

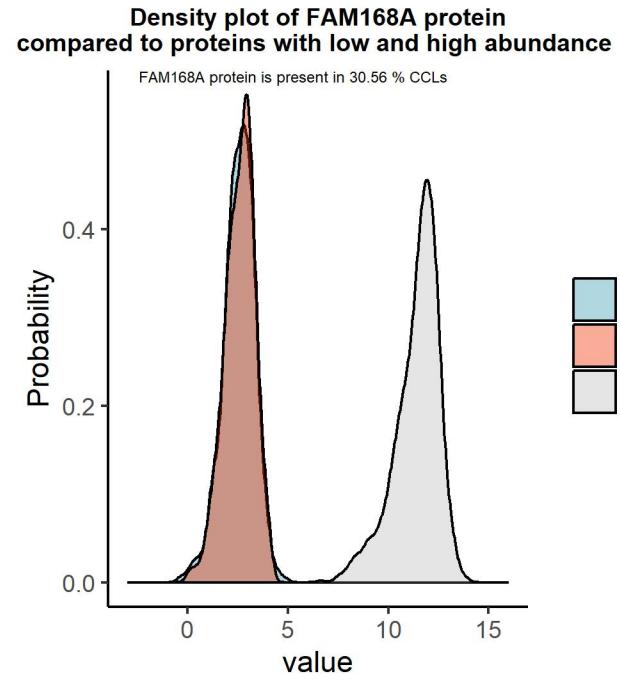
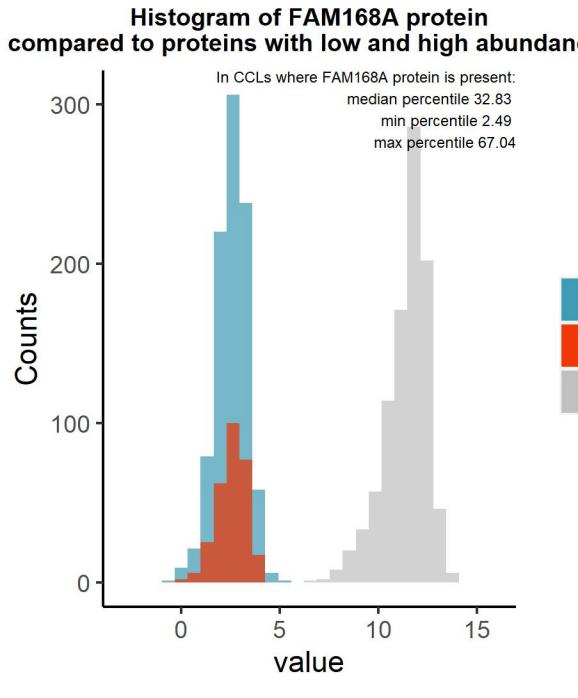
FAM168A

Protein name: F168A ; UNIPROT: Q92567 ; Gene name: family with sequence similarity 168 member A

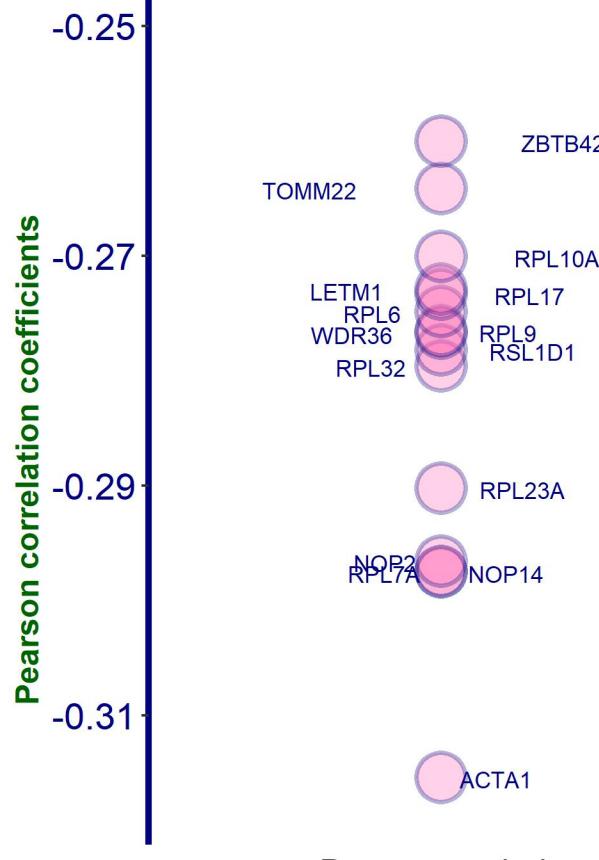
Ligandable: NA ; Ligandable_by_Chem: NA ; Is_enzyme: NA (<https://cansar.ai/>)

Sanger Institute Protein Database 2 (DB2), protein presence is less certain

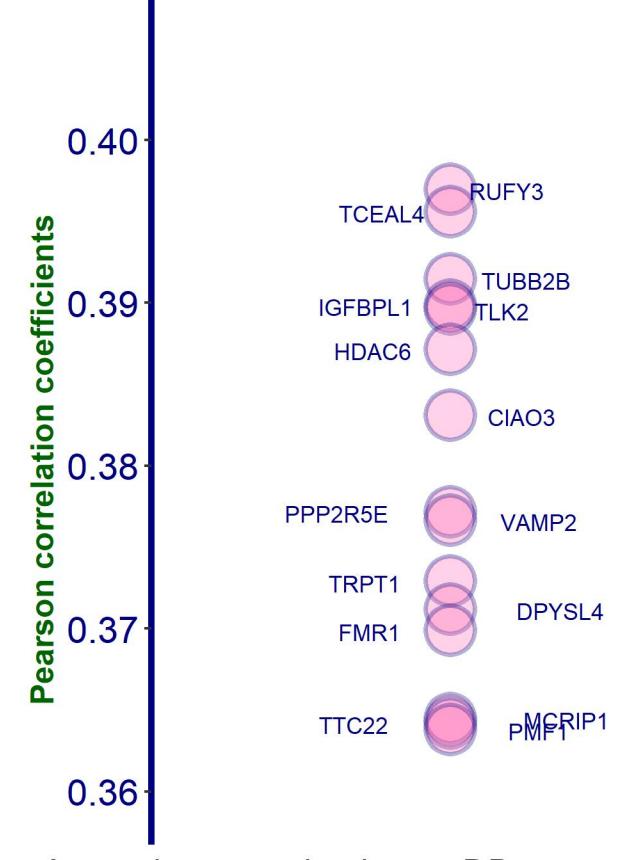
8498 proteins in same 949 CCLs



Negative correlations of FAM168A protein, DB2

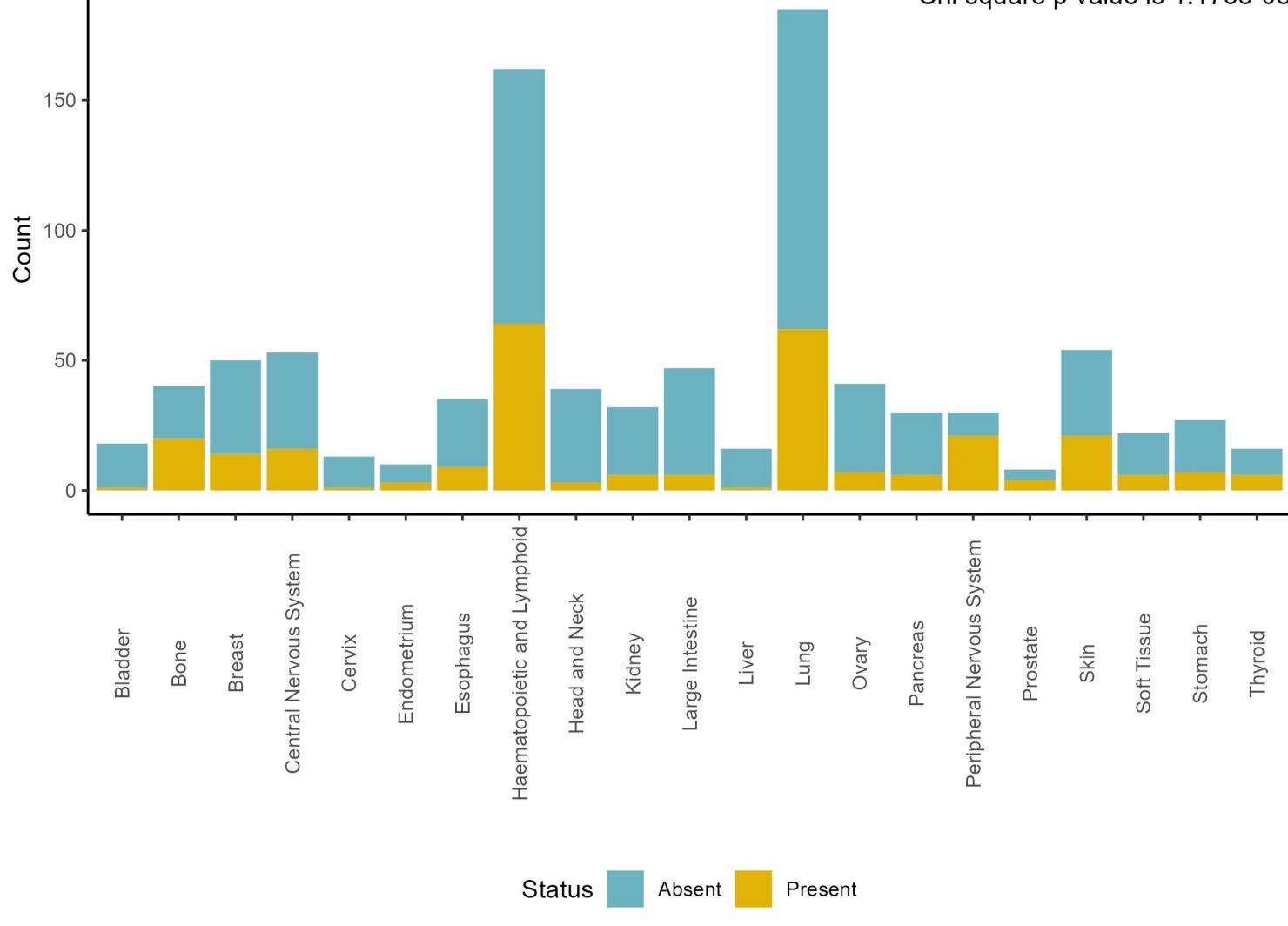
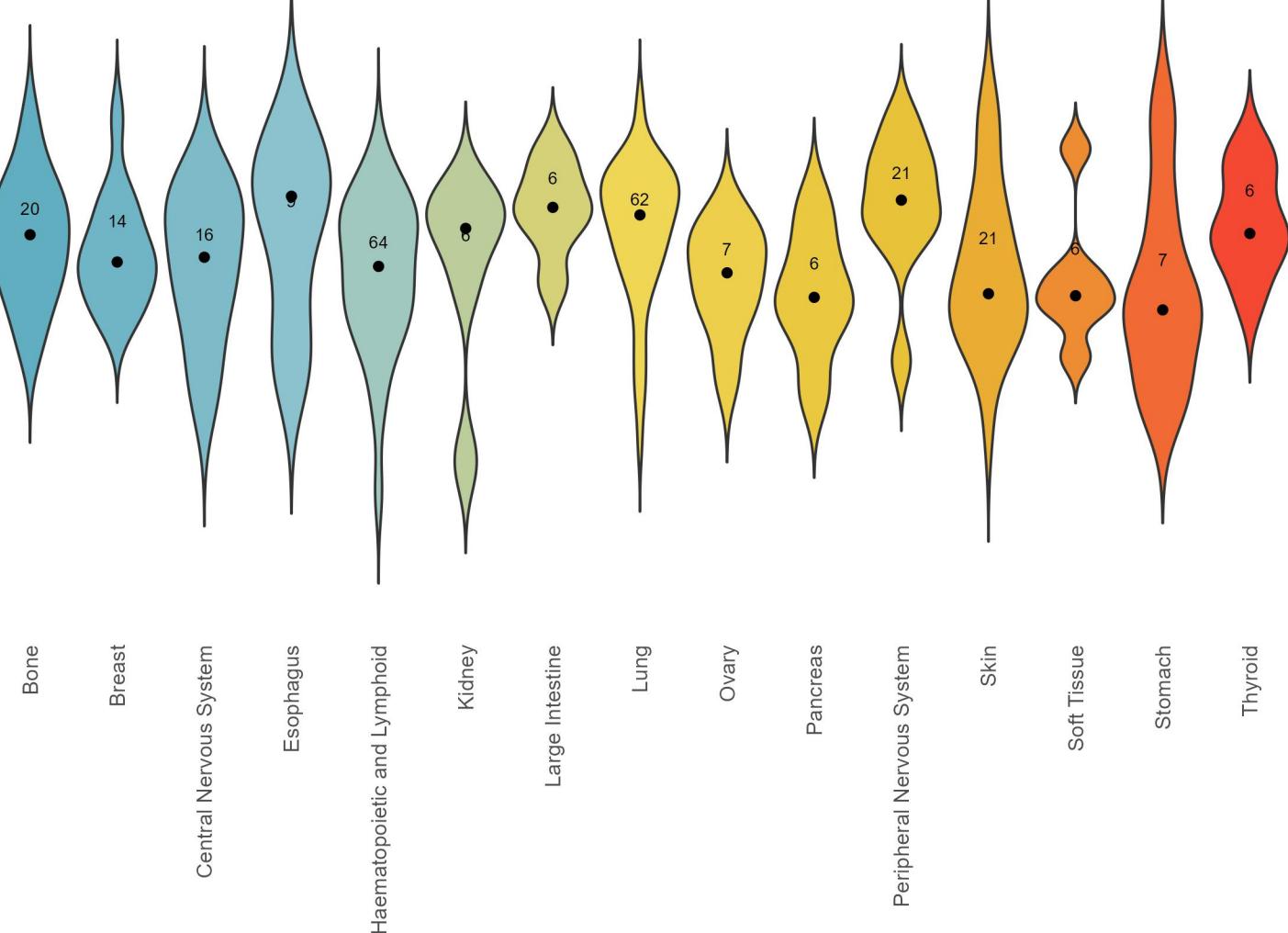


Positive correlations of FAM168A protein, DB2



Amount of FAM168A protein, number of CCLs where it is present by tissue, DB2

ANOVA p value is 2.796e-02

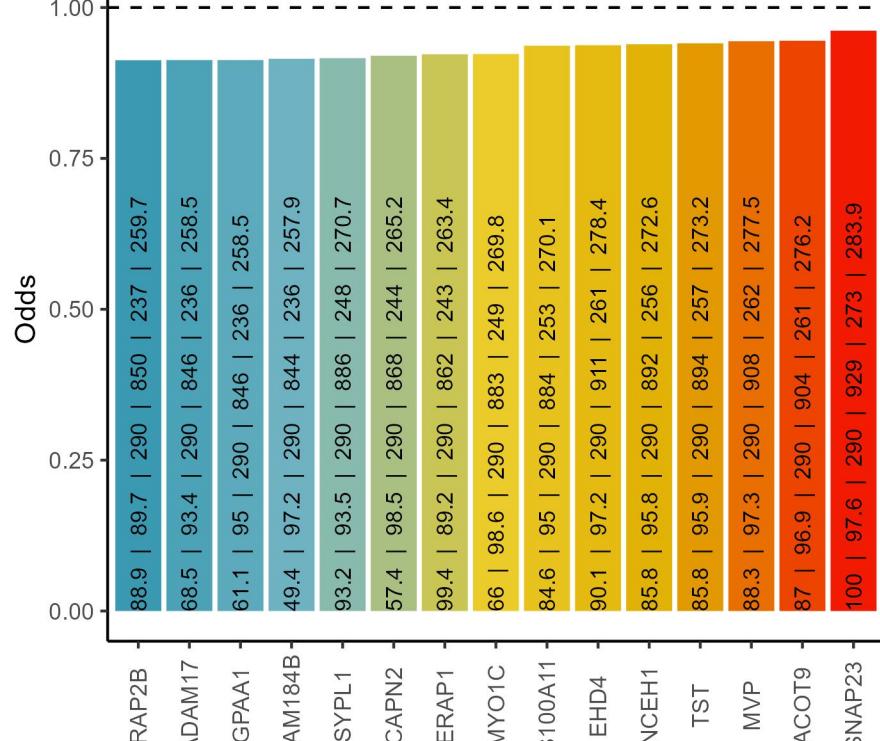


Cooccurrence with FAM168A protein, DB2

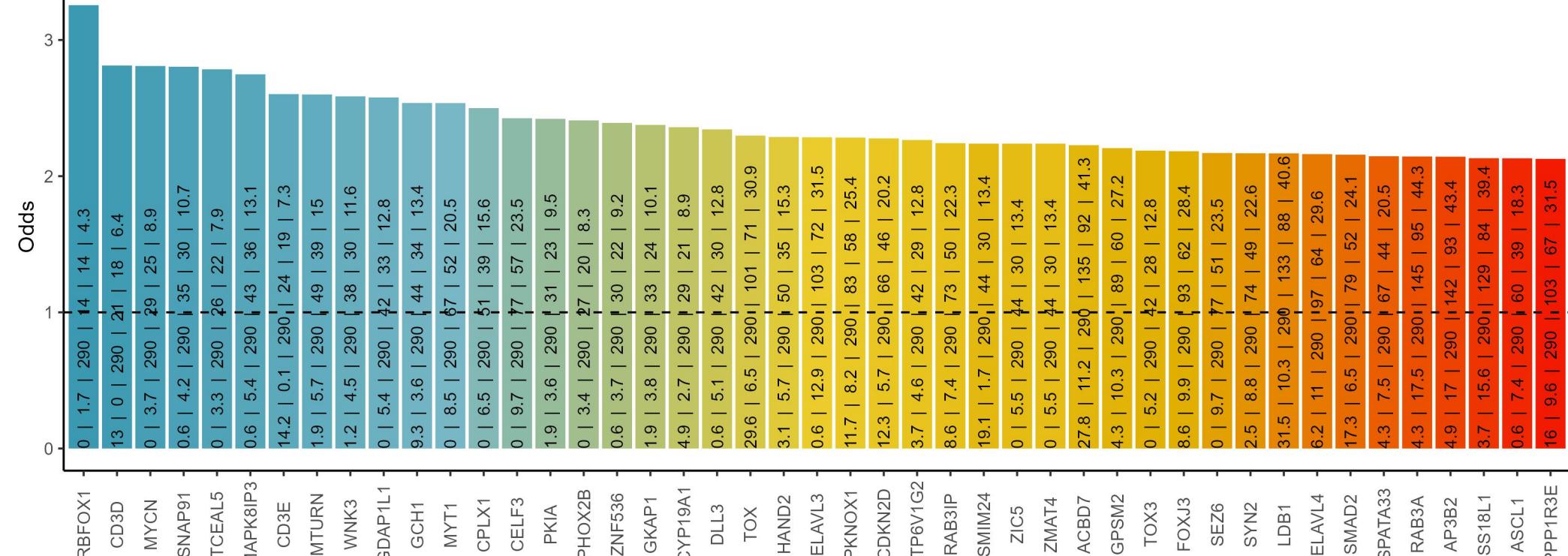
% of FAM168A in blood cancers: 39.5 ; % of FAM168A in solid cancers: 28.7

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of FAM168A | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

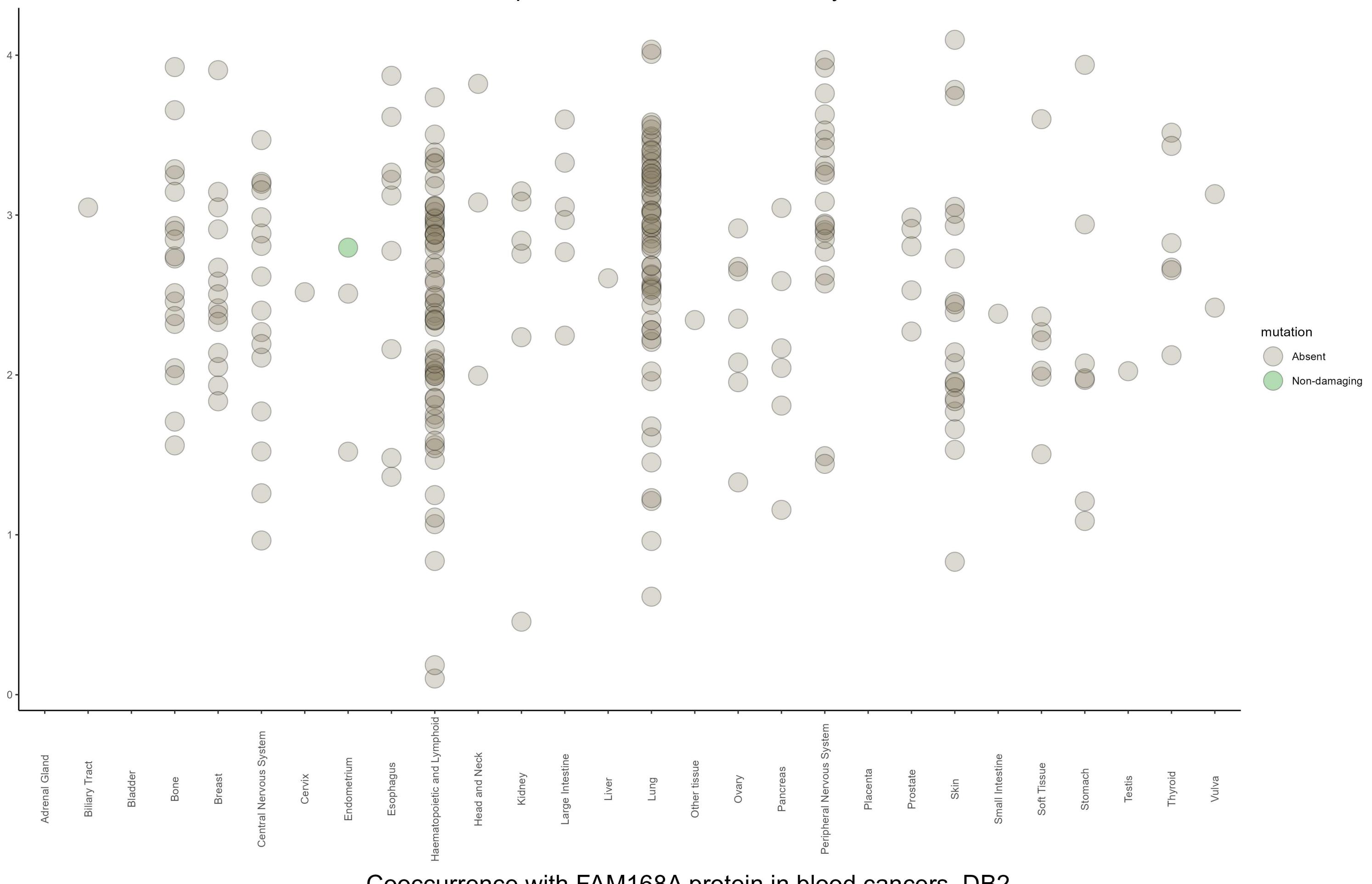
Negative cooccurrence



Positive cooccurrence

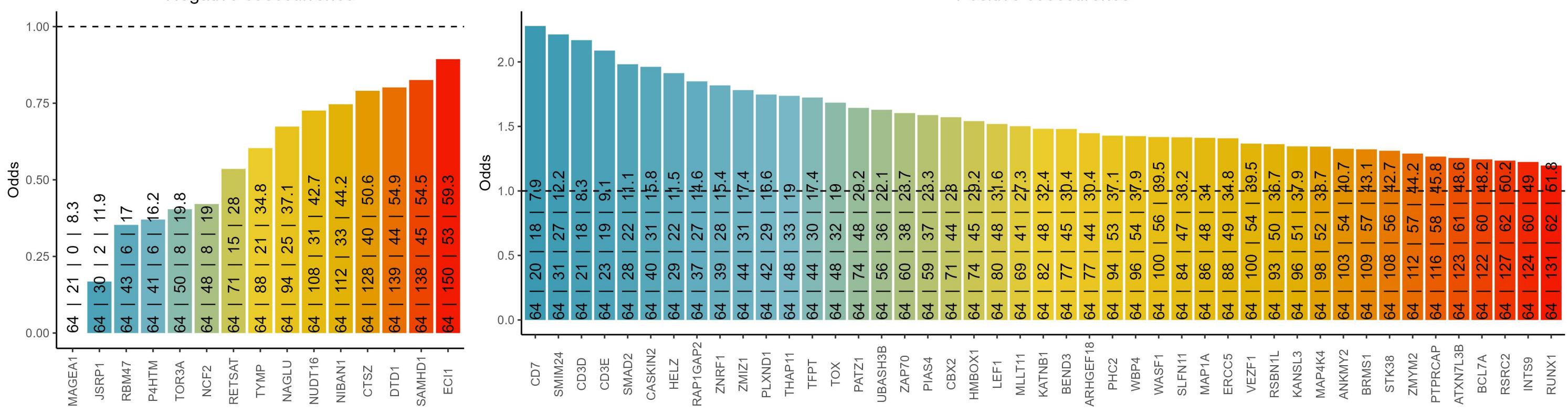


Amount of FAM168A protein and mutation status by tissue, DB2



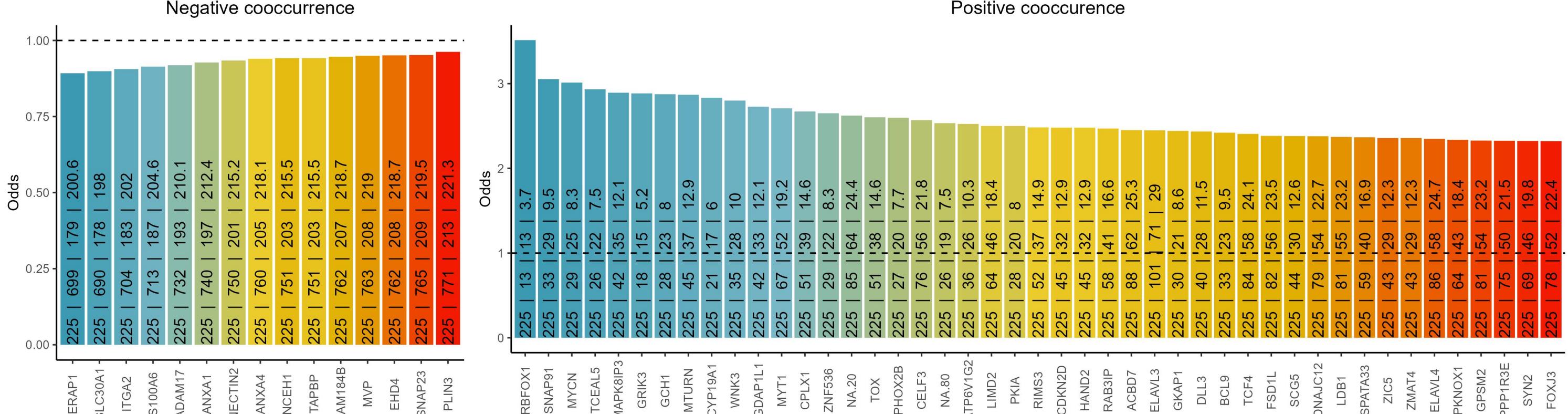
Cooccurrence with FAM168A protein in blood cancers, DB2

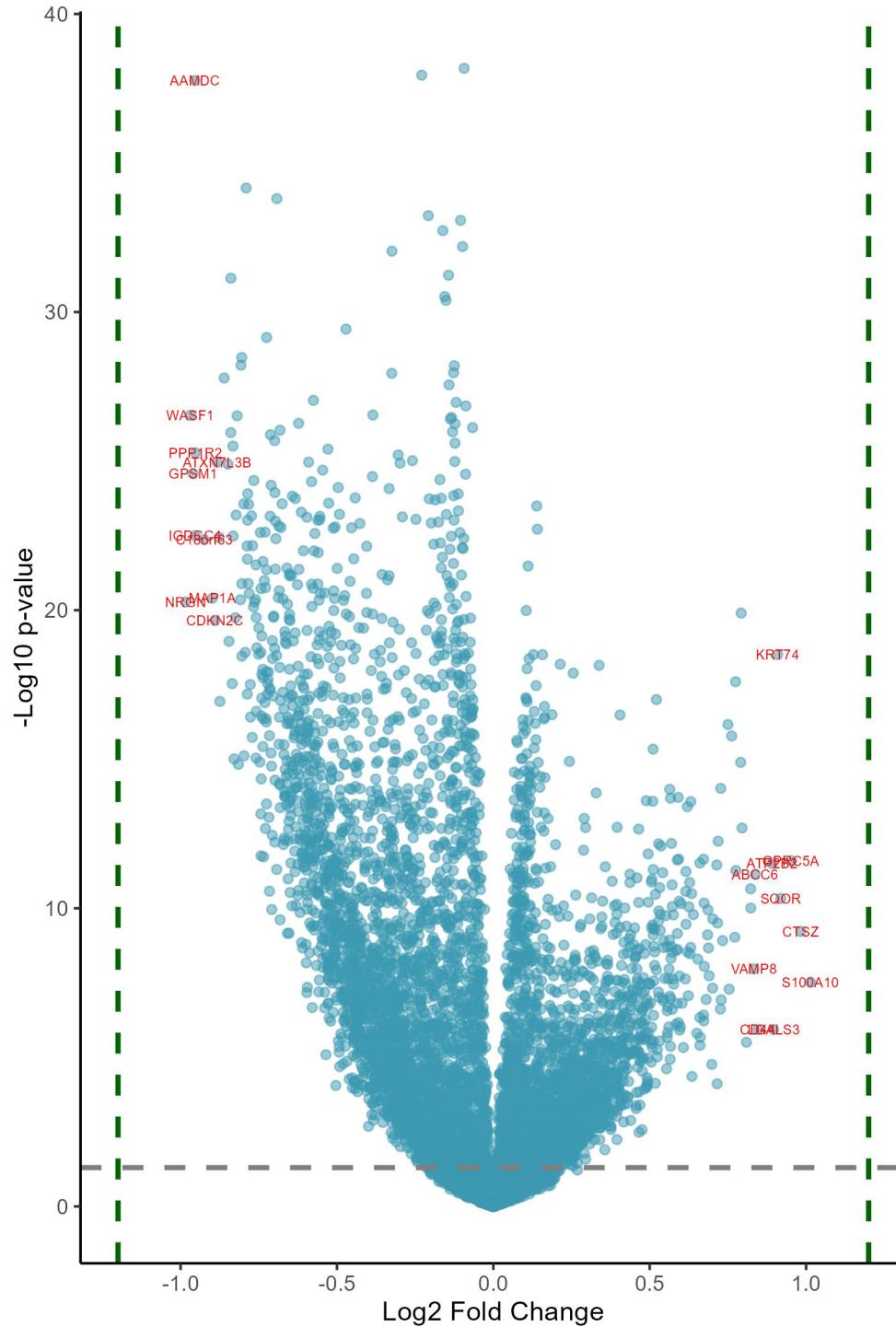
The text in the bars: incidence of FAM168A | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Cooccurrence with FAM168A protein in solid cancers, DB2

The text in the bars: incidence of FAM168A | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

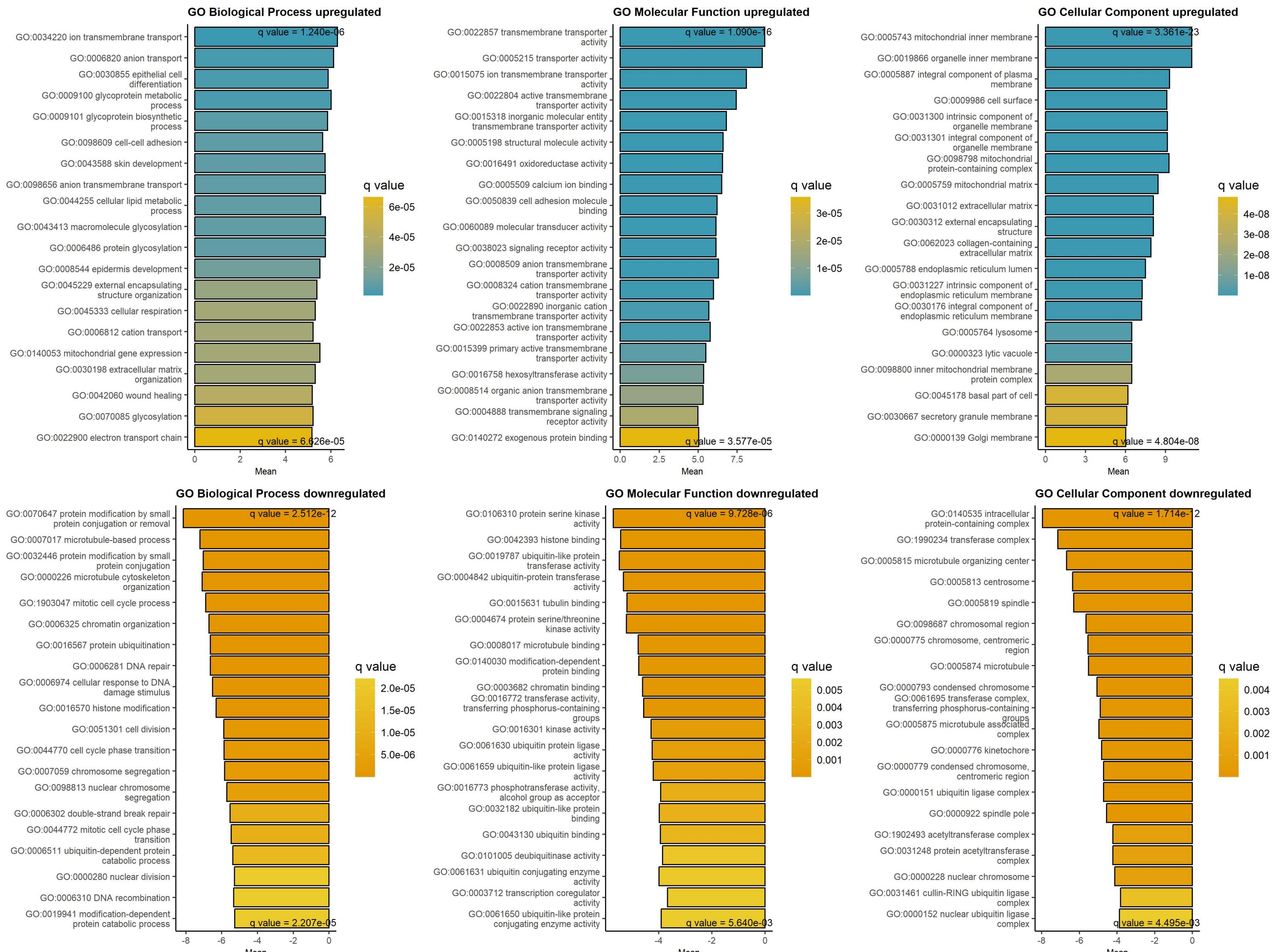


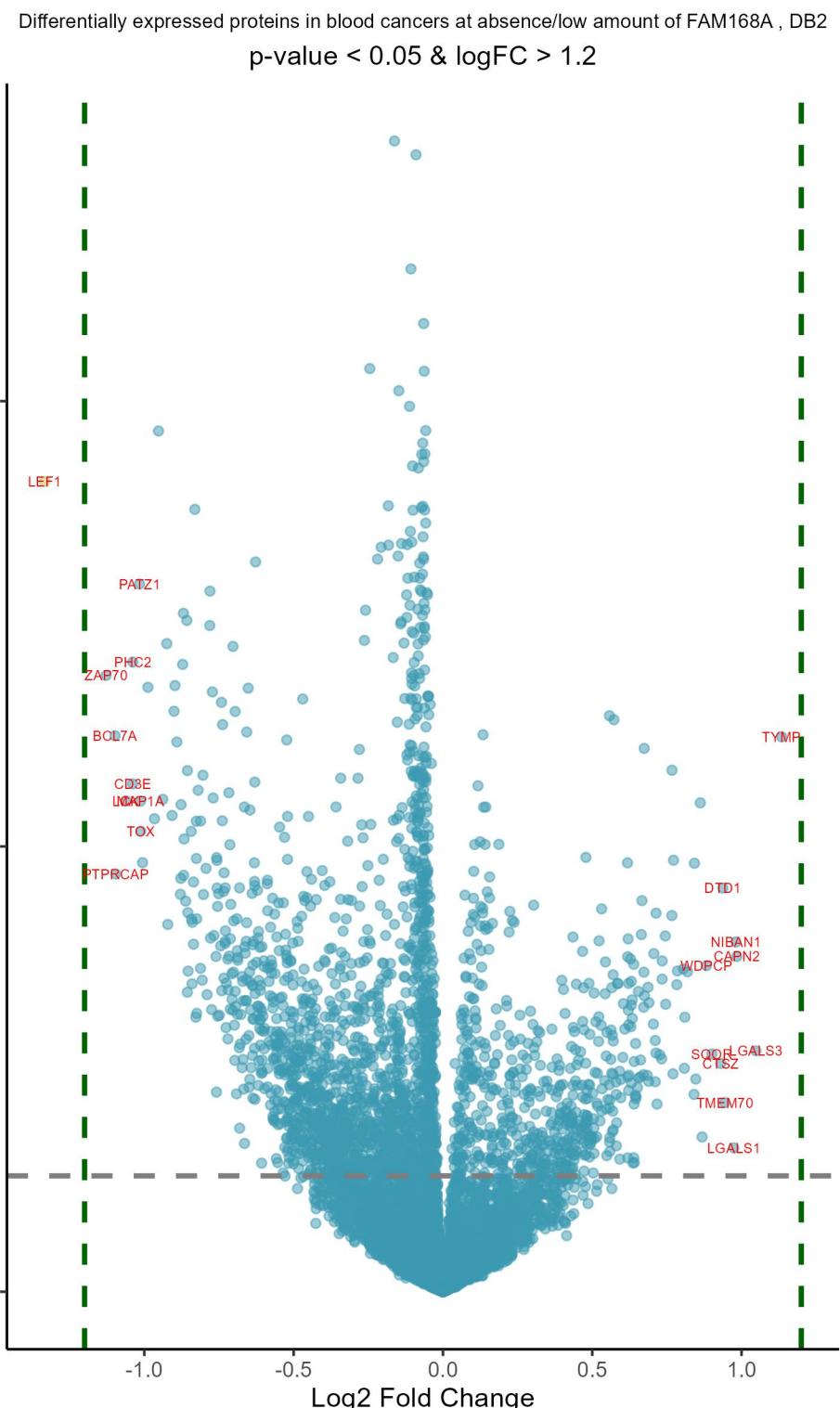


Downregulated at low/absent FAM168A Upregulated at low/absent FAM168A

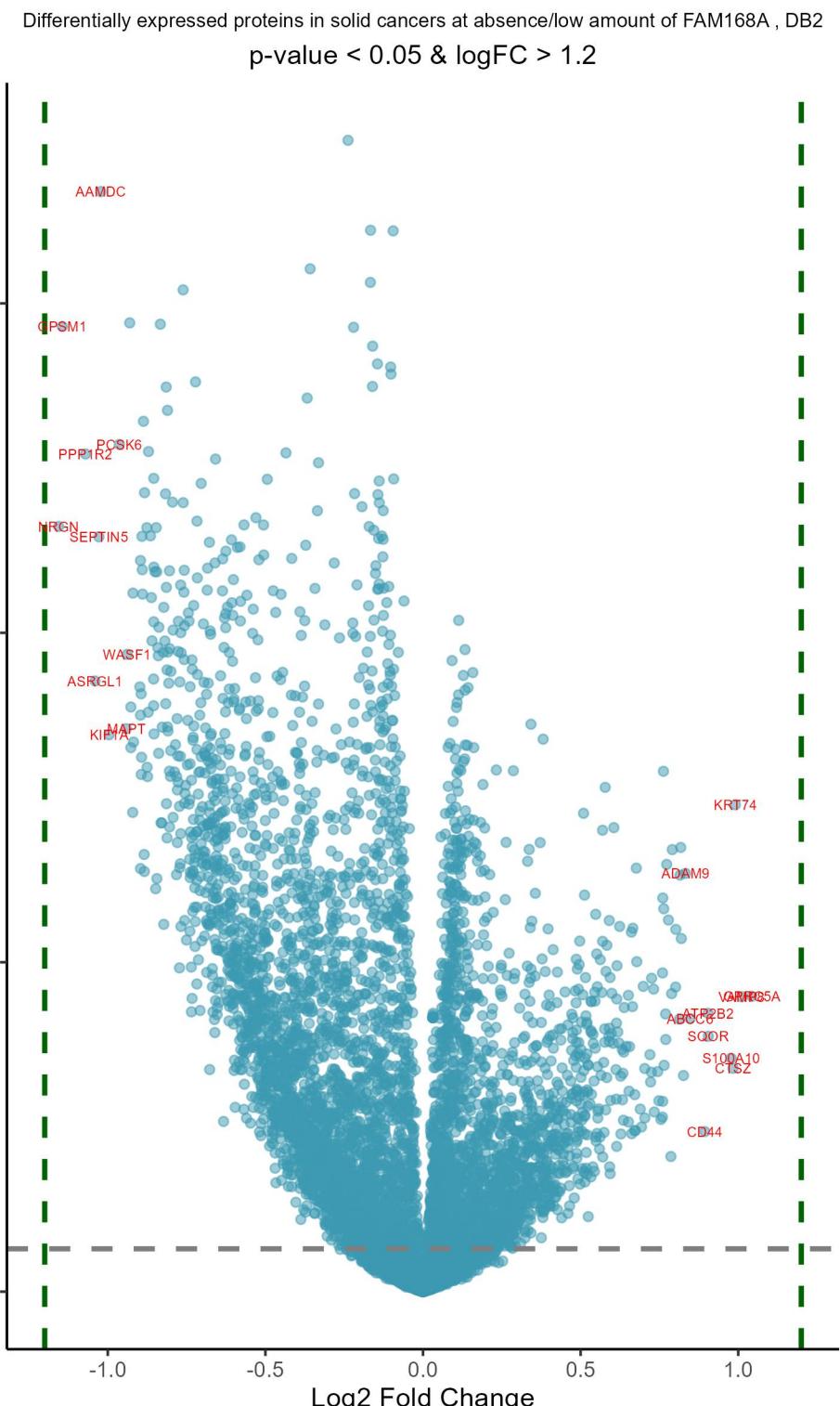
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.98	2.55e-19	NRGN	neurogranin	1.01	1.28e-07	S100A10	S100 calcium binding protein A10
-0.97	8.31e-25	WASF1	WASP family member 1	0.98	3.39e-09	CTSZ	cathepsin Z
-0.96	4.17e-23	GPM1	G protein signaling modulator 1	0.95	2.13e-11	GPRC5A	G protein-coupled receptor class C
-0.95	3.58e-35	AAMDC	adipogenesis associated Mth938 doma	0.92	3.24e-10	SQOR	sulfide quinone oxidoreductase
-0.95	2.47e-21	IGDCC4	immunoglobulin superfamily DCC subc	0.91	9.84e-18	KRT74	keratin 74
-0.95	9.99e-24	PPP1R2	protein phosphatase 1 regulatory in	0.9	3.84e-06	LGALS3	galectin 3
-0.92	3.21e-21	C18orf63	chromosome 18 open reading frame 63	0.89	2.62e-11	ATP2B2	ATPase plasma membrane Ca2+ transpo
-0.9	1.98e-19	MAP1A	microtubule associated protein 1A	0.85	3.84e-06	CD44	CD44 molecule (Indian blood group)
-0.89	9.17e-19	CDKN2C	cyclin dependent kinase inhibitor 2	0.84	5.70e-11	ABCC6	ATP binding cassette subfamily C me
-0.88	1.86e-23	ATXN7L3B	ataxin 7 like 3B	0.83	5.02e-08	VAMP8	vesicle associated membrane protein
-0.88	2.76e-21	DCAF16	DDB1 and CUL4 associated factor 16	0.82	6.39e-10	PCLO	piccolo presynaptic cytomatrix prot
-0.87	2.61e-16	GNG2	G protein subunit gamma 2	0.82	1.61e-10	ADAM9	ADAM metallopeptidase domain 9
-0.86	5.92e-26	HIRIP3	HIRA interacting protein 3	0.81	9.56e-06	CAVIN1	caveolae associated protein 1
-0.85	2.06e-23	PCSK6	proprotein convertase subtilisin/ke	0.8	2.06e-12	SDC4	syndecan 4
-0.85	3.98e-18	SRR	serine racemase	0.79	5.58e-19	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-b
-0.84	2.44e-24	MZT1	mitotic spindle organizing protein	0.79	1.96e-14	CACUL1	CDK2 associated cullin domain 1
-0.84	4.71e-29	PDE6D	phosphodiesterase 6D	0.78	4.30e-11	CDCP1	CUB domain containing protein 1
-0.83	7.56e-17	TCF3	transcription factor 3	0.77	6.64e-17	RETSAT	retinol saturase
-0.83	6.24e-24	SMYD3	SET and MYND domain containing 3	0.77	5.20e-09	EPHA2	EPH receptor A2
-0.83	2.55e-21	HAUS1	HAUS augmin like complex subunit 1	0.76	2.98e-15	TCHHL1	trichohyalin like 1
-0.83	1.54e-14	ASRGL1	asparaginase and isoasparyl peptid	0.75	2.12e-07	NT5E	5'-nucleotidase ecto
-0.82	7.61e-19	SSNA1	SS nuclear autoantigen 1	0.75	1.31e-15	ASB2	ankyrin repeat and SOCS box contain
-0.82	6.66e-22	HDHD2	haloacid dehalogenase like hydrolas	0.73	6.60e-09	EPS8L2	EPS8 like 2
-0.82	8.42e-25	GPATCH11	G-patch domain containing 11	0.73	4.57e-07	ANXA3	annexin A3
-0.82	2.24e-14	MLLT11	MLLT11 transcription factor 7 cofac	0.73	1.25e-13	B4GALT5	beta-1,4-galactosyltransferase 5
-0.81	2.17e-19	DPYSL4	dihydropyrimidinase like 4	0.73	8.77e-07	PROCR	protein C receptor
-0.81	2.64e-26	PANK4	pantothenate kinase 4 (inactive)	0.72	5.31e-12	RBM47	RNA binding motif protein 47
-0.8	1.56e-26	TLE5	TLE family member 5, transcriptiona	0.72	1.88e-09	AXL	AXL receptor tyrosine kinase
-0.8	7.24e-20	GPALPP1	GPALPP motifs containing 1	0.72	1.86e-04	S100A6	S100 calcium binding protein A6

GAGE analysis on upregulated and downregulated proteins at low/absent FAM168A protein, DB2



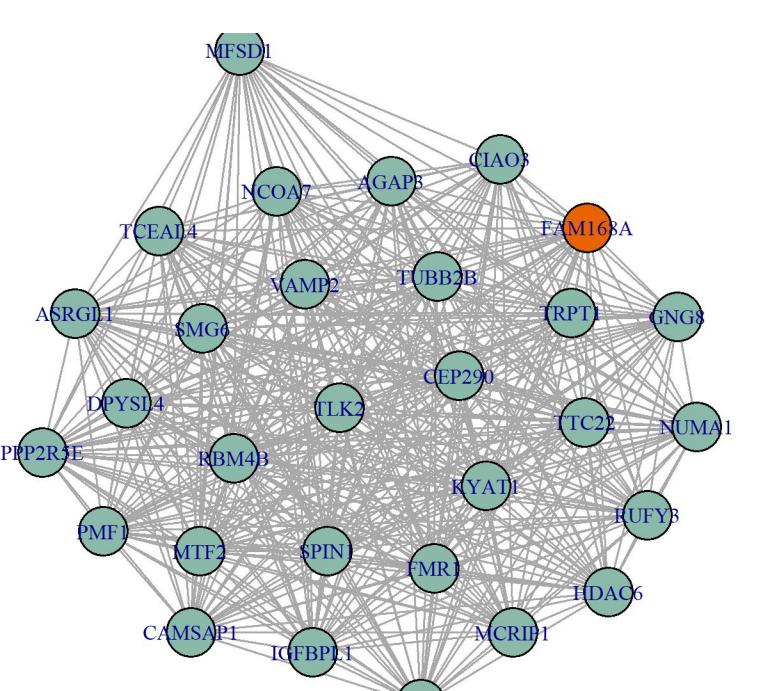


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.33	3.71e-07	LEF1	lymphoid enhancer binding factor 1	1.13	4.12e-05	TYMP	thymidine phosphorylase
-1.13	1.21e-05	ZAP70	zeta chain of T cell receptor assoc	1.05	1.37e-02	LGALS3	galectin 3
-1.1	4.05e-05	BCL7A	BAF chromatin remodeling complex su	0.98	3.03e-03	CAPN2	calpain 2
-1.1	6.24e-04	PTPRCAP	protein tyrosine phosphatase recept	0.98	2.28e-03	NIBAN1	niban apoptosis regulator 1
-1.06	1.49e-04	LCK	LCK proto-oncogene, Src family tyro	0.97	8.84e-02	LGALS1	galectin 1
-1.04	1.04e-04	CD3E	CD3 epsilon subunit of T-cell recep	0.94	3.77e-02	TMEM70	transmembrane protein 70
-1.04	9.34e-06	PHC2	polyhomeotic homolog 2	0.94	8.15e-04	DTD1	D-aminoacyl-tRNA deacylase 1
-1.02	2.20e-06	PATZ1	POZ/BTB and AT hook containing zinc	0.93	1.76e-02	CTSZ	cathepsin Z
-1.01	1.49e-04	MAP1A	microtubule associated protein 1A	0.9	1.47e-02	SQOR	sulfide quinone oxidoreductase
-1.01	2.65e-04	TOX	thymocyte selection associated high	0.88	3.52e-03	WDPCP	WD repeat containing planar cell po
-1.01	5.03e-04	MLLT11	MLLT11 transcription factor 7 cofac	0.87	7.23e-02	S100A6	S100 calcium binding protein A6
-0.99	1.53e-05	WASF1	WASP family member 1	0.86	1.54e-04	NAGLU	N-acetyl-alpha-glucosaminidase
-0.97	2.05e-04	BCL11B	BAF chromatin remodeling complex su	0.85	2.37e-02	DENN5B	DENN domain containing 5B
-0.95	1.64e-07	ATXN7L3B	ataxin 7 like 3B	0.84	5.06e-04	FLVCR1	FLVCR heme transporter 1
-0.94	1.44e-04	CBX2	chromobox 2	0.84	3.21e-02	KIF5C	kinesin family member 5C
-0.92	6.18e-06	RUNX1	RUNX family transcription factor 1	0.82	4.02e-03	SAMHD1	SAM and HD domain containing deoxyn
-0.92	1.60e-03	PTK7	protein tyrosine kinase 7 (inactive	0.81	6.97e-03	JUNB	JunB proto-oncogene, AP-1 transcrip
-0.91	1.95e-04	SASH3	SAM and SH3 domain containing 3	0.81	1.95e-02	NLRP1	NLR family pyrin domain containing
-0.9	2.41e-05	MACROD1	mono-ADP ribosylhydrolase 1	0.81	3.77e-03	GPAA1	glycosylphosphatidylinositol anchor
-0.9	1.50e-05	SMIM24	small integral membrane protein 24	0.79	3.95e-03	ATP6V0A1	ATPase H+ transporting V0 subunit a
-0.89	4.64e-05	SSBP2	single stranded DNA binding protein	0.78	5.04e-03	IKBIP	IKBKB interacting protein
-0.88	9.15e-04	BCL11A	BAF chromatin remodeling complex su	0.77	4.81e-04	RETSAT	retinol saturase
-0.88	6.82e-04	SCML2	Scm polycomb group protein like 2	0.77	2.15e-02	SIM2	SIM bHLH transcription factor 2
-0.88	1.59e-04	SLFN11	schlafen family member 11	0.77	8.42e-05	RBM47	RNA binding motif protein 47
-0.87	9.69e-06	KANSL3	KAT8 regulatory NSL complex subunit	0.77	1.36e-03	NUDT16	nudix hydrolase 16
-0.87	3.67e-06	CD3D	CD3 delta subunit of T-cell recepto	0.75	6.30e-03	IL4I1	interleukin 4 induced 1
-0.87	6.44e-04	SH2D1A	SH2 domain containing 1A	0.74	2.03e-03	PARVB	parvin beta
-0.87	3.07e-04	GNB4	G protein subunit beta 4	0.73	3.24e-03	PLOD1	procollagen-lysine,2-oxoglutarate 5
-0.86	1.03e-03	ERG	ETS transcription factor ERG	0.73	4.60e-03	SIL1	SIL1 nucleotide exchange factor

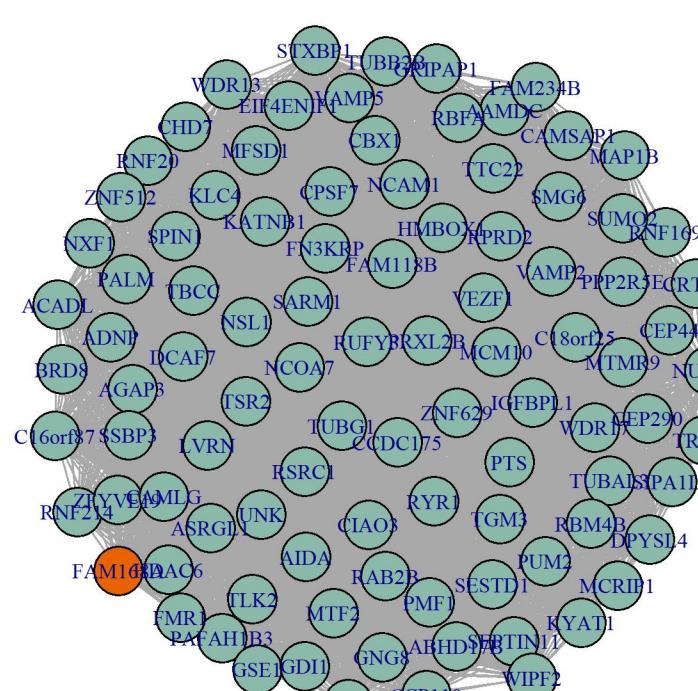


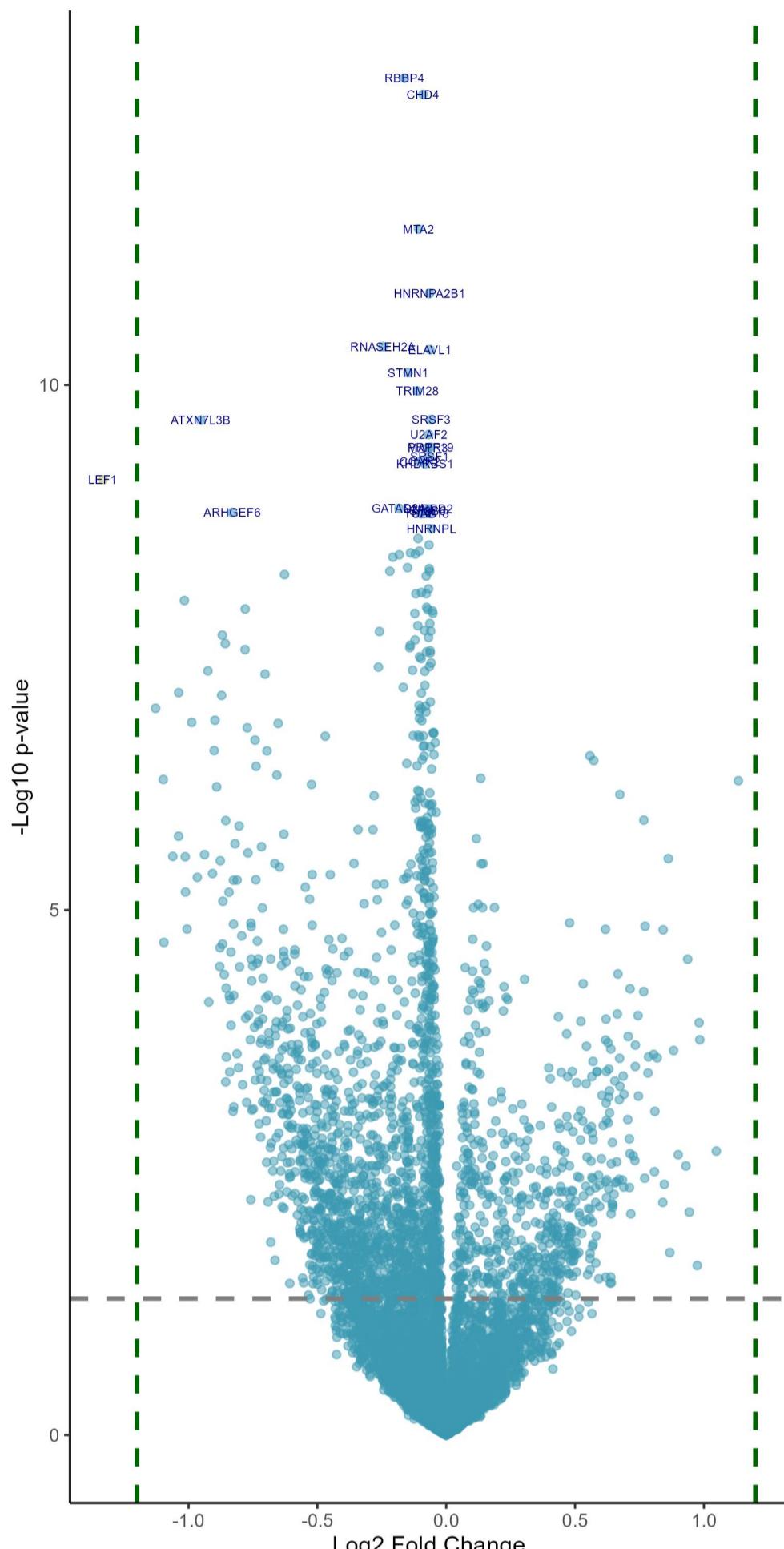
Downregulated in solid cancers at low/absent FAM168A				Upregulated in solid cancers at low/absent FAM168A			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.16	1.02e-21	NRGN	neurogranin	1.04	6.38e-09	GPRC5A	G protein-coupled receptor class C
-1.14	3.71e-27	GPSM1	G protein signaling modulator 1	1.01	6.59e-09	VAMP8	vesicle associated membrane protein
-1.07	1.20e-23	PPP1R2	protein phosphatase 1 regulatory in	0.99	3.13e-14	KRT74	keratin 74
-1.04	1.33e-17	ASRGL1	asparaginase and isoaspartyl peptid	0.98	6.65e-07	CTSZ	cathepsin Z
-1.03	1.82e-21	SEPTIN5	septin 5	0.98	3.45e-07	S100A10	S100 calcium binding protein A10
-1.02	1.13e-30	AAMDC	adipogenesis associated Mth938 doma	0.91	8.36e-08	SQOR	sulfide quinone oxidoreductase
-1	3.94e-16	KIF1A	kinesin family member 1A	0.9	1.91e-08	ATP2B2	ATPase plasma membrane Ca2+ transpo
-0.96	6.97e-24	PCSK6	proprotein convertase subtilisin/ke	0.89	4.02e-05	CD44	CD44 molecule (Indian blood group)
-0.94	2.65e-16	MAPT	microtubule associated protein tau	0.85	2.66e-08	ABCC6	ATP binding cassette subfamily C me
-0.94	2.38e-18	WASF1	WASP family member 1	0.83	2.40e-12	ADAM9	ADAM metallopeptidase domain 9
-0.93	3.59e-27	PDE6D	phosphodiesterase 6D	0.83	1.06e-06	ICAM1	intercellular adhesion molecule 1
-0.93	6.68e-17	C18orf63	chromosome 18 open reading frame 63	0.82	1.57e-10	TAP2	transporter 2, ATP binding cassette
-0.93	8.83e-16	IGDCC4	immunoglobulin superfamily DCC subc	0.82	4.63e-13	ASB2	ankyrin repeat and SOCS box contain
-0.92	5.09e-14	NCAM1	neural cell adhesion molecule 1	0.82	2.67e-12	TCHHL1	trichohyalin like 1
-0.92	5.37e-20	DPYSL4	dihydropyrimidinase like 4	0.81	2.74e-08	EPHA2	EPH receptor A2
-0.92	6.33e-16	SOGA1	suppressor of glucose, autophagy as	0.8	8.67e-11	SDC4	syndecan 4
-0.9	1.90e-17	DCAF16	DDB1 and CUL4 associated factor 16	0.8	3.56e-09	CDCP1	CUB domain containing protein 1
-0.9	7.64e-21	MZT1	mitotic spindle organizing protein	0.79	5.31e-13	CTSG	cathepsin G
-0.9	1.77e-12	CRMP1	collapsin response mediator protein	0.79	5.45e-09	IL18	interleukin 18
-0.9	1.11e-16	SARM1	sterile alpha and TIR motif contain	0.79	2.01e-04	CAVIN1	caveolae associated protein 1
-0.89	2.97e-17	ARAP1	ArfGAP with RhoGAP domain, ankyrin	0.78	4.75e-11	TAP1	transporter 1, ATP binding cassette
-0.89	4.60e-15	SEPTIN3	septin 3	0.77	1.35e-12	B4GALT5	beta-1,4-galactosyltransferase 5
-0.89	1.58e-15	CDKN2C	cyclin dependent kinase inhibitor 2	0.77	1.03e-07	KRT80	keratin 80
-0.89	1.80e-21	HIRIP3	HIRA interacting protein 3	0.77	1.99e-08	F3	coagulation factor III, tissue fact
-0.89	1.34e-20	USP13	ubiquitin specific peptidase 13	0.76	5.48e-07	PCLO	piccolo presynaptic cytomatrix prot
-0.89	5.71e-20	HDHD2	haloacid dehalogenase like hydrolas	0.76	2.30e-11	S100P	S100 calcium binding protein P
-0.89	1.45e-24	MAPRE3	microtubule associated protein RP/E	0.76	3.78e-15	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-b
-0.88	7.20e-13	DPYSL5	dihydropyrimidinase like 5	0.76	1.15e-11	CACUL1	CDK2 associated cullin domain 1
-0.88	2.13e-12	CPAPB1	cellular retinoic acid binding prot	0.76	5.71e-06	NT5E	5'-nucleotidase ecto-

FAM168A network, DB2, all Pearson $r \geq 0.35$



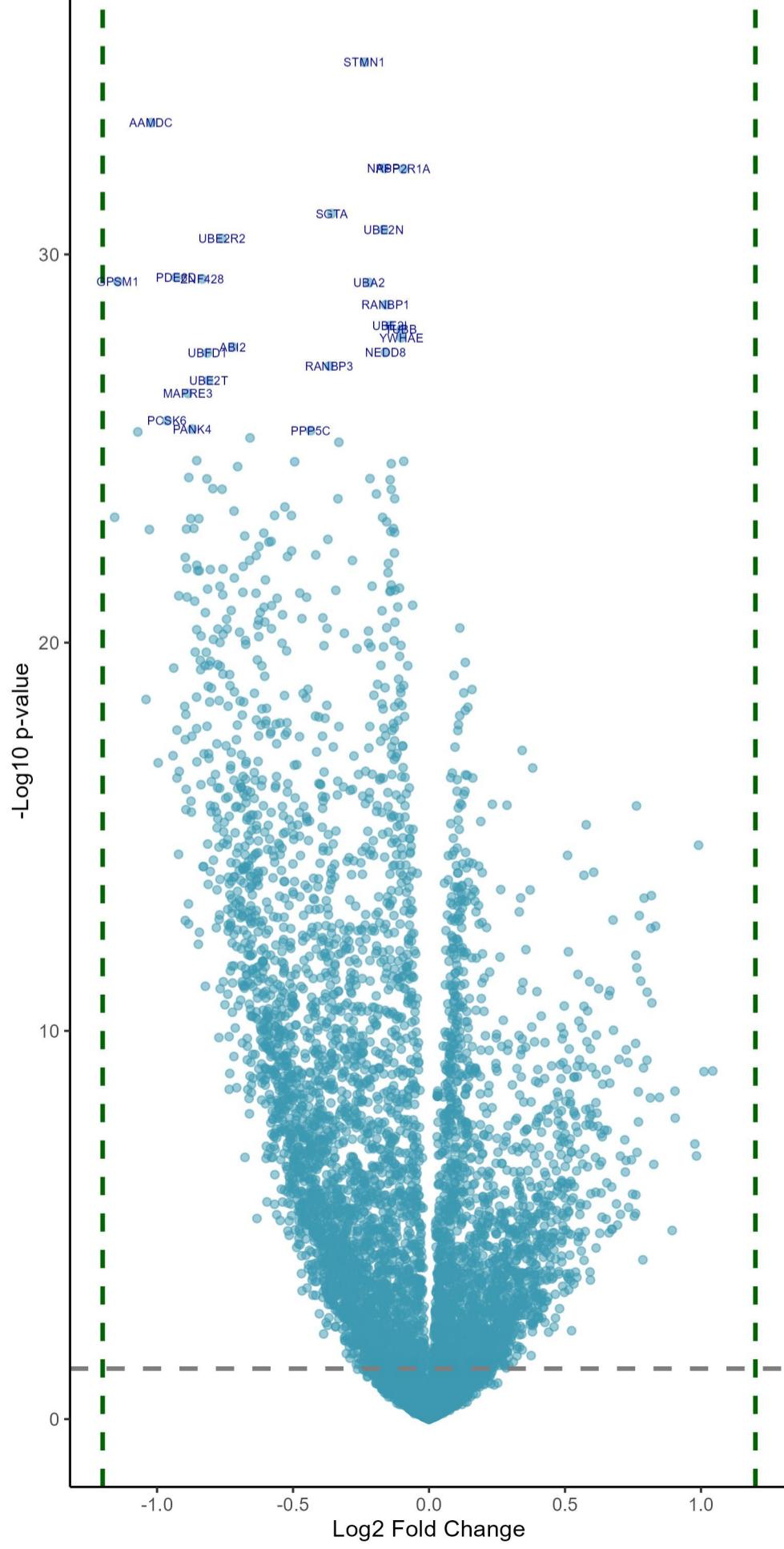
FAM168A network, DB2, all Pearson $r \geq 0.3$





Sorted by p values!
Downregulated in blood cancers at low/absent FAM168A Upregulated in blood cancers at low/absent FAM168A

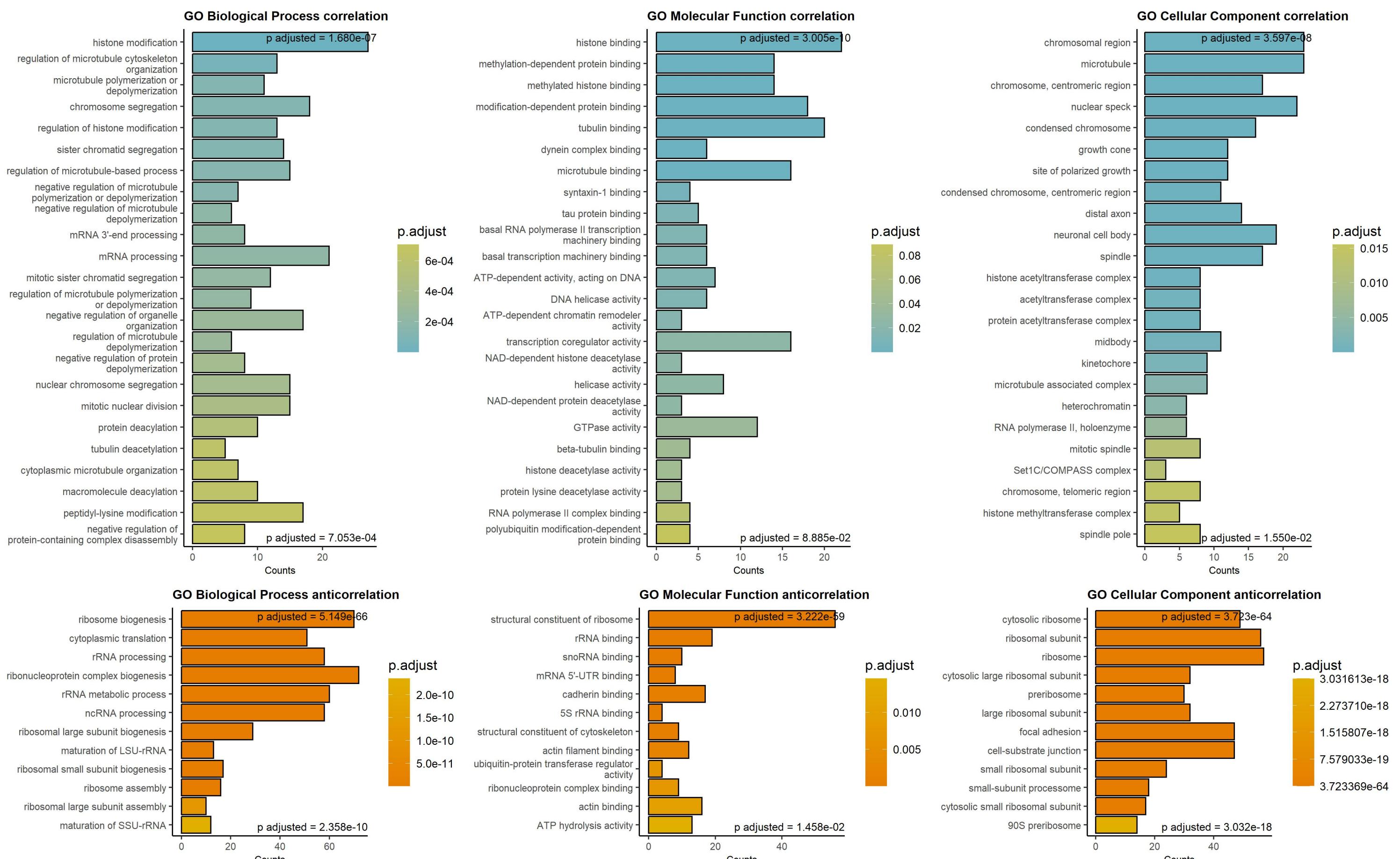
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.16	4.77e-10	RBBP4	RB binding protein 4, chromatin rem	0.56	2.62e-05	MAGEA1	MAGE family member A1
-0.09	4.77e-10	CHD4	chromodomain helicase DNA binding p	0.57	2.84e-05	SQSTM1	sequestosome 1
-0.11	6.85e-09	MTA2	metastasis associated 1 family memb	0.13	3.98e-05	UQCRCB	ubiquinol-cytochrome c reductase bi
-0.06	2.25e-08	HNRNPA2B1	heterogeneous nuclear ribonucleopro	1.13	4.12e-05	TYMP	thymidine phosphorylase
-0.24	5.51e-08	RNASEH2A	ribonuclease H2 subunit A	0.67	5.30e-05	JSRP1	junctional sarcoplasmic reticulum p
-0.06	5.51e-08	ELAVL1	ELAV like RNA binding protein 1	0.77	8.42e-05	RBM47	RNA binding motif protein 47
-0.15	7.99e-08	STMN1	stathmin 1	0.12	1.08e-04	UQCRC2	ubiquinol-cytochrome c reductase co
-0.11	1.06e-07	TRIM28	tripartite motif containing 28	0.86	1.54e-04	NAGLU	N-acetyl-alpha-glucosaminidase
-0.06	1.64e-07	SRSF3	serine and arginine rich splicing f	0.14	1.65e-04	SRPRB	SRP receptor subunit beta
-0.95	1.64e-07	ATXN7L3B	ataxin 7 like 3B	0.14	1.65e-04	LMAN2	lectin, mannose binding 2
-0.07	2.06e-07	U2AF2	U2 small nuclear RNA auxiliary fact	0.12	3.23e-04	DNAJB11	DnaJ heat shock protein family (Hsp
-0.06	2.36e-07	PRPF19	pre-mRNA processing factor 19	0.19	3.43e-04	MYDGF	myeloid derived growth factor
-0.07	2.36e-07	MATR3	matrin 3	0.14	3.43e-04	MRPL4	mitochondrial ribosomal protein L4
-0.06	2.66e-07	SRSF1	serine and arginine rich splicing f	0.11	3.43e-04	CLPP	caseinolytic mitochondrial matrix p
-0.1	2.78e-07	CCAR2	cell cycle and apoptosis regulator	0.48	4.62e-04	SEC11C	SEC11 homolog C, signal peptidase c
-0.08	2.78e-07	KHDRBS1	KH RNA binding domain containing, s	0.77	4.81e-04	RETSAT	retinol saturase
-1.33	3.71e-07	LEF1	lymphoid enhancer binding factor 1	0.62	5.03e-04	ECI1	enoyl-CoA delta isomerase 1
-0.18	5.85e-07	GATA2D2A	GATA zinc finger domain containing	0.84	5.06e-04	FLVCR1	FLVCR heme transporter 1
-0.07	5.85e-07	SNRPD2	small nuclear ribonucleoprotein D2	0.1	5.96e-04	PPIB	peptidylprolyl isomerase B
-0.07	5.85e-07	SF3B6	splicing factor 3b subunit 6	0.16	6.62e-04	MOGS	mannosyl-oligosaccharide glucosidas
-0.83	5.85e-07	ARHGEF6	Rac/Cdc42 guanine nucleotide exchan	0.94	8.15e-04	DTD1	D-aminoacyl-tRNA deacylase 1
-0.06	5.85e-07	SAP18	Sin3A associated protein 18	0.15	8.75e-04	NCSTN	nicastrin
-0.1	5.85e-07	TUBB	tubulin beta class I	0.07	9.24e-04	UQCRC1	ubiquinol-cytochrome c reductase co
-0.06	7.82e-07	HNRNPL	heterogeneous nuclear ribonucleopro	0.16	9.80e-04	CISD2	CDGSH iron sulfur domain 2
-0.11	9.32e-07	PPP1CA	protein phosphatase 1 catalytic sub	0.1	9.83e-04	NDUFB1	NADH:ubiquinone oxidoreductase subu
-0.07	1.03e-06	NONO	non-POU domain containing octamer b	0.67	1.02e-03	CFTR	CF transmembrane conductance regula
-0.1	1.12e-06	HNRNPA0	heterogeneous nuclear ribonucleopro	0.3	1.12e-03	DHODH	dihydroorotate dehydrogenase (quino
-0.14	1.12e-06	MACROH2A1	macroH2A.1 histone	0.13	1.14e-03	CYC1	cytochrome c1
-0.12	1.12e-06	PDS5A	PDS5 cohesin associated factor A	0.13	1.18e-03	PLCH1	phospholipase C eta 1
-0.18	1.12e-06	ACOT7	acyl-CoA thioesterase 7	0.53	1.19e-03	ATP7A	ATPase copper transporting alpha
-0.21	1.14e-06	RNASEH2C	ribonuclease H2 subunit C	0.22	1.26e-03	MRPL48	mitochondrial ribosomal protein L48
-0.15	1.38e-06	SMARCB1	SWI/SNF related, matrix associated,	0.13	1.30e-03	NDUFB2	NADH:ubiquinone oxidoreductase subu
-0.07	1.38e-06	THRAP3	thyroid hormone receptor associated	0.71	1.30e-03	NCF2	neutrophil cytosolic factor 2
-0.22	1.38e-06	SCAF4	SR-related CTD associated factor 4	0.1	1.33e-03	MRPL13	mitochondrial ribosomal protein L13
-0.06	1.38e-06	SRRT	serrate, RNA effector molecule	0.77	1.36e-03	NUDT16	nudix hydrolase 16
-0.63	1.44e-06	TRIM24	tripartite motif containing 24	0.11	1.40e-03	HSP90B1	heat shock protein 90 beta family m
-0.08	1.45e-06	PNN	pinin, desmosome associated protein	0.23	1.50e-03	PGM3	phosphoglucomutase 3
-0.07	1.88e-06	RBM39	RNA binding motif protein 39	0.24	1.54e-03	MTIF2	mitochondrial translational initiat
0.1	1.94e-06	NASP	nuclear autoantigenic sperm protein	0.09	1.54e-03	EDD20	endoplasmic reticulum protein 20



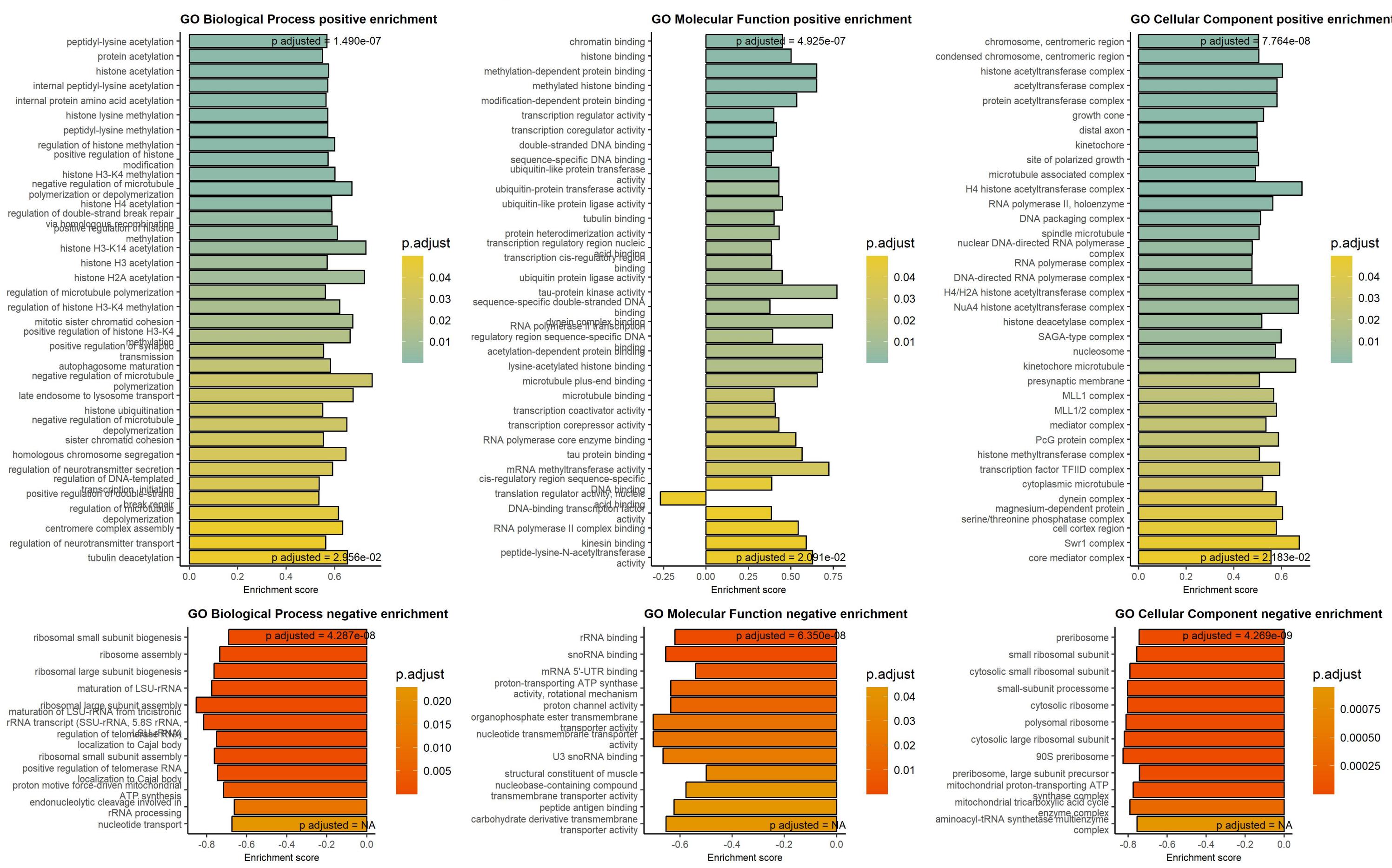
Sorted by p values!
Downregulated in solid cancers at low/absent FAM168A Upregulated in solid cancers at low/absent FAM168A

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.24	4.69e-32	STMN1	stathmin 1	0.11	2.94e-19	TMED9	transmembrane p24 trafficking prote
-1.02	1.13e-30	AAMDC	adipogenesis associated Mth938 doma	0.13	1.80e-18	LMAN2	lectin, mannose binding 2
-0.17	1.05e-29	NASP	nuclear autoantigenic sperm protein	0.09	3.59e-18	RAB1A	RAB1A, member RAS oncogene family
-0.09	1.05e-29	PPP2R1A	protein phosphatase 2 scaffold subu	0.16	7.78e-18	TM9SF3	transmembrane 9 superfamily member
-0.36	1.24e-28	SGTA	small glutamine rich tetratricopept	0.13	9.35e-18	SSR4	signal sequence receptor subunit 4
-0.17	2.76e-28	UBE2N	ubiquitin conjugating enzyme E2 N	0.14	1.98e-17	RPN2	ribophorin II
-0.76	4.07e-28	UBE2R2	ubiquitin conjugating enzyme E2 R2	0.13	2.34e-17	SRPRB	SRP receptor subunit beta
-0.93	3.59e-27	PDE6D	phosphodiesterase 6D	0.11	3.15e-17	GTPBP4	GTP binding protein 4
-0.83	3.59e-27	ZNF428	zinc finger protein 428	0.11	5.05e-17	DDOST	dolichyl-diphosphooligosaccharide--
-1.14	3.71e-27	GPSM1	G protein signaling modulator 1	0.11	6.81e-17	NCLN	nicalin
-0.22	3.71e-27	UBA2	ubiquitin like modifier activating	0.1	1.66e-16	VDAC1	voltage dependent anion channel 1
-0.16	1.28e-26	RANBP1	RAN binding protein 1	0.34	2.00e-16	SUCLG2	succinate-CoA ligase GDP-forming su
-0.14	4.10e-26	UBE2I	ubiquitin conjugating enzyme E2 I	0.38	5.22e-16	MYO1C	myosin IC
-0.1	4.77e-26	TUBB	tubulin beta class I	0.09	6.89e-16	RAB10	RAB10, member RAS oncogene family
-0.1	7.32e-26	YWHAE	tyrosine 3-monooxygenase/trypophan	0.13	7.53e-16	TMOD3	tropomodulin 3
-0.72	1.19e-25	ABI2	abl interactor 2	0.14	7.77e-16	POLDIP2	DNA polymerase delta interacting pr
-0.16	1.52e-25	NEDD8	NEDD8 ubiquitin like modifier	0.08	8.69e-16	RPN1	ribophorin I
-0.81	1.52e-25	UBFD1	ubiquitin family domain containing	0.16	8.82e-16	ACADVL	acyl-CoA dehydrogenase very long ch
-0.37	3.14e-25	RANBP3	RAN binding protein 3	0.1	9.62e-16	MRPL13	mitochondrial ribosomal protein L13
-0.81	7.03e-25	UBE2T	ubiquitin conjugating enzyme E2 T	0.13	1.75e-15	OGDH	oxoglutarate dehydrogenase
-0.89	1.45e-24	MAPRE3	microtubule associated protein RP/E	0.1	1.75e-15	SSR1	signal sequence receptor subunit 1
-0.96	6.97e-24	PCSK6	proprotein convertase subtilisin/ke	0.13	2.06e-15	FAF2	Fas associated factor family member
-0.87	1.10e-23	PANK4	pantothenate kinase 4 (inactive)	0.11	3.33e-15	RRS1	ribosome biogenesis regulator 1 hom
-0.43	1.15e-23	PPP5C	protein phosphatase 5 catalytic sub	0.23	3.52e-15	SSR3	signal sequence receptor subunit 3
-1.07	1.20e-23	PPP1R2	protein phosphatase 1 regulatory in	0.12	3.62e-15	ALDH18A1	aldehyde dehydrogenase 18 family me
-0.66	1.65e-23	TMEM263	transmembrane protein 263	0.29	3.68e-15	PLEC	plectin
-0.33	2.06e-23	ANP32E	acidic nuclear phosphoprotein 32 fa	0.76	3.78e-15	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-b
-0.85	5.90e-23	TLE5	TLE family member 5, transcriptiona	0.11	4.18e-15	TMED10	transmembrane p24 trafficking prote
-0.09	5.90e-23	STIP1	stress induced phosphoprotein 1	0.11	8.04e-15	RRP1	ribosomal RNA processing 1
-0.49	5.90e-23	CARHSP1	calcium regulated heat stable prote	0.19	8.64e-15	TBL2	transducin beta like 2
-0.14	6.43e-23	FEN1	flap structure-specific endonucleas	0.08	9.74e-15	CANX	calnexin
-0.7	7.41e-23	RNF					

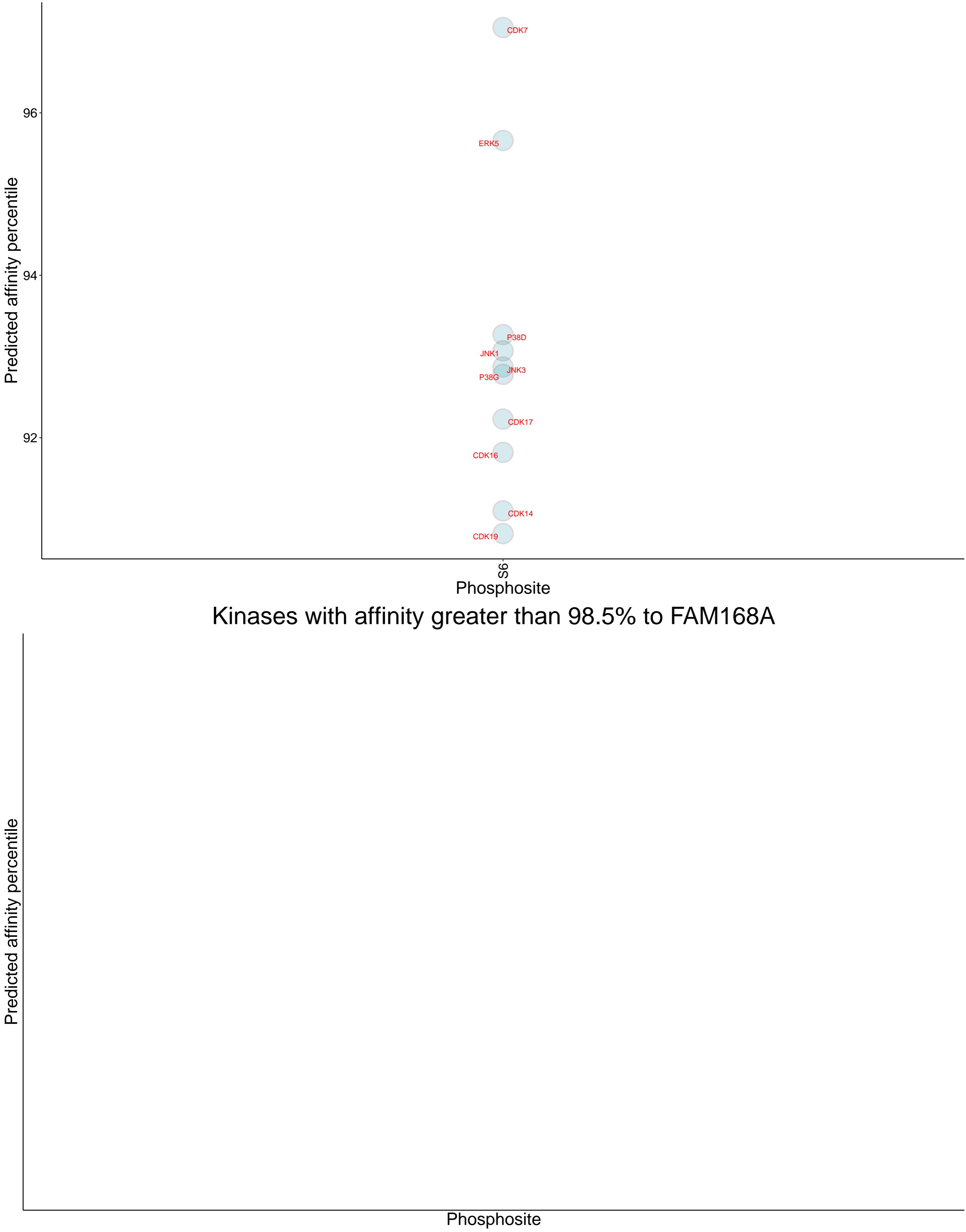
Top 250 correlation coefficients overrepresentation, FAM168A protein, DB2



Gene Set Enrichment analysis on protein correlation coefficients, FAM168A protein, DB2

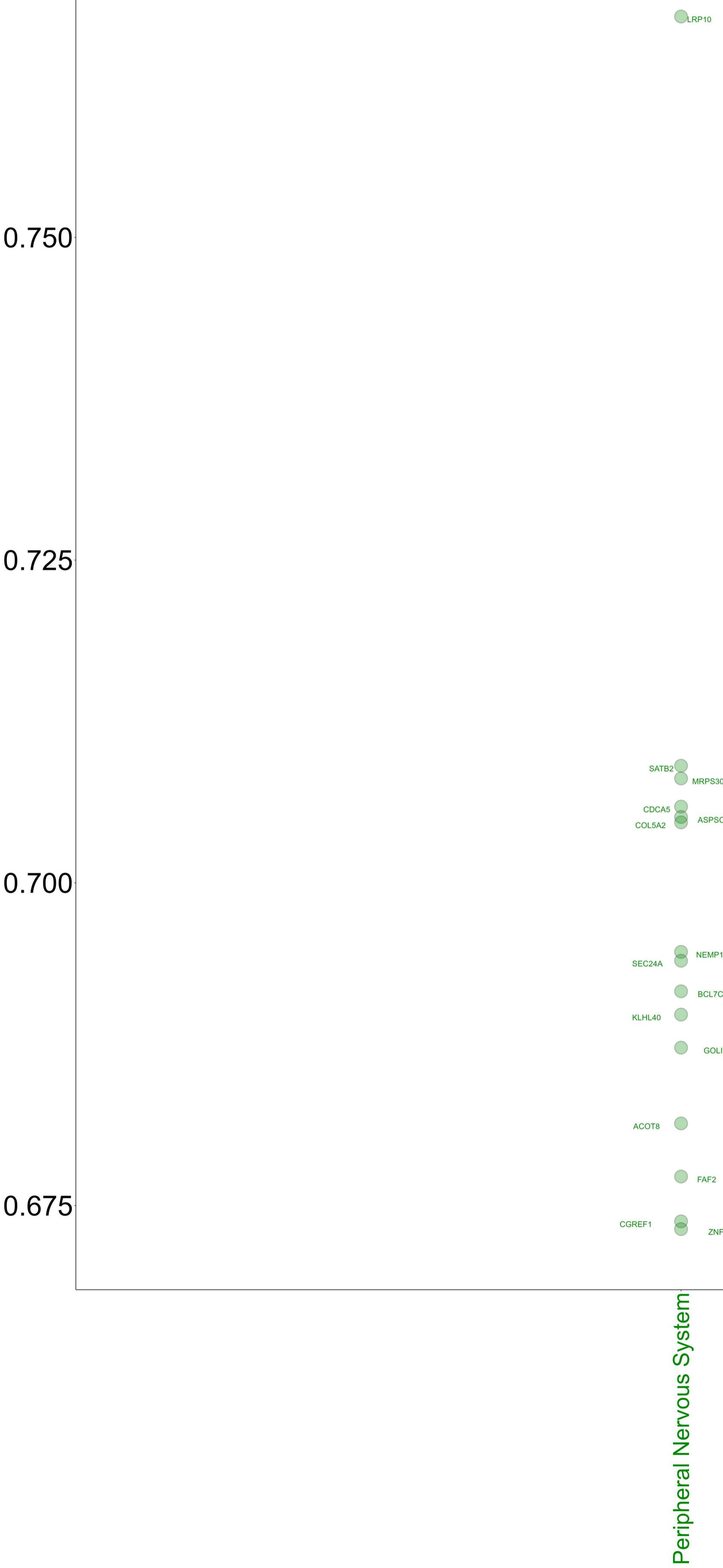


Top 10 kinases for each phosphosite in FAM168A



Top 15 positive correlation coefficients for FAM168A protein by tissue, DB2

Beware of false positives in tissues with small number of samples



Peripheral Nervous System