

BAG6

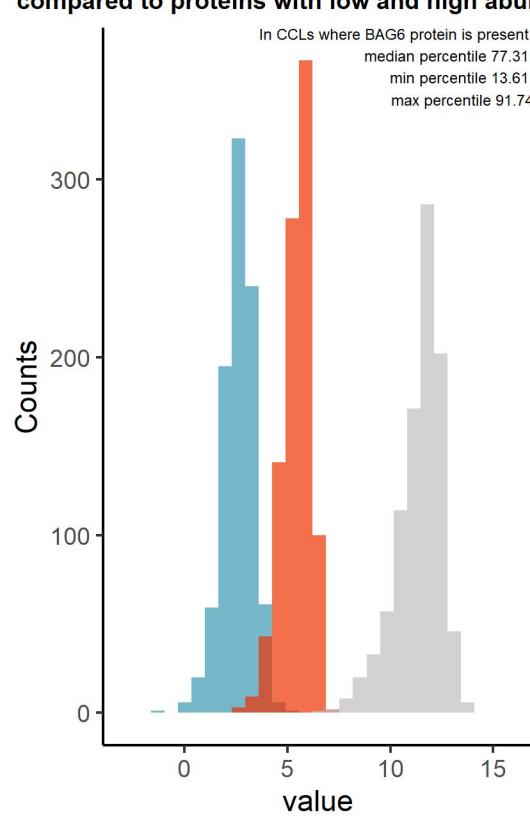
Protein name: BAG6 ; UNIPROT: P46379 ; Gene name: BAG cochaperone 6

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

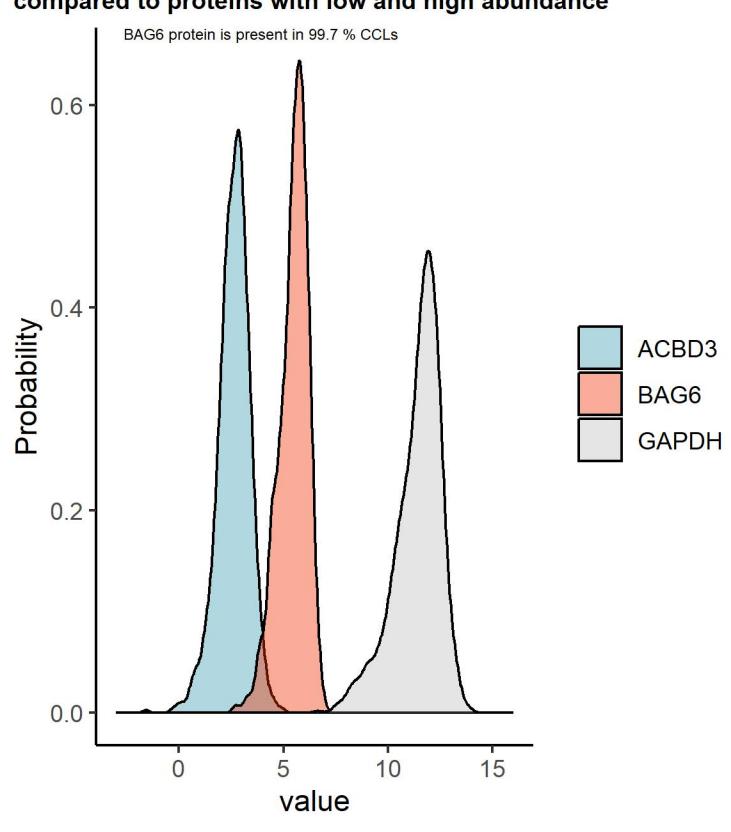
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

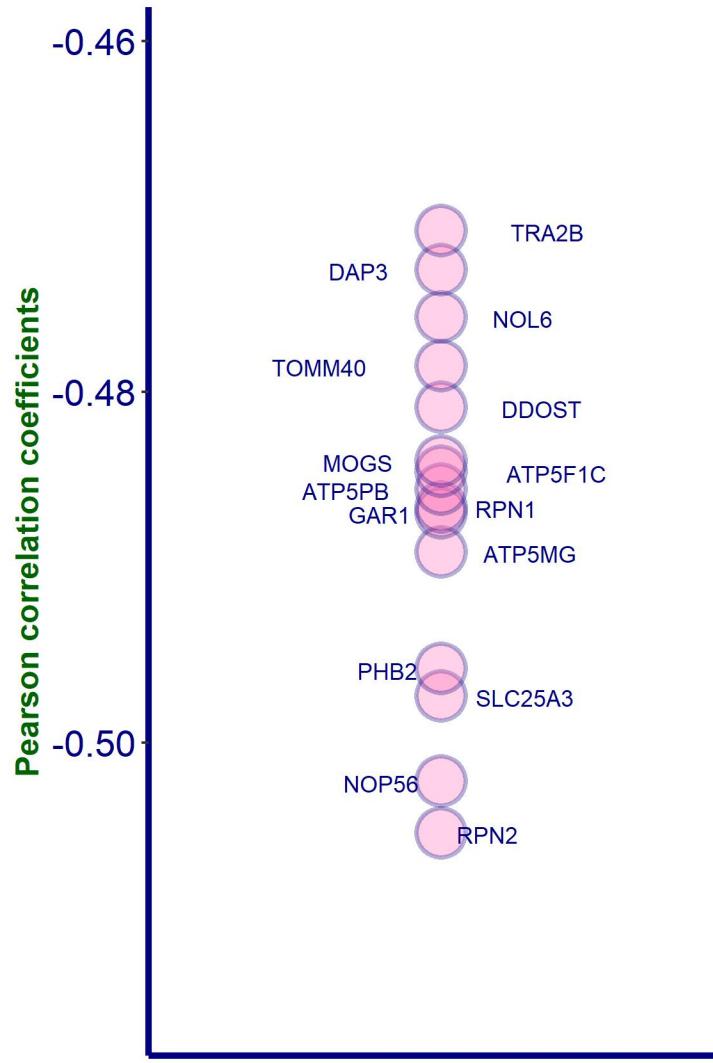
Histogram of BAG6 protein compared to proteins with low and high abundance



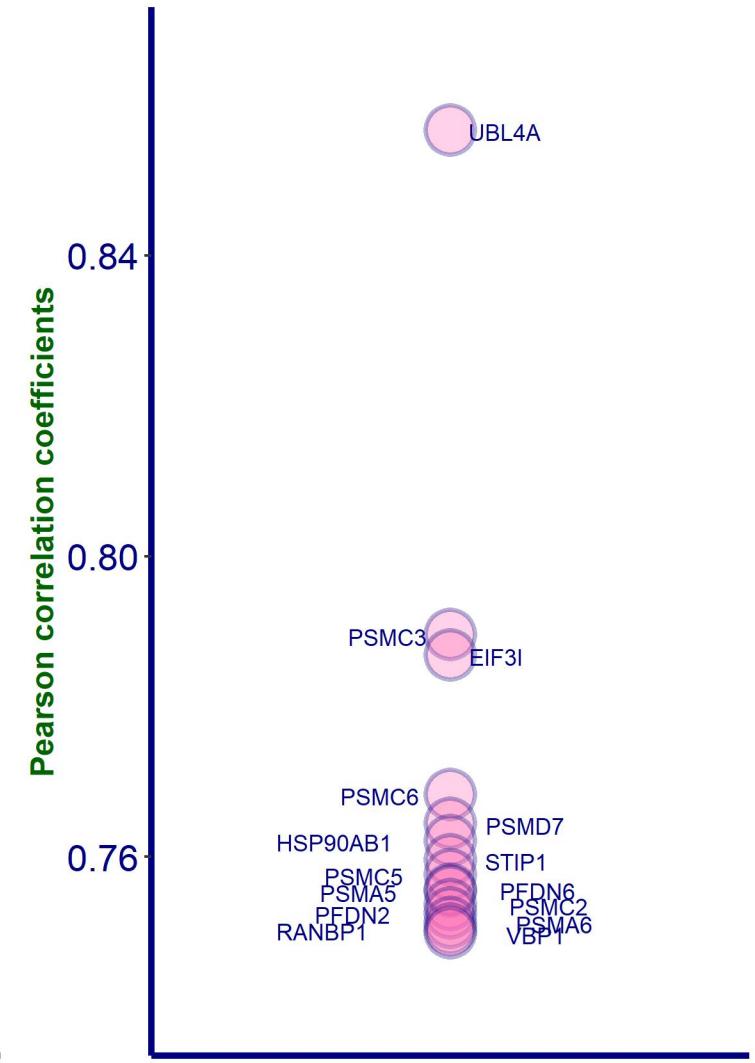
Density plot of BAG6 protein compared to proteins with low and high abundance



Top negative correlations of BAG6 protein, DB1

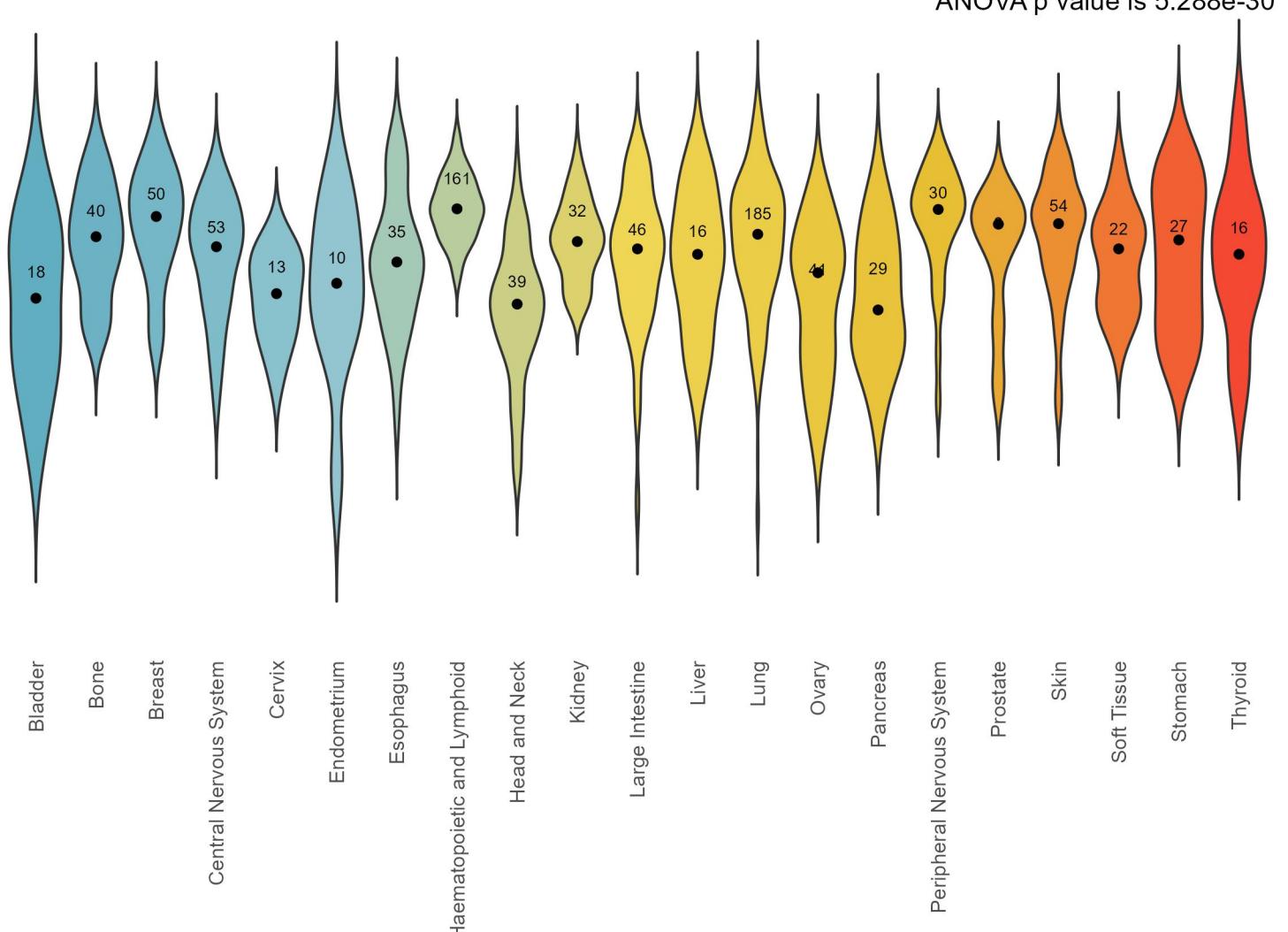


Top positive correlations of BAG6 protein, DB1



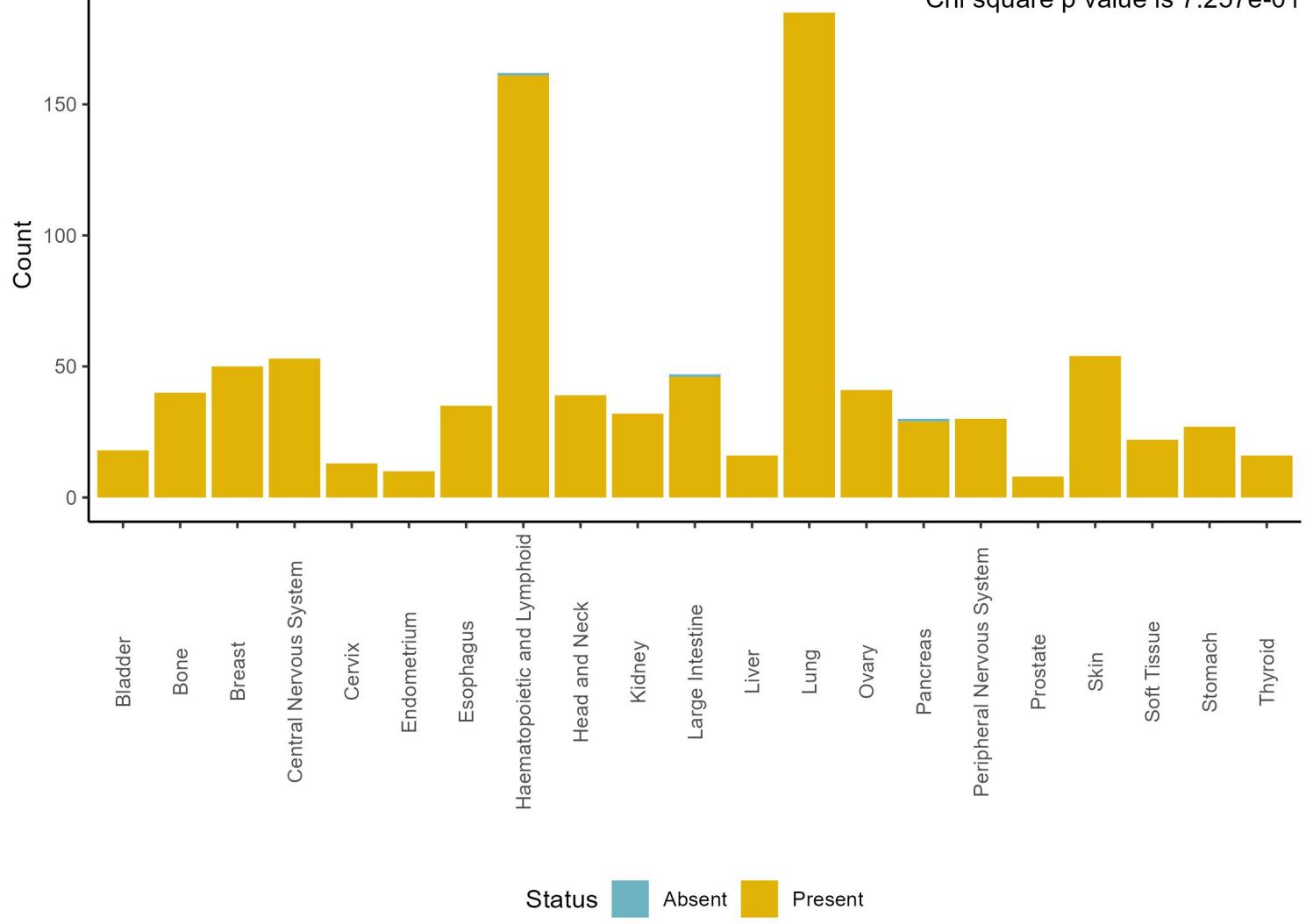
Amount of BAG6 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 5.288e-30



Present and absent BAG6 protein counts by tissue, DB1

Chi square p value is 7.257e-01

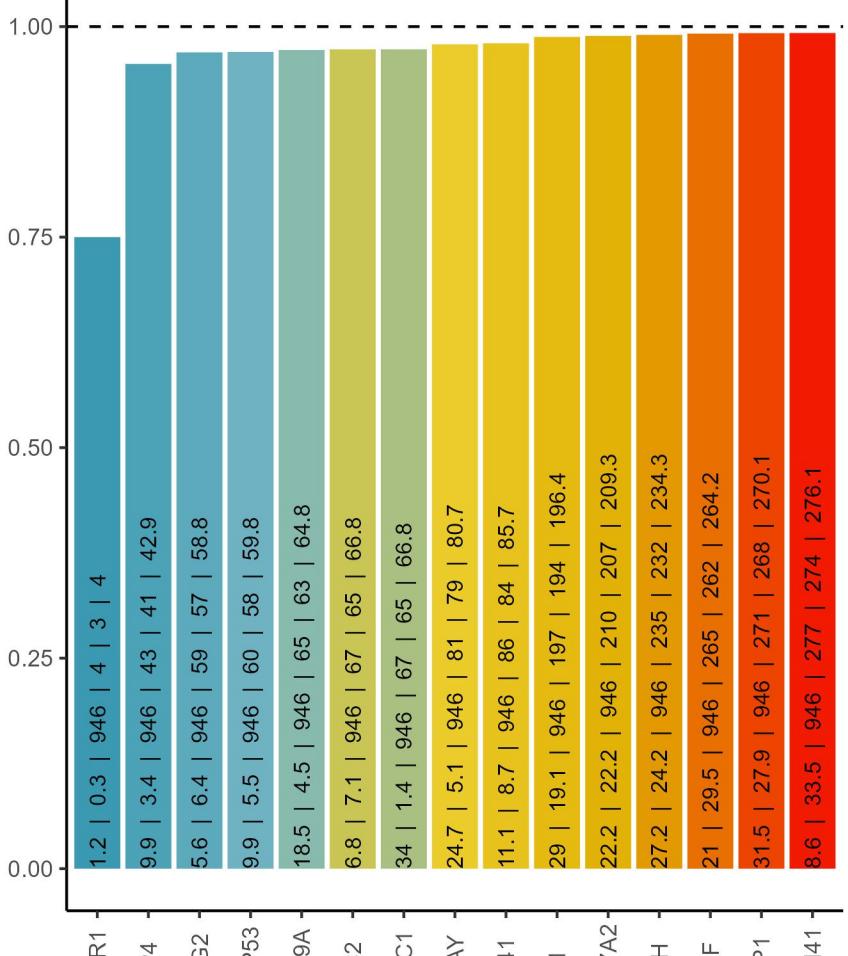


Cooccurrence with BAG6 protein, DB1

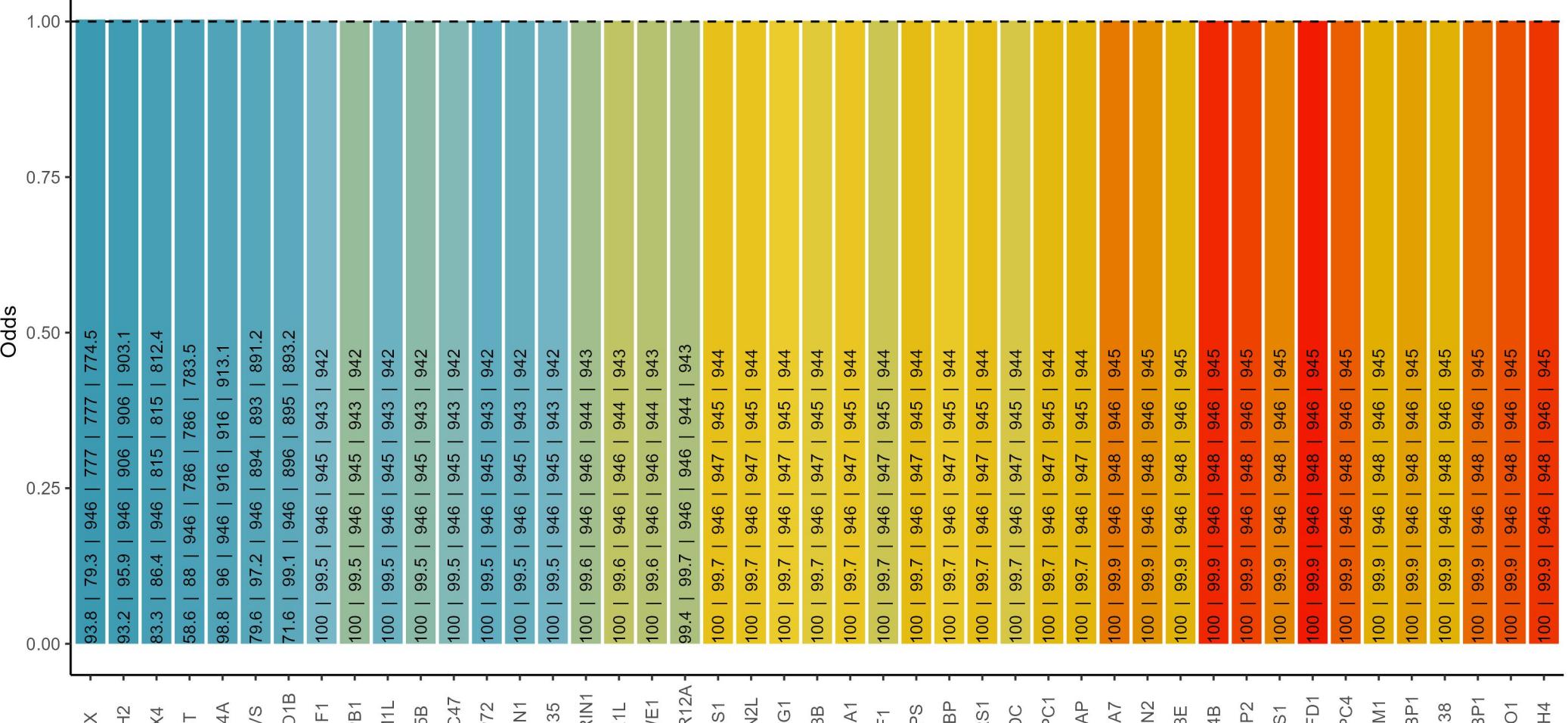
% of BAG6 in blood cancers: 99.4 ; % of BAG6 in solid cancers: 99.7

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of BAG6 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

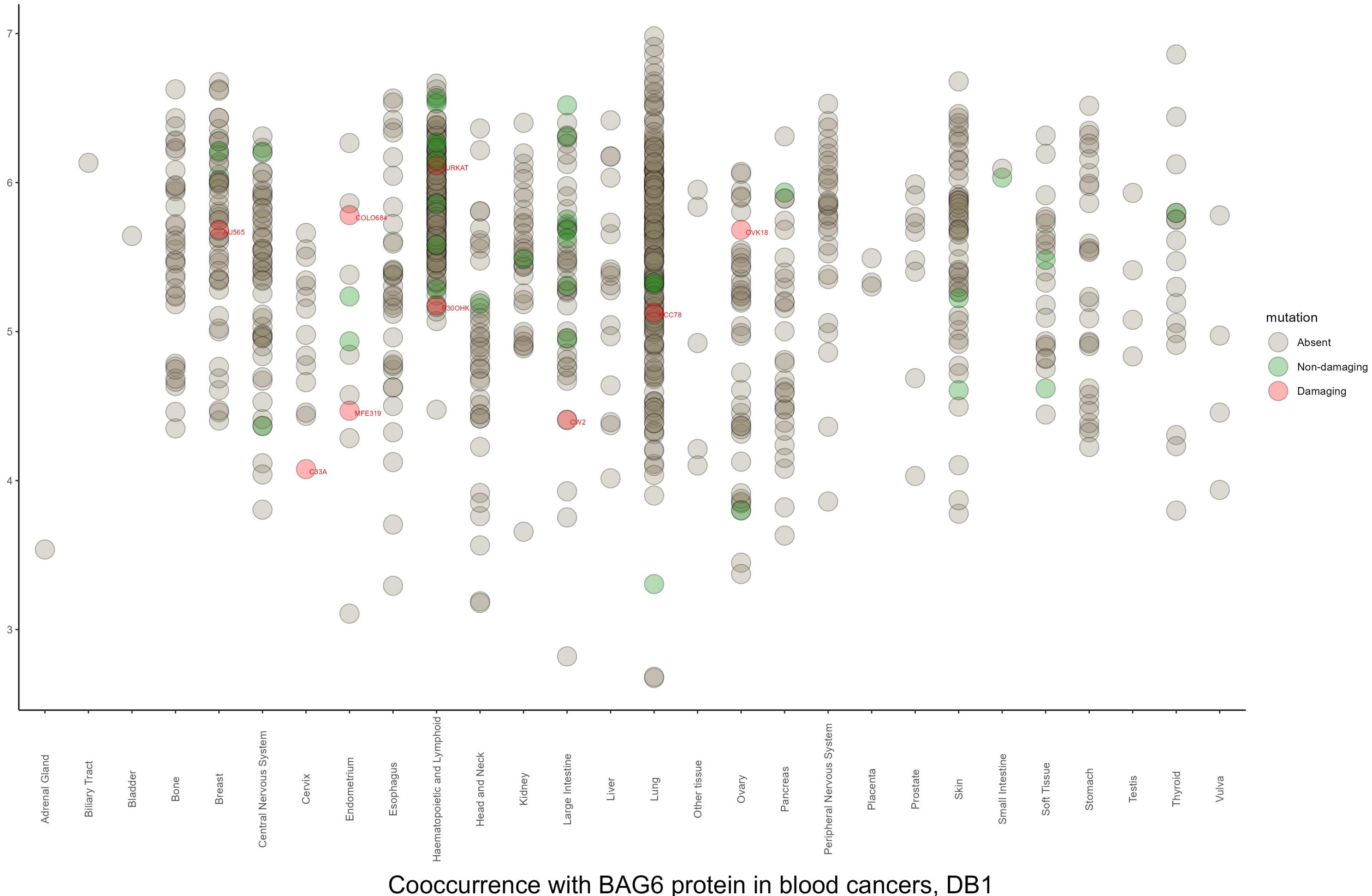
Negative cooccurrence



Positive cooccurrence



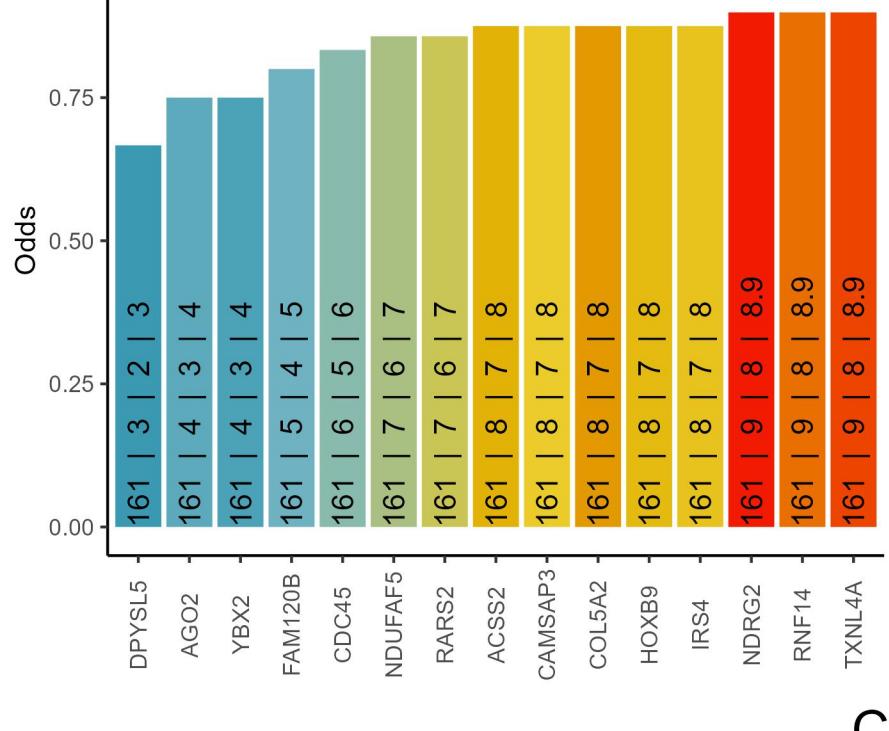
Amount of BAG6 protein and mutation status by tissue, DB1



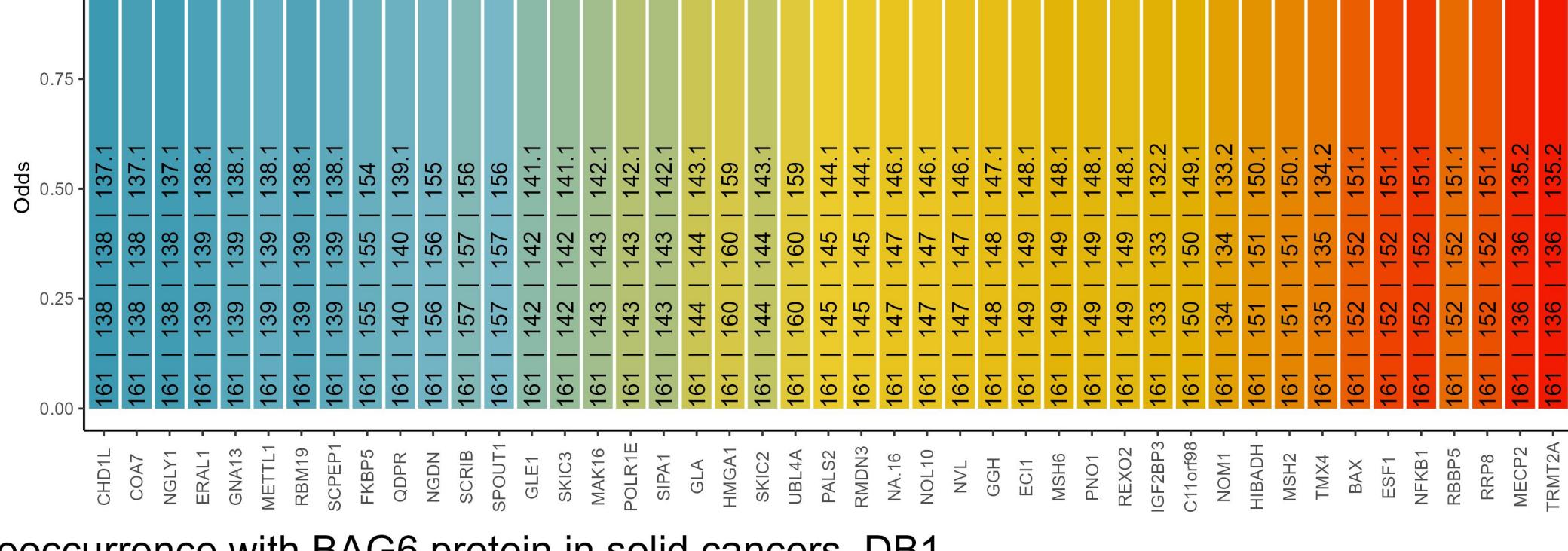
Cooccurrence with BAG6 protein in blood cancers, DB1

The text in the bars: incidence of BAG6 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



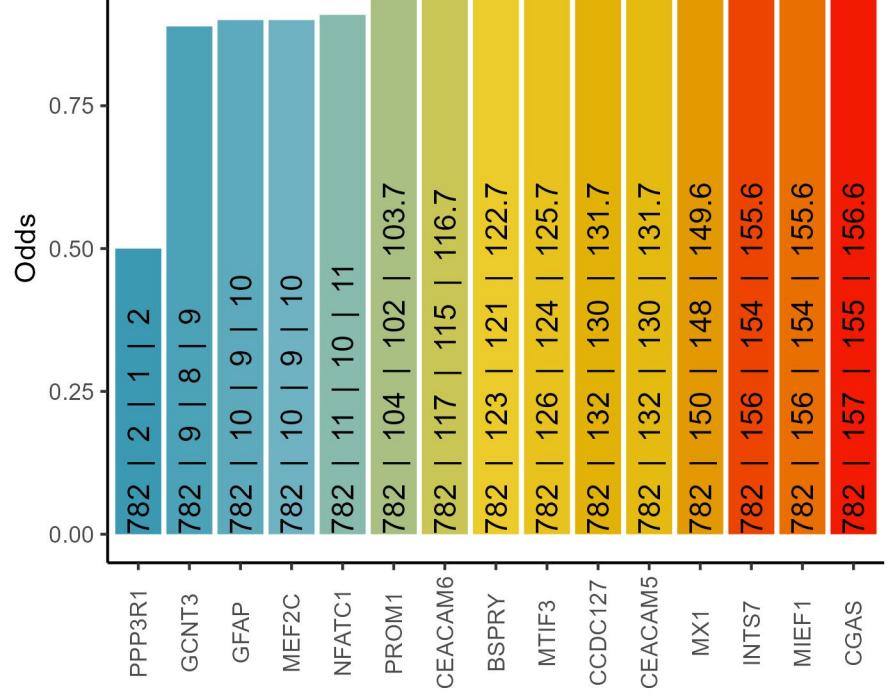
Positive cooccurrence



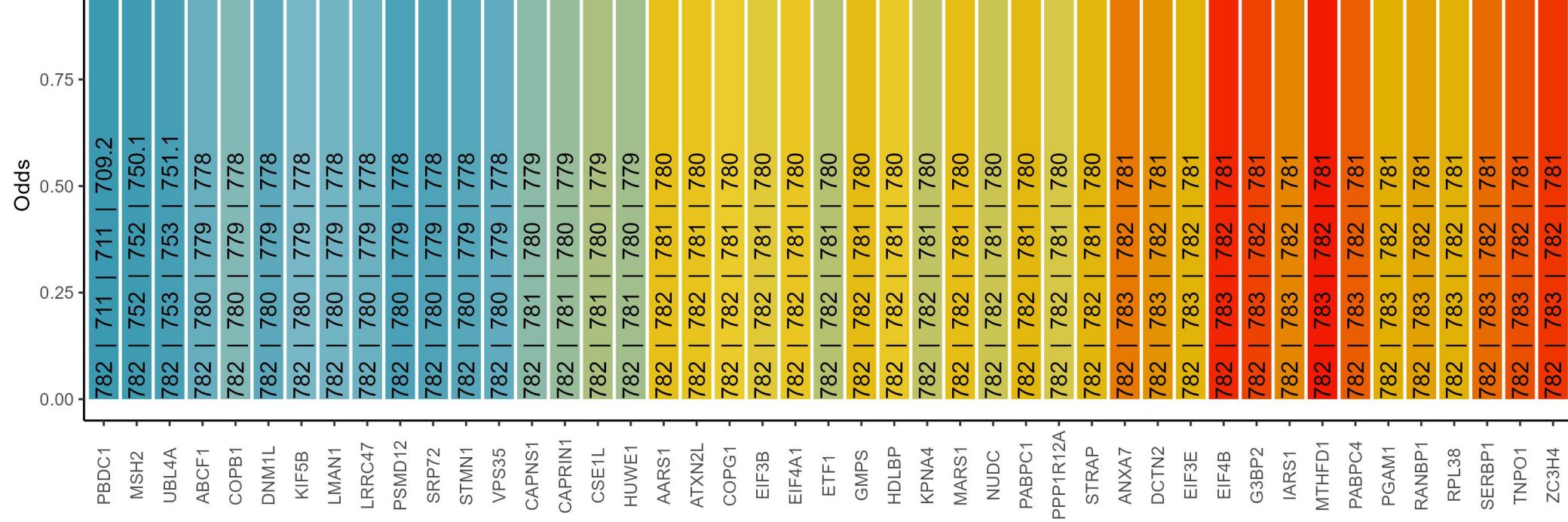
Cooccurrence with BAG6 protein in solid cancers, DB1

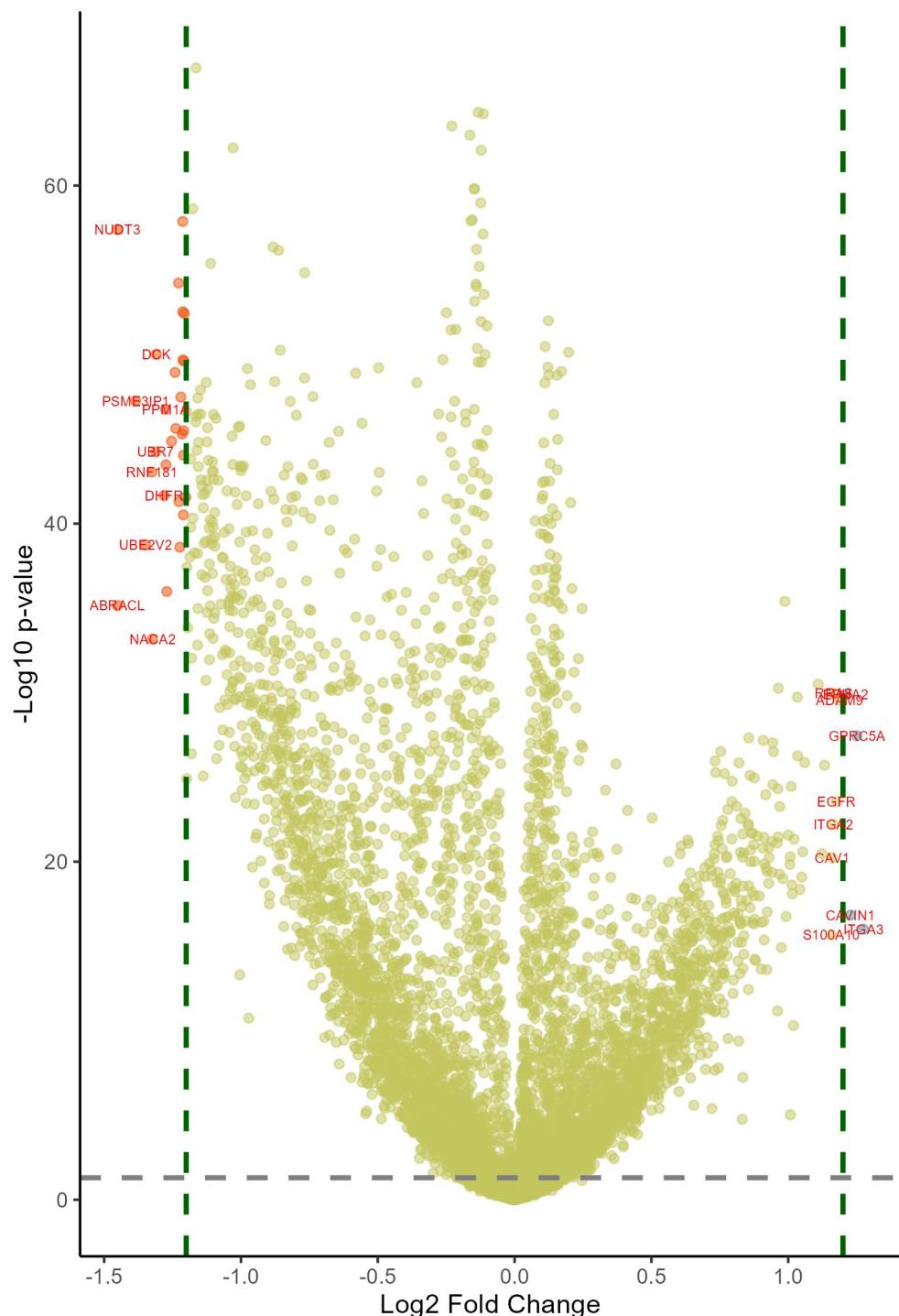
The text in the bars: incidence of BAG6 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



Positive cooccurrence

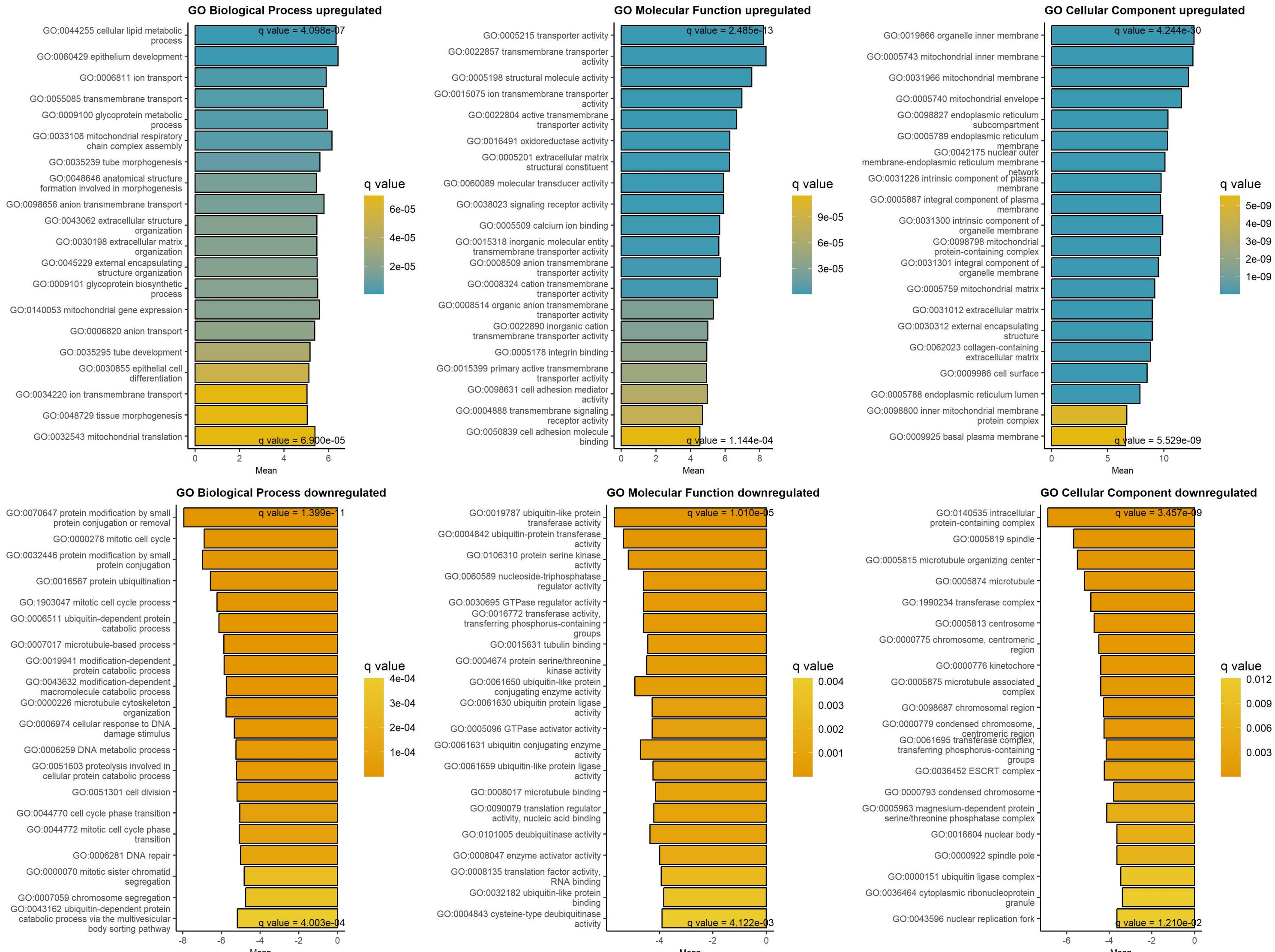




Downregulated at low/absent BAG6 Upregulated at low/absent BAG6

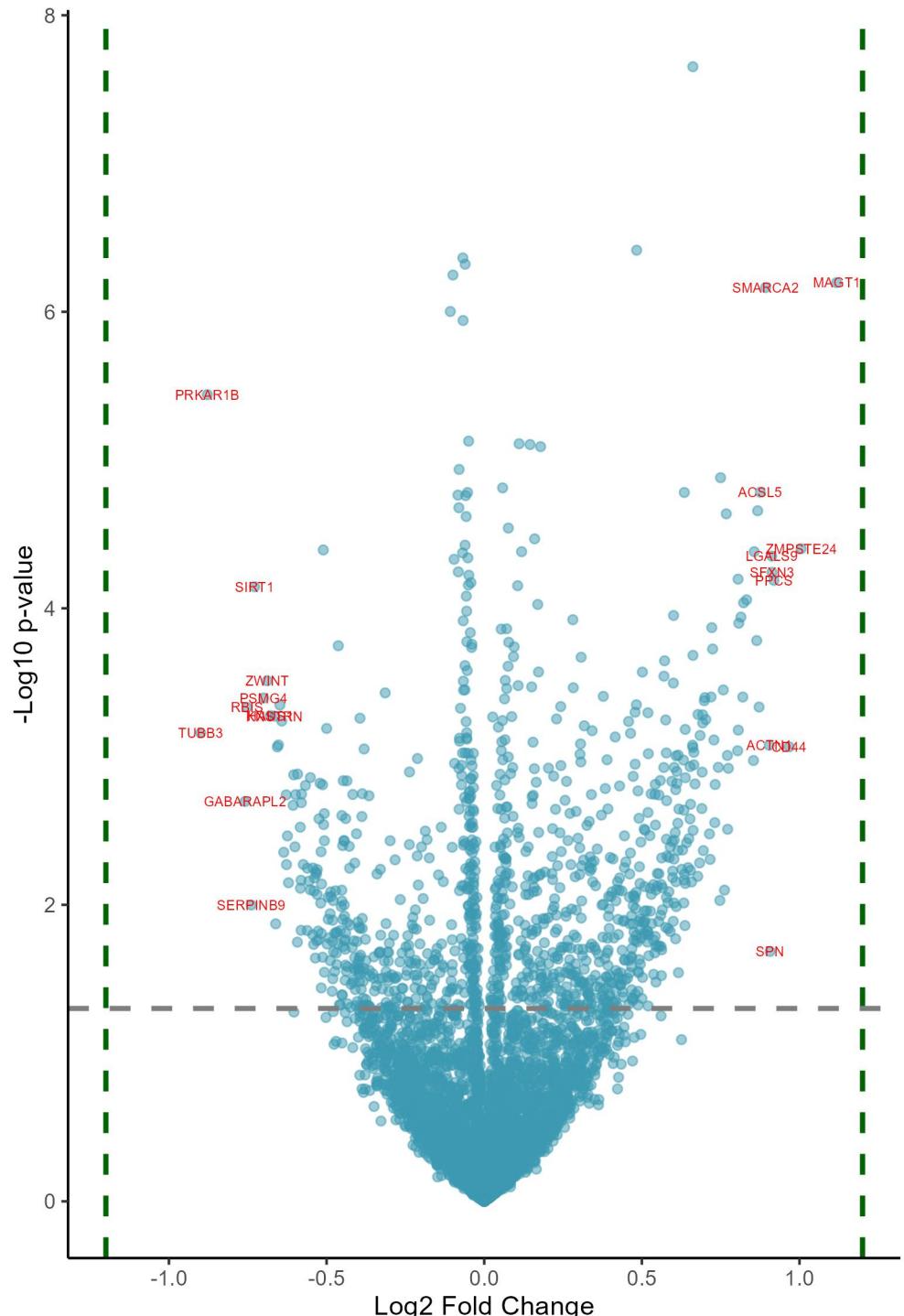
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.45	1.46e-34	ABRACL	ABRA C-terminal like	1.28	4.30e-16	ITGA3	integrin subunit alpha 3
-1.45	1.67e-55	NUDT3	nudix hydrolase 3	1.25	3.90e-27	GPRC5A	G protein-coupled receptor class C
-1.38	5.57e-46	PSME3IP1	proteasome activator subunit 3 inte	1.23	6.76e-17	CAVIN1	caveolae associated protein 1
-1.35	5.49e-38	UBE2V2	ubiquitin conjugating enzyme E2 V2	1.21	1.60e-29	EPHA2	EPH receptor A2
-1.33	4.62e-42	RNF181	ring finger protein 181	1.19	3.66e-29	ADAM9	ADAM metallopeptidase domain 9
-1.32	1.22e-32	NACA2	nascent polypeptide associated comp	1.18	2.14e-23	EGFR	epidermal growth factor receptor
-1.31	3.57e-43	UBR7	ubiquitin protein ligase E3 compone	1.17	1.42e-29	RRAS	RAS related
-1.31	1.56e-48	DCK	deoxycytidine kinase	1.16	4.27e-22	ITGA2	integrin subunit alpha 2
-1.28	9.09e-41	DHFR	dihydrofolate reductase	1.16	3.55e-20	CAV1	caveolin 1
-1.28	1.64e-45	PPM1A	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe	1.16	8.86e-16	S100A10	S100 calcium binding protein A10
-1.27	1.90e-42	COPS7B	COP9 signalosome subunit 7B	1.13	1.81e-25	UQCR10	ubiquinol-cytochrome c reductase, c
-1.27	2.40e-35	PBK	PDZ binding kinase	1.12	2.03e-20	AP2S1	adaptor related protein complex 2 s
-1.25	9.02e-44	PPM1B	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe	1.11	4.49e-30	SDC4	syndecan 4
-1.24	1.44e-47	CCDC43	coiled-coil domain containing 43	1.06	1.26e-25	CD151	CD151 molecule (Raph blood group)
-1.24	1.77e-44	PITHD1	PITH domain containing 1	1.05	1.63e-20	PPIC	peptidylprolyl isomerase C
-1.23	1.61e-52	GINS4	GINS complex subunit 4	1.05	4.42e-19	ITGB4	integrin subunit beta 4
-1.23	1.98e-40	ARMC6	armadillo repeat containing 6	1.04	2.25e-18	KRT17	keratin 17
-1.22	7.45e-38	PPP6R1	protein phosphatase 6 regulatory su	1.03	5.37e-26	MBOAT7	membrane bound O-acyltransferase do
-1.22	3.37e-46	GRIPAP1	GRIP1 associated protein 1	1.03	2.35e-29	FNDC3B	fibronectin type III domain contain
-1.22	3.59e-44	RABEP1	rabaptin, RAB GTPase binding effect	1.02	3.03e-21	GPX8	glutathione peroxidase 8 (putative)
-1.21	5.90e-56	DOHH	deoxyhypusine hydroxylase	1.02	1.42e-10	GNG12	G protein subunit gamma 12
-1.21	6.62e-51	NUDT1	nudix hydrolase 1	1.01	4.06e-18	NT5E	5'-nucleotidase ecto
-1.21	3.15e-48	EIPR1	EARP complex and GARP complex inter	1.01	1.28e-18	DSG2	desmoglein 2
-1.21	1.10e-39	UBE2T	ubiquitin conjugating enzyme E2 T	1.01	2.91e-24	F3	coagulation factor III, tissue fact
-1.21	5.51e-43	TP53RK	TP53 regulating kinase	1.01	1.73e-05	KRT18	keratin 18
-1.21	2.38e-44	KIAA1143	KIAA1143	1	1.78e-21	KRT80	keratin 80
-1.21	3.53e-48	TACC3	transforming acidic coiled-coil con	1.01	8.33e-20	MMP14	matrix metallopeptidase 14
-1.21	7.94e-51	AARS1	alanyl-tRNA synthetase domain conta	1	1.78e-21	KRT80	keratin 80
-1.2	1.12e-40	UBA5	ubiquitin like modifier activating	0.99	8.06e-17	S100A16	S100 calcium binding protein A16

GAGE analysis on upregulated and downregulated proteins at low/absent BAG6 protein, DB1



Differentially expressed proteins in blood cancers at absence/low amount of BAG6 , DB1

p-value < 0.05 & logFC > 1.2

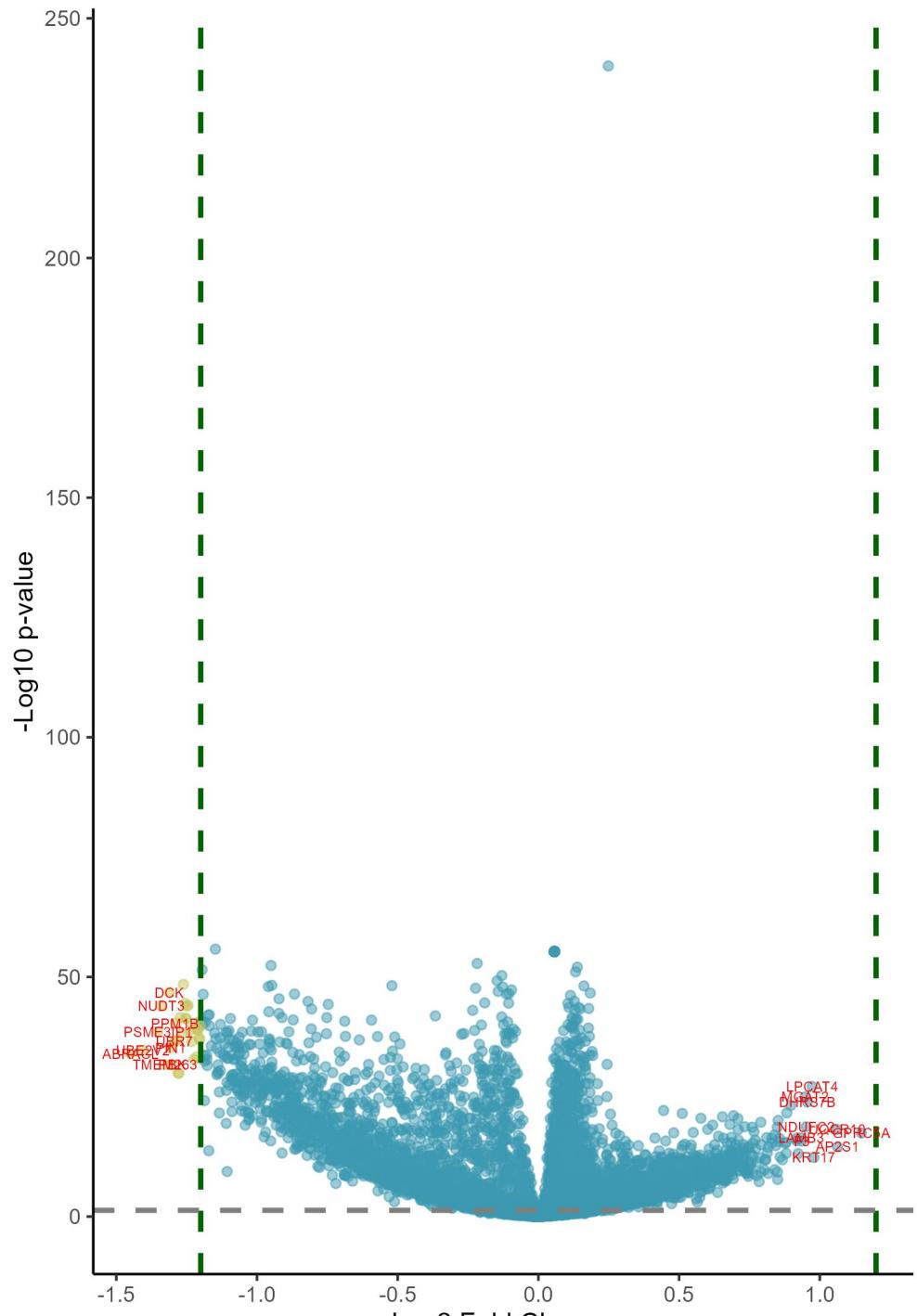


Downregulated in blood cancers at low/absent BAG6 Upregulated in blood cancers at low/absent BAG6

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.9	3.57e-02	TUBB3	tubulin beta 3 class III	1.12	6.51e-04	MAGT1	magnesium transporter 1
-0.88	2.41e-03	PRKAR1B	protein kinase cAMP-dependent type	1.01	8.03e-03	ZMPSTE24	zinc metallopeptidase STE24
-0.76	5.52e-02	GABARAPL2	GABA type A receptor associated pro	0.97	3.92e-02	CD44	CD44 molecule (Indian blood group)
-0.75	3.00e-02	RBIS	ribosomal biogenesis factor	0.92	1.00e-02	PPCS	phosphopantethenoylcysteine synthet
-0.74	1.27e-01	SERPINB9	serpin family B member 9	0.91	9.51e-03	SFXN3	sideroflexin 3
-0.73	1.01e-02	SIRT1	sirtuin 1	0.91	8.18e-03	LGALS9	galectin 9
-0.7	2.79e-02	PSMG4	proteasome assembly chaperone 4	0.91	1.84e-01	SPN	sialophorin
-0.69	2.51e-02	ZWINT	ZW10 interacting kinetochore protei	0.9	3.87e-02	ACTN1	actinin alpha 1
-0.68	3.21e-02	HAUS1	HAUS augmin like complex subunit 1	0.89	6.51e-04	SMARCA2	SWI/SNF related, matrix associated,
-0.67	3.21e-02	KNSTRN	kinetochore localized astrin (SPAG5	0.88	5.25e-03	ACSL5	acyl-CoA synthetase long chain fami
-0.66	1.50e-01	IGF2BP1	insulin like growth factor 2 mRNA b	0.87	3.00e-02	BIN2	bridging integrator 2
-0.66	3.92e-02	ARL2BP	ADP ribosylation factor like GTPase	0.87	5.90e-03	DGLUCY	D-glutamate cyclase
-0.65	3.87e-02	CCNB2	cyclin B2	0.86	1.76e-02	PIGK	phosphatidylinositol glycan anchor
-0.65	2.99e-02	DLGAP5	DLG associated protein 5	0.86	8.03e-03	DUSP23	dual specificity phosphatase 23
-0.64	3.22e-02	RANBP10	RAN binding protein 10	0.85	4.21e-02	GSN	gelsolin
-0.64	8.42e-02	CEP43	centrosomal protein 43	0.83	1.19e-02	MYO1F	myosin IF
-0.63	5.20e-02	GINS2	GINS complex subunit 2	0.82	1.22e-02	CHID1	chitinase domain containing 1
-0.63	9.38e-02	CHMP5	charged multivesicular body protein	0.82	2.79e-02	UNC13D	unc-13 homolog D
-0.62	7.50e-02	ETS1	ETS proto-oncogene 1, transcription	0.81	1.41e-02	DAD1	defender against cell death 1
-0.62	1.07e-01	GLCCI1	glucocorticoid induced 1	0.81	1.47e-02	ARRB1	arrestin beta 1
-0.61	5.74e-02	C1orf52	chromosome 1 open reading frame 52	0.81	3.50e-02	GLB1	galactosidase beta 1
-0.6	4.62e-02	PDCD2L	programmed cell death 2 like	0.81	1.00e-02	MFN2	mitofusin 2
-0.6	2.97e-01	MZB1	marginal zone B and B1 cell specifi	0.8	4.05e-02	ARF4	ADP ribosylation factor 4
-0.6	8.06e-02	MYH11	myosin heavy chain 11	0.77	4.36e-02	SERPINH1	serpin family H member 1
-0.6	5.20e-02	DTNBP1	dystrobrelin binding protein 1	0.77	7.07e-02	STOM	stomatin
-0.59	1.73e-01	GCSH	glycine cleavage system protein H	0.77	4.08e-02	ITGA5	integrin subunit alpha 5
-0.59	4.60e-02	PEX1	peroxisomal biogenesis factor 1	0.77	5.90e-03	TEX10	testis expressed 10
-0.58	6.96e-02	PBK	PDZ binding kinase	0.76	1.12e-01	RTN4	reticulon 4
-0.58	1.11e-01	KIF23	kinesin family member 23	0.76	2.63e-02	LPCAT2	lysophosphatidylcholine acyltransfe

Differentially expressed proteins in solid cancers at absence/low amount of BAG6 , DB1

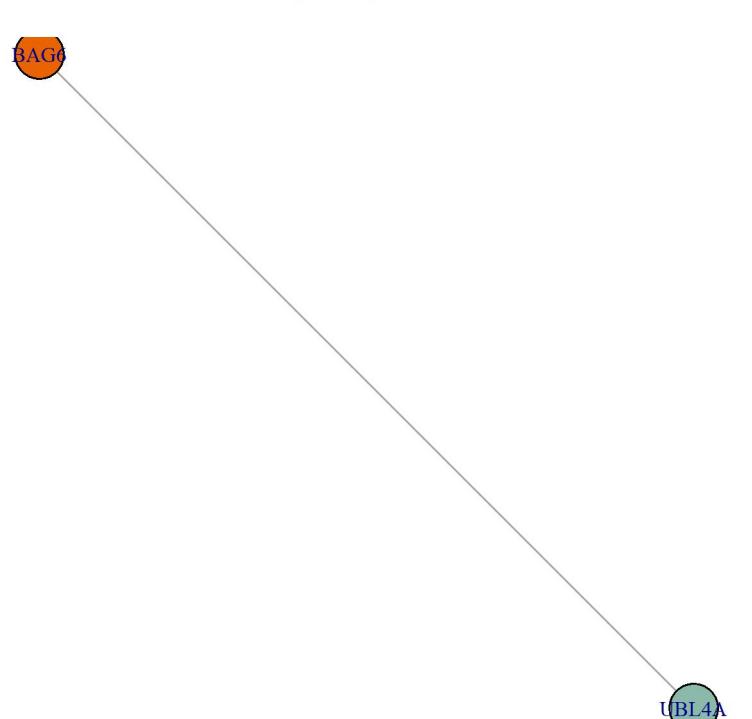
p-value < 0.05 & logFC > 1.2



Downregulated in solid cancers at low/absent BAG6 Upregulated in solid cancers at low/absent BAG6

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.45	2.54e-33	ABRACL	ABRA C-terminal like	1.15	2.04e-17	GPRC5A	G protein-coupled receptor class C
-1.41	5.06e-34	UBE2V2	ubiquitin conjugating enzyme E2 V2	1.06	1.30e-14	AP2S1	adaptor related protein complex 2 s
-1.35	1.20e-37	PSME3IP1	proteasome activator subunit 3 inte	1.06	4.00e-18	UQCR10	ubiquinol-cytochrome c reductase, c
-1.34	6.46e-43	NUDT3	nudix hydrolase 3	0.98	1.74e-12	KRT17	keratin 17
-1.33	3.83e-31	TMEM263	transmembrane protein 263	0.97	9.05e-27	LPCAT4	lysophosphatidylcholine acyltransfe
-1.31	1.17e-45	DCK	deoxyctydine kinase	0.96	1.23e-23	DHRS7B	dehydrogenase/reductase 7B
-1.31	1.64e-34	PIN1	peptidylprolyl cis/trans isomerase,	0.95	1.15e-18	NDUFC2	NADH:ubiquinone oxidoreductase subu
-1.3	3.64e-31	PBK	PDZ binding kinase	0.95	1.06e-24	MGAT2	alpha-1,6-mannosyl-glycoprotein 2-b
-1.29	7.87e-36	UBR7	ubiquitin protein ligase E3 compone	0.94	9.29e-16	F3	coagulation factor III, tissue fact
-1.29	2.34e-39	PPM1B	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe	0.93	2.01e-16	LAMB3	laminin subunit beta 3
-1.28	1.82e-29	FKBP1A	FKBP prolyl isomerase 1A	0.92	3.02e-13	KRT5	keratin 5
-1.28	4.04e-36	PITHD1	PITH domain containing 1	0.92	7.49e-16	EPHA2	EPH receptor A2
-1.28	2.15e-29	CLNS1A	chloride nucleotide-sensitive chann	0.91	2.83e-16	LAMC2	laminin subunit gamma 2
-1.27	1.51e-40	PPP1R14B	protein phosphatase 1 regulatory in	0.9	5.76e-23	LAMA3	laminin subunit alpha 3
-1.26	2.00e-37	PPM1A	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe	0.88	1.90e-21	MRPS10	mitochondrial ribosomal protein S10
-1.26	2.61e-47	TBCC	tubulin folding cofactor C	0.88	2.84e-13	KRT80	keratin 80
-1.26	1.90e-43	PHPT1	phosphohistidine phosphatase 1	0.88	1.63e-15	MRPS18C	mitochondrial ribosomal protein S18
-1.25	2.12e-40	NUDCD3	NudC domain containing 3	0.88	2.51e-15	UXS1	UDP-glucuronate decarboxylase 1
-1.25	2.86e-40	CCDC43	coiled-coil domain containing 43	0.87	5.27e-12	MISP	mitotic spindle positioning
-1.25	6.82e-43	NUDT1	nudix hydrolase 1	0.86	1.46e-12	LCLAT1	lysocardiolipin acyltransferase 1
-1.24	4.94e-43	AARSD1	alanyl-tRNA synthetase domain conta	0.86	2.51e-16	RAP2B	RAP2B, member of RAS oncogene famil
-1.24	5.57e-38	WASL	WASP like actin nucleation promotin	0.85	1.14e-15	SDC4	syndecan 4
-1.23	9.36e-36	FN3KRP	fructosamine 3 kinase related prote	0.85	6.02e-20	SGPL1	sphingosine-1-phosphate lyase 1
-1.22	3.86e-32	ENSA	endosulfine alpha	0.85	4.61e-08	CAVIN1	caveolae associated protein 1
-1.22	2.16e-38	PCYT2	phosphate cytidylyltransferase 2, e	0.85	1.55e-09	ITGA3	integrin subunit alpha 3
-1.21	1.06e-32	CZIB	CXXC motif containing zinc binding	0.85	1.55e-18	FNDC3B	fibronectin type III domain contain
-1.21	2.28e-38	LZIC	leucine zipper and CTNNBIP1 domain	0.84	7.41e-15	RRAS2	RAS related 2
-1.21	4.73e-38	UBE2C	ubiquitin conjugating enzyme E2 C	0.84	4.96e-10	BRI3BP	BRI3 binding protein
-1.21	1.10e-39	PPP2R5D	protein phosphatase 2 regulatory su	0.84	5.34e-17	ERGIC2	ERGIC and golgi 2

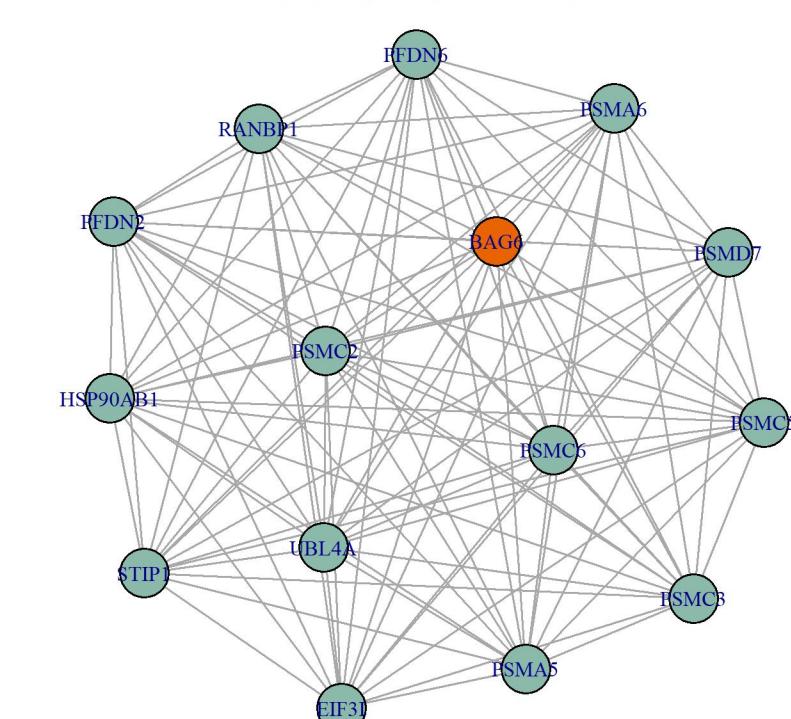
BAG6 network, DB1, all Pearson r > 0.85

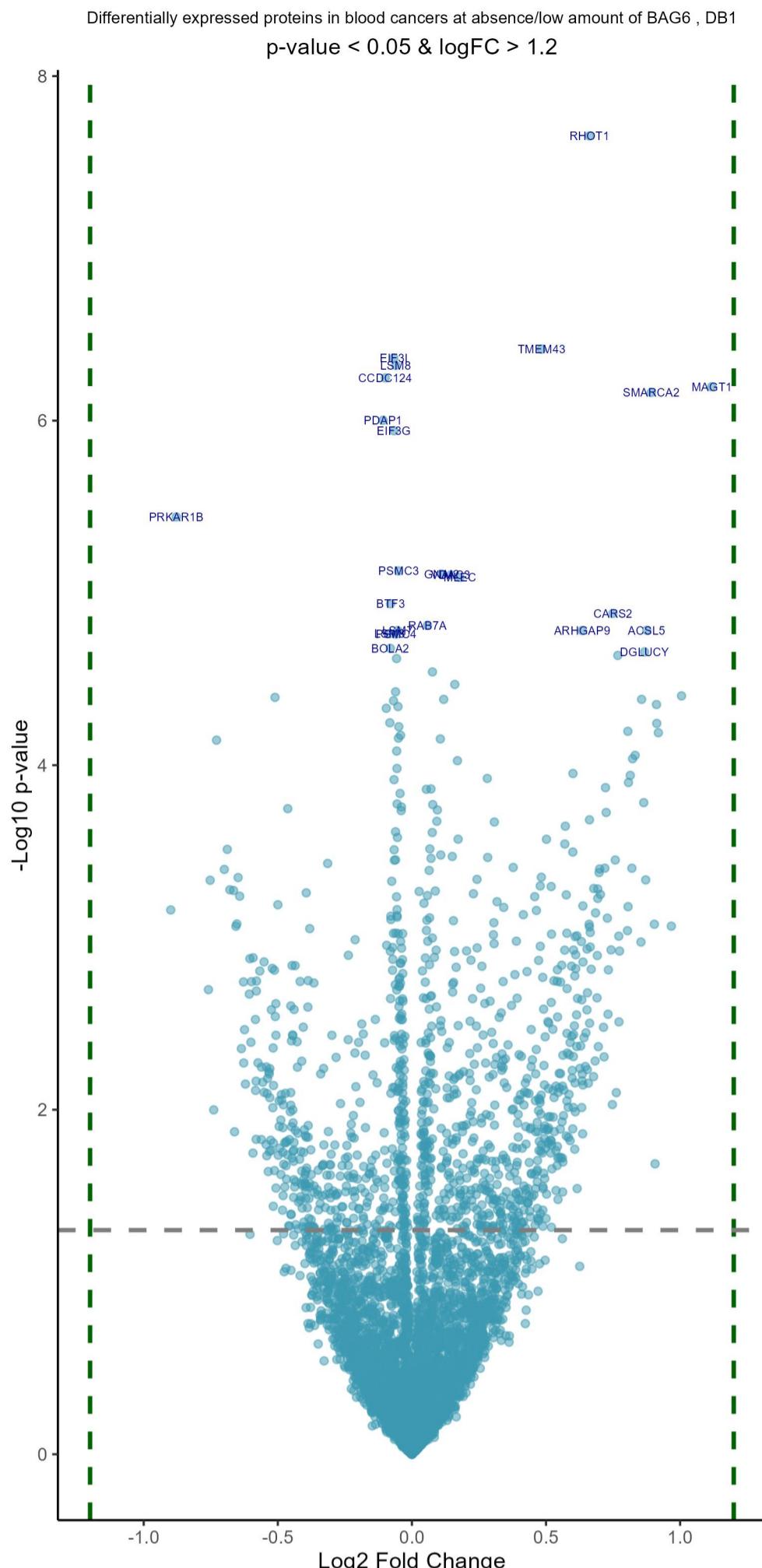


BAG6 network, DB1, all Pearson r > 0.8

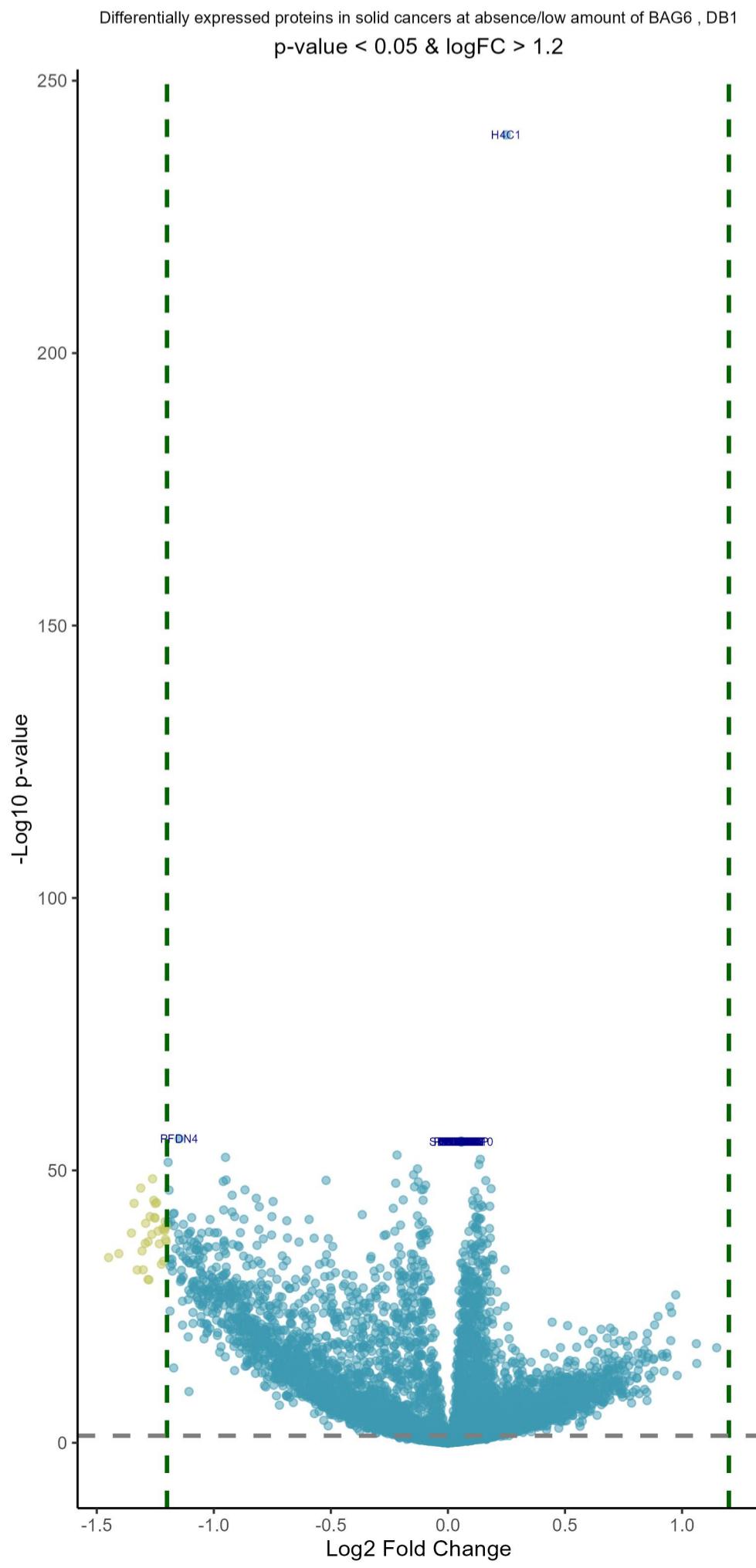


BAG6 network, DB1, all Pearson r > 0.75



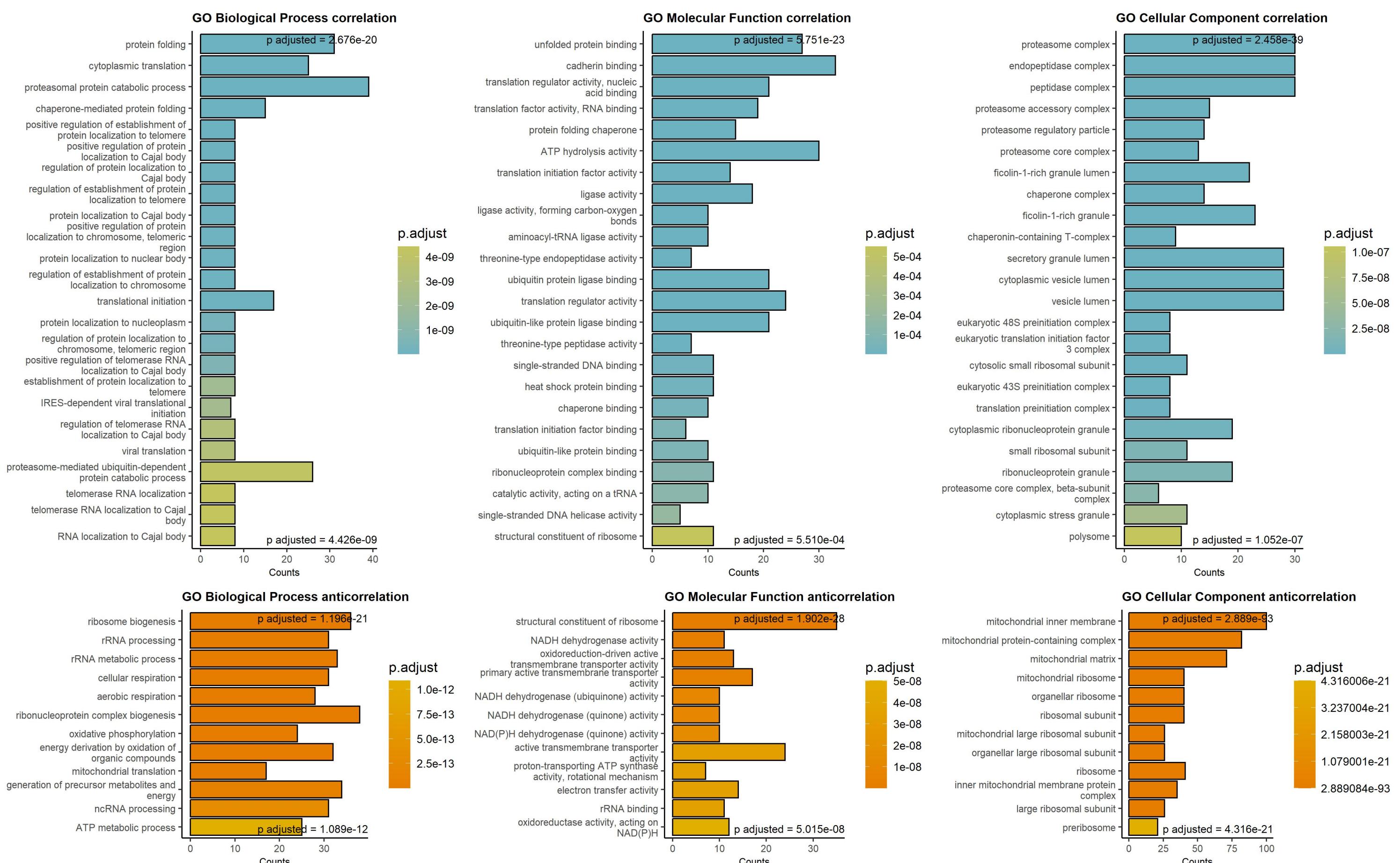


Sorted by p values!							
Downregulated in blood cancers at low/absent BAG6				Upregulated in blood cancers at low/absent BAG6			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.07	6.51e-04	EIF3I	eukaryotic translation initiation f	0.66	1.48e-04	RHOT1	ras homolog family member T1
-0.06	6.51e-04	LSM8	LSM8 homolog, U6 small nuclear RNA	0.48	6.51e-04	TMEM43	transmembrane protein 43
-0.1	6.51e-04	CCDC124	coiled-coil domain containing 124	1.12	6.51e-04	MAGT1	magnesium transporter 1
-0.11	8.27e-04	PDGFA1	PDGFA associated protein 1	0.89	6.51e-04	SMARCA2	SWI/SNF related, matrix associated,
-0.07	8.46e-04	EIF3G	eukaryotic translation initiation f	0.11	3.86e-03	GNAI2	G protein subunit alpha i2
-0.88	2.41e-03	PRKAR1B	protein kinase cAMP-dependent type	0.15	3.86e-03	VDAC3	voltage dependent anion channel 3
-0.05	3.86e-03	PSMC3	proteasome 26S subunit, ATPase 3	0.18	3.86e-03	MLEC	malectin
-0.08	5.13e-03	BTF3	basic transcription factor 3	0.75	5.25e-03	CARS2	cysteinyl-tRNA synthetase 2, mitoch
-0.05	5.25e-03	LSM7	LSM7 homolog, U6 small nuclear RNA	0.06	5.25e-03	RAB7A	RAB7A, member RAS oncogene family
-0.08	5.25e-03	LSM3	LSM3 homolog, U6 small nuclear RNA	0.88	5.25e-03	ACSL5	acyl-CoA synthetase long chain fami
-0.06	5.25e-03	PSMC4	proteasome 26S subunit, ATPase 4	0.63	5.25e-03	ARHGAP9	Rho GTPase activating protein 9
-0.08	5.90e-03	BOLA2	bola family member 2	0.87	5.90e-03	DGLUCY	D-glutamate cyclase
-0.06	5.92e-03	PFDN6	prefoldin subunit 6	0.77	5.90e-03	TEX10	testis expressed 10
-0.06	8.03e-03	POLR2C	RNA polymerase II subunit C	0.08	6.83e-03	RPN1	ribophorin I
-0.51	8.03e-03	EEPD1	endonuclease/exonuclease/phosphatas	0.16	7.80e-03	RPN2	ribophorin II
-0.07	8.03e-03	EIF4H	eukaryotic translation initiation f	1.01	8.03e-03	ZMPSTE24	zinc metallopeptidase STE24
-0.05	8.18e-03	AIMP1	aminoacyl tRNA synthetase complex i	0.86	8.03e-03	DUSP23	dual specificity phosphatase 23
-0.1	8.18e-03	CIAPIN1	cytokine induced apoptosis inhibito	0.12	8.03e-03	DDOST	dolichyl-diphosphooligosaccharide--
-0.08	9.51e-03	PSMD9	proteasome 26S subunit, non-ATPase	0.91	8.18e-03	LGALS9	galectin 9
-0.05	9.70e-03	PSMC5	proteasome 26S subunit, ATPase 5	0.91	9.51e-03	SFXN3	sideroflexin 3
-0.04	1.01e-02	PSMC2	proteasome 26S subunit, ATPase 2	0.81	1.00e-02	MFN2	mitofusin 2
-0.05	1.01e-02	PSMC1	proteasome 26S subunit, ATPase 1	0.92	1.00e-02	PPCS	phosphopantethenoylcysteine synthet
-0.73	1.01e-02	SIRT1	sirtuin 1	0.11	1.01e-02	UGGT1	UDP-glucose glycoprotein glucosyltr
-0.06	1.15e-02	RPS28	ribosomal protein S28	0.83	1.19e-02	MYO1F	myosin IF
-0.06	1.34e-02	ELOB	elongin B	0.82	1.22e-02	CHID1	chitinase domain containing 1
-0.07	1.44e-02	SUPT5H	SPT5 homolog, DSIF elongation facto	0.17	1.23e-02	GLYR1	glyoxylate reductase 1 homolog
-0.04	1.59e-02	TCERG1	transcription elongation regulator	0.6	1.40e-02	ATL3	atlastin GTPase 3
-0.06	1.76e-02	TTC1	tetratricopeptide repeat domain 1	0.81	1.41e-02	DAD1	defender against cell death 1
-0.04	1.79e-02	CCT2	chaperonin containing TCP1 subunit	0.28	1.44e-02	ACADVL	acyl-CoA dehydrogenase very long ch
-0.46	1.80e-02	PPM1A	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe	0.81	1.47e-02	ARRB1	arrestin beta 1
-0.04	1.80e-02	EIF3F	eukaryotic translation initiation f	0.72	1.53e-02	PTGR3	prostaglandin reductase 3
-0.06	2.18e-02	DNAJA2	DnaJ heat shock protein family (Hsp	0.07	1.53e-02	METAP1	methionyl aminopeptidase 1
-0.05	2.30e-02	SKP1	S-phase kinase associated protein 1	0.05	1.53e-02	RAB10	RAB10, member RAS oncogene family
-0.69	2.51e-02	ZWINT	ZW10 interacting kinetochore protei	0.86	1.76e-02	PIGK	phosphatidylinositol glycan anchor
-0.07	2.51e-02	RANBP1	RAN binding protein 1	0.08	1.76e-02	HP1BP3	heterochromatin protein 1 binding p
-0.06	2.63e-02	NACA	nascent polypeptide associated comp	0.09	1.80e-02	ARHGAP1	Rho GTPase activating protein 1
-0.07	2.63e-02	PDCD5	programmed cell death 5	0.72	1.81e-02	ERMP1	endoplasmic reticulum metallopeptid
-0.31	2.72e-02	WNK1	WNK lysine deficient protein kinase	0.66	1.97e-02	CD33	CD33 molecule
-0.7	2.78e-02	PSMC4	proteasome assembly chaperone 4	0.09	1.97e-02	MACROH2A1	macroH2A.1 histone

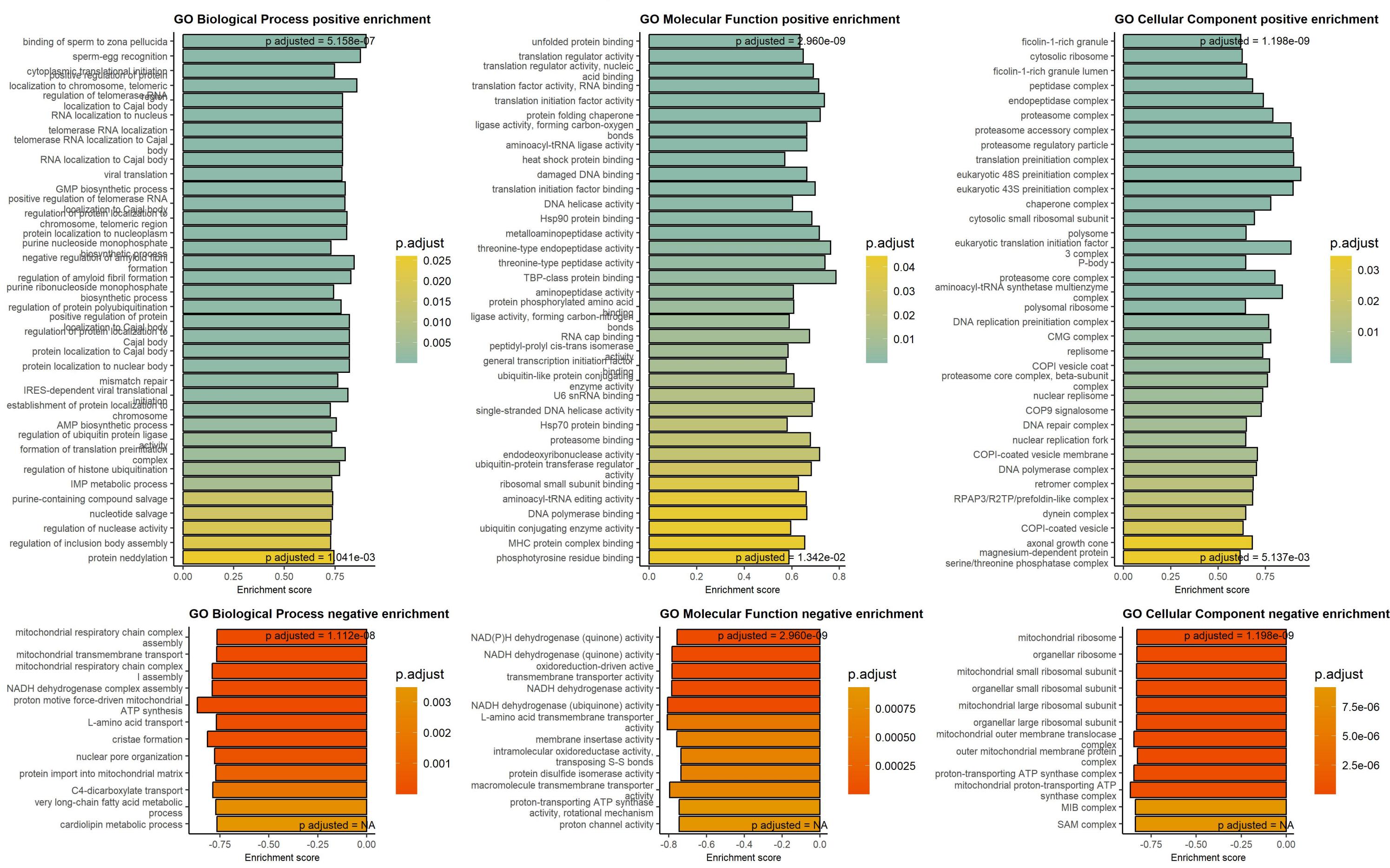


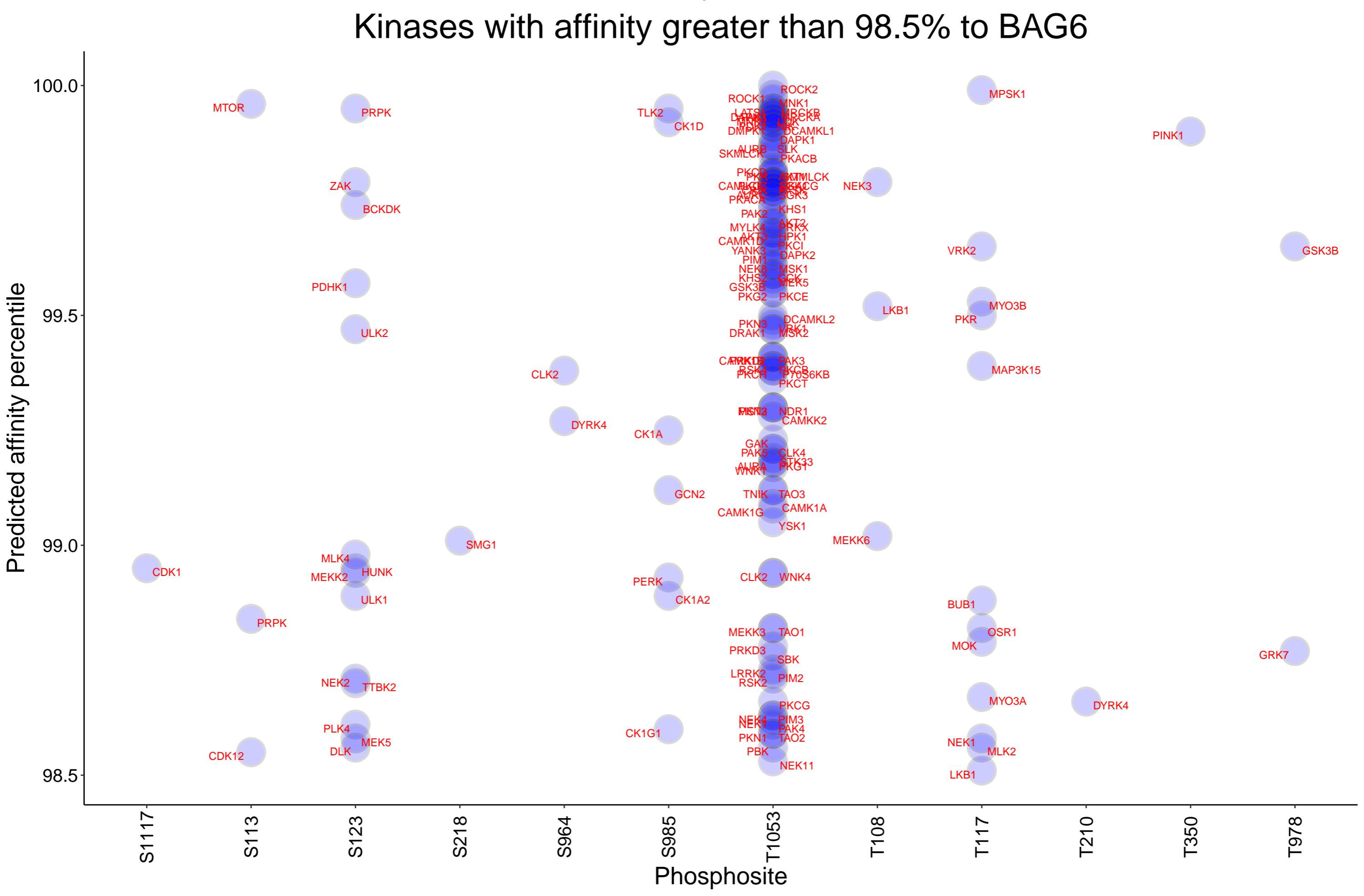
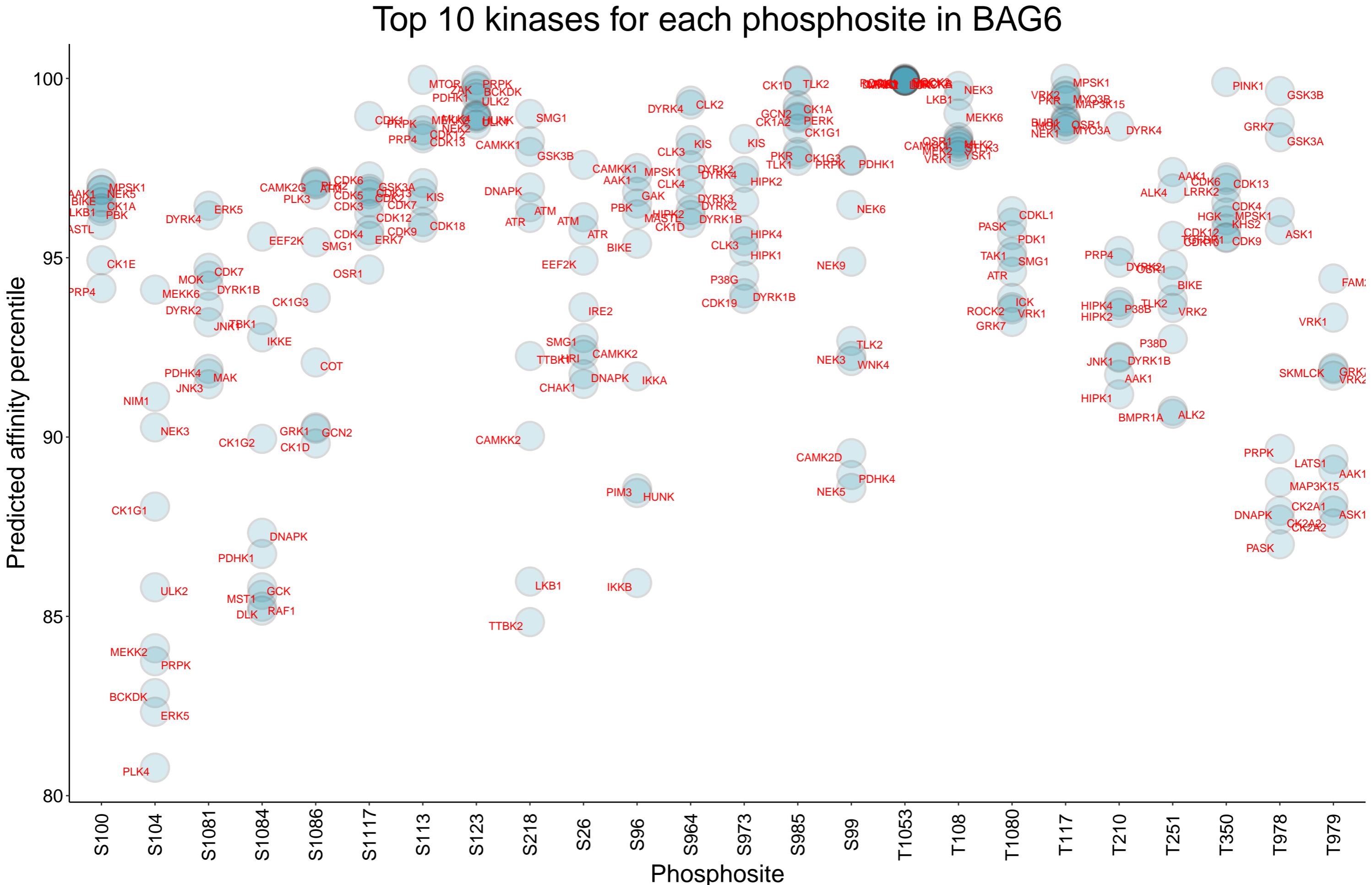
Sorted by p values!							
Downregulated in solid cancers at low/absent BAG6				Upregulated in solid cancers at low/absent BAG6			
FC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
15	4.12e-54	PFDN4	prefoldin subunit 4	0.25	5.72e-237	H4C1	H4 clustered histone 1
22	1.22e-51	EIF3I	eukaryotic translation initiation f	0.06	4.12e-54	PTPRCAP	protein tyrosine phosphatase recept
95	3.20e-51	PPP5C	protein phosphatase 5 catalytic sub	0.06	4.12e-54	HBE1	hemoglobin subunit epsilon 1
2	2.52e-50	NUBP2	NUBP iron-sulfur cluster assembly f	0.06	4.12e-54	SERPINB10	serpin family B member 10
13	3.92e-49	PSMA5	proteasome 20S subunit alpha 5	0.06	4.12e-54	IGLL1	immunoglobulin lambda like polypept
15	4.65e-48	PSMD7	proteasome 26S subunit, non-ATPase	0.06	4.12e-54	CRYBB1	crystallin beta B1
26	2.61e-47	TBCC	tubulin folding cofactor C	0.06	4.12e-54	ITGA2B	integrin subunit alpha 2b
95	4.19e-47	ZPR1	ZPR1 zinc finger	0.06	4.12e-54	ACAP1	ArfGAP with coiled-coil, ankyrin re
52	4.84e-47	UBL4A	ubiquitin like 4A	0.06	4.12e-54	NCF4	neutrophil cytosolic factor 4
96	7.50e-47	ARFGAP2	ADP ribosylation factor GTPase acti	0.06	4.12e-54	SP140	SP140 nuclear body protein
13	8.64e-47	PSMA6	proteasome 20S subunit alpha 6	0.06	4.12e-54	PSTPIP1	proline-serine-threonine phosphatas
22	1.54e-46	DCTN2	dynactin subunit 2	0.06	4.12e-54	STAB1	stabilin 1
1	3.49e-46	PSMC3	proteasome 26S subunit, ATPase 3	0.06	4.12e-54	SELPLG	selectin P ligand
14	7.00e-46	PSMA3	proteasome 20S subunit alpha 3	0.06	4.12e-54	RCSD1	RCSD domain containing 1
31	1.17e-45	DCK	deoxycytidine kinase	0.06	4.12e-54	STAT5A	signal transducer and activator of
1	2.05e-45	PSMC6	proteasome 26S subunit, ATPase 6	0.06	4.12e-54	CTSW	cathepsin W
11	2.35e-45	PSMC5	proteasome 26S subunit, ATPase 5	0.06	4.12e-54	GIMAP6	GTPase, IMAP family member 6
37	2.41e-45	GIGYF2	GRB10 interacting GYF protein 2	0.06	4.12e-54	GZMB	granzyme B
19	2.70e-45	OTUD6B	OTU deubiquitinase 6B	0.06	4.12e-54	HK3	hexokinase 3
92	2.25e-44	NAA10	N-alpha-acetyltransferase 10, NatA	0.06	4.12e-54	TUBA8	tubulin alpha 8
32	7.86e-44	RANBP3	RAN binding protein 3	0.06	4.12e-54	CR2	complement C3d receptor 2
19	1.58e-43	TRAPPC3	trafficking protein particle comple	0.06	4.12e-54	POU2F2	POU class 2 homeobox 2
11	1.81e-43	PSMC4	proteasome 26S subunit, ATPase 4	0.06	4.12e-54	AZU1	azurocidin 1
26	1.90e-43	PHPT1	phosphohistidine phosphatase 1	0.06	4.12e-54	CD48	CD48 molecule
75	3.02e-43	UBXN1	UBX domain protein 1	0.06	4.12e-54	SKAP2	src kinase associated phosphoprotei
24	4.94e-43	AARSD1	alanyl-tRNA synthetase domain conta	0.06	4.12e-54	CCL17	C-C motif chemokine ligand 17
34	6.46e-43	NUDT3	nudix hydrolase 3	0.06	4.12e-54	ADA2	adenosine deaminase 2
25	6.82e-43	NUDT1	nudix hydrolase 1	0.06	4.12e-54	CD3E	CD3 epsilon subunit of T-cell recep
31	2.68e-42	TIPRL	TOR signaling pathway regulator	0.06	4.12e-54	RNASE2	ribonuclease A family member 2
23	4.99e-42	RANBP1	RAN binding protein 1	0.06	4.12e-54	TEX11	testis expressed 11
96	9.88e-42	ILKAP	ILK associated serine/threonine pho	0.06	4.12e-54	PLEK	pleckstrin
92	2.22e-41	IRGQ	immunity related GTPase Q	0.06	4.12e-54	CD300A	CD300a molecule
17	3.93e-41	CASP3	caspase 3	0.06	4.12e-54	GZMA	granzyme A
17	4.97e-41	DOHH	deoxyhypusine hydroxylase	0.06	4.12e-54	SIGLEC12	sialic acid binding Ig like lectin
37	6.91e-41	PFDN2	prefoldin subunit 2	0.06	4.12e-54	SMIM24	small integral membrane protein 24
13	1.13e-40	CCT6A	chaperonin containing TCP1 subunit	0.06	4.12e-54	ALOX15	arachidonate 15-lipoxygenase
27	1.51e-40	PPP1R14B	protein phosphatase 1 regulatory in	0.06	4.12e-54	GZMM	granzyme M
91	1.52e-40	HGH1	HGH1 homolog	0.06	4.12e-54	ARHGAP9	Rho GTPase activating protein 9
75	1.52e-40	MTRN	metabolism related	0.06	4.12e-54	NINJ2	neurofibromatosis 2

Top 250 correlation coefficients overrepresentation, BAG6 protein, DB1



Gene Set Enrichment analysis on protein correlation coefficients, BAG6 protein, DB1





Top 15 positive correlation coefficients for BAG6 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

