

ATAD5

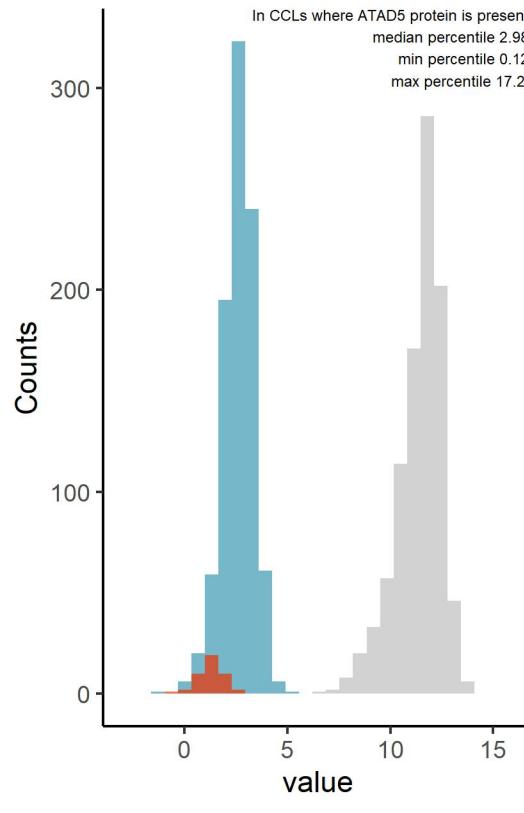
Protein name: ATAD5 ; UNIPROT: Q96QE3 ; Gene name: ATPase family AAA domain containing 5

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

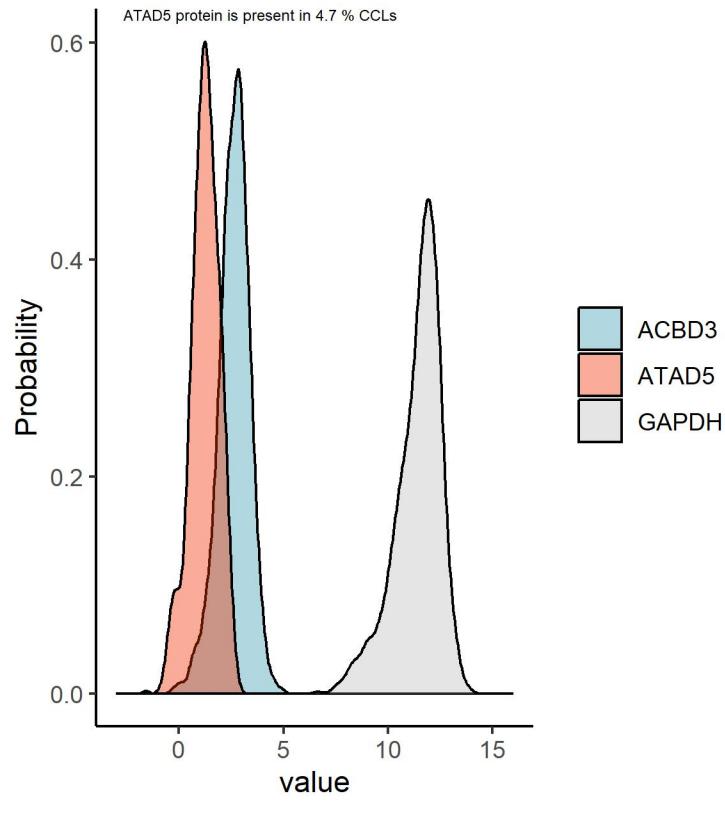
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

Histogram of ATAD5 protein compared to proteins with low and high abundance

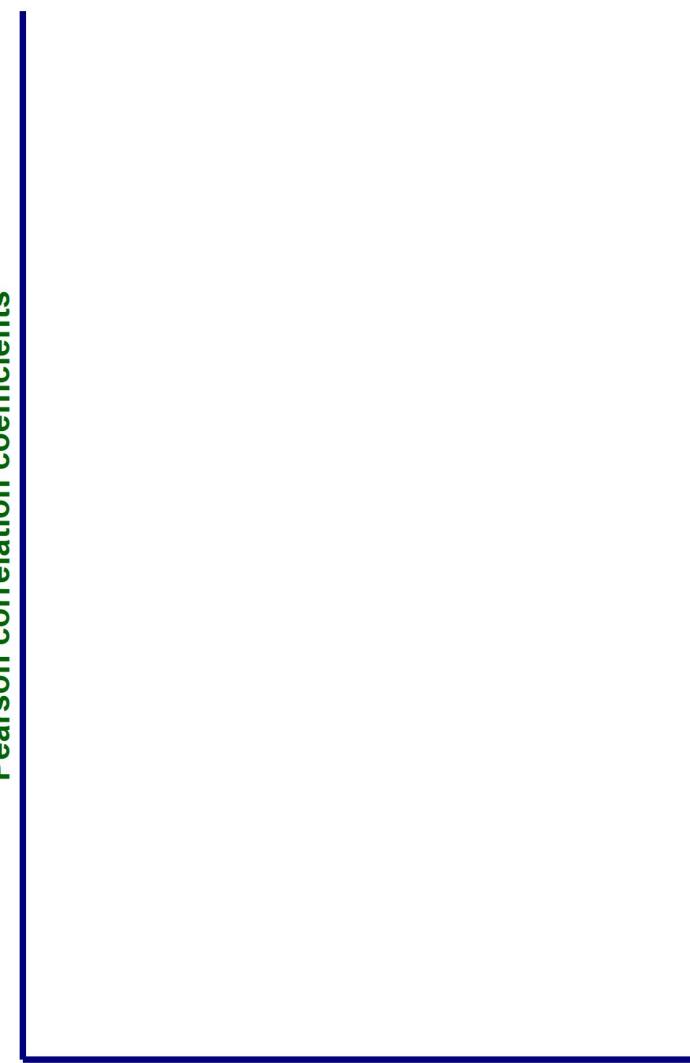


Density plot of ATAD5 protein compared to proteins with low and high abundance



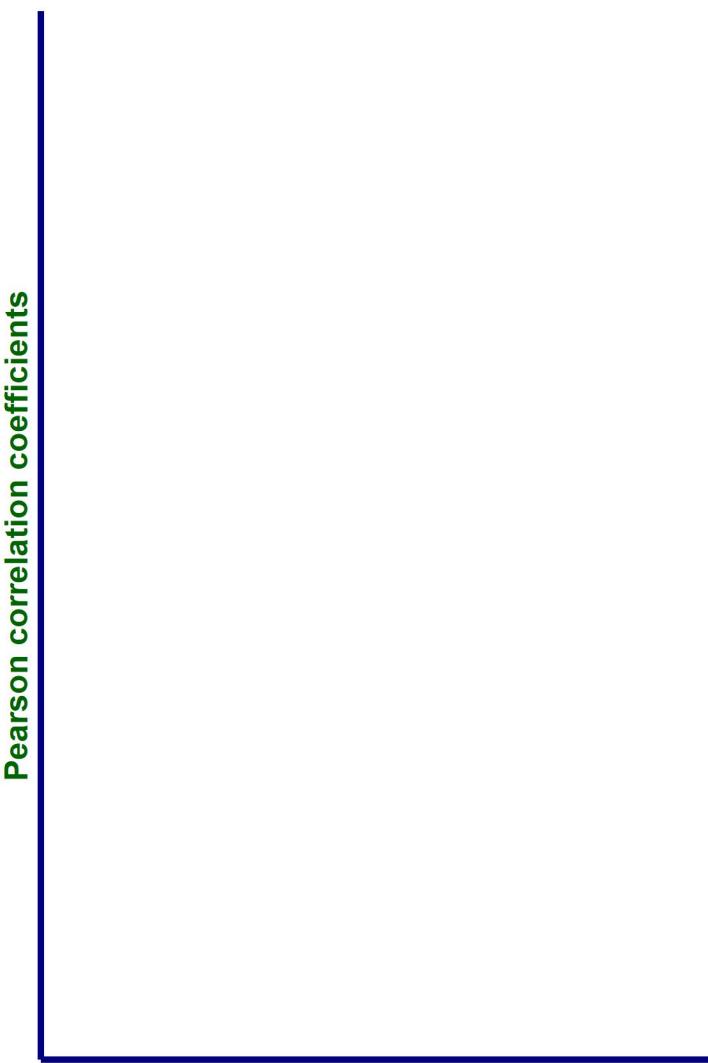
Top negative correlations of ATAD5 protein, DB1

Pearson correlation coefficients

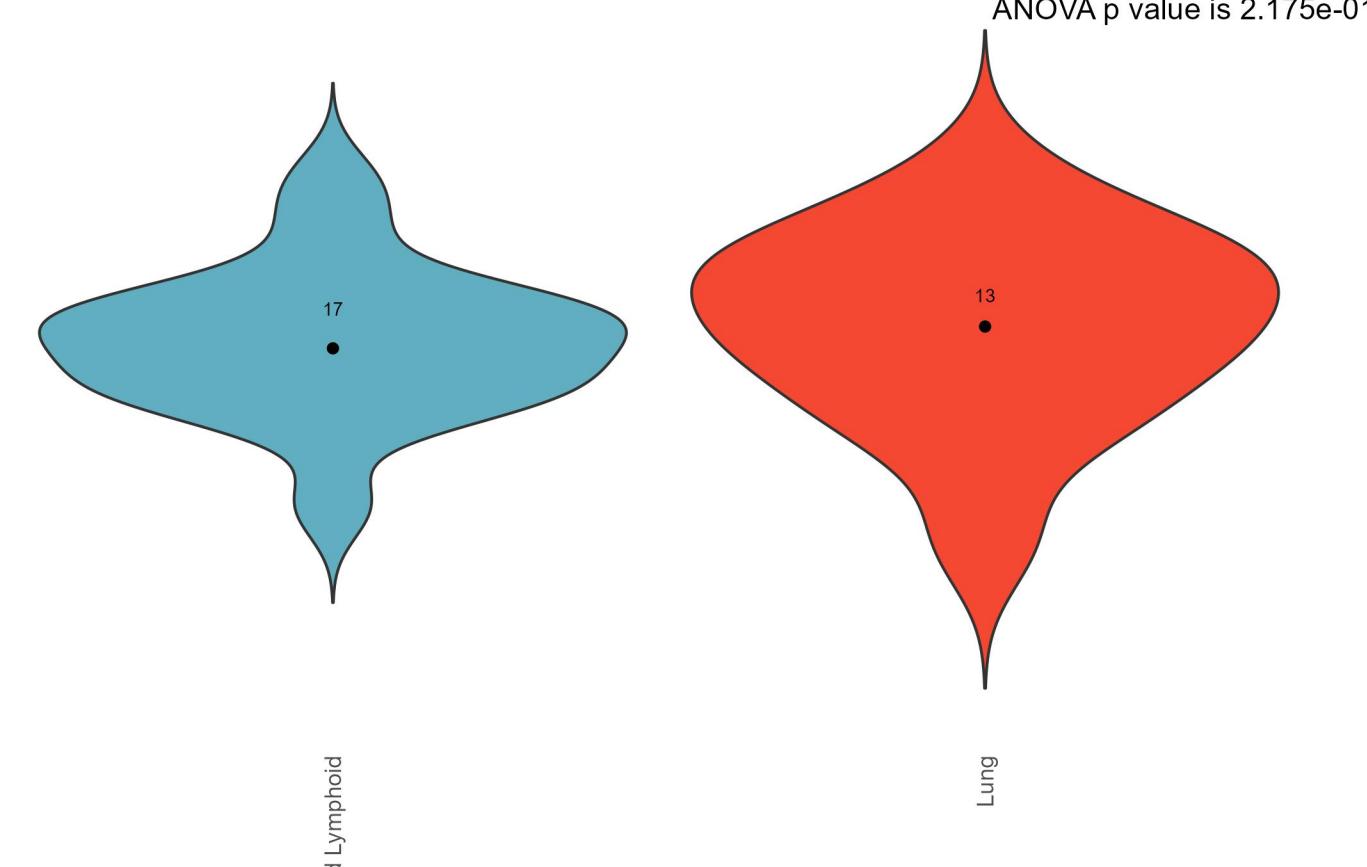


Top positive correlations of ATAD5 protein, DB1

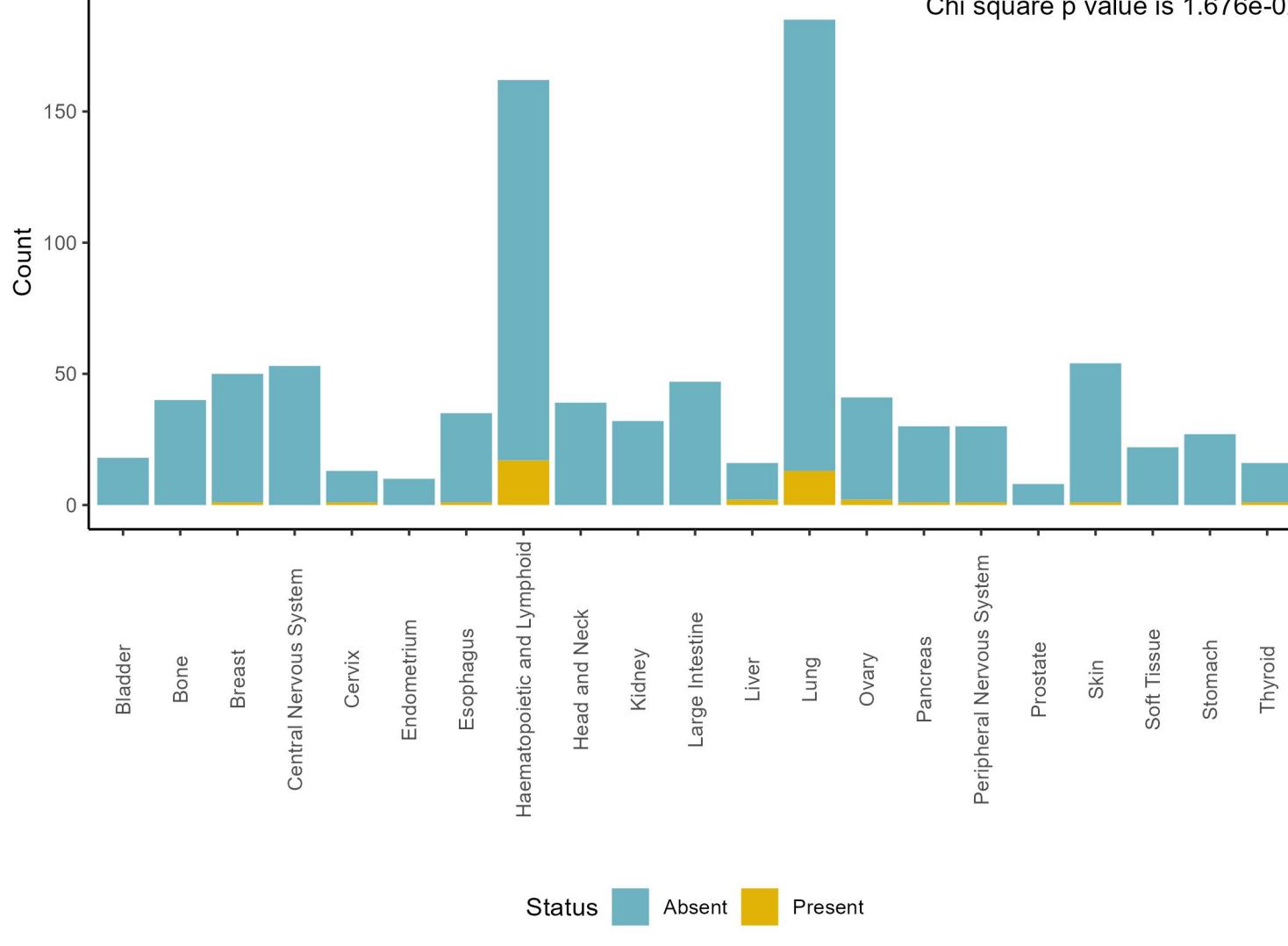
Pearson correlation coefficients



Amount of ATAD5 protein, number of CCLs where it is present by tissue, DB1



Present and absent ATAD5 protein counts by tissue, DB1

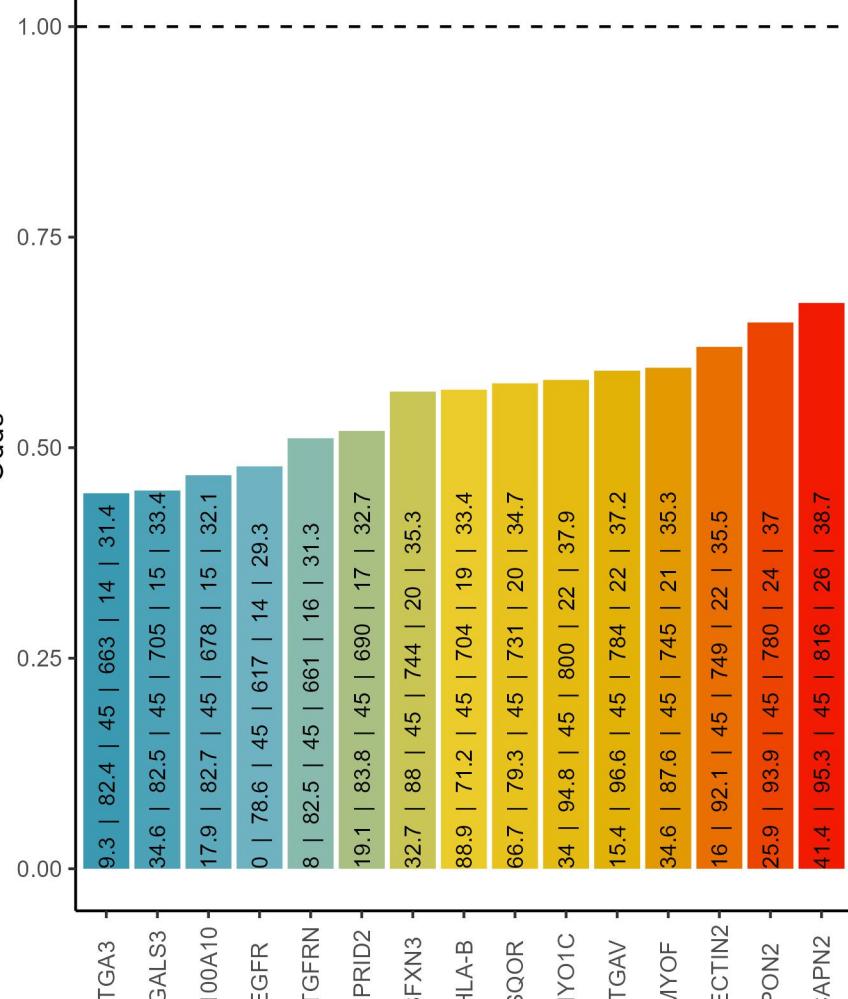


Cooccurrence with ATAD5 protein, DB1

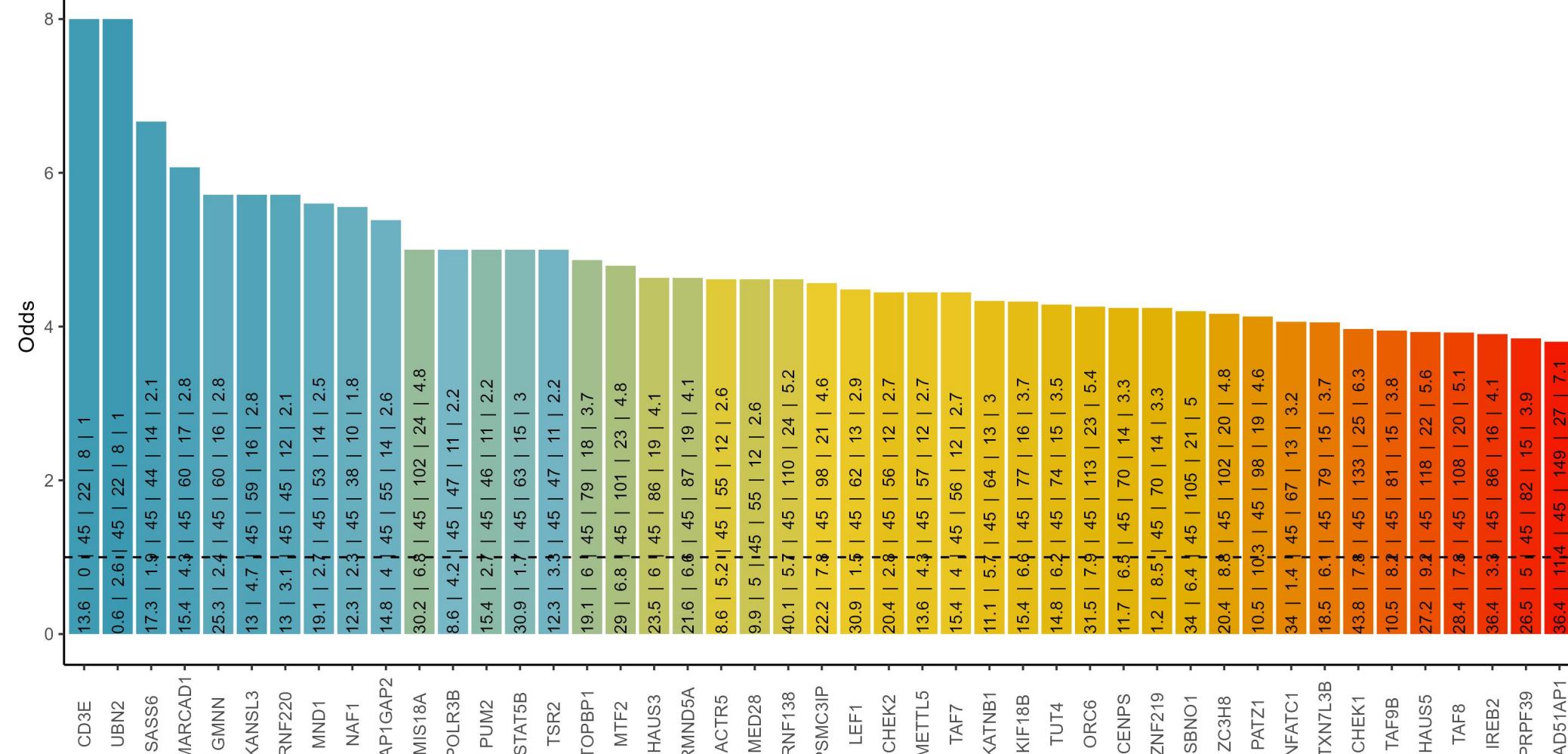
% of ATAD5 in blood cancers: 10.5 ; % of ATAD5 in solid cancers: 3.4

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ATAD5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

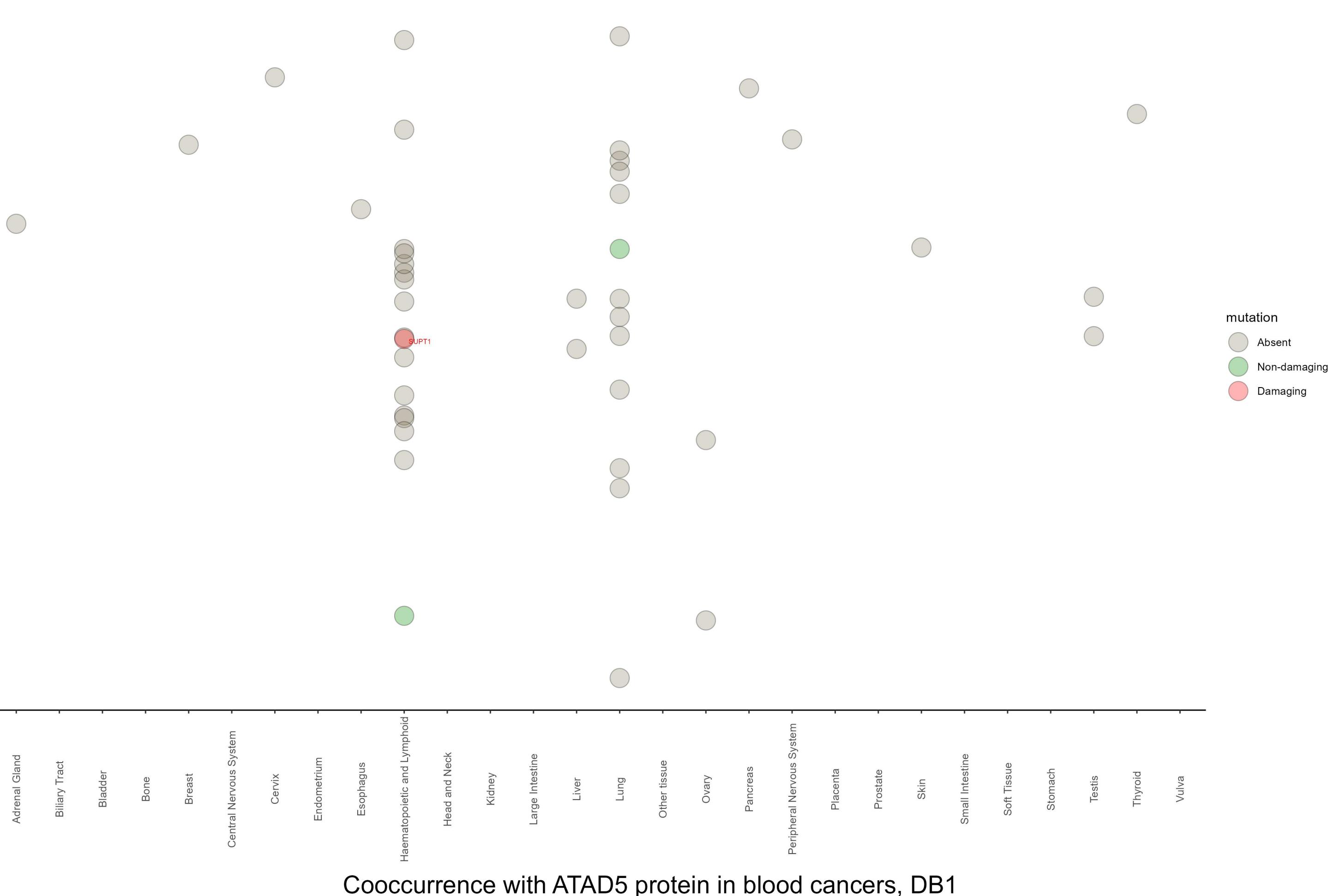
Negative cooccurrence



Positive cooccurrence



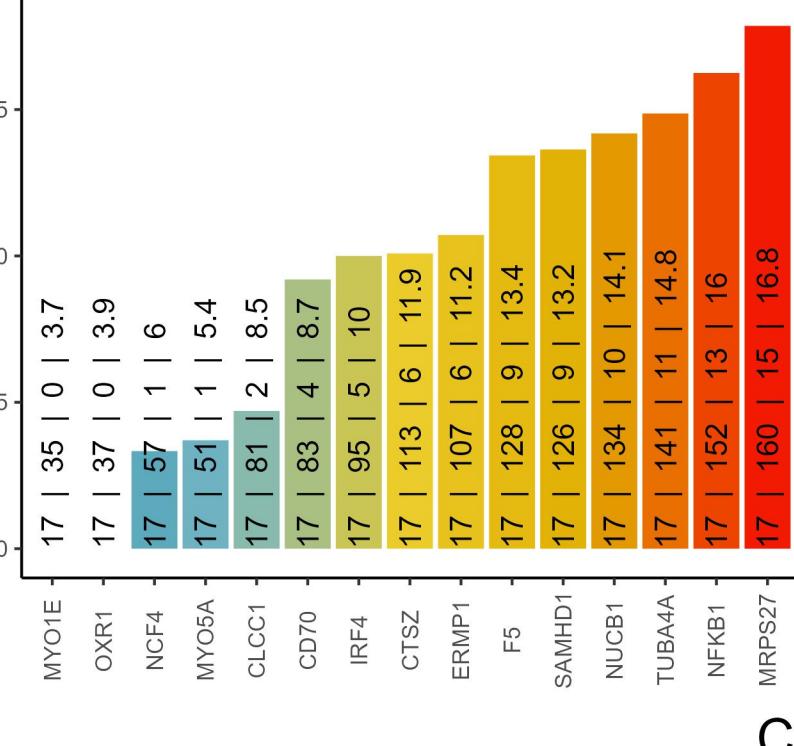
Amount of ATAD5 protein and mutation status by tissue, DB1



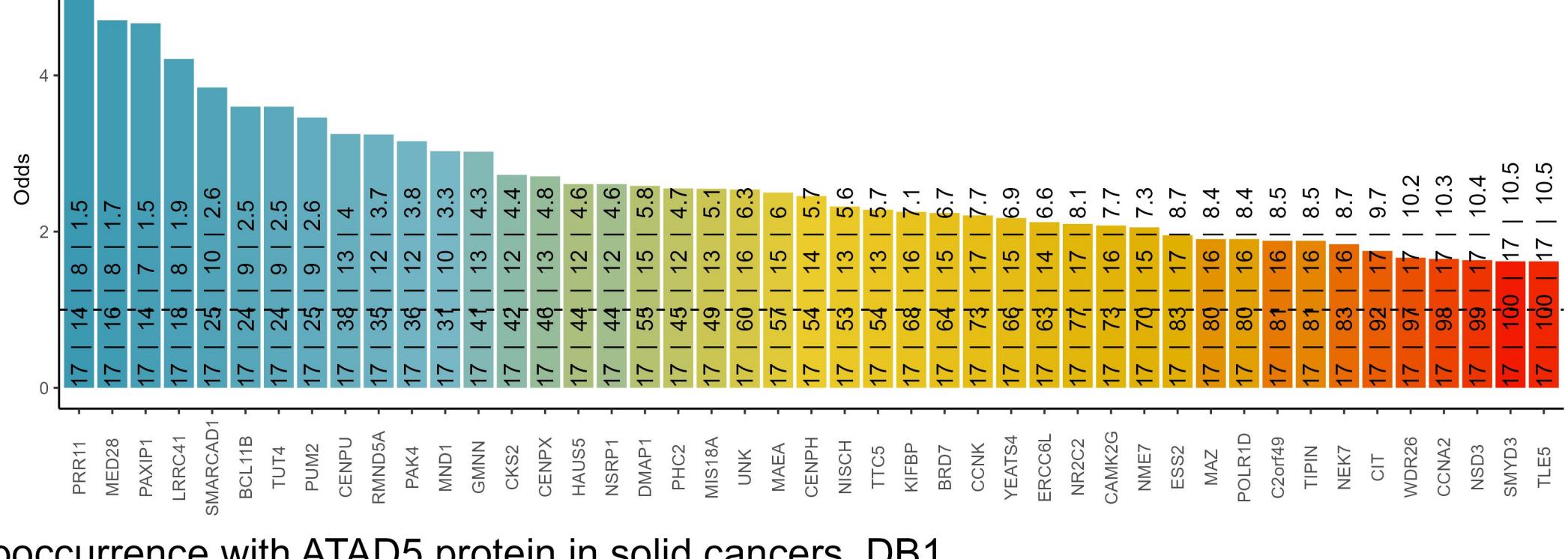
Cooccurrence with ATAD5 protein in blood cancers, DB1

The text in the bars: incidence of ATAD5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



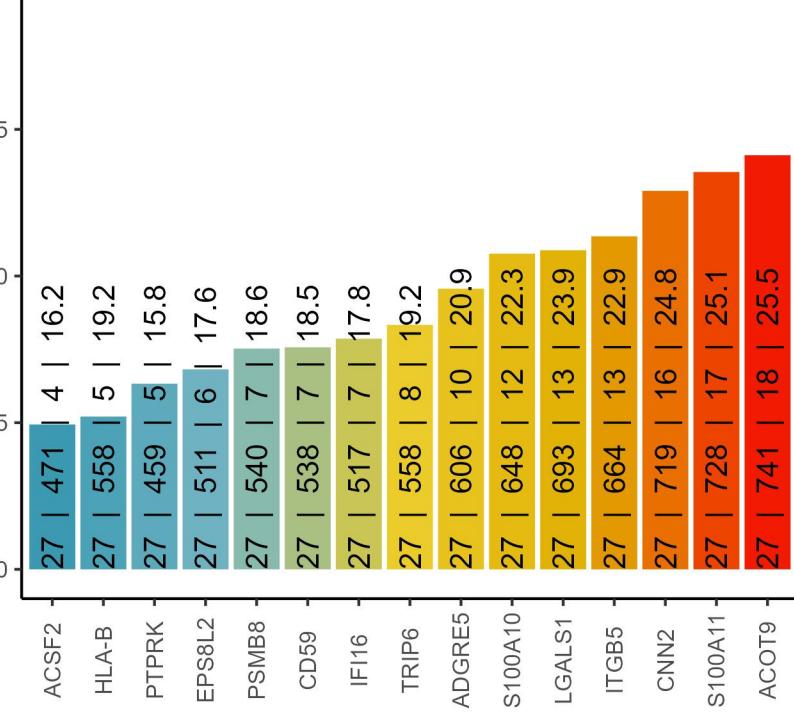
Positive cooccurrence



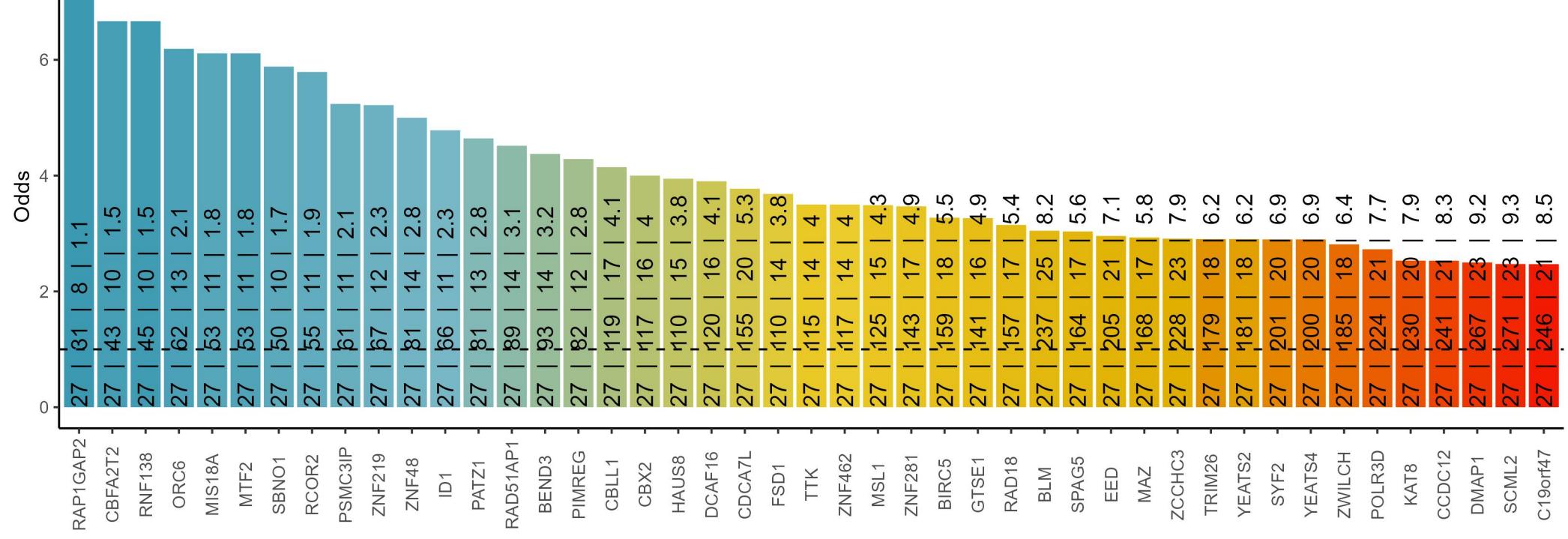
Cooccurrence with ATAD5 protein in solid cancers, DB1

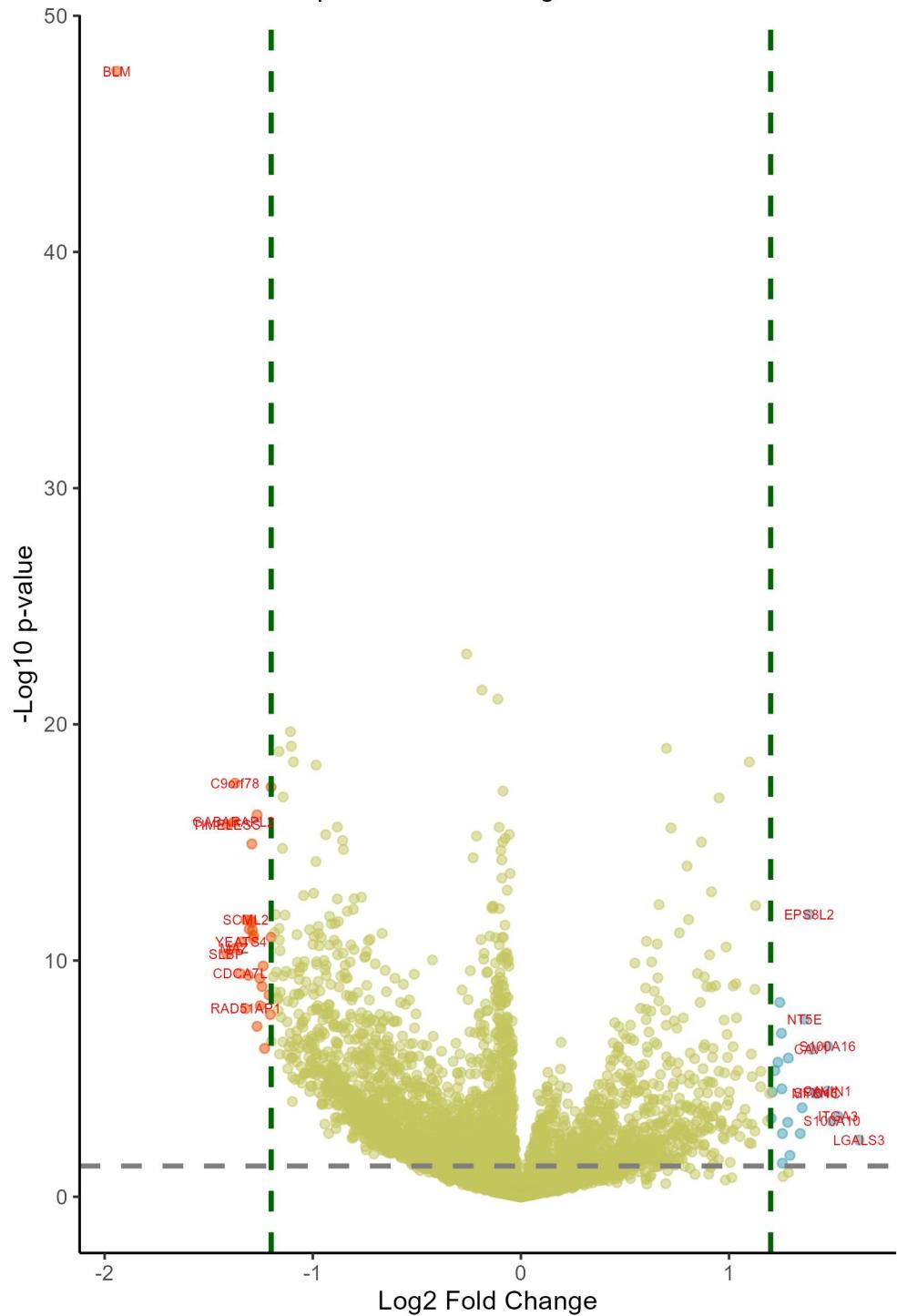
The text in the bars: incidence of ATAD5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



Positive cooccurrence



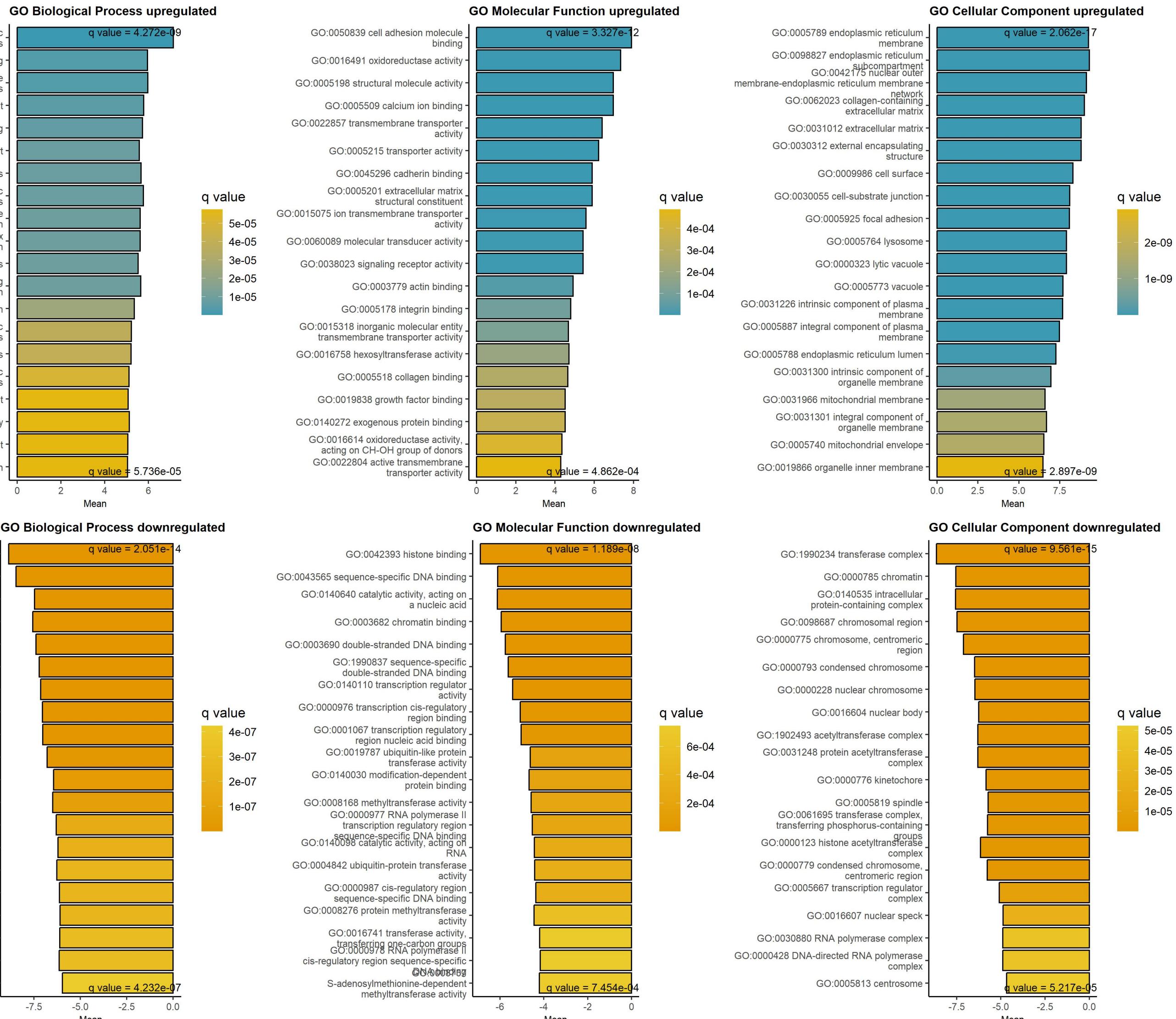


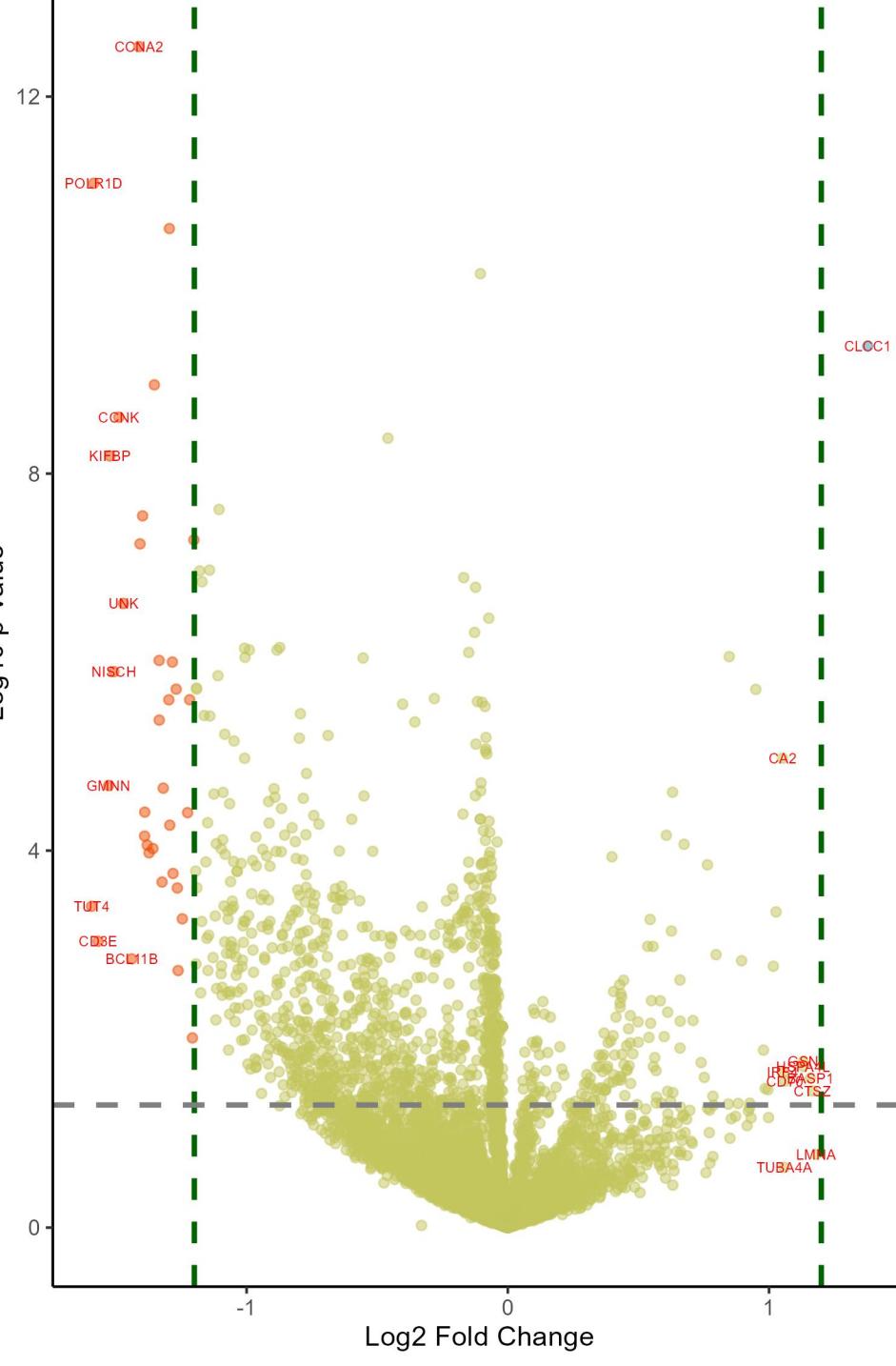
Downregulated at low/absent ATAD5

Upregulated at low/absent ATAD5

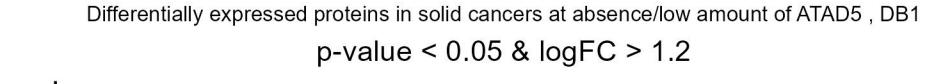
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.94	7.40e-45	BLM	BLM RecQ like helicase	1.62	1.44e-02	LGALS3	galectin 3
-1.41	3.18e-09	SLBP	stem-loop binding protein	1.52	2.20e-03	ITGA3	integrin subunit alpha 3
-1.41	5.83e-14	TIMELESS	timeless circadian regulator	1.49	3.21e-03	S100A10	S100 calcium binding protein A10
-1.38	4.80e-14	GABARPL2	GABA type A receptor associated pro	1.47	6.74e-06	S100A16	S100 calcium binding protein A16
-1.38	2.03e-09	MAZ	MYC associated zinc finger protein	1.47	2.82e-04	CAVIN1	caveolae associated protein 1
-1.37	1.58e-15	C9orf78	chromosome 9 open reading frame 78	1.42	3.32e-04	MYO1C	myosin IC
-1.35	1.58e-08	CDCA7L	cell division cycle associated 7 li	1.42	3.24e-04	SFXN3	sideroflexin 3
-1.34	1.19e-09	YEATS4	YEATS domain containing 4	1.4	8.79e-06	CAV1	caveolin 1
-1.32	3.00e-07	RAD51AP1	RAD51 associated protein 1	1.39	1.31e-10	EPS8L2	EPS8 like 2
-1.32	2.03e-10	SCML2	Scm polycomb group protein like 2	1.36	7.34e-07	NT5E	5'-nucleotidase ecto
-1.31	1.85e-08	RAD18	RAD18 E3 ubiquitin protein ligase	1.35	1.10e-03	SQOR	sulfide quinone oxidoreductase
-1.31	4.50e-10	POLR3D	RNA polymerase III subunit D	1.34	8.70e-03	MYOF	myoferlin
-1.3	2.03e-10	SNRNP27	small nuclear ribonucleoprotein U4/U6/U8/U11	1.29	4.77e-02	PLP2	proteolipid protein 2
-1.29	2.47e-13	BRD3	bromodomain containing 3	1.28	1.76e-01	S100A6	S100 calcium binding protein A6
-1.29	2.47e-10	CCDC12	coiled-coil domain containing 12	1.28	1.79e-05	RRAS	RAS related
-1.29	4.72e-10	CORO1A	coronin 1A	1.28	3.54e-03	ITGAV	integrin subunit alpha V
-1.29	9.32e-10	TDP2	tyrosyl-DNA phosphodiesterase 2	1.26	2.39e-01	LGALS1	galectin 1
-1.28	7.57e-10	ZCCHC3	zinc finger CCHC-type containing 3	1.26	8.71e-03	CTSZ	cathepsin Z
-1.27	2.51e-14	ZMYM3	zinc finger MYM-type containing 3	1.26	8.67e-02	GNG12	G protein subunit gamma 12
-1.27	1.30e-06	DCAF16	DDB1 and CUL4 associated factor 16	1.25	2.34e-04	EGFR	epidermal growth factor receptor
-1.25	2.30e-08	BRD7	bromodomain containing 7	1.25	2.32e-06	ITGB4	integrin subunit beta 4
-1.25	2.31e-07	GTSE1	G2 and S-phase expressed 1	1.24	1.74e-07	MMP14	matrix metallopeptidase 14
-1.24	4.64e-08	POLR1D	RNA polymerase I and III subunit D	1.23	2.57e-05	ADAM9	ADAM metallopeptidase domain 9
-1.24	8.45e-09	RNASEH2B	ribonuclease H2 subunit B	1.22	5.11e-05	CD151	CD151 molecule (Raph blood group)
-1.23	8.15e-06	ORC6	origin recognition complex subunit	1.21	3.08e-04	CD59	CD59 molecule (CD59 blood group)
-1.21	9.39e-08	SPC25	SPC25 component of NDC80 kinetochor	1.2	2.61e-03	NQO1	NAD(P)H quinone dehydrogenase 1
-1.2	4.93e-07	SPAG5	sperm associated antigen 5	1.19	3.37e-04	PPIC	peptidylprolyl isomerase C
-1.2	8.39e-10	STK4	serine/threonine kinase 4	1.18	3.15e-03	NECTIN2	nectin cell adhesion molecule 2
-1.2	2.15e-15	EZH2	enhancer of zeste 2 polycomb repres	1.15	5.47e-05	ITPRID2	ITPR interacting domain containing

GAGE analysis on upregulated and downregulated proteins at low/absent ATAD5 protein, DB1





logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.59	1.42e-02	TUT4	terminal uridylyl transferase 4	1.38	4.91e-07	CLCC1	chloride channel CLIC like 1
-1.59	1.84e-08	POLR1D	RNA polymerase I and III subunit D	1.18	4.19e-01	LMNA	lamin A/C
-1.57	2.21e-02	CD3E	CD3 epsilon subunit of T-cell recep	1.17	1.52e-01	CTSZ	cathepsin Z
-1.53	2.12e-03	GMNN	geminin DNA replication inhibitor	1.16	1.20e-01	BASP1	brain abundant membrane attached si
-1.52	4.32e-06	KIFBP	kinesin family binding protein	1.13	9.73e-02	HSPA4L	heat shock protein family A (Hsp70)
-1.51	2.54e-04	NISCH	nischarin	1.13	8.83e-02	GSN	gelsolin
-1.49	2.09e-06	CCNK	cyclin K	1.06	1.28e-01	CD70	CD70 molecule
-1.47	7.94e-05	UNK	unk zinc finger	1.06	5.04e-01	TUBA4A	tubulin alpha 4a
-1.44	2.87e-02	BCL11B	BAF chromatin remodeling complex su	1.05	1.09e-01	IRF4	interferon regulatory factor 4
-1.41	9.80e-10	CCNA2	cyclin A2	1.05	1.14e-03	CA2	carbonic anhydrase 2
-1.41	2.64e-05	PLCG1	phospholipase C gamma 1	1.03	1.53e-02	ERMP1	endoplasmic reticulum metallopeptid
-1.4	1.56e-05	MAZ	MYC associated zinc finger protein	1.02	3.23e-02	LGALS3	galectin 3
-1.39	4.86e-03	CENPUP	centromere protein U	1	2.36e-01	MTAP	methylthioadenosine phosphorylase
-1.39	3.33e-03	MIS18A	MIS18 kinetochore protein A	1	1.49e-01	NUCB1	nucleobindin 1
-1.38	5.59e-03	ZAP70	zeta chain of T cell receptor assoc	0.99	1.46e-01	F5	coagulation factor V
-1.37	6.22e-03	PHC2	polyhomeotic homolog 2	0.98	7.16e-02	PLP2	proteolipid protein 2
-1.36	6.01e-03	LEF1	lymphoid enhancer binding factor 1	0.95	3.41e-04	NCF4	neutrophil cytosolic factor 4
-1.35	1.09e-06	SLBP	stem-loop binding protein	0.93	2.37e-01	MVP	major vault protein
-1.33	2.06e-04	ZMAT2	zinc finger matrin-type 2	0.93	1.88e-01	IGF2BP2	insulin like growth factor 2 mRNA b
-1.33	5.60e-04	BRD7	bromodomain containing 7	0.93	2.02e-01	SQOR	sulfide quinone oxidoreductase
-1.32	9.88e-03	CENPX	centromere protein X	0.92	2.12e-01	SAMHD1	SAM and HD domain containing deoxyn
-1.32	2.22e-03	MAEA	macrophage erythroblast attacher, E	0.92	2.69e-01	DTD1	D-aminoacyl-tRNA deacylase 1
-1.3	4.07e-04	CAMK2G	calcium/calmodulin dependent protei	0.89	2.95e-02	PLOD3	procollagen-lysine,2-oxoglutarate 5
-1.3	4.18e-08	BLM	BLM RecQ like helicase	0.88	1.88e-01	CTSS	cathepsin S
-1.29	4.01e-03	IREB2	iron responsive element binding pro	0.87	2.32e-01	HSPA2	heat shock protein family A (Hsp70)
-1.28	2.07e-04	C2orf49	chromosome 2 open reading frame 49	0.86	2.40e-01	STOM	stomatin
-1.28	8.55e-03	LCK	LCK proto-oncogene, Src family tyro	0.85	3.27e-01	ALB	albumin
-1.27	3.41e-04	BRD3	bromodomain containing 3	0.85	2.00e-04	NME3	NME/NM23 nucleoside diphosphate kin
-1.27	1.10e-02	STK38	serine/threonine kinase 38	0.84	1.90e-01	GPD2	glycerol-3-phosphate dehydrogenase

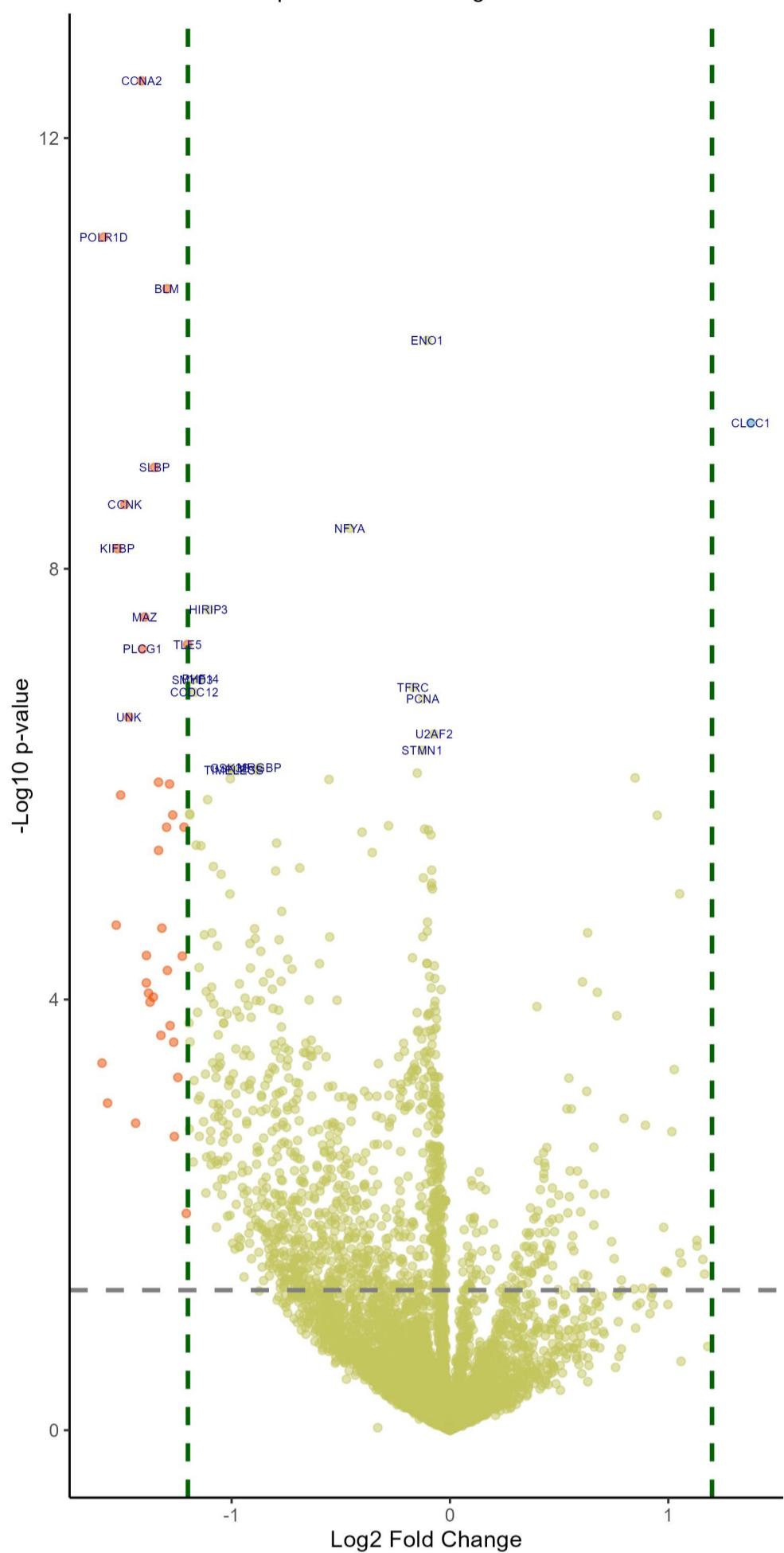


Downregulated in solid cancers at low/absent ATAD5 Upregulated in solid cancers at low/absent ATAD5

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2	1.52e-25	BLM	BLM RecQ like helicase	1.83	3.96e-01	LGALS1	galectin 1
-1.54	2.45e-06	CDCA7L	cell division cycle associated 7 li	1.8	1.92e-08	HLA-B	major histocompatibility complex, c
-1.52	2.14e-09	SCML2	Scm polycomb group protein like 2	1.74	2.78e-05	CD59	CD59 molecule (CD59 blood group)
-1.44	3.24e-15	EZH2	enhancer of zeste 2 polycomb repres	1.52	1.23e-07	PSMB8	proteasome 20S subunit beta 8
-1.41	1.23e-04	DCAF16	DDB1 and CUL4 associated factor 16	1.44	3.09e-05	TRIP6	thyroid hormone receptor interactor
-1.39	7.31e-05	CRMP1	collapsin response mediator protein	1.44	1.02e-04	ADGRE5	adhesion G protein-coupled receptor
-1.37	6.06e-04	ASRGL1	asparagine and isoaspartyl peptid	1.43	1.12e-02	B2M	beta-2-microglobulin
-1.34	1.69e-05	YEATS4	YEATS domain containing 4	1.42	1.52e-01	S100A10	S100 calcium binding protein A10
-1.33	4.16e-05	YEATS2	YEATS domain containing 2	1.41	2.43e-02	SQOR	sulfide quinone oxidoreductase
-1.32	2.04e-06	TIMELESS	timeless circadian regulator	1.4	8.81e-02	CAVIN1	caveolae associated protein 1
-1.31	8.63e-09	ZMYM3	zinc finger MYM-type containing 3	1.4	9.13e-05	PSMB9	proteasome 20S subunit beta 9
-1.3	2.27e-08	BRD3	bromodomain containing 3	1.4	5.33e-05	IFI16	interferon gamma inducible protein
-1.29	1.31e-05	POLR3D	RNA polymerase III subunit D	1.39	2.61e-02	S100A16	S100 calcium binding protein A16
-1.28	7.08e-06	ZMYM4	zinc finger MYM-type containing 4	1.39	4.78e-03	NT5E	5'-nucleotidase ecto
-1.28	2.58e-04	RAD51AP1	RAD51 associated protein 1	1.38	4.83e-04	EPS8L2	EPS8 like 2
-1.27	2.22e-04	GLDC	glycine decarboxylase	1.36	1.82e-01	ITGA3	integrin subunit alpha 3
-1.27	1.68e-04	SPAG5	sperm associated antigen 5	1.35	1.64e-01	CD44	CD44 molecule (Indian blood group)
-1.26	4.98e-06	C9orf78	chromosome 9 open reading frame 78	1.35	4.87e-08	TAP2	transporter 2, ATP binding cassette
-1.26	4.37e-04	ORC6	origin recognition complex subunit	1.33	5.04e-01	S100A11	S100 calcium binding protein A11
-1.26	1.58e-05	SPINDOC	spindlin interactor and repressor o	1.32	2.78e-01	LGALS3	galectin 3
-1.25	7.83e-08	ZNF24	zinc finger protein 24	1.31	1.20e-01	ITGB5	integrin subunit beta 5
-1.25	1.35e-08	UPF3B	UPF3B regulator of nonsense mediate	1.3	2.97e-02	CAV1	caveolin 1
-1.25	1.37e-05	PEG10	paternally expressed 10	1.28	2.73e-08	ACSF2	acyl-CoA synthetase family member 2
-1.24	5.12e-05	SNRNP27	small nuclear ribonucleoprotein U4/	1.28	4.92e-09	LPCAT2	lysophosphatidylcholine acyltransfe
-1.24	9.16e-05	EED	embryonic ectoderm development	1.26	1.52e-11	TACSTD2	tumor associated calcium signal tra
-1.24	7.83e-05	ZNF768	zinc finger protein 768	1.26	1.41e-03	TAP1	transporter 1, ATP binding cassette
-1.24	4.86e-05	ZCCHC3	zinc finger CCHC-type containing 3	1.25	8.98e-03	CD151	CD151 molecule (Raph blood group)
-1.24	1.70e-03	KIF5C	kinesin family member 5C	1.25	7.32e-22	CYBRD1	cytochrome b reductase 1
-1.23	4.68e-05	GABARPL2	GABA type A receptor associated pro	1.24	7.92e-05	SP100	SP100 nuclear antigen

ATAD5 network, DB1, no Pearson r > 0.3

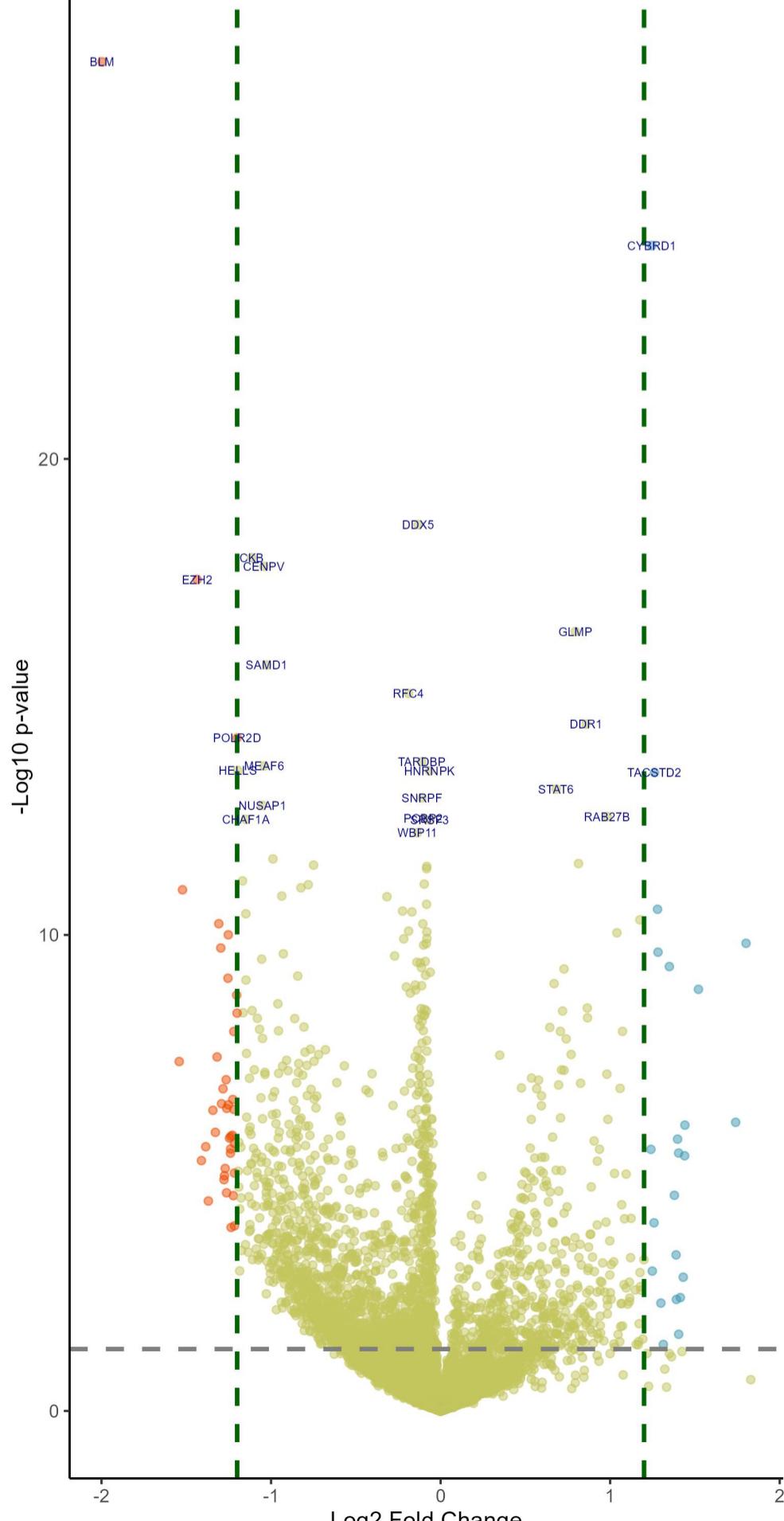
Differentially expressed proteins in blood cancers at absence/low amount of ATAD5 , DB1
p-value < 0.05 & logFC > 1.2



Sorted by p values!
Downregulated in blood cancers at low/absent ATAD5 Upregulated in blood cancers at low/absent ATAD5

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.41	9.80e-10	CCNA2	cyclin A2	1.38	4.91e-07	CLCC1	chloride channel CLIC like 1
-1.59	1.84e-08	POLR1D	RNA polymerase I and III subunit D	0.85	2.00e-04	NME3	NME/NM23 nucleoside diphosphate kin
-1.3	4.18e-08	BLM	BLM RecQ like helicase	0.95	3.41e-04	NCF4	neutrophil cytosolic factor 4
-0.11	1.01e-07	ENO1	enolase 1	1.05	1.14e-03	CA2	carbonic anhydrase 2
-1.35	1.09e-06	SLBP	stem-loop binding protein	0.63	2.32e-03	OXR1	oxidation resistance 1
-1.49	2.09e-06	CCNK	cyclin K	0.61	4.81e-03	MYO1E	myosin IE
-0.46	3.11e-06	NFYA	nuclear transcription factor Y subu	0.67	5.54e-03	MYO5A	myosin VA
-1.52	4.32e-06	KIFBP	kinesin family binding protein	0.4	6.61e-03	MRPS27	mitochondrial ribosomal protein S27
-1.11	1.45e-05	HIRIP3	HIRA interacting protein 3	0.76	7.30e-03	METTL7A	methyltransferase like 7A
-1.4	1.56e-05	MAZ	MYC associated zinc finger protein	1.03	1.53e-02	ERMP1	endoplasmic reticulum metallopeptid
-1.2	2.58e-05	TLE5	TLE family member 5, transcriptiona	0.54	1.66e-02	SH2B2	SH2B adaptor protein 2
-1.41	2.64e-05	PLCG1	phospholipase C gamma 1	0.63	1.94e-02	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-b
-1.14	4.48e-05	PHF14	PHD finger protein 14	0.54	2.34e-02	ALDH1L2	aldehyde dehydrogenase 1 family mem
-1.18	4.48e-05	SMYD3	SET and MYND domain containing 3	0.56	2.34e-02	IRF5	interferon regulatory factor 5
-0.17	4.97e-05	TFRC	transferrin receptor	0.8	2.69e-02	TYMP	thymidine phosphorylase
-1.17	5.19e-05	CCDC12	coiled-coil domain containing 12	0.89	2.95e-02	PLOD3	procollagen-lysine,2-oxoglutarate 5
-0.12	5.63e-05	PCNA	proliferating cell nuclear antigen	1.02	3.23e-02	LGALS3	galectin 3
-1.47	7.94e-05	UNK	unk zinc finger	0.66	4.17e-02	TRADD	TNFRSF1A associated via death domai
-0.07	1.08e-04	U2AF2	U2 small nuclear RNA auxiliary fact	0.44	4.17e-02	GLT8D1	glycosyltransferase 8 domain contai
-0.13	1.46e-04	STMN1	stathmin 1	0.43	4.45e-02	SLC25A46	solute carrier family 25 member 46
-0.87	1.91e-04	MRGBP	MRG domain binding protein	0.41	4.52e-02	DNAJB2	DnaJ heat shock protein family (Hsp
-1.01	1.91e-04	GSK3B	glycogen synthase kinase 3 beta	0.43	4.52e-02	SHTN1	shootin 1
-0.99	1.91e-04	TIMELESS	timeless circadian regulator	0.44	4.52e-02	HMOX1	heme oxygenase 1
-0.88	1.91e-04	RTN4	reticulon 4	0.55	4.52e-02	BCS1L	BCS1 homolog, ubiquinol-cytochrome
-0.15	1.95e-04	RBBP4	RB binding protein 4, chromatin rem	0.58	4.52e-02	MCAM	melanoma cell adhesion molecule
-1.01	2.00e-04	BRD2	bromodomain containing 2	0.13	4.52e-02	DNAJA3	DnaJ heat shock protein family (Hsp
-0.55	2.00e-04	PRPF18	pre-mRNA processing factor 18	0.43	4.52e-02	ITGAV	integrin subunit alpha V
-1.33	2.06e-04	ZMAT2	zinc finger matrin-type 2	0.43	4.52e-02	HACL1	2-hydroxyacyl-CoA lyase 1
-1.28	2.07e-04	C2orf49	chromosome 2 open reading frame 49	0.1	4.52e-02	AFG3L2	AFG3 like matrix AAA peptidase subu
-1.51	2.54e-04	NISCH	nischarin	0.61	4.52e-02	GPAA1	glycosylphosphatidylinositol anchor
-1.11	2.73e-04	GID8	GID complex subunit 8 homolog	0.1	4.52e-02	NDUFS3	NADH:ubiquinone oxidoreductase core
-1.19	3.41e-04	URM1	ubiquitin related modifier 1	0.14	4.52e-02	UQCRC2	ubiquinol-cytochrome c reductase co
-1.27	3.41e-04	BRD3	bromodomain containing 3	0.47	4.52e-02	RAB24	RAB24, member RAS oncogene family
-1.19	3.41e-04	SPC25	SPC25 component of NDC80 kinetochor	0.41	4.52e-02	CGN	cingulin
-0.28	4.07e-04	SCYL2	SCY1 like pseudokinase 2	0.16	4.52e-02	FKBP2	FKBP prolyl isomerase 2
-1.22	4.07e-04	GTSE1	G2 and S-phase expressed 1	0.71	4.52e-02	ALDH2	aldehyde dehydrogenase 2 family mem
-1.3	4.07e-04	CAMK2G	calcium/calmodulin dependent protei	0.66	4.52e-02	ACOT8	acyl-CoA thioesterase 8
-0.12	4.12e-04	CNBP	CCHC-type zinc finger nucleic acid	0.5	4.52e-02	RPP25	ribonuclease P and MRP subunit p25
-0.1	4.12e-04	NASP	nuclear autoantigenic sperm protein	0.55	4.52e-02	IE173	interferon induced protein with tet

Differentially expressed proteins in solid cancers at absence/low amount of ATAD5 , DB1
p-value < 0.05 & logFC > 1.2

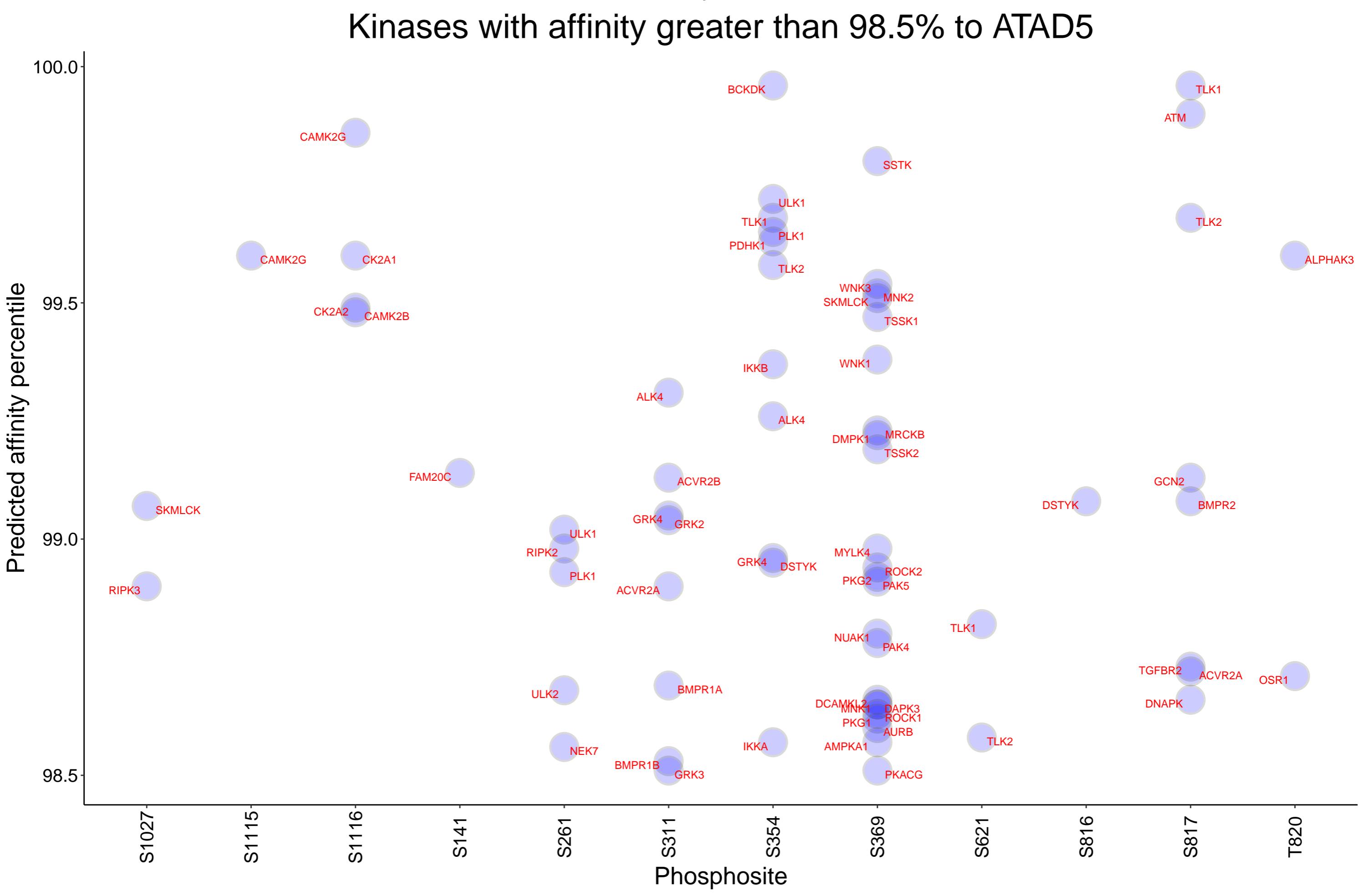
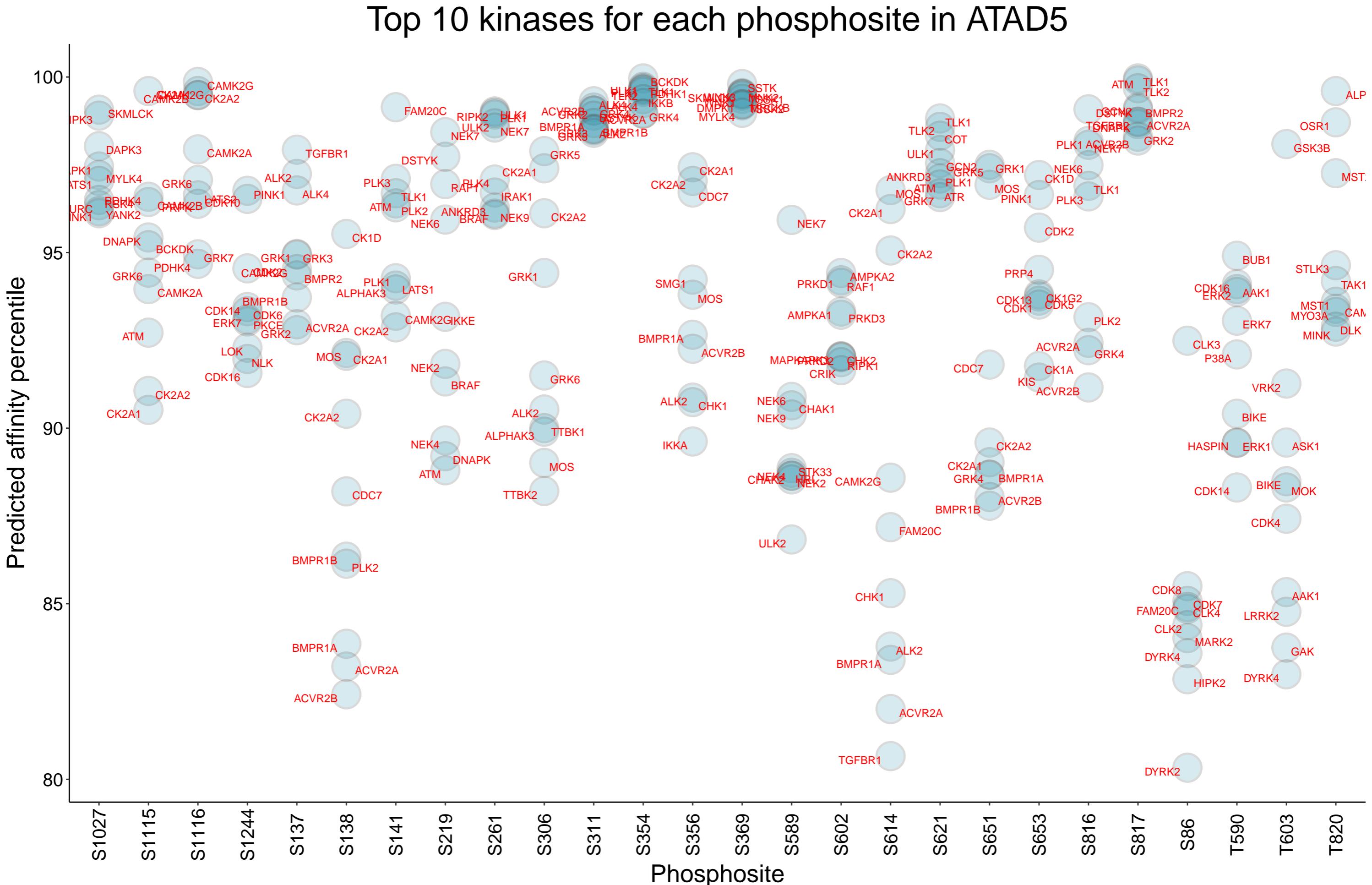


Sorted by p values!
Downregulated in solid cancers at low/absent ATAD5 Upregulated in solid cancers at low/absent ATAD5

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2	1.52e-25	BLM	BLM RecQ like helicase	1.25	7.32e-22	CYBRD1	cytochrome b reductase 1
-0.13	3.98e-16	DDX5	DEAD-box helicase 5	0.8	3.52e-14	GLMP	glycosylated lysosomal membrane pro
-1.11	1.58e-15	CKB	creatine kinase B	0.86	2.26e-12	DDR1	discoidin domain receptor tyrosine
-1.04	2.00e-15	CENPV	centromere protein V	1.26	1.52e-11	TACSTD2	tumor associated calcium signal tra
-1.44	3.24e-15	EZH2	enhancer of zeste 2 polycomb repres	0.68	3.18e-11	STAT6	signal transducer and activator of
-1.03	1.57e-13	SAMD1	sterile alpha motif domain containi	0.98	1.03e-10	RAB27B	RAB27B, member RAS oncogene family
-0.19	5.61e-13	RFC4	replication factor C subunit 4	0.81	7.80e-10	TYMP	thymidine phosphorylase
-1.2	4.03e-12	POLR2D	RNA polymerase II subunit D	1.28	4.92e-09	LPCAT2	lysophosphatidylcholine acyltransfe
-0.11	1.17e-11	TARDBP	TAR DNA binding protein	1.18	7.45e-09	RAC2	Rac family small GTPase 2
-1.04	1.34e-11	MEAF6	MYST/Esa1 associated factor 6	1.04	1.25e-08	GALE	UDP-galactose-4-epimerase
-1.2	1.49e-11	HELLS	helicase, lymphoid specific	1.8	1.92e-08	HLA-B	major histocompatibility complex, c
-0.06	1.49e-11	HNRNPK	heterogeneous nuclear ribonucleopro	1.28	2.73e-08	ACSF2	acyl-CoA synthetase family member 2
-0.11	4.61e-11	SNRPF	small nuclear ribonucleoprotein pol	1.35	4.87e-08	TAP2	transporter 2, ATP binding cassette
-1.05	6.29e-11	NUSAP1	nucleolar and spindle associated pr	0.73	5.31e-08	ALDH3B1	aldehyde dehydrogenase 3 family mem
-0.1	1.06e-10	PCBP2	poly(rC) binding protein 2	0.67	9.87e-08	NQO2	N-ribosyldihydronicotinamide:quinon
-1.15	1.06e-10	CHAF1A	chromatin assembly factor 1 subunit	1.52	1.23e-07	PSMB8	proteasome 20S subunit beta 8
-0.06	1.06e-10	SRSF3	serine and arginine rich splicing f	0.87	2.85e-07	PDLIM2	PDZ and LIM domain 2
-0.14	1.90e-10	WBP11	WW domain binding protein 11	0.72	3.10e-07	KRT13	keratin 13
-0.99	6.47e-10	SUZ12	SUZ12 polycomb repressive complex 2	0.87	4.02e-07	GOLGA1	golgin A1
-0.75	8.10e-10	PPHLN1	peripherin 1	0.64	5.94e-07	PSMB10	proteasome 20S subunit beta 10
-0.08	8.33e-10	HNRNPM	heterogeneous nuclear ribonucleopro	1.07	6.82e-07	PTPRK	protein tyrosine phosphatase recept
-0.08	8.99e-10	SFPQ	splicing factor proline and glutami	0.71	6.82e-07	TRIM16	tripartite motif containing 16
-1.17	1.57e-09	GNL3L	G protein nucleolar 3 like	0.74	9.55e-07	GSDME	gasdermin E
-0.1	1.77e-09	HNRNPH1	heterogeneous nuclear ribonucleopro	0.77	1.86e-06	IFI35	interferon induced protein 35
-0.78	1.78e-09	BAX	BCL2 associated X, apoptosis regula	0.35	1.91e-06	PICALM	phosphatidylinositol binding clathr
-0.82	2.00e-09	PPP1CC	protein phosphatase 1 catalytic sub	0.71	3.44e-06	SSH3	slingshot protein phosphatase 3
-1.52	2.14e-09	SCML2	Scm polycomb group protein like 2	0.73	3.49e-06	KRT6A	keratin 6A
-0.94	2.82e-09	FRG1	FSHD region gene 1	0.98	4.02e-06	TNC	tenascin C
-0.32	2.82e-09	PSIP1	PC4 and SFRS1 interacting protein 1	0.54	4.66e-06	ABCC3	ATP binding cassette subfamily C me
-0.08	3.98e-09	HNRNPA1	heterogeneous nuclear ribonucleopro	0.58	5.02e-06	IFIT3	interferon induced protein with tet
-0.22	5.23e-09	CELF1	CUGBP Elav-like family member 1</td				

Insufficient number of paired observations in DB1 for ATAD5

Insufficient number of paired observations in DB1 for ATAD5



No sufficient paired observations in DB1 for ATAD5