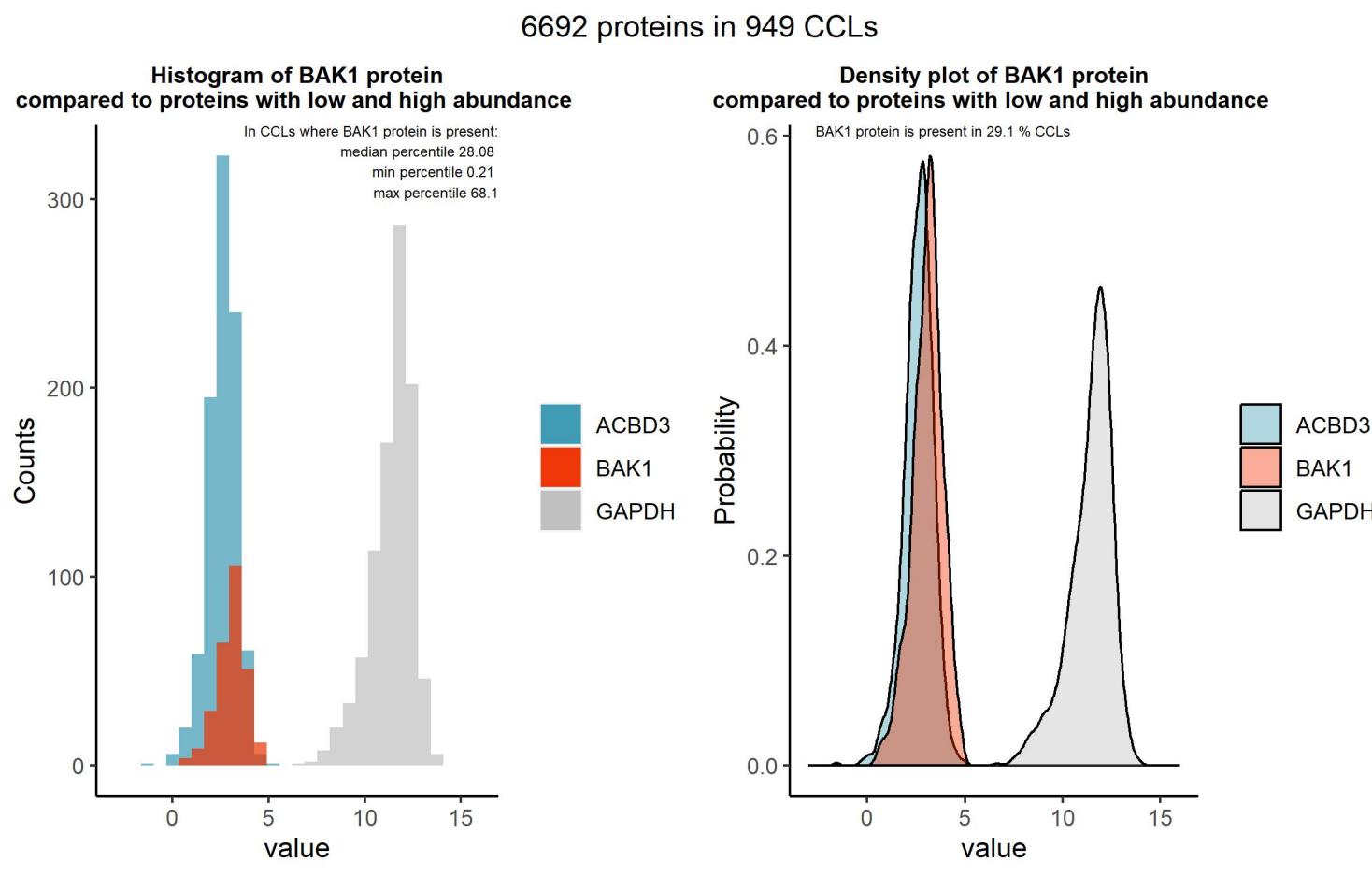


BAK1

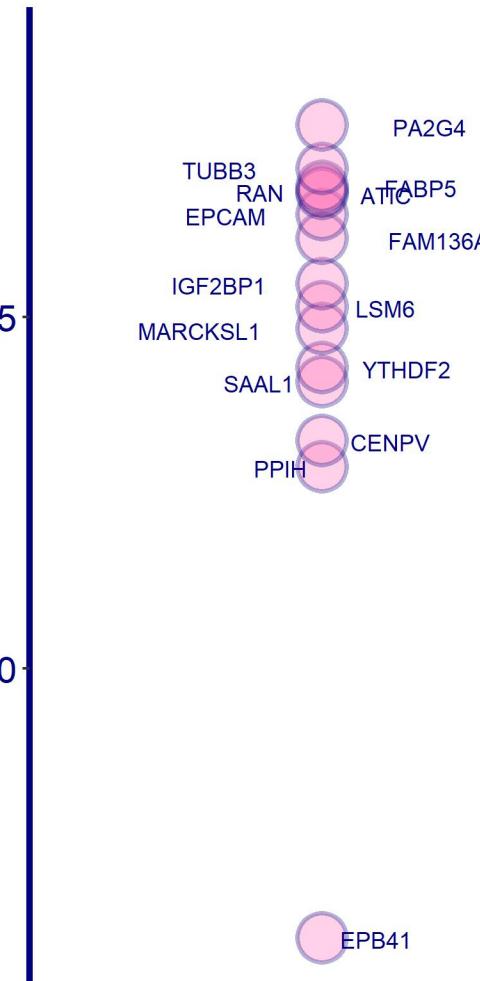
Protein name: BAK ; UNIPROT: Q16611 ; Gene name: BCL2 antagonist/killer 1

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

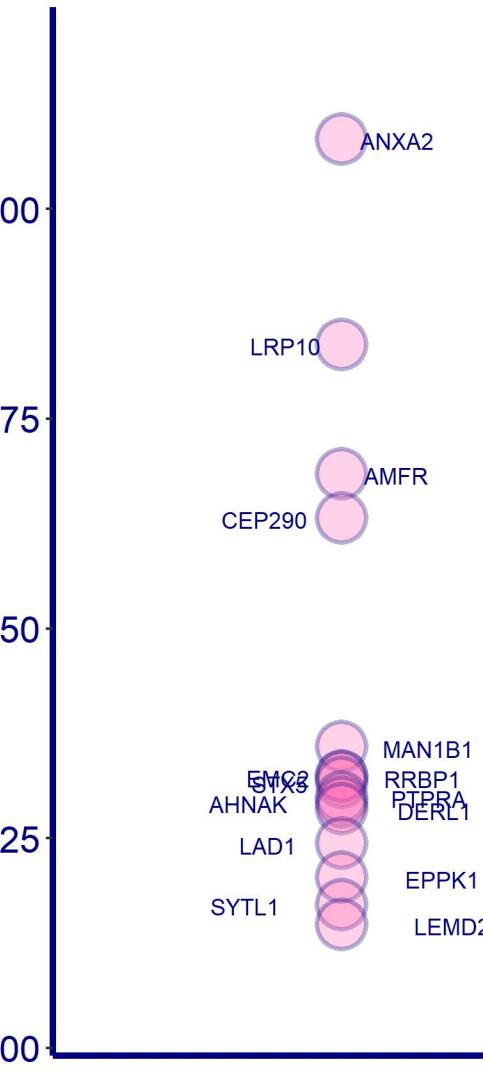
Sanger Institute Protein Database 1 (DB1), protein presence is certain



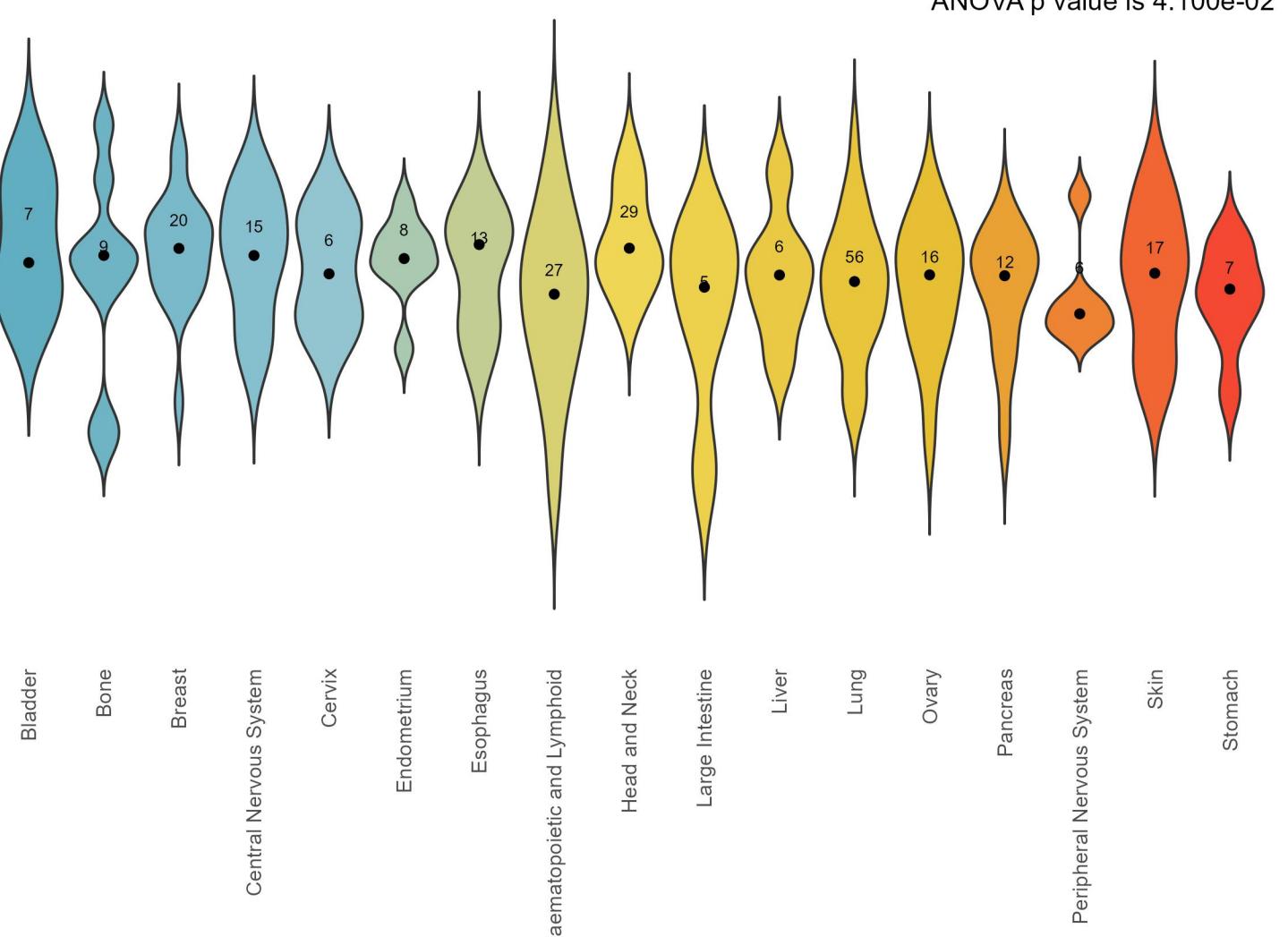
Top negative correlations of BAK1 protein, DB1



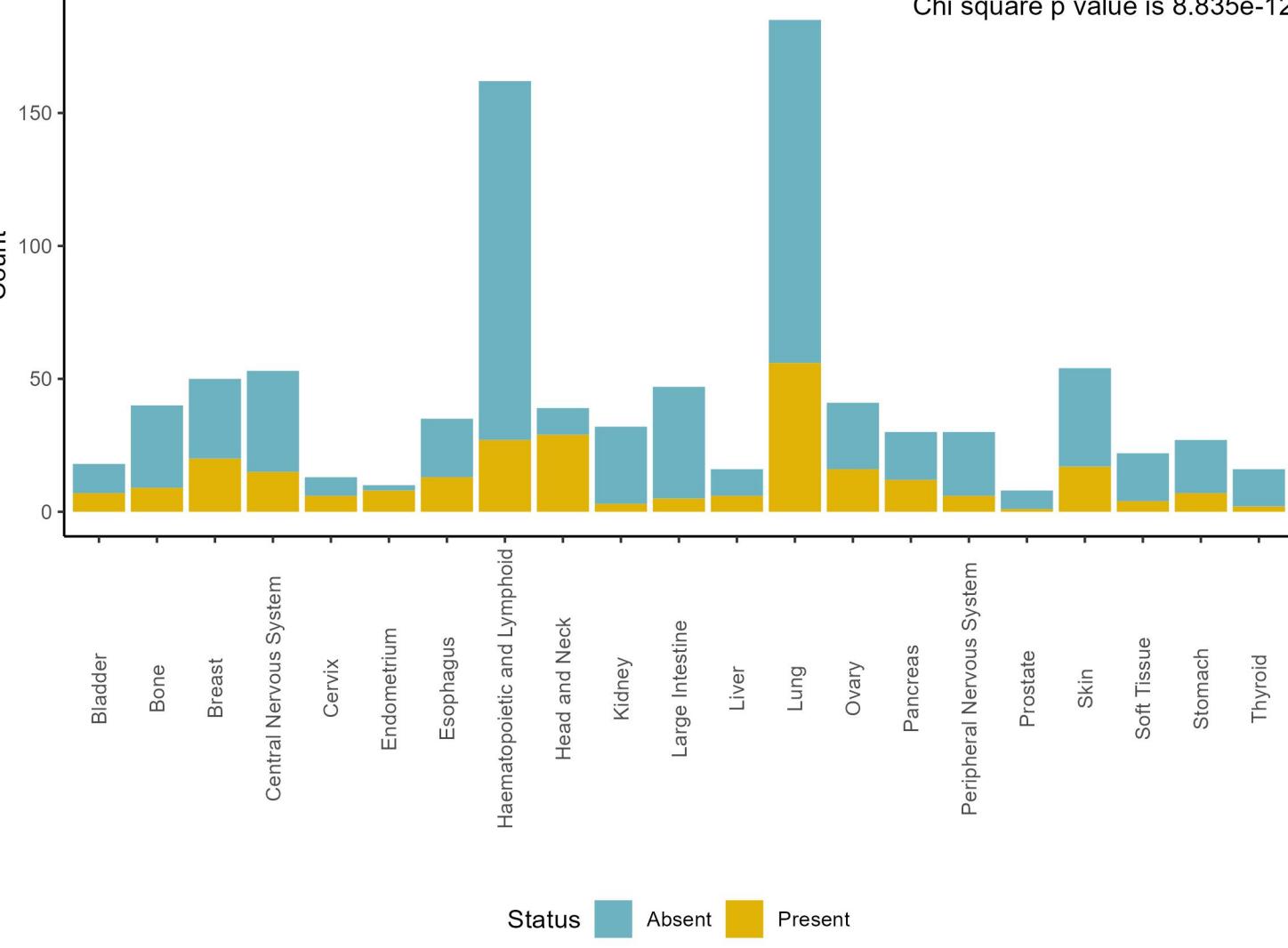
Top positive correlations of BAK1 protein, DB1



Amount of BAK1 protein, number of CCLs where it is present by tissue, DB1



Present and absent BAK1 protein counts by tissue, DB1

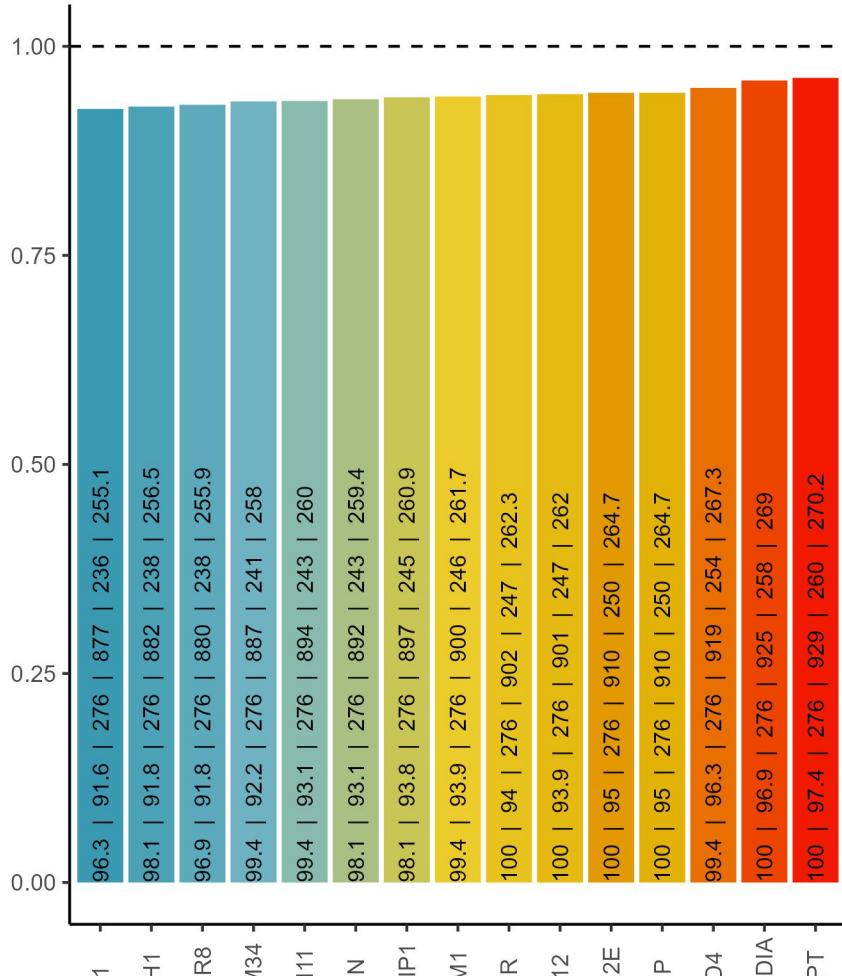


Cooccurrence with BAK1 protein, DB1

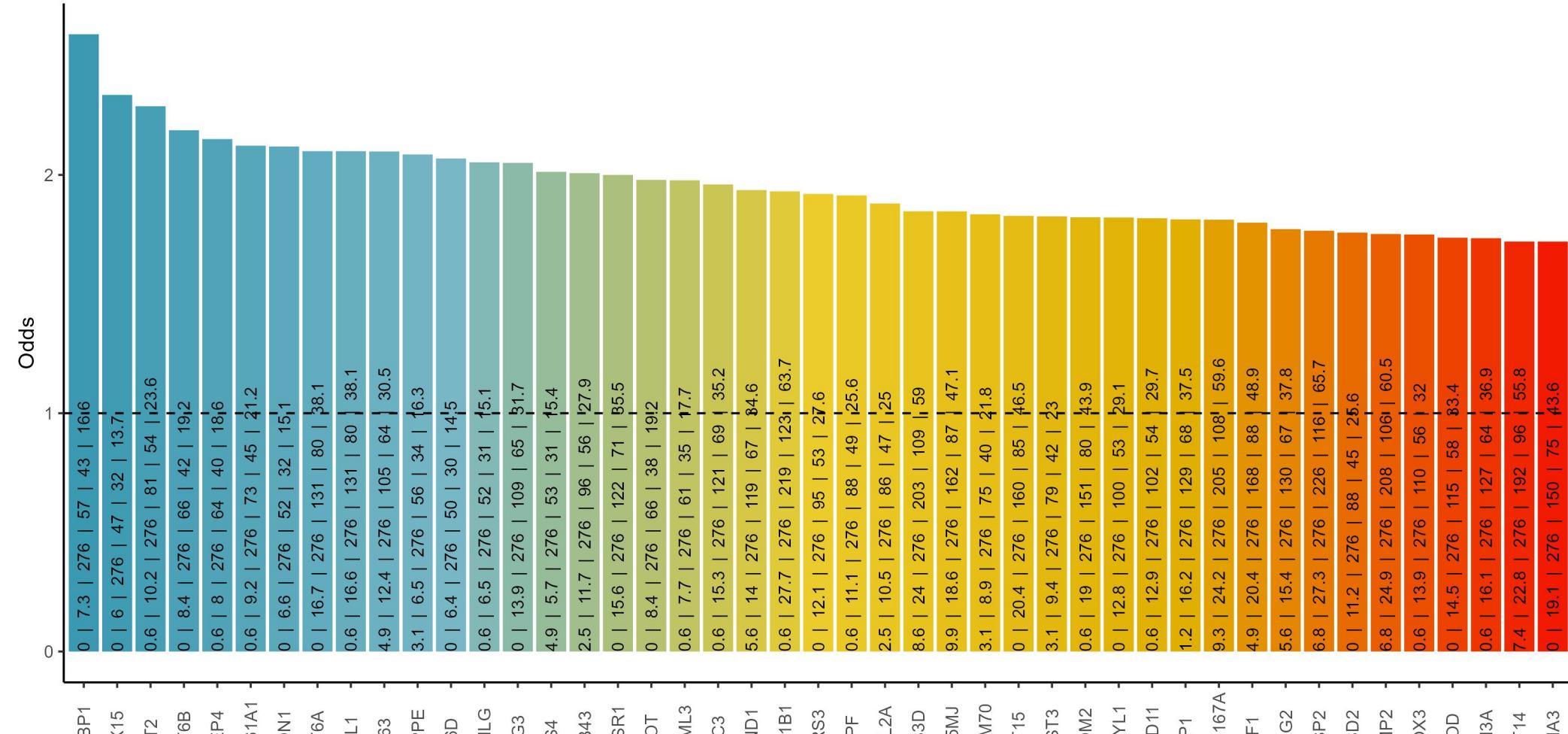
% of BAK1 in blood cancers: 16.7 ; % of BAK1 in solid cancers: 31.8

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of BAK1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

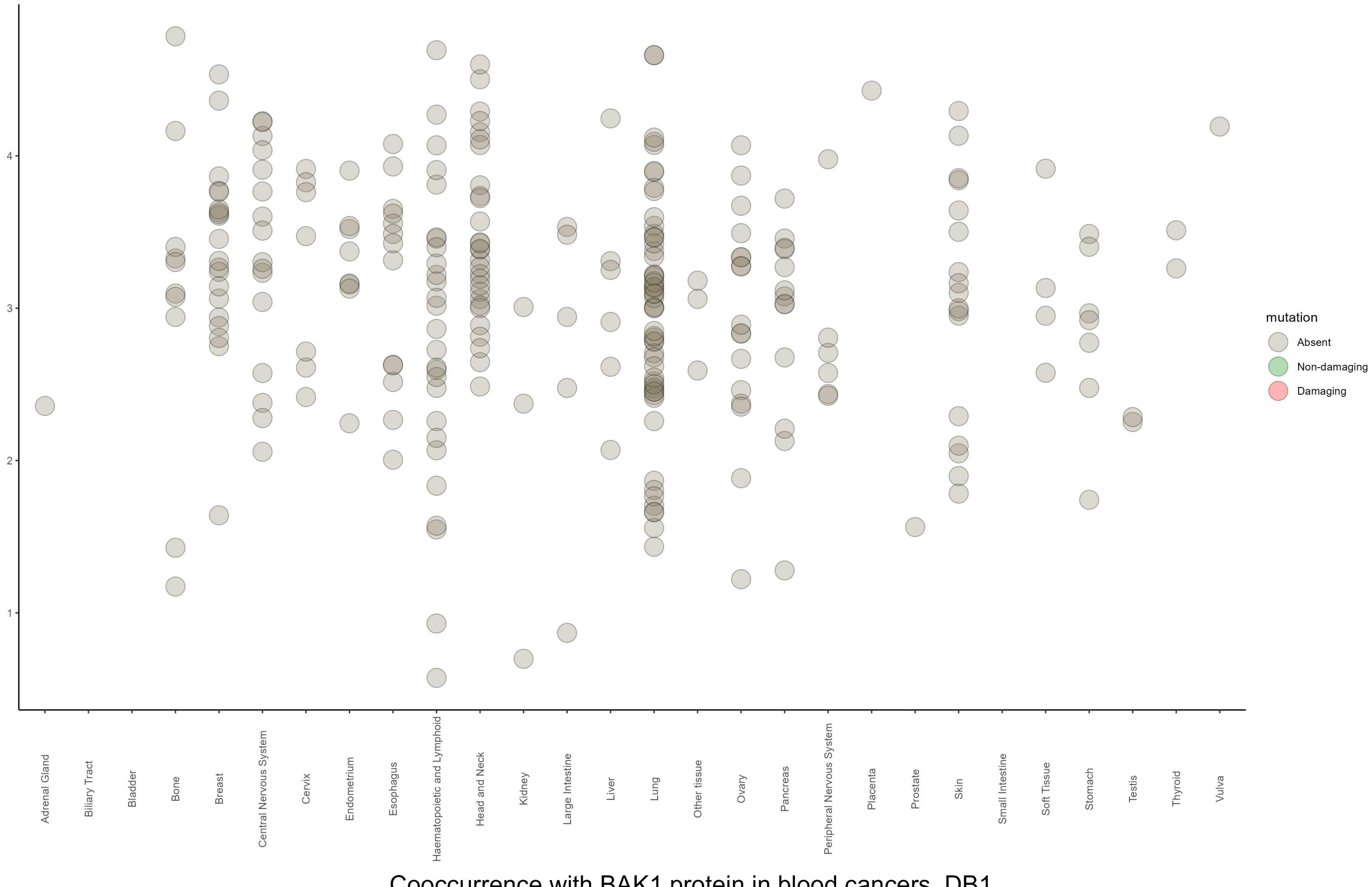
Negative cooccurrence



Positive cooccurrence

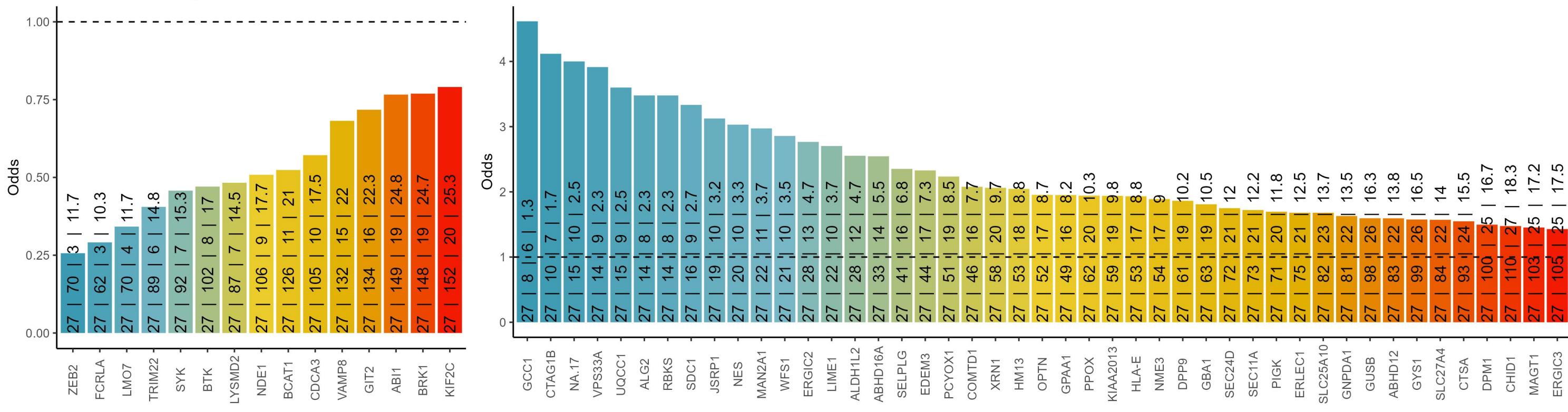


Amount of BAK1 protein and mutation status by tissue, DB1



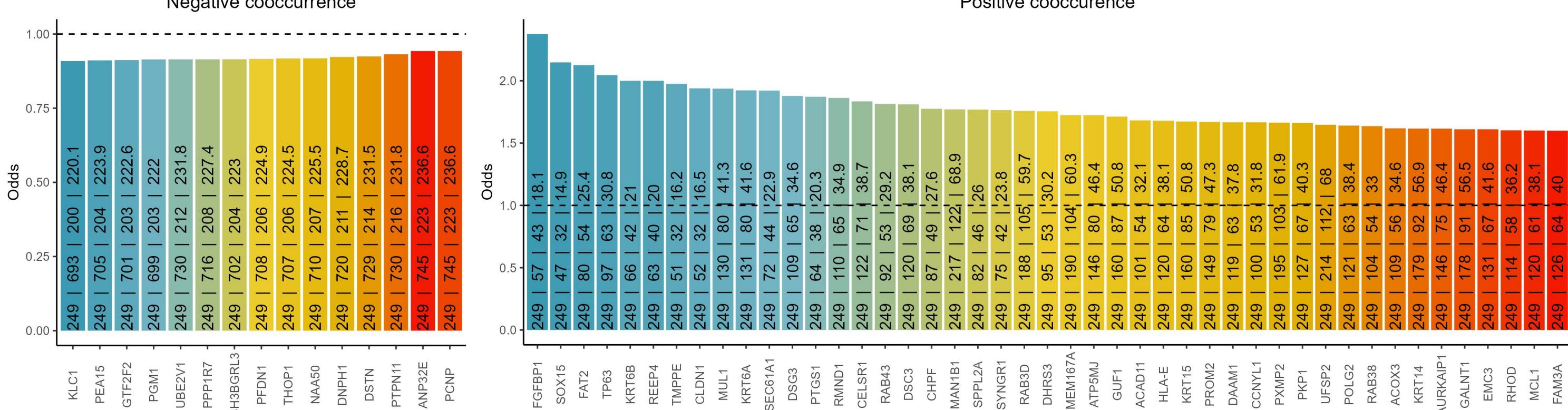
Cooccurrence with BAK1 protein in blood cancers, DB1

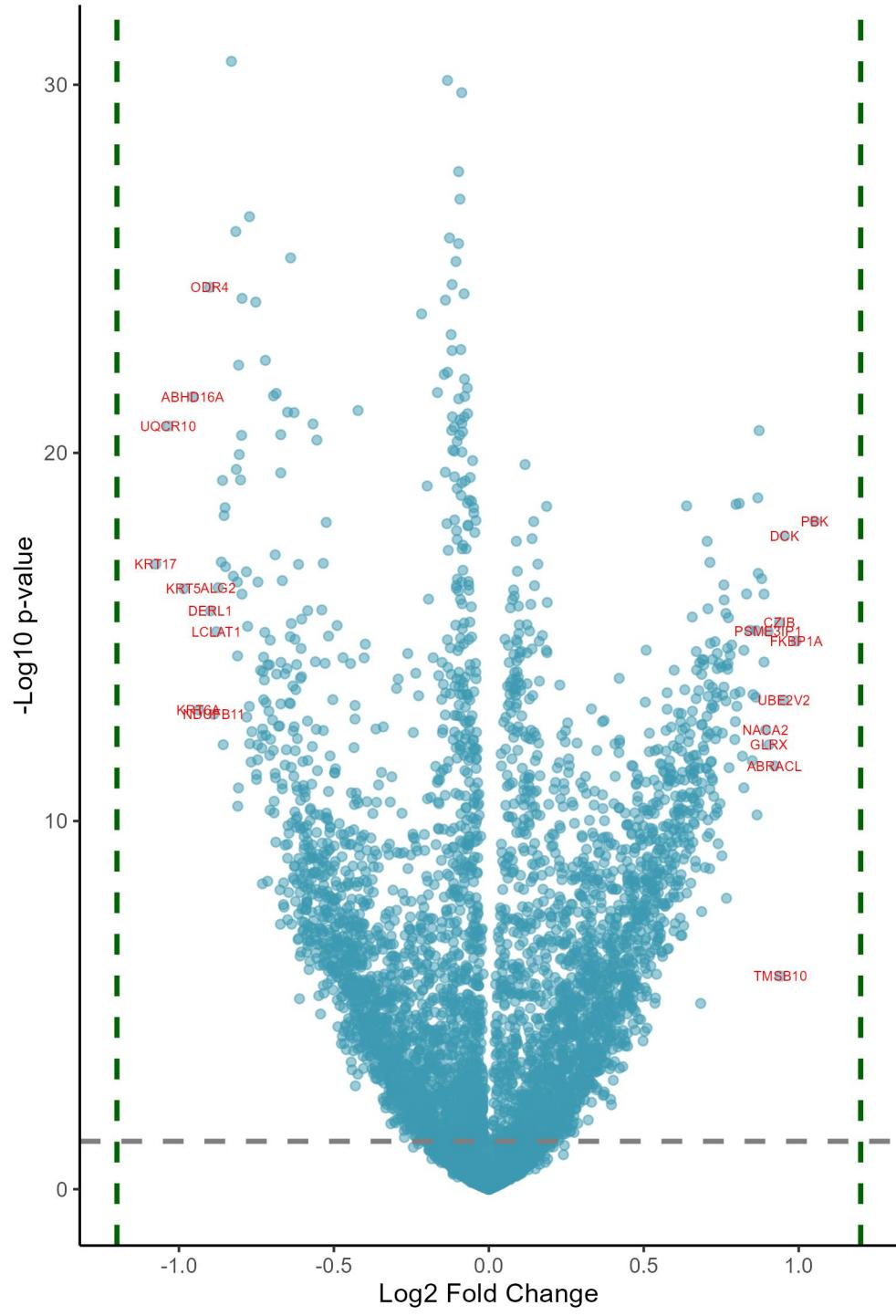
The text in the bars: incidence of BAK1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Cooccurrence with BAK1 protein in solid cancers, DB1

The text in the bars: incidence of BAK1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

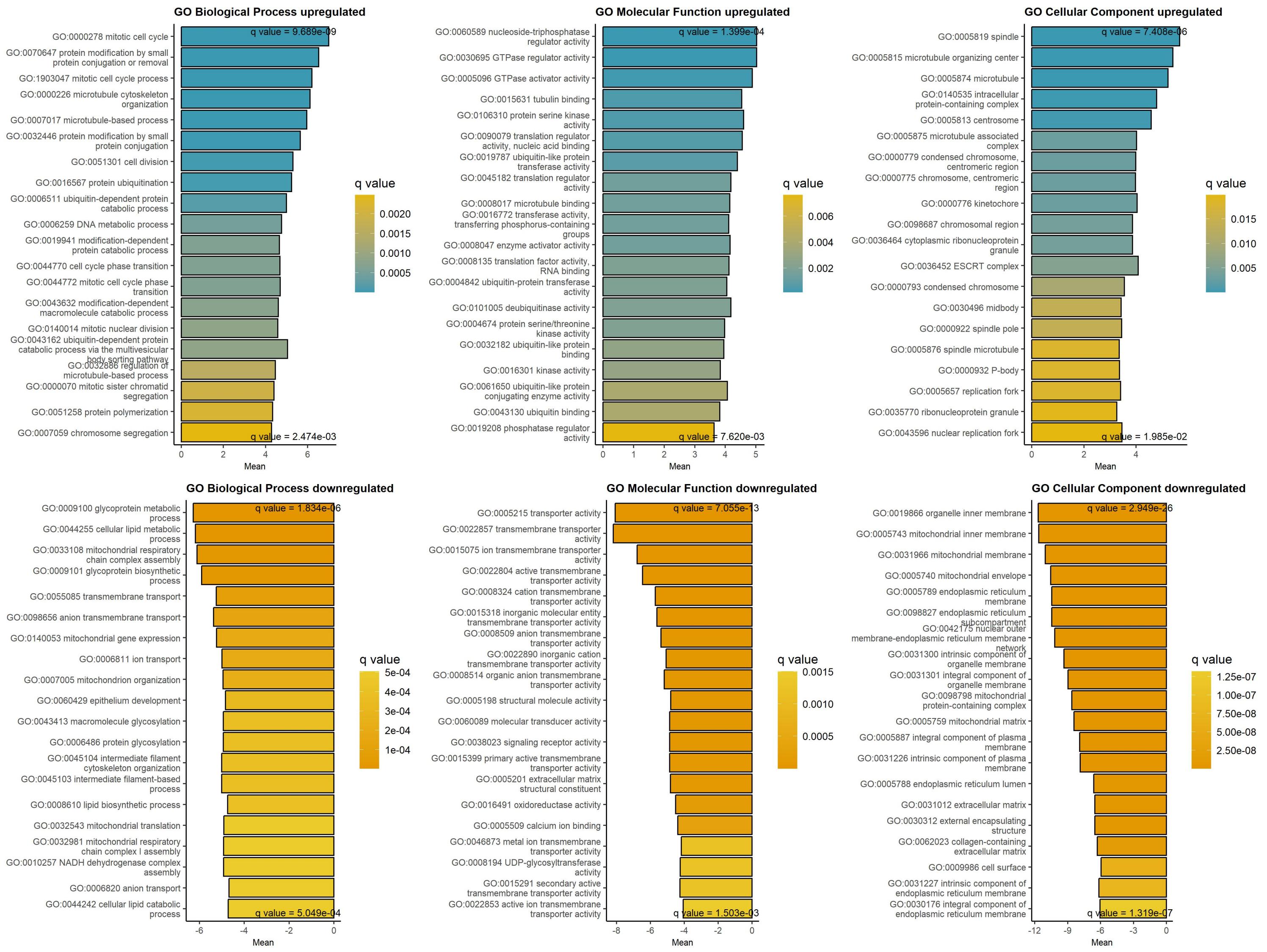


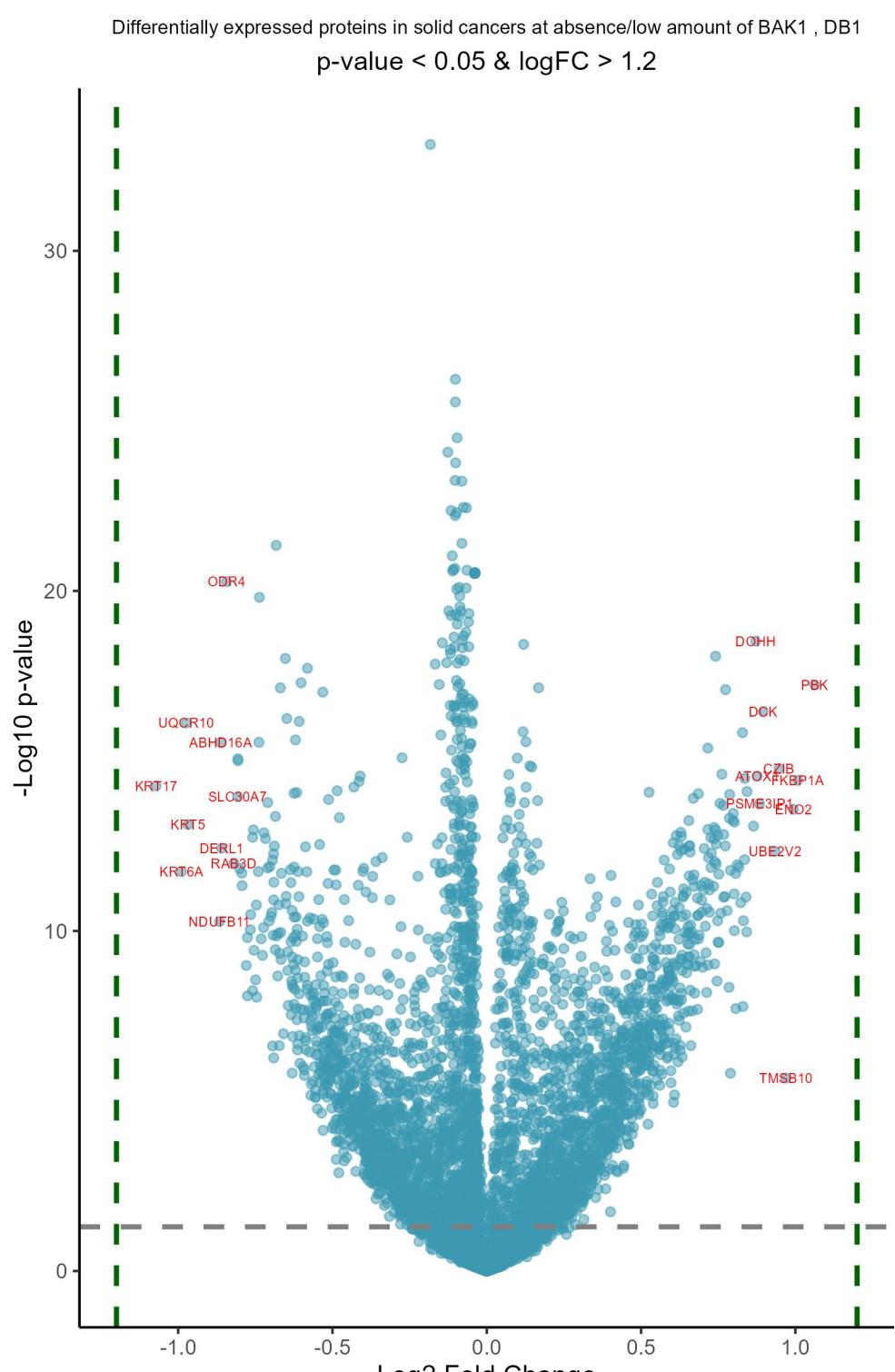
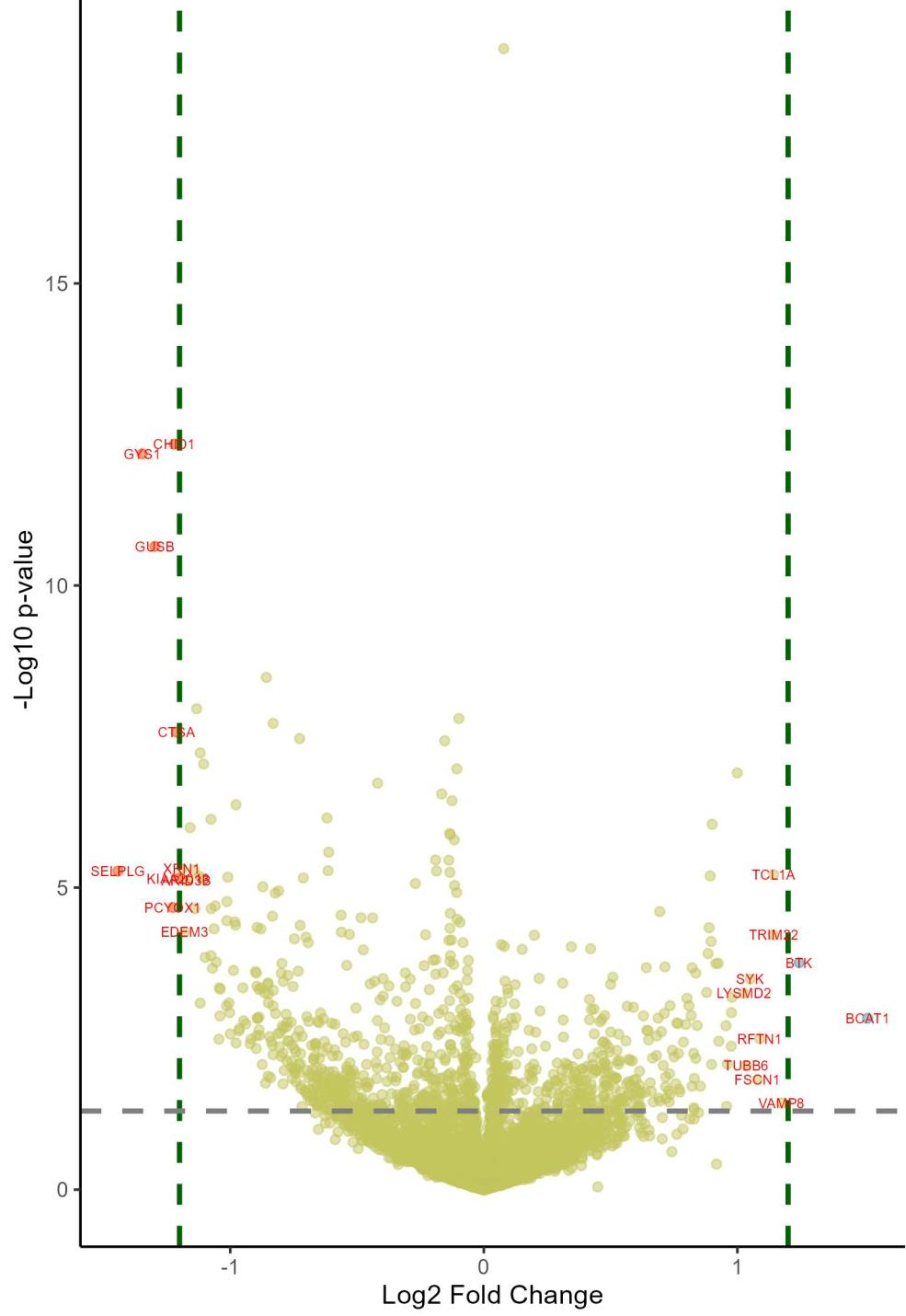


Downregulated at low/absent BAK1 Upregulated at low/absent BAK1

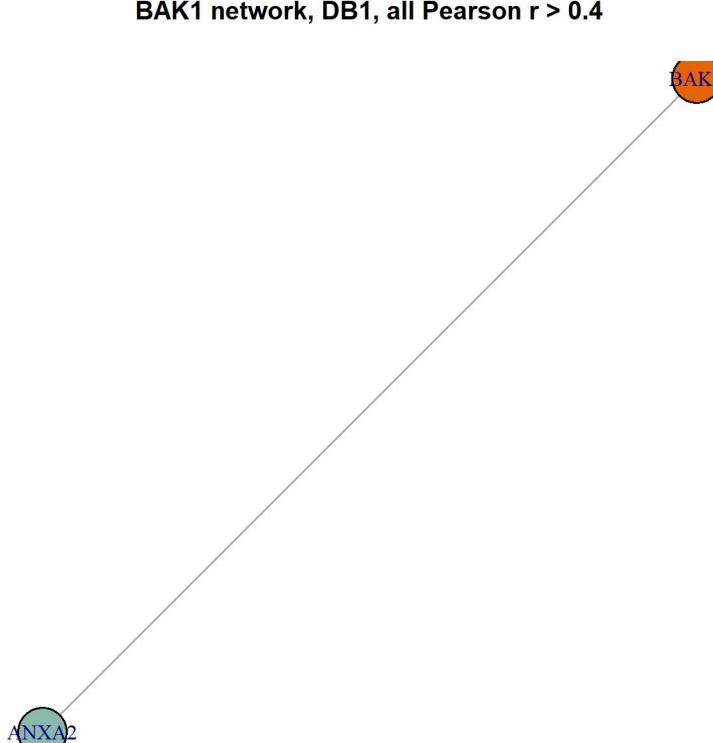
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.07	6.47e-16	KRT17	keratin 17	1.05	5.57e-17	PBK	PDZ binding kinase
-1.04	2.81e-19	UQCR10	ubiquinol-cytochrome c reductase, c	0.99	4.71e-14	FKBP1A	FKBP prolyl isomerase 1A
-0.98	2.53e-15	KRT5	keratin 5	0.95	1.28e-16	DCK	deoxycytidine kinase
-0.95	6.02e-20	ABHD16A	abhydrolase domain containing 16A,	0.95	1.08e-12	UBE2V2	ubiquitin conjugating enzyme E2 V2
-0.94	1.88e-12	KRT6A	keratin 6A	0.94	5.67e-06	TMSB10	thymosin beta 10
-0.9	1.52e-22	ODR4	odr-4 GPCR localization factor homo	0.94	1.71e-14	CZIB	CXXC motif containing zinc binding
-0.9	8.72e-15	DERL1	derlin 1	0.92	4.22e-11	ABRACL	ABRA C-terminal like
-0.89	2.41e-12	NDUFB11	NADH:ubiquinone oxidoreductase subu	0.9	1.29e-11	GLRX	glutaredoxin
-0.88	2.82e-14	LCLAT1	lysocardiolipin acyltransferase 1	0.9	2.78e-14	PSME3IP1	proteasome activator subunit 3 inte
-0.87	2.40e-15	ALG2	ALG2 alpha-1,3/1,6-mannosyltransfer	0.89	5.72e-12	NACA2	nascent polypeptide associated comp
-0.86	5.89e-16	MTCH1	mitochondrial carrier 1	0.89	1.44e-13	AK6	adenylate kinase 6
-0.86	5.65e-18	DHRS7B	dehydrogenase/reductase 7B	0.89	3.38e-15	CORO7	coronin 7
-0.86	1.28e-11	AP2S1	adaptor related protein complex 2 s	0.88	1.50e-15	SAAL1	serum amyloid A like 1
-0.85	4.04e-17	GGCX	gamma-glutamyl carboxylase	0.87	3.51e-19	DOHH	deoxyhypusine hydroxylase
-0.85	2.53e-17	ERGIC2	ERGIC and golgi 2	0.87	1.10e-15	RPE	ribulose-5-phosphate-3-epimerase
-0.85	7.48e-16	PIGT	phosphatidylinositol glycan anchor	0.87	1.54e-17	GINS4	GINS complex subunit 4
-0.83	7.70e-28	ERLEC1	endoplasmic reticulum lectin 1	0.87	6.37e-10	ZNF706	zinc finger protein 706
-0.82	1.29e-15	SLC30A7	solute carrier family 30 member 7	0.86	2.69e-14	PPP6R1	protein phosphatase 6 regulatory su
-0.82	8.07e-24	SEC11A	SEC11 homolog A, signal peptidase c	0.86	9.24e-13	RNASEH2C	ribonuclease H2 subunit C
-0.81	3.12e-18	TMEM33	transmembrane protein 33	0.85	7.99e-13	RPIA	ribose 5-phosphate isomerase A
-0.81	1.75e-15	UQCC1	ubiquinol-cytochrome c reductase co	0.85	3.12e-11	ENO2	enolase 2
-0.81	1.04e-13	LAMA5	laminin subunit alpha 5	0.84	2.66e-14	RNF181	ring finger protein 181
-0.81	3.92e-10	TACSTD2	tumor associated calcium signal tra	0.83	3.38e-15	RNASEH2A	ribonuclease H2 subunit A
-0.81	1.41e-10	CERS2	ceramide synthase 2	0.82	7.73e-14	ATOX1	antioxidant 1 copper chaperone
-0.81	1.15e-20	GPAA1	glycosylphosphatidylinositol anchor	0.82	1.40e-10	PIN1	peptidylprolyl cis/trans isomerase,
-0.81	1.29e-18	PTPMT1	protein tyrosine phosphatase mitoch	0.82	2.42e-11	PPP2CA	protein phosphatase 2 catalytic sub
-0.8	5.54e-18	DAD1	defender against cell death 1	0.81	7.07e-13	DHFR	dihydrofolate reductase
-0.8	4.36e-19	KIAA2013	KIAA2013	0.81	2.07e-17	ZFAND6	zinc finger AN1-type containing 6
-0.8	3.38e-15	SLC25A4	solute carrier family 25 member 4	0.8	1.52e-12	MCRIP1	MAPK regulated corepressor interact

GAGE analysis on upregulated and downregulated proteins at low/absent BAK1 protein, DB1

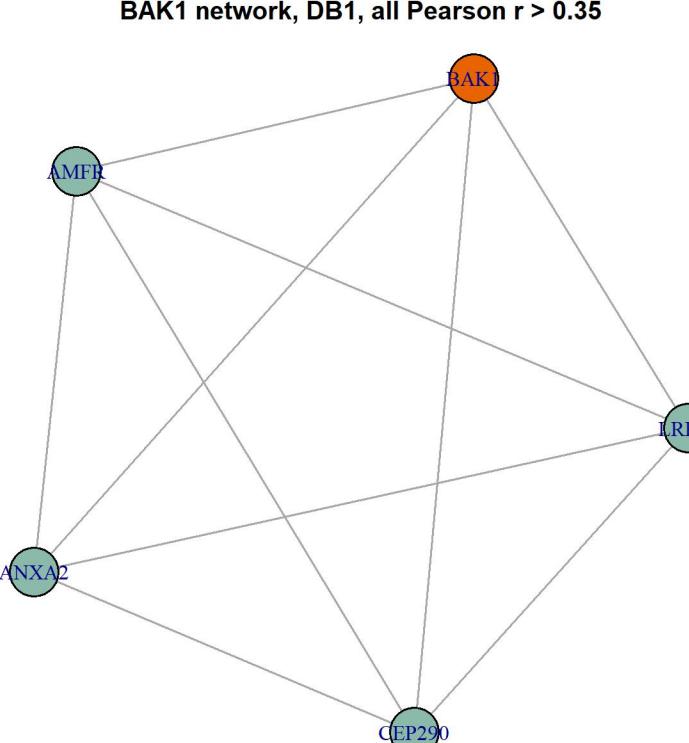




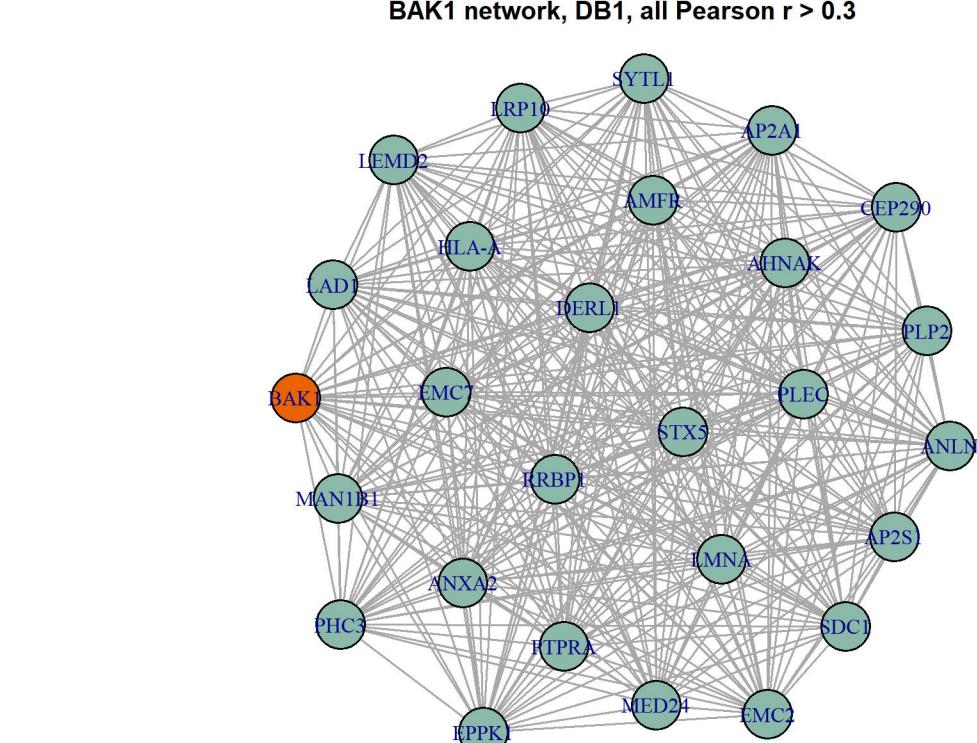
BAK1 network, DB1, all Pearson r > 0.4



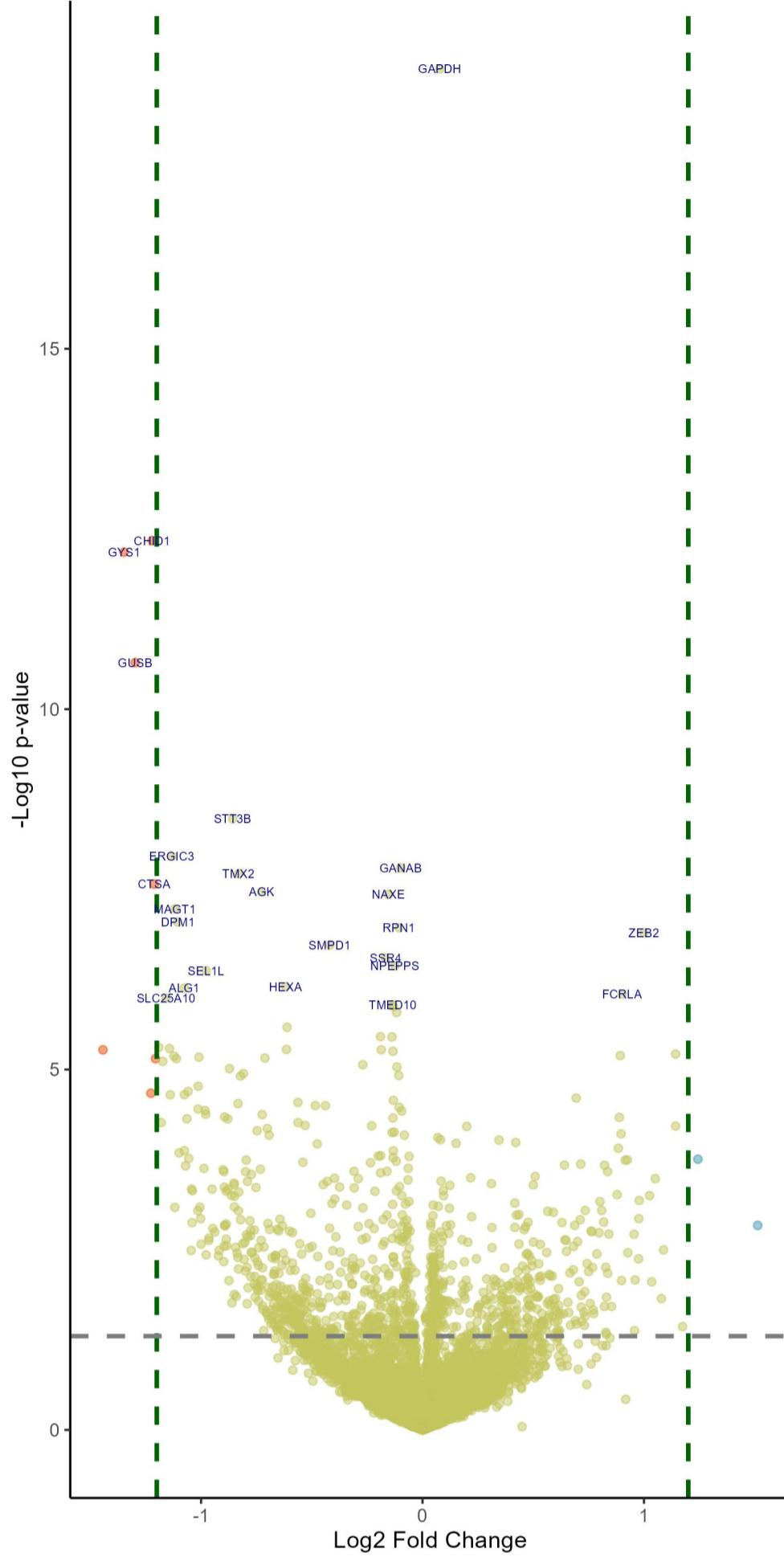
BAK1 network, DB1, all Pearson r > 0.35



BAK1 network, DB1, all Pearson r > 0.3



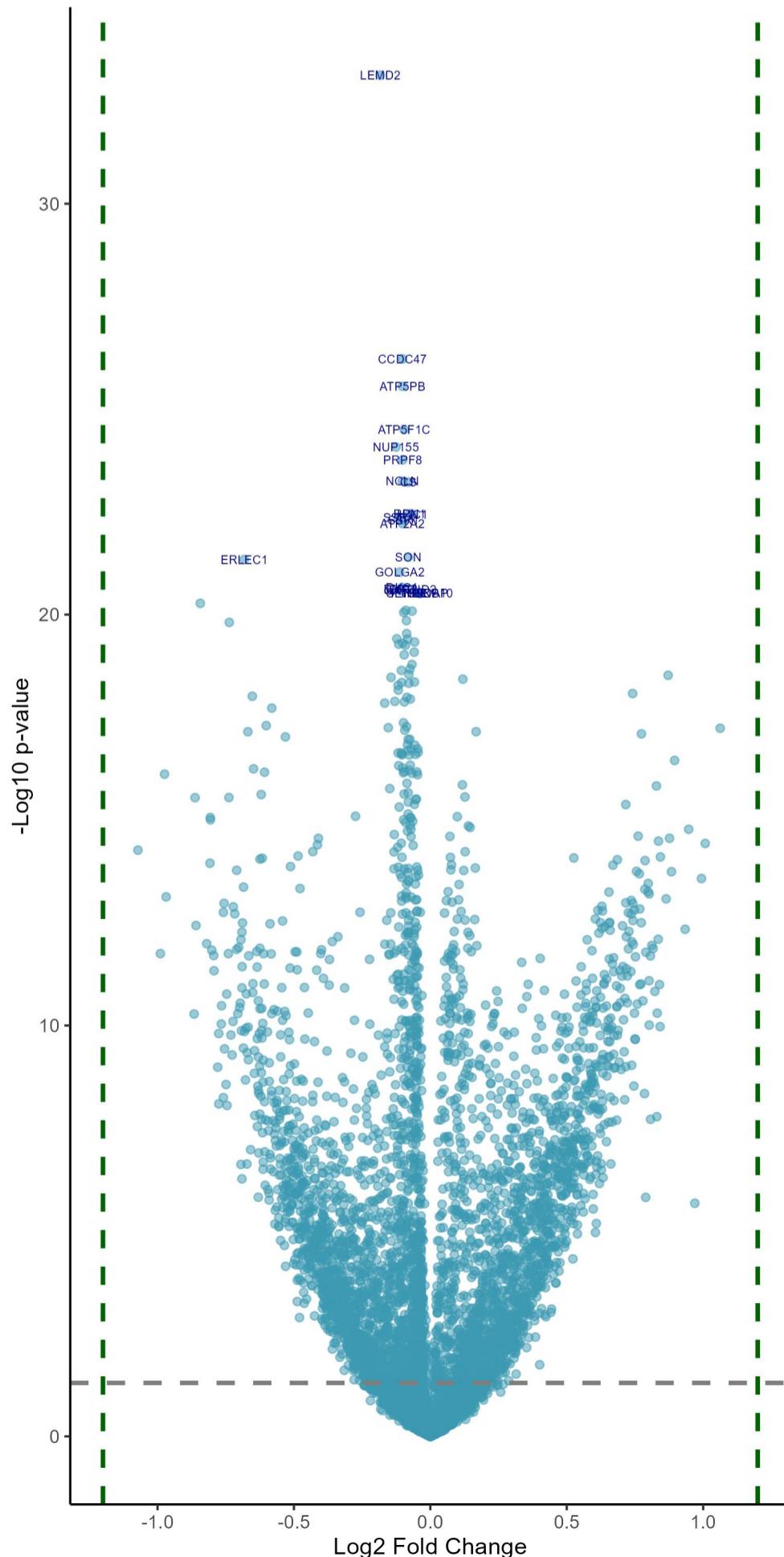
Differentially expressed proteins in blood cancers at absence/low amount of BAK1 , DB1
p-value < 0.05 & logFC > 1.2



Sorted by p values!
Downregulated in blood cancers at low/absent BAK1 Upregulated in blood cancers at low/absent BAK1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.22	1.02e-09	CHID1	chitinase domain containing 1	0.08	4.33e-16	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
-1.35	1.10e-09	GYS1	glycogen synthase 1	1	5.27e-05	ZEB2	zinc finger E-box binding homeobox
-1.3	3.00e-08	GUSB	glucuronidase beta	0.9	2.59e-04	FCRLA	Fc receptor like A
-0.86	3.68e-06	STT3B	STT3 oligosaccharyltransferase comp	1.14	1.09e-03	TCL1A	TCL1 family AKT coactivator A
-1.13	1.04e-05	ERGIC3	ERGIC and golgi 3	0.89	1.09e-03	PRKAR2B	protein kinase cAMP-dependent type I
-0.1	1.32e-05	GANAB	glucosidase II alpha subunit	0.69	2.95e-03	LAPTM5	lysosomal protein transmembrane 5
-0.83	1.42e-05	TMX2	thioredoxin related transmembrane p	0.89	4.45e-03	NDE1	nudE neurodevelopment protein 1
-1.21	1.78e-05	CTSA	cathepsin A	1.14	5.24e-03	TRIM22	tripartite motif containing 22
-0.73	2.06e-05	AGK	acylglycerol kinase	0.2	5.24e-03	GATA2A	GATA zinc finger domain containing 2A
-0.15	2.06e-05	NAXE	NAD(P)HX epimerase	0.9	6.25e-03	LMO7	LIM domain 7
-1.12	3.02e-05	MAGT1	magnesium transporter 1	0.07	6.81e-03	IK	IK cytokine
-1.11	4.28e-05	DPM1	dolichyl-phosphate mannosyltransfer	0.08	7.18e-03	MFAP1	microfibril associated protein 1
-0.11	4.79e-05	RPN1	ribophorin I	0.35	7.20e-03	NCAPH	non-SMC condensin I complex subunit B
-0.42	7.33e-05	SMPD1	sphingomyelin phosphodiesterase 1	0.42	7.68e-03	TTC38	tetratricopeptide repeat domain 38
-0.17	1.04e-04	SSR4	signal sequence receptor subunit 4	0.15	7.81e-03	SCP2	sterol carrier protein 2
-0.13	1.28e-04	NPEPPS	aminopeptidase puromycin sensitive	0.88	8.93e-03	CD19	CD19 molecule
-0.98	1.41e-04	SEL1L	SEL1L adaptor subunit of ERAD E3 ub	1.24	1.15e-02	BTK	Bruton tyrosine kinase
-0.62	2.24e-04	HEXA	hexosaminidase subunit alpha	0.92	1.16e-02	PAX5	paired box 5
-1.08	2.24e-04	ALG1	ALG1 chitobiosyldiphosphodolichol b	0.92	1.16e-02	IGHM	immunoglobulin heavy constant mu
-1.16	2.82e-04	SLC25A10	solute carrier family 25 member 10	0.71	1.26e-02	MRFAP1	Morf4 family associated protein 1
-0.13	3.37e-04	TMED10	transmembrane p24 trafficking prote	0.64	1.29e-02	NFATC1	nuclear factor of activated T cells
-0.13	3.41e-04	PDIA4	protein disulfide isomerase family	0.82	1.29e-02	CD40	CD40 molecule
-0.12	3.98e-04	HSP90B1	heat shock protein 90 beta family m	0.84	1.45e-02	TPM1	tropomyosin 1
-0.61	6.16e-04	ATP6V0D1	ATPase H+ transporting V0 subunit d	0.51	1.64e-02	MYL4	myosin light chain 4
-0.19	7.80e-04	RPN2	ribophorin II	0.22	1.70e-02	SH3BGRL	SH3 domain binding glutamate rich p
-0.14	7.80e-04	DDOST	dolichyl-diphosphooligosaccharide--	1.05	1.71e-02	SYK	spleen associated tyrosine kinase
-1.19	1.01e-03	XRN1	5'-3' exoribonuclease 1	0.08	1.81e-02	GMPS	guanine monophosphate synthase
-1.14	1.01e-03	SEC11A	SEC11 homolog A, signal peptidase c	0.31	1.91e-02	MAPK1	mitogen-activated protein kinase 1
-0.61	1.01e-03	HEXB	hexosaminidase subunit beta	0.5	1.95e-02	MACROH2A2	macroH2A.2 histone
-0.19	1.01e-03	MYDGF	myeloid derived growth factor	0.12	1.96e-02	PGLS	6-phosphogluconolactonase
-1.44	1.01e-03	SELPLG	selectin P ligand	0.09	2.16e-02	CAPZA1	capping actin protein of muscle Z-I
-0.13	1.03e-03	BCAP31	B cell receptor associated protein	0.88	2.38e-02	MS4A1	membrane spanning 4-domains A1
-1.12	1.09e-03	GNPDA1	glucosamine-6-phosphate deaminase 1	1.03	2.40e-02	LYSMD2	LysM domain containing 2
-1.01	1.09e-03	CLPTM1L	CLPTM1 like	0.1	2.40e-02	BTF3	basic transcription factor 3
-0.71	1.09e-03	NDUFB3	NADH:ubiquinone oxidoreductase subu	0.98	2.74e-02	IGF2BP1	insulin like growth factor 2 mRNA b
-1.11	1.09e-03	ERLEC1	endoplasmic reticulum lectin 1	0.8	2.81e-02	KIF2C	kinesin family member 2C
-1.21	1.09e-03	KIAA2013	KIAA2013	0.42	2.92e-02	APP	amyloid beta precursor protein
-1.17	1.17e-03	ARID3B	AT-rich interaction domain 3B	0.05	3.03e-02	TARDBP	TAR DNA binding protein
0.27	1.27e-03	APHGEF11	Rho guanine nucleotide exchange fac	0.07	3.13e-02	HSP90AA1	heat shock protein family A (Hsp70)

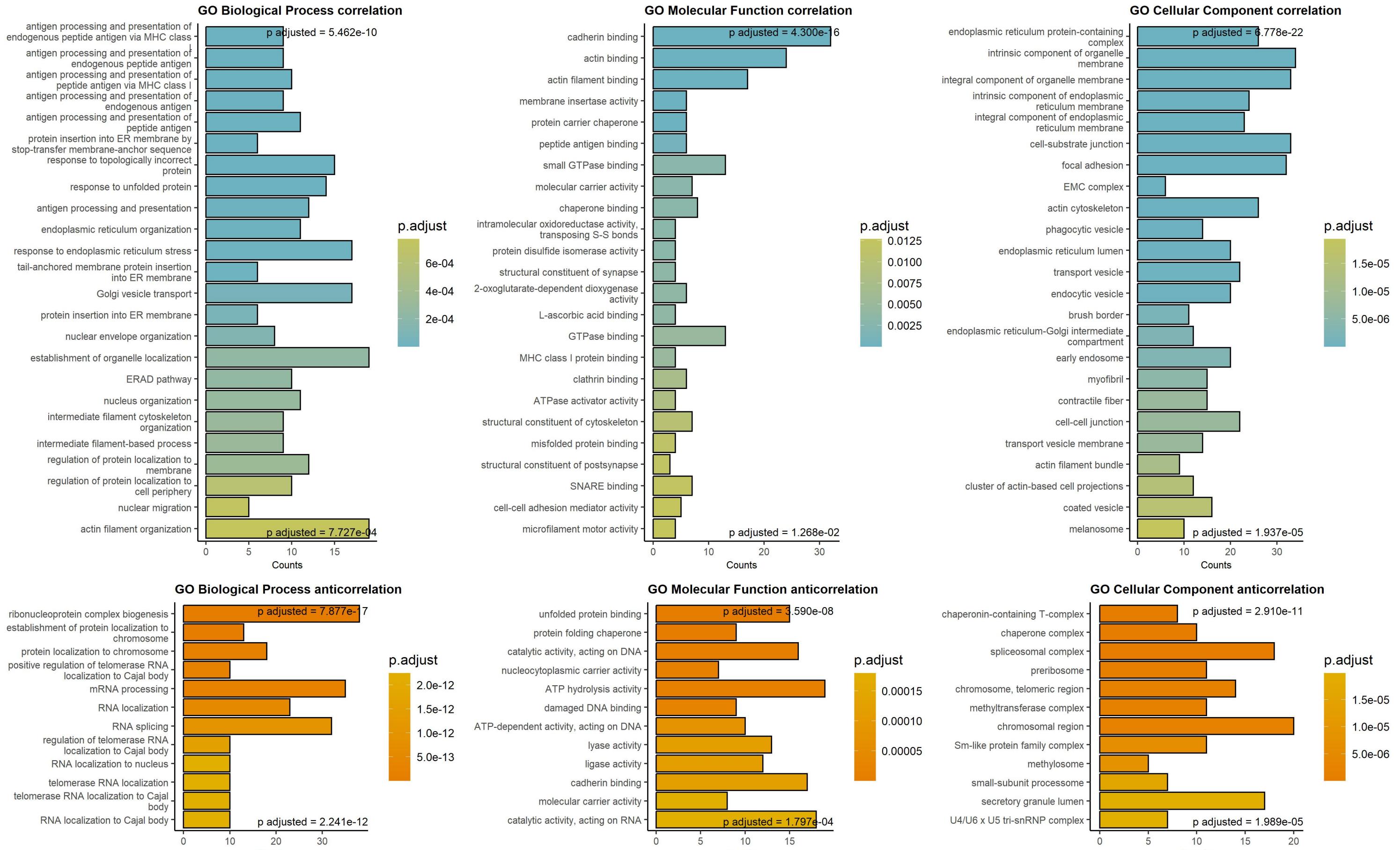
Differentially expressed proteins in solid cancers at absence/low amount of BAK1 , DB1
p-value < 0.05 & logFC > 1.2



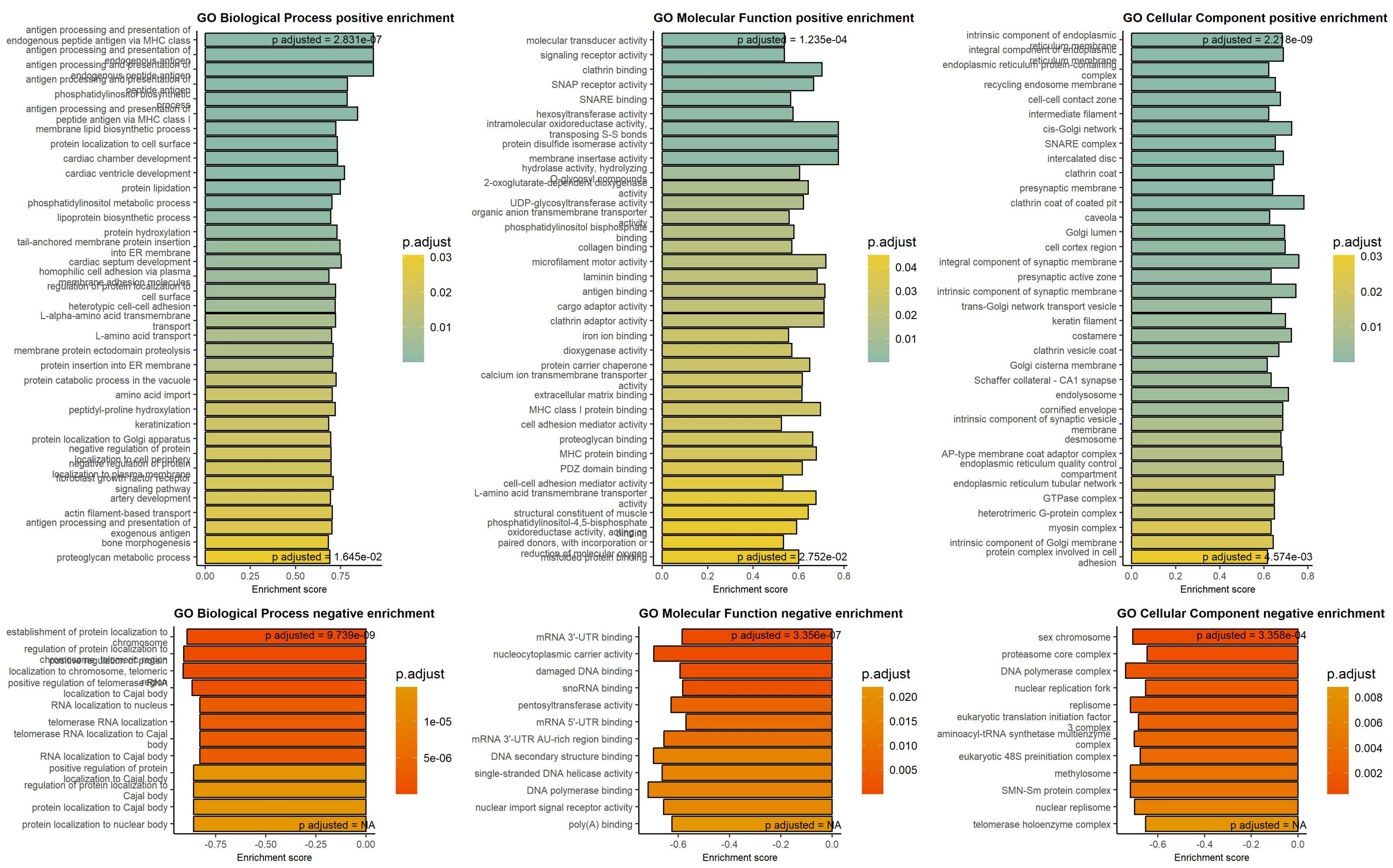
Sorted by p values!
Downregulated in solid cancers at low/absent BAK1 Upregulated in solid cancers at low/absent BAK1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.18	2.49e-30	LEMD2	LEM domain nuclear envelope protein	0.87	1.65e-17	DOHH	deoxyhypusine hydroxylase
-0.1	1.33e-23	CCDC47	coiled-coil domain containing 47	0.12	2.01e-17	DTYMK	deoxythymidylate kinase
-0.1	4.63e-23	ATP5PB	ATP synthase peripheral stalk-membr	0.74	4.29e-17	SHPK	sedoheptulokinase
-0.1	4.21e-22	ATP5F1C	ATP synthase F1 subunit gamma	1.06	2.75e-16	PBK	PDZ binding kinase
-0.13	9.24e-22	NUP155	nucleoporin 155	0.17	3.27e-16	ATIC	5-aminoimidazole-4-carboxamide ribo
-0.1	1.62e-21	PRPF8	pre-mRNA processing factor 8	0.77	3.66e-16	ZFAND6	zinc finger AN1-type containing 6
-0.1	4.39e-21	NCLN	nicalin	0.9	1.46e-15	DCK	deoxycytidine kinase
-0.08	4.39e-21	CS	citrate synthase	0.12	5.29e-15	PCNA	proliferating cell nuclear antigen
-0.08	2.17e-20	RPN1	ribophorin I	0.83	5.58e-15	GINS4	GINS complex subunit 4
-0.07	2.17e-20	H4C1	H4				

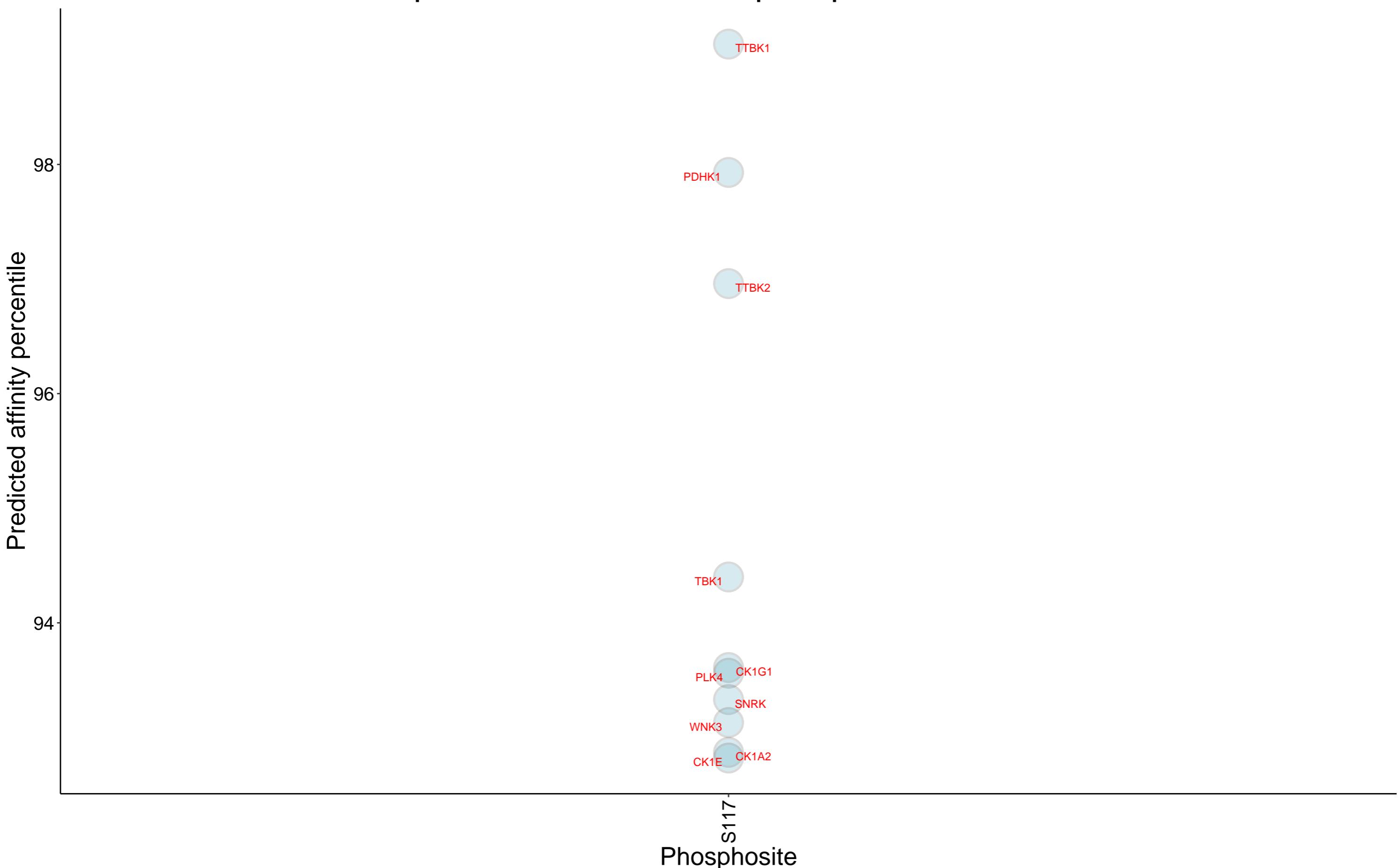
Top 250 correlation coefficients overrepresentation, BAK1 protein, DB1



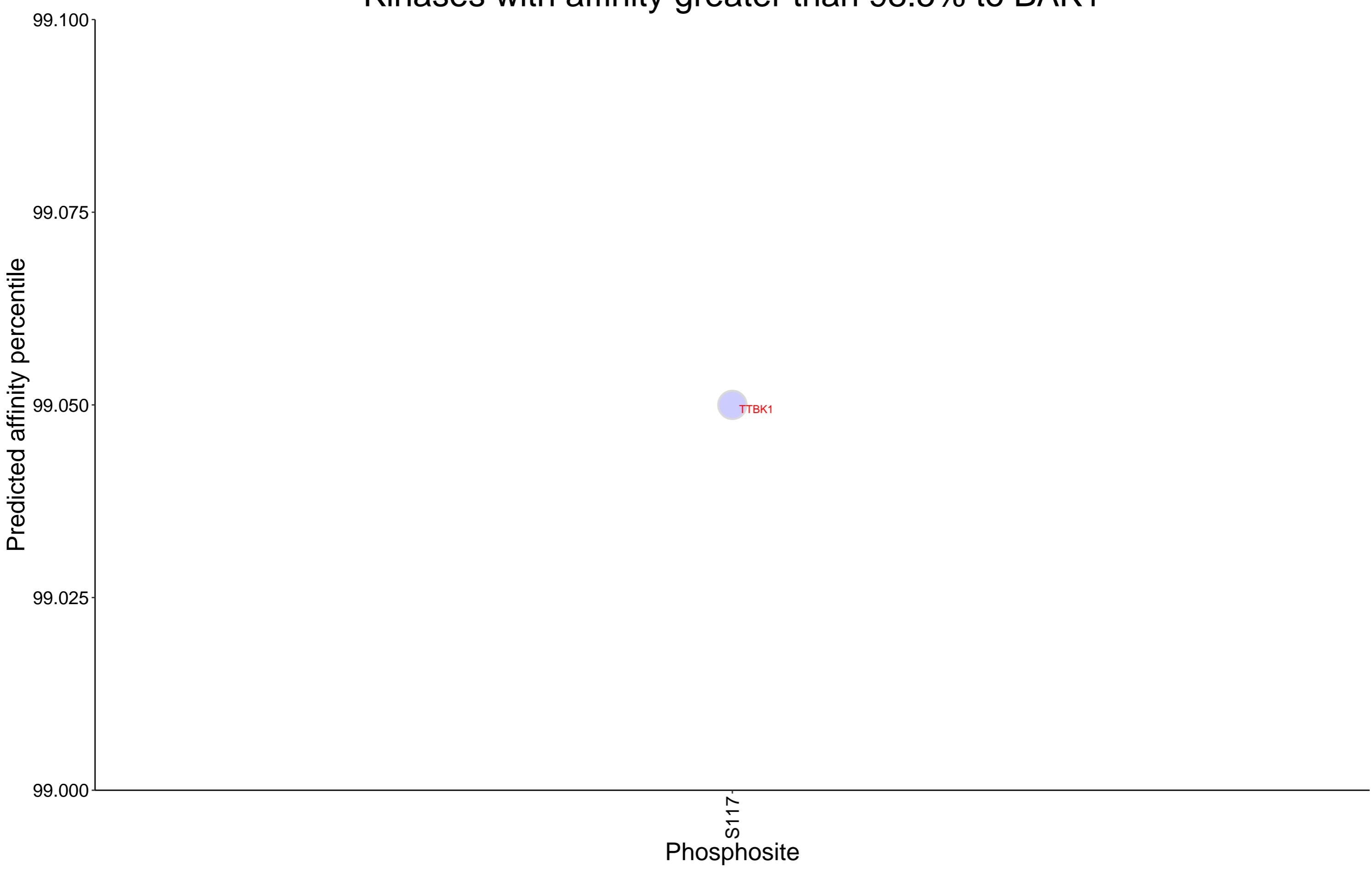
Gene Set Enrichment analysis on protein correlation coefficients, BAK1 protein, DB1



Top 10 kinases for each phosphosite in BAK1



Kinases with affinity greater than 98.5% to BAK1



Top 15 positive correlation coefficients for BAK1 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

