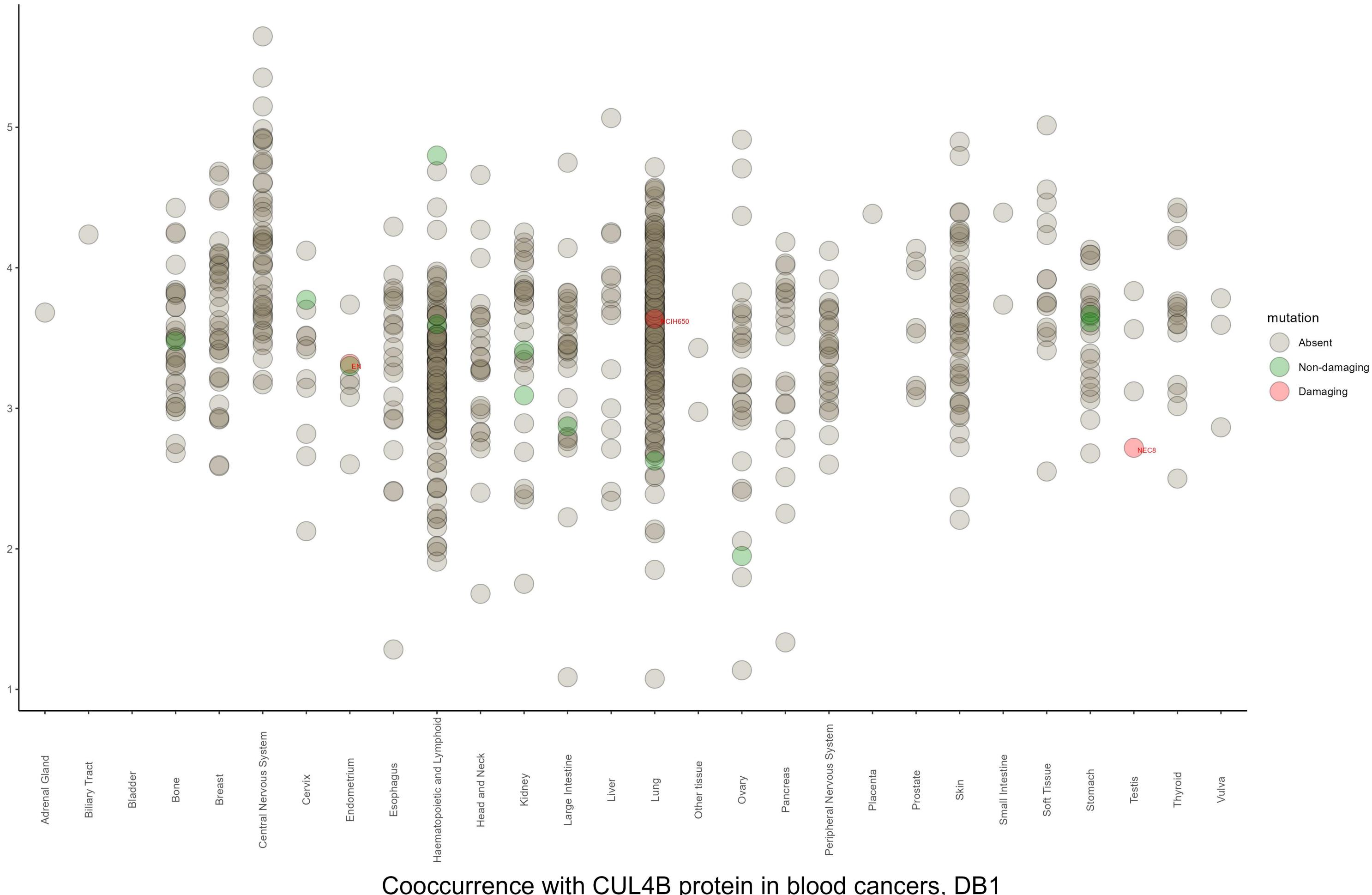
Negative cooccurrence



Positive cooccurrence

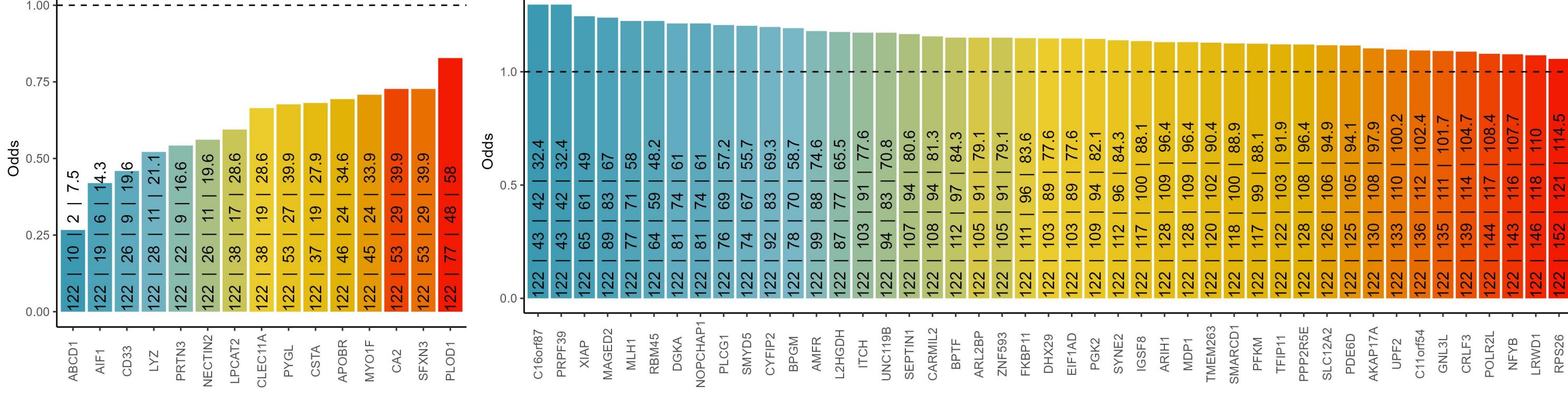


Amount of CUL4B protein and mutation status by tissue, DB1



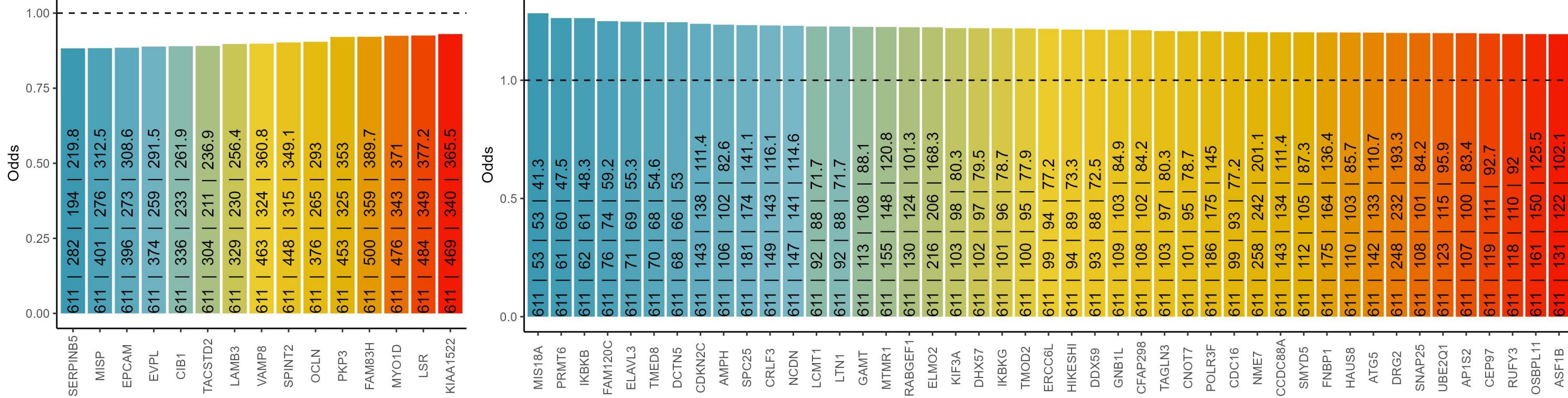
Cooccurrence with CUL4B protein in blood cancers, DB1

The text in the bars: incidence of CUL4B | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

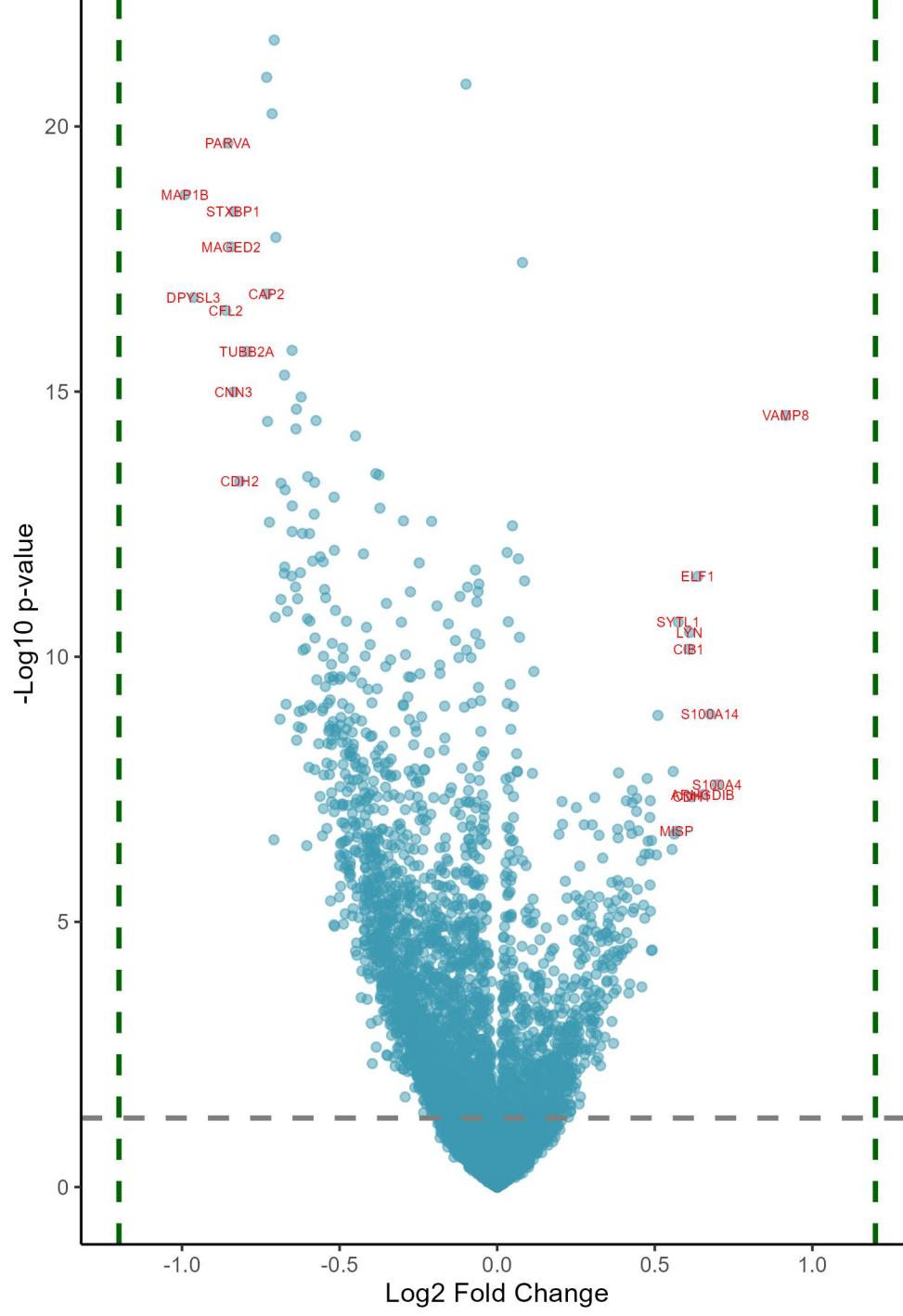


Cooccurrence with CUL4B protein in solid cancers, DB1

The text in the bars: incidence of CUL4B | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

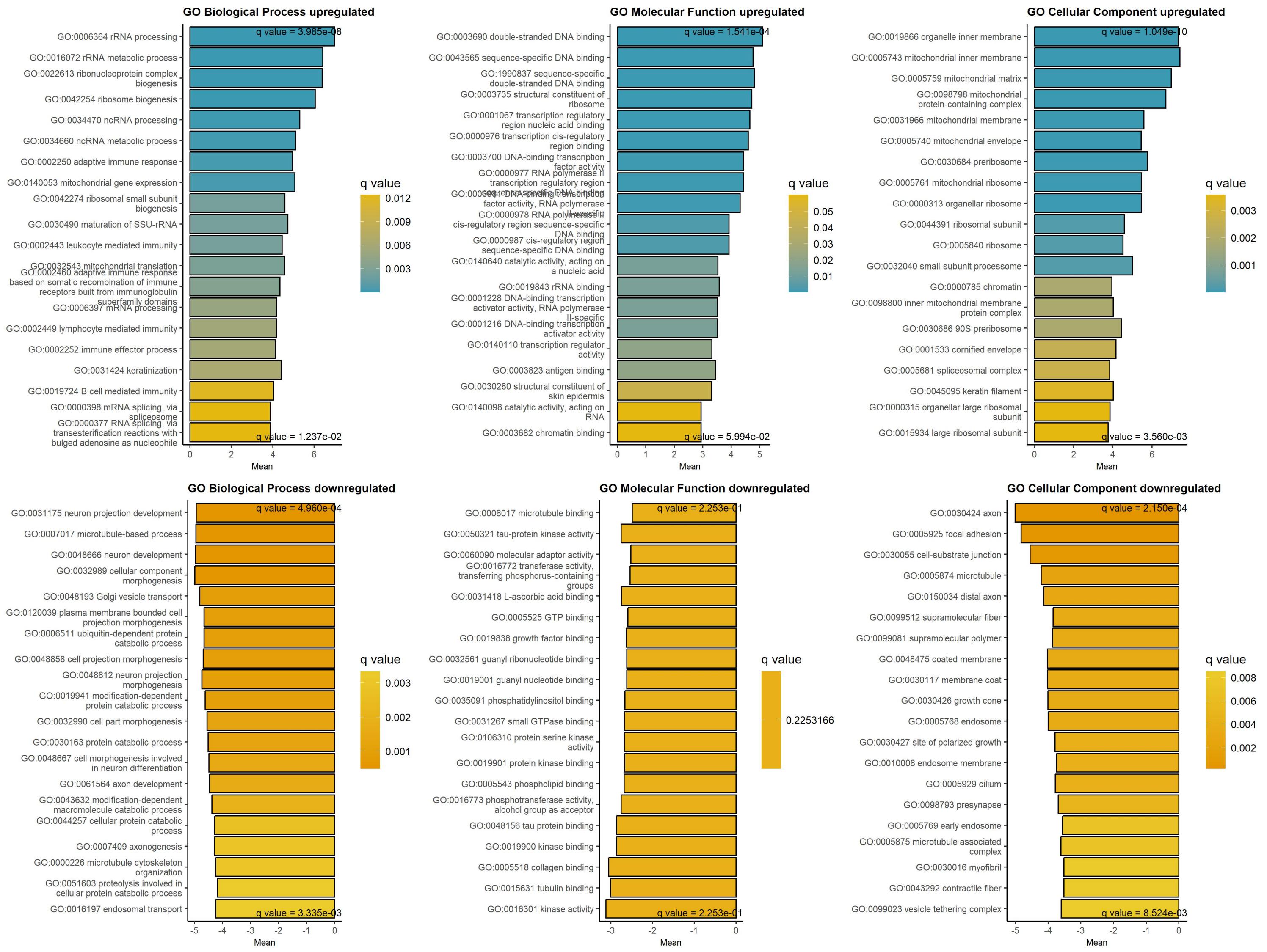


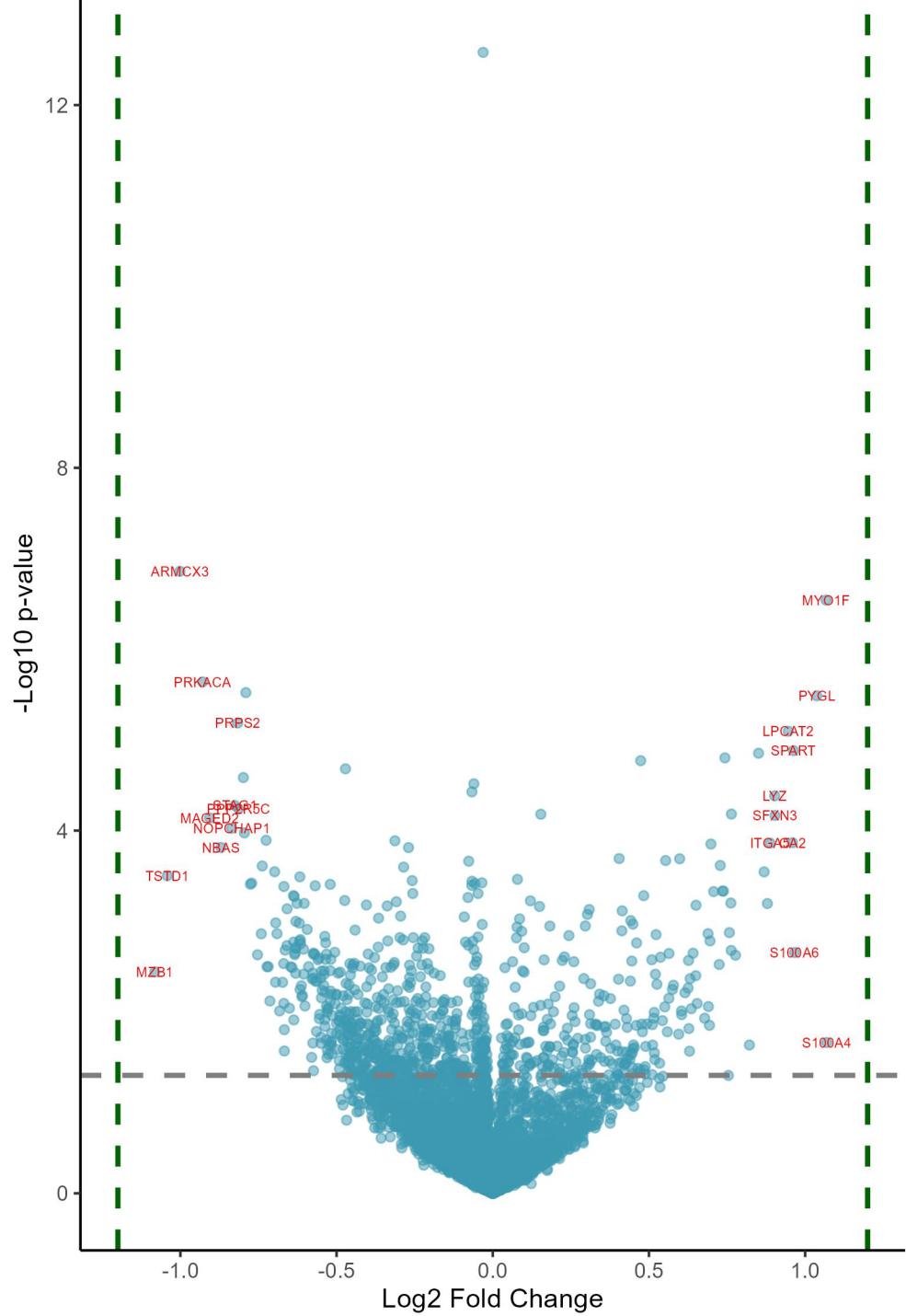
Downregulated at low/absent CUL4B Upregulated at low/absent CUL4B



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.99	1.84e-16	MAP1B	microtubule associated protein 1B	0.92	8.90e-13	VAMP8	vesicle associated membrane protein
-0.96	8.59e-15	DPYSL3	dihydropyrimidinase like 3	0.7	6.92e-07	S100A4	S100 calcium binding protein A4
-0.86	1.40e-14	CFL2	cofilin 2	0.68	5.49e-08	S100A14	S100 calcium binding protein A14
-0.85	2.27e-17	PARVA	parvin alpha	0.65	9.98e-07	ARHGDIB	Rho GDP dissociation inhibitor beta
-0.84	1.25e-15	MAGED2	MAGE family member D2	0.64	3.57e-10	ELF1	E74 like ETS transcription factor 1
-0.84	3.34e-16	STXBP1	syntaxin binding protein 1	0.62	1.07e-06	CDH1	cadherin 1
-0.84	3.74e-13	CNN3	calponin 3	0.61	2.79e-09	LYN	LYN proto-oncogene, Src family tyro
-0.82	1.13e-11	CDH2	cadherin 2	0.61	5.13e-09	CIB1	calcium and integrin binding 1
-0.79	7.28e-14	TUBB2A	tubulin beta 2A class IIa	0.57	1.85e-09	SYTL1	synaptotagmin like 1
-0.73	7.97e-15	CAP2	cyclase associated actin cytoskeleton	0.57	3.63e-06	MISP	mitotic spindle positioning
-0.73	2.63e-18	OCRL	OCRL inositol polyphosphate-5-phosp	0.56	4.04e-06	LAD1	ladinin 1
-0.73	1.05e-12	RHEB	Ras homolog, mTORC1 binding	0.56	4.35e-07	RAB25	RAB25, member RAS oncogene family
-0.72	4.96e-11	FERMT2	FERM domain containing kindlin 2	0.55	6.88e-06	SPINT2	serine peptidase inhibitor, Kunitz
-0.71	7.65e-18	GDI1	GDP dissociation inhibitor 1	0.51	5.78e-08	C1orf131	chromosome 1 open reading frame 131
-0.71	4.86e-06	UCHL1	ubiquitin C-terminal hydrolase L1	0.51	8.40e-06	RNASET2	ribonuclease T2
-0.71	7.82e-19	WDR44	WD repeat domain 44	0.49	2.50e-04	AGR2	anterior gradient 2, protein disulp
-0.7	1.62e-09	NNMT	nicotinamide N-methyltransferase	0.49	4.99e-06	CDH3	cadherin 3
-0.7	9.14e-16	APPL2	adaptor protein, phosphotyrosine in	0.49	2.55e-04	BRI3BP	BRI3 binding protein
-0.69	6.64e-08	PRAF2	PRA1 domain family member 2	0.49	6.34e-05	SPINT1	serine peptidase inhibitor, Kunitz
-0.69	8.12e-10	ENO2	enolase 2	0.49	1.22e-06	DSC2	desmocollin 2
-0.69	1.15e-11	FHL1	four and a half LIM domains 1	0.48	2.52e-05	HPDL	4-hydroxyphenylpyruvate dioxygenase
-0.68	3.25e-10	FAM114A1	family with sequence similarity 114	0.48	2.22e-06	ITGB6	integrin subunit beta 6
-0.67	1.91e-13	PHLD1	pleckstrin homology like domain fam	0.48	8.09e-06	EVPL	envoplakin
-0.67	2.59e-10	WASL	WASP like actin nucleation promotin	0.48	5.08e-06	HCL51	hematopoietic cell-specific Lyn sub
-0.67	1.48e-11	AK1	adenylate kinase 1	0.48	5.51e-07	GALNT3	polypeptide N-acetylgalactosaminylt
-0.67	3.93e-08	CALD1	caldesmon 1	0.47	8.17e-06	ST14	ST14 transmembrane serine protease
-0.67	1.26e-09	HPCAL1	hippocalcin like 1	0.47	8.18e-05	EPCAM	epithelial cell adhesion molecule
-0.65	3.57e-10	TUBB3	tubulin beta 3 class III	0.46	5.16e-05	FAM83H	family with sequence similarity 83
-0.65	7.28e-14	FAM50A	family with sequence similarity 50	0.46	9.55e-04	LCP1	lymphocyte cytosolic protein 1

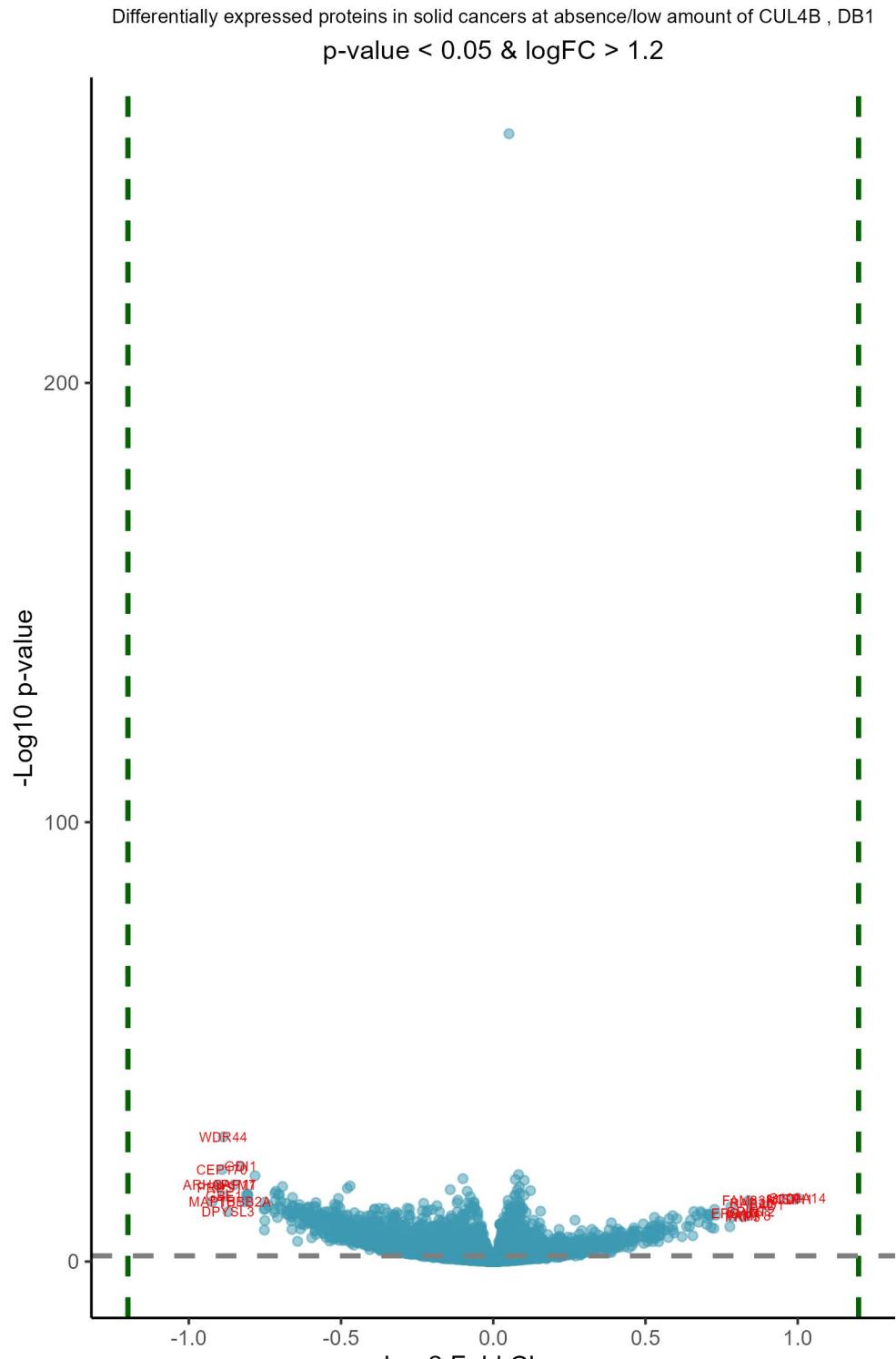
GAGE analysis on upregulated and downregulated proteins at low/absent CUL4B protein, DB1





Downregulated in blood cancers at low/absent CUL4B Upregulated in blood cancers at low/absent CUL4B

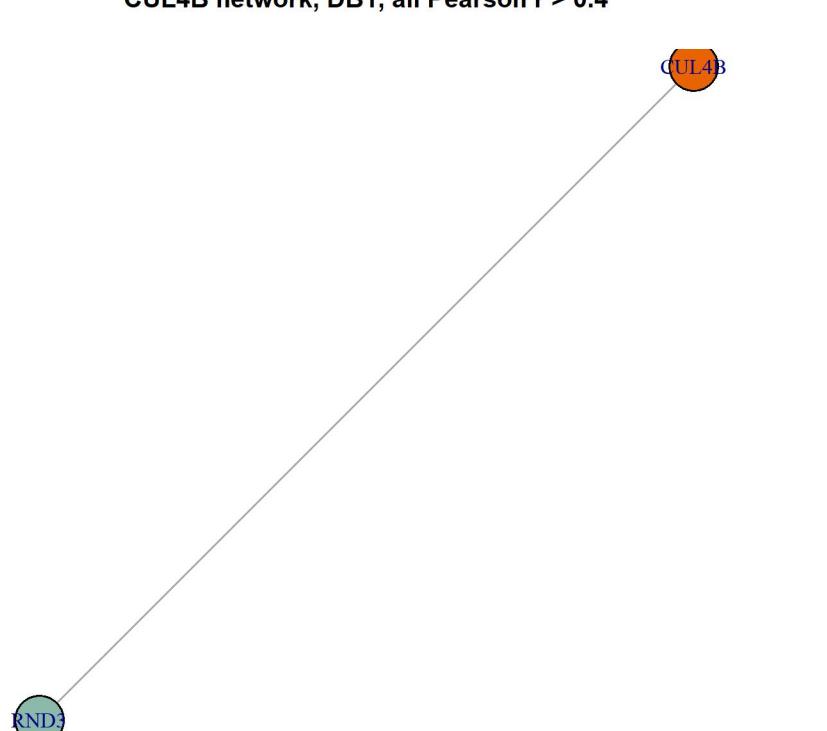
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.08	1.24e-01	MZB1	marginal zone B and B1 cell specific	1.07	2.78e-01	S100A4	S100 calcium binding protein A4
-1.04	4.87e-02	TSTD1	thiosulfate sulfurtransferase like	1.07	4.78e-04	MYO1F	myosin IF
-1	3.07e-04	ARMCX3	armadillo repeat containing X-linker	1.04	3.10e-03	PYGL	glycogen phosphorylase L
-0.93	3.05e-03	PRKACA	protein kinase cAMP-activated catalytic	0.97	1.07e-01	S100A6	S100 calcium binding protein A6
-0.91	2.01e-02	MAGED2	MAGE family member D2	0.96	8.48e-03	SPART	spartin
-0.87	3.11e-02	NBAS	NBAS subunit of NRZ tethering complex	0.96	3.02e-02	CA2	carbonic anhydrase 2
-0.84	2.51e-02	NOPCHAP1	NOP protein chaperone 1	0.95	5.94e-03	LPCAT2	lysophosphatidylcholine acyltransferase
-0.83	1.85e-02	STAG1	stromal antigen 1	0.9	1.97e-02	SFXN3	sideroflexin 3
-0.82	5.42e-03	PRPS2	phosphoribosyl pyrophosphate synthetase	0.9	1.53e-02	LYZ	lysozyme
-0.81	1.91e-02	PPP2R5C	protein phosphatase 2 regulatory subunit	0.89	3.02e-02	ITGA5	integrin subunit alpha 5
-0.8	1.15e-02	CYFIP2	cytoplasmic FMR1 interacting protein	0.88	5.97e-02	ZYX	zyxin
-0.8	2.71e-02	MTA3	metastasis associated 1 family member	0.87	4.52e-02	NDRG1	N-myc downstream regulated 1
-0.79	3.10e-03	STX5	syntaxin 5	0.85	8.48e-03	APOBR	apolipoprotein B receptor
-0.78	5.00e-02	STAT2	signal transducer and activator of transcription 2	0.82	2.80e-01	SPN	sialophorin
-0.77	5.00e-02	PFKM	phosphofructokinase, muscle	0.78	1.08e-01	LAT2	linker for activation of T cells fa
-0.75	1.07e-01	ENO2	enolase 2	0.76	1.97e-02	MRC2	mannose receptor C type 2
-0.74	9.14e-02	TMEM263	transmembrane protein 263	0.76	1.05e-01	RNASET2	ribonuclease T2
-0.74	4.19e-02	HIP1R	huntingtin interacting protein 1 related	0.76	5.97e-02	CTBP2	C-terminal binding protein 2
-0.73	3.02e-02	SYVN1	synoviolin 1	0.76	9.14e-02	RAB27A	RAB27A, member RAS oncogene family
-0.72	1.17e-01	IKZF3	IKAROS family zinc finger 3	0.75	3.61e-01	LGALS1	galectin 1
-0.72	1.17e-01	MYH10	myosin heavy chain 10	0.74	8.67e-03	CD33	CD33 molecule
-0.71	1.81e-01	SEPTIN1	septin 1	0.74	5.40e-02	ARRB1	arrestin beta 1
-0.7	4.52e-02	L2HGDH	L-2-hydroxyglutarate dehydrogenase	0.74	5.40e-02	ARSB	arylsulfatase B
-0.7	1.40e-01	SAR1B	secretion associated Ras related GTPase	0.73	4.19e-02	PRTN3	proteinase 3
-0.69	8.01e-02	MAP4K1	mitogen-activated protein kinase kinase 1	0.72	1.16e-01	RALB	RAS like proto-oncogene B
-0.69	9.14e-02	PEG10	paternally expressed 10	0.71	5.40e-02	ZEB2	zinc finger E-box binding homeobox
-0.68	2.00e-01	RABIF	RAB interacting factor	0.7	3.02e-02	NECTIN2	nectin cell adhesion molecule 2
-0.67	1.40e-01	CD79B	CD79b molecule	0.7	9.61e-02	CLEC11A	C-type lectin domain containing 11A
-0.67	1.16e-01	CFAP20	cilia and flagella associated protein	0.69	2.30e-01	ANXA1	annexin A1



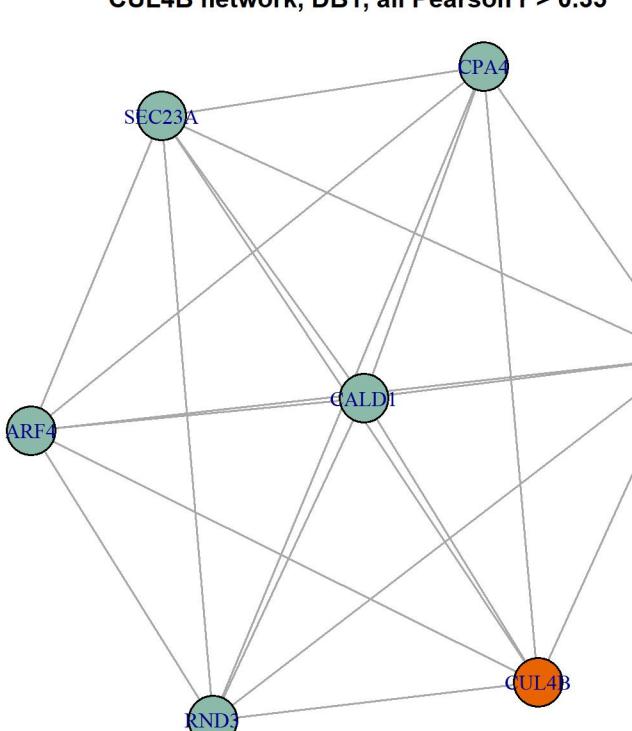
Downregulated in solid cancers at low/absent CUL4B Upregulated in solid cancers at low/absent CUL4B

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.92	3.45e-12	MAP1B	microtubule associated protein 1B	1	7.15e-13	S100A14	S100 calcium binding protein A14
-0.9	5.76e-15	PRPS1	phosphoribosyl pyrophosphate synthetase	0.99	1.09e-12	CDH1	cadherin 1
-0.9	2.07e-15	ARHGAP17	Rho GTPase activating protein 17	0.95	1.09e-12	MISP	mitotic spindle positioning
-0.89	1.50e-18	CEP170	centrosomal protein 170	0.9	1.61e-11	LAD1	ladinin 1
-0.89	9.61e-26	WDR44	WD repeat domain 44	0.85	6.11e-12	RAB25	RAB25, member RAS oncogene family
-0.88	2.60e-13	GBE1	1,4-alpha-glucan branching enzyme 1	0.85	2.24e-10	SPINT2	serine peptidase inhibitor, Kunitz
-0.87	2.40e-10	DPYSL3	dihydropyrimidinase like 3	0.84	1.99e-12	FAM83H	family with sequence similarity 83
-0.85	2.07e-15	AP1M1	adaptor related protein complex 1 subunit	0.84	1.30e-09	VAMP8	vesicle associated membrane protein
-0.83	3.20e-19	GDI1	GDP dissociation inhibitor 1	0.82	2.03e-09	PKP3	plakophilin 3
-0.82	3.60e-12	TUBB2A	tubulin beta 2A class IIa	0.8	4.73e-10	EPCAM	epithelial cell adhesion molecule
-0.81	1.48e-13	UAP1	UDP-N-acetylglucosamine pyrophosphoryl transferase 1	0.78	2.38e-09	SPINT1	serine peptidase inhibitor, Kunitz
-0.81	9.49e-14	MCRIP1	MAPK regulated corepressor interactant	0.78	2.76e-11	EVPL	envoplakin
-0.81	2.07e-13	STXBP1	syntaxin binding protein 1	0.78	1.50e-07	AGR2	anterior gradient 2, protein disulfide isomerase
-0.81	2.53e-12	MAGED2	MAGE family member D2	0.73	1.05e-09	CDH3	cadherin 3
-0.78	2.83e-17	FAM50A	family with sequence similarity 50	0.73	8.64e-11	DSC2	desmocollin 2
-0.75	8.39e-11	FERMT2	FERM domain containing kindlin 2	0.72	3.24e-07	CKMT1A	creatine kinase, mitochondrial 1A
-0.75	7.33e-07	TMSB10	thymosin beta 10	0.72	2.12e-07	TACSTD2	tumor associated calcium signal transducer 2
-0.75	1.17e-08	CDH2	cadherin 2	0.71	1.22e-09	ESRP1	epithelial splicing regulatory protein
-0.75	3.85e-12	PPM1F	protein phosphatase, Mg2+/Mn2+ dependent	0.71	8.35e-10	ITGB6	integrin subunit beta 6
-0.75	7.28e-11	CBL	Cbl proto-oncogene	0.71	4.44e-09	TRIM29	tripartite motif containing 29
-0.74	1.79e-11	PARVA	parvin alpha	0.7	6.50e-10	ST14	ST14 transmembrane serine protease
-0.72	8.41e-11	C11orf68	chromosome 11 open reading frame 68	0.7	5.52e-08	LSR	lipolysis stimulated lipoprotein receptor
-0.72	2.88e-10	CCDC50	coiled-coil domain containing 50	0.69	4.80e-10	LYN	LYN proto-oncogene, Src family tyrosine kinase
-0.72	8.39e-14	MAP7D1	MAP7 domain containing 1	0.68	2.24e-10	GALNT3	polypeptide N-acetylgalactosaminyltransferase
-0.71	2.18e-12	PPP2R5D	protein phosphatase 2 regulatory subunit	0.67	2.35e-08	CGN	cingulin
-0.71	3.05e-14	OCRL	OCRL inositol polyphosphate-5-phosphatase	0.67	1.30e-09	PATJ	PATJ crumbs cell polarity complex component
-0.71	2.89e-09	ENO2	enolase 2	0.66	2.26e-10	SYTL1	synaptotagmin like 1
-0.71	1.31e-13	TBCD	tubulin folding cofactor D	0.66	9.77e-06	KRT17	keratin 17
-0.7	2.40e-11	MAP2K2	mitogen-activated protein kinase kinase 2	0.65	1.04e-08	CIB1	calcium and integrin binding 1

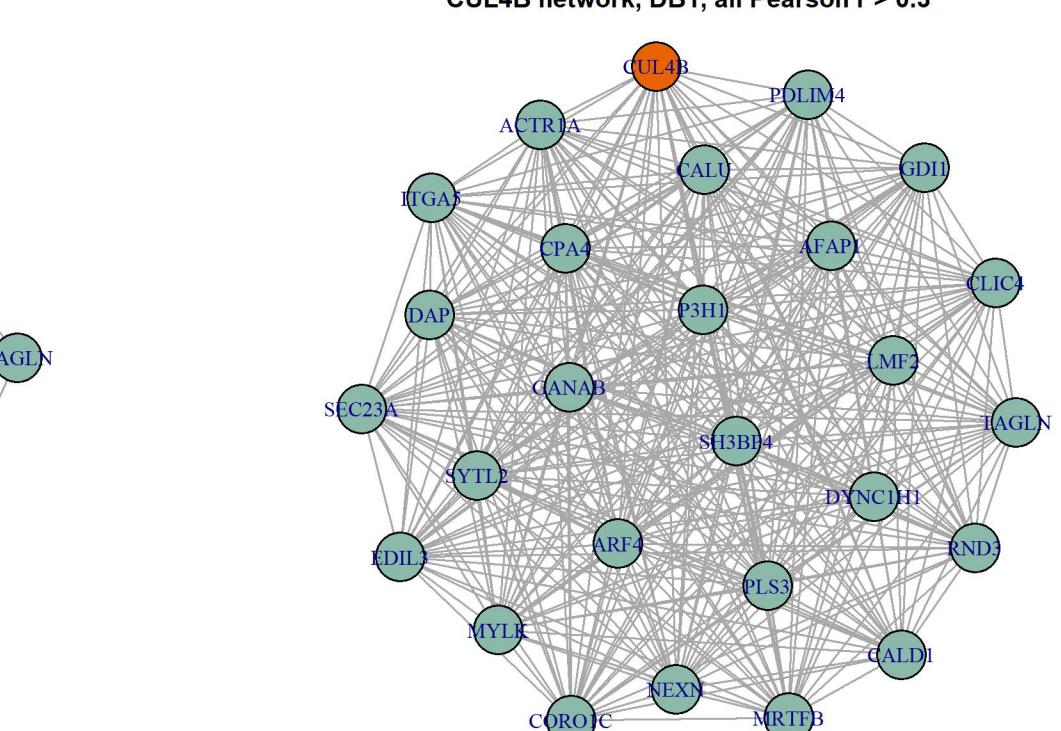
CUL4B network, DB1, all Pearson r > 0.4



CUL4B network, DB1, all Pearson r > 0.35

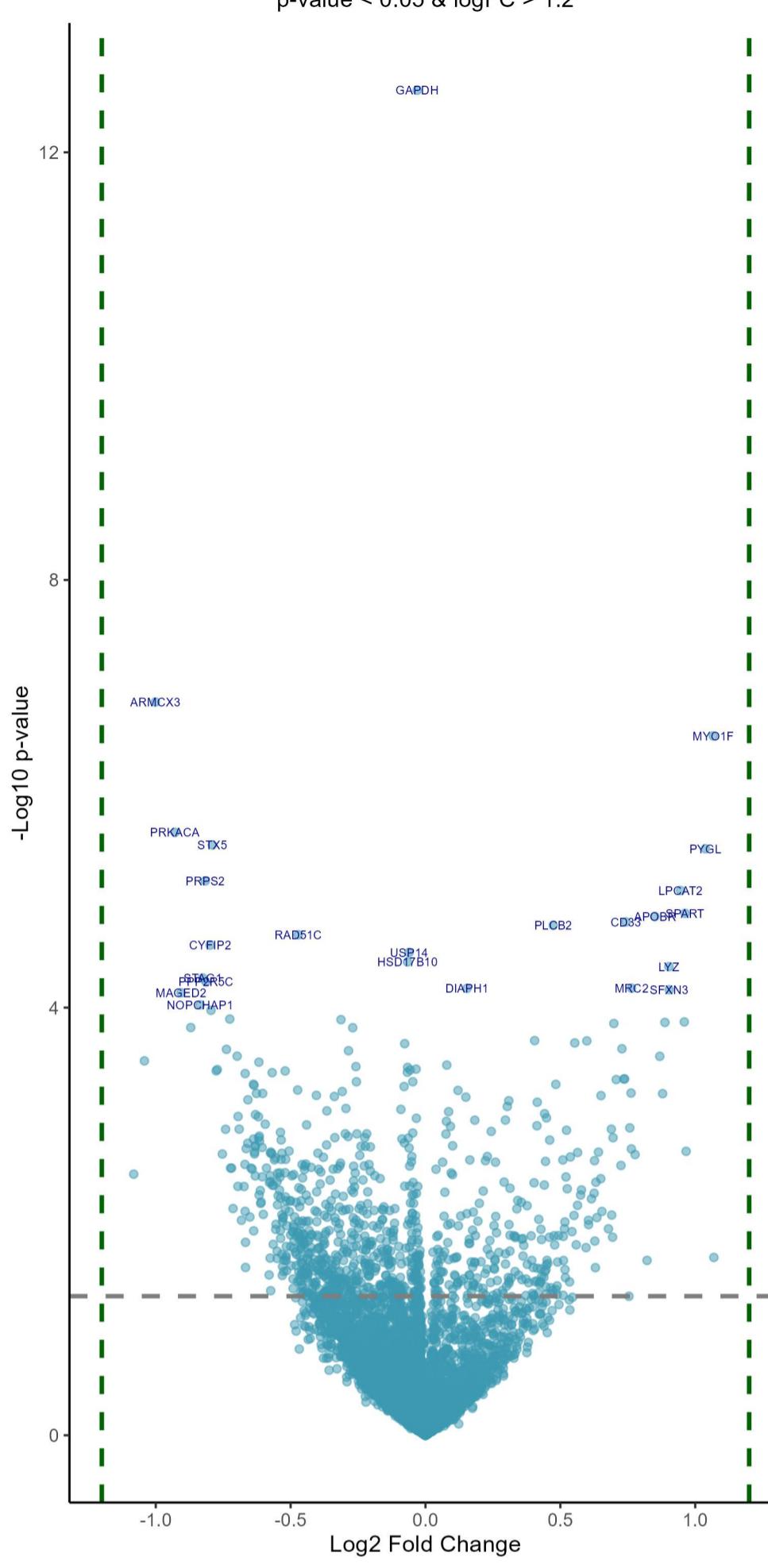


CUL4B network, DB1, all Pearson r > 0.3



Sorted by p values!

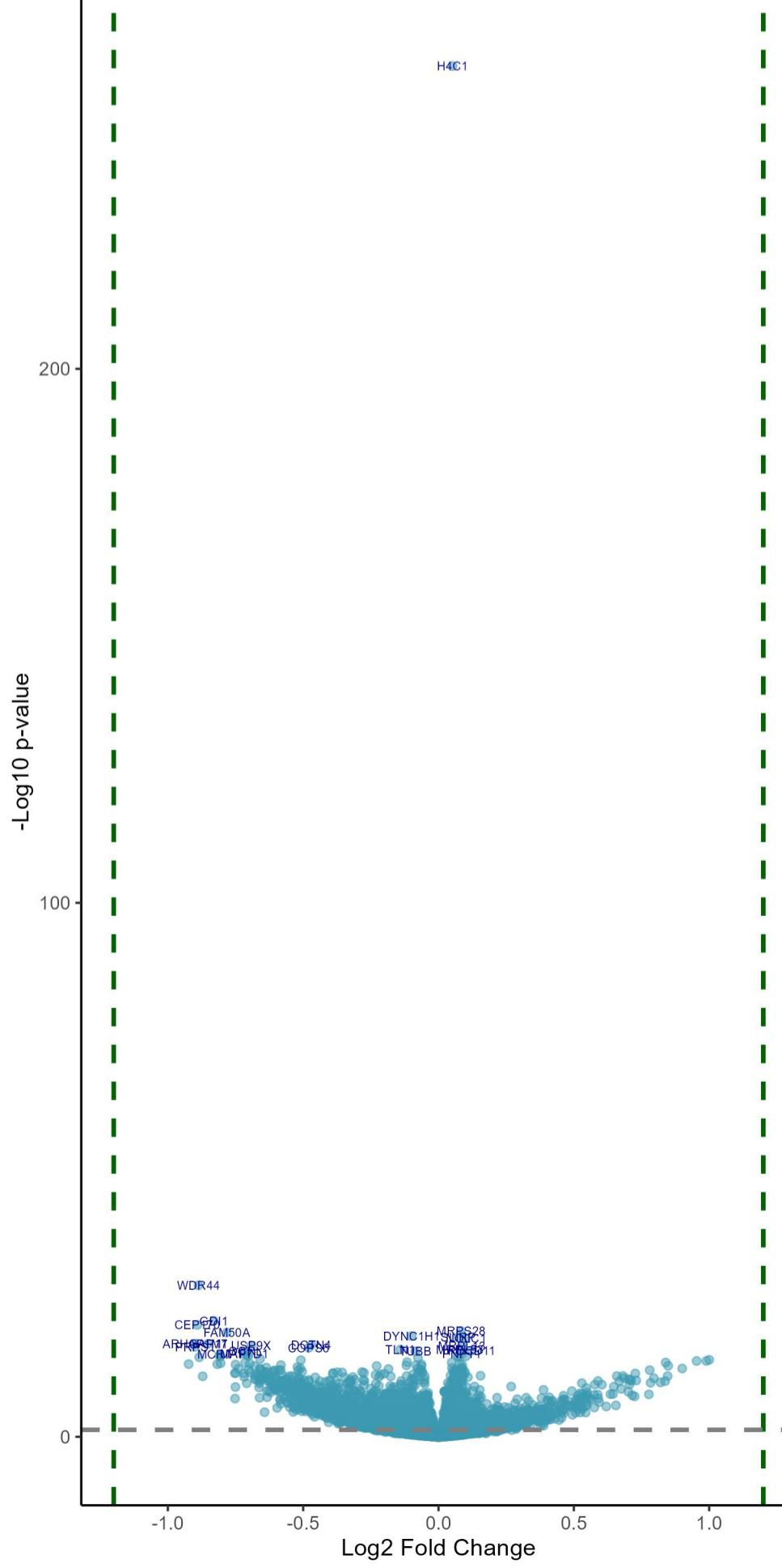
Downregulated in blood cancers at low/absent CUL4B Upregulated in blood cancers at low/absent CUL4B



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.03	8.73e-10	GAPDH	glyceraldehyde-3-phosphate dehydrog	1.07	4.78e-04	MYO1F	myosin IF
-1	3.07e-04	ARMX3	armadillo repeat containing X-linker	1.04	3.10e-03	PYGL	glycogen phosphorylase L
-0.93	3.05e-03	PRKACA	protein kinase cAMP-activated catal	0.95	5.94e-03	LPCAT2	lysophosphatidylcholine acyltransfe
-0.79	3.10e-03	STX5	syntaxin 5	0.96	8.48e-03	SPART	spartin
-0.82	5.42e-03	PRPS2	phosphoribosyl pyrophosphate synthe	0.85	8.48e-03	APOBR	apolipoprotein B receptor
-0.47	9.90e-03	RAD51C	RAD51 paralog C	0.74	8.67e-03	CD33	CD33 molecule
-0.8	1.15e-02	CYFIP2	cytoplasmic FMR1 interacting protei	0.47	8.67e-03	PLCB2	phospholipase C beta 2
-0.06	1.27e-02	USP14	ubiquitin specific peptidase 14	0.9	1.53e-02	LYZ	lysozyme
-0.07	1.46e-02	HSD17B10	hydroxysteroid 17-beta dehydrogenas	0.76	1.97e-02	MRC2	mannose receptor C type 2
-0.83	1.85e-02	STAG1	stromal antigen 1	0.15	1.97e-02	DIAPH1	diaphanous related formin 1
-0.81	1.91e-02	PPP2R5C	protein phosphatase 2 regulatory su	0.9	1.97e-02	SFXN3	sideroflexin 3
-0.91	2.01e-02	MAGED2	MAGE family member D2	0.96	3.02e-02	CA2	carbonic anhydrase 2
-0.84	2.51e-02	NOPCHAP1	NOP protein chaperone 1	0.89	3.02e-02	ITGA5	integrin subunit alpha 5
-0.8	2.71e-02	MTA3	metastasis associated 1 family memb	0.7	3.02e-02	NECTIN2	nectin cell adhesion molecule 2
-0.73	3.02e-02	SYVN1	synoviolin 1	0.4	3.89e-02	UXS1	UDP-glucuronate decarboxylase 1
-0.31	3.02e-02	PEX5	peroxisomal biogenesis factor 5	0.6	3.89e-02	MPO	myeloperoxidase
-0.87	3.11e-02	NBAS	NBAS subunit of NRZ tethering compl	0.55	3.91e-02	AIF1	allograft inflammatory factor 1
-0.27	3.11e-02	NKAP	NFKB activating protein	0.73	4.19e-02	PRTN3	proteinase 3
-0.08	3.91e-02	GOT2	glutamic-oxaloacetic transaminase 2	0.87	4.52e-02	NDRG1	N-myc downstream regulated 1
-0.74	4.19e-02	HIP1R	huntingtin interacting protein 1 re	0.08	5.00e-02	MRPL1	mitochondrial ribosomal protein L1
-0.29	4.20e-02	LYSMD1	LysM domain containing 1	0.74	5.40e-02	ARRB1	arrestin beta 1
-0.7	4.52e-02	L2HGDH	L-2-hydroxyglutarate dehydrogenase	0.74	5.40e-02	ARSB	arylsulfatase B
-1.04	4.87e-02	TSTD1	thiosulfate sulfurtransferase like	0.71	5.40e-02	ZEB2	zinc finger E-box binding homeobox
-0.62	4.89e-02	COMTD1	catechol-O-methyltransferase domain	0.48	5.60e-02	SUMF1	sulfatase modifying factor 1
-0.26	5.00e-02	SPAST	spastin	0.12	5.97e-02	GFUS	GDP-L-fucose synthase
-0.07	5.00e-02	COPZ1	COPI coat complex subunit zeta 1	0.76	5.97e-02	CTBP2	C-terminal binding protein 2
-0.03	5.00e-02	H4C1	H4 clustered histone 1	0.88	5.97e-02	ZYX	zyxin
-0.77	5.00e-02	PFKM	phosphofructokinase, muscle	0.65	6.06e-02	FHL3	four and a half LIM domains 3
-0.06	5.00e-02	PPA1	inorganic pyrophosphatase 1	0.15	6.09e-02	VASP	vasodilator stimulated phosphoprote
-0.78	5.00e-02	STAT2	signal transducer and activator of	0.31	6.41e-02	STAB1	stabilin 1
-0.52	5.00e-02	NFYB	nuclear transcription factor Y subu	0.41	6.54e-02	RAB44	RAB44, member RAS oncogene family
-0.07	5.00e-02	USP7	ubiquitin specific peptidase 7	0.3	7.07e-02	SEPTIN5	septin 5
-0.57	5.00e-02	NTMT1	N-terminal Xaa-Pro-Lys N-methyltran	0.09	7.54e-02	PLPBP	pyridoxal phosphate binding protein
-0.67	5.00e-02	RAB30	RAB30, member RAS oncogene family	0.44	7.78e-02	GMPR	guanosine monophosphate reductase
-0.05	5.47e-02	UBA1	ubiquitin like modifier activating	0.45	8.10e-02	ITGA2B	integrin subunit alpha 2b
-0.26	5.47e-02	BMI1	BMI1 proto-oncogene, polycomb ring	0.3	8.25e-02	TPBG	trophoblast glycoprotein
-0.64	5.60e-02	PEX1	peroxisomal biogenesis factor 1	0.18	8.25e-02	CTSC	cathepsin C
-0.64	5.63e-02	RUFY3	RUN and FYVE domain containing 3	0.08	8.37e-02	TXNDC12	thioredoxin domain containing 12
0.09	5.68e-02	RAB21	RAB21, member RAS oncogene family	0.11	9.91e-02	D5E6	D5E6 guanine nucleotide exchange fo

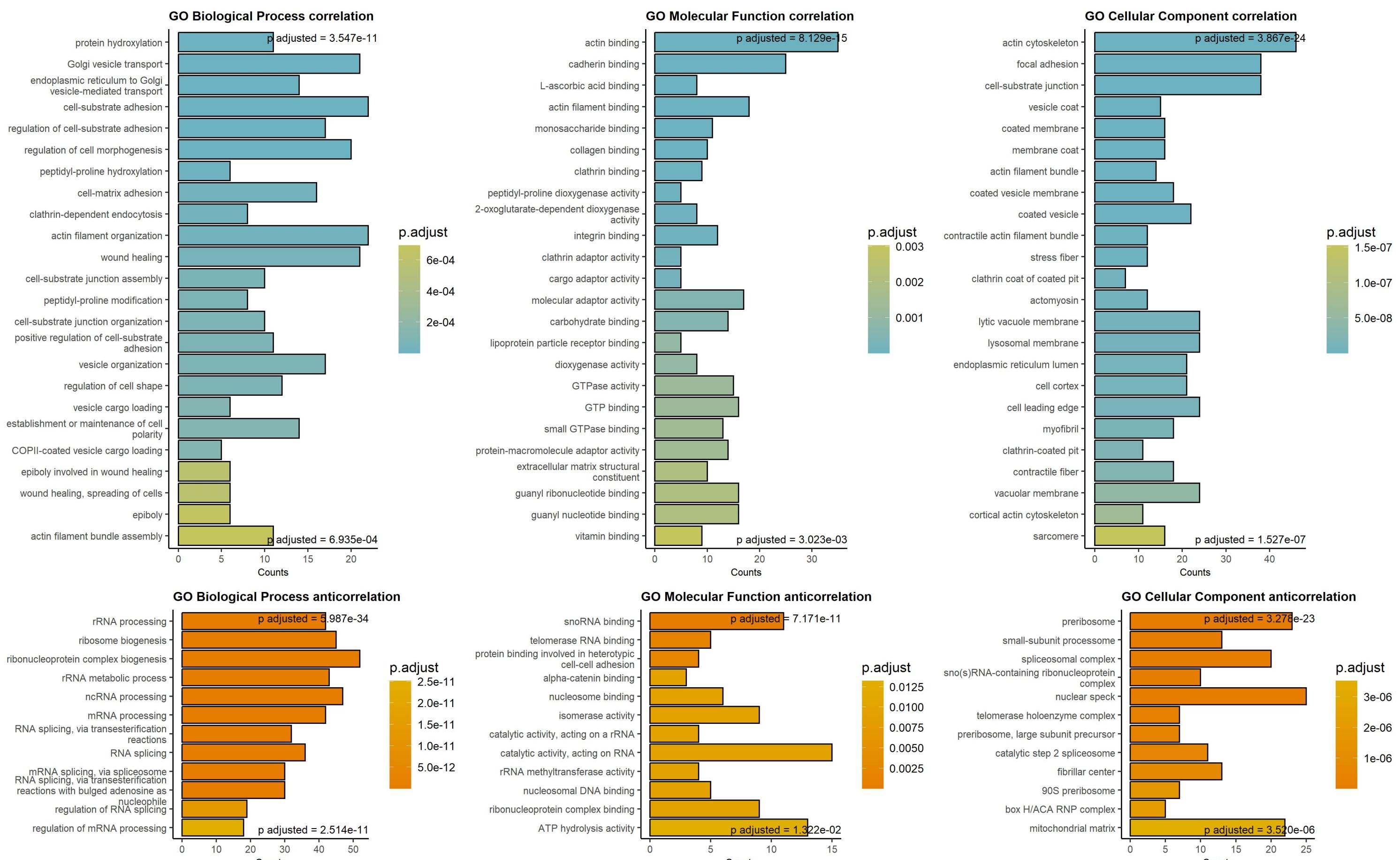
Sorted by p values!

Downregulated in solid cancers at low/absent CUL4B Upregulated in solid cancers at low/absent CUL4B

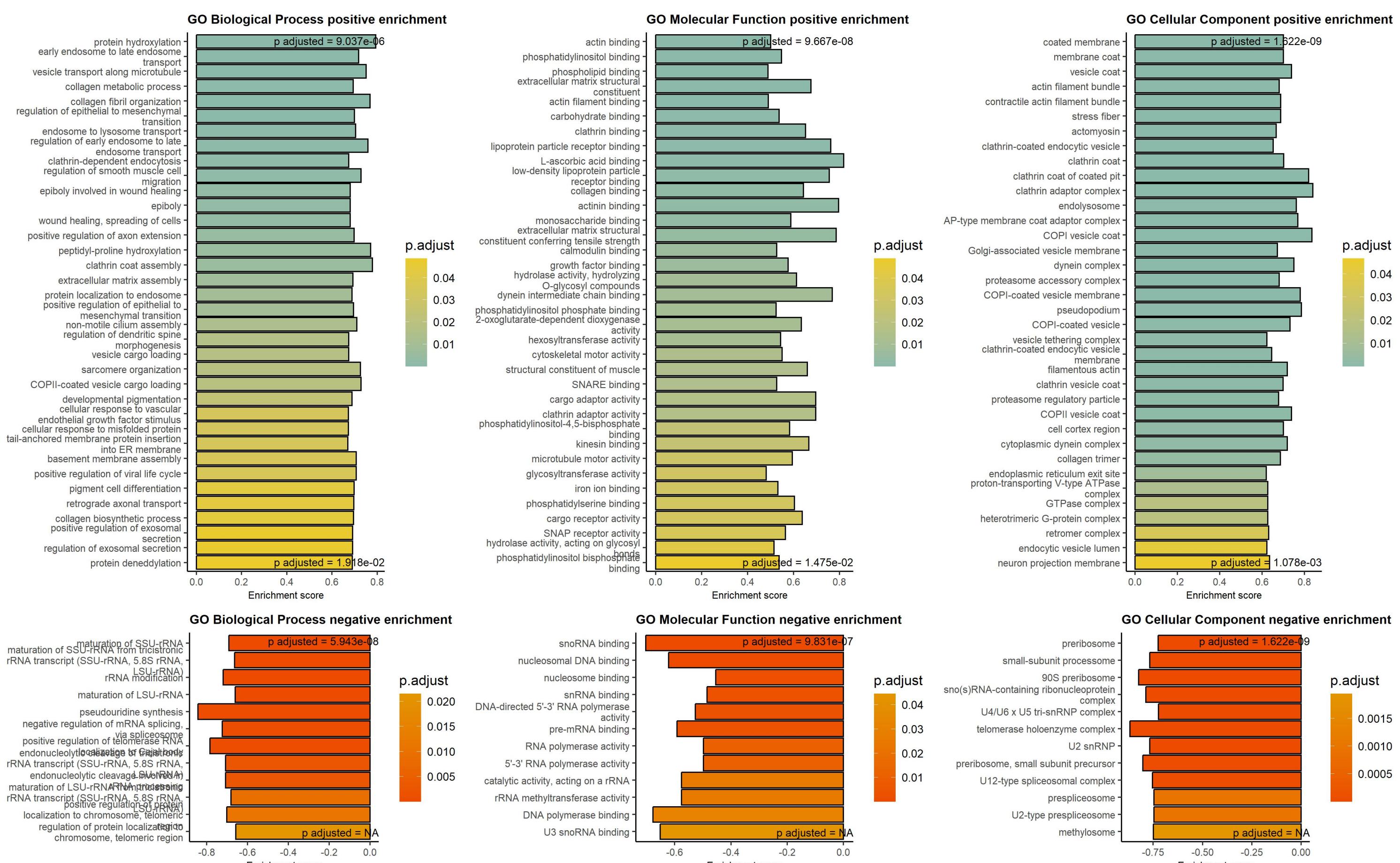


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.89	9.61e-26	WDR44	WD repeat domain 44	0.05	1.32e-253	H4C1	H4 clustered histone 1
-0.83	3.20e-19	GDI1	GDP dissociation inhibitor 1	0.08	1.77e-17	MRPS28	mitochondrial ribosomal protein S28
-0.89	1.50e-18	CEP170	centrosomal protein 170	0.07	1.54e-16	SLIRP	SRA stem-loop interacting RNA bindi
-0.78	2.83e-17	FAM50A	family with sequence similarity 50	0.1	2.25e-16	NOLC1	nucleolar and coiled-body phosphopr
-0.1	1.13e-16	DYNC1H1	dynein cytoplasmic 1 heavy chain 1	0.09	4.36e-15	MRPL13	mitochondrial ribosomal protein L13
-0.9	2.07e-15	ARHGAP17	Rho GTPase activating protein 17	0.08	1.68e-14	MRPL53	mitochondrial ribosomal protein L53
-0.85	2.07e-15	AP1M1	adaptor related protein complex 1 s	0.12	2.41e-14	PDCD11	programmed cell death 11
-0.47	3.19e-15	DCTN4	dynactin subunit 4	0.09	8.39e-14	PNPT1	polyribonucleotide nucleotidyltrans
-0.69	4.10e-15	USP9X	ubiquitin specific peptidase 9 X-li	0.07	1.76e-13	LRPPRC	leucine rich pentatricopeptide repe
-0.9	5.76e-15	PRPS1	phosphoribosyl pyrophosphate synthet	0.1	1.84e-13	NOP2	NOP2 nucleolar protein
-0.48	8.52e-15	COPS6	COP9 signalosome subunit 6	0.07	2.30e-13	MRPL43	mitochondrial ribosomal protein L43
-0.14	1.65e-14	TLN1	talin 1	1	7.15e-13	S100A14	S100 calcium binding protein A14
-0.09	3.05e-14	TUBB	tubulin beta class I	0.99	1.09e-12	CDH1	cadherin 1
-0.71	3.05e-14	OCRL	OCRL inositol polyphosphate-5-phosp	0.95	1.09e-12	MISP	mitotic spindle positioning
-0.72	8.39e-14	MAP7D1	MAP7 domain containing 1	0.05	1.99e-12	HSPD1	heat shock protein family D (Hsp60)
-0.81	9.49e-14	MCRIP1	MAPK regulated corepressor interact	0.84	1.99e-12	FAM83H	family with sequence similarity 83
-0.71	1.31e-13	TBCD	tubulin folding cofactor D	0.08	2.53e-12	CLPX	caseinolytic mitochondrial matrix p
-0.81	1.48e-13	UAP1	UDP-N-acetylglucosamine pyrophospho	0.09	3.85e-12	DDX21	DExD-box helicase 21
-0.7	1.63e-13	EIF4G3	eukaryotic translation initiation f	0.85	6.11e-12	RAB25	RAB25, member RAS oncogene family
-0.81	2.07e-13	STXBP1	syntaxin binding protein 1	0.05	1.41e-11	HSPA9	heat shock protein family A (Hsp70)
-0.88	2.60e-13	GBE1	1,4-alpha-glucan branching enzyme 1	0.09	1.51e-11	GFM1	G elongation factor mitochondrial 1
-0.08	3.21e-13	PSMD1	proteasome 26S subunit, non-ATPase	0.08	1.61e-11	RRS1	ribosome biogenesis regulator 1 hom
-0.66	4.97e-13	RECQL	RecQ like helicase	0.9	1.61e-11	LAD1	ladinin 1
-0.51	7.97e-13	CLIC4	chloride intracellular channel 4	0.08	1.89e-11	FTSJ3	FtsJ RNA 2'-O-methyltransferase 3
-0.12	1.74e-12	CAP1	cyclase associated actin cytoskelet	0.06	2.75e-11	MRPL12	mitochondrial ribosomal protein L12
-0.71	2.18e-12	PPP2R5D	protein phosphatase 2 regulatory su	0.07	2.76e-11	MRPL39	mitochondrial ribosomal protein L39
-0.81	2.53e-12	MAGED2	MAGE family member D2	0.78	2.76e-11	EVPL	envoplakin
-0.7	2.81e-12	MAP2K1	mitogen-activated protein kinase ki	0.05	3.29e-11	COX5A	cytochrome c oxidase subunit 5A
-0.92	3.45e-12	MAP1B	microtubule associated protein 1B	0.1	4.77e-11	WDR43	WD repeat domain 43
-0.82	3.60e-12	TUBB2A	tubulin beta 2A class IIa	0.			

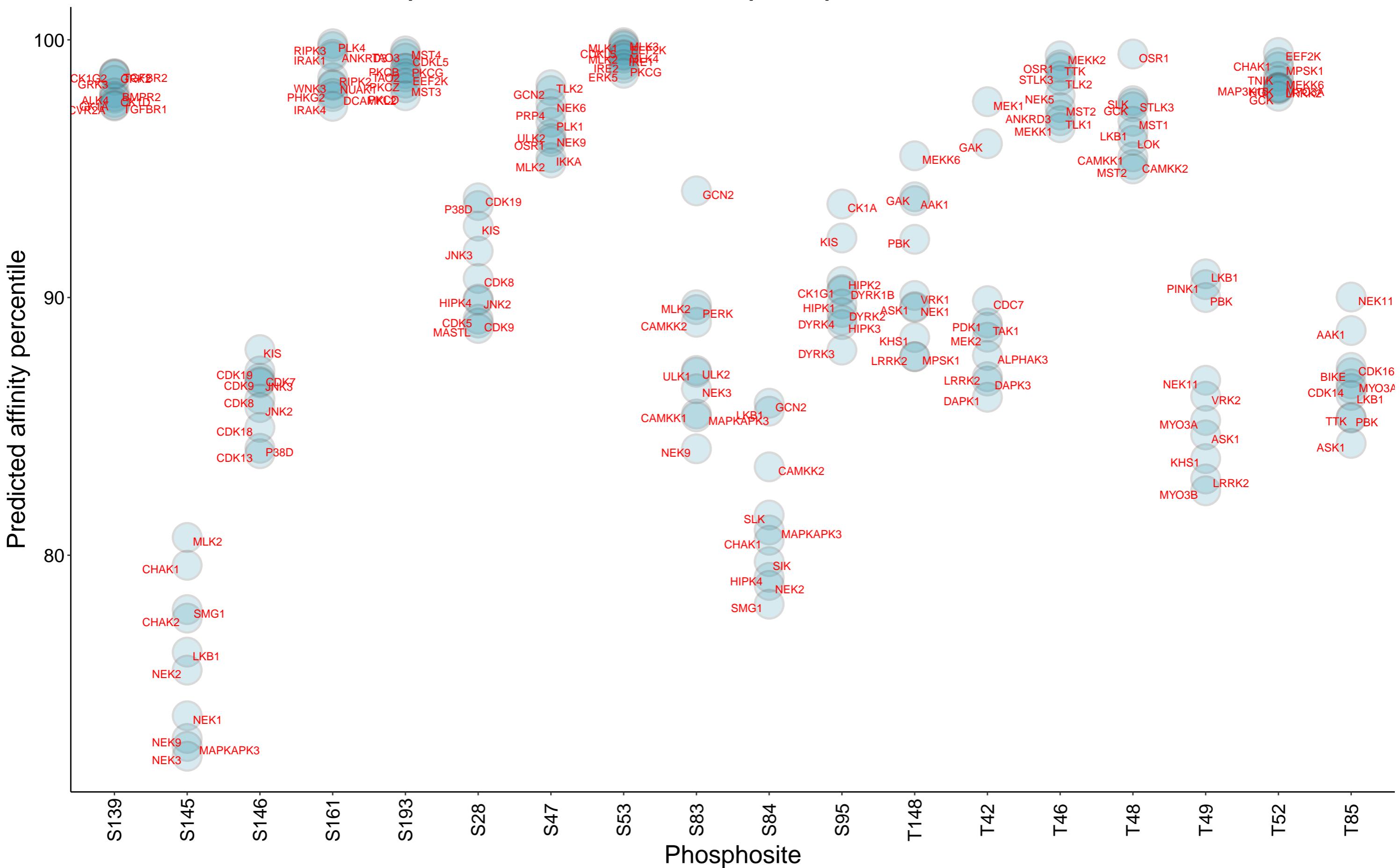
Top 250 correlation coefficients overrepresentation, CUL4B protein, DB1



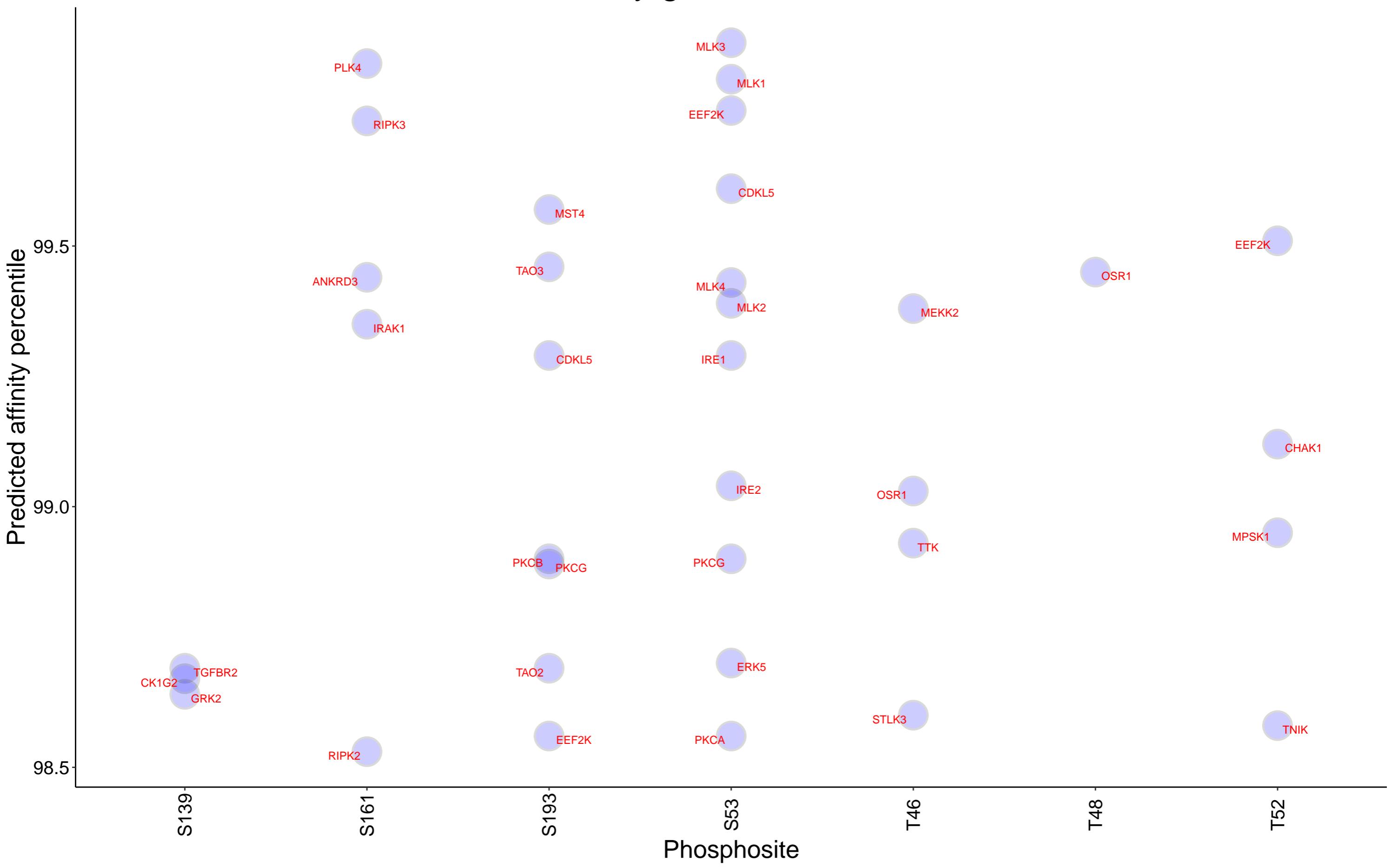
Gene Set Enrichment analysis on protein correlation coefficients, CUL4B protein, DB1



Top 10 kinases for each phosphosite in CUL4B



Kinases with affinity greater than 98.5% to CUL4B



Top 15 positive correlation coefficients for CUL4B protein by tissue, DB1

Beware of false positives in tissues with small number of samples

