

BAX

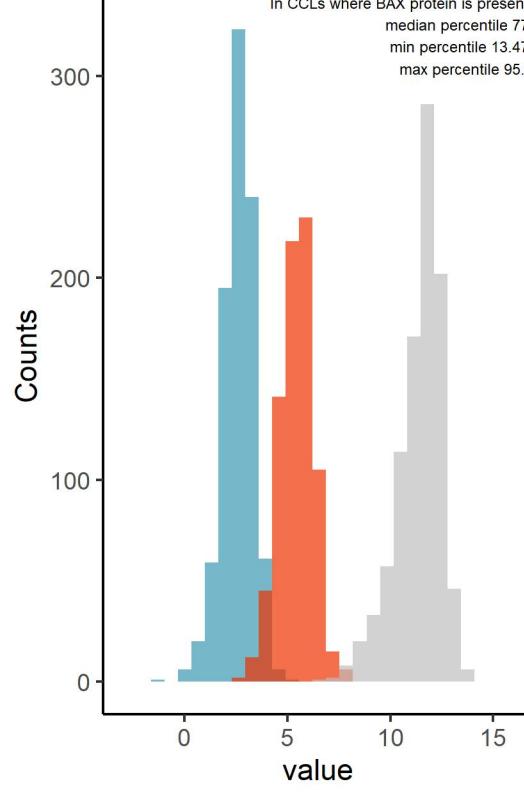
Protein name: BAX ; UNIPROT: Q07812 ; Gene name: BCL2 associated X, apoptosis regulator

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

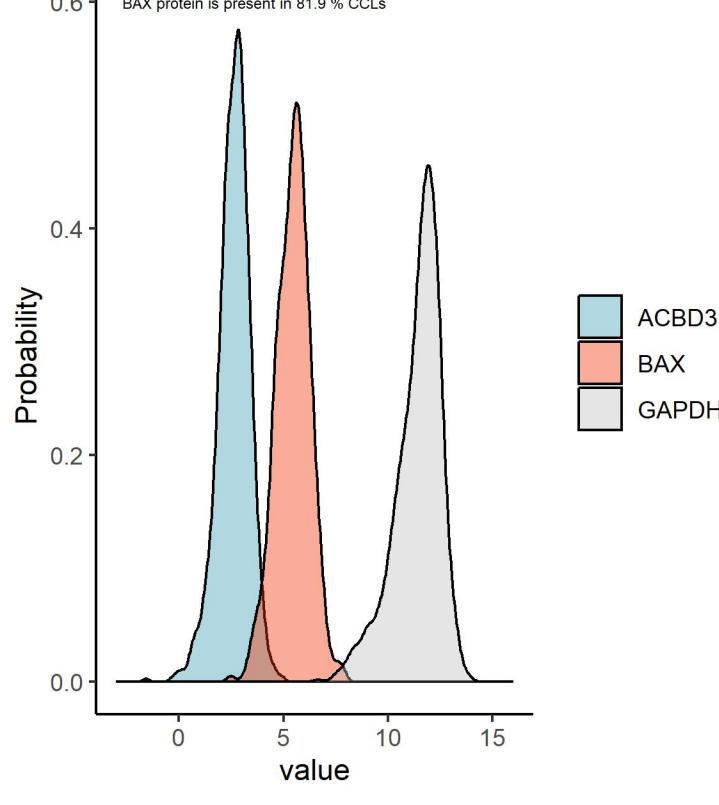
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

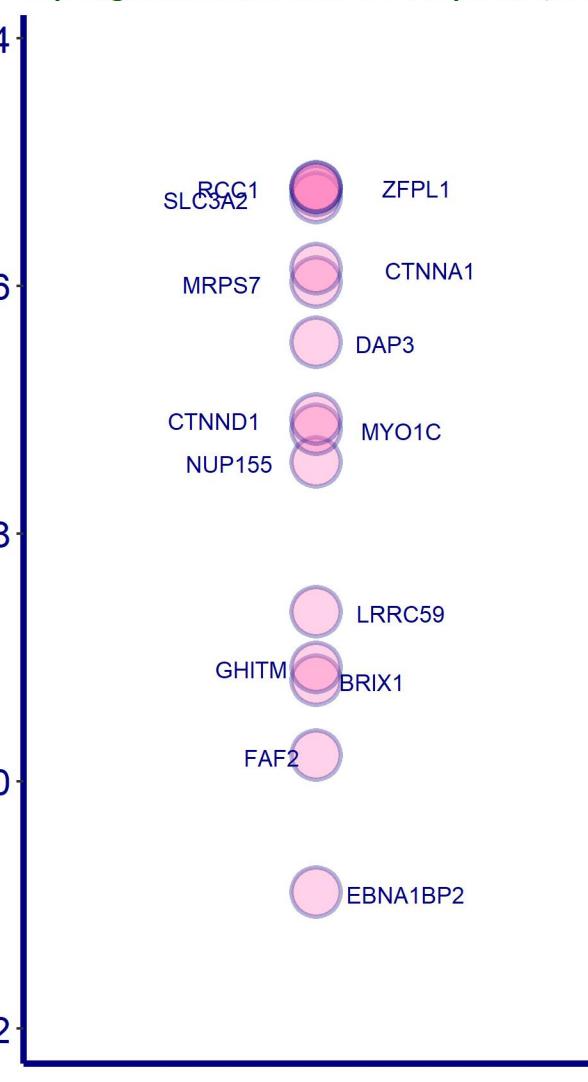
Histogram of BAX protein compared to proteins with low and high abundance



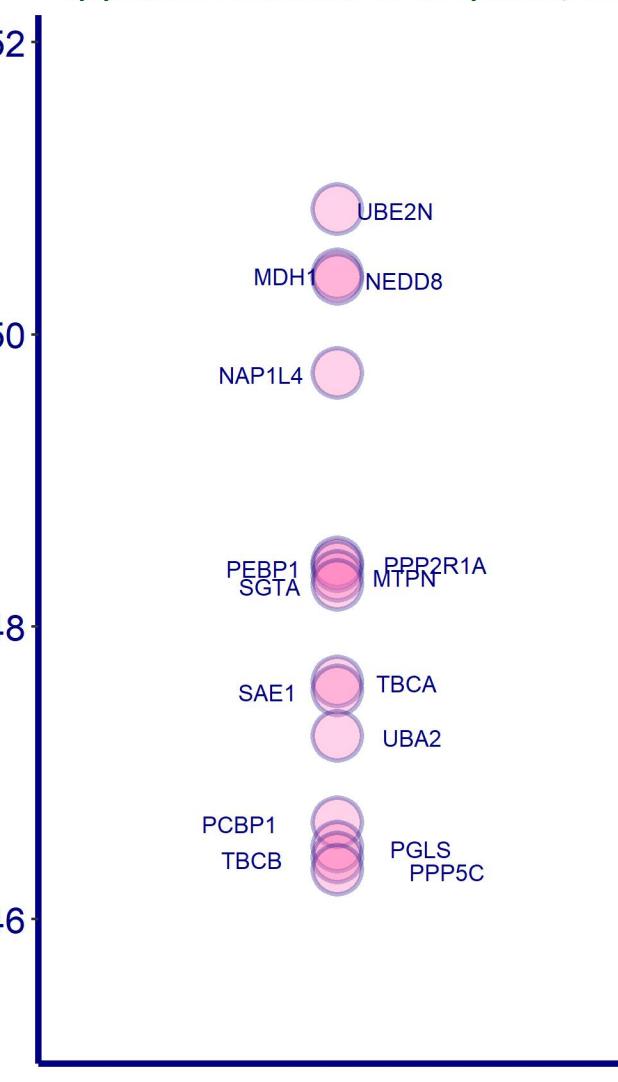
Density plot of BAX protein compared to proteins with low and high abundance



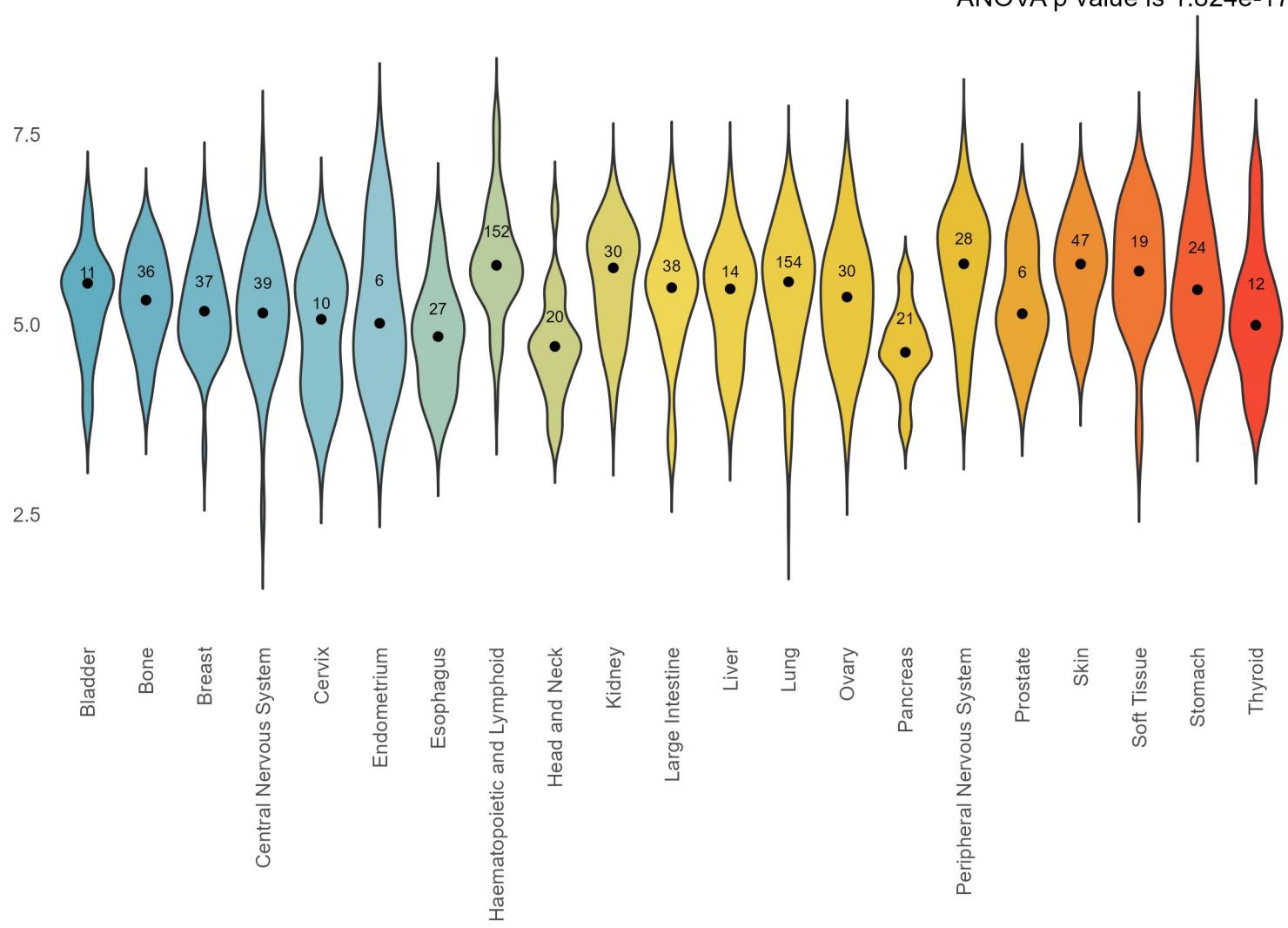
Top negative correlations of BAX protein, DB1



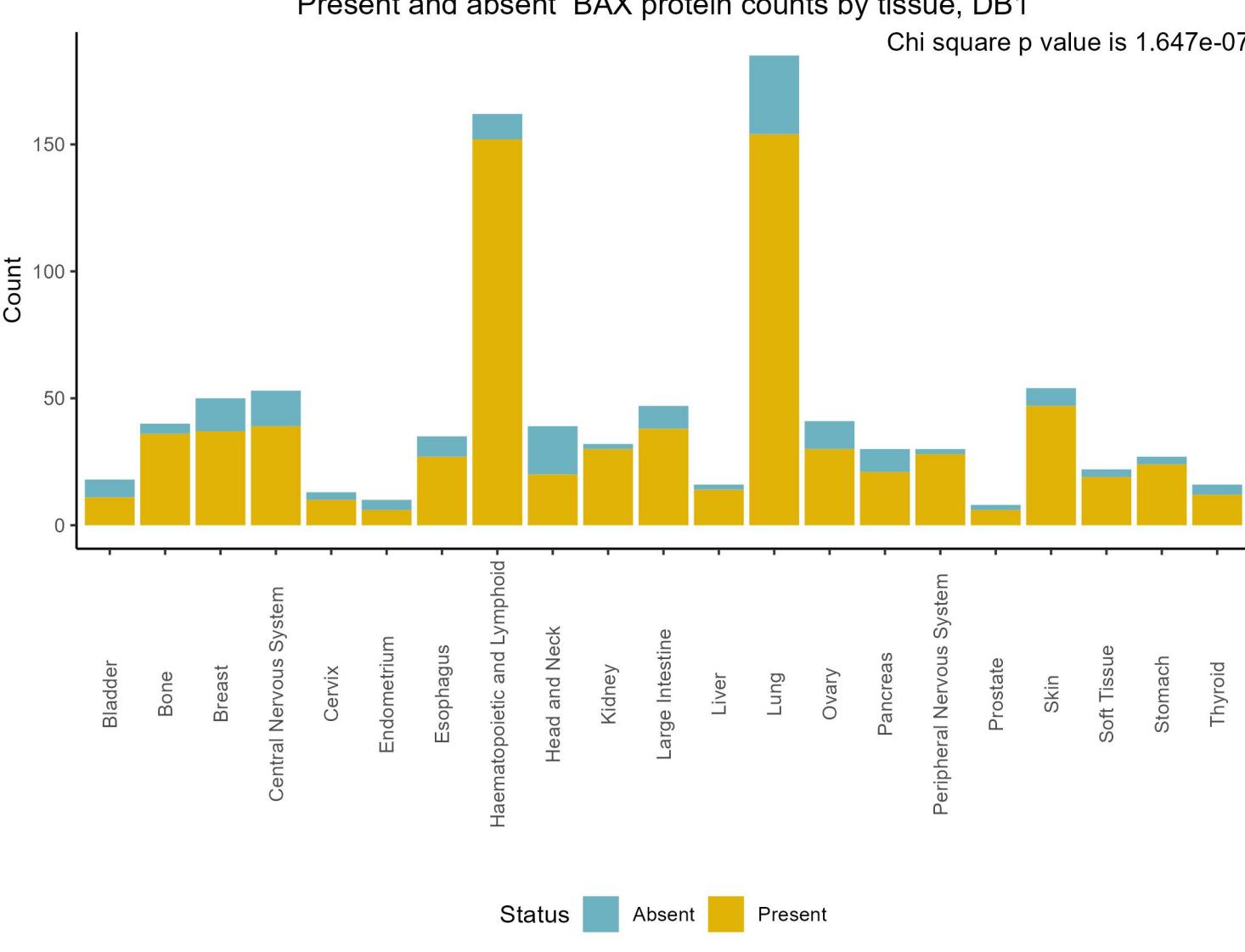
Top positive correlations of BAX protein, DB1



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



Present and absent BAX protein counts by tissue, DB1

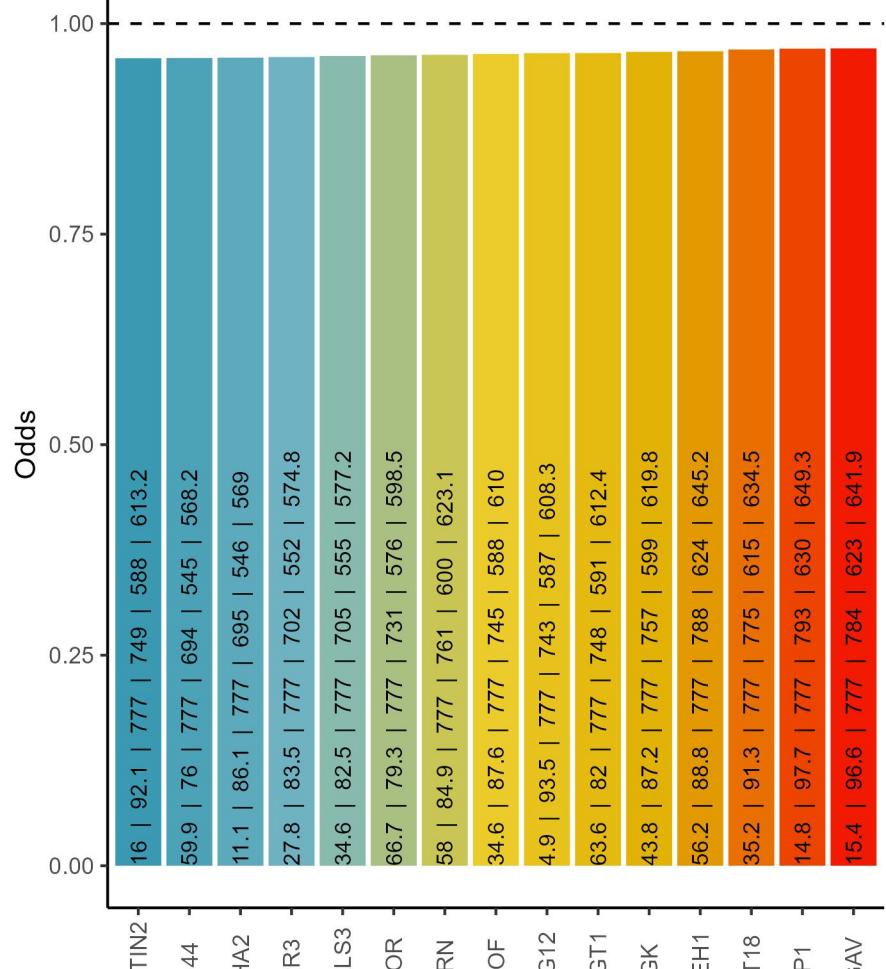


Cooccurrence with BAX protein, DB1

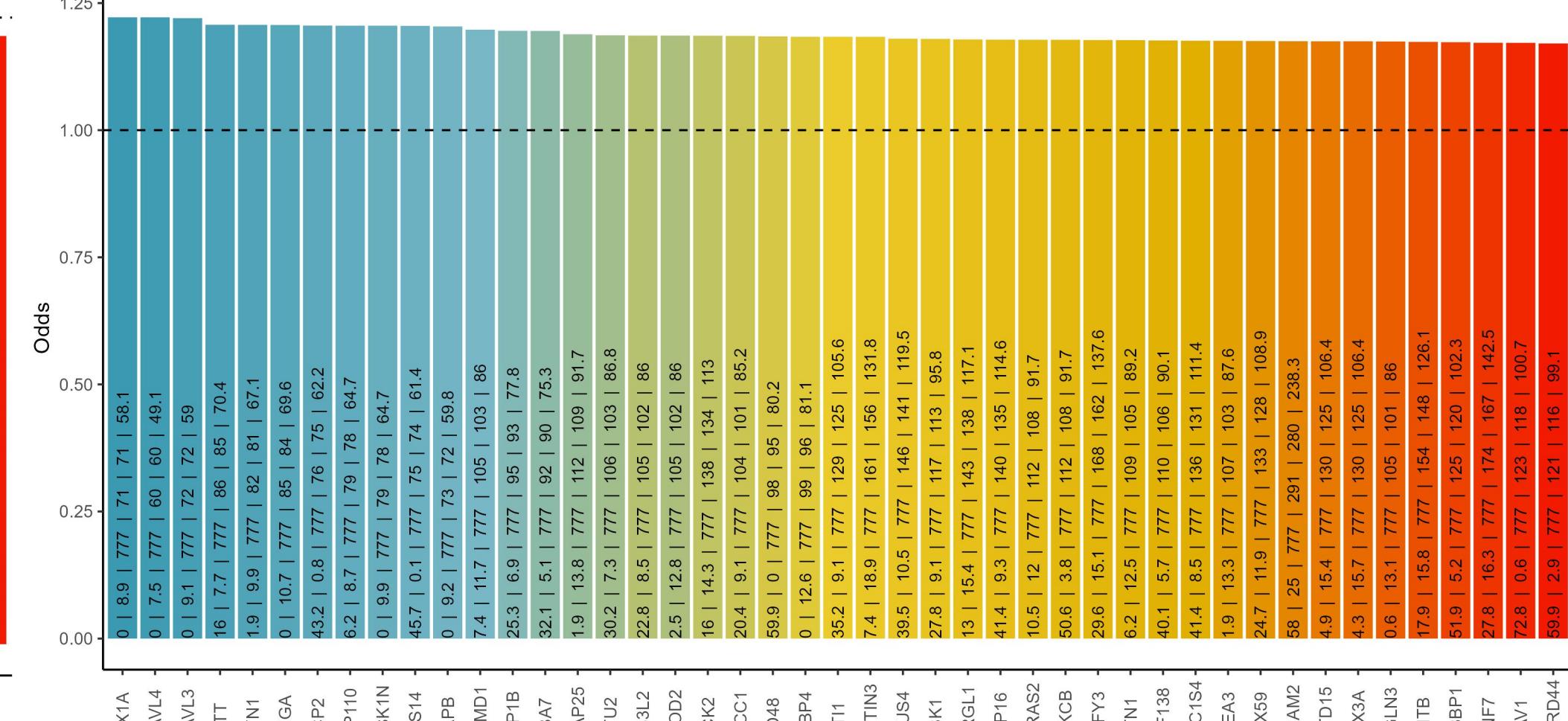
% of BAX in blood cancers: 93.8 ; % of BAX in solid cancers: 79.3

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

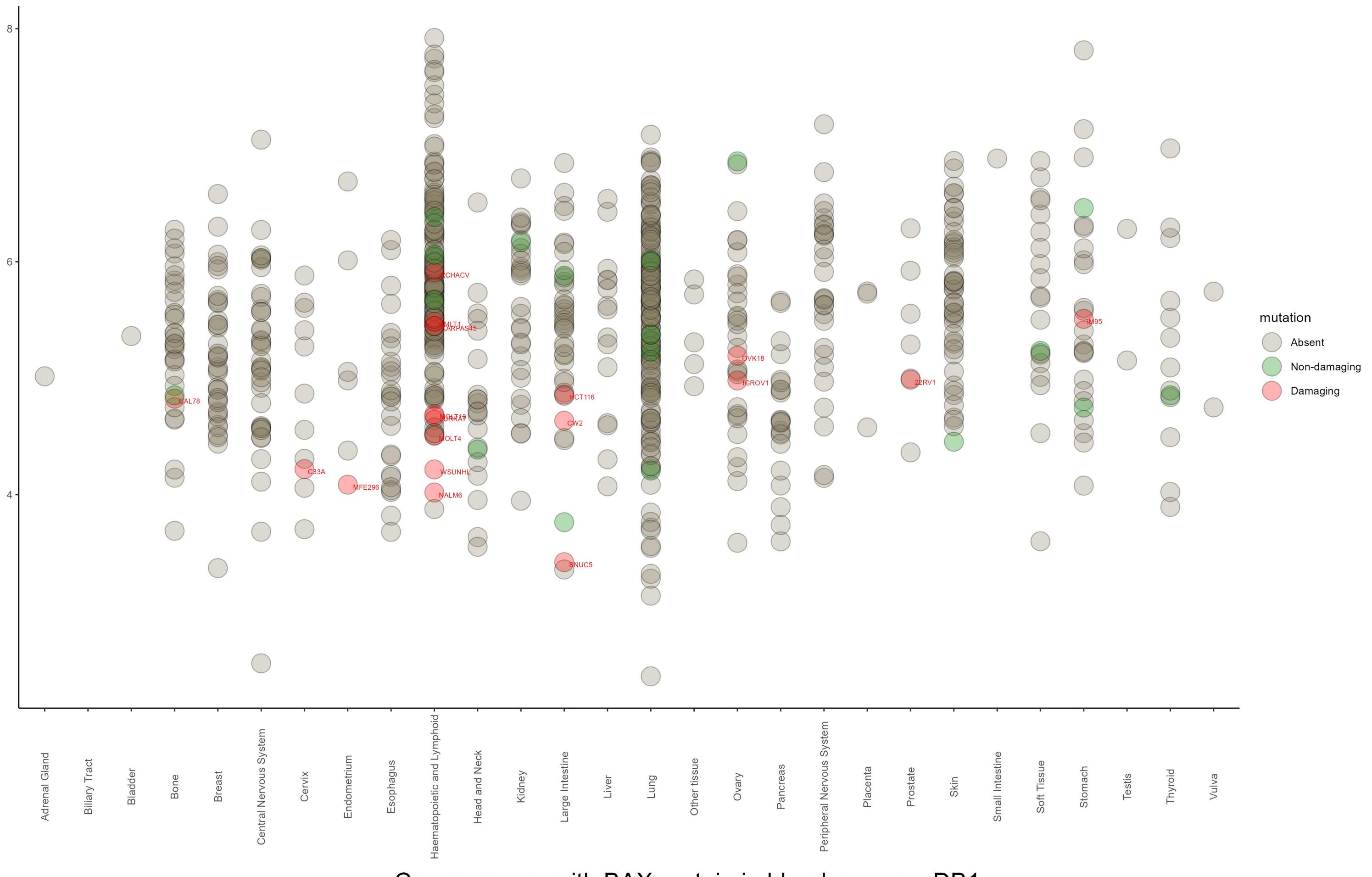
Negative cooccurrence



Positive cooccurrence



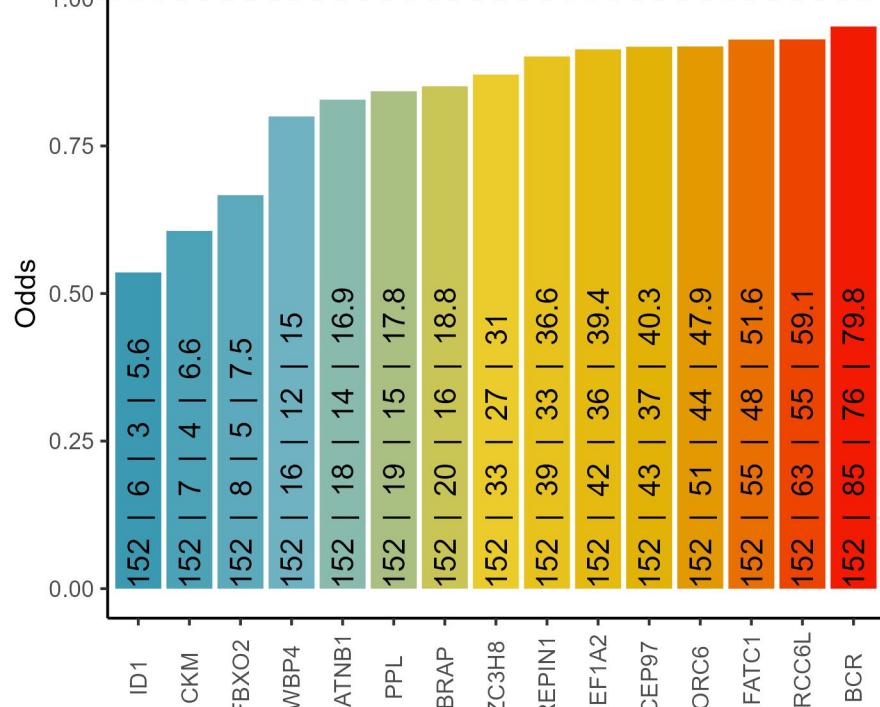
Amount of BAX protein and mutation status by tissue, DB1



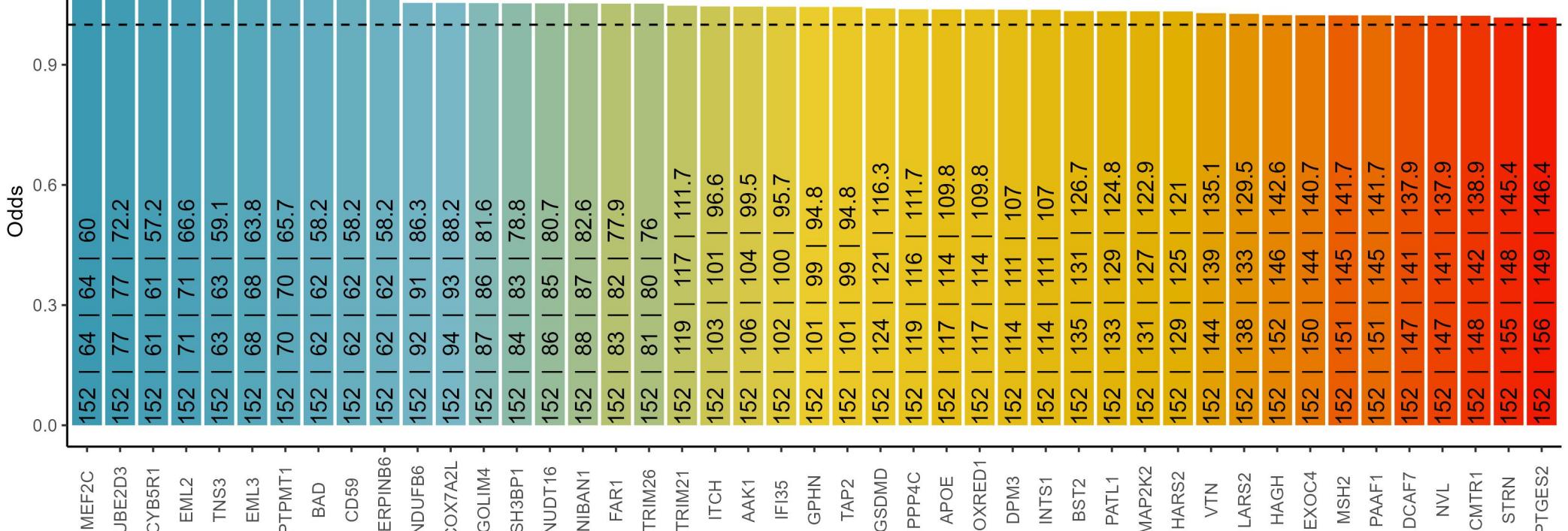
Cooccurrence with BAX protein in blood cancers, DB1

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

Negative cooccurrence



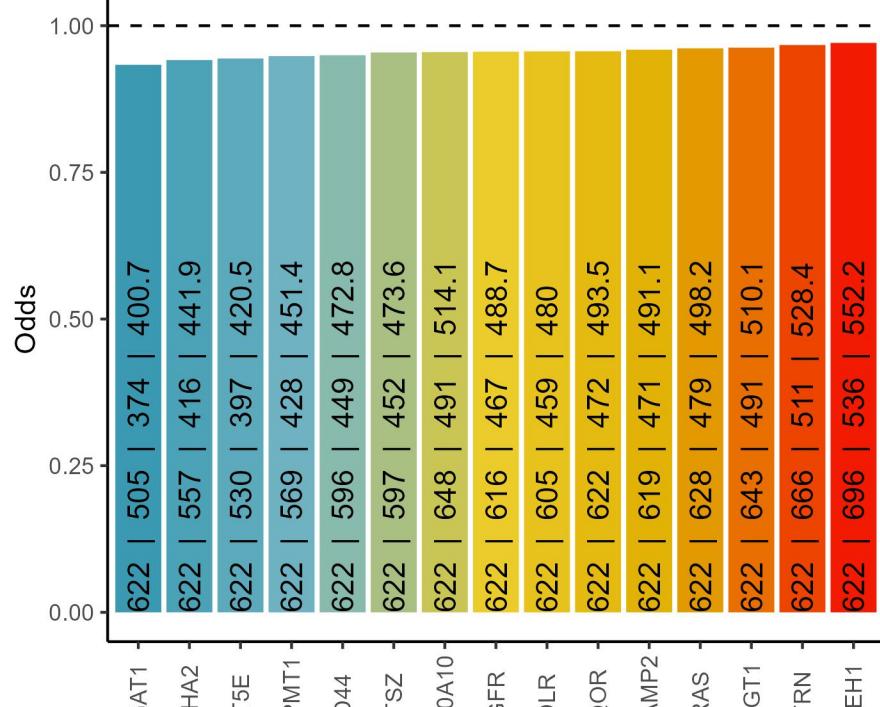
Positive cooccurrence



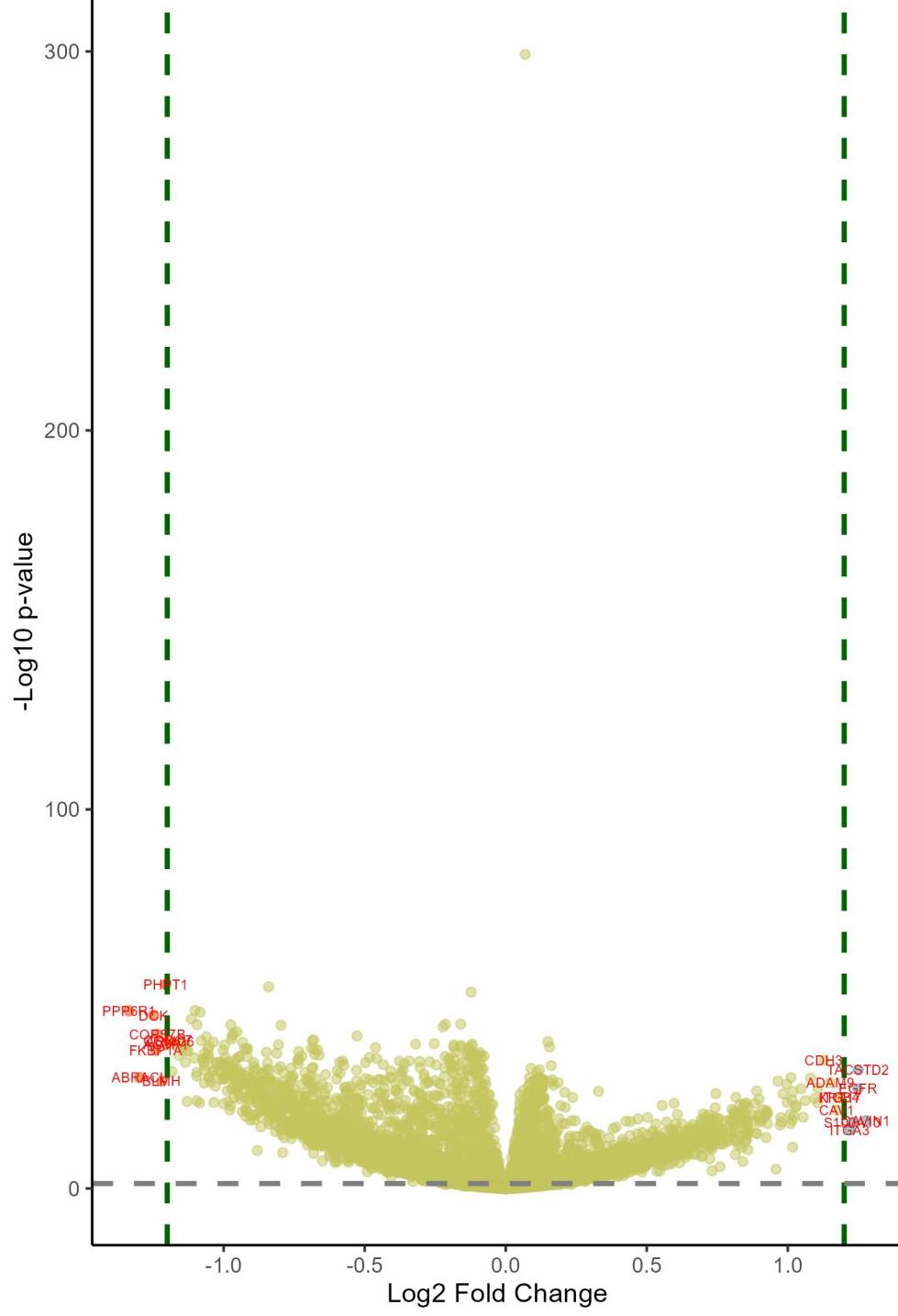
Cooccurrence with BAX protein in solid cancers, DB1

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

Negative cooccurrence

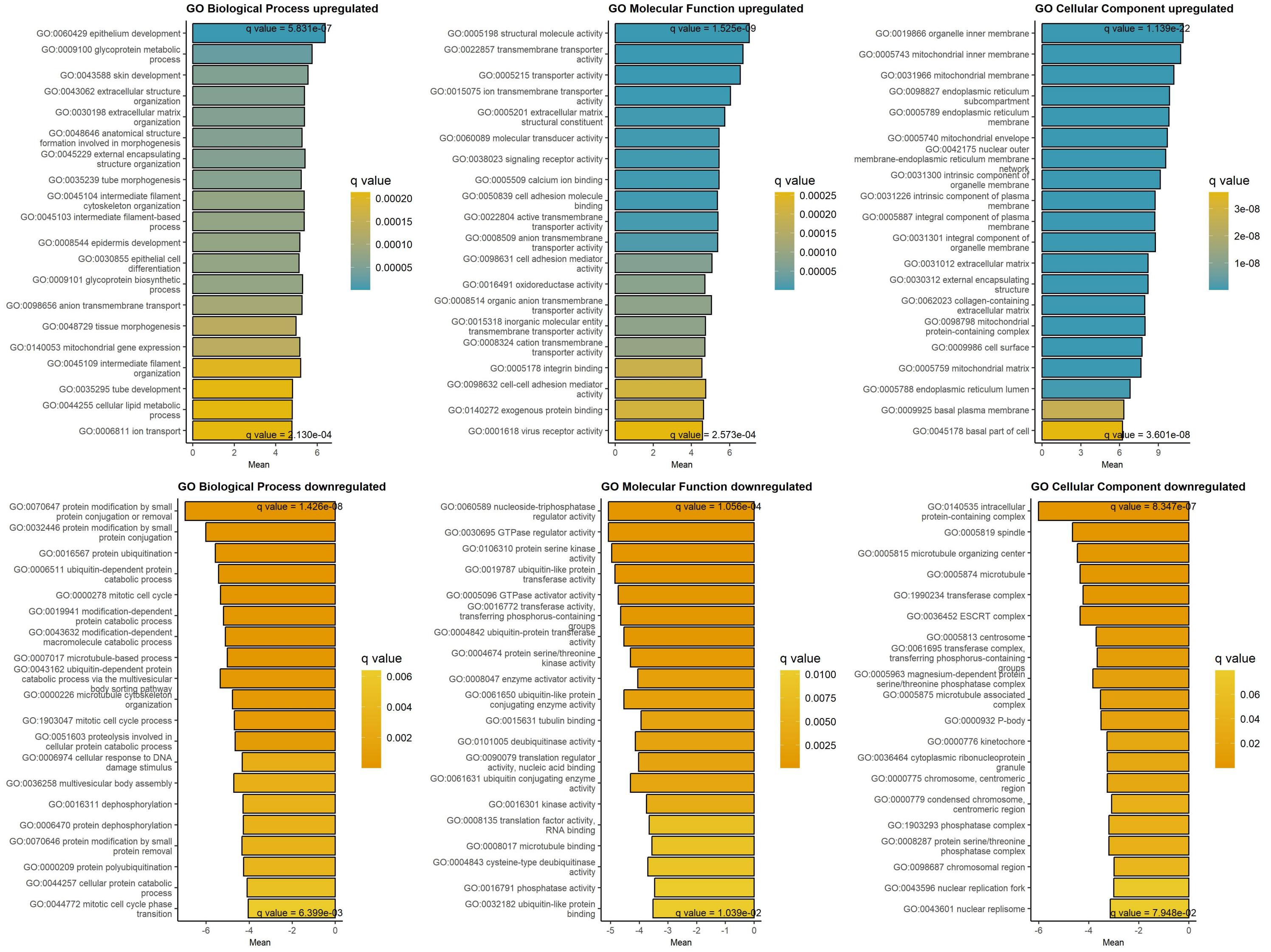


Downregulated at low/absent BAX Upregulated at low/absent BAX



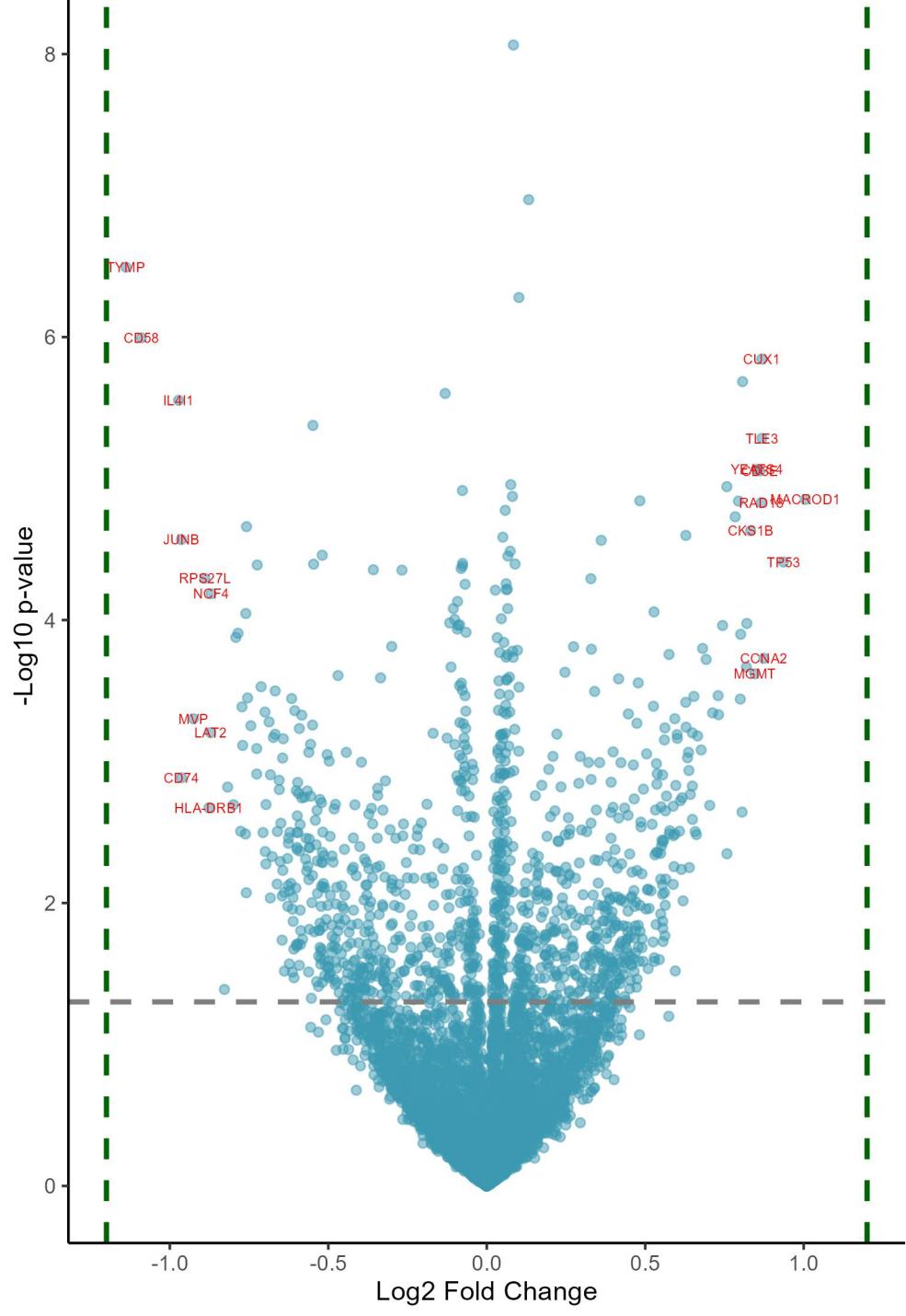
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.34	1.26e-44	PPP6R1	protein phosphatase 6 regulatory su	1.28	1.02e-17	CAVIN1	caveolae associated protein 1
-1.3	1.55e-28	ABRACL	ABRA C-terminal like	1.25	1.98e-30	TACSTD2	tumor associated calcium signal tra
-1.25	1.60e-43	DCK	deoxycytidine kinase	1.25	9.36e-26	EGFR	epidermal growth factor receptor
-1.24	4.00e-35	FKBP1A	FKBP prolyl isomerase 1A	1.23	2.69e-17	S100A10	S100 calcium binding protein A10
-1.23	7.94e-39	COPS7B	COP9 signalosome subunit 7B	1.22	2.20e-15	ITGA3	integrin subunit alpha 3
-1.22	1.16e-27	BLMH	bleomycin hydrolase	1.19	1.92e-23	KRT17	keratin 17
-1.21	3.08e-51	PHPT1	phosphohistidine phosphatase 1	1.18	1.40e-23	ITGB4	integrin subunit beta 4
-1.2	1.92e-36	ACYP1	acylphosphatase 1	1.17	2.16e-20	CAV1	caveolin 1
-1.2	1.89e-37	CORO7	coronin 7	1.15	2.84e-27	ADAM9	ADAM metallopeptidase domain 9
-1.19	4.31e-37	ARMC6	armadillo repeat containing 6	1.13	1.03e-32	CDH3	cadherin 3
-1.18	6.15e-30	UBE2V2	ubiquitin conjugating enzyme E2 V2	1.11	5.73e-26	KRT80	keratin 80
-1.17	3.06e-36	HDHD2	haloacid dehalogenase like hydrolas	1.11	3.06e-22	PPIC	peptidylprolyl isomerase C
-1.16	6.86e-34	NUDT3	nudix hydrolase 3	1.1	2.34e-23	MISP	mitotic spindle positioning
-1.14	9.68e-36	PPM1A	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe	1.08	2.12e-28	LAMB3	laminin subunit beta 3
-1.14	1.66e-36	CZIB	CXXC motif containing zinc binding	1.06	9.10e-23	EPHA2	EPH receptor A2
-1.14	3.16e-36	PDXP	pyridoxal phosphatase	1.05	1.31e-18	ITGA2	integrin subunit alpha 2
-1.14	3.12e-32	STK4	serine/threonine kinase 4	1.05	9.18e-26	F3	coagulation factor III, tissue fact
-1.13	7.54e-35	PPM1B	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe	1.03	1.45e-21	GPX8	glutathione peroxidase 8 (putative)
-1.13	1.48e-22	ZNF706	zinc finger protein 706	1.03	3.73e-21	KRT5	keratin 5
-1.13	5.32e-35	SMAP2	small ArfGAP2	1.02	6.97e-19	PKP3	plakophilin 3
-1.11	1.41e-42	AARSD1	alanyl-tRNA synthetase domain conta	1.02	4.61e-25	SDC4	syndecan 4
-1.1	2.55e-33	PIN1	peptidylprolyl cis/trans isomerase,	1.02	4.46e-11	GNG12	G protein subunit gamma 12
-1.1	1.15e-44	DOHH	deoxyhypusine hydroxylase	1.02	7.78e-18	GPRC5A	G protein-coupled receptor class C
-1.1	7.05e-29	PSME3IP1	proteasome activator subunit 3 inte	1.01	6.03e-23	RRAS	RAS related
-1.1	8.63e-30	RPIA	ribose 5-phosphate isomerase A	1.01	1.64e-28	ERGIC2	ERGIC and golgi 2
-1.09	9.54e-23	CORO1A	coronin 1A	1.01	5.19e-17	S100A16	S100 calcium binding protein A16
-1.09	3.07e-41	CHMP4A	charged multivesicular body protein	1.01	2.14e-19	S100A14	S100 calcium binding protein A14
-1.09	3.48e-22	NACA2	nascent polypeptide associated comp	1	2.49e-22	TPBG	trophoblast glycoprotein
-1.08	2.63e-44	CASP3	caspase 3	1	5.98e-27	FNDC3B	fibronectin type III domain contain

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



Differentially expressed proteins in blood cancers at absence/low amount of BAX , DB1

p-value < 0.05 & logFC > 1.2

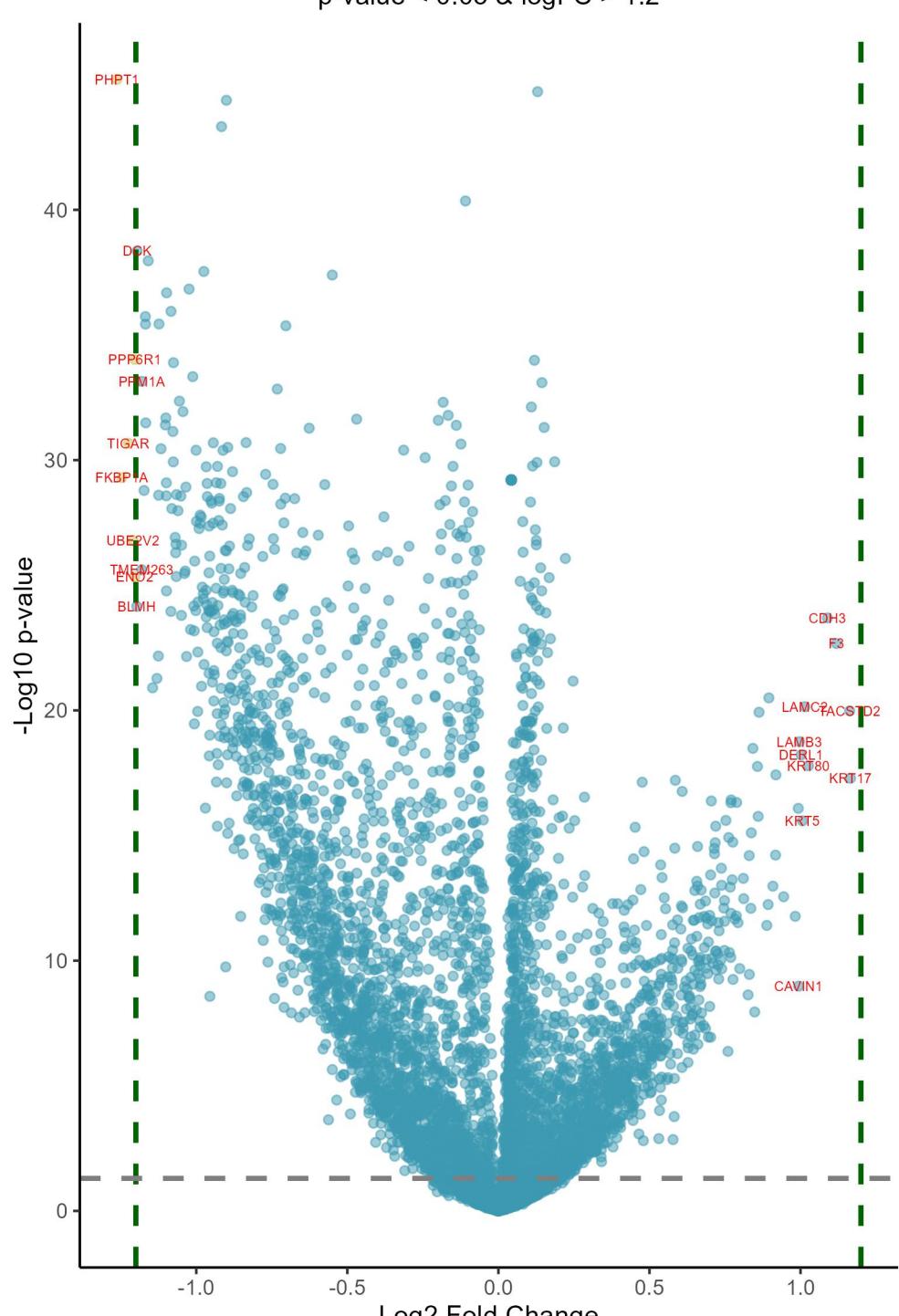


Downregulated in blood cancers at low/absent BAX Upregulated in blood cancers at low/absent BAX

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.14	5.33e-04	TYMP	thymidine phosphorylase	1.01	4.47e-03	MACROD1	mono-ADP ribosylhydrolase 1
-1.09	1.12e-03	CD58	CD58 molecule	0.94	7.03e-03	TP53	tumor protein p53
-0.97	1.86e-03	IL4I1	interleukin 4 induced 1	0.87	1.53e-02	CCNA2	cyclin A2
-0.96	6.05e-03	JUNB	JunB proto-oncogene, AP-1 transcript	0.87	2.88e-03	TLE3	TLE family member 3, transcriptional
-0.96	4.12e-02	CD74	CD74 molecule	0.87	1.36e-03	CUX1	cut like homeobox 1
-0.93	2.63e-02	MVP	major vault protein	0.87	4.47e-03	RAD18	RAD18 E3 ubiquitin protein ligase
-0.89	7.71e-03	RPS27L	ribosomal protein S27 like	0.86	4.19e-03	CD3E	CD3 epsilon subunit of T-cell receptor
-0.88	5.35e-02	HLA-DRB1	major histocompatibility complex, c	0.85	4.19e-03	YEATS4	YEATS domain containing 4
-0.87	2.94e-02	LAT2	linker for activation of T cells fa	0.85	1.85e-02	MGMT	O-6-methylguanine-DNA methyltransferase
-0.87	8.66e-03	NCF4	neutrophil cytosolic factor 4	0.83	5.97e-03	CKS1B	CDC28 protein kinase regulatory sub
-0.83	2.45e-01	LGALS1	galectin 1	0.82	1.17e-02	MAZ	MYC associated zinc finger protein
-0.82	4.44e-02	CTTN	cortactin	0.82	1.70e-02	SCML2	Scm polycomb group protein like 2
-0.8	5.19e-02	STOM	stomatin	0.81	1.72e-03	CCNB1	cyclin B1
-0.79	1.30e-02	ACOT9	acyl-CoA thioesterase 9	0.81	5.44e-02	DBN1	drebrin 1
-0.78	1.27e-02	MYO1C	myosin IC	0.8	1.27e-02	MAP1A	microtubule associated protein 1A
-0.78	6.60e-02	CTSZ	cathepsin Z	0.8	2.21e-02	LEF1	lymphoid enhancer binding factor 1
-0.77	2.42e-02	ABHD12	abhydrolase domain containing 12, I	0.79	4.47e-03	MORC2	MORC family CW-type zinc finger 2
-0.77	3.22e-02	ENTPD1	ectonucleoside triphosphate diphosphorylase	0.78	5.16e-03	OGFOD1	2-oxoglutarate and iron dependent oxygenase
-0.76	6.67e-02	PLEK	pleckstrin	0.76	7.85e-02	IGF2BP1	insulin like growth factor 2 mRNA binding protein b
-0.76	1.09e-02	MYO6	myosin VI	0.76	4.47e-03	CKAP2	cytoskeleton associated protein 2
-0.76	1.09e-01	CD70	CD70 molecule	0.74	1.17e-02	CCDC12	coiled-coil domain containing 12
-0.76	5.82e-03	EML2	EMAP like 2	0.73	2.52e-02	CFAP298	cilia and flagella associated protein
-0.75	2.21e-02	PRKCD	protein kinase C delta	0.73	2.17e-02	CHEK1	checkpoint kinase 1
-0.74	2.81e-02	ACSL1	acyl-CoA synthetase long chain family	0.71	2.51e-02	TCF12	transcription factor 12
-0.73	4.02e-02	PLXNB2	plexin B2	0.7	5.22e-02	TCF3	transcription factor 3
-0.73	3.32e-02	SPRYD4	SPRY domain containing 4	0.69	1.54e-02	KIF20A	kinesin family member 20A
-0.72	7.03e-03	NCF2	neutrophil cytosolic factor 2	0.68	1.46e-02	BCL11B	BAF chromatin remodeling complex sub
-0.71	2.02e-02	TOR1A	torsin family 1 member A	0.68	3.34e-02	TLE5	TLE family member 5, transcriptional
-0.71	6.60e-02	MX1	MX dynamin like GTPase 1	0.67	2.96e-02	RNF138	ring finger protein 138

Differentially expressed proteins in solid cancers at absence/low amount of BAX , DB1

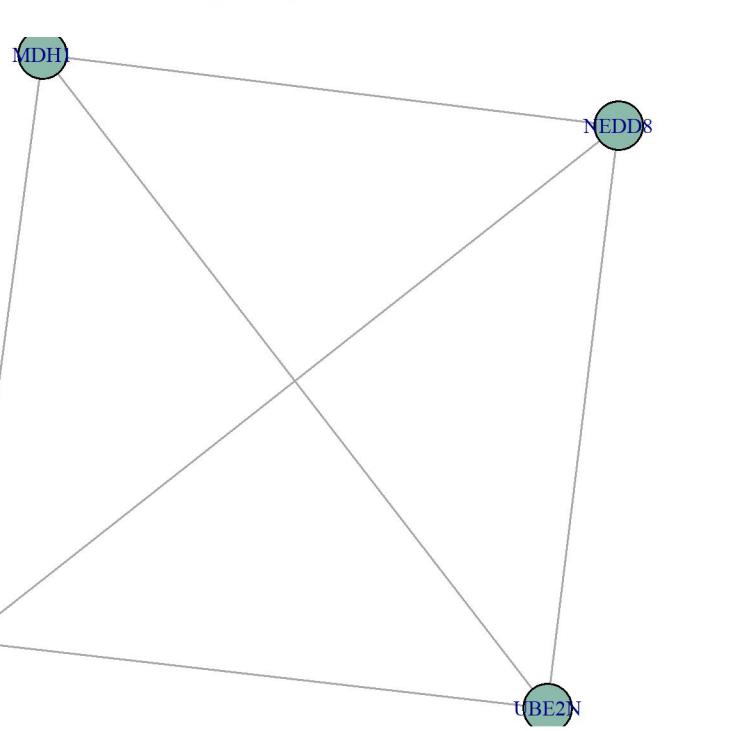
p-value < 0.05 & logFC > 1.2



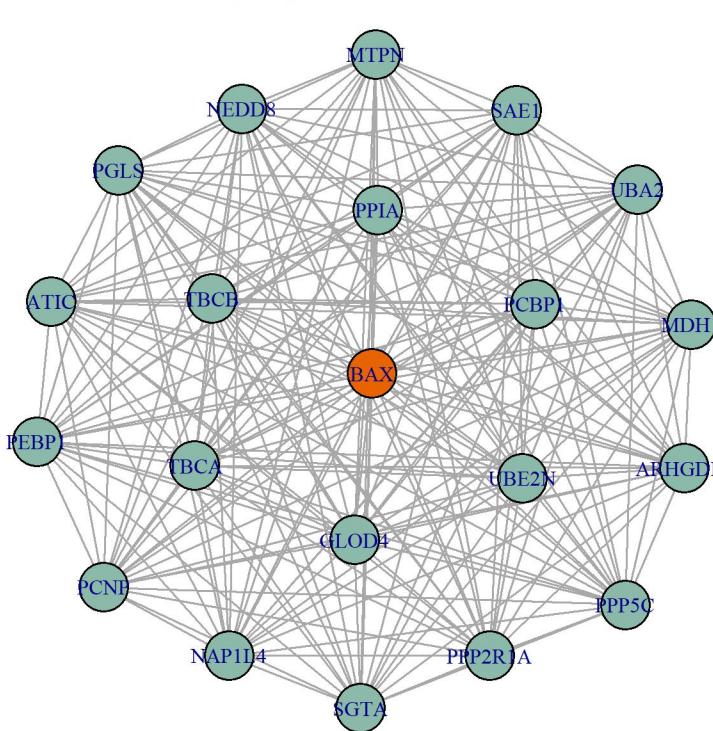
Downregulated in solid cancers at low/absent BAX Upregulated in solid cancers at low/absent BAX

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.26	2.05e-42	PHPT1	phosphohistidine phosphatase 1	1.17	4.96e-17	KRT17	keratin 17
-1.25	2.98e-28	FKBP1A	FKBP prolyl isomerase 1A	1.16	1.42e-19	TACSTD2	tumor associated calcium signal tra
-1.22	3.45e-29	TIGAR	TP53 induced glycolysis regulatory	1.12	3.92e-22	F3	coagulation factor III, tissue fact
-1.21	5.39e-26	UBE2V2	ubiquitin conjugating enzyme E2 V2	1.09	4.38e-23	CDH3	cadherin 3
-1.2	3.53e-32	PPP6R1	protein phosphatase 6 regulatory su	1.03	1.66e-17	KRT80	keratin 80
-1.2	1.29e-24	ENO2	enolase 2	1.01	9.86e-20	LAMC2	laminin subunit gamma 2
-1.2	1.65e-23	BLMH	bleomycin hydrolase	1.01	2.08e-15	KRT5	keratin 5
-1.2	4.17e-36	DCK	deoxyctydine kinase	1	6.40e-18	DERL1	derlin 1
-1.18	6.89e-25	TMEM263	transmembrane protein 263	1	2.02e-18	LAMB3	laminin subunit beta 3
-1.18	2.15e-31	PPM1A	protein phosphatase, Mg2+/Mn2+ depe	0.99	4.02e-09	CAVIN1	caveole associated protein 1
-1.17	7.28e-28	PIN1	peptidylprolyl cis/trans isomerase,	0.99	6.93e-16	THBS1	thrombospondin 1
-1.17	8.76e-34	WASL	WASP like actin nucleation promotin	0.98	8.79e-12	CAV1	caveolin 1
-1.17	1.53e-33	ATOX1	antioxidant 1 copper chaperone	0.94	1.60e-12	ITGB4	integrin subunit beta 4
-1.17	6.54e-30	CZIB	CXXC motif containing zinc binding	0.92	3.68e-17	JUNB	JunB proto-oncogene, AP-1 transcrip
-1.16	9.04e-36	ADI1	acireductone dioxygenase 1	0.92	4.16e-14	EGFR	epidermal growth factor receptor
-1.14	1.88e-20	ZNF706	zinc finger protein 706	0.91	6.35e-13	MISP	mitotic spindle positioning
-1.13	8.27e-21	ABRACL	ABRA C-terminal like	0.9	4.54e-20	PTPMT1	protein tyrosine phosphatase mitoch
-1.13	1.16e-21	TUBB2B	tubulin beta 2B class IIb	0.89	3.17e-12	S100A10	S100 calcium binding protein A10
-1.12	1.11e-27	ACYP1	acylphosphatase 1	0.89	1.95e-11	S100A14	S100 calcium binding protein A14
-1.12	1.53e-33	AARS1	alanyl-tRNA synthetase domain conta	0.86	1.59e-19	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-b
-1.12	5.18e-29	COPS7B	COP9 signalosome subunit 7B	0.86	1.40e-15	ITGB6	integrin subunit beta 6
-1.1	7.70e-30	CCDC43	coiled-coil domain containing 43	0.86	1.77e-17	ERGIC2	ERGIC and golgi 2
-1.1	4.59e-30	SMAD4	SMAD family member 4	0.85	3.87e-08	CD44	CD44 molecule (Indian blood group)
-1.1	1.16e-27	PPM1B	protein phosphatase, Mg2+/Mn2+ depe	0.84	3.59e-18	DHRS7B	dehydrogenase/reductase 7B
-1.1	3.81e-28	FN3KRP	fructosamine 3 kinase related prote	0.84	5.94e-15	SDC4	syndecan 4
-1.1	4.31e-24	ITPA	inosine triphosphatase	0.84	4.42e-12	SQOR	sulfide quinone oxidoreductase
-1.1	1.15e-34	DOHH	deoxyhypusine hydroxylase	0.83	1.44e-09	GPRC5A	G protein-coupled receptor class C
-1.08	2.51e-23	TUBB2A	tubulin beta 2A class IIa	0.83	4.35e-14	TGFBI	transforming growth factor beta ind
-1.08	5.81e-34	CASP3	caspase 3	0.83	8.69e-09	ITGA3	integrin subunit alpha 3

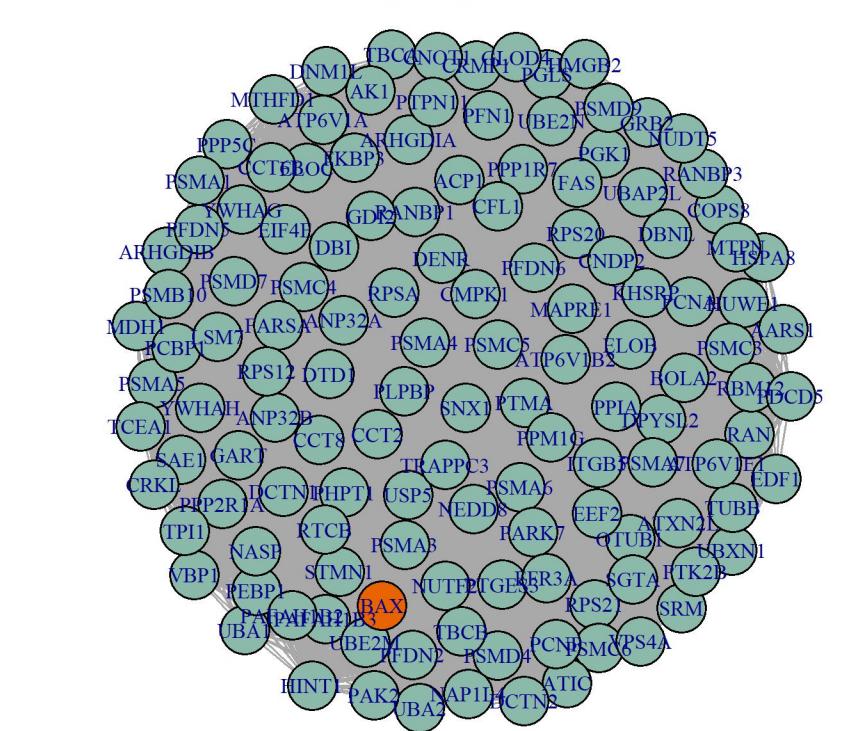
BAX network, DB1, all Pearson r > 0.5

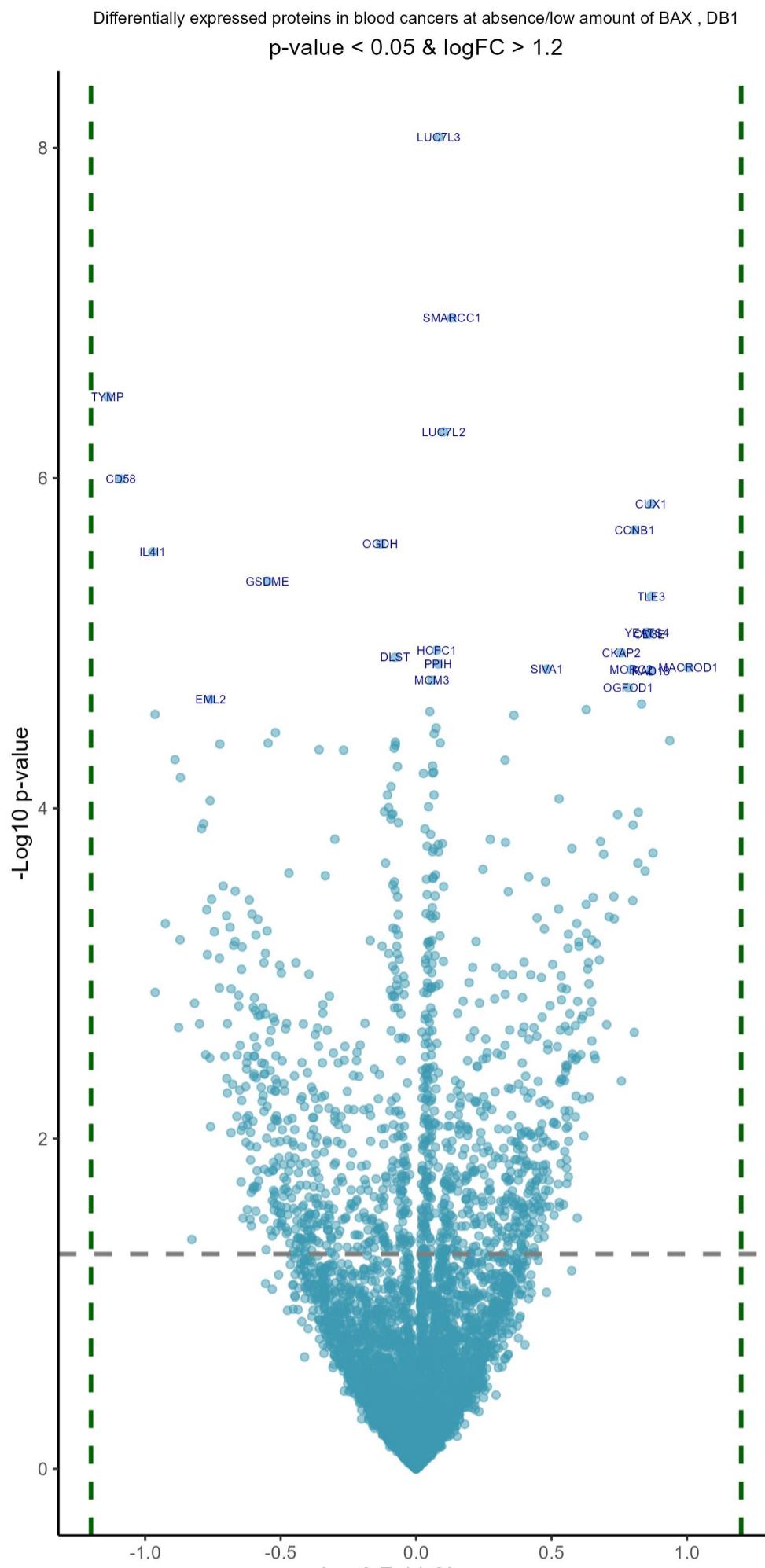


BAX network, DB1, all Pearson r > 0.45

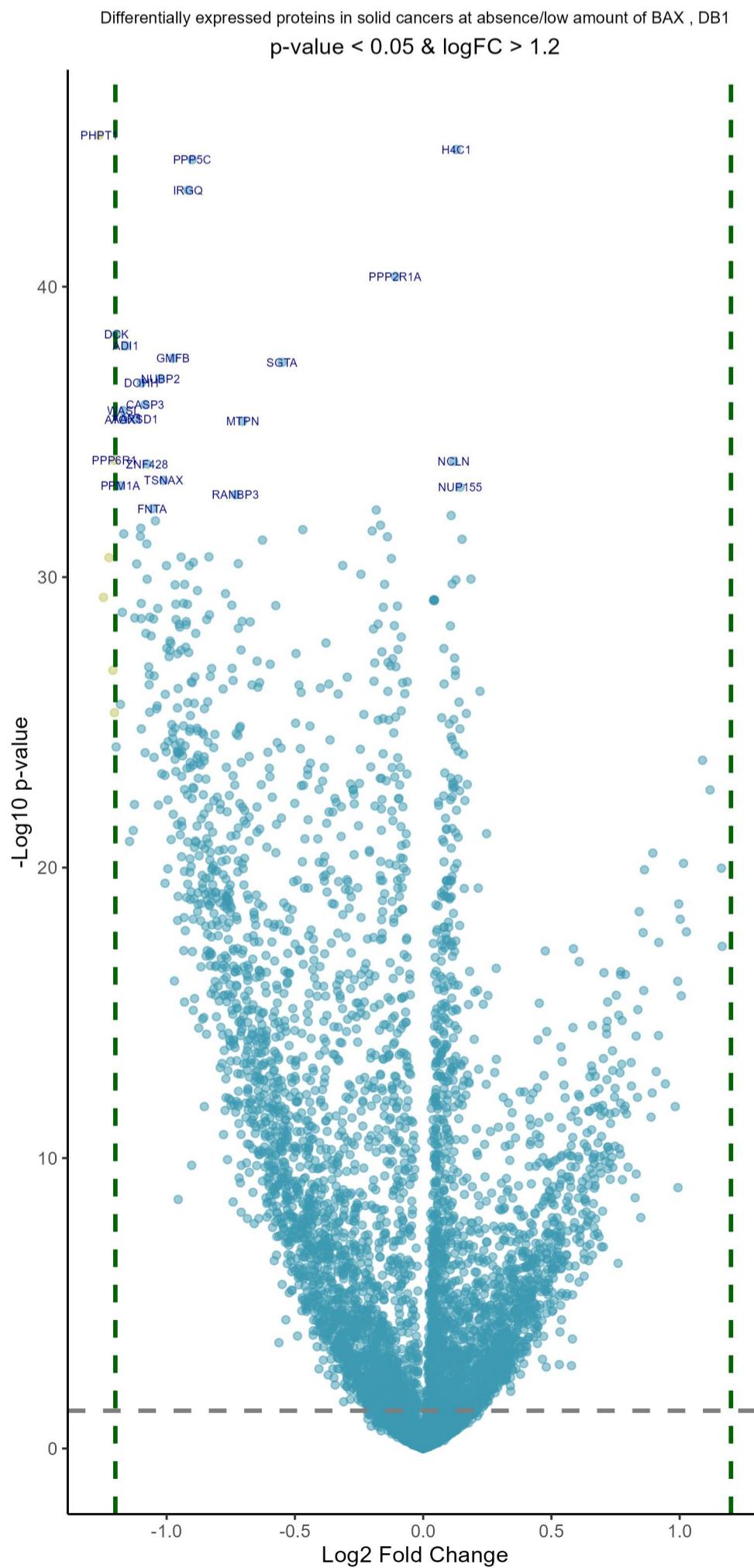


BAX network, DB1, all Pearson r > 0.4

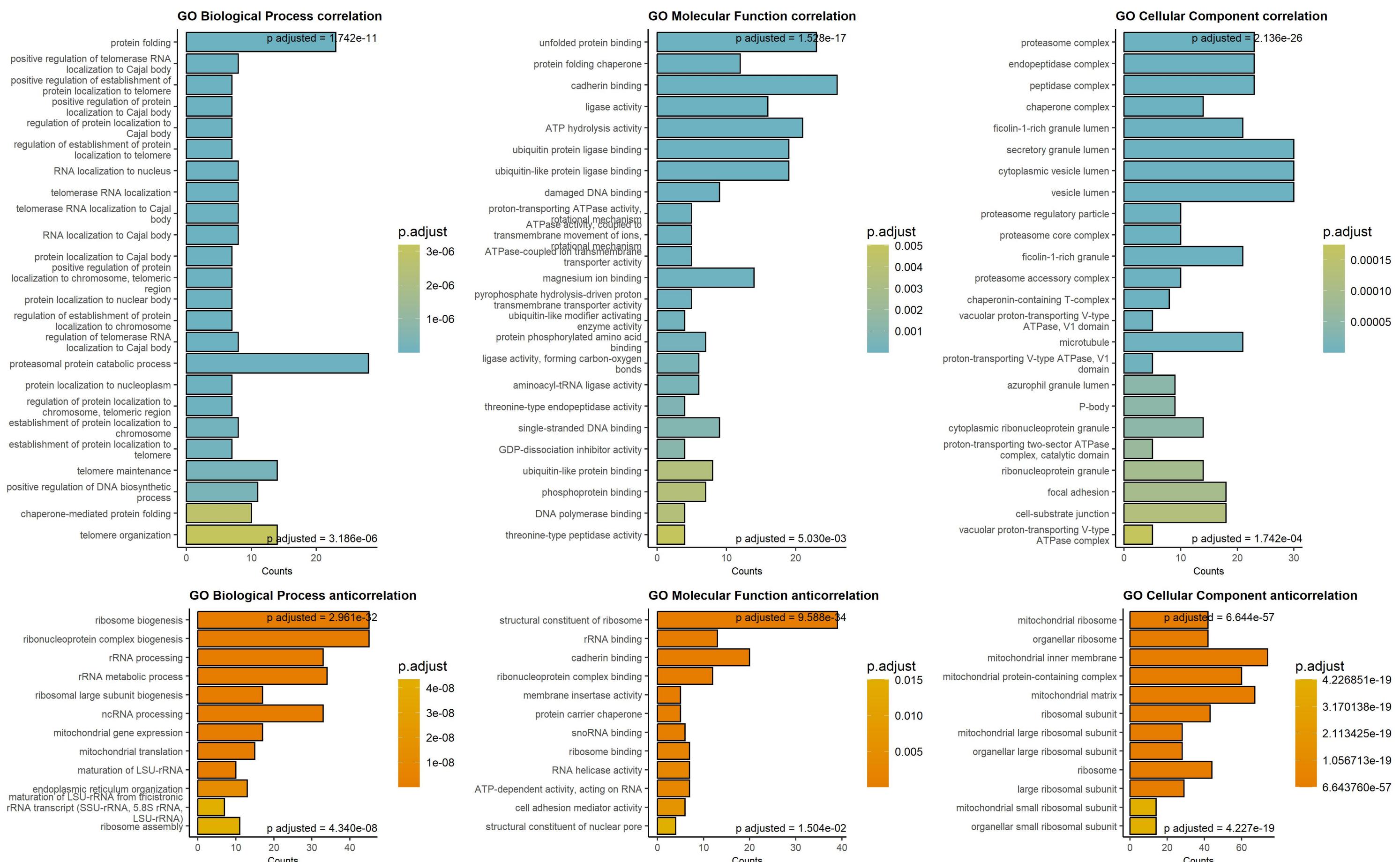




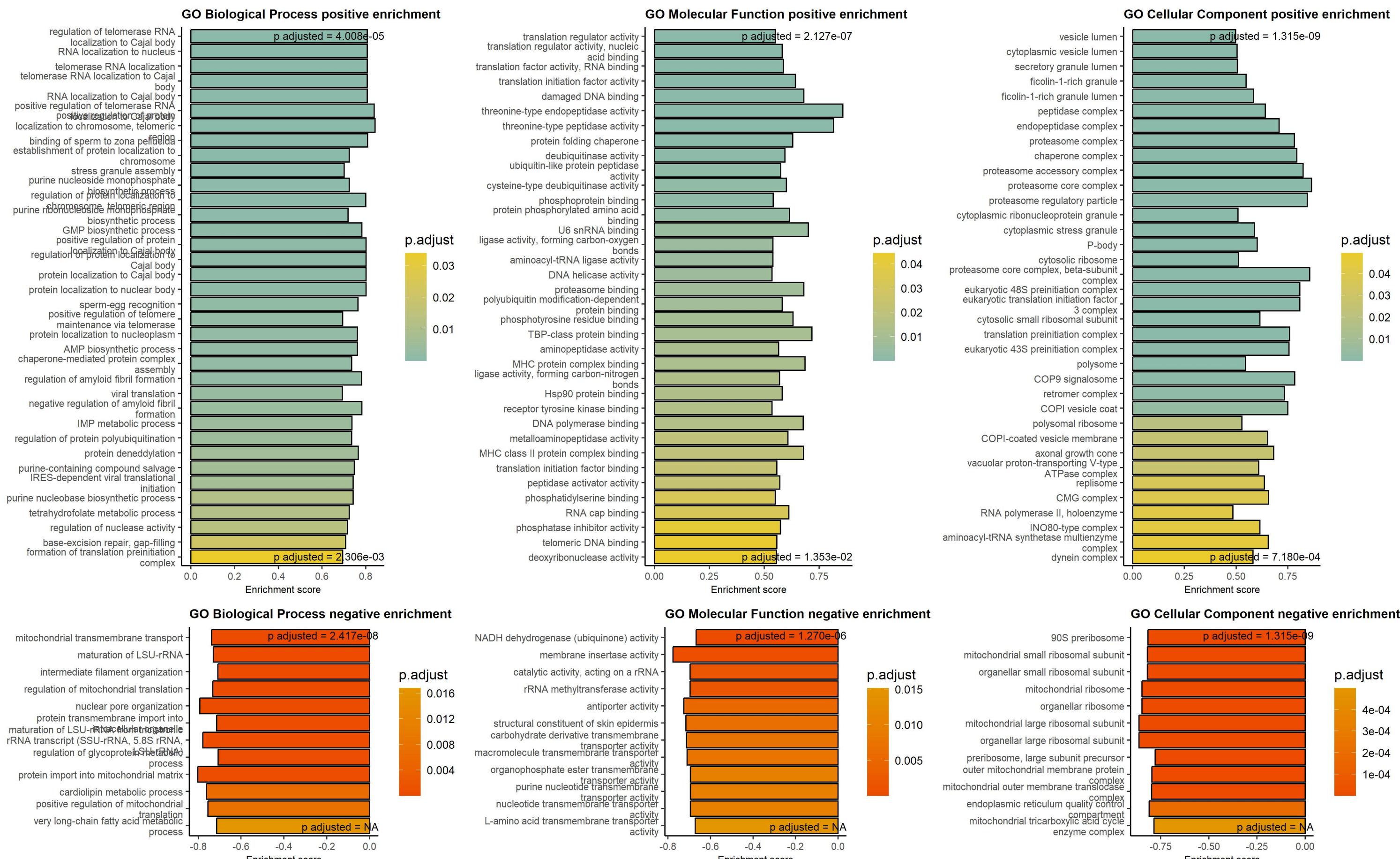
Sorted by p values!							
Downregulated in blood cancers at low/absent BAX				Upregulated in blood cancers at low/absent BAX			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.14	5.33e-04	TYMP	thymidine phosphorylase	0.08	2.87e-05	LUC7L3	LUC7 like 3 pre-mRNA splicing facto
-1.09	1.12e-03	CD58	CD58 molecule	0.13	2.37e-04	SMARCC1	SWI/SNF related, matrix associated,
-0.13	1.85e-03	OGDH	oxoglutarate dehydrogenase	0.1	6.98e-04	LUC7L2	LUC7 like 2, pre-mRNA splicing fact
-0.97	1.86e-03	IL4I1	interleukin 4 induced 1	0.87	1.36e-03	CUX1	cut like homeobox 1
-0.55	2.55e-03	GSDME	gasdermin E	0.81	1.72e-03	CCNB1	cyclin B1
-0.08	4.47e-03	DLST	dihydrolipoamide S-succinyltransfer	0.87	2.88e-03	TLE3	TLE family member 3, transcriptiona
-0.76	5.82e-03	EML2	EMAP like 2	0.85	4.19e-03	YEATS4	YEATS domain containing 4
-0.96	6.05e-03	JUNB	JunB proto-oncogene, AP-1 transcrip	0.86	4.19e-03	CD3E	CD3 epsilon subunit of T-cell recep
-0.52	7.03e-03	FLOT2	flotillin 2	0.08	4.47e-03	HCFC1	host cell factor C1
-0.08	7.03e-03	NDUFS3	NADH:ubiquinone oxidoreductase core	0.76	4.47e-03	CKAP2	cytoskeleton associated protein 2
-0.55	7.03e-03	GM2A	GM2 ganglioside activator	0.08	4.47e-03	PPIH	peptidylprolyl isomerase H
-0.72	7.03e-03	NCF2	neutrophil cytosolic factor 2	1.01	4.47e-03	MACROD1	mono-ADP ribosylhydrolase 1
-0.08	7.03e-03	LAMTOR1	late endosomal/lysosomal adaptor, M	0.48	4.47e-03	SIVA1	SIVA1 apoptosis inducing factor
-0.08	7.03e-03	ARPC4	actin related protein 2/3 complex s	0.79	4.47e-03	MORC2	MORC family CW-type zinc finger 2
-0.36	7.03e-03	HAAO	3-hydroxyanthranilate 3,4-dioxygena	0.87	4.47e-03	RAD18	RAD18 E3 ubiquitin protein ligase
-0.27	7.03e-03	RAB3GAP2	RAB3 GTPase activating non-catalyti	0.06	4.85e-03	MCM3	minichromosome maintenance complex
-0.89	7.71e-03	RPS27L	ribosomal protein S27 like	0.78	5.16e-03	OGFOD1	2-oxoglutarate and iron dependent o
-0.07	8.07e-03	COX6C	cytochrome c oxidase subunit 6C	0.83	5.97e-03	CKS1B	CDC28 protein kinase regulatory sub
-0.87	8.66e-03	NCF4	neutrophil cytosolic factor 4	0.63	6.05e-03	BCOR	BCL6 corepressor
-0.09	9.63e-03	ACTN4	actinin alpha 4	0.05	6.05e-03	CHD4	chromodomain helicase DNA binding p
-0.11	1.04e-02	UGGT1	UDP-glucose glycoprotein glucosyltr	0.36	6.05e-03	UBE2S	ubiquitin conjugating enzyme E2 S
-0.76	1.09e-02	MYO6	myosin VI	0.07	6.99e-03	CNBP	CCHC-type zinc finger nucleic acid
-0.1	1.15e-02	UQCRCB	ubiquinol-cytochrome c reductase bi	0.07	7.03e-03	MCM6	minichromosome maintenance complex
-0.12	1.17e-02	CYC1	cytochrome c1	0.94	7.03e-03	TP53	tumor protein p53
-0.09	1.17e-02	CLPP	caseinolytic mitochondrial matrix p	0.09	7.03e-03	PSMB6	proteasome 20S subunit beta 6
-0.09	1.17e-02	ATP1A1	ATPase Na+/K+ transporting subunit	0.33	7.71e-03	PGM2L1	phosphoglucomutase 2 like 1
-0.09	1.22e-02	UQCRC2	ubiquinol-cytochrome c reductase co	0.06	8.07e-03	MCM4	minichromosome maintenance complex
-0.07	1.27e-02	UQCRC1	ubiquinol-cytochrome c reductase co	0.06	8.35e-03	MCM2	minichromosome maintenance complex
-0.78	1.27e-02	MYO1C	myosin IC	0.06	8.35e-03	NOLC1	nucleolar and coiled-body phosphopr
-0.79	1.30e-02	ACOT9	acyl-CoA thioesterase 9	0.03	8.35e-03	SNRPD3	small nuclear ribonucleoprotein D3
-0.3	1.44e-02	SPATA20	spermatogenesis associated 20	0.07	1.04e-02	EDC4	enhancer of mRNA decapping 4
-0.11	1.70e-02	NDUFA13	NADH:ubiquinone oxidoreductase subu	0.53	1.08e-02	TAF8	TATA-box binding protein associated
-0.47	1.89e-02	ECI1	enoyl-CoA delta isomerase 1	0.05	1.15e-02	ZNF207	zinc finger protein 207
-0.34	1.91e-02	PLS1	plastin 1	0.82	1.17e-02	MAZ	MYC associated zinc finger protein
-0.08	1.95e-02	HDLBP	high density lipoprotein binding pr	0.74	1.17e-02	CCDC12	coiled-coil domain containing 12
-0.09	2.02e-02	ACTR3	actin related protein 3	0.8	1.27e-02	MAP1A	microtubule associated protein 1A
-0.71	2.02e-02	TOR1A	torsin family 1 member A	0.03	1.30e-02	HNRNPA1	heterogeneous nuclear ribonucleopro
-0.08	2.10e-02	ARPC2	actin related protein 2/3 complex s	0.05	1.39e-02	MCM7	minichromosome maintenance complex
-0.67	2.10e-02	XPC	XPC complex subunit, DNA damage rec	0.27	1.44e-02	TRBL1XPC1	TRBL1 X receptor 1



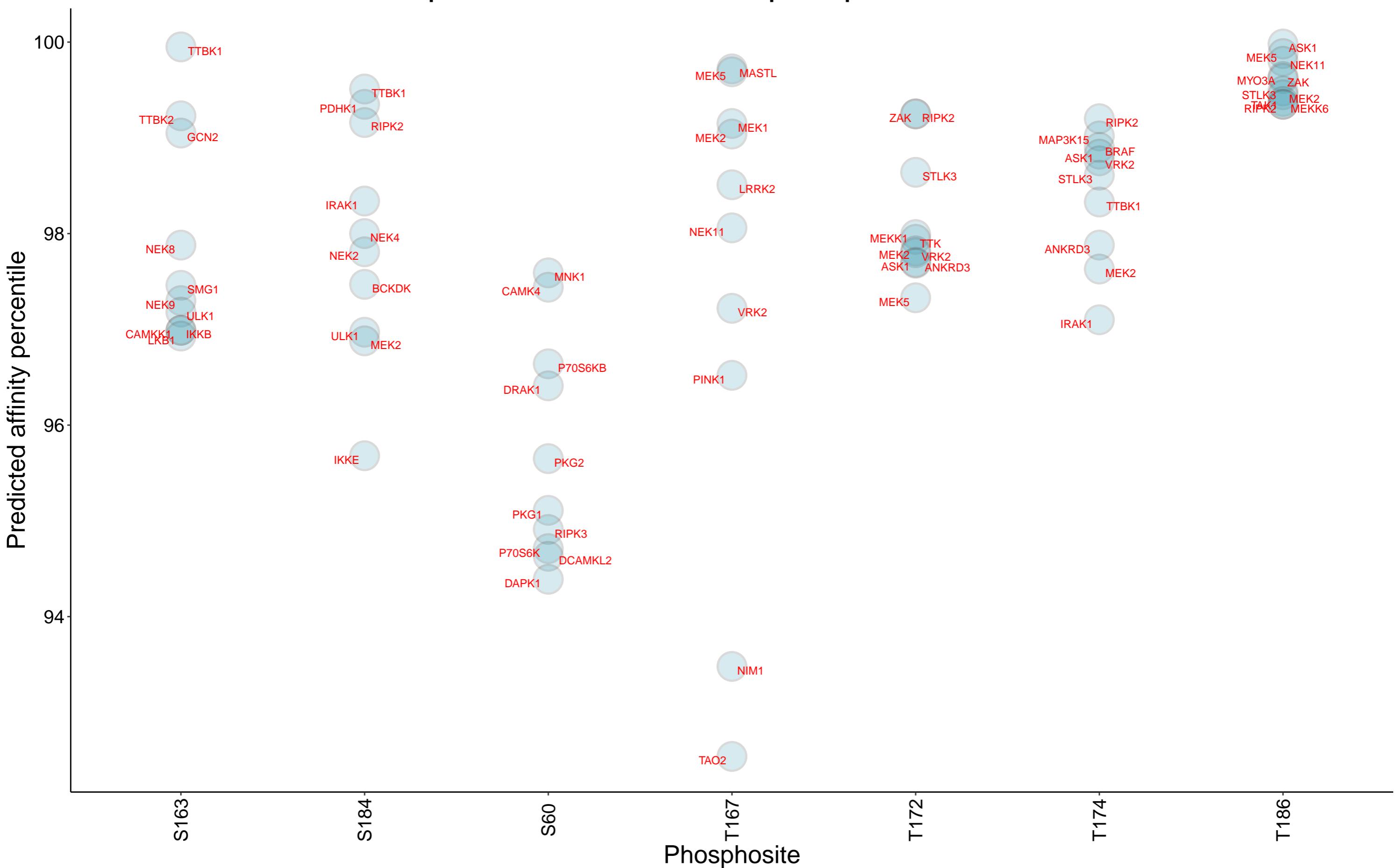
Top 250 correlation coefficients overrepresentation, BAX protein, DB1



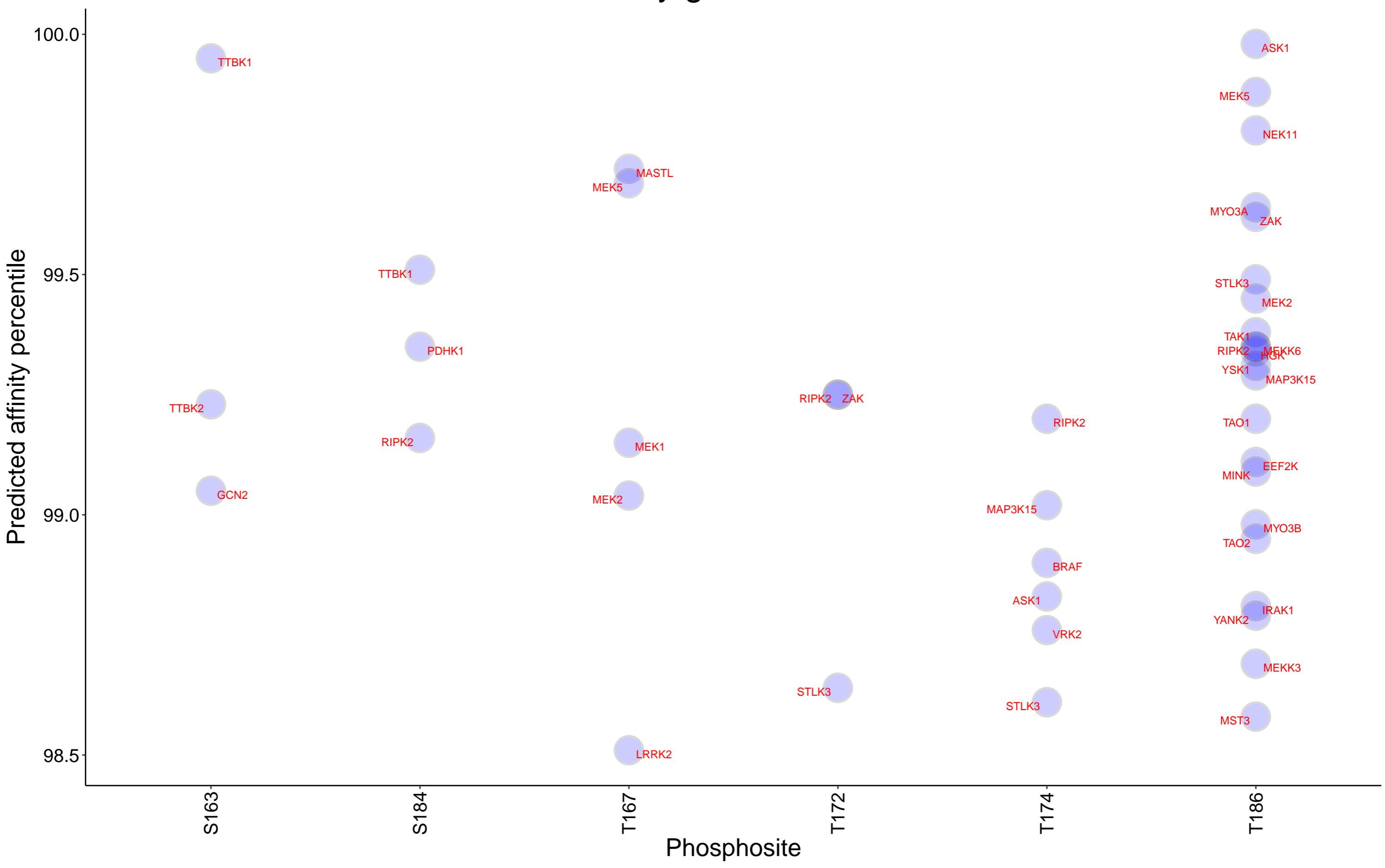
Gene Set Enrichment analysis on protein correlation coefficients, BAX protein, DB1



Top 10 kinases for each phosphosite in BAX



Kinases with affinity greater than 98.5% to BAX



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

Beware of false positives in tissues with small number of samples

