

CENPS

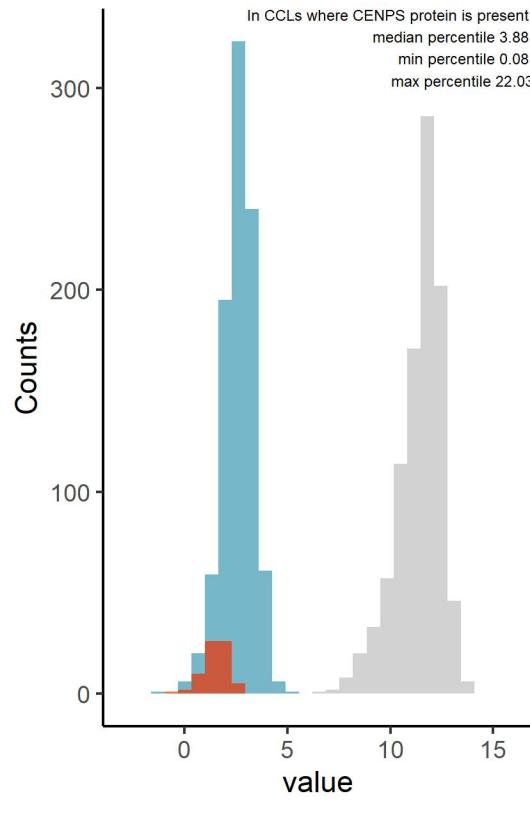
Protein name: CENPS ; UNIPROT: Q8N2Z9 ; Gene name: centromere protein S

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

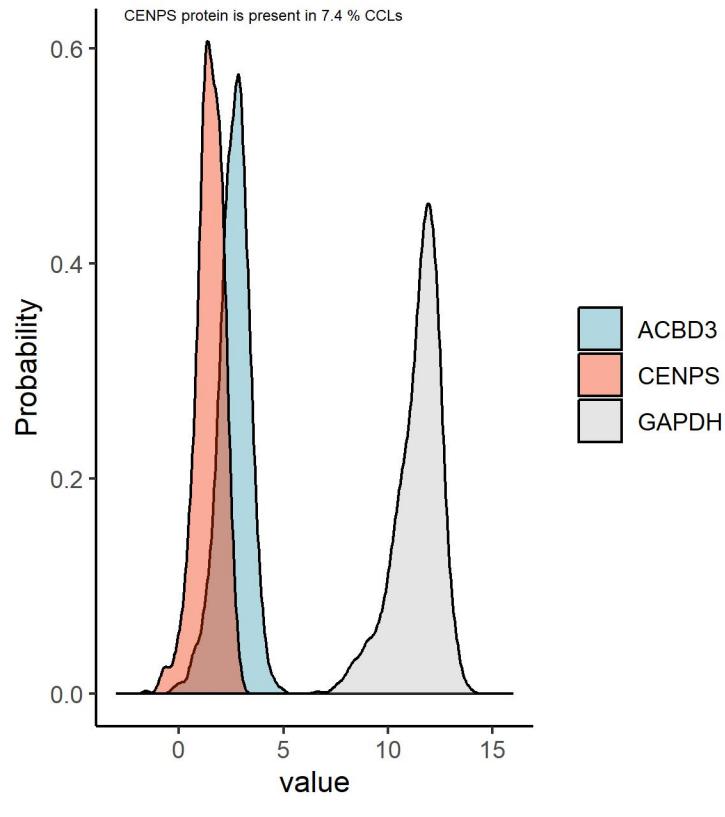
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

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



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



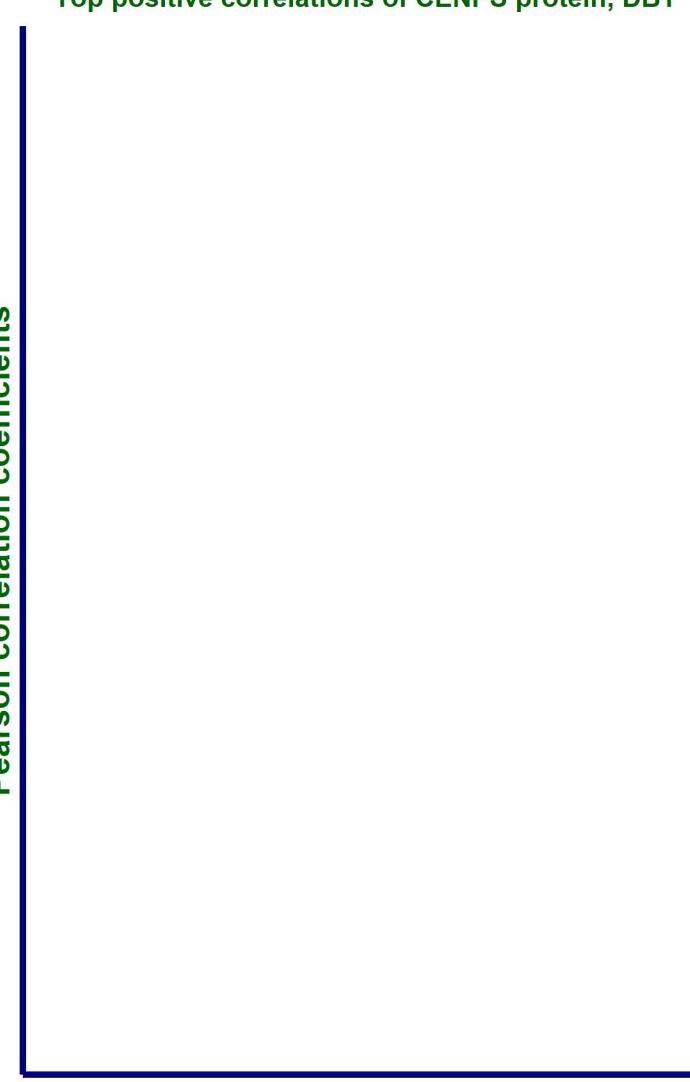
Top negative correlations of CENPS protein, DB1

Pearson correlation coefficients



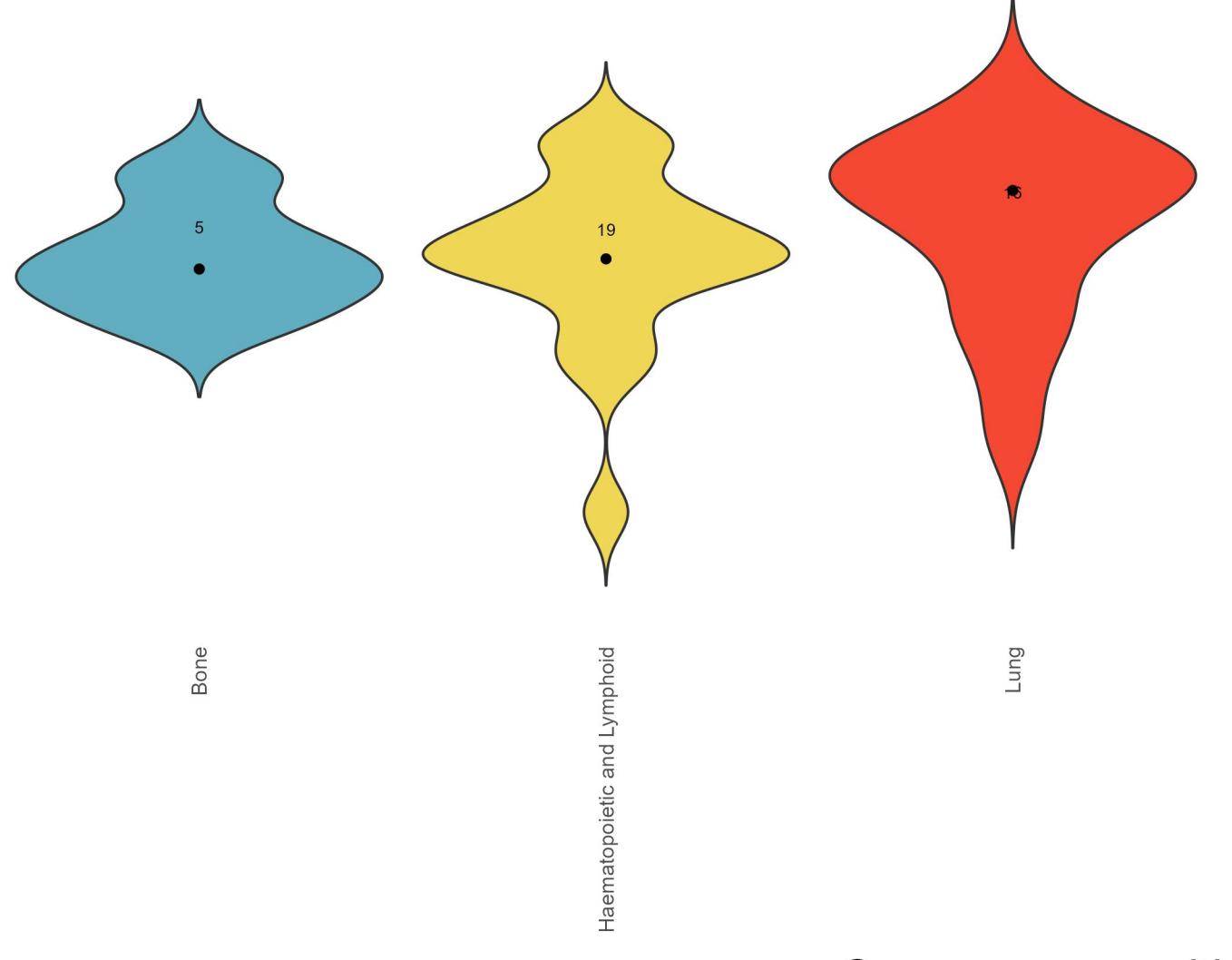
Top positive correlations of CENPS protein, DB1

Pearson correlation coefficients



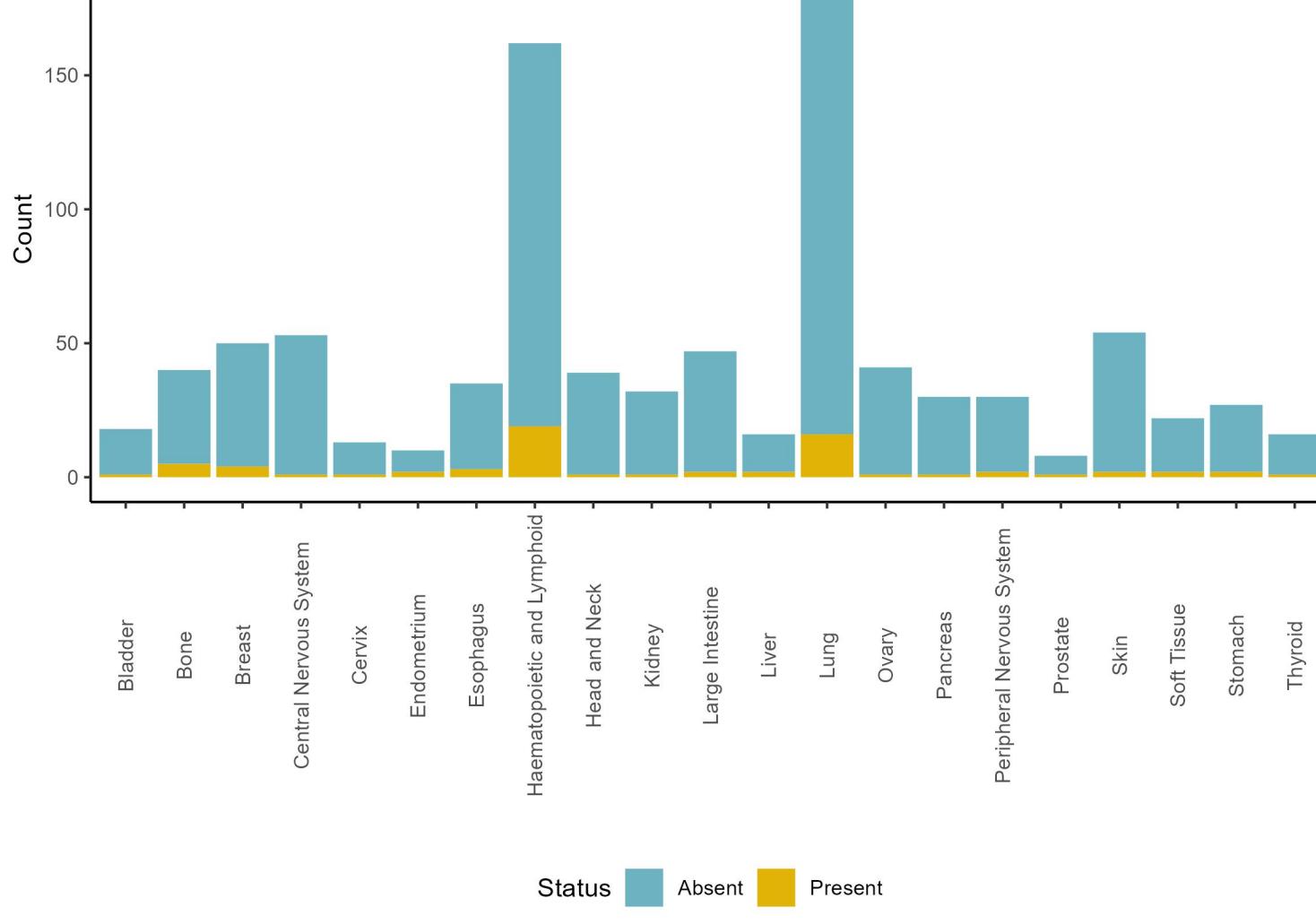
Amount of CENPS protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 5.625e-01



Present and absent CENPS protein counts by tissue, DB1

Chi square p value is 5.829e-01

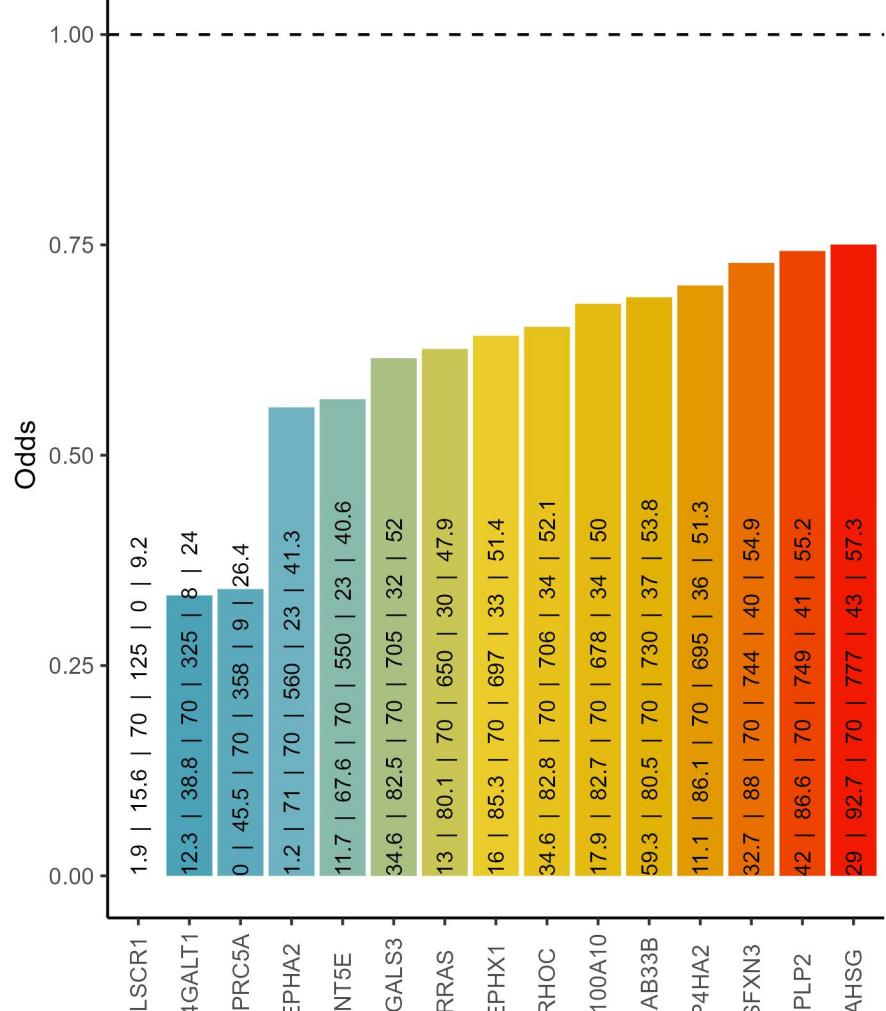


Cooccurrence with CENPS protein, DB1

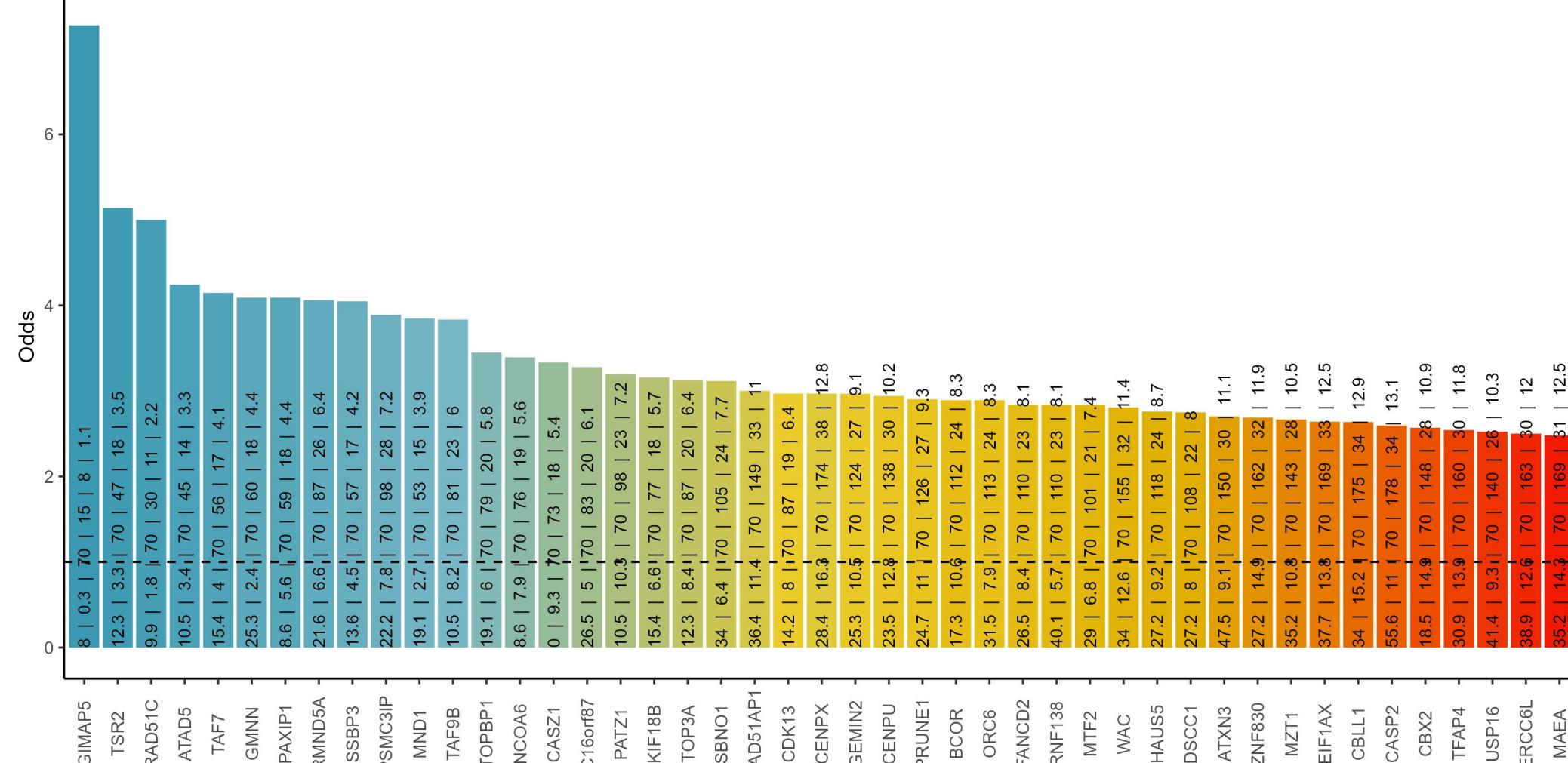
% of CENPS in blood cancers: 11.7 ; % of CENPS in solid cancers: 6.5

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

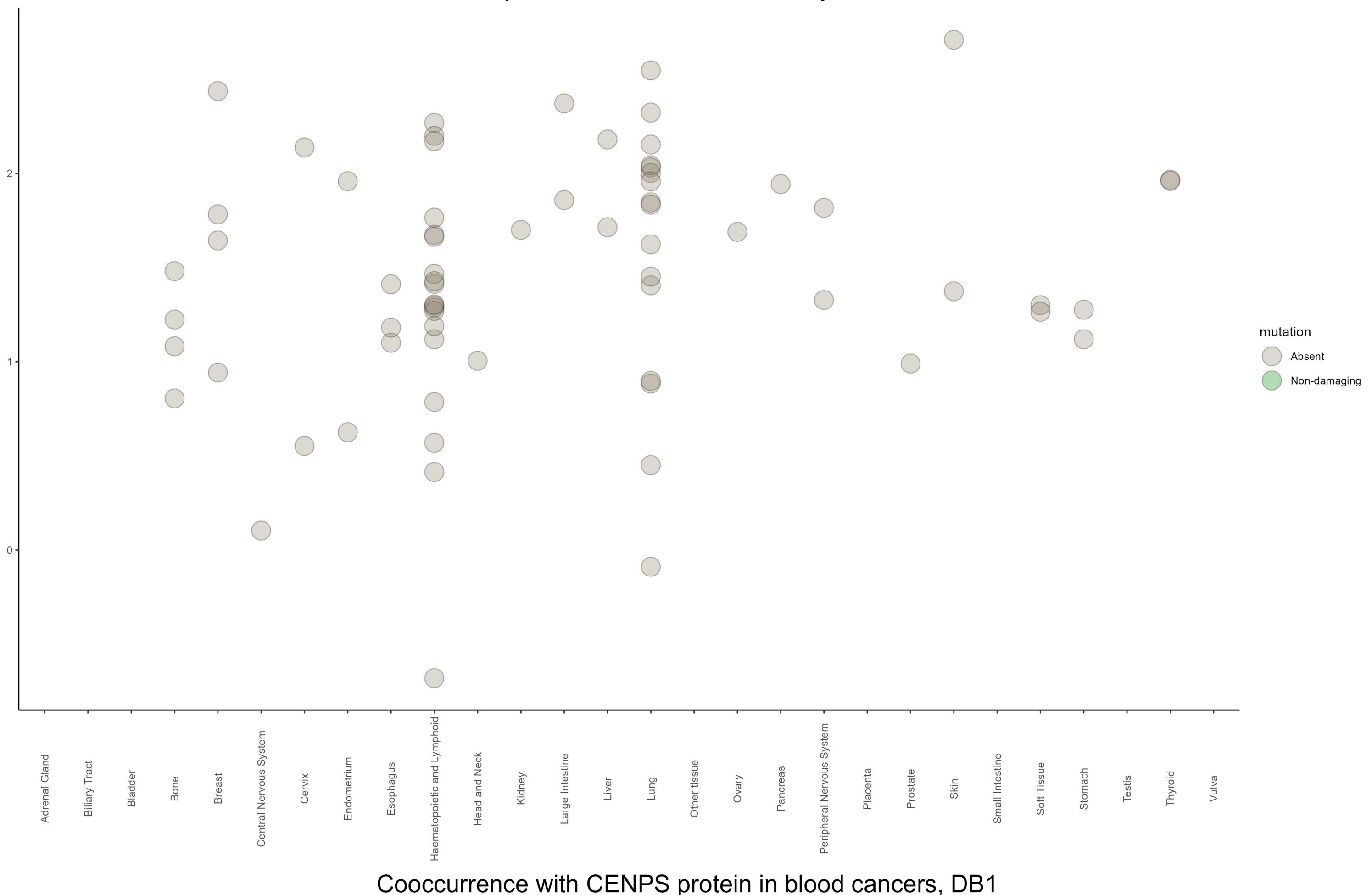
Negative cooccurrence



Positive cooccurrence

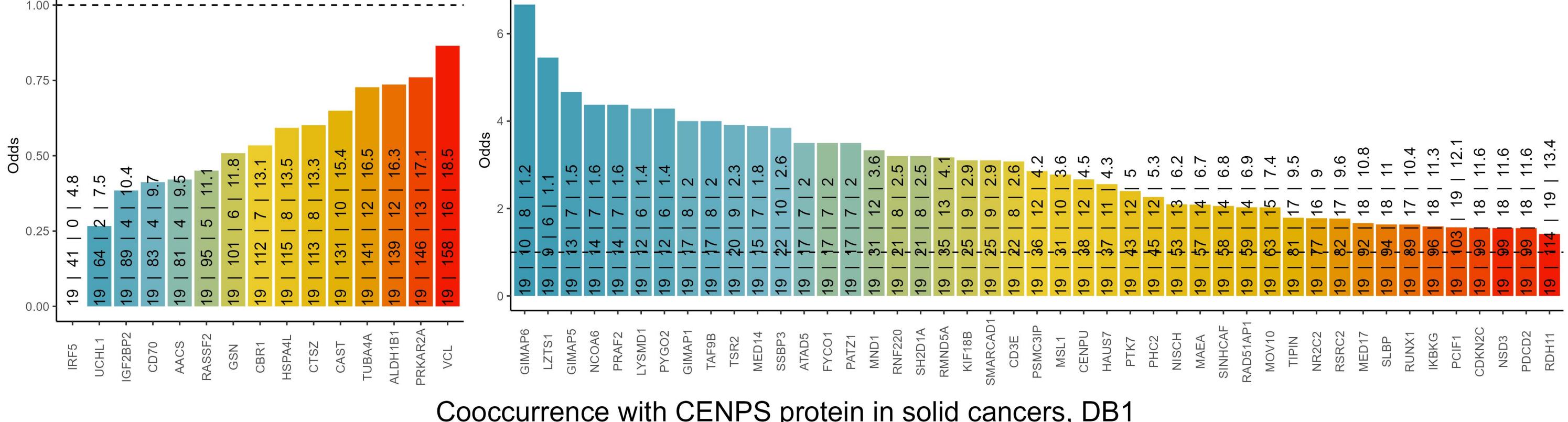


Amount of CENPS protein and mutation status by tissue, DB1



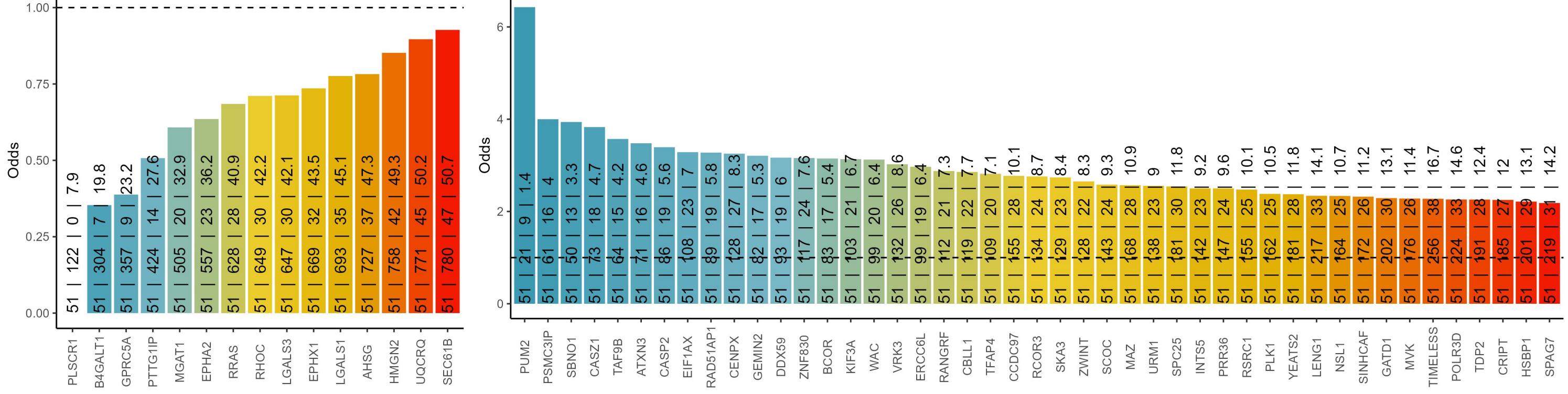
Cooccurrence with CENPS protein in blood cancers, DB1

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

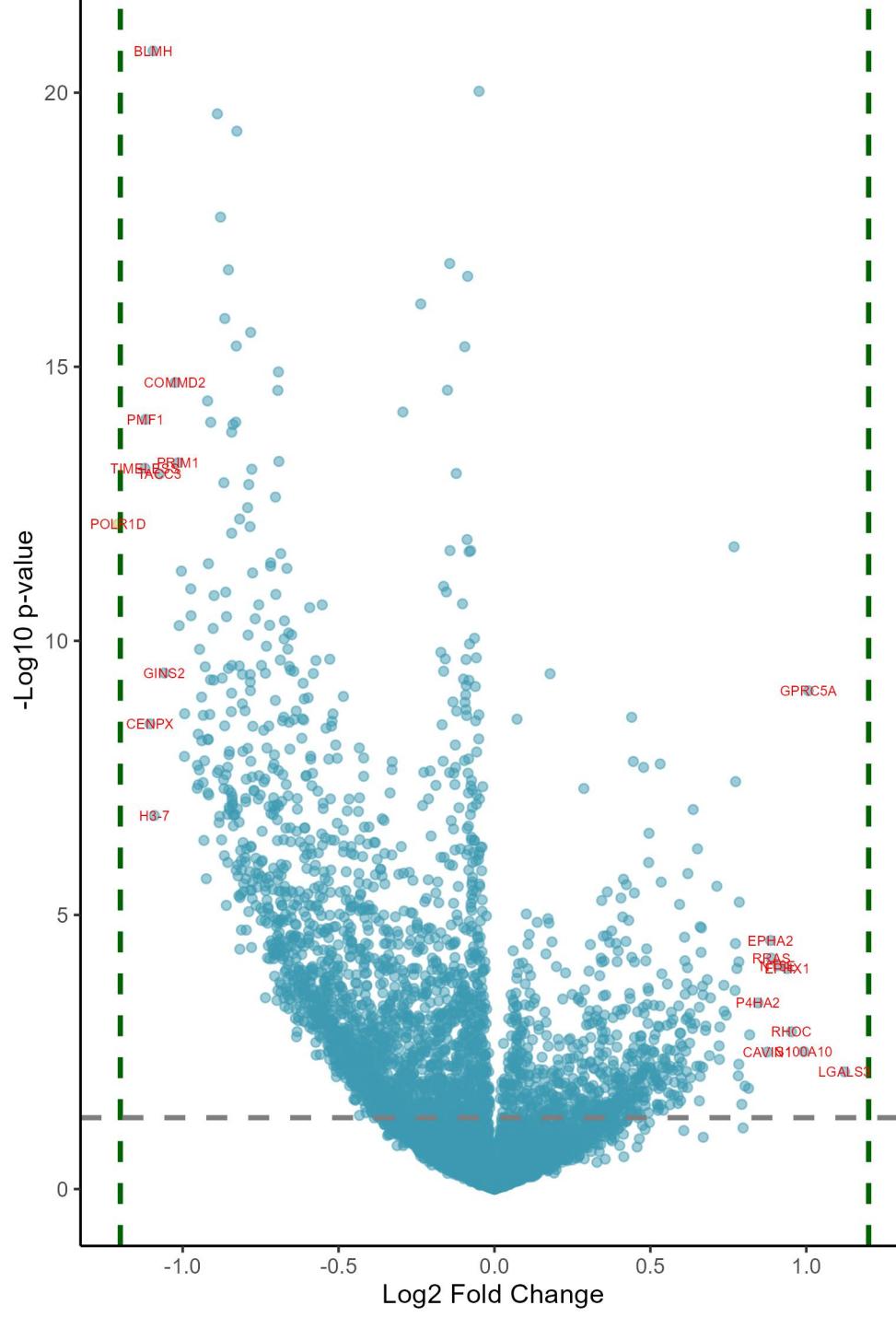


Cooccurrence with CENPS protein in solid cancers, DB1

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

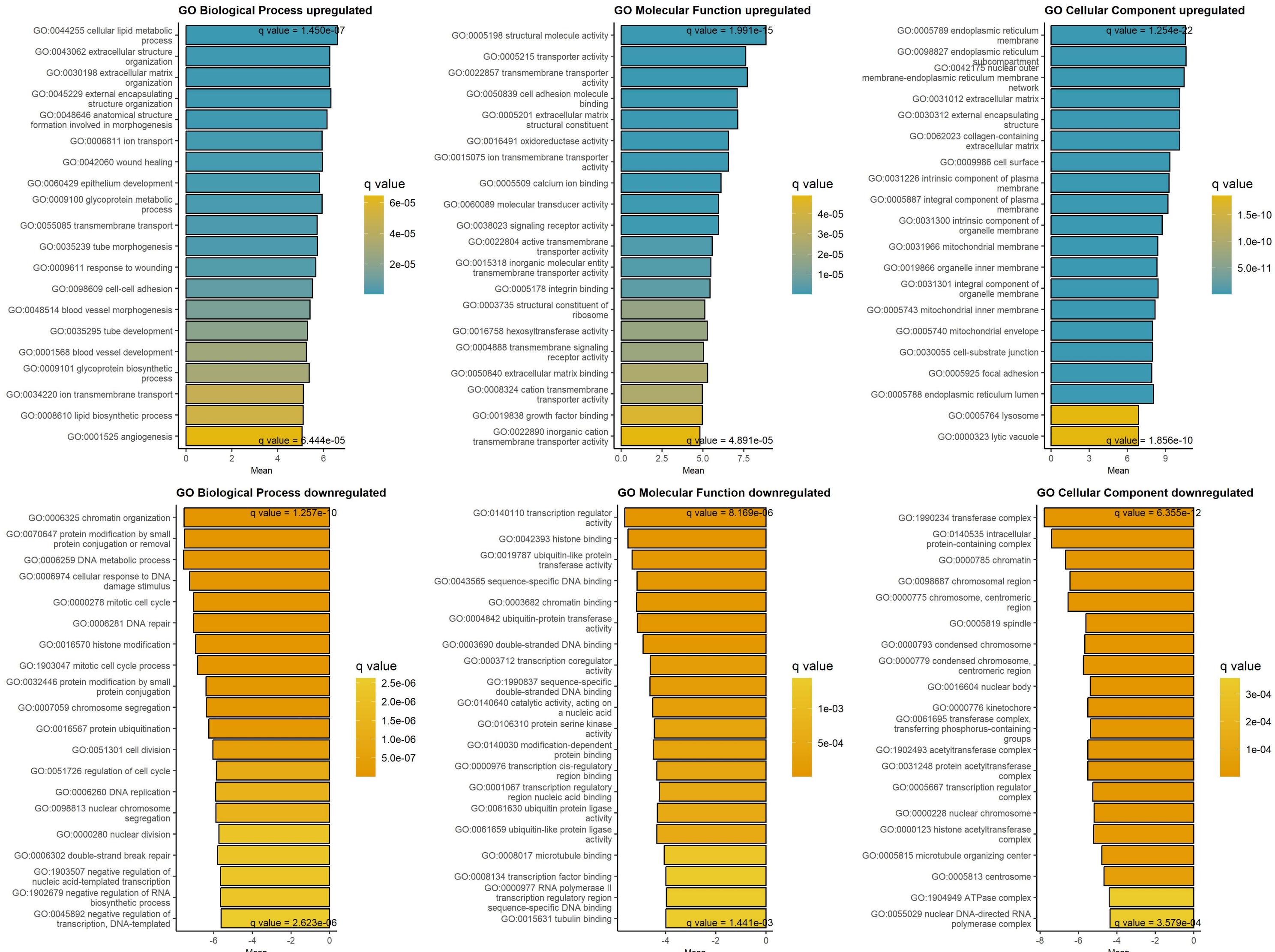


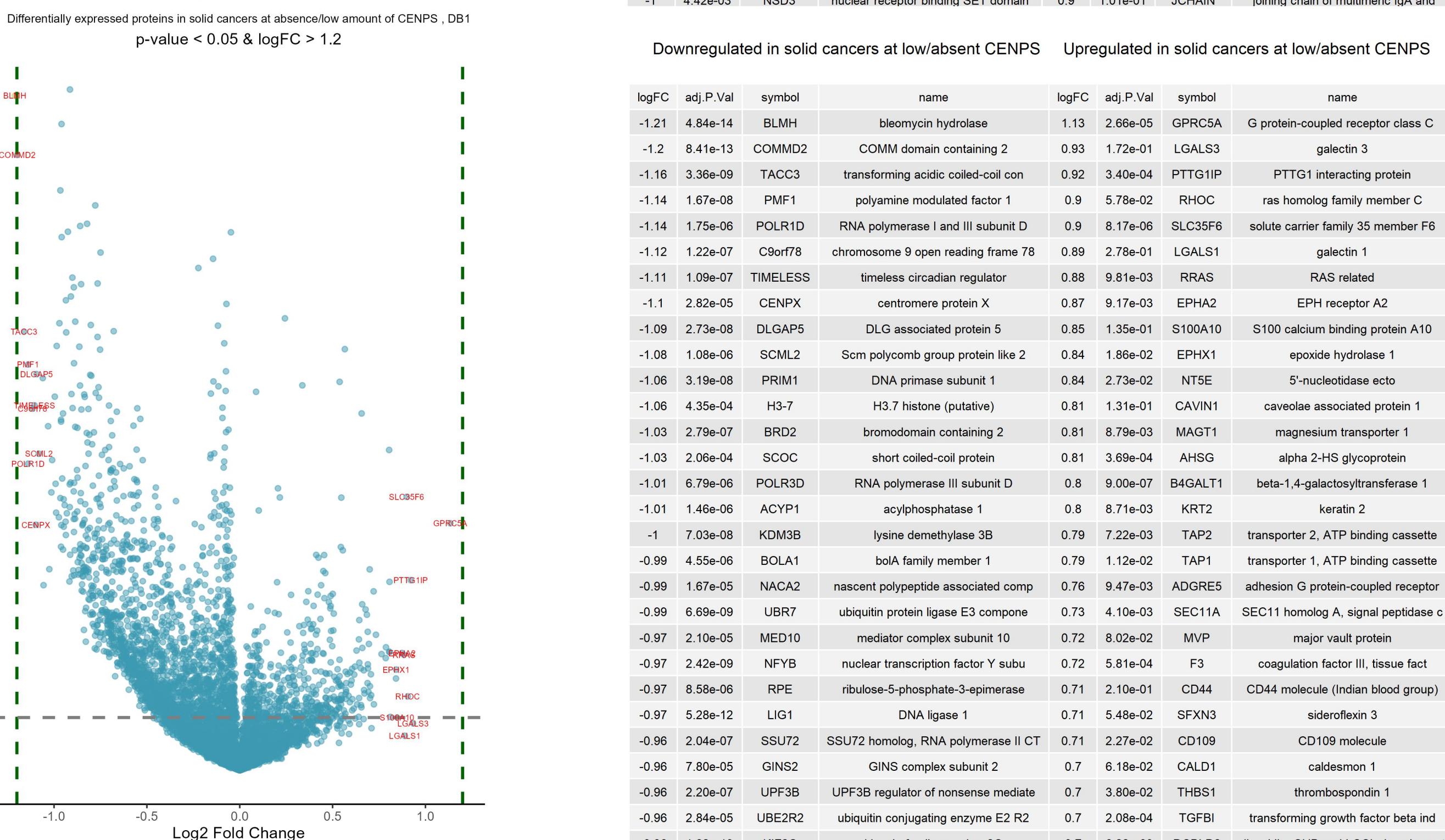
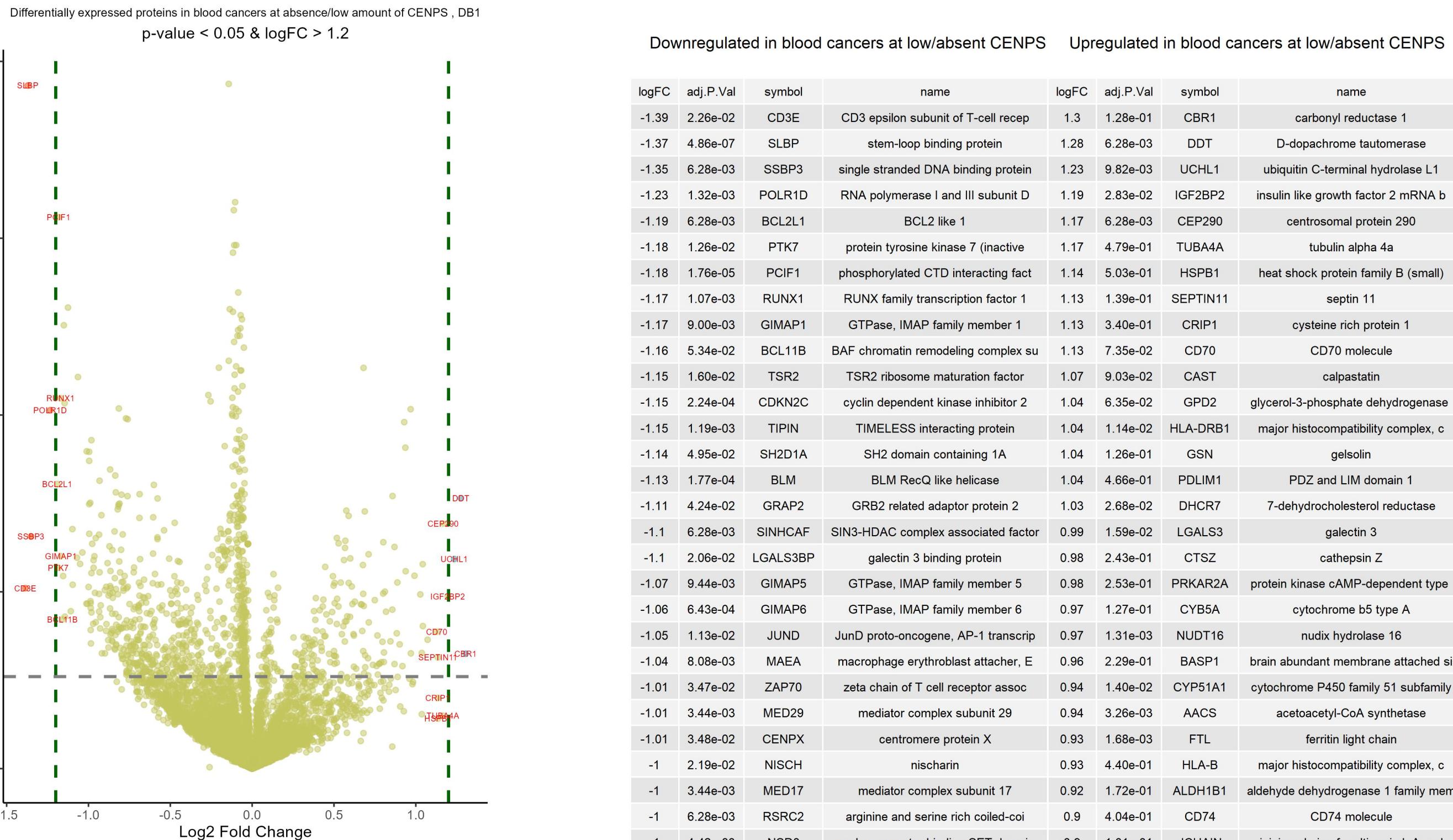
Downregulated at low/absent CENPS Upregulated at low/absent CENPS



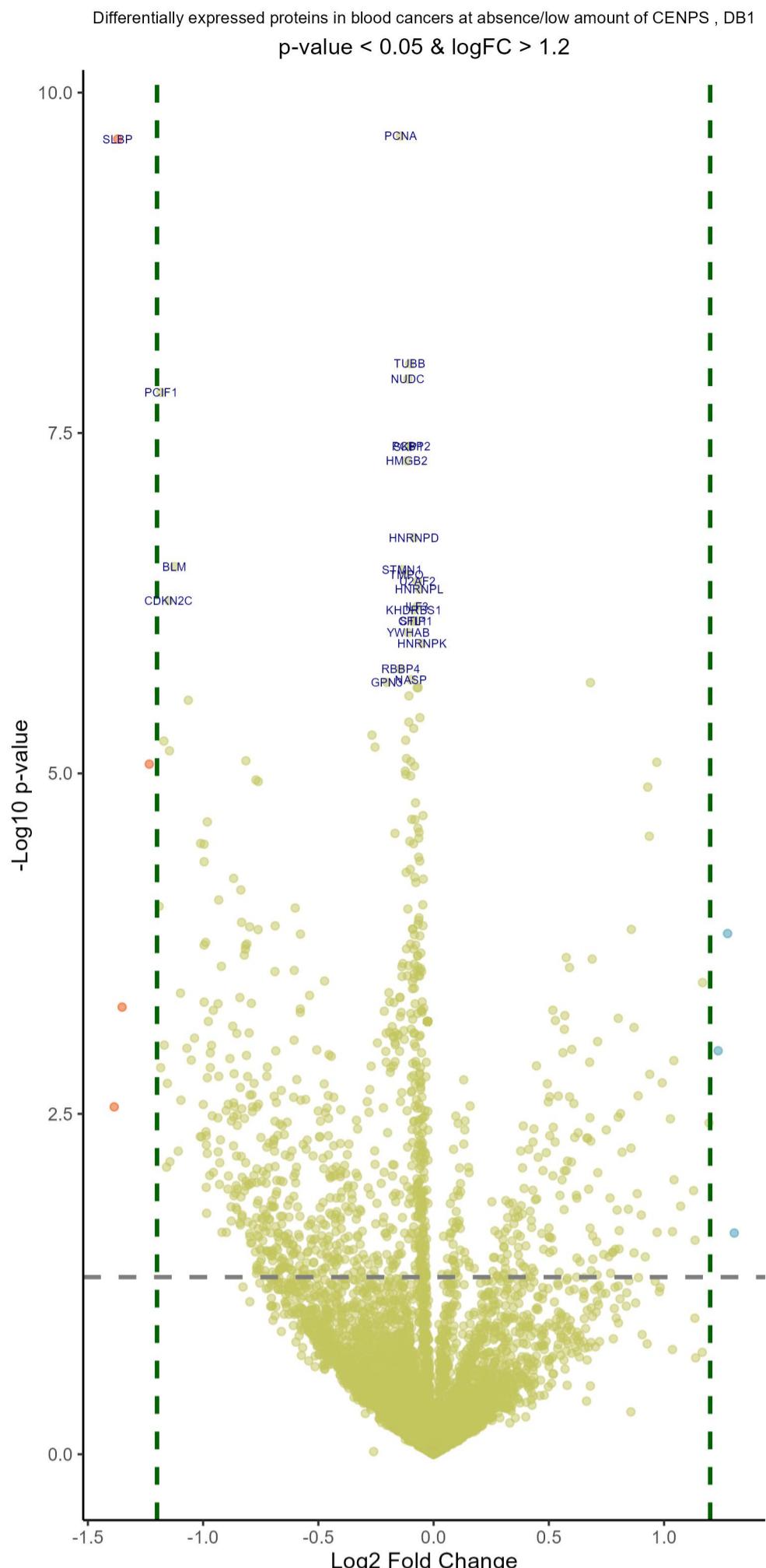
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.21	1.33e-10	POLR1D	RNA polymerase I and III subunit D	1.12	2.61e-02	LGALS3	galectin 3
-1.12	1.69e-11	TIMELESS	timeless circadian regulator	1.01	4.92e-08	GPRC5A	G protein-coupled receptor class C
-1.12	2.88e-12	PMF1	polyamine modulated factor 1	0.99	6.80e-03	RHOC	ras homolog family member C
-1.1	1.53e-07	CENPX	centromere protein X	0.95	6.80e-03	EPHX1	epoxide hydrolase 1
-1.09	5.74e-18	BLMH	bleomycin hydrolase	0.94	8.17e-04	NT5E	5'-nucleotidase ecto
-1.09	3.72e-06	H3-7	H3.7 histone (putative)	0.91	7.42e-04	RRAS	RAS related
-1.07	1.94e-11	TACC3	transforming acidic coiled-coil con	0.89	5.69e-04	EPHA2	EPH receptor A2
-1.06	2.72e-08	GINS2	GINS complex subunit 2	0.89	3.11e-04	CAVIN1	caveolae associated protein 1
-1.02	8.05e-13	COMMD2	COMM domain containing 2	0.88	1.35e-02	P4HA2	prolyl 4-hydroxylase subunit alpha
-1.02	1.39e-11	PRIM1	DNA primase subunit 1	0.85	2.62e-03	ITGA3	neutral cholesterol ester hydrolase
-1.01	5.23e-09	C9orf78	chromosome 9 open reading frame 78	0.82	7.57e-03	SFXN3	sideroflexin 3
-1	7.11e-10	BRD2	bromodomain containing 2	0.81	4.51e-02	NCEH1	integrin subunit alpha 3
-0.99	5.08e-07	BLM	BLM RecQ like helicase	0.8	4.17e-02	LGALS1	galectin 1
-0.99	1.13e-07	SPC25	SPC25 component of NDC80 kinetochor	0.8	1.62e-01	PLP2	proteolipid protein 2
-0.97	1.41e-09	ACYP1	acylphosphatase 1	0.79	7.57e-02	PTTG1IP	PTTG1 interacting protein
-0.97	3.73e-09	DLGAP5	DLG associated protein 5	0.79	8.18e-05	RAB33B	RAB33B, member RAS oncogene family
-0.95	1.49e-06	MAZ	MYC associated zinc finger protein	0.78	6.40e-04	MVP	major vault protein
-0.95	6.80e-07	GABARAPL2	GABA type A receptor associated pro	0.78	2.03e-02	CTSZ	cathepsin Z
-0.95	2.23e-07	POLR3D	RNA polymerase III subunit D	0.78	2.98e-02	CD109	CD109 molecule
-0.95	1.31e-06	CEP43	centrosomal protein 43	0.78	8.17e-04	SLC35F6	solute carrier family 35 member F6
-0.95	8.00e-07	SNRNP27	small nuclear ribonucleoprotein U4/U6	0.77	1.18e-06	AHSG	alpha 2-HS glycoprotein
-0.95	1.23e-08	RWDD1	RWD domain containing 1	0.77	3.44e-04	MAGT1	magnesium transporter 1
-0.94	6.18e-08	BRD3	bromodomain containing 3	0.77	1.73e-03	B4GALT1	beta-1,4-galactosyltransferase 1
-0.94	2.85e-07	ZCCHC3	zinc finger CCHC-type containing 3	0.77	3.12e-10	CD151	CD151 molecule (Raph blood group)
-0.93	1.21e-06	HIRIP3	HIRA interacting protein 3	0.74	3.91e-03	THBS1	thrombospondin 1
-0.93	1.17e-07	NUDT3	nudix hydrolase 3	0.74	3.46e-03	ADAM9	ADAM metallopeptidase domain 9
-0.93	9.38e-06	SLBP	stem-loop binding protein	0.74	1.45e-03	ADAM9	ADAM metallopeptidase domain 9
-0.93	5.87e-07	LENG1	leukocyte receptor cluster member 1	0.72	5.78e-03	S100A16	S100 calcium binding protein A16
-0.93	2.22e-08	BRD8	bromodomain containing 8	0.72	1.73e-02	S100A16	S100 calcium binding protein A16

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

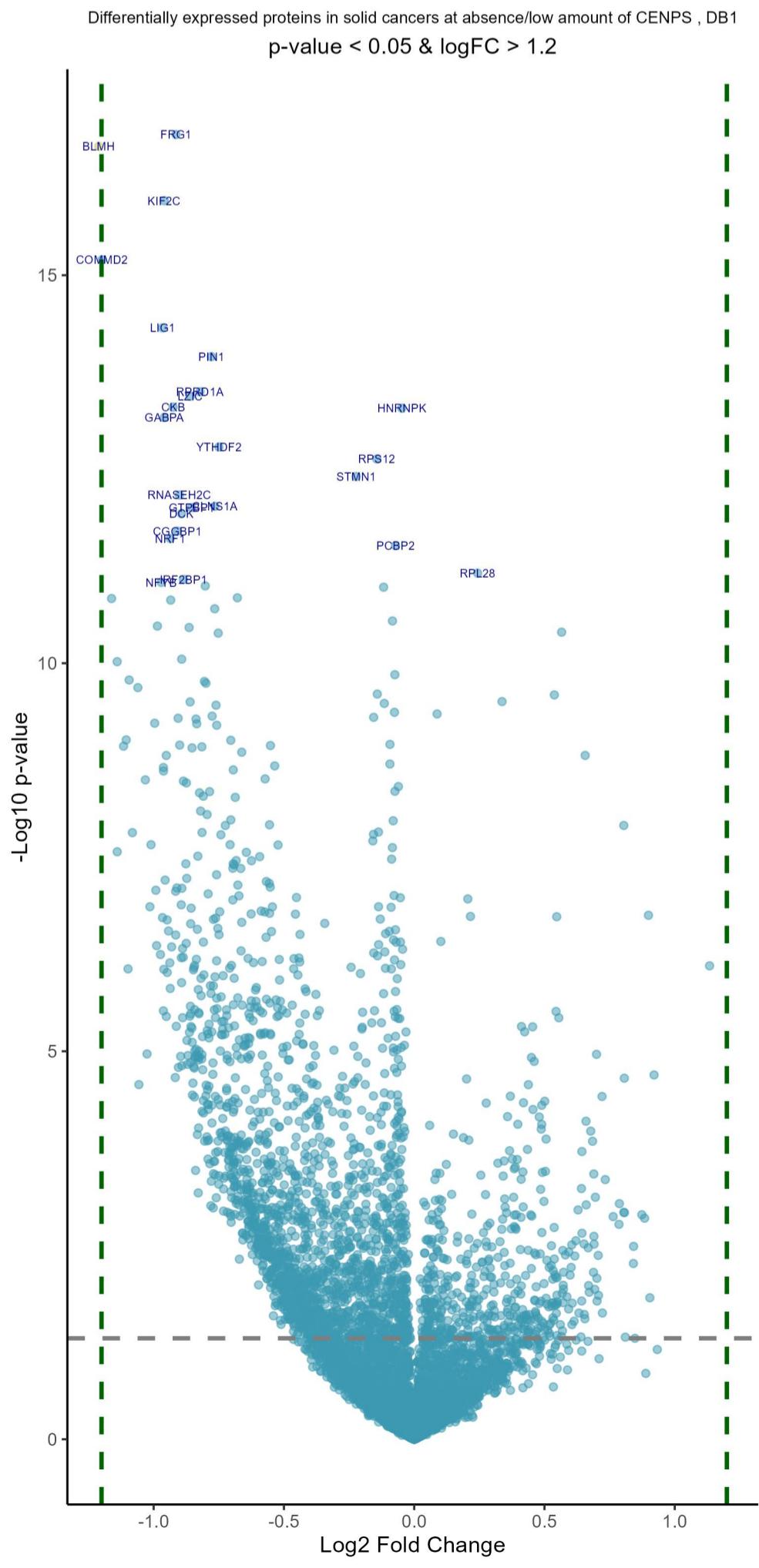




CENPS network-DB1-no Pearson r > 0.3



Sorted by p values!							
Downregulated in blood cancers at low/absent CENPS				Upregulated in blood cancers at low/absent CENPS			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.14	4.86e-07	PCNA	proliferating cell nuclear antigen	0.68	5.51e-04	IRF5	interferon regulatory factor 5
-1.37	4.86e-07	SLBP	stem-loop binding protein	0.97	1.31e-03	NUDT16	nudix hydrolase 16
-0.1	1.63e-05	TUBB	tubulin beta class I	0.93	1.68e-03	FTL	ferritin light chain
-0.11	1.69e-05	NUDC	nuclear distribution C, dynein comp	0.94	3.26e-03	AACS	acetoacetyl-CoA synthetase
-1.18	1.76e-05	PCIF1	phosphorylated CTD interacting fact	0.86	6.28e-03	TYMP	thymidine phosphorylase
-0.1	3.30e-05	PCBP2	poly(rC) binding protein 2	1.28	6.28e-03	DDT	D-dopachrome tautomerase
-0.11	3.30e-05	SKP1	S-phase kinase associated protein 1	0.58	6.28e-03	CD9	CD9 molecule
-0.12	3.74e-05	HMGB2	high mobility group box 2	0.69	6.28e-03	HOMER3	homer scaffold protein 3
-0.08	1.23e-04	HNRNPD	heterogeneous nuclear ribonucleopro	0.59	6.28e-03	MRTFA	myocardin related transcription fac
-1.13	1.77e-04	BLM	BLM RecQ like helicase	1.17	6.28e-03	CEP290	centrosomal protein 290
-0.14	1.77e-04	STMN1	stathmin 1	0.52	6.28e-03	POU2F2	POU class 2 homeobox 2
-0.12	1.78e-04	TMPO	thymopoietin	0.57	6.28e-03	PALD1	phosphatase domain containing palad
-0.07	1.84e-04	U2AF2	U2 small nuclear RNA auxiliary fact	0.8	6.28e-03	ALDH2	aldehyde dehydrogenase 2 family mem
-0.06	1.96e-04	HNRNPL	heterogeneous nuclear ribonucleopro	0.53	6.28e-03	DDAH1	dimethylarginine dimethylaminohydro
-1.15	2.24e-04	CDKN2C	cyclin dependent kinase inhibitor 2	0.87	6.91e-03	CD22	CD22 molecule
-0.07	2.32e-04	ILF3	interleukin enhancer binding factor	0.57	7.11e-03	BPHL	biphenyl hydrolase like
-0.09	2.33e-04	KHDRBS1	KH RNA binding domain containing, s	0.71	8.53e-03	KANK1	KN motif and ankyrin repeat domains
-0.08	2.53e-04	STIP1	stress induced phosphoprotein 1	0.6	9.64e-03	ABLM1	actin binding LIM protein 1
-0.09	2.53e-04	CFL1	cofilin 1	1.23	9.82e-03	UCHL1	ubiquitin C-terminal hydrolase L1
-0.11	2.93e-04	YWHAB	tyrosine 3-monooxygenase/tryptophan	0.56	1.01e-02	CCDC88B	coiled-coil domain containing 88B
-0.05	3.37e-04	HNRNPK	heterogeneous nuclear ribonucleopro	1.04	1.14e-02	HLA-DRB1	major histocompatibility complex, c
-0.14	4.95e-04	RBBP4	RB binding protein 4, chromatin rem	0.68	1.17e-02	SYVN1	synoviolin 1
-0.1	5.51e-04	NASP	nuclear autoantigenic sperm protein	0.45	1.23e-02	GLT8D1	glycosyltransferase 8 domain contai
-0.2	5.51e-04	GPN3	GPN-loop GTPase 3	0.94	1.40e-02	CYP51A1	cytochrome P450 family 51 subfamily
-0.07	5.58e-04	SF3B1	splicing factor 3b subunit 1	0.13	1.52e-02	MRPL13	mitochondrial ribosomal protein L13
-0.07	5.58e-04	NONO	non-POU domain containing octamer b	0.99	1.59e-02	LGALS3	galectin 3
-0.11	6.18e-04	TRIM28	tripartite motif containing 28	0.49	1.61e-02	ZCCHC9	zinc finger CCHC-type containing 9
-1.06	6.43e-04	GIMAP6	GTPase, IMAP family member 6	0.89	1.94e-02	HDHD3	haloacid dehalogenase like hydrolas
-0.06	8.36e-04	PRPF19	pre-mRNA processing factor 19	0.54	1.95e-02	RAB30	RAB30, member RAS oncogene family
-0.11	8.73e-04	BANF1	BAF nuclear assembly factor 1	0.5	1.96e-02	MAP3K20	mitogen-activated protein kinase ki
-0.09	9.41e-04	PTGES3	prostaglandin E synthase 3	0.59	1.96e-02	NRBF2	nuclear receptor binding factor 2
-0.27	1.02e-03	APPL2	adaptor protein, phosphotyrosine in	0.5	2.11e-02	SLC27A2	solute carrier family 27 member 2
-0.12	1.07e-03	ERH	ERH mRNA splicing and mitosis facto	0.61	2.17e-02	GLDC	glycine decarboxylase
-1.17	1.07e-03	RUNX1	RUNX family transcription factor 1	0.16	2.24e-02	PNP	purine nucleoside phosphorylase
-0.25	1.15e-03	SCYL2	SCY1 like pseudokinase 2	0.81	2.49e-02	MS4A1	membrane spanning 4-domains A1
-1.15	1.19e-03	TIPIN	TIMELESS interacting protein	0.1	2.59e-02	AFG3L2	AFG3 like matrix AAA peptidase subu
-0.12	1.31e-03	PPIH	peptidylprolyl isomerase H	0.8	2.62e-02	CTPS2	CTP synthase 2
-0.81	1.31e-03	ASF1B	anti-silencing function 1B histone	0.68	2.65e-02	GOLIM4	golgi integral membrane protein 4
0.1	1.31e-03	DSME1	proto-oncogene activator subunit 1	1.03	2.68e-02	DHCR7	7-dihydrocholesterol reductase

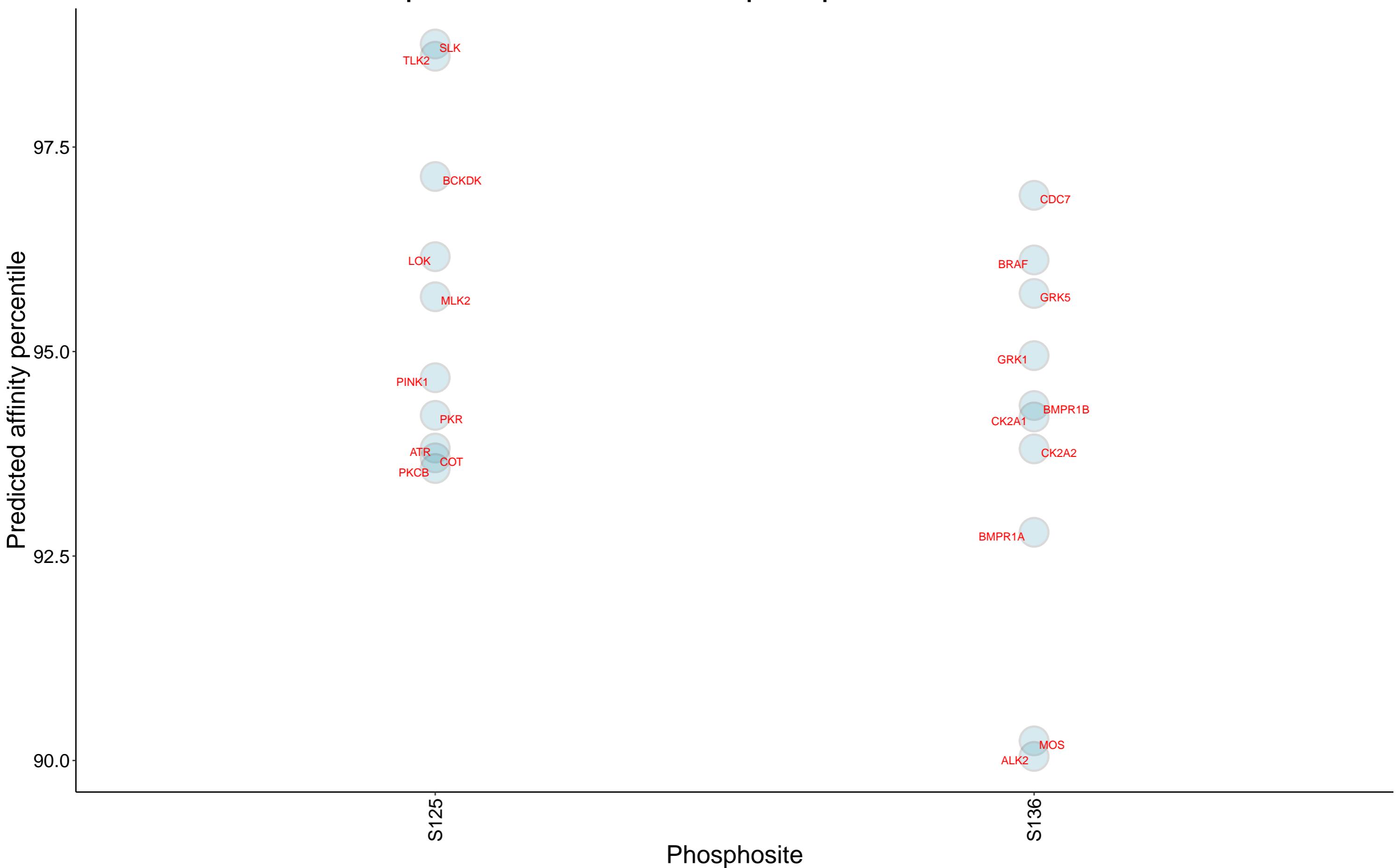


Sorted by p values!							
Downregulated in solid cancers at low/absent CENPS				Upregulated in solid cancers at low/absent CENPS			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
0.91	4.84e-14	FRG1	FSHD region gene 1	0.24	1.99e-09	RPL28	ribosomal protein L28
1.21	4.84e-14	BLMH	bleomycin hydrolase	0.57	7.56e-09	ABCD1	ATP binding cassette subfamily D member 1
0.96	1.82e-13	KIF2C	kinesin family member 2C	0.54	3.78e-08	PLSCR1	phospholipid scramblase 1
-1.2	8.41e-13	COMM2	COMM domain containing 2	0.34	4.46e-08	SEC61B	SEC61 translocon subunit beta
0.97	5.28e-12	LIG1	DNA ligase 1	0.09	5.87e-08	RPL34	ribosomal protein L34
0.78	1.06e-11	PIN1	peptidylprolyl cis/trans isomerase, endoplasmic reticulum-associated	0.66	1.49e-07	ALDH3B1	aldehyde dehydrogenase 3 family member 1
0.82	2.65e-11	RPRD1A	regulation of nuclear pre-mRNA domain	0.8	9.00e-07	B4GALT1	beta-1,4-galactosyltransferase 1
0.86	2.67e-11	LZIC	leucine zipper and CTNNBIP1 domain	0.21	5.57e-06	PICALM	phosphatidylinositol binding clathrin-associated protein
0.93	3.13e-11	CKB	creatine kinase B	0.9	8.17e-06	SLC35F6	solute carrier family 35 member F6
0.05	3.13e-11	HNRNPK	heterogeneous nuclear ribonucleoprotein K	0.22	8.39e-06	FAF2	Fas associated factor family member 2
0.96	3.77e-11	GABPA	GA binding protein transcription factor alpha	0.55	8.41e-06	MICAL2	microtubule associated monooxygenase 2
0.75	8.36e-11	YTHDF2	YTH N6-methyladenosine RNA binding	0.1	1.53e-05	RAB1A	RAB1A, member RAS oncogene family
0.14	1.11e-10	RPS12	ribosomal protein S12	1.13	2.66e-05	GPRC5A	G protein-coupled receptor class C member 5
0.22	1.74e-10	STMN1	stathmin 1	0.54	7.84e-05	CLCN7	chloride voltage-gated channel 7
-0.9	2.82e-10	RNASEH2C	ribonuclease H2 subunit C	0.56	8.83e-05	SCEL	scilillin
0.77	3.65e-10	CLNS1A	chloride nucleotide-sensitive channel	0.41	1.09e-04	COL4A1	collagen type IV alpha 1 chain
0.85	3.65e-10	GTPBP1	GTP binding protein 1	0.45	1.10e-04	COL7A1	collagen type VII alpha 1 chain
0.89	4.13e-10	DCK	deoxycytidine kinase	0.42	1.24e-04	ABCC3	ATP binding cassette subfamily C member 3
0.91	6.61e-10	CGGBP1	CGG triplet repeat binding protein	0.7	2.08e-04	TGFBI	transforming growth factor beta induced
0.94	7.82e-10	NRF1	nuclear respiratory factor 1	0.45	2.19e-04	UQCRC2	ubiquinol-cytochrome c reductase complex II
0.07	9.20e-10	PCBP2	poly(rC) binding protein 2	0.46	2.39e-04	XYLT2	xylosyltransferase 2
0.89	2.30e-09	IRF2BP1	interferon regulatory factor 2 bind	0.92	3.40e-04	PTTG1IP	PTTG1 interacting protein
0.97	2.42e-09	NFYB	nuclear transcription factor Y subunit B	0.81	3.69e-04	AHSG	alpha 2-HS glycoprotein
-0.8	2.58e-09	NTMT1	N-terminal Xaa-Pro-Lys N-methyltransferase	0.2	3.75e-04	RPL13A	ribosomal protein L13a
0.12	2.58e-09	PCNA	proliferating cell nuclear antigen	0.44	4.35e-04	SLC39A11	solute carrier family 39 member 11
0.68	3.36e-09	UBQLN2	ubiquilin 2	0.37	5.79e-04	RAB5A	RAB5A, member RAS oncogene family
1.16	3.36e-09	TACC3	transforming acidic coiled-coil con	0.72	5.81e-04	F3	coagulation factor III, tissue factor
0.93	3.40e-09	DERPC	DERPC proline and glycine rich nucleic acid binding protein	0.5	6.53e-04	CAV2	caveolin 2
0.77	4.26e-09	ENSA	endosulfine alpha	0.42	6.75e-04	PLA2G15	phospholipase A2 group XV
0.08	5.93e-09	SKP1	S-phase kinase associated protein 1	0.28	6.79e-04	HMGN1	high mobility group nucleosome binding protein 1
0.99	6.69e-09	UBR7	ubiquitin protein ligase E3 component	0.49	7.14e-04	HKDC1	hexokinase domain containing 1
0.86	6.77e-09	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.46	7.89e-04	COL5A1	collagen type V alpha 1 chain
0.75	7.56e-09	MED30	mediator complex subunit 30	0.36	9.38e-04	ATP11A	ATPase phospholipid transporting 11A
0.89	1.59e-08	NHLRC2	NHL repeat containing 2	0.48	9.44e-04	LAMA3	laminin subunit alpha 3
1.14	1.67e-08	PMF1	polyamine modulated factor 1	0.66	1.05e-03	UPP1	uridine phosphorylase 1
0.07	2.39e-08	RUVBL1	RuvB like AAA ATPase 1	0.4	1.13e-03	TMEM167A	transmembrane protein 167A
1.09	2.73e-08	DLGAP5	DLG associated protein 5	0.49	1.14e-03	HMGN2	high mobility group nucleosomal binding protein 2
0.81	2.78e-08	CFDP1	craniofacial development protein 1	0.06	1.16e-03	CLTC	clathrin heavy chain
0.8	2.82e-08	HNRNPL	heterogeneous nuclear ribonucleoprotein L	0.49	1.27e-03	LCN2	lipocalin 2

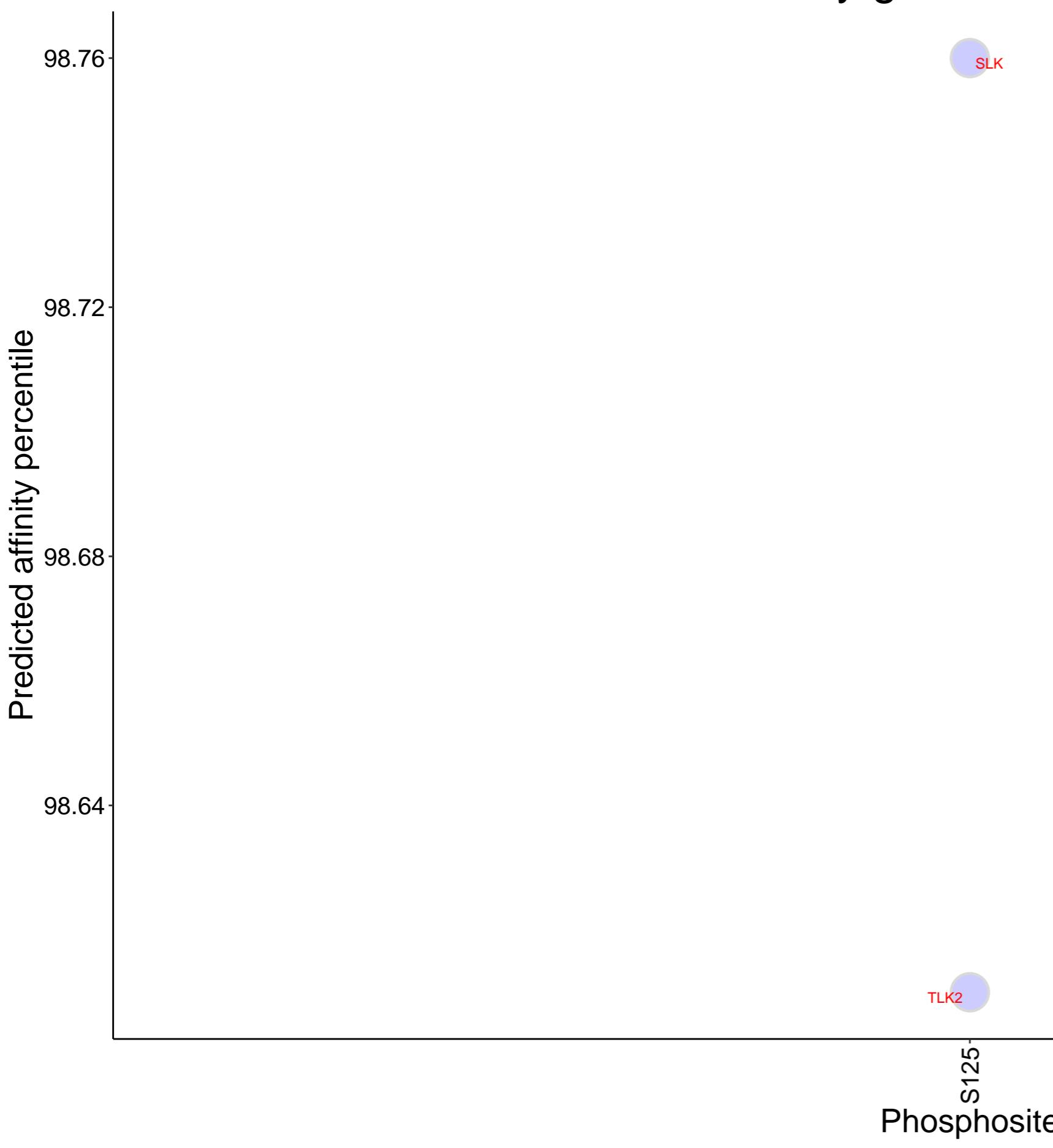
Insufficient number of paired observations in DB1 for CENPS

Insufficient number of paired observations in DB1 for CENPS

Top 10 kinases for each phosphosite in CENPS



Kinases with affinity greater than 98.5% to CENPS



No sufficient paired observations in DB1 for CENPS