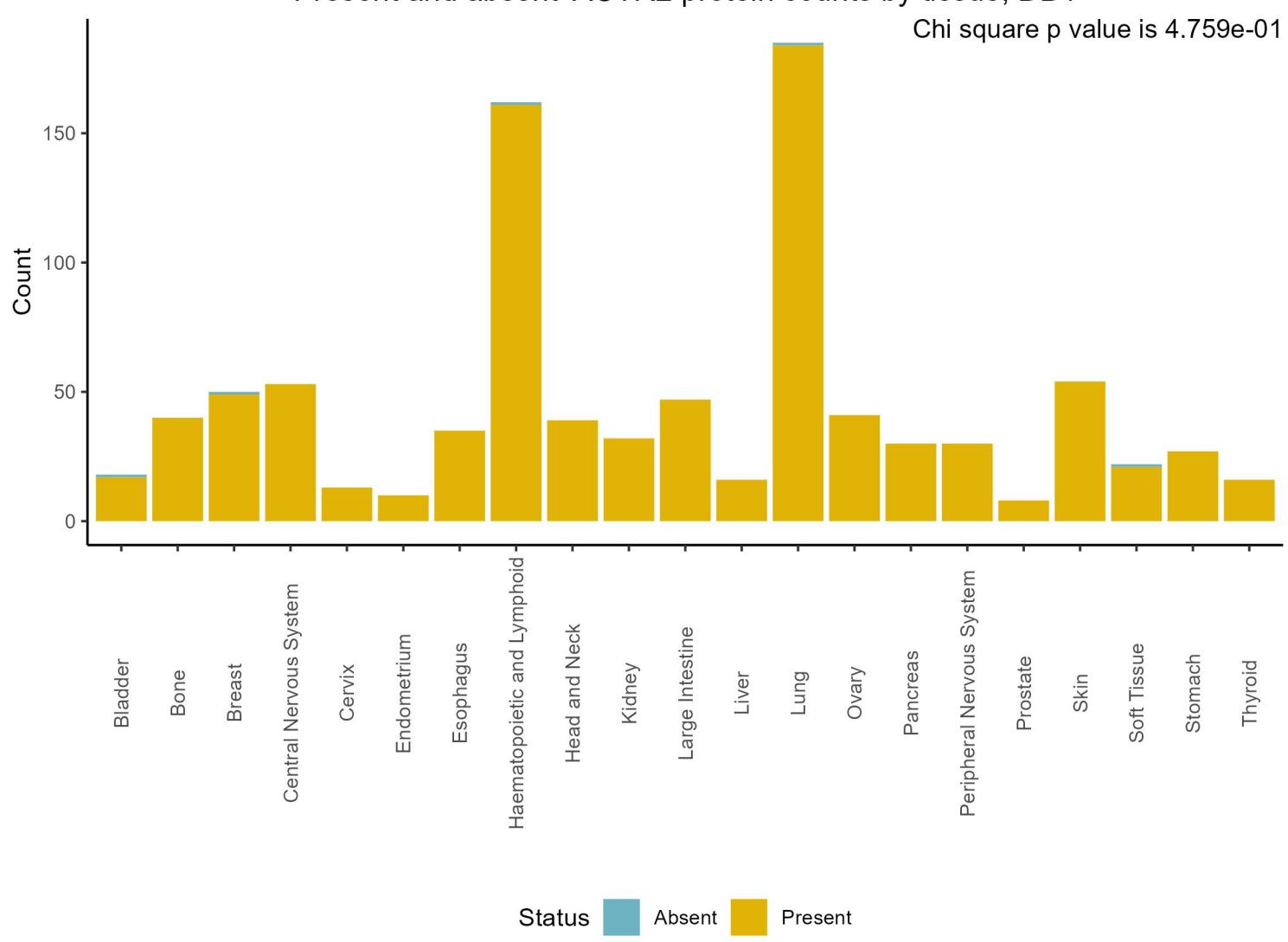
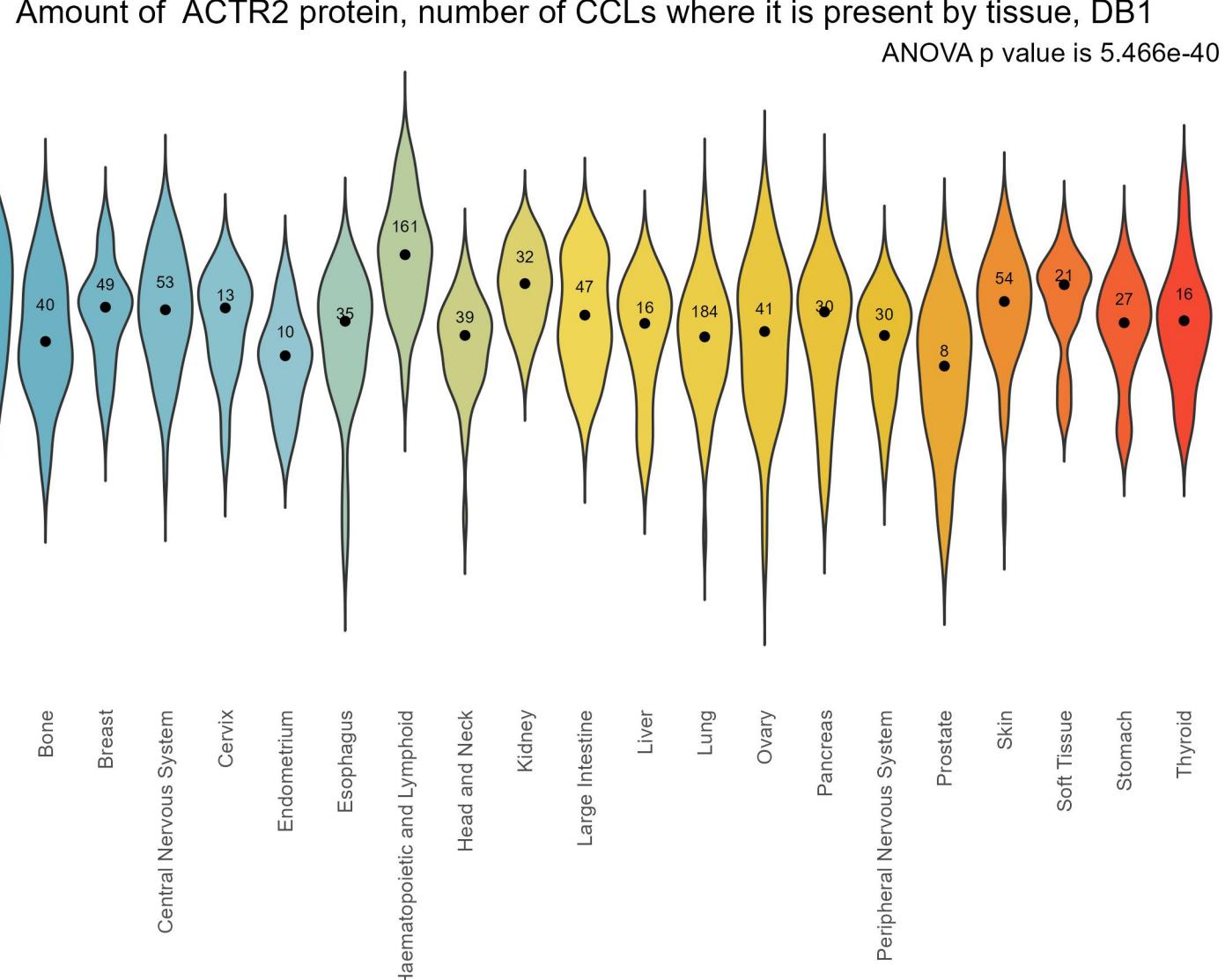
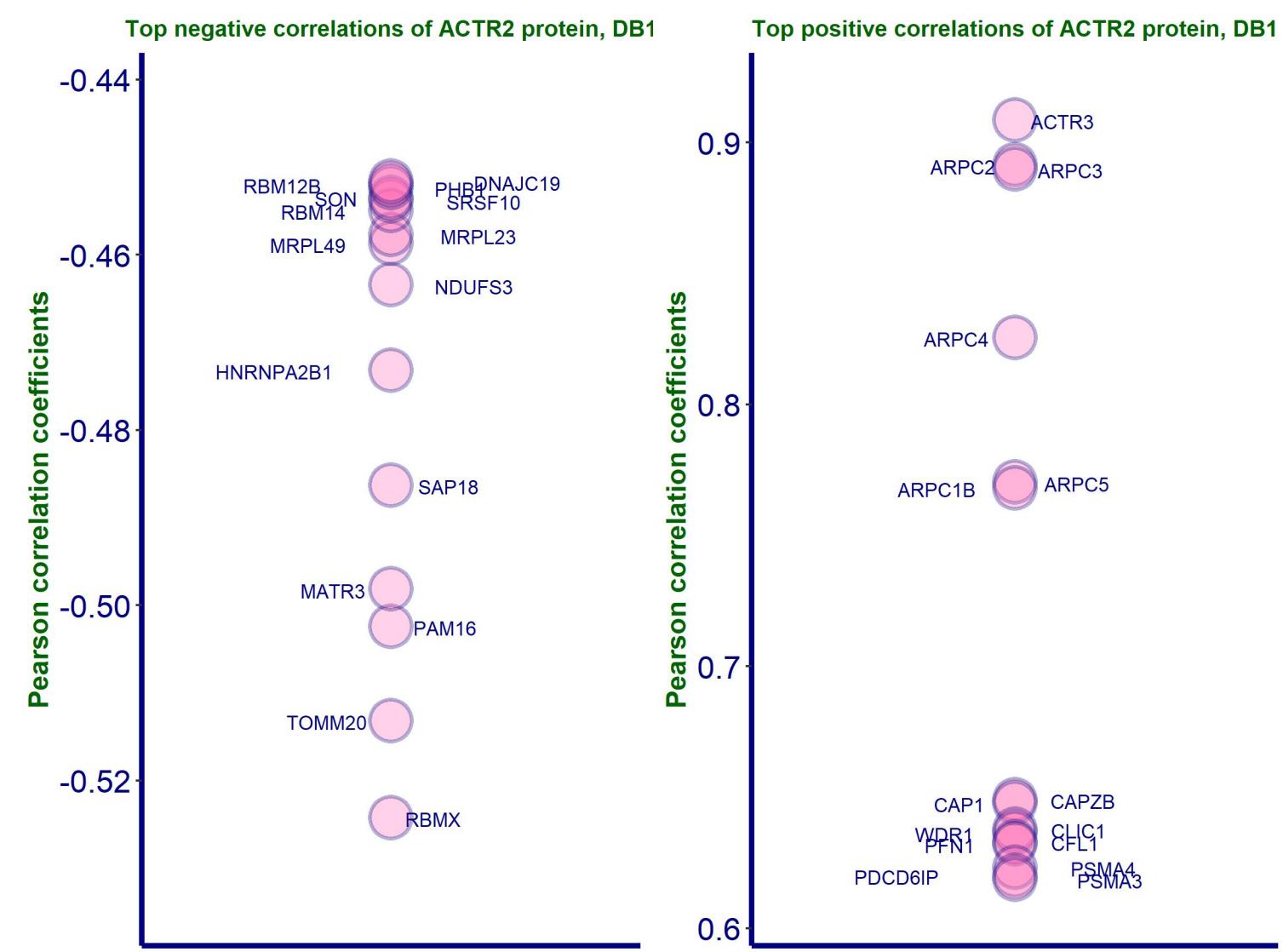
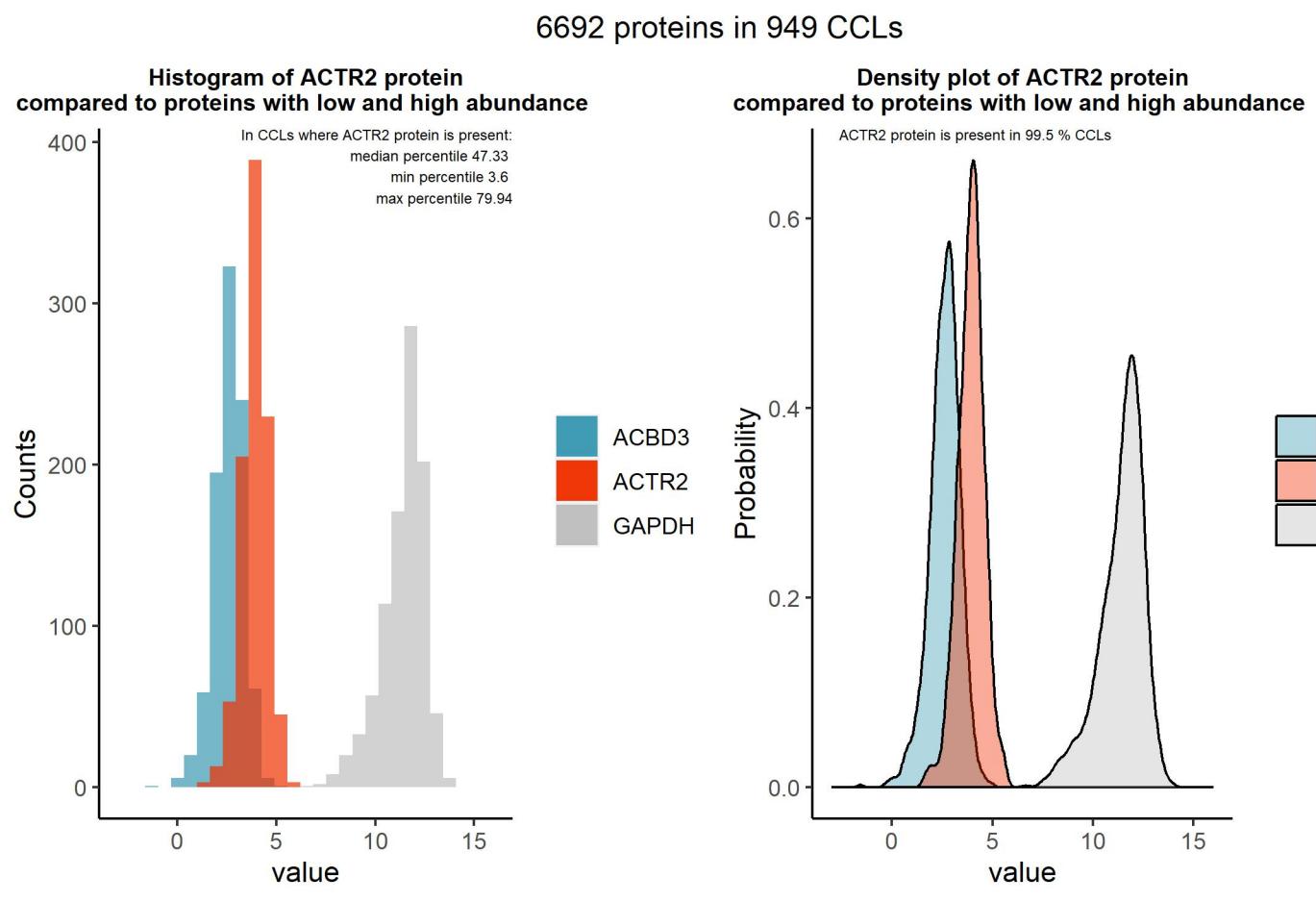


ACTR2

Protein name: ARP2 ; UNIPROT: P61160 ; Gene name: actin related protein 2

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

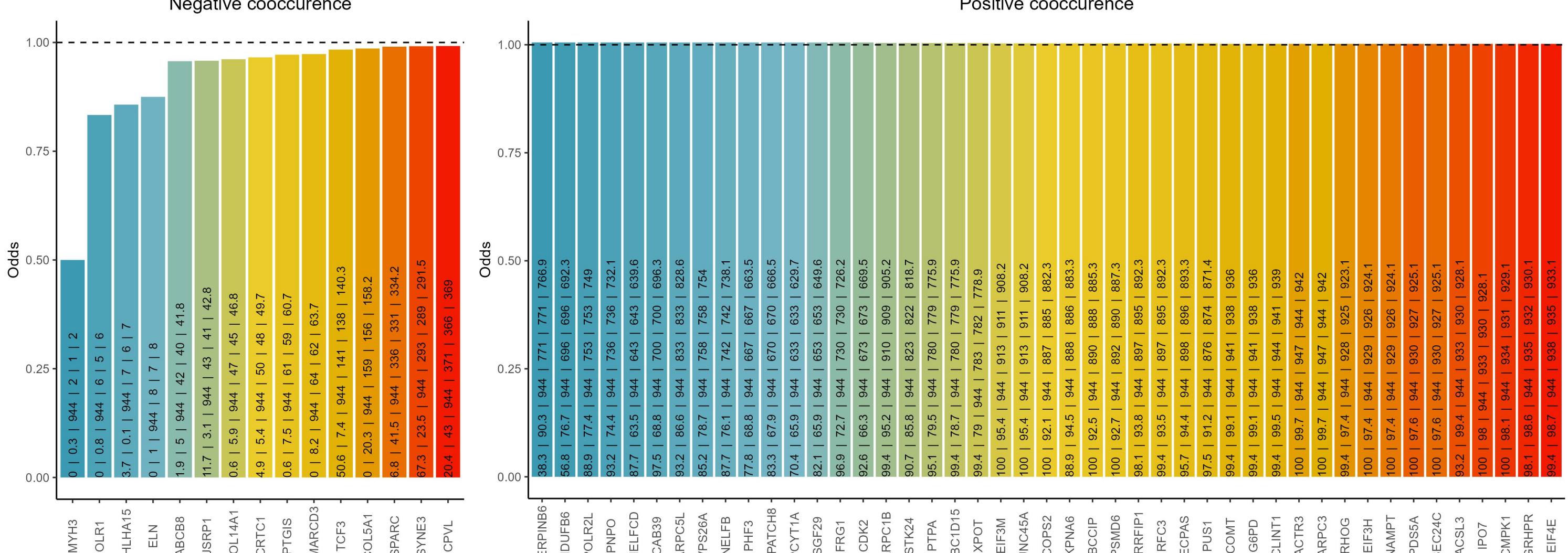
Sanger Institute Protein Database 1 (DB1), protein presence is certain



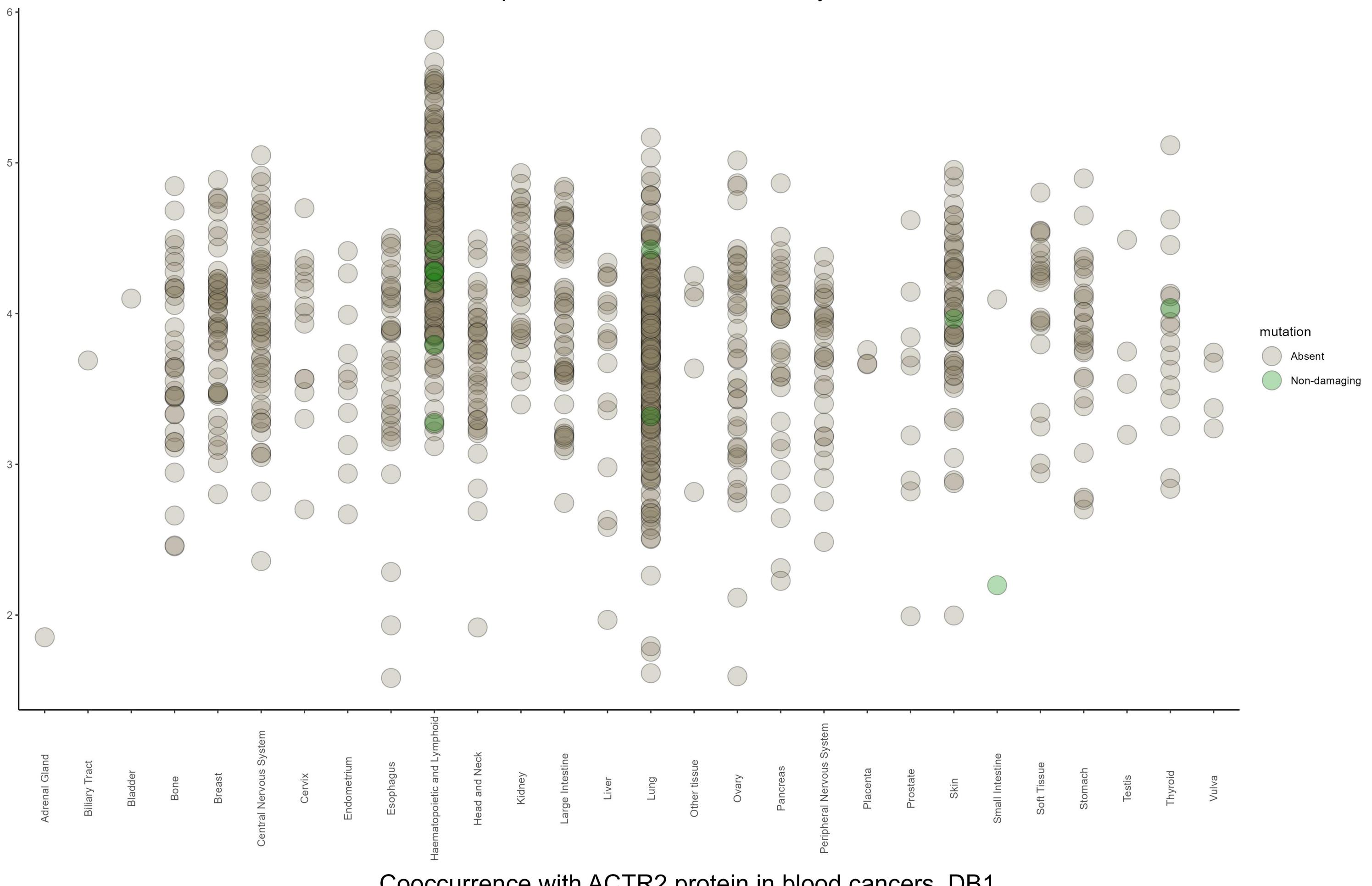
Cooccurrence with ACTR2 protein, DB1

% of ACTR2 in blood cancers: 99.4 ; % of ACTR2 in solid cancers: 99.5
of Protein 2 in solid cancers | Incidence of ACTB2 | Incidence of Protein

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ACTR2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

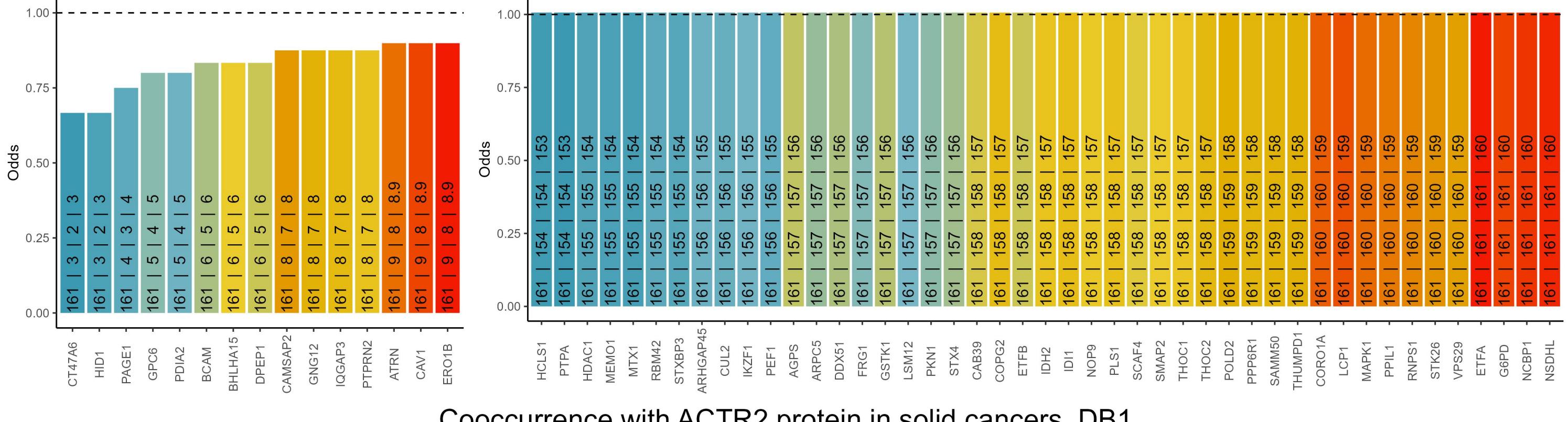


Amount of ACTR2 protein and mutation status by tissue, DB1



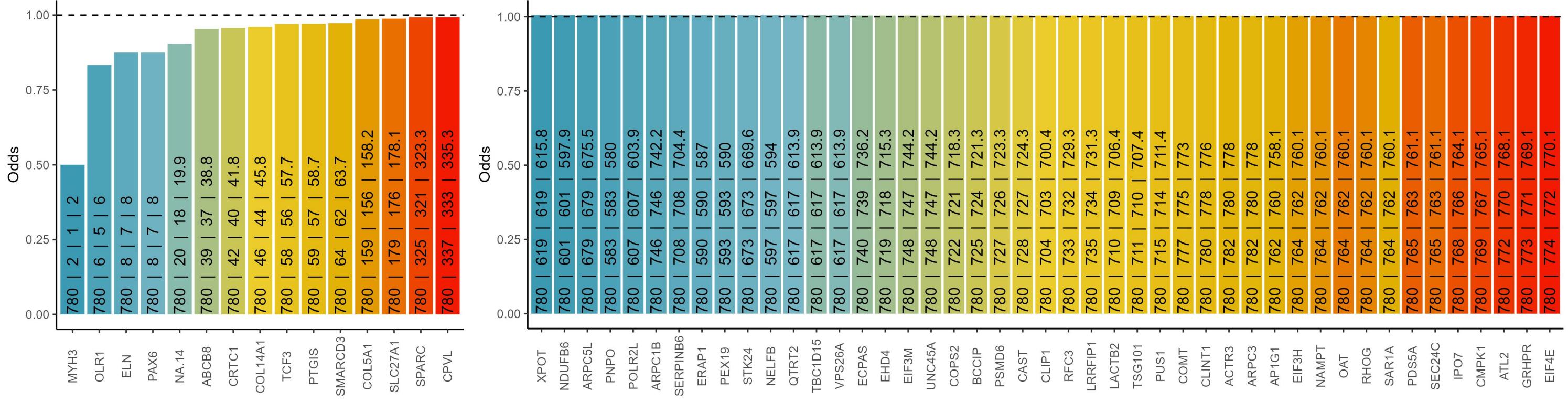
Cooccurrence with ACTR2 protein in blood cancers, DB1

The text in the bars: incidence of ACTR2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

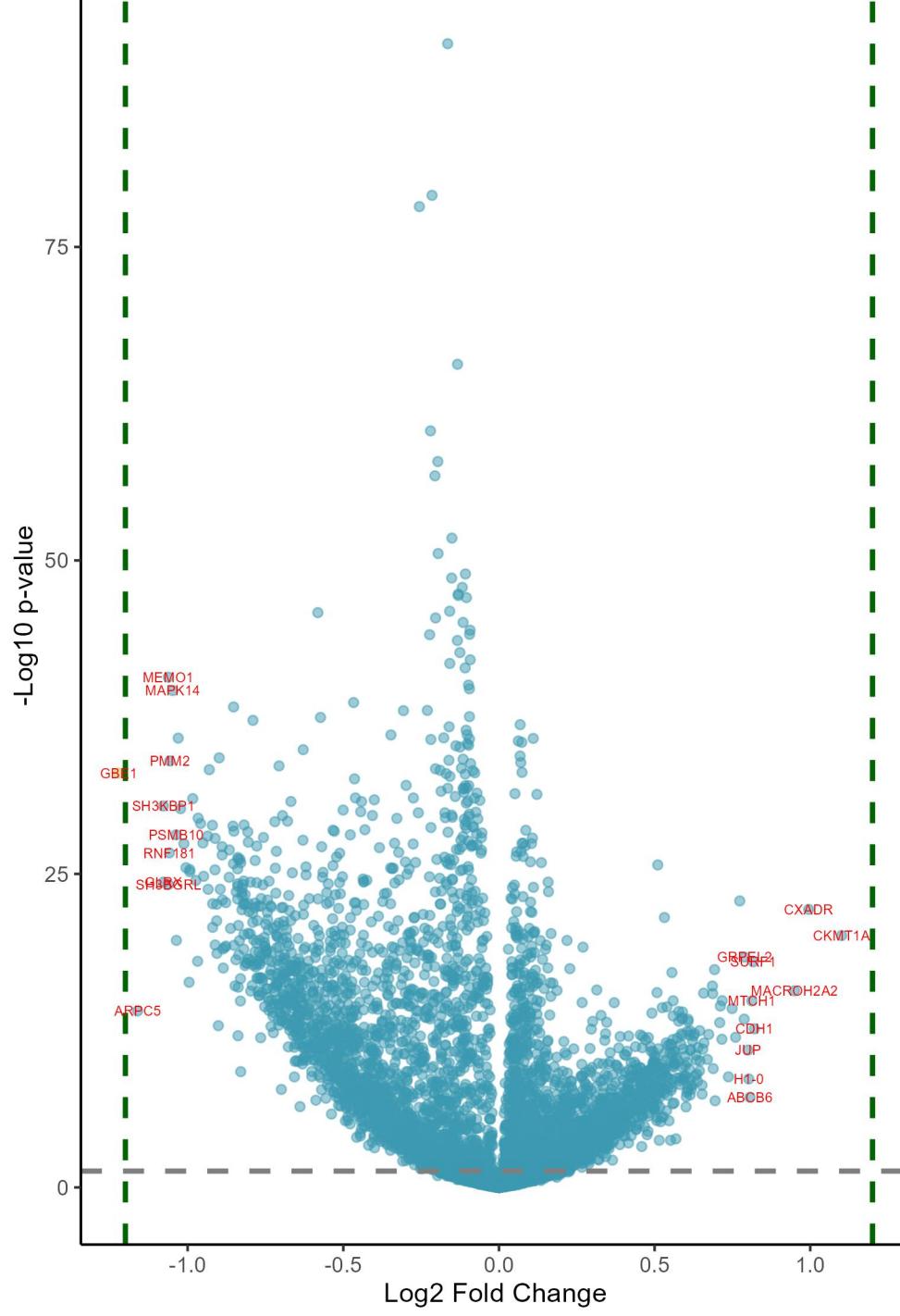


Cooccurrence with ACTR2 protein in solid cancers, DB1

The text in the bars: incidence of ACTR2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

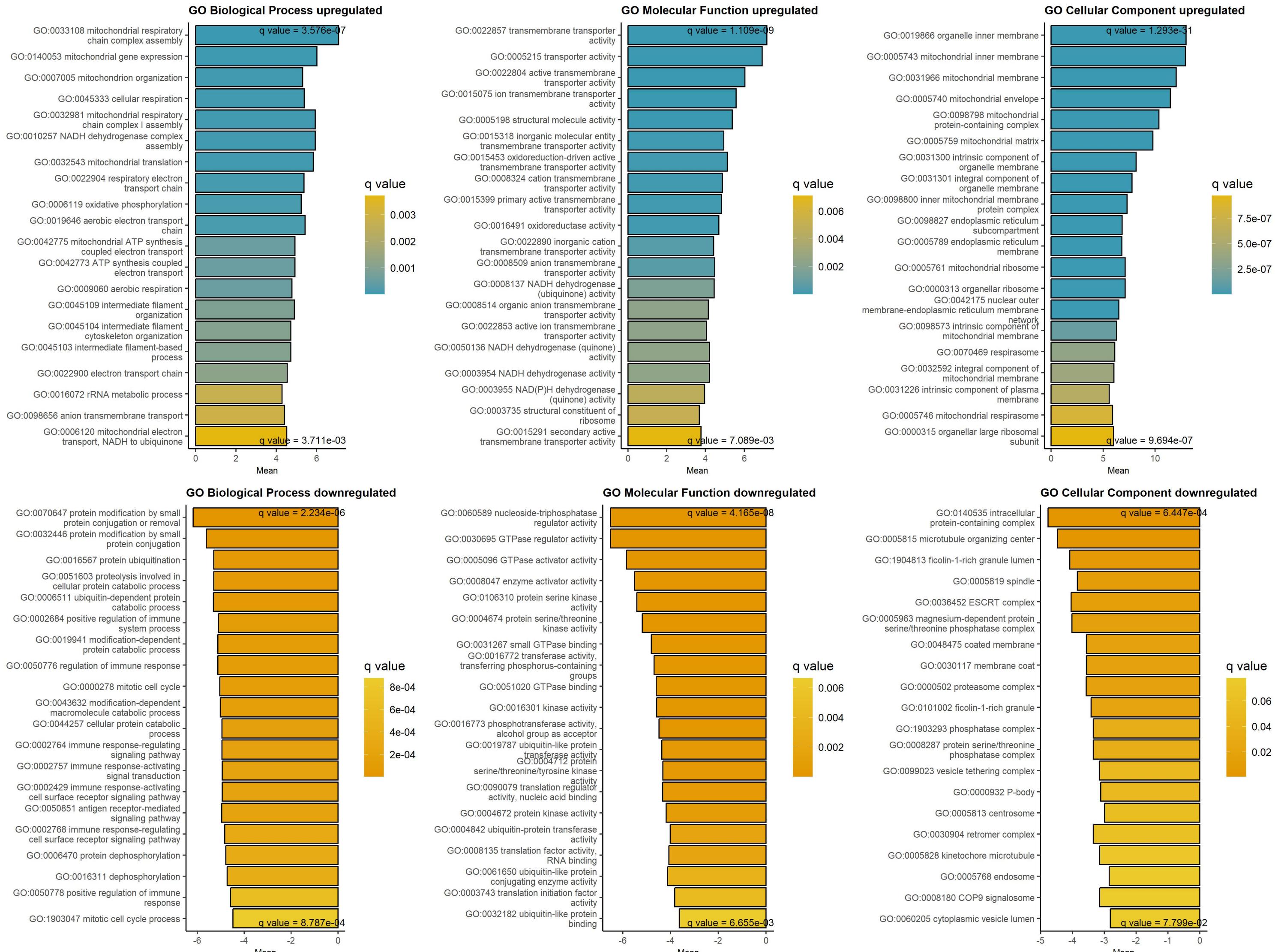


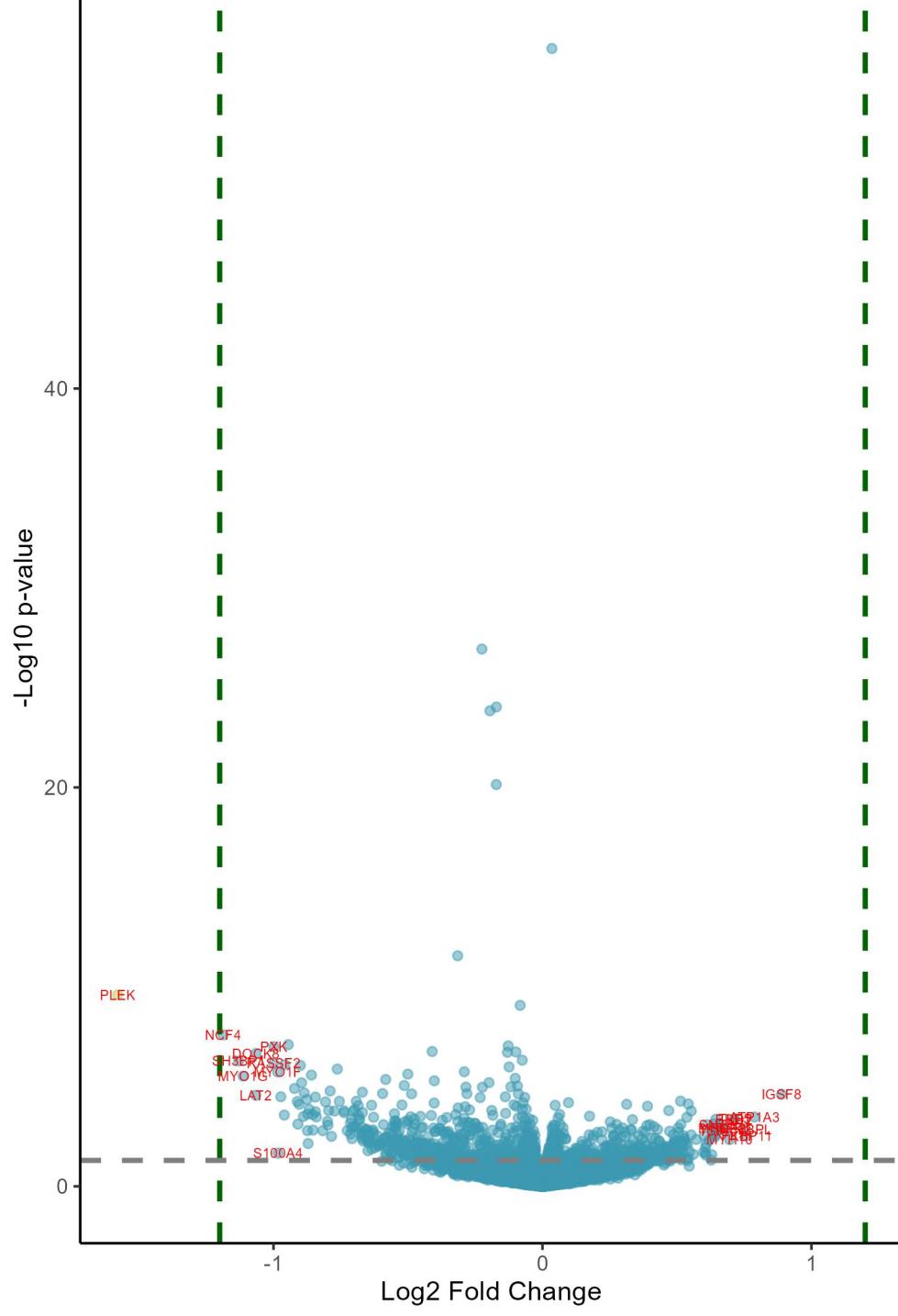
Downregulated at low/absent ACTR2 Upregulated at low/absent ACTR2



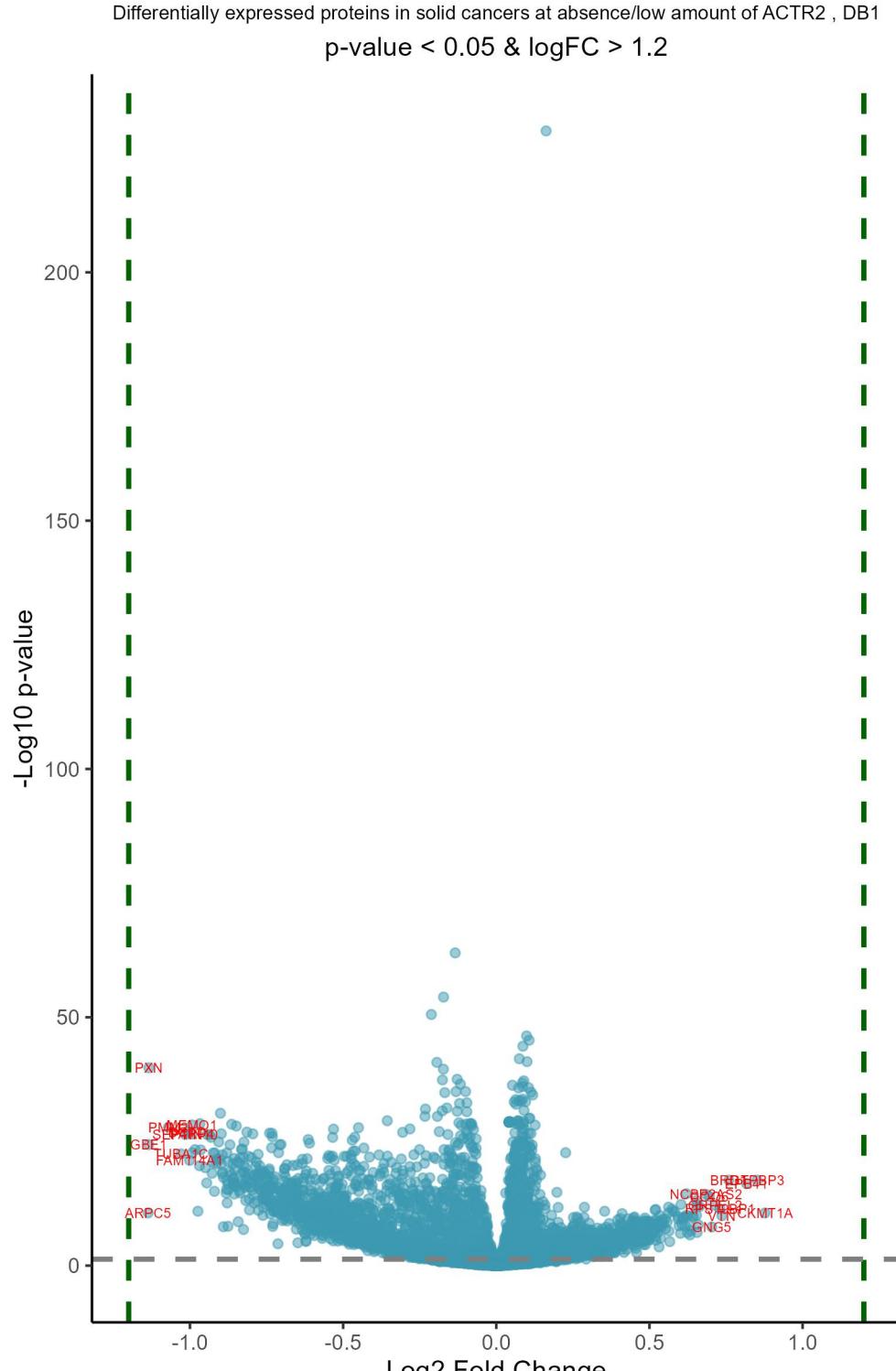
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.22	8.47e-32	GBE1	1,4-alpha-glucan branching enzyme 1	1.1	1.32e-19	CKMT1A	creatine kinase, mitochondrial 1A
-1.16	6.08e-14	ARPC5	actin related protein 2/3 complex s	0.99	1.38e-21	CXADR	CXADR Ig-like cell adhesion molecule
-1.08	1.26e-23	GLRX	glutaredoxin	0.95	1.86e-15	MACROH2A2	macroH2A.2 histone
-1.08	2.56e-29	SH3KBP1	SH3 domain containing kinase bindin	0.82	1.36e-12	CDH1	cadherin 1
-1.06	4.71e-39	MEMO1	mediator of cell motility 1	0.82	1.22e-17	SURF1	SURF1 cytochrome c oxidase assembly
-1.06	1.87e-23	SH3BGR1	SH3 domain binding glutamate rich p	0.81	1.05e-14	MTCH1	mitochondrial carrier 1
-1.06	7.96e-26	RNF181	ring finger protein 181	0.81	2.17e-07	ABCB6	ATP binding cassette subfamily B me
-1.06	1.06e-32	PMM2	phosphomannomutase 2	0.8	8.71e-09	H1-0	H1.0 linker histone
-1.05	4.92e-38	MAPK14	mitogen-activated protein kinase 14	0.8	5.63e-11	JUP	junction plakoglobin
-1.04	3.63e-27	PSMB10	proteasome 20S subunit beta 10	0.79	5.47e-18	GRPEL2	GrpE like 2, mitochondrial
-1.04	3.05e-19	ABRACL	ABRA C-terminal like	0.79	2.54e-13	EPCAM	epithelial cell adhesion molecule
-1.03	2.14e-34	STK10	serine/threonine kinase 10	0.77	3.25e-22	EXD2	exonuclease 3'-5' domain containing
-1.02	4.10e-29	DCK	deoxyribonucleoside kinase	0.76	6.01e-12	SPINT1	serine peptidase inhibitor, Kunitz
-1.01	1.67e-26	IRF3	interferon regulatory factor 3	0.75	4.01e-14	GNG10	G protein subunit gamma 10
-1.01	1.04e-24	PSMB8	proteasome 20S subunit beta 8	0.74	6.03e-09	CKB	creatine kinase B
-1	4.22e-16	ARHGDIB	Rho GDP dissociation inhibitor beta	0.72	1.02e-14	GTPBP3	GTP binding protein 3, mitochondria
-0.99	2.07e-24	PPP6R1	protein phosphatase 6 regulatory subunit	0.72	8.48e-12	TMEM205	transmembrane protein 205
-0.99	1.43e-24	FAH	fumarylacetoacetate hydrolase	0.71	2.56e-14	CHCHD6	coiled-coil-helix-coiled-coil-helix
-0.98	7.07e-30	BCL10	BCL10 immune signaling adaptor	0.71	4.66e-13	PRXL2A	peroxiredoxin like 2A
-0.97	9.43e-24	RPE	ribulose-5-phosphate-3-epimerase	0.69	3.91e-07	NDUFB11	NADH:ubiquinone oxidoreductase subunit
-0.97	1.13e-17	NACA2	nascent polypeptide associated complex	0.69	4.74e-17	TDRKH	tudor and KH domain containing
-0.97	2.09e-28	DCTD	dCMP deaminase	0.69	1.43e-09	SPINT2	serine peptidase inhibitor, Kunitz
-0.96	5.22e-28	NFKB1	nuclear factor kappa B subunit 1	0.69	2.94e-15	APP	amyloid beta precursor protein
-0.95	1.49e-26	NECAP2	NECAP endocytosis associated 2	0.69	7.98e-16	MFN1	mitofusin 1
-0.95	4.67e-24	TAOK3	TAO kinase 3	0.67	3.65e-12	SMARCA1	SWI/SNF related, matrix associated, chromatin-remodeling complex
-0.94	4.55e-27	PCYT2	phosphate cytidylyltransferase 2, e	0.67	2.86e-10	NDUFB2	NADH:ubiquinone oxidoreductase subunit
-0.93	4.34e-23	WIPF1	WAS/WASL interacting protein family	0.66	1.63e-11	ESRP1	epithelial splicing regulatory protein
-0.93	4.81e-32	STAT6	signal transducer and activator of transcription 6	0.66	2.75e-15	BRD1	bromodomain containing 1
-0.92	7.05e-28	OSTF1	osteoclast stimulating factor 1	0.65	4.73e-11	CTNNB1	catenin beta 1

GAGE analysis on upregulated and downregulated proteins at low/absent ACTR2 protein, DB1



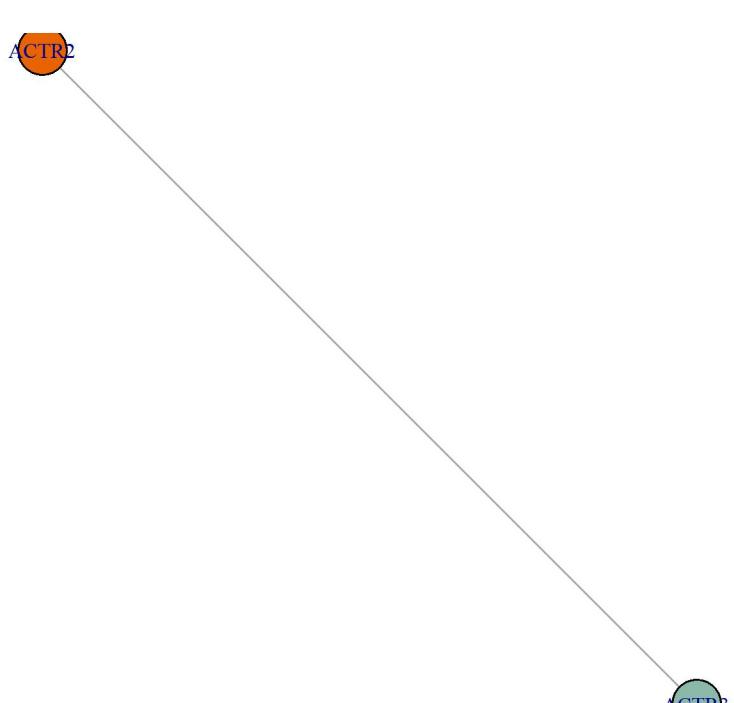


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.58	2.07e-07	PLEK	pleckstrin	0.89	3.33e-03	IGSF8	immunoglobulin superfamily member 8
-1.19	1.68e-05	NCF4	neutrophil cytosolic factor 4	0.79	2.08e-02	ATP1A3	ATPase Na+/K+ transporting subunit
-1.13	1.81e-04	SH3BP1	SH3 domain binding protein 1	0.76	7.10e-02	FKBP11	FKBP prolyl isomerase 11
-1.11	6.79e-04	MYO1G	myosin IG	0.75	4.80e-02	IRF2BPL	interferon regulatory factor 2 bind
-1.07	3.73e-03	LAT2	linker for activation of T cells fa	0.71	2.39e-02	TLE5	TLE family member 5, transcriptiona
-1.07	8.47e-05	DOCK8	dedicator of cytokinesis 8	0.71	2.41e-02	BRD2	bromodomain containing 2
-1	2.20e-04	RASSF2	Ras association domain family membe	0.7	9.01e-02	MYH10	myosin heavy chain 10
-1	5.11e-05	PXK	PX domain containing serine/threoni	0.68	5.16e-02	TSPAN3	tetraspanin 3
-0.98	4.69e-04	MYO1F	myosin IF	0.67	4.32e-02	MFGE8	milk fat globule EGF and factor V/V
-0.98	2.02e-01	S100A4	S100 calcium binding protein A4	0.66	3.59e-02	SNTB2	syntrophin beta 2
-0.97	4.23e-03	CSTA	cystatin A	0.66	4.30e-02	RAD18	RAD18 E3 ubiquitin protein ligase
-0.96	1.83e-02	ZYX	zyxin	0.65	4.54e-02	TCF12	transcription factor 12
-0.96	2.48e-04	WDFY4	WDFY family member 4	0.64	2.41e-02	SRPK2	SRSF protein kinase 2
-0.94	4.76e-05	MNDA	myeloid cell nuclear differentiatio	0.64	5.12e-02	LENG1	leukocyte receptor cluster member 1
-0.92	2.06e-03	PRKCD	protein kinase C delta	0.64	6.68e-02	MAZ	MYC associated zinc finger protein
-0.91	6.28e-03	GPD2	glycerol-3-phosphate dehydrogenase	0.64	7.54e-02	PFKM	phosphofructokinase, muscle
-0.91	3.53e-02	ITGB2	integrin subunit beta 2	0.64	3.47e-02	RNF169	ring finger protein 169
-0.9	7.79e-03	PLCG2	phospholipase C gamma 2	0.63	4.90e-02	PSMG4	proteasome assembly chaperone 4
-0.9	2.63e-04	TAOK3	TAO kinase 3	0.63	4.32e-02	BRD7	bromodomain containing 7
-0.9	1.26e-03	ANKRD44	ankyrin repeat domain 44	0.63	2.18e-01	TSTD1	thiosulfate sulfurtransferase like
-0.89	2.00e-02	RALB	RAS like proto-oncogene B	0.63	3.02e-01	MZB1	marginal zone B and B1 cell specifi
-0.89	3.22e-03	ARSB	arylsulfatase B	0.62	9.35e-02	MPZL1	myelin protein zero like 1
-0.88	5.39e-03	LYZ	lysozyme	0.61	3.57e-02	SIRT1	sirtuin 1
-0.87	5.12e-02	VAMP8	vesicle associated membrane protein	0.61	1.17e-01	ACP2	acid phosphatase 2, lysosomal
-0.87	1.72e-02	DOK3	docking protein 3	0.61	2.23e-01	CASP6	caspase 6
-0.87	1.16e-01	COTL1	coactosin like F-actin binding prot	0.61	2.02e-01	GTSF1	gamete specific factor 1
-0.87	1.17e-02	SYK	spleen associated tyrosine kinase	0.61	1.49e-01	SMC1B	structural maintenance of chromosom
-0.86	6.28e-04	PRTN3	proteinase 3	0.6	7.04e-02	HIP1R	huntingtin interacting protein 1 re
-0.85	1.75e-02	PTK2B	protein tyrosine kinase 2 beta	0.6	1.89e-01	LGALS3BP	galectin 3 binding protein

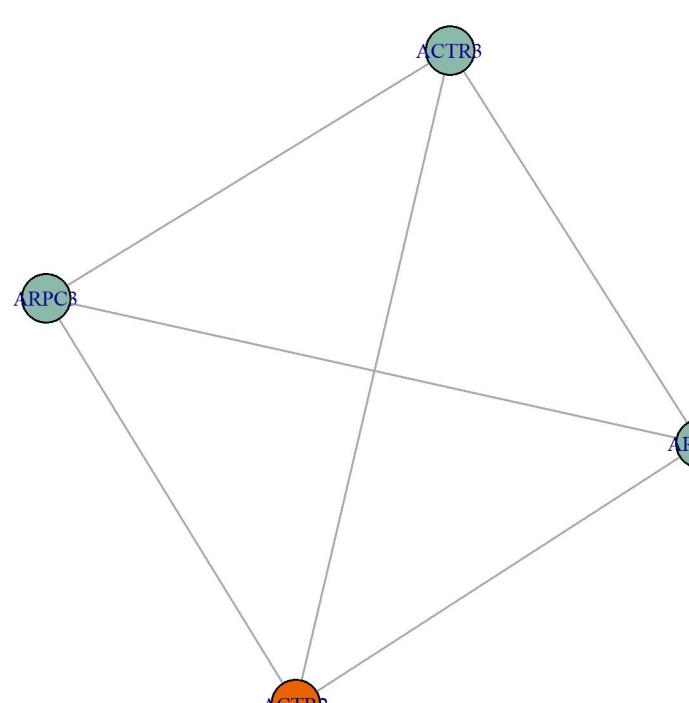


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.14	1.44e-10	ARPC5	actin related protein 2/3 complex s	0.88	1.46e-10	CKMT1A	creatine kinase, mitochondrial 1A
-1.13	1.41e-23	GBE1	1,4-alpha-glucan branching enzyme 1	0.85	8.85e-17	GTPBP3	GTP binding protein 3, mitochondria
-1.13	8.11e-38	PXN	paxillin	0.82	3.67e-16	EPB41	erythrocyte membrane protein band 4
-1.07	6.42e-27	PMM2	phosphomannomutase 2	0.76	8.92e-17	BRD1	bromodomain containing 1
-1.03	8.61e-22	TUBA1C	tubulin alpha 1c	0.74	5.01e-10	VTN	vitronectin
-1.02	1.55e-25	SEPTIN10	septin 10	0.73	2.40e-11	RPS19BP1	ribosomal protein S19 binding prote
-1.01	4.88e-26	DCTD	dCMP deaminase	0.71	5.37e-12	GRPEL2	GrpE like 2, mitochondrial
-1	1.40e-20	FAM114A1	family with sequence similarity 114	0.7	6.90e-08	GNG5	G protein subunit gamma 5
-0.99	2.09e-27	MEMO1	mediator of cell motility 1	0.7	1.09e-13	COQ6	coenzyme Q6, monooxygenase
-0.99	1.20e-25	PARP4	poly(ADP-ribose) polymerase family	0.69	4.47e-14	NCBP2AS2	NCBP2 antisense 2 (head to head)
-0.99	5.18e-22	PARVA	parvin alpha	0.66	9.25e-12	MEAF6	MYST/Esa1 associated factor 6
-0.98	1.27e-22	GALE	UDP-galactose-4-epimerase	0.66	2.62e-08	H2AX	H2A.X variant histone
-0.97	6.99e-11	CBR3	carbonyl reductase 3	0.66	7.88e-07	MACROH2A2	macroH2A.2 histone
-0.97	1.58e-19	FAH	fumarylacetoacetate hydrolase	0.65	5.08e-12	YTHDC1	YTH domain containing 1
-0.97	1.21e-27	LIMS1	LIM zinc finger domain containing 1	0.65	4.37e-10	CENPV	centromere protein V
-0.97	1.46e-22	NECAP2	NECAP endocytosis associated 2	0.65	6.63e-13	ZNF384	zinc finger protein 384
-0.95	3.67e-19	IRF3	interferon regulatory factor 3	0.64	7.75e-10	SURF1	SURF1 cytochrome c oxidase assembly
-0.95	2.99e-16	FHL2	four and a half LIM domains 2	0.64	5.72e-10	MBD1	methyl-CpG binding domain protein 1
-0.94	1.56e-25	MAPK14	mitogen-activated protein kinase 14	0.64	3.48e-07	MRPL54	mitochondrial ribosomal protein L54
-0.94	1.60e-25	SWAP70	switching B cell complex subunit SW	0.63	2.27e-06	CDH1	cadherin 1
-0.93	5.40e-25	AAK1	AP2 associated kinase 1	0.63	4.26e-08	CXADR	CXADR Ig-like cell adhesion molecul
-0.93	4.22e-18	ACY1	aminoacylase 1	0.62	5.02e-10	TMEM209	transmembrane protein 209
-0.92	5.52e-22	PDLIM2	PDZ and LIM domain 2	0.62	8.54e-07	SPINT1	serine peptidase inhibitor, Kunitz
-0.92	3.99e-20	TNS3	tensin 3	0.62	3.39e-14	DNMT3A	DNA methyltransferase 3 alpha
-0.92	1.18e-14	UBE2Z	ubiquitin conjugating enzyme E2 Z	0.62	4.27e-10	ABT1	activator of basal transcription 1
-0.92	5.78e-22	SCYL1	SCY1 like pseudokinase 1	0.62	4.42e-08	GNG10	G protein subunit gamma 10
-0.91	6.58e-20	OPTN	optineurin	0.61	9.42e-10	COQ7	coenzyme Q7, hydroxylase
-0.91	7.82e-21	PCYT2	phosphate cytidylyltransferase 2, e	0.61	1.31e-09	COQ8A	coenzyme Q8A
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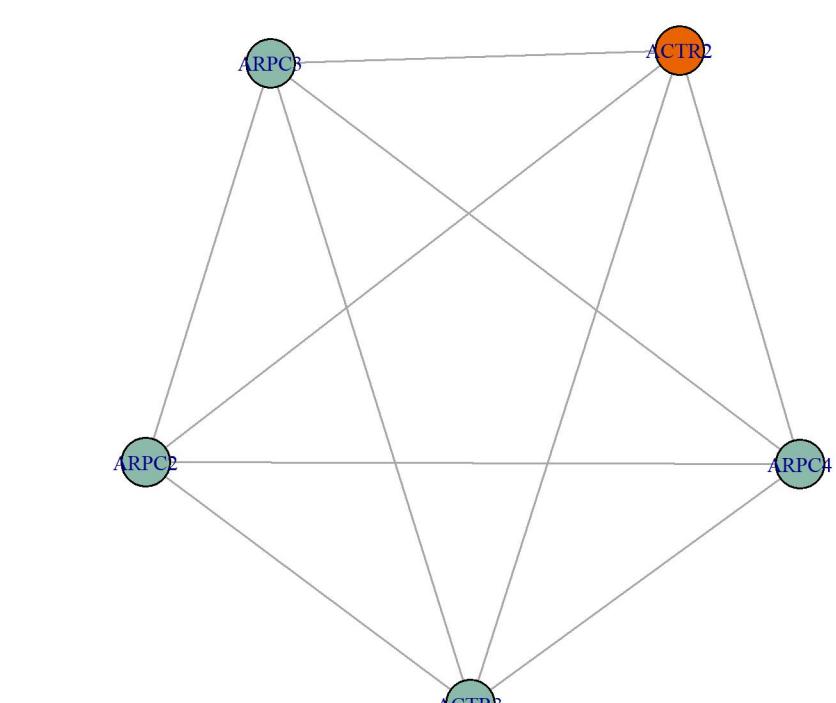
ACTR2 network, DB1, all Pearson r > 0.9

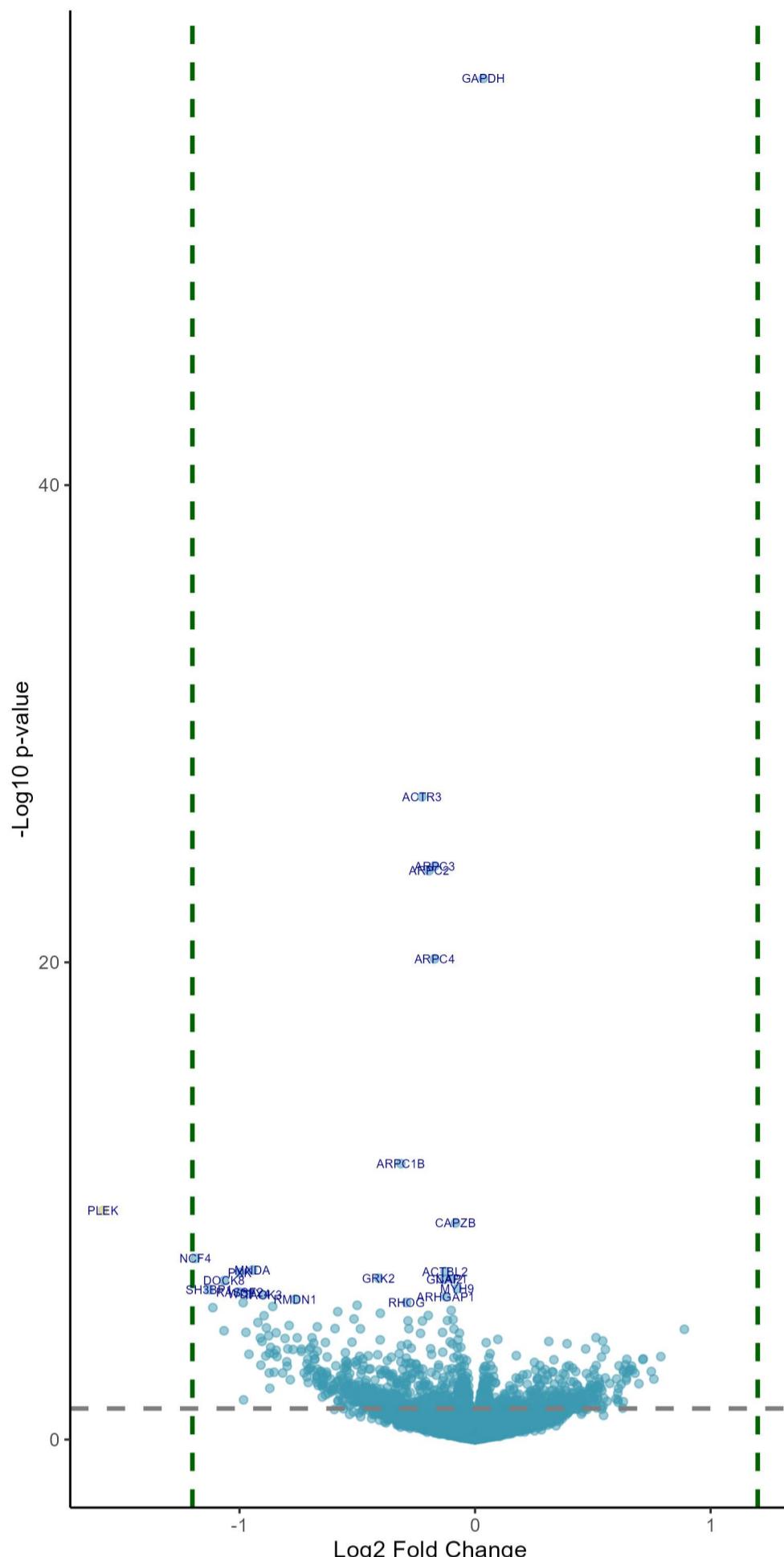


ACTR2 network, DB1, all Pearson r > 0.85



ACTR2 network, DB1, all Pearson r > 0.8

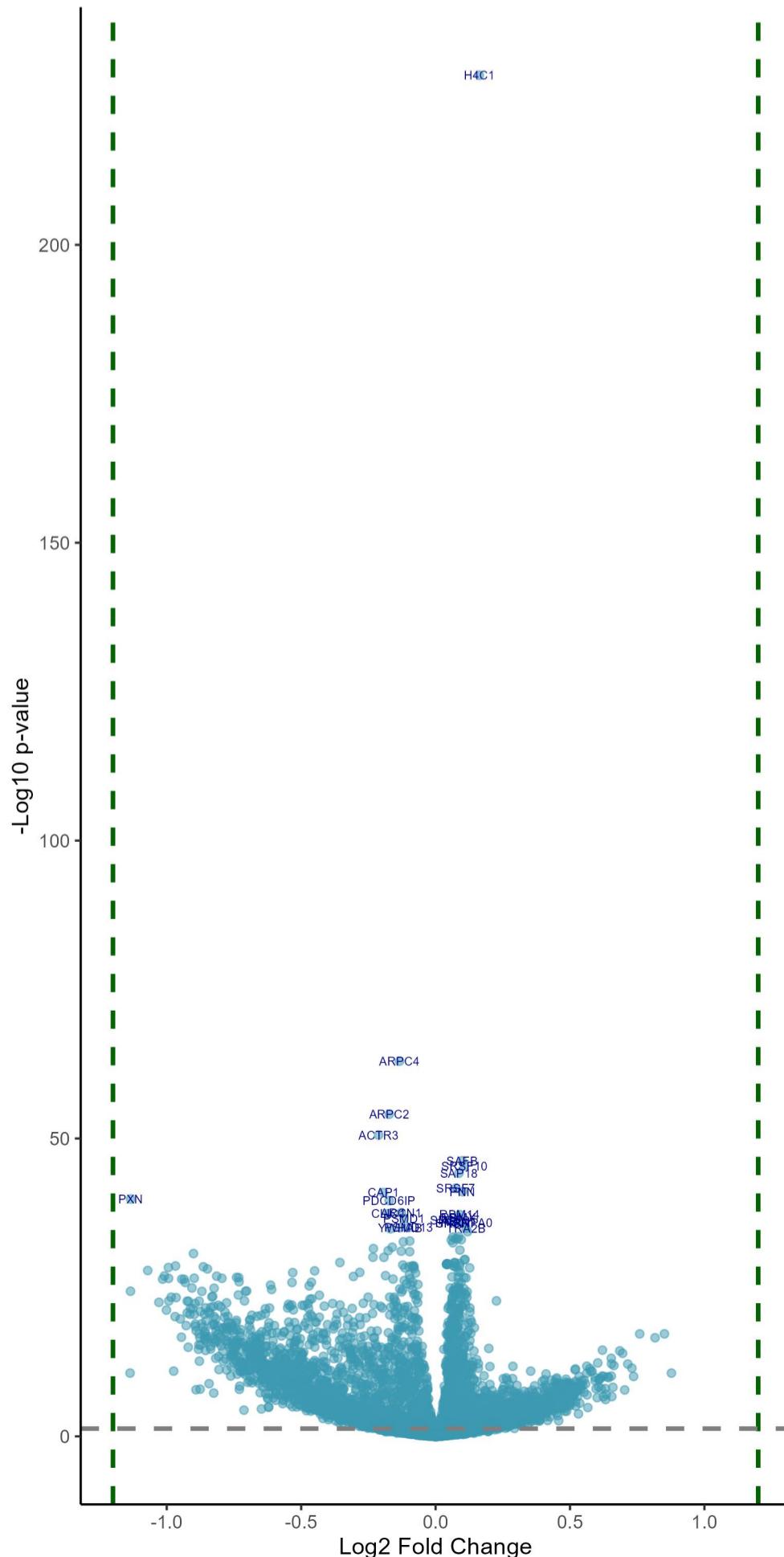




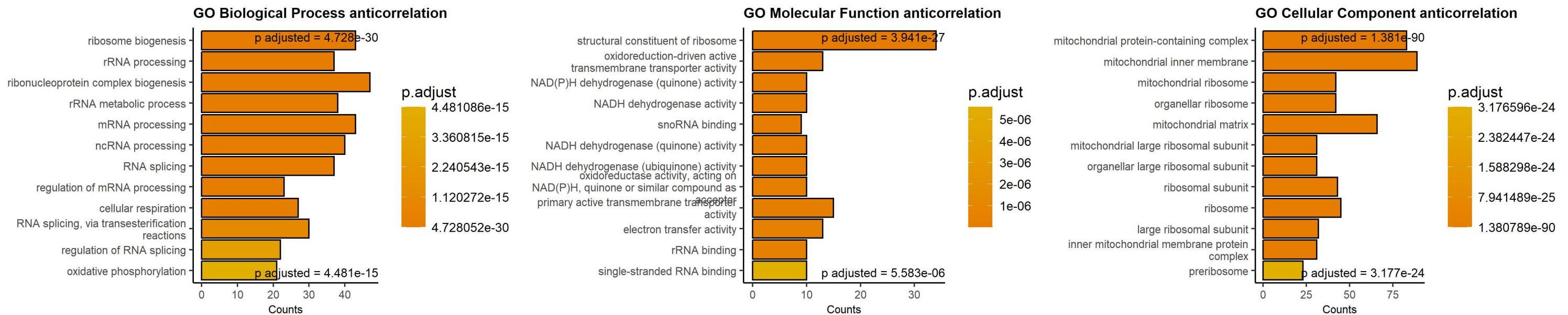
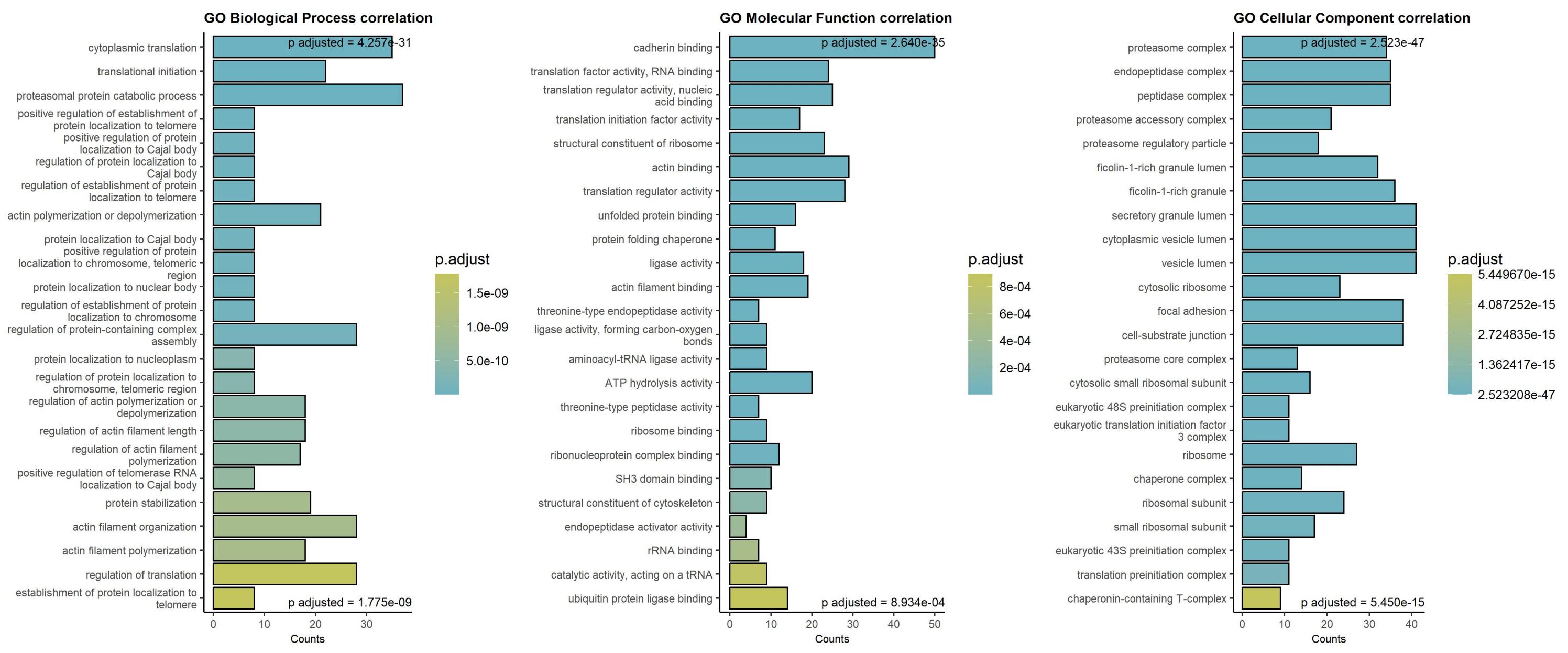
Sorted by p values!

Downregulated in blood cancers at low/absent ACTR2 Upregulated in blood cancers at low/absent ACTR2

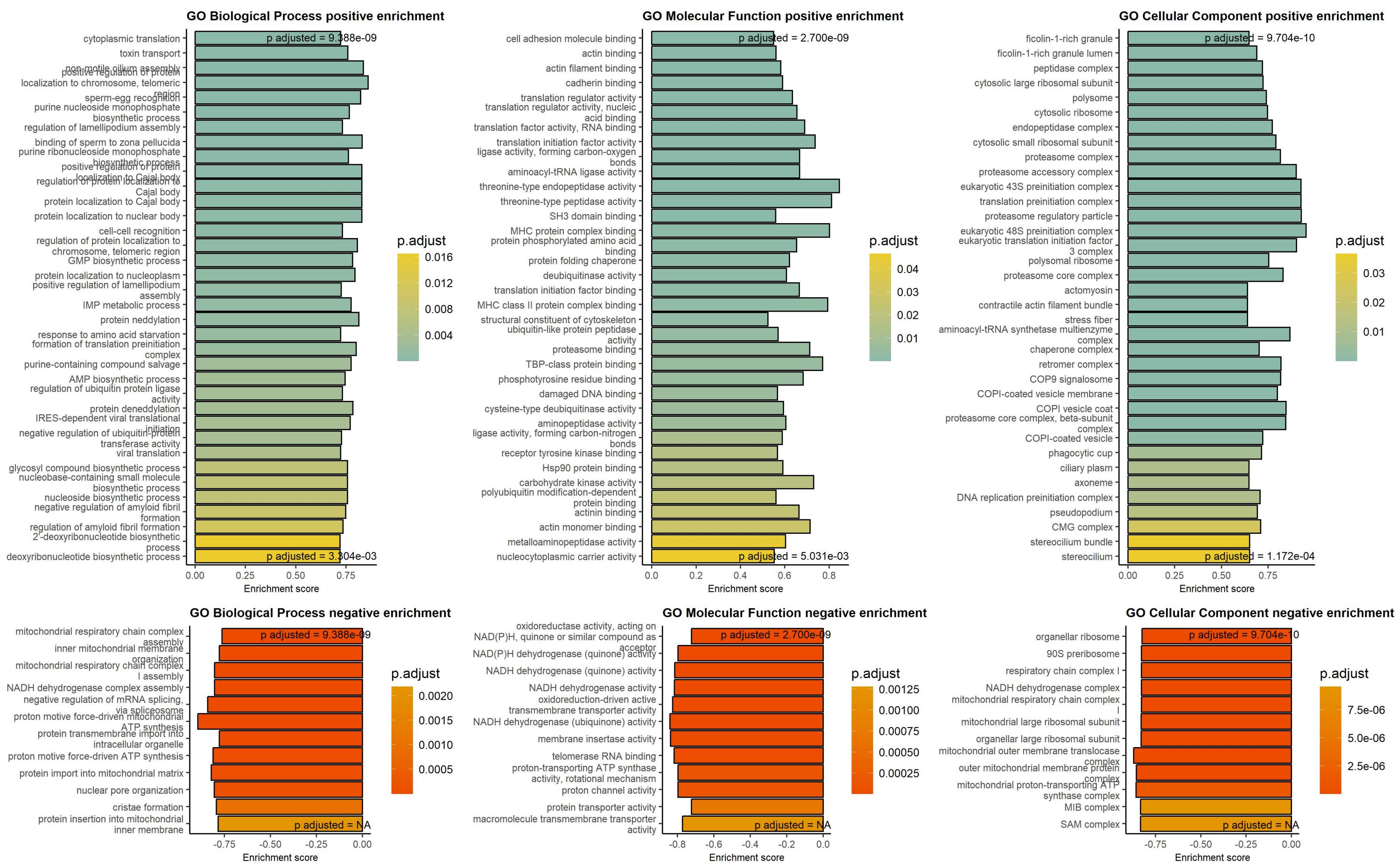
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.23	3.84e-24	ACTR3	actin related protein 3	0.03	5.99e-54	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
-0.17	2.05e-21	ARPC3	actin related protein 2/3 complex subunit 3	0.89	3.33e-03	IGSF8	immunoglobulin superfamily member 8
-0.2	2.39e-21	ARPC2	actin related protein 2/3 complex subunit 2	0.51	6.25e-03	PSMC3IP	PSMC3 interacting protein
-0.17	9.50e-18	ARPC4	actin related protein 2/3 complex subunit 4	0.1	6.91e-03	PGRMC2	progesterone receptor membrane component
-0.32	2.61e-09	ARPC1B	actin related protein 2/3 complex subunit 1B	0.54	7.68e-03	SUPT4H1	SPT4 homolog, DSIF elongation factor
-1.58	2.07e-07	PLEK	pleckstrin homology domain containing protein	0.31	7.79e-03	GIMAP6	GTPase, IMAP family member 6
-0.08	6.23e-07	CAPZB	capping actin protein of muscle Z-line	0.05	8.24e-03	HNRPDL	heterogeneous nuclear ribonucleoprotein D
-1.19	1.68e-05	NCF4	neutrophil cytosolic factor 4	0.39	8.90e-03	UCKL1	uridine-cytidine kinase 1 like 1
-0.94	4.76e-05	MNDA	myeloid cell nuclear differentiation antigen	0.47	1.27e-02	PAIP2	poly(A) binding protein interacting protein 2
-0.13	5.04e-05	ACTBL2	actin beta like 2	0.55	1.29e-02	SPATA5L1	spematogenesis associated 5 like 1
-1	5.11e-05	PXK	PX domain containing serine/threonine kinase	0.06	1.75e-02	SUPT5H	SPT5 homolog, DSIF elongation factor
-0.41	7.89e-05	GRK2	G protein-coupled receptor kinase 2	0.18	2.00e-02	CALU	calumenin
-0.1	7.89e-05	CAP1	cyclase associated actin cytoskeleton-associated protein	0.79	2.08e-02	ATP1A3	ATPase Na+/K+ transporting subunit alpha 3
-0.13	7.89e-05	GNAI2	G protein subunit alpha i2	0.54	2.11e-02	SPATA5	spematogenesis associated 5
-1.07	8.47e-05	DOCK8	dedicator of cytokinesis 8	0.06	2.21e-02	SSBP1	single stranded DNA binding protein
-0.08	1.75e-04	MYH9	myosin heavy chain 9	0.71	2.39e-02	TLE5	TLE family member 5, transcriptional regulator
-1.13	1.81e-04	SH3BP1	SH3 domain binding protein 1	0.64	2.41e-02	SRPK2	SRSF protein kinase 2
-1	2.20e-04	RASSF2	Ras association domain family member	0.71	2.41e-02	BRD2	bromodomain containing 2
-0.96	2.48e-04	WDFY4	WDFY family member 4	0.33	2.45e-02	ZNF512B	zinc finger protein 512B
-0.9	2.63e-04	TAOK3	TAO kinase 3	0.25	2.95e-02	PTPRK	protein tyrosine phosphatase receptor type K
-0.12	2.97e-04	ARHGAP1	Rho GTPase activating protein 1	0.64	3.47e-02	RNF169	ring finger protein 169
-0.76	3.65e-04	RMDN1	regulator of microtubule dynamics 1	0.28	3.56e-02	LZTS1	leucine zipper tumor suppressor 1
-0.29	4.69e-04	RHOG	ras homolog family member G	0.51	3.56e-02	SLC38A2	solute carrier family 38 member 2
-0.98	4.69e-04	MYO1F	myosin IF	0.4	3.56e-02	KCMF1	potassium channel modulatory factor
-0.5	5.82e-04	RNASE2	ribonuclease A family member 2	0.07	3.56e-02	SMARCE1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily E, member 1
-0.86	6.28e-04	PRTN3	proteinase 3	0.61	3.57e-02	SIRT1	sirtuin 1
-1.11	6.79e-04	MYO1G	myosin IG	0.66	3.59e-02	SNTB2	syntrophin beta 2
-0.1	8.56e-04	GRB2	growth factor receptor bound protein 2	0.05	3.67e-02	PFDN6	prefoldin subunit 6
-0.58	9.37e-04	BST1	bone marrow stromal cell antigen 1	0.04	3.69e-02	SAFB	scaffold attachment factor B
-0.4	1.06e-03	ARPC5	actin related protein 2/3 complex subunit 5	0.39	3.78e-02	TOP3A	DNA topoisomerase III alpha
-0.2	1.26e-03	VASP	vasodilator stimulated phosphoprotein	0.41	4.08e-02	GUK1	guanylate kinase 1
-0.9	1.26e-03	ANKRD44	ankyrin repeat domain 44	0.66	4.30e-02	RAD18	RAD18 E3 ubiquitin protein ligase
-0.51	1.68e-03	CEBPA	CCAAT enhancer binding protein alpha	0.08	4.32e-02	NSFL1C	NSFL1 cofactor
-0.09	1.73e-03	HADHA	hydroxyacyl-CoA dehydrogenase trifluoroacetyl transferase	0.3	4.32e-02	CENPS	centromere protein S
-0.12	1.83e-03	PNP	purine nucleoside phosphorylase	0.04	4.32e-02	DDX46	DEAD-box helicase 46
-0.28	1.83e-03	RAC2	Rac family small GTPase 2	0.5	4.32e-02	FMR1	FMRP translational regulator 1
-0.22	1.83e-03	OSTF1	osteoclast stimulating factor 1	0.26	4.32e-02	ERCC6	ERCC excision repair 6, chromatin reorganization factor
-0.92	2.06e-03	PRKCD	protein kinase C delta	0.67	4.32e-02	MFGE8	milk fat globule EGF and factor V/V
0.79	2.60e-03	ARMND	armadillo repeat containing 9	0.63	4.32e-02	RBD7	hemedomain containing 7



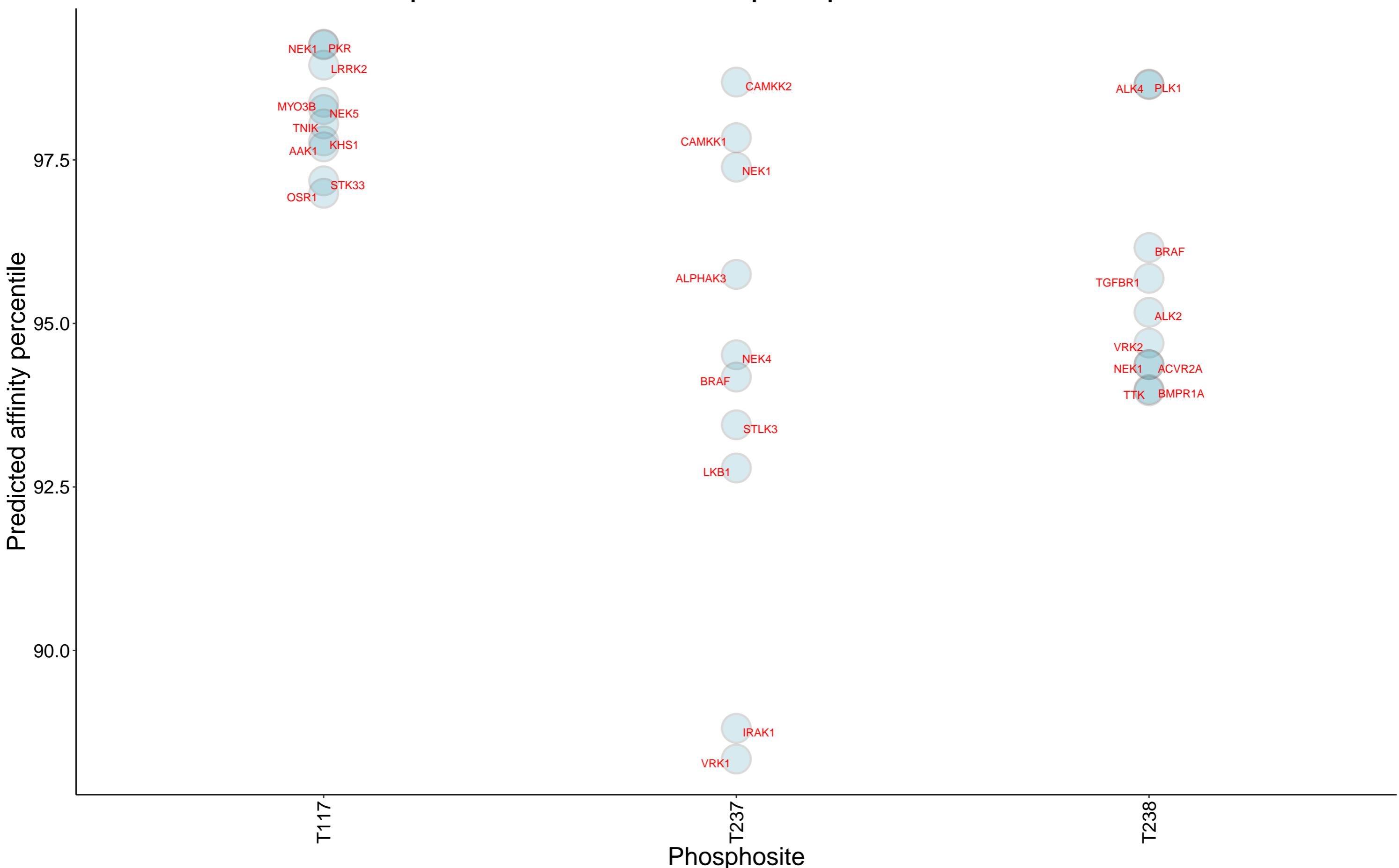
Top 250 correlation coefficients overrepresentation, ACTR2 protein, DB1



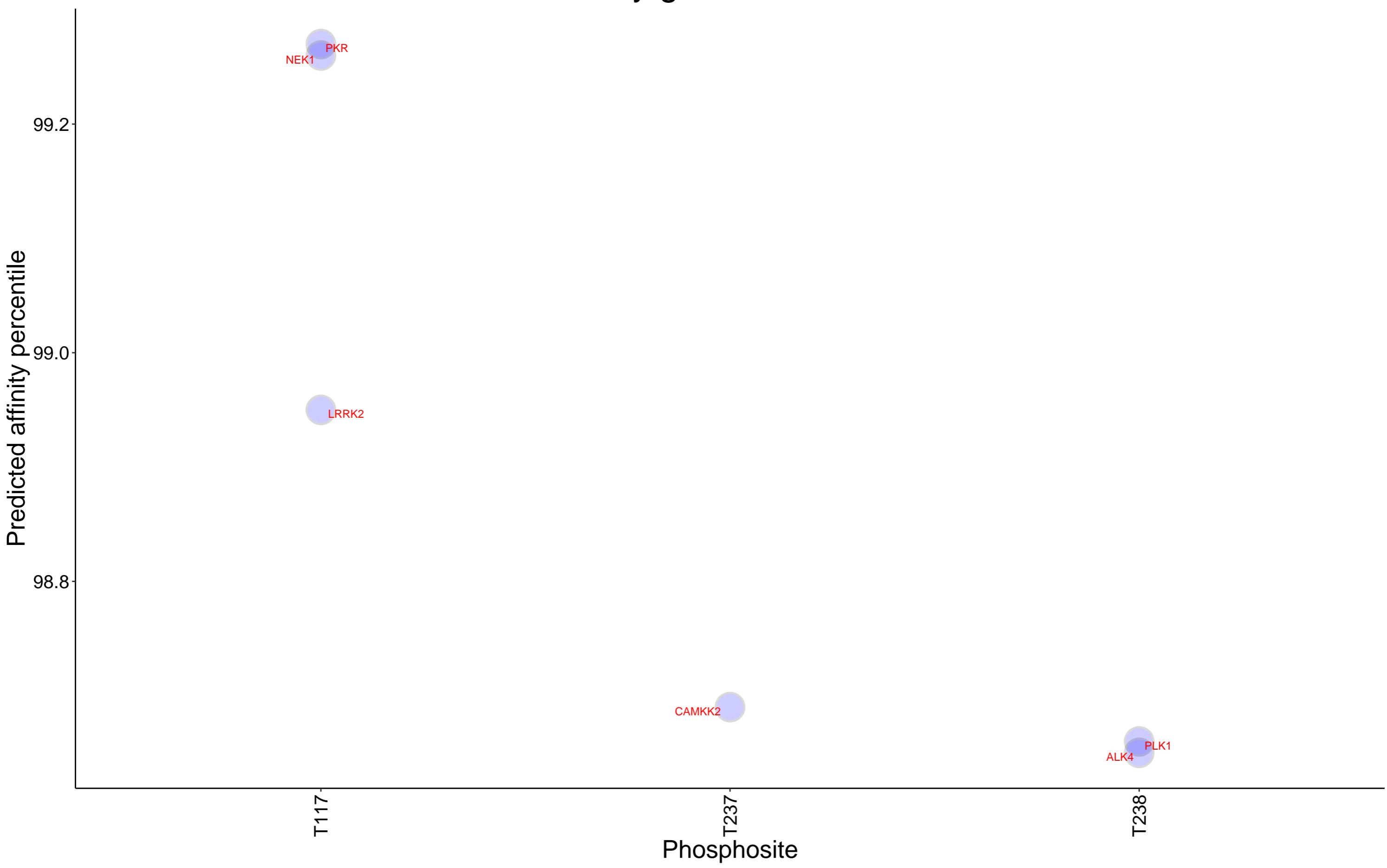
Gene Set Enrichment analysis on protein correlation coefficients, ACTR2 protein, DB1



Top 10 kinases for each phosphosite in ACTR2



Kinases with affinity greater than 98.5% to ACTR2



Top 15 positive correlation coefficients for ACTR2 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

