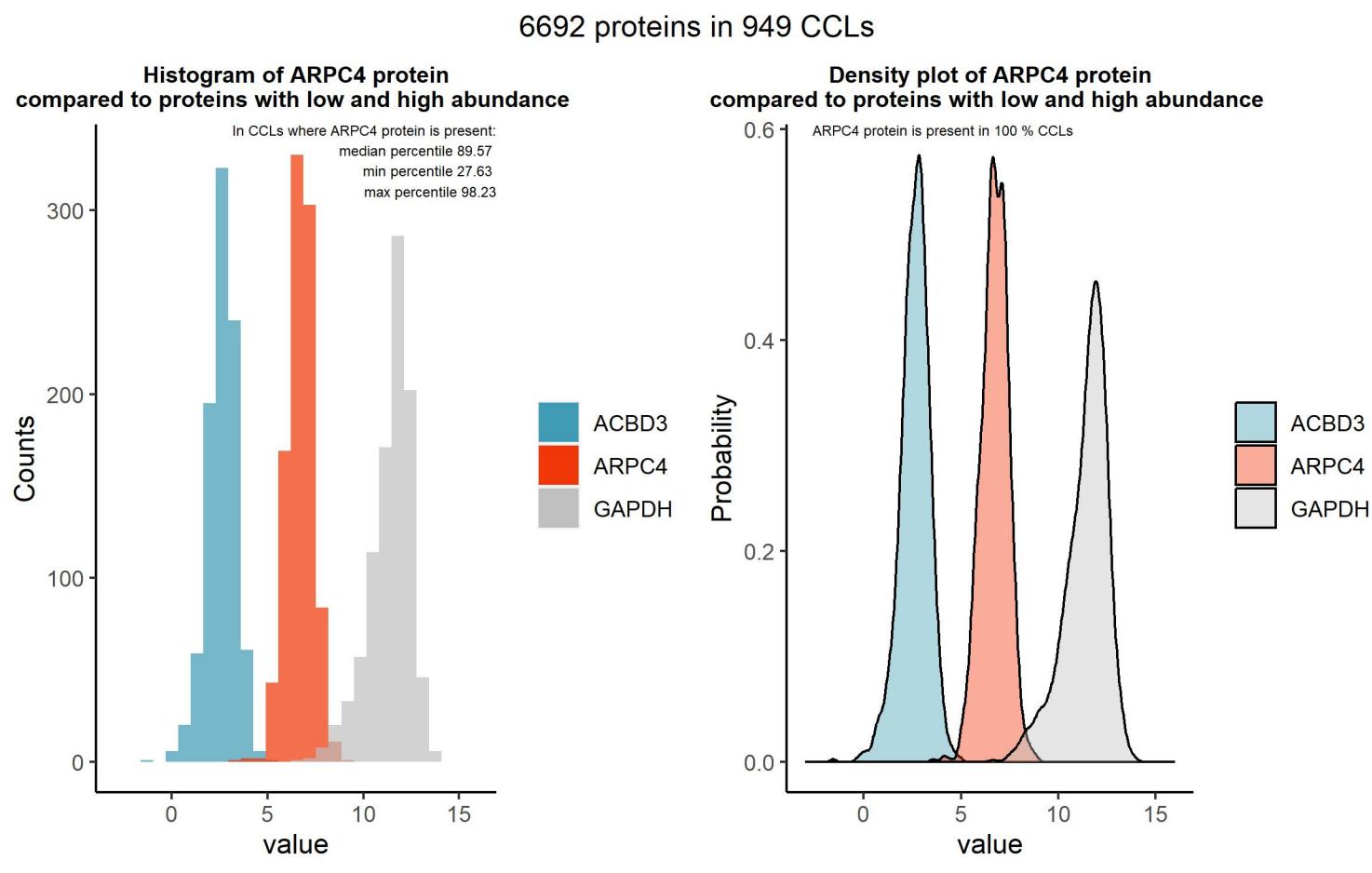


ARPC4

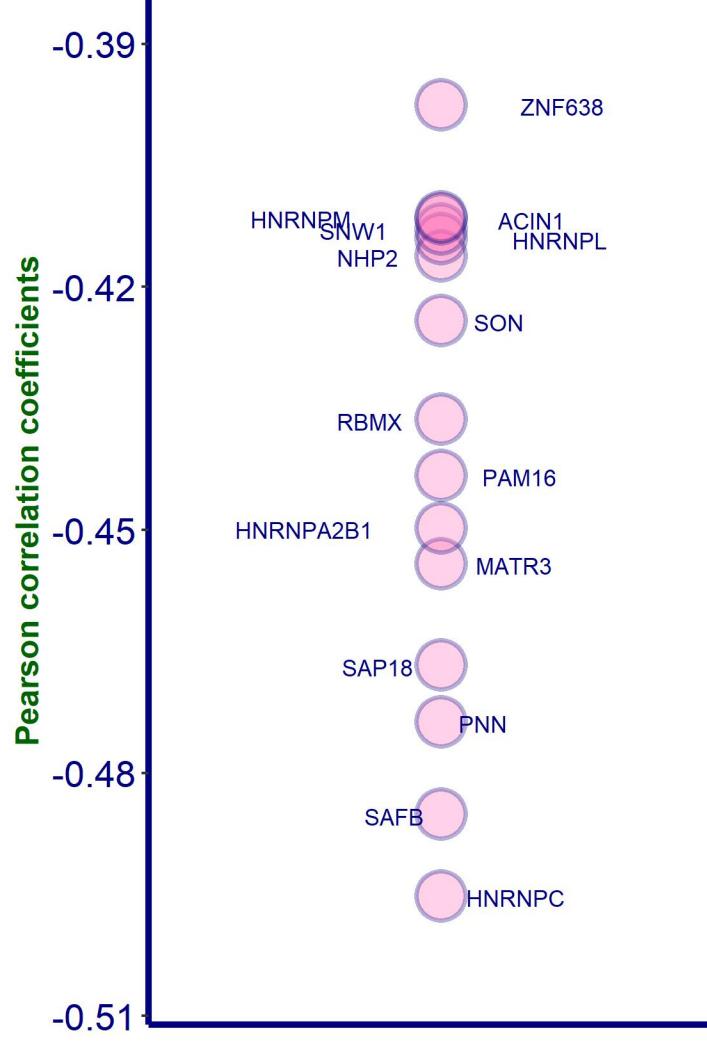
Protein name: ARPC4 ; UNIPROT: P59998 ; Gene name: actin related protein 2/3 complex subunit 4

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

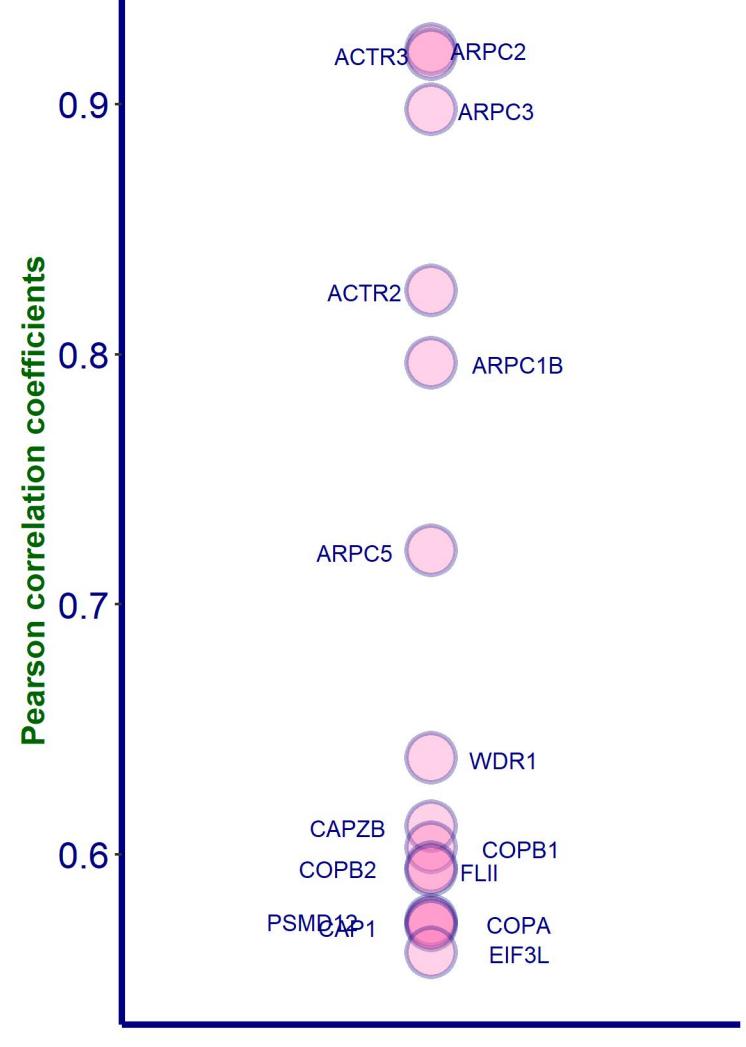
Sanger Institute Protein Database 1 (DB1), protein presence is certain



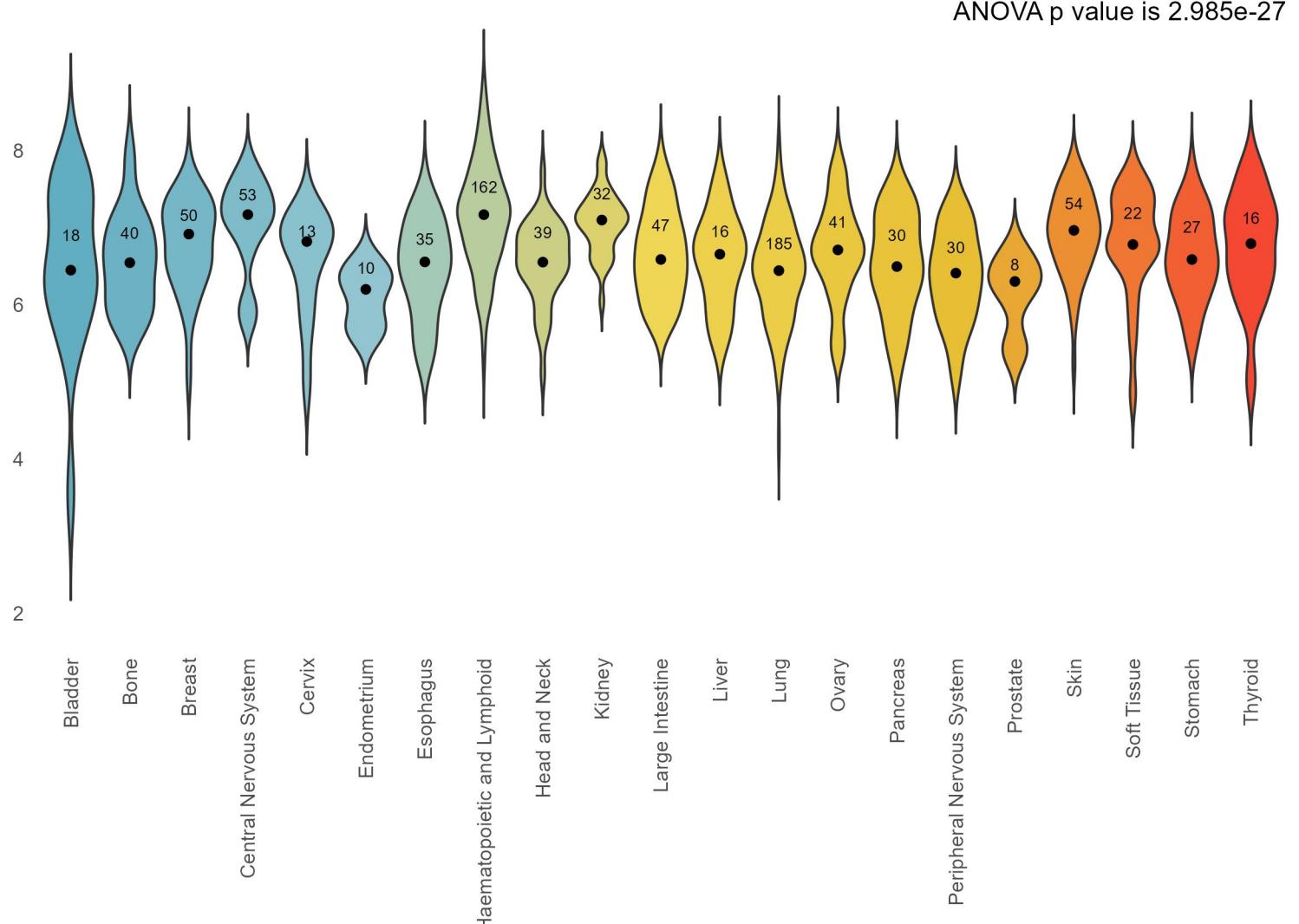
Top negative correlations of ARPC4 protein, DB1



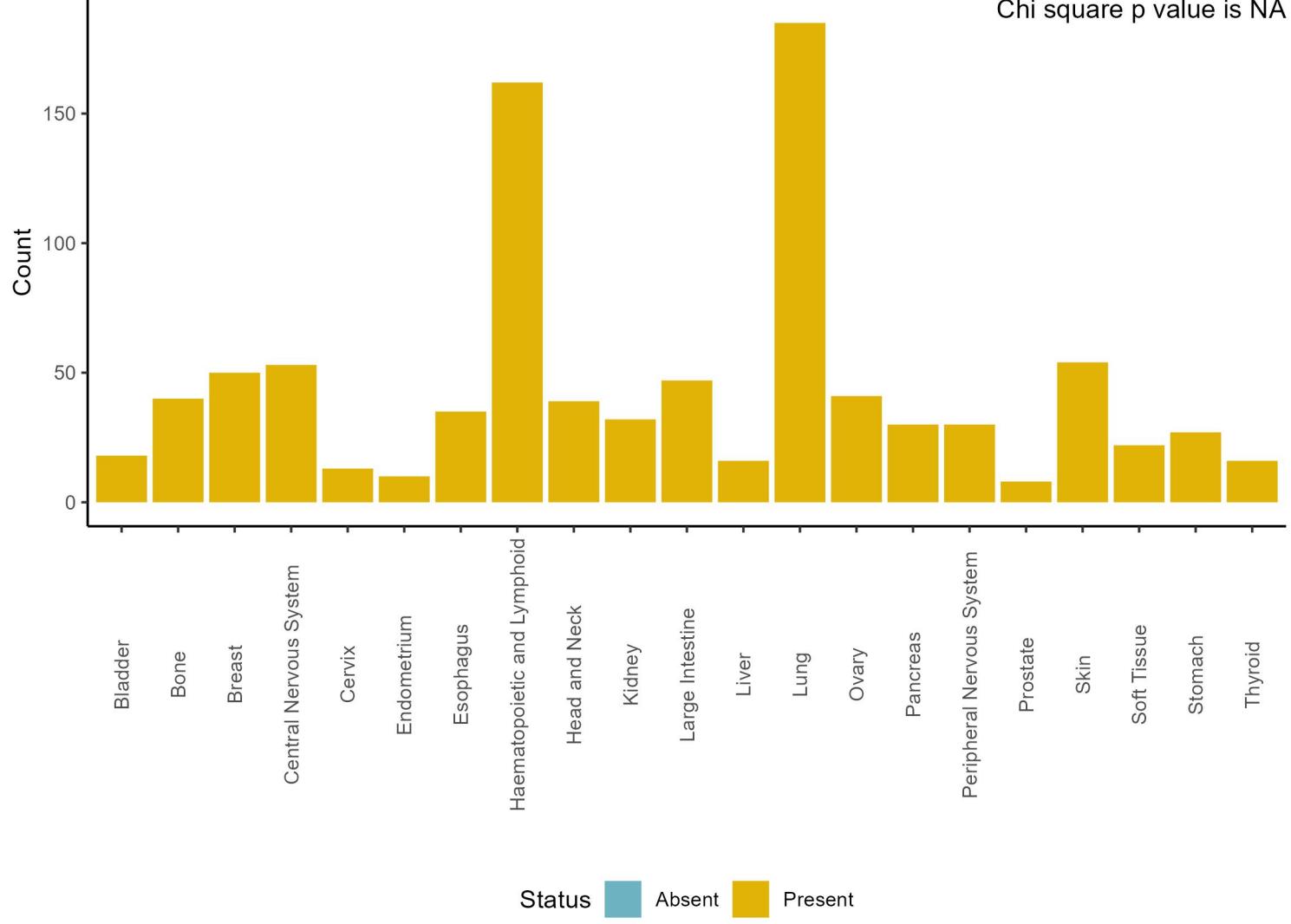
Top positive correlations of ARPC4 protein, DB1



Amount of ARPC4 protein, number of CCLs where it is present by tissue, DB1



Present and absent ARPC4 protein counts by tissue, DB1

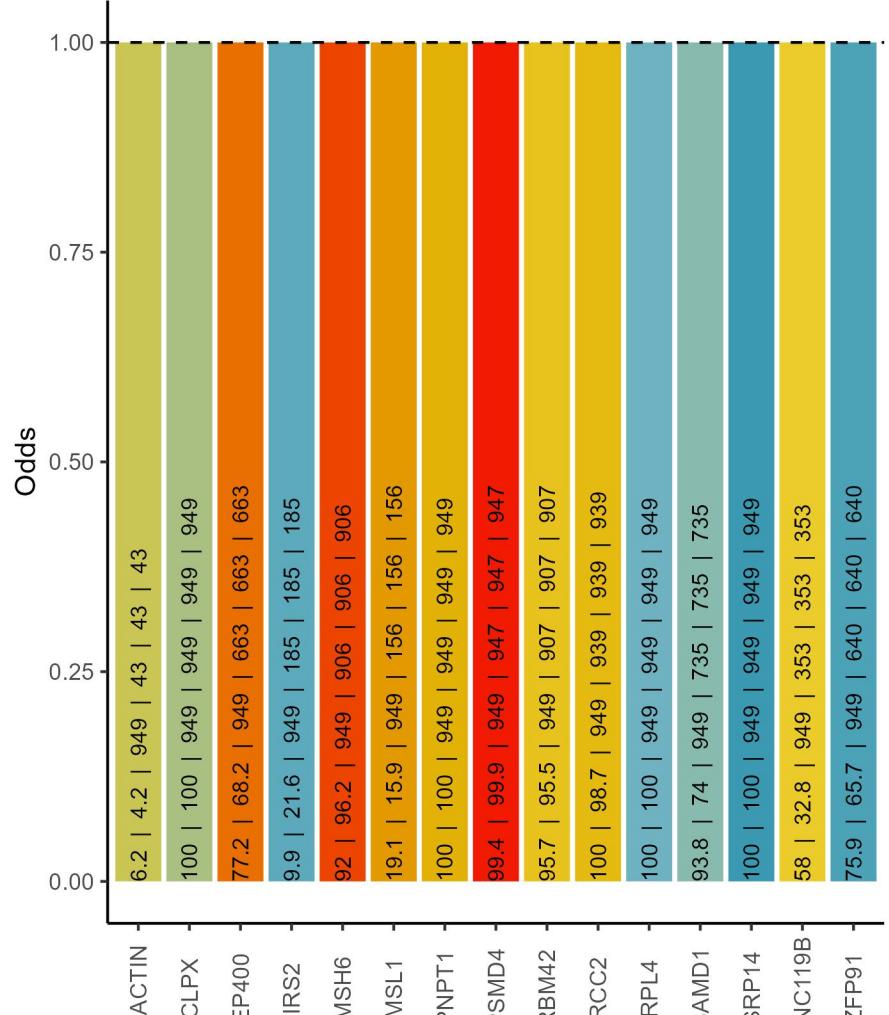


Cooccurrence with ARPC4 protein, DB1

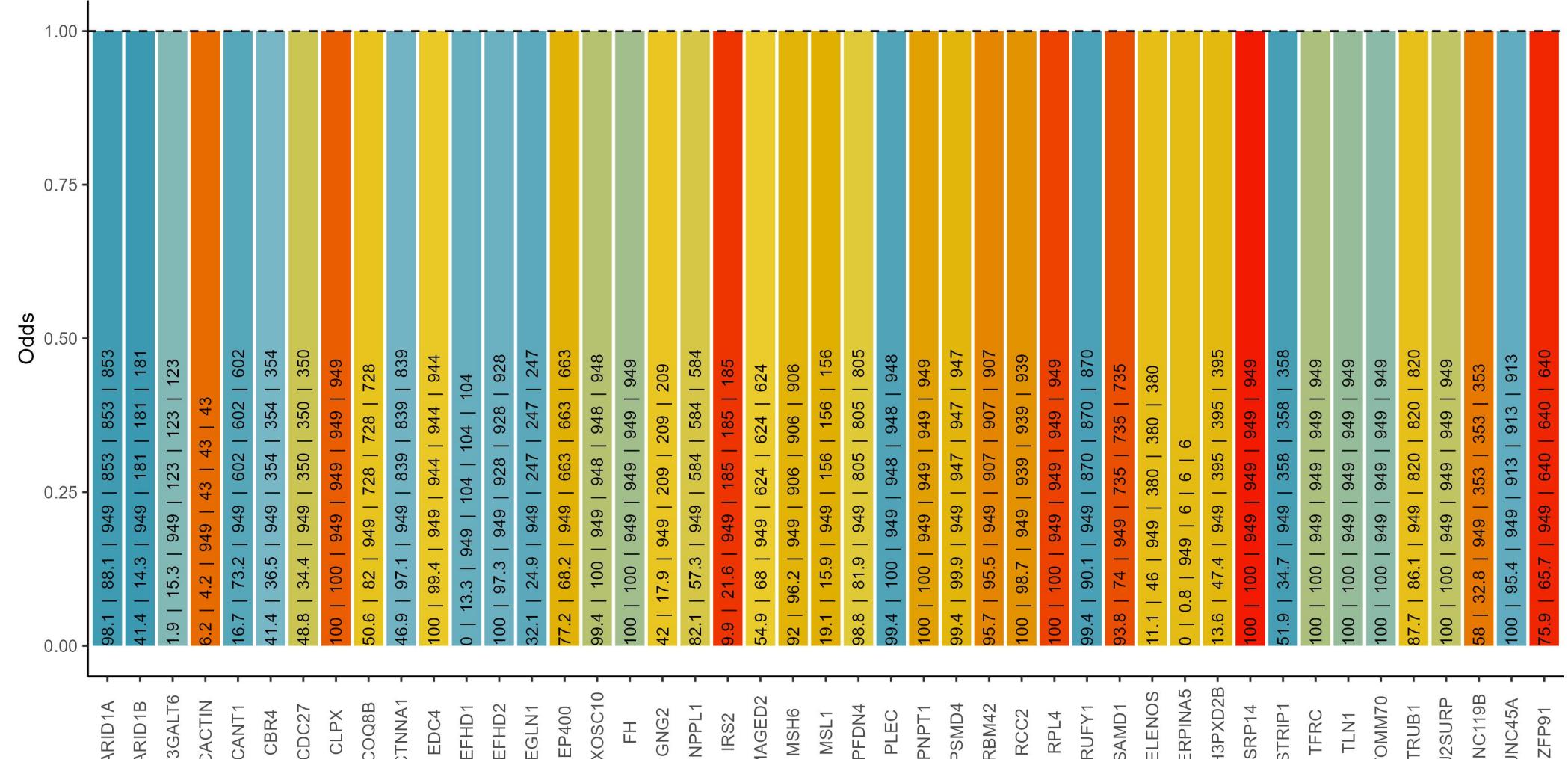
% of ARPC4 in blood cancers: 100 ; % of ARPC4 in solid cancers: 100

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ARPC4 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

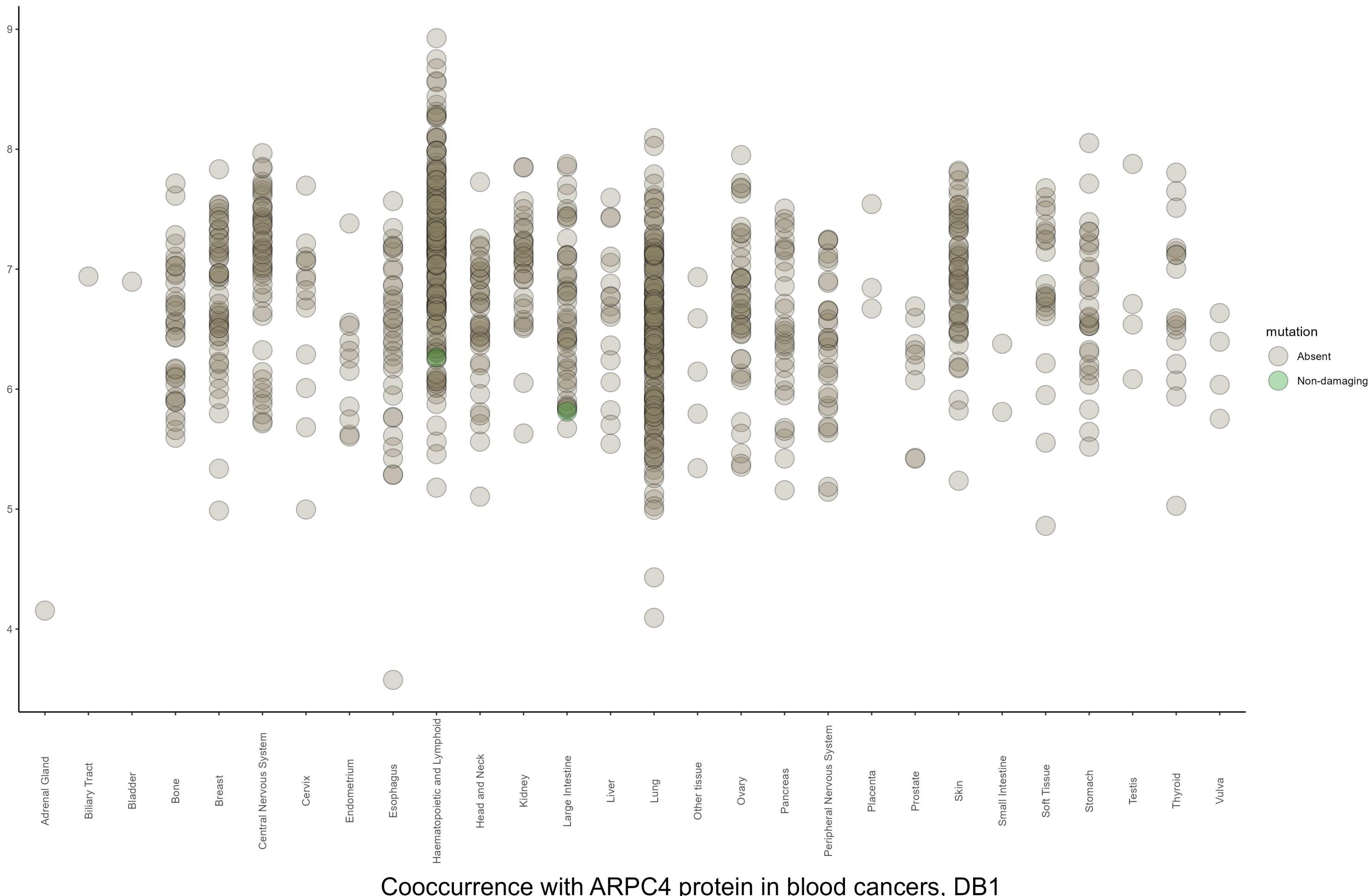
Negative cooccurrence



Positive cooccurrence



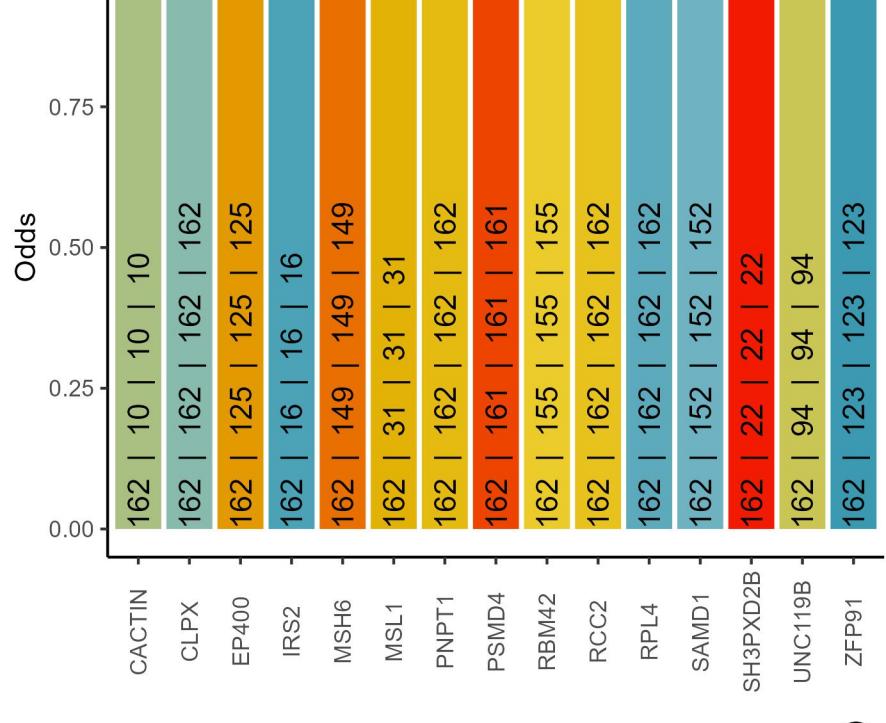
Amount of ARPC4 protein and mutation status by tissue, DB1



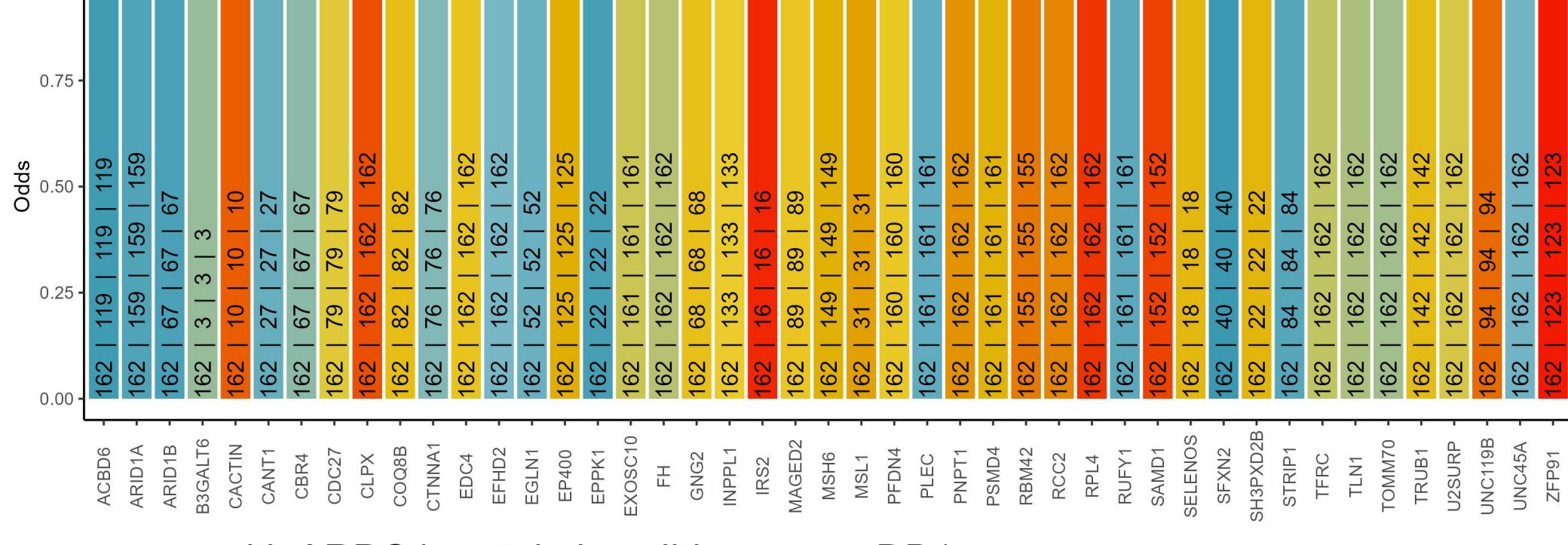
Cooccurrence with ARPC4 protein in blood cancers, DB1

The text in the bars: incidence of ARPC4 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



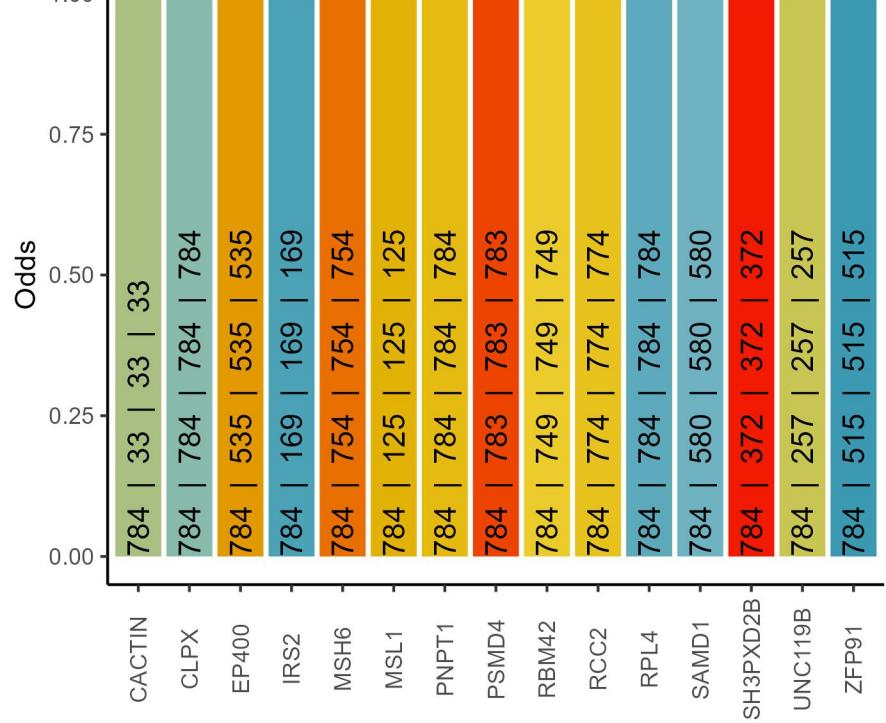
Positive cooccurrence



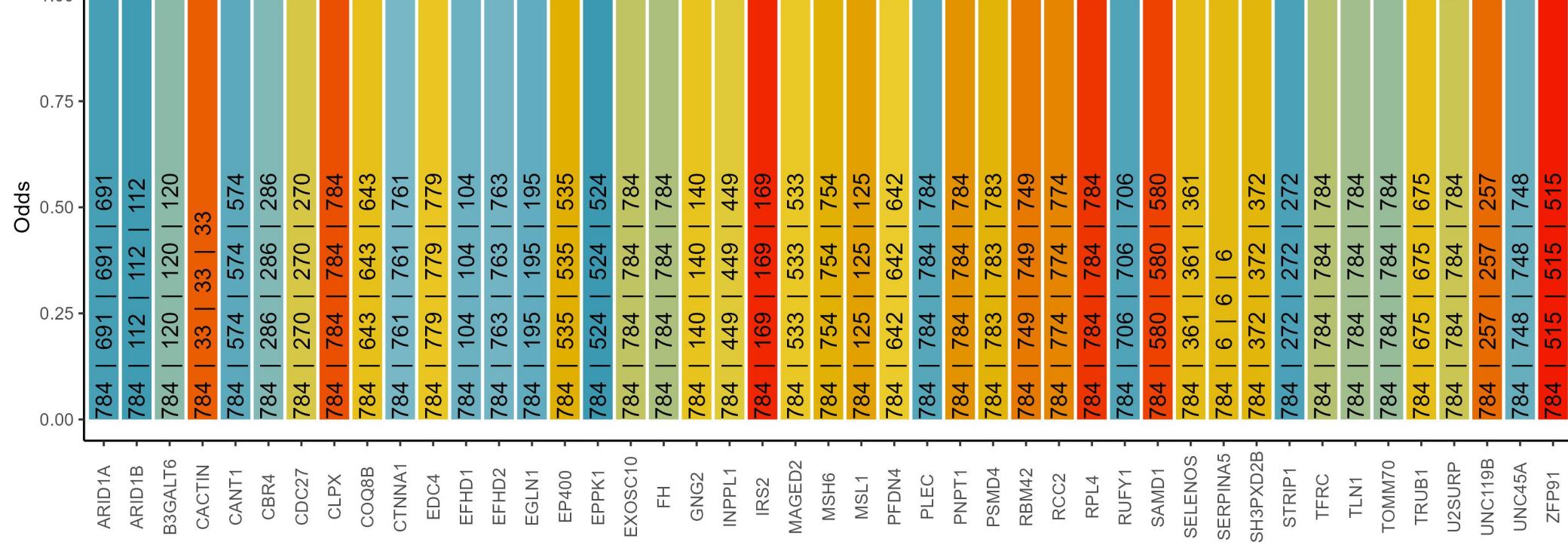
Cooccurrence with ARPC4 protein in solid cancers, DB1

The text in the bars: incidence of ARPC4 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

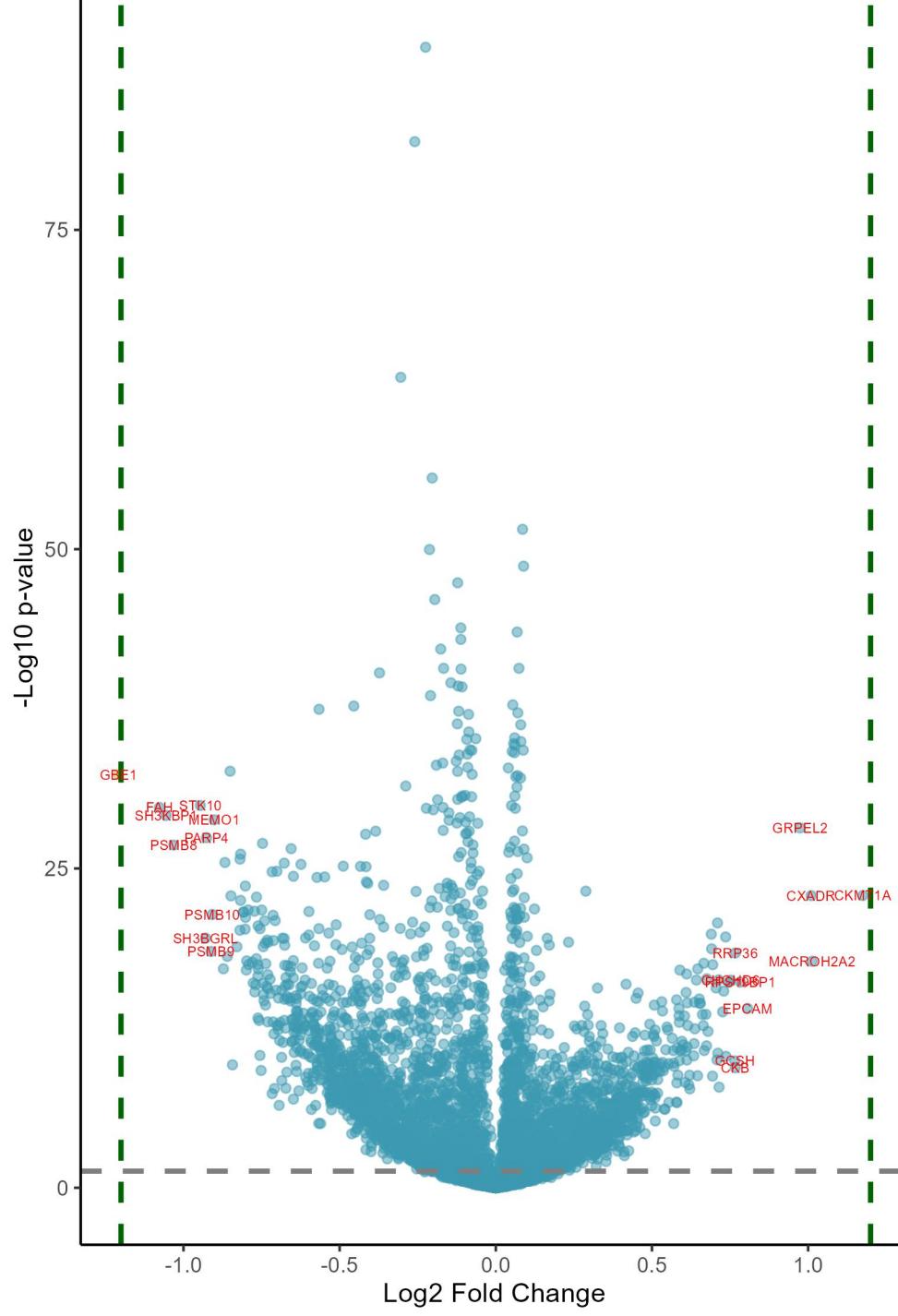
Negative cooccurrence



Positive cooccurrence

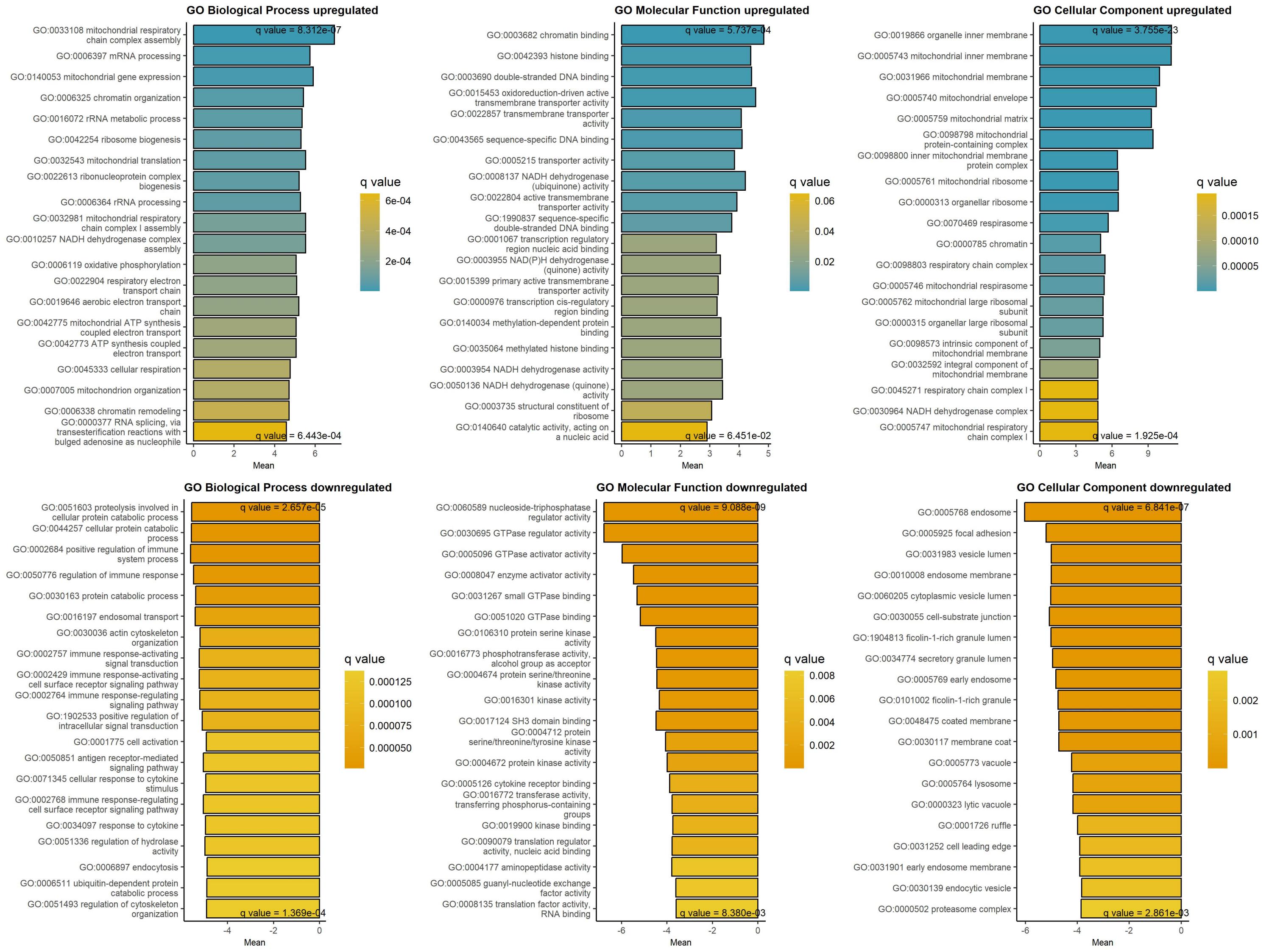


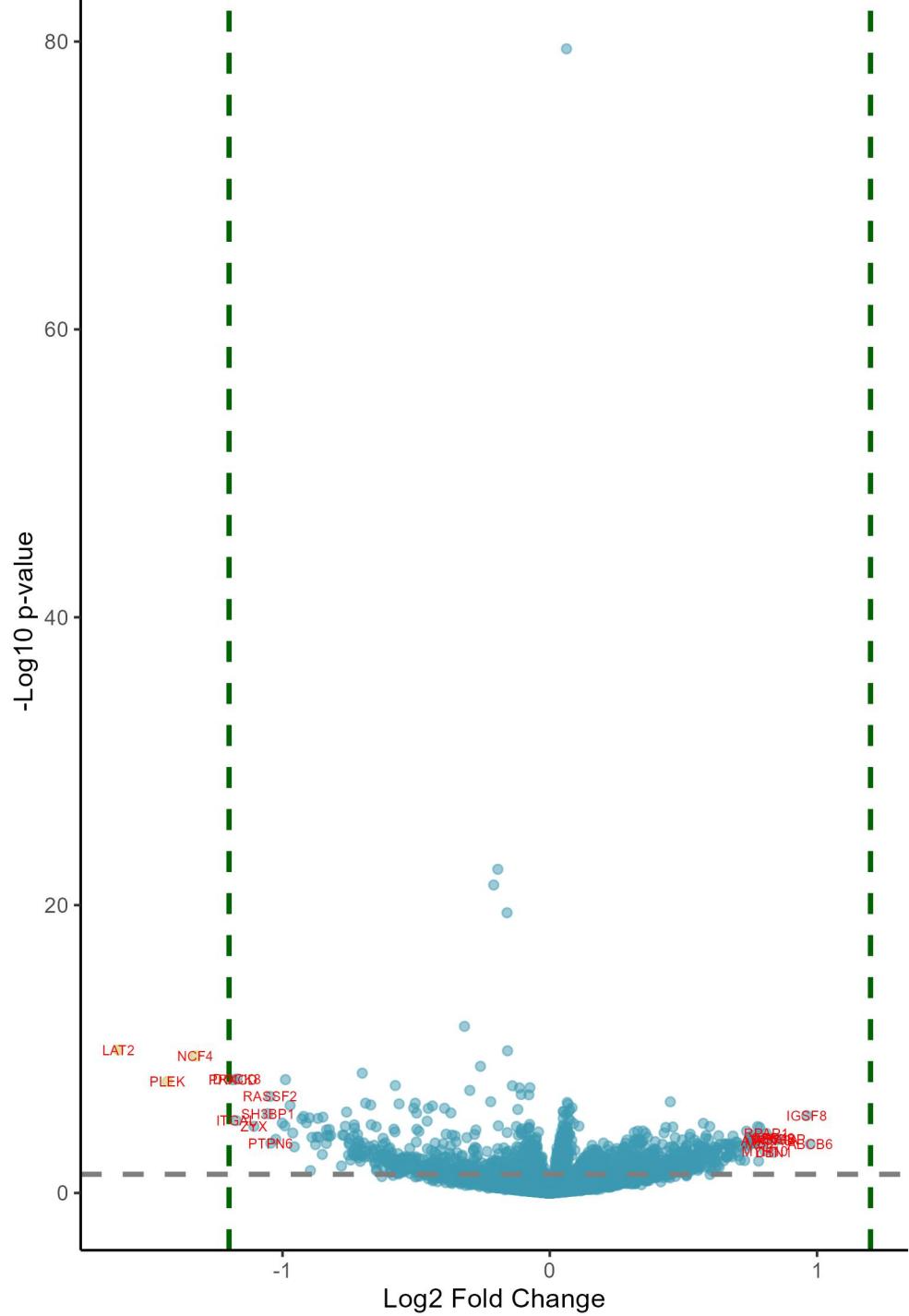
Downregulated at low/absent ARPC4 Upregulated at low/absent ARPC4



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.21	5.50e-31	GBE1	1,4-alpha-glucan branching enzyme 1	1.18	6.14e-22	CKMT1A	creatine kinase, mitochondrial 1A
-1.08	1.62e-28	FAH	fumarylacetoacetate hydrolase	1.01	4.51e-17	MACROH2A2	macroH2A.2 histone
-1.06	6.37e-28	SH3KBP1	SH3 domain containing kinase bindin	1.01	6.20e-22	CXADR	CXADR Ig-like cell adhesion molecule
-1.03	1.03e-25	PSMB8	proteasome 20S subunit beta 8	0.97	5.40e-27	GRPEL2	GrpE like 2, mitochondrial
-0.95	1.18e-28	STK10	serine/threonine kinase 10	0.81	1.24e-13	EPCAM	epithelial cell adhesion molecule
-0.93	8.56e-19	SH3BGRL	SH3 domain binding glutamate rich p	0.78	1.51e-15	RPS19BP1	ribosomal protein S19 binding prote
-0.93	2.87e-26	PARP4	poly(ADP-ribose) polymerase family	0.77	1.11e-17	RRP36	ribosomal RNA processing 36
-0.91	8.51e-18	PSMB9	proteasome 20S subunit beta 9	0.77	2.61e-09	CKB	creatine kinase B
-0.91	1.54e-20	PSMB10	proteasome 20S subunit beta 10	0.77	8.52e-10	GCSH	glycine cleavage system protein H
-0.9	1.35e-27	MEMO1	mediator of cell motility 1	0.75	1.08e-15	CHCHD6	coiled-coil-helix-coiled-coil-helix
-0.87	1.58e-16	GLRX	glutaredoxin	0.75	1.55e-15	GTPBP3	GTP binding protein 3, mitochondria
-0.87	2.09e-24	TRIM21	tripartite motif containing 21	0.74	3.99e-10	CDH1	cadherin 1
-0.86	1.99e-17	CDK6	cyclin dependent kinase 6	0.74	7.08e-19	TDRKH	tudor and KH domain containing
-0.85	3.24e-31	NAGK	N-acetylglucosamine kinase	0.73	6.87e-15	CENPV	centromere protein V
-0.85	6.46e-22	PCYT2	phosphate cytidylyltransferase 2, e	0.73	2.25e-13	PRXL2A	peroxiredoxin like 2A
-0.84	1.63e-09	ARPC5	actin related protein 2/3 complex s	0.71	6.80e-08	H1-0	H1.0 linker histone
-0.83	3.73e-18	TAOK3	TAO kinase 3	0.71	1.04e-15	ZNF280C	zinc finger protein 280C
-0.82	2.24e-19	GYS1	glycogen synthase 1	0.71	2.38e-10	SPINT1	serine peptidase inhibitor, Kunitz
-0.82	1.16e-24	LIMS1	LIM zinc finger domain containing 1	0.71	6.48e-20	KIF1A	kinesin family member 1A
-0.82	1.41e-21	OSTF1	osteoclast stimulating factor 1	0.71	7.08e-10	SPINT2	serine peptidase inhibitor, Kunitz
-0.82	4.90e-25	GMPPB	GDP-mannose pyrophosphorylase B	0.71	4.02e-15	SCML2	Scm polycomb group protein like 2
-0.81	1.06e-20	LPXN	leupaxin	0.69	8.03e-17	NCBP2AS2	NCBP2 antisense 2 (head to head)
-0.81	1.01e-20	SCYL1	SCY1 like pseudokinase 1	0.69	1.07e-08	JUP	junction plakoglobin
-0.8	1.86e-19	NFKB1	nuclear factor kappa B subunit 1	0.69	5.36e-18	KNOP1	lysine rich nucleolar protein 1
-0.8	1.20e-22	RSU1	Ras suppressor protein 1	0.69	4.38e-19	PODXL2	podocalyxin like 2
-0.8	2.52e-20	SWAP70	switching B cell complex subunit SW	0.68	6.00e-12	SPTBN2	spectrin beta, non-erythrocytic 2
-0.8	1.94e-16	WIPF1	WAS/WASL interacting protein family	0.68	8.60e-16	CCDC137	coiled-coil domain containing 137
-0.8	4.22e-17	C11orf68	chromosome 11 open reading frame 68	0.67	6.88e-11	INA	internexin neuronal intermediate fi
-0.79	7.26e-21	ALAD	aminolevulinate dehydratase	0.67	3.42e-13	EPB41	erythrocyte membrane protein band 4

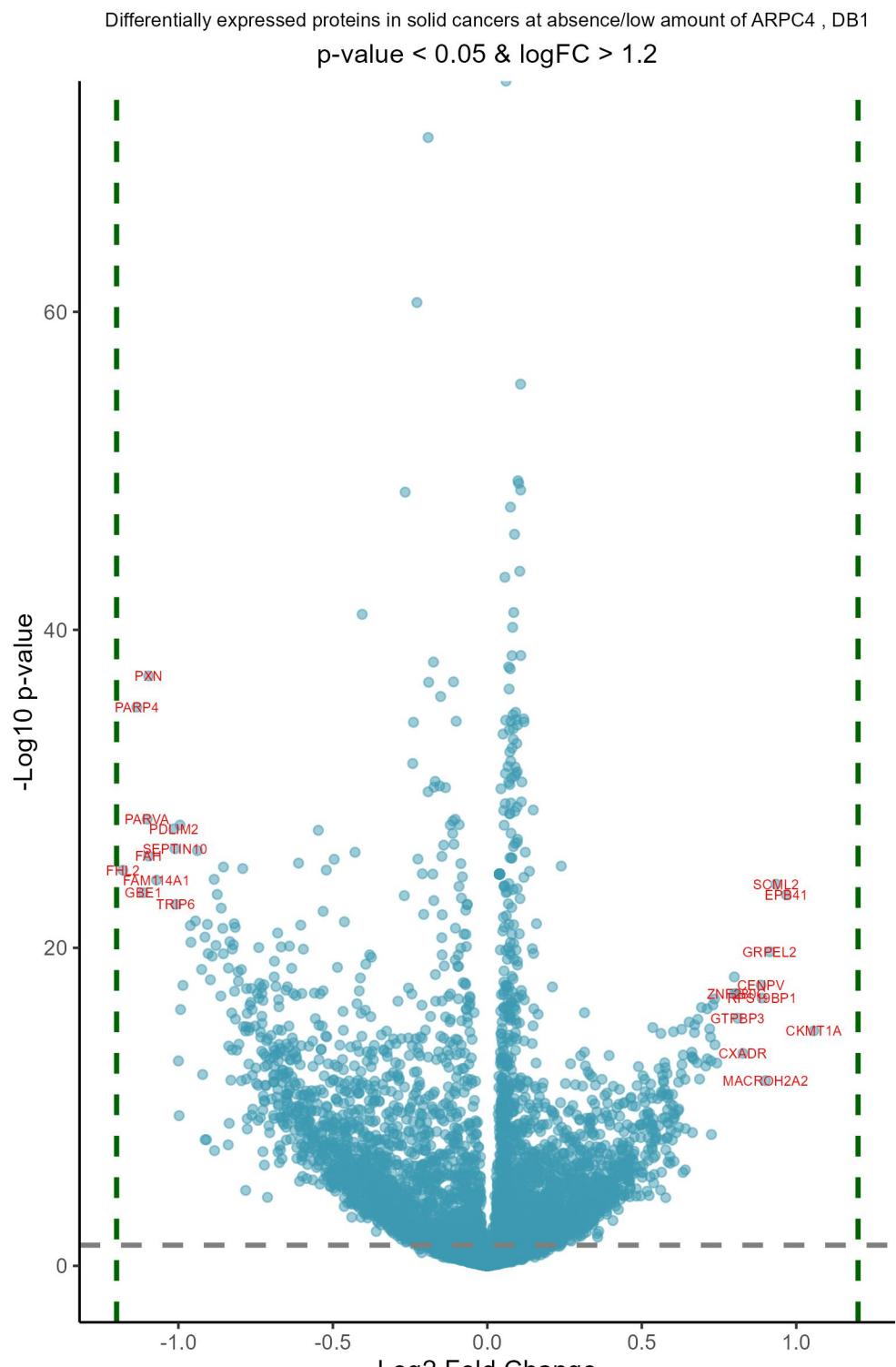
GAGE analysis on upregulated and downregulated proteins at low/absent ARPC4 protein, DB1





Downregulated in blood cancers at low/absent ARPC4 Upregulated in blood cancers at low/absent ARPC4

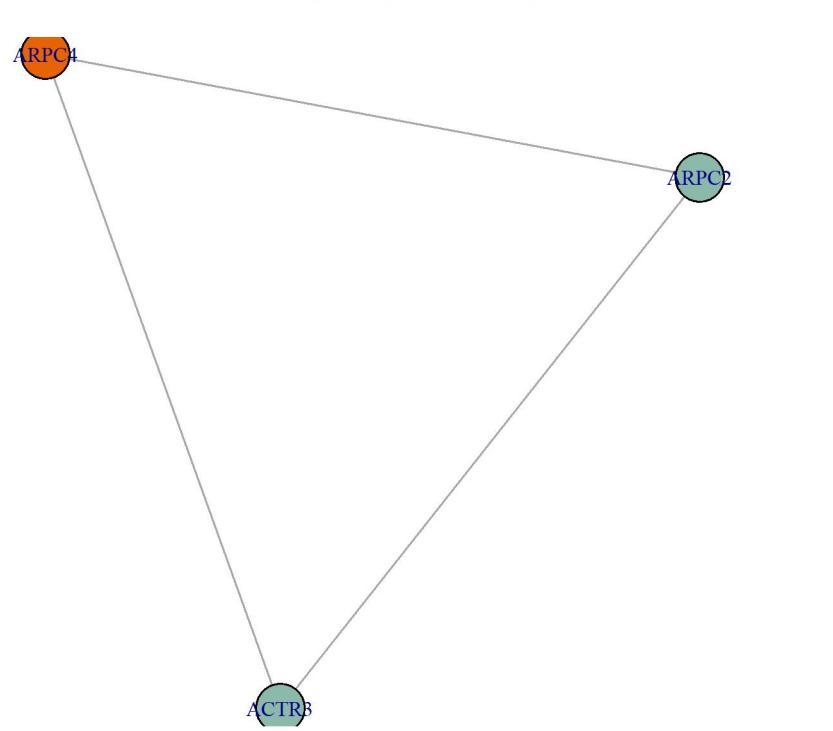
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.61	1.09e-07	LAT2	linker for activation of T cells fa	0.97	1.18e-02	ABCB6	ATP binding cassette subfamily B me
-1.43	7.90e-06	PLEK	pleckstrin	0.96	5.72e-04	IGSF8	immunoglobulin superfamily member 8
-1.33	2.19e-07	NCF4	neutrophil cytosolic factor 4	0.86	7.50e-03	MRGBP	MRG domain binding protein
-1.19	6.45e-06	PRKCD	protein kinase C delta	0.85	7.84e-03	ASF1A	anti-silencing function 1A histone
-1.17	1.10e-03	ITGAL	integrin subunit alpha L	0.84	2.57e-02	DBN1	drebrin 1
-1.17	6.45e-06	DOCK8	dedicator of cytokinesis 8	0.84	6.81e-03	CEP43	centrosomal protein 43
-1.11	2.15e-03	ZYX	zyxin	0.81	8.39e-03	ATP1A3	ATPase Na+/K+ transporting subunit
-1.06	4.44e-04	SH3BP1	SH3 domain binding protein 1	0.81	4.27e-03	RPAP1	RNA polymerase II associated protei
-1.05	5.60e-05	RASSF2	Ras association domain family membe	0.8	2.24e-02	MYH10	myosin heavy chain 10
-1.04	1.10e-02	PTPN6	protein tyrosine phosphatase non-re	0.79	1.10e-02	MSI2	musashi RNA binding protein 2
-1.03	7.67e-03	ITGB2	integrin subunit beta 2	0.79	2.32e-03	RNF169	ring finger protein 169
-1	1.53e-03	PLCG2	phospholipase C gamma 2	0.78	5.43e-03	PPP2R5C	protein phosphatase 2 regulatory su
-0.99	2.14e-03	PTK2B	protein tyrosine kinase 2 beta	0.78	5.76e-02	TSTD1	thiosulfate sulfurtransferase like
-0.99	6.45e-06	MNDA	myeloid cell nuclear differentiatio	0.78	2.15e-03	MORC2	MORC family CW-type zinc finger 2
-0.97	1.72e-04	ANKRD44	ankyrin repeat domain 44	0.77	7.88e-03	MAP1A	microtubule associated protein 1A
-0.96	4.15e-03	MYO1G	myosin IG	0.77	1.08e-02	TSPAN3	tetraspanin 3
-0.96	1.53e-02	ICAM3	intercellular adhesion molecule 3	0.76	6.48e-03	BRD2	bromodomain containing 2
-0.93	8.77e-04	MYO1F	myosin IF	0.76	1.08e-02	MAZ	MYC associated zinc finger protein
-0.92	6.49e-04	VAV1	vav guanine nucleotide exchange fac	0.76	5.11e-03	BRD7	bromodomain containing 7
-0.91	1.50e-03	LYZ	lysozyme	0.75	8.29e-03	TCF12	transcription factor 12
-0.9	7.86e-04	UBA7	ubiquitin like modifier activating	0.75	7.11e-03	SNTB2	syntrophin beta 2
-0.9	1.46e-01	S100A4	S100 calcium binding protein A4	0.75	1.32e-02	GTSE1	G2 and S-phase expressed 1
-0.89	6.25e-03	TRIM22	tripartite motif containing 22	0.74	1.12e-02	MFGE8	milk fat globule EGF and factor V/V
-0.88	1.24e-02	PYCARD	PYD and CARD domain containing	0.74	1.81e-02	POLR2F	RNA polymerase II, I and III subuni
-0.87	5.97e-03	GPD2	glycerol-3-phosphate dehydrogenase	0.74	3.39e-03	SKA3	spindle and kinetochore associated
-0.87	8.30e-04	WDFY4	WDFY family member 4	0.73	5.48e-02	TUBB3	tubulin beta 3 class III
-0.86	6.25e-03	SFXN3	sideroflexin 3	0.71	1.42e-02	SDAD1	SDA1 domain containing 1
-0.85	3.21e-02	VAMP8	vesicle associated membrane protein	0.71	5.34e-02	LGALS3BP	galectin 3 binding protein
-0.85	7.11e-04	PRTN3	proteinase 3	0.71	3.65e-02	IRF2BPL	interferon regulatory factor 2 bind



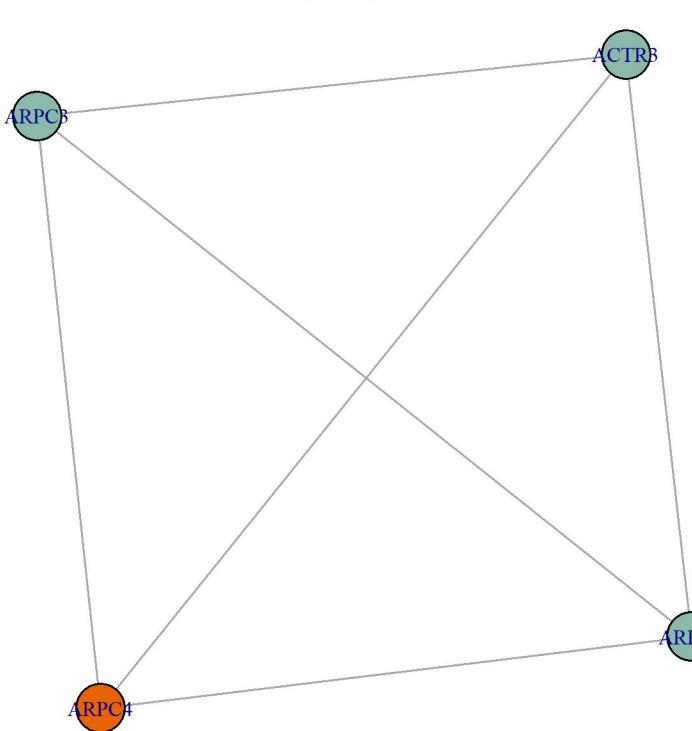
Downregulated in solid cancers at low/absent ARPC4 Upregulated in solid cancers at low/absent ARPC4

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.18	8.11e-24	FHL2	four and a half LIM domains 2	1.06	2.52e-14	CKMT1A	creatine kinase, mitochondrial 1A
-1.13	1.80e-33	PARP4	poly(ADP-ribose) polymerase family	0.97	1.49e-22	EPB41	erythrocyte membrane protein band 4
-1.11	1.11e-22	GBE1	1,4-alpha-glucan branching enzyme 1	0.93	3.38e-23	SCML2	Scm polycomb group protein like 2
-1.1	7.43e-27	PARVA	parvin alpha	0.91	4.45e-19	GRPEL2	GrpE like 2, mitochondrial
-1.1	1.20e-24	FAH	fumarylacetoacetate hydrolase	0.9	2.25e-11	MACROH2A2	macroH2A.2 histone
-1.1	2.39e-35	PXN	paxillin	0.89	2.78e-16	RPS19BP1	ribosomal protein S19 binding prote
-1.07	1.88e-23	FAM114A1	family with sequence similarity 114	0.89	4.79e-17	CENPV	centromere protein V
-1.01	2.75e-26	PDLIM2	PDZ and LIM domain 2	0.83	5.40e-13	CXADR	CXADR Ig-like cell adhesion molecu
-1.01	4.34e-25	SEPTIN10	septin 10	0.81	4.42e-15	GTPBP3	GTP binding protein 3, mitochondria
-1.01	5.73e-22	TRIP6	thyroid hormone receptor interactor	0.81	1.55e-16	ZNF280C	zinc finger protein 280C
-1	1.51e-12	S100A10	S100 calcium binding protein A10	0.8	1.53e-17	KIF1A	kinesin family member 1A
-1	2.50e-09	NQO1	NAD(P)H quinone dehydrogenase 1	0.8	1.55e-16	MEAF6	MYST/Esa1 associated factor 6
-0.99	1.64e-26	TRIOBP	TRIO and F-actin binding protein	0.74	2.03e-12	CRMP1	collapsin response mediator protein
-0.99	1.33e-15	NNMT	nicotinamide N-methyltransferase	0.74	1.71e-13	COQ7	coenzyme Q7, hydroxylase
-0.99	5.01e-17	EHD2	EH domain containing 2	0.74	3.10e-16	ZMYM3	zinc finger MYM-type containing 3
-0.96	1.15e-20	SH3KBP1	SH3 domain containing kinase bindin	0.73	7.24e-16	ZNF384	zinc finger protein 384
-0.96	1.21e-19	PSMB8	proteasome 20S subunit beta 8	0.73	3.11e-08	GNG5	G protein subunit gamma 5
-0.94	6.07e-21	TNS3	tensin 3	0.72	1.49e-12	SNRNP27	small nuclear ribonucleoprotein U4/
-0.94	5.65e-25	MYO1E	myosin IE	0.72	5.96e-14	NSD3	nuclear receptor binding SET domain
-0.92	5.30e-18	TUBA1C	tubulin alpha 1c	0.72	1.95e-14	COQ6	coenzyme Q6, monooxygenase
-0.92	9.87e-12	TGM2	transglutaminase 2	0.71	1.14e-12	COQ8A	coenzyme Q8A
-0.91	5.79e-20	GYS1	glycogen synthase 1	0.71	1.20e-15	COQ3	coenzyme Q3, methyltransferase
-0.91	6.24e-08	LGALS3	galectin 3	0.71	3.02e-12	RRP36	ribosomal RNA processing 36
-0.91	6.27e-08	CAVIN1	caveolae associated protein 1	0.69	1.01e-15	TCF20	transcription factor 20
-0.91	9.81e-21	DAB2	DAB adaptor protein 2	0.69	1.84e-11	VPS72	vacuolar protein sorting 72 homolog
-0.9	5.74e-19	GALE	UDP-galactose-4-epimerase	0.68	5.10e-15	KAT7	lysine acetyltransferase 7
-0.9	2.27e-17	MVP	major vault protein	0.68	1.96e-12	DPYSL5	dihydropyrimidinase like 5
-0.89	8.24e-19	SPATS2L	spermatogenesis associated serine r	0.67	1.12e-14	KNOP1	lysine rich nucleolar protein 1
-0.88	1.70e-23	TGFB11	transforming growth factor beta 1 i	0.67	3.19e-14	TDRKH	tudor and KH domain containing

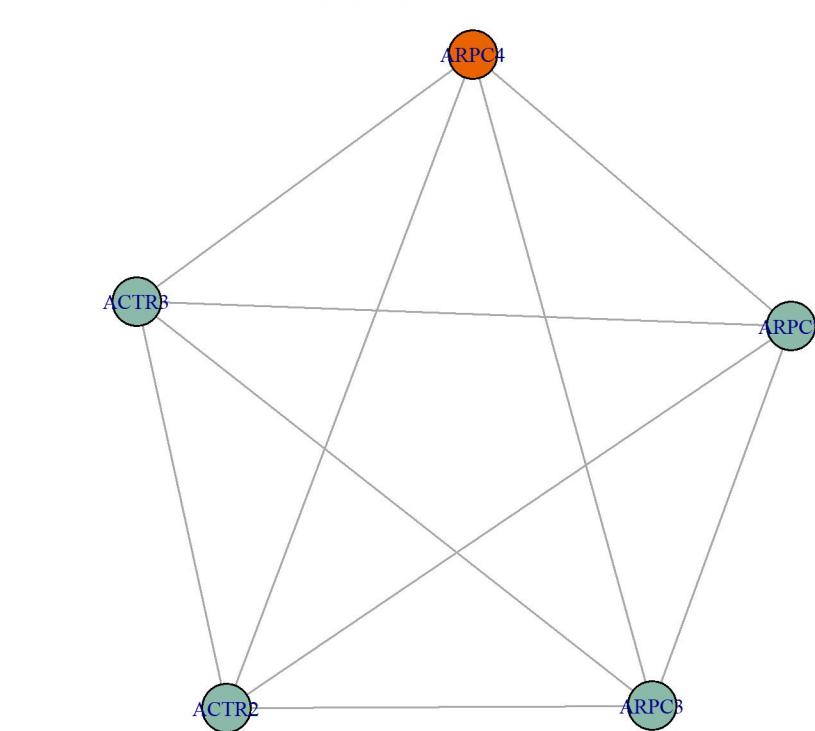
ARPC4 network, DB1, all Pearson r > 0.9

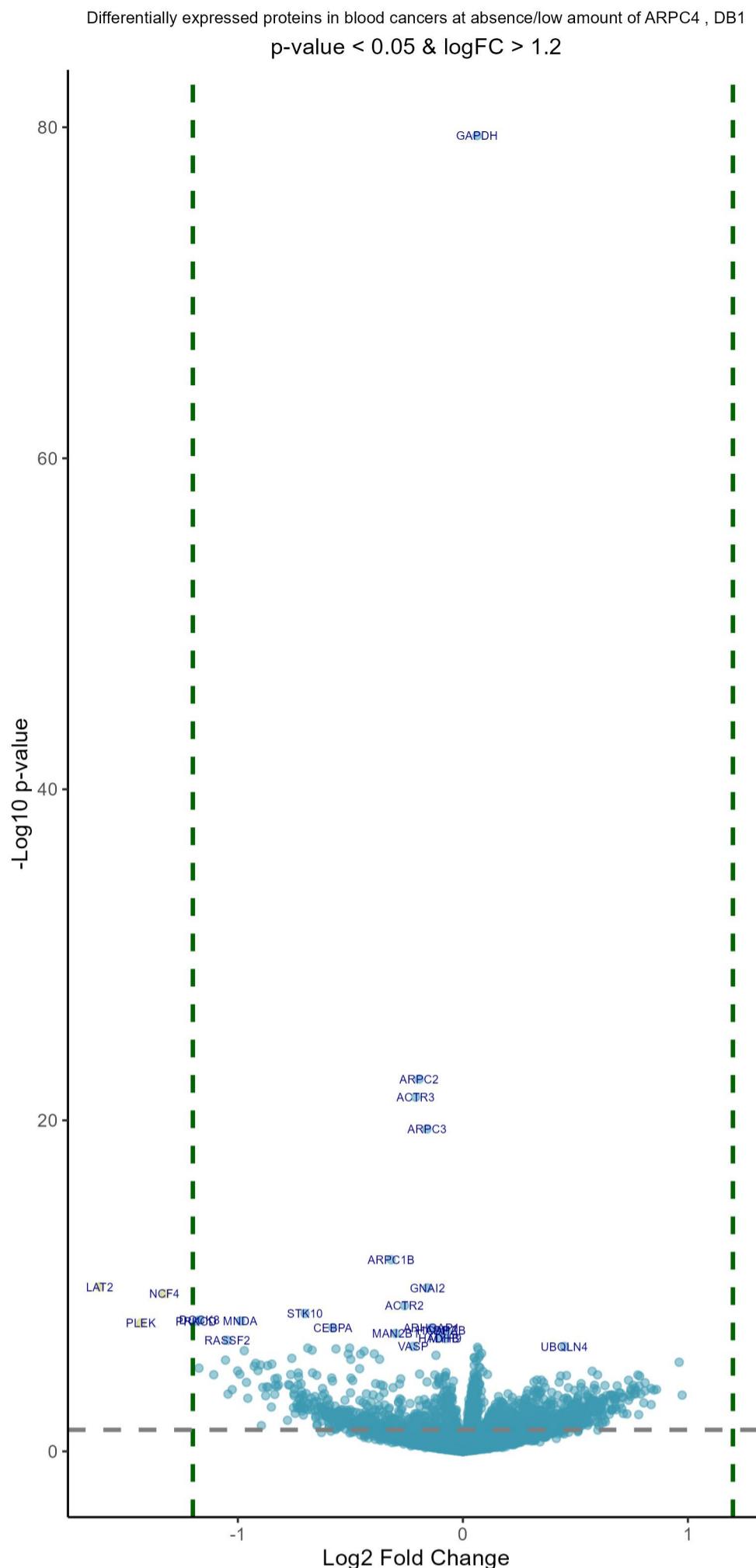


ARPC4 network, DB1, all Pearson r > 0.85

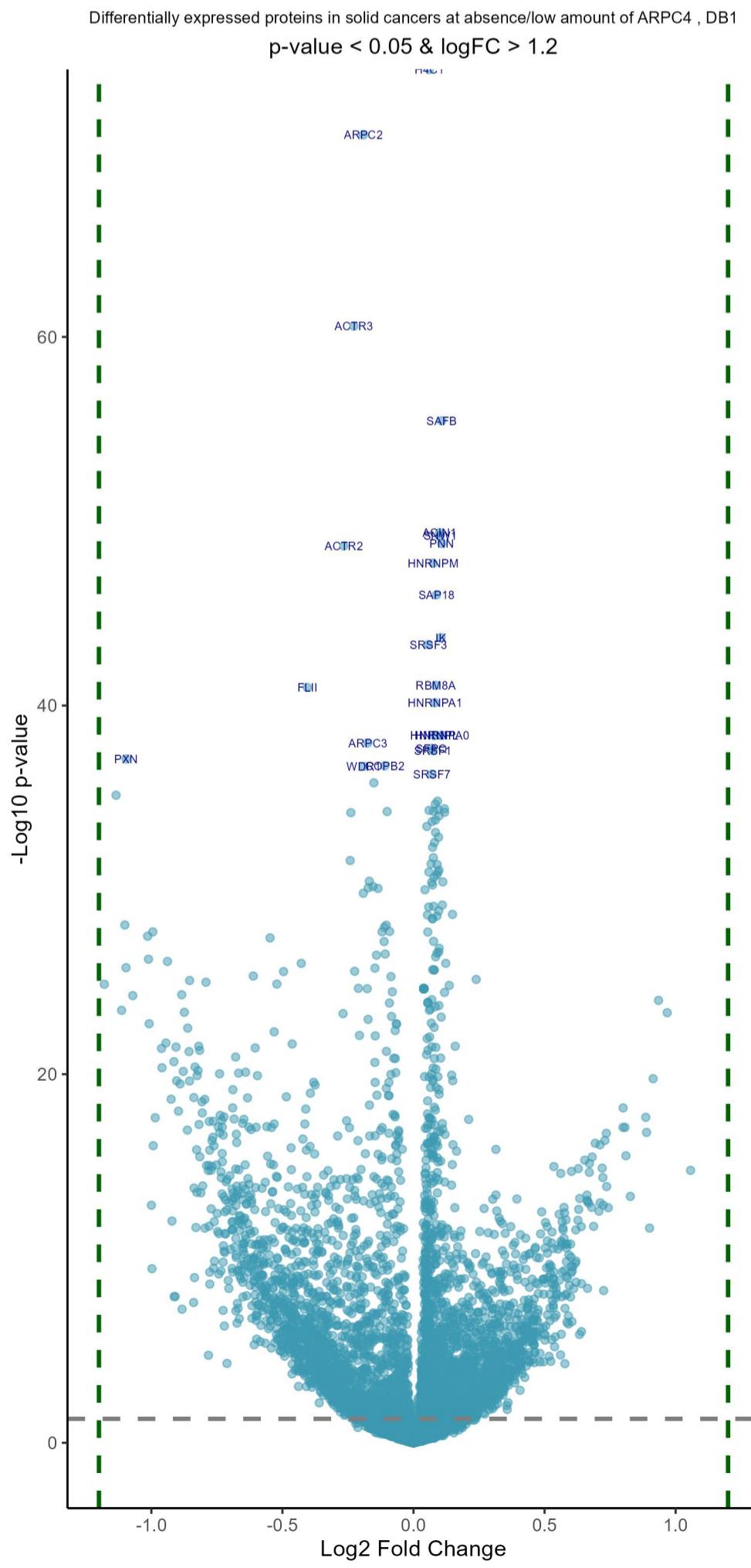


ARPC4 network, DB1, all Pearson r > 0.8

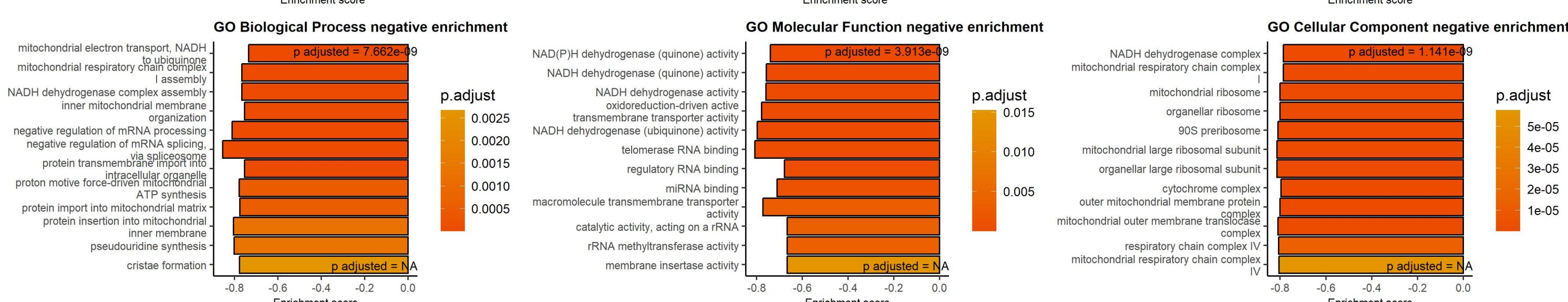
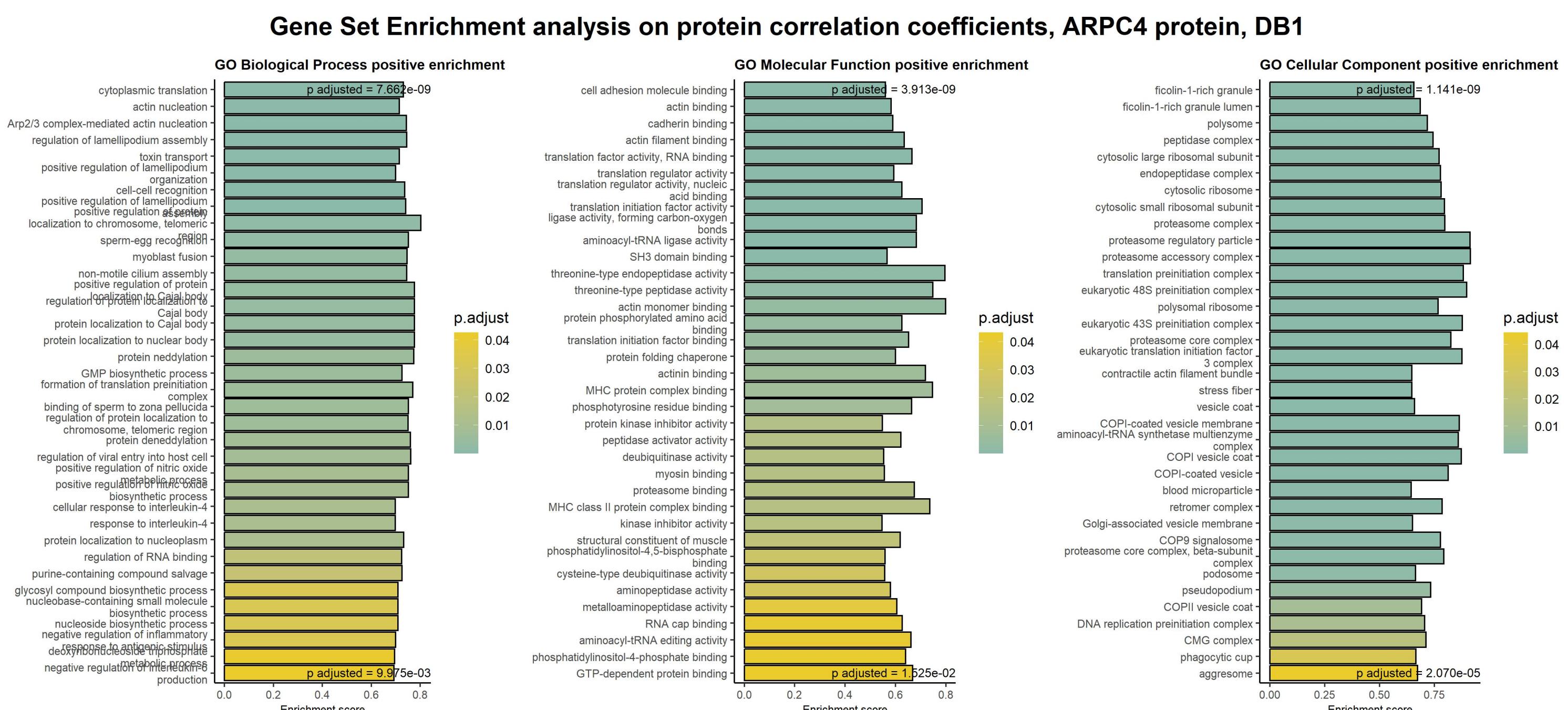
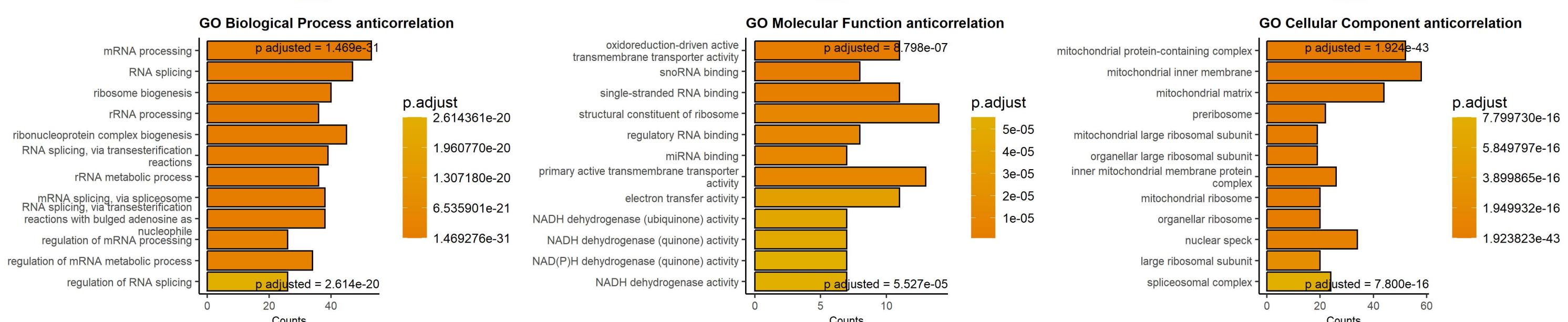
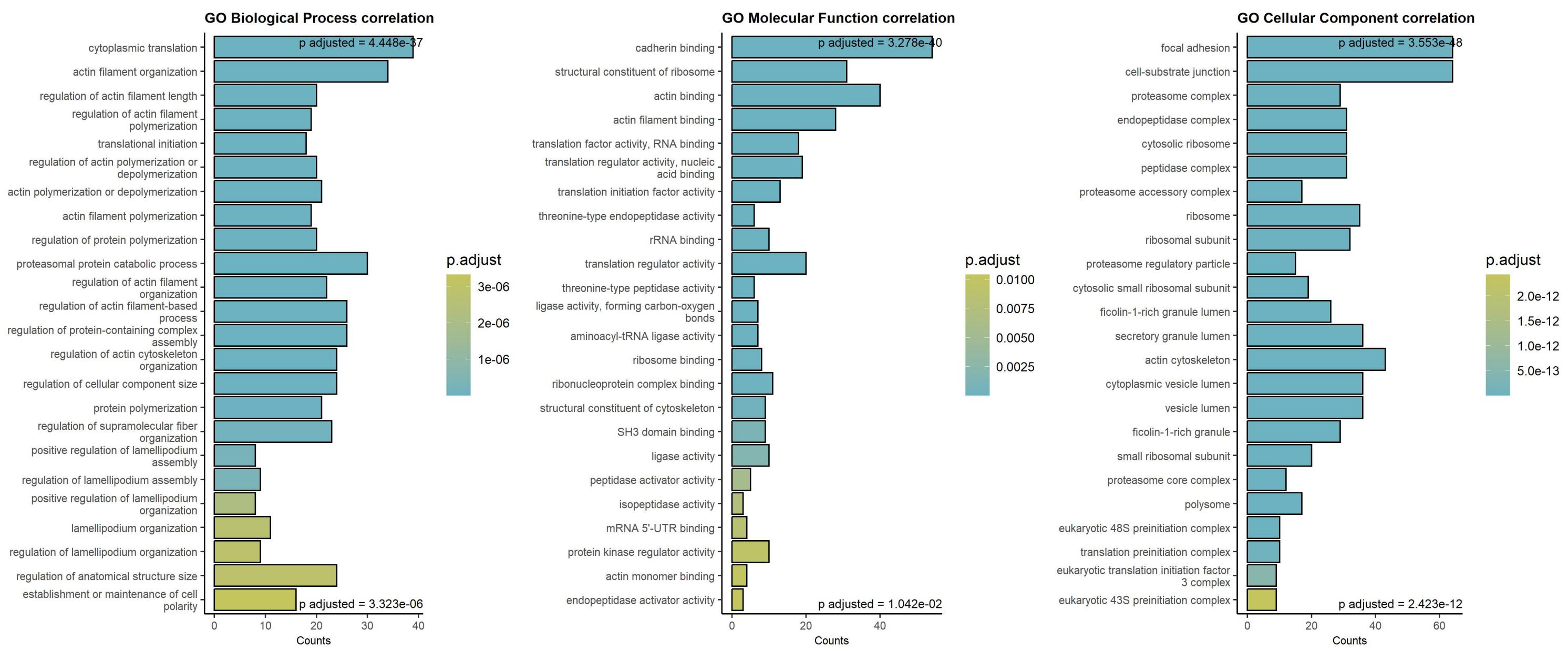




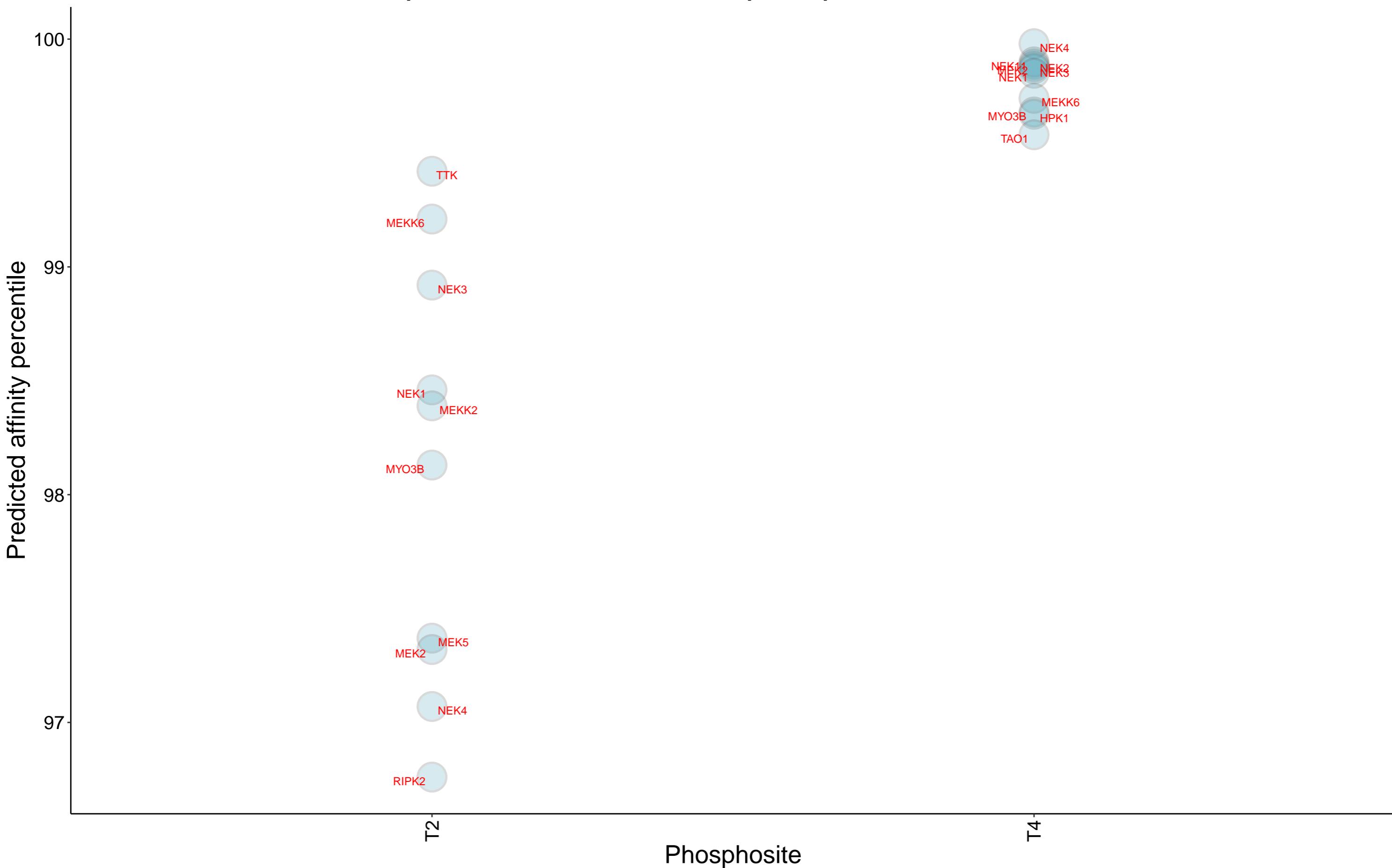
Sorted by p values!							
Downregulated in blood cancers at low/absent ARPC4				Upregulated in blood cancers at low/absent ARPC4			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.19	7.17e-20	ARPC2	actin related protein 2/3 complex s	0.06	2.13e-76	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
-0.21	6.62e-19	ACTR3	actin related protein 3	0.45	1.23e-04	UBQLN4	ubiquilin 4
-0.16	4.50e-17	ARPC3	actin related protein 2/3 complex s	0.07	1.31e-04	PHF5A	PHD finger protein 5A
-0.32	2.92e-09	ARPC1B	actin related protein 2/3 complex s	0.07	1.52e-04	PFDN6	prefoldin subunit 6
-1.61	1.09e-07	LAT2	linker for activation of T cells fa	0.08	2.35e-04	SUPT5H	SPT5 homolog, DSIF elongation factor
-0.16	1.10e-07	GNAI2	G protein subunit alpha i2	0.07	2.76e-04	PFDN2	prefoldin subunit 2
-1.33	2.19e-07	NCF4	neutrophil cytosolic factor 4	0.05	3.56e-04	SF3A1	splicing factor 3a subunit 1
-0.26	1.05e-06	ACTR2	actin related protein 2	0.07	3.56e-04	CACYBP	calcyclin binding protein
-0.7	2.83e-06	STK10	serine/threonine kinase 10	0.05	3.56e-04	PSMC3	proteasome 26S subunit, ATPase 3
-1.17	6.45e-06	DOCK8	dedicator of cytokinesis 8	0.06	5.03e-04	RBM8A	RNA binding motif protein 8A
-0.99	6.45e-06	MNDA	myeloid cell nuclear differentiatio	0.96	5.72e-04	IGSF8	immunoglobulin superfamily member
-1.19	6.45e-06	PRKCD	protein kinase C delta	0.05	8.13e-04	STIP1	stress induced phosphoprotein 1
-1.43	7.90e-06	PLEK	pleckstrin	0.07	9.41e-04	PFDN5	prefoldin subunit 5
-0.58	1.38e-05	CEBPA	CCAAT enhancer binding protein alph	0.08	1.05e-03	CSTF2	cleavage stimulation factor subunit
-0.14	1.38e-05	ARHGAP1	Rho GTPase activating protein 1	0.57	1.57e-03	SUPT4H1	SPT4 homolog, DSIF elongation fact
-0.07	1.74e-05	CAPZB	capping actin protein of muscle Z-I	0.09	1.61e-03	ZC3H4	zinc finger CCCH-type containing 4
-0.11	1.74e-05	HADHA	hydroxyacyl-CoA dehydrogenase trifu	0.05	1.95e-03	RUVBL1	RuvB like AAA ATPase 1
-0.3	2.48e-05	MAN2B1	mannosidase alpha class 2B member 1	0.11	2.15e-03	PAFAH1B3	platelet activating factor acetylhy
-0.11	4.52e-05	HADHB	hydroxyacyl-CoA dehydrogenase trifu	0.05	2.15e-03	HNRNPDL	heterogeneous nuclear ribonucleoprote
-0.08	4.56e-05	MYH9	myosin heavy chain 9	0.6	2.15e-03	PRCC	proline rich mitotic checkpoint con
-1.05	5.60e-05	RASSF2	Ras association domain family membe	0.78	2.15e-03	MORC2	MORC family CW-type zinc finger 2
-0.22	1.23e-04	VASP	vasodilator stimulated phosphoprote	0.06	2.15e-03	NUDC	nuclear distribution C, dynein comp
-0.5	1.37e-04	F13A1	coagulation factor XIII A chain	0.46	2.23e-03	SIVA1	SIVA1 apoptosis inducing factor
-0.69	1.37e-04	TTC9	tetratricopeptide repeat domain 9	0.43	2.31e-03	TIMM9	translocase of inner mitochondrial
-0.56	1.48e-04	TNFAIP2	TNF alpha induced protein 2	0.79	2.32e-03	RNF169	ring finger protein 169
-0.67	1.65e-04	CES1	carboxylesterase 1	0.06	2.34e-03	ANP32A	acidic nuclear phosphoprotein 32 fa
-0.97	1.72e-04	ANKRD44	ankyrin repeat domain 44	0.05	2.57e-03	SRSF11	serine and arginine rich splicing f
-0.44	1.80e-04	ARHGAP45	Rho GTPase activating protein 45	0.07	2.95e-03	ENY2	ENY2 transcription and export comp
-0.51	2.39e-04	SERPINB10	serpin family B member 10	0.04	3.28e-03	DDX46	DEAD-box helicase 46
-0.39	2.39e-04	GRK2	G protein-coupled receptor kinase 2	0.06	3.33e-03	VBP1	VHL binding protein 1
-0.45	2.41e-04	PRAM1	PML-RARA regulated adaptor molecule	0.33	3.35e-03	PGM2L1	phosphoglucomutase 2 like 1
-0.12	2.74e-04	PDCD6	programmed cell death 6	0.35	3.35e-03	GLRX5	glutaredoxin 5
-0.76	3.70e-04	RMDN1	regulator of microtubule dynamics 1	0.74	3.39e-03	SKA3	spindle and kinetochore associated
-0.37	4.11e-04	CORO1A	coronin 1A	0.05	3.45e-03	PNN	pinin, desmosome associated protein
-0.5	4.11e-04	RNASE2	ribonuclease A family member 2	0.07	3.93e-03	EDC4	enhancer of mRNA decapping 4
-1.06	4.44e-04	SH3BP1	SH3 domain binding protein 1	0.32	3.93e-03	GIMAP6	GTPase, IMAP family member 6
-0.92	6.49e-04	VAV1	vav guanine nucleotide exchange fac	0.43	4.09e-03	WBP2	WW domain binding protein 2
-0.85	7.11e-04	PRTN3	proteinase 3	0.36	4.19e-03	LARP4	La ribonucleoprotein 4
0.9	7.86e-04	UBA7	ubiquitin like modifier activating	0.81	4.27e-03	DDAD1	RNA polymerase II associated protein



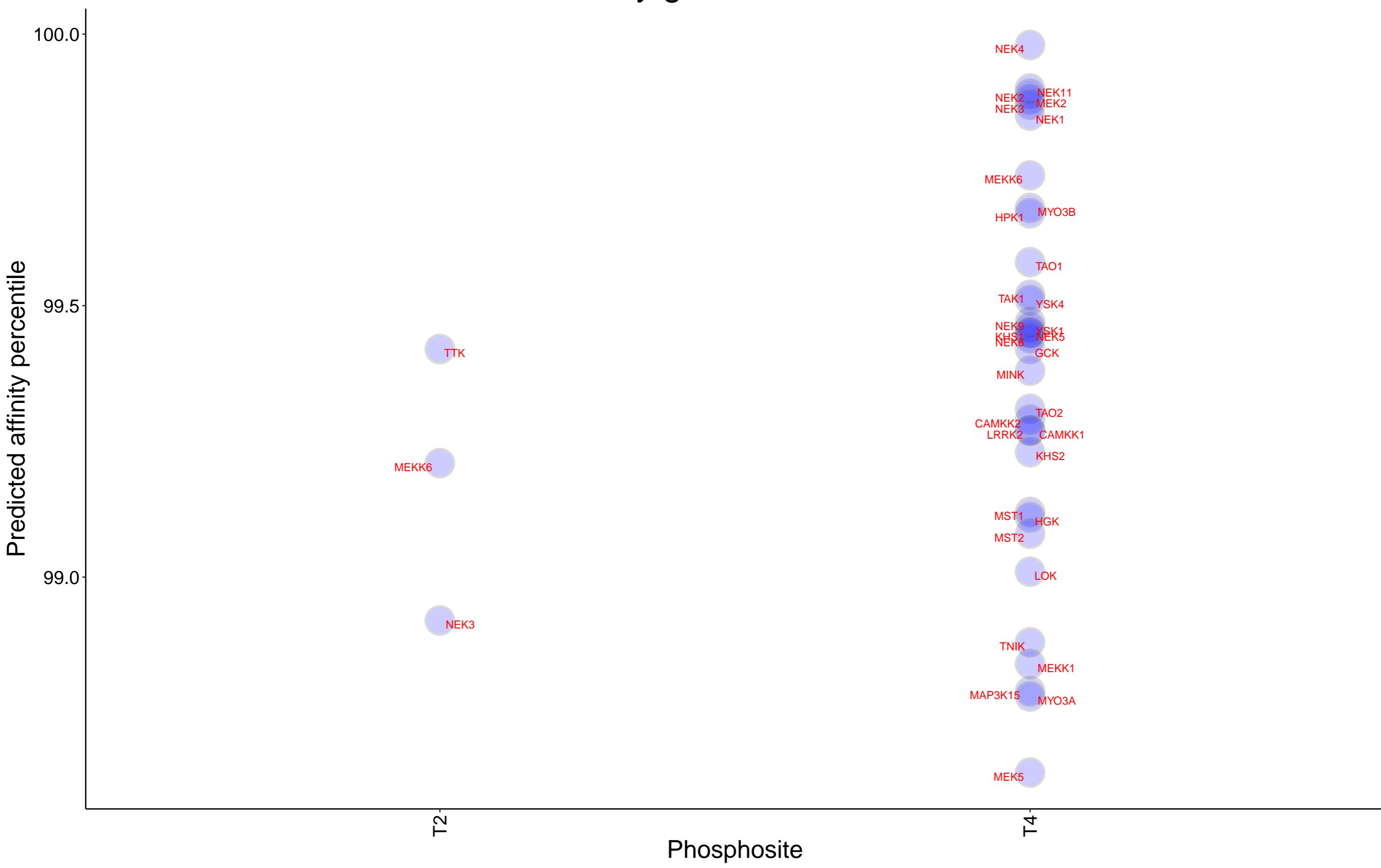
Top 250 correlation coefficients overrepresentation, ARPC4 protein, DB1



Top 10 kinases for each phosphosite in ARPC4



Kinases with affinity greater than 98.5% to ARPC4



Top 15 positive correlation coefficients for ARPC4 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

