

CETN2

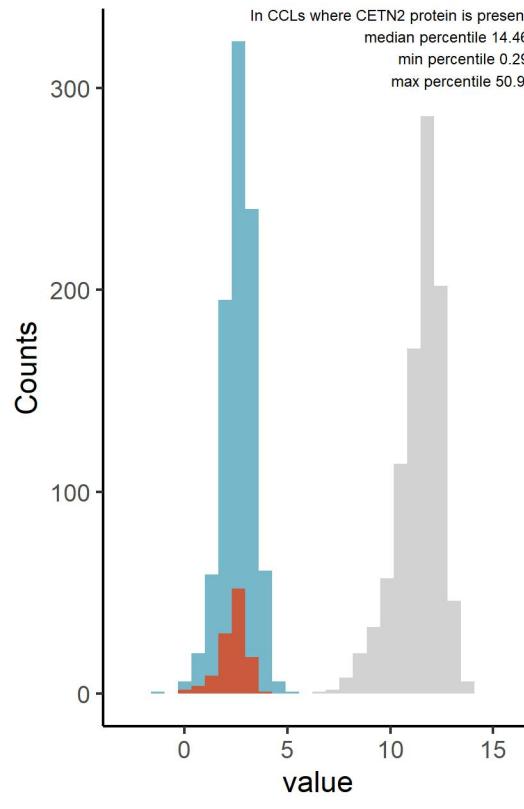
Protein name: CETN2 ; UNIPROT: P41208 ; Gene name: centrin 2

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

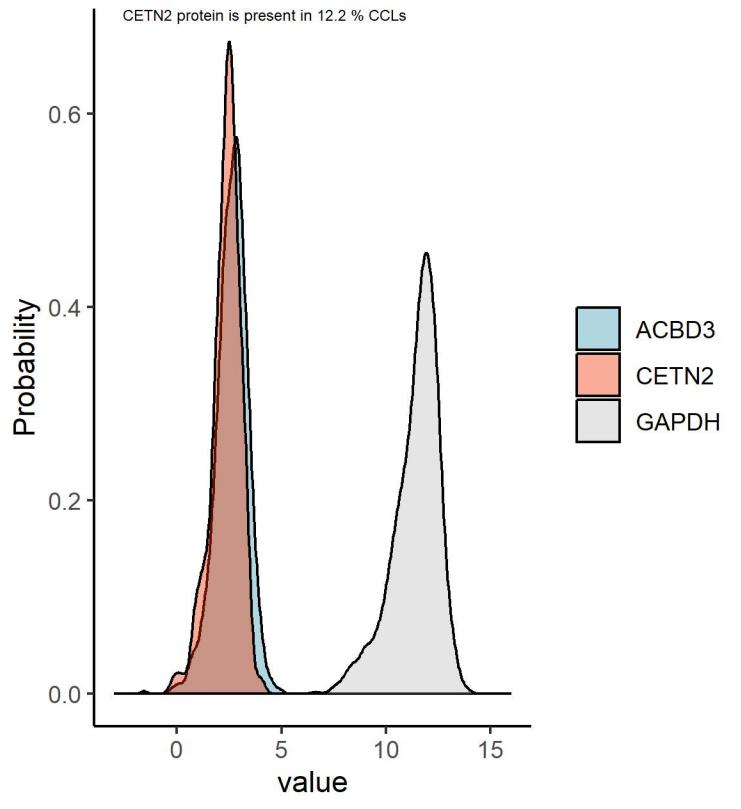
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

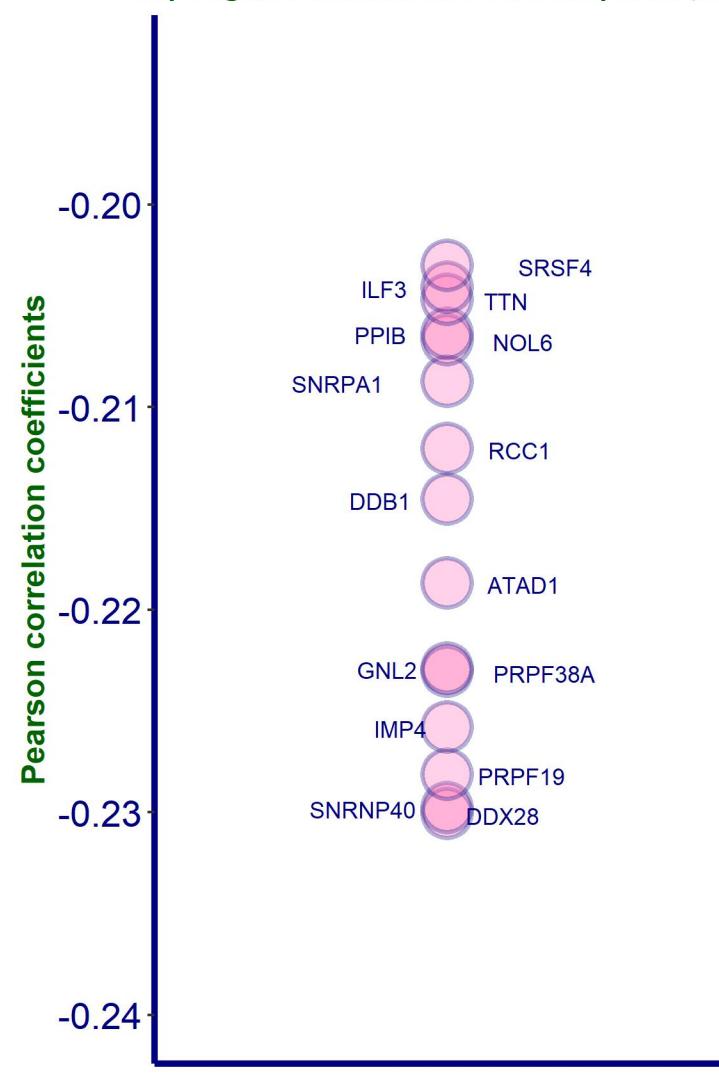
Histogram of CETN2 protein compared to proteins with low and high abundance



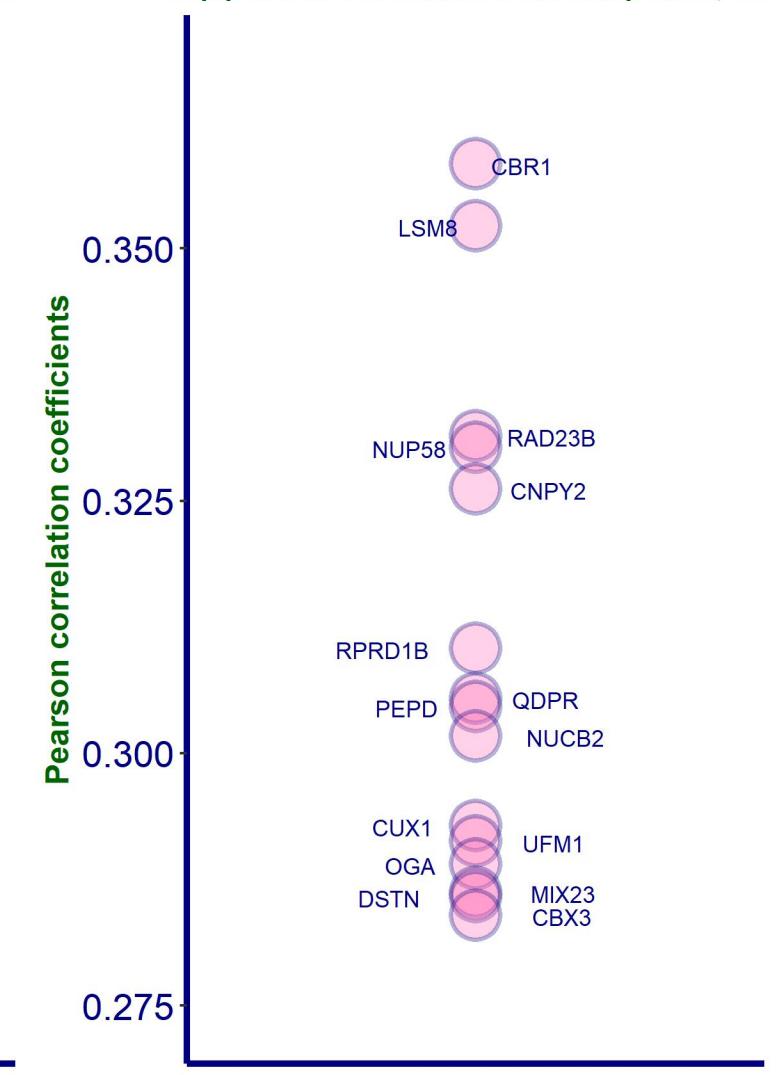
Density plot of CETN2 protein compared to proteins with low and high abundance



Top negative correlations of CETN2 protein, DB1

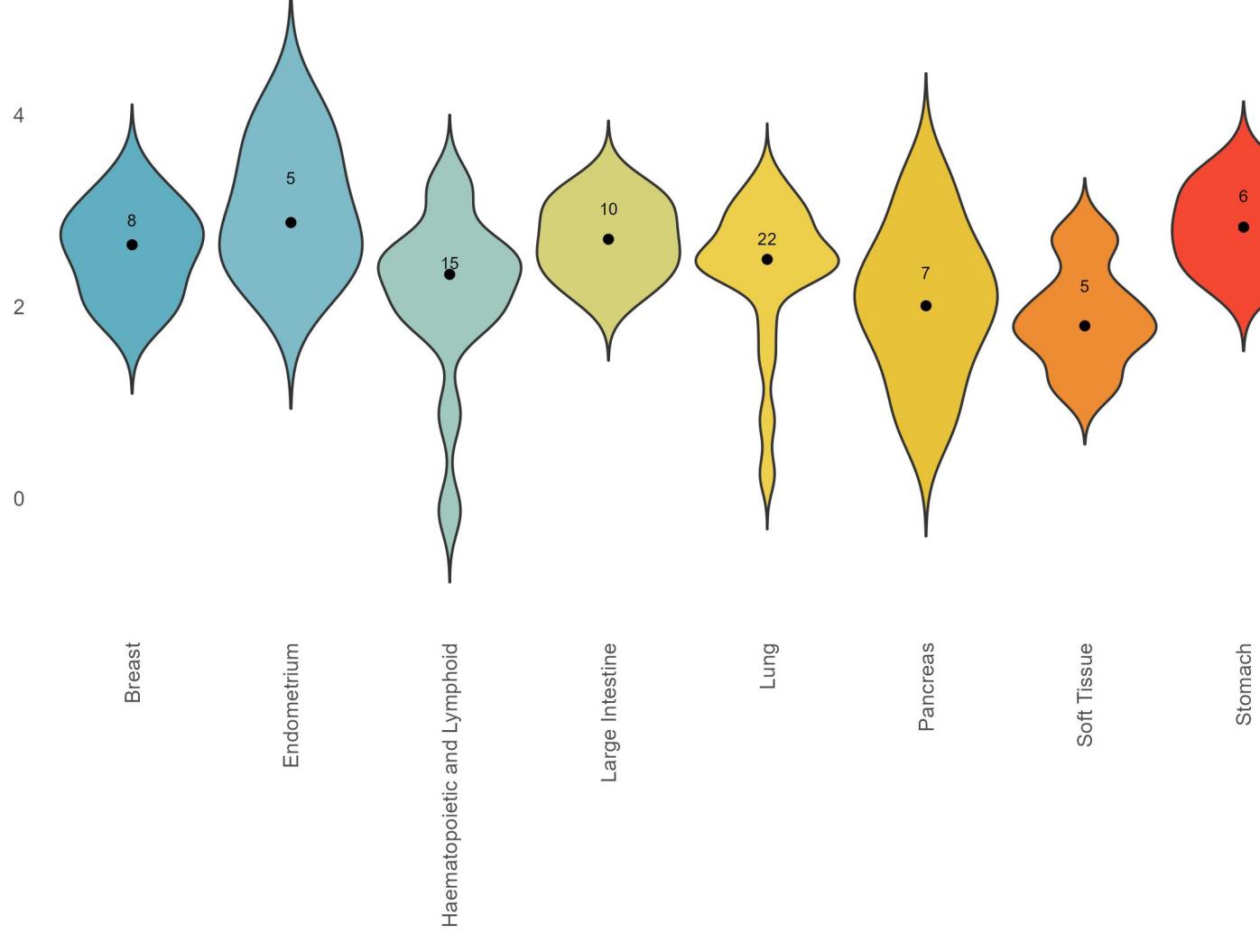


Top positive correlations of CETN2 protein, DB1



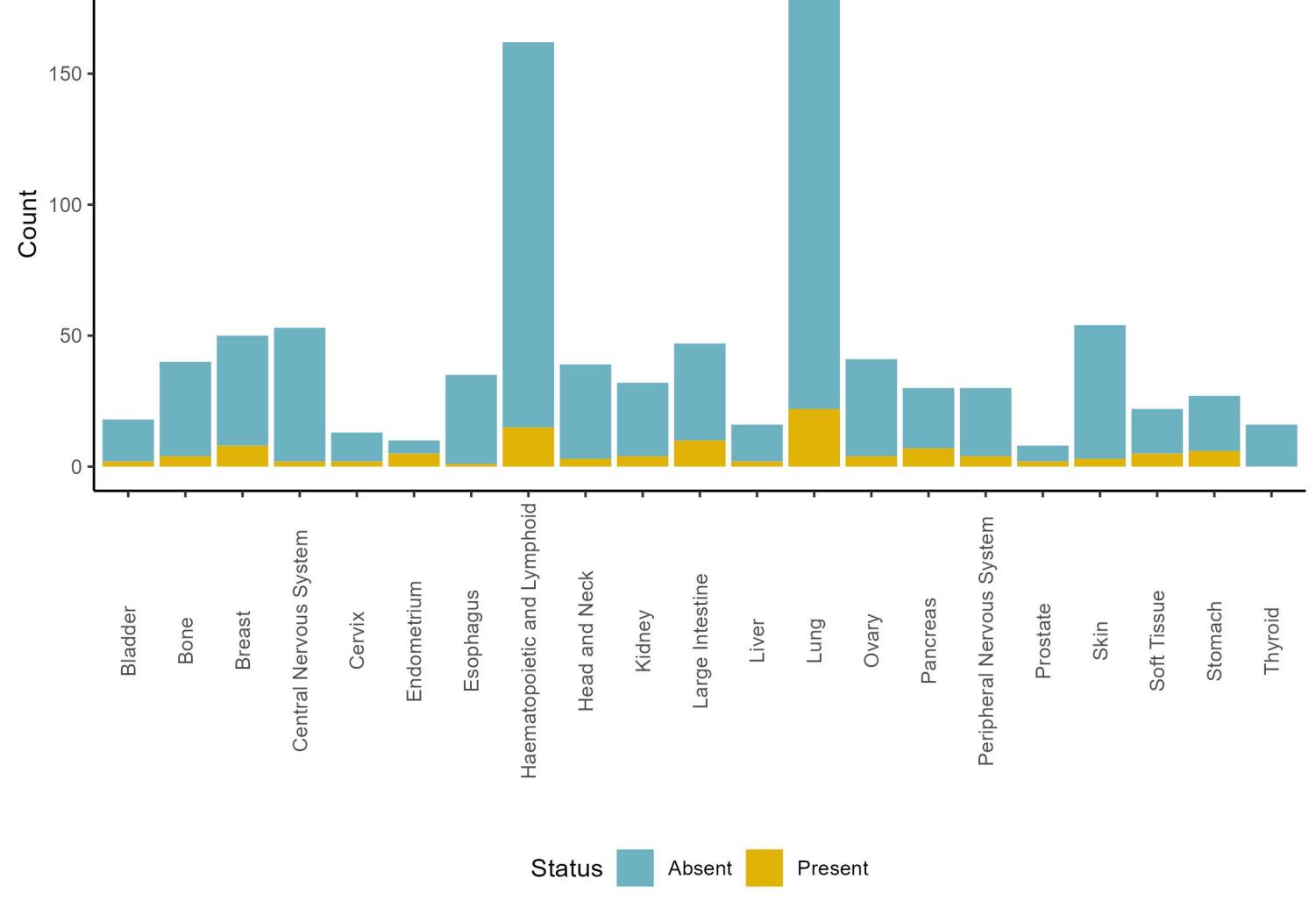
Amount of CETN2 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 6.619e-02



Present and absent CETN2 protein counts by tissue, DB1

Chi square p value is 3.459e-03

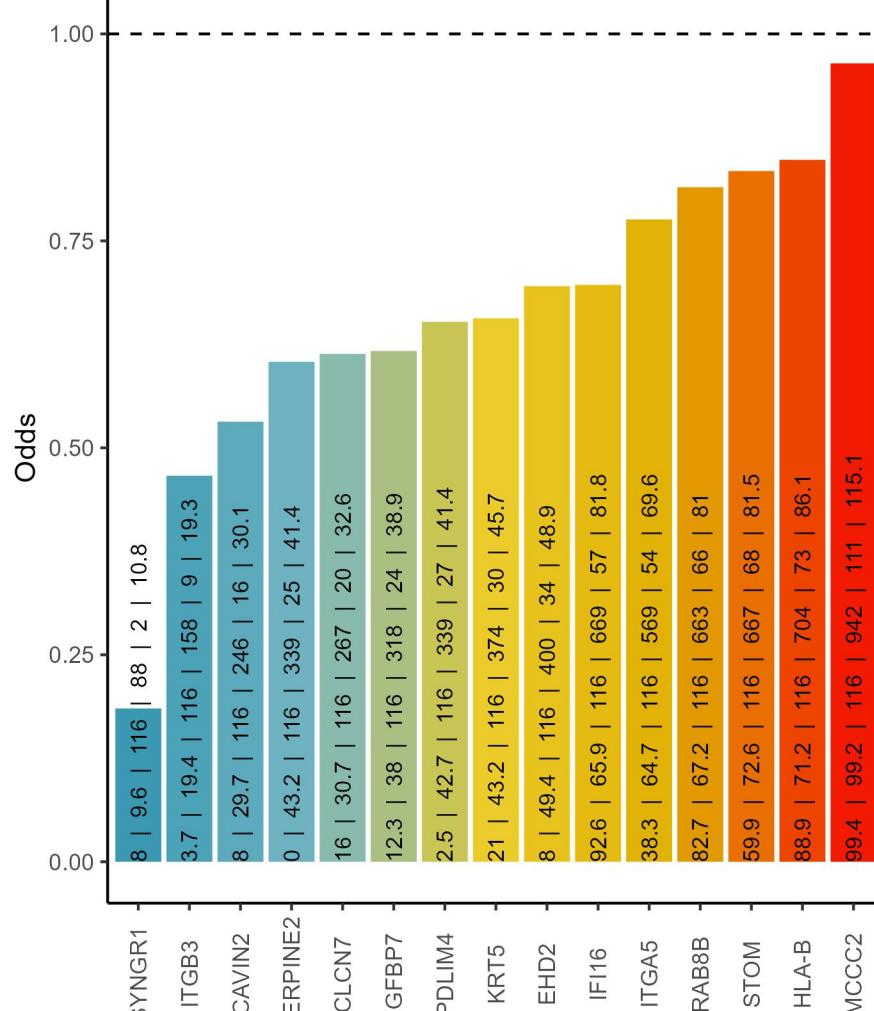


Cooccurrence with CETN2 protein, DB1

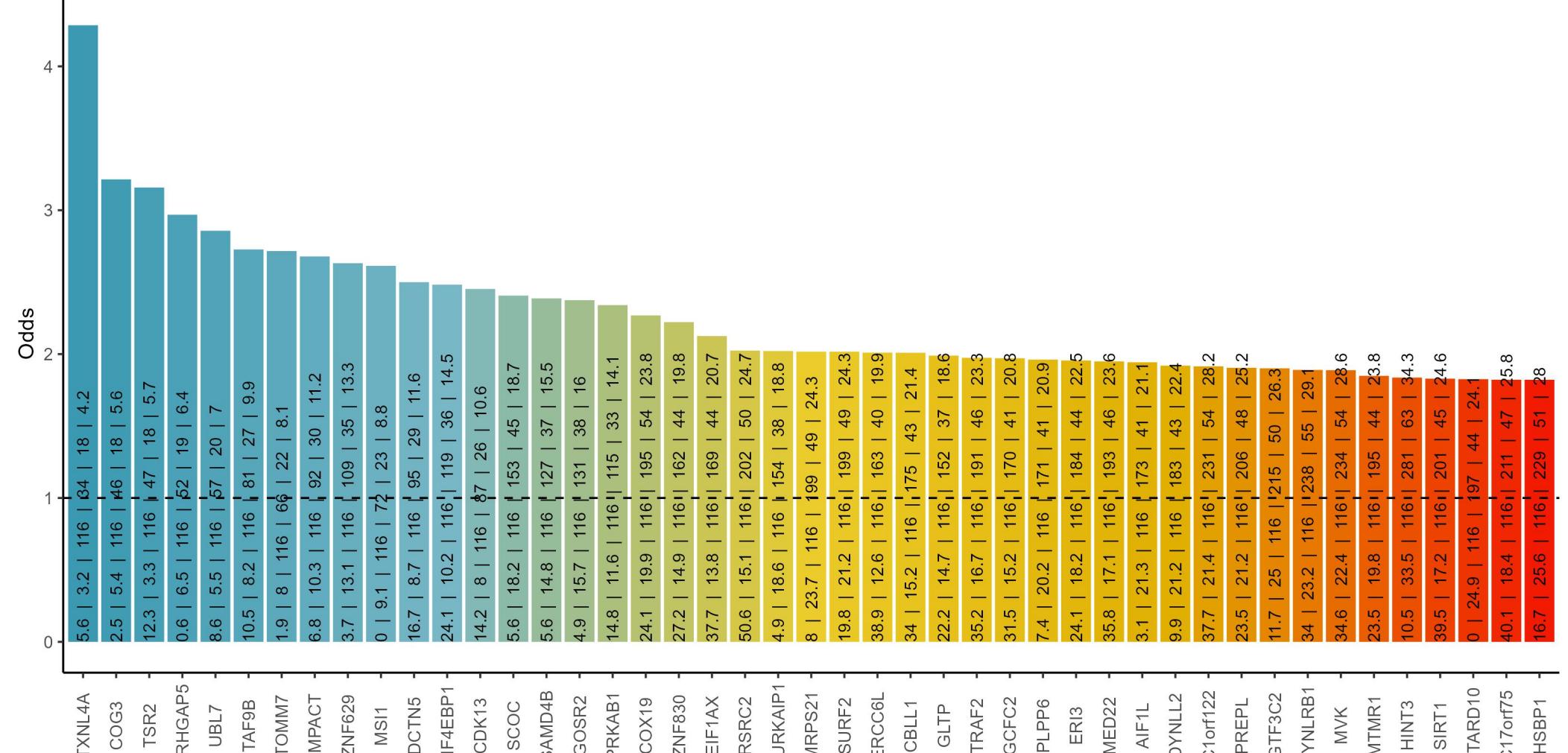
% of CETN2 in blood cancers: 9.3 ; % of CETN2 in solid cancers: 12.9

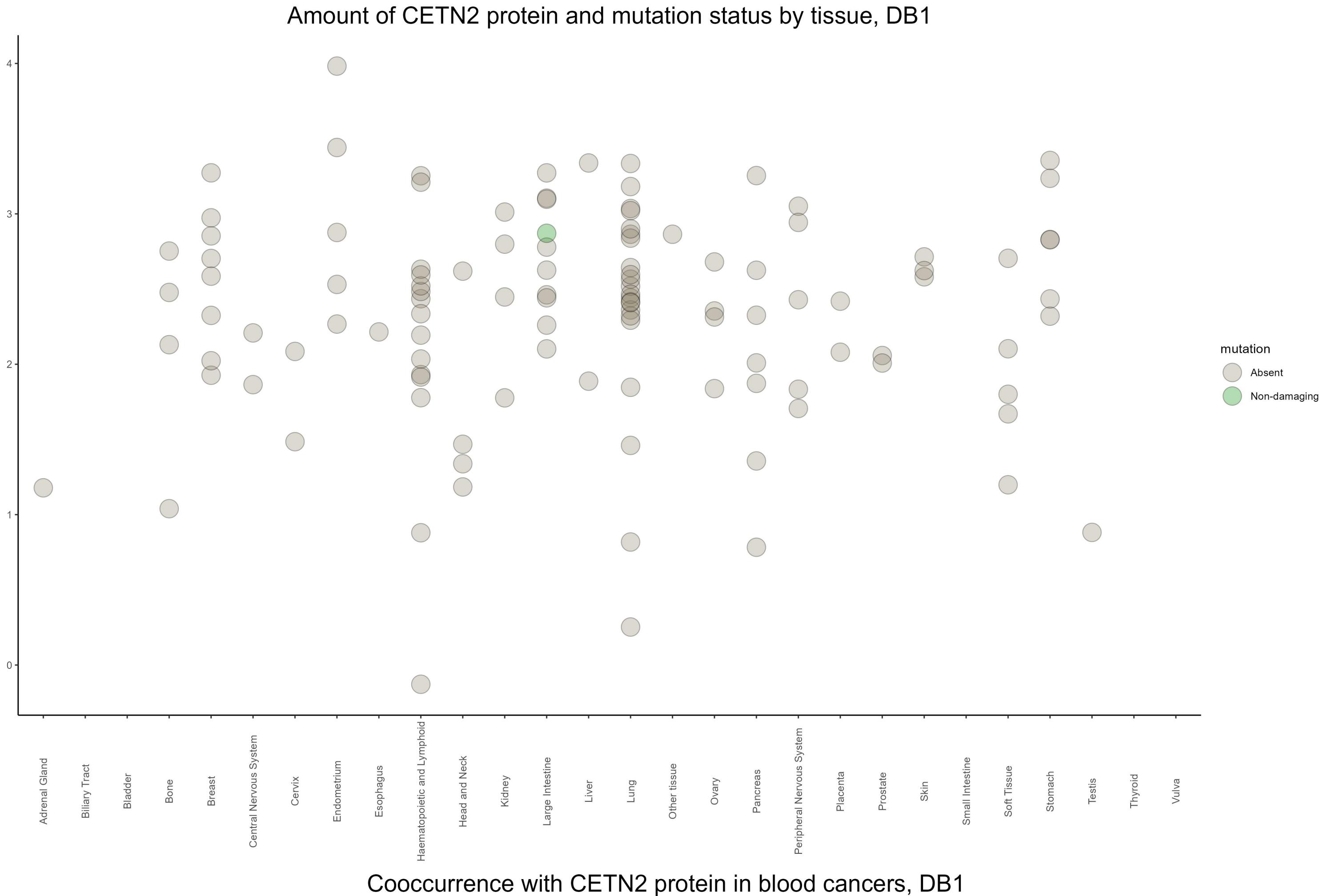
Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CETN2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



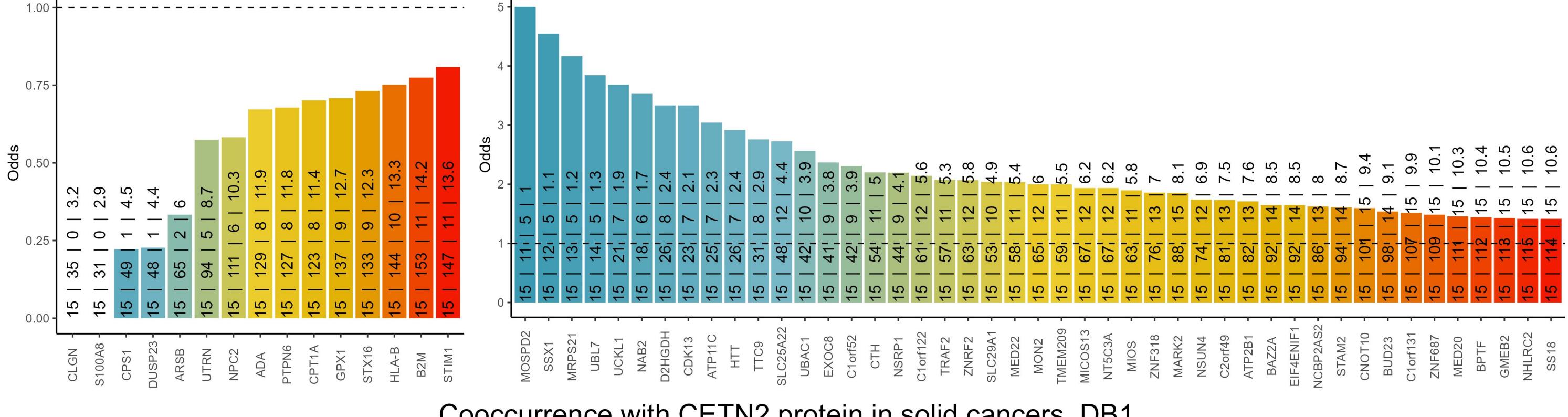
Positive cooccurrence





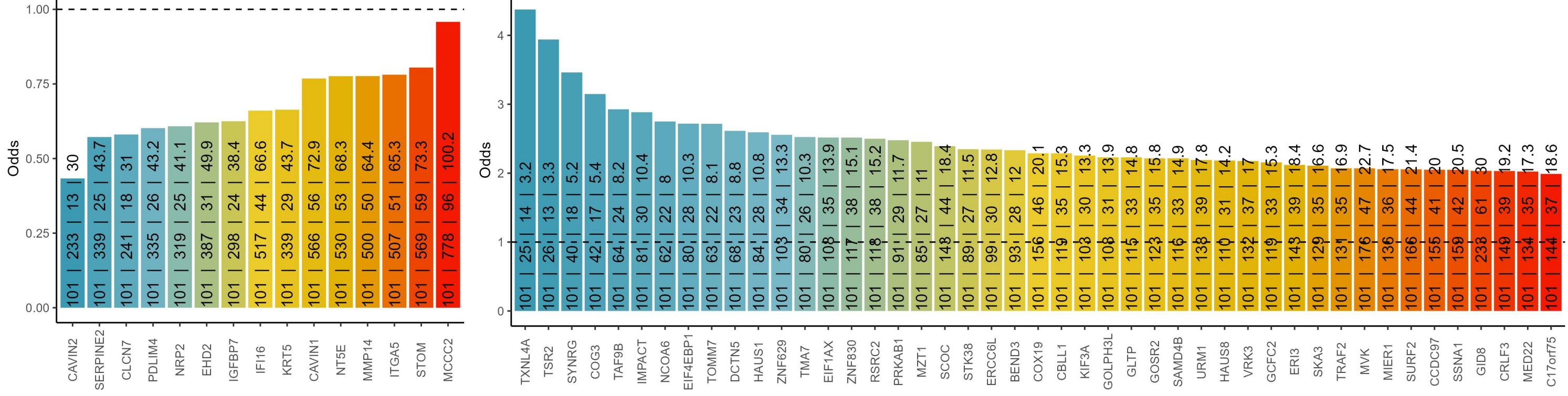
ncidence of CETN2 | incidence of Protein 2 | observed cooccurrence | e

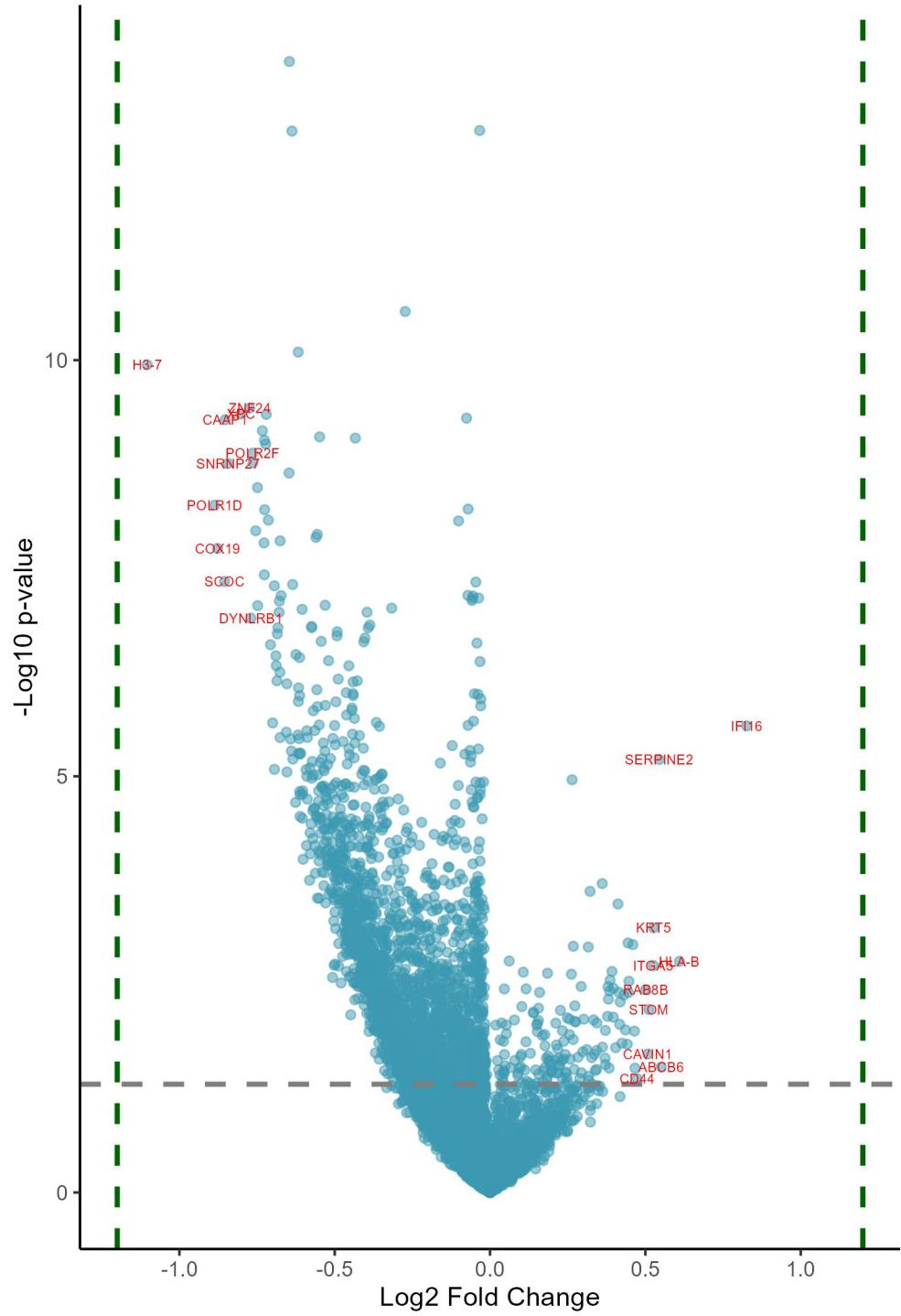
Positive cooccurrence



Incidence of CETN2 | incidence of Protein 2 | observed cooccurrence | e

Positive cooccurrence

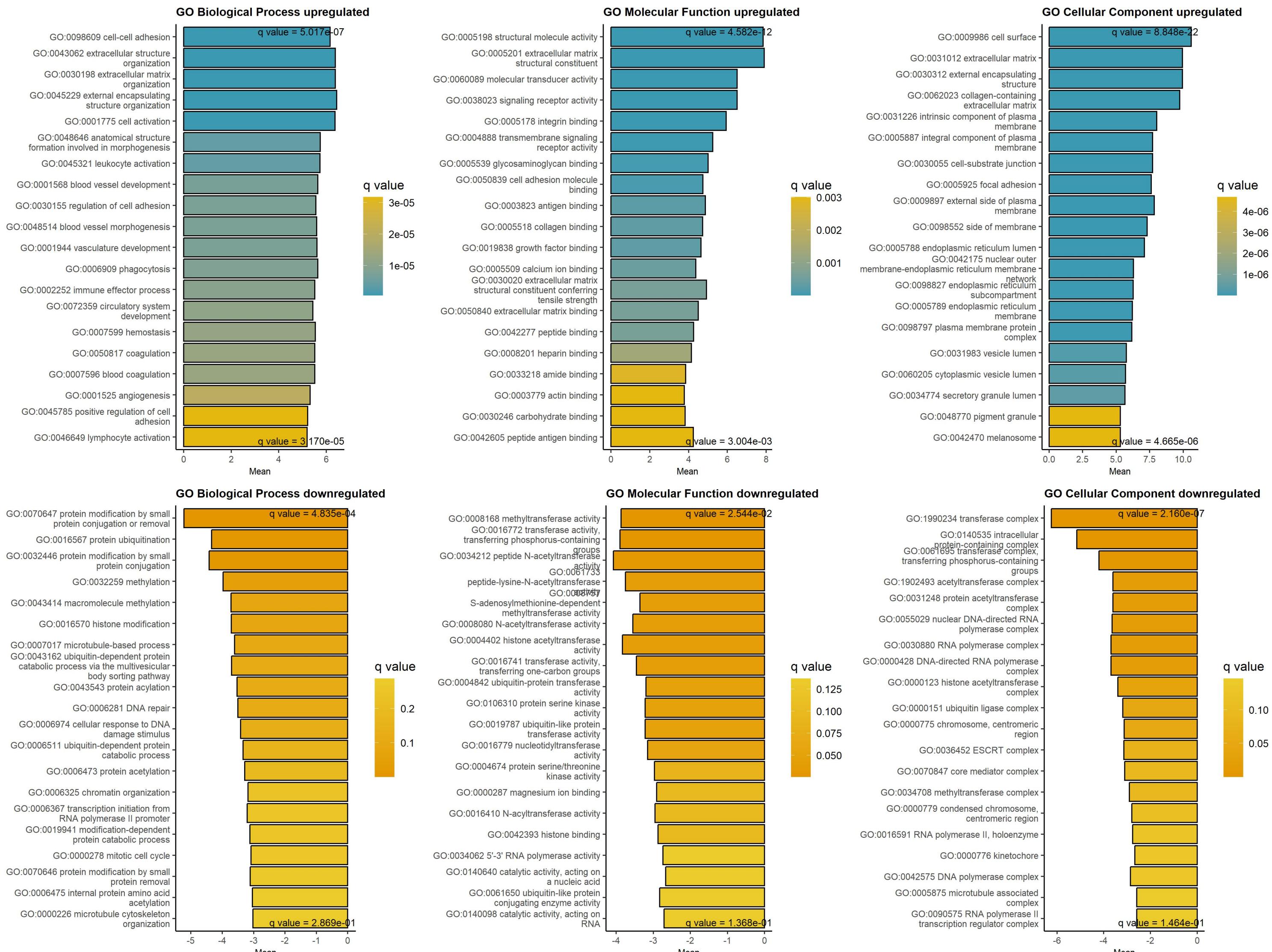


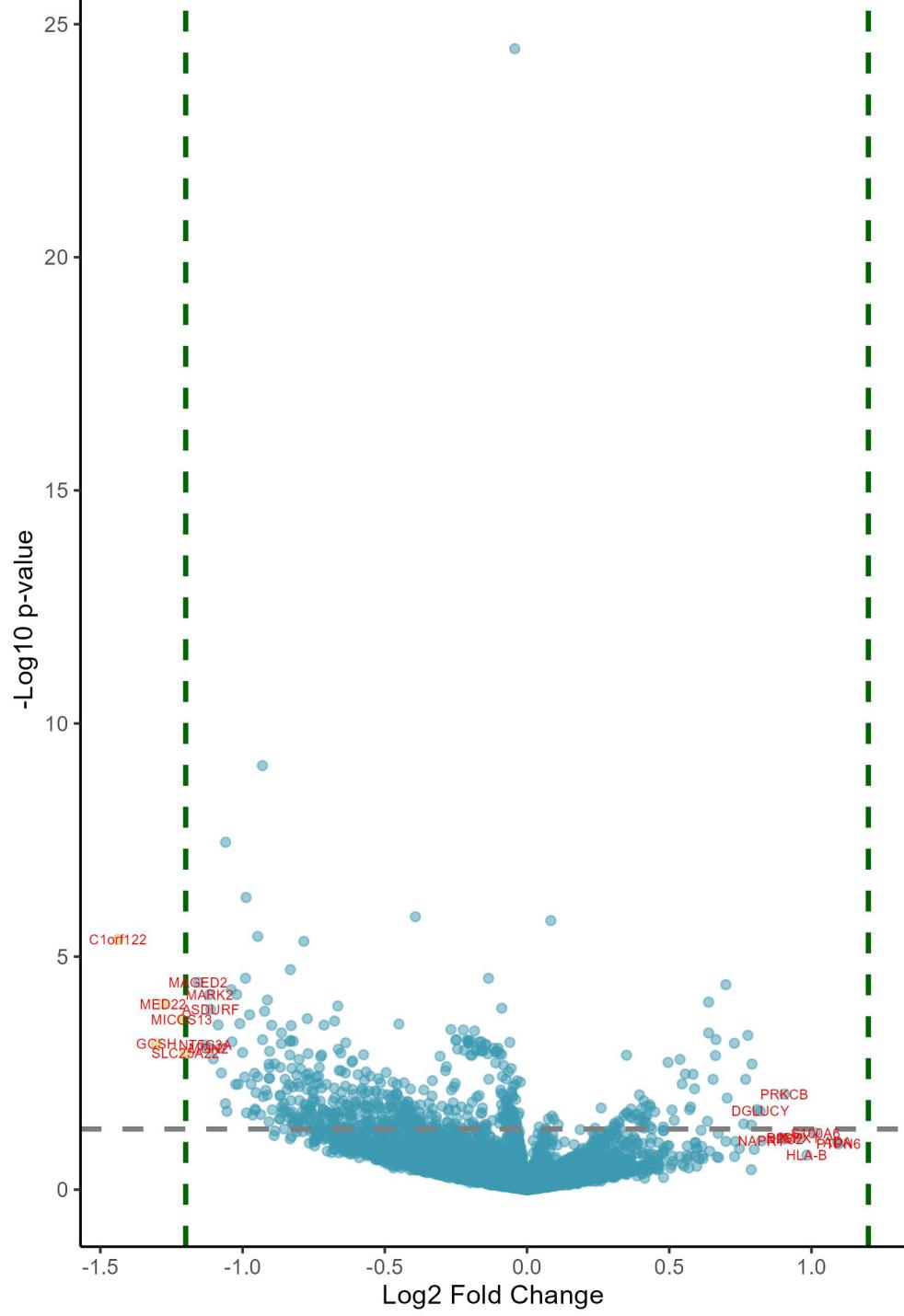


Downregulated at low/absent CETN2 Upregulated at low/absent CETN2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.1	1.08e-07	H3-7	H3.7 histone (putative)	0.83	1.58e-04	IFI16	interferon gamma inducible protein
-0.89	1.60e-06	POLR1D	RNA polymerase I and III subunit D	0.61	1.31e-02	HLA-B	major histocompatibility complex, c
-0.88	3.68e-06	COX19	cytochrome c oxidase assembly facto	0.55	9.69e-02	ABCB6	ATP binding cassette subfamily B me
-0.85	8.56e-06	SCOC	short coiled-coil protein	0.54	3.02e-04	SERPINE2	serpin family E member 2
-0.85	2.88e-07	CAAP1	caspase activity and apoptosis inhi	0.53	6.95e-03	KRT5	keratin 5
-0.84	5.79e-07	SNRNP27	small nuclear ribonucleoprotein U4/U6	0.53	1.42e-02	ITGA5	integrin subunit alpha 5
-0.8	2.88e-07	XPC	XPC complex subunit, DNA damage rec	0.51	3.24e-02	STOM	stomatin
-0.77	2.88e-07	ZNF24	zinc finger protein 24	0.51	7.56e-02	CAVIN1	caveolae associated protein 1
-0.77	1.61e-05	DYNLRB1	dynein light chain roadblock-type 1	0.5	2.21e-02	RAB8B	RAB8B, member RAS oncogene family
-0.76	4.85e-07	POLR2F	RNA polymerase II, I and III subuni	0.47	1.21e-01	CD44	CD44 molecule (Indian blood group)
-0.76	5.79e-07	UBE2Z	ubiquitin conjugating enzyme E2 Z	0.47	9.90e-02	MSN	moesin
-0.75	2.67e-06	CTPS2	CTP synthase 2	0.46	4.90e-02	NT5E	5'-nucleotidase ecto
-0.75	1.03e-06	GID8	GID complex subunit 8 homolog	0.46	9.55e-03	PDILM4	PDZ and LIM domain 4
-0.75	1.26e-05	GCSH	glycine cleavage system protein H	0.45	1.89e-02	IGFBP7	insulin like growth factor binding
-0.73	3.62e-07	ZNF706	zinc finger protein 706	0.45	2.33e-02	LPCAT2	lysophosphatidylcholine acyltransfe
-0.73	3.26e-06	DYNLL1	dynein light chain LC8-type 1	0.44	9.27e-03	TNC	tenascin C
-0.73	7.42e-06	TXN2	thioredoxin 2	0.44	6.33e-02	RAC2	Rac family small GTPase 2
-0.73	3.81e-07	ARFIP2	ADP ribosylation factor interacting	0.44	4.79e-02	B2M	beta-2-microglobulin
-0.73	1.67e-06	CNOT10	CCR4-NOT transcription complex subu	0.43	2.44e-02	EHD2	EH domain containing 2
-0.72	3.99e-07	MARK2	microtubule affinity regulating kin	0.42	6.21e-02	KRT17	keratin 17
-0.72	2.88e-07	MED29	mediator complex subunit 29	0.42	2.78e-02	ADGRE5	adhesion G protein-coupled receptor
-0.71	2.10e-06	PIN4	peptidylprolyl cis/trans isomerase,	0.42	1.69e-01	LGALS1	galectin 1
-0.71	2.68e-05	C1orf122	chromosome 1 open reading frame 122	0.42	4.31e-02	CD109	CD109 molecule
-0.7	1.52e-04	GABARPL2	GABA type A receptor associated pro	0.42	2.32e-02	NNMT	nicotinamide N-methyltransferase
-0.69	8.99e-06	MED20	mediator complex subunit 20	0.41	4.43e-03	CAVIN2	caveolae associated protein 2
-0.69	3.73e-04	C20orf27	chromosome 20 open reading frame 27	0.4	6.76e-02	MMP14	matrix metallopeptidase 14
-0.69	3.54e-05	PHC2	polyhomeotic homolog 2	0.4	2.16e-02	SYNM	synemin
-0.69	4.34e-05	MED10	mediator complex subunit 10	0.4	3.74e-02	SPARC	secreted protein acidic and cystein
-0.69	6.23e-05	HOOK1	hook microtubule tethering protein	0.39	1.58e-02	NRP2	neuropilin 2

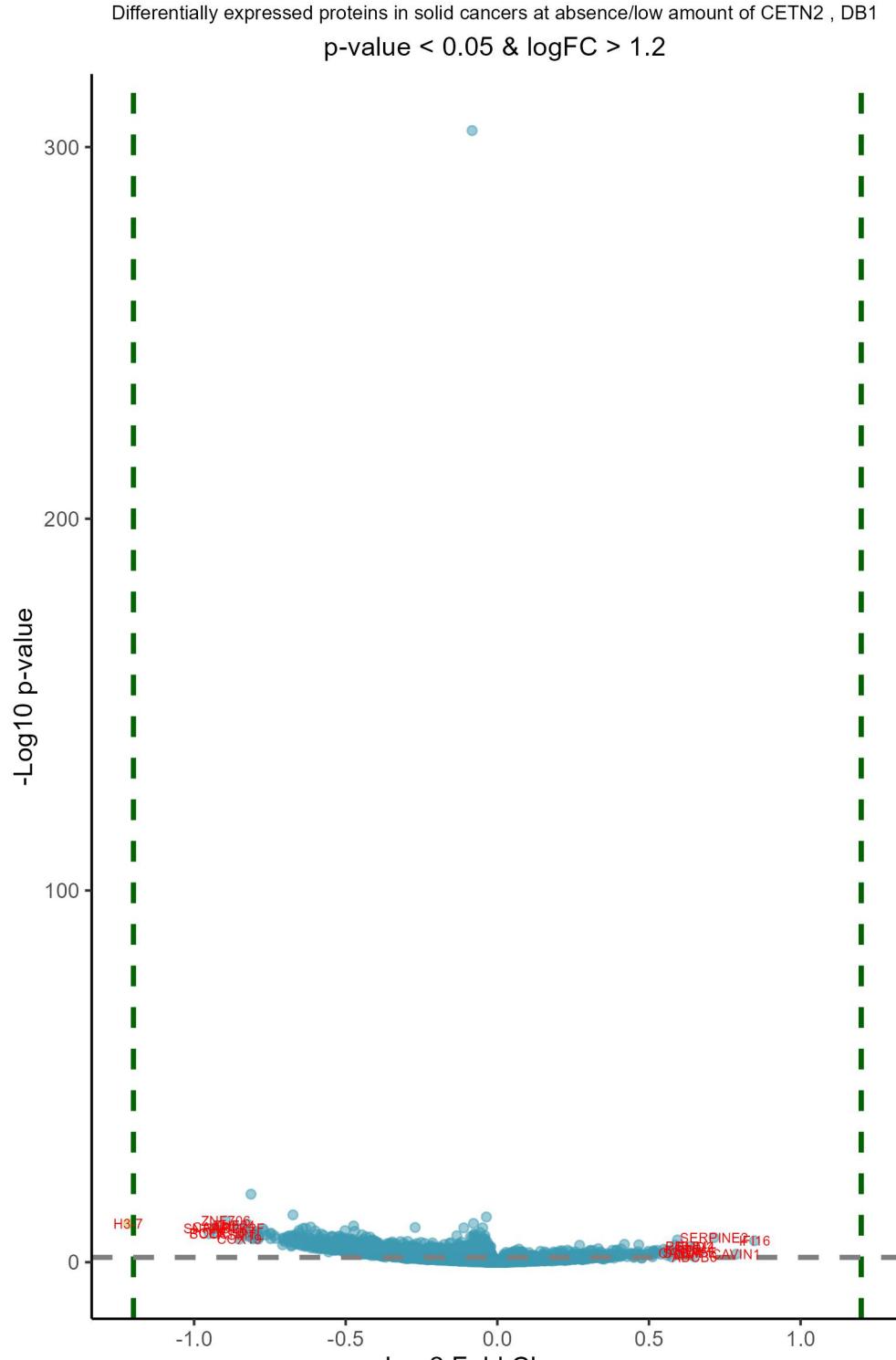
GAGE analysis on upregulated and downregulated proteins at low/absent CETN2 protein, DB1





Downregulated in blood cancers at low/absent CETN2 Upregulated in blood cancers at low/absent CETN2

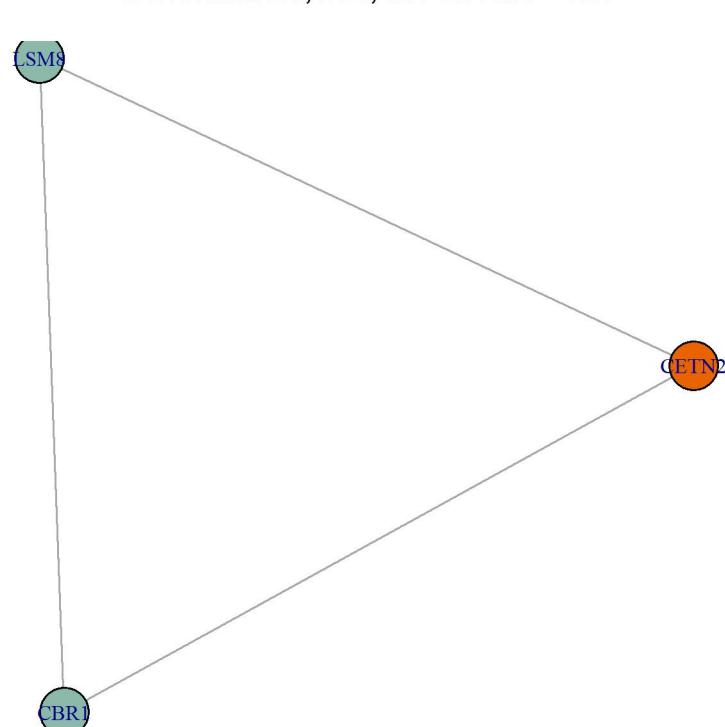
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.44	3.14e-03	C1orf122	chromosome 1 open reading frame 122	1.1	7.27e-01	PTPN6	protein tyrosine phosphatase non-re
-1.3	7.96e-02	GCSH	glycine cleavage system protein H	1.09	7.12e-01	ADA	adenosine deaminase
-1.28	3.29e-02	MED22	mediator complex subunit 22	1.01	6.29e-01	S100A6	S100 calcium binding protein A6
-1.21	5.32e-02	MICOS13	mitochondrial contact site and cris	0.98	8.29e-01	HLA-B	major histocompatibility complex, c
-1.2	9.16e-02	SLC25A22	solute carrier family 25 member 22	0.96	6.87e-01	GPX1	glutathione peroxidase 1
-1.16	1.70e-02	MAGED2	MAGE family member D2	0.91	6.99e-01	NPC2	NPC intracellular cholesterol trans
-1.13	8.05e-02	NT5C3A	5'-nucleotidase, cytosolic IIIA	0.9	3.01e-01	PRKCB	protein kinase C beta
-1.12	8.84e-02	MON2	MON2 homolog, regulator of endosome	0.89	6.82e-01	B2M	beta-2-microglobulin
-1.12	2.41e-02	MARK2	microtubule affinity regulating kin	0.82	7.07e-01	NAPRT	nicotinate phosphoribosyltransferas
-1.11	3.75e-02	ASDURF	ASNSD1 upstream open reading frame	0.82	4.34e-01	DGLUCY	D-glutamate cyclase
-1.1	1.05e-01	ZNRF2	zinc and ring finger 2	0.81	4.25e-01	H1-0	H1.0 linker histone
-1.09	5.76e-02	ATP2B1	ATPase plasma membrane Ca ²⁺ transpo	0.8	7.85e-01	GSDMD	gasdermin D
-1.08	8.84e-02	SIRT1	sirtuin 1	0.79	1.25e-01	ARSB	arylsulfatase B
-1.07	1.69e-01	VPS37C	VPS37C subunit of ESCRT-I	0.79	5.55e-01	NDRG1	N-myc downstream regulated 1
-1.06	3.84e-01	COX19	cytochrome c oxidase assembly facto	0.79	9.06e-01	S100A4	S100 calcium binding protein A4
-1.06	5.86e-05	SS18	SS18 subunit of BAF chromatin remod	0.78	7.94e-02	CPS1	carbamoyl-phosphate synthase 1
-1.05	4.34e-01	LAMTOR5	late endosomal/lysosomal adaptor, M	0.77	1.97e-01	GPX7	glutathione peroxidase 7
-1.04	2.13e-02	BUD23	BUD23 rRNA methyltransferase and ri	0.76	5.50e-01	UTRN	utrophin
-1.04	7.96e-02	C2orf49	chromosome 2 open reading frame 49	0.75	7.81e-01	CPT1A	carnitine palmitoyltransferase 1A
-1.02	2.24e-01	CTH	cystathione gamma-lyase	0.73	7.12e-01	ATL3	atlakin GTPase 3
-1.02	2.41e-02	CHMP5	charged multivesicular body protein	0.73	8.39e-01	PABPC1L	poly(A) binding protein cytoplasmic
-1.02	2.24e-01	C20orf27	chromosome 20 open reading frame 27	0.73	7.96e-02	DUSP23	dual specificity phosphatase 23
-1.01	5.76e-02	EIF4ENIF1	eukaryotic translation initiation f	0.7	3.35e-01	SFXN3	sideroflexin 3
-1	9.16e-02	FYTTD1	forty-two-three domain containing 1	0.7	7.12e-01	ALDH4A1	aldehyde dehydrogenase 4 family mem
-0.99	1.86e-01	TMEM209	transmembrane protein 209	0.7	1.78e-02	CLGN	calmegin
-0.99	1.50e-02	C1orf131	chromosome 1 open reading frame 131	0.67	8.43e-01	ACTN1	actinin alpha 1
-0.99	7.20e-04	PFKM	phosphofructokinase, muscle	0.67	6.32e-01	ALG5	ALG5 dolichyl-phosphate beta-glucos
-0.99	4.43e-01	EIF4EBP1	eukaryotic translation initiation f	0.67	8.39e-01	IQGAP2	IQ motif containing GTPase activati
-0.98	4.54e-02	CNOT10	CCR4-NOT transcription complex subu	0.66	7.96e-02	PTPRJ	protein tyrosine phosphatase recept



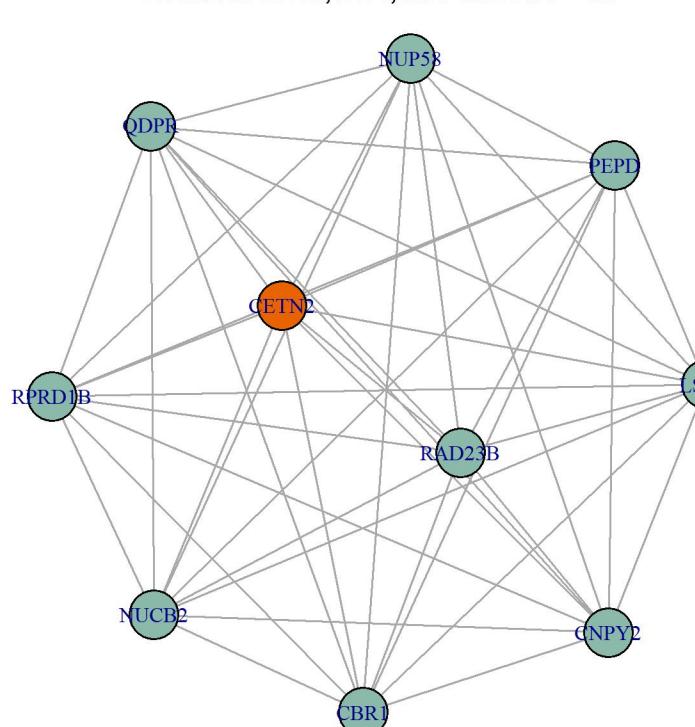
Downregulated in solid cancers at low/absent CETN2 Upregulated in solid cancers at low/absent CETN2

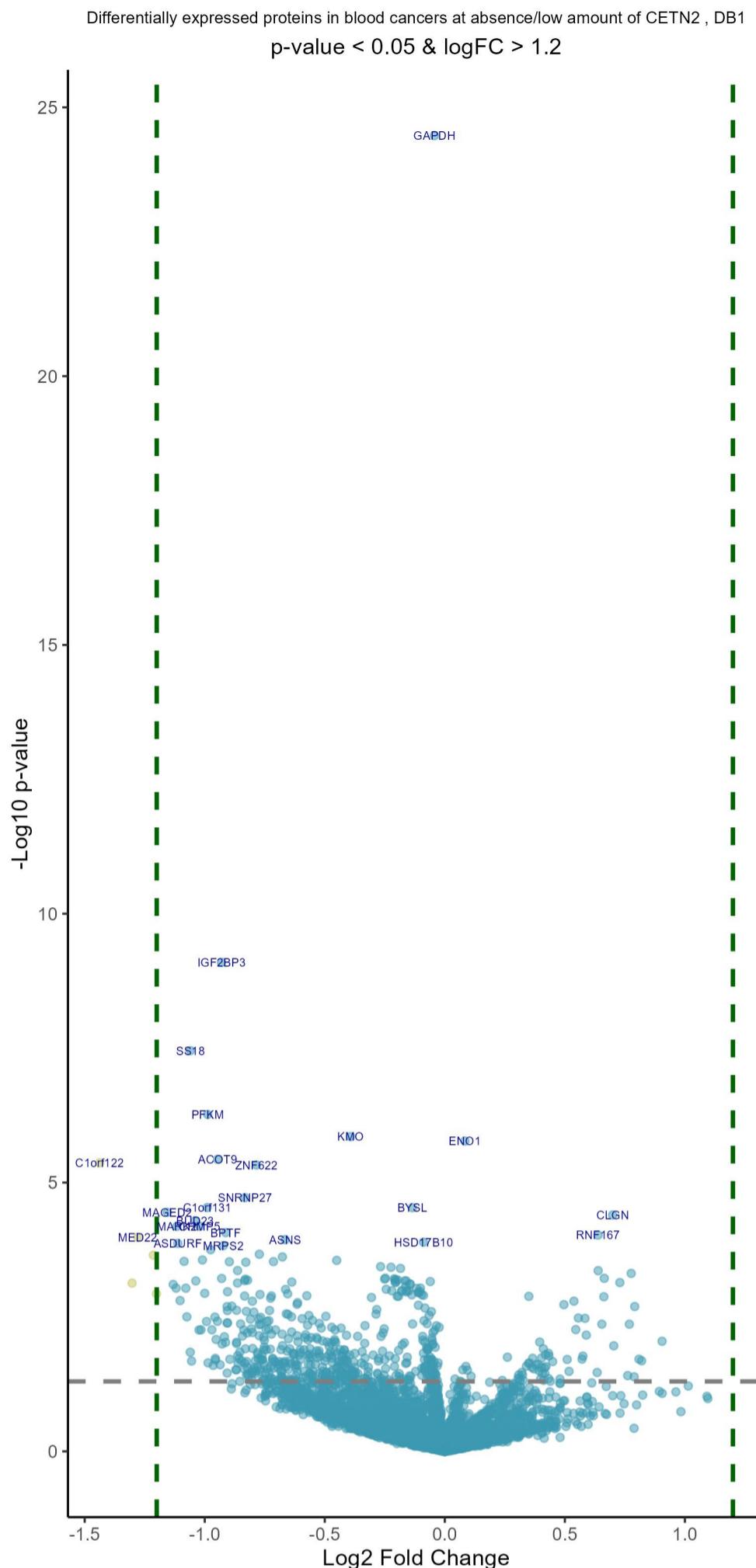
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.22	3.39e-08	H3-7	H3.7 histone (putative)	0.85	8.96e-05	IFI16	interferon gamma inducible protein
-0.95	3.71e-06	SCOC	short coiled-coil protein	0.79	3.13e-02	CAVIN1	caveolae associated protein 1
-0.93	1.74e-07	CAAP1	caspase activity and apoptosis inhi	0.71	2.28e-05	SERPINE2	serpin family E member 2
-0.93	2.88e-07	SNRNP27	small nuclear ribonucleoprotein U4/U	0.67	1.30e-02	NT5E	5'-nucleotidase ecto
-0.93	3.14e-06	POLR1D	RNA polymerase I and III subunit D	0.65	1.52e-03	EHD2	EH domain containing 2
-0.9	8.34e-09	ZNF706	zinc finger protein 706	0.65	1.07e-01	ABCB6	ATP binding cassette subfamily B me
-0.87	9.32e-08	ZNF24	zinc finger protein 24	0.64	1.11e-03	PDLM4	PDZ and LIM domain 4
-0.86	2.88e-07	POLR2F	RNA polymerase II, I and III subuni	0.61	1.96e-02	STOM	stomatin
-0.85	4.23e-05	COX19	cytochrome c oxidase assembly facto	0.61	5.41e-03	KRT5	keratin 5
-0.85	6.65e-06	ASMTL	acetylserotonin O-methyltransferase	0.6	1.77e-02	CALD1	caldesmon 1
-0.83	6.73e-07	GID8	GID complex subunit 8 homolog	0.59	6.16e-05	CAVIN2	caveolae associated protein 2
-0.83	1.21e-05	GSPT2	G1 to S phase transition 2	0.59	1.44e-02	MMP14	matrix metallopeptidase 14
-0.83	3.39e-08	MED29	mediator complex subunit 29	0.59	6.24e-04	NRP2	neuropilin 2
-0.81	1.09e-15	ENSA	endosulfine alpha	0.58	1.19e-02	ITGA5	integrin subunit alpha 5
-0.81	1.36e-06	XPC	XPC complex subunit, DNA damage rec	0.58	1.10e-01	CD44	CD44 molecule (Indian blood group)
-0.81	2.48e-05	GABARPL2	GABA type A receptor associated pro	0.57	5.77e-03	SPARC	secreted protein acidic and cystein
-0.81	3.48e-05	NACA2	nascent polypeptide associated comp	0.56	1.85e-02	PLOD2	procollagen-lysine,2-oxoglutarate 5
-0.8	6.90e-06	MED10	mediator complex subunit 10	0.56	5.27e-02	CAV1	caveolin 1
-0.79	1.20e-06	PIN4	peptidylprolyl cis/trans isomerase,	0.56	6.78e-03	NNMT	nicotinamide N-methyltransferase
-0.79	3.10e-06	CTPS2	CTP synthase 2	0.55	3.59e-03	TNC	tenascin C
-0.79	4.29e-05	DYNLRB1	dynein light chain roadblock-type 1	0.54	3.29e-02	KRT17	keratin 17
-0.79	1.21e-05	C11orf54	chromosome 11 open reading frame 54	0.53	5.85e-03	F3	coagulation factor III, tissue fact
-0.79	1.63e-05	C9orf78	chromosome 9 open reading frame 78	0.53	2.20e-02	RAB8B	RAB8B, member RAS oncogene family
-0.77	2.97e-07	ARFIP2	ADP ribosylation factor interacting	0.52	1.46e-02	IGFBP7	insulin like growth factor binding
-0.77	9.63e-07	SSU72	SSU72 homolog, RNA polymerase II CT	0.52	7.58e-03	PRNP	prion protein
-0.76	7.30e-06	UBE2Z	ubiquitin conjugating enzyme E2 Z	0.52	7.93e-03	FNDC3B	fibronectin type III domain contain
-0.75	4.48e-06	CNOT10	CCR4-NOT transcription complex subu	0.52	1.56e-02	LPCAT2	lysophosphatidylcholine acyltransfe
-0.75	3.43e-05	HOOK1	hook microtubule tethering protein	0.51	1.03e-01	MSN	moesin
-0.75	3.10e-06	HPF1	histone PARylation factor 1	0.51	4.05e-02	HLA-B	major histocompatibility complex, c

CETN2 network, DB1, all Pearson r > 0.35

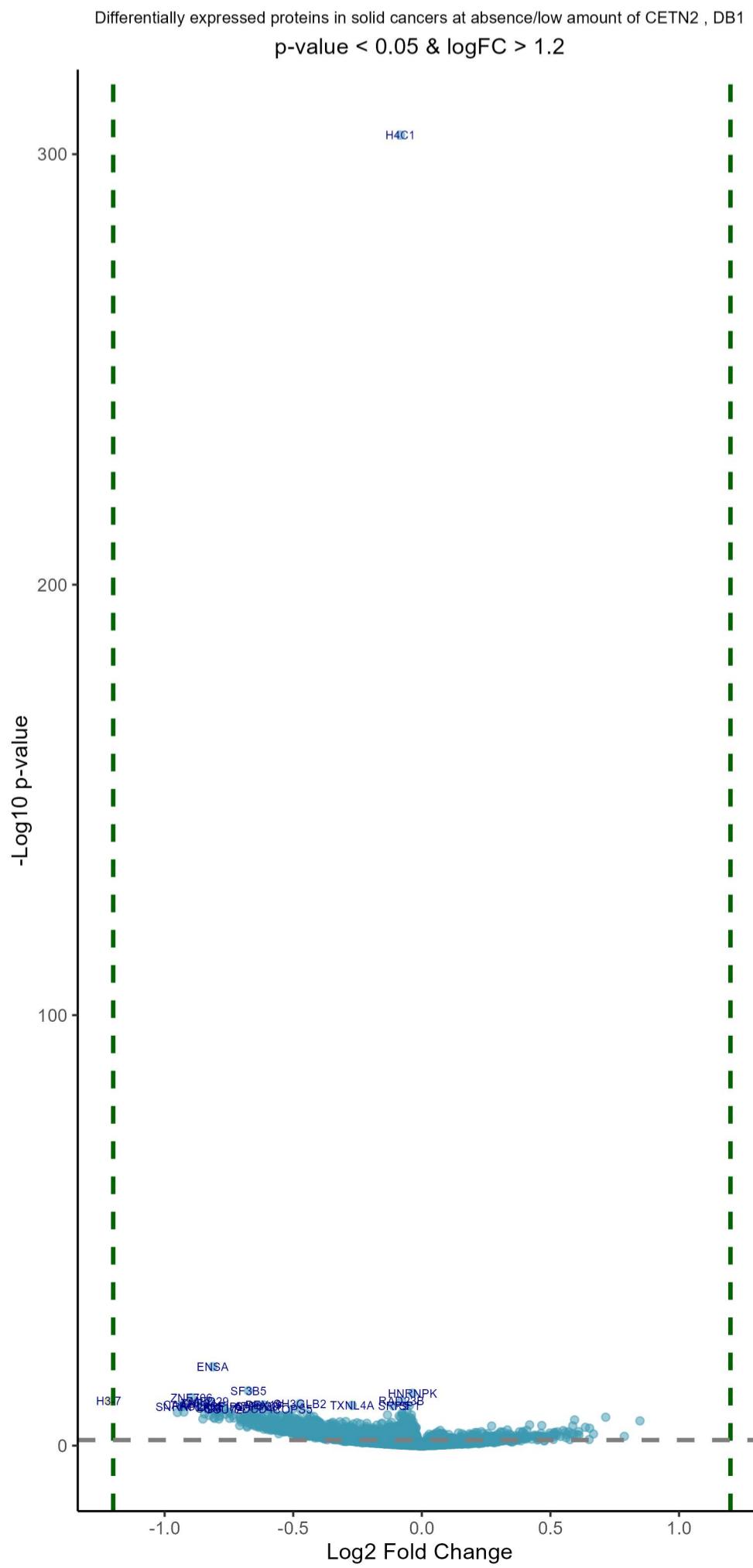


CETN2 network, DB1, all Pearson r > 0.3



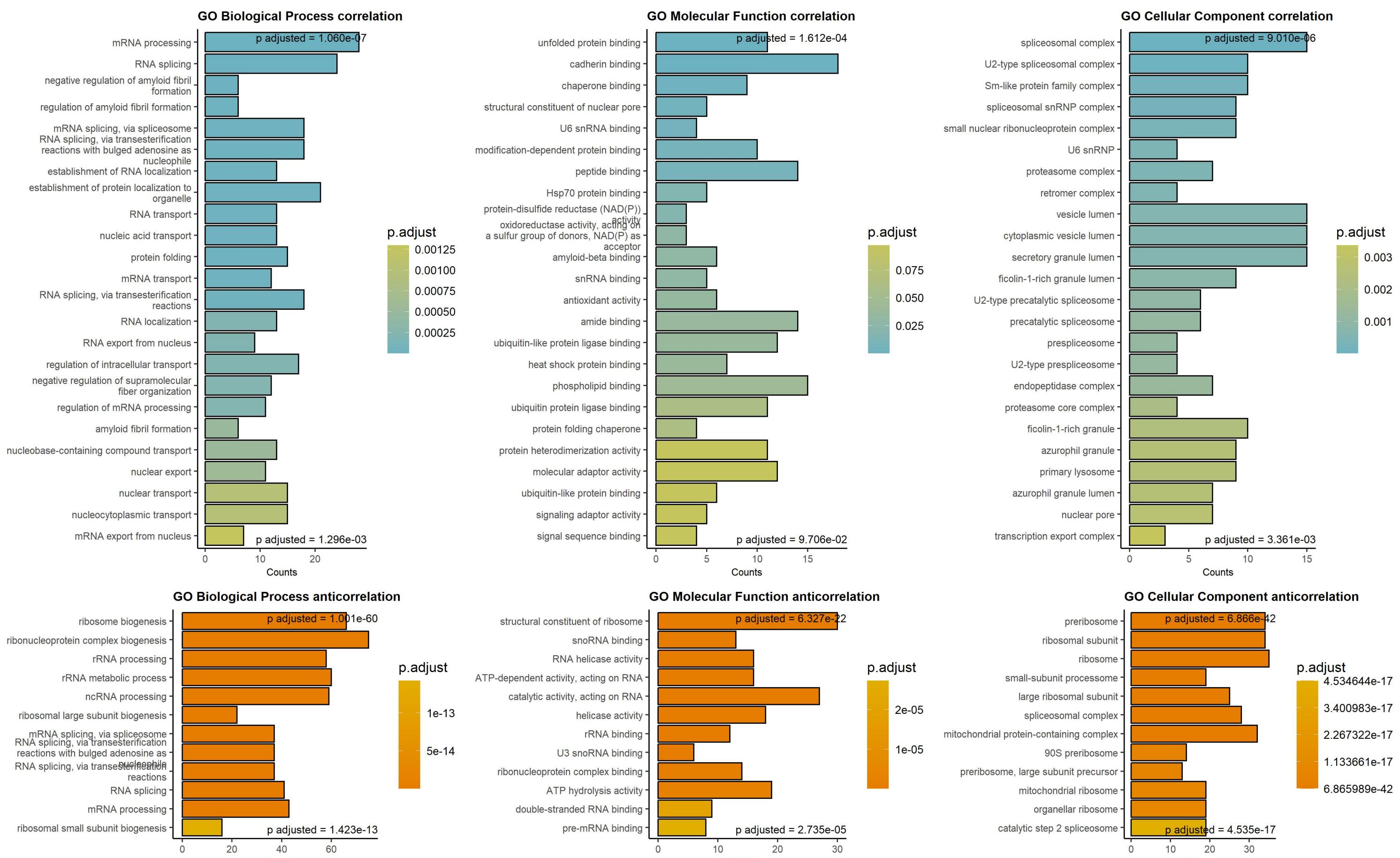


Sorted by p values!							
Downregulated in blood cancers at low/absent CETN2				Upregulated in blood cancers at low/absent CETN2			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.04	1.12e-21	GAPDH	glyceraldehyde-3-phosphate dehydrog	0.08	1.61e-03	ENO1	enolase 1
-0.93	1.78e-06	IGF2BP3	insulin like growth factor 2 mRNA b	0.7	1.78e-02	CLGN	calmegin
-1.06	5.86e-05	SS18	SS18 subunit of BAF chromatin remod	0.64	3.15e-02	RNF167	ring finger protein 167
-0.99	7.20e-04	PFKM	phosphofructokinase, muscle	0.64	7.24e-02	S100A8	S100 calcium binding protein A8
-0.39	1.55e-03	KMO	kynurenine 3-monooxygenase	0.78	7.94e-02	CPS1	carbamoyl-phosphate synthase 1
-0.95	3.07e-03	ACOT9	acyl-CoA thioesterase 9	0.66	7.96e-02	PTPRJ	protein tyrosine phosphatase recep
-1.44	3.14e-03	C1orf122	chromosome 1 open reading frame 122	0.73	7.96e-02	DUSP23	dual specificity phosphatase 23
-0.78	3.14e-03	ZNF622	zinc finger protein 622	0.35	9.16e-02	VPS4B	vacuolar protein sorting 4 homolog
-0.83	1.15e-02	SNRNP27	small nuclear ribonucleoprotein U4/	0.66	9.22e-02	CTSG	cathepsin G
-0.99	1.50e-02	C1orf131	chromosome 1 open reading frame 131	0.54	1.06e-01	ERG	ETS transcription factor ERG
-0.14	1.50e-02	BYSL	bystin like	0.5	1.19e-01	CD109	CD109 molecule
-1.16	1.70e-02	MAGED2	MAGE family member D2	0.79	1.25e-01	ARSB	arylsulfatase B
-1.04	2.13e-02	BUD23	BUD23 rRNA methyltransferase and ri	0.56	1.73e-01	VAMP5	vesicle associated membrane protei
-1.02	2.41e-02	CHMP5	charged multivesicular body protein	0.58	1.74e-01	TRAF3IP3	TRAF3 interacting protein 3
-1.12	2.41e-02	MARK2	microtubule affinity regulating kin	0.65	1.97e-01	MYLK	myosin light chain kinase
-0.91	2.99e-02	BPTF	bromodomain PHD finger transcriptio	0.77	1.97e-01	GPX7	glutathione peroxidase 7
-1.28	3.29e-02	MED22	mediator complex subunit 22	0.55	2.24e-01	PRTN3	proteinase 3
-0.67	3.48e-02	ASNS	asparagine synthetase (glutamine-hy	0.59	2.61e-01	HOMER3	homer scaffold protein 3
-0.09	3.72e-02	HSD17B10	hydroxysteroid 17-beta dehydrogenas	0.9	3.01e-01	PRKCB	protein kinase C beta
-1.11	3.75e-02	ASDURF	ASNSD1 upstream open reading frame	0.4	3.03e-01	RAP1GAP2	RAP1 GTPase activating protein 2
-0.92	3.96e-02	MRPS2	mitochondrial ribosomal protein S2	0.7	3.35e-01	SFXN3	sideroflexin 3
-0.98	4.54e-02	CNOT10	CCR4-NOT transcription complex subu	0.41	3.62e-01	CST3	cystatin C
-0.77	5.31e-02	HMGN5	high mobility group nucleosome bind	0.43	3.92e-01	CTHRC1	collagen triple helix repeat contai
-1.21	5.32e-02	MICOS13	mitochondrial contact site and cris	0.42	4.03e-01	PSMB8	proteasome 20S subunit beta 8
-0.68	5.54e-02	DTD1	D-aminoacyl-tRNA deacylase 1	0.43	4.08e-01	MPO	myeloperoxidase
-1.01	5.76e-02	EIF4ENIF1	eukaryotic translation initiation f	0.57	4.08e-01	GNAQ	G protein subunit alpha q
-0.45	5.76e-02	RPLP1	ribosomal protein lateral stalk sub	0.26	4.21e-01	LMAN1	lectin, mannose binding 1
-1.09	5.76e-02	ATP2B1	ATPase plasma membrane Ca2+ transpo	0.4	4.25e-01	IGFBP7	insulin like growth factor binding
-0.71	5.76e-02	ABHD11	abhydrolase domain containing 11	0.37	4.25e-01	CDC42BPB	CDC42 binding protein kinase beta
-0.9	5.76e-02	UBE2Z	ubiquitin conjugating enzyme E2 Z	0.57	4.25e-01	CLEC11A	C-type lectin domain containing 11A
-0.83	5.76e-02	SMARCD1	SWI/SNF related, matrix associated,	0.81	4.25e-01	H1-0	H1.0 linker histone
-0.27	6.77e-02	OGDHL	oxoglutarate dehydrogenase L	0.51	4.25e-01	MYO6	myosin VI
-0.22	6.77e-02	MOXD1	monooxygenase DBH like 1	0.82	4.34e-01	DGLUCY	D-glutamate cyclase
-0.18	6.91e-02	AMER2	APC membrane recruitment protein 2	0.45	4.34e-01	SLC27A2	solute carrier family 27 member 2
-0.86	7.24e-02	CWC22	CWC22 spliceosome associated protei	0.35	4.43e-01	FUCA1	alpha-L-fucosidase 1
-0.25	7.96e-02	SPOCK2	SPARC (osteonectin), cwcv and kazal	0.35	4.45e-01	SORBS3	sorbin and SH3 domain containing
-0.93	7.96e-02	ARMC10	armadillo repeat containing 10	0.39	4.54e-01	SERPINB8	serpin family B member 8
-0.21	7.96e-02	TMEM200A	transmembrane protein 200A	0.38	4.56e-01	PALM	paralemmin
-0.25	7.96e-02	EGRBP	E _{gr} gamma binding protein	0.34	4.75e-01	PRAS	PRAS related

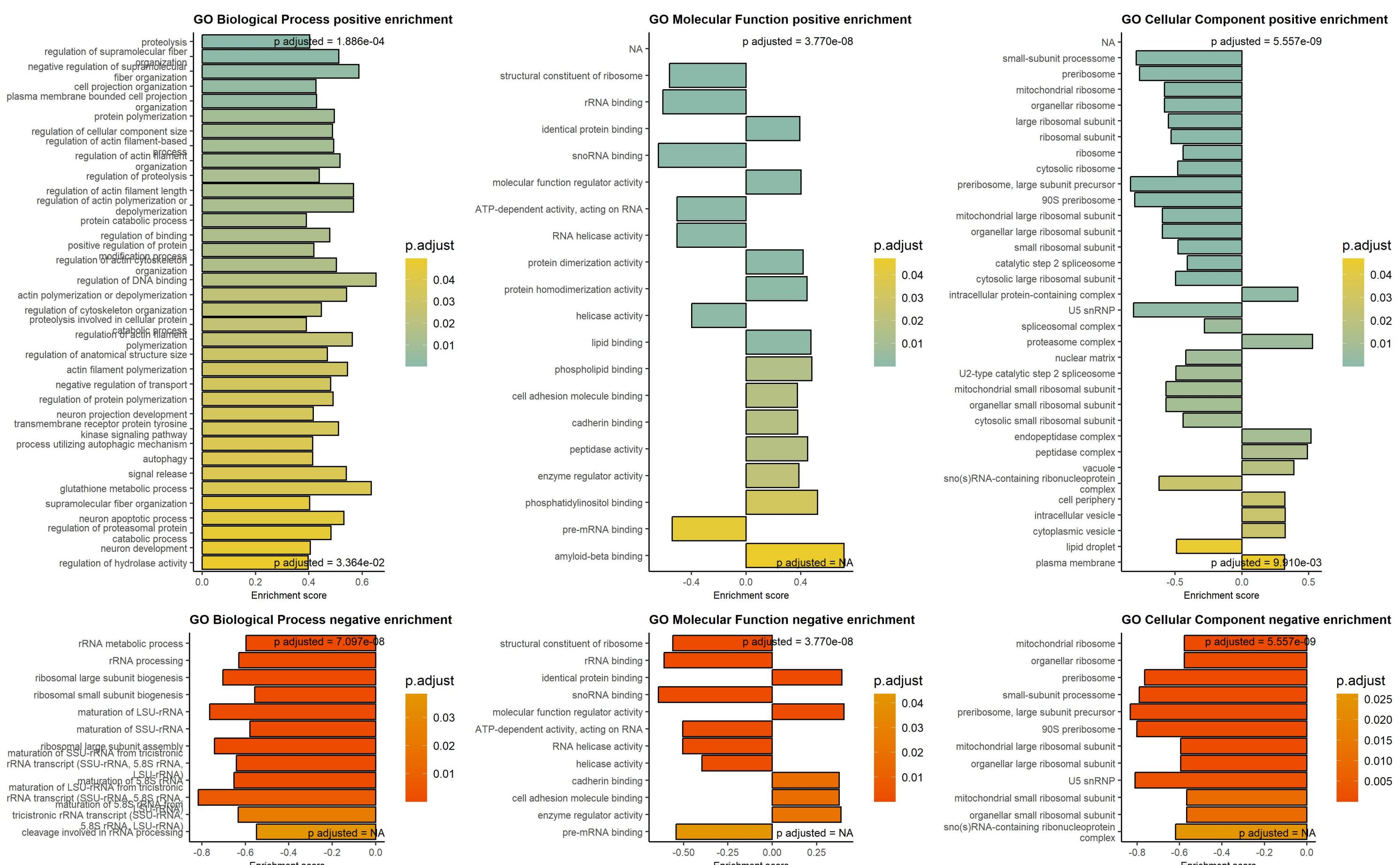


Sorted by p values!							
Downregulated in solid cancers at low/absent CETN2				Upregulated in solid cancers at low/absent CETN2			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.08	1.23e-301	H4C1	H4 clustered histone 1	0.71	2.28e-05	SERPINE2	serpin family E member 2
-0.81	1.09e-15	ENSA	endosulfine alpha	0.59	6.16e-05	CAVIN2	caveolae associated protein 2
-0.67	2.98e-10	SF3B5	splicing factor 3b subunit 5	0.85	8.96e-05	IFI16	interferon gamma inducible protein
-0.04	8.91e-10	HNRNPK	heterogeneous nuclear ribonucleoprotein K	0.42	4.36e-04	COL5A1	collagen type V alpha 1 chain
-0.9	8.34e-09	ZNF706	zinc finger protein 706	0.47	5.50e-04	MYL9	myosin light chain 9
-0.08	3.39e-08	RAD23B	RAD23 homolog B, nucleotide excision repair protein	0.59	6.24e-04	NRP2	neuropilin 2
-1.22	3.39e-08	H3-7	H3.7 histone (putative)	0.27	6.74e-04	SYNGR1	synaptogyrin 1
-0.83	3.39e-08	MED29	mediator complex subunit 29	0.64	1.11e-03	PDLIM4	PDZ and LIM domain 4
-0.87	9.32e-08	ZNF24	zinc finger protein 24	0.65	1.52e-03	EHD2	EH domain containing 2
-0.47	1.06e-07	SH3GLB2	SH3 domain containing GRB2 like, endoplasmic reticulum associated	0.33	2.92e-03	ITGB3	integrin subunit beta 3
-0.93	1.74e-07	CAAP1	caspase activity and apoptosis inhibitor 1	0.41	3.26e-03	TRIM16	tripartite motif containing 16
-0.62	1.74e-07	PEX19	peroxisomal biogenesis factor 19	0.07	3.40e-03	SSR4	signal sequence receptor subunit 4
-0.27	2.13e-07	TXNL4A	thioredoxin like 4A	0.55	3.59e-03	TNC	tenascin C
-0.05	2.39e-07	SF1	splicing factor 1	0.39	5.25e-03	CDH13	cadherin 13
-0.11	2.39e-07	SRP9	signal recognition particle 9	0.61	5.41e-03	KRT5	keratin 5
-0.63	2.75e-07	ATP6V1F	ATPase H+ transporting V1 subunit F	0.23	5.60e-03	SGCD	sarcoglycan delta
-0.64	2.88e-07	SAP130	Sin3A associated protein 130	0.31	5.71e-03	COL7A1	collagen type VII alpha 1 chain
-0.86	2.88e-07	POLR2F	RNA polymerase II, I and III subunit F	0.38	5.71e-03	KRT14	keratin 14
-0.93	2.88e-07	SNRNP27	small nuclear ribonucleoprotein U4/6snRNA	0.57	5.77e-03	SPARC	secreted protein acidic and cysteine rich
-0.77	2.97e-07	ARFIP2	ADP ribosylation factor interacting protein 2	0.53	5.85e-03	F3	coagulation factor III, tissue factor
-0.83	6.73e-07	GID8	GID complex subunit 8 homolog	0.06	6.53e-03	EMC2	ER membrane protein complex subunit 2
-0.65	8.31e-07	PDCD4	programmed cell death 4	0.32	6.59e-03	ARMCX4	armadillo repeat containing X-linker
-0.5	8.88e-07	COPS5	COP9 signalosome subunit 5	0.56	6.78e-03	NNMT	nicotinamide N-methyltransferase
-0.77	9.63e-07	SSU72	SSU72 homolog, RNA polymerase II C-terminal	0.39	7.50e-03	EDIL3	EGF like repeats and discoidin domain containing 3
-0.6	1.05e-06	CLNS1A	chloride nucleotide-sensitive channel	0.52	7.58e-03	PRNP	prion protein
-0.79	1.20e-06	PIN4	peptidylprolyl cis/trans isomerase, neuronal	0.21	7.63e-03	PLAU	plasminogen activator, urokinase type
-0.47	1.20e-06	CUL3	cullin 3	0.21	7.70e-03	OASL	2'-5'-oligoadenylate synthetase like
-0.81	1.36e-06	XPC	XPC complex subunit, DNA damage recognition	0.52	7.93e-03	FNDC3B	fibronectin type III domain containing 3
-0.06	1.99e-06	SKP1	S-phase kinase associated protein 1	0.31	8.40e-03	DSG3	desmoglein 3
-0.65	2.41e-06	TIMM10	translocase of inner mitochondrial membrane	0.14	9.11e-03	MCCC2	methylcrotonyl-CoA carboxylase subunit
-0.75	3.10e-06	HPF1	histone PARylation factor 1	0.5	9.25e-03	SYNM	synemin
-0.79	3.10e-06	CTPS2	CTP synthase 2	0.46	1.06e-02	TGFBI	transforming growth factor beta induced
-0.93	3.14e-06	POLR1D	RNA polymerase I and III subunit D	0.05	1.08e-02	ACTBL2	actin beta like 2
-0.95	3.71e-06	SCOC	short coiled-coil protein	0.24	1.11e-02	PLAUR	plasminogen activator, urokinase receptor
-0.75	4.48e-06	CNOT10	CCR4-NOT transcription complex subunit 10	0.08	1.11e-02	SPTBN1	spectrin beta, non-erythrocytic 1
-0.58	4.61e-06	C17orf49	chromosome 17 open reading frame 49	0.26	1.12e-02	KYNU	kynureninase
-0.08	4.61e-06	ERH	ERH mRNA splicing and mitosis factor	0.08	1.19e-02	COLGALT1	collagen beta(1-O)galactosyltransferase
-0.6	6.24e-06	FRG1	FSHD region gene 1	0.58	1.19e-02	ITGA5	integrin subunit alpha 5
-0.27	6.25e-06	HPXNZ	HPX-like zinc finger 7	0.19	1.19e-02	SKAP1	skap1-associated protein 1

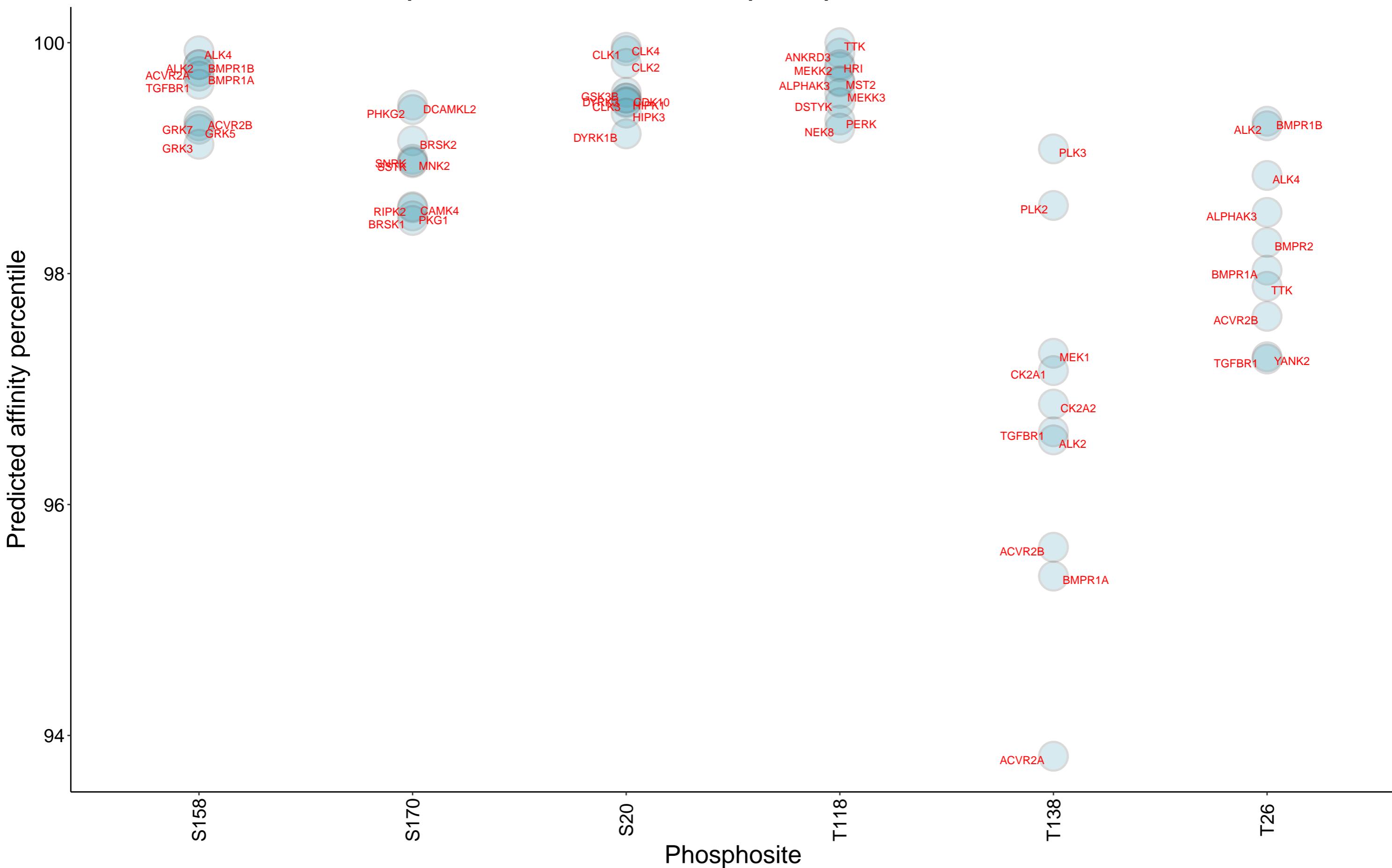
Top 250 correlation coefficients overrepresentation, CETN2 protein, DB1



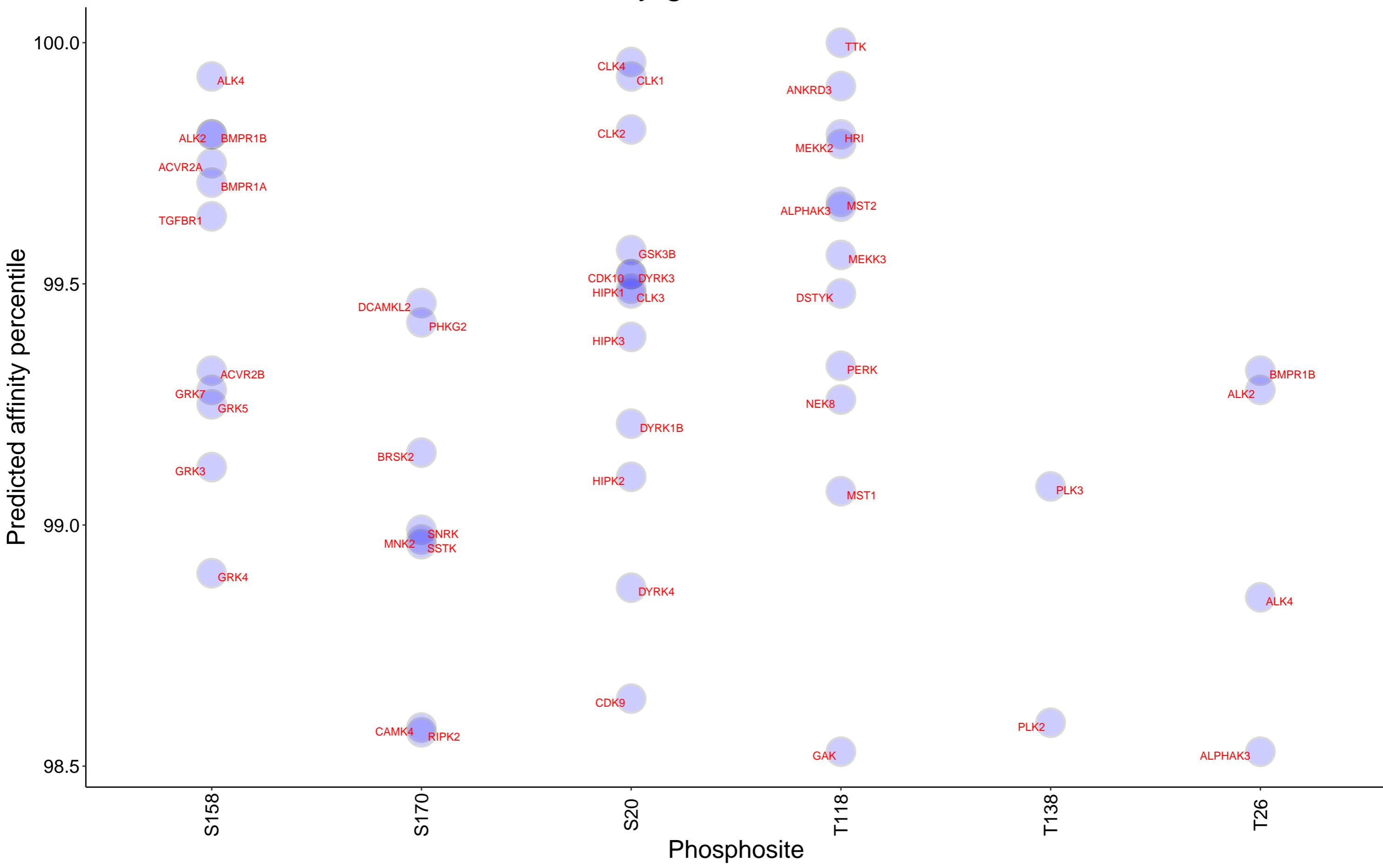
Gene Set Enrichment analysis on protein correlation coefficients, CETN2 protein, DB1



Top 10 kinases for each phosphosite in CETN2



Kinases with affinity greater than 98.5% to CETN2



No sufficient paired observations in DB1 for CETN2