

ACTL6A

Protein name: ACTL6A ;

UNIPROT: O96019 ;

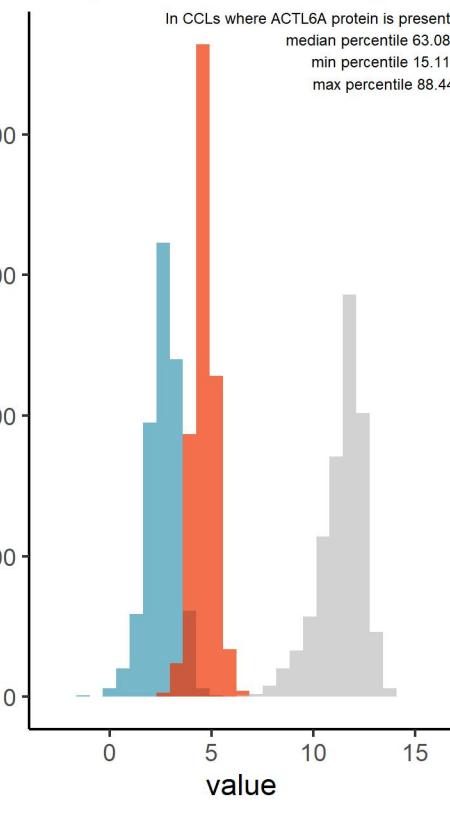
Gene name: actin like 6A

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

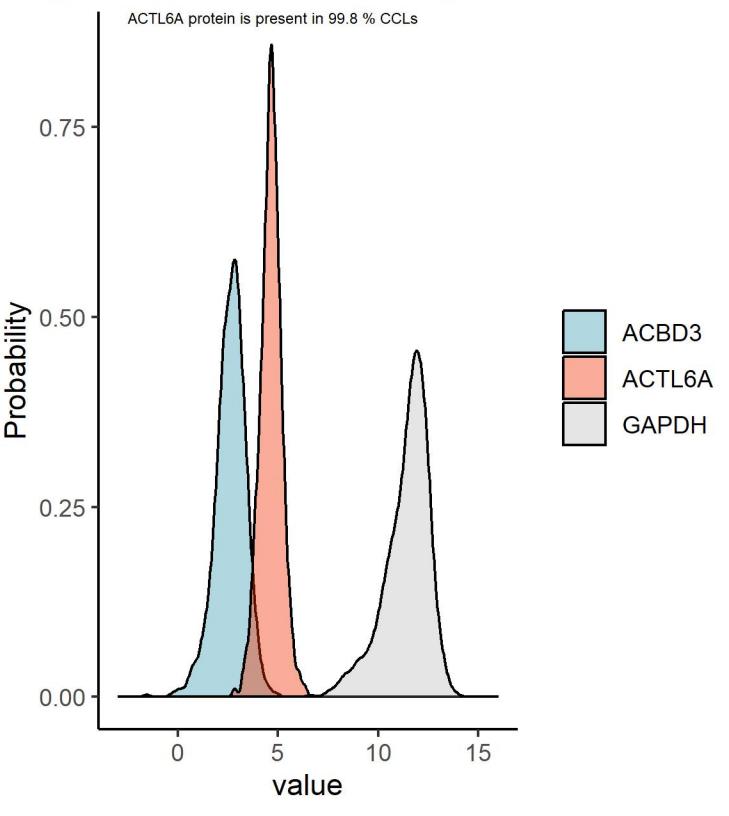
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

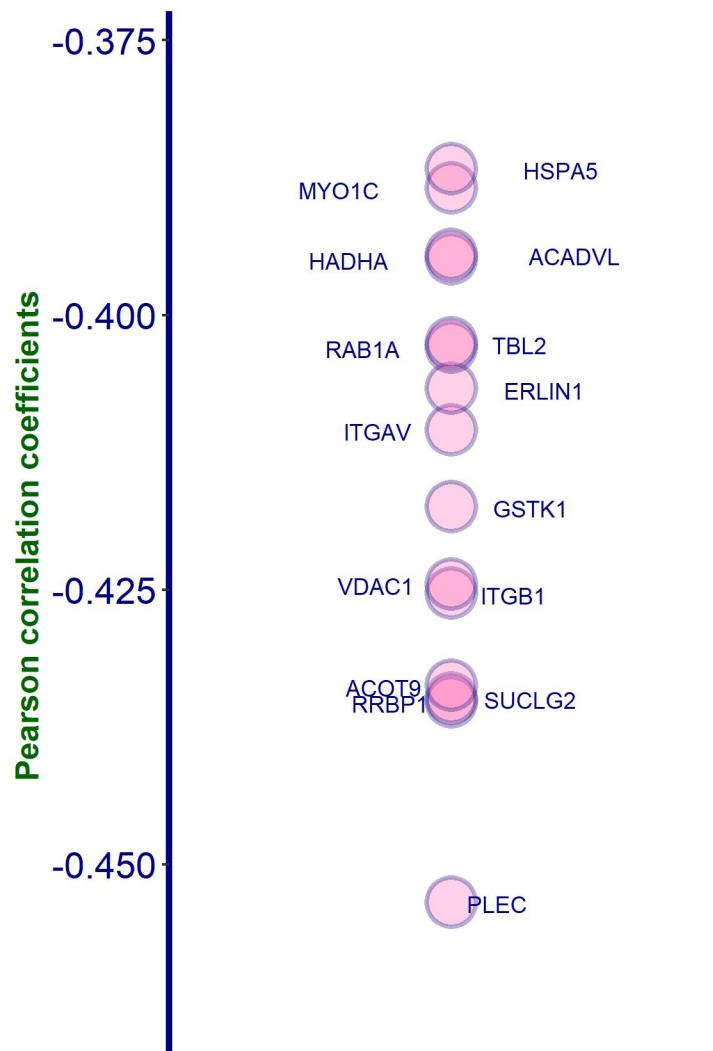
Histogram of ACTL6A protein compared to proteins with low and high abundance



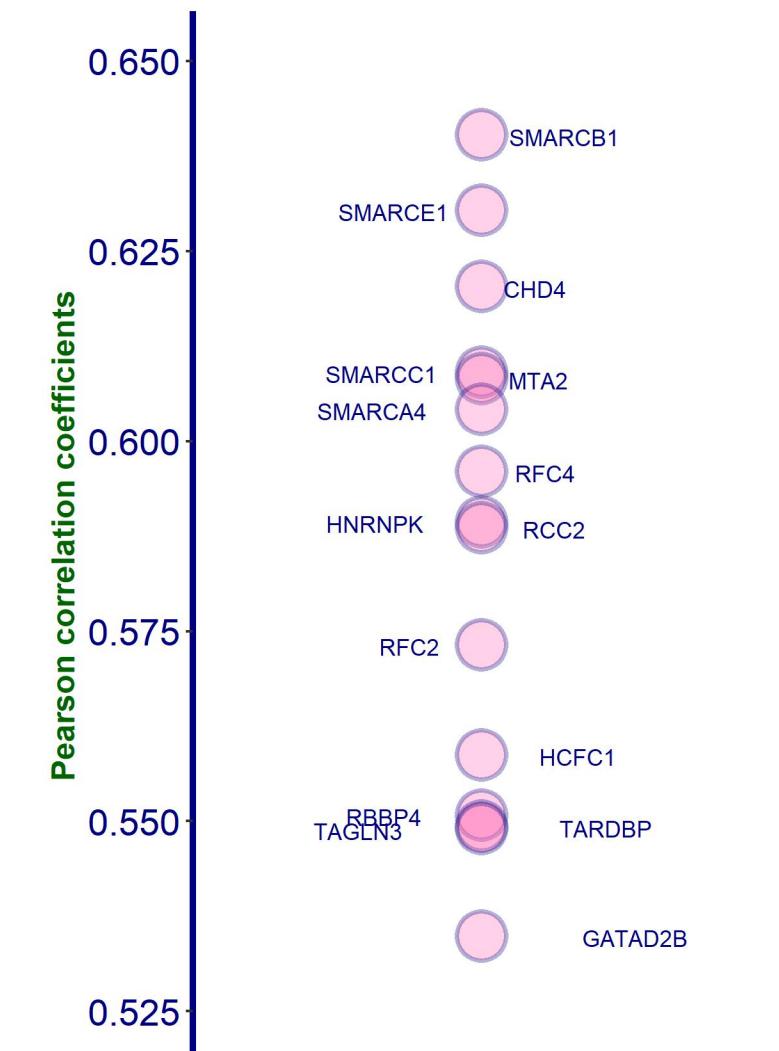
Density plot of ACTL6A protein compared to proteins with low and high abundance



Top negative correlations of ACTL6A protein, DE

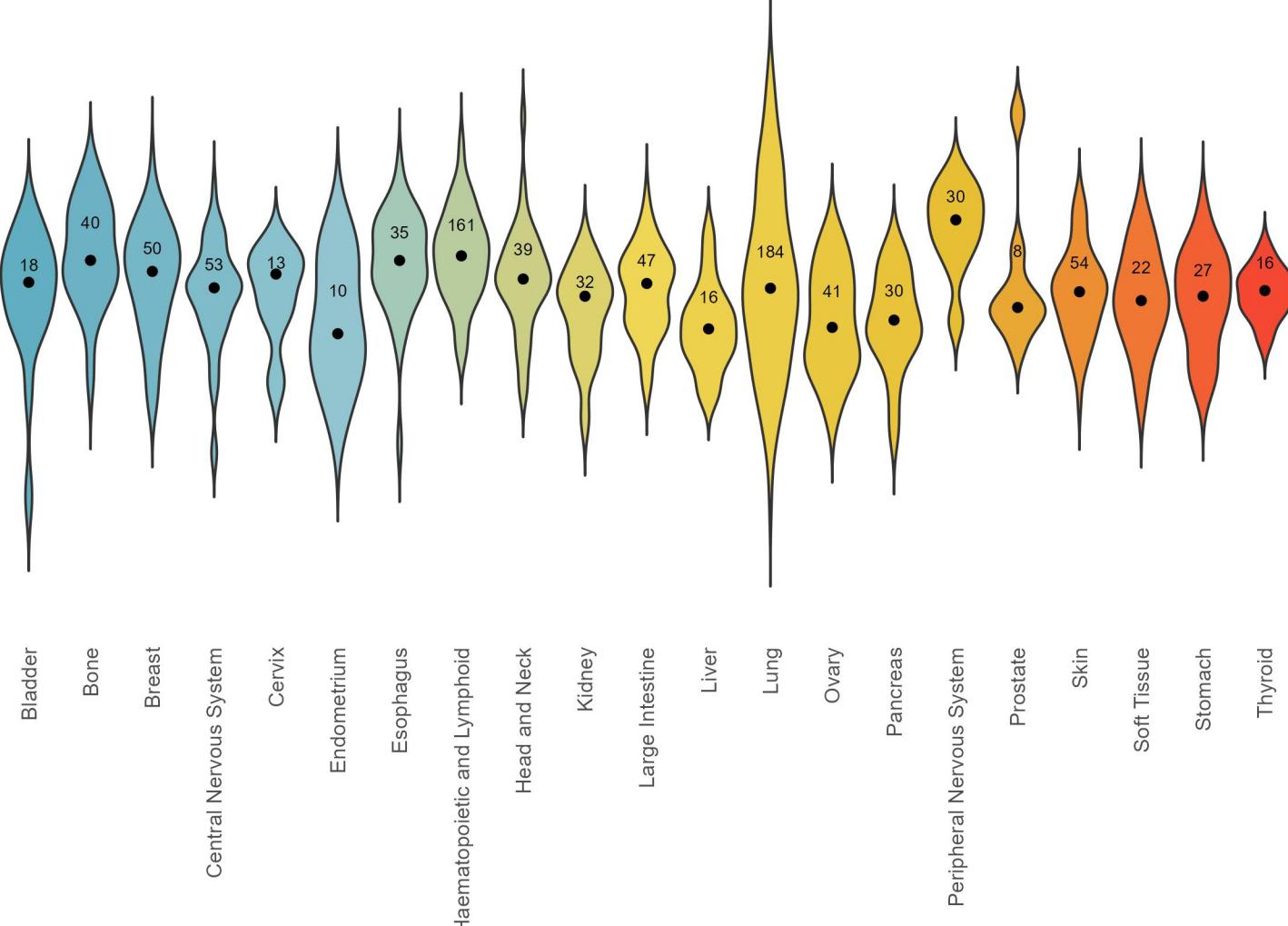


Top positive correlations of ACTL6A protein, DB



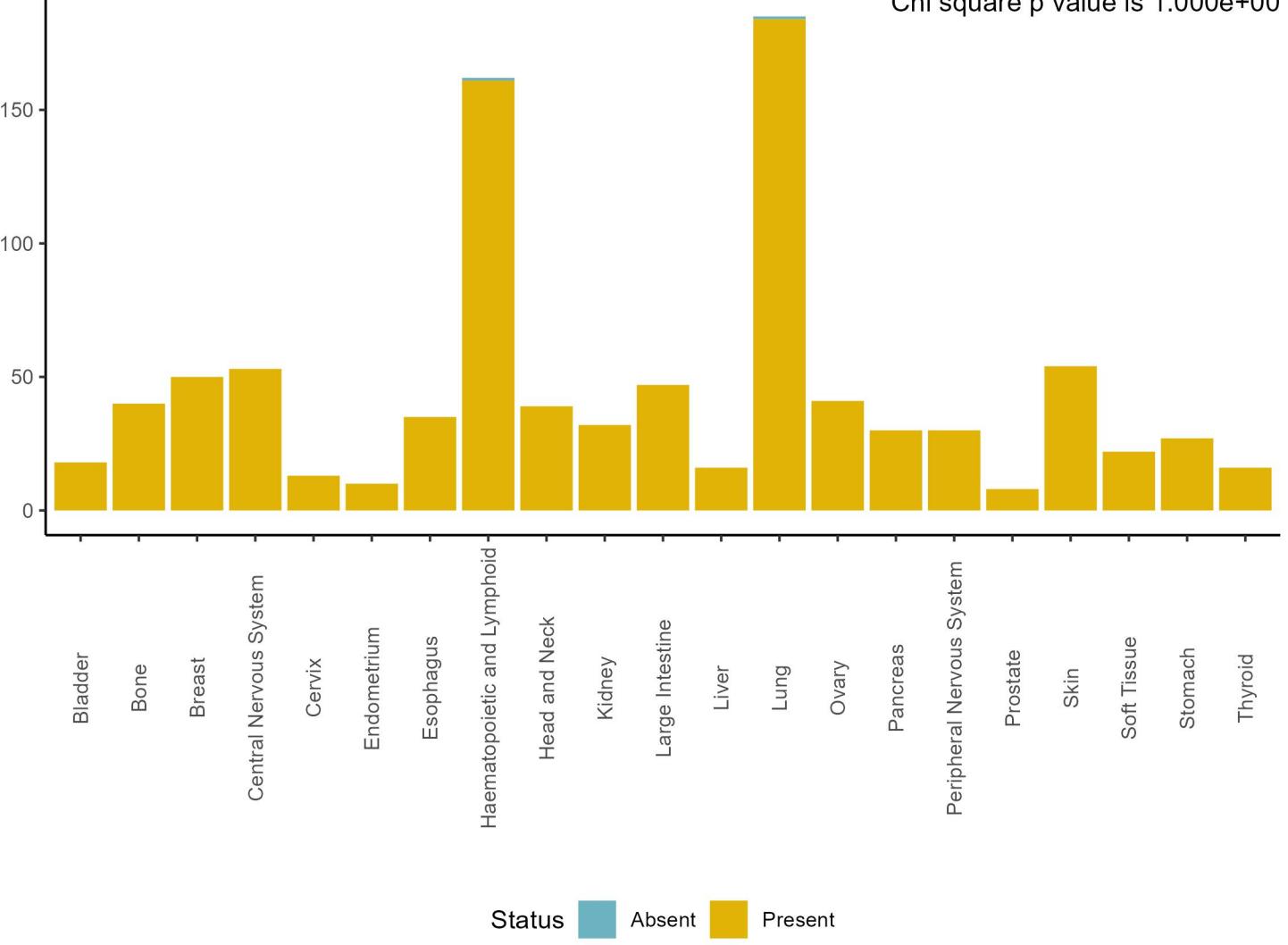
Amount of ACTL6A protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 6.333e-18



Present and absent ACTL6A protein counts by tissue, DB1

Chi square p value is 1.000e+00

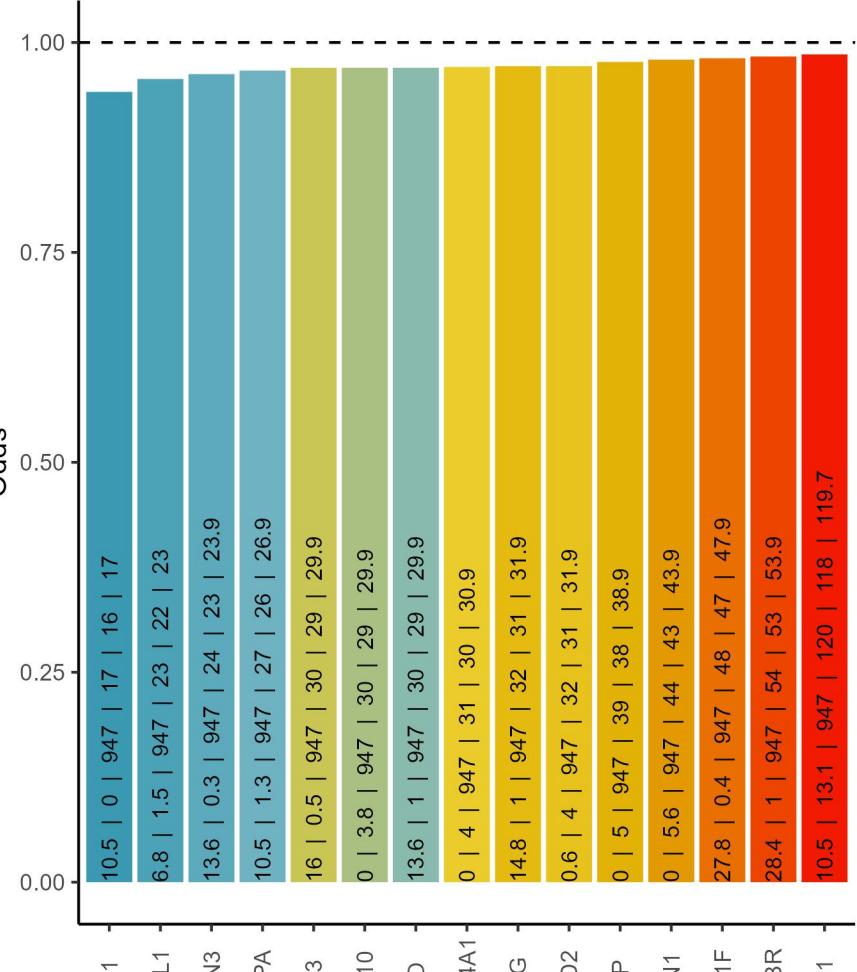


Cooccurrence with ACTL6A protein, DB1

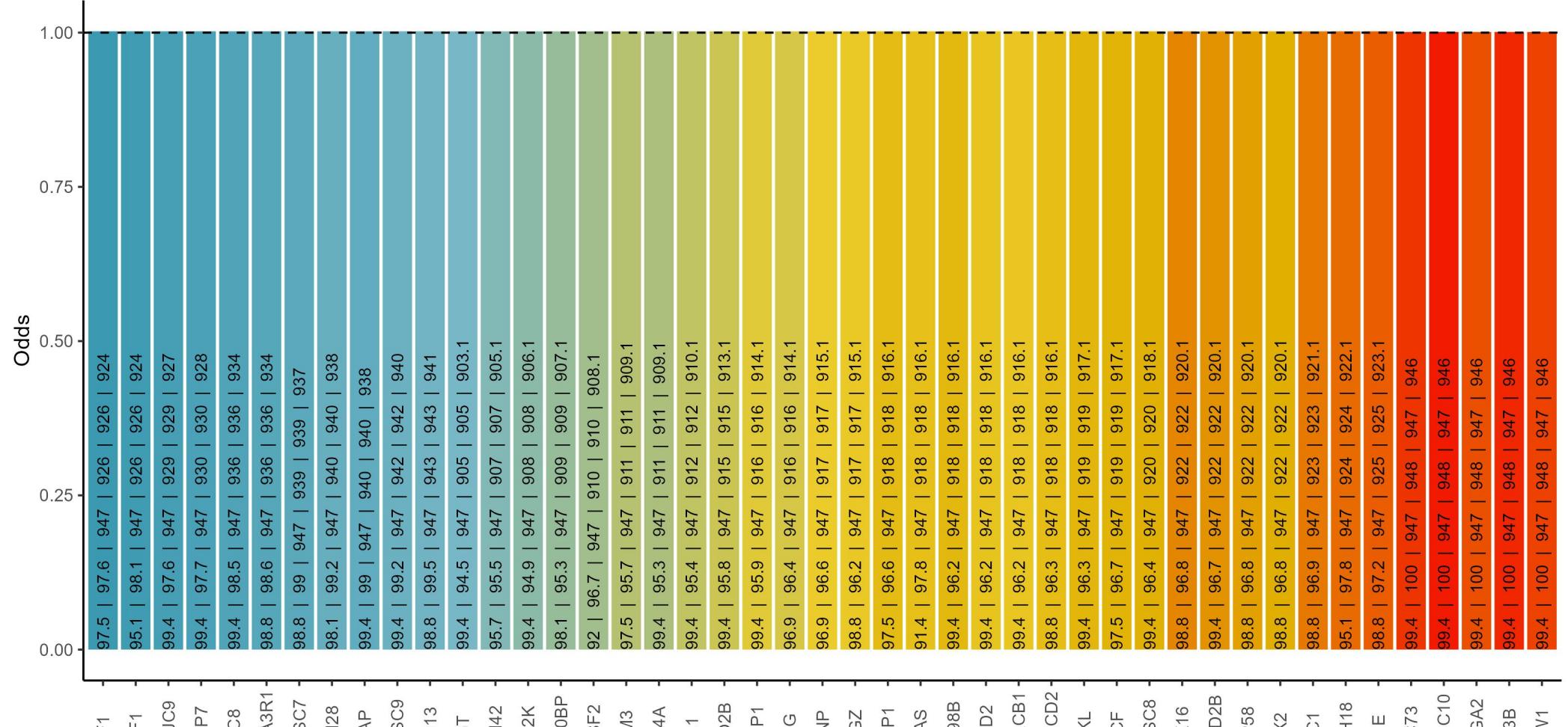
% of ACTL6A in blood cancers: 99.4 ; % of ACTL6A in solid cancers: 99.9

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ACTL6A | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

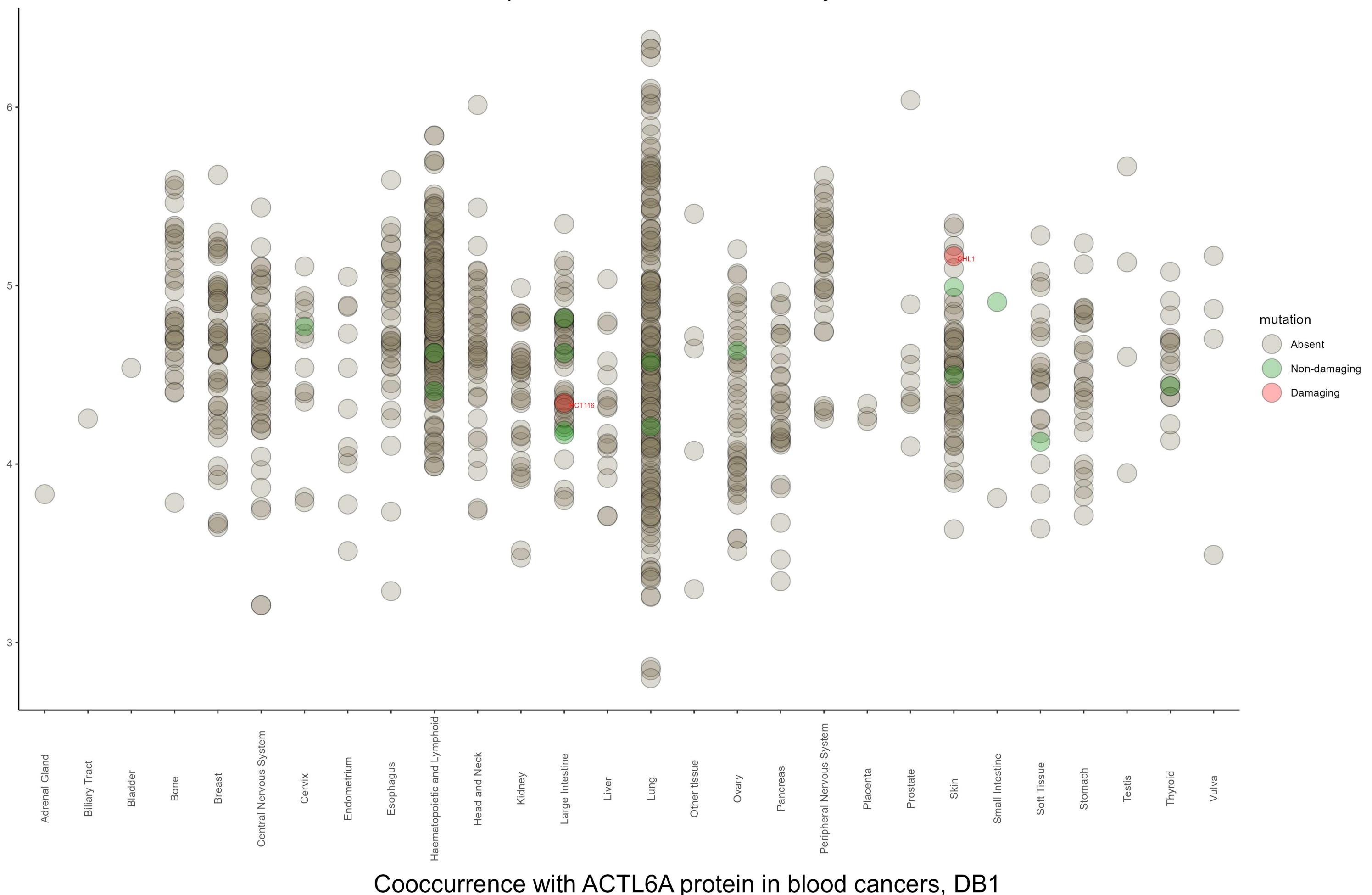
Negative cooccurrence



Positive cooccurrence



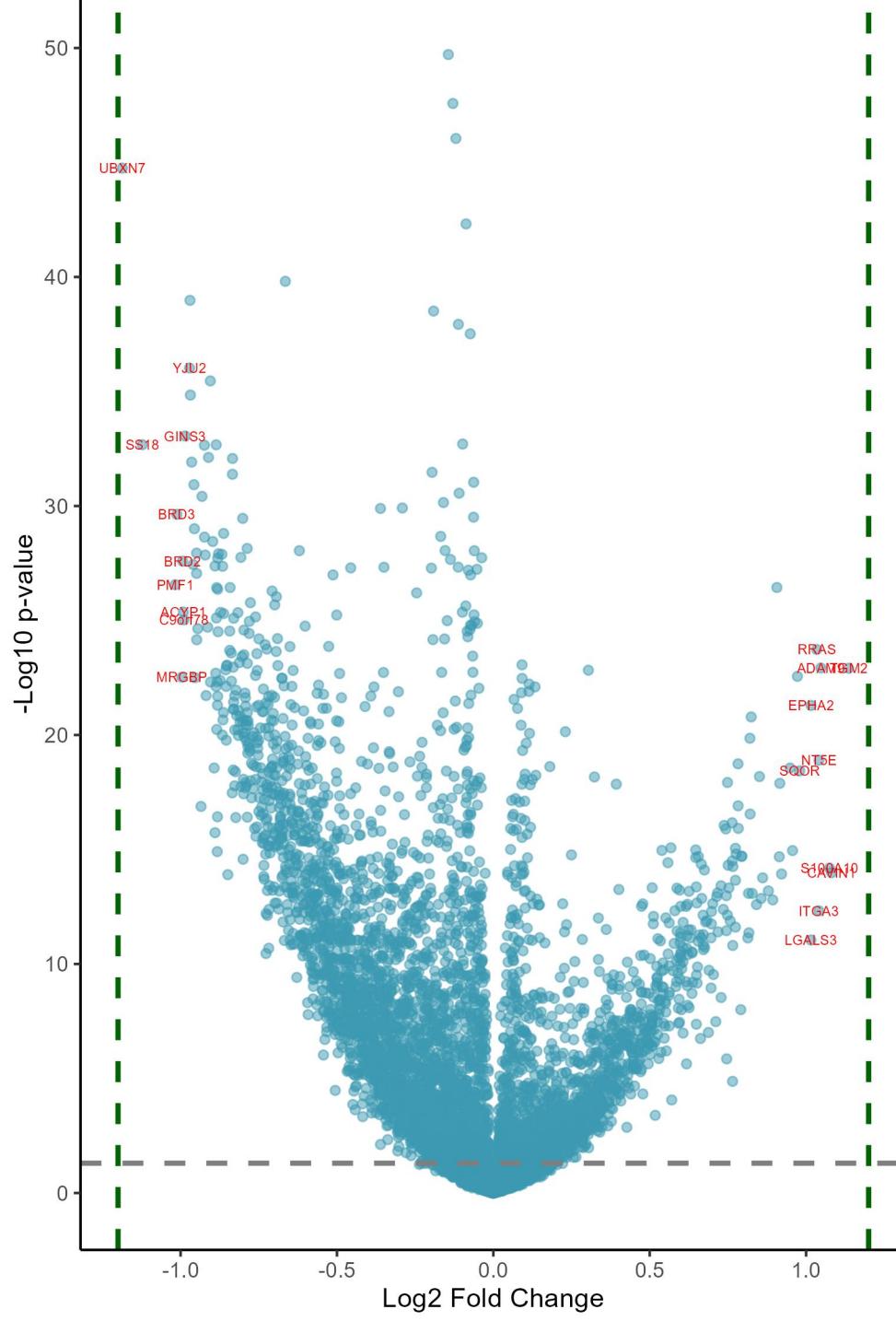
Amount of ACTL6A protein and mutation status by tissue, DB1



Cooccurrence with ACTL6A protein in blood cancers, DB1

The text in the bars: incidence of ACTL6A | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

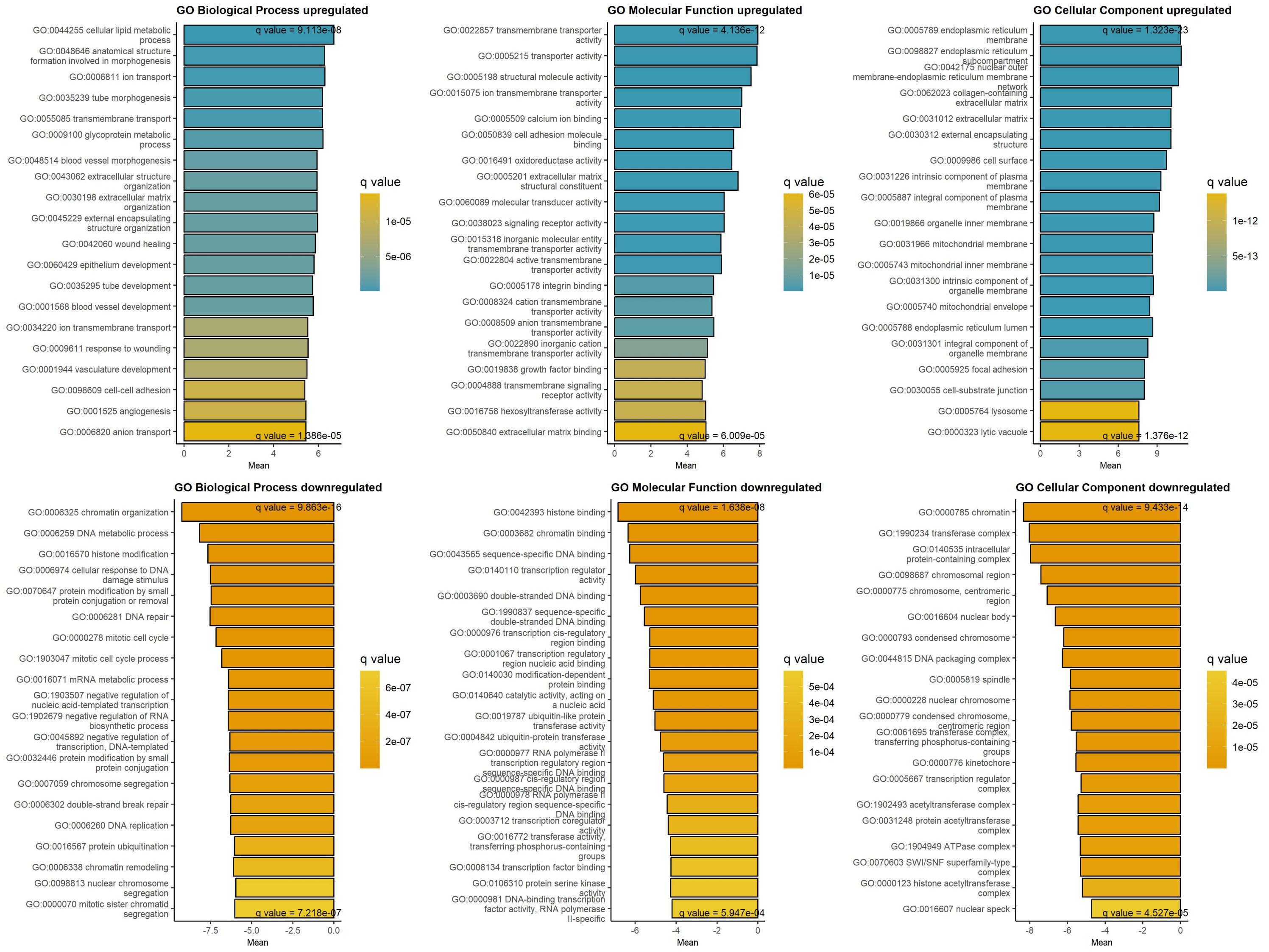




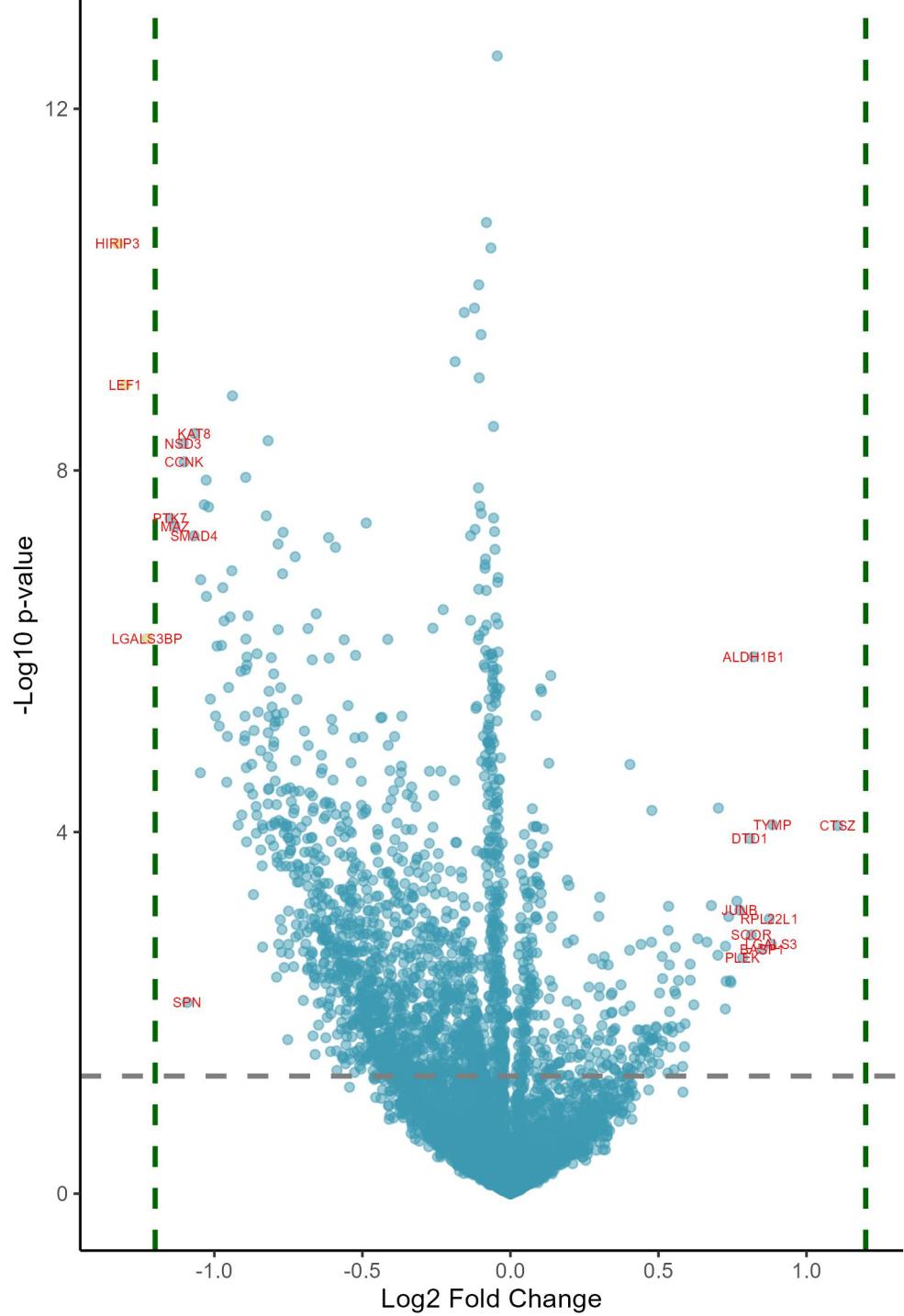
Downregulated at low/absent ACTL6A Upregulated at low/absent ACTL6A

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.19	2.33e-42	UBXN7	UBX domain protein 7	1.14	6.35e-22	TGM2	transglutaminase 2
-1.12	7.76e-31	SS18	SS18 subunit of BAF chromatin remod	1.08	1.03e-13	CAVIN1	caveolae associated protein 1
-1.02	2.79e-25	PMF1	polyamine modulated factor 1	1.07	6.70e-14	S100A10	S100 calcium binding protein A10
-1.01	4.82e-28	BRD3	bromodomain containing 3	1.05	6.20e-22	ADAM9	ADAM metallopeptidase domain 9
-1	1.42e-21	MRGBP	MRG domain binding protein	1.04	2.88e-18	NT5E	5'-nucleotidase ecto
-0.99	3.26e-26	BRD2	bromodomain containing 2	1.04	3.55e-12	ITGA3	integrin subunit alpha 3
-0.99	3.74e-24	ACYP1	acylphosphatase 1	1.03	1.10e-22	RRAS	RAS related
-0.99	7.20e-24	C9orf78	chromosome 9 open reading frame 78	1.02	1.84e-20	EPHA2	EPH receptor A2
-0.99	3.91e-31	GINS3	GINS complex subunit 3	1.02	5.42e-11	LGALS3	galectin 3
-0.97	5.23e-34	YJU2	YJU2 splicing factor homolog	0.98	7.67e-18	SQOR	sulfide quinone oxidoreductase
-0.97	8.69e-37	TRIM24	tripartite motif containing 24	0.97	1.31e-21	CTSL	cathepsin L
-0.97	6.78e-33	SAMD1	sterile alpha motif domain containi	0.96	1.28e-14	NCEH1	neutral cholesterol ester hydrolase
-0.96	3.67e-30	POU2F1	POU class 2 homeobox 1	0.95	5.87e-18	GPX8	glutathione peroxidase 8 (putative)
-0.96	4.51e-26	EPB41	erythrocyte membrane protein band 4	0.92	1.15e-13	MYOF	myoferlin
-0.96	3.00e-29	NRF1	nuclear respiratory factor 1	0.92	2.43e-17	AXL	AXL receptor tyrosine kinase
-0.96	1.87e-27	SMARCD1	SWI/SNF related, matrix associated,	0.91	2.31e-14	RHOC	ras homolog family member C
-0.95	1.48e-21	PSME3IP1	proteasome activator subunit 3 inte	0.91	3.59e-25	RAB11FIP5	RAB11 family interacting protein 5
-0.95	1.73e-26	PDCL	phosducin like	0.89	1.27e-12	CAV1	caveolin 1
-0.95	9.42e-26	RNASEH2B	ribonuclease H2 subunit B	0.88	5.62e-13	CTSZ	cathepsin Z
-0.95	4.30e-23	ARMC6	armadillo repeat containing 6	0.86	1.65e-13	EGFR	epidermal growth factor receptor
-0.94	1.59e-23	UBE2T	ubiquitin conjugating enzyme E2 T	0.86	1.11e-12	GPRC5A	G protein-coupled receptor class C
-0.93	2.07e-16	CORO1A	coronin 1A	0.85	1.30e-17	MBOAT7	membrane bound O-acyltransferase do
-0.93	9.00e-29	TLE3	TLE family member 3, transcriptiona	0.84	1.98e-12	S100A16	S100 calcium binding protein A16
-0.92	7.76e-31	TIMELESS	timeless circadian regulator	0.83	6.99e-13	CAVIN3	caveolae associated protein 3
-0.92	4.01e-27	HIRIP3	HIRA interacting protein 3	0.82	5.25e-20	GGCX	gamma-glutamyl carboxylase
-0.92	1.96e-26	PRIM1	DNA primase subunit 1	0.82	4.24e-16	MVP	major vault protein
-0.92	7.50e-21	NUDT3	nudix hydrolase 3	0.82	3.67e-19	RETSAT	retinol saturase
-0.91	1.38e-23	USP13	ubiquitin specific peptidase 13	0.82	2.81e-11	PROCR	protein C receptor
-0.91	2.50e-30	KAT8	lysine acetyltransferase 8	0.82	6.97e-13	PPIC	peptidylprolyl isomerase C

GAGE analysis on upregulated and downregulated proteins at low/absent ACTL6A protein, DB1

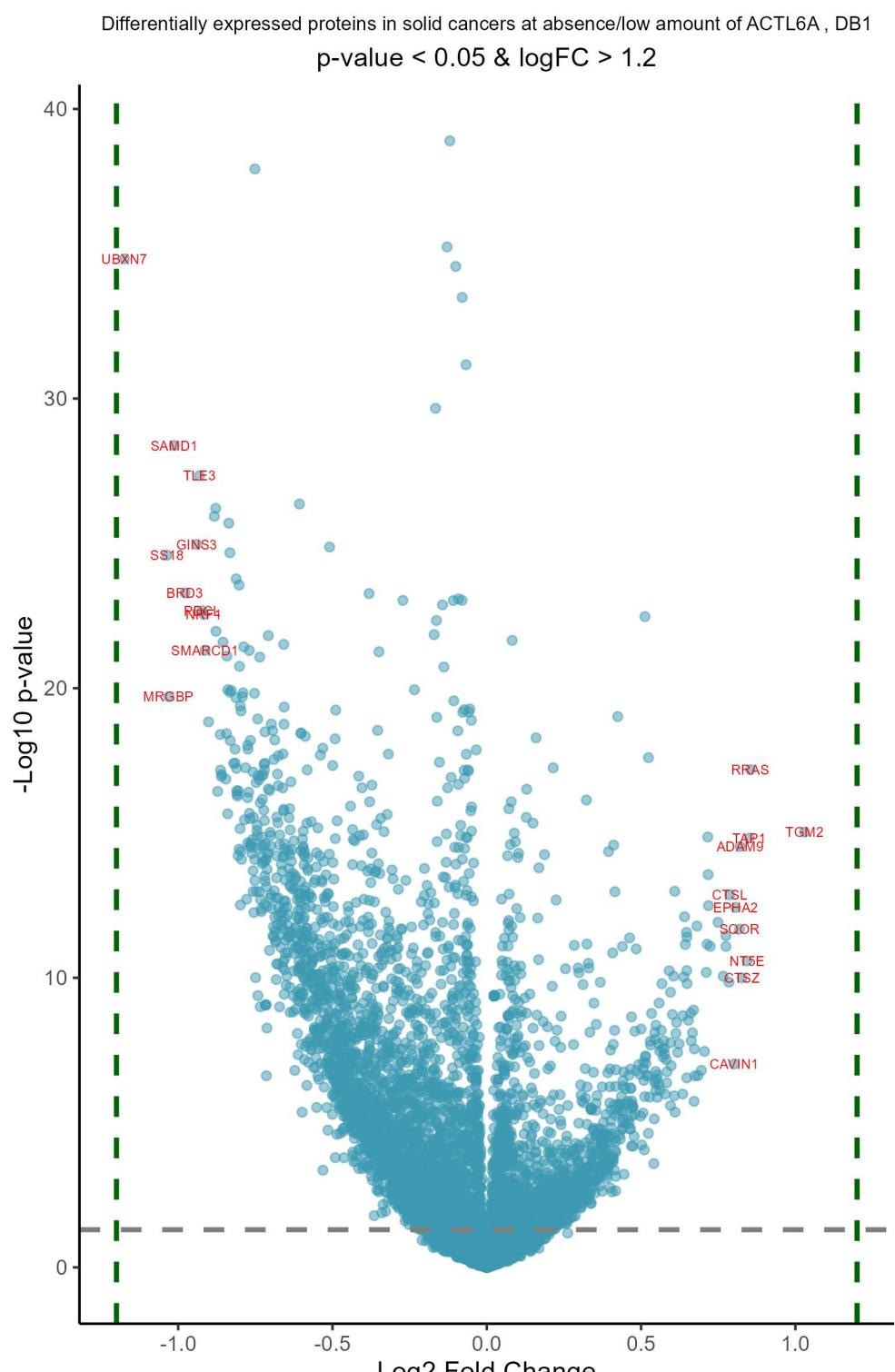


p-value < 0.05 & logFC > 1.2



Downregulated in blood cancers at low/absent ACTL6A Upregulated in blood cancers at low/absent ACTL6A

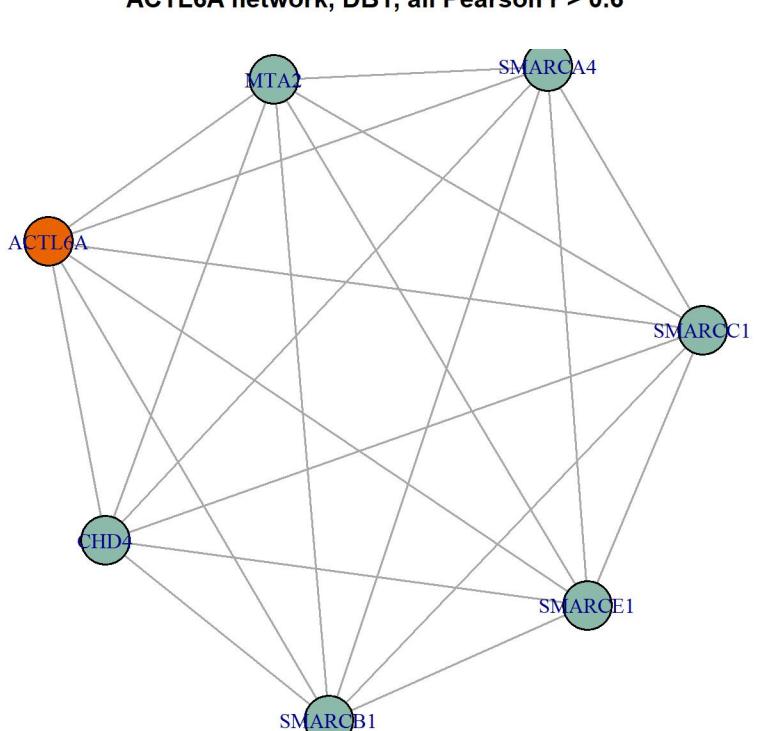
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.33	5.75e-08	HIRIP3	HIRA interacting protein 3	1.11	2.06e-03	CTSZ	cathepsin Z
-1.3	6.87e-07	LEF1	lymphoid enhancer binding factor 1	0.89	2.04e-03	TYMP	thymidine phosphorylase
-1.23	6.99e-05	LGALS3BP	galectin 3 binding protein	0.88	1.67e-02	LGALS3	galectin 3
-1.15	8.35e-06	PTK7	protein tyrosine kinase 7 (inactive)	0.87	1.10e-02	RPL22L1	ribosomal protein L22 like 1
-1.13	9.55e-06	MAZ	MYC associated zinc finger protein	0.85	1.82e-02	BASP1	brain abundant membrane attached si
-1.11	2.09e-06	NSD3	nuclear receptor binding SET domain	0.82	9.30e-05	ALDH1B1	aldehyde dehydrogenase 1 family mem
-1.1	3.15e-06	CCNK	cyclin K	0.81	1.44e-02	SQOR	sulfide quinone oxidoreductase
-1.09	4.15e-02	SPN	sialophorin	0.81	2.54e-03	DTD1	D-aminoacyl-tRNA deacylase 1
-1.07	1.03e-05	SMAD4	SMAD family member 4	0.78	2.10e-02	PLEK	pleckstrin
-1.07	1.85e-06	KAT8	lysine acetyltransferase 8	0.77	9.33e-03	JUNB	JunB proto-oncogene, AP-1 transcrip
-1.05	7.72e-04	SLBP	stem-loop binding protein	0.76	7.89e-03	ATP6V0A1	ATPase H ⁺ transporting V0 subunit a
-1.05	2.29e-05	ZAP70	zeta chain of T cell receptor assoc	0.74	3.26e-02	MVP	major vault protein
-1.03	7.33e-06	AAMDC	adipogenesis associated Mth938 doma	0.74	3.16e-02	STOM	stomatin
-1.03	4.48e-06	KMT2A	lysine methyltransferase 2A	0.74	1.05e-02	SAMHD1	SAM and HD domain containing deoxyn
-1.03	3.16e-05	LENG1	leukocyte receptor cluster member 1	0.73	3.20e-02	CA2	carbonic anhydrase 2
-1.02	7.33e-06	SMARCD1	SWI/SNF related, matrix associated,	0.73	1.73e-02	SYNGR2	synaptogyrin 2
-1.01	2.01e-04	DCAF16	DDB1 and CUL4 associated factor 16	0.73	4.15e-02	HLA-DQB1	major histocompatibility complex, c
-1	2.76e-04	FLI1	Fli-1 proto-oncogene, ETS transcrip	0.7	1.49e-03	BCS1L	BCS1 homolog, ubiquinol-cytochrome
-0.99	7.99e-05	CHEK1	checkpoint kinase 1	0.7	1.99e-02	IKBIP	IKBKB interacting protein
-0.98	3.27e-04	HDGFL3	HDGF like 3	0.68	8.54e-03	ASNS	asparagine synthetase (glutamine-hy
-0.98	7.96e-05	BRD2	bromodomain containing 2	0.66	1.62e-02	ARSB	arylsulfatase B
-0.97	2.69e-05	CASP2	caspase 2	0.63	1.52e-02	GOLM1	golgi membrane protein 1
-0.97	5.21e-05	MED20	mediator complex subunit 20	0.62	4.15e-02	NCEH1	neutral cholesterol ester hydrolase
-0.96	9.30e-04	ASF1A	anti-silencing function 1A histone	0.61	3.15e-02	PRKCD	protein kinase C delta
-0.96	3.94e-04	LZTFL1	leucine zipper transcription factor	0.61	2.37e-02	DPM1	dolichyl-phosphate mannosyltransfer
-0.95	1.64e-04	ZNF148	zinc finger protein 148	0.59	4.80e-02	NIBAN1	niban apoptosis regulator 1
-0.95	4.95e-05	BRD1	bromodomain containing 1	0.59	7.59e-02	HLA-DPA1	major histocompatibility complex, c
-0.94	1.95e-05	MAEA	macrophage erythroblast attacher, E	0.58	1.80e-01	LGALS1	galectin 1
-0.94	8.29e-07	C11orf54	chromosome 11 open reading frame 54	0.58	1.11e-01	PLP2	proteolipid protein 2



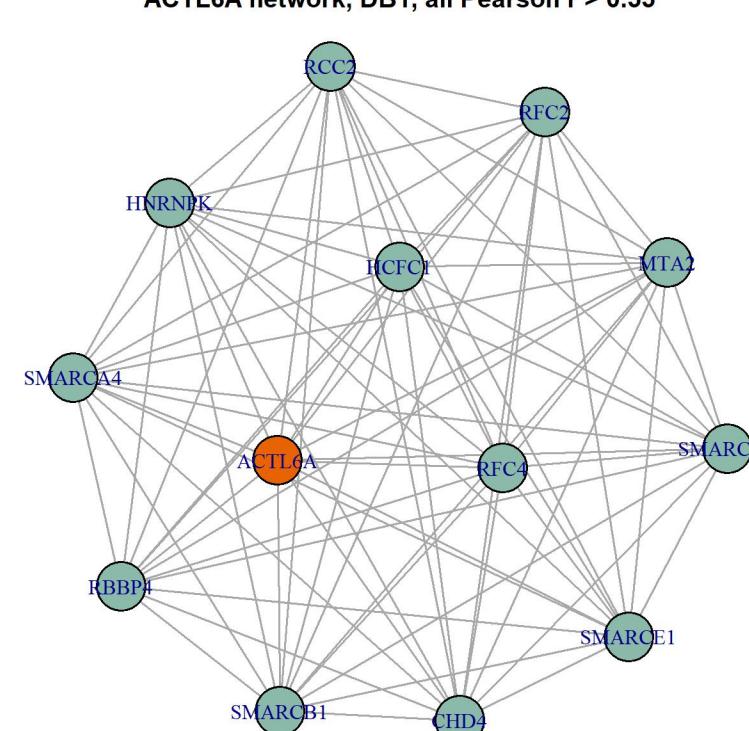
Downregulated in solid cancers at low/absent ACTL6A Upregulated in solid cancers at low/absent ACTL6A

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.17	1.98e-32	UBXN7	UBX domain protein 7	1.03	3.33e-14	TGM2	transglutaminase 2
-1.04	8.93e-23	SS18	SS18 subunit of BAF chromatin remod	0.85	4.04e-16	RRAS	RAS related
-1.03	2.42e-18	MRGBP	MRG domain binding protein	0.85	5.04e-14	TAP1	transporter 1, ATP binding cassette
-1.01	2.76e-26	SAMD1	sterile alpha motif domain containi	0.84	2.98e-10	NT5E	5'-nucleotidase ecto
-0.98	1.56e-21	BRD3	bromodomain containing 3	0.83	9.98e-10	CTSZ	cathepsin Z
-0.94	4.48e-23	GINS3	GINS complex subunit 3	0.82	8.92e-14	ADAM9	ADAM metallopeptidase domain 9
-0.93	2.77e-25	TLE3	TLE family member 3, transcriptiona	0.82	3.06e-11	CAVIN1	caveolae associated protein 1
-0.92	4.82e-21	PDCL	phosducin like	0.81	6.54e-12	EPHA2	EPH receptor A2
-0.92	6.27e-21	NRF1	nuclear respiratory factor 1	0.8	4.82e-07	CAVIN1	caveolae associated protein 1
-0.91	8.08e-20	SMARCD1	SWI/SNF related, matrix associated,	0.79	2.63e-12	CTSL	cathepsin L
-0.9	1.41e-17	BRD2	bromodomain containing 2	0.78	1.36e-09	S100A10	S100 calcium binding protein A10
-0.88	5.50e-24	DCAF7	DDB1 and CUL4 associated factor 7	0.78	5.01e-11	GPX8	glutathione peroxidase 8 (putative)
-0.88	3.15e-24	TRIM24	tripartite motif containing 24	0.78	1.06e-10	TAP2	transporter 2, ATP binding cassette
-0.88	2.19e-20	BPTF	bromodomain PHD finger transcriptio	0.77	8.80e-10	AXL	AXL receptor tyrosine kinase
-0.87	1.75e-15	DERPC	DERPC proline and glycine rich nucl	0.75	1.92e-11	NCEH1	neutral cholesterol ester hydrolase
-0.86	3.33e-17	POLE3	DNA polymerase epsilon 3, accessory	0.72	1.05e-10	RHOC	ras homolog family member C
-0.86	4.05e-16	CRMP1	collapsin response mediator protein	0.72	5.76e-12	FGF2	fibroblast growth factor 2
-0.86	6.11e-16	UBE2T	ubiquitin conjugating enzyme E2 T	0.72	6.28e-13	RETSAT	retinol saturase
-0.86	5.46e-16	C9orf78	chromosome 9 open reading frame 78	0.72	4.66e-14	RAB11FIP5	RAB11 family interacting protein 5
-0.85	4.62e-20	DPYSL5	dihydropyrimidinase like 5	0.71	9.12e-11	LACTB	lactamase beta
-0.85	7.37e-16	ZNF148	zinc finger protein 148	0.71	6.71e-10	UXS1	UDP-glucuronate decarboxylase 1
-0.84	3.18e-17	GABPA	GA binding protein transcription fa	0.71	1.91e-07	ICAM1	intercellular adhesion molecule 1
-0.84	1.21e-19	TLE5	TLE family member 5, transcriptiona	0.7	7.67e-07	GPRC5A	G protein-coupled receptor class C
-0.84	9.08e-15	PMF1	polyamine modulated factor 1	0.68	1.13e-06	AP2S1	adaptor related protein complex 2 s
-0.84	1.57e-18	DBR1	debranching RNA lariats 1	0.68	2.51e-11	GGCX	gamma-glutamyl carboxylase
-0.84	8.86e-24	MBD3	methyl-CpG binding domain protein 3	0.67	1.15e-06	ITGA3	integrin subunit alpha 3
-0.83	1.83e-18	PRIM1	DNA primase subunit 1	0.67	1.60e-07	NNMT	nicotinamide N-methyltransferase
-0.83	7.79e-23	TRIM33	tripartite motif containing 33	0.67	7.37e-06	CD44	CD44 molecule (Indian blood group)
-0.83	5.04e-17	PPP4R2	protein phosphatase 4 regulatory su	0.67	9.34e-09	CYBRD1	cytochrome b reductase 1

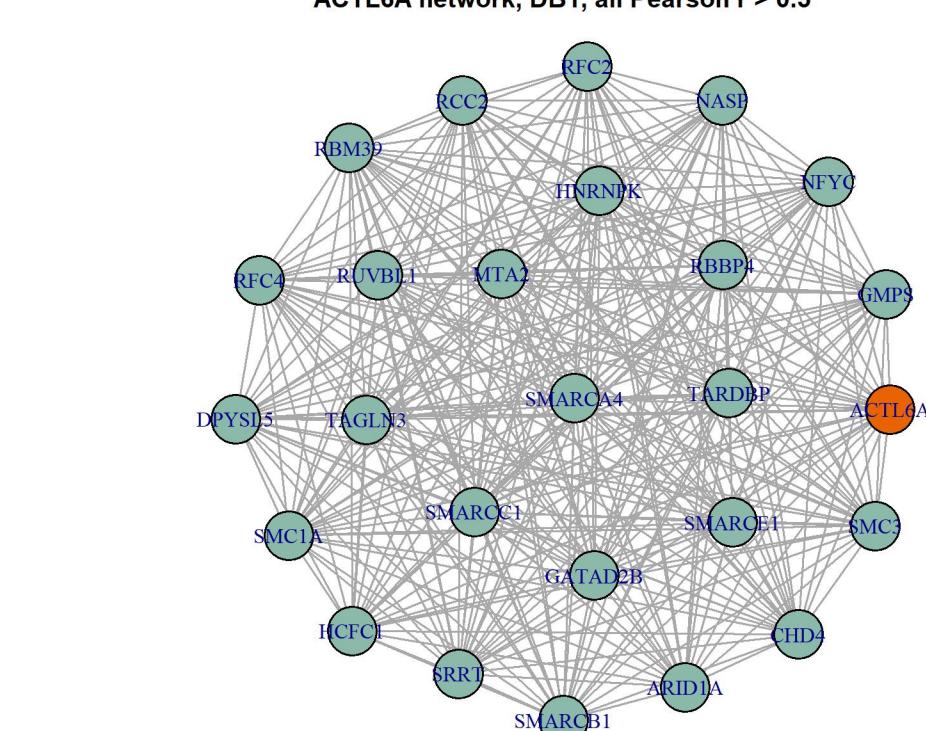
ACTL6A network, DB1, all Pearson r > 0.6

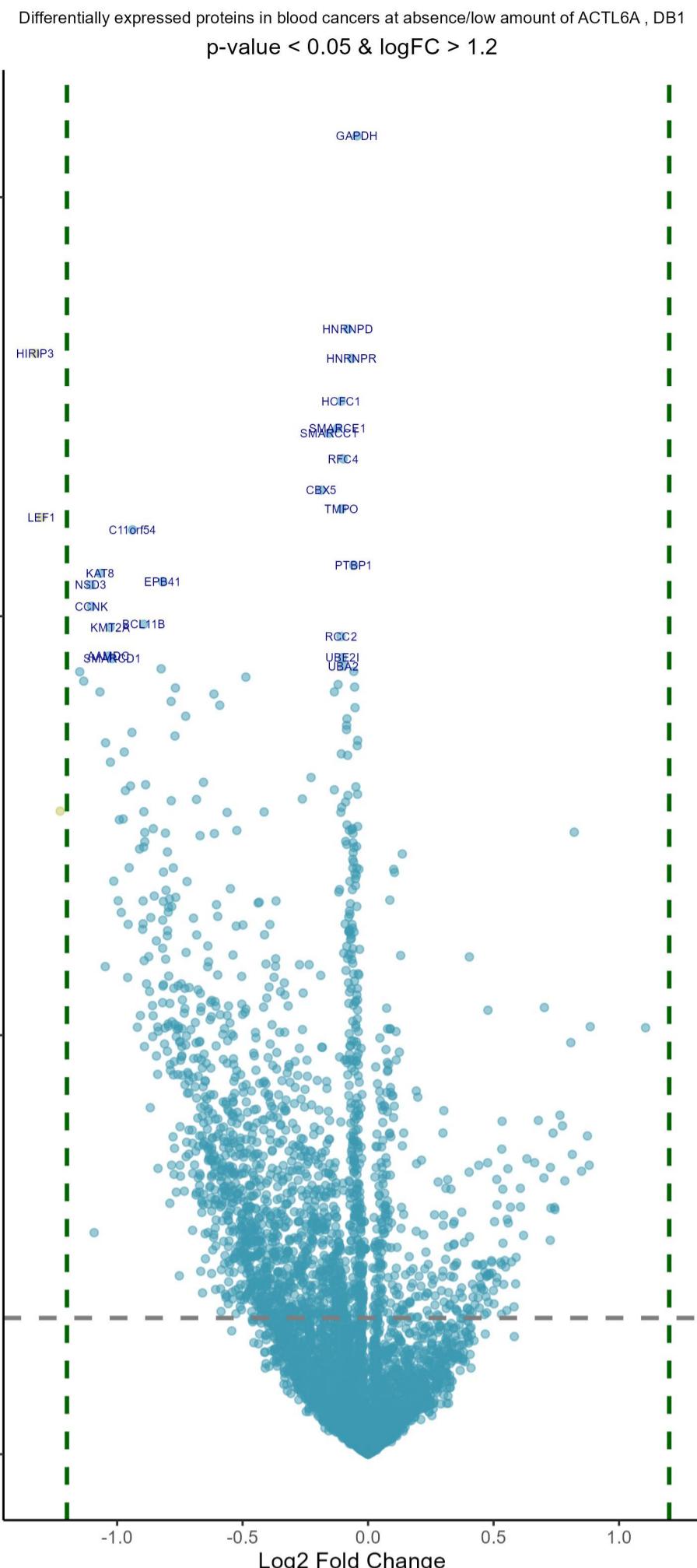


ACTL6A network, DB1, all Pearson r > 0.55

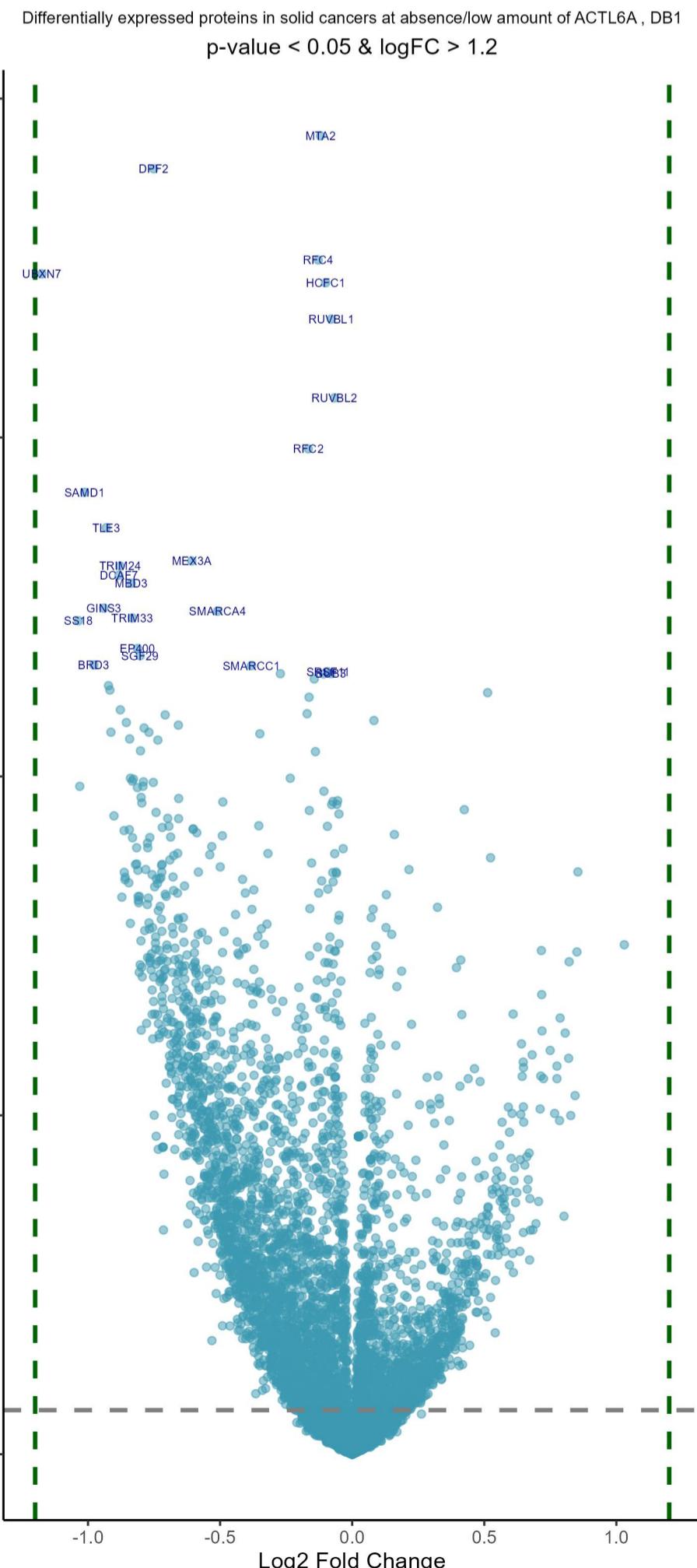


ACTL6A network, DB1, all Pearson r > 0.5



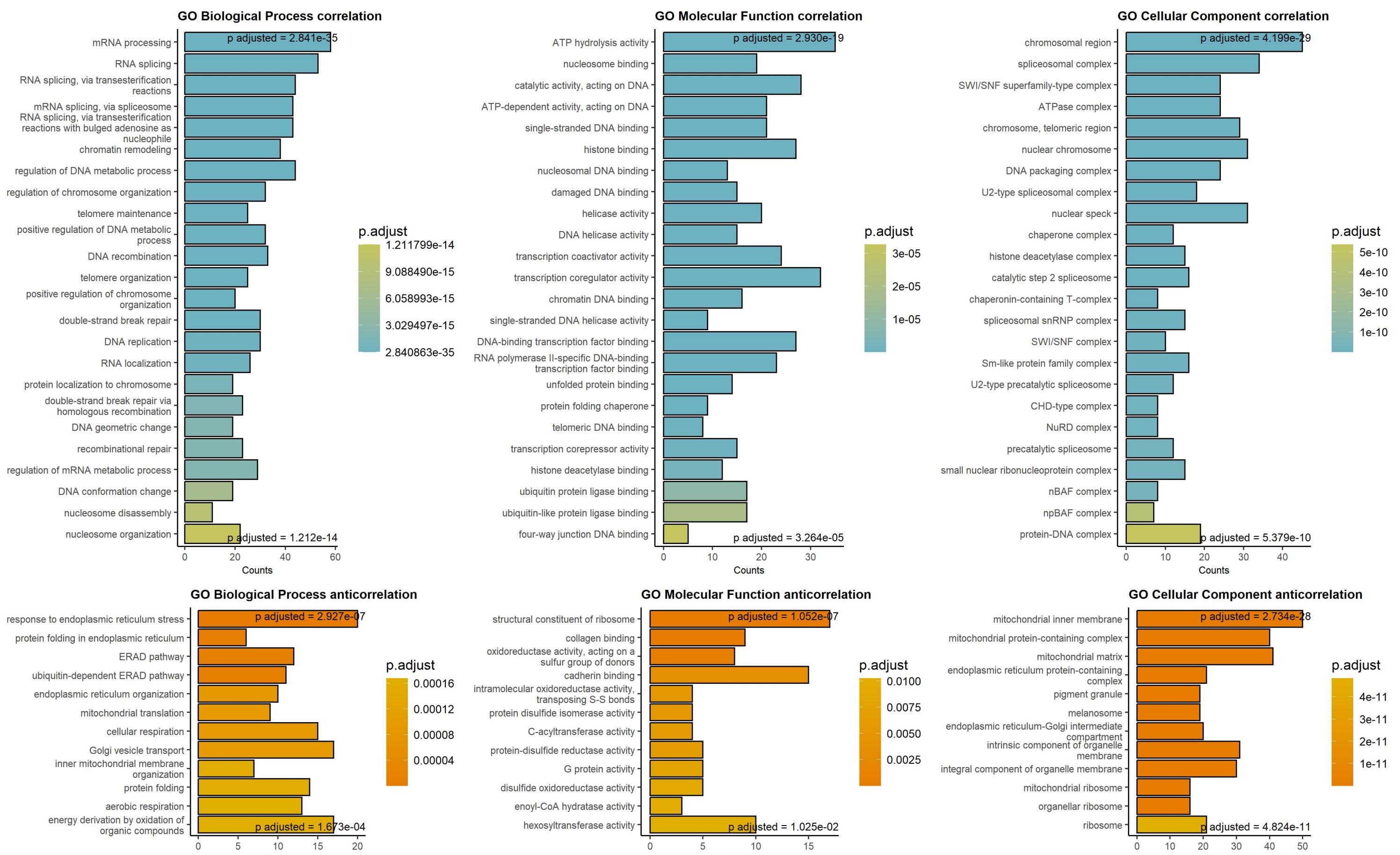


Sorted by p values!							
Downregulated in blood cancers at low/absent ACTL6A				Upregulated in blood cancers at low/absent ACTL6A			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.04	1.73e-09	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	0.82	9.30e-05	ALDH1B1	aldehyde dehydrogenase 1 family member 1
-0.08	5.75e-08	HNRNPD	heterogeneous nuclear ribonucleoprotein D	0.14	1.27e-04	HEATR1	HEAT repeat containing 1
-1.33	5.75e-08	HIRIP3	HIRA interacting protein 3	0.1	1.65e-04	CLPP	caseinolytic mitochondrial matrix peptidase, propeptidase
-0.07	5.75e-08	HNRNPR	heterogeneous nuclear ribonucleoprotein R	0.11	1.74e-04	PCD11	programmed cell death 11
-0.11	1.18e-07	HCFC1	host cell factor C1	0.09	2.76e-04	GTPBP4	GTP binding protein 4
-0.12	1.70e-07	SMARCE1	SWI/SNF related, matrix associated, chromatin-remodeling complex subunit E1	0.13	6.55e-04	NDUFA13	NADH:ubiquinone oxidoreductase subunit 13
-0.16	1.70e-07	SMARCC1	SWI/SNF related, matrix associated, chromatin-remodeling complex subunit C1	0.4	6.68e-04	CD274	CD274 molecule
-0.1	2.62e-07	RFC4	replication factor C subunit 4	0.7	1.49e-03	BCS1L	BCS1 homolog, ubiquinol-cytochrome c reductase subunit 1
-0.19	4.63e-07	CBX5	chromobox 5	0.07	1.50e-03	PHB2	prohibitin 2
-0.11	6.29e-07	TMPO	thymopoietin	0.48	1.55e-03	ECI1	enoyl-CoA delta isomerase 1
-1.3	6.87e-07	LEF1	lymphoid enhancer binding factor 1	0.89	2.04e-03	TYMP	thymidine phosphorylase
-0.94	8.29e-07	C11orf54	chromosome 11 open reading frame 54	1.11	2.06e-03	CTSZ	cathepsin Z
-0.06	1.67e-06	PTBP1	polypyrimidine tract binding protein 1	0.09	2.06e-03	MRPL13	mitochondrial ribosomal protein L13
-1.07	1.85e-06	KAT8	lysine acetyltransferase 8	0.08	2.06e-03	RRP12	ribosomal RNA processing 12 homolog
-0.82	2.08e-06	EPB41	erythrocyte membrane protein band 4	0.09	2.07e-03	MRPL19	mitochondrial ribosomal protein L19
-1.11	2.09e-06	NSD3	nuclear receptor binding SET domain	0.11	2.14e-03	OGDH	oxoglutarate dehydrogenase
-1.1	3.15e-06	CCNK	cyclin K	0.05	2.36e-03	RSL1D1	ribosomal L1 domain containing 1
-0.89	4.41e-06	BCL11B	BAF chromatin remodeling complex subunit 11B	0.81	2.54e-03	DTD1	D-aminoacyl-tRNA deacylase 1
-1.03	4.48e-06	KMT2A	lysine methyltransferase 2A	0.07	2.82e-03	LAMTOR1	late endosomal/lysosomal adaptor, MAP62 and XPO1 interactor
-0.11	5.18e-06	RCC2	regulator of chromosome condensin complex subunit 2	0.12	2.97e-03	PPIF	peptidylprolyl isomerase F
-1.03	7.33e-06	AAMDC	adipogenesis associated Mfh938 domain containing	0.11	3.31e-03	RPL13A	ribosomal protein L13a
-0.1	7.33e-06	UBE2I	ubiquitin conjugating enzyme E2 I	0.08	3.42e-03	SLC25A3	solute carrier family 25 member 3
-1.02	7.33e-06	SMARCD1	SWI/SNF related, matrix associated, chromatin-remodeling complex subunit D1	0.08	3.50e-03	HADHA	hydroxyacyl-CoA dehydrogenase trifunctional protein
-0.1	8.29e-06	UBA2	ubiquitin like modifier activating enzyme 2	0.03	3.67e-03	RPS7	ribosomal protein S7
-0.82	8.35e-06	PHF3	PHD finger protein 3	0.08	3.87e-03	HADHB	hydroxyacyl-CoA dehydrogenase trifunctional protein B
-0.06	8.35e-06	NONO	non-POU domain containing octamer b	0.08	3.92e-03	HSPA5	heat shock protein family A (Hsp70) member 5
-1.15	8.35e-06	PTK7	protein tyrosine kinase 7 (inactive)	0.04	4.79e-03	RPL6	ribosomal protein L6
-0.49	9.06e-06	KANSL3	KAT8 regulatory NSL complex subunit	0.09	5.09e-03	UTP4	UTP4 small subunit processome component
-1.13	9.55e-06	MAZ	MYC associated zinc finger protein	0.19	5.44e-03	MAN2B1	mannosidase alpha class 2B member 1
-0.12	9.95e-06	RBBP4	RB binding protein 4, chromatin remodelling complex subunit	0.05	5.48e-03	RPL7	ribosomal protein L7
-0.05	1.01e-05	TARDBP	TAR DNA binding protein	0.09	5.57e-03	IPO4	importin 4
-0.77	1.01e-05	CBX2	chromobox 2	0.07	5.57e-03	AIFM1	apoptosis inducing factor mitochondrial
-0.13	1.03e-05	NUMA1	nuclear mitotic apparatus protein 1	0.1	5.82e-03	LMAN2	lectin, mannose binding 2
-1.07	1.03e-05	SMAD4	SMAD family member 4	0.09	5.82e-03	PNP	purine nucleoside phosphorylase
-0.61	1.05e-05	DCAF7	DDB1 and CUL4 associated factor 7	0.2	5.96e-03	NOL6	nucleolar protein 6
-0.78	1.20e-05	PIN4	peptidylprolyl cis/trans isomerase, NIMA-interacting 4	0.05	6.33e-03	RPS16	ribosomal protein S16
-0.59	1.27e-05	UBXN7	UBX domain protein 7	0.06	6.81e-03	TRAP1	TNF receptor associated protein 1
-0.05	1.31e-05	CPSF6	cleavage and polyadenylation specific 6	0.1	6.90e-03	CYC1	cytochrome c1
-0.73	1.50e-05	ORICH1	glutamine rich 1	0.05	6.90e-03	PDI 27	ribosomal protein L27

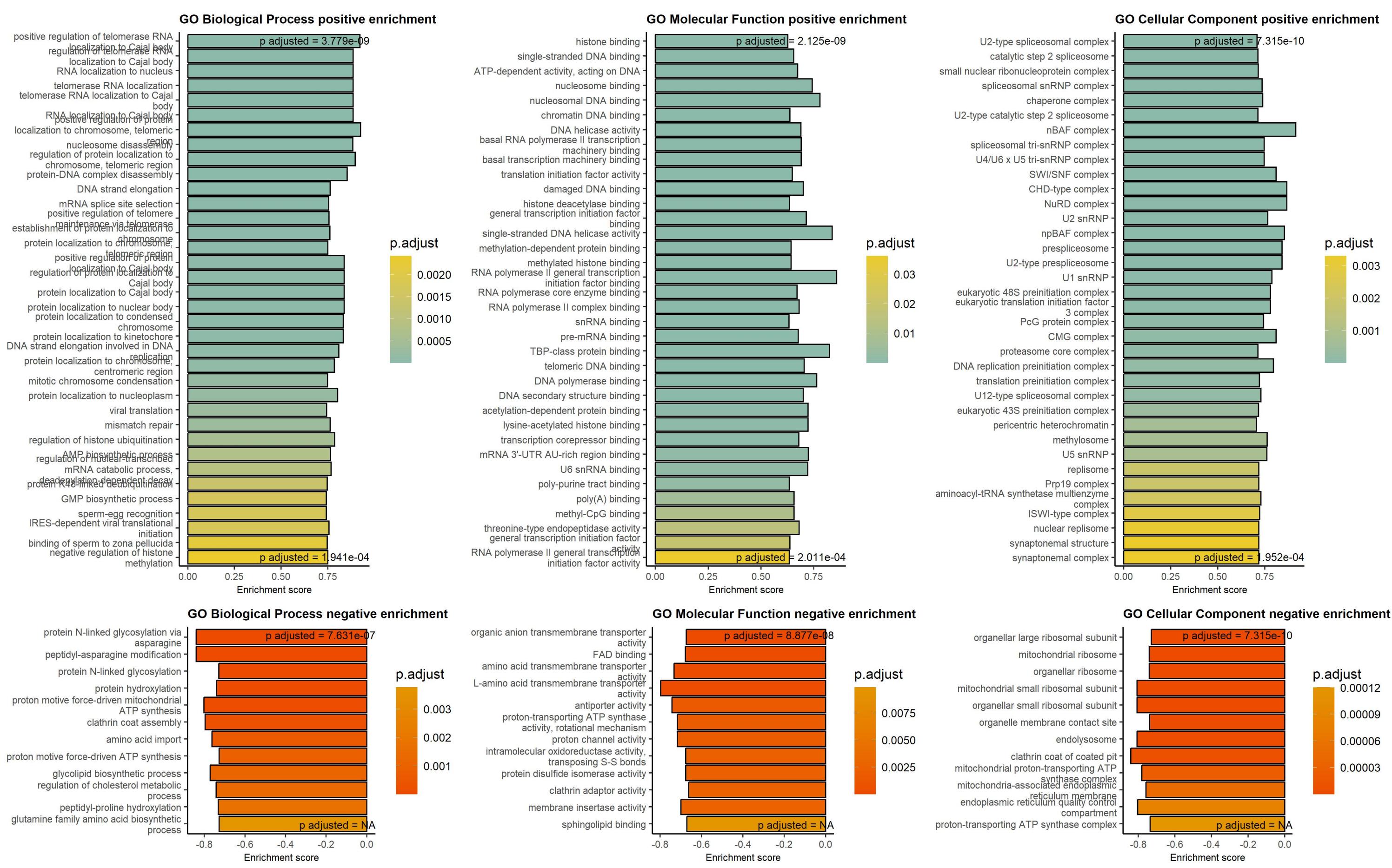


Sorted by p values!							
Downregulated in solid cancers at low/absent ACTL6A				Upregulated in solid cancers at low/absent ACTL6A			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.12	4.20e-36	MTA2	metastasis associated 1 family memb	0.51	7.25e-21	MYO1C	myosin IC
-0.75	2.62e-35	DPF2	double PHD fingers 2	0.08	4.14e-20	RAB1A	RAB1A, member RAS oncogene family
-0.13	9.61e-33	RFC4	replication factor C subunit 4	0.42	9.79e-18	GSTK1	glutathione S-transferase kappa 1
-1.17	1.98e-32	UBXN7	UBX domain protein 7	0.16	4.26e-17	ITGB1	integrin subunit beta 1
-0.1	3.02e-32	HCFC1	host cell factor C1	0.52	1.74e-16	PON2	paraoxonase 2
-0.08	3.05e-31	RUVBL1	RuvB like AAA ATPase 1	0.22	3.56e-16	PLEC	plectin
-0.07	5.61e-29	RUVBL2	RuvB like AAA ATPase 2	0.85	4.04e-16	RRAS	RAS related
-0.17	1.60e-27	RFC2	replication factor C subunit 2	0.13	1.52e-15	ACADVL	acyl-CoA dehydrogenase very long ch
-1.01	2.76e-26	SAMD1	sterile alpha motif domain containi	0.32	3.33e-15	SUCLG2	succinate-CoA ligase GDP-forming su
-0.93	2.77e-25	TLE3	TLE family member 3, transcriptiona	0.08	3.75e-15	HADHA	hydroxyacyl-CoA dehydrogenase trifu
-0.61	2.43e-24	MEX3A	mex-3 RNA binding family member A	0.07	6.34e-15	VDAC1	voltage dependent anion channel 1
-0.88	3.15e-24	TRIM24	tripartite motif containing 24	0.13	1.18e-14	PICALM	phosphatidylinositol binding clathr
-0.88	5.50e-24	DCAF7	DDB1 and CUL4 associated factor 7	0.15	1.76e-14	LMNA	lamin A/C
-0.84	8.86e-24	MBD3	methyl-CpG binding domain protein 3	1.03	3.33e-14	TGM2	transglutaminase 2
-0.94	4.48e-23	GINS3	GINS complex subunit 3	0.09	3.59e-14	PGRMC2	progesterone receptor membrane comp
-0.51	5.21e-23	SMARCA4	SWI/SNF related, matrix associated,	0.72	4.66e-14	RAB11FIP5	RAB11 family interacting protein 5
-0.83	7.79e-23	TRIM33	tripartite motif containing 33	0.85	5.04e-14	TAP1	transporter 1, ATP binding cassette
-1.04	8.93e-23	SS18	SS18 subunit of BAF chromatin remod	0.09	6.44e-14	SSR4	signal sequence receptor subunit 4
-0.81	5.58e-22	EP400	E1A binding protein p400	0.08	7.92e-14	HADHB	hydroxyacyl-CoA dehydrogenase trifu
-0.8	8.73e-22	SGF29	SAGA complex associated factor 29	0.41	8.13e-14	RALB	RAS like proto-oncogene B
-0.98	1.56e-21	BRD3	bromodomain containing 3	0.82	8.92e-14	ADAM9	ADAM metallopeptidase domain 9
-0.38	1.56e-21	SMARCC1	SWI/SNF related, matrix associated,	0.39	1.25e-13	ITGAV	integrin subunit alpha V
-0.09	2.28e-21	SRSF11	serine and arginine rich splicing f	0.1	1.41e-13	RPN2	ribophorin II
-0.08	2.33e-21	BUB3	BUB3 mitotic checkpoint protein	0.19	1.52e-13	AHNAK	AHNAK nucleoprotein
-0.27	2.33e-21	RCC2	regulator of chromosome condensatio	0.07	1.65e-13	P4HB	prolyl 4-hydroxylase subunit beta
-0.11	2.33e-21	CHD4	chromodomain helicase DNA binding p	0.1	1.85e-13	AP2A1	adaptor related protein complex 2 s
-0.14	3.16e-21	GMPS	guanine monophosphate synthase	0.17	3.86e-13	HIBADH	3-hydroxyisobutyrate dehydrogenase
-0.92	4.82e-21	PDCL	phosducin like	0.72	6.28e-13	RETSAT	retinol saturase
-0.92	6.27e-21	NRF1	nuclear respiratory factor 1	0.61	2.09e-12	UTRN	utrophin
-0.16	9.57e-21	NASP	nuclear autoantigenic sperm protein	0.42	2.15e-12	ACOT9	acyl-CoA thioesterase 9
-0.88	2.19e-20	BPTF	bromodomain PHD finger transcriptio	0.07	2.53e-12	AP2B1	adaptor related protein complex 2 s
-0.17	2.76e-20	SMARCE1	SWI/SNF related, matrix associated,	0.79	2.63e-12	CTSL	cathepsin L
-0.71	2.91e-20	ZMYM2	zinc finger MYM-type containing 2	0.05	3.62e-12	CLTC	clathrin heavy chain
-0.85	4.62e-20	DPYSL5	dihydropyrimidinase like 5	0.22	3.82e-12	HEXB	hexosaminidase subunit beta
-0.66	5.37e-20	PBRM1	polybromo 1	0.72	5.76e-12	FGF2	fibroblast growth factor 2
-0.79	6.35e-20	SUGP1	SURP and G-patch domain containing	0.81	6.54e-12	EPHA2	EPH receptor A2
-0.91	8.08e-20	SMARCD1	SWI/SNF related, matrix associated,	0.1	7.09e-12	ESYT1	extended synaptotagmin 1
-0.77	8.08e-20	YJU2	YJU2 splicing factor homolog	0.64	1.29e-11	PNPLA6	patatin like phospholipase domain c

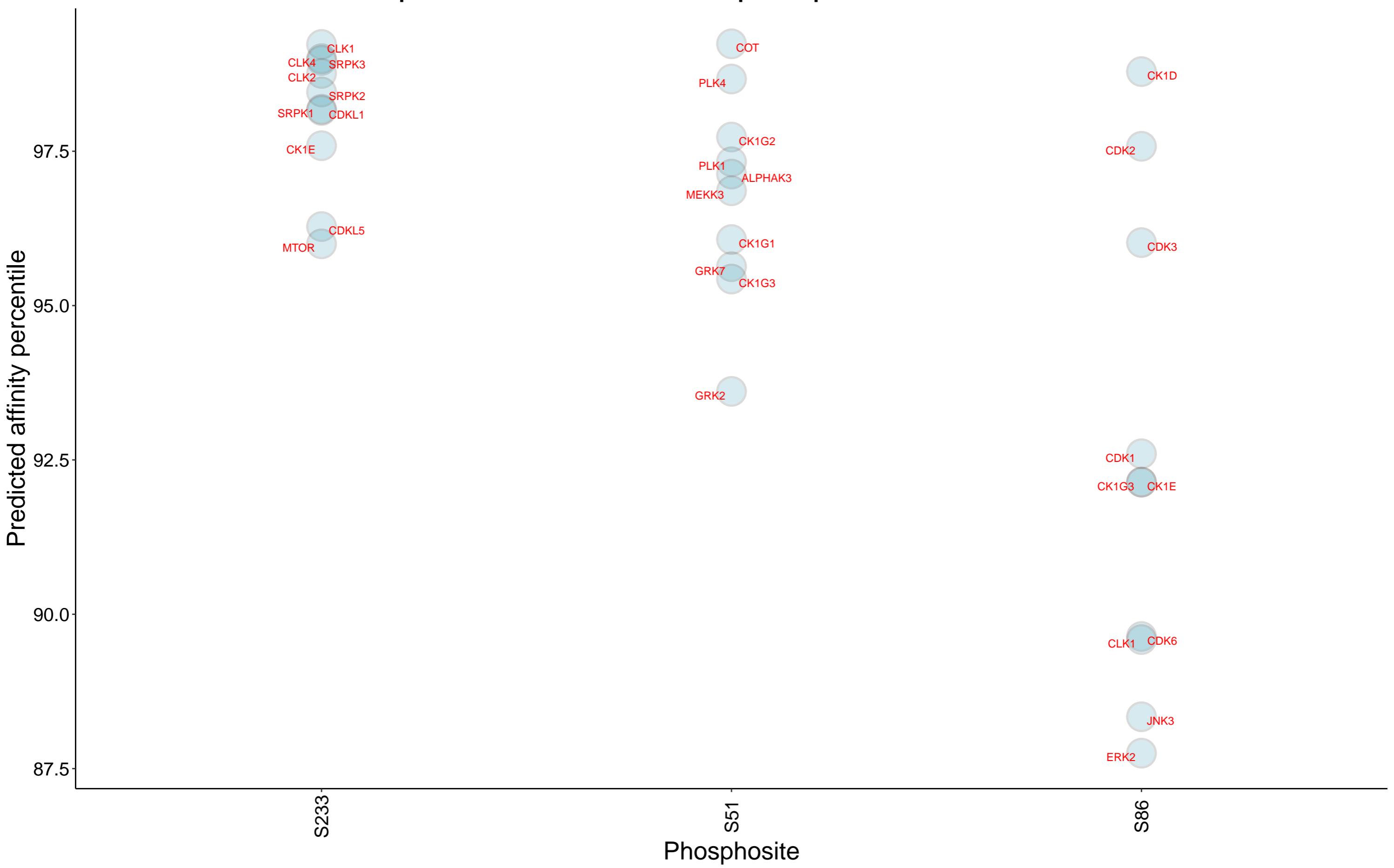
Top 250 correlation coefficients overrepresentation, ACTL6A protein, DB1



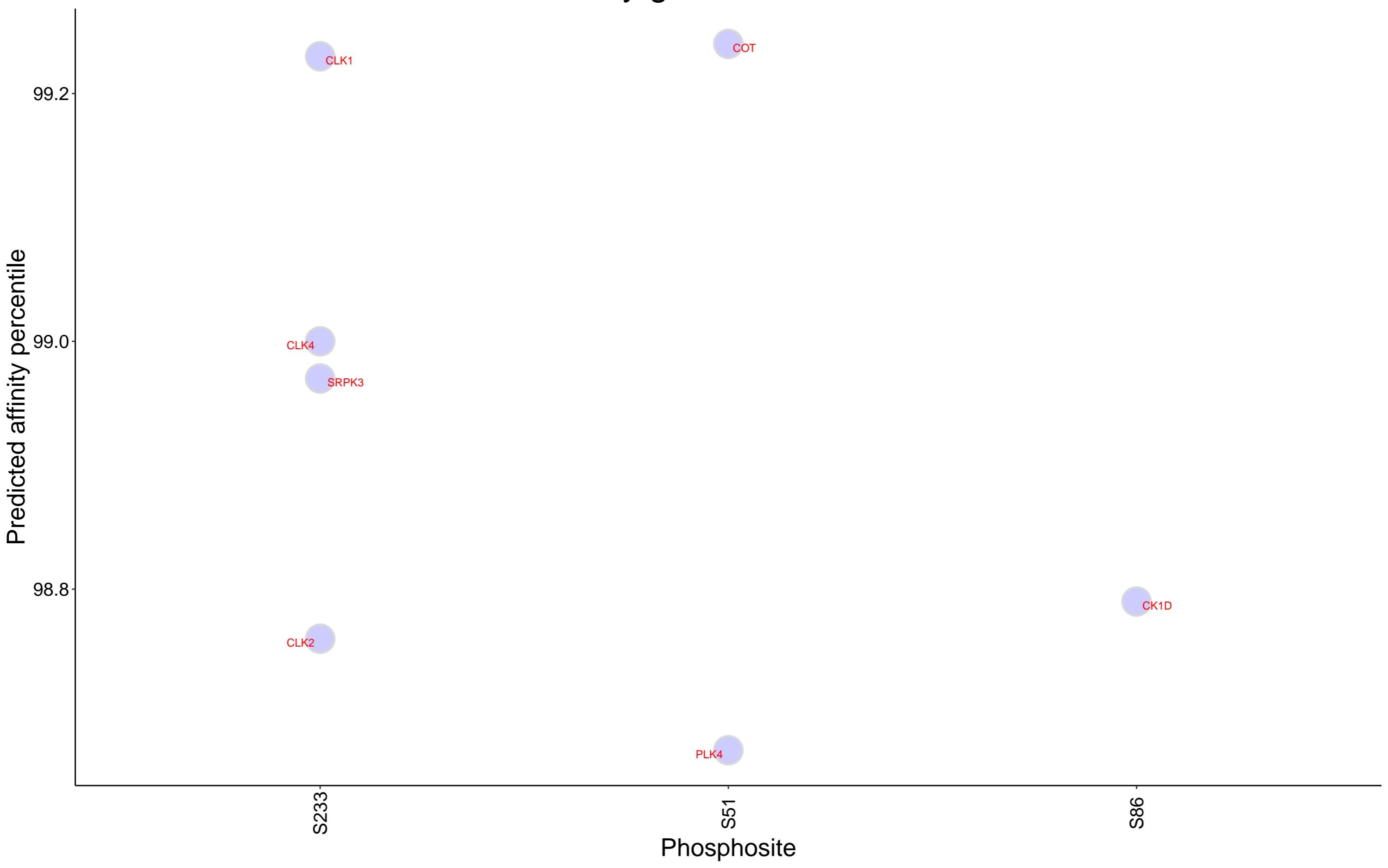
Gene Set Enrichment analysis on protein correlation coefficients, ACTL6A protein, DB1



Top 10 kinases for each phosphosite in ACTL6A



Kinases with affinity greater than 98.5% to ACTL6A



Top 15 positive correlation coefficients for ACTL6A protein by tissue, DB1

Beware of false positives in tissues with small number of samples

