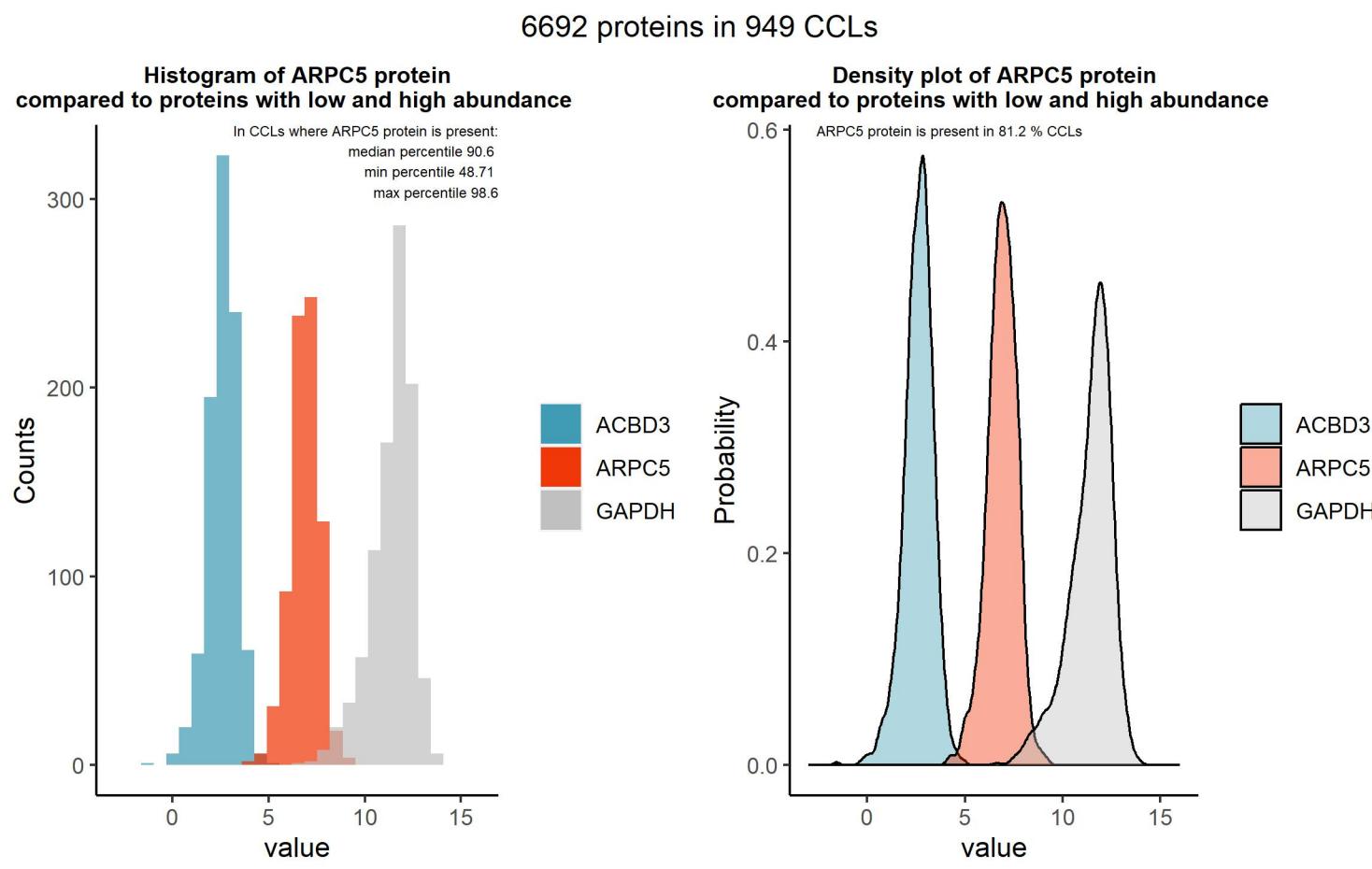


# ARPC5

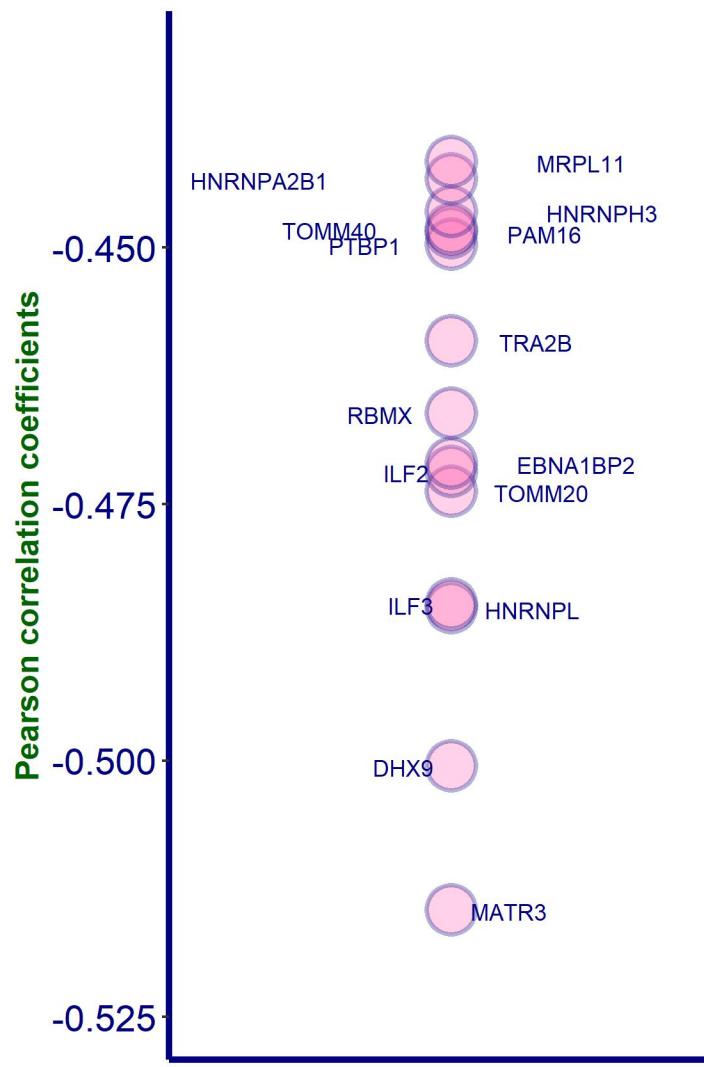
Protein name: ARPC5 ; UNIPROT: O15511 ; Gene name: actin related protein 2/3 complex subunit 5

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

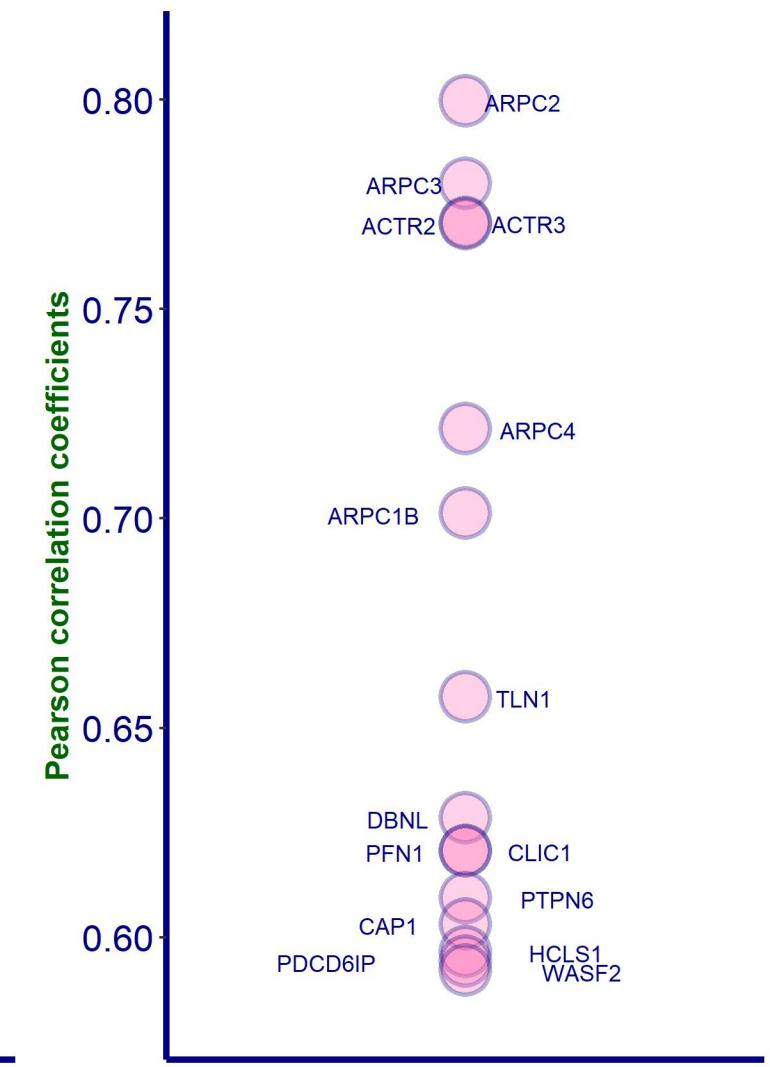
## Sanger Institute Protein Database 1 (DB1), protein presence is certain



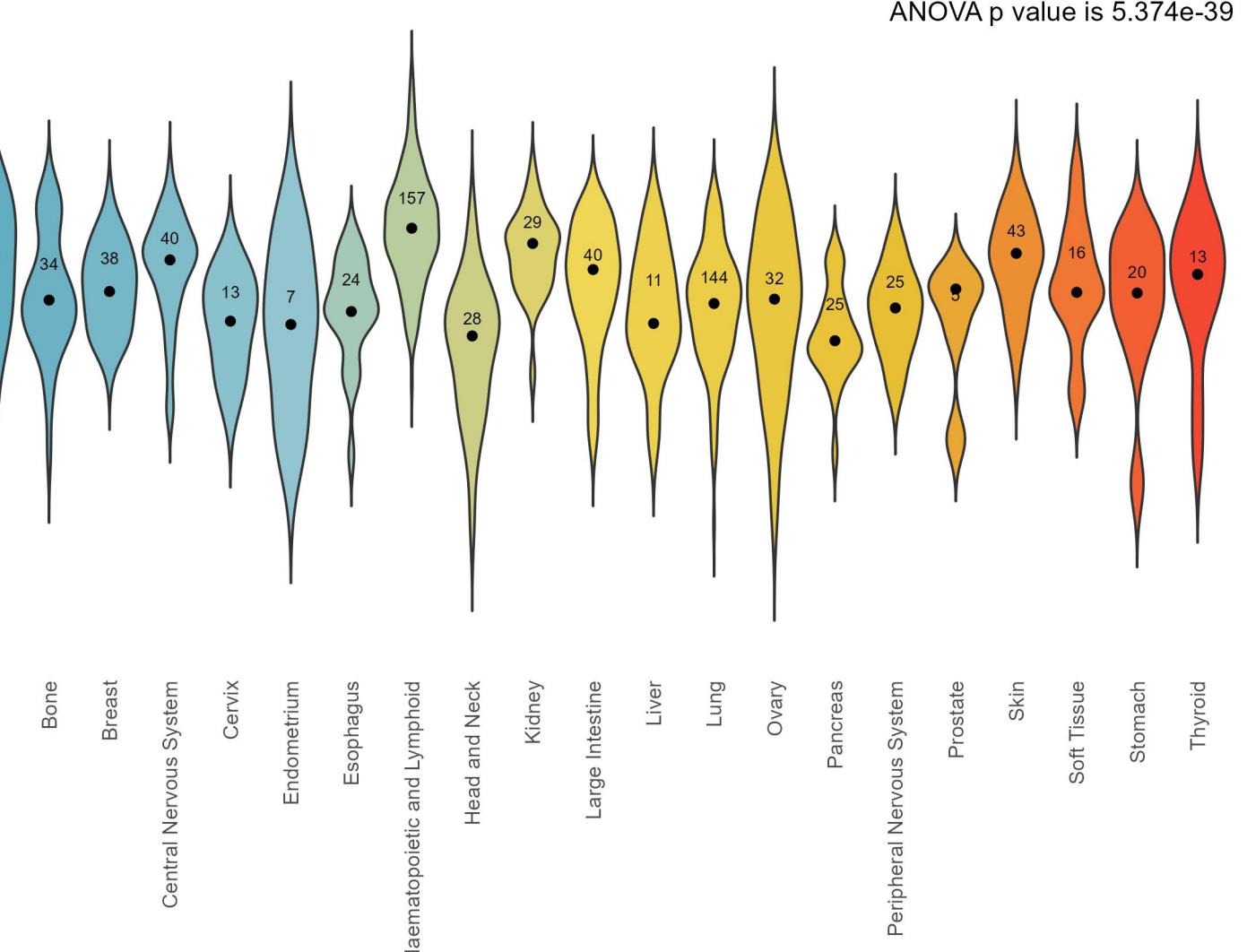
Top negative correlations of ARPC5 protein, DB



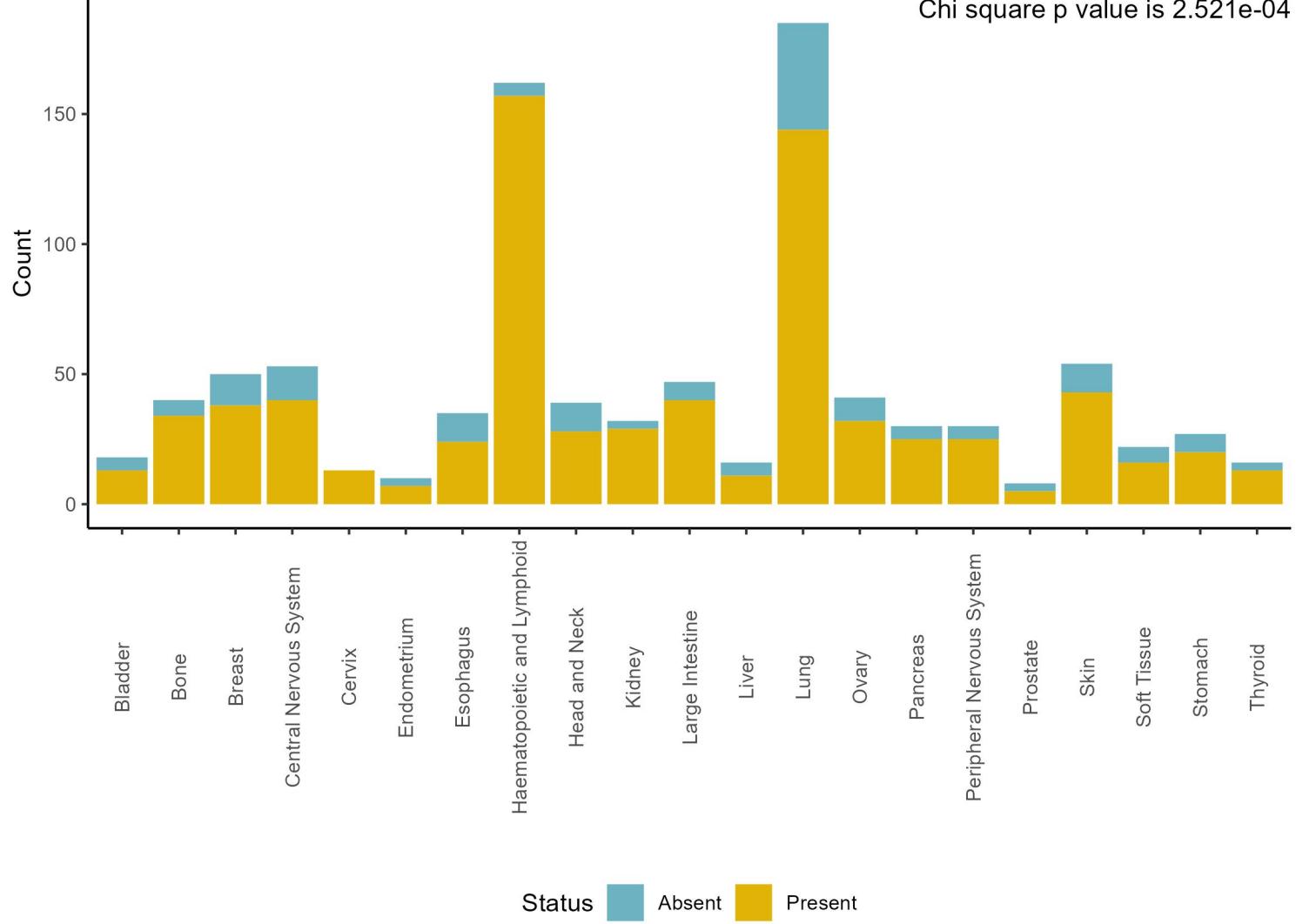
Top positive correlations of ARPC5 protein, DB



## Amount of ARPC5 protein, number of CCLs where it is present by tissue, DB1



## Present and absent ARPC5 protein counts by tissue, DB1

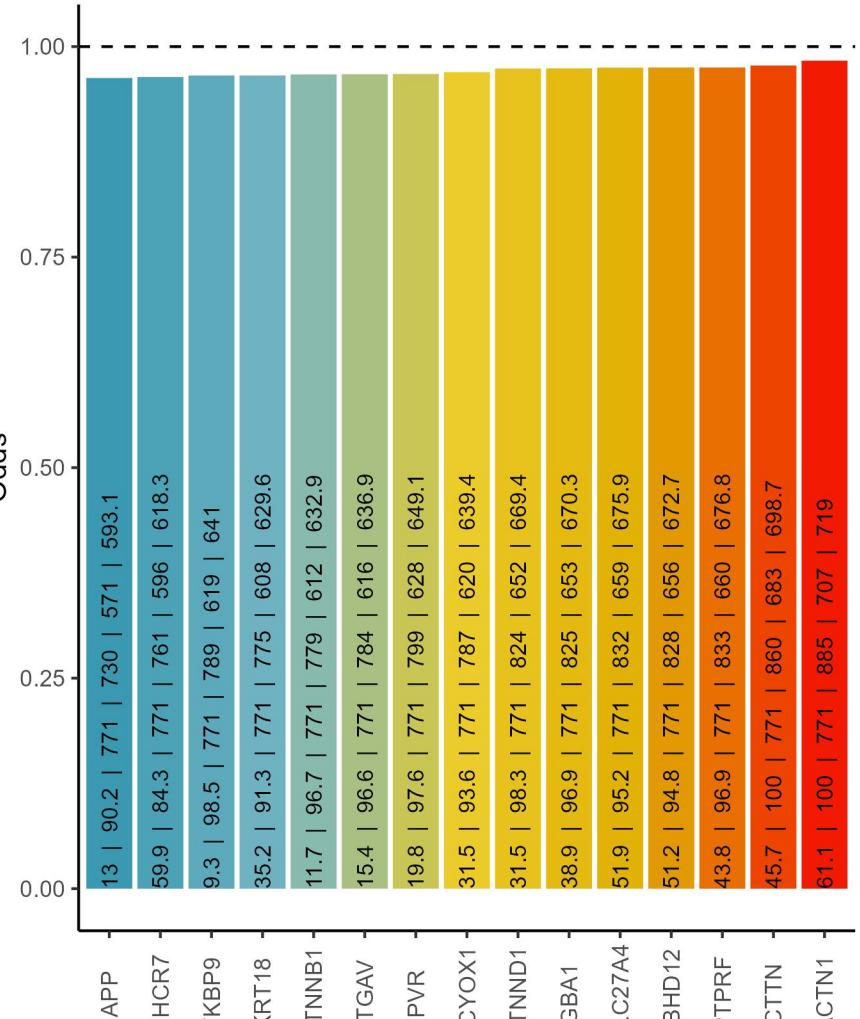


## Cooccurrence with ARPC5 protein, DB1

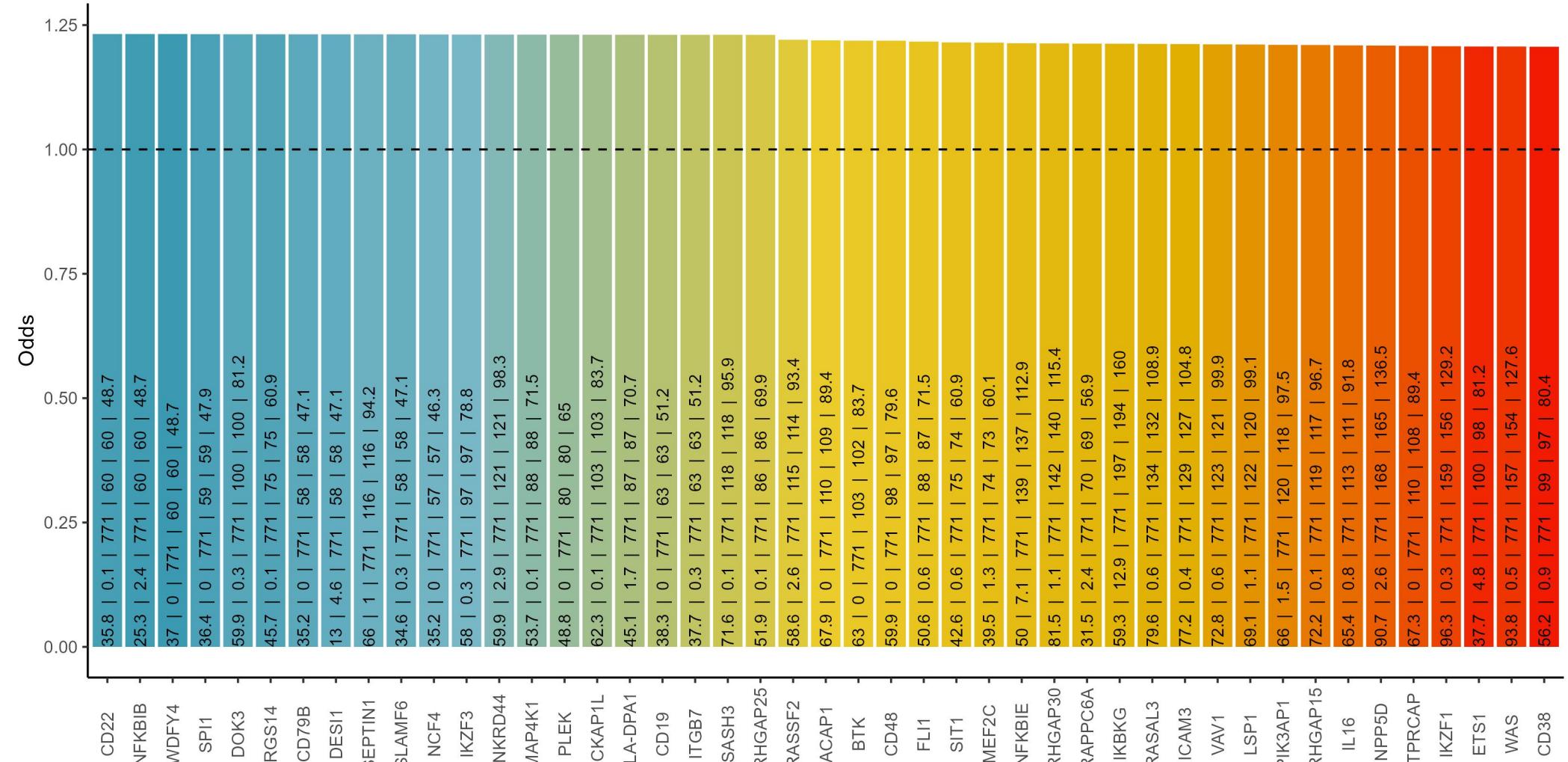
% of ARPC5 in blood cancers: 96.9 ; % of ARPC5 in solid cancers: 77.9

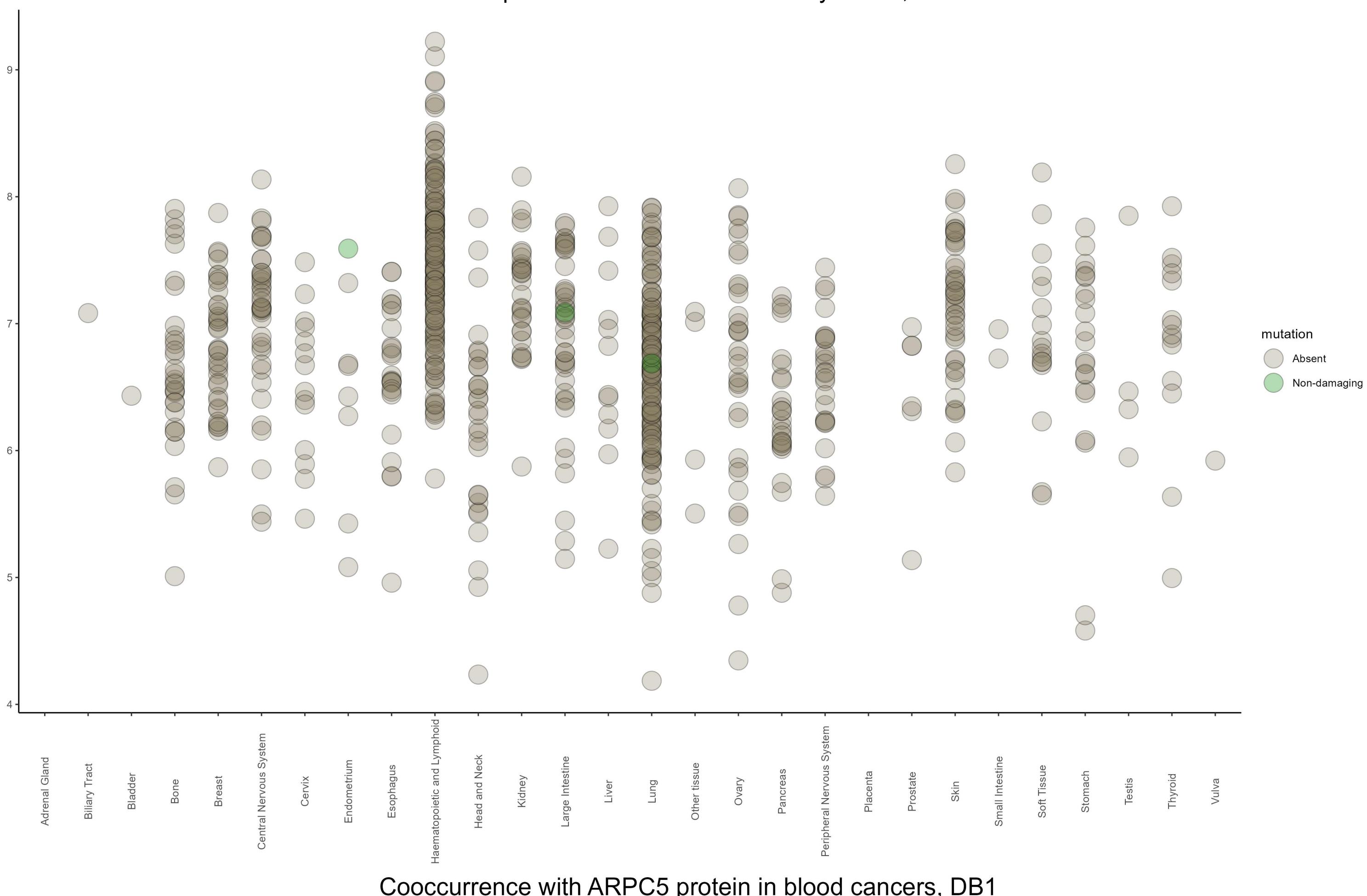
Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ARPC5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

### Negative cooccurrence



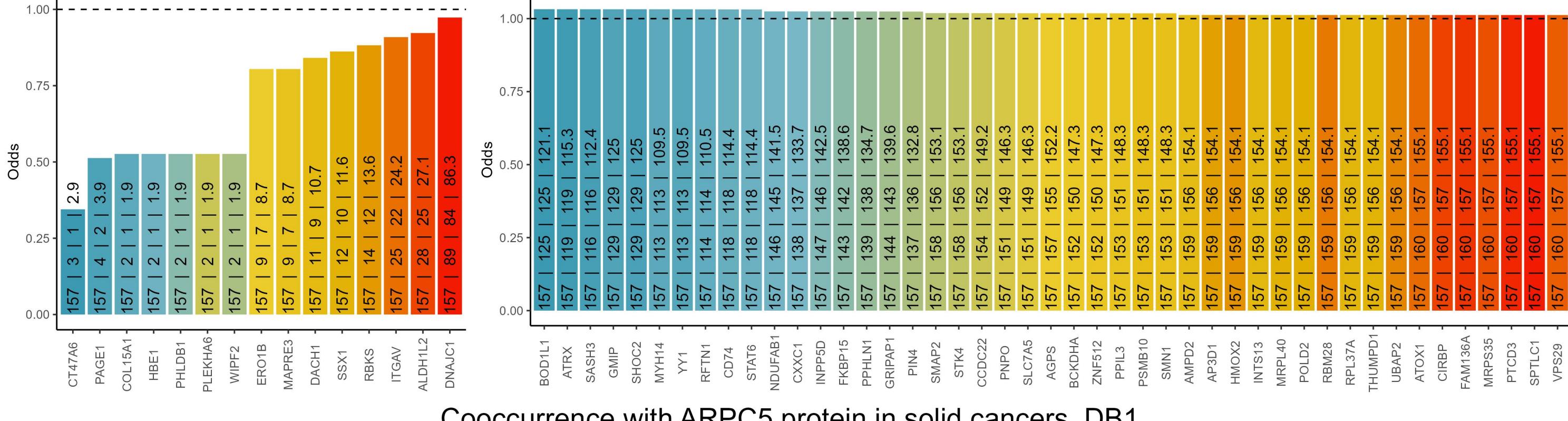
### Positive cooccurrence





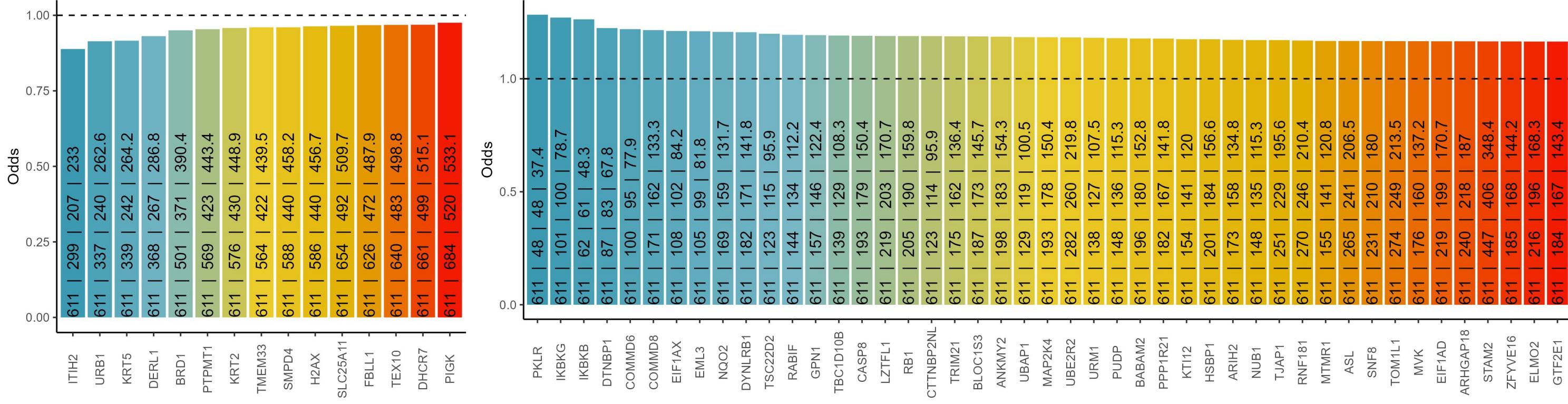
ncidence of ARPC5 | incidence of Protein 2 | observed cooccurrence | e

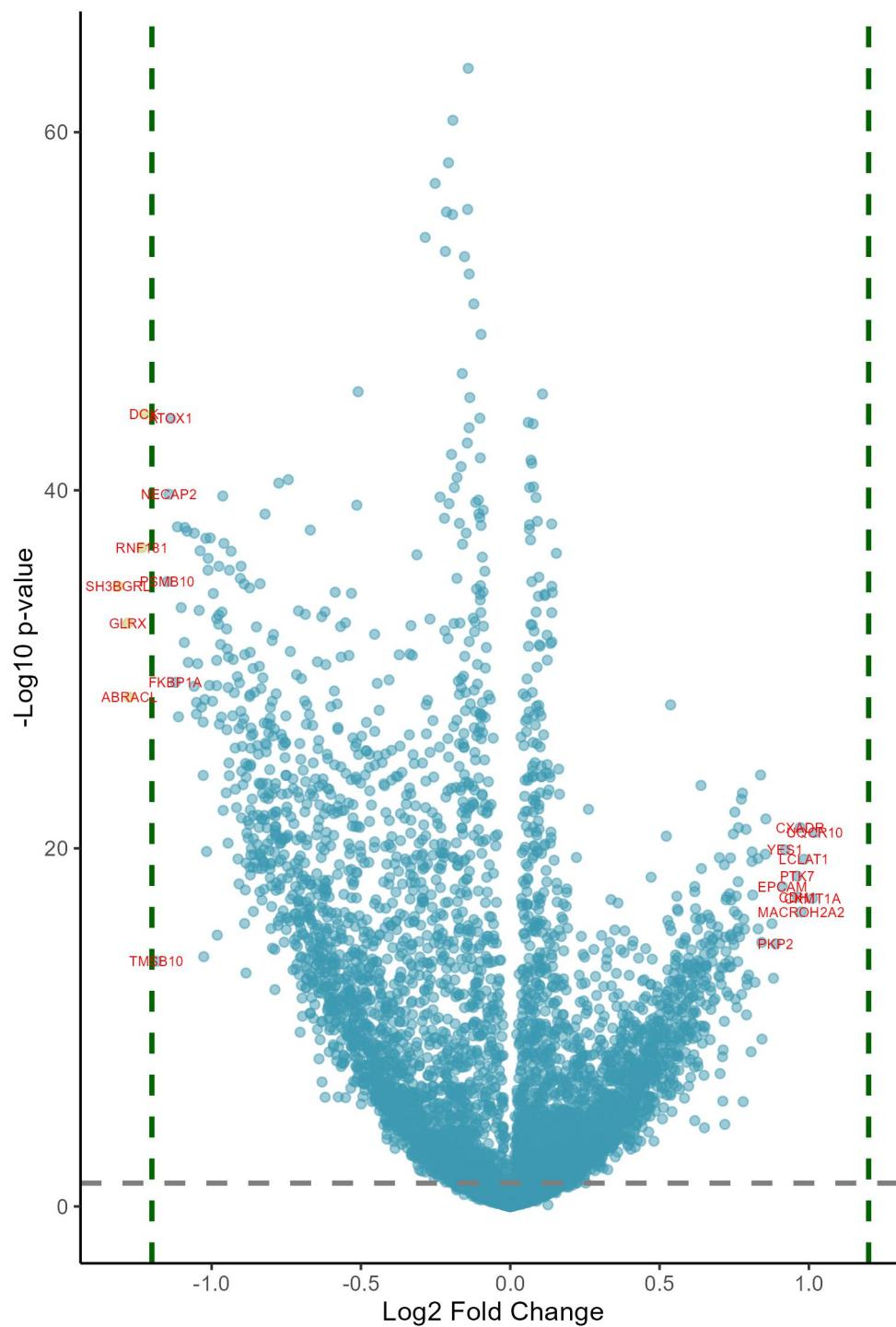
negative cooccurrence Positive cooccurrence



incidence of ARPC5 | incidence of Protein 2 | observed cooccurrence | e

negative cooccurrence Positive cooccurrence

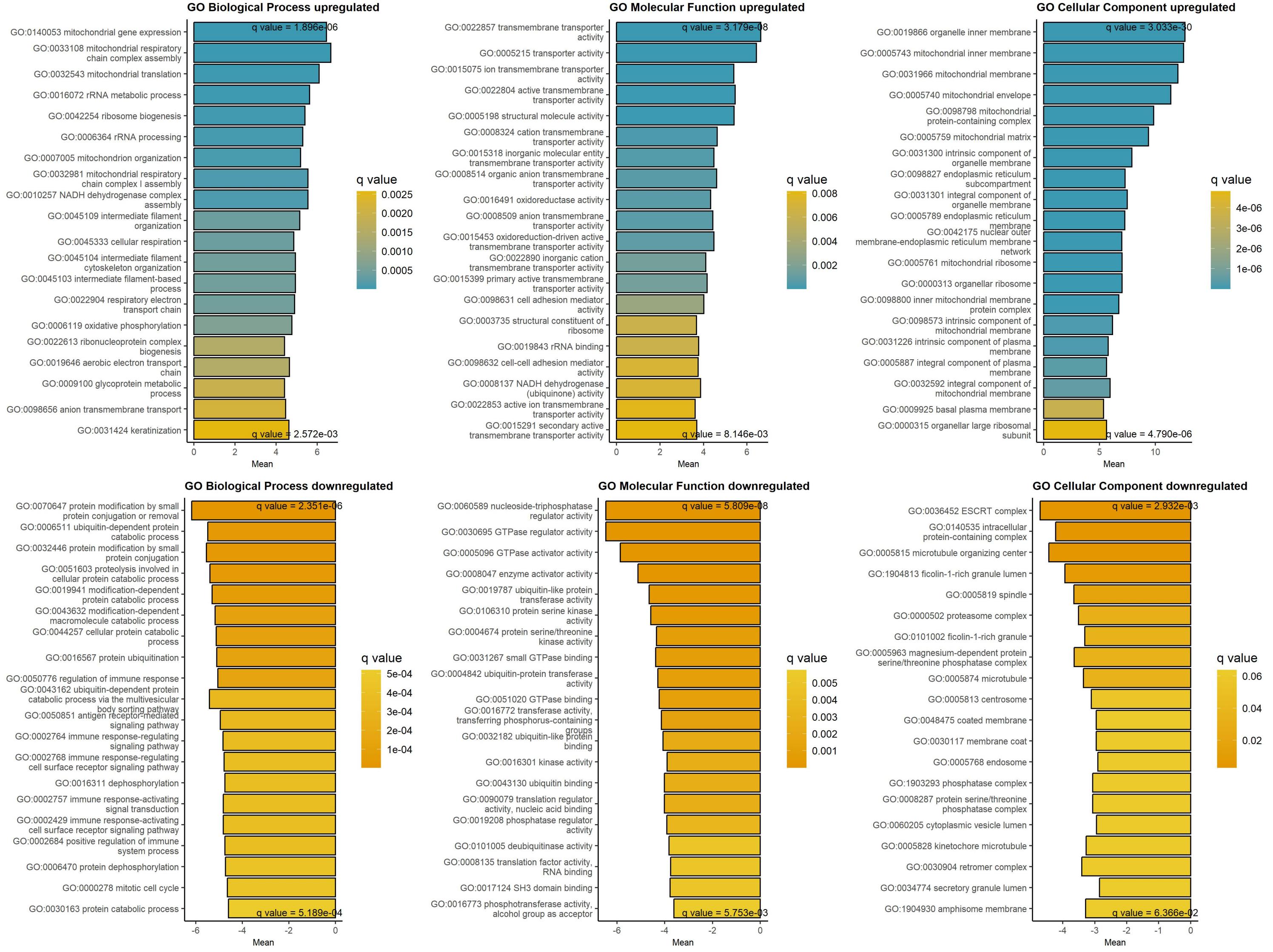


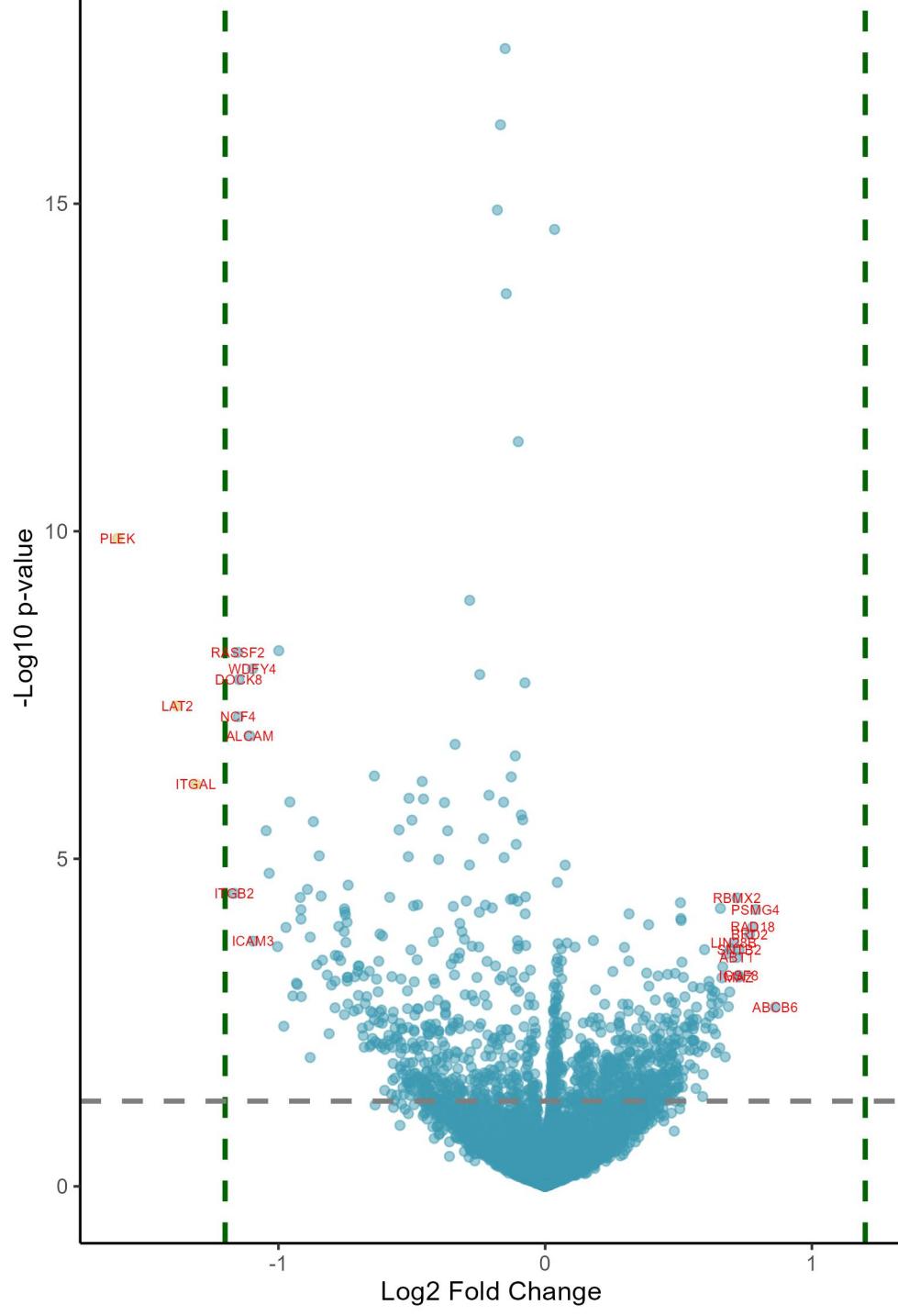


## Downregulated at low/absent ARPC5 Upregulated at low/absent ARPC5

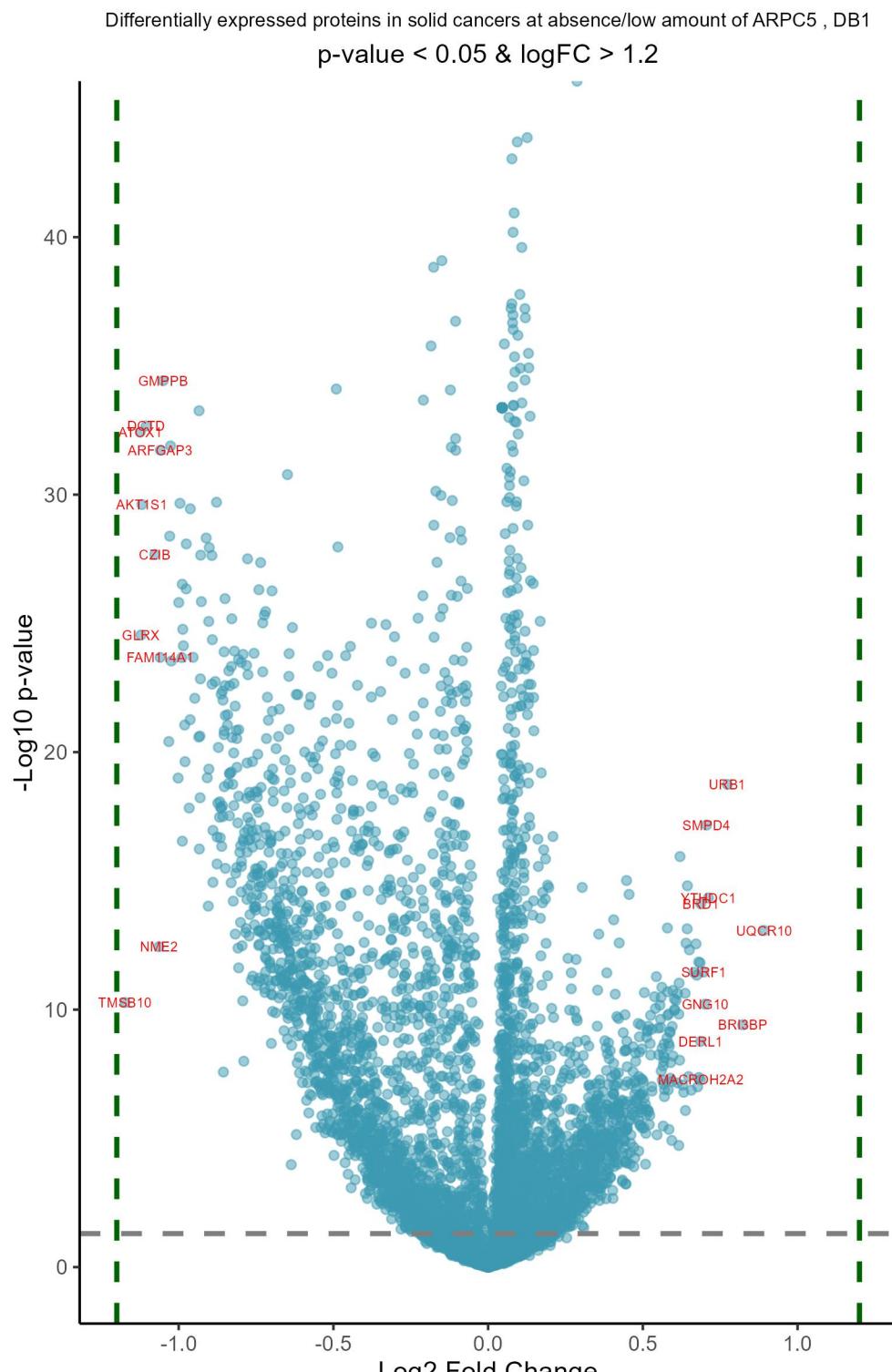
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.31	1.73e-33	SH3BGR1	SH3 domain binding glutamate rich p	1.02	1.58e-20	UQCRC10	ubiquinol-cytochrome c reductase, c
-1.28	1.51e-31	GLRX	glutaredoxin	1.01	5.10e-17	CKMT1A	creatine kinase, mitochondrial 1A
-1.28	1.20e-27	ABRACL	ABRA C-terminal like	0.98	4.13e-19	LCLAT1	lysocardiolipin acyltransferase 1
-1.23	1.58e-35	RNF181	ring finger protein 181	0.97	2.74e-16	MACROH2A2	macroH2A2 histone
-1.23	1.94e-42	DCK	deoxycytidine kinase	0.97	8.69e-21	CXADR	CXADR Ig-like cell adhesion molecule
-1.18	1.15e-13	TMSB10	thymosin beta 10	0.96	4.41e-17	CDH1	cadherin 1
-1.15	1.01e-33	PSMB10	proteasome 20S subunit beta 10	0.96	3.29e-18	PTK7	protein tyrosine kinase 7 (inactive)
-1.14	2.98e-38	NECAP2	NECAP endocytosis associated 2	0.92	1.32e-19	YES1	YES proto-oncogene 1, Src family ty
-1.14	3.04e-42	ATOX1	antioxidant 1 copper chaperone	0.91	1.19e-17	EPCAM	epithelial cell adhesion molecule
-1.12	2.02e-28	FKBP1A	FKBP prolyl isomerase 1A	0.89	1.35e-14	PKP2	plakophilin 2
-1.11	1.33e-36	CZIB	CXXC motif containing zinc binding	0.88	9.19e-13	JUP	junction plakoglobin
-1.11	1.28e-26	GBE1	1,4-alpha-glucan branching enzyme 1	0.88	1.15e-15	SPINT1	serine peptidase inhibitor, Kunitz
-1.1	2.36e-32	WIPF1	WAS/WASL interacting protein family	0.86	2.99e-21	GRPEL2	GrpE like 2, mitochondrial
-1.09	1.54e-30	ABHD14B	abhydrolase domain containing 14B	0.85	2.24e-19	SURF1	SURF1 cytochrome c oxidase assembly
-1.09	1.43e-36	DCTD	dCMP deaminase	0.84	1.61e-09	NDUFB11	NADH:ubiquinone oxidoreductase subu
-1.08	2.17e-36	PCYT2	phosphate cytidylyltransferase 2, e	0.84	1.14e-14	BCAM	basal cell adhesion molecule (Luthe
-1.08	1.72e-29	UBE2L6	ubiquitin conjugating enzyme E2 L6	0.84	1.50e-23	MFN1	mitofusin 1
-1.06	3.23e-28	RPE	ribulose-5-phosphate-3-epimerase	0.83	2.19e-15	MTCH1	mitochondrial carrier 1
-1.06	2.70e-36	RABEP2	rabaptin, RAB GTPase binding effect	0.83	3.79e-19	ATPAF1	ATP synthase mitochondrial F1 compl
-1.05	9.26e-27	PSMB8	proteasome 20S subunit beta 8	0.82	1.51e-12	PKP3	plakophilin 3
-1.05	2.27e-27	PPP6R1	protein phosphatase 6 regulatory su	0.81	3.37e-17	ESRP1	epithelial splicing regulatory prot
-1.05	2.01e-29	CASP7	caspase 7	0.81	1.70e-19	LRRC8A	leucine rich repeat containing 8 VR
-1.04	3.34e-32	PIN1	peptidylprolyl cis/trans isomerase,	0.81	5.35e-19	TMTC3	transmembrane O-mannosyltransferase
-1.04	2.35e-35	STK10	serine/threonine kinase 10	0.81	7.74e-09	H1-0	H1.0 linker histone
-1.03	3.92e-27	SH3KBP1	SH3 domain containing kinase bindin	0.8	6.11e-13	EPPK1	epiplakin 1
-1.03	2.40e-26	STK4	serine/threonine kinase 4	0.79	2.04e-12	TACSTD2	tumor associated calcium signal tra
-1.03	1.56e-23	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.79	1.01e-12	KRT5	keratin 5
-1.03	6.61e-14	NME2	NME/NM23 nucleoside diphosphate kin	0.79	8.22e-11	KRT17	keratin 17
-1.02	1.60e-27	CORO7	coronin 7	0.79	1.08e-20	MRPS10	mitochondrial ribosomal protein S10

## GAGE analysis on upregulated and downregulated proteins at low/absent ARPC5 protein, DB1



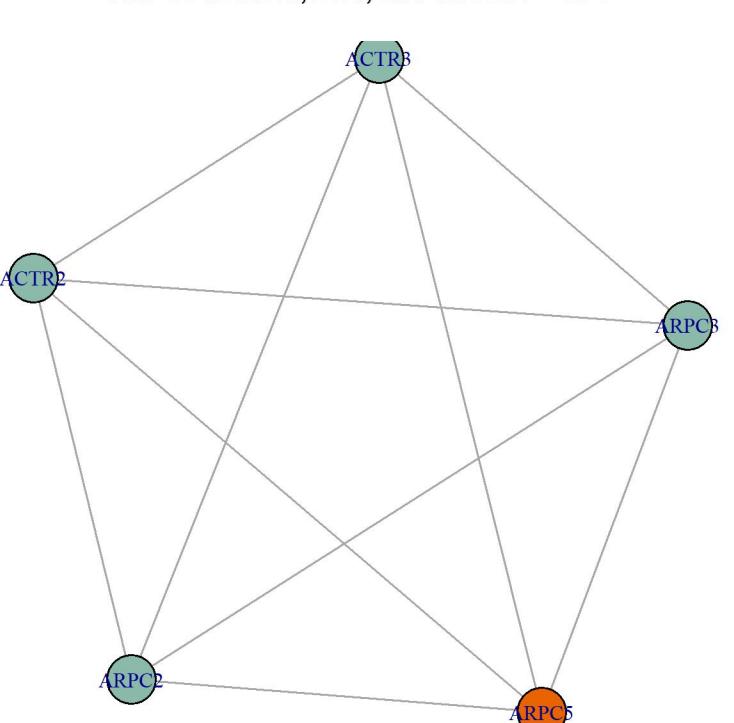


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.6	1.22e-07	PLEK	pleckstrin	0.86	5.36e-02	ABCB6	ATP binding cassette subfamily B me
-1.38	2.06e-05	LAT2	linker for activation of T cells fa	0.79	5.75e-03	PSMG4	proteasome assembly chaperone 4
-1.31	2.01e-04	ITGAL	integrin subunit alpha L	0.78	8.93e-03	RAD18	RAD18 E3 ubiquitin protein ligase
-1.17	4.49e-03	ITGB2	integrin subunit beta 2	0.77	1.08e-02	BRD2	bromodomain containing 2
-1.15	4.69e-06	RASSF2	Ras association domain family membe	0.73	1.46e-02	SNTB2	syntrophin beta 2
-1.15	2.82e-05	NCF4	neutrophil cytosolic factor 4	0.73	2.71e-02	MAZ	MYC associated zinc finger protein
-1.15	9.39e-06	DOCK8	dedicator of cytokinesis 8	0.73	2.71e-02	IGSF8	immunoglobulin superfamily member 8
-1.11	5.19e-05	ALCAM	activated leukocyte cell adhesion m	0.72	4.77e-03	RBMX2	RNA binding motif protein X-linked
-1.1	7.65e-06	WDFY4	WDFY family member 4	0.72	1.83e-02	ABT1	activator of basal transcription 1
-1.1	1.28e-02	ICAM3	intercellular adhesion molecule 3	0.71	1.30e-02	LIN28B	lin-28 homolog B
-1.05	6.71e-04	SH3BP1	SH3 domain binding protein 1	0.69	1.45e-02	UAP1	UDP-N-acetylglucosamine pyrophospho
-1.03	2.40e-03	GCA	grancalcin	0.69	3.79e-02	AIDA	axin interactor, dorsalization asso
-1	1.41e-02	CTSZ	cathepsin Z	0.69	5.34e-02	MSI2	musashi RNA binding protein 2
-1	4.69e-06	MNDA	myeloid cell nuclear differentiatio	0.68	1.66e-02	CHD1	chromodomain helicase DNA binding p
-0.98	7.91e-02	COTL1	coactosin like F-actin binding prot	0.68	1.40e-01	RABIF	RAB interacting factor
-0.97	8.95e-03	RNASET2	ribonuclease T2	0.67	2.20e-02	SORT1	sortilin 1
-0.96	3.07e-04	ANKRD44	ankyrin repeat domain 44	0.66	4.39e-02	MFGE8	milk fat globule EGF and factor V/V
-0.95	4.21e-02	CD44	CD44 molecule (Indian blood group)	0.66	2.72e-02	TDRKH	tudor and KH domain containing
-0.93	3.07e-02	VAMP8	vesicle associated membrane protein	0.66	5.75e-03	SUN1	Sad1 and UNC84 domain containing 1
-0.93	3.19e-02	BASP1	brain abundant membrane attached si	0.65	1.17e-01	ISYNA1	inositol-3-phosphate synthase 1
-0.92	4.77e-03	EVL	Enah/Vasp-like	0.65	4.97e-02	GIPC1	GIPC PDZ domain containing family m
-0.92	5.75e-03	PLCG2	phospholipase C gamma 2	0.65	6.06e-02	MAP1A	microtubule associated protein 1A
-0.92	7.29e-03	PTK2B	protein tyrosine kinase 2 beta	0.64	1.29e-01	MYH10	myosin heavy chain 10
-0.91	4.24e-02	PTPN6	protein tyrosine phosphatase non-re	0.64	8.95e-02	ACP2	acid phosphatase 2, lysosomal
-0.89	3.98e-03	PRKCD	protein kinase C delta	0.64	3.79e-02	BRD7	bromodomain containing 7
-0.88	1.41e-01	LSP1	lymphocyte specific protein 1	0.63	5.99e-02	RPP25L	ribonuclease P/MRP subunit p25 like
-0.88	1.16e-02	TRIM22	tripartite motif containing 22	0.63	8.11e-02	TRMT61A	tRNA methyltransferase 61A
-0.87	5.30e-04	SH3KBP1	SH3 domain containing kinase bindin	0.63	3.70e-02	PRKAR1B	protein kinase cAMP-dependent type
-0.86	2.10e-02	PYCARD	PYD and CARD domain containing	0.63	4.24e-02	UTP25	UTP25 small subunit processome comp

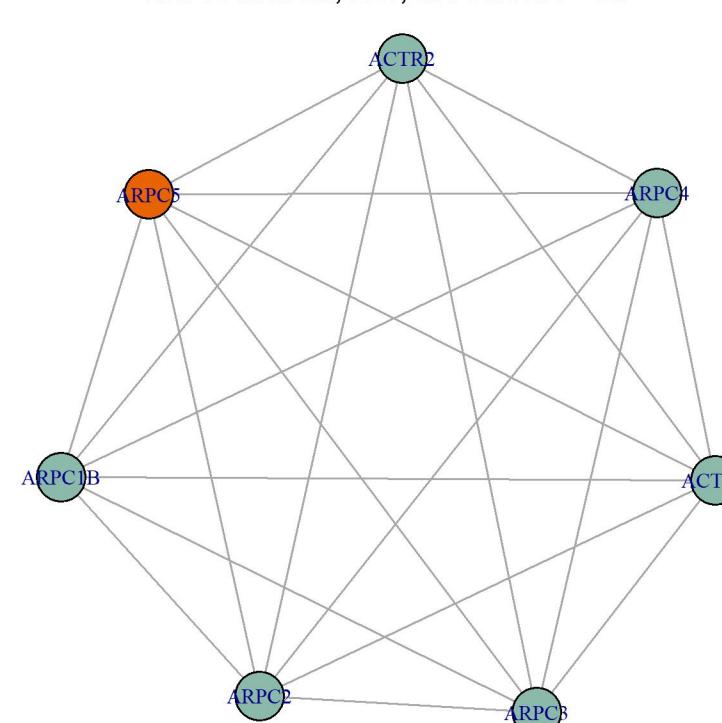


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.17	2.96e-10	TMSB10	thymosin beta 10	0.89	6.75e-13	UQCR10	ubiquinol-cytochrome c reductase, c
-1.12	2.01e-31	ATOX1	antioxidant 1 copper chaperone	0.82	1.96e-09	BRI3BP	BRI3 binding protein
-1.12	8.91e-24	GLRX	glutaredoxin	0.77	2.83e-18	URB1	URB1 ribosome biogenesis homolog
-1.12	1.10e-28	AKT1S1	AKT1 substrate 1	0.71	4.30e-14	YTHDC1	YTH domain containing 1
-1.11	1.17e-31	DCTD	dCMP deaminase	0.71	9.09e-17	SMPD4	sphingomyelin phosphodiesterase 4
-1.08	8.59e-27	CZIB	CXXC motif containing zinc binding	0.7	3.39e-10	GNG10	G protein subunit gamma 10
-1.06	2.65e-12	NME2	NME/NM23 nucleoside diphosphate kin	0.7	2.28e-11	SURF1	SURF1 cytochrome c oxidase assembly
-1.06	5.97e-23	FAM114A1	family with sequence similarity 114	0.69	7.11e-14	BRD1	bromodomain containing 1
-1.06	9.70e-31	ARFGAP3	ADP ribosylation factor GTPase acti	0.69	2.07e-07	MACROH2A2	macroH2A.2 histone
-1.05	8.63e-33	GMPPB	GDP-mannose pyrophosphorylase B	0.69	8.04e-09	DERL1	derlin 1
-1.03	7.41e-20	FKBP1A	FKBP prolyl isomerase 1A	0.69	1.05e-11	RRP36	ribosomal RNA processing 36
-1.03	1.78e-27	DCK	deoxyctydine kinase	0.68	1.71e-07	KRT5	keratin 5
-1.03	6.74e-31	PXN	paxillin	0.68	9.67e-12	TMEM209	transmembrane protein 209
-1.02	8.08e-23	PIN1	peptidylprolyl cis/trans isomerase,	0.68	3.77e-07	CDH1	cadherin 1
-1	1.65e-18	GBE1	1,4-alpha-glucan branching enzyme 1	0.67	2.97e-11	TMEM33	transmembrane protein 33
-1	5.42e-25	PCYT2	phosphate cytidylyltransferase 2, e	0.67	2.09e-12	MRPS10	mitochondrial ribosomal protein S10
-1	9.97e-29	AAK1	AP2 associated kinase 1	0.67	2.35e-11	PHF2	PHD finger protein 2
-0.99	5.99e-23	PMM2	phosphomannomutase 2	0.66	5.01e-07	GNG5	G protein subunit gamma 5
-0.99	1.13e-25	FAM114A2	family with sequence similarity 114	0.65	3.47e-12	CWC22	CWC22 spliceosome associated protei
-0.99	3.52e-16	ABRACL	ABRA C-terminal like	0.65	1.59e-07	LCLAT1	lysocardiolipin acyltransferase 1
-0.99	5.38e-24	WASL	WASP like actin nucleation promotin	0.64	1.56e-14	DDX31	DEAD-box helicase 31
-0.98	2.24e-23	NECAP2	NECAP endocytosis associated 2	0.64	5.83e-13	SLC16A1	solute carrier family 16 member 1
-0.98	1.81e-20	ABHD14B	abhydrolase domain containing 14B	0.64	1.97e-12	NCPBP2AS2	NCPBP2 antisense 2 (head to head)
-0.98	4.15e-19	SH3BGRL	SH3 domain binding glutamate rich p	0.64	2.76e-06	CKMT1A	creatine kinase, mitochondrial 1A
-0.98	1.69e-25	STAM2	signal transducing adaptor molecule	0.64	1.36e-10	ABCB7	ATP binding cassette subfamily B me
-0.98	3.45e-27	HOOK3	hook microtubule tethering protein	0.63	5.96e-07	SPINT1	serine peptidase inhibitor, Kunitz
-0.97	2.12e-17	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.63	3.29e-07	EPCAM	epithelial cell adhesion molecule
-0.96	1.15e-20	RNF181	ring finger protein 181	0.62	1.28e-15	TEX10	testis expressed 10
-0.96	1.59e-28	LPP	LIM domain containing preferred tra	0.62	3.92e-08	ESRP1	epithelial splicing regulatory prot

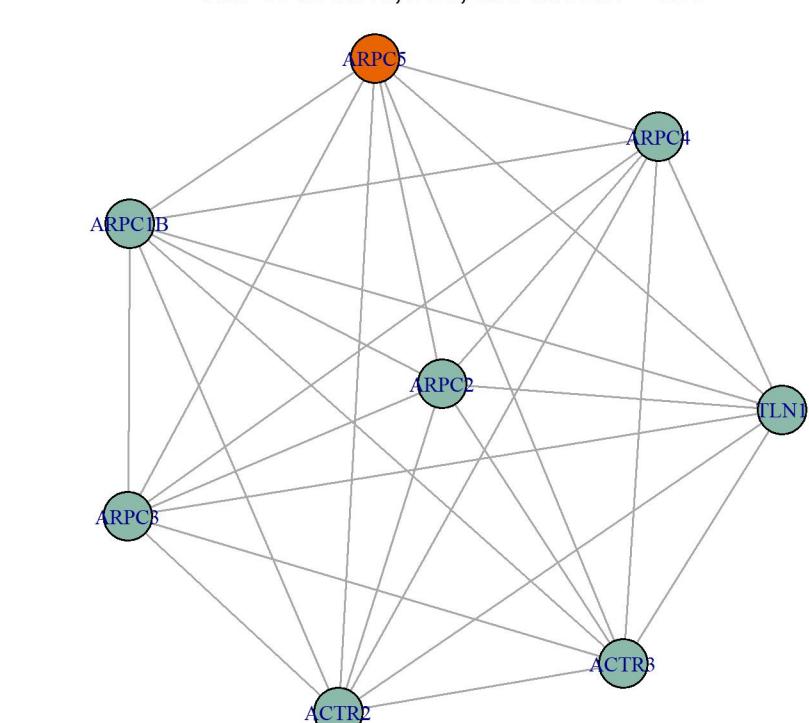
ARPC5 network, DB1, all Pearson r &gt; 0.75

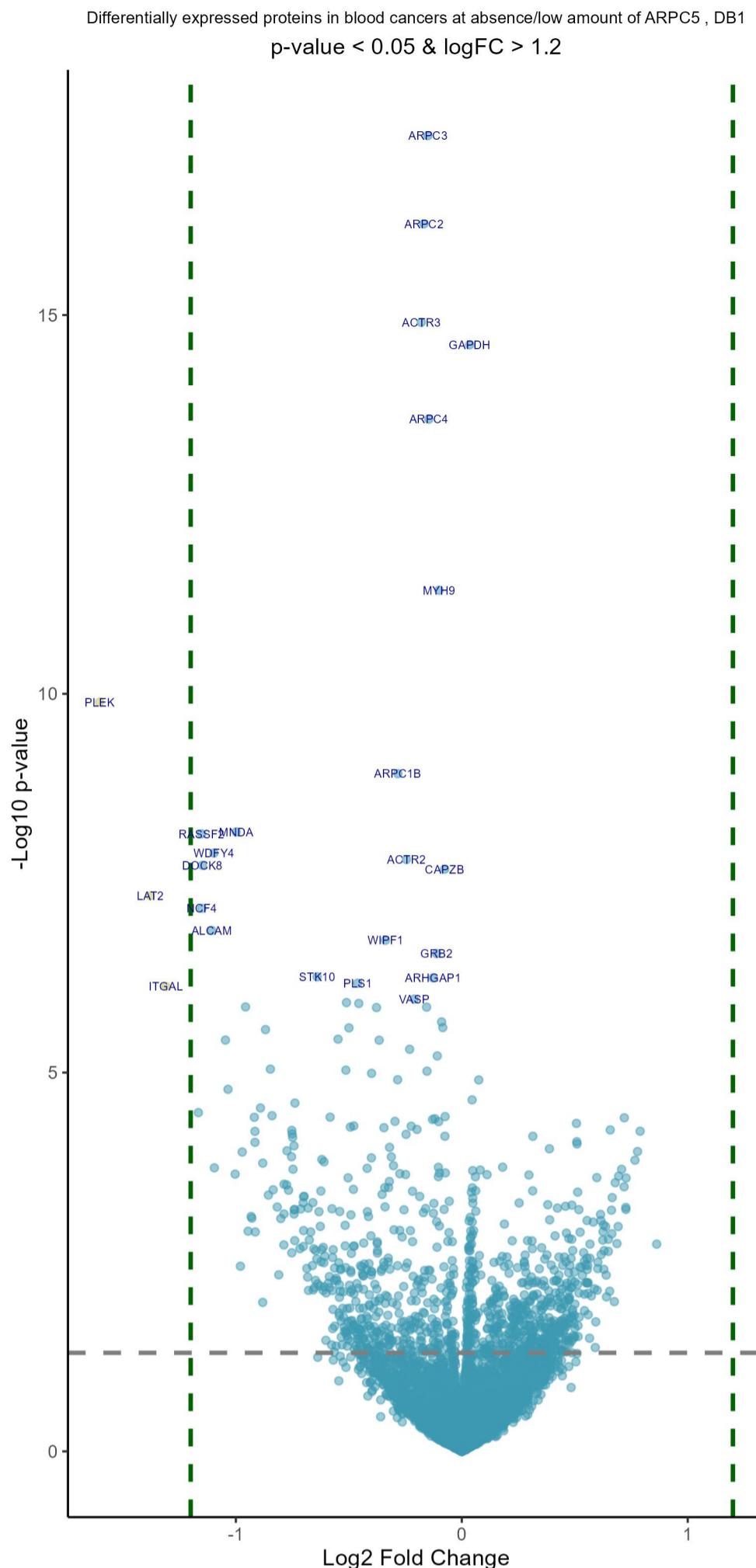


ARPC5 network, DB1, all Pearson r &gt; 0.7

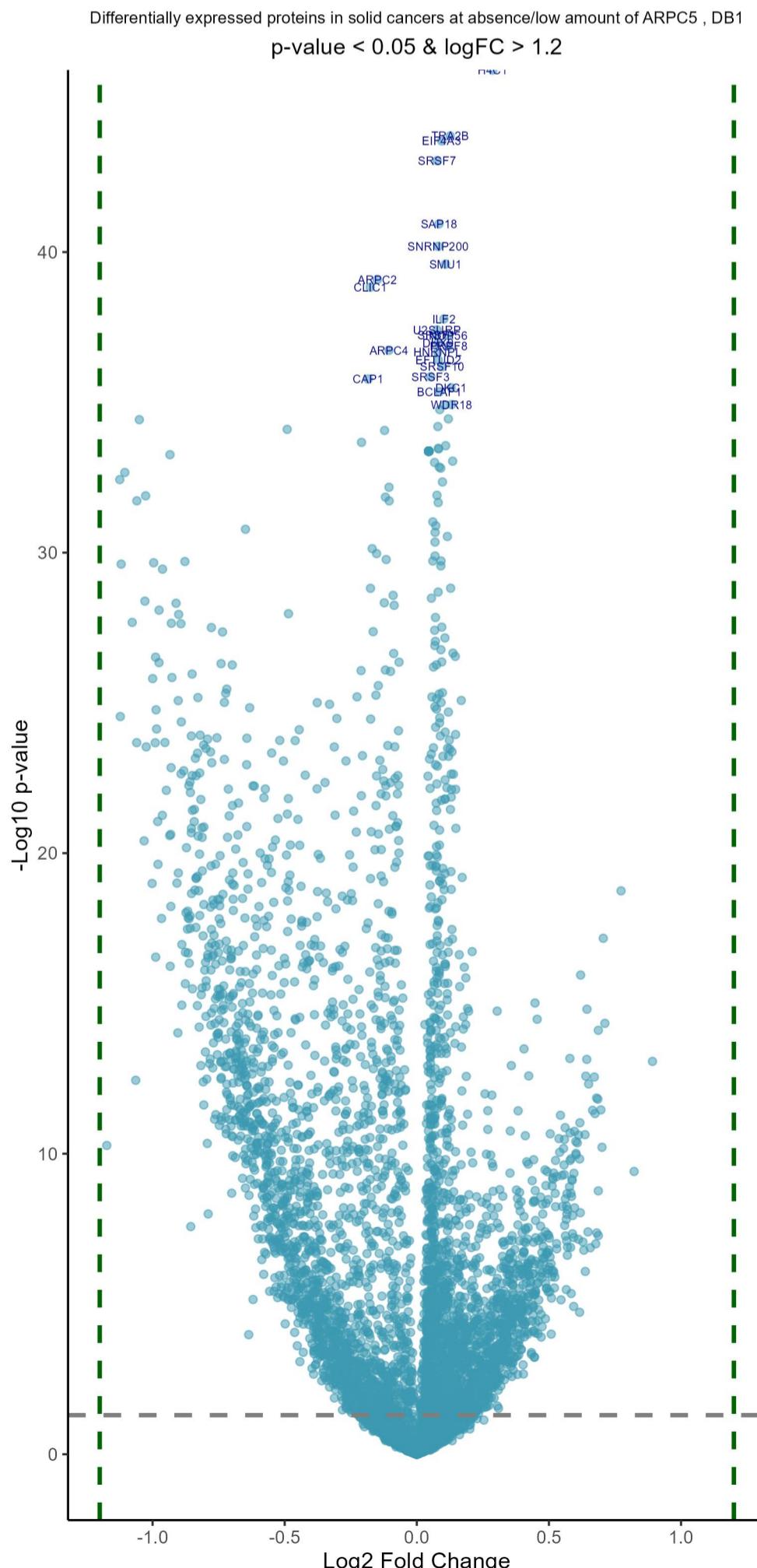


ARPC5 network, DB1, all Pearson r &gt; 0.65



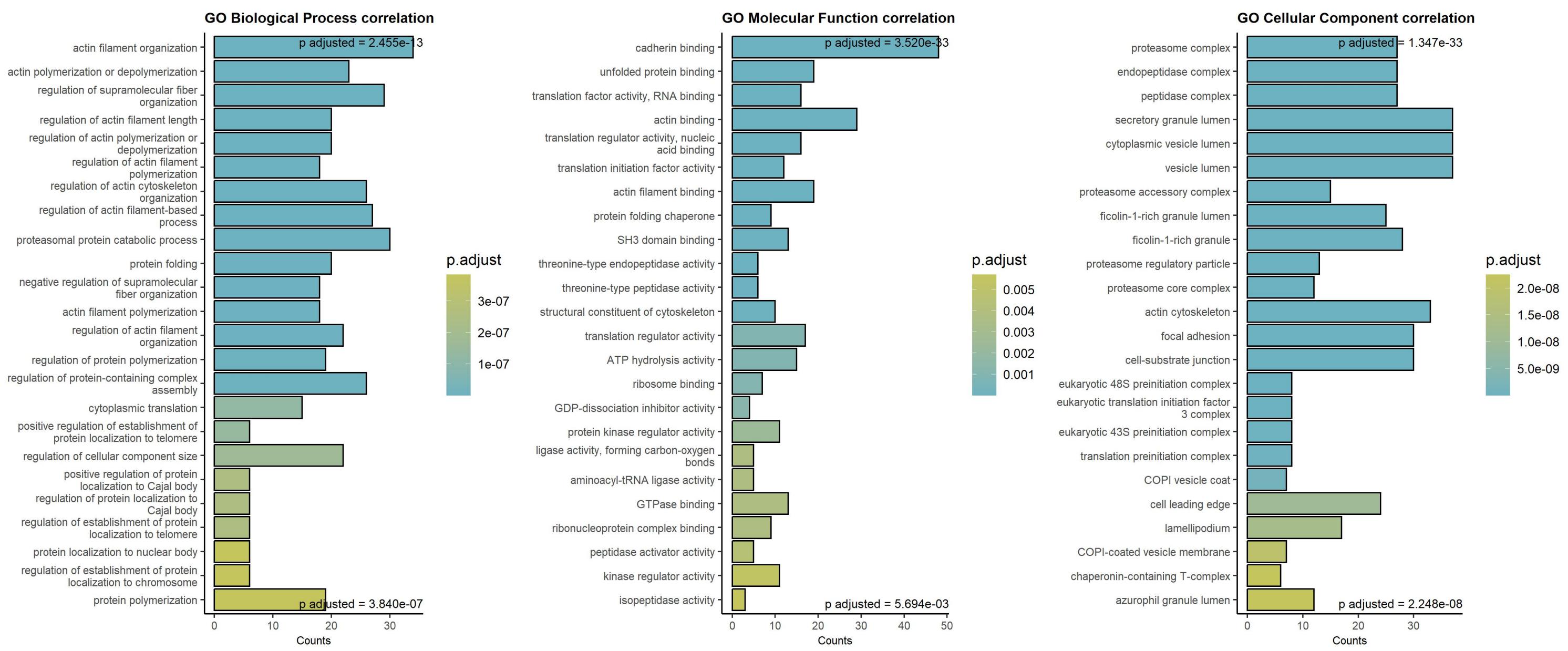


Sorted by p values!							
Downregulated in blood cancers at low/absent ARPC5				Upregulated in blood cancers at low/absent ARPC5			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.15	2.85e-14	ARPC3	actin related protein 2/3 complex s	0.04	4.10e-12	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
-0.17	2.08e-13	ARPC2	actin related protein 2/3 complex s	0.08	1.85e-03	SUPT5H	SPT5 homolog, DSIF elongation factor
-0.18	2.77e-12	ACTR3	actin related protein 3	0.05	3.24e-03	DDX46	DEAD-box helicase 46
-0.15	3.15e-11	ARPC4	actin related protein 2/3 complex s	0.72	4.77e-03	RBMX2	RNA binding motif protein X-linked
-0.1	4.75e-09	MYH9	myosin heavy chain 9	0.51	5.19e-03	PRAF2	PRA1 domain family member 2
-1.6	1.22e-07	PLEK	pleckstrin	0.66	5.75e-03	SUN1	Sad1 and UNC84 domain containing 1
-0.28	9.42e-07	ARPC1B	actin related protein 2/3 complex s	0.79	5.75e-03	PSMG4	proteasome assembly chaperone 4
-1	4.69e-06	MNDA	myeloid cell nuclear differentiation antigen	0.31	6.31e-03	GIMAP6	GTPase, IMAP family member 6
-1.15	4.69e-06	RASSF2	Ras association domain family member	0.51	7.24e-03	YOD1	YOD1 deubiquitinase
-1.1	7.65e-06	WDFY4	WDFY family member 4	0.51	7.55e-03	GRPEL2	GrpE like 2, mitochondrial
-0.25	8.53e-06	ACTR2	actin related protein 2	0.39	8.42e-03	P4HTM	prolyl 4-hydroxylase, transmembrane
-1.15	9.39e-06	DOCK8	dedicator of cytokinesis 8	0.78	8.93e-03	RAD18	RAD18 E3 ubiquitin protein ligase
-0.08	9.81e-06	CAPZB	capping actin protein of muscle Z-I	0.77	1.08e-02	BRD2	bromodomain containing 2
-1.38	2.06e-05	LAT2	linker for activation of T cells fa	0.18	1.27e-02	CALU	calumenin
-1.15	2.82e-05	NCF4	neutrophil cytosolic factor 4	0.71	1.30e-02	LIN28B	lin-28 homolog B
-1.11	5.19e-05	ALCAM	activated leukocyte cell adhesion molecule	0.08	1.31e-02	BAZ1B	bromodomain adjacent to zinc finger
-0.34	6.60e-05	WIPF1	WAS/WASL interacting protein family	0.05	1.32e-02	RBM8A	RNA binding motif protein 8A
-0.11	9.39e-05	GRB2	growth factor receptor bound protein 2	0.11	1.41e-02	PABPC4	poly(A) binding protein cytoplasmic
-0.64	1.78e-04	STK10	serine/threonine kinase 10	0.3	1.41e-02	LZTS1	leucine zipper tumor suppressor 1
-0.13	1.78e-04	ARHGAP1	Rho GTPase activating protein 1	0.69	1.45e-02	UAP1	UDP-N-acetylglucosamine pyrophosphorylase
-0.46	1.91e-04	PLS1	plastin 1	0.06	1.45e-02	SSBP1	single stranded DNA binding protein
-1.31	2.01e-04	ITGAL	integrin subunit alpha L	0.6	1.46e-02	ZGPAT	zinc finger CCCH-type and G-patch domain
-0.21	2.85e-04	VASP	vasodilator stimulated phosphoprotein	0.73	1.46e-02	SNTB2	syntrophin beta 2
-0.51	3.01e-04	SERPINB10	serpin family B member 10	0.68	1.66e-02	CHD1	chromodomain helicase DNA binding protein
-0.46	3.01e-04	PRAM1	PML-RARA regulated adaptor molecule	0.72	1.83e-02	ABT1	activator of basal transcription 1
-0.96	3.07e-04	ANKRD44	ankyrin repeat domain 44	0.05	1.84e-02	PRPF4	pre-mRNA processing factor 4
-0.16	3.07e-04	EFHD2	EF-hand domain family member D2	0.06	1.93e-02	RAE1	ribonucleic acid export 1
-0.38	3.07e-04	CORO1A	coronin 1A	0.31	1.93e-02	REPIN1	replication initiator 1
-0.09	4.60e-04	CAP1	cyclase associated actin cytoskeleton	0.51	1.95e-02	SH3PXD2B	SH3 and PX domains 2B
-0.08	5.17e-04	MYL6	myosin light chain 6	0.04	1.95e-02	RBM14	RNA binding motif protein 14
-0.5	5.17e-04	RNASE2	ribonuclease A family member 2	0.67	2.20e-02	SORT1	sortilin 1
-0.87	5.30e-04	SH3KBP1	SH3 domain containing kinase bindin	0.05	2.22e-02	PSMC4	proteasome 26S subunit, ATPase 4
-0.55	6.71e-04	WAS	WASP actin nucleation promoting factor	0.25	2.49e-02	PTPRK	protein tyrosine phosphatase receptor
-1.05	6.71e-04	SH3BP1	SH3 domain binding protein 1	0.05	2.49e-02	DDX23	DEAD-box helicase 23
-0.37	6.71e-04	GRK2	G protein-coupled receptor kinase 2	0.38	2.58e-02	CHTF18	chromosome transmission fidelity factor
-0.23	8.61e-04	OSTF1	osteoclast stimulating factor 1	0.49	2.60e-02	SNIP1	Smad nuclear interacting protein 1
-0.11	1.03e-03	ACTBL2	actin beta like 2	0.46	2.67e-02	KIF14	kinesin family member 14
-0.85	1.50e-03	PIK3R1	phosphoinositide-3-kinase regulator	0.73	2.71e-02	IGSF8	immunoglobulin superfamily member 8
-0.51	1.51e-03	CERD1	CCAAT enhancer binding protein alpha	0.12	2.71e-02	IPWD1	leucine rich repeats and WD repeat

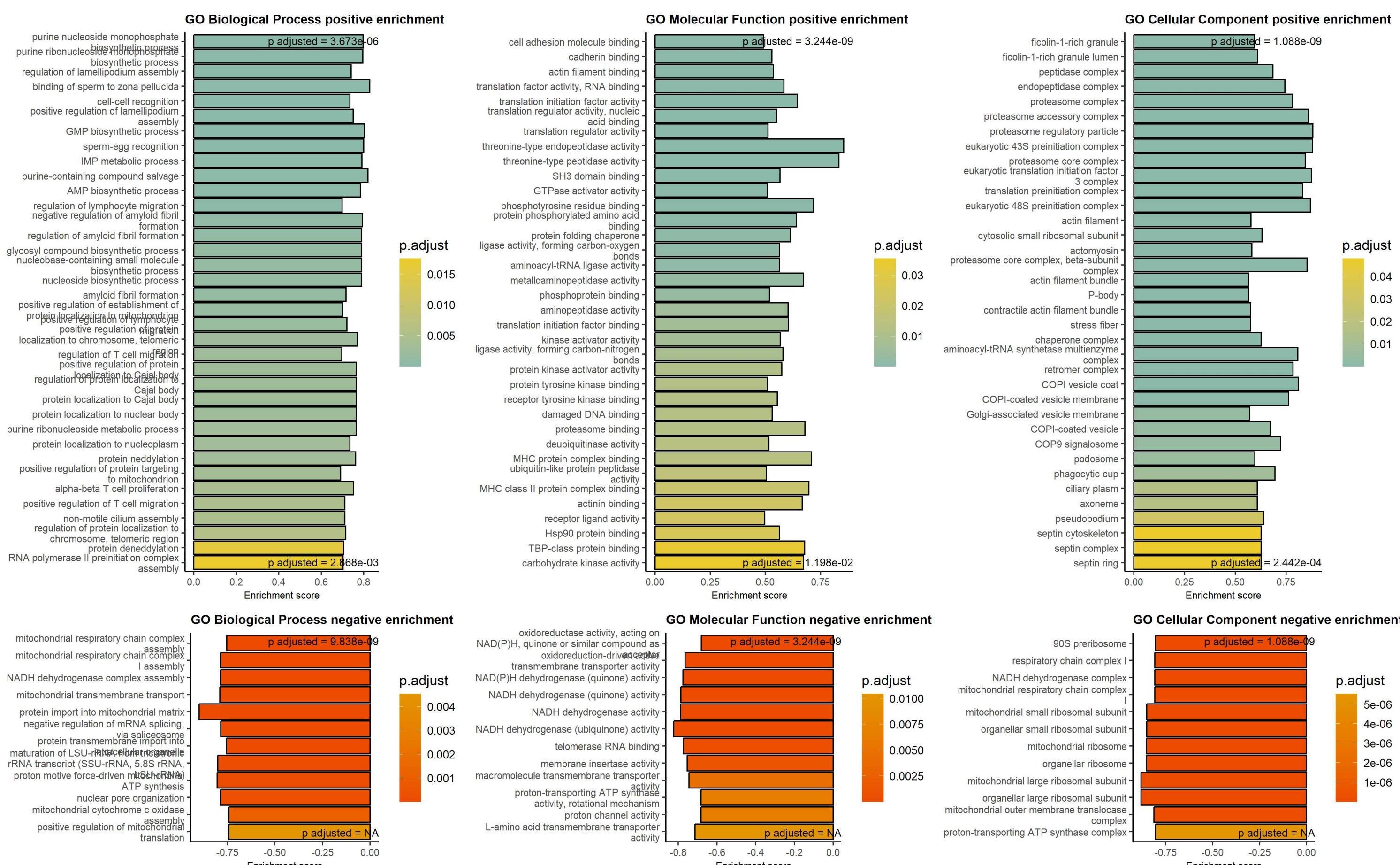


Sorted by p values!							
Downregulated in solid cancers at low/absent ARPC5				Upregulated in solid cancers at low/absent ARPC5			
C	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
5	6.06e-37	ARPC2	actin related protein 2/3 complex s	0.29	0.00e+00	H4C1	H4 clustered histone 1
8	9.80e-37	CLIC1	chloride intracellular channel 1	0.13	3.02e-41	TRA2B	transformer 2 beta homolog
1	7.22e-35	ARPC4	actin related protein 2/3 complex s	0.09	3.33e-41	EIF4A3	eukaryotic translation initiation f
8	5.08e-34	CAP1	cyclase associated actin cytoskelet	0.08	1.21e-40	SRSF7	serine and arginine rich splicing f
5	8.63e-33	GMPPB	GDP-mannose pyrophosphorylase B	0.08	1.27e-38	SAP18	Sin3A associated protein 18
9	1.70e-32	DBNL	drebrin like	0.08	6.14e-38	SNRNP200	small nuclear ribonucleoprotein U5
2	1.79e-32	ARCN1	archain 1	0.11	2.09e-37	SMU1	SMU1 DNA replication regulator and
1	2.42e-32	TLN1	talin 1	0.1	1.01e-35	ILF2	interleukin enhancer binding factor
3	3.13e-32	PTPN23	protein tyrosine phosphatase non-re	0.08	2.14e-35	U2SURP	U2 snRNP associated SURP domain co
1	1.17e-31	DCTD	dCMP deaminase	0.07	2.83e-35	SRSF1	serine and arginine rich splicing f
2	2.01e-31	ATOX1	antioxidant 1 copper chaperone	0.12	2.83e-35	NOP56	NOP56 ribonucleoprotein
1	3.55e-31	PSMA6	proteasome 20S subunit alpha 6	0.08	4.70e-35	DHX9	DExH-box helicase 9
3	6.74e-31	PXN	paxillin	0.12	5.61e-35	PRPF8	pre-mRNA processing factor 8
2	7.38e-31	PSMA3	proteasome 20S subunit alpha 3	0.08	7.86e-35	HNRNPL	heterogeneous nuclear ribonucleopro
6	9.70e-31	ARFGAP3	ADP ribosylation factor GTPase acti	0.08	1.36e-34	EFTUD2	elongation factor Tu GTP binding do
1	9.70e-31	PSMA5	proteasome 20S subunit alpha 5	0.1	2.16e-34	SRSF10	serine and arginine rich splicing f
5	8.28e-30	MTPN	myotrophin	0.05	4.44e-34	SRSF3	serine and arginine rich splicing f
7	3.55e-29	ACTR3	actin related protein 3	0.13	9.43e-34	DKC1	dyskerin pseudouridine synthase 1
5	5.15e-29	PDCD6IP	programmed cell death 6 interacting	0.09	1.23e-33	BCLAF1	BCL2 associated transcription facto
2	7.99e-29	PSMD7	proteasome 26S subunit, non-ATPase	0.13	3.13e-33	WDR18	WD repeat domain 18
8	9.13e-29	DUSP3	dual specificity phosphatase 3	0.1	3.13e-33	DHX15	DEAH-box helicase 15
	9.97e-29	AAK1	AP2 associated kinase 1	0.09	4.28e-33	RBM14	RNA binding motif protein 14
2	1.10e-28	AKT1S1	AKT1 substrate 1	0.12	8.44e-33	SNRNP40	small nuclear ribonucleoprotein U5
6	1.59e-28	LPP	LIM domain containing preferred tra	0.08	1.41e-32	ILF3	interleukin enhancer binding factor
8	6.82e-28	DCTN2	dynactin subunit 2	0.11	2.42e-32	NOP58	NOP58 ribonucleoprotein
9	1.16e-27	PSMA2	proteasome 20S subunit alpha 2	0.08	2.42e-32	RBMX	RNA binding motif protein X-linked
3	1.78e-27	DCK	deoxycytidine kinase	0.08	2.42e-32	MATR3	matrin 3
2	2.01e-27	CFL1	cofilin 1	0.05	2.42e-32	PTPRCAP	protein tyrosine phosphatase recept
1	2.06e-27	NUBP2	NUBP iron-sulfur cluster assembly f	0.05	2.42e-32	HBE1	hemoglobin subunit epsilon 1
9	2.40e-27	PSMC4	proteasome 26S subunit, ATPase 4	0.05	2.42e-32	SERPINB10	serpin family B member 10
8	3.45e-27	HOOK3	hook microtubule tethering protein	0.05	2.42e-32	IGLL1	immunoglobulin lambda like polypept
9	4.50e-27	SNX1	sorting nexin 1	0.05	2.42e-32	CRYBB1	crystallin beta B1
9	4.73e-27	RAP1GDS1	Rap1 GTPase-GDP dissociation stimul	0.05	2.42e-32	ITGA2B	integrin subunit alpha 2b
8	8.59e-27	CZIB	CXXC motif containing zinc binding	0.05	2.42e-32	ACAP1	ArfGAP with coiled-coil, ankyrin re
3	9.16e-27	CCDC22	coiled-coil domain containing 22	0.05	2.42e-32	NCF4	neutrophil cytosolic factor 4
9	9.38e-27	C12orf57	chromosome 12 open reading frame 57	0.05	2.42e-32	SP140	SP140 nuclear body protein
8	1.25e-26	EXOC4	exocyst complex component 4	0.05	2.42e-32	PSTPIP1	proline-serine-threonine phosphatas
7	1.69e-26	WDR1	WD repeat domain 1	0.05	2.42e-32	STAB1	stabilin 1

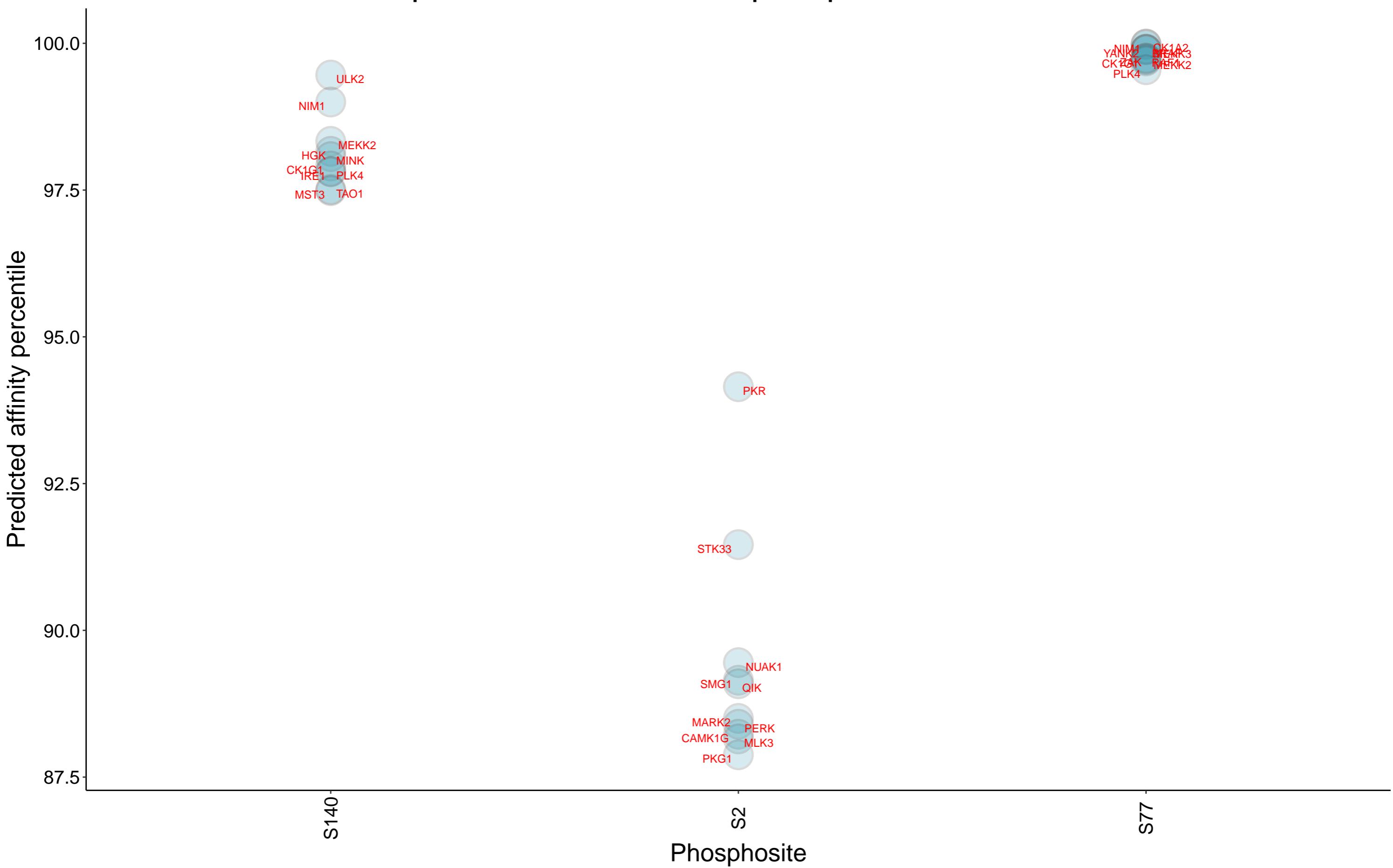
# Top 250 correlation coefficients overrepresentation, ARPC5 protein, DB1



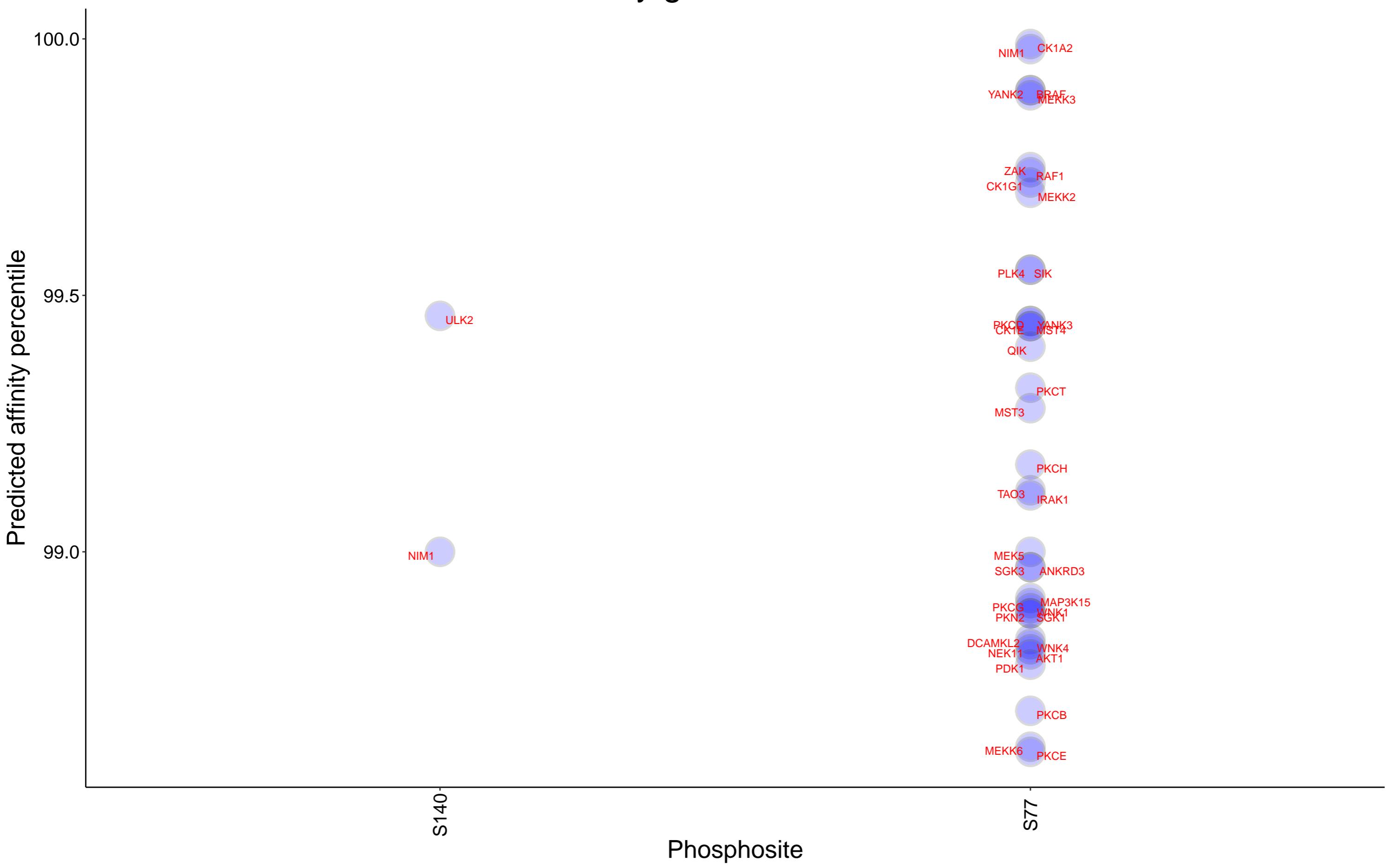
## Gene Set Enrichment analysis on protein correlation coefficients, ARPC5 protein, DB1



# Top 10 kinases for each phosphosite in ARPC5



## Kinases with affinity greater than 98.5% to ARPC5



## Top 15 positive correlation coefficients for ARPC5 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

