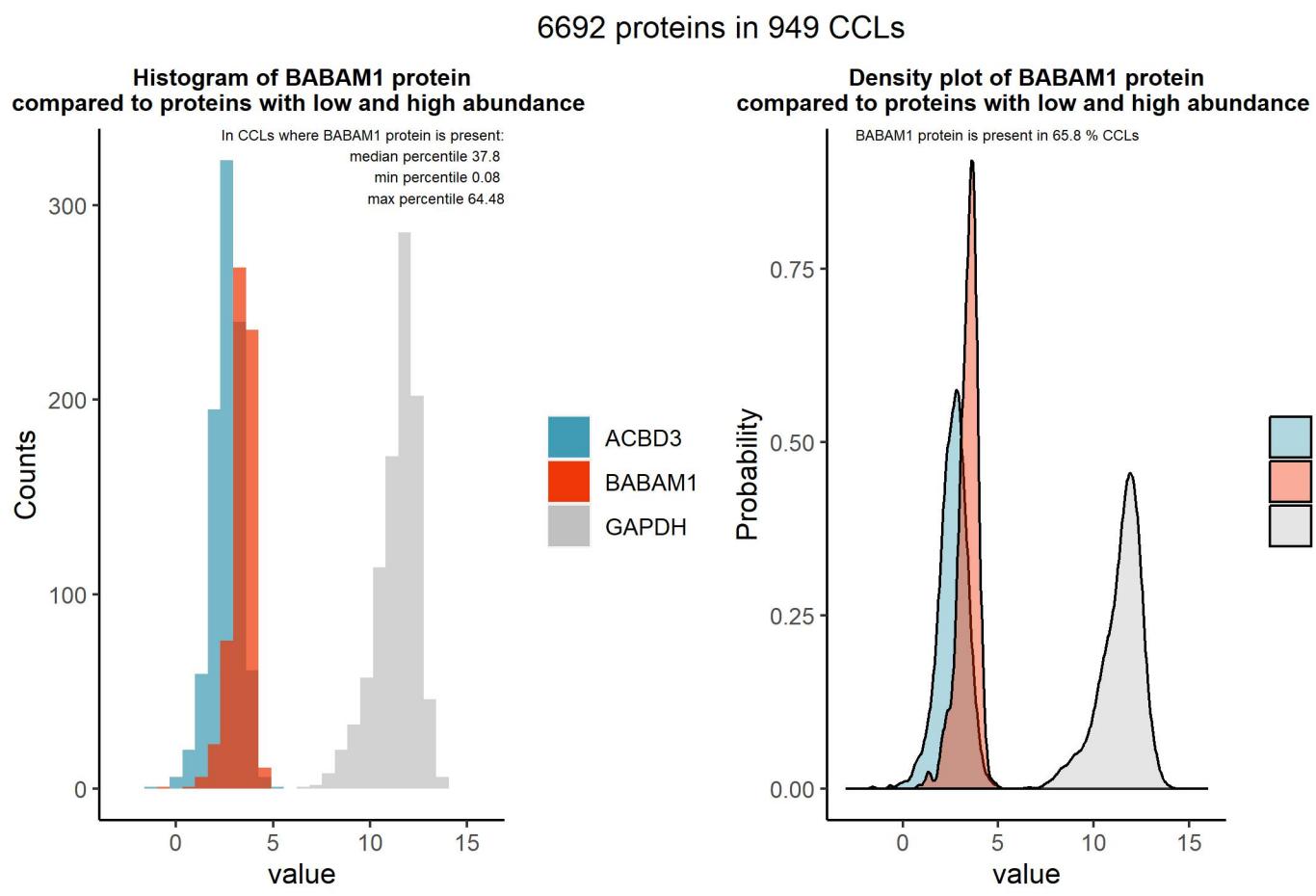


BABAM1

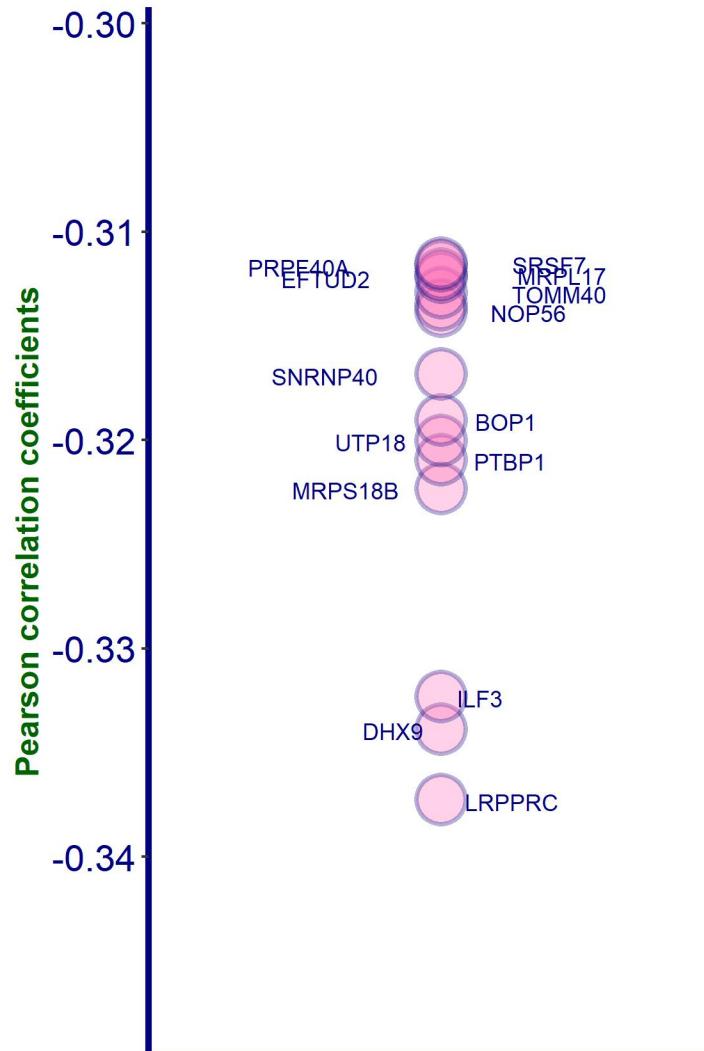
Protein name: BABA1 ; UNIPROT: Q9NWV8 ; Gene name: BRISC and BRCA1 A complex member 1

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

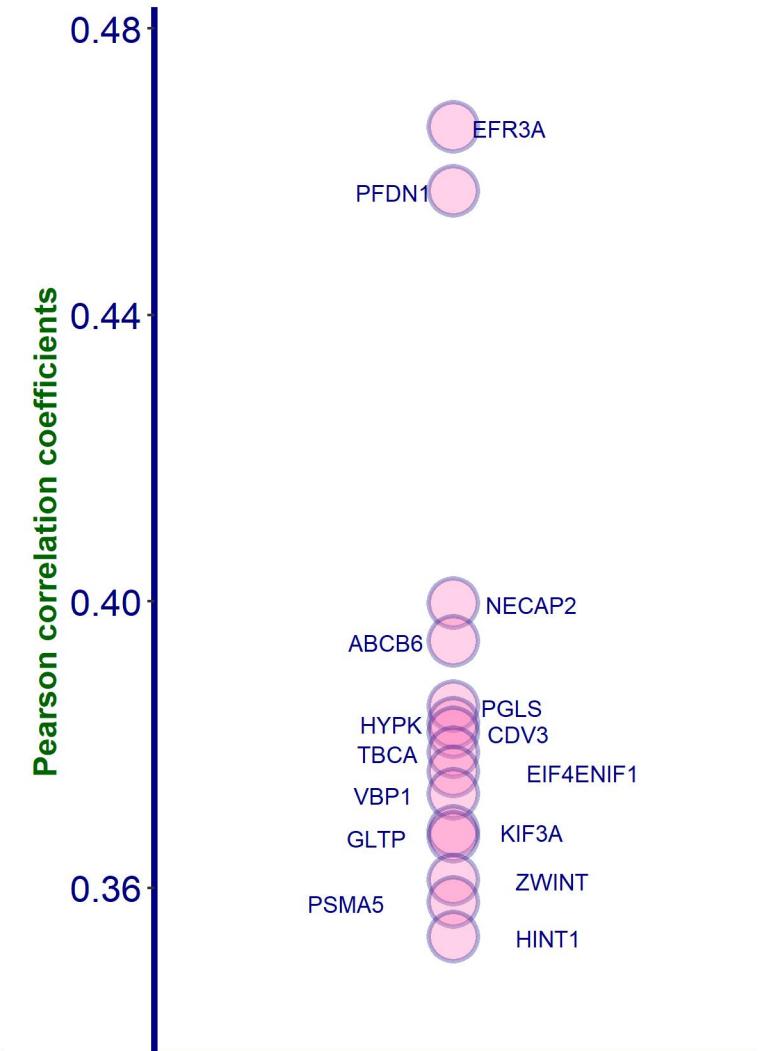
Sanger Institute Protein Database 1 (DB1), protein presence is certain



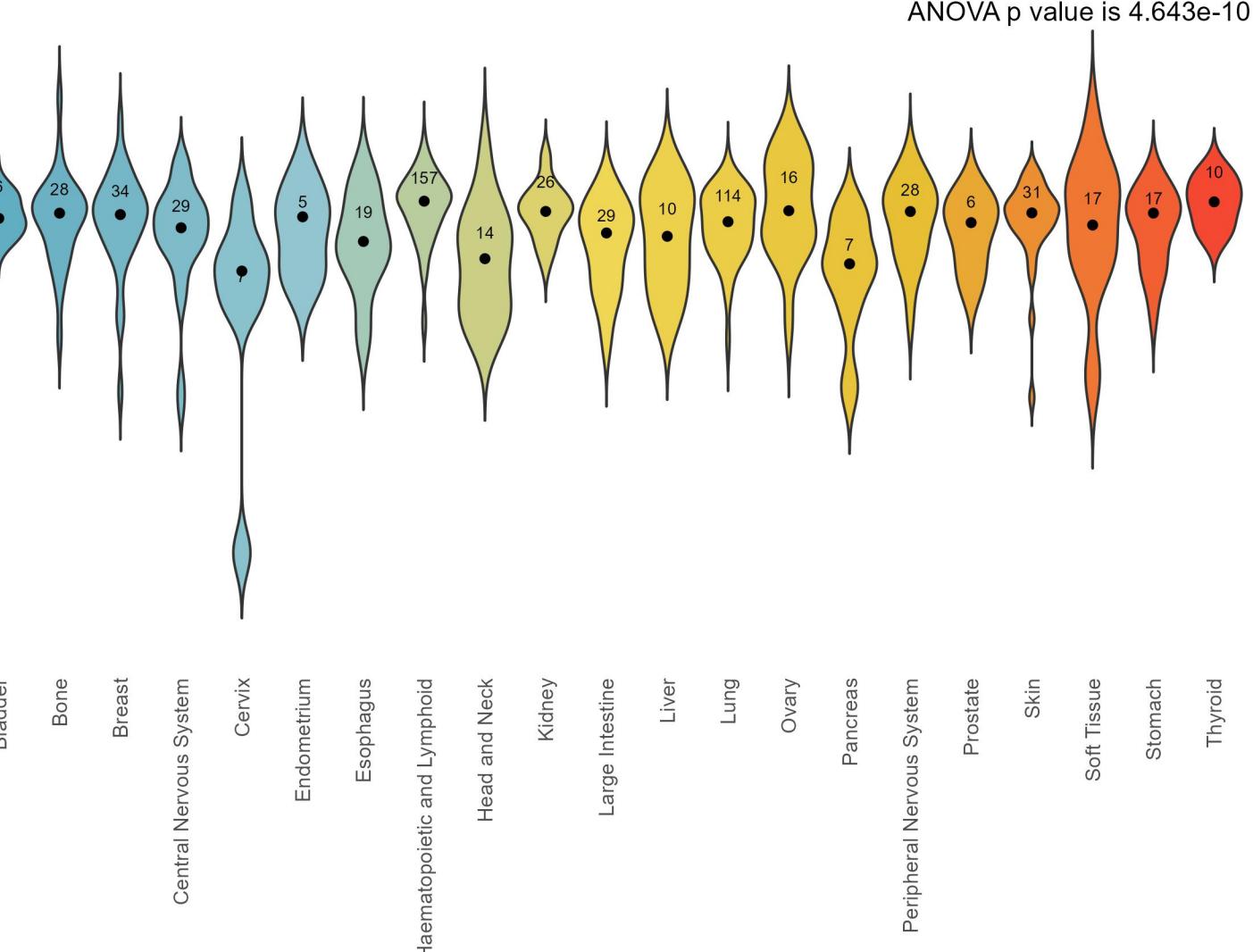
Top negative correlations of BABAM1 protein, DB



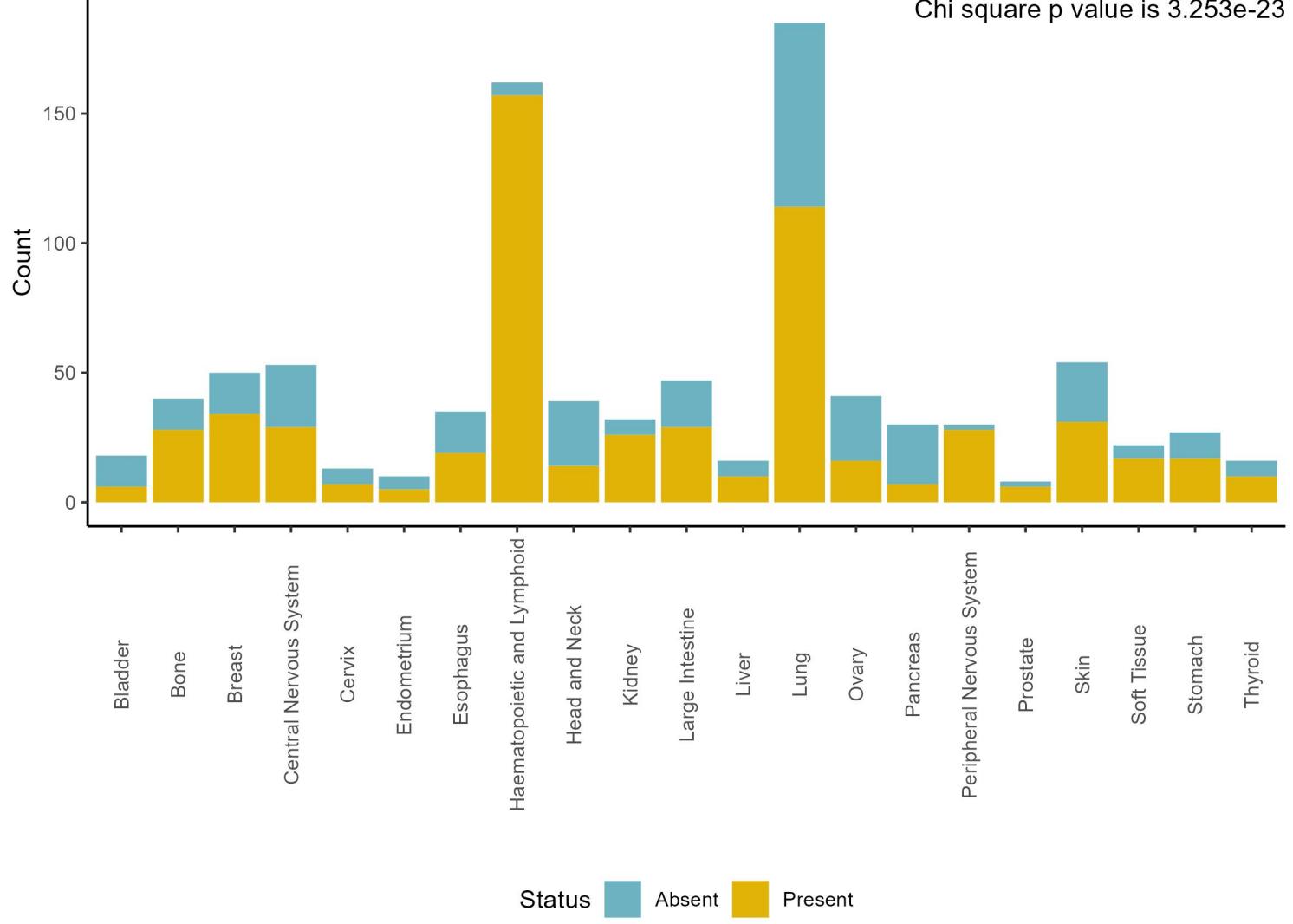
Top positive correlations of BABAM1 protein, DB



Amount of BABAM1 protein, number of CCLs where it is present by tissue, DB1



Present and absent BABAM1 protein counts by tissue, DB1

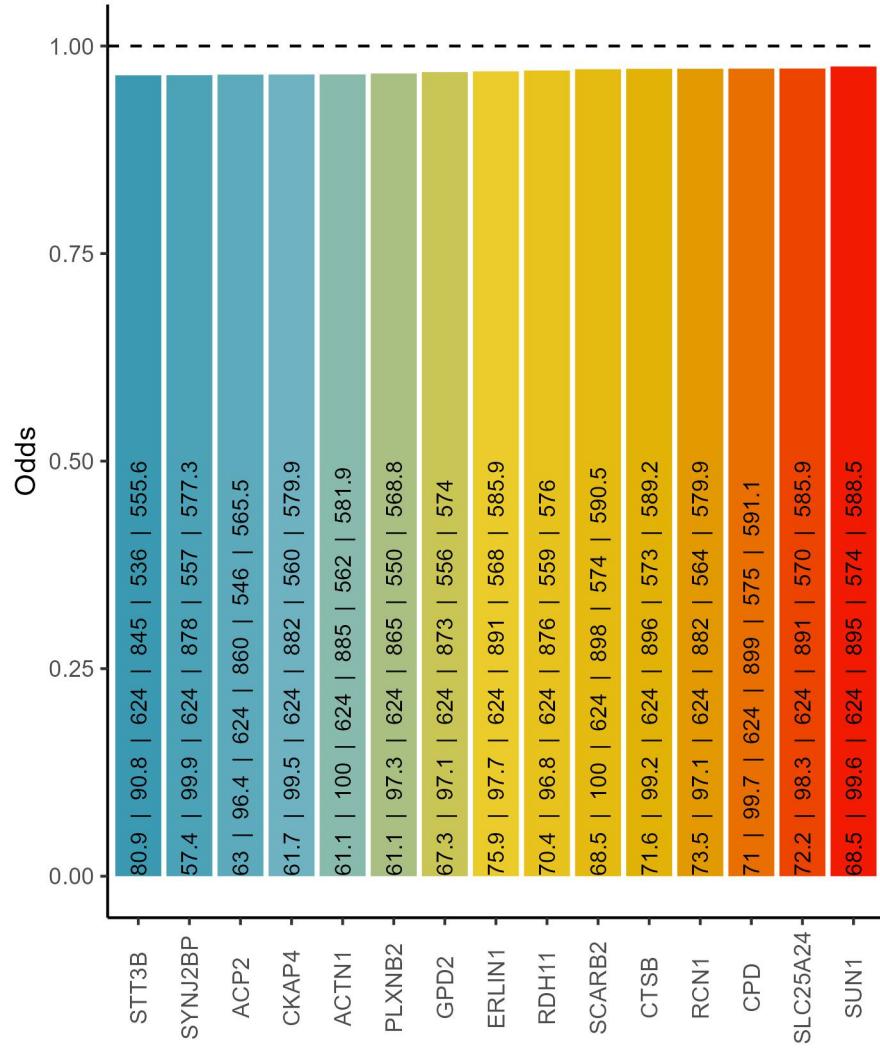


Cooccurrence with BABAM1 protein, DB1

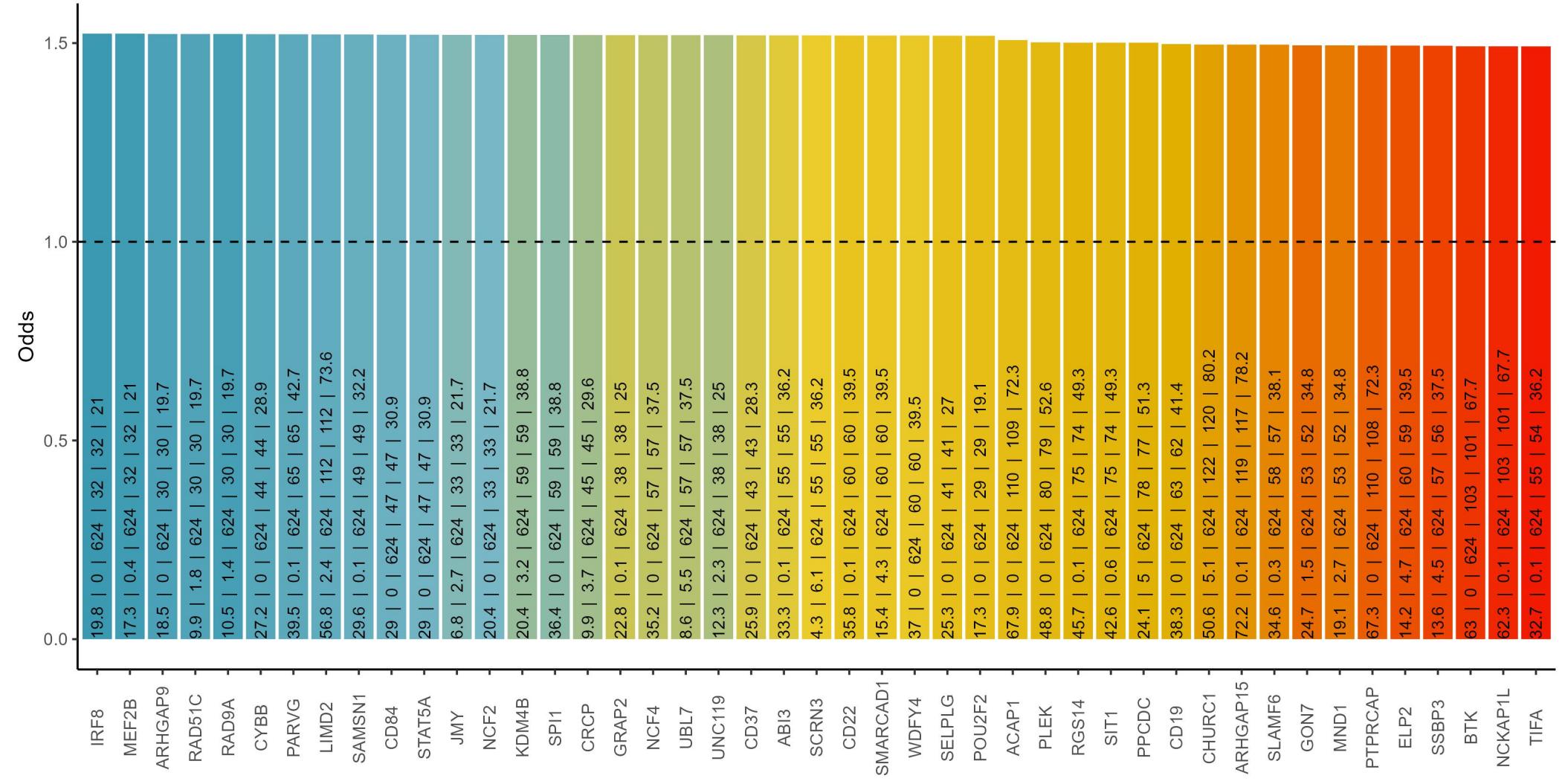
% of BABAM1 in blood cancers: 96.9 ; % of BABAM1 in solid cancers: 59.3

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of BABAM1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

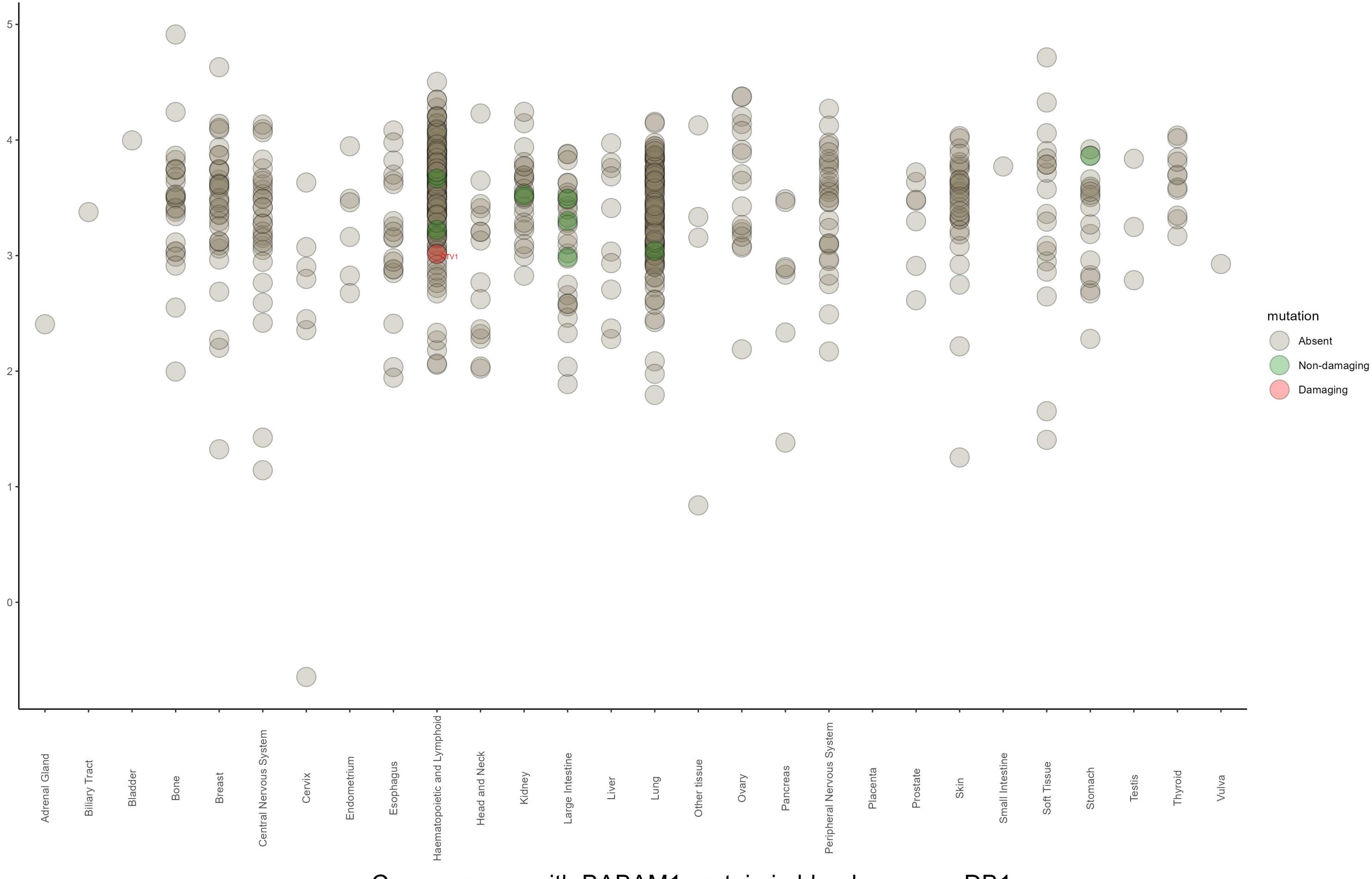
Negative cooccurrence



Positive cooccurrence



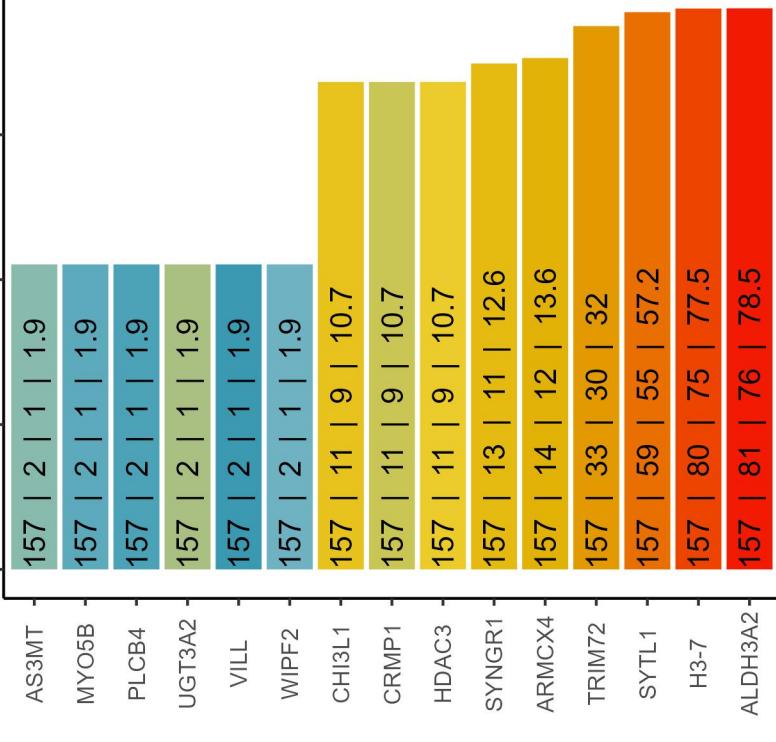
Amount of BABAM1 protein and mutation status by tissue, DB1



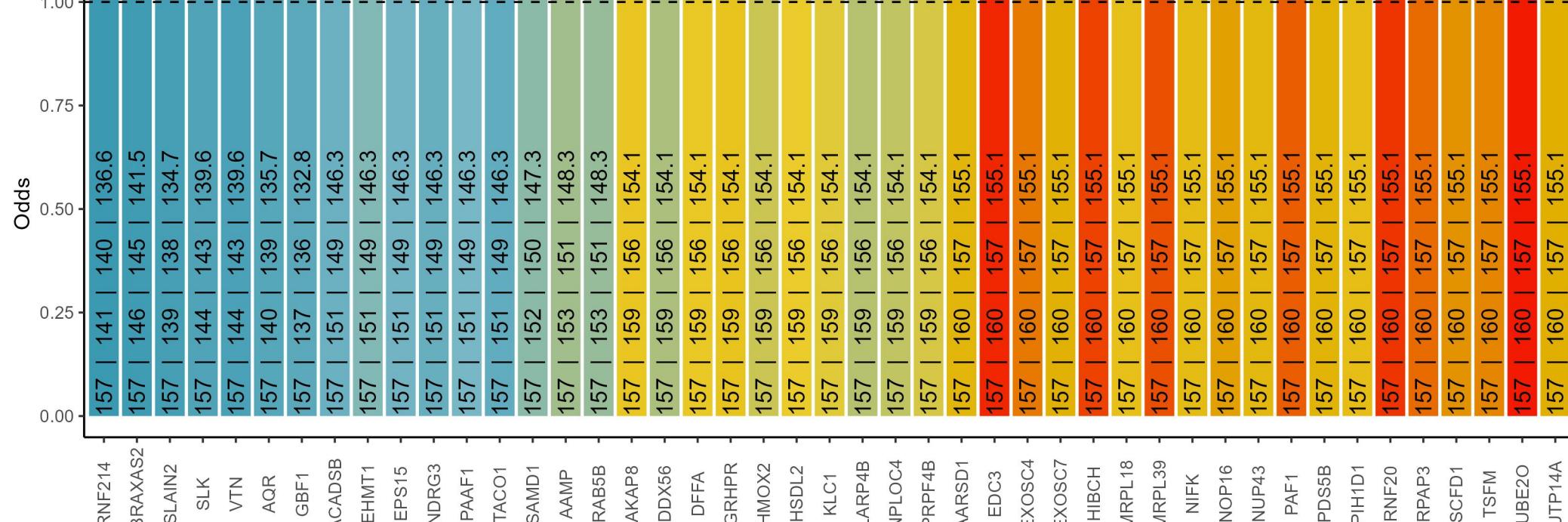
Cooccurrence with BABAM1 protein in blood cancers, DB1

The text in the bars: incidence of BABAM1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



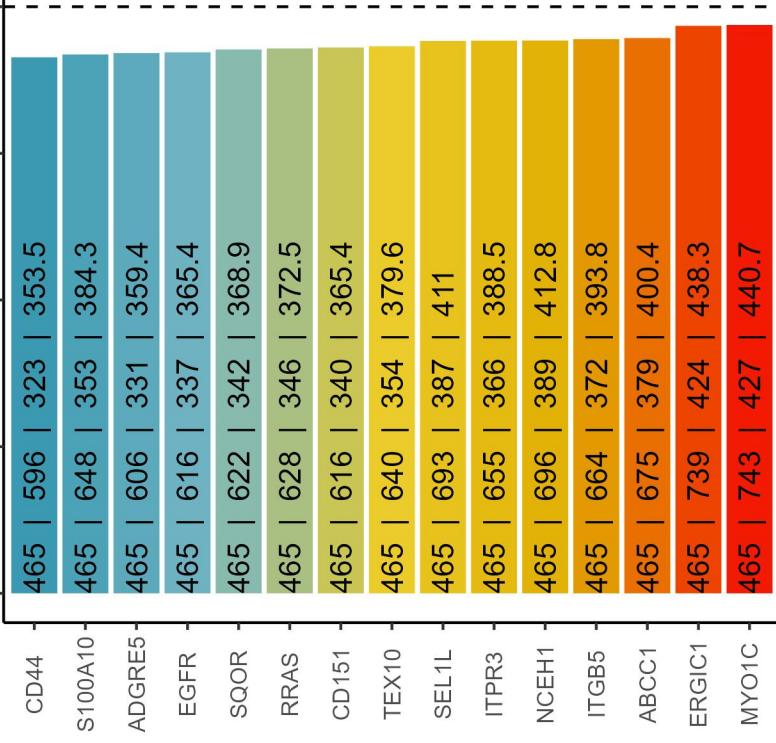
Positive cooccurrence



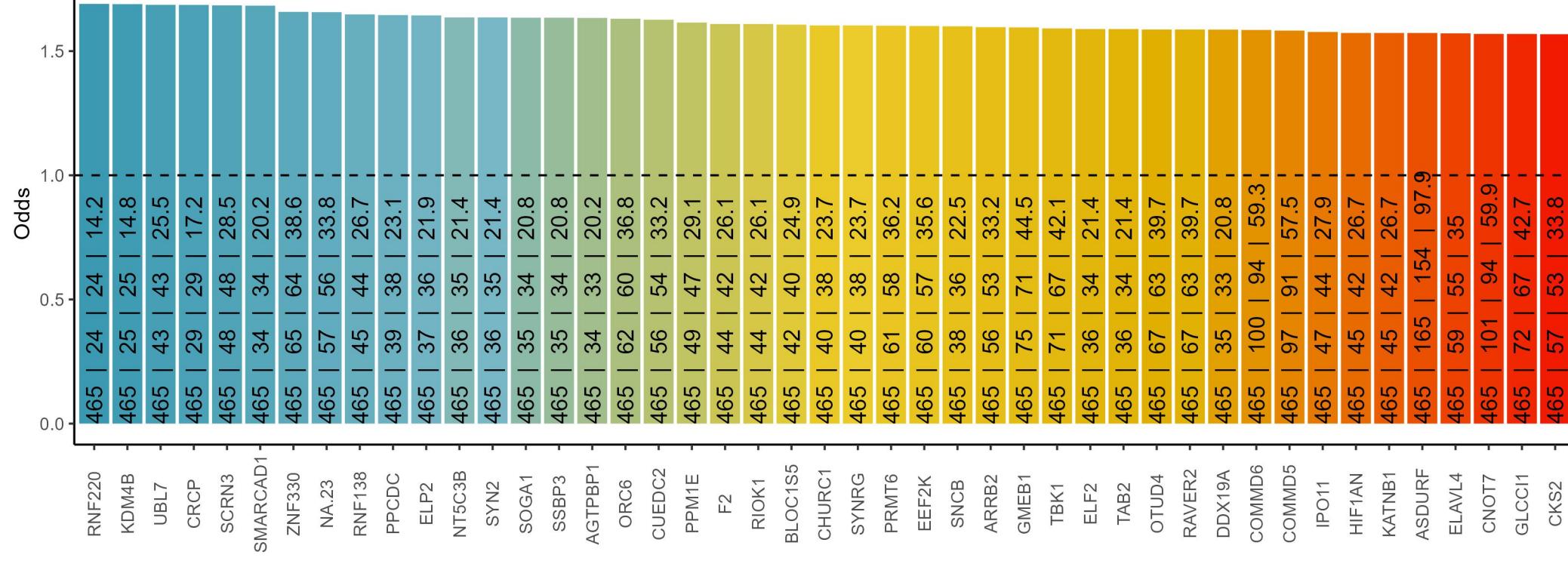
Cooccurrence with BABAM1 protein in solid cancers, DB1

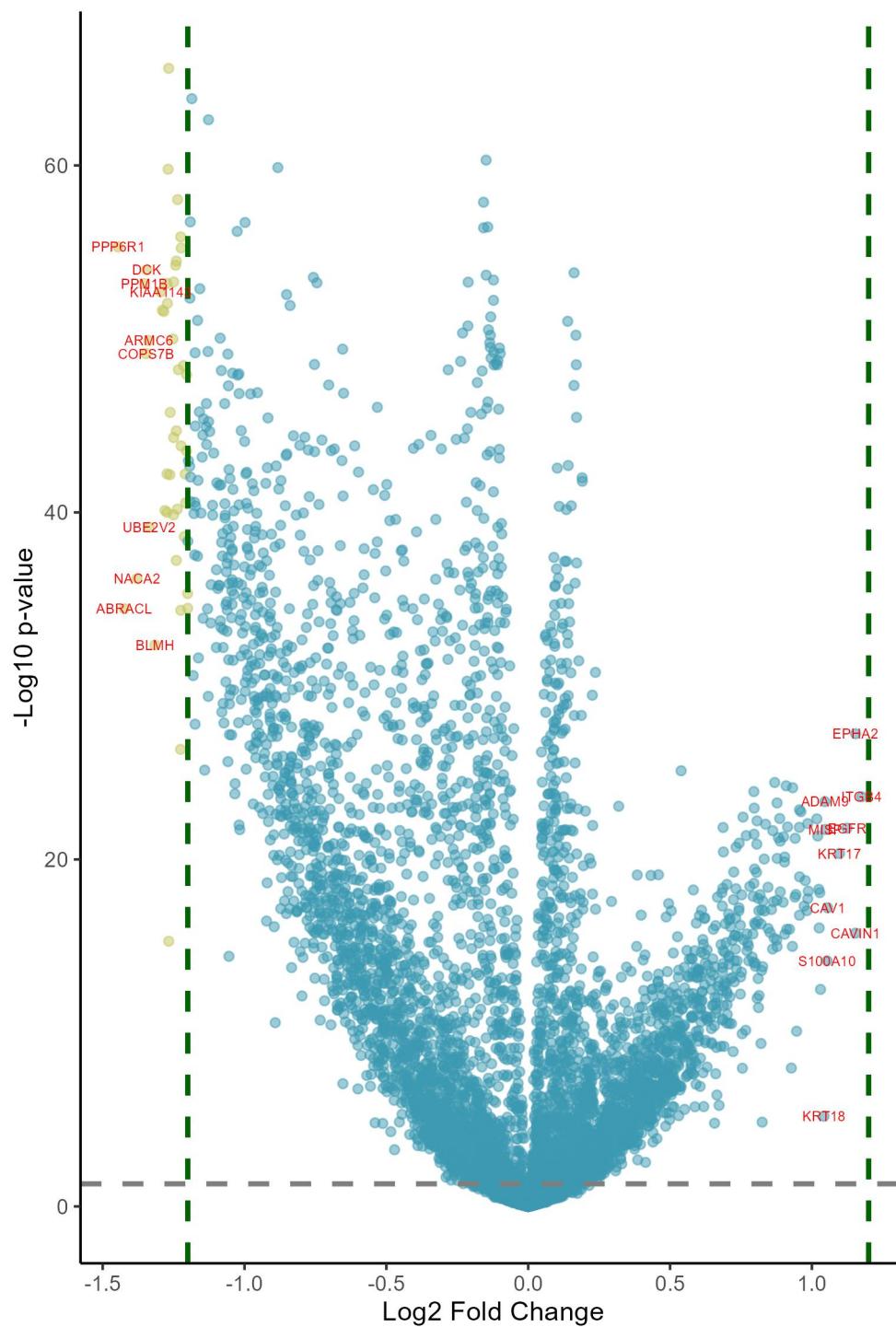
The text in the bars: incidence of BABAM1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



Positive cooccurrence

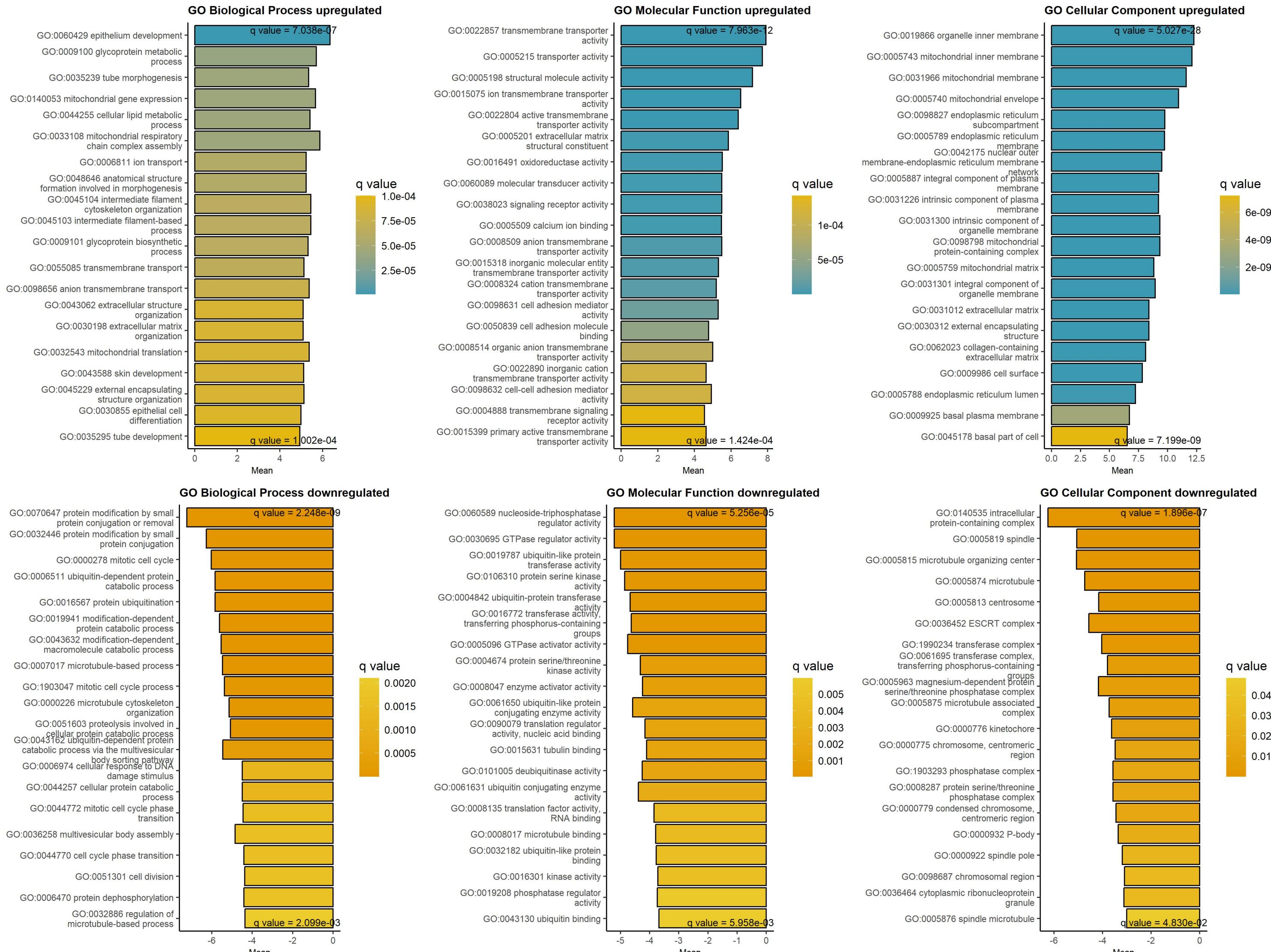


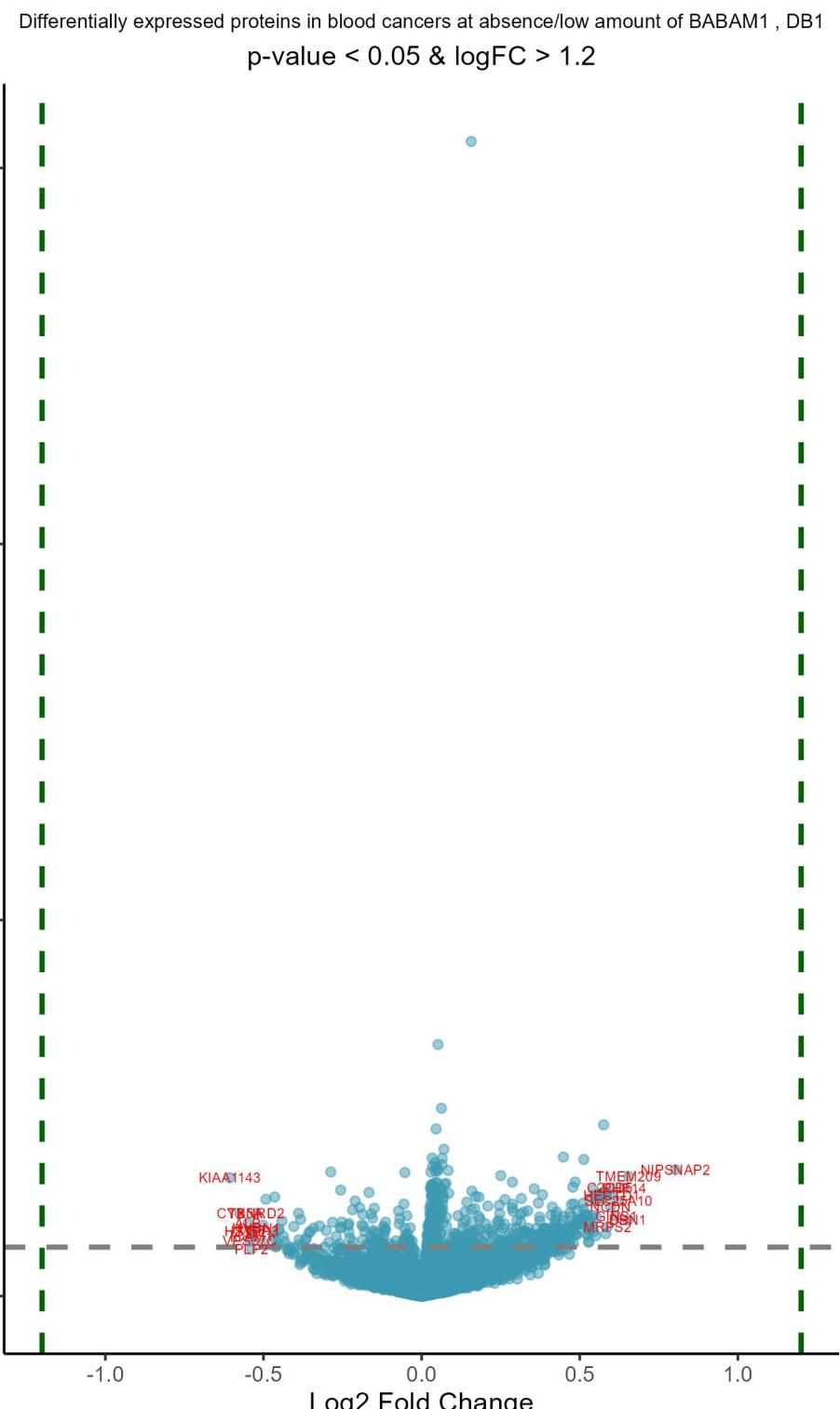


Downregulated at low/absent BABAM1 Upregulated at low/absent BABAM1

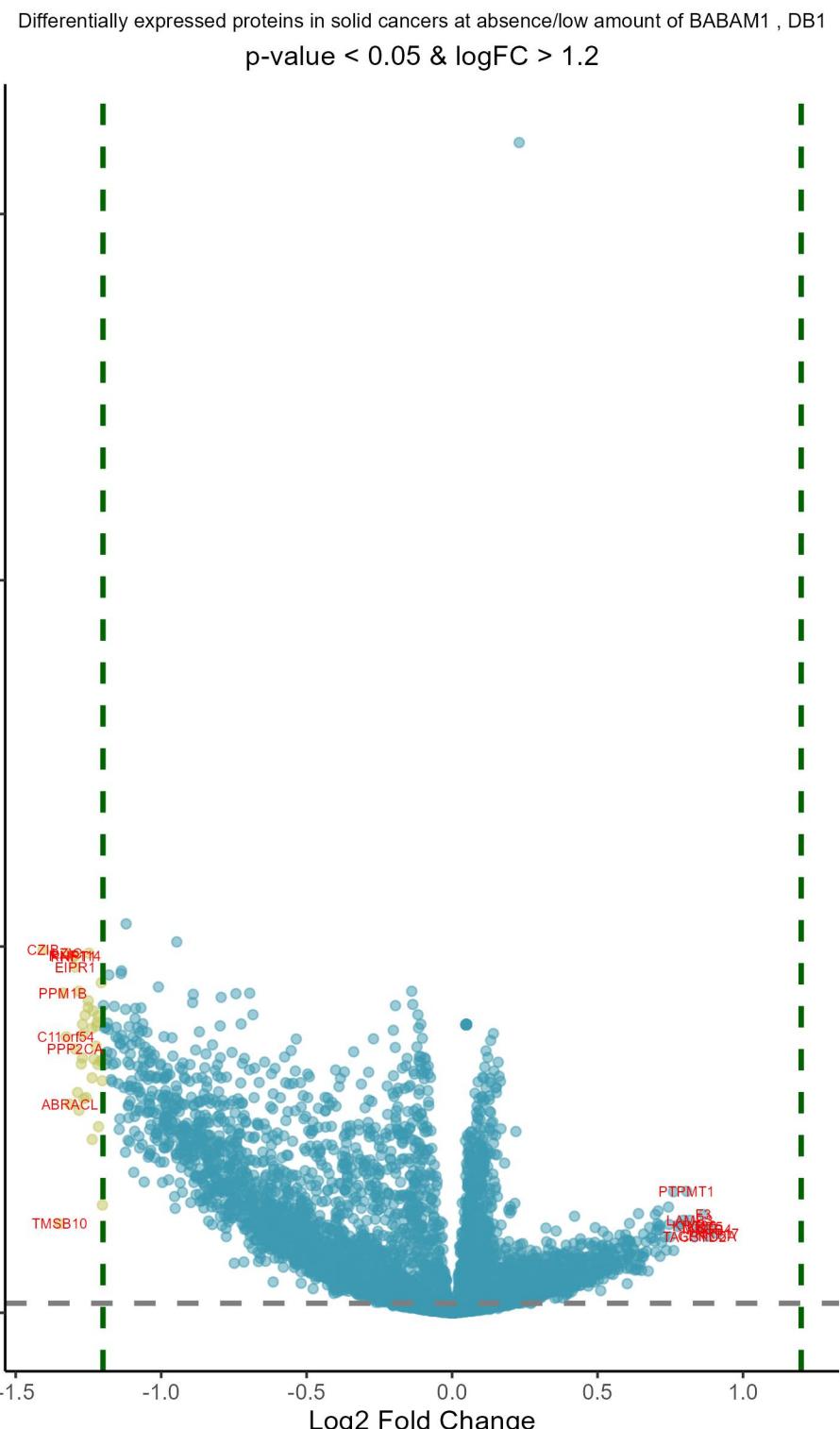
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.45	2.06e-53	PPP6R1	protein phosphatase 6 regulatory su	1.18	1.94e-23	ITGB4	integrin subunit beta 4
-1.42	6.74e-34	ABRACL	ABRA C-terminal like	1.15	5.85e-27	EPHA2	EPH receptor A2
-1.38	1.54e-35	NACA2	nascent polypeptide associated comp	1.15	7.99e-16	CAVIN1	caveolae associated protein 1
-1.35	1.48e-51	PPM1B	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe	1.12	1.09e-21	EGFR	epidermal growth factor receptor
-1.35	8.06e-48	COPS7B	COP9 signalosome subunit 7B	1.1	2.83e-20	KRT17	keratin 17
-1.35	3.41e-52	DCK	deoxycytidine kinase	1.06	3.08e-17	CAV1	caveolin 1
-1.34	1.68e-48	ARMC6	armadillo repeat containing 6	1.05	2.81e-14	S100A10	S100 calcium binding protein A10
-1.34	2.26e-38	UBE2V2	ubiquitin conjugating enzyme E2 V2	1.05	1.29e-21	MISP	mitotic spindle positioning
-1.32	6.66e-32	BLMH	bleomycin hydrolase	1.05	3.64e-23	ADAM9	ADAM metallopeptidase domain 9
-1.3	4.13e-51	KIAA1143	KIAA1143	1.04	1.25e-05	KRT18	keratin 18
-1.29	3.98e-50	RABEP1	rabaptin, RAB GTPase binding effect	1.03	1.11e-12	ITGA3	integrin subunit alpha 3
-1.28	4.60e-50	CZIB	CXXC motif containing zinc binding	1.03	4.43e-18	ITGA2	integrin subunit alpha 2
-1.28	2.78e-39	C11orf54	chromosome 11 open reading frame 54	1.03	4.14e-16	JUP	junction plakoglobin
-1.27	1.48e-51	ARPP19	cAMP regulated phosphoprotein 19	1.02	2.89e-18	GPRC5A	G protein-coupled receptor class C
-1.27	3.52e-39	PSME3IP1	proteasome activator subunit 3 inte	1.02	2.93e-21	BCAM	basal cell adhesion molecule (Luthe
-1.27	2.76e-41	UBR7	ubiquitin protein ligase E3 compone	1.02	3.29e-22	KRT80	keratin 80
-1.27	1.69e-50	GRIPAP1	GRIP1 associated protein 1	0.99	3.65e-18	CDH1	cadherin 1
-1.27	1.57e-57	NUBP1	NUBP iron-sulfur cluster assembly f	0.99	9.64e-18	DSG2	desmoglein 2
-1.27	8.42e-63	DOHH	deoxyhypusine hydroxylase	0.99	6.05e-22	FAM83H	family with sequence similarity 83
-1.27	2.28e-15	TMSB10	thymosin beta 10	0.98	4.46e-17	NT5E	5'-nucleotidase ecto
-1.26	3.04e-41	NUDT3	nudix hydrolase 3	0.98	9.31e-19	TACSTD2	tumor associated calcium signal tra
-1.26	1.23e-44	PPM1A	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe	0.97	2.50e-17	PKP2	plakophilin 2
-1.25	1.39e-48	PIN1	peptidylprolyl cis/trans isomerase,	0.96	1.31e-22	SDC4	syndecan 4
-1.25	4.74e-39	CBL	Cbl proto-oncogene	0.96	5.77e-19	GPX8	glutathione peroxidase 8 (putative)
-1.25	2.96e-43	PPP2CA	protein phosphatase 2 catalytic sub	0.96	8.00e-17	PKP3	plakophilin 3
-1.25	1.37e-51	EIPR1	EARP complex and GARP complex inter	0.96	1.03e-22	NECTIN2	nectin cell adhesion molecule 2
-1.24	1.97e-52	ATOX1	antioxidant 1 copper chaperone	0.96	9.87e-22	F3	coagulation factor III, tissue fact
-1.24	1.53e-36	RNF181	ring finger protein 181	0.95	2.37e-10	GNG12	G protein subunit gamma 12
-1.24	1.21e-52	RNF114	ring finger protein 114	0.94	5.65e-18	KRT5	keratin 5

GAGE analysis on upregulated and downregulated proteins at low/absent BABAM1 protein, DB1



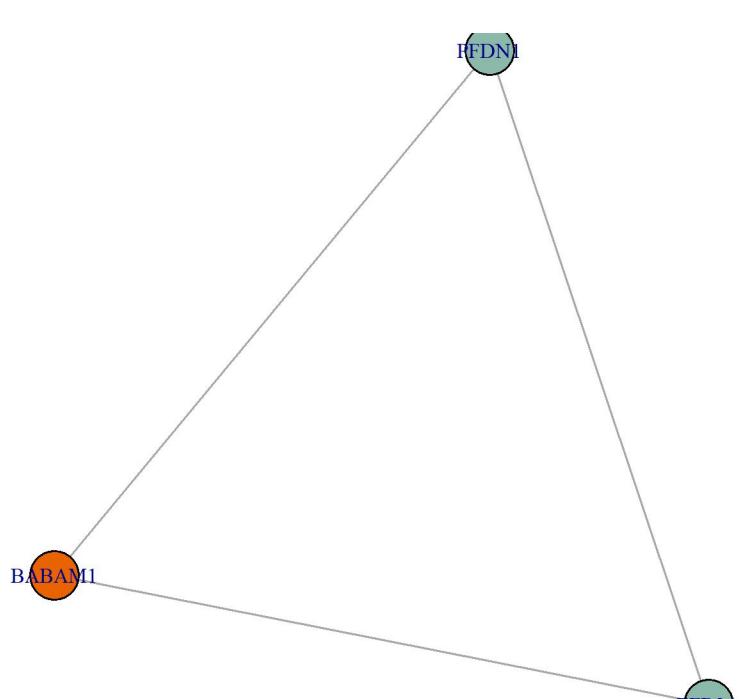


Downregulated in blood cancers at low/absent BABAM1				Upregulated in blood cancers at low/absent BABAM1			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.61	1.83e-01	KIAA1143	KIAA1143	0.8	1.50e-01	NIPSNAP2	nipsnap homolog 2
-0.58	3.30e-01	CYB5A	cytochrome b5 type A	0.65	1.76e-01	TMEM209	transmembrane protein 209
-0.55	3.96e-01	ALB	albumin	0.65	3.70e-01	DBN1	drebrin 1
-0.54	5.14e-01	VPS37C	VPS37C subunit of ESCRT-I	0.64	2.07e-01	PHF14	PHD finger protein 14
-0.54	5.77e-01	PLP2	proteolipid protein 2	0.62	2.44e-01	SLC25A10	solute carrier family 25 member 10
-0.54	4.66e-01	ICAM1	intercellular adhesion molecule 1	0.62	3.34e-01	GINS1	GINS complex subunit 1
-0.54	4.31e-01	HS1BP3	HCLS1 binding protein 3	0.6	2.25e-01	HECTD1	HECT domain E3 ubiquitin protein li
-0.54	4.22e-01	MFF	mitochondrial fission factor	0.6	2.91e-01	NCDN	neurochondrin
-0.52	3.30e-01	TXNRD2	thioredoxin reductase 2	0.6	2.07e-01	C2CD5	C2 calcium dependent domain contain
-0.52	4.14e-01	HVCN1	hydrogen voltage gated channel 1	0.59	4.14e-01	MRPS2	mitochondrial ribosomal protein S2
-0.5	4.03e-01	PBXIP1	PBX homeobox interacting protein 1	0.58	2.25e-01	CNOT10	CCR4-NOT transcription complex subu
-0.5	5.20e-01	SCAMP2	secretory carrier membrane protein	0.58	2.17e-01	EED	embryonic ectoderm development
-0.49	2.33e-01	RAP1A	RAP1A, member of RAS oncogene famil	0.58	4.41e-01	DPYD	dihydropyrimidine dehydrogenase
-0.47	4.49e-01	BSDC1	BSD domain containing 1	0.58	3.72e-02	NLE1	notchless homolog 1
-0.47	4.80e-01	ARSB	arylsulfatase B	0.57	2.29e-01	MARK2	microtubule affinity regulating kin
-0.46	2.25e-01	IGFBP7	insulin like growth factor binding	0.57	2.19e-01	CCDC137	coiled-coil domain containing 137
-0.46	5.44e-01	NCEH1	neutral cholesterol ester hydrolase	0.56	2.17e-01	TCF20	transcription factor 20
-0.46	5.44e-01	MRPS18C	mitochondrial ribosomal protein S18	0.55	2.35e-01	GTPBP10	GTP binding protein 10
-0.45	4.31e-01	FHOD1	formin homology 2 domain containing	0.55	3.42e-01	RBM15B	RNA binding motif protein 15B
-0.45	5.34e-01	ATP1A3	ATPase Na+/K+ transporting subunit	0.55	2.31e-01	NUDT16L1	nudix hydrolase 16 like 1
-0.45	4.18e-01	NFKBIE	NFKB inhibitor epsilon	0.55	4.56e-01	ENO2	enolase 2
-0.44	3.72e-01	MAGEA4	MAGE family member A4	0.54	4.32e-01	EI24	EI24 autophagy associated transmemb
-0.44	4.63e-01	H2AX	H2A.X variant histone	0.54	2.07e-01	DDX28	DEAD-box helicase 28
-0.43	5.15e-01	MED22	mediator complex subunit 22	0.54	3.31e-01	EARS2	glutamyl-tRNA synthetase 2, mitocho
-0.42	5.80e-01	EVL	Enah/Vasp-like	0.54	2.31e-01	POLR2G	RNA polymerase II subunit G
-0.42	5.80e-01	CHMP5	charged multivesicular body protein	0.53	4.19e-01	CEP43	centrosomal protein 43
-0.42	5.44e-01	BORCS7	BLOC-1 related complex subunit 7	0.53	3.97e-01	AIDA	axin interactor, dorsalization asso
-0.42	6.18e-01	ALDH2	aldehyde dehydrogenase 2 family mem	0.53	4.01e-01	MAZ	MYC associated zinc finger protein
-0.41	5.77e-01	GATM	glycine amidinotransferase	0.53	3.70e-01	ACOX1	acyl-CoA oxidase 1

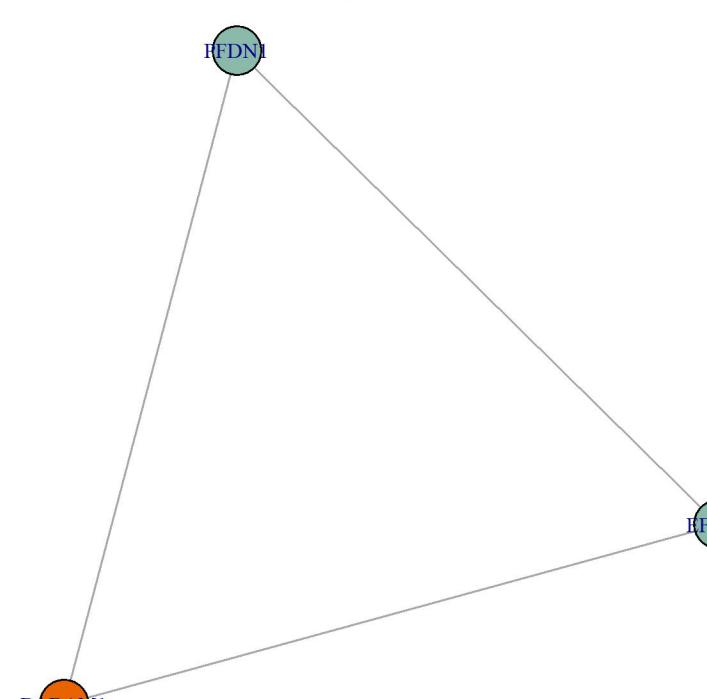


Downregulated in solid cancers at low/absent BABAM1				Upregulated in solid cancers at low/absent BABAM1			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.41	3.90e-47	CZIB	CXXC motif containing zinc binding	0.91	5.99e-11	KRT17	keratin 17
-1.35	3.12e-12	TMSB10	thymosin beta 10	0.89	1.71e-11	ITGB4	integrin subunit beta 4
-1.34	8.20e-42	PPM1B	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe	0.88	1.42e-10	GPRC5A	G protein-coupled receptor class C
-1.33	9.91e-37	C11orf54	chromosome 11 open reading frame 54	0.87	9.21e-12	KRT5	keratin 5
-1.32	8.00e-47	LZIC	leucine zipper and CTNNBIP1 domain	0.86	1.89e-13	F3	coagulation factor III, tissue fact
-1.31	5.81e-28	ABRACL	ABRA C-terminal like	0.85	1.43e-11	MISP	mitotic spindle positioning
-1.3	1.54e-46	PHPT1	phosphohistidine phosphatase 1	0.83	6.26e-12	KRT80	keratin 80
-1.3	1.53e-46	RNF114	ring finger protein 114	0.83	1.71e-10	TACSTD2	tumor associated calcium signal tra
-1.3	4.11e-35	PPP2CA	protein phosphatase 2 catalytic sub	0.82	1.12e-12	LAMB3	laminin subunit beta 3
-1.3	4.30e-45	EIPR1	EARP complex and GARP complex inter	0.81	1.57e-16	PTPMT1	protein tyrosine phosphatase mitoch
-1.29	1.81e-29	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.8	1.06e-12	UXS1	UDP-glucuronate decarboxylase 1
-1.28	5.13e-42	ATOX1	antioxidant 1 copper chaperone	0.78	3.41e-12	CDH3	cadherin 3
-1.28	3.77e-27	BLMH	bleomycin hydrolase	0.78	7.32e-12	LAMC2	laminin subunit gamma 2
-1.27	3.48e-33	CBL	Cbl proto-oncogene	0.76	1.04e-08	S100A14	S100 calcium binding protein A14
-1.27	5.83e-34	PIN1	peptidylprolyl cis/trans isomerase,	0.76	1.81e-16	LPCAT4	lysophosphatidylcholine acyltransfe
-1.27	2.45e-38	FN3KRP	fructosamine 3 kinase related prote	0.75	1.70e-10	LPCAT2	lysophosphatidylcholine acyltransfe
-1.27	4.86e-37	PITHD1	PITH domain containing 1	0.75	3.80e-12	SDC4	syndecan 4
-1.27	1.20e-28	TMEM263	transmembrane protein 263	0.74	1.91e-14	DHRS7B	dehydrogenase/reductase 7B
-1.26	4.47e-39	MRI1	methylthioribose-1-phosphate isomer	0.74	9.53e-09	NT5E	5'-nucleotidase ecto
-1.26	8.00e-29	FKBP1A	FKBP prolyl isomerase 1A	0.73	1.68e-10	EPHA2	EPH receptor A2
-1.25	4.70e-40	PPP1R14B	protein phosphatase 1 regulatory in	0.72	9.26e-10	DERL1	derlin 1
-1.25	7.19e-41	DCK	deoxycytidine kinase	0.71	5.98e-08	CDH1	cadherin 1
-1.25	8.00e-47	DOHH	deoxyhypusine hydroxylase	0.71	5.25e-12	COL17A1	collagen type XVII alpha 1 chain
-1.24	7.52e-38	ARMC6	armadillo repeat containing 6	0.71	1.85e-11	RAP2B	RAP2B, member of RAS oncogene fami
-1.24	2.14e-31	PSME3IP1	proteasome activator subunit 3 inte	0.71	7.34e-12	SURF1	SURF1 cytochrome c oxidase assembly
-1.24	2.39e-23	VPS37C	VPS37C subunit of ESCRT-I	0.71	6.16e-14	MRPS10	mitochondrial ribosomal protein S10
-1.23	1.26e-39	RABEP1	rabaptin, RAB GTPase binding effect	0.71	3.14e-12	ERGIC2	ERGIC and golgi 2
-1.23	7.97e-34	ENSA	endosulfine alpha	0.7	2.25e-11	SCAMP2	secretory carrier membrane protein
-1.22	1.62e-35	IFT27	intraflagellar transport 27	0.7	1.62e-08	UQCRC10	ubiquinol cytochrome c reductase, c

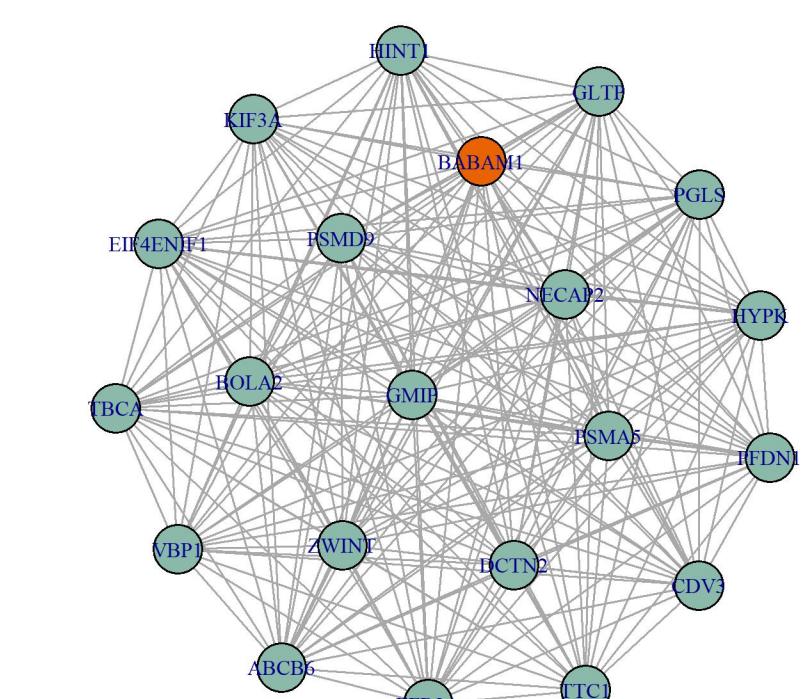
BABAM1 network, DB1, all Pearson $r > 0.45$

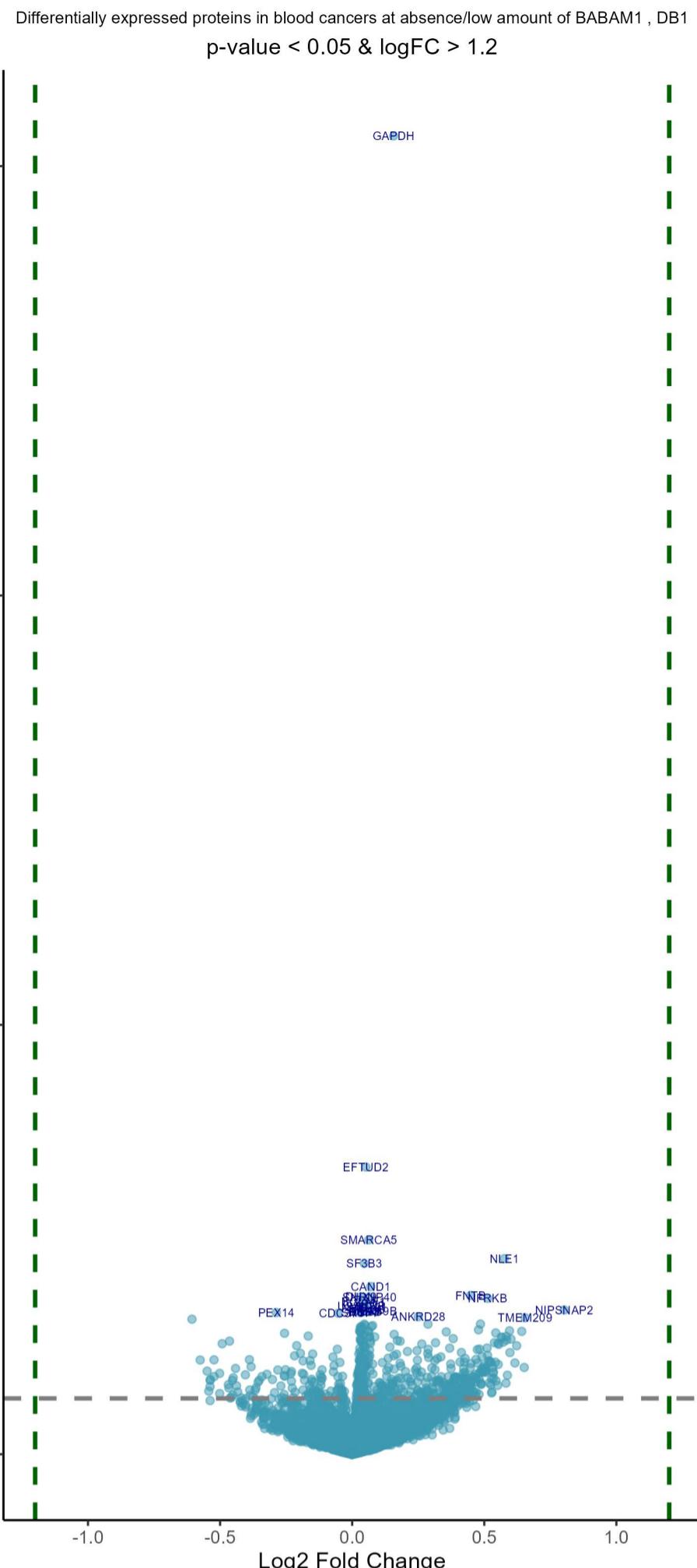


BABAM1 network, DB1, all Pearson $r > 0.4$

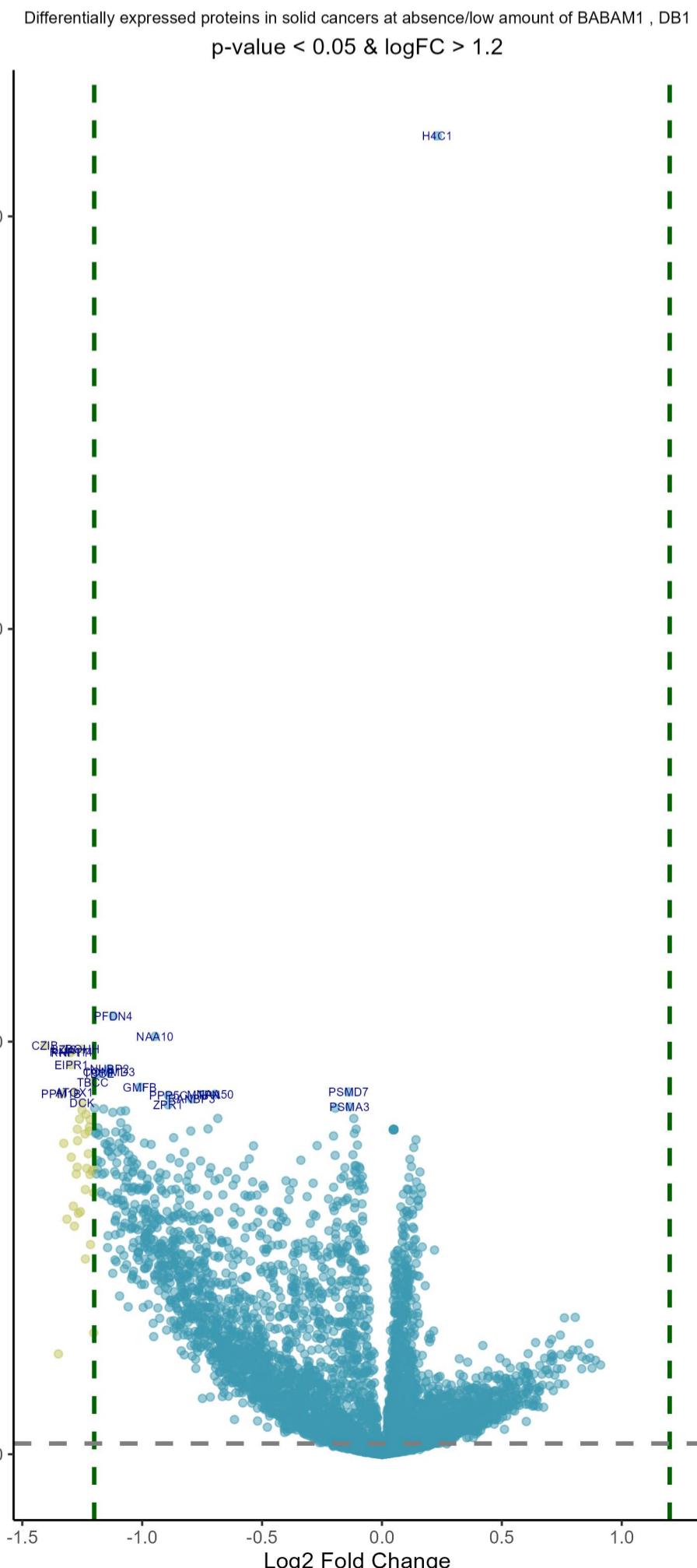


BABAM1 network, DB1, all Pearson r > 0.35

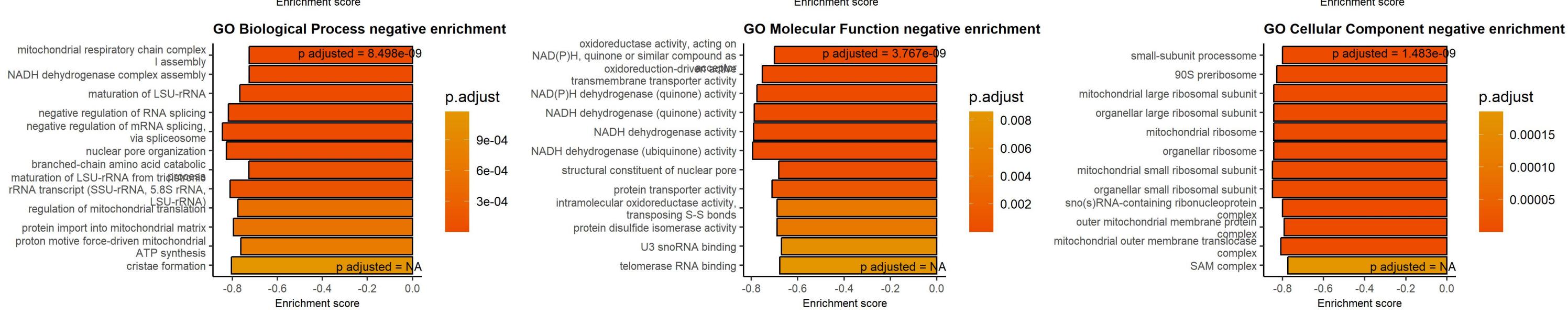
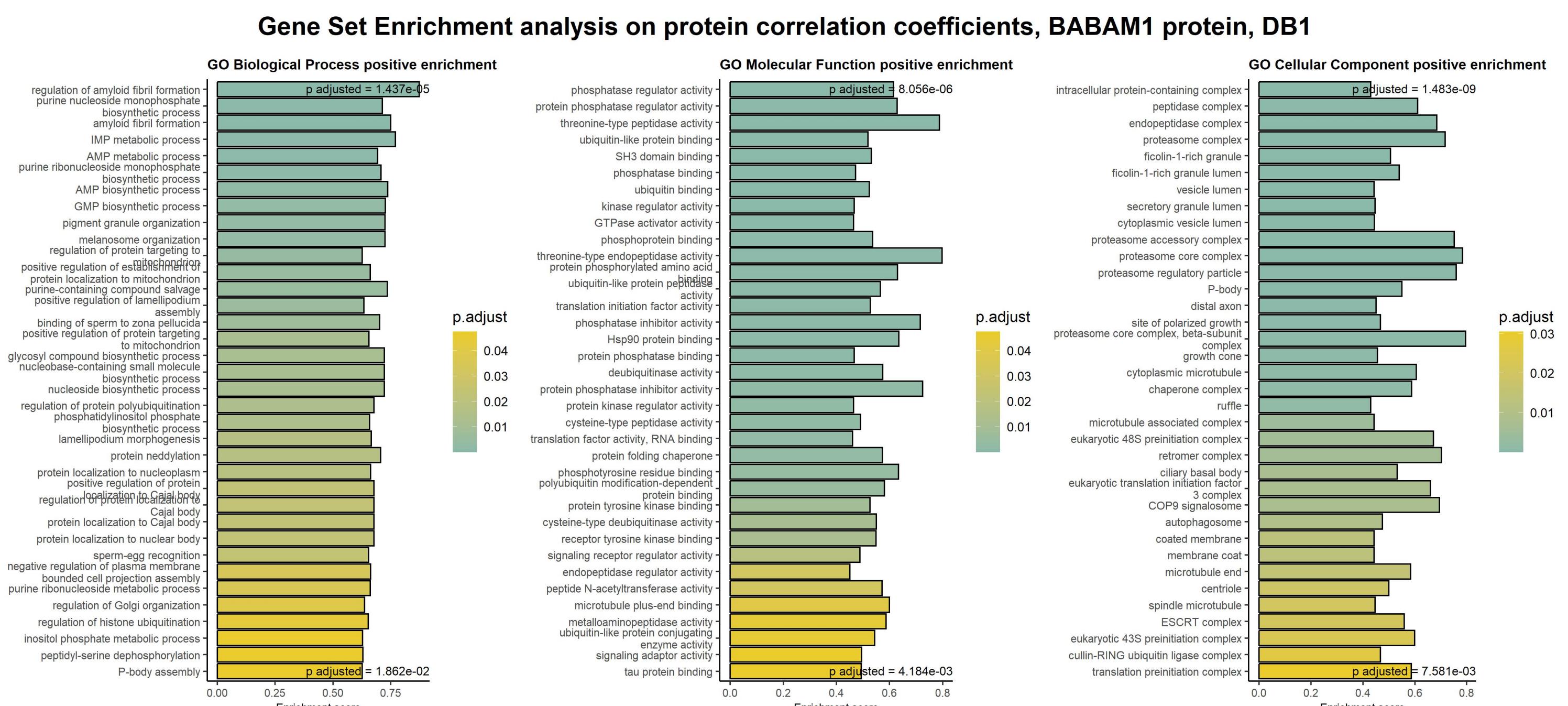
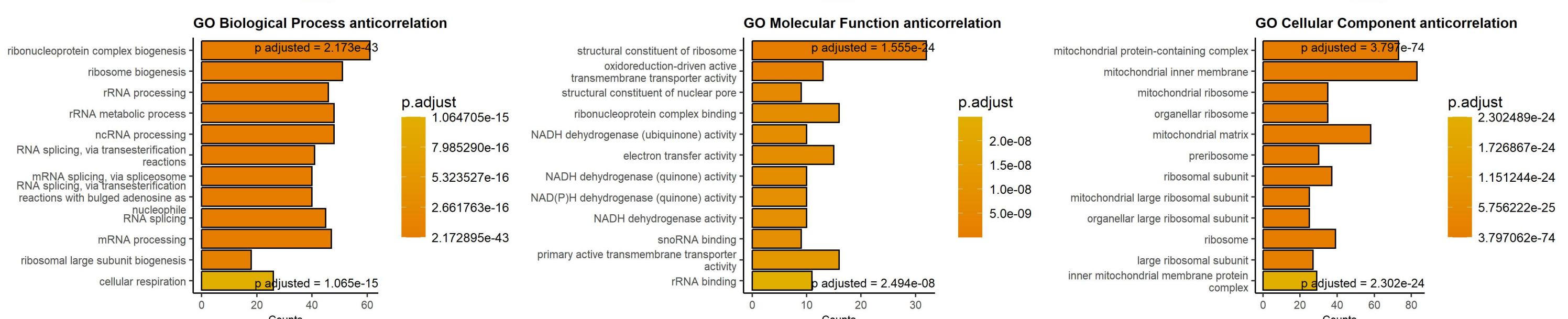
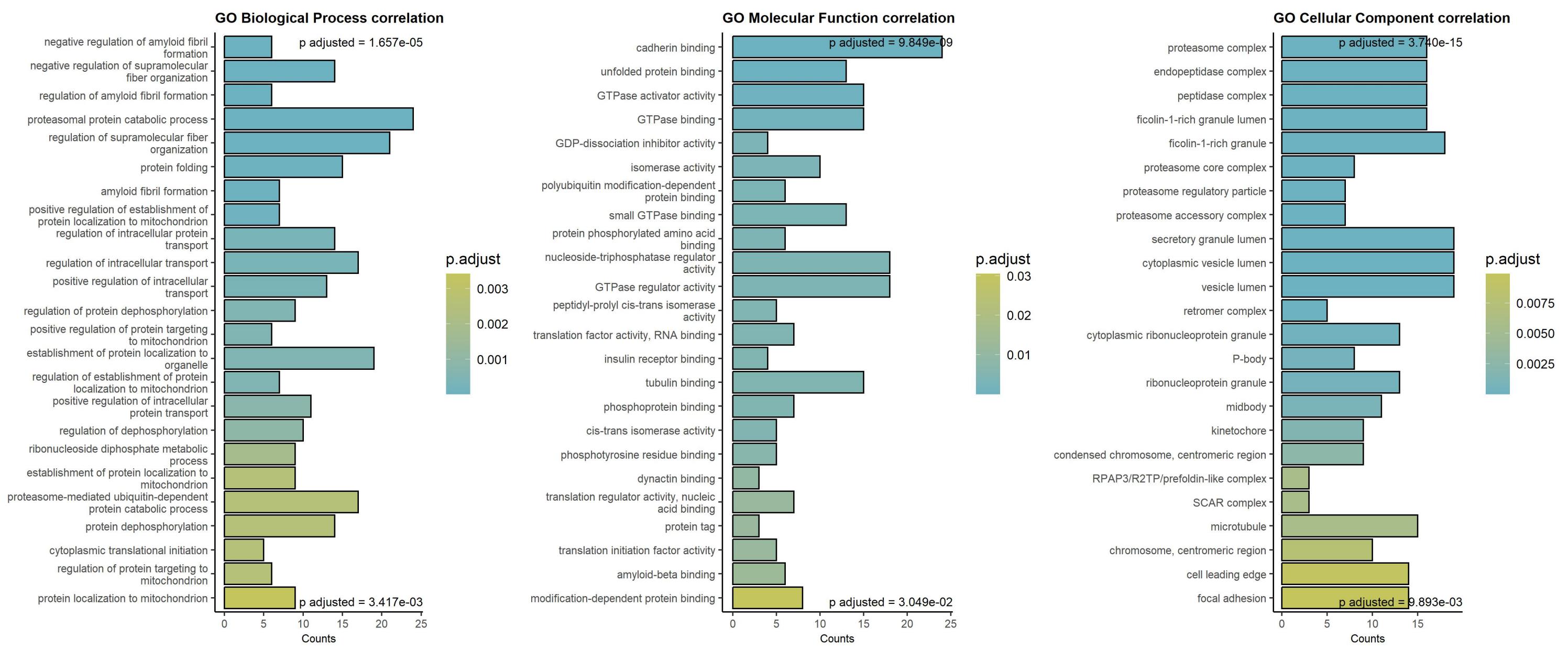




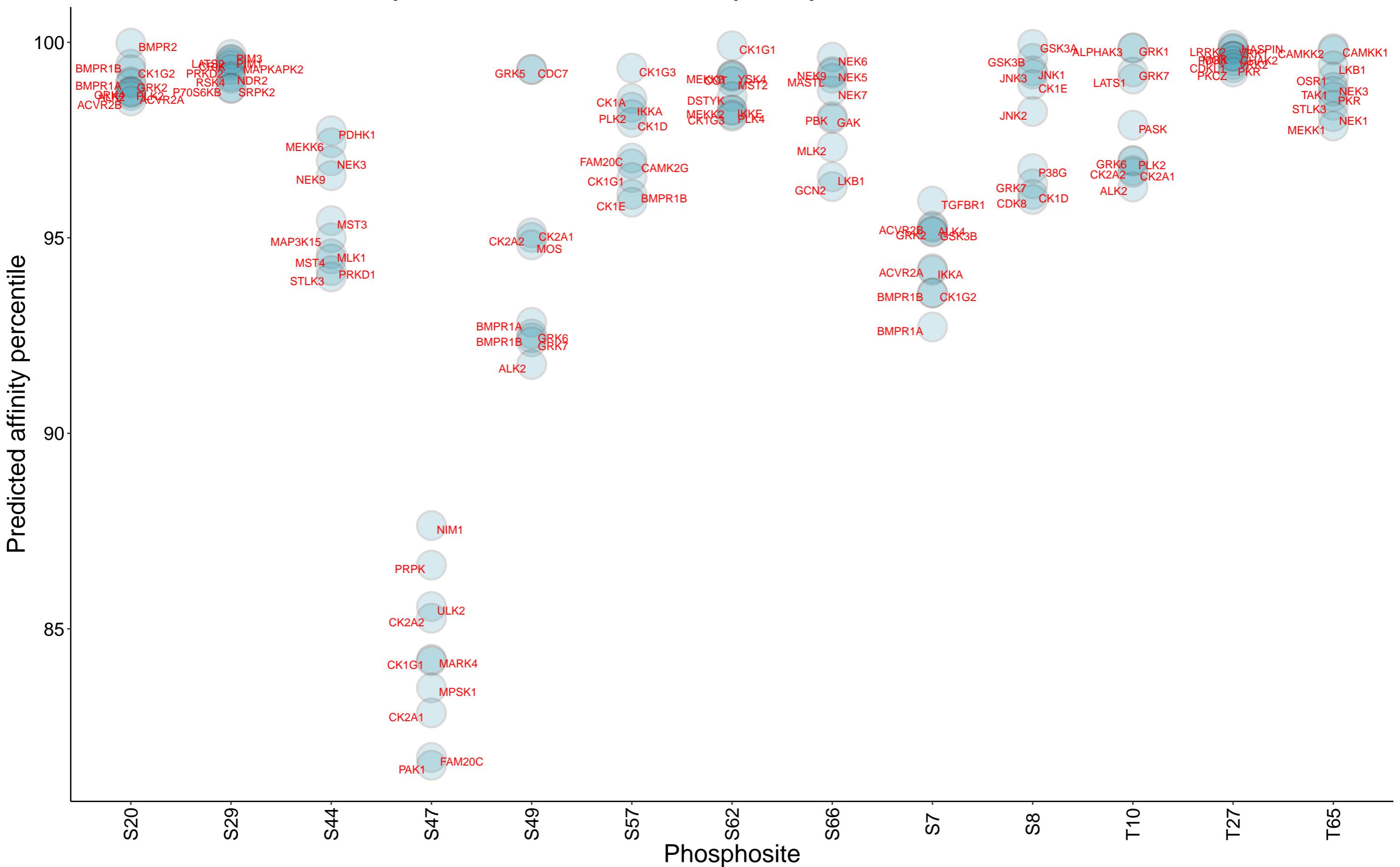
Sorted by p values!							
Downregulated in blood cancers at low/absent BABAM1				Upregulated in blood cancers at low/absent BABAM1			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.29	1.50e-01	PEX14	peroxisomal biogenesis factor 14	0.16	1.32e-27	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
-0.05	1.50e-01	CDC37	cell division cycle 37, HSP90 cocha	0.05	4.54e-04	EFTUD2	elongation factor Tu GTP binding domain
-0.61	1.83e-01	KIAA1143	KIAA1143	0.06	1.69e-02	SMARCA5	SWI/SNF related, matrix associated, chromatin rearranger 5
-0.26	2.07e-01	ADPRS	ADP-ribosylserine hydrolase	0.58	3.72e-02	NLE1	notchless homolog 1
-0.17	2.17e-01	MAN2B1	mannosidase alpha class 2B member 1	0.05	3.98e-02	SF3B3	splicing factor 3b subunit 3
-0.46	2.25e-01	IGFBP7	insulin like growth factor binding protein 7	0.07	1.18e-01	CAND1	cullin associated and neddylation domain
-0.49	2.33e-01	RAP1A	RAP1A, member of RAS oncogene family	0.45	1.41e-01	FNTB	farnesyltransferase, CAAX box, beta
-0.21	2.44e-01	ZFYVE16	zinc finger FYVE-type containing 16	0.03	1.41e-01	DHX9	DExH-box helicase 9
-0.06	2.63e-01	CMPK1	cytidine/uridine monophosphate kinase	0.07	1.41e-01	SNRNP40	small nuclear ribonucleoprotein U5
-0.2	2.99e-01	SRSF2	serine and arginine rich splicing factor 2	0.51	1.41e-01	NFRKB	nuclear factor related to kappaB binding
-0.15	2.99e-01	OSTF1	osteoclast stimulating factor 1	0.04	1.50e-01	BCLAF1	BCL2 associated transcription factor 1
-0.22	3.09e-01	MOB4	MOB family member 4, phoceanin	0.06	1.50e-01	XPO1	exportin 1
-0.07	3.16e-01	TRIR	telomerase RNA component interactin	0.04	1.50e-01	U2SURP	U2 snRNP associated SURP domain containing protein
-0.39	3.30e-01	RPL36AL	ribosomal protein L36a like	0.05	1.50e-01	NUDT21	nudix hydrolase 21
-0.52	3.30e-01	TXNRD2	thioredoxin reductase 2	0.05	1.50e-01	TRA2B	transformer 2 beta homolog
-0.58	3.30e-01	CYB5A	cytochrome b5 type A	0.8	1.50e-01	NIPSNAP2	nipsnap homolog 2
-0.16	3.31e-01	RAD23A	RAD23 homolog A, nucleotide excision repair protein	0.08	1.50e-01	DDX39B	DExD-box helicase 39B
-0.19	3.31e-01	TXNDC15	thioredoxin domain containing 15	0.05	1.50e-01	EIF3B	eukaryotic translation initiation factor 3 subunit B
-0.05	3.31e-01	GET3	guided entry of tail-anchored protein 3	0.04	1.50e-01	BUB3	BUB3 mitotic checkpoint protein
-0.16	3.54e-01	SNAP29	synaptosome associated protein 29	0.03	1.50e-01	SRSF7	serine and arginine rich splicing factor 7
-0.07	3.55e-01	FKBP2	FKBP prolyl isomerase 2	0.25	1.74e-01	ANKRD28	ankyrin repeat domain 28
-0.38	3.69e-01	PSME3IP1	proteasome activator subunit 3 interacting protein 1	0.65	1.76e-01	TMEM209	transmembrane protein 209
-0.44	3.72e-01	MAGEA4	MAGE family member A4	0.49	2.07e-01	TYMS	thymidylate synthetase
-0.25	3.82e-01	PDXDC1	pyridoxal dependent decarboxylase domain	0.29	2.07e-01	GTPBP8	GTP binding protein 8 (putative)
-0.11	3.82e-01	EIF2B4	eukaryotic translation initiation factor 2B subunit 4	0.05	2.07e-01	RPS15A	ribosomal protein S15a
-0.28	3.82e-01	PLPP6	phospholipid phosphatase 6	0.05	2.07e-01	SSRP1	structure specific recognition protein
-0.55	3.96e-01	ALB	albumin	0.08	2.07e-01	EIF4A1	eukaryotic translation initiation factor 4A1
-0.23	3.97e-01	RNF126	ring finger protein 126	0.03	2.07e-01	RPL38	ribosomal protein L38
-0.07	3.97e-01	EPS15L1	epidermal growth factor receptor pathway associated	0.07	2.07e-01	PRPF8	pre-mRNA processing factor 8
-0.19	4.01e-01	TBL1XR1	TBL1X receptor 1	0.04	2.07e-01	DDB1	damage specific DNA binding protein
-0.5	4.03e-01	PBXIP1	PBX homeobox interacting protein 1	0.03	2.07e-01	SRSF6	serine and arginine rich splicing factor 6
-0.23	4.03e-01	RAB5A	RAB5A, member RAS oncogene family	0.03	2.07e-01	SRRT	serrate, RNA effector molecule
-0.32	4.08e-01	RRAS	RAS related	0.48	2.07e-01	NUP160	nucleoporin 160
-0.18	4.08e-01	TARS2	threonyl-tRNA synthetase 2, mitochondrial	0.6	2.07e-01	C2CD5	C2 calcium dependent domain containing
-0.12	4.12e-01	SCAMP3	secretory carrier membrane protein 3	0.03	2.07e-01	PTBP1	polypyrimidine tract binding protein
-0.4	4.12e-01	SQSTM1	sequestosome 1	0.03	2.07e-01	HNRNPL	heterogeneous nuclear ribonucleoprotein
-0.26	4.14e-01	CCS	copper chaperone for superoxide dismutase	0.03	2.07e-01	U2AF2	U2 small nuclear RNA auxiliary factor
-0.26	4.14e-01	AAMP	angiogenesis associated migratory cell protein	0.06	2.07e-01	UBE2I	ubiquitin conjugating enzyme E2 I
-0.04	4.14e-01	TTC1	tetratricopeptide repeat domain 1	0.64	2.07e-01	RHE14	RHD finger protein 14



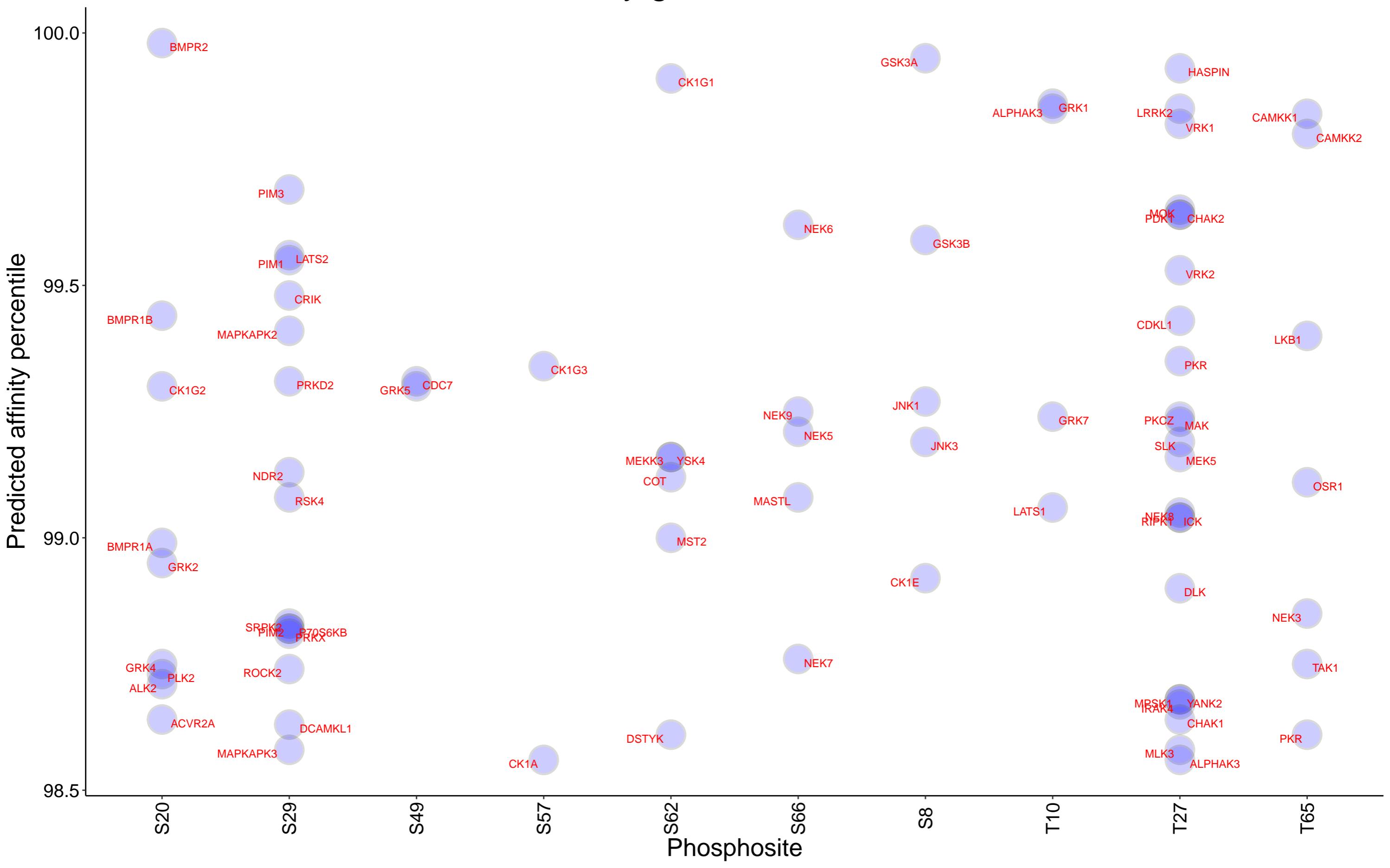
Top 250 correlation coefficients overrepresentation, BABAM1 protein, DB1



Top 10 kinases for each phosphosite in BABAM1



Kinases with affinity greater than 98.5% to BABAM1



Top 15 positive correlation coefficients for BABAM1 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

