

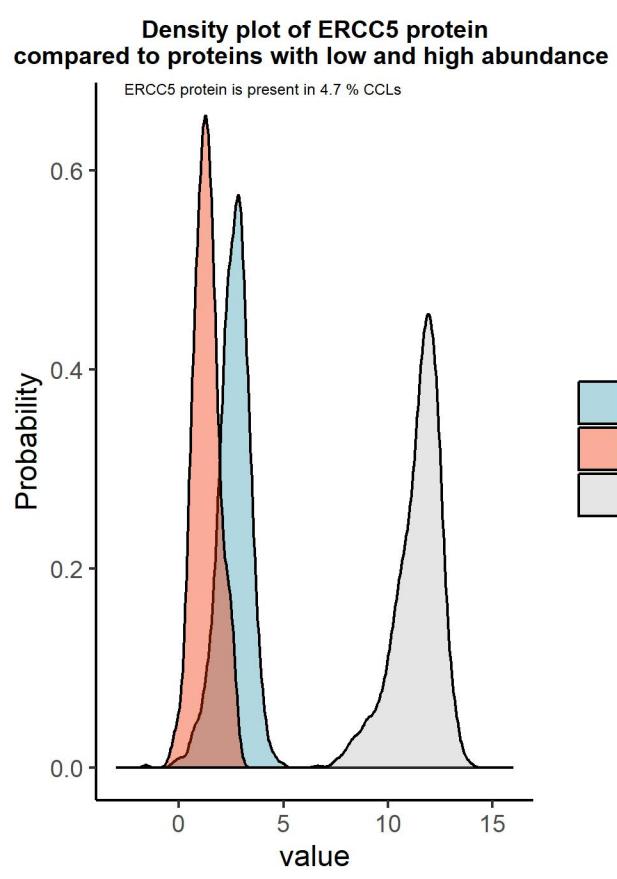
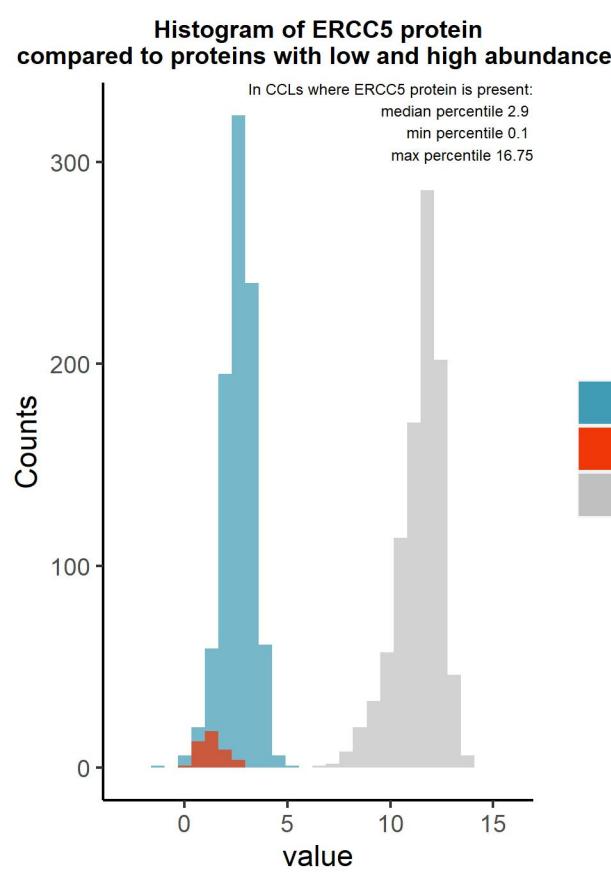
ERCC5

Protein name: ERCC5 ; UNIPROT: P28715 ; Gene name: ERCC excision repair 5, endonuclease

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

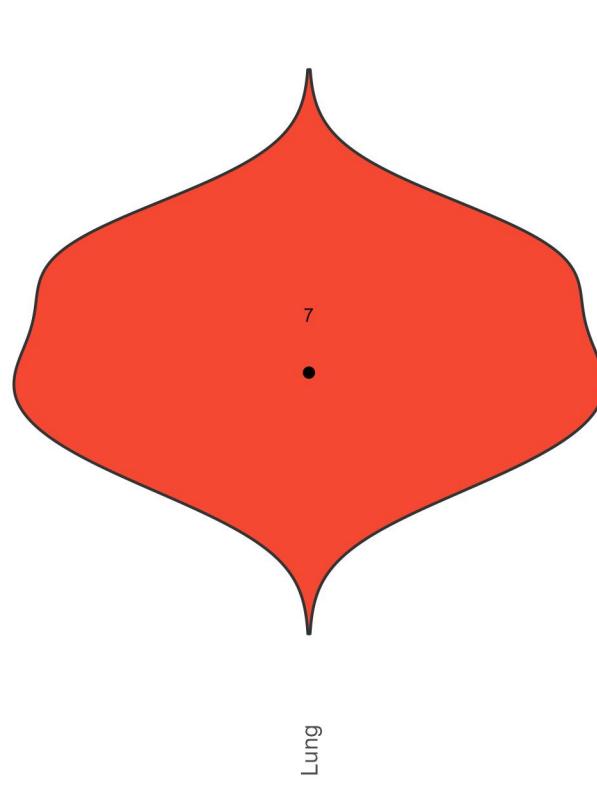
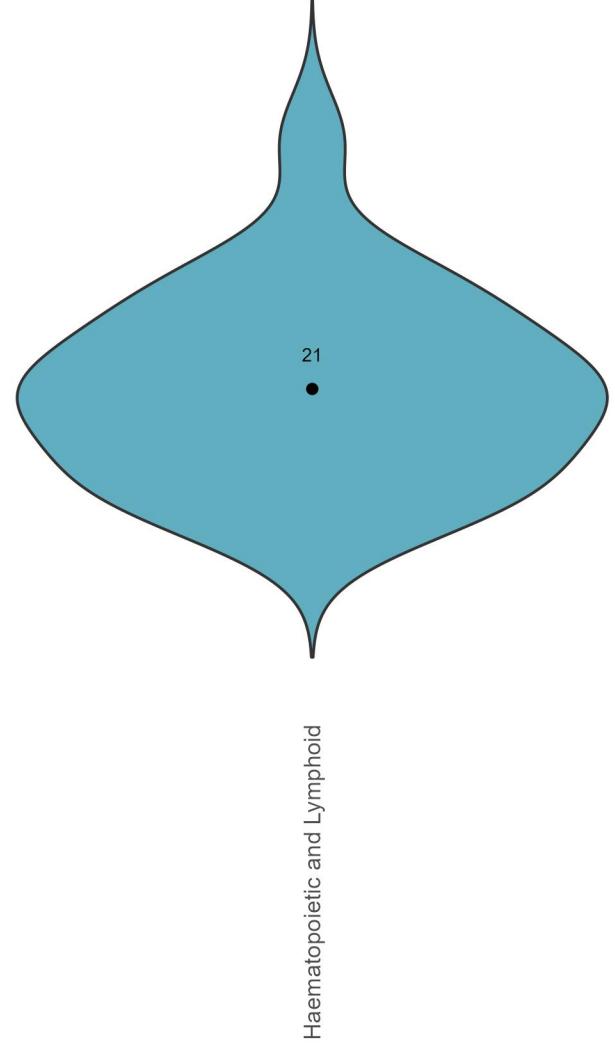
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs



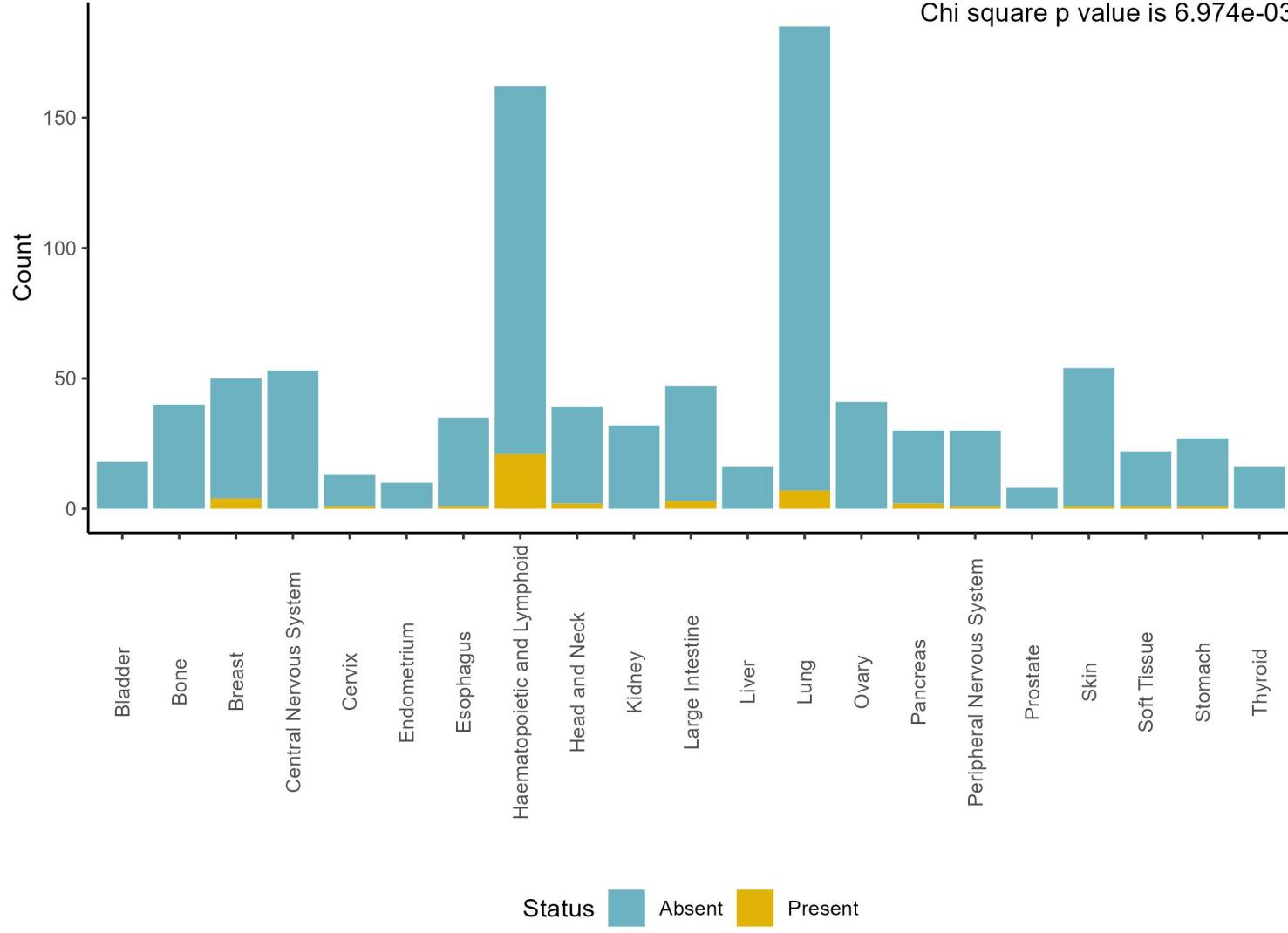
Amount of ERCC5 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 3.694e-01



Present and absent ERCC5 protein counts by tissue, DB1

Chi square p value is 6.974e-03

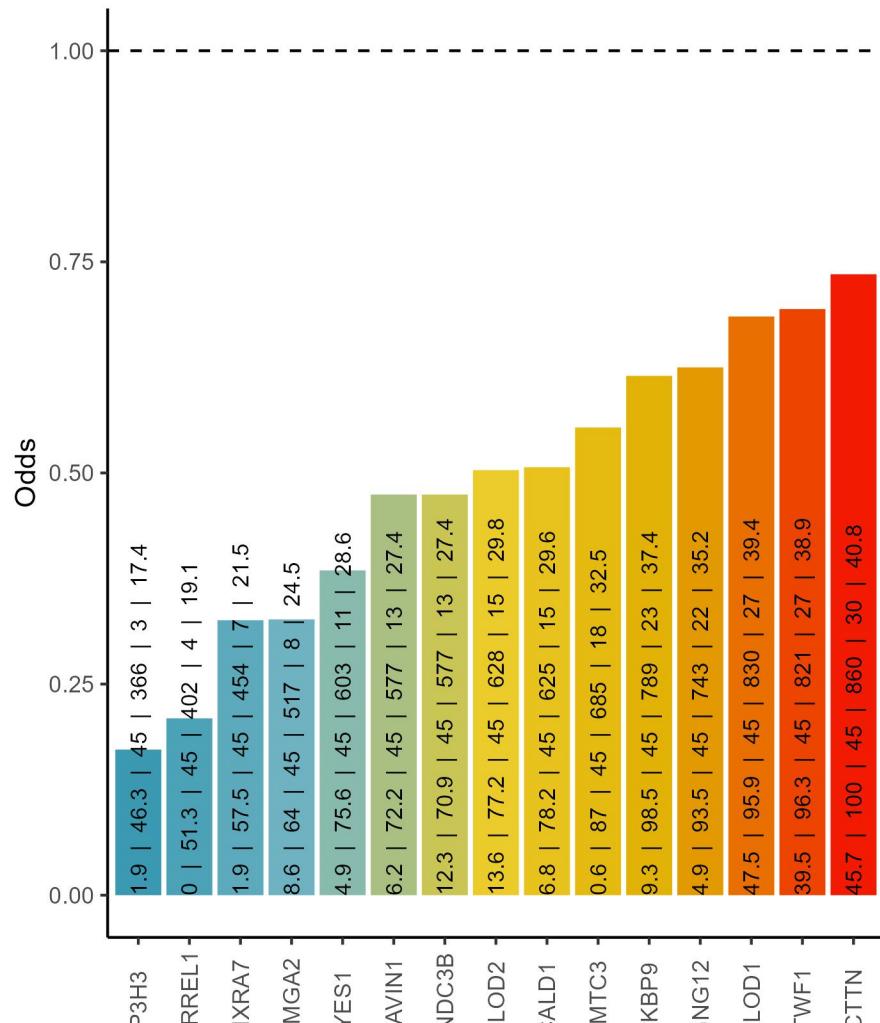


Cooccurrence with ERCC5 protein, DB1

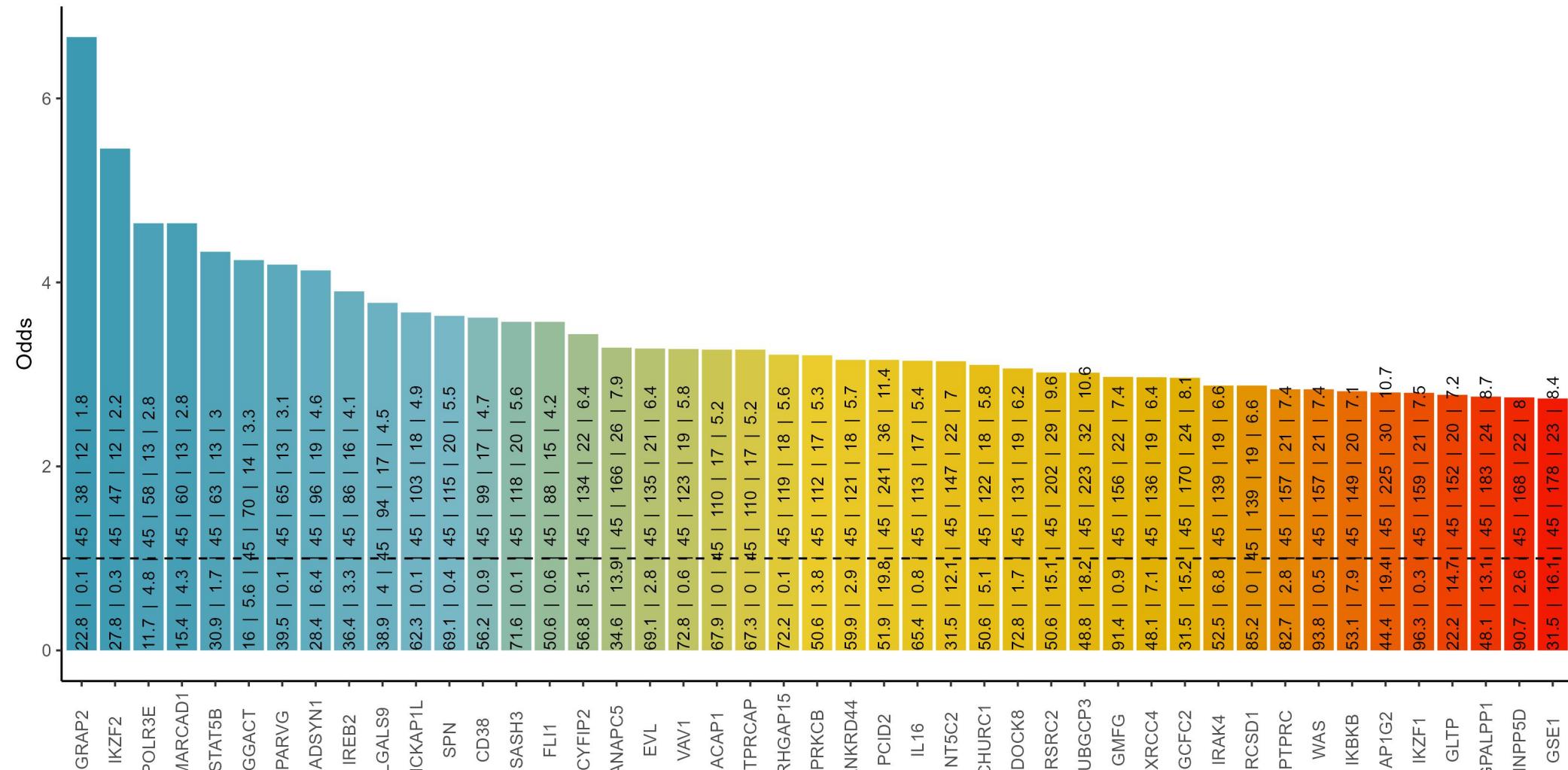
% of ERCC5 in blood cancers: 13 ; % of ERCC5 in solid cancers: 3.1

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ERCC5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

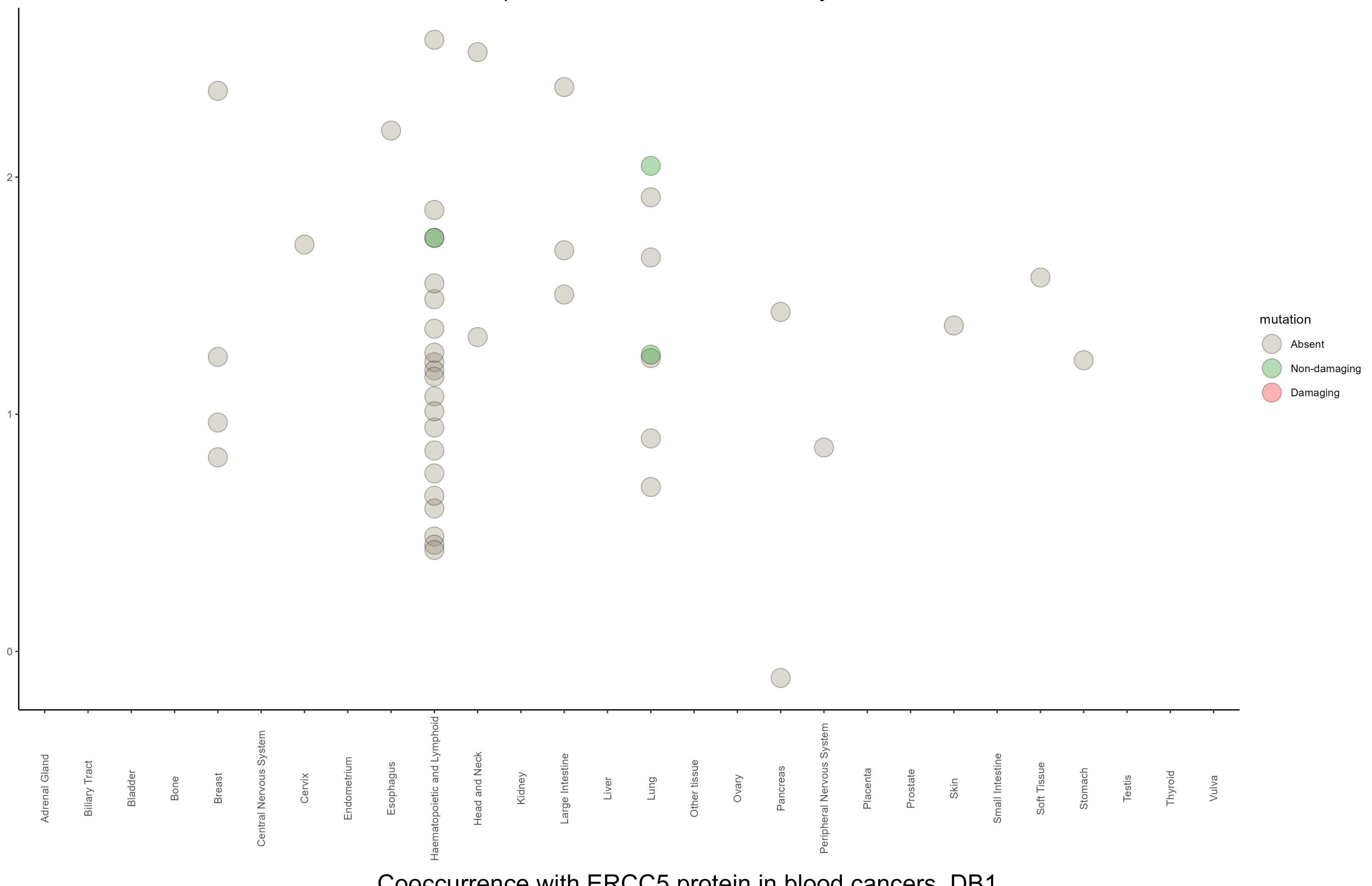
Negative cooccurrence



Positive cooccurrence

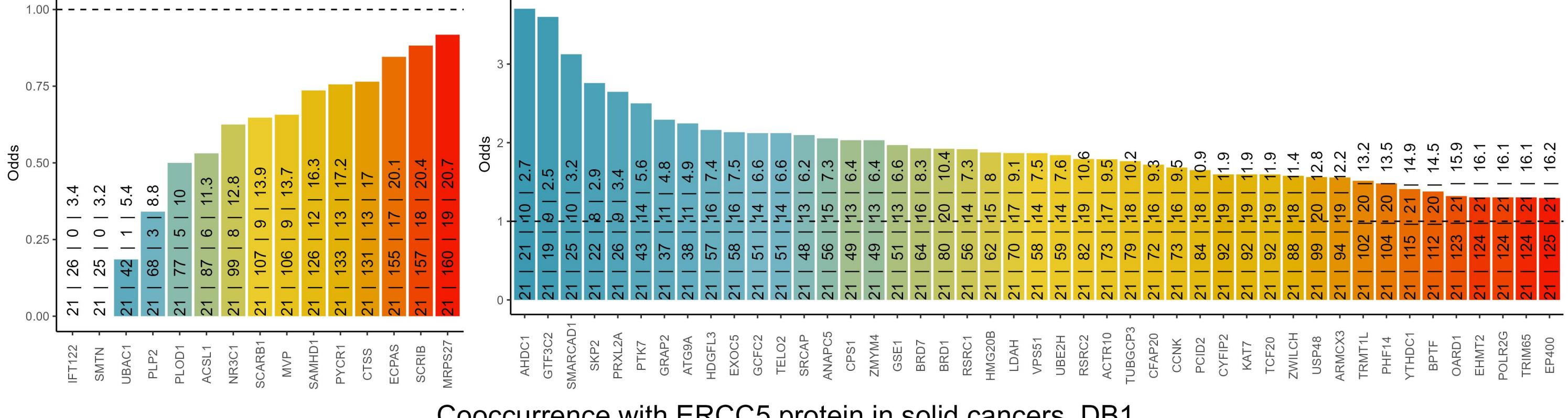


Amount of ERCC5 protein and mutation status by tissue, DB1



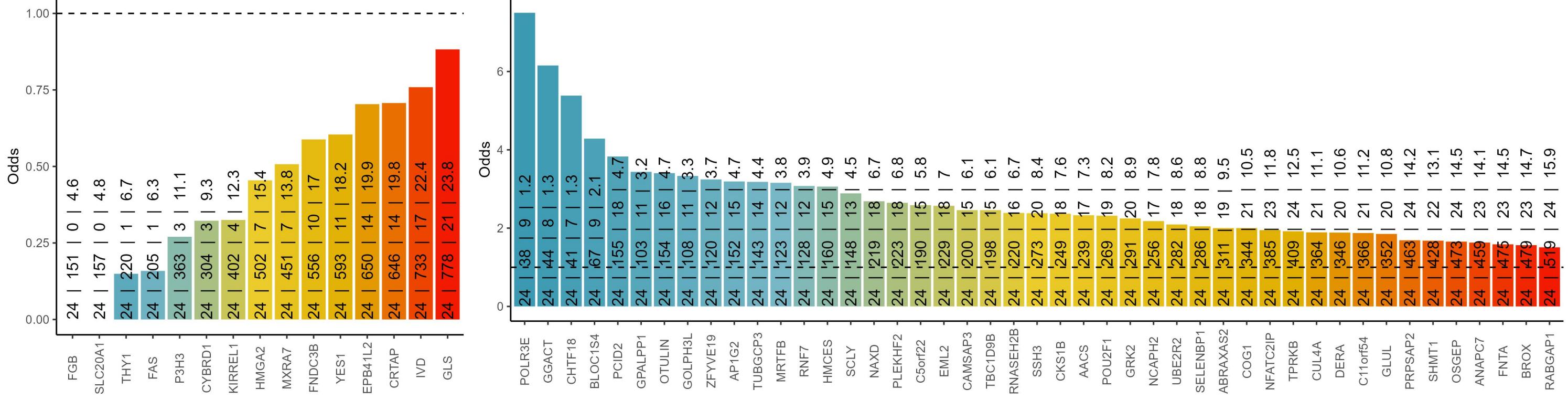
Cooccurrence with ERCC5 protein in blood cancers, DB1

The text in the bars: incidence of ERCC5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

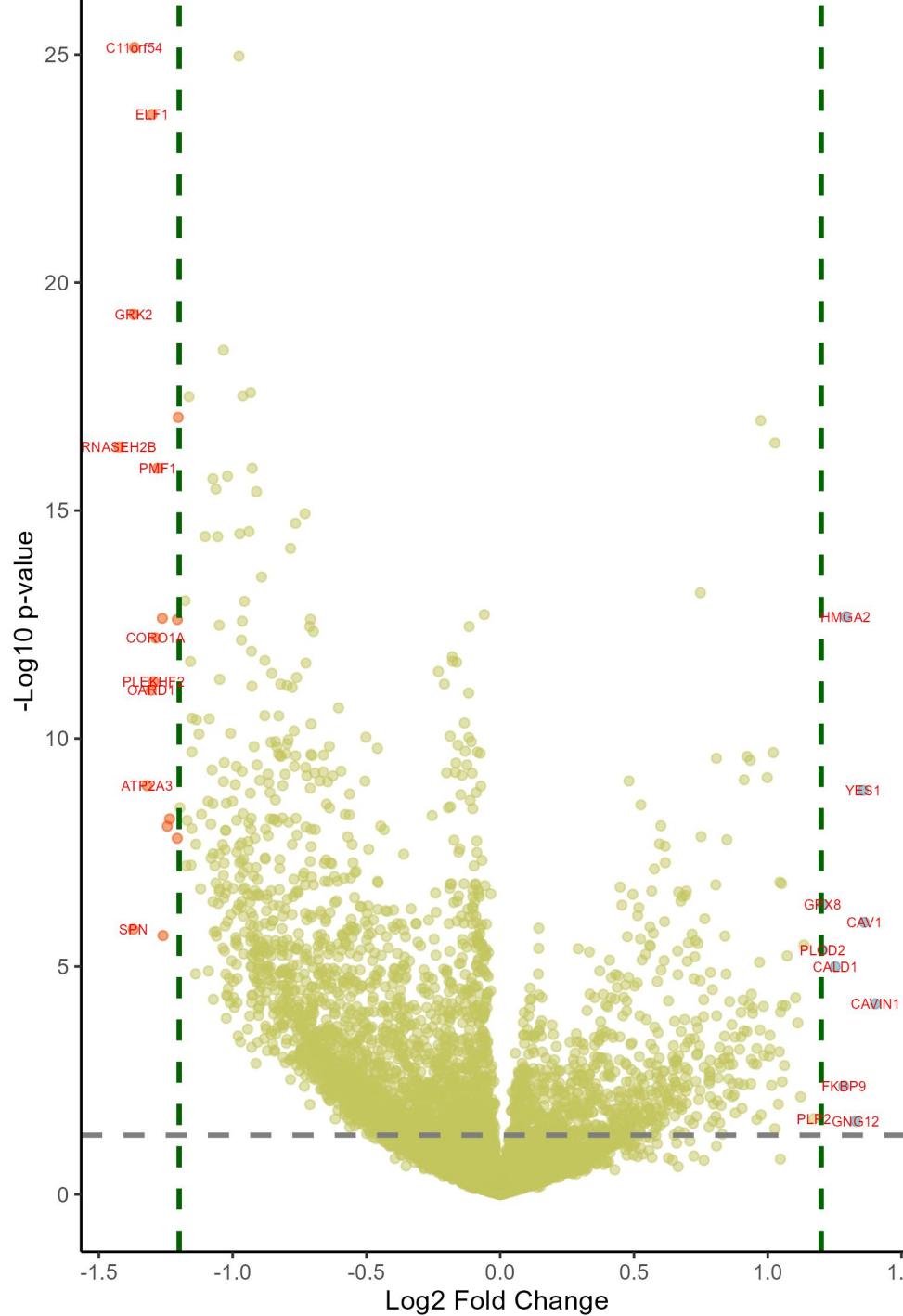


Cooccurrence with ERCC5 protein in solid cancers, DB1

The text in the bars: incidence of ERCC5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

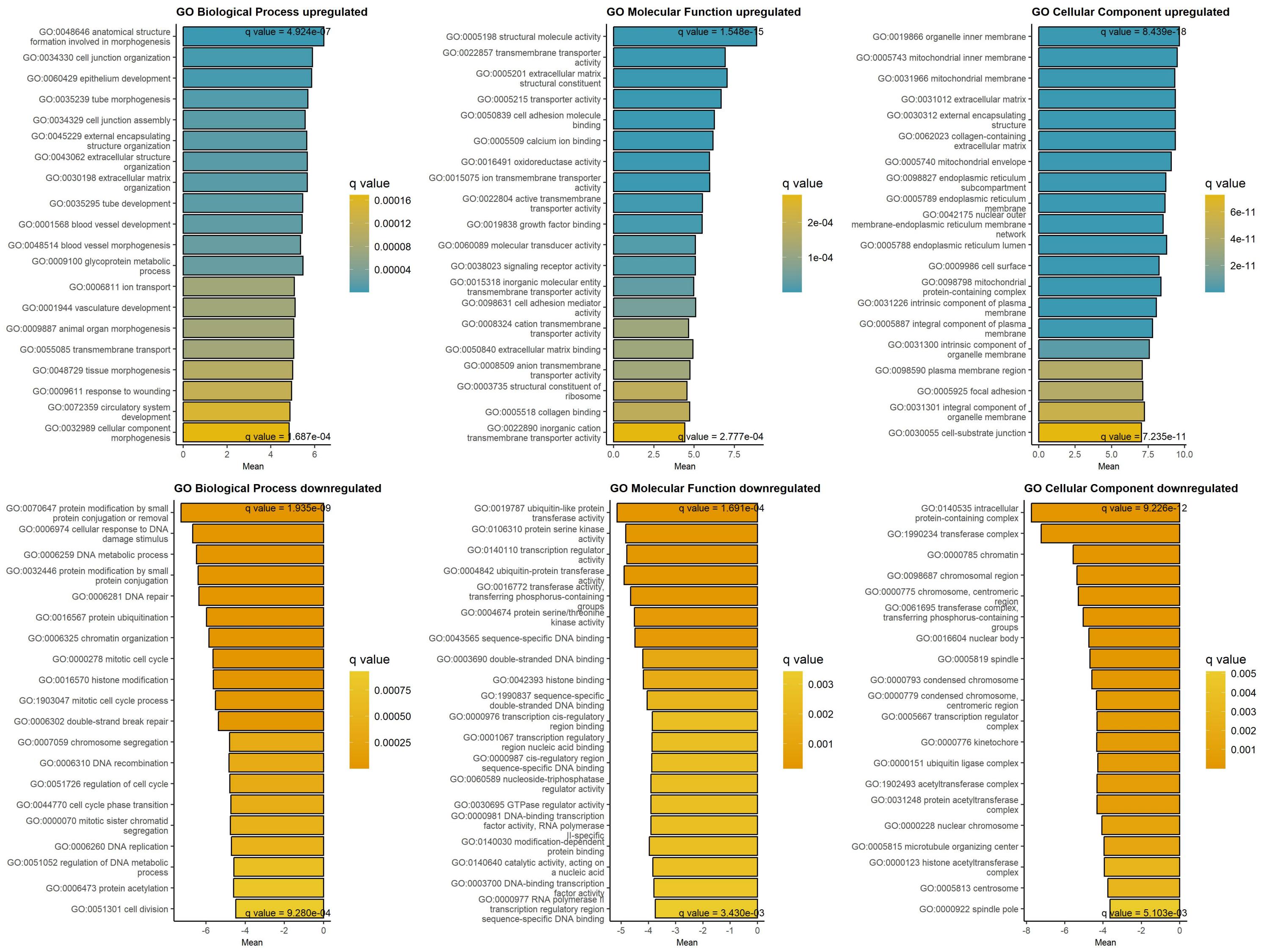


Downregulated at low/absent ERCC5 Upregulated at low/absent ERCC5

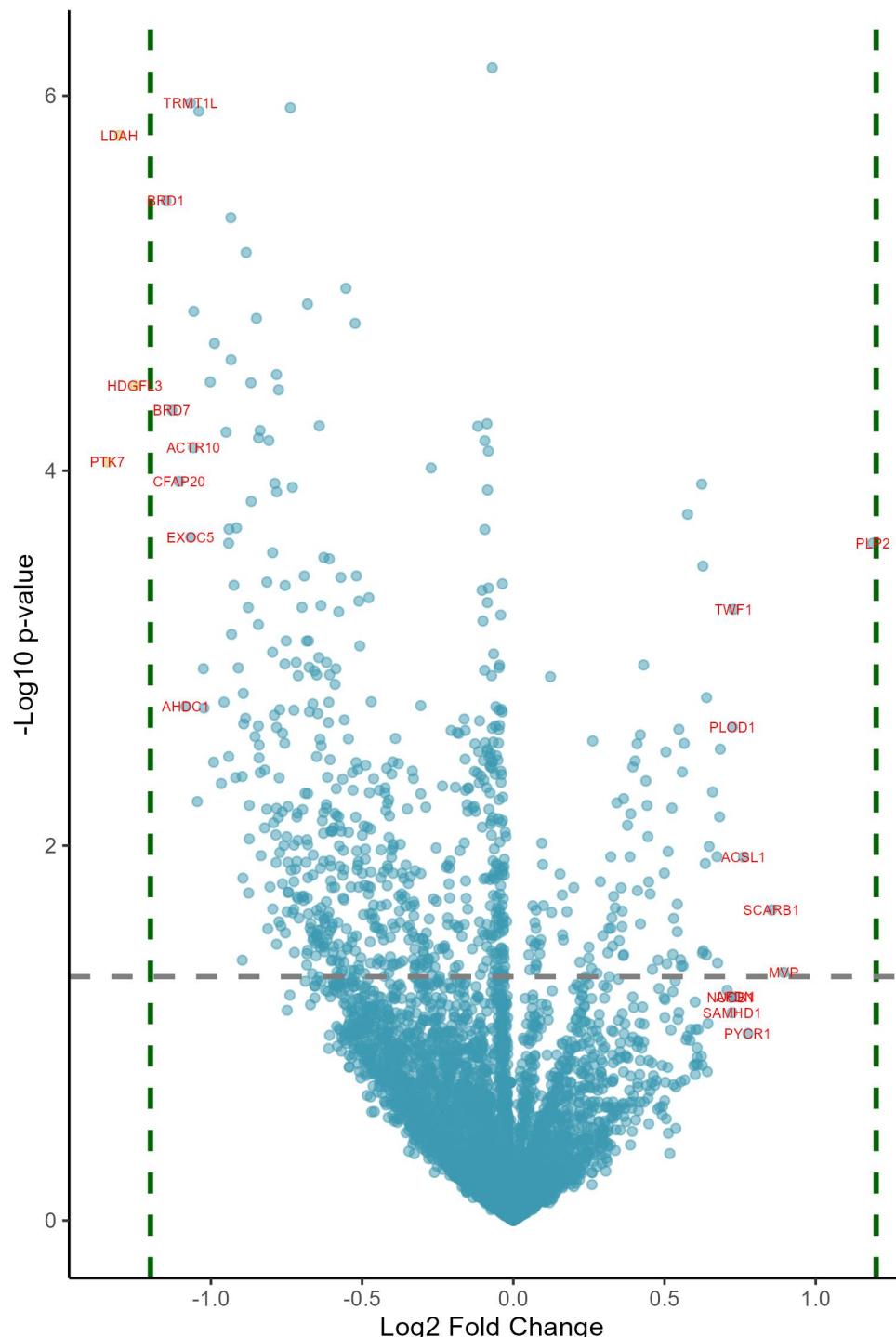


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.43	2.08e-14	RNASEH2B	ribonuclease H2 subunit B	1.4	5.46e-04	CAVIN1	caveolae associated protein 1
-1.37	2.55e-05	SPN	sialophorin	1.36	1.92e-05	CAV1	caveolin 1
-1.37	6.62e-17	GRK2	G protein-coupled receptor kinase 2	1.36	6.70e-08	YES1	YES proto-oncogene 1, Src family ty
-1.32	5.40e-08	ATP2A3	ATPase sarcoplasmic/endoplasmic ret	1.29	4.42e-11	HMGAA2	high mobility group AT-hook 2
-1.3	9.67e-10	OARD1	O-acyl-ADP-ribose deacylase 1	1.28	1.60e-02	FKBP9	FKBP prolyl isomerase 9
-1.3	3.41e-21	ELF1	E74 like ETS transcription factor 1	1.25	1.18e-04	CALD1	caldesmon 1
-1.3	7.01e-10	PLEKHF2	pleckstrin homology and FYVE domain	1.21	5.83e-05	PLOD2	procollagen-lysine,2-oxoglutarate 5
-1.29	1.01e-10	CORO1A	coronin 1A	1.21	9.13e-06	GPX8	glutathione peroxidase 8 (putative)
-1.28	5.23e-14	PMF1	polyamine modulated factor 1	1.17	5.89e-02	PLP2	proteolipid protein 2
-1.26	4.65e-11	POU2F1	POU class 2 homeobox 1	1.14	4.81e-05	EPHA2	EPH receptor A2
-1.26	3.33e-05	GMFG	glia maturation factor gamma	1.12	2.45e-02	ITGA3	integrin subunit alpha 3
-1.24	3.20e-07	SLBP	stem-loop binding protein	1.11	1.20e-03	P4HA2	prolyl 4-hydroxylase subunit alpha
-1.24	2.36e-07	PTPN6	protein tyrosine phosphatase non-re	1.1	4.24e-04	PLOD1	procollagen-lysine,2-oxoglutarate 5
-1.21	5.41e-07	REL	REL proto-oncogene, NF- κ B subunit	1.07	7.36e-05	TMTCS3	transmembrane O-mannosyltransferase
-1.21	4.67e-11	ARHGEF7	Rho guanine nucleotide exchange fac	1.07	5.87e-04	LAMB1	laminin subunit beta 1
-1.2	6.03e-15	NFATC2IP	nuclear factor of activated T cells	1.06	7.01e-03	FKBP10	FKBP prolyl isomerase 10
-1.2	1.45e-07	TUBGCP3	tubulin gamma complex associated pr	1.05	5.86e-04	ADAM9	ADAM metallopeptidase domain 9
-1.18	2.17e-11	ARMC6	armadillo repeat containing 6	1.05	1.35e-02	PVR	PVR cell adhesion molecule
-1.17	1.78e-06	AP1G2	adaptor related protein complex 1 s	1.05	3.90e-06	FNDC3B	fibronectin type III domain contain
-1.17	2.47e-07	PGK2	phosphoglycerate kinase 2	1.05	7.61e-04	RRAS	RAS related
-1.16	2.34e-15	TPRKB	TP53RK binding protein	1.05	2.87e-01	KRT18	keratin 18
-1.16	2.90e-10	DERA	deoxyribose-phosphate aldolase	1.05	3.69e-06	CTSL	cathepsin L
-1.16	1.74e-06	HMGNS	high mobility group nucleosome bind	1.04	4.01e-03	CRTAP	cartilage associated protein
-1.15	3.54e-07	UBE2L6	ubiquitin conjugating enzyme E2 L6	1.04	3.31e-02	MYOF	myoferlin
-1.15	1.50e-08	UBE2R2	ubiquitin conjugating enzyme E2 R2	1.03	1.83e-14	P3H3	prolyl 3-hydroxylase 3
-1.15	3.65e-09	DBR1	debranching RNA lariats 1	1.03	8.78e-02	CTTN	cortactin
-1.14	1.56e-04	PTPRC	protein tyrosine phosphatase recept	1.02	1.52e-08	MXRA7	matrix remodeling associated 7
-1.14	7.04e-07	PSMB10	proteasome 20S subunit beta 10	1.01	1.57e-02	ITGAV	integrin subunit alpha V

GAGE analysis on upregulated and downregulated proteins at low/absent ERCC5 protein, DB1



p-value < 0.05 & logFC > 1.2

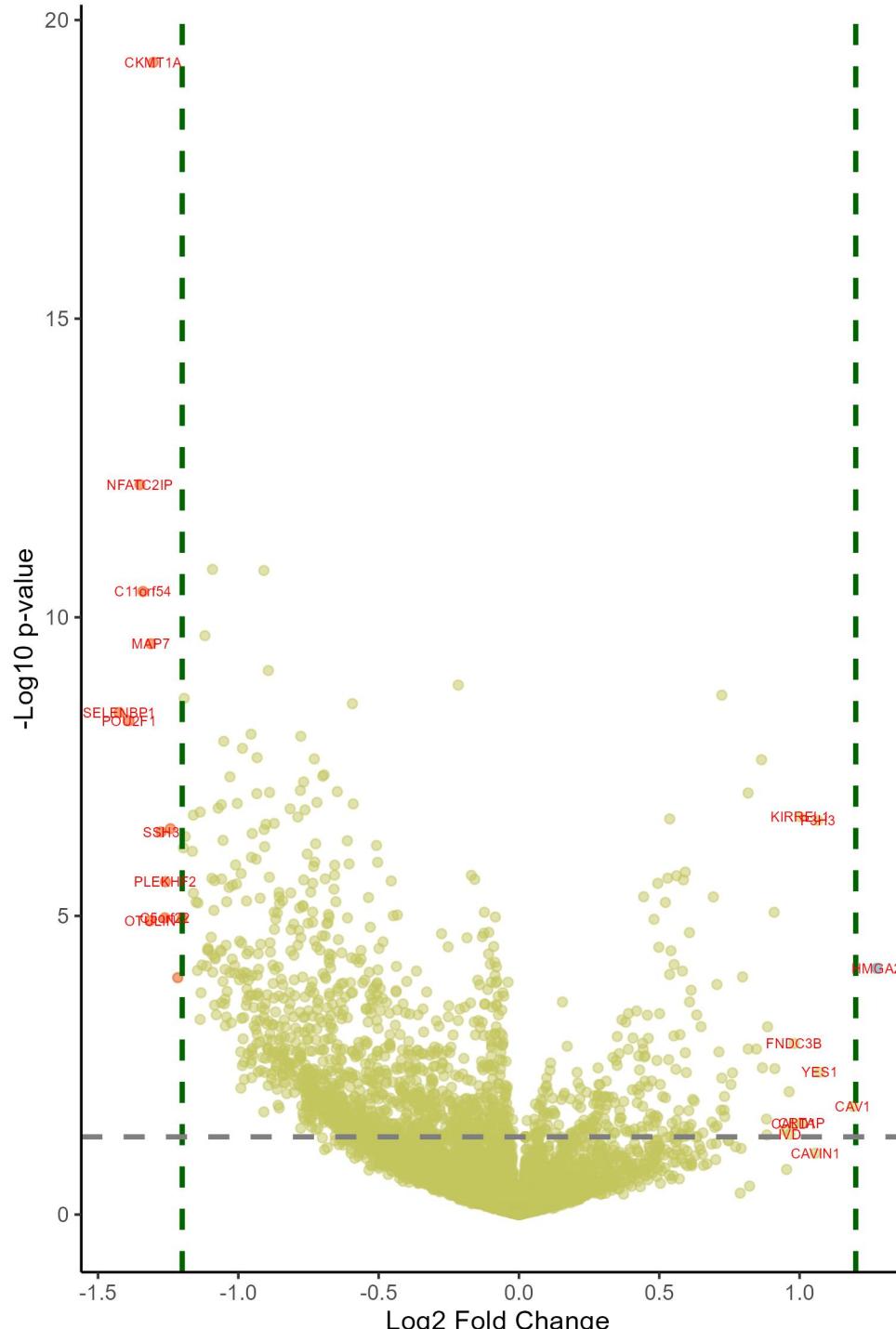


Downregulated in blood cancers at low/absent ERCC5 Upregulated in blood cancers at low/absent ERCC5

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.34	1.81e-02	PTK7	protein tyrosine kinase 7 (inactive)	1.19	3.38e-02	PLP2	proteolipid protein 2
-1.3	1.81e-03	LDAH	lipid droplet associated hydrolase	0.89	4.65e-01	MVP	major vault protein
-1.25	1.17e-02	HDGFL3	HDGF like 3	0.85	3.28e-01	SCARB1	scavenger receptor class B member 1
-1.15	3.45e-03	BRD1	bromodomain containing 1	0.78	5.45e-01	PYCR1	pyrroline-5-carboxylate reductase 1
-1.13	1.44e-02	BRD7	bromodomain containing 7	0.76	2.41e-01	ACSL1	acyl-CoA synthetase long chain fami
-1.11	2.12e-02	CFAP20	cilia and flagella associated prote	0.73	5.17e-01	AFDN	afadin, adherens junction formation
-1.08	1.12e-01	AHDC1	AT-hook DNA binding motif containin	0.73	5.37e-02	TWF1	twinfilin actin binding protein 1
-1.07	1.61e-03	TRMT1L	tRNA methyltransferase 1 like	0.73	1.22e-01	PLOD1	procollagen-lysine,2-oxoglutarate 5
-1.07	3.27e-02	EXOC5	exocyst complex component 5	0.72	5.45e-01	SAMHD1	SAM and HD domain containing deoxyn
-1.06	1.62e-02	ACTR10	actin related protein 10	0.72	5.17e-01	NUCB1	nucleobindin 1
-1.06	7.78e-03	SPN	sialophorin	0.71	5.01e-01	CTTN	cortactin
-1.05	1.72e-01	GRAP2	GRB2 related adaptor protein 2	0.68	1.34e-01	SUN1	Sad1 and UNC84 domain containing 1
-1.04	1.61e-03	PHF14	PHD finger protein 14	0.68	1.83e-01	MYOF	myoferlin
-1.02	8.42e-02	TELO2	telomere maintenance 2	0.68	4.39e-01	CAPN2	calpain 2
-1.02	1.12e-01	SRCAP	Snf2 related CREBBP activator prote	0.67	2.41e-01	NR3C1	nuclear receptor subfamily 3 group
-1	1.17e-02	ARMCX3	armadillo repeat containing X-linke	0.66	1.60e-01	CD58	CD58 molecule
-0.99	1.40e-01	NDUFB11	NADH:ubiquinone oxidoreductase subu	0.65	2.24e-01	UQCRCFS1	ubiquinol-cytochrome c reductase, R
-0.99	9.28e-03	USP48	ubiquitin specific peptidase 48	0.64	5.45e-01	SCARB2	scavenger receptor class B member 2
-0.97	1.53e-01	CPS1	carbamoyl-phosphate synthase 1	0.64	5.45e-01	CTSZ	cathepsin Z
-0.96	1.11e-01	E124	E124 autophagy associated transmemb	0.64	1.08e-01	LSR	lipolysis stimulated lipoprotein re
-0.95	1.53e-02	KAT7	lysine acetyltransferase 7	0.64	4.17e-01	MFF	mitochondrial fission factor
-0.94	3.38e-02	TUBGCP3	tubulin gamma complex associated pr	0.63	2.51e-01	JUNB	JunB proto-oncogene, AP-1 transcrip
-0.94	1.39e-01	ZMYM4	zinc finger MYM-type containing 4	0.63	4.09e-01	PLOD3	procollagen-lysine,2-oxoglutarate 5
-0.94	3.04e-02	RSRC2	arginine and serine rich coiled-coi	0.63	4.13e-02	SRXN1	sulfiredoxin 1
-0.93	3.72e-03	GSK3B	glycogen synthase kinase 3 beta	0.63	4.15e-01	VAMP7	vesicle associated membrane protein
-0.93	1.06e-02	PGK2	phosphoglycerate kinase 2	0.63	5.45e-01	TUBB6	tubulin beta 6 class V
-0.93	6.79e-02	CCNK	cyclin K	0.62	2.12e-02	UBAC1	UBA domain containing 1
-0.92	4.62e-02	ACSS1	acyl-CoA synthetase short chain fam	0.62	5.45e-01	TUBB3	tubulin beta 3 class III
-0.92	1.48e-01	LGALS9	galectin 9	0.61	5.45e-01	CTSS	cathepsin S

Differentially expressed proteins in solid cancers at absence/low amount of ERCC5 , DB1

p-value < 0.05 & logFC > 1.2

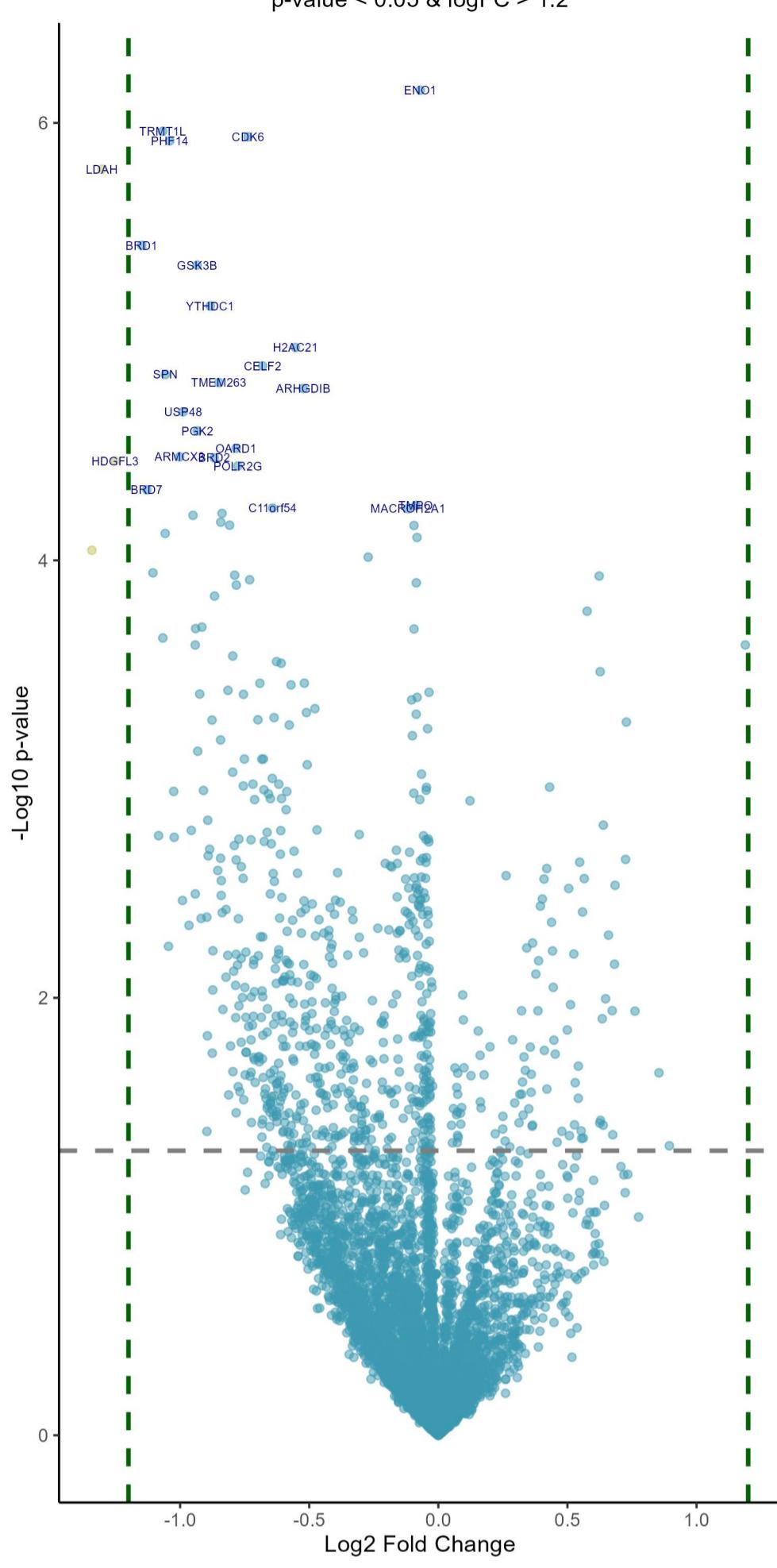


Downregulated in solid cancers at low/absent ERCC5 Upregulated in solid cancers at low/absent ERCC5

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.42	1.87e-06	SELENBP1	selenium binding protein 1	1.27	2.52e-03	HMGAA2	high mobility group AT-hook 2
-1.39	2.38e-06	POU2F1	POU class 2 homeobox 1	1.19	1.07e-01	CAV1	caveolin 1
-1.35	1.33e-09	NFATC2IP	nuclear factor of activated T cells	1.07	4.39e-02	YES1	YES proto-oncogene 1, Src family ty
-1.34	4.10e-08	C11orf54	chromosome 11 open reading frame 54	1.07	3.80e-05	P3H3	prolyl 3-hydroxylase 3
-1.31	6.35e-04	OTULIN	OTU deubiquitinase with linear link	1.06	3.00e-01	CAVIN1	caveolae associated protein 1
-1.31	2.30e-07	MAP7	microtubule associated protein 7	1.01	1.59e-01	CRTAP	cartilage associated protein
-1.3	1.70e-16	CKMT1A	creatine kinase, mitochondrial 1A	1	3.49e-05	KIRREL1	kirre like nephrin family adhesion
-1.28	5.31e-05	SSH3	slingshot protein phosphatase 3	0.98	2.06e-02	FNDC3B	fibronectin type III domain contain
-1.26	5.88e-04	C5orf22	chromosome 5 open reading frame 22	0.98	1.62e-01	CALD1	caldesmon 1
-1.26	2.14e-04	PLEKH2	pleckstrin homology and FYVE domain	0.97	2.05e-01	IVD	isovaleryl-CoA dehydrogenase
-1.24	4.90e-05	GRK2	G protein-coupled receptor kinase 2	0.96	7.43e-02	ITGA5	integrin subunit alpha 5
-1.22	3.23e-03	AP1G2	adaptor related protein complex 1 s	0.95	4.21e-01	MSN	moesin
-1.2	6.02e-04	NAXD	NAD(P)HX dehydratase	0.95	1.88e-01	EPB41L2	erythrocyte membrane protein band 4
-1.2	8.43e-05	POLB	DNA polymerase beta	0.91	4.03e-02	AXL	AXL receptor tyrosine kinase
-1.19	1.26e-06	TPRK2	TP53RK binding protein	0.91	5.06e-04	CYBRD1	cytochrome b reductase 1
-1.19	6.12e-05	PMF1	polyamine modulated factor 1	0.89	1.23e-02	COL12A1	collagen type XII alpha 1 chain
-1.16	9.48e-05	DERA	deoxyribose-phosphate aldolase	0.88	2.07e-01	STOM	stomatin
-1.16	2.96e-04	C9orf78	chromosome 9 open reading frame 78	0.88	1.46e-01	GPX8	glutathione peroxidase 8 (putative)
-1.16	3.41e-05	CUL4A	cullin 4A	0.87	3.94e-02	MXRA7	matrix remodeling associated 7
-1.15	3.78e-04	GRIPAP1	GRIP1 associated protein 1	0.86	7.33e-06	THY1	Thy-1 cell surface antigen
-1.15	2.67e-03	PCID2	PCI domain containing 2	0.85	2.41e-02	SPARC	secreted protein acidic and cystein
-1.14	3.84e-04	PPCS	phosphopantethenoylcysteine synthet	0.82	5.69e-01	LGALS1	galectin 1
-1.14	1.00e-02	MRTFB	myocardin related transcription fac	0.82	2.41e-02	NOTCH2	notch receptor 2
-1.14	3.10e-05	ELF1	E74 like ETS transcription factor 1	0.82	1.92e-05	CCN1	cellular communication network fact
-1.13	4.86e-03	STARD10	StAR related lipid transfer domain	0.8	3.17e-03	NEXN	nexilin F-actin binding protein
-1.13	2.30e-03	CAMSAP3	calmodulin regulated spectrin assoc	0.79	2.70e-01	FN1	fibronectin 1
-1.12	1.93e-07	BROX	BRO1 domain and CAAX motif containi	0.79	6.38e-01	VIM	vimentin
-1.11	2.37e-03	EIF1	eukaryotic translation initiation f	0.77	2.60e-01	IKBIP	IKBKB interacting protein
-1.11	1.52e-03	EML2	EMAP like 2	0.76	4.44e-02	UXS1	UDP-glucuronate decarboxylase 1

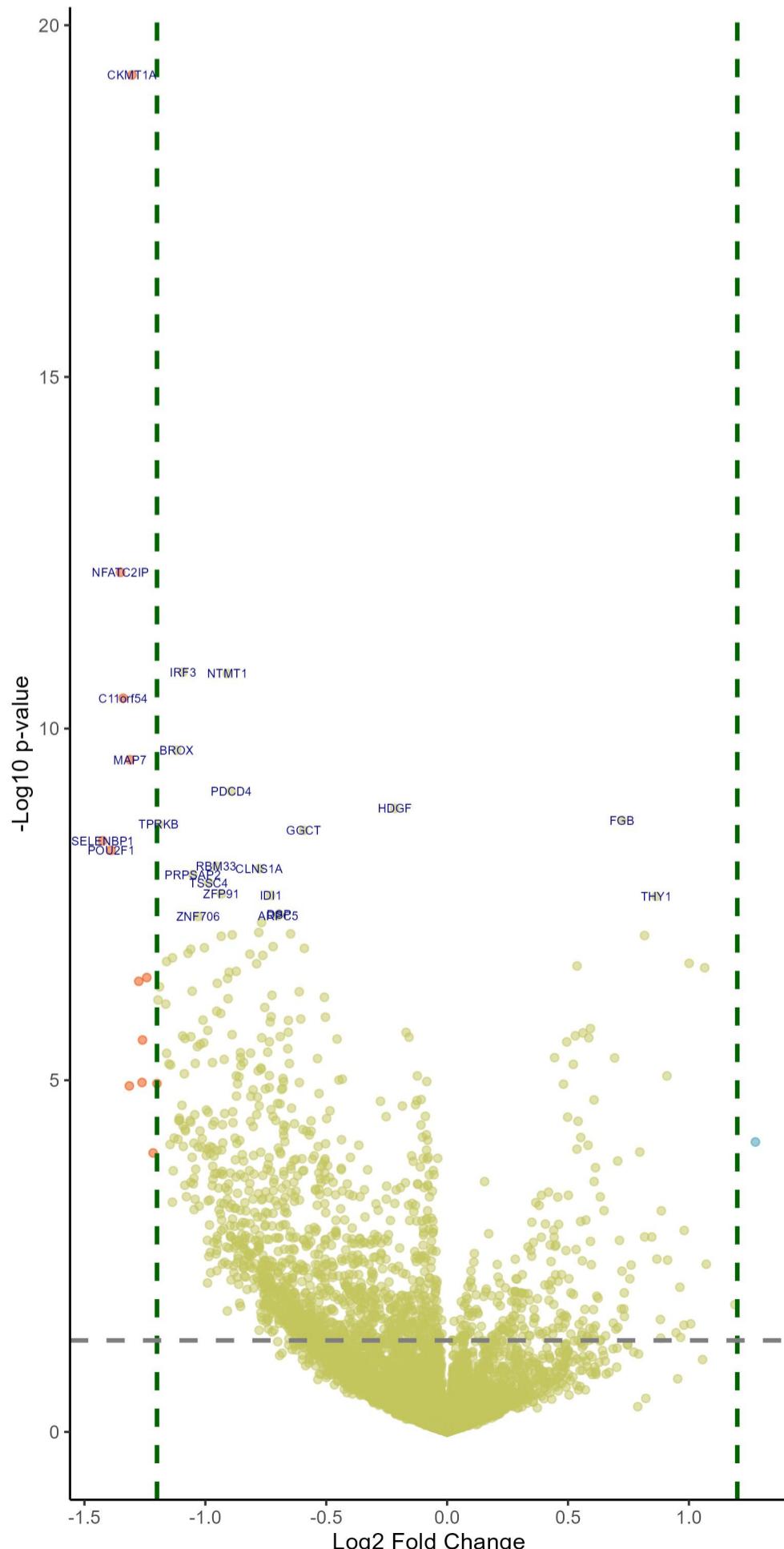
ERCC5 network, DB1, no Pearson r > 0.3

Differentially expressed proteins in blood cancers at absence/low amount of ERCC5 , DB1 p-value < 0.05 & logFC ≥ 1.2



Sorted by p values!							
Downregulated in blood cancers at low/absent ERCC5				Upregulated in blood cancers at low/absent ERCC5			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.07	1.61e-03	ENO1	enolase 1	0.62	2.12e-02	UBAC1	UBA domain containing 1
-1.07	1.61e-03	TRMT1L	tRNA methyltransferase 1 like	0.58	2.70e-02	IFT122	intraflagellar transport 122
-0.74	1.61e-03	CDK6	cyclin dependent kinase 6	1.19	3.38e-02	PLP2	proteolipid protein 2
-1.04	1.61e-03	PHF14	PHD finger protein 14	0.63	4.13e-02	SRXN1	sulfiredoxin 1
-1.3	1.81e-03	LDAH	lipid droplet associated hydrolase	0.73	5.37e-02	TWF1	twinfilin actin binding protein 1
-1.15	3.45e-03	BRD1	bromodomain containing 1	0.43	8.42e-02	SMTN	smoothelin
-0.93	3.72e-03	GSK3B	glycogen synthase kinase 3 beta	0.12	8.61e-02	CLPP	caseinolytic mitochondrial matrix p
-0.88	5.07e-03	YTHDC1	YTH domain containing 1	0.64	1.08e-01	LSR	lipolysis stimulated lipoprotein re
-0.55	7.07e-03	H2AC21	H2A clustered histone 21	0.73	1.22e-01	PLOD1	procollagen-lysine,2-oxoglutarate 5
-0.68	7.78e-03	CELF2	CUGBP Elav-like family member 2	0.55	1.22e-01	AGAP3	ArfGAP with GTPase domain, ankyrin
-1.06	7.78e-03	SPN	sialophorin	0.42	1.25e-01	PLOD2	procollagen-lysine,2-oxoglutarate 5
-0.85	7.78e-03	TMEM263	transmembrane protein 263	0.26	1.29e-01	MRPS27	mitochondrial ribosomal protein S27
-0.52	7.78e-03	ARHGDI	Rho GDP dissociation inhibitor beta	0.57	1.29e-01	ECPAS	Ecm29 proteasome adaptor and scuff
-0.99	9.28e-03	USP48	ubiquitin specific peptidase 48	0.41	1.29e-01	SLC9A3R2	SLC9A3 regulator 2
-0.93	1.06e-02	PGK2	phosphoglycerate kinase 2	0.68	1.34e-01	SUN1	Sad1 and UNC84 domain containing 1
-0.78	1.17e-02	OARD1	O-acyl-ADP-ribose deacetylase 1	0.5	1.36e-01	AGA	aspartylglucosaminidase
-1	1.17e-02	ARMCX3	armadillo repeat containing X-linker	0.4	1.40e-01	PXN	paxillin
-0.87	1.17e-02	BRD2	bromodomain containing 2	0.4	1.44e-01	IL1RAP	interleukin 1 receptor accessory pr
-1.25	1.17e-02	HDGFL3	HDGF like 3	0.56	1.46e-01	SPATS2L	spermatogenesis associated serine r
-0.78	1.17e-02	POLR2G	RNA polymerase II subunit G	0.44	1.50e-01	NQO1	NAD(P)H quinone dehydrogenase 1
-1.13	1.44e-02	BRD7	bromodomain containing 7	0.66	1.60e-01	CD58	CD58 molecule
-0.09	1.53e-02	TMPO	thymopoietin	0.37	1.68e-01	FUCA1	alpha-L-fucosidase 1
-0.64	1.53e-02	C11orf54	chromosome 11 open reading frame 54	0.34	1.74e-01	ASB6	ankyrin repeat and SOCS box contain
-0.12	1.53e-02	MACROH2A1	macroH2A.1 histone	0.44	1.76e-01	STX11	syntaxin 11
-0.84	1.53e-02	DAXX	death domain associated protein	0.52	1.77e-01	MYO6	myosin VI
-0.95	1.53e-02	KAT7	lysine acetyltransferase 7	0.39	1.80e-01	JSRP1	junctional sarcoplasmic reticulum p
-0.84	1.54e-02	SASH3	SAM and SH3 domain containing 3	0.68	1.83e-01	MYOF	myoferlin
-0.81	1.54e-02	PMF1	polyamine modulated factor 1	0.38	1.95e-01	CTSL	cathepsin L
-0.09	1.54e-02	CAND1	cullin associated and neddylation d	0.45	2.09e-01	SCRIB	scribble planar cell polarity prote
-1.06	1.62e-02	ACTR10	actin related protein 10	0.09	2.20e-01	HYPK	huntingtin interacting protein K
-0.08	1.63e-02	MTA2	metastasis associated 1 family memb	0.65	2.24e-01	UQCRCFS1	ubiquinol-cytochrome c reductase, R
-1.34	1.81e-02	PTK7	protein tyrosine kinase 7 (inactive	0.51	2.31e-01	MINPP1	multiple inositol-polyphosphate pho
-0.27	1.89e-02	ZNF219	zinc finger protein 219	0.67	2.41e-01	NR3C1	nuclear receptor subfamily 3 group
-1.11	2.12e-02	CFAP20	cilia and flagella associated prote	0.39	2.41e-01	CDKN2A	cyclin dependent kinase inhibitor 2
-0.79	2.12e-02	LANCL1	LanC like 1	0.32	2.41e-01	NT5E	5'-nucleotidase ecto
-0.73	2.15e-02	EHMT2	euchromatic histone lysine methyltr	0.76	2.41e-01	ACSL1	acyl-CoA synthetase long chain fami
-0.09	2.16e-02	HNRNPA0	heterogeneous nuclear ribonucleopro	0.63	2.51e-01	JUNB	JunB proto-oncogene, AP-1 transcrip
-0.78	2.16e-02	ZMYM3	zinc finger MYM-type containing 3	0.1	2.53e-01	DNAJA3	DnaJ heat shock protein family (Hsp
-0.87	2.36e-02	ASE1A	anti-silencing function 1A histone	0.5	2.60e-01	GOLM1	golgi membrane protein 1

Differentially expressed proteins in solid cancers at absence/low amount of ERCC5 , DB1
p-value < 0.05 & logFC > 1.2

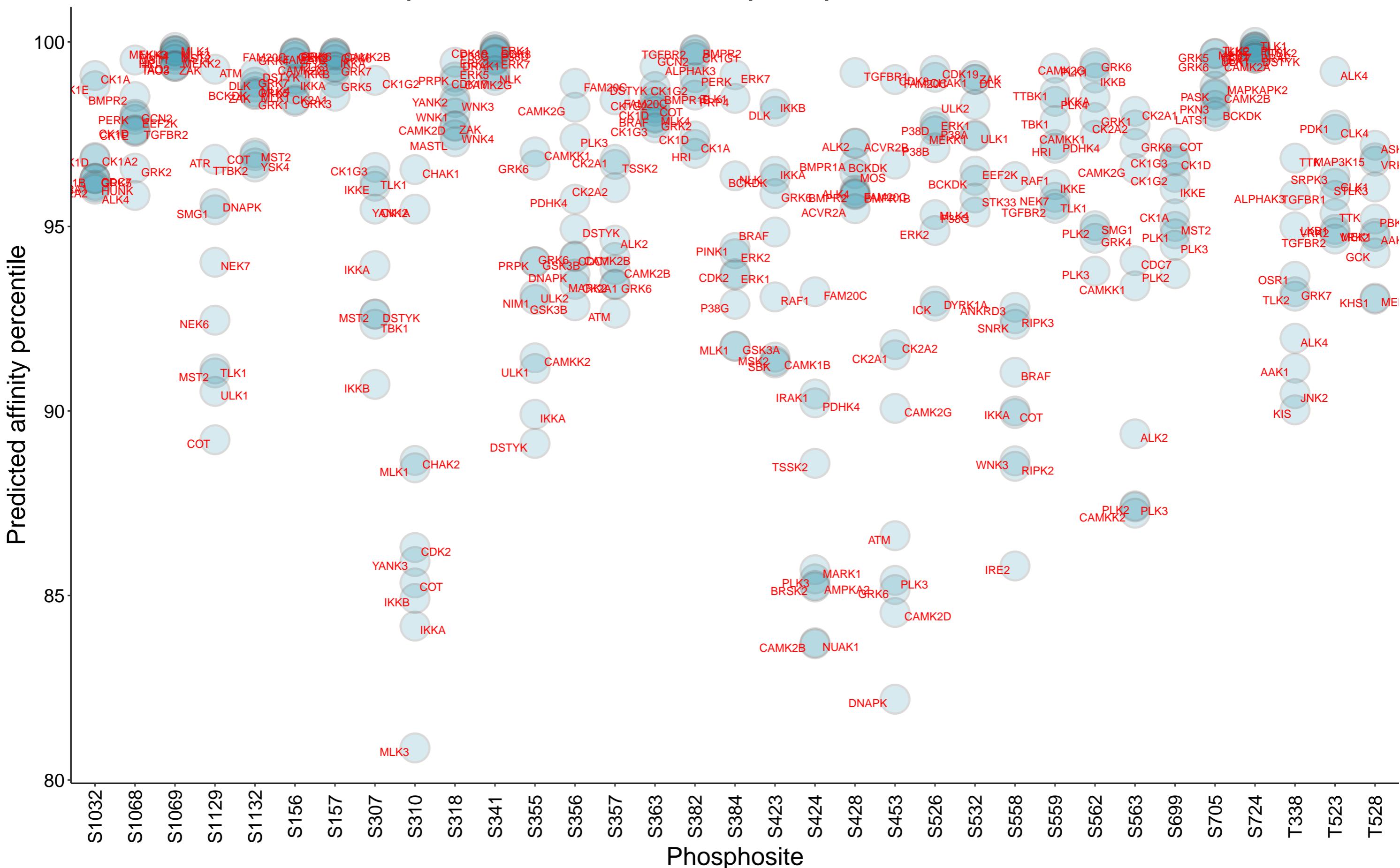


Sorted by p values!							
Downregulated in solid cancers at low/absent ERCC5				Upregulated in solid cancers at low/absent ERCC5			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.3	1.70e-16	CKMT1A	creatine kinase, mitochondrial 1A	0.72	1.22e-06	FGB	fibrinogen beta chain
1.35	1.33e-09	NFATC2IP	nuclear factor of activated T cells	0.86	7.33e-06	THY1	Thy-1 cell surface antigen
1.09	2.19e-08	IRF3	interferon regulatory factor 3	0.82	1.92e-05	CCN1	cellular communication network fact
0.91	2.19e-08	NTMT1	N-terminal Xaa-Pro-Lys N-methyltran	1	3.49e-05	KIRREL1	kirre like nephrin family adhesion
1.34	4.10e-08	C11orf54	chromosome 11 open reading frame 54	0.54	3.67e-05	SLC20A1	solute carrier family 20 member 1
1.12	1.93e-07	BROX	BRO1 domain and CAAX motif containi	1.07	3.80e-05	P3H3	prolyl 3-hydroxylase 3
1.31	2.30e-07	MAP7	microtubule associated protein 7	0.59	1.80e-04	FAS	Fas cell surface death receptor
0.89	5.75e-07	PDCD4	programmed cell death 4	0.56	1.96e-04	CDH6	cadherin 6
0.22	9.07e-07	HDGF	heparin binding growth factor	0.53	2.07e-04	VCAN	versican
1.19	1.26e-06	TPRKB	TP53RK binding protein	0.59	2.07e-04	ARHGAP29	Rho GTPase activating protein 29
0.59	1.43e-06	GGCT	gamma-glutamylcyclotransferase	0.49	2.23e-04	SLC19A1	solute carrier family 19 member 1
1.42	1.87e-06	SELENBP1	selenium binding protein 1	0.44	3.33e-04	PRR11	proline rich 11
1.39	2.38e-06	POU2F1	POU class 2 homeobox 1	0.69	3.33e-04	COL1A2	collagen type I alpha 2 chain
0.95	3.76e-06	RBM33	RNA binding motif protein 33	0.52	3.80e-04	SHROOM3	shroom family member 3
0.78	3.83e-06	CLNS1A	chloride nucleotide-sensitive chann	0.91	5.06e-04	CYBRD1	cytochrome b reductase 1
1.05	4.40e-06	PRPSAP2	phosphoribosyl pyrophosphate synthe	0.48	6.05e-04	MSRB3	methionine sulfoxide reductase B3
0.99	5.47e-06	TSSC4	tumor suppressing subtransferable c	0.61	9.23e-04	COL1A1	collagen type I alpha 1 chain
0.93	7.33e-06	ZFP91	ZFP91 zinc finger protein, atypical	0.5	1.41e-03	MOXD1	monooxygenase DBH like 1
0.73	7.33e-06	IDI1	isopentenyl-diphosphate delta isome	0.54	1.53e-03	ITGA4	integrin subunit alpha 4
0.69	1.25e-05	DSP	desmoplakin	0.55	2.28e-03	SEMA3C	semaphorin 3C
-0.7	1.25e-05	ARPC5	actin related protein 2/3 complex s	1.27	2.52e-03	HMG2	high mobility group AT-hook 2
1.03	1.25e-05	ZNF706	zinc finger protein 706	0.58	2.71e-03	NF2	NF2, moesin-ezrin-radixin like (MER)
0.77	1.46e-05	CHRAC1	chromatin accessibility complex sub	0.54	2.96e-03	PIEZ01	piezo type mechanosensitive ion cha
0.78	1.92e-05	ADK	adenosine kinase	0.8	3.17e-03	NEXN	nexilin F-actin binding protein
0.65	1.92e-05	STK24	serine/threonine kinase 24	0.71	3.81e-03	EPDR1	ependymin related 1
0.89	1.92e-05	IAH1	isoamyl acetate hydrolyzing esteras	0.61	4.56e-03	ITIH3	inter-alpha-trypsin inhibitor heavy
0.93	1.92e-05	UBXN7	UBX domain protein 7	0.61	6.26e-03	GPC4	glycan 4
0.72	2.60e-05	OSTF1	osteoclast stimulating factor 1	0.15	6.26e-03	KHSRP	KH-type splicing regulatory protein
-1	2.60e-05	OSGEP	O-sialoglycoprotein endopeptidase	0.42	7.87e-03	ANTXR2	ANTXR cell adhesion molecule 2
0.59	2.60e-05	PCBD1	pterin-4 alpha-carbinolamine dehydr	0.39	8.50e-03	PTPRG	protein tyrosine phosphatase recept
1.06	2.61e-05	GMDS	GDP-mannose 4,6-dehydratase	0.5	8.50e-03	XYLT2	xylosyltransferase 2
1.07	2.89e-05	SHMT1	serine hydroxymethyltransferase 1	0.63	8.79e-03	SIRPA	signal regulatory protein alpha
0.82	2.90e-05	DCAF7	DDB1 and CUL4 associated factor 7	0.46	8.84e-03	ANTXR1	ANTXR cell adhesion molecule 1
0.76	2.94e-05	ENOPH1	enolase-phosphatase 1	0.37	1.01e-02	NOMO1	NODAL modulator 1
1.14	3.10e-05	ELF1	E74 like ETS transcription factor 1	0.38	1.07e-02	PLAUR	plasminogen activator, urokinase re
1.16	3.41e-05	CUL4A	cullin 4A	0.65	1.23e-02	GLS	glutaminase
0.79	3.49e-05	UBAC2	UBA domain containing 2	0.89	1.23e-02	COL12A1	collagen type XII alpha 1 chain
0.87	4.18e-05	NME2	NME/NM23 nucleoside diphosphate kin	0.57	1.59e-02	SERPINE1	serpin family E member 1

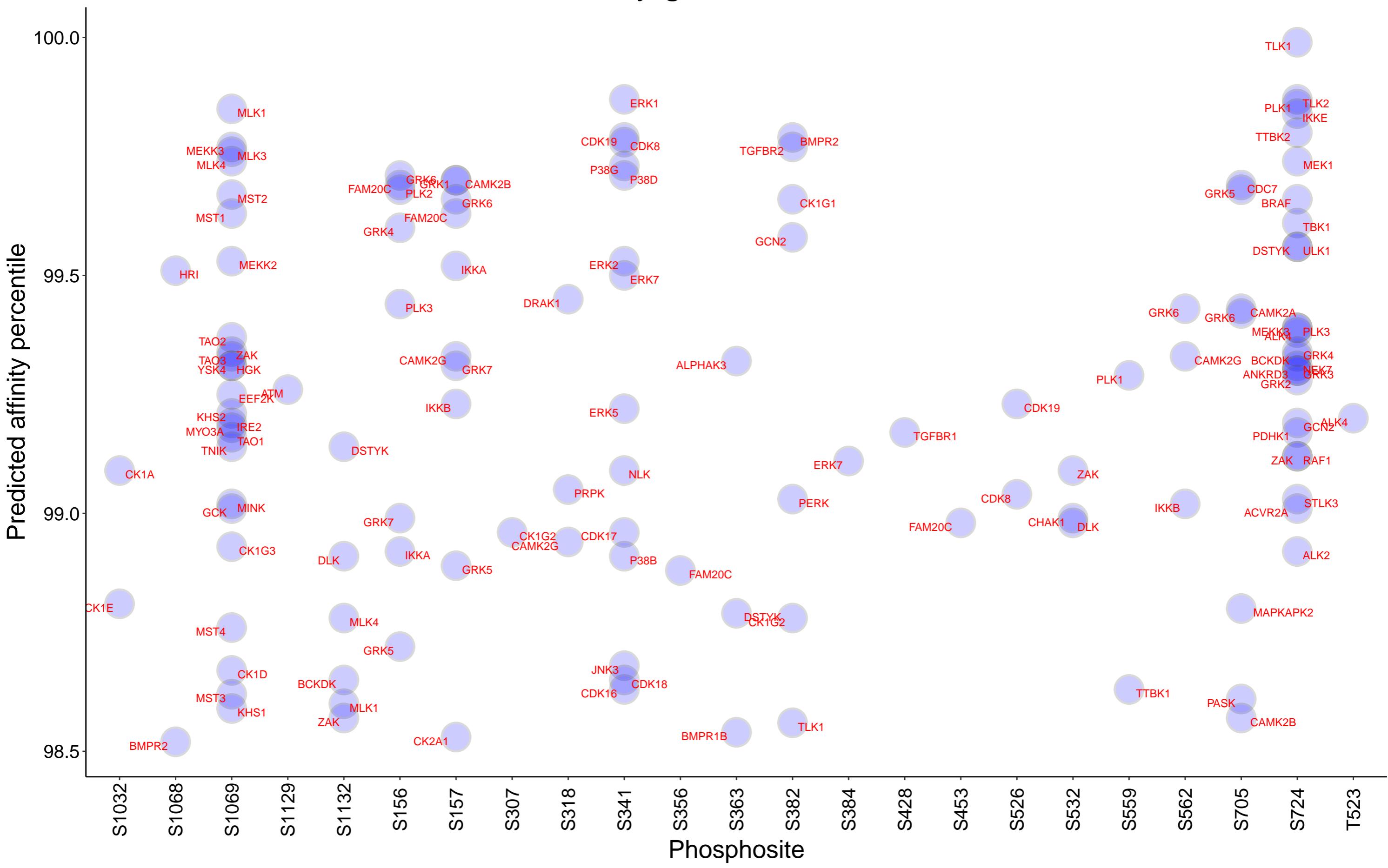
Insufficient number of paired observations in DB1 for ERCC5

Insufficient number of paired observations in DB1 for ERCC5

Top 10 kinases for each phosphosite in ERCC5



Kinases with affinity greater than 98.5% to ERCC5



No sufficient paired observations in DB1 for ERCC5