

# ATF2

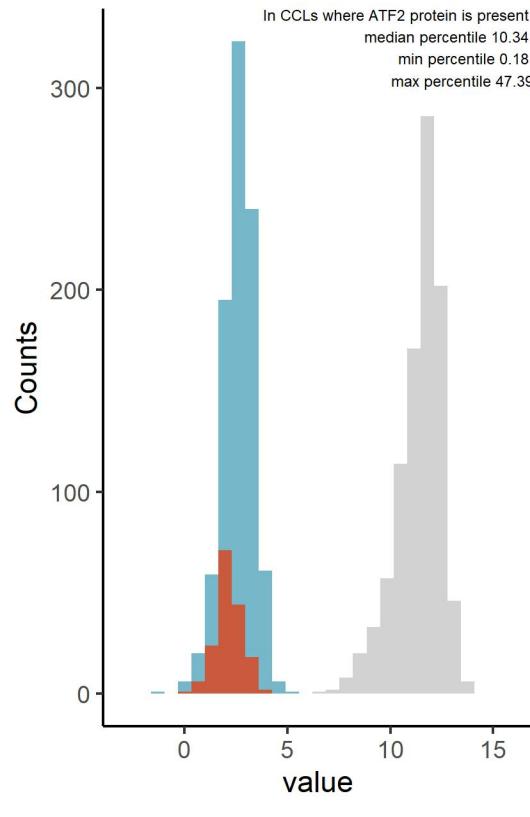
Protein name: ATF2 ; UNIPROT: P15336 ; Gene name: activating transcription factor 2

Ligandable: NA ; Ligandable\_by\_Chem: Yes ; Is\_enzyme: NA (<https://cansar.ai/>)

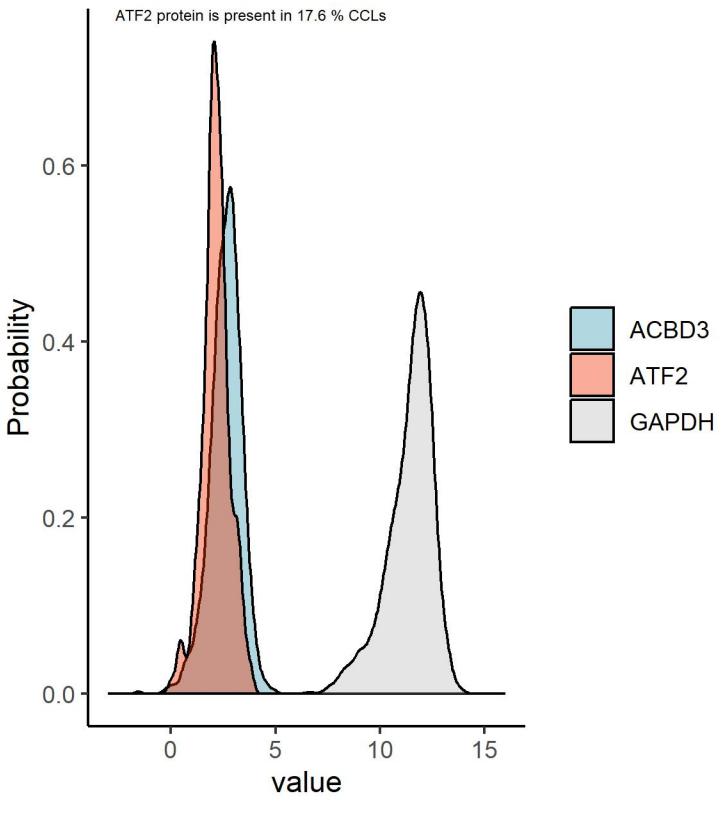
## Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

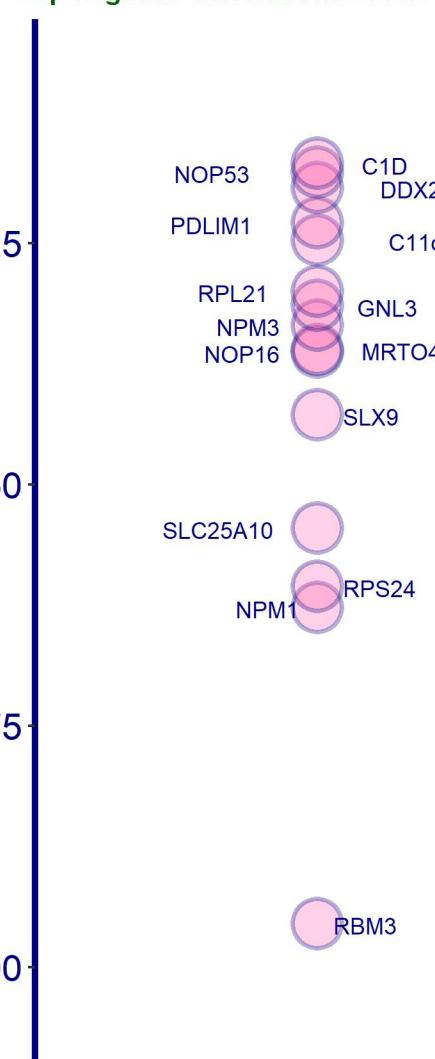
Histogram of ATF2 protein compared to proteins with low and high abundance



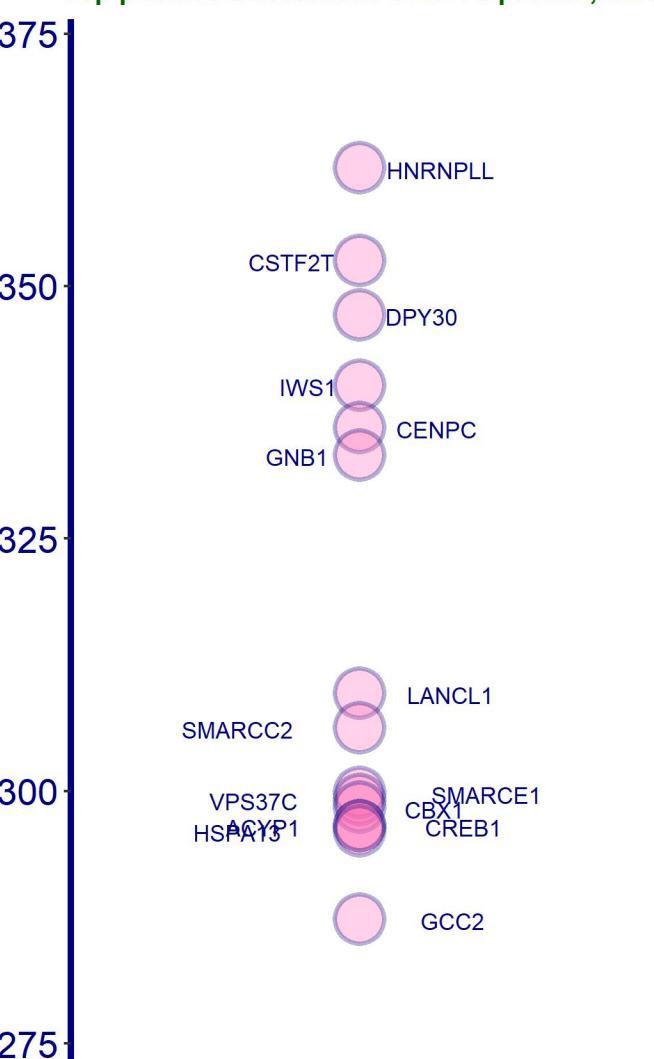
Density plot of ATF2 protein compared to proteins with low and high abundance



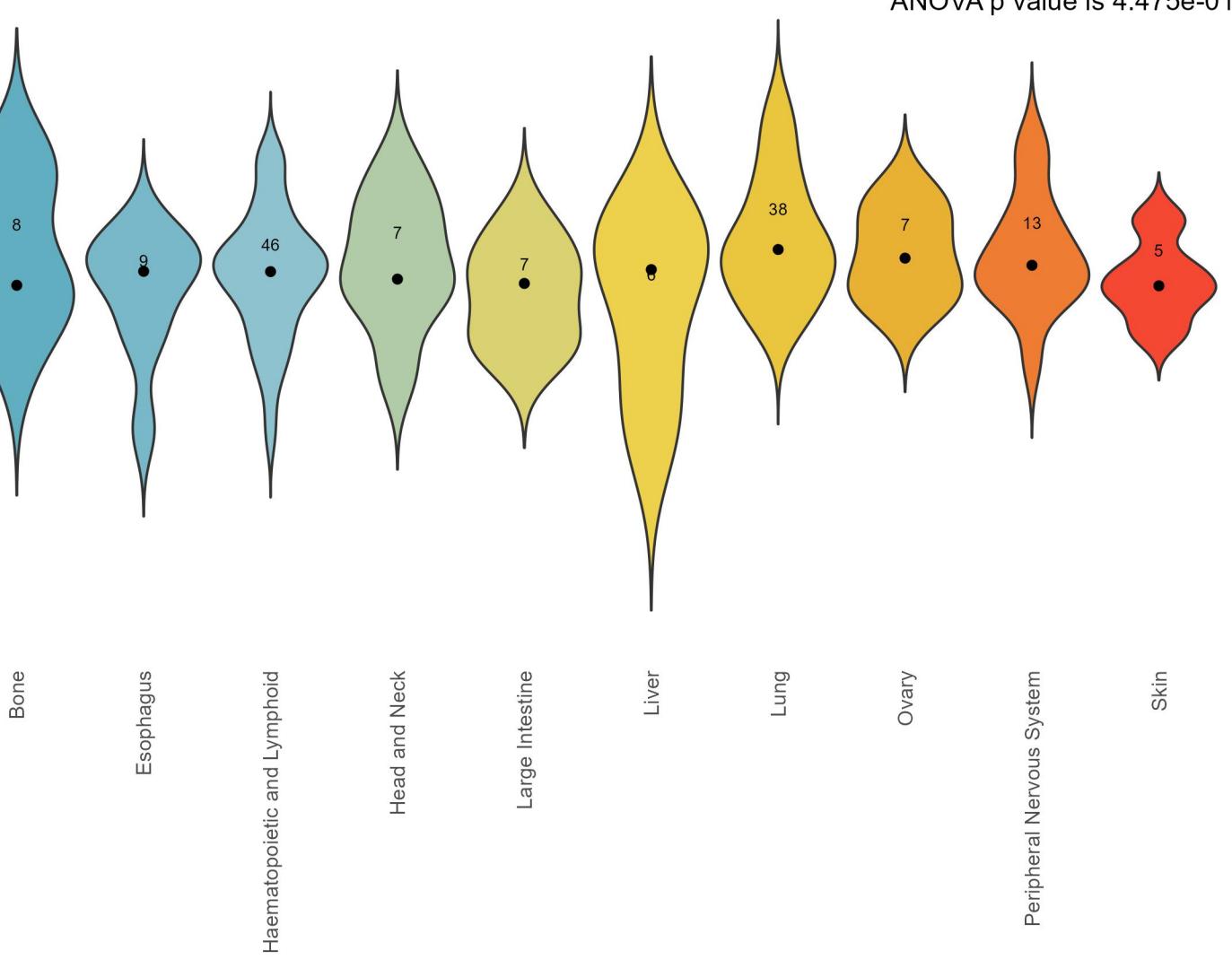
Top negative correlations of ATF2 protein, DB1



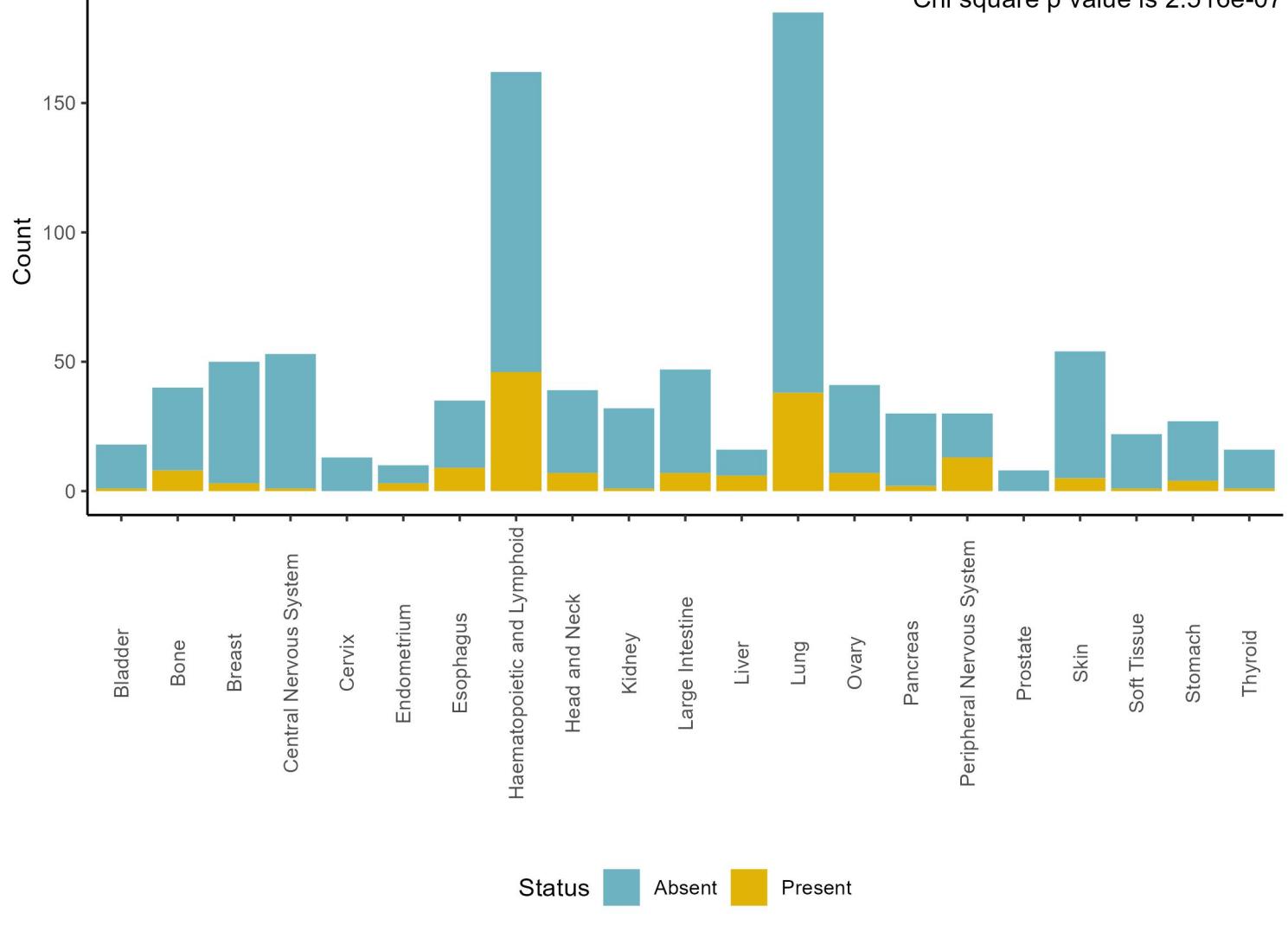
Top positive correlations of ATF2 protein, DB1



Amount of ATF2 protein, number of CCLs where it is present by tissue, DB1



Present and absent ATF2 protein counts by tissue, DB1

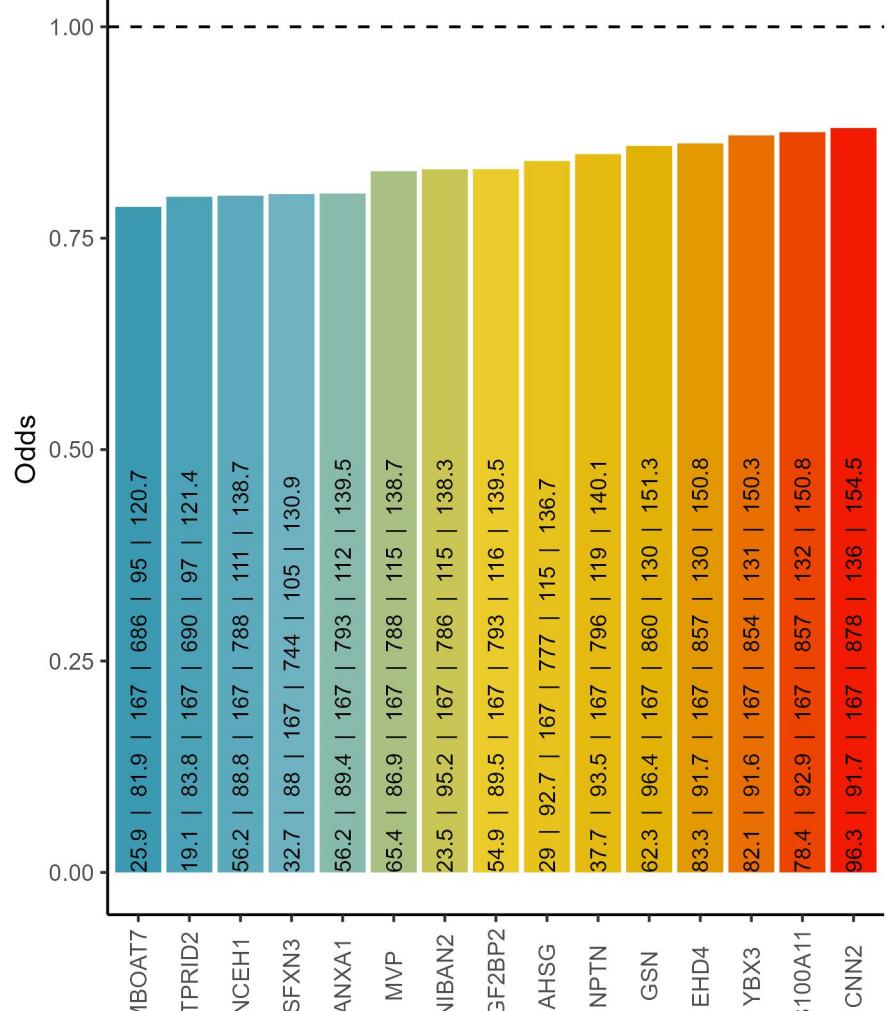


## Cooccurrence with ATF2 protein, DB1

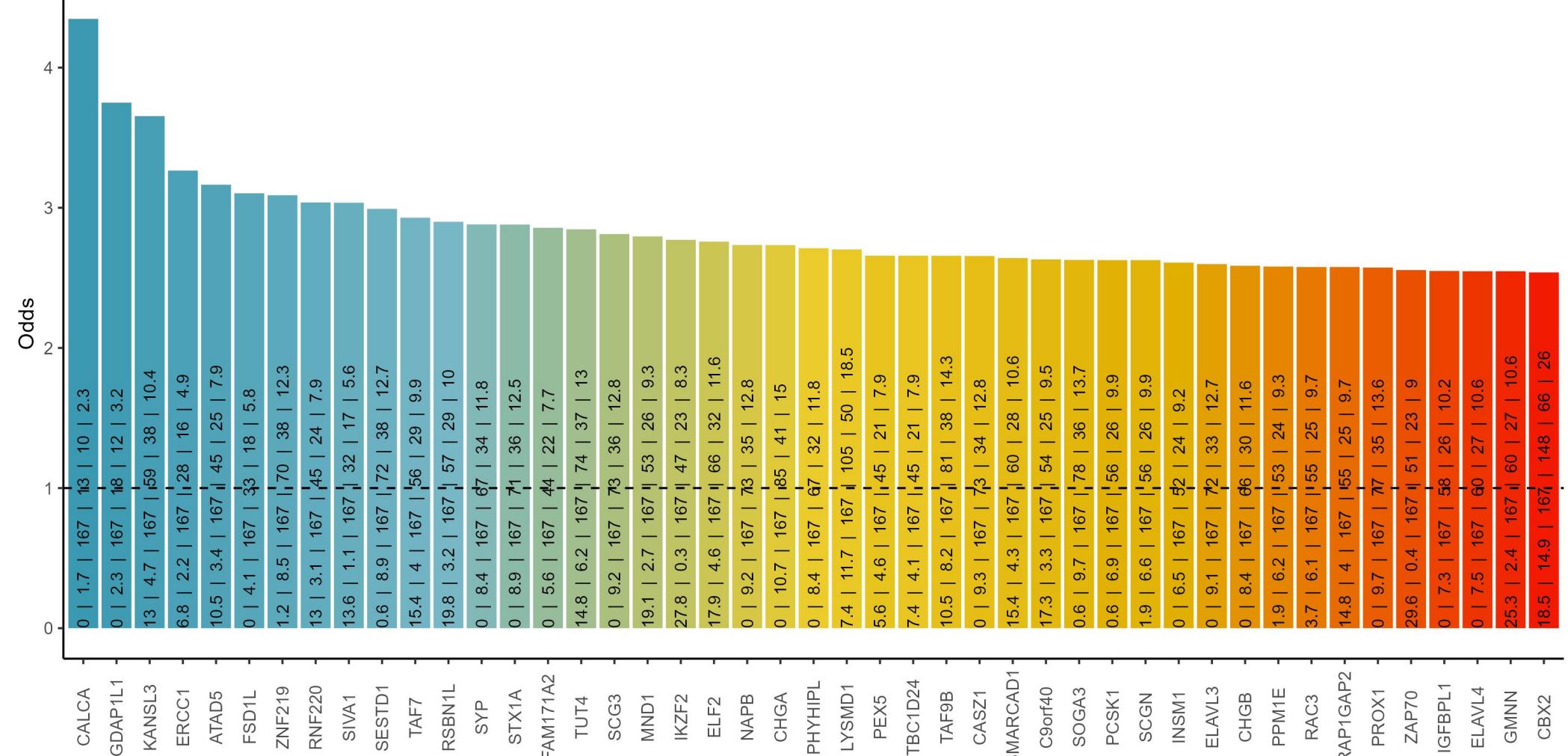
% of ATF2 in blood cancers: 28.4 ; % of ATF2 in solid cancers: 15.3

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ATF2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

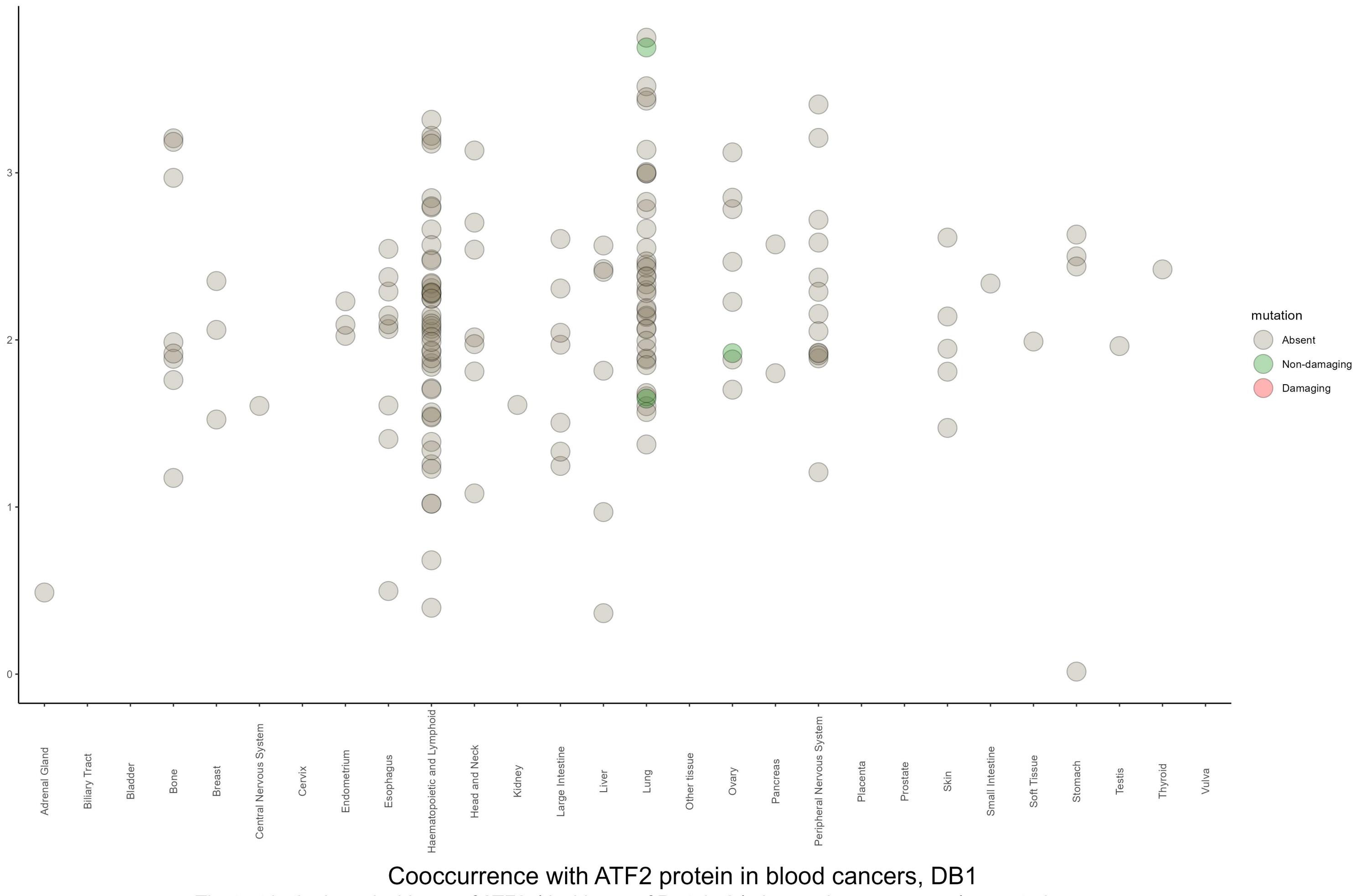
Negative cooccurrence



Positive cooccurrence

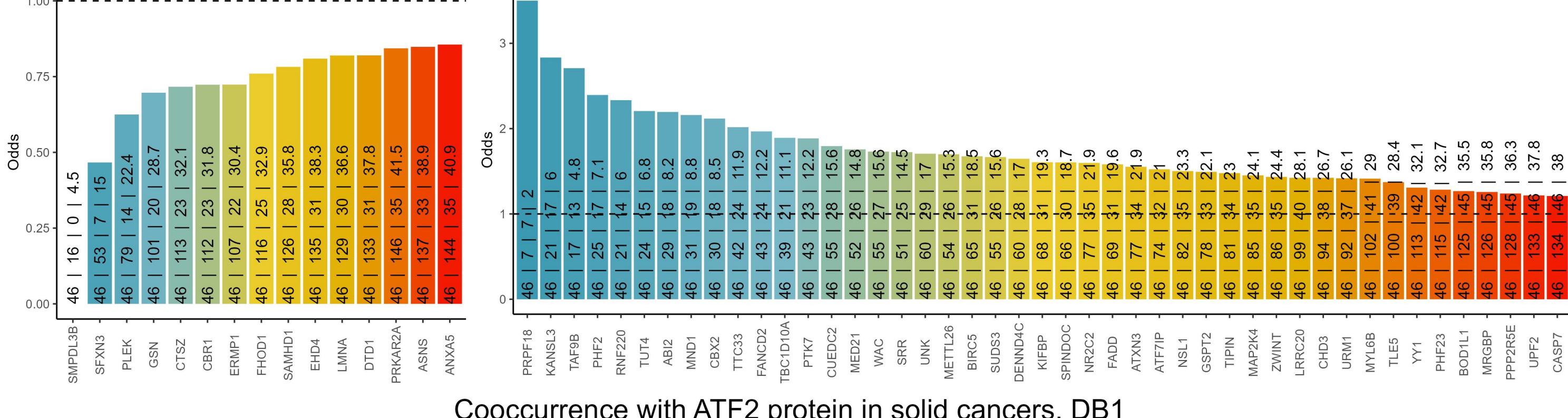


# Amount of ATF2 protein and mutation status by tissue, DB1



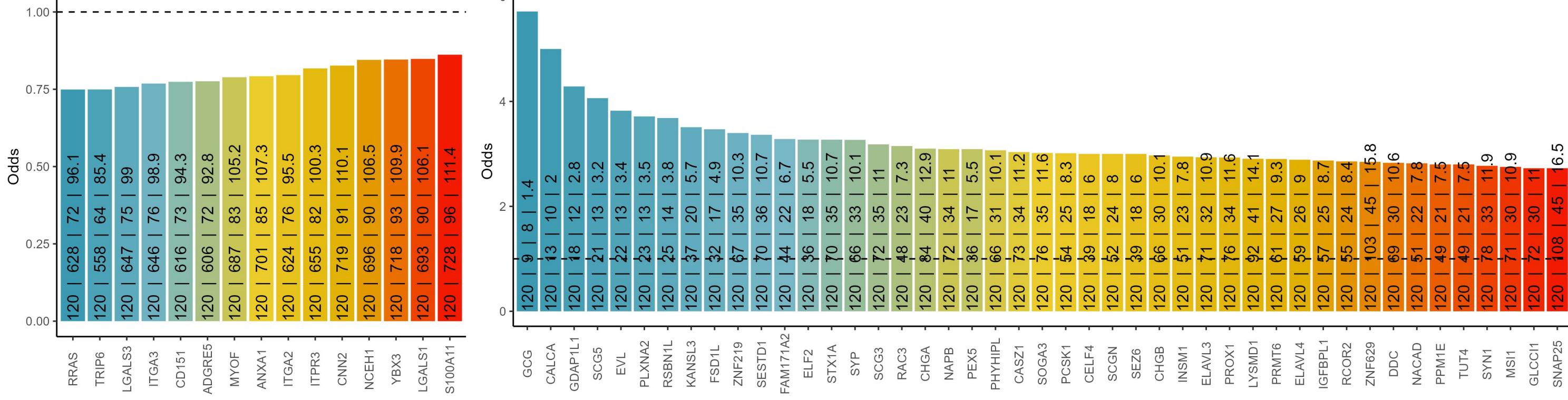
## Cooccurrence with ATF2 protein in blood cancers, DB1

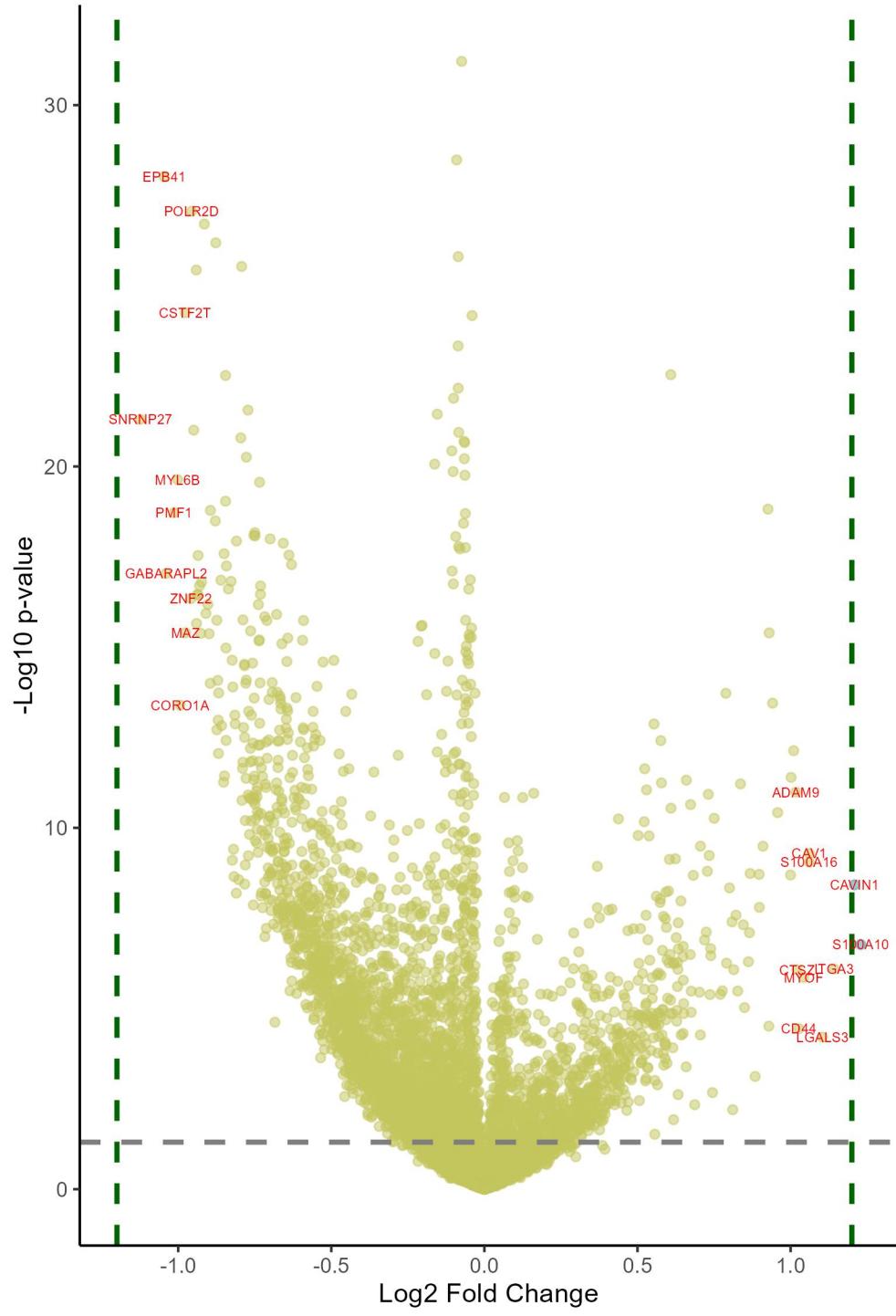
The text in the bars: incidence of ATF2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



## Cooccurrence with ATF2 protein in solid cancers, DB1

The text in the bars: incidence of ATF2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence





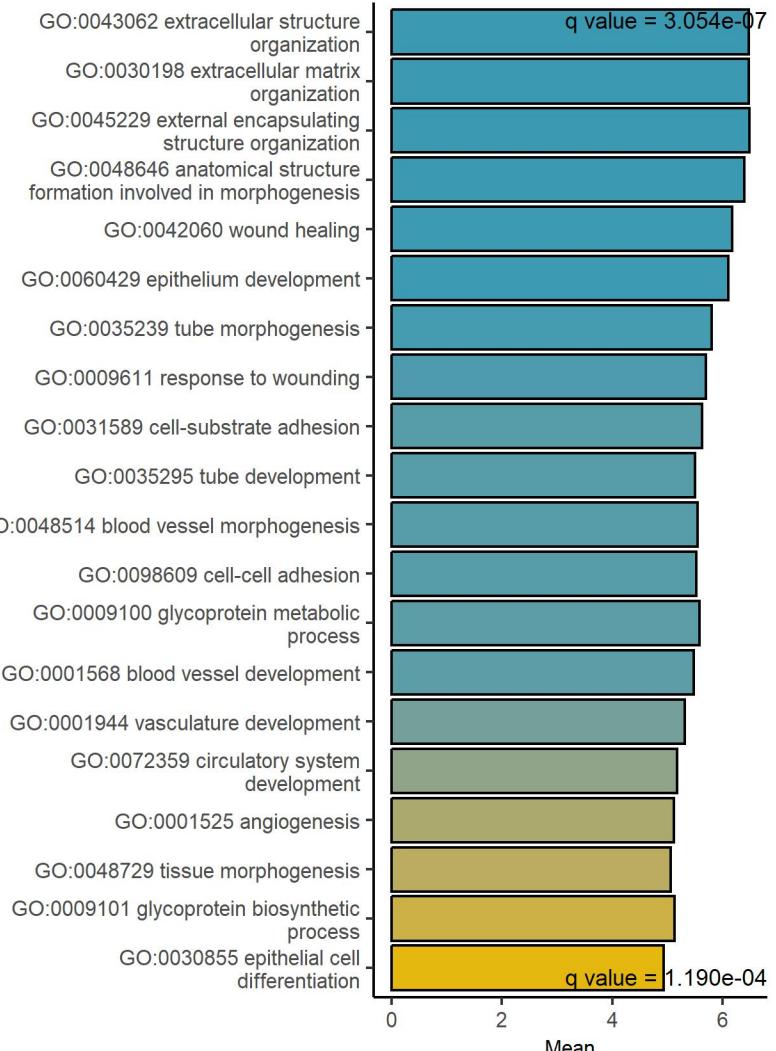
## Downregulated at low/absent ATF2

## Upregulated at low/absent ATF2

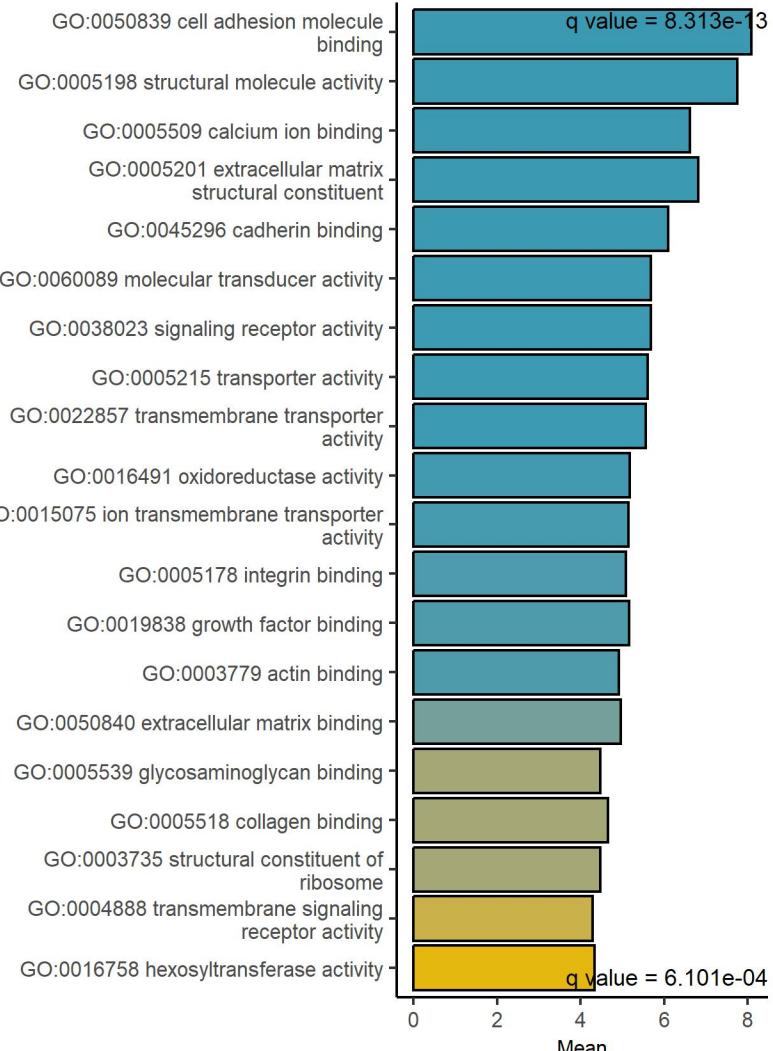
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.12	1.65e-19	SNRNP27	small nuclear ribonucleoprotein U4/64	1.23	1.48e-06	S100A10	S100 calcium binding protein A10
-1.05	1.58e-25	EPB41	erythrocyte membrane protein band 4	1.21	5.44e-08	CAVIN1	caveolae associated protein 1
-1.04	1.07e-15	GABARAPL2	GABA type A receptor associated protein	1.14	5.93e-06	ITGA3	integrin subunit alpha 3
-1.01	3.42e-17	PMF1	polyamine modulated factor 1	1.1	2.61e-04	LGALS3	galectin 3
-1	4.79e-18	MYL6B	myosin light chain 6B	1.06	9.08e-09	CAV1	caveolin 1
-0.99	1.87e-12	CORO1A	coronin 1A	1.06	1.53e-08	S100A16	S100 calcium binding protein A16
-0.98	3.34e-22	CSTF2T	cleavage stimulation factor subunit	1.04	9.53e-06	MYOF	myoferlin
-0.98	3.08e-14	MAZ	MYC associated zinc finger protein	1.03	1.63e-04	CD44	CD44 molecule (Indian blood group)
-0.96	4.31e-15	ZNF22	zinc finger protein 22	1.02	6.13e-06	CTSZ	cathepsin Z
-0.96	1.15e-24	POLR2D	RNA polymerase II subunit D	1.02	2.76e-10	ADAM9	ADAM metallopeptidase domain 9
-0.95	3.13e-19	ZMYM3	zinc finger MYM-type containing 3	1.01	2.56e-11	FHL2	four and a half LIM domains 2
-0.94	2.43e-23	MRGBP	MRG domain binding protein	1	1.18e-10	EPHA2	EPH receptor A2
-0.94	1.82e-14	MDP1	magnesium dependent phosphatase 1	1	3.13e-08	PROCR	protein C receptor
-0.94	3.46e-15	LRRC20	leucine rich repeat containing 20	0.96	8.87e-10	GPX8	glutathione peroxidase 8 (putative)
-0.94	3.40e-15	ZCCHC3	zinc finger CCHC-type containing 3	0.94	1.67e-12	CTSL	cathepsin L
-0.94	3.65e-16	POLR2F	RNA polymerase II, I and III subunits	0.93	3.08e-14	AXL	AXL receptor tyrosine kinase
-0.93	2.10e-15	BRD2	bromodomain containing 2	0.93	1.41e-04	NCEH1	neutral cholesterol ester hydrolase
-0.93	3.15e-14	COPS7B	COP9 signalosome subunit 7B	0.93	2.88e-17	RAB11FIP5	RAB11 family interacting protein 5
-0.92	1.73e-15	KAT8	lysine acetyltransferase 8	0.91	6.06e-09	THBS1	thrombospondin 1
-0.91	2.16e-24	UBXN7	UBX domain protein 7	0.9	1.89e-07	NT5E	5'-nucleotidase ecto
-0.91	1.06e-14	ACYP1	acylphosphatase 1	0.9	3.04e-08	RRAS	RAS related
-0.9	6.14e-15	CCDC12	coiled-coil domain containing 12	0.88	2.32e-03	ANXA1	annexin A1
-0.9	3.17e-14	POU2F1	POU class 2 homeobox 1	0.87	2.89e-08	MMP14	matrix metalloproteinase 14
-0.9	5.56e-13	NSL1	NSL1 component of MIS12 kinetochore	0.87	7.53e-07	PPIC	peptidylprolyl isomerase C
-0.89	3.03e-17	BPTF	bromodomain PHD finger transcriptio	0.86	3.98e-06	ITGA2	integrin subunit alpha 2
-0.88	5.47e-17	PCF11	PCF11 cleavage and polyadenylation	0.85	5.05e-05	RHOC	ras homolog family member C
-0.88	6.14e-24	SCAF8	SR-related CTD associated factor 8	0.85	4.86e-07	ITGB4	integrin subunit beta 4
-0.87	1.52e-14	ZNF24	zinc finger protein 24	0.84	1.71e-10	FNDC3B	fibronectin type III domain contain
-0.87	7.69e-12	SUDS3	SDS3 homolog, SIN3A corepressor com	0.83	2.02e-05	SQOR	sulfide quinone oxidoreductase

## GAGE analysis on upregulated and downregulated proteins at low/absent ATF2 protein, DB1

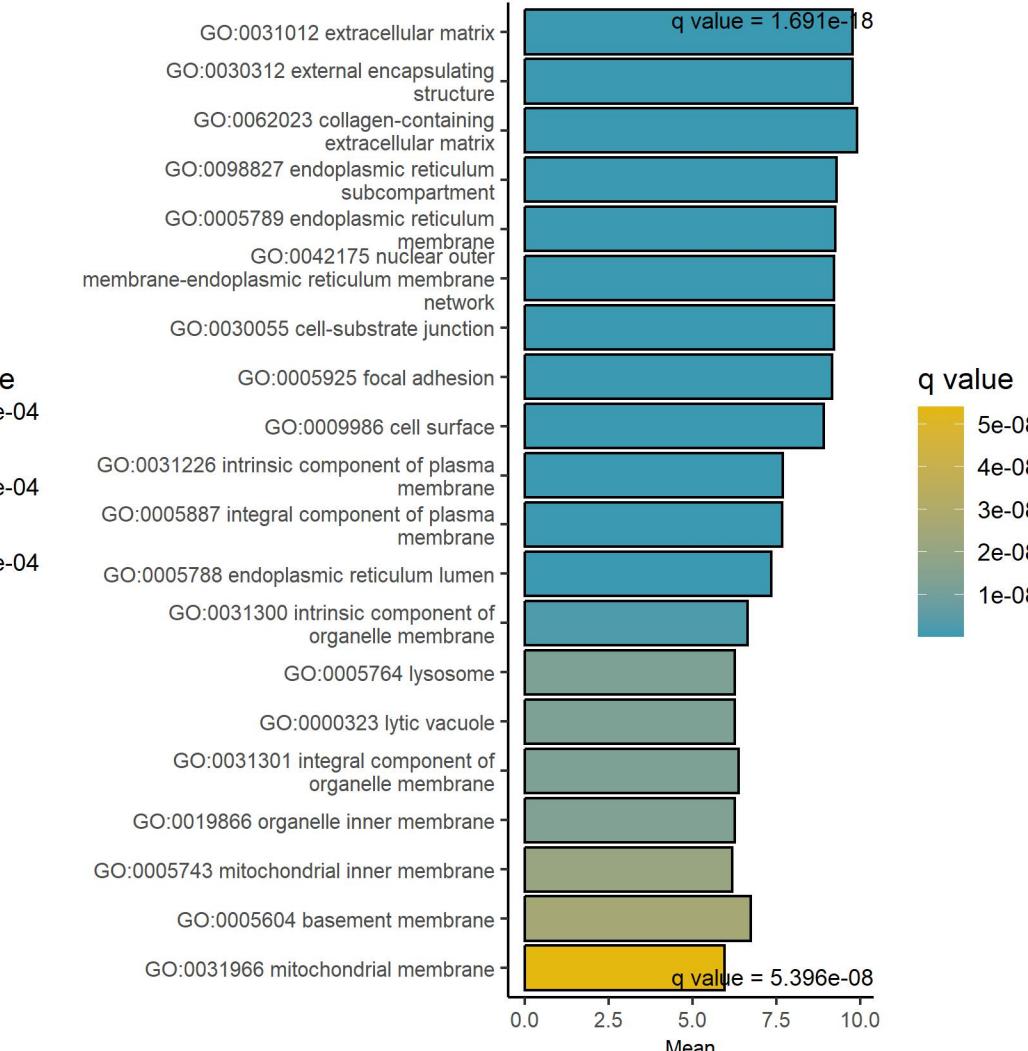
## GO Biological Process upregulated



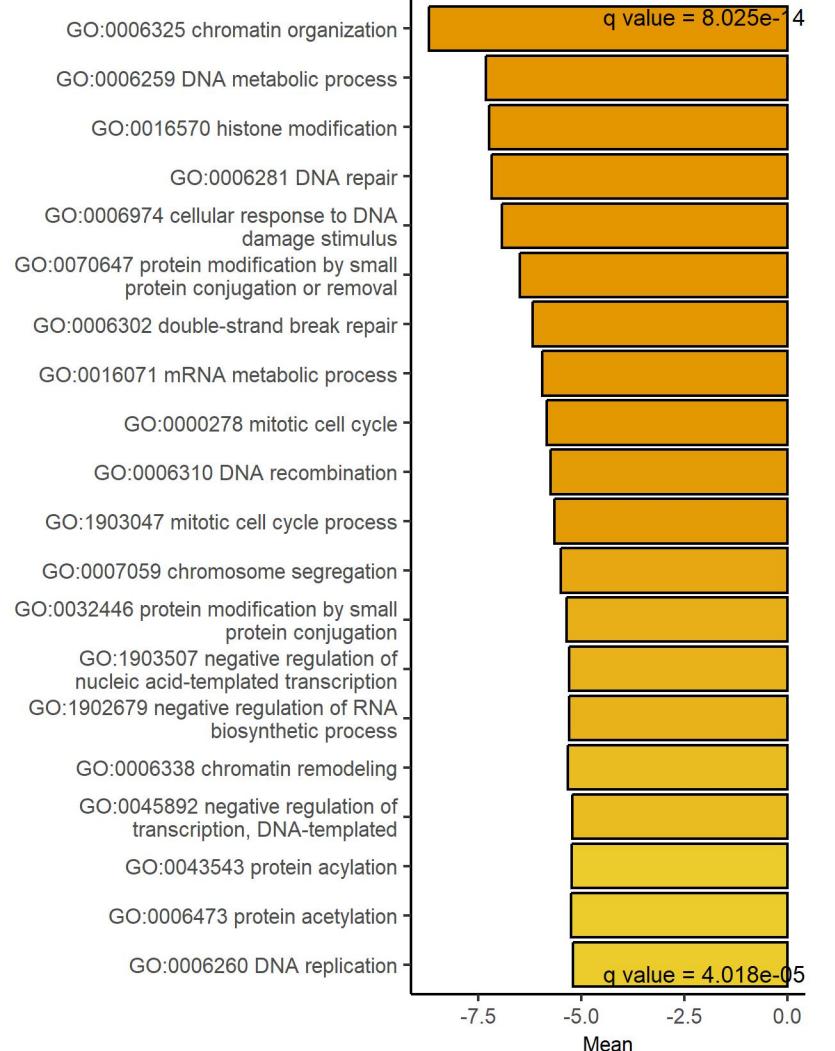
## GO Molecular Function upregulated



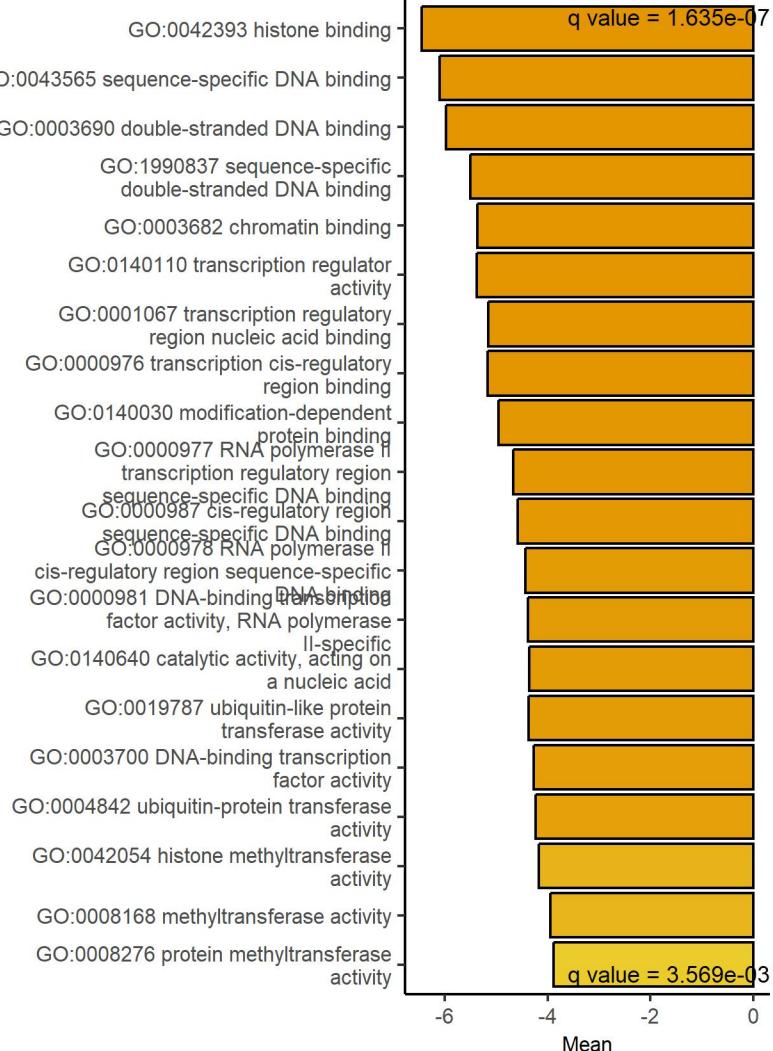
## GO Cellular Component upregulated



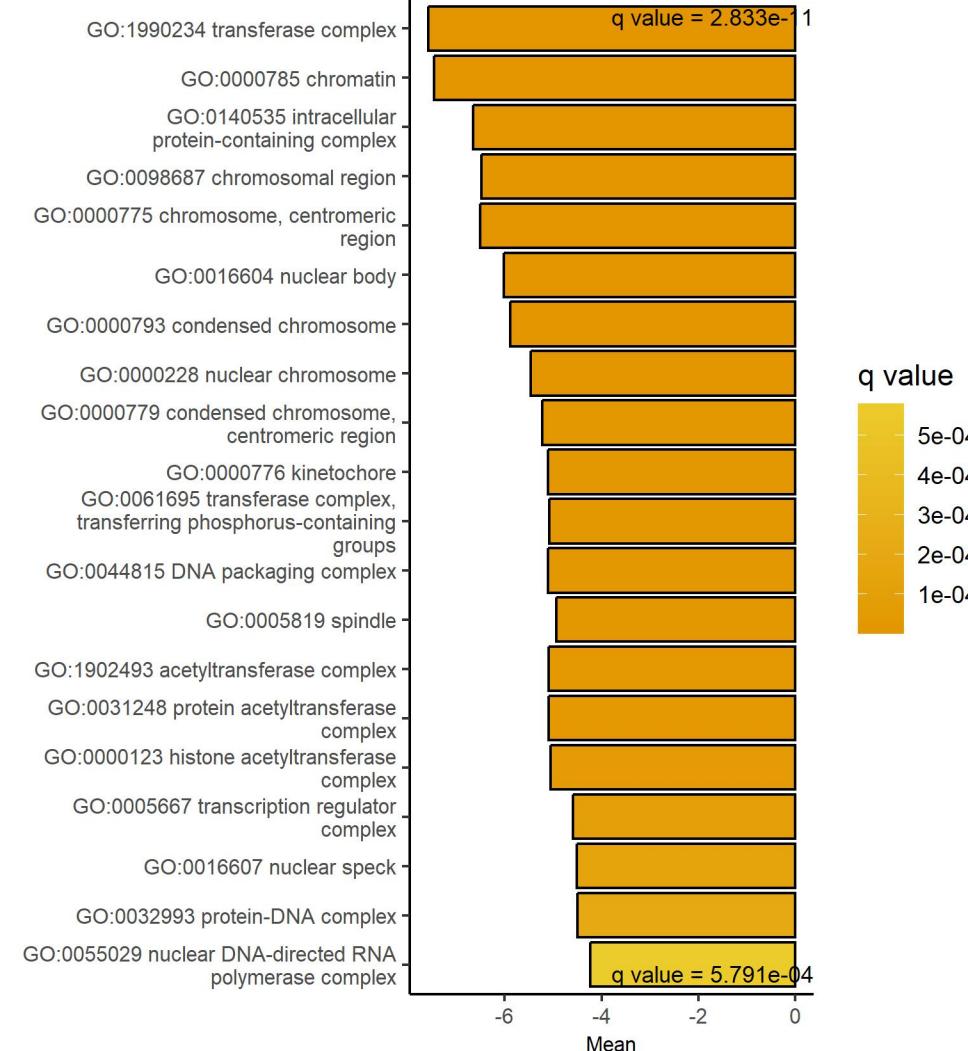
## GO Biological Process downregulated

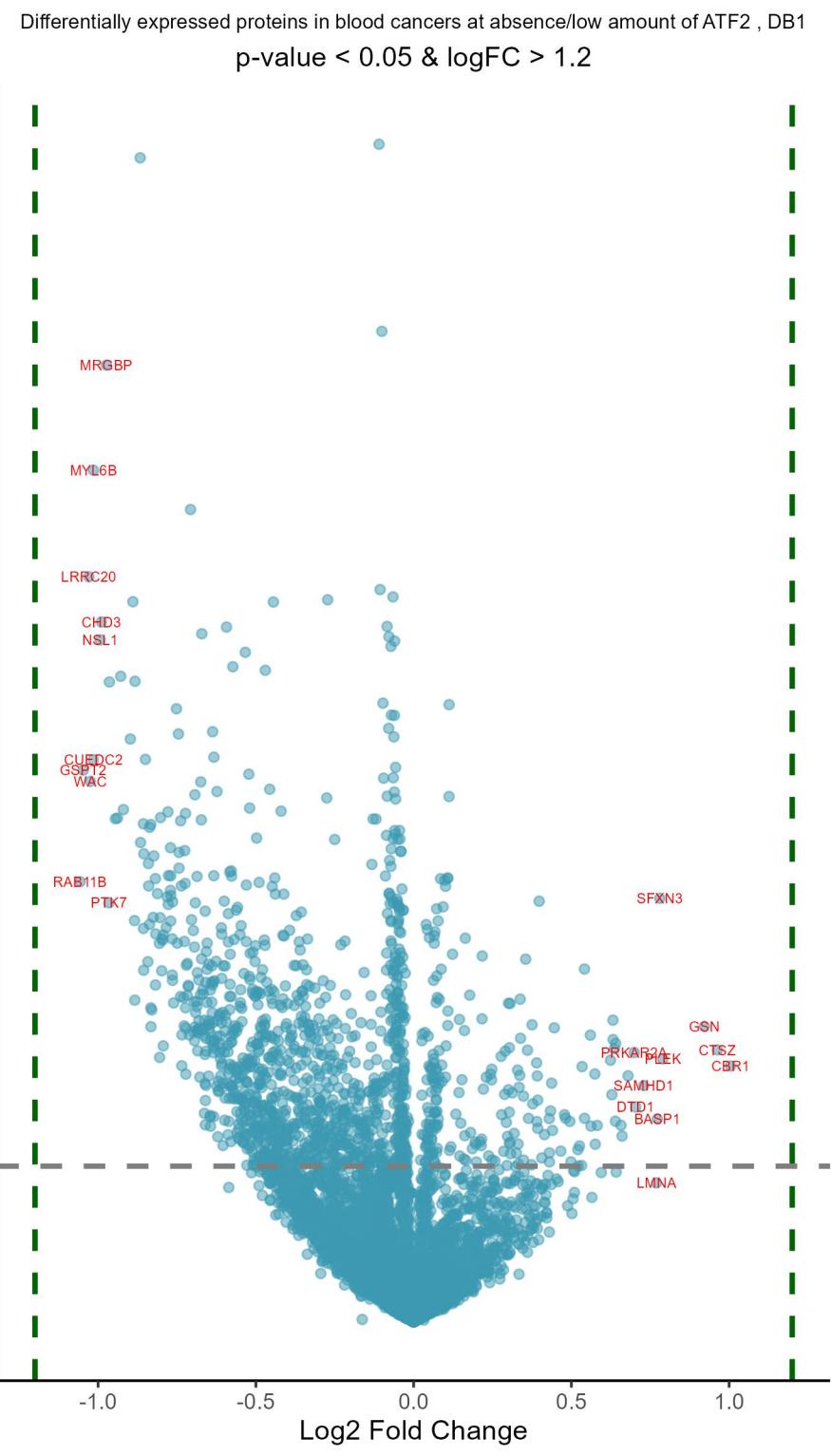


## GO Molecular Function downregulated

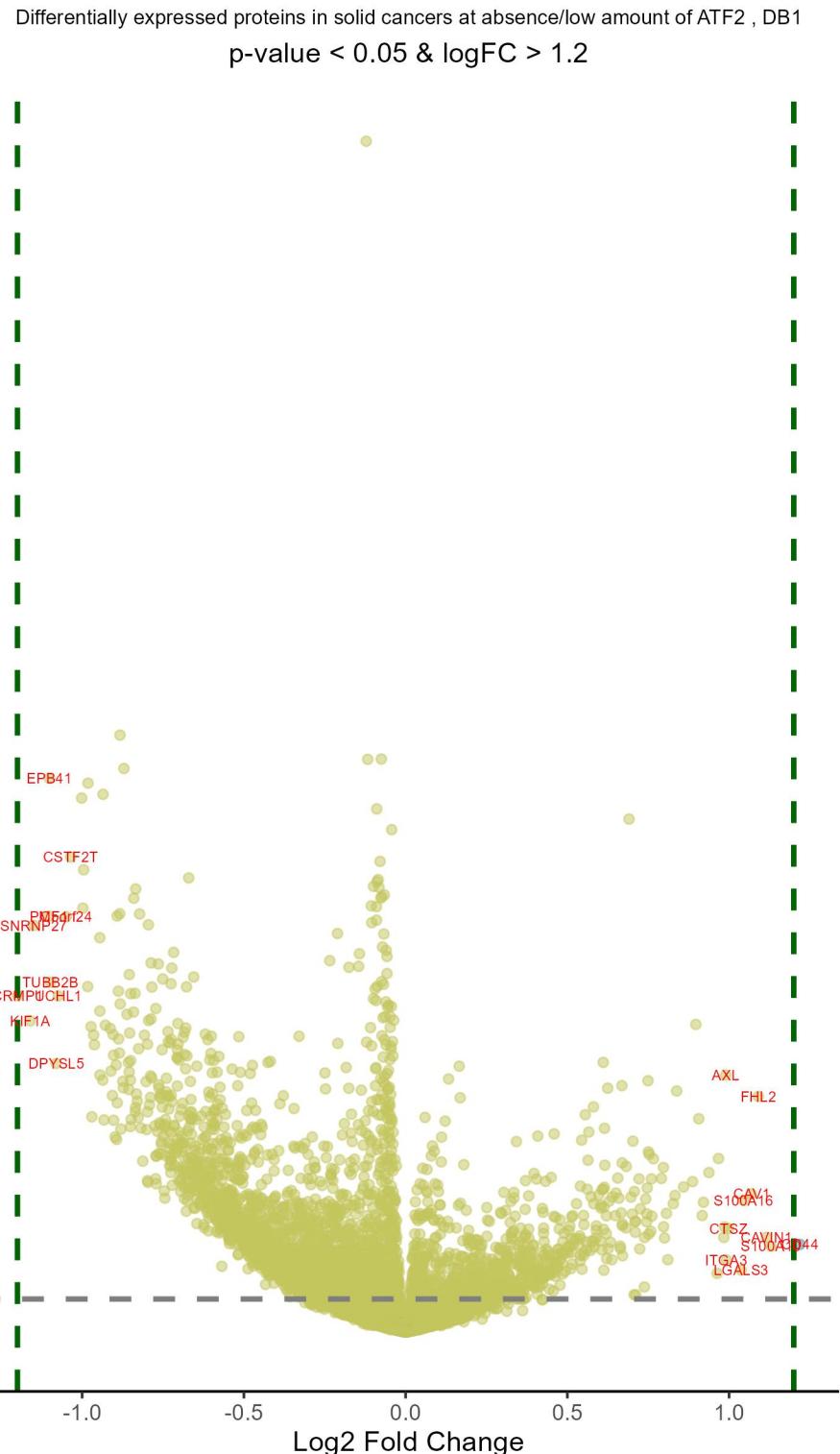


## GO Cellular Component downregulated



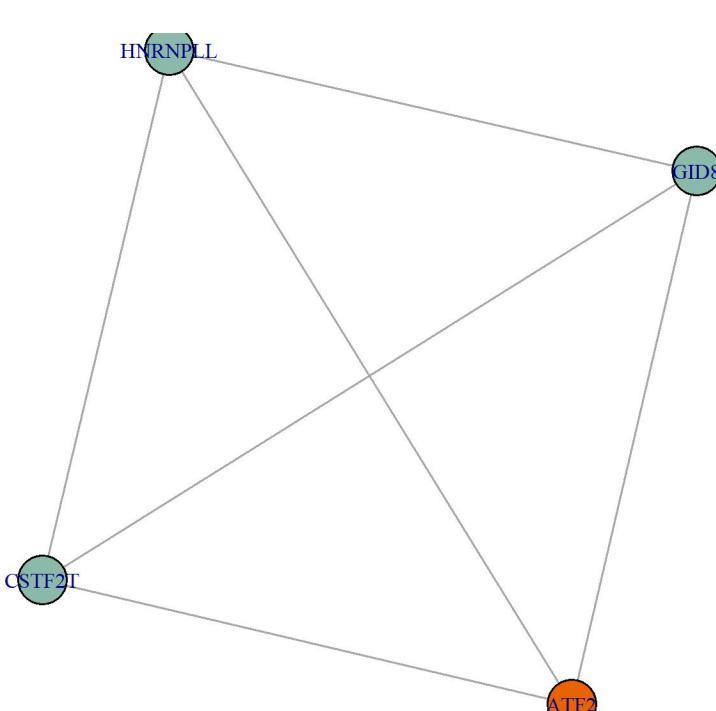


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.06	1.29e-02	RAB11B	RAB11B, member RAS oncogene family	1	8.03e-02	CBR1	carbonyl reductase 1
-1.05	3.87e-03	GSPT2	G1 to S phase transition 2	0.96	6.74e-02	CTSZ	cathepsin Z
-1.03	4.91e-04	LRRC20	leucine rich repeat containing 20	0.92	5.45e-02	GSN	gelsolin
-1.02	4.34e-03	WAC	WW domain containing adaptor with c	0.79	7.41e-02	PLEK	pleckstrin
-1.02	3.33e-03	CUEDC2	CUE domain containing 2	0.78	1.52e-02	SFXN3	sideroflexin 3
-1.01	8.43e-05	MYL6B	myosin light chain 6B	0.77	1.45e-01	BASP1	brain abundant membrane attached si
-0.99	6.78e-04	NSL1	NSL1 component of MIS12 kinetochore	0.77	2.36e-01	LMNA	lamin A/C
-0.99	6.47e-04	CHD3	chromodomain helicase DNA binding p	0.73	9.81e-02	SAMHD1	SAM and HD domain containing deoxyn
-0.97	1.34e-05	MRGBP	MRG domain binding protein	0.7	1.28e-01	DTD1	D-aminoacyl-tRNA deacylase 1
-0.97	1.55e-02	PTK7	protein tyrosine kinase 7 (inactive	0.7	6.82e-02	PRKAR2A	protein kinase cAMP-dependent type
-0.96	1.10e-03	BIRC5	baculoviral IAP repeat containing 5	0.68	8.96e-02	CA2	carbonic anhydrase 2
-0.95	6.41e-03	GTF2E1	general transcription factor IIIE su	0.66	1.71e-01	SQOR	sulfide quinone oxidoreductase
-0.94	6.41e-03	CCDC117	coiled-coil domain containing 117	0.66	1.53e-01	NDUFB2	NADH:ubiquinone oxidoreductase subu
-0.93	1.07e-03	TLE5	TLE family member 5, transcriptiona	0.64	2.36e-01	ANXA5	annexin A5
-0.92	6.10e-03	KIFBP	kinesin family binding protein	0.64	6.24e-02	FHOD1	formin homology 2 domain containing
-0.9	2.41e-03	URM1	ubiquitin related modifier 1	0.64	1.48e-01	ASNS	asparagine synthetase (glutamine-hy
-0.89	4.91e-04	YY1	YY1 transcription factor	0.64	6.66e-02	EHD4	EH domain containing 4
-0.88	1.86e-02	ZAP70	zeta chain of T cell receptor assoc	0.63	5.99e-02	ERMP1	endoplasmic reticulum metallopeptid
-0.88	4.17e-02	TUT4	terminal uridylyl transferase 4	0.63	5.21e-02	TNS3	tensin 3
-0.88	1.10e-03	HMGN5	high mobility group nucleosome bind	0.63	1.09e-01	RAB33B	RAB33B, member RAS oncogene family
-0.87	4.13e-07	CASP7	caspase 7	0.62	7.54e-02	TFB2M	transcription factor B2, mitochondr
-0.87	8.19e-03	RANGRF	RAN guanine nucleotide release fact	0.59	2.36e-01	MVP	major vault protein
-0.86	6.71e-03	TIMM10	translocase of inner mitochondrial	0.58	1.53e-01	ALG1	ALG1 chitobiosyldiphosphodolichol b
-0.86	2.03e-02	CD38	CD38 molecule	0.58	1.87e-01	NIBAN1	niban apoptosis regulator 1
-0.86	3.11e-02	LEF1	lymphoid enhancer binding factor 1	0.57	8.77e-02	CKB	creatine kinase B
-0.86	9.35e-03	AMDHD2	amidohydrolase domain containing 2	0.57	2.50e-01	DDT	D-dopachrome tautomerase
-0.85	3.33e-03	TMEM263	transmembrane protein 263	0.56	1.54e-01	KCNAB2	potassium voltage-gated channel sub
-0.84	2.89e-02	ZC3HAV1L	zinc finger CCCH-type containing, a	0.56	5.78e-02	LYZ	lysozyme
-0.84	1.09e-02	C2orf49	chromosome 2 open reading frame 49	0.54	1.44e-01	PLOD3	procollagen-lysine,2-oxoglutarate 5

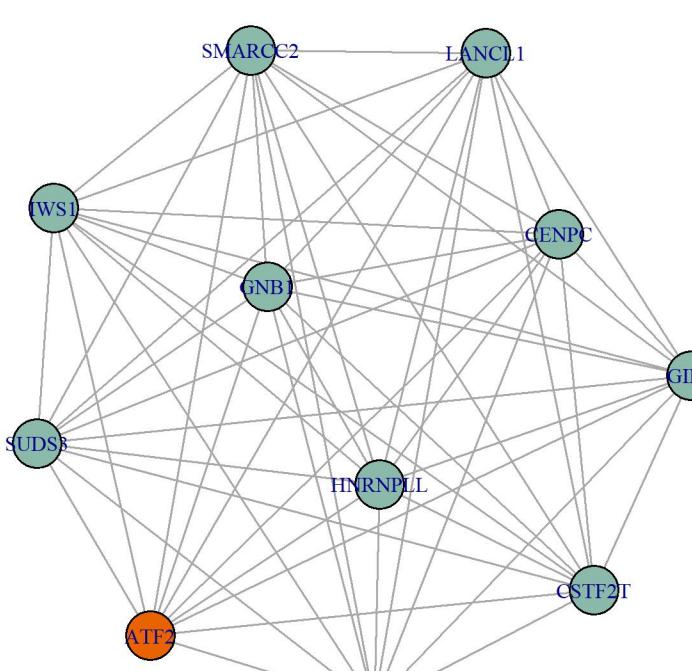


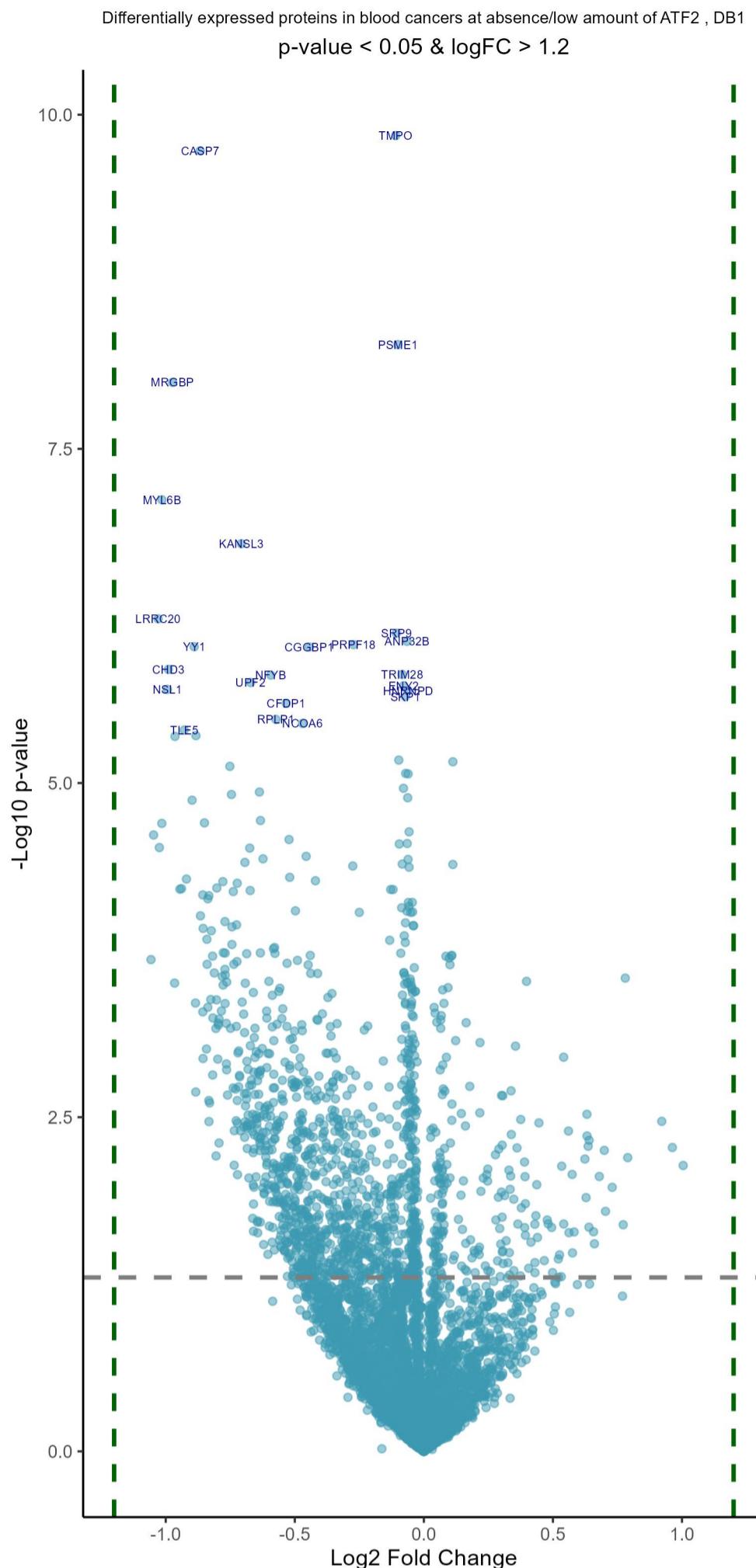
Downregulated in solid cancers at low/absent ATF2				Upregulated in solid cancers at low/absent ATF2			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.2	4.81e-12	CRMP1	collapsin response mediator protein	1.22	1.64e-03	CD44	CD44 molecule (Indian blood group)
-1.16	3.74e-11	KIF1A	kinesin family member 1A	1.13	1.89e-03	S100A10	S100 calcium binding protein A10
-1.15	1.45e-14	SNRNP27	small nuclear ribonucleoprotein U4/	1.12	9.45e-04	CAVIN1	caveolae associated protein 1
-1.1	7.25e-15	PMF1	polyamine modulated factor 1	1.09	1.53e-08	FHL2	four and a half LIM domains 2
-1.1	1.19e-19	EPB41	erythrocyte membrane protein band 4	1.07	3.50e-05	CAV1	caveolin 1
-1.1	1.69e-12	TUBB2B	tubulin beta 2B class IIb	1.04	5.67e-05	S100A16	S100 calcium binding protein A16
-1.08	1.09e-09	DPYSL5	dihydropyrimidinase like 5	1.04	1.13e-02	LGALS3	galectin 3
-1.07	4.85e-12	UCHL1	ubiquitin C-terminal hydrolase L1	1	4.89e-04	CTSZ	cathepsin Z
-1.05	7.34e-15	C5orf24	chromosome 5 open reading frame 24	0.99	5.27e-03	ITGA3	integrin subunit alpha 3
-1.04	7.67e-17	CSTF2T	cleavage stimulation factor subunit	0.99	2.75e-09	AXL	AXL receptor tyrosine kinase
-1	5.04e-19	POLR2D	RNA polymerase II subunit D	0.99	4.36e-04	RHOC	ras homolog family member C
-1	3.96e-15	ZMYM3	zinc finger MYM-type containing 3	0.98	9.56e-04	MYOF	myoferlin
-1	2.16e-16	CKB	creatine kinase B	0.97	2.13e-06	EPHA2	EPH receptor A2
-0.98	2.34e-12	BRD2	bromodomain containing 2	0.96	1.45e-02	ANXA1	annexin A1
-0.98	1.63e-19	UBXN7	UBX domain protein 7	0.94	6.29e-06	ADAM9	ADAM metallopeptidase domain 9
-0.97	6.07e-11	DNMT3A	DNA methyltransferase 3 alpha	0.92	6.57e-05	NT5E	5'-nucleotidase ecto
-0.97	7.72e-08	ASRGL1	asparaginase and isoaspartyl peptid	0.92	1.82e-04	PROCR	protein C receptor
-0.96	1.17e-10	ZNF768	zinc finger protein 768	0.91	9.06e-08	CTSL	cathepsin L
-0.96	2.41e-10	SMC1B	structural maintenance of chromosom	0.9	5.06e-11	RAB11FIP5	RAB11 family interacting protein 5
-0.95	4.12e-14	BPTF	bromodomain PHD finger transcriptio	0.89	1.29e-05	GPX8	glutathione peroxidase 8 (putative)
-0.95	1.71e-11	POLR2F	RNA polymerase II, I and III subuni	0.86	2.00e-05	THBS1	thrombospondin 1
-0.95	2.75e-09	MAZ	MYC associated zinc finger protein	0.84	9.88e-09	NNMT	nicotinamide N-methyltransferase
-0.94	4.18e-09	PRR36	proline rich 36	0.83	3.92e-05	RRAS	RAS related
-0.94	3.99e-19	SCAF8	SR-related CTD associated factor 8	0.83	7.34e-05	TGM2	transglutaminase 2
-0.93	9.78e-08	CHGA	chromogranin A	0.81	5.23e-03	NCEH1	neutral cholesterol ester hydrolase
-0.93	5.36e-11	MYL6B	myosin light chain 6B	0.81	1.55e-04	ICAM1	intercellular adhesion molecule 1
-0.91	6.87e-11	POU2F1	POU class 2 homeobox 1	0.8	9.96e-04	SQOR	sulfide quinone oxidoreductase
-0.91	2.04e-09	SUDS3	SDS3 homolog, SIN3A corepressor com	0.8	4.30e-04	STOM	stomatin
-0.91	1.43e-08	GABARAPL2	GABA type A receptor associated pro	0.8	4.24e-06	SP100	SP100 nuclear antigen

ATE2 network, DB1, all Pearson  $r \geq 0.35$

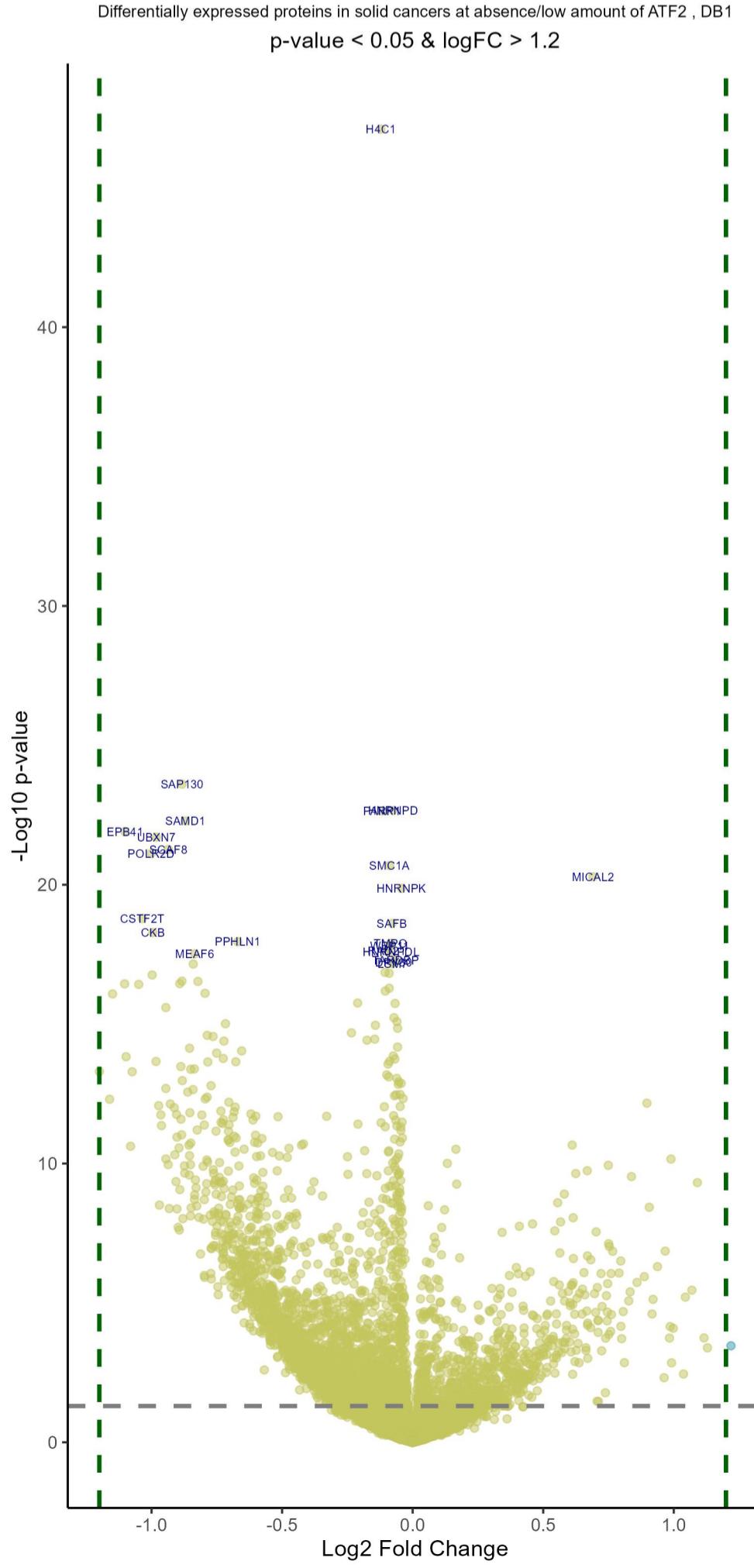


ATE2 network, DB1, all Pearson  $r \geq 0.3$



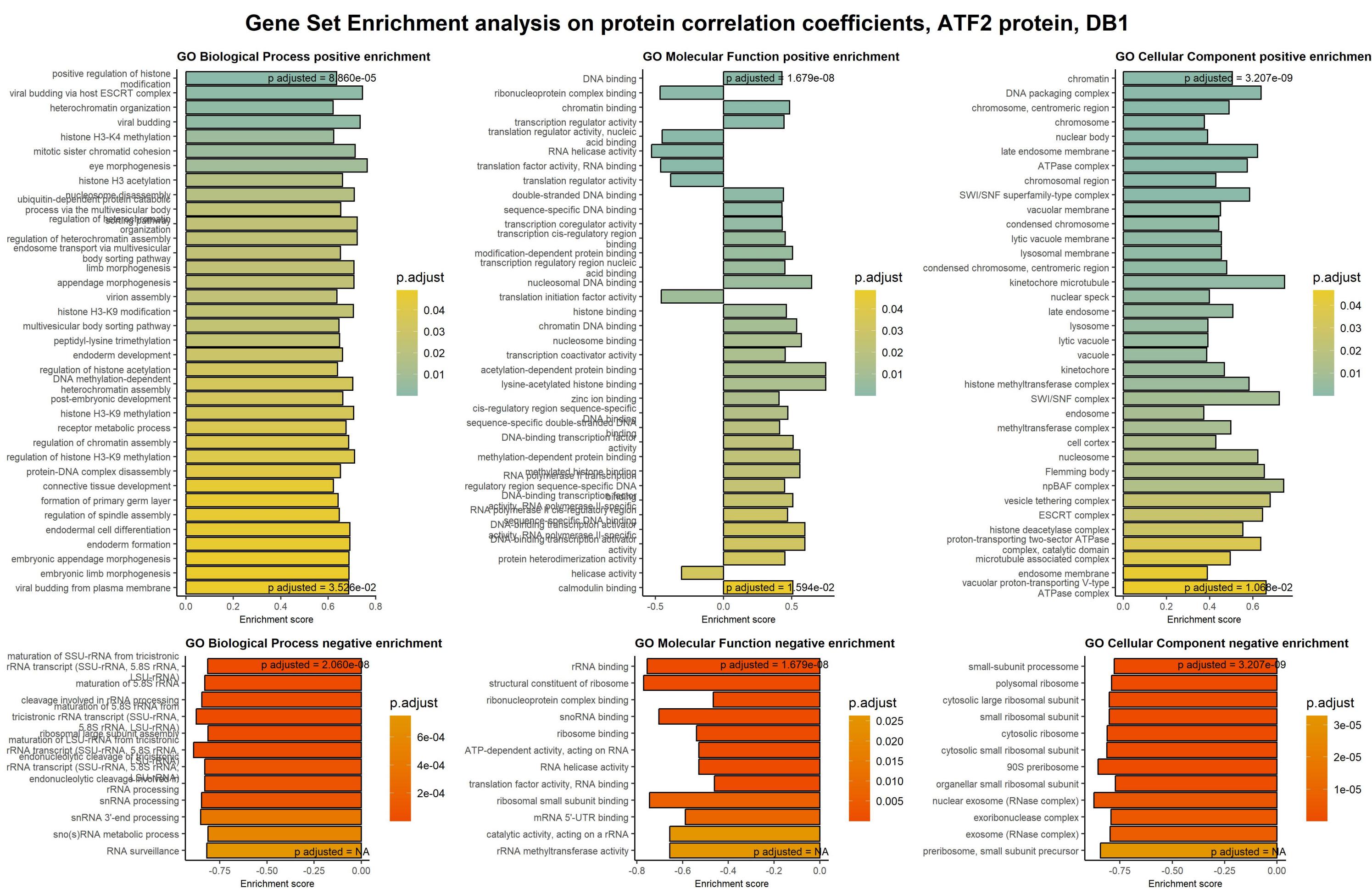
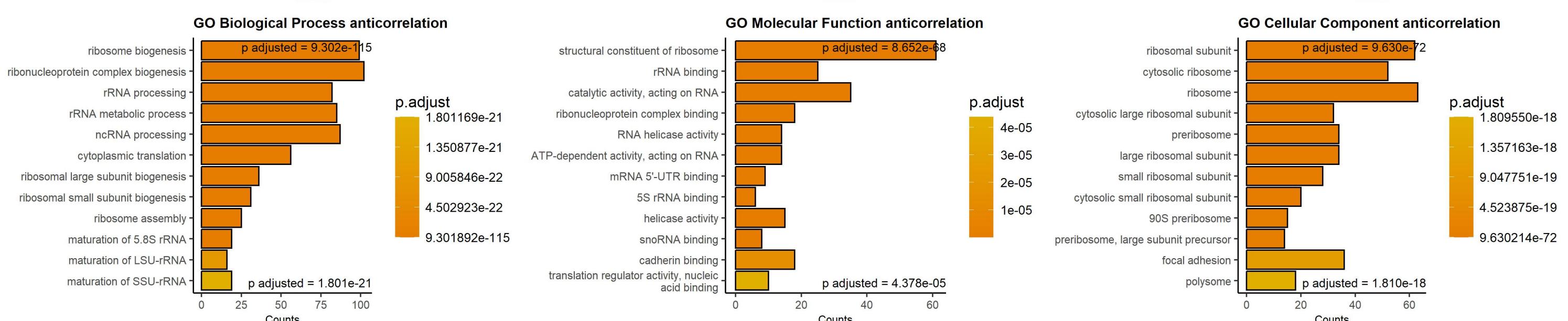
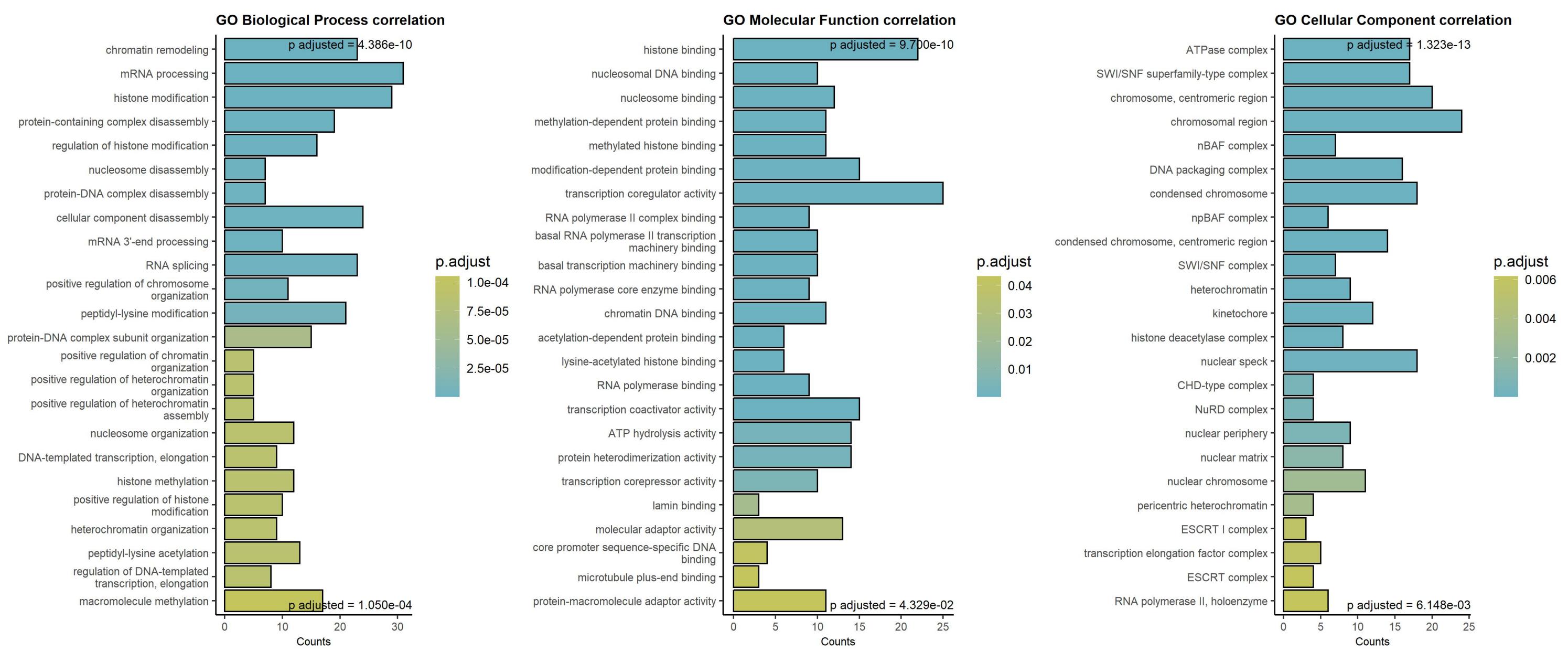


Sorted by p values!							
Downregulated in blood cancers at low/absent ATF2				Upregulated in blood cancers at low/absent ATF2			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.11	4.13e-07	TMPO	thymopoietin	0.11	1.59e-03	MRT04	MRT4 homolog, ribosome maturation f
-0.87	4.13e-07	CASP7	caspase 7	0.11	5.10e-03	PDCD11	programmed cell death 11
-0.1	8.72e-06	PSME1	proteasome activator subunit 1	0.11	1.24e-02	UQCRC2	ubiquinol-cytochrome c reductase co
-0.97	1.34e-05	MRGBP	MRG domain binding protein	0.11	1.24e-02	UTP4	UTP4 small subunit processome compo
-1.01	8.43e-05	MYL6B	myosin light chain 6B	0.09	1.24e-02	RRS1	ribosome biogenesis regulator 1 hom
-0.71	1.54e-04	KANSL3	KAT8 regulatory NSL complex subunit	0.1	1.27e-02	HADHA	hydroxyacyl-CoA dehydrogenase trifu
-1.03	4.91e-04	LRRC20	leucine rich repeat containing 20	0.1	1.33e-02	DNAJA3	DnaJ heat shock protein family (Hsp
-0.11	4.91e-04	SRP9	signal recognition particle 9	0.78	1.52e-02	SFXN3	sideroflexin 3
-0.07	4.91e-04	ANP32B	acidic nuclear phosphoprotein 32 fa	0.4	1.55e-02	SMPDL3B	sphingomyelin phosphodiesterase aci
-0.27	4.91e-04	PRPF18	pre-mRNA processing factor 18	0.09	1.62e-02	HADHB	hydroxyacyl-CoA dehydrogenase trifu
-0.89	4.91e-04	YY1	YY1 transcription factor	0.07	1.64e-02	UQCRC1	ubiquinol-cytochrome c reductase co
-0.44	4.91e-04	CGGBP1	CGG triplet repeat binding protein	0.08	1.86e-02	RRP1	ribosomal RNA processing 1
-0.99	6.47e-04	CHD3	chromodomain helicase DNA binding p	0.04	1.92e-02	RPS18	ribosomal protein S18
-0.08	6.47e-04	TRIM28	tripartite motif containing 28	0.04	2.06e-02	RPS23	ribosomal protein S23
-0.59	6.47e-04	NFYB	nuclear transcription factor Y subu	0.07	2.10e-02	QARS1	glutaminyl-tRNA synthetase 1
-0.67	6.78e-04	UPF2	UPF2 regulator of nonsense mediated	0.07	2.17e-02	ETF1	eukaryotic translation termination
-0.08	6.78e-04	ENY2	ENY2 transcription and export compl	0.05	2.24e-02	RSL1D1	ribosomal L1 domain containing 1
-0.99	6.78e-04	NSL1	NSL1 component of MIS12 kinetochore	0.16	2.24e-02	DCXR	dicarbonyl and L-xylulose reductase
-0.06	6.78e-04	HNRNP <span style="font-variant: small-caps;">D</span>	heterogeneous nuclear ribonucleopro	0.07	2.27e-02	PES1	pescadillo ribosomal biogenesis fac
-0.07	7.15e-04	SKP1	S-phase kinase associated protein 1	0.12	2.62e-02	CYC1	cytochrome c1
-0.53	7.65e-04	CFDP1	craniofacial development protein 1	0.22	2.69e-02	POP1	POP1 homolog, ribonuclease P/MRP su
-0.57	9.66e-04	RPLP1	ribosomal protein lateral stalk sub	0.36	2.81e-02	ABCF3	ATP binding cassette subfamily F me
-0.47	9.92e-04	NCOA6	nuclear receptor coactivator 6	0.54	3.11e-02	PRTN3	proteinase 3
-0.93	1.07e-03	TLE5	TLE family member 5, transcriptiona	0.09	3.11e-02	MRPL19	mitochondrial ribosomal protein L19
-0.88	1.10e-03	HMGN5	high mobility group nucleosome bind	0.07	3.34e-02	BOP1	BOP1 ribosomal biogenesis factor
-0.96	1.10e-03	BIRC5	baculoviral IAP repeat containing 5	0.06	3.52e-02	SRM	spermidine synthase
-0.1	1.59e-03	OXSR1	oxidative stress responsive kinase	0.18	4.04e-02	ATP6AP1	ATPase H <sup>+</sup> transporting accessory pr
-0.75	1.66e-03	UBE2R2	ubiquitin conjugating enzyme E2 R2	0.08	4.07e-02	AIFM1	apoptosis inducing factor mitochond
-0.07	1.77e-03	PFN1	profilin 1	0.34	4.12e-02	SLC25A19	solute carrier family 25 member 19
-0.06	1.77e-03	RBM8A	RNA binding motif protein 8A	0.08	4.13e-02	MRPL13	mitochondrial ribosomal protein L13
-0.08	2.21e-03	YWHAE	tyrosine 3-monooxygenase/tryptophan	0.07	4.27e-02	MRPL17	mitochondrial ribosomal protein L17
-0.64	2.28e-03	ORC2	origin recognition complex subunit	0.3	4.27e-02	RAB11FIP5	RAB11 family interacting protein 5
-0.75	2.31e-03	PHF23	PHD finger protein 23	0.31	4.27e-02	GHITM	growth hormone inducible transmembr
-0.06	2.38e-03	WBP11	WW domain binding protein 11	0.11	4.66e-02	NDUFA13	NADH:ubiquinone oxidoreductase subu
-0.9	2.41e-03	URM1	ubiquitin related modifier 1	0.22	5.15e-02	MRPL15	mitochondrial ribosomal protein L15
-0.63	3.33e-03	BOD1L1	biorientation of chromosomes in cel	0.15	5.18e-02	TBL3	transducin beta like 3
-0.85	3.33e-03	TMEM263	transmembrane protein 263	0.63	5.21e-02	TNS3	tensin 3
-1.02	3.33e-03	CUEDC2	CUE domain containing 2	0.38	5.39e-02	TOR1B	torsin family 1 member B
-0.06	3.76e-03	LSMA1	LSMA homolog, U6 small nuclear RNA	0.11	5.41e-02	SSPA1	signal sequence receptor subunit 1

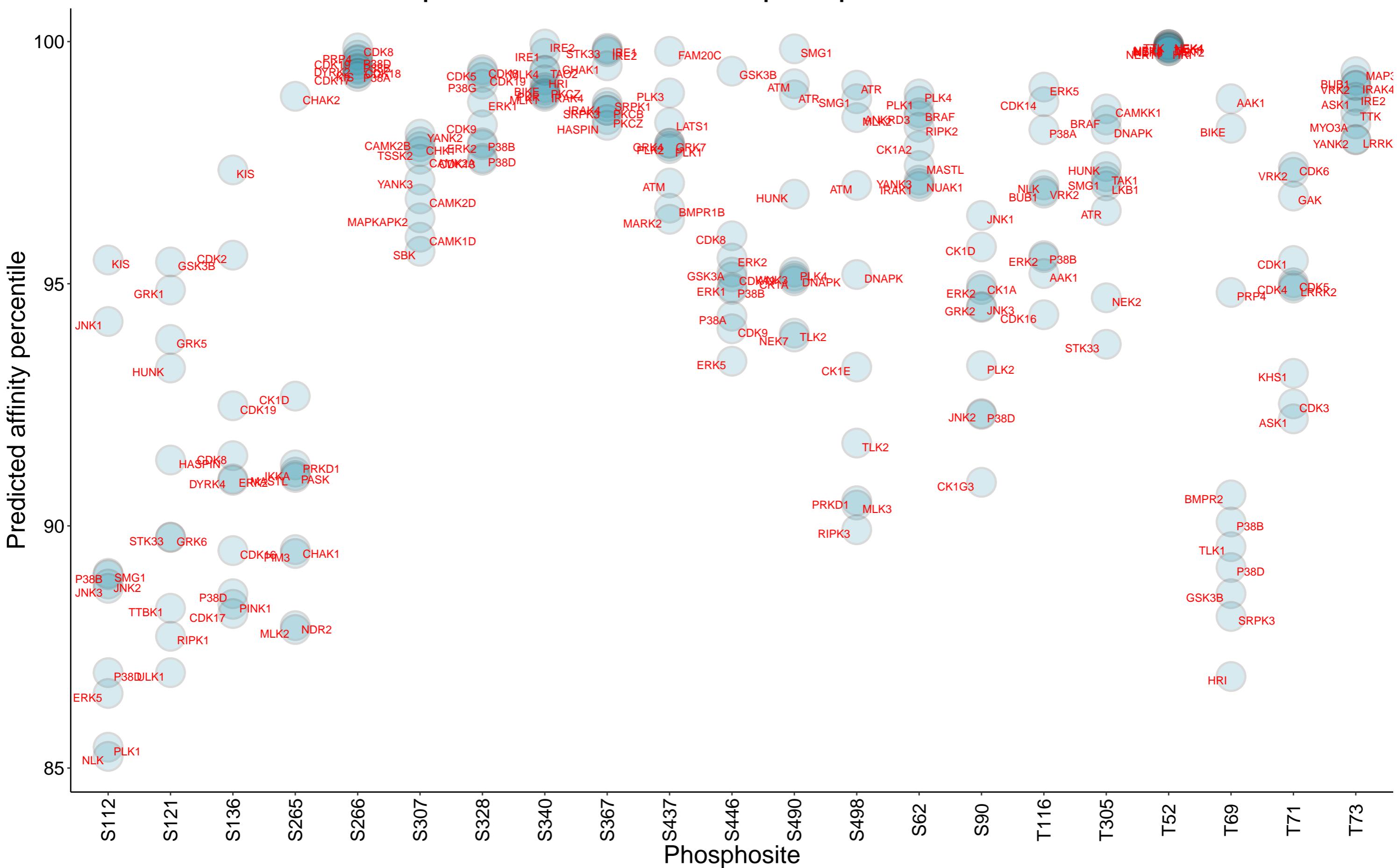


Sorted by p values!							
Downregulated in solid cancers at low/absent ATF2				Upregulated in solid cancers at low/absent ATF2			
C	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
2	2.63e-44	H4C1	H4 clustered histone 1	0.69	2.86e-18	MICAL2	microtubule associated monooxygenases
8	5.46e-21	SAP130	Sin3A associated protein 130	0.9	5.06e-11	RAB11FIP5	RAB11 family interacting protein 5
8	2.98e-20	HNRNPD	heterogeneous nuclear ribonucleoprotein D	0.61	1.00e-09	JUN	Jun proto-oncogene, AP-1 transcript
2	2.98e-20	PARP1	poly(ADP-ribose) polymerase 1	0.17	1.35e-09	PICALM	phosphatidylinositol binding clathrin
7	5.71e-20	SAMD1	sterile alpha motif domain containin	0.99	2.75e-09	AXL	AXL receptor tyrosine kinase
1	1.19e-19	EPB41	erythrocyte membrane protein band 4	0.13	3.81e-09	IQGAP1	IQ motif containing GTPase activati
8	1.63e-19	UBXN7	UBX domain protein 7	0.75	4.38e-09	NEXN	nexilin F-actin binding protein
4	3.99e-19	SCAF8	SR-related CTD associated factor 8	0.67	6.56e-09	MYO1E	myosin IE
	5.04e-19	POLR2D	RNA polymerase II subunit D	0.62	7.96e-09	DAB2	DAB adaptor protein 2
9	1.23e-18	SMC1A	structural maintenance of chromosom	0.84	9.88e-09	NNMT	nicotinamide N-methyltransferase
4	6.91e-18	HNRNPK	heterogeneous nuclear ribonucleoprotein K	1.09	1.53e-08	FHL2	four and a half LIM domains 2
4	7.67e-17	CSTF2T	cleavage stimulation factor subunit	0.17	1.69e-08	ACTN4	actinin alpha 4
8	1.08e-16	SAFB	scaffold attachment factor B	0.58	3.54e-08	SERPINE1	serpin family E member 1
	2.16e-16	CKB	creatine kinase B	0.56	6.55e-08	CCDC9B	coiled-coil domain containing 9B
7	4.30e-16	PPHLN1	periphilin 1	0.06	8.14e-08	CLTC	clathrin heavy chain
8	4.74e-16	TMPO	thymopoietin	0.91	9.06e-08	CTSL	cathepsin L
9	5.37e-16	WBP11	WW domain binding protein 11	0.12	1.08e-07	AP2A1	adaptor related protein complex 2 s
1	7.88e-16	RAD21	RAD21 cohesin complex component	0.61	1.91e-07	CCN1	cellular communication network fact
8	8.22e-16	HNRNPDL	heterogeneous nuclear ribonucleoprotein D	0.57	2.58e-07	FGF2	fibroblast growth factor 2
3	9.09e-16	MEAF6	MYST/Esa1 associated factor 6	0.46	2.98e-07	MLPH	melanophilin
7	1.50e-15	TARDBP	TAR DNA binding protein	0.41	3.51e-07	LOXL2	lysyl oxidase like 2
7	1.68e-15	DPY30	dpy-30 histone methyltransferase co	0.11	3.83e-07	MYL6	myosin light chain 6
8	1.78e-15	LSM7	LSM7 homolog, U6 small nuclear RNA	0.54	4.92e-07	MYL9	myosin light chain 9
4	1.78e-15	RBBP6	RB binding protein 6, ubiquitin lig	0.7	5.33e-07	PARP4	poly(ADP-ribose) polymerase family
1	3.44e-15	ZNF638	zinc finger protein 638	0.34	5.50e-07	LPXN	leupaxin
9	3.56e-15	HCFC1	host cell factor C1	0.08	7.72e-07	AP2B1	adaptor related protein complex 2 s
	3.96e-15	ZMYM3	zinc finger MYM-type containing 3	0.09	1.17e-06	ACTBL2	actin beta like 2
8	6.31e-15	NRF1	nuclear respiratory factor 1	0.75	1.24e-06	COL12A1	collagen type XII alpha 1 chain
2	6.31e-15	EP400	E1A binding protein p400	0.75	1.51e-06	DCBLD2	discoidin, CUB and LCCL domain cont
9	7.25e-15	MRGBP	MRG domain binding protein	0.08	1.73e-06	VDAC1	voltage dependent anion channel 1
1	7.25e-15	PMF1	polyamine modulated factor 1	0.97	2.13e-06	EPHA2	EPH receptor A2
5	7.34e-15	C5orf24	chromosome 5 open reading frame 24	0.77	2.16e-06	FNDC3B	fibronectin type III domain contain
9	9.78e-15	SMC3	structural maintenance of chromosom	0.56	2.40e-06	FSTL1	follistatin like 1
1	1.20e-14	FUS	FUS RNA binding protein	0.11	2.74e-06	TMOD3	tropomodulin 3
3	1.41e-14	CENPV	centromere protein V	0.67	2.94e-06	SH3KBP1	SH3 domain containing kinase bindin
5	1.45e-14	SNRNP27	small nuclear ribonucleoprotein U4/	0.18	3.40e-06	ACTN1	actinin alpha 1
1	2.97e-14	H1-10	H1.10 linker histone	0.62	3.56e-06	RBMS2	RNA binding motif single stranded i
7	3.01e-14	SNRPF	small nuclear ribonucleoprotein pol	0.68	3.89e-06	SERPINE2	serpin family E member 2
5	4.12e-14	BPTE	bp10.1 in RHD5 protein complex	0.0	4.24e-06	GP100	GP100 antigen presentation

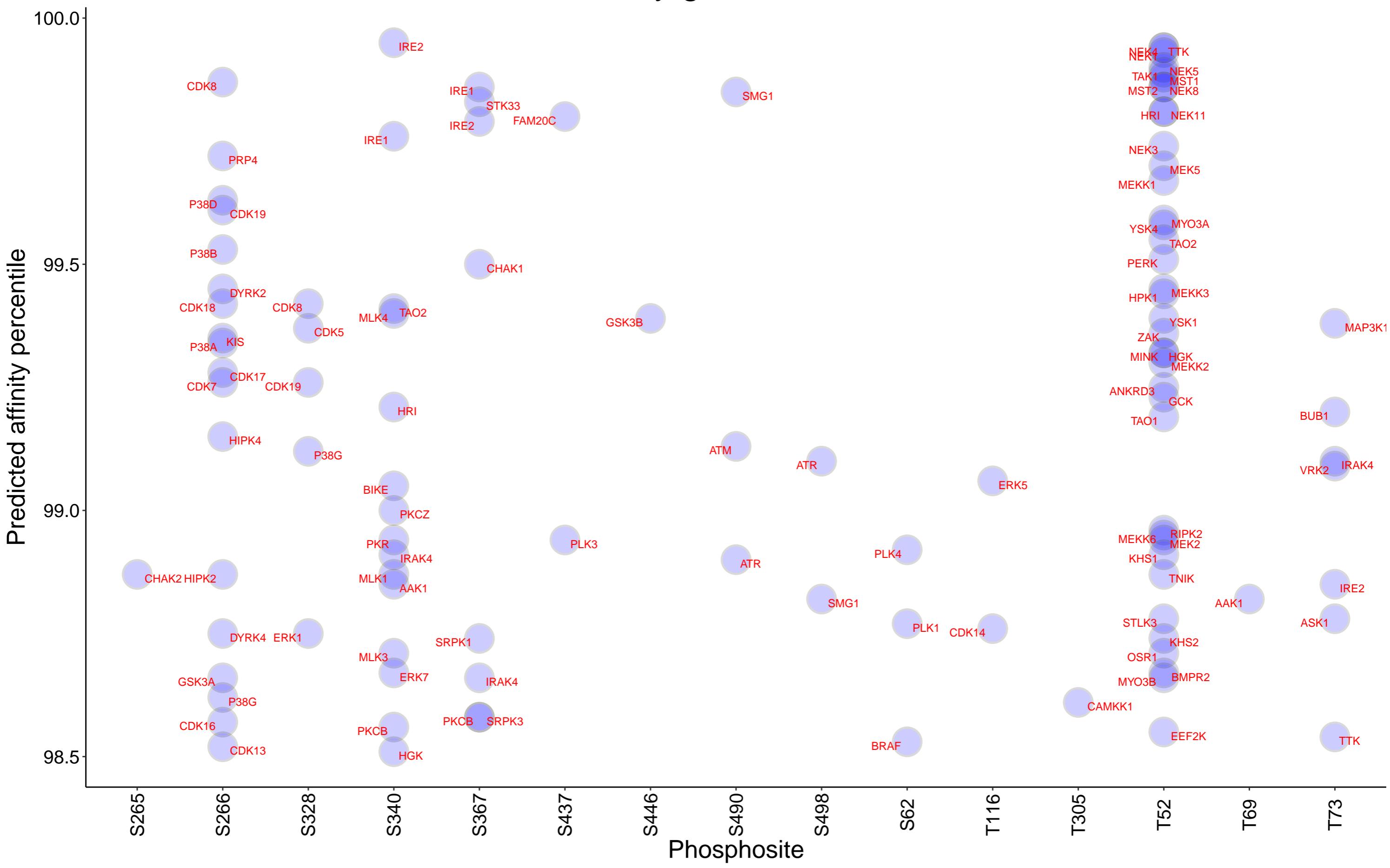
# Top 250 correlation coefficients overrepresentation, ATF2 protein, DB1



# Top 10 kinases for each phosphosite in ATF2



Kinases with affinity greater than 98.5% to ATF2



No sufficient paired observations in DB1 for ATF2