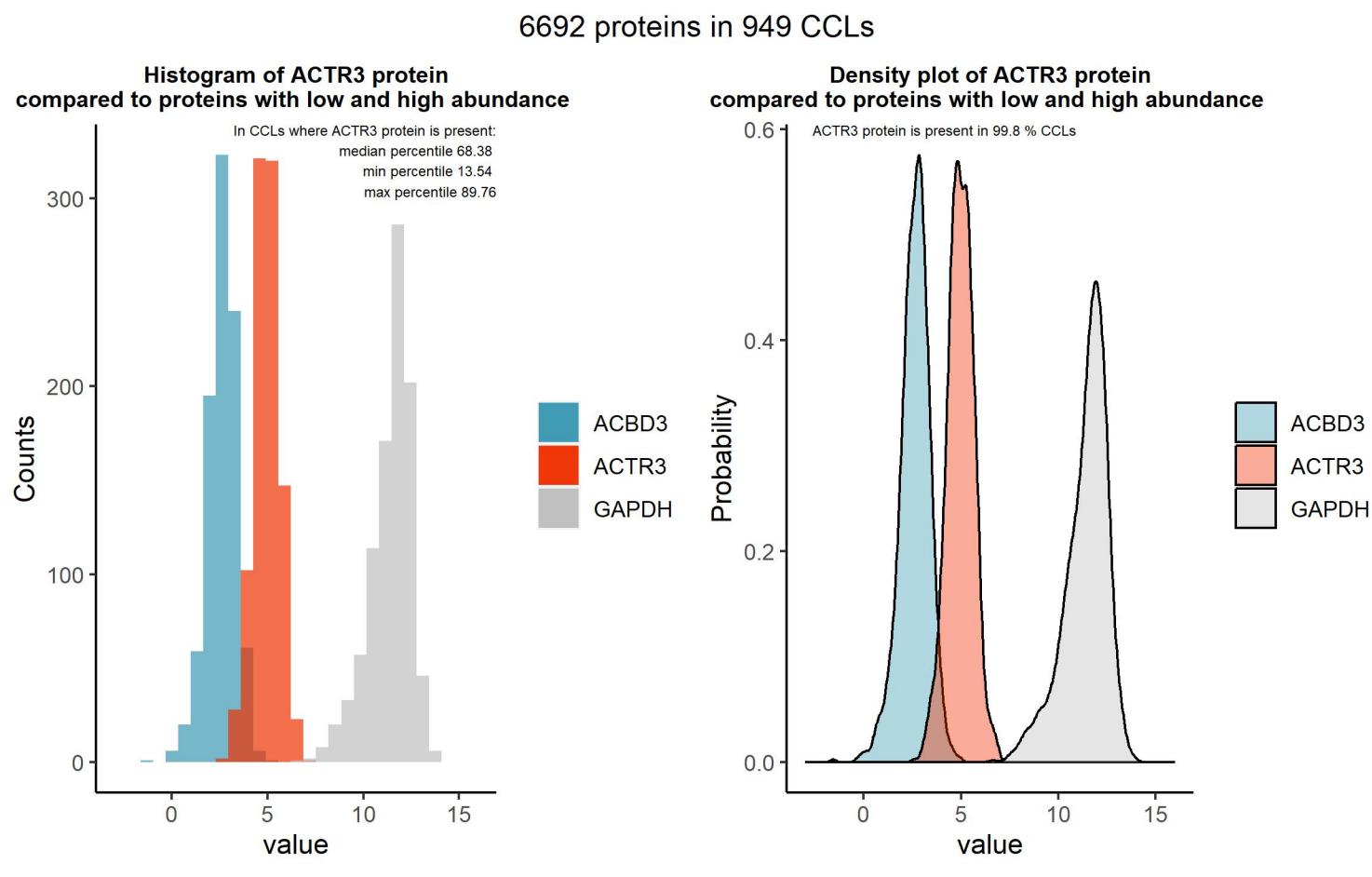


ACTR3

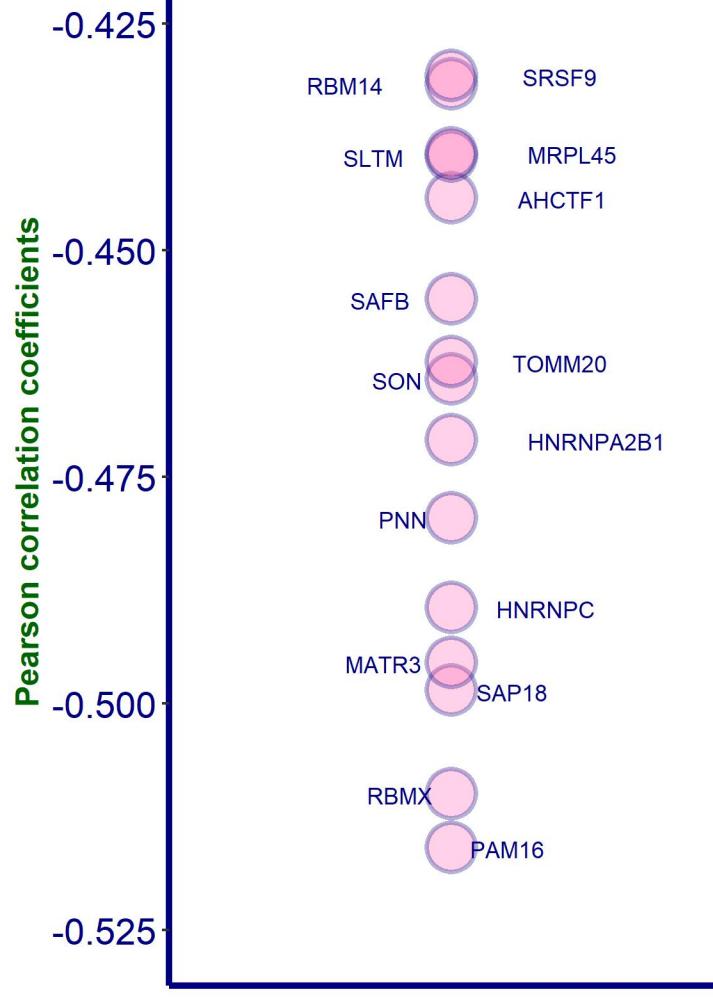
Protein name: ARP3 ; UNIPROT: P61158 ; Gene name: actin related protein 3

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

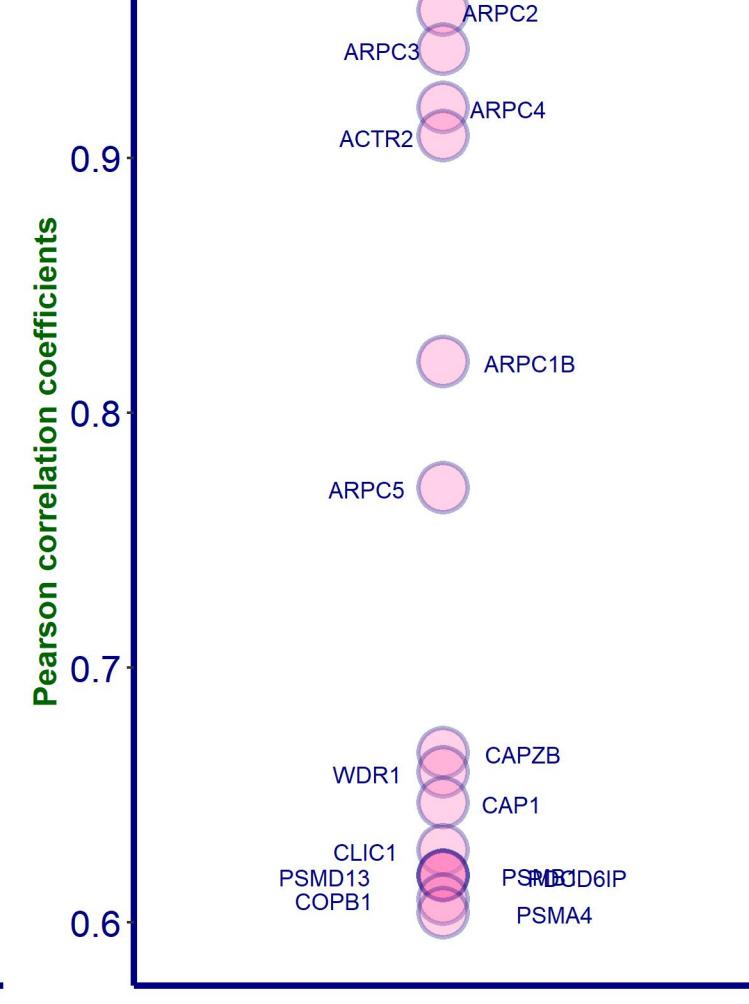
Sanger Institute Protein Database 1 (DB1), protein presence is certain



Top negative correlations of ACTR3 protein, DB1

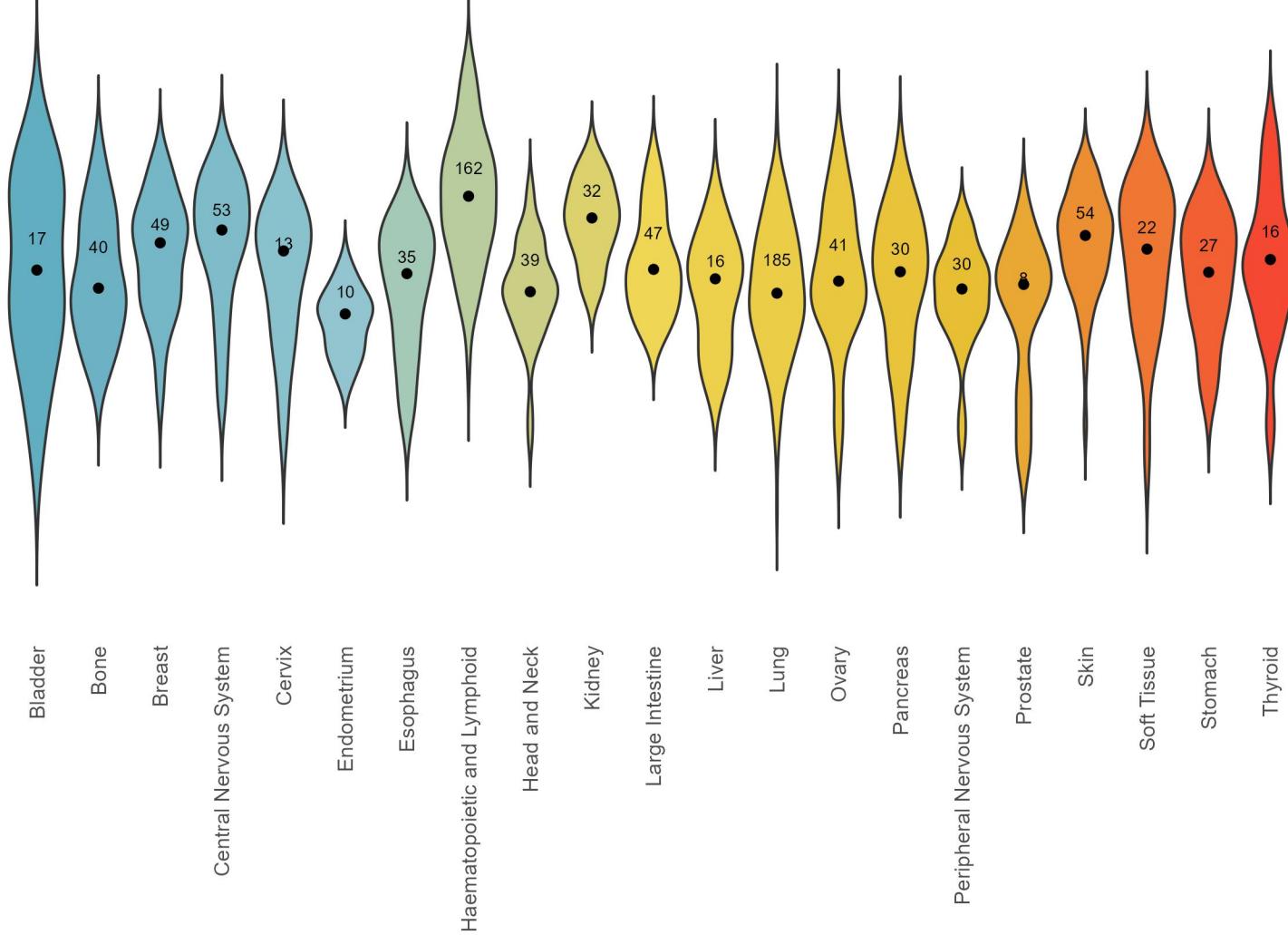


Top positive correlations of ACTR3 protein, DB1



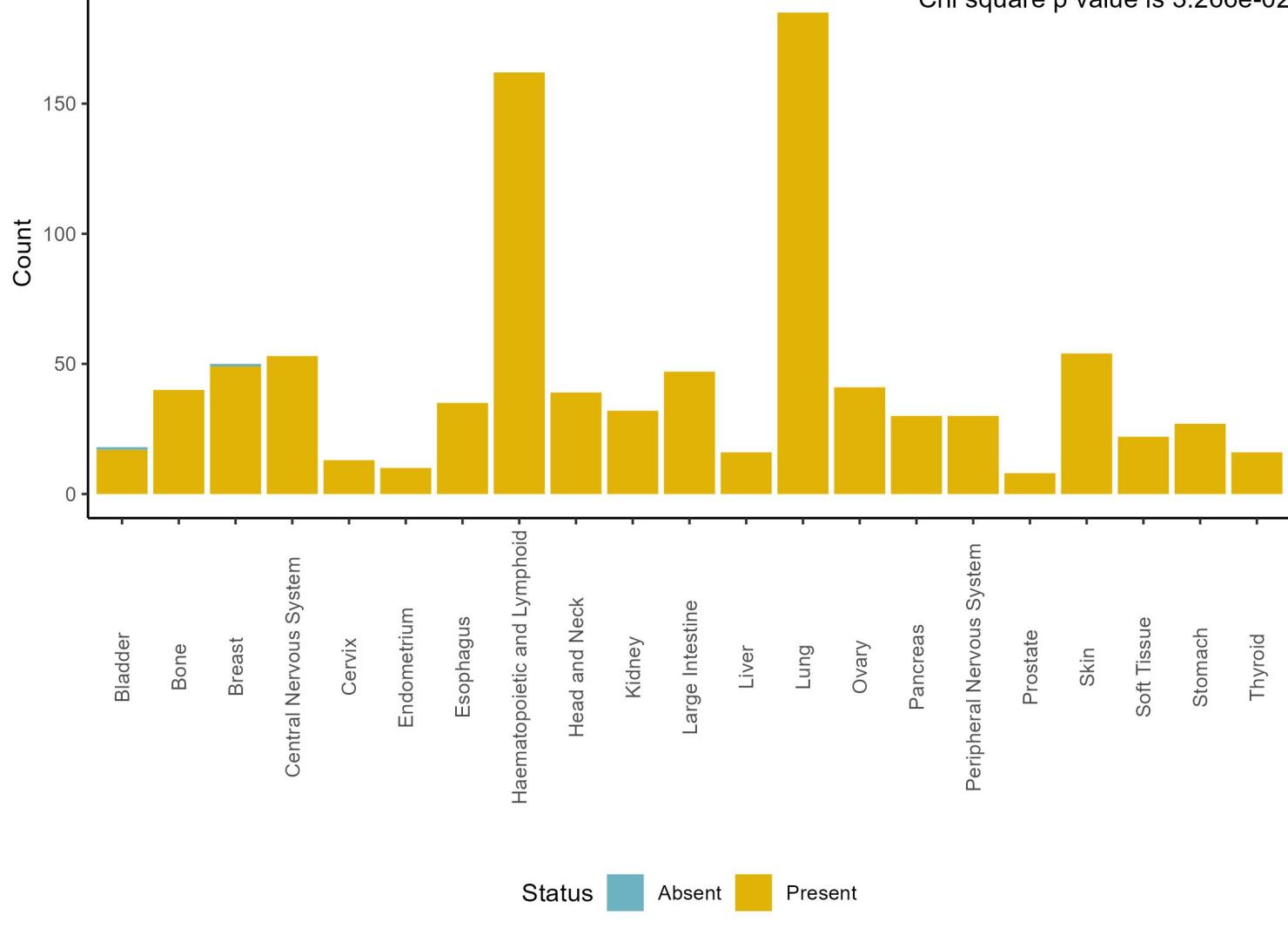
Amount of ACTR3 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 1.855e-41



Present and absent ACTR3 protein counts by tissue, DB1

Chi square p value is 3.266e-02

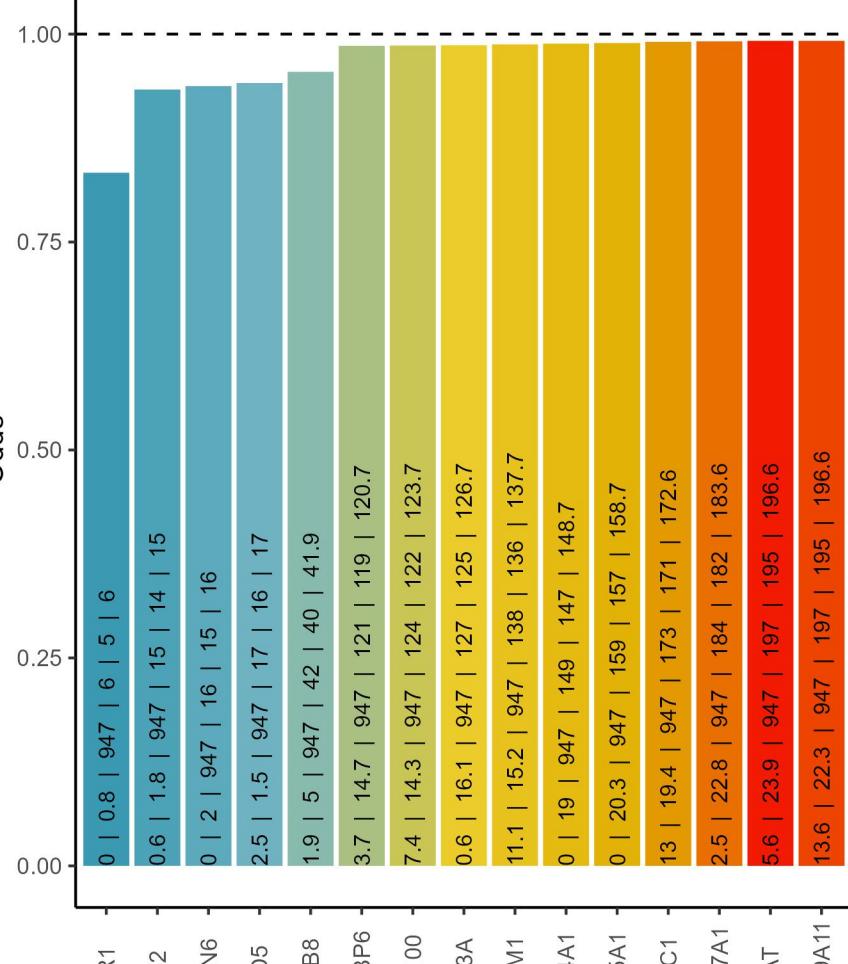


Cooccurrence with ACTR3 protein, DB1

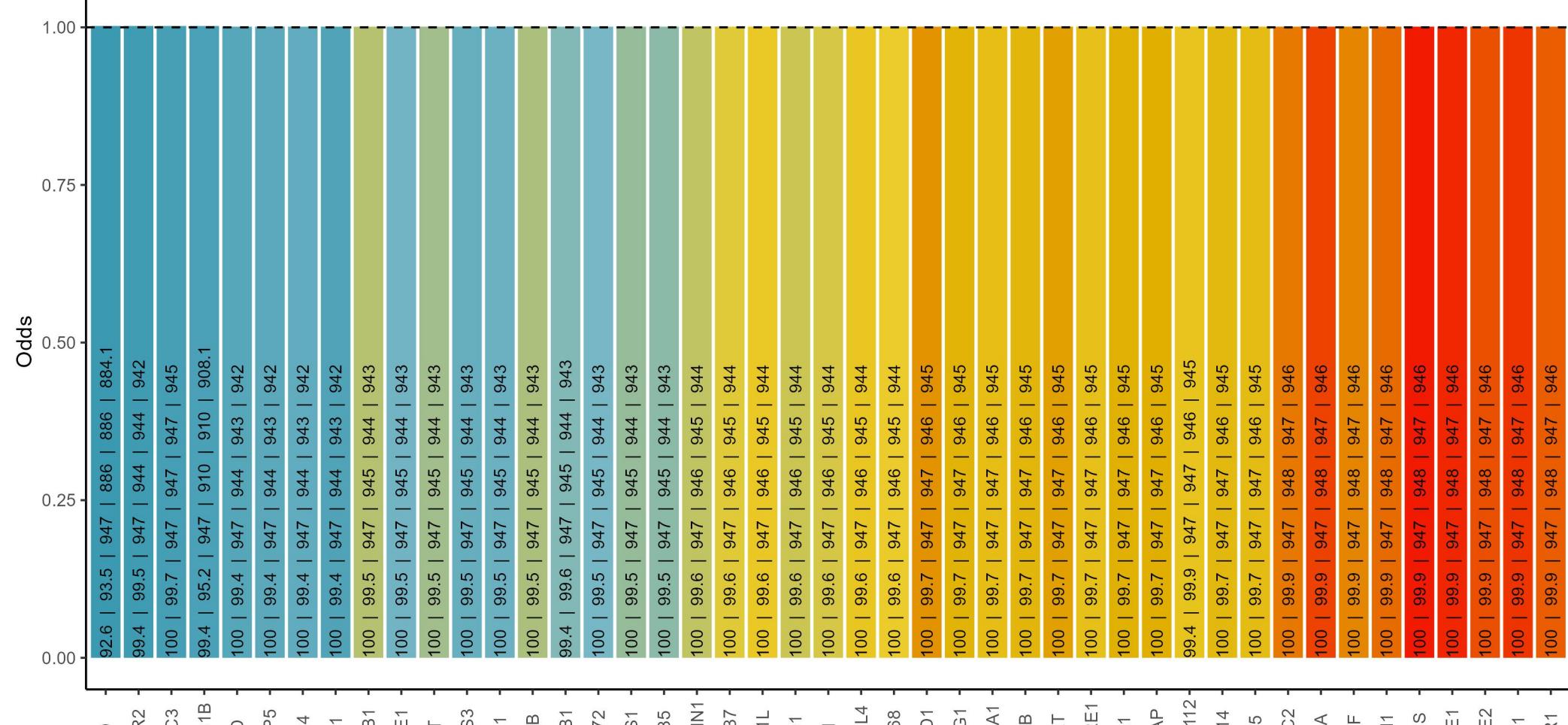
% of ACTR3 in blood cancers: 100 ; % of ACTR3 in solid cancers: 99.7

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ACTR3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

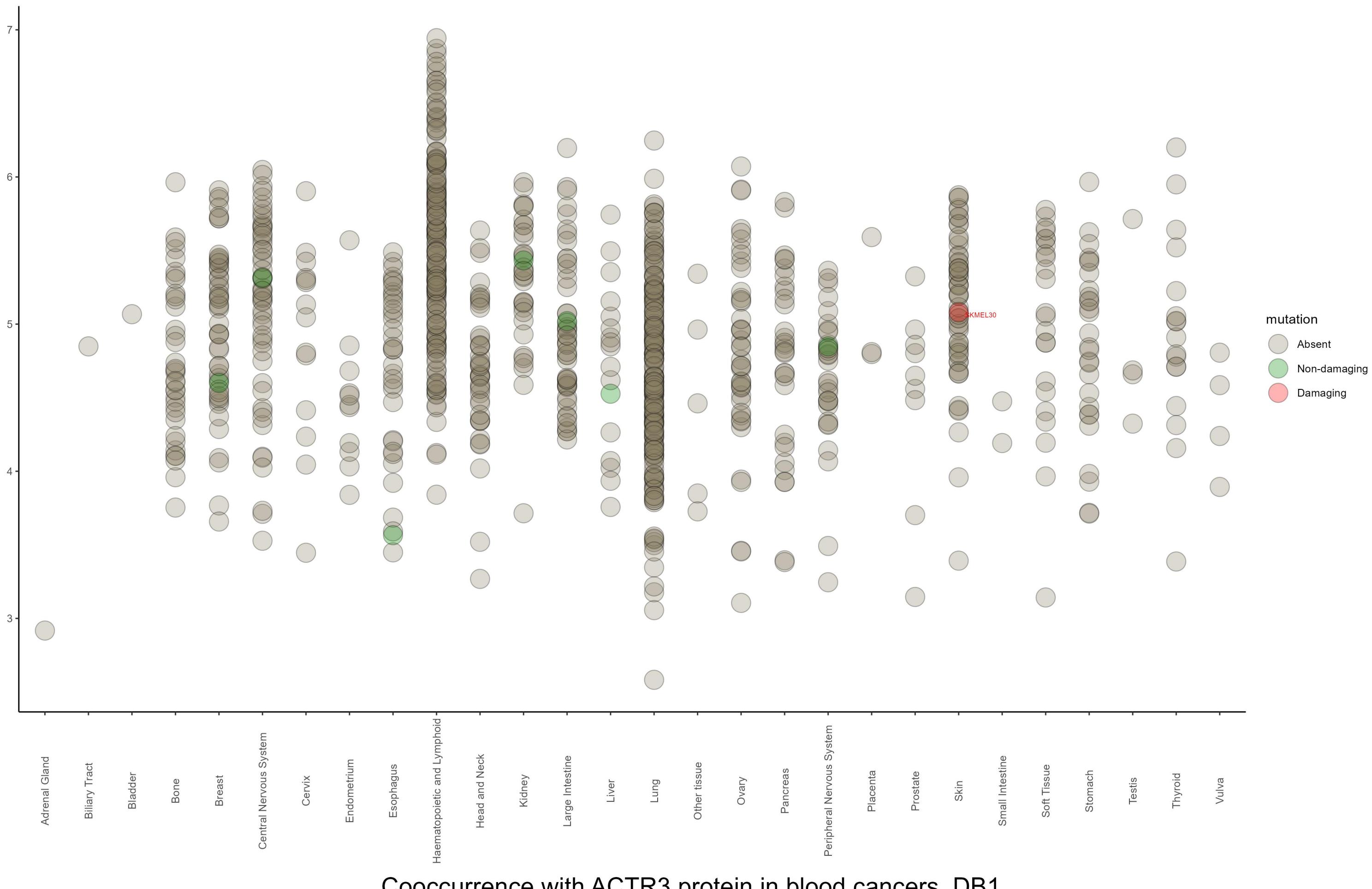
Negative cooccurrence



Positive cooccurrence



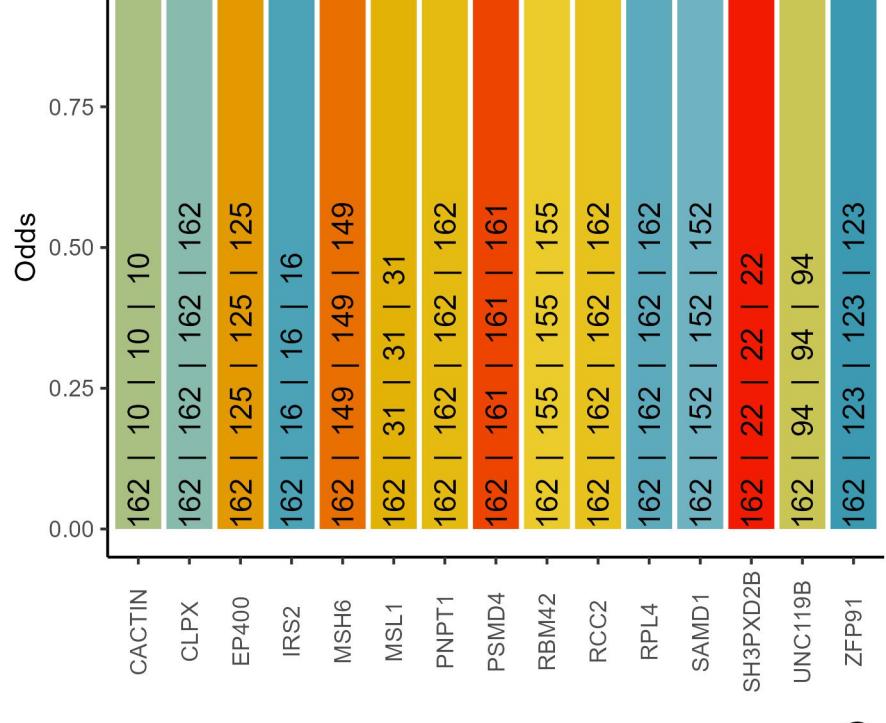
Amount of ACTR3 protein and mutation status by tissue, DB1



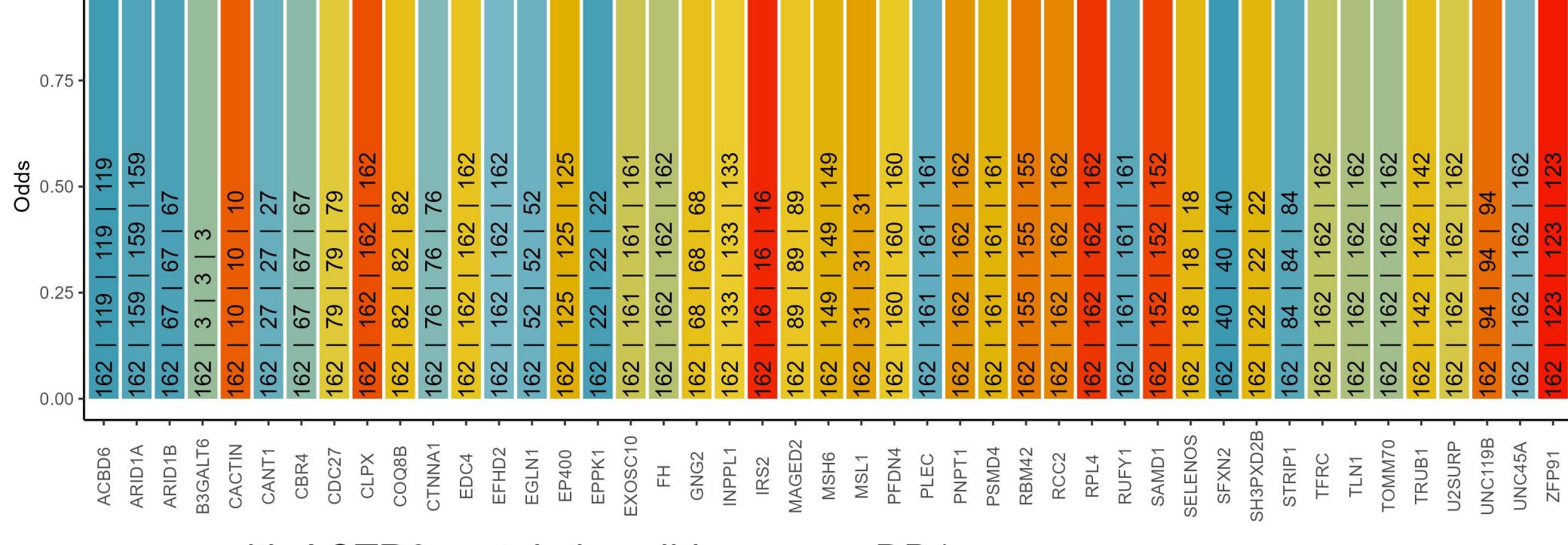
Cooccurrence with ACTR3 protein in blood cancers, DB1

The text in the bars: incidence of ACTR3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



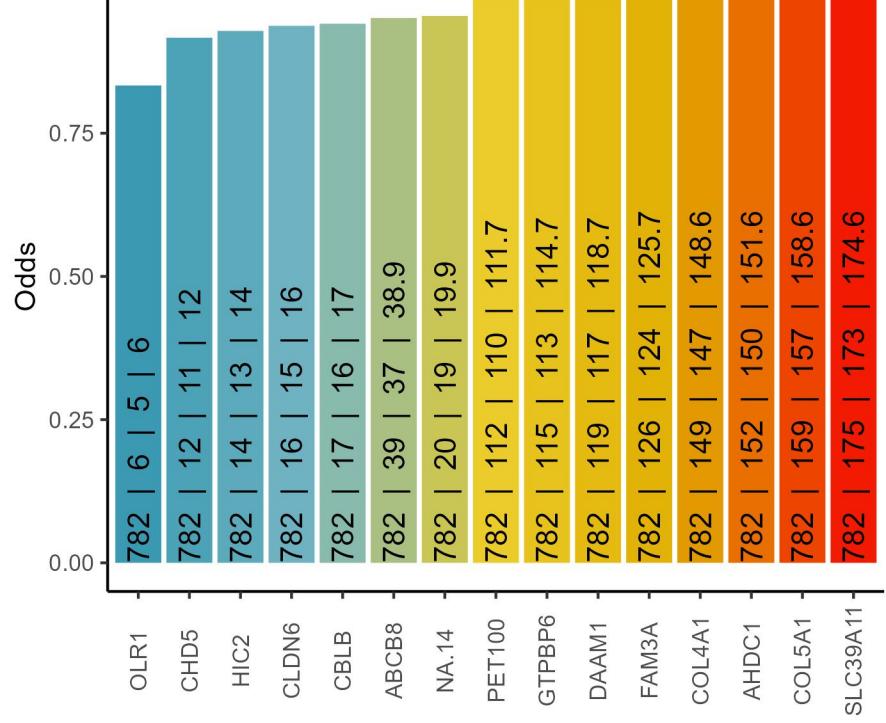
Positive cooccurrence



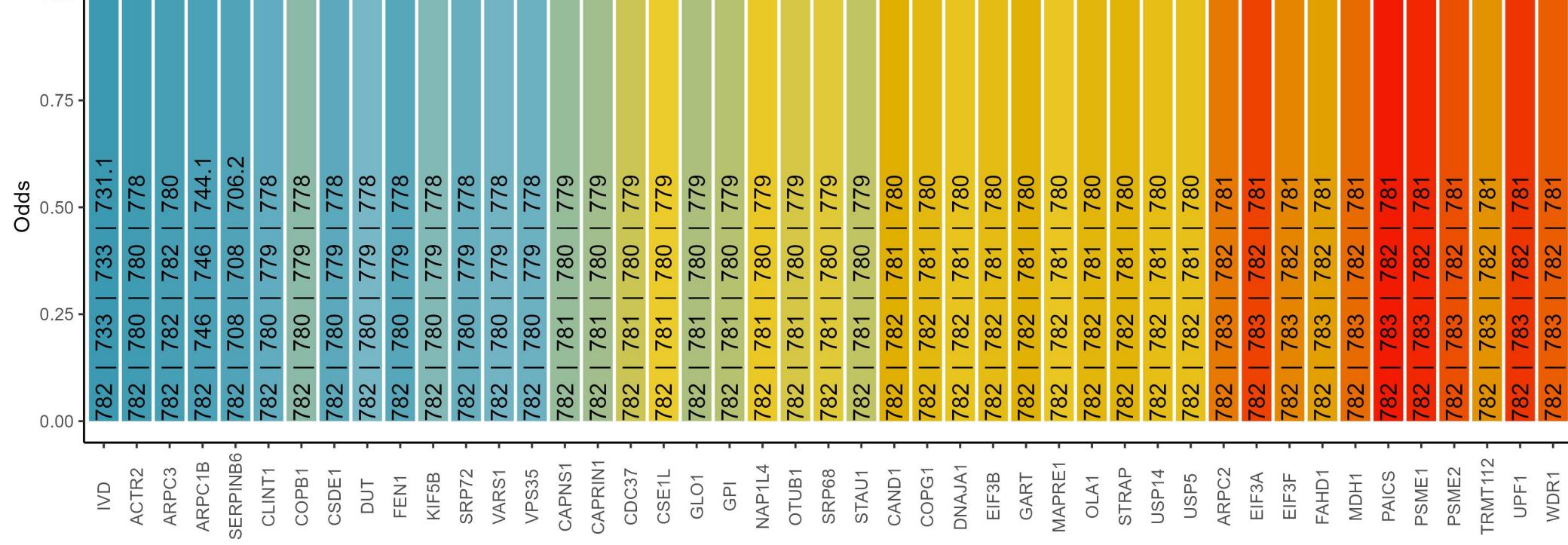
Cooccurrence with ACTR3 protein in solid cancers, DB1

The text in the bars: incidence of ACTR3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

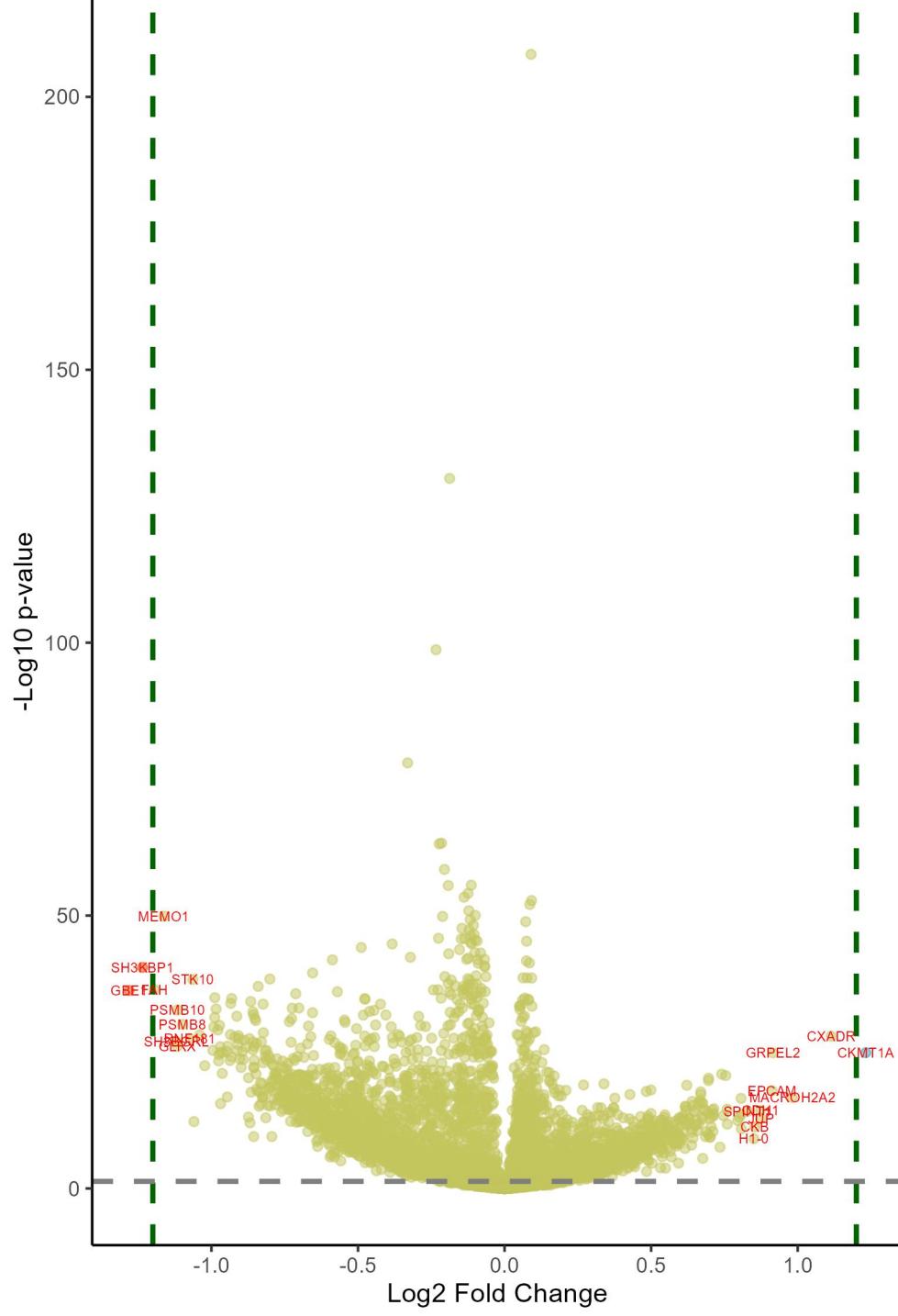
Negative cooccurrence



Positive cooccurrence

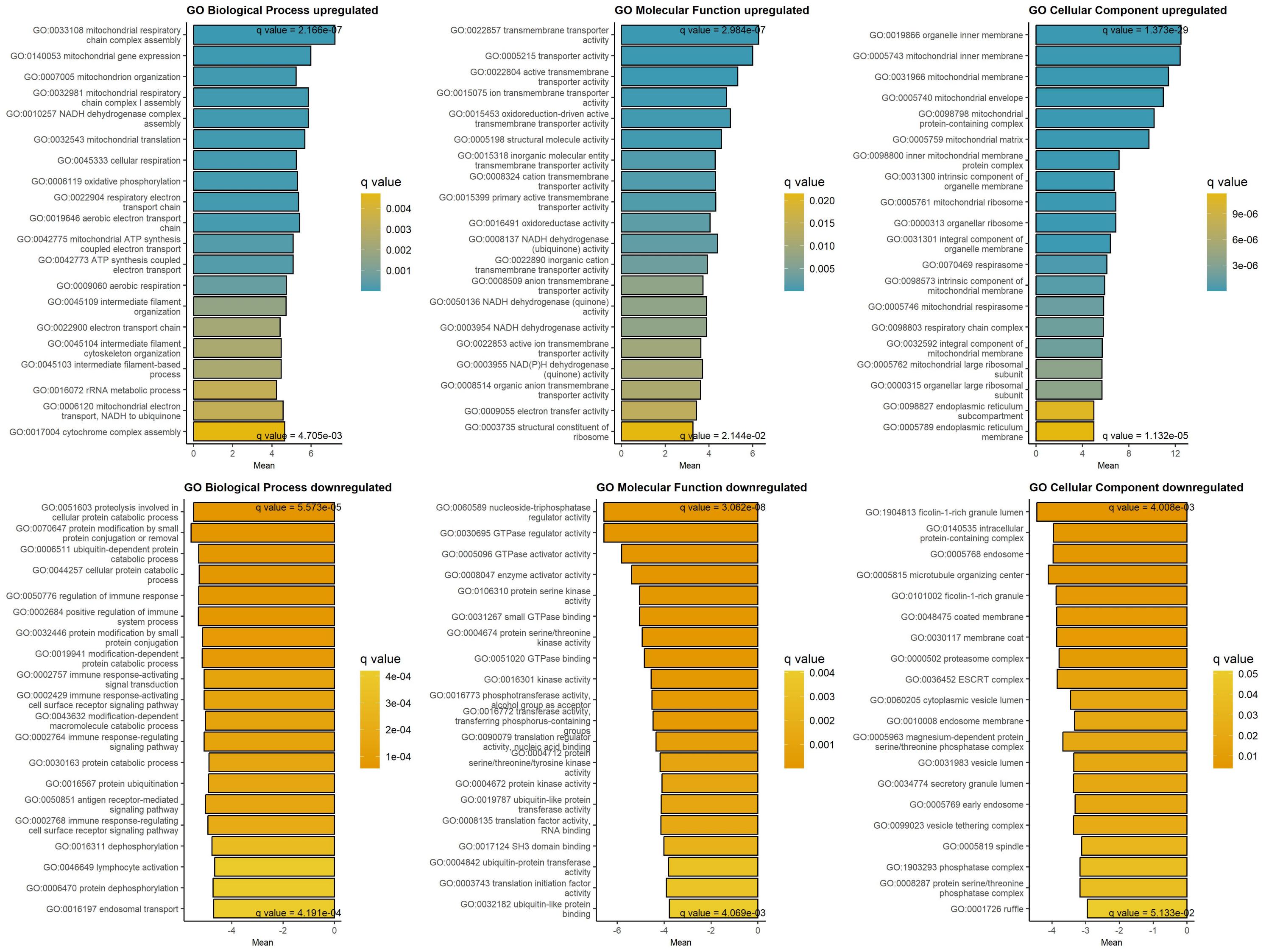


Downregulated at low/absent ACTR3 Upregulated at low/absent ACTR3

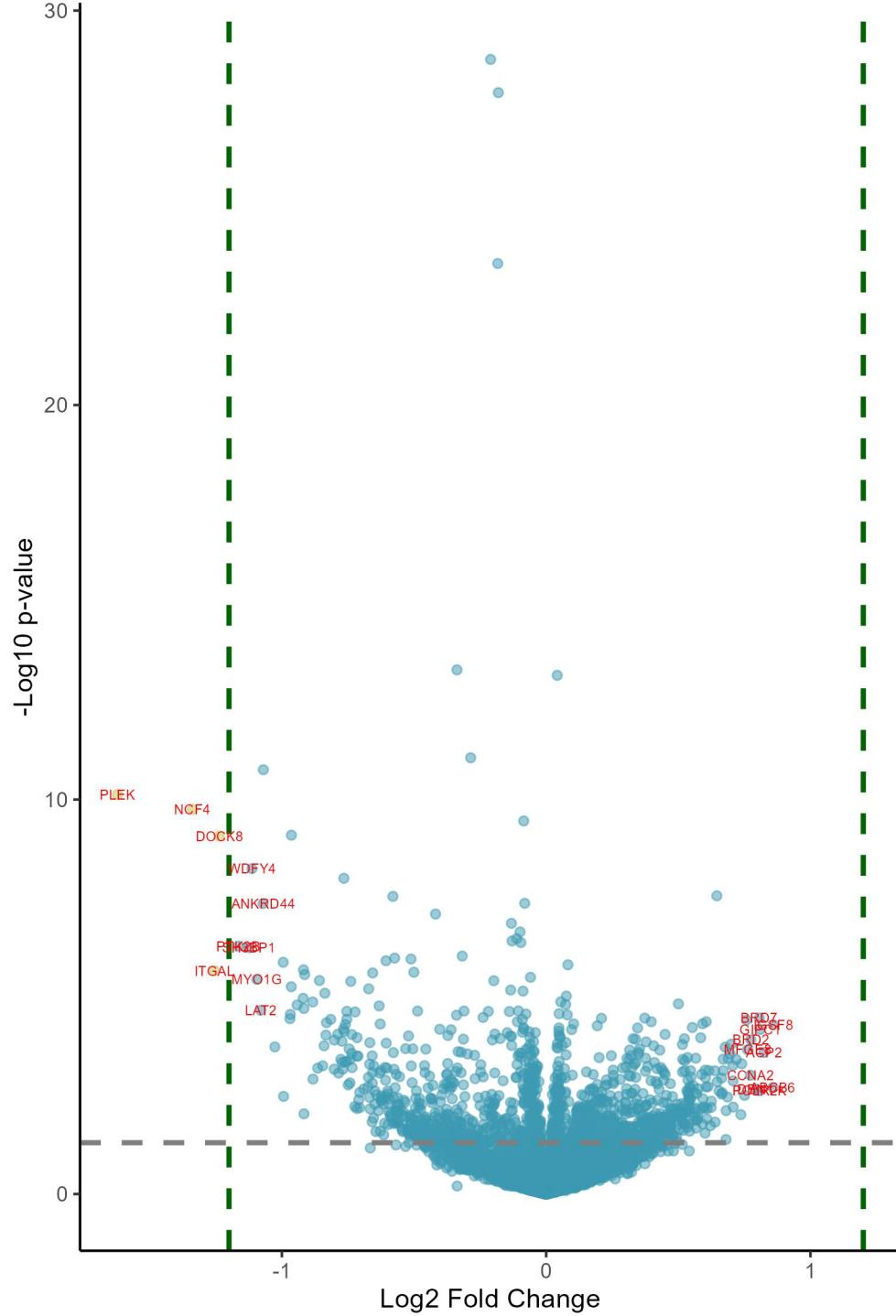


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.28	4.55e-35	GBE1	1,4-alpha-glucan branching enzyme 1	1.23	3.21e-24	CKMT1A	creatine kinase, mitochondrial 1A
-1.23	4.06e-39	SH3KBP1	SH3 domain containing kinase bindin	1.11	4.65e-27	CXADR	CXADR Ig-like cell adhesion molecule
-1.2	3.23e-35	FAH	fumarylacetoacetate hydrolase	0.98	2.16e-16	MACROH2A2	macroH2A.2 histone
-1.16	5.12e-48	MEMO1	mediator of cell motility 1	0.92	3.49e-24	GRPEL2	GrpE like 2, mitochondrial
-1.12	4.00e-26	SH3BGRL	SH3 domain binding glutamate rich p	0.91	1.35e-17	EPCAM	epithelial cell adhesion molecule
-1.12	2.59e-25	GLRX	glutaredoxin	0.87	9.73e-13	JUP	junction plakoglobin
-1.12	1.07e-31	PSMB10	proteasome 20S subunit beta 10	0.87	3.65e-14	CDH1	cadherin 1
-1.1	3.71e-29	PSMB8	proteasome 20S subunit beta 8	0.85	2.65e-11	CKB	creatine kinase B
-1.07	1.20e-26	RNF181	ring finger protein 181	0.85	2.97e-09	H1-0	H1.0 linker histone
-1.06	5.61e-37	STK10	serine/threonine kinase 10	0.83	4.78e-14	SPINT1	serine peptidase inhibitor, Kunitz
-1.06	3.15e-12	ARPC5	actin related protein 2/3 complex s	0.81	5.73e-11	GCSH	glycine cleavage system protein H
-1.04	2.88e-27	UBE2L6	ubiquitin conjugating enzyme E2 L6	0.81	1.63e-13	MRPL54	mitochondrial ribosomal protein L54
-1.02	6.31e-22	PSMB9	proteasome 20S subunit beta 9	0.81	2.93e-16	GNG10	G protein subunit gamma 10
-1	1.30e-24	PPP6R1	protein phosphatase 6 regulatory su	0.8	5.39e-13	EPPK1	epiplakin 1
-0.99	1.10e-28	PMM2	phosphomannomutase 2	0.8	2.02e-12	SPINT2	serine peptidase inhibitor, Kunitz
-0.99	2.18e-30	PCYT2	phosphate cytidylyltransferase 2, e	0.76	8.82e-12	UQCR10	ubiquinol-cytochrome c reductase, c
-0.99	8.11e-34	MAPK14	mitogen-activated protein kinase 14	0.76	2.21e-14	SLC25A4	solute carrier family 25 member 4
-0.98	7.36e-32	TRIM21	tripartite motif containing 21	0.75	3.33e-20	TDRKH	tudor and KH domain containing
-0.98	3.72e-28	NECAP2	NECAP endocytosis associated 2	0.75	2.95e-13	CGN	cingulin
-0.98	8.94e-23	CDK6	cyclin dependent kinase 6	0.74	1.94e-20	EXD2	exonuclease 3'-5' domain containing
-0.97	6.82e-24	RPE	ribulose-5-phosphate-3-epimerase	0.73	9.33e-08	NDUFB11	NADH:ubiquinone oxidoreductase subu
-0.97	5.78e-29	NFKB1	nuclear factor kappa B subunit 1	0.71	1.78e-14	CNTN1	contactin 1
-0.97	2.98e-25	TAOK3	TAO kinase 3	0.71	2.46e-13	ESRP1	epithelial splicing regulatory prot
-0.97	2.40e-15	ARHGDIB	Rho GDP dissociation inhibitor beta	0.71	1.22e-13	SURF1	SURF1 cytochrome c oxidase assembly
-0.97	2.94e-24	IRF3	interferon regulatory factor 3	0.71	1.64e-10	LSR	lipolysis stimulated lipoprotein re
-0.96	1.43e-20	GSDMD	gasdermin D	0.71	4.29e-13	PRXL2A	peroxiredoxin like 2A
-0.96	3.08e-24	WIPF1	WAS/WASL interacting protein family	0.71	3.21e-14	CHCHD6	coiled-coil-helix-coiled-coil-helix
-0.95	1.91e-24	EXOC2	exocyst complex component 2	0.7	2.38e-11	MTCH1	mitochondrial carrier 1
-0.95	1.73e-16	ABRACL	ABRA C-terminal like	0.7	1.57e-09	ALDH2	aldehyde dehydrogenase 2 family mem

GAGE analysis on upregulated and downregulated proteins at low/absent ACTR3 protein, DB1



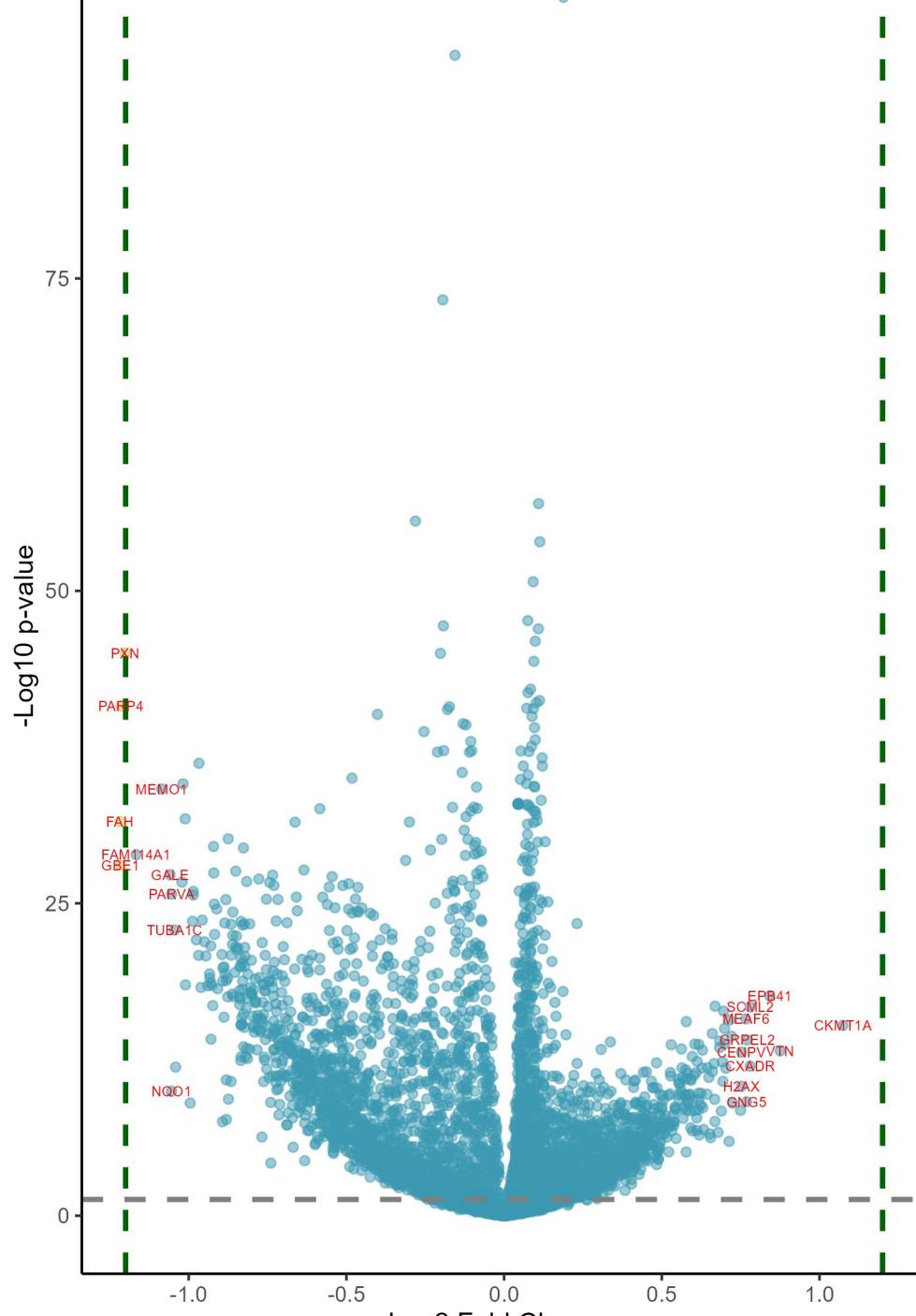
p-value < 0.05 & logFC > 1.2



Downregulated in blood cancers at low/absent ACTR3 Upregulated in blood cancers at low/absent ACTR3

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.62	5.51e-08	PLEK	pleckstrin	0.86	3.86e-03	IGSF8	immunoglobulin superfamily member 8
-1.34	1.18e-07	NCF4	neutrophil cytosolic factor 4	0.86	3.79e-02	ABCB6	ATP binding cassette subfamily B me
-1.25	4.13e-04	ITGAL	integrin subunit alpha L	0.82	1.05e-02	ACP2	acid phosphatase 2, lysosomal
-1.24	4.32e-07	DOCK8	dedicator of cytokinesis 8	0.81	4.60e-03	GIPC1	GIPC PDZ domain containing family m
-1.16	1.33e-04	PTK2B	protein tyrosine kinase 2 beta	0.81	4.27e-02	POLR2K	RNA polymerase II, I and III subuni
-1.13	1.41e-04	SH3BP1	SH3 domain binding protein 1	0.81	3.15e-03	BRD7	bromodomain containing 7
-1.11	2.69e-06	WDFY4	WDFY family member 4	0.79	3.99e-02	DBN1	drebrin 1
-1.1	6.01e-04	MYO1G	myosin IG	0.77	6.48e-03	BRD2	bromodomain containing 2
-1.08	2.45e-03	LAT2	linker for activation of T cells fa	0.77	2.37e-02	CCNA2	cyclin A2
-1.07	1.51e-05	ANKRD44	ankyrin repeat domain 44	0.76	9.47e-03	MFGE8	milk fat globule EGF and factor V/V
-1.07	1.46e-08	MNDA	myeloid cell nuclear differentiatio	0.76	3.26e-03	MORC2	MORC family CW-type zinc finger 2
-1.03	8.67e-03	ITGB2	integrin subunit beta 2	0.75	5.05e-02	FKBP11	FKBP prolyl isomerase 11
-1	2.78e-04	MYO1F	myosin IF	0.74	1.63e-02	MAZ	MYC associated zinc finger protein
-0.99	5.25e-02	COTL1	coactosin like F-actin binding prot	0.74	9.83e-02	TSTD1	thiosulfate sulfurtransferase like
-0.97	3.19e-03	CSTA	cystatin A	0.72	1.35e-02	TCF12	transcription factor 12
-0.97	2.73e-03	PLCG2	phospholipase C gamma 2	0.71	7.72e-02	CTTN	cortactin
-0.96	8.41e-04	PRKCD	protein kinase C delta	0.71	2.91e-02	ATP1A3	ATPase Na+/K+ transporting subunit
-0.96	4.32e-07	PRTN3	proteinase 3	0.71	1.75e-02	RPAP1	RNA polymerase II associated protei
-0.94	1.96e-03	CTSG	cathepsin G	0.7	7.74e-03	KIF20A	kinesin family member 20A
-0.92	1.45e-03	NCKAP1L	NCK associated protein 1 like	0.7	1.10e-02	KNSTRN	kinetochore localized astrin (SPAG5
-0.92	4.04e-04	PXK	PX domain containing serine/threoni	0.69	1.31e-02	KNOP1	lysine rich nucleolar protein 1
-0.92	2.30e-03	SORL1	sortilin related receptor 1	0.69	5.40e-02	IRF2BPL	interferon regulatory factor 2 bind
-0.92	9.60e-02	LSP1	lymphocyte specific protein 1	0.68	8.48e-02	LGALS3BP	galectin 3 binding protein
-0.91	4.78e-04	FAM107B	family with sequence similarity 107	0.68	2.14e-01	RPLP1	ribosomal protein lateral stalk sub
-0.88	1.73e-03	ACSL5	acyl-CoA synthetase long chain fami	0.68	8.70e-03	C12orf57	chromosome 12 open reading frame 57
-0.88	2.73e-02	PTPN6	protein tyrosine phosphatase non-re	0.67	2.04e-02	SNTB2	syntrophin beta 2
-0.86	1.89e-02	ZYX	zyxin	0.67	1.35e-02	RNF169	ring finger protein 169
-0.86	6.20e-04	IKBKB	inhibitor of nuclear factor kappa B	0.67	4.60e-02	ZMAT2	zinc finger matrin-type 2
-0.85	1.76e-02	RALB	RAS like proto-oncogene B	0.66	4.83e-02	CEP43	centrosomal protein 43

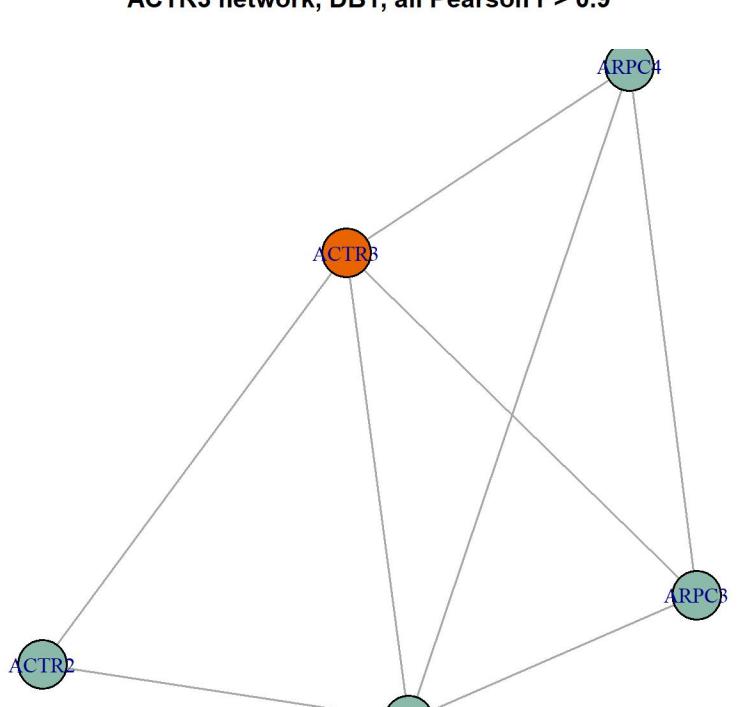
p-value < 0.05 & logFC > 1.2



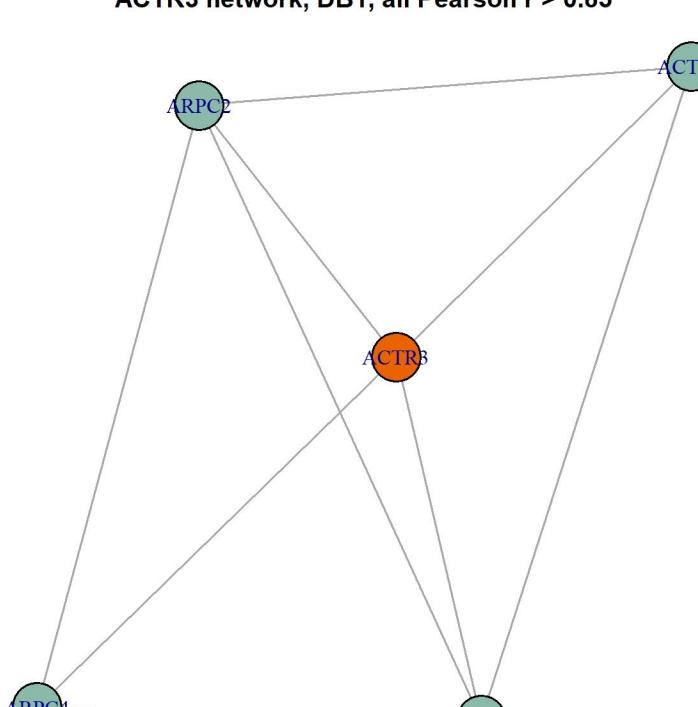
Downregulated in solid cancers at low/absent ACTR3 Upregulated in solid cancers at low/absent ACTR3

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.22	1.27e-30	FAH	fumarylacetoacetate hydrolase	1.07	6.20e-15	CKMT1A	creatine kinase, mitochondrial 1A
-1.22	3.36e-27	GBE1	1,4-alpha-glucan branching enzyme 1	0.88	5.18e-13	VTN	vitronectin
-1.21	5.56e-39	PARP4	poly(ADP-ribose) polymerase family	0.84	3.44e-17	EPB41	erythrocyte membrane protein band 4
-1.2	4.77e-43	PXN	paxillin	0.78	7.54e-12	CXADR	CXADR Ig-like cell adhesion molecul
-1.17	4.90e-28	FAM114A1	family with sequence similarity 114	0.78	2.38e-16	SCML2	Scm polycomb group protein like 2
-1.09	8.99e-33	MEMO1	mediator of cell motility 1	0.77	7.81e-14	GRPEL2	GrpE like 2, mitochondrial
-1.06	1.83e-26	GALE	UDP-galactose-4-epimerase	0.77	3.72e-09	GNG5	G protein subunit gamma 5
-1.05	5.71e-25	PARVA	parvin alpha	0.77	1.98e-15	MEAF6	MYST/Esa1 associated factor 6
-1.05	5.84e-10	NQO1	NAD(P)H quinone dehydrogenase 1	0.75	2.55e-10	H2AX	H2A.X variant histone
-1.05	3.26e-22	TUBA1C	tubulin alpha 1c	0.75	6.62e-13	CENPV	centromere protein V
-1.04	8.97e-12	CBR3	carbonyl reductase 3	0.75	1.66e-08	MACROH2A2	macroH2A.2 histone
-1.02	6.88e-26	SEPTIN10	septin 10	0.72	4.73e-09	MRPL54	mitochondrial ribosomal protein L54
-1.02	3.78e-33	LPP	LIM domain containing preferred tra	0.72	4.08e-14	NSD3	nuclear receptor binding SET domain
-1.01	7.85e-31	GMPPB	GDP-mannose pyrophosphorylase B	0.71	2.45e-15	ZNF384	zinc finger protein 384
-1.01	5.03e-18	FHL2	four and a half LIM domains 2	0.71	3.56e-06	NDUFB11	NADH:ubiquinone oxidoreductase subu
-1	4.71e-09	ARPC5	actin related protein 2/3 complex s	0.7	1.10e-11	GTPBP3	GTP binding protein 3, mitochondria
-0.99	6.89e-23	PMM2	phosphomannomutase 2	0.7	1.48e-13	KIF1A	kinesin family member 1A
-0.99	6.66e-25	DCTD	dCMP deaminase	0.7	1.09e-14	NCBP2AS2	NCBP2 antisense 2 (head to head)
-0.99	3.52e-25	PDLIM2	PDZ and LIM domain 2	0.7	5.08e-16	TCF20	transcription factor 20
-0.98	1.90e-21	SH3KBP1	SH3 domain containing kinase bindin	0.69	1.05e-10	CNTN1	contactin 1
-0.97	2.88e-20	TRIP6	thyroid hormone receptor interactor	0.69	3.58e-12	COQ7	coenzyme Q7, hydroxylase
-0.97	1.01e-34	PTPN23	protein tyrosine phosphatase non-re	0.69	1.89e-08	EPCAM	epithelial cell adhesion molecule
-0.96	7.94e-18	GLRX	glutaredoxin	0.68	9.47e-14	BRD1	bromodomain containing 1
-0.96	5.57e-23	PCYT2	phosphate cytidylyltransferase 2, e	0.68	2.92e-13	COQ6	coenzyme Q6, monooxygenase
-0.95	2.63e-21	TNS3	tensin 3	0.68	7.49e-07	GCSH	glycine cleavage system protein H
-0.95	3.19e-20	EXOC2	exocyst complex component 2	0.67	2.11e-16	DNMT3A	DNA methyltransferase 3 alpha
-0.94	5.96e-18	SH3BGRL	SH3 domain binding glutamate rich p	0.67	1.14e-07	SPINT1	serine peptidase inhibitor, Kunitz
-0.93	7.37e-19	PSMB8	proteasome 20S subunit beta 8	0.67	2.42e-09	GNG10	G protein subunit gamma 10
-0.93	1.57e-18	IRF3	interferon regulatory factor 3	0.67	4.82e-12	HPSE	heparanase

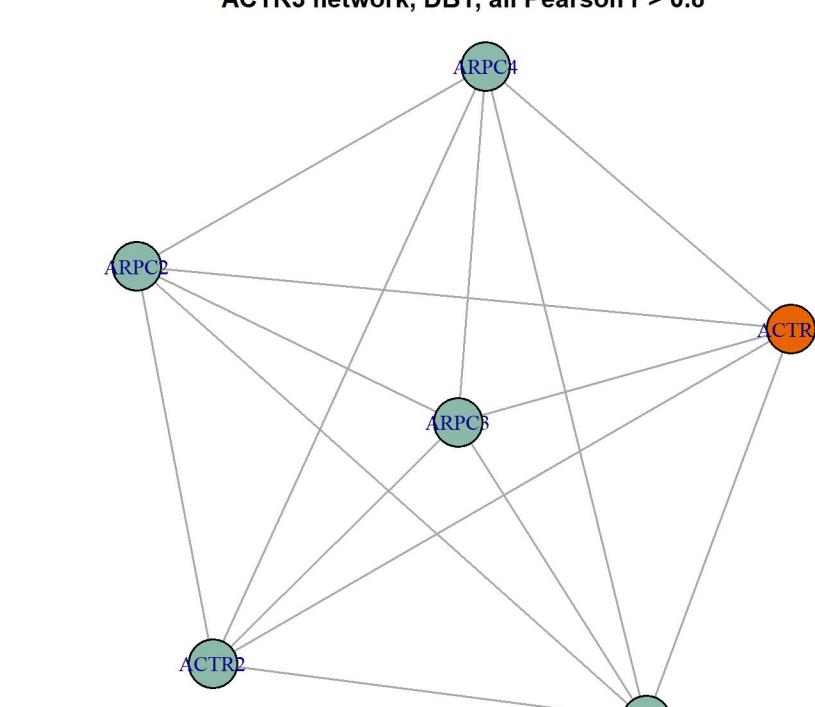
ACTR3 network, DB1, all Pearson r > 0.9



ACTR3 network, DB1, all Pearson r > 0.85

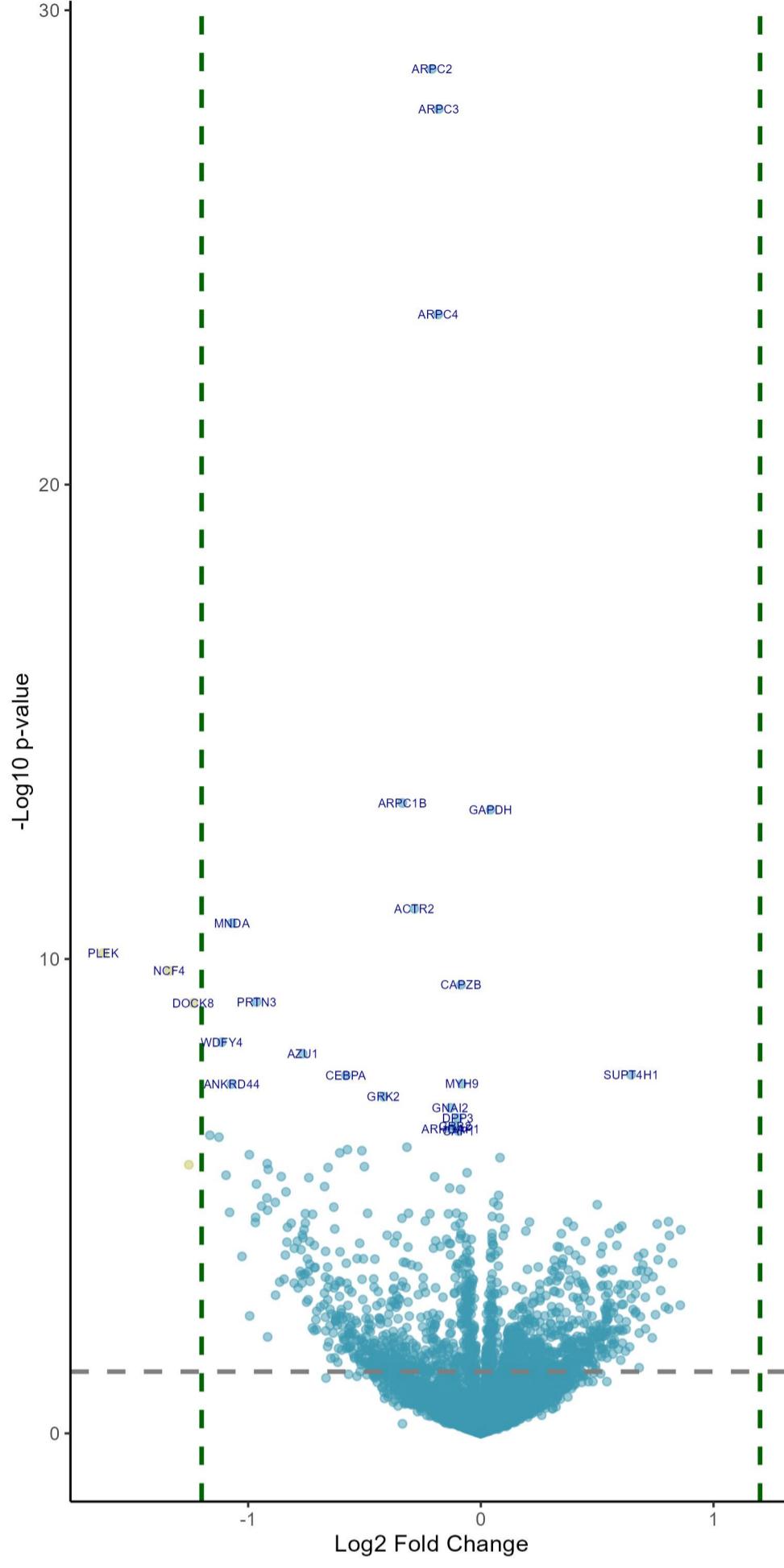


ACTR3 network, DB1, all Pearson r > 0.8



Differentially expressed proteins in blood cancers at absence/low amount of ACTR3 , DB1

p-value < 0.05 & logFC > 1.2



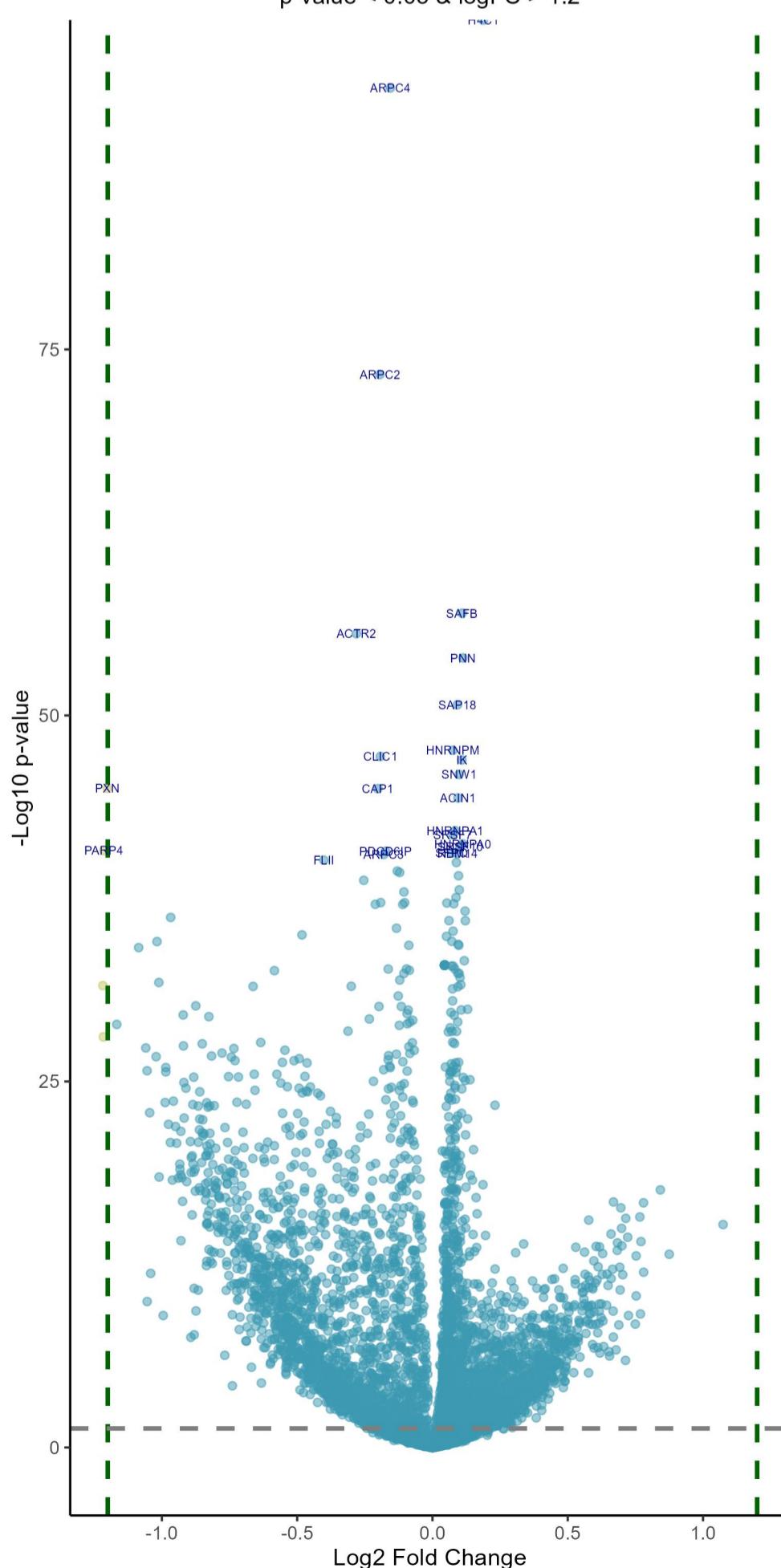
Sorted by p values!

Downregulated in blood cancers at low/absent ACTR3 Upregulated in blood cancers at low/absent ACTR3

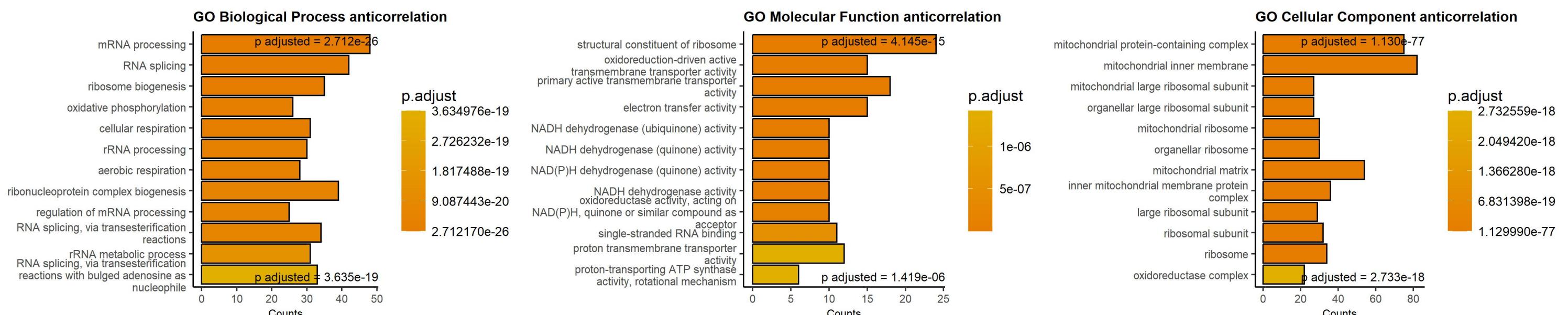
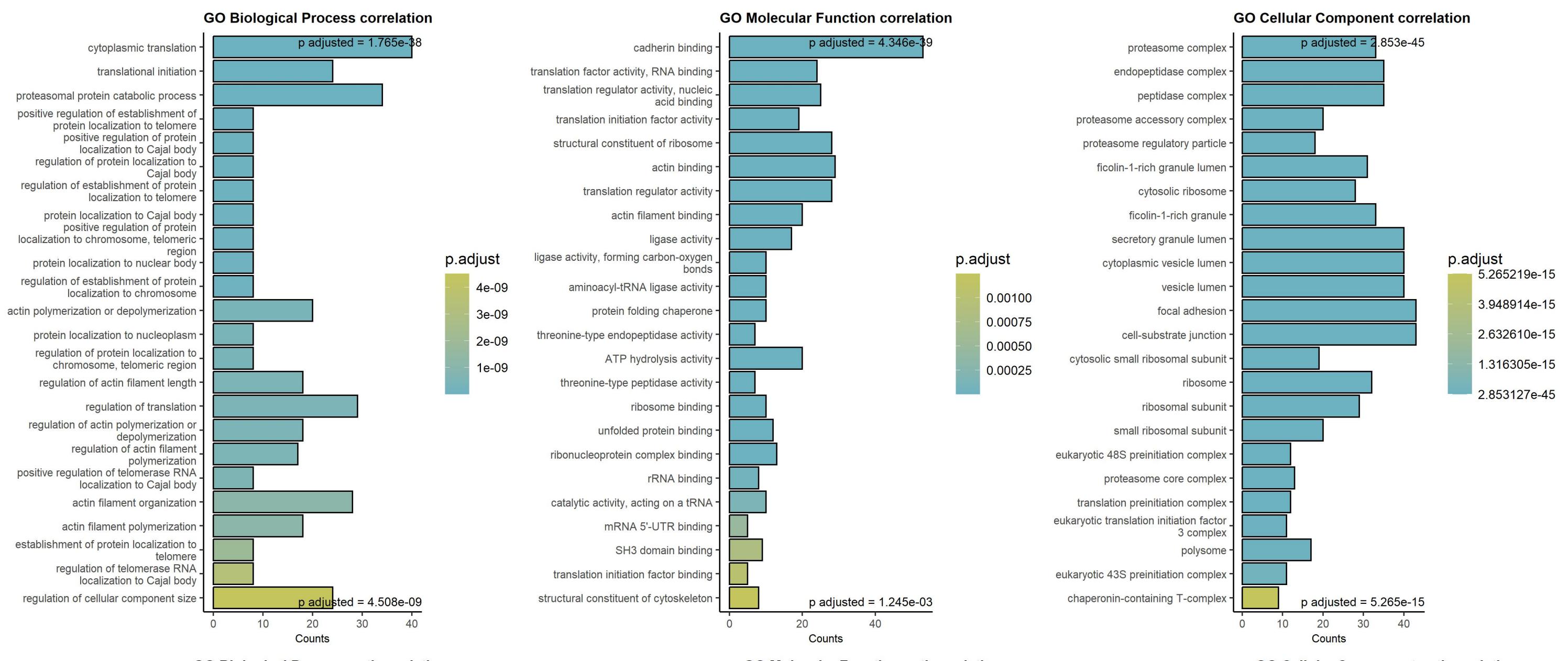
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.21	5.75e-26	ARPC2	actin related protein 2/3 complex s	0.04	7.86e-11	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
-0.18	2.67e-25	ARPC3	actin related protein 2/3 complex s	0.65	1.12e-05	SUPT4H1	SPT4 homolog, DSIF elongation factor
-0.18	4.28e-21	ARPC4	actin related protein 2/3 complex s	0.08	3.11e-04	SUPT5H	SPT5 homolog, DSIF elongation factor
-0.34	6.85e-11	ARPC1B	actin related protein 2/3 complex s	0.08	1.30e-03	CSTF2	cleavage stimulation factor subunit
-0.29	8.31e-09	ACTR2	actin related protein 2	0.06	1.73e-03	ATXN2L	ataxin 2 like
-1.07	1.46e-08	MNDA	myeloid cell nuclear differentiation	0.5	1.90e-03	GUK1	guanylate kinase 1
-1.62	5.51e-08	PLEK	pleckstrin	0.07	1.94e-03	RAE1	ribonucleic acid export 1
-1.34	1.18e-07	NCF4	neutrophil cytosolic factor 4	0.05	2.70e-03	EIF4B	eukaryotic translation initiation factor
-0.08	2.11e-07	CAPZB	capping actin protein of muscle Z-I	0.08	2.77e-03	LSM3	LSM3 homolog, U6 small nuclear RNA
-0.96	4.32e-07	PRIN3	proteinase 3	0.81	3.15e-03	BRD7	bromodomain containing 7
-1.24	4.32e-07	DOCK8	dedicator of cytokinesis 8	0.37	3.15e-03	LARP4	La ribonucleoprotein 4
-1.11	2.69e-06	WDFY4	WDFY family member 4	0.21	3.15e-03	PGRMC1	progesterone receptor membrane component
-0.77	4.40e-06	AZU1	azurocidin 1	0.76	3.26e-03	MORC2	MORC family CW-type zinc finger 2
-0.58	1.12e-05	CEBPA	CCAAT enhancer binding protein alph	0.61	3.48e-03	SPATA5	spermatogenesis associated 5
-0.08	1.51e-05	MYH9	myosin heavy chain 9	0.4	3.48e-03	P4HTM	prolyl 4-hydroxylase, transmembrane
-1.07	1.51e-05	ANKRD44	ankyrin repeat domain 44	0.59	3.79e-03	SPATA5L1	spermatogenesis associated 5 like 1
-0.42	2.65e-05	GRK2	G protein-coupled receptor kinase 2	0.1	3.79e-03	PAFAH1B3	platelet activating factor acetylhydrolase, membrane bound
-0.13	4.36e-05	GNAI2	G protein subunit alpha i2	0.86	3.86e-03	IGSF8	immunoglobulin superfamily member 8
-0.1	6.87e-05	DPP3	dipeptidyl peptidase 3	0.19	4.06e-03	CALU	calumenin
-0.11	9.71e-05	GRB2	growth factor receptor bound protein 2	0.55	4.41e-03	SH3PXD2B	SH3 and PX domains 2B
-0.13	1.07e-04	ARHGAP1	Rho GTPase activating protein 1	0.05	4.41e-03	HNRNPDL	heterogeneous nuclear ribonucleoprotein D-like
-0.1	1.12e-04	CAP1	cyclase associated actin cytoskeleton	0.35	4.41e-03	GLRX5	glutaredoxin 5
-1.16	1.33e-04	PTK2B	protein tyrosine kinase 2 beta	0.81	4.60e-03	GIPC1	GIPC PDZ domain containing family m
-1.13	1.41e-04	SH3BP1	SH3 domain binding protein 1	0.1	4.60e-03	PGRMC2	progesterone receptor membrane component
-0.32	2.20e-04	WIPF1	WAS/WASL interacting protein family	0.05	4.96e-03	SAFB	scaffold attachment factor B
-0.57	2.39e-04	WAS	WASP actin nucleation promoting factor	0.45	5.52e-03	KCMF1	potassium channel modulatory factor
-0.51	2.44e-04	SERPINB10	serpin family B member 10	0.05	5.52e-03	SON	SON DNA and RNA binding protein
-0.61	2.62e-04	STK10	serine/threonine kinase 10	0.05	6.01e-03	PSMC4	proteasome 26S subunit, ATPase 4
-1	2.78e-04	MYO1F	myosin IF	0.05	6.01e-03	PHF5A	PHD finger protein 5A
-0.92	4.04e-04	PXK	PX domain containing serine/threonine kinase	0.58	6.06e-03	SLC38A2	solute carrier family 38 member 2
-1.25	4.13e-04	ITGAL	integrin subunit alpha L	0.33	6.25e-03	LEMD3	LEM domain containing 3
-0.5	4.41e-04	RNASE2	ribonuclease A family member 2	0.52	6.25e-03	SMTN	smoothelin
-0.66	4.47e-04	TTC9	tetratricopeptide repeat domain 9	0.34	6.32e-03	NIT1	nitrilase 1
-0.91	4.78e-04	FAM107B	family with sequence similarity 107	0.77	6.48e-03	BRD2	bromodomain containing 2
-0.06	5.47e-04	RPL4	ribosomal protein L4	0.38	7.05e-03	C19orf53	chromosome 19 open reading frame 53
-1.1	6.01e-04	MYO1G	myosin IG	0.08	7.27e-03	SMARCE1	SWI/SNF related, matrix associated, chromatin rearranging factor
-0.86	6.20e-04	IKBKB	inhibitor of nuclear factor kappa B	0.04	7.56e-03	PSMC3	proteasome 26S subunit, ATPase 3
-0.2	6.20e-04	VASP	vasodilator stimulated phosphoprotein	0.7	7.74e-03	KIF20A	kinesin family member 20A
0.74	6.30e-04	RMND1	regulator of microtubule dynamics 1	0.52	7.80e-03	C5orf24	chromosome 5 open reading frame 24

Differentially expressed proteins in solid cancers at absence/low amount of ACTR3 , DB1

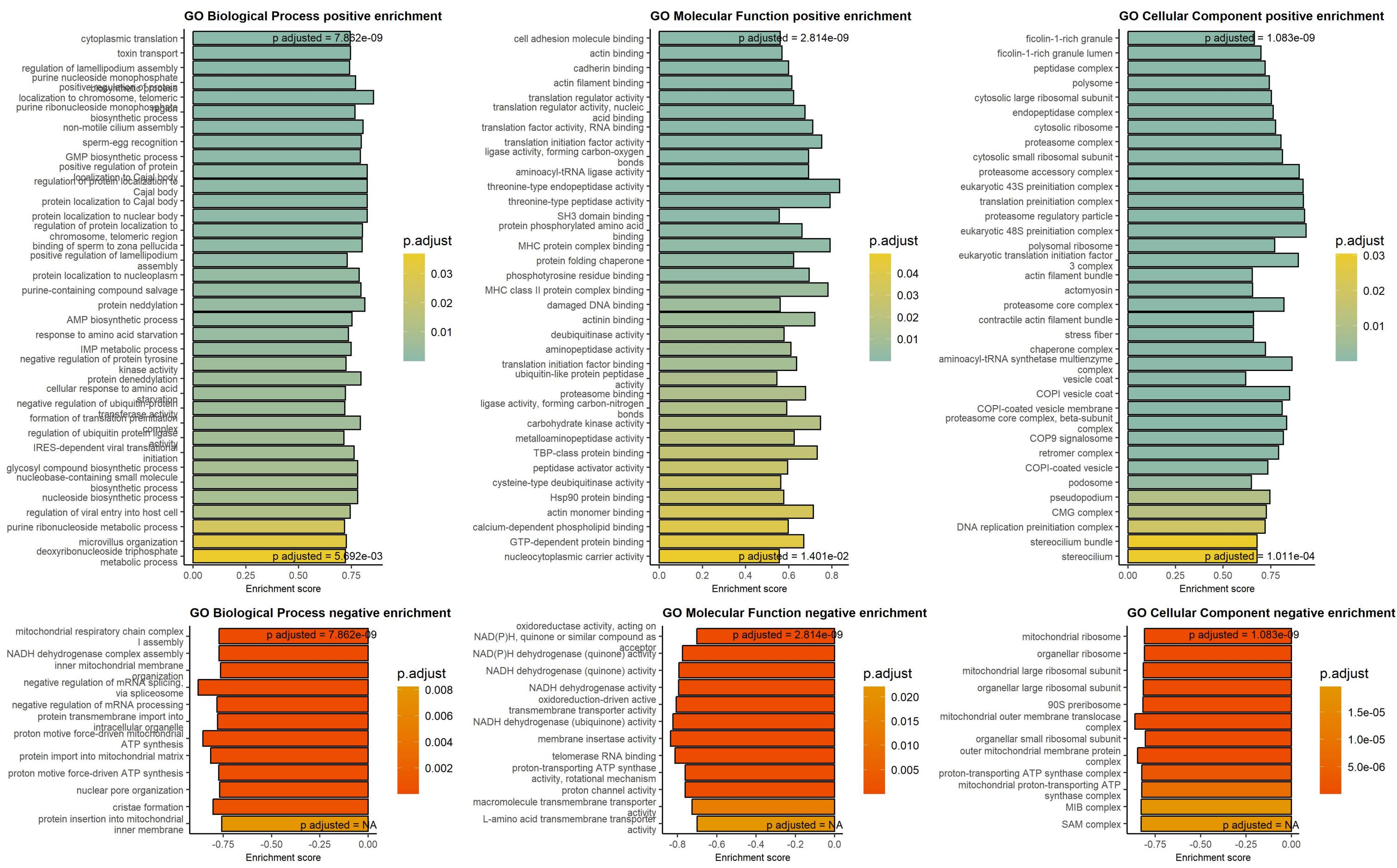
p-value < 0.05 & logFC > 1.2



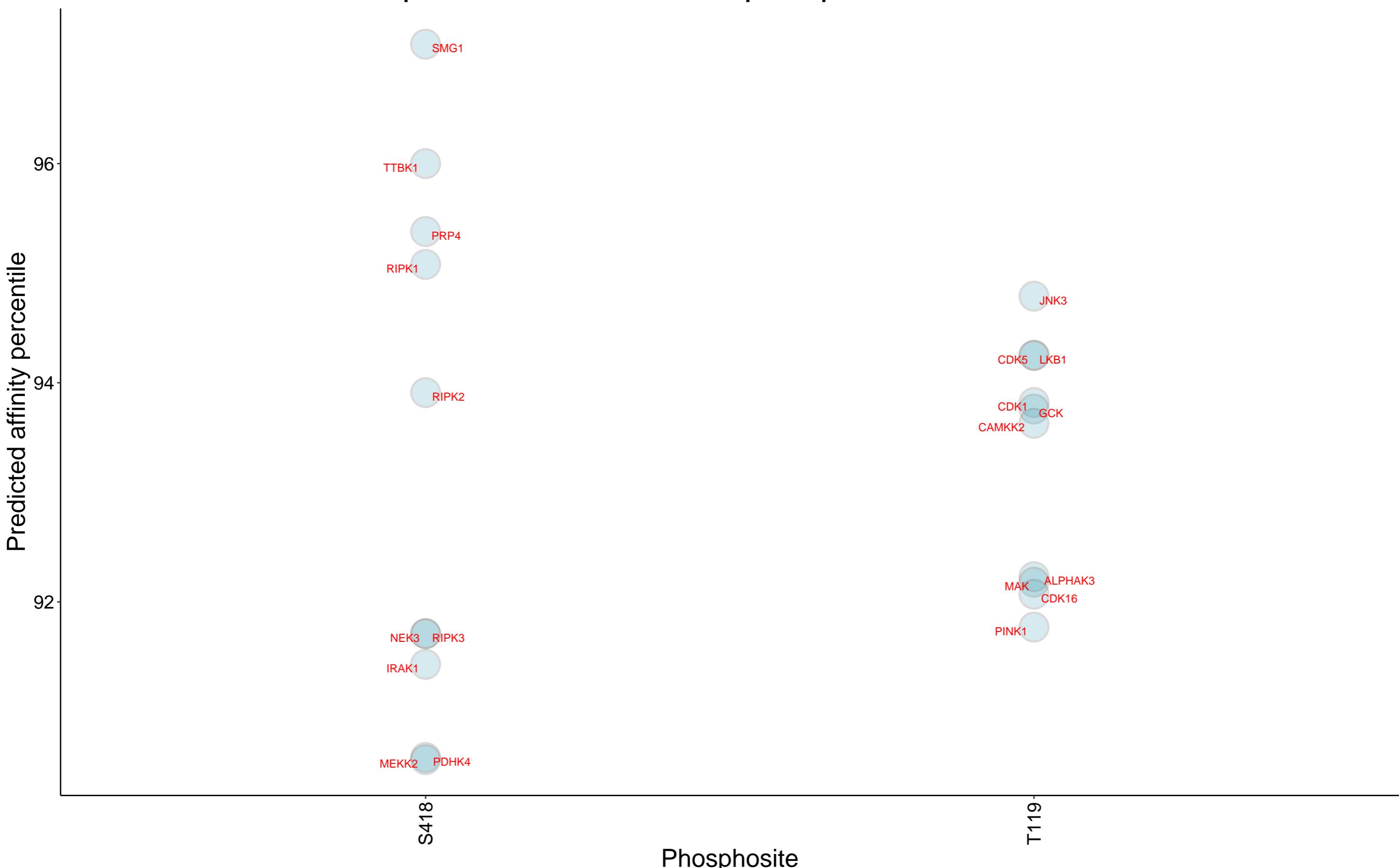
Top 250 correlation coefficients overrepresentation, ACTR3 protein, DB1



Gene Set Enrichment analysis on protein correlation coefficients, ACTR3 protein, DB1



Top 10 kinases for each phosphosite in ACTR3



Kinases with affinity greater than 98.5% to ACTR3

Top 15 positive correlation coefficients for ACTR3 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

