

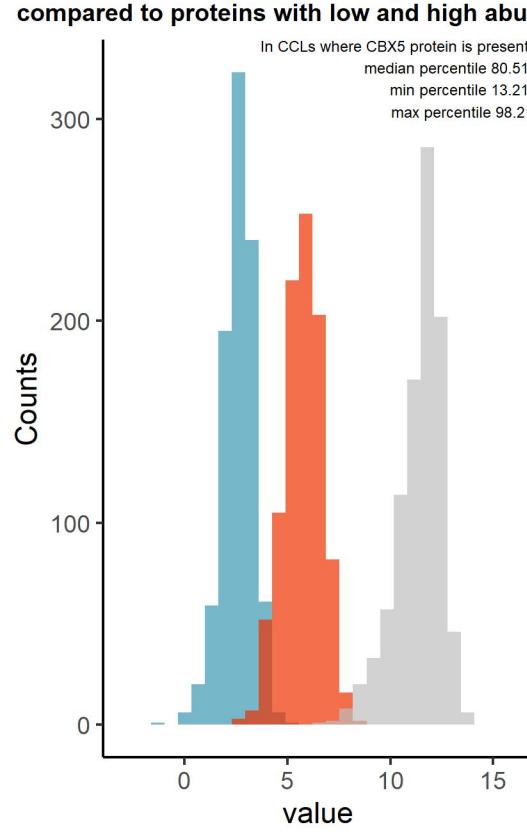
CBX5

Protein name: CBX5 ; UNIPROT: P45973 ; Gene name: chromobox 5
 Ligandable: NA ; Ligandable_by_Chem: NA ; Is_enzyme: NA (<https://cansar.ai/>)

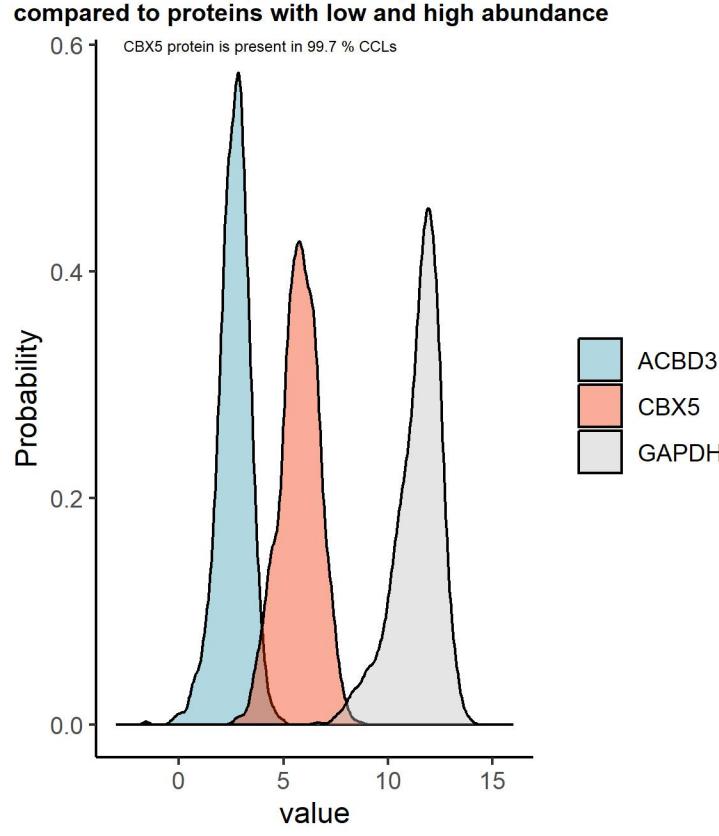
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

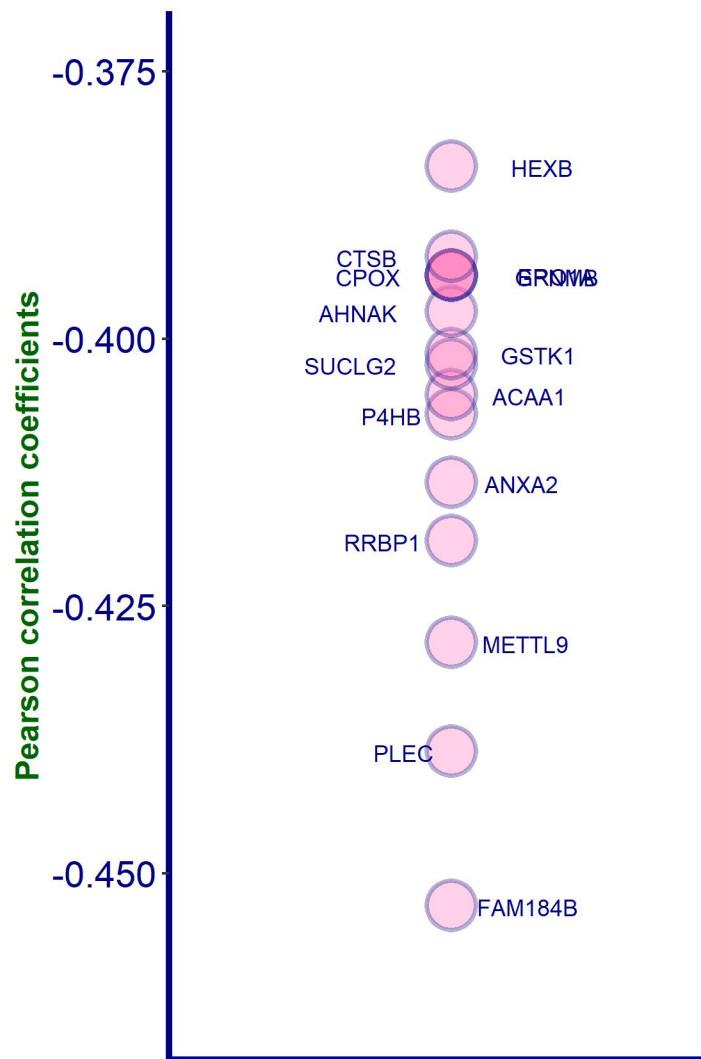
Histogram of CBX5 protein compared to proteins with low and high abundance



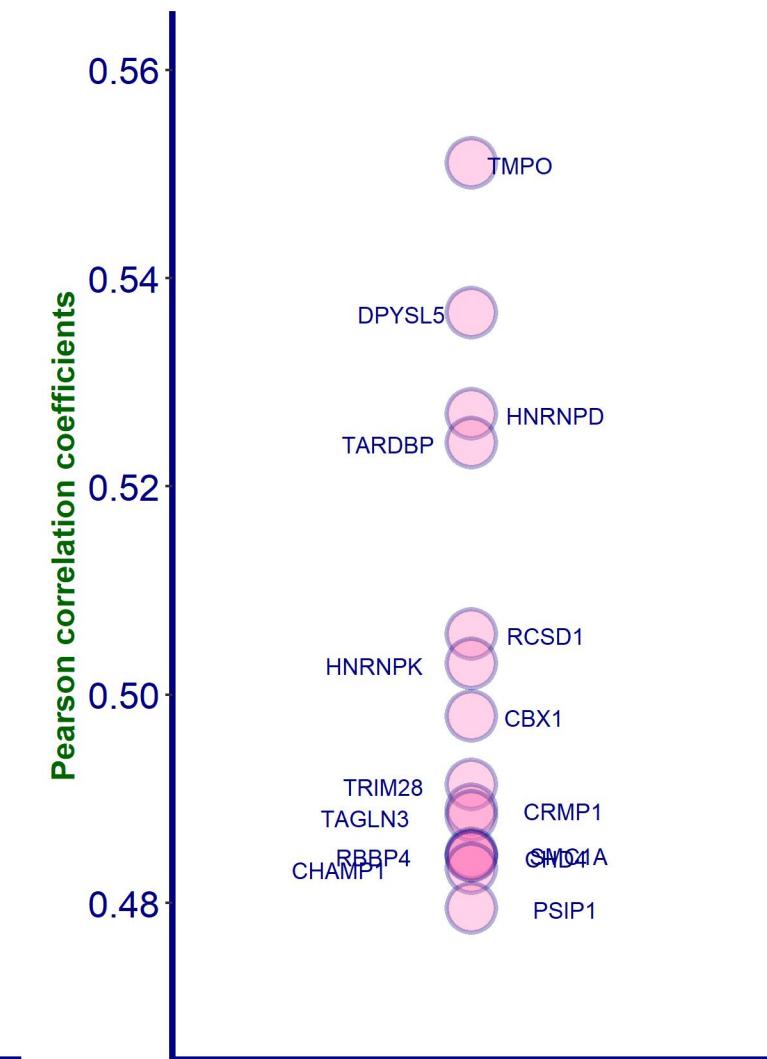
Density plot of CBX5 protein compared to proteins with low and high abundance



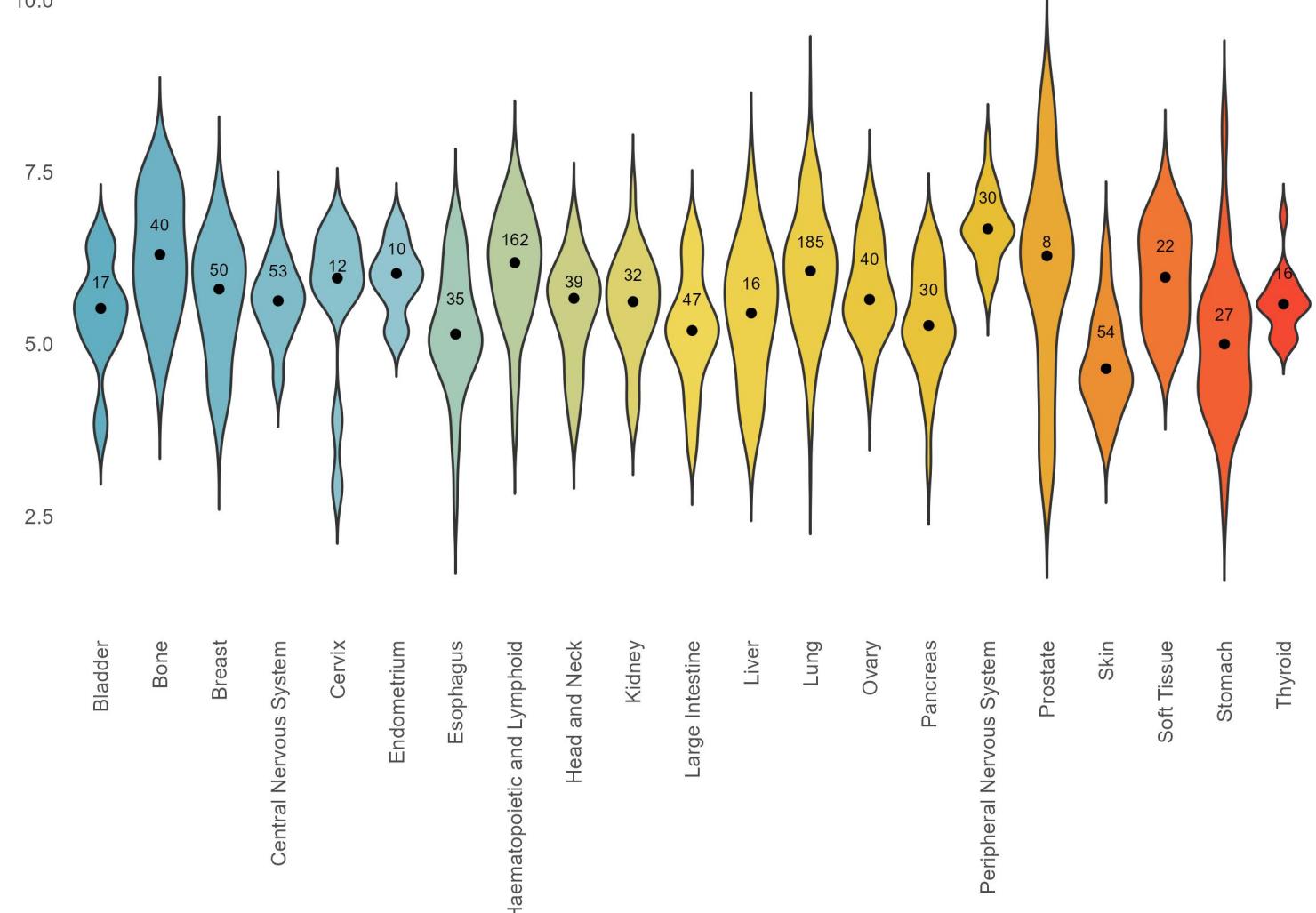
Top negative correlations of CBX5 protein, DB1



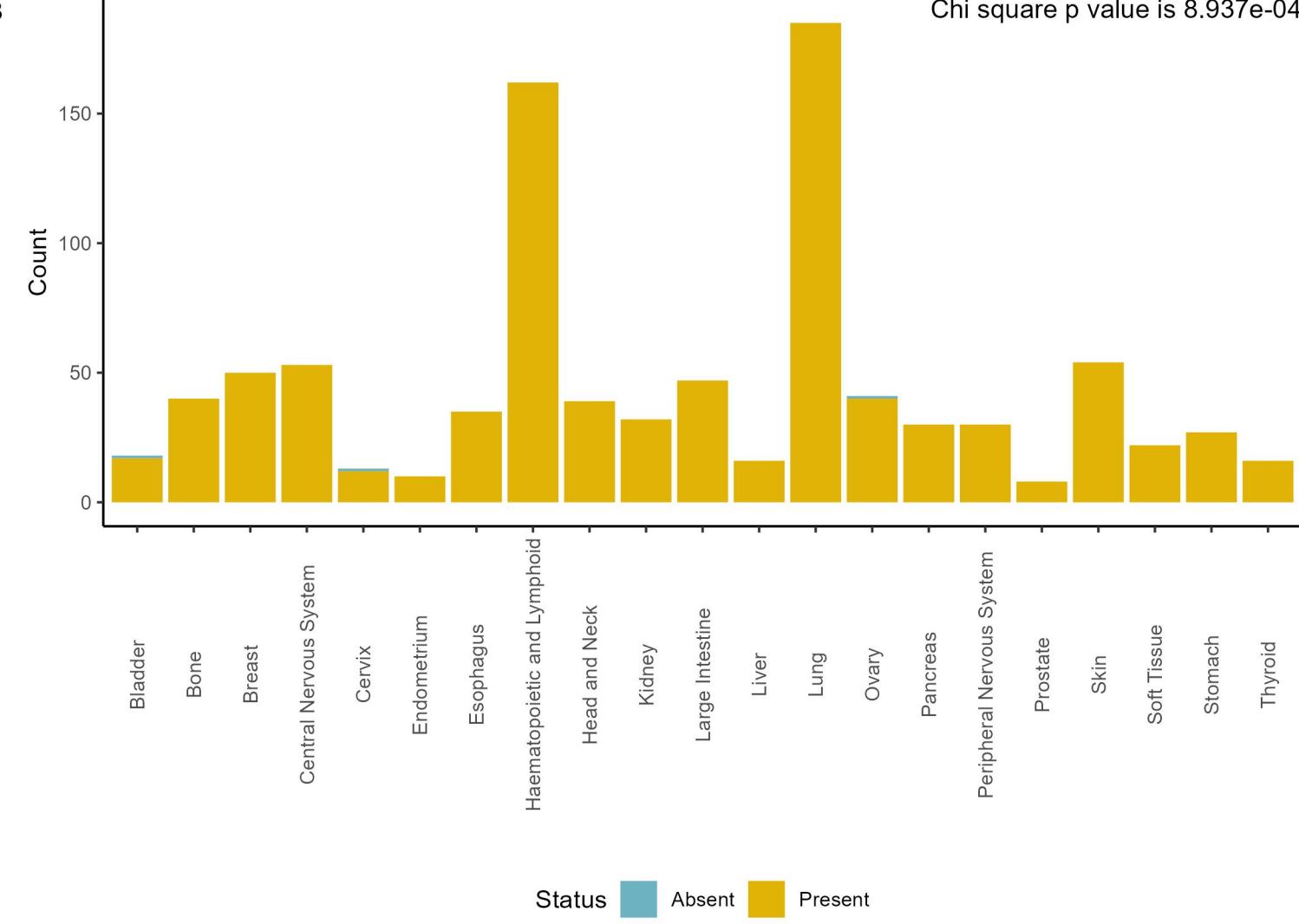
Top positive correlations of CBX5 protein, DB1



Amount of CBX5 protein, number of CCLs where it is present by tissue, DB1



Present and absent CBX5 protein counts by tissue, DB1

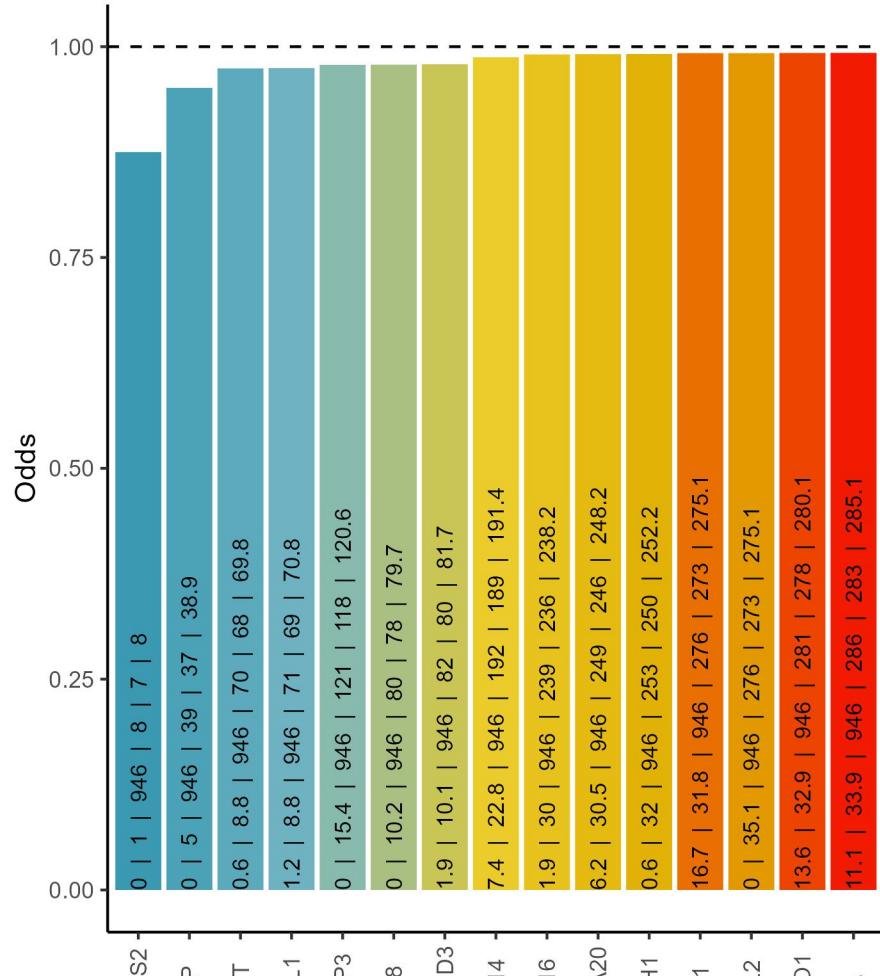


Cooccurrence with CBX5 protein, DB1

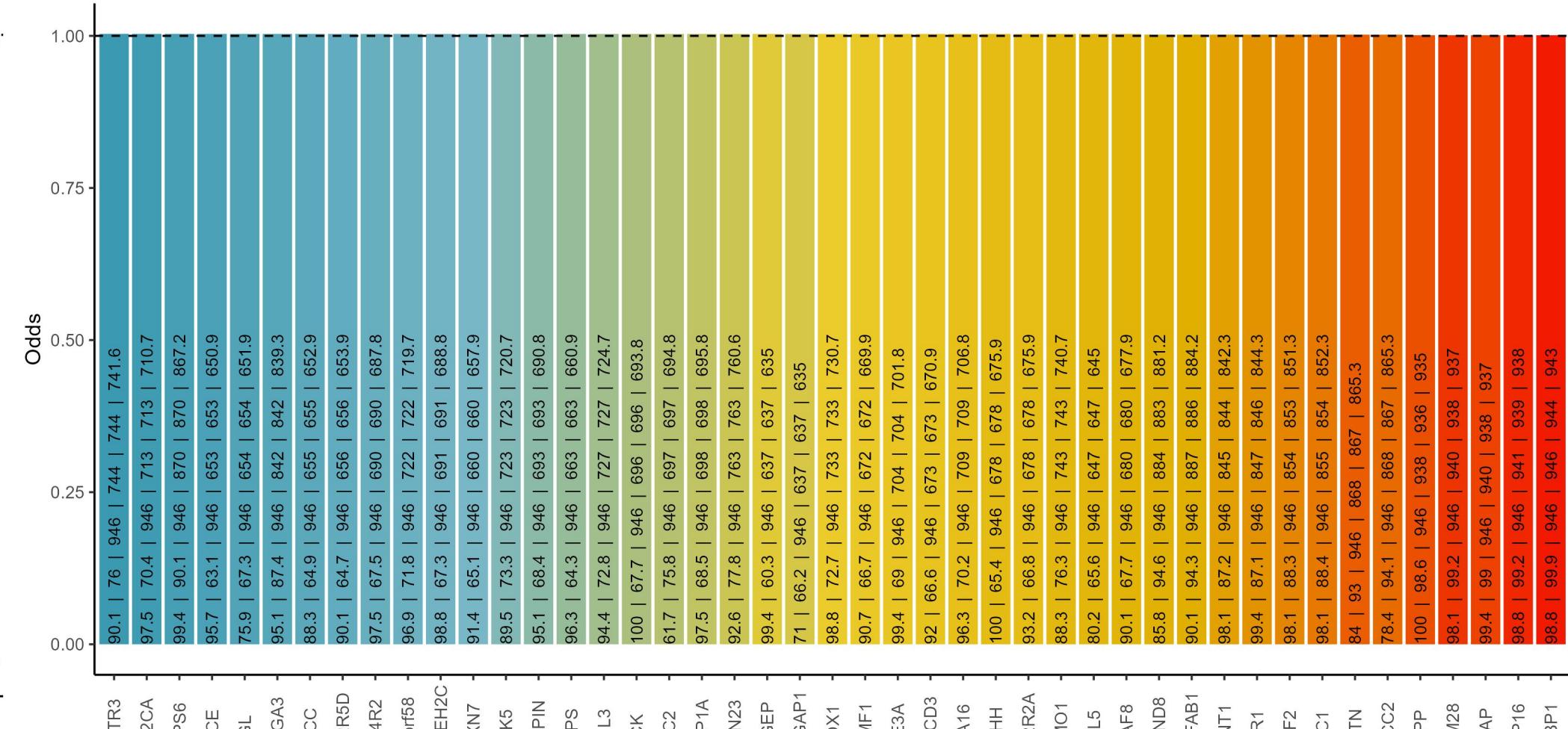
% of CBX5 in blood cancers: 100 ; % of CBX5 in solid cancers: 99.6

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CBX5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

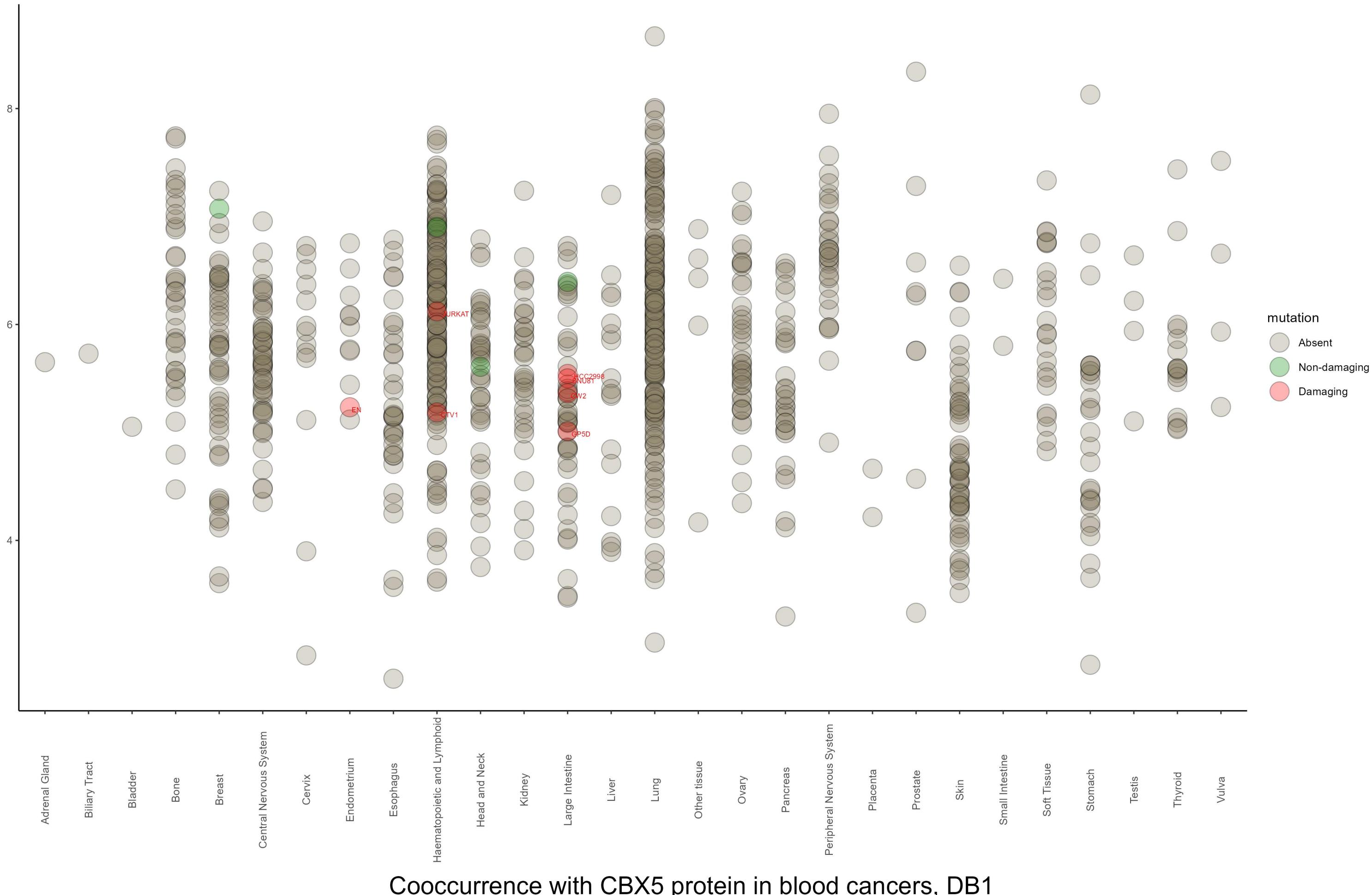
Negative cooccurrence



Positive cooccurrence



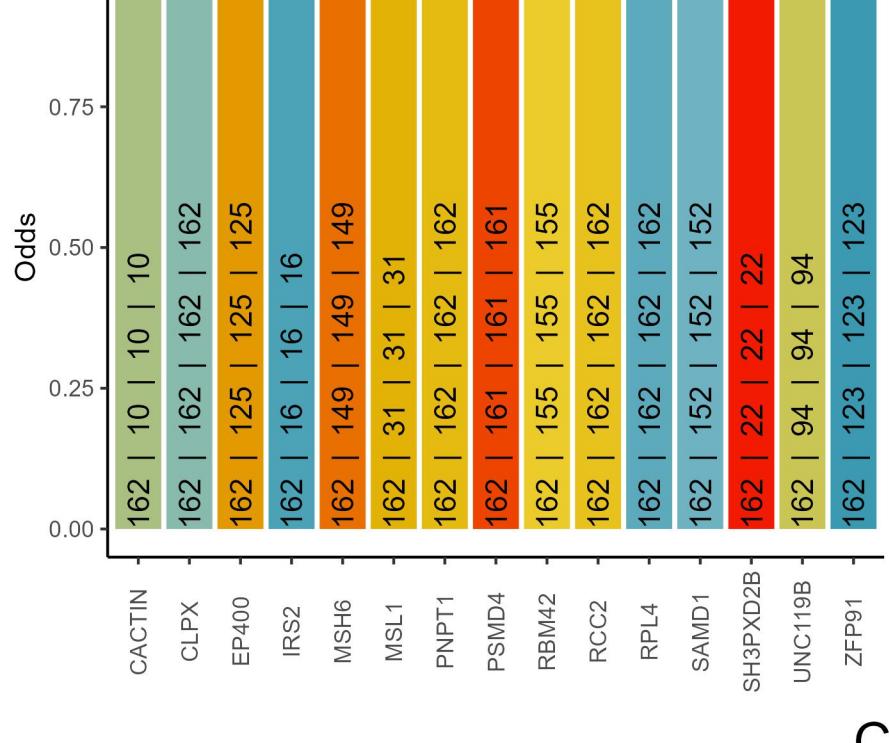
Amount of CBX5 protein and mutation status by tissue, DB1



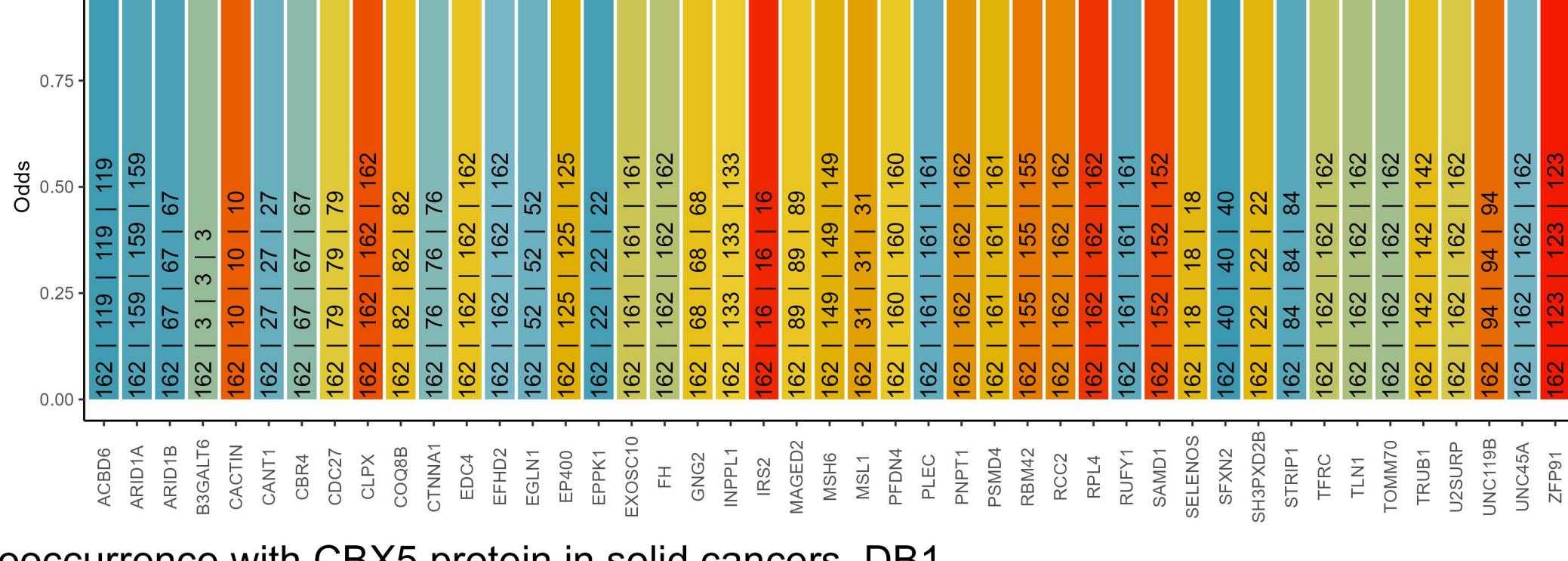
Cooccurrence with CBX5 protein in blood cancers, DB1

The text in the bars: incidence of CBX5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



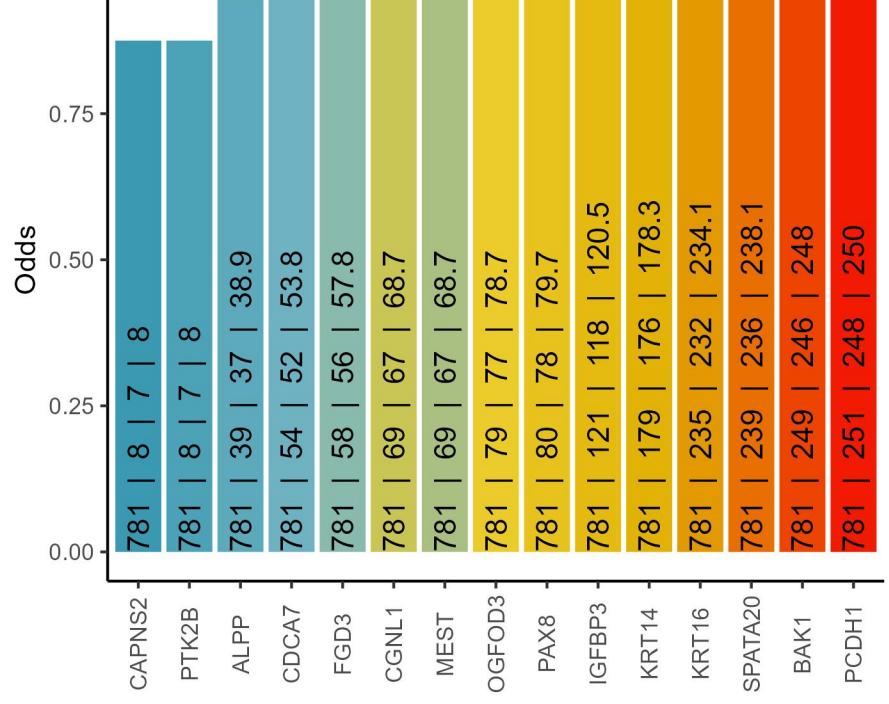
Positive cooccurrence



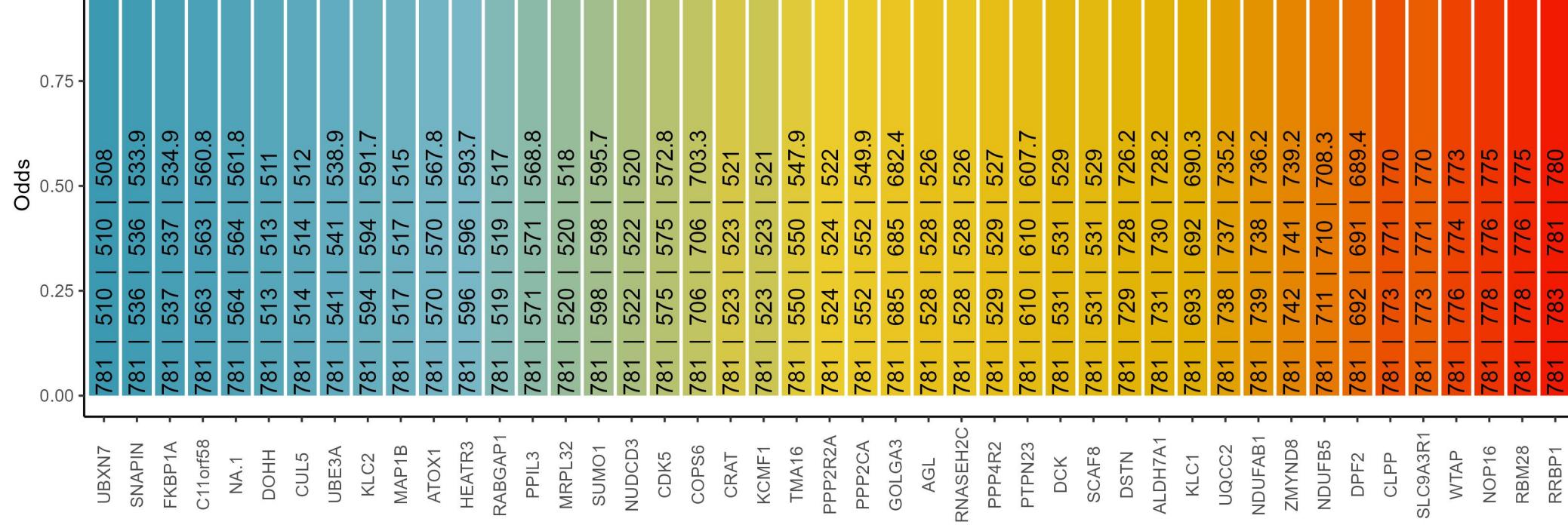
Cooccurrence with CBX5 protein in solid cancers, DB1

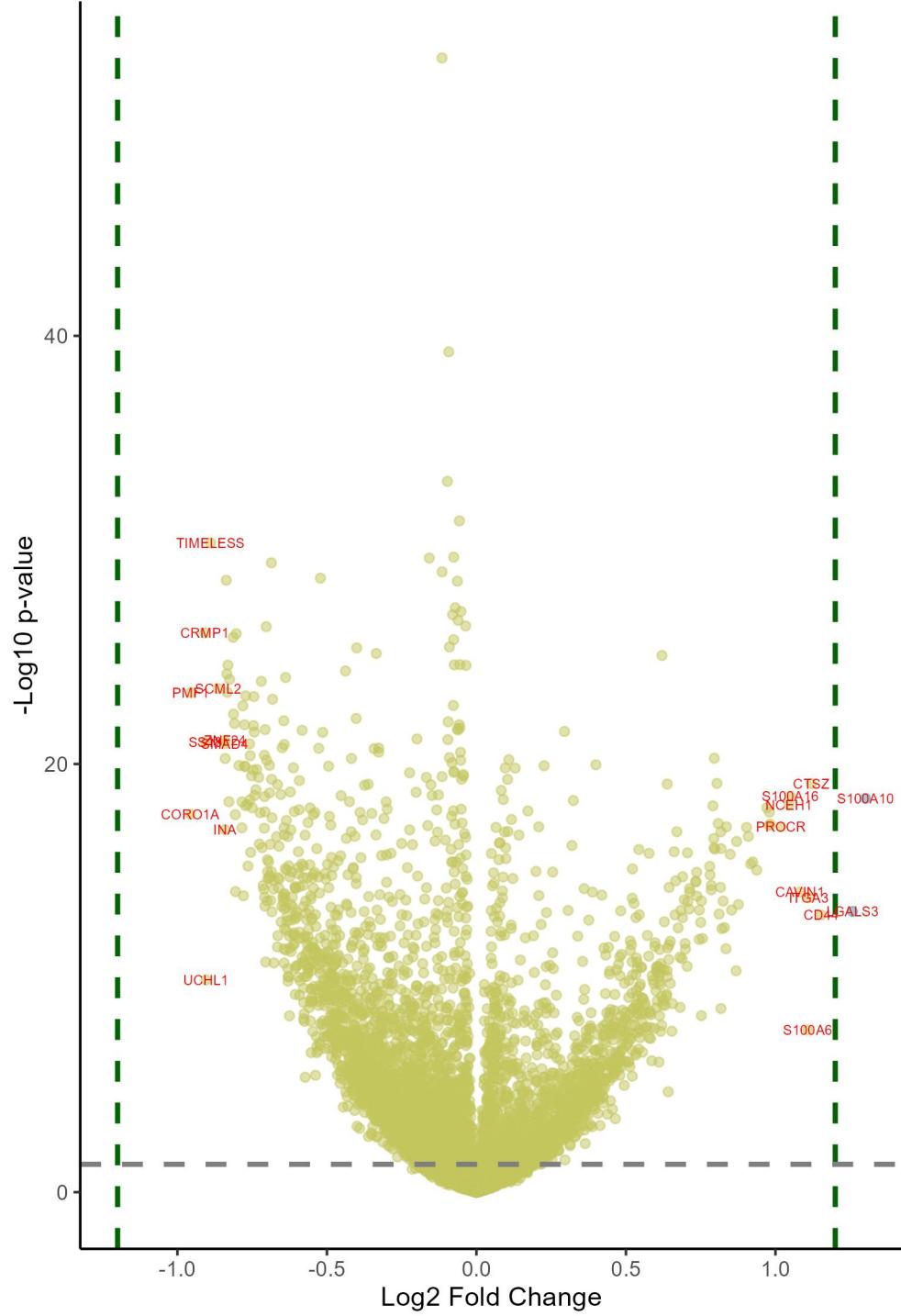
The text in the bars: incidence of CBX5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



Positive cooccurrence



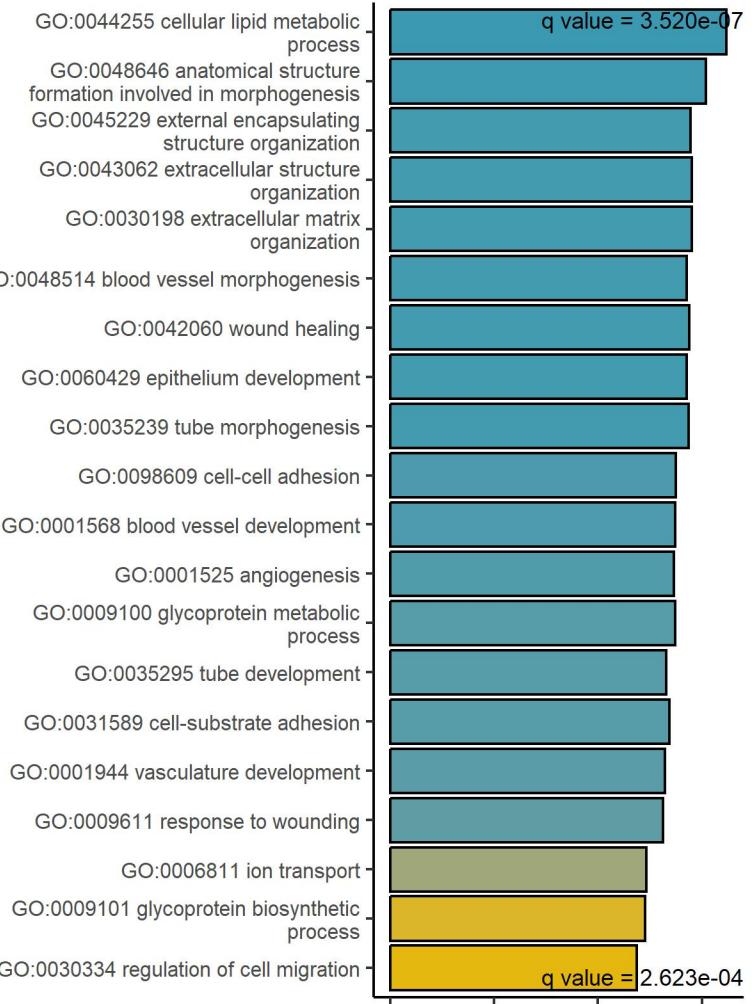


Downregulated at low/absent CBX5 Upregulated at low/absent CBX5

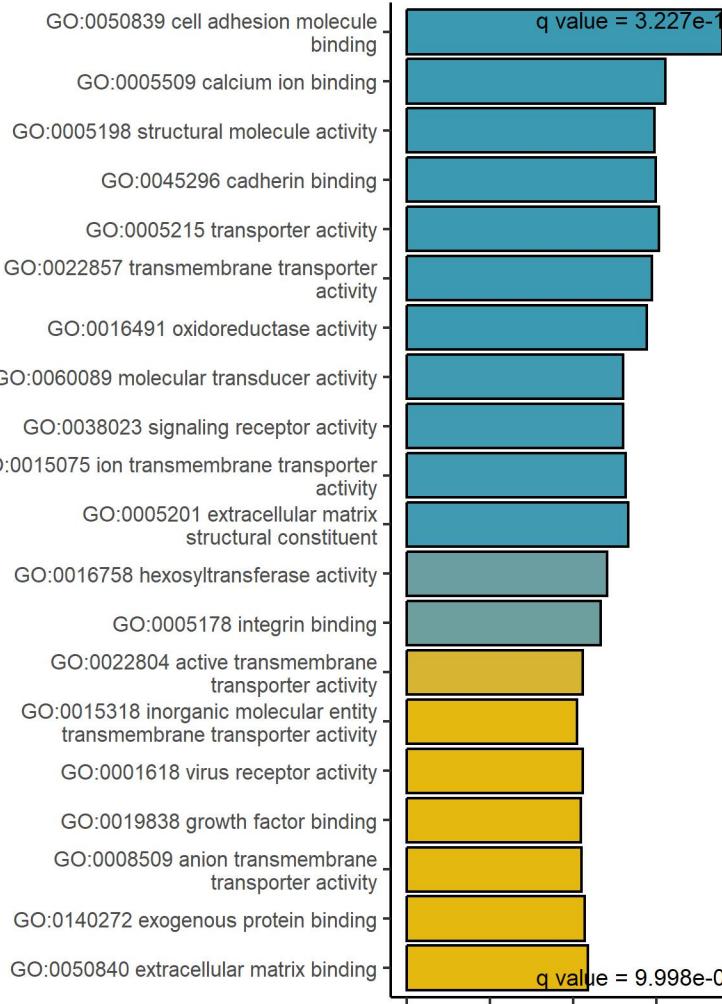
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.96	9.42e-17	CORO1A	coronin 1A	1.3	2.09e-17	S100A10	S100 calcium binding protein A10
-0.95	7.84e-22	PMF1	polyamine modulated factor 1	1.26	1.30e-12	LGALS3	galectin 3
-0.91	2.46e-24	CRMP1	collapsin response mediator protein	1.15	1.82e-12	CD44	CD44 molecule (Indian blood group)
-0.91	9.70e-20	SS18	SS18 subunit of BAF chromatin remod	1.12	4.98e-18	CTSZ	cathepsin Z
-0.9	1.16e-09	UCHL1	ubiquitin C-terminal hydrolase L1	1.11	3.29e-13	ITGA3	integrin subunit alpha 3
-0.89	5.17e-28	TIMELESS	timeless circadian regulator	1.11	1.60e-07	S100A6	S100 calcium binding protein A6
-0.86	5.37e-22	SCML2	Scm polycomb group protein like 2	1.08	1.94e-13	CAVIN1	caveolae associated protein 1
-0.84	1.14e-19	SMAD4	SMAD family member 4	1.05	1.65e-17	S100A16	S100 calcium binding protein A16
-0.84	4.27e-16	INA	internexin neuronal intermediate fi	1.04	3.87e-17	NCEH1	neutral cholesterol ester hydrolase
-0.84	8.27e-20	ZNF24	zinc finger protein 24	1.02	3.27e-16	PROCR	protein C receptor
-0.84	4.68e-19	BRD3	bromodomain containing 3	0.98	2.55e-16	NT5E	5'-nucleotidase ecto
-0.84	1.45e-26	TRIM24	tripartite motif containing 24	0.98	7.85e-17	CD59	CD59 molecule (CD59 blood group)
-0.83	1.25e-22	ZNF428	zinc finger protein 428	0.98	2.89e-16	TGM2	transglutaminase 2
-0.83	7.84e-22	NSD3	nuclear receptor binding SET domain	0.97	5.28e-17	CAVIN3	caveolae associated protein 3
-0.83	5.31e-23	SAMD1	sterile alpha motif domain containi	0.94	2.28e-14	MYOF	myoferlin
-0.83	2.88e-17	SNRNP27	small nuclear ribonucleoprotein U4/U	0.92	1.03e-14	ITGA2	integrin subunit alpha 2
-0.83	2.12e-22	NSD2	nuclear receptor binding SET domain	0.92	1.26e-14	EGFR	epidermal growth factor receptor
-0.81	3.65e-24	MAZ	MYC associated zinc finger protein	0.91	8.15e-16	SQOR	sulfide quinone oxidoreductase
-0.81	6.92e-21	EZH2	enhancer of zeste 2 polycomb repres	0.9	3.45e-16	EPHA2	EPH receptor A2
-0.81	1.75e-20	HIRIP3	HIRA interacting protein 3	0.88	6.54e-13	GPRC5A	G protein-coupled receptor class C
-0.81	9.76e-17	HDHD2	haloacid dehalogenase like hydrolas	0.87	1.34e-15	ADAM9	ADAM metallopeptidase domain 9
-0.81	1.85e-13	TUBB2B	tubulin beta 2B class IIb	0.87	4.71e-10	ANXA1	annexin A1
-0.8	2.61e-24	SPINDOC	spindlin interactor and repressor o	0.85	1.14e-12	RHOC	ras homolog family member C
-0.79	9.10e-19	SMARCD1	SWI/SNF related, matrix associated,	0.85	4.76e-15	FHL2	four and a half LIM domains 2
-0.78	3.55e-16	USP11	ubiquitin specific peptidase 11	0.84	3.27e-16	MVP	major vault protein
-0.78	2.91e-17	EPB41	erythrocyte membrane protein band 4	0.83	5.30e-11	CAV1	caveolin 1
-0.78	2.89e-21	ZMYM3	zinc finger MYM-type containing 3	0.83	6.50e-12	ITGB4	integrin subunit beta 4
-0.78	2.80e-13	GABARPL2	GABA type A receptor associated pro	0.83	4.66e-13	MMP14	matrix metallopeptidase 14
-0.78	9.41e-19	NUSAP1	nucleolar and spindle associated pr	0.82	7.25e-12	ANXA3	annexin A3

GAGE analysis on upregulated and downregulated proteins at low/absent CBX5 protein, DB1

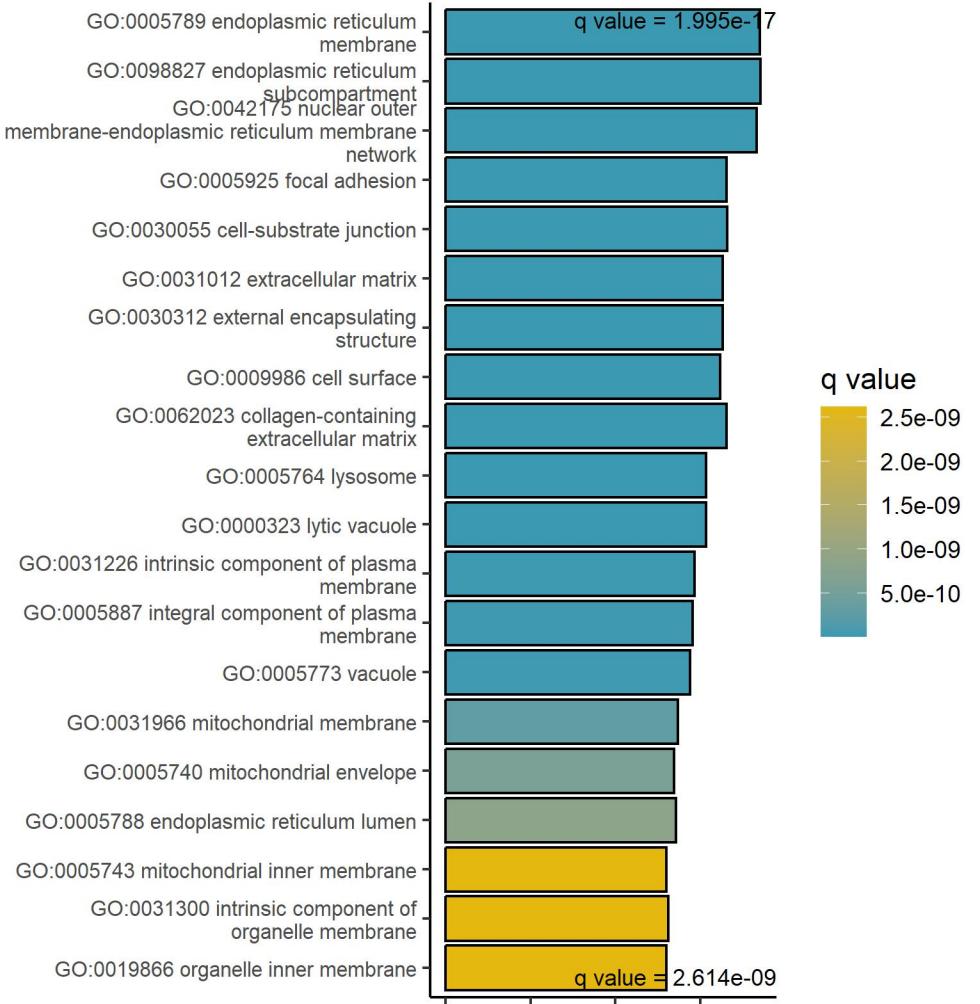
GO Biological Process upregulated



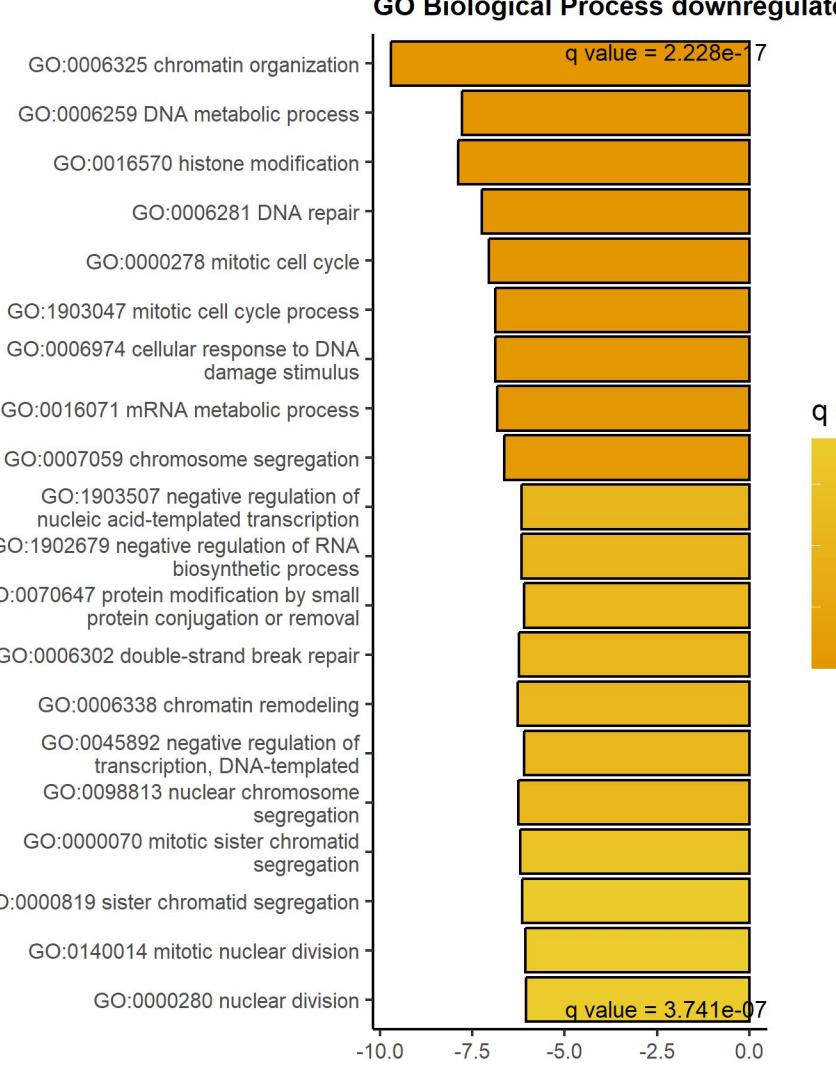
GO Molecular Function upregulated



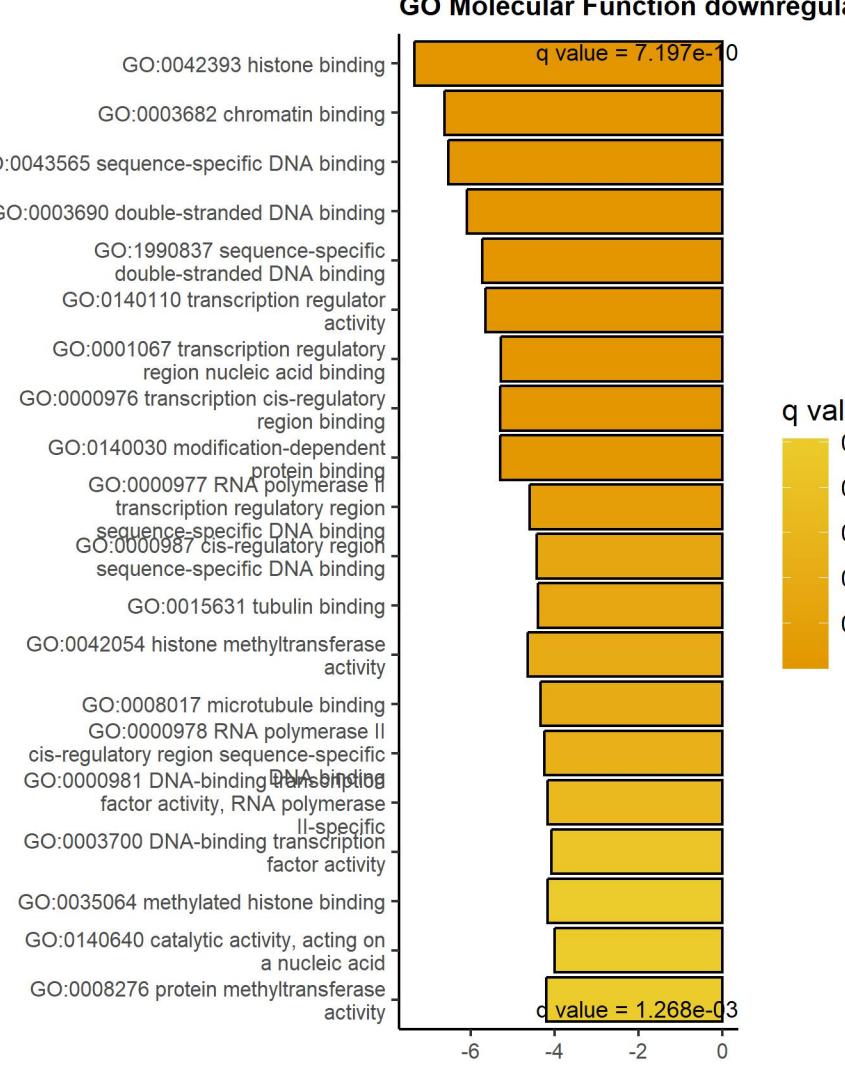
GO Cellular Component upregulated

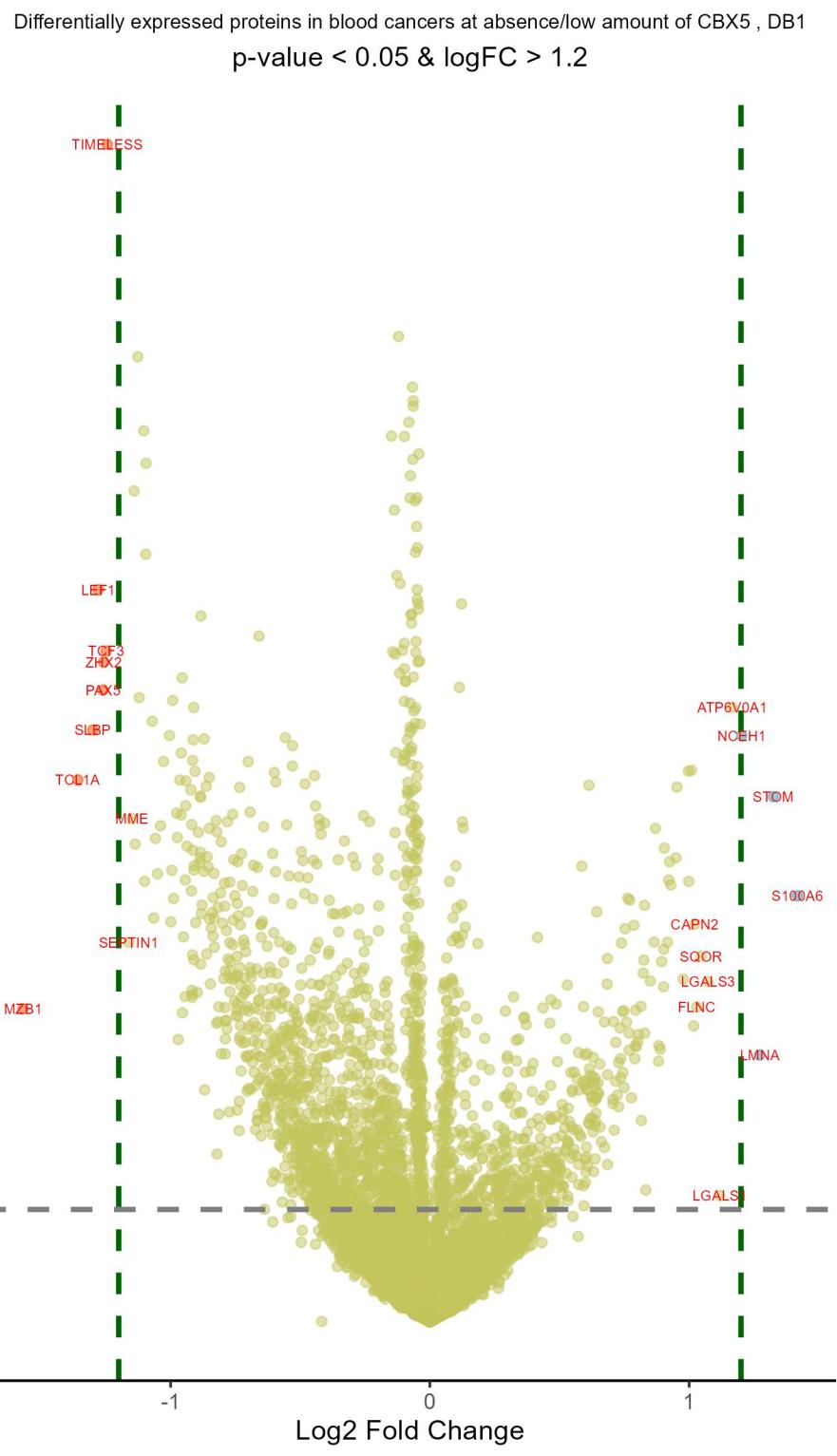


GO Biological Process downregulated

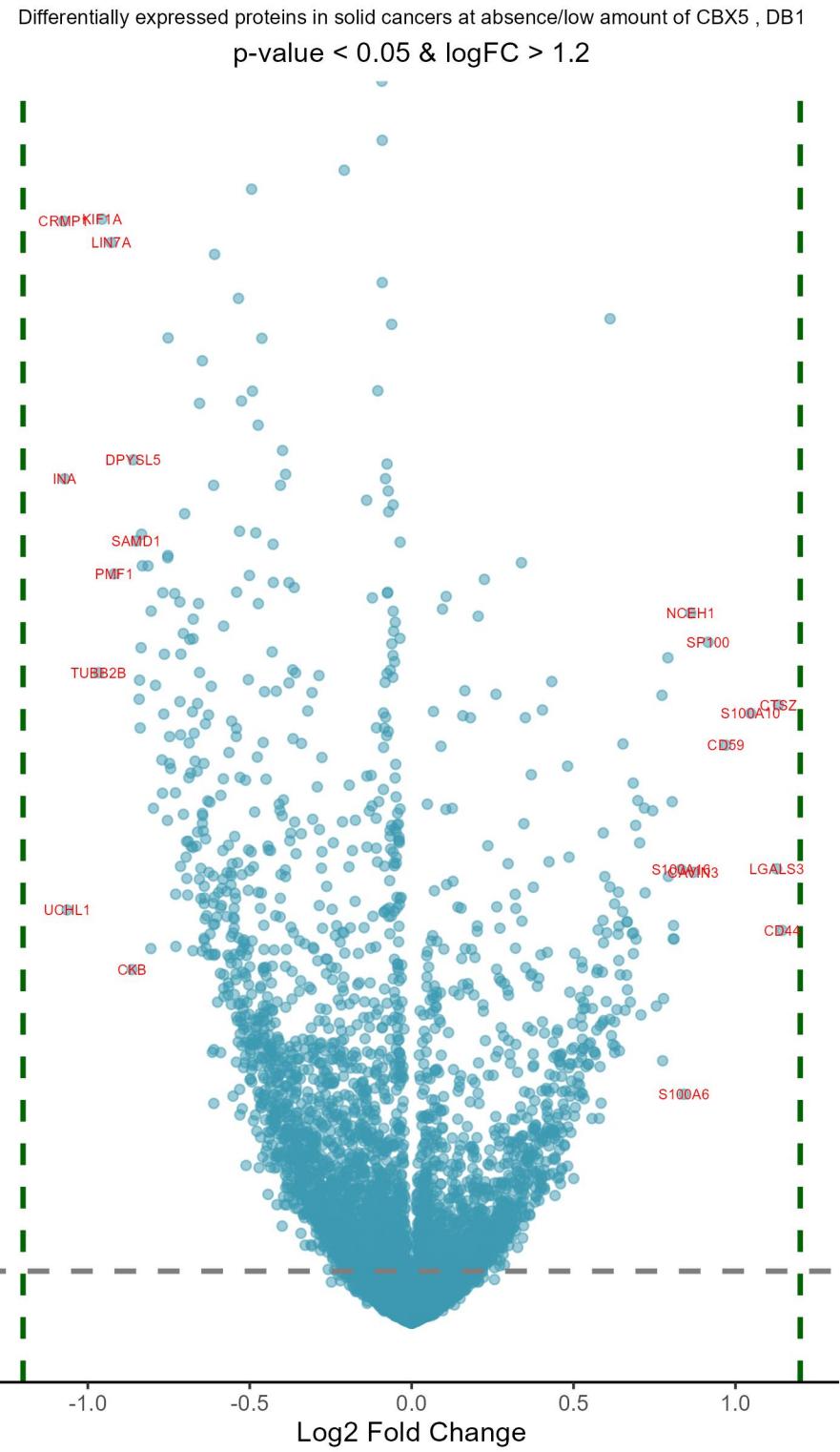


GO Molecular Function downregulated





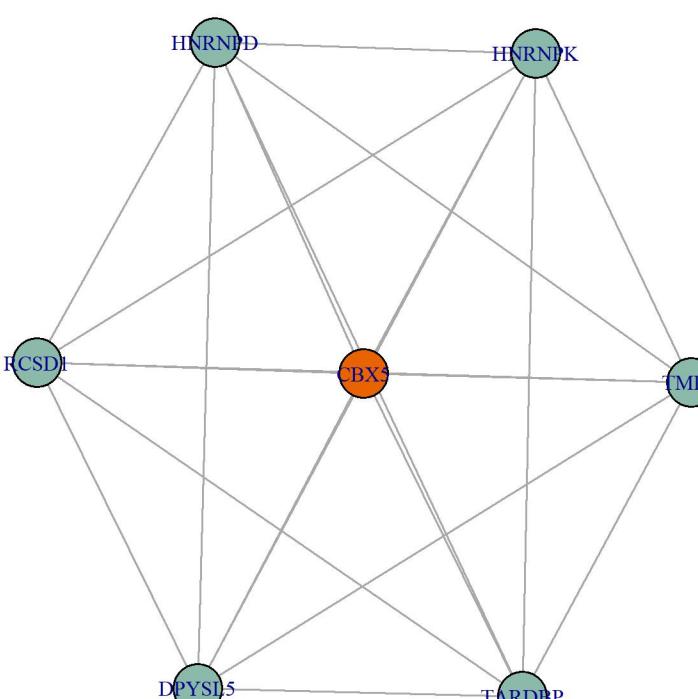
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.57	3.34e-03	MZB1	marginal zone B and B1 cell specific	1.42	3.36e-04	S100A6	S100 calcium binding protein A6
-1.36	3.53e-05	TCL1A	TCL1 family AKT coactivator A	1.32	4.74e-05	STOM	stomatin
-1.3	1.35e-05	SLBP	stem-loop binding protein	1.27	8.05e-03	LMNA	lamin A/C
-1.28	7.88e-07	LEF1	lymphoid enhancer binding factor 1	1.2	1.50e-05	NCEH1	neutral cholesterol ester hydrolase
-1.26	5.82e-06	PAX5	paired box 5	1.17	8.31e-06	ATP6V0A1	ATPase H ⁺ transporting V0 subunit a
-1.26	3.25e-06	ZHX2	zinc fingers and homeoboxes 2	1.12	9.54e-02	LGALS1	galectin 1
-1.25	2.74e-06	TCF3	transcription factor 3	1.07	2.00e-03	LGALS3	galectin 3
-1.24	7.65e-11	TIMELESS	timeless circadian regulator	1.05	1.18e-03	SQOR	sulfide quinone oxidoreductase
-1.16	8.89e-04	SEPTIN1	septin 1	1.03	3.24e-03	FLNC	filamin C
-1.15	7.62e-05	MME	membrane metalloendopeptidase	1.02	6.07e-04	CAPN2	calpain 2
-1.14	9.91e-08	KAT8	lysine acetyltransferase 8	1.02	4.59e-03	ANXA1	annexin A1
-1.14	1.20e-04	GABARPL2	GABA type A receptor associated pro	1.01	2.96e-05	EML3	EMAP like 3
-1.13	1.10e-08	ASF1B	anti-silencing function 1B histone	1	2.41e-04	PLBD2	phospholipase B domain containing 2
-1.12	7.00e-06	MAZ	MYC associated zinc finger protein	1	2.99e-05	DUSP3	dual specificity phosphatase 3
-1.1	3.37e-08	BIRC5	baculoviral IAP repeat containing 5	0.98	1.91e-03	CA2	carbonic anhydrase 2
-1.1	2.41e-04	SASH3	SAM and SH3 domain containing 3	0.95	3.95e-05	ERMP1	endoplasmic reticulum metallopeptid
-1.1	3.57e-07	NCAPH2	non-SMC condensin II complex subuni	0.95	1.57e-04	PLOD3	procollagen-lysine,2-oxoglutarate 5
-1.09	5.41e-08	PDE6D	phosphodiesterase 6D	0.93	2.61e-04	DTD1	D-aminoacyl-tRNA deacylase 1
-1.07	1.15e-05	FAIM	Fas apoptotic inhibitory molecule	0.92	1.66e-04	SIL1	SIL1 nucleotide exchange factor
-1.06	5.29e-04	CD38	CD38 molecule	0.92	2.37e-04	NUDT19	nudix hydrolase 19
-1.06	1.07e-04	CD19	CD19 molecule	0.92	8.89e-04	PYGL	glycogen phosphorylase L
-1.05	2.07e-04	CD81	CD81 molecule	0.9	1.30e-04	CMBL	carboxymethylenebutenolidase homolo
-1.04	8.36e-05	DCAF16	DDB1 and CUL4 associated factor 16	0.9	1.01e-03	SPART	spartin
-1.03	2.46e-05	GPALPP1	GPALPP motifs containing 1	0.9	2.19e-03	NIBAN1	niban apoptosis regulator 1
-1	1.50e-05	SYNE2	spectrin repeat containing nuclear	0.89	1.31e-03	TYMP	thymidine phosphorylase
-1	5.76e-04	CD79B	CD79b molecule	0.89	7.20e-03	ZYX	zyxin
-1	1.96e-04	SCML2	Scm polycomb group protein like 2	0.88	6.68e-03	GSN	gelsolin
-0.99	7.41e-06	YY1	YY1 transcription factor	0.88	9.03e-03	MVP	major vault protein
-0.99	3.55e-04	GINS1	GINS complex subunit 1	0.87	8.65e-05	LRPAP1	LDL receptor related protein associ



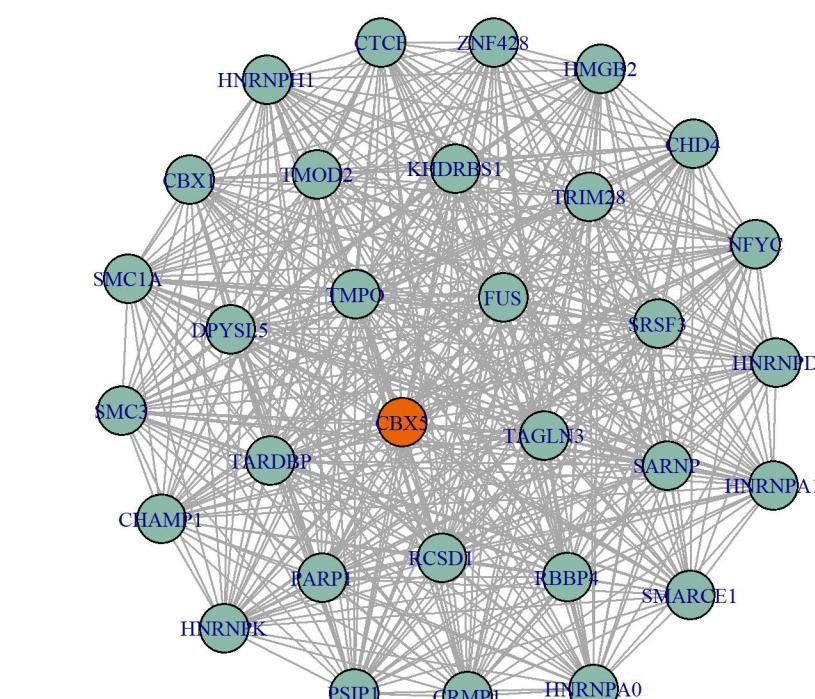
Downregulated in solid cancers at low/absent CBX5				Upregulated in solid cancers at low/absent CBX5			
C	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
7	2.37e-25	CRMP1	collapsin response mediator protein	1.14	2.68e-09	CD44	CD44 molecule (Indian blood group antigen)
7	1.75e-19	INA	internexin neuronal intermediate filament protein	1.13	2.03e-14	CTSZ	cathepsin Z
6	9.18e-10	UCHL1	ubiquitin C-terminal hydrolase L1	1.13	1.07e-10	LGALS3	galectin 3
7	3.91e-15	TUBB2B	tubulin beta 2B class IIb	1.05	3.10e-14	S100A10	S100 calcium binding protein A10
6	2.37e-25	KIF1A	kinesin family member 1A	0.97	1.61e-13	CD59	CD59 molecule (CD59 blood group antigen)
3	7.14e-25	LIN7A	lin-7 homolog A, crumbs cell polarity gene family, member A	0.92	7.81e-16	SP100	SP100 nuclear antigen
2	2.47e-17	PMF1	polyamine modulated factor 1	0.87	1.28e-10	CAVIN3	caveolae associated protein 3
6	2.04e-08	CKB	creatine kinase B	0.86	1.68e-16	NCEH1	neutral cholesterol ester hydrolase 1
6	6.88e-20	DPYSL5	dihydropyrimidinase like 5	0.84	1.28e-05	S100A6	S100 calcium binding protein A6
5	4.50e-18	SAMD1	sterile alpha motif domain containing 1	0.83	1.11e-10	S100A16	S100 calcium binding protein A16
4	1.50e-14	HDGFL3	HDGF like 3	0.81	4.21e-09	ICAM1	intercellular adhesion molecule 1
4	5.63e-15	SS18	SS18 subunit of BAF chromatin remod	0.81	2.10e-09	NT5E	5'-nucleotidase ecto
4	6.61e-14	CLGN	calmegin	0.81	4.18e-09	TGM2	transglutaminase 2
4	1.05e-15	BRD3	bromodomain containing 3	0.8	3.33e-12	ALDH1A3	aldehyde dehydrogenase 1 family, member 3
3	3.12e-18	NSD2	nuclear receptor binding SET domain	0.79	1.58e-10	SQOR	sulfide quinone oxidoreductase
3	1.60e-17	SCML2	Scm polycomb group protein like 2	0.79	1.76e-15	MVP	major vault protein
1	1.60e-17	ZMYM4	zinc finger MYM-type containing 4	0.78	9.39e-08	ITGA3	integrin subunit alpha 3
1	6.91e-09	MACROH2A2	macroH2A.2 histone	0.78	2.28e-06	CAVIN1	caveolae associated protein 1
3	1.53e-16	NSD3	nuclear receptor binding SET domain	0.77	1.20e-14	RETSAT	retinol saturase
3	4.69e-12	FADS2	fatty acid desaturase 2	0.76	1.37e-07	GPRC5A	G protein-coupled receptor class C member 5A
9	7.27e-15	MAP1A	microtubule associated protein 1A	0.74	5.27e-12	PSMB8	proteasome 20S subunit beta type 8
7	3.61e-13	ADD2	adducin 2	0.72	3.79e-10	RHOC	ras homolog family member C
7	2.13e-12	MAP2	microtubule associated protein 2	0.72	4.68e-12	MYOF	myoferlin
7	6.26e-17	ZMYM3	zinc finger MYM-type containing 3	0.71	2.19e-07	PROCR	protein C receptor
7	3.21e-14	RPRD1A	regulation of nuclear pre-mRNA doma	0.7	2.77e-11	EPS8	epidermal growth factor receptor-binding protein 8
6	1.47e-15	ZNF428	zinc finger protein 428	0.7	3.18e-12	PARP4	Poly(ADP-ribose) polymerase family, member 4
5	8.70e-12	CDKN2A	cyclin dependent kinase inhibitor 2A	0.69	4.23e-09	DCBLD2	discoidin, CUB and LCCL domain containing 2
5	1.07e-17	TRIM24	tripartite motif containing 24	0.69	1.12e-11	SPATS2L	spermatogenesis associated 2
5	9.63e-18	SPINDOC	spindlin interactor and repressor 2	0.69	3.04e-09	EHL2	four and a half LIM domains containing 2

CBX5 network, DB1, all Pearson r > 0.55

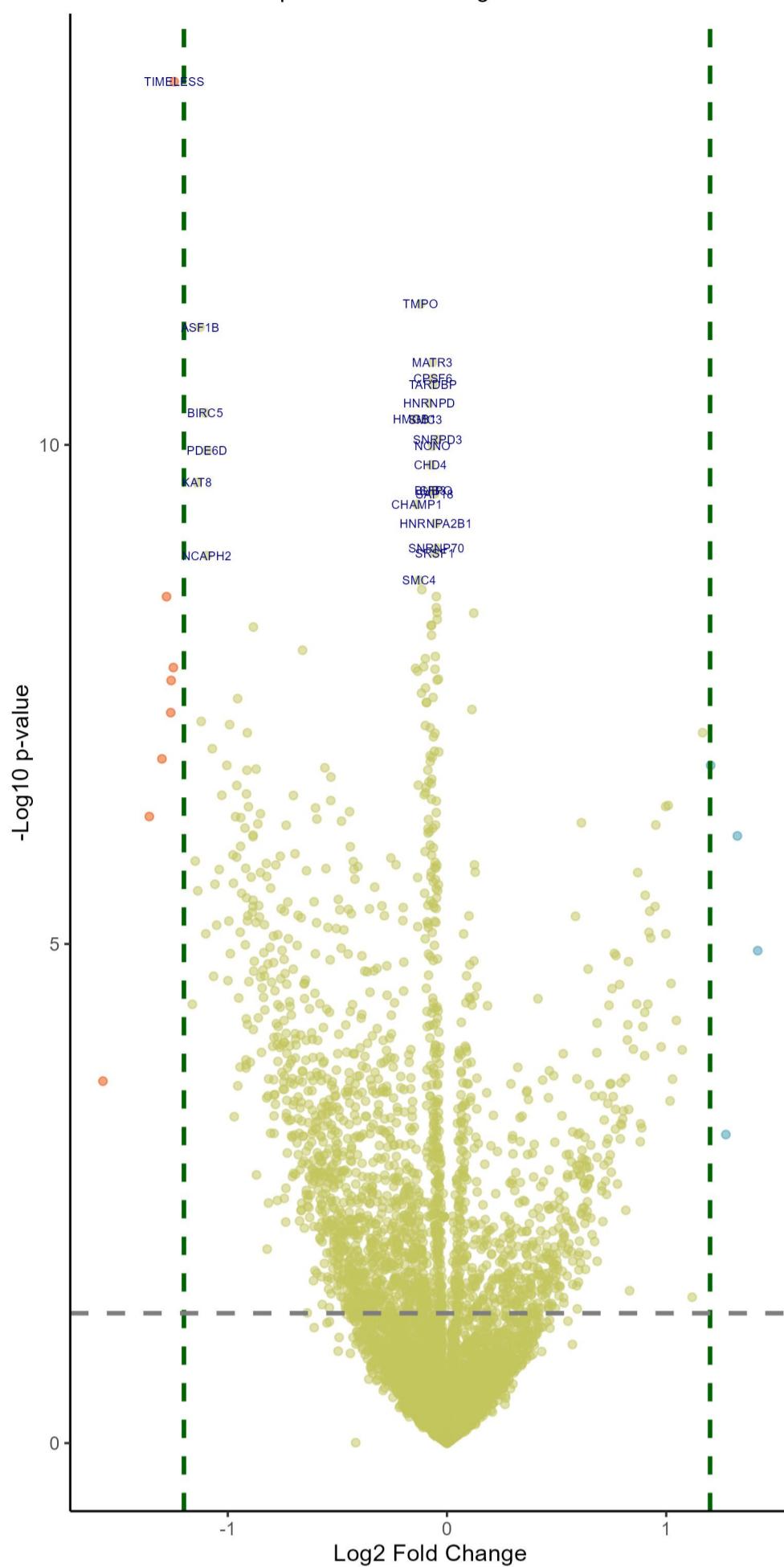
CBX5 network, DB1, all Pearson r > 0.5



CBX5 network, DB1, all Pearson r > 0.45

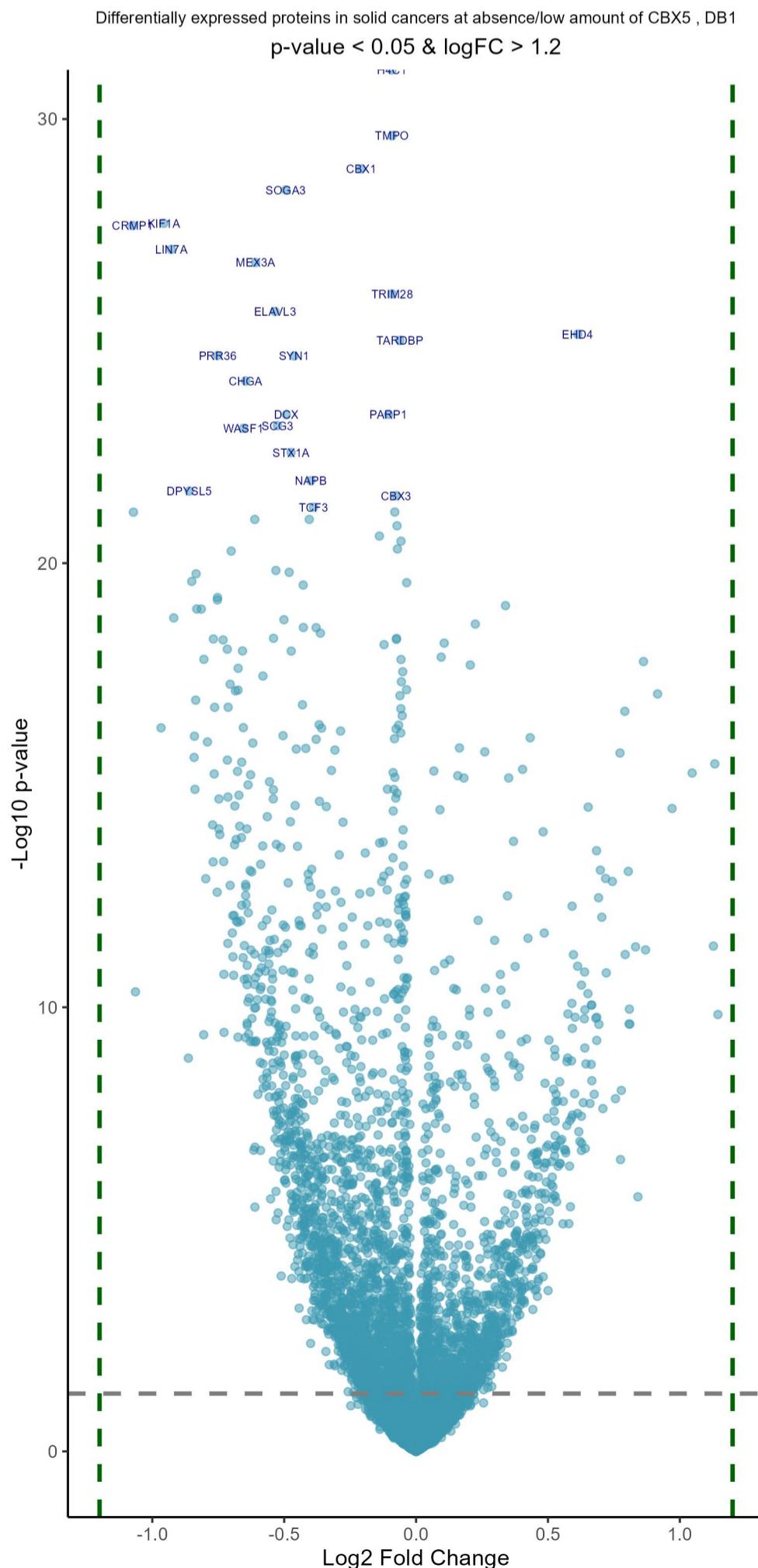


Differentially expressed proteins in blood cancers at absence/low amount of CBX5 , DB1
p-value < 0.05 & logFC > 1.2



Sorted by p values!
Downregulated in blood cancers at low/absent CBX5 Upregulated in blood cancers at low/absent CBX5

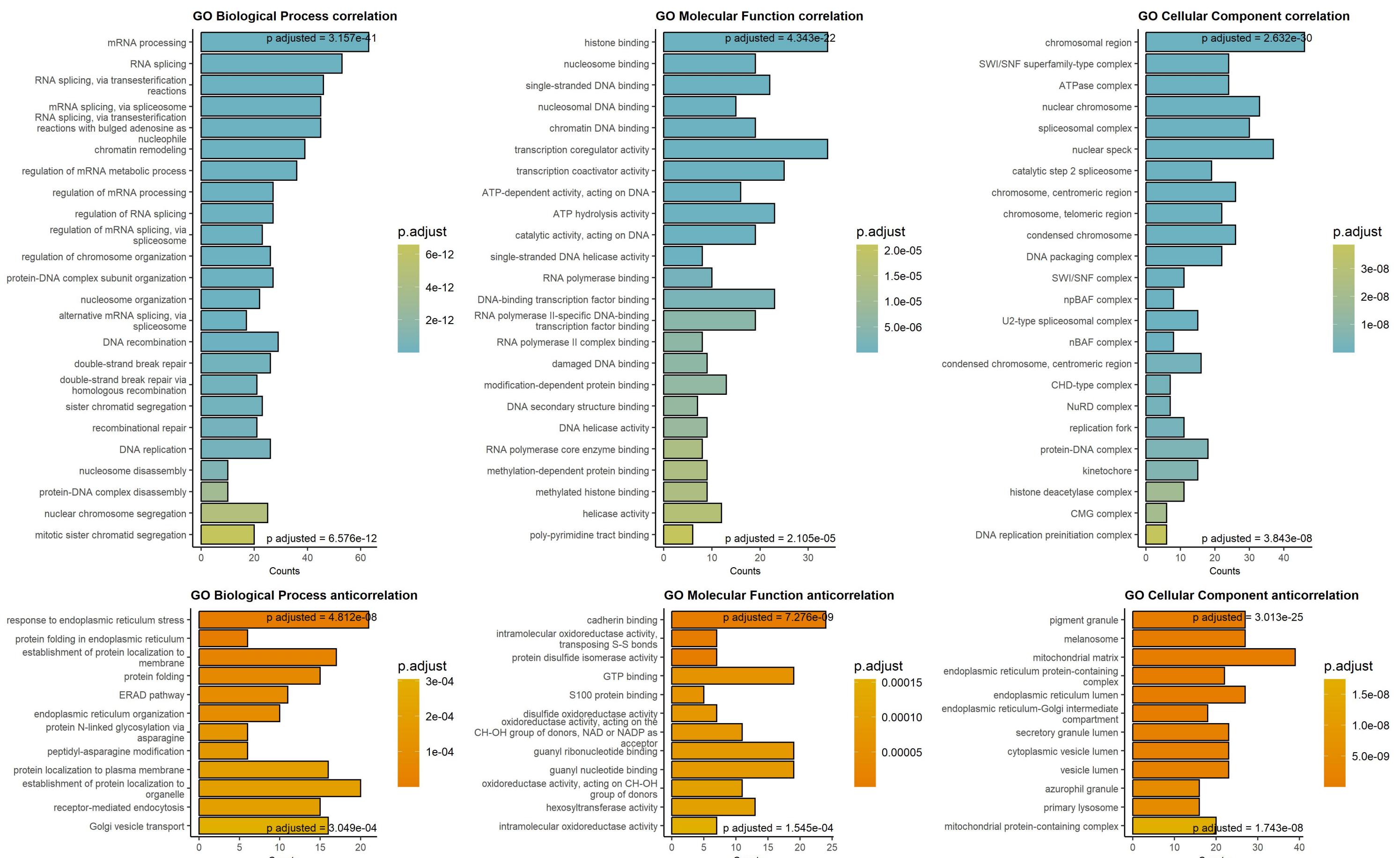
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.24	7.65e-11	TIMELESS	timeless circadian regulator	0.12	1.04e-06	HADHA	hydroxyacyl-CoA dehydrogenase trifluoromethylbenzyl ester
-0.12	8.59e-09	TMPO	thymopoietin	0.11	5.52e-06	HADHB	hydroxyacyl-CoA dehydrogenase trifluoromethylbenzyl ester
-1.13	1.10e-08	ASF1B	anti-silencing function 1B histone	1.17	8.31e-06	ATP6V0A1	ATPase H ⁺ transporting V0 subunit a
-0.07	1.98e-08	MATR3	matrin 3	1.2	1.50e-05	NCEH1	neutral cholesterol ester hydrolase
-0.06	2.36e-08	CPSF6	cleavage and polyadenylation specific	1.01	2.96e-05	EML3	EMAP like 3
-0.06	2.36e-08	TARDBP	TAR DNA binding protein	1	2.99e-05	DUSP3	dual specificity phosphatase 3
-0.08	3.18e-08	HNRNPD	heterogeneous nuclear ribonucleoprotein D	0.61	3.87e-05	SLC35F6	solute carrier family 35 member F6
-1.1	3.37e-08	BIRC5	baculoviral IAP repeat containing 5	0.95	3.95e-05	ERMP1	endoplasmic reticulum metallopeptidase 1
-0.15	3.37e-08	HMGB1	high mobility group box 1	1.32	4.74e-05	STOM	stomatin
-0.1	3.37e-08	SMC3	structural maintenance of chromosomal	0.13	7.96e-05	BCAP31	B cell receptor associated protein
-0.04	4.91e-08	SNRPD3	small nuclear ribonucleoprotein D3	0.13	8.65e-05	UGGT1	UDP-glucose glycoprotein glucosyltransferase 1
-0.07	5.25e-08	NONO	non-POU domain containing octamer b	0.87	8.65e-05	LRPAP1	LDL receptor related protein associated with PAP1
-1.09	5.41e-08	PDE6D	phosphodiesterase 6D	0.9	1.30e-04	CMBL	carboxymethylenebutenolidase homolog
-0.07	7.04e-08	CHD4	chromodomain helicase DNA binding protein 4	0.95	1.57e-04	PLOD3	procollagen-lysine,2-oxoglutarate 5
-1.14	9.91e-08	KAT8	lysine acetyltransferase 8	0.92	1.66e-04	SIL1	SIL1 nucleotide exchange factor
-0.05	1.06e-07	SFPQ	splicing factor proline and glutami	0.1	1.80e-04	HDLBP	high density lipoprotein binding protein
-0.08	1.06e-07	BUB3	BUB3 mitotic checkpoint protein	0.59	1.80e-04	IL1RAP	interleukin 1 receptor accessory protein
-0.06	1.09e-07	SAP18	Sin3A associated protein 18	0.92	2.37e-04	NUDT19	nudix hydrolase 19
-0.14	1.32e-07	CHAMP1	chromosome alignment maintaining ph	1	2.41e-04	PLBD2	phospholipase B domain containing 2
-0.05	1.94e-07	HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2B1	0.08	2.41e-04	UQCRC1	ubiquinol-cytochrome c reductase complex I
-0.05	3.28e-07	SNRP70	small nuclear ribonucleoprotein U1	0.93	2.61e-04	DTD1	D-aminoacyl-tRNA deacylase 1
-0.06	3.53e-07	SRSF1	serine and arginine rich splicing factor	1.42	3.36e-04	S100A6	S100 calcium binding protein A6
-1.1	3.57e-07	NCAPH2	non-SMC condensin II complex subunit	0.76	3.55e-04	BCS1L	BCS1 homolog, ubiquinol-cytochrome c reductase complex I
-0.13	6.05e-07	SMC4	structural maintenance of chromosomal	0.77	3.64e-04	ALDH1B1	aldehyde dehydrogenase 1 family member
-0.11	7.21e-07	SMARCE1	SWI/SNF related, matrix associated, chromatin	0.12	4.02e-04	SRPRB	SRP receptor subunit beta
-0.05	7.88e-07	ELAVL1	ELAV like RNA binding protein 1	0.83	4.04e-04	FHOD1	formin homology 2 domain containing 1
-1.28	7.88e-07	LEF1	lymphoid enhancer binding factor 1	0.1	4.28e-04	ACTN4	actinin alpha 4
-0.05	9.82e-07	HNRNPL	heterogeneous nuclear ribonucleoprotein L	0.64	4.67e-04	DNAJC3	DnaJ heat shock protein family (Hsp 70) homologues
-0.04	1.04e-06	SRSF3	serine and arginine rich splicing factor	0.09	5.26e-04	GPI	glucose-6-phosphate isomerase
-0.04	1.17e-06	HNRNPK	heterogeneous nuclear ribonucleoprotein K	1.02	6.07e-04	CAPN2	calpain 2
-0.07	1.26e-06	PNN	pinin, desmosome associated protein	0.79	6.15e-04	STAT3	signal transducer and activator of transcription 3
-0.07	1.26e-06	HNRNPH1	heterogeneous nuclear ribonucleoprotein H1	0.14	6.43e-04	P4HB	prolyl 4-hydroxylase subunit beta
-0.88	1.27e-06	MEAF6	MYST/Esa1 associated factor 6	0.75	6.65e-04	CLPTM1	CLPTM1 regulator of GABA type A receptor
-0.07	1.49e-06	IK	IK cytokine	0.13	7.71e-04	CYC1	cytochrome c1
-0.66	2.05e-06	PSMC3IP	PSMC3 interacting protein	0.1	7.91e-04	AP2A1	adaptor related protein complex 2 subunit alpha
-0.05	2.31e-06	HNRNPM	heterogeneous nuclear ribonucleoprotein M	0.42	8.06e-04	RAB11FIP5	RAB11 family interacting protein 5
-0.1	2.36e-06	SMC1A	structural maintenance of chromosomal	0.11	8.07e-04	UQCRC2	ubiquinol-cytochrome c reductase bi
-0.11	2.74e-06	FUS	FUS RNA binding protein	0.09	8.71e-04	AP2B1	adaptor related protein complex 2 subunit beta
1.25	2.74e-06	TCE3	transcription factor 3	0.97	9.89e-04	DUSP23	dual specificity phosphatase 23



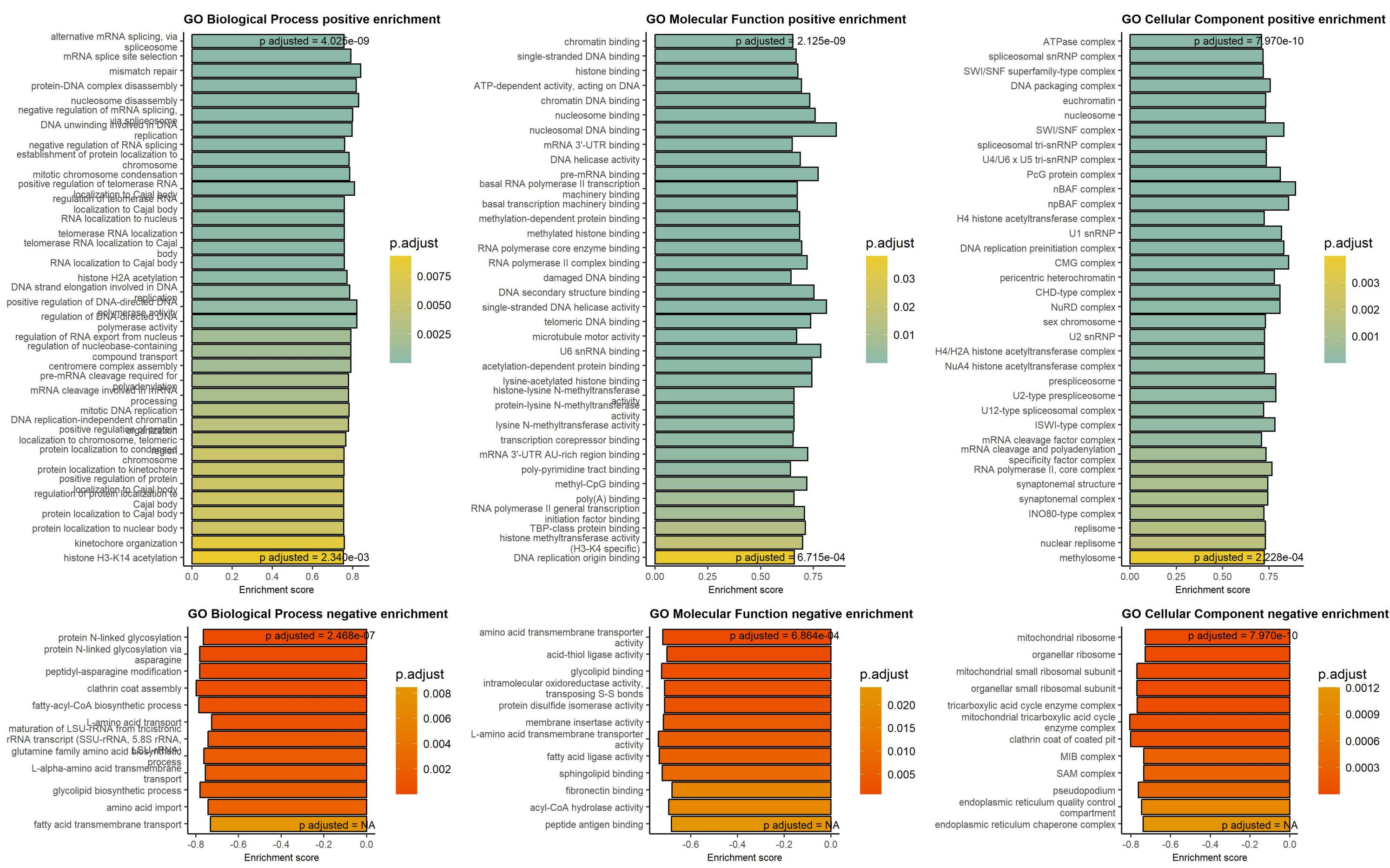
Sorted by p values!
Downregulated in solid cancers at low/absent CBX5 Upregulated in solid cancers at low/absent CBX5

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.09	0.00e+00	H4C1	H4 clustered histone 1	0.61	3.87e-23	EHD4	EH domain containing 4
-0.09	5.24e-27	TMPO	thymopoietin	0.34	1.40e-17	SUCLG2	succinate-CoA ligase GDP-forming subunit
-0.21	2.20e-26	CBX1	chromobox 1	0.22	3.26e-17	PLEC	plectin
-0.49	5.26e-26	SOGA3	SOGA family member 3	0.11	7.37e-17	IQGAP1	IQ motif containing GTPase activating protein
-0.96	2.37e-25	KIF1A	kinesin family member 1A	0.1	1.40e-16	TPD52L2	TPD52 like 2
-1.07	2.37e-25	CRMP1	collapsin response mediator protein	0.86	1.68e-16	NCEH1	neutral cholesterol ester hydrolase
-0.93	7.14e-25	LIN7A	lin-7 homolog A, crumbs cell polarity	0.21	1.98e-16	AHNAK	AHNAK nucleoprotein
-0.61	1.26e-24	MEX3A	mex-3 RNA binding family member A	0.92	7.81e-16	SP100	SP100 nuclear antigen
-0.09	5.75e-24	TRIM28	tripartite motif containing 28	0.79	1.76e-15	MVP	major vault protein
-0.53	1.30e-23	ELAVL3	ELAV like RNA binding protein 3	0.43	6.04e-15	MYO1C	myosin IC
-0.06	4.92e-23	TARDBP	TAR DNA binding protein	0.16	9.72e-15	LMNA	lamin A/C
-0.75	9.56e-23	PRR36	proline rich 36	0.26	1.15e-14	CTSB	cathepsin B
-0.46	9.56e-23	SYN1	synapsin I	0.77	1.20e-14	RETSAT	retinol saturase
-0.65	3.28e-22	CHGA	chromogranin A	1.13	2.03e-14	CTSZ	cathepsin Z
-0.1	1.67e-21	PARP1	poly(ADP-ribose) polymerase 1	0.4	2.68e-14	ARPC4	actin related protein 2/3 complex subunit alpha
-0.49	1.67e-21	DCX	doublecortin	0.07	2.87e-14	SQSTM1	sequestosome 1
-0.53	2.80e-21	SCG3	secretogranin III	1.05	3.10e-14	S100A10	S100 calcium binding protein A10
-0.65	3.05e-21	WASF1	WASP family member 1	0.16	3.47e-14	ACTN1	actinin alpha 1
-0.47	1.02e-20	STX1A	syntaxin 1A	0.35	3.81e-14	ETHE1	ETHE1 persulfide dioxygenase
-0.4	4.21e-20	NAPB	NSF attachment protein beta	0.18	3.81e-14	CPOX	coproporphyrinogen oxidase
-0.86	6.88e-20	DPYSL5	dihydropyrimidinase like 5	0.65	1.51e-13	STK10	serine/threonine kinase 10
-0.08	8.41e-20	CBX3	chromobox 3	0.97	1.61e-13	CD59	CD59 molecule (CD59 blood group)
-0.39	1.46e-19	TCF3	transcription factor 3	0.09	1.71e-13	MYL6	myosin light chain 6
-0.08	1.75e-19	HNRNPA0	heterogeneous nuclear ribonucleoprotein A	0.48	5.01e-13	YBX3	Y-box binding protein 3
-1.07	1.75e-19	INA	internexin neuronal intermediate filament	0.37	7.99e-13	GSTK1	glutathione S-transferase kappa 1
-0.41	2.37e-19	ZNF219	zinc finger protein 219	0.68	1.22e-12	CCDC9B	coiled-coil domain containing 9B
-0.61	2.37e-19	CBX2	chromobox 2	0.7	3.18e-12	PARP4	poly(ADP-ribose) polymerase family
-0.07	3.19e-19	LMNB1	lamin B1	0.8	3.33e-12	ALDH1A3	aldehyde dehydrogenase 1 family member
-0.14	5.26e-19	RBBP4	RB binding protein 4, chromatin remodeller	0.05	3.77e-12	EIF6	eukaryotic translation initiation factor 6
-0.06	6.65e-19	HNRNPA1	heterogeneous nuclear ribonucleoprotein A	0.72	4.68e-12	MYOF	myoferlin
-0.07	9.64e-19	SMC1A	structural maintenance of chromosomal	0.13	4.69e-12	CTSD	cathepsin D
-0.7	1.05e-18	SEPTIN3	septin 3	0.11	4.94e-12	ACTN4	actinin alpha 4
-0.53	2.77e-18	SNAP25	synaptosome associated protein 25	0.74	5.27e-12	PSMB8	proteasome 20S subunit beta 8
-0.48	2.97e-18	PROX1	prospero homeobox 1	0.35	1.03e-11</		

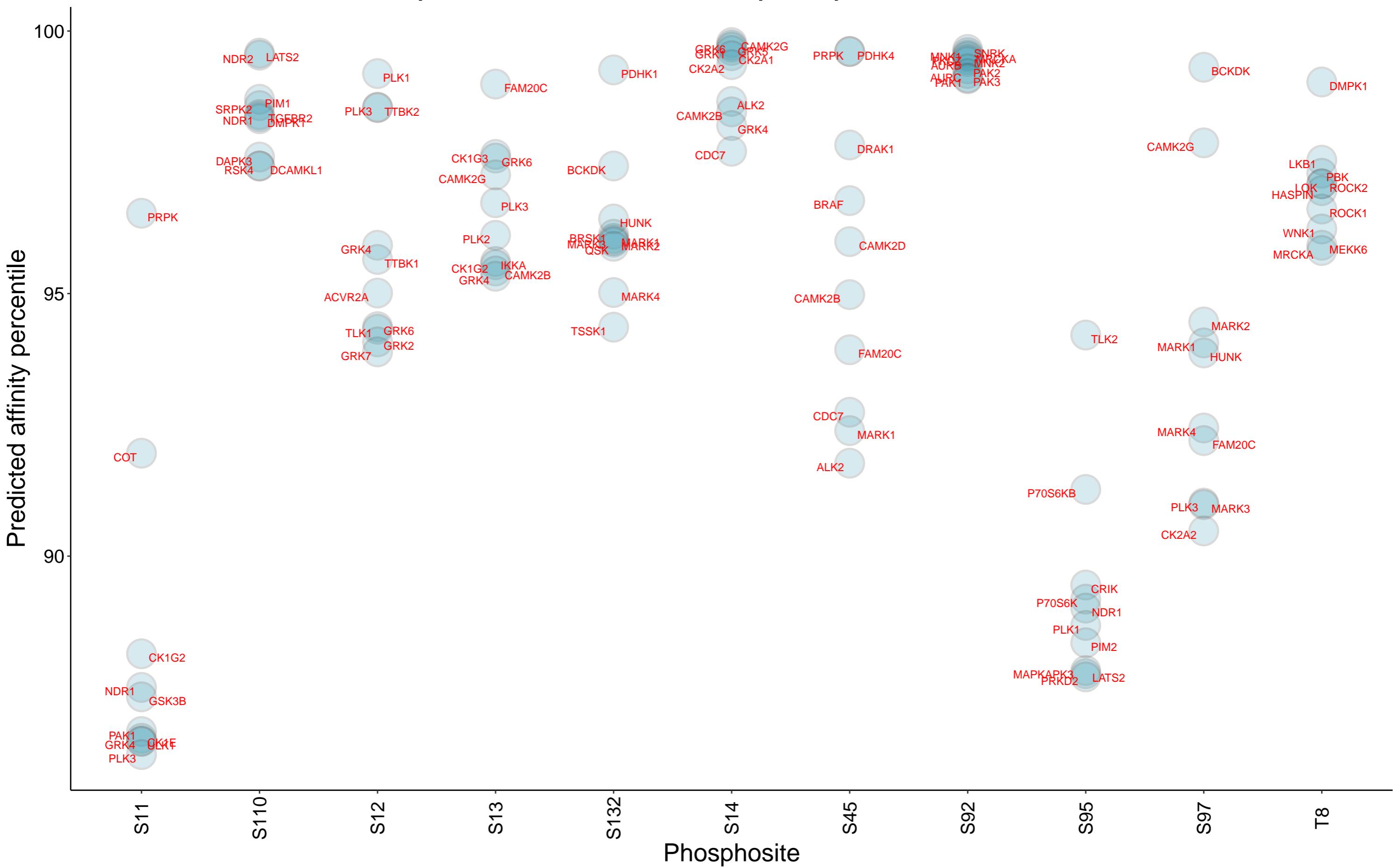
Top 250 correlation coefficients overrepresentation, CBX5 protein, DB1



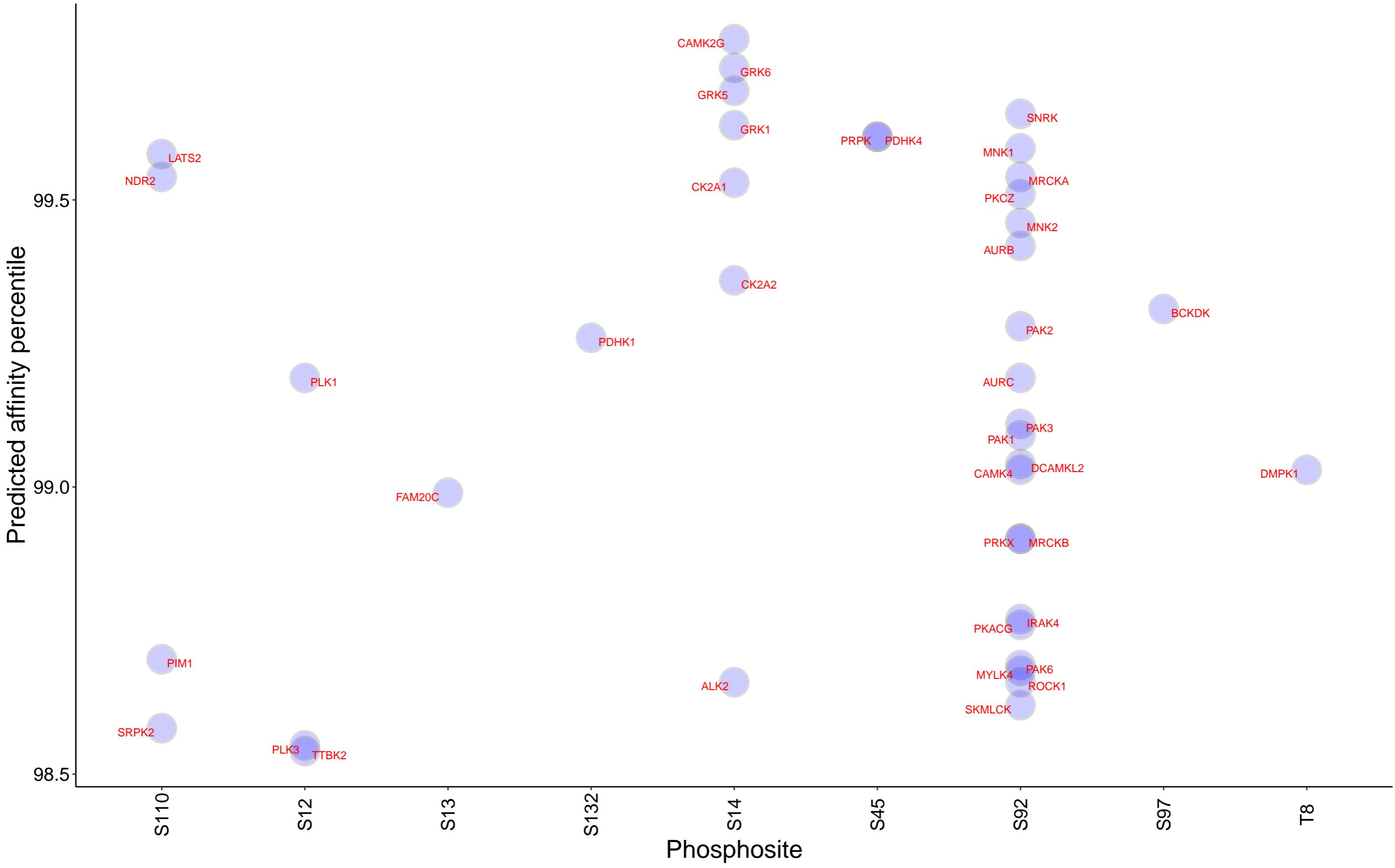
Gene Set Enrichment analysis on protein correlation coefficients, CBX5 protein, DB1



Top 10 kinases for each phosphosite in CBX5



Kinases with affinity greater than 98.5% to CBX5



Top 15 positive correlation coefficients for CBX5 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

