

# CUL4A

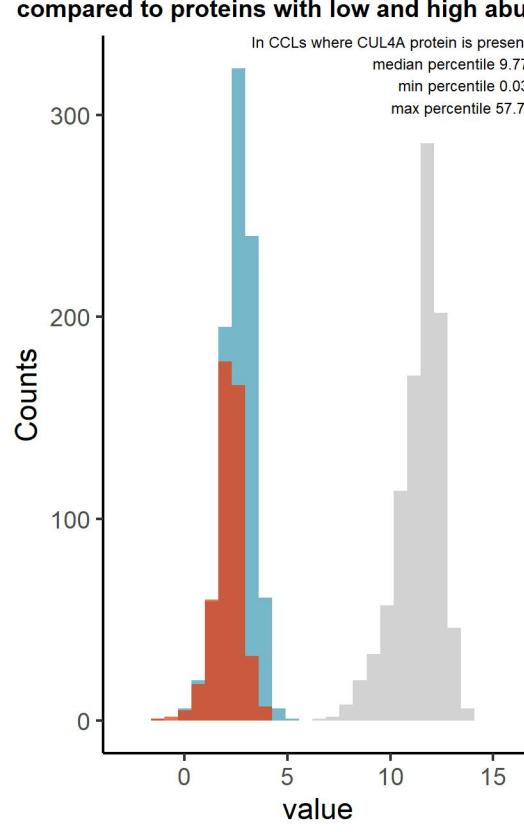
Protein name: CUL4A ; UNIPROT: Q13619 ; Gene name: cullin 4A

Ligandable: Yes ; Ligandable\_by\_Chem: NA ; Is\_enzyme: NA (<https://cansar.ai/>)

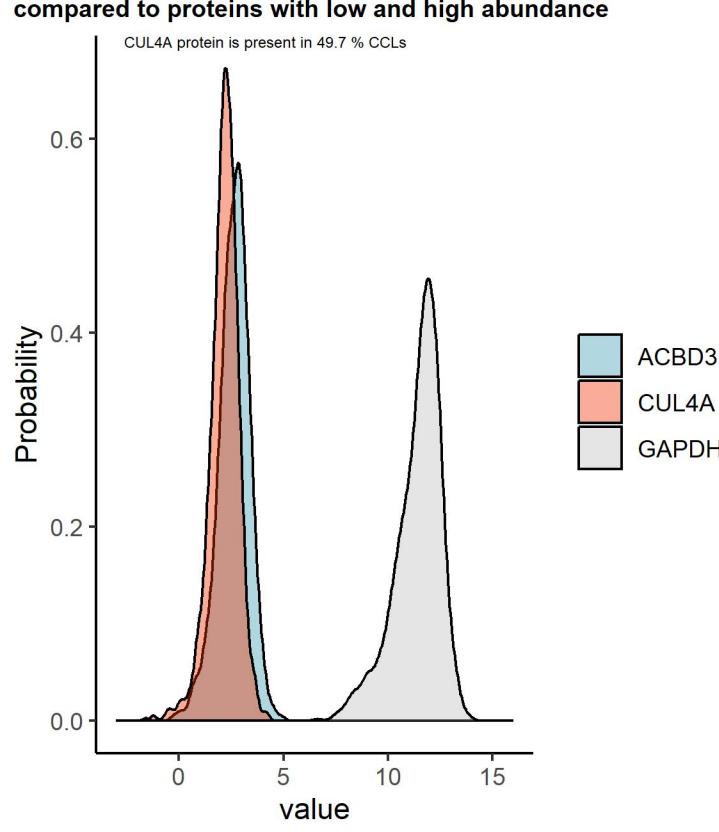
## Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

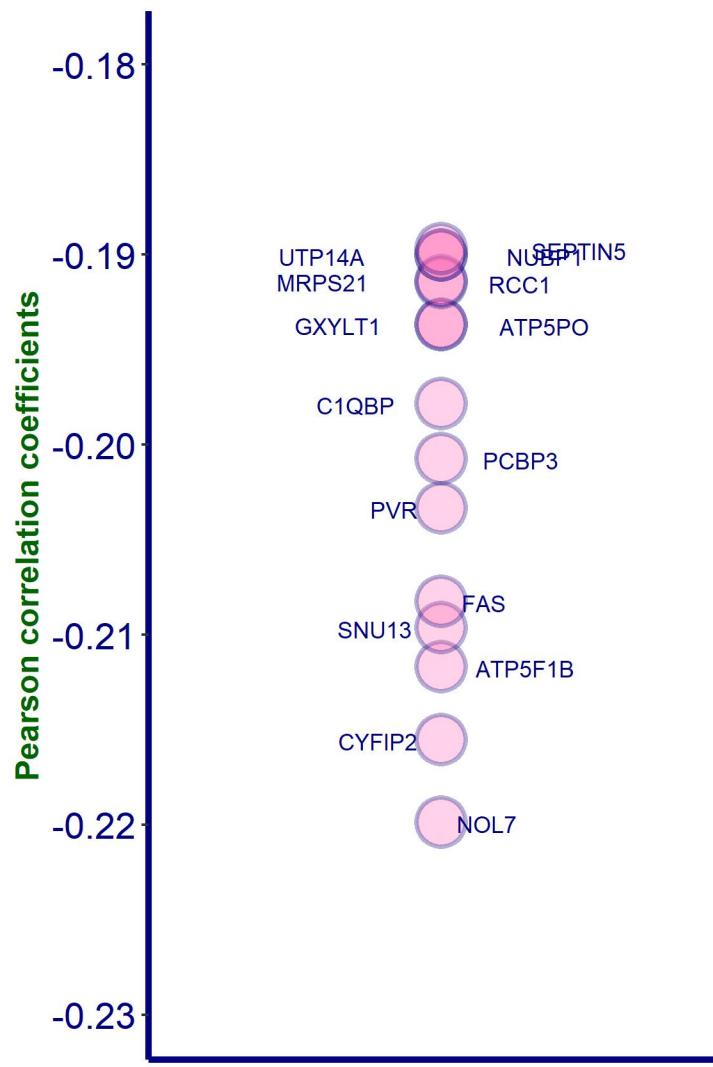
### Histogram of CUL4A protein compared to proteins with low and high abundance



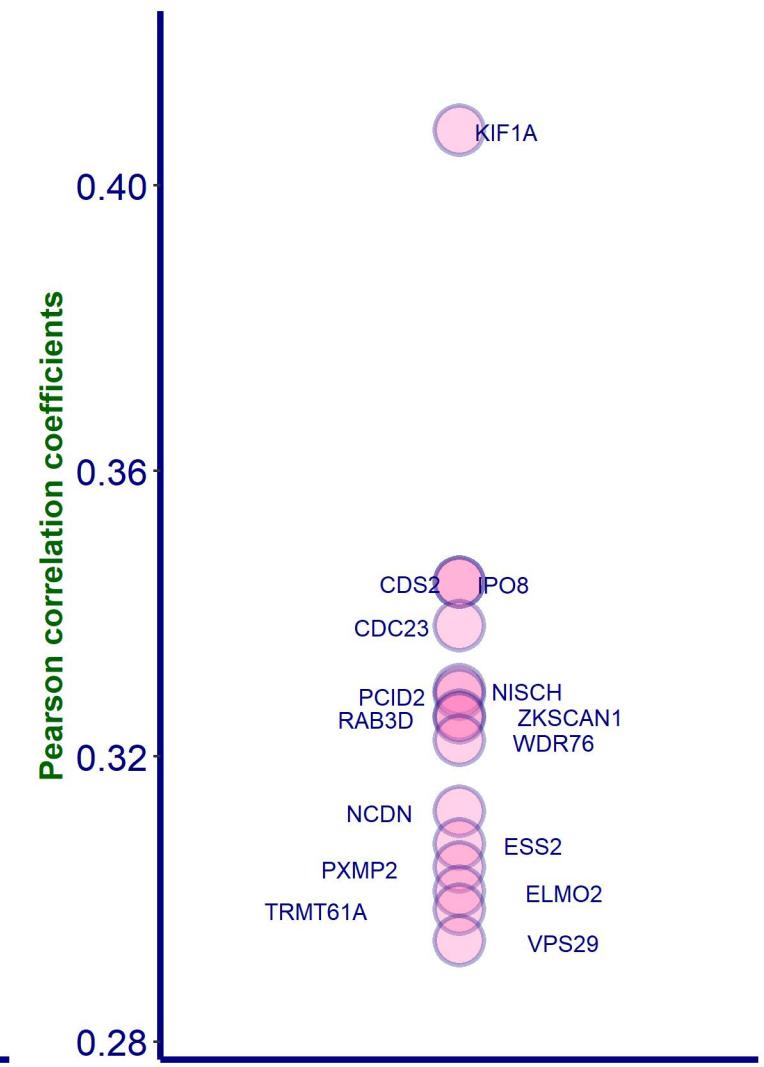
### Density plot of CUL4A protein compared to proteins with low and high abundance



### Top negative correlations of CUL4A protein, DB1

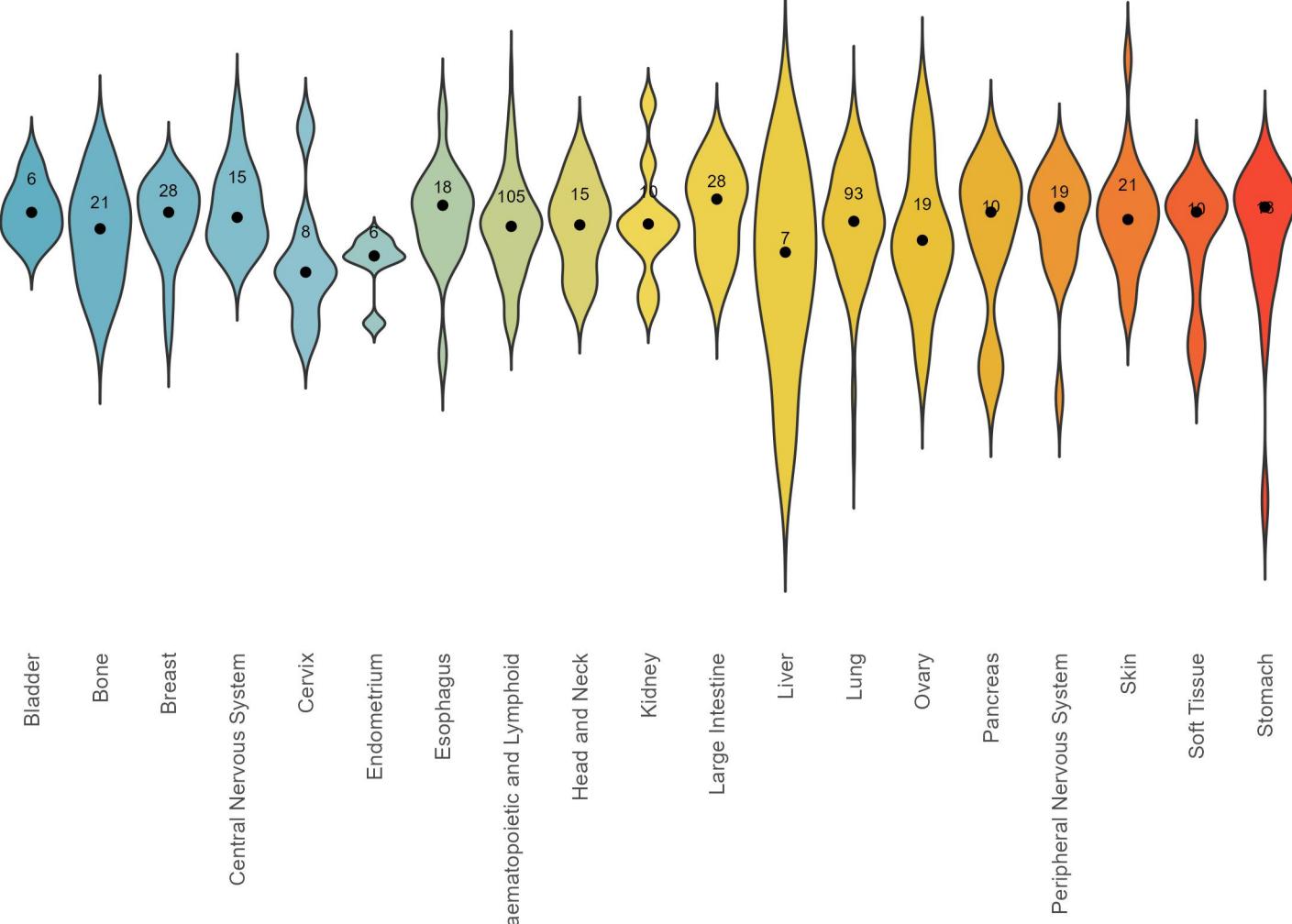


### Top positive correlations of CUL4A protein, DB1



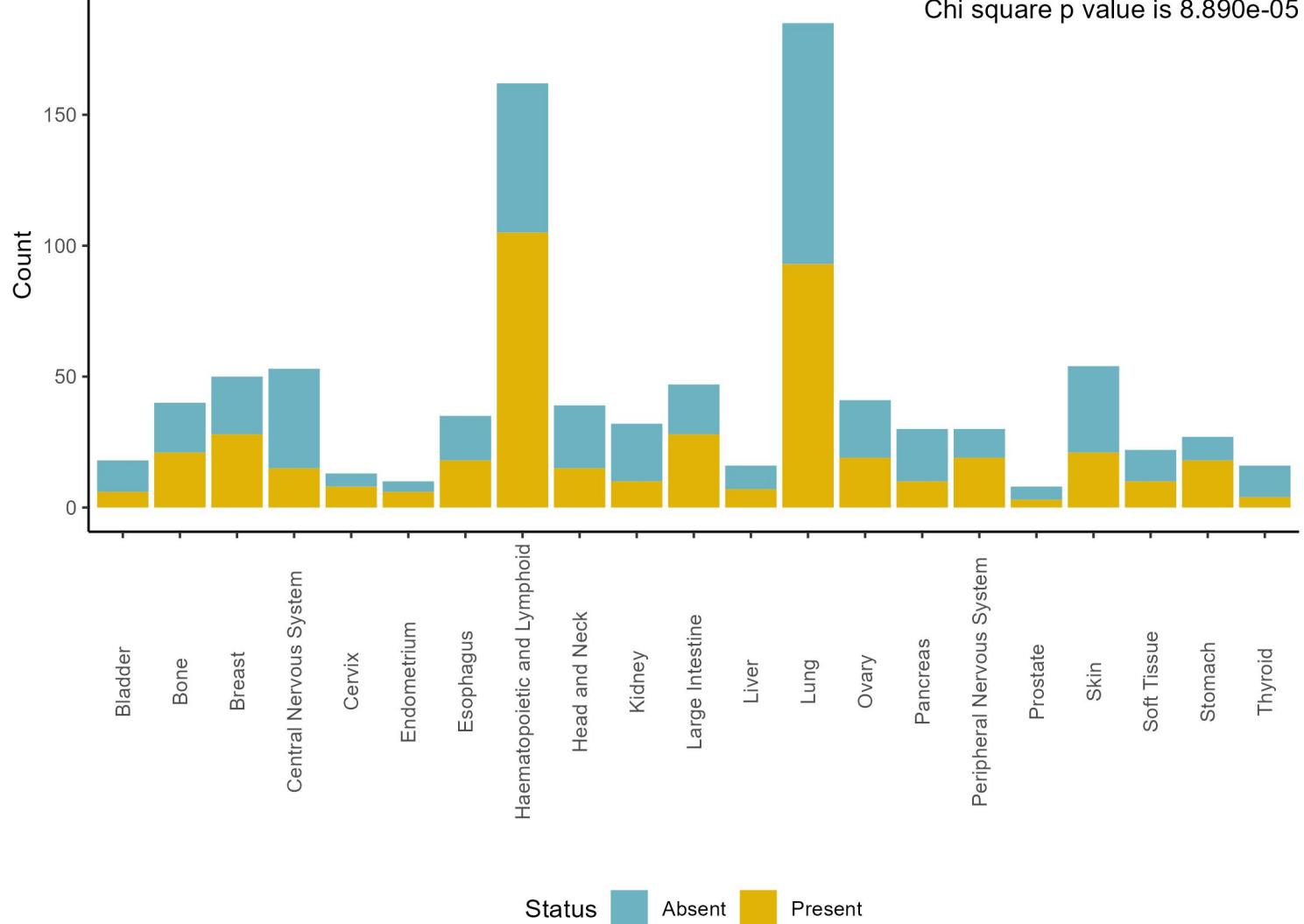
## Amount of CUL4A protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 5.109e-01



## Present and absent CUL4A protein counts by tissue, DB1

Chi square p value is 8.890e-05

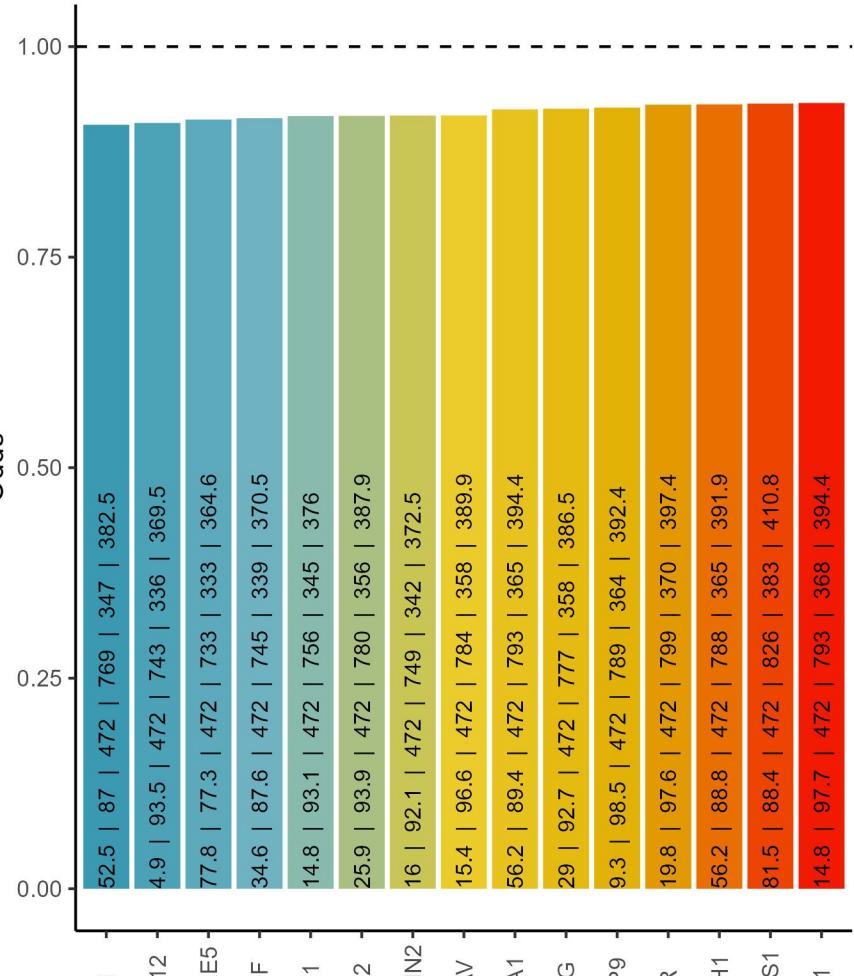


## Cooccurrence with CUL4A protein, DB1

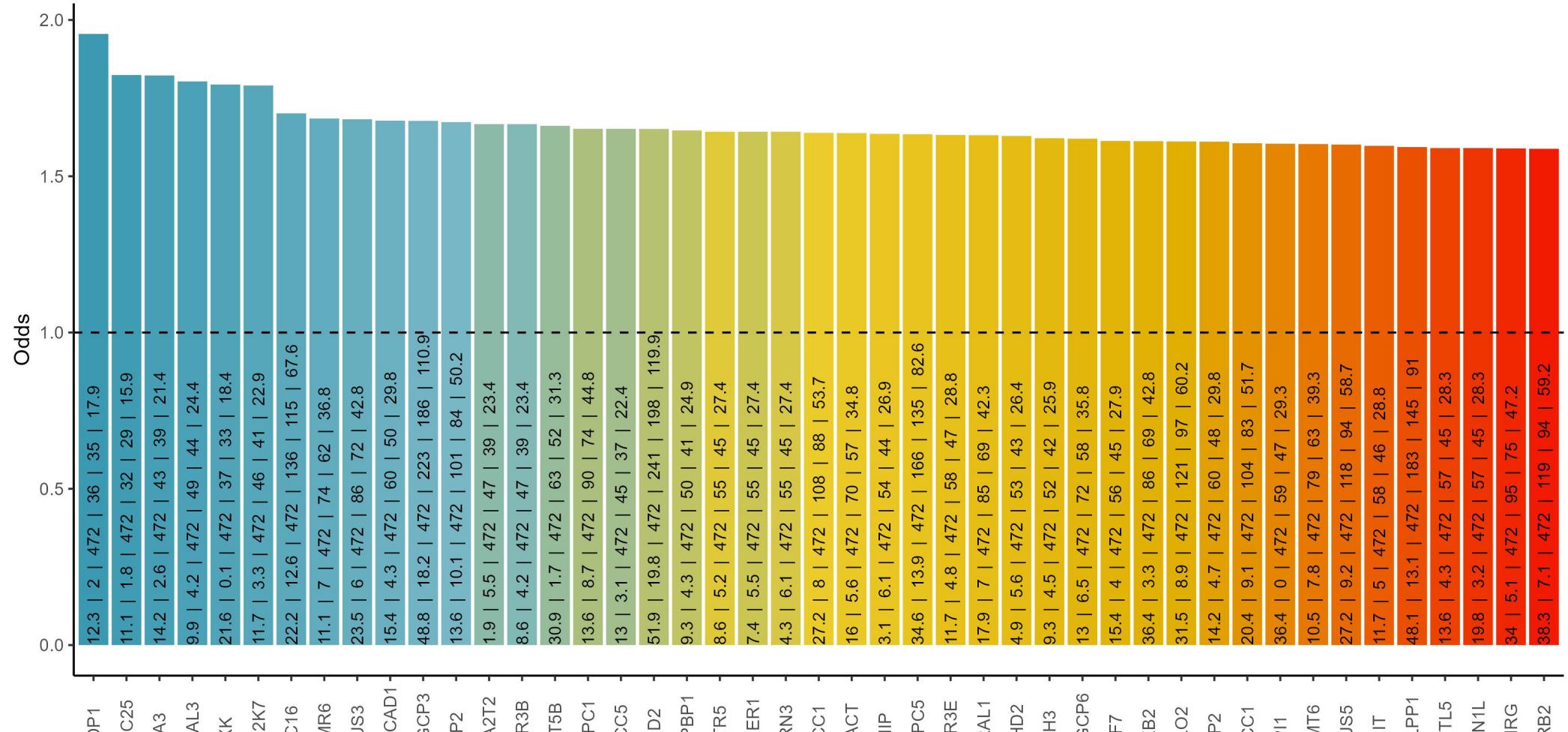
% of CUL4A in blood cancers: 64.8 ; % of CUL4A in solid cancers: 46.4

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CUL4A | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

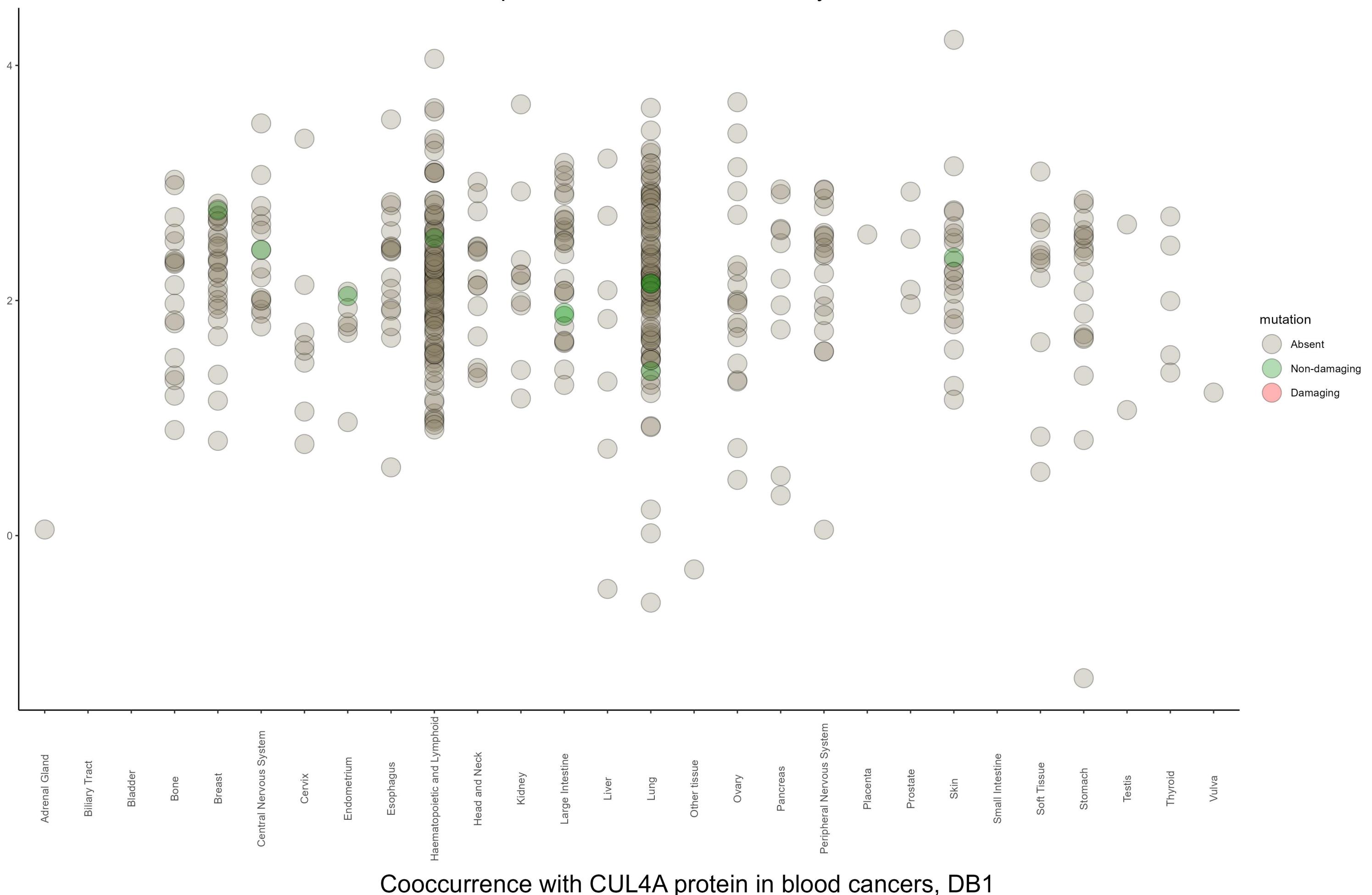
### Negative cooccurrence



### Positive cooccurrence

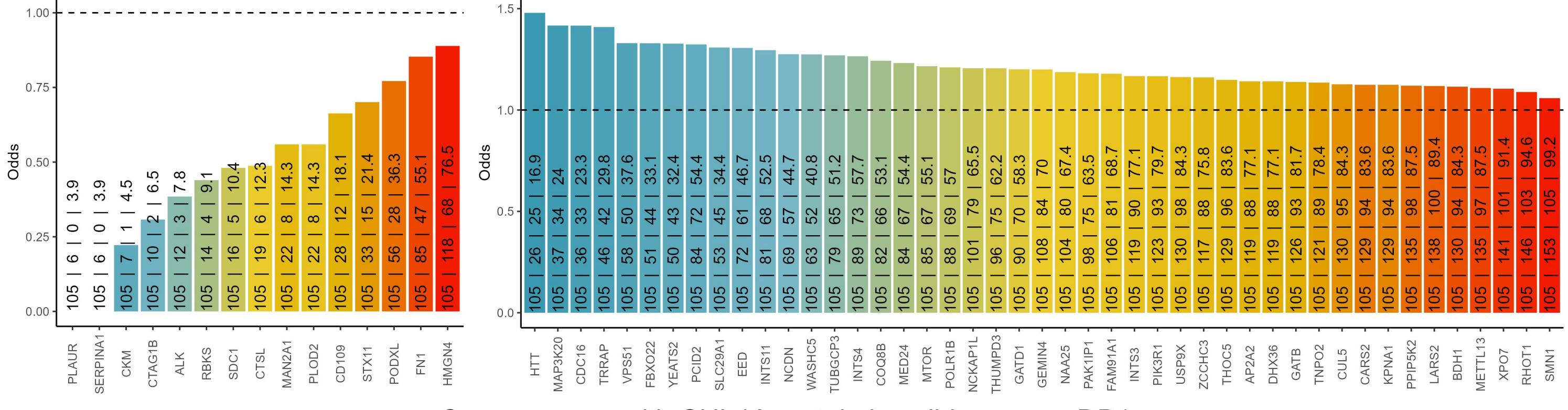


# Amount of CUL4A protein and mutation status by tissue, DB1



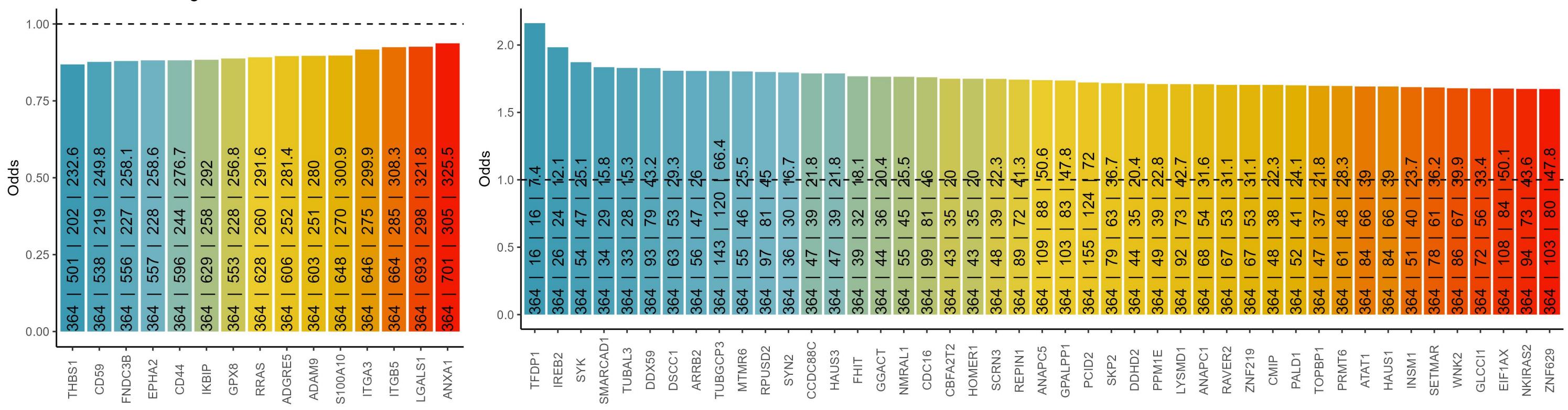
## Cooccurrence with CUL4A protein in blood cancers, DB1

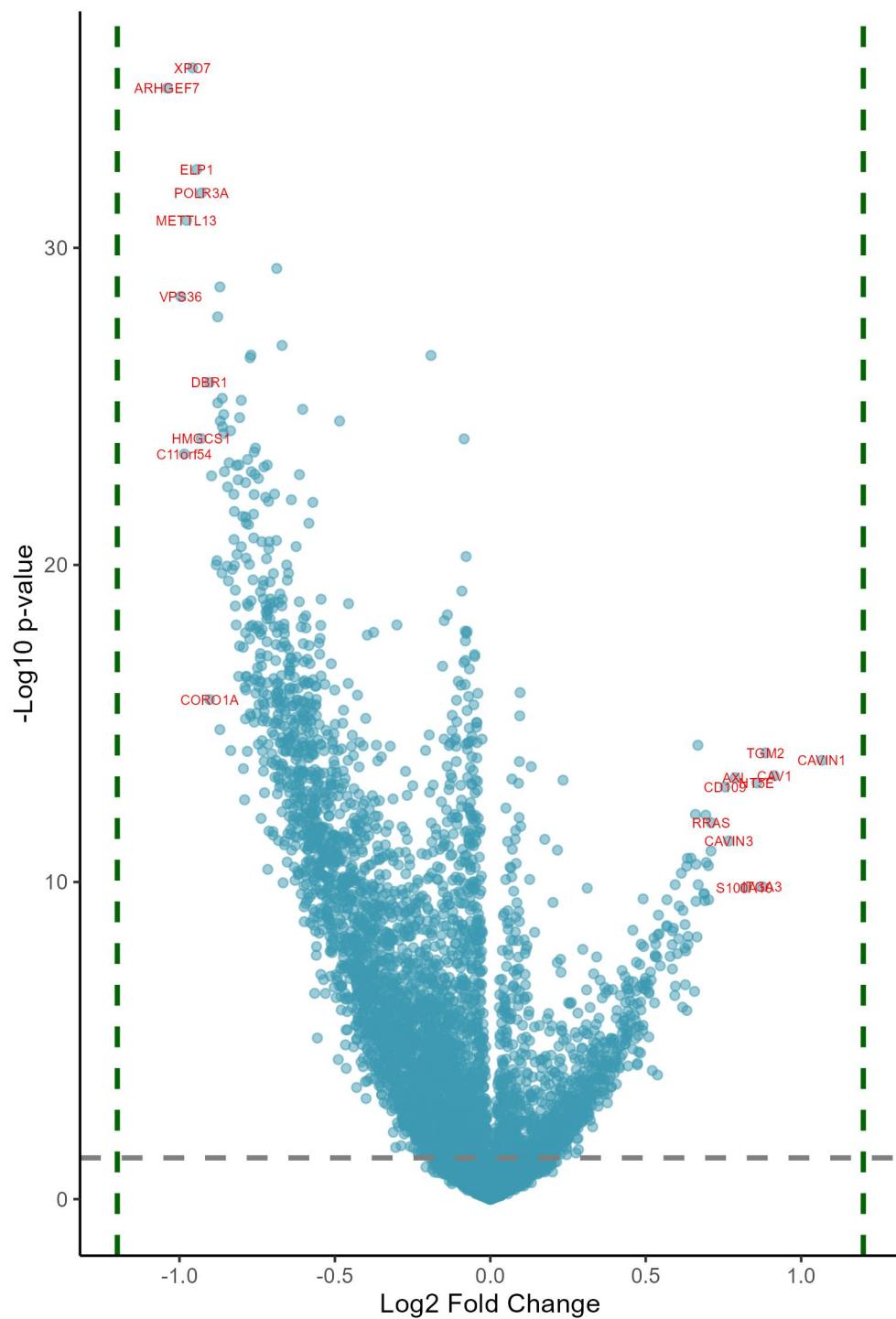
The text in the bars: incidence of CUL4A | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



## Cooccurrence with CUL4A protein in solid cancers, DB1

The text in the bars: incidence of CUL4A | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

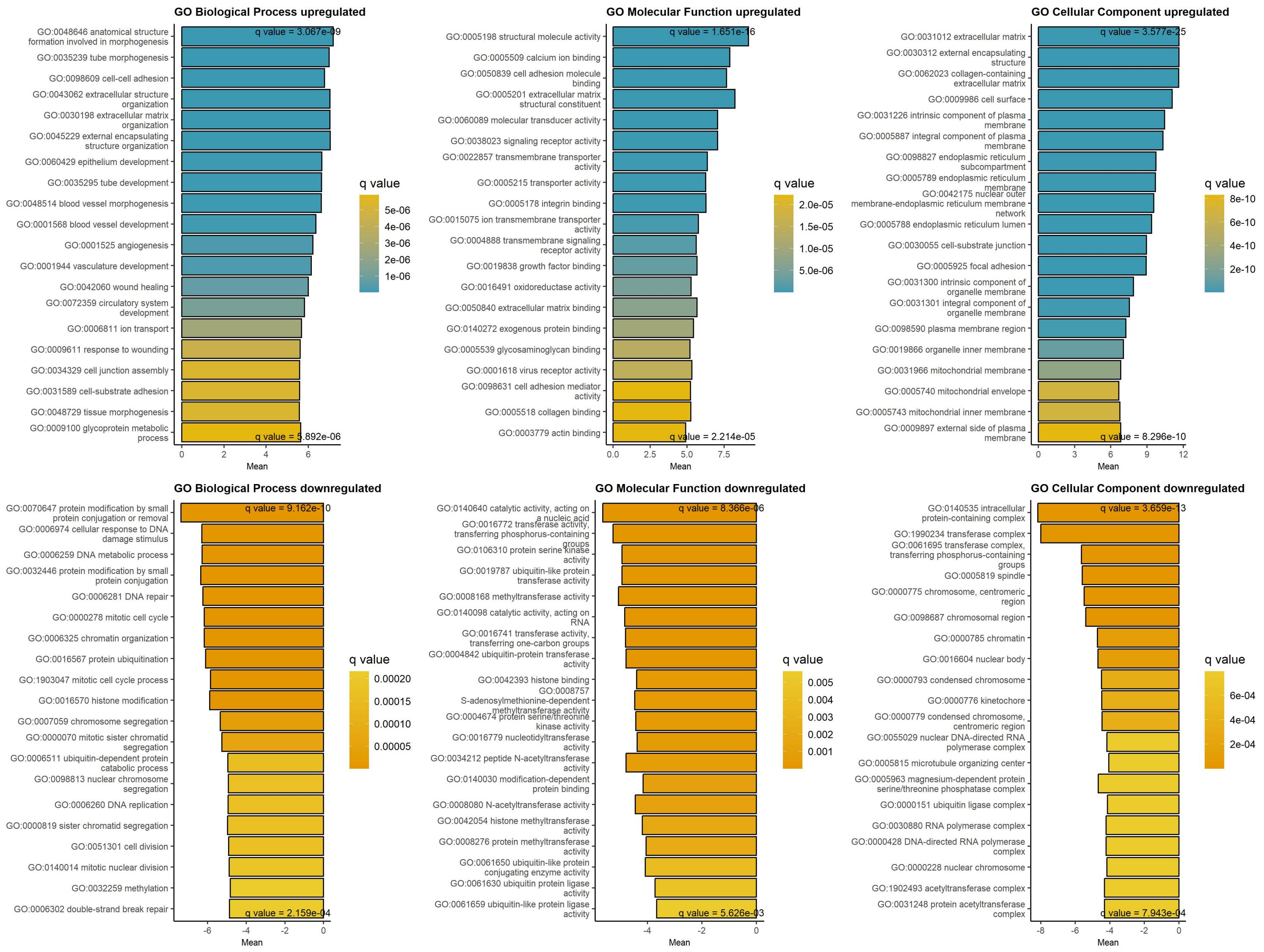


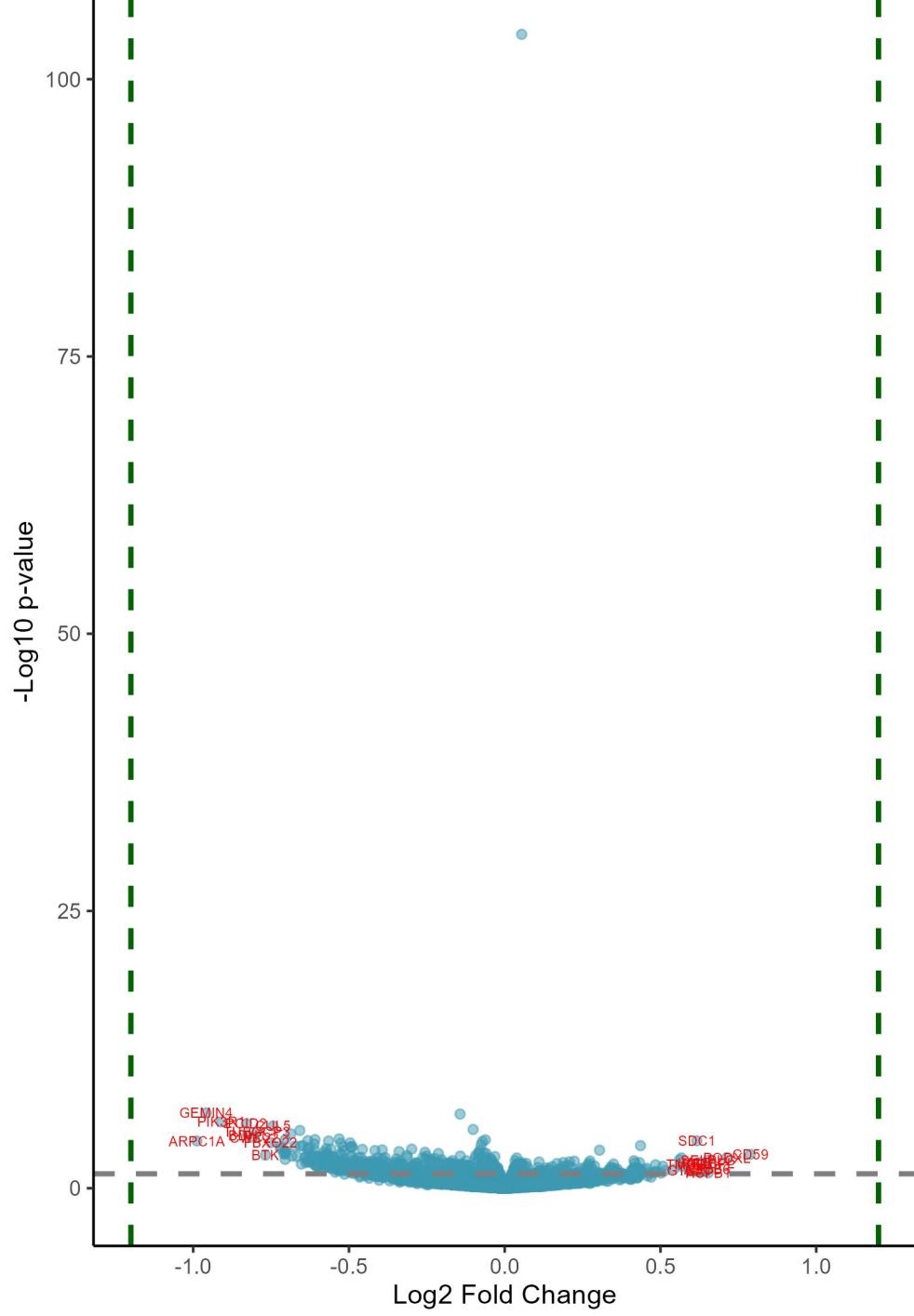


### Downregulated at low/absent CUL4A Upregulated at low/absent CUL4A

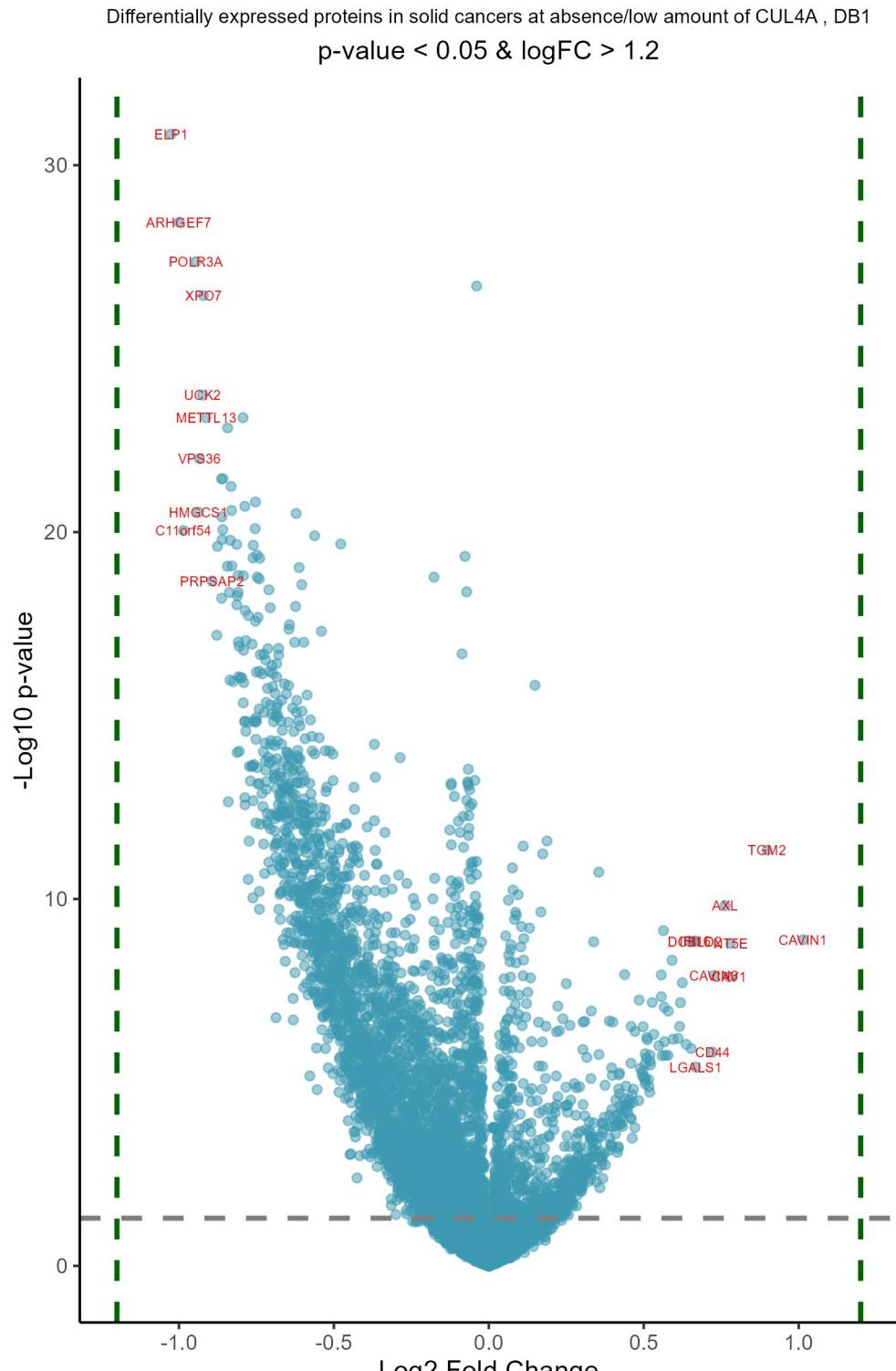
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.04	2.03e-32	ARHGEF7	Rho guanine nucleotide exchange fac	1.07	2.41e-13	CAVIN1	caveolae associated protein 1
-1	2.54e-26	VPS36	vacuolar protein sorting 36 homolog	0.91	6.63e-13	CAV1	caveolin 1
-0.98	6.83e-22	C11orf54	chromosome 11 open reading frame 54	0.89	1.44e-13	TGM2	transglutaminase 2
-0.98	1.51e-28	METTL13	methyltransferase 13, eEF1A lysine	0.88	1.00e-09	ITGA3	integrin subunit alpha 3
-0.96	7.04e-33	XPO7	exportin 7	0.86	1.05e-12	NT5E	5'-nucleotidase ecto
-0.94	5.62e-30	ELP1	elongator acetyltransferase complex	0.82	1.08e-09	S100A10	S100 calcium binding protein A10
-0.93	2.51e-22	HMGCS1	3-hydroxy-3-methylglutaryl-CoA synt	0.79	7.49e-13	AXL	AXL receptor tyrosine kinase
-0.93	2.46e-29	POLR3A	RNA polymerase III subunit A	0.77	4.82e-11	CAVIN3	caveolae associated protein 3
-0.9	7.78e-24	DBR1	debranching RNA lariats 1	0.76	1.36e-12	CD109	CD109 molecule
-0.9	4.96e-15	CORO1A	coronin 1A	0.71	1.47e-11	RRAS	RAS related
-0.9	2.46e-21	PRPSAP2	phosphoribosyl pyrophosphate synthetase	0.71	9.25e-11	PLOD2	procollagen-lysine,2-oxoglutarate 5
-0.88	8.78e-19	NUDT3	nudix hydrolase 3	0.7	2.41e-09	ITGA2	integrin subunit alpha 2
-0.88	6.70e-19	COPS7B	COP9 signalosome subunit 7B	0.7	2.47e-10	EPHA2	EPH receptor A2
-0.88	9.98e-26	KDM3B	lysine demethylase 3B	0.69	1.99e-10	ADAM9	ADAM metallopeptidase domain 9
-0.88	2.88e-23	UBFD1	ubiquitin family domain containing	0.69	9.01e-12	DCBLD2	discoidin, CUB and LCCL domain cont
-0.87	3.35e-14	NACA2	nascent polypeptide associated comp	0.69	2.56e-09	CD59	CD59 molecule (CD59 blood group)
-0.87	1.42e-26	EIF2B2	eukaryotic translation initiation f	0.69	1.65e-09	MMP14	matrix metallopeptidase 14
-0.87	8.41e-23	EIF2B5	eukaryotic translation initiation f	0.69	1.58e-09	THBS1	thrombospondin 1
-0.86	1.49e-18	SNRNP27	small nuclear ribonucleoprotein U4/U6	0.67	8.77e-10	HMGAA2	high mobility group AT-hook 2
-0.86	2.30e-23	UCK2	uridine-cytidine kinase 2	0.67	8.98e-14	RAB11FIP5	RAB11 family interacting protein 5
-0.86	1.20e-22	ELP3	elongator acetyltransferase complex	0.66	2.90e-08	S100A16	S100 calcium binding protein A16
-0.86	1.84e-22	GABPA	GA binding protein transcription fa	0.66	2.24e-10	IKBIP	IKBKB interacting protein
-0.86	6.01e-23	CARM1	coactivator associated arginine met	0.66	2.66e-09	GPX8	glutathione peroxidase 8 (putative)
-0.86	1.95e-21	UBXN7	UBX domain protein 7	0.66	8.58e-12	FNDC3B	fibronectin type III domain contain
-0.85	9.28e-19	GRK2	G protein-coupled receptor kinase 2	0.66	1.14e-06	GNG12	G protein subunit gamma 12
-0.85	5.01e-21	POLA2	DNA polymerase alpha 2, accessory s	0.65	1.50e-10	FN1	fibronectin 1
-0.84	2.47e-18	APIP	APAF1 interacting protein	0.64	2.80e-08	PPIC	peptidylprolyl isomerase C
-0.84	1.21e-21	LIG1	DNA ligase 1	0.64	4.86e-08	MYOF	myoferlin
-0.84	1.56e-22	HAT1	histone acetyltransferase 1	0.63	1.52e-10	ITGAV	integrin subunit alpha V

### GAGE analysis on upregulated and downregulated proteins at low/absent CUL4A protein, DB1





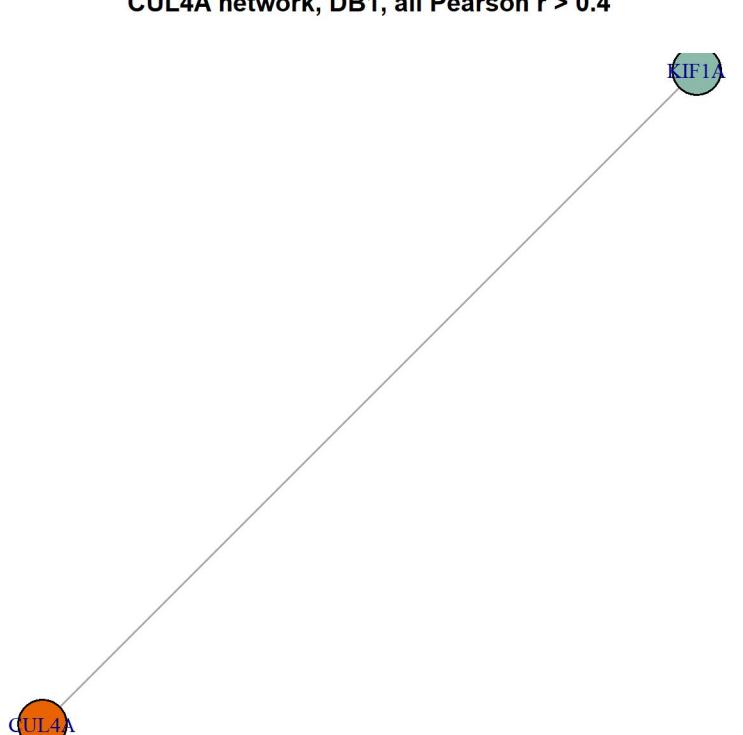
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.99	1.74e-02	ARPC1A	actin related protein 2/3 complex s	0.79	8.69e-02	CD59	CD59 molecule (CD59 blood group)
-0.96	3.40e-04	GEMIN4	gem nuclear organelle associated pr	0.71	1.19e-01	PODXL	podocalyxin like
-0.91	1.39e-03	PIK3R1	phosphoinositide-3-kinase regulator	0.65	3.78e-01	HSPB1	heat shock protein family B (small)
-0.83	1.63e-03	PCID2	PCI domain containing 2	0.65	1.54e-01	SELPLG	selectin P ligand
-0.83	8.91e-03	BDH1	3-hydroxybutyrate dehydrogenase 1	0.65	2.94e-01	ABCB6	ATP binding cassette subfamily B me
-0.8	1.39e-02	CWC22	CWC22 spliceosome associated protei	0.65	1.86e-01	IRF2BPL	interferon regulatory factor 2 bind
-0.8	5.55e-03	TUBGCP3	tubulin gamma complex associated pr	0.62	1.74e-01	ALB	albumin
-0.77	9.78e-02	BTK	Bruton tyrosine kinase	0.62	1.74e-02	SDC1	syndecan 1
-0.75	2.27e-02	FBXO22	F-box protein 22	0.6	1.96e-01	TMUB1	transmembrane and ubiquitin like do
-0.74	2.31e-03	CUL5	cullin 5	0.59	3.20e-01	GTSF1	gameteocyte specific factor 1
-0.72	4.40e-02	UBAC2	UBA domain containing 2	0.57	2.33e-01	TRIP10	thyroid hormone receptor interactor
-0.72	3.46e-02	INTS11	integrator complex subunit 11	0.57	1.20e-01	LRRKIP2	LRR binding FLII interacting protei
-0.71	8.01e-02	SMYD3	SET and MYND domain containing 3	0.56	1.49e-01	ARFGAP3	ADP ribosylation factor GTPase acti
-0.71	6.54e-02	ZEB2	zinc finger E-box binding homeobox	0.54	2.95e-01	PLD3	phospholipase D family member 3
-0.71	5.32e-02	DNAJC10	DnaJ heat shock protein family (Hsp	0.51	3.23e-01	SYNJ2BP	synaptjanin 2 binding protein
-0.7	1.44e-01	STARD9	StAR related lipid transfer domain	0.51	2.32e-01	EHBP1L1	EH domain binding protein 1 like 1
-0.7	1.70e-02	CARS2	cysteinyl-tRNA synthetase 2, mitoch	0.5	3.84e-01	FKBP11	FKBP prolyl isomerase 11
-0.7	7.35e-02	POLR1B	RNA polymerase I subunit B	0.49	3.50e-01	CLCC1	chloride channel CLIC like 1
-0.7	8.32e-02	NCKAP1L	NCK associated protein 1 like	0.48	2.01e-01	C12orf57	chromosome 12 open reading frame 57
-0.7	6.78e-02	TRAPP/C5	trafficking protein particle comple	0.48	3.48e-01	HLA-DRB4	major histocompatibility complex, c
-0.69	7.58e-03	INTS3	integrator complex subunit 3	0.48	3.84e-01	DHRS4	dehydrogenase/reductase 4
-0.68	1.07e-01	LANCL1	LanC like 1	0.47	5.19e-01	CD70	CD70 molecule
-0.67	3.46e-02	IBA57	iron-sulfur cluster assembly factor	0.46	3.90e-01	SPTY2D1	SPT2 chromatin protein domain conta
-0.67	1.10e-01	HSD17B11	hydroxysteroid 17-beta dehydrogenas	0.46	4.72e-01	IRF4	interferon regulatory factor 4
-0.66	4.58e-03	USP9X	ubiquitin specific peptidase 9 X-li	0.46	2.69e-01	LDLR	low density lipoprotein receptor
-0.66	3.46e-02	GATB	glutamyl-tRNA amidotransferase subu	0.45	3.13e-01	RNF149	ring finger protein 149
-0.65	1.92e-01	MRPS2	mitochondrial ribosomal protein S2	0.44	3.75e-01	TNS3	tensin 3
-0.65	3.33e-02	MAP3K20	mitogen-activated protein kinase ki	0.44	3.27e-01	FAM3C	FAM3 metabolism regulating signalin
-0.64	1.19e-01	RASSF2	Ras association domain family membe	0.44	3.33e-02	PKP2	plakophilin 2



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.03	4.76e-28	ELP1	elongator acetyltransferase complex	1.01	1.29e-08	CAVIN1	caveolae associated protein 1
-1	7.98e-26	ARHGEF7	Rho guanine nucleotide exchange fac	0.9	8.73e-11	TGM2	transglutaminase 2
-0.99	2.61e-18	C11orf54	chromosome 11 open reading frame 54	0.78	1.56e-08	NT5E	5'-nucleotidase ecto
-0.95	7.09e-25	POLR3A	RNA polymerase III subunit A	0.78	1.01e-07	CAV1	caveolin 1
-0.94	1.06e-18	HMGCS1	3-hydroxy-3-methylglutaryl-CoA synt	0.76	1.91e-09	AXL	AXL receptor tyrosine kinase
-0.93	6.01e-20	VPS36	vacuolar protein sorting 36 homolog	0.73	9.34e-08	CAVIN3	caveolae associated protein 3
-0.92	1.74e-21	UCK2	uridine-cytidine kinase 2	0.72	6.99e-06	CD44	CD44 molecule (Indian blood group)
-0.92	3.95e-24	XPO7	exportin 7	0.67	1.64e-05	LGALS1	galectin 1
-0.91	5.61e-21	METTL13	methyltransferase 13, eEF1A lysine	0.67	1.38e-08	IFI16	interferon gamma inducible protein
-0.89	3.33e-17	PRPSAP2	phosphoribosyl pyrophosphate synthe	0.66	1.41e-08	DCBLD2	discoidin, CUB and LCCL domain cont
-0.88	7.07e-16	NTMT1	N-terminal Xaa-Pro-Lys N-methyltran	0.65	5.71e-06	ITGA3	integrin subunit alpha 3
-0.88	5.42e-18	UBXN7	UBX domain protein 7	0.65	1.40e-08	IKBIP	IKBKB interacting protein
-0.86	1.81e-19	NHLRC2	NHL repeat containing 2	0.64	4.49e-06	ICAM1	intercellular adhesion molecule 1
-0.86	8.46e-17	GSK3B	glycogen synthase kinase 3 beta	0.62	1.38e-07	CD109	CD109 molecule
-0.86	1.27e-18	UBFD1	ubiquitin family domain containing	0.62	4.27e-07	HMGA2	high mobility group AT-hook 2
-0.86	4.24e-18	GABPA	GA binding protein transcription fa	0.62	1.64e-06	THBS1	thrombospondin 1
-0.86	2.60e-18	DBR1	debranching RNA lariats 1	0.61	3.24e-06	S100A10	S100 calcium binding protein A10
-0.86	1.81e-19	CARM1	coactivator associated arginine met	0.59	3.38e-06	MMP14	matrix metallopeptidase 14
-0.84	1.58e-17	POLA2	DNA polymerase alpha 2, accessory s	0.59	4.00e-08	RRAS	RAS related
-0.84	9.59e-21	EIF2B2	eukaryotic translation initiation f	0.58	6.90e-07	SP100	SP100 nuclear antigen
-0.84	6.36e-12	POLR2F	RNA polymerase II, I and III subuni	0.58	8.42e-06	CD59	CD59 molecule (CD59 blood group)
-0.84	6.11e-17	IRF2BP2	interferon regulatory factor 2 bind	0.57	8.32e-06	KRT80	keratin 80
-0.84	8.22e-15	BRD2	bromodomain containing 2	0.57	3.86e-06	EHD2	EH domain containing 2
-0.83	4.26e-18	ELP3	elongator acetyltransferase complex	0.57	5.52e-07	NRP1	neuropilin 1
-0.83	2.70e-19	PPP2R2A	protein phosphatase 2 regulatory su	0.56	7.71e-09	RAB11FIP5	RAB11 family interacting protein 5
-0.83	1.01e-18	KDM3B	lysine demethylase 3B	0.56	8.58e-06	RAC2	Rac family small GTPase 2
-0.83	1.58e-17	LIG1	DNA ligase 1	0.56	3.07e-07	APOL2	apolipoprotein L2
-0.83	8.97e-15	APIP	APAF1 interacting protein	0.56	9.06e-08	ADGRE5	adhesion G protein-coupled receptor
-0.81	5.12e-18	NELFCD	negative elongation factor complex	0.55	4.88e-06	EPHA2	EPH receptor A2

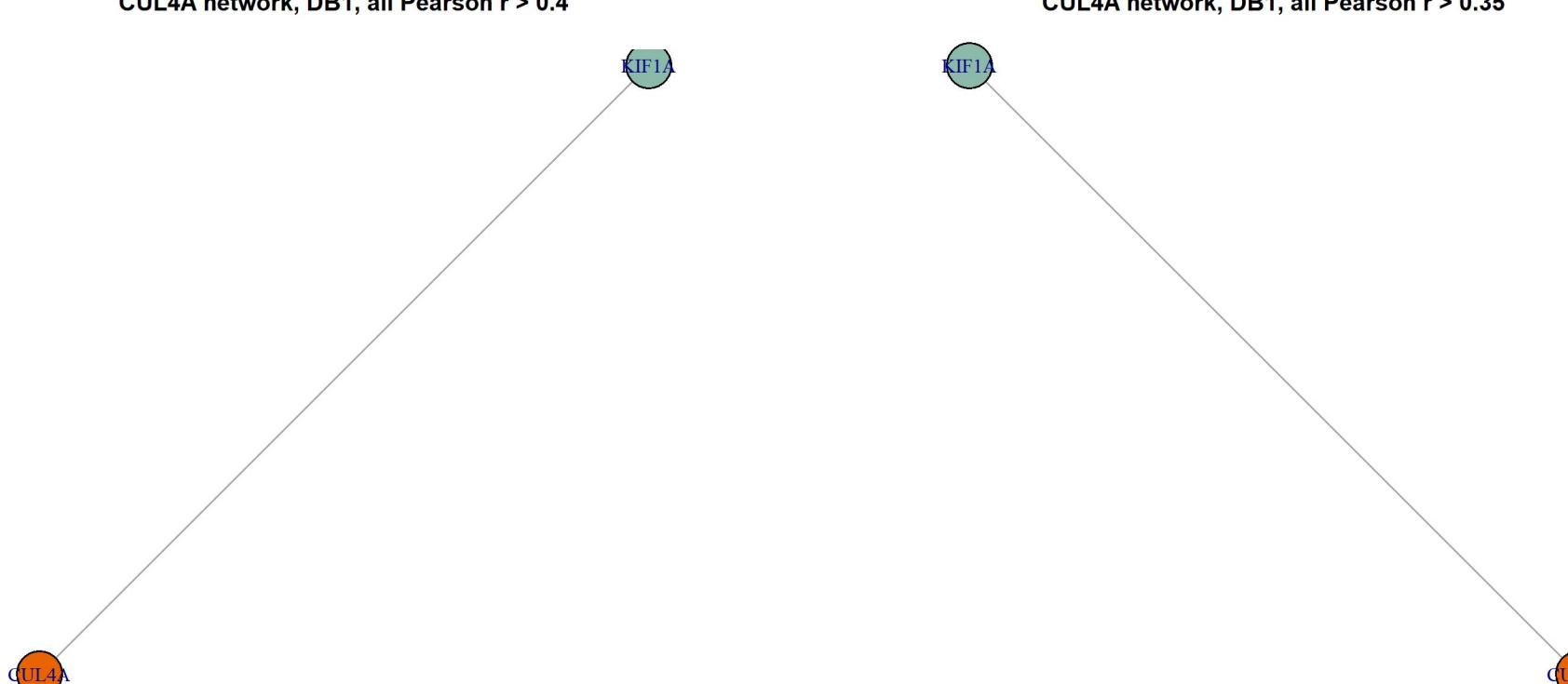
CUL4A network, DB1, all Pearson r &gt; 0.4

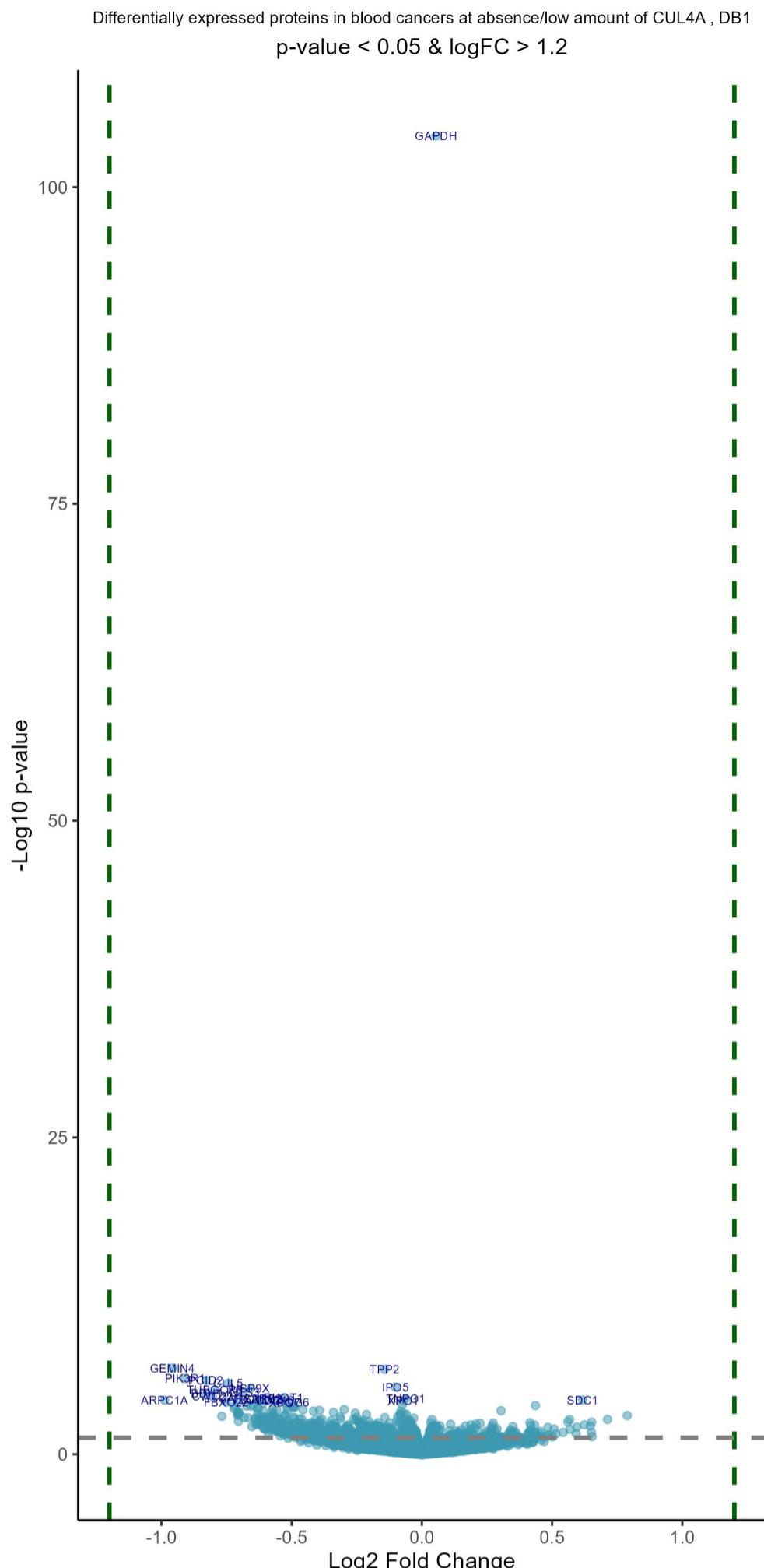
KIF1A



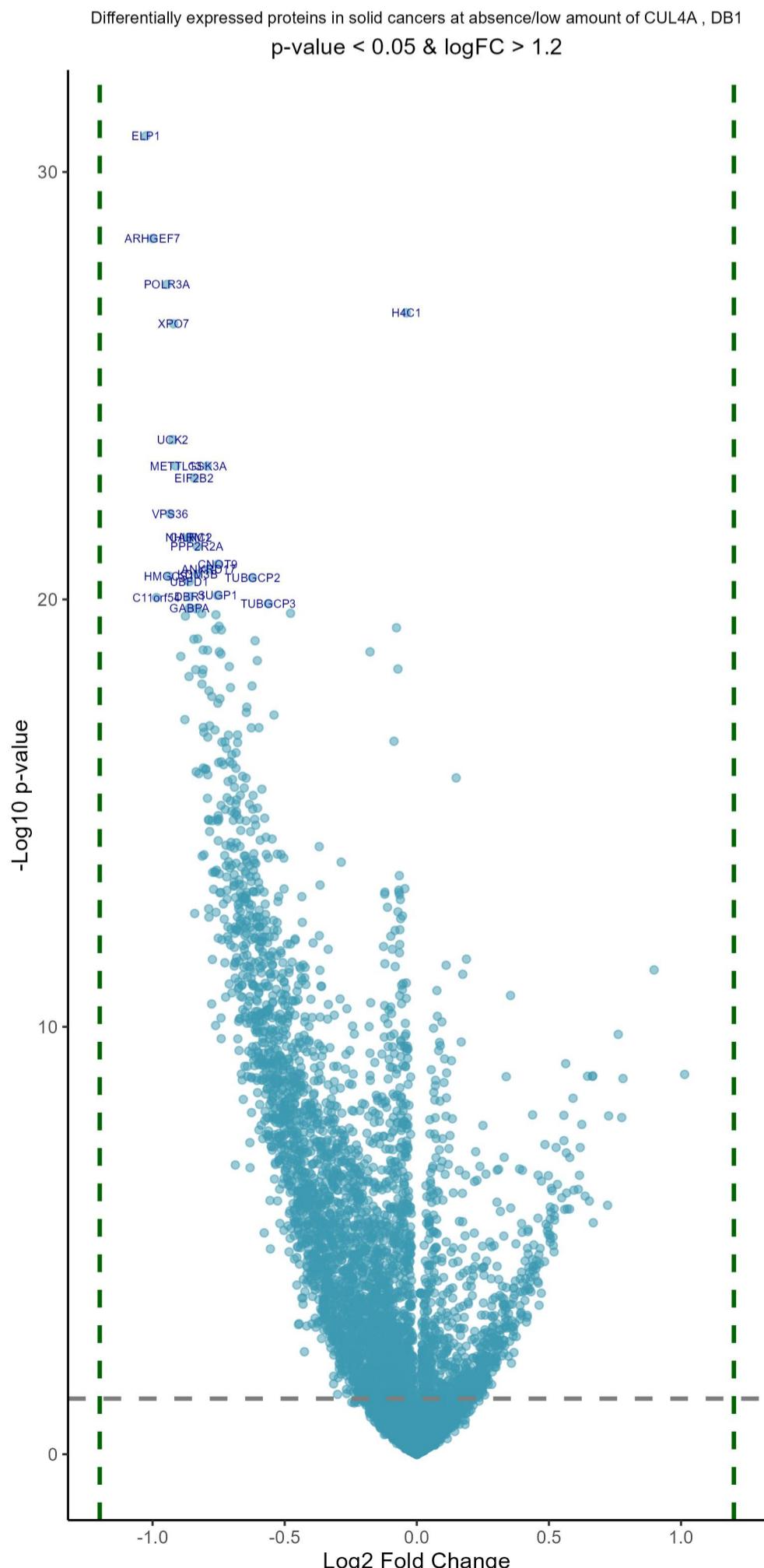
CUL4A network, DB1, all Pearson r &gt; 0.35

CUL4A



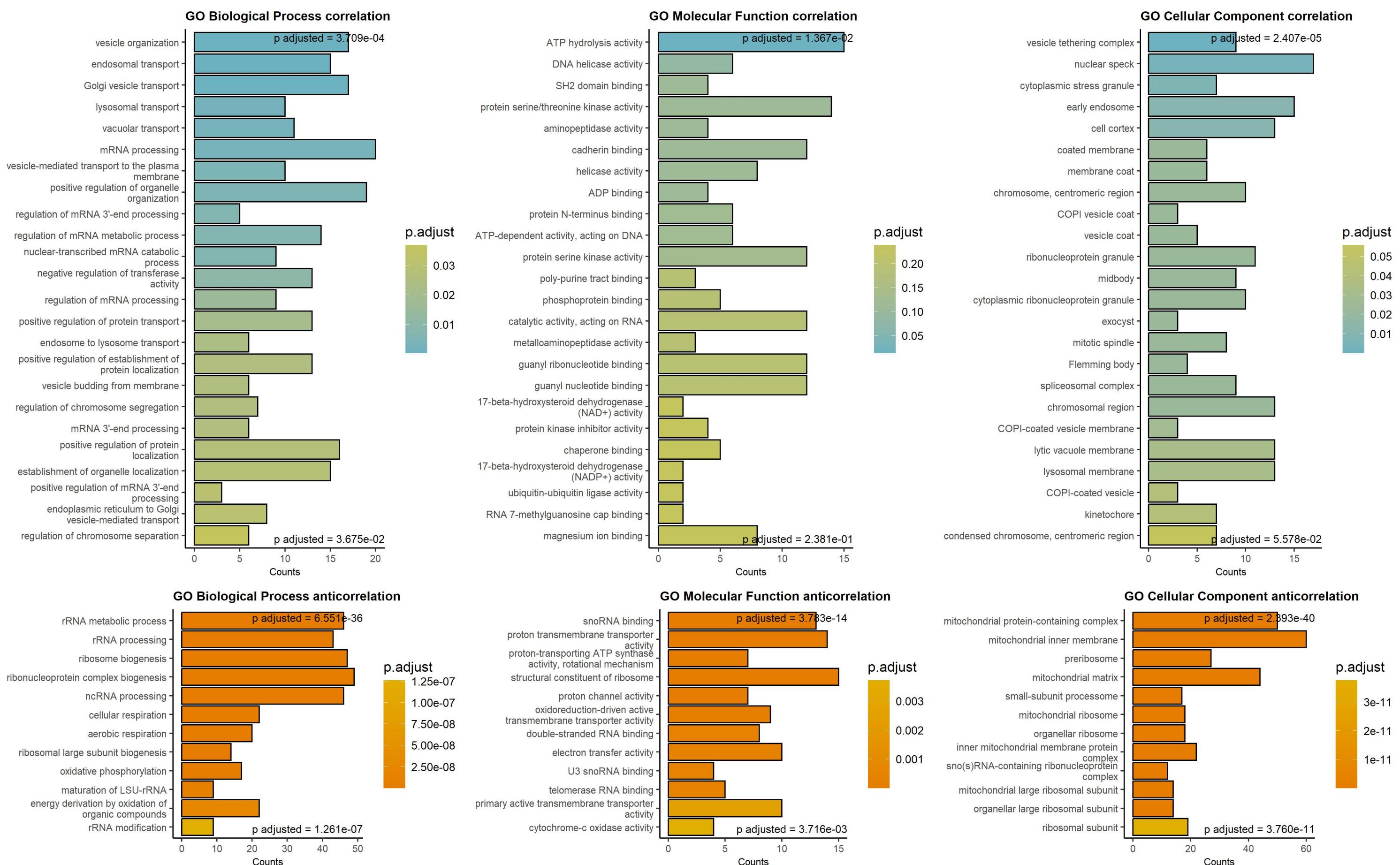


Downregulated in blood cancers at low/absent CUL4A				Upregulated in blood cancers at low/absent CUL4A			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.96	3.40e-04	GEMIN4	gem nuclear organelle associated pr	0.05	6.02e-101	GAPDH	glyceraldehyde-3-phosphate dehydrog
-0.14	3.40e-04	TPP2	tripeptidyl peptidase 2	0.62	1.74e-02	SDC1	syndecan 1
-0.91	1.39e-03	PIK3R1	phosphoinositide-3-kinase regulator	0.44	3.33e-02	PKP2	plakophilin 2
-0.83	1.63e-03	PCID2	PCI domain containing 2	0.3	5.32e-02	RNF126	ring finger protein 126
-0.74	2.31e-03	CUL5	cullin 5	0.79	8.69e-02	CD59	CD59 molecule (CD59 blood group)
-0.1	4.19e-03	IPO5	importin 5	0.71	1.19e-01	PODXL	podocalyxin like
-0.66	4.58e-03	USP9X	ubiquitin specific peptidase 9 X-li	0.57	1.20e-01	LRRKIP2	LRR binding FLII interacting protei
-0.8	5.55e-03	TUBGCP3	tubulin gamma complex associated pr	0.04	1.20e-01	PSMC5	proteasome 26S subunit, ATPase 5
-0.69	7.58e-03	INTS3	integrator complex subunit 3	0.56	1.49e-01	ARFGAP3	ADP ribosylation factor GTPase acti
-0.83	8.91e-03	BDH1	3-hydroxybutyrate dehydrogenase 1	0.65	1.54e-01	SELPLG	selectin P ligand
-0.8	1.39e-02	CWC22	CWC22 spliceosome associated protei	0.03	1.55e-01	PSMC3	proteasome 26S subunit, ATPase 3
-0.53	1.68e-02	RHOT1	ras homolog family member T1	0.41	1.55e-01	PHC3	polyhomeotic homolog 3
-0.61	1.70e-02	LARS2	leucyl-tRNA synthetase 2, mitochond	0.27	1.59e-01	SERPINA1	serpin family A member 1
-0.7	1.70e-02	CARS2	cysteinyl-tRNA synthetase 2, mitoch	0.22	1.62e-01	IRS4	insulin receptor substrate 4
-0.06	1.70e-02	TNPO1	transportin 1	0.21	1.73e-01	PLAUR	plasminogen activator, urokinase re
-0.63	1.74e-02	TBC1D13	TBC1 domain family member 13	0.11	1.74e-01	MYDGF	myeloid derived growth factor
-0.99	1.74e-02	ARPC1A	actin related protein 2/3 complex s	0.19	1.74e-01	TXNDC5	thioredoxin domain containing 5
-0.57	1.74e-02	CDC16	cell division cycle 16	0.62	1.74e-01	ALB	albumin
-0.07	1.81e-02	XPO1	exportin 1	0.05	1.74e-01	RNF40	ring finger protein 40
-0.75	2.27e-02	FBXO22	F-box protein 22	0.43	1.74e-01	MAN2A1	mannosidase alpha class 2A member 1
-0.5	2.27e-02	COG6	component of oligomeric golgi compl	0.42	1.81e-01	PLOD2	procollagen-lysine,2-oxoglutarate 5
-0.53	2.35e-02	XPO7	exportin 7	0.27	1.84e-01	PABIR1	PP2A Aalpha (PPP2R1A) and B55A (PPP
-0.61	2.61e-02	PPIP5K2	diphosphoinositol pentakisphosphate	0.04	1.84e-01	RPS28	ribosomal protein S28
-0.08	2.96e-02	RCC2	regulator of chromosome condensatio	0.07	1.86e-01	PDIA4	protein disulfide isomerase family
-0.65	3.33e-02	MAP3K20	mitogen-activated protein kinase ki	0.17	1.86e-01	TM9SF1	transmembrane 9 superfamily member
-0.67	3.46e-02	IBA57	iron-sulfur cluster assembly factor	0.65	1.86e-01	IRF2BPL	interferon regulatory factor 2 bind
-0.66	3.46e-02	GATB	glutamyl-tRNA amidotransferase subu	0.05	1.88e-01	DCTN2	dynactin subunit 2
-0.72	3.46e-02	INTS11	integrator complex subunit 11	0.35	1.92e-01	NOL3	nucleolar protein 3
-0.5	3.50e-02	RPUSD3	RNA pseudouridine synthase D3	0.05	1.96e-01	SSR1	signal sequence receptor subunit 1
-0.49	3.50e-02	NELFB	negative elongation factor complex	0.6	1.96e-01	TMUB1	transmembrane and ubiquitin like do
-0.52	3.50e-02	MEPCE	methylphosphate capping enzyme	0.04	1.96e-01	PSMC4	proteasome 26S subunit, ATPase 4
-0.49	3.70e-02	DOCK2	dedicator of cytokinesis 2	0.48	2.01e-01	C12orf57	chromosome 12 open reading frame 57
-0.63	4.13e-02	TDP2	tyrosyl-DNA phosphodiesterase 2	0.06	2.02e-01	NUDT5	nudix hydrolase 5
-0.63	4.13e-02	MED24	mediator complex subunit 24	0.27	2.05e-01	CAV1	caveolin 1
-0.72	4.40e-02	UBAC2	UBA domain containing 2	0.04	2.13e-01	EIF3G	eukaryotic translation initiation f
-0.57	4.49e-02	KPNA1	karyopherin subunit alpha 1	0.2	2.15e-01	NRP1	neuropilin 1
-0.3	4.77e-02	COIL	coilin	0.29	2.30e-01	C19orf53	chromosome 19 open reading frame 53
-0.56	4.77e-02	INTS4	integrator complex subunit 4	0.28	2.30e-01	P4HTM	prolyl 4-hydroxylase, transmembrane
-0.16	4.81e-02	SKB2	S phase kinase associated protein 2	0.51	2.32e-01	EGRB1L1	EH domain binding protein 1 like 1

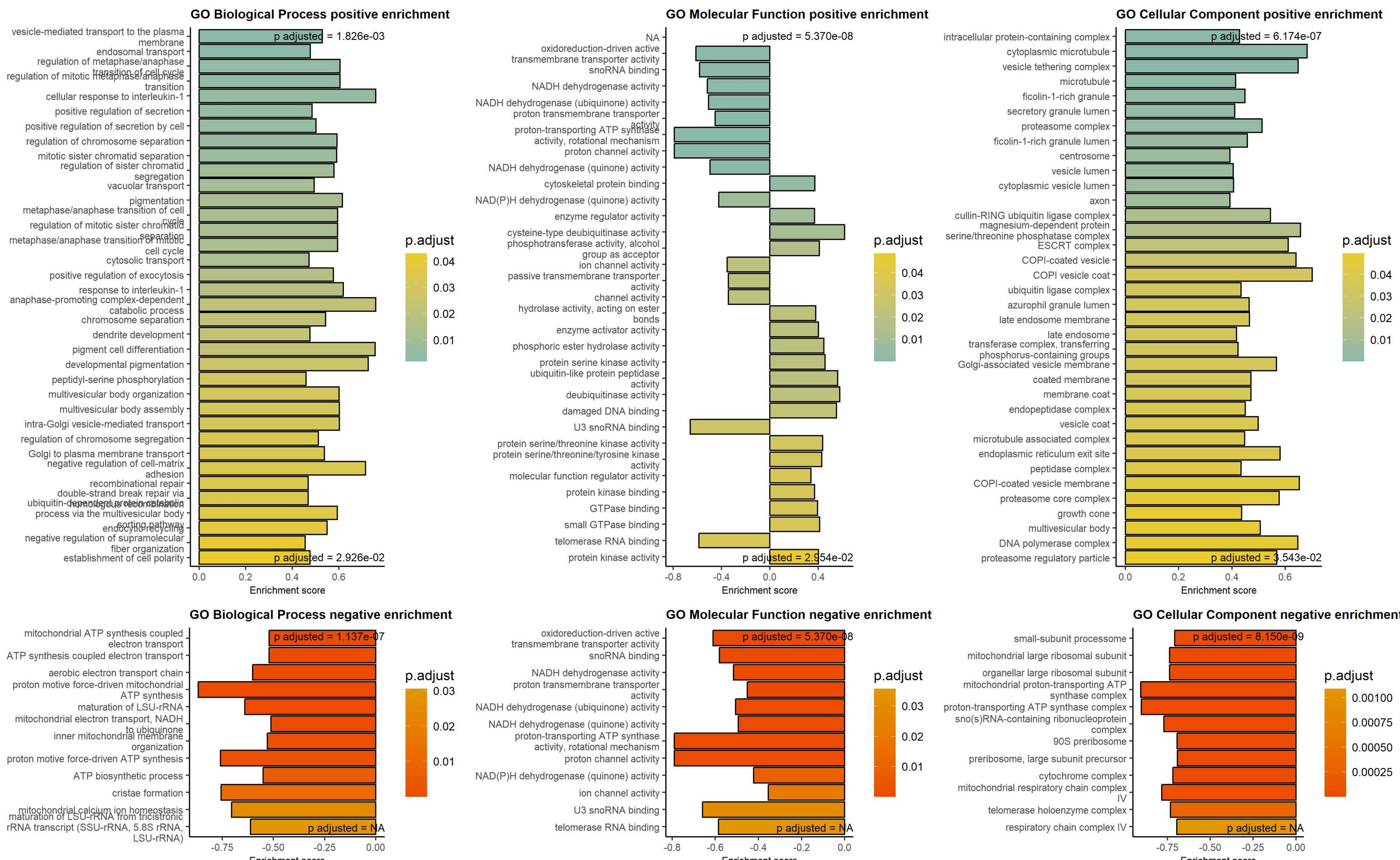


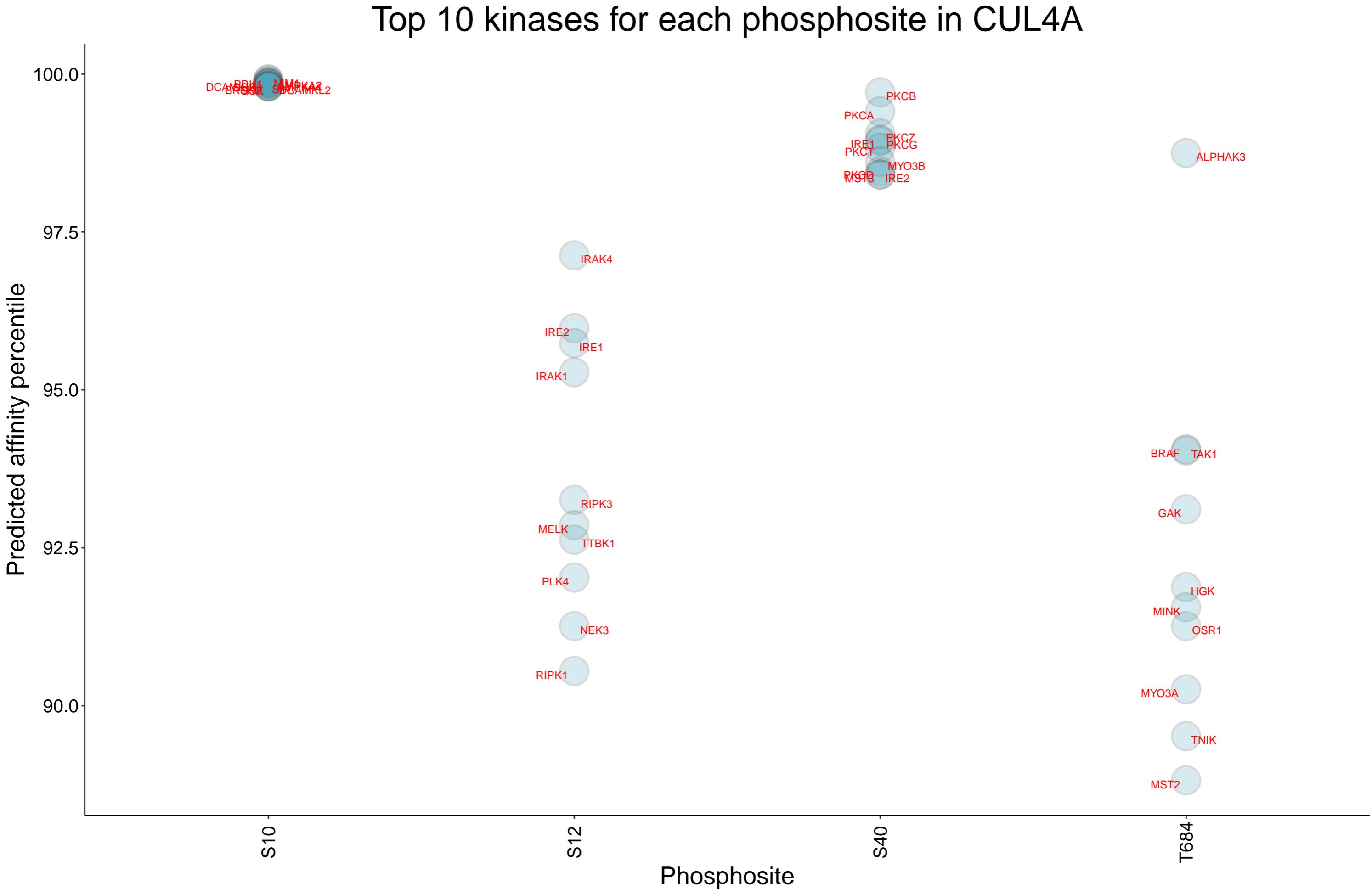
Sorted by p values!							
Downregulated in solid cancers at low/absent CUL4A				Upregulated in solid cancers at low/absent CUL4A			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.03	4.76e-28	ELP1	elongator acetyltransferase complex	0.15	1.09e-14	ITGB1	integrin subunit beta 1
-1	7.98e-26	ARHGEF7	Rho guanine nucleotide exchange fac	0.19	5.33e-11	PLEC	plectin
-0.95	7.09e-25	POLR3A	RNA polymerase III subunit A	0.11	7.03e-11	PICALM	phosphatidylinositol binding clathr
-0.04	2.62e-24	H4C1	H4 clustered histone 1	0.9	8.73e-11	TGM2	transglutaminase 2
-0.92	3.95e-24	XPO7	exportin 7	0.17	1.08e-10	AHNAK	AHNAK nucleoprotein
-0.92	1.74e-21	UCK2	uridine-cytidine kinase 2	0.08	2.35e-10	PGRMC2	progesterone receptor membrane comp
-0.91	5.61e-21	METTL13	methyltransferase 13, eEF1A lysine	0.35	3.00e-10	ITGAV	integrin subunit alpha V
-0.79	5.61e-21	GSK3A	glycogen synthase kinase 3 alpha	0.08	8.06e-10	SSR4	signal sequence receptor subunit 4
-0.84	9.59e-21	EIF2B2	eukaryotic translation initiation f	0.09	1.03e-09	CALU	calumenin
-0.93	6.01e-20	VPS36	vacuolar protein sorting 36 homolog	0.06	1.42e-09	AP2B1	adaptor related protein complex 2 s
-0.86	1.81e-19	CARM1	coactivator associated arginine met	0.76	1.91e-09	AXL	AXL receptor tyrosine kinase
-0.86	1.81e-19	NHLRC2	NHL repeat containing 2	0.17	2.77e-09	ESYT2	extended synaptotagmin 2
-0.83	2.70e-19	PPP2R2A	protein phosphatase 2 regulatory su	0.09	2.82e-09	TMOD3	tropomodulin 3
-0.75	6.66e-19	CNOT9	CCR4-NOT transcription complex subu	0.09	3.32e-09	SEC22B	SEC22 homolog B, vesicle traffickin
-0.79	8.21e-19	ANKRD17	ankyrin repeat domain 17	0.08	4.18e-09	AP2A1	adaptor related protein complex 2 s
-0.83	1.01e-18	KDM3B	lysine demethylase 3B	0.11	6.18e-09	ZFPL1	zinc finger protein like 1
-0.94	1.06e-18	HMGCS1	3-hydroxy-3-methylglutaryl-CoA synt	0.13	6.72e-09	RTN4	reticulon 4
-0.62	1.09e-18	TUBGCP2	tubulin gamma complex associated pr	0.56	7.71e-09	RAB11FIP5	RAB11 family interacting protein 5
-0.86	1.27e-18	UBFD1	ubiquitin family domain containing	0.05	1.02e-08	P4HB	prolyl 4-hydroxylase subunit beta
-0.75	2.54e-18	SUGP1	SURP and G-patch domain containing	0.11	1.20e-08	NUCB1	nucleobindin 1
-0.86	2.60e-18	DBR1	debranching RNA lariats 1	1.01	1.29e-08	CAVIN1	caveolae associated protein 1
-0.99	2.61e-18	C11orf54	chromosome 11 open reading frame 54	0.67	1.38e-08	IFI16	interferon gamma inducible protein
-0.56	3.49e-18	TUBGCP3	tubulin gamma complex associated pr	0.65	1.40e-08	IKBIP	IKBKB interacting protein
-0.86	4.24e-18	GABPA	GA binding protein transcription fa	0.66	1.41e-08	DCBLD2	discoidin, CUB and LCCL domain cont
-0.83	4.26e-18	ELP3	elongator acetyltransferase complex	0.34	1.43e-08	RALB	RAS like proto-oncogene B
-0.48	5.12e-18	TPP2	tripeptidyl peptidase 2	0.78	1.56e-08	NT5E	5'-nucleotidase ecto
-0.81	5.12e-18	NELFCD	negative elongation factor complex	0.07	1.68e-08	MYL6	myosin light chain 6
-0.76	5.24e-18	RBBP6	RB binding protein 6, ubiquitin lig	0.1	1.86e-08	FAF2	Fas associated factor family member
-0.88	5.42e-18	UBXN7	UBX domain protein 7	0.07	2.16e-08	TOR1AIP1	torsin 1A interacting protein 1
-0.75	9.08e-18	DCAF7	DDB1 and CUL4 associated factor 7	0.06	2.99e-08	EMD	emerin
-0.08	9.55e-18	USP7	ubiquitin specific peptidase 7	0.11	3.94e-08	MYH9	myosin heavy chain 9
-0.76	1.01e-17	DCP1A	decapping mRNA 1A	0.59	4.00e-08	RRAS	RAS related
-0.74	1.01e-17	NCAPD3	non-SMC condensin II complex subuni	0.07	4.37e-08	MYDGF	myeloid derived growth factor
-0.83	1.58e-17	LIG1	DNA ligase 1	0.09	4.64e-08	EMC7	ER membrane protein complex subunit
-0.84	1.58e-17	POLA2	DNA polymerase alpha 2, accessory s	0.44	8.87e-08	LAMC1	laminin subunit gamma 1
-0.61	1.67e-17	CUL1	cullin 1	0.56	9.06e-08	ADGRE5	adhesion G protein-coupled receptor
-0.81	2.64e-17	HAT1	histone acetyltransferase 1	0.73	9.34e-08	CAVIN3	caveolae associated protein 3
-0.79	2.64e-17	TPRKB	TP53RK binding protein	0.11	9.46e-08	FLNA	filamin A
-0.75	2.70e-17	METTL13	methyltransferase 13, N2a methyltran	0.79	1.01e-07	CAV1	catenin, arm

# Top 250 correlation coefficients overrepresentation, CUL4A protein, DB1

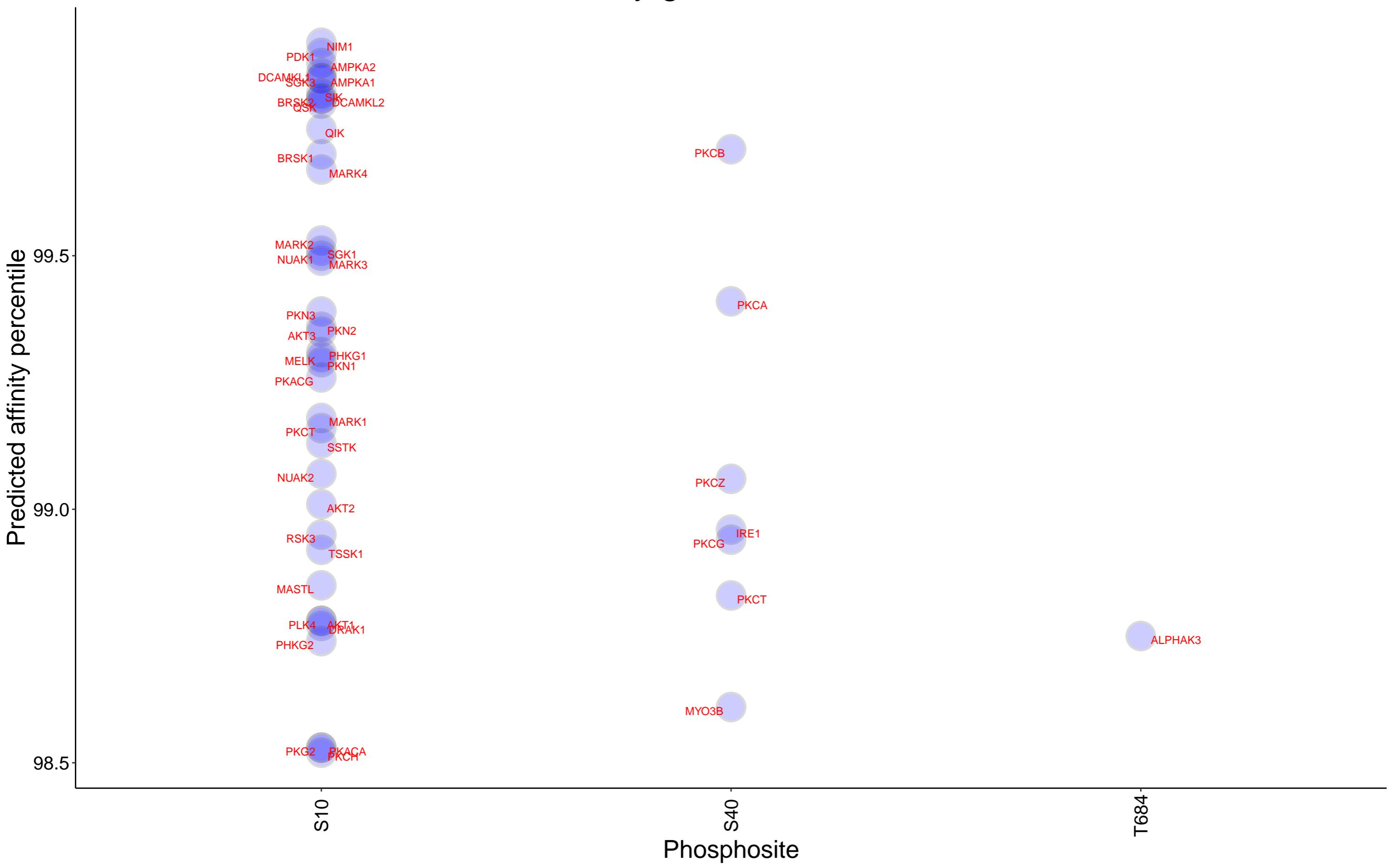


## Gene Set Enrichment analysis on protein correlation coefficients, CUL4A protein, DB1





# Kinases with affinity greater than 98.5% to CUL4A



# Top 15 positive correlation coefficients for CUL4A protein by tissue, DB1

Beware of false positives in tissues with small number of samples

