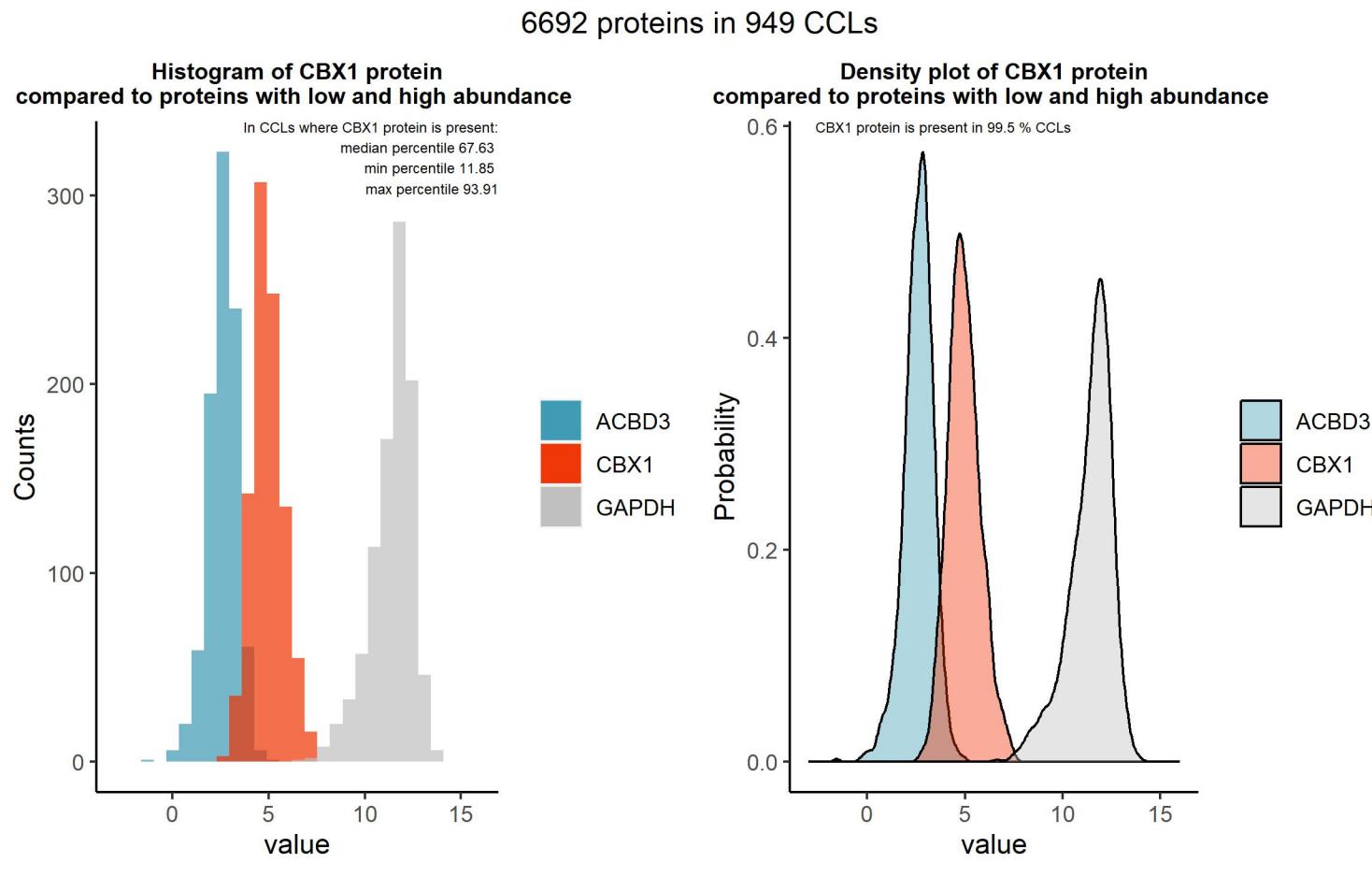


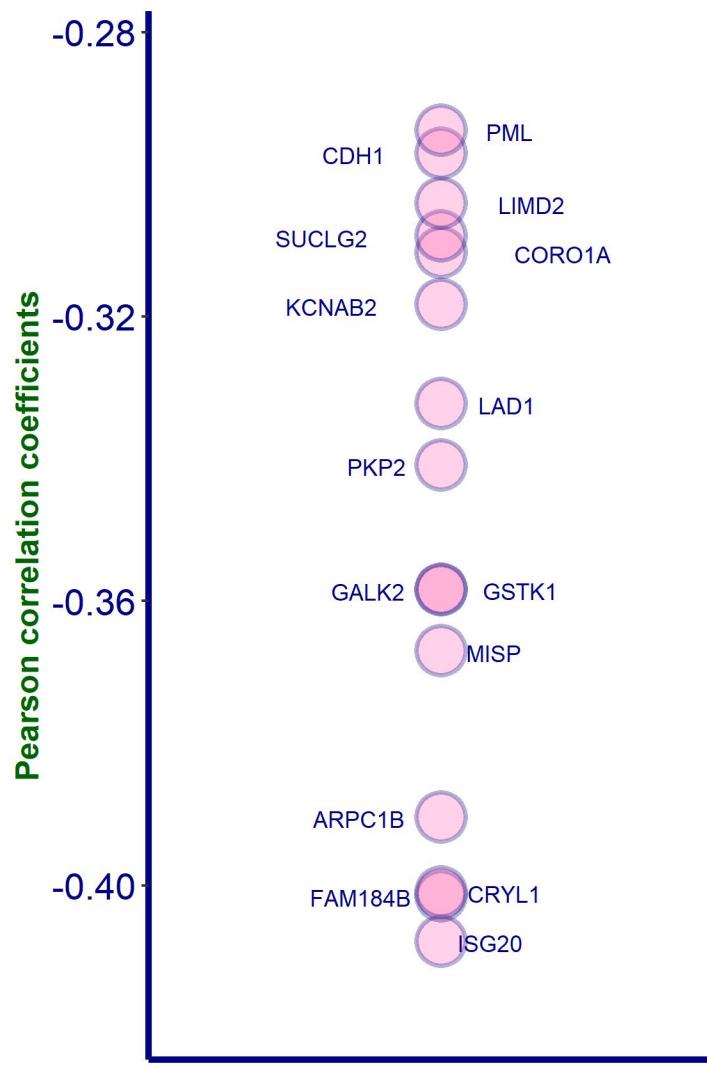
# CBX1

Protein name: CBX1 ; UNIPROT: P83916 ; Gene name: chromobox 1  
 Ligandable: NA ; Ligandable\_by\_Chem: NA ; Is\_enzyme: NA (<https://cansar.ai/>)

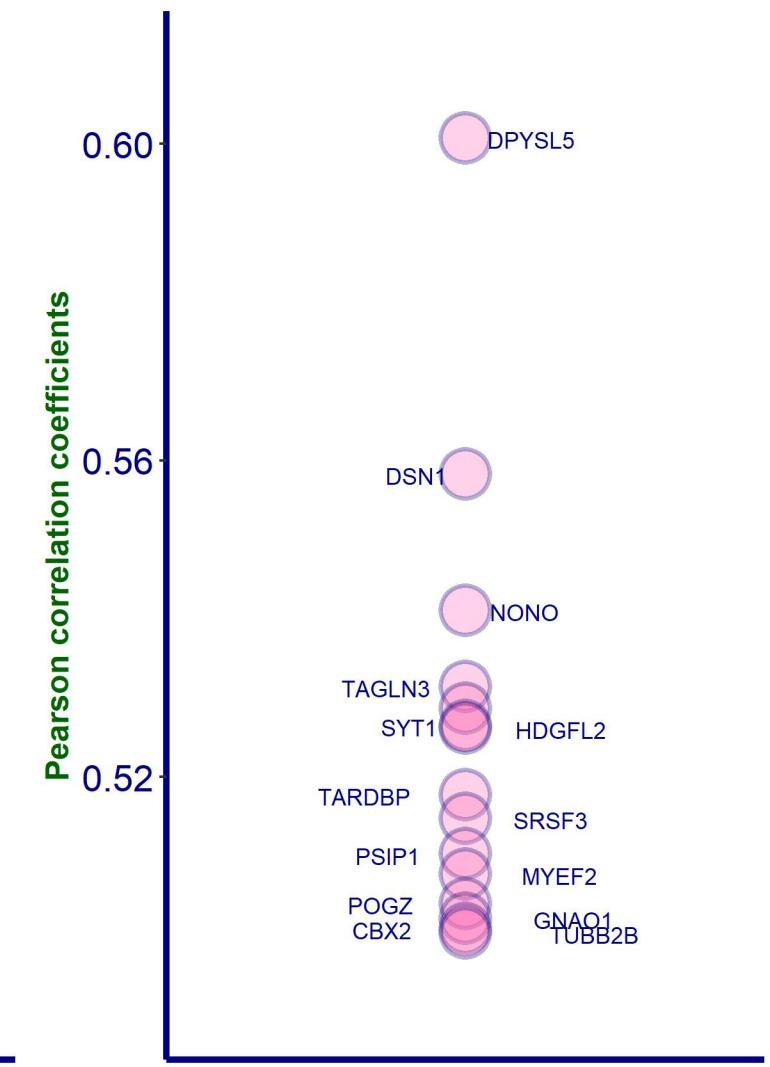
## Sanger Institute Protein Database 1 (DB1), protein presence is certain



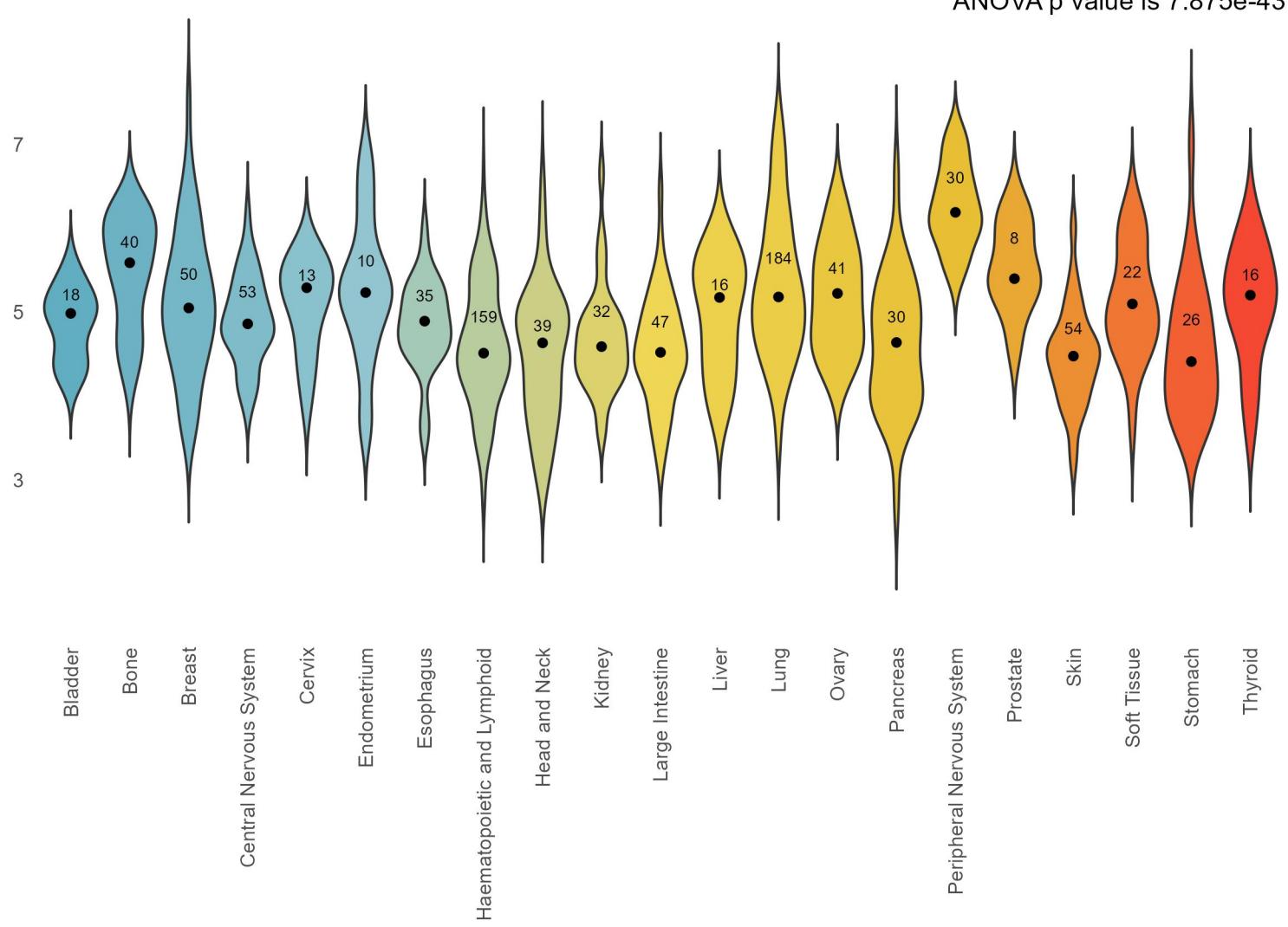
## Top negative correlations of CBX1 protein, DB1



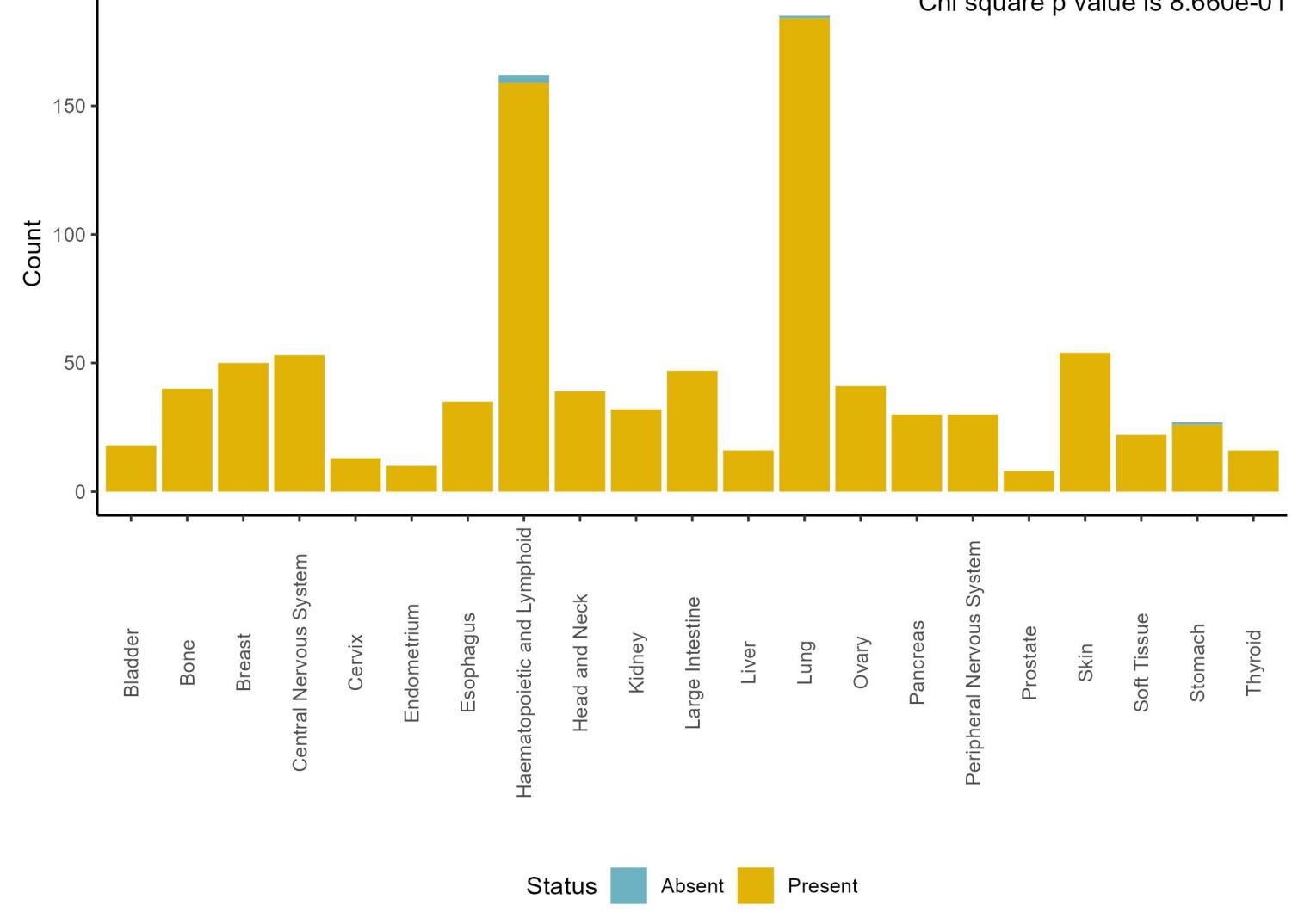
## Top positive correlations of CBX1 protein, DB1



## Amount of CBX1 protein, number of CCLs where it is present by tissue, DB1



## Present and absent CBX1 protein counts by tissue, DB1

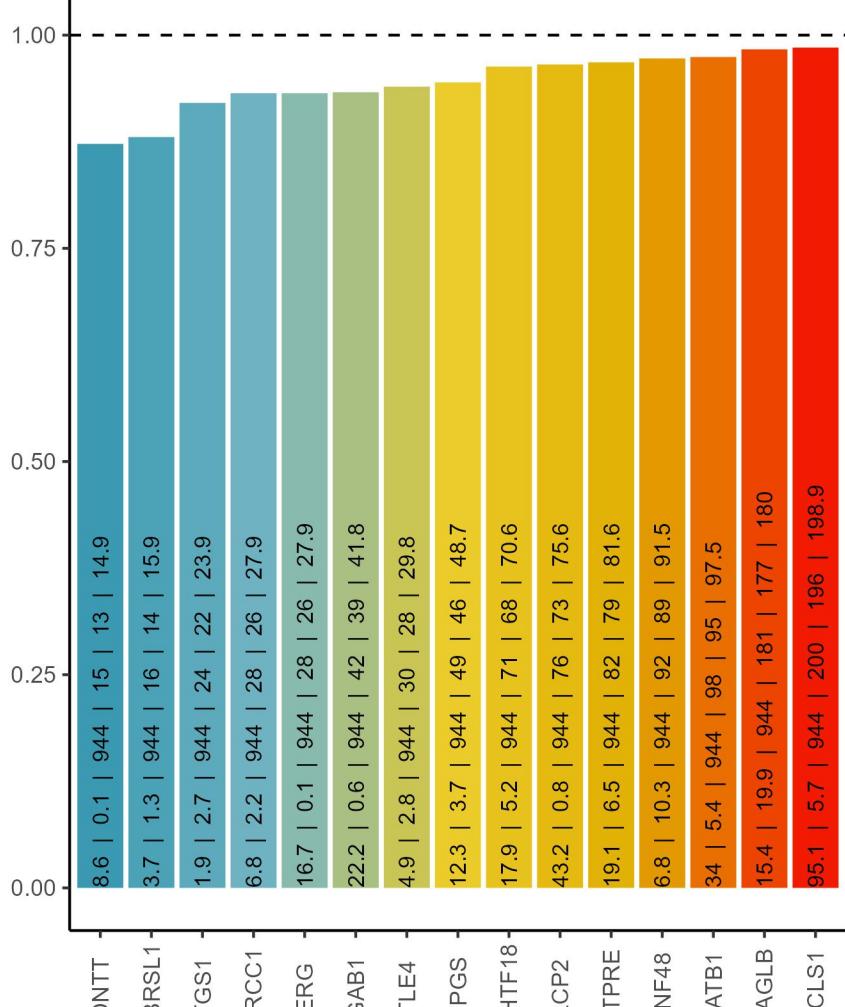


## Cooccurrence with CBX1 protein, DB1

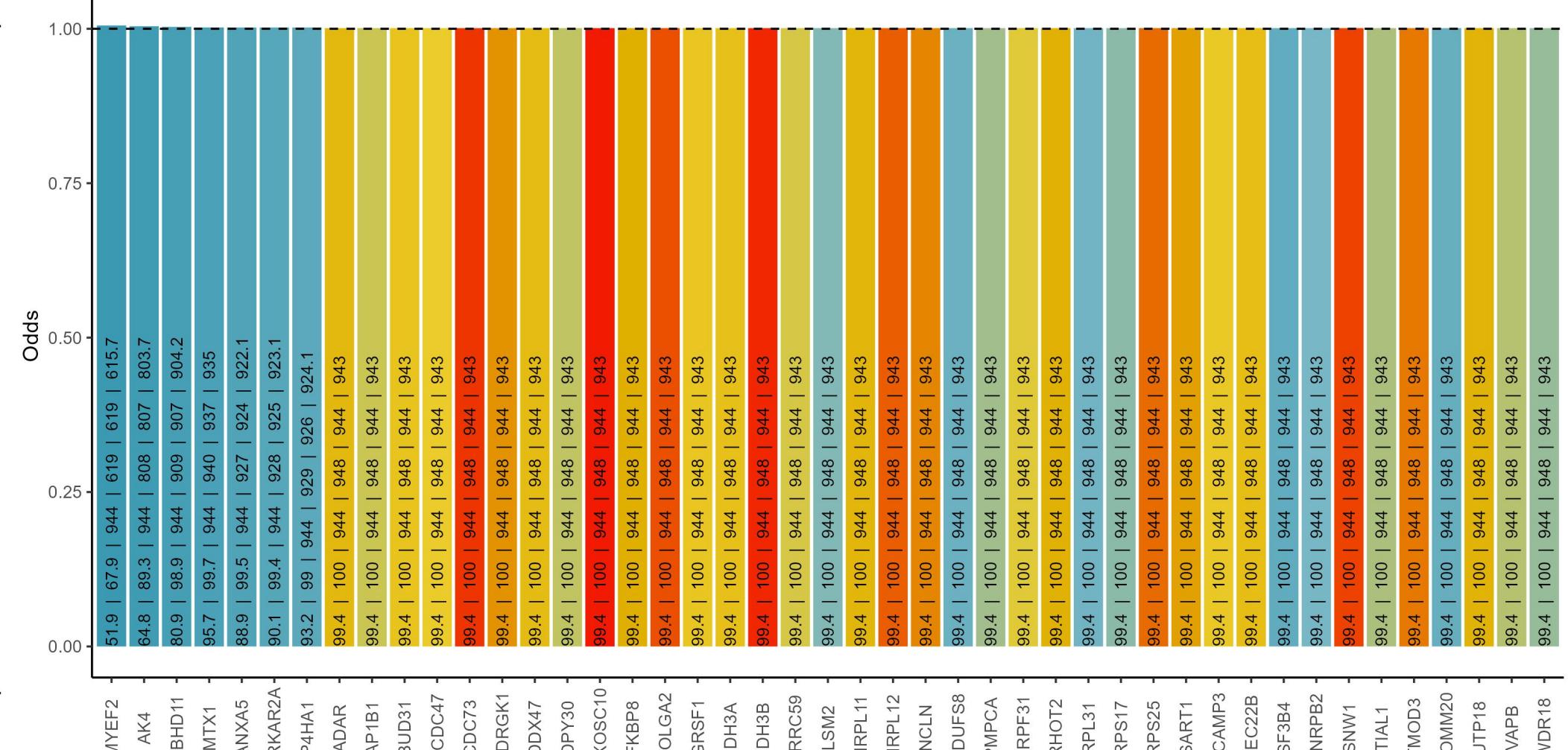
% of CBX1 in blood cancers: 98.1 ; % of CBX1 in solid cancers: 99.7

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CBX1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

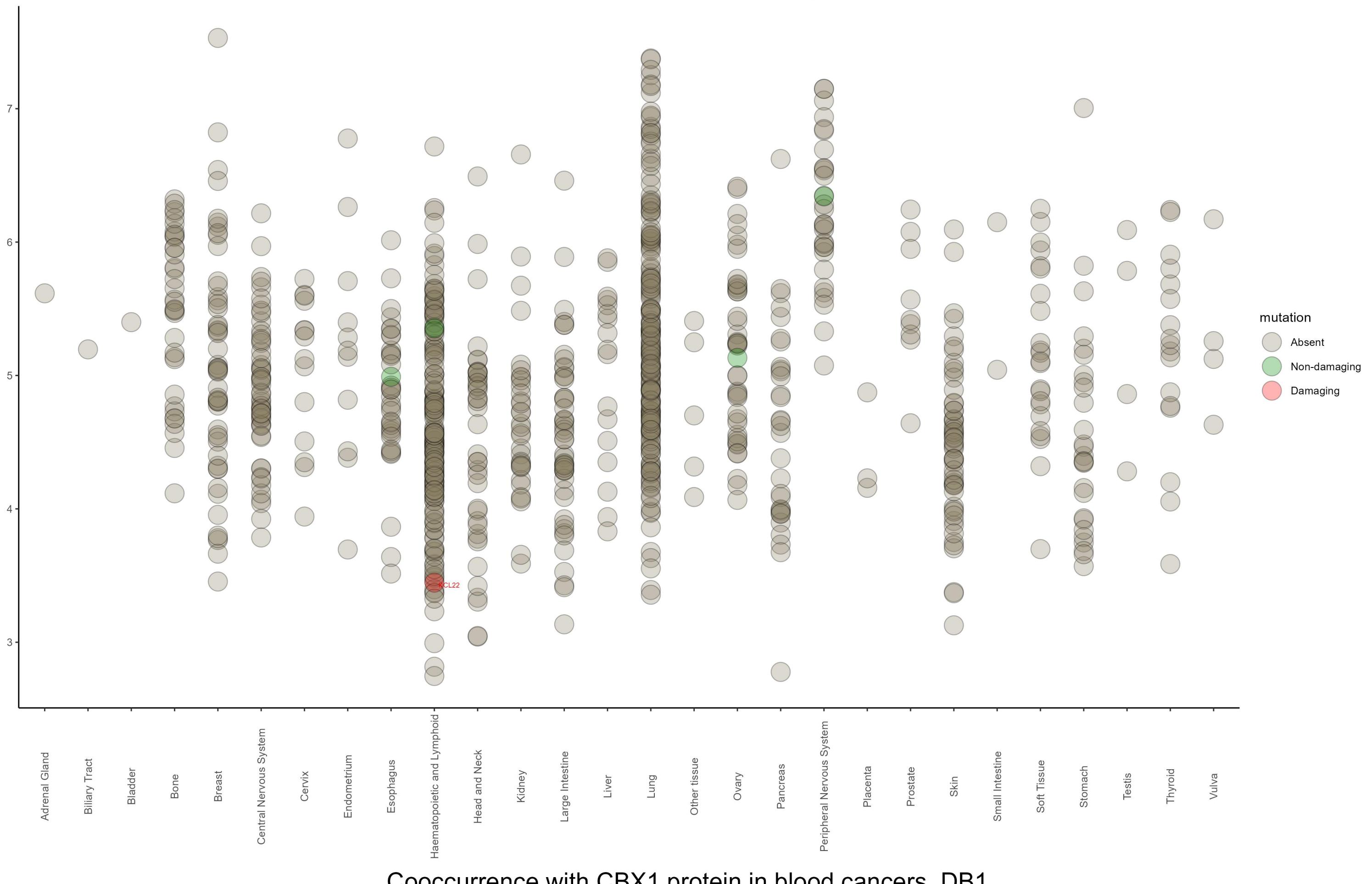
### Negative cooccurrence



### Positive cooccurrence

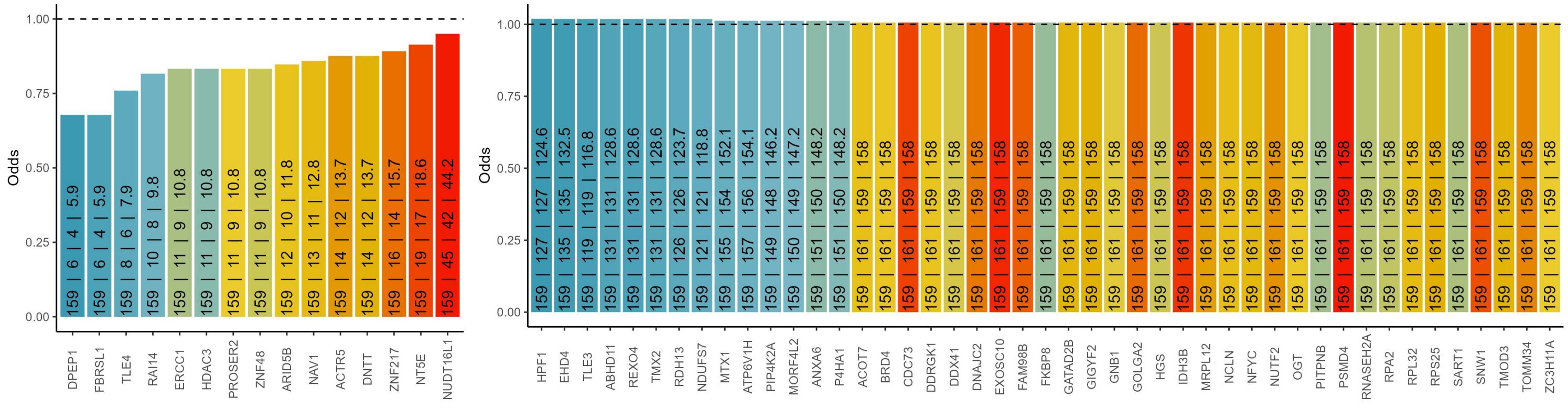


# Amount of CBX1 protein and mutation status by tissue, DB1



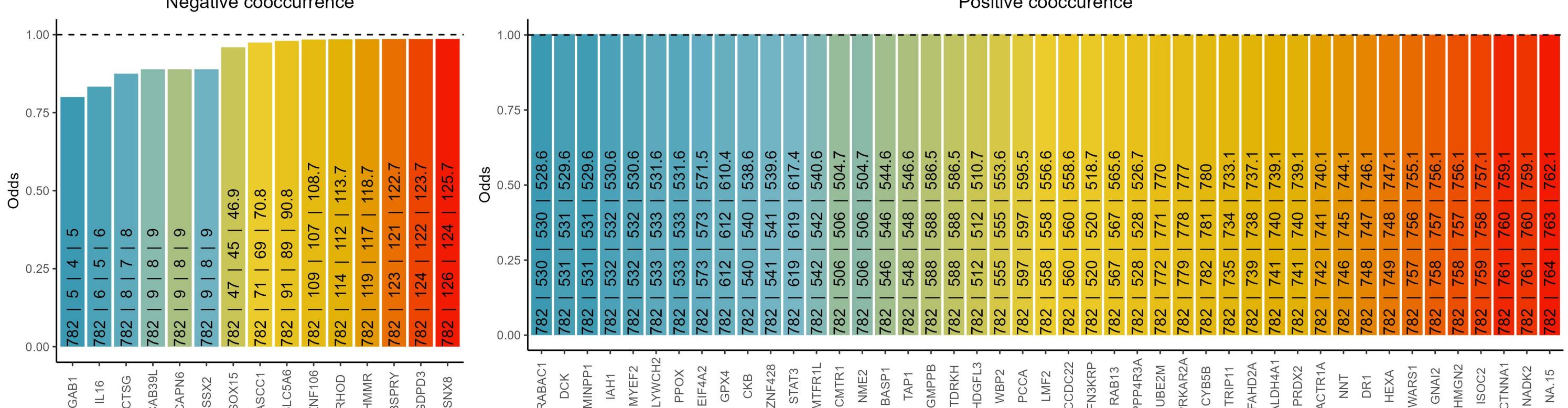
## Cooccurrence with CBX1 protein in blood cancers, DB1

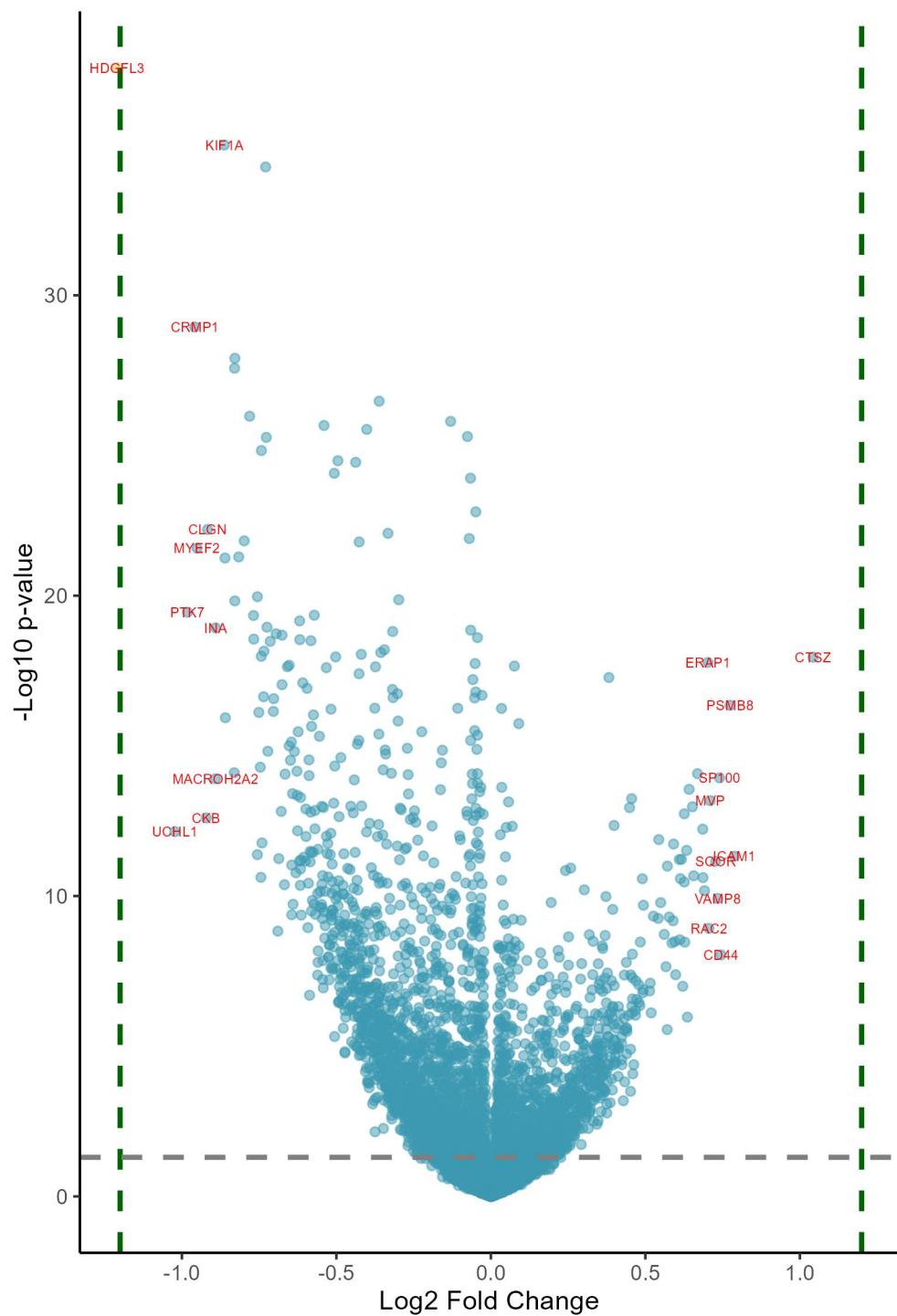
The text in the bars: incidence of CBX1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



## Cooccurrence with CBX1 protein in solid cancers, DB1

The text in the bars: incidence of CBX1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

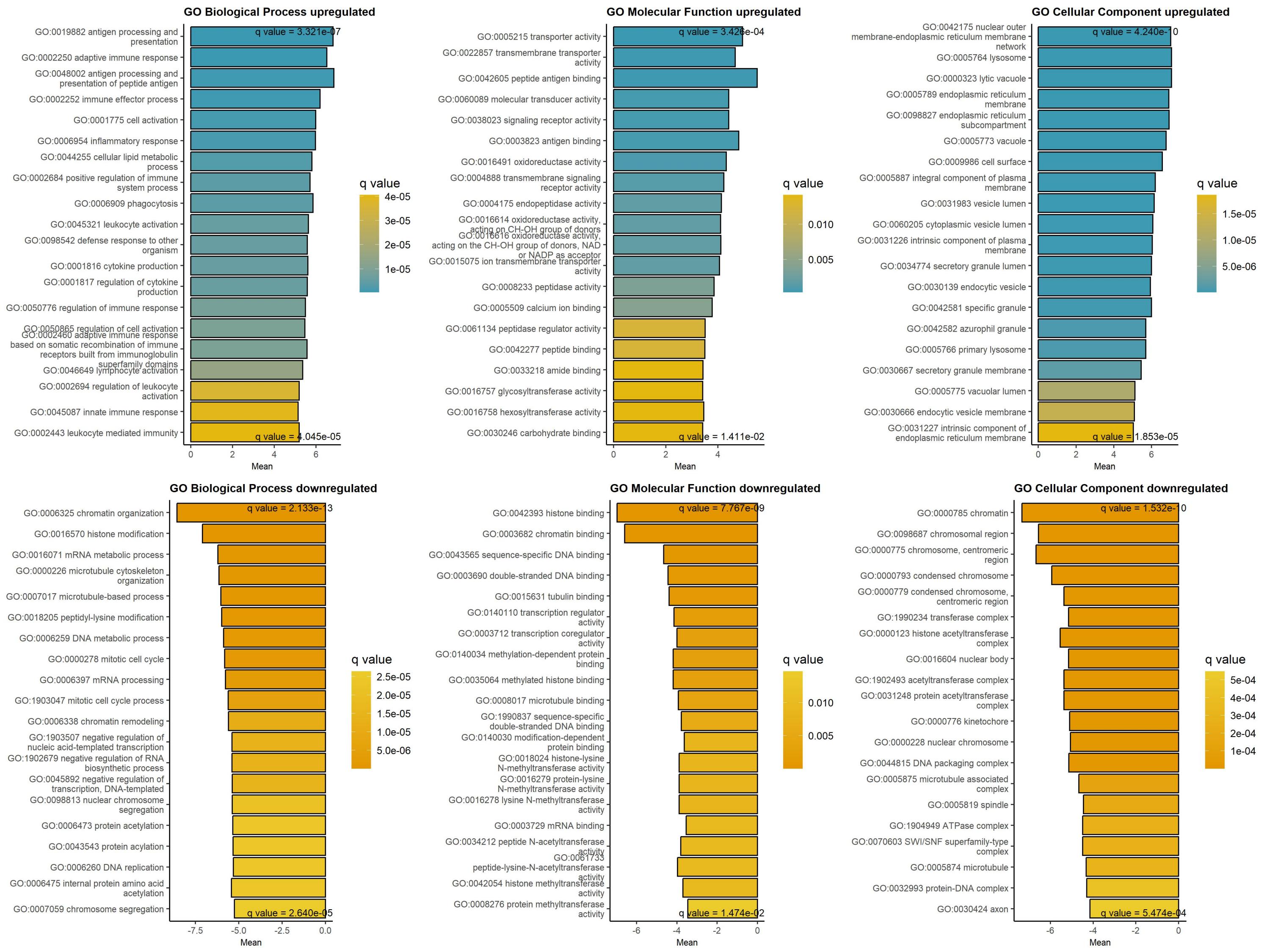




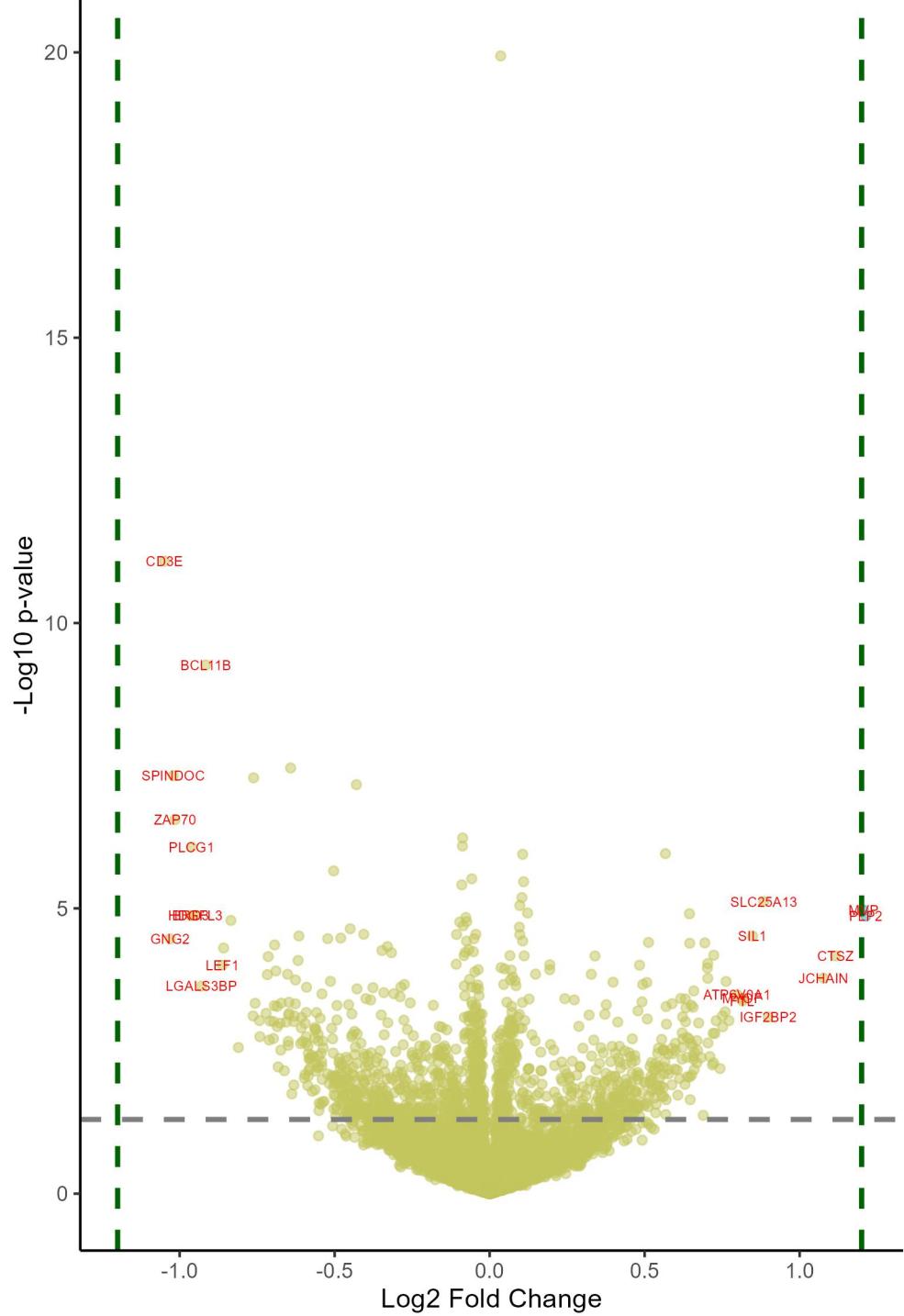
## Downregulated at low/absent CBX1 Upregulated at low/absent CBX1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.21	8.84e-35	HDGFL3	HDGF like 3	1.04	1.40e-16	CTSZ	cathepsin Z
-1.02	2.70e-11	UCHL1	ubiquitin C-terminal hydrolase L1	0.79	1.49e-10	ICAM1	intercellular adhesion molecule 1
-0.98	7.36e-18	PTK7	protein tyrosine kinase 7 (inactive)	0.77	3.97e-15	PSMB8	proteasome 20S subunit beta 8
-0.96	1.51e-26	CRMP1	collapsin response mediator protein	0.75	1.28e-07	CD44	CD44 molecule (Indian blood group)
-0.95	6.75e-20	MYEF2	myelin expression factor 2	0.74	6.36e-13	SP100	SP100 nuclear antigen
-0.92	1.02e-11	CKB	creatine kinase B	0.73	2.74e-09	VAMP8	vesicle associated membrane protein
-0.92	1.98e-20	CLGN	calmegin	0.73	2.08e-10	SQOR	sulfide quinone oxidoreductase
-0.89	6.76e-13	MACROH2A2	macroH2A.2 histone	0.71	3.25e-12	MVP	major vault protein
-0.89	2.13e-17	INA	internexin neuronal intermediate fil	0.71	2.08e-08	RAC2	Rac family small GTPase 2
-0.86	2.20e-32	KIF1A	kinesin family member 1A	0.7	2.06e-16	ERAP1	endoplasmic reticulum aminopeptidase
-0.86	1.32e-19	BRD3	bromodomain containing 3	0.69	1.62e-09	HLA-B	major histocompatibility complex, c
-0.86	9.31e-15	TUBB2B	tubulin beta 2B class IIb	0.69	6.60e-10	TAP2	transporter 2, ATP binding cassette
-0.83	4.62e-13	CRIP2	cysteine rich protein 2	0.69	2.26e-11	PSMB10	proteasome 20S subunit beta 10
-0.83	2.54e-25	SPINDOC	spindlin interactor and repressor o	0.67	4.85e-13	CTSS	cathepsin S
-0.83	1.38e-25	KAT7	lysine acetyltransferase 7	0.66	5.89e-10	PSMB9	proteasome 20S subunit beta 9
-0.83	3.21e-18	PALM	paralemmin	0.65	4.95e-12	ACSL5	acyl-CoA synthetase long chain fami
-0.82	1.26e-19	ZNF280C	zinc finger protein 280C	0.64	1.46e-12	TCIRG1	T cell immune regulator 1, ATPase H
-0.8	4.15e-20	TSPYL5	TSPY like 5	0.64	9.09e-06	LGALS3	galectin 3
-0.78	7.85e-24	DPYSL5	dihydropyrimidinase like 5	0.63	1.01e-10	RPS27L	ribosomal protein S27 like
-0.77	8.97e-18	KIF5C	kinesin family member 5C	0.63	5.40e-08	FKBP11	FKBP prolyl isomerase 11
-0.77	4.33e-17	SCML2	Scm polycomb group protein like 2	0.63	7.73e-12	ADGRE5	adhesion G protein-coupled receptor
-0.76	1.33e-10	MAP1B	microtubule associated protein 1B	0.63	8.97e-10	PYCARD	PYD and CARD domain containing
-0.76	2.48e-18	NSD2	nuclear receptor binding SET domain	0.62	1.12e-06	BST2	bone marrow stromal cell antigen 2
-0.75	6.32e-15	ABI2	abl interactor 2	0.62	1.84e-10	GALE	UDP-galactose-4-epimerase
-0.75	3.11e-13	PMF1	polyamine modulated factor 1	0.61	7.11e-10	CD74	CD74 molecule
-0.74	6.52e-10	PFN2	profilin 2	0.61	4.58e-08	LPCAT2	lysophosphatidylcholine acyltransfe
-0.74	1.36e-16	GPRIN1	G protein regulated inducer of neur	0.61	1.86e-10	B2M	beta-2-microglobulin
-0.74	6.52e-23	SPIN1	spindlin 1	0.6	5.01e-07	CD59	CD59 molecule (CD59 blood group)
-0.74	5.97e-11	ISYNA1	inositol-3-phosphate synthase 1	0.6	5.21e-08	RNASET2	ribonuclease T2

## GAGE analysis on upregulated and downregulated proteins at low/absent CBX1 protein, DB1



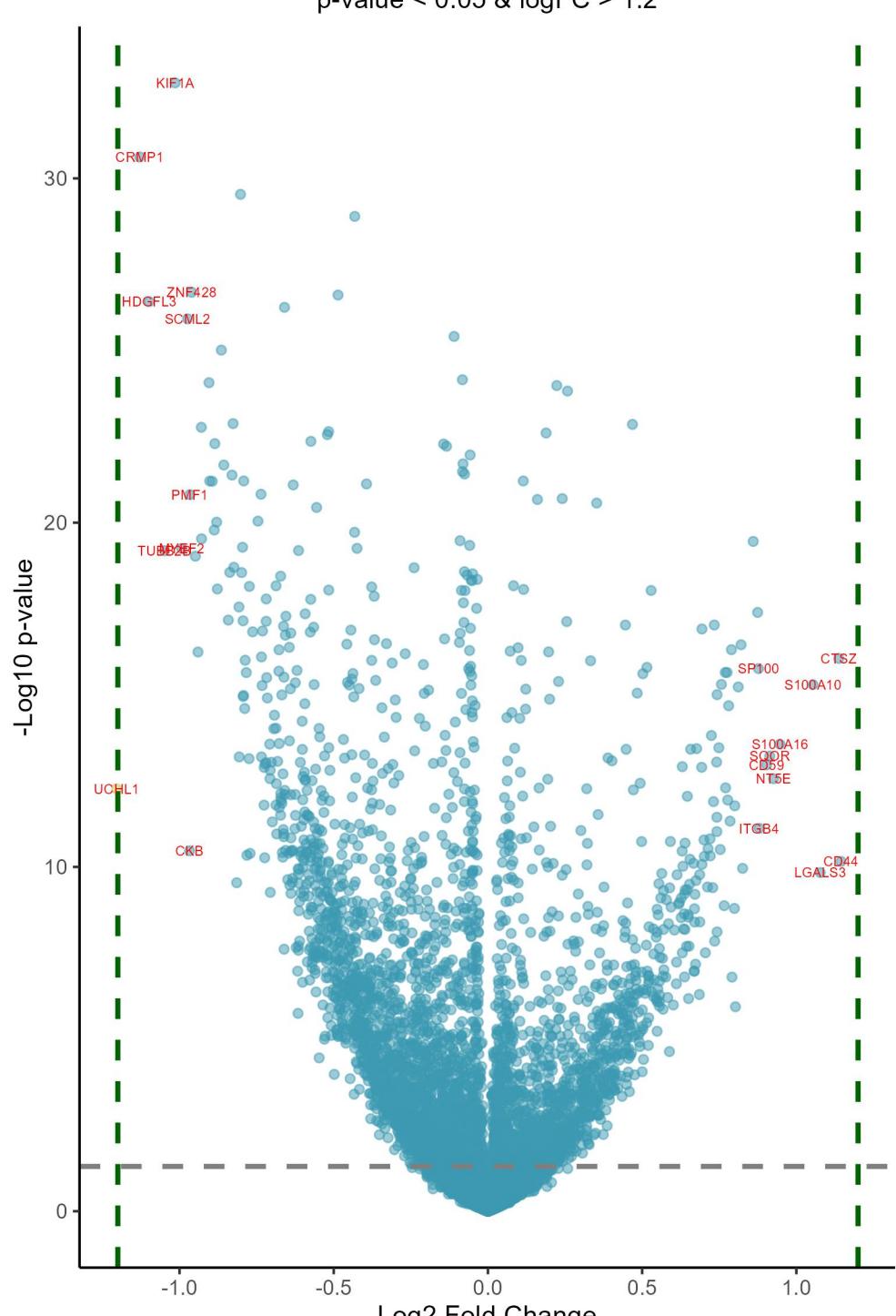
p-value &lt; 0.05 &amp; logFC &gt; 1.2



Downregulated in blood cancers at low/absent CBX1 Upregulated in blood cancers at low/absent CBX1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.05	1.82e-08	CD3E	CD3 epsilon subunit of T-cell recep	1.21	3.35e-03	PLP2	proteolipid protein 2
-1.03	5.17e-03	GNG2	G protein subunit gamma 2	1.21	3.24e-03	MVP	major vault protein
-1.02	4.89e-05	SPINDOC	spindlin interactor and repressor o	1.12	7.20e-03	CTSZ	cathepsin Z
-1.01	2.06e-04	ZAP70	zeta chain of T cell receptor assoc	1.08	1.31e-02	JCHAIN	joining chain of multimeric IgA and
-0.97	3.35e-03	BRD3	bromodomain containing 3	0.9	3.05e-02	IGF2BP2	insulin like growth factor 2 mRNA b
-0.96	4.66e-04	PLCG1	phospholipase C gamma 1	0.88	2.54e-03	SLC25A13	solute carrier family 25 member 13
-0.95	3.35e-03	HDGFL3	HDGF like 3	0.85	5.09e-03	SIL1	SIL1 nucleotide exchange factor
-0.93	1.53e-02	LGALS3BP	galectin 3 binding protein	0.82	2.24e-02	FTL	ferritin light chain
-0.92	9.02e-07	BCL11B	BAF chromatin remodeling complex su	0.81	2.13e-02	MYOF	myoferlin
-0.86	9.40e-03	LEF1	lymphoid enhancer binding factor 1	0.8	1.92e-02	ATP6V0A1	ATPase H <sup>+</sup> transporting V0 subunit a
-0.86	6.33e-03	GRAP2	GRB2 related adaptor protein 2	0.77	3.29e-02	NCEH1	neutral cholesterol ester hydrolase
-0.83	3.72e-03	SPIN1	spindlin 1	0.76	1.40e-02	GPAA1	glycosylphosphatidylinositol anchor
-0.81	5.85e-02	SEPTIN1	septin 1	0.76	2.85e-02	PLXNB2	plexin B2
-0.76	3.03e-02	LGALS9	galectin 9	0.75	3.71e-02	SYNGR2	synaptogyrin 2
-0.76	4.89e-05	SH2D1A	SH2 domain containing 1A	0.75	3.03e-02	SAMHD1	SAM and HD domain containing deoxyn
-0.76	2.32e-02	ELMO2	engulfment and cell motility 2	0.74	8.75e-02	CBR1	carbonyl reductase 1
-0.74	3.29e-02	BCL2L1	BCL2 like 1	0.73	3.29e-02	ALG1	ALG1 chitobiosyldiphosphodolichol b
-0.74	4.59e-02	MPP1	MAGUK p55 scaffold protein 1	0.73	4.25e-02	IKBIP	IKBKB interacting protein
-0.72	2.95e-02	LANC1	LanC like 1	0.72	7.20e-03	TIMM21	translocase of inner mitochondrial
-0.72	1.18e-02	OARD1	O-acyl-ADP-ribose deacetylase 1	0.72	7.70e-02	PLEK	pleckstrin
-0.71	7.27e-03	TCF20	transcription factor 20	0.72	4.25e-02	CISD1	CDGSH iron sulfur domain 1
-0.71	4.99e-02	MRGBP	MRG domain binding protein	0.72	8.12e-02	TUBB6	tubulin beta 6 class V
-0.71	3.29e-02	PTK7	protein tyrosine kinase 7 (inactive)	0.71	6.73e-02	SAR1B	secretion associated Ras related GT
-0.7	4.83e-02	CFAP20	cilia and flagella associated prote	0.7	5.33e-02	HIGD2A	HIG1 hypoxia inducible domain famil
-0.7	3.29e-02	MAP1A	microtubule associated protein 1A	0.7	1.31e-02	MGAT2	alpha-1,6-mannosyl-glycoprotein 2-b
-0.69	2.38e-02	SDCBP	syndecan binding protein	0.7	9.34e-03	GOLM4	golgi integral membrane protein 4
-0.69	5.82e-03	IKZF2	IKAROS family zinc finger 2	0.7	1.02e-02	CLPTM1	CLPTM1 regulator of GABA type A rec
-0.69	1.08e-02	KAT7	lysine acetyltransferase 7	0.69	5.55e-03	AUP1	AUP1 lipid droplet regulating VL
-0.69	2.41e-02	NSL1	NSL1 component of MIS12 kinetochore	0.69	1.99e-01	LGALS1	galectin 1

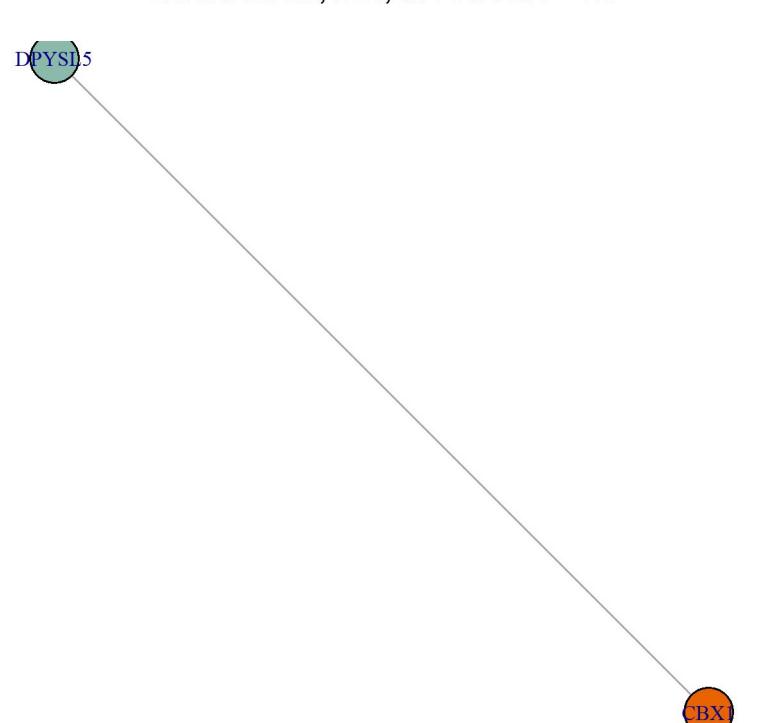
p-value &lt; 0.05 &amp; logFC &gt; 1.2



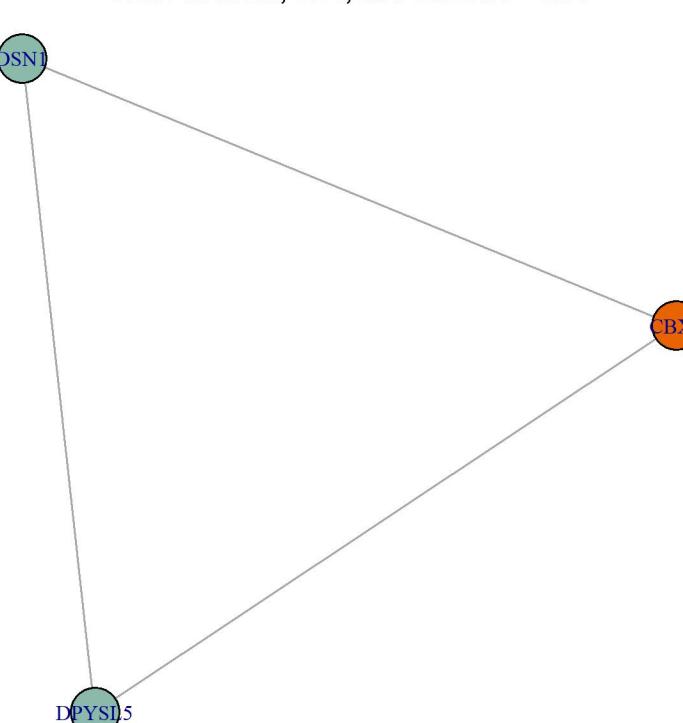
Downregulated in solid cancers at low/absent CBX1 Upregulated in solid cancers at low/absent CBX1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.2	1.32e-11	UCHL1	ubiquitin C-terminal hydrolase L1	1.14	1.04e-09	CD44	CD44 molecule (Indian blood group)
-1.13	5.29e-28	CRMP1	collapsin response mediator protein	1.14	4.73e-15	CTSZ	cathepsin Z
-1.1	3.16e-24	HDGFL3	HDGF like 3	1.08	2.01e-09	LGALS3	galectin 3
-1.05	7.62e-18	TUBB2B	tubulin beta 2B class IIb	1.05	2.21e-14	S100A10	S100 calcium binding protein A10
-1.01	5.59e-30	KIF1A	kinesin family member 1A	0.95	8.91e-13	S100A16	S100 calcium binding protein A16
-0.99	6.88e-18	MYEF2	myelin expression factor 2	0.93	7.17e-12	NT5E	5'-nucleotidase ecto
-0.97	7.96e-24	SCML2	Scm polycomb group protein like 2	0.91	1.83e-12	SQOR	sulfide quinone oxidoreductase
-0.97	5.60e-10	CKB	creatine kinase B	0.9	3.03e-12	CD59	CD59 molecule (CD59 blood group)
-0.97	2.55e-19	PMF1	polyamine modulated factor 1	0.88	1.49e-10	ITGB4	integrin subunit beta 4
-0.96	2.25e-24	ZNF428	zinc finger protein 428	0.88	8.72e-15	SP100	SP100 nuclear antigen
-0.95	1.08e-17	CLGN	calmodulin	0.87	3.13e-16	NCEH1	neutral cholesterol ester hydrolase
-0.94	3.17e-15	INA	internexin neuronal intermediate fil	0.86	4.57e-18	MVP	major vault protein
-0.93	5.95e-21	ZNF280C	zinc finger protein 280C	0.83	1.57e-09	ICAM1	intercellular adhesion molecule 1
-0.93	3.99e-18	PALM	paramelemin	0.82	2.09e-15	MYOF	myoferlin
-0.9	4.09e-22	DPYSL5	dihydropyrimidinase like 5	0.81	2.52e-14	PSMB8	proteasome 20S subunit beta 8
-0.9	1.16e-19	TSPYL5	TSPY like 5	0.8	6.38e-06	S100A6	S100 calcium binding protein A6
-0.89	1.16e-19	MEAF6	MYST/Esa1 associated factor 6	0.8	3.66e-11	TAP2	transporter 2, ATP binding cassette
-0.89	2.31e-18	KIF5C	kinesin family member 5C	0.8	1.75e-08	GPRC5A	G protein-coupled receptor class C
-0.89	1.38e-20	NSD2	nuclear receptor binding SET domain	0.79	1.09e-06	CAVIN1	caveolae associated protein 1
-0.88	1.40e-18	RPRD1A	regulation of nuclear pre-mRNA doma	0.79	2.82e-15	TCIRG1	T cell immune regulator 1, ATPase H
-0.88	7.59e-17	ADD2	adducin 2	0.78	9.52e-11	LPCAT2	lysophosphatidylcholine acyltransfe
-0.86	5.38e-23	SPINDOC	spindlin interactor and repressor o	0.78	7.89e-14	EPS8	epidermal growth factor receptor pa
-0.86	4.86e-20	LUC7L	LUC7 like	0.78	2.62e-11	S100P	S100 calcium binding protein P
-0.84	5.05e-16	BRD3	bromodomain containing 3	0.78	1.08e-14	ENDOD1	endonuclease domain containing 1
-0.84	2.97e-17	PDCL	phosducin like	0.77	1.26e-11	SERPINB1	serpin family B member 1
-0.83	8.61e-20	ZMYM3	zinc finger MYM-type containing 3	0.77	1.08e-14	ADGRE5	adhesion G protein-coupled receptor
-0.83	5.16e-21	KAT7	lysine acetyltransferase 7	0.77	1.48e-08	CAVIN3	caveolae associated protein 3
-0.82	2.23e-17	NSD3	nuclear receptor binding SET domain	0.76	2.21e-14	PARP4	poly(ADP-ribose) polymerase family
-0.81	3.70e-09	MACROH2A2	macroH2A.2 histone	0.75	5.26e-10	ITGA2	integrin subunit alpha 2

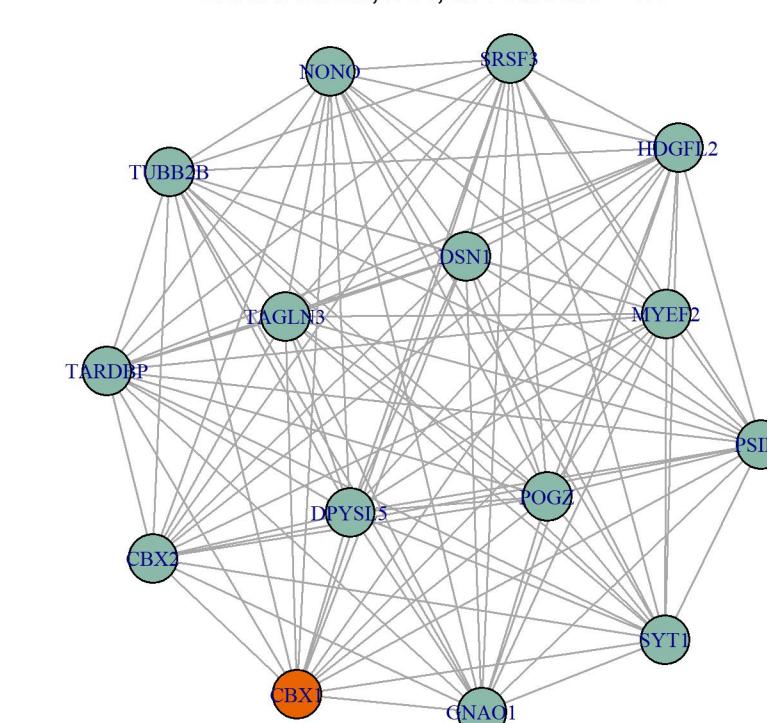
CBX1 network, DB1, all Pearson r &gt; 0.6



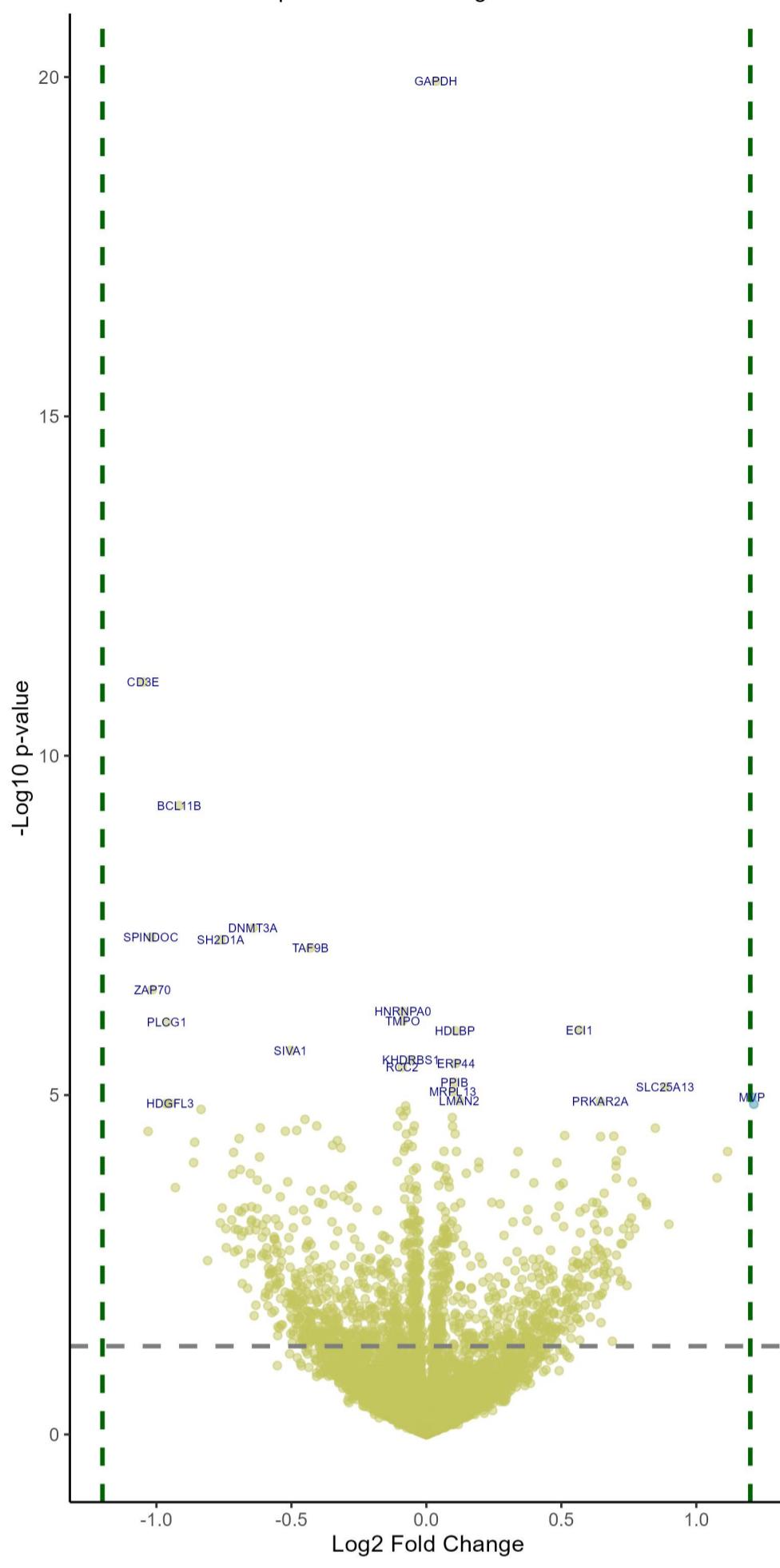
CBX1 network, DB1, all Pearson r &gt; 0.55



CBX1 network, DB1, all Pearson r &gt; 0.5



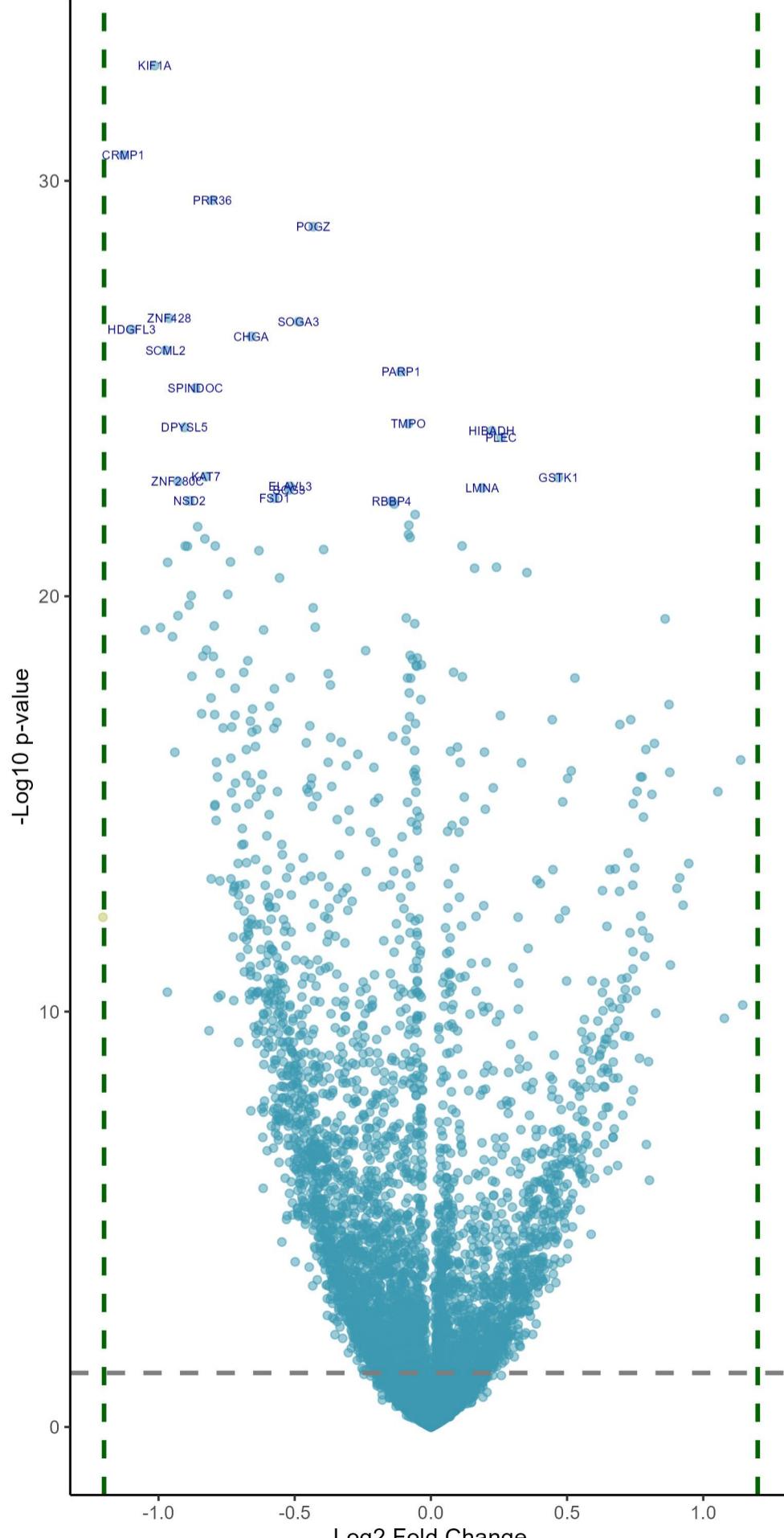
Differentially expressed proteins in blood cancers at absence/low amount of CBX1 , DB1  
p-value < 0.05 & logFC > 1.2



Sorted by p values!  
Downregulated in blood cancers at low/absent CBX1 Upregulated in blood cancers at low/absent CBX1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.05	1.82e-08	CD3E	CD3 epsilon subunit of T-cell recep	0.04	7.66e-17	GAPDH	glyceraldehyde-3-phosphate dehydrog
-0.92	9.02e-07	BCL11B	BAF chromatin remodeling complex su	0.57	5.35e-04	ECI1	enoyl-CoA delta isomerase 1
-0.64	4.61e-05	DNMT3A	DNA methyltransferase 3 alpha	0.11	5.35e-04	HDLBP	high density lipoprotein binding pr
-1.02	4.89e-05	SPINDOC	spindlin interactor and repressor o	0.11	1.34e-03	ERP44	endoplasmic reticulum protein 44
-0.76	4.89e-05	SH2D1A	SH2 domain containing 1A	0.1	2.26e-03	PIPIB	peptidylprolyl isomerase B
-0.43	5.64e-05	TAF9B	TATA-box binding protein associated	0.88	2.54e-03	SLC25A13	solute carrier family 25 member 13
-1.01	2.06e-04	ZAP70	zeta chain of T cell receptor assoc	0.1	2.82e-03	MRPL13	mitochondrial ribosomal protein L13
-0.09	3.88e-04	HNRNPA0	heterogeneous nuclear ribonucleopro	1.21	3.24e-03	MVP	major vault protein
-0.09	4.66e-04	TMPO	thymopoietin	0.12	3.35e-03	LMAN2	lectin, mannose binding 2
-0.96	4.66e-04	PLCG1	phospholipase C gamma 1	0.64	3.35e-03	PRKAR2A	protein kinase cAMP-dependent type
-0.5	9.76e-04	SIVA1	SIVA1 apoptosis inducing factor	1.21	3.35e-03	PLP2	proteolipid protein 2
-0.06	1.26e-03	KHDRBS1	KH RNA binding domain containing, s	0.1	4.31e-03	DNAJA3	DnaJ heat shock protein family (Hsp
-0.09	1.43e-03	RCC2	regulator of chromosome condensatio	0.1	5.03e-03	ATP1A1	ATPase Na+/K+ transporting subunit
-0.95	3.35e-03	HDGFL3	HDGF like 3	0.85	5.09e-03	SIL1	SIL1 nucleotide exchange factor
-0.97	3.35e-03	BRD3	bromodomain containing 3	0.11	5.42e-03	MRPL38	mitochondrial ribosomal protein L38
-0.08	3.43e-03	TRIM28	tripartite motif containing 28	0.51	5.55e-03	FKBP9	FKBP prolyl isomerase 9
-0.83	3.72e-03	SPIN1	spindlin 1	0.69	5.55e-03	AUP1	AUP1 lipid droplet regulating VLDL
-0.07	3.72e-03	HCFC1	host cell factor C1	0.65	5.55e-03	CFL2	cofilin 2
-0.1	3.72e-03	RBBP4	RB binding protein 4, chromatin rem	0.72	7.20e-03	TIMM21	translocase of inner mitochondrial
-0.09	4.19e-03	SMARCE1	SWI/SNF related, matrix associated,	0.07	7.20e-03	SRM	spermidine synthase
-0.45	4.46e-03	GINS3	GINS complex subunit 3	0.11	7.20e-03	OGDH	oxoglutarate dehydrogenase
-0.04	5.03e-03	NONO	non-POU domain containing octamer b	1.12	7.20e-03	CTSZ	cathepsin Z
-0.41	5.03e-03	MND1	meiotic nuclear divisions 1	0.34	7.20e-03	ECPAS	Ecm29 proteasome adaptor and scanno
-0.11	5.03e-03	PAFAH1B3	platelet activating factor acetylhy	0.7	9.34e-03	GOLM4	golgi integral membrane protein 4
-0.62	5.09e-03	TAF4	TATA-box binding protein associated	0.19	9.40e-03	IMPDH1	inosine monophosphate dehydrogenase
-0.48	5.17e-03	GIMAP1	GTPase, IMAP family member 1	0.48	9.40e-03	RBM47	RNA binding motif protein 47
-0.52	5.17e-03	DHX40	DEAH-box helicase 40	0.04	1.02e-02	RPS18	ribosomal protein S18
-0.05	5.17e-03	CHD4	chromodomain helicase DNA binding p	0.7	1.02e-02	CLPTM1	CLPTM1 regulator of GABA type A rec
-1.03	5.17e-03	GNG2	G protein subunit gamma 2	0.05	1.04e-02	TUFM	Tu translation elongation factor, m
-0.07	5.42e-03	SMC1A	structural maintenance of chromosom	0.19	1.05e-02	SPCS2	signal peptidase complex subunit 2
-0.69	5.82e-03	IKZF2	IKAROS family zinc finger 2	0.07	1.06e-02	TRAP1	TNF receptor associated protein 1
-0.33	6.11e-03	PGM2L1	phosphoglucomutase 2 like 1	0.15	1.17e-02	MYDGF	myeloid derived growth factor
-0.86	6.33e-03	GRAP2	GRB2 related adaptor protein 2	0.33	1.17e-02	ABCF3	ATP binding cassette subfamily F me
-0.07	6.61e-03	TUBB	tubulin beta class I	0.07	1.28e-02	MRPL17	mitochondrial ribosomal protein L17
-0.35	6.74e-03	MAPT	microtubule associated protein tau	1.08	1.31e-02	JCHAIN	joining chain of multimeric IgA and
-0.05	6.94e-03	RBM8A	RNA binding motif protein 8A	0.7	1.31e-02	MGAT2	alpha-1,6-mannosyl-glycoprotein 2-b
-0.08	6.98e-03	HDGFL2	HDGF like 2	0.07	1.36e-02	TMED9	transmembrane p24 trafficking prote
-0.32	6.98e-03	GIMAP6	GTPase, IMAP family member 6	0.08	1.39e-02	ACO2	aconitase 2
0.09	7.20e-03	RCNA	proliferating cell nuclear antigen	0.76	1.40e-02	GRAA1	glucosylcerabidiglyceride anchor

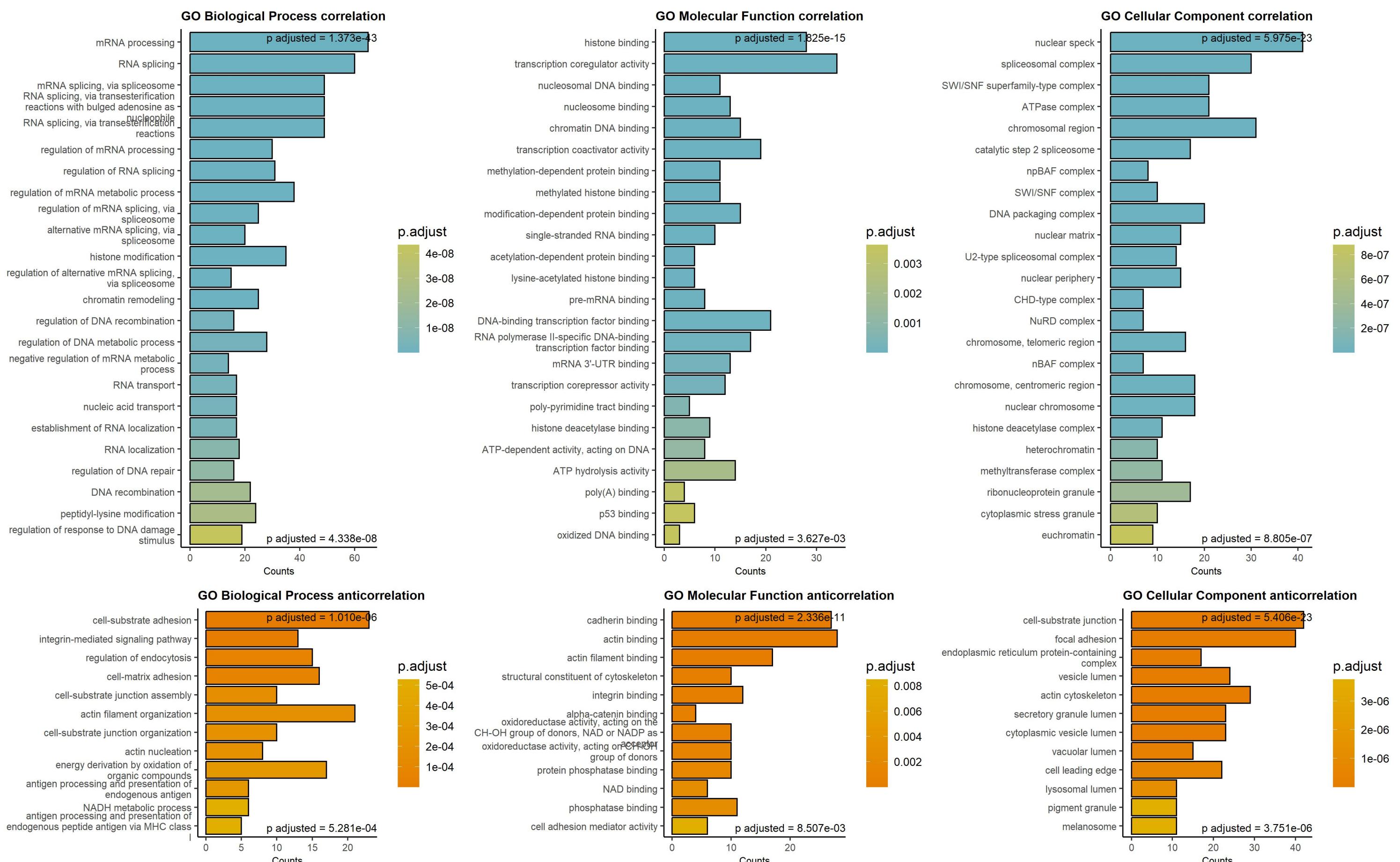
Differentially expressed proteins in solid cancers at absence/low amount of CBX1 , DB1  
p-value < 0.05 & logFC > 1.2



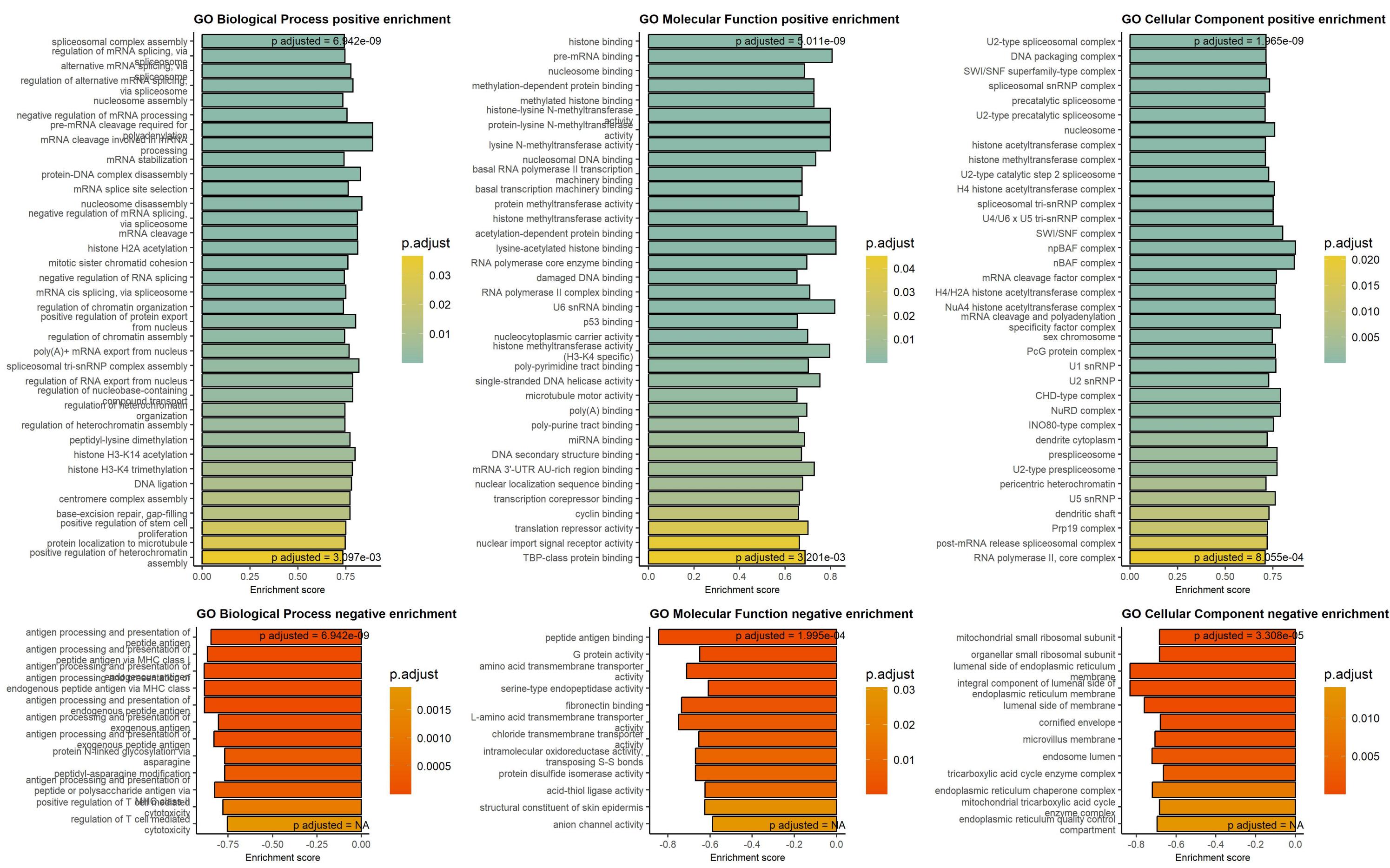
Sorted by p values!  
Downregulated in solid cancers at low/absent CBX1 Upregulated in solid cancers at low/absent CBX1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.01	5.59e-30	KIF1A	kinesin family member 1A	0.22	4.62e-22	HIBADH	3-hydroxyisobutyrate dehydrogenase
-1.13	5.29e-28	CRMP1	collapsin response mediator protein	0.26	6.24e-22	PLEC	plectin
-0.8	4.84e-27	PRR36	proline rich 36	0.47	5.16e-21	GSTK1	glutathione S-transferase kappa 1
-0.43	1.69e-26	POGZ	pogo transposable element derived w	0.19	7.86e-21	LMNA	lamin A/C
-0.96	2.25e-24	ZNF428	zinc finger protein 428	0.11	1.16e-19	IQGAP1	IQ motif containing GTPase activati
-0.49	2.33e-24	SOGA3	SOGA family member 3	0.24	3.25e-19	ESYT2	extended synaptotagmin 2
-1.1	3.16e-24	HDGFL3	HDGF like 3	0.16	3.36e-19	CTSD	cathepsin D
-0.66	4.12e-24	CHGA	chromogranin A	0.35	4.16e-19	SUCLG2	succinate-CoA ligase GDP-forming su
-0.97	7.96e-24	SCML2	Scm polycomb group protein like 2	0.86	4.57e-18	MVP	major vault protein
-0.11	2.36e-23	PARP1	Poly(ADP-ribose) polymerase 1	0.08	6.39e-17	RAC1	Rac family small GTPase 1
-0.86	5.38e-23	SPINDOC	spindlin interactor and repressor o	0.12	7.71e-17	OGDH	oxoglutarate dehydrogenase
-0.08	3.61e-22	TMPO	thymopoietin	0.53	7.90e-17	EHD4	EH domain containing 4
-0.9	4.09e-22	DPYSL5	dihydropyrimidinase like 5	0.87	3.13e-16	NCEH1	neutral cholesterol ester hydrolase
-0.83	5.16e-21	KAT7	lysine acetyltransferase 7	0.26	5.40e-16	HEXB	hexosaminidase subunit beta
-0.93	5.95e-21	ZNF280C	zinc finger protein 280C	0.73	6.58e-16	ITPR3	inositol 1,4,5-trisphosphate recept
-0.52	7.52e-21	ELAVL3	ELAV like RNA binding protein 3	0.45	6.58e-16	MYO1C	myosin IC
-0.52	8.37e-21	SCG3	secretogranin III	0.69	8.23e-16	ITPRID2	ITPR interacting domain containing
-0.57	1.25e-20	FSD1	fibronectin type III and SPRY domai	0.82	2.09e-15	MYOF	myoferlin
-0.89	1.38e-20	NSD2	nuclear receptor binding SET domain	0.1	2.51e-15	ATP1A1	ATPase Na+/K+ transporting subunit
-0.14	1.38e-20	RBBP4	RB binding protein 4, chromatin rem	0.79	2.82e-15	TCIRG1	T cell immune regulator 1, ATPase H
-0.13	1.54e-20	HDGFL2	HDGF like 2	0.07	3.05e-15	VDAC1	voltage dependent anion channel 1
-0.06	2.66e-20	TARDBP	TAR DNA binding protein	0.2	3.16e-15	AHNAK	AHNAK nucleoprotein
-0.08	4.64e-20	HCFC1	host cell factor C1	1.14	4.73e-15	CTSZ	cathepsin Z
-0.86	4.86e-20	LUC7L	LUC7 like	0.11	5.29e-15	RPN2	ribophorin II
-0.08	7.27e-20	TRIM28	tripartite motif containing 28	0.33	5.36e-15	ANXA2	annexin A2
-0.08	8.26e-20	HNRNPDL	heterogeneous nuclear ribonucleopro	0.52	8.12e-15	TMEM214	transmembrane protein 214
-0.83	8.61e-20	ZMYM3	zinc finger MYM-type containing 3	0.88	8.72e-15	SP100	SP100 nuclear antigen
-0.79	1.16e-19	TRIM24	tripartite motif containing 24	0.77	1.08e-14	ADGRE5	adhesion G protein-coupled receptor
-0.9	1.16e-19	TSPYL5	TSPY like 5	0.78	1.08e-14	ENDOD1	endonuclease domain containing 1
-0.89	1.16e-19	MEAF6	MYST/Esa1 associated factor 6	0.5	1.15e-14	YBX3	Y-box binding protein 3
-0.39	1.35e-19	NAPB	NSF attachment protein beta	0.23	1.86e-14	FAM3C	FAM3 metabolism regulating signalin
-0.63	1.40e-19	WASF1	WASP family member 1	0.76	2.21e-14	PARP4	Poly(ADP-ribose) polymerase family

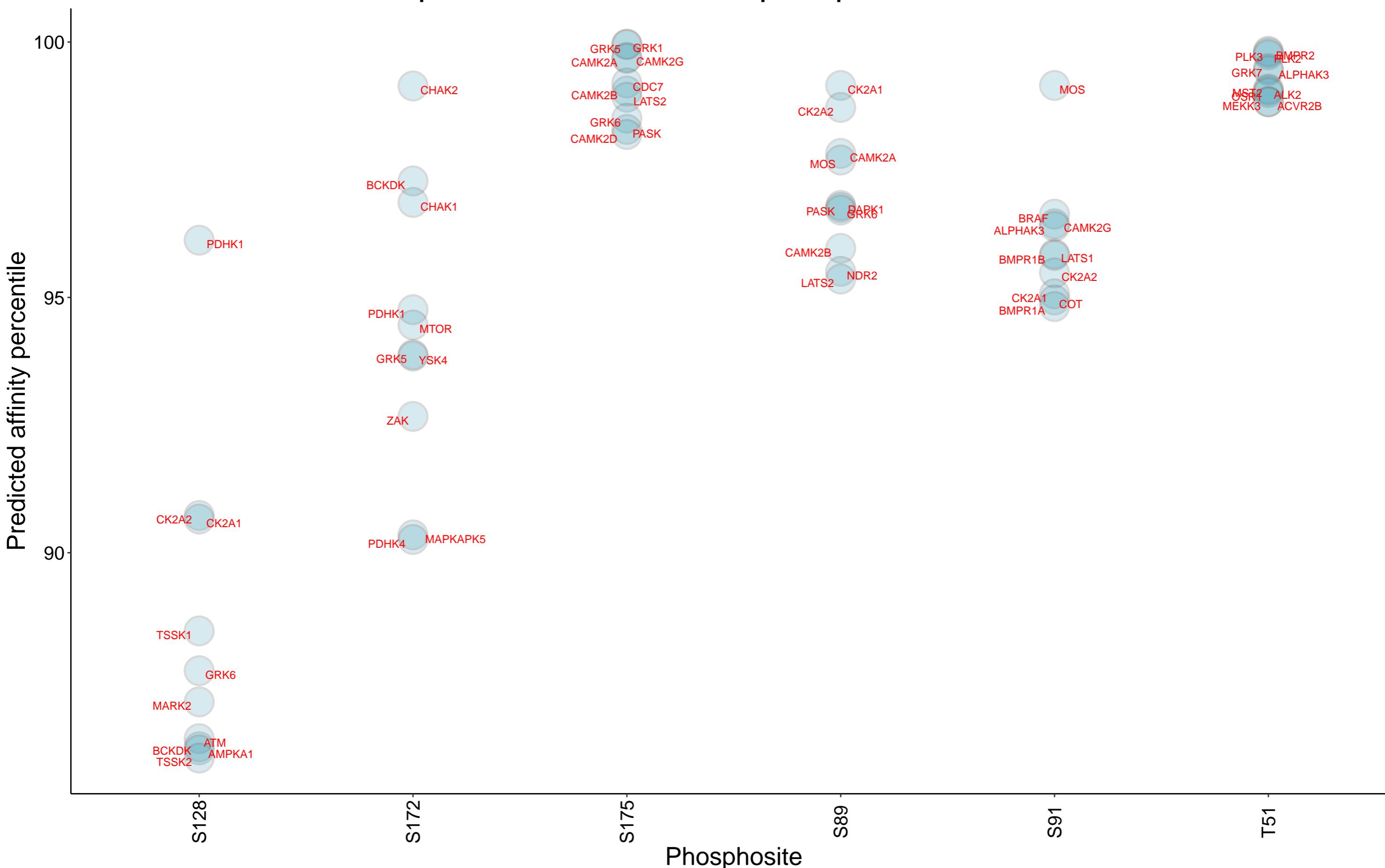
# Top 250 correlation coefficients overrepresentation, CBX1 protein, DB1



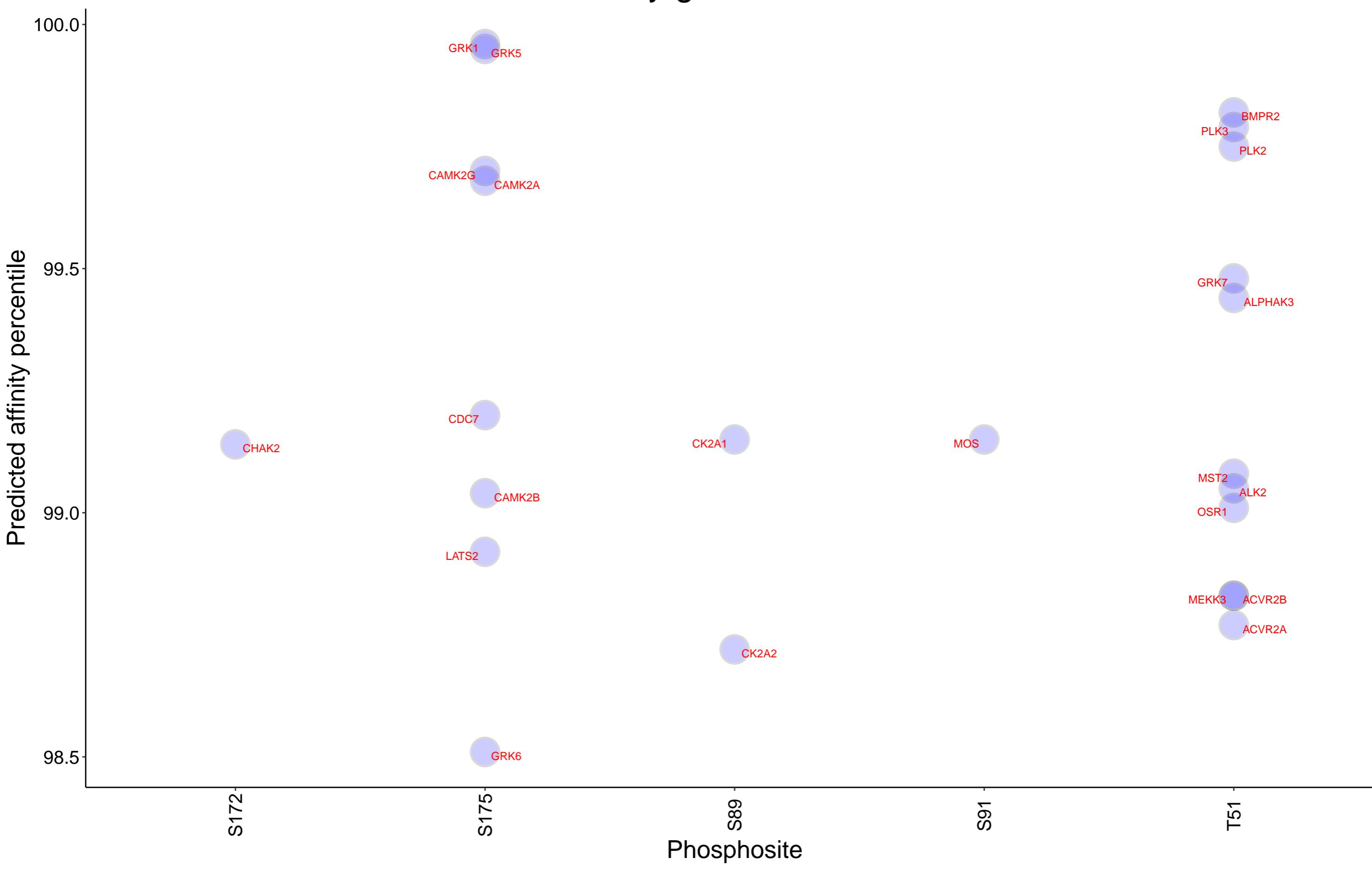
# Gene Set Enrichment analysis on protein correlation coefficients, CBX1 protein, DB1



# Top 10 kinases for each phosphosite in CBX1



## Kinases with affinity greater than 98.5% to CBX1



## Top 15 positive correlation coefficients for CBX1 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

