

ERCC1

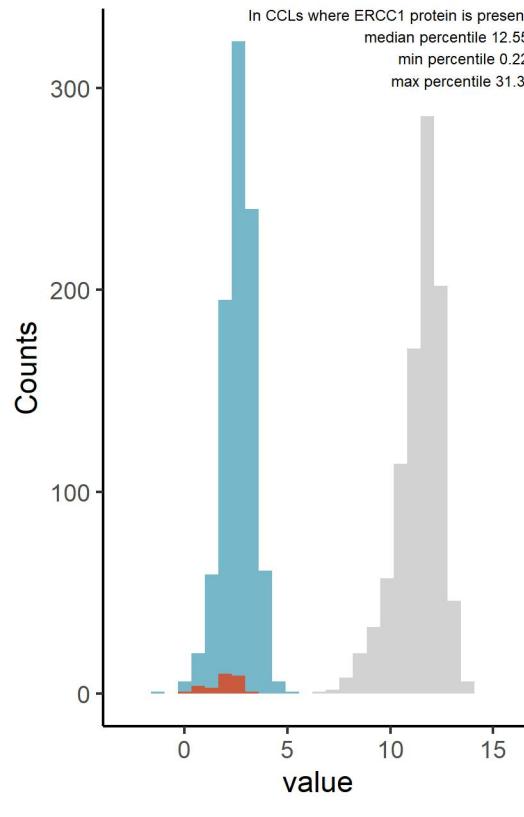
Protein name: ERCC1 ; UNIPROT: P07992 ; Gene name: ERCC excision repair 1, endonuclease non-catalytic subunit

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

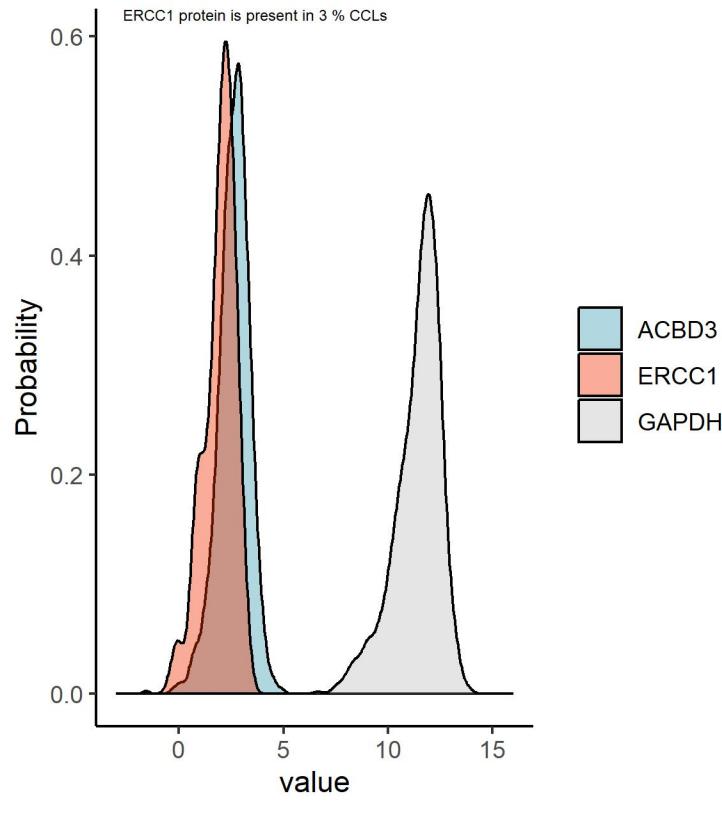
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

Histogram of ERCC1 protein compared to proteins with low and high abundance



Density plot of ERCC1 protein compared to proteins with low and high abundance



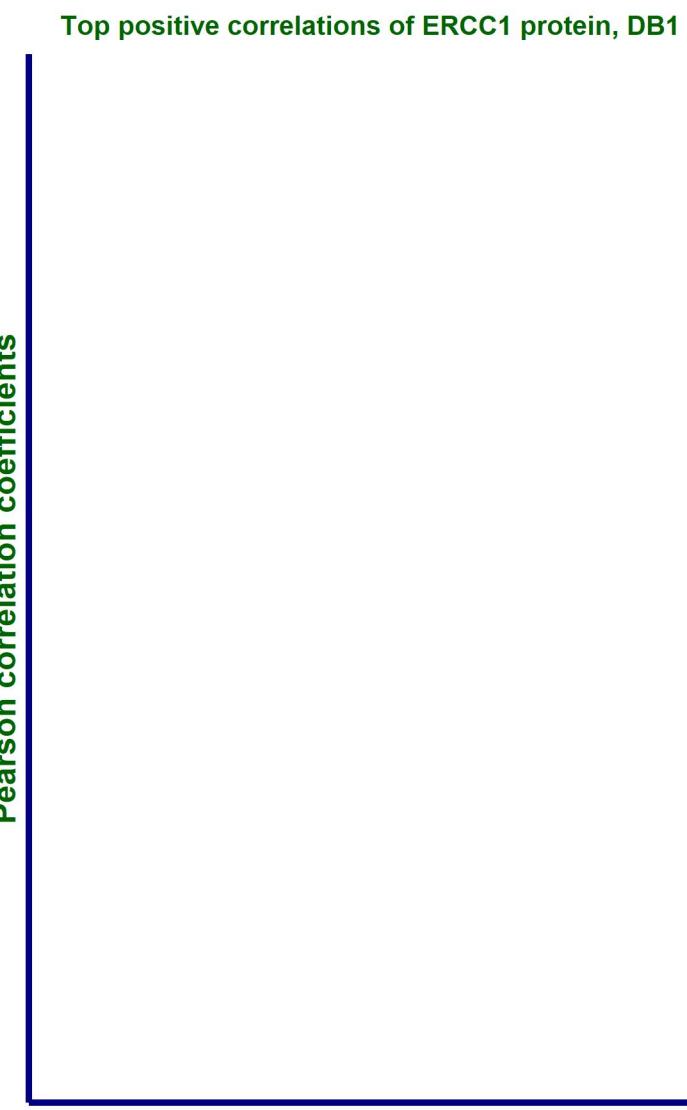
Top negative correlations of ERCC1 protein, DB1

Pearson correlation coefficients



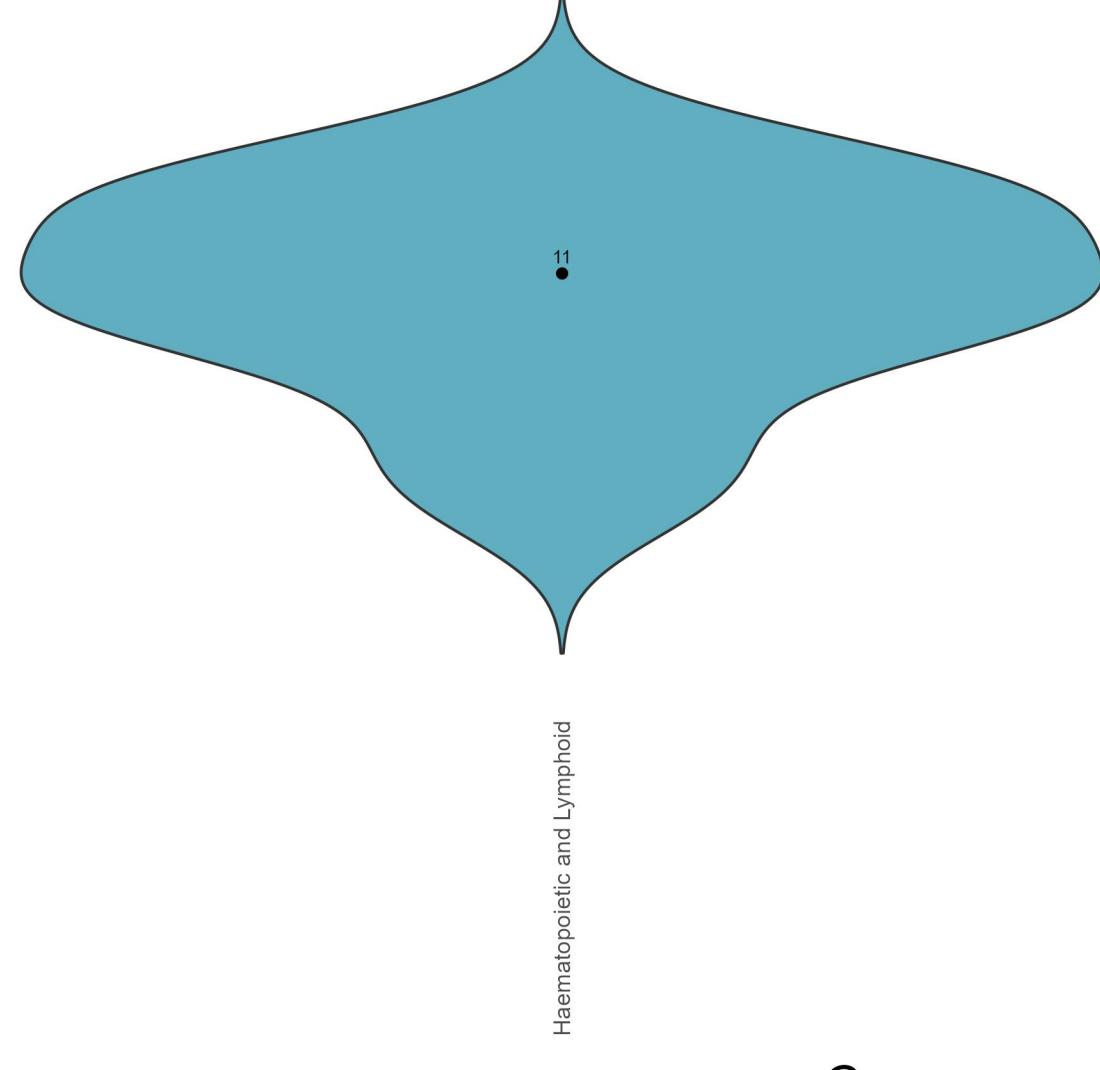
Top positive correlations of ERCC1 protein, DB1

Pearson correlation coefficients



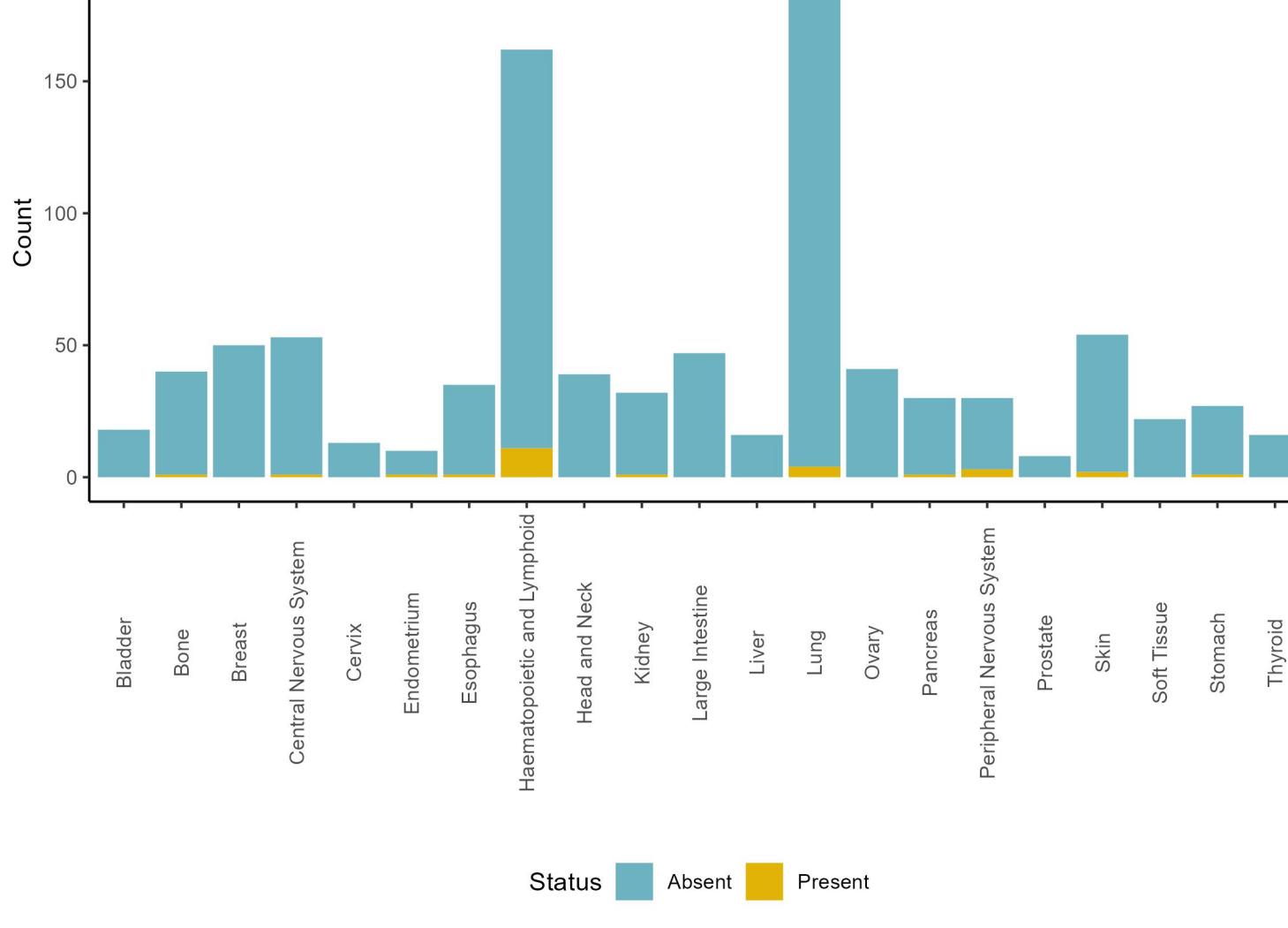
Amount of ERCC1 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 1.125e-01



Present and absent ERCC1 protein counts by tissue, DB1

Chi square p value is 2.156e-01

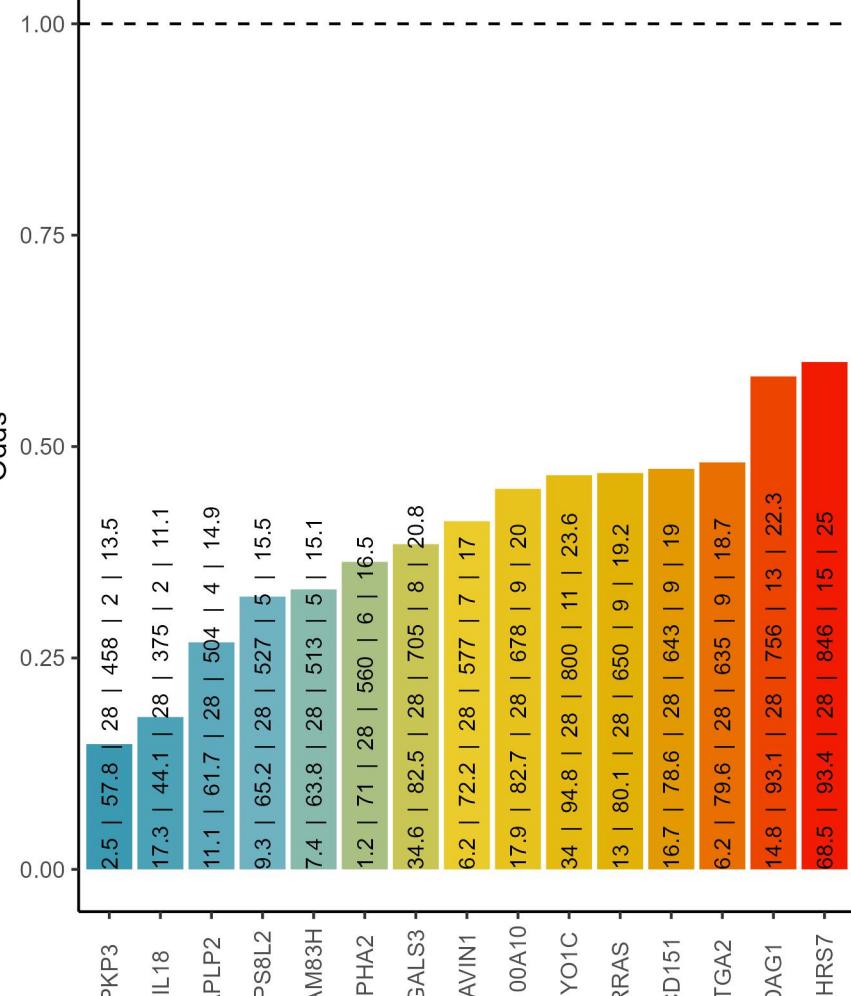


Cooccurrence with ERCC1 protein, DB1

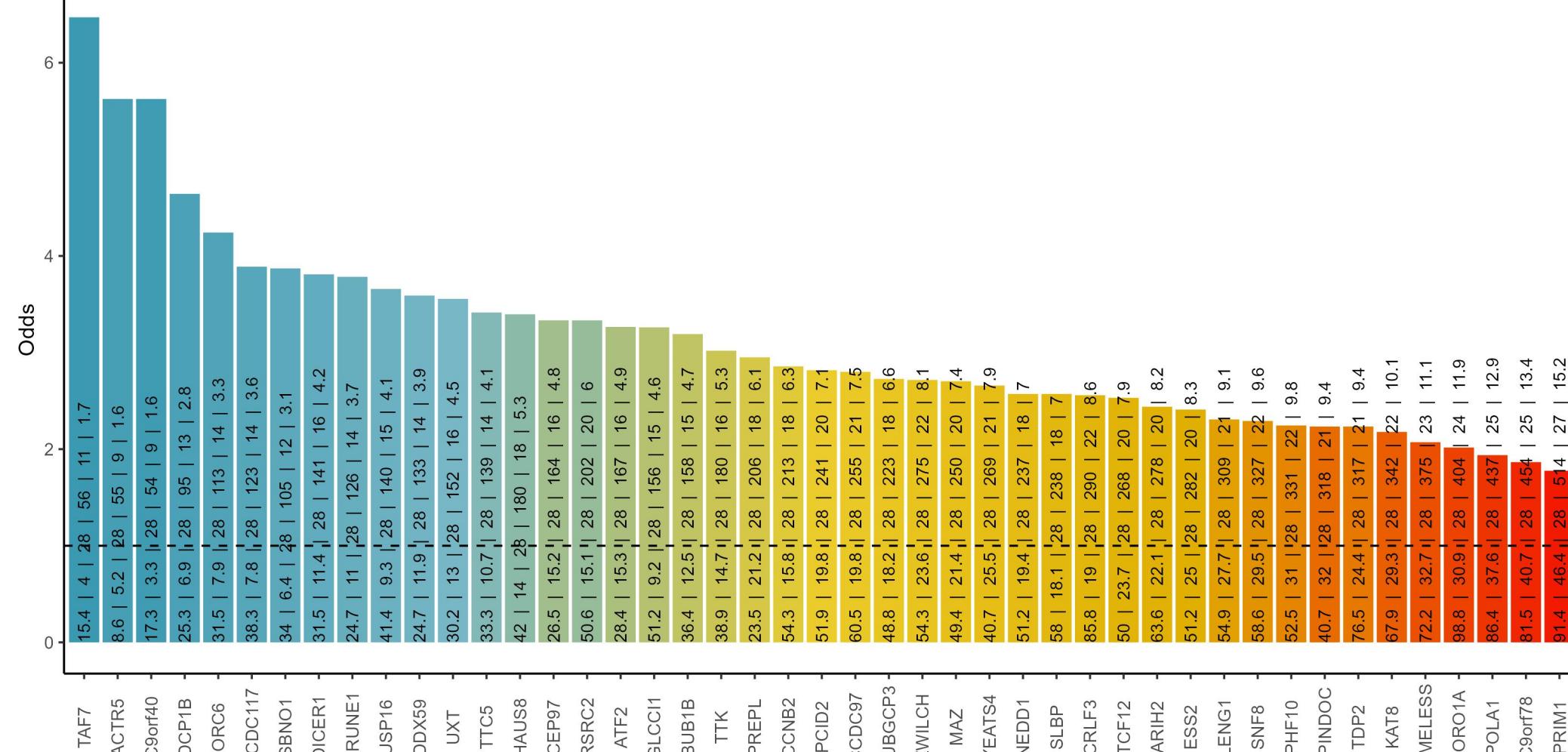
% of ERCC1 in blood cancers: 6.8 ; % of ERCC1 in solid cancers: 2.2

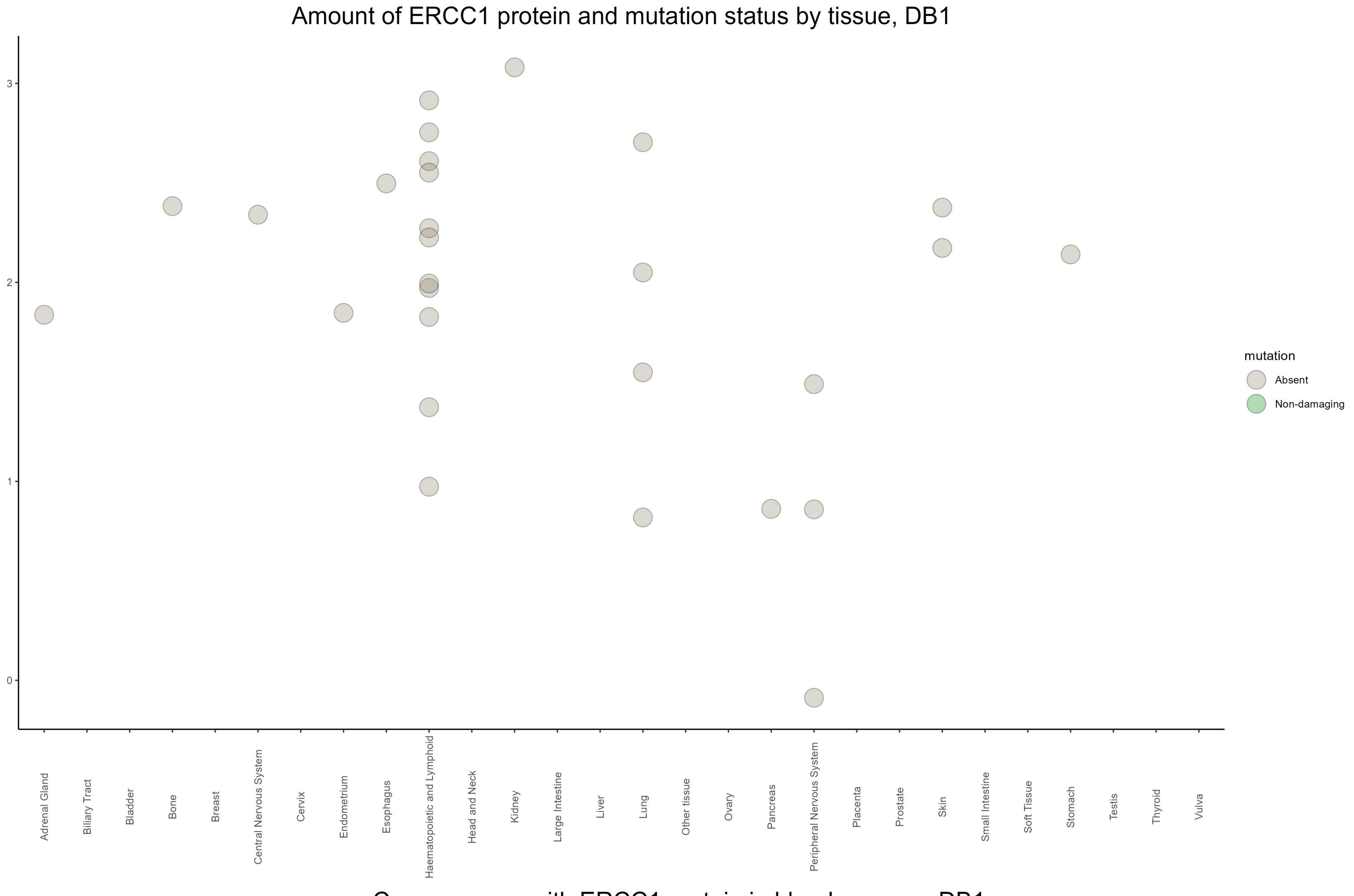
Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ERCC1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



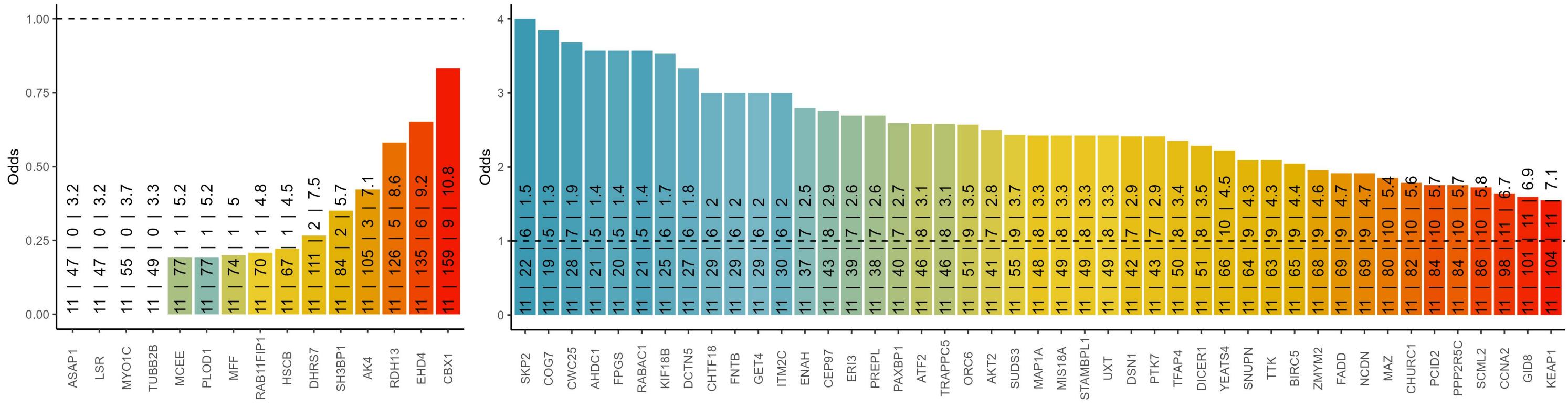
Positive cooccurrence





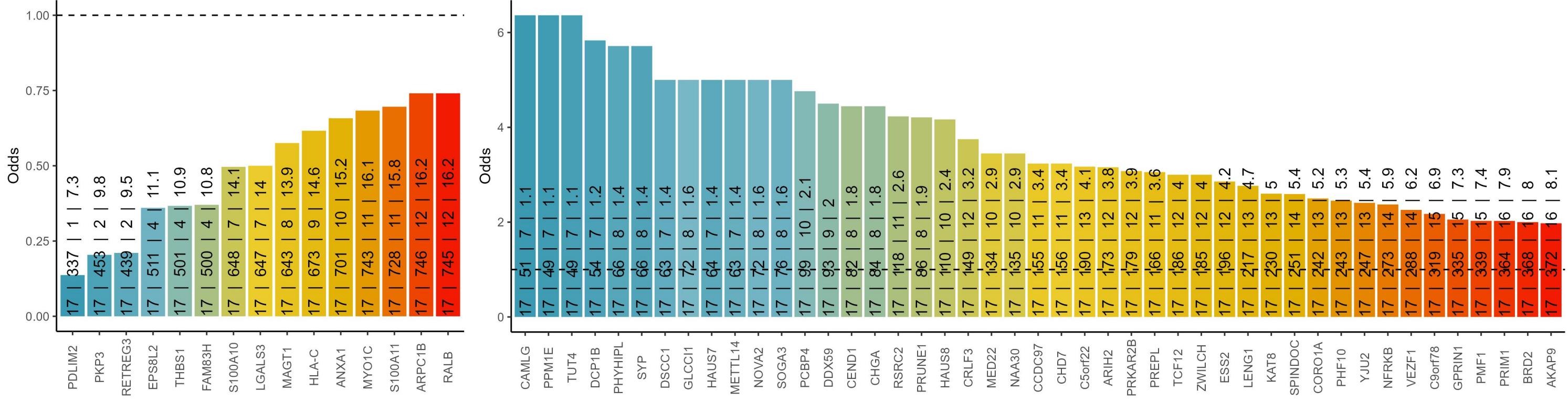
incidence of ERCC1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

negative cooccurrence Positive cooccurrence

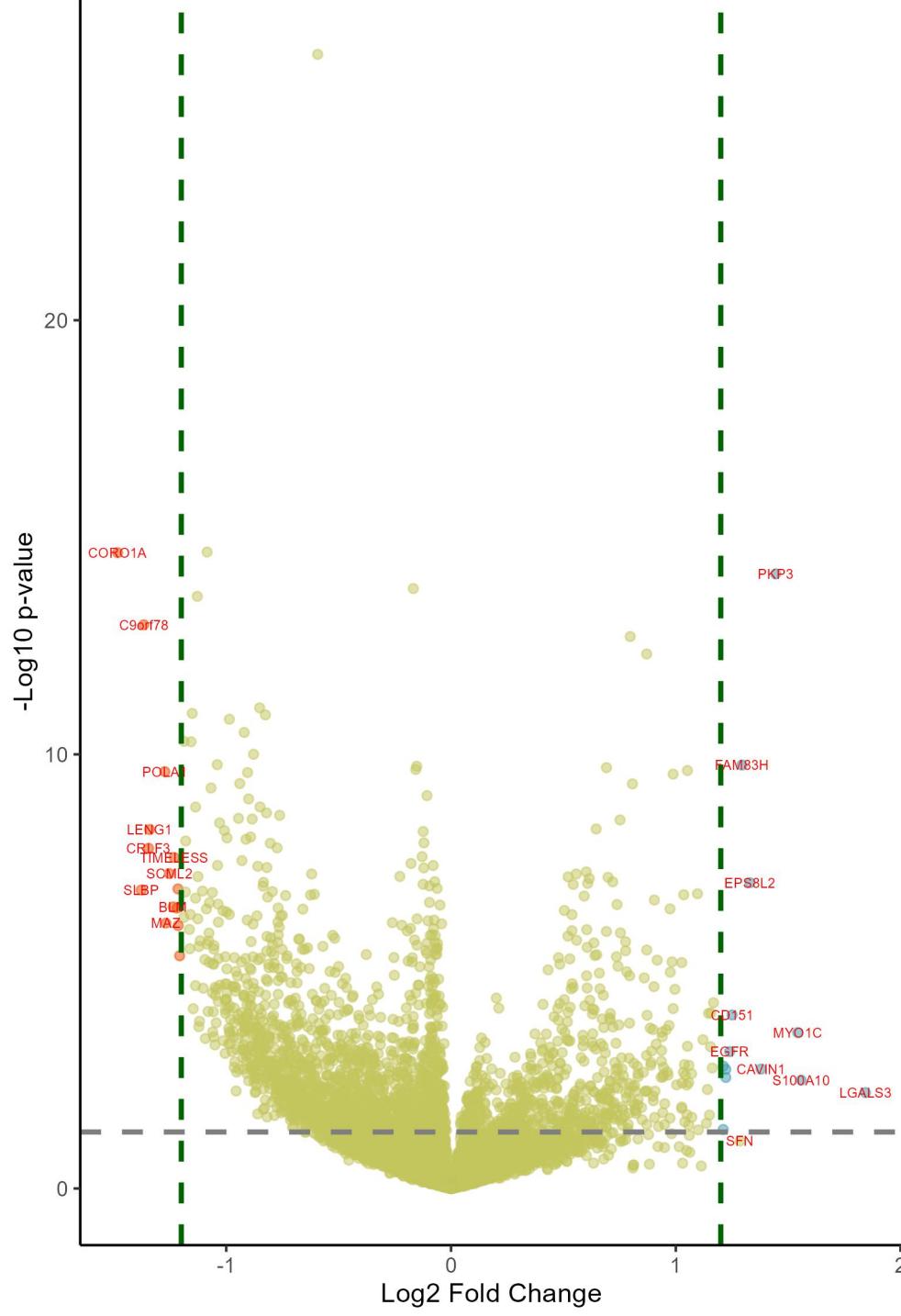


incidence of ERCC1 | incidence of Protein 2 | observed cooccurrence | e

negative cooccurrence Positive cooccurrence

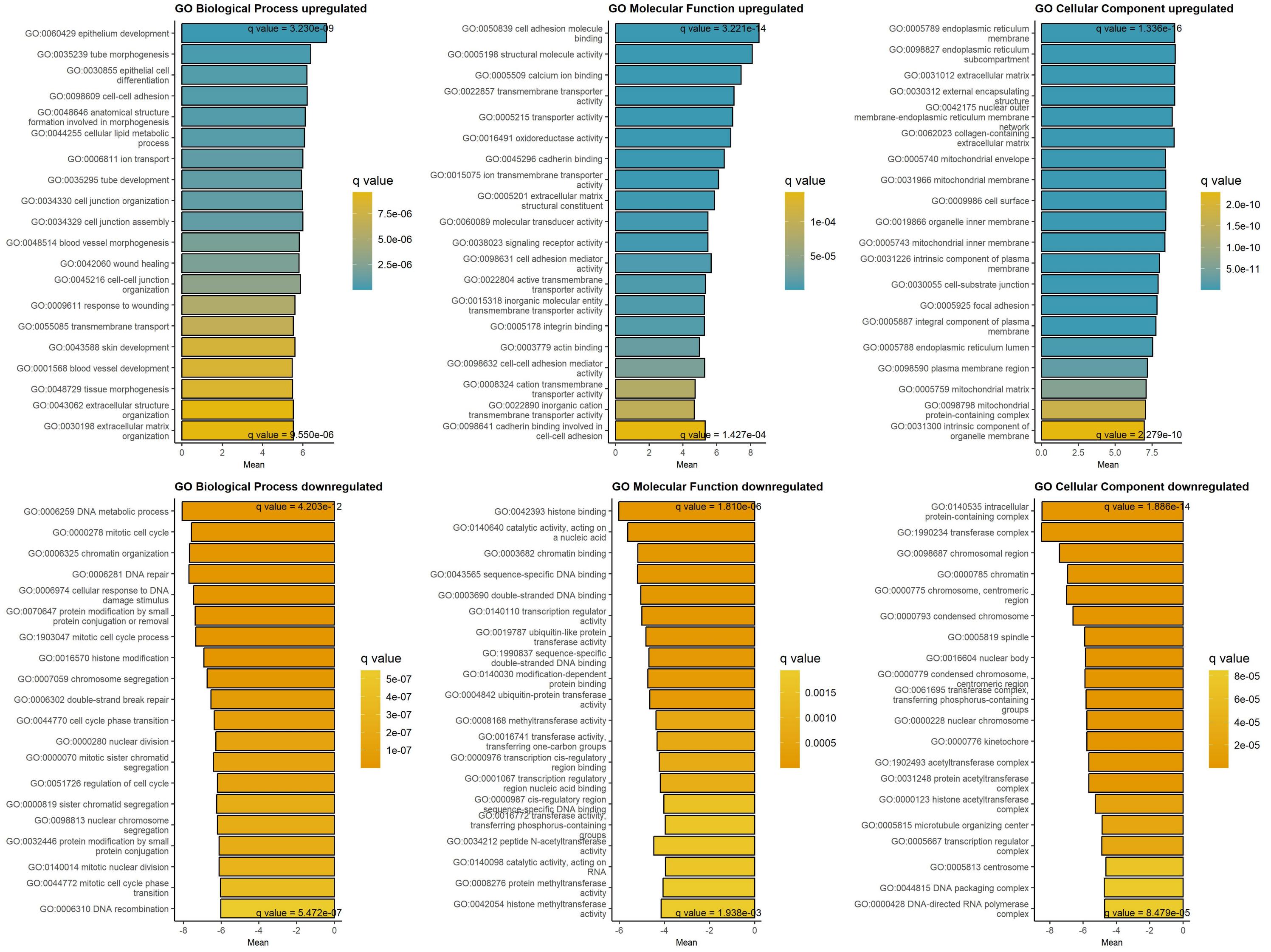


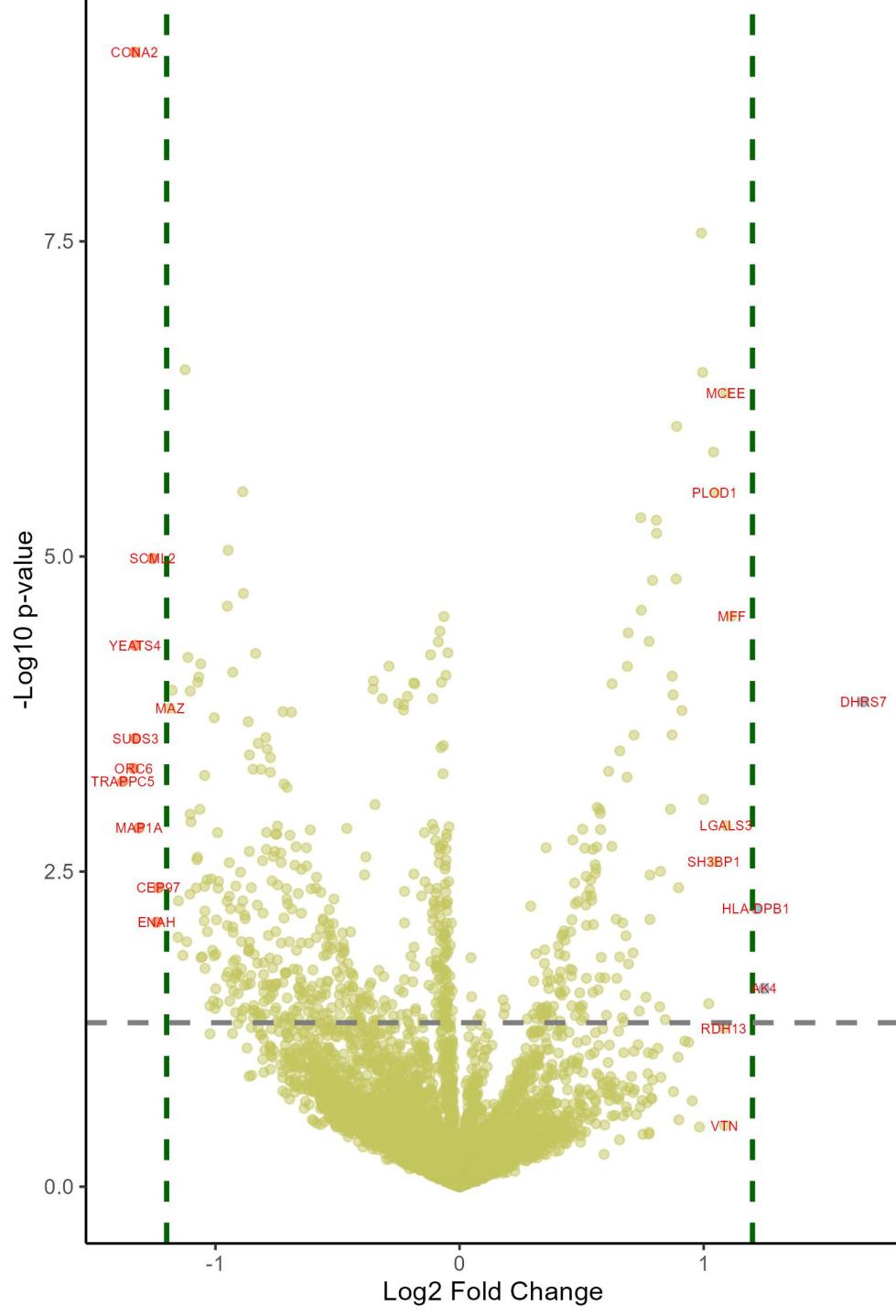
Downregulated at low/absent ERCC1 Upregulated at low/absent ERCC1



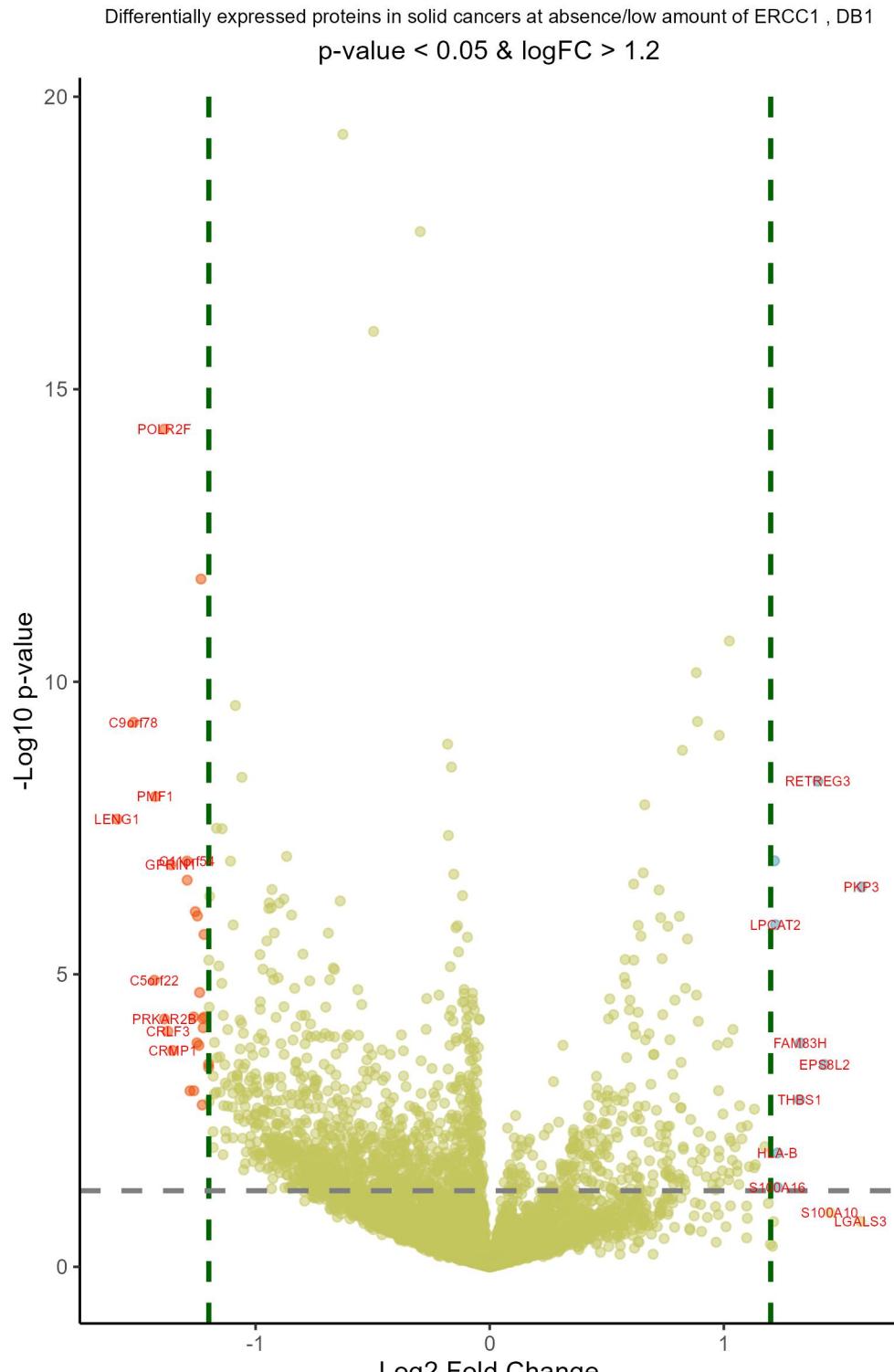
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.48	3.76e-12	CORO1A	coronin 1A	1.84	3.34e-02	LGALS3	galectin 3
-1.38	1.08e-05	SLBP	stem-loop binding protein	1.56	2.13e-02	S100A10	S100 calcium binding protein A10
-1.37	8.61e-11	C9orf78	chromosome 9 open reading frame 78	1.54	3.50e-03	MYO1C	myosin IC
-1.35	1.86e-06	CRLF3	cytokine receptor like factor 3	1.44	9.23e-12	PKP3	plakophilin 3
-1.34	8.54e-07	LENG1	leukocyte receptor cluster member 1	1.38	1.42e-02	CAVIN1	caveolae associated protein 1
-1.27	6.65e-08	POLA1	DNA polymerase alpha 1, catalytic s	1.33	8.14e-06	EPS8L2	EPS8 like 2
-1.27	4.10e-05	MAZ	MYC associated zinc finger protein	1.29	5.87e-08	FAM83H	family with sequence similarity 83
-1.25	5.85e-06	SCML2	Scm polycomb group protein like 2	1.29	1.93e-01	SFN	stratifin
-1.24	2.16e-05	BLM	BLM RecQ like helicase	1.25	1.72e-03	CD151	CD151 molecule (Raph blood group)
-1.23	2.93e-06	TIMELESS	timeless circadian regulator	1.24	7.34e-03	EGFR	epidermal growth factor receptor
-1.22	2.24e-05	ZWILCH	zwilch kinetochore protein	1.22	1.95e-02	DHRS7	dehydrogenase/reductase 7
-1.21	1.03e-05	SNRNP27	small nuclear ribonucleoprotein U4/U6/U11	1.22	1.43e-02	ITGA2	integrin subunit alpha 2
-1.21	4.54e-05	YEATS4	YEATS domain containing 4	1.21	1.28e-02	S100A16	S100 calcium binding protein A16
-1.21	1.52e-04	GSPT2	G1 to S phase transition 2	1.21	1.27e-01	NCEH1	neutral cholesterol ester hydrolase
-1.19	3.28e-05	RNASEH2B	ribonuclease H2 subunit B	1.17	1.06e-03	BCAM	basal cell adhesion molecule (Luthe)
-1.19	2.00e-08	PRIM1	DNA primase subunit 1	1.16	1.36e-02	CAV1	caveolin 1
-1.18	1.16e-05	VPS36	vacuolar protein sorting 36 homolog	1.16	1.61e-03	EPHA2	EPH receptor A2
-1.18	1.37e-06	PMF1	polyamine modulated factor 1	1.15	6.12e-03	RRAS	RAS related
-1.16	5.39e-05	SNF8	SNF8 subunit of ESCRT-II	1.15	7.51e-02	CTS2	cathepsin Z
-1.16	1.16e-04	TCF12	transcription factor 12	1.15	1.63e-03	THBS1	thrombospondin 1
-1.16	2.92e-05	NCAPH2	non-SMC condensin II complex subunit A	1.14	3.01e-02	JUP	junction plakoglobin
-1.16	2.00e-08	PDXP	pyridoxal phosphatase	1.14	1.02e-01	ITGA3	integrin subunit alpha 3
-1.15	6.30e-09	EZH2	enhancer of zeste 2 polycomb repressor complex subunit	1.12	4.70e-03	ANXA3	annexin A3
-1.15	1.34e-03	C20orf27	chromosome 20 open reading frame 27	1.11	4.74e-01	KRT8	keratin 8
-1.14	5.27e-04	RSRC2	arginine and serine rich coiled-coil containing protein 2	1.1	1.29e-01	FKBP9	FKBP prolyl isomerase 9
-1.14	3.20e-07	ZNF24	zinc finger protein 24	1.1	1.24e-05	CDH1	cadherin 1
-1.14	1.45e-05	SMAD4	SMAD family member 4	1.07	8.14e-02	RHOC	ras homolog family member C
-1.13	2.18e-11	UBE2T	ubiquitin conjugating enzyme E2 T	1.07	1.71e-02	MYO1B	myosin IB
-1.13	3.47e-05	TYMS	thymidylate synthetase	1.06	2.91e-01	ANXA1	annexin A1

GAGE analysis on upregulated and downregulated proteins at low/absent ERCC1 protein, DB1



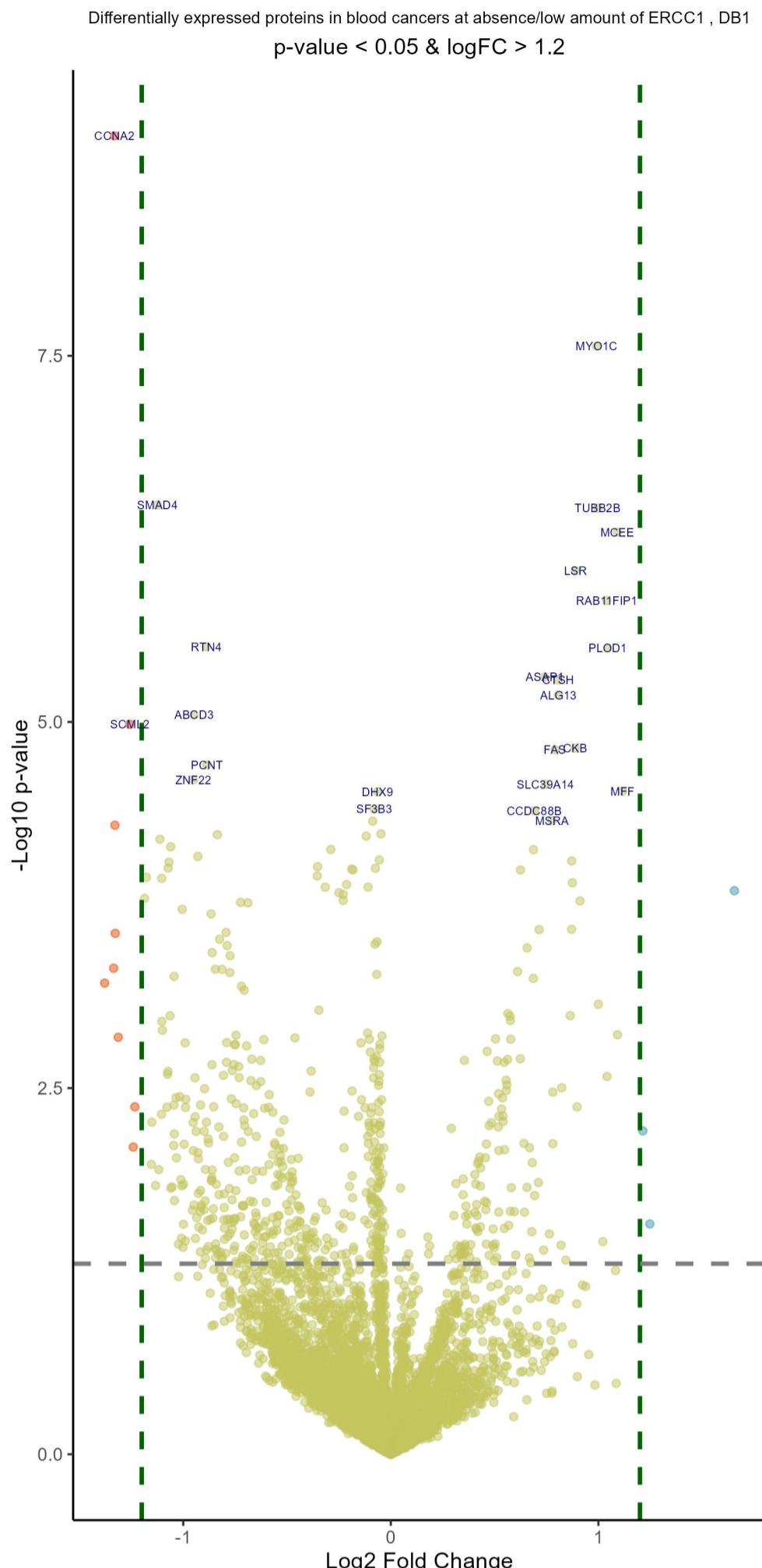


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.38	4.98e-02	TRAPPC5	trafficking protein particle comple	1.66	1.82e-02	DHRS7	dehydrogenase/reductase 7
-1.34	4.33e-02	ORC6	origin recognition complex subunit	1.25	4.27e-01	AK4	adenylate kinase 4
-1.33	3.31e-06	CCNA2	cyclin A2	1.21	1.99e-01	HLA-DPB1	major histocompatibility complex, c
-1.33	1.25e-02	YEATS4	YEATS domain containing 4	1.12	9.05e-03	MFF	mitochondrial fission factor
-1.33	2.84e-02	SUDS3	SDS3 homolog, SIN3A corepressor com	1.09	9.61e-02	LGALS3	galectin 3
-1.31	9.61e-02	MAP1A	microtubule associated protein 1A	1.09	5.61e-04	MCEE	methylmalonyl-CoA epimerase
-1.26	4.60e-03	SCML2	Scm polycomb group protein like 2	1.09	9.14e-01	VTN	vitronectin
-1.24	2.31e-01	ENAH	ENAH actin regulator	1.08	5.70e-01	RDH13	retinol dehydrogenase 13
-1.23	1.65e-01	CEP97	centrosomal protein 97	1.04	2.08e-03	PLOD1	procollagen-lysine,2-oxoglutarate 5
-1.19	1.94e-02	MAZ	MYC associated zinc finger protein	1.04	1.30e-01	SH3BP1	SH3 domain binding protein 1
-1.18	1.65e-02	PPP2R5C	protein phosphatase 2 regulatory su	1.04	1.23e-03	RAB11FIP1	RAB11 family interacting protein 1
-1.15	2.64e-01	PTK7	protein tyrosine kinase 7 (inactive)	1.02	4.88e-01	EHD4	EH domain containing 4
-1.15	1.85e-01	ATF2	activating transcription factor 2	1	6.70e-02	HLA-DRB3	major histocompatibility complex, c
-1.13	3.17e-01	ERI3	ERI1 exoribonuclease family member	1	4.61e-04	TUBB2B	tubulin beta 2B class IIb
-1.12	4.61e-04	SMAD4	SMAD family member 4	0.99	6.02e-05	MYO1C	myosin IC
-1.12	2.79e-01	PAXBP1	PAX3 and PAX7 binding protein 1	0.98	9.14e-01	ANXA6	annexin A6
-1.11	1.36e-02	SLBP	stem-loop binding protein	0.95	9.08e-01	CD74	CD74 molecule
-1.1	1.75e-01	DICER1	dicer 1, ribonuclease III	0.94	6.44e-01	TES	testin LIM domain protein
-1.1	1.65e-02	KAT7	lysine acetyltransferase 7	0.92	6.36e-01	DDT	D-dopachrome tautomerase
-1.1	8.10e-02	XRCC4	X-ray repair cross complementing 4	0.91	1.94e-02	TYMP	thymidine phosphorylase
-1.1	9.22e-02	FADD	Fas associated via death domain	0.9	9.14e-01	LSP1	lymphocyte specific protein 1
-1.08	1.65e-01	SCAMP1	secretory carrier membrane protein	0.9	1.65e-01	CA2	carbonic anhydrase 2
-1.08	1.28e-01	TTK	TTK protein kinase	0.9	7.20e-01	CTSS	cathepsin S
-1.07	1.24e-01	SNUPN	snurportin 1	0.89	8.81e-04	LSR	lipolysis stimulated lipoprotein re
-1.07	1.55e-02	MGMT	O-6-methylguanine-DNA methyltransfe	0.89	6.05e-03	CKB	creatine kinase B
-1.07	1.55e-02	TLE5	TLE family member 5, transcriptiona	0.88	8.71e-01	CTSZ	cathepsin Z
-1.06	7.62e-02	CHURC1	churchill domain containing 1	0.87	1.74e-02	HSCB	HscB mitochondrial iron-sulfur clus
-1.06	1.46e-02	GID8	GID complex subunit 8 homolog	0.87	1.55e-02	SIL1	SIL1 nucleotide exchange factor
-1.06	3.19e-01	FANCD2	FA complementation group D2	0.87	2.76e-02	BORCS7	BLOC-1 related complex subunit 7

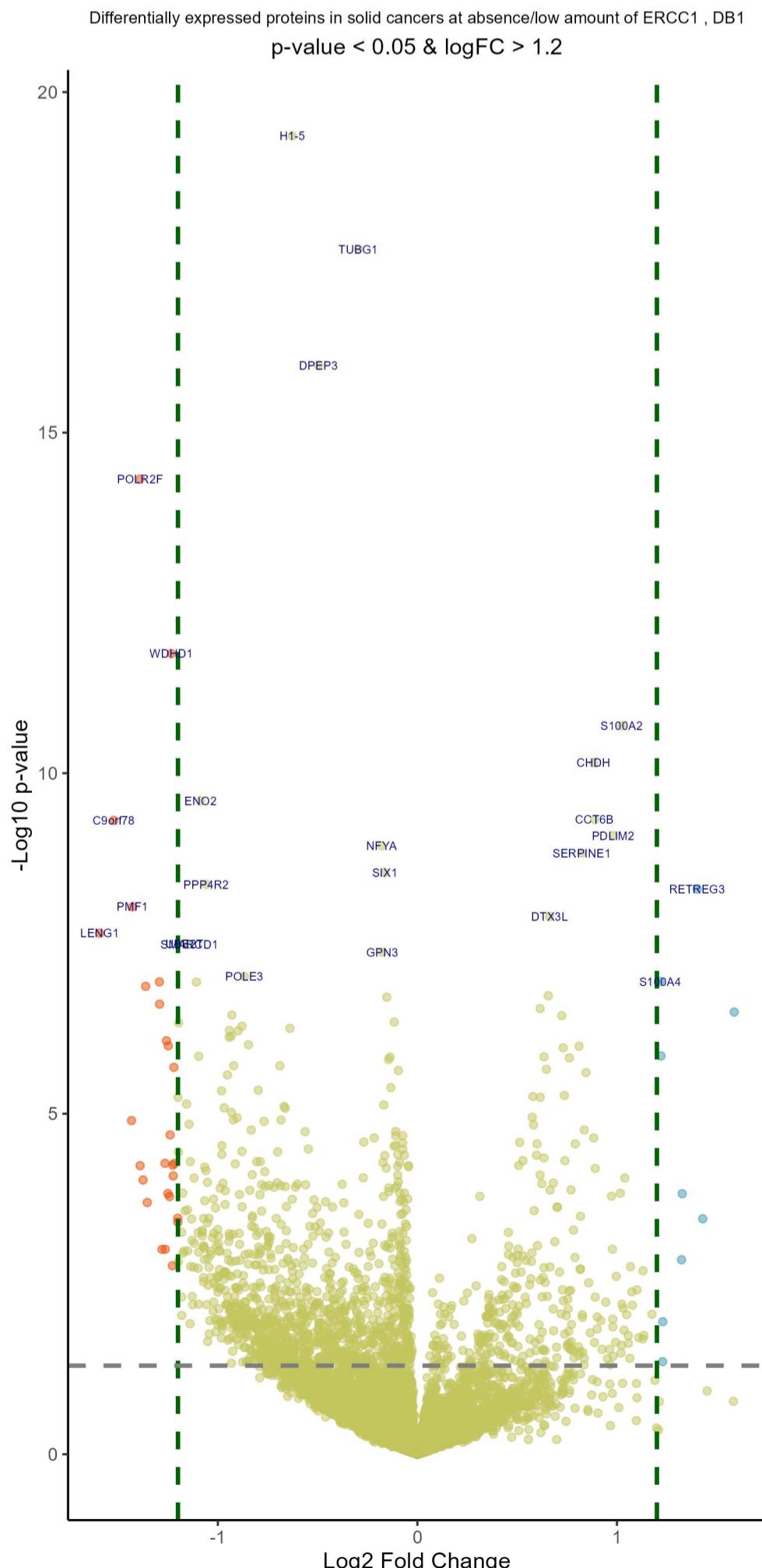


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.59	7.41e-06	LENG1	leukocyte receptor cluster member 1	1.59	6.47e-05	PKP3	plakophilin 3
-1.52	2.98e-07	C9orf78	chromosome 9 open reading frame 78	1.58	4.19e-01	LGALS3	galectin 3
-1.43	1.06e-03	C5orf22	chromosome 5 open reading frame 22	1.45	3.54e-01	S100A10	S100 calcium binding protein A10
-1.43	3.38e-06	PMF1	polyamine modulated factor 1	1.43	1.09e-02	EPS8L2	EPS8 like 2
-1.39	6.37e-12	POLR2F	RNA polymerase II, I and III subuni	1.4	1.96e-06	RETREG3	reticulophagy regulator family memb
-1.39	3.10e-03	PRKAR2B	protein kinase cAMP-dependent type	1.33	5.84e-03	FAM83H	family with sequence similarity 83
-1.37	4.49e-03	CRLF3	cytokine receptor like factor 3	1.32	2.79e-02	THBS1	thrombospondin 1
-1.36	3.19e-05	GPRIN1	G protein regulated inducer of neur	1.23	9.66e-02	HLA-B	major histocompatibility complex, c
-1.35	7.18e-03	CRMP1	collapsin response mediator protein	1.23	2.04e-01	S100A16	S100 calcium binding protein A16
-1.29	2.86e-05	C11orf54	chromosome 11 open reading frame 54	1.22	1.89e-04	LPCAT2	lysophosphatidylcholine acyltransfe
-1.29	5.27e-05	BRD2	bromodomain containing 2	1.22	2.86e-05	S100A4	S100 calcium binding protein A4
-1.28	2.22e-02	INTS7	integrator complex subunit 7	1.21	4.20e-01	CD44	CD44 molecule (Indian blood group)
-1.26	3.00e-03	USP13	ubiquitin specific peptidase 13	1.21	6.96e-01	S100A11	S100 calcium binding protein A11
-1.26	2.22e-02	PCBP4	poly(rC) binding protein 4	1.2	6.65e-01	LGALS1	galectin 1
-1.26	1.28e-04	GTPBP3	GTP binding protein 3, mitochondria	1.19	2.93e-01	CTSZ	cathepsin Z
-1.25	5.84e-03	BLM	BLM RecQ like helicase	1.17	8.59e-02	VAMP8	vesicle associated membrane protein
-1.25	1.45e-04	PRIM1	DNA primase subunit 1	1.13	1.25e-01	CD151	CD151 molecule (Raph blood group)
-1.24	6.20e-03	CORO1A	coronin 1A	1.13	3.54e-02	CDH1	cadherin 1
-1.24	1.56e-03	POLA1	DNA polymerase alpha 1, catalytic s	1.13	1.32e-01	ITGB4	integrin subunit beta 4
-1.23	1.94e-09	WDHD1	WD repeat and HMG-box DNA binding p	1.11	1.30e-01	ANXA3	annexin A3
-1.23	3.18e-02	MED22	mediator complex subunit 22	1.1	5.37e-02	PSMB8	proteasome 20S subunit beta 8
-1.23	3.10e-03	NCAPH2	non-SMC condensin II complex subuni	1.1	3.94e-01	CAVIN1	caveolae associated protein 1
-1.22	4.04e-03	SMC1B	structural maintenance of chromosom	1.1	5.86e-01	ANXA1	annexin A1
-1.22	2.43e-04	PDXP	pyridoxal phosphatase	1.1	3.11e-01	HLA-C	major histocompatibility complex, c
-1.22	3.00e-03	TIMELESS	timeless circadian regulator	1.08	7.31e-02	PIGT	phosphatidylinositol glycan anchor
-1.2	1.08e-02	MAP2	microtubule associated protein 2	1.07	5.54e-02	TAP2	transporter 2, ATP binding cassette
-1.2	1.22e-02	TCF12	transcription factor 12	1.07	3.24e-02	LAD1	ladinin 1
-1.2	5.61e-04	BUD23	BUD23 rRNA methyltransferase and ri	1.06	1.93e-01	CD59	CD59 molecule (CD59 blood group)
-1.2	2.33e-03	UBFD1	ubiquitin family domain containing	1.06	1.44e-01	EPHA2	EPH receptor A2

ERCC1 network, DB1, no Pearson r > 0.3



Sorted by p values!							
Downregulated in blood cancers at low/absent ERCC1				Upregulated in blood cancers at low/absent ERCC1			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.33	3.31e-06	CCNA2	cyclin A2	0.99	6.02e-05	MYO1C	myosin IC
-1.12	4.61e-04	SMAD4	SMAD family member 4	1	4.61e-04	TUBB2B	tubulin beta 2B class IIb
-0.89	2.08e-03	RTN4	reticulon 4	1.09	5.61e-04	MCEE	methylmalonyl-CoA epimerase
-0.95	4.24e-03	ABCD3	ATP binding cassette subfamily D me	0.89	8.81e-04	LSR	lipolysis stimulated lipoprotein re
-1.26	4.60e-03	SCML2	Scm polycomb group protein like 2	1.04	1.23e-03	RAB11FIP1	RAB11 family interacting protein 1
-0.89	7.26e-03	PCNT	pericentrin	1.04	2.08e-03	PLOD1	procollagen-lysine,2-oxoglutarate 5
-0.95	8.69e-03	ZNF22	zinc finger protein 22	0.74	2.86e-03	ASAP1	ArfGAP with SH3 domain, ankyrin rep
-0.06	9.05e-03	DHX9	DExH-box helicase 9	0.81	2.86e-03	CTSH	cathepsin H
-0.08	1.12e-02	SF3B3	splicing factor 3b subunit 3	0.81	3.35e-03	ALG13	ALG13 UDP-N-acetylglucosaminyltrans
-0.09	1.22e-02	BUB3	BUB3 mitotic checkpoint protein	0.89	6.05e-03	CKB	creatine kinase B
-1.33	1.25e-02	YEATS4	YEATS domain containing 4	0.79	6.05e-03	FAS	Fas cell surface death receptor
-0.05	1.34e-02	SNRPD3	small nuclear ribonucleoprotein D3	0.74	8.88e-03	SLC39A14	solute carrier family 39 member 14
-0.84	1.34e-02	SNRNP27	small nuclear ribonucleoprotein U4/	1.12	9.05e-03	MFF	mitochondrial fission factor
-0.12	1.34e-02	CKAP5	cytoskeleton associated protein 5	0.69	1.12e-02	CCDC88B	coiled-coil domain containing 88B
-1.11	1.36e-02	SLBP	stem-loop binding protein	0.78	1.22e-02	MSRA	methionine sulfoxide reductase A
-1.06	1.46e-02	GID8	GID complex subunit 8 homolog	0.69	1.46e-02	MYO1D	myosin ID
-0.29	1.46e-02	S100A14	S100 calcium binding protein A14	0.87	1.55e-02	SIL1	SIL1 nucleotide exchange factor
-0.93	1.55e-02	MRPL21	mitochondrial ribosomal protein L21	0.62	1.55e-02	PRORP	protein only RNase P catalytic subu
-0.06	1.55e-02	SRSF7	serine and arginine rich splicing f	0.87	1.74e-02	HSCB	HscB mitochondrial iron-sulfur clus
-1.07	1.55e-02	TLE5	TLE family member 5, transcriptiona	1.66	1.82e-02	DHRS7	dehydrogenase/reductase 7
-0.35	1.55e-02	FRMD8	FERM domain containing 8	0.91	1.94e-02	TYMP	thymidine phosphorylase
-1.07	1.55e-02	MGMT	O-6-methylguanine-DNA methyltransfe	0.87	2.76e-02	BORCS7	BLOC-1 related complex subunit 7
-0.07	1.55e-02	RBM39	RNA binding motif protein 39	0.71	2.76e-02	HVCN1	hydrogen voltage gated channel 1
-0.19	1.55e-02	SESTD1	SEC14 and spectrin domain containin	0.66	3.31e-02	CLIC2	chloride intracellular channel 2
-0.18	1.55e-02	CCDC85C	coiled-coil domain containing 85C	0.61	4.43e-02	ARSA	arylsulfatase A
-0.35	1.65e-02	STMN2	stathmin 2	0.69	4.68e-02	IL4I1	interleukin 4 induced 1
-1.18	1.65e-02	PPP2R5C	protein phosphatase 2 regulatory su	1	6.70e-02	HLA-DRB3	major histocompatibility complex, c
-1.1	1.65e-02	KAT7	lysine acetyltransferase 7	0.56	7.58e-02	SPECC1	sperm antigen with calponin homolog
-0.21	1.75e-02	SERPINB5	serpin family B member 5	0.86	7.62e-02	NT5C	5', 3'-nucleotidase, cytosolic
-0.11	1.75e-02	HNRNPUL1	heterogeneous nuclear ribonucleopro	0.57	7.62e-02	SYNE1	spectrin repeat containing nuclear
-0.32	1.75e-02	KRT80	keratin 80	0.58	8.08e-02	BAIAP2L1	BAR/IMD domain containing adaptor p
-0.25	1.84e-02	GALNT3	polypeptide N-acetylgalactosaminylt	1.09	9.61e-02	LGALS3	galectin 3
-0.23	1.85e-02	SLC12A4	solute carrier family 12 member 4	0.5	9.61e-02	FAM234A	family with sequence similarity 234
-1.19	1.94e-02	MAZ	MYC associated zinc finger protein	0.58	9.61e-02	TRAF1	TNF receptor associated factor 1
-0.23	1.94e-02	MGAT3	beta-1,4-mannosyl-glycoprotein 4-be	0.46	1.06e-01	AK2	adenylate kinase 2
-0.72	1.94e-02	CHMP1B	charged multivesicular body protein	0.62	1.13e-01	NCOA7	nuclear receptor coactivator 7
-0.69	1.94e-02	CDK6	cyclin dependent kinase 6	0.56	1.13e-01	MCL1	MCL1 apoptosis regulator, BCL2 fami
-1	2.11e-02	KEAP1	kelch like ECH associated protein 1	0.35	1.13e-01	NDUFV1	NADH:ubiquinone oxidoreductase core
-0.87	2.23e-02	EGR3	EVVE_PbcGEF and PH domain containi	0.51	1.13e-01	ETS1	Ets-Like Protein 2' O-methyltransferase 1



Sorted by p values!							
Downregulated in solid cancers at low/absent ERCC1				Upregulated in solid cancers at low/absent ERCC1			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.63	1.46e-16	H1-5	H1.5 linker histone, cluster member	1.02	1.91e-08	S100A2	S100 calcium binding protein A2
-0.3	4.48e-15	TUBG1	tubulin gamma 1	0.88	5.82e-08	CHDH	choline dehydrogenase
-0.5	1.70e-13	DPEP3	dipeptidase 3	0.89	2.98e-07	CCT6B	chaperonin containing TCP1 subunit
-1.39	6.37e-12	POLR2F	RNA polymerase II, I and III subuni	0.98	4.57e-07	PDLM2	PDZ and LIM domain 2
-1.23	1.94e-09	WDHD1	WD repeat and HMG-box DNA binding p	0.82	7.05e-07	SERPINE1	serpin family E member 1
-1.09	1.88e-07	ENO2	enolase 2	1.4	1.96e-06	RETREG3	reticulophagy regulator family memb
-1.52	2.98e-07	C9orf78	chromosome 9 open reading frame 78	0.66	4.44e-06	DTX3L	deltex E3 ubiquitin ligase 3L
-0.18	5.95e-07	NFYA	nuclear transcription factor Y subu	1.22	2.86e-05	S100A4	S100 calcium binding protein A4
-0.16	1.27e-06	SIX1	SIX homeobox 1	0.66	4.24e-05	GRHL2	grainyhead like transcription facto
-1.06	1.78e-06	PPP4R2	protein phosphatase 4 regulatory su	0.62	5.94e-05	FZD6	frizzled class receptor 6
-1.43	3.38e-06	PMF1	polyamine modulated factor 1	1.59	6.47e-05	PKP3	plakophilin 3
-1.59	7.41e-06	LENG1	leukocyte receptor cluster member 1	0.72	6.89e-05	KRT4	keratin 4
-1.17	9.81e-06	UBE2T	ubiquitin conjugating enzyme E2 T	0.81	1.45e-04	IFI35	interferon induced protein 35
-1.14	9.81e-06	SMARCD1	SWI/SNF related, matrix associated,	0.73	1.49e-04	AP1M2	adaptor related protein complex 1 s
-0.18	1.23e-05	GPN3	GPN-loop GTPase 3	1.22	1.89e-04	LPCAT2	lysophosphatidylcholine acyltransfe
-0.87	2.67e-05	POLE3	DNA polymerase epsilon 3, accessory	0.63	1.89e-04	PLCD3	phospholipase C delta 3
-1.29	2.86e-05	C11orf54	chromosome 11 open reading frame 54	0.76	1.90e-04	PYCARD	PYD and CARD domain containing
-1.11	2.86e-05	CREB1	cAMP responsive element binding pro	0.65	2.55e-04	CPA4	carboxypeptidase A4
-1.36	3.19e-05	GPRIN1	G protein regulated inducer of neur	0.84	2.76e-04	DSC2	desmocollin 2
-0.15	4.31e-05	RFC4	replication factor C subunit 4	0.74	5.52e-04	KRT6A	keratin 6A
-1.29	5.27e-05	BRD2	bromodomain containing 2	0.58	5.61e-04	LXN	latexin
-0.93	6.89e-05	CEP170	centrosomal protein 170	0.62	5.61e-04	SLC44A2	solute carrier family 44 member 2
-0.12	8.33e-05	PRPF4	pre-mRNA processing factor 4	0.58	1.00e-03	COL7A1	collagen type VII alpha 1 chain
-1.2	8.34e-05	EZH2	enhancer of zeste 2 polycomb repres	0.58	1.18e-03	PROM2	prominin 2
-0.88	9.06e-05	FRG1	FSHD region gene 1	0.84	1.37e-03	GALNT7	polypeptide N-acetylgalactosaminylt
-0.64	9.51e-05	TUBB3	tubulin beta 3 class III	0.88	1.66e-03	MAN2A1	mannosidase alpha class 2A member 1
-0.94	9.83e-05	MRGBP	MRG domain binding protein	0.51	1.88e-03	UBL3	ubiquitin like 3
-0.9	9.83e-05	CKB	creatine kinase B	0.6	1.92e-03	PIEZ01	piezo type mechanosensitive ion cha
-0.93	1.15e-04	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.79	1.92e-03	TRIM29	tripartite motif containing 29
-0.94	1.16e-04	MORC2	MORC family CW-type zinc finger 2	0.6	2.51e-03	ESRP2	epithelial splicing regulatory prot
-1.26	1.28e-04	GTPBP3	GTP binding protein 3, mitochondria	0.63	2.69e-03	PLXNA1	plexin A1
-0.85	1.43e-04	KIF11	kinesin family member 11	0.53	2.91e-03	SIAE	sialic acid acetylesterase
-1.25	1.45e-04	PRIM1	DNA primase subunit 1	0.74	2.91e-03	SLC35B2	solute carrier family 35 member B2
-1.1	1.89e-04	CCDC50	coiled-coil domain containing 50	0.51	3.10e-03	PECR	peroxisomal trans-2-enoyl-CoA reduc
-0.14	1.89e-04	PCNA	proliferating cell nuclear antigen	0.89	3.28e-03	RBM47	RNA binding motif protein 47
-0.14	1.97e-04	SUPT6H	SPT6 homolog, histone chaperone and	0.61	3.98e-03	SURF4	surfeit 4
-0.92	2.35e-04	MTFR1L	mitochondrial fission regulator 1 l	1.04	4.24e-03	IL18	interleukin 18
-0.69	2.35e-04	PPAT	phosphoribosyl pyrophosphate amidot	0.68	4.82e-03	GALNT3	polypeptide N-acetylgalactosaminylt

Insufficient number of paired observations in DB1 for ERCC1

Insufficient number of paired observations in DB1 for ERCC1

No information on Ser/Thr kinase phosphorylation sites for ERCC1

No information on Ser/Thr kinase phosphorylation sites for ERCC1

No sufficient paired observations in DB1 for ERCC1