

# CLSPN

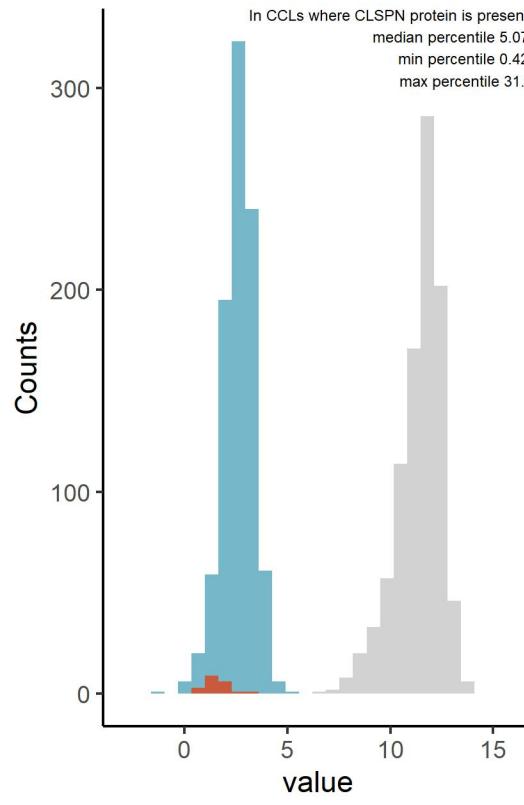
Protein name: CLSPN ; UNIPROT: Q9HAW4 ; Gene name: claspin

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

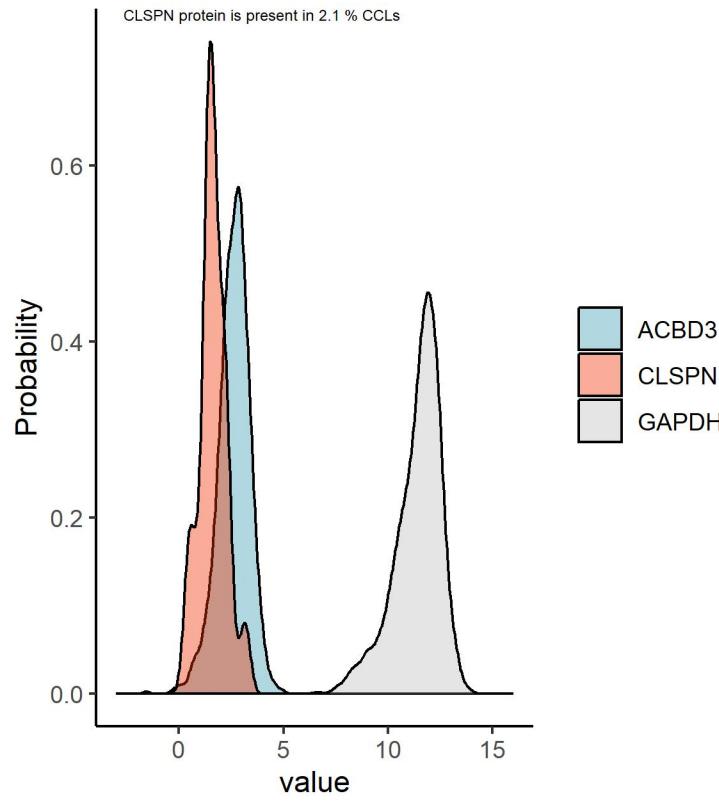
## Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

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



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



Top negative correlations of CLSPN protein, DB1

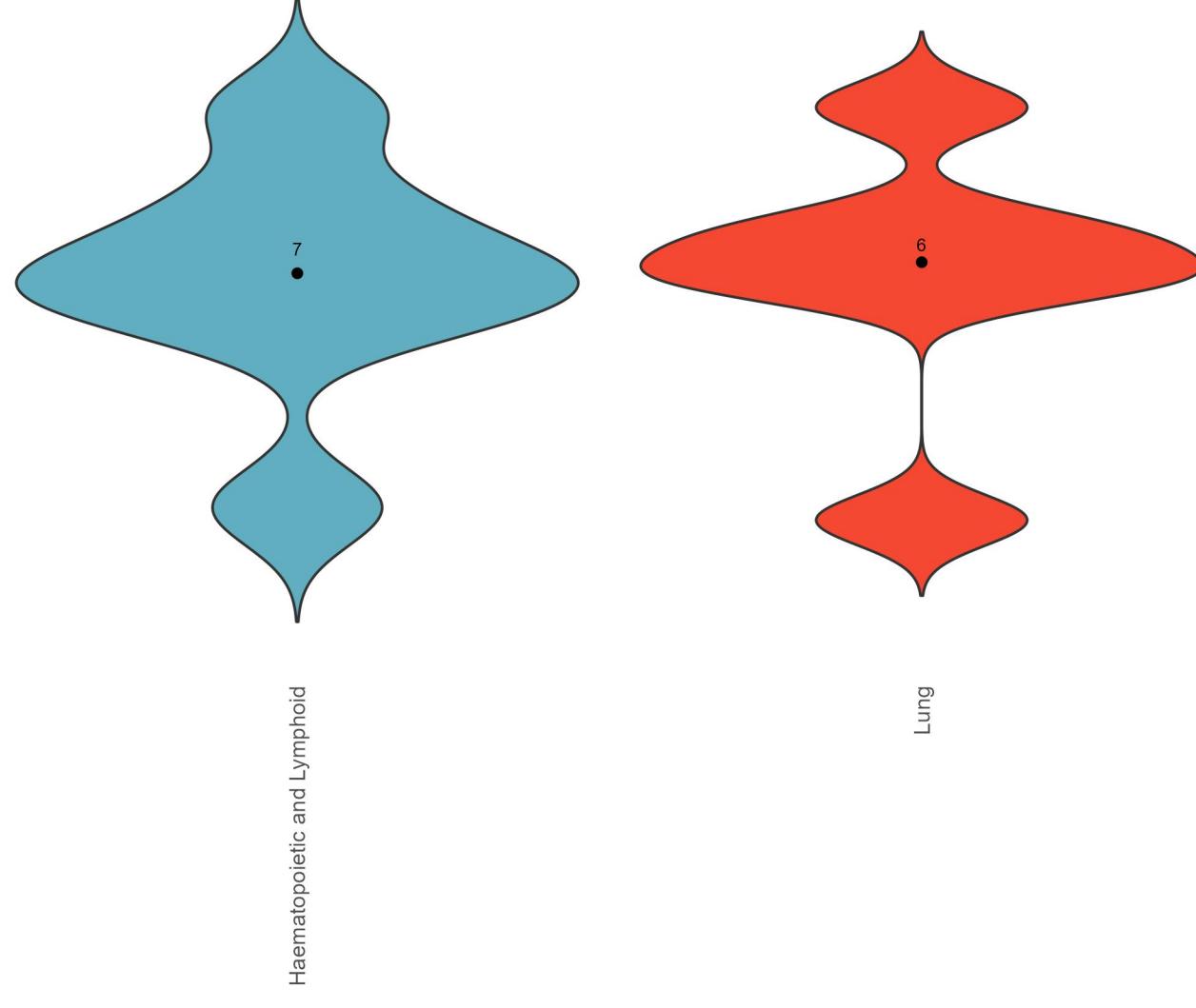
Pearson correlation coefficients

Top positive correlations of CLSPN protein, DB1

Pearson correlation coefficients

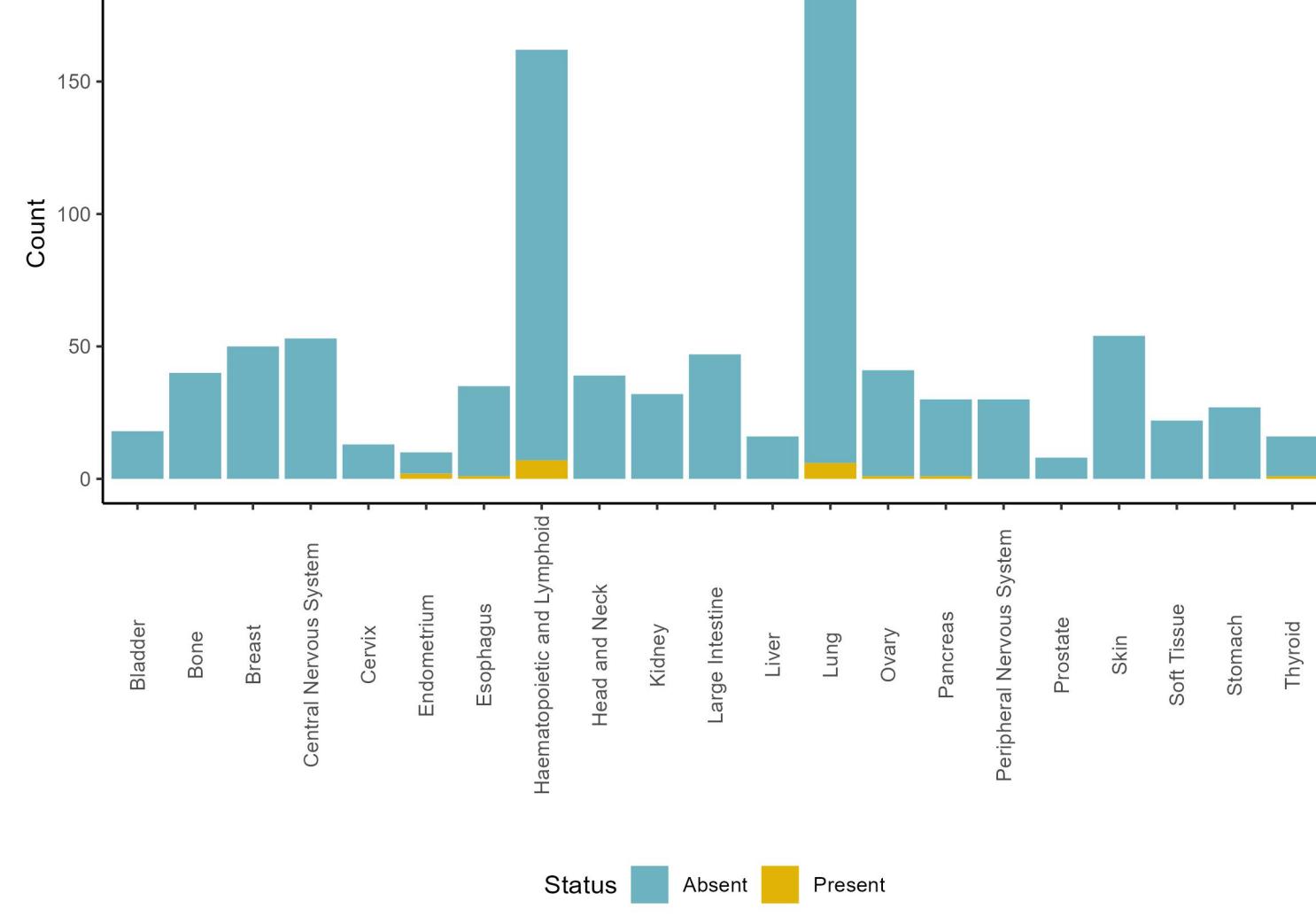
Amount of CLSPN protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 5.310e-01



Present and absent CLSPN protein counts by tissue, DB1

Chi square p value is 3.591e-02

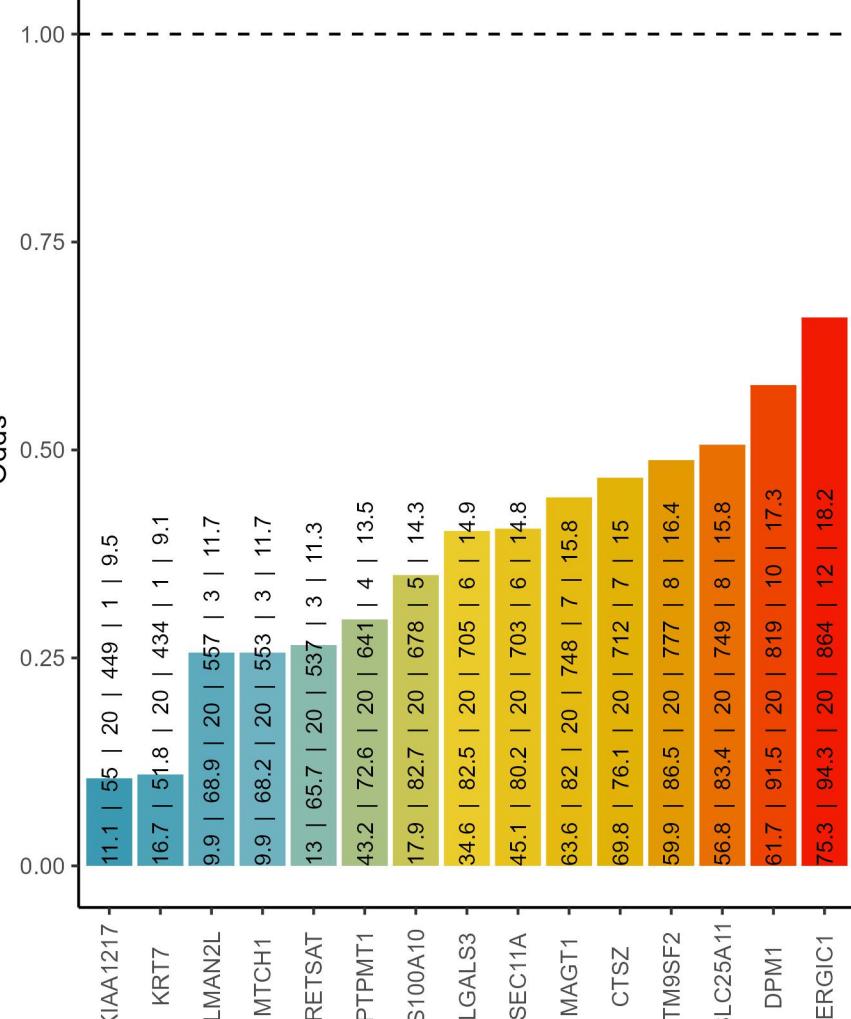


Cooccurrence with CLSPN protein, DB1

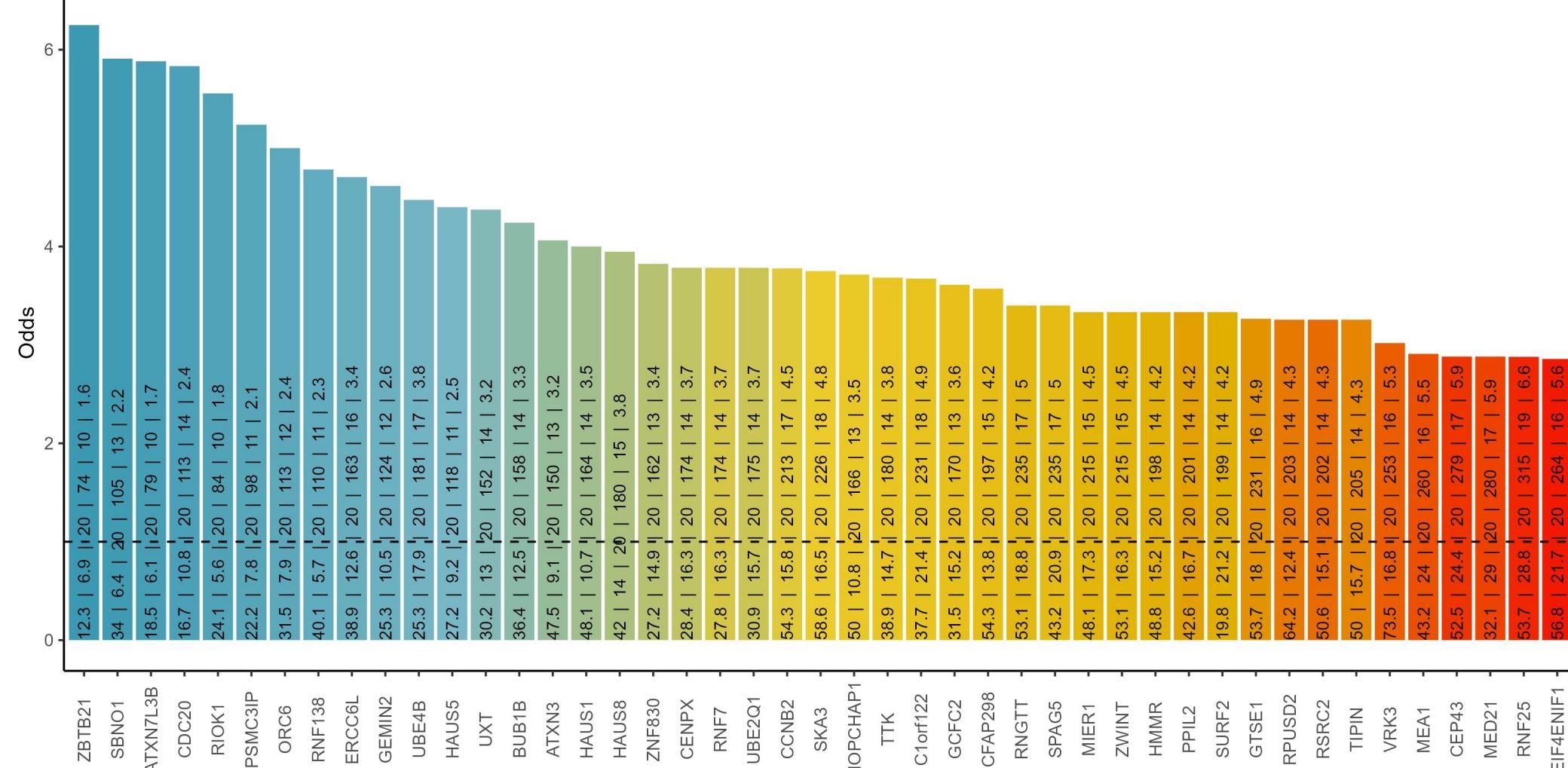
% of CLSPN in blood cancers: 4.3 ; % of CLSPN in solid cancers: 1.7

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

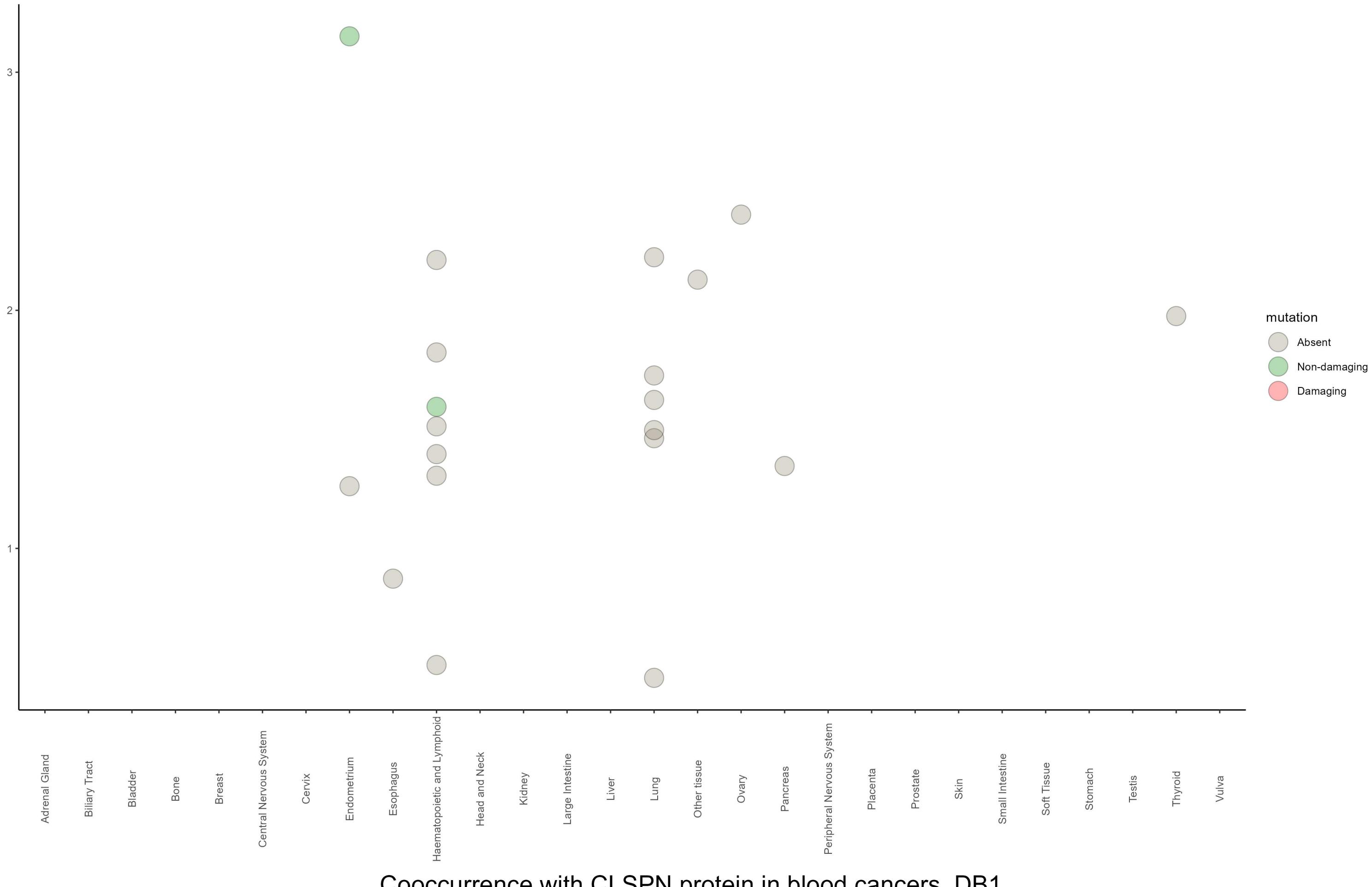
Negative cooccurrence



Positive cooccurrence

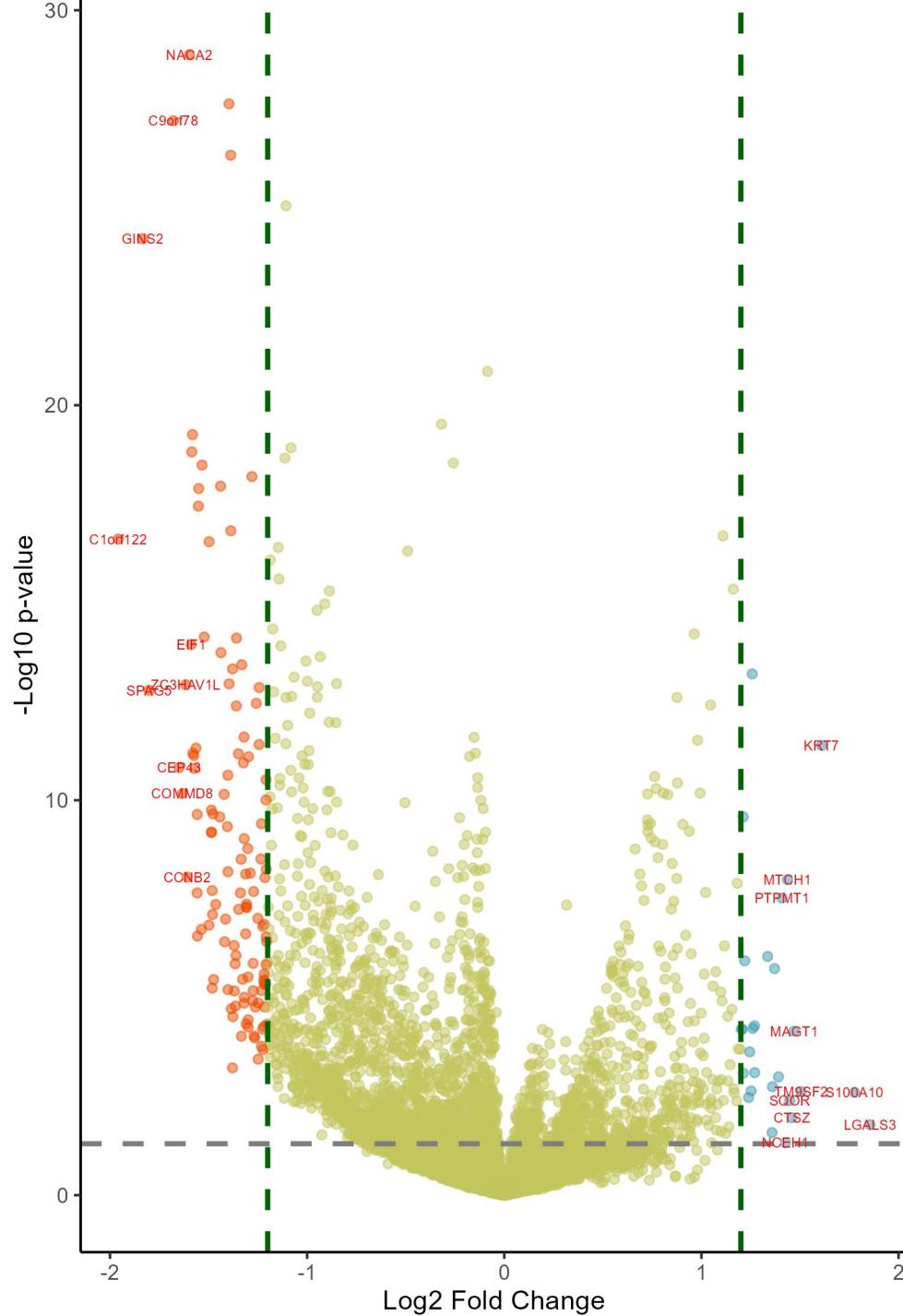


# Amount of CLSPN protein and mutation status by tissue, DB1



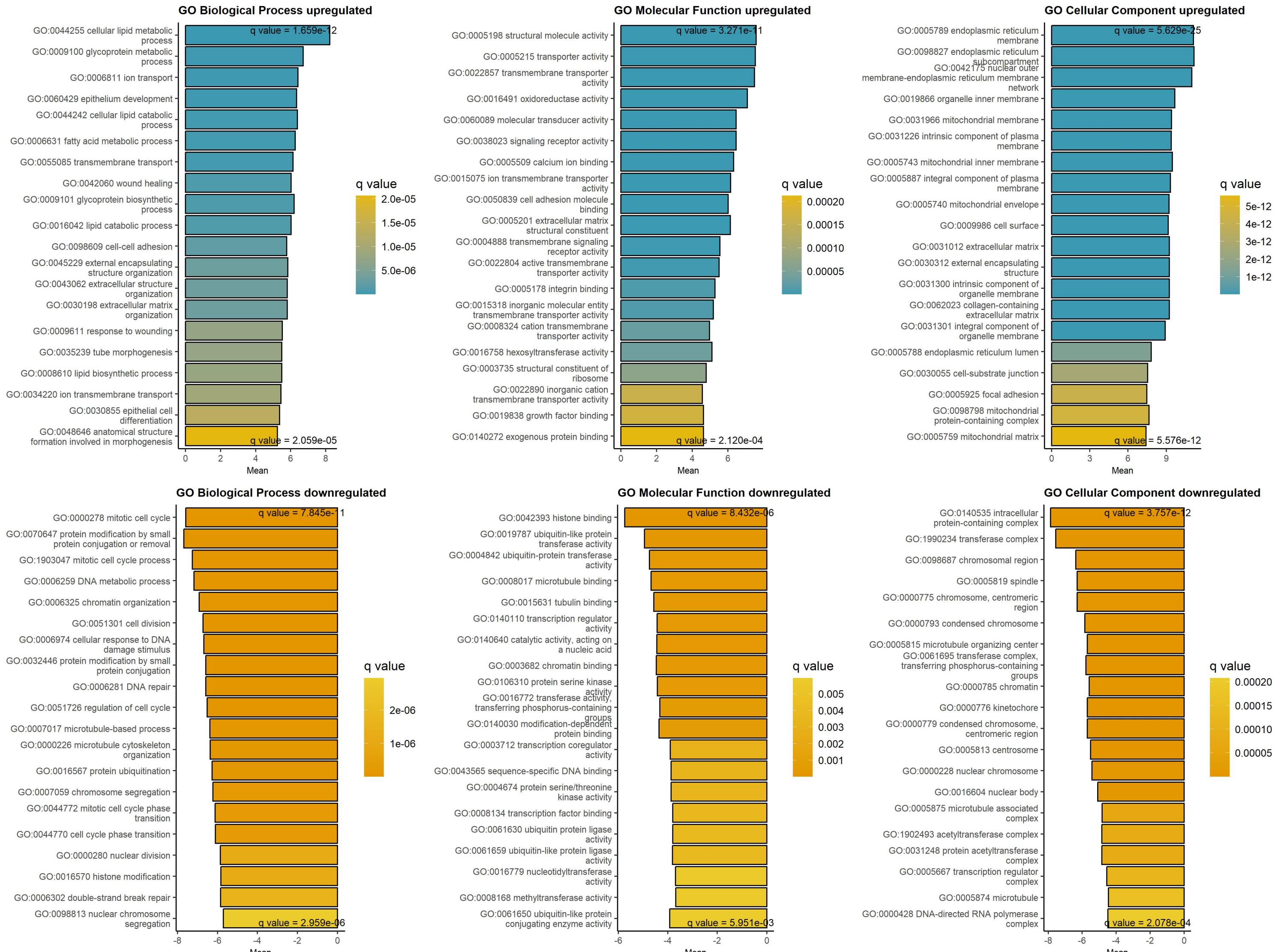
## Downregulated at low/absent CLSPN

## Upregulated at low/absent CLSPN



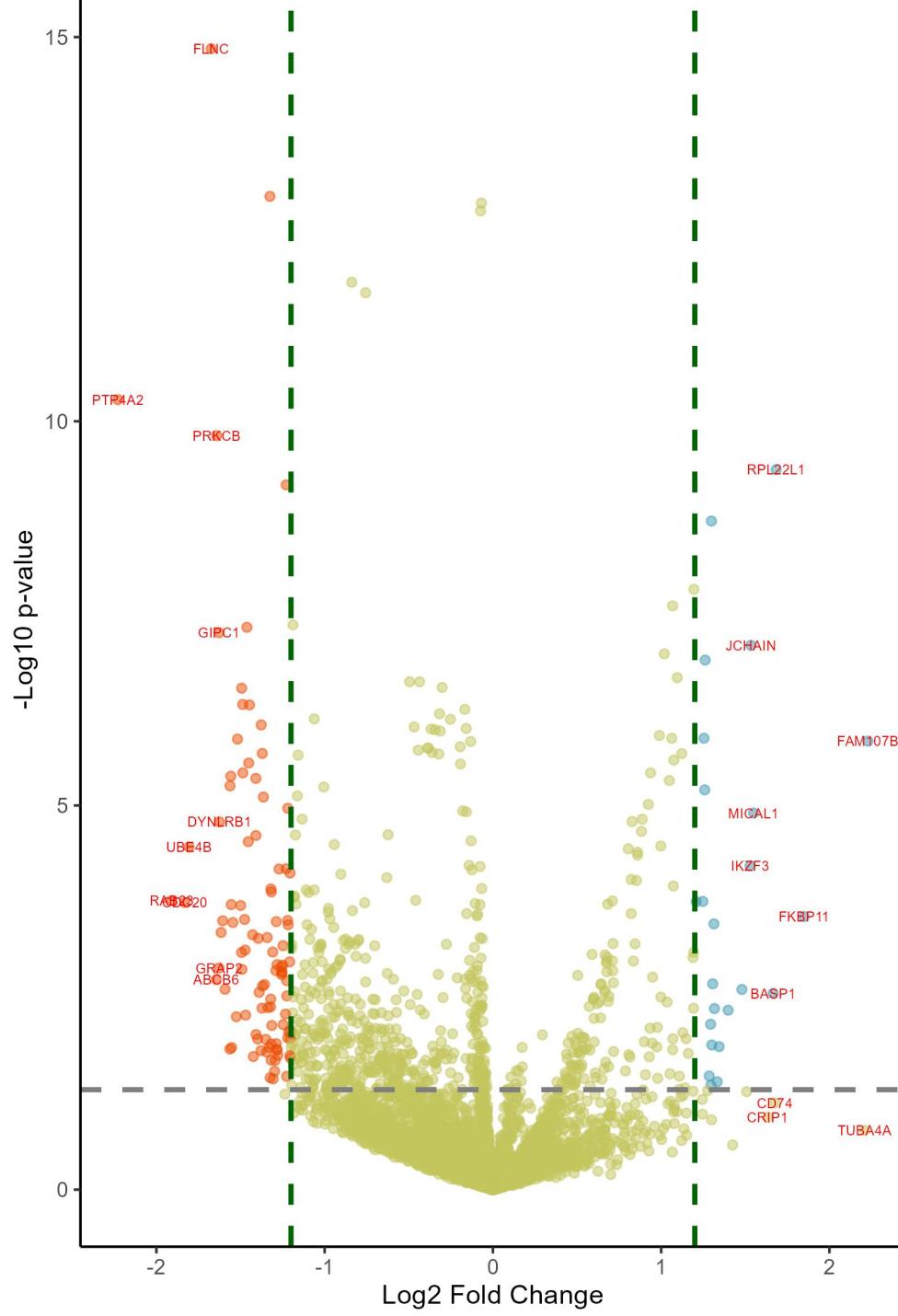
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.96	7.40e-15	C1orf122	chromosome 1 open reading frame 122	1.86	5.65e-02	LGALS3	galectin 3
-1.83	5.77e-22	GINS2	GINS complex subunit 2	1.78	1.31e-02	S100A10	S100 calcium binding protein A10
-1.8	2.15e-11	SPAG5	sperm associated antigen 5	1.61	3.91e-10	KRT7	keratin 7
-1.68	1.04e-24	C9orf78	chromosome 9 open reading frame 78	1.51	1.26e-02	TM9SF2	transmembrane 9 superfamily member
-1.65	1.20e-09	CEP43	centrosomal protein 43	1.47	6.75e-04	MAGT1	magnesium transporter 1
-1.63	4.41e-09	COMM8	COMM domain containing 8	1.46	4.11e-02	CTSZ	cathepsin Z
-1.62	1.66e-11	ZC3HAV1L	zinc finger CCCH-type containing, a	1.45	1.89e-02	SQOR	sulfide quinone oxidoreductase
-1.61	3.27e-07	CCNB2	cyclin B2	1.44	3.69e-07	MTCH1	mitochondrial carrier 1
-1.6	4.42e-26	NACA2	nascent polypeptide associated comp	1.43	1.25e-01	NCEH1	neutral cholesterol ester hydrolase
-1.59	2.12e-12	EIF1	eukaryotic translation initiation f	1.41	9.73e-07	PTPMT1	protein tyrosine phosphatase mitoch
-1.59	8.40e-17	TACC3	transforming acidic coiled-coil con	1.39	6.25e-03	S100A16	S100 calcium binding protein A16
-1.58	3.69e-17	PCLAF	PCNA clamp associated factor	1.37	3.28e-05	SEC11A	SEC11 homolog A, signal peptidase c
-1.58	5.81e-10	POLR3D	RNA polymerase III subunit D	1.36	9.99e-03	SCAMP2	secretory carrier membrane protein
-1.57	6.48e-10	KNSTRN	kinetochore localized astrin (SPAG5)	1.36	8.00e-02	ITGA3	integrin subunit alpha 3
-1.57	1.24e-09	RNF25	ring finger protein 25	1.34	1.82e-05	MMP14	matrix metallopeptidase 14
-1.56	4.51e-10	CDC34	cell division cycle 34, ubiquitin c	1.27	5.05e-03	RRAS	RAS related
-1.56	7.41e-07	SKA3	spindle and kinetochore associated	1.27	5.23e-04	AP2S1	adaptor related protein complex 2 s
-1.56	1.28e-08	C2orf49	chromosome 2 open reading frame 49	1.26	5.92e-04	DAD1	defender against cell death 1
-1.56	6.73e-06	ERCC6L	ERCC excision repair 6 like, spindl	1.26	9.83e-12	LMAN2L	lectin, mannose binding 2 like
-1.55	1.26e-15	YRDC	yrdC N6-threonylcarbamoyltransferas	1.25	1.22e-02	ERGIC1	endoplasmic reticulum-golgi interme
-1.55	4.76e-16	POMP	proteasome maturation protein	1.24	1.87e-03	GPAA1	glycosylphosphatidylinositol anchor
-1.54	4.80e-06	UBE4B	ubiquitination factor E4B	1.24	1.66e-02	EGFR	epidermal growth factor receptor
-1.53	1.45e-16	DLGAP5	DLG associated protein 5	1.22	2.28e-05	FNDC3B	fibronectin type III domain contain
-1.52	1.44e-12	RNF181	ring finger protein 181	1.21	5.22e-03	KRT2	keratin 2
-1.5	3.87e-06	GTSE1	G2 and S-phase expressed 1	1.21	1.46e-08	RETSAT	retinol saturase
-1.5	8.25e-15	TXLNG	taxilin gamma	1.21	6.16e-04	DPM1	dolichyl-phosphate mannosyltransfer
-1.49	3.20e-08	POLR1D	RNA polymerase I and III subunit D	1.2	6.10e-04	LMF2	lipase maturation factor 2
-1.49	1.01e-08	CKS1B	CDC28 protein kinase regulatory sub	1.2	1.64e-03	DHTKD1	dehydrogenase E1 and transketolase
-1.48	3.24e-08	PDRG1	p53 and DNA damage regulated 1	1.19	1.60e-03	SLC25A11	solute carrier family 25 member 11

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

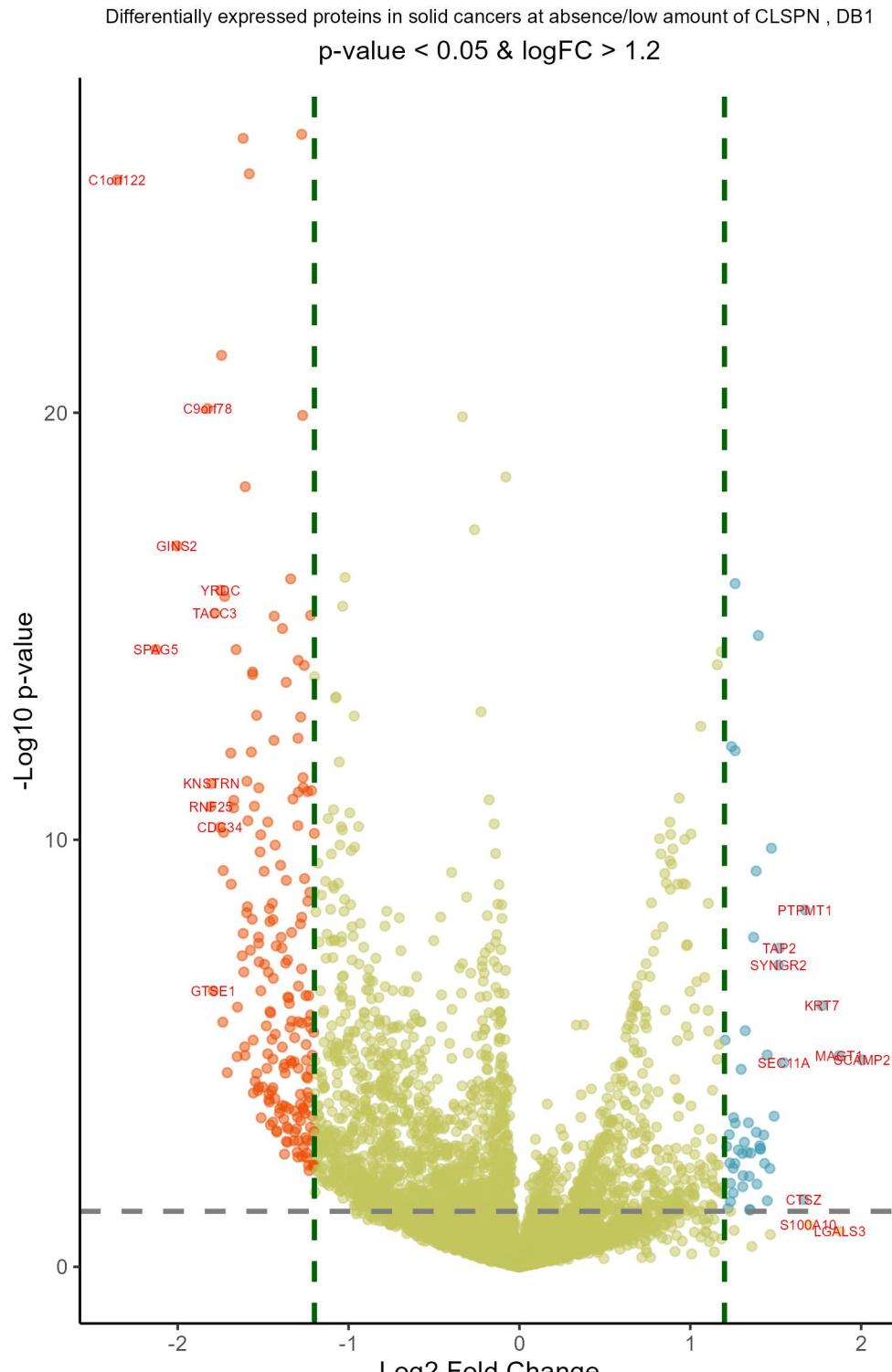


p-value &lt; 0.05 &amp; logFC &gt; 1.2

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



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.23	4.36e-08	PTP4A2	protein tyrosine phosphatase 4A2	2.23	2.27e-04	FAM107B	family with sequence similarity 107
-1.91	1.07e-02	RAB23	RAB23, member RAS oncogene family	2.21	7.20e-01	TUBA4A	tubulin alpha 4a
-1.83	1.09e-02	CDC20	cell division cycle 20	1.85	1.46e-02	FKBP11	FKBP prolyl isomerase 11
-1.81	2.78e-03	UBE4B	ubiquitination factor E4B	1.68	2.83e-07	RPL22L1	ribosomal protein L22 like 1
-1.67	4.71e-12	FLNC	filamin C	1.68	5.34e-01	CD74	CD74 molecule
-1.64	5.58e-02	ABCB6	ATP binding cassette subfamily B me	1.67	7.39e-02	BASP1	brain abundant membrane attached si
-1.64	1.14e-07	PRKCB	protein kinase C beta	1.63	6.28e-01	CRIP1	cysteine rich protein 1
-1.63	4.45e-02	GRAP2	GRB2 related adaptor protein 2	1.55	1.19e-03	MICAL1	microtubule associated monooxygenases
-1.63	2.20e-05	GIPC1	GIPC PDZ domain containing family m	1.53	3.04e-05	JCHAIN	joining chain of multimeric IgA and
-1.62	1.47e-03	DYNLRB1	dynein light chain roadblock-type 1	1.53	4.61e-03	IKZF3	IKAROS family zinc finger 3
-1.62	2.15e-02	FANCD2	FA complementation group D2	1.51	4.51e-01	MTAP	methylthioadenosine phosphorylase
-1.61	1.61e-02	CENPX	centromere protein X	1.48	6.87e-02	IRF4	interferon regulatory factor 4
-1.59	6.86e-02	FADS1	fatty acid desaturase 1	1.42	7.20e-01	HLA-B	major histocompatibility complex, c
-1.56	2.21e-01	MYL4	myosin light chain 4	1.4	1.03e-01	MEF2D	myocyte enhancer factor 2D
-1.56	6.05e-04	ZC3HAV1L	zinc finger CCCH-type containing, a	1.34	2.13e-01	CD70	CD70 molecule
-1.56	4.77e-04	CRYZL1	crystallin zeta like 1	1.33	3.79e-01	SQOR	sulfide quinone oxidoreductase
-1.56	1.10e-02	GNAQ	G protein subunit alpha q	1.32	9.95e-02	PIK3AP1	phosphoinositide-3-kinase adaptor p
-1.55	2.15e-01	TUT4	terminal uridyl transferase 4	1.31	1.72e-02	TRIM22	tripartite motif containing 22
-1.55	1.67e-02	GSE1	Gse1 coiled-coil protein	1.31	6.06e-02	LAT2	linker for activation of T cells fa
-1.53	1.17e-01	ATXN7L3B	ataxin 7 like 3B	1.3	2.06e-01	STK10	serine/threonine kinase 10
-1.52	2.22e-04	ANLN	anillin actin binding protein	1.3	6.53e-01	DTD1	D-aminoacyl-tRNA deacylase 1
-1.5	1.12e-02	CUEDC2	CUE domain containing 2	1.3	1.10e-06	SNTB1	syntrophin beta 1
-1.49	3.21e-02	TRIT1	tRNA isopentenyltransferase 1	1.3	4.04e-01	CAMK2D	calcium/calmodulin dependent protei
-1.49	7.91e-05	GNB1L	G protein subunit beta 1 like	1.29	1.40e-01	HLA-DPB1	major histocompatibility complex, c
-1.49	4.58e-02	CMPK2	cytidine/uridine monophosphate kina	1.29	3.45e-01	PLCG2	phospholipase C gamma 2
-1.49	1.21e-04	NOPCHAP1	NOP protein chaperone 1	1.28	4.41e-01	RFTN1	raftlin, lipid raft linker 1
-1.49	4.39e-04	HNRNPLL	heterogeneous nuclear ribonucleopro	1.26	4.26e-05	PAX5	paired box 5
-1.48	1.57e-02	LGALS3BP	galectin 3 binding protein	1.26	6.62e-04	TCL1A	TCL1 family AKT coactivator A
-1.47	3.05e-02	UBE2Q1	ubiquitin conjugating enzyme E2 Q1	1.25	2.22e-04	HLA-DRB3	major histocompatibility complex, c



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.35	4.69e-23	C1orf122	chromosome 1 open reading frame 122	2.01	2.33e-04	SCAMP2	secretory carrier membrane protein
-2.13	8.99e-13	SPAG5	sperm associated antigen 5	1.88	3.14e-01	LGALS3	galectin 3
-2.01	6.71e-15	GINS2	GINS complex subunit 2	1.87	1.93e-04	MAGT1	magnesium transporter 1
-1.83	7.57e-18	C9orf78	chromosome 9 open reading frame 78	1.77	2.04e-05	KRT7	keratin 7
-1.81	1.80e-09	RNF25	ring finger protein 25	1.69	2.51e-01	S100A10	S100 calcium binding protein A10
-1.8	6.26e-10	KNSTRN	kinetochore localized astrin (SPAG5)	1.67	2.25e-07	PTPMT1	protein tyrosine phosphatase mitoch
-1.79	1.02e-05	GTSE1	G2 and S-phase expressed 1	1.66	9.83e-02	CTSZ	cathepsin Z
-1.78	1.65e-13	TACC3	transforming acidic coiled-coil con	1.55	2.61e-04	SEC11A	SEC11 homolog A, signal peptidase c
-1.75	4.59e-09	CDC34	cell division cycle 34, ubiquitin c	1.52	1.33e-06	TAP2	transporter 2, ATP binding cassette
-1.75	5.59e-14	YRDC	yrdC N6-threonylcarbamoyltransferas	1.52	2.97e-06	SYNGR2	synaptogyrin 2
-1.74	5.02e-19	NACA2	nascent polypeptide associated comp	1.49	2.93e-03	MTCH1	mitochondrial carrier 1
-1.74	4.22e-05	CCNB2	cyclin B2	1.47	1.22e-08	RETSAT	retinol saturase
-1.73	3.60e-08	NECAP1	NECAP endocytosis associated 1	1.47	3.57e-01	NCEH1	neutral cholesterol ester hydrolase
-1.73	5.85e-09	NCAPH2	non-SMC condensin II complex subuni	1.47	2.83e-02	ENDOD1	endonuclease domain containing 1
-1.72	7.42e-14	TXLNG	taxilin gamma	1.45	1.03e-01	TM9SF2	transmembrane 9 superfamily member
-1.71	4.16e-04	WAC	WW domain containing adaptor with c	1.45	1.86e-04	CANT1	calcium activated nucleotidase 1
-1.69	1.32e-10	PCLAF	PCNA clamp associated factor	1.44	2.29e-02	ARL6IP1	ADP ribosylation factor like GTPase
-1.69	6.67e-08	CKS1B	CDC28 protein kinase regulatory sub	1.43	6.70e-03	AGRN	agrin
-1.67	1.89e-09	ACBD6	acyl-CoA binding domain containing	1.41	1.25e-02	MMP14	matrix metallopeptidase 14
-1.67	1.32e-09	TRMT61A	tRNA methyltransferase 61A	1.41	1.18e-02	KRT2	keratin 2
-1.66	8.99e-13	DLGAP5	DLG associated protein 5	1.41	1.07e-02	GPAA1	glycosylphosphatidylinositol anchor
-1.65	1.99e-04	HAUS8	HAUS augmin like complex subunit 8	1.4	4.57e-13	S100A14	S100 calcium binding protein A14
-1.65	2.17e-05	GTF2E1	general transcription factor IIIE su	1.39	5.29e-02	CD59	CD59 molecule (CD59 blood group)
-1.62	1.94e-06	PDRG1	p53 and DNA damage regulated 1	1.39	5.87e-03	DAD1	defender against cell death 1
-1.62	8.33e-24	BLMH	bleomycin hydrolase	1.39	3.66e-08	LPCAT2	lysophosphatidylcholine acyltransfe
-1.62	6.97e-07	EIF1	eukaryotic translation initiation f	1.37	8.14e-07	LMAN2L	lectin, mannose binding 2 like
-1.61	4.18e-06	POLR3D	RNA polymerase III subunit D	1.36	5.34e-01	ANXA1	annexin A1
-1.61	1.30e-04	SGTB	small glutamine rich tetratricopept	1.35	1.45e-02	ERBIN	erbB2 interacting protein
-1.61	1.90e-04	SKA3	spindle and kinetochore associated	1.35	1.45e-01	SQOR	sulfide quinone oxidoreductase

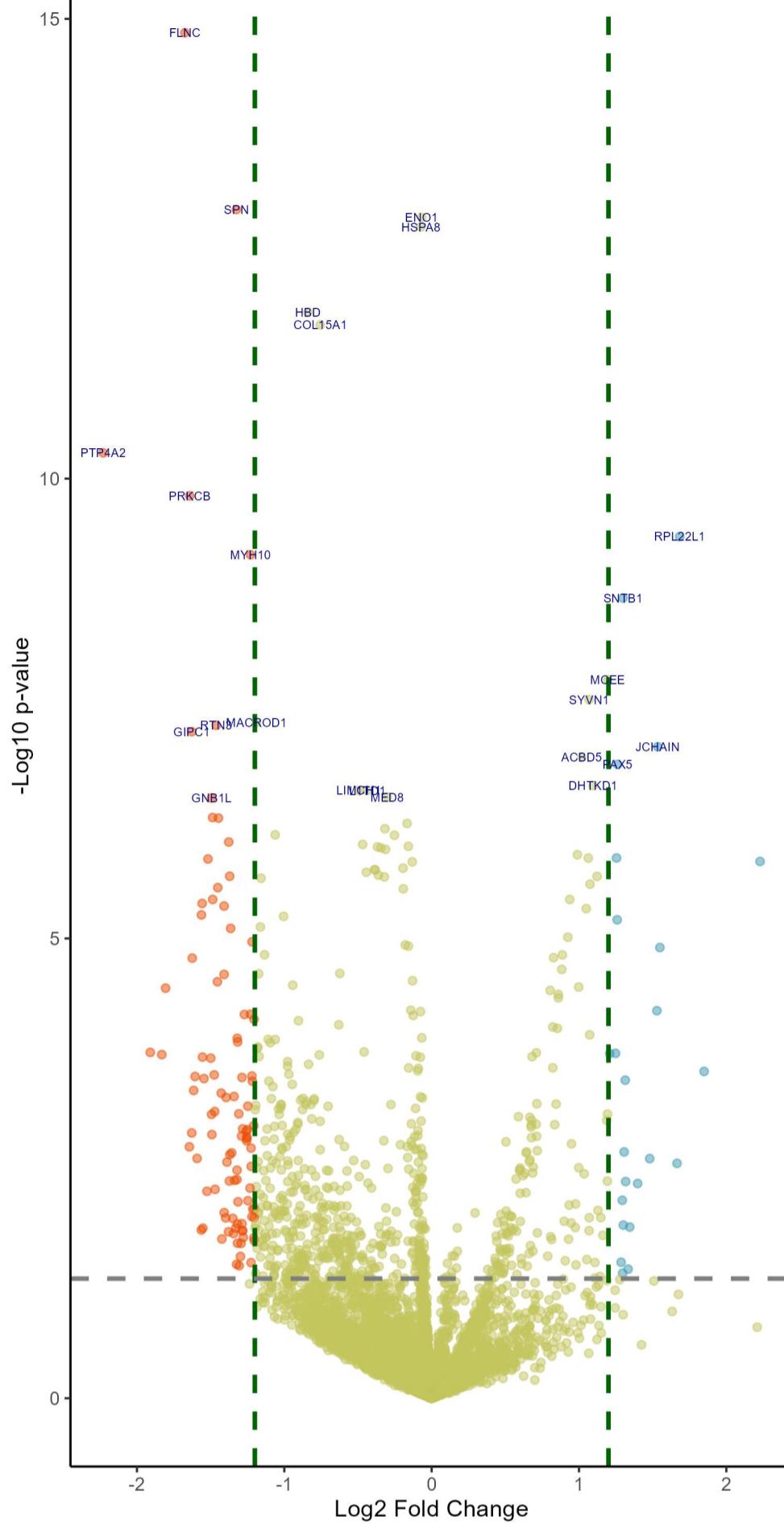
CLSPN network, DB1, no Pearson r &gt; 0.3

Differentially expressed proteins in blood cancers at absence/low amount of CLSPN , DB1

p-value &lt; 0.05 &amp; logFC &gt; 1.2

Sorted by p values!

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



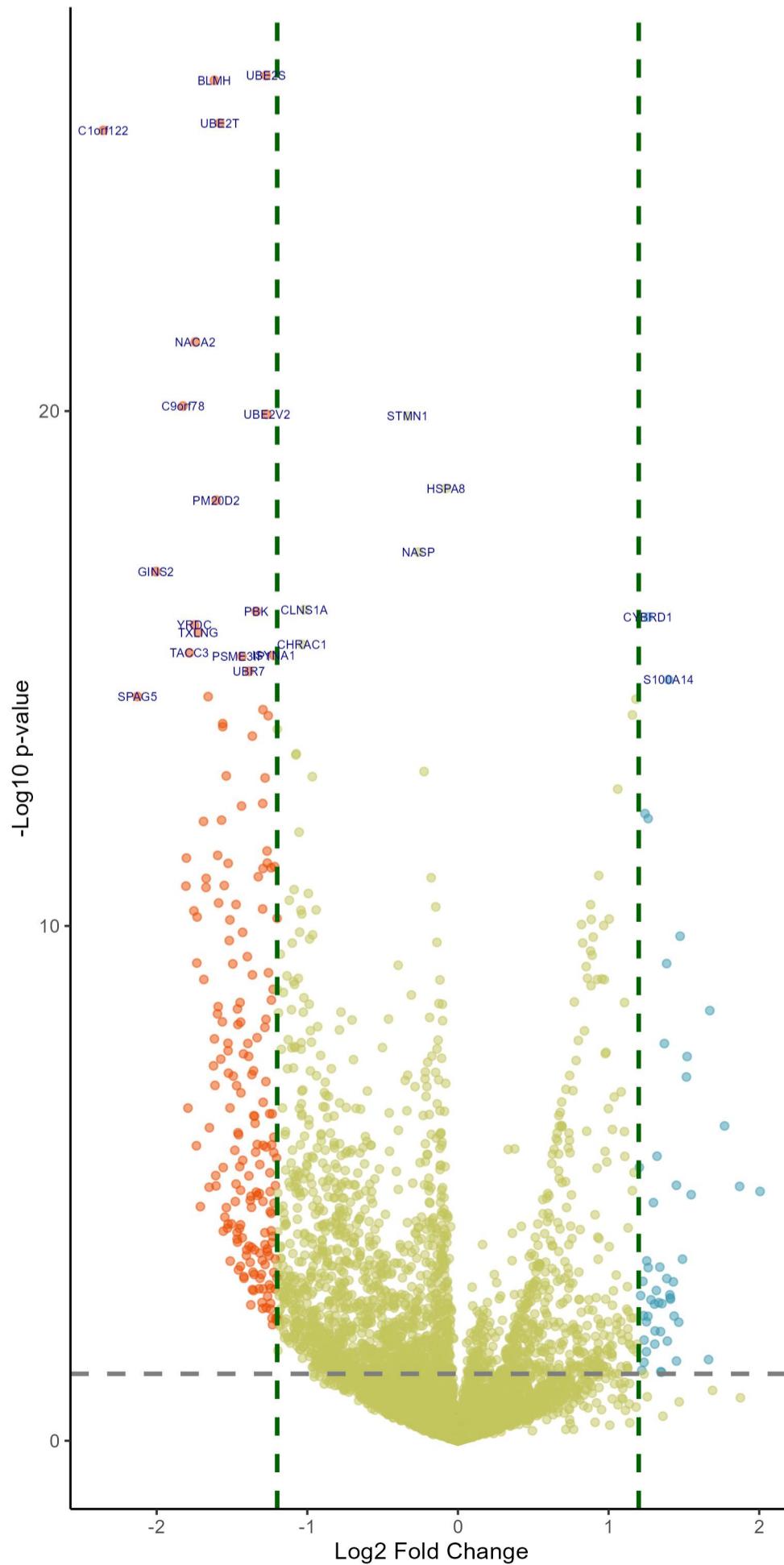
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.67	4.71e-12	FLNC	filamin C	1.68	2.83e-07	RPL22L1	ribosomal protein L22 like 1
-1.33	2.40e-10	SPN	sialophorin	1.3	1.10e-06	SNTB1	syntrophin beta 1
-0.07	2.40e-10	ENO1	enolase 1	1.19	7.85e-06	MCEE	methylmalonyl-CoA epimerase
-0.07	2.43e-10	HSPA8	heat shock protein family A (Hsp70)	1.07	1.20e-05	SYVN1	synoviolin 1
-0.84	1.72e-09	HBD	hemoglobin subunit delta	1.53	3.04e-05	JCHAIN	joining chain of multimeric IgA and
-0.76	2.02e-09	COL15A1	collagen type XV alpha 1 chain	1.02	3.72e-05	ACBD5	acyl-CoA binding domain containing
-2.23	4.36e-08	PTP4A2	protein tyrosine phosphatase 4A2	1.26	4.26e-05	PAX5	paired box 5
-1.64	1.14e-07	PRKCB	protein kinase C beta	1.1	6.88e-05	DHTKD1	dehydrogenase E1 and transketolase
-1.23	4.07e-07	MYH10	myosin heavy chain 10	0.99	2.15e-04	SYTL1	synaptotagmin like 1
-1.19	1.98e-05	MACROD1	mono-ADP ribosylhydrolase 1	1.25	2.22e-04	HLA-DRB3	major histocompatibility complex, c
-1.46	2.00e-05	RTN3	reticulon 3	1.06	2.22e-04	NCF4	neutrophil cytosolic factor 4
-1.63	2.20e-05	GIPC1	GIPC PDZ domain containing family m	2.23	2.27e-04	FAM107B	family with sequence similarity 107
-0.5	7.11e-05	LIMCH1	LIM and calponin homology domains 1	1.12	2.79e-04	CD79B	CD79b molecule
-0.44	7.11e-05	L1TD1	LINE1 type transposase domain conta	1.07	3.22e-04	TYMP	thymidine phosphorylase
-0.3	7.91e-05	MED8	mediator complex subunit 8	0.94	4.39e-04	GPT2	glutamic--pyruvic transaminase 2
-1.49	7.91e-05	GNB1L	G protein subunit beta 1 like	1.05	5.25e-04	SFXN3	sideroflexin 3
-1.49	1.21e-04	NOPCHAP1	NOP protein chaperone 1	1.26	6.62e-04	TCL1A	TCL1 family AKT coactivator A
-1.45	1.21e-04	CEP43	centrosomal protein 43	0.92	9.77e-04	GNG7	G protein subunit gamma 7
-0.17	1.33e-04	PGD	phosphogluconate dehydrogenase	1.55	1.19e-03	MICAL1	microtubule associated monooxygenas
-0.32	1.47e-04	ANTXR1	ANTXR cell adhesion molecule 1	0.89	1.39e-03	IFI30	IFI30 lysosomal thiol reductase
-1.06	1.62e-04	APOE	apolipoprotein E	0.83	1.47e-03	TIFA	TRAF interacting protein with forkh
-0.25	1.62e-04	IFT46	intraflagellar transport 46	0.88	1.92e-03	FAIM	Fas apoptotic inhibitory molecule
-1.38	1.86e-04	MAGED2	MAGE family member D2	1	2.74e-03	MX1	MX dynamin like GTPase 1
-0.47	1.91e-04	LRATD2	LRAT domain containing 2	0.8	2.90e-03	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-b
-0.16	1.91e-04	KANK4	KN motif and ankyrin repeat domains	0.86	3.17e-03	FHL1	four and a half LIM domains 1
-0.37	1.91e-04	GLUD2	glutamate dehydrogenase 2	0.86	3.42e-03	SLC25A4	solute carrier family 25 member 4
-0.34	1.91e-04	ECHDC3	enoyl-CoA hydratase domain containi	1.53	4.61e-03	IKZF3	IKAROS family zinc finger 3
-0.31	1.93e-04	NOL12	nucleolar protein 12	0.82	6.36e-03	HOMER3	homer scaffold protein 3
-1.52	2.22e-04	ANLN	anillin actin binding protein	0.85	6.50e-03	CYBB	cytochrome b-245 beta chain
-0.13	2.27e-04	NUDC	nuclear distribution C, dynein comp	1.07	7.57e-03	PDK1	pyruvate dehydrogenase kinase 1
-0.19	2.60e-04	CTNNBL1	catenin beta like 1	0.71	1.07e-02	RELB	RELB proto-oncogene, NF- $\kappa$ B subunit
-0.39	2.60e-04	FLG	filaggrin	1.25	1.07e-02	ZHX2	zinc fingers and homeoboxes 2
-0.38	2.60e-04	AXL	AXL receptor tyrosine kinase	1.21	1.07e-02	ANKRD44	ankyrin repeat domain 44
-0.44	2.70e-04	HIC2	HIC ZBTB transcriptional repressor	0.68	1.10e-02	SNX4	sorting nexin 4
-0.36	2.79e-04	PLCD1	phospholipase C delta 1	0.82	1.37e-02	SEPLIG	selectin P ligand
-1.37	2.79e-04	LYSMD2	LysM domain containing 2	1.85	1.46e-02	FKBP11	FKBP prolyl isomerase 11
-0.32	2.79e-04	VAMP3	vesicle associated membrane protein	1.31	1.72e-02	TRIM22	tripartite motif containing 22
-1.16	2.83e-04	COMM8	COMM domain containing 8	0.71	2.73e-02	GCHFR	GTP cyclohydrolase I feedback regul
1.45	3.45e-04	C2orf10	chromosome 2 open reading frame 10	0.84	2.73e-02	CSTA	cystatin A

Differentially expressed proteins in solid cancers at absence/low amount of CLSPN , DB1

p-value &lt; 0.05 &amp; logFC &gt; 1.2

Sorted by p values!

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

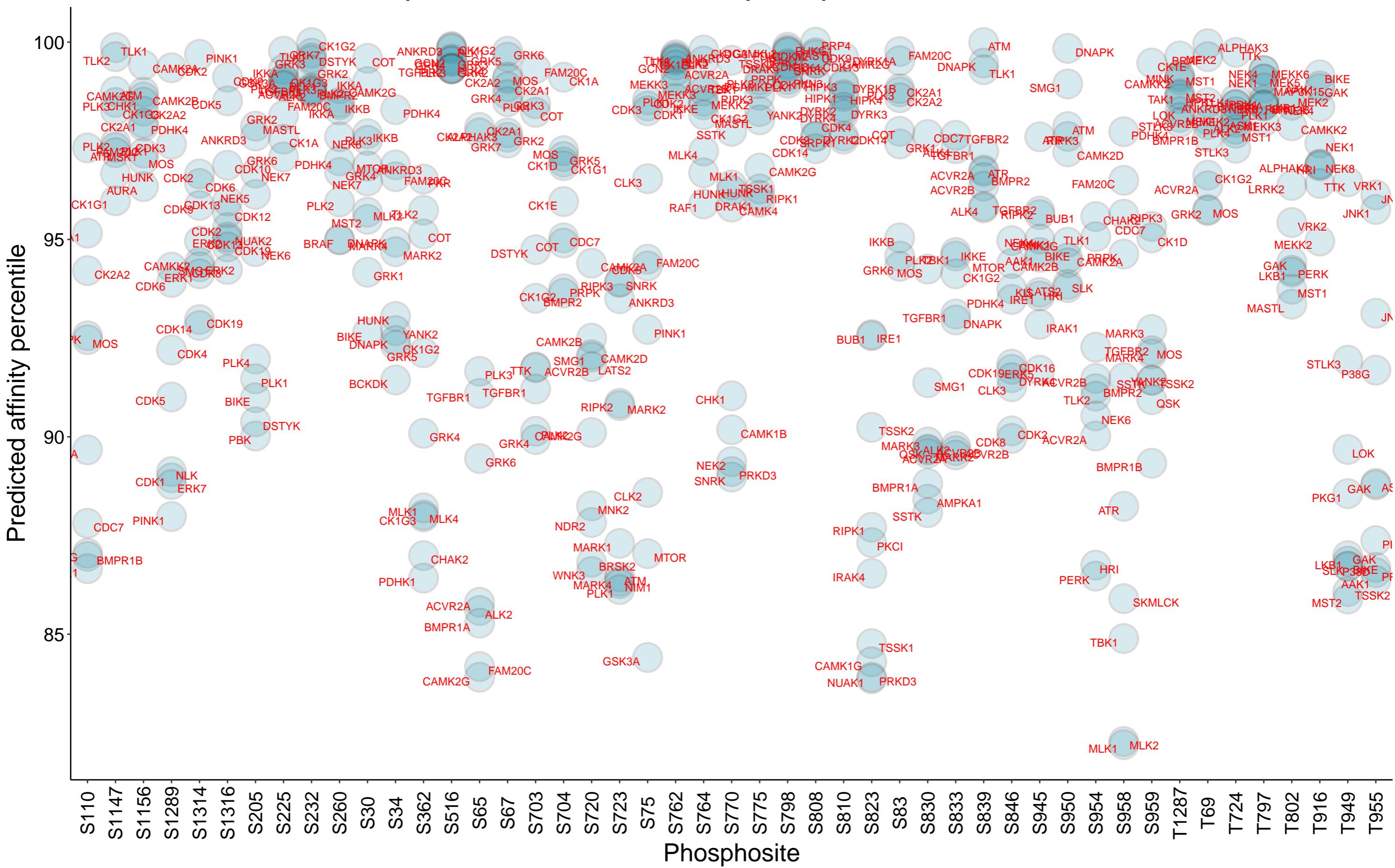


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.27	8.33e-24	UBE2S	ubiquitin conjugating enzyme E2 S	1.26	4.16e-14	CYBRD1	cytochrome b reductase 1
-1.62	8.33e-24	BLMH	bleomycin hydrolase	1.4	4.57e-13	S100A14	S100 calcium binding protein A14
-1.58	4.24e-23	UBE2T	ubiquitin conjugating enzyme E2 T	1.18	9.71e-13	NEXN	nexilin F-actin binding protein
-2.35	4.69e-23	C1orf122	chromosome 1 open reading frame 122	1.16	1.83e-12	TGFBI	transforming growth factor beta ind
-1.74	5.02e-19	NACA2	nascent polypeptide associated comp	1.06	3.57e-11	DSC2	desmocollin 2
-1.83	7.57e-18	C9orf78	chromosome 9 open reading frame 78	1.24	9.93e-11	KIAA1217	KIAA1217
-1.27	9.18e-18	UBE2V2	ubiquitin conjugating enzyme E2 V2	1.26	1.21e-10	KRT85	keratin 85
-0.33	9.18e-18	STMN1	stathmin 1	0.93	1.23e-09	ACSS1	acyl-CoA synthetase short chain fam
-0.08	2.13e-16	HSPA8	heat shock protein family A (Hsp70)	0.88	3.73e-09	AP1M2	adaptor related protein complex 1 s
-1.6	3.26e-16	PM20D2	peptidase M20 domain containing 2	1	6.26e-09	PRSS8	serine protease 8
-0.26	3.04e-15	NASP	nuclear autoantigenic sperm protein	0.88	6.31e-09	TRIM16	tripartite motif containing 16
-2.01	6.71e-15	GINS2	GINS complex subunit 2	0.82	7.71e-09	TMEM87A	transmembrane protein 87A
-1.02	3.42e-14	CLNS1A	chloride nucleotide-sensitive chann	0.97	7.95e-09	KRT16	keratin 16
-1.34	3.44e-14	PBK	PDZ binding kinase	1.47	1.22e-08	RETSAT	retinol saturase
-1.75	5.59e-14	YRDC	yrdC N6-threonylcarbamoyltransferas	0.9	1.26e-08	TMEM63A	transmembrane protein 63A
-1.72	7.42e-14	TXLNG	taxilin gamma	0.83	1.56e-08	CLCN7	chloride voltage-gated channel 7
-1.03	1.19e-13	CHRAC1	chromatin accessibility complex sub	0.88	2.19e-08	DDR1	discoidin domain receptor tyrosine
-1.78	1.65e-13	TACC3	transforming acidic coiled-coil con	0.89	2.59e-08	GALNT3	polypeptide N-acetylgalactosaminyt
-1.22	1.76e-13	ISYNA1	inositol-3-phosphate synthase 1	1.39	3.66e-08	LPCAT2	lysophosphatidylcholine acyltransfe
-1.44	1.76e-13	PSME3IP1	proteasome activator subunit 3 inte	0.85	4.05e-08	ALD3B1	aldehyde dehydrogenase 3 family mem
-1.39	3.27e-13	UBR7	ubiquitin protein ligase E3 compone	0.86	6.54e-08	FUCA2	alpha-L-fucosidase 2
-2.13	8.99e-13	SPAG5	sperm associated antigen 5	0.96	6.64e-08	S100P	S100 calcium binding protein P
-1.66	8.99e-13	DLGAP5	DLG associated protein 5	0.92	6.67e-08	ITGB6	integrin subunit beta 6
-1.29	1.49e-12	UCK2	uridine-cytidine kinase 2	0.97	6.67e-08	ANO6	anoctamin 6
-1.26	1.83e-12	UBE2C	ubiquitin conjugating enzyme E2 C	0.88	8.43e-08	MAOA	monoamine oxidase A
-1.56	2.52e-12	CCNB1	cyclin B1	0.77	1.65e-07	GALNS	galactosamine (N-acetyl)-6-sulfatas
-1.56	2.80e-12	POLA2	DNA polymerase alpha 2, accessory s	1.11	1.66e-07	ALG2	ALG2 alpha-1,3/1,6-mannosyltransfer
-1.2	3.05e-12	KIF2C	kinesin family member 2C	1.67	2.25e-07	PTPMT1	protein tyrosine phosphatase mitoch
-1.37	4.01e-12	SAAL1	serum amyloid A like 1	0.84	4.94e-07	SERPINE1	serpin family E member 1
-1.07	8.58e-12	NTMT1	N-terminal Xaa-Pro-Lys N-methyltran	0.8	7.34e-07	BET1L	Bet1 golgi vesicular membrane traff
-1.08	8.82e-12	RRM2	ribonucleotide reductase regulatory	1.37	8.14e-07	LMAN2L	lectin, mannose binding 2 like
-0.22	1.80e-11	CDC45	cell division cycle 45	0.98	1.14e-06	GALNT7	polypeptide N-acetylgalactosaminyt
-1.54	2.13e-11	NFATC2IP	nuclear factor of activated T cells	0.98	1.20e-06		

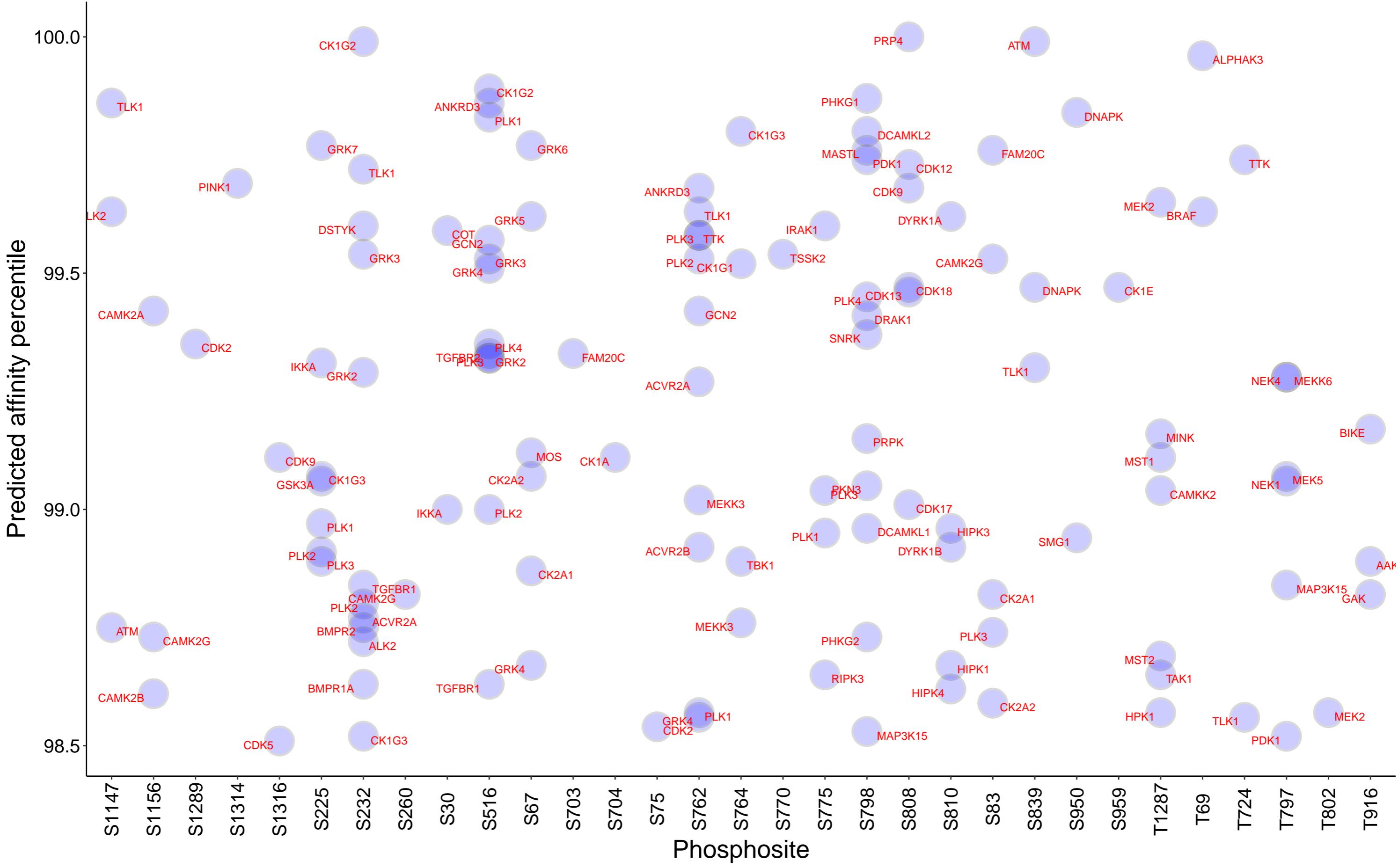
Insufficient number of paired observations in DB1 for CLSPN

Insufficient number of paired observations in DB1 for CLSPN

# Top 10 kinases for each phosphosite in CLSPN



Kinases with affinity greater than 98.5% to CLSPN



No sufficient paired observations in DB1 for CLSPN