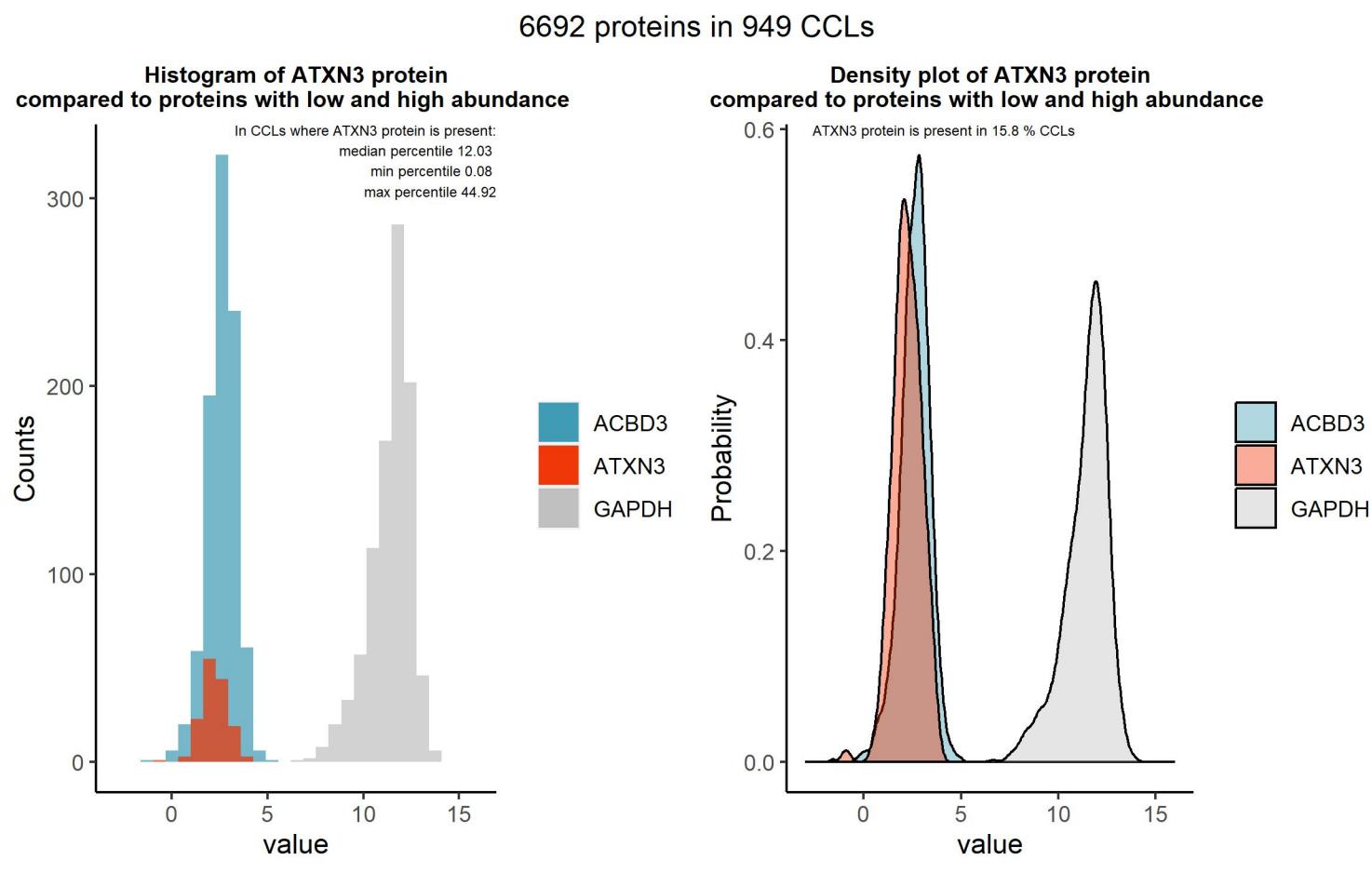


ATXN3

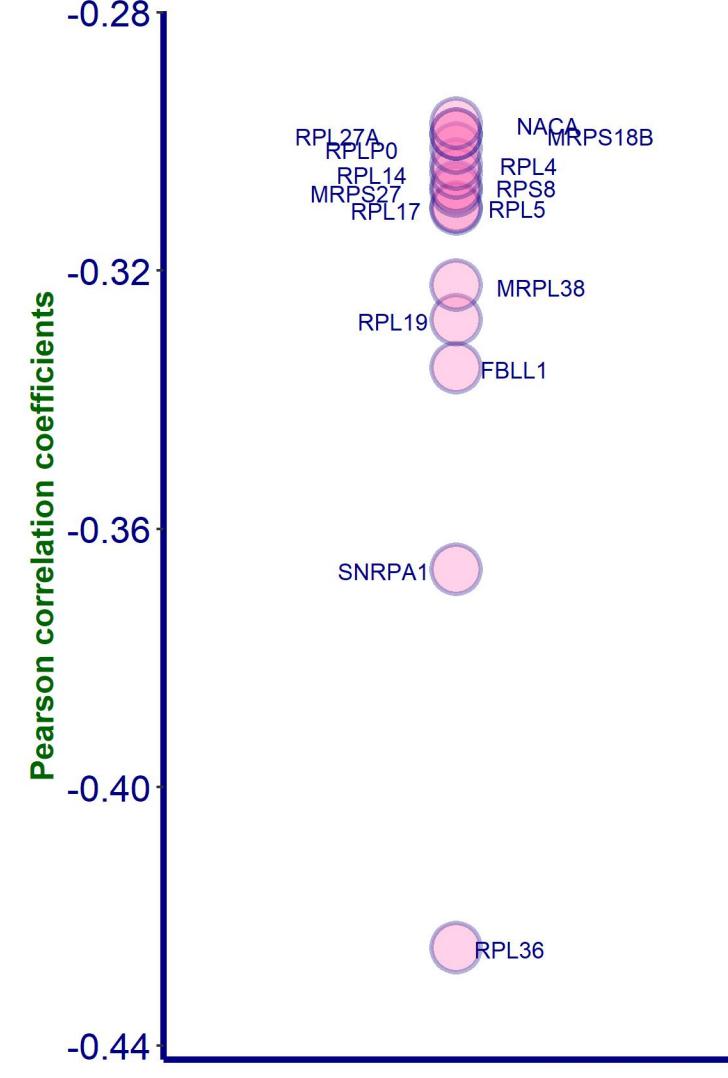
Protein name: ATX3 ; UNIPROT: P54252 ; Gene name: ataxin 3

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

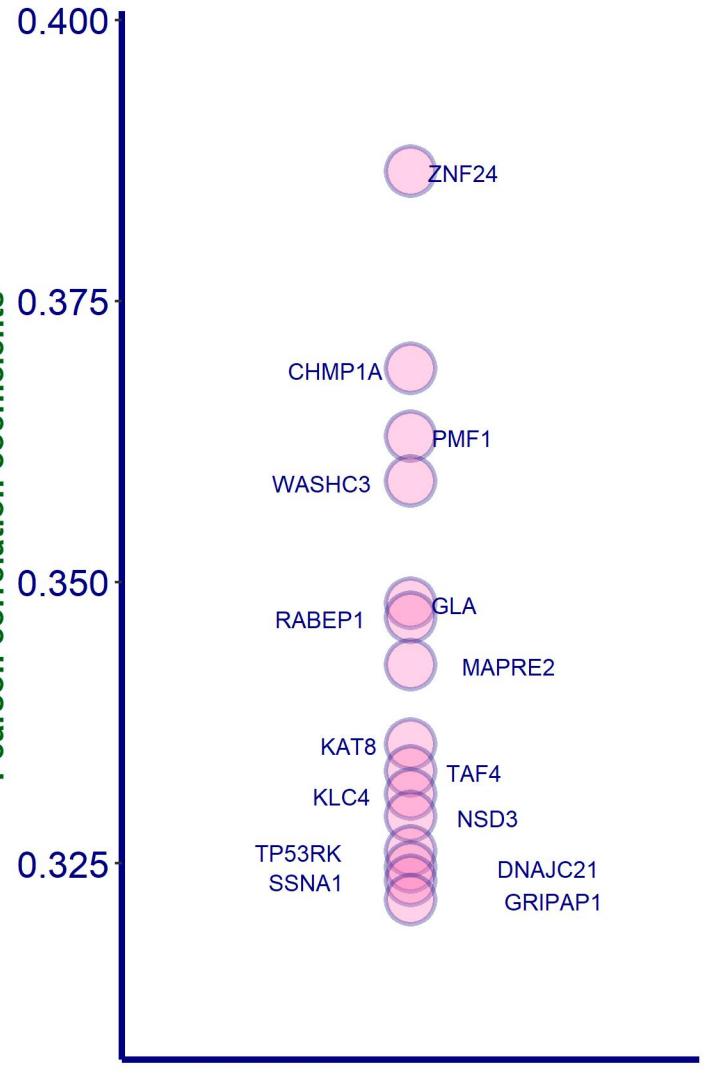
Sanger Institute Protein Database 1 (DB1), protein presence is certain



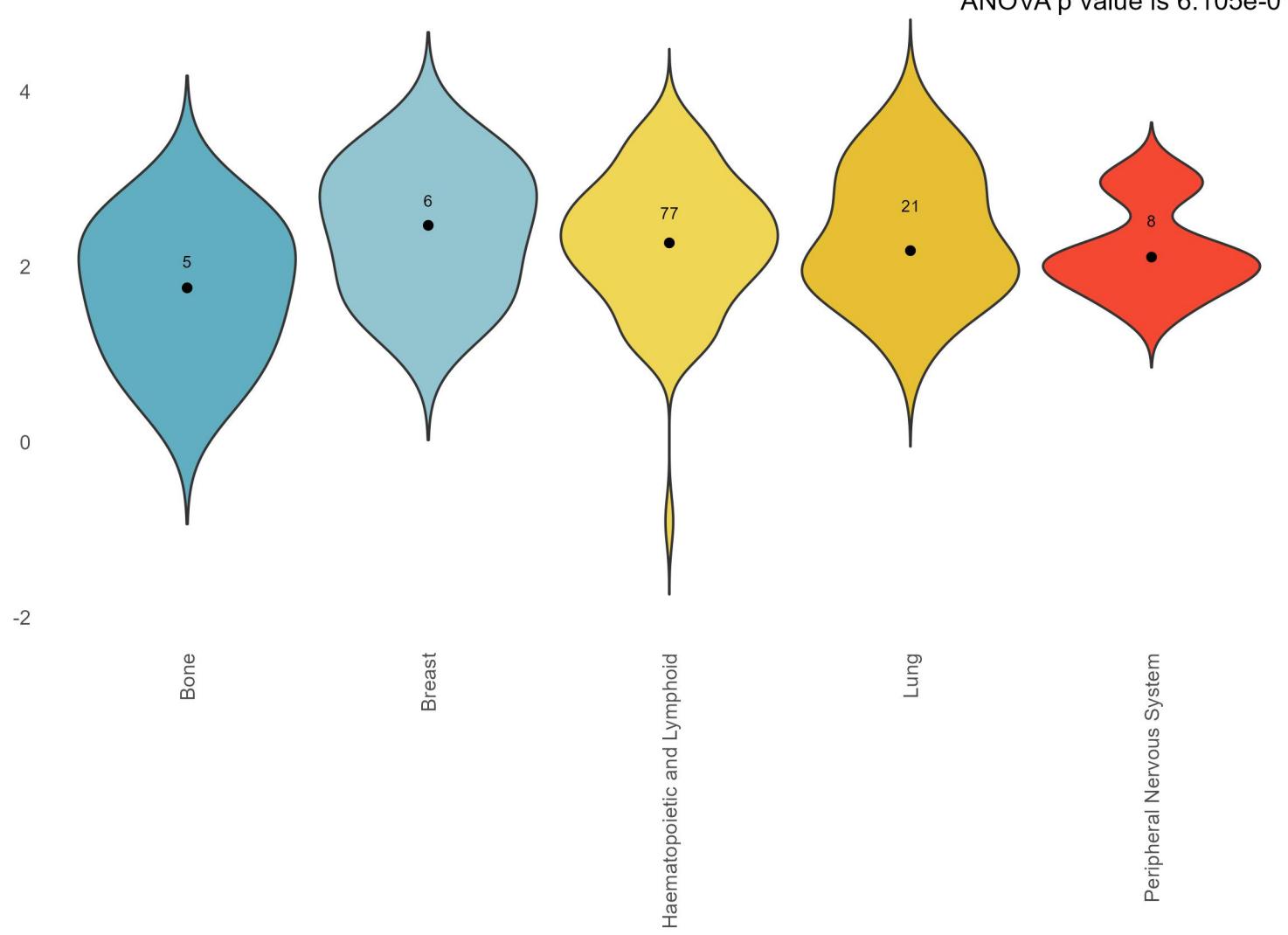
Top negative correlations of ATXN3 protein, DB1



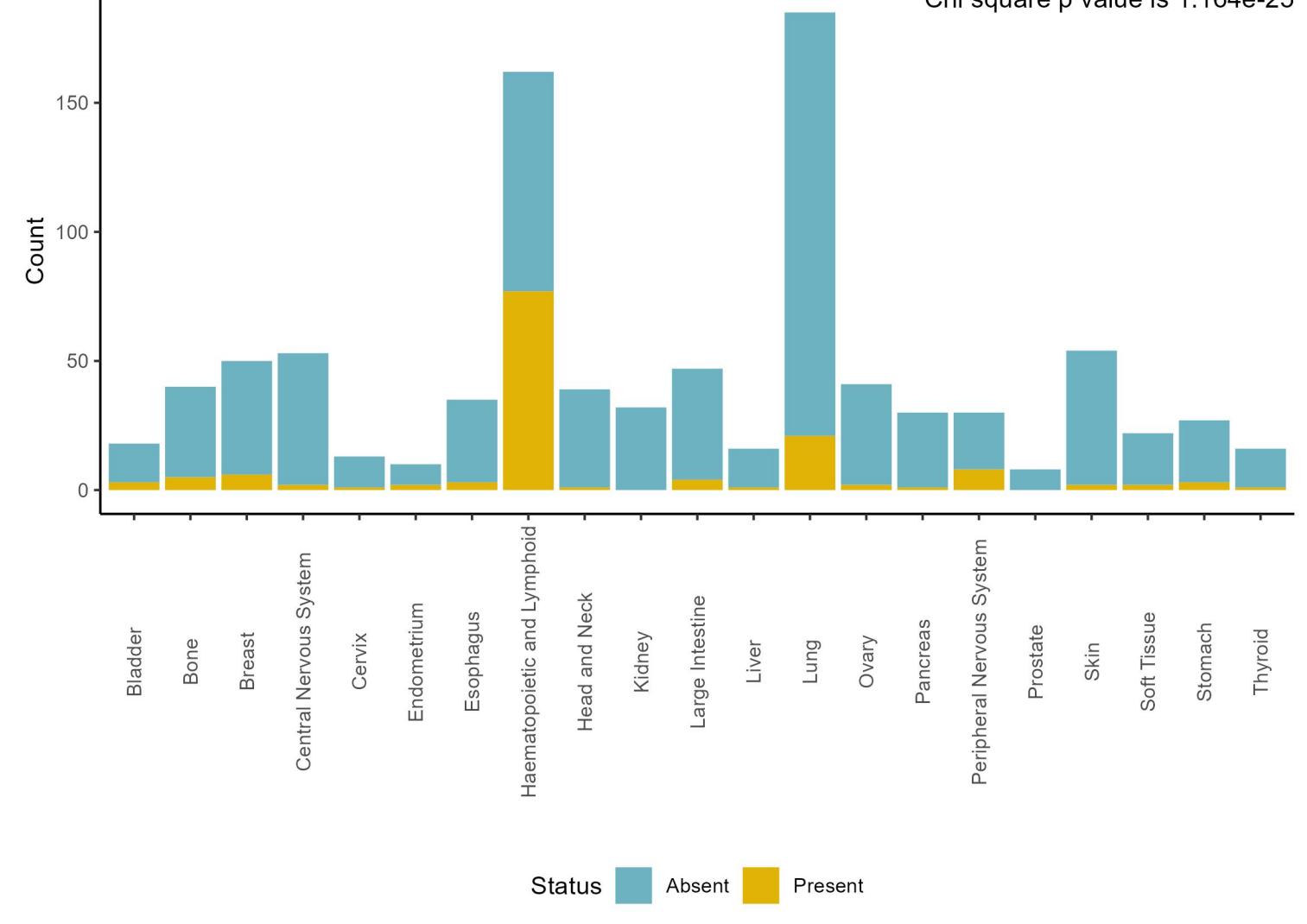
Top positive correlations of ATXN3 protein, DB1



Amount of ATXN3 protein, number of CCLs where it is present by tissue, DB1



Present and absent ATXN3 protein counts by tissue, DB1

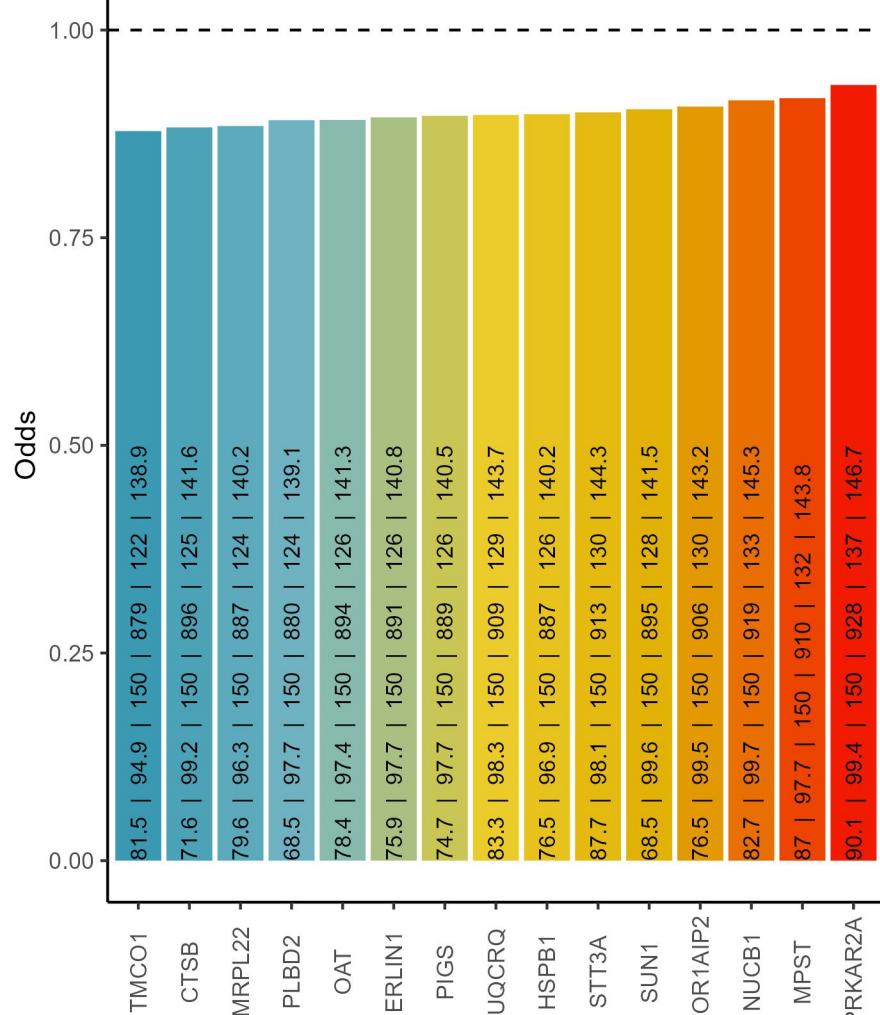


Cooccurrence with ATXN3 protein, DB1

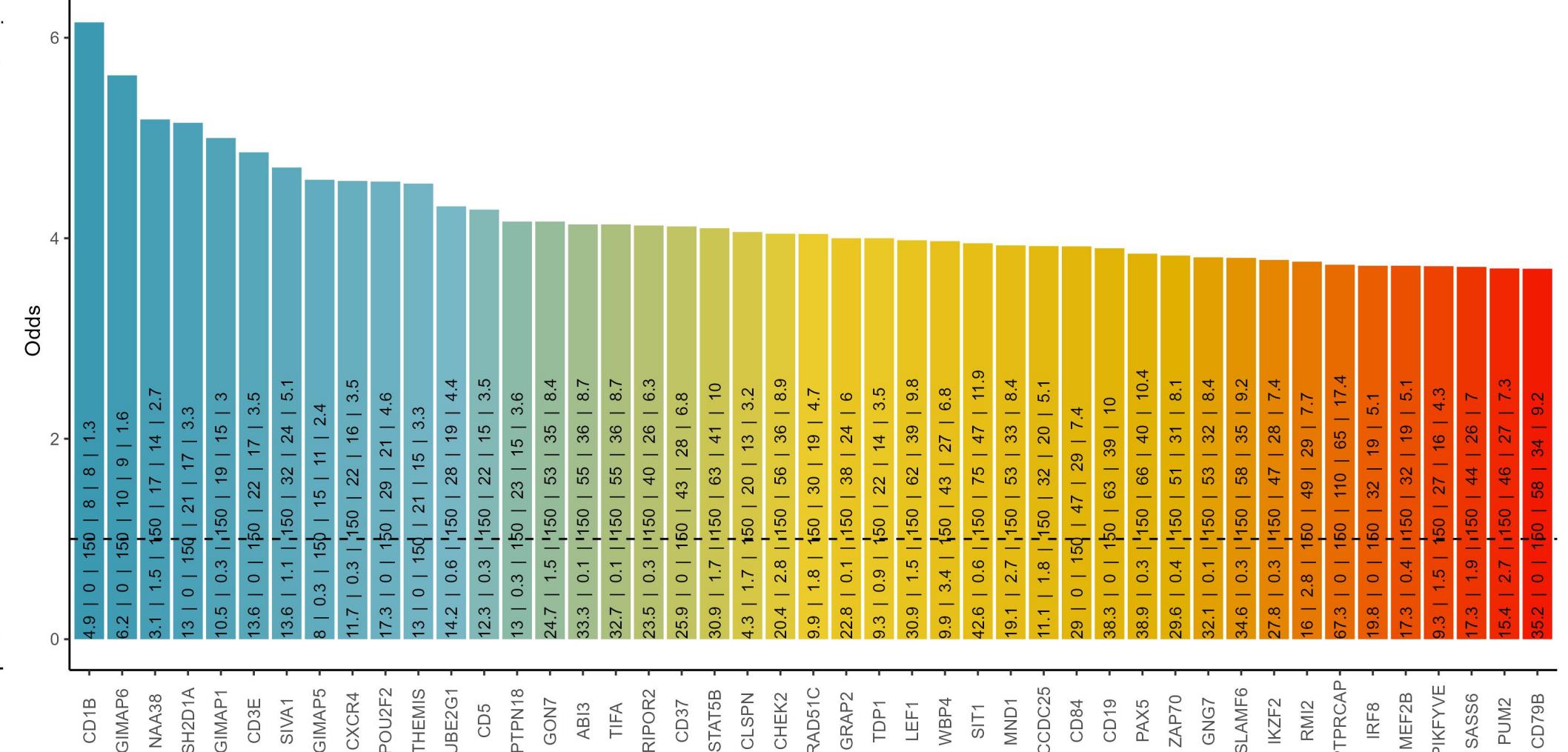
% of ATXN3 in blood cancers: 47.5 ; % of ATXN3 in solid cancers: 9.1

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ATXN3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

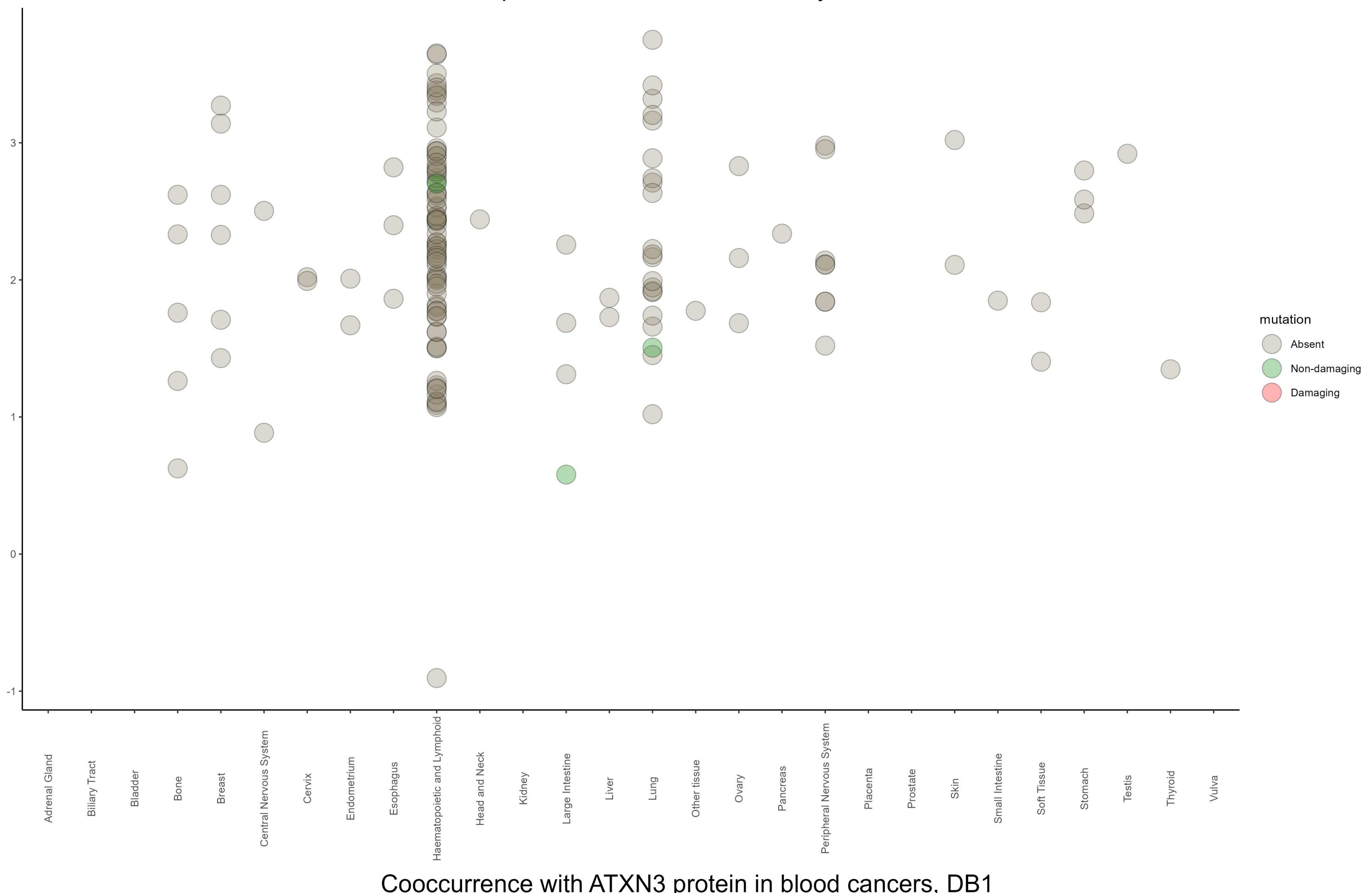
Negative cooccurrence



Positive cooccurrence

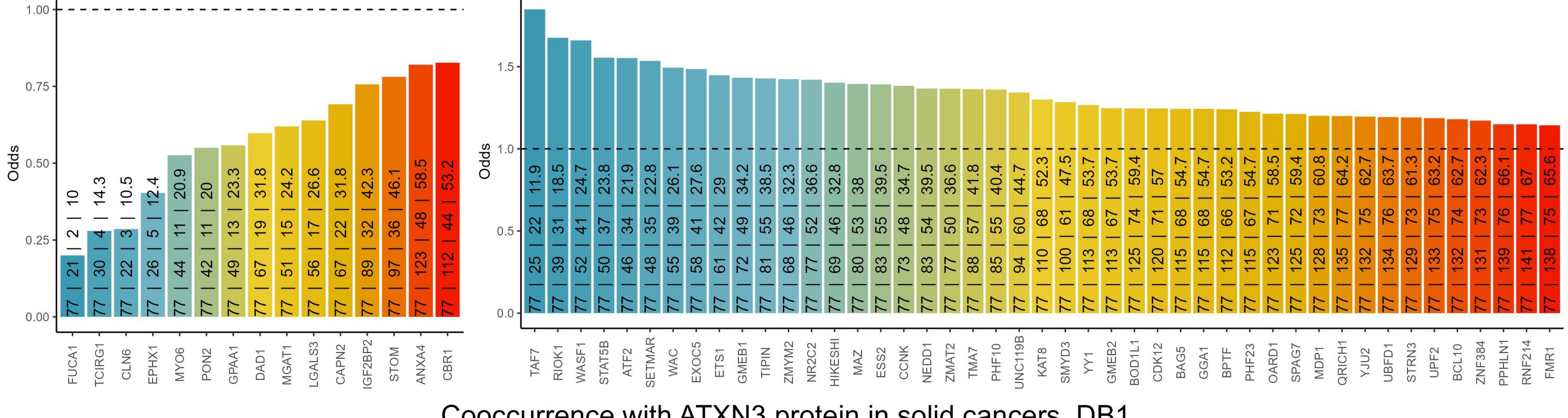


Amount of ATXN3 protein and mutation status by tissue, DB1



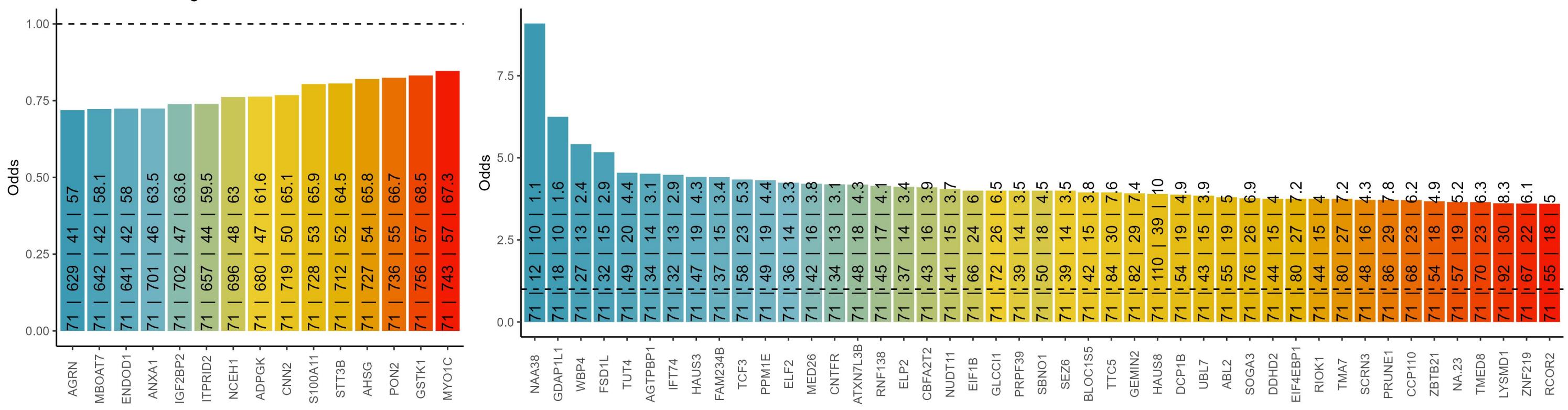
Cooccurrence with ATXN3 protein in blood cancers, DB1

The text in the bars: incidence of ATXN3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

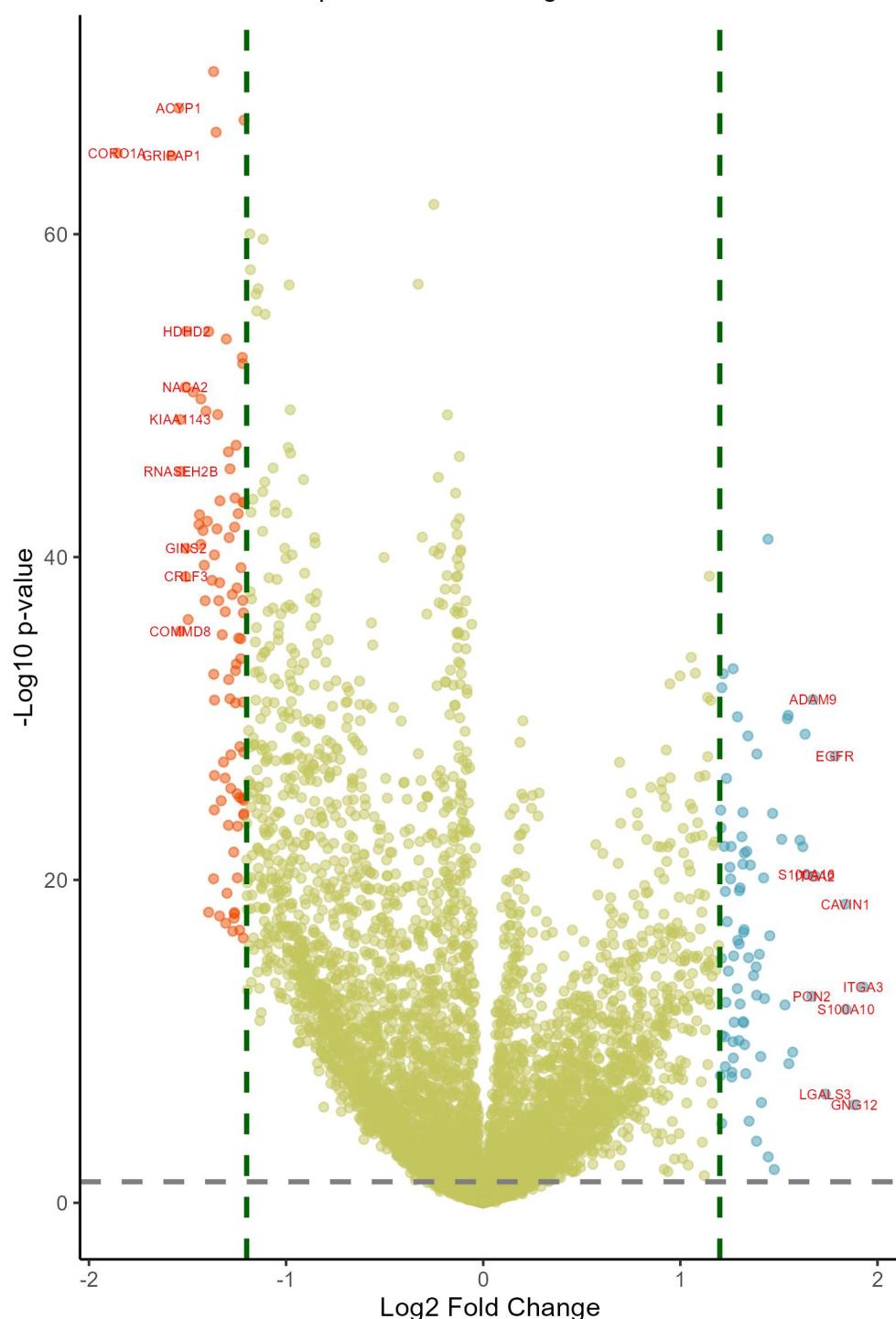


Cooccurrence with ATXN3 protein in solid cancers, DB1

The text in the bars: incidence of ATXN3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



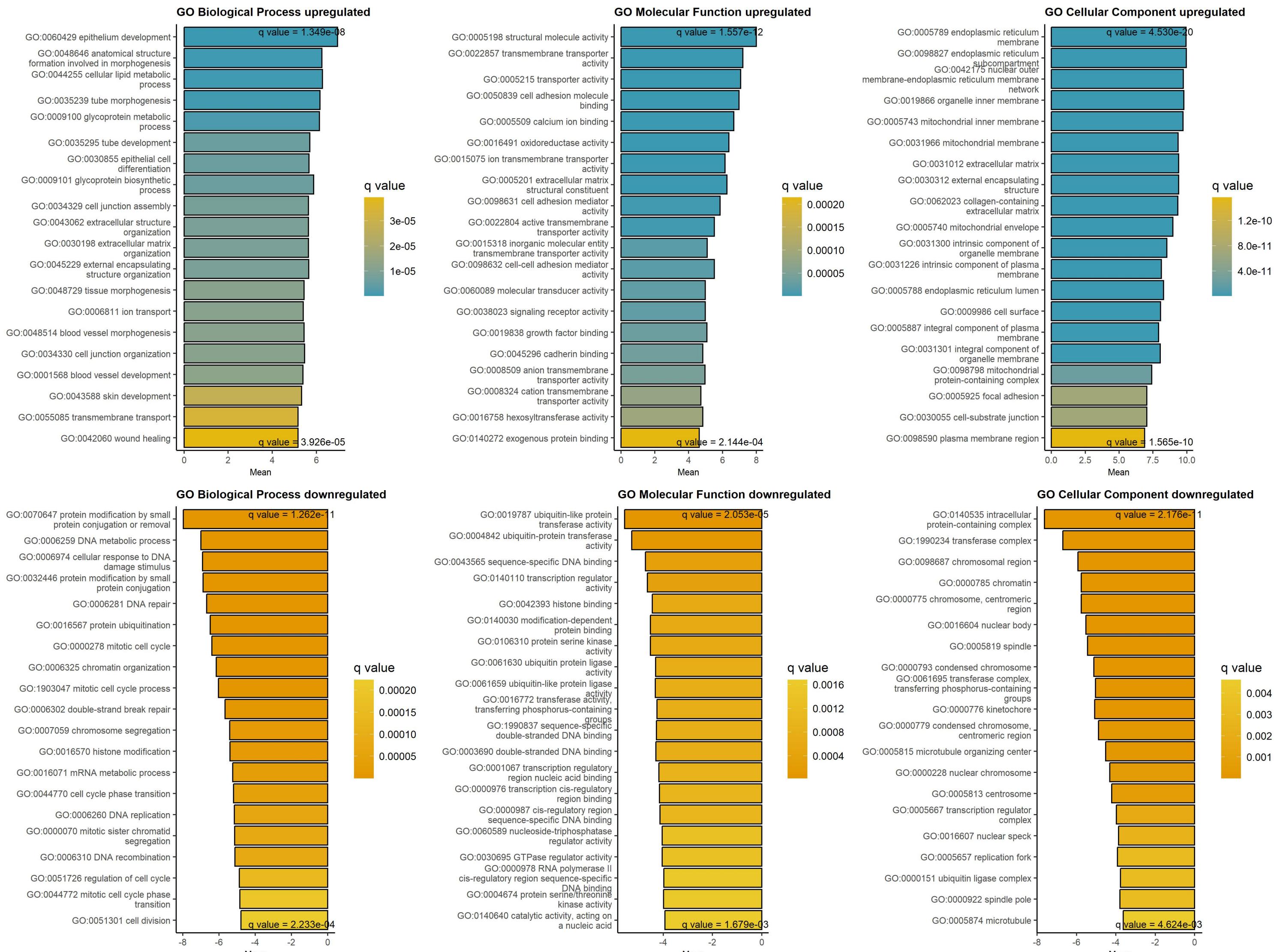
Differentially expressed proteins at absence/low amount of ATXN3 , DB1
p-value < 0.05 & logFC > 1.2

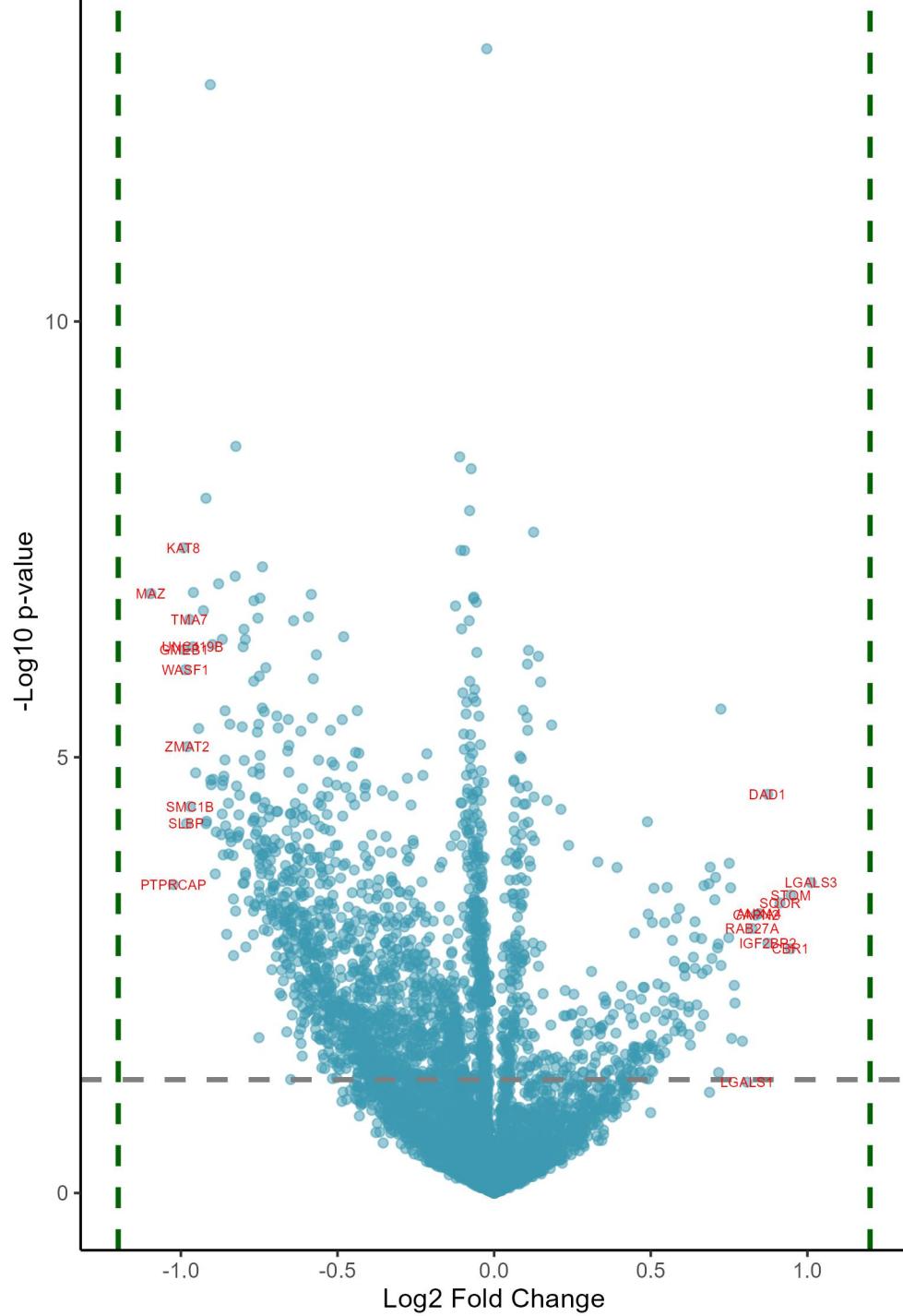


Downregulated at low/absent ATXN3 Upregulated at low/absent ATXN3

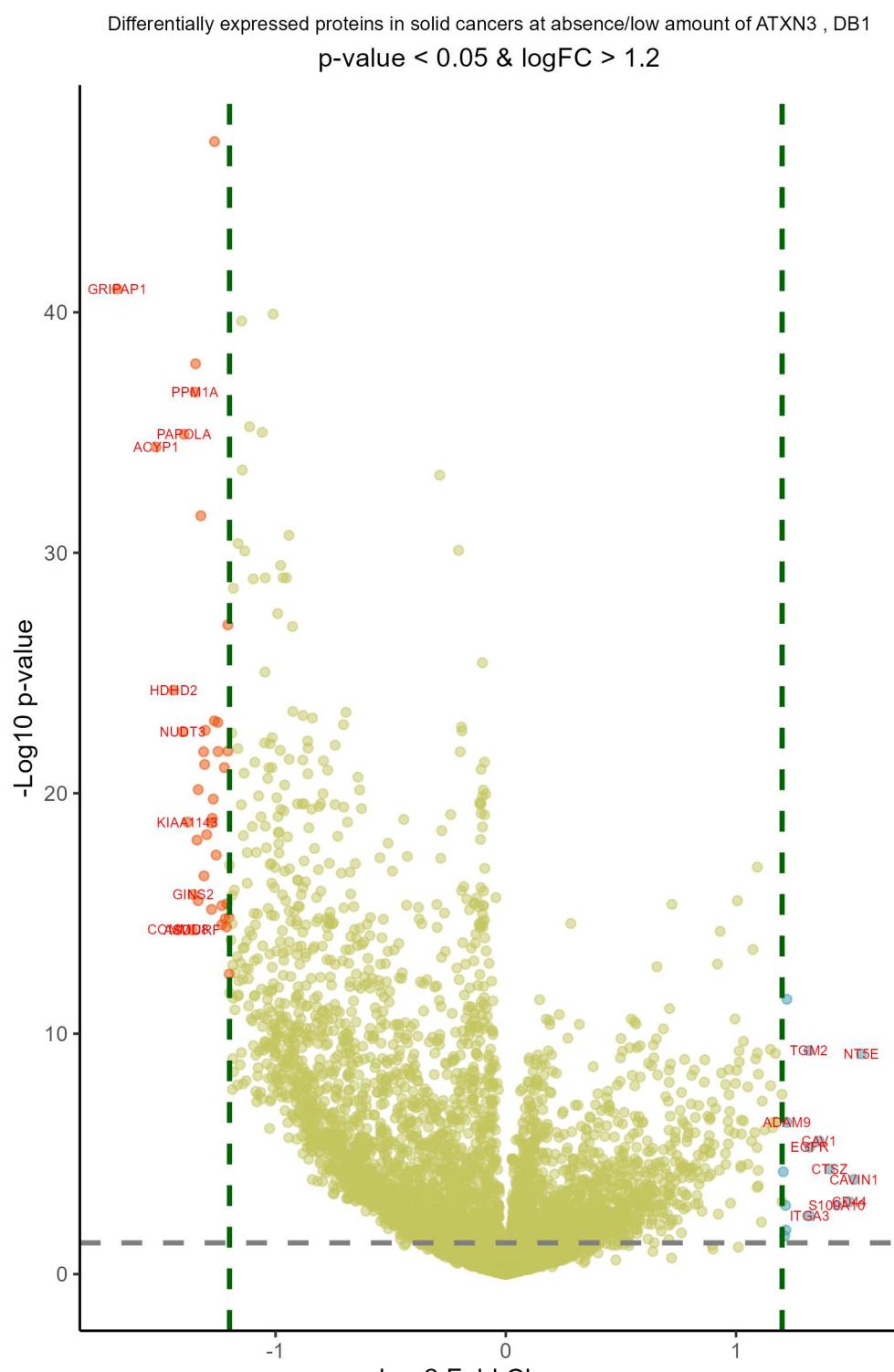
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.86	1.04e-62	CORO1A	coronin 1A	1.93	2.43e-13	ITGA3	integrin subunit alpha 3
-1.58	1.30e-62	GRIPAP1	GRIP1 associated protein 1	1.88	2.20e-06	GNG12	G protein subunit gamma 12
-1.54	3.41e-65	ACYP1	acylphosphatase 1	1.84	4.95e-12	S100A10	S100 calcium binding protein A10
-1.54	1.98e-34	COMMID8	COMM domain containing 8	1.84	3.03e-18	CAVIN1	caveolae associated protein 1
-1.54	6.76e-47	KIAA1143	KIAA1143	1.78	5.22e-27	EGFR	epidermal growth factor receptor
-1.53	8.69e-44	RNASEH2B	ribonuclease H2 subunit B	1.74	5.09e-07	LGALS3	galectin 3
-1.51	8.74e-49	NACA2	nascent polypeptide associated comp	1.68	6.52e-20	ITGA2	integrin subunit alpha 2
-1.51	1.21e-37	CRLF3	cytokine receptor like factor 3	1.67	2.26e-30	ADAM9	ADAM metallopeptidase domain 9
-1.51	2.68e-39	GINS2	GINS complex subunit 2	1.67	8.56e-13	PON2	paraoxonase 2
-1.5	3.74e-52	HDHD2	haloacid dehalogenase like hydrolas	1.64	5.27e-20	S100A16	S100 calcium binding protein A16
-1.5	3.98e-35	SSNA1	SS nuclear autoantigen 1	1.63	2.59e-28	NT5E	5'-nucleotidase ecto
-1.47	1.64e-48	NUDT3	nudix hydrolase 3	1.62	1.16e-21	CAV1	caveolin 1
-1.44	1.11e-40	UBE2R2	ubiquitin conjugating enzyme E2 R2	1.61	4.79e-22	PPIC	peptidylprolyl isomerase C
-1.44	2.95e-41	SPAG7	sperm associated antigen 7	1.57	1.69e-09	MYOF	myoferlin
-1.43	1.58e-39	SEPTIN6	septin 6	1.55	8.07e-09	FKBP9	FKBP prolyl isomerase 9
-1.43	4.26e-48	ARMC6	armadillo repeat containing 6	1.55	1.93e-29	EPHA2	EPH receptor A2
-1.42	2.46e-40	STK4	serine/threonine kinase 4	1.54	3.03e-29	GPX8	glutathione peroxidase 8 (putative)
-1.42	2.62e-38	RNF113A	ring finger protein 113A	1.53	2.72e-12	ITGAV	integrin subunit alpha V
-1.41	3.21e-36	MDP1	magnesium dependent phosphatase 1	1.51	4.23e-22	RRAS	RAS related
-1.41	2.25e-47	C11orf54	chromosome 11 open reading frame 54	1.48	1.34e-02	KRT18	keratin 18
-1.4	7.23e-41	GRK2	G protein-coupled receptor kinase 2	1.47	1.24e-23	ITGB4	integrin subunit beta 4
-1.39	9.12e-18	GMFG	glia maturation factor gamma	1.45	2.25e-16	P4HA2	prolyl 4-hydroxylase subunit alpha
-1.39	3.74e-52	ABRACL	ABRA C-terminal like	1.45	2.45e-03	S100A6	S100 calcium binding protein A6
-1.38	1.98e-37	POU2F1	POU class 2 homeobox 1	1.44	7.69e-40	FNDC3B	fibronectin type III domain contain
-1.37	9.38e-20	HCLS1	hematopoietic cell-specific Lyn sub	1.43	1.15e-12	SFXN3	sideroflexin 3
-1.37	2.81e-67	UBR7	ubiquitin protein ligase E3 compone	1.42	8.36e-20	CD151	CD151 molecule (Raph blood group)
-1.37	7.12e-32	GABARPL2	GABA type A receptor associated pro	1.41	1.59e-06	NCEH1	neutral cholesterol ester hydrolase
-1.36	7.67e-24	CDKN2C	cyclin dependent kinase inhibitor 2	1.41	3.03e-09	CTNNB1	catenin beta 1
-1.36	7.30e-26	WIPF1	WAS/WASL interacting protein family	1.4	2.81e-15	EPHX1	epoxide hydrolase 1

GAGE analysis on upregulated and downregulated proteins at low/absent ATXN3 protein, DB1



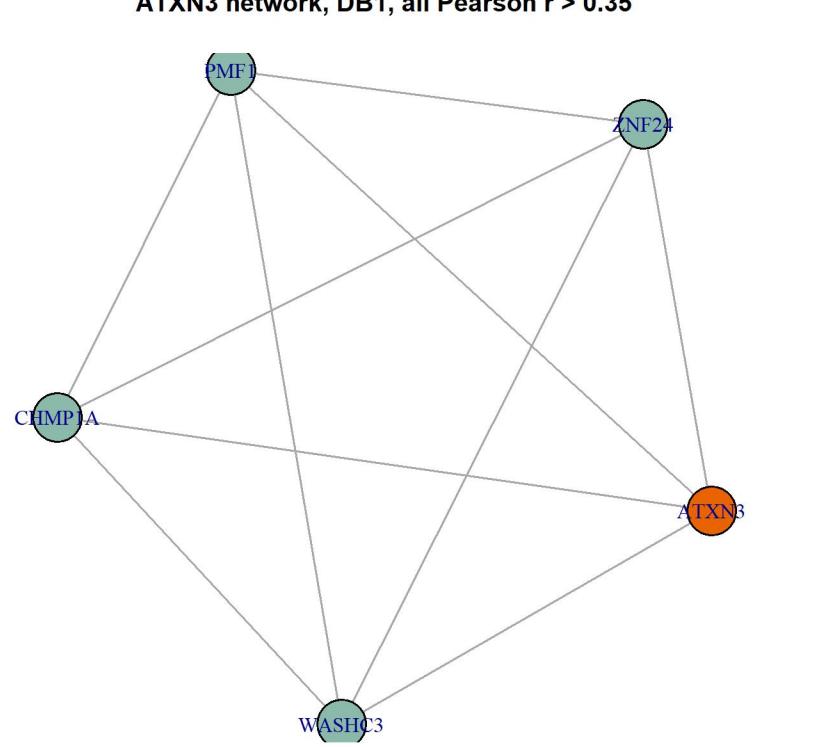


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.1	4.80e-05	MAZ	MYC associated zinc finger protein	1.01	4.91e-03	LGALS3	galectin 3
-1.02	5.03e-03	PTPRCAP	protein tyrosine phosphatase recept	0.95	6.12e-03	STOM	stomatin
-0.99	2.36e-05	KAT8	lysine acetyltransferase 8	0.95	1.52e-02	CBR1	carbonyl reductase 1
-0.99	9.87e-05	GMEB1	glucocorticoid modulatory element b	0.91	7.08e-03	SQOR	sulfide quinone oxidoreductase
-0.99	1.43e-04	WASF1	WASP family member 1	0.87	1.37e-02	IGF2BP2	insulin like growth factor 2 mRNA b
-0.98	1.92e-03	SLBP	stem-loop binding protein	0.87	1.29e-03	DAD1	defender against cell death 1
-0.98	5.92e-04	ZMAT2	zinc finger matrin-type 2	0.85	8.35e-03	ANXA4	annexin A4
-0.97	6.02e-05	TMA7	translation machinery associated 7	0.84	8.57e-03	CAPN2	calpain 2
-0.97	1.49e-03	SMC1B	structural maintenance of chromosom	0.82	1.06e-02	RAB27A	RAB27A, member RAS oncogene family
-0.96	9.44e-05	UNC119B	unc-119 lipid binding chaperone B	0.81	1.38e-01	LGALS1	galectin 1
-0.96	4.80e-05	YY1	YY1 transcription factor	0.79	5.98e-02	LMNA	lamin A/C
-0.95	9.39e-04	DCAF16	DDB1 and CUL4 associated factor 16	0.77	2.72e-02	PLP2	proteolipid protein 2
-0.94	4.15e-04	SMYD3	SET and MYND domain containing 3	0.77	2.60e-02	MVP	major vault protein
-0.93	5.53e-05	PHF10	PHD finger protein 10	0.76	5.66e-02	S100A6	S100 calcium binding protein A6
-0.92	1.01e-05	MDP1	magnesium dependent phosphatase 1	0.75	5.34e-03	PLOD3	procollagen-lysine,2-oxoglutarate 5
-0.92	1.92e-03	SIT1	signaling threshold regulating tran	0.75	3.51e-03	GPAA1	glycosylphosphatidylinositol anchor
-0.92	1.90e-03	LEF1	lymphoid enhancer binding factor 1	0.75	1.25e-02	PIGK	phosphatidylinositol glycan anchor
-0.91	4.26e-10	QRICH1	glutamine rich 1	0.72	2.03e-02	NIBAN1	niban apoptosis regulator 1
-0.9	1.05e-03	PLEKHG2	pleckstrin homology and FYVE domain	0.72	3.19e-04	TCIRG1	T cell immune regulator 1, ATPase H
-0.9	1.12e-03	TMED8	transmembrane p24 trafficking prote	0.72	1.14e-01	S100A11	S100 calcium binding protein A11
-0.9	9.42e-05	OARD1	O-acyl-ADP-ribose deacetylase 1	0.72	1.39e-02	ALG1	ALG1 chitobiosyldiphosphodolichol b
-0.9	1.04e-03	DGKA	diacylglycerol kinase alpha	0.71	1.50e-02	ATP6V0A1	ATPase H+ transporting V0 subunit a
-0.89	4.22e-03	GTF2E1	general transcription factor IIIE su	0.71	4.50e-03	NME3	NME/NM23 nucleoside diphosphate kin
-0.89	2.22e-03	STK39	serine/threonine kinase 39	0.7	6.66e-03	PON2	paraoxonase 2
-0.88	4.54e-05	PPHLN1	peripherin 1	0.7	1.79e-02	TYMP	thymidine phosphorylase
-0.87	2.31e-03	RANGRF	RAN guanine nucleotide release fact	0.69	3.72e-03	MGAT2	alpha-1,6-mannosyl-glycoprotein 2-b
-0.87	1.69e-03	LRRC20	leucine rich repeat containing 20	0.69	1.67e-01	S100A4	S100 calcium binding protein A4
-0.87	8.45e-05	GGA1	golgi associated, gamma adaptin ear	0.69	4.99e-03	MYO6	myosin VI
-0.87	1.12e-03	ZNF148	zinc finger protein 148	0.68	2.19e-02	SFXN3	sideroflexin 3

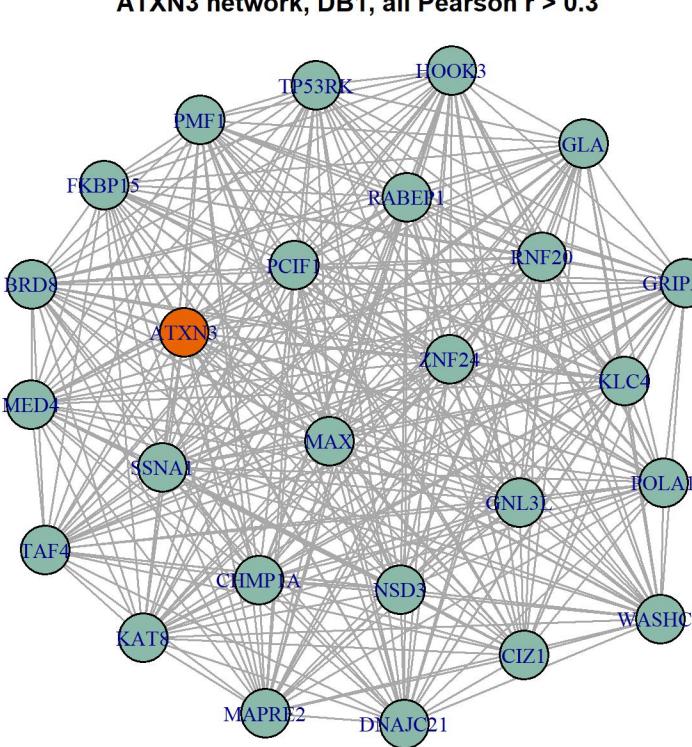


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.69	2.34e-38	GRIPAP1	GRIP1 associated protein 1	1.54	7.77e-09	NTSE	5'-nucleotidase ecto
-1.52	2.44e-32	ACYP1	acylphosphatase 1	1.51	3.99e-04	CAVIN1	caveolae associated protein 1
-1.44	1.15e-22	HDHD2	haloacid dehalogenase like hydrolas	1.49	2.73e-03	CD44	CD44 molecule (Indian blood group)
-1.42	1.32e-13	COMM8	COMM domain containing 8	1.44	3.57e-03	S100A10	S100 calcium binding protein A10
-1.4	4.45e-21	NUDT3	nudix hydrolase 3	1.41	1.63e-04	CTSZ	cathepsin Z
-1.4	7.85e-33	PAPOLA	poly(A) polymerase alpha	1.36	1.55e-05	CAV1	caveolin 1
-1.38	1.03e-17	KIAA1143	KIAA1143	1.32	2.59e-05	EGFR	epidermal growth factor receptor
-1.36	1.37e-13	ASDURF	ASNSD1 upstream open reading frame	1.32	8.90e-03	ITGA3	integrin subunit alpha 3
-1.36	6.75e-15	GINS2	GINS complex subunit 2	1.32	5.84e-09	TGM2	transglutaminase 2
-1.35	1.98e-34	PPM1A	protein phosphatase, Mg2+/Mn2+ depe	1.22	3.01e-06	ADAM9	ADAM metallopeptidase domain 9
-1.35	1.52e-35	UBR7	ubiquitin protein ligase E3 compone	1.22	6.68e-11	FNDC3B	fibronectin type III domain contain
-1.34	5.01e-17	UBE2R2	ubiquitin conjugating enzyme E2 R2	1.22	2.95e-02	LGALS3	galectin 3
-1.34	1.17e-14	NECAP1	NECAP endocytosis associated 1	1.22	3.70e-03	MYOF	myoferlin
-1.34	6.64e-19	ARMC6	armadillo repeat containing 6	1.21	4.77e-02	ANXA1	annexin A1
-1.32	1.37e-29	ABRACL	ABRA C-terminal like	1.2	2.06e-04	S100A16	S100 calcium binding protein A16
-1.31	2.33e-20	C11orf54	chromosome 11 open reading frame 54	1.2	2.55e-07	MAGT1	magnesium transporter 1
-1.31	1.26e-15	CDC34	cell division cycle 34, ubiquitin c	1.2	2.66e-03	ITGB5	integrin subunit beta 5
-1.31	7.04e-20	RABEP1	rabaptin, RAB GTPase binding effect	1.17	7.46e-09	TAP2	transporter 2, ATP binding cassette
-1.31	4.12e-21	PIN4	peptidyl/prolyl cis/trans isomerase,	1.16	3.03e-06	EPHA2	EPH receptor A2
-1.3	3.11e-17	NACA2	nascent polypeptide associated comp	1.16	3.06e-06	GPX8	glutathione peroxidase 8 (putative)
-1.28	1.10e-17	CHD8	chromodomain helicase DNA binding p	1.16	4.90e-06	CD151	CD151 molecule (Raph blood group)
-1.28	2.42e-14	SPAG7	sperm associated antigen 7	1.15	1.22e-07	GPRC5A	G protein-coupled receptor class C
-1.27	7.34e-18	CHMP5	charged multivesicular body protein	1.15	5.21e-09	CAVIN3	caveolae associated protein 3
-1.27	1.47e-18	PDCL	phosducin like	1.12	5.94e-06	ICAM1	intercellular adhesion molecule 1
-1.27	1.86e-21	RNF214	ring finger protein 214	1.11	4.72e-07	CD109	CD109 molecule
-1.26	2.65e-44	UBE2V2	ubiquitin conjugating enzyme E2 V2	1.11	1.51e-02	NCEH1	neutral cholesterol ester hydrolase
-1.26	1.97e-16	UBFD1	ubiquitin family domain containing	1.1	4.56e-08	ERAP1	endoplasmic reticulum aminopeptidases
-1.25	2.08e-21	BLMH	bleomycin hydrolase	1.1	6.96e-04	SQOR	sulfide quinone oxidoreductase
-1.25	2.33e-20	POLA2	DNA polymerase alpha 2, accessory s	1.1	1.84e-04	PPIC	peptidylprolyl isomerase C

ATXN3 network, DB1, all Pearson r > 0.35

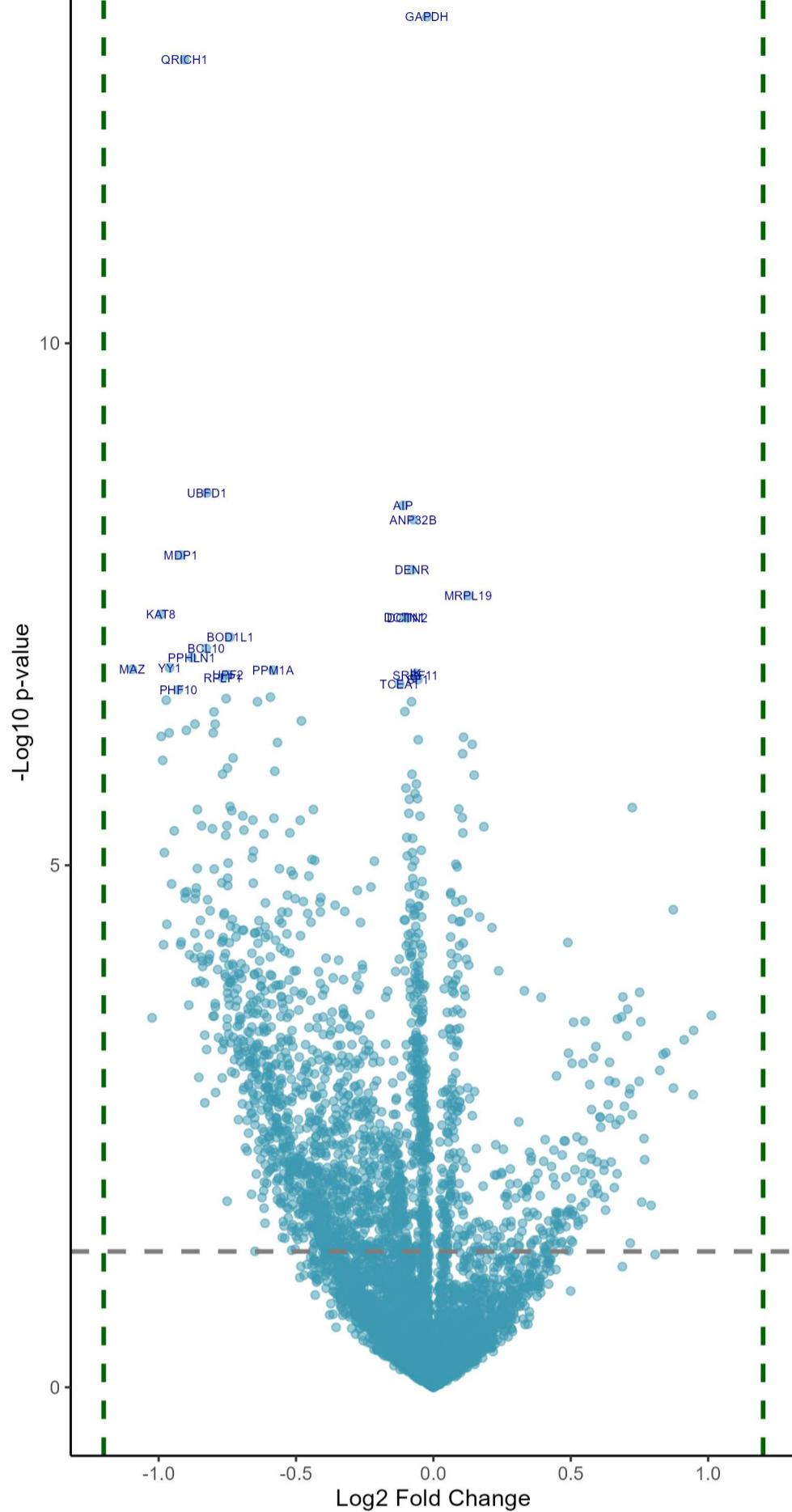


ATXN3 network, DB1, all Pearson r > 0.3



Sorted by p values!

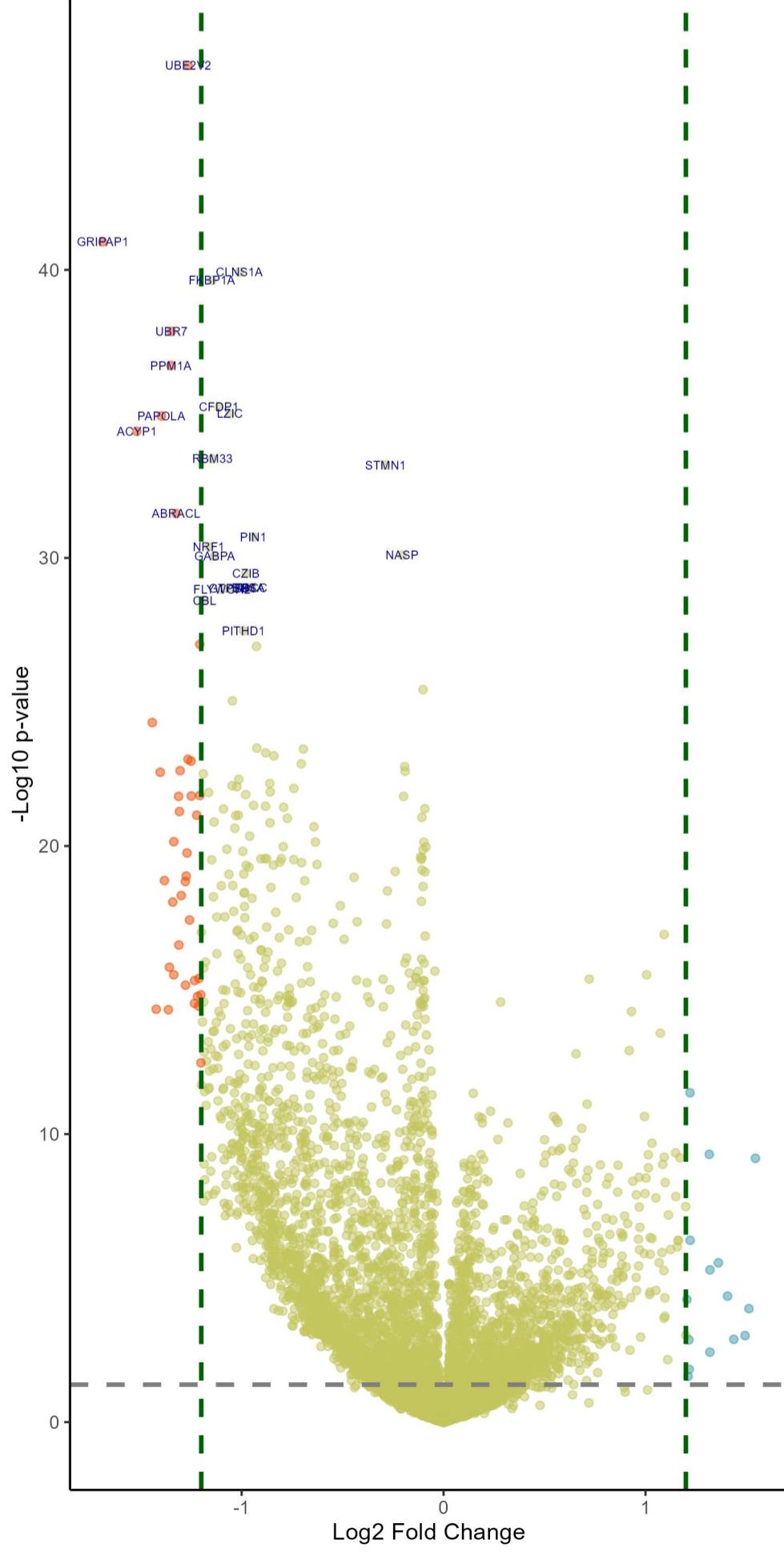
Downregulated in blood cancers at low/absent ATXN3 Upregulated in blood cancers at low/absent ATXN3



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.02	2.48e-10	GAPDH	glyceraldehyde-3-phosphate dehydrog	0.13	1.93e-05	MRPL19	mitochondrial ribosomal protein L19
-0.91	4.26e-10	QRICH1	glutamine rich 1	0.11	9.87e-05	HADHA	hydroxyacyl-CoA dehydrogenase triflu
-0.82	4.51e-06	UBFD1	ubiquitin family domain containing	0.14	1.07e-04	LMAN2	lectin, mannose binding 2
-0.11	4.75e-06	AIP	aryl hydrocarbon receptor interacti	0.11	1.29e-04	HADHB	hydroxyacyl-CoA dehydrogenase triflu
-0.07	5.43e-06	ANP32B	acidic nuclear phosphoprotein 32 fa	0.15	1.79e-04	SSR4	signal sequence receptor subunit 4
-0.92	1.01e-05	MDP1	magnesium dependent phosphatase 1	0.72	3.19e-04	TCIRG1	T cell immune regulator 1, ATPase H
-0.08	1.23e-05	DENR	density regulated re-initiation and	0.09	3.19e-04	PSMD12	proteasome 26S subunit, non-ATPase
-0.99	2.36e-05	KAT8	lysine acetyltransferase 8	0.1	3.52e-04	MRPL13	mitochondrial ribosomal protein L13
-0.11	2.36e-05	DCTN1	dynactin subunit 1	0.18	3.95e-04	RPN2	ribophorin II
-0.09	2.36e-05	DCTN2	dynactin subunit 2	0.11	4.24e-04	VARS1	valyl-tRNA synthetase 1
-0.74	3.34e-05	BOD1L1	biorientation of chromosomes in cel	0.08	6.98e-04	WDR12	WD repeat domain 12
-0.83	3.98e-05	BCL10	BCL10 immune signaling adaptor	0.09	7.24e-04	PDIA6	protein disulfide isomerase family
-0.88	4.54e-05	PPHLN1	periphilin 1	0.06	1.05e-03	COPB2	COPI coat complex subunit beta 2
-0.96	4.80e-05	YY1	YY1 transcription factor	0.06	1.07e-03	CANX	calnexin
-1.1	4.80e-05	MAZ	MYC associated zinc finger protein	0.11	1.12e-03	TMED10	transmembrane p24 trafficking prote
-0.58	4.80e-05	PPM1A	protein phosphatase, Mg2+/Mn2+ depe	0.08	1.16e-03	RPN1	ribophorin I
-0.06	4.80e-05	IK	IK cytokine	0.87	1.29e-03	DAD1	defender against cell death 1
-0.75	4.80e-05	UPF2	UPF2 regulator of nonsense mediated	0.13	1.31e-03	DDOST	dolichyl-diphosphooligosaccharide--
-0.07	4.80e-05	SRSF11	serine and arginine rich splicing f	0.17	1.38e-03	MLEC	malectin
-0.77	4.82e-05	RPLP1	ribosomal protein lateral stalk sub	0.07	1.43e-03	COPB1	COPI coat complex subunit beta 1
-0.06	4.82e-05	SF1	splicing factor 1	0.1	1.44e-03	UQCRC2	ubiquinol-cytochrome c reductase co
-0.12	5.09e-05	TCEA1	transcription elongation factor A1	0.09	1.44e-03	HDLBP	high density lipoprotein binding pr
-0.93	5.53e-05	PHF10	PHD finger protein 10	0.21	1.57e-03	SPCS2	signal peptidase complex subunit 2
-0.59	6.02e-05	ACYP1	acylphosphatase 1	0.06	1.75e-03	EIF3D	eukaryotic translation initiation f
-0.75	6.02e-05	YJU2	YJU2 splicing factor homolog	0.49	1.90e-03	FUCA1	alpha-L-fucosidase 1
-0.97	6.02e-05	TMA7	translation machinery associated 7	0.11	1.90e-03	MRPL38	mitochondrial ribosomal protein L38
-0.64	6.02e-05	RNF214	ring finger protein 214	0.09	1.95e-03	ATP2A2	ATPase sarcoplasmic/endoplasmic ret
-0.08	6.02e-05	ENY2	ENY2 transcription and export compl	0.06	2.21e-03	ETF1	eukaryotic translation termination
-0.1	7.06e-05	OXSR1	oxidative stress responsive kinase	0.09	2.31e-03	COPG1	COPI coat complex subunit gamma 1
-0.8	7.06e-05	SPAG7	sperm associated antigen 7	0.12	2.34e-03	CYC1	cytochrome c1
-0.48	8.34e-05	PPP4R3A	protein phosphatase 4 regulatory su	0.07	2.54e-03	GANAB	glucosidase II alpha subunit
-0.87	8.45e-05	GGA1	golgi associated, gamma adaptin ear	0.13	2.54e-03	P4HB	prolyl 4-hydroxylase subunit beta
-0.79	8.45e-05	CDK12	cyclin dependent kinase 12	0.24	2.75e-03	MRPL15	mitochondrial ribosomal protein L15
-0.9	9.42e-05	OARD1	O-acyl-ADP-ribose deacetylase 1	0.09	2.86e-03	NUP155	nucleoporin 155
-0.8	9.44e-05	BAG5	BAG cochaperone 5	0.08	3.05e-03	MRTO4	MRT4 homolog, ribosome maturation f
-0.96	9.44e-05	UNC119B	unc-119 lipid binding chaperone B	0.05	3.05e-03	RPS16	ribosomal protein S16
-0.99	9.87e-05	GMEB1	glucocorticoid modulatory element b	0.07	3.19e-03	PHB2	prohibitin 2
-0.06	1.02e-04	ACIN1	apoptotic chromatin condensation in	0.07	3.19e-03	EIF3L	eukaryotic translation initiation f
0.57	1.06e-04	ZNF706	zinc finger protein 706	0.04	3.36e-03	ACKK1	receptor for activated C kinase 1

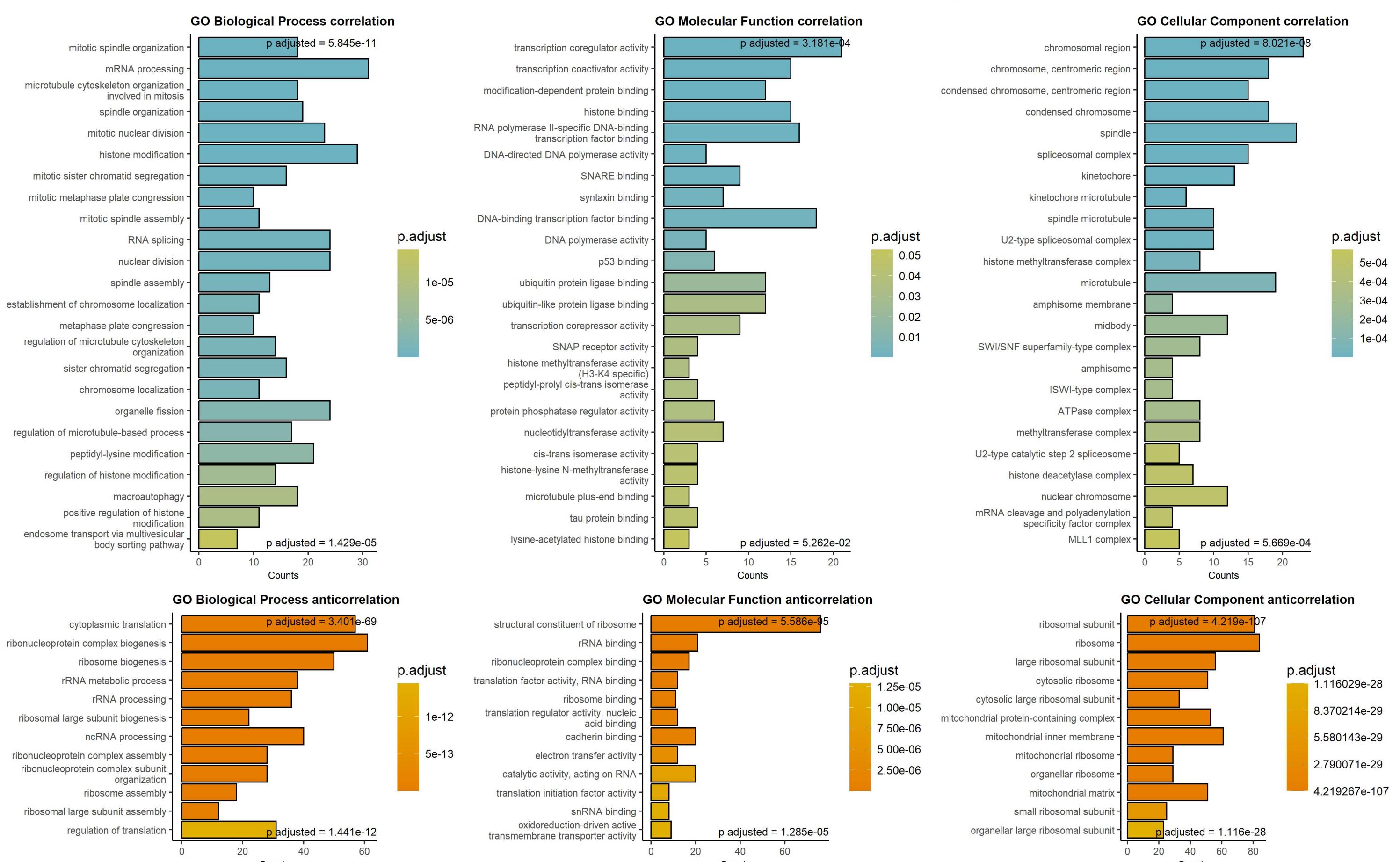
Sorted by p values!

Downregulated in solid cancers at low/absent ATXN3 Upregulated in solid cancers at low/absent ATXN3

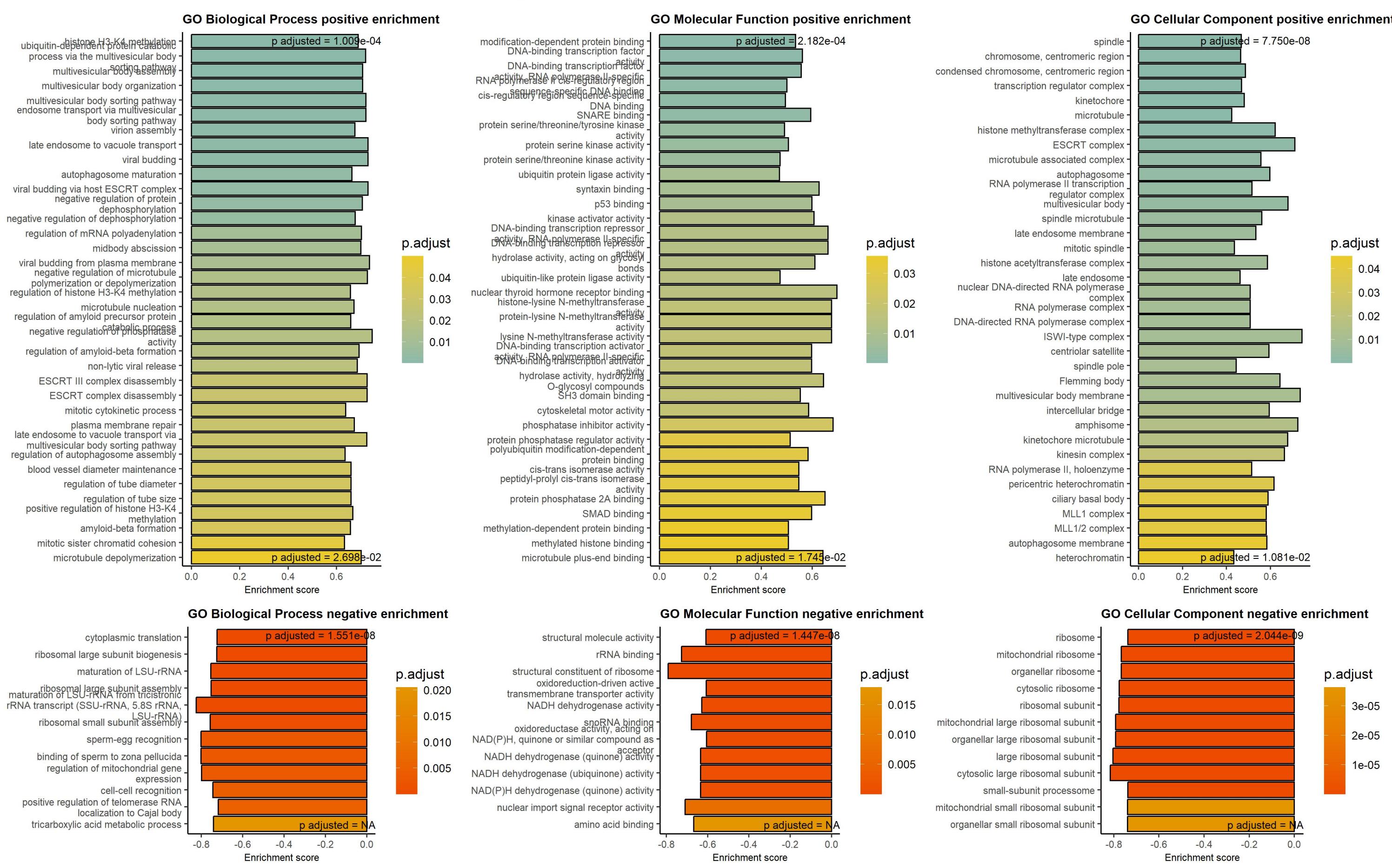


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.26	2.65e-44	UBE2V2	ubiquitin conjugating enzyme E2 V2	1.09	5.82e-16	UXS1	UDP-glucuronate decarboxylase 1
-1.69	2.34e-38	GRIPAP1	GRIP1 associated protein 1	1.01	1.17e-14	F3	coagulation factor III, tissue fact
-1.01	1.98e-37	CLNS1A	chloride nucleotide-sensitive chann	0.72	1.61e-14	CAV2	caveolin 2
-1.15	3.05e-37	FKBP1A	FKBP prolyl isomerase 1A	0.28	8.10e-14	FAF2	Fas associated factor family member
-1.35	1.52e-35	UBR7	ubiquitin protein ligase E3 compone	0.93	1.56e-13	TGFBI	transforming growth factor beta ind
-1.35	1.98e-34	PPM1A	protein phosphatase, Mg2+/Mn2+ depe	1.07	7.90e-13	DCBLD2	discoidin, CUB and LCCL domain cont
-1.11	4.76e-33	CFDP1	craniofacial development protein 1	0.92	2.87e-12	NEXN	nexilin F-actin binding protein
-1.06	7.21e-33	LZIC	leucine zipper and CTNNBIP1 domain	0.66	3.64e-12	LAMA3	laminin subunit alpha 3
-1.4	7.85e-33	PAPOLA	poly(A) polymerase alpha	1.22	6.68e-11	FNDC3B	fibronectin type III domain contain
-1.52	2.44e-32	ACYP1	acylphosphatase 1	0.15	6.95e-11	NCLN	nicalin
-1.14	1.99e-31	RBM33	RNA binding motif protein 33	0.71	1.54e-10	KRT6A	keratin 6A
-0.29	3.02e-31	STMN1	stathmin 1	0.23	2.59e-10	MLEC	malectin
-1.32	1.37e-29	ABRACL	ABRA C-terminal like	0.55	3.81e-10	ITGB3	integrin subunit beta 3
-0.94	8.25e-29	PIN1	peptidyl/prolyl cis/trans isomerase,	1	3.81e-10	IGFBP7	insulin like growth factor binding
-1.16	1.71e-28	NRF1	nuclear respiratory factor 1	0.18	3.87e-10	LMAN2	lectin, mannose binding 2
-0.21	3.13e-28	NASP	nuclear autoantigenic sperm protein	0.19	4.29e-10	MRPL47	mitochondrial ribosomal protein L47
-1.13	3.13e-28	GABPA	GA binding protein transcription fa	0.56	4.72e-10	BCAP29	B cell receptor associated protein
-0.98	1.18e-27	CZIB	CXXC motif containing zinc binding	0.57	5.85e-10	SLFN5	schlafin family member 5
-0.97	3.36e-27	ENSA	endosulfine alpha	0.32	6.03e-10	SEC61B	SEC61 translocon subunit beta
-0.95	3.36e-27	TBCC	tubulin folding cofactor C	0.19	6.08e-10	RPN2	ribophorin II
-1.04	3.36e-27	GTPBP1	GTP binding protein 1	0.68	8.85e-10	SERpine1	serpin family E member 1
-1.1	3.50e-27	FLYWCH2	FLYWCH family member 2	0.27	1.98e-09	SPCS2	signal peptidase complex subunit 2
-1.18	8.27e-27	CBL	Cbl proto-oncogene	0.5	2.02e-09	HLA-E	major histocompatibility complex, c
-0.99	8.95e-26	PITHD1	PITH domain containing 1	0.65	2.08e-09	ALDH3B1	aldehyde dehydrogenase 3 family mem
-1.21	2.55e-25	PRPSAP2	phosphoribosyl pyrophosphate synthe	1.03	2.59e-09	RETSAT	retinol saturase
-0.93	2.88e-25	C12orf57	chromosome 12 open reading frame 57	0.64	3.55e-09	KRT14	keratin 14
-0.1	8.83e-24	HSP90AA1	heat shock protein 90 alpha family	0.58	3.76e-09	MICAL2	microtubule associated monoxygenas
-1.05	2.09e-23	RNASEH2C	ribonuclease H2 subunit C	0.57	4.46e-09	DYSF	dysferlin
-1.44	1.15e-22	HDHD2	haloacid dehalogenase like hydrolas	0.54	4.53e-09	GPAT3	glycerol-3-phosphate acyltransferas
-0.92	8.58e-22	GPHN	gephyrin	1.15	5.21e-09	CAVIN3	caveolae associated protein 3
-0.69	8.94e-22	GMFB	glia maturation factor beta	1.32	5.84e-09	TGM2	transglutaminase 2
-0.88	1.17e-21	ENOPH1	enolase-phosphatase 1	0.18</td			

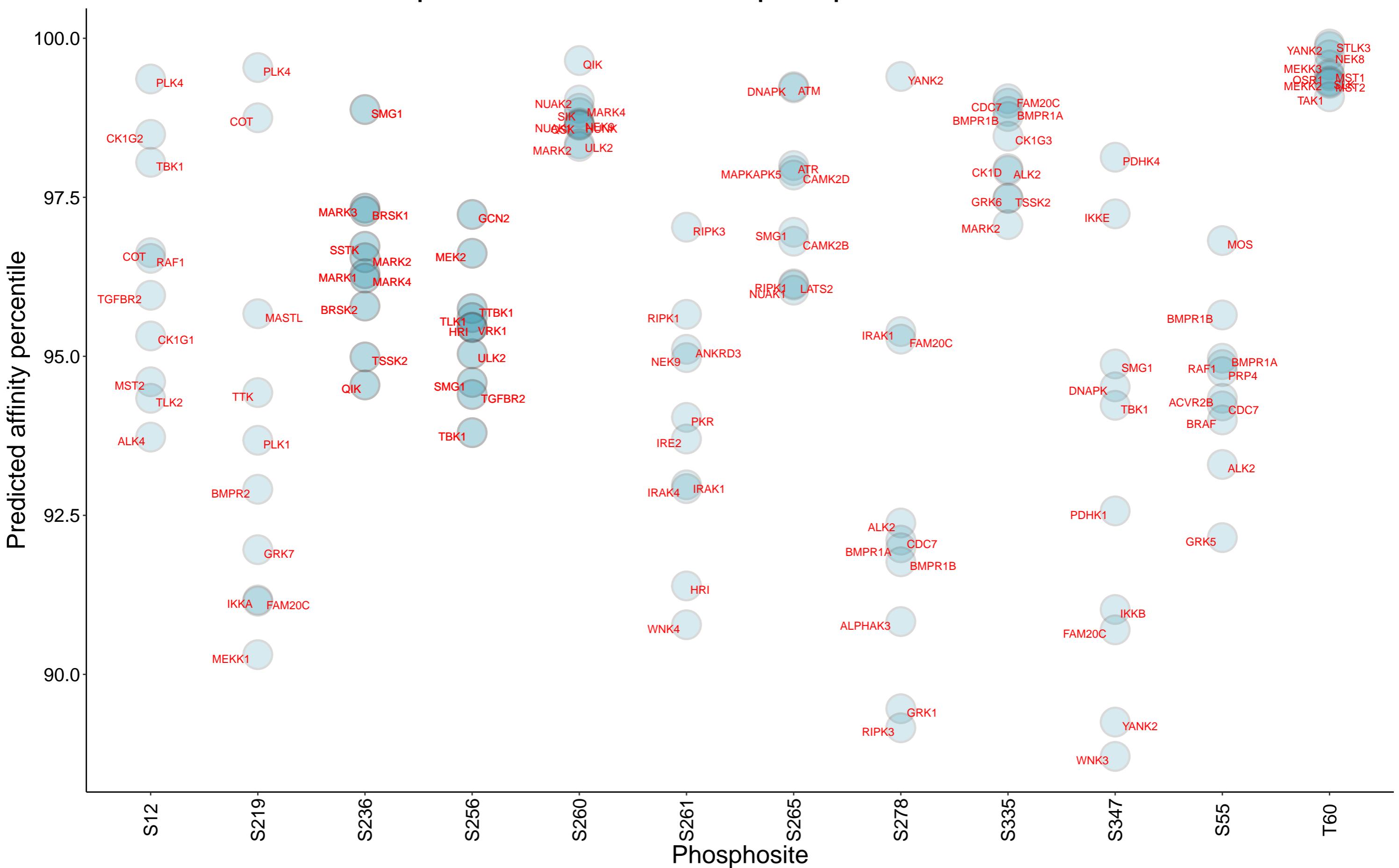
Top 250 correlation coefficients overrepresentation, ATXN3 protein, DB1



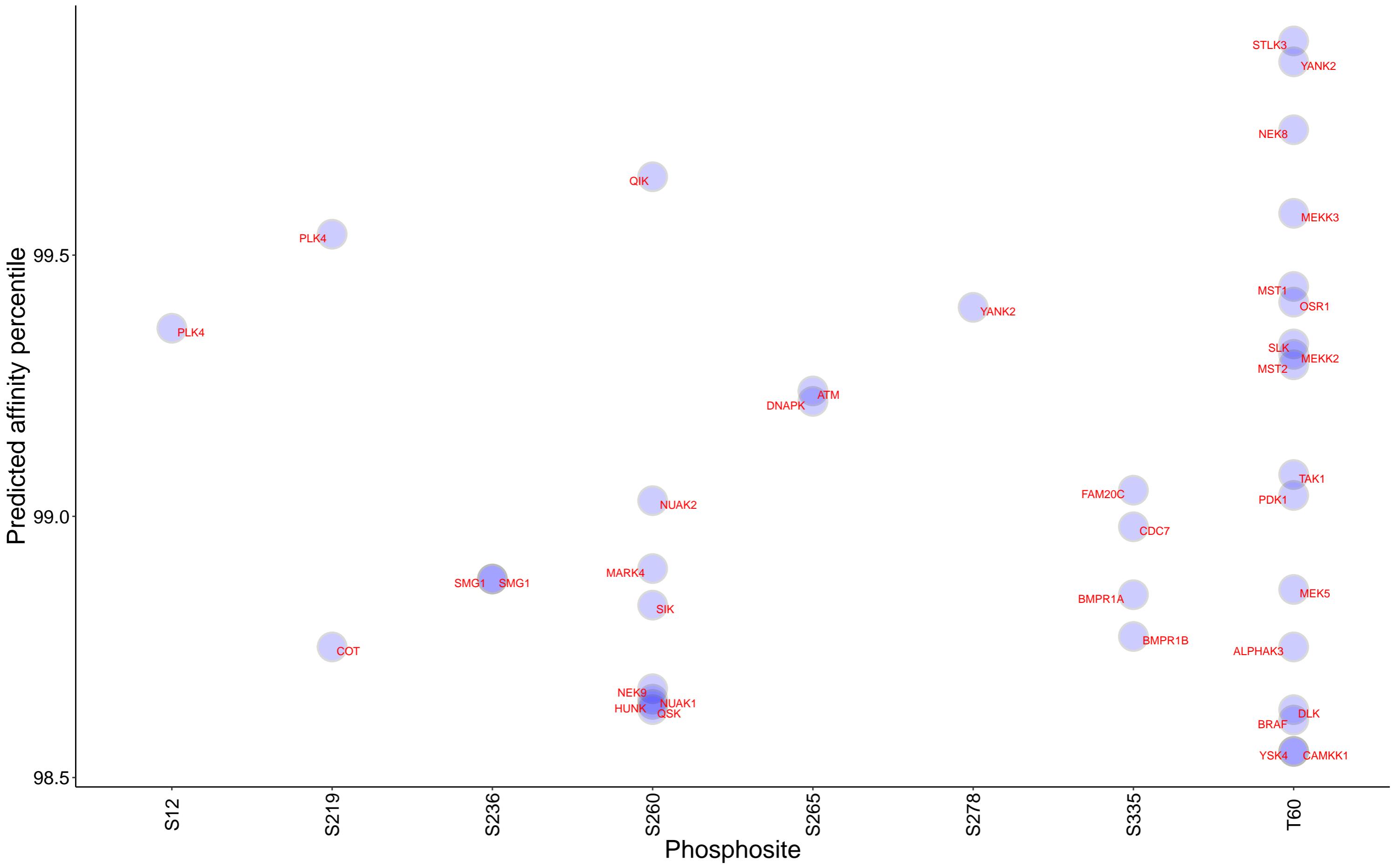
Gene Set Enrichment analysis on protein correlation coefficients, ATXN3 protein, DB1



Top 10 kinases for each phosphosite in ATXN3



Kinases with affinity greater than 98.5% to ATXN3



No sufficient paired observations in DB1 for ATXN3