

ARPC1A

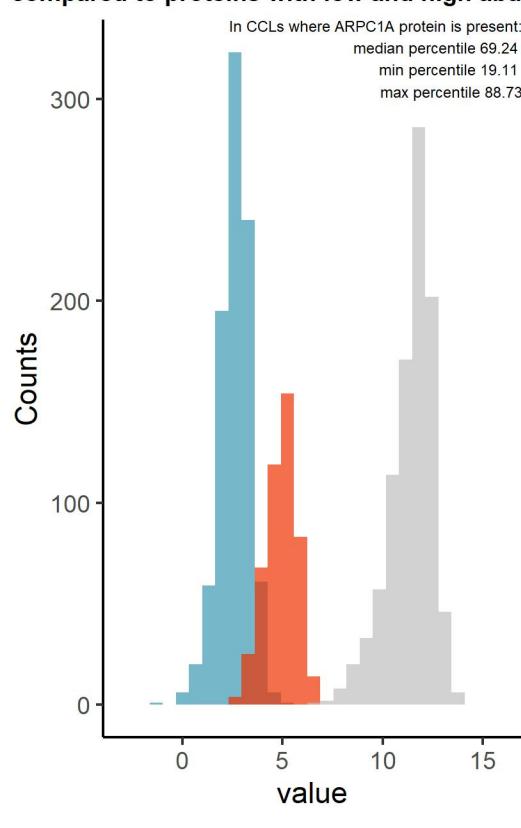
Protein name: ARC1A ; UNIPROT: Q92747 ; Gene name: actin related protein 2/3 complex subunit 1A

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

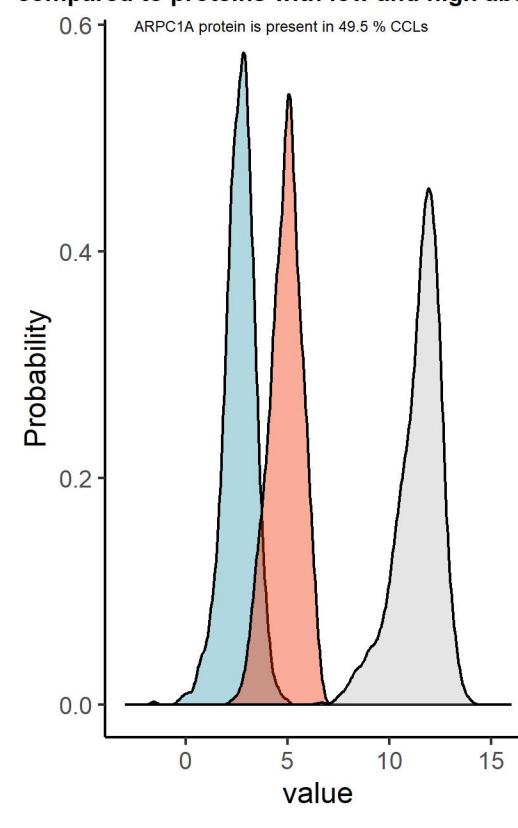
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

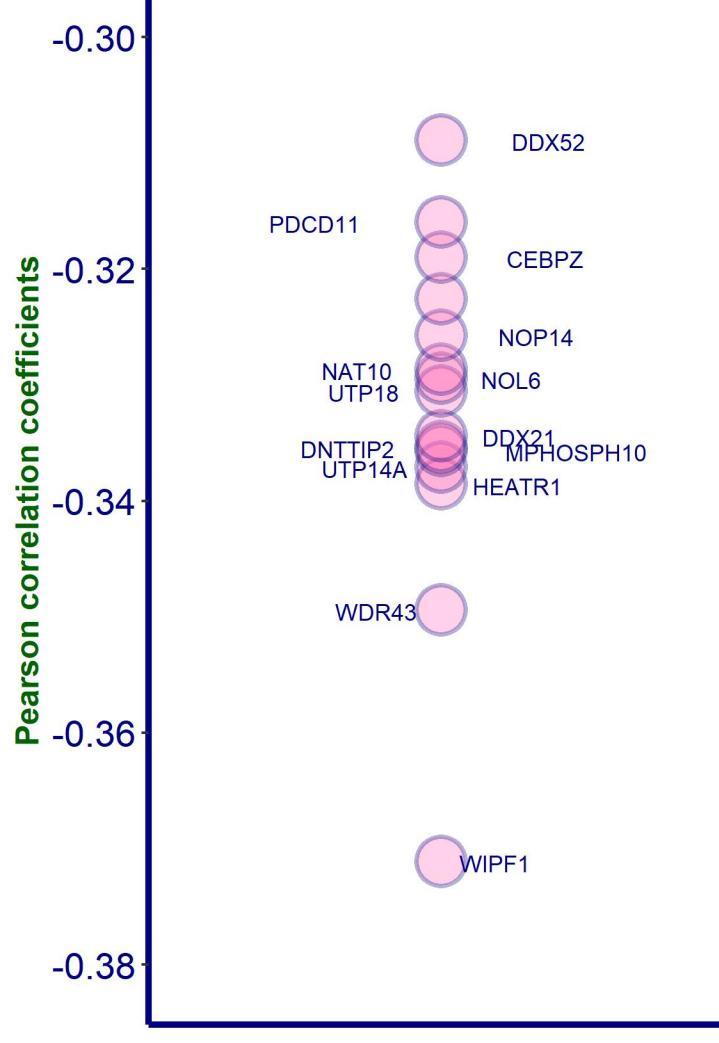
Histogram of ARPC1A protein compared to proteins with low and high abundance



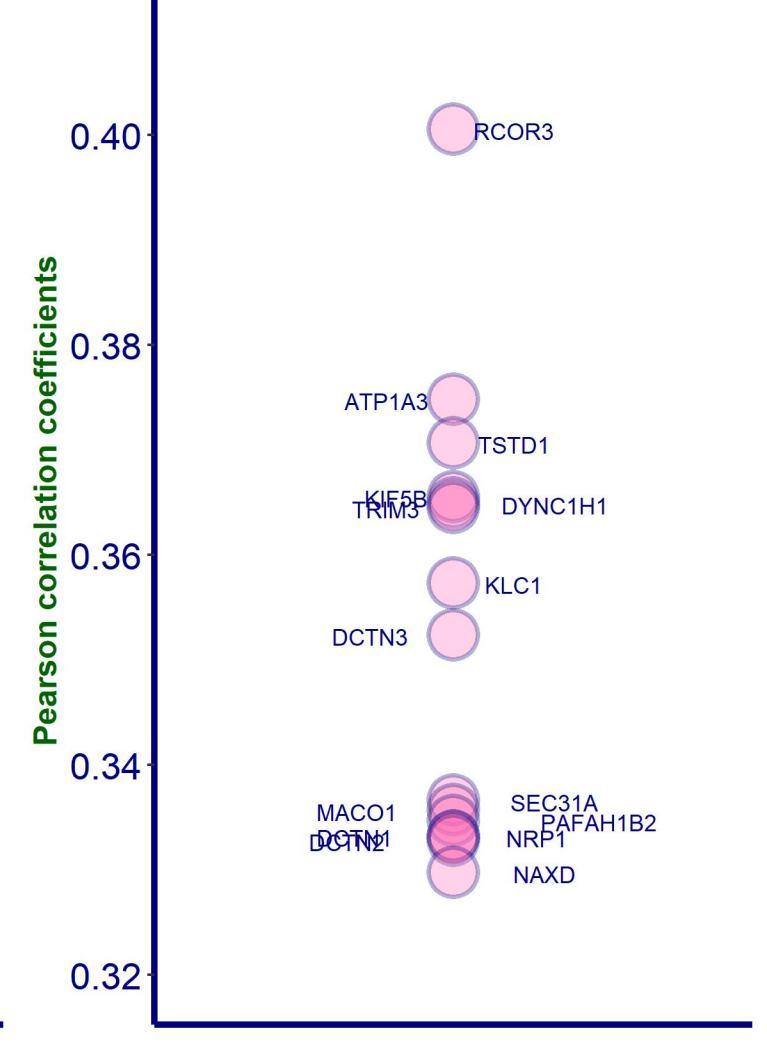
Density plot of ARPC1A protein compared to proteins with low and high abundance



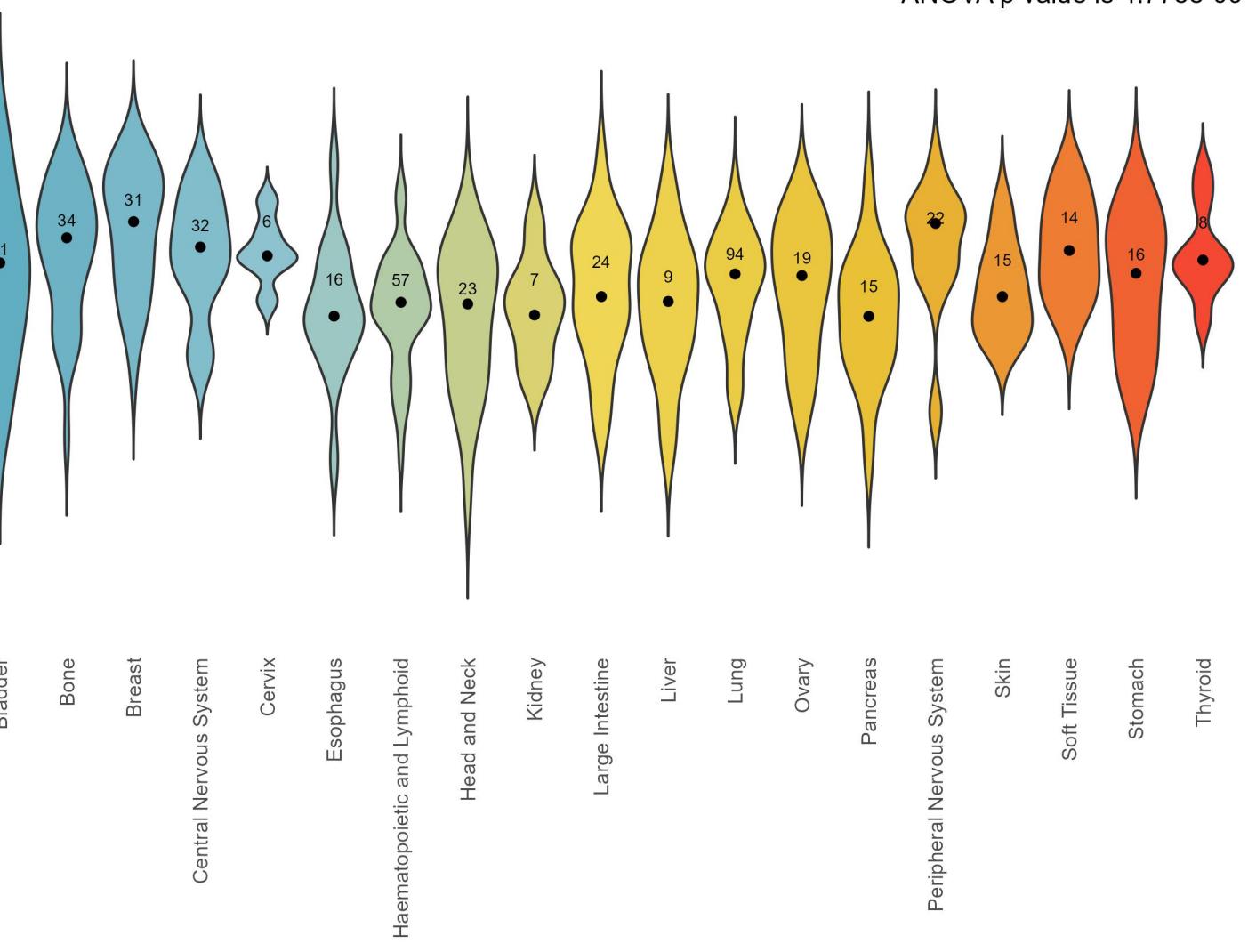
Top negative correlations of ARPC1A protein, DB1



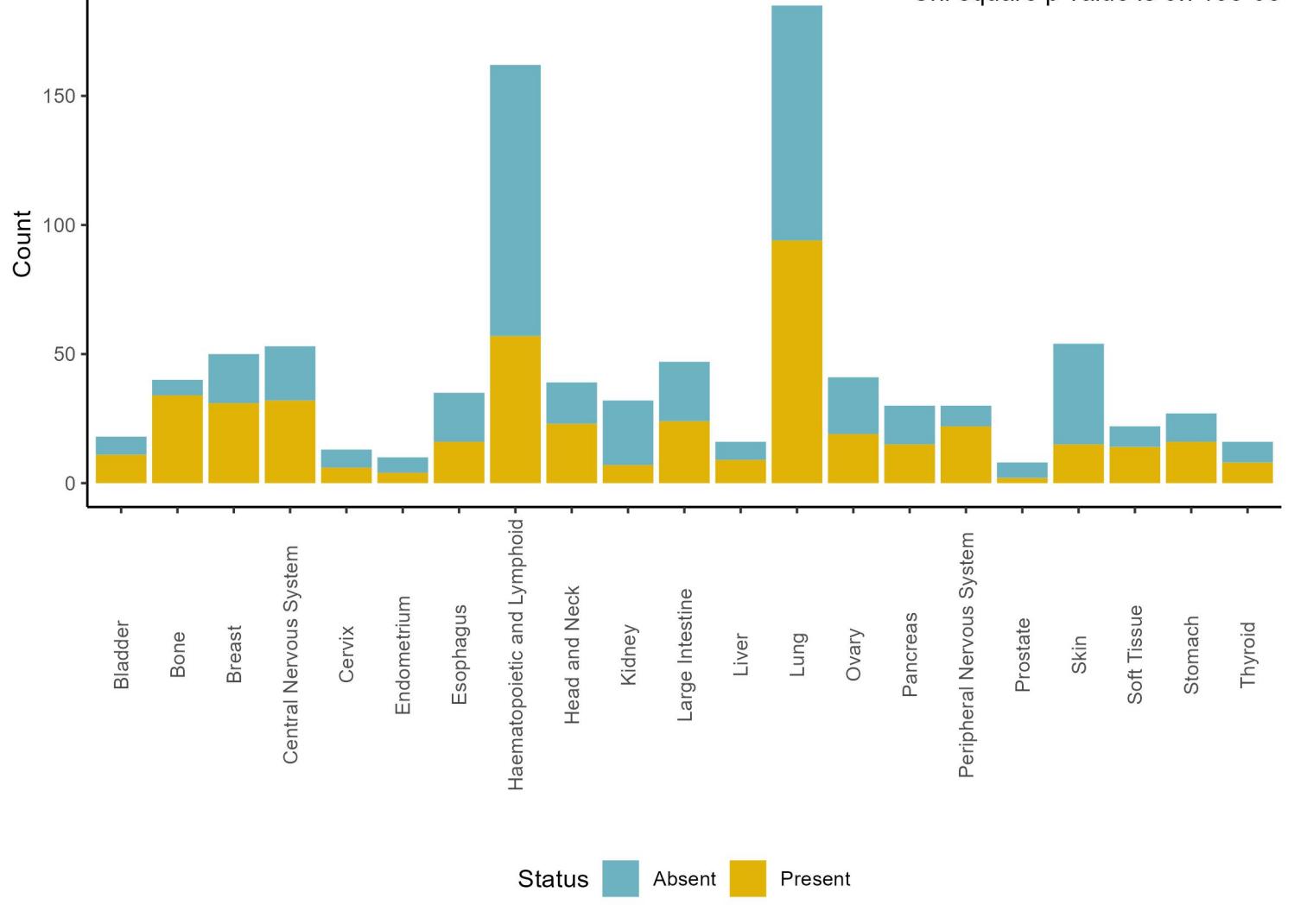
Top positive correlations of ARPC1A protein, DB1



Amount of ARPC1A protein, number of CCLs where it is present by tissue, DB1



Present and absent ARPC1A protein counts by tissue, DB1

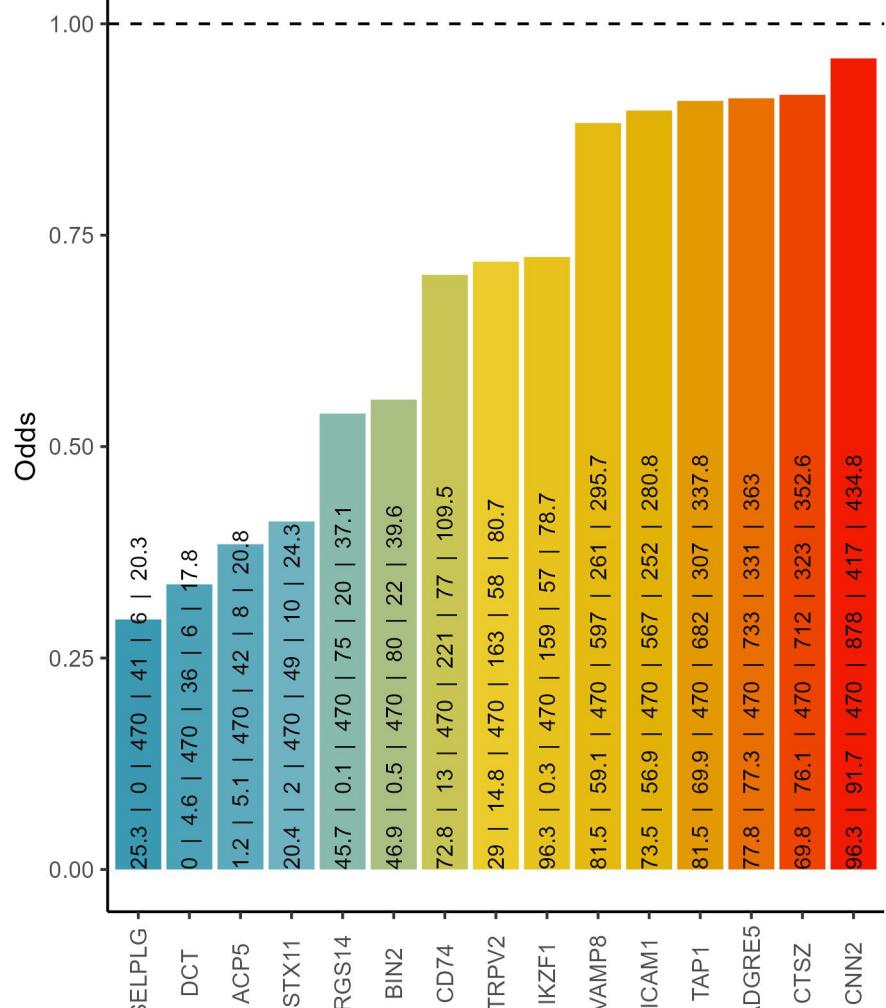


Cooccurrence with ARPC1A protein, DB1

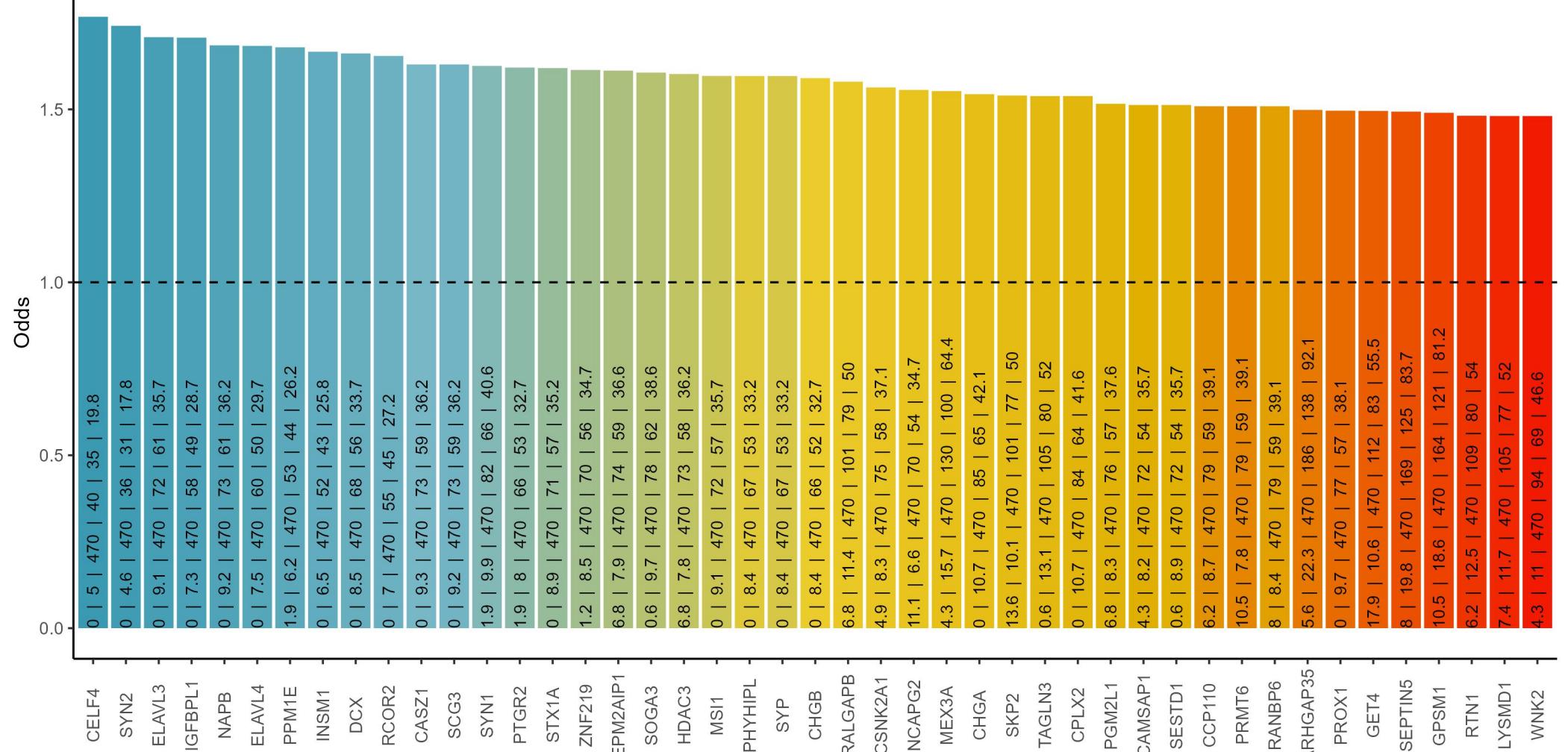
% of ARPC1A in blood cancers: 35.2 ; % of ARPC1A in solid cancers: 52.3

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ARPC1A | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

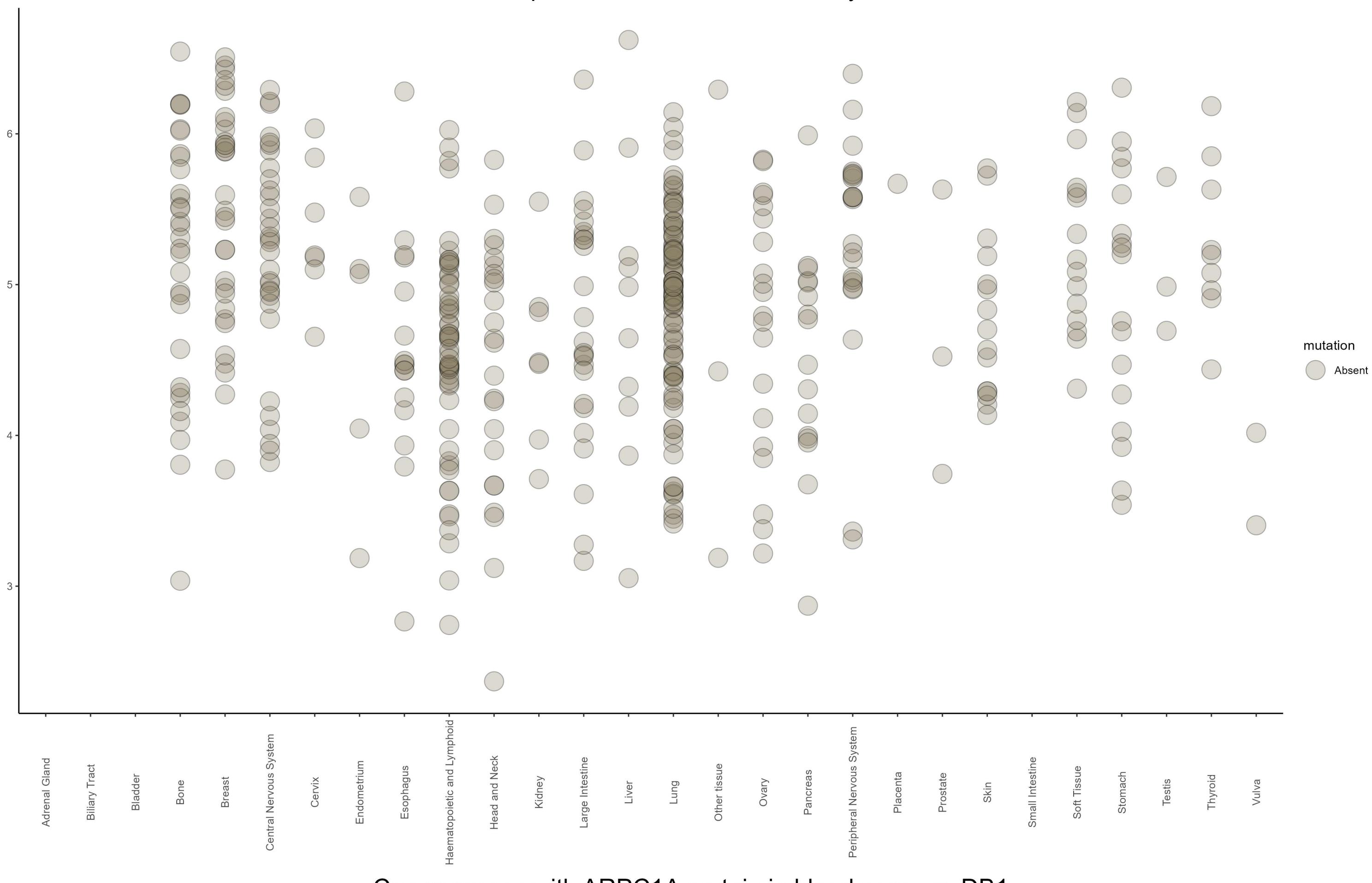
Negative cooccurrence



Positive cooccurrence

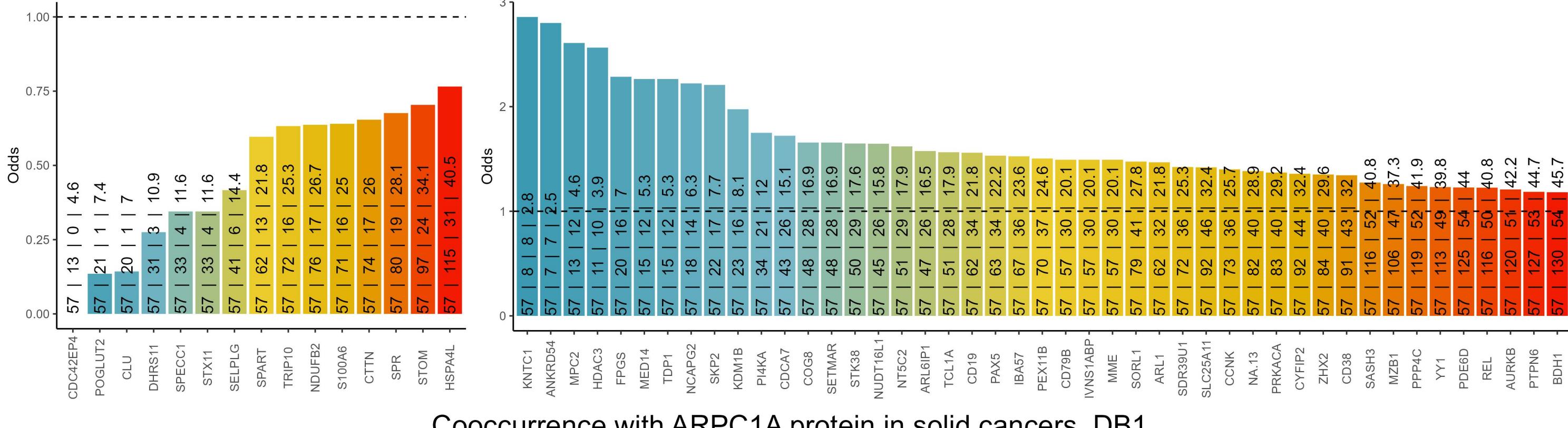


Amount of ARPC1A protein and mutation status by tissue, DB1



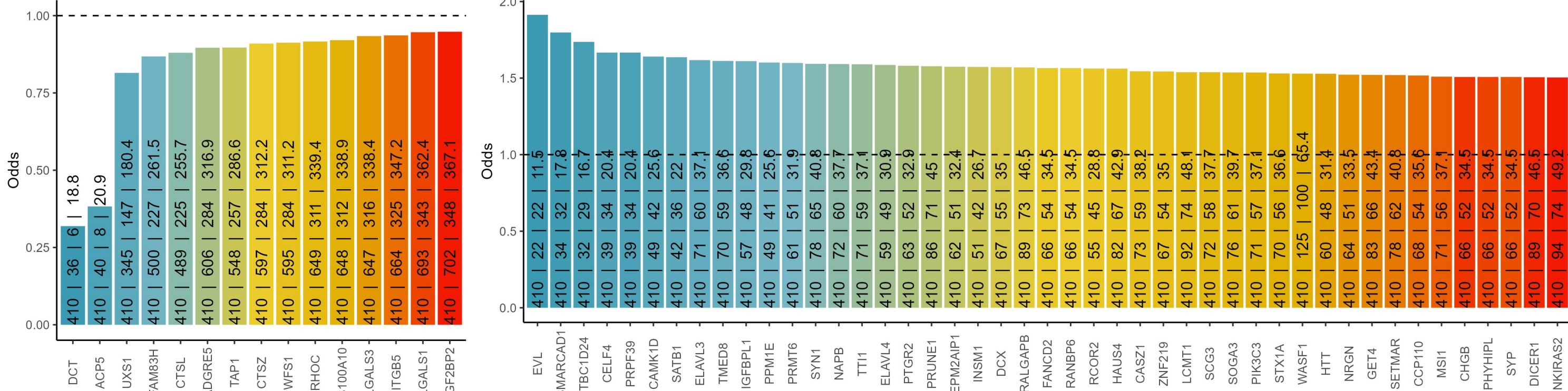
Cooccurrence with ARPC1A protein in blood cancers, DB1

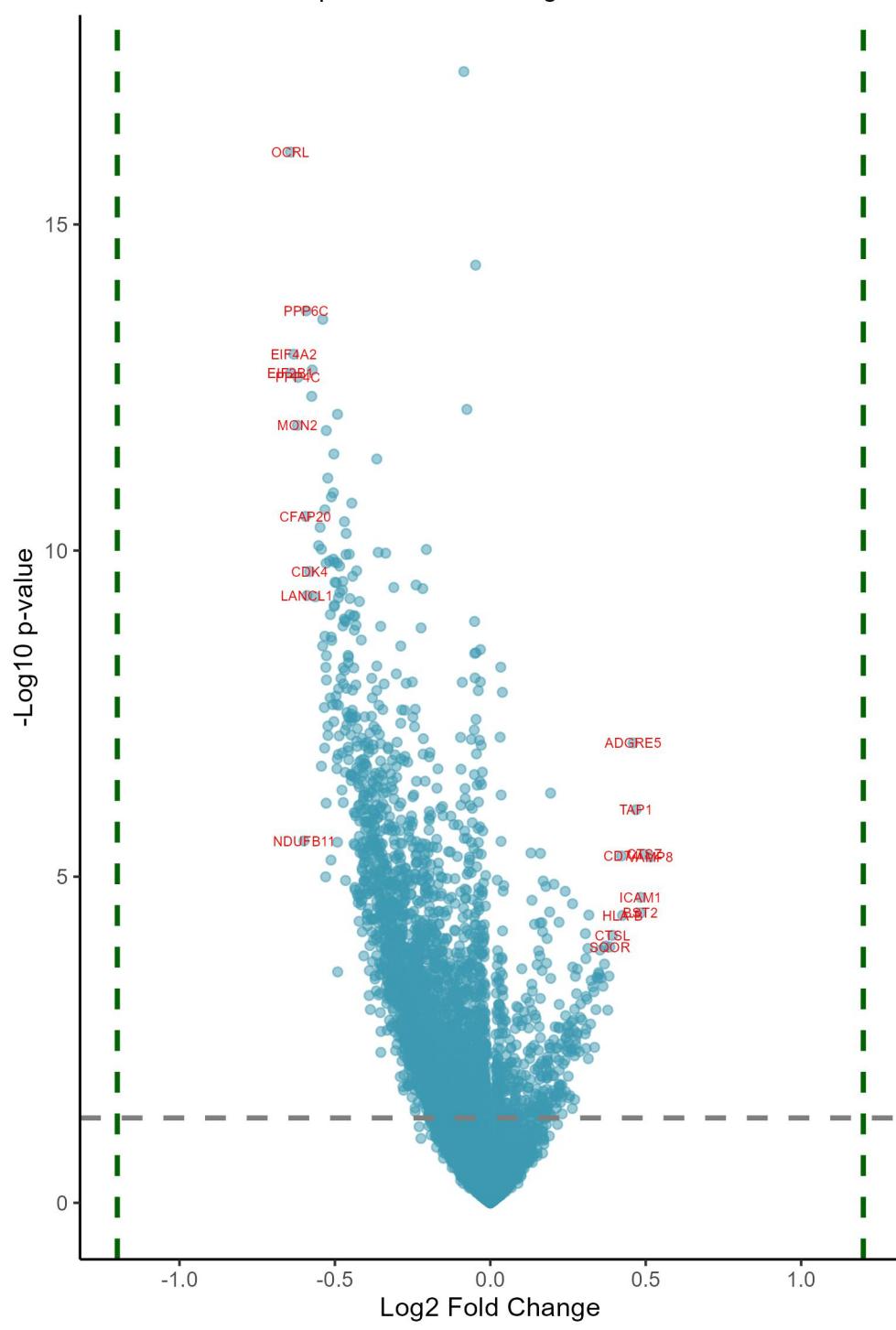
The text in the bars: incidence of ARPC1A | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Cooccurrence with ARPC1A protein in solid cancers, DB1

The text in the bars: incidence of ARPC1A | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

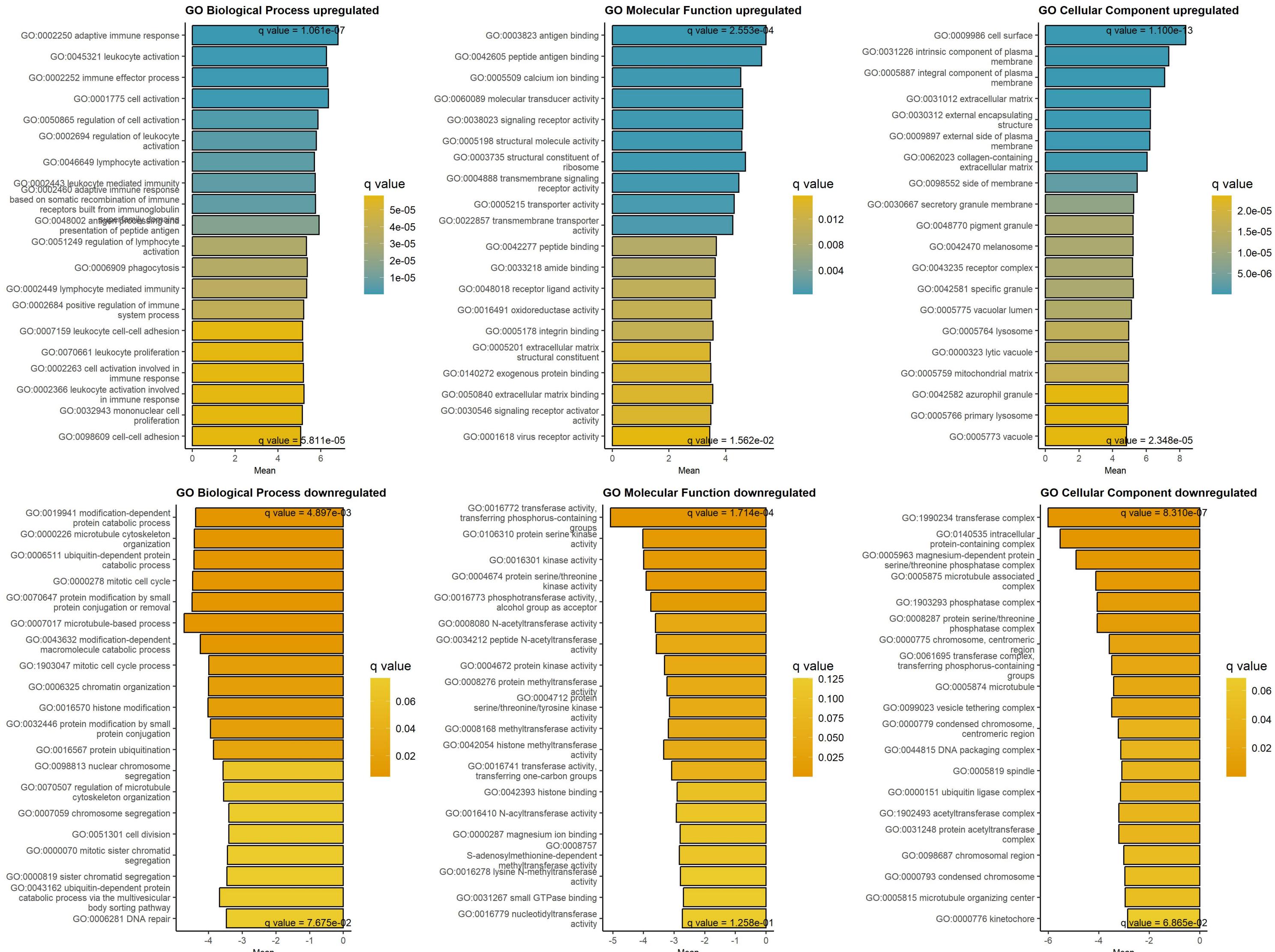




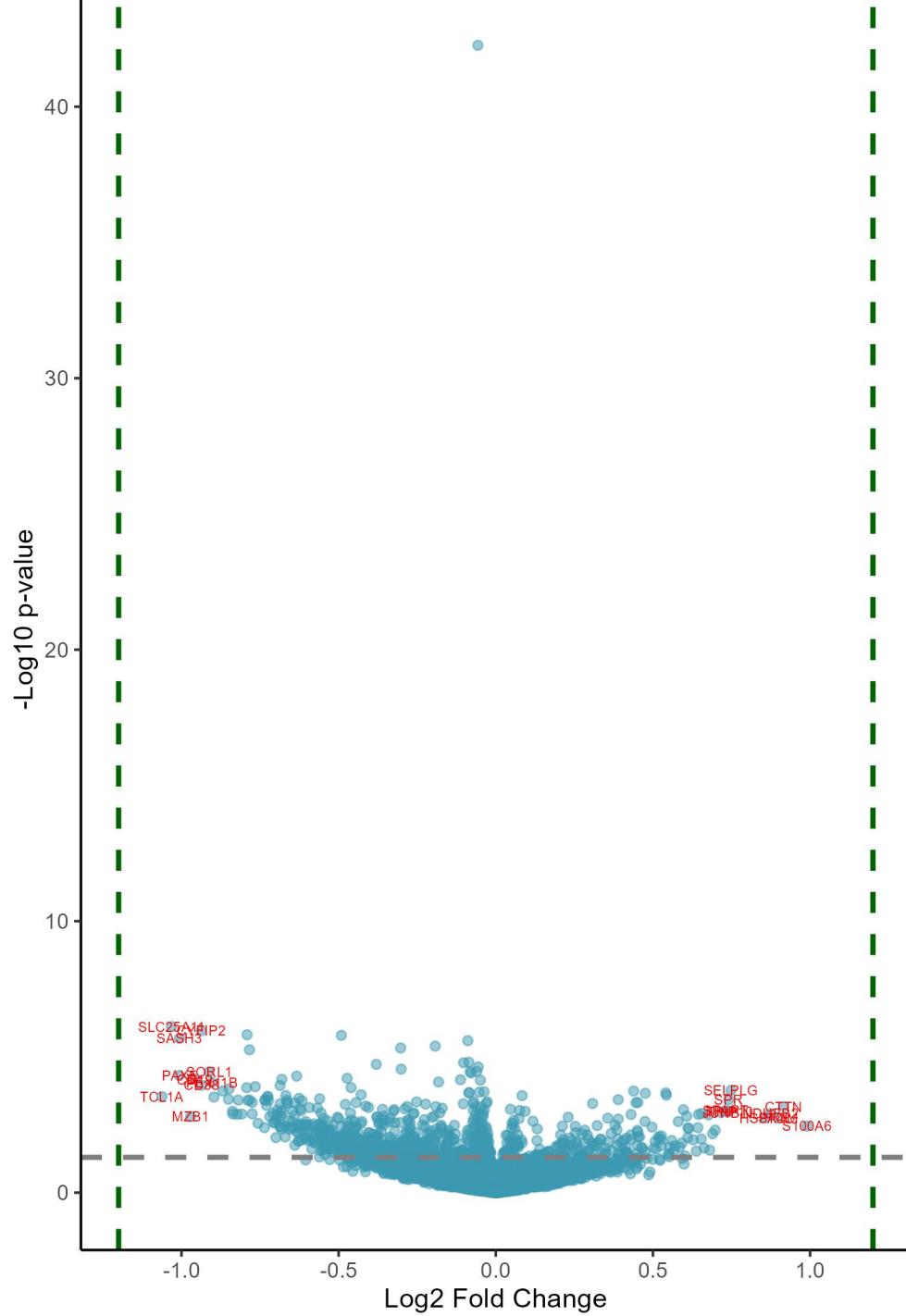
Downregulated at low/absent ARPC1A Upregulated at low/absent ARPC1A

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.64	1.72e-13	OCRL	OCRL inositol polyphosphate-5-phosphatase	0.52	8.18e-05	VAMP8	vesicle associated membrane protein
-0.64	1.40e-10	EIF2B1	eukaryotic translation initiation factor 2B subunit 1	0.5	7.58e-05	CTSZ	cathepsin Z
-0.63	9.27e-11	EIF4A2	eukaryotic translation initiation factor 4A2	0.48	2.42e-04	ICAM1	intercellular adhesion molecule 1
-0.62	5.71e-10	MON2	MON2 homolog, regulator of endosome	0.48	3.75e-04	BST2	bone marrow stromal cell antigen 2
-0.62	1.47e-10	PPP4C	protein phosphatase 4 catalytic subunit	0.47	2.26e-05	TAP1	transporter 1, ATP binding cassette
-0.6	5.42e-05	NDUFB11	NADH:ubiquinone oxidoreductase subunit 11	0.46	3.74e-06	ADGRE5	adhesion G protein-coupled receptor
-0.59	8.64e-09	CFAP20	cilia and flagella associated protein 20	0.43	4.01e-04	HLA-B	major histocompatibility complex, class I B
-0.59	2.80e-11	PPP6C	protein phosphatase 6 catalytic subunit	0.42	7.98e-05	CD74	CD74 molecule
-0.59	6.38e-08	LANCL1	LanC like 1	0.39	7.05e-04	CTSL	cathepsin L
-0.58	3.39e-08	CDK4	cyclin dependent kinase 4	0.38	9.72e-04	SQOR	sulfide quinone oxidoreductase
-0.57	2.61e-10	DYNLL1	dynein light chain LC8-type 1	0.38	2.14e-03	FKBP11	FKBP prolyl isomerase 11
-0.57	1.40e-10	NAA25	N-alpha-acetyltransferase 25, NatB	0.38	5.46e-03	RAC2	Rac family small GTPase 2
-0.56	6.54e-08	BRD3	bromodomain containing 3	0.37	9.49e-04	CELF2	CUGBP Elav-like family member 2
-0.55	2.07e-08	EIF2B5	eukaryotic translation initiation factor 2B subunit 5	0.37	1.55e-03	CD70	CD70 molecule
-0.55	1.17e-08	PRKACA	protein kinase cAMP-activated catalytic subunit	0.36	2.82e-03	RHOC	ras homolog family member C
-0.54	7.00e-06	PFN2	profilin 2	0.36	2.26e-03	LGALS1	galectin 1
-0.54	2.21e-08	TLE5	TLE family member 5, transcriptional regulator	0.35	1.06e-03	ITGB5	integrin subunit beta 5
-0.54	2.54e-07	ABI2	abl interactor 2	0.35	2.04e-03	PSMB9	proteasome 20S subunit beta 9
-0.54	3.16e-11	PPP2R5E	protein phosphatase 2 regulatory subunit B	0.35	1.95e-03	PSMB10	proteasome 20S subunit beta 10
-0.53	1.48e-06	DDAH1	dimethylarginine dimethylaminohydrolase	0.35	2.28e-03	UXS1	UDP-glucuronate decarboxylase 1
-0.53	4.28e-06	ARL6IP1	ADP ribosylation factor like GTPase	0.34	2.22e-03	SH3KBP1	SH3 domain containing kinase bindin
-0.53	1.93e-07	AK1	adenylate kinase 1	0.34	5.38e-03	STOM	stomatin
-0.53	7.17e-09	CUL5	cullin 5	0.34	1.55e-02	LGALS3	galectin 3
-0.53	1.43e-04	CKB	creatine kinase B	0.33	3.27e-03	SP100	SP100 nuclear antigen
-0.53	4.76e-07	PRPSAP2	phosphoribosyl pyrophosphate synthetase	0.33	2.87e-03	MELTF	melanotransferrin
-0.53	2.74e-08	NHLRC2	NHL repeat containing 2	0.32	2.41e-03	FMNL1	formin like 1
-0.53	1.91e-05	BLMH	bleomycin hydrolase	0.32	8.11e-03	TAP2	transporter 2, ATP binding cassette
-0.53	6.41e-10	EXOC6B	exocyst complex component 6B	0.32	3.97e-04	TAPBP	TAP binding protein
-0.53	3.35e-07	NT5DC2	5'-nucleotidase domain containing 2	0.32	2.11e-02	CD44	CD44 molecule (Indian blood group)

GAGE analysis on upregulated and downregulated proteins at low/absent ARPC1A protein, DB1

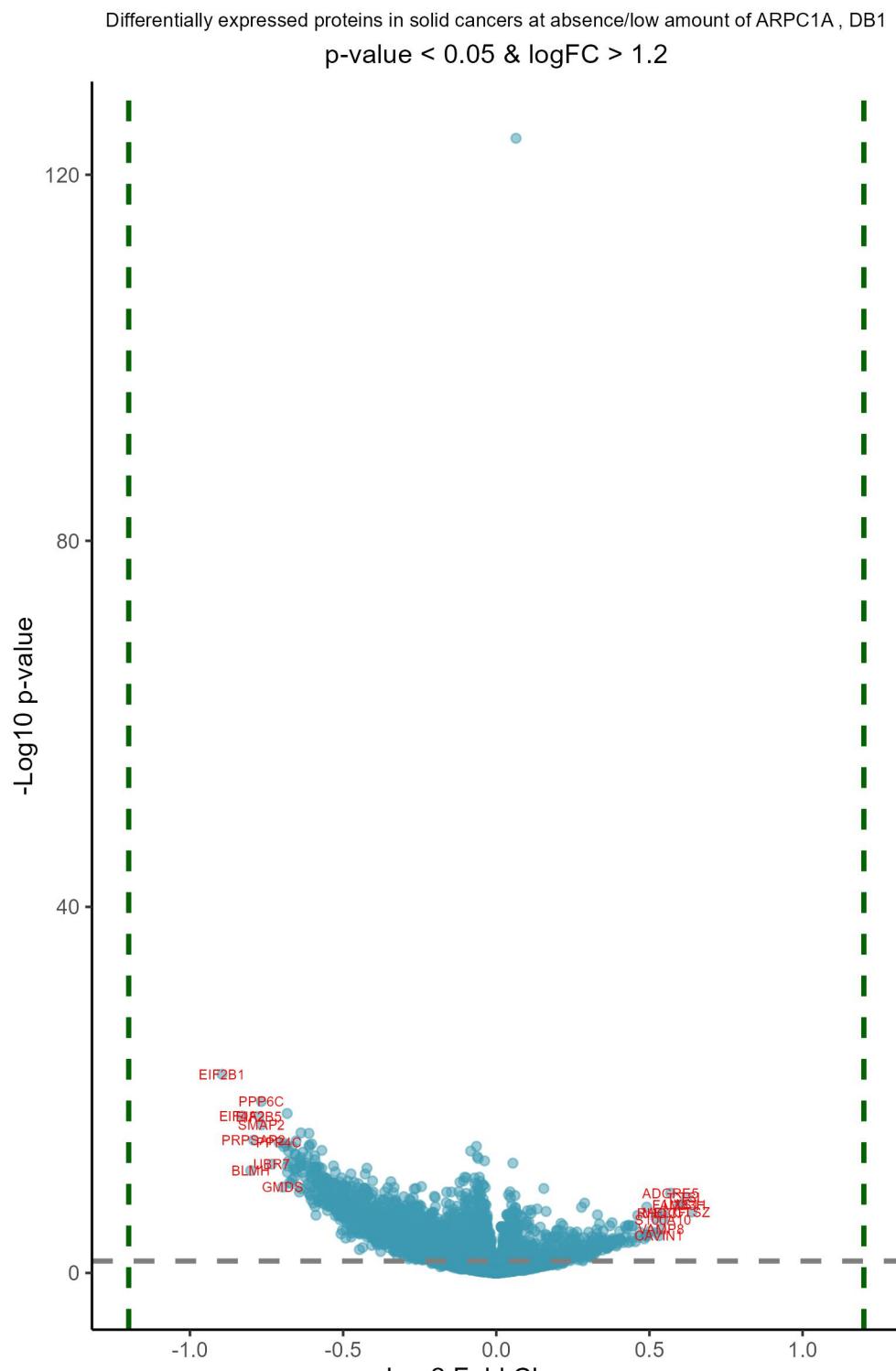


p-value < 0.05 & logFC > 1.2



Downregulated in blood cancers at low/absent ARPC1A Upregulated in blood cancers at low/absent ARPC1A

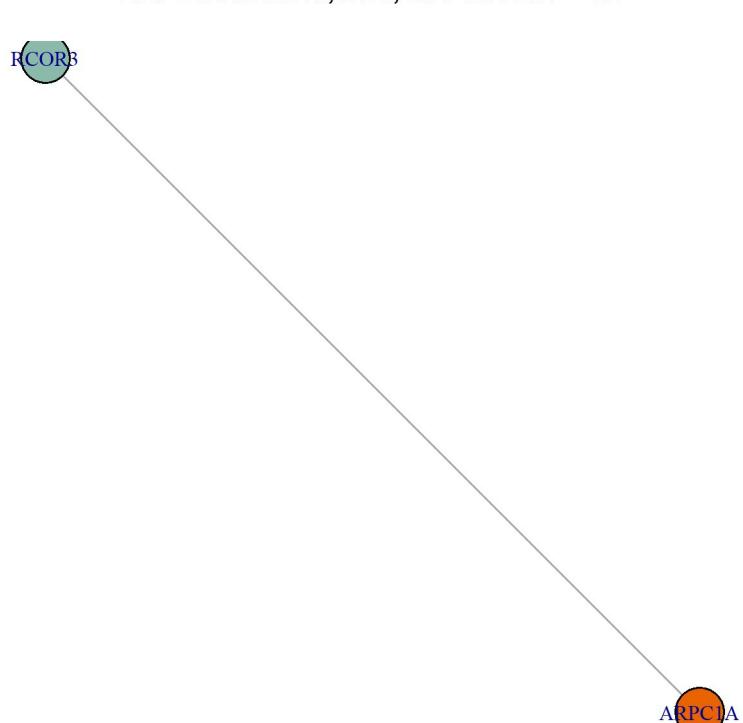
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.06	3.83e-02	TCL1A	TCL1 family AKT coactivator A	0.99	1.11e-01	S100A6	S100 calcium binding protein A6
-1.03	1.70e-03	SLC25A11	solute carrier family 25 member 11	0.92	5.22e-02	CTTN	cortactin
-1.01	1.96e-03	SASH3	SAM and SH3 domain containing 3	0.9	8.03e-02	STOM	stomatin
-1.01	1.53e-02	PAX5	paired box 5	0.87	6.67e-02	NDUFB2	NADH:ubiquinone oxidoreductase subu
-0.97	7.46e-02	MZB1	marginal zone B and B1 cell specifi	0.86	8.00e-02	HSPA4L	heat shock protein family A (Hsp70)
-0.96	1.78e-02	CD19	CD19 molecule	0.75	3.15e-02	SEPL1G	selectin P ligand
-0.94	1.78e-03	CYFIP2	cytoplasmic FMR1 interacting protei	0.74	6.09e-02	TRIP10	thyroid hormone receptor interactor
-0.94	2.41e-02	CD38	CD38 molecule	0.74	4.17e-02	SPR	sepiapterin reductase
-0.91	1.25e-02	SORL1	sortilin related receptor 1	0.73	6.04e-02	SPART	spartin
-0.9	2.01e-02	PEX11B	peroxisomal biogenesis factor 11 be	0.72	6.57e-02	JUNB	JunB proto-oncogene, AP-1 transcrip
-0.9	3.87e-02	SEPTIN1	septin 1	0.7	1.29e-01	IRF2BPL	interferon regulatory factor 2 bind
-0.87	3.17e-02	ZHX2	zinc fingers and homeoboxes 2	0.69	1.55e-01	CA2	carbonic anhydrase 2
-0.85	4.17e-02	IRAG2	inositol 1,4,5-triphosphate recepto	0.68	2.66e-01	ANXA1	annexin A1
-0.85	2.84e-02	STK38	serine/threonine kinase 38	0.68	6.89e-02	FHOD1	formin homology 2 domain containing
-0.84	6.09e-02	CD79B	CD79b molecule	0.66	2.51e-01	IGF2BP2	insulin like growth factor 2 mRNA b
-0.84	6.67e-02	MME	membrane metalloendopeptidase	0.65	6.67e-02	DUSP3	dual specificity phosphatase 3
-0.82	6.72e-02	CD22	CD22 molecule	0.65	1.85e-01	CAPN2	calpain 2
-0.82	4.17e-02	TCF3	transcription factor 3	0.64	6.72e-02	EML3	EMAP like 3
-0.81	6.70e-02	TMEM123	transmembrane protein 123	0.64	1.16e-01	TYMP	thymidine phosphorylase
-0.79	2.66e-02	NCKAP1L	NCK associated protein 1 like	0.64	2.77e-01	LGALS3	galectin 3
-0.79	1.78e-03	PDE6D	phosphodiesterase 6D	0.63	1.87e-01	PLBD2	phospholipase B domain containing 2
-0.79	4.17e-02	SUDS3	SDS3 homolog, SIN3A corepressor com	0.61	1.22e-01	TNFRSF8	TNF receptor superfamily member 8
-0.78	3.29e-03	PPP4C	protein phosphatase 4 catalytic sub	0.61	1.17e-01	NEU1	neuraminidase 1
-0.78	4.17e-02	COG8	component of oligomeric golgi compl	0.61	1.76e-01	ACY1	aminoacylase 1
-0.78	6.67e-02	ARL6IP1	ADP ribosylation factor like GTPase	0.61	7.33e-02	SLC30A1	solute carrier family 30 member 1
-0.77	4.42e-02	ARL1	ADP ribosylation factor like GTPase	0.6	3.22e-01	FLNC	filamin C
-0.77	2.58e-02	EED	embryonic ectoderm development	0.6	4.36e-01	LMNA	lamin A/C
-0.76	9.85e-02	AKAP12	A-kinase anchoring protein 12	0.6	5.87e-02	CMBL	carboxymethylenebutenolidase homolo
-0.74	1.16e-01	IGLL1	immunoglobulin lambda like polypept	0.59	3.59e-01	CD70	CD70 molecule



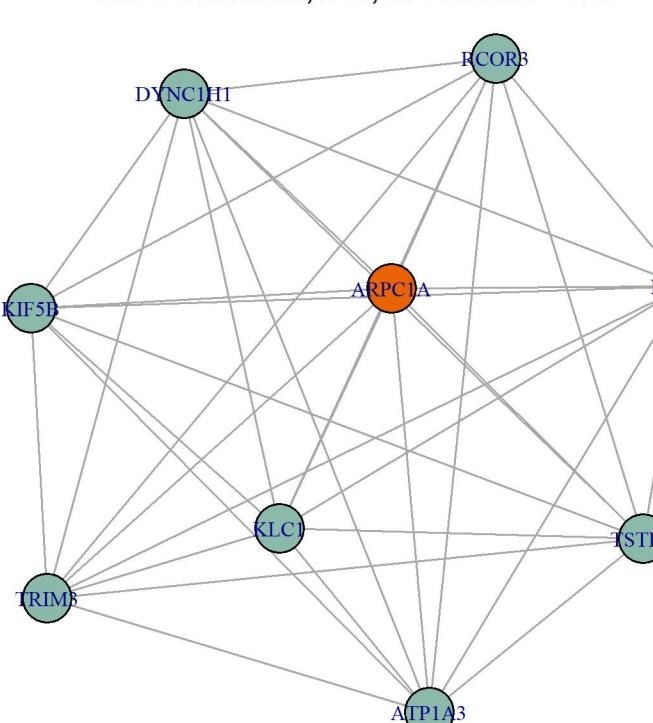
Downregulated in solid cancers at low/absent ARPC1A Upregulated in solid cancers at low/absent ARPC1A

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.9	4.31e-19	EIF2B1	eukaryotic translation initiation f	0.64	3.13e-06	CTS2	cathepsin Z
-0.83	7.73e-15	EIF4A2	eukaryotic translation initiation f	0.62	1.66e-07	CTS1	cathepsin L
-0.8	7.22e-10	BLMH	bleomycin hydrolase	0.6	7.04e-07	UXS1	UDP-glucuronate decarboxylase 1
-0.79	1.89e-12	PRPSAP2	phosphoribosyl pyrophosphate synthe	0.6	8.03e-07	FAM83H	family with sequence similarity 83
-0.78	7.77e-15	EIF2B5	eukaryotic translation initiation f	0.57	6.80e-08	ADGRE5	adhesion G protein-coupled receptor
-0.77	2.97e-16	PPP6C	protein phosphatase 6 catalytic sub	0.55	3.60e-06	MELTF	melanotransferrin
-0.77	5.28e-14	SMAP2	small ArfGAP2	0.54	1.50e-05	S100A10	S100 calcium binding protein A10
-0.73	2.03e-10	UBR7	ubiquitin protein ligase E3 compone	0.54	1.05e-04	VAMP8	vesicle associated membrane protein
-0.71	2.85e-12	PPP4C	protein phosphatase 4 catalytic sub	0.53	4.30e-04	CAVIN1	caveolae associated protein 1
-0.7	2.04e-08	GMDS	GDP-mannose 4,6-dehydratase	0.53	4.07e-06	RHOC	ras homolog family member C
-0.69	5.09e-12	FNTA	farnesyltransferase, CAAX box, alph	0.52	2.14e-04	ICAM1	intercellular adhesion molecule 1
-0.69	3.09e-12	MAPK14	mitogen-activated protein kinase 14	0.52	1.08e-05	TAP1	transporter 1, ATP binding cassette
-0.69	4.57e-12	TLE5	TLE family member 5, transcriptiona	0.5	1.56e-04	LGALS3	galectin 3
-0.68	3.05e-10	PDXP	pyridoxal phosphatase	0.49	3.62e-04	ITGB4	integrin subunit beta 4
-0.68	4.97e-15	CNOT9	CCR4-NOT transcription complex subu	0.49	1.15e-06	WFS1	wolframin ER transmembrane glycopro
-0.68	1.03e-09	CDK4	cyclin dependent kinase 4	0.49	5.29e-04	CAVIN3	caveolae associated protein 3
-0.68	1.16e-10	RNF214	ring finger protein 214	0.49	3.47e-04	PROCR	protein C receptor
-0.68	1.33e-11	ELP1	elongator acetyltransferase complex	0.48	8.39e-04	CD44	CD44 molecule (Indian blood group)
-0.67	8.38e-09	LANCL1	LanC like 1	0.47	1.93e-04	LGALS1	galectin 1
-0.67	1.47e-10	DYNLT1	dynein light chain Tctex-type 1	0.47	5.65e-04	NTSE	5'-nucleotidase ecto
-0.67	1.12e-08	MAD2L1	mitotic arrest deficient 2 like 1	0.46	6.34e-06	ADAM17	ADAM metallopeptidase domain 17
-0.67	5.09e-12	XPO7	exportin 7	0.45	1.57e-03	BST2	bone marrow stromal cell antigen 2
-0.67	5.03e-09	HMGCS1	3-hydroxy-3-methylglutaryl-CoA synt	0.45	5.26e-05	ANXA1	annexin A1
-0.66	5.43e-10	GTPBP1	GTP binding protein 1	0.44	6.45e-04	ITGA3	integrin subunit alpha 3
-0.66	3.22e-09	GSK3B	glycogen synthase kinase 3 beta	0.44	6.05e-05	ITGB5	integrin subunit beta 5
-0.66	2.46e-11	PPP2R2A	protein phosphatase 2 regulatory su	0.44	1.38e-03	MISP	mitotic spindle positioning
-0.66	5.73e-10	MON2	MON2 homolog, regulator of endosome	0.43	5.36e-05	NCEH1	neutral cholesterol ester hydrolase
-0.65	2.92e-11	USP15	ubiquitin specific peptidase 15	0.43	1.86e-03	ANXA3	annexin A3
-0.65	4.75e-10	PSMG1	proteasome assembly chaperone 1	0.43	4.90e-05	HKDC1	hexokinase domain containing 1

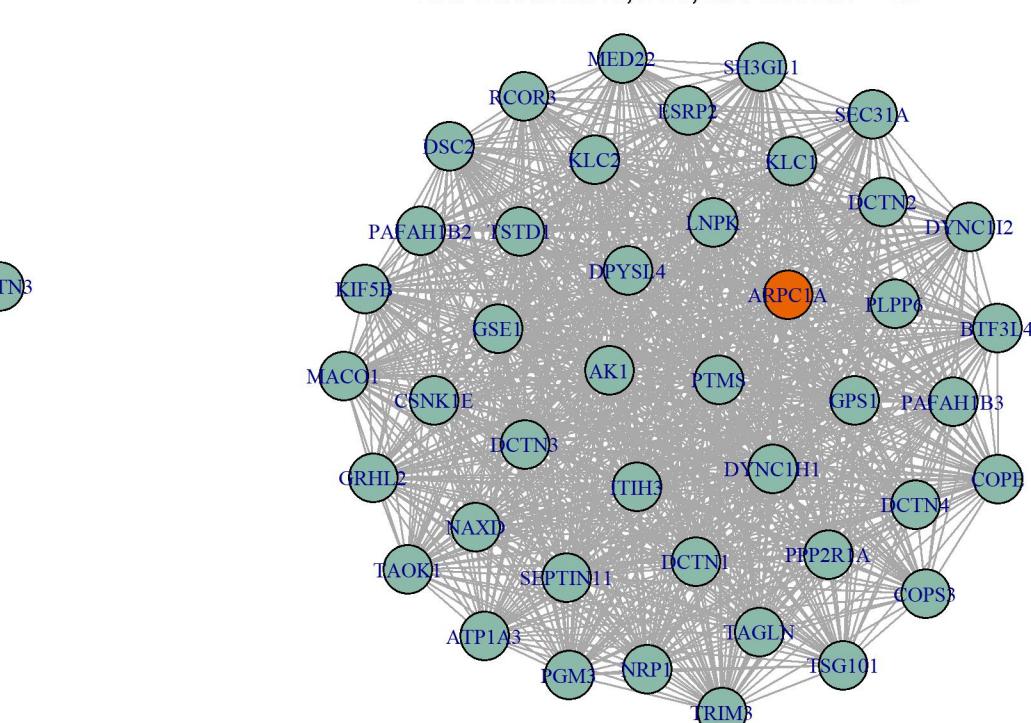
ARPC1A network, DB1, all Pearson r > 0.4

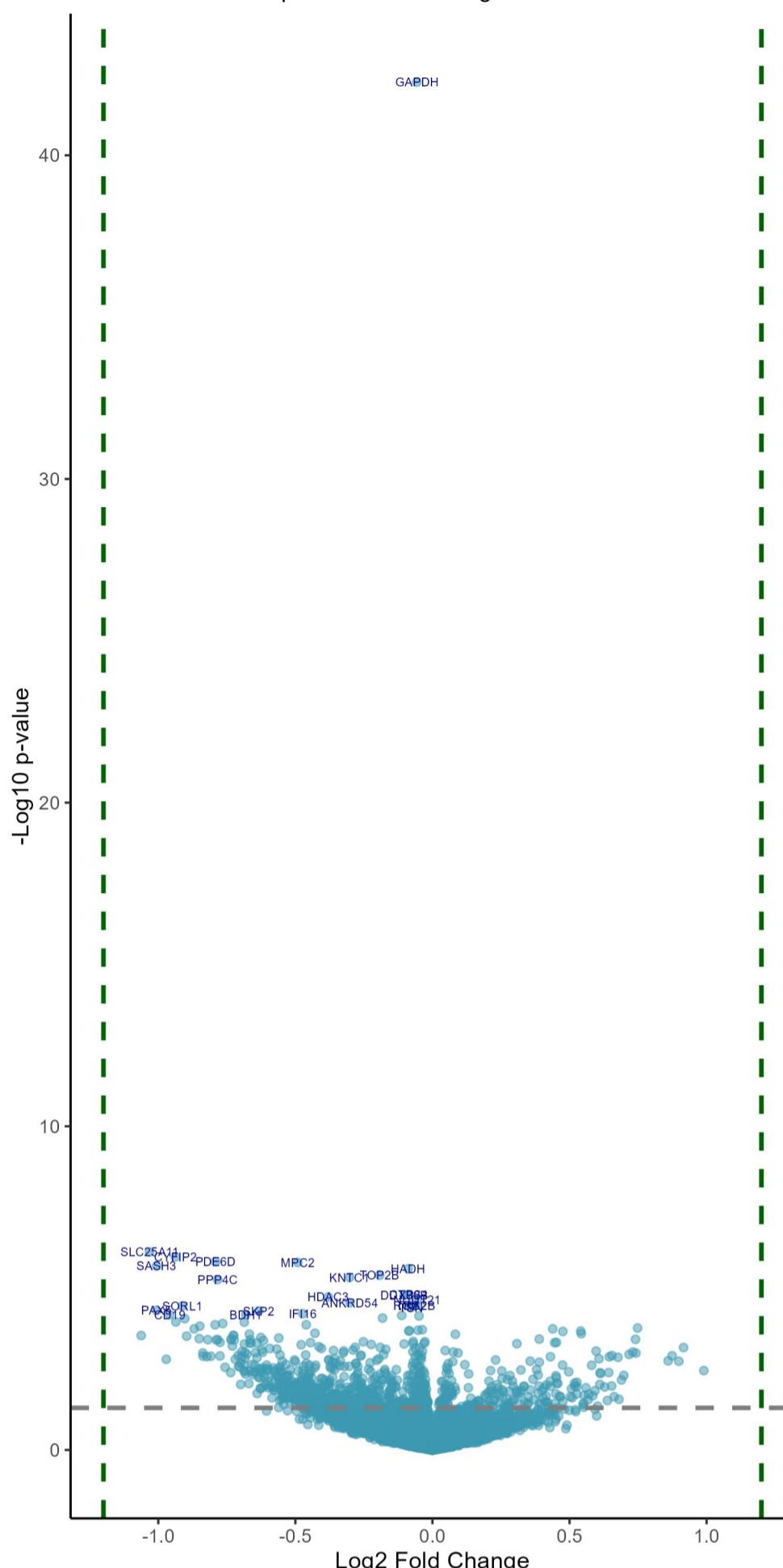


ARPC1A network, DB1, all Pearson r > 0.35

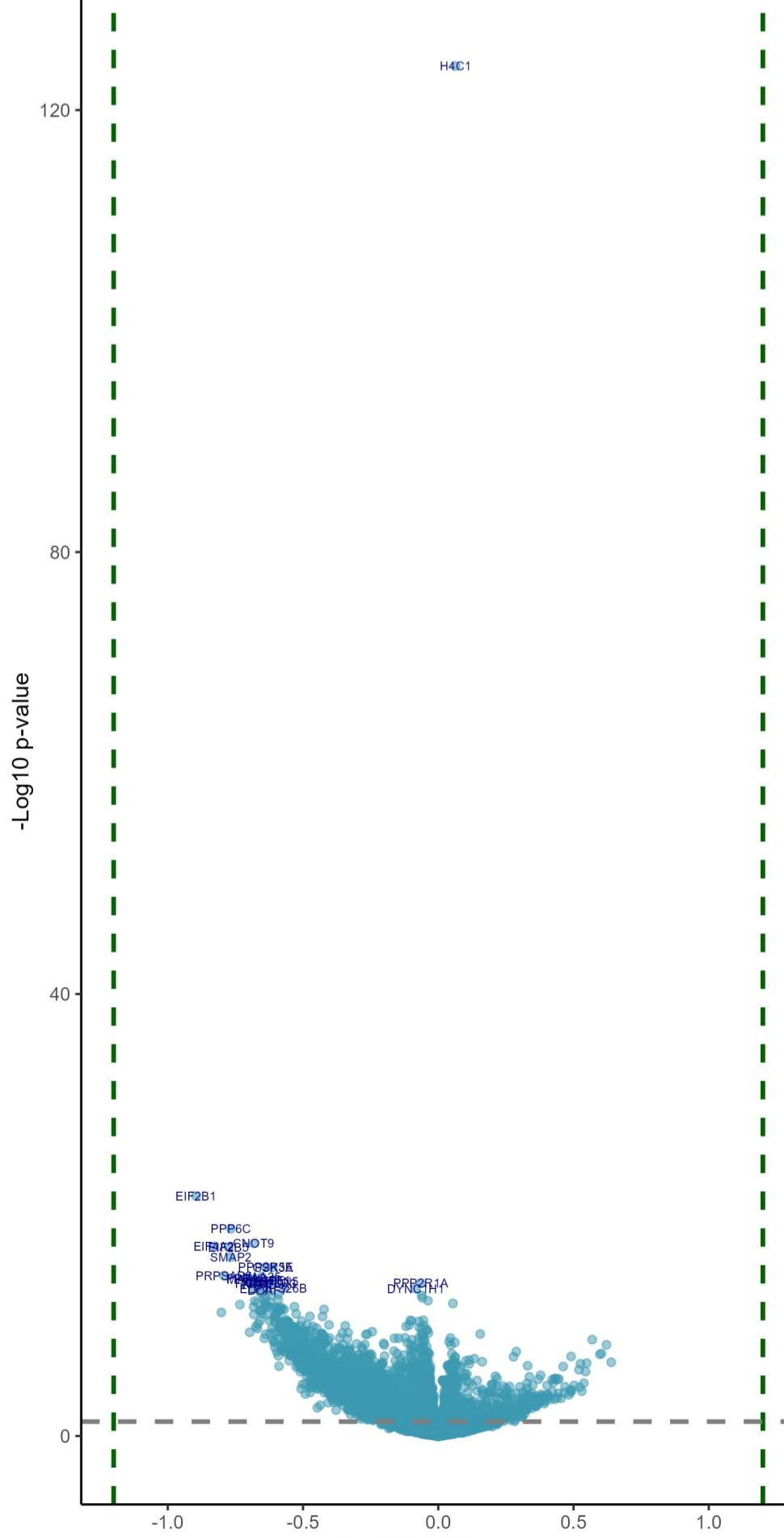


ARPC1A network, DB1, all Pearson r > 0.3

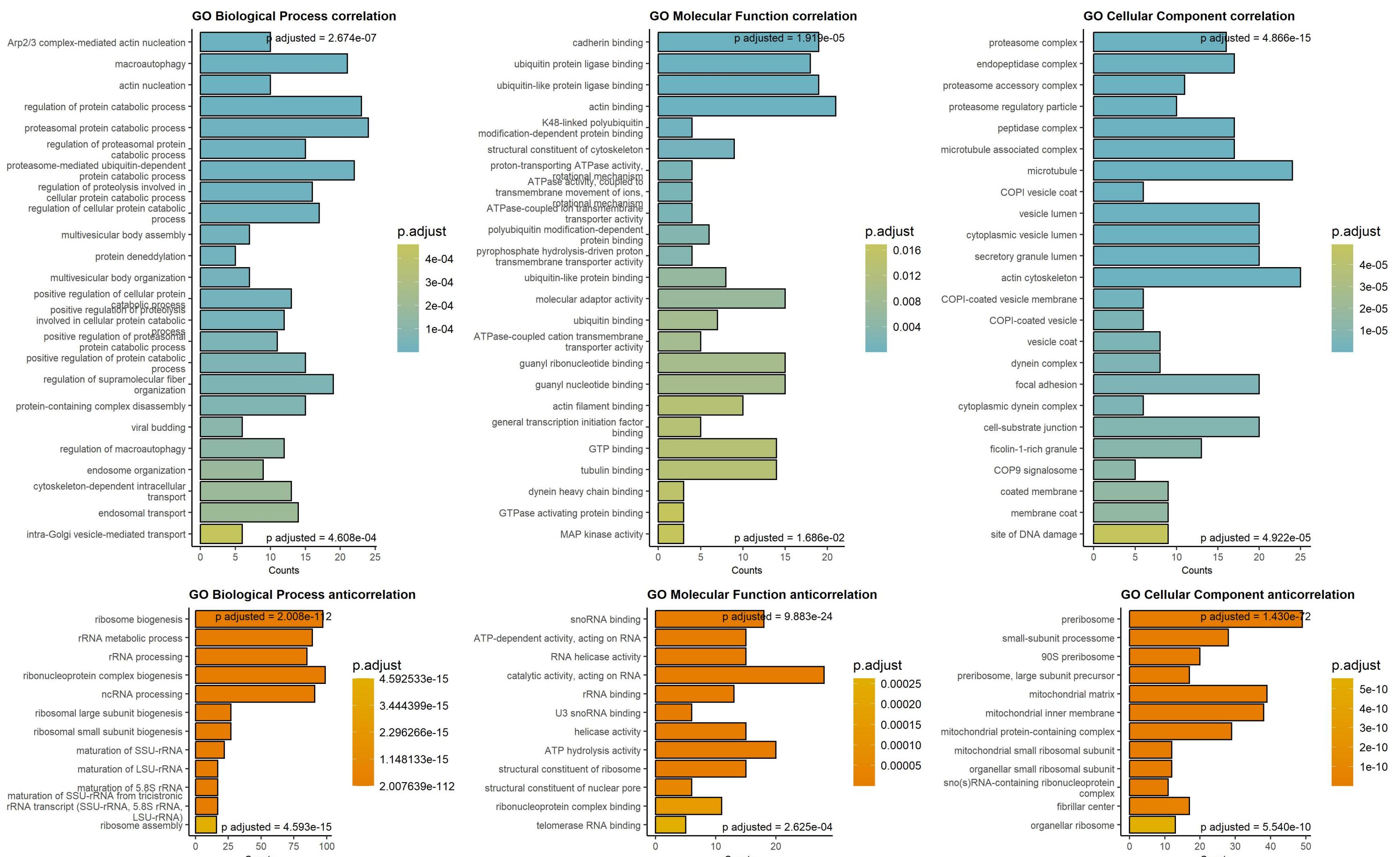


Sorted by p values!
Downregulated in blood cancers at low/absent ARPC1A Upregulated in blood cancers at low/absent ARPC1A

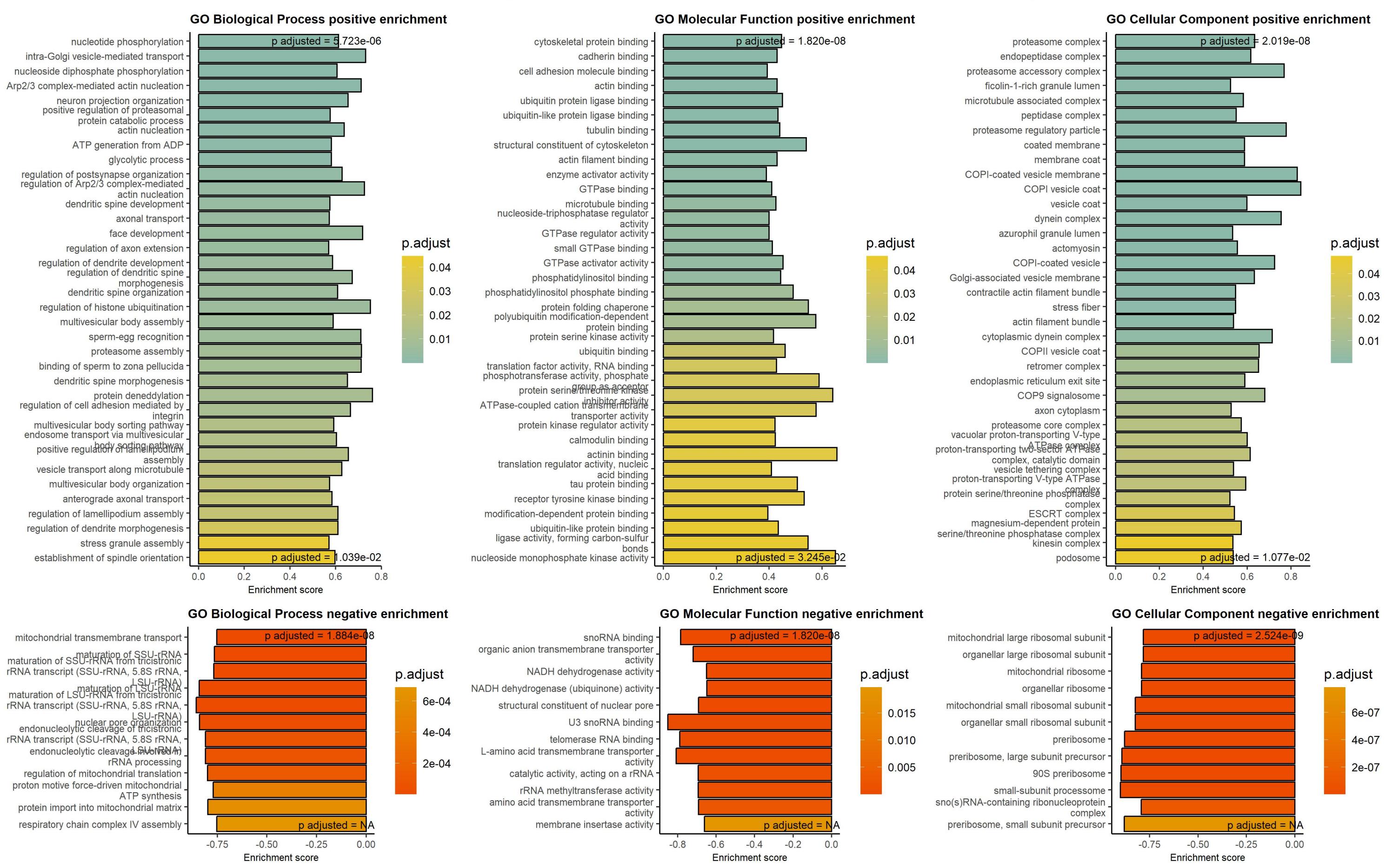
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.06	1.81e-39	GAPDH	glyceraldehyde-3-phosphate dehydrog	0.75	3.15e-02	SEPLG	selectin P ligand
-1.03	1.70e-03	SLC25A11	solute carrier family 25 member 11	0.44	3.17e-02	POGLUT2	protein O-glucosyltransferase 2
-0.94	1.78e-03	CYFIP2	cytoplasmic FMR1 interacting protei	0.54	3.28e-02	STX11	syntaxin 11
-0.79	1.78e-03	PDE6D	phosphodiesterase 6D	0.48	3.29e-02	DHRS11	dehydrogenase/reductase 11
-0.49	1.78e-03	MPC2	mitochondrial pyruvate carrier 2	0.54	3.69e-02	SPECC1	sperm antigen with calponin homolog
-1.01	1.96e-03	SASH3	SAM and SH3 domain containing 3	0.08	3.69e-02	SDHB	succinate dehydrogenase complex iro
-0.09	2.09e-03	HADH	hydroxyacyl-CoA dehydrogenase	0.39	4.17e-02	NOTCH2	notch receptor 2
-0.19	2.96e-03	TOP2B	DNA topoisomerase II beta	0.74	4.17e-02	SPR	sepiapterin reductase
-0.3	3.12e-03	KNTC1	kinetochore associated 1	0.45	4.42e-02	CGN	cingulin
-0.78	3.29e-03	PPP4C	protein phosphatase 4 catalytic sub	0.45	4.42e-02	CLU	clusterin
-0.09	8.38e-03	CTPS1	CTP synthase 1	0.31	4.44e-02	CDC42EP4	CDC42 effector protein 4
-0.1	8.38e-03	DDX39B	DExD-box helicase 39B	0.92	5.22e-02	CTTN	cortactin
-0.38	8.91e-03	HDAC3	histone deacetylase 3	0.05	5.82e-02	TUFM	Tu translation elongation factor, m
-0.06	1.04e-02	NUDT21	nudix hydrolase 21	0.6	5.87e-02	CMBL	carboxymethylenebutenolidase homolo
-0.3	1.17e-02	ANKRD54	ankyrin repeat domain 54	0.08	6.04e-02	EBNA1BP2	EBNA1 binding protein 2
-0.06	1.25e-02	TRA2B	transformer 2 beta homolog	0.73	6.04e-02	SPART	spartin
-0.08	1.25e-02	RCC2	regulator of chromosome condensatio	0.09	6.09e-02	UQCRB	ubiquinol-cytochrome c reductase bi
-0.91	1.25e-02	SORL1	sortilin related receptor 1	0.74	6.09e-02	TRIP10	thyroid hormone receptor interactor
-0.08	1.31e-02	TSN	translin	0.72	6.57e-02	JUNB	JunB proto-oncogene, AP-1 transcrip
-1.01	1.53e-02	PAX5	paired box 5	0.65	6.67e-02	DUSP3	dual specificity phosphatase 3
-0.63	1.54e-02	SKP2	S-phase kinase associated protein 2	0.87	6.67e-02	NDUFB2	NADH:ubiquinone oxidoreductase subu
-0.47	1.78e-02	IFI16	interferon gamma inducible protein	0.43	6.72e-02	NAGLU	N-acetyl-alpha-glucosaminidase
-0.68	1.78e-02	BDH1	3-hydroxybutyrate dehydrogenase 1	0.64	6.72e-02	EML3	EMAP like 3
-0.96	1.78e-02	CD19	CD19 molecule	0.68	6.89e-02	FHOD1	formin homology 2 domain containing
-0.11	1.78e-02	LRRC40	leucine rich repeat containing 40	0.61	7.33e-02	SLC30A1	solute carrier family 30 member 1
-0.05	1.78e-02	CHD4	chromodomain helicase DNA binding p	0.23	7.61e-02	FLNA	filamin A
-0.18	1.99e-02	DCK	deoxyribonucleic kinase	0.86	8.00e-02	HSPA4L	heat shock protein family A (Hsp70)
-0.9	2.01e-02	PEX11B	peroxisomal biogenesis factor 11 be	0.36	8.03e-02	NOL3	nucleolar protein 3
-0.94	2.41e-02	CD38	CD38 molecule	0.9	8.03e-02	STOM	stomatin
-0.69	2.41e-02	RCSD1	RCSD domain containing 1	0.07	8.13e-02	NMT1	N-myristoyltransferase 1
-0.77	2.58e-02	EED	embryonic ectoderm development	0.39	8.34e-02	S100P	S100 calcium binding protein P
-0.46	2.66e-02	FPGS	fattyacylglycerol synthase	0.06	8.79e-02	CIAO1	cytosolic iron-sulfur assembly comp
-0.79	2.66e-02	NCKAP1L	NCK associated protein 1 like	0.12	9.20e-02	UQCRH	ubiquinol-cytochrome c reductase hi
-0.85	2.84e-02	STK38	serine/threonine kinase 38	0.47	9.24e-02	REEP6	receptor accessory protein 6
-0.87	3.17e-02	ZHX2	zinc fingers and homeoboxes 2	0.58	9.24e-02	CD320	CD320 molecule
-0.04	3.28e-02	PTBP1	polypyrimidine tract binding protei	0.05	9.85e-02	HARS1	histidyl-tRNA synthetase 1
-0.05	3.28e-02	HNRNPA3	heterogeneous nuclear ribonucleoprotein	0.06	1.06e-01	UQCRC1	ubiquinol-cytochrome c reductase co
-0.09	3.28e-02	WDR5	WD repeat domain 5	0.38	1.06e-01	CTSL	cathepsin L
0.00	3.28e-02	CHAMP1	chromosome alignment maintaining ph	0.22	1.08e-01	GDE1	glycophosphoinositide phosphodiester



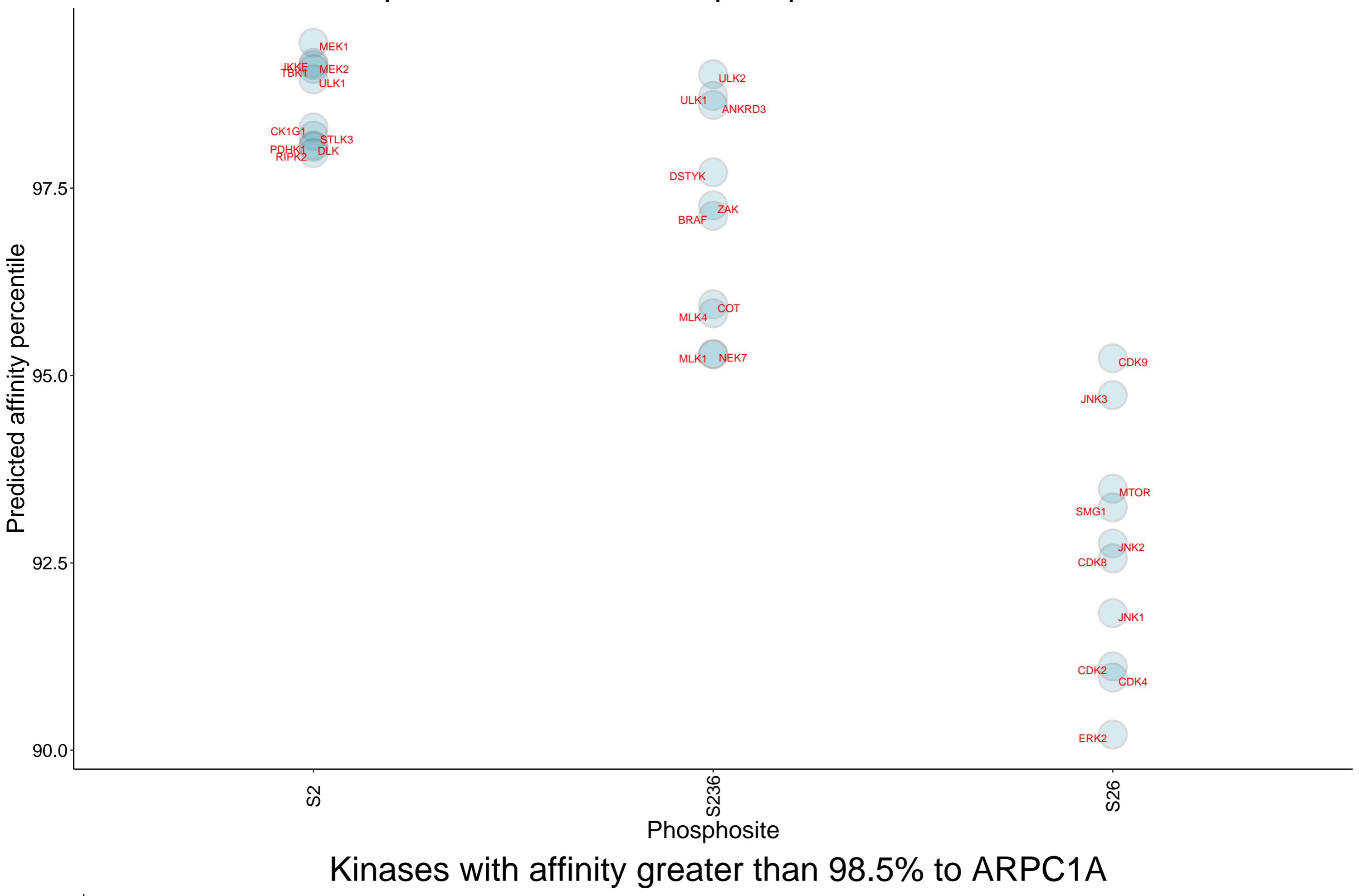
Top 250 correlation coefficients overrepresentation, ARPC1A protein, DB1



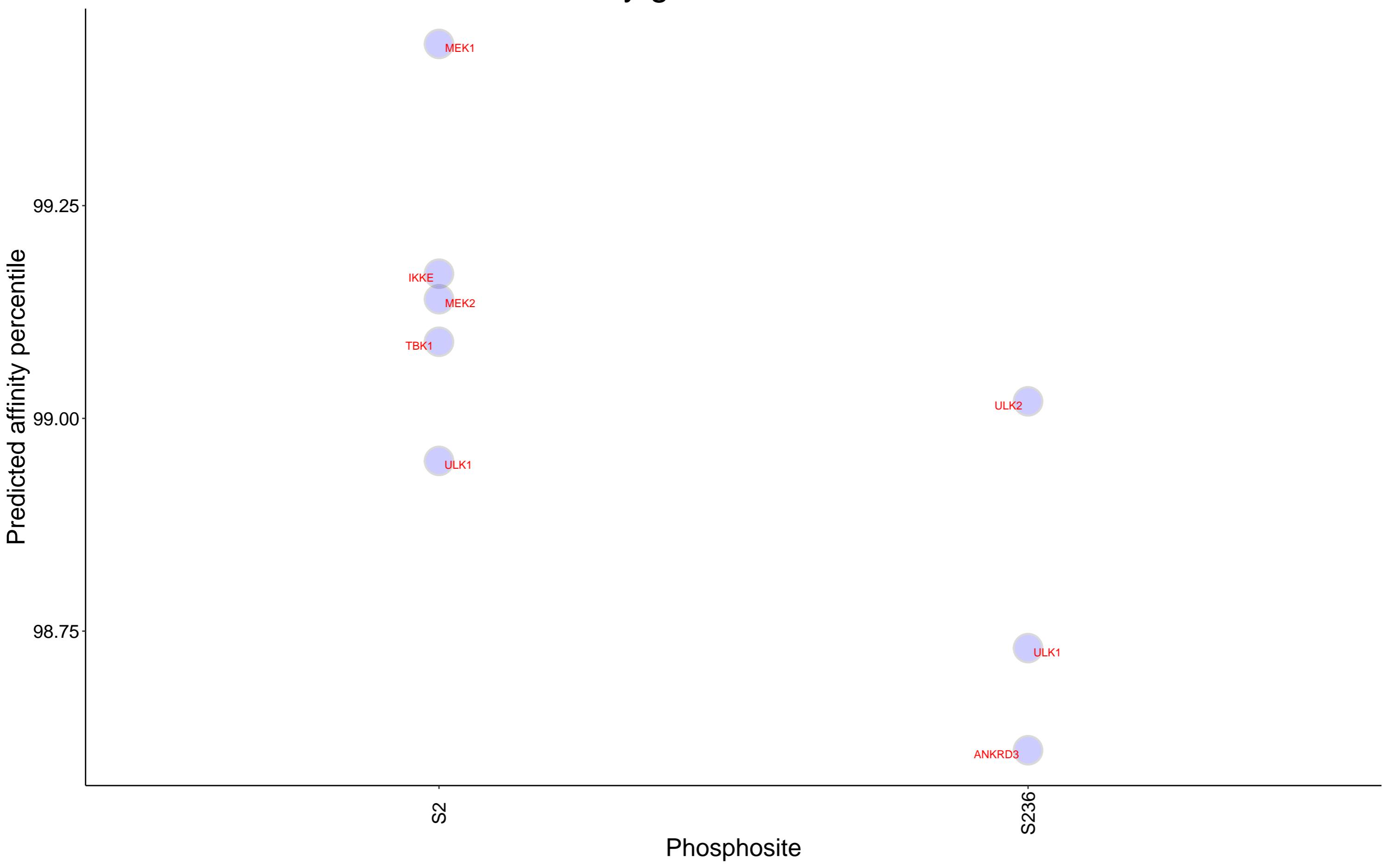
Gene Set Enrichment analysis on protein correlation coefficients, ARPC1A protein, DB1



Top 10 kinases for each phosphosite in ARPC1A



Kinases with affinity greater than 98.5% to ARPC1A



Top 15 positive correlation coefficients for ARPC1A protein by tissue, DB1

Beware of false positives in tissues with small number of samples

