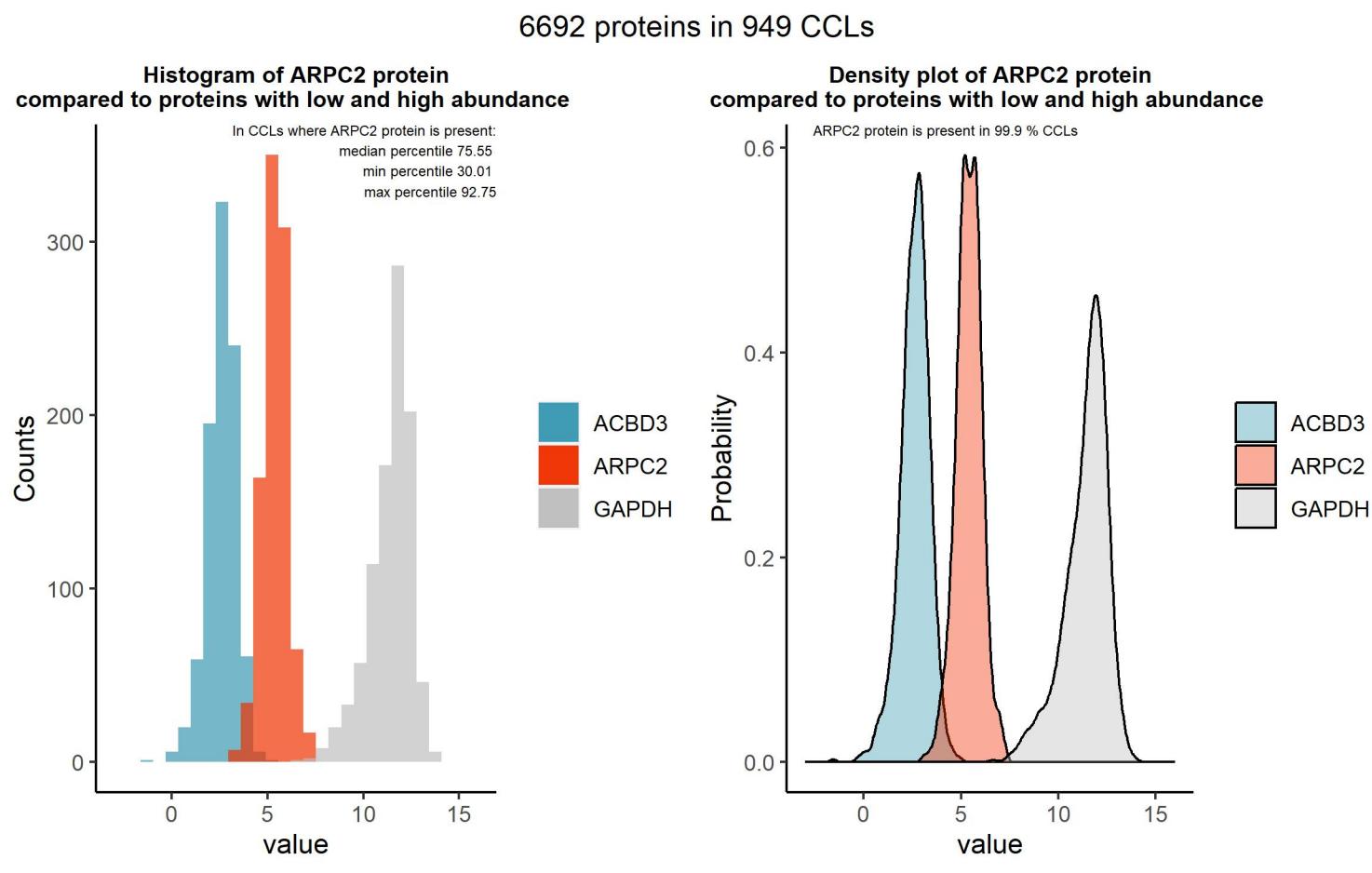


# ARPC2

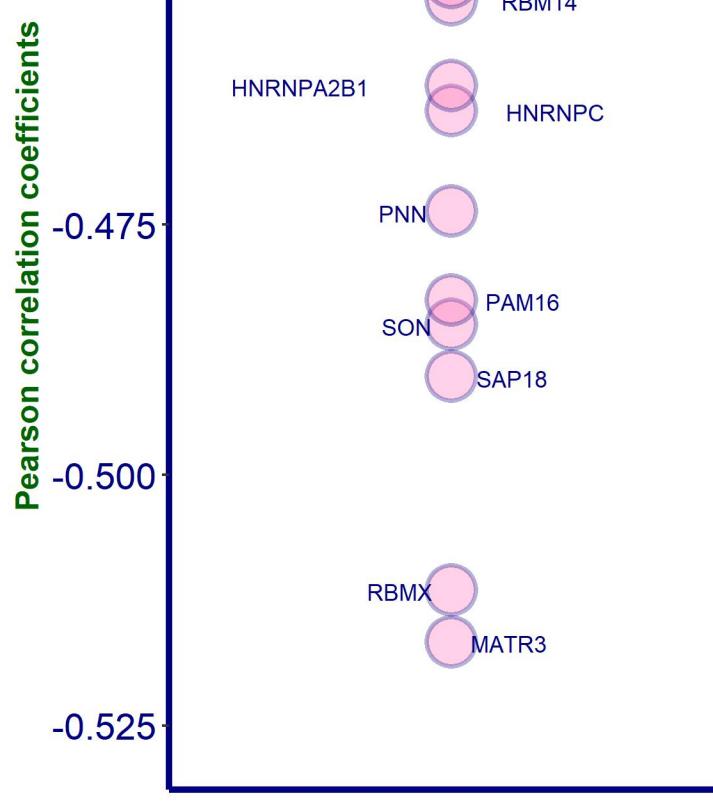
Protein name: ARPC2 ; UNIPROT: O15144 ; Gene name: actin related protein 2/3 complex subunit 2

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

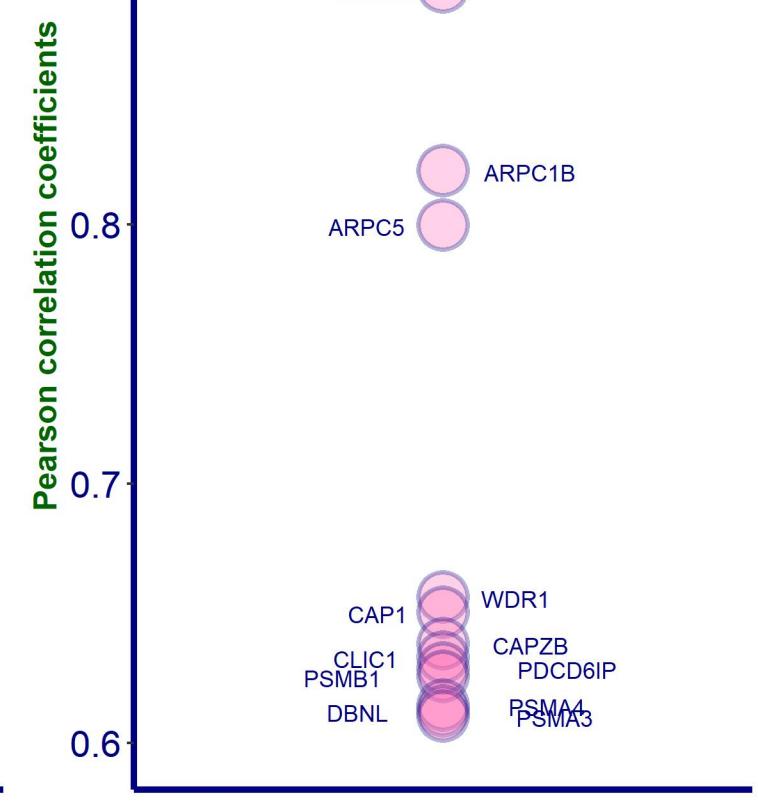
## Sanger Institute Protein Database 1 (DB1), protein presence is certain



## Top negative correlations of ARPC2 protein, DB1

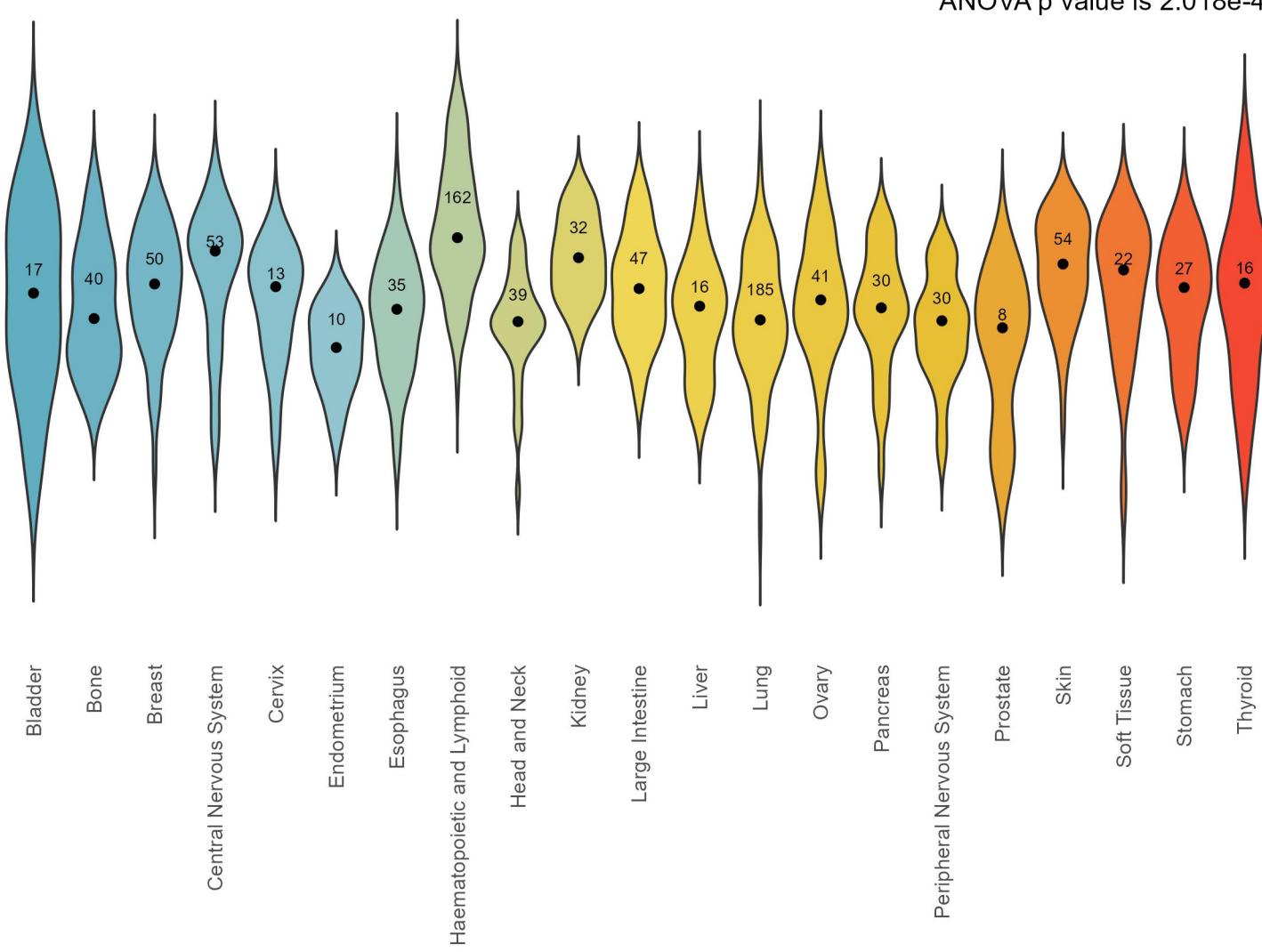


## Top positive correlations of ARPC2 protein, DB1



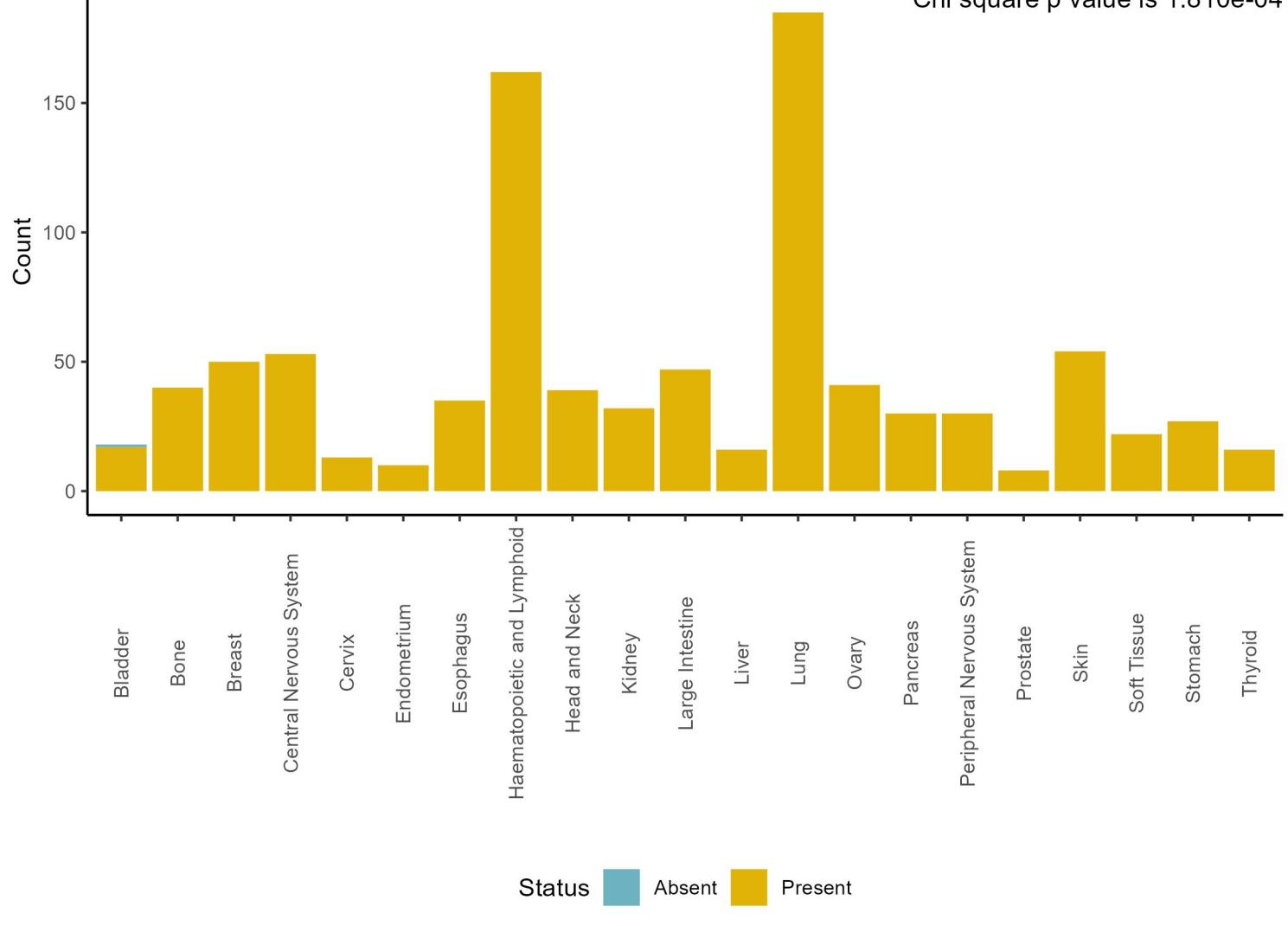
## Amount of ARPC2 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 2.018e-41



## Present and absent ARPC2 protein counts by tissue, DB1

Chi square p value is 1.810e-04

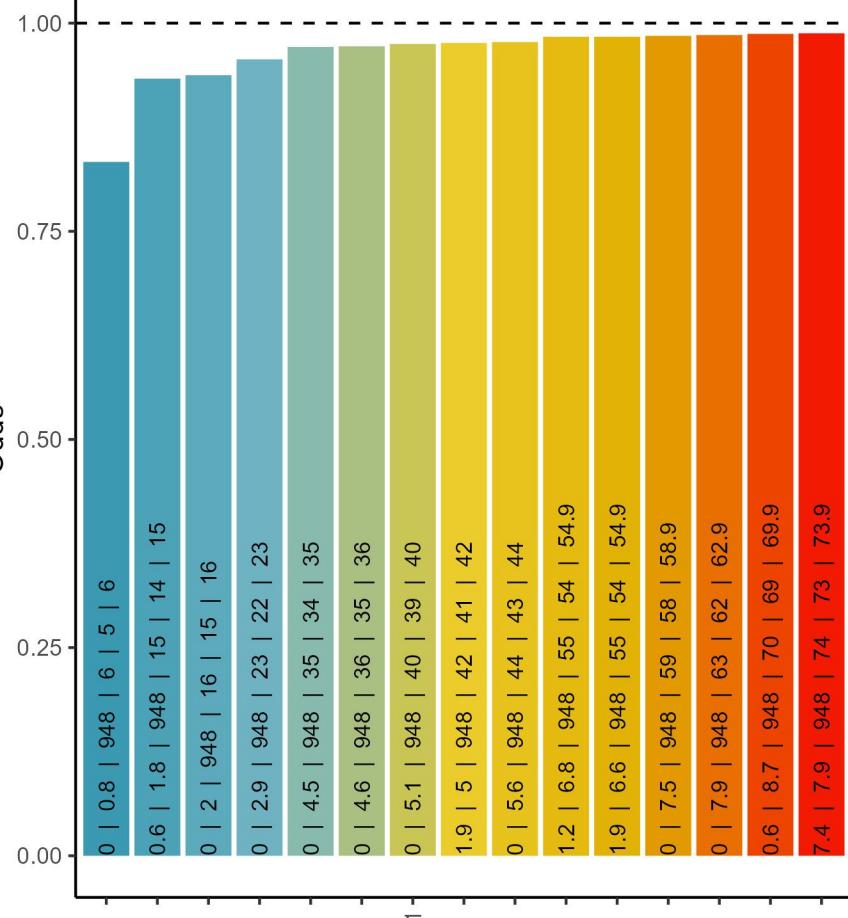


## Cooccurrence with ARPC2 protein, DB1

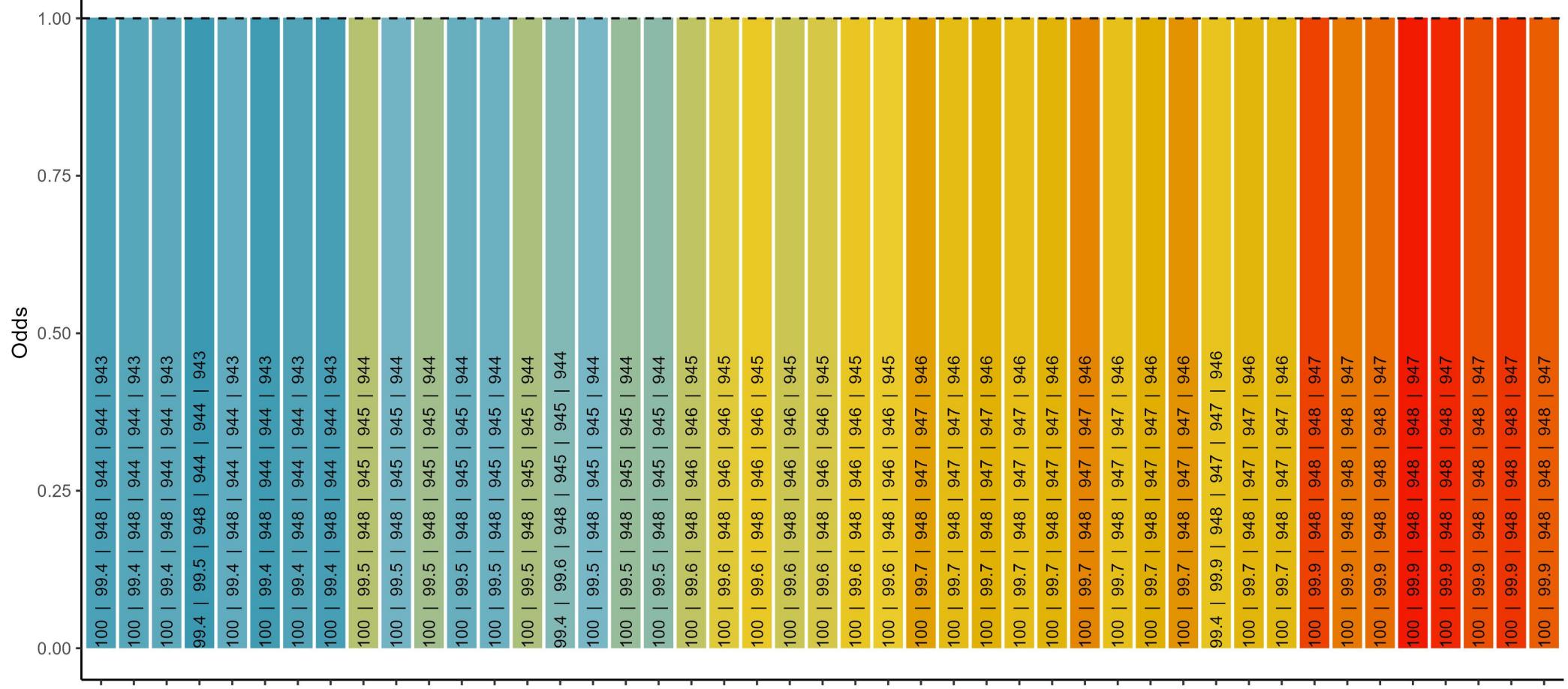
% of ARPC2 in blood cancers: 100 ; % of ARPC2 in solid cancers: 99.9

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ARPC2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

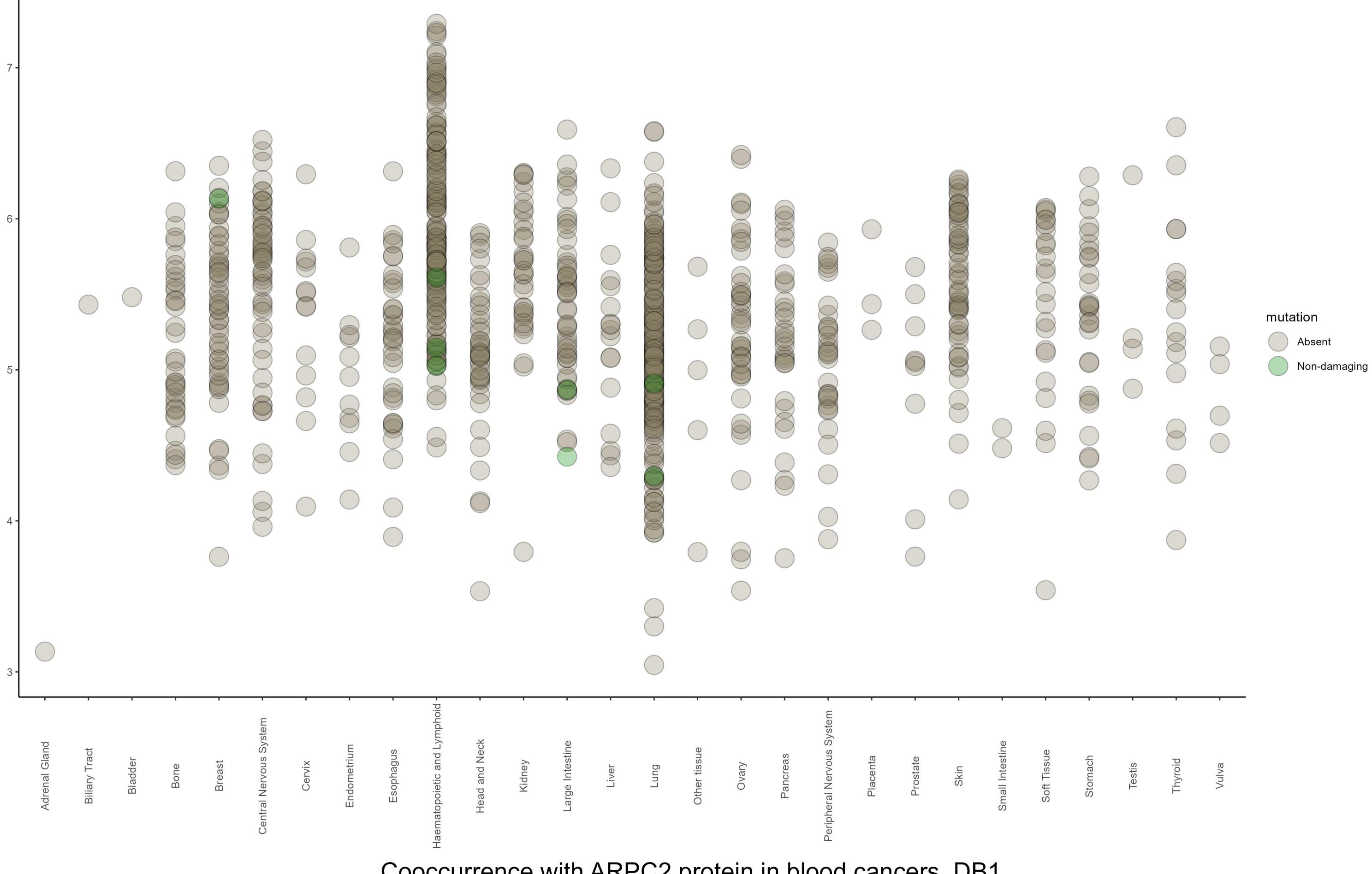
### Negative cooccurrence



### Positive cooccurrence



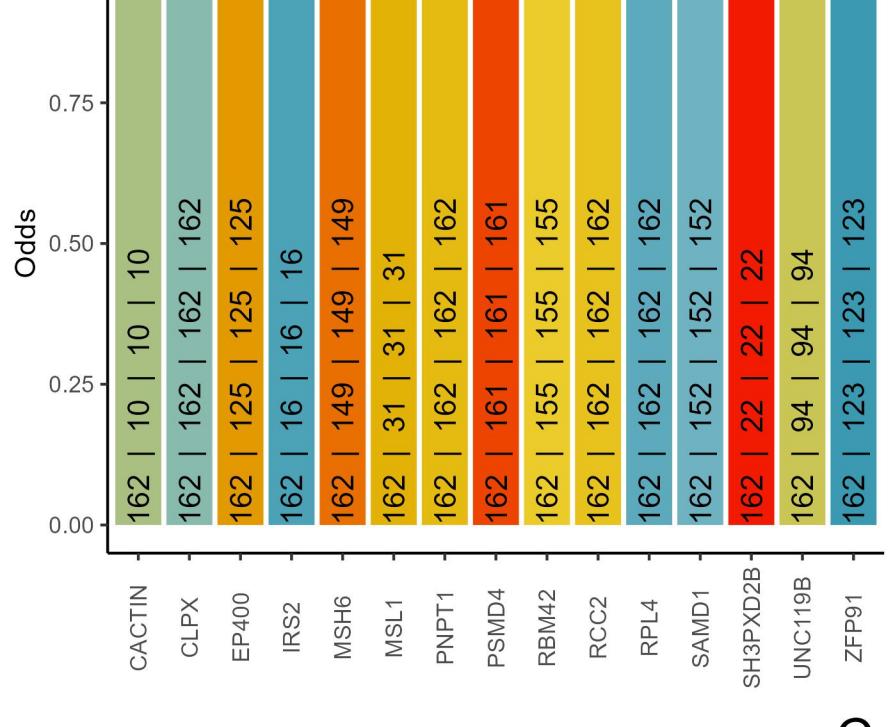
# Amount of ARPC2 protein and mutation status by tissue, DB1



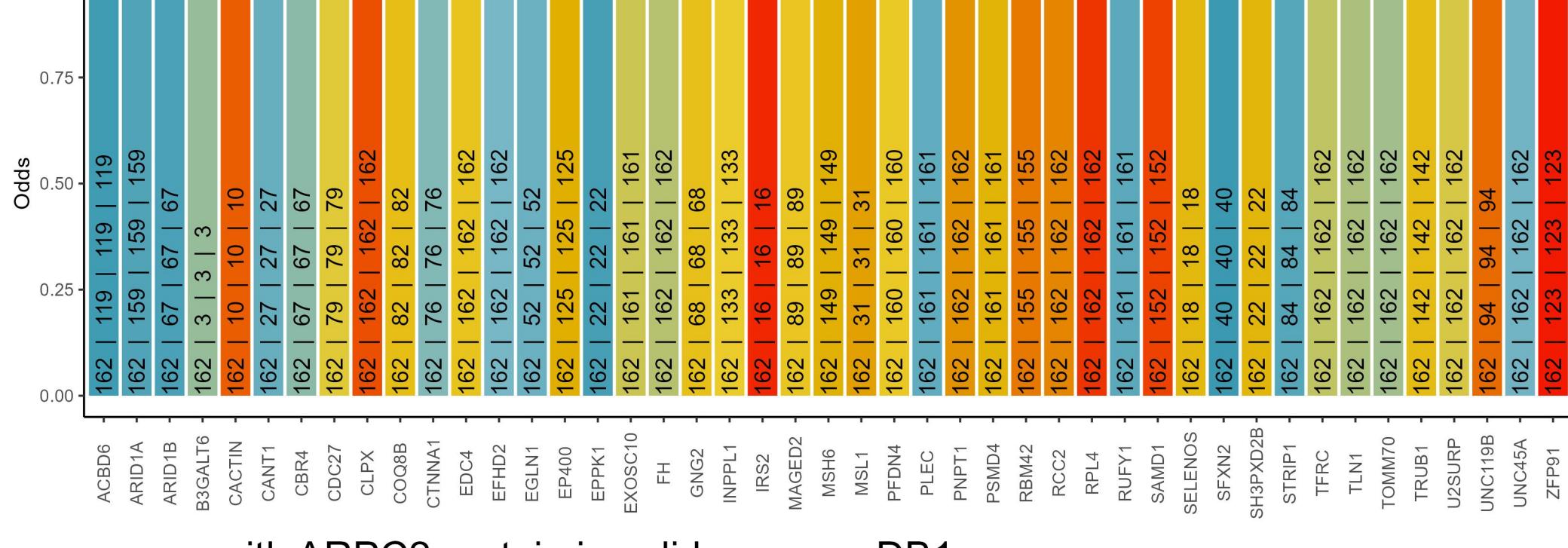
## Cooccurrence with ARPC2 protein in blood cancers, DB1

The text in the bars: incidence of ARPC2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

### Negative cooccurrence



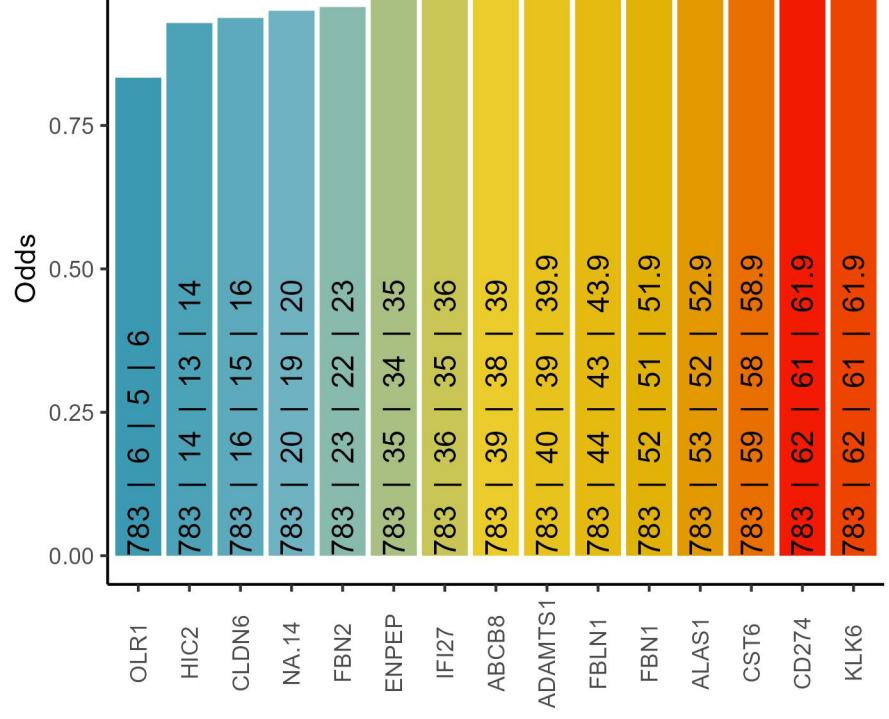
### Positive cooccurrence



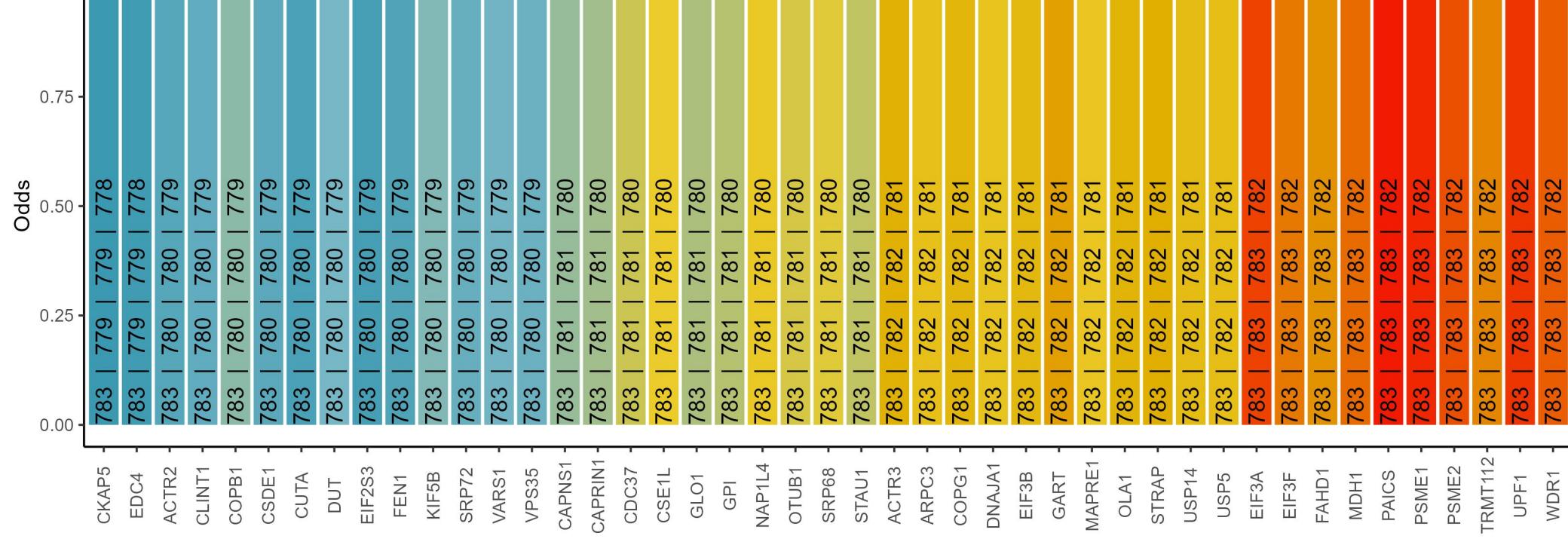
## Cooccurrence with ARPC2 protein in solid cancers, DB1

The text in the bars: incidence of ARPC2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

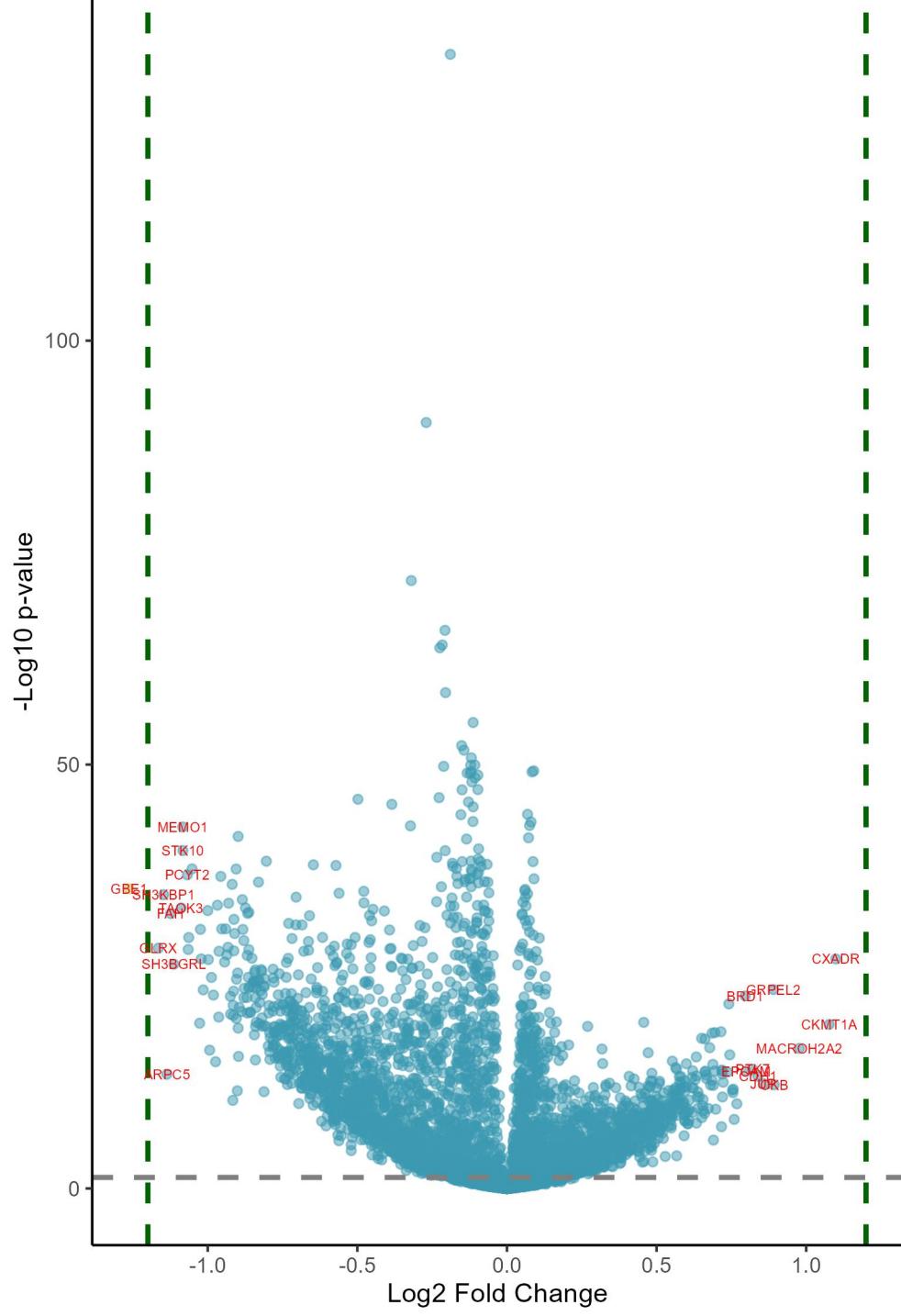
### Negative cooccurrence



### Positive cooccurrence

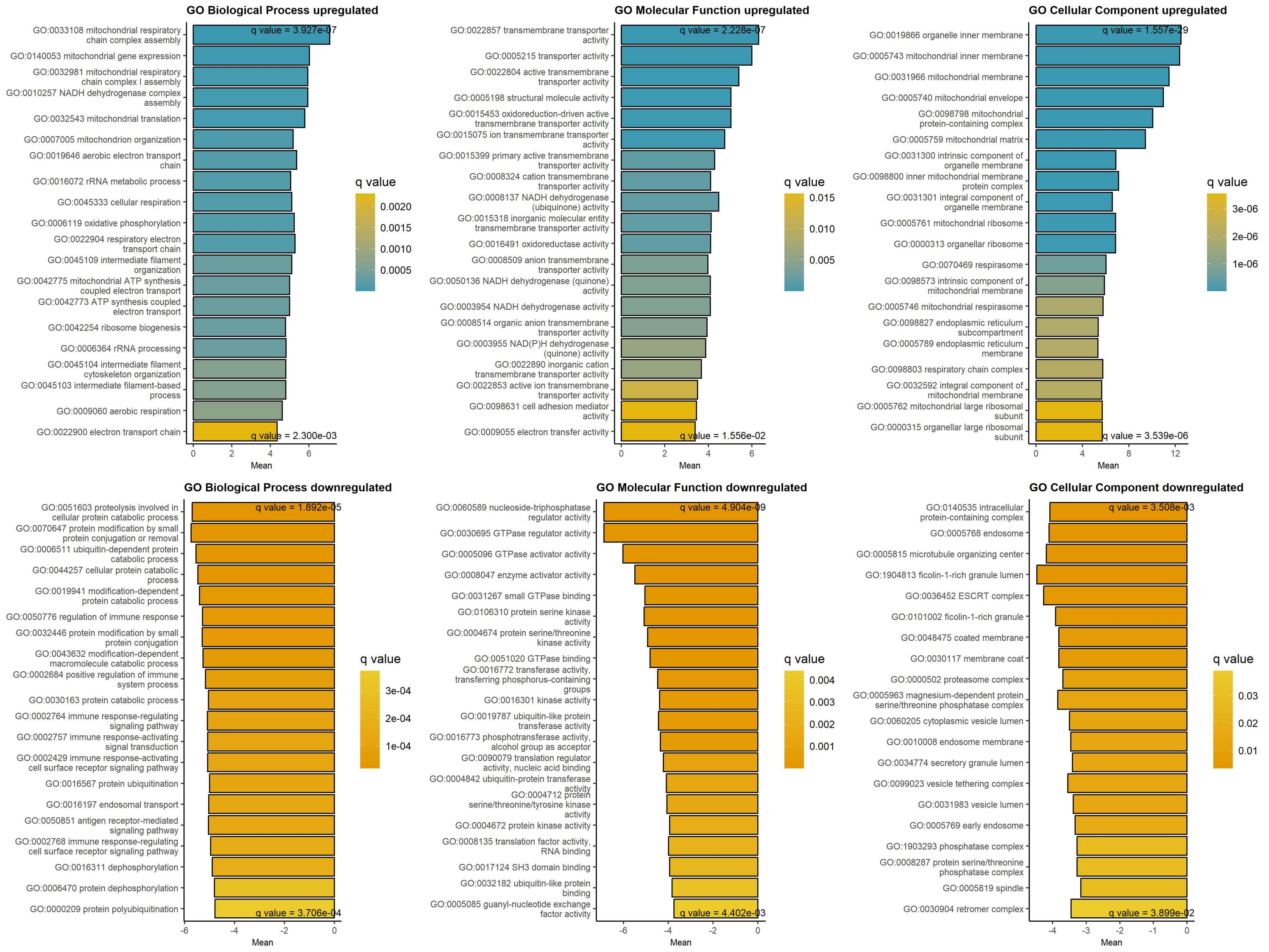


## Downregulated at low/absent ARPC2 Upregulated at low/absent ARPC2



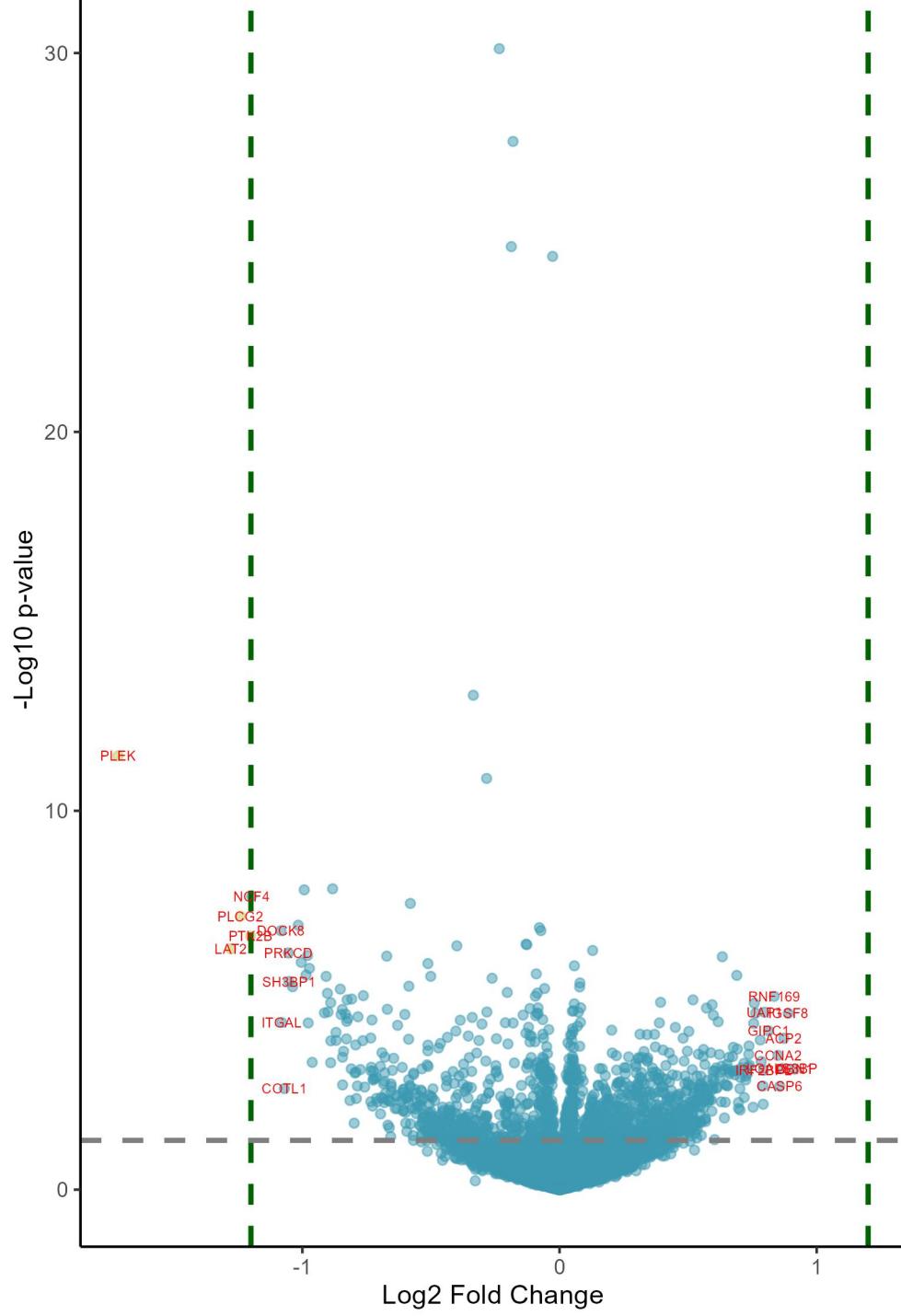
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.26	3.73e-34	GBE1	1,4-alpha-glucan branching enzyme 1	1.1	2.67e-26	CXADR	CXADR Ig-like cell adhesion molecule
-1.17	1.73e-27	GLRX	glutaredoxin	1.08	5.93e-19	CKMT1A	creatine kinase, mitochondrial 1A
-1.15	1.71e-33	SH3KBP1	SH3 domain containing kinase bindin	0.98	2.74e-16	MACROH2A2	macroH2A.2 histone
-1.14	2.17e-13	ARPC5	actin related protein 2/3 complex s	0.89	3.36e-12	CKB	creatine kinase B
-1.12	2.21e-31	FAH	fumarylacetoacetate hydrolase	0.89	7.46e-23	GRPEL2	GrpE like 2, mitochondrial
-1.11	1.06e-25	SH3BGRL	SH3 domain binding glutamate rich p	0.86	2.75e-12	JUP	junction plakoglobin
-1.09	5.14e-32	TAOK3	TAO kinase 3	0.84	3.88e-13	CDH1	cadherin 1
-1.08	4.11e-41	MEMO1	mediator of cell motility 1	0.82	6.05e-14	PTK7	protein tyrosine kinase 7 (inactive)
-1.08	2.21e-38	STK10	serine/threonine kinase 10	0.8	1.08e-13	EPCAM	epithelial cell adhesion molecule
-1.07	1.05e-35	PCYT2	phosphate cytidylyltransferase 2, e	0.8	4.01e-22	BRD1	bromodomain containing 1
-1.07	2.42e-27	PSMB8	proteasome 20S subunit beta 8	0.77	4.58e-10	GCSH	glycine cleavage system protein H
-1.06	1.06e-28	PSMB10	proteasome 20S subunit beta 10	0.76	2.61e-08	H1-0	H1.0 linker histone
-1.05	2.30e-36	TRIM21	tripartite motif containing 21	0.76	1.02e-11	EPPK1	epiplakin 1
-1.03	4.38e-19	ABRACL	ABRA C-terminal like	0.76	2.59e-11	SPINT2	serine peptidase inhibitor, Kunitz
-1.02	1.29e-29	DCK	deoxycytidine kinase	0.75	1.33e-11	UQCR10	ubiquinol-cytochrome c reductase, c
-1.02	2.66e-26	UBE2L6	ubiquitin conjugating enzyme E2 L6	0.74	1.45e-15	CHCHD6	coiled-coil-helix-coiled-coil-helix
-1.02	8.13e-23	GSDMD	gasdermin D	0.74	3.05e-21	TCF20	transcription factor 20
-1	1.04e-31	ATOX1	antioxidant 1 copper chaperone	0.74	1.24e-13	SLC25A4	solute carrier family 25 member 4
-1	3.13e-26	WIPF1	WAS/WASL interacting protein family	0.72	1.75e-12	CGN	cingulin
-0.99	4.37e-16	ARHGDIB	Rho GDP dissociation inhibitor beta	0.72	7.82e-11	SPINT1	serine peptidase inhibitor, Kunitz
-0.99	3.19e-24	PPP6R1	protein phosphatase 6 regulatory su	0.72	9.14e-14	SMARCA1	SWI/SNF related, matrix associated,
-0.98	3.11e-22	RNF181	ring finger protein 181	0.72	2.07e-13	PRXL2A	peroxiredoxin like 2A
-0.97	8.50e-15	LCP1	lymphocyte cytosolic protein 1	0.72	7.34e-14	SURF1	SURF1 cytochrome c oxidase assembly
-0.97	2.63e-32	MAPK14	mitogen-activated protein kinase 14	0.72	1.72e-07	NDUFB11	NADH:ubiquinone oxidoreductase subu
-0.96	8.99e-20	PSMB9	proteasome 20S subunit beta 9	0.72	3.85e-18	TDRKH	tudor and KH domain containing
-0.96	3.80e-27	NECAP2	NECAP endocytosis associated 2	0.7	1.89e-09	PKP2	plakophilin 2
-0.96	1.56e-35	GMPPB	GDP-mannose pyrophosphorylase B	0.7	4.79e-18	EXD2	exonuclease 3'-5' domain containing
-0.95	1.16e-29	OSTF1	osteoclast stimulating factor 1	0.69	9.48e-14	CNTN1	contactin 1
-0.94	6.06e-26	PMM2	phosphomannomutase 2	0.69	5.43e-06	ABCB6	ATP binding cassette subfamily B me

## GAGE analysis on upregulated and downregulated proteins at low/absent ARPC2 protein, DB1

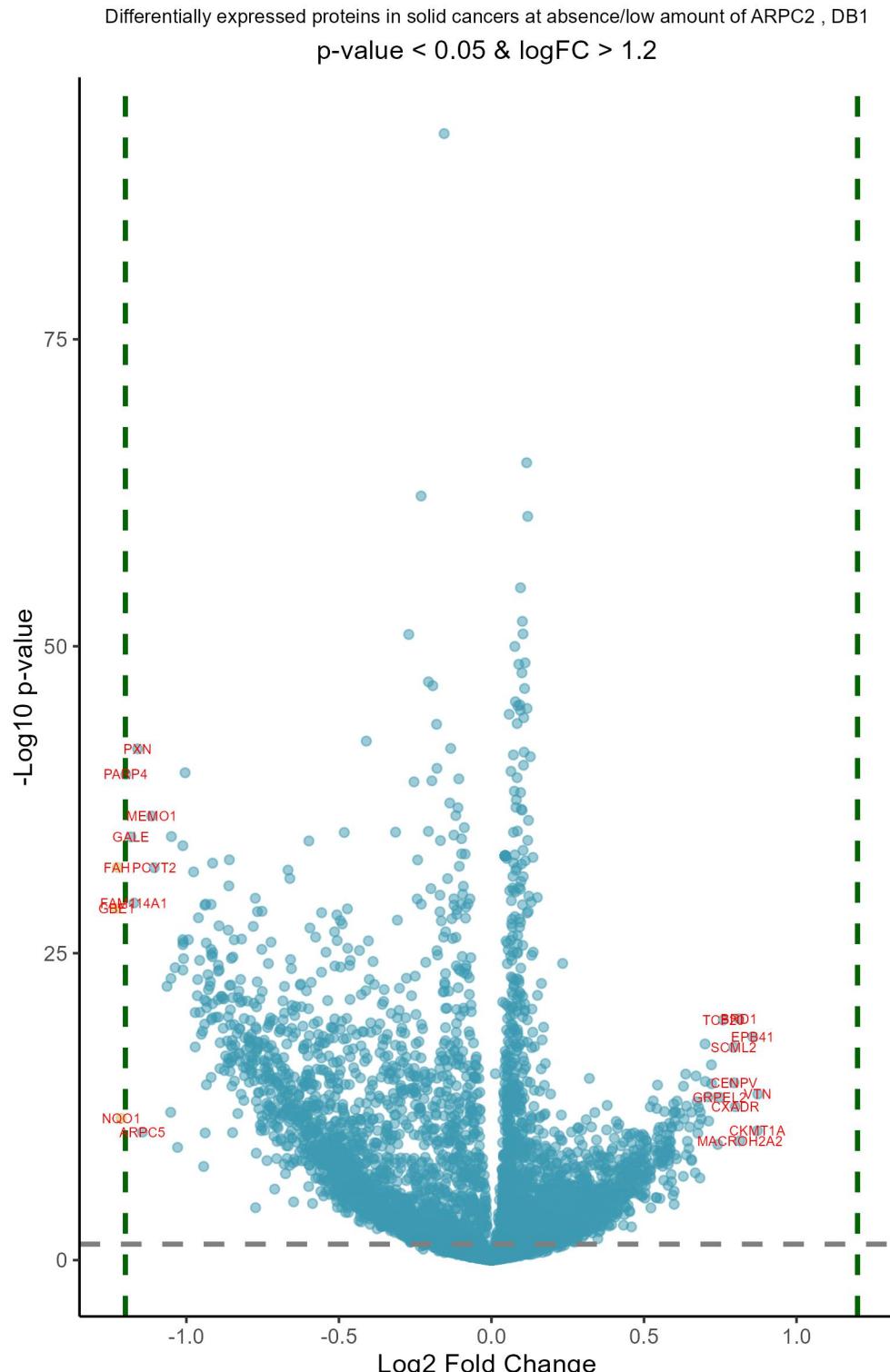


p-value &lt; 0.05 &amp; logFC &gt; 1.2

Downregulated in blood cancers at low/absent ARPC2 Upregulated in blood cancers at low/absent ARPC2

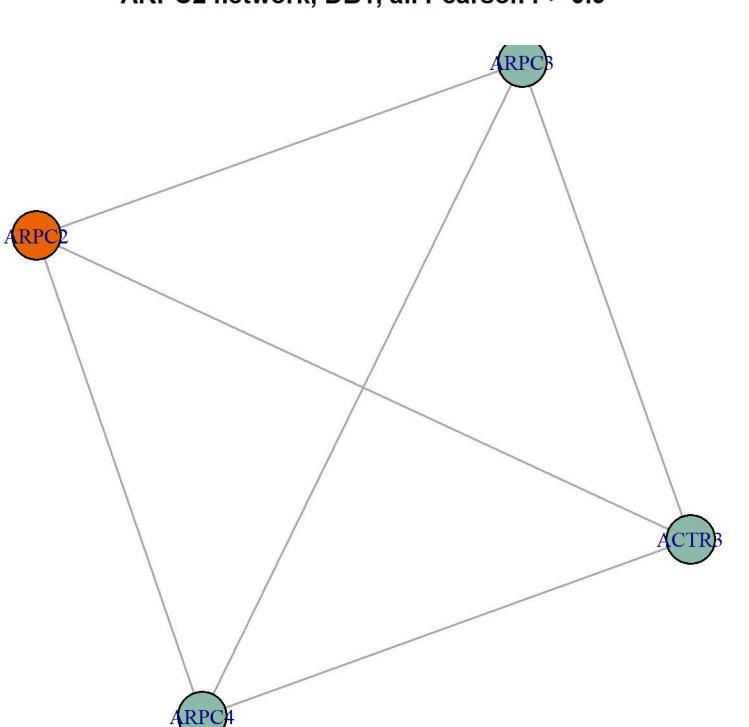


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.72	3.35e-09	PLEK	pleckstrin	0.91	1.84e-02	DBN1	drebrin 1
-1.28	1.33e-04	LAT2	linker for activation of T cells fa	0.89	1.98e-03	IGSF8	immunoglobulin superfamily member 8
-1.24	3.09e-05	PLCG2	phospholipase C gamma 2	0.87	5.43e-03	ACP2	acid phosphatase 2, lysosomal
-1.2	7.47e-05	PTK2B	protein tyrosine kinase 2 beta	0.87	1.81e-02	LGALS3BP	galectin 3 binding protein
-1.2	1.08e-05	NCF4	neutrophil cytosolic factor 4	0.86	3.11e-02	CASP6	caspase 6
-1.08	5.72e-05	DOCK8	dedicator of cytokinesis 8	0.85	1.15e-02	CCNA2	cyclin A2
-1.08	2.79e-03	ITGAL	integrin subunit alpha L	0.83	1.05e-03	RNF169	ring finger protein 169
-1.07	3.40e-02	COTL1	coactosin like F-actin binding prot	0.81	4.06e-03	GIPC1	GIPC PDZ domain containing family m
-1.05	1.57e-04	PRKCD	protein kinase C delta	0.8	1.97e-03	UAP1	UDP-N-acetylglucosamine pyrophospho
-1.05	5.63e-04	SH3BP1	SH3 domain binding protein 1	0.79	1.89e-02	IRF2BPL	interferon regulatory factor 2 bind
-1.04	7.06e-04	SYK	spleen associated tyrosine kinase	0.79	6.13e-02	TSTD1	thiosulfate sulfurtransferase like
-1.02	5.00e-05	WDFY4	WDFY family member 4	0.79	3.09e-02	FKBP11	FKBP prolyl isomerase 11
-1	2.37e-04	MYO1F	myosin IF	0.78	1.44e-02	CEP43	centrosomal protein 43
-0.99	8.12e-06	MNDA	myeloid cell nuclear differentiatio	0.78	5.79e-03	TCF12	transcription factor 12
-0.99	4.31e-04	NCKAP1L	NCK associated protein 1 like	0.76	1.98e-03	C12orf57	chromosome 12 open reading frame 57
-0.98	1.75e-04	ANKRD44	ankyrin repeat domain 44	0.76	1.42e-03	CCNB1	cyclin B1
-0.98	2.79e-03	DOK3	docking protein 3	0.76	2.84e-03	MORC2	MORC family CW-type zinc finger 2
-0.97	3.11e-04	RASSF2	Ras association domain family membe	0.75	6.76e-02	ABCB6	ATP binding cassette subfamily B me
-0.96	1.50e-02	CTSZ	cathepsin Z	0.74	1.65e-02	MAZ	MYC associated zinc finger protein
-0.91	1.98e-03	CYBB	cytochrome b-245 beta chain	0.74	7.54e-03	BRD7	bromodomain containing 7
-0.91	4.33e-04	CTSS	cathepsin S	0.74	1.09e-02	TLE5	TLE family member 5, transcriptiona
-0.9	9.30e-04	VAV1	vav guanine nucleotide exchange fac	0.73	1.74e-02	GTSE1	G2 and S-phase expressed 1
-0.9	1.97e-03	LYZ	lysozyme	0.73	2.02e-02	BOLA1	bolA family member 1
-0.89	1.52e-02	ZYX	zyxin	0.72	2.18e-02	ATP1A3	ATPase Na+/K+ transporting subunit
-0.89	1.41e-03	ACSL5	acyl-CoA synthetase long chain fami	0.72	2.46e-02	BAG3	BAG cochaperone 3
-0.89	5.89e-03	MYO1G	myosin IG	0.72	4.83e-02	MYH10	myosin heavy chain 10
-0.88	8.12e-06	RMDN1	regulator of microtubule dynamics 1	0.72	1.55e-02	RPAP1	RNA polymerase II associated protei
-0.87	4.30e-03	PIK3AP1	phosphoinositide-3-kinase adaptor p	0.71	1.79e-02	MFGE8	milk fat globule EGF and factor V/V
-0.87	5.86e-03	GPD2	glycerol-3-phosphate dehydrogenase	0.7	2.28e-02	RBIS	ribosomal biogenesis factor

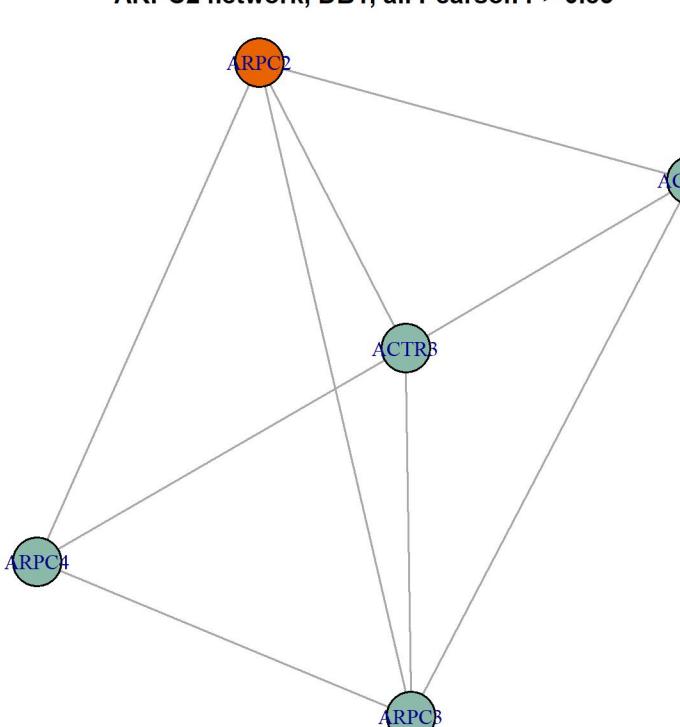


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.23	7.47e-28	GBE1	1,4-alpha-glucan branching enzyme 1	0.87	2.35e-13	VTN	vitronectin
-1.23	4.33e-31	FAH	fumarylacetoacetate hydrolase	0.87	1.61e-10	CKMT1A	creatine kinase, mitochondrial 1A
-1.21	1.77e-11	NQO1	NAD(P)H quinone dehydrogenase 1	0.86	8.60e-18	EPB41	erythrocyte membrane protein band 4
-1.2	4.96e-38	PARP4	poly(ADP-ribose) polymerase family	0.81	9.70e-10	MACROH2A2	macroH2A.2 histone
-1.18	3.79e-33	GALE	UDP-galactose-4-epimerase	0.81	3.49e-19	BRD1	bromodomain containing 1
-1.17	2.87e-28	FAM114A1	family with sequence similarity 114	0.8	2.24e-12	CXADR	CXADR Ig-like cell adhesion molecul
-1.16	5.36e-40	PXN	paxillin	0.8	3.12e-14	CENPV	centromere protein V
-1.14	2.04e-10	ARPC5	actin related protein 2/3 complex s	0.79	5.65e-17	SCML2	Scm polycomb group protein like 2
-1.11	8.96e-35	MEMO1	mediator of cell motility 1	0.76	4.34e-19	TCF20	transcription factor 20
-1.11	4.58e-31	PCYT2	phosphate cytidylyltransferase 2, e	0.75	4.17e-13	GRPEL2	GrpE like 2, mitochondrial
-1.06	1.01e-21	GLRX	glutaredoxin	0.74	1.86e-09	MRPL54	mitochondrial ribosomal protein L54
-1.05	6.05e-12	CBR3	carbonyl reductase 3	0.72	3.68e-14	NSD3	nuclear receptor binding SET domain
-1.05	2.49e-22	TUBA1C	tubulin alpha 1c	0.72	1.28e-15	ZNF384	zinc finger protein 384
-1.05	3.57e-33	GMPPB	GDP-mannose pyrophosphorylase B	0.71	2.86e-11	CNTN1	contactin 1
-1.04	3.52e-23	TRIP6	thyroid hormone receptor interactor	0.71	3.84e-13	ZNF280C	zinc finger protein 280C
-1.03	3.14e-09	TMSB10	thymosin beta 10	0.7	2.44e-14	ZMYM4	zinc finger MYM-type containing 4
-1.01	2.22e-25	SEPTIN10	septin 10	0.7	3.08e-17	PHF3	PHD finger protein 3
-1.01	1.80e-32	LPP	LIM domain containing preferred tra	0.69	2.00e-11	MBD1	methyl-CpG binding domain protein 1
-1.01	5.33e-23	PARVA	parvin alpha	0.68	5.82e-12	COQ7	coenzyme Q7, hydroxylase
-1.01	5.38e-25	ATOX1	antioxidant 1 copper chaperone	0.68	7.11e-07	CKB	creatine kinase B
-1.01	3.40e-25	ACO1	aconitase 1	0.68	5.20e-11	GTPBP3	GTP binding protein 3, mitochondria
-1.01	6.79e-24	PMM2	phosphomannomutase 2	0.68	2.57e-12	MEAF6	MYST/Esa1 associated factor 6
-1	3.80e-38	PTPN23	protein tyrosine phosphatase non-re	0.68	2.52e-10	SLC25A4	solute carrier family 25 member 4
-0.99	2.25e-25	DCTD	dCMP deaminase	0.67	9.21e-13	YTHDC1	YTH domain containing 1
-0.98	9.64e-31	DNPEP	aspartyl aminopeptidase	0.67	9.32e-15	KNOP1	lysine rich nucleolar protein 1
-0.97	1.13e-19	ACY1	aminoacylase 1	0.67	2.86e-07	GNG5	G protein subunit gamma 5
-0.97	5.24e-17	FHL2	four and a half LIM domains 2	0.66	3.26e-08	INA	internexin neuronal intermediate fi
-0.96	5.51e-21	SH3KBP1	SH3 domain containing kinase bindin	0.66	5.90e-12	KIF1A	kinesin family member 1A
-0.96	2.98e-22	OPTN	optineurin	0.66	2.55e-08	H2AX	H2A.X variant histone

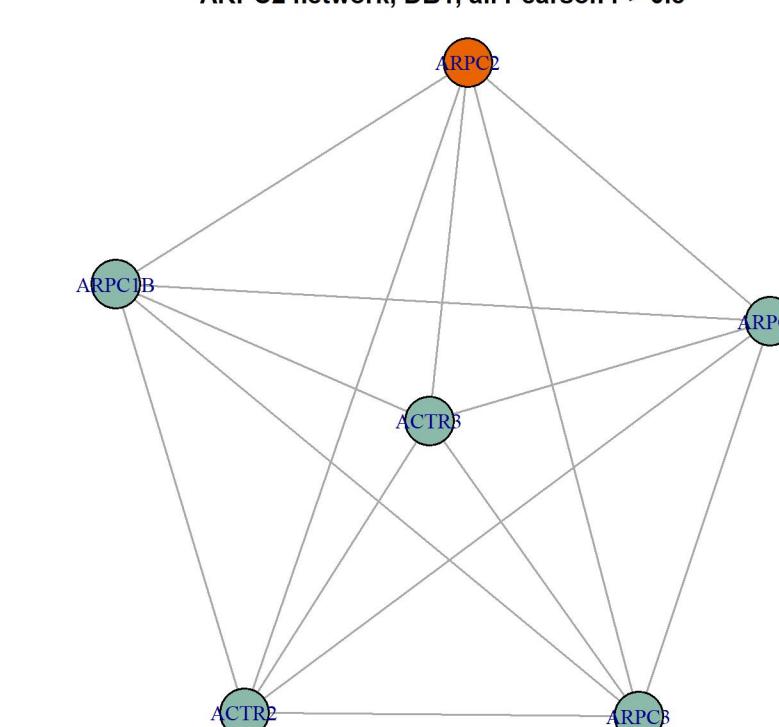
ARPC2 network, DB1, all Pearson r &gt; 0.9

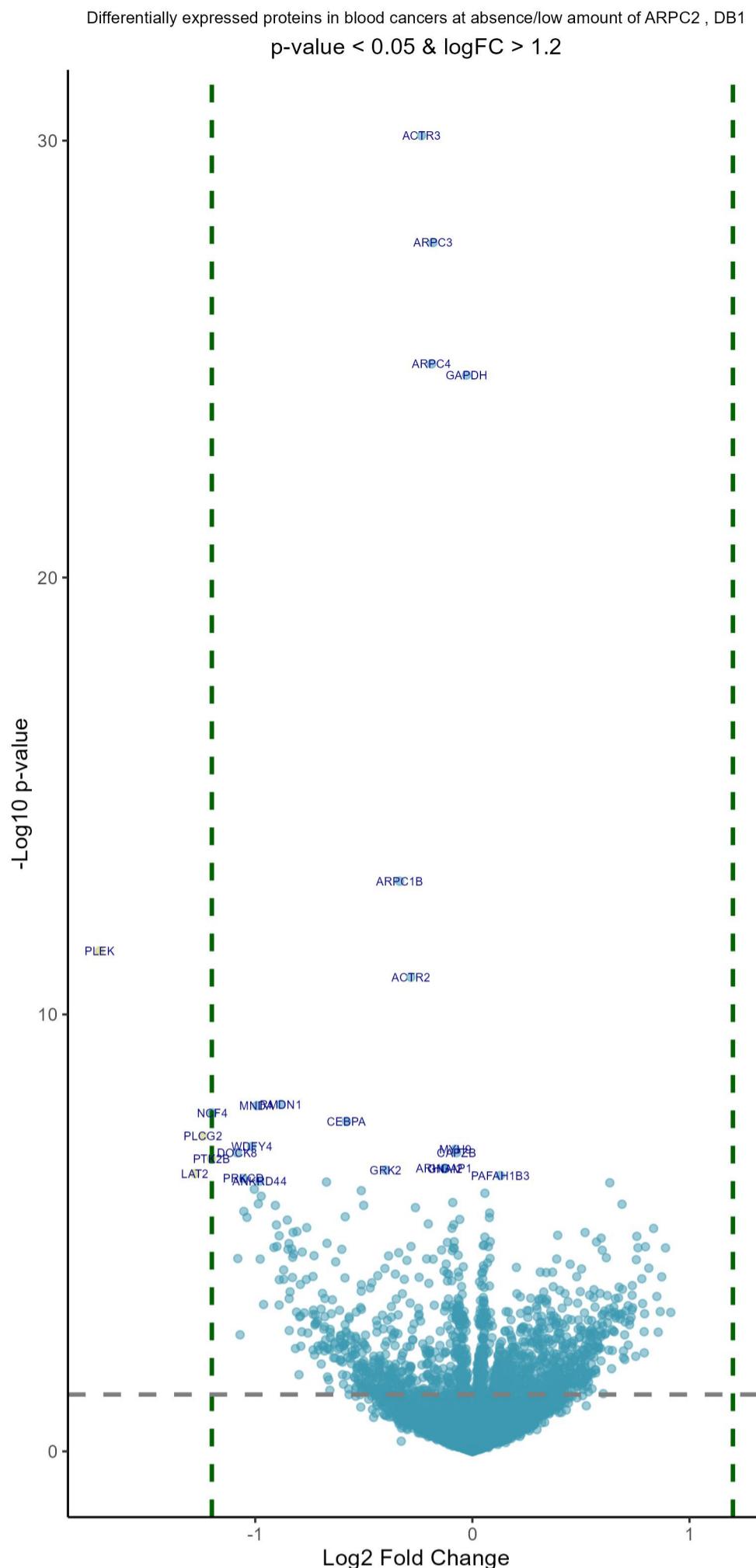


ARPC2 network, DB1, all Pearson r &gt; 0.85

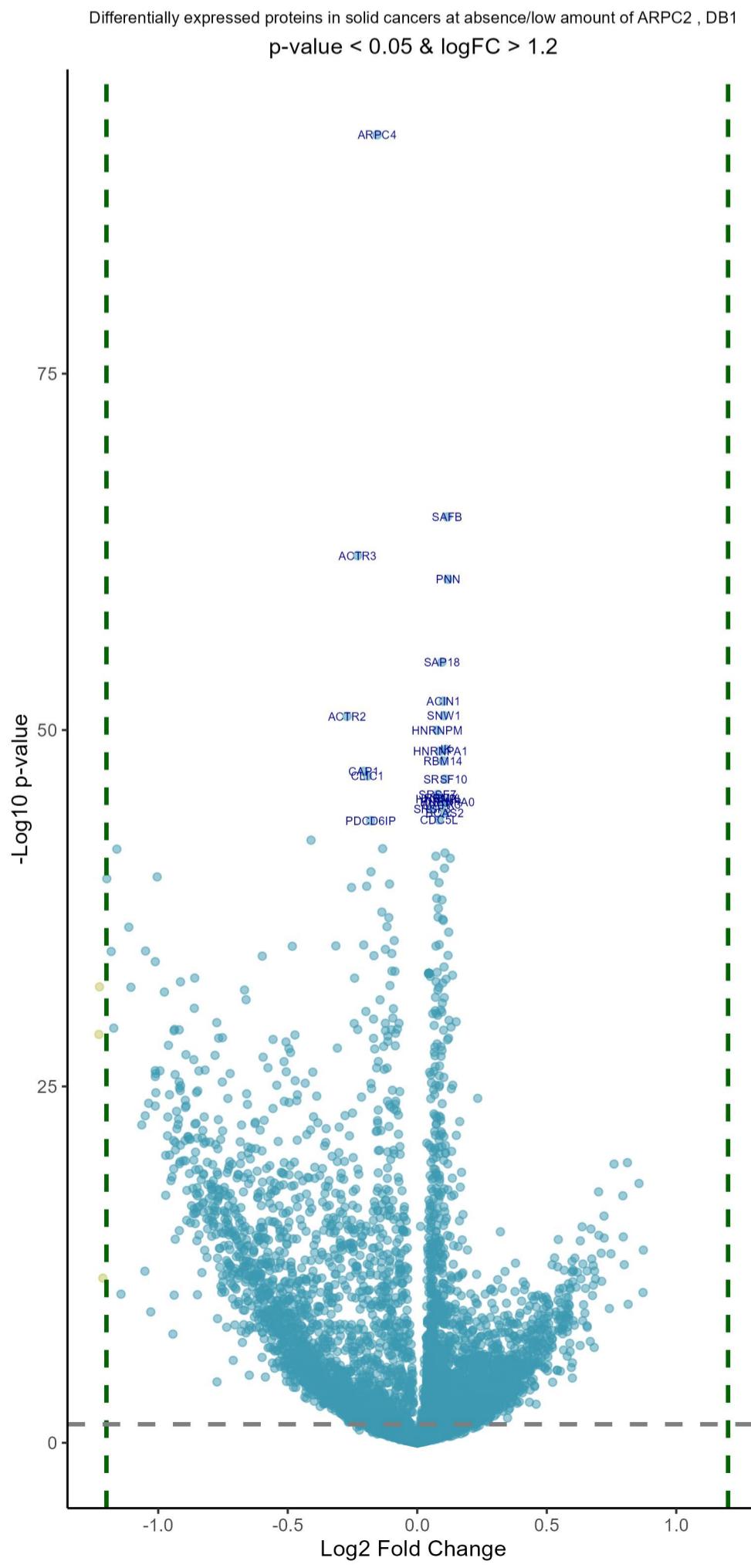


ARPC2 network, DB1, all Pearson r &gt; 0.8

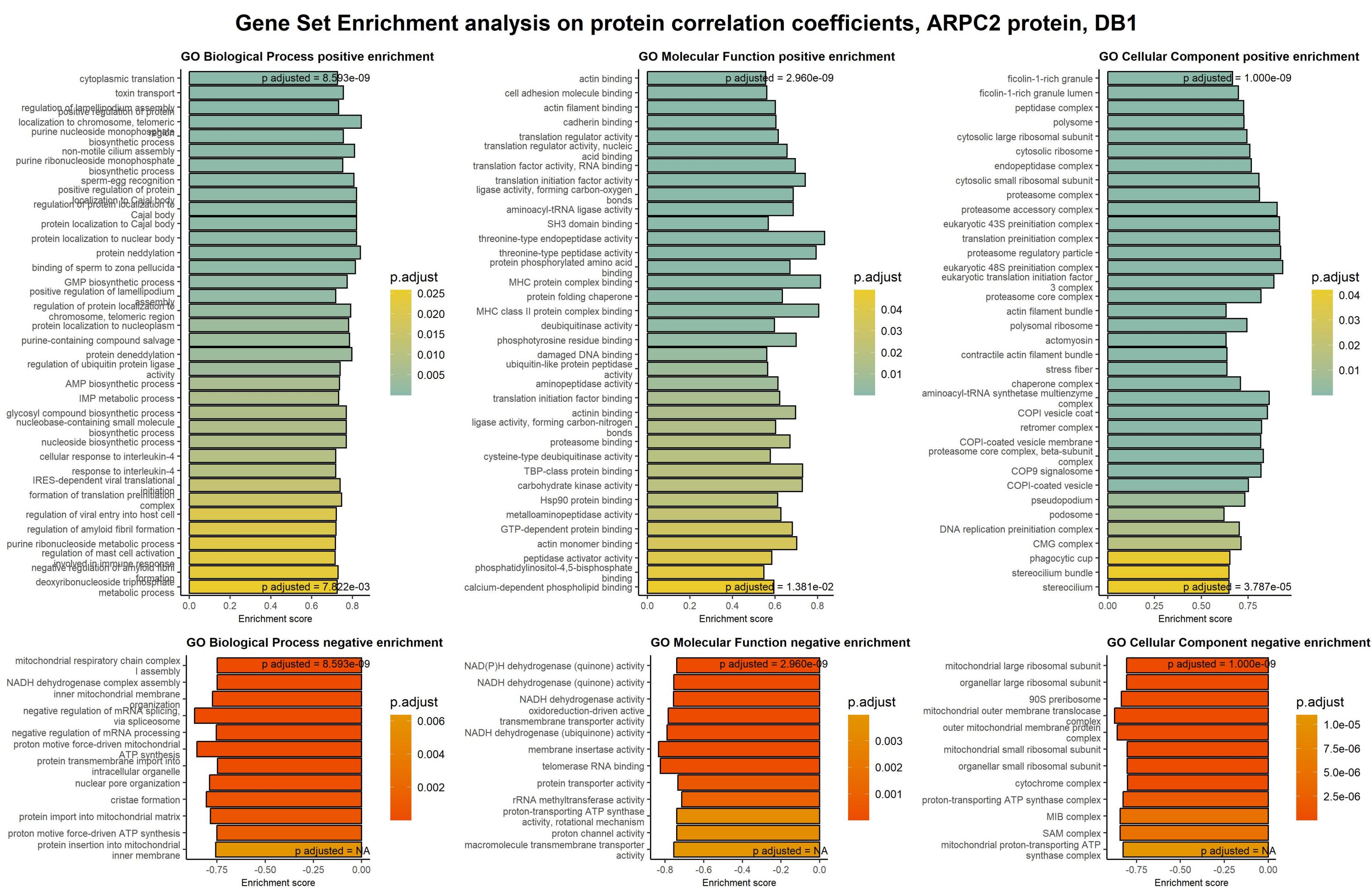
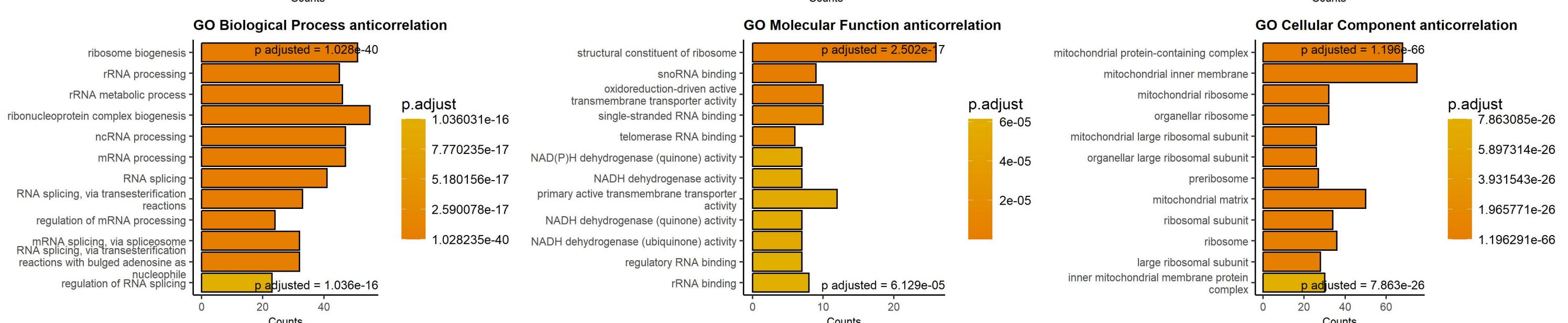
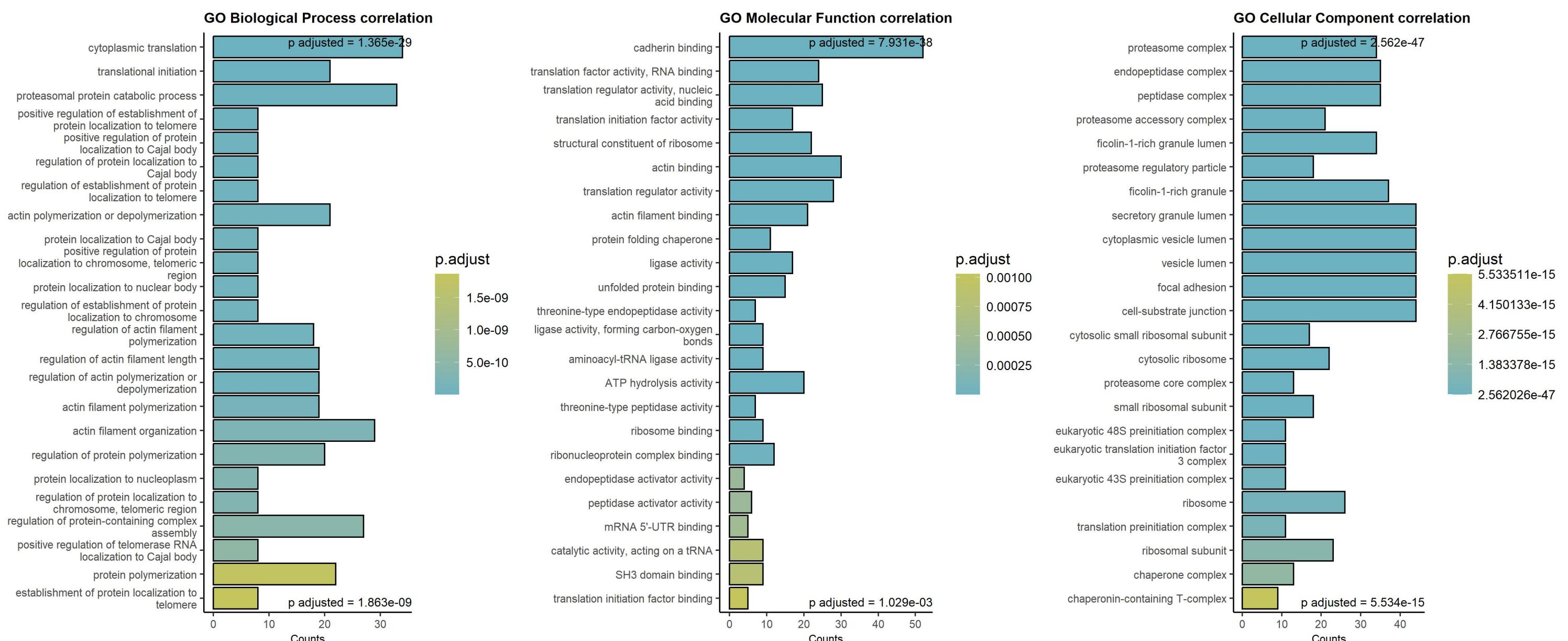




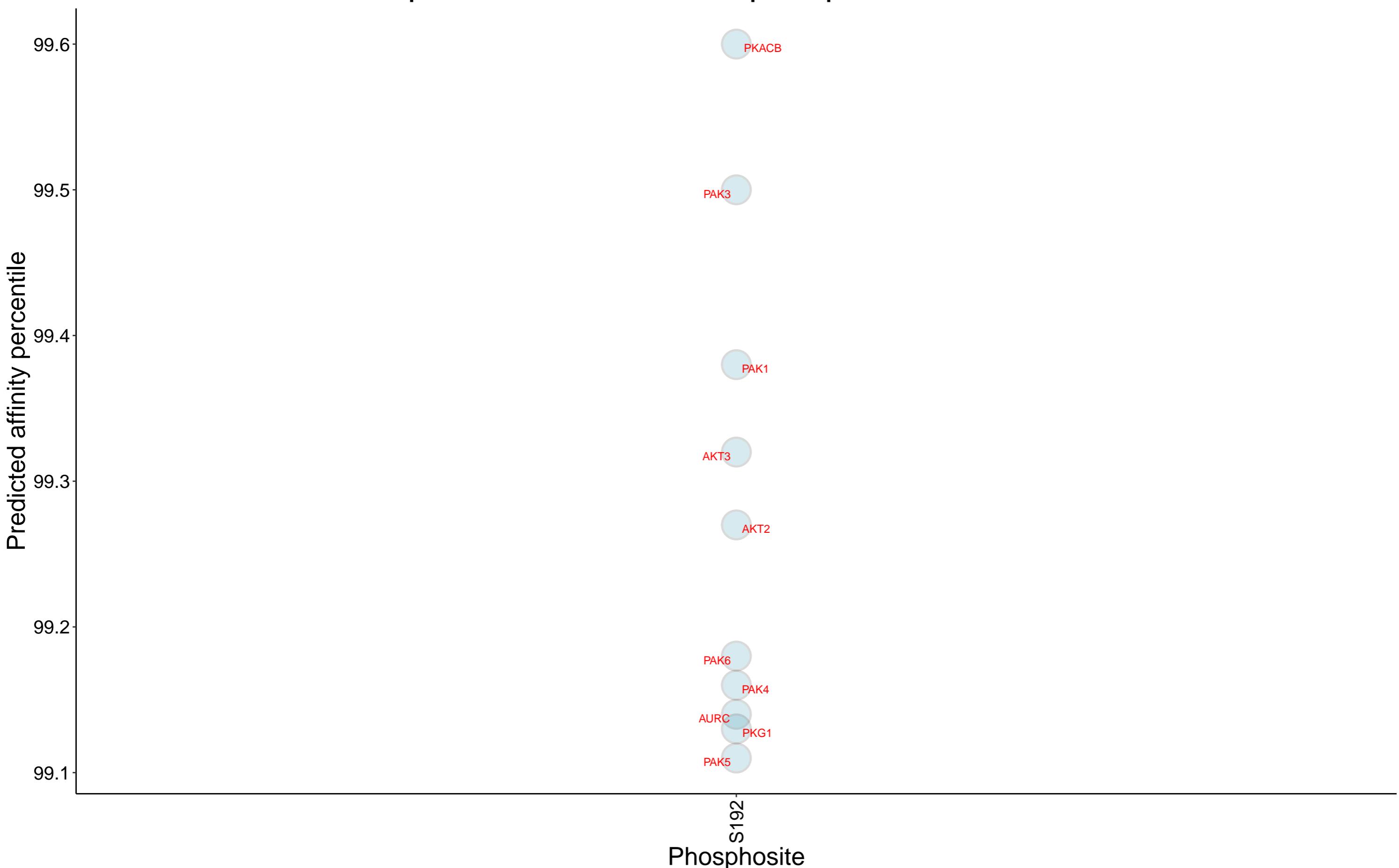
Sorted by p values!							
Downregulated in blood cancers at low/absent ARPC2				Upregulated in blood cancers at low/absent ARPC2			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.23	2.55e-27	ACTR3	actin related protein 3	0.13	1.41e-04	PAFAH1B3	platelet activating factor acetylhydrolase, membrane attack complex subunit
-0.18	4.78e-25	ARPC3	actin related protein 2/3 complex subunit 3	0.63	1.75e-04	SMTN	smoothelin
-0.19	2.14e-22	ARPC4	actin related protein 2/3 complex subunit 4	0.06	2.74e-04	HNRNPDL	heterogeneous nuclear ribonucleoprotein D/L-like
-0.03	3.10e-22	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	0.69	4.31e-04	SPATA5	spermatogenesis associated 5
-0.34	9.89e-11	ARPC1B	actin related protein 2/3 complex subunit 1B	0.08	5.98e-04	SUPT5H	SPT5 homolog, DSIF elongation factor
-1.72	3.35e-09	PLEK	pleckstrin	0.08	7.06e-04	RAE1	ribonucleic acid export 1
-0.28	1.16e-08	ACTR2	actin related protein 2	0.83	1.05e-03	RNF169	ring finger protein 169
-0.88	8.12e-06	RMDN1	regulator of microtubule dynamics 1	0.52	1.23e-03	RPL36AL	ribosomal protein L36a like
-0.99	8.12e-06	MNDA	myeloid cell nuclear differentiation antigen	0.39	1.40e-03	LARP4	La ribonucleoprotein 4
-1.2	1.08e-05	NCF4	neutrophil cytosolic factor 4	0.76	1.42e-03	CCNB1	cyclin B1
-0.58	1.55e-05	CEBPA	CCAAT enhancer binding protein alpha	0.06	1.45e-03	PHF5A	PHD finger protein 5A
-1.24	3.09e-05	PLCG2	phospholipase C gamma 2	0.59	1.51e-03	SH3PXD2B	SH3 and PX domains 2B
-1.02	5.00e-05	WDFY4	WDFY family member 4	0.08	1.76e-03	LSM3	LSM3 homolog, U6 small nuclear RNA
-0.08	5.40e-05	MYH9	myosin heavy chain 9	0.57	1.76e-03	SUPT4H1	SPT4 homolog, DSIF elongation factor
-0.07	5.72e-05	CAPZB	capping actin protein of muscle Z-line	0.05	1.94e-03	ATXN2L	ataxin 2 like
-1.08	5.72e-05	DOCK8	dedicator of cytokinesis 8	0.05	1.95e-03	EIF4B	eukaryotic translation initiation factor 4B
-1.2	7.47e-05	PTK2B	protein tyrosine kinase 2 beta	0.07	1.97e-03	CSTF2	cleavage stimulation factor subunit 2B
-0.13	1.14e-04	ARHGAP1	Rho GTPase activating protein 1	0.8	1.97e-03	UAP1	UDP-N-acetylglucosamine pyrophosphoryl transferase 1
-0.13	1.14e-04	GNAI2	G protein subunit alpha i2	0.76	1.98e-03	C12orf57	chromosome 12 open reading frame 57
-0.4	1.16e-04	GRK2	G protein-coupled receptor kinase 2	0.89	1.98e-03	IGSF8	immunoglobulin superfamily member 8
-1.28	1.33e-04	LAT2	linker for activation of T cells fa	0.6	2.07e-03	PRCC	proline rich mitotic checkpoint component
-1.05	1.57e-04	PRKCD	protein kinase C delta	0.62	2.76e-03	STEEP1	STING1 ER exit protein 1
-0.98	1.75e-04	ANKRD44	ankyrin repeat domain 44	0.08	2.79e-03	SMARCE1	SWI/SNF related, matrix associated, chromatin rearranging protein 1
-0.67	1.75e-04	CES1	carboxylesterase 1	0.39	2.79e-03	UBQLN4	ubiquilin 4
-1	2.37e-04	MYO1F	myosin IF	0.76	2.84e-03	MORC2	MORC family CW-type zinc finger 2
-0.51	2.47e-04	SERPINB10	serpin family B member 10	0.07	3.25e-03	EIF5	eukaryotic translation initiation factor 5
-0.97	3.11e-04	RASSF2	Ras association domain family member 2	0.45	3.43e-03	SIVA1	SIVA1 apoptosis inducing factor
-0.09	4.19e-04	CAP1	cyclase associated actin cytoskeleton-associated protein 1	0.05	3.68e-03	PNN	pinin, desmosome associated protein
-0.99	4.31e-04	NCKAP1L	NCK associated protein 1 like	0.2	3.94e-03	PGRMC1	progesterone receptor membrane component 1
-0.5	4.33e-04	RNASE2	ribonuclease A family member 2	0.81	4.06e-03	GIPC1	GIPC PDZ domain containing family member 1
-0.91	4.33e-04	CTSS	cathepsin S	0.05	4.09e-03	SRRM2	serine/arginine repetitive matrix 2
-0.26	4.73e-04	MAN2B1	mannosidase alpha class 2B member 1	0.5	4.11e-03	ZNRD2	zinc ribbon domain containing 2
-1.05	5.63e-04	SH3BP1	SH3 domain binding protein 1	0.31	4.65e-03	GIMAP6	GTPase, IMAP family member 6
-0.59	7.06e-04	STK10	serine/threonine kinase 10	0.37	4.65e-03	ZBTB21	zinc finger and BTB domain containing 21
-1.04	7.06e-04	SYK	spleen associated tyrosine kinase	0.05	4.65e-03	SAFB	scaffold attachment factor B
-0.06	7.60e-04	RPL4	ribosomal protein L4	0.34	4.68e-03	GLRX5	glutaredoxin 5
-0.85	7.68e-04	PRTN3	proteinase 3	0.04	4.77e-03	DDX46	DEAD-box helicase 46
-0.2	9.21e-04	ACAD9	acyl-CoA dehydrogenase family member 9	0.48	5.43e-03	ANKRD17	ankyrin repeat domain 17
-0.09	9.30e-04	PABPA1	PABPA1, PABPA1-like, PABPA1-like 1	0.87	5.43e-03	ACP2	acid phosphatase 2, lysosomal



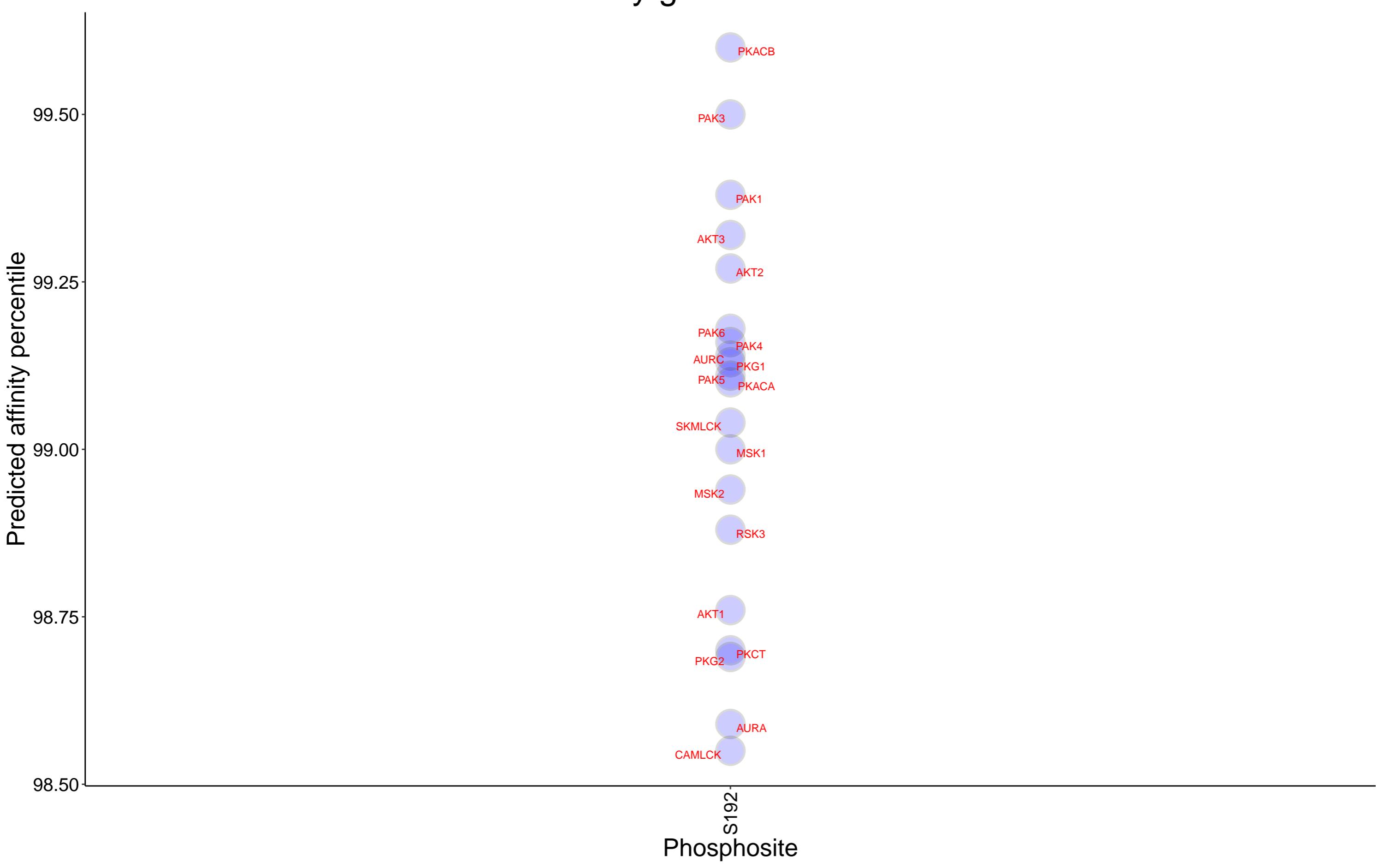
# Top 250 correlation coefficients overrepresentation, ARPC2 protein, DB1



# Top 10 kinases for each phosphosite in ARPC2



Kinases with affinity greater than 98.5% to ARPC2



# Top 15 positive correlation coefficients for ARPC2 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

