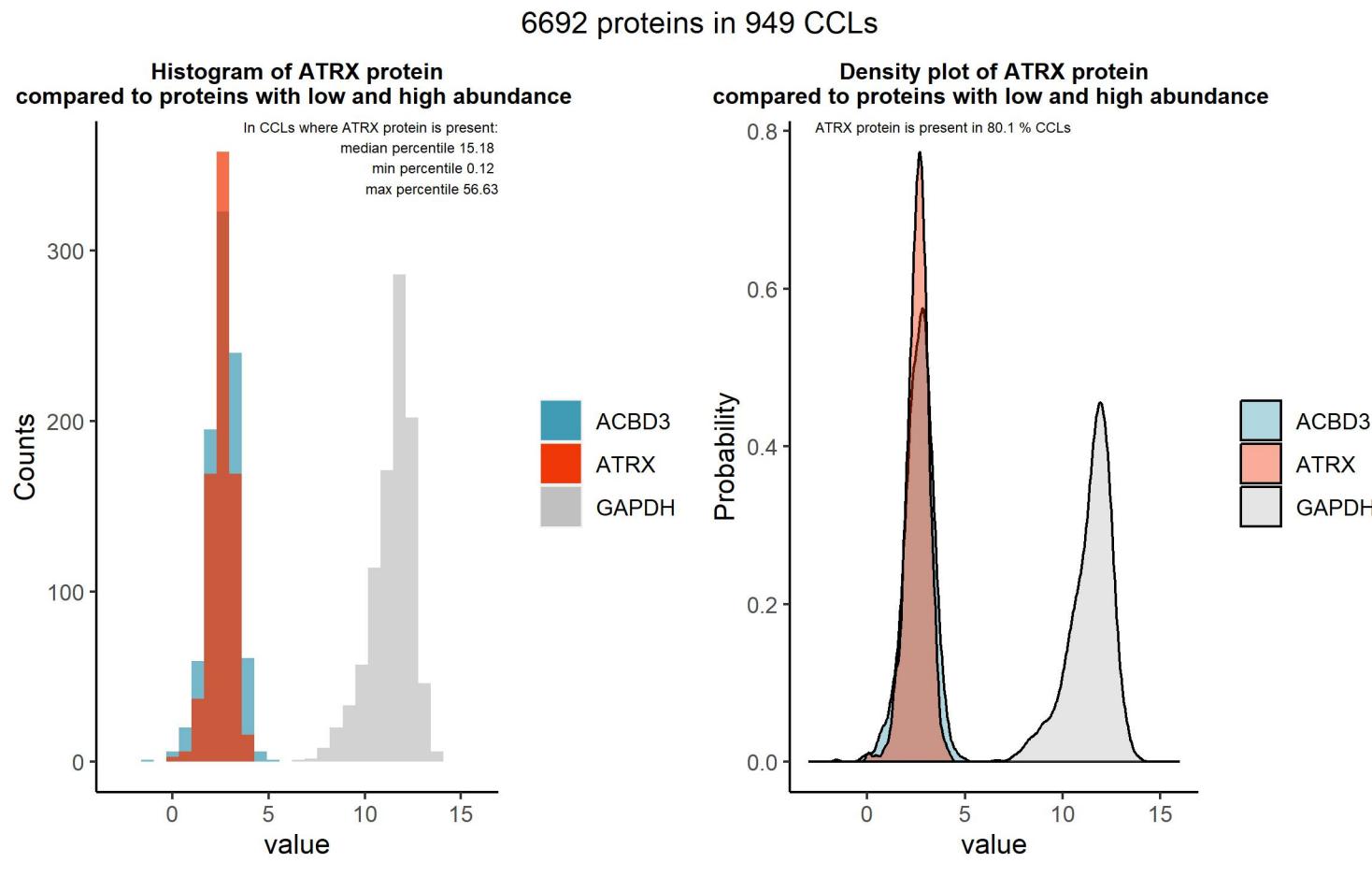


# ATRX

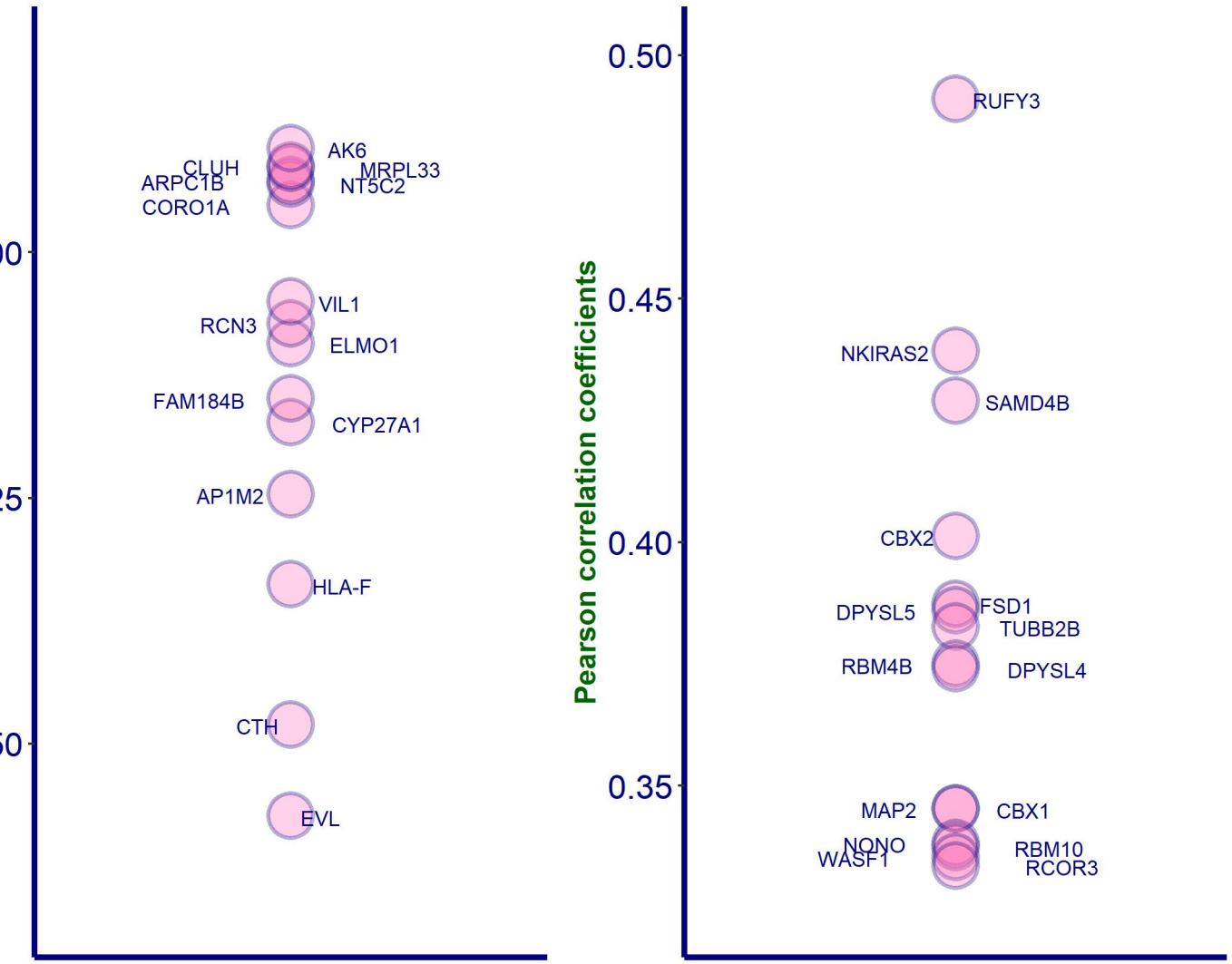
Protein name: ATRX ; UNIPROT: P46100 ; Gene name: ATRX chromatin remodeler

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

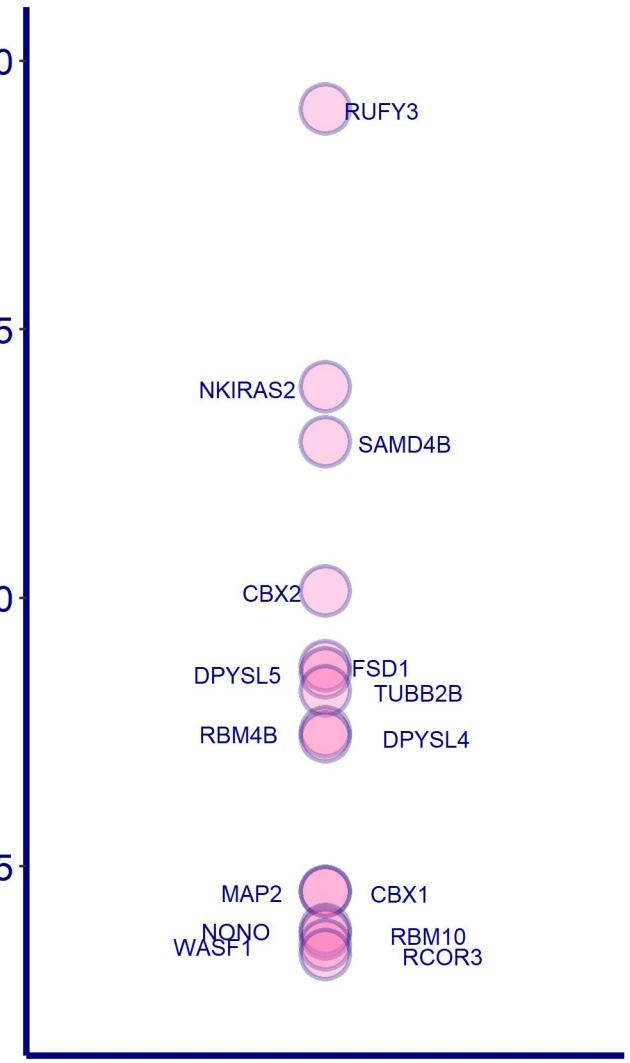
## Sanger Institute Protein Database 1 (DB1), protein presence is certain



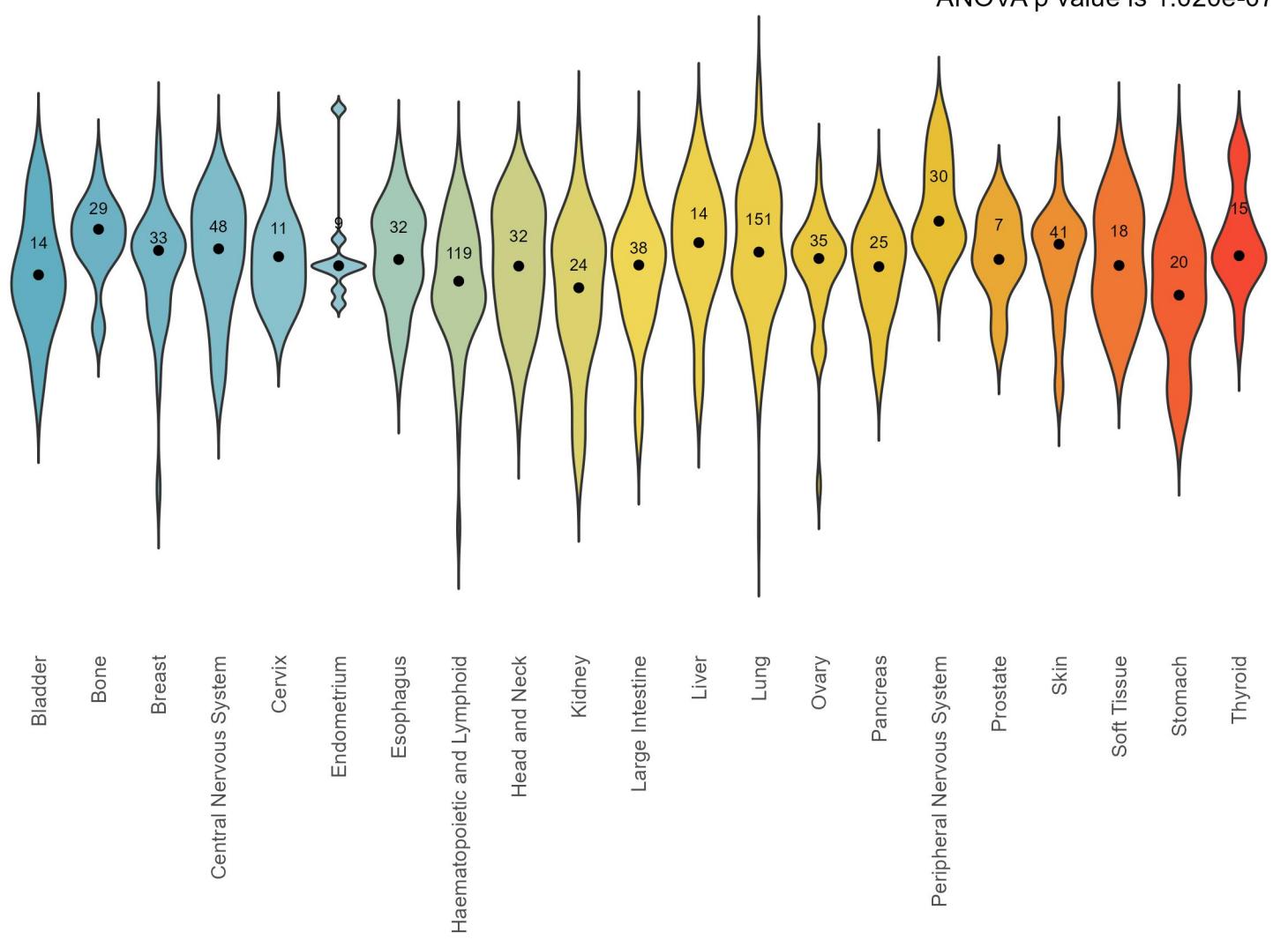
Top negative correlations of ATRX protein, DB1



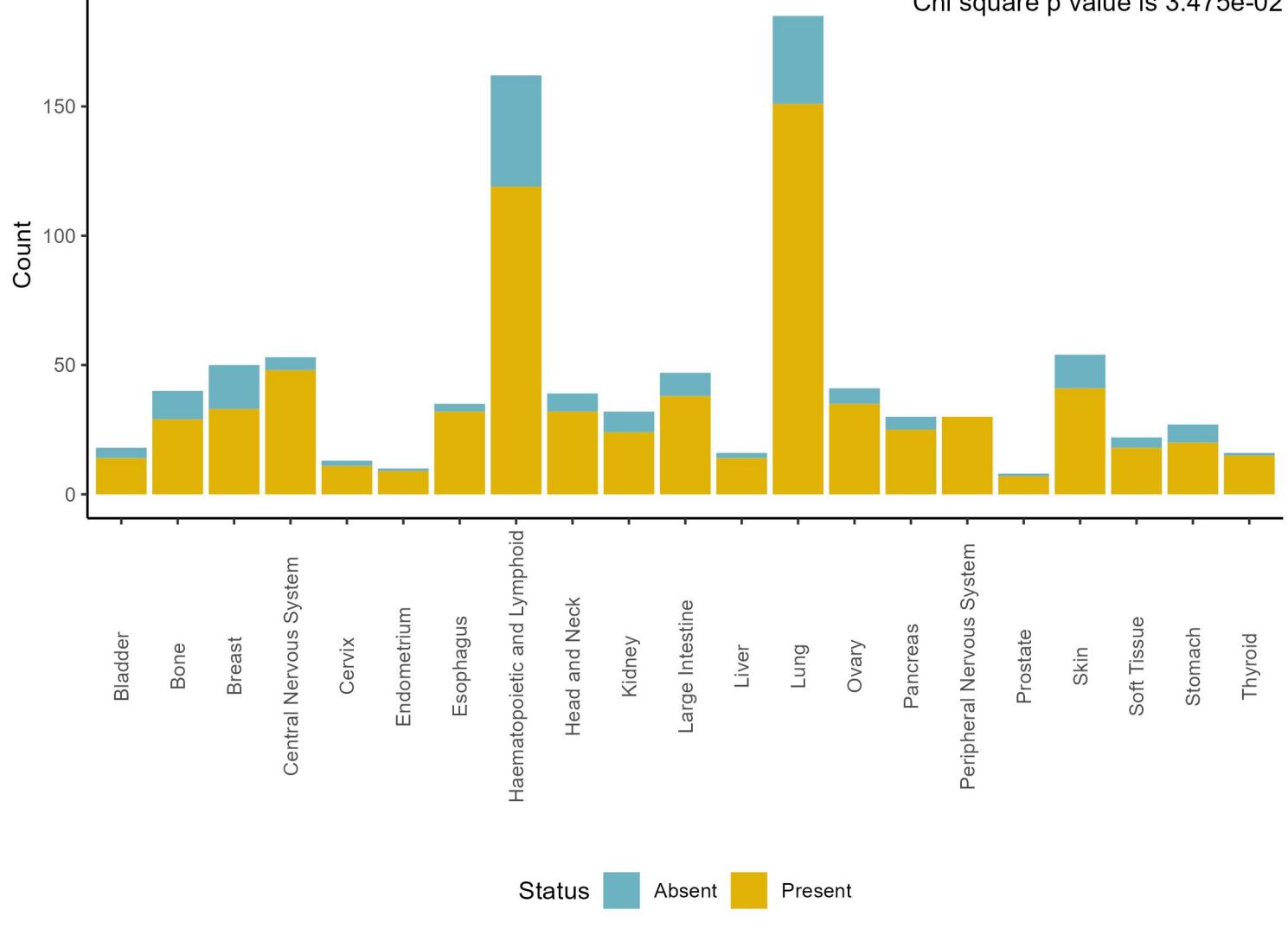
Top positive correlations of ATRX protein, DB1



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



## Present and absent ATRX protein counts by tissue, DB1

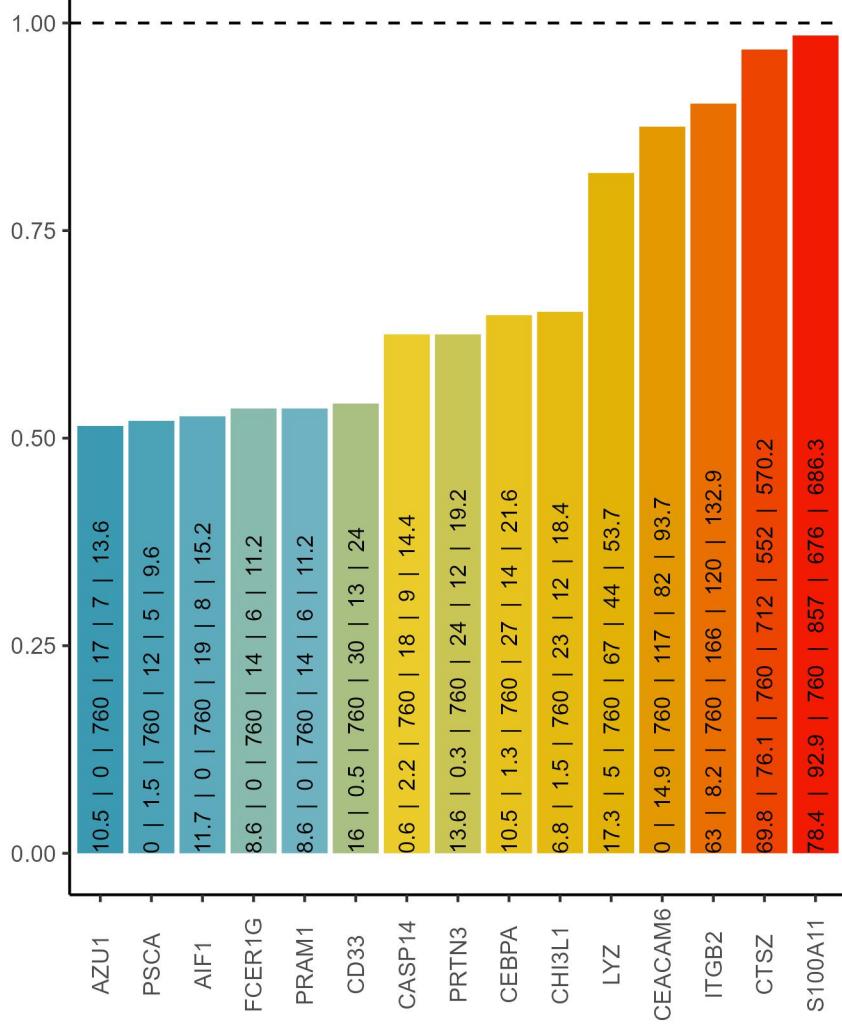


## Cooccurrence with ATRX protein, DB1

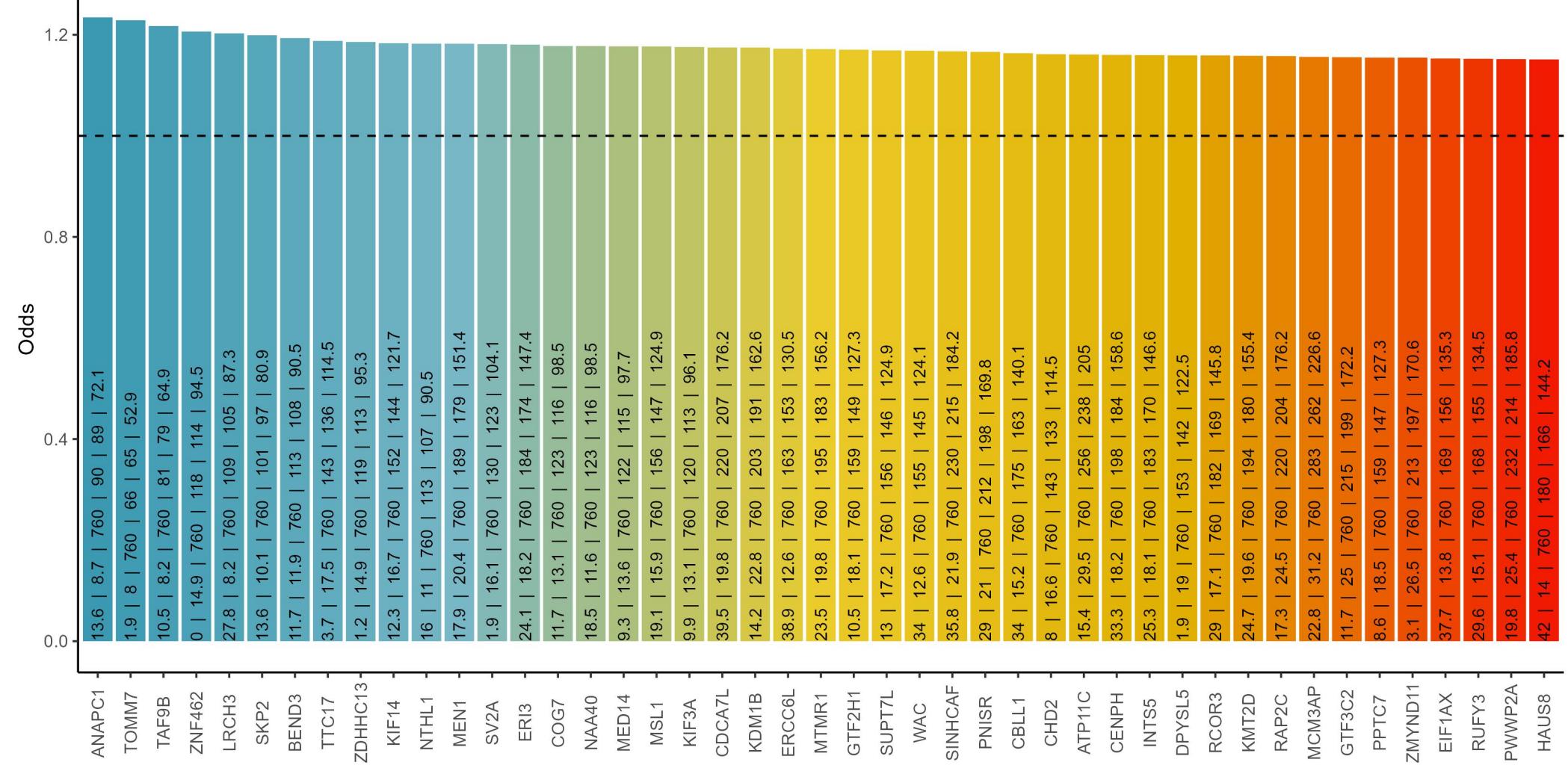
% of ATRX in blood cancers: 73.5 ; % of ATRX in solid cancers: 81.5

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

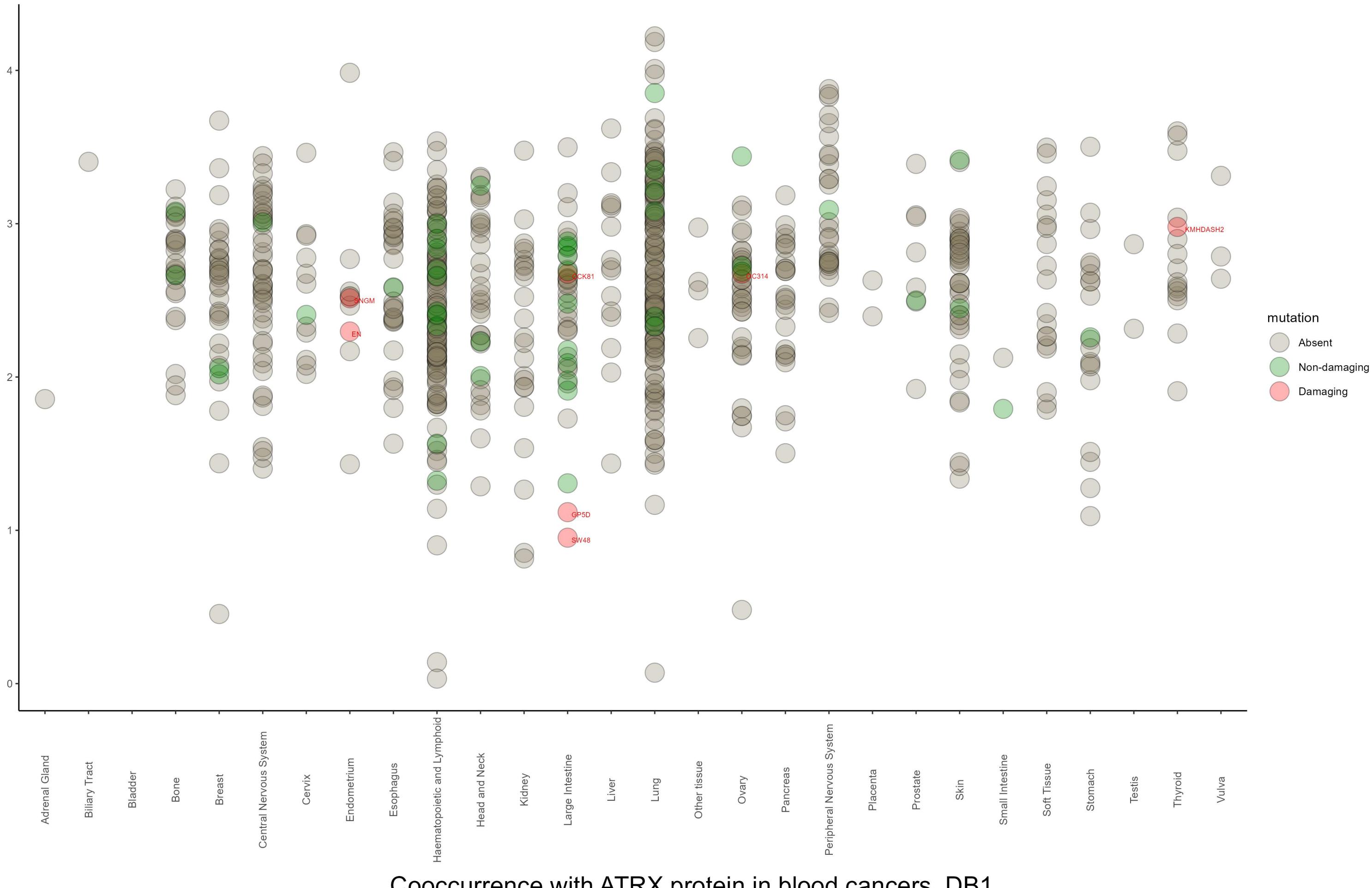
### Negative cooccurrence



### Positive cooccurrence

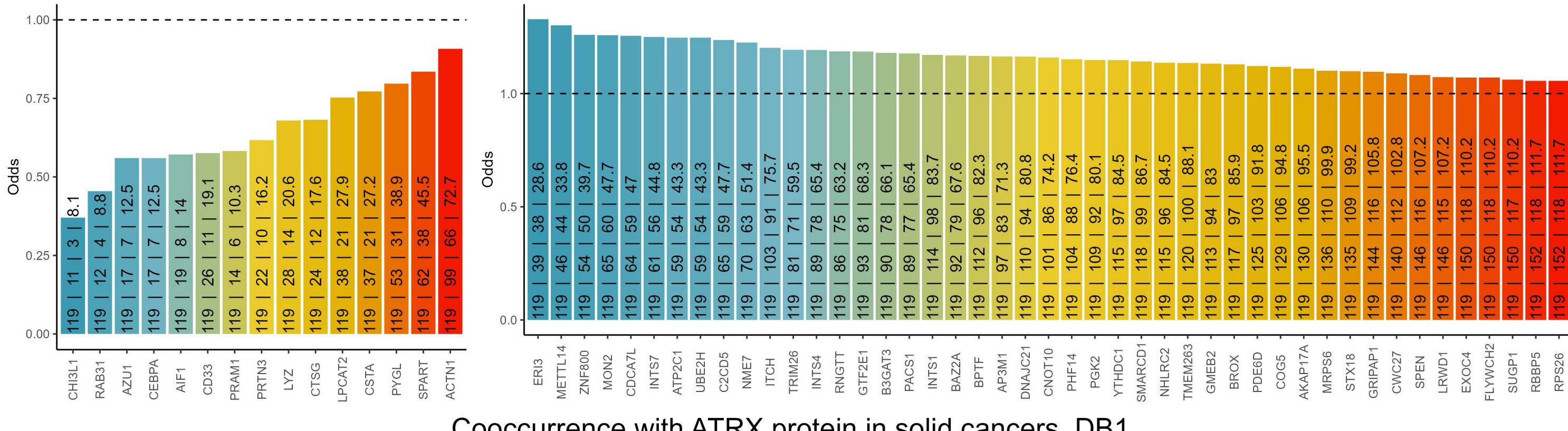


# Amount of ATRX protein and mutation status by tissue, DB1



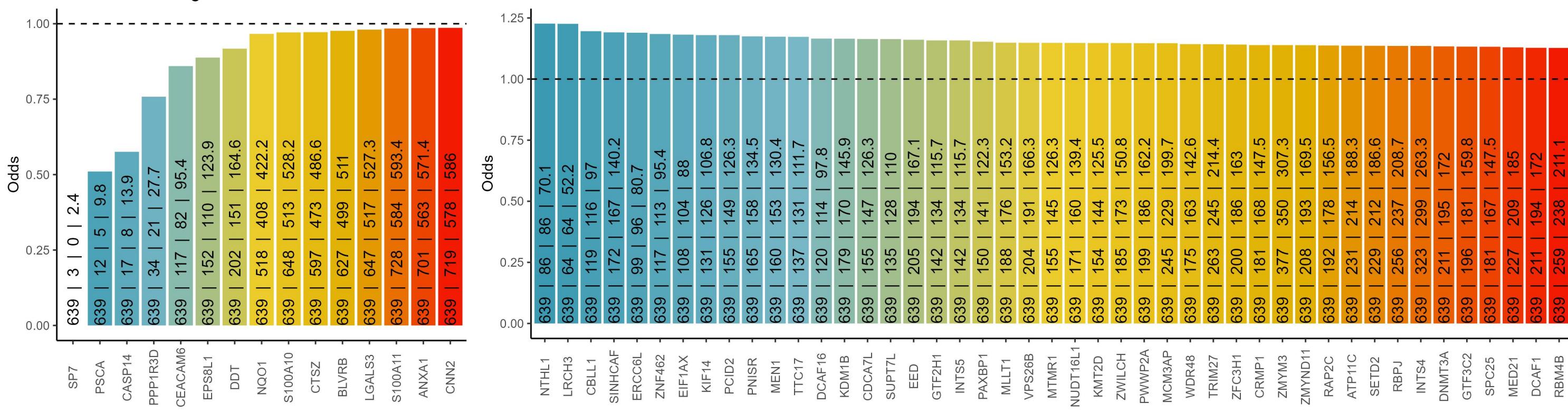
## Cooccurrence with ATRX protein in blood cancers, DB1

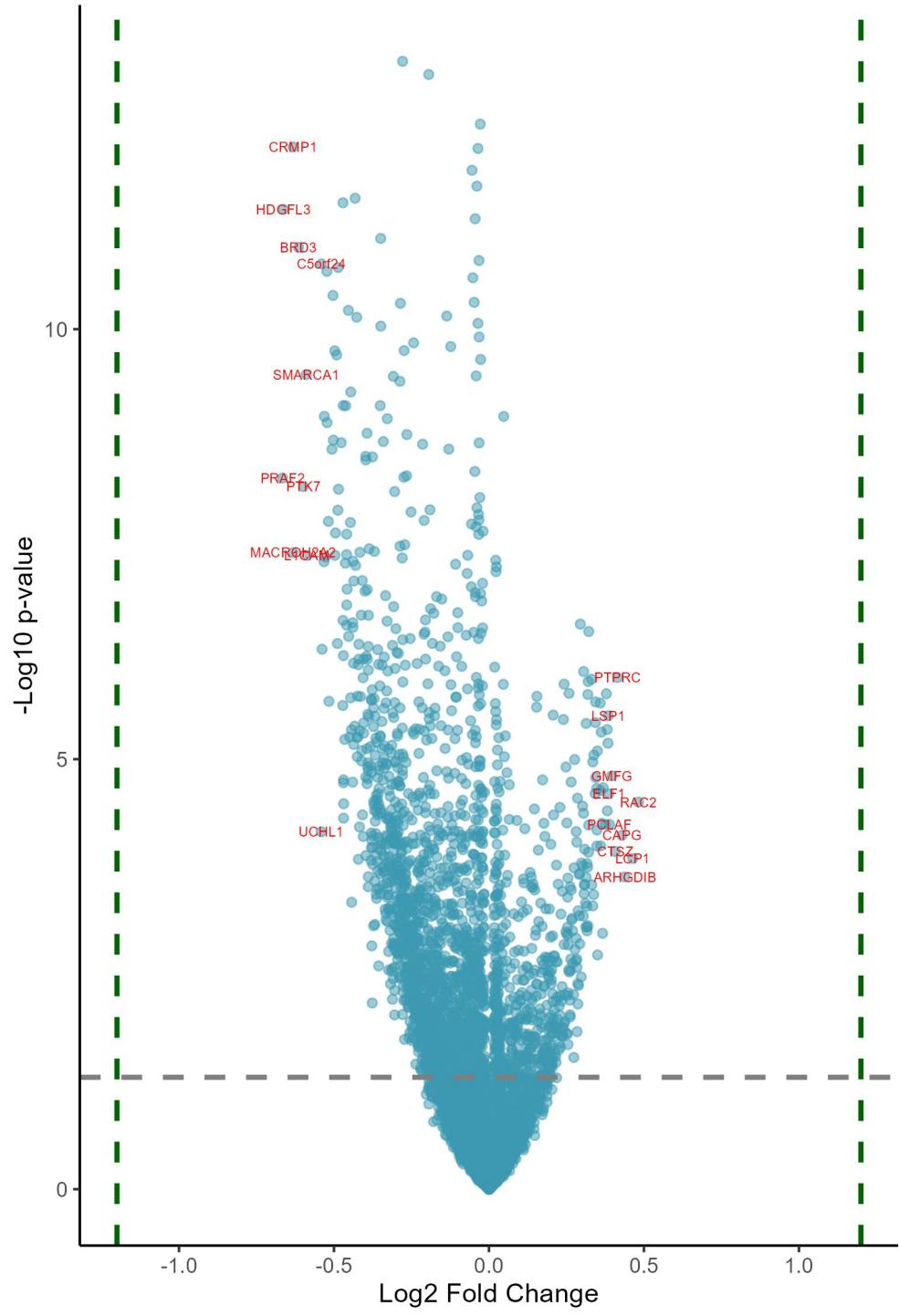
The text in the bars: incidence of ATRX | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



## Cooccurrence with ATRX protein in solid cancers, DB1

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



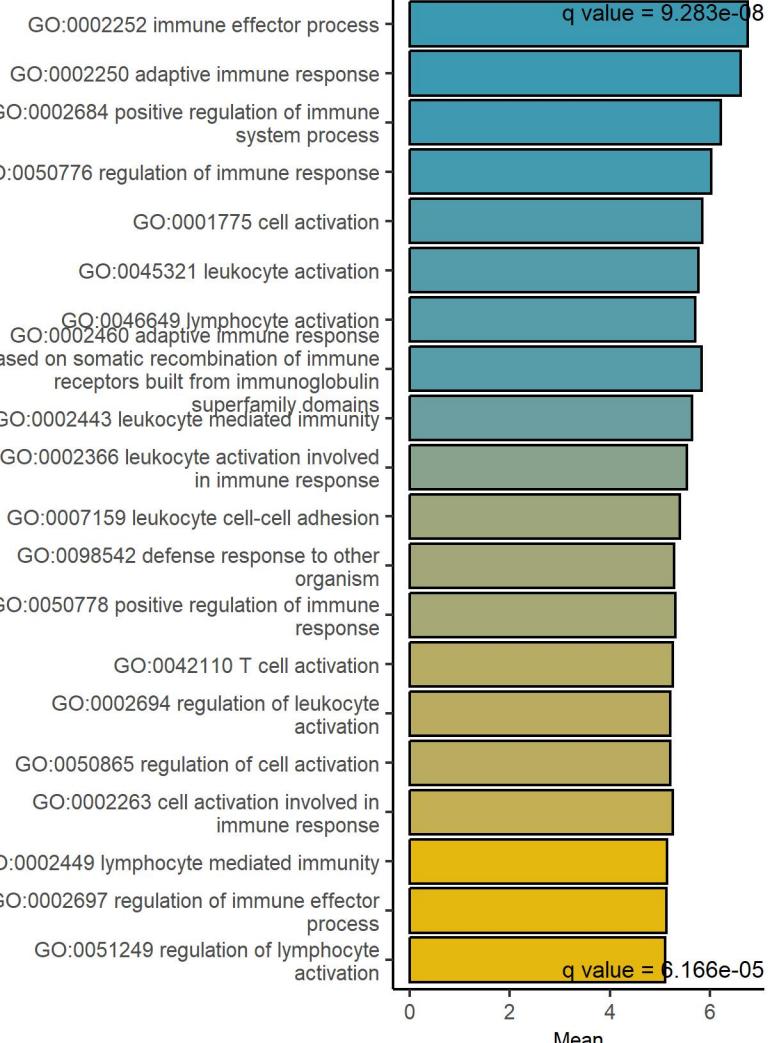


## Downregulated at low/absent ATRX      Upregulated at low/absent ATRX

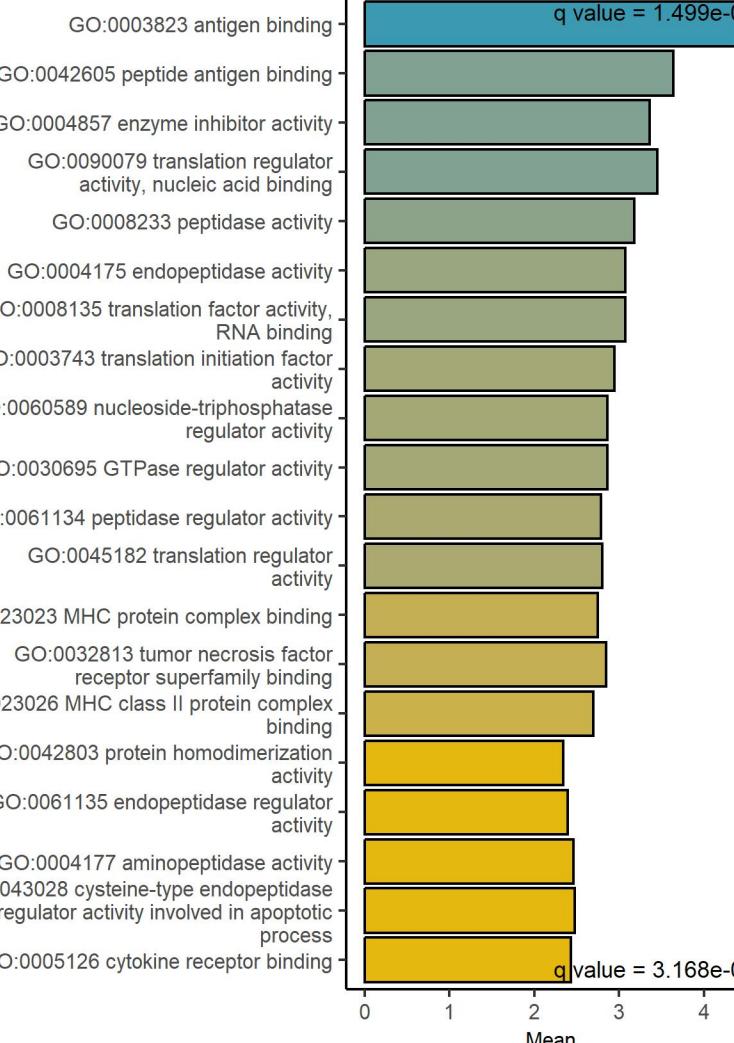
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.67	5.76e-07	PRAF2	PRA1 domain family member 2	0.48	5.31e-04	RAC2	Rac family small GTPase 2
-0.66	2.45e-09	HDGL3	HDGF like 3	0.46	1.62e-03	LCP1	lymphocyte cytosolic protein 1
-0.63	8.78e-10	CRMP1	collapsin response mediator protein	0.44	2.32e-03	ARHGDI1B	Rho GDP dissociation inhibitor beta
-0.63	3.03e-06	MACROH2A2	macroH2A.2 histone	0.43	1.03e-03	CAPG	capping actin protein, gelsolin like
-0.61	5.33e-09	BRD3	bromodomain containing 3	0.41	4.19e-05	PTPRC	protein tyrosine phosphatase receptor
-0.6	7.12e-07	PTK7	protein tyrosine kinase 7 (inactive)	0.41	1.39e-03	CTSZ	cathepsin Z
-0.59	6.36e-08	SMARCA1	SWI/SNF related, matrix associated,	0.4	3.10e-04	GMFG	glia maturation factor gamma
-0.59	3.12e-06	L1CAM	L1 cell adhesion molecule	0.39	8.28e-04	PCLAF	PCNA clamp associated factor
-0.54	9.60e-04	UCHL1	ubiquitin C-terminal hydrolase L1	0.39	4.43e-04	ELF1	E74 like ETS transcription factor 1
-0.54	7.24e-09	C5orf24	chromosome 5 open reading frame 24	0.38	9.08e-05	LSP1	lymphocyte specific protein 1
-0.54	2.32e-05	CRIP2	cysteine rich protein 2	0.38	1.55e-04	SPN	sialophorin
-0.53	3.50e-06	MYEF2	myelin expression factor 2	0.38	6.34e-04	HCLS1	hematopoietic cell-specific Lyn sub
-0.53	1.56e-07	ABCB7	ATP binding cassette subfamily B member	0.38	1.20e-04	ARHGAP45	Rho GTPase activating protein 45
-0.53	3.22e-06	THY1	Thy-1 cell surface antigen	0.38	5.91e-05	ICAM3	intercellular adhesion molecule 3
-0.52	7.86e-09	KIF1A	kinesin family member 1A	0.38	8.28e-04	TAOK3	TAO kinase 3
-0.52	1.77e-07	SUDS3	SDS3 homolog, SIN3A corepressor complex	0.37	3.94e-04	ZFAND1	zinc finger AN1-type containing 1
-0.52	1.55e-06	HIP1	huntingtin interacting protein 1	0.37	7.42e-03	VAMP8	vesicle associated membrane protein
-0.52	6.83e-05	MAP1B	microtubule associated protein 1B	0.36	8.06e-04	GALE	UDP-galactose-4-epimerase
-0.51	3.01e-07	PHF2	PHD finger protein 2	0.36	1.25e-04	INPP5D	inositol polyphosphate-5-phosphatase
-0.5	1.35e-08	KAT7	lysine acetyltransferase 7	0.36	1.24e-03	CA2	carbonic anhydrase 2
-0.5	2.65e-07	B3GAT3	beta-1,3-glucuronidyltransferase 3	0.36	4.14e-04	STK10	serine/threonine kinase 10
-0.5	3.71e-08	DPYSL5	dihydropyrimidinase like 5	0.36	6.99e-05	WAS	WASP actin nucleation promoting factor
-0.5	3.12e-06	MAP2	microtubule associated protein 2	0.35	1.16e-02	ICAM1	intercellular adhesion molecule 1
-0.5	1.97e-06	BPHL	biphenyl hydrolase like	0.35	1.84e-04	CASP8	caspase 8
-0.49	4.02e-08	OCRL	OCRL inositol polyphosphate-5-phosphatase	0.35	9.32e-04	PTPN6	protein tyrosine phosphatase non-receptor type 6
-0.49	2.06e-05	GSTM3	glutathione S-transferase mu 3	0.35	1.24e-03	PTER	phosphotriesterase related
-0.49	1.23e-06	KIF5C	kinesin family member 5C	0.35	3.98e-04	ELMO1	engulfment and cell motility 1
-0.49	7.50e-09	SPIN1	spindlin 1	0.34	3.20e-04	RCSD1	RCSD domain containing 1
-0.49	7.54e-07	NSD3	nuclear receptor binding SET domain	0.34	6.87e-05	MYO1G	myosin Ig

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

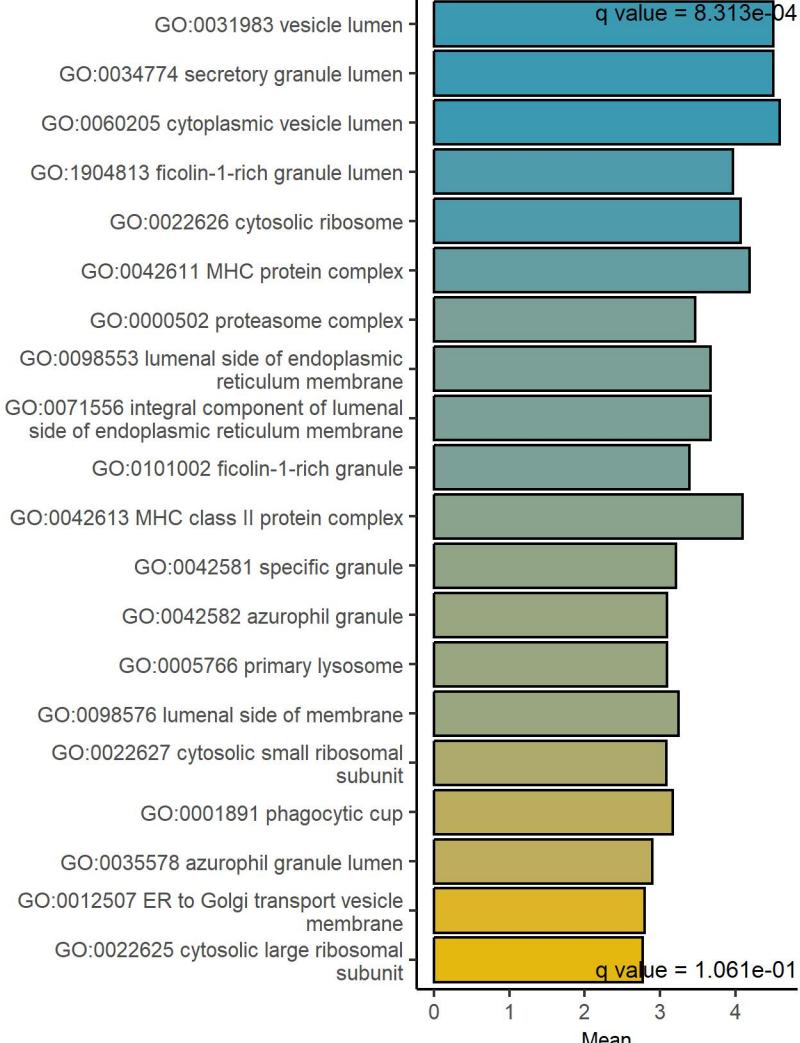
## GO Biological Process upregulated



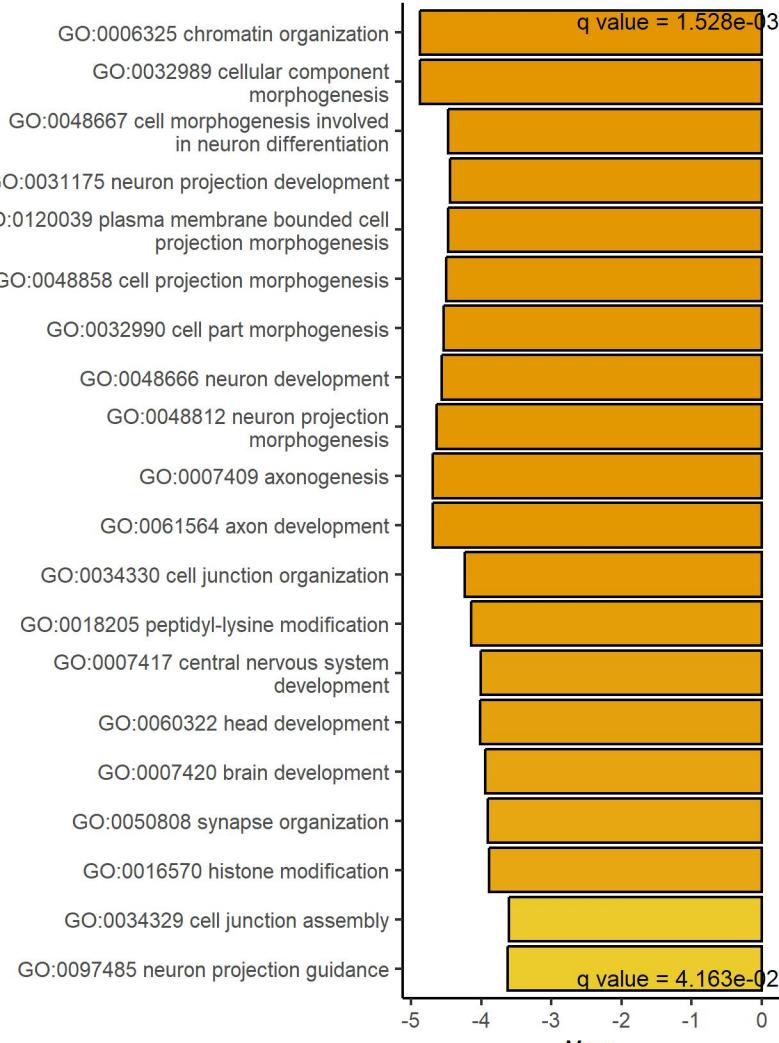
## GO Molecular Function upregulated



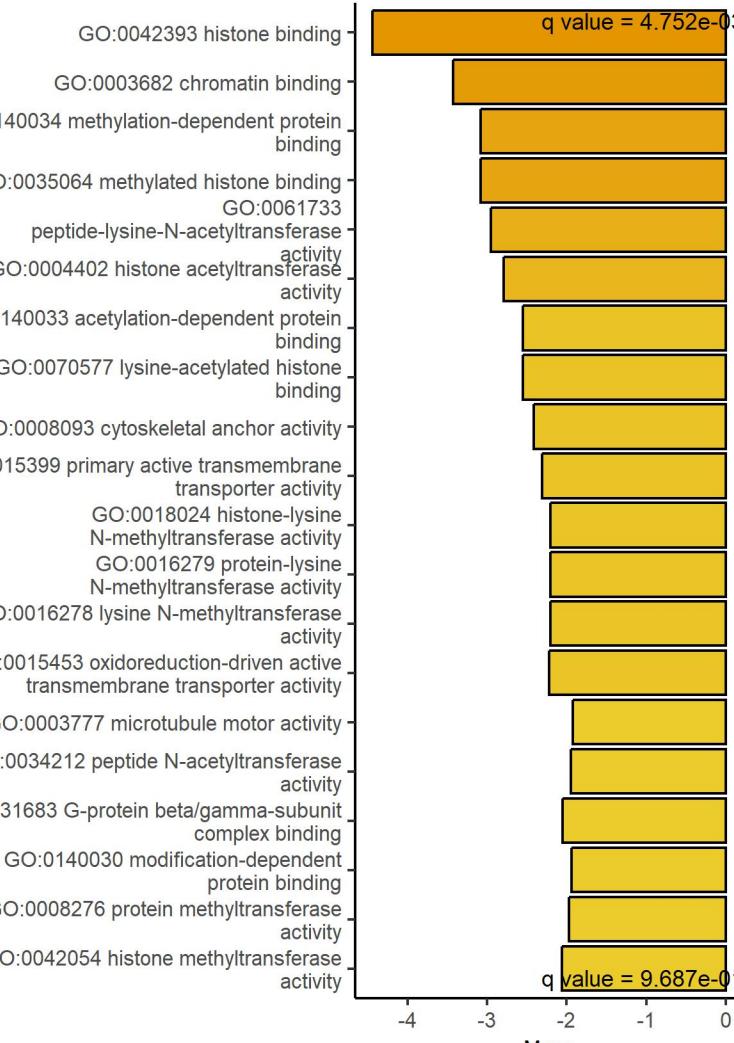
## GO Cellular Component upregulated



## GO Biological Process downregulated

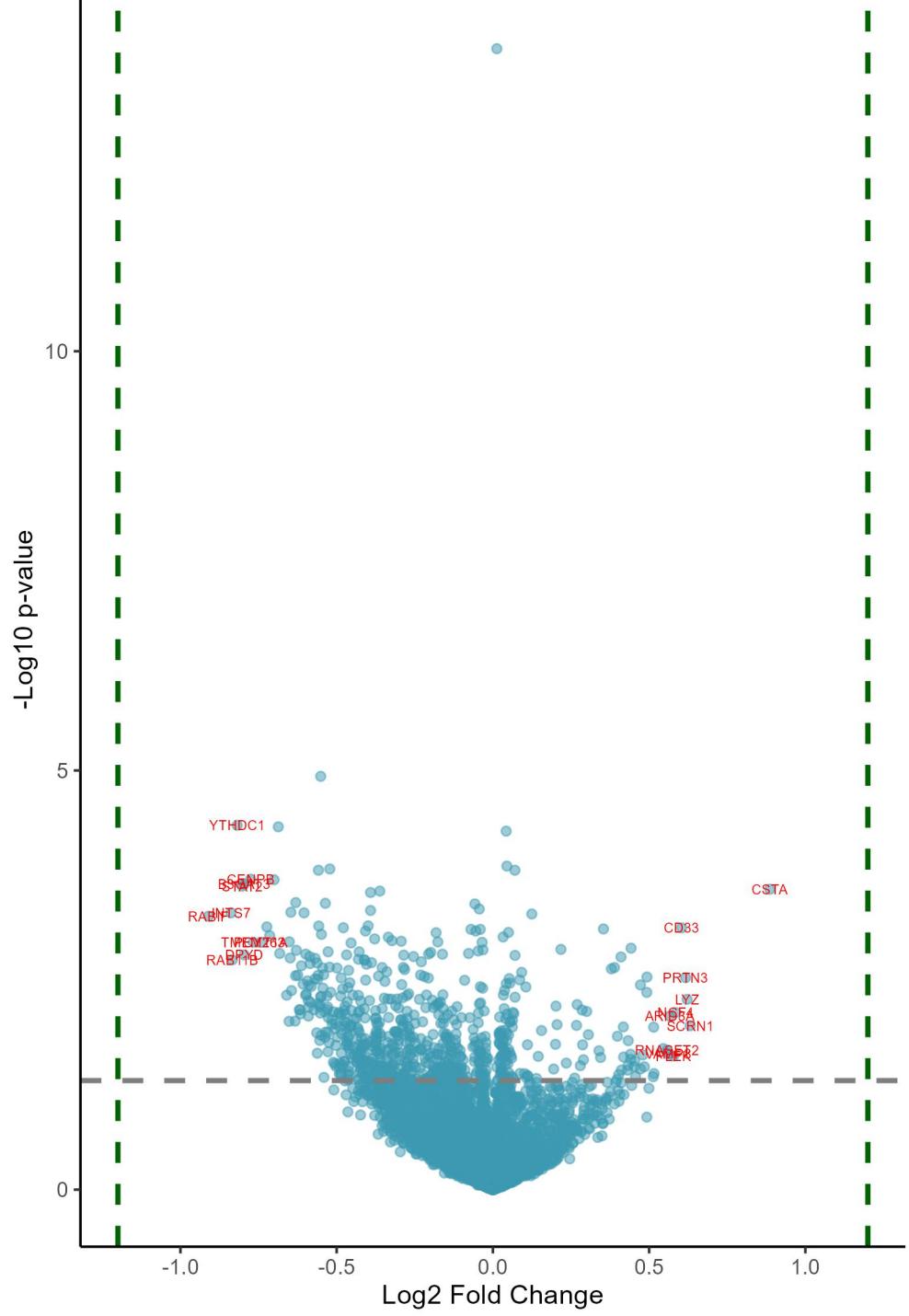


## GO Molecular Function downregulated

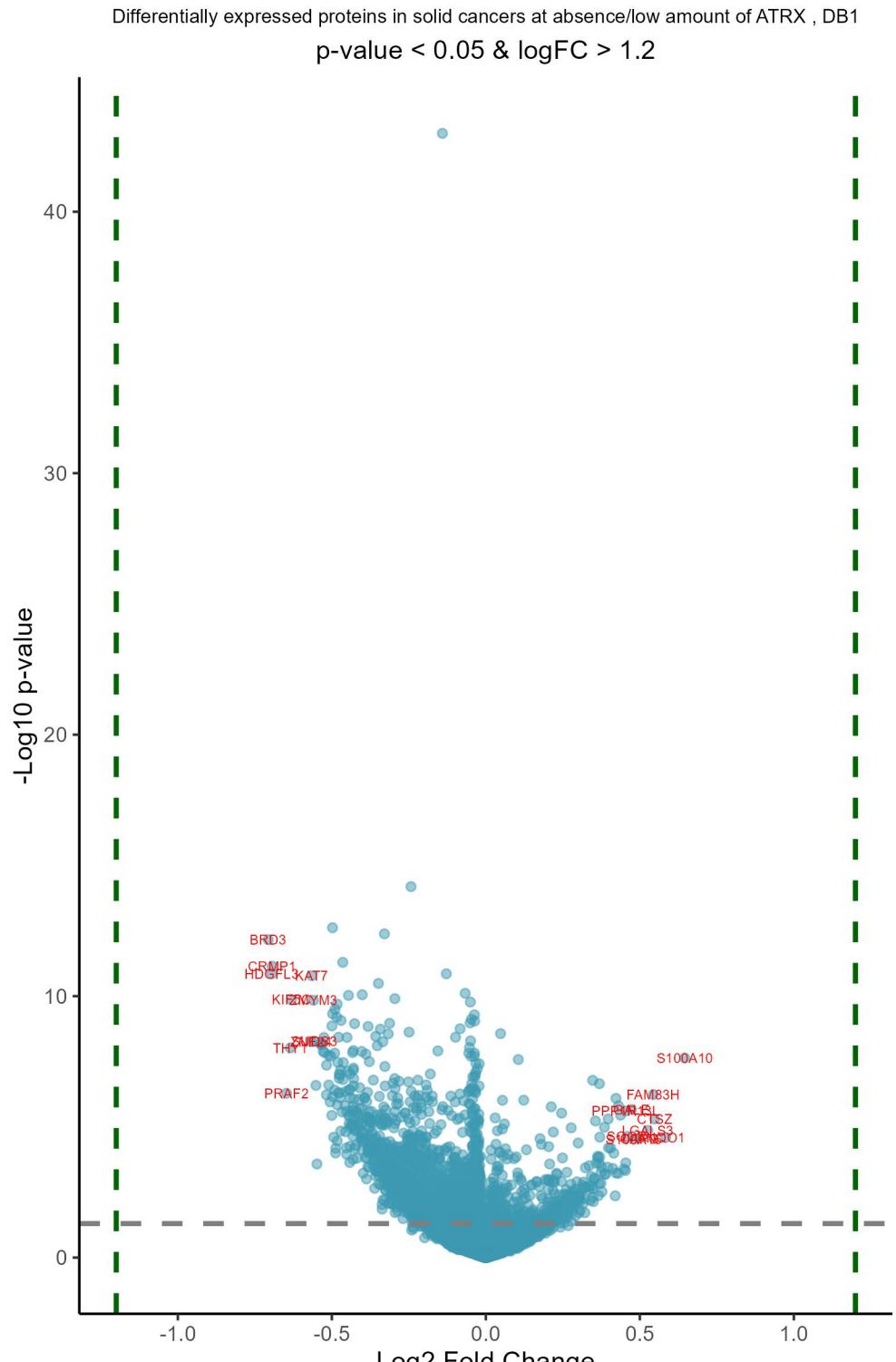


p-value &lt; 0.05 &amp; logFC &gt; 1.2

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

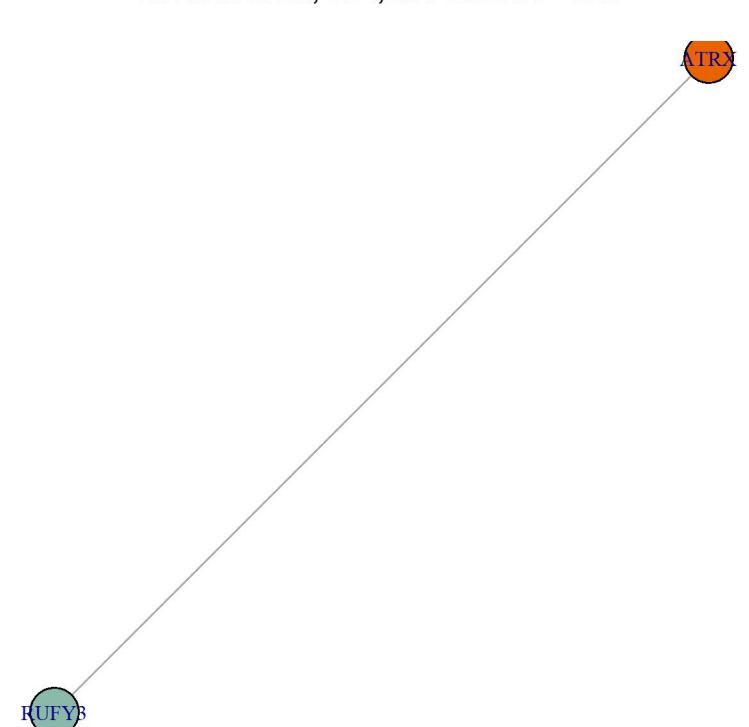


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.91	1.35e-01	RABIF	RAB interacting factor	0.89	1.12e-01	CSTA	cystatin A
-0.84	1.32e-01	INTS7	integrator complex subunit 7	0.63	2.87e-01	SCRN1	secernin 1
-0.83	1.56e-01	RAB11B	RAB11B, member RAS oncogene family	0.62	2.32e-01	LYZ	lysozyme
-0.82	5.87e-02	YTHDC1	YTH domain containing 1	0.62	1.88e-01	PRTN3	proteinase 3
-0.8	1.12e-01	STAT2	signal transducer and activator of	0.6	1.46e-01	CD33	CD33 molecule
-0.8	1.12e-01	B3GAT3	beta-1,3-glucuronyltransferase 3	0.59	2.55e-01	NCF4	neutrophil cytosolic factor 4
-0.8	1.55e-01	DPYD	dihydropyrimidine dehydrogenase	0.58	3.24e-01	PLEK	pleckstrin
-0.78	1.11e-01	CENPB	centromere protein B	0.57	2.63e-01	ARID3A	AT-rich interaction domain 3A
-0.77	1.46e-01	TMEM263	transmembrane protein 263	0.56	3.24e-01	VAMP8	vesicle associated membrane protein
-0.74	1.46e-01	PCYT1A	phosphate cytidyltransferase 1A,	0.56	3.24e-01	RNASET2	ribonuclease T2
-0.72	1.46e-01	IRAK4	interleukin 1 receptor associated k	0.55	3.24e-01	CTSG	cathepsin G
-0.71	1.46e-01	AUH	AU RNA binding methylglutaconyl-CoA	0.52	3.24e-01	CTSZ	cathepsin Z
-0.7	1.11e-01	COX6A1	cytochrome c oxidase subunit 6A1	0.51	2.90e-01	S100A8	S100 calcium binding protein A8
-0.69	5.87e-02	MRPS10	mitochondrial ribosomal protein S10	0.51	3.24e-01	TUBB6	tubulin beta 6 class V
-0.68	1.55e-01	RETREG3	reticulophagy regulator family memb	0.5	3.24e-01	COTL1	coactosin like F-actin binding prot
-0.66	2.27e-01	RUNX1	RUNX family transcription factor 1	0.49	1.88e-01	MTO1	mitochondrial tRNA translation opti
-0.65	2.77e-01	GNG2	G protein subunit gamma 2	0.49	4.51e-01	S100A4	S100 calcium binding protein A4
-0.65	1.46e-01	MPRIP	myosin phosphatase Rho interacting	0.49	2.24e-01	AZU1	azurocidin 1
-0.65	1.56e-01	SNRNP27	small nuclear ribonucleoprotein U4/	0.48	3.24e-01	MRPL54	mitochondrial ribosomal protein L54
-0.65	1.32e-01	ARFGAP3	ADP ribosylation factor GTPase acti	0.48	3.24e-01	AKT1S1	AKT1 substrate 1
-0.64	2.16e-01	CFAP20	cilia and flagella associated prote	0.47	2.00e-01	CES1	carboxylesterase 1
-0.63	2.76e-01	TAP2	transporter 2, ATP binding cassette	0.47	3.24e-01	PLCG2	phospholipase C gamma 2
-0.63	1.87e-01	TAP1	transporter 1, ATP binding cassette	0.46	3.24e-01	PYGL	glycogen phosphorylase L
-0.63	1.30e-01	RFX5	regulatory factor X5	0.45	3.24e-01	MYH11	myosin heavy chain 11
-0.63	1.55e-01	ARL2BP	ADP ribosylation factor like GTPase	0.45	3.24e-01	LPCAT2	lysophosphatidylcholine acyltransfe
-0.62	1.86e-01	F5	coagulation factor V	0.44	3.24e-01	TUBA1C	tubulin alpha 1c
-0.62	2.54e-01	SYNJ2BP	synaptojanin 2 binding protein	0.44	1.55e-01	PLD2	phospholipase D2
-0.62	2.54e-01	PODXL	podocalyxin like	0.44	3.24e-01	MNDA	myeloid cell nuclear differentiatio
-0.62	2.56e-01	FTL	ferritin light chain	0.44	3.24e-01	ASNS	asparagine synthetase (glutamine-hy

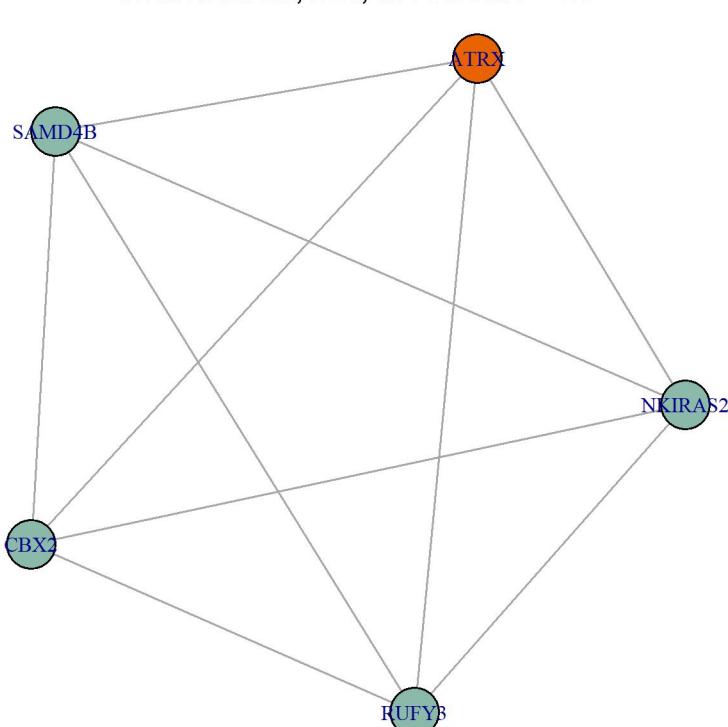


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.71	7.66e-10	BRD3	bromodomain containing 3	0.65	2.30e-06	S100A10	S100 calcium binding protein A10
-0.7	9.39e-09	HDGFL3	HDGF like 3	0.58	5.46e-04	NQO1	NAD(P)H quinone dehydrogenase 1
-0.69	5.95e-09	CRMP1	collapsin response mediator protein	0.55	1.49e-04	CTSZ	cathepsin Z
-0.65	2.74e-05	PRAF2	PRA1 domain family member 2	0.54	2.99e-05	FAM83H	family with sequence similarity 83
-0.63	1.22e-06	THY1	Thy-1 cell surface antigen	0.53	3.34e-04	LGALS3	galectin 3
-0.63	5.32e-08	KIF5C	kinesin family member 5C	0.5	5.88e-04	CAPG	capping actin protein, gelsolin lik
-0.57	8.00e-07	ZNF24	zinc finger protein 24	0.48	6.22e-04	S100A16	S100 calcium binding protein A16
-0.57	1.00e-08	KAT7	lysine acetyltransferase 7	0.47	8.19e-05	GALE	UDP-galactose-4-epimerase
-0.56	5.32e-08	ZMYM3	zinc finger MYM-type containing 3	0.46	5.16e-04	SQOR	sulfide quinone oxidoreductase
-0.56	8.00e-07	SUDS3	SDS3 homolog, SIN3A corepressor com	0.45	8.91e-05	PPP1R13L	protein phosphatase 1 regulatory su
-0.55	1.67e-05	MYEF2	myelin expression factor 2	0.45	3.00e-03	ANXA3	annexin A3
-0.55	3.24e-03	UCHL1	ubiquitin C-terminal hydrolase L1	0.45	4.94e-03	CD44	CD44 molecule (Indian blood group)
-0.54	9.50e-07	KIF1A	kinesin family member 1A	0.45	4.53e-03	ICAM1	intercellular adhesion molecule 1
-0.53	9.50e-07	DPYSL5	dihydropyrimidinase like 5	0.44	1.17e-04	ADGRE5	adhesion G protein-coupled receptor
-0.53	9.05e-07	NSD2	nuclear receptor binding SET domain	0.43	6.39e-05	MVP	major vault protein
-0.53	1.55e-06	NSD3	nuclear receptor binding SET domain	0.43	5.98e-03	S100A6	S100 calcium binding protein A6
-0.53	6.04e-07	SARM1	sterile alpha and TIR motif contain	0.42	5.84e-03	MISP	mitotic spindle positioning
-0.52	1.65e-06	SCML2	Scm polycomb group protein like 2	0.42	3.77e-05	S100A11	S100 calcium binding protein A11
-0.52	3.07e-05	MAP2	microtubule associated protein 2	0.42	2.51e-02	KRT7	keratin 7
-0.52	3.92e-06	MTFR1L	mitochondrial fission regulator 1 l	0.42	1.57e-03	DSG2	desmoglein 2
-0.51	1.93e-06	C5orf24	chromosome 5 open reading frame 24	0.41	4.38e-03	CD59	CD59 molecule (CD59 blood group)
-0.51	1.64e-05	USP11	ubiquitin specific peptidase 11	0.4	1.12e-03	RHOC	ras homolog family member C
-0.51	4.74e-05	PMF1	polyamine modulated factor 1	0.4	1.12e-03	HTATIP2	HIV-1 Tat interactive protein 2
-0.5	2.02e-06	UHRF2	ubiquitin like with PHD and ring fi	0.4	1.49e-04	BAG3	BAG cochaperone 3
-0.5	1.18e-04	MSI2	musashi RNA binding protein 2	0.4	4.04e-03	NDRG1	N-myc downstream regulated 1
-0.5	2.97e-07	SPINDOC	spindlin interactor and repressor o	0.39	6.27e-03	EPS8L2	EPS8 like 2
-0.5	4.02e-10	RBM4B	RNA binding motif protein 4B	0.39	6.32e-03	LGALS1	galectin 1
-0.5	1.44e-07	DNMT3A	DNA methyltransferase 3 alpha	0.38	2.59e-04	BLVRB	biliverdin reductase B
-0.5	3.41e-05	ADD2	adducin 2	0.38	1.92e-02	CAVIN3	caveolae associated protein 3

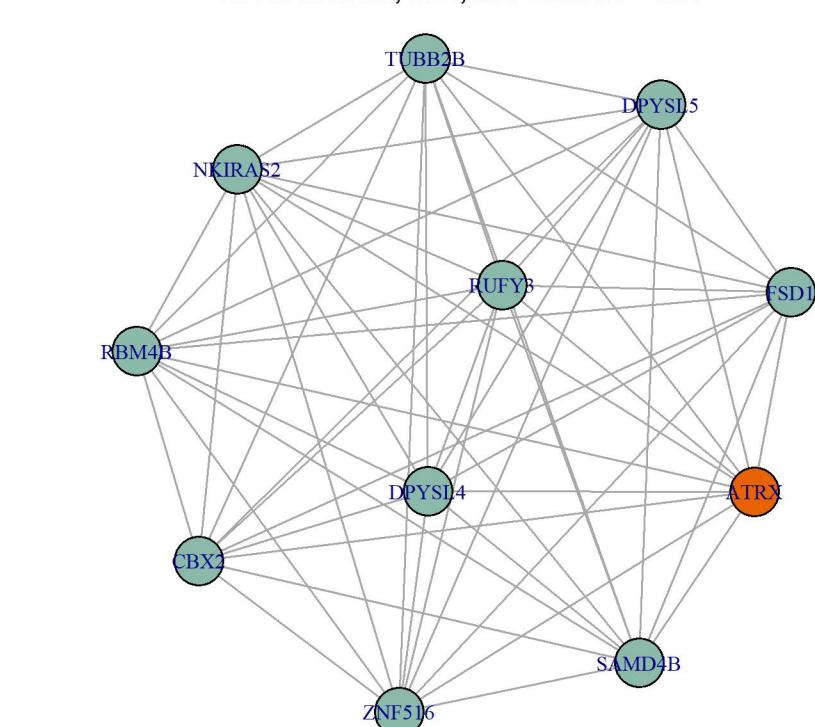
ATRX network, DB1, all Pearson r &gt; 0.45



ATRX network, DB1, all Pearson r &gt; 0.4



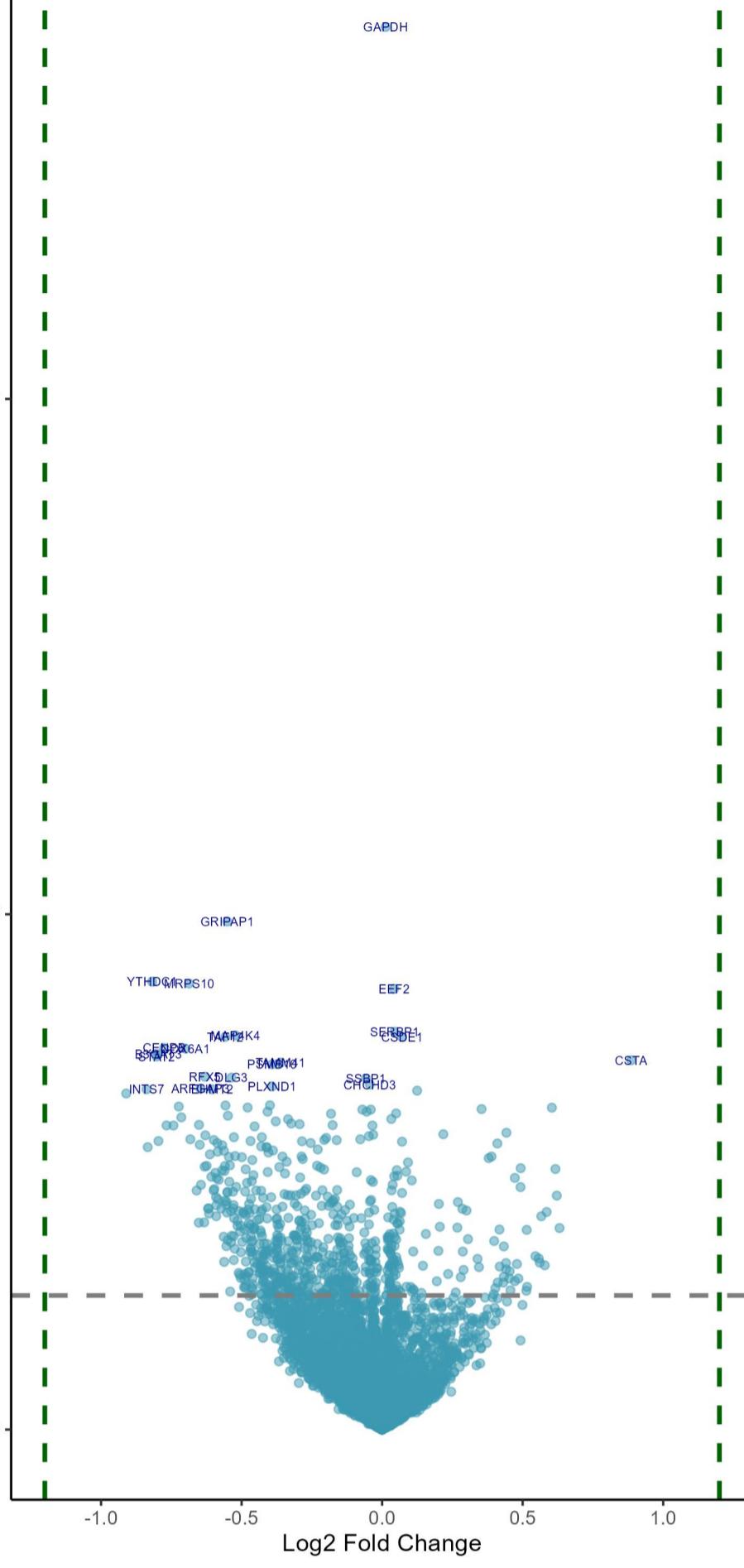
ATRX network, DB1, all Pearson r &gt; 0.35



Sorted by p values!

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

-Log10 p-value

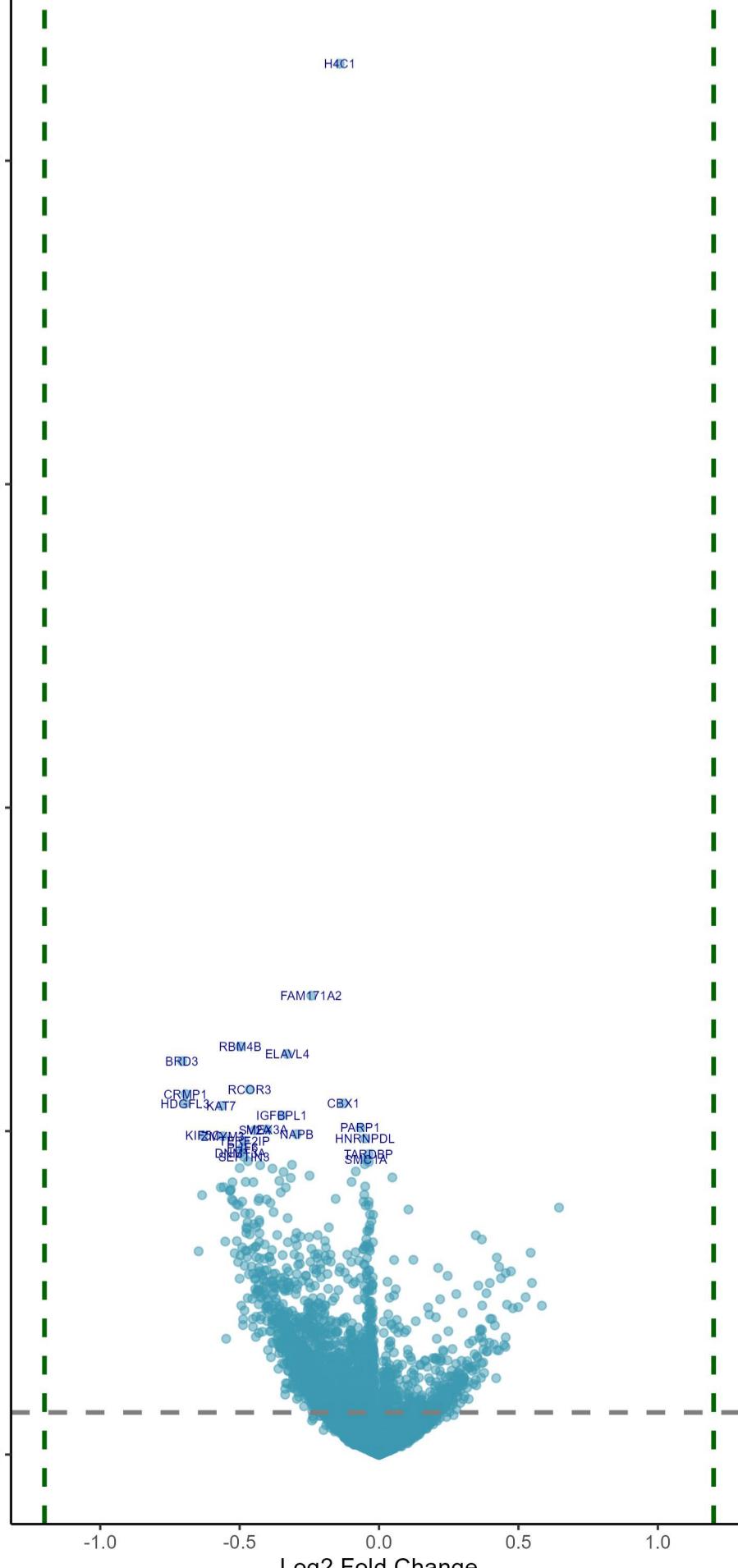


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.55	2.60e-02	GRIPAP1	GRIP1 associated protein 1	0.01	8.19e-11	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
-0.82	5.87e-02	YTHDC1	YTH domain containing 1	0.04	5.87e-02	EEF2	eukaryotic translation elongation factor 2
-0.69	5.87e-02	MRPS10	mitochondrial ribosomal protein S10	0.04	1.03e-01	SERBP1	SERPINE1 mRNA binding protein 1
-0.52	1.03e-01	MAP4K4	mitogen-activated protein kinase kinase 4	0.07	1.03e-01	CSDE1	cold shock domain containing E1
-0.56	1.03e-01	TAF12	TATA-box binding protein associated factor 12	0.89	1.12e-01	CSTA	cystatin A
-0.78	1.11e-01	CENPB	centromere protein B	0.12	1.32e-01	CLUH	clustered mitochondria homolog
-0.7	1.11e-01	COX6A1	cytochrome c oxidase subunit 6A1	0.6	1.46e-01	CD33	CD33 molecule
-0.8	1.12e-01	B3GAT3	beta-1,3-glucuronidyltransferase 3	0.35	1.46e-01	WASL	WASP like actin nucleation promoting factor
-0.8	1.12e-01	STAT2	signal transducer and activator of transcription 2	0.05	1.46e-01	PSME3	proteasome activator subunit 3
-0.36	1.12e-01	TAMM41	TAMM41 mitochondrial translocator protein	0.03	1.46e-01	HSP90AB1	heat shock protein 90 alpha family member B1
-0.39	1.12e-01	PSMB10	proteasome 20S subunit beta 10	0.44	1.55e-01	PLD2	phospholipase D2
-0.63	1.30e-01	RFX5	regulatory factor X5	0.22	1.55e-01	VRK2	VRK serine/threonine kinase 2
-0.54	1.30e-01	DLG3	discs large MAGUK scaffold protein 3	0.07	1.55e-01	PSMB6	proteasome 20S subunit beta 6
-0.06	1.30e-01	SSBP1	single stranded DNA binding protein 1	0.41	1.55e-01	IMPA2	inositol monophosphatase 2
-0.04	1.32e-01	CHCHD3	coiled-coil-helix-coiled-coil-helix motif containing 3	0.39	1.68e-01	CEBPA	CCAAT enhancer binding protein alpha
-0.39	1.32e-01	PLXND1	plexin D1	0.38	1.70e-01	RAB44	RAB44, member RAS oncogene family
-0.65	1.32e-01	ARFGAP3	ADP ribosylation factor GTPase activating protein 3	0.09	1.79e-01	BCCIP	BRCA2 and CDKN1A interacting protein
-0.84	1.32e-01	INTS7	integrator complex subunit 7	0.49	1.88e-01	MTO1	mitochondrial tRNA translation optimizes
-0.6	1.32e-01	EHMT2	euchromatic histone lysine methyltransferase 2	0.62	1.88e-01	PRTN3	proteinase 3
-0.91	1.35e-01	RABIF	RAB interacting factor	0.05	1.88e-01	PSMB7	proteasome 20S subunit beta 7
-0.4	1.46e-01	MSL1	MSL complex subunit 1	0.09	1.89e-01	ATG3	autophagy related 3
-0.56	1.46e-01	HSPB11	heat shock protein family B (small)	0.05	1.97e-01	BTF3	basic transcription factor 3
-0.72	1.46e-01	IRAK4	interleukin 1 receptor associated kinase 4	0.04	1.98e-01	CDC37	cell division cycle 37, HSP90 cochaperone
-0.48	1.46e-01	IFI16	interferon gamma inducible protein 16	0.47	2.00e-01	CES1	carboxylesterase 1
-0.07	1.46e-01	HP1BP3	heterochromatin protein 1 binding protein 3	0.11	2.05e-01	DOHH	deoxyhypusine hydroxylase
-0.04	1.46e-01	RBM14	RNA binding motif protein 14	0.04	2.16e-01	PABPC1	poly(A) binding protein cytoplasmic 1
-0.41	1.46e-01	SPEN	spen family transcriptional repressor	0.49	2.24e-01	AZU1	azurocidin 1
-0.05	1.46e-01	HSD17B10	hydroxysteroid 17-beta dehydrogenase 10	0.03	2.27e-01	RPS21	ribosomal protein S21
-0.18	1.46e-01	POGZ	pogo transposable element derived protein	0.07	2.29e-01	DRG1	developmentally regulated GTP binding protein
-0.55	1.46e-01	WDR44	WD repeat domain 44	0.62	2.32e-01	LYZ	lysozyme
-0.71	1.46e-01	AUH	AU RNA binding methylglutaryl-CoA	0.27	2.46e-01	ITM2B	integral membrane protein 2B
-0.33	1.46e-01	WDR70	WD repeat domain 70	0.2	2.51e-01	GAPVD1	GTPase activating protein and VPS9
-0.38	1.46e-01	FLYWCH2	FLYWCH family member 2	0.04	2.52e-01	PDCD6IP	programmed cell death 6 interacting protein
-0.32	1.46e-01	RBBP5	RB binding protein 5, histone lysine acetyltransferase 5	0.29	2.54e-01	MED26	mediator complex subunit 26
-0.29	1.46e-01	LEMD3	LEM domain containing 3	0.3	2.54e-01	ATG7	autophagy related 7
-0.65	1.46e-01	MPRIP	myosin phosphatase Rho interacting protein	0.06	2.55e-01	ATP6V1G1	ATPase H <sup>+</sup> transporting V1 subunit G
-0.18	1.46e-01	LLRRC41	leucine rich repeat containing 41	0.59	2.55e-01	NCF4	neutrophil cytosolic factor 4
-0.77	1.46e-01	TMEM263	transmembrane protein 263	0.07	2.56e-01	IPO4	importin 4
0.74	1.46e-01	DCLRE1A	phosphotidylserine transferase 1A	0.04	2.56e-01	OARS1	glutaminyl tRNA synthetase 1

Sorted by p values!

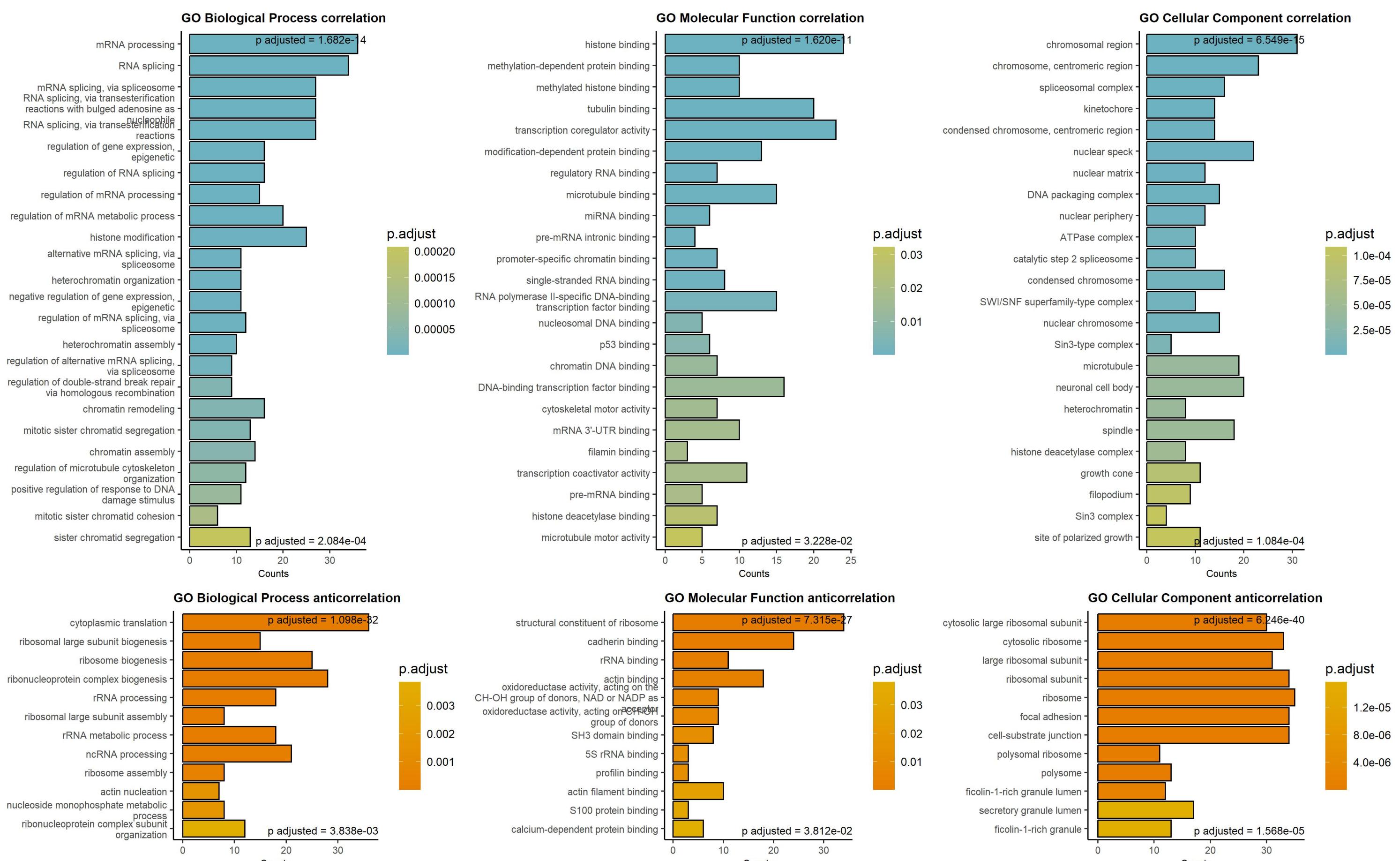
Downregulated in solid cancers at low/absent ATRX Upregulated in solid cancers at low/absent ATRX

-Log10 p-value

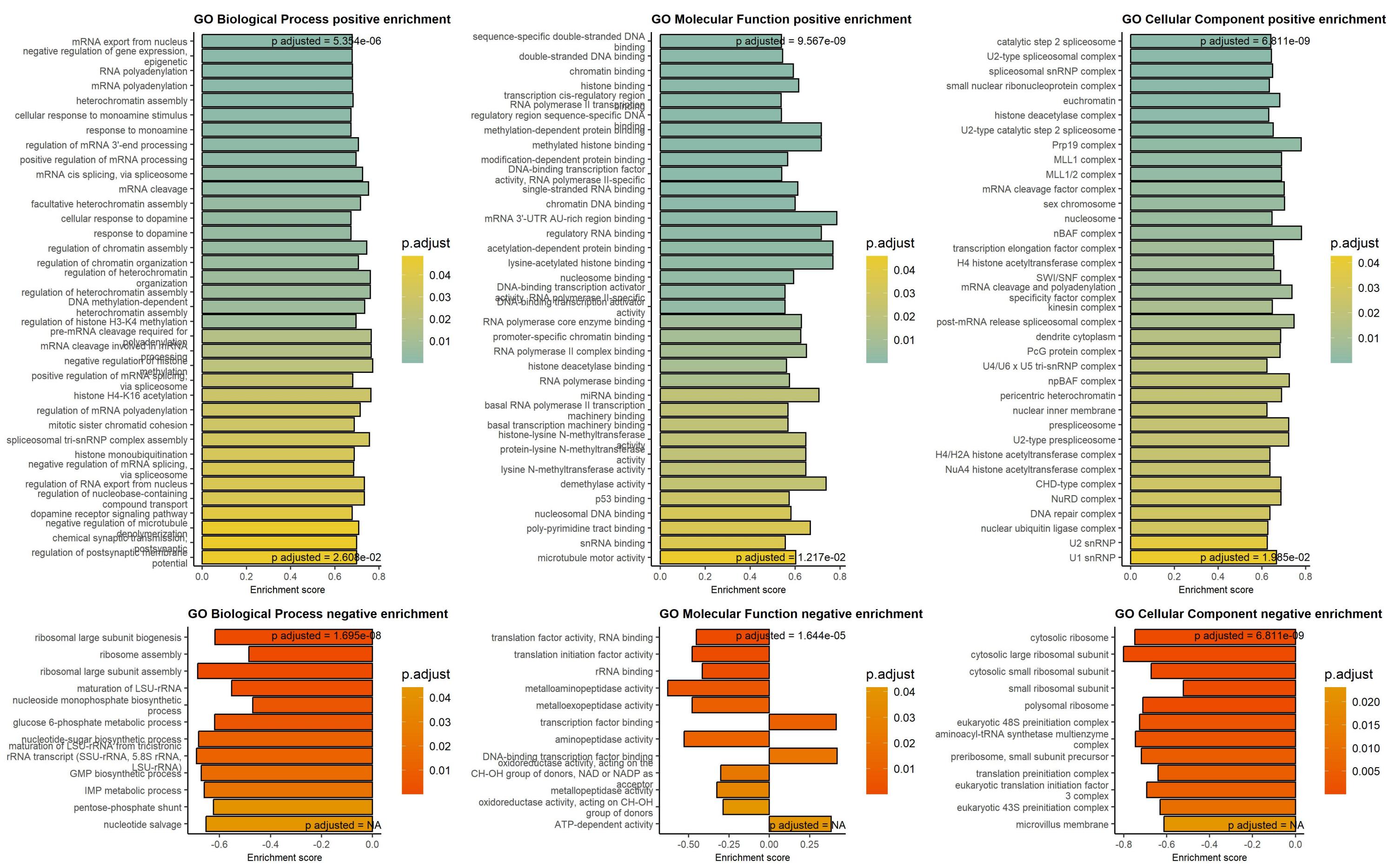


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.14	3.34e-40	H4C1	H4 clustered histone 1	0.05	5.00e-07	EEF1D	eukaryotic translation elongation factor 1D
-0.24	1.44e-11	FAM171A2	family with sequence similarity 171	0.65	2.30e-06	S100A10	S100 calcium binding protein A10
-0.5	4.02e-10	RBM4B	RNA binding motif protein 4B	0.11	2.60e-06	LMNA	lamin A/C
-0.33	5.51e-10	ELAVL4	ELAV like RNA binding protein 4	0.35	1.16e-05	YBX3	Y-box binding protein 3
-0.71	7.66e-10	BRD3	bromodomain containing 3	0.37	1.49e-05	CNN2	calponin 2
-0.46	4.86e-09	RCOR3	REST corepressor 3	0.54	2.99e-05	FAM83H	family with sequence similarity 83
-0.69	5.95e-09	CRMP1	collapsin response mediator protein 1	0.42	3.77e-05	S100A11	S100 calcium binding protein A11
-0.13	9.39e-09	CBX1	chromobox 1	0.12	4.28e-05	PLEC	plectin
-0.7	9.39e-09	HDGFL3	HDGF like 3	0.05	4.29e-05	TPD52L2	TPD52 like 2
-0.57	1.00e-08	KAT7	lysine acetyltransferase 7	0.43	6.39e-05	MVP	major vault protein
-0.35	1.81e-08	IGFBPL1	insulin like growth factor binding protein 1	0.21	6.78e-05	ANXA2	annexin A2
-0.07	4.00e-08	PARP1	poly(ADP-ribose) polymerase 1	0.47	8.19e-05	GALE	UDP-galactose-4-epimerase
-0.4	4.15e-08	MEX3A	mex-3 RNA binding family member A	0.45	8.91e-05	PPP1R13L	protein phosphatase 1 regulatory subunit 13L
-0.45	4.15e-08	SV2A	synaptic vesicle glycoprotein 2A	0.25	1.02e-04	SQSTM1	sequestosome 1
-0.3	5.18e-08	NAPB	NSF attachment protein beta	0.44	1.17e-04	ADGRE5	adhesion G protein-coupled receptor E
-0.63	5.32e-08	KIF5C	kinesin family member 5C	0.03	1.40e-04	EIF6	eukaryotic translation initiation factor 6
-0.56	5.32e-08	ZMYM3	zinc finger MYM-type containing 3	0.55	1.49e-04	CTS2	cathepsin Z
-0.05	5.90e-08	HNRNPD1	heterogeneous nuclear ribonucleoprotein D1	0.4	1.49e-04	BAG3	BAG co-chaperone 3
-0.48	6.75e-08	TERF2IP	TERF2 interacting protein	0.36	1.71e-04	CASP8	caspase 8
-0.49	1.01e-07	PHF6	PHD finger protein 6	0.06	2.06e-04	TMOD3	tropomodulin 3
-0.5	1.44e-07	DNMT3A	DNA methyltransferase 3 alpha	0.38	2.59e-04	BLVRB	biliverdin reductase B
-0.04	1.50e-07	TARDBP	TAR DNA binding protein	0.28	2.73e-04	EHD4	EH domain containing 4
-0.48	1.76e-07	SEPTIN3	septin 3	0.05	2.96e-04	IQQAP1	IQ motif containing GTPase activating protein 1
-0.05	2.02e-07	SMC1A	structural maintenance of chromosomes 1A	0.53	3.34e-04	LGALS3	galectin 3
-0.47	2.18e-07	VEZF1	vascular endothelial zinc finger 1	0.04	3.42e-04	P4HB	prolyl 4-hydroxylase subunit beta
-0.04	2.21e-07	RSRF1	serine and arginine rich splicing factor 1	0.22	3.71e-04	PLIN3	perilipin 3

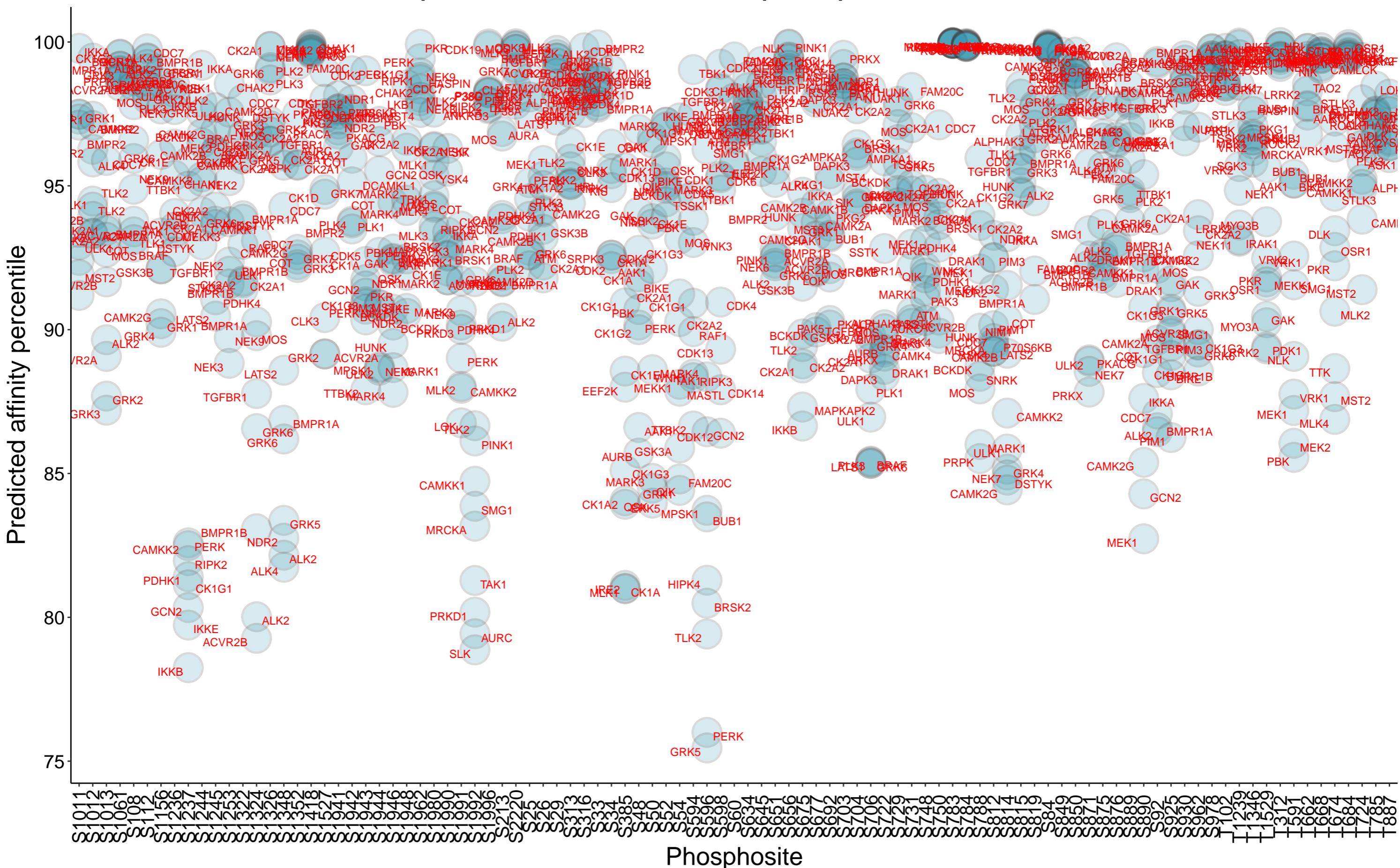
# Top 250 correlation coefficients overrepresentation, ATRX protein, DB1



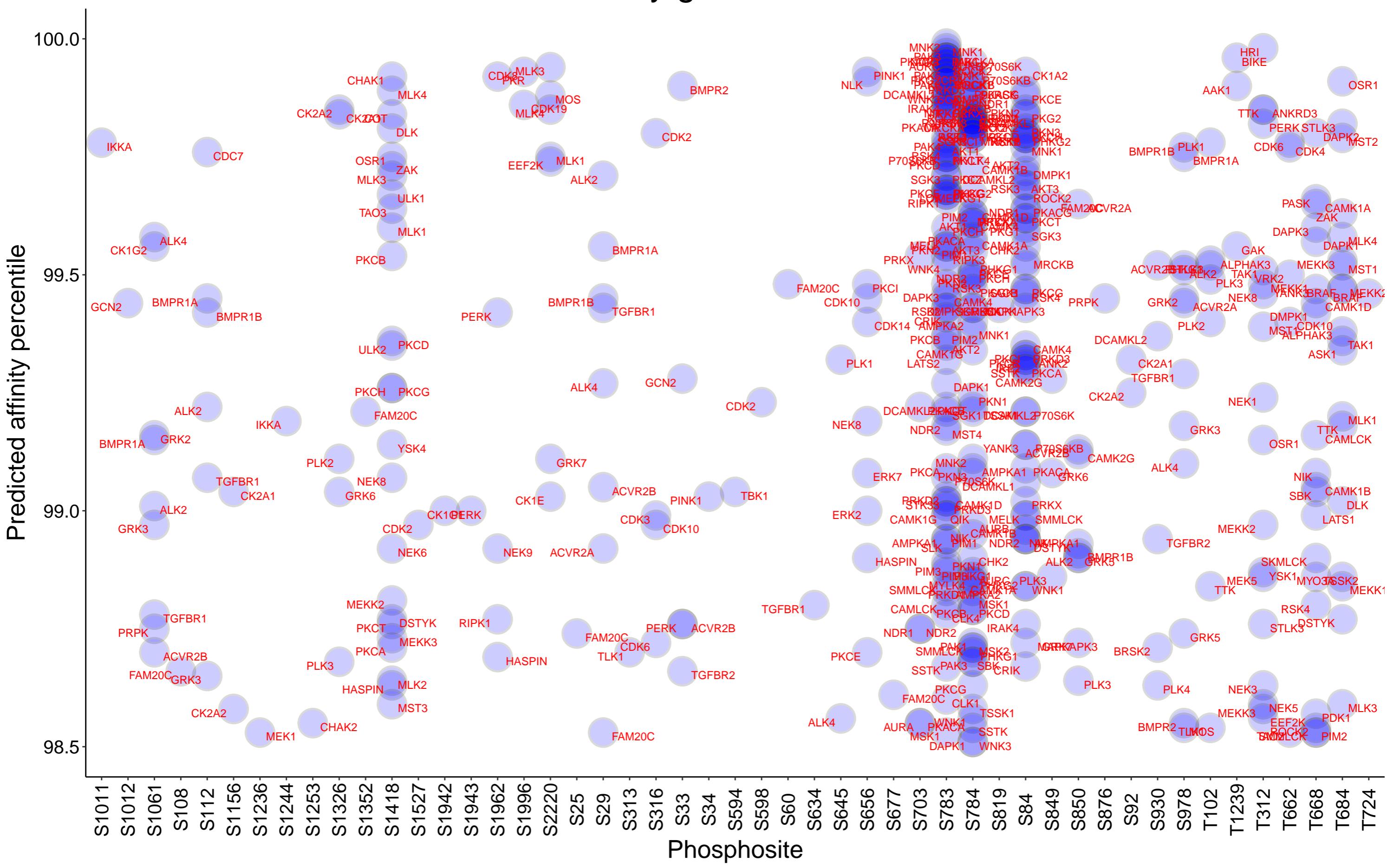
# Gene Set Enrichment analysis on protein correlation coefficients, ATRX protein, DB1



# Top 10 kinases for each phosphosite in ATRX



## Kinases with affinity greater than 98.5% to ATRX



## Top 15 positive correlation coefficients for ATRX protein by tissue, DB1

Beware of false positives in tissues with small number of samples

