

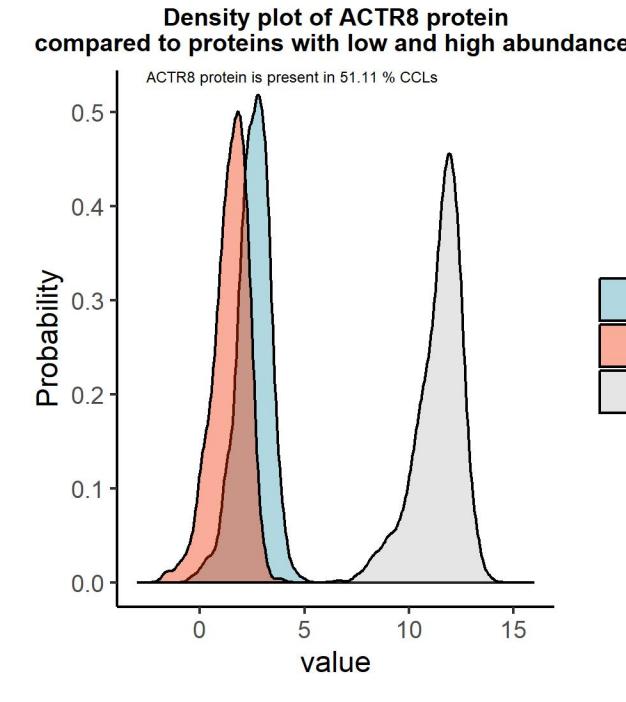
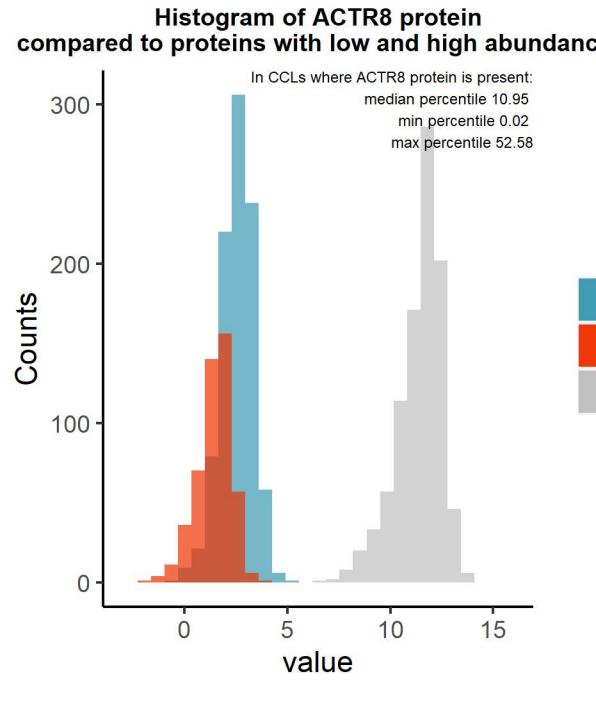
ACTR8

Protein name: ARP8 ; UNIPROT: Q9H981 ; Gene name: actin related protein 8

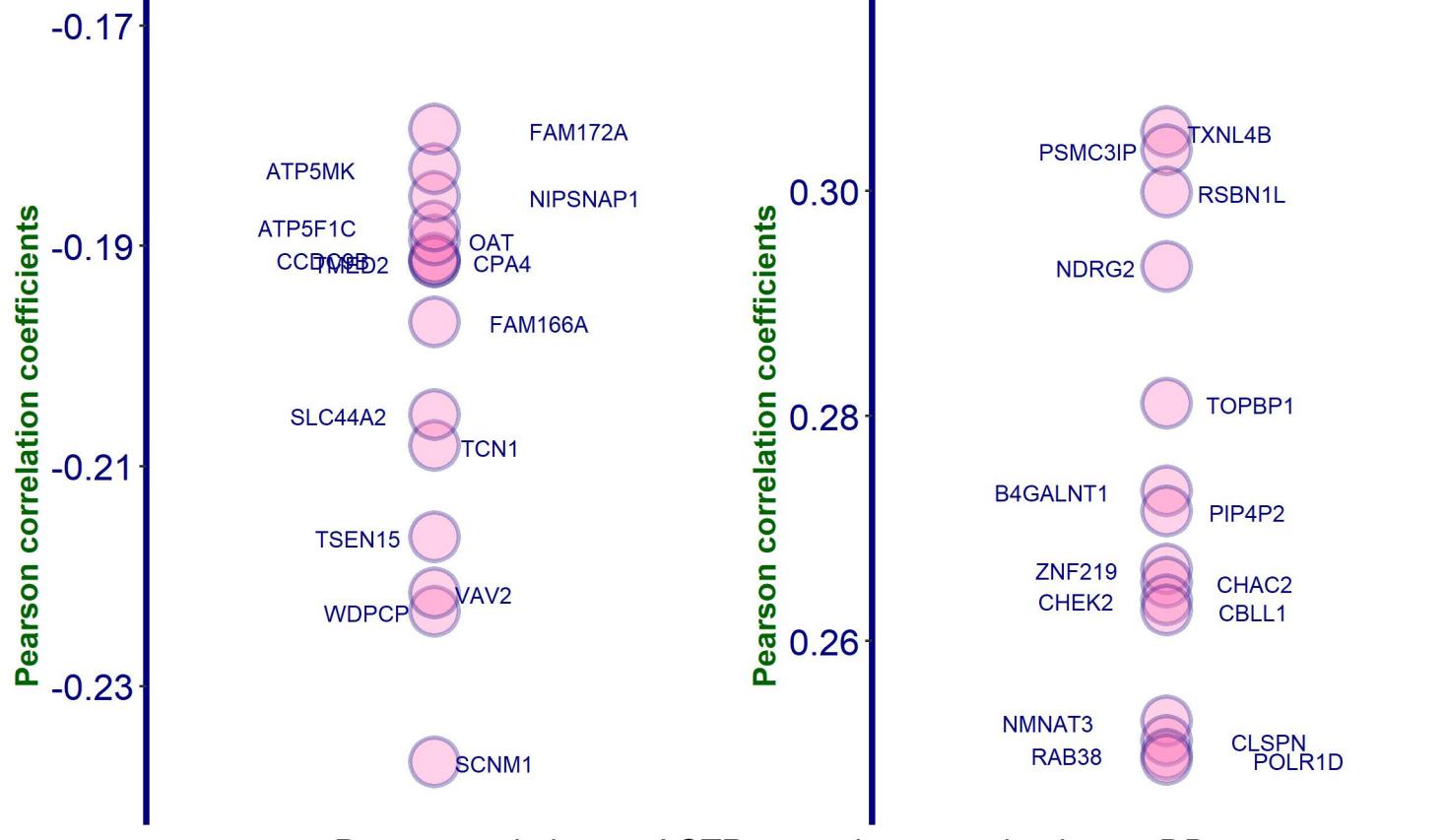
Ligandable: NA ; Ligandable_by_Chem: NA ; Is_enzyme: NA (<https://cansar.ai/>)

Sanger Institute Protein Database 2 (DB2), protein presence is less certain

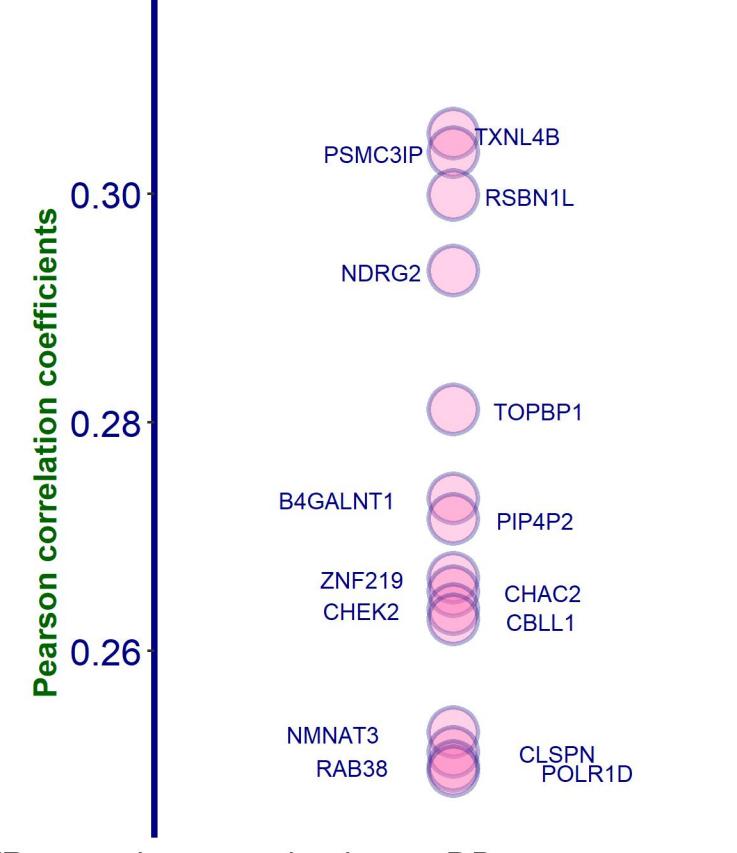
8498 proteins in same 949 CCLs



Negative correlations of ACTR8 protein, DB2

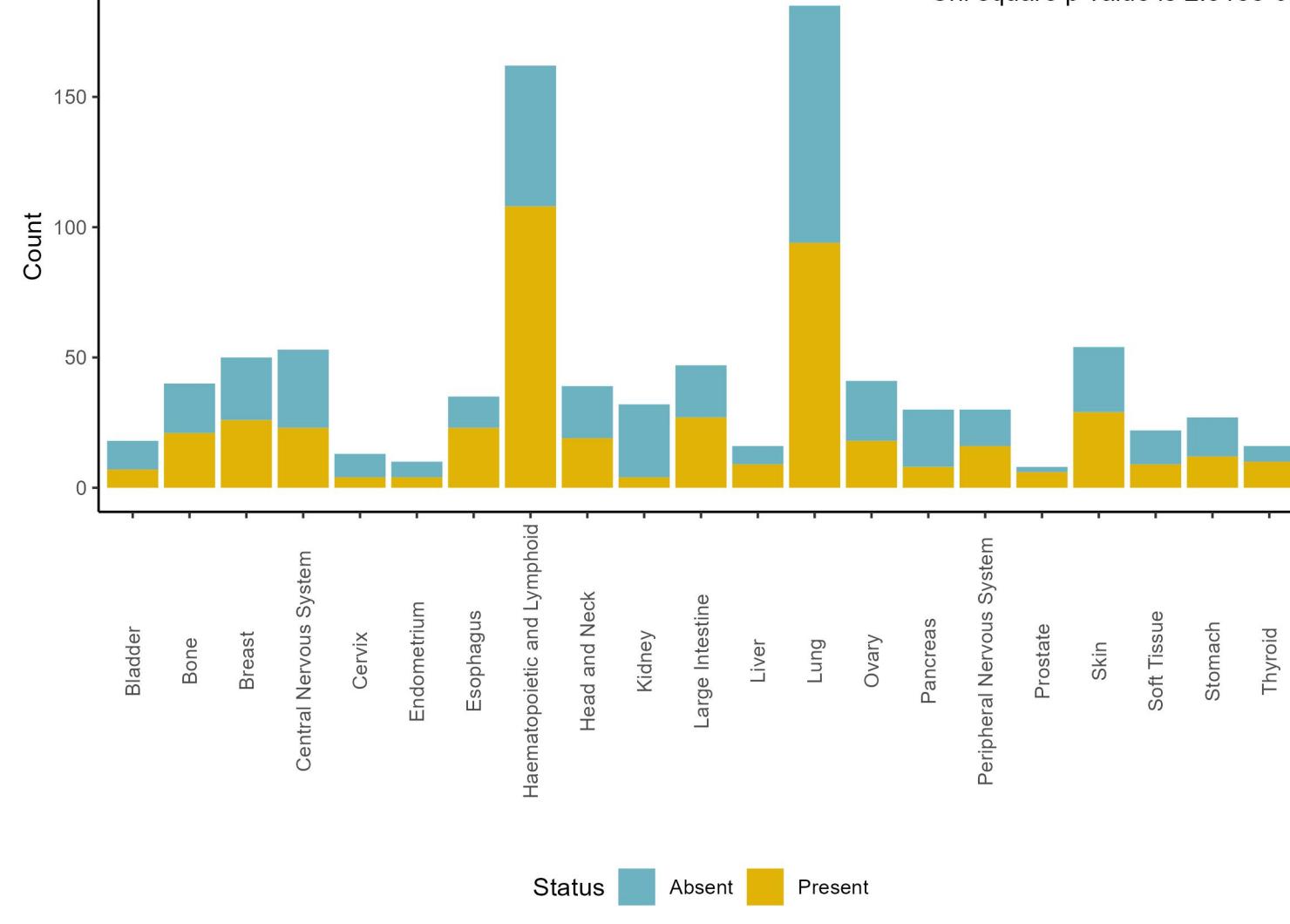
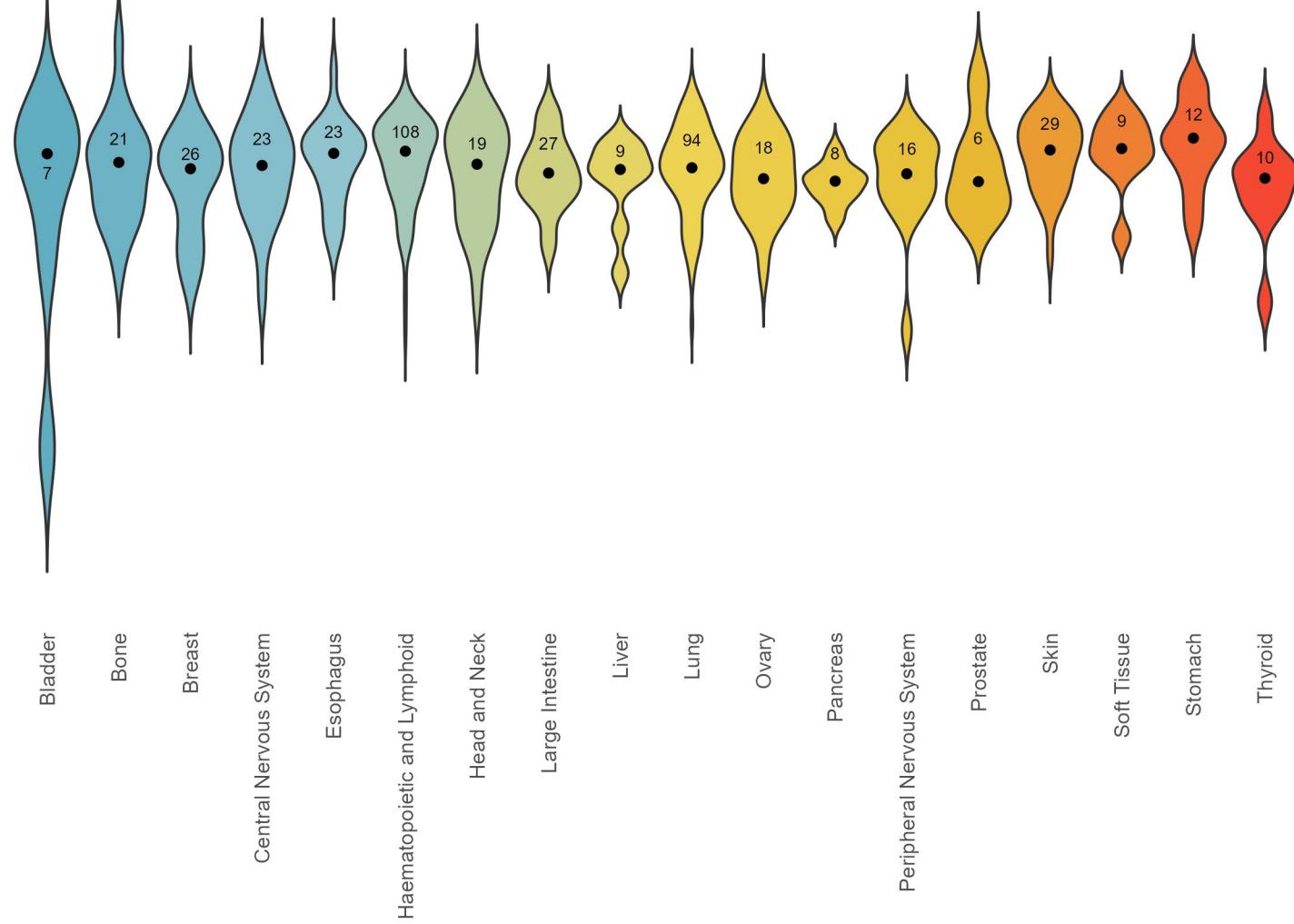


Positive correlations of ACTR8 protein, DB2



Amount of ACTR8 protein, number of CCLs where it is present by tissue, DB2

ANOVA p value is 2.369e-01

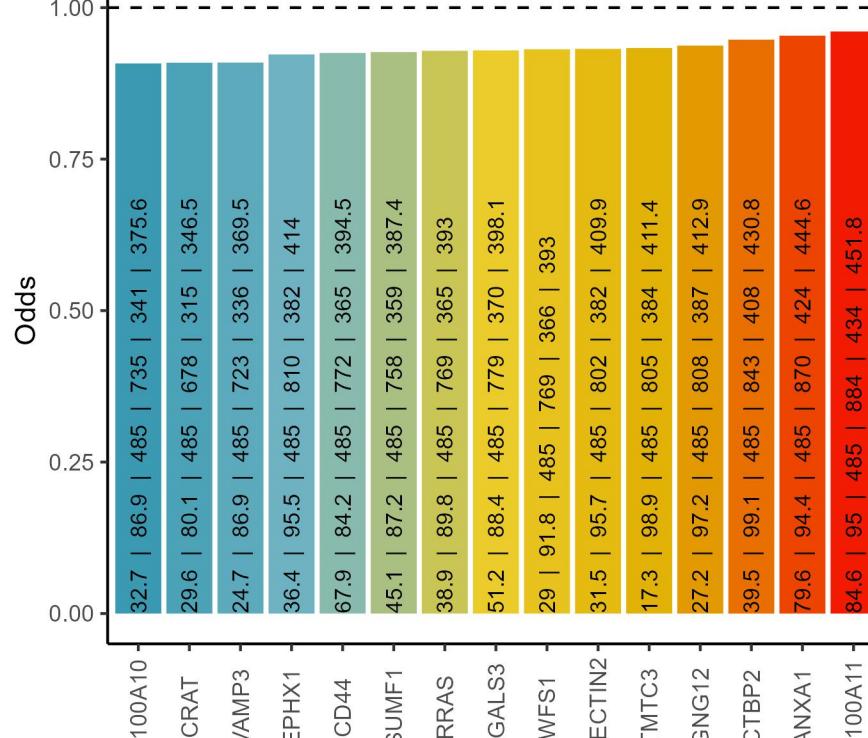


Cooccurrence with ACTR8 protein, DB2

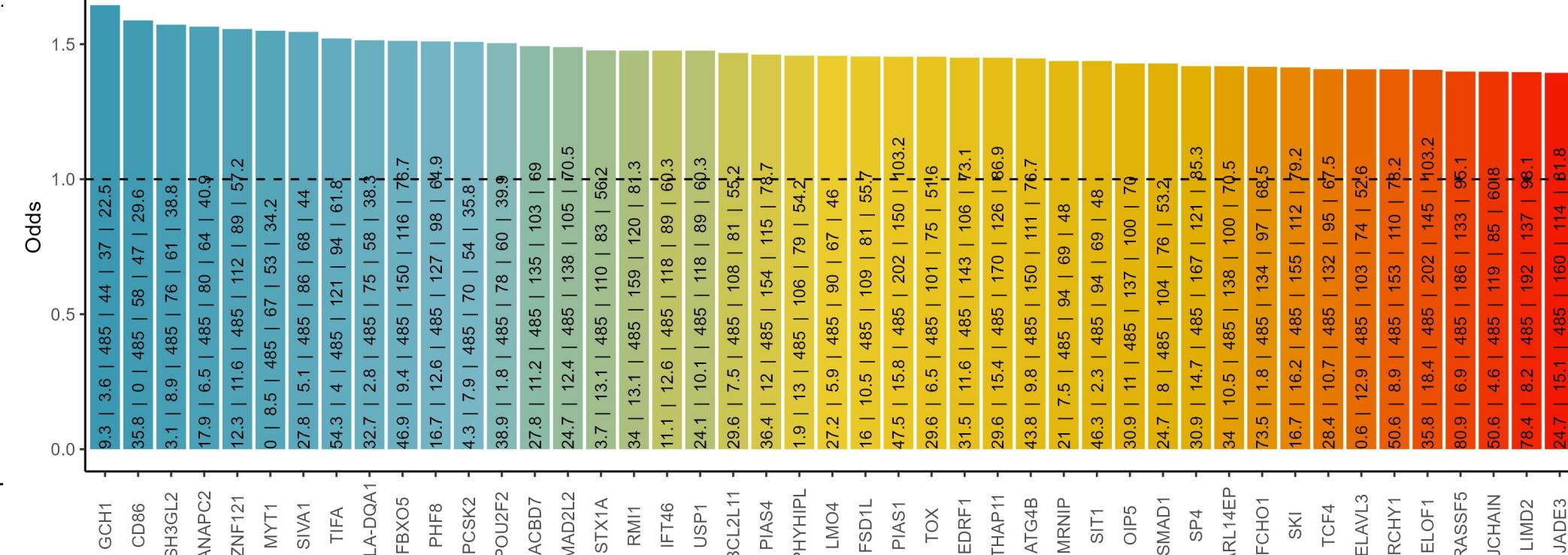
% of ACTR8 in blood cancers: 66.7 ; % of ACTR8 in solid cancers: 47.8

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ACTR8 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

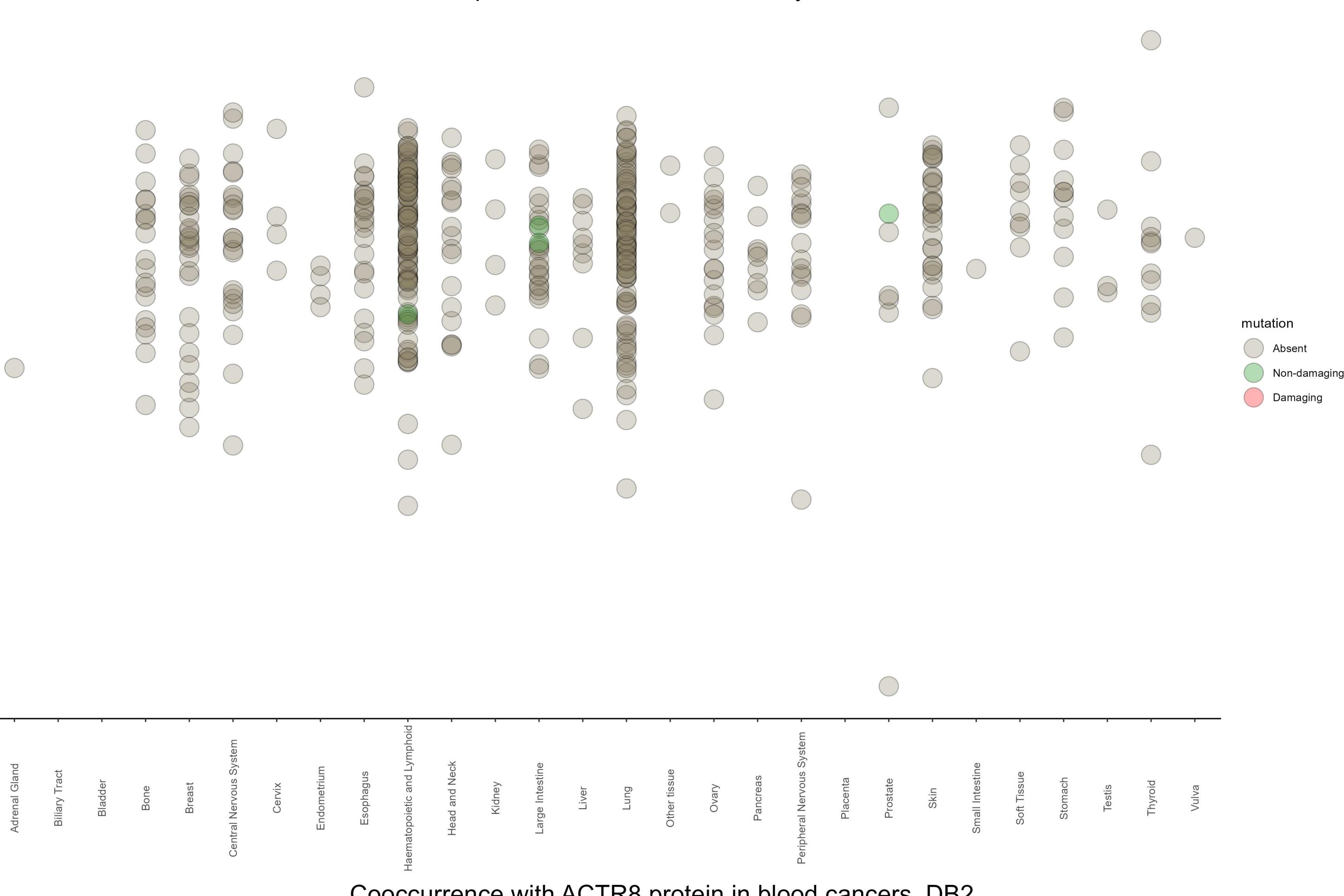
Negative cooccurrence



Positive cooccurrence

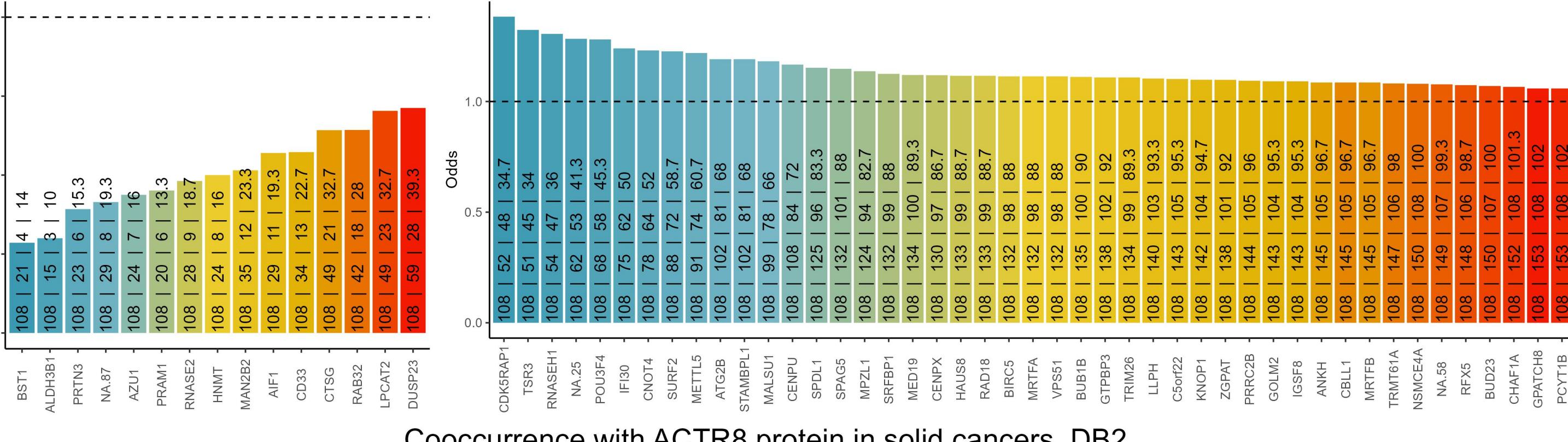


Amount of ACTR8 protein and mutation status by tissue, DB2



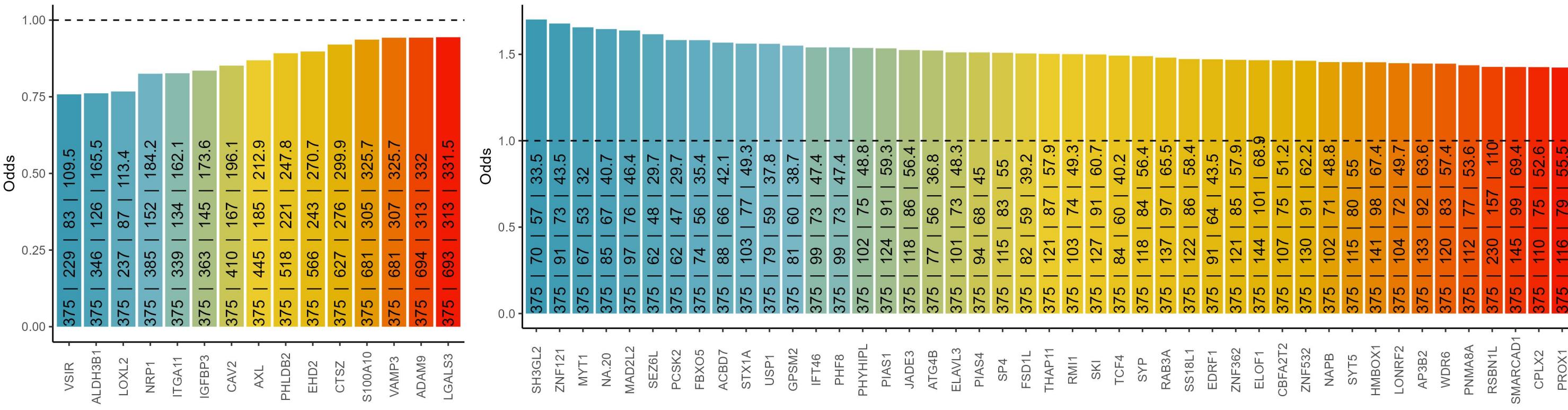
Cooccurrence with ACTR8 protein in blood cancers, DB2

The text in the bars: incidence of ACTR8 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

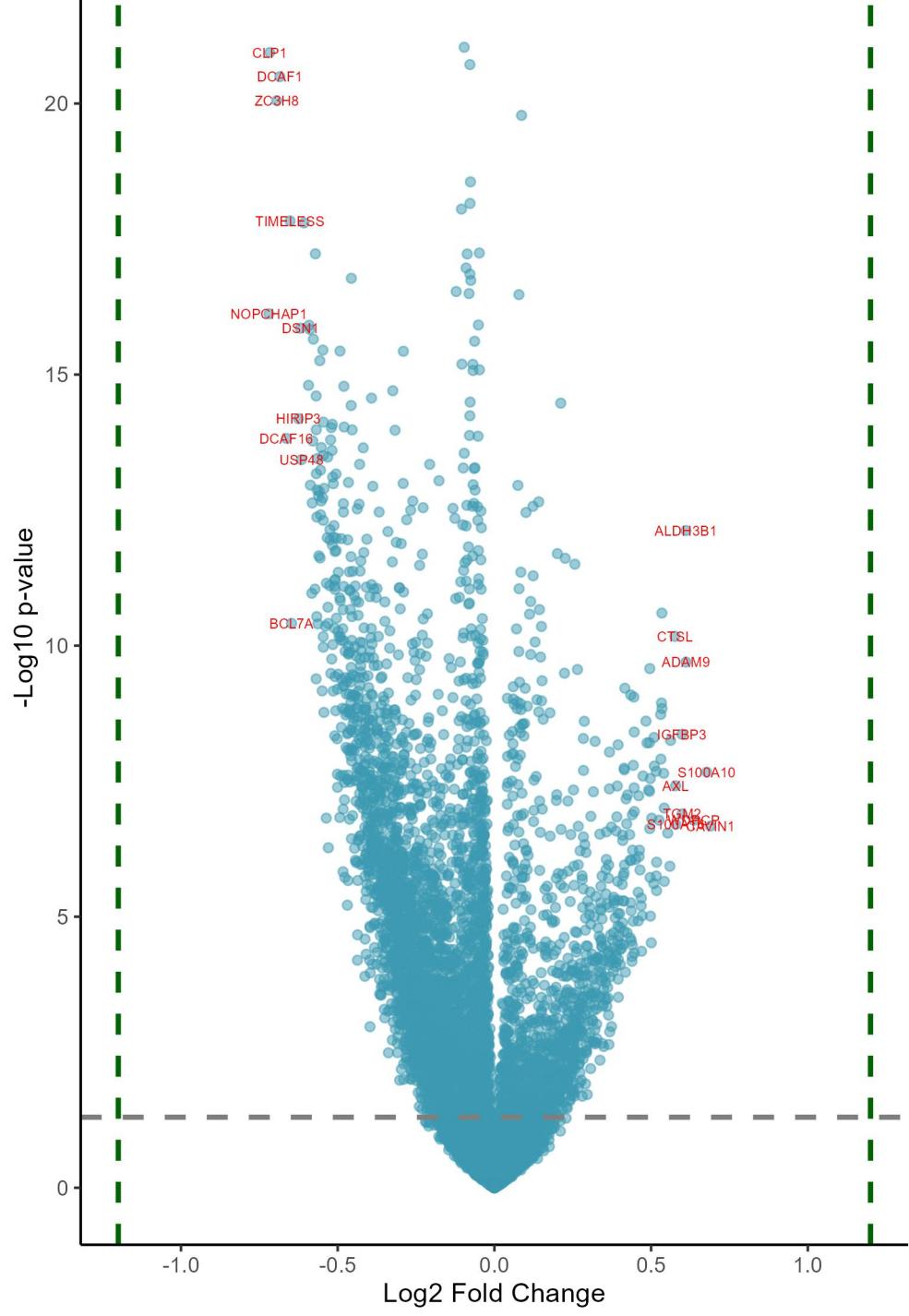


Cooccurrence with ACTR8 protein in solid cancers, DB2

The text in the bars: incidence of ACTR8 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



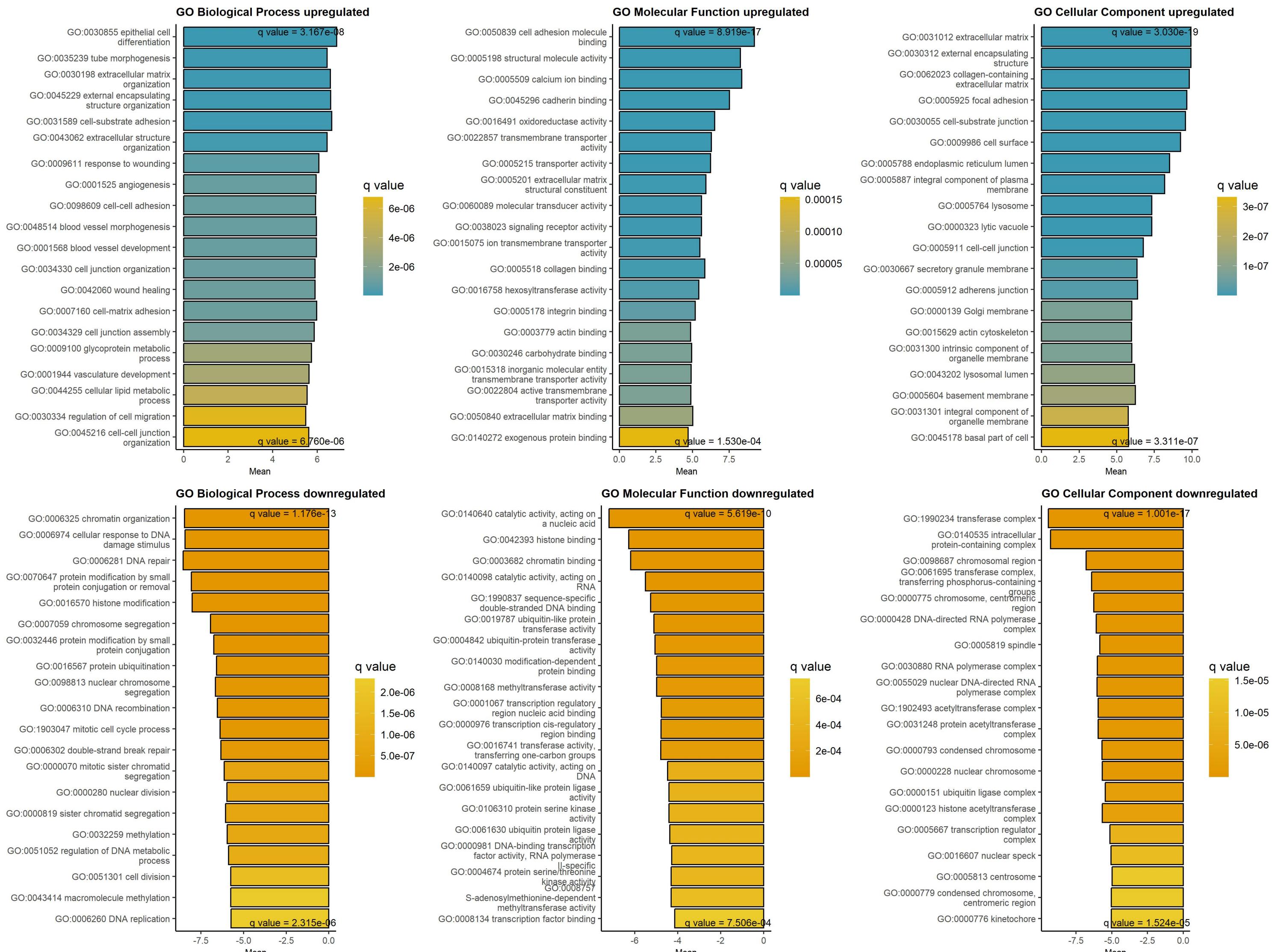
Differentially expressed proteins at absence/low amount of ACTR8 , DB2
p-value < 0.05 & logFC > 1.2



Downregulated at low/absent ACTR8 Upregulated at low/absent ACTR8

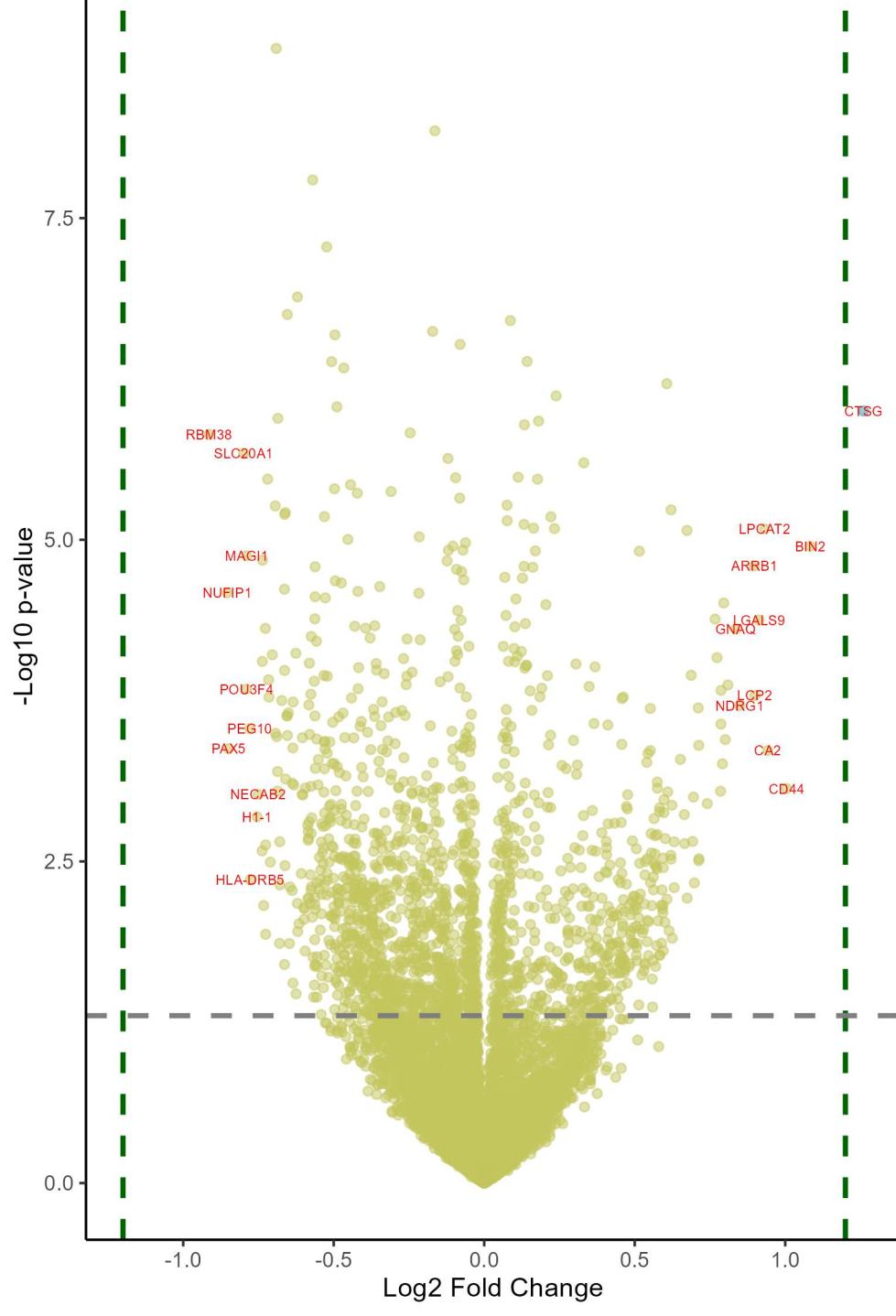
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.72	2.75e-14	NOPCHAP1	NOP protein chaperone 1	0.69	2.08e-06	CAVIN1	caveolae associated protein 1
-0.72	3.20e-18	CLP1	cleavage factor polyribonucleotide	0.68	3.05e-07	S100A10	S100 calcium binding protein A10
-0.69	1.24e-17	ZC3H8	zinc finger CCCH-type containing 8	0.64	1.68e-06	WDPCP	WD repeat containing planar cell po
-0.68	5.35e-18	DCAF1	DDB1 and CUL4 associated factor 1	0.61	5.96e-09	ADAM9	ADAM metallopeptidase domain 9
-0.66	2.21e-12	DCAF16	DDB1 and CUL4 associated factor 16	0.61	5.21e-11	ALDH3B1	aldehyde dehydrogenase 3 family mem
-0.65	1.11e-15	TIMELESS	timeless circadian regulator	0.6	1.34e-06	TGM2	transglutaminase 2
-0.65	1.52e-09	BCL7A	BAF chromatin remodeling complex su	0.6	7.80e-08	IGFBP3	insulin like growth factor binding
-0.62	1.16e-12	HIRIP3	HIRA interacting protein 3	0.58	1.95e-06	S100A16	S100 calcium binding protein A16
-0.62	4.49e-14	DSN1	DSN1 component of MIS12 kinetochore	0.58	4.92e-07	AXL	AXL receptor tyrosine kinase
-0.62	4.64e-12	USP48	ubiquitin specific peptidase 48	0.58	2.44e-09	CTSL	cathepsin L
-0.61	1.11e-15	CCDC12	coiled-coil domain containing 12	0.56	9.67e-08	FHL2	four and a half LIM domains 2
-0.59	3.47e-13	TDP2	tyrosyl-DNA phosphodiesterase 2	0.56	8.87e-06	CD44	CD44 molecule (Indian blood group)
-0.59	4.13e-14	UBE2T	ubiquitin conjugating enzyme E2 T	0.55	2.69e-06	IGFBP7	insulin like growth factor binding
-0.59	4.56e-14	ARIH2	ariadne RBR E3 ubiquitin protein li	0.54	1.52e-05	CAV1	caveolin 1
-0.59	1.12e-11	RBM38	RNA binding motif protein 38	0.54	1.09e-06	KRT74	keratin 74
-0.58	4.92e-10	TYMS	thymidylate synthetase	0.54	3.18e-07	NRP1	neuropilin 1
-0.58	2.08e-11	GTF2A1	general transcription factor IIA su	0.53	3.22e-08	RRAS	RAS related
-0.58	2.38e-12	CCNB2	cyclin B2	0.53	1.03e-09	EPHX1	epoxide hydrolase 1
-0.58	6.65e-14	NSL1	NSL1 component of MIS12 kinetochore	0.53	2.63e-08	PHLDB2	pleckstrin homology like domain fam
-0.57	4.26e-10	NUFIP1	nuclear FMR1 interacting protein 1	0.53	1.92e-07	RAB32	RAB32, member RAS oncogene family
-0.57	3.33e-15	CBLL1	Cbl proto-oncogene like 1	0.53	3.89e-08	CRAT	carnitine O-acetyltransferase
-0.57	1.09e-08	PPP1R2	protein phosphatase 1 regulatory in	0.53	1.68e-06	EHD2	EH domain containing 2
-0.57	5.06e-13	RAD51C	RAD51 paralog C	0.52	7.75e-06	KRT80	keratin 80
-0.57	1.65e-12	SURF2	surfeit 2	0.52	2.12e-05	LGALS3	galectin 3
-0.57	7.61e-12	WRAP53	WD repeat containing antisense to T	0.52	1.25e-05	ABCC6	ATP binding cassette subfamily C me
-0.57	1.17e-09	CDK5R2	cyclin dependent kinase 5 regulator	0.52	2.96e-07	TCHH1	trichohyalin like 1
-0.57	3.21e-11	GTSE1	G2 and S-phase expressed 1	0.51	2.47e-07	TRPM4	transient receptor potential cation
-0.57	1.30e-11	TLK2	tousled like kinase 2	0.51	8.70e-08	ANXA1	annexin A1
-0.57	4.49e-12	CARMIL2	capping protein regulator and myosi	0.51	1.64e-05	NT5E	5'-nucleotidase ecto

GAGE analysis on upregulated and downregulated proteins at low/absent ACTR8 protein, DB2

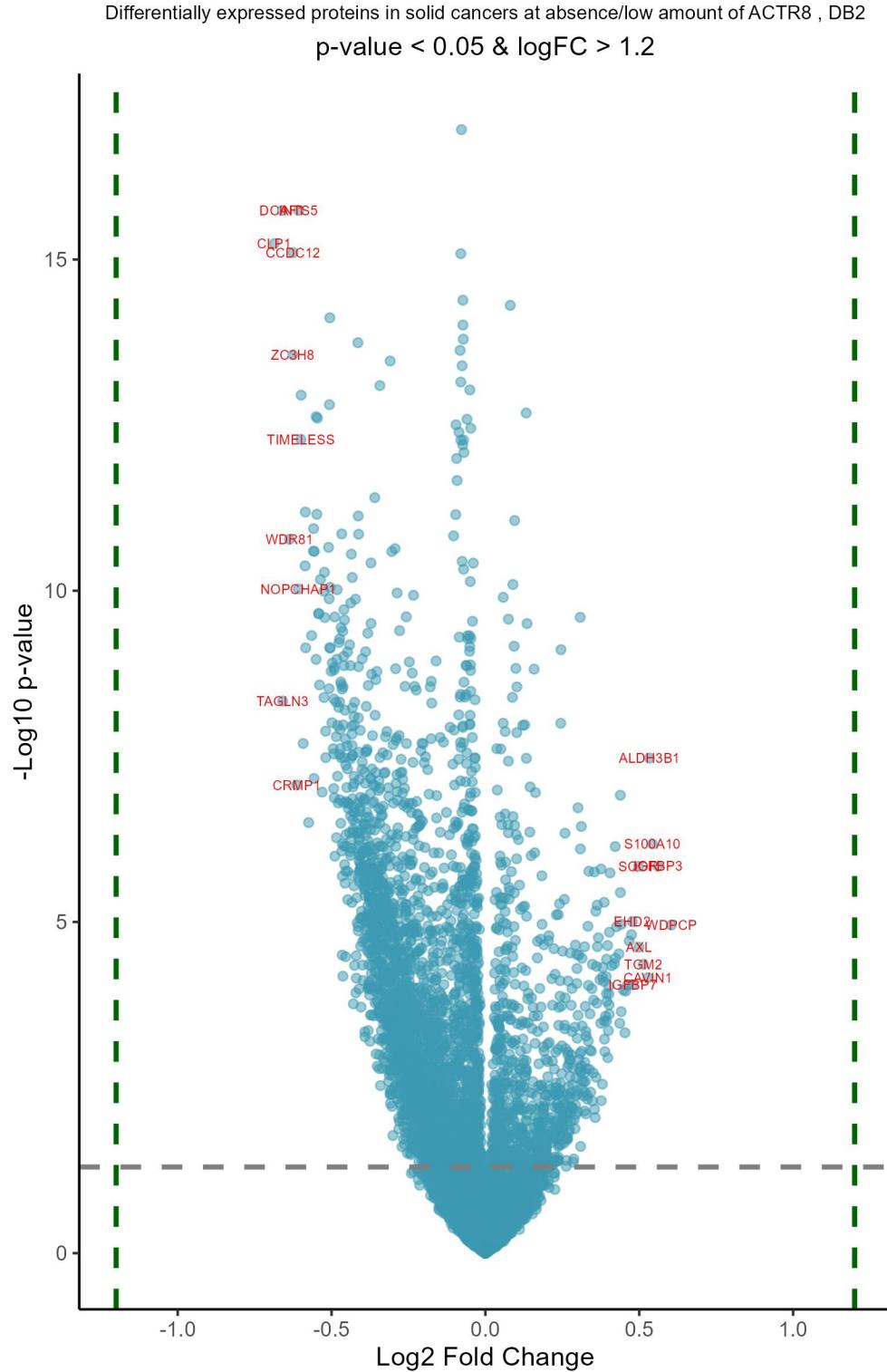


p-value < 0.05 & logFC > 1.2

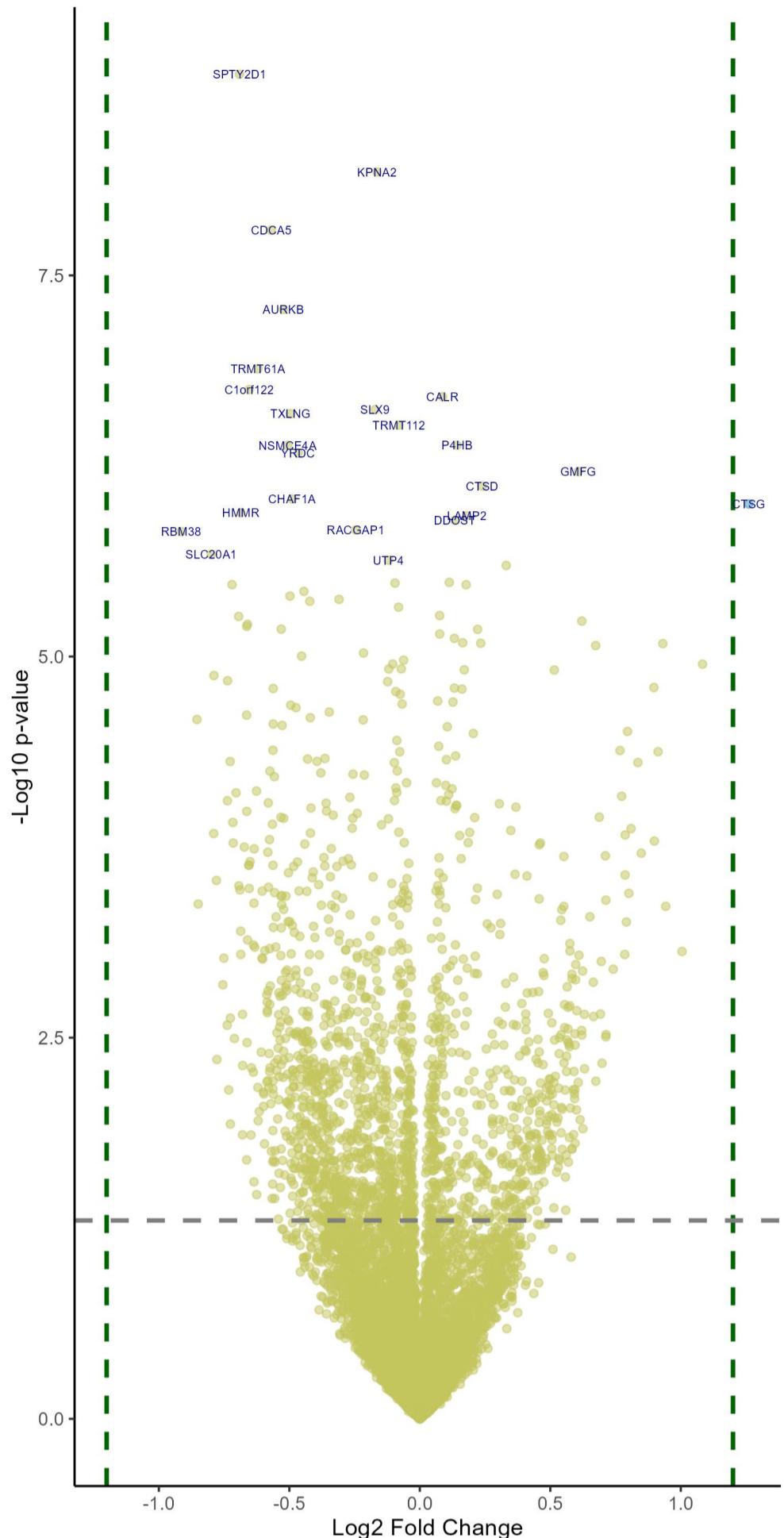
Downregulated in blood cancers at low/absent ACTR8 Upregulated in blood cancers at low/absent ACTR8



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.91	5.51e-04	RBM38	RNA binding motif protein 38	1.26	4.64e-04	CTSG	cathepsin G
-0.85	2.86e-03	NUFIP1	nuclear FMR1 interacting protein 1	1.08	1.77e-03	BIN2	bridging integrator 2
-0.85	1.57e-02	PAX5	paired box 5	1	2.50e-02	CD44	CD44 molecule (Indian blood group)
-0.8	7.43e-04	SLC20A1	solute carrier family 20 member 1	0.94	1.58e-02	CA2	carbonic anhydrase 2
-0.79	8.41e-03	POU3F4	POU class 3 homeobox 4	0.93	1.46e-03	LPCAT2	lysophosphatidylcholine acyltransfe
-0.79	1.92e-03	MAGI1	membrane associated guanylate kinases	0.91	4.05e-03	LGALS9	galectin 9
-0.78	1.31e-02	PEG10	paternally expressed 10	0.9	9.17e-03	LCP2	lymphocyte cytosolic protein 2
-0.78	6.12e-02	HLA-DRB5	major histocompatibility complex, c	0.9	2.14e-03	ARRB1	arrestin beta 1
-0.75	3.35e-02	H1-1	H1.1 linker histone, cluster member	0.85	1.02e-02	NDRG1	N-myc downstream regulated 1
-0.75	2.64e-02	NECA2B	N-terminal EF-hand calcium binding	0.84	4.37e-03	GNAQ	G protein subunit alpha q
-0.74	4.68e-02	CD40	CD40 molecule	0.81	8.09e-03	DUSP23	dual specificity phosphatase 23
-0.74	6.40e-03	SPDL1	spindle apparatus coiled-coil prote	0.8	1.45e-02	HPCAL1	hippocalcin like 1
-0.74	2.04e-03	SURF2	surfeit 2	0.8	3.24e-03	ANXA4	annexin A4
-0.73	7.61e-02	PADI2	peptidyl arginine deiminase 2	0.79	1.87e-02	LYZ	lysozyme
-0.73	4.37e-03	WRAP53	WD repeat containing antisense to T	0.79	8.54e-03	PECAM1	platelet and endothelial cell adhes
-0.73	4.39e-02	IRF4	interferon regulatory factor 4	0.79	1.25e-02	PARVG	parvin gamma
-0.73	1.02e-01	IGF2BP1	insulin like growth factor 2 mRNA b	0.79	2.57e-02	ME1	malic enzyme 1
-0.72	9.42e-04	UBAP1	ubiquitin associated protein 1	0.77	6.21e-03	PSTPIP2	proline-serine-threonine phosphatas
-0.72	7.59e-03	MALSU1	mitochondrial assembly of ribosomal	0.77	4.05e-03	PRTN3	proteinase 3
-0.72	9.20e-03	PHF20L1	PHD finger protein 20 like 1	0.74	2.98e-02	MYO1F	myosin IF
-0.71	5.15e-02	MCAM	melanoma cell adhesion molecule	0.71	5.00e-02	PYCARD	PYD and CARD domain containing
-0.7	6.01e-03	ORC6	origin recognition complex subunit	0.71	1.52e-02	APOBR	apolipoprotein B receptor
-0.69	1.23e-03	SPAG5	sperm associated antigen 5	0.71	5.10e-02	CAPN2	calpain 2
-0.69	1.39e-02	SRXN1	sulfiredoxin 1	0.71	1.06e-02	NIPSNAP3A	nipsnap homolog 3A
-0.69	6.34e-06	SPTY2D1	SPT2 chromatin protein domain conta	0.7	6.32e-02	ACTN1	actinin alpha 1
-0.69	1.43e-02	FLVCR1	FLVCR heme transporter 1	0.7	2.72e-02	SIRPA	signal regulatory protein alpha
-0.69	2.08e-02	MCL1	MCL1 apoptosis regulator, BCL2 fami	0.69	4.30e-02	SPART	spartin
-0.69	2.57e-02	ETS1	ETS proto-oncogene 1, transcription	0.69	7.24e-03	VPS26B	VPS26, retromer complex component B
-0.69	5.00e-04	HMMR	hyaluronan mediated motility recept	0.67	7.09e-02	ITGB2	integrin subunit beta 2

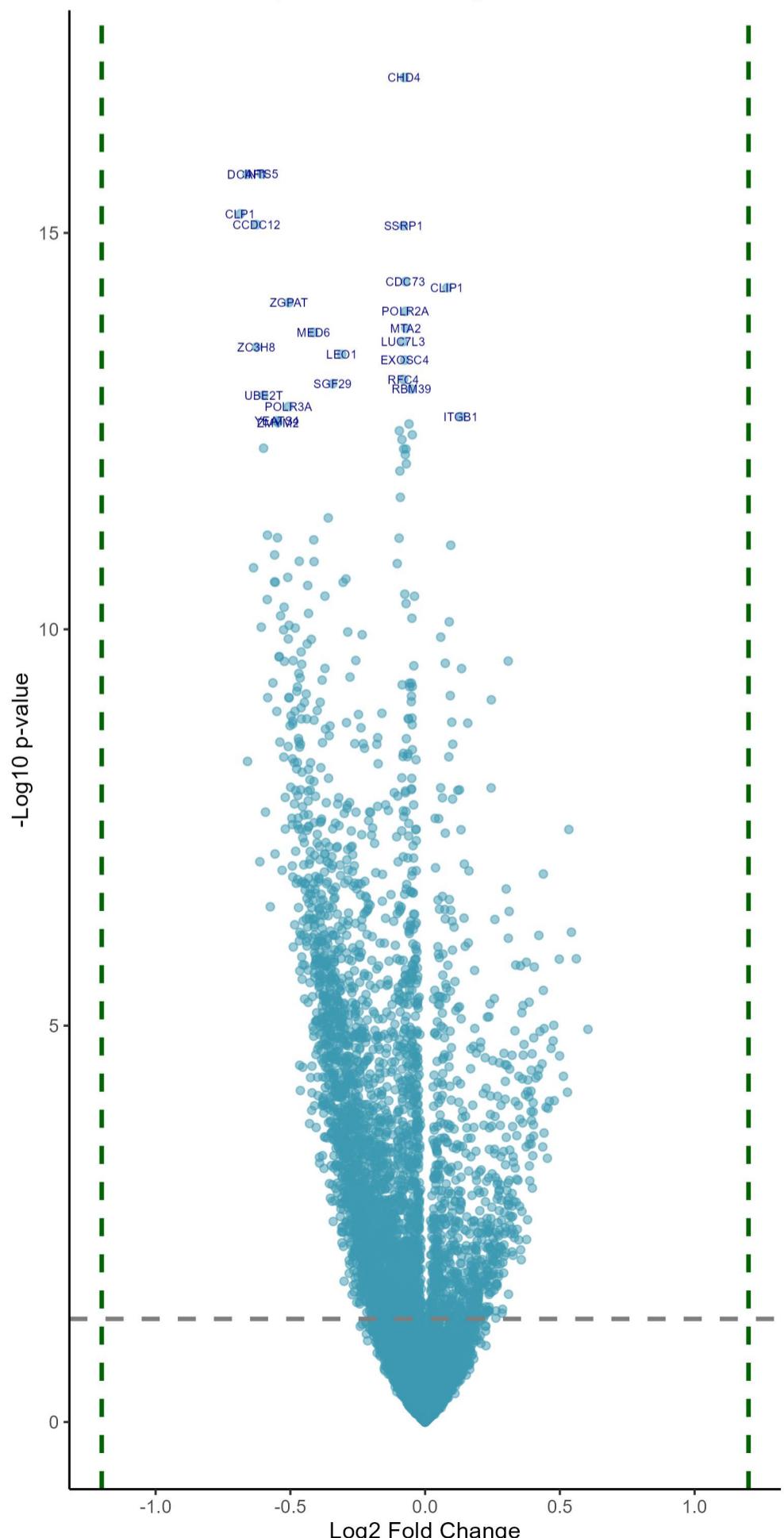


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-0.69	9.62e-13	CLP1	cleavage factor polyribonucleotide	0.6	1.19e-04	WDPCP	WD repeat containing planar cell po
-0.66	3.82e-13	DCAF1	DDB1 and CUL4 associated factor 1	0.56	2.43e-05	IGFBP3	insulin like growth factor binding
-0.66	2.50e-07	TAGLN3	transgelin 3	0.54	1.31e-05	S100A10	S100 calcium binding protein A10
-0.64	2.98e-09	WDR81	WD repeat domain 81	0.53	1.20e-06	ALDH3B1	aldehyde dehydrogenase 3 family mem
-0.63	1.54e-11	ZC3H8	zinc finger CCCH-type containing 8	0.53	5.16e-04	CAVIN1	caveolae associated protein 1
-0.63	9.75e-13	CCDC12	coiled-coil domain containing 12	0.51	3.52e-04	TGM2	transglutaminase 2
-0.61	2.60e-06	CRMP1	collapsin response mediator protein	0.5	2.18e-04	AXL	AXL receptor tyrosine kinase
-0.61	1.21e-08	NOPCHAP1	NOP protein chaperone 1	0.5	2.44e-05	SQOR	sulfide quinone oxidoreductase
-0.61	3.82e-13	INTS5	integrator complex subunit 5	0.48	6.32e-04	IGFBP7	insulin like growth factor binding
-0.6	1.39e-10	TIMELESS	timeless circadian regulator	0.48	1.09e-04	EHD2	EH domain containing 2
-0.6	4.44e-11	UBE2T	ubiquitin conjugating enzyme E2 T	0.47	1.53e-04	HLA-B	major histocompatibility complex, c
-0.59	8.23e-07	BCL7A	BAF chromatin remodeling complex su	0.47	1.82e-04	NRP1	neuropilin 1
-0.59	6.18e-09	HIRIP3	HIRA interacting protein 3	0.46	6.40e-04	KRT80	keratin 80
-0.59	1.43e-09	POLR3F	RNA polymerase III subunit F	0.46	7.59e-04	CTSZ	cathepsin Z
-0.58	5.97e-08	DCAF16	DDB1 and CUL4 associated factor 16	0.45	2.48e-03	NNMT	nicotinamide N-methyltransferase
-0.57	7.38e-06	CPVL	carboxypeptidase vitellogenin like	0.45	7.38e-04	KRT74	keratin 74
-0.56	4.36e-08	NKIRAS2	NFKB inhibitor interacting Ras like	0.44	1.17e-04	CAV2	caveolin 2
-0.56	4.11e-09	DSN1	DSN1 component of MIS12 kinetochore	0.44	1.36e-03	AKR1D1	aldo-keto reductase family 1 member
-0.56	2.24e-09	SURF2	surfeit 2	0.44	3.46e-06	ADAM9	ADAM metallopeptidase domain 9
-0.56	2.17e-06	ASRGL1	asparaginase and isoaspartyl peptid	0.44	4.85e-05	PHLDB2	pleckstrin homology like domain fam
-0.56	4.11e-09	POLR3C	RNA polymerase III subunit C	0.44	1.90e-03	CD44	CD44 molecule (Indian blood group)
-0.55	8.18e-08	USP48	ubiquitin specific peptidase 48	0.43	2.60e-04	TCHHL1	trichohyalin like 1
-0.55	8.22e-11	YEATS4	YEATS domain containing 4	0.43	1.25e-04	KRT79	keratin 79
-0.55	1.48e-09	NSL1	NSL1 component of MIS12 kinetochore	0.42	2.95e-04	RAB7B	RAB7B, member RAS oncogene family
-0.55	8.28e-11	ZMYM2	zinc finger MYM-type containing 2	0.42	1.40e-05	CTS1	cathepsin L
-0.54	2.46e-08	BEND3	BEN domain containing 3	0.42	3.47e-04	ITGA3	integrin subunit alpha 3
-0.54	2.46e-08	TOP3A	DNA topoisomerase III alpha	0.41	3.67e-04	CCN1	cellular communication network fact
-0.54	1.63e-07	LYRM2	LYR motif containing 2	0.41	2.85e-05	ANXA1	annexin A1
-0.54	9.28e-09	EED	embryonic ectoderm development	0.4	1.42e-04	LOXL2	lysyl oxidase like 2



Sorted by p values!
Downregulated in blood cancers at low/absent ACTR8 Upregulated in blood cancers at low/absent ACTR8

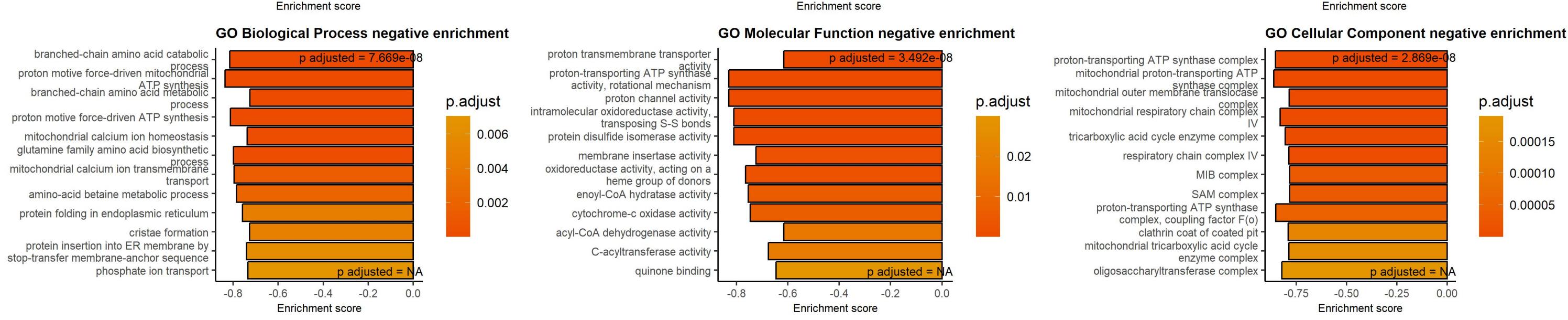
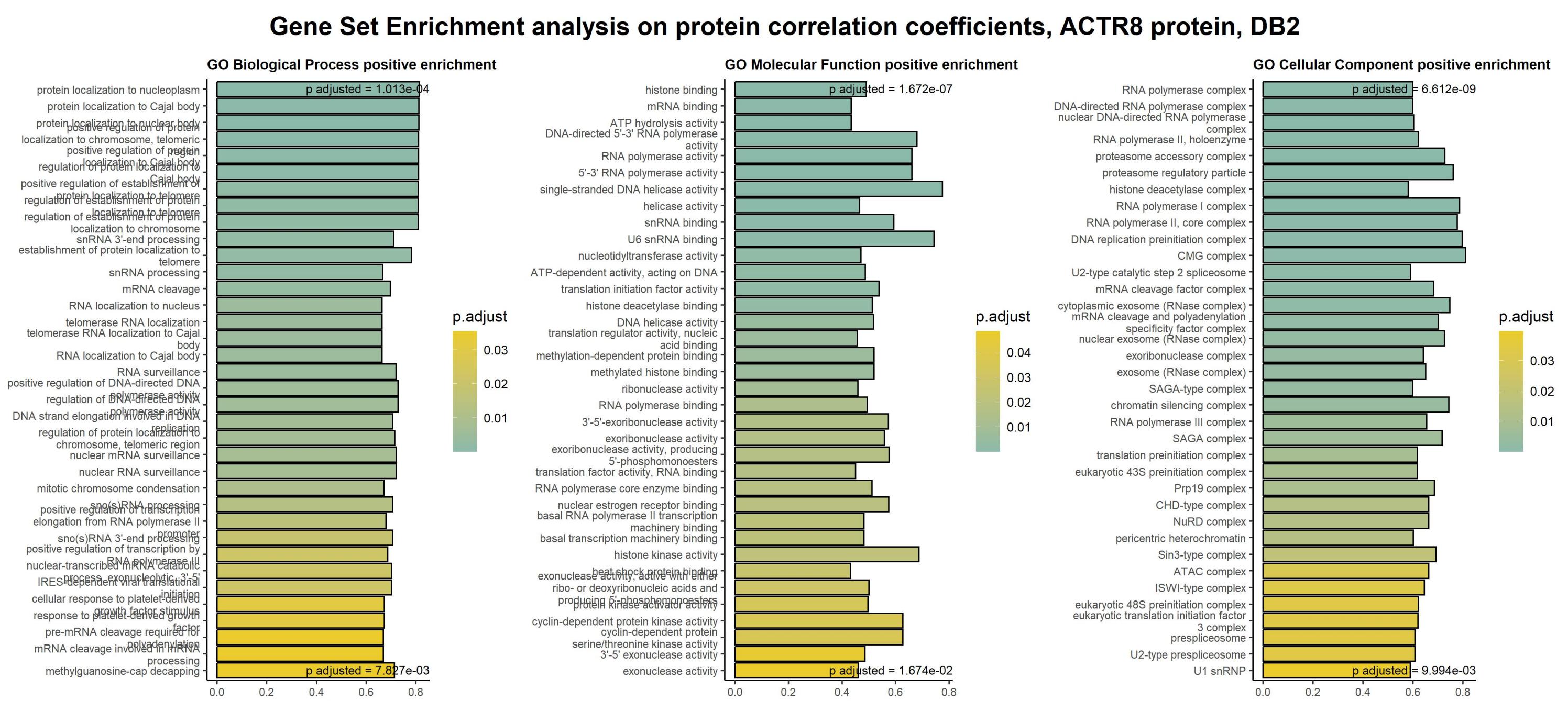
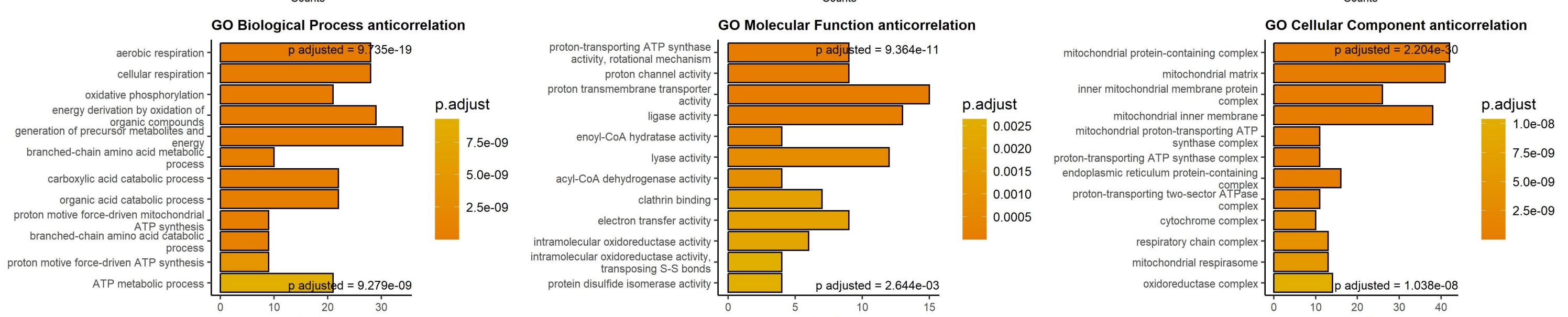
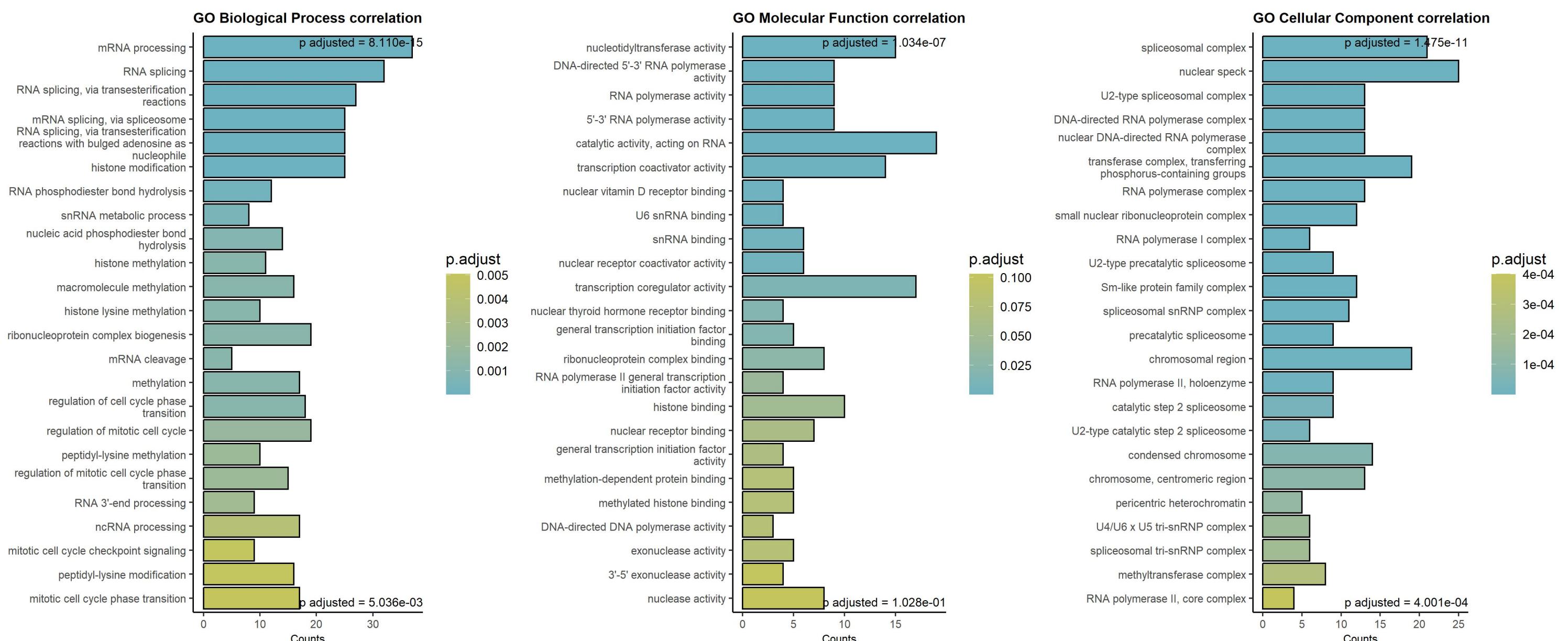
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.69	6.34e-06	SPTY2D1	SPT2 chromatin protein domain conta	0.09	2.07e-04	CALR	calreticulin
-0.16	1.85e-05	KPNA2	karyopherin subunit alpha 2	0.14	2.65e-04	P4HB	prolyl 4-hydroxylase subunit beta
-0.57	3.34e-05	CDC45	cell division cycle associated 5	0.61	3.41e-04	GMFG	glia maturation factor gamma
-0.52	8.85e-05	AURKB	aurora kinase B	0.24	3.98e-04	CTSD	cathepsin D
-0.62	1.81e-04	TRMT61A	tRNA methyltransferase 61A	1.26	4.64e-04	CTSG	cathepsin G
-0.65	2.07e-04	C1orf122	chromosome 1 open reading frame 122	0.18	5.00e-04	LAMP2	lysosomal associated membrane prote
-0.17	2.14e-04	SLX9	SLX9 ribosome biogenesis factor	0.13	5.09e-04	DDOST	dolichyl-diphosphooligosaccharide--
-0.5	2.14e-04	TXLNG	taxilin gamma	0.33	8.12e-04	PFKL	phosphofructokinase, liver type
-0.08	2.31e-04	TRMT112	tRNA methyltransferase activator su	0.11	9.42e-04	LAMP1	lysosomal associated membrane prote
-0.51	2.65e-04	NSMCE4A	NSE4 homolog A, SMC5-SMC6 complex c	0.18	9.42e-04	RPN2	ribophorin II
-0.47	2.76e-04	YRDC	yrdC N6-threonylcarbamoyltransf	0.08	1.23e-03	HNRNPUL1	heterogeneous nuclear ribonucleop
-0.49	4.56e-04	CHAF1A	chromatin assembly factor 1 subunit	0.62	1.29e-03	BST1	bone marrow stromal cell antigen 1
-0.69	5.00e-04	HMMR	hyaluronan mediated motility recept	0.22	1.32e-03	GNS	glucosamine (N-acetyl)-6-sulfatase
-0.25	5.51e-04	RACGAP1	Rac GTPase activating protein 1	0.08	1.38e-03	TPM3	tropomyosin 3
-0.91	5.51e-04	RBM38	RNA binding motif protein 38	0.13	1.44e-03	VPS25	vacuolar protein sorting 25 homolog
-0.8	7.43e-04	SLC20A1	solute carrier family 20 member 1	0.16	1.46e-03	PREP	prolyl endopeptidase
-0.12	7.81e-04	UTP4	UTP4 small subunit processome compo	0.23	1.46e-03	ACADVL	acyl-CoA dehydrogenase very long ch
-0.1	9.42e-04	CCDC124	coiled-coil domain containing 124	0.93	1.46e-03	LPCAT2	lysophosphatidylcholine acyltransfe
-0.72	9.42e-04	UBAP1	ubiquitin associated protein 1	0.67	1.48e-03	OR8B8	olfactory receptor family 8 subfami
-0.44	1.01e-03	RPS19BP1	ribosomal protein S19 binding prote	1.08	1.77e-03	BIN2	bridging integrator 2
-0.5	1.05e-03	STARD7	STAR related lipid transfer domain	0.17	1.80e-03	SUB1	SUB1 regulator of transcription
-0.31	1.07e-03	LARP4	La ribonucleoprotein 4	0.52	1.80e-03	MAN2B2	mannosidase alpha class 2B member 2
-0.42	1.07e-03	ABT1	activator of basal transcription 1	0.9	2.14e-03	ARRB1	arrestin beta 1
-0.08	1.13e-03	CPSF2	cleavage and polyadenylation specif	0.13	2.14e-03	VDAC3	voltage dependent anion channel 3
-0.69	1.23e-03	SPAG5	sperm associated antigen 5	0.16	2.14e-03	RAB2A	RAB2A, member RAS oncogene family
-0.66	1.32e-03	BIRC5	baculoviral IAP repeat containing 5	0.07	2.44e-03	TALDO1	transaldolase 1
-0.66	1.32e-03	HAUS8	HAUS augmin like complex subunit 8	0.13	2.44e-03	NNT	nicotinamide nucleotide transhydrog
-0.53	1.32e-03	DPH5	diphthamide biosynthesis 5	0.11	3.06e-03	UGGT1	UDP-glucose glycoprotein glucosyltr
-0.22	1.62e-03	SLC2A1	solute carrier family 2 member 1	0.8	3.24e-03	ANXA4	annexin A4
-0.45	1.66e-03	RRP36	ribosomal RNA processing 36	0.2	3.30e-03	CAT	catalase
-0.06	1.73e-03	SRRM2	serine/arginine repetitive matrix 2	0.07	3.91e-03	RPN1	ribophorin I
-0.1	1.77e-03	CD2BP2	CD2 cytoplasmic tail binding protei	0.77	4.05e-03	PRTN3	proteinase 3
-0.07	1.80e-03	NUP35	nucleoporin 35	0.91	4.05e-03	LGALS9	galectin 9
-0.12	1.80e-03	NCAPH	non-SMC condensin I complex subunit	0.14	4.26e-03	MMUT	methylmalonyl-CoA mutase
-0.79	1.92e-03	MAGI1	membrane associated guanylate kinas	0.1	4.36e-03	BCAP31	B cell receptor associated protein
-0.74	2.04e-03	SURF2	surfeit 2	0.84	4.37e-03	GNAQ	G protein subunit alpha q
-0.12	2.04e-03	UTP14A	UTP14A small subunit processome com	0.06	5.47e-03	GANAB	glucosidase II alpha subunit
-0.56	2.14e-03	MRTFB	myocardin related transcription fac	0.1	5.63e-03	RAB11B	RAB11B, member RAS oncogene family
0.00	2.18e-02	HSDA1A	heat shock protein family A (Hsp70)	0.12	5.81e-02	TRIM25	trinicotinic acid containing 25



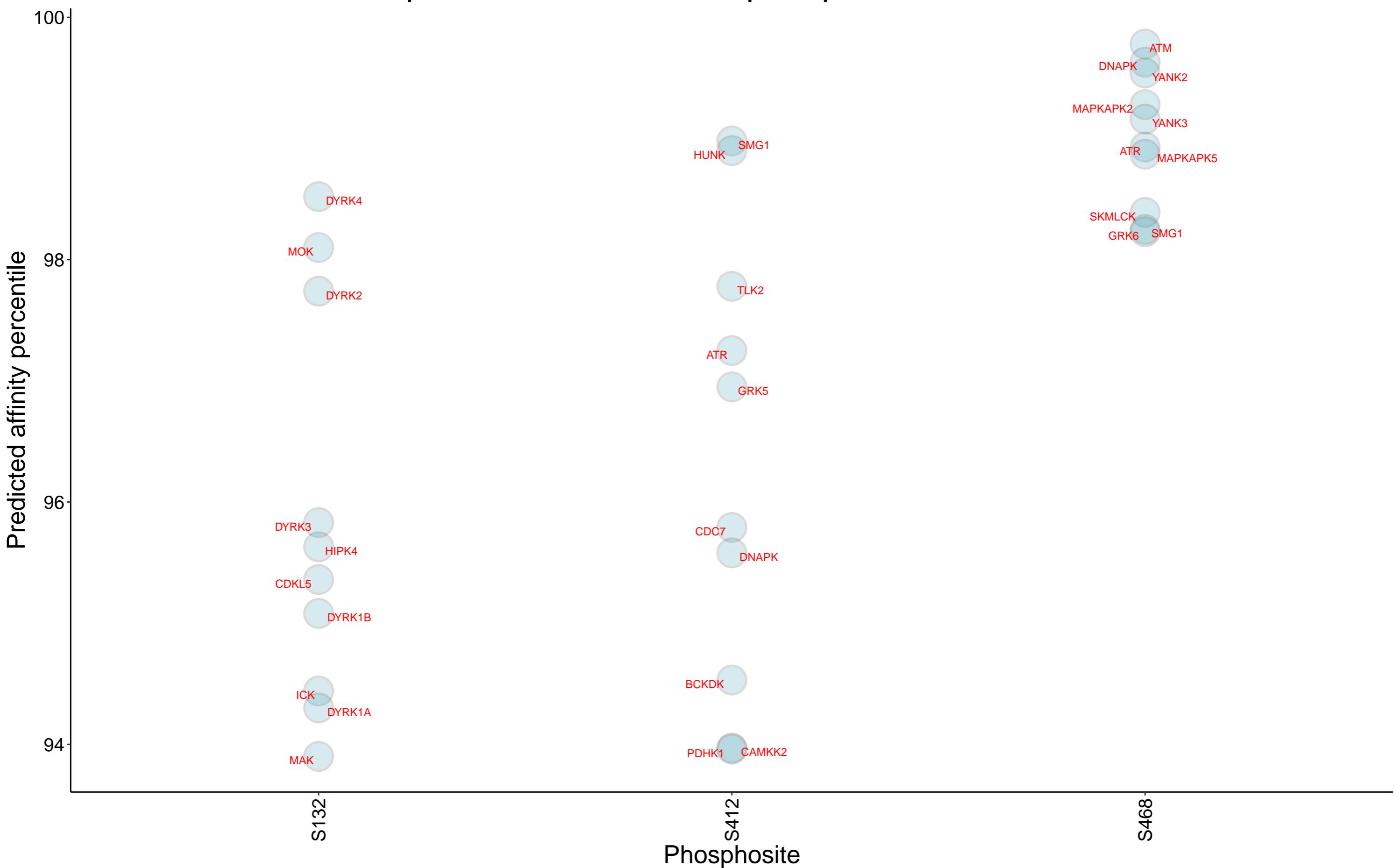
Sorted by p values!
Downregulated in solid cancers at low/absent ACTR8 Upregulated in solid cancers at low/absent ACTR8

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.08	4.58e-14	CHD4	chromodomain helicase DNA binding p	0.08	4.58e-12	CLIP1	CAP-Gly domain containing linker pr
-0.61	3.82e-13	INTS5	integrator complex subunit 5	0.13	7.55e-11	ITGB1	integrin subunit beta 1
-0.66	3.82e-13	DCAF1	DDB1 and CUL4 associated factor 1	0.1	1.73e-09	TMOD3	tropomodulin 3
-0.69	9.62e-13	CLP1	cleavage factor polyribonucleotide	0.09	1.07e-08	GOLGB1	golgin B1
-0.63	9.75e-13	CCDC12	coiled-coil domain containing 12	0.06	1.50e-08	P4HB	prolyl 4-hydroxylase subunit beta
-0.08	9.75e-13	SSRP1	structure specific recognition prot	0.31	2.66e-08	RHOC	ras homolog family member C
-0.07	4.30e-12	CDC73	cell division cycle 73	0.07	2.77e-08	MYL6	myosin light chain 6
-0.51	6.34e-12	ZGPAT	zinc finger CCCH-type and G-patch d	0.14	3.08e-08	AHNAK	AHNAK nucleoprotein
-0.07	7.41e-12	POLR2A	RNA polymerase II subunit A	0.09	5.80e-08	TM9SF3	transmembrane 9 superfamily member
-0.07	1.11e-11	MTA2	metastasis associated 1 family memb	0.25	6.24e-08	ITGA5	integrin subunit alpha V
-0.41	1.16e-11	MED6	mediator complex subunit 6	0.1	1.02e-07	MYH9	myosin heavy chain 9
-0.08	1.41e-11	LUC7L3	LUC7 like 3 pre-mRNA splicing facto	0.16	1.03e-07	PLEC	plectin
-0.63	1.54e-11	ZC3H8	zinc finger CCCH-type containing 8	0.1	1.66e-07	LASP1	LIM and SH3 protein 1
-0.31	1.78e-11	LEO1	LEO1 homolog, Paf1/RNA polymerase I	0.09	2.25e-07	ACTN4	actinin alpha 4
-0.08	1.98e-11	EXOSC4	exosome component 4	0.06	4.90e-07	AP2B1	adaptor related protein complex 2 s
-0.08	3.28e-11	RFC4	replication factor C subunit 4	0.24	4.90e-07	PLIN3	perilipin 3
-0.34	3.52e-11	SGF29	SAGA complex associated factor 29	0.13	5.07e-07	FLNB	filamin B
-0.05	3.89e-11	RBM39	RNA binding motif protein 39	0.12	5.07e-07	GALNT2	polypeptide N-acetylgalactosaminylt
-0.6	4.44e-11	UBE2T	ubiquitin conjugating enzyme E2 T	0.06	5.94e-07	PGRMC2	progesterone receptor membrane comp
-0.51	5.90e-11	POLR3A	RNA polymerase III subunit A	0.1	6.13e-07	VCL	vinculin
-0.55	8.22e-11	YEATS4	YEATS domain containing 4	0.04	9.49e-07	CDC42	cell division cycle 42
-0.55	8.28e-11	ZMYM2	zinc finger MYM-type containing 2	0.05	9.53e-07	RAB1A	RAB1A, member RAS oncogene family
-0.06	8.28e-11	CSTF1	cleavage stimulation factor subunit	0.53	1.20e-06	ALDH3B1	aldehyde dehydrogenase 3 family mem
-0.1	9.70e-11	RFC2	replication factor C subunit 2	0.13	1.20e-06	HEXB	hexosaminidase subunit beta
-0.05	1.05e-10	POLR2E	RNA polymerase II, I and III subuni	0.07	1.30e-06	AP2A1	adaptor related protein complex 2 s
-0.09	1.17e-10	SMARCA5	SWI/SNF related, matrix associated,	0.15	2.75e-06	TPM1	tropomyosin 1
-0.6	1.39e-10	TIMELESS	timeless circadian regulator	0.04	3.00e-06	HSPA5	heat shock protein family A (Hsp70)
-0.07	1.39e-10	SUPT6H	SPT6 homolog, histone chaperone and	0.16	3.21e-06	ERLIN1	ER lipid raft associated 1
-0.08	1.39e-10	ACTL6A	actin like 6A	0.44	3.46e-06	ADAM9	ADAM metallopeptidase domain 9
-0.07	1.59e-10	PARP1	poly(ADP-ribose) polymerase 1	0.3	4.86e-06	MBOAT7	membrane bound O-acyltransferase do
-0.07	2.01e-10	SUPT16H	SPT16 homolog, facilitates chromati	0.06	5.7		

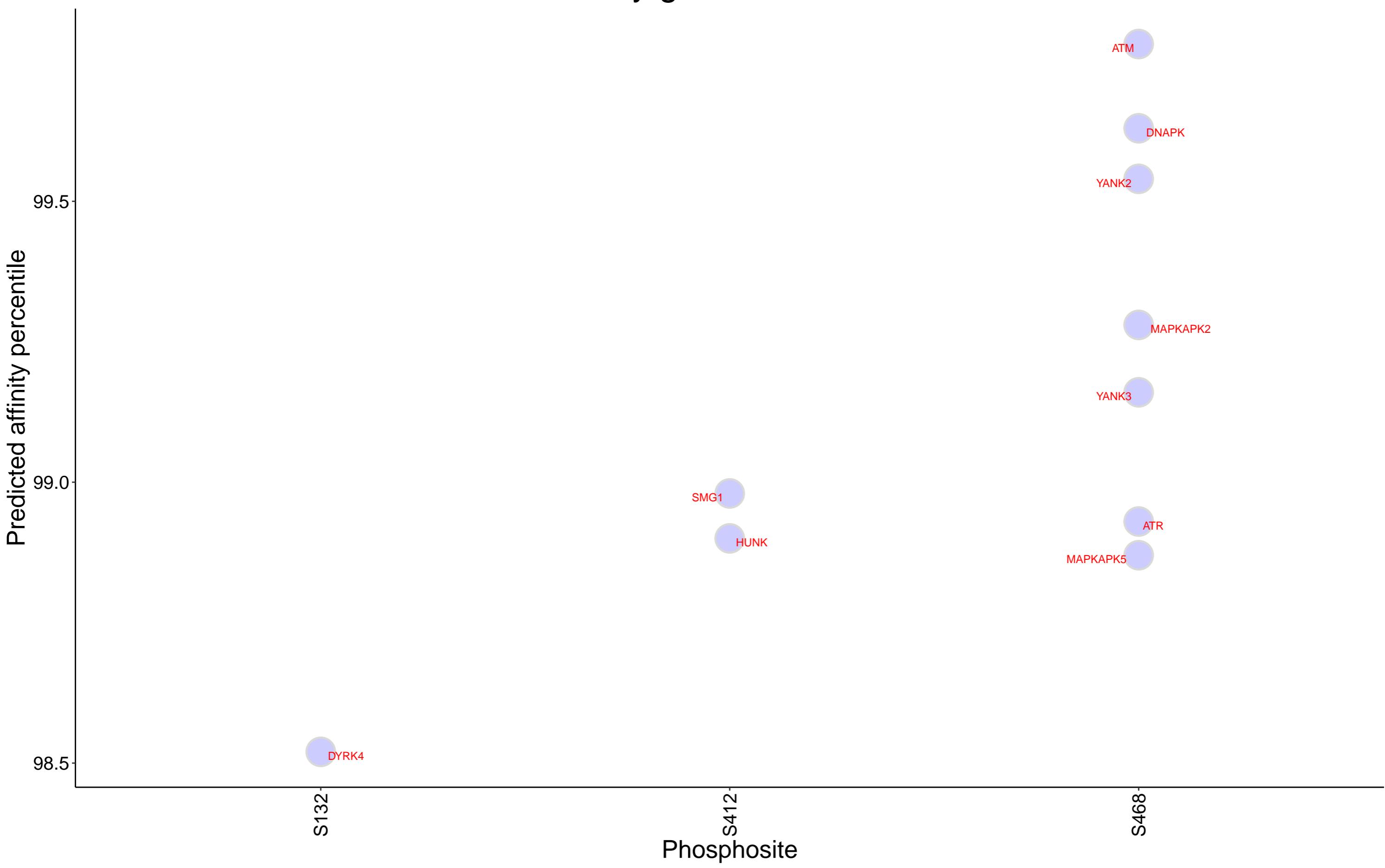
Top 250 correlation coefficients overrepresentation, ACTR8 protein, DB2



Top 10 kinases for each phosphosite in ACTR8



Kinases with affinity greater than 98.5% to ACTR8



Top 15 positive correlation coefficients for ACTR8 protein by tissue, DB2

Beware of false positives in tissues with small number of samples

