

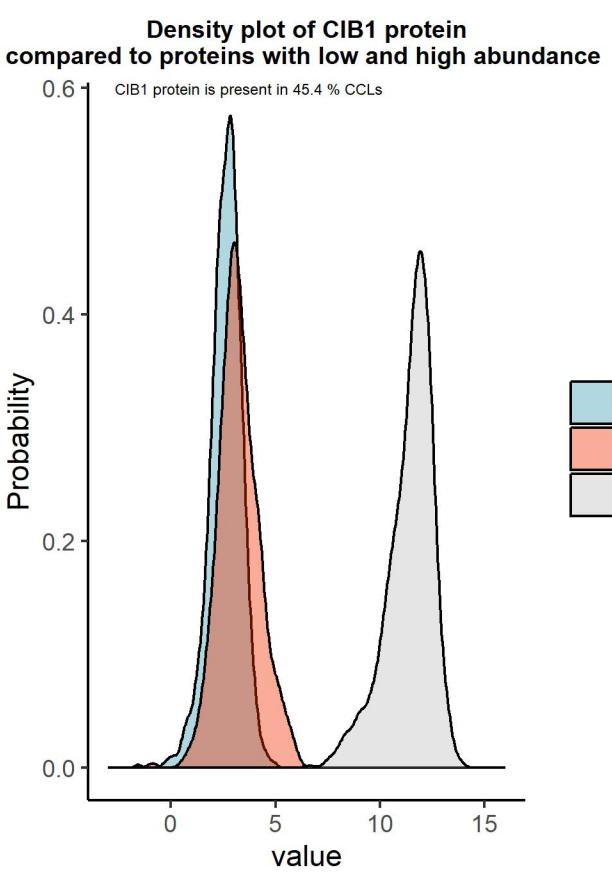
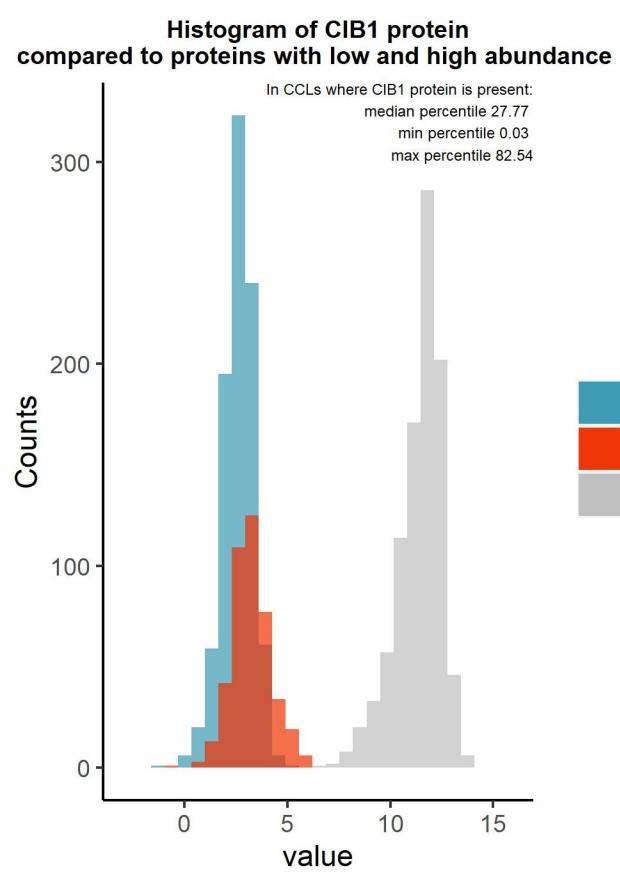
# CIB1

Protein name: CIB1 ; UNIPROT: Q99828 ; Gene name: calcium and integrin binding 1

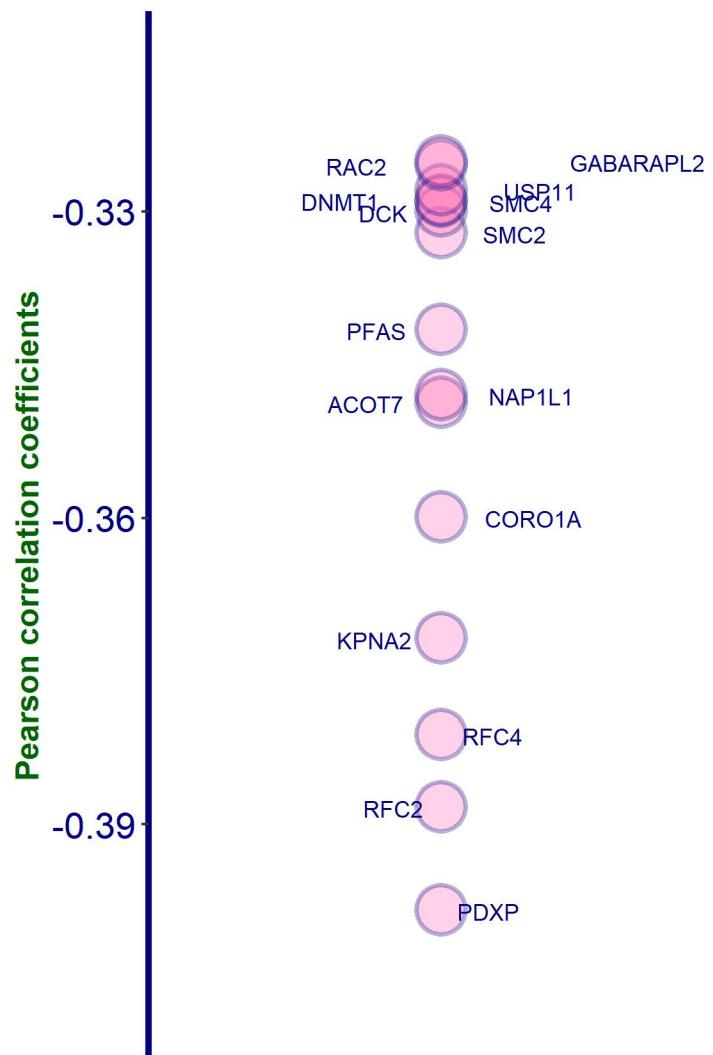
Ligandable: Yes ; Ligandable\_by\_Chem: NA ; Is\_enzyme: NA (<https://cansar.ai/>)

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

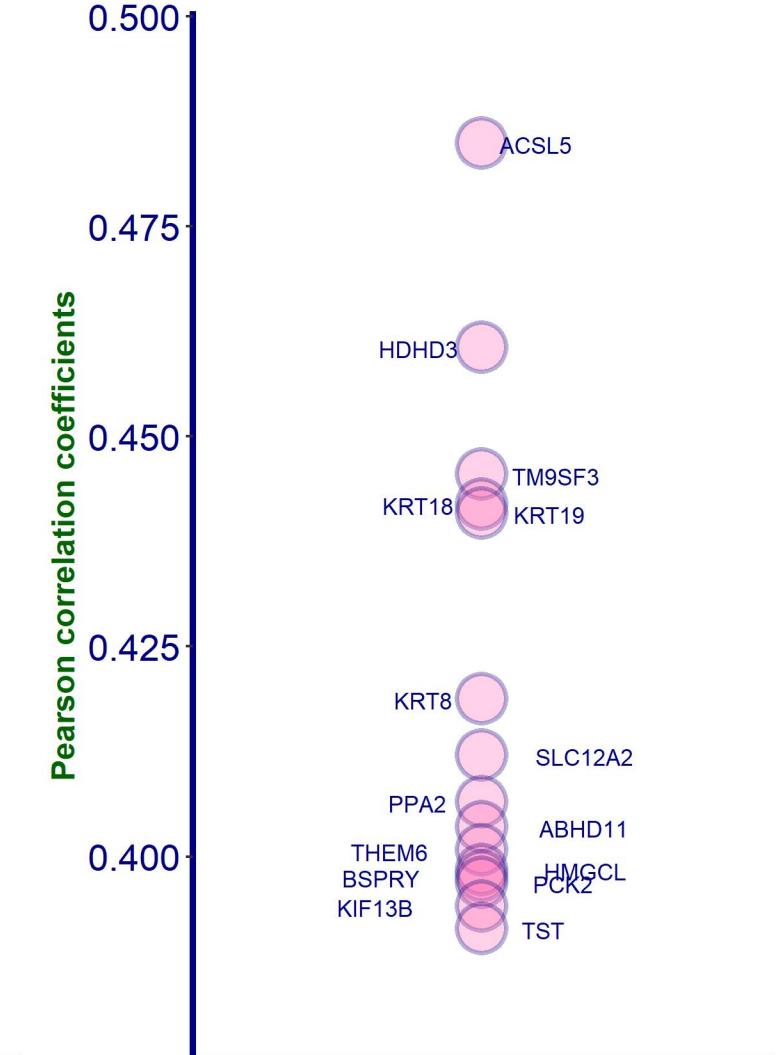
6692 proteins in 949 CCLs



### Top negative correlations of CIB1 protein, DB1

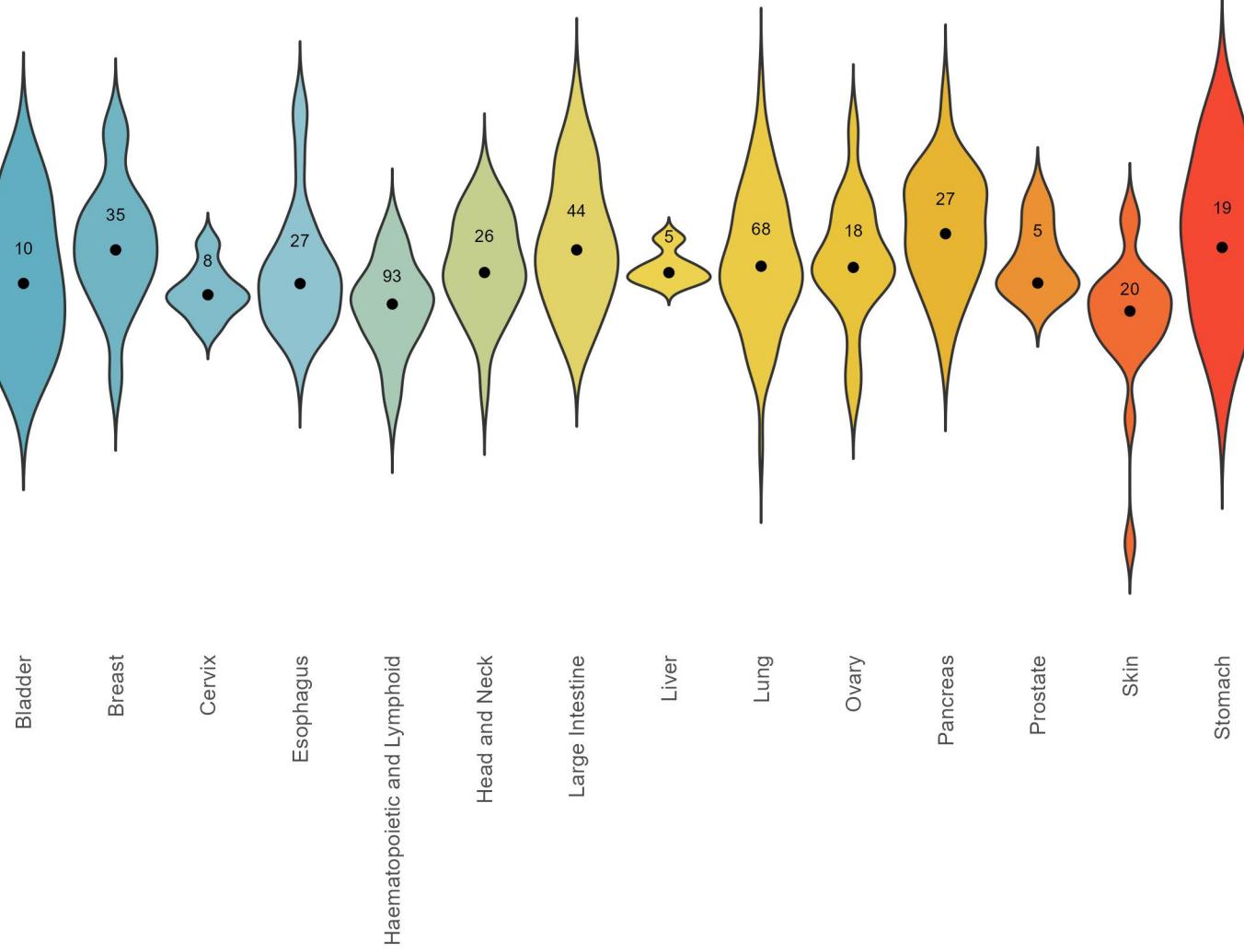


### Top positive correlations of CIB1 protein, DB1



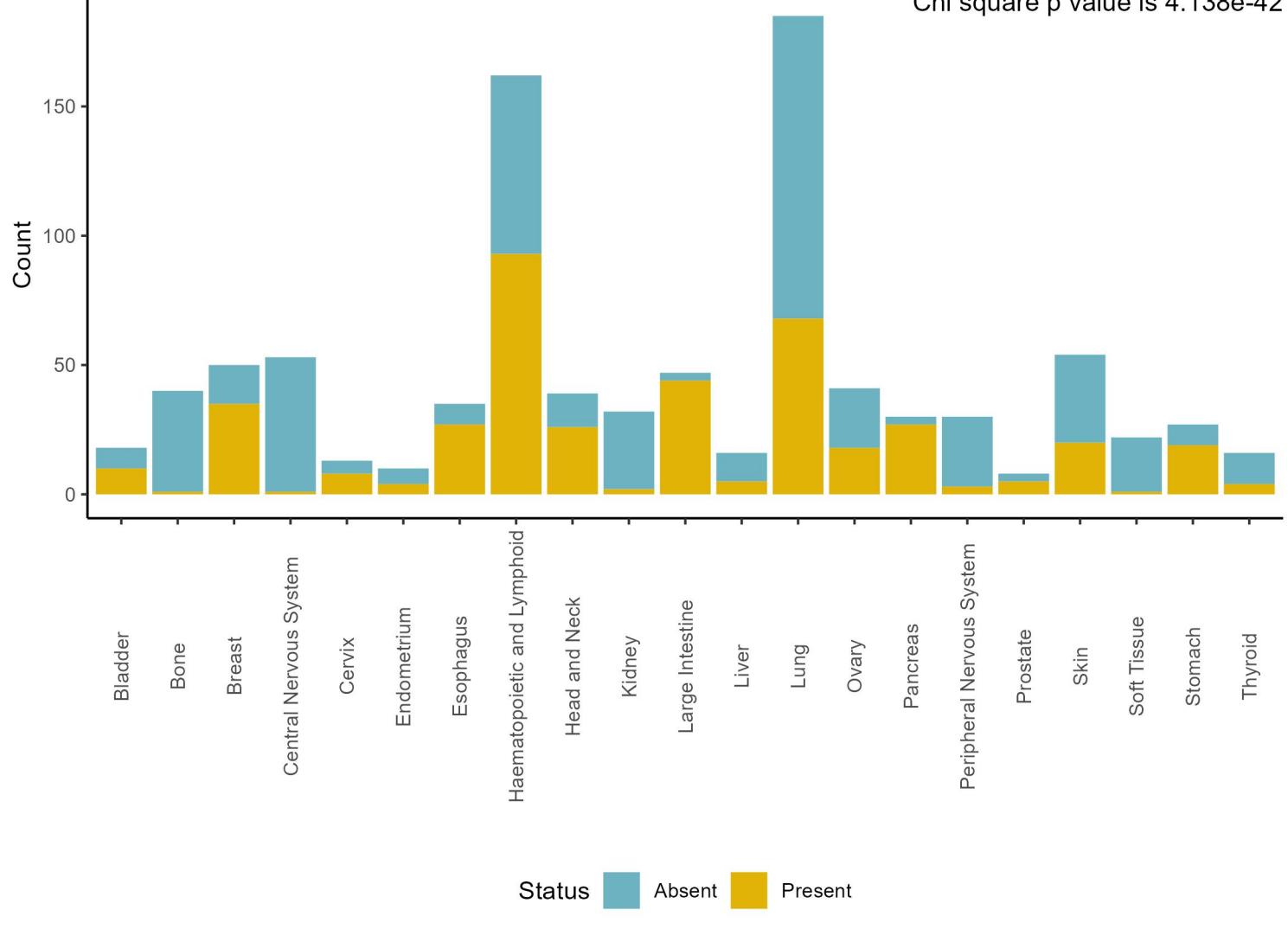
## Amount of CIB1 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 9.098e-11



## Present and absent CIB1 protein counts by tissue, DB1

Chi square p value is 4.138e-42

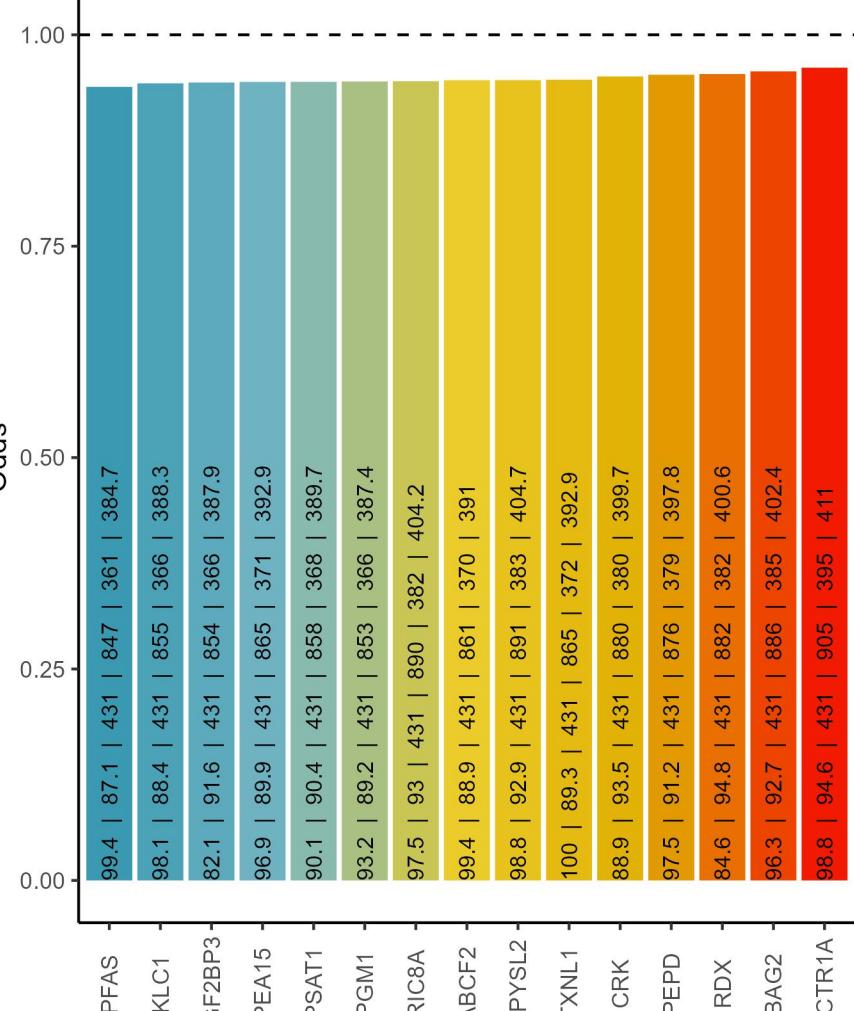


## Cooccurrence with CIB1 protein, DB1

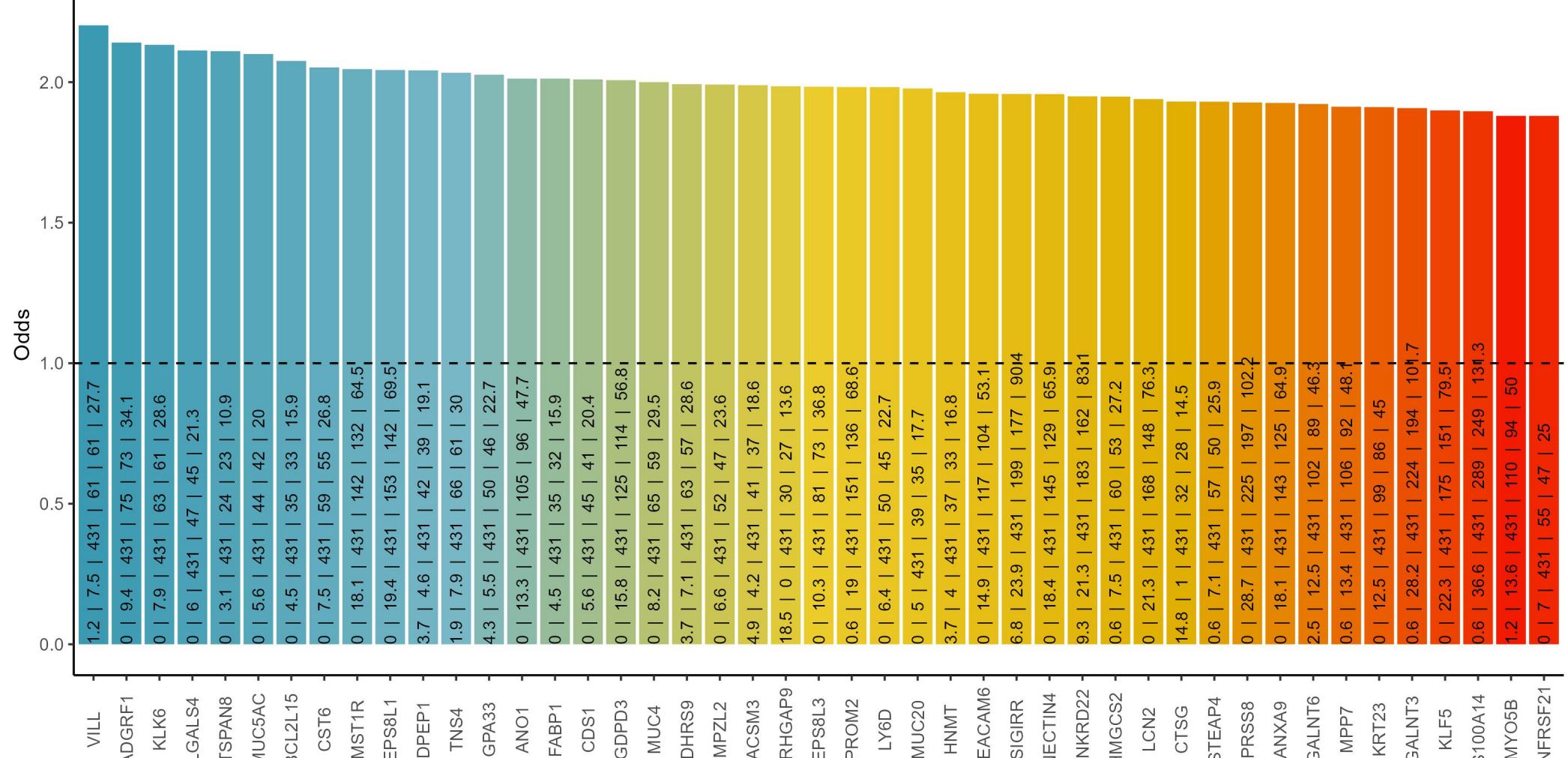
% of CIB1 in blood cancers: 57.4 ; % of CIB1 in solid cancers: 42.9

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CIB1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

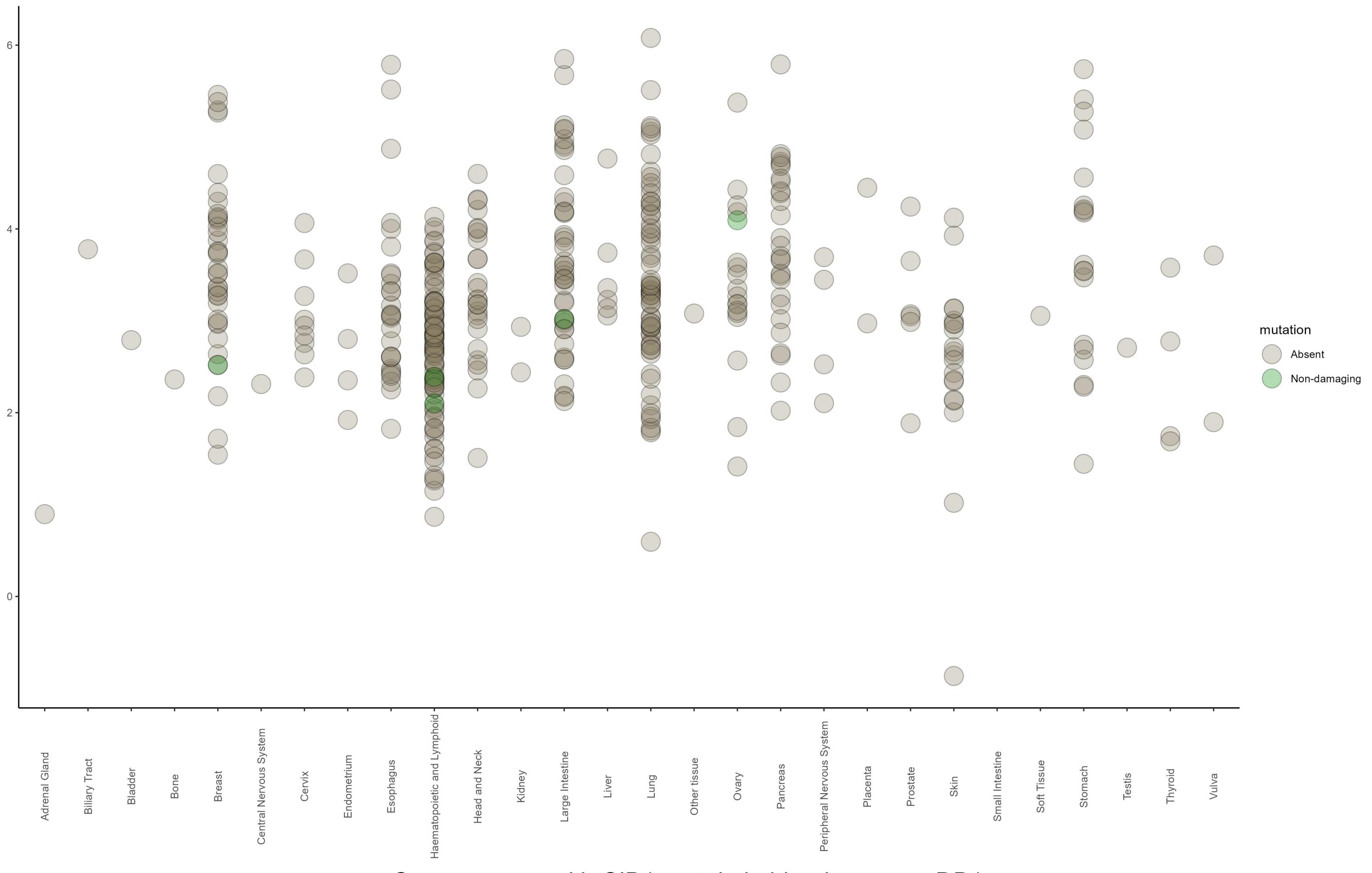
### Negative cooccurrence



### Positive cooccurrence



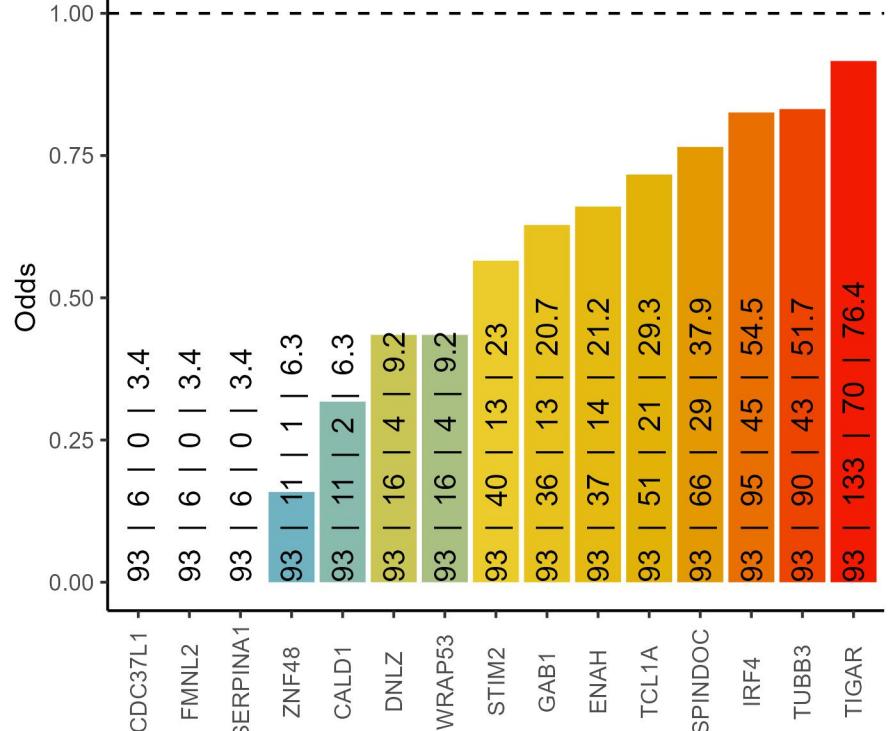
# Amount of CIB1 protein and mutation status by tissue, DB1



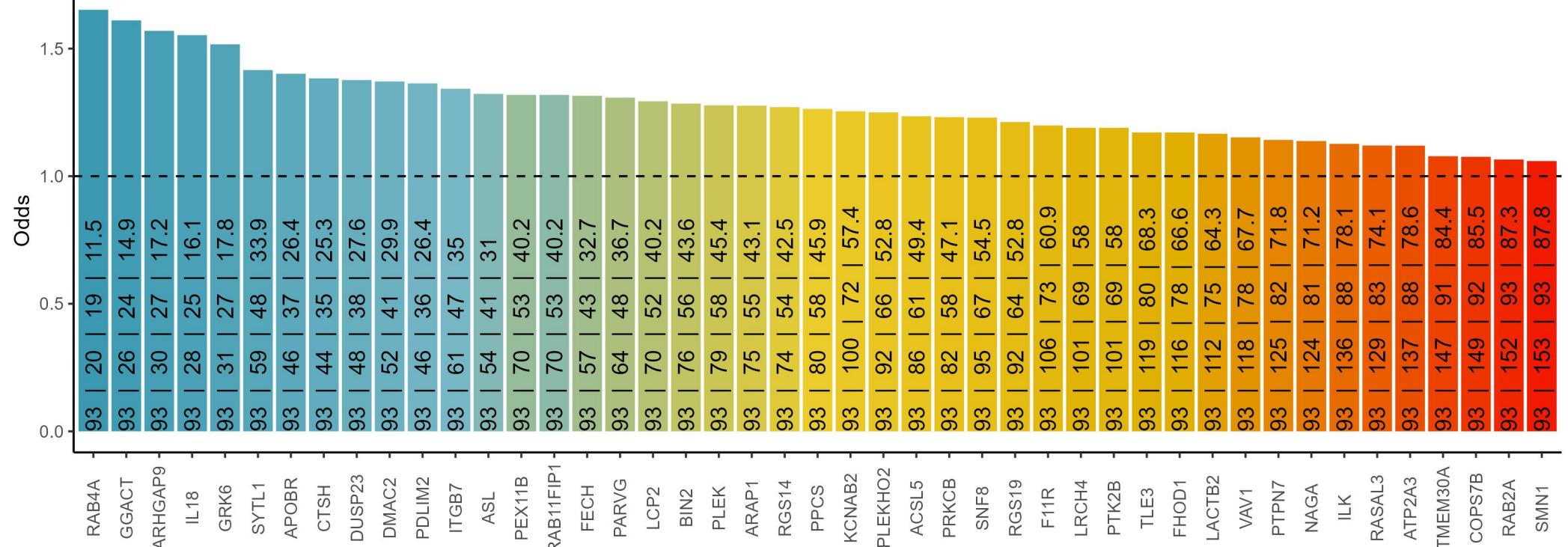
## Cooccurrence with CIB1 protein in blood cancers, DB1

The text in the bars: incidence of CIB1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



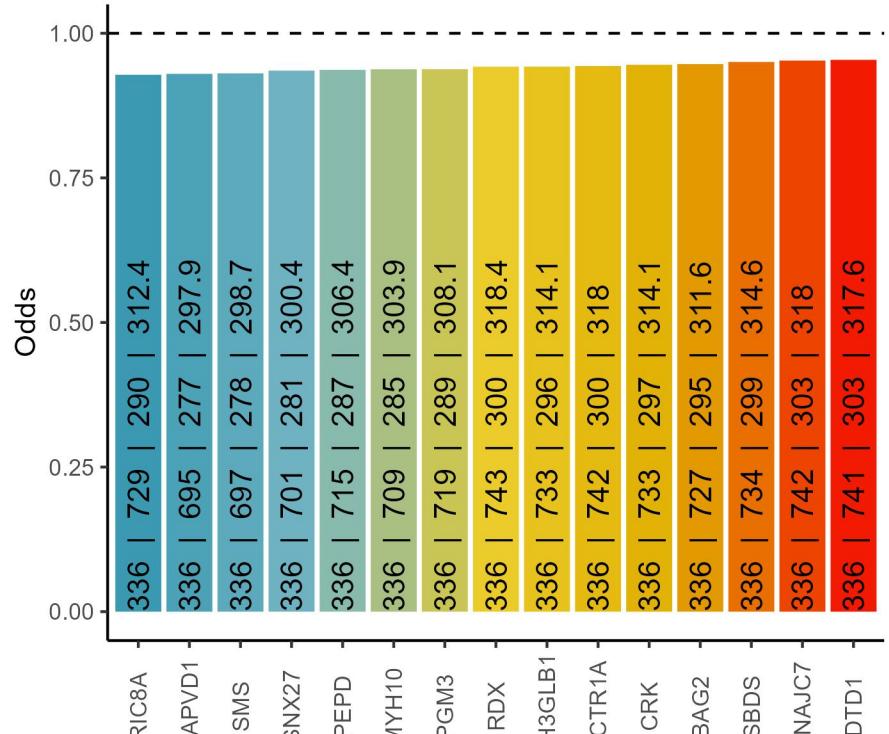
Positive cooccurrence



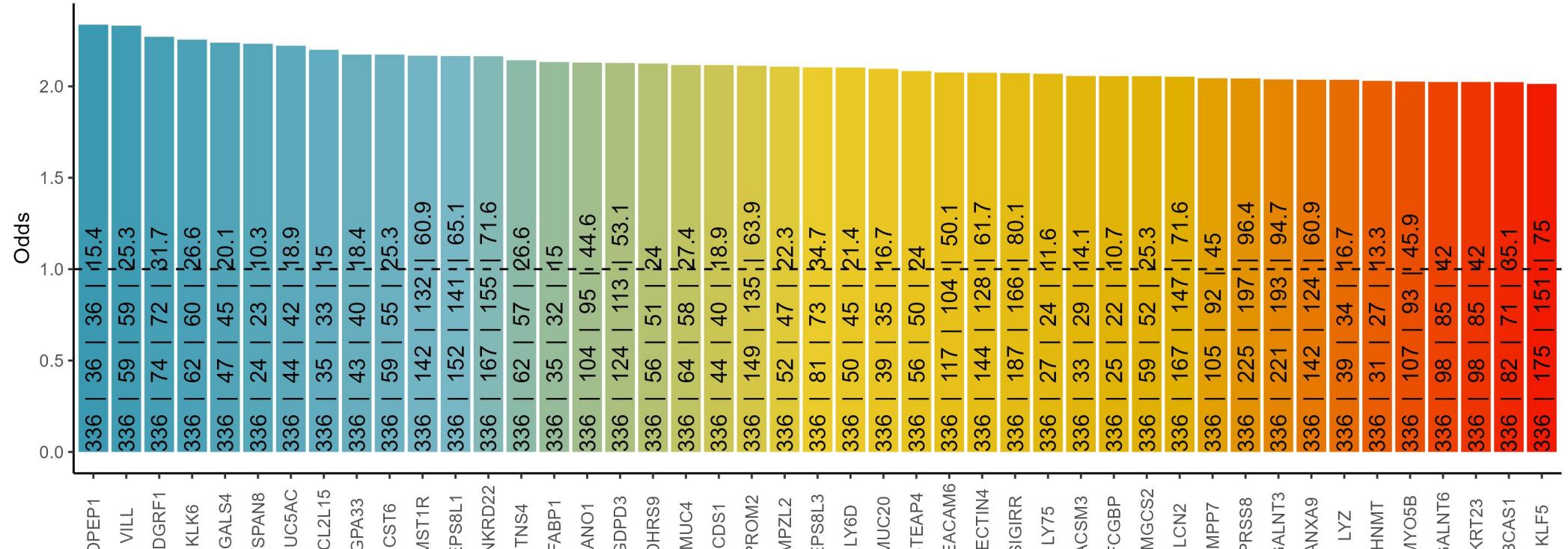
## Cooccurrence with CIB1 protein in solid cancers, DB1

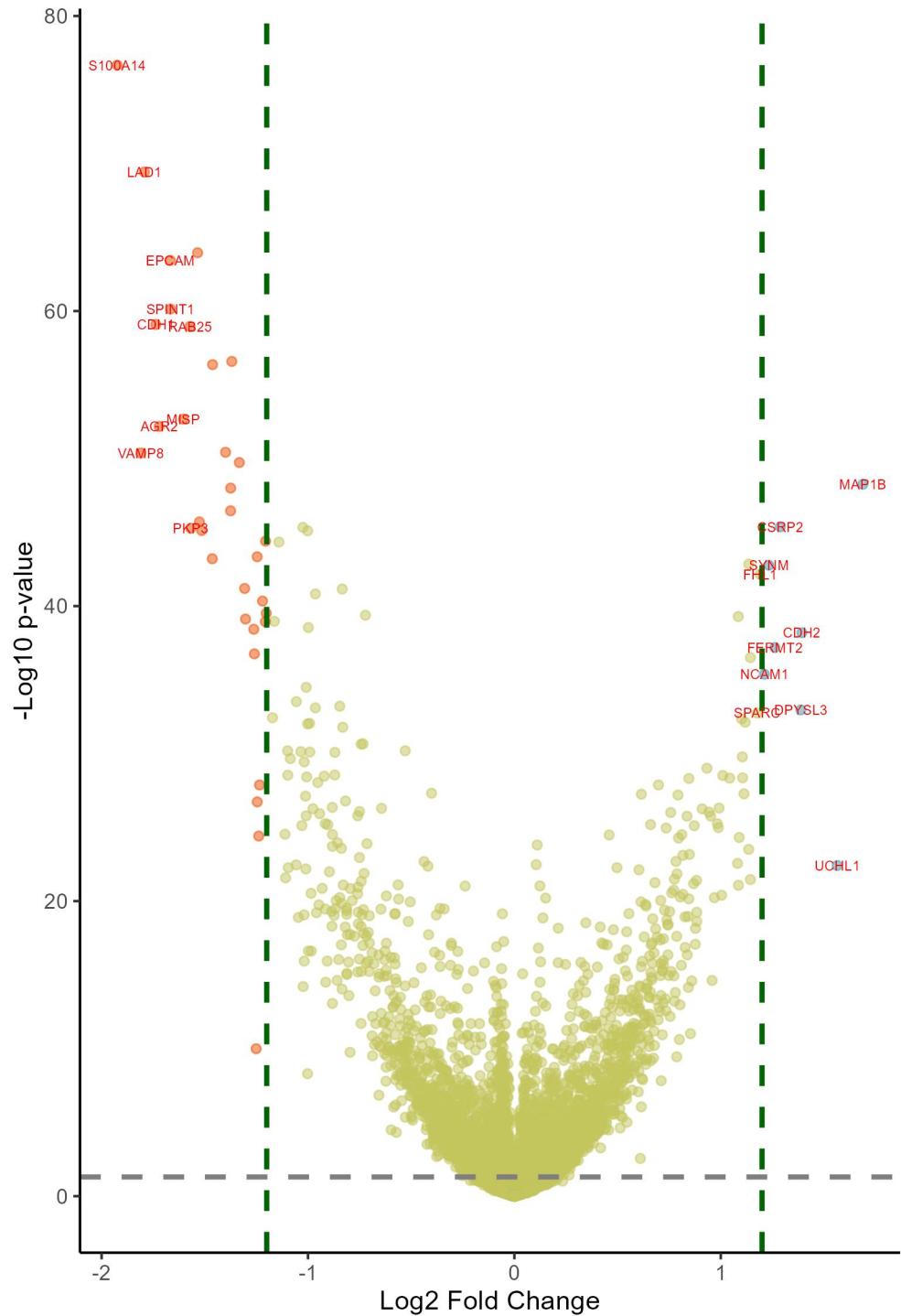
The text in the bars: incidence of CIB1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



Positive cooccurrence

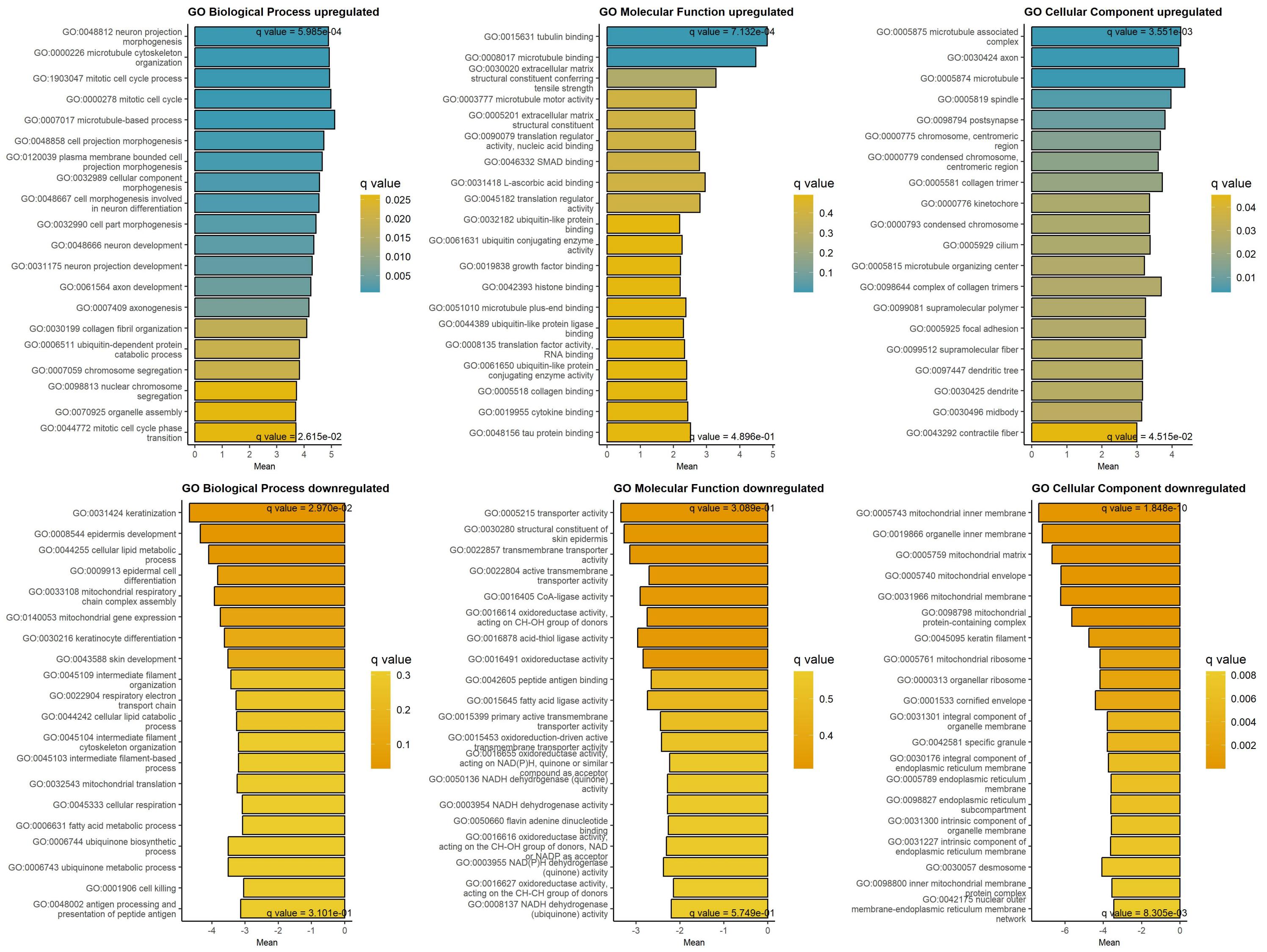


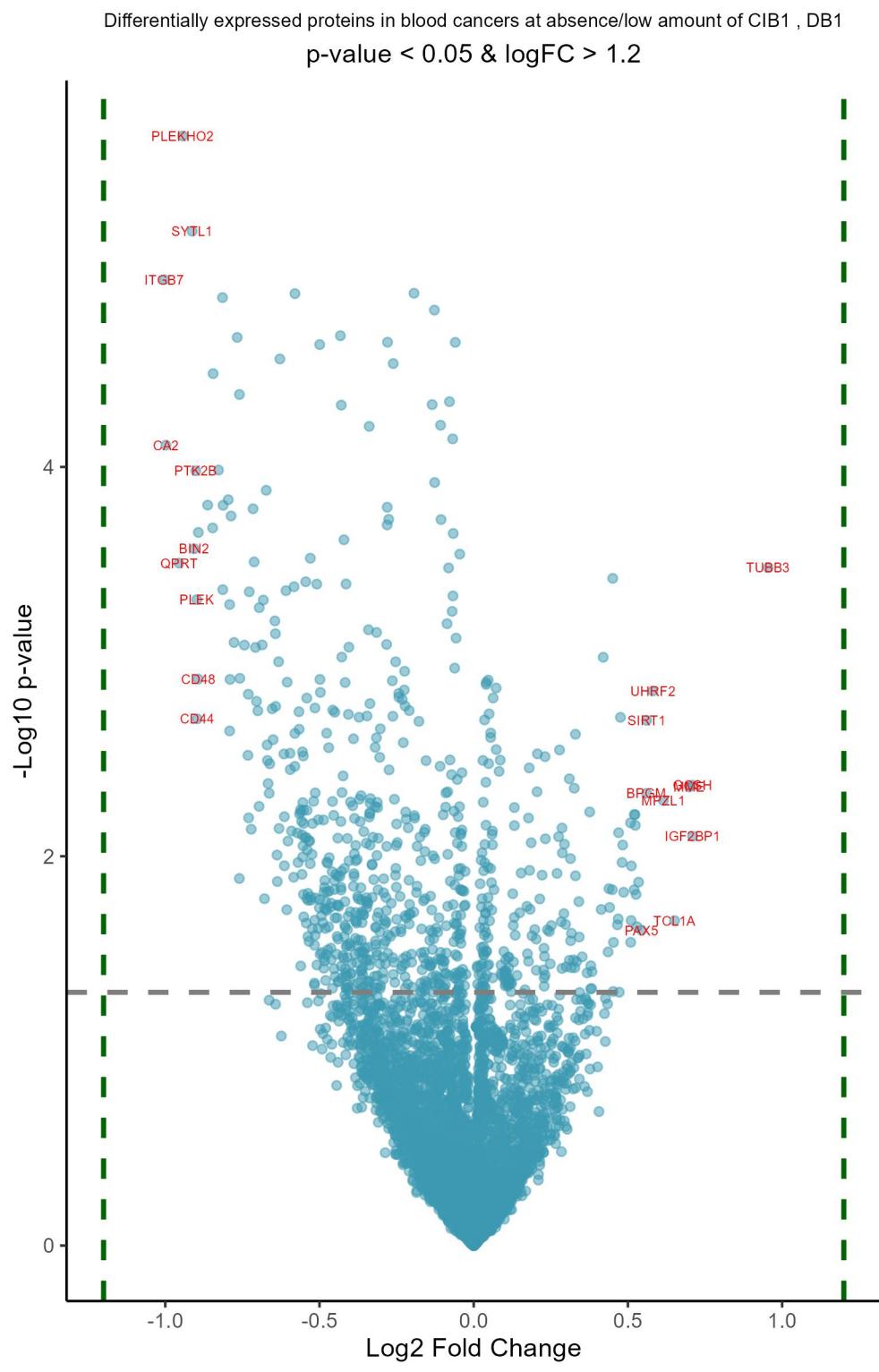


## Downregulated at low/absent CIB1 Upregulated at low/absent CIB1

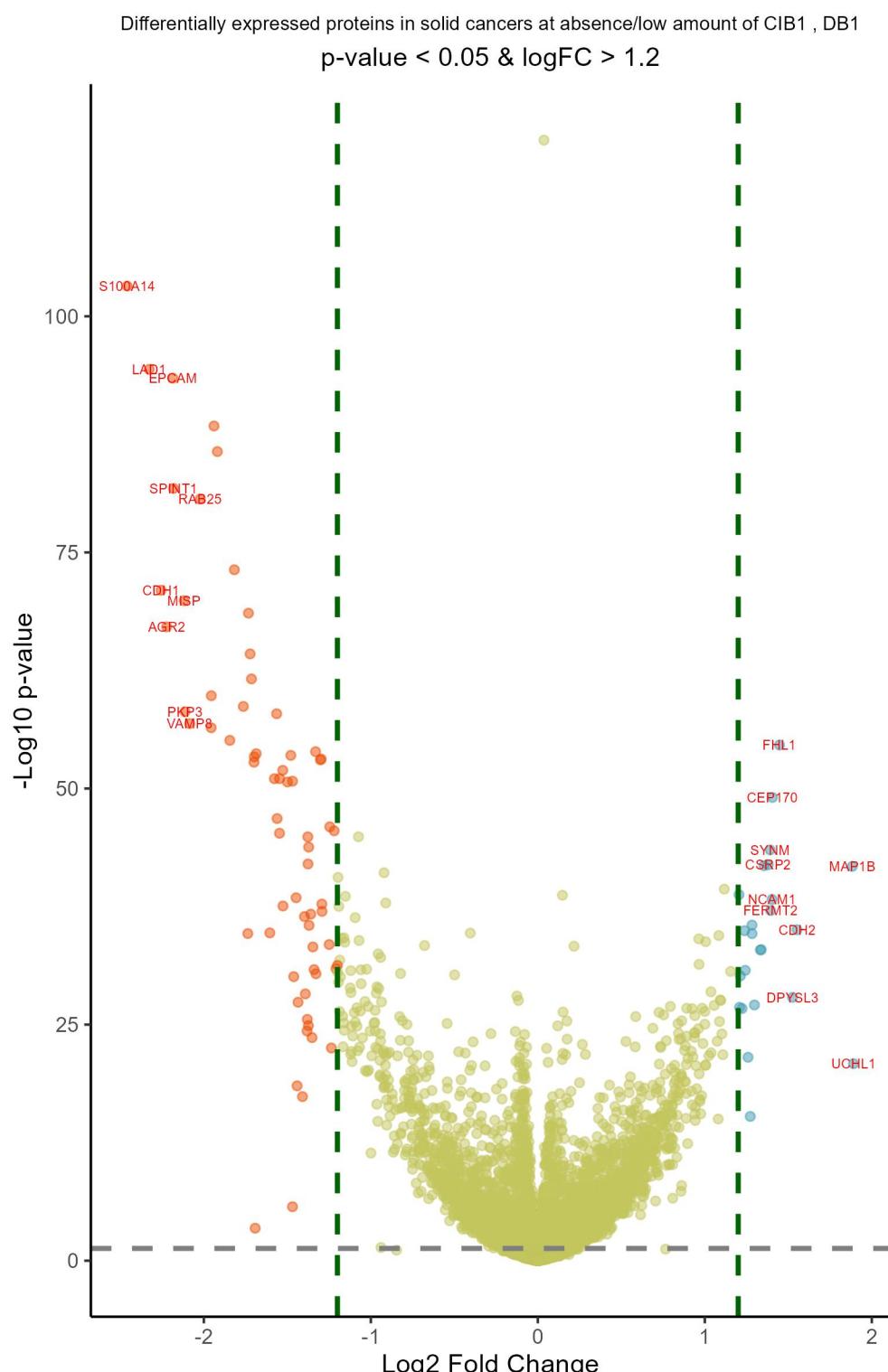
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.92	7.15e-74	S100A14	S100 calcium binding protein A14	1.69	2.31e-46	MAP1B	microtubule associated protein 1B
-1.81	2.00e-48	VAMP8	vesicle associated membrane protein	1.56	1.95e-21	UCHL1	ubiquitin C-terminal hydrolase L1
-1.79	8.38e-67	LAD1	ladinin 1	1.39	9.71e-37	CDH2	cadherin 2
-1.74	7.73e-57	CDH1	cadherin 1	1.39	1.37e-31	DPYSL3	dihydropyrimidinase like 3
-1.72	3.68e-50	AGR2	anterior gradient 2, protein disulf	1.29	1.40e-43	CSRP2	cysteine and glycine rich protein 2
-1.67	4.94e-61	EPCAM	epithelial cell adhesion molecule	1.26	9.48e-36	FERMT2	FERM domain containing kindlin 2
-1.67	8.06e-58	SPINT1	serine peptidase inhibitor, Kunitz	1.23	3.80e-41	SYNM	synemin
-1.6	1.29e-50	MISP	mitotic spindle positioning	1.21	5.80e-34	NCAM1	neural cell adhesion molecule 1
-1.57	9.20e-57	RAB25	RAB25, member RAS oncogene family	1.19	1.50e-40	FHL1	four and a half LIM domains 1
-1.57	1.61e-43	PKP3	plakophilin 3	1.18	2.18e-31	SPARC	secreted protein acidic and cystein
-1.53	1.86e-61	ST14	ST14 transmembrane serine protease	1.14	4.37e-35	THY1	Thy-1 cell surface antigen
-1.53	6.91e-44	SPINT2	serine peptidase inhibitor, Kunitz	1.14	1.61e-20	CALD1	caldesmon 1
-1.52	2.19e-43	TACSTD2	tumor associated calcium signal tra	1.14	3.29e-41	CEP170	centrosomal protein 170
-1.46	1.47e-41	LSR	lipolysis stimulated lipoprotein re	1.14	1.69e-22	PRAF2	PRA1 domain family member 2
-1.46	2.84e-54	EVPL	envoplakin	1.12	8.67e-31	TUBB2A	tubulin beta 2A class IIa
-1.4	1.92e-48	ESRP1	epithelial splicing regulatory prot	1.11	4.22e-26	TUBB2B	tubulin beta 2B class IIb
-1.38	1.28e-44	S100P	S100 calcium binding protein P	1.11	3.76e-27	MAGED2	MAGE family member D2
-1.37	3.95e-46	PRSS8	serine protease 8	1.1	1.63e-28	STXBP1	syntaxin binding protein 1
-1.37	1.93e-54	SYTL1	synaptotagmin like 1	1.1	5.22e-31	P3H3	prolyl 3-hydroxylase 3
-1.33	8.25e-48	PATJ	PATJ crumbs cell polarity complex c	1.09	2.78e-23	ENO2	enolase 2
-1.31	1.33e-39	CDH3	cadherin 3	1.09	3.74e-20	CNN3	calponin 3
-1.3	1.29e-37	SERPINB5	serpin family B member 5	1.08	8.89e-38	CAP2	cyclase associated actin cytoskelet
-1.26	5.77e-37	CGN	cingulin	1.08	1.43e-21	CFL2	cofilin 2
-1.26	2.51e-35	FAM83H	family with sequence similarity 83	1.04	3.89e-27	MRC2	mannose receptor C type 2
-1.25	1.12e-09	KRT19	keratin 19	1.01	2.73e-27	AIDA	axin interactor, dorsalization asso
-1.25	1.12e-41	MAP7	microtubule associated protein 7	1	1.64e-19	TUBB3	tubulin beta 3 class III
-1.25	1.41e-25	ITGB4	integrin subunit beta 4	0.99	3.58e-25	SPART	spartin
-1.24	2.24e-23	BRI3BP	BRI3 binding protein	0.99	6.35e-24	MXRA7	matrix remodeling associated 7
-1.23	1.09e-26	PKP2	plakophilin 2	0.98	3.63e-24	CACNA2D1	calcium voltage-gated channel auxil

## GAGE analysis on upregulated and downregulated proteins at low/absent CIB1 protein, DB1

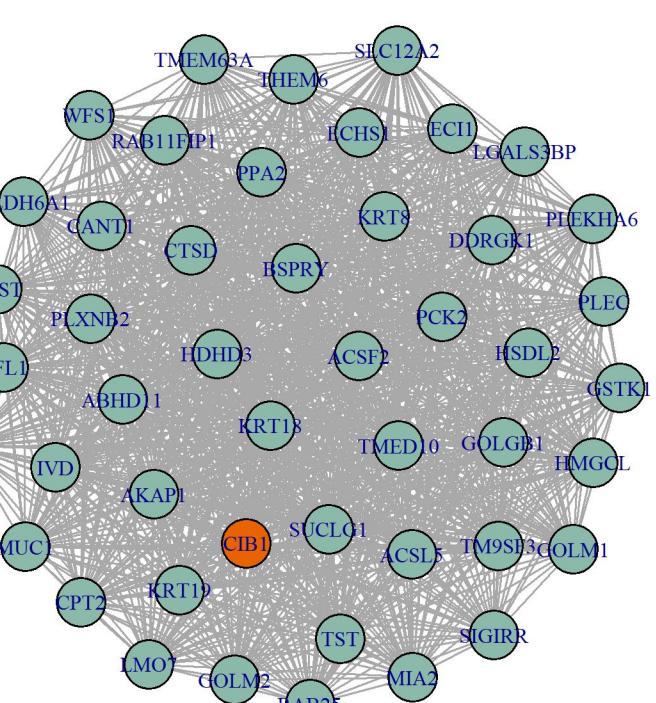
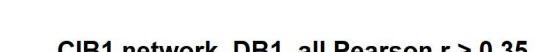
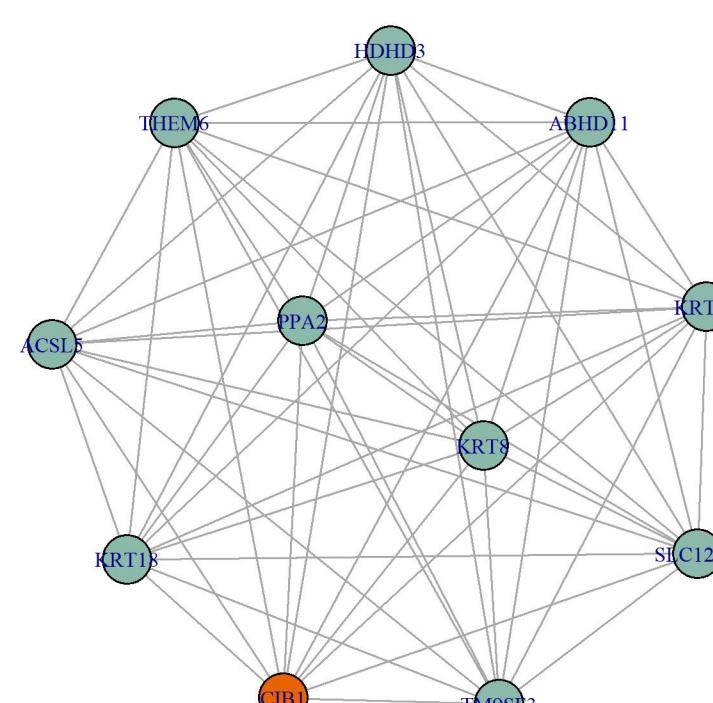
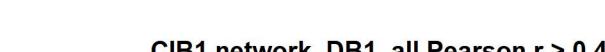
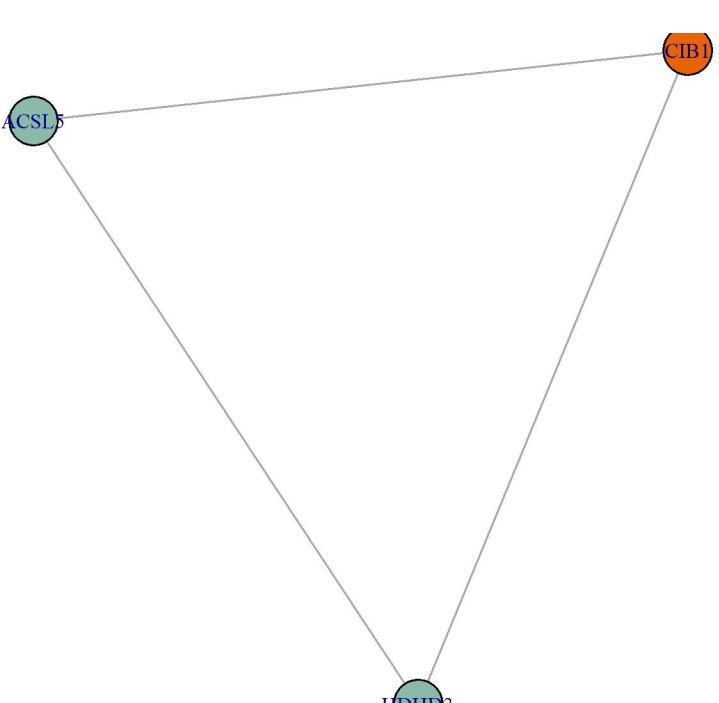


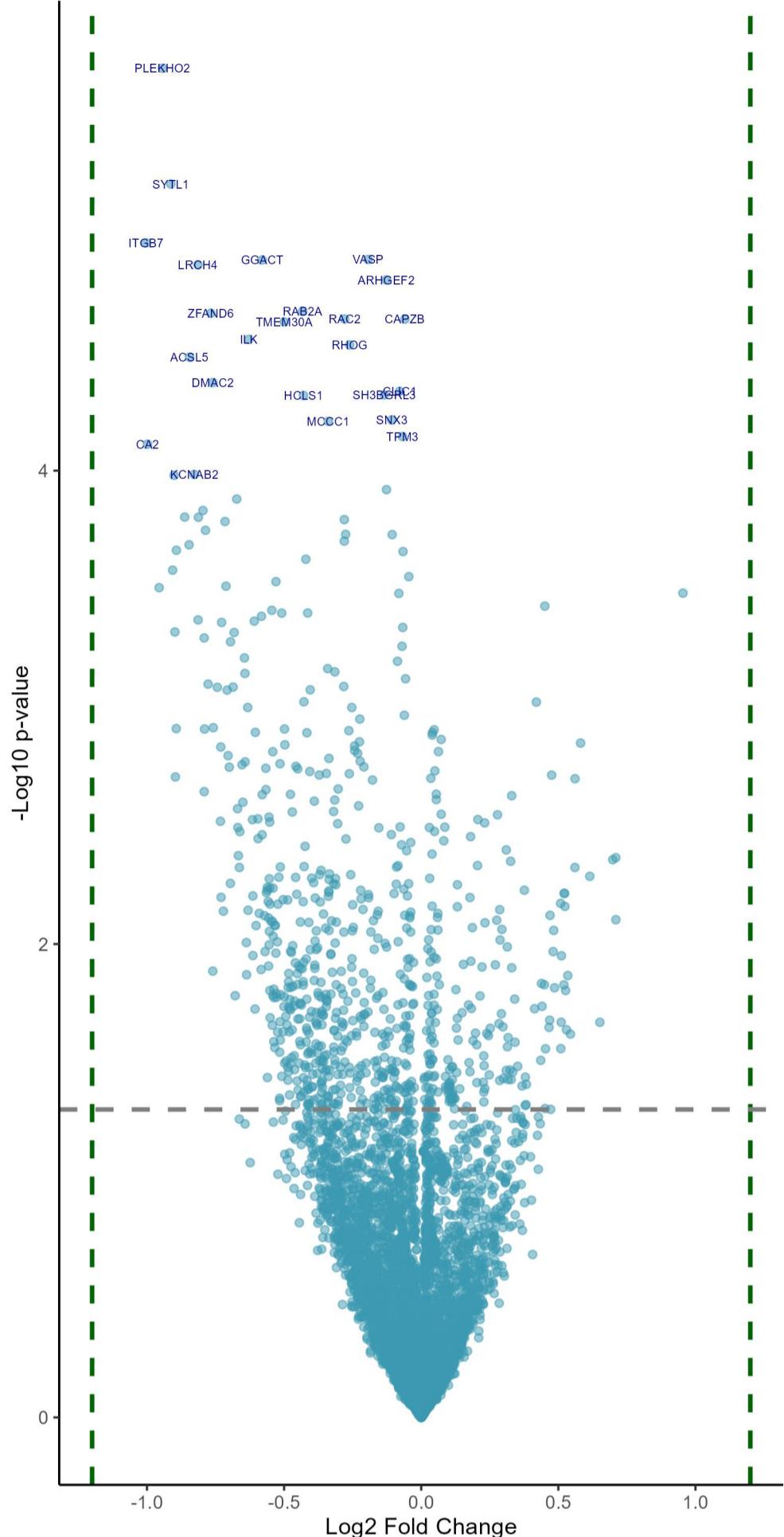


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1	1.20e-02	ITGB7	integrin subunit beta 7	0.95	4.57e-02	TUBB3	tubulin beta 3 class III
-1	2.14e-02	CA2	carbonic anhydrase 2	0.71	2.10e-01	IGF2BP1	insulin like growth factor 2 mRNA b
-0.96	4.51e-02	QPRT	quinolinate phosphoribosyltransfera	0.71	1.72e-01	GCSH	glycine cleavage system protein H
-0.94	6.63e-03	PLEKHO2	pleckstrin homology domain containi	0.7	1.74e-01	MME	membrane metalloendopeptidase
-0.91	1.20e-02	SYTL1	synaptotagmin like 1	0.65	3.14e-01	TCL1A	TCL1 family AKT coactivator A
-0.91	4.17e-02	BIN2	bridging integrator 2	0.61	1.88e-01	MPZL1	myelin protein zero like 1
-0.9	2.68e-02	PTK2B	protein tyrosine kinase 2 beta	0.58	1.01e-01	UHRF2	ubiquitin like with PHD and ring fi
-0.9	5.44e-02	PLEK	pleckstrin	0.56	1.11e-01	SIRT1	sirtuin 1
-0.9	1.11e-01	CD44	CD44 molecule (Indian blood group)	0.56	1.79e-01	BPGM	bisphosphoglycerate mutase
-0.89	9.57e-02	CD48	CD48 molecule	0.54	3.25e-01	PAX5	paired box 5
-0.89	3.65e-02	LCP2	lymphocyte cytosolic protein 2	0.53	2.68e-01	CDCA3	cell division cycle associated 3
-0.86	3.30e-02	SYNJ2BP	synaptojanin 2 binding protein	0.53	3.23e-01	AFDN	afadin, adherens junction formation
-0.85	3.60e-02	PRKCB	protein kinase C beta	0.53	2.85e-01	PFKM	phosphofructokinase, muscle
-0.84	1.38e-02	ACSL5	acyl-CoA synthetase long chain fami	0.52	2.01e-01	TIGAR	TP53 induced glycolysis regulatory
-0.83	2.68e-02	KCNAB2	potassium voltage-gated channel sub	0.52	1.96e-01	PBK	PDZ binding kinase
-0.81	1.20e-02	LRCH4	leucine rich repeats and calponin h	0.52	1.96e-01	SPINDOC	spindlin interactor and repressor o
-0.81	5.20e-02	PPCS	phosphopantethenoylcysteine synthet	0.52	2.80e-01	SETD7	SET domain containing 7, histone ly
-0.81	3.30e-02	PARVG	parvin gamma	0.51	2.45e-01	GNE	glucosamine (UDP-N-acetyl)-2-epimer
-0.8	3.30e-02	PTPN7	protein tyrosine phosphatase non-re	0.51	3.14e-01	ATP1A3	ATPase Na+/K+ transporting subunit
-0.79	5.64e-02	ARAP1	ArfGAP with RhoGAP domain, ankyrin	0.51	3.25e-01	GLCCI1	glucocorticoid induced 1
-0.79	1.22e-01	ITGAL	integrin subunit alpha L	0.51	2.00e-01	STIM2	stromal interaction molecule 2
-0.79	9.57e-02	SCAMP2	secretory carrier membrane protein	0.49	2.82e-01	GPT2	glutamic--pyruvic transaminase 2
-0.79	3.44e-02	DUSP23	dual specificity phosphatase 23	0.48	2.15e-01	SKA3	spindle and kinetochore associated
-0.78	7.60e-02	F11R	F11 receptor	0.48	2.41e-01	SLC4A7	solute carrier family 4 member 7
-0.77	1.20e-02	ZFAND6	zinc finger AN1-type containing 6	0.48	1.10e-01	GAB1	GRB2 associated binding protein 1
-0.76	2.63e-01	COTL1	coactosin like F-actin binding prot	0.47	3.25e-01	MYH10	myosin heavy chain 10
-0.76	1.60e-02	DMAC2	distal membrane arm assembly compon	0.47	2.07e-01	PALLD	palladin, cytoskeletal associated p
-0.76	9.57e-02	TES	testin LIM domain protein	0.47	3.13e-01	ZNF280C	zinc finger protein 280C
-0.74	7.60e-02	PEX11B	peroxisomal biogenesis factor 11 be	0.47	3.20e-01	RAD18	RAD18 E3 ubiquitin protein ligase

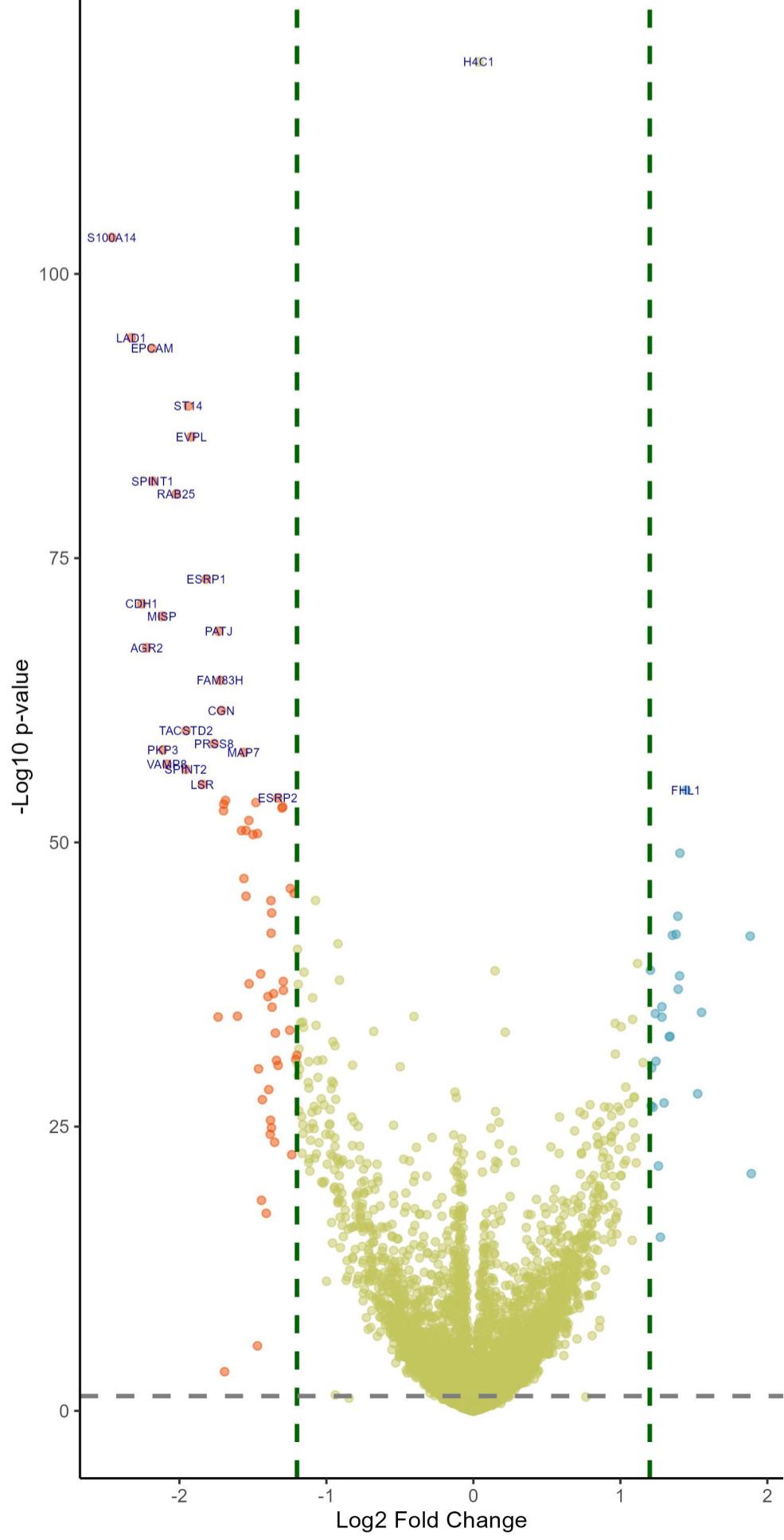


Downregulated in solid cancers at low/absent CIB1				Upregulated in solid cancers at low/absent CIB1			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.46	1.40e-100	S100A14	S100 calcium binding protein A14	1.89	3.73e-20	UCHL1	ubiquitin C-terminal hydrolase L1
-2.33	6.92e-92	LAD1	ladinin 1	1.88	2.39e-40	MAP1B	microtubule associated protein 1B
-2.26	6.17e-69	CDH1	cadherin 1	1.55	8.63e-34	CDH2	cadherin 2
-2.22	3.63e-65	AGR2	anterior gradient 2, protein disulf	1.53	7.38e-27	DPYSL3	dihydropyrimidinase like 3
-2.19	4.77e-91	EPCAM	epithelial cell adhesion molecule	1.45	6.87e-53	FHL1	four and a half LIM domains 1
-2.18	1.38e-79	SPINT1	serine peptidase inhibitor, Kunitz	1.41	1.59e-47	CEP170	centrosomal protein 170
-2.12	7.17e-68	MISP	mitotic spindle positioning	1.4	6.42e-37	NCAM1	neural cell adhesion molecule 1
-2.11	2.61e-56	PKP3	plakophilin 3	1.39	8.85e-36	FERMT2	FERM domain containing kindlin 2
-2.09	4.28e-55	VAMP8	vesicle associated membrane protein	1.39	4.62e-42	SYNM	synemisin
-2.02	1.66e-78	RAB25	RAB25, member RAS oncogene family	1.38	1.69e-40	CSRP2	cysteine and glycine rich protein 2
-1.96	1.11e-54	SPINT2	serine peptidase inhibitor, Kunitz	1.35	2.06e-40	THY1	Thy-1 cell surface antigen
-1.96	5.82e-58	TACSTD2	tumor associated calcium signal tra	1.34	8.95e-32	SPARC	secreted protein acidic and cystein
-1.94	4.55e-86	ST14	ST14 transmembrane serine protease	1.33	9.50e-32	MAGED2	MAGE family member D2
-1.92	2.00e-83	EVPL	envoplakin	1.3	4.45e-26	ENO2	enolase 2
-1.84	2.29e-53	LSR	lipolysis stimulated lipoprotein re	1.28	2.09e-33	TUBB2A	tubulin beta 2A class Ila
-1.82	4.56e-71	ESRP1	epithelial splicing regulatory prot	1.28	2.85e-34	MRC2	mannose receptor C type 2
-1.76	7.54e-57	PRSS8	serine protease 8	1.27	7.78e-15	ANXA6	annexin A6
-1.74	2.08e-33	ITGB4	integrin subunit beta 4	1.26	8.22e-21	PRAF2	PRA1 domain family member 2
-1.73	1.39e-66	PATJ	PATJ crumbs cell polarity complex c	1.24	1.23e-29	STXBP1	syntaxin binding protein 1
-1.72	2.47e-62	FAM83H	family with sequence similarity 83	1.24	1.09e-33	SPART	spartin
-1.71	1.04e-59	CGN	cingulin	1.22	9.90e-26	TUBB2B	tubulin beta 2B class IIb
-1.7	3.55e-51	SERPINB5	serpin family B member 5	1.21	4.46e-29	P3H3	prolyl 3-hydroxylase 3
-1.7	1.05e-51	S100P	S100 calcium binding protein P	1.21	7.65e-26	ARHGAP17	Rho GTPase activating protein 17
-1.69	8.62e-04	KRT19	keratin 19	1.2	2.20e-37	CAP2	cyclase associated actin cytoskelet
-1.69	5.27e-52	CDH3	cadherin 3	1.15	1.56e-29	AIDA	axin interactor, dorsalization asso
-1.6	1.83e-33	PKP2	plakophilin 2	1.12	5.74e-38	MAP1A	microtubule associated protein 1A
-1.58	1.80e-49	DSC2	desmocollin 2	1.11	4.56e-21	CNN3	calponin 3
-1.56	4.04e-56	MAP7	microtubule associated protein 7	1.1	3.67e-23	CFL2	cofilin 2



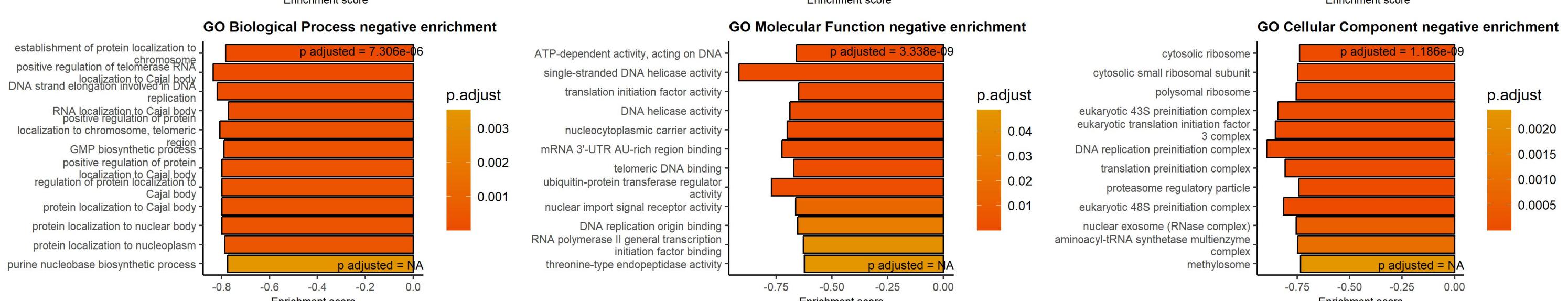
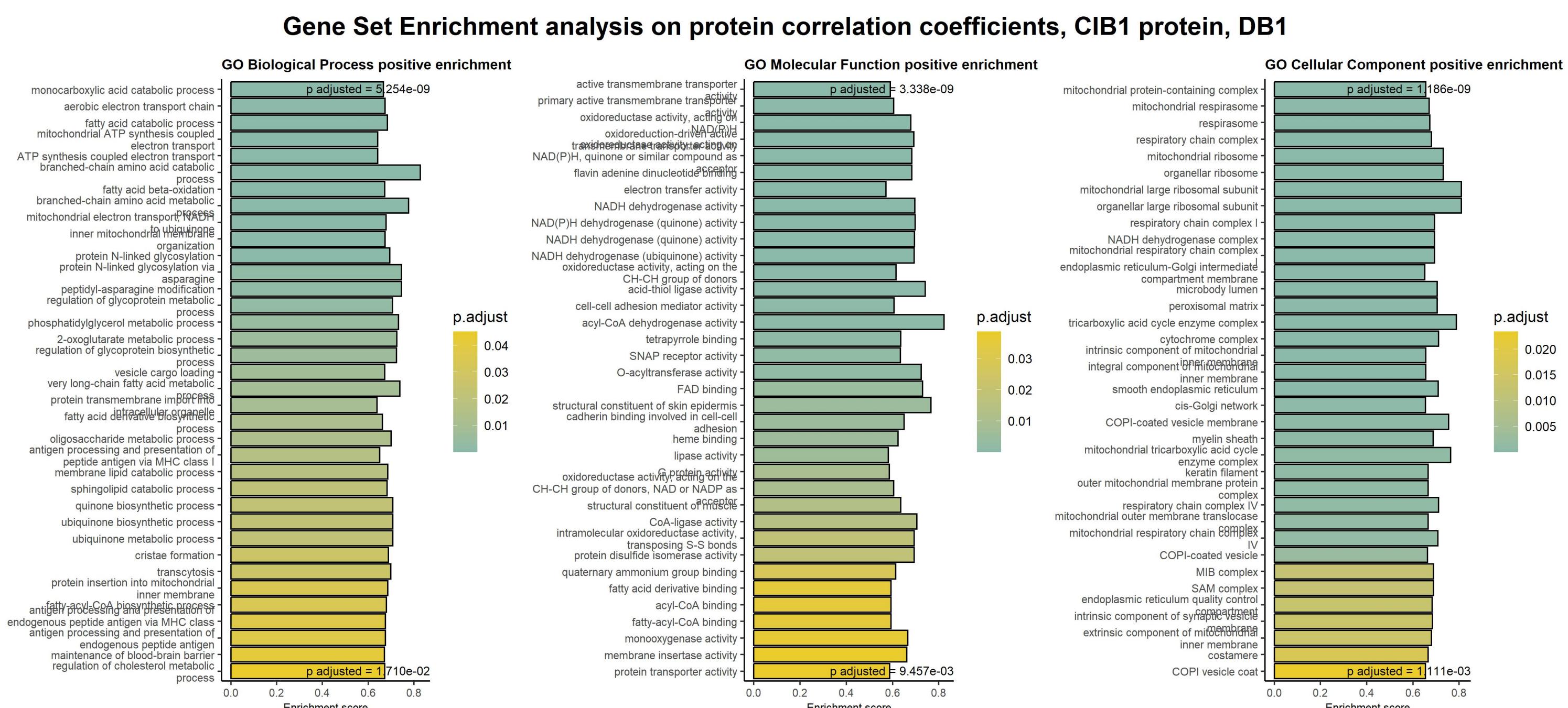
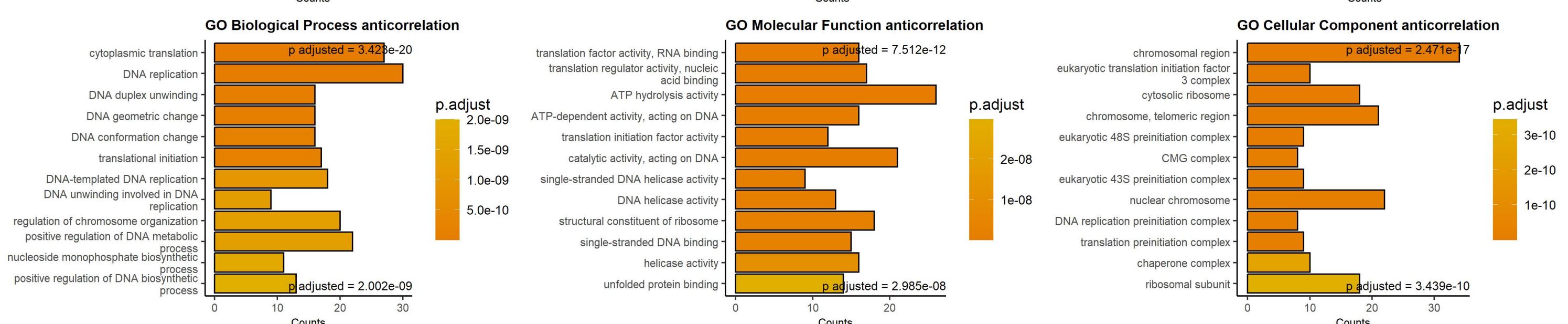
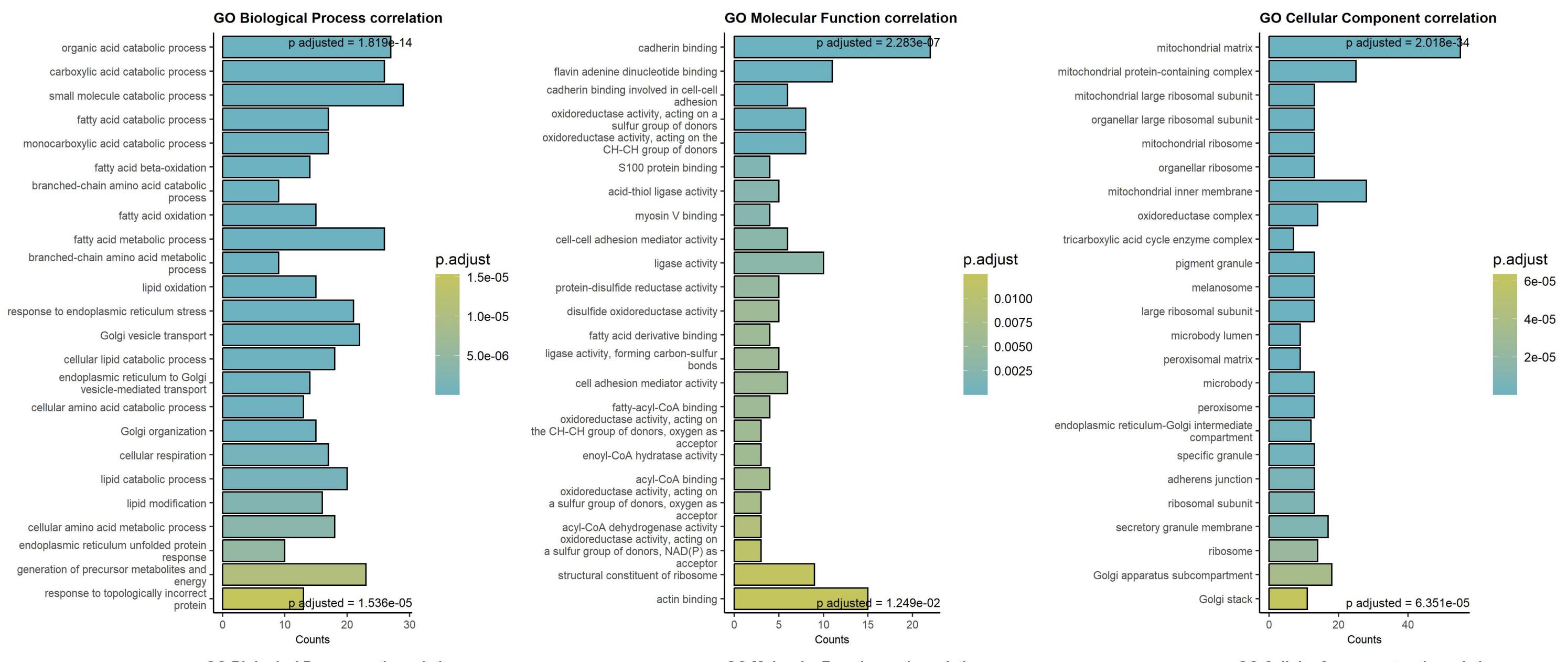
Sorted by p values!  
Downregulated in blood cancers at low/absent CIB1 Upregulated in blood cancers at low/absent CIB1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.94	6.63e-03	PLEKH02	pleckstrin homology domain containi	0.95	4.57e-02	TUBB3	tubulin beta 3 class III
-0.91	1.20e-02	SYTL1	synaptotagmin like 1	0.45	5.07e-02	ITGA3	integrin subunit alpha 3
-1	1.20e-02	ITGB7	integrin subunit beta 7	0.42	8.31e-02	PGM1	phosphoglucomutase 1
-0.19	1.20e-02	VASP	vasodilator stimulated phosphoprote	0.05	9.57e-02	SSRP1	structure specific recognition prot
-0.58	1.20e-02	GGACT	gamma-glutamylamine cyclotransferas	0.04	9.57e-02	IK	IK cytokine
-0.81	1.20e-02	LRCH4	leucine rich repeats and calponin h	0.04	9.68e-02	CPSF3	cleavage and polyadenylation specif
-0.13	1.20e-02	ARHGEF2	Rho/Rac guanine nucleotide exchange	0.07	9.99e-02	GAPDH	glyceraldehyde-3-phosphate dehydrog
-0.43	1.20e-02	RAB2A	RAB2A, member RAS oncogene family	0.58	1.01e-01	UHRF2	ubiquitin like with PHD and ring fi
-0.77	1.20e-02	ZFAND6	zinc finger AN1-type containing 6	0.06	1.03e-01	NOP2	NOP2 nucleolar protein
-0.28	1.20e-02	RAC2	Rac family small GTPase 2	0.05	1.10e-01	DNAJC7	Dnaj heat shock protein family (Hsp
-0.06	1.20e-02	CAPZB	capping actin protein of muscle Z-I	0.48	1.10e-01	GAB1	GRB2 associated binding protein 1
-0.5	1.20e-02	TMEM30A	transmembrane protein 30A	0.04	1.11e-01	PRPF40A	pre-mRNA processing factor 40 homol
-0.63	1.30e-02	ILK	integrin linked kinase	0.56	1.11e-01	SIRT1	sirtuin 1
-0.26	1.30e-02	RHOG	ras homolog family member G	0.06	1.22e-01	TCOF1	treacle ribosome biogenesis factor
-0.84	1.38e-02	ACSL5	acyl-CoA synthetase long chain fami	0.33	1.23e-01	WRAP53	WD repeat containing antisense to T
-0.76	1.60e-02	DMAC2	distal membrane arm assembly compon	0.05	1.26e-01	ACP1	acid phosphatase 1
-0.08	1.60e-02	CLIC1	chloride intracellular channel 1	0.07	1.37e-01	SLC3A2	solute carrier family 3 member 2
-0.13	1.60e-02	SH3BGR3	SH3 domain binding glutamate rich p	0.28	1.37e-01	SERPINA1	serpin family A member 1
-0.43	1.60e-02	HCLS1	hematopoietic cell-specific Lyn sub	0.21	1.40e-01	CAB39L	calcium binding protein 39 like
-0.11	1.87e-02	SNX3	sorting nexin 3	0.23	1.41e-01	CDC37L1	cell division cycle 37 like 1
-0.34	1.87e-02	MCCC1	methylcrotonyl-CoA carboxylase subu	0.09	1.42e-01	TOP2A	DNA topoisomerase II alpha
-0.07	2.07e-02	TPM3	tropomyosin 3	0.03	1.42e-01	H4C1	H4 clustered histone 1
-1	2.14e-02	CA2	carbonic anhydrase 2	0.05	1.46e-01	USP39	ubiquitin specific peptidase 39
-0.83	2.68e-02	KCNAB2	potassium voltage-gated channel sub	0.18	1.50e-01	FMNL2	formin like 2
-0.9	2.68e-02	PTK2B	protein tyrosine kinase 2 beta	0.08	1.53e-01	KPNA2	karyopherin subunit alpha 2
-0.13	2.96e-02	CSK	C-terminal Src kinase	0.31	1.63e-01	ALK	ALK receptor tyrosine kinase
-0.67	3.13e-02	IL18	interleukin 18	0.04	1.68e-01	SRRM2	serine/arginine repetitive matrix 2
-0.8	3.30e-02	PTPN7	protein tyrosine phosphatase non-re	0.71	1.72e-01	GCSH	glycine cleavage system protein H
-0.86	3.30e-02	SYNJ2BP	synaptosomal 2 binding protein	0.7	1.74e-01	MME	membrane metalloendopeptidase
-0.81	3.30e-02	PARVG	parvin gamma	0.33	1.76e-01	RANBP6	RAN binding protein 6
-0.28	3.30e-02	SLC9A3R1	SLC9A3 regulator 1	0.21	1.79e-01	ZNF48	zinc finger protein 48
-0.72	3.30e-02	FHOD1	formin homology 2 domain containing	0.56	1.79e-01	BPGM	bisphosphoglycerate mutase
-0.79	3.44e-02	DUSP23	dual specificity phosphatase 23	0.61	1.88e-01	MPZL1	myelin protein zero like 1
-0.28	3.44e-02	SIGIRR	single Ig and TIR domain containing	0.03	1.88e-01	RBM39	RNA binding motif protein 39
-0.11	3.44e-02	GSR	glutathione-disulfide reductase	0.13	1.92e-01	FZD6	frizzled class receptor 6
-0.28	3.57e-02	RGS3	regulator of G protein signaling 3	0.38	1.95e-01	BZW2	basic leucine zipper and W2 domains
-0.85	3.60e-02	PRKCB	protein kinase C beta	0.52	1.96e-01	SPINDOC	spindlin interactor and repressor o
-0.89	3.65e-02	LCP2	lymphocyte cytosolic protein 2	0.52	1.96e-01	PBK	PDZ binding kinase
0.07	3.65e-02	TLN1	talin 1	0.19	1.96e-01	SLC14A2	solute carrier family 14 member 2

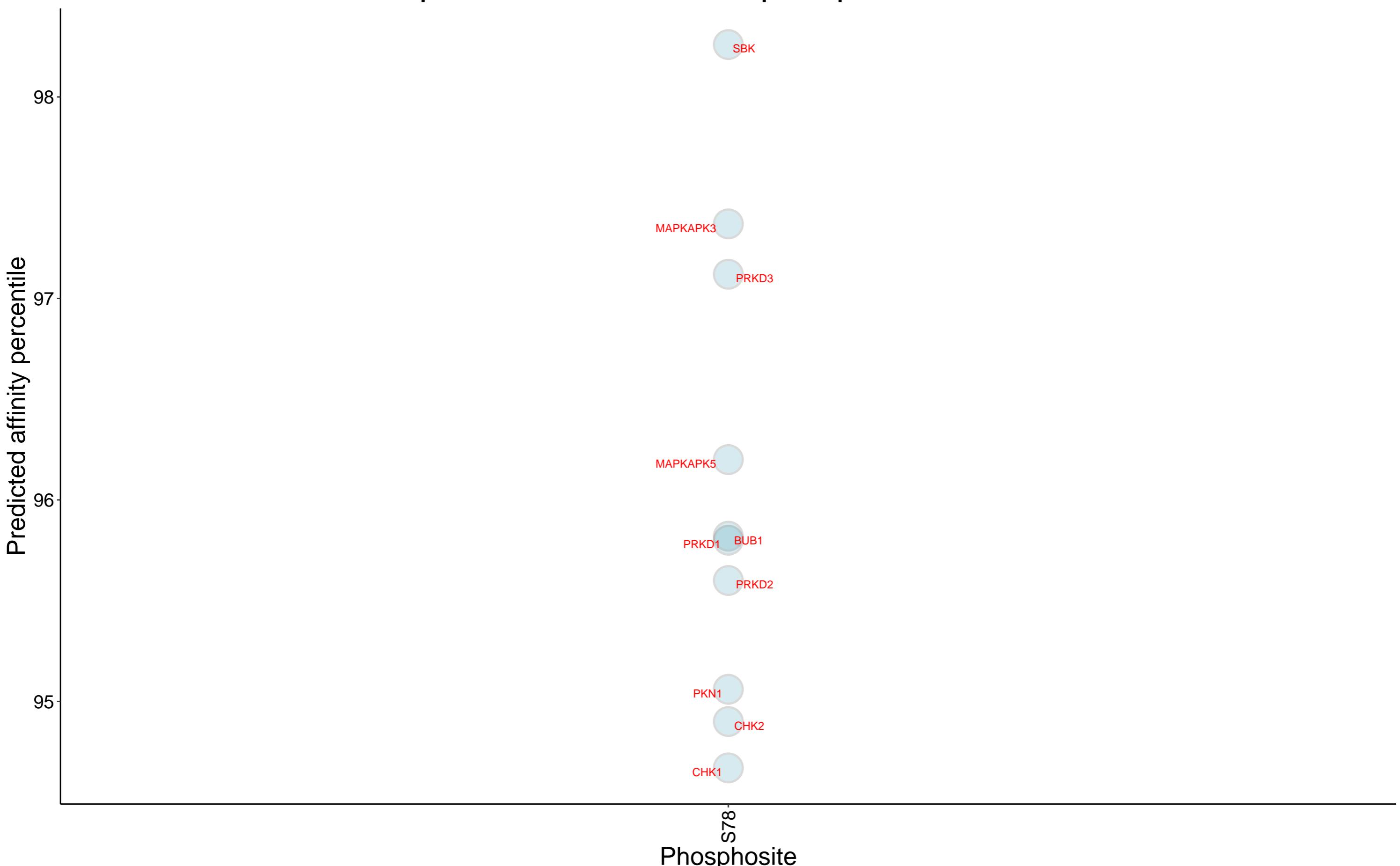
Sorted by p values!  
Downregulated in solid cancers at low/absent CIB1 Upregulated in solid cancers at low/absent CIB1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.46	1.40e-100	S100A14	S100 calcium binding protein A14	0.04	7.40e-116	H4C1	H4 clustered histone 1
-2.33	6.92e-92	LAD1	ladin 1	1.45	6.87e-53	FHL1	four and a half LIM domains 1
-2.19	4.77e-91	EPCAM	epithelial cell adhesion molecule	1.41	1.59e-47	CEP170	centrosomal protein 170
-1.94	4.55e-86	ST14	ST14 transmembrane serine protease	1.39	4.62e-42	SYNM	synemin
-1.92	2.00e-83	EVPL	envoplakin	1.38	1.69e-40	CSRP2	cysteine and glycine rich protein 2
-2.18	1.38e-79	SPINT1	serine peptidase inhibitor, Kunitz	1.35	2.06e-40	THY1	Thy-1 cell surface antigen
-2.02	1.66e-78	RAB25	RAB25, member RAS oncogene family	1.88	2.39e-40	MAP1B	microtubule associated protein 1B
-1.82	4.56e-71	ESRP1	epithelial splicing regulatory prot	1.12	5.74e-38	MAP1A	microtubule associated protein 1A
-2.26	6.17e-69	CDH1	cadherin 1	1.2	2.20e-37	CAP2	cyclase associated actin cytoskelet
-2.12	7.17e-68	MISP	mitotic spindle positioning	0.15	2.47e-37	TUBB	tubulin beta class I
-1.73	1.39e-66	PATJ	PATJ crumbs cell polarity complex c	1.4	6.42e-37	NCAM1	neural cell adhesion molecule 1
-2.22	3.63e-65	AGR2	anterior gradient 2, protein disulp	1.39	8.85e-36	FERMT2	FERM domain containing kindlin 2
-1.72	2.47e-62	FAM83H	family with sequence similarity 83	1.28	2.85e-34	MRC2	mannose receptor C type 2
-1.71	1.04e-59	CGN	cingulin	1.55	8.63e-34	CDH2	cadherin 2
-1.96	5.82e-58	TACSTD2	tumor associated calcium signal tra	1.24	1.09e-33	SPART	spartin
-1.76	7.54e-57	PRSS8	serine protease 8	1.28	2.09e-33	TUBB2A	tubulin beta 2A class Iia
-2.11	2.61e-56	PKP3	plakophilin 3	1.08	3.31e-33	HOOK3	hook microtubule tethering protein
-1.56	4.04e-56	MAP7	microtubule associated protein 7	0.96	7.13e-33	TBC1D13	TBC1 domain family member 13
-2.09	4.28e-55	VAMP8	vesicle associated membrane protein	1.01	1.38e-32	PLCG1	phospholipase C gamma 1
-1.96	1.11e-54	SPINT2	serine peptidase inhibitor, Kunitz	0.22	3.91e-32	TLN1	talin 1
-1.84	2.29e-53	LSR	lipolysis stimulated lipoprotein re	1.34	8.95e-32	SPARC	secreted protein acidic and cystein
-1.33	3.35e-52	ESRP2	epithelial splicing regulatory prot	1.33	9.50e-32	MAGED2	MAGE family member D2
-1.69	5.27e-52	CDH3	cadherin 3	0.97	3.04e-30	SARM1	sterile alpha and TIR motif contain
-1.48	7.62e-52	AP1M2	adaptor related protein complex 1 s	1.24	1.23e-29	STXBP1	syntaxin binding protein 1
-1.7	1.05e-51	S100P	S100 calcium binding protein P	1.15	1.56e-29	AIDA	axin interactor, dorsalization asso
-1.3	1.74e-51	ANKRD22	ankyrin repeat domain 22	1.21	4.46e-29	P3H3	prolyl 3-hydroxylase 3
-1.3	2.09e-51	LRRC1	leucine rich repeat containing 1	1.04	2.00e-27	MAP7D1	MAP7 domain containing 1
-1.7	3.55e-51	SERPINB5	serpin family B member 5	1.53	7.38e-27	DPYSL3	dihydropyrimidinase like 3
-1.53	2.47e-50	LLGL2	LLGL scribble cell polarity complex	1.09	1.40e-26	FKBP7	FKBP prolyl isomerase 7
-1.55	1.80e-49	GALNT3	polypeptide N-acetylgalactosaminylt	1.1	1.53e-26	PPM1F	protein phosphatase, Mg2+/Mn2+ depe
-1.58	1.80e-49	DSC2	desmocollin 2	1.3	4.45e-26	ENO2	enolase 2
-1.47	3.19e-49	SYTL1	synaptotagmin like 1	1.06	4.99e-26	GLIPR2	GLI pathogenesis related 2
-1.5	3.77e-49	RBM47	RNA binding motif protein 47	0.79	6.35e-26	LOX	lysyl oxidase
-1.56	2.66e-45	LAMB3	laminin subunit beta 3	1.21	7.65e-26	ARHGAP17	Rho GTPase activating protein 1

# Top 250 correlation coefficients overrepresentation, CIB1 protein, DB1



# Top 10 kinases for each phosphosite in CIB1



Kinases with affinity greater than 98.5% to CIB1



# Top 15 positive correlation coefficients for CIB1 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

