

ERCC3

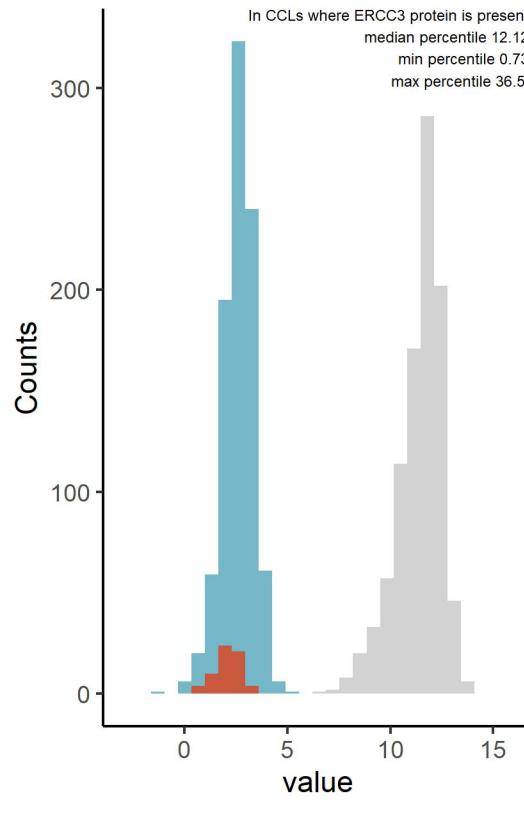
Protein name: ERCC3 ; UNIPROT: P19447 ; Gene name: ERCC excision repair 3, TFIIH core complex helicase subunit

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

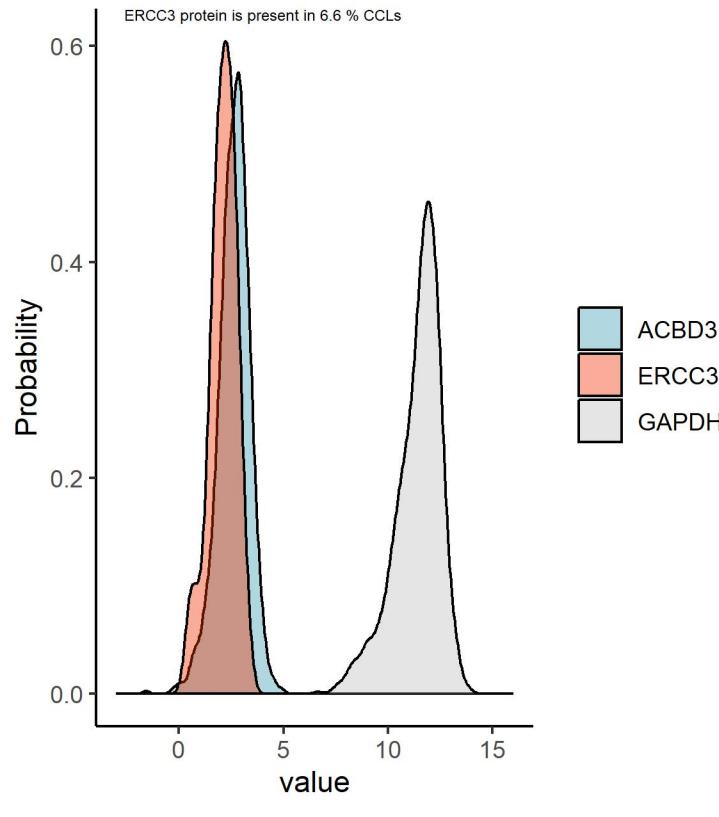
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

Histogram of ERCC3 protein compared to proteins with low and high abundance



Density plot of ERCC3 protein compared to proteins with low and high abundance



Top negative correlations of ERCC3 protein, DB1

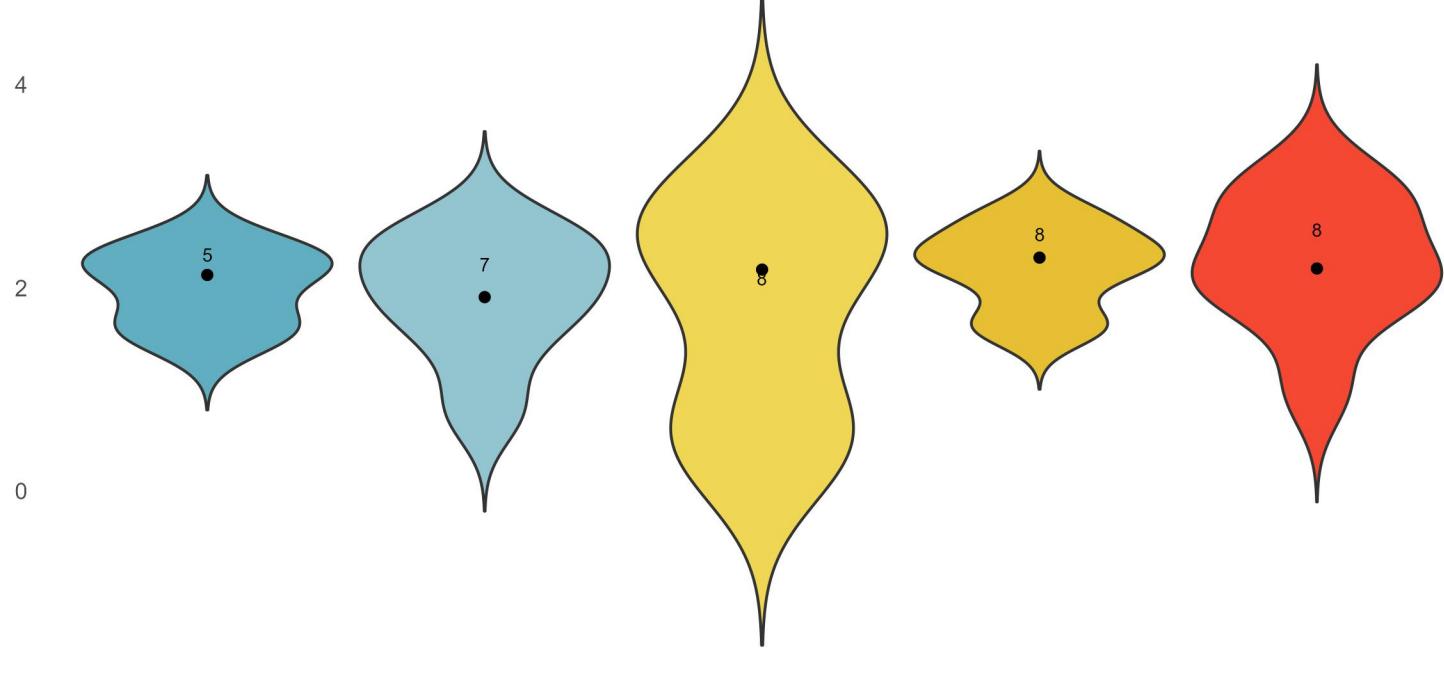
Pearson correlation coefficients

Top positive correlations of ERCC3 protein, DB1

Pearson correlation coefficients

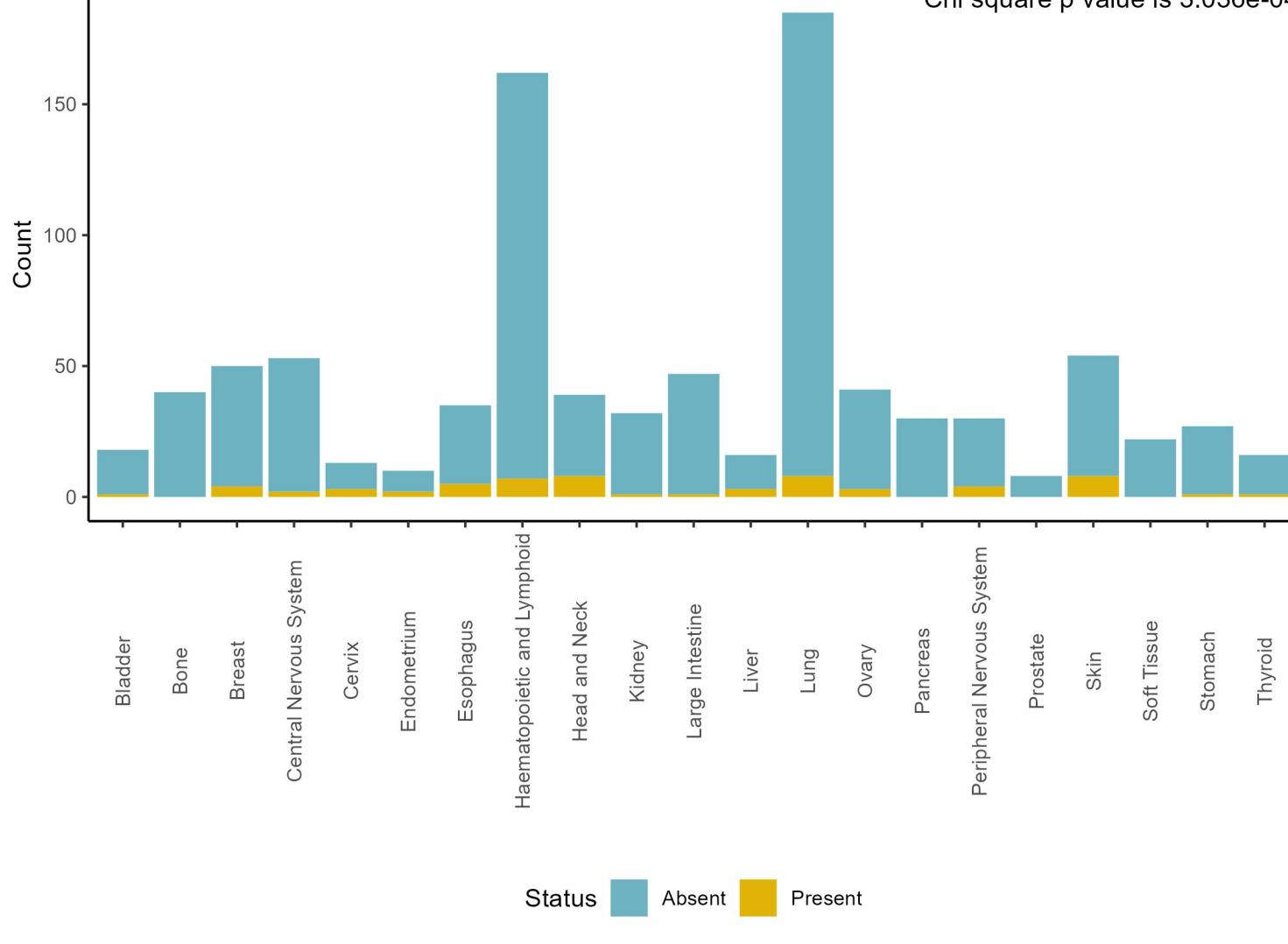
Amount of ERCC3 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 7.608e-01



Present and absent ERCC3 protein counts by tissue, DB1

Chi square p value is 3.036e-04

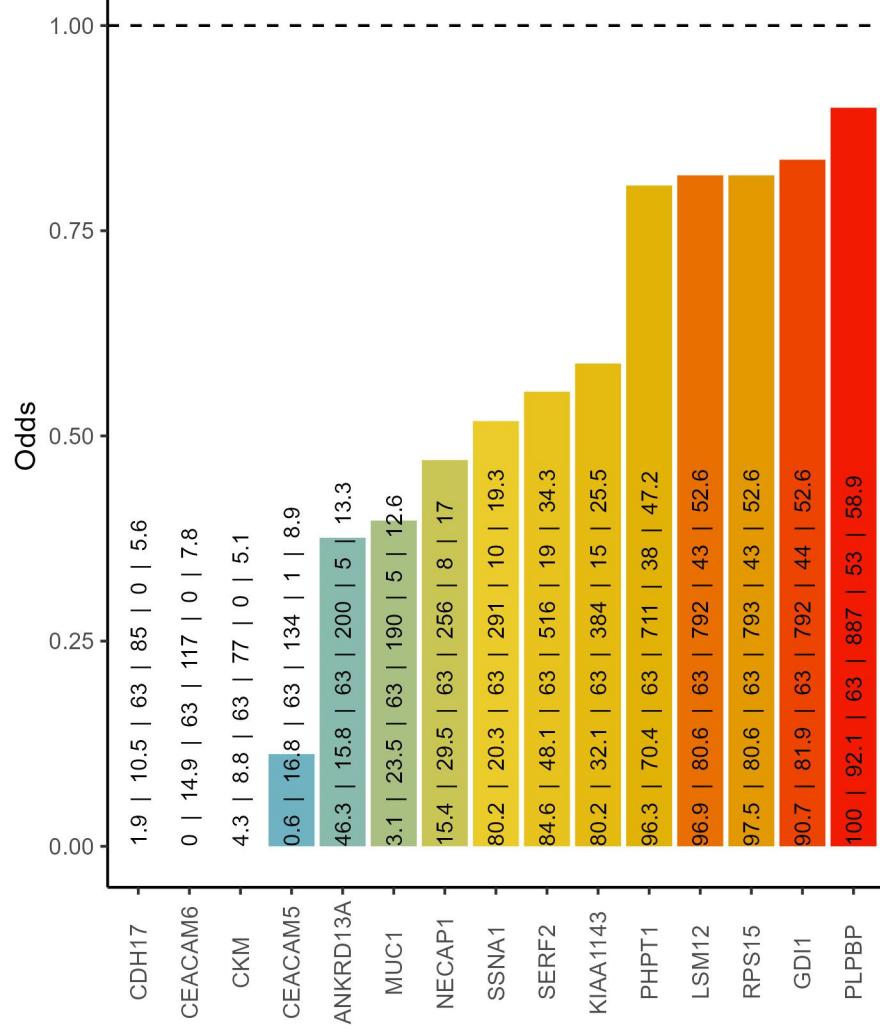


Cooccurrence with ERCC3 protein, DB1

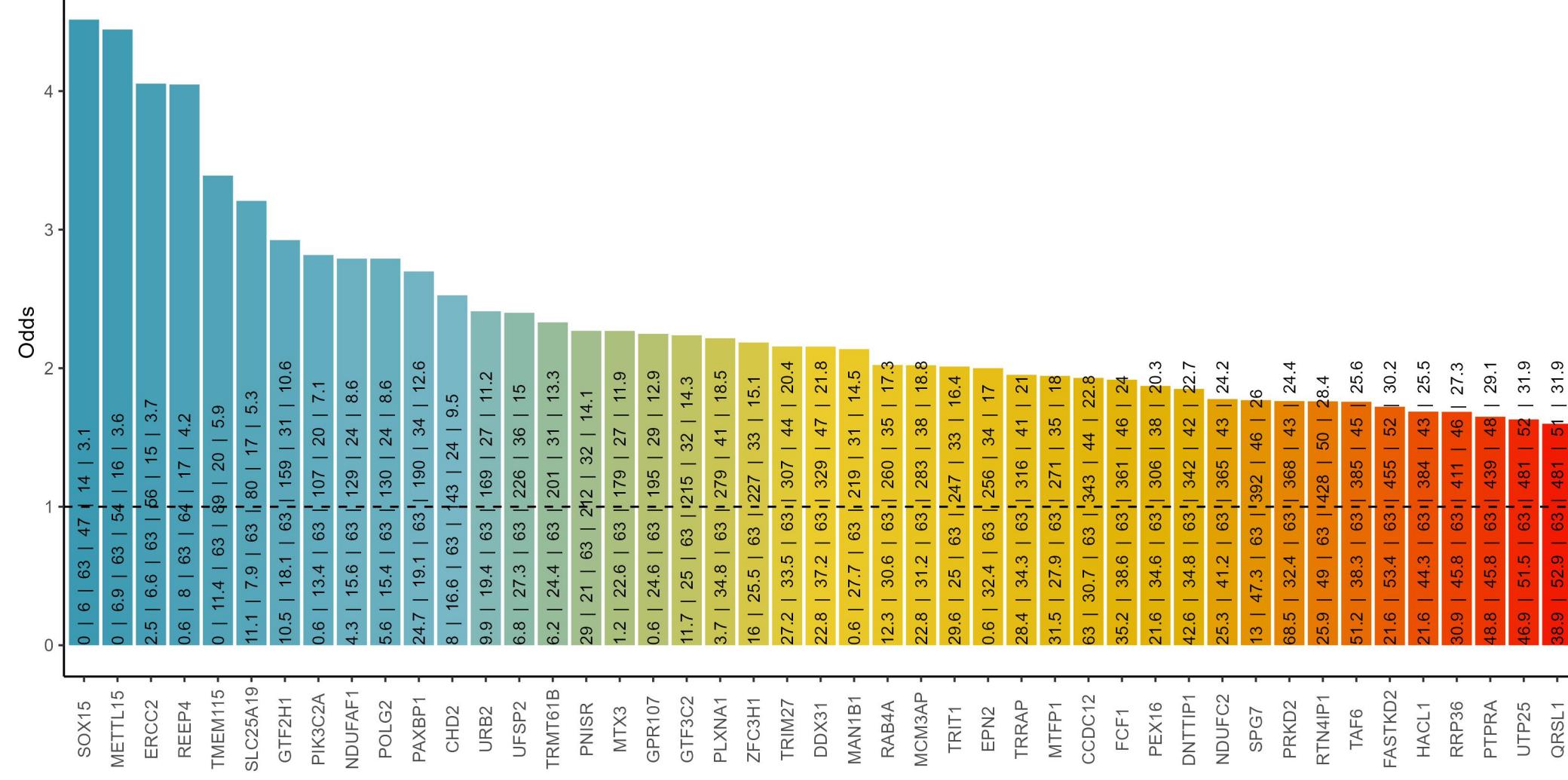
% of ERCC3 in blood cancers: 4.3 ; % of ERCC3 in solid cancers: 7.1

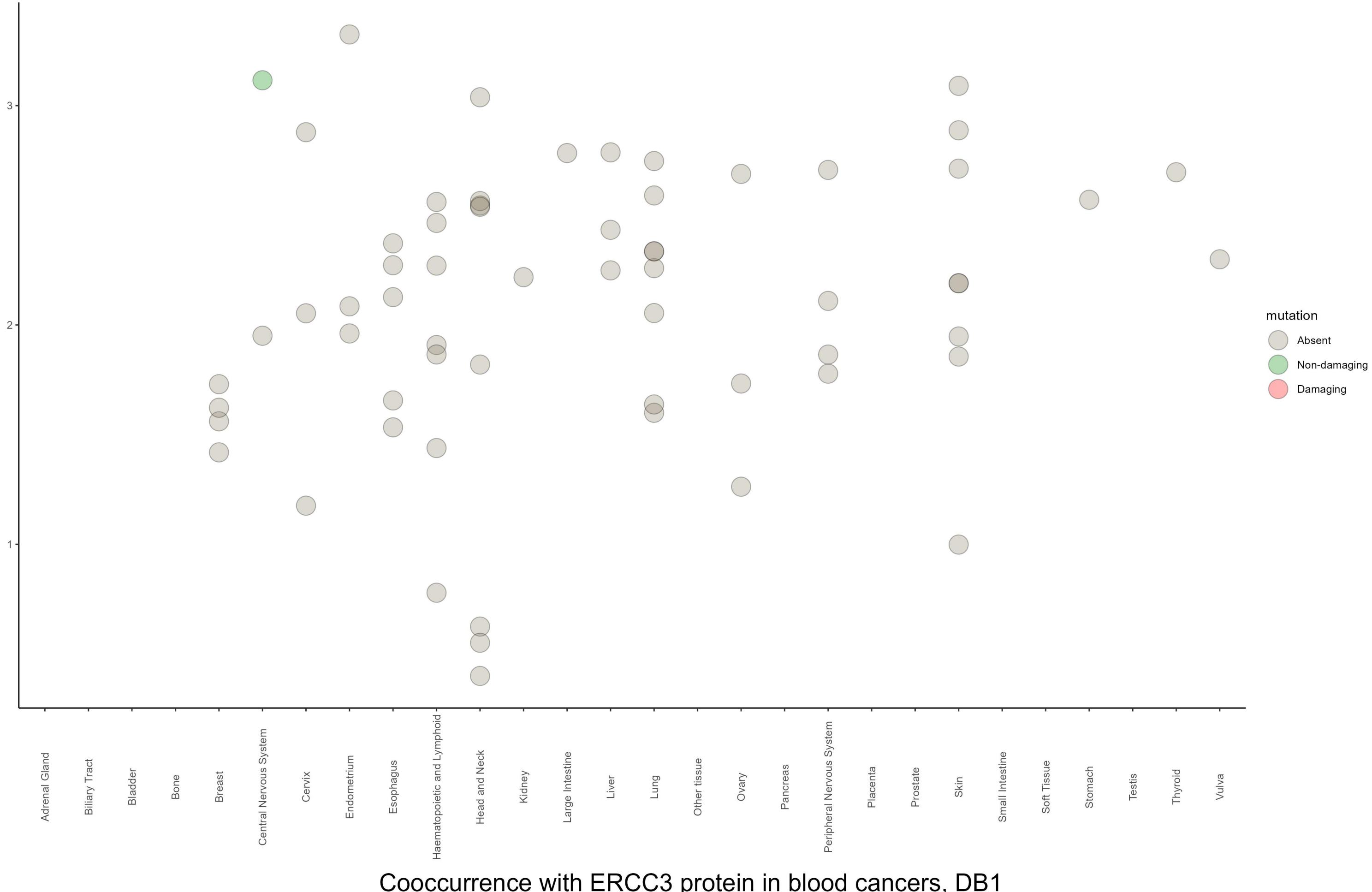
Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ERCC3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



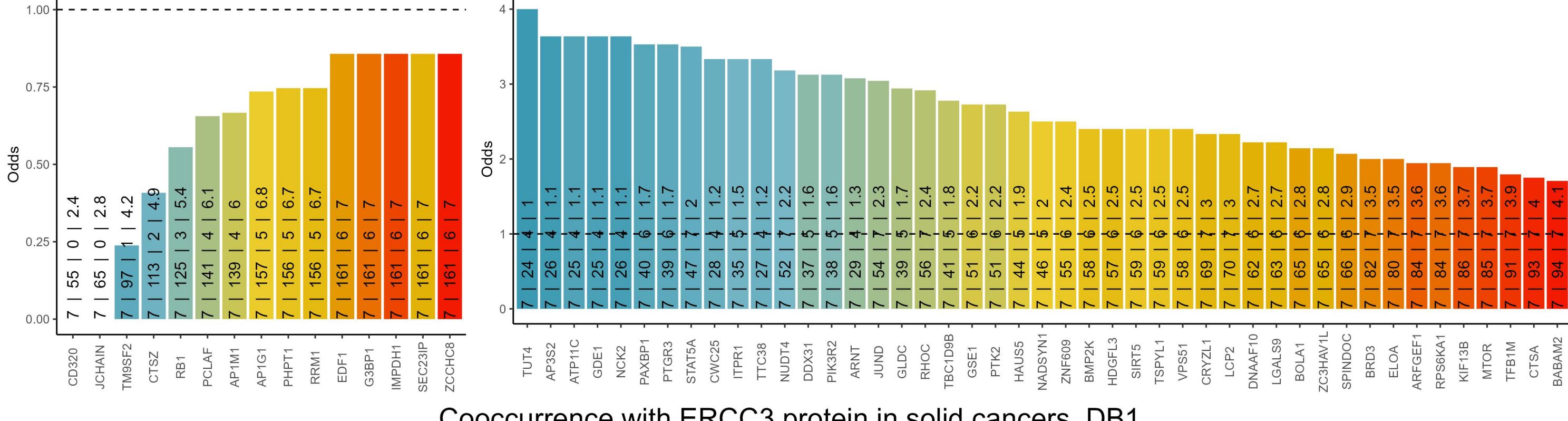
Positive cooccurrence





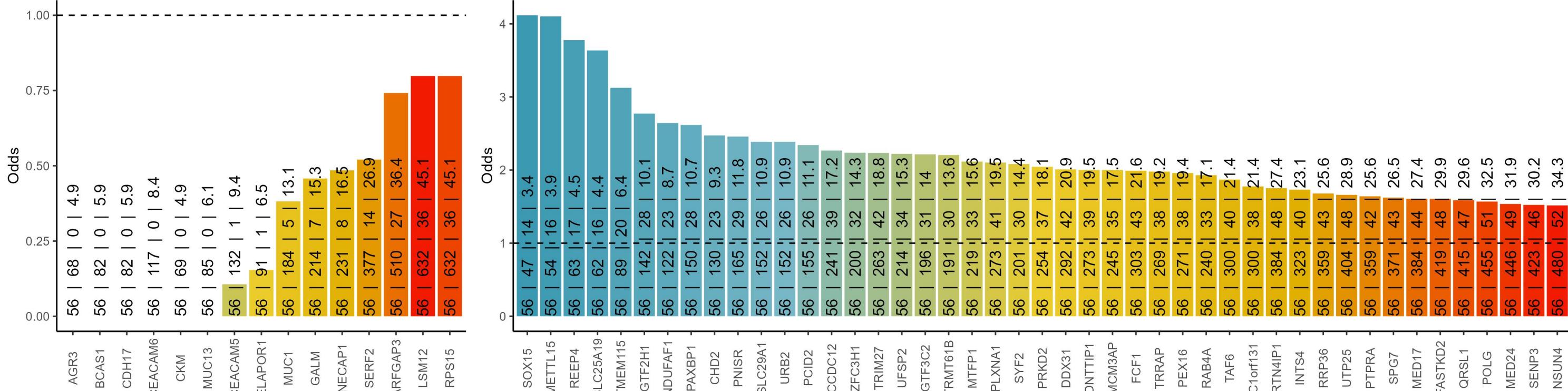
ncidence of ERCC3 | incidence of Protein 2 | observed cooccurrence | ex

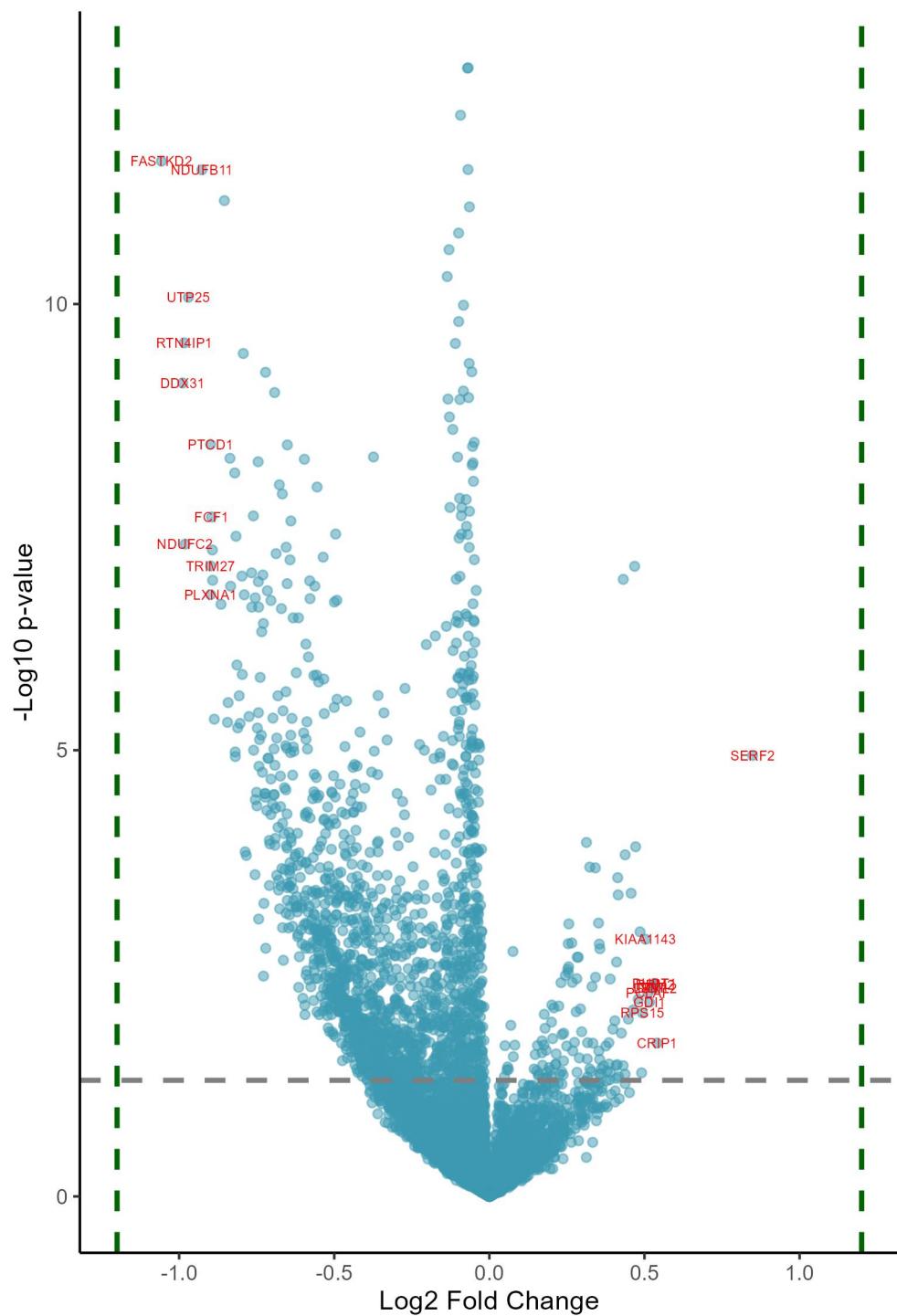
negative cooccurrence Positive cooccurrence



Incidence of ERCC3 | incidence of Protein 2 | observed cooccurrence | e

negative cooccurrence Positive cooccurrence

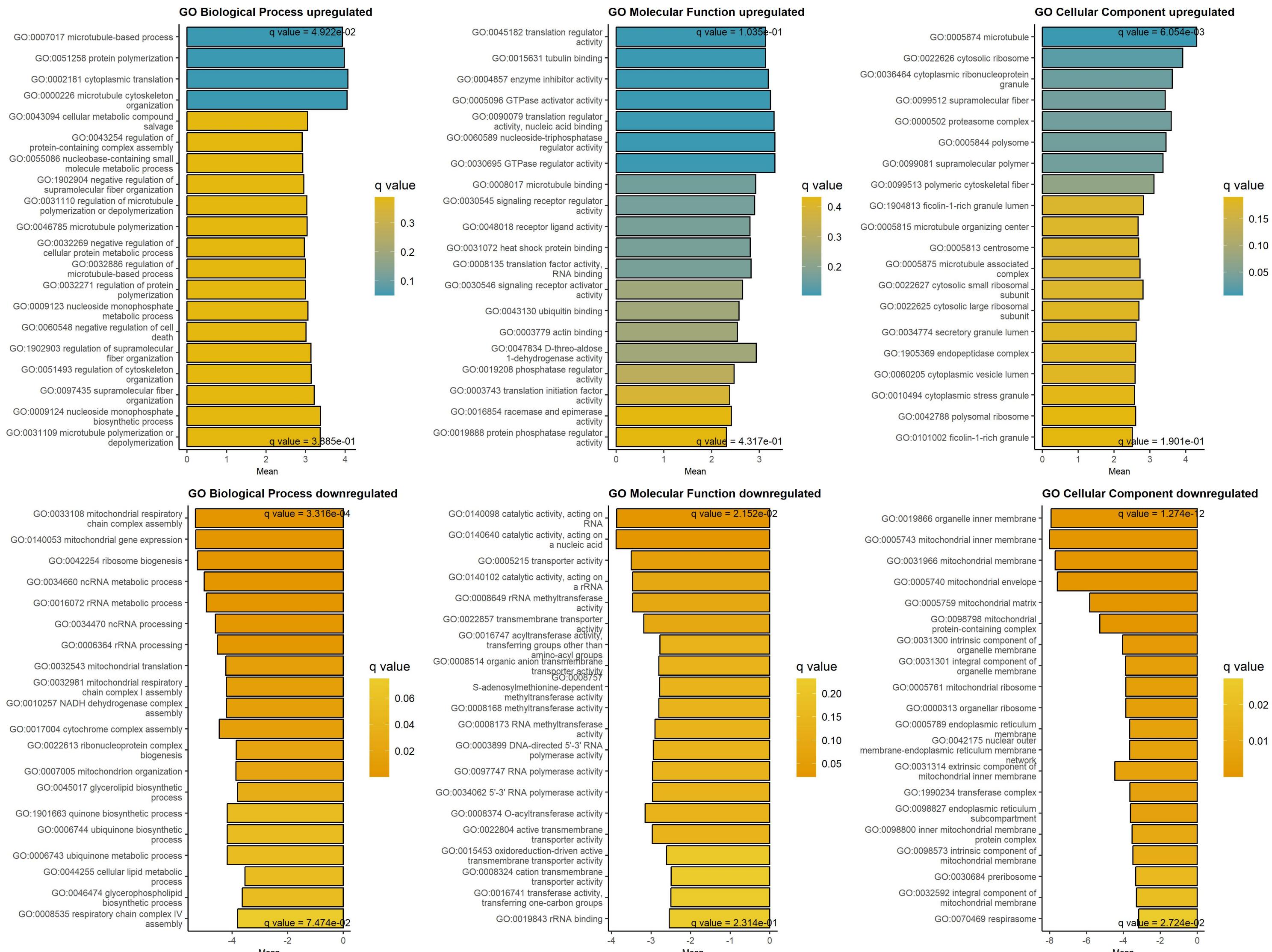




Downregulated at low/absent ERCC3 Upregulated at low/absent ERCC3

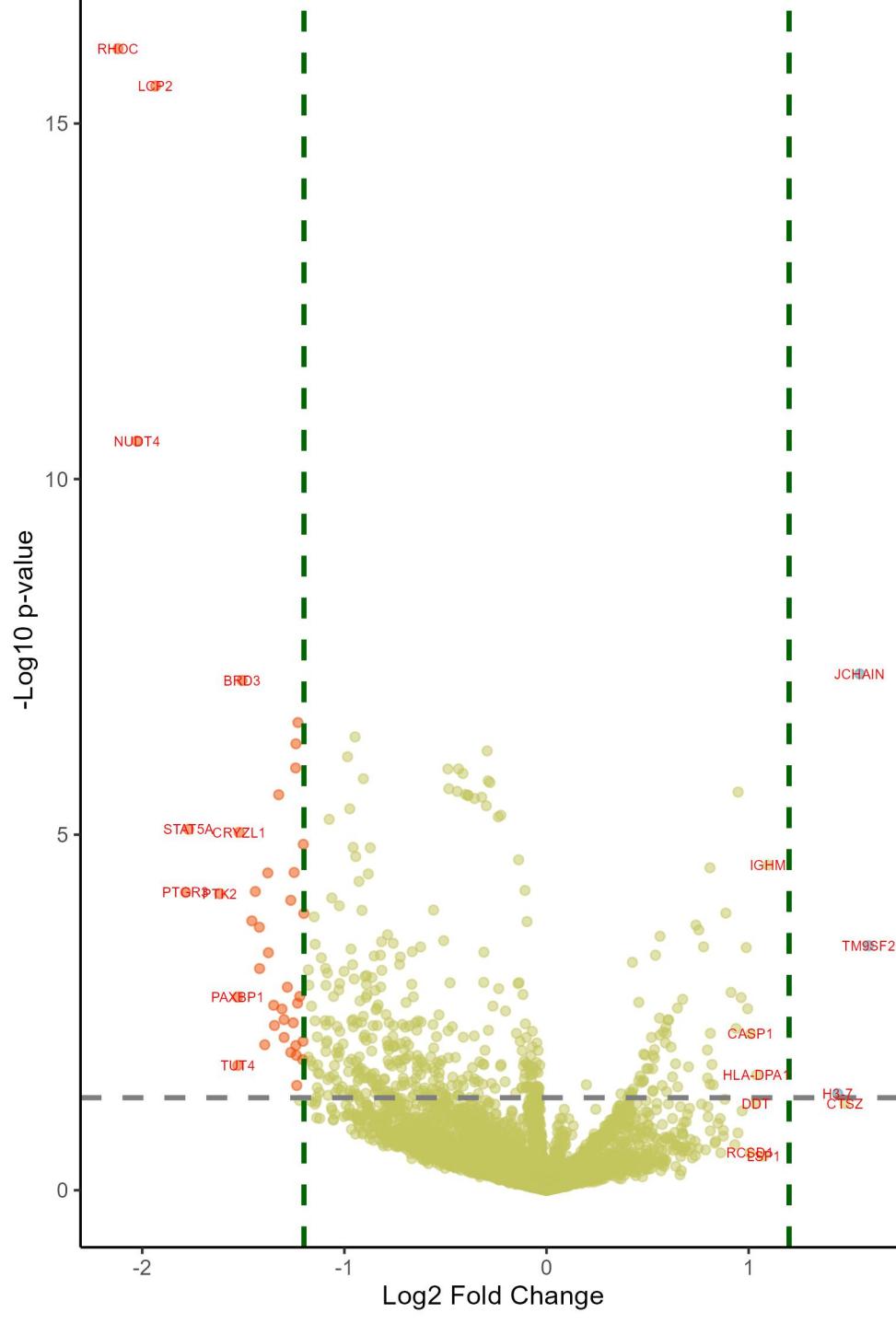
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.06	2.98e-09	FASTKD2	FAST kinase domains 2	0.85	3.63e-04	SERF2	small EDRK-rich factor 2
-0.99	2.32e-07	DDX31	DEAD-box helicase 31	0.54	9.40e-02	CRIP1	cysteine rich protein 1
-0.98	1.08e-07	RTN4IP1	reticulon 4 interacting protein 1	0.53	3.17e-02	RRM2	ribonucleotide reductase regulatory
-0.98	5.34e-06	NDUFC2	NADH:ubiquinone oxidoreductase subu	0.53	3.37e-02	LSM12	LSM12 homolog
-0.97	4.30e-08	UTP25	UTP25 small subunit processome comp	0.53	3.07e-02	PHPT1	phosphohistidine phosphatase 1
-0.93	2.98e-09	NDUFB11	NADH:ubiquinone oxidoreductase subu	0.52	3.34e-02	DDT	D-dopachrome tautomerase
-0.9	1.40e-05	PLXNA1	plexin A1	0.52	4.44e-02	GDI1	GDP dissociation inhibitor 1
-0.9	7.88e-07	PTCD1	pentatricopeptide repeat domain 1	0.51	3.72e-02	PCLAF	PCNA clamp associated factor
-0.9	8.25e-06	TRIM27	tripartite motif containing 27	0.5	1.34e-02	KIAA1143	KIAA1143
-0.9	3.05e-06	FCF1	FCF1 rRNA-processing protein	0.49	5.34e-02	RPS15	ribosomal protein S15
-0.89	5.92e-06	CCDC12	coiled-coil domain containing 12	0.49	1.60e-01	ABRACL	ABRA C-terminal like
-0.89	1.08e-05	RRP36	ribosomal RNA processing 36	0.49	1.16e-02	SRA1	steroid receptor RNA activator 1
-0.89	1.82e-04	PNISR	PNN interacting serine and arginine	0.48	4.21e-02	ARFGAP3	ADP ribosylation factor GTPase acti
-0.86	1.66e-05	PTPRA	protein tyrosine phosphatase recept	0.47	2.31e-03	CDKN2C	cyclin dependent kinase inhibitor 2
-0.85	5.76e-09	CCDC59	coiled-coil domain containing 59	0.47	8.25e-06	CEACAM5	CEA cell adhesion molecule 5
-0.84	1.94e-04	PAXBP1	PAX3 and PAX7 binding protein 1	0.46	5.07e-02	EIF1	eukaryotic translation initiation f
-0.84	1.28e-04	AP2S1	adaptor related protein complex 2 s	0.46	5.80e-03	SSNA1	SS nuclear autoantigen 1
-0.84	9.86e-07	POLG	DNA polymerase gamma, catalytic sub	0.45	2.26e-01	CEP290	centrosomal protein 290
-0.83	1.18e-05	TMEM209	transmembrane protein 209	0.45	6.03e-02	FLYWCH2	FLYWCH family member 2
-0.82	1.27e-06	NSUN4	NOP2/Sun RNA methyltransferase 4	0.44	2.66e-03	NECAP1	NECAP endocytosis associated 1
-0.82	3.38e-04	CFAP20	cilia and flagella associated prote	0.44	1.93e-01	GLRX	glutaredoxin
-0.82	3.70e-04	TRABD	TraB domain containing	0.44	1.64e-01	CORO1A	coronin 1A
-0.82	4.51e-06	QRSL1	glutaminyl-tRNA amidotransferase su	0.43	1.06e-05	CEACAM6	CEA cell adhesion molecule 6
-0.81	6.20e-05	MCM3AP	minichromosome maintenance complex	0.43	1.42e-01	PDXDC1	pyridoxal dependent decarboxylase d
-0.81	2.19e-04	UFSP2	UFM1 specific peptidase 2	0.43	7.78e-02	ZNF428	zinc finger protein 428
-0.81	1.13e-04	LCLAT1	lysocardiolipin acyltransferase 1	0.42	2.51e-01	ZNF706	zinc finger protein 706
-0.8	1.98e-04	SOAT1	sterol O-acyltransferase 1	0.42	1.71e-01	CHMP2B	charged multivesicular body protein
-0.8	1.01e-05	LLPH	LLP homolog, long-term synaptic fac	0.42	6.02e-03	RBIS	ribosomal biogenesis factor
-0.8	7.53e-05	TRRAP	transformation/transcription domain	0.41	4.30e-03	MUC1	mucin 1, cell surface associated

GAGE analysis on upregulated and downregulated proteins at low/absent ERCC3 protein, DB1

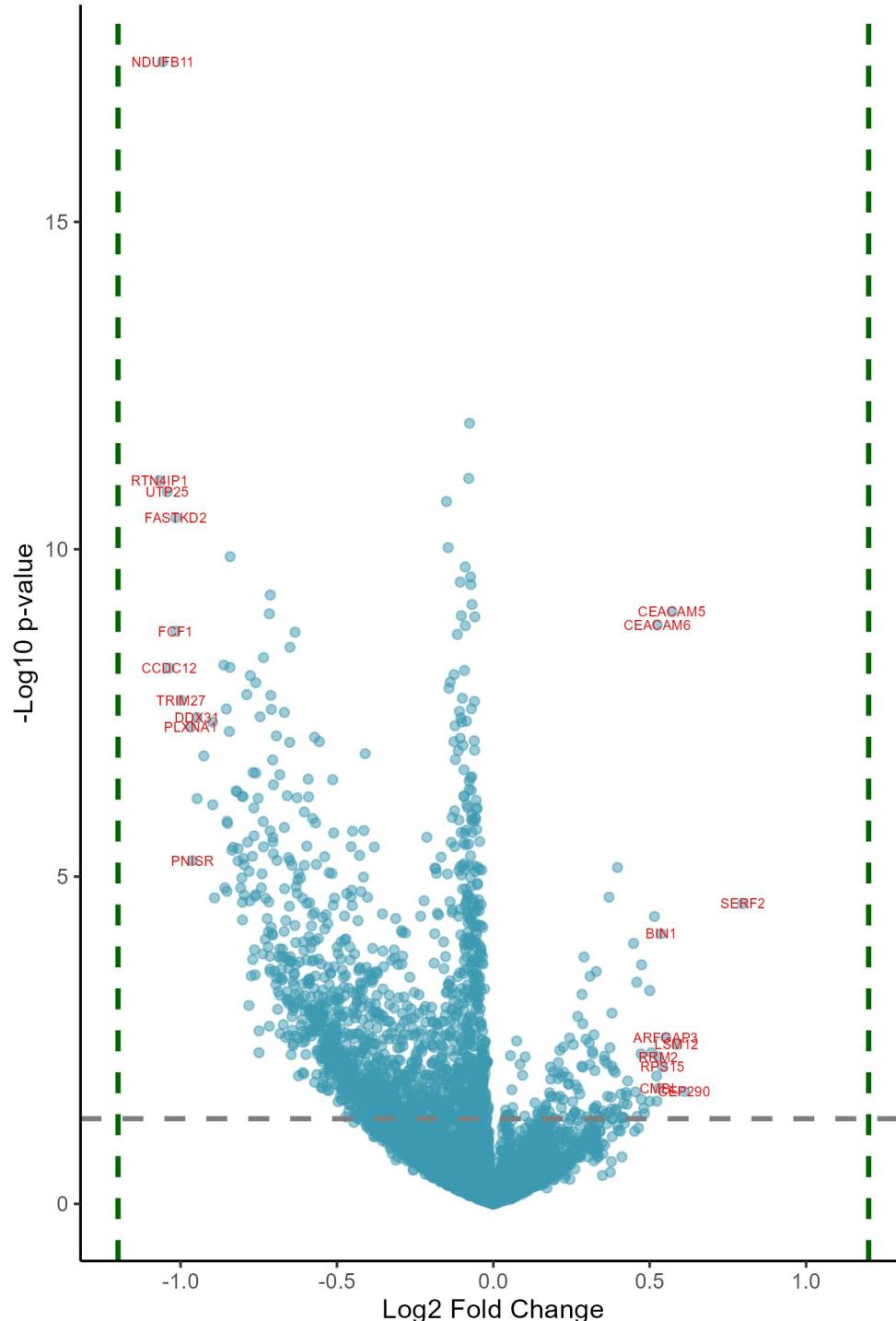


p-value < 0.05 & logFC > 1.2

Downregulated in blood cancers at low/absent ERCC3 Upregulated in blood cancers at low/absent ERCC3

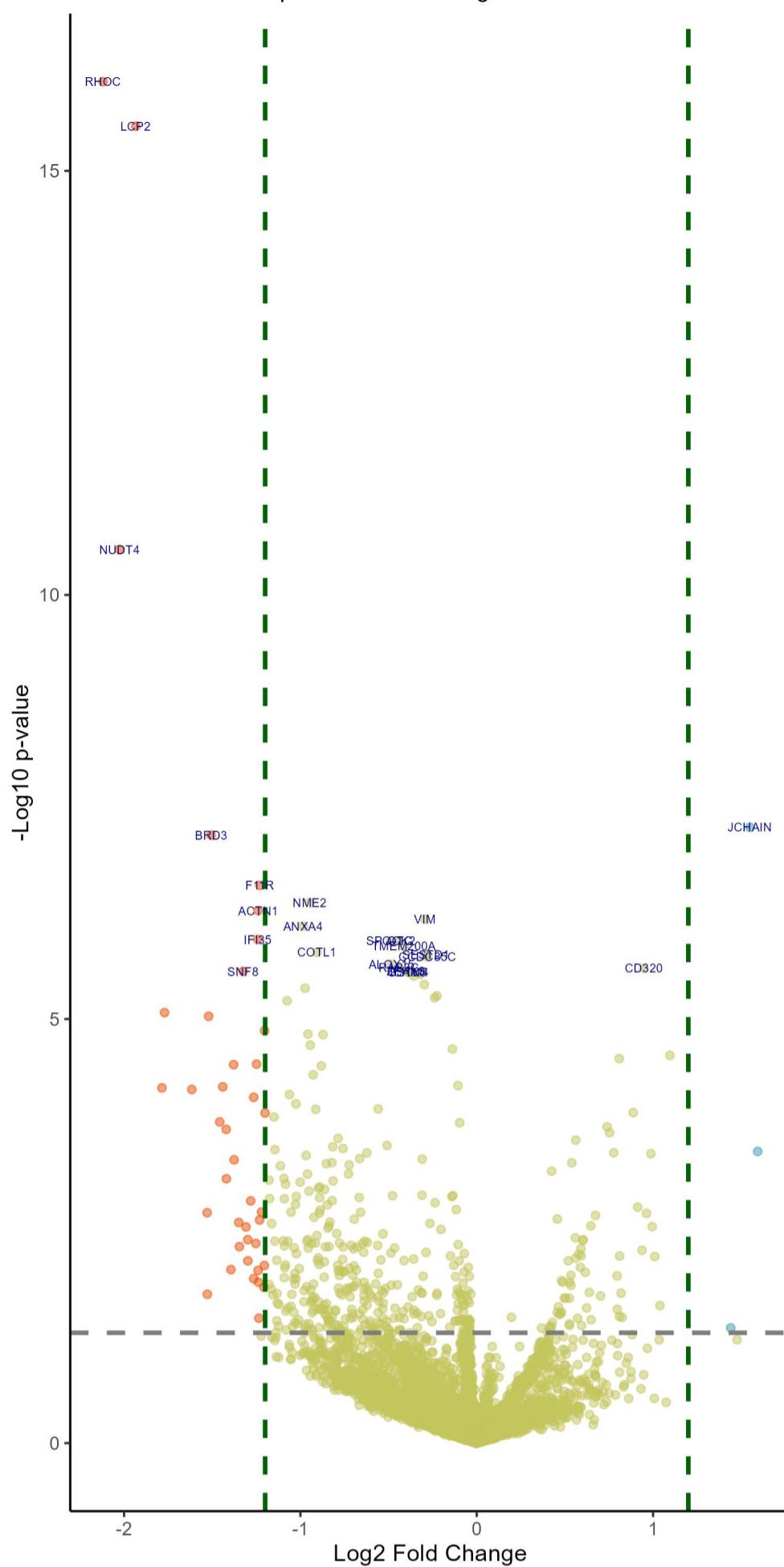


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.12	2.95e-13	RHOC	ras homolog family member C	1.59	3.51e-02	TM9SF2	transmembrane 9 superfamily member
-2.03	4.85e-08	NUDT4	nudix hydrolase 4	1.55	7.29e-05	JCHAIN	joining chain of multimeric IgA and cathepsin Z
-1.93	6.58e-13	LCP2	lymphocyte cytosolic protein 2	1.48	8.08e-01	CTSZ	H3.7 histone (putative)
-1.79	8.98e-03	PTGR3	prostaglandin reductase 3	1.44	7.06e-01	H3-7	immunoglobulin heavy constant mu
-1.77	1.69e-03	STAT5A	signal transducer and activator of	1.1	4.46e-03	IGHM	lymphocyte specific protein 1
-1.62	9.18e-03	PTK2	protein tyrosine kinase 2	1.07	9.45e-01	LSP1	D-dopachrome tautomerase
-1.53	1.11e-01	PAXBP1	PAX3 and PAX7 binding protein 1	1.04	5.19e-01	HLA-DPA1	major histocompatibility complex, c
-1.53	4.35e-01	TUT4	terminal uridylyl transferase 4	1.03	8.08e-01	DDT	caspase 1
-1.52	1.82e-03	CRYZL1	crystallin zeta like 1	1.01	2.39e-01	CASP1	RCSD1
-1.51	7.52e-05	BRD3	bromodomain containing 3	1.01	9.45e-01	TMED8	RCSD domain containing 1
-1.46	1.87e-02	LGALS9	galectin 9	0.99	1.44e-01	MCEE	methylmalonyl-CoA epimerase
-1.44	8.91e-03	UNC13D	unc-13 homolog D	0.99	3.57e-02	RB1	ubiquitin conjugating enzyme E2 J1
-1.42	2.18e-02	ZC3HAV1L	zinc finger CCCH-type containing, a	0.97	8.70e-01	SNTB1	RB transcriptional corepressor 1
-1.42	5.91e-02	BMP2K	BMP2 inducible kinase	0.96	1.11e-01	GLDC	syntrophin beta 1
-1.39	2.99e-01	GLDC	glycine decarboxylase	0.95	7.49e-04	CD320	CD320 molecule
-1.38	5.34e-03	RPS6KA1	ribosomal protein S6 kinase A1	0.95	9.45e-01	SLC25A1	solute carrier family 25 member 1
-1.38	4.00e-02	BOLA1	bola family member 1	0.94	2.13e-01	UBE2J1	ubiquitin clasp associated factor
-1.35	1.34e-01	LGALS3BP	galactosidase 3 binding protein	0.93	9.45e-01	PCLAF	PCNA clamp associated factor
-1.35	2.02e-01	JUND	JunD proto-oncogene, AP-1 transcript	0.91	1.01e-01	BPBM	bisphosphoglycerate mutase
-1.33	7.49e-04	SNF8	SNF8 subunit of ESCRT-II	0.89	1.52e-02	EEF1A2	eukaryotic translation elongation f
-1.31	1.45e-01	TSPYLI1	TSPY like 1	0.88	7.64e-01	GLCCI1	glucocorticoid induced 1
-1.3	1.91e-01	SERPINB6	serpin family B member 6	0.87	9.45e-01	DLG1	discs large MAGUK scaffold protein
-1.3	2.52e-01	FTL	ferritin light chain	0.87	9.45e-01	KRT8	keratin 8
-1.28	8.83e-02	RAB11FIP1	RAB11 family interacting protein 1	0.86	9.45e-01	RALYL	RALY RNA binding protein like
-1.27	3.44e-01	CMPK2	cytidine/uridine monophosphate kina	0.86	9.05e-01	RRM1	ribonucleotide reductase catalytic
-1.27	1.09e-02	CASP6	caspase 6	0.85	9.45e-01	AP1M1	adaptor related protein complex 1 s
-1.25	1.96e-01	VPS51	VPS51 subunit of GARP complex	0.84	9.45e-01	SS18	SS18 subunit of BAF chromatin remod
-1.25	5.34e-03	FSCN1	fascin actin-bundling protein 1	0.83	9.45e-01	F5	coagulation factor V
-1.24	5.67e-04	IFI35	interferon induced protein 35	0.82	6.23e-01	CD59	CD59 molecule (CD59 blood group)

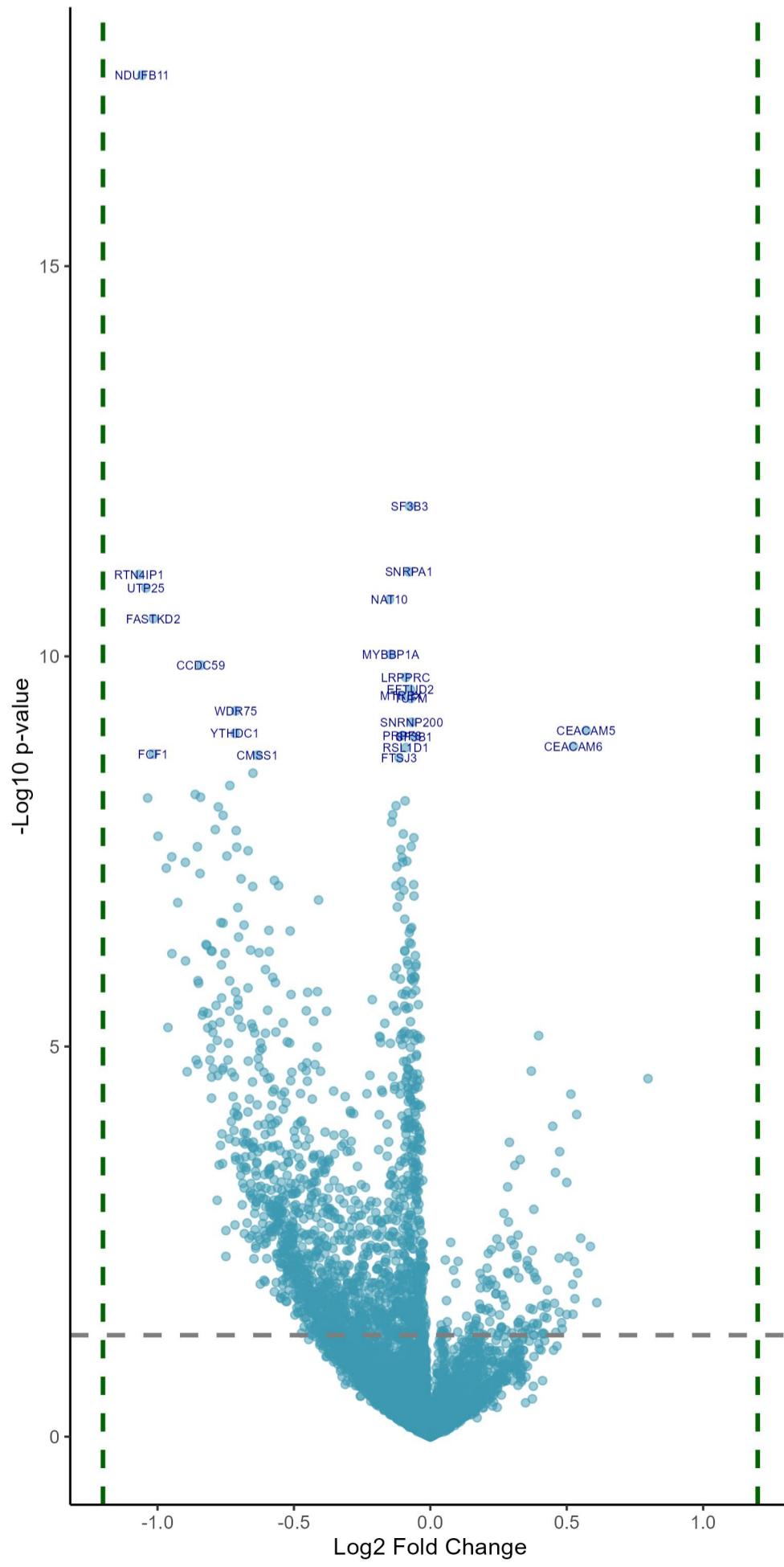
Differentially expressed proteins in solid cancers at absence/low amount of ERCC3 , DB1
p-value < 0.05 & logFC > 1.2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.07	1.19e-08	RTN4IP1	reticulon 4 interacting protein 1	0.8	7.60e-04	SERF2	small EDRK-rich factor 2
-1.06	1.19e-14	NDUFB11	NADH:ubiquinone oxidoreductase subu	0.61	9.63e-02	CEP290	centrosomal protein 290
-1.04	1.47e-08	UTP25	UTP25 small subunit processome comp	0.59	3.13e-02	LSM12	LSM12 homolog
-1.04	1.45e-06	CCDC12	coiled-coil domain containing 12	0.57	3.49e-07	CEACAM5	CEA cell adhesion molecule 5
-1.02	5.12e-07	FCF1	FCF1 rRNA-processing protein	0.55	2.62e-02	ARFGAP3	ADP ribosylation factor GTPase acti
-1.02	2.74e-08	FASTKD2	FAST kinase domains 2	0.54	5.15e-02	RPS15	ribosomal protein S15
-1	3.36e-06	TRIM27	tripartite motif containing 27	0.54	1.75e-03	BIN1	bridging integrator 1
-0.97	6.37e-06	PLXNA1	plexin A1	0.53	8.88e-02	CMBL	carboxymethylenebutenolide homolo
-0.96	2.49e-04	PNISR	PNN interacting serine and arginine	0.53	4.38e-02	RRM2	ribonucleotide reductase regulatory
-0.95	5.13e-06	DDX31	DEAD-box helicase 31	0.52	4.46e-07	CEACAM6	CEA cell adhesion molecule 6
-0.95	4.67e-05	NDUFC2	NADH:ubiquinone oxidoreductase subu	0.52	1.22e-01	ENO2	enolase 2
-0.93	1.42e-05	RRP36	ribosomal RNA processing 36	0.52	6.53e-02	GDI1	GDP dissociation inhibitor 1
-0.9	5.58e-06	BRI3BP	BRI3 binding protein	0.52	1.07e-03	MUC1	mucin 1, cell surface associated
-0.9	5.61e-05	PEX16	peroxisomal biogenesis factor 16	0.51	3.89e-02	SELENBP1	selenium binding protein 1
-0.89	6.67e-04	KRT5	keratin 5	0.5	7.90e-03	SRA1	steroid receptor RNA activator 1
-0.86	1.40e-06	POLG	DNA polymerase gamma, catalytic sub	0.5	1.23e-01	PDXDC1	pyridoxal dependent decarboxylase d
-0.86	5.17e-04	CFAP20	cilia and flagella associated prote	0.48	1.66e-01	ABRACL	ABRA C-terminal like
-0.85	4.22e-06	PTCD1	pentatricopeptide repeat domain 1	0.48	1.46e-01	CRIP1	cysteine rich protein 1
-0.85	8.64e-05	TRRAP	transformation/transcription domain	0.47	3.98e-03	NECAP1	NECAP endocytosis associated 1
-0.85	5.68e-04	TRABD	Trab domain containing	0.47	1.17e-01	C19orf25	chromosome 19 open reading frame 25
-0.85	9.00e-05	RPS19BP1	ribosomal protein S19 binding prote	0.47	4.05e-02	ROCK2	Rho associated coiled-coil containi
-0.84	7.33e-06	QRSL1	glutaminyl-tRNA amidotransferase su	0.46	2.34e-01	MAP1B	microtubule associated protein 1B
-0.84	1.45e-06	NSUN4	NOP2/Sun RNA methyltransferase 4	0.46	1.77e-01	TMEM263	transmembrane protein 263
-0.84	8.63e-08	CCDC59	coiled-coil domain containing 59	0.46	6.31e-03	MAP1A	microtubule associated protein 1A
-0.84	1.85e-04	PTPRA	protein tyrosine phosphatase recept	0.46	9.77e-02	PHPT1	phosphohistidine phosphatase 1
-0.83	1.69e-04	DNTTIP1	deoxyribonucleotidyltransferase termina	0.45	2.52e-01	RPL36A	ribosomal protein L36a
-0.82	3.99e-05	SENP3	SUMO specific peptidase 3	0.45	2.28e-03	GALM	galactose mutarotase
-0.82	4.06e-05	C1D	C1D nuclear receptor corepressor	0.43	7.36e-02	PLPBP	pyridoxal phosphate binding protein
-0.82	2.49e-04	MCM3AP	minichromosome maintenance complex	0.43	1.32e-01	DUSP23	dual specificity phosphatase 23

ERCC3 network, DB1, no Pearson r > 0.3

Sorted by p values!
Downregulated in blood cancers at low/absent ERCC3 Upregulated in blood cancers at low/absent ERCC3

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.12	2.95e-13	RHOC	ras homolog family member C	1.55	7.29e-05	JCHAIN	joining chain of multimeric IgA and
-1.93	6.58e-13	LCP2	lymphocyte cytosolic protein 2	0.95	7.49e-04	CD320	CD320 molecule
-2.03	4.85e-08	NUDT4	nudix hydrolase 4	1.1	4.46e-03	IGHM	immunoglobulin heavy constant mu
-1.51	7.52e-05	BRD3	bromodomain containing 3	0.81	4.74e-03	FNDC3A	fibronectin type III domain contain
-1.23	2.52e-04	F11R	F11 receptor	0.89	1.52e-02	EEF1A2	eukaryotic translation elongation f
-0.95	3.51e-04	NME2	NME/NM23 nucleoside diphosphate kin	0.74	2.07e-02	KCTD5	potassium channel tetramerization d
-1.24	3.90e-04	ACTN1	actinin alpha 1	0.75	2.34e-02	SLC12A9	solute carrier family 12 member 9
-0.29	4.42e-04	VIM	vimentin	0.56	2.79e-02	G3BP1	G3BP stress granule assembly factor
-0.98	4.85e-04	ANXA4	annexin A4	1.59	3.51e-02	TM9SF2	transmembrane 9 superfamily member
-1.24	5.67e-04	IFI35	interferon induced protein 35	0.78	3.55e-02	MCAM	melanoma cell adhesion molecule
-0.44	5.67e-04	OTC	ornithine transcarbamylase	0.99	3.57e-02	MCEE	methylmalonyl-CoA epimerase
-0.49	5.67e-04	SPOCK2	SPARC (osteonectin), cwcv and kazal	0.54	4.23e-02	EDF1	endothelial differentiation related
-0.41	6.13e-04	TMEM200A	transmembrane protein 200A	0.42	5.05e-02	SEC23IP	SEC23 interacting protein
-0.91	6.79e-04	COTL1	coactosin like F-actin binding prot	0.91	1.01e-01	BPGM	bisphosphoglycerate mutase
-0.29	6.84e-04	SESTD1	SEC14 and spectrin domain containin	0.96	1.11e-01	SNTB1	syntrophin beta 1
-0.28	6.84e-04	CCDC85C	coiled-coil domain containing 85C	0.67	1.16e-01	CLGN	calmegin
-0.48	7.49e-04	ALOX15	arachidonate 15-lipoxygenase	0.46	1.26e-01	ZCCHC8	zinc finger CCHC-type containing 8
-0.44	7.49e-04	RAB3C	RAB3C, member RAS oncogene family	0.65	1.43e-01	ST14	ST14 transmembrane serine protease
-0.4	7.49e-04	ZFHX3	zinc finger homeobox 3	0.99	1.44e-01	TMED8	transmembrane p24 trafficking prote
-1.33	7.49e-04	SNF8	SNF8 subunit of ESCRT-II	0.56	1.86e-01	IMPDH1	inosine monophosphate dehydrogenase
-0.39	7.49e-04	GSTM4	glutathione S-transferase mu 4	0.6	1.91e-01	CWF19L2	CWF19 like cell cycle control facto
-0.39	7.49e-04	ICAM5	intercellular adhesion molecule 5	0.6	1.91e-01	ARSA	arylsulfatase A
-0.32	7.61e-04	SH2D4A	SH2 domain containing 4A	0.59	2.06e-01	CEPB	CCAAT enhancer binding protein beta
-0.36	7.65e-04	LAMA5	laminin subunit alpha 5	0.94	2.13e-01	UBE2J1	ubiquitin conjugating enzyme E2 J1
-0.3	9.31e-04	B4GALNT1	beta-1,4-N-acetyl-galactosaminyltra	0.58	2.29e-01	FADS1	fatty acid desaturase 1
-0.97	9.94e-04	ZYX	zyxin	0.59	2.37e-01	AGA	aspartylglucosaminidase
-0.23	1.18e-03	TMTC3	transmembrane O-mannosyltransferase	0.81	2.37e-01	ATXN3	ataxin 3
-0.24	1.21e-03	STXBP4	syntaxin binding protein 4	1.01	2.39e-01	CASP1	caspase 1
-1.08	1.27e-03	ISG15	ISG15 ubiquitin like modifier	0.56	2.46e-01	KRT5	keratin 5
-1.77	1.69e-03	STAT5A	signal transducer and activator of	0.52	2.52e-01	PEX16	peroxisomal biogenesis factor 16
-1.52	1.82e-03	CRYZL1	crystallin zeta like 1	0.59	2.88e-01	PCBP3	poly(rC) binding protein 3
-1.2	2.60e-03	ARMC10	armadillo repeat containing 10	0.62	3.08e-01	BORCS8-MEF2B	BORCS8-MEF2B readthrough
-0.96	2.75e-03	DBN1	drebrin 1	0.53	3.28e-01	VKORC1L1	vitamin K epoxide reductase complex
-0.87	2.75e-03	EPB41L2	erythrocyte membrane protein band 4	0.8	3.30e-01	TNS3	tensin 3
-0.94	3.55e-03	CYB5A	cytochrome b5 type A	0.48	3.61e-01	GEMIN2	gem nuclear organelle associated pr
-0.14	3.84e-03	GPR107	G protein-coupled receptor 107	0.49	3.70e-01	NAGLU	N-acetyl-alpha-glucosaminidase
-1.25	5.34e-03	FSCN1	fascin actin-bundling protein 1	0.53	3.70e-01	TCIRG1	T cell immune regulator 1, ATPase H
-1.38	5.34e-03	RPS6KA1	ribosomal protein S6 kinase A1	0.53	3.88e-01	SH2B2	SH2B adaptor protein 2
0.89	5.39e-03	IIMMA1	IIM domain and actin binding 1	0.64	4.21e-01	CTSG	cathepsin G

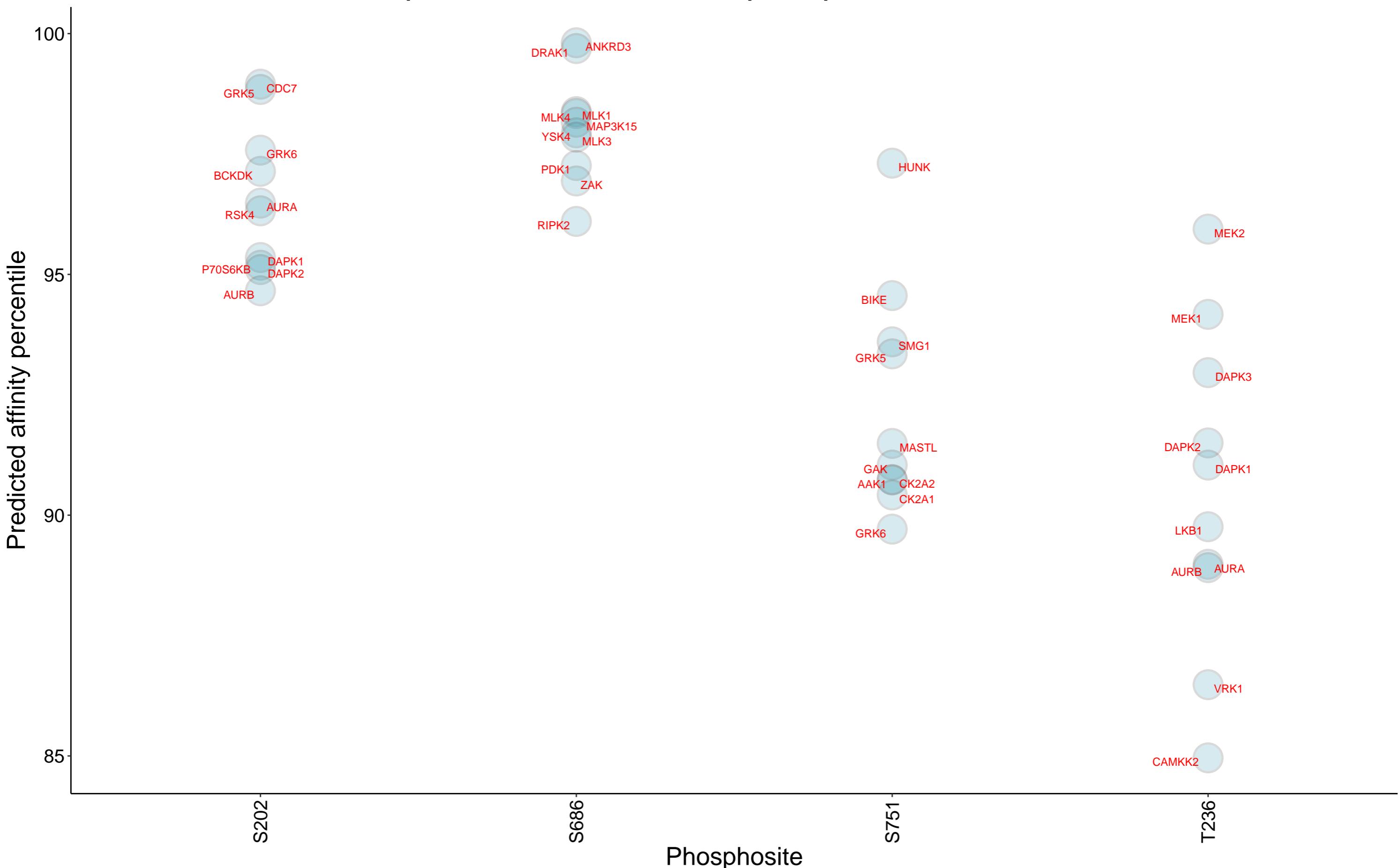
Sorted by p values!
Downregulated in solid cancers at low/absent ERCC3 Upregulated in solid cancers at low/absent ERCC3

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.06	1.19e-14	NDUFB11	NADH:ubiquinone oxidoreductase subu	0.57	3.49e-07	CEACAM5	CEA cell adhesion molecule 5
-0.08	2.64e-09	SF3B3	splicing factor 3b subunit 3	0.52	4.46e-07	CEACAM6	CEA cell adhesion molecule 6
-0.08	1.19e-08	SNRPA1	small nuclear ribonucleoprotein pol	0.4	2.93e-04	MUC13	mucin 13, cell surface associated
-1.07	1.19e-08	RTN4IP1	reticulon 4 interacting protein 1	0.37	6.60e-04	CDH17	cadherin 17
-1.04	1.47e-08	UTP25	UTP25 small subunit processome comp	0.8	7.60e-04	SERF2	small EDRK-rich factor 2
-0.15	1.77e-08	NAT10	N-acetyltransferase 10	0.52	1.07e-03	MUC1	mucin 1, cell surface associated
-1.02	2.74e-08	FASTKD2	FAST kinase domains 2	0.54	1.75e-03	BIN1	bridging integrator 1
-0.14	6.97e-08	MYBBP1A	MYB binding protein 1a	0.45	2.28e-03	GALM	galactose mutarotase
-0.84	8.63e-08	CCDC59	coiled-coil domain containing 59	0.29	3.28e-03	BCAS1	brain enriched myelin associated pr
-0.09	1.12e-07	LRPPRC	leucine rich pentatricopeptide repe	0.47	3.98e-03	NECAP1	NECAP endocytosis associated 1
-0.07	1.47e-07	EFTUD2	elongation factor Tu GTP binding do	0.33	4.78e-03	ABCC3	ATP binding cassette subfamily C me
-0.11	1.62e-07	MTREX	Mtr4 exosome RNA helicase	0.31	5.36e-03	AGR3	anterior gradient 3, protein disulp
-0.07	1.64e-07	TUFM	Tu translation elongation factor, m	0.46	6.31e-03	MAP1A	microtubule associated protein 1A
-0.71	2.22e-07	WDR75	WD repeat domain 75	0.5	7.90e-03	SRA1	steroid receptor RNA activator 1
-0.07	2.90e-07	SNRNP200	small nuclear ribonucleoprotein U5	0.28	8.72e-03	CKM	creative kinase, M-type
-0.72	3.58e-07	YTHDC1	YTH domain containing 1	0.38	1.41e-02	WRAP73	WD repeat containing, antisense to
-0.1	3.58e-07	PRPF8	pre-mRNA processing factor 8	0.27	1.52e-02	ELAPOR1	endosome-lysosome associated apopto
-0.06	3.58e-07	SF3B1	splicing factor 3b subunit 1	0.29	1.85e-02	ALPL	alkaline phosphatase, biominaliz
-0.09	4.46e-07	RSL1D1	ribosomal L1 domain containing 1	0.32	2.46e-02	WASHC3	WASH complex subunit 3
-1.02	5.12e-07	FCF1	FCF1 rRNA-processing protein	0.55	2.62e-02	ARFGAP3	ADP ribosylation factor GTPase acti
-0.63	5.12e-07	CMSS1	cms1 ribosomal small subunit homolo	0.24	2.67e-02	HMGCS2	3-hydroxy-3-methylglutaryl-Co synt
-0.11	5.31e-07	FTSJ3	FtsJ RNA 2'-O-methyltransferase 3	0.3	2.74e-02	FBP1	fructose-bisphosphatase 1
-0.65	8.03e-07	PPP1CC	protein phosphatase 1 catalytic sub	0.07	2.87e-02	DTYMK	deoxythymidine kinase
-0.74	1.11e-06	PTPMT1	protein tyrosine phosphatase mitoch	0.31	3.03e-02	SSNA1	SS nuclear autoantigen 1
-0.86	1.40e-06	POLG	DNA polymerase gamma, catalytic sub	0.59	3.13e-02	LSM12	LSM12 homolog
-0.84	1.45e-06	NSUN4	NOP2/Sun RNA methyltransferase 4	0.26	3.14e-02	ANKRD13A	ankyrin repeat domain 13A
-1.04	1.45e-06	CCDC12	coiled-coil domain containing 12	0.22	3.36e-02	ARFGEF3	ARFGEF family member 3
-0.09	1.53e-06	NOP56	NOP56 ribonucleoprotein	0.37	3.42e-02	SRSF2	serine and arginine rich splicing f
-0.13	1.71e-06	UTP18	UTP18 small subunit processome comp	0.21	3.68e-02	VILL	villin like
-0.78	1.72e-06	CWC22	CWC22 spliceosome associated protei	0.32	3.76e-02	CDKN2C	cyclin dependent kinase inhibitor 2
-0.14	2.07e-06	DDX18	DEAD-box helicase 18				

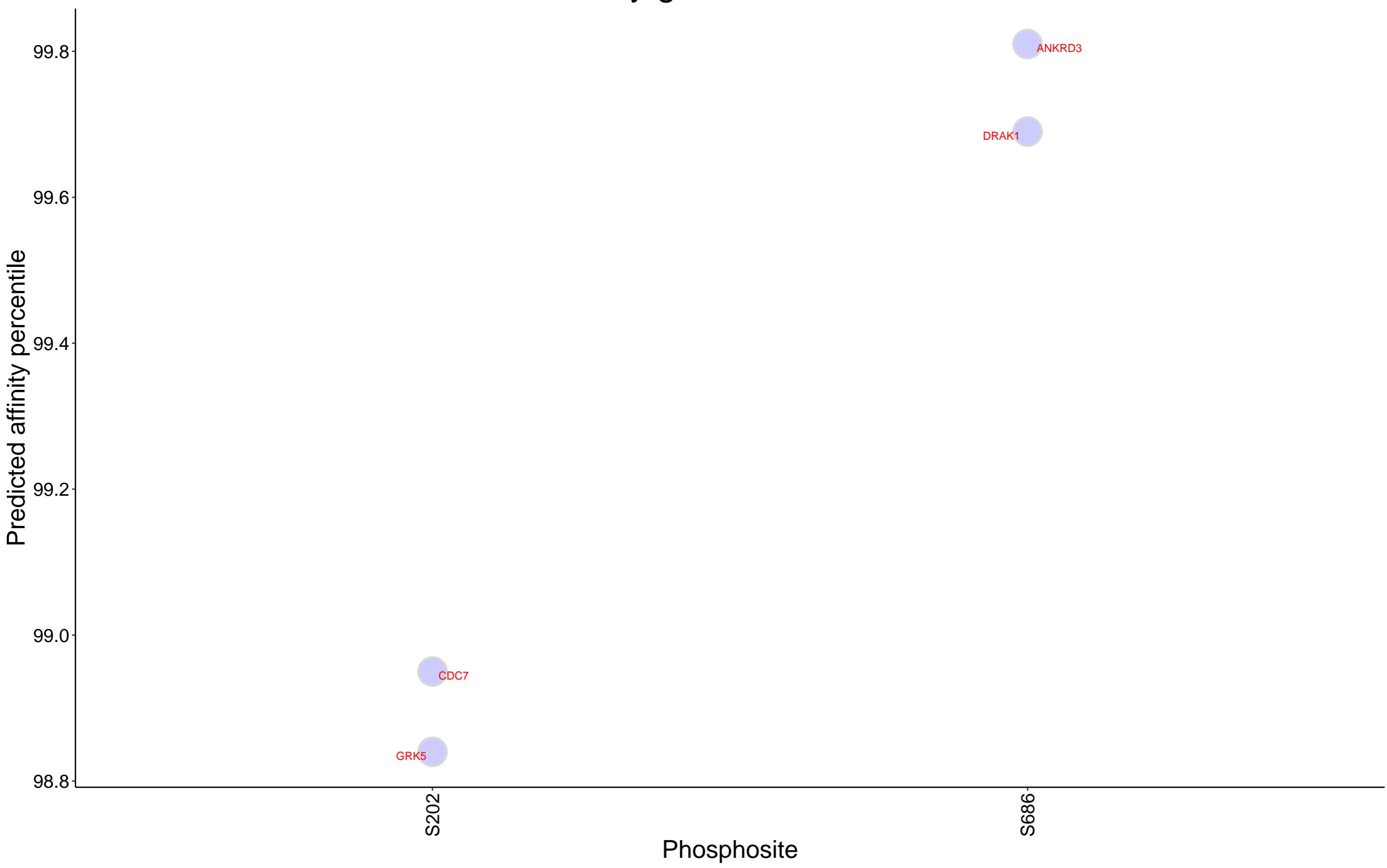
Insufficient number of paired observations in DB1 for ERCC3

Insufficient number of paired observations in DB1 for ERCC3

Top 10 kinases for each phosphosite in ERCC3



Kinases with affinity greater than 98.5% to ERCC3



No sufficient paired observations in DB1 for ERCC3