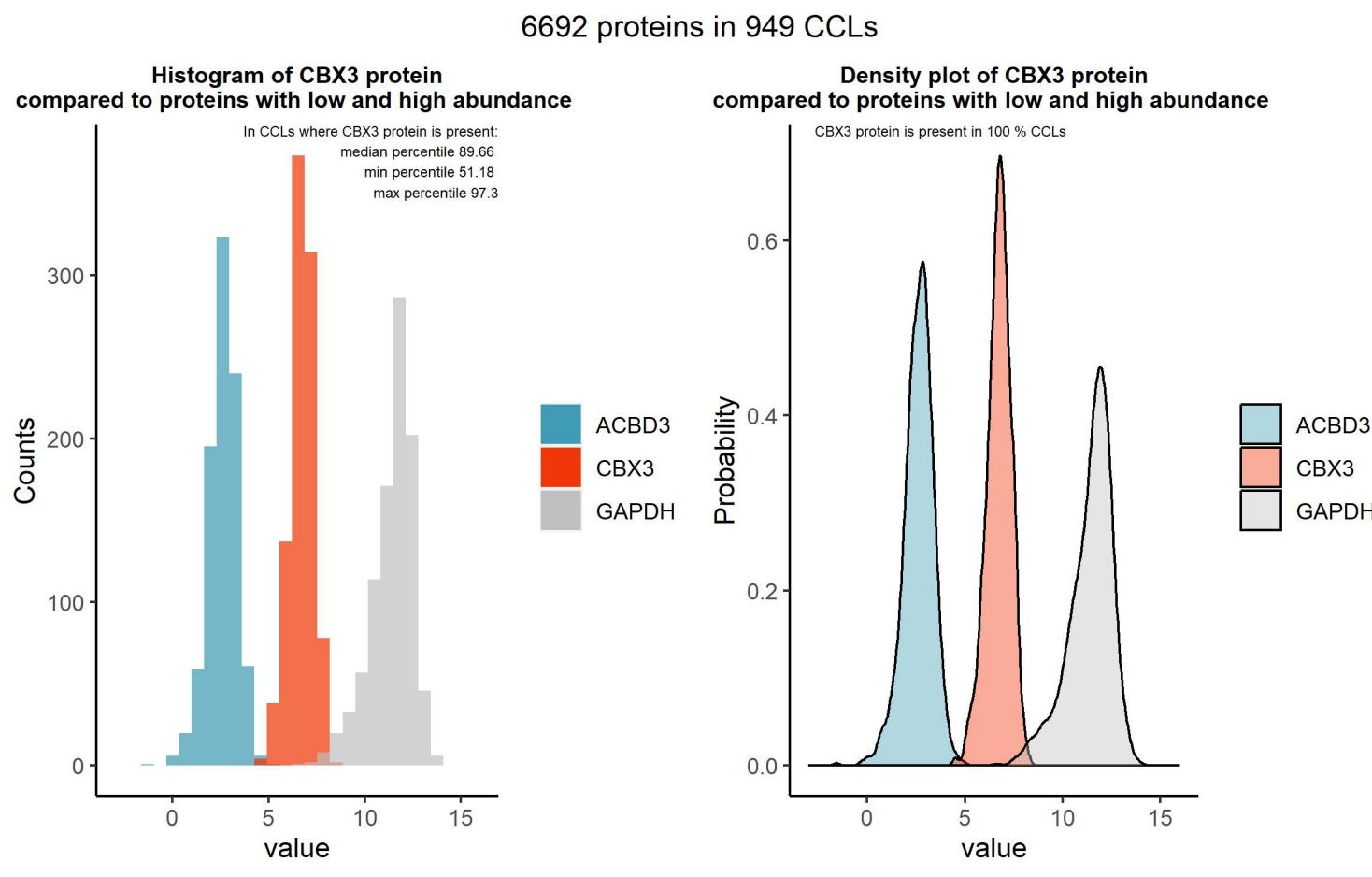


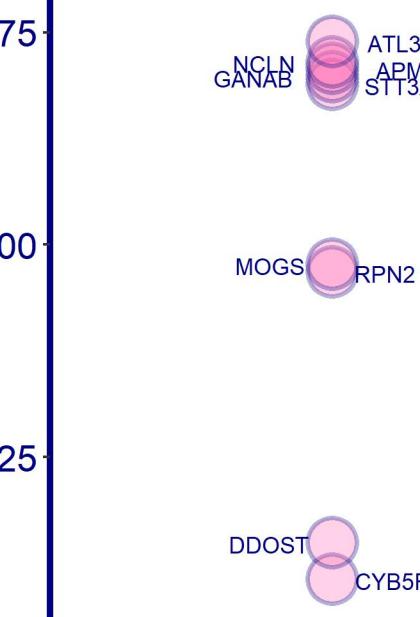
CBX3

Protein name: CBX3 ; UNIPROT: Q13185 ; Gene name: chromobox 3
 Ligandable: Yes ; Ligandable_by_Chem: NA ; Is_enzyme: NA (<https://cansar.ai/>)

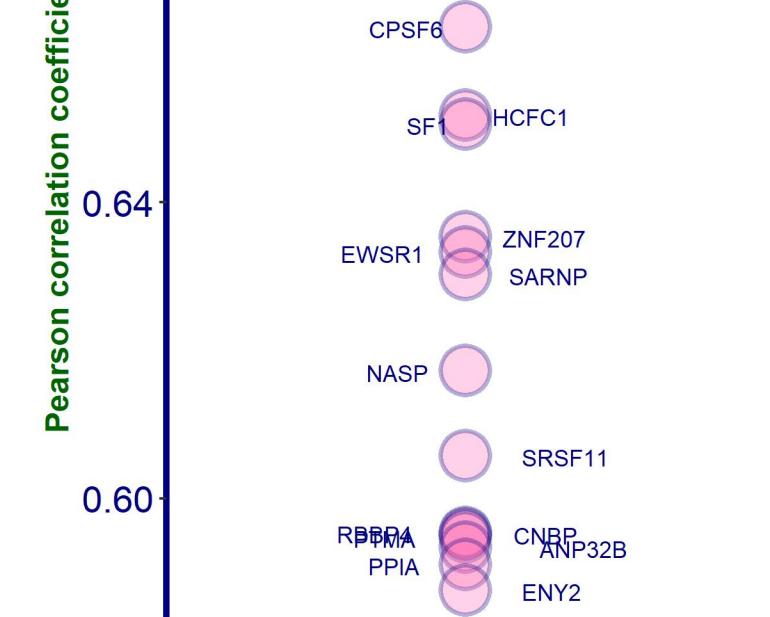
Sanger Institute Protein Database 1 (DB1), protein presence is certain



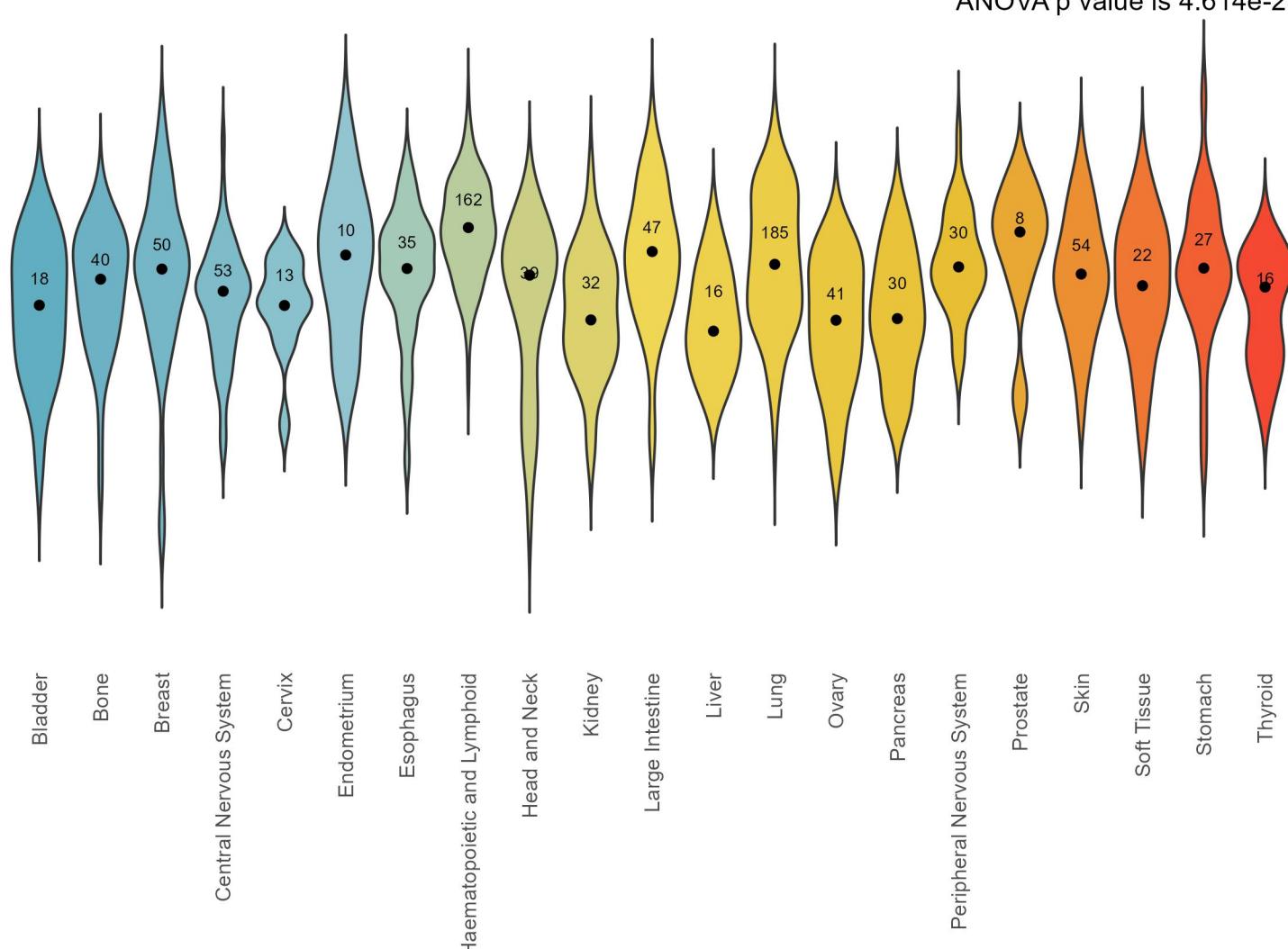
Top negative correlations of CBX3 protein, DB1



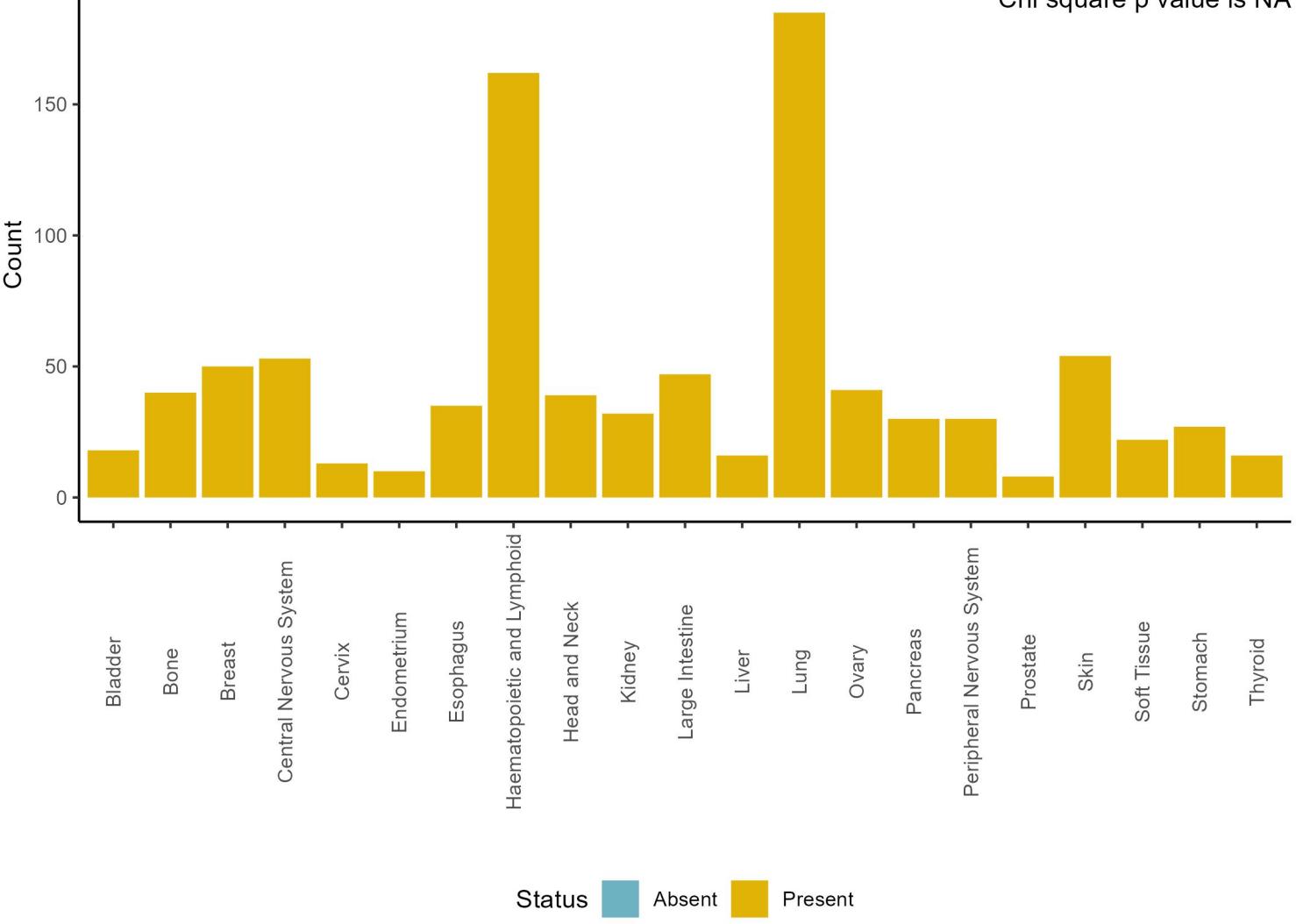
Top positive correlations of CBX3 protein, DB1



Amount of CBX3 protein, number of CCLs where it is present by tissue, DB1



Present and absent CBX3 protein counts by tissue, DB1

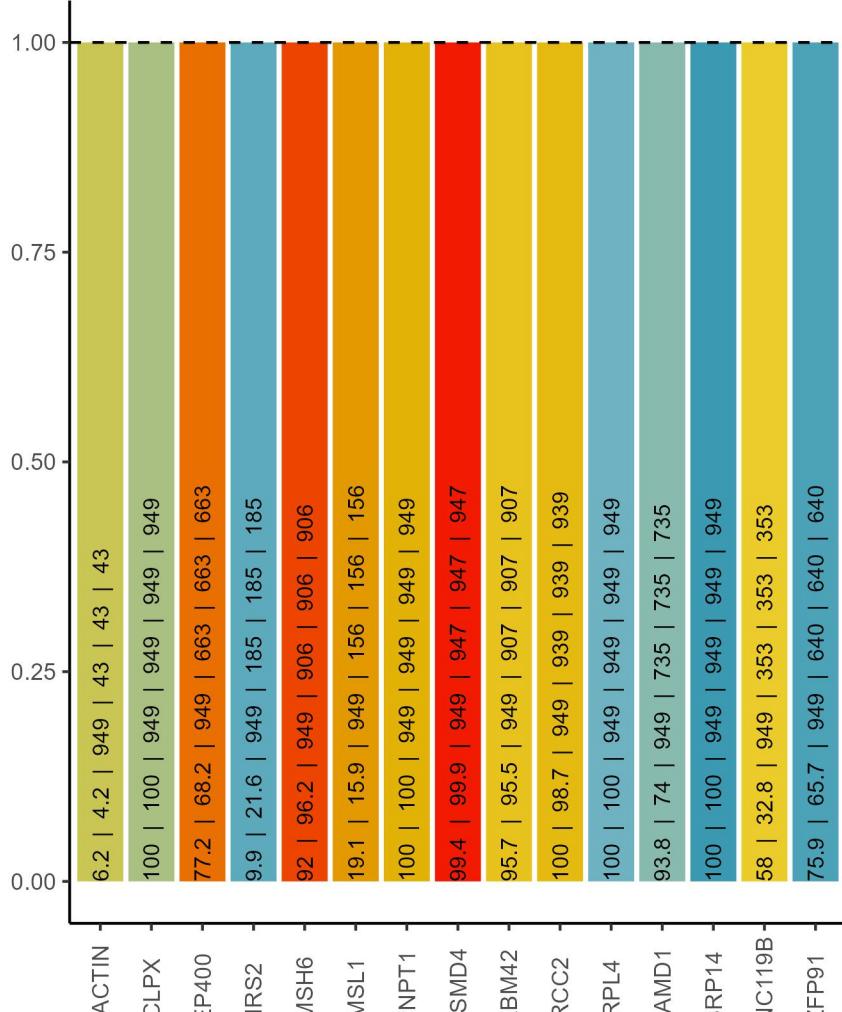


Cooccurrence with CBX3 protein, DB1

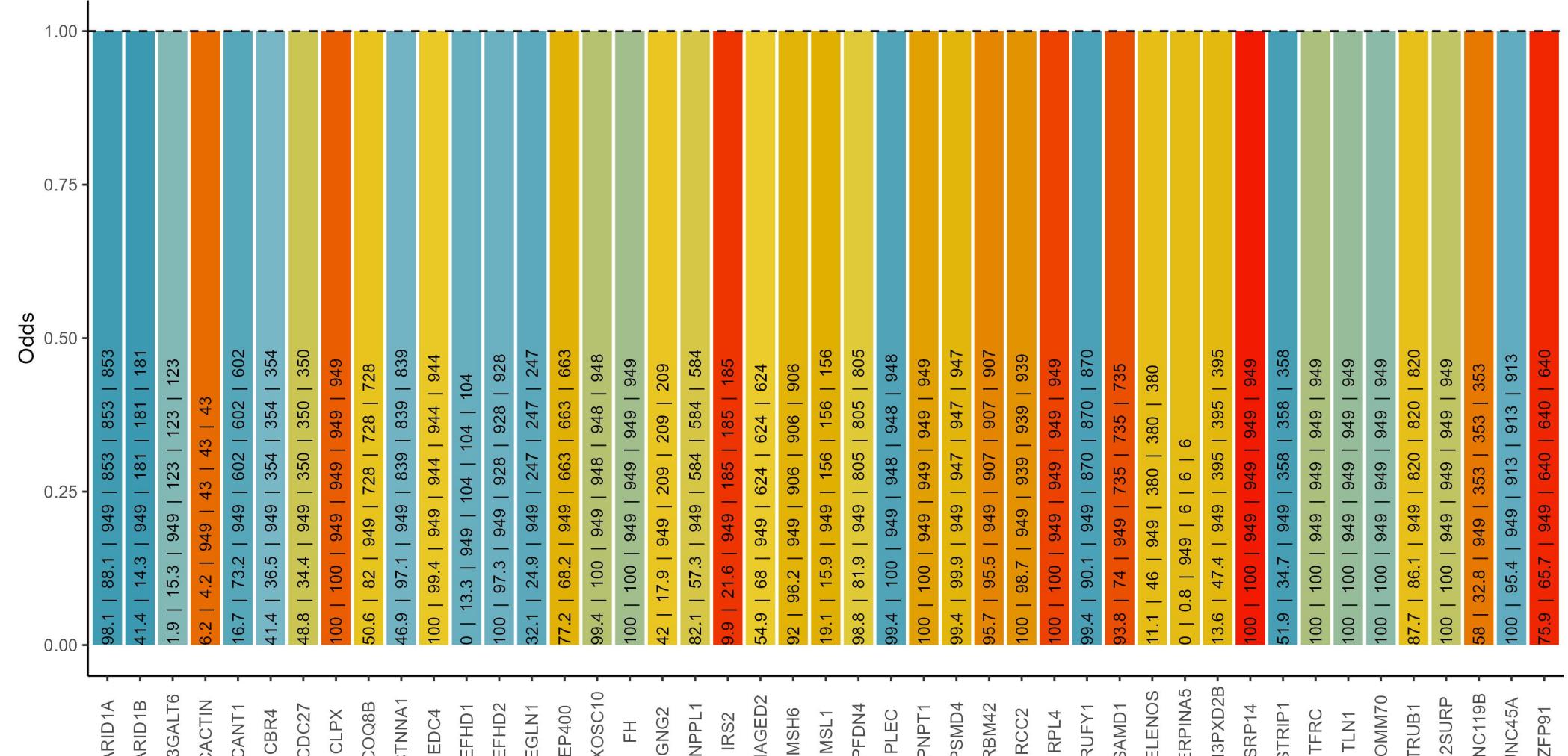
% of CBX3 in blood cancers: 100 ; % of CBX3 in solid cancers: 100

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CBX3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

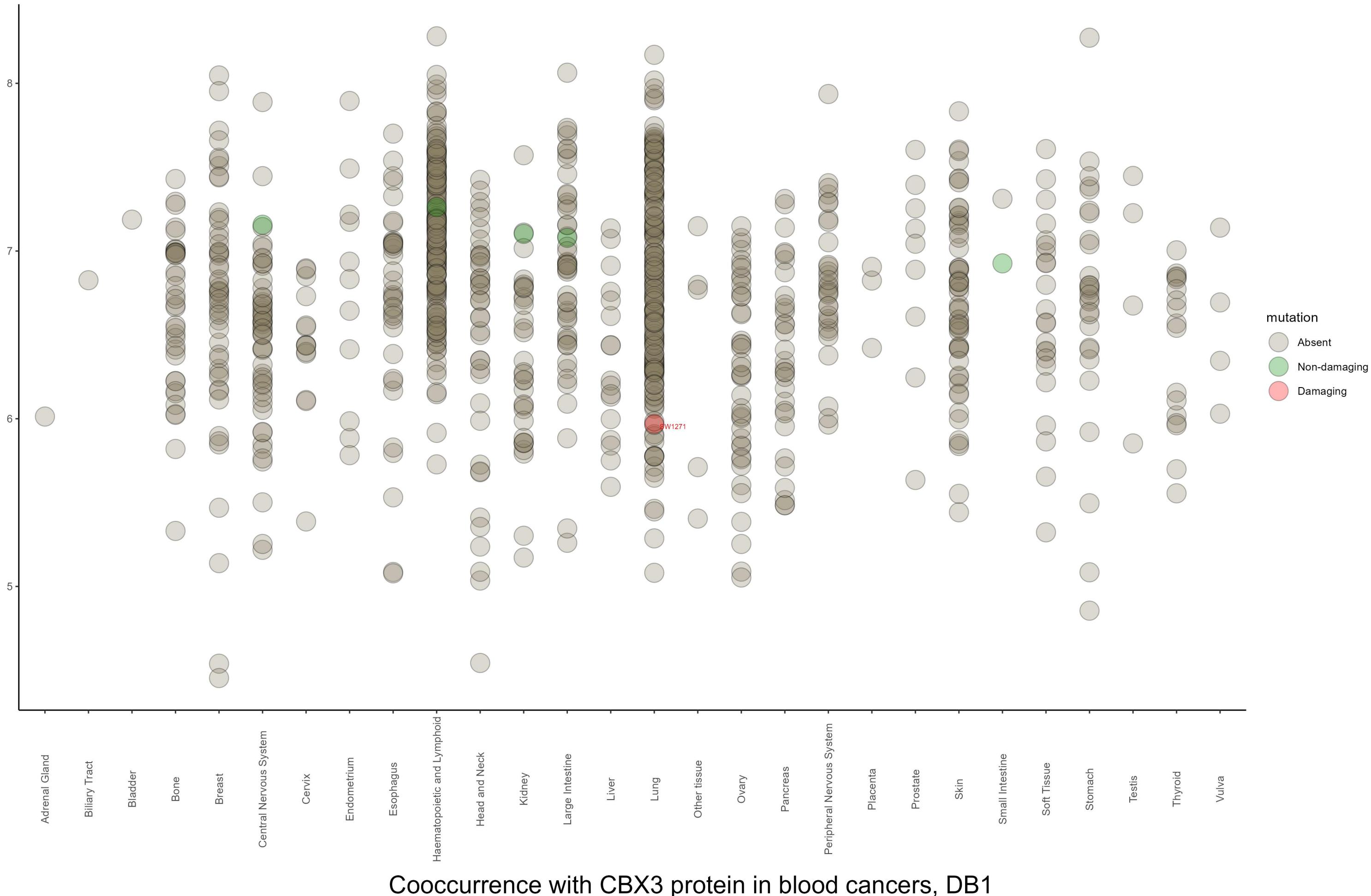
Negative cooccurrence



Positive cooccurrence



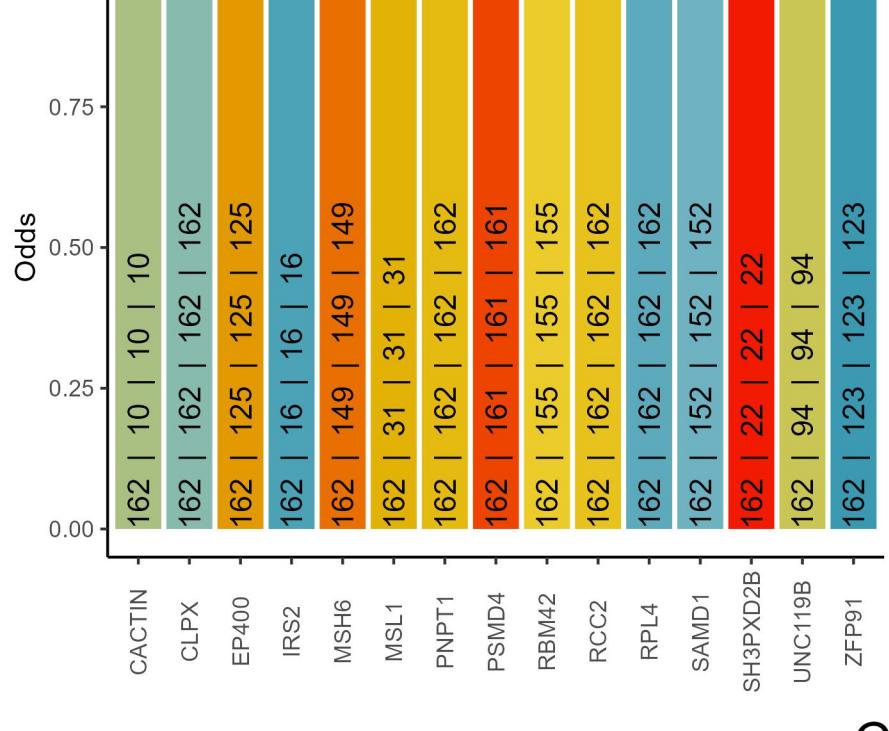
Amount of CBX3 protein and mutation status by tissue, DB1



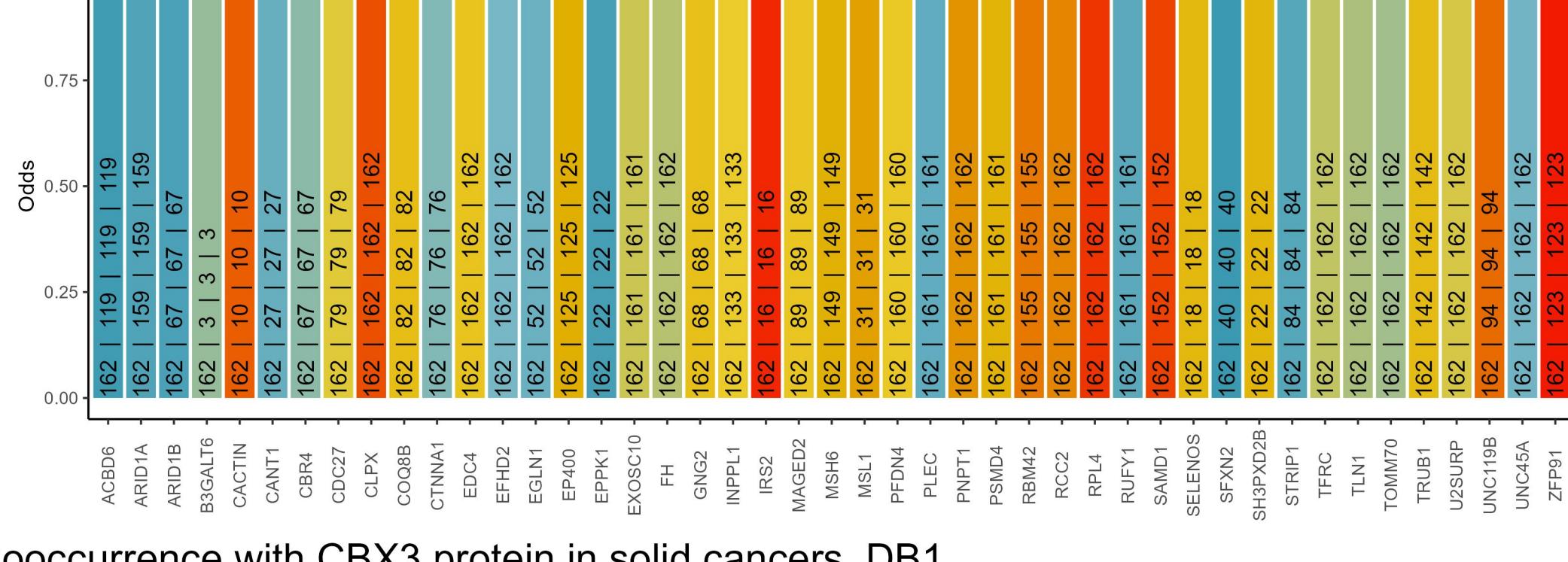
Cooccurrence with CBX3 protein in blood cancers, DB1

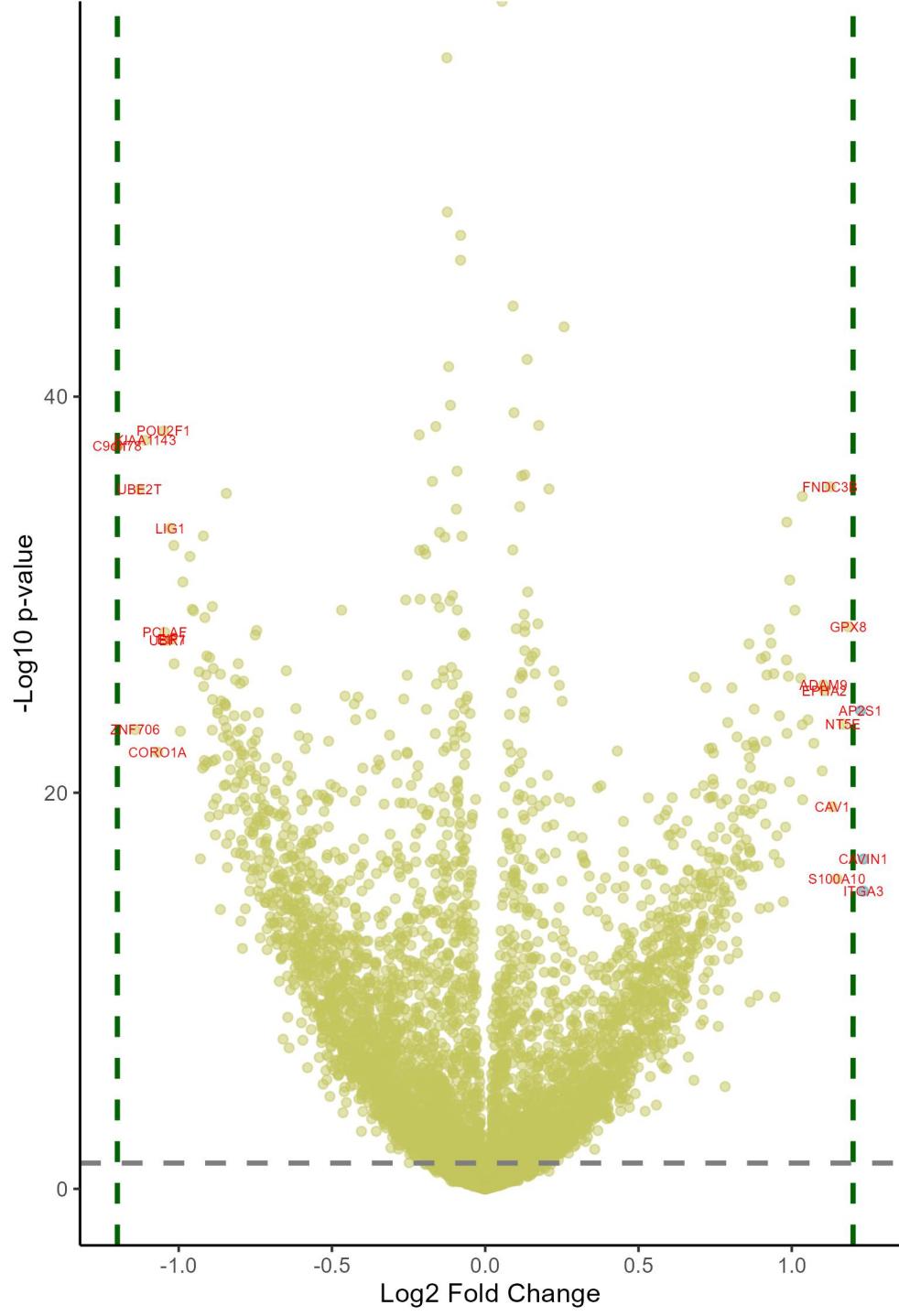
The text in the bars: incidence of CBX3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



Positive cooccurrence

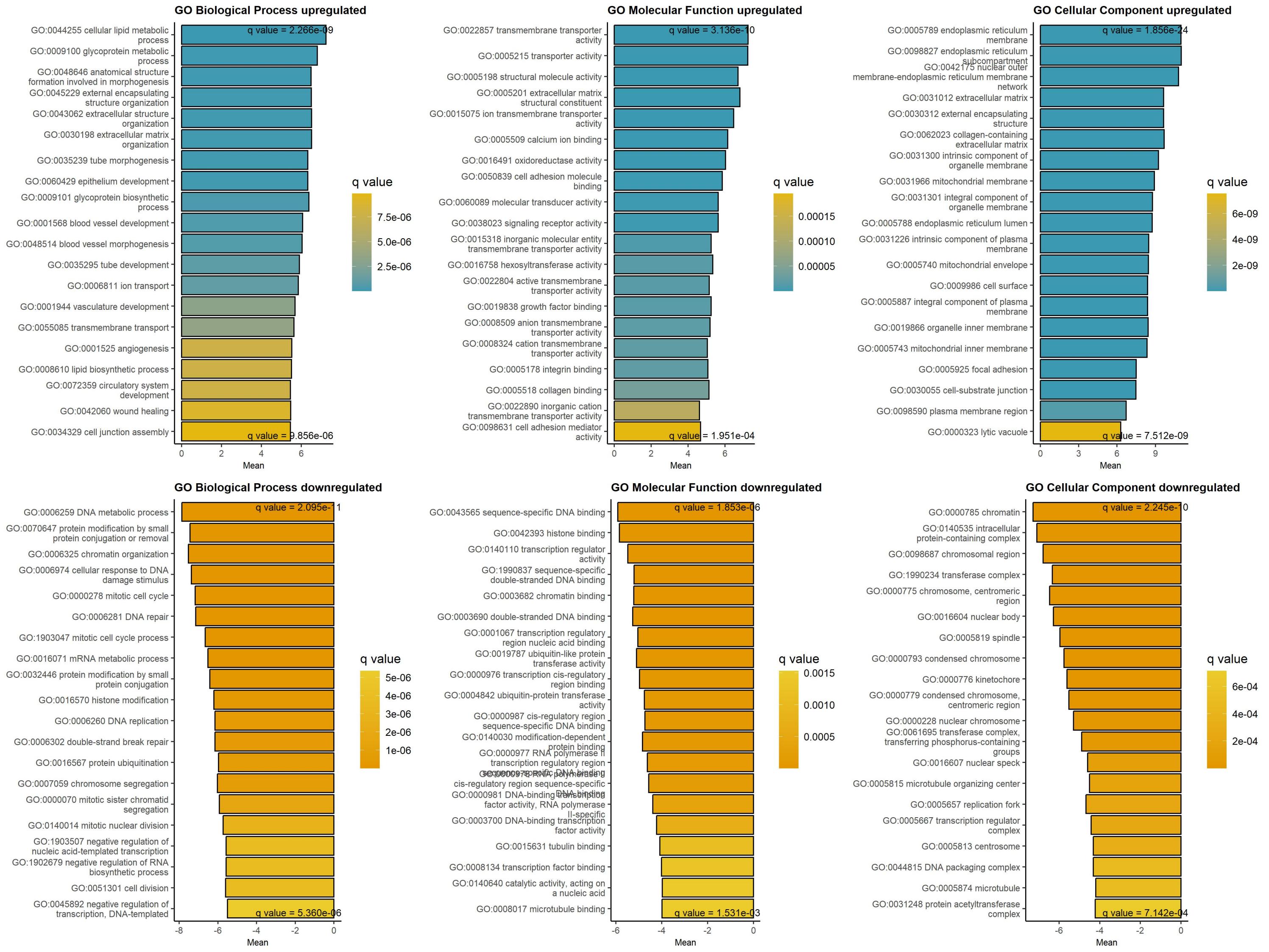


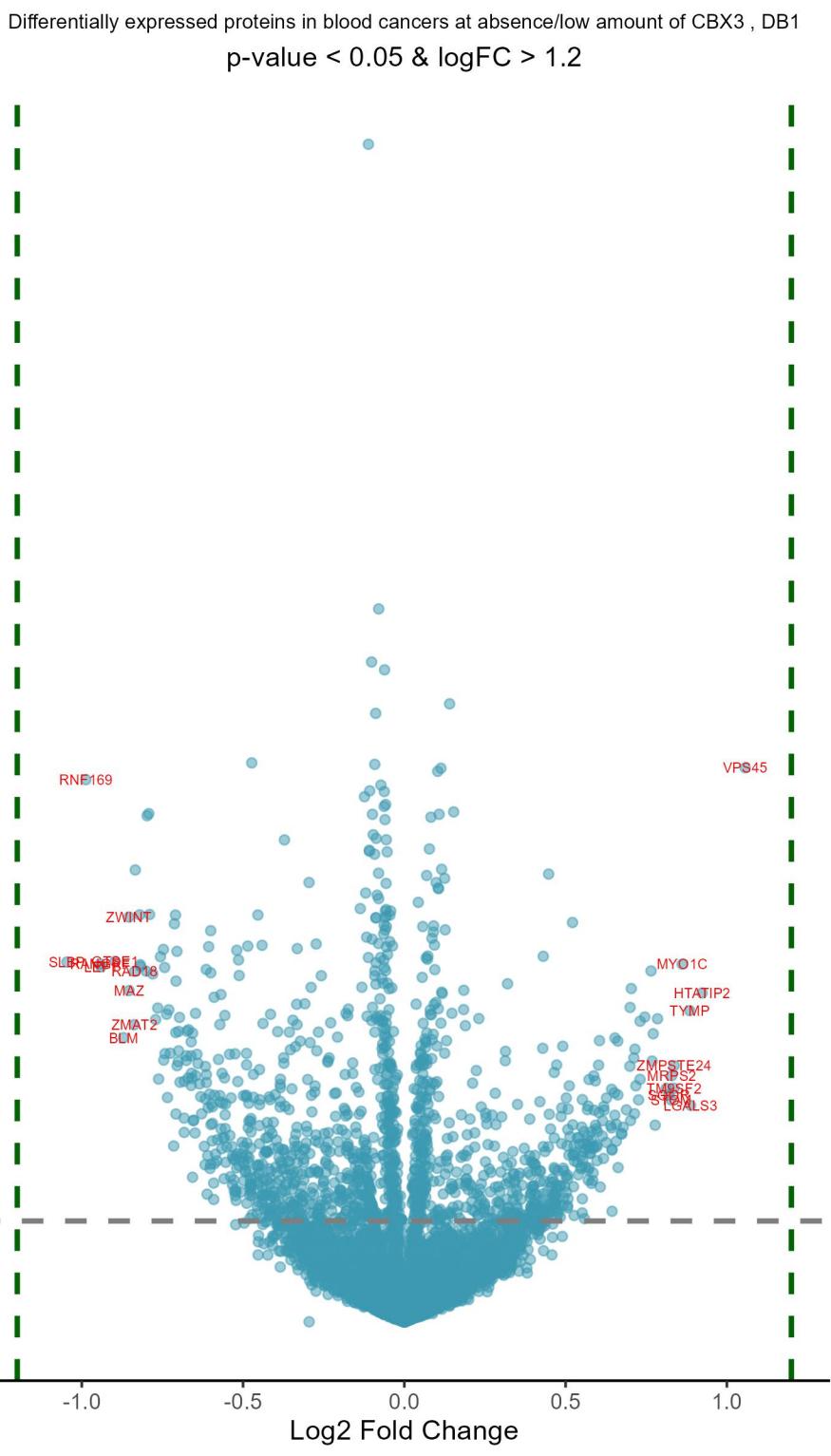


Downregulated at low/absent CBX3 Upregulated at low/absent CBX3

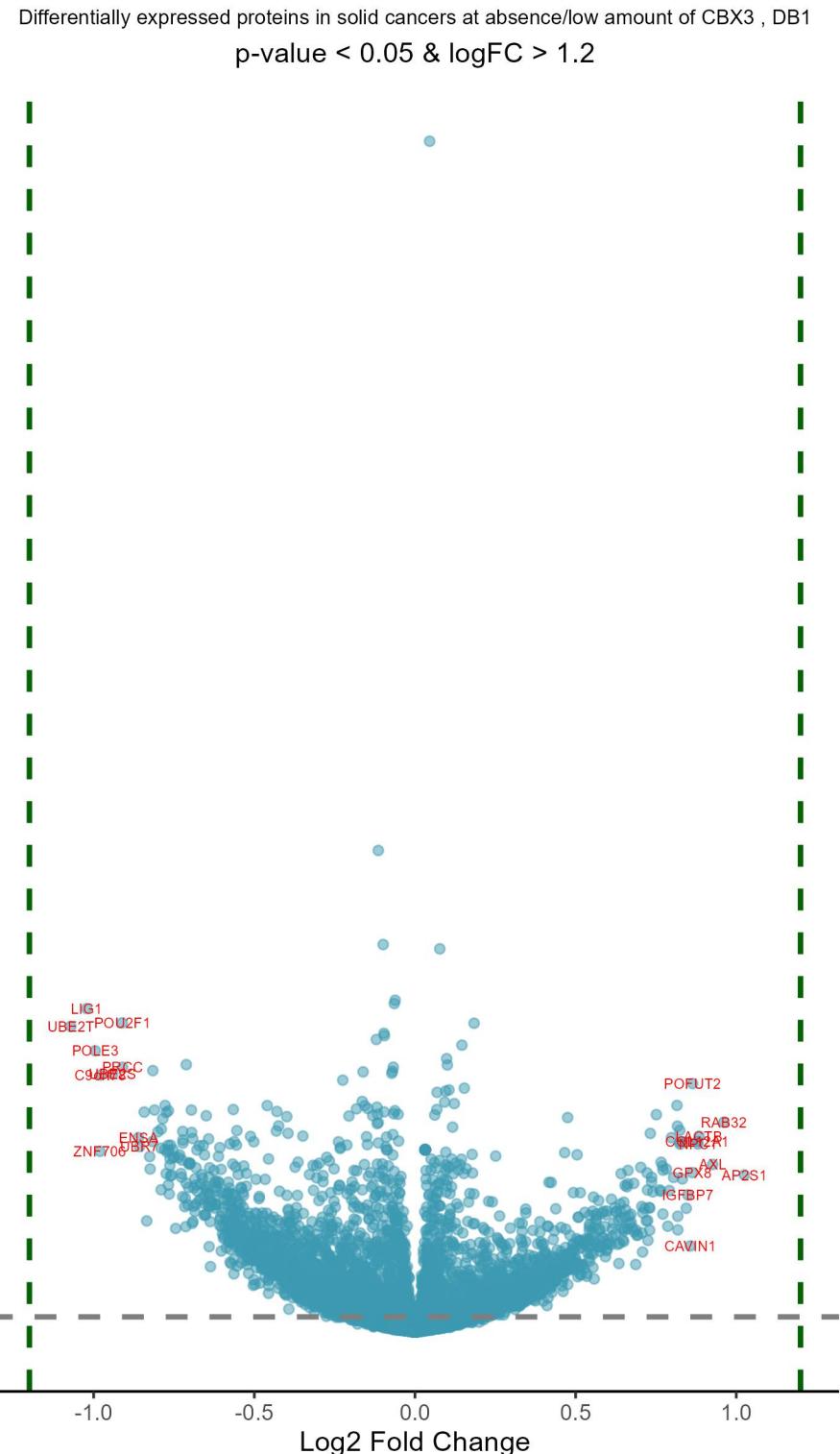
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.2	1.17e-35	C9orf78	chromosome 9 open reading frame 78	1.23	9.52e-15	ITGA3	integrin subunit alpha 3
-1.14	2.80e-22	ZNF706	zinc finger protein 706	1.23	3.08e-16	CAVIN1	caveolae associated protein 1
-1.13	1.29e-33	UBE2T	ubiquitin conjugating enzyme E2 T	1.22	3.53e-23	AP2S1	adaptor related protein complex 2 s
-1.11	6.27e-36	KIAA1143	KIAA1143	1.18	4.56e-27	GPX8	glutathione peroxidase 8 (putative)
-1.07	3.03e-21	CORO1A	coronin 1A	1.17	1.53e-22	NT5E	5'-nucleotidase ecto
-1.05	2.40e-36	POU2F1	POU class 2 homeobox 1	1.15	2.54e-15	S100A10	S100 calcium binding protein A10
-1.04	7.97e-27	PCLAF	PCNA clamp associated factor	1.13	1.06e-18	CAV1	caveolin 1
-1.04	1.89e-26	UBR7	ubiquitin protein ligase E3 compone	1.13	1.04e-33	FNDC3B	fibronectin type III domain contain
-1.03	9.56e-32	LIG1	DNA ligase 1	1.11	4.06e-24	EPHA2	EPH receptor A2
-1.02	1.73e-26	EIF1	eukaryotic translation initiation f	1.1	2.13e-24	ADAM9	ADAM metallopeptidase domain 9
-1.02	6.07e-31	POLE3	DNA polymerase epsilon 3, accessory	1.1	2.29e-20	EGFR	epidermal growth factor receptor
-1.01	2.44e-25	SS18	SS18 subunit of BAF chromatin remod	1.07	1.20e-21	MMP14	matrix metallopeptidase 14
-0.99	3.28e-22	SERF2	small EDKR-rich factor 2	1.05	9.37e-23	AXL	AXL receptor tyrosine kinase
-0.99	3.53e-29	POLE4	DNA polymerase epsilon 4, accessory	1.04	5.05e-19	PPIC	peptidylprolyl isomerase C
-0.96	1.90e-30	PRCC	proline rich mitotic checkpoint con	1.03	2.67e-33	LMAN2L	lectin, mannose binding 2 like
-0.96	6.94e-28	SSNA1	SS nuclear autoantigen 1	1.03	1.60e-22	RRAS	RAS related
-0.95	7.77e-28	UBE2S	ubiquitin conjugating enzyme E2 S	1.03	1.05e-24	RAB32	RAB32, member RAS oncogene family
-0.93	5.78e-25	NFATC2IP	nuclear factor of activated T cells	1.01	7.38e-28	ERGIC2	ERGIC and golgi 2
-0.93	3.01e-16	NACA2	nascent polypeptide associated comp	0.99	2.88e-29	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-b
-0.92	1.68e-20	DHFR	dihydrofolate reductase	0.99	7.66e-20	P4HA2	prolyl 4-hydroxylase subunit alpha
-0.92	2.18e-31	STEEP1	STING1 ER exit protein 1	0.99	8.70e-25	COL12A1	collagen type XII alpha 1 chain
-0.92	2.53e-24	RNASEH2B	ribonuclease H2 subunit B	0.98	4.13e-22	NPC1	NPC intracellular cholesterol trans
-0.92	7.40e-21	ACYP1	acylphosphatase 1	0.98	4.83e-32	SEC11A	SEC11 homolog A, signal peptidase c
-0.91	1.63e-27	GINS4	GINS complex subunit 4	0.98	1.63e-25	HSPG2	heparan sulfate proteoglycan 2
-0.91	1.28e-20	PMF1	polyamine modulated factor 1	0.98	9.50e-18	CAVIN3	caveolae associated protein 3
-0.91	7.73e-25	SSU72	SSU72 homolog, RNA polymerase II CT	0.97	3.06e-14	NCEH1	neutral cholesterol ester hydrolase
-0.91	1.08e-25	RNASEH2A	ribonuclease H2 subunit A	0.96	6.03e-23	LACTB	lactamase beta
-0.91	9.17e-21	RNASEH2C	ribonuclease H2 subunit C	0.96	4.39e-16	TGM2	transglutaminase 2
-0.9	1.26e-25	NUSAP1	nucleolar and spindle associated pr	0.95	2.45e-17	THBS1	thrombospondin 1

GAGE analysis on upregulated and downregulated proteins at low/absent CBX3 protein, DB1



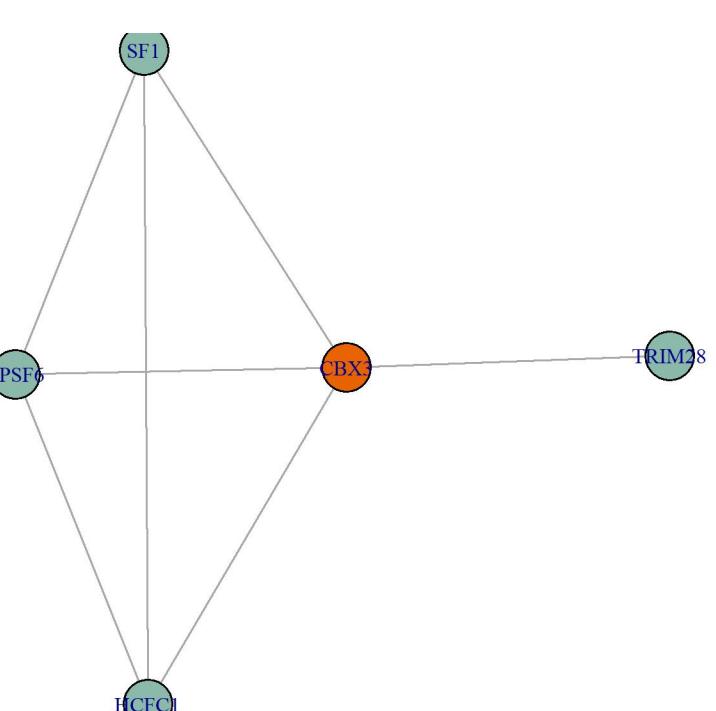


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
1.05	1.47e-03	SLBP	stem-loop binding protein	1.06	4.34e-05	VPS45	vacuolar protein sorting 45 homolog
0.99	5.16e-05	RNF169	ring finger protein 169	0.92	2.73e-03	HTATIP2	HIV-1 Tat interactive protein 2
0.94	1.52e-03	RANGRF	RAN guanine nucleotide release fact	0.89	2.57e-02	LGALS3	galectin 3
0.94	1.60e-03	LEF1	lymphoid enhancer binding factor 1	0.88	4.06e-03	TYMP	thymidine phosphorylase
0.9	1.46e-03	GTSE1	G2 and S-phase expressed 1	0.86	1.52e-03	MYO1C	myosin IC
0.87	6.76e-03	BLM	BLM RecQ like helicase	0.84	1.15e-02	ZMPSTE24	zinc metallopeptidase STE24
0.85	6.37e-04	ZWINT	ZW10 interacting kinetochore protei	0.84	1.84e-02	TM9SF2	transmembrane 9 superfamily member
0.85	2.58e-03	MAZ	MYC associated zinc finger protein	0.83	1.42e-02	MRPS2	mitochondrial ribosomal protein S2
0.84	5.10e-03	ZMAT2	zinc finger matrin-type 2	0.83	2.29e-02	STOM	stomatin
0.84	1.69e-03	RAD18	RAD18 E3 ubiquitin protein ligase	0.82	2.14e-02	SQOR	sulfide quinone oxidoreductase
0.83	2.65e-04	RCOR1	REST corepressor 1	0.81	1.84e-02	SAR1B	secretion associated Ras related GT
0.82	6.37e-04	KIAA1143	KIAA1143	0.79	4.64e-03	TIMMDC1	translocase of inner mitochondrial
0.82	1.53e-03	HAUS1	HAUS augmin like complex subunit 1	0.78	3.84e-02	MVP	major vault protein
0.82	1.60e-03	BRD7	bromodomain containing 7	0.77	6.19e-03	LAETCB	lactamase beta
0.8	1.69e-03	CCDC12	coiled-coil domain containing 12	0.77	1.08e-02	PCCB	propionyl-CoA carboxylase subunit b
0.8	8.16e-05	MEAF6	MYST/Esa1 associated factor 6	0.76	1.69e-03	FAM91A1	family with sequence similarity 91
0.79	8.16e-05	CHAF1A	chromatin assembly factor 1 subunit	0.75	4.51e-03	BCAT2	branched chain amino acid transamin
0.79	6.37e-04	BIRC5	baculoviral IAP repeat containing 5	0.73	4.81e-03	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-b
0.78	1.79e-03	ATF7IP	activating transcription factor 7 i	0.73	1.54e-02	NDUFB6	NADH:ubiquinone oxidoreductase subu
0.77	4.73e-03	H2AX	H2A.X variant histone	0.73	2.29e-02	MAGT1	magnesium transporter 1
0.76	3.93e-03	CEP131	centrosomal protein 131	0.72	1.74e-02	ACSL1	acyl-CoA synthetase long chain fami
0.76	1.54e-02	SS18	SS18 subunit of BAF chromatin remod	0.71	8.58e-03	PLOD1	procollagen-lysine,2-oxoglutarate 5
0.76	1.36e-03	MRFAP1	Morf4 family associated protein 1	0.71	3.04e-02	SYNGR2	synaptogyrin 2
0.75	1.17e-03	TIPIN	TIMELESS interacting protein	0.71	1.02e-02	TMED2	transmembrane p24 trafficking prote
0.75	1.07e-02	SETD7	SET domain containing 7, histone ly	0.7	2.48e-03	NDUFAF7	NADH:ubiquinone oxidoreductase comp
0.74	1.61e-03	ASF1B	anti-silencing function 1B histone	0.7	3.49e-02	NBAS	NBAS subunit of NRZ tethering compl
0.74	9.36e-03	ZAP70	zeta chain of T cell receptor assoc	0.7	3.89e-03	EML2	EMAP like 2
0.74	4.36e-03	CASP2	caspase 2	0.7	1.16e-02	PTPMT1	protein tyrosine phosphatase mitoch
0.73	2.21e-02	TCF3	transcription factor 3	0.69	2.81e-02	RPS27L	ribosomal protein S27 like

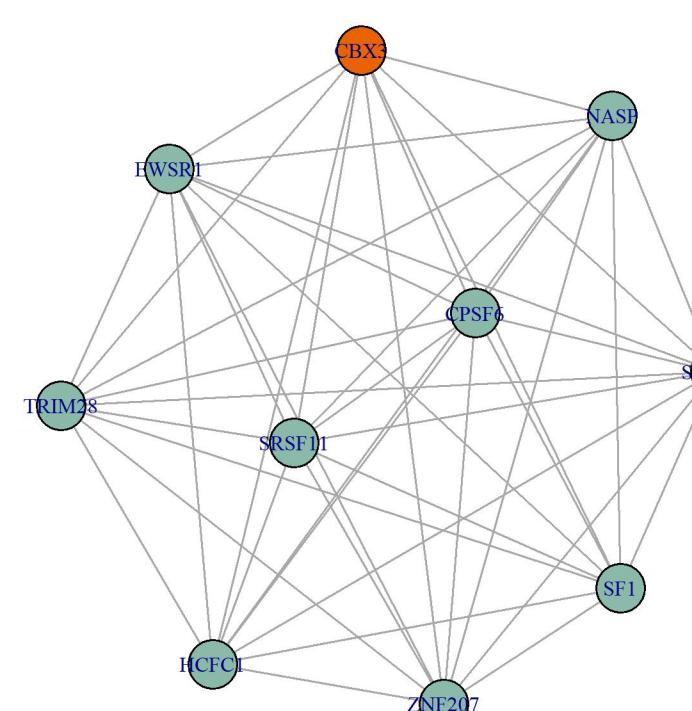


Downregulated in solid cancers at low/absent CBX3				Upregulated in solid cancers at low/absent CBX3			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
1.07	2.19e-24	UBE2T	ubiquitin conjugating enzyme E2 T	1.03	6.07e-13	AP2S1	adaptor related protein complex 2 s
1.02	8.56e-26	LIG1	DNA ligase 1	0.96	7.14e-17	RAB32	RAB32, member RAS oncogene family
-1	1.93e-22	POLE3	DNA polymerase epsilon 3, accessory	0.93	8.91e-14	AXL	AXL receptor tyrosine kinase
0.98	7.63e-15	ZNF706	zinc finger protein 706	0.88	9.39e-16	LACTB	lactamase beta
0.98	1.43e-20	C9orf78	chromosome 9 open reading frame 78	0.88	3.50e-15	NPC1	NPC intracellular cholesterol trans
0.94	1.16e-20	UBE2S	ubiquitin conjugating enzyme E2 S	0.88	2.33e-15	COL12A1	collagen type XII alpha 1 chain
0.91	1.27e-24	POU2F1	POU class 2 homeobox 1	0.86	7.38e-20	POFUT2	protein O-fucosyltransferase 2
0.91	3.93e-21	PRCC	proline rich mitotic checkpoint con	0.86	3.92e-13	GPX8	glutathione peroxidase 8 (putative)
0.86	1.17e-15	ENSA	endosulfine alpha	0.86	2.55e-07	CAVIN1	caveolae associated protein 1
0.86	5.48e-15	UBR7	ubiquitin protein ligase E3 compone	0.85	2.33e-11	IGFBP7	insulin like growth factor binding
0.84	1.19e-17	NUSAP1	nucleolar and spindle associated pr	0.84	2.79e-10	NT5E	5'-nucleotidase ecto
0.83	2.78e-09	CKMT1A	creatine kinase, mitochondrial 1A	0.84	2.44e-15	HSPG2	heparan sulfate proteoglycan 2
0.83	2.07e-14	PMF1	polyamine modulated factor 1	0.83	1.27e-12	EPHA2	EPH receptor A2
0.82	2.03e-13	CLNS1A	chloride nucleotide-sensitive chann	0.82	3.62e-15	FSTL1	follistatin like 1
0.82	2.37e-15	UBXN7	UBX domain protein 7	0.82	3.34e-16	FNDC3B	fibronectin type III domain contain
0.82	7.25e-21	TRIM24	tripartite motif containing 24	0.82	2.44e-15	ERGIC2	ERGIC and golgi 2
0.81	8.86e-18	KIAA1143	KIAA1143	0.82	1.42e-08	CAV1	caveolin 1
-0.8	4.16e-16	SAP130	Sin3A associated protein 130	0.82	1.18e-09	CAVIN3	caveolae associated protein 3
0.79	5.72e-15	NFATC2IP	nuclear factor of activated T cells	0.82	1.48e-16	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-b
0.79	9.34e-12	PBK	PDZ binding kinase	0.82	4.38e-18	LMAN2L	lectin, mannose binding 2 like
0.79	2.56e-16	TSEN34	tRNA splicing endonuclease subunit	0.81	9.60e-13	TGFBI	transforming growth factor beta ind
0.78	3.64e-17	POLD3	DNA polymerase delta 3, accessory s	0.8	1.17e-15	GOLT1B	golgi transport 1B
0.78	5.72e-15	UBE2C	ubiquitin conjugating enzyme E2 C	0.79	1.06e-11	CYBRD1	cytochrome b reductase 1
0.78	4.38e-18	DNAJC17	DnaJ heat shock protein family (Hsp	0.79	7.30e-09	ICAM1	intercellular adhesion molecule 1
0.77	4.74e-13	SS18	SS18 subunit of BAF chromatin remod	0.78	2.05e-13	SERPINE1	serpin family E member 1
0.77	1.28e-17	IRF2BP1	interferon regulatory factor 2 bind	0.77	2.52e-13	IER3IP1	immediate early response 3 interact
0.77	8.92e-15	POLE4	DNA polymerase epsilon 4, accessory	0.77	8.06e-10	MMP14	matrix metallopeptidase 14
0.77	4.36e-15	NUDT1	nudix hydrolase 1	0.77	1.19e-13	CCN1	cellular communication network fact
0.77	9.87e-18	PHF23	PHD finger protein 23	0.77	6.01e-14	KIRREL1	kirre like nephrin family adhesion

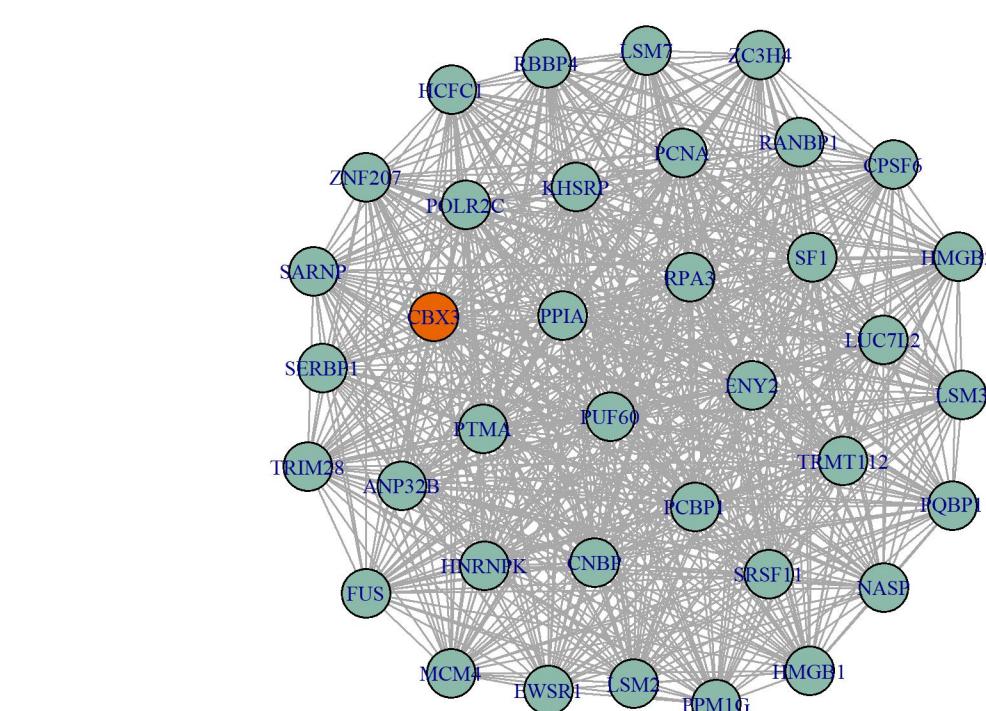
CBX3 network, DB1, all Pearson r > 0.65

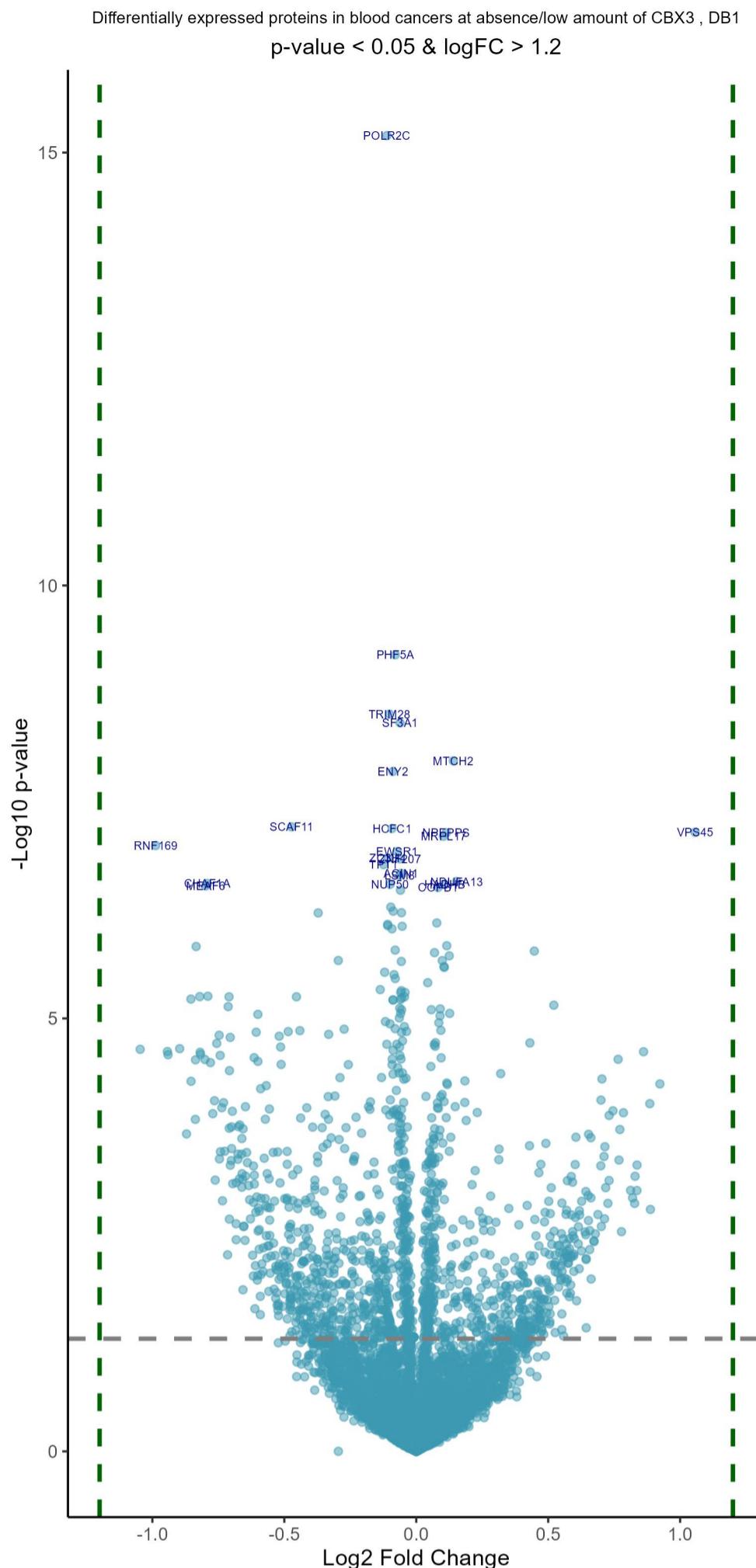


CBX3 network, DB1, all Pearson $r > 0.6$

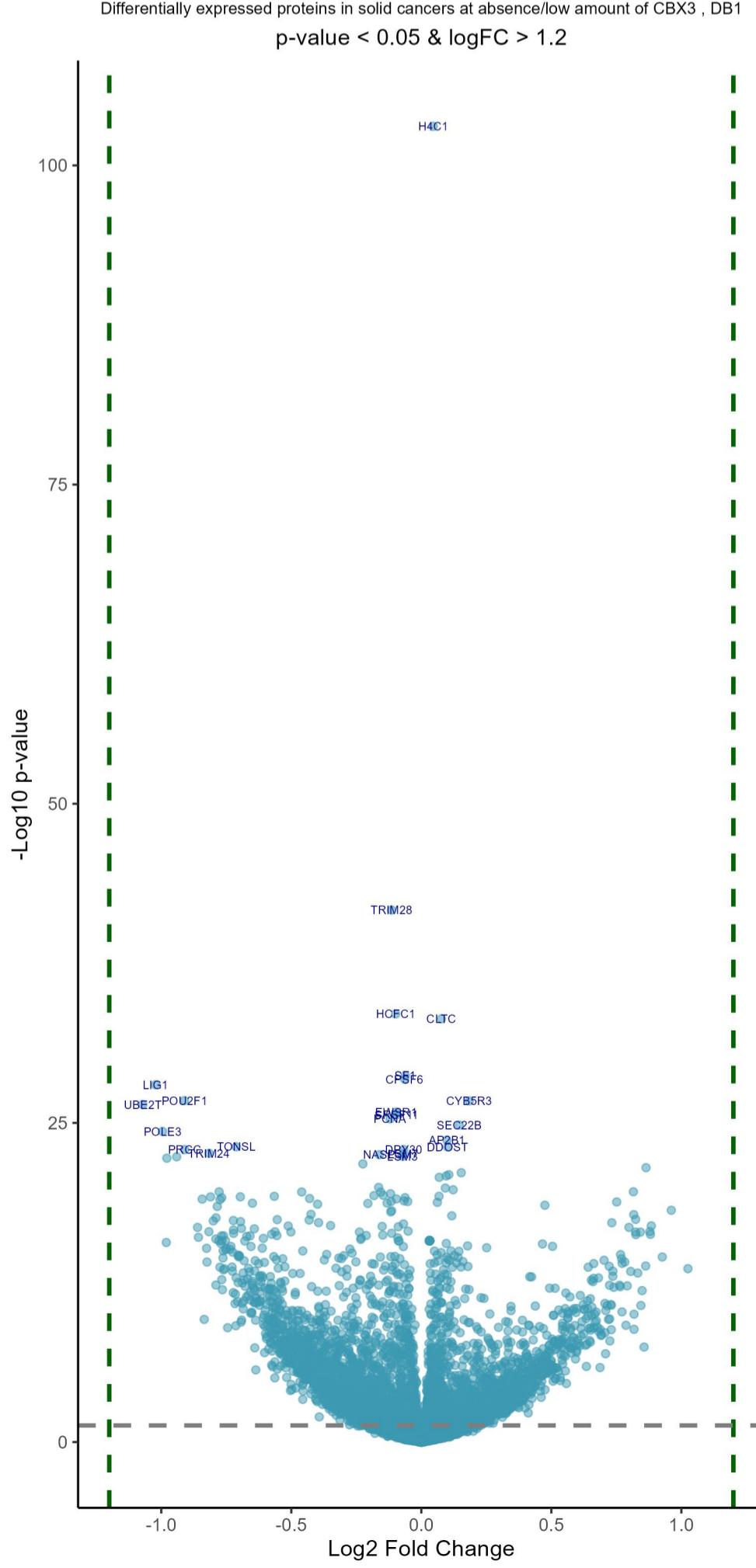


CBX3 network, DB1, all Pearson $r > 0.55$



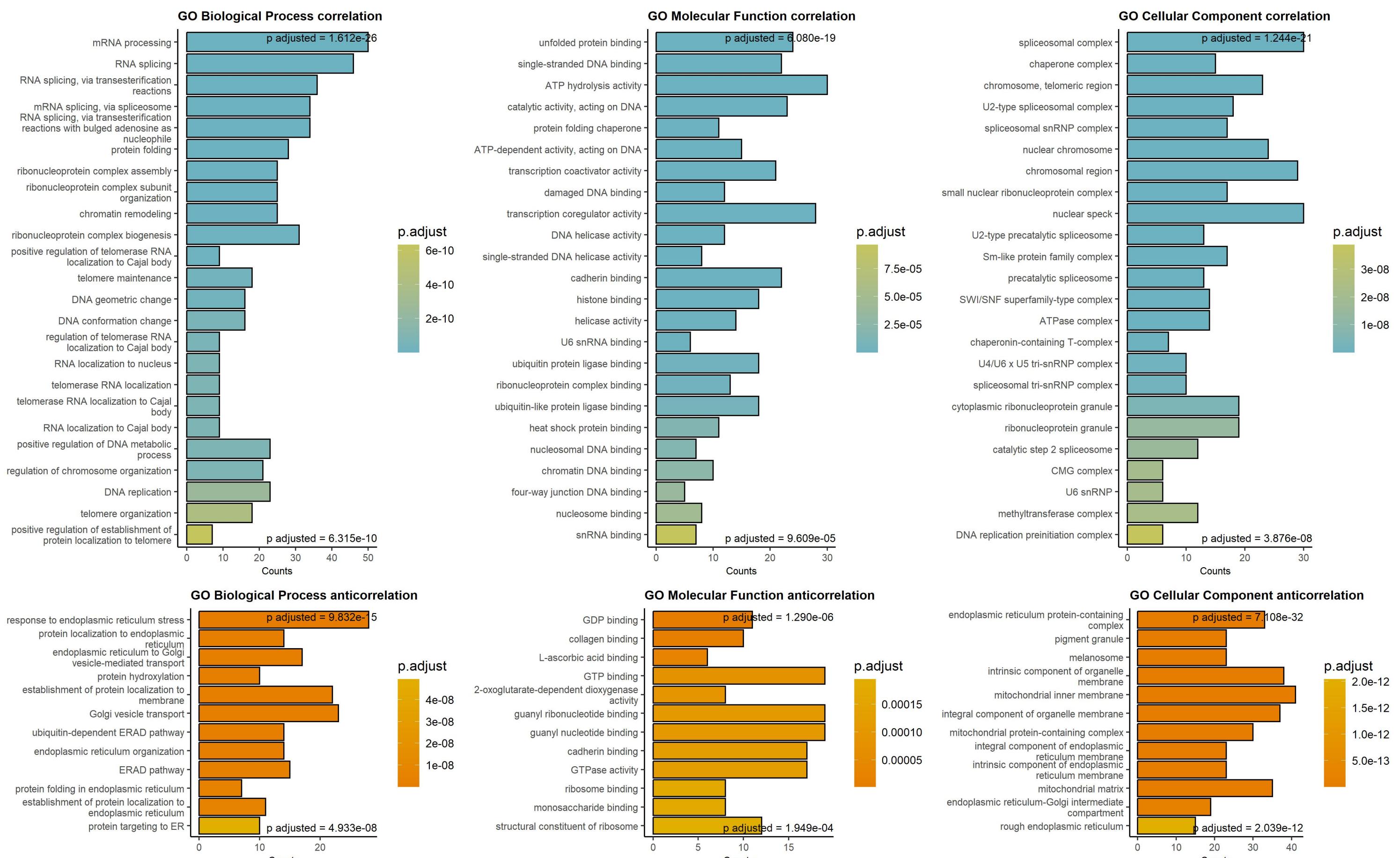


Sorted by p values!							
Downregulated in blood cancers at low/absent CBX3				Upregulated in blood cancers at low/absent CBX3			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.11	2.12e-12	POLR2C	RNA polymerase II subunit C	0.14	1.18e-05	MTCH2	mitochondrial carrier 2
-0.08	1.40e-06	PHF5A	PHD finger protein 5A	1.06	4.34e-05	VPS45	vacuolar protein sorting 45 homolog
-0.1	5.08e-06	TRIM28	tripartite motif containing 28	0.11	4.34e-05	NPEPPS	aminopeptidase puromycin sensitive
-0.06	5.13e-06	SF3A1	splicing factor 3a subunit 1	0.1	4.36e-05	MRPL17	mitochondrial ribosomal protein L17
-0.09	1.34e-05	ENY2	ENY2 transcription and export compl	0.15	8.16e-05	NDUFA13	NADH:ubiquinone oxidoreductase subu
-0.47	4.34e-05	SCAF11	SR-related CTD associated factor 11	0.11	8.16e-05	HADHB	hydroxyacyl-CoA dehydrogenase triflu
-0.09	4.34e-05	HCFC1	host cell factor C1	0.08	8.18e-05	COPB1	COPI coat complex subunit beta 1
-0.99	5.16e-05	RNF169	ring finger protein 169	0.08	1.69e-04	CLTC	clathrin heavy chain
-0.07	5.63e-05	EWSR1	EWS RNA binding protein 1	0.12	2.65e-04	NDUFS2	NADH:ubiquinone oxidoreductase core
-0.11	5.97e-05	ZC3H4	zinc finger CCCH-type containing 4	0.45	2.84e-04	IFIH1	interferon induced with helicase C
-0.06	5.97e-05	ZNF207	zinc finger protein 207	0.07	2.89e-04	COPB2	COPI coat complex subunit beta 2
-0.12	6.55e-05	TPT1	tumor protein, translationally-cont	0.12	3.07e-04	MRPL38	mitochondrial ribosomal protein L38
-0.06	7.79e-05	ACIN1	apoptotic chromatin condensation in	0.1	3.32e-04	ATP5PB	ATP synthase peripheral stalk-membr
-0.06	7.82e-05	LSM8	LSM8 homolog, U6 small nuclear RNA	0.11	3.72e-04	MRPL19	mitochondrial ribosomal protein L19
-0.79	8.16e-05	CHAF1A	chromatin assembly factor 1 subunit	0.11	3.72e-04	PDCD11	programmed cell death 11
-0.1	8.16e-05	NUP50	nucleoporin 50	0.04	5.14e-04	RPS18	ribosomal protein S18
-0.8	8.16e-05	MEAF6	MYST/Esa1 associated factor 6	0.52	7.19e-04	RAP2C	RAP2C, member of RAS oncogene fam
-0.06	8.46e-05	HNRNPDL	heterogeneous nuclear ribonucleopro	0.09	7.55e-04	ACLY	ATP citrate lyase
-0.1	1.28e-04	FUS	FUS RNA binding protein	0.06	7.55e-04	PSMD8	proteasome 26S subunit, non-ATPase
-0.09	1.34e-04	TMPO	thymopoietin	0.13	8.08e-04	DDOST	dolichyl-diphosphooligosaccharide--
-0.06	1.34e-04	TPR	translocated promoter region, nucle	0.09	8.38e-04	ATP5F1C	ATP synthase F1 subunit gamma
-0.37	1.34e-04	POLE3	DNA polymerase epsilon 3, accessory	0.09	9.69e-04	PSMD12	proteasome 26S subunit, non-ATPase
-0.11	1.69e-04	RBBP4	RB binding protein 4, chromatin rem	0.09	1.11e-03	HADHA	hydroxyacyl-CoA dehydrogenase triflu
-0.11	1.69e-04	DUT	deoxyuridine triphosphatase	0.07	1.36e-03	UBR4	ubiquitin protein ligase E3 compone
-0.05	1.69e-04	SF1	splicing factor 1	0.43	1.36e-03	ADPRH	ADP-ribosylarginine hydrolase
-0.09	1.75e-04	RNF40	ring finger protein 40	0.07	1.36e-03	ETF1	eukaryotic translation termination
-0.83	2.65e-04	RCOR1	REST corepressor 1	0.07	1.41e-03	UQCRC1	ubiquinol-cytochrome c reductase co
-0.08	2.84e-04	NASP	nuclear autoantigenic sperm protein	0.86	1.52e-03	MYO1C	myosin IC
-0.3	3.32e-04	GINS4	GINS complex subunit 4	0.09	1.68e-03	GCN1	GCN1 activator of EIF2AK4
-0.06	3.32e-04	CHD4	chromodomain helicase DNA binding p	0.76	1.69e-03	FAM91A1	family with sequence similarity 91
-0.12	4.14e-04	NUMA1	nuclear mitotic apparatus protein 1	0.06	1.92e-03	COPA	COPI coat complex subunit alpha
-0.08	4.33e-04	CAPRIN1	cell cycle associated protein 1	0.32	2.24e-03	EMC1	ER membrane protein complex subunit
-0.08	4.70e-04	RPA3	replication protein A3	0.7	2.48e-03	NDUFAF7	NADH:ubiquinone oxidoreductase comp
-0.14	6.06e-04	MKI67	marker of proliferation Ki-67	0.18	2.57e-03	NDUFV1	NADH:ubiquinone oxidoreductase core
-0.06	6.11e-04	PNN	pinin, desmosome associated protein	0.12	2.68e-03	HEATR1	HEAT repeat containing 1
-0.04	6.19e-04	SAP18	Sin3A associated protein 18	0.92	2.73e-03	HTATIP2	HIV-1 Tat interactive protein 2
-0.06	6.19e-04	ANP32B	acidic nuclear phosphoprotein 32 fa	0.12	2.75e-03	ME2	malic enzyme 2
-0.79	6.37e-04	BIRC5	baculoviral IAP repeat containing 5	0.1	3.49e-03	DRG1	developmentally regulated GTP bindi
-0.82	6.37e-04	KIAA1143	KIAA1143	0.01	3.61e-03	PSMD11	proteasome 26S subunit, non-ATPase

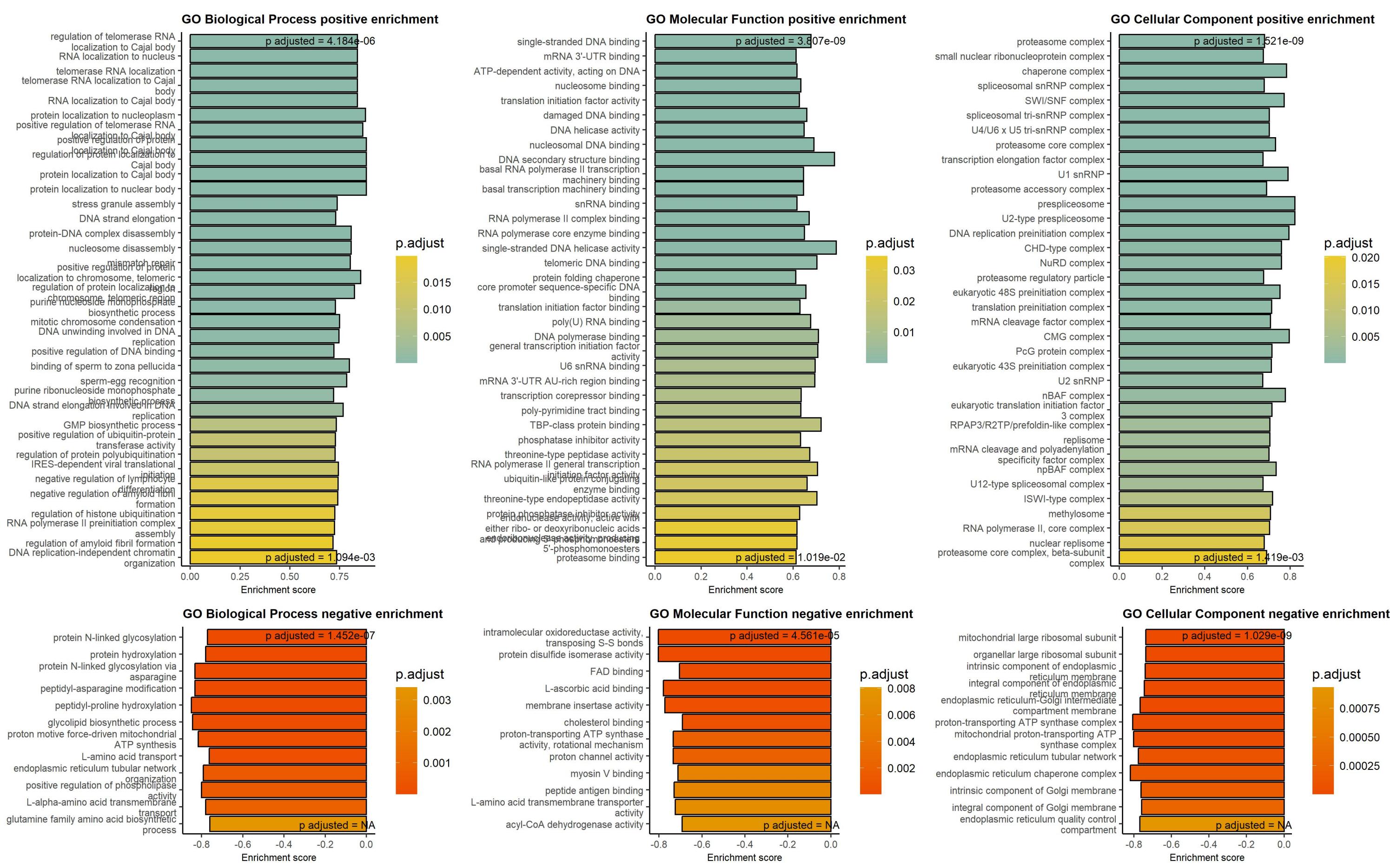


Sorted by p values!							
Downregulated in solid cancers at low/absent CBX3				Upregulated in solid cancers at low/absent CBX3			
C	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
1	4.71e-39	TRIM28	tripartite motif containing 28	0.05	2.89e-100	H4C1	H4 clustered histone 1
1	4.90e-31	HCFC1	host cell factor C1	0.08	9.28e-31	CLTC	clathrin heavy chain
6	2.16e-26	SF1	splicing factor 1	0.18	1.27e-24	CYB5R3	cytochrome b5 reductase 3
6	3.64e-26	CPSF6	cleavage and polyadenylation specif	0.15	6.67e-23	SEC22B	SEC22 homolog B, vesicle traffickin
2	8.56e-26	LIG1	DNA ligase 1	0.1	8.73e-22	AP2B1	adaptor related protein complex 2 s
1	1.27e-24	POU2F1	POU class 2 homeobox 1	0.1	2.74e-21	DDOST	dolichyl-diphosphooligosaccharide--
7	2.19e-24	UBE2T	ubiquitin conjugating enzyme E2 T	0.86	7.38e-20	POFUT2	protein O-fucosyltransferase 2
1	7.93e-24	EWSR1	EWS RNA binding protein 1	0.15	1.77e-19	MOGS	mannosyl-oligosaccharide glucosidase
1	1.18e-23	SRSF11	serine and arginine rich splicing f	0.11	2.44e-19	PGRMC2	progesterone receptor membrane com
2	2.30e-23	PCNA	proliferating cell nuclear antigen	0.1	2.99e-19	NCLN	nicalin
	1.93e-22	POLE3	DNA polymerase epsilon 3, accessory	0.07	3.71e-19	GANAB	glucosidase II alpha subunit
1	2.73e-21	TONSL	tonsoku like, DNA repair protein	0.09	2.41e-18	TMED9	transmembrane p24 trafficking prote
7	3.93e-21	DPY30	dpy-30 histone methyltransferase co	0.12	3.20e-18	RPN2	ribophorin II
1	3.93e-21	PRCC	proline rich mitotic checkpoint con	0.82	4.38e-18	LMAN2L	lectin, mannose binding 2 like
2	7.25e-21	TRIM24	tripartite motif containing 24	0.07	8.33e-18	RPL27	ribosomal protein L27
7	8.01e-21	LSM7	LSM7 homolog, U6 small nuclear RNA	0.75	1.82e-17	SEC11A	SEC11 homolog A, signal peptidase
6	8.60e-21	NASP	nuclear autoantigenic sperm protein	0.06	1.93e-17	RPL15	ribosomal protein L15
7	1.10e-20	LSM3	LSM3 homolog, U6 small nuclear RNA	0.48	2.96e-17	ANO10	anoctamin 10
4	1.16e-20	UBE2S	ubiquitin conjugating enzyme E2 S	0.96	7.14e-17	RAB32	RAB32, member RAS oncogene fami
8	1.43e-20	C9orf78	chromosome 9 open reading frame 78	0.82	1.48e-16	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-b
2	3.86e-20	PTMA	prothymosin alpha	0.12	1.80e-16	ESYT1	extended synaptotagmin 1
6	2.20e-18	MCM6	minichromosome maintenance complex	0.82	3.34e-16	FNDC3B	fibronectin type III domain contain
8	4.38e-18	DNAJC17	DnaJ heat shock protein family (Hsp	0.73	5.58e-16	ANO6	anoctamin 6
6	4.39e-18	PPP1R8	protein phosphatase 1 regulatory su	0.88	9.39e-16	LACTB	lactamase beta
6	4.39e-18	RANBP1	RAN binding protein 1	0.8	1.17e-15	GOLT1B	golgi transport 1B
2	5.76e-18	TRMT112	tRNA methyltransferase activator su	0.88	2.33e-15	COL12A1	collagen type XII alpha 1 chain
5	7.37e-18	MCM4	minichromosome maintenance complex	0.82	2.44e-15	ERGIC2	ERGIC and golgi 2
8	7.64e-18	CNBP	CCHC-type zinc finger nucleic acid	0.84	2.44e-15	HSPG2	heparan sulfate proteoglycan 2
7	8.33e-18	RNF20	ring finger protein 20	0.88	3.50e-15	NPC1	NPC intracellular cholesterol trans
7	8.86e-18	C11orf58	chromosome 11 open reading frame 58	0.82	3.62e-15	FSTL1	follistatin like 1
1	8.86e-18	KIAA1143	KIAA1143	0.03	5.72e-15	PTPRCAP	protein tyrosine phosphatase recept
6	9.87e-18	DDX46	DEAD-box helicase 46	0.03	5.72e-15	HBE1	hemoglobin subunit epsilon 1
7	9.87e-18	PHF23	PHD finger protein 23	0.03	5.72e-15	SERPINB10	serpin family B member 10
3	1.10e-17	PQBP1	polyglutamine binding protein 1	0.03	5.72e-15	IGLL1	immunoglobulin lambda like polypept
1	1.18e-17	PPIA	peptidylprolyl isomerase A	0.03	5.72e-15	CRYBB1	crystallin beta B1
4	1.19e-17	NUSAP1	nucleolar and spindle associated pr	0.03	5.72e-15	ITGA2B	integrin subunit alpha 2b
7	1.28e-17	IRF2BP1	interferon regulatory factor 2 bind	0.03	5.72e-15	ACAP1	ArfGAP with coiled-coil, ankyrin re
7	1.59e-17	LSM2	LSM2 homolog, U6 small nuclear RNA	0.03	5.72e-15	NCF4	neutrophil cytosolic factor 4
6	1.72e-17	ZC3H14	zinc finger CCCH-type containing 14	0.03	5.72e-15	SP140	SP140, nuclear factor 1B

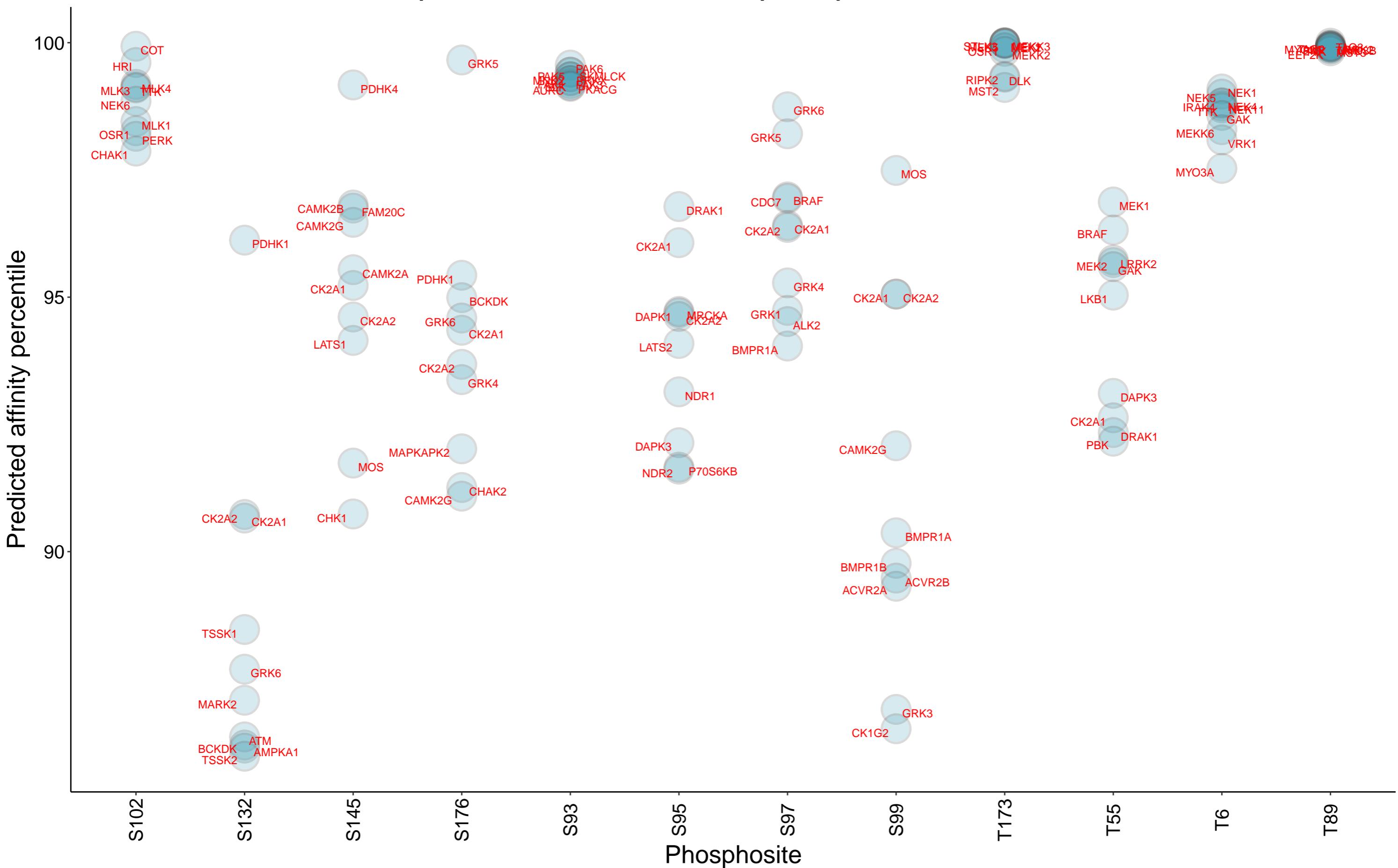
Top 250 correlation coefficients overrepresentation, CBX3 protein, DB1



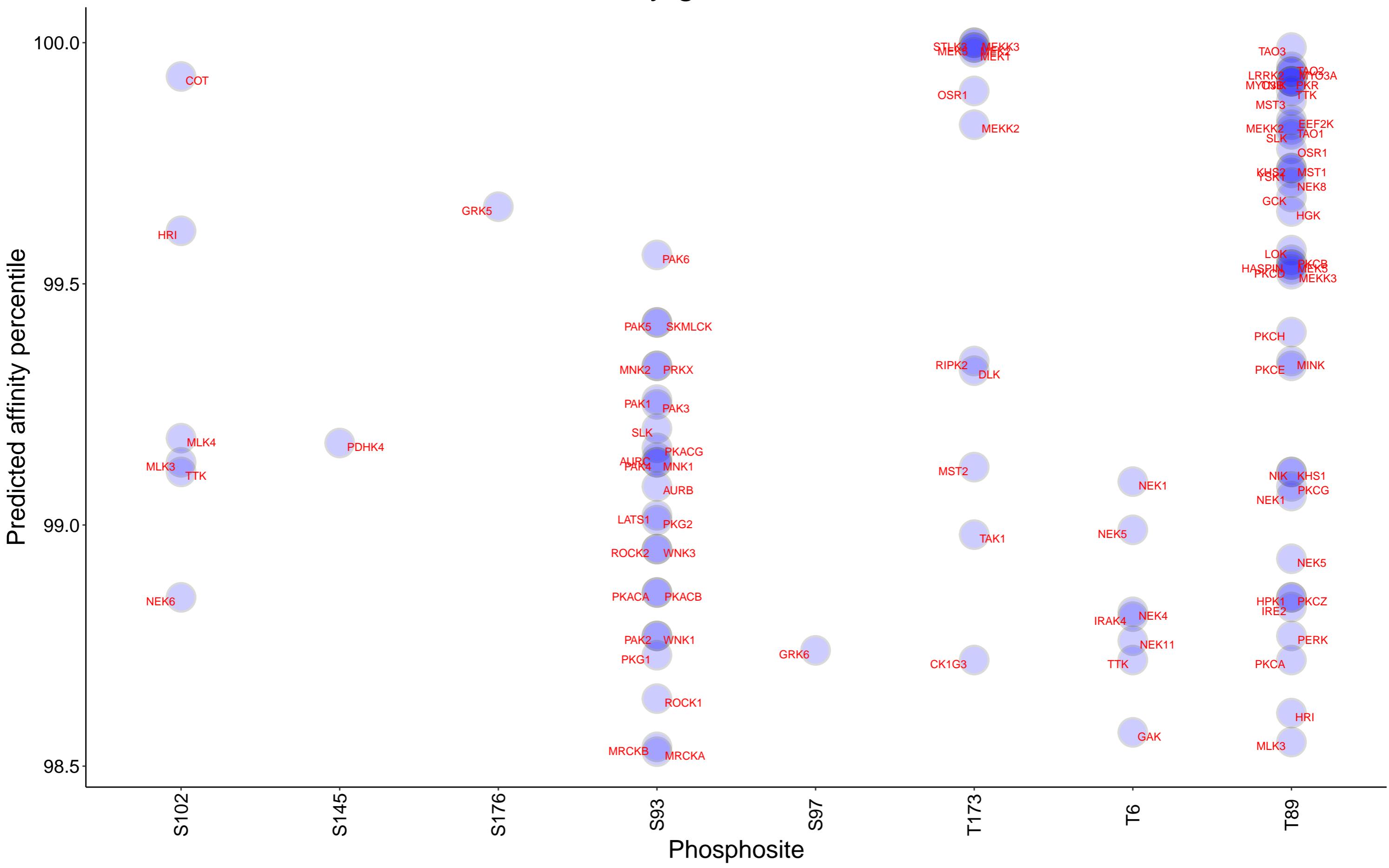
Gene Set Enrichment analysis on protein correlation coefficients, CBX3 protein, DB1



Top 10 kinases for each phosphosite in CBX3



Kinases with affinity greater than 98.5% to CBX3



Top 15 positive correlation coefficients for CBX3 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

