

ARMT1

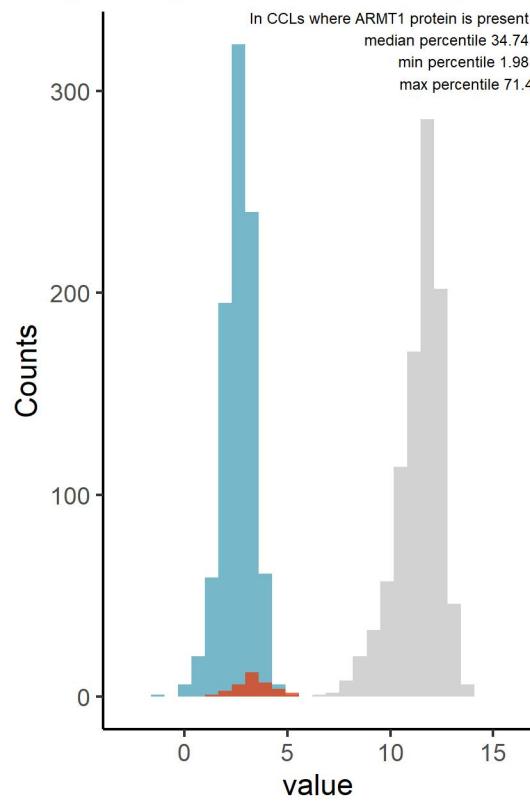
Protein name: ARMT1 ; UNIPROT: Q9H993 ; Gene name: acidic residue methyltransferase 1

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

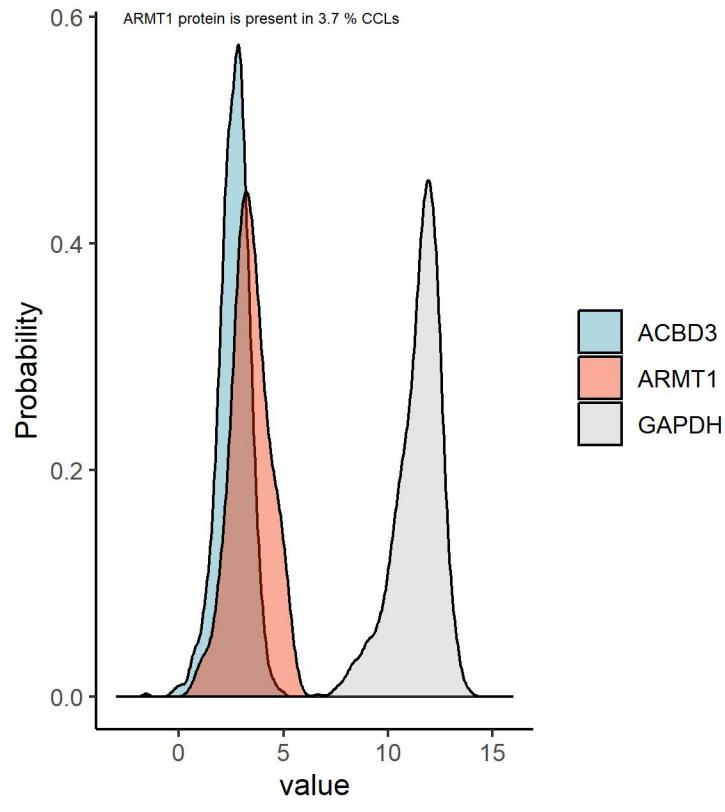
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

Histogram of ARMT1 protein compared to proteins with low and high abundance



Density plot of ARMT1 protein compared to proteins with low and high abundance



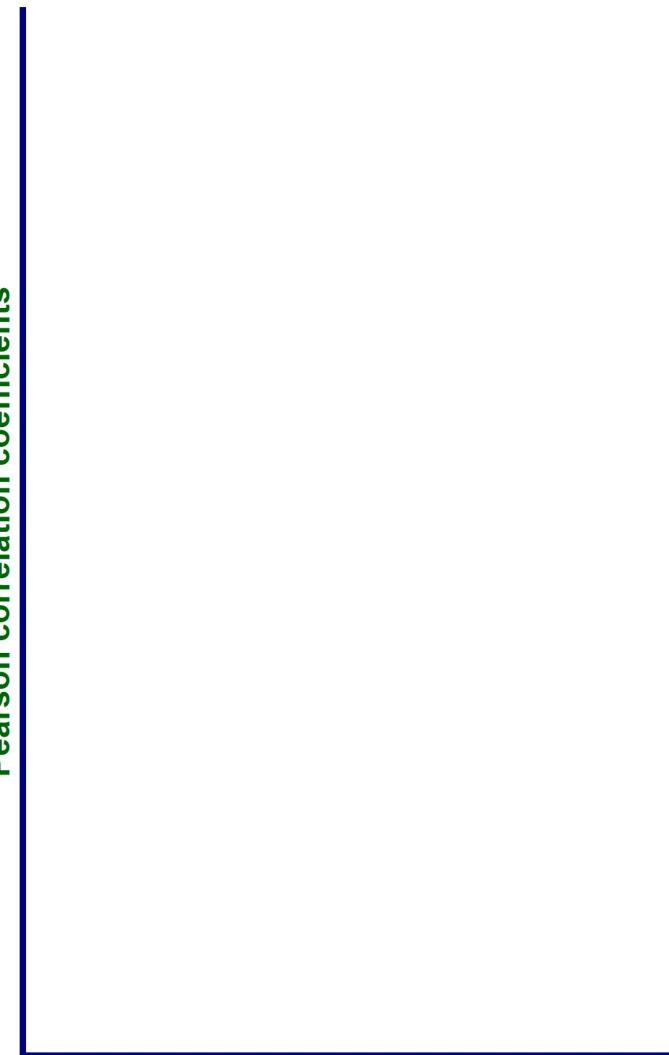
Top negative correlations of ARMT1 protein, DB1

Pearson correlation coefficients



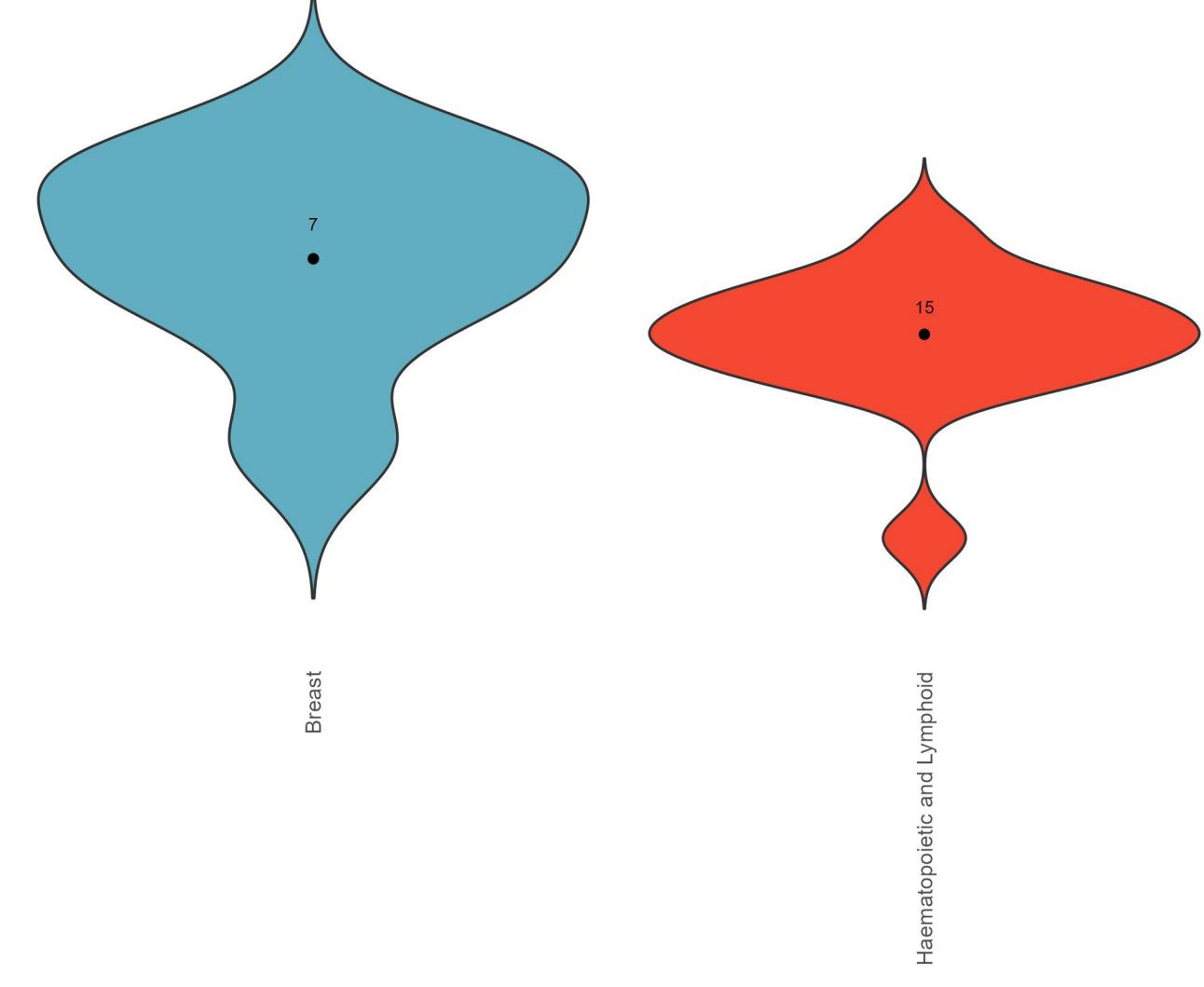
Top positive correlations of ARMT1 protein, DB1

Pearson correlation coefficients



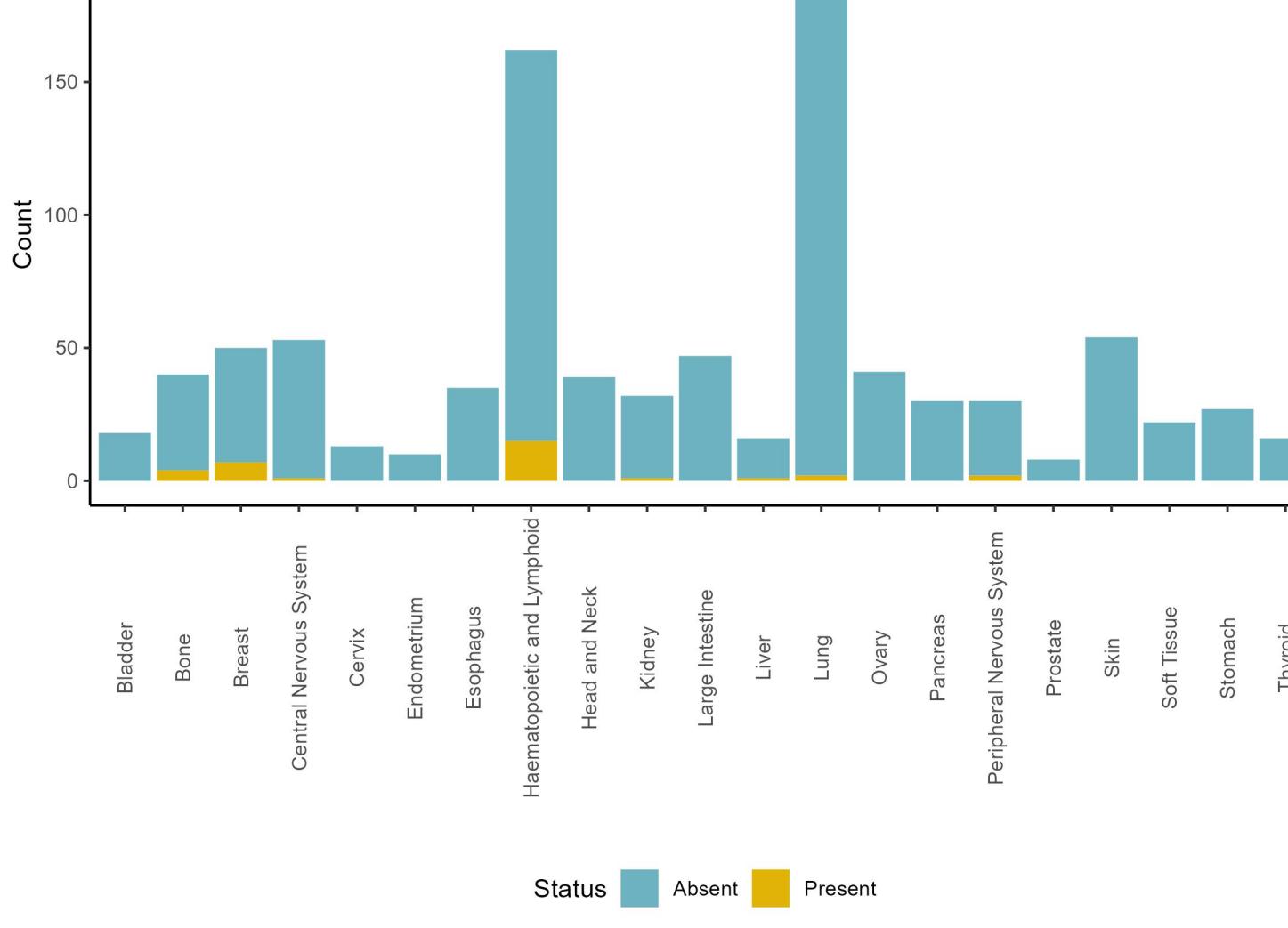
Amount of ARMT1 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 5.664e-02



Present and absent ARMT1 protein counts by tissue, DB1

Chi square p value is 5.184e-05

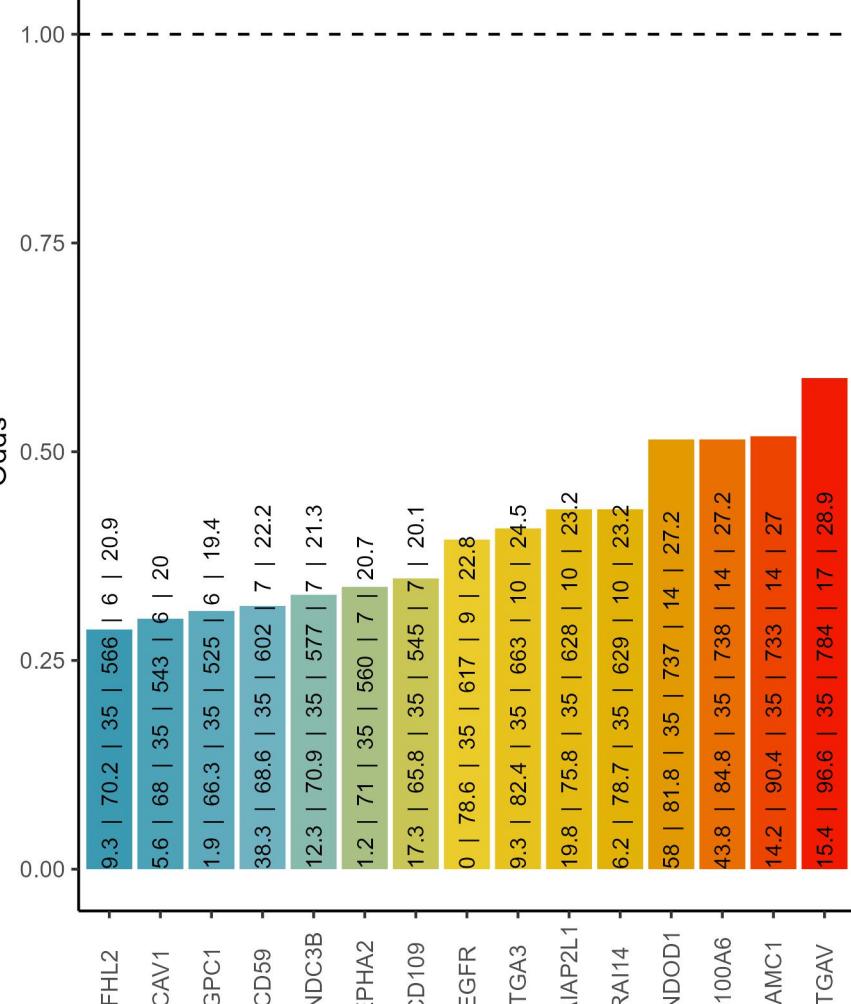


Cooccurrence with ARMT1 protein, DB1

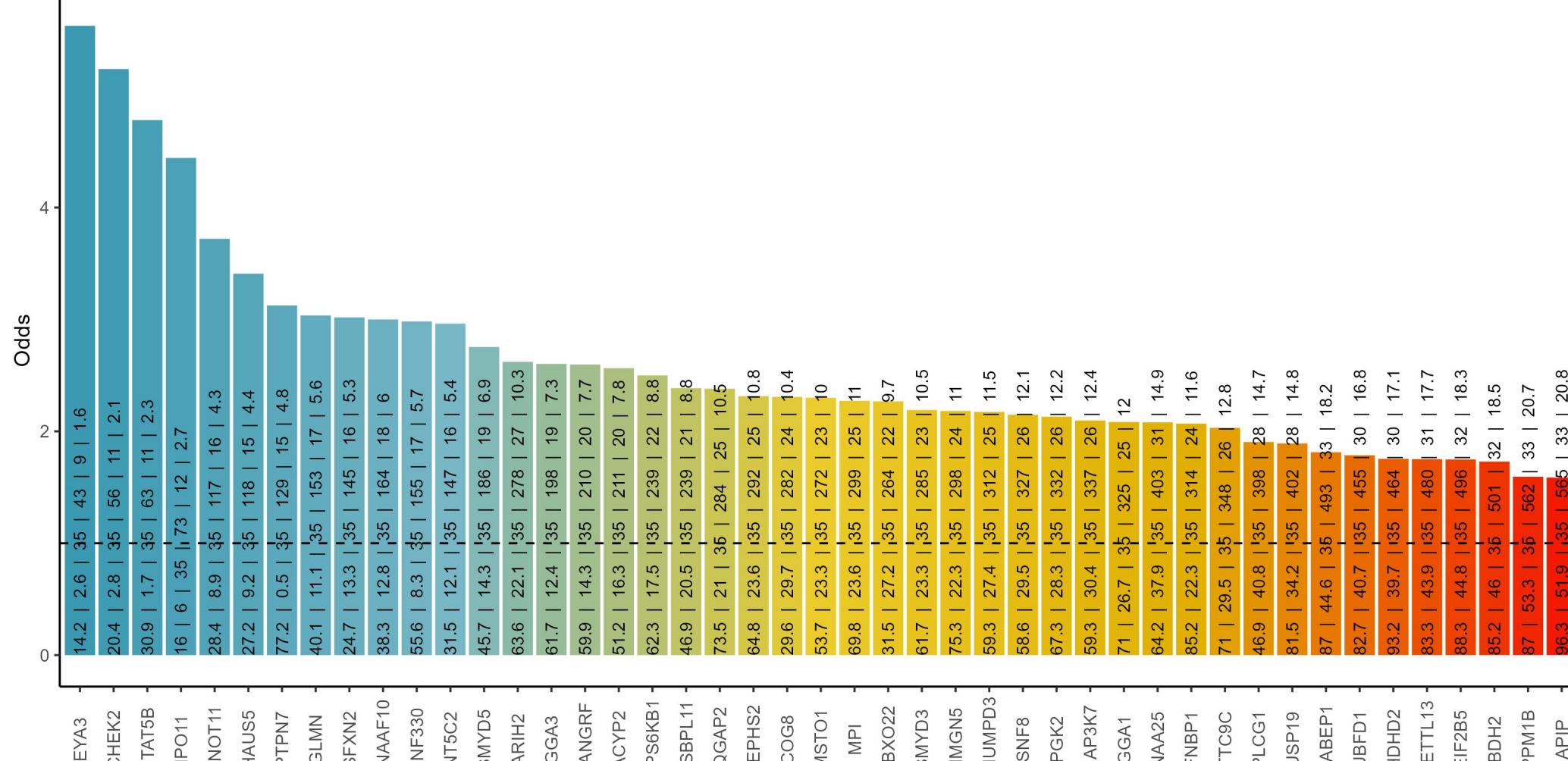
% of ARMT1 in blood cancers: 9.3 ; % of ARMT1 in solid cancers: 2.6

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ARMT1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

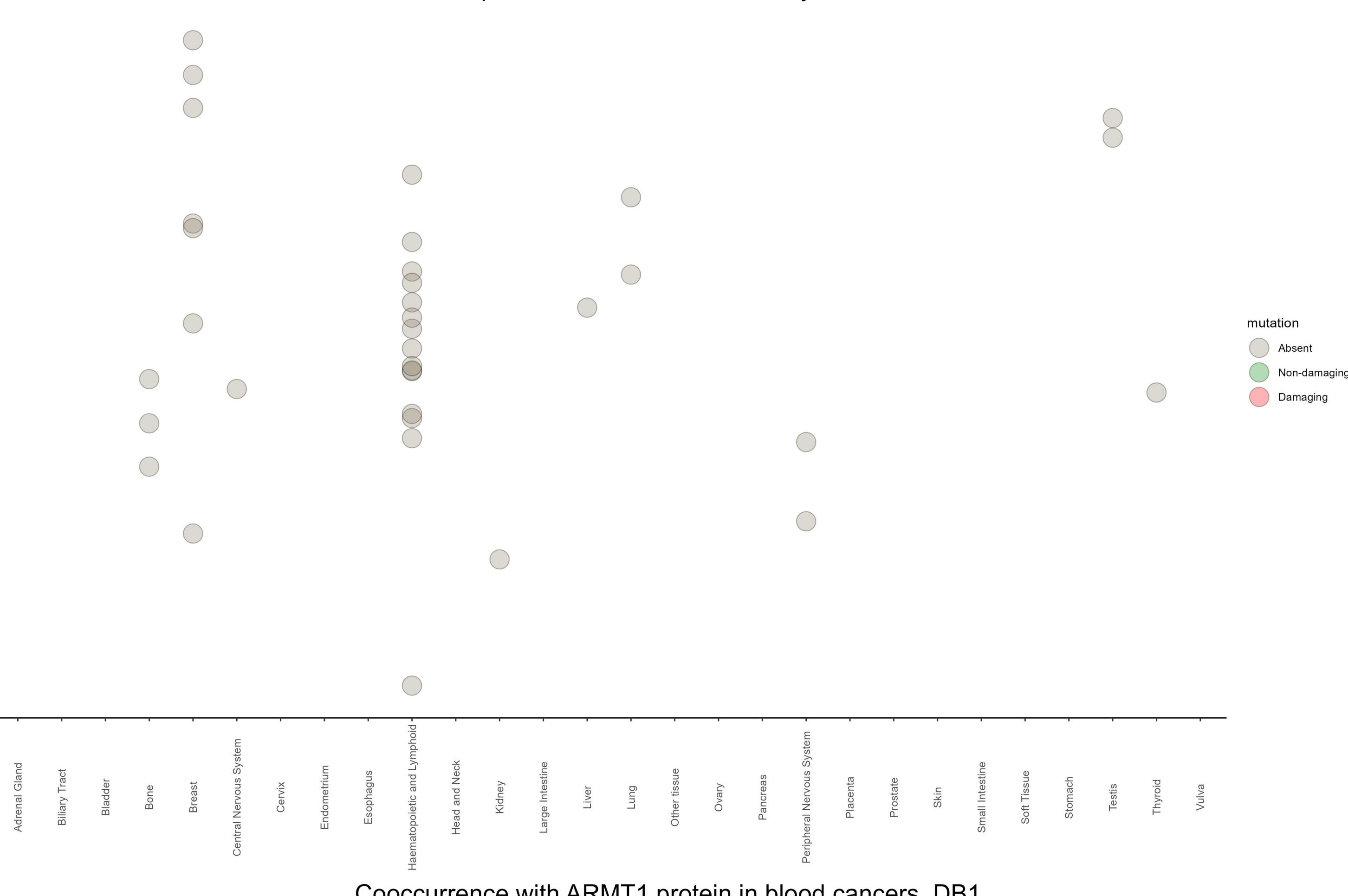
Negative cooccurrence



Positive cooccurrence



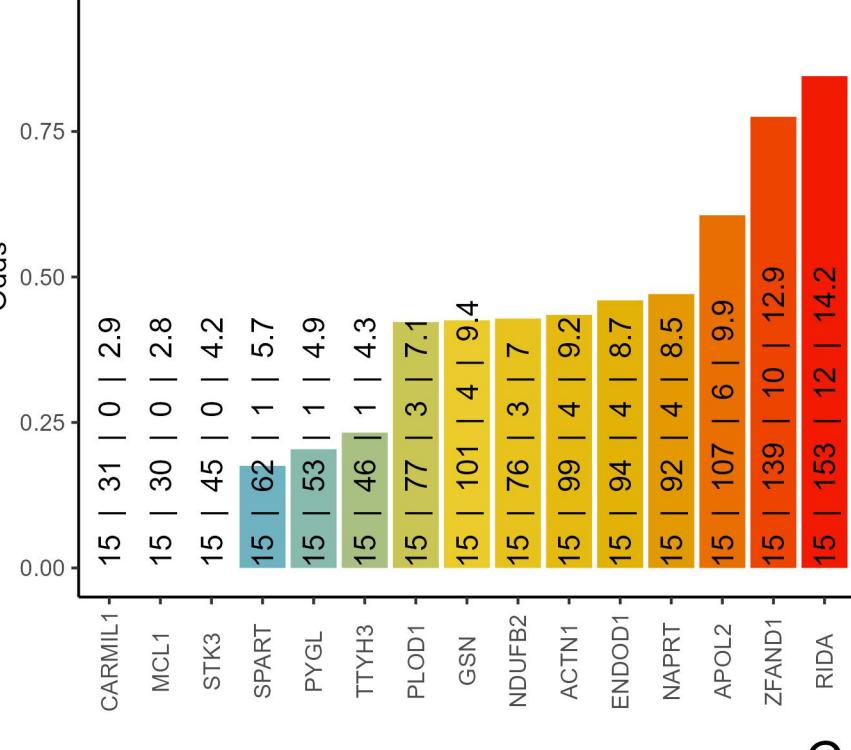
Amount of ARMT1 protein and mutation status by tissue, DB1



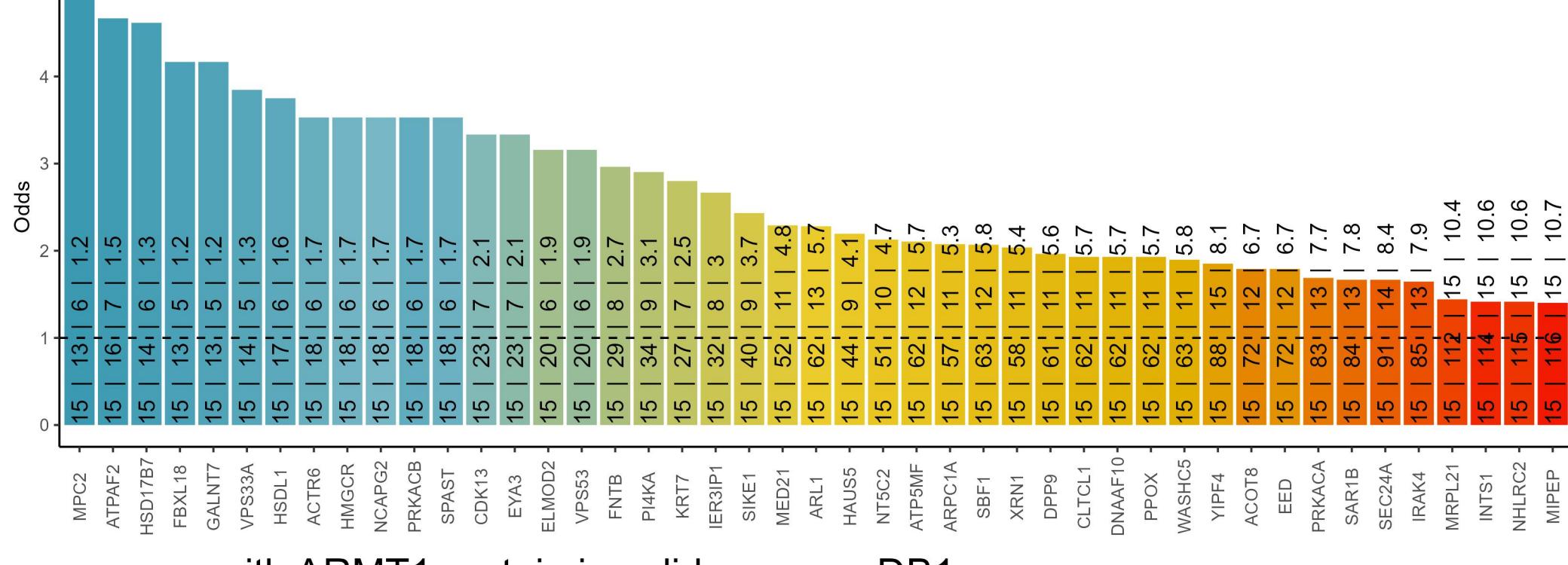
Cooccurrence with ARMT1 protein in blood cancers, DB1

The text in the bars: incidence of ARMT1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



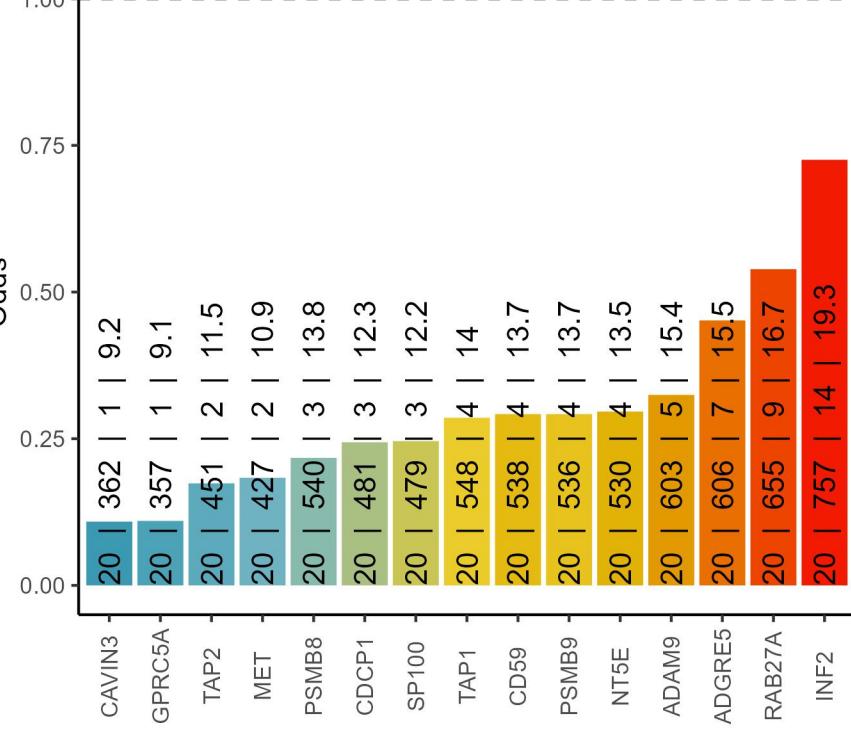
Positive cooccurrence



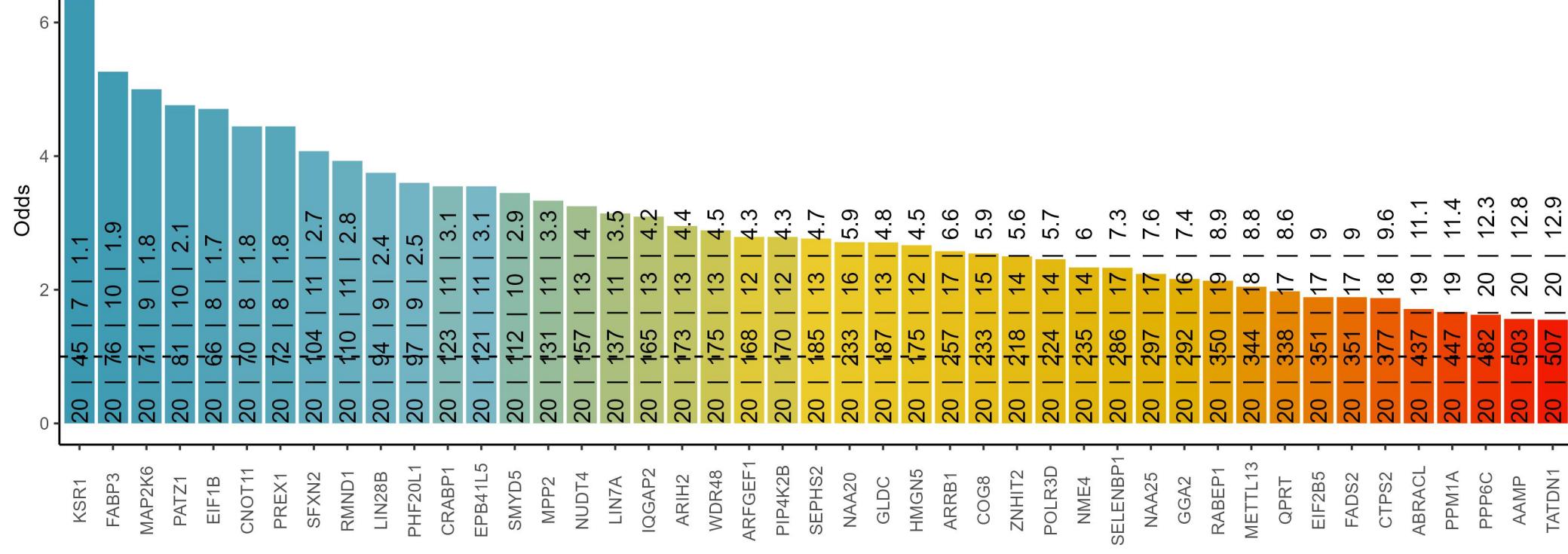
Cooccurrence with ARMT1 protein in solid cancers, DB1

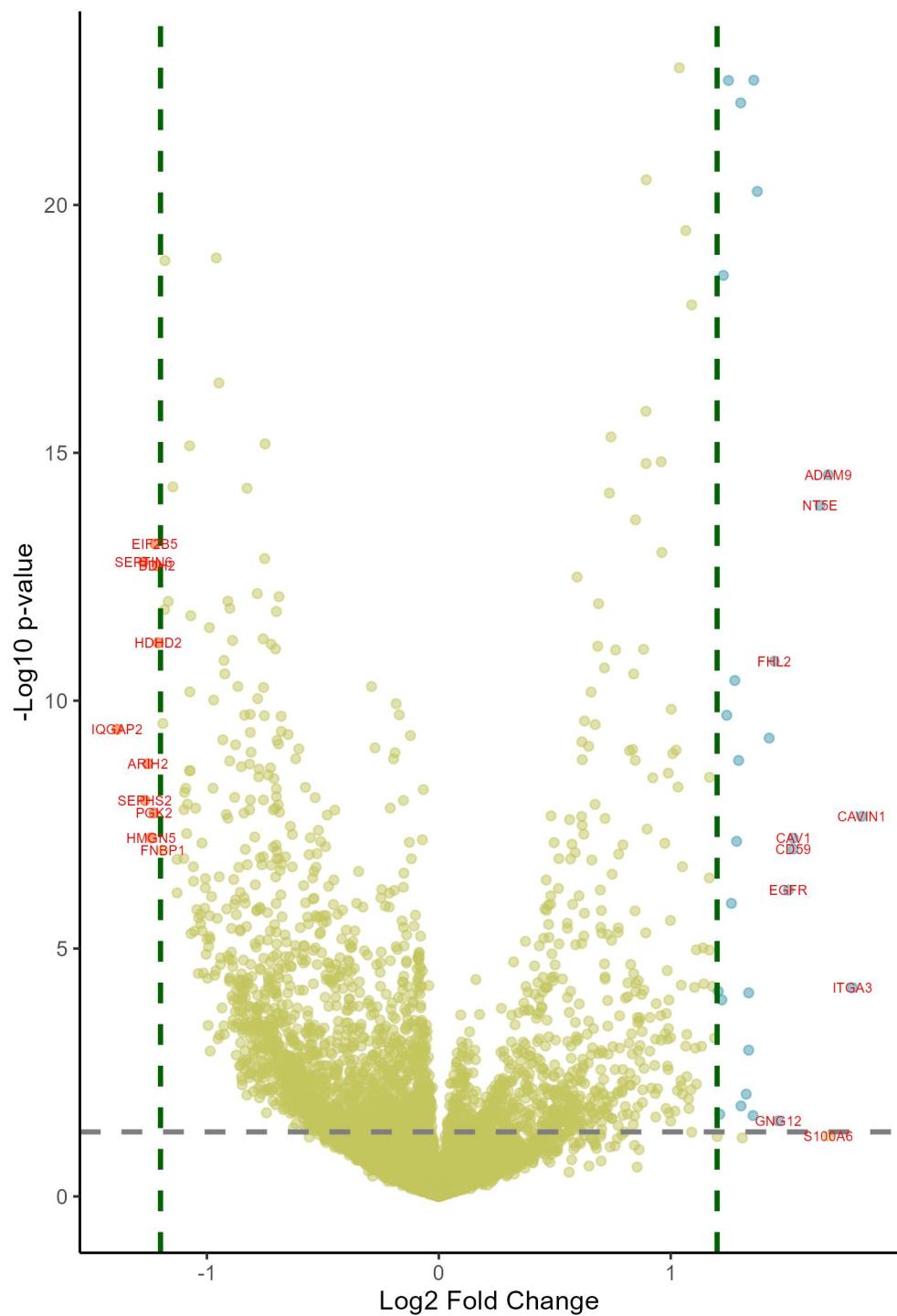
The text in the bars: incidence of ARMT1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



Positive cooccurrence

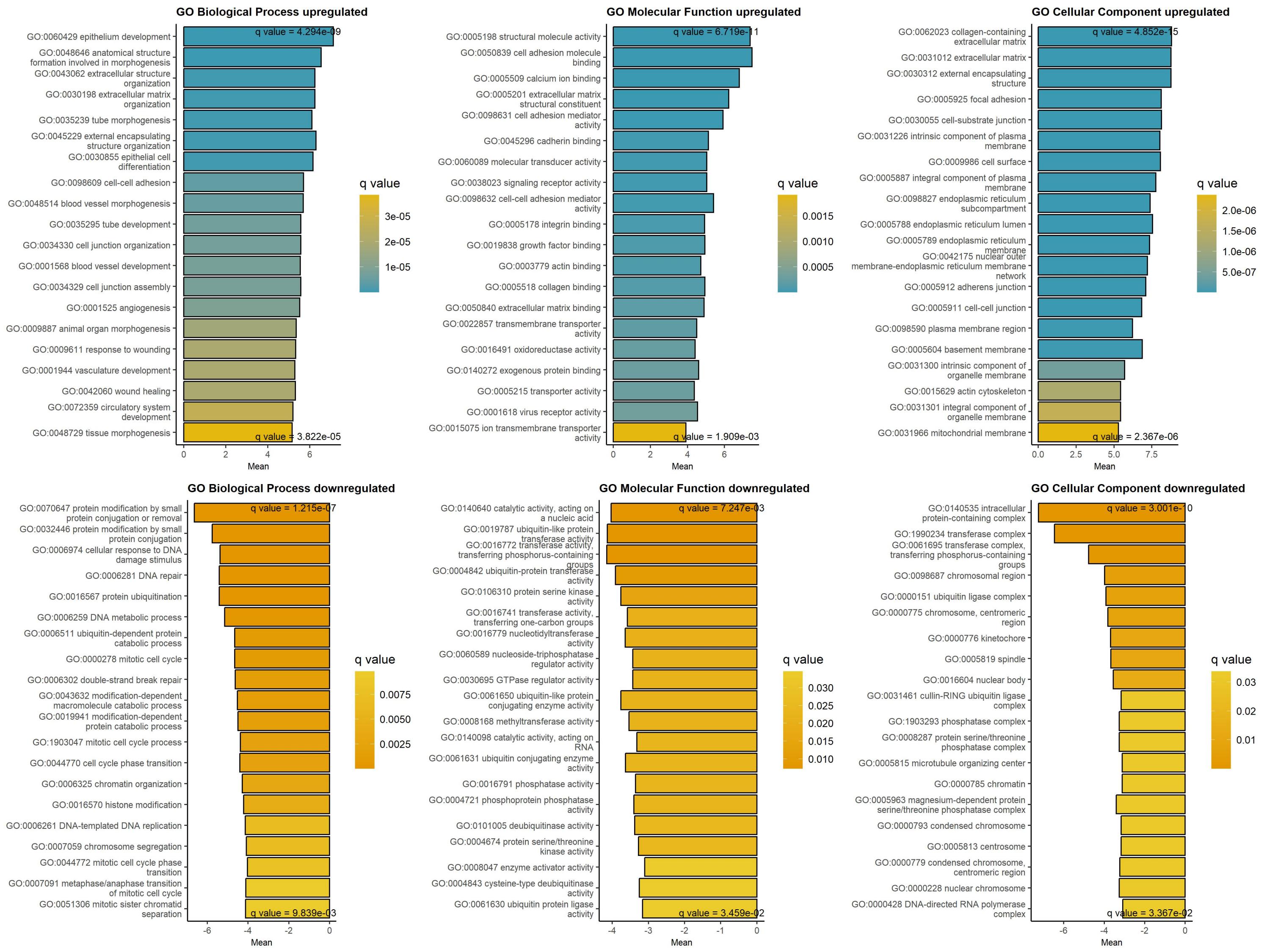


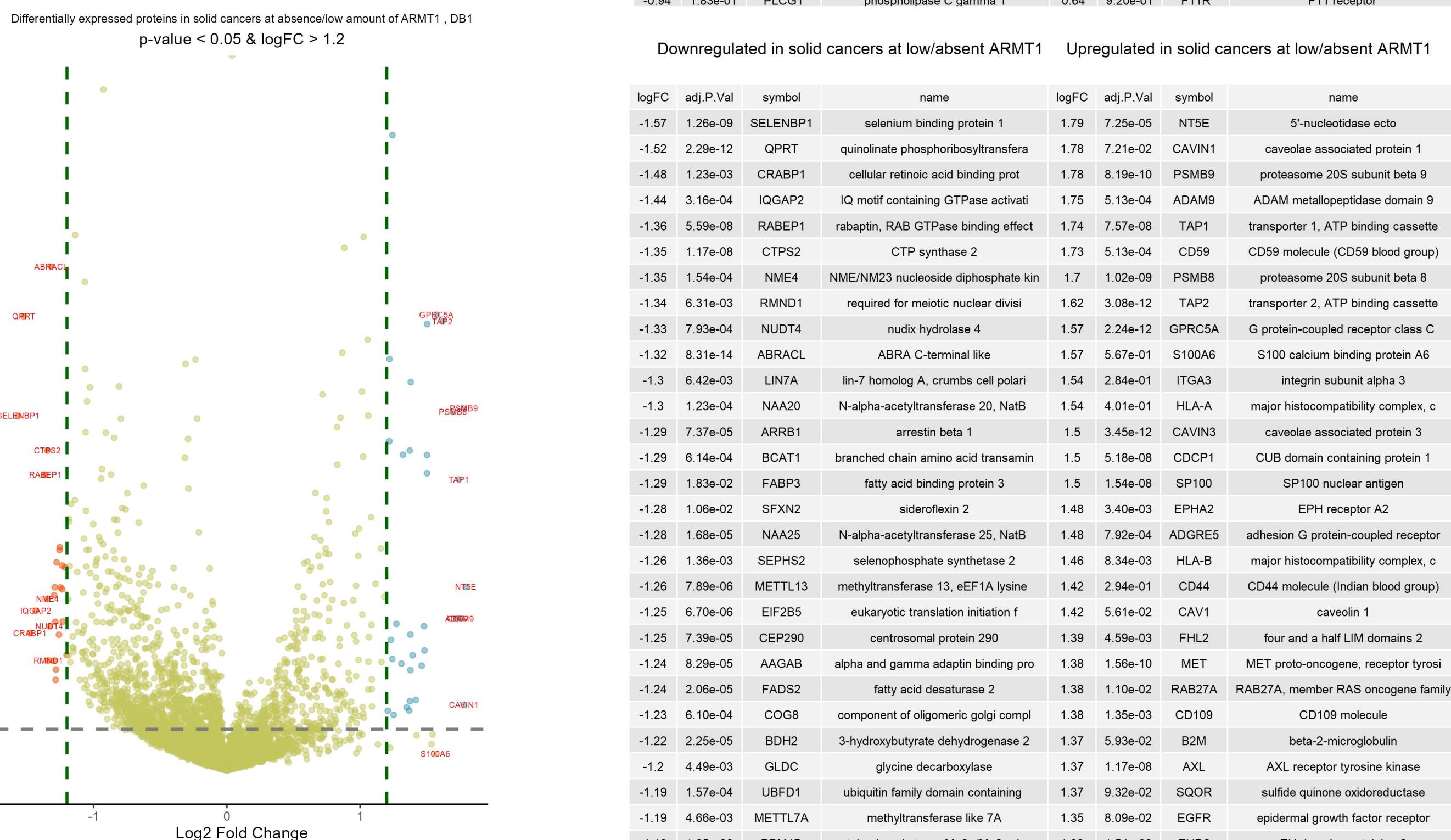
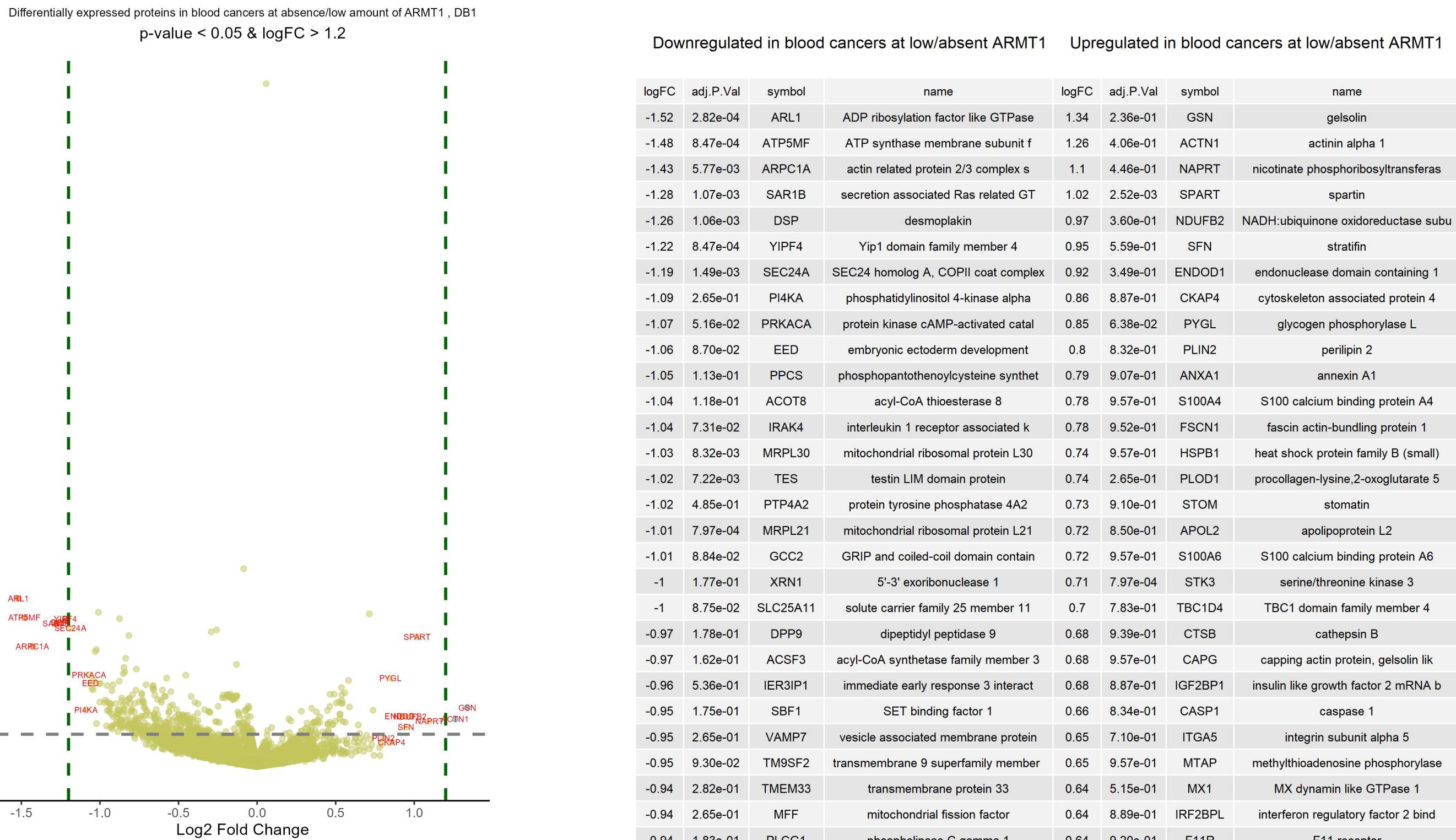


Downregulated at low/absent ARMT1 Upregulated at low/absent ARMT1

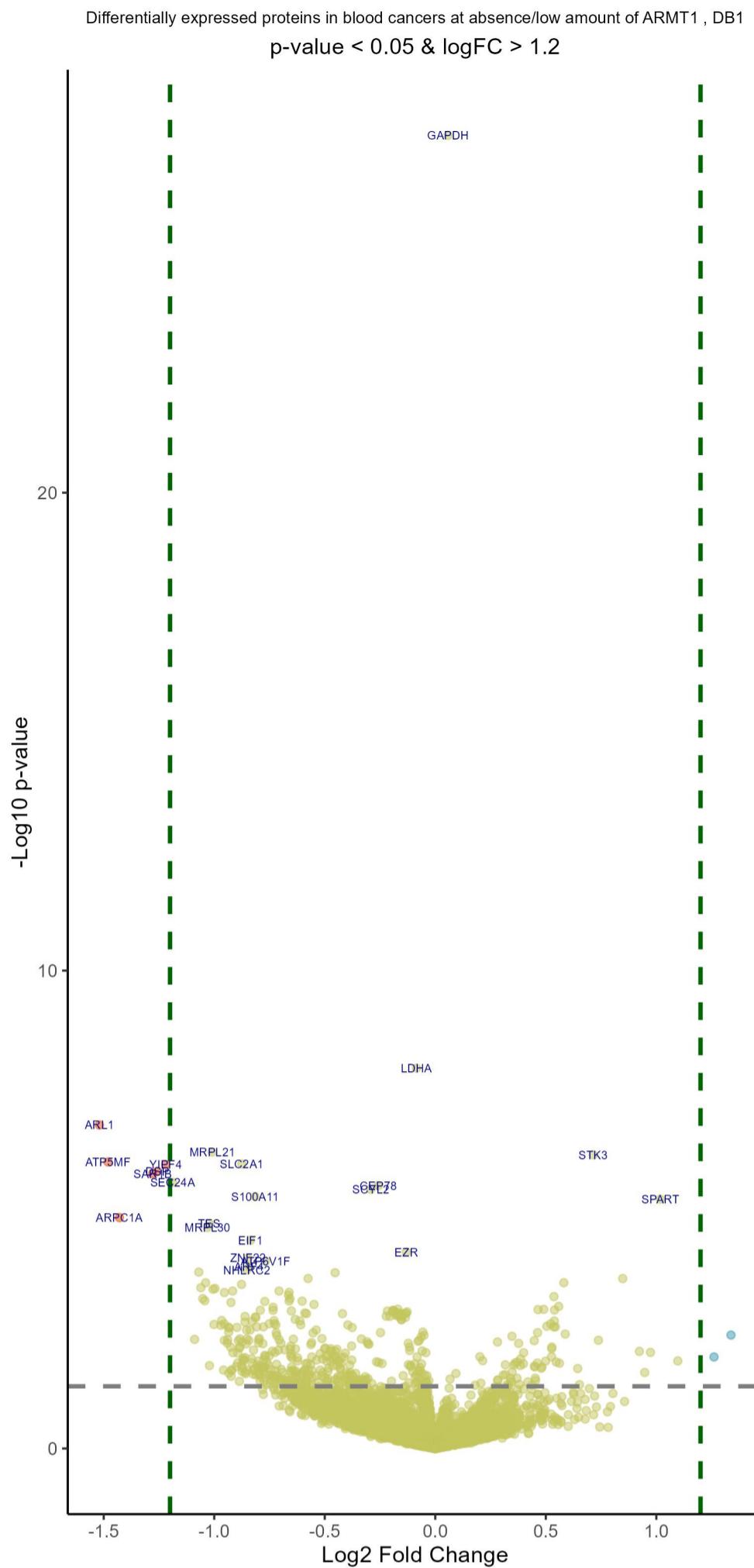
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.39	3.40e-08	IQGAP2	IQ motif containing GTPase activati	1.82	9.98e-07	CAVIN1	caveolae associated protein 1
-1.27	3.68e-11	SEPTIN6	septin 6	1.78	8.36e-04	ITGA3	integrin subunit alpha 3
-1.27	5.45e-07	SEPHS2	selenophosphate synthetase 2	1.68	1.55e-01	S100A6	S100 calcium binding protein A6
-1.25	1.24e-07	ARIH2	ariadne RBR E3 ubiquitin protein li	1.68	9.19e-13	ADAM9	ADAM metallopeptidase domain 9
-1.24	2.47e-06	HMGNS	high mobility group nucleosome bind	1.64	3.20e-12	NT5E	5'-nucleotidase ecto
-1.23	8.87e-07	PGK2	phosphoglycerate kinase 2	1.53	2.50e-06	CAV1	caveolin 1
-1.22	1.76e-11	EIF2B5	eukaryotic translation initiation f	1.53	3.82e-06	CD59	CD59 molecule (CD59 blood group)
-1.22	4.20e-11	BDH2	3-hydroxybutyrate dehydrogenase 2	1.51	1.99e-05	EGFR	epidermal growth factor receptor
-1.21	1.03e-09	HDHD2	haloacid dehalogenase like hydrolas	1.46	9.40e-02	GNG12	G protein subunit gamma 12
-1.19	4.03e-06	FNBP1	formin binding protein 1	1.45	2.08e-09	FHL2	four and a half LIM domains 2
-1.19	2.66e-08	NAA25	N-alpha-acetyltransferase 25, NatB	1.42	4.79e-08	EPHA2	EPH receptor A2
-1.18	2.54e-10	RABEP1	rabaptin, RAB GTPase binding effect	1.37	5.07e-18	CDCP1	CUB domain containing protein 1
-1.18	8.83e-17	BLMH	bleomycin hydrolase	1.36	5.12e-20	GPRC5A	G protein-coupled receptor class C
-1.17	1.89e-10	C11orf54	chromosome 11 open reading frame 54	1.36	7.91e-02	LGALS3	galectin 3
-1.15	1.54e-12	PPM1B	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe	1.34	1.02e-03	LAMC1	laminin subunit gamma 1
-1.13	2.24e-05	BCAT1	branched chain amino acid transamin	1.34	8.60e-03	ITGAV	integrin subunit alpha V
-1.13	5.63e-06	CORO1A	coronin 1A	1.33	3.98e-02	FKBP9	FKBP prolyl isomerase 9
-1.1	5.52e-06	PPCS	phosphopantethenylcysteine synthet	1.31	1.65e-01	ANXA1	annexin A1
-1.1	7.86e-07	TUBB4A	tubulin beta 4A class IVa	1.3	5.88e-02	CD44	CD44 molecule (Indian blood group)
-1.1	3.97e-07	NUDT3	nudix hydrolase 3	1.3	1.16e-19	CAVIN3	caveolae associated protein 3
-1.09	3.36e-07	SMAP2	small ArfGAP2	1.29	1.09e-07	CD109	CD109 molecule
-1.09	2.10e-06	AAGAB	alpha and gamma adaptin binding pro	1.28	2.86e-06	RAI14	retinoic acid induced 14
-1.08	6.40e-07	UBFD1	ubiquitin family domain containing	1.28	4.74e-09	GPC1	glycan 1
-1.07	1.62e-07	RWDD1	RWD domain containing 1	1.26	3.43e-05	GPX8	glutathione peroxidase 8 (putative)
-1.07	2.83e-13	ABRACL	ABRA C-terminal like	1.25	5.12e-20	MET	MET proto-oncogene, receptor tyrosi
-1.07	7.44e-09	MSI2	musashi RNA binding protein 2	1.24	1.93e-08	FNDC3B	fibronectin type III domain contain
-1.07	1.62e-07	EIF2B1	eukaryotic translation initiation f	1.23	1.60e-16	AXL	AXL receptor tyrosine kinase
-1.07	3.22e-10	APIP	APAF1 interacting protein	1.22	1.34e-03	PROCR	protein C receptor
-1.07	1.08e-04	GALM	galactose mutarotase	1.21	7.56e-02	NCEH1	neutral cholesterol ester hydrolase

GAGE analysis on upregulated and downregulated proteins at low/absent ARMT1 protein, DB1

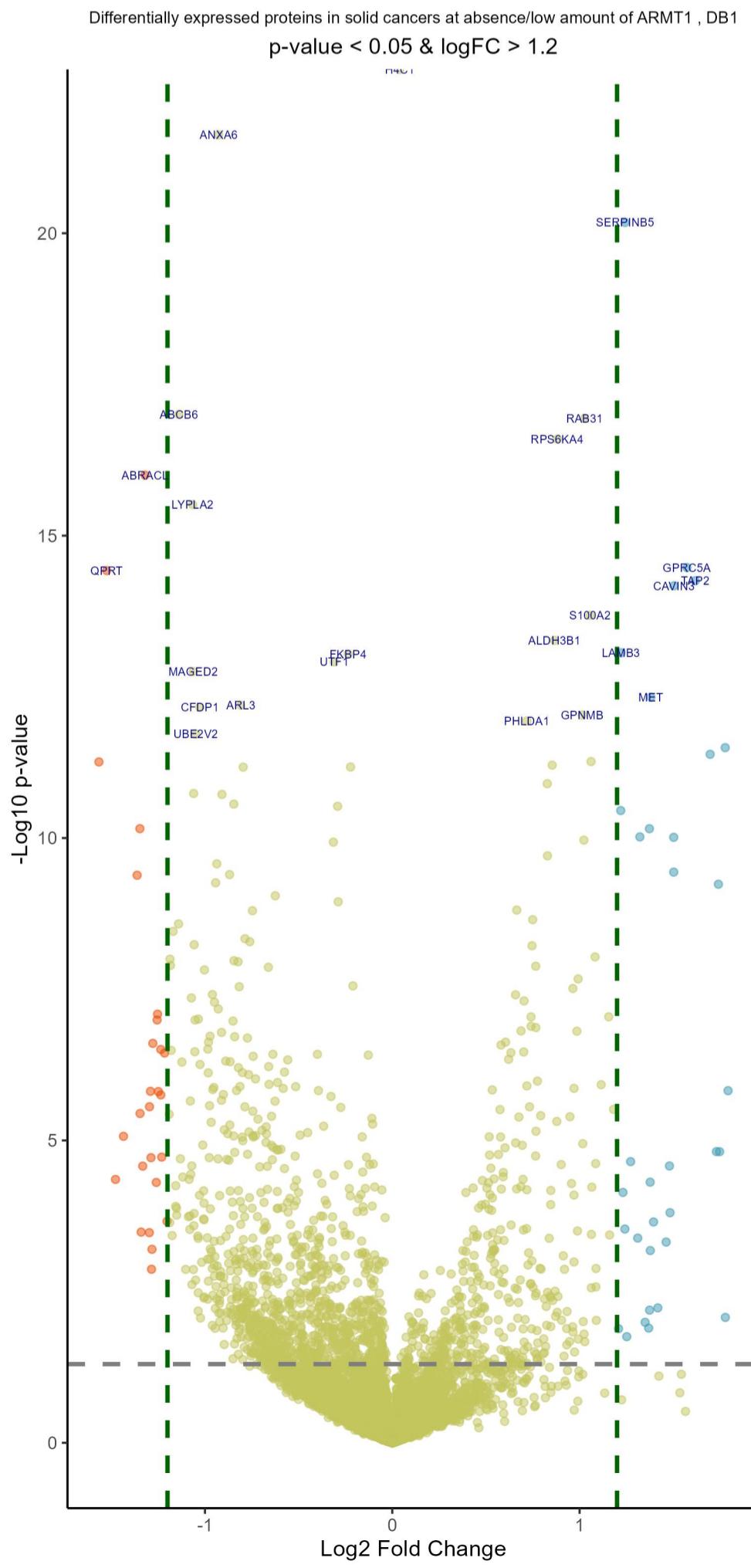




ARMT1 network, DB1, no Pearson r > 0.3



Sorted by p values!							
Downregulated in blood cancers at low/absent ARMT1				Upregulated in blood cancers at low/absent ARMT1			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.09	2.44e-05	LDHA	lactate dehydrogenase A	0.06	1.11e-24	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
-1.52	2.82e-04	ARL1	ADP ribosylation factor like GTPase	0.71	7.97e-04	STK3	serine/threonine kinase 3
-1.01	7.97e-04	MRPL21	mitochondrial ribosomal protein L21	1.02	2.52e-03	SPART	spartin
-1.48	8.47e-04	ATP5MF	ATP synthase membrane subunit f	0.85	6.38e-02	PYGL	glycogen phosphorylase L
-0.88	8.47e-04	SLC2A1	solute carrier family 2 member 1	0.58	7.31e-02	MCL1	MCL1 apoptosis regulator, BCL2 family
-1.22	8.47e-04	YIPF4	Yip1 domain family member 4	0.54	1.07e-01	TMOD1	tropomodulin 1
-1.26	1.06e-03	DSP	desmoplakin	0.56	1.42e-01	NECTIN2	nectin cell adhesion molecule 2
-1.28	1.07e-03	SAR1B	secretion associated Ras related GT	0.49	1.42e-01	SNX9	sorting nexin 9
-1.19	1.49e-03	SEC24A	SEC24 homolog A, COPII coat complex	0.46	1.42e-01	CARMIL1	capping protein regulator and myosin
-0.26	1.62e-03	CEP78	centrosomal protein 78	0.54	1.42e-01	CD33	CD33 molecule
-0.29	1.79e-03	SCYL2	SCY1 like pseudokinase 2	0.54	1.63e-01	SLAMF1	signaling lymphocytic activation molecule
-0.82	2.37e-03	S100A11	S100 calcium binding protein A11	0.52	1.75e-01	COL1A1	collagen type I alpha 1 chain
-1.43	5.77e-03	ARPC1A	actin related protein 2/3 complex s	0.5	1.83e-01	FCGR2B	Fc gamma receptor IIb
-1.02	7.22e-03	TES	testin LIM domain protein	0.54	1.83e-01	FDX2	ferredoxin 2
-1.03	8.32e-03	MRPL30	mitochondrial ribosomal protein L30	0.54	1.83e-01	TTYH3	tweety family member 3
-0.84	1.46e-02	EIF1	eukaryotic translation initiation f	0.46	2.17e-01	NME4	NME/NM23 nucleoside diphosphate kinase
-0.13	2.46e-02	EZR	ezrin	0.59	2.27e-01	IFIT3	interferon induced protein with tet
-0.85	3.12e-02	ZNF22	zinc finger protein 22	1.34	2.36e-01	GSN	gelsolin
-0.77	3.46e-02	ATP6V1F	ATPase H+ transporting V1 subunit F	0.35	2.44e-01	EEA1	early endosome antigen 1
-0.84	4.33e-02	ARF4	ADP ribosylation factor 4	0.74	2.65e-01	PLOD1	procollagen-lysine,2-oxoglutarate 5
-0.85	4.87e-02	NHLRC2	NHL repeat containing 2	0.45	2.65e-01	GNAI1	G protein subunit alpha i1
-1.07	5.16e-02	PRKACA	protein kinase cAMP-activated catal	0.28	2.76e-01	HSD17B4	hydroxysteroid 17-beta dehydrogenase
-0.45	5.16e-02	YBX2	Y-box binding protein 2	0.38	2.82e-01	NPEPL1	aminopeptidase like 1
-0.58	6.38e-02	PTBP2	polypyrimidine tract binding protei	0.53	3.17e-01	PTGR3	prostaglandin reductase 3
-1.04	7.31e-02	IRAK4	interleukin 1 receptor associated k	0.53	3.28e-01	AASS	aminoacidate-semialdehyde synthase
-0.88	7.66e-02	PITPNA	phosphatidylinositol transfer prote	0.92	3.49e-01	ENDOD1	endonuclease domain containing 1
-1.06	8.70e-02	EED	embryonic ectoderm development	0.97	3.60e-01	NDUFB2	NADH:ubiquinone oxidoreductase sub
-1	8.75e-02	SLC25A11	solute carrier family 25 member 11	0.4	3.60e-01	SLC9A3R2	SLC9A3 regulator 2
-1.01	8.84e-02	GCC2	GRIP and coiled-coil domain contain	0.2	4.06e-01	BAG6	BAG cochaperone 6
-0.92	9.12e-02	ARMC10	armadillo repeat containing 10	0.53	4.06e-01	UBAP1	ubiquitin associated protein 1
-0.71	9.12e-02	OAT	ornithine aminotransferase	1.26	4.06e-01	ACTN1	actinin alpha 1
-0.66	9.30e-02	TMX2	thioredoxin related transmembrane p	0.39	4.27e-01	THEMIS2	thymocyte selection associated fami
-0.95	9.30e-02	TM9SF2	transmembrane 9 superfamily member	0.21	4.46e-01	DIS3	DIS3 homolog, exosome endoribonucle
-0.66	1.03e-01	POLR2F	RNA polymerase II, I and III subuni	1.1	4.46e-01	NAPRT	nicotinate phosphoribosyltransferas
-1.05	1.13e-01	PPCS	phosphopantethenoylcysteine synthet	0.5	4.46e-01	RAB9A	RAB9A, member RAS oncogene famil
-0.66	1.13e-01	USP19	ubiquitin specific peptidase 19	0.55	4.53e-01	CTNND1	catenin delta 1
-1.04	1.18e-01	ACOT8	acyl-CoA thioesterase 8	0.37	4.54e-01	APP	amyloid beta precursor protein
-0.66	1.18e-01	SLC1A4	solute carrier family 1 member 4	0.46	4.65e-01	NCF2	neutrophil cytosolic factor 2
-0.6	1.18e-01	LRRC8B	ubiquitin like domain containing CT	0.36	4.65e-01	LVI75	lymphocyte antigen 75

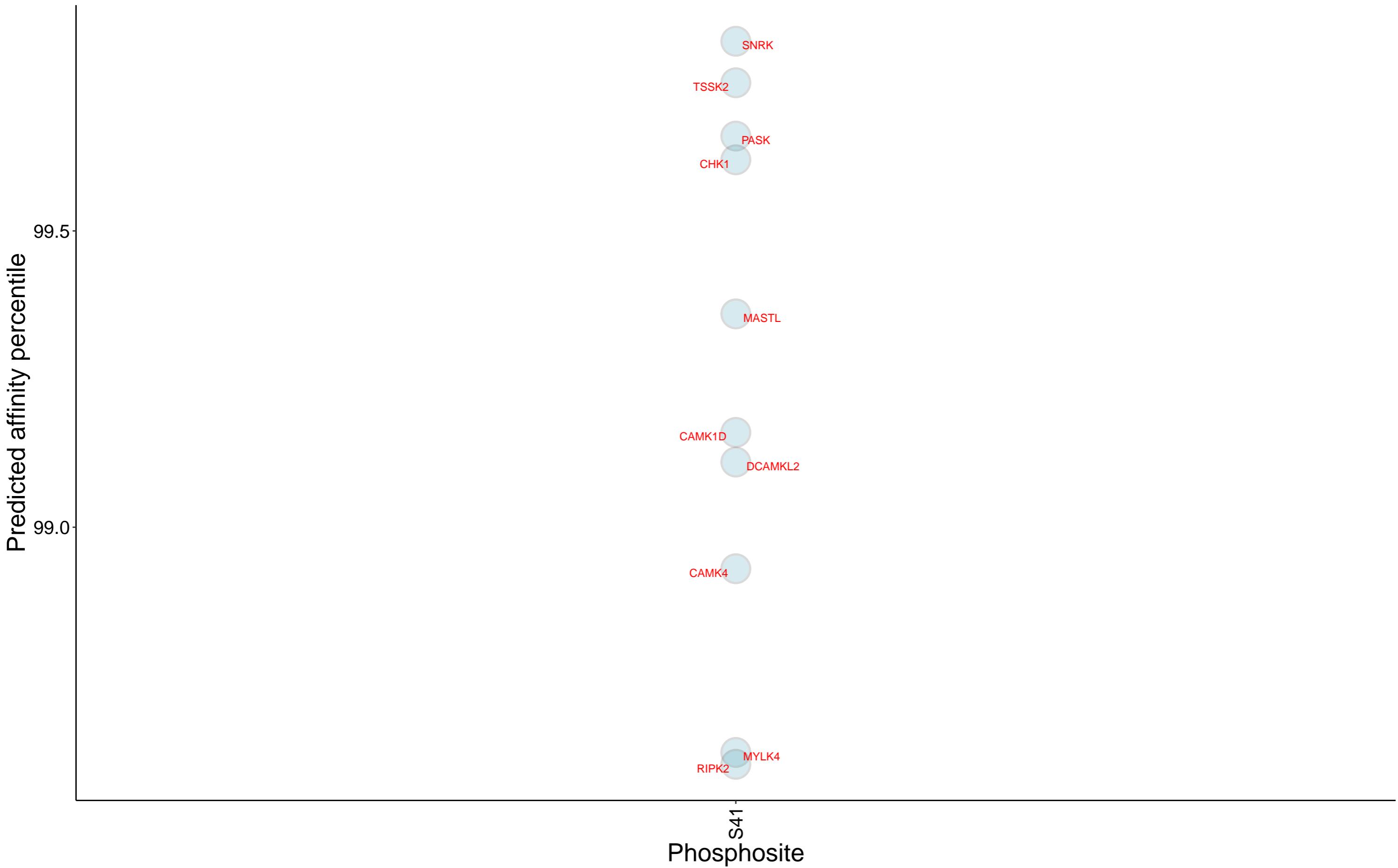


Sorted by p values!							
Downregulated in solid cancers at low/absent ARMT1				Upregulated in solid cancers at low/absent ARMT1			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
0.93	5.23e-19	ANXA6	annexin A6	0.04	0.00e+00	H4C1	H4 clustered histone 1
1.14	1.27e-14	ABCB6	ATP binding cassette subfamily B me	1.24	1.10e-17	SERPINB5	serpin family B member 5
1.32	8.31e-14	ABRACL	ABRA C-terminal like	1.03	1.27e-14	RAB31	RAB31, member RAS oncogene fam
1.07	2.27e-13	LYPLA2	lysophospholipase 2	0.88	2.41e-14	RPS6KA4	ribosomal protein S6 kinase A4
1.52	2.29e-12	QPRT	quinolinate phosphoribosyltransfera	1.57	2.24e-12	GPRC5A	G protein-coupled receptor class C
0.24	3.54e-11	FKBP4	FKBP prolyl isomerase 4	1.62	3.08e-12	TAP2	transporter 2, ATP binding cassette
0.31	4.51e-11	UTF1	undifferentiated embryonic cell tra	1.5	3.45e-12	CAVIN3	caveolae associated protein 3
1.06	6.20e-11	MAGED2	MAGE family member D2	1.06	9.88e-12	S100A2	S100 calcium binding protein A2
0.81	2.02e-10	ARL3	ADP ribosylation factor like GTPase	0.87	2.39e-11	ALDH3B1	aldehyde dehydrogenase 3 family me
1.03	2.08e-10	CFDP1	craniofacial development protein 1	1.22	3.54e-11	LAMB3	laminin subunit beta 3
1.05	5.06e-10	UBE2V2	ubiquitin conjugating enzyme E2 V2	1.38	1.56e-10	MET	MET proto-oncogene, receptor tyros
1.57	1.26e-09	SELENBP1	selenium binding protein 1	1.01	2.68e-10	GPNMB	glycoprotein nmb
0.22	1.40e-09	FASN	fatty acid synthase	0.72	3.22e-10	PHLDA1	pleckstrin homology like domain fam
-0.8	1.40e-09	ARPC5	actin related protein 2/3 complex s	1.78	8.19e-10	PSMB9	proteasome 20S subunit beta 9
1.06	3.59e-09	FLYWCH2	FLYWCH family member 2	1.7	1.02e-09	PSMB8	proteasome 20S subunit beta 8
0.91	3.61e-09	CZIB	CXXC motif containing zinc binding	1.06	1.26e-09	EHBP1L1	EH domain binding protein 1 like 1
0.85	5.08e-09	DDI2	DNA damage inducible 1 homolog 2	0.85	1.38e-09	OSBPL3	oxysterol binding protein like 3
0.29	5.36e-09	TBR1	T-box brain transcription factor 1	0.83	2.55e-09	CDH13	cadherin 13
1.35	1.17e-08	CTPS2	CTP synthase 2	1.22	6.15e-09	DCBLD2	discoidin, CUB and LCCL domain co
0.31	1.77e-08	PEBP1	phosphatidylethanolamine binding pr	1.37	1.17e-08	AXL	AXL receptor tyrosine kinase
0.94	3.86e-08	AKT1S1	AKT1 substrate 1	1.32	1.54e-08	EHD2	EH domain containing 2
0.87	5.57e-08	ENSA	endosulfine alpha	1.5	1.54e-08	SP100	SP100 nuclear antigen
1.36	5.59e-08	RABEP1	rabaptin, RAB GTPase binding effect	1.02	1.68e-08	TGFBI	transforming growth factor beta ind
0.94	7.31e-08	DHTKD1	dehydrogenase E1 and transketolase	0.83	2.91e-08	JUN	Jun proto-oncogene, AP-1 transcript
0.62	1.15e-07	BTF3L4	basic transcription factor 3 like 4	1.5	5.18e-08	CDCP1	CUB domain containing protein 1
0.29	1.42e-07	MIF	macrophage migration inhibitory fac	1.74	7.57e-08	TAP1	transporter 1, ATP binding cassette
0.75	1.92e-07	LSM1	LSM1 homolog, mRNA degradation asso	0.66	1.91e-07	SYNE3	spectrin repeat containing nuclear
1.14	3.07e-07	PPM1A	protein phosphatase, Mg2+/Mn2+ depe	0.75	2.66e-07	LCN2	lipocalin 2
1.17	4.00e-07	BLMH	bleomycin hydrolase	0.75	6.48e-07	ALDH3A1	aldehyde dehydrogenase 3 family me
0.79	5.21e-07	PIN1	peptidylprolyl cis/trans isomerase,	1.08	9.75e-07	NNMT	nicotinamide N-methyltransferase
0.76	5.74e-07	PTPA	protein phosphatase 2 phosphatase a	0.77	1.29e-06	ZNF800	zinc finger protein 800
1.06	6.33e-07	REEP6	receptor accessory protein 6	0.99	2.00e-06	ERAP2	endoplasmic reticulum aminopeptida
1.19	1.05e-06	PPM1B	protein phosphatase, Mg2+/Mn2+ depe	0.96	2.76e-06	MME	membrane metalloendopeptidase
0.85	1.09e-06	PAXX	PAXX non-homologous end joining fac	0.66	3.42e-06	CGAS	cyclic GMP-AMP synthase
0.82	1.12e-06	ZNRD2	zinc ribbon domain containing 2	0.7	4.21e-06	LAMA3	laminin subunit alpha 3
1.18	1.27e-06	MSI2	musashi RNA binding protein 2	1.16	7.27e-06	IL18	interleukin 18
0.66	1.32e-06	PSPH	phosphoserine phosphatase	0.74	7.27e-06	HPSE	heparanase
-1	1.44e-06	AGL	amylo-alpha-1, 6-glucosidase, 4-alp	0.74	9.80e-06	PLEKHG3	pleckstrin homology and RhoGEF do
0.21	2.57e-06	GLC1	glucosidase, 1, 4-beta-glucosidase	0.77	1.22e-05	KRT2A	keratin 2A

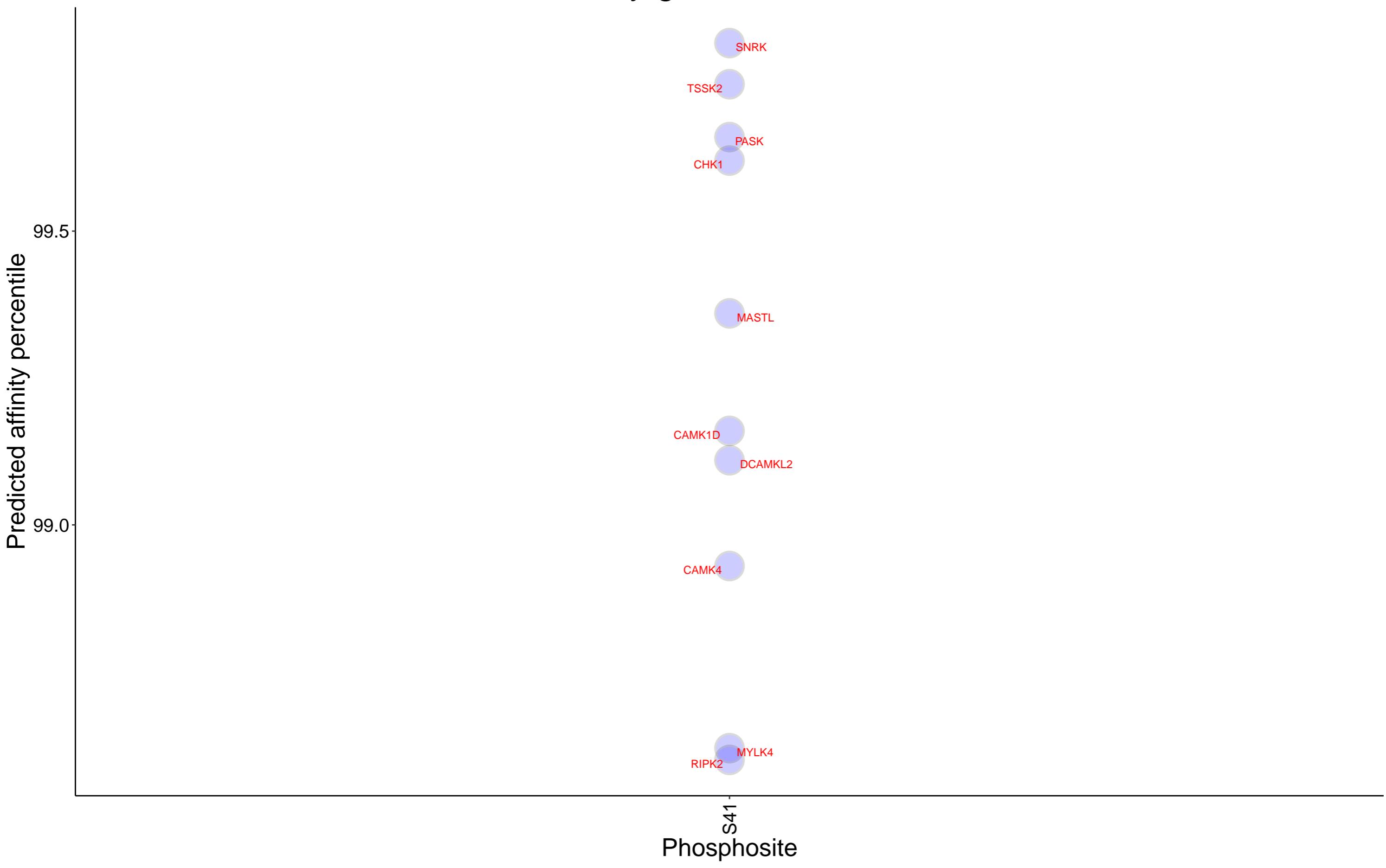
Insufficient number of paired observations in DB1 for ARMT1

Insufficient number of paired observations in DB1 for ARMT1

Top 10 kinases for each phosphosite in ARMT1



Kinases with affinity greater than 98.5% to ARMT1



No sufficient paired observations in DB1 for ARMT1