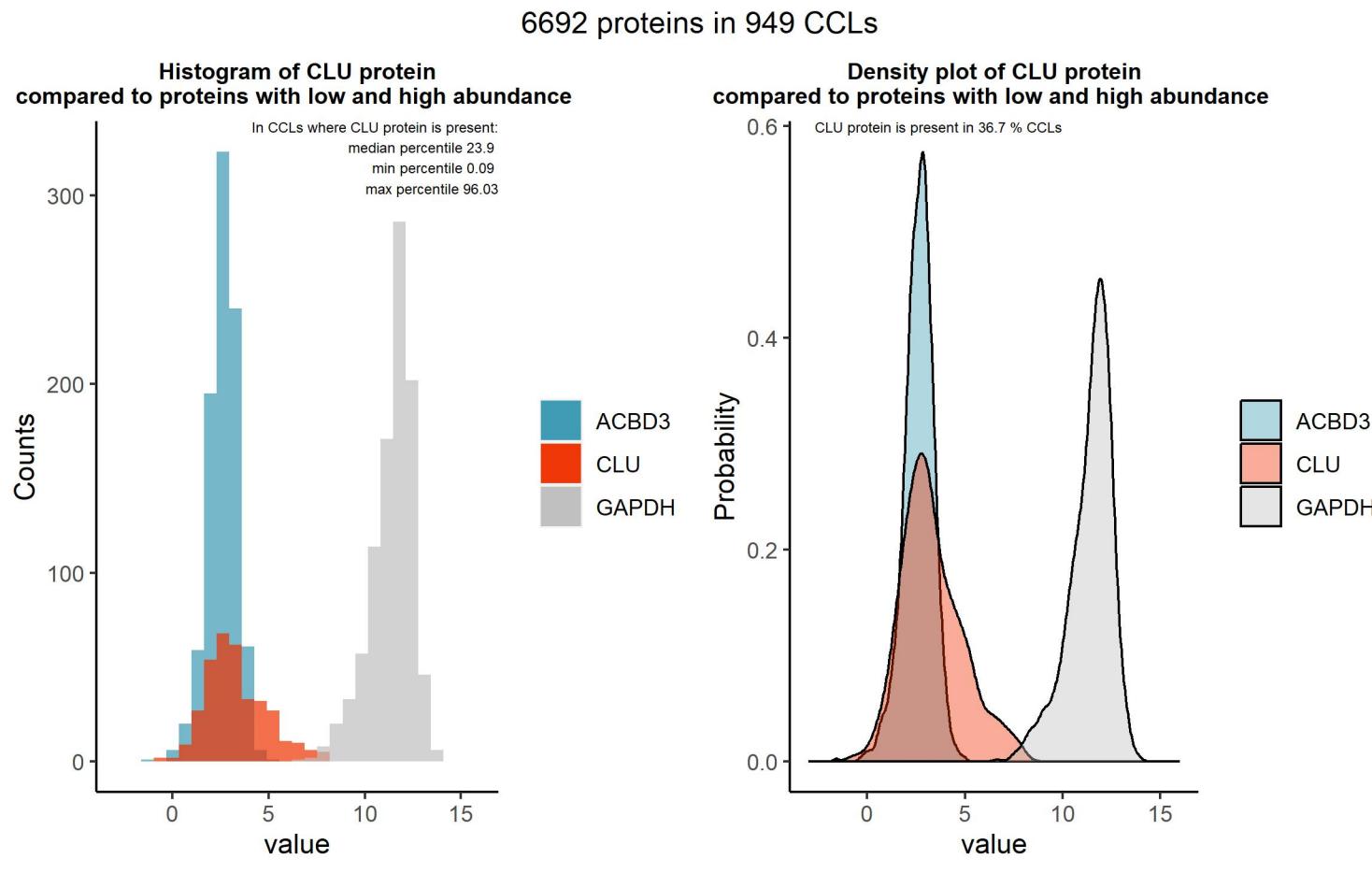


CLU

Protein name: CLUS ; UNIPROT: P10909 ; Gene name: clusterin

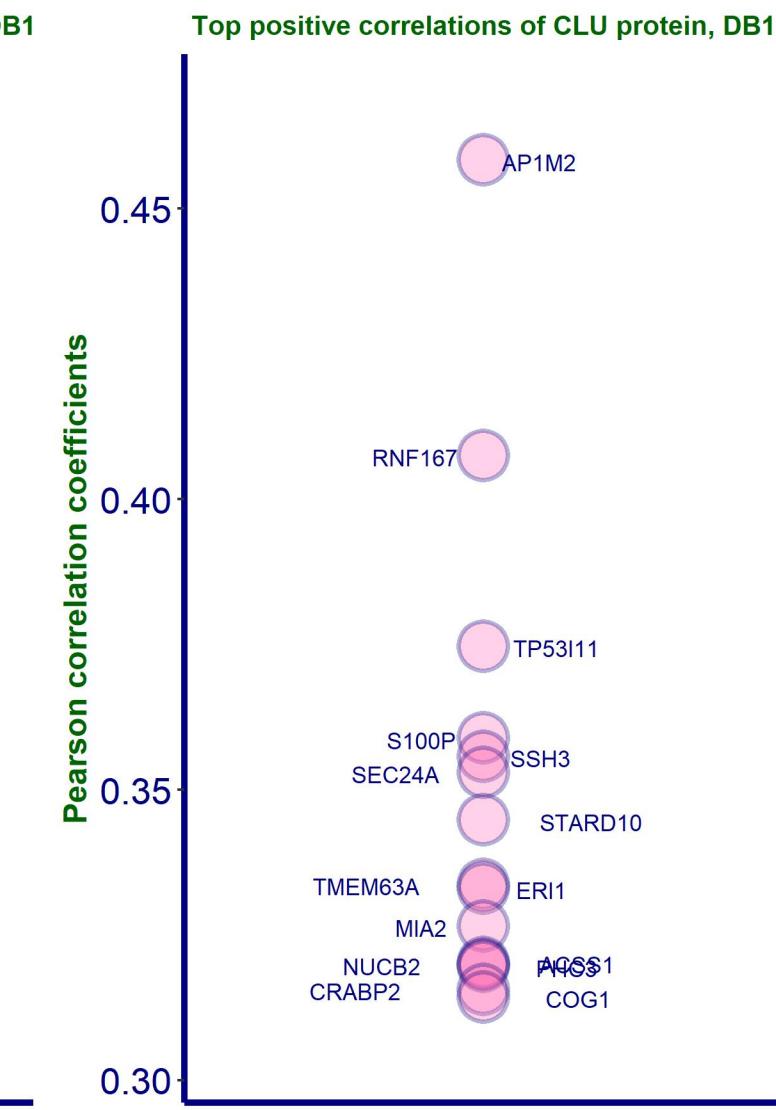
Ligandable: NA ; Ligandable_by_Chem: NA ; Is_enzyme: NA (<https://cansar.ai/>)

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



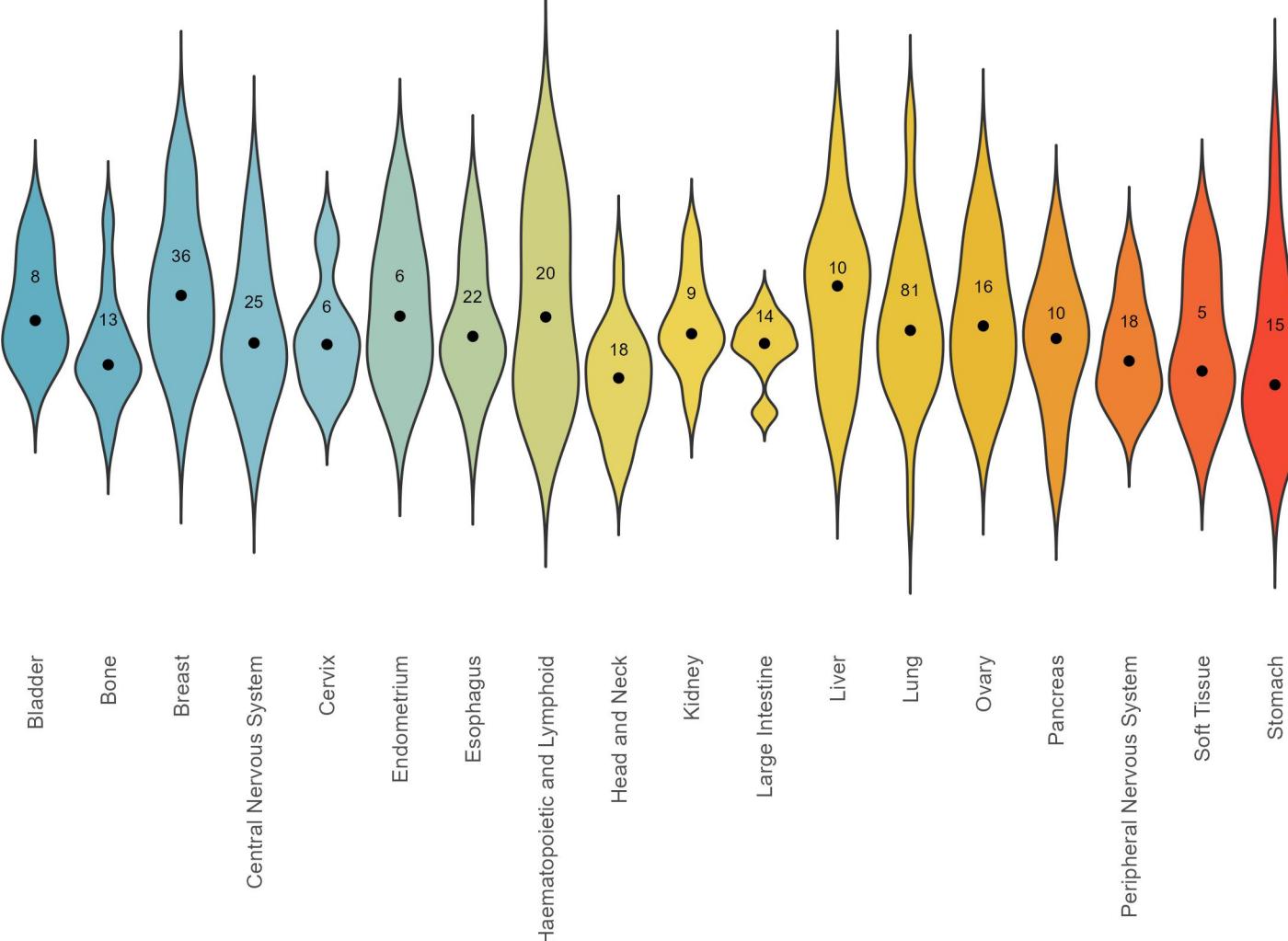
Top negative correlations of CLU protein, DB1

NOC4L
NOP58
ACTN1
ACTL6A
ILF3
UTP18
WDR74



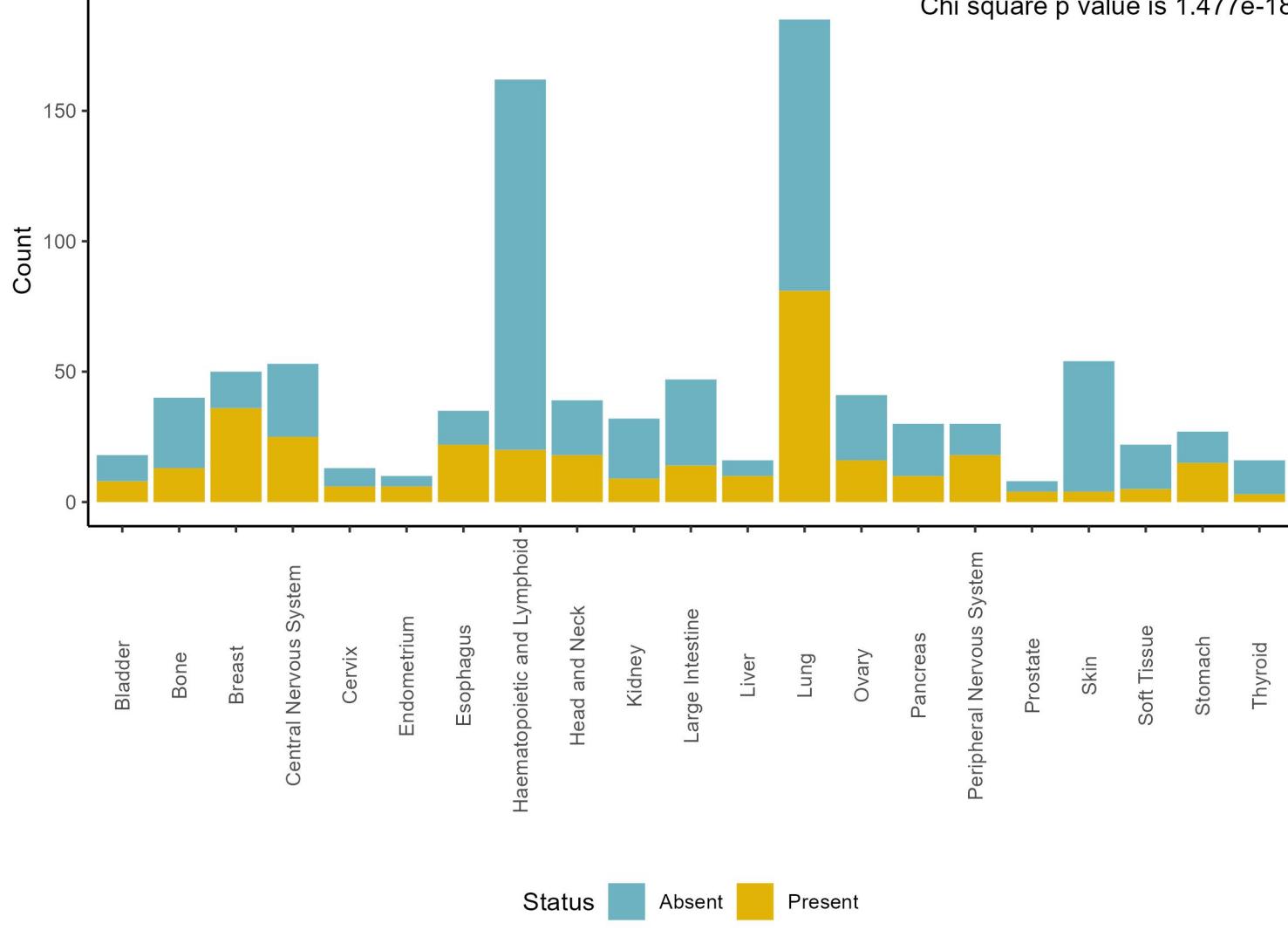
Amount of CLU protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 2.629e-02



Present and absent CLU protein counts by tissue, DB1

Chi square p value is 1.477e-18

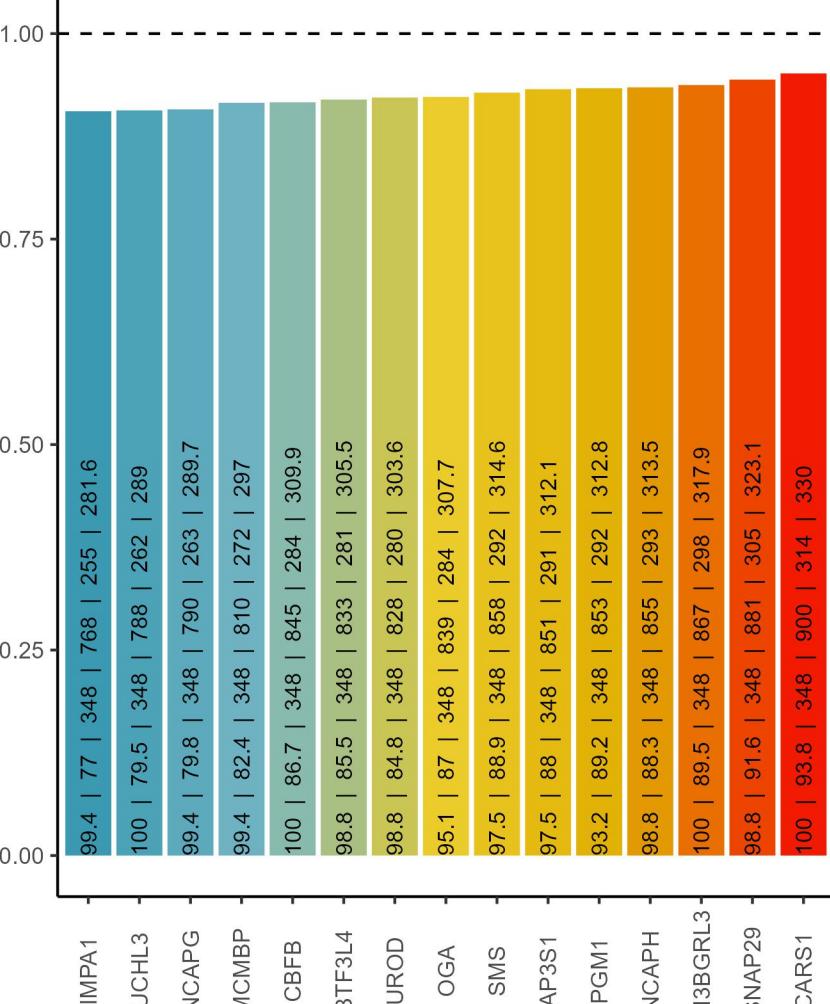


Cooccurrence with CLU protein, DB1

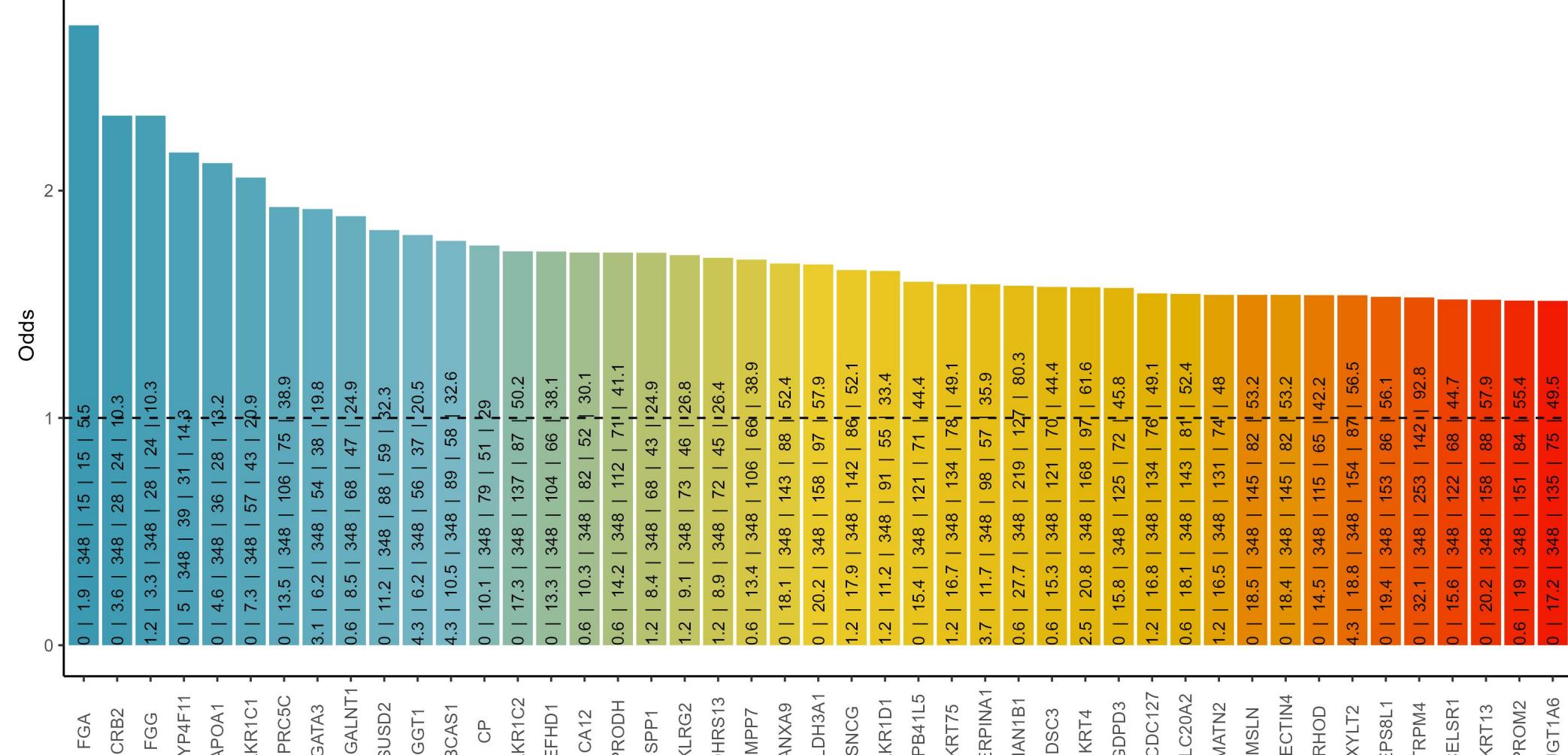
% of CLU in blood cancers: 12.3 ; % of CLU in solid cancers: 41.8

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

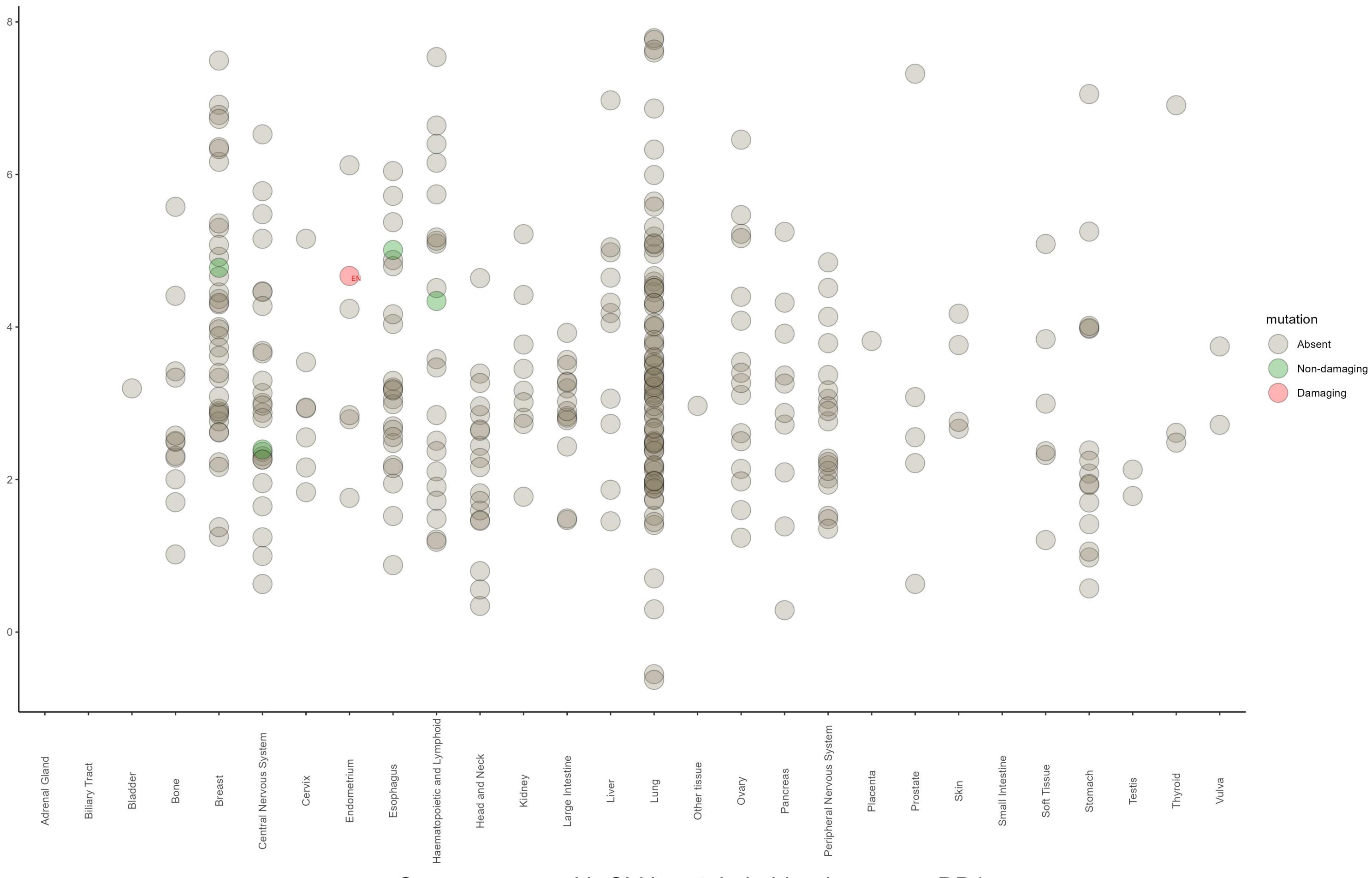
Negative cooccurrence



Positive cooccurrence

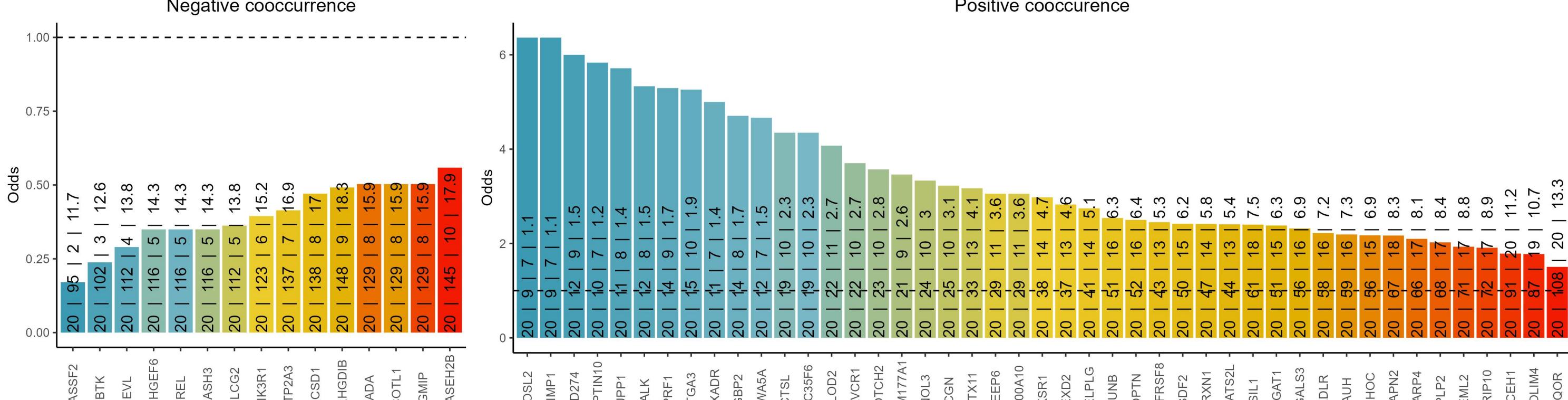


Amount of CLU protein and mutation status by tissue, DB1



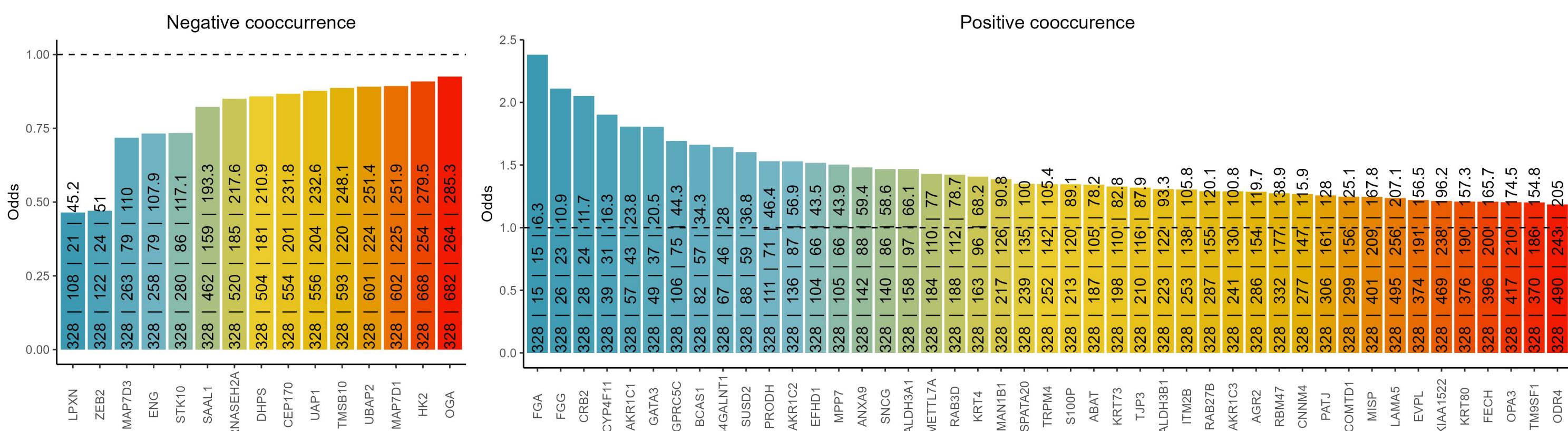
Cooccurrence with CLU protein in blood cancers, DB1

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

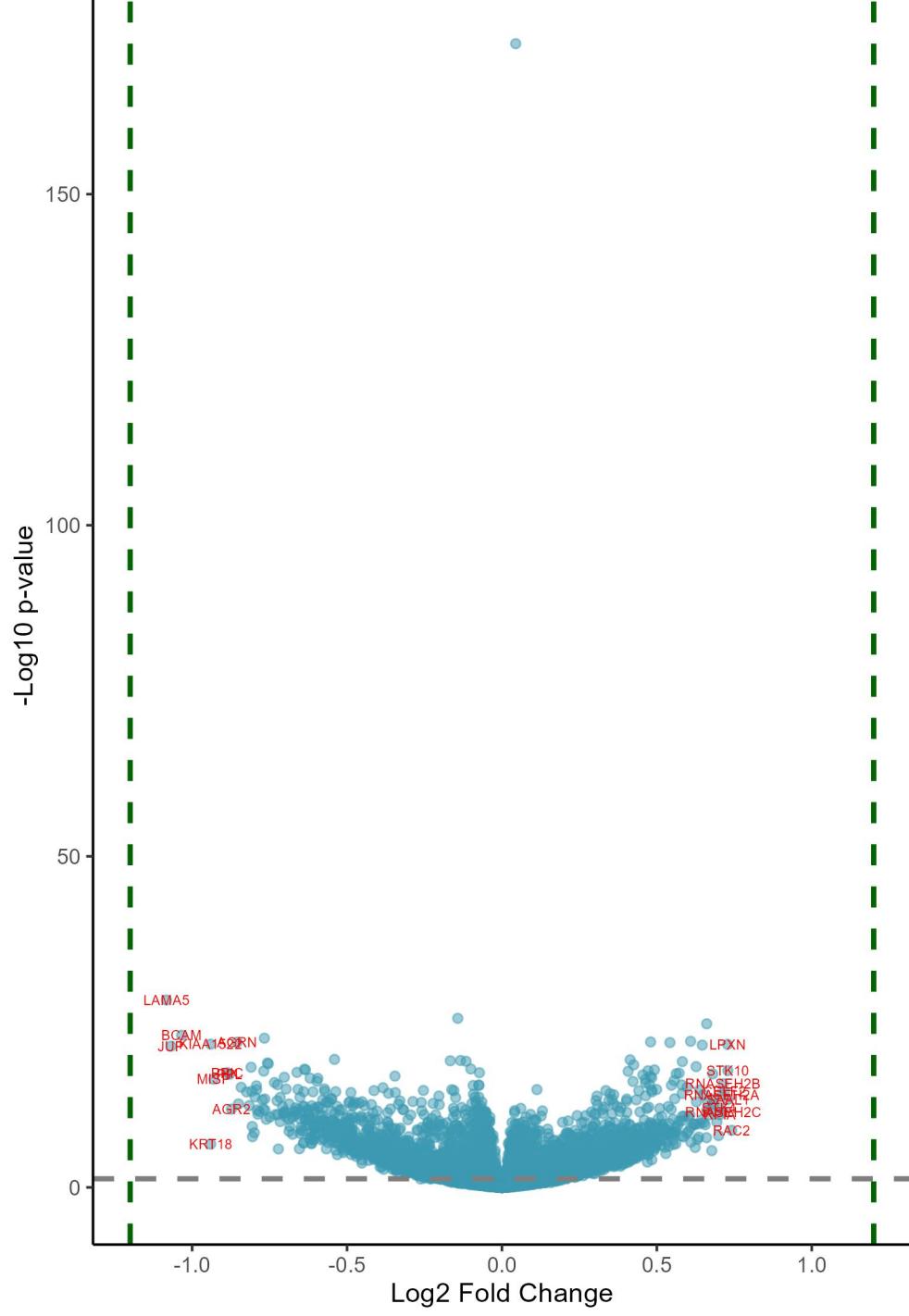


Cooccurrence with CLU protein in solid cancers, DB1

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

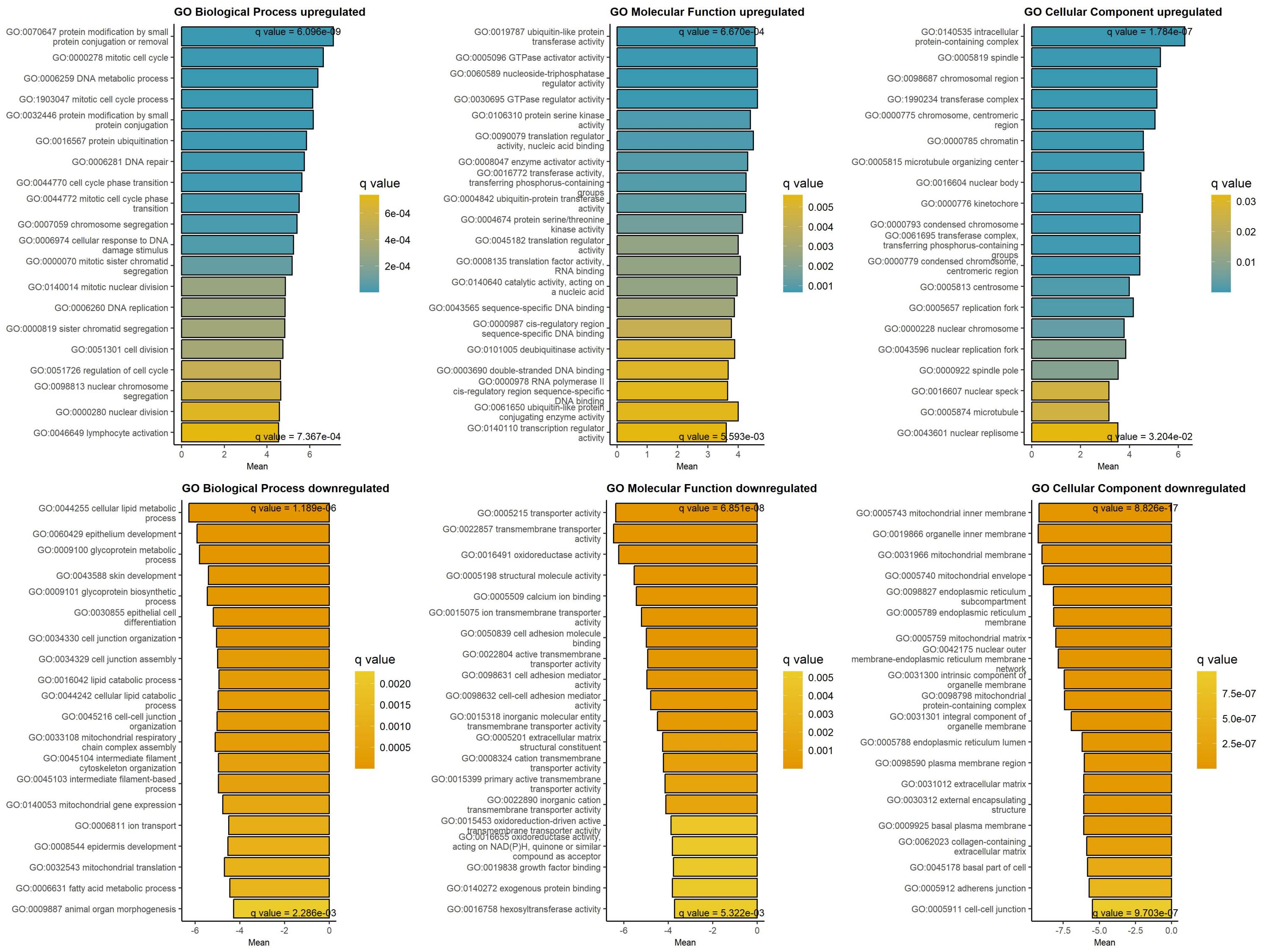


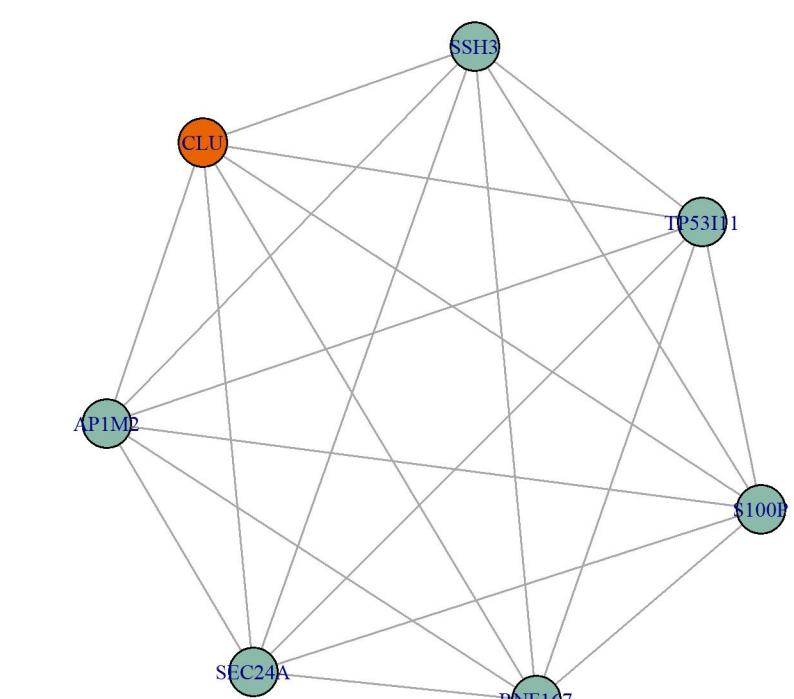
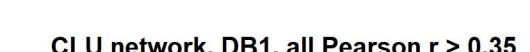
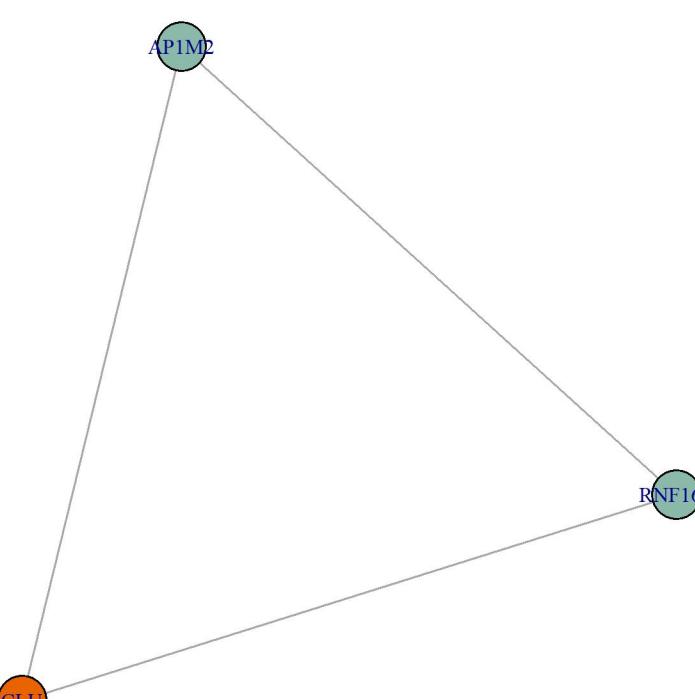
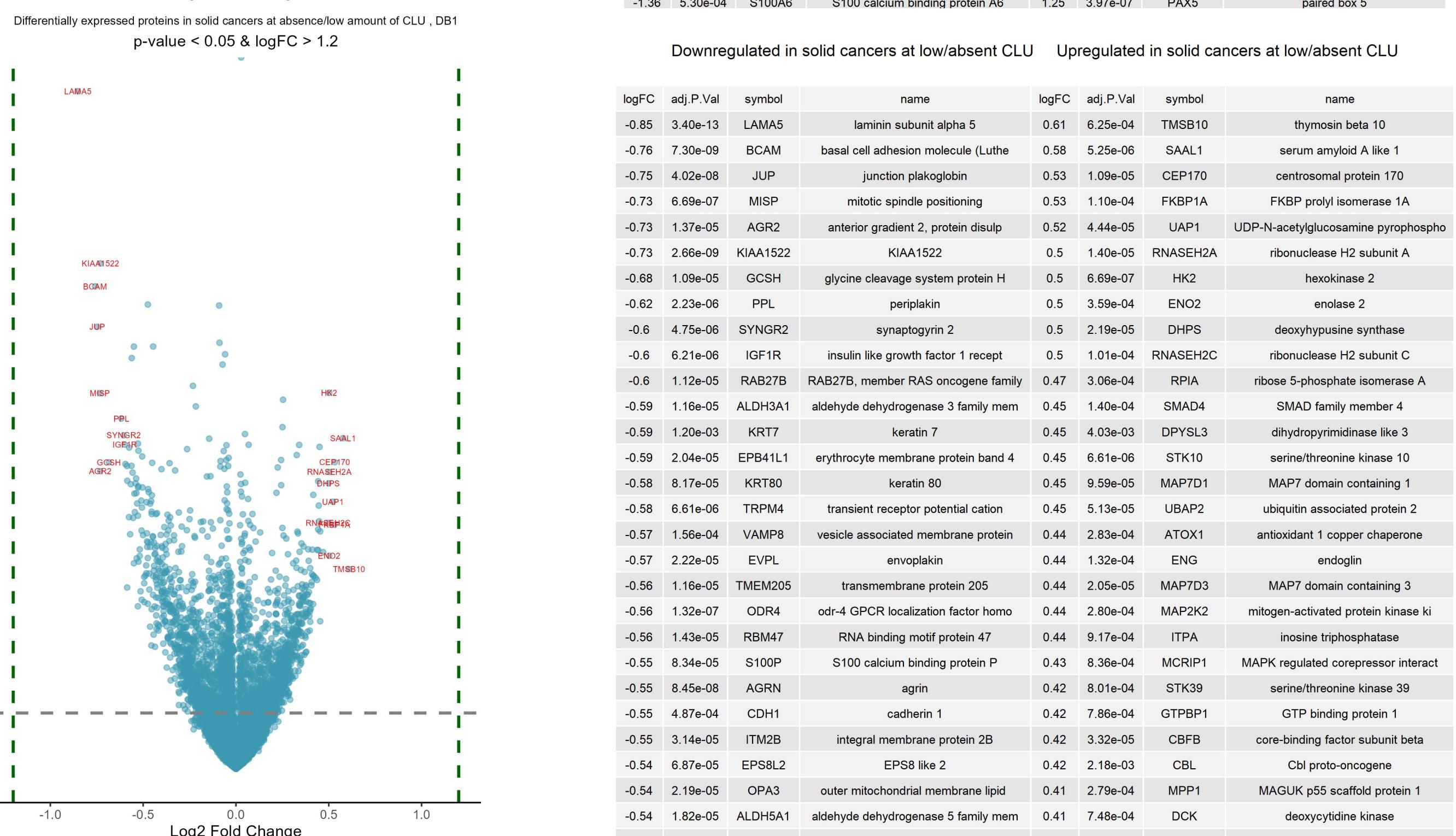
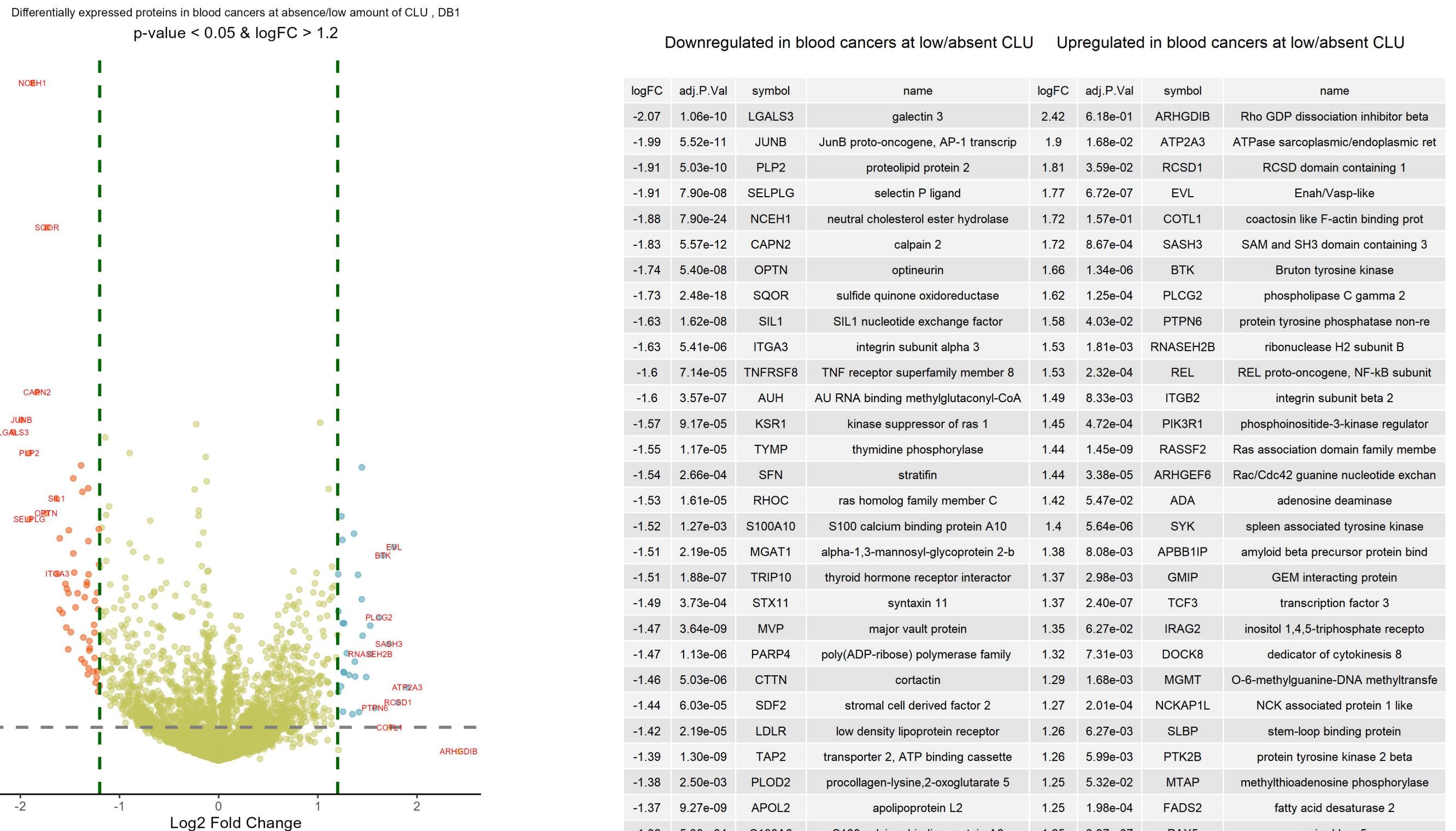
Downregulated at low/absent CLU Upregulated at low/absent CLU



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.08	1.12e-25	LAMA5	laminin subunit alpha 5	0.74	3.37e-08	RAC2	Rac family small GTPase 2
-1.07	2.06e-19	JUP	junction plakoglobin	0.73	3.12e-12	SAAL1	serum amyloid A like 1
-1.03	1.19e-20	BCAM	basal cell adhesion molecule (Luthe)	0.73	4.93e-16	STK10	serine/threonine kinase 10
-0.94	1.30e-19	KIAA1522	KIAA1522	0.73	1.30e-19	LPXN	leupaxin
-0.94	2.05e-06	KRT18	keratin 18	0.72	2.41e-13	CELF2	CUGBP Elav-like family member 2
-0.93	6.15e-15	MISP	mitotic spindle positioning	0.72	1.22e-10	RNASEH2C	ribonuclease H2 subunit C
-0.89	8.62e-16	PPIC	peptidylprolyl isomerase C	0.71	2.69e-14	RNASEH2B	ribonuclease H2 subunit B
-0.88	1.37e-15	PPL	periplakin	0.71	7.93e-13	RNASEH2A	ribonuclease H2 subunit A
-0.87	5.70e-11	AGR2	anterior gradient 2, protein disulf	0.7	2.89e-10	RPIA	ribose 5-phosphate isomerase A
-0.85	7.94e-20	AGRN	agrin	0.7	3.76e-11	STK4	serine/threonine kinase 4
-0.85	1.16e-11	ITGA3	integrin subunit alpha 3	0.7	1.62e-07	ARHGDIB	Rho GDP dissociation inhibitor beta
-0.84	7.77e-14	EPB41L1	erythrocyte membrane protein band 4	0.69	2.75e-09	FKBP1A	FKBP prolyl isomerase 1A
-0.82	2.89e-13	EPS8L2	EPS8 like 2	0.68	1.29e-11	SMAP2	small ArfGAP2
-0.82	1.98e-11	PKP3	plakophilin 3	0.68	2.94e-12	WIPF1	WAS/WASL interacting protein family
-0.81	1.82e-16	EPHX1	epoxide hydrolase 1	0.68	1.20e-15	GMFG	glia maturation factor gamma
-0.81	2.48e-13	DSG2	desmoglein 2	0.68	7.81e-11	ARMC6	armadillo repeat containing 6
-0.81	1.05e-08	KRT7	keratin 7	0.68	1.52e-05	TMSB10	thymosin beta 10
-0.81	2.20e-07	SFN	stratifin	0.67	3.06e-10	DCK	deoxyctidine kinase
-0.8	6.75e-08	KRT19	keratin 19	0.66	5.44e-12	DUS3L	dihydrouridine synthase 3 like
-0.8	1.41e-12	EGFR	epidermal growth factor receptor	0.66	8.27e-11	PDXP	pyridoxal phosphatase
-0.79	4.72e-14	TMEM205	transmembrane protein 205	0.66	2.60e-22	RCSD1	RCSD domain containing 1
-0.79	1.57e-13	IGF1R	insulin like growth factor 1 receptor	0.66	2.92e-07	ZNF706	zinc finger protein 706
-0.79	7.23e-11	S100A10	S100 calcium binding protein A10	0.66	6.20e-09	SEPTIN6	septin 6
-0.79	2.56e-10	CDH1	cadherin 1	0.65	3.26e-09	UBR7	ubiquitin protein ligase E3 compone
-0.78	1.16e-10	ITGB4	integrin subunit beta 4	0.65	6.84e-13	HCLS1	hematopoietic cell-specific Lyn sub
-0.77	3.36e-12	CD276	CD276 molecule	0.65	1.53e-19	INPP5D	inositol polyphosphate-5-phosphatas
-0.77	5.25e-11	KRT80	keratin 80	0.64	1.40e-09	SH3KBP1	SH3 domain containing kinase bindin
-0.77	5.58e-16	WFS1	wolframin ER transmembrane glycopro	0.64	4.47e-09	PPP6R1	protein phosphatase 6 regulatory su
-0.77	2.79e-20	ITGA5	integrin subunit alpha V	0.64	1.73e-13	FERMT3	FERM domain containing kindlin 3

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

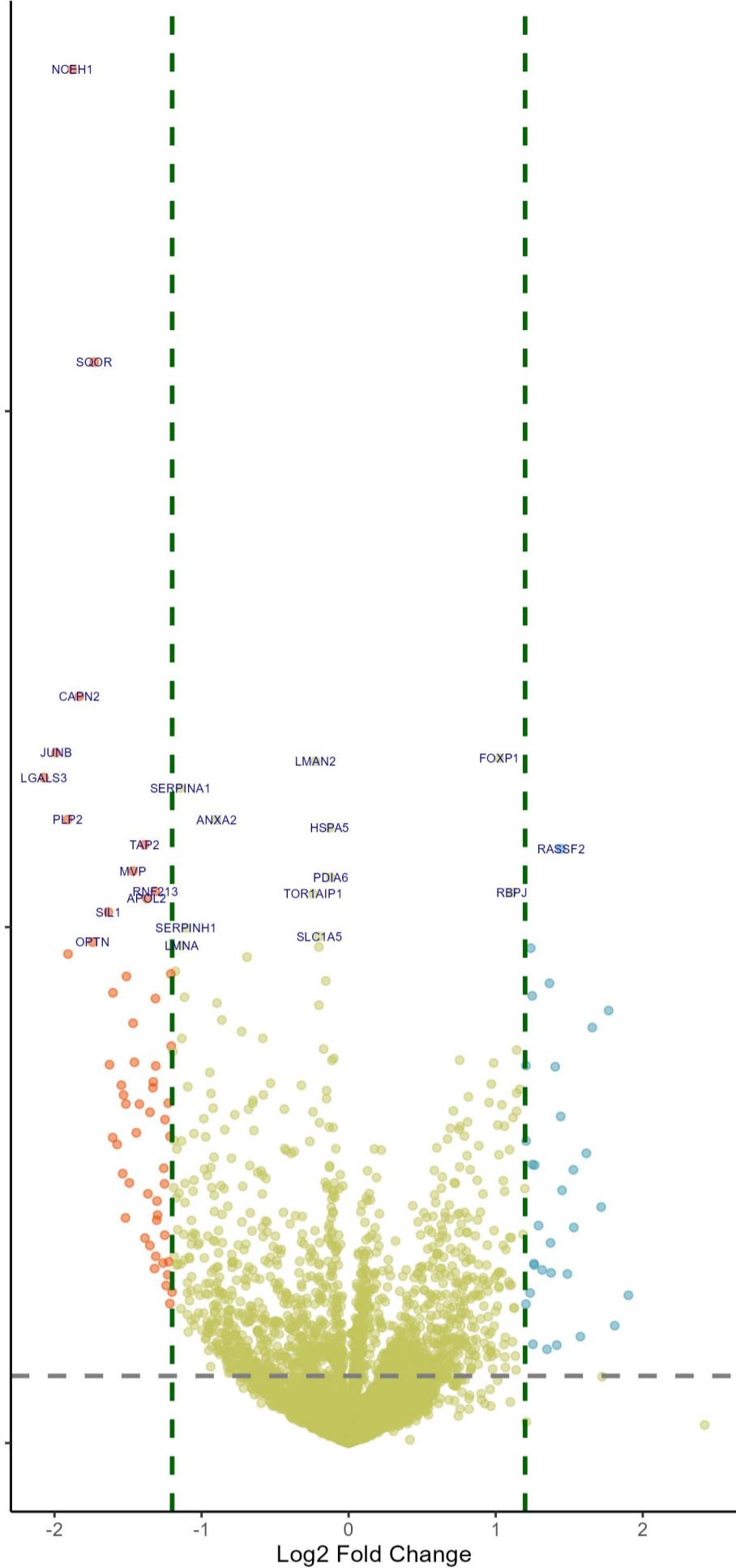




Sorted by p values!

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

-Log10 p-value

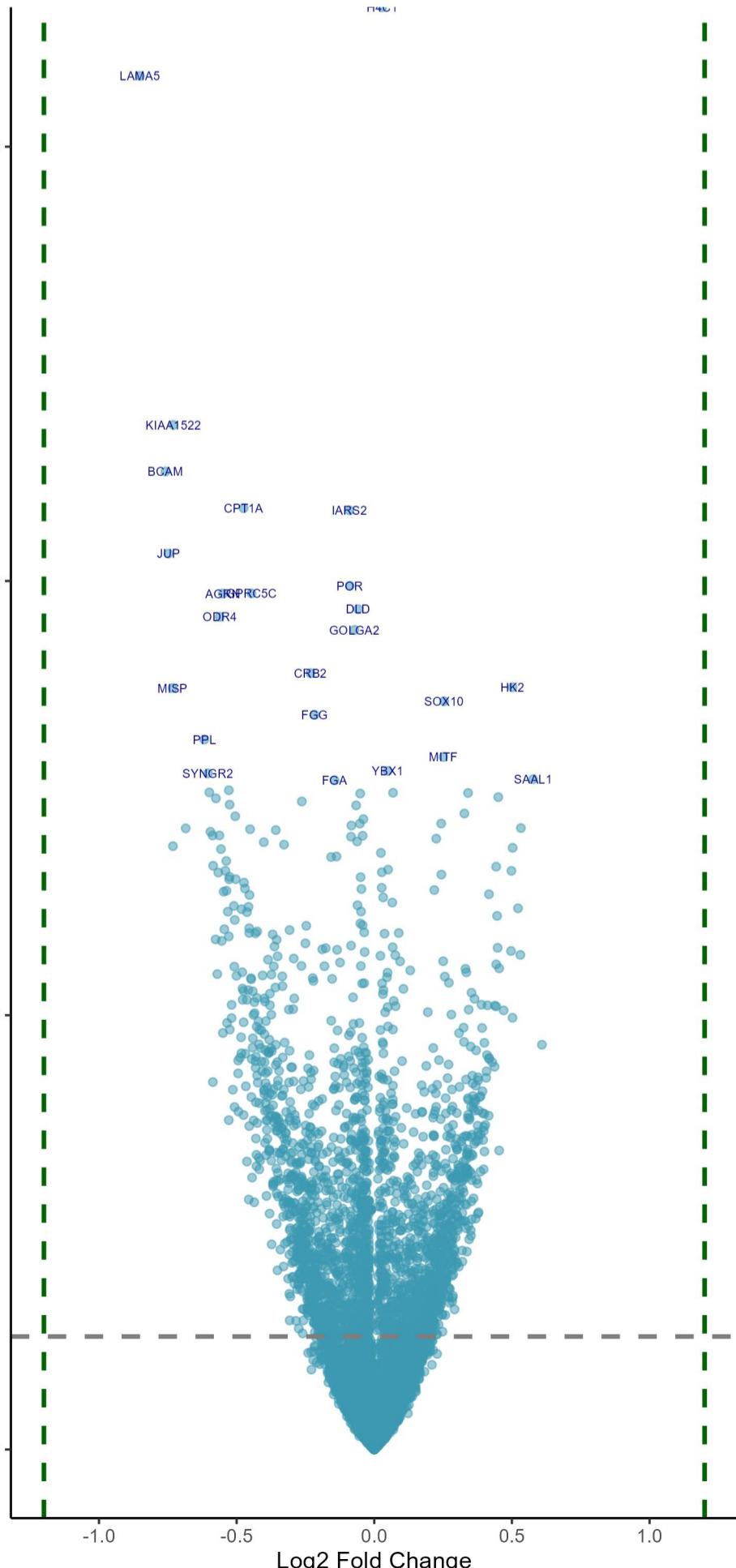


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.88	7.90e-24	NCEH1	neutral cholesterol ester hydrolase	1.02	5.80e-11	FOXP1	forkhead box P1
-1.73	2.48e-18	SQOR	sulfide quinone oxidoreductase	1.44	1.45e-09	RASSF2	Ras association domain family membe
-1.83	5.57e-12	CAPN2	calpain 2	1.11	7.85e-09	RBPJ	recombination signal binding protei
-1.99	5.52e-11	JUNB	JunB proto-oncogene, AP-1 transcript	1.24	6.30e-08	CYFIP2	cytoplasmic FMR1 interacting protei
-0.23	5.80e-11	LMAN2	lectin, mannose binding 2	1.37	2.40e-07	TCF3	transcription factor 3
-2.07	1.06e-10	LGALS3	galectin 3	1.25	3.97e-07	PAX5	paired box 5
-1.14	1.49e-10	SERPINA1	serpin family A member 1	1.77	6.72e-07	EVL	Enah/Vasp-like
-1.91	5.03e-10	PLP2	proteolipid protein 2	1.66	1.34e-06	BTK	Bruton tyrosine kinase
-0.9	5.03e-10	ANXA2	annexin A2	1.14	3.22e-06	CD19	CD19 molecule
-0.13	6.62e-10	HSPA5	heat shock protein family A (Hsp70)	0.75	4.72e-06	ZMYM2	zinc finger MYM-type containing 2
-1.39	1.30e-09	TAP2	transporter 2, ATP binding cassette	0.99	5.12e-06	FCRLA	Fc receptor like A
-1.47	3.64e-09	MVP	major vault protein	1.21	5.53e-06	SORL1	sortilin related receptor 1
-0.12	4.51e-09	PDI6	protein disulfide isomerase family	1.4	5.64e-06	SYK	spleen associated tyrosine kinase
-1.32	7.85e-09	RNF213	ring finger protein 213	0.97	1.14e-05	TTF2	transcription termination factor 2
-0.24	7.85e-09	TOR1AIP1	torsin 1A interacting protein 1	1.16	1.34e-05	KIF15	kinesin family member 15
-1.37	9.27e-09	APOL2	apolipoprotein L2	1.14	1.55e-05	CD22	CD22 molecule
-1.63	1.62e-08	SIL1	SIL1 nucleotide exchange factor	0.81	1.73e-05	NFATC1	nuclear factor of activated T cells
-1.11	3.14e-08	SERPINH1	serpin family H member 1	0.95	2.15e-05	LEF1	lymphoid enhancer binding factor 1
-0.2	4.39e-08	SLC1A5	solute carrier family 1 member 5	1.04	2.23e-05	ZWILCH	zwilch kinetochore protein
-1.74	5.40e-08	OPTN	optineurin	0.71	2.79e-05	RIPOR2	RHO family interacting cell polariz
-1.13	6.05e-08	LMNA	lamin A/C	1.14	2.79e-05	ARPC1A	actin related protein 2/3 complex s
-0.2	6.19e-08	SSR4	signal sequence receptor subunit 4	1.44	3.38e-05	ARHGEF6	Rac/Cdc42 guanine nucleotide exchan
-1.91	7.90e-08	SELPLG	selectin P ligand	1.12	3.52e-05	MME	membrane metalloendopeptidase
-0.69	8.71e-08	FLOT1	flotillin 1	0.81	4.15e-05	PLD4	phospholipase D family member 4
-1.18	1.59e-07	SCARB2	scavenger receptor class B member 2	1.01	4.68e-05	ALDH2	aldehyde dehydrogenase 2 family mem
-1.21	1.73e-07	ERGIC3	ERGIC and golgi 3	1.06	4.85e-05	CD79B	CD79b molecule
-1.51	1.88e-07	TRIP10	thyroid hormone receptor interactor	0.76	4.88e-05	CPNE2	copine 2
-0.16	2.23e-07	STOML2	stomatin like 2	0.69	5.14e-05	ACTR1B	actin related protein 1B
-1.6	3.57e-07	AUH	AU RNA binding methylglutaconyl-CoA	0.75	5.36e-05	PXK	PX domain containing serine/threoni
-1.12	4.11e-07	NFKB2	nuclear factor kappa B subunit 2	0.79	6.82e-05	TIFA	TRAF interacting protein with forkh
-1.31	4.24e-07	GOLIM4	golgi integral membrane protein 4	0.67	7.53e-05	NT5C2	5'-nucleotidase, cytosolic II
-0.9	5.06e-07	ALB	albumin	1.21	8.00e-05	TCL1A	TCL1 family AKT coactivator A
-0.2	5.43e-07	IARS2	isoleucyl-tRNA synthetase 2, mitoch	0.88	9.69e-05	SPI1	Spi-1 proto-oncogene
-0.86	9.97e-07	EHD4	EH domain containing 4	0.6	1.05e-04	RTN4IP1	reticulon 4 interacting protein 1
-1.47	1.13e-06	PARP4	poly(ADP-ribose) polymerase family	0.18	1.07e-04	RCC2	regulator of chromosome condensatio
-0.73	1.56e-06	SERPINB4	serpin family B member 4	1.09	1.10e-04	MS4A1	membrane spanning 4-domains A1
-1.13	2.03e-06	PLD3	phospholipase D family member 3	0.22	1.11e-04	GGCT	gamma-glutamylcyclotransferase
-0.58	2.03e-06	SERPINB3	serpin family B member 3	1.62	1.25e-04	PLCG2	phospholipase C gamma 2
1.21	2.81e-06	ACPD2	acid phosphatase 2, lysosomal	1.02	1.32e-04	CASPD2	caspase 2

Sorted by p values!

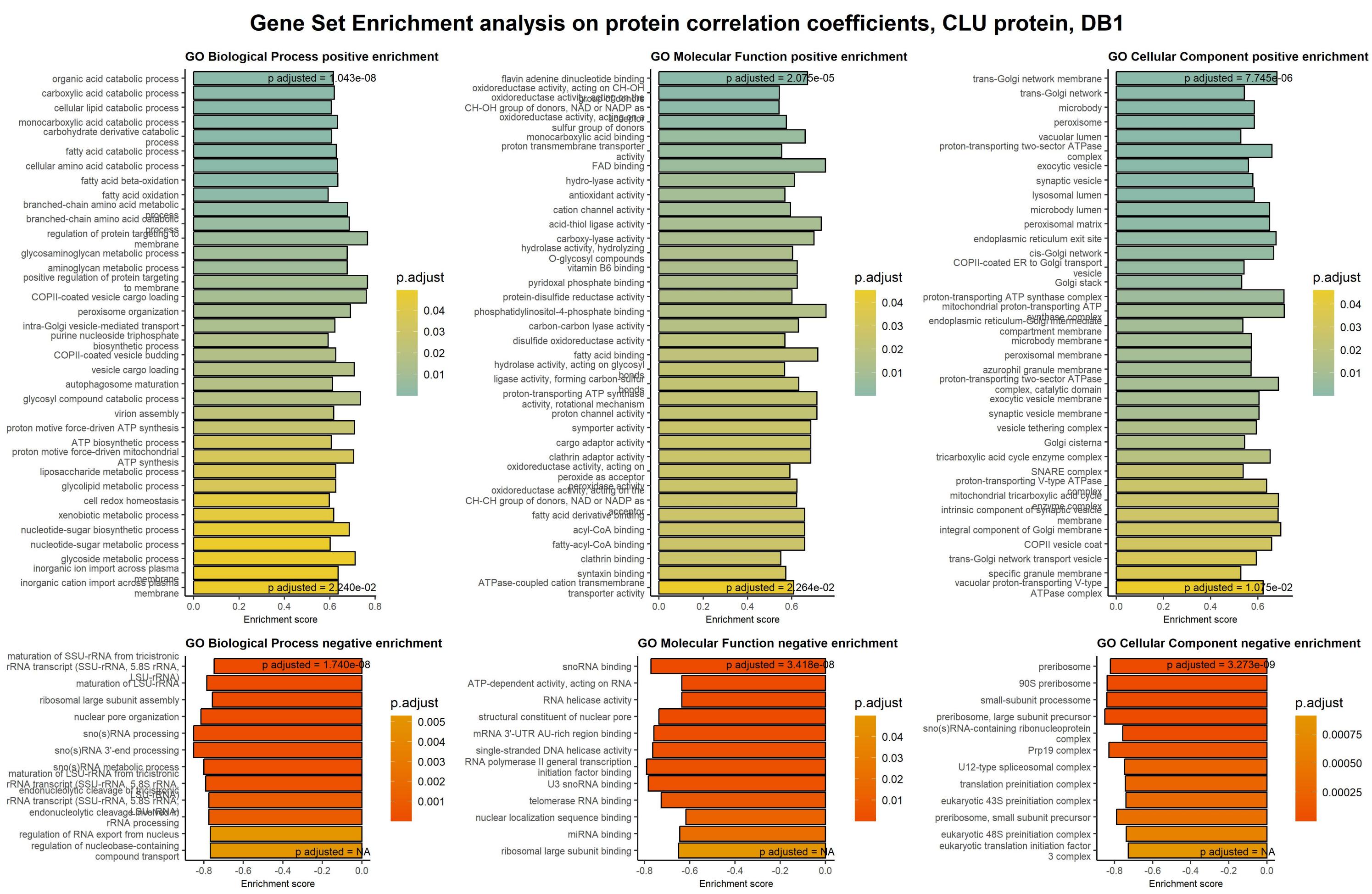
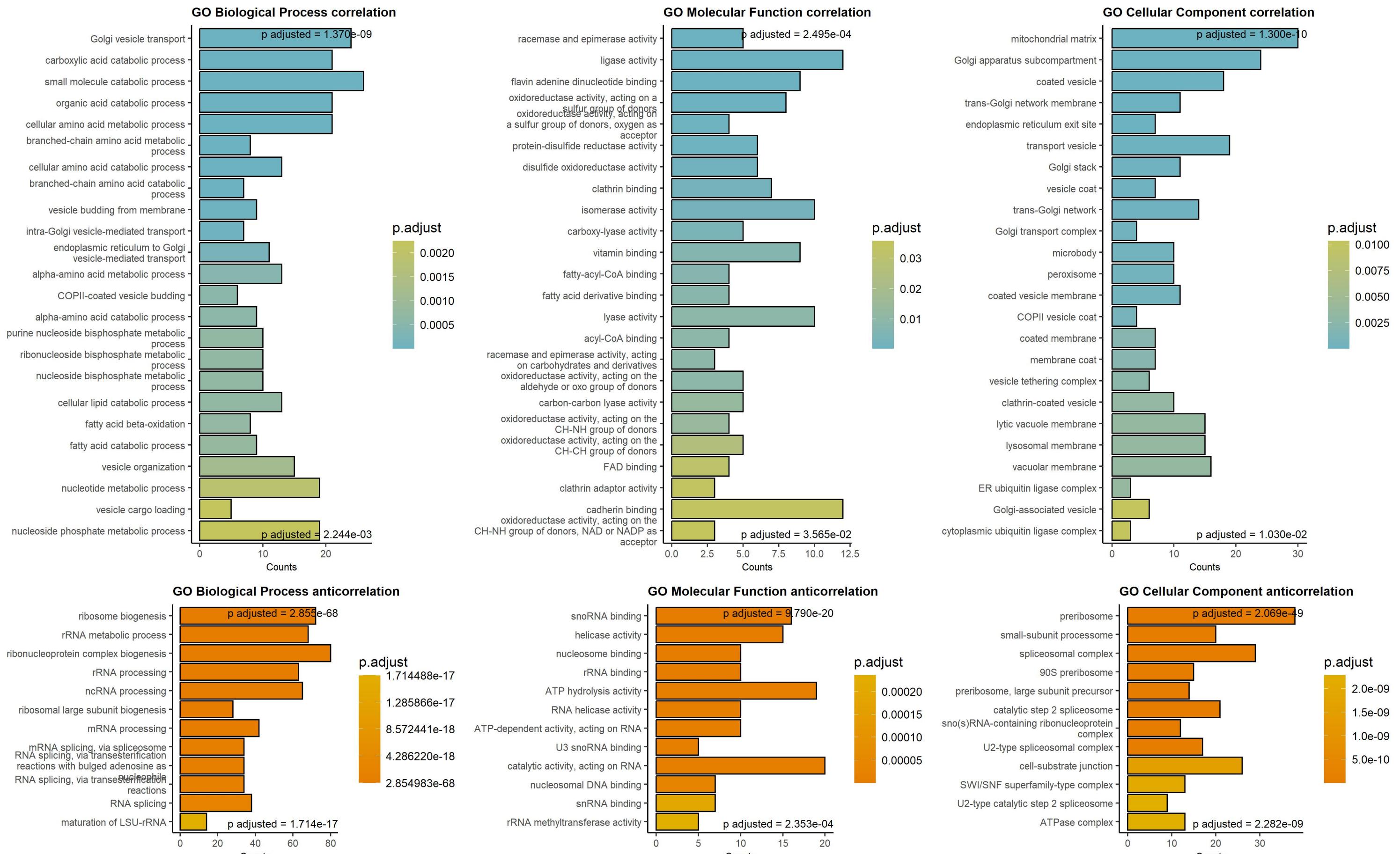
Downregulated in solid cancers at low/absent CLU Upregulated in solid cancers at low/absent CLU

-Log10 p-value

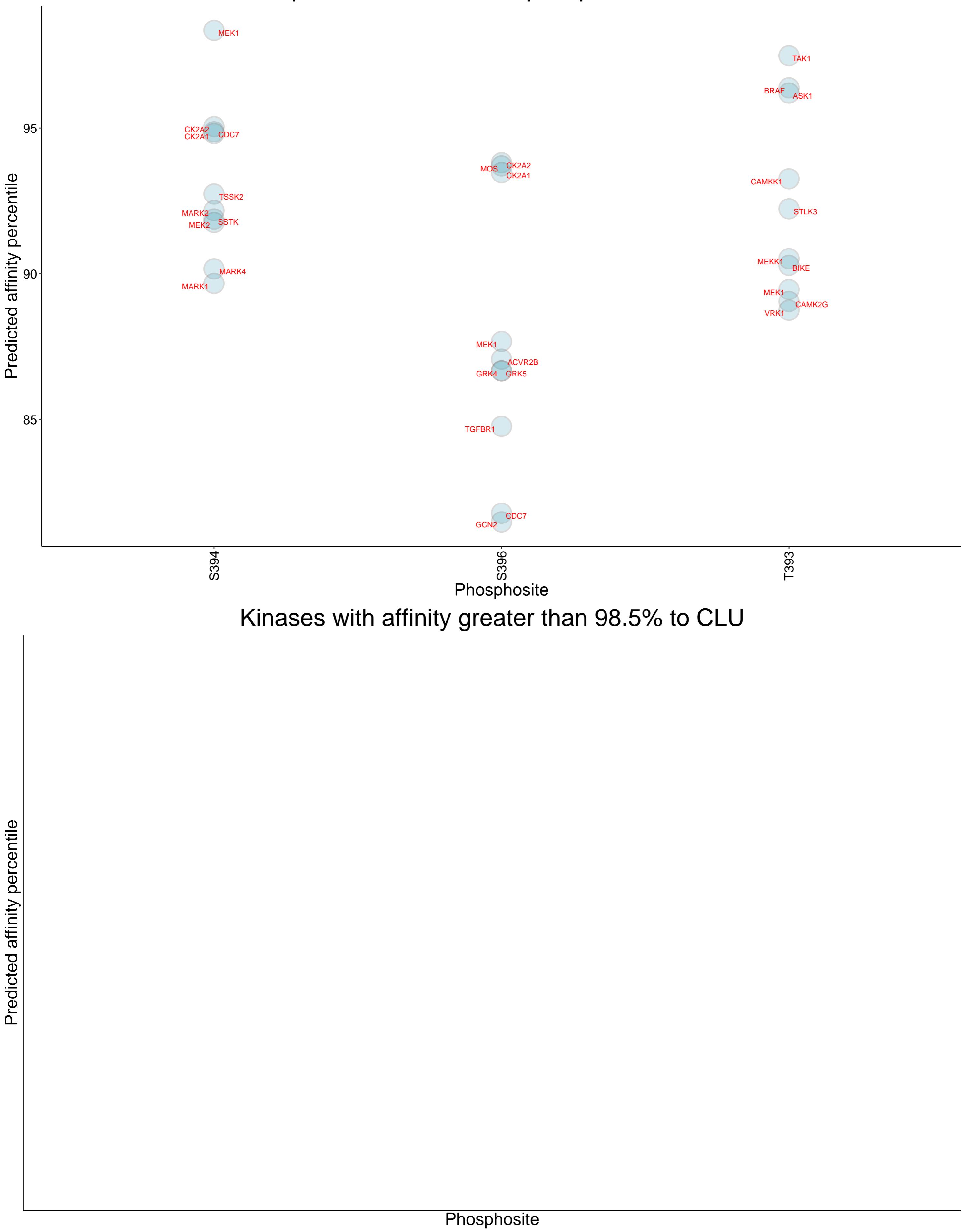


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.85	3.40e-13	LAMA5	laminin subunit alpha 5	0.03	0.00e+00	H4C1	H4 clustered histone 1
-0.73	2.66e-09	KIAA1522	KIAA1522	0.5	6.69e-07	HK2	hexokinase 2
-0.76	7.30e-09	BCAM	basal cell adhesion molecule (Luthe	0.25	8.98e-07	SOX10	SRY-box transcription factor 10
-0.47	1.46e-08	CPT1A	carnitine palmitoyltransferase 1A	0.25	3.36e-06	MITF	melanocyte inducing transcription f
-0.09	1.46e-08	IARS2	isoleucyl-tRNA synthetase 2, mitoch	0.05	4.65e-06	YBX1	Y-box binding protein 1
-0.75	4.02e-08	JUP	junction plakoglobin	0.58	5.25e-06	SAAL1	serum amyloid A like 1
-0.09	8.40e-08	POR	cytochrome p450 oxidoreductase	0.07	6.21e-06	PCNA	proliferating cell nuclear antigen
-0.45	8.45e-08	GPRC5C	G protein-coupled receptor class C	0.34	6.21e-06	LPXN	leupaxin
-0.55	8.45e-08	AGRN	agrin	0.45	6.61e-06	STK10	serine/threonine kinase 10
-0.06	1.17e-07	DLD	dihydrolipoamide dehydrogenase	0.33	8.79e-06	ZEB2	zinc finger E-box binding homeobox
-0.56	1.32e-07	ODR4	odr-4 GPCR localization factor homo	0.24	1.03e-05	PMEL	premelanosome protein
-0.07	1.74e-07	GOLGA2	golgin A2	0.53	1.09e-05	CEP170	centrosomal protein 170
-0.23	5.11e-07	CRB2	crumbs cell polarity complex compon	0.23	1.21e-05	DCT	dopachrome tautomerase
-0.73	6.69e-07	MISP	mitotic spindle positioning	0.5	1.40e-05	RNASEH2A	ribonuclease H2 subunit A
-0.22	1.22e-06	FGG	fibrinogen gamma chain	0.02	1.55e-05	RPS25	ribosomal protein S25
-0.62	2.23e-06	PPL	periplakin	0.44	2.05e-05	MAP7D3	MAP7 domain containing 3
-0.6	4.75e-06	SYNGR2	synaptogyrin 2	0.05	2.19e-05	EIF2S2	eukaryotic translation initiation f
-0.14	5.25e-06	FGA	fibrinogen alpha chain	0.5	2.19e-05	DHPS	deoxyhypusine synthase
-0.53	6.21e-06	AKR1C2	aldo-keto reductase family 1 member	0.03	2.22e-05	RPS3A	ribosomal protein S3A
-0.6	6.21e-06	IGF1R	insulin like growth factor 1 recept	0.24	2.31e-05	S100B	S100 calcium binding protein B
-0.05	6.21e-06	ATP5F1C	ATP synthase F1 subunit gamma	0.03	3.02e-05	RPS14	ribosomal protein S14
-0.58	6.61e-06	TRPM4	transient receptor potential cation	0.22	3.08e-05	MLANA	melan-A
-0.26	6.96e-06	APOA1	apolipoprotein A1	0.42	3.32e-05	CBFB	core-binding factor subunit beta
-0.53	7.29e-06	FECH	ferrochelatase	0.03	3.53e-05	RPS17	ribosomal protein S17
-0.07	7.29e-06	KTN1	kinectin 1	0.07	3.99e-05	EIF3F	eukaryotic translation initiation f
-0.51	9.20e-06	METTL7A	methyltransferase like 7A	0.52	4.44e-05	UAP1	UDP-N-acetylglucosamine pyrophospho
-0.04	9.66e-06	PRDX3	peroxiredoxin 3	0.45	5.13e-05	UBAP2	ubiquitin associated protein 2
-0.05	1.03e-05	VAPA	VAMP associated protein A	0.09	7.22e-05	GART	phosphoribosylglycinamide formyltra
-0.08	1.06e-05	ACADVL	acyl-CoA dehydrogenase very long ch	0.04	7.22e-05	RPSA	ribosomal protein SA
-0.68	1.09e-05	GCSH	glycine cleavage system protein H	0.07	9.53e-05	PGK1	phosphoglycerate kinase 1

Top 250 correlation coefficients overrepresentation, CLU protein, DB1



Top 10 kinases for each phosphosite in CLU



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

Beware of false positives in tissues with small number of samples

