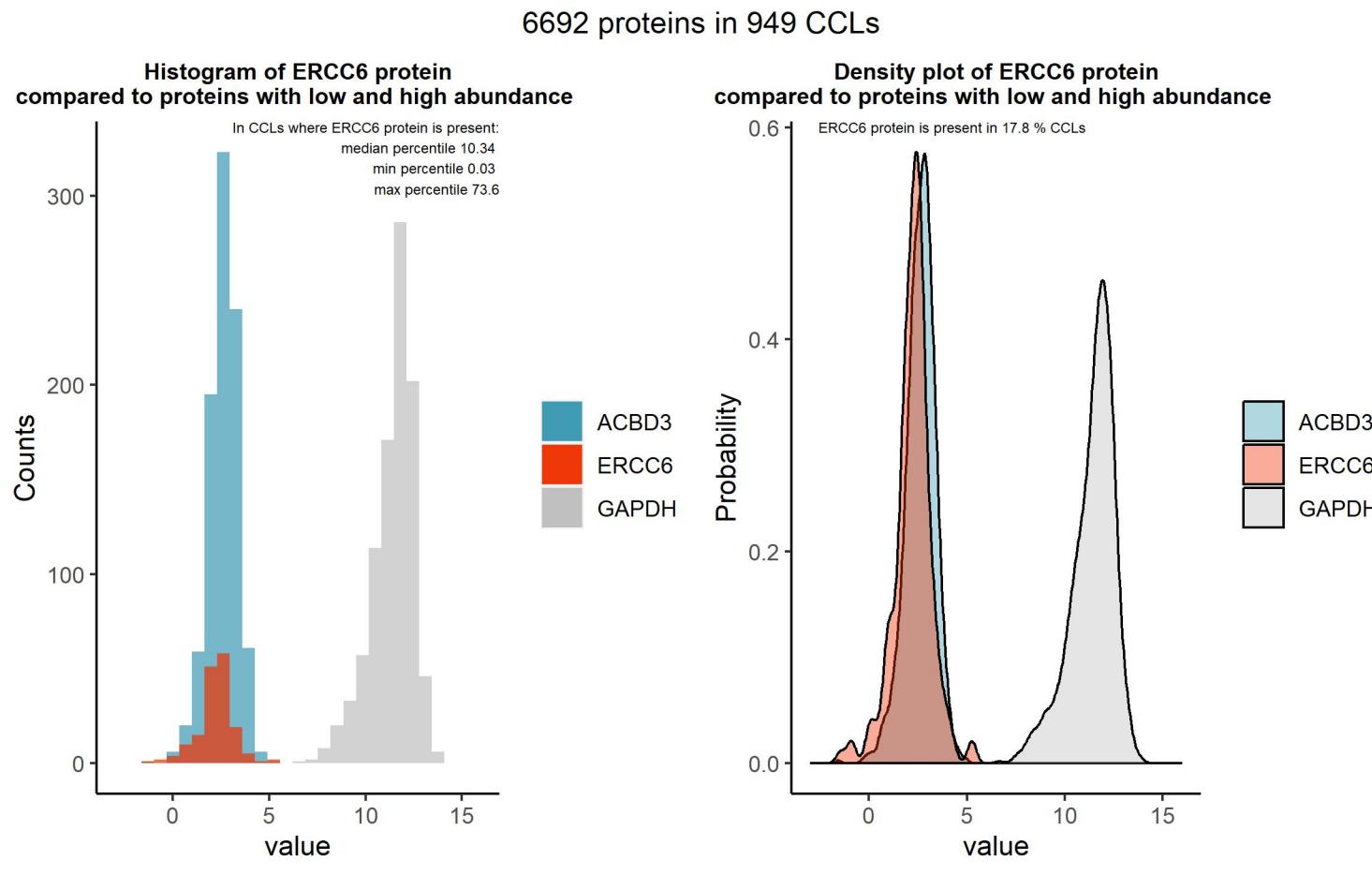


ERCC6

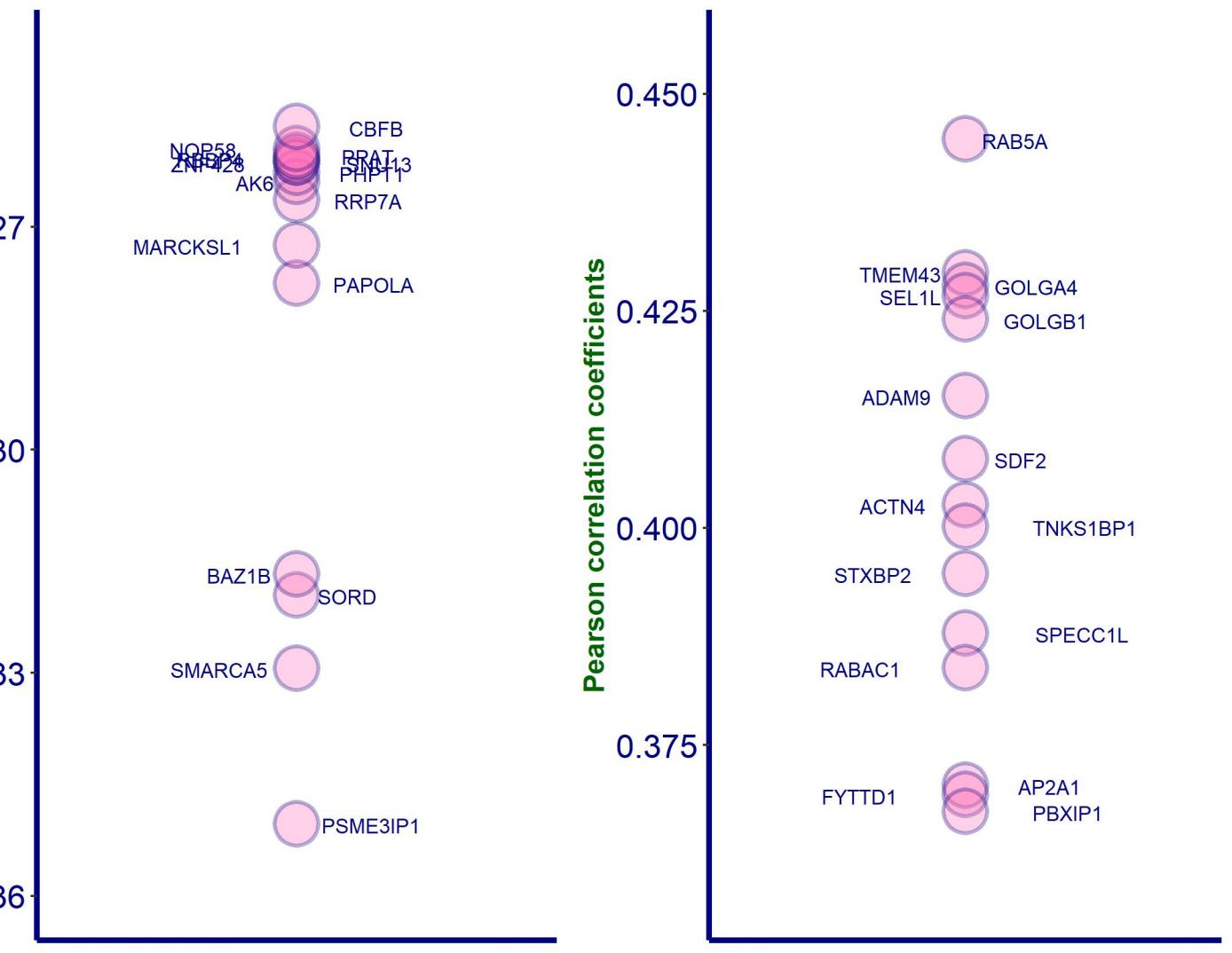
Protein name: ERCC6 ; UNIPROT: Q03468 ; Gene name: ERCC excision repair 6, chromatin remodeling factor

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

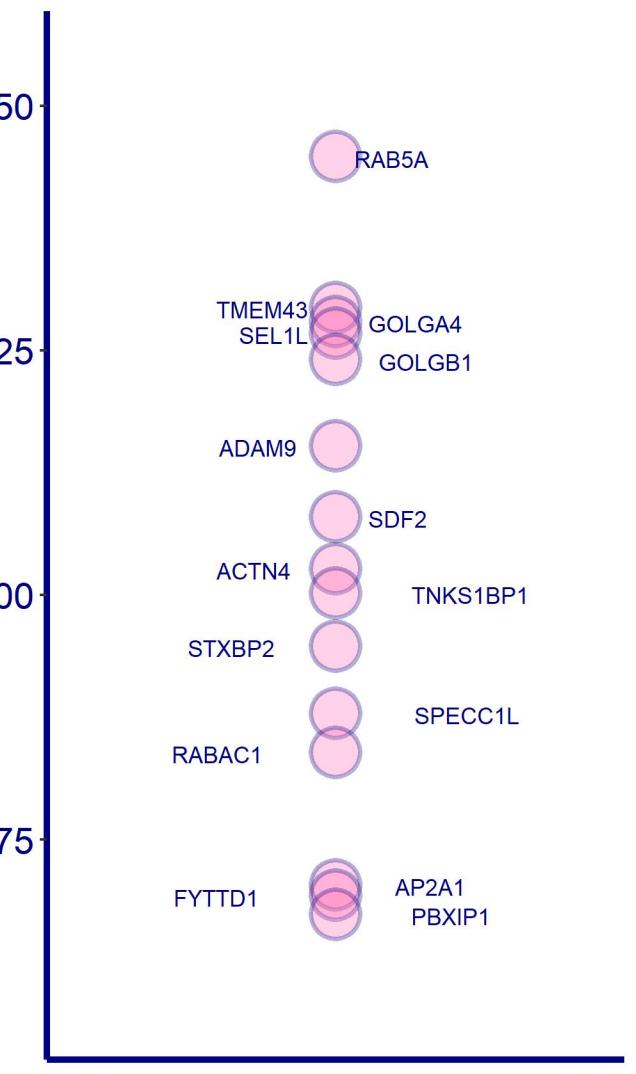
Sanger Institute Protein Database 1 (DB1), protein presence is certain



Top negative correlations of ERCC6 protein, DB1

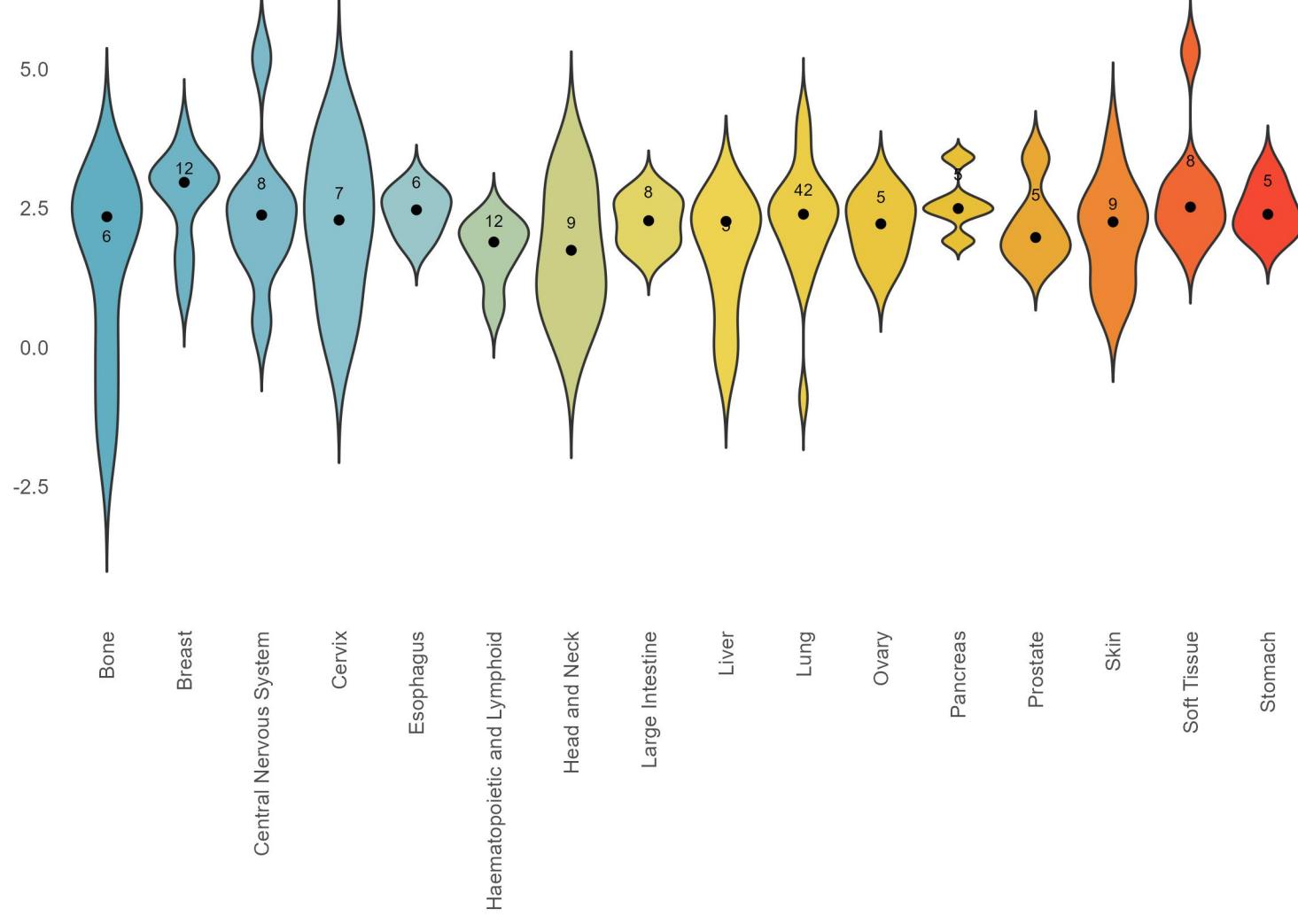


Top positive correlations of ERCC6 protein, DB1



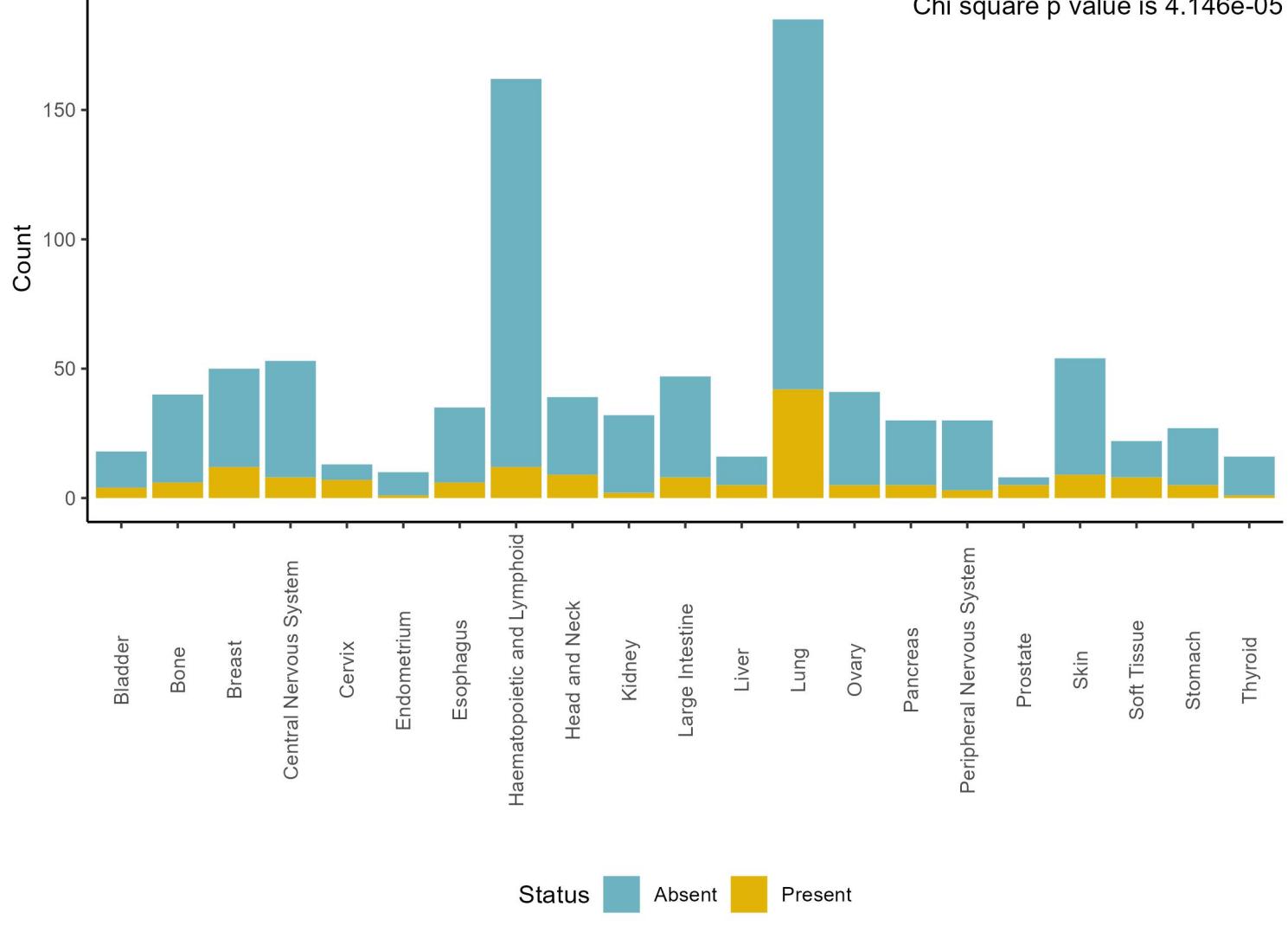
Amount of ERCC6 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 3.649e-01



Present and absent ERCC6 protein counts by tissue, DB1

Chi square p value is 4.146e-05

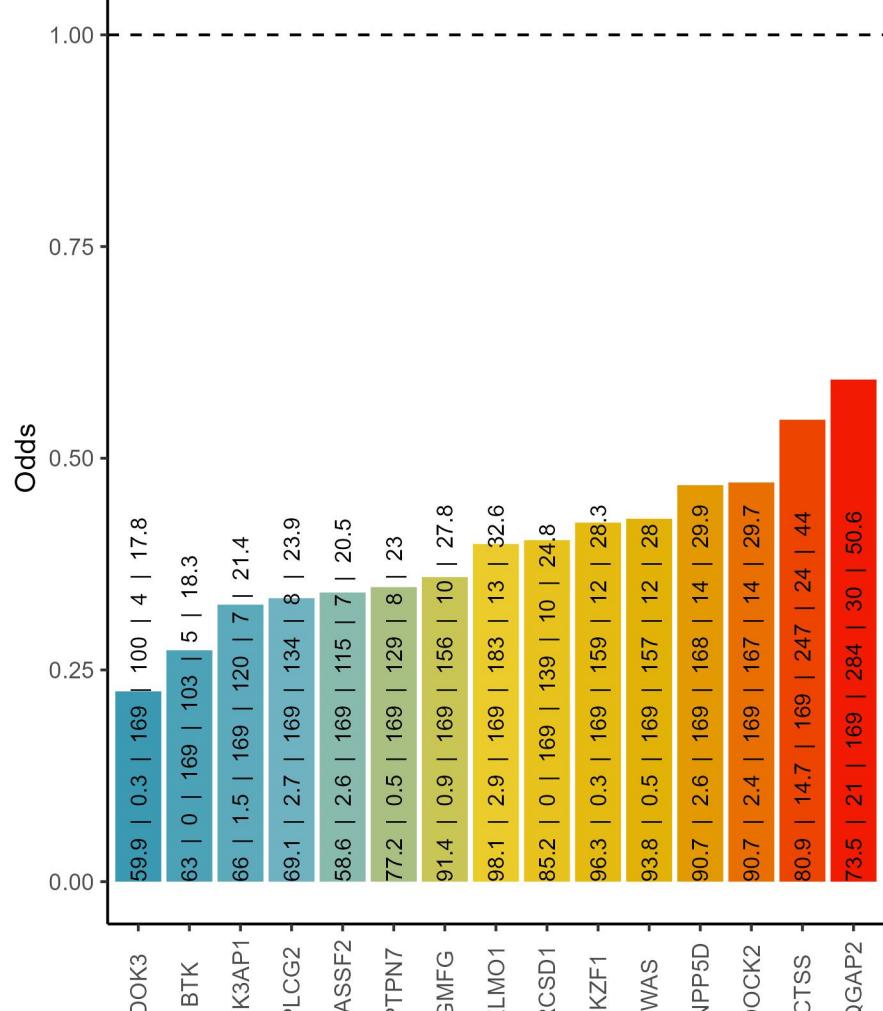


Cooccurrence with ERCC6 protein, DB1

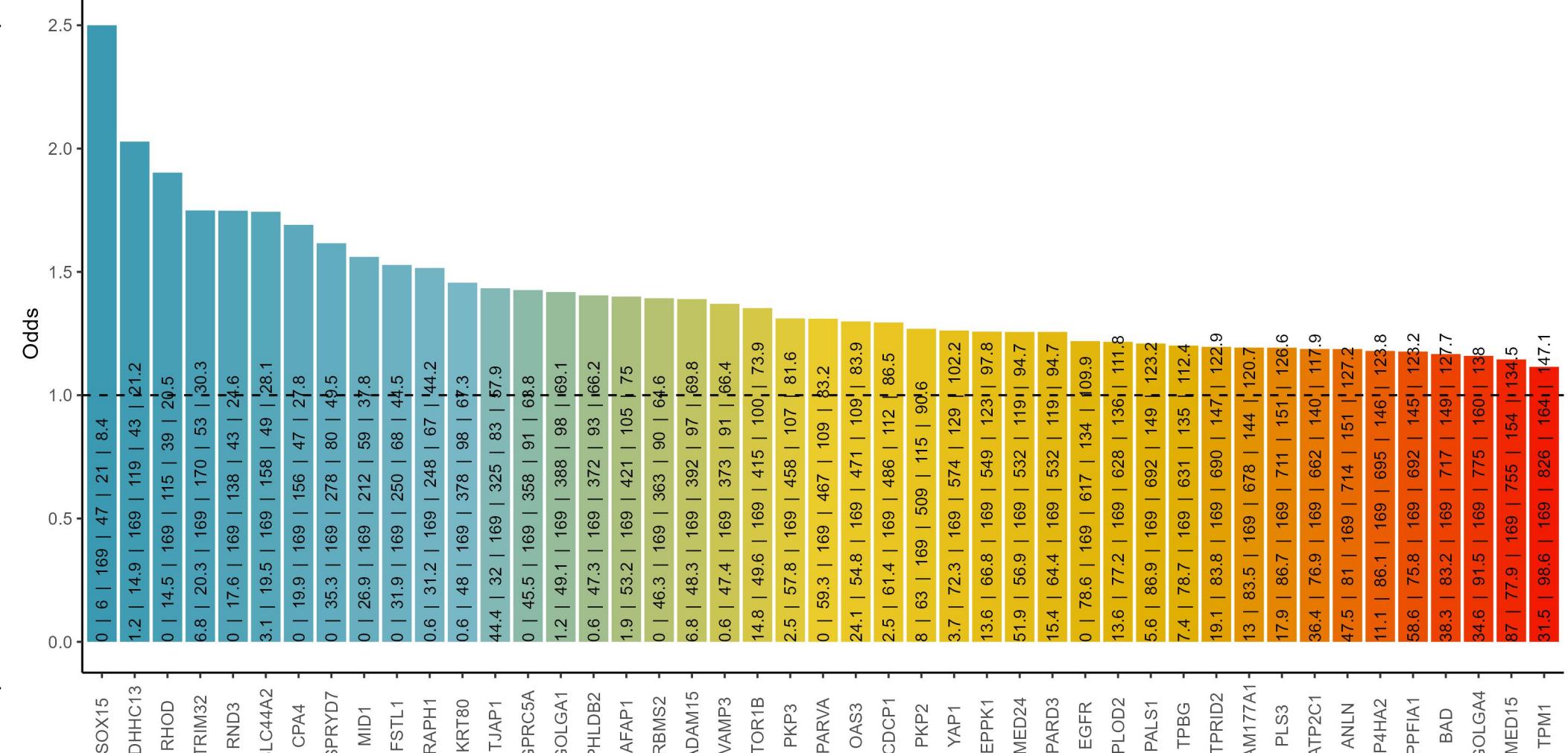
% of ERCC6 in blood cancers: 7.4 ; % of ERCC6 in solid cancers: 19.9

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ERCC6 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

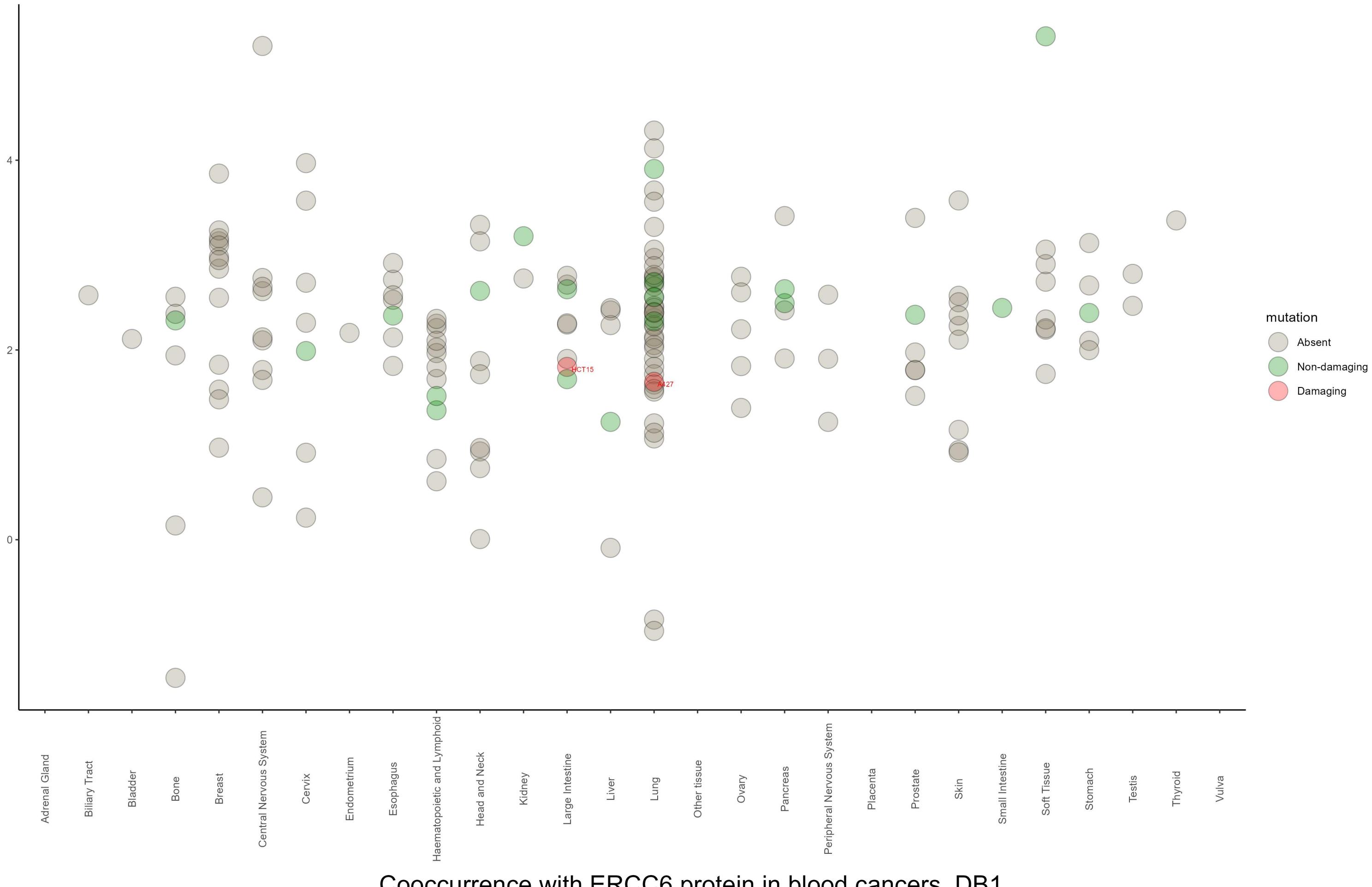
Negative cooccurrence



Positive cooccurrence

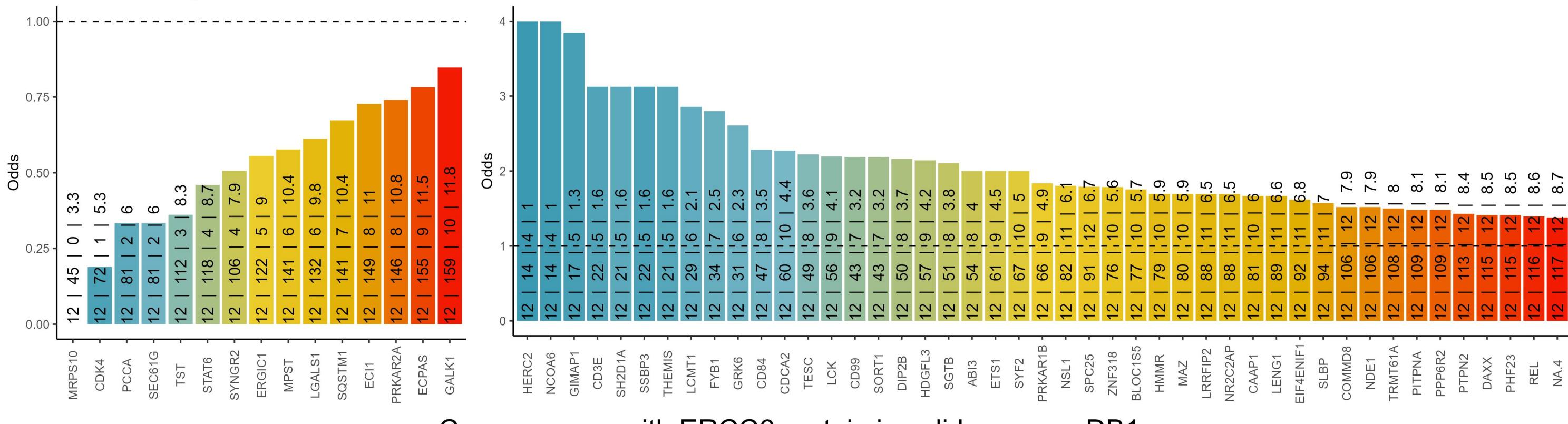


Amount of ERCC6 protein and mutation status by tissue, DB1



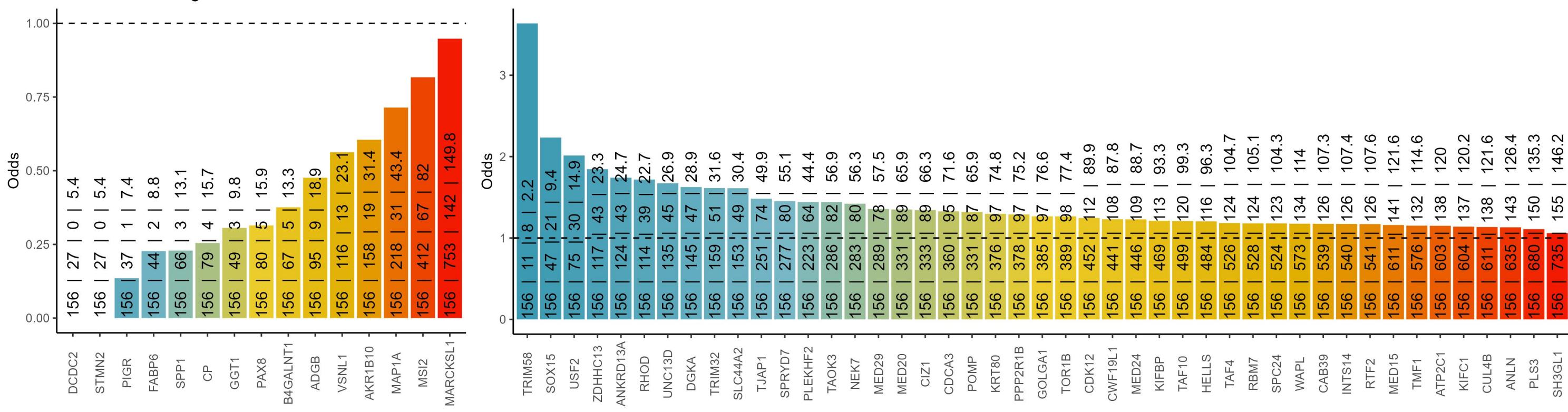
Cooccurrence with ERCC6 protein in blood cancers, DB1

The text in the bars: incidence of ERCC6 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

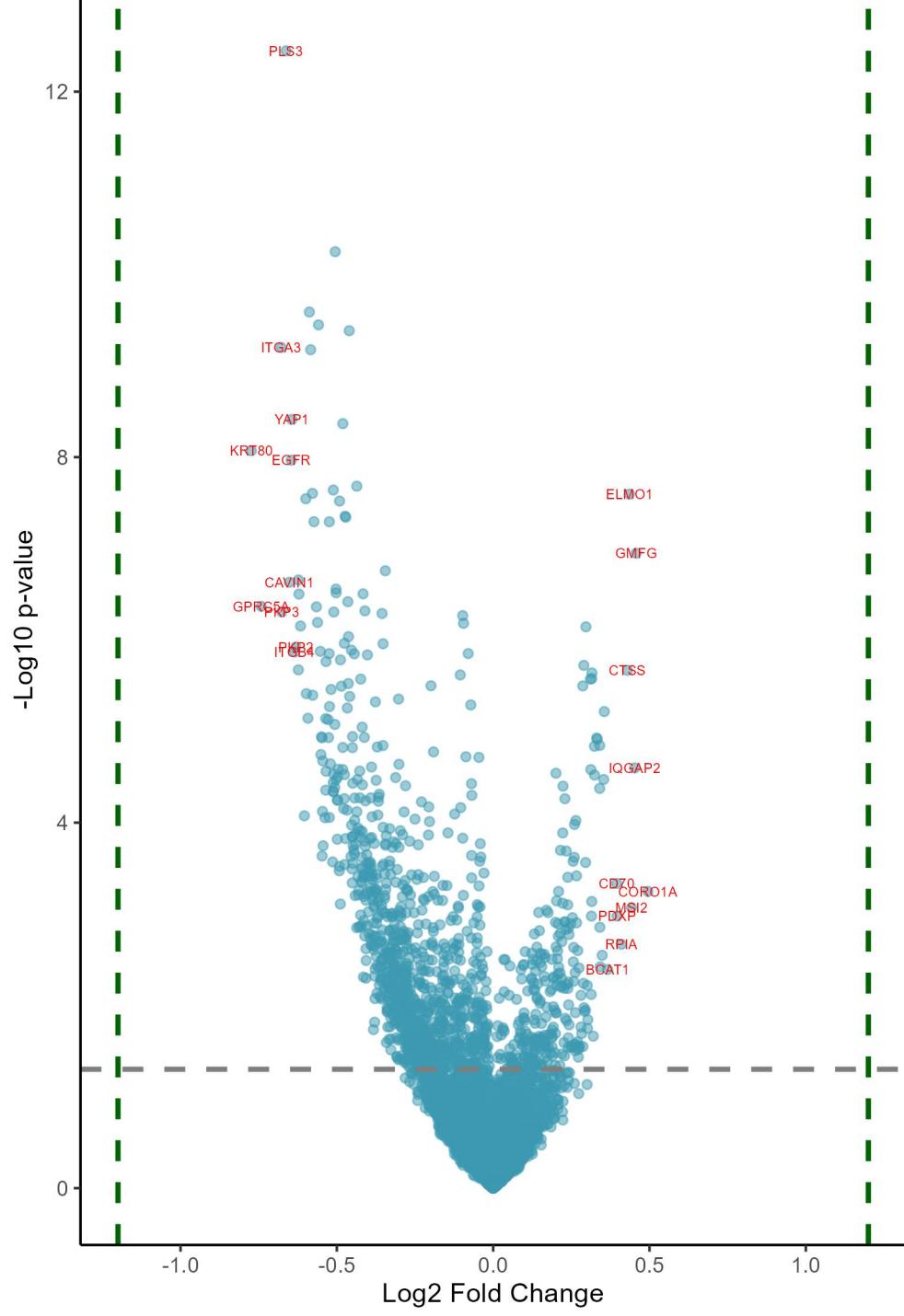


Cooccurrence with ERCC6 protein in solid cancers, DB1

The text in the bars: incidence of ERCC6 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



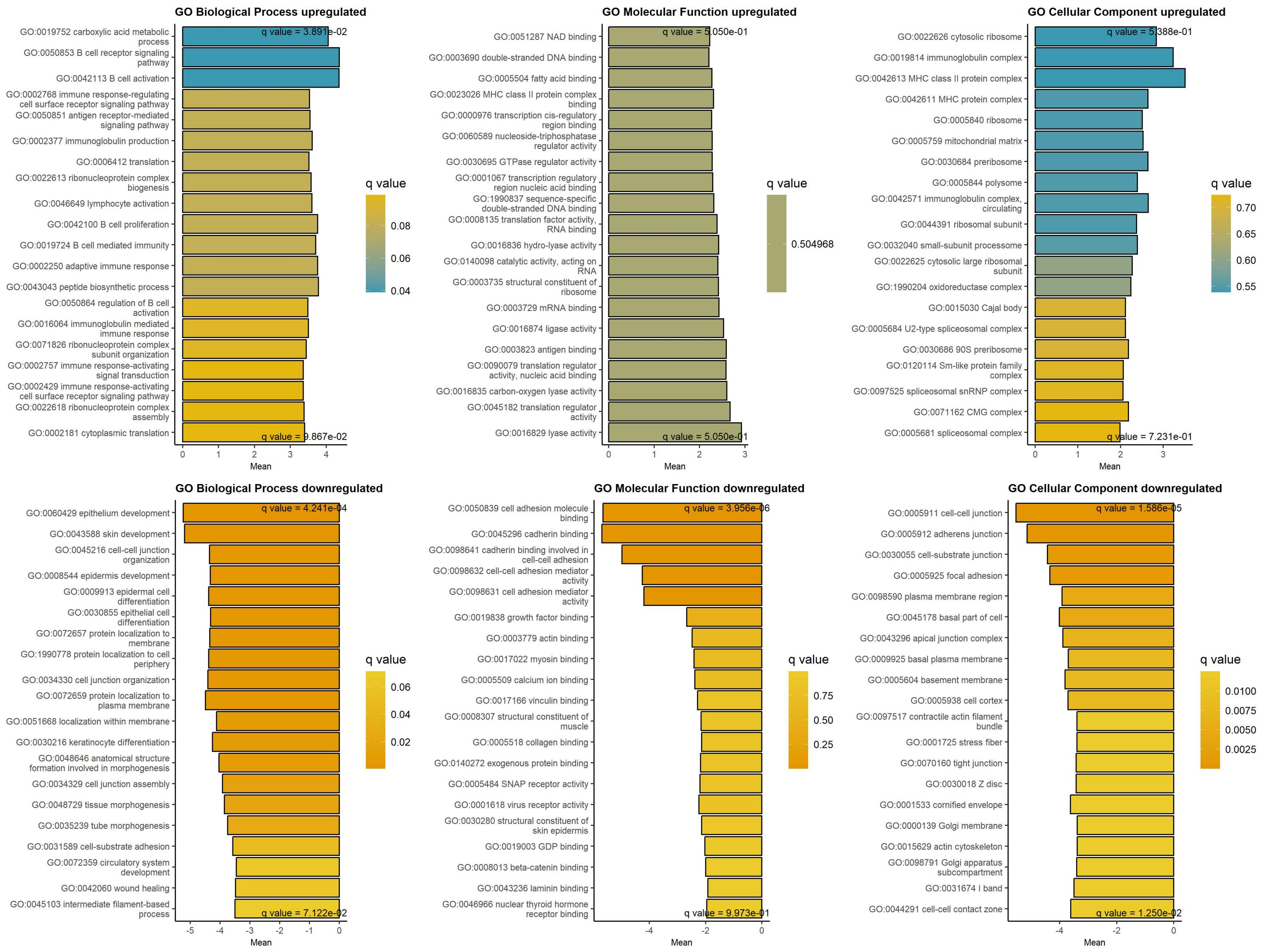
Differentially expressed proteins at absence/low amount of ERCC6 , DB1
p-value < 0.05 & logFC > 1.2

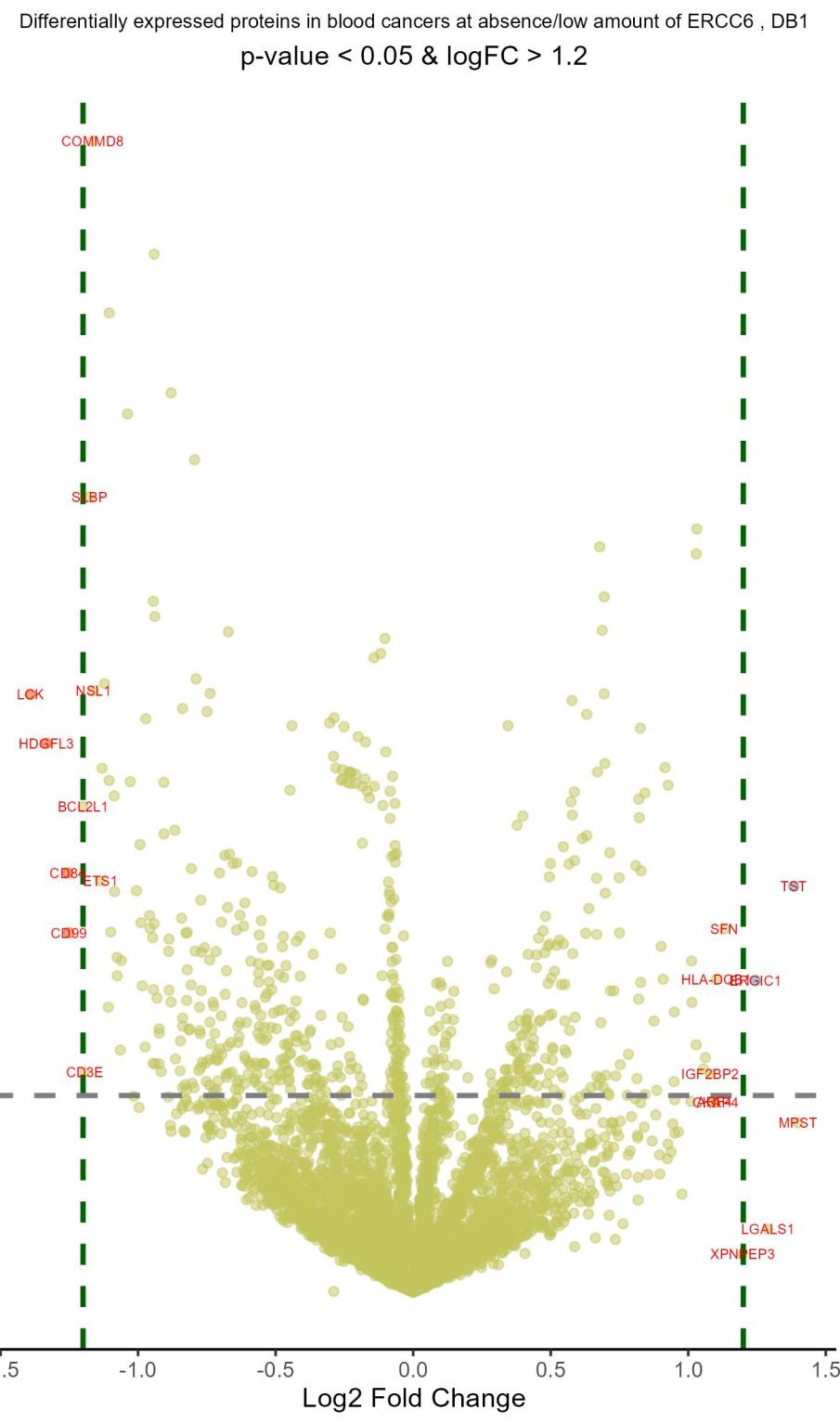


Downregulated at low/absent ERCC6 Upregulated at low/absent ERCC6

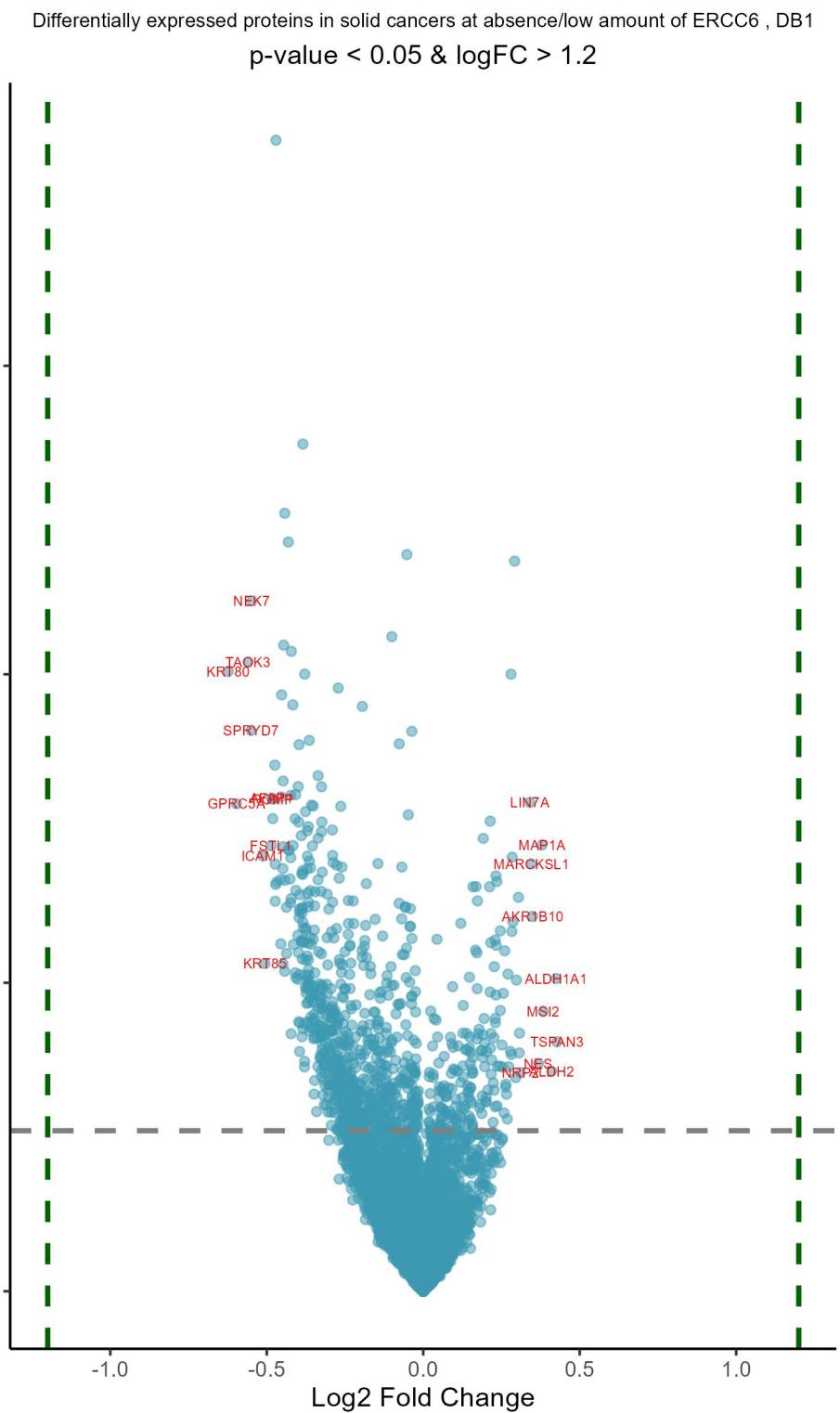
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.77	5.14e-06	KRT80	keratin 80	0.49	1.37e-02	CORO1A	coronin 1A
-0.74	8.75e-05	GPRC5A	G protein-coupled receptor class C	0.46	3.25e-05	GMFG	glia maturation factor gamma
-0.68	5.55e-07	ITGA3	integrin subunit alpha 3	0.45	1.61e-03	IQGAP2	IQ motif containing GTPase activati
-0.68	9.14e-05	PKP3	plakophilin 3	0.44	1.80e-02	MSI2	musashi RNA binding protein 2
-0.66	1.19e-09	PLS3	plastin 3	0.44	1.05e-05	ELMO1	engulfment and cell motility 1
-0.65	5.99e-05	CAVIN1	caveolae associated protein 1	0.43	2.47e-04	CTSS	cathepsin S
-0.65	5.97e-06	EGFR	epidermal growth factor receptor	0.41	3.43e-02	RPIA	ribose 5-phosphate isomerase A
-0.64	2.86e-06	YAP1	Yes1 associated transcriptional reg	0.4	2.11e-02	PDXP	pyridoxal phosphatase
-0.64	1.82e-04	ITGB4	integrin subunit beta 4	0.4	1.19e-02	CD70	CD70 molecule
-0.63	1.73e-04	PKP2	plakophilin 2	0.37	5.10e-02	BCAT1	branched chain amino acid transamin
-0.62	2.47e-04	ANXA3	annexin A3	0.36	5.26e-04	INPP5D	inositol polyphosphate-5-phosphatas
-0.62	5.88e-05	AFAP1	actin filament associated protein 1	0.35	1.92e-03	ARHGAP45	Rho GTPase activating protein 45
-0.62	6.99e-05	KRT19	keratin 19	0.35	4.03e-02	WIPF1	WAS/WASL interacting protein family
-0.62	1.14e-04	SPRYD7	SPRY domain containing 7	0.34	4.85e-02	BDH2	3-hydroxybutyrate dehydrogenase 2
-0.6	3.66e-03	KRT85	keratin 85	0.34	2.55e-02	DGLUCY	D-glutamate cyclase
-0.6	1.12e-05	TPBG	trophoblast glycoprotein	0.34	2.21e-03	SPN	sialophorin
-0.6	3.74e-04	CAV1	caveolin 1	0.34	1.05e-03	RCSD1	RCSD domain containing 1
-0.59	6.12e-04	L1CAM	L1 cell adhesion molecule	0.33	9.12e-04	IKZF1	IKAROS family zinc finger 1
-0.59	4.29e-07	ITGA6	integrin subunit alpha 6	0.33	8.95e-04	WAS	WASP actin nucleation promoting fac
-0.58	5.55e-07	ITPRID2	ITPR interacting domain containing	0.32	1.77e-03	ICAM3	intercellular adhesion molecule 3
-0.58	1.05e-05	KRT18	keratin 18	0.32	1.05e-03	DOCK2	dedicator of cytokinesis 2
-0.58	3.83e-04	CDCP1	CUB domain containing protein 1	0.32	1.50e-01	SH3BGR	SH3 domain binding glutamate rich p
-0.57	1.54e-05	PXN	paxillin	0.32	2.59e-04	PTPN7	protein tyrosine phosphatase non-re
-0.57	8.75e-05	PPP1R13L	protein phosphatase 1 regulatory su	0.32	1.62e-02	LPXN	leupaxin
-0.56	1.09e-04	PLOD2	procollagen-lysine,2-oxoglutarate 5	0.32	2.83e-04	PLCG2	phospholipase C gamma 2
-0.56	4.58e-07	ANLN	anillin actin binding protein	0.31	2.11e-02	FERMT3	FERM domain containing kindlin 3
-0.55	1.82e-04	ADAM9	ADAM metallopeptidase domain 9	0.31	7.58e-02	TYMS	thymidylate synthetase
-0.55	1.23e-03	NT5E	5'-nucleotidase ecto	0.31	1.63e-03	ARHGAP30	Rho GTPase activating protein 30
-0.55	8.95e-04	EPPK1	epiplakin 1	0.31	2.83e-04	IRF4	interferon regulatory factor 4

GAGE analysis on upregulated and downregulated proteins at low/absent ERCC6 protein, DB1

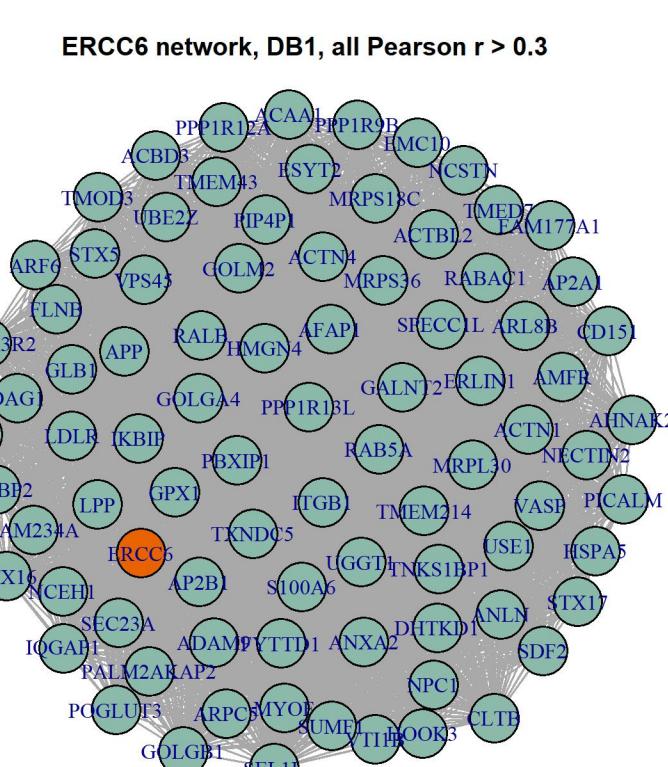
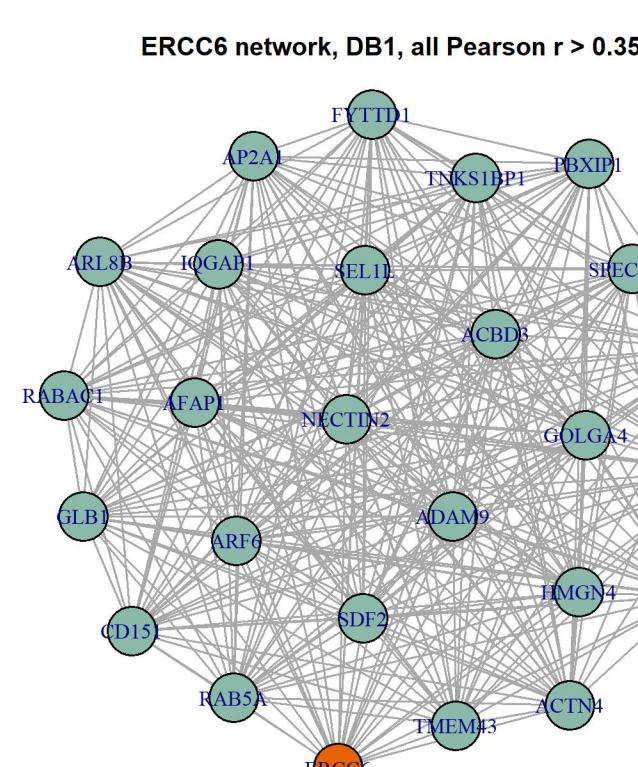
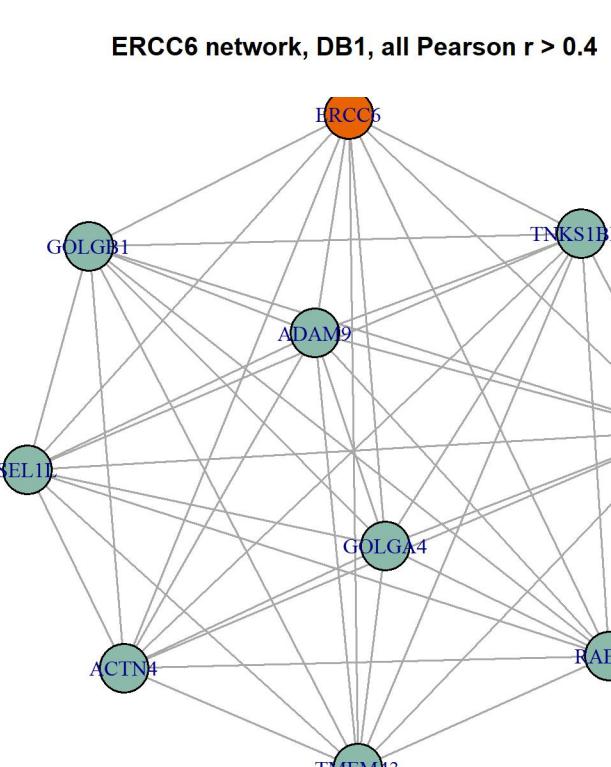


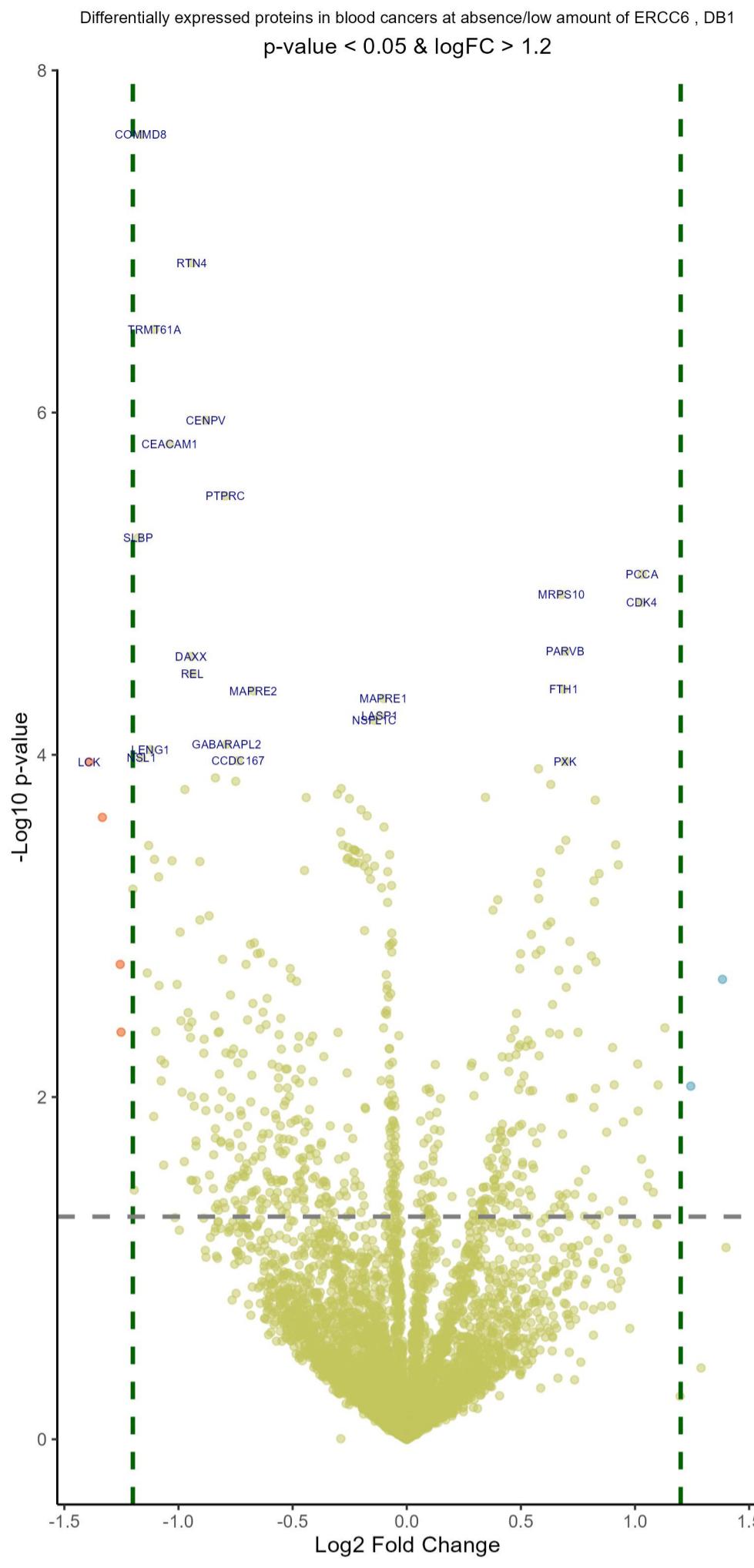


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.39	2.93e-02	LCK	LCK proto-oncogene, Src family tyro	1.4	6.42e-01	MPST	mercaptopyruvate sulfurtransferase
-1.33	3.96e-02	HDGFL3	HDGF like 3	1.38	1.19e-01	TST	thiosulfate sulfurtransferase
-1.26	1.04e-01	CD84	CD84 molecule	1.29	9.33e-01	LGALS1	galectin 1
-1.25	1.85e-01	CD99	CD99 molecule (Xg blood group)	1.24	2.71e-01	ERGIC1	endoplasmic reticulum-golgi interme
-1.2	5.34e-02	BCL2L1	BCL2 like 1	1.2	9.33e-01	XPNPEP3	X-prolyl aminopeptidase 3
-1.19	5.09e-01	CD3E	CD3 epsilon subunit of T-cell recep	1.13	1.85e-01	SFN	stratin
-1.18	4.48e-03	SLBP	stem-loop binding protein	1.1	2.68e-01	HLA-DQB1	major histocompatibility complex, c
-1.16	7.88e-05	COMMD8	COMM domain containing 8	1.1	5.82e-01	CKAP4	cytoskeleton associated protein 4
-1.16	2.93e-02	NSL1	NSL1 component of MIS12 kinetochore	1.1	5.80e-01	ARF4	ADP ribosylation factor 4
-1.14	1.12e-01	ETS1	ETS proto-oncogene 1, transcription	1.08	5.11e-01	IGF2BP2	insulin like growth factor 2 mRNA b
-1.13	4.65e-02	CAAP1	caspase activity and apoptosis inhi	1.06	4.83e-01	SYNGR2	synaptogyrin 2
-1.12	2.93e-02	LENG1	leukocyte receptor cluster member 1	1.06	5.01e-01	QPRT	quinolinate phosphoribosyltransfера
-1.11	3.36e-01	FYN1	FYN binding protein 1	1.03	6.51e-03	PCCA	propionyl-CoA carboxylase subunit a
-1.11	4.65e-02	MTA3	metastasis associated 1 family memb	1.03	7.79e-03	CDK4	cyclin dependent kinase 4
-1.1	5.43e-04	TRMT61A	tRNA methyltransferase 61A	1.03	4.36e-01	MAGT1	magnesium transporter 1
-1.1	1.85e-01	MED10	mediator complex subunit 10	1.01	3.21e-01	ETV6	ETS variant transcription factor 6
-1.09	4.92e-02	SMC1B	structural maintenance of chromosom	1.01	2.28e-01	HLA-DPA1	major histocompatibility complex, c
-1.09	1.25e-01	CDCA2	cell division cycle associated 2	1.01	5.79e-01	DHRS7	dehydrogenase/reductase 7
-1.08	2.23e-01	ELMO2	engulfment and cell motility 2	0.98	8.52e-01	TMED5	transmembrane p24 trafficking prote
-1.08	2.61e-01	TESC	tescalcin	0.96	6.58e-01	TUBB6	tubulin beta 6 class V
-1.06	4.52e-01	GRAP2	GRB2 related adaptor protein 2	0.95	6.62e-01	ECI1	enoyl-CoA delta isomerase 1
-1.06	2.28e-01	ABI3	ABI family member 3	0.95	5.78e-01	SCARB2	scavenger receptor class B member 2
-1.04	1.69e-03	CEACAM1	CEA cell adhesion molecule 1	0.95	3.52e-01	STAT6	signal transducer and activator of
-1.03	4.65e-02	EIF4ENIF1	eukaryotic translation initiation f	0.95	5.24e-01	MECR	mitochondrial trans-2-enoyl-CoA red
-1.02	5.67e-01	SH2D1A	SH2 domain containing 1A	0.94	6.46e-01	IRF4	interferon regulatory factor 4
-1.01	1.25e-01	BLOC1S5	biogenesis of lysosomal organelles	0.94	7.23e-01	ARL8B	ADP ribosylation factor like GTPase
-1	5.93e-01	BCL11B	BAF chromatin remodeling complex su	0.93	4.65e-02	SEC61G	SEC61 translocon subunit gamma
-0.99	8.31e-02	SPC25	SPC25 component of NDC80 kinetochor	0.93	6.99e-01	SERPINH1	serpin family H member 1
-0.99	1.74e-01	PLCG1	phospholipase C gamma 1	0.92	7.42e-01	ASNS	asparagine synthetase (glutamine-hy

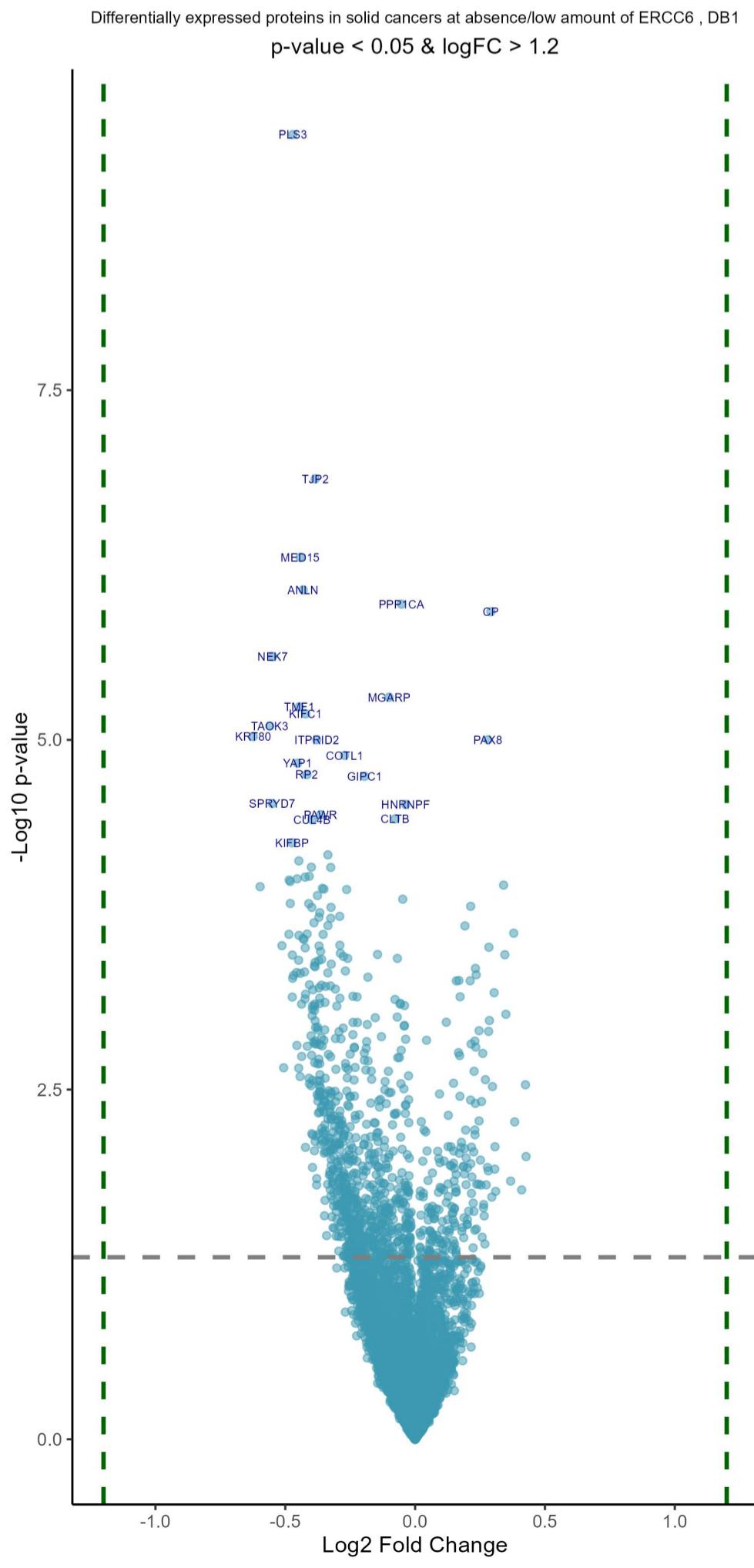


Downregulated in solid cancers at low/absent ERCC6				Upregulated in solid cancers at low/absent ERCC6			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.62	4.43e-03	KRT80	keratin 80	0.43	1.63e-01	TSPAN3	tetraspanin 3
-0.6	2.00e-02	GPRC5A	G protein-coupled receptor class C	0.42	9.16e-02	ALDH1A1	aldehyde dehydrogenase 1 family mem
-0.56	4.40e-03	TAOK3	TAO kinase 3	0.41	2.11e-01	ALDH2	aldehyde dehydrogenase 2 family mem
-0.55	9.17e-03	SPRYD7	SPRY domain containing 7	0.38	1.24e-01	MSI2	musashi RNA binding protein 2
-0.55	2.11e-03	NEK7	NIMA related kinase 7	0.38	2.86e-02	MAP1A	microtubule associated protein 1A
-0.51	3.14e-02	ICAM1	intercellular adhesion molecule 1	0.37	2.00e-01	NES	nestin
-0.51	7.81e-02	KRT85	keratin 85	0.35	4.95e-02	AKR1B10	aldo-keto reductase family 1 member
-0.49	2.86e-02	FSTL1	follistatin like 1	0.35	3.28e-02	MARCKSL1	MARCKS like 1
-0.49	2.00e-02	AFAP1	actin filament associated protein 1	0.34	2.00e-02	LIN7A	lin-7 homolog A, crumbs cell polariz
-0.48	2.00e-02	POMP	proteasome maturation protein	0.31	2.14e-01	NRP2	neuropilin 2
-0.48	2.28e-02	CDCA3	cell division cycle associated 3	0.31	1.52e-01	ELMOD2	ELMO domain containing 2
-0.47	1.45e-02	KIFBP	kinesin family binding protein	0.31	1.79e-01	SNTB1	syntrophin beta 1
-0.47	4.33e-02	PKP3	plakophilin 3	0.3	4.23e-02	GGT7	gamma-glutamyltransferase 7
-0.47	3.28e-02	PKP2	plakophilin 2	0.3	9.31e-02	CEACAM5	CEA cell adhesion molecule 5
-0.47	3.74e-02	ANXA3	annexin A3	0.3	2.21e-01	GTPBP3	GTP binding protein 3, mitochondria
-0.47	1.56e-06	PLS3	plastin 3	0.29	1.15e-03	CP	ceruloplasmin
-0.47	3.65e-02	ITGB4	integrin subunit beta 4	0.29	5.29e-02	CDH6	cadherin 6
-0.46	3.61e-02	JUNB	JunB proto-oncogene, AP-1 transcrip	0.28	3.14e-02	METTL7B	methyltransferase like 7B
-0.46	6.36e-02	IL18	interleukin 18	0.28	5.71e-02	NEFL	neurofilament light chain
-0.45	2.00e-02	GSK3B	glycogen synthase kinase 3 beta	0.28	1.83e-01	GPC4	glypican 4
-0.45	5.74e-03	YAP1	Yes1 associated transcriptional reg	0.28	4.43e-03	PAX8	paired box 8
-0.45	3.31e-02	KRT19	keratin 19	0.28	1.77e-01	DGLUCY	D-glutamate cyclase
-0.45	7.82e-02	NACA2	nascent polypeptide associated comp	0.27	2.04e-01	PCCA	propionyl-CoA carboxylase subunit a
-0.45	1.81e-02	PPP1R13L	protein phosphatase 1 regulatory su	0.27	8.79e-02	VWA8	von Willebrand factor A domain cont
-0.45	2.86e-02	HOMER3	homer scaffold protein 3	0.27	3.03e-01	CLGN	calmegin
-0.45	3.86e-03	TMF1	TATA element modulatory factor 1	0.27	2.51e-01	PEG10	paternally expressed 10
-0.44	8.57e-02	PRNP	prion protein	0.26	2.33e-01	CRMP1	collapsin response mediator protein
-0.44	8.24e-04	MED15	mediator complex subunit 15	0.26	2.39e-01	AGL	amylo-alpha-1, 6-glucosidase, 4-alp
-0.44	3.61e-02	SVIP	small VCP interacting protein	0.26	6.82e-02	UGT1A6	UDP glucuronosyltransferase family



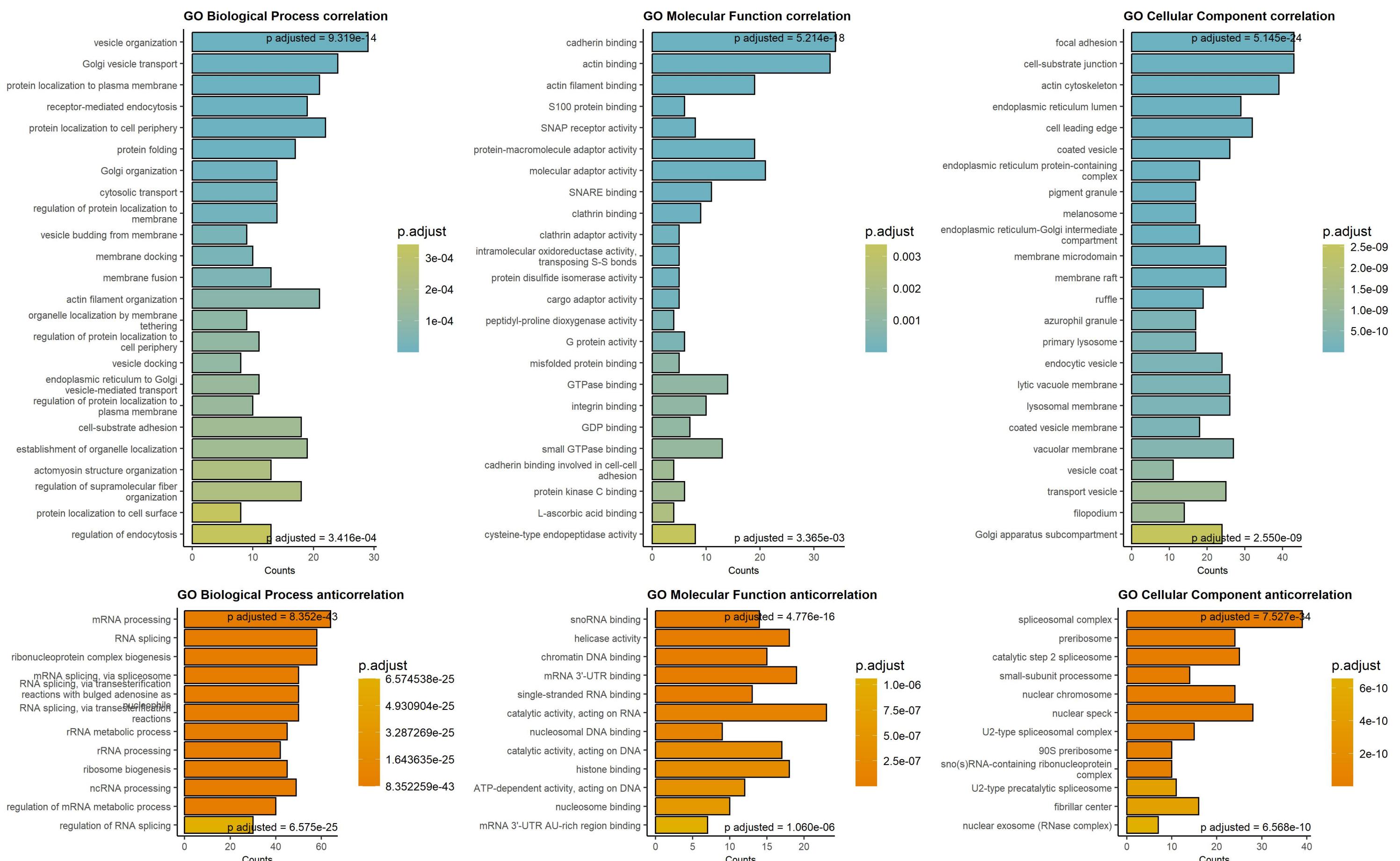


Sorted by p values!							
Downregulated in blood cancers at low/absent ERCC6				Upregulated in blood cancers at low/absent ERCC6			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.16	7.88e-05	COMM8	COMM domain containing 8	1.03	6.51e-03	PCCA	propionyl-CoA carboxylase subunit alpha
-0.94	2.95e-04	RTN4	reticulon 4	0.68	7.69e-03	MRPS10	mitochondrial ribosomal protein S10
-1.1	5.43e-04	TRMT61A	tRNA methyltransferase 61A	1.03	7.79e-03	CDK4	cyclin dependent kinase 4
-0.88	1.47e-03	CENPV	centromere protein V	0.69	1.36e-02	PARVB	parvin beta
-1.04	1.69e-03	CEACAM1	CEA cell adhesion molecule 1	0.69	1.76e-02	FTH1	ferritin heavy chain 1
-0.79	2.92e-03	PTPRC	protein tyrosine phosphatase recept	0.69	2.93e-02	PXK	PX domain containing serine/threonine
-1.18	4.48e-03	SLBP	stem-loop binding protein	0.58	3.09e-02	CHCHD1	coiled-coil-helix-coiled-coil-helix
-0.94	1.36e-02	DAXX	death domain associated protein	0.63	3.40e-02	GLTP	glycolipid transfer protein
-0.94	1.59e-02	REL	REL proto-oncogene, NF- κ B subunit	0.34	3.40e-02	SEC23IP	SEC23 interacting protein
-0.67	1.76e-02	MAPRE2	microtubule associated protein RP/E	0.83	3.40e-02	ARL1	ADP ribosylation factor like GTPase
-0.1	1.83e-02	MAPRE1	microtubule associated protein RP/E	0.7	4.65e-02	IGLL1	immunoglobulin lambda like polypep
-0.12	2.18e-02	LASP1	LIM and SH3 protein 1	0.92	4.65e-02	ACOX1	acyl-CoA oxidase 1
-0.14	2.20e-02	NSFL1C	NSFL1 cofactor	0.67	4.65e-02	TRIM72	tripartite motif containing 72
-0.79	2.89e-02	GABARAPL2	GABA type A receptor associated pro	0.93	4.65e-02	SEC61G	SEC61 translocon subunit gamma
-1.12	2.93e-02	LENG1	leukocyte receptor cluster member 1	0.59	4.76e-02	UBASH3B	ubiquitin associated and SH3 domain
-1.16	2.93e-02	NSL1	NSL1 component of MIS12 kinetochore	0.84	4.77e-02	PNPLA6	patatin like phospholipase domain c
-0.74	2.93e-02	CCDC167	coiled-coil domain containing 167	0.82	5.02e-02	TMEM205	transmembrane protein 205
-1.39	2.93e-02	LCK	LCK proto-oncogene, Src family tyro	0.57	5.15e-02	KRT5	keratin 5
-0.84	3.36e-02	AAGAB	alpha and gamma adaptin binding pro	0.58	5.98e-02	IER3IP1	immediate early response 3 interact
-0.75	3.39e-02	GINS2	GINS complex subunit 2	0.4	6.00e-02	MCCC2	methylcrotonyl-CoA carboxylase sub
-0.29	3.40e-02	TCEAL4	transcription elongation factor A I	0.82	6.06e-02	CTBP2	C-terminal binding protein 2
-0.97	3.40e-02	C1D	C1D nuclear receptor corepressor	0.38	6.63e-02	MYG1	MYG1 exonuclease
-0.3	3.40e-02	CSRP3	cysteine and glycine rich protein 3	0.63	7.51e-02	S100A8	S100 calcium binding protein A8
-0.44	3.40e-02	GSTP1	glutathione S-transferase pi 1	0.62	7.77e-02	PLS3	plastin 3
-0.25	3.40e-02	DTNA	dystrobrevin alpha	0.55	8.39e-02	VKORC1L1	vitamin K epoxide reductase comple
-0.2	3.77e-02	TH	tyrosine hydroxylase	0.71	9.06e-02	FAIM	Fas apoptotic inhibitory molecu
-0.17	3.96e-02	FRA10AC1	FRA10A associated CGG repeat 1	0.59	9.61e-02	S100A10	S100 calcium binding protein A10
-1.33	3.96e-02	HDGFL3	HDGF like 3	0.5	9.64e-02	NAGLU	N-acetyl-alpha-glucosaminidase
-0.1	4.39e-02	PCNA	proliferating cell nuclear antigen	0.57	9.64e-02	FERMT2	FERM domain containing kindlin 2
-0.29	4.59e-02	KRT80	keratin 80	0.81	9.77e-02	SFXN3	sideroflexin 3
-0.28	4.65e-02	ALOX15	arachidonate 15-lipoxygenase	0.83	1.04e-01	FTL	ferritin light chain
-1.13	4.65e-02	CAAP1	caspase activity and apoptosis inhi	0.5	1.09e-01	MFN1	mitofusin 1
-0.26	4.65e-02	RAB3C	RAB3C, member RAS oncogene family	0.75	1.09e-01	SMPD4	sphingomyelin phosphodiesterase 4
-0.23	4.65e-02	ZFHX3	zinc finger homeobox 3	0.67	1.09e-01	ACADS	acyl-CoA dehydrogenase short chain
-0.23	4.65e-02	GSTM4	glutathione S-transferase mu 4	1.38	1.19e-01	TST	thiosulfate sulfurtransferase
-0.23	4.65e-02	ICAM5	intercellular adhesion molecule 5	0.7	1.27e-01	ARL6IP1	ADP ribosylation factor like GTPase
-0.21	4.65e-02	LAMA5	laminin subunit alpha 5	0.64	1.51e-01	PON2	paraoxonase 2
-0.07	4.65e-02	TUBB	tubulin beta class I	0.48	1.64e-01	GET4	guided entry of tail-anchored prote
-0.26	4.65e-02	HIC2	HIC-ZBTB transcriptional repressor	1.13	1.85e-01	SEN	stratifin

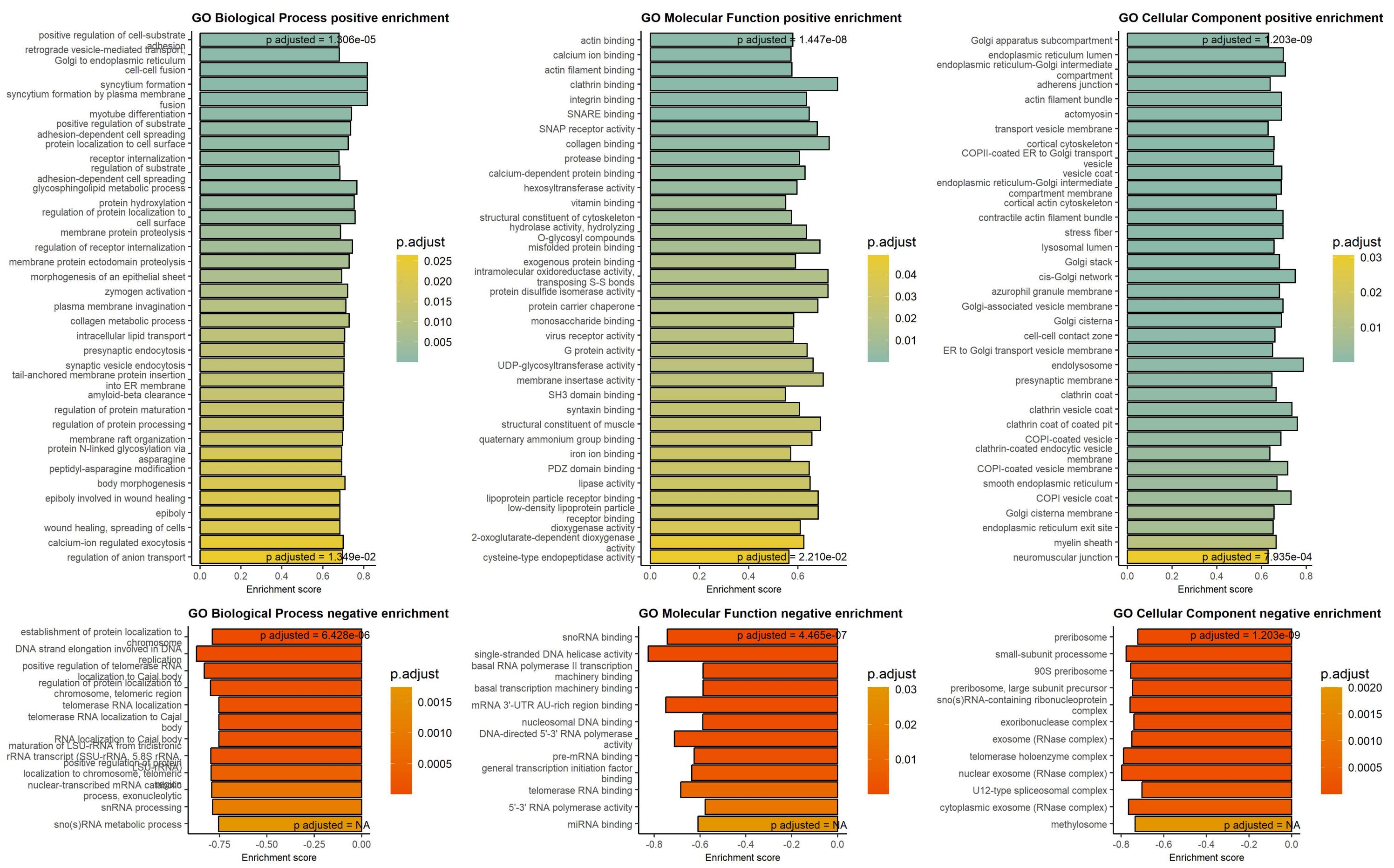


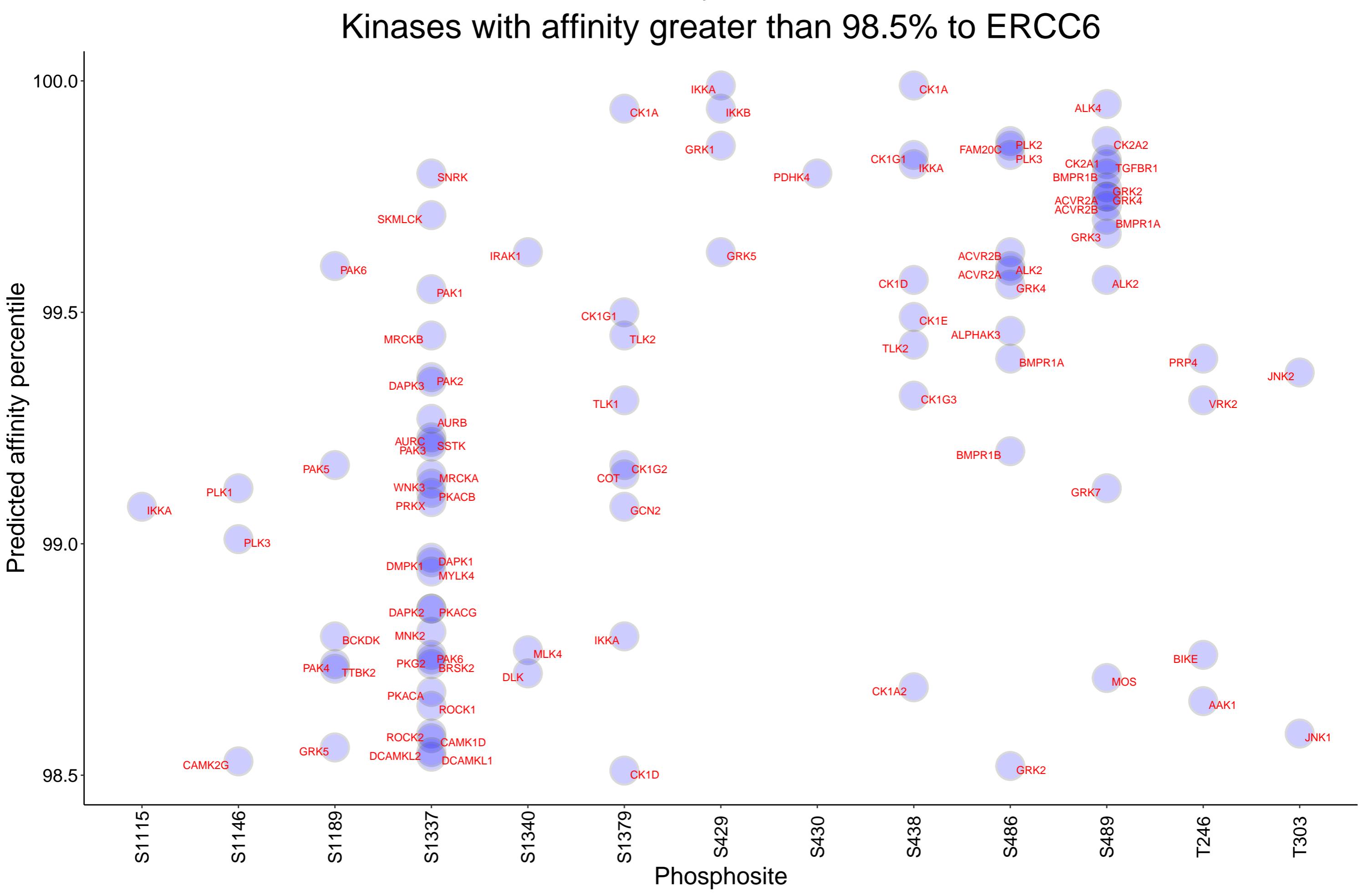
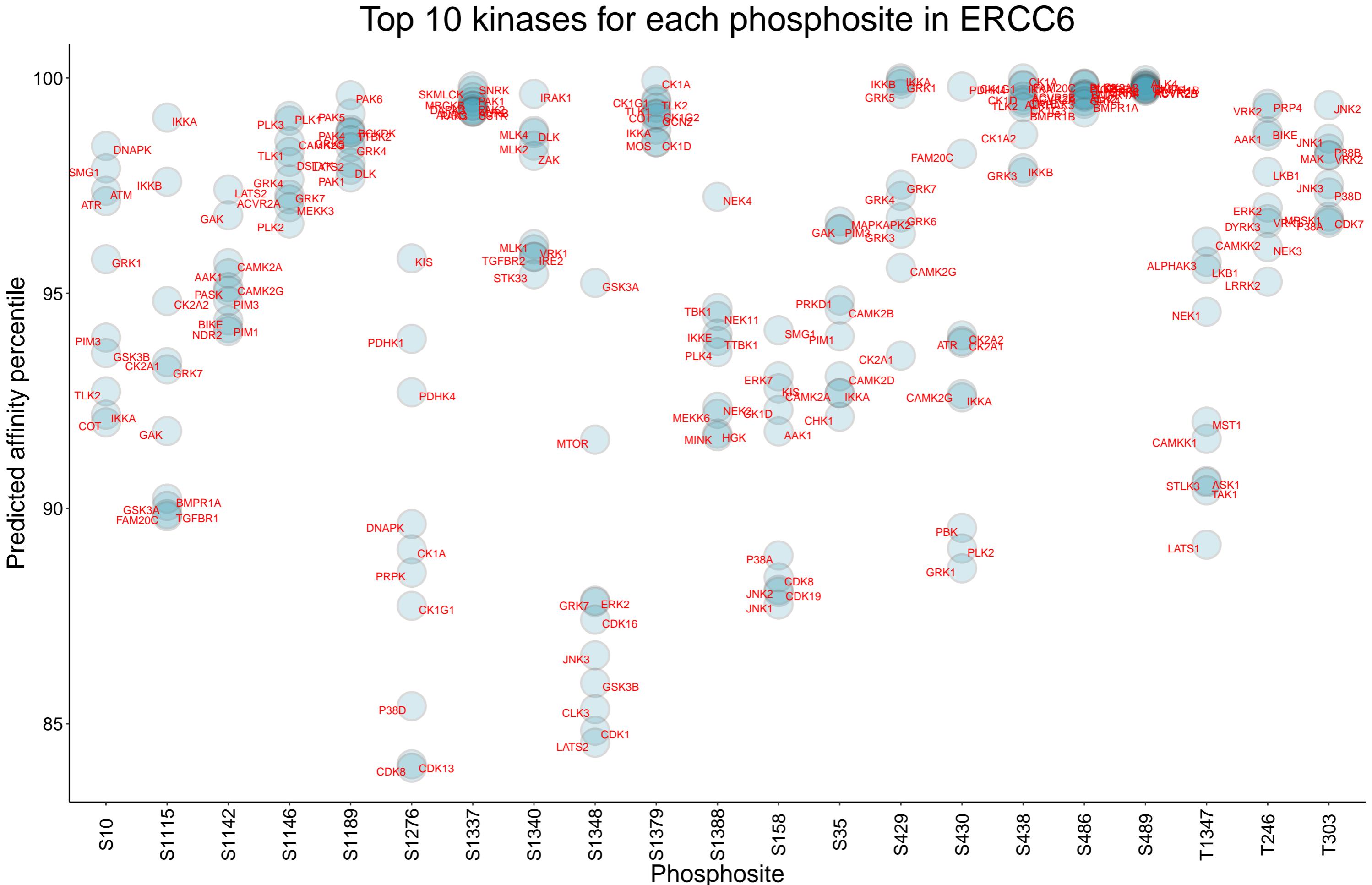
Sorted by p values!							
Downregulated in solid cancers at low/absent ERCC6				Upregulated in solid cancers at low/absent ERCC6			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
0.47	1.56e-06	PLS3	plastin 3	0.29	1.15e-03	CP	ceruloplasmin
0.38	3.02e-04	TJP2	tight junction protein 2	0.28	4.43e-03	PAX8	paired box 8
0.44	8.24e-04	MED15	mediator complex subunit 15	0.34	2.00e-02	LIN7A	lin-7 homolog A, crumbs cell polarity
0.43	1.13e-03	ANLN	anillin actin binding protein	0.21	2.28e-02	SPP1	secreted phosphoprotein 1
0.05	1.15e-03	PPP1CA	protein phosphatase 1 catalytic sub	0.19	2.68e-02	B4GALNT1	beta-1,4-N-acetyl-galactosaminyltr
0.55	2.11e-03	NEK7	NIMA related kinase 7	0.38	2.86e-02	MAP1A	microtubule associated protein 1A
-0.1	3.66e-03	MGARP	mitochondria localized glutamic aci	0.28	3.14e-02	METTL7B	methyltransferase like 7B
0.45	3.86e-03	TMF1	TATA element modulatory factor 1	0.35	3.28e-02	MARCKSL1	MARCKS like 1
0.42	3.94e-03	KIFC1	kinesin family member C1	0.23	3.53e-02	ADGB	androglobin
0.56	4.40e-03	TAOK3	TAO kinase 3	0.24	3.65e-02	LIN28B	lin-28 homolog B
0.62	4.43e-03	KRT80	keratin 80	0.17	3.77e-02	INTS9	integrator complex subunit 9
0.38	4.43e-03	ITPRID2	ITPR interacting domain containing	0.21	3.77e-02	CEND1	cell cycle exit and neuronal differ
0.27	5.37e-03	COTL1	coactosin like F-actin binding prot	0.16	3.77e-02	PIGR	polymeric immunoglobulin receptor
0.45	5.74e-03	YAP1	Yes1 associated transcriptional reg	0.3	4.23e-02	GGT7	gamma-glutamyltransferase 7
0.42	6.37e-03	RP2	RP2 activator of ARL3 GTPase	0.17	4.33e-02	STMN2	stathmin 2
0.19	6.37e-03	GIPC1	GIPC PDZ domain containing family m	0.35	4.95e-02	AKR1B10	aldo-keto reductase family 1 membe
0.55	9.17e-03	SPRYD7	SPRY domain containing 7	0.29	5.29e-02	CDH6	cadherin 6
0.04	9.17e-03	HNRNPF	heterogeneous nuclear ribonucleopro	0.12	5.32e-02	DCDC2	doublecortin domain containing 2
0.36	1.03e-02	PAWR	pro-apoptotic WT1 regulator	0.25	5.70e-02	CLYBL	citramaly-CoA lyase
0.08	1.03e-02	CLTB	clathrin light chain B	0.28	5.71e-02	NEFL	neurofilament light chain
-0.4	1.03e-02	CUL4B	cullin 4B	0.04	6.18e-02	ACO2	aconitase 2
0.47	1.45e-02	KIFBP	kinesin family binding protein	0.23	6.19e-02	CA12	carbonic anhydrase 12
0.34	1.70e-02	ITGA6	integrin subunit alpha 6	0.22	6.29e-02	ARID3B	AT-rich interaction domain 3B
0.45	1.81e-02	PPP1R13L	protein phosphatase 1 regulatory su	0.23	6.37e-02	ENO3	enolase 3
-0.4	1.87e-02	RTF2	replication termination factor 2	0.17	6.82e-02	FABP6	fatty acid binding protein 6
0.33	1.87e-02	KDM2A	lysine demethylase 2A	0.26	6.82e-02	UGT1A6	UDP glucuronosyltransferase family
0.41	2.00e-02	PXN	paxillin	0.17	6.91e-02	GGT1	gamma-glutamyltransferase 1
0.42	2.00e-02	CIT	citron rho-interacting serine/threo	0.23	7.98e-02	ALPL	alkaline phosphatase, biomimetic
0.45	2.00e-02	GSK3B	glycogen synthase kinase 3 beta	0.27	8.79e-02	VWA8	von Willebrand factor A domain con
0.49	2.00e-02	AFAP1	actin filament associated protein 1	0.15	9.05e-02	DMTN	dematin actin binding protein
0.48	2.00e-02	POMP	proteasome maturation protein	0.42	9.16e-02	ALDH1A1	aldehyde dehydrogenase 1 family me
-0.6	2.00e-02	GPRC5A	G protein-coupled receptor class C	0.3	9.31e-02	CEACAM5	CEA cell adhesion molecule 5
0.36	2.00e-02	WAPL	WAPL cohesin release factor	0.09	9.88e-02	SAMD11	sterile alpha motif domain containi
0.35	2.00e-02	CSNK1A1	casein kinase 1 alpha 1	0.17	9.93e-02	NOVA2	NOVA alternative splicing regulator
0.26	2.00e-02	SEPTIN8	septin 8	0.21	1.03e-01	EPS8L3	EPS8 like 3
0.38	2.16e-02	TJAP1	tight junction associated protein 1	0.26	1.03e-01	ITGB3	integrin subunit beta 3
0.05	2.23e-02	CTNNBL1	catenin beta like 1	0.23	1.05e-01	NEO1	neogenin 1
0.48	2.28e-02	CDCA3	cell division cycle associated 3	0.13	1.17e-01	IL4I1	interleukin 4 induced 1
0.41	2.28e-02	CDK12	cyclin dependent kinase 12	0.25	1.23e-01	SYT1	synaptotagmin 1

Top 250 correlation coefficients overrepresentation, ERCC6 protein, DB1



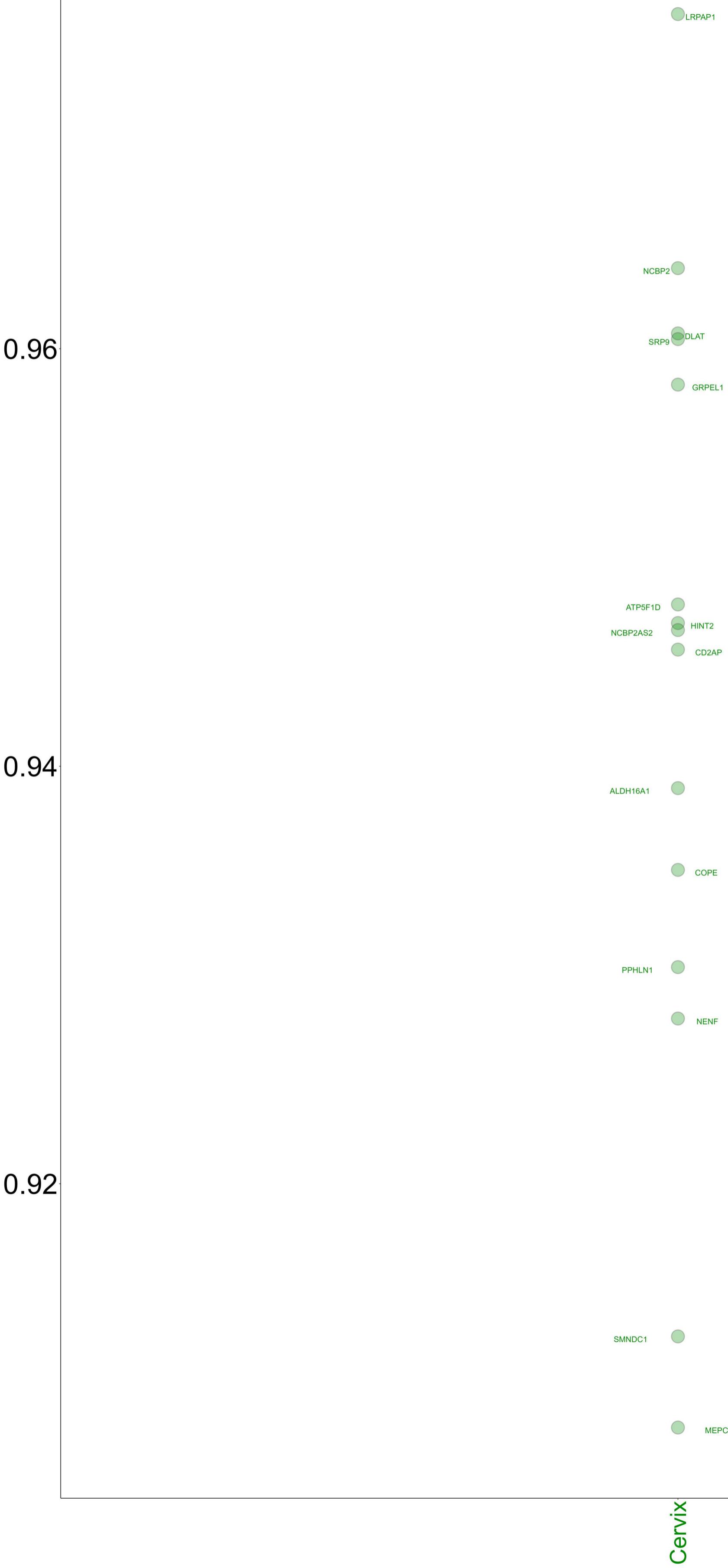
Gene Set Enrichment analysis on protein correlation coefficients, ERCC6 protein, DB1





Top 15 positive correlation coefficients for ERCC6 protein by tissue, DB1

Beware of false positives in tissues with small number of samples



Cervix