

ARPC3

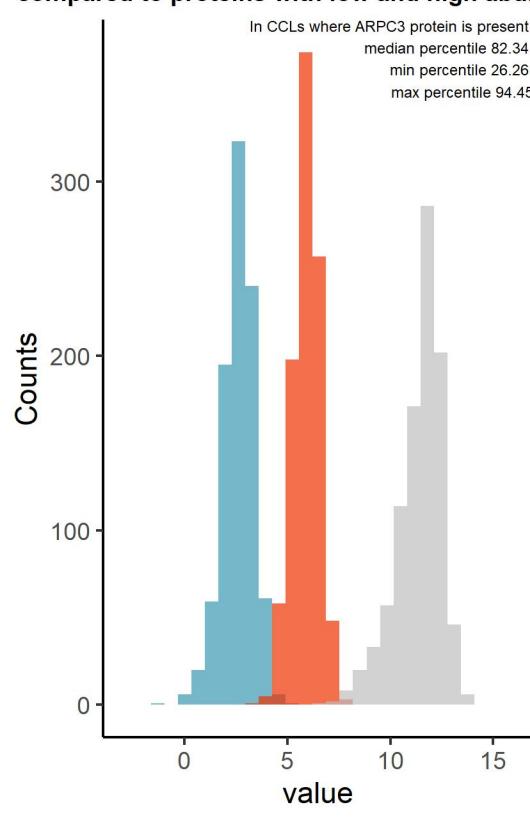
Protein name: ARPC3 ; UNIPROT: O15145 ; Gene name: actin related protein 2/3 complex subunit 3

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

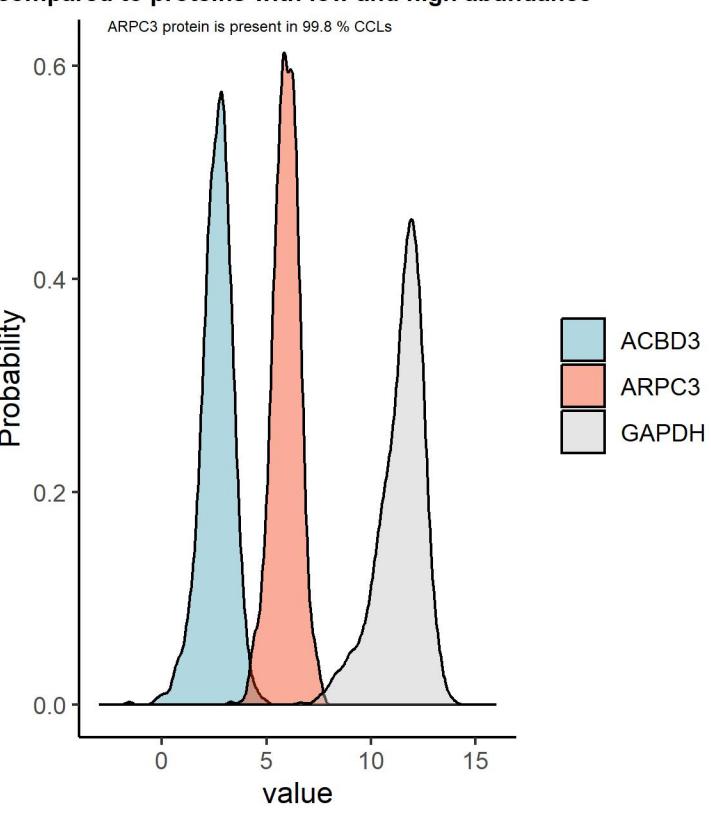
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

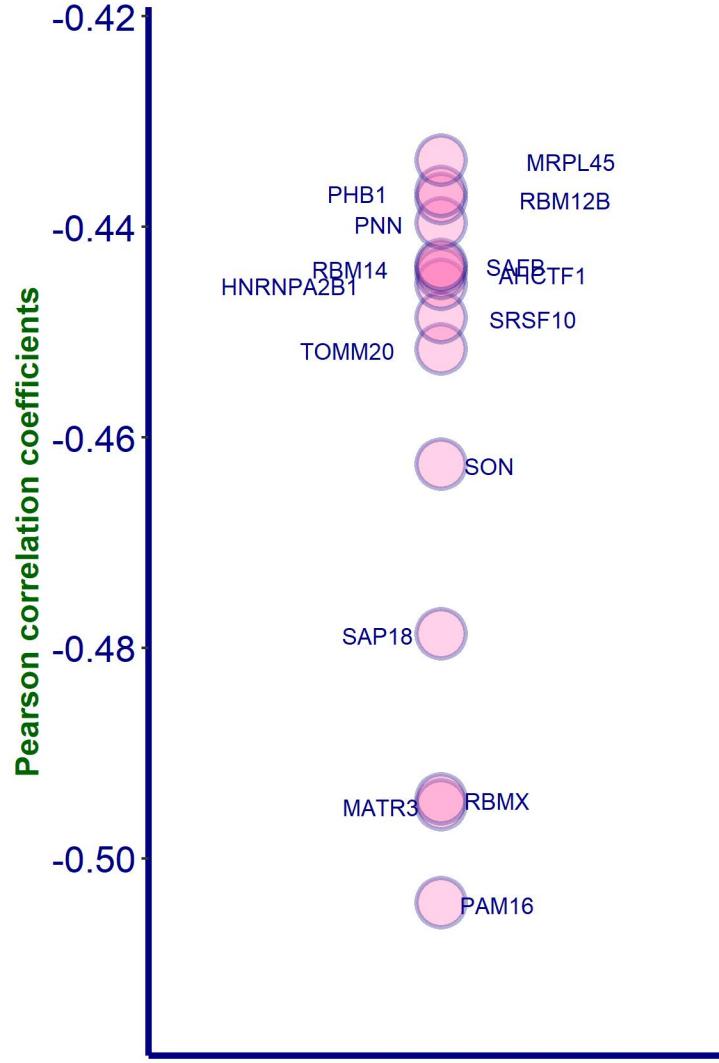
Histogram of ARPC3 protein compared to proteins with low and high abundance



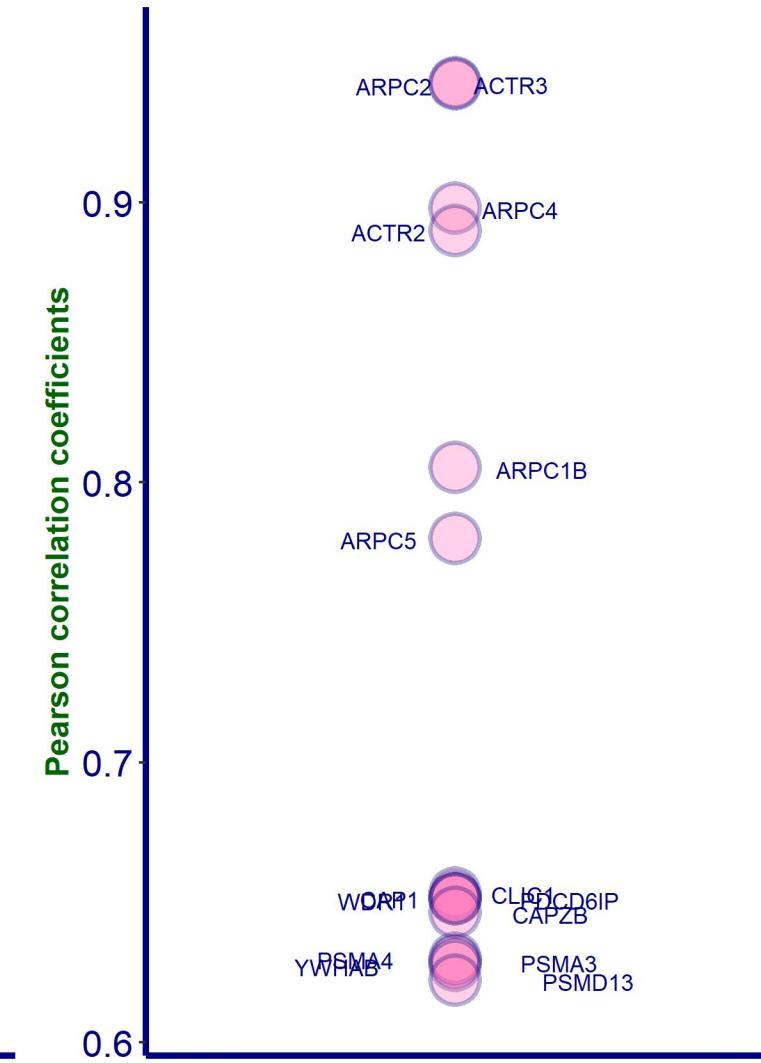
Density plot of ARPC3 protein compared to proteins with low and high abundance



Top negative correlations of ARPC3 protein, DB1

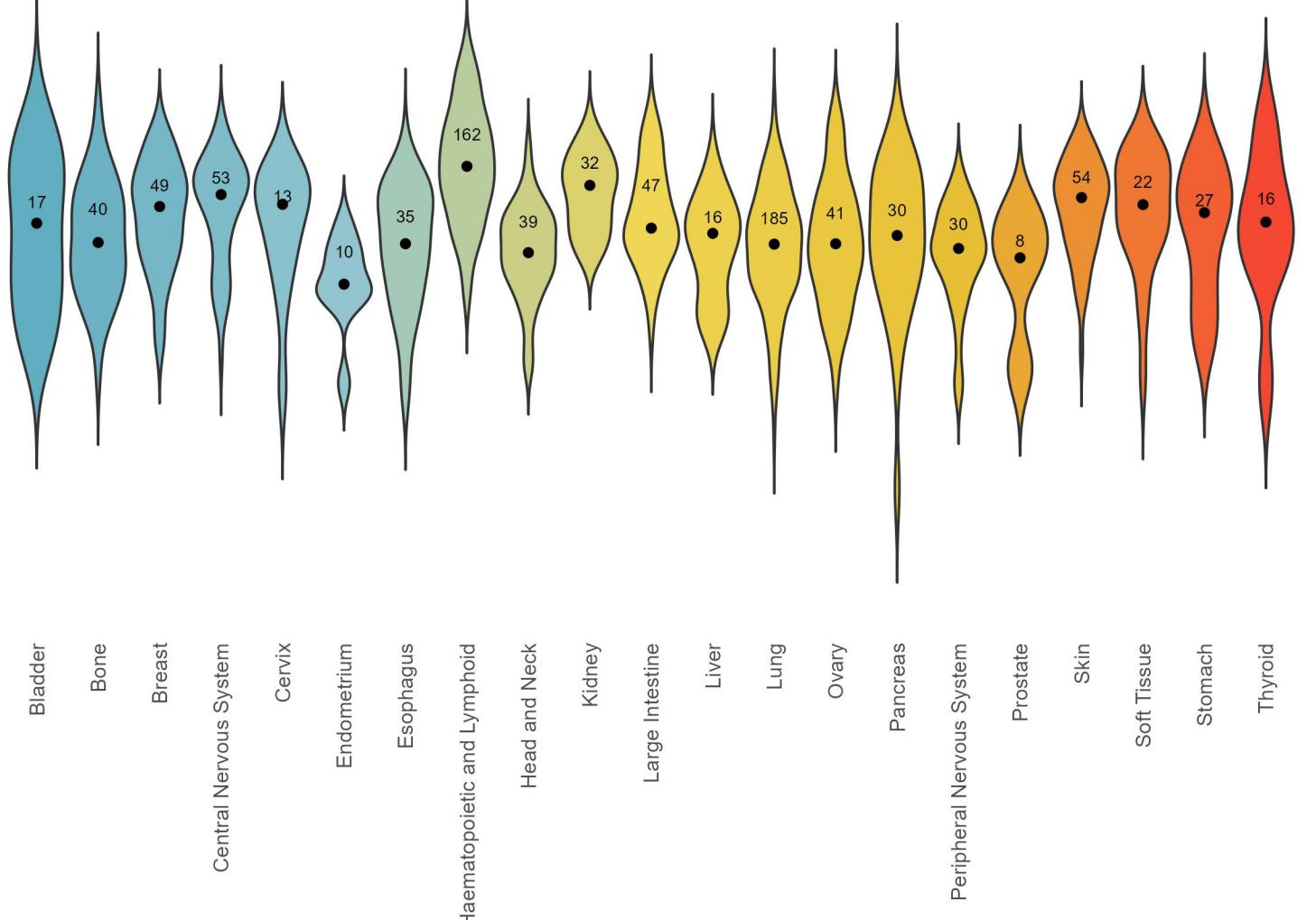


Top positive correlations of ARPC3 protein, DB1



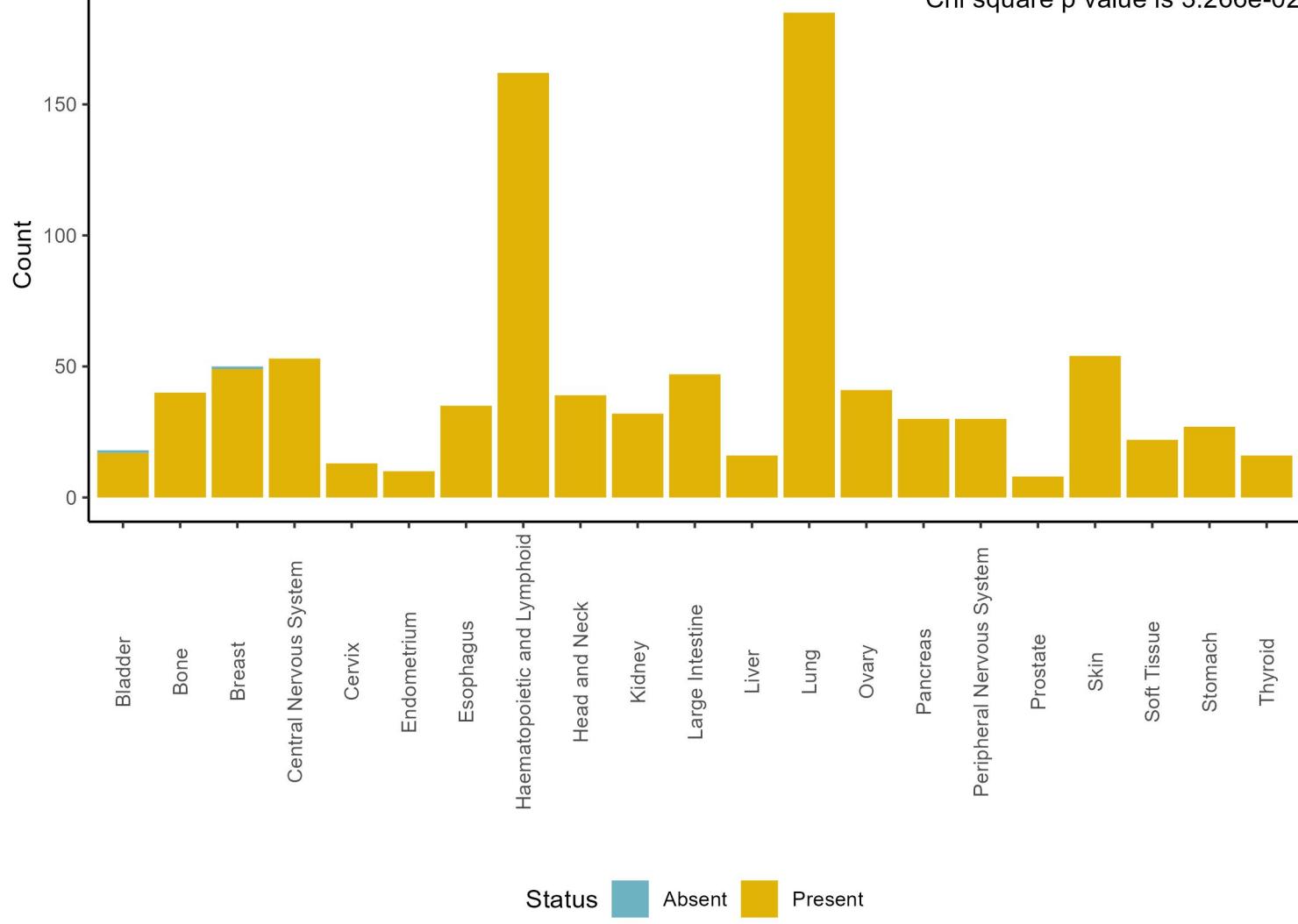
Amount of ARPC3 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 2.198e-40



Present and absent ARPC3 protein counts by tissue, DB1

Chi square p value is 3.266e-02

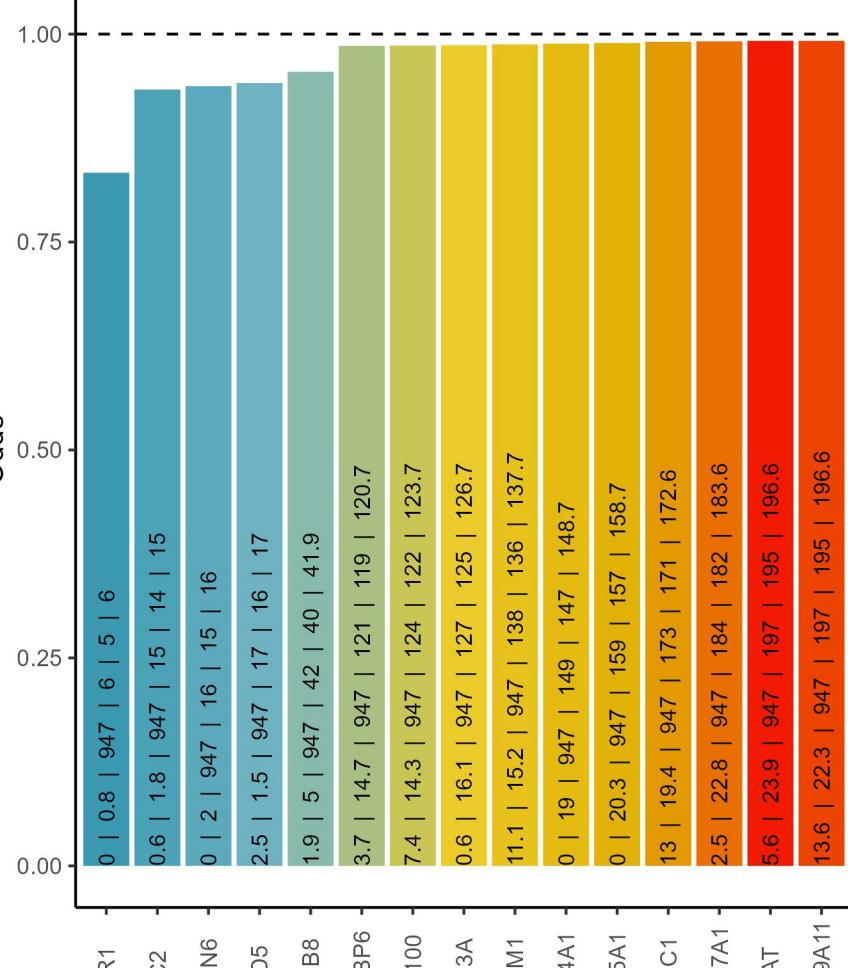


Cooccurrence with ARPC3 protein, DB1

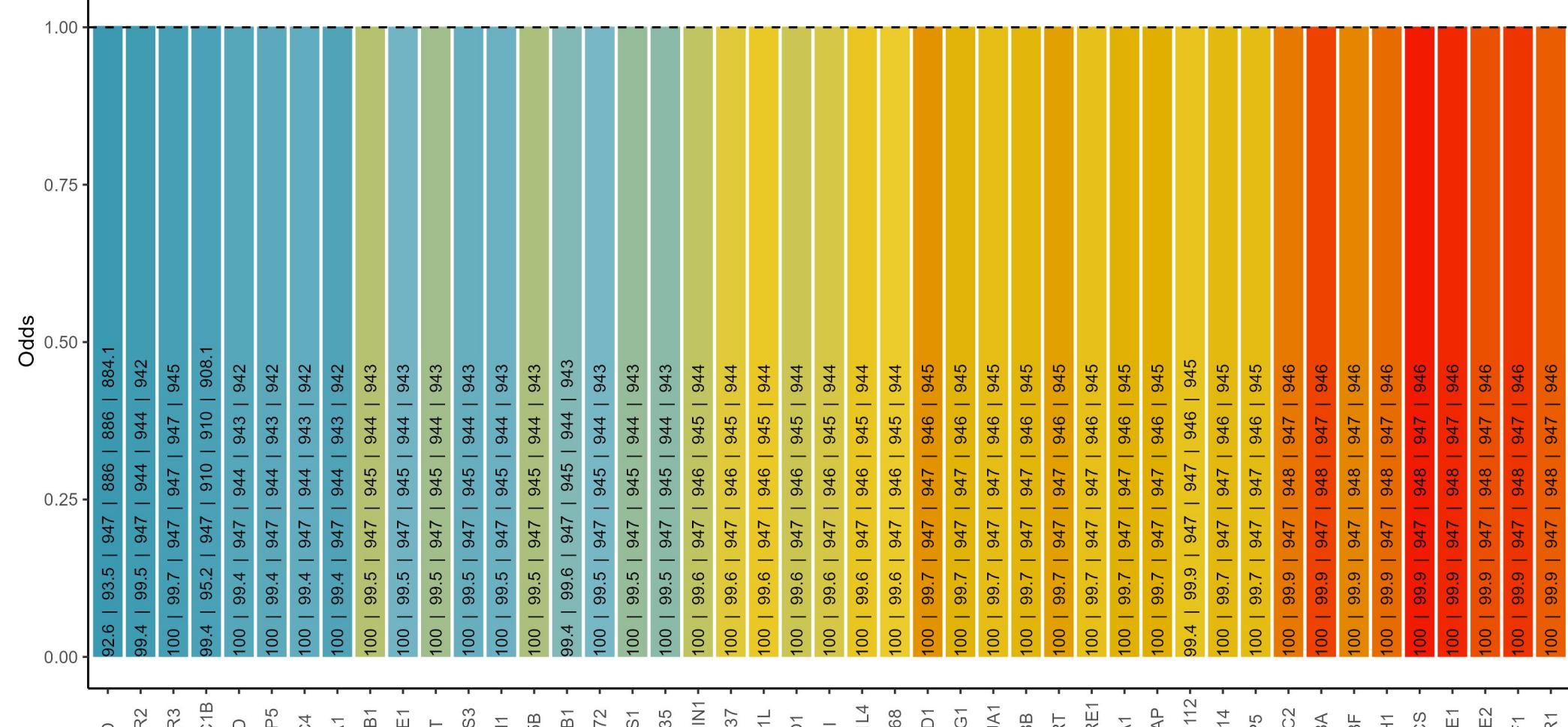
% of ARPC3 in blood cancers: 100 ; % of ARPC3 in solid cancers: 99.7

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ARPC3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

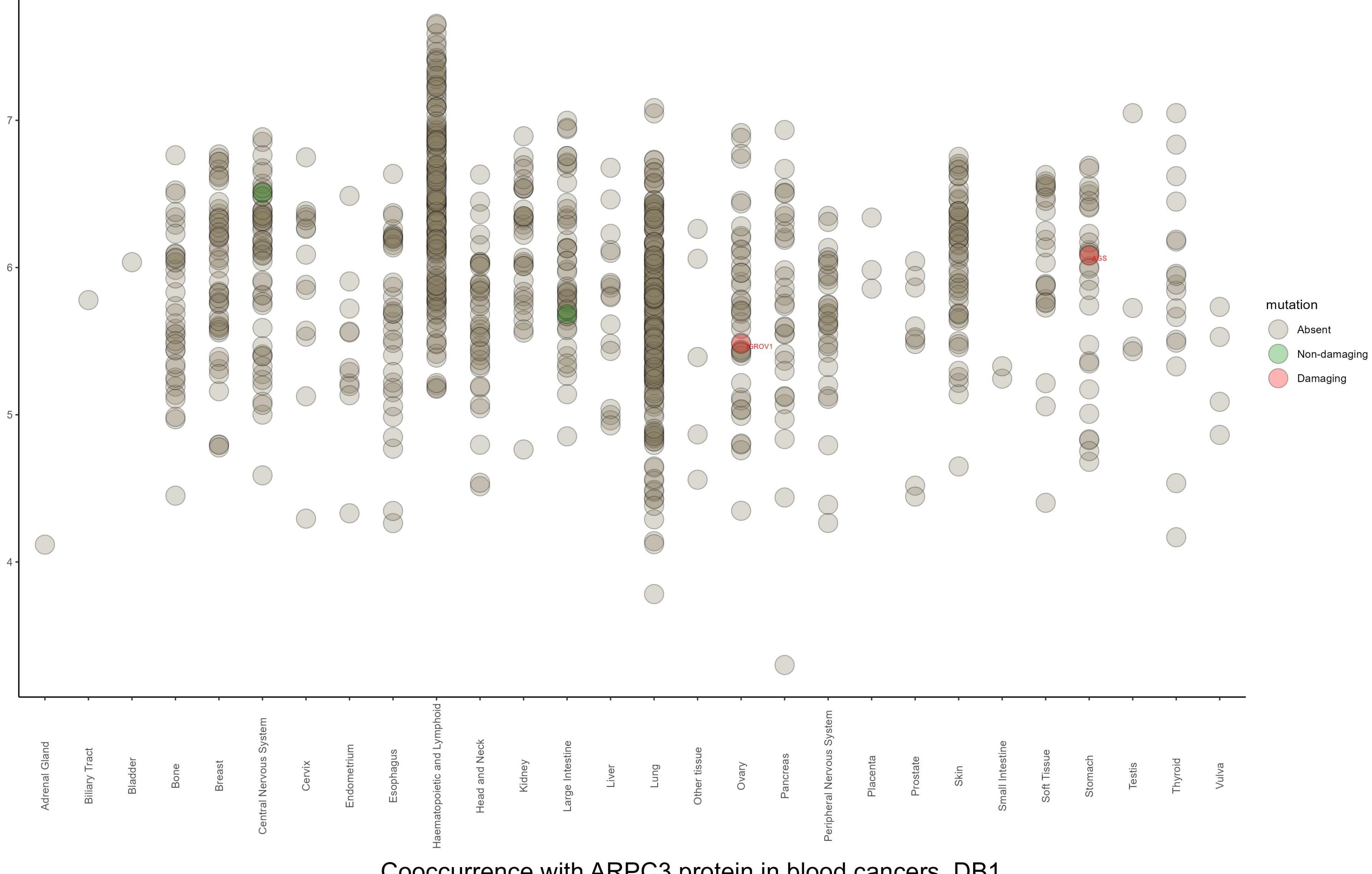
Negative cooccurrence



Positive cooccurrence



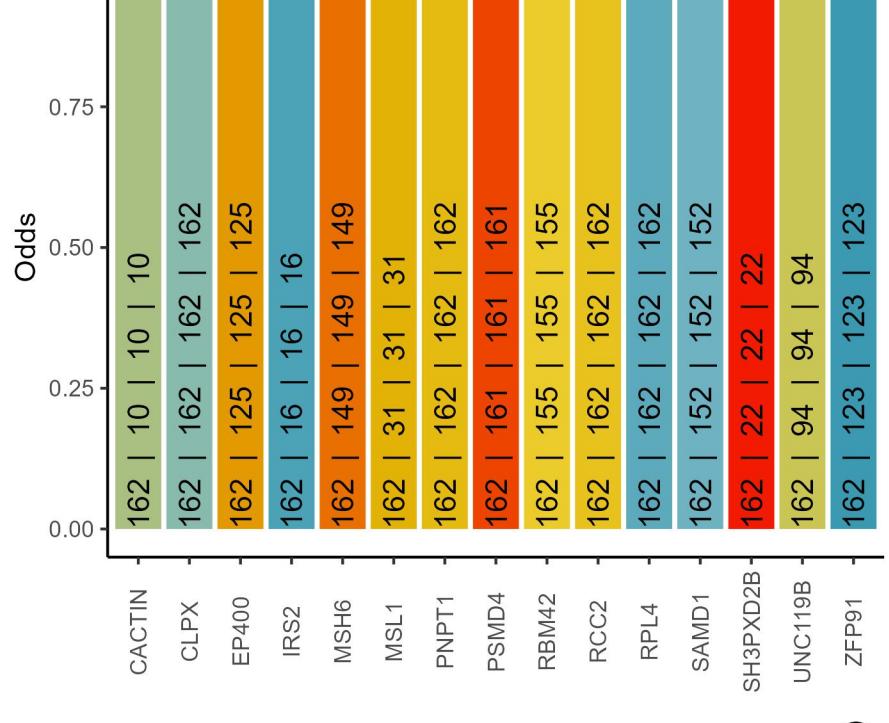
Amount of ARPC3 protein and mutation status by tissue, DB1



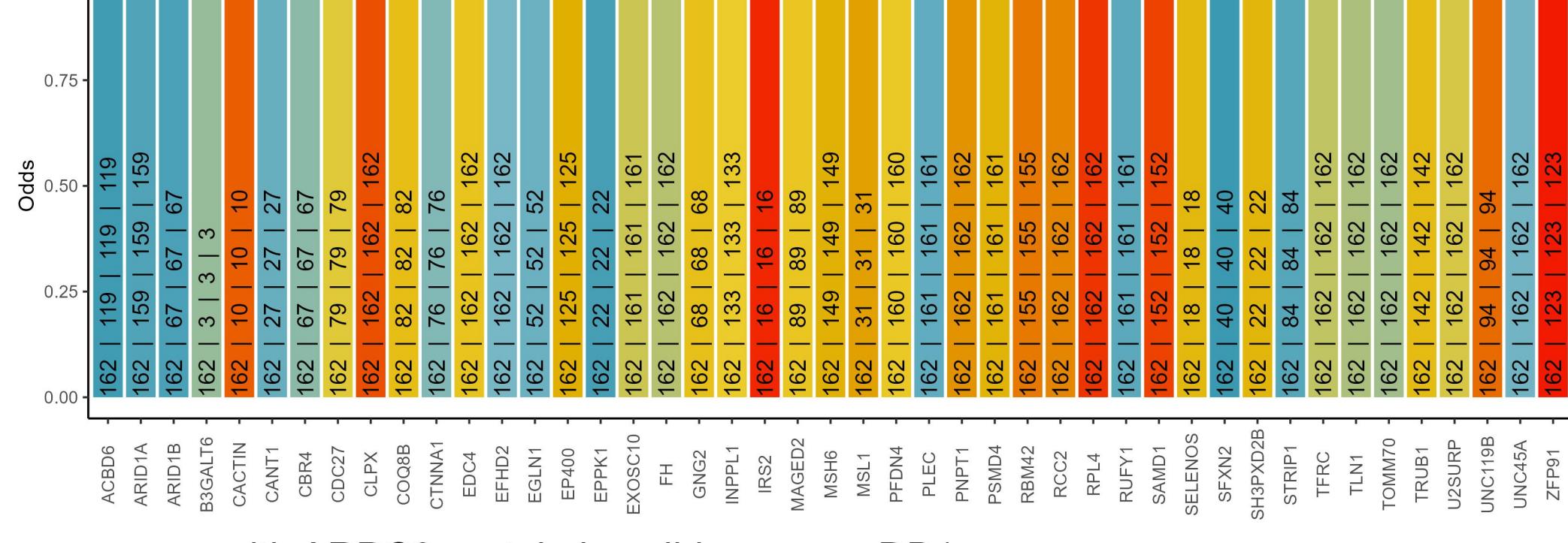
Cooccurrence with ARPC3 protein in blood cancers, DB1

The text in the bars: incidence of ARPC3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



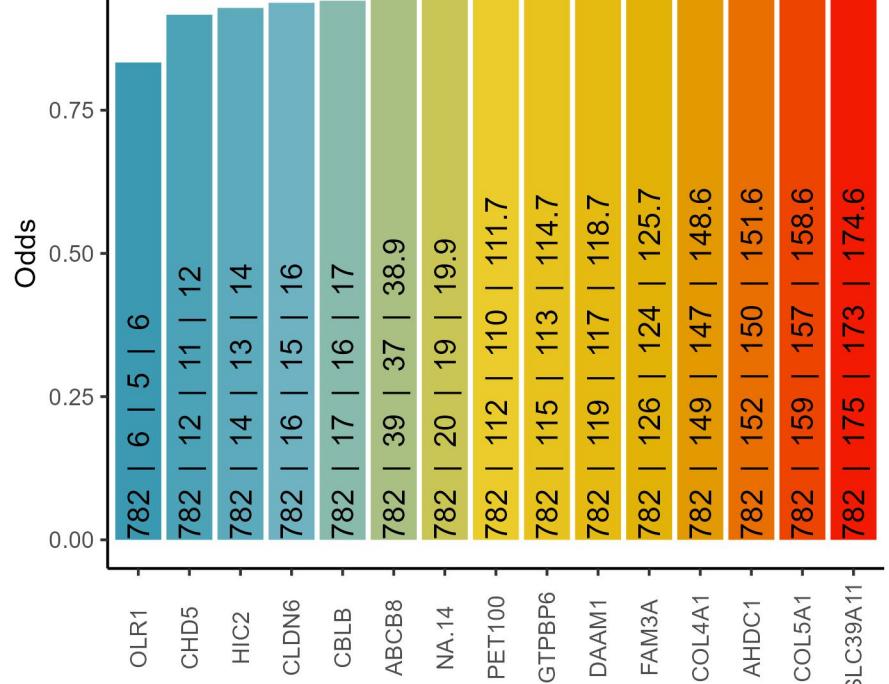
Positive cooccurrence



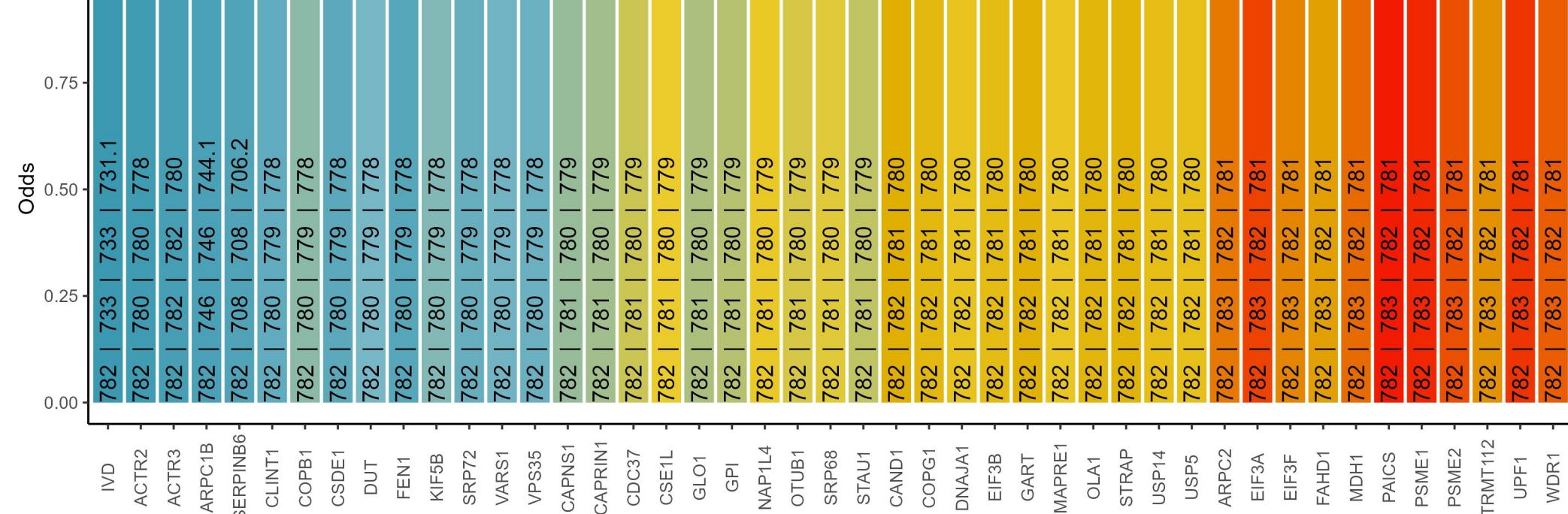
Cooccurrence with ARPC3 protein in solid cancers, DB1

The text in the bars: incidence of ARPC3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

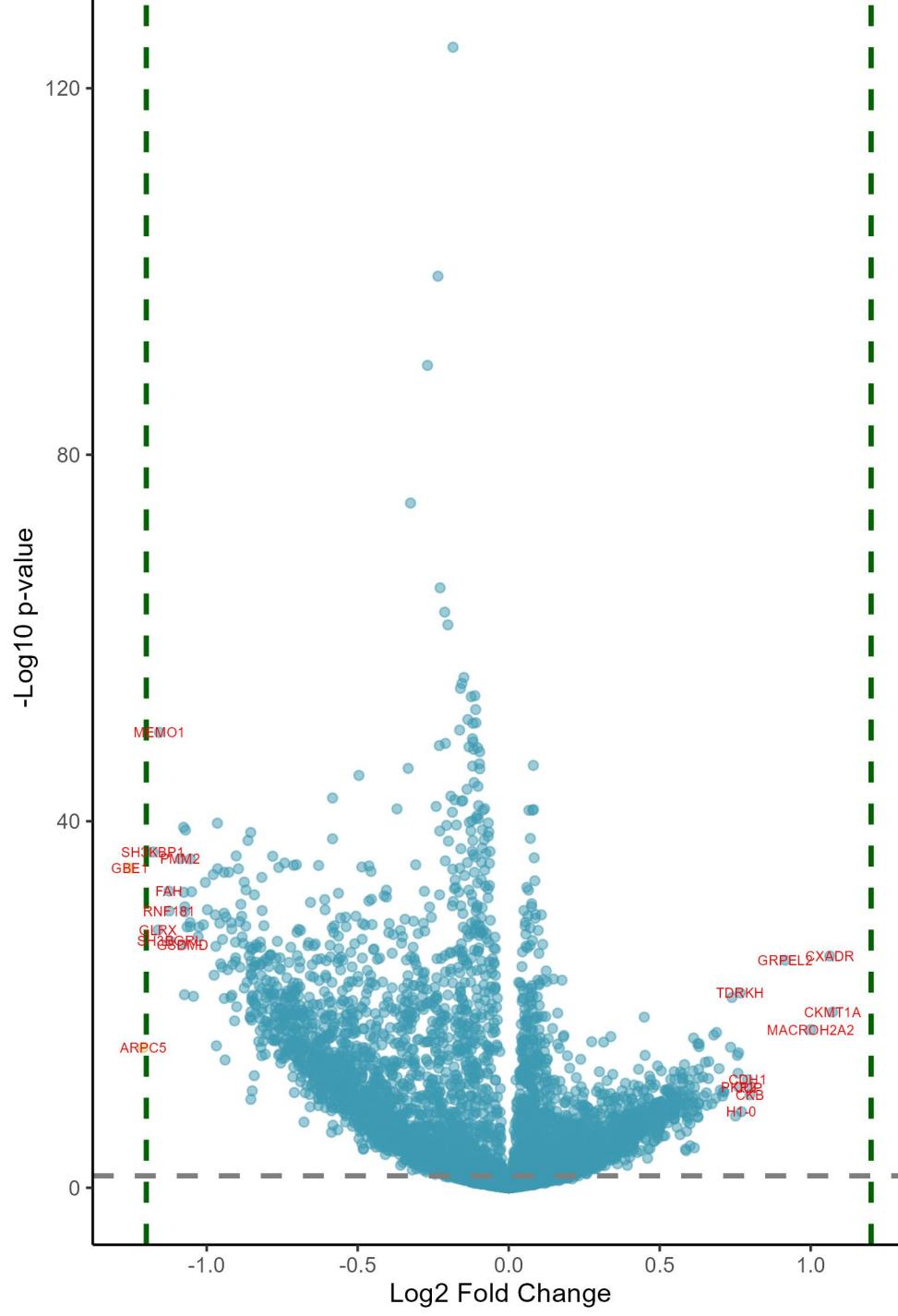
Negative cooccurrence



Positive cooccurrence

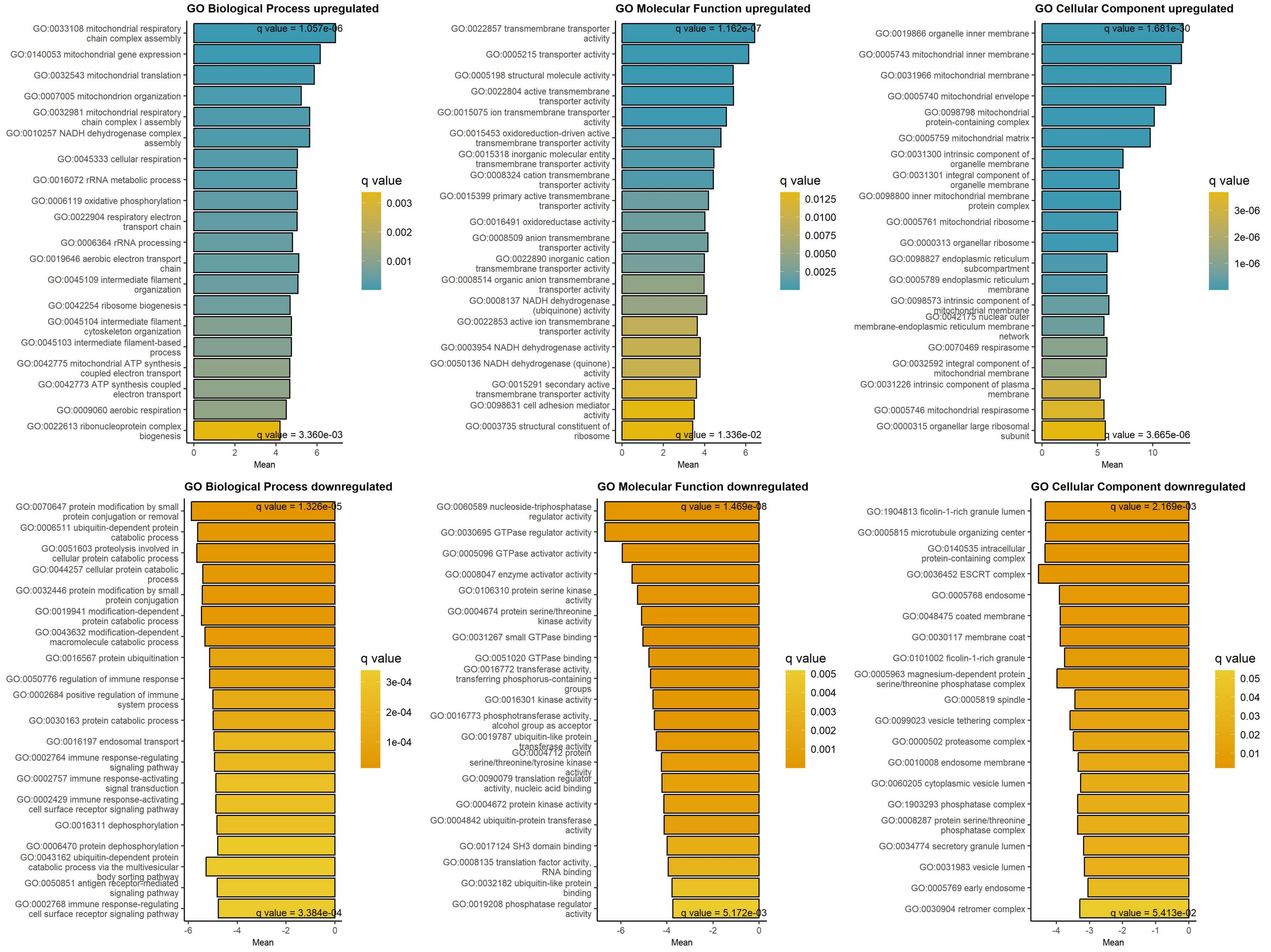


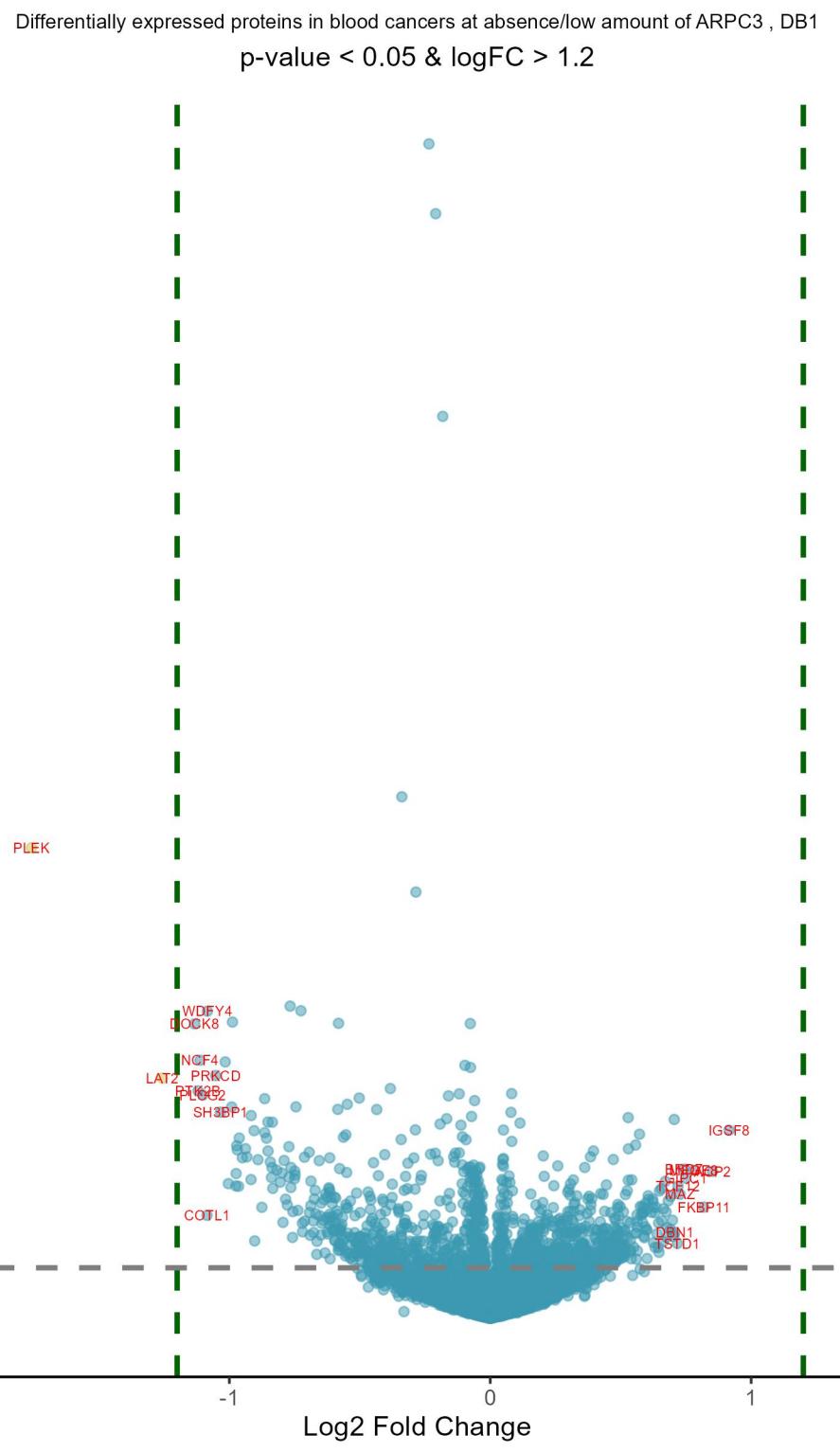
Downregulated at low/absent ARPC3 Upregulated at low/absent ARPC3



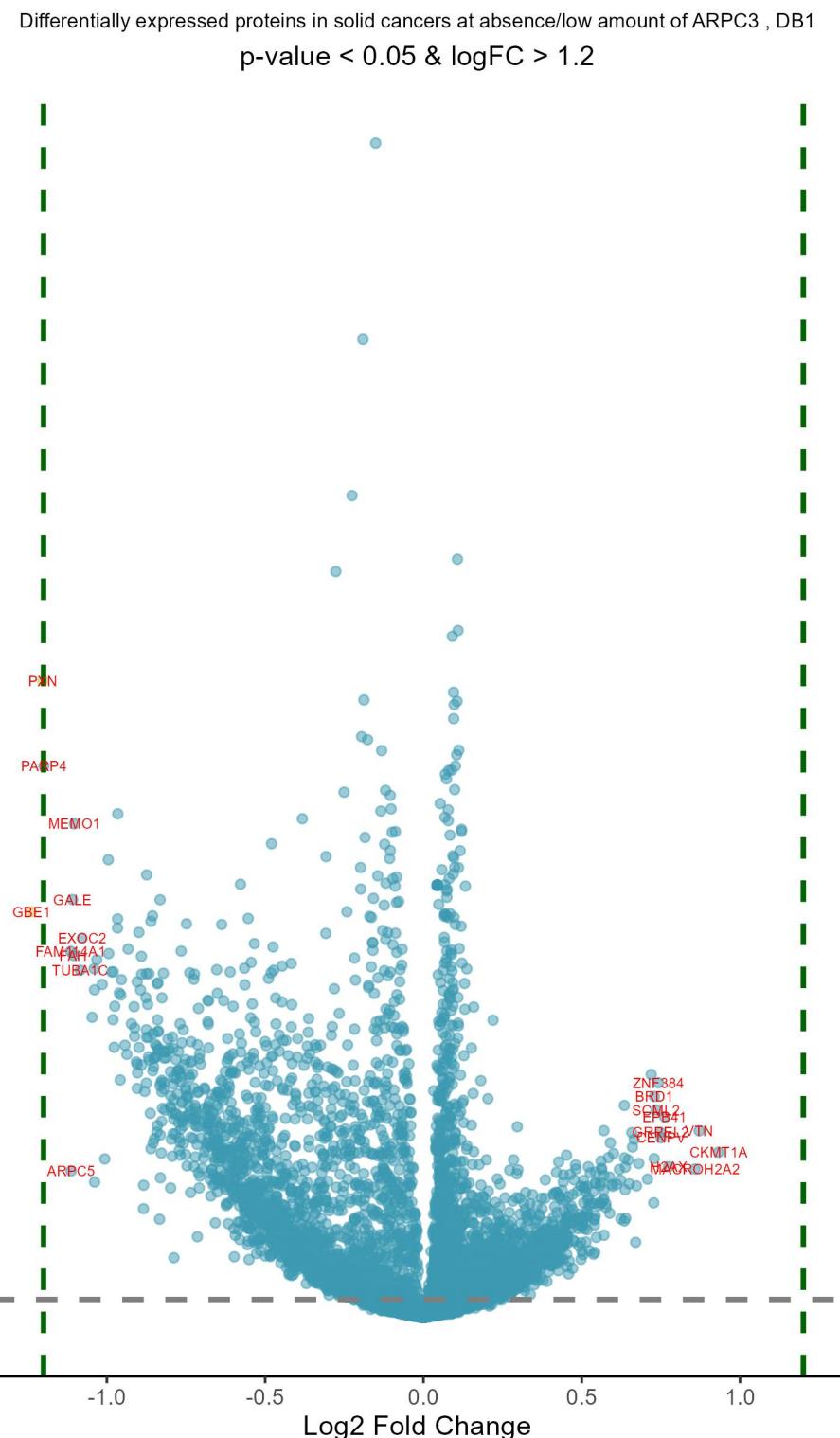
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.25	8.64e-34	GBE1	1,4-alpha-glucan branching enzyme 1	1.07	7.32e-19	CKMT1A	creatine kinase, mitochondrial 1A
-1.21	3.72e-15	ARPC5	actin related protein 2/3 complex s	1.06	1.14e-24	CXADR	CXADR Ig-like cell adhesion molecule
-1.18	1.96e-35	SH3KBP1	SH3 domain containing kinase bindin	1	5.01e-17	MACROH2A2	macroH2A.2 histone
-1.16	2.32e-27	GLRX	glutaredoxin	0.92	3.10e-24	GRPEL2	GrpE like 2, mitochondrial
-1.16	7.11e-48	MEMO1	mediator of cell motility 1	0.8	3.18e-10	CKB	creatine kinase B
-1.13	2.20e-31	FAH	fumarylacetoacetate hydrolase	0.8	6.01e-11	JUP	junction plakoglobin
-1.12	2.56e-29	RNF181	ring finger protein 181	0.79	8.37e-12	CDH1	cadherin 1
-1.12	3.18e-26	SH3BGR	SH3 domain binding glutamate rich p	0.77	1.83e-08	H1-0	H1.0 linker histone
-1.09	9.37e-35	PMM2	phosphomannomutase 2	0.77	8.03e-21	TDRKH	tudor and KH domain containing
-1.08	7.61e-26	GSDMD	gasdermin D	0.76	4.99e-11	PKP2	plakophilin 2
-1.08	5.05e-38	STK10	serine/threonine kinase 10	0.76	1.29e-14	GNG10	G protein subunit gamma 10
-1.08	2.83e-31	TAOK3	TAO kinase 3	0.76	1.81e-12	EPCAM	epithelial cell adhesion molecule
-1.07	1.22e-20	ABRACL	ABRA C-terminal like	0.76	2.41e-14	SLC25A4	solute carrier family 25 member 4
-1.07	3.23e-29	PSMB10	proteasome 20S subunit beta 10	0.75	5.19e-08	NDUFB11	NADH:ubiquinone oxidoreductase subunit
-1.07	9.46e-30	IRF3	interferon regulatory factor 3	0.74	2.33e-20	EXD2	exonuclease 3'-5' domain containing
-1.07	9.81e-38	TRIM21	tripartite motif containing 21	0.73	3.41e-15	CHCHD6	coiled-coil-helix-coiled-coil-helix
-1.07	1.14e-27	PSMB8	proteasome 20S subunit beta 8	0.71	1.65e-10	UQCRC10	ubiquinol-cytochrome c reductase, c
-1.06	4.10e-28	UBE2L6	ubiquitin conjugating enzyme E2 L6	0.71	1.38e-10	SPINT1	serine peptidase inhibitor, Kunitz
-1.05	1.05e-27	PPP6R1	protein phosphatase 6 regulatory subunit	0.71	4.39e-10	SPINT2	serine peptidase inhibitor, Kunitz
-1.05	1.00e-34	PCYT2	phosphate cytidylyltransferase 2, e	0.7	1.05e-10	PTK7	protein tyrosine kinase 7 (inactive)
-1.05	2.54e-31	DCK	deoxyribonucleoside kinase	0.7	5.84e-13	SMARCA1	SWI/SNF related, matrix associated, chromatin-remodeling complex
-1.04	1.78e-20	NACA2	nascent polypeptide associated comp	0.69	9.92e-17	BRD1	bromodomain containing 1
-1.03	1.16e-26	RPE	ribulose-5-phosphate-3-epimerase	0.69	7.45e-10	LSR	lipolysis stimulated lipoprotein receptor
-1.03	1.15e-27	WIPF1	WAS/WASL interacting protein family	0.68	1.83e-16	NCBP2AS2	NCBP2 antisense 2 (head to head)
-1.01	6.86e-28	EXOC2	exocyst complex component 2	0.67	2.70e-09	MISP	mitotic spindle positioning
-1	2.71e-32	ATOX1	antioxidant 1 copper chaperone	0.66	1.07e-13	CASK	calcium/calmodulin dependent serine
-1	1.93e-29	NECAP2	NECAP endocytosis associated 2	0.66	6.48e-12	SURF1	SURF1 cytochrome c oxidase assembly
-0.98	4.06e-33	MAPK14	mitogen-activated protein kinase 14	0.66	4.00e-09	EPPK1	epiplakin 1
-0.98	1.14e-22	TIGAR	TP53 induced glycolysis regulatory	0.65	1.97e-10	CGN	cingulin

GAGE analysis on upregulated and downregulated proteins at low/absent ARPC3 protein, DB1



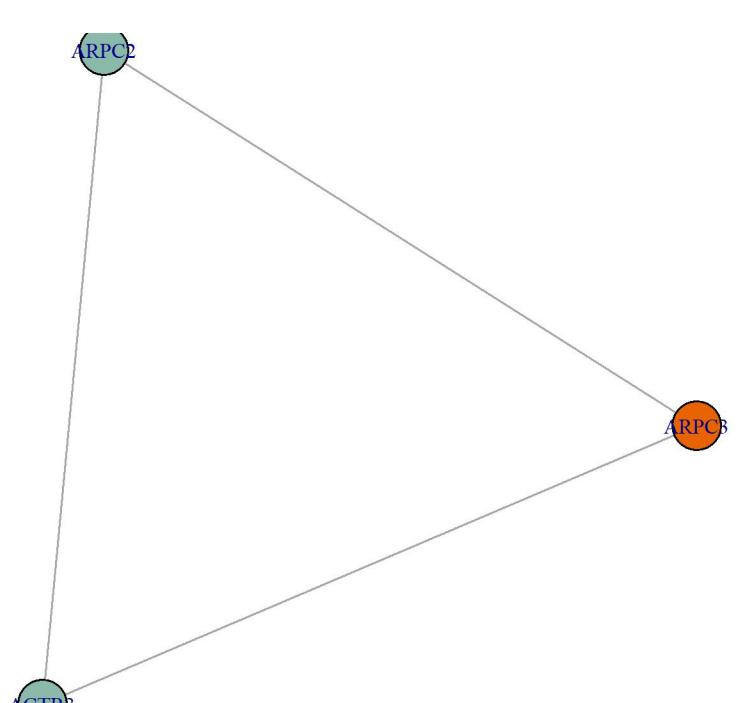


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.76	7.87e-10	PLEK	pleckstrin	0.92	1.89e-03	IGSF8	immunoglobulin superfamily member 8
-1.26	2.10e-04	LAT2	linker for activation of T cells fa	0.85	9.54e-03	ACP2	acid phosphatase 2, lysosomal
-1.13	1.19e-05	DOCK8	dedicator of cytokinesis 8	0.82	3.42e-02	FKBP11	FKBP prolyl isomerase 11
-1.12	4.07e-04	PTK2B	protein tyrosine kinase 2 beta	0.78	9.10e-03	MFGE8	milk fat globule EGF and factor V/V
-1.11	9.66e-05	NCF4	neutrophil cytosolic factor 4	0.75	1.21e-02	GIPC1	GIPC PDZ domain containing family m
-1.1	4.60e-04	PLCG2	phospholipase C gamma 2	0.74	8.71e-03	BRD7	bromodomain containing 7
-1.09	4.56e-02	COTL1	coactosin like F-actin binding prot	0.73	2.18e-02	MAZ	MYC associated zinc finger protein
-1.08	7.86e-06	WDFY4	WDFY family member 4	0.72	1.63e-02	TCF12	transcription factor 12
-1.05	1.90e-04	PRKCD	protein kinase C delta	0.72	1.21e-01	TSTD1	thiosulfate sulfurtransferase like
-1.03	8.94e-04	SH3BP1	SH3 domain binding protein 1	0.71	8.24e-02	DBN1	drebrin 1
-1.02	1.00e-04	ANKRD44	ankyrin repeat domain 44	0.71	1.20e-03	RPL36A	ribosomal protein L36a
-1	1.47e-02	BASP1	brain abundant membrane attached si	0.7	9.36e-02	GTSF1	gametocyte specific factor 1
-0.99	7.31e-04	SORL1	sortilin related receptor 1	0.7	5.57e-02	CCNA2	cyclin A2
-0.99	1.19e-05	MNDA	myeloid cell nuclear differentiatio	0.69	2.34e-02	RPAP1	RNA polymerase II associated protei
-0.98	1.62e-02	CTSZ	cathepsin Z	0.69	7.52e-02	MYH10	myosin heavy chain 10
-0.97	1.03e-02	ITGAL	integrin subunit alpha L	0.68	2.75e-02	ZAP70	zeta chain of T cell receptor assoc
-0.97	3.77e-03	CSTA	cystatin A	0.68	7.13e-02	SMC1B	structural maintenance of chromosom
-0.97	4.50e-03	DOK3	docking protein 3	0.68	9.69e-02	LGALS3BP	galectin 3 binding protein
-0.96	1.63e-02	ITGB2	integrin subunit beta 2	0.67	4.02e-02	RBIS	ribosomal biogenesis factor
-0.96	2.62e-03	SYK	spleen associated tyrosine kinase	0.67	1.34e-02	MORC2	MORC family CW-type zinc finger 2
-0.95	5.91e-03	SWAP70	switching B cell complex subunit SW	0.66	3.60e-02	CD3E	CD3 epsilon subunit of T-cell recep
-0.94	4.33e-03	MYO1G	myosin IG	0.66	1.14e-01	PTMS	parathymosin
-0.93	5.84e-03	BTK	Bruton tyrosine kinase	0.66	5.72e-02	ZMAT2	zinc finger matrin-type 2
-0.92	1.28e-02	MS4A1	membrane spanning 4-domains A1	0.66	1.78e-02	TNKS1BP1	tankyrase 1 binding protein 1
-0.92	1.05e-03	RASSF2	Ras association domain family membe	0.65	1.92e-02	HMGN4	high mobility group nucleosomal bin
-0.91	1.91e-03	MYO1F	myosin IF	0.65	1.56e-01	ABCB6	ATP binding cassette subfamily B me
-0.9	1.12e-01	LSP1	lymphocyte specific protein 1	0.65	6.06e-02	ATP1A3	ATPase Na+/K+ transporting subunit
-0.89	6.24e-03	GPD2	glycerol-3-phosphate dehydrogenase	0.64	1.34e-01	POLR2K	RNA polymerase II, I and III subuni
-0.88	3.42e-02	PTPN6	protein tyrosine phosphatase non-re	0.64	8.66e-02	IRF2BPL	interferon regulatory factor 2 bind

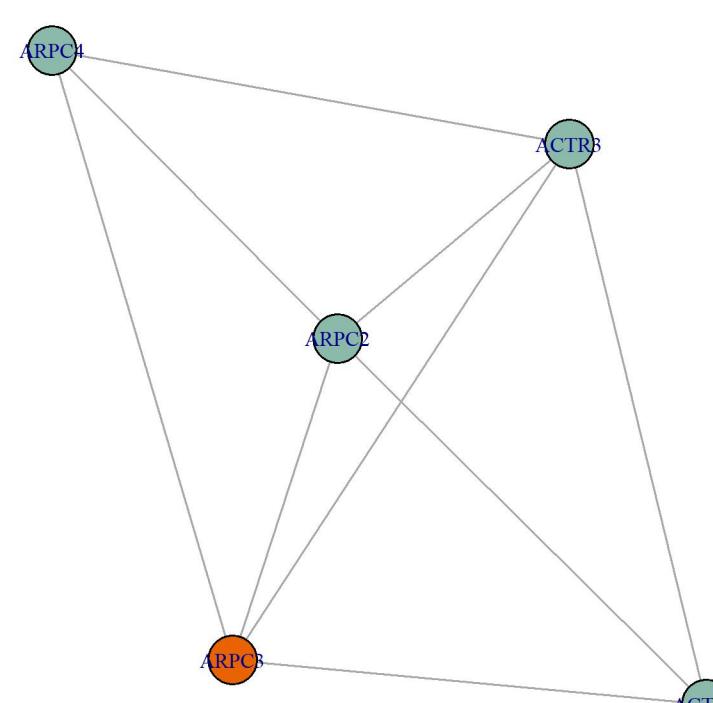


Downregulated in solid cancers at low/absent ARPC3				Upregulated in solid cancers at low/absent ARPC3			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.24	2.95e-28	GBE1	1,4-alpha-glucan branching enzyme 1	0.93	9.09e-12	CKMT1A	creatine kinase, mitochondrial 1A
-1.2	1.36e-43	PXN	paxillin	0.87	3.18e-13	VTN	vitronectin
-1.2	7.81e-38	PARP4	poly(ADP-ribose) polymerase family	0.86	1.27e-10	MACROH2A2	macroH2A.2 histone
-1.11	1.61e-25	FAM114A1	family with sequence similarity 114	0.77	8.72e-11	H2AX	H2A.X variant histone
-1.11	1.71e-10	ARPC5	actin related protein 2/3 complex s	0.76	3.53e-14	EPB41	erythrocyte membrane protein band 4
-1.11	4.13e-29	GALE	UDP-galactose-4-epimerase	0.75	9.59e-13	CENPV	centromere protein V
-1.11	3.19e-25	FAH	fumarylacetoacetate hydrolase	0.75	4.01e-13	GRPEL2	GrpE like 2, mitochondrial
-1.1	5.94e-34	MEMO1	mediator of cell motility 1	0.74	1.71e-16	ZNF384	zinc finger protein 384
-1.08	3.29e-24	TUBA1C	tubulin alpha 1c	0.73	1.25e-14	SCML2	Scm polycomb group protein like 2
-1.08	2.03e-26	EXOC2	exocyst complex component 2	0.73	1.46e-15	BRD1	bromodomain containing 1
-1.05	5.90e-21	GLRX	glutaredoxin	0.73	2.49e-11	RPS19BP1	ribosomal protein S19 binding prote
-1.04	2.66e-24	PARVA	parvin alpha	0.73	2.51e-08	GNG5	G protein subunit gamma 5
-1.04	7.29e-23	IRF3	interferon regulatory factor 3	0.72	4.62e-17	TCF20	transcription factor 20
-1.04	9.82e-10	NQO1	NAD(P)H quinone dehydrogenase 1	0.71	6.27e-10	CXADR	CXADR Ig-like cell adhesion molecu
-1.03	6.19e-25	PMM2	phosphomannomutase 2	0.68	5.29e-11	GTPBP3	GTP binding protein 3, mitochondria
-1.01	3.07e-23	SH3KBP1	SH3 domain containing kinase bindin	0.67	1.79e-09	GNG10	G protein subunit gamma 10
-1.01	2.58e-11	CBR3	carbonyl reductase 3	0.67	1.18e-05	NDUFB11	NADH:ubiquinone oxidoreductase sub
-1	1.63e-31	LPP	LIM domain containing preferred tra	0.67	1.20e-12	COQ6	coenzyme Q6, monooxygenase
-0.99	2.33e-25	DCTD	dCMP deaminase	0.66	4.05e-12	KIF1A	kinesin family member 1A
-0.98	4.24e-24	SEPTIN10	septin 10	0.66	4.22e-13	NCBP2AS2	NCBP2 antisense 2 (head to head)
-0.98	8.63e-21	TRIP6	thyroid hormone receptor interactor	0.65	1.31e-09	SLC25A4	solute carrier family 25 member 4
-0.98	4.27e-24	PCYT2	phosphate cytidylyltransferase 2, e	0.65	3.07e-11	MEAF6	MYST/Esa1 associated factor 6
-0.98	6.71e-19	TIGAR	TP53 induced glycolysis regulatory	0.64	2.79e-07	MRPL54	mitochondrial ribosomal protein L54
-0.97	9.89e-22	AKT1S1	AKT1 substrate 1	0.64	9.47e-11	ZNF280C	zinc finger protein 280C
-0.97	3.89e-27	AAK1	AP2 associated kinase 1	0.64	3.26e-09	CNTN1	contactin 1
-0.97	8.91e-28	GMPPB	GDP-mannose pyrophosphorylase B	0.64	2.18e-11	YTHDC1	YTH domain containing 1
-0.97	1.28e-34	PTPN23	protein tyrosine phosphatase non-re	0.63	6.04e-15	DNMT3A	DNA methyltransferase 3 alpha
-0.96	1.21e-22	ATOX1	antioxidant 1 copper chaperone	0.63	4.29e-07	UQCR10	ubiquinol-cytochrome c reductase, c

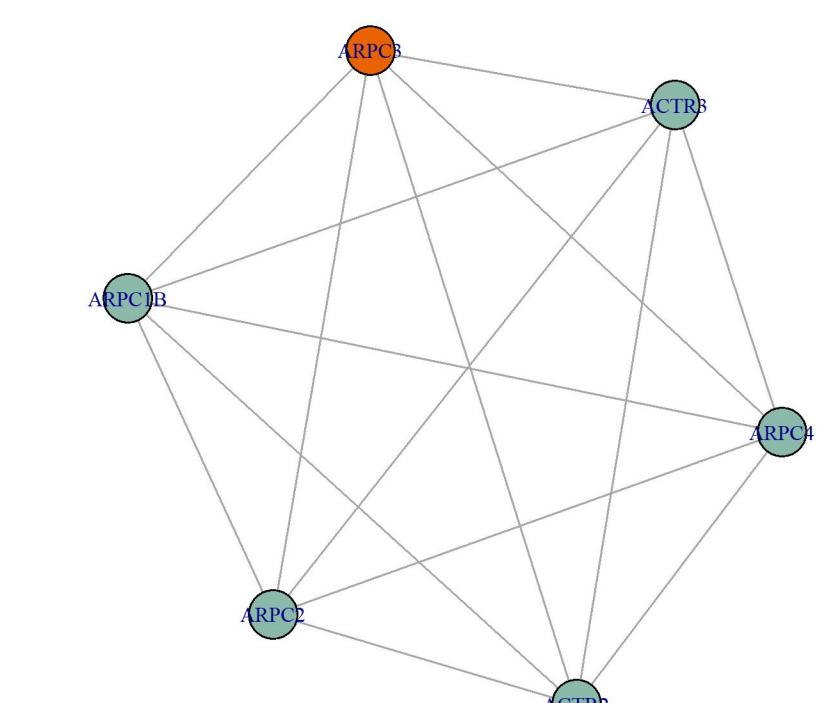
ARPC3 network, DB1, all Pearson $r \geq 0.9$

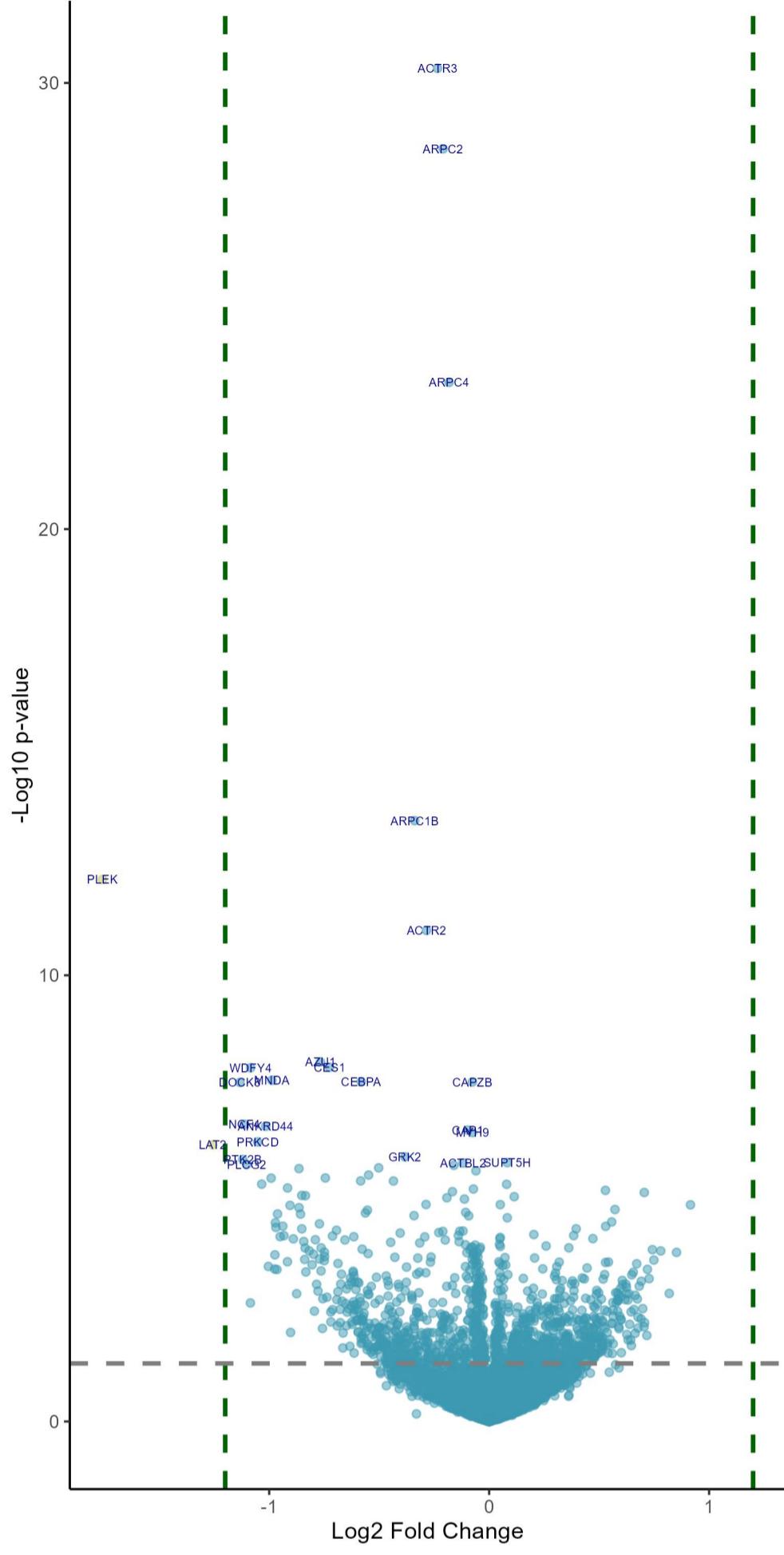


ARPC3 network- DB1, all Pearson r > 0.85



ARPC3 network, DB1, all Pearson $r \geq 0.8$

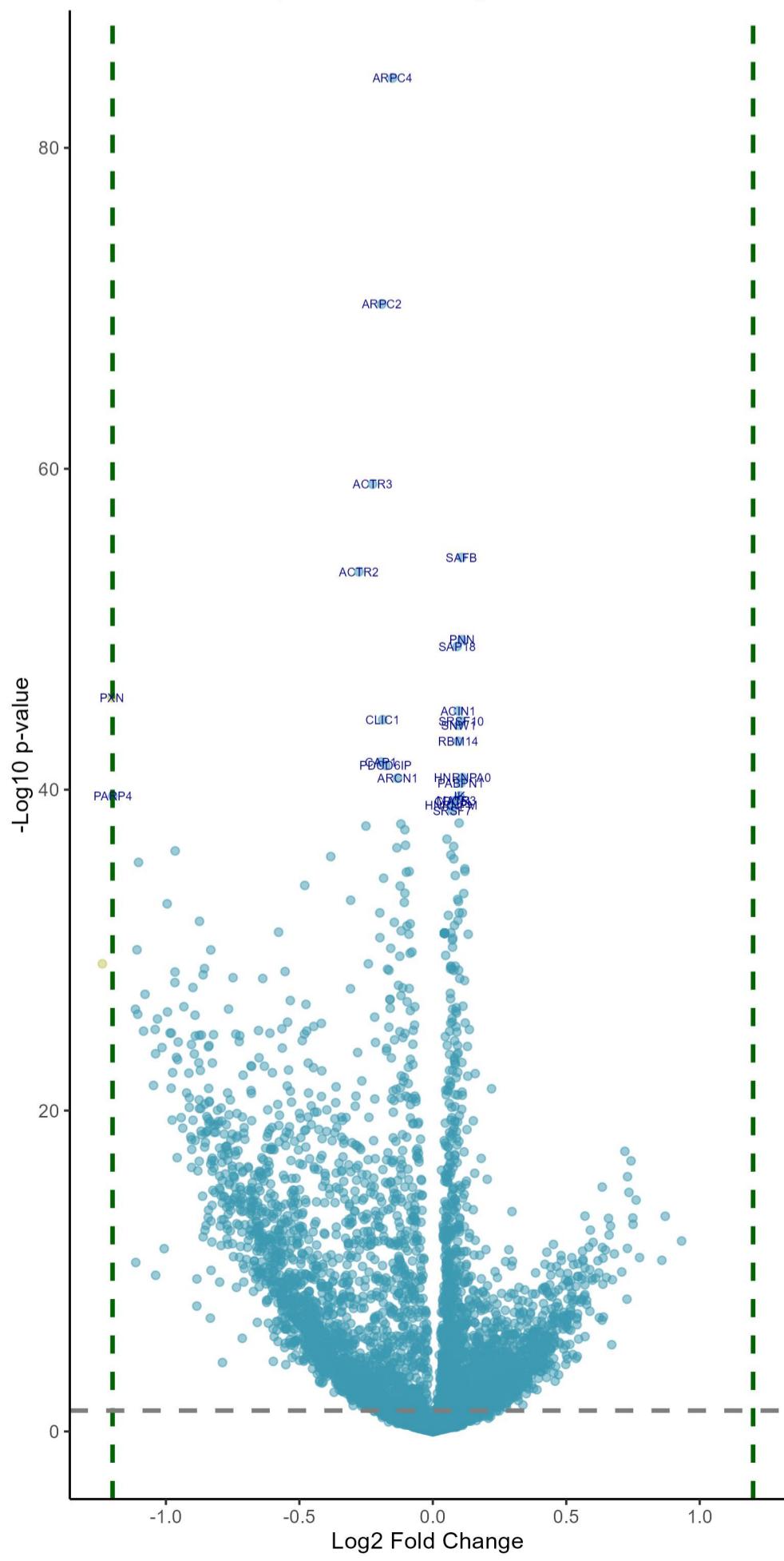




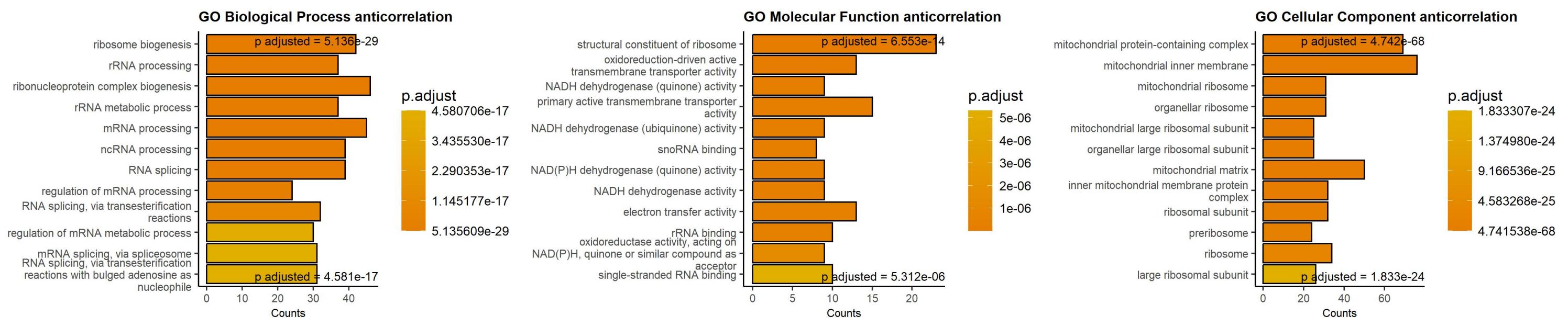
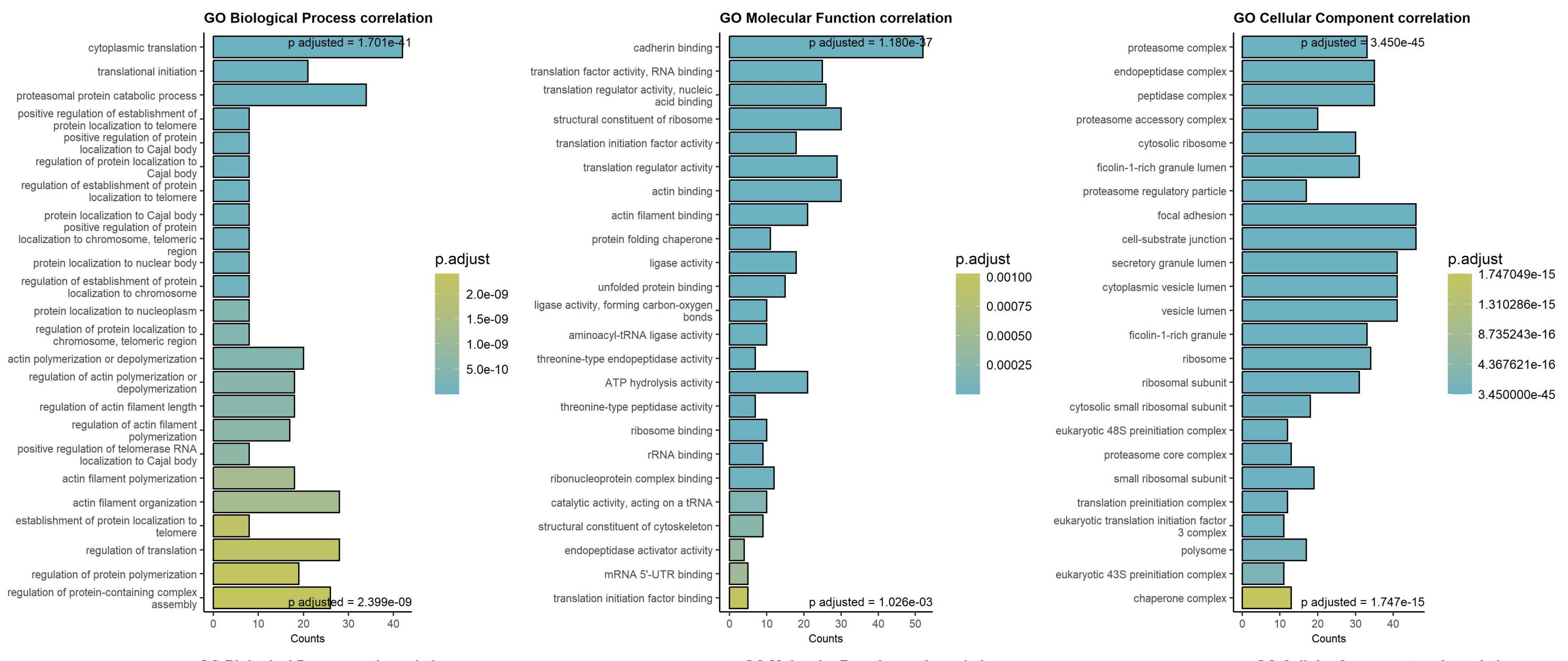
Sorted by p values!

Downregulated in blood cancers at low/absent ARPC3 Upregulated in blood cancers at low/absent ARPC3

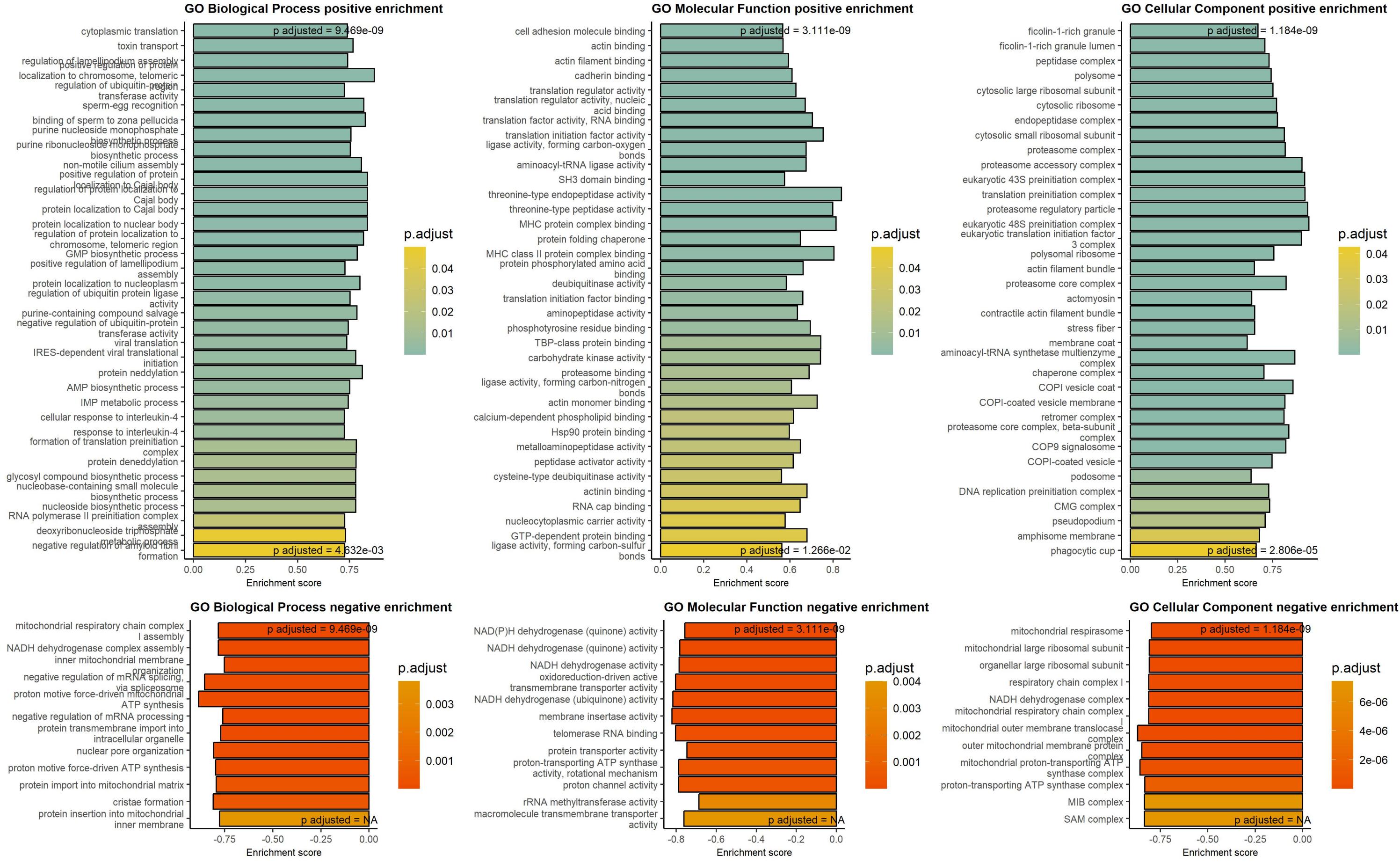
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.23	1.57e-27	ACTR3	actin related protein 3	0.08	4.46e-04	SUPT5H	SPT5 homolog, DSIF elongation facto
-0.21	6.65e-26	ARPC2	actin related protein 2/3 complex s	0.08	8.94e-04	CSTF2	cleavage stimulation factor subunit
-0.18	8.55e-21	ARPC4	actin related protein 2/3 complex s	0.53	1.13e-03	RPL36AL	ribosomal protein L36a like
-0.34	4.56e-11	ARPC1B	actin related protein 2/3 complex s	0.71	1.20e-03	RPL36A	ribosomal protein L36a
-1.76	7.87e-10	PLEK	pleckstrin	0.11	1.38e-03	PAFAH1B3	platelet activating factor acetylhy
-0.28	9.40e-09	ACTR2	actin related protein 2	0.05	1.89e-03	EIF4B	eukaryotic translation initiation f
-0.77	7.26e-06	AZU1	azurocidin 1	0.92	1.89e-03	IGSF8	immunoglobulin superfamily member 8
-0.73	7.86e-06	CES1	carboxylesterase 1	0.57	2.27e-03	SMTN	smoothelin
-1.08	7.86e-06	WDFY4	WDFY family member 4	0.08	3.01e-03	SMARCE1	SWI/SNF related, matrix associated,
-0.99	1.19e-05	MNDA	myeloid cell nuclear differentiatio	0.56	3.67e-03	SUPT4H1	SPT4 homolog, DSIF elongation facto
-0.58	1.19e-05	CEBPA	CCAAT enhancer binding protein alph	0.53	4.33e-03	RBM6	RNA binding motif protein 6
-0.08	1.19e-05	CAPZB	capping actin protein of muscle Z-I	0.4	4.71e-03	P4HTM	prolyl 4-hydroxylase, transmembrane
-1.13	1.19e-05	DOCK8	dedicator of cytokinesis 8	0.2	5.73e-03	PGRMC1	progesterone receptor membrane comp
-1.11	9.66e-05	NCF4	neutrophil cytosolic factor 4	0.38	5.84e-03	RNF2	ring finger protein 2
-1.02	1.00e-04	ANKRD44	ankyrin repeat domain 44	0.05	6.01e-03	ATXN2L	ataxin 2 like
-0.1	1.16e-04	CAP1	cyclase associated actin cytoskelet	0.47	6.24e-03	NDRG3	NDRG family member 3
-0.08	1.24e-04	MYH9	myosin heavy chain 9	0.05	6.24e-03	SON	SON DNA and RNA binding protein
-1.05	1.90e-04	PRKCD	protein kinase C delta	0.05	7.60e-03	HNRNPDL	heterogeneous nuclear ribonucleopro
-1.26	2.10e-04	LAT2	linker for activation of T cells fa	0.26	8.00e-03	SRSF2	serine and arginine rich splicing f
-0.38	3.72e-04	GRK2	G protein-coupled receptor kinase 2	0.05	8.10e-03	PHF5A	PHD finger protein 5A
-1.12	4.07e-04	PTK2B	protein tyrosine kinase 2 beta	0.36	8.25e-03	ZBTB21	zinc finger and BTB domain containi
-0.12	4.46e-04	ACTBL2	actin beta like 2	0.74	8.71e-03	BRD7	bromodomain containing 7
-1.1	4.60e-04	PLCG2	phospholipase C gamma 2	0.78	9.10e-03	MFGE8	milk fat globule EGF and factor V/V
-0.16	4.64e-04	CSK	C-terminal Src kinase	0.85	9.54e-03	ACP2	acid phosphatase 2, lysosomal
-0.5	5.10e-04	RNASE2	ribonuclease A family member 2	0.07	1.12e-02	LSM3	LSM3 homolog, U6 small nuclear RNA
-0.86	5.10e-04	PRTN3	proteinase 3	0.21	1.13e-02	PQBP1	polyglutamine binding protein 1
-0.06	5.52e-04	RPL4	ribosomal protein L4	0.75	1.21e-02	GIPC1	GIPC PDZ domain containing family m
-0.55	6.65e-04	WAS	WASP actin nucleation promoting fac	0.04	1.28e-02	SAFB	scaffold attachment factor B
-0.74	7.31e-04	RMDN1	regulator of microtubule dynamics 1	0.54	1.28e-02	TAF4	TATA-box binding protein associated
-0.99	7.31e-04	SORL1	sortilin related receptor 1	0.32	1.28e-02	FXR2	FMR1 autosomal homolog 2
-0.58	7.98e-04	BST1	bone marrow stromal cell antigen 1	0.53	1.29e-02	PRCC	proline rich mitotic checkpoint con
-0.44	7.98e-04	VCL	vinculin	0.05	1.34e-02	WBP11	WW domain binding protein 11
-1.03	8.94e-04	SH3BP1	SH3 domain binding protein 1	0.67	1.34e-02	MORC2	MORC family CW-type zinc finger 2
-0.92	1.05e-03	RASSF2	Ras association domain family membe	0.08	1.39e-02	ZC3H4	zinc finger CCCH-type containing 4
-0.07	1.08e-03	CLTC	clathrin heavy chain	0.06	1.40e-02	RAE1	ribonucleic acid export 1
-0.17	1.17e-03	IDH1	isocitrate dehydrogenase (NADP(+))	0.31	1.47e-02	LEMD3	LEM domain containing 3
-0.85	1.34e-03	CTSS	cathepsin S	0.45	1.55e-02	GUK1	guanylate kinase 1
-0.84	1.34e-03	TAOK3	TAO kinase 3	0.24	1.61e-02	TMEM9	transmembrane protein 9
0.19	1.42e-03	VASD	vasodilator stimulated phosphoprotein	0.72	1.63e-02	TCE12	transcription factor 12



Top 250 correlation coefficients overrepresentation, ARPC3 protein, DB1



Gene Set Enrichment analysis on protein correlation coefficients, ARPC3 protein, DB1



No information on Ser/Thr kinase phosphorylation sites for ARPC3

No information on Ser/Thr kinase phosphorylation sites for ARPC3

Top 15 positive correlation coefficients for ARPC3 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

