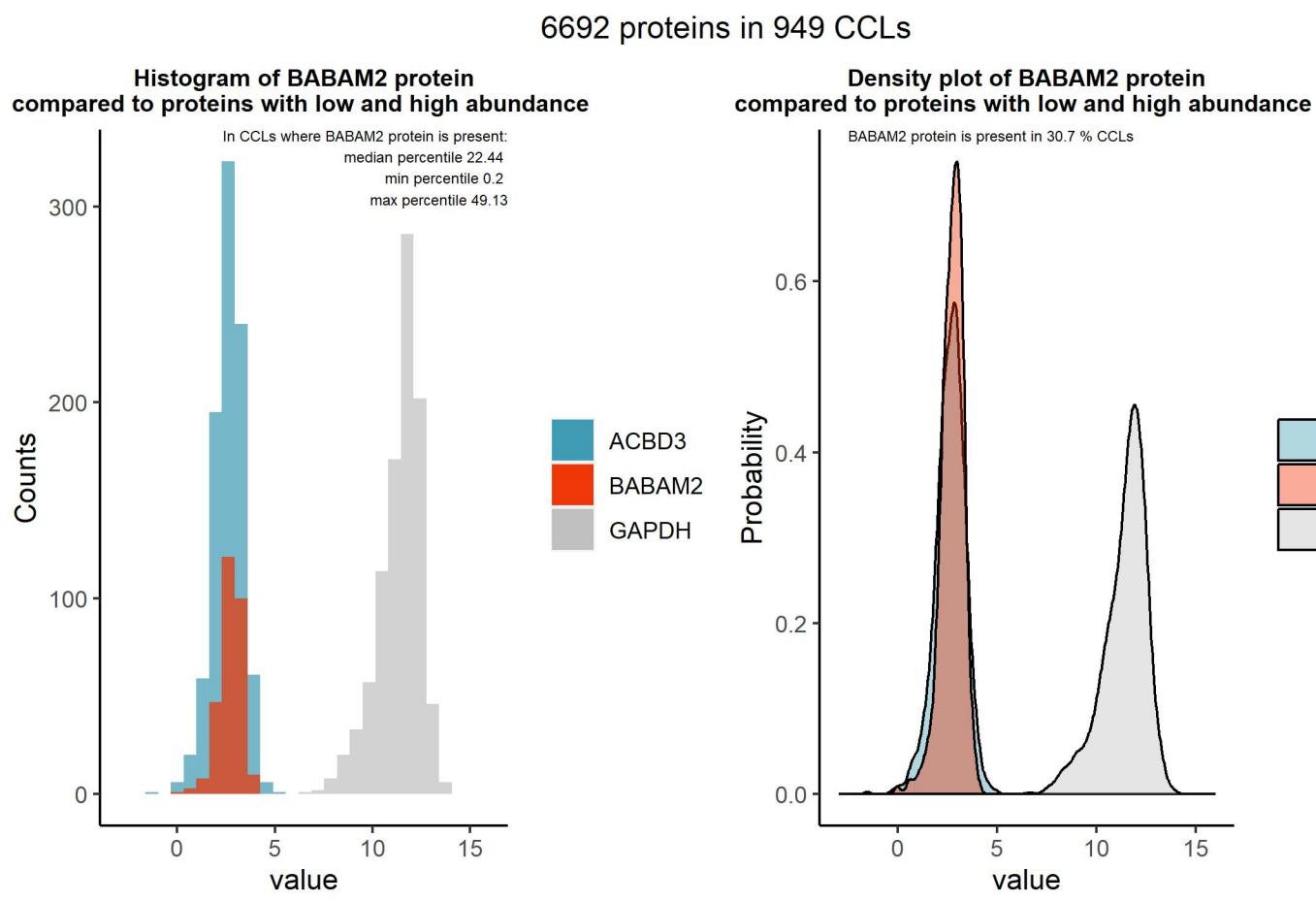


BABAM2

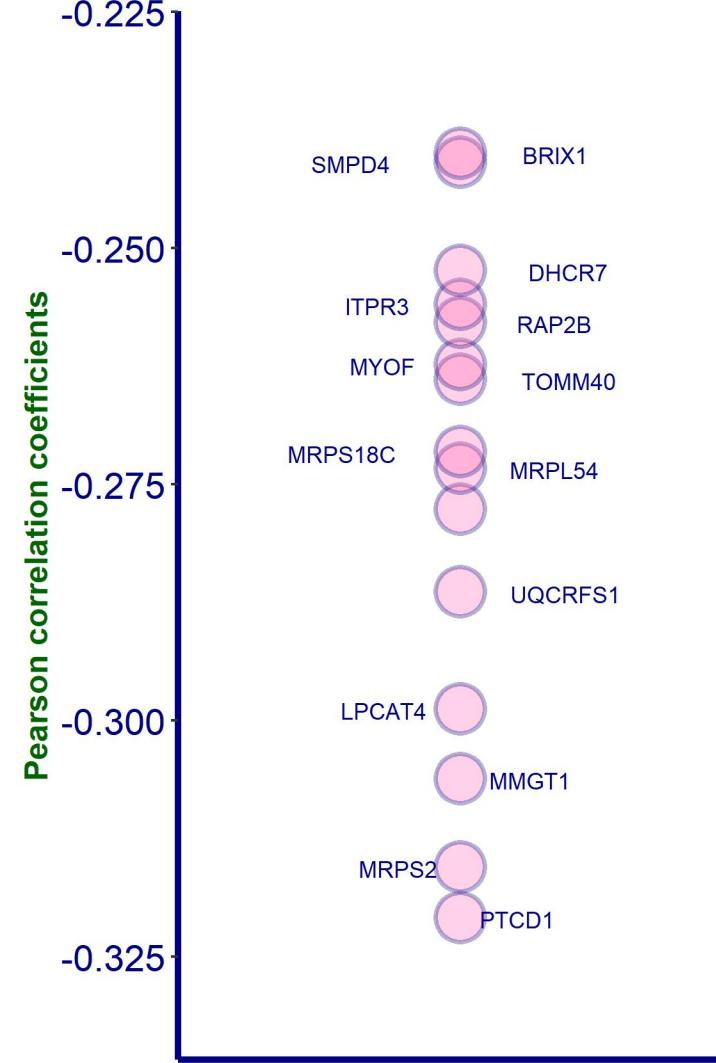
Protein name: BABA2 ; UNIPROT: Q9NXR7 ; Gene name: BRISC and BRCA1 A complex member 2

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

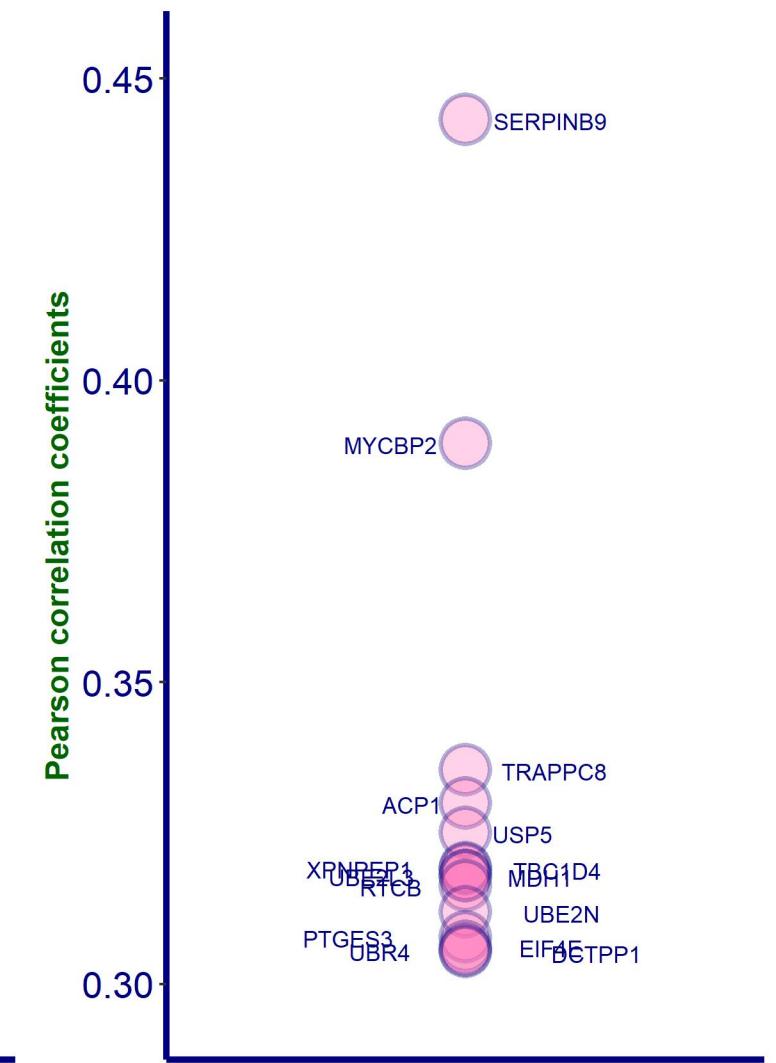
Sanger Institute Protein Database 1 (DB1), protein presence is certain



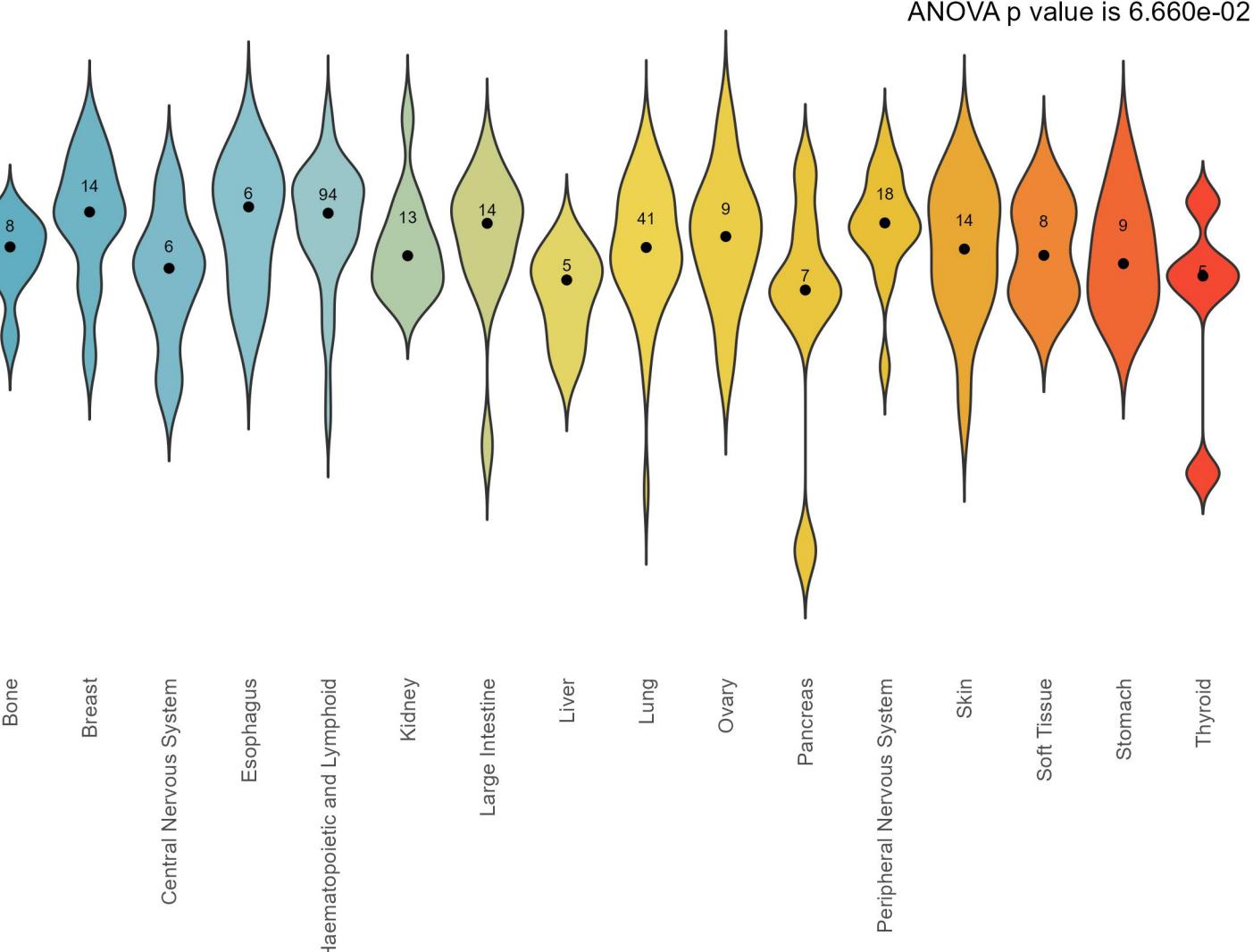
Top negative correlations of BABAM2 protein, DB1



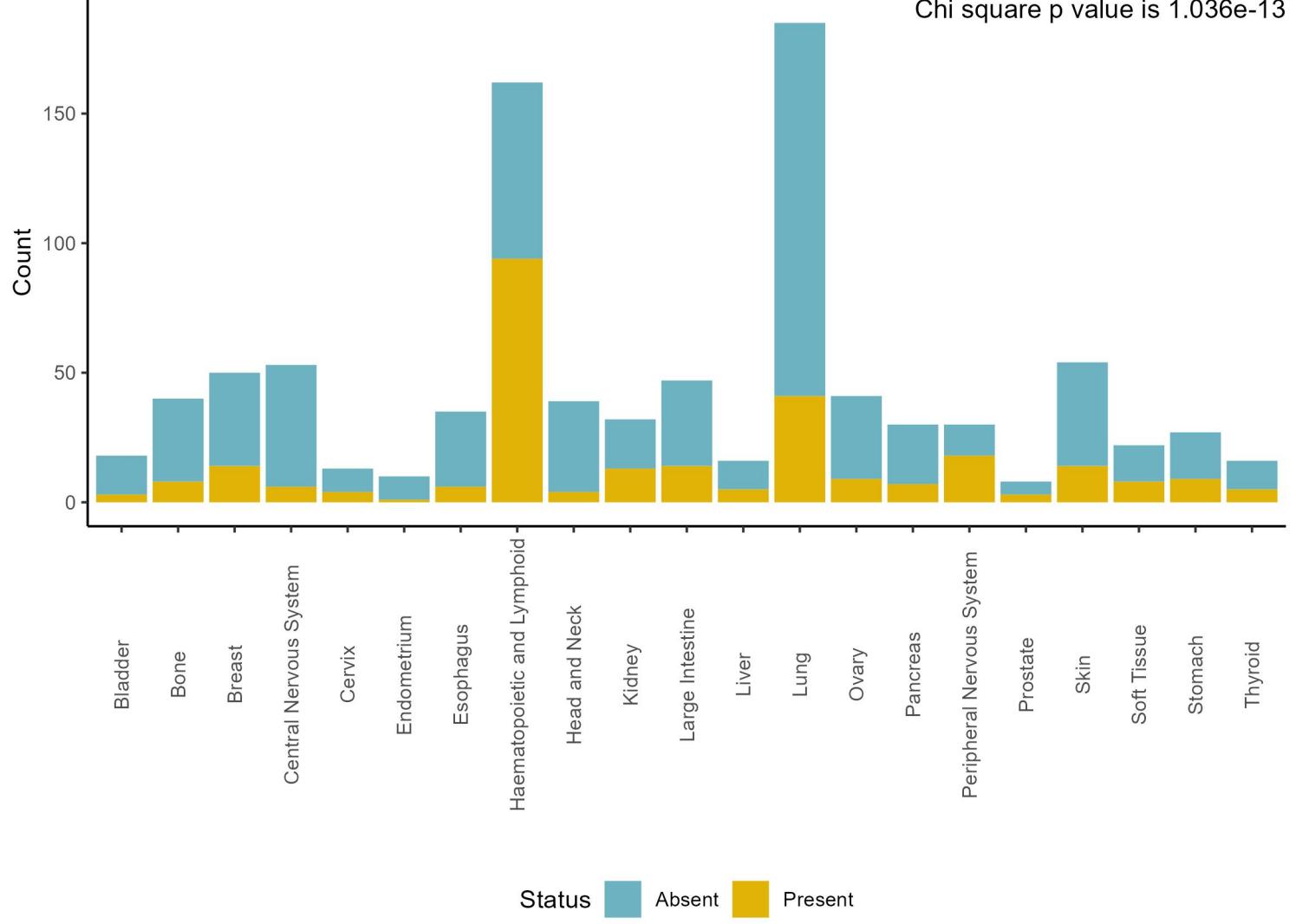
Top positive correlations of BABAM2 protein, DB1



Amount of BABAM2 protein, number of CCLs where it is present by tissue, DB1



Present and absent BABAM2 protein counts by tissue, DB1

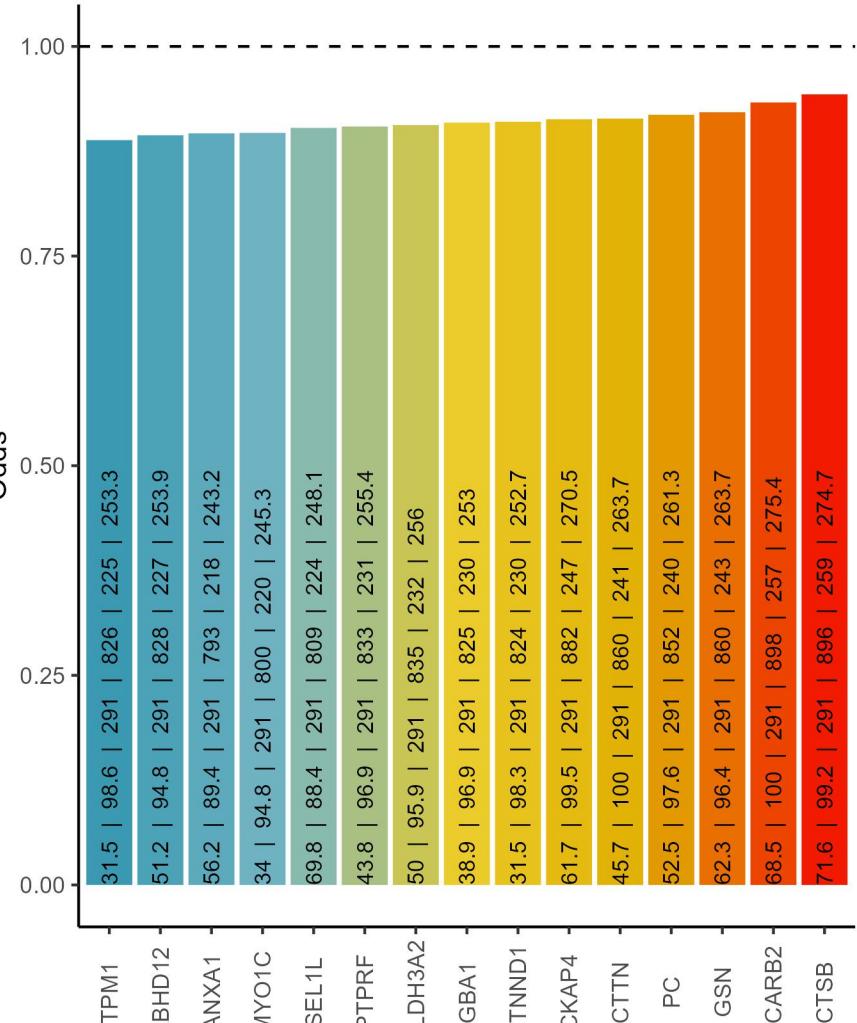


Cooccurrence with BABAM2 protein, DB1

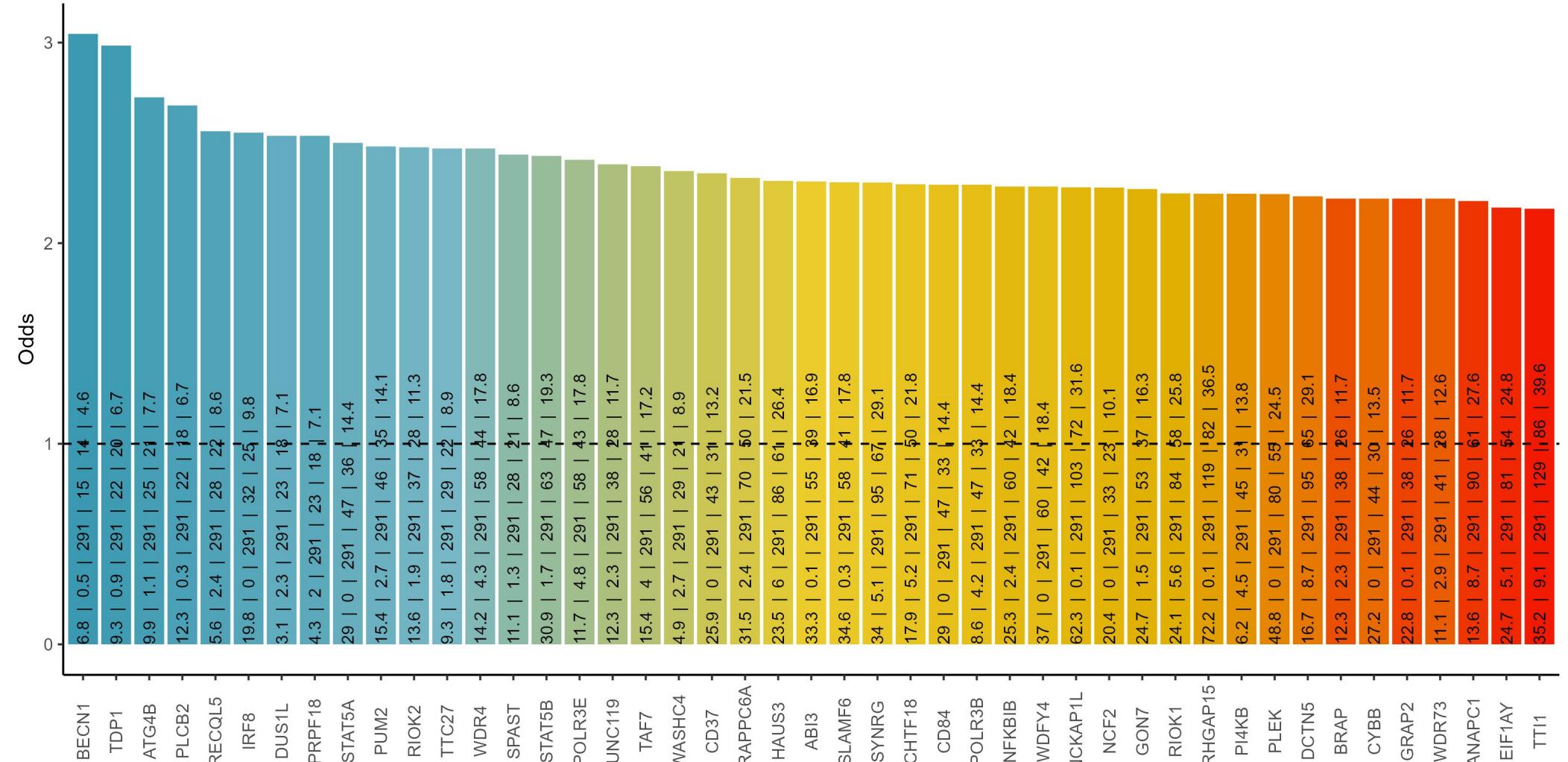
% of BABAM2 in blood cancers: 58 ; % of BABAM2 in solid cancers: 25

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of BABAM2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

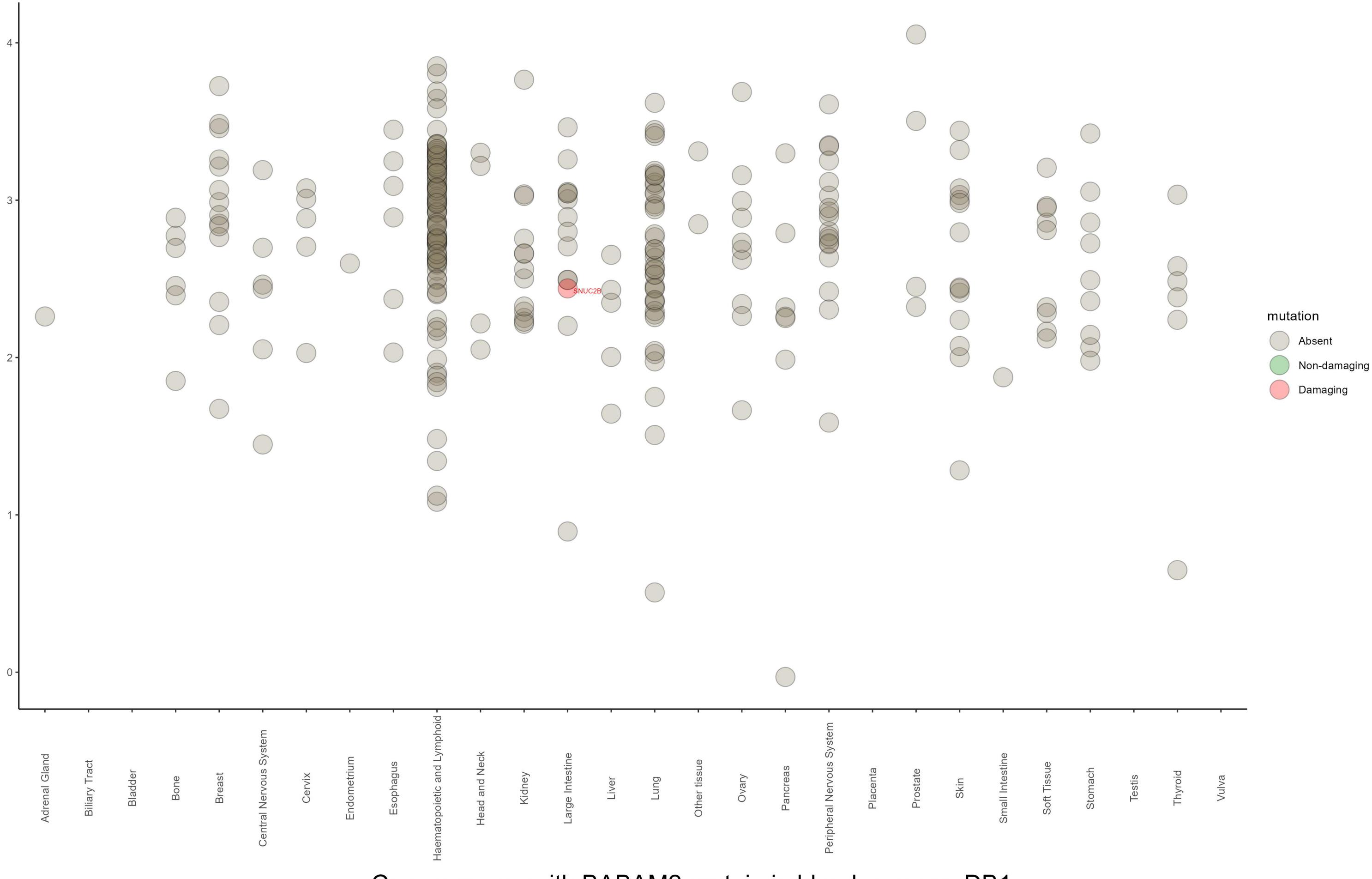
Negative cooccurrence



Positive cooccurrence

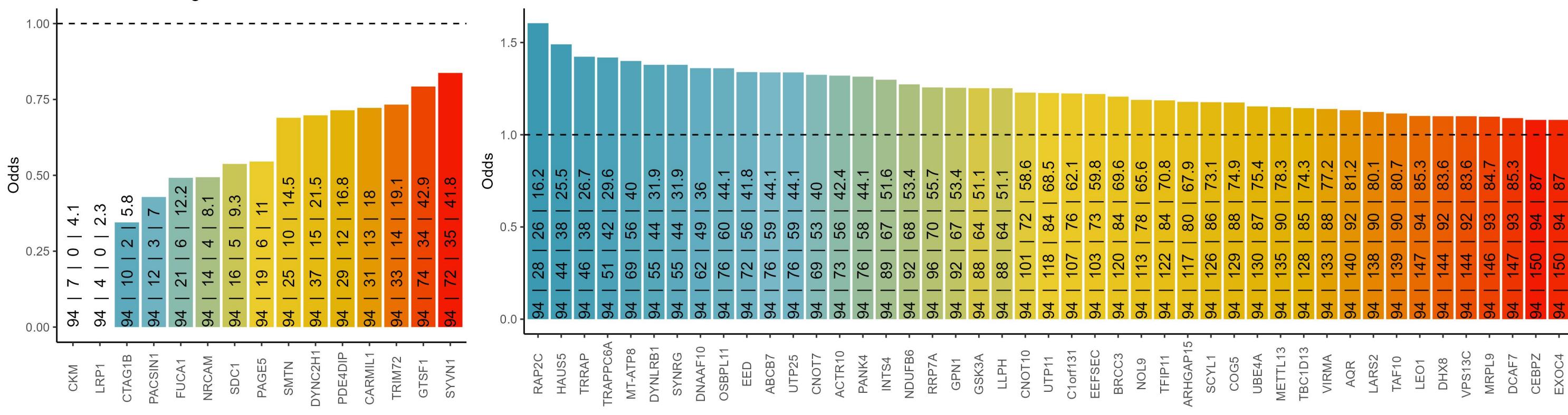


Amount of BABAM2 protein and mutation status by tissue, DB1



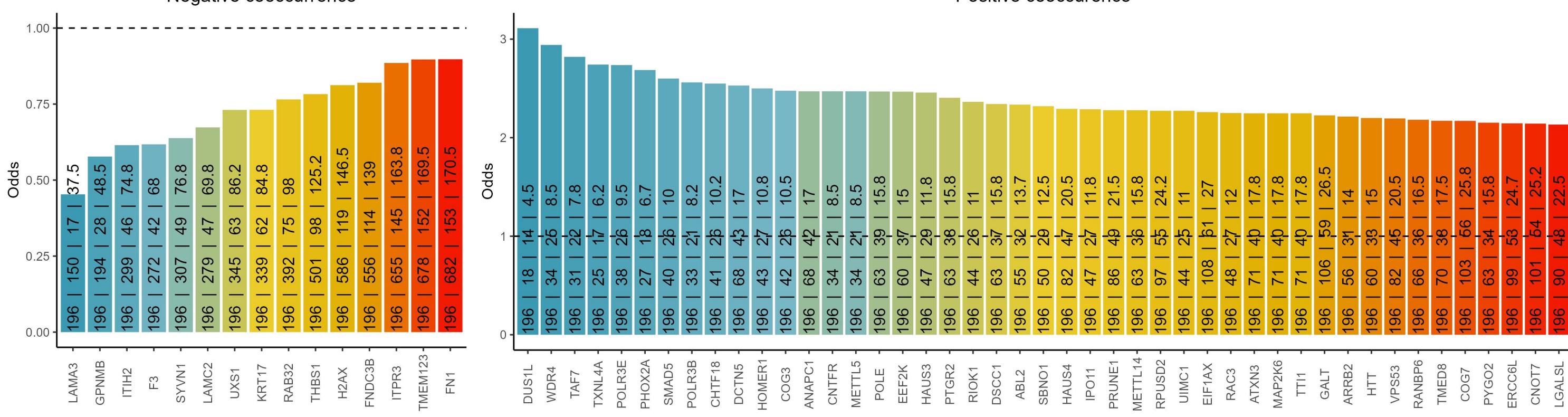
Cooccurrence with BABAM2 protein in blood cancers, DB1

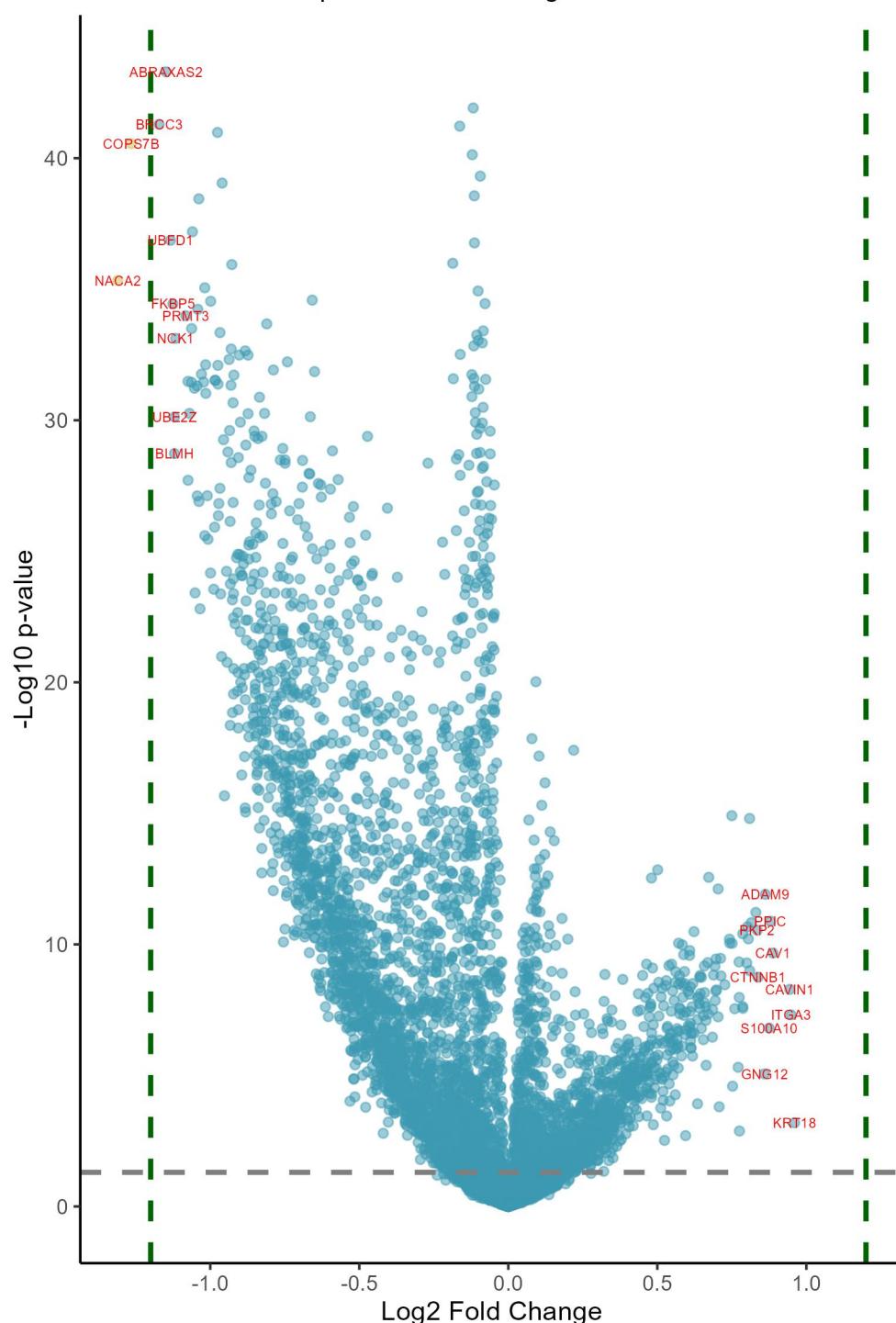
The text in the bars: incidence of BABAM2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Cooccurrence with BABAM2 protein in solid cancers, DB1

The text in the bars: incidence of BABAM2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

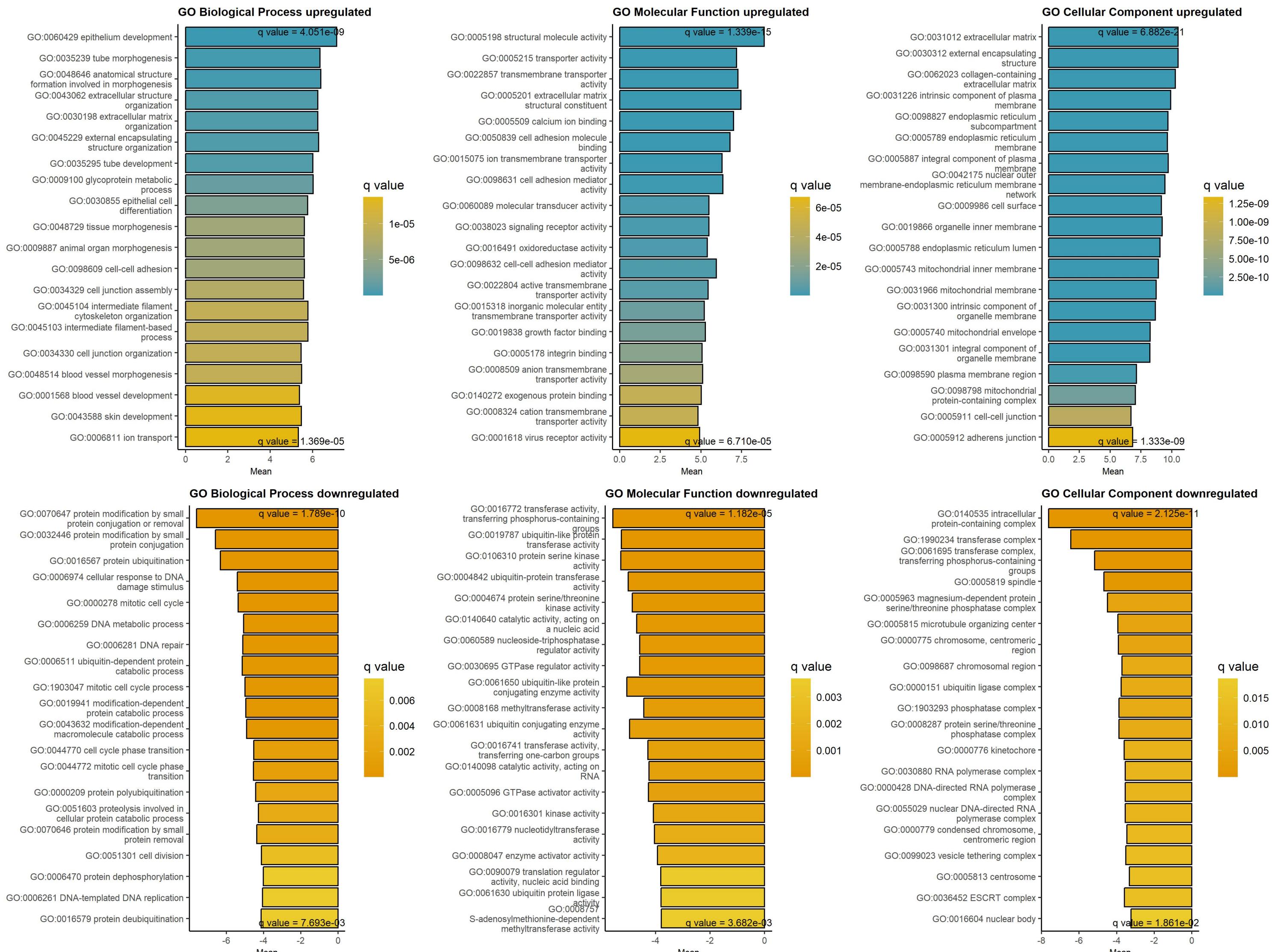




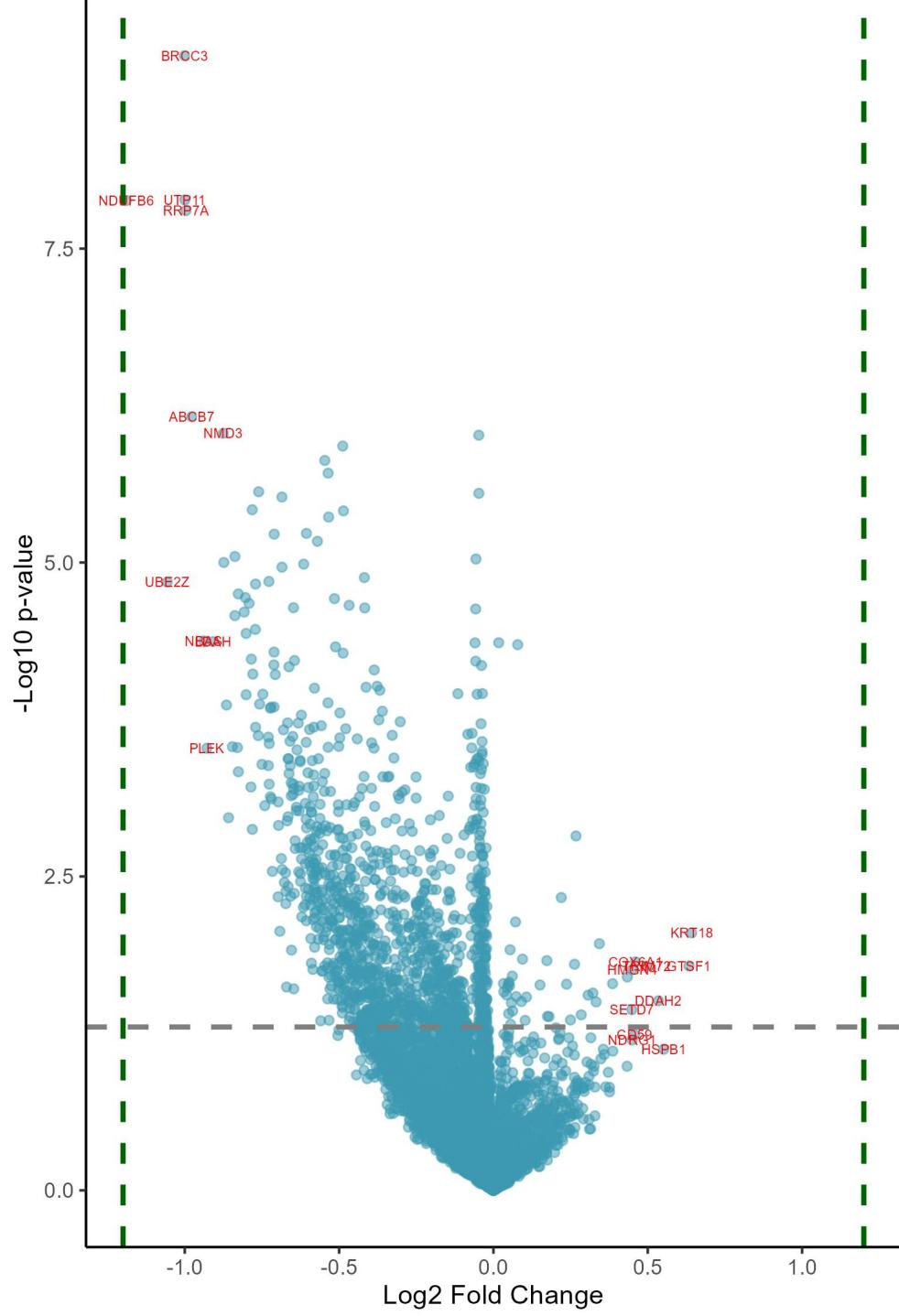
Downregulated at low/absent BABAM2 Upregulated at low/absent BABAM2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.31	1.73e-33	NACA2	nascent polypeptide associated comp	0.96	1.36e-03	KRT18	keratin 18
-1.27	2.65e-38	COPS7B	COP9 signalosome subunit 7B	0.95	1.77e-07	ITGA3	integrin subunit alpha 3
-1.17	8.00e-39	BRCC3	BRCA1/BRCA2-containing complex subu	0.94	2.16e-08	CAVIN1	caveolae associated protein 1
-1.15	1.68e-40	ABRAXAS2	abraxas 2, BRISC complex subunit	0.89	1.04e-09	CAV1	caveolin 1
-1.13	6.53e-35	UBFD1	ubiquitin family domain containing	0.88	7.34e-11	PPIC	peptidylprolyl isomerase C
-1.13	1.00e-32	FKBP5	FKBP prolyl isomerase 5	0.88	5.34e-07	S100A10	S100 calcium binding protein A10
-1.12	1.32e-27	BLMH	bleomycin hydrolase	0.86	7.63e-12	ADAM9	ADAM metallopeptidase domain 9
-1.12	6.76e-29	UBE2Z	ubiquitin conjugating enzyme E2 Z	0.86	2.41e-05	GNG12	G protein subunit gamma 12
-1.12	1.56e-31	NCK1	NCK adaptor protein 1	0.84	7.86e-09	CTNNB1	catenin beta 1
-1.08	2.63e-32	PRMT3	protein arginine methyltransferase	0.83	1.54e-10	PKP2	plakophilin 2
-1.07	3.97e-30	COMMD2	COMM domain containing 2	0.83	3.49e-11	MMP14	matrix metallopeptidase 14
-1.07	1.14e-26	C11orf54	chromosome 11 open reading frame 54	0.82	8.22e-11	THBS1	thrombospondin 1
-1.07	5.15e-29	RWDD1	RWD domain containing 1	0.81	4.59e-09	EGFR	epidermal growth factor receptor
-1.06	4.15e-30	PSME3IP1	proteasome activator subunit 3 inte	0.81	1.39e-14	FNDC3B	fibronectin type III domain contain
-1.06	7.55e-32	EIF2B5	eukaryotic translation initiation f	0.81	3.16e-10	EPHX1	epoxide hydrolase 1
-1.06	3.29e-35	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.8	1.16e-10	EPHA2	EPH receptor A2
-1.05	6.44e-30	EIF2B1	eukaryotic translation initiation f	0.8	2.39e-09	ITGB4	integrin subunit beta 4
-1.05	1.09e-22	GTF2E1	general transcription factor IIIE su	0.79	1.04e-07	FKBP9	FKBP prolyl isomerase 9
-1.04	5.44e-30	METTL13	methyltransferase 13, eEF1A lysine	0.79	2.07e-10	BCAM	basal cell adhesion molecule (Luthe
-1.04	4.04e-26	DHFR	dihydrofolate reductase	0.79	8.93e-08	JUP	junction plakoglobin
-1.04	1.56e-32	TBC1D5	TBC1 domain family member 5	0.78	2.66e-03	KRT8	keratin 8
-1.04	1.97e-36	EIPR1	EARP complex and GARP complex inter	0.77	4.19e-08	ITGA2	integrin subunit alpha 2
-1.04	6.47e-26	ARMC6	armadillo repeat containing 6	0.77	2.20e-09	KRT17	keratin 17
-1.03	4.07e-22	SEPTIN6	septin 6	0.77	1.41e-05	PLP2	proteolipid protein 2
-1.03	2.47e-30	RABGTA	Rab geranylgeranyltransferase subun	0.76	1.07e-07	ITGA6	integrin subunit alpha 6
-1.02	4.15e-30	GMPR2	guanosine monophosphate reductase 2	0.75	6.65e-05	LGALS3	galectin 3
-1.02	1.05e-24	GRK2	G protein-coupled receptor kinase 2	0.75	4.60e-10	MISP	mitotic spindle positioning
-1.02	3.09e-33	CNOT2	CCR4-NOT transcription complex subu	0.75	1.10e-14	F3	coagulation factor III, tissue fact
-1.02	1.18e-30	SSU72	SSU72 homolog, RNA polymerase II CT	0.74	4.48e-10	MTCH1	mitochondrial carrier 1

GAGE analysis on upregulated and downregulated proteins at low/absent BABAM2 protein, DB1

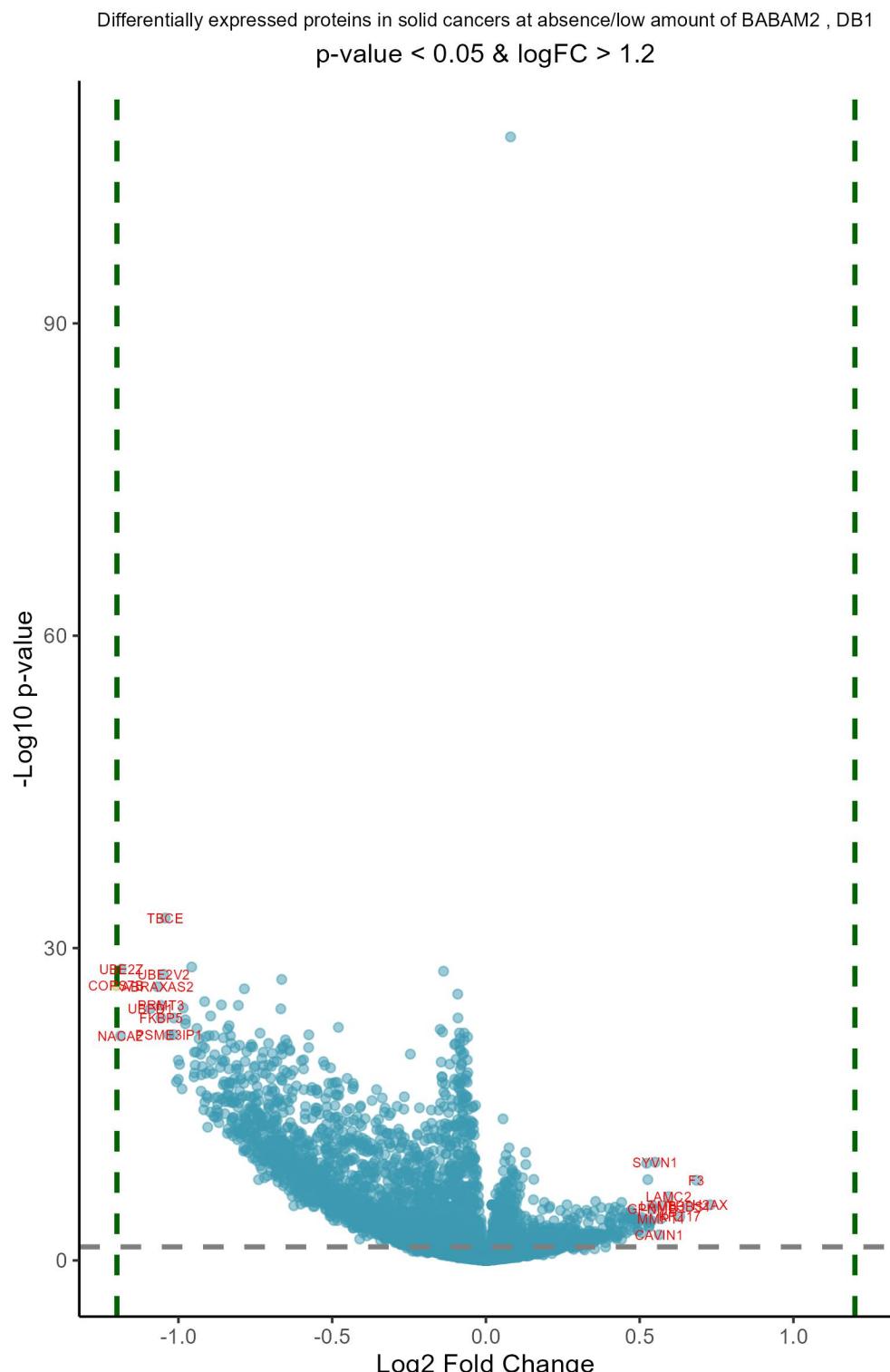


p-value < 0.05 & logFC > 1.2



Downregulated in blood cancers at low/absent BABAM2 Upregulated in blood cancers at low/absent BABAM2

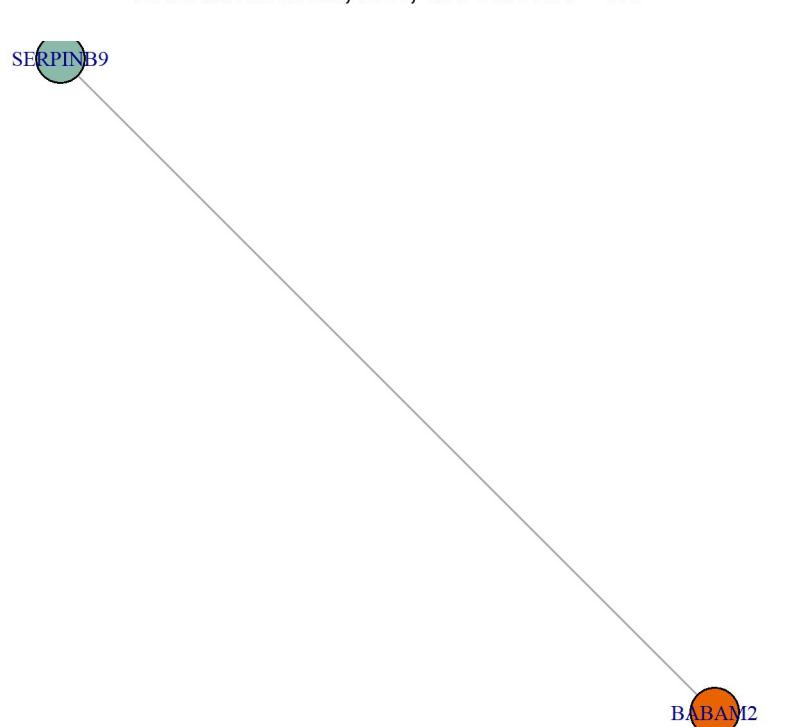
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.19	2.09e-05	NDUFB6	NADH:ubiquinone oxidoreductase subu	0.64	1.05e-01	KRT18	keratin 18
-1.06	3.40e-03	UBE2Z	ubiquitin conjugating enzyme E2 Z	0.63	1.48e-01	GTSF1	gametocyte specific factor 1
-1	3.06e-06	BRCC3	BRCA1/BRCA2-containing complex subu	0.55	3.11e-01	HSPB1	heat shock protein family B (small)
-1	2.09e-05	UTP11	UTP11 small subunit processome comp	0.53	2.04e-01	DDAH2	dimethylarginine dimethylaminohydro
-1	2.09e-05	RRP7A	ribosomal RNA processing 7 homolog	0.5	1.48e-01	TRIM72	tripartite motif containing 72
-0.98	7.65e-04	ABC B7	ATP binding cassette subfamily B me	0.46	1.42e-01	COX6A1	cytochrome c oxidase subunit 6A1
-0.94	6.45e-03	NBAS	NBAS subunit of NRZ tethering compl	0.46	2.73e-01	CD59	CD59 molecule (CD59 blood group)
-0.93	1.87e-02	PLEK	pleckstrin	0.45	1.54e-01	HMGN4	high mobility group nucleosomal bin
-0.91	6.45e-03	LDAH	lipid droplet associated hydrolase	0.45	2.84e-01	NDRG1	N-myc downstream regulated 1
-0.88	8.05e-04	NMD3	NMD3 ribosome export adaptor	0.45	2.23e-01	SETD7	SET domain containing 7, histone ly
-0.87	2.85e-03	MRPS30	mitochondrial ribosomal protein S30	0.43	1.63e-01	PAGE5	PAGE family member 5
-0.86	1.30e-02	ARAP1	ArfGAP with RhoGAP domain, ankyrin	0.43	3.60e-01	IGF2BP2	insulin like growth factor 2 mRNA b
-0.86	3.73e-02	POLR1D	RNA polymerase I and III subunit D	0.39	3.15e-01	DNAJC1	DnaJ heat shock protein family (Hsp
-0.85	1.87e-02	UBE2G2	ubiquitin conjugating enzyme E2 G2	0.39	1.73e-01	CTHRC1	collagen triple helix repeat contai
-0.84	4.51e-03	ABCC1	ATP binding cassette subfamily C me	0.38	4.58e-01	H1-0	H1.0 linker histone
-0.84	2.83e-03	PIK3R4	phosphoinositide-3-kinase regulator	0.38	4.42e-01	CBR3	carbonyl reductase 3
-0.83	1.87e-02	PCYT1A	phosphate cytidylyltransferase 1A,	0.37	3.81e-01	CCNA2	cyclin A2
-0.83	3.94e-03	TMEM209	transmembrane protein 209	0.36	4.40e-01	PTMS	parathymosin
-0.83	2.39e-02	ATP5MF	ATP synthase membrane subunit f	0.36	3.24e-01	BCR	BCR activator of RhoGEF and GTPase
-0.81	4.34e-03	ACTR10	actin related protein 10	0.36	3.11e-01	ITGA6	integrin subunit alpha 6
-0.8	4.03e-03	CNOT10	CCR4-NOT transcription complex subu	0.35	3.40e-01	MINPP1	multiple inositol-polyphosphate pho
-0.8	5.95e-03	AP1S1	adaptor related protein complex 1 s	0.34	1.17e-01	FUCA1	alpha-L-fucosidase 1
-0.8	1.12e-02	NAA20	N-alpha-acetyltransferase 20, NatB	0.33	2.07e-01	SP3	Sp3 transcription factor
-0.79	4.21e-03	TRAPP6A	trafficking protein particle comple	0.33	4.40e-01	FBLL1	fibrillarin like 1
-0.79	2.77e-02	HIGD2A	HIG1 hypoxia inducible domain famil	0.33	4.84e-01	JCHAIN	joining chain of multimeric IgA and
-0.78	7.81e-03	LLPH	LLP homolog, long-term synaptic fac	0.33	3.60e-01	H2AX	H2A.X variant histone
-0.78	1.61e-03	DNAJC13	DnaJ heat shock protein family (Hsp	0.32	3.78e-01	NIBAN2	niban apoptosis regulator 2
-0.78	4.08e-02	GTF2E1	general transcription factor II E su	0.32	1.91e-01	SMTN	smoothelin
-0.78	8.94e-03	NOL9	nucleolar protein 9	0.32	3.57e-01	SYVN1	synoviolin 1



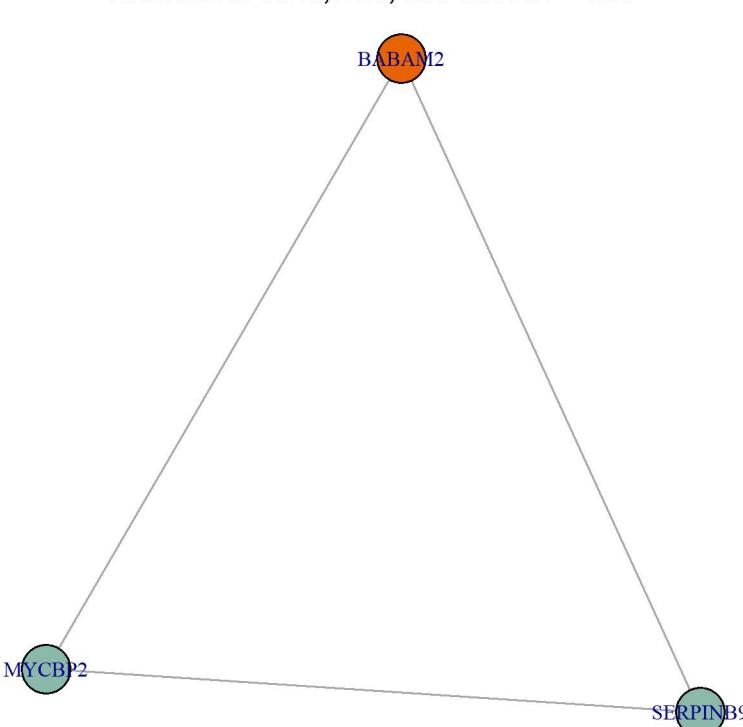
Downregulated in solid cancers at low/absent BABAM2 Upregulated in solid cancers at low/absent BABAM2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.2	3.07e-24	COPS7B	COP9 signalosome subunit 7B	0.73	1.98e-05	H2AX	H2A.X variant histone
-1.19	4.34e-20	NACA2	nascent polypeptide associated comp	0.68	1.30e-07	F3	coagulation factor III, tissue fact
-1.19	1.39e-25	UBE2Z	ubiquitin conjugating enzyme E2 Z	0.66	2.83e-05	THBS1	thrombospondin 1
-1.09	2.41e-22	UBFD1	ubiquitin family domain containing	0.63	2.11e-04	KRT17	keratin 17
-1.07	3.48e-24	ABRAXAS2	abraxas 2, BRISC complex subunit	0.59	3.81e-06	LAMC2	laminin subunit gamma 2
-1.06	1.52e-21	FKBP5	FKBP prolyl isomerase 5	0.57	2.38e-05	LAMB3	laminin subunit beta 3
-1.06	1.33e-22	PRMT3	protein arginine methyltransferase	0.57	3.44e-04	MMP14	matrix metallopeptidase 14
-1.05	3.15e-25	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.56	8.49e-03	CAVIN1	caveolae associated protein 1
-1.04	2.88e-30	TBCE	tubulin folding cofactor E	0.55	3.28e-09	SYVN1	synoviolin 1
-1.03	4.11e-20	PSME3IP1	proteasome activator subunit 3 inte	0.54	4.71e-05	GPNMB	glycoprotein nmb
-1.02	3.94e-20	BRCC3	BRCA1/BRCA2-containing complex subu	0.54	2.11e-05	FNDC3B	fibronectin type III domain contain
-1.01	1.52e-21	LANCL1	LanC like 1	0.54	4.88e-04	KRT5	keratin 5
-1.01	3.07e-16	BLMH	bleomycin hydrolase	0.53	7.14e-04	MISP	mitotic spindle positioning
-1	1.87e-16	C11orf54	chromosome 11 open reading frame 54	0.53	1.82e-03	GNG5	G protein subunit gamma 5
-1	4.53e-18	NCK1	NCK adaptor protein 1	0.53	1.47e-03	PKP2	plakophilin 2
-1	1.00e-17	RWDD1	RWD domain containing 1	0.53	1.15e-07	ITIH2	inter-alpha-trypsin inhibitor heavy
-0.99	1.26e-15	NME2	NME/NM23 nucleoside diphosphate kin	0.52	8.19e-04	TMEM123	transmembrane protein 123
-0.98	2.24e-22	EIPR1	EARP complex and GARP complex inter	0.52	4.21e-04	IGFBP7	insulin like growth factor binding
-0.98	2.13e-21	CNOT2	CCR4-NOT transcription complex subu	0.52	4.11e-09	LAMA3	laminin subunit alpha 3
-0.98	5.02e-21	PDCL3	phosducin like 3	0.51	6.15e-03	CAV1	caveolin 1
-0.96	1.10e-25	VPS25	vacuolar protein sorting 25 homolog	0.51	2.49e-04	RAB32	RAB32, member RAS oncogene family
-0.95	1.19e-16	COMM2	COMM domain containing 2	0.5	4.30e-04	PTTG1IP	PTTG1 interacting protein
-0.95	9.11e-19	SSU72	SSU72 homolog, RNA polymerase II CT	0.5	4.00e-03	ITGB4	integrin subunit beta 4
-0.95	5.40e-17	EIF2B1	eukaryotic translation initiation f	0.49	3.80e-03	ICAM1	intercellular adhesion molecule 1
-0.95	1.16e-17	EIF2B5	eukaryotic translation initiation f	0.49	7.75e-04	CD109	CD109 molecule
-0.94	8.92e-19	BABAM1	BRISC and BRCA1 A complex member 1	0.49	5.43e-04	FN1	fibronectin 1
-0.94	1.23e-20	YTHDF3	YTH N6-methyladenosine RNA binding	0.49	2.34e-04	COL12A1	collagen type XII alpha 1 chain
-0.93	7.39e-20	EIF2D	eukaryotic translation initiation f	0.49	3.66e-04	H1-1	H1.1 linker histone, cluster member
-0.93	1.37e-18	TBC1D5	TBC1 domain family member 5	0.48	1.03e-03	MTCH1	mitochondrial carrier 1

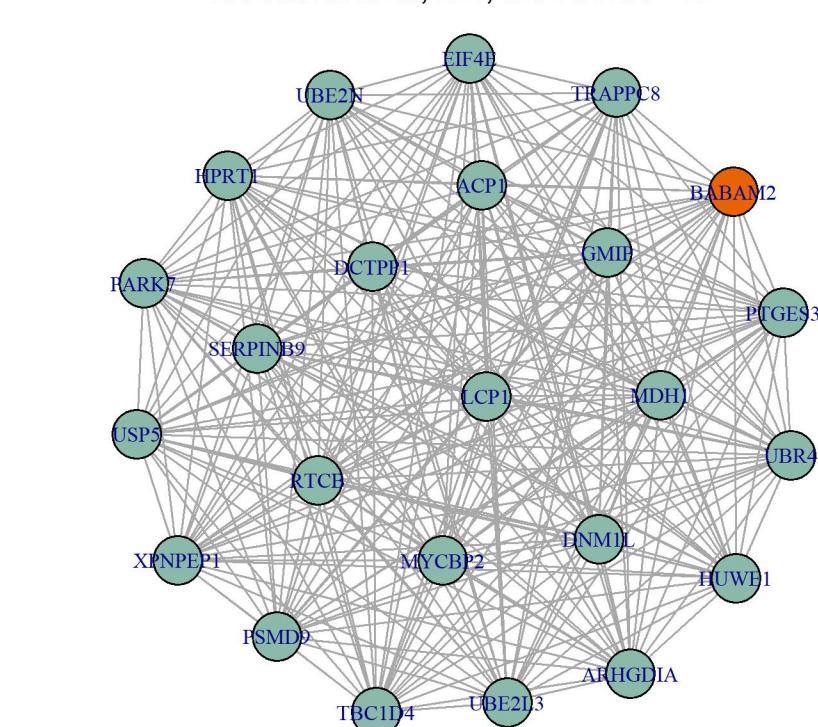
BABAM2 network, DB1, all Pearson r > 0.4

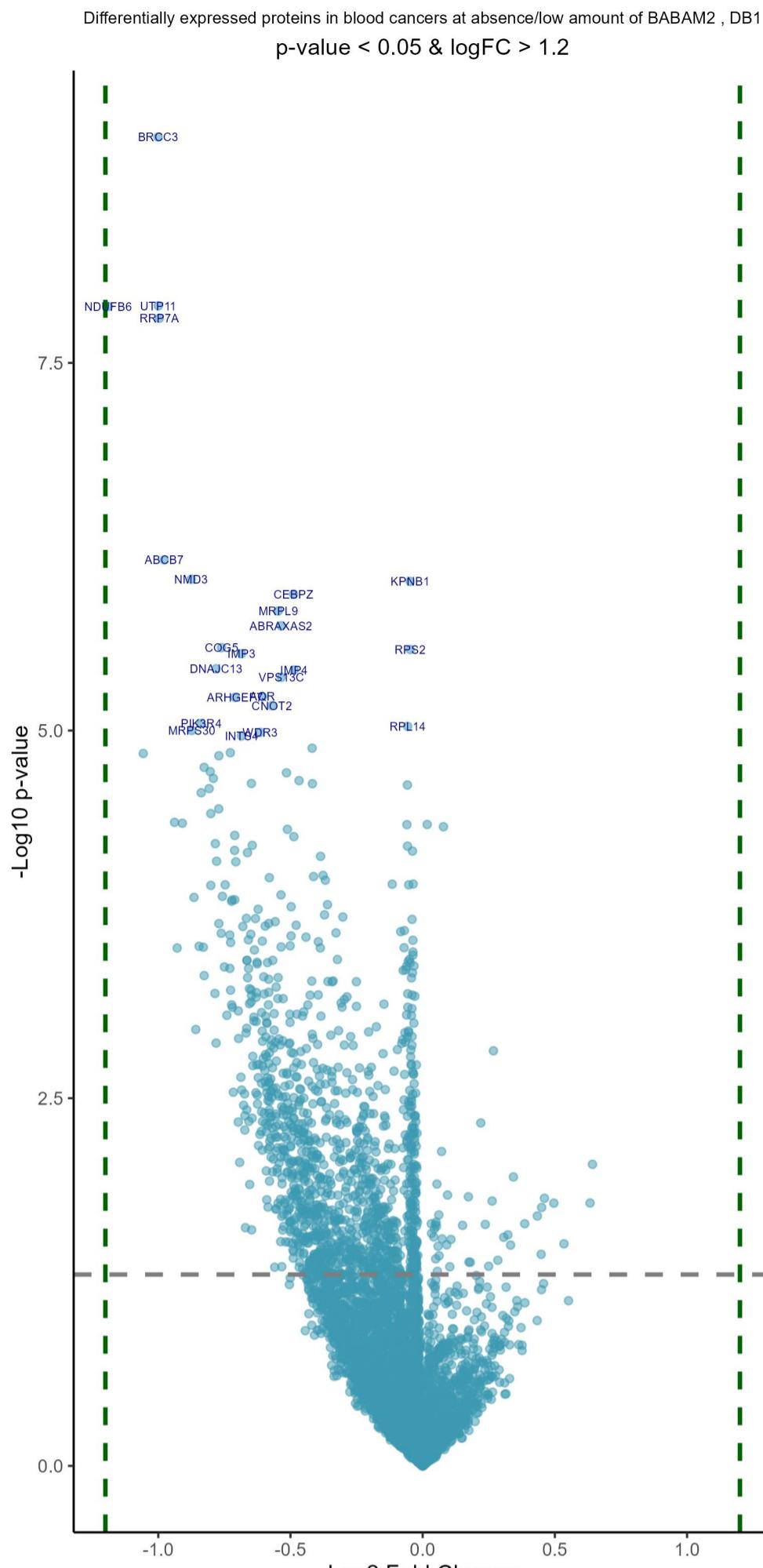


BABAM2 network, DB1, all Pearson r > 0.35

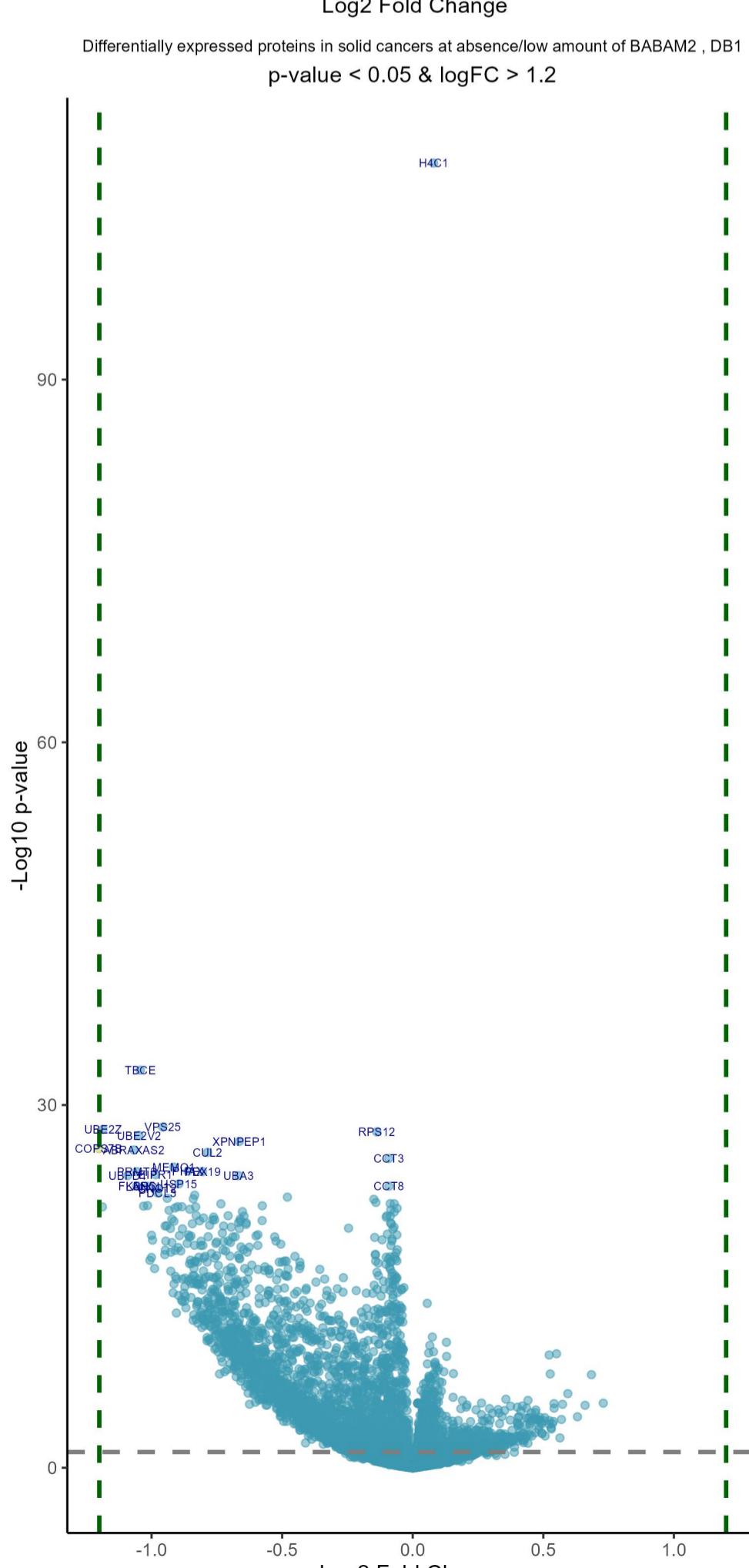


BABAM2 network, DB1, all Pearson r > 0.3



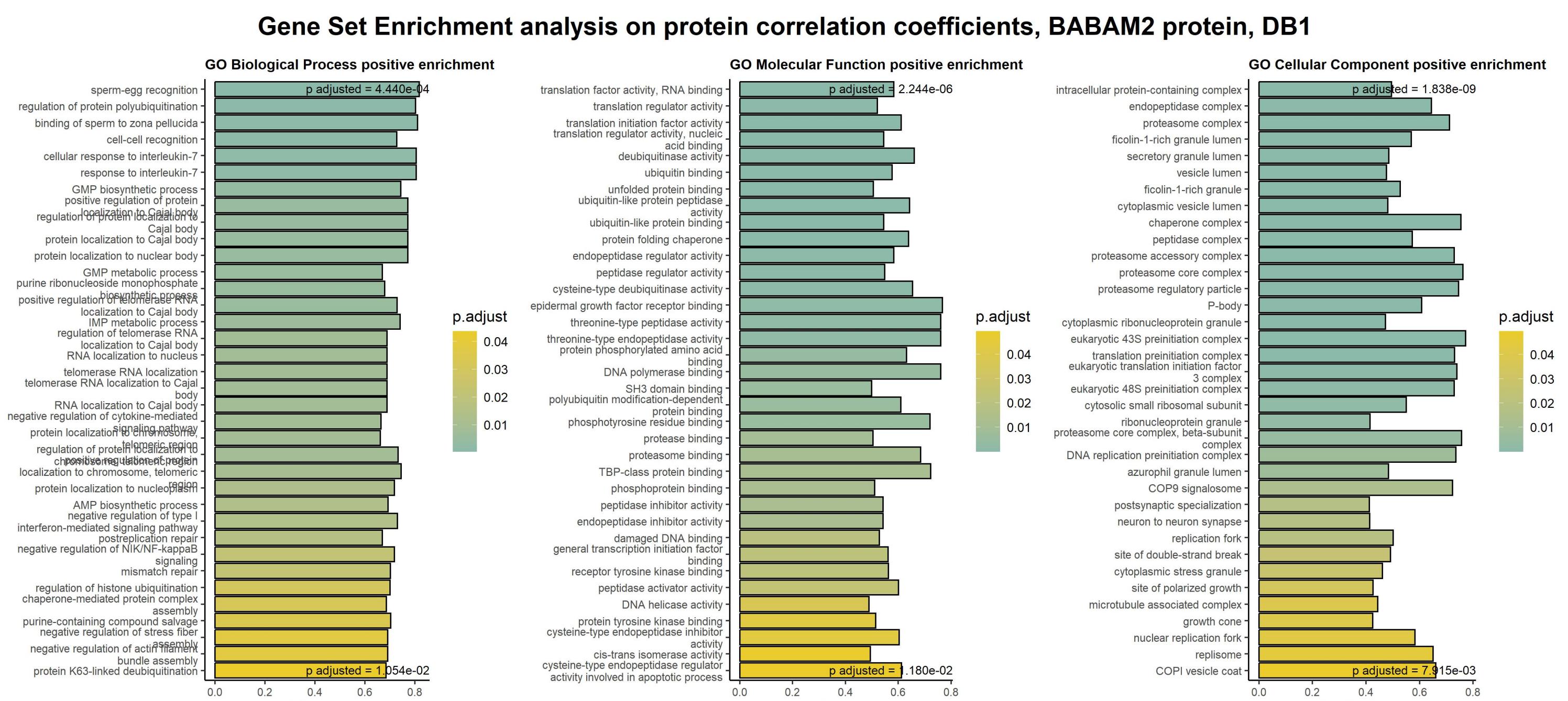
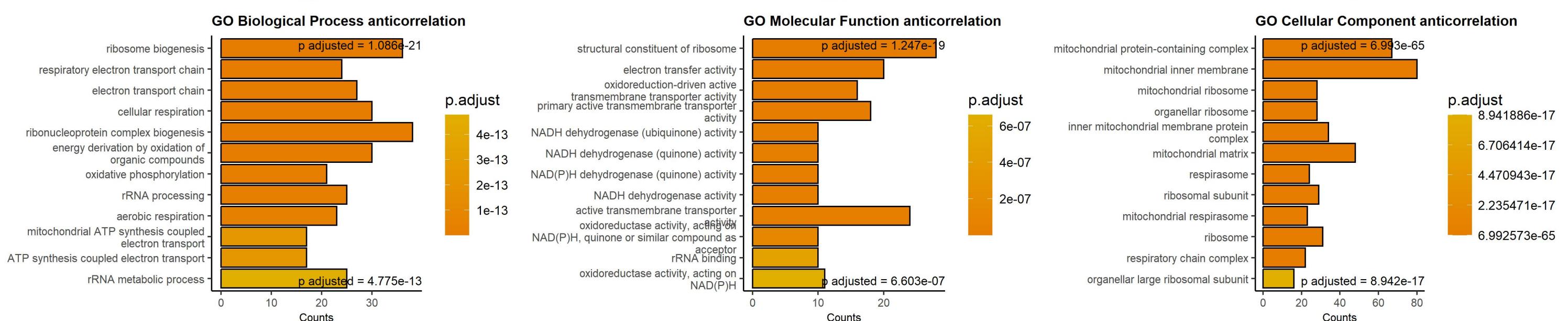
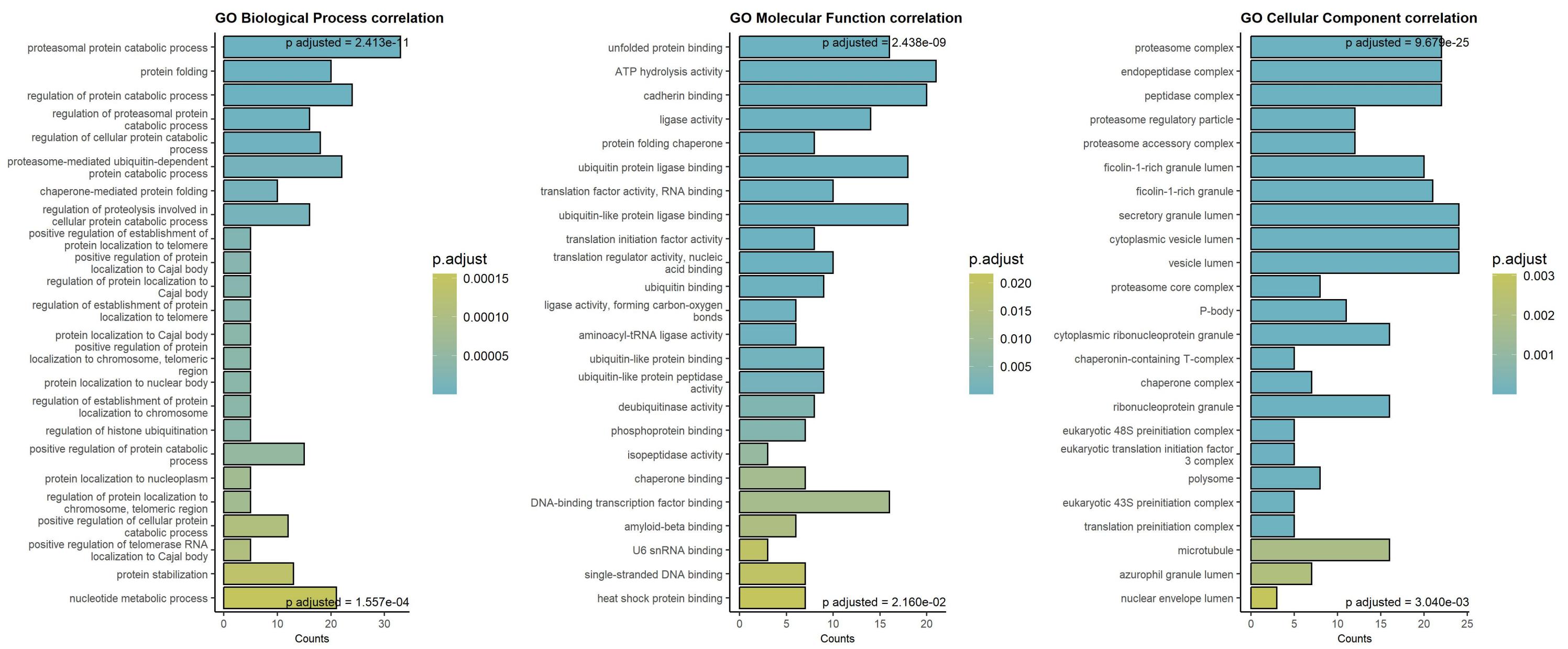


Sorted by p values!							
Downregulated in blood cancers at low/absent BABAM2				Upregulated in blood cancers at low/absent BABAM2			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1	3.06e-06	BRCC3	BRCA1/BRCA2-containing complex subunit	0.02	6.45e-03	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
-1	2.09e-05	UTP11	UTP11 small subunit processome component	0.08	6.52e-03	RNF40	ring finger protein 40
-1.19	2.09e-05	NDUFB6	NADH:ubiquinone oxidoreductase subunit	0.27	4.35e-02	CKM	creatine kinase, M-type
-1	2.09e-05	RRP7A	ribosomal RNA processing 7 homolog	0.22	7.67e-02	ABL1	ABL proto-oncogene 1, non-receptor tyrosine kinase
-0.98	7.65e-04	ABCB7	ATP binding cassette subfamily B member	0.07	9.37e-02	FKBP2	FKBP prolyl isomerase 2
-0.88	8.05e-04	NMD3	NMD3 ribosome export adaptor	0.64	1.05e-01	KRT18	keratin 18
-0.05	8.05e-04	KPNB1	karyopherin subunit beta 1	0.34	1.17e-01	FUCA1	alpha-L-fucosidase 1
-0.49	8.73e-04	CEBPZ	CCAAT enhancer binding protein zeta	0.05	1.24e-01	ENO1	enolase 1
-0.55	1.02e-03	MRPL9	mitochondrial ribosomal protein L9	0.09	1.38e-01	MYDGF	myeloid derived growth factor
-0.54	1.17e-03	ABRAXAS2	abraxas 2, BRISC complex subunit	0.17	1.40e-01	CRYBB1	crystallin beta B1
-0.76	1.43e-03	COG5	component of oligomeric golgi complex	0.46	1.42e-01	COX6A1	cytochrome c oxidase subunit 6A1
-0.05	1.43e-03	RPS2	ribosomal protein S2	0.26	1.45e-01	NRCAM	neuronal cell adhesion molecule
-0.69	1.43e-03	IMP3	IMP U3 small nucleolar ribonucleoprotein	0.63	1.48e-01	GTSF1	gameteocyte specific factor 1
-0.78	1.61e-03	DNAJC13	DnaJ heat shock protein family (Hsp)	0.5	1.48e-01	TRIM72	tripartite motif containing 72
-0.49	1.61e-03	IMP4	IMP U3 small nucleolar ribonucleoprotein	0.45	1.54e-01	HMGN4	high mobility group nucleosomal binding protein 4
-0.53	1.70e-03	VPS13C	vacuolar protein sorting 13 homolog	0.06	1.61e-01	TRIR	telomerase RNA component interactor
-0.61	2.08e-03	AQR	aquarius intron-binding spliceosoma	0.43	1.63e-01	PAGE5	PAGE family member 5
-0.71	2.08e-03	ARHGEF7	Rho guanine nucleotide exchange factor	0.05	1.71e-01	HYPK	huntingtin interacting protein K
-0.57	2.25e-03	CNOT2	CCR4-NOT transcription complex subunit	0.03	1.73e-01	CBX3	chromobox 3
-0.84	2.83e-03	PIK3R4	phosphoinositide-3-kinase regulator	0.39	1.73e-01	CTHRC1	collagen triple helix repeat containing 1
-0.06	2.83e-03	RPL14	ribosomal protein L14	0.05	1.74e-01	ZC3H4	zinc finger CCCH-type containing 4
-0.87	2.85e-03	MRPS30	mitochondrial ribosomal protein S30	0.24	1.74e-01	GNG12	G protein subunit gamma 12
-0.61	2.85e-03	WDR3	WD repeat domain 3	0.15	1.76e-01	TXNDC5	thioredoxin domain containing 5
-0.69	2.90e-03	INTS4	integrator complex subunit 4	0.05	1.77e-01	SET	SET nuclear proto-oncogene
-0.42	3.37e-03	UTP20	UTP20 small subunit processome component	0.04	1.81e-01	SMARCE1	SWI/SNF related, matrix associated, chromatin rearranger 1
-0.73	3.40e-03	SCYL1	SCY1 like pseudokinase 1	0.03	1.88e-01	POLR2C	RNA polymerase II subunit C
-1.06	3.40e-03	UBE2Z	ubiquitin conjugating enzyme E2 Z	0.32	1.91e-01	SMTN	smoothelin
-0.77	3.40e-03	PANK4	pantothenate kinase 4 (inactive)	0.04	1.94e-01	PRKCSH	protein kinase C substrate 80K-H
-0.83	3.94e-03	TMEM209	transmembrane protein 209	0.31	1.94e-01	PHC3	polyhomeotic homolog 3
-0.8	4.03e-03	CNOT10	CCR4-NOT transcription complex subunit	0.07	1.97e-01	MDC1	mediator of DNA damage checkpoint 1
-0.52	4.03e-03	RAP2C	RAP2C, member of RAS oncogene family	0.11	1.97e-01	NCSTN	nicastrin
-0.79	4.21e-03	TRAPPC6A	trafficking protein particle complex	0.53	2.04e-01	DDAH2	dimethylarginine dimethylaminohydrolase 2
-0.47	4.21e-03	LEO1	LEO1 homolog, Paf1/RNA polymerase I	0.09	2.07e-01	LYAR	Ly1 antibody reactive
-0.65	4.21e-03	METTL13	methyltransferase 13, eEF1A lysine	0.33	2.07e-01	SP3	Sp3 transcription factor
-0.42	4.21e-03	GTF3C2	general transcription factor IIIC subunit	0.06	2.10e-01	SNX3	sorting nexin 3
-0.06	4.21e-03	RARS1	arginyl-tRNA synthetase 1	0.45	2.23e-01	SETD7	SET domain containing 7, histone lysine methyltransferase
-0.81	4.34e-03	ACTR10	actin related protein 10	0.06	2.25e-01	SLC1A5	solute carrier family 1 member 5
-0.84	4.51e-03	ABCC1	ATP binding cassette subfamily C member	0.05	2.31e-01	TXNDC12	thioredoxin domain containing 12
-0.77	5.67e-03	EEBD	embryonic ectoderm development	0.28	2.32e-01	H1_10	H1_10 linker histone

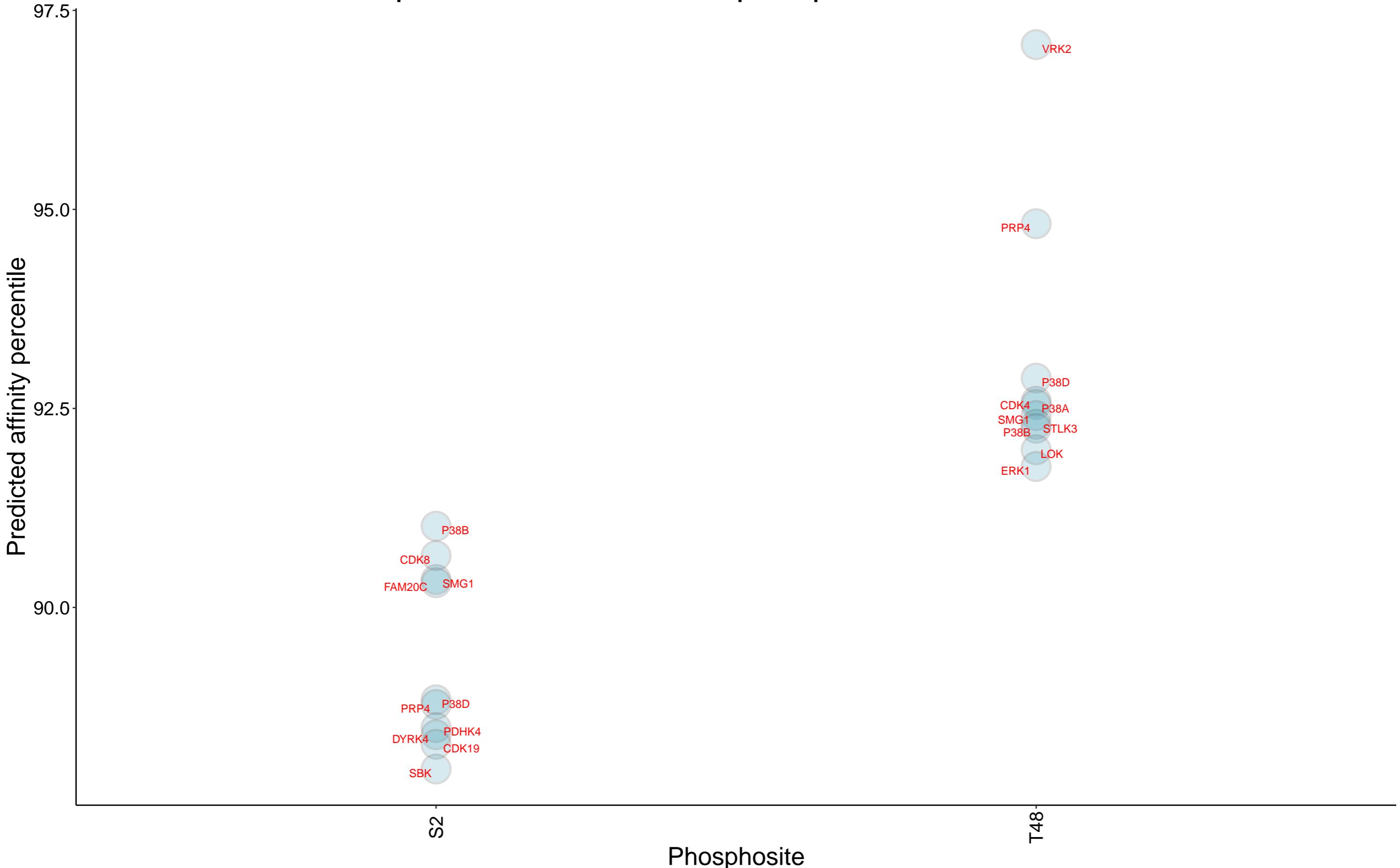


Sorted by p values!							
Downregulated in solid cancers at low/absent BABAM2				Upregulated in solid cancers at low/absent BABAM2			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
1.04	2.88e-30	TBCE	tubulin folding cofactor E	0.08	4.07e-105	H4C1	H4 clustered histone 1
0.96	1.10e-25	VPS25	vacuolar protein sorting 25 homolog	0.06	5.03e-13	SNRPB2	small nuclear ribonucleoprotein pol
1.19	1.39e-25	UBE2Z	ubiquitin conjugating enzyme E2 Z	0.08	1.75e-10	LMNB2	lamin B2
0.14	1.85e-25	RPS12	ribosomal protein S12	0.13	4.42e-10	LEMD2	LEM domain nuclear envelope protein
1.05	3.15e-25	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.07	7.68e-10	PABPN1	poly(A) binding protein nuclear 1
0.66	8.59e-25	XPNPEP1	X-prolyl aminopeptidase 1	0.08	2.32e-09	NCLN	nicalin
-1.2	3.07e-24	COPS7B	COP9 signalosome subunit 7B	0.06	2.88e-09	RPN1	ribophorin I
1.07	3.48e-24	ABRAXAS2	abraxas 2, BRISC complex subunit	0.55	3.28e-09	SYVN1	synoviolin 1
0.79	4.95e-24	CUL2	cullin 2	0.52	4.11e-09	LAMA3	laminin subunit alpha 3
0.09	1.46e-23	CCT3	chaperonin containing TCP1 subunit	0.13	5.25e-09	ZFPL1	zinc finger protein like 1
0.91	7.01e-23	MEMO1	mediator of cell motility 1	0.09	1.44e-08	PLRG1	pleiotropic regulator 1
0.86	1.33e-22	PHAX	phosphorylated adaptor for RNA expo	0.08	1.94e-08	DDRGK1	DDRGK domain containing 1
0.81	1.33e-22	PEX19	peroxisomal biogenesis factor 19	0.06	1.96e-08	SRSF10	serine and arginine rich splicing f
1.06	1.33e-22	PRMT3	protein arginine methyltransferase	0.09	2.66e-08	SSR4	signal sequence receptor subunit 4
0.98	2.24e-22	EIPR1	EARP complex and GARP complex inter	0.09	3.63e-08	RAB14	RAB14, member RAS oncogene family
1.09	2.41e-22	UBFD1	ubiquitin family domain containing	0.1	3.93e-08	ESYT1	extended synaptotagmin 1
0.67	2.41e-22	UBA3	ubiquitin like modifier activating	0.1	6.07e-08	RPN2	ribophorin II
-0.9	1.10e-21	USP15	ubiquitin specific peptidase 15	0.12	7.62e-08	GOLGB1	golgin B1
1.06	1.52e-21	FKBP5	FKBP prolyl isomerase 5	0.16	1.09e-07	TOR1AIP2	torsin 1A interacting protein 2
0.09	1.52e-21	CCT8	chaperonin containing TCP1 subunit	0.08	1.10e-07	GOLGA2	golgin A2
1.01	1.52e-21	LANCL1	LanC like 1	0.53	1.15e-07	ITIH2	inter-alpha-trypsin inhibitor heavy
0.98	2.13e-21	CNOT2	CCR4-NOT transcription complex subu	0.68	1.30e-07	F3	coagulation factor III, tissue fact
0.98	5.02e-21	PDCL3	phosducin like 3	0.08	1.36e-07	SPTLC1	serine palmitoyltransferase long ch
0.83	7.27e-21	PGP	phosphoglycolate phosphatase	0.06	1.66e-07	RALY	RALY heterogeneous nuclear ribonucl
0.48	1.02e-20	BCCIP	BRCA2 and CDKN1A interacting protei	0.09	1.95e-07	SRPRB	SRP receptor subunit beta
0.94	1.23e-20	YTHDF3	YTH N6-methyladenosine RNA binding	0.06	2.00e-07	NUP153	nucleoporin 153
0.84	1.30e-20	CZIB	CXXC motif containing zinc binding	0.07	2.66e-07	MRPL13	mitochondrial ribosomal protein L13
0.15	1.40e-20	ATIC	5-aminoimidazole-4-carboxamide ribo	0.06	2.89e-07	CCDC47	coiled-coil domain containing 47
0.14	2.45e-20	FARSB	phenylalanyl-tRNA synthetase subuni	0.07	4.04e-07	HNRNPUL2	heterogeneous nuclear ribonucleopro
0.09	2.92e-20	CCT7	chaperonin containing TCP1 subunit	0.1	4.64e-07	NDUFA13	NADH:ubiquinone oxidoreductase subu
0.07	2.92e-20	RPS2	ribosomal protein S2	0.11	5.15e-07	FAF2	Fas associated factor family member
0.73	2.92e-20	EXOC7	exocyst complex component 7	0.05	5.32e-07	GANAB	glucosidase II alpha subunit
1.02	3.94e-20	BRCC3	BRCA1/BRCA2-containing complex subu	0.07	6.51e-07	LAMTOR1	late endosomal/lysosomal adaptor, M
0.58	3.96e-20	PFAS	phosphoribosylformylglycinamidine s	0.04	6.88e-07	SAP18	Sin3A associated protein 18
1.03	4.11e-20	PSME3IP1	proteasome activator subunit 3 inte	0.09	8.07e-07	MRPL23	mitochondrial ribosomal protein L23
-0.9	4.34e-20	GABPA	GA binding protein transcription fa	0.05	1.50e-06	NUP98	nucleoporin 98 and 96 precursor
0.88	4.34e-20	NTMT1	N-terminal Xaa-Pro-Lys N-methyltran	0.07	1.66e-06	DDOST	dolichyl-diphosphooligosaccharide--
1.19	4.34e-20	NACA2	nascent polypeptide associated comp	0.1	2.06e-06	MLEC	malectin
0.20	4.34e-20	ENCA	endoplasmic reticulum 15 kDa	0.07	2.06e-06	NUP155	large ribosomal subunit

Top 250 correlation coefficients overrepresentation, BABAM2 protein, DB1



Top 10 kinases for each phosphosite in BABAM2



Kinases with affinity greater than 98.5% to BABAM2

Top 15 positive correlation coefficients for BABAM2 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

