

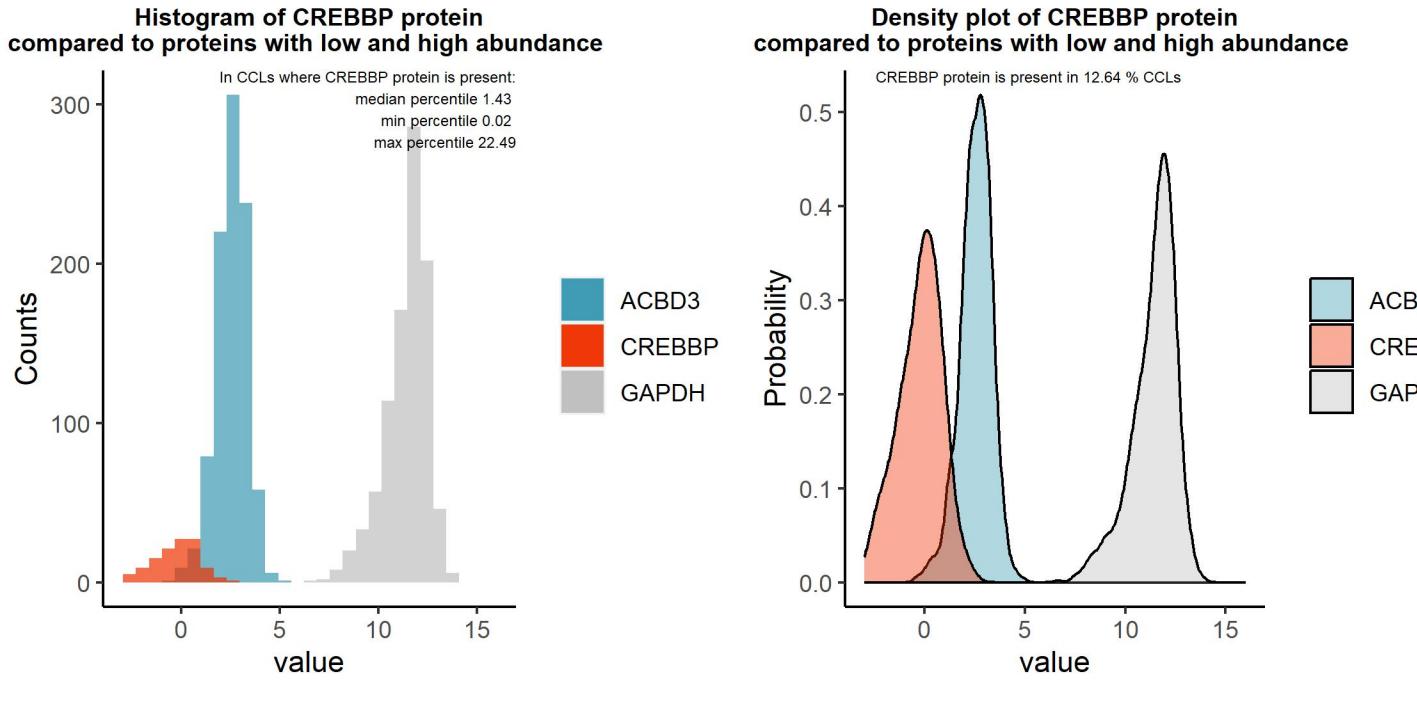
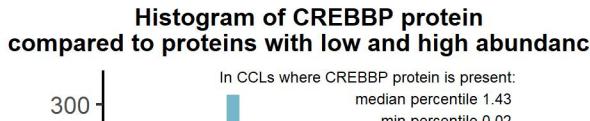
CREBBP

Protein name: CBP ; UNIPROT: Q92793 ; Gene name: CREB binding protein

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

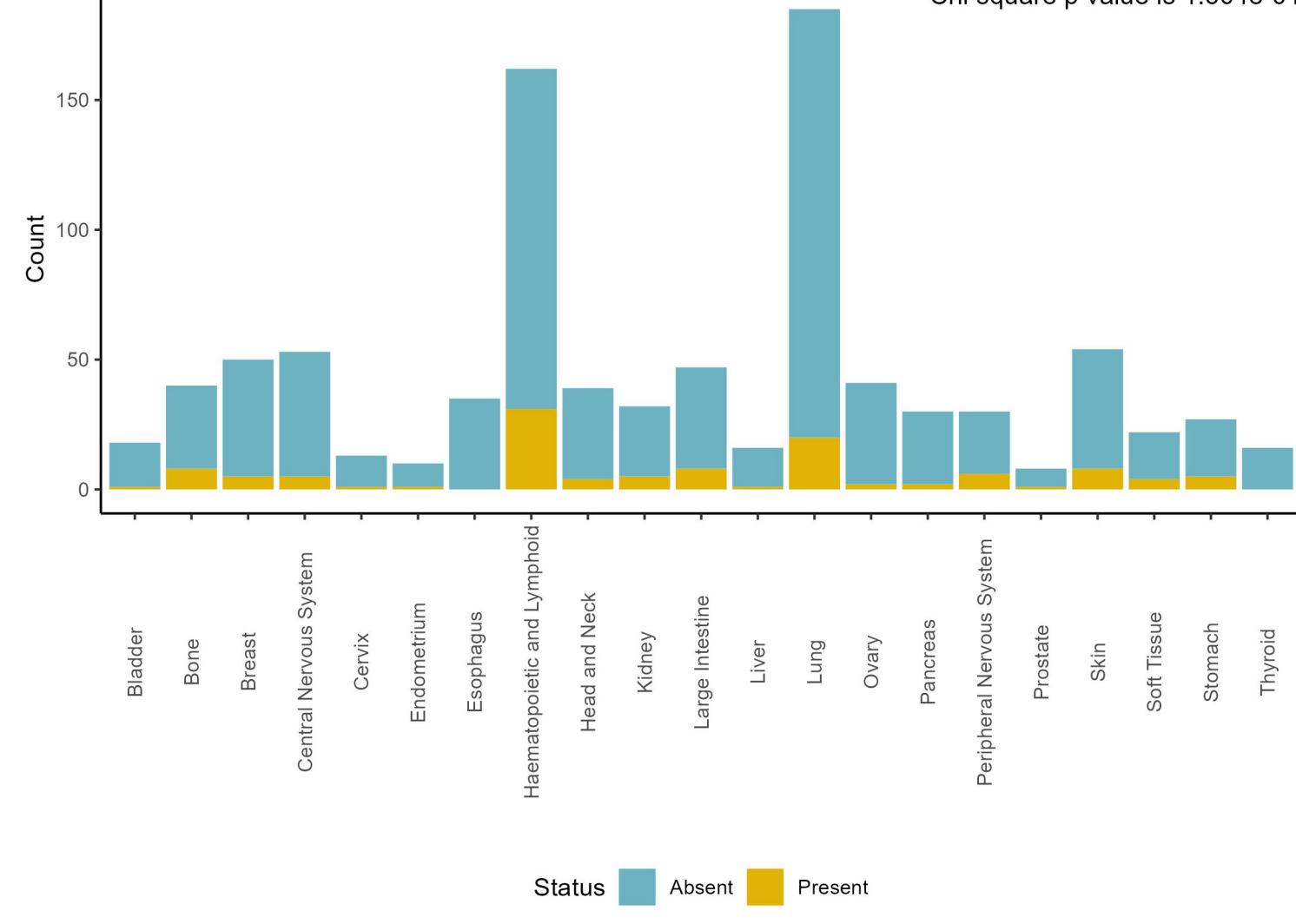
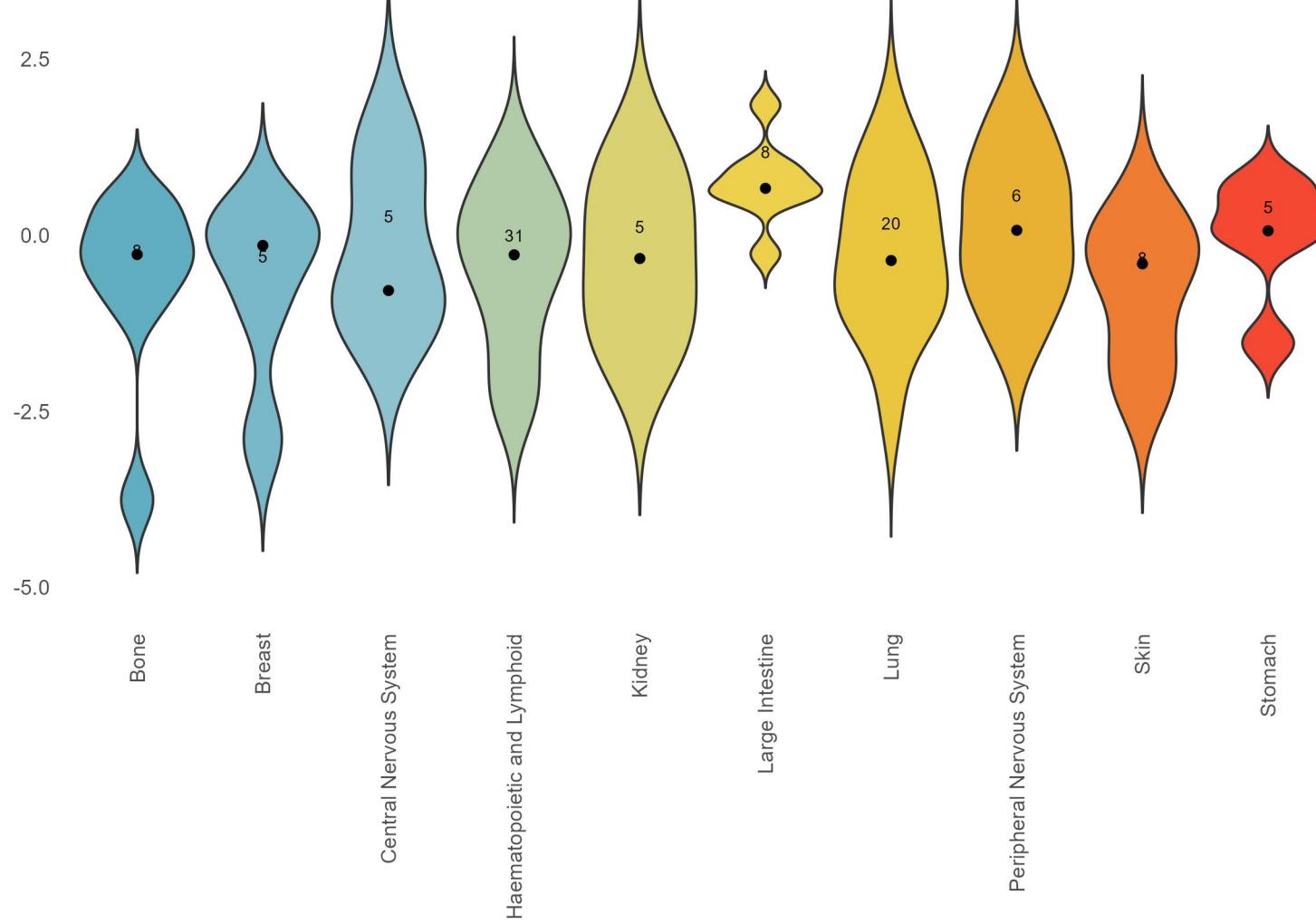
Sanger Institute Protein Database 2 (DB2), protein presence is less certain

8498 proteins in same 949 CCLs



Amount of CREBBP protein, number of CCLs where it is present by tissue, DB2

ANOVA p value is 3.924e-01

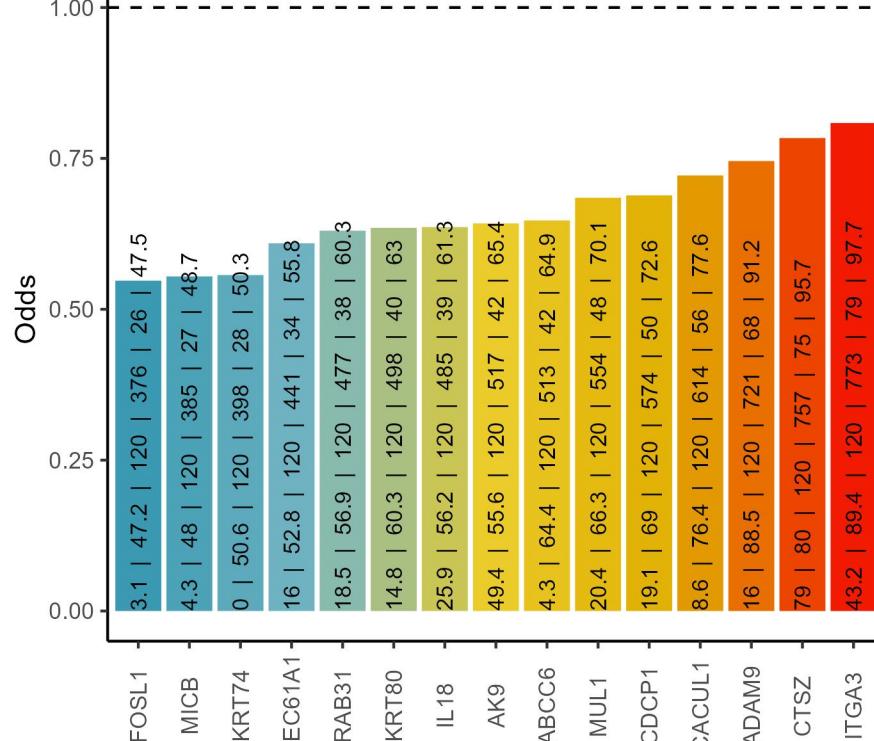


Cooccurrence with CREBBP protein, DB2

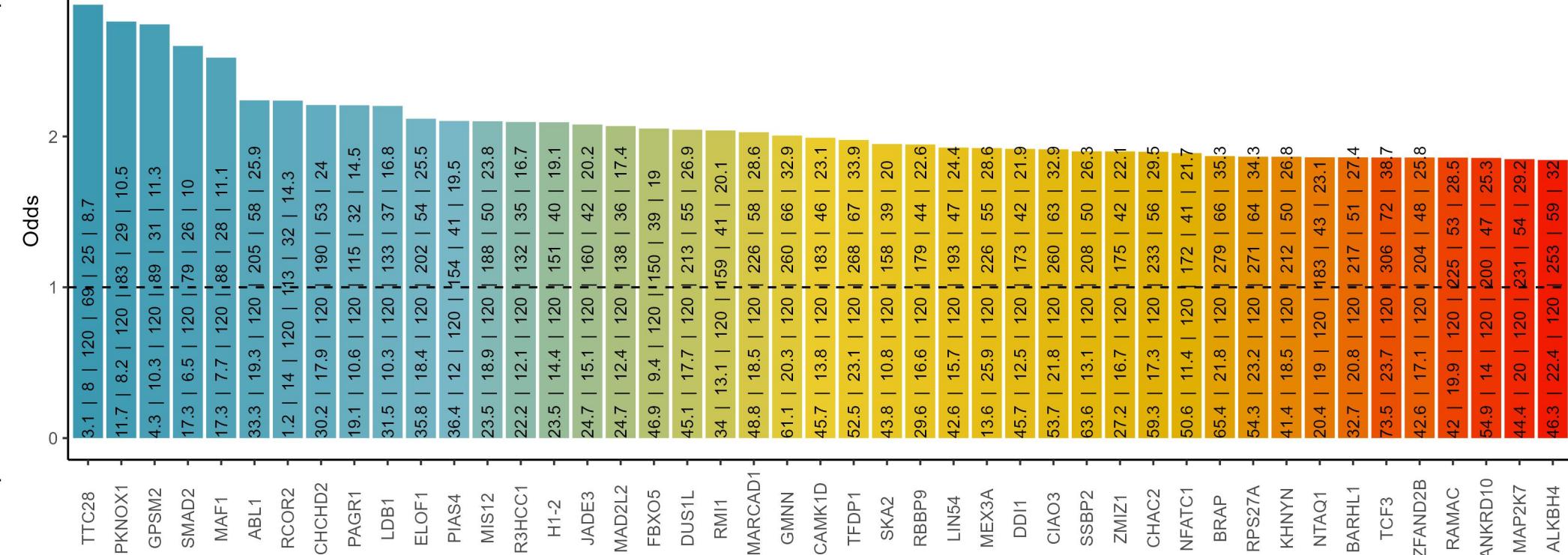
% of CREBBP in blood cancers: 19.1 ; % of CREBBP in solid cancers: 11.2

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

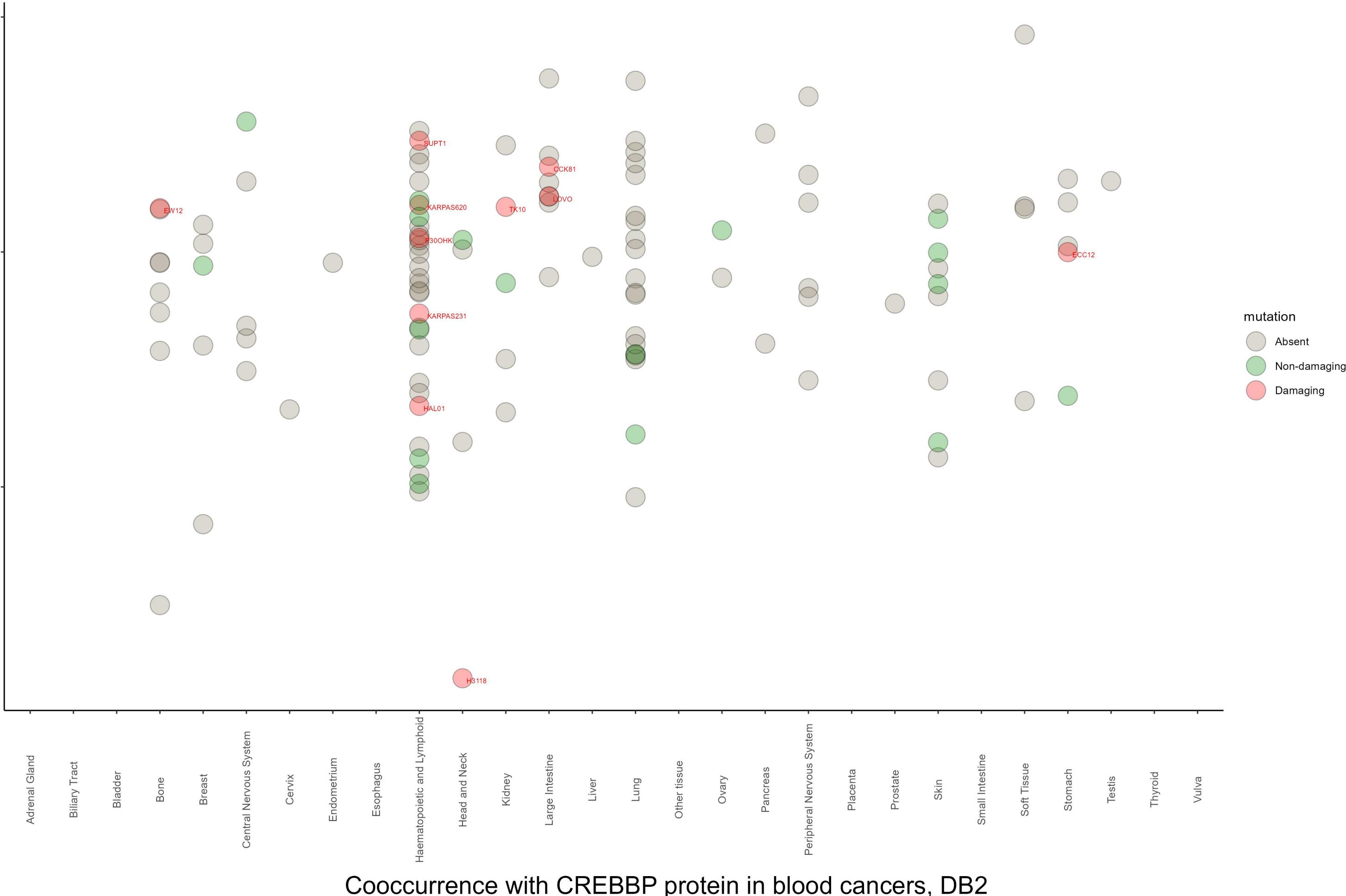
Negative cooccurrence



Positive cooccurrence



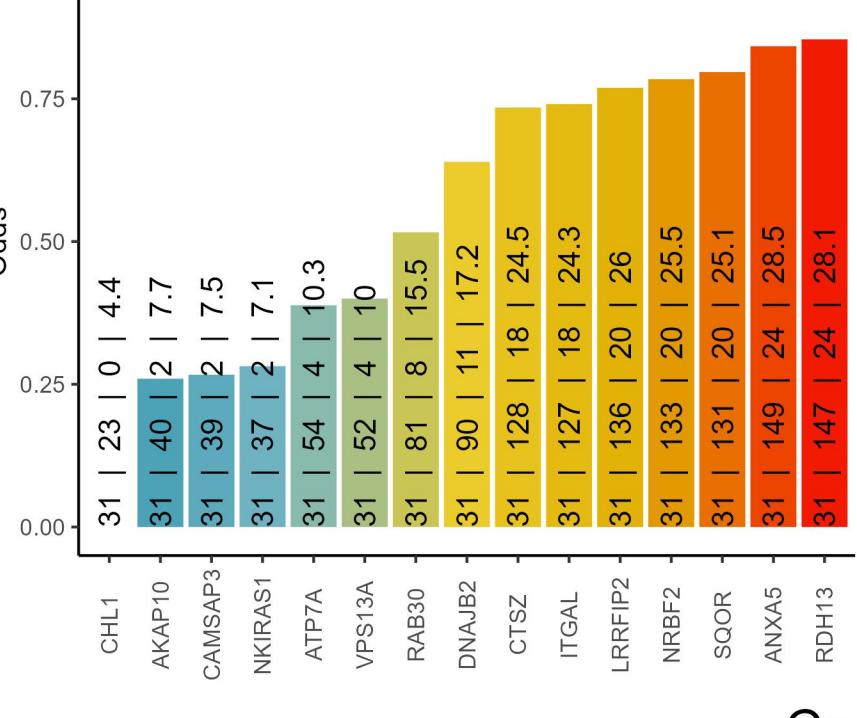
Amount of CREBBP protein and mutation status by tissue, DB2



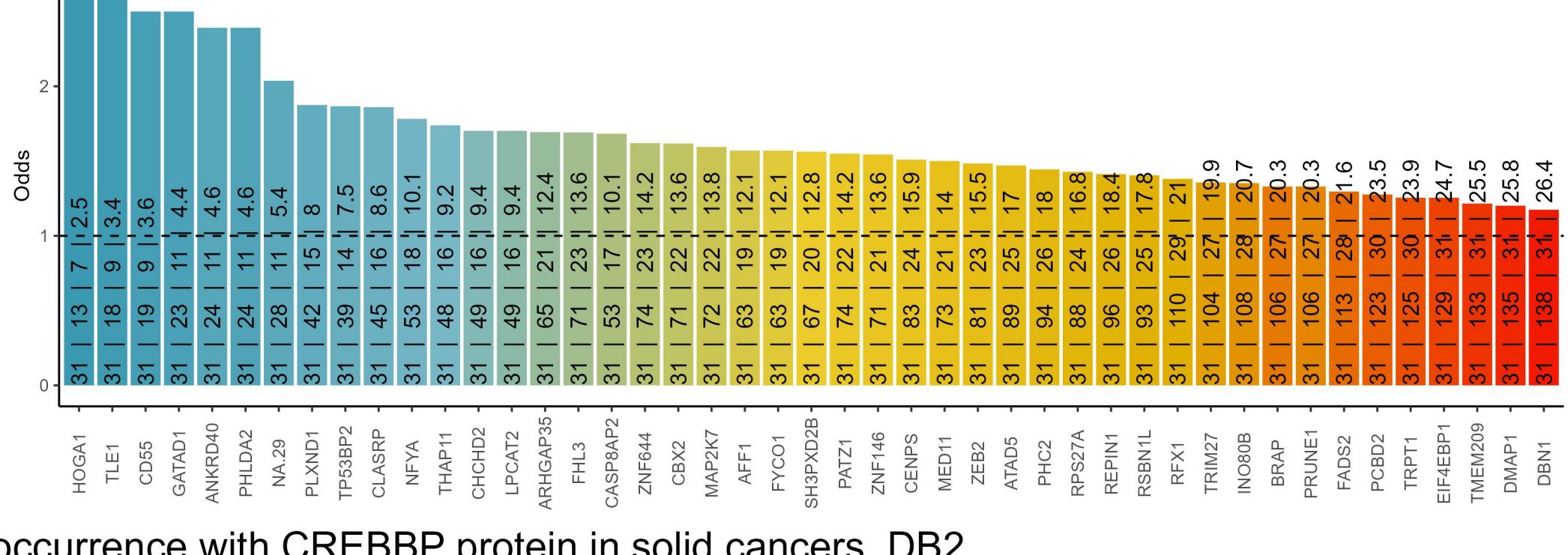
Cooccurrence with CREBBP protein in blood cancers, DB2

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

Negative cooccurrence



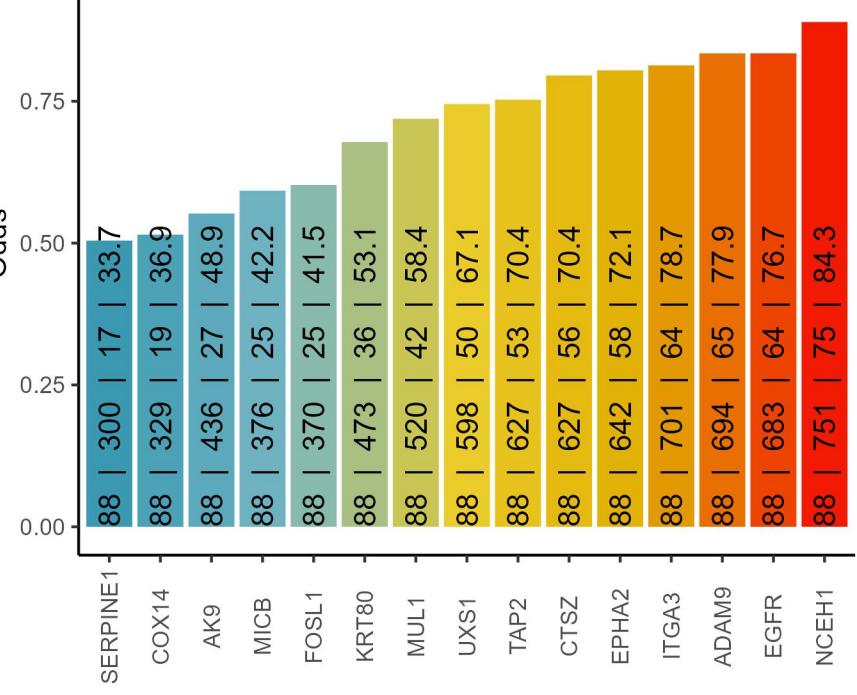
Positive cooccurrence



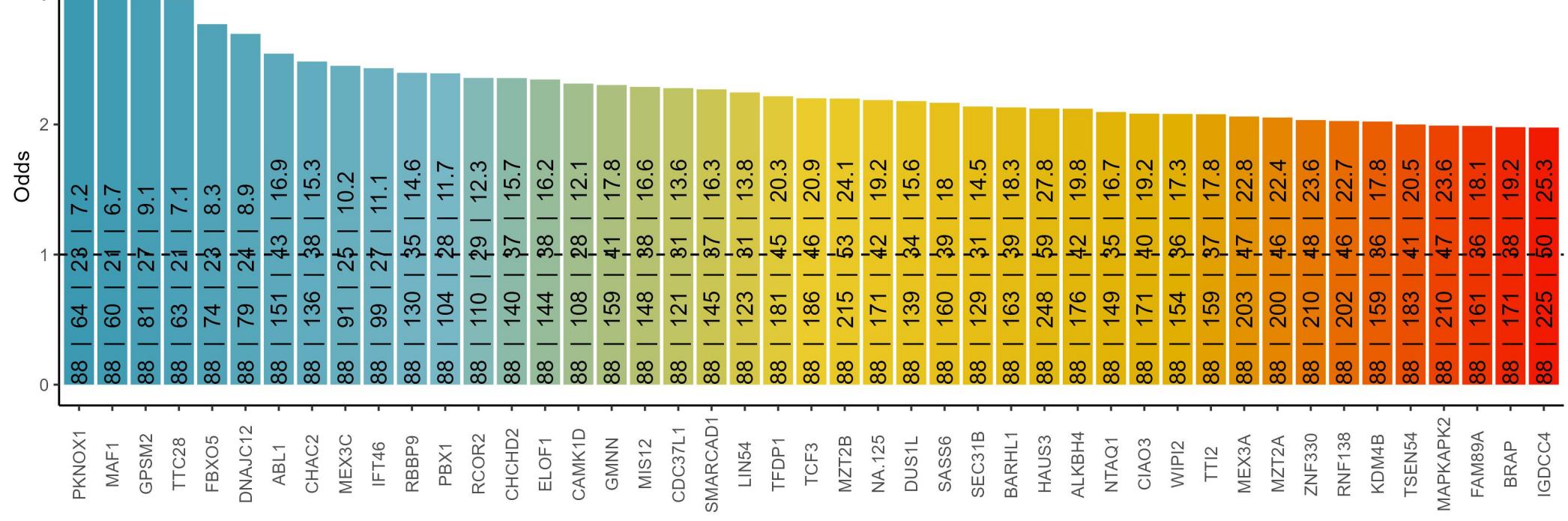
Cooccurrence with CREBBP protein in solid cancers, DB2

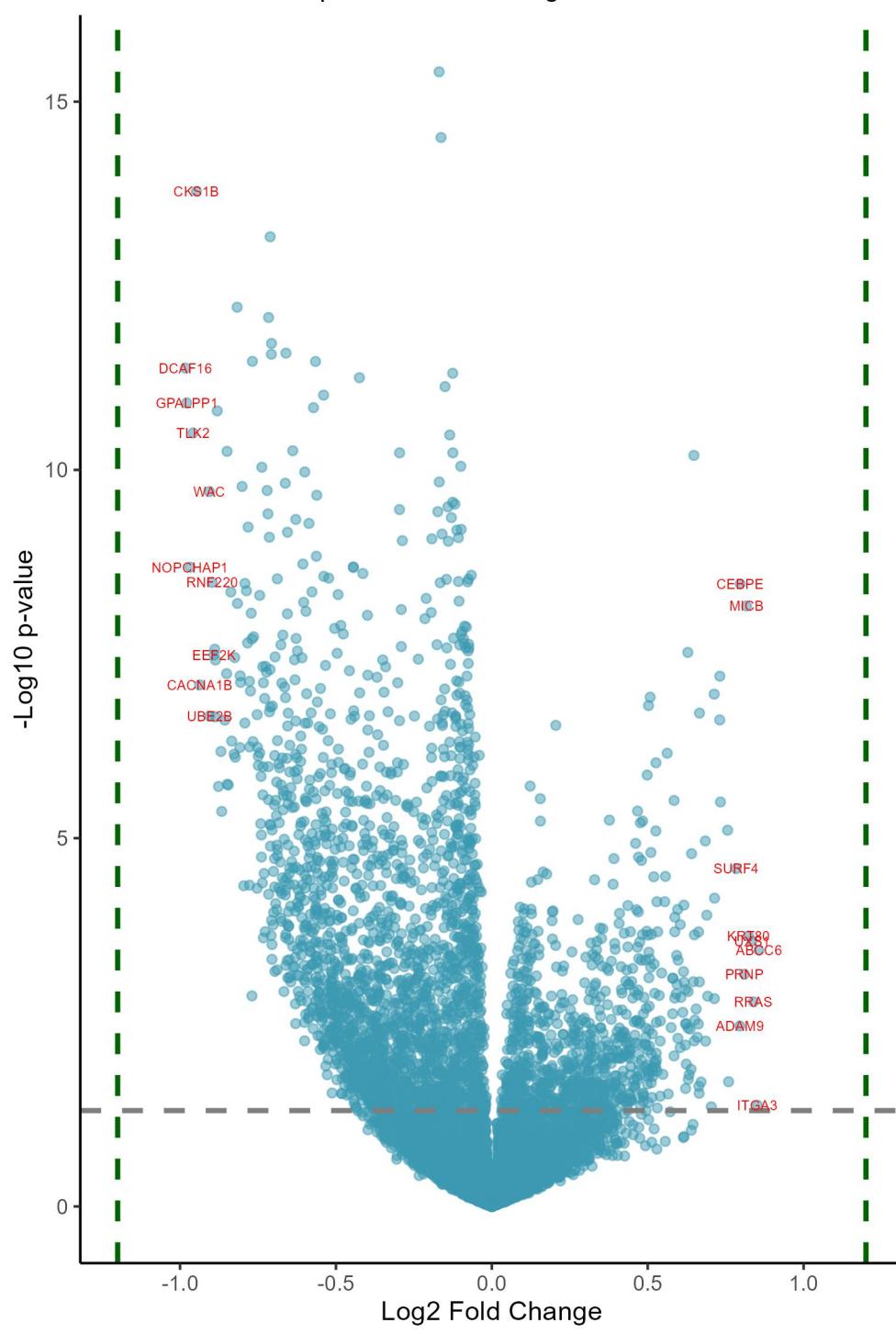
The text in the bars: incidence of CREBBP | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



Positive cooccurrence

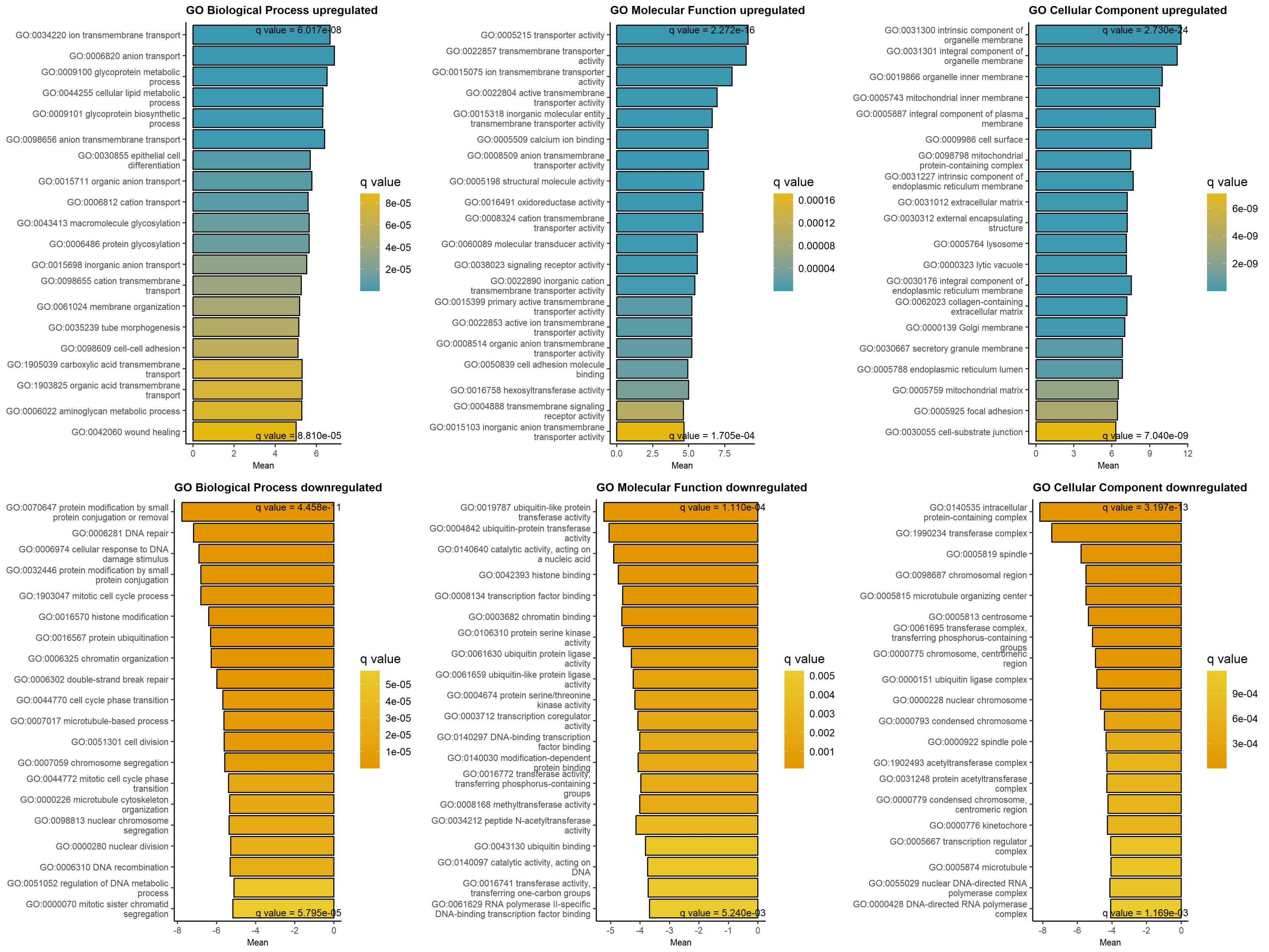




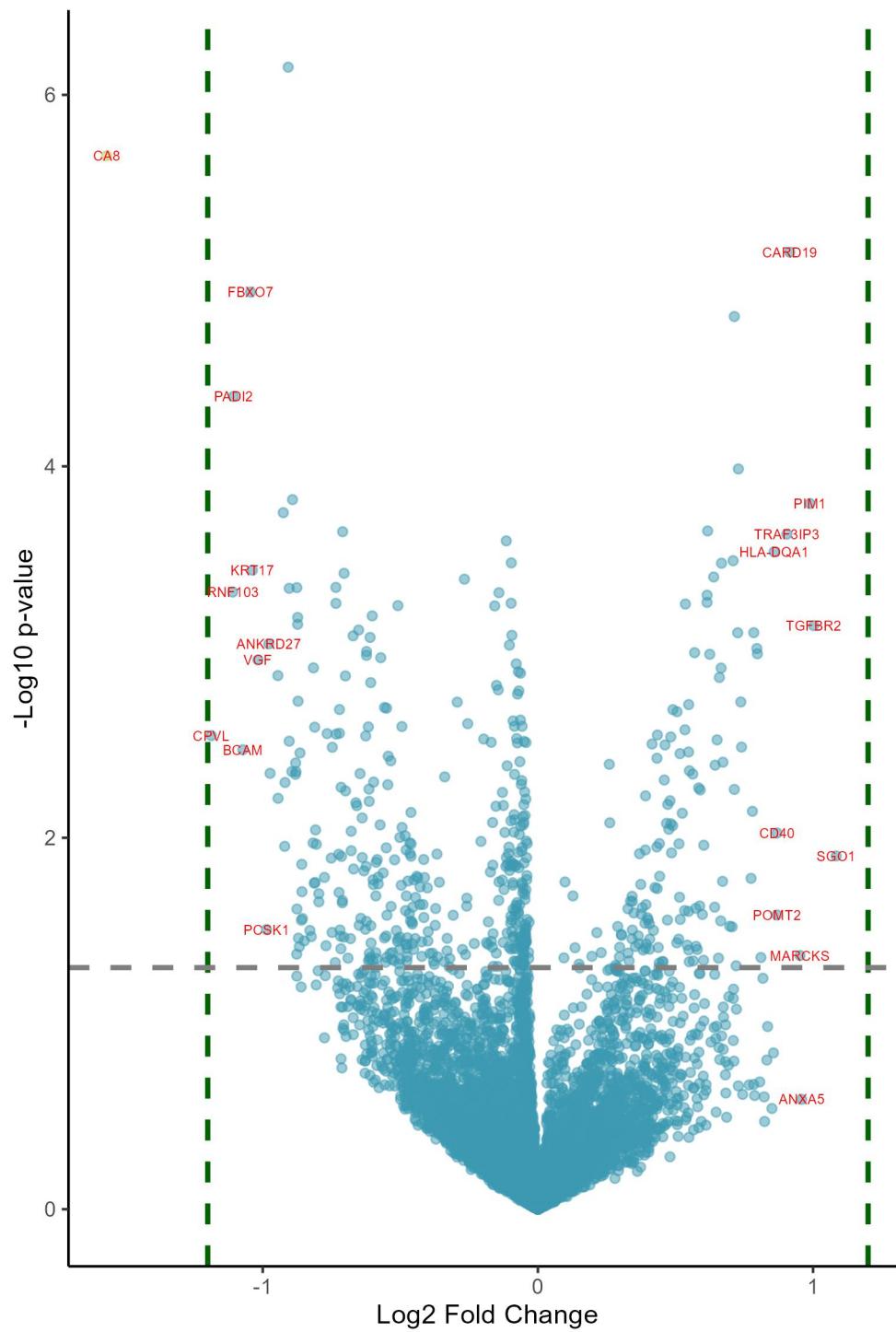
Downregulated at low/absent CREBBP Upregulated at low/absent CREBBP

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.98	2.66e-09	DCAF16	DDB1 and CUL4 associated factor 16	0.86	3.04e-03	ABCC6	ATP binding cassette subfamily C me
-0.98	5.71e-09	GPALPP1	GPALPP motifs containing 1	0.85	1.21e-01	ITGA3	integrin subunit alpha 3
-0.97	2.95e-07	NOPCHAP1	NOP protein chaperone 1	0.84	1.05e-02	RRAS	RAS related
-0.96	1.25e-08	TLK2	tousled like kinase 2	0.83	2.43e-03	UXS1	UDP-glucuronate decarboxylase 1
-0.95	3.44e-11	CKS1B	CDC28 protein kinase regulatory sub	0.82	7.08e-07	KRT80	keratin 80
-0.94	4.63e-06	CACNA1B	calcium voltage-gated channel subun	0.82	1.05e-02	MICB	MHC class I polypeptide-related seq
-0.91	4.70e-08	WAC	WW domain containing adaptor with c	0.81	5.46e-03	PRNP	prion protein
-0.9	9.78e-06	UBE2B	ubiquitin conjugating enzyme E2 B	0.8	4.06e-07	CEBPE	CCAAT enhancer binding protein epsi
-0.9	4.00e-07	RNF220	ring finger protein 220	0.8	1.90e-02	ADAM9	ADAM metallopeptidase domain 9
-0.89	2.28e-06	EEF2K	eukaryotic elongation factor 2 kina	0.78	3.96e-04	SURF4	surfeit 4
-0.89	2.00e-06	ATXN7L3B	ataxin 7 like 3B	0.76	7.12e-02	CAV1	caveolin 1
-0.89	9.85e-06	MBIP	MAP3K12 binding inhibitory protein	0.76	1.55e-04	IGFBP3	insulin like growth factor binding
-0.89	2.53e-06	PARG	poly(ADP-ribose) glycohydrolase	0.73	7.71e-05	MOSPD2	motile sperm domain containing 2
-0.88	6.60e-09	CEP104	centrosomal protein 104	0.73	3.77e-06	SERPINE1	serpin family E member 1
-0.88	5.38e-05	IGDCC4	immunoglobulin superfamily DCC subc	0.73	1.06e-05	FOSL1	FOS like 1, AP-1 transcription fact
-0.87	2.34e-05	PABIR1	PP2A Aalpha (PPP2R1A) and B55A (PPP	0.71	8.34e-04	RAB11FIP5	RAB11 family interacting protein 5
-0.87	9.75e-05	TCF3	transcription factor 3	0.71	9.80e-03	IGFBP7	insulin like growth factor binding
-0.86	1.07e-05	FTSJ1	FtsJ RNA 2'-O-methyltransferase 1	0.71	5.83e-06	MUL1	mitochondrial E3 ubiquitin protein
-0.85	3.59e-06	HAUS1	HAUS augmin like complex subunit 1	0.7	1.25e-01	CTSZ	cathepsin Z
-0.85	1.89e-08	TRPC3	transient receptor potential cation	0.69	9.22e-03	LACTB	lactamase beta
-0.85	5.10e-05	RNF138	ring finger protein 138	0.69	1.27e-03	MGST3	microsomal glutathione S-transferas
-0.85	5.22e-05	FBXO30	F-box protein 30	0.69	2.71e-02	TDRD5	tudor domain containing 5
-0.84	5.00e-07	RM12	RecQ mediated genome instability 2	0.68	2.02e-04	SLC12A4	solute carrier family 12 member 4
-0.83	1.83e-05	FERMT3	FERM domain containing kindlin 3	0.67	7.17e-02	PKP3	plakophilin 3
-0.83	2.50e-05	RAD51AP1	RAD51 associated protein 1	0.67	9.32e-06	MFSD10	major facilitator superfamily domai
-0.82	2.44e-06	SSNA1	SS nuclear autoantigen 1	0.67	6.55e-03	SLC35B2	solute carrier family 35 member B2
-0.82	2.65e-05	ELP2	elongator acetyltransferase complex	0.67	9.25e-02	SQOR	sulfide quinone oxidoreductase
-0.82	8.61e-10	GTF2A1	general transcription factor IIA su	0.66	7.92e-02	STOM	stomatin
-0.82	6.64e-07	ZSWIM8	zinc finger SWIM-type containing 8	0.66	1.94e-03	TCIRG1	T cell immune regulator 1, ATPase H

GAGE analysis on upregulated and downregulated proteins at low/absent CREBBP protein, DB2

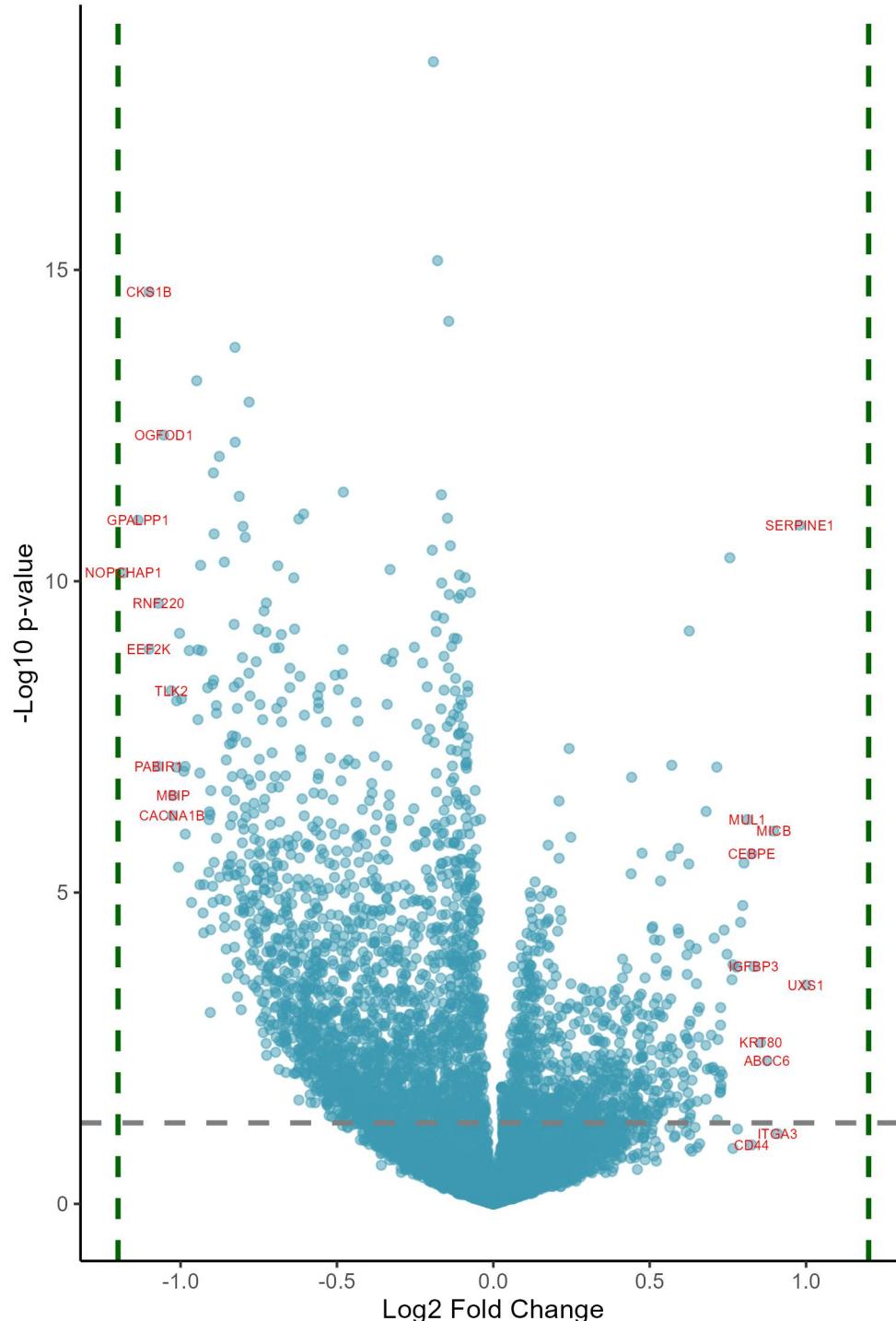


p-value < 0.05 & logFC > 1.2



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

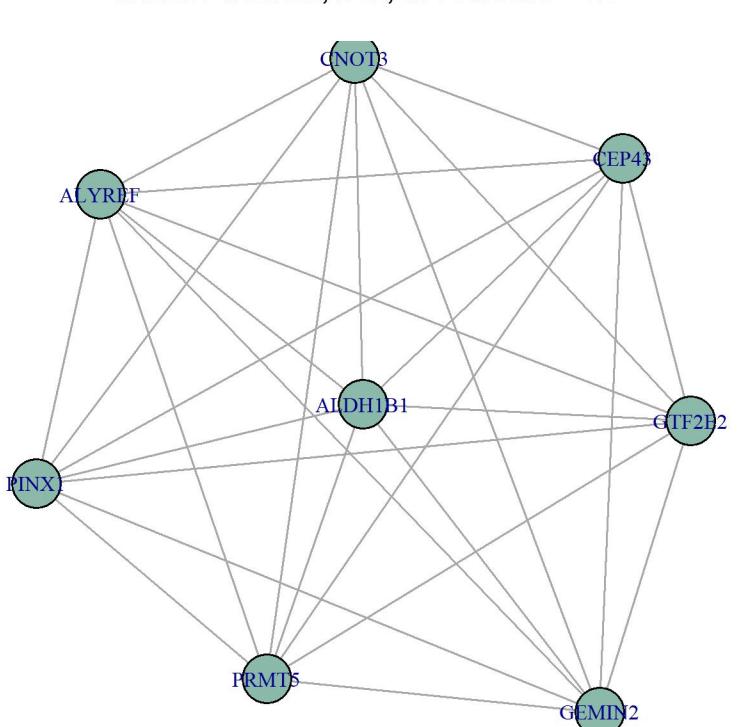
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.57	5.93e-03	CA8	carbonic anhydrase 8	1.08	5.04e-01	SGO1	shugoshin 1
-1.19	2.56e-01	CPVL	carboxypeptidase vitellogenin like	1	1.55e-01	TGFBR2	transforming growth factor beta rec
-1.11	1.35e-01	RNF103	ring finger protein 103	0.99	1.33e-01	PIM1	Pim-1 proto-oncogene, serine/threon
-1.11	5.02e-02	PADI2	peptidyl arginine deiminase 2	0.96	9.62e-01	ANXA5	annexin A5
-1.07	2.65e-01	BCAM	basal cell adhesion molecule (Luthe	0.95	7.79e-01	MARCKS	myristoylated alanine rich protein
-1.04	1.93e-02	FBXO7	F-box protein 7	0.91	1.47e-02	CARD19	caspase recruitment domain family m
-1.04	1.35e-01	KRT17	keratin 17	0.9	1.35e-01	TRAF3IP3	TRAF3 interacting protein 3
-1.02	1.68e-01	VGF	VGF nerve growth factor inducible	0.87	4.46e-01	CD40	CD40 molecule
-0.99	7.36e-01	PCSK1	proprotein convertase subtilisin/ke	0.87	6.83e-01	POMT2	protein O-mannosyltransferase 2
-0.98	1.63e-01	ANKRD27	ankyrin repeat domain 27	0.86	1.35e-01	HLA-DQA1	major histocompatibility complex, c
-0.97	3.02e-01	FBXL20	F-box and leucine rich repeat prote	0.86	9.62e-01	KRT7	keratin 7
-0.95	1.81e-01	DNAH5	dynein axonemal heavy chain 5	0.85	9.62e-01	HERC1	HECT and RLD domain containing E3 u
-0.94	3.59e-01	AHRR	aryl-hydrocarbon receptor repressor	0.83	9.62e-01	HLA-DPA1	major histocompatibility complex, c
-0.93	1.35e-01	ASPA	aspartoacylase	0.83	9.62e-01	CAMK2D	calcium/calmodulin dependent protei
-0.92	4.86e-01	CTBP2	C-terminal binding protein 2	0.82	9.62e-01	SEPTIN14	septin 14
-0.92	3.22e-01	MVB12A	multivesicular body subunit 12A	0.82	9.62e-01	UCHL1	ubiquitin C-terminal hydrolase L1
-0.91	2.97e-03	PYCARD	PYD and CARD domain containing	0.82	8.46e-01	STAT2	signal transducer and activator of
-0.9	2.56e-01	MAP3K20	mitogen-activated protein kinase ki	0.81	7.82e-01	HLA-F	major histocompatibility complex, c
-0.9	1.35e-01	ITGA6	integrin subunit alpha 6	0.81	9.62e-01	IRF4	interferon regulatory factor 4
-0.89	3.02e-01	GAN	gigaxonin	0.8	1.64e-01	IL4I1	interleukin 4 induced 1
-0.89	1.33e-01	DDAH2	dimethylarginine dimethylaminohydro	0.8	1.64e-01	GNG12	G protein subunit gamma 12
-0.88	3.02e-01	KIF14	kinesin family member 14	0.79	9.62e-01	CTSZ	cathepsin Z
-0.88	2.88e-01	SPI1	Spi-1 proto-oncogene	0.78	1.55e-01	PKP3	plakophilin 3
-0.88	3.02e-01	PATZ1	POZ/BTB and AT hook containing zinc	0.78	9.62e-01	TUT7	terminal uridylyl transferase 7
-0.88	7.69e-01	SIRPA	signal regulatory protein alpha	0.78	3.94e-01	GLDC	glycine decarboxylase
-0.88	8.41e-01	LAMA2	laminin subunit alpha 2	0.77	5.70e-01	TARBP1	TAR (HIV-1) RNA binding protein 1
-0.88	1.35e-01	PPP2CB	protein phosphatase 2 catalytic sub	0.77	9.62e-01	CD48	CD48 molecule
-0.88	6.62e-01	CLASRP	CLK4 associating serine/arginine ri	0.74	9.62e-01	SERPINB9	serpin family B member 9
-0.87	1.55e-01	VMA21	vacuolar ATPase assembly factor VMA	0.74	2.59e-01	MALT1	MALT1 paracaspase

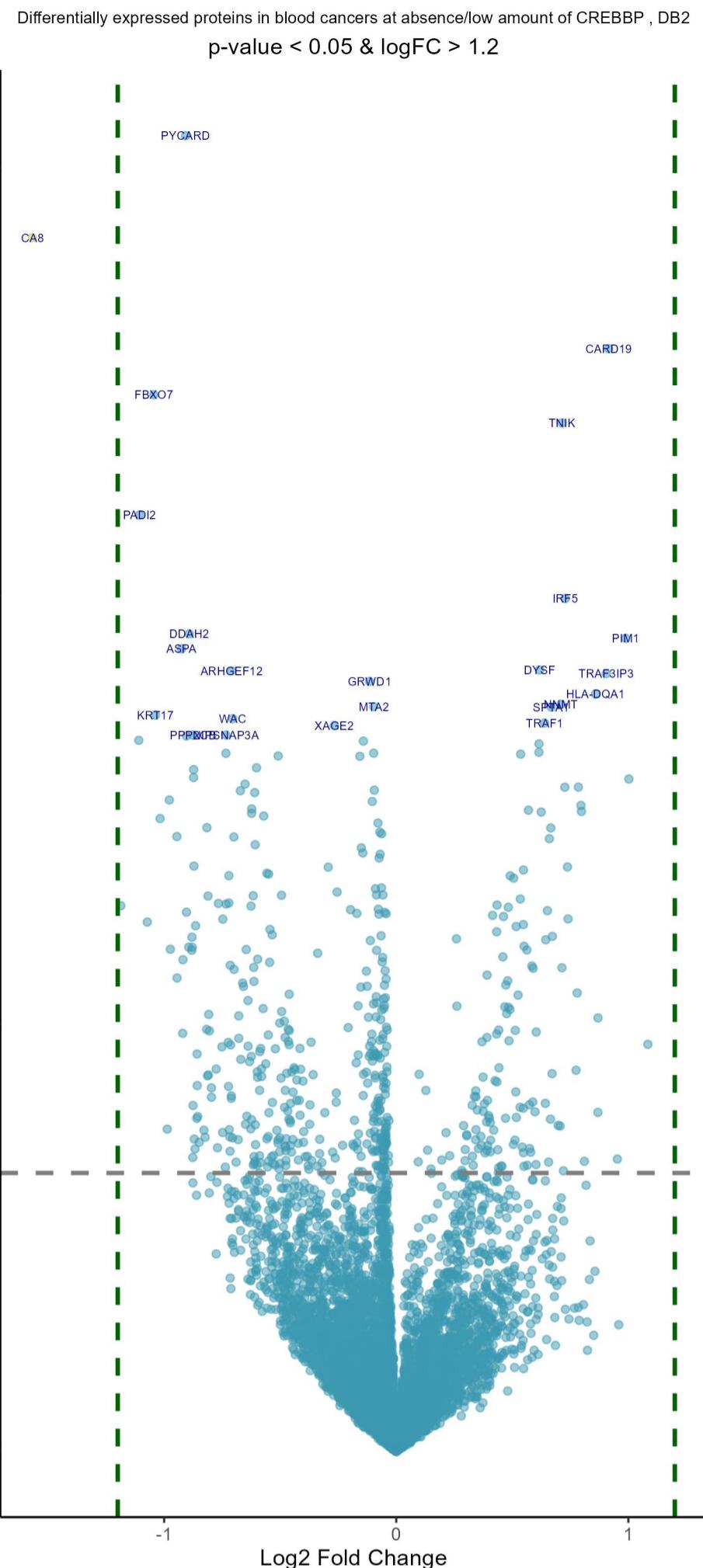
Differentially expressed proteins in solid cancers at absence/low amount of CREBBP , DB2
p-value < 0.05 & logFC > 1.2

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

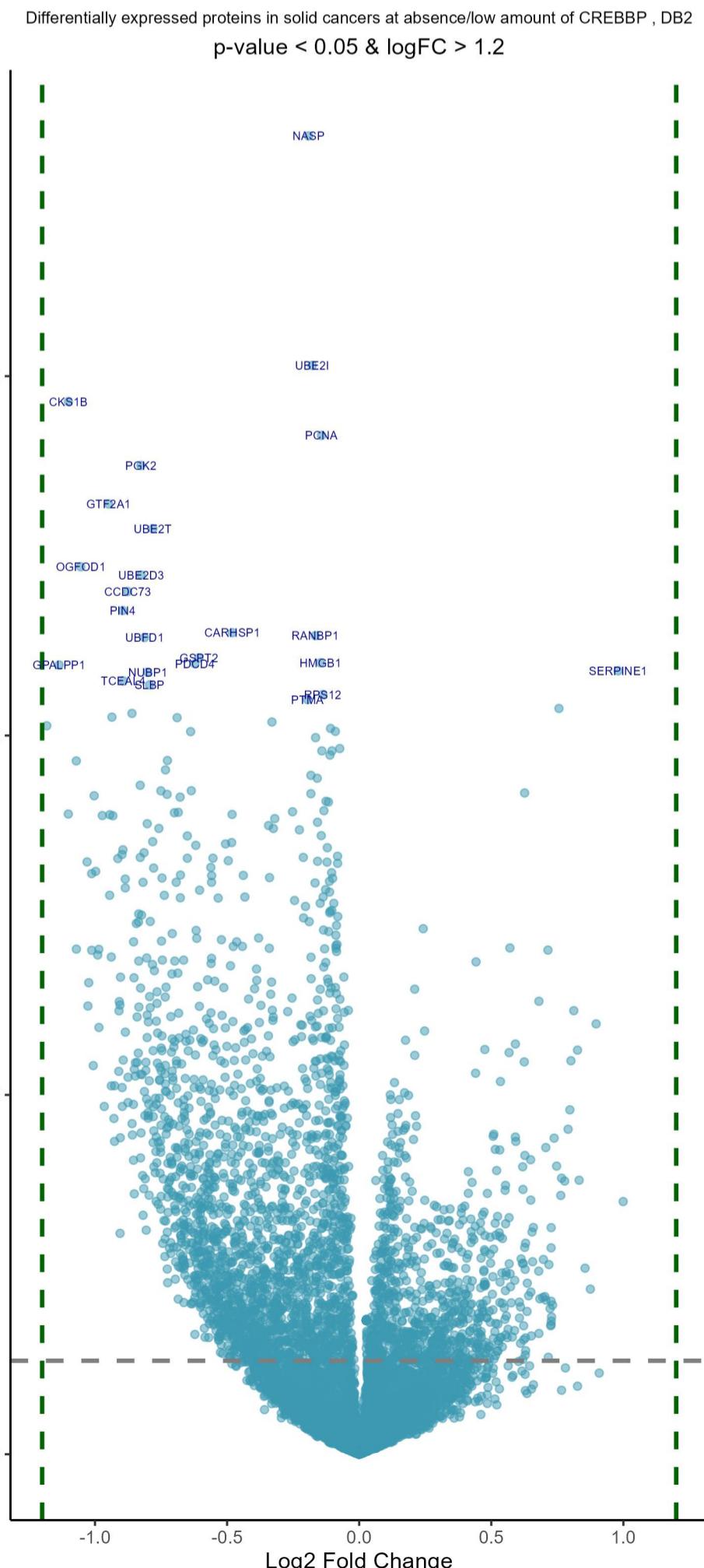
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.18	1.97e-08	NOPCHAP1	NOP protein chaperone 1	1	2.94e-03	UXS1	UDP-glucuronate decarboxylase 1
-1.14	4.59e-09	GPALPP1	GPALPP motifs containing 1	0.98	5.24e-09	SERPINE1	serpin family E member 1
-1.1	1.73e-07	EEF2K	eukaryotic elongation factor 2 kina	0.91	1.81e-01	ITGA3	integrin subunit alpha 3
-1.1	4.72e-12	CKS1B	CDC28 protein kinase regulatory sub	0.9	3.52e-05	MICB	MHC class I polypeptide-related seq
-1.07	4.60e-08	RNF220	ring finger protein 220	0.87	2.53e-02	ABCC6	ATP binding cassette subfamily C me
-1.07	5.05e-06	PABIR1	PP2A Aalpha (PPP2R1A) and B55A (PPP	0.85	1.51e-02	KRT80	keratin 80
-1.05	4.18e-10	OGFOD1	2-oxoglutarate and iron dependent o	0.83	1.68e-03	IGFBP3	insulin like growth factor binding
-1.03	5.36e-07	TLK2	tousled like kinase 2	0.83	2.43e-01	CD44	CD44 molecule (Indian blood group)
-1.03	2.27e-05	CACNA1B	calcium voltage-gated channel subun	0.83	6.74e-05	CEBPE	CCAAT enhancer binding protein epsi
-1.02	1.22e-05	MBIP	MAP3K12 binding inhibitory protein	0.81	2.54e-05	MUL1	mitochondrial E3 ubiquitin protein
-1.01	7.26e-07	DCAF16	DDB1 and CUL4 associated factor 16	0.8	8.66e-05	QPCTL	glutaminyl-peptide cyclotransferase
-1.01	5.15e-06	ATXN7L3B	ataxin 7 like 3B	0.8	2.93e-04	FOSL1	FOS like 1, AP-1 transcription fact
-1.01	9.68e-05	ASRGL1	asparaginase and isoaspartyl peptid	0.79	4.76e-04	MOSPD2	motile sperm domain containing 2
-1	1.13e-07	UBAC1	UBA domain containing 1	0.78	1.62e-01	CAV1	caveolin 1
-1	6.90e-07	ERCC6L	ERCC excision repair 6 like, spindl	0.78	1.71e-03	TCIRG1	T cell immune regulator 1, ATPase H
-0.99	5.90e-06	HAUS7	HAUS augmin like complex subunit 7	0.77	1.60e-03	AKAP6	A-kinase anchoring protein 6
-0.99	5.06e-06	HAUS1	HAUS augmin like complex subunit 1	0.77	2.65e-01	CAVIN1	caveolae associated protein 1
-0.99	3.86e-05	FBXO30	F-box protein 30	0.76	2.50e-03	HLA-E	major histocompatibility complex, c
-0.97	1.73e-07	UBAP1	ubiquitin associated protein 1	0.76	1.35e-08	MICA	MHC class I polypeptide-related seq
-0.96	2.68e-04	IGDCC4	immunoglobulin superfamily DCC subc	0.75	1.20e-03	SLC12A4	solute carrier family 12 member 4
-0.95	7.18e-11	GTF2A1	general transcription factor IIA su	0.74	5.85e-04	SMPD1	sphingomyelin phosphodiesterase 1
-0.94	1.23e-06	RMI2	RecQ mediated genome instability 2	0.73	3.75e-02	IGFBP7	insulin like growth factor binding
-0.94	1.73e-07	CEP104	centrosomal protein 104	0.73	5.05e-02	RRAS	RAS related
-0.94	6.26e-06	SMYD5	SMYD family member 5	0.73	5.50e-02	PRNP	prion protein
-0.94	1.62e-04	CRMP1	collapsin response mediator protein	0.73	5.62e-03	SLC35B2	solute carrier family 35 member B2
-0.94	1.63e-08	TRPC3	transient receptor potential cation	0.73	9.21e-03	SURF4	surfeit 4
-0.93	1.73e-07	PPP4R3B	protein phosphatase 4 regulatory su	0.73	5.94e-02	CAVIN3	caveolae associated protein 3
-0.93	3.60e-04	PCBP4	poly(rC) binding protein 4	0.73	3.44e-02	APOL2	apolipoprotein L2
-0.93	6.43e-04	SMARCAD1	SWI/SNF-related, matrix-associated	0.72	6.10e-02	ADAM9	ADAM metallopeptidase domain 9

CREBBP network, DB2, all Pearson r > 0.3



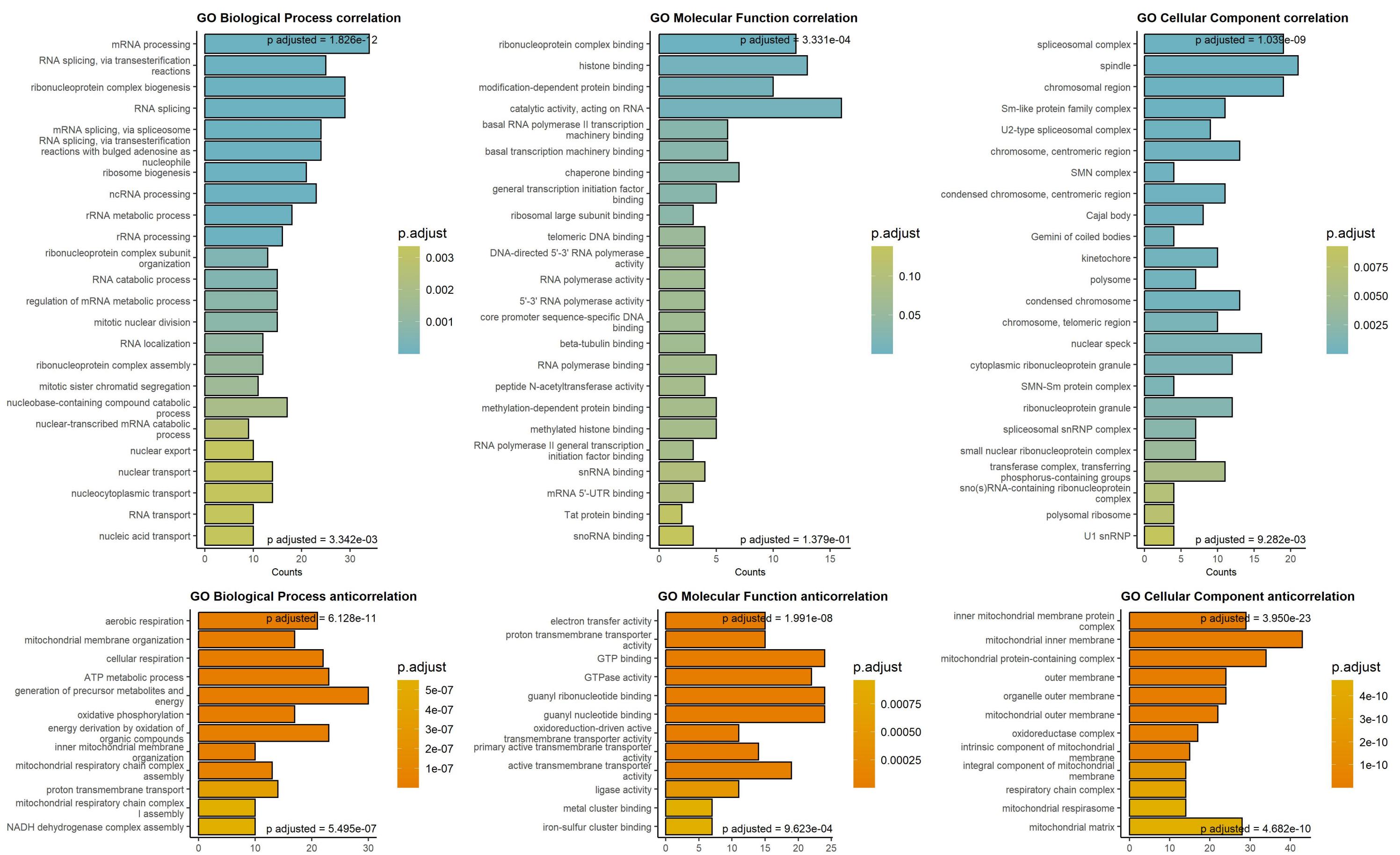


Sorted by p values!							
Downregulated in blood cancers at low/absent CREBBP				Upregulated in blood cancers at low/absent CREBBP			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.91	2.97e-03	PYCARD	PYD and CARD domain containing	0.91	1.47e-02	CARD19	caspase recruitment domain family member 19
-1.57	5.93e-03	CA8	carbonic anhydrase 8	0.71	2.18e-02	TNIK	TRAF2 and NCK interacting kinase
-1.04	1.93e-02	FBXO7	F-box protein 7	0.73	1.08e-01	IRF5	interferon regulatory factor 5
-1.11	5.02e-02	PADI2	peptidyl arginine deiminase 2	0.99	1.33e-01	PIM1	Pim-1 proto-oncogene, serine/threonine kinase 1
-0.89	1.33e-01	DDAH2	dimethylarginine dimethylaminohydroxylase 2	0.62	1.35e-01	DYSF	dysferlin
-0.93	1.35e-01	ASPA	aspartoacylase	0.9	1.35e-01	TRAF3IP3	TRAF3 interacting protein 3
-0.71	1.35e-01	ARHGEF12	Rho guanine nucleotide exchange factor	0.86	1.35e-01	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1
-0.11	1.35e-01	GRWD1	glutamate rich WD repeat containing	0.71	1.35e-01	NNMT	nicotinamide N-methyltransferase
-0.1	1.35e-01	MTA2	metastasis associated 1 family member	0.67	1.35e-01	SPTA1	spectrin alpha, erythrocytic 1
-1.04	1.35e-01	KRT17	keratin 17	0.64	1.35e-01	TRAF1	TNF receptor associated factor 1
-0.7	1.35e-01	WAC	WW domain containing adaptor with caspase recruitment domain	0.61	1.35e-01	TBC1D24	tubulin folding cofactor E like
-0.27	1.35e-01	XAGE2	X antigen family member 2	0.61	1.35e-01	ARHGAP12	Rho GTPase activating protein 12
-0.73	1.35e-01	NIPSNAP3A	nipsnap homolog 3A	0.54	1.35e-01	KIAA1217	KIAA1217
-0.88	1.35e-01	PPP2CB	protein phosphatase 2 catalytic subunit B	1	1.55e-01	TGFBR2	transforming growth factor beta receptor type 2
-0.9	1.35e-01	ITGA6	integrin subunit alpha 6	0.78	1.55e-01	PKP3	plakophilin 3
-1.11	1.35e-01	RNF103	ring finger protein 103	0.73	1.55e-01	ACTL6B	actin like 6B
-0.14	1.35e-01	PPFIA2	PTPRF interacting protein alpha 2	0.8	1.64e-01	GNG12	G protein subunit gamma 12
-0.1	1.35e-01	UBE2M	ubiquitin conjugating enzyme E2 M	0.57	1.64e-01	BTN2A1	butyrophilin subfamily 2 member A1
-0.73	1.35e-01	MTF2	metal response element binding protein 2	0.8	1.64e-01	IL4I1	interleukin 4 induced 1
-0.51	1.35e-01	DPPA2	developmental pluripotency associated 2	0.62	1.64e-01	EBI3	Epstein-Barr virus induced 3
-0.16	1.35e-01	RHOQ	ras homolog family member Q	0.67	1.76e-01	UBIAD1	UbiA prenyltransferase domain containing 1
-0.6	1.47e-01	RNF5	ring finger protein 5	0.66	1.82e-01	BIN1	bridging integrator 1
-0.87	1.47e-01	SUPT7L	SPT7 like, STAGA complex subunit gamma	0.74	2.19e-01	SLC25A20	solute carrier family 25 member 20
-0.87	1.55e-01	VMA21	vacuolar ATPase assembly factor VMA21	0.55	2.23e-01	DENND4A	DENN domain containing 4A
-0.65	1.55e-01	TMEM209	transmembrane protein 209	0.49	2.25e-01	PTPRG	protein tyrosine phosphatase receptor type G
-0.09	1.55e-01	C11orf96	chromosome 11 open reading frame 96	0.51	2.28e-01	AGFG2	ArfGAP with FG repeats 2
-0.67	1.55e-01	DBN1	drebrin 1	0.53	2.55e-01	ZC2HC1A	zinc finger C2HC-type containing 1A
-0.61	1.55e-01	TFCP2	transcription factor CP2	0.43	2.56e-01	NUBPL	NUBP iron-sulfur cluster assembly factor
-0.98	1.63e-01	ANKRD27	ankyrin repeat domain 27	0.48	2.56e-01	HABP4	hyaluronan binding protein 4
-0.1	1.63e-01	UBA2	ubiquitin like modifier activating enzyme 2	0.65	2.56e-01	RELB	RELB proto-oncogene, NF-kB subunit B
-0.62	1.64e-01	SERPINH1	serpin family H member 1	0.41	2.56e-01	AKAP10	A-kinase anchoring protein 10
-0.62	1.64e-01	XPO4	exportin 4	0.46	2.57e-01	RAB11FIP5	RAB11 family interacting protein 5
-0.57	1.66e-01	DCAF16	DDB1 and CUL4 associated factor 16	0.74	2.59e-01	MALT1	MALT1 paracaspase
-1.02	1.68e-01	VGF	VGFR nerve growth factor inducible	0.55	2.70e-01	ACP6	acid phosphatase 6, lysophosphatidic acid phosphatase
-0.08	1.73e-01	H3-5	H3.5 histone	0.52	2.70e-01	CDCP1	CUB domain containing protein 1
-0.82	1.76e-01	NADSYN1	NAD synthetase 1	0.43	2.81e-01	SP140	SP140 nuclear body protein
-0.07	1.81e-01	PA2G4	proliferation-associated 2G4	0.67	2.87e-01	KIAA0319L	KIAA0319 like
-0.06	1.81e-01	ILF3	interleukin enhancer binding factor 3	0.26	2.90e-01	MTX2	metaxin 2
-0.95	1.81e-01	DNAH5	dynamin exon 16 heavy chain 5	0.61	2.90e-01	TUBR2	tubulin alpha 2

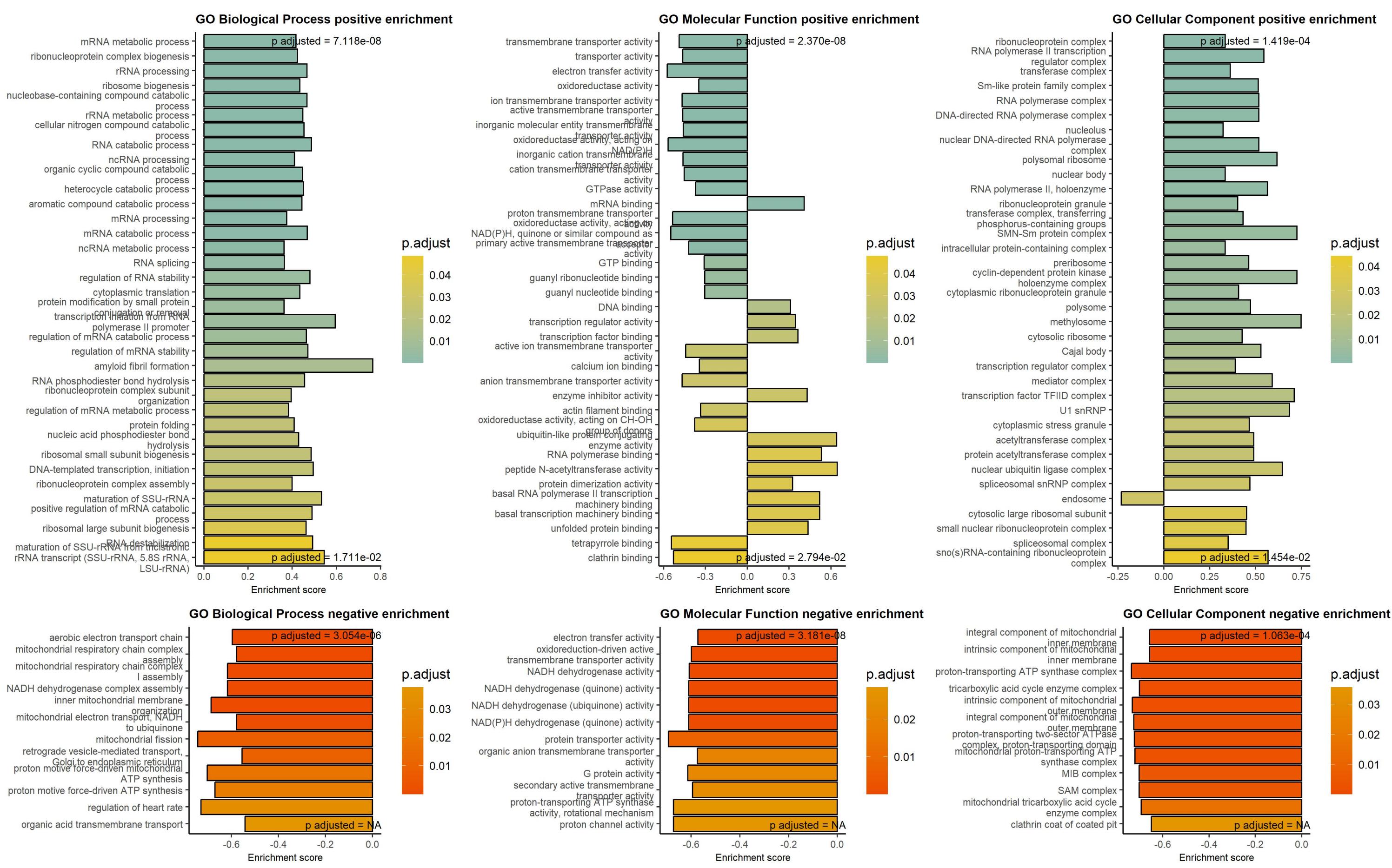


Sorted by p values!							
Downregulated in solid cancers at low/absent CREBBP				Upregulated in solid cancers at low/absent CREBBP			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.19	1.90e-15	NASP	nuclear autoantigenic sperm protein	0.98	5.24e-09	SERPINE1	serpin family E member 1
-0.18	1.98e-12	UBE2I	ubiquitin conjugating enzyme E2 I	0.76	1.35e-08	MICA	MHC class I polypeptide-related seq
-1.1	4.72e-12	CKS1B	CDC28 protein kinase regulatory sub	0.63	1.10e-07	MCUR1	mitochondrial calcium uniporter reg
-0.14	1.12e-11	PCNA	proliferating cell nuclear antigen	0.24	3.02e-06	AP2S1	adaptor related protein complex 2 s
-0.83	2.44e-11	PGK2	phosphoglycerate kinase 2	0.57	4.99e-06	SGPP1	sphingosine-1-phosphate phosphatase
-0.95	7.18e-11	GTF2A1	general transcription factor II A su	0.71	5.15e-06	CMTM6	CKLF like MARVEL transmembrane dom
-0.78	1.39e-10	UBE2T	ubiquitin conjugating enzyme E2 T	0.44	6.98e-06	TMPPE	transmembrane protein with metallopr
-1.05	4.18e-10	OGFOD1	2-oxoglutarate and iron dependent o	0.21	1.43e-05	ATP6AP1	ATPase H+ transporting accessory pr
-0.83	4.89e-10	UBE2D3	ubiquitin conjugating enzyme E2 D3	0.68	1.99e-05	SLC39A7	solute carrier family 39 member 7
-0.88	7.53e-10	CCDC73	coiled-coil domain containing 73	0.81	2.54e-05	MUL1	mitochondrial E3 ubiquitin protein
-0.9	1.27e-09	PIN4	peptidylprolyl cis/trans isomerase,	0.9	3.52e-05	MICB	MHC class I polypeptide-related seq
-0.48	2.38e-09	CARHSP1	calcium regulated heat stable prote	0.25	4.17e-05	ACADVL	acyl-CoA dehydrogenase very long ch
-0.17	2.42e-09	RANBP1	RAN binding protein 1	0.18	5.21e-05	RAB15	RAB15, member RAS oncogene family
-0.81	2.42e-09	UBFD1	ubiquitin family domain containing	0.59	5.71e-05	PLAUR	plasminogen activator, urokinase re
-0.61	4.35e-09	GSPT2	G1 to S phase transition 2	0.48	6.64e-05	STBD1	starch binding domain 1
-0.15	4.59e-09	HMGB1	high mobility group box 1	0.83	6.74e-05	CEBPE	CCAAT enhancer binding protein epsi
-0.62	4.59e-09	PDCD4	programmed cell death 4	0.57	7.12e-05	CELSR1	cadherin EGF LAG seven-pass G-type
-1.14	4.59e-09	GPALPP1	GPALPP motifs containing 1	0.21	7.64e-05	LEMD2	LEM domain nuclear envelope protein
-0.8	5.24e-09	NUBP1	NUBP iron-sulfur cluster assembly f	0.8	8.66e-05	QPCTL	glutaminyl-peptide cyclotransferase
-0.89	6.62e-09	TCEAL4	transcription elongation factor A I	0.62	8.86e-05	SEC61A1	SEC61 translocon subunit alpha 1
-0.79	7.16e-09	SLBP	stem-loop binding protein	0.44	1.19e-04	OSMR	oncostatin M receptor
-0.14	9.37e-09	RPS12	ribosomal protein S12	0.53	1.45e-04	TINAGL1	tubulointerstitial nephritis antige
-0.2	1.06e-08	PTMA	prothymosin alpha	0.13	1.49e-04	UFL1	UFM1 specific ligase 1
-0.86	1.52e-08	POU2F1	POU class 2 homeobox 1	0.17	1.88e-04	RPN2	ribophorin II
-0.94	1.63e-08	TRPC3	transient receptor potential cation	0.12	2.01e-04	ATP5F1C	ATP synthase F1 subunit gamma
-0.69	1.63e-08	LUC7L	LUC7 like	0.19	2.02e-04	TMED4	transmembrane p24 trafficking prote
-0.33	1.81e-08	SGTA	small glutamine rich tetratricopept	0.12	2.27e-04	SAMM50	SAMM50 sorting and assembly machine
-1.18	1.97e-08	NOPCHAP1	NOP protein chaperone 1	0.15	2.27e-04	SPCS3	signal peptidase complex subunit 3
-0.11	2.08e-08	ZNF207	zinc finger protein 207	0.8	2.93e-04	FOSL1	FOS like 1, AP-1 transcription fact
-0.09	2.17e-08	PPIA	peptidylprolyl isomerase A	0.15	3.25e-04	SSR4	signal sequence receptor subunit 4
-0.64	2.17e-08	ADI1	acireductone dioxygenase 1	0.21	3.41e-04	EMC1	ER membrane protein complex subunit
-0.17	2.56e-08	NEDD8	NEDD8 ubiquitin like modifier	0.12	3.54e-04	NCLN	nicalin
-0.07	3.52e-08	HSP90AB1	heat shock protein 90 alpha family	0.12	4.27e-04	DDOST	dolichyl-diphosphooligosaccharide--
-0.1	3.60e-08	TPI1	triosephosphate isomerase 1	0.18	4.30e-04	RAB5B	RAB5B, member RAS oncogene family
-0.14	3.60e-08	PSME3	proteasome activator subunit 3	0.22	4.39e-04	CYB5R3	cytochrome b5 reductase 3
-0.11	4.01e-08	SRSF11	serine and arginine rich splicing f	0.17	4.61e-04	ZFPL1	zinc finger protein like 1
-0.73	4.60e-08	COPS7B	COP9 signalosome subunit 7B	0.79	4.76e-04	MOSPD2	motile sperm domain containing 2
-1.07	4.60e-08	RNF220	ring finger protein 220	0.17	4.88e-04	MTX1	metaxin 1
-0.70	5.22e-08	PPF1	phosphatase 5 homolog 1, C-terminal	0.15	5.22e-04	FAF2	Fractalkine-like family member 2

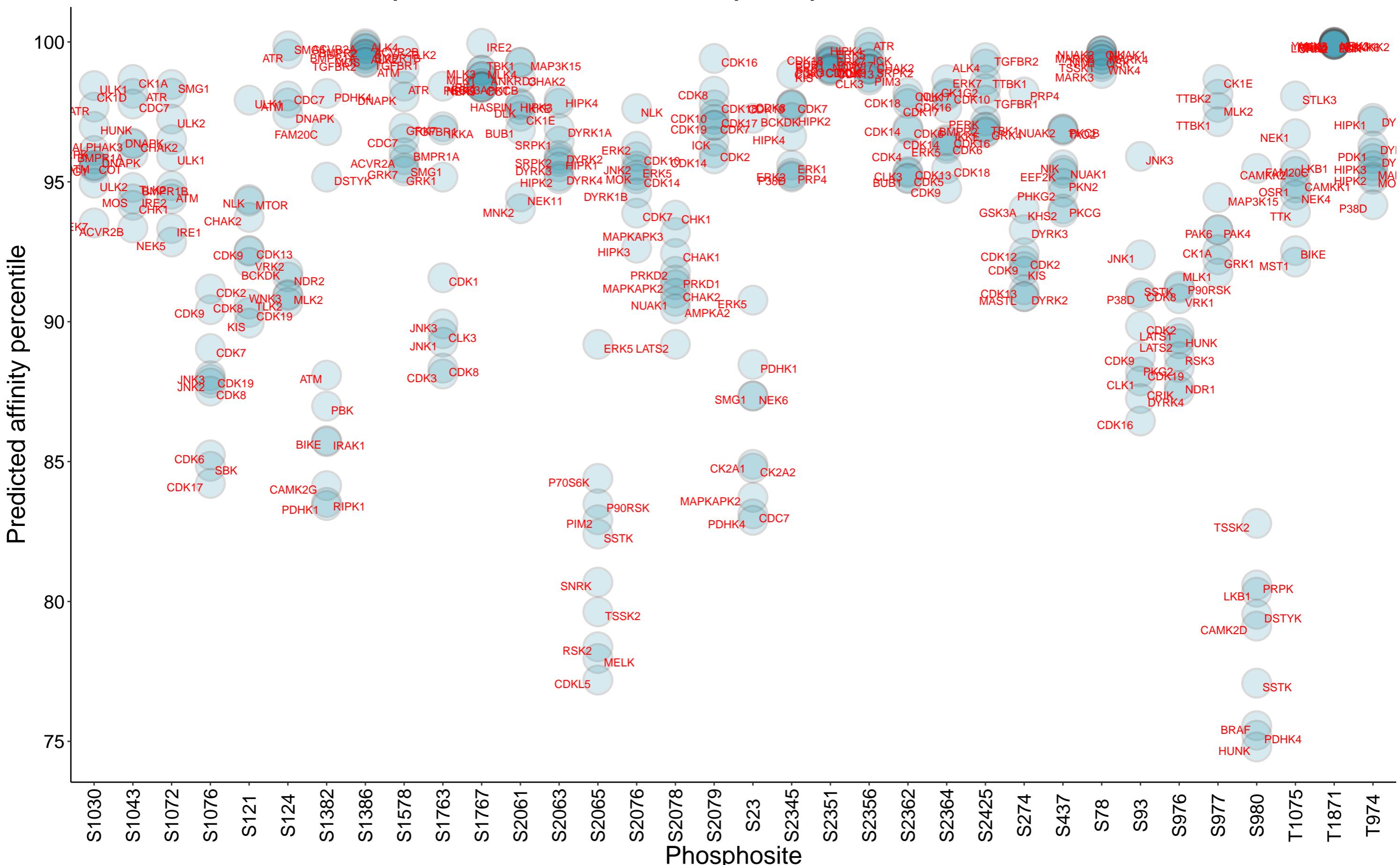
Top 250 correlation coefficients overrepresentation, CREBBP protein, DB2



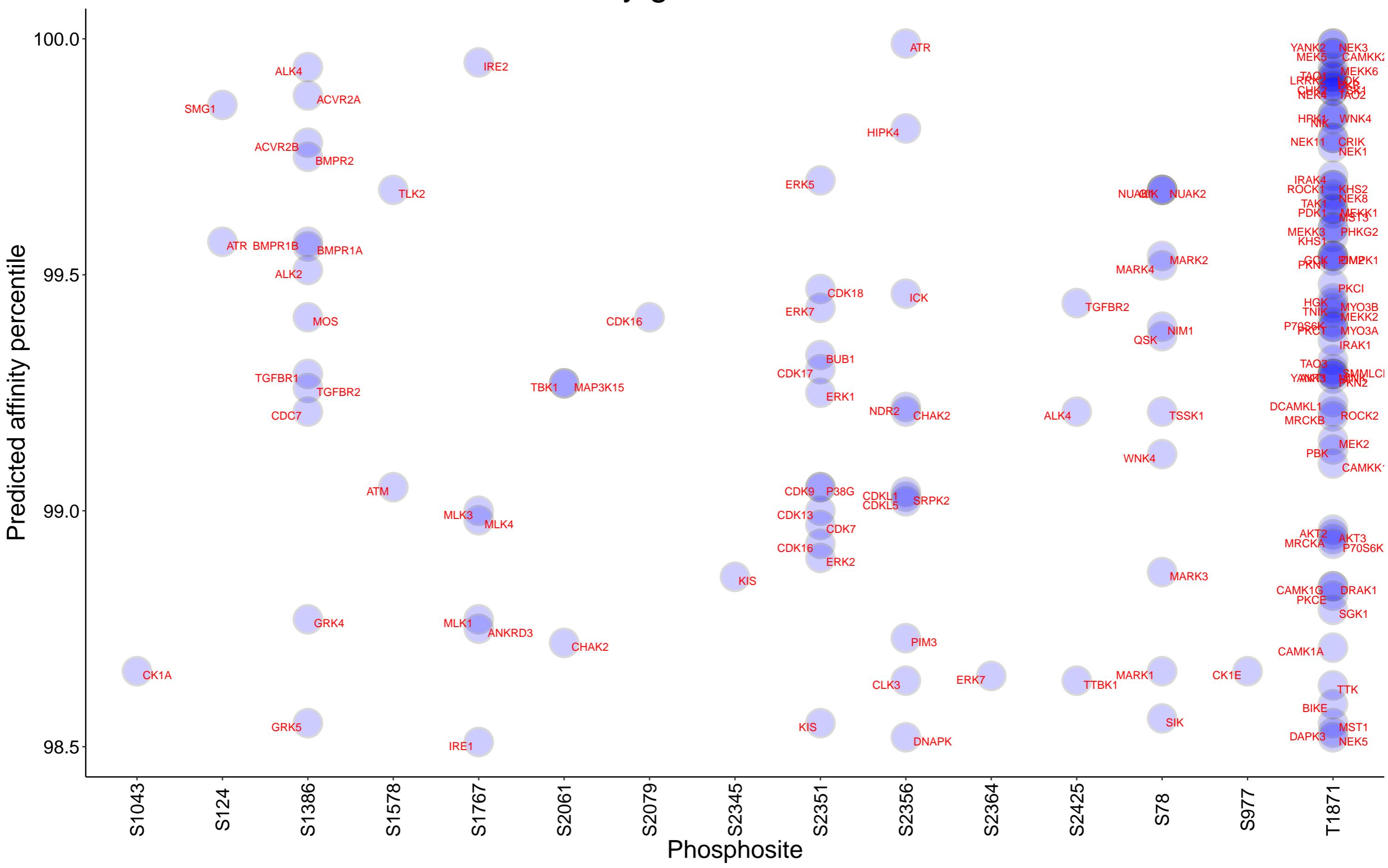
Gene Set Enrichment analysis on protein correlation coefficients, CREBBP protein, DB2



Top 10 kinases for each phosphosite in CREBBP



Kinases with affinity greater than 98.5% to CREBBP



No sufficient number of paired observations in DB2 for CREBBP