

# ERCC2

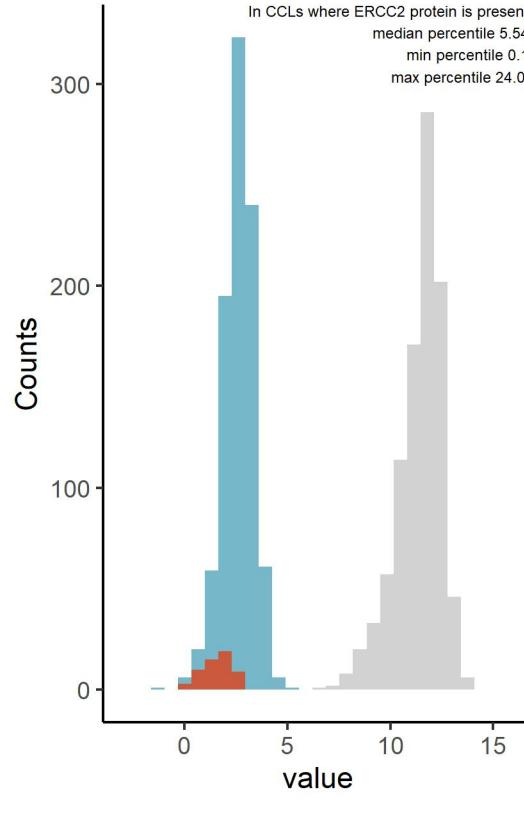
Protein name: ERCC2 ; UNIPROT: P18074 ; Gene name: ERCC excision repair 2, TFIIH core complex helicase subunit

Ligandable: Yes ; Ligandable\_by\_Chem: Yes ; Is\_enzyme: Yes (<https://cansar.ai/>)

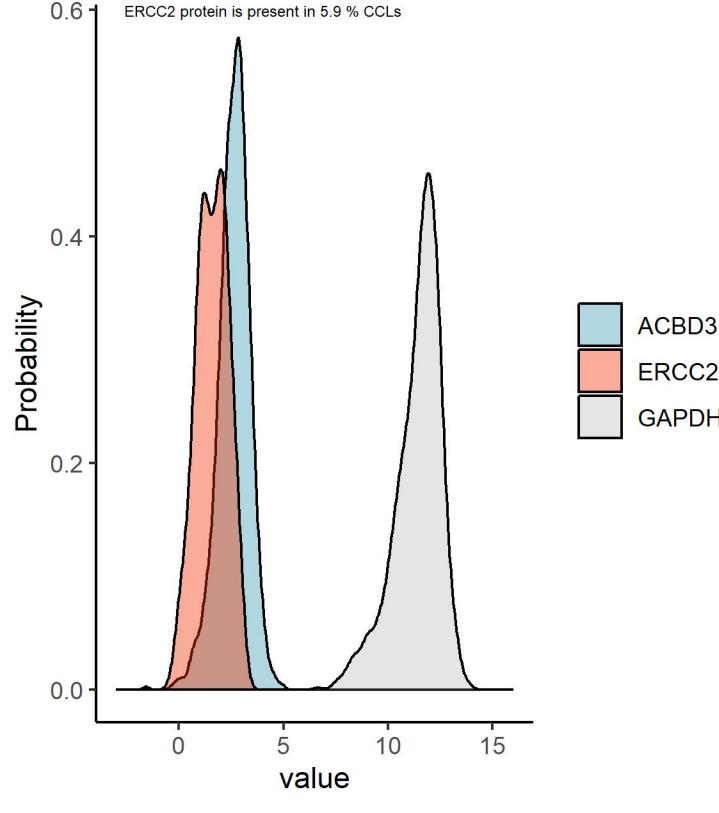
## Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

Histogram of ERCC2 protein compared to proteins with low and high abundance



Density plot of ERCC2 protein compared to proteins with low and high abundance



Top negative correlations of ERCC2 protein, DB1

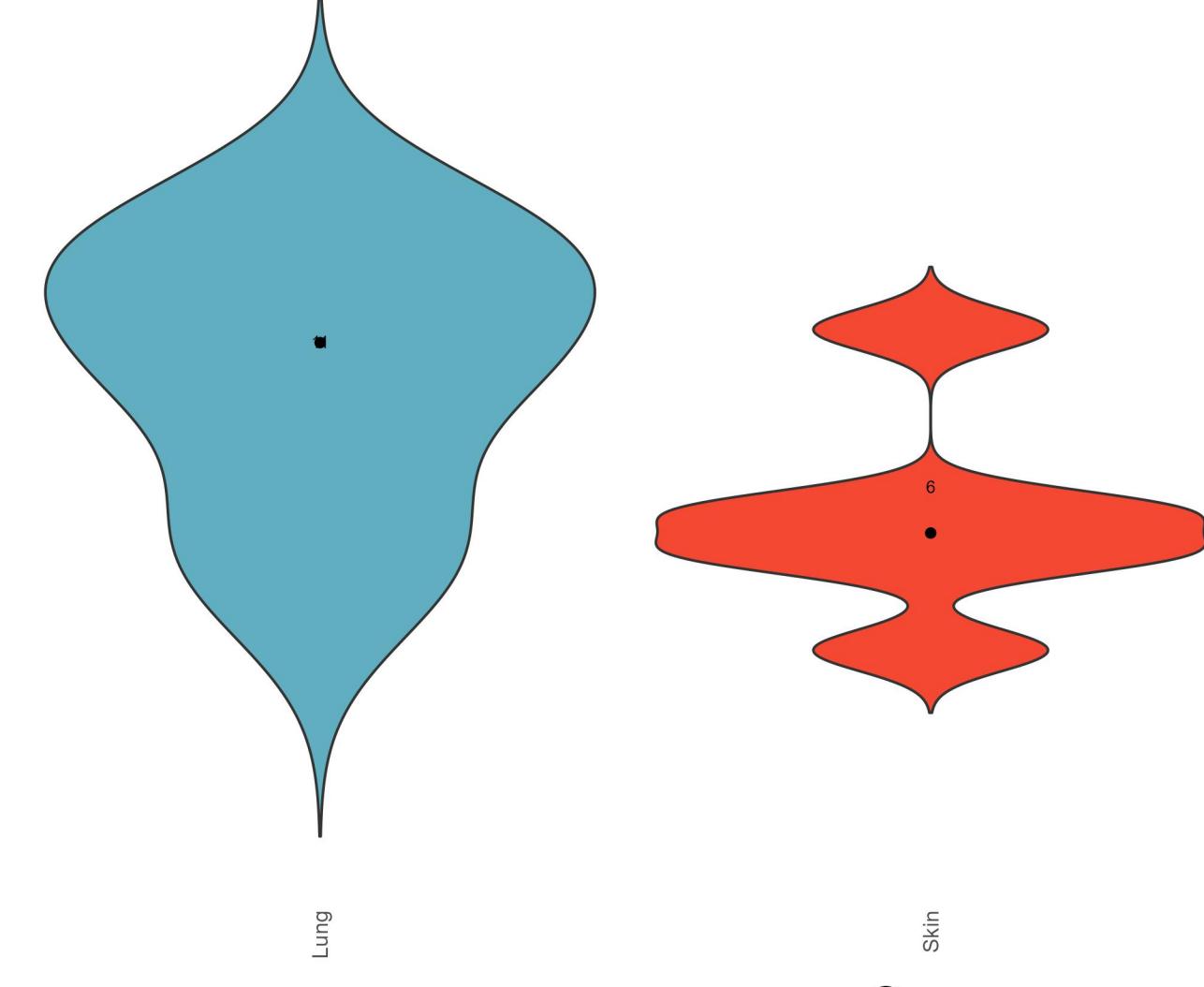
Pearson correlation coefficients

Top positive correlations of ERCC2 protein, DB1

Pearson correlation coefficients

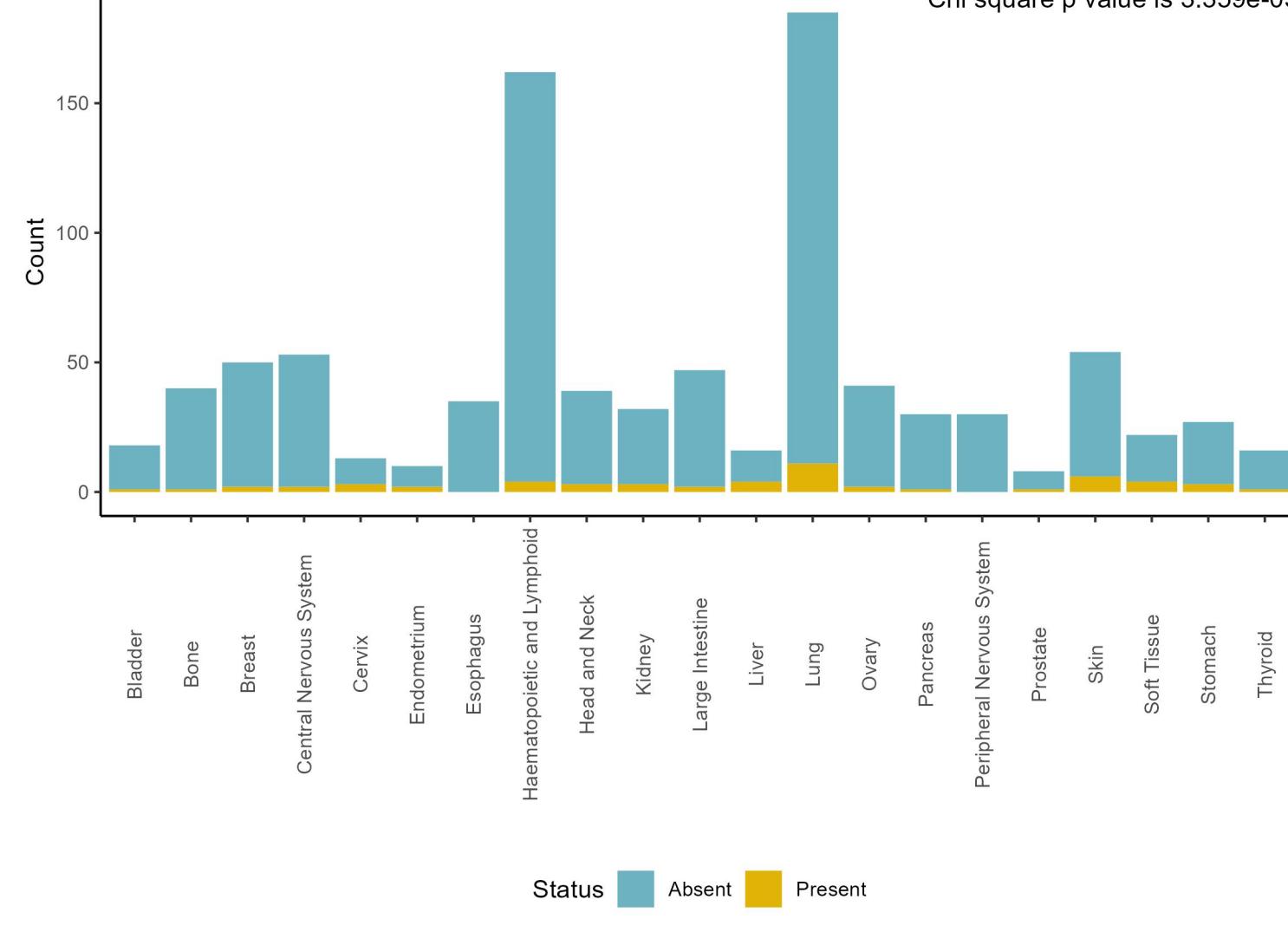
Amount of ERCC2 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 5.327e-01



Present and absent ERCC2 protein counts by tissue, DB1

Chi square p value is 3.359e-03

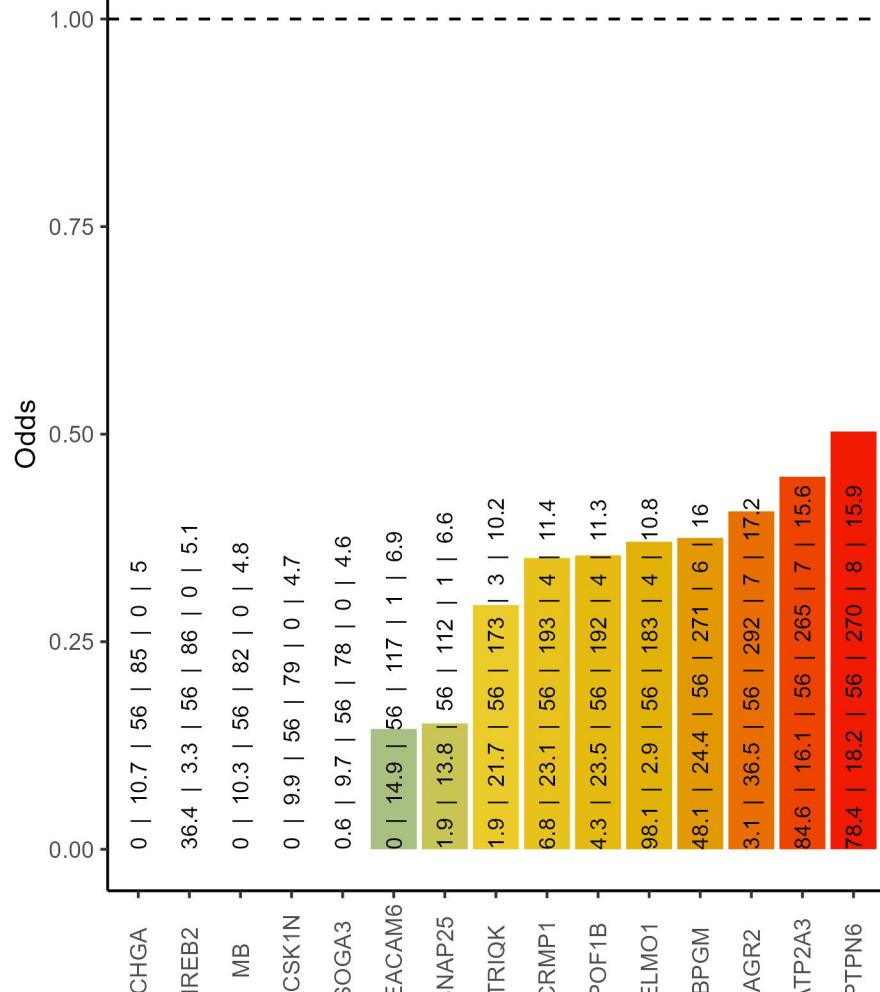


## Cooccurrence with ERCC2 protein, DB1

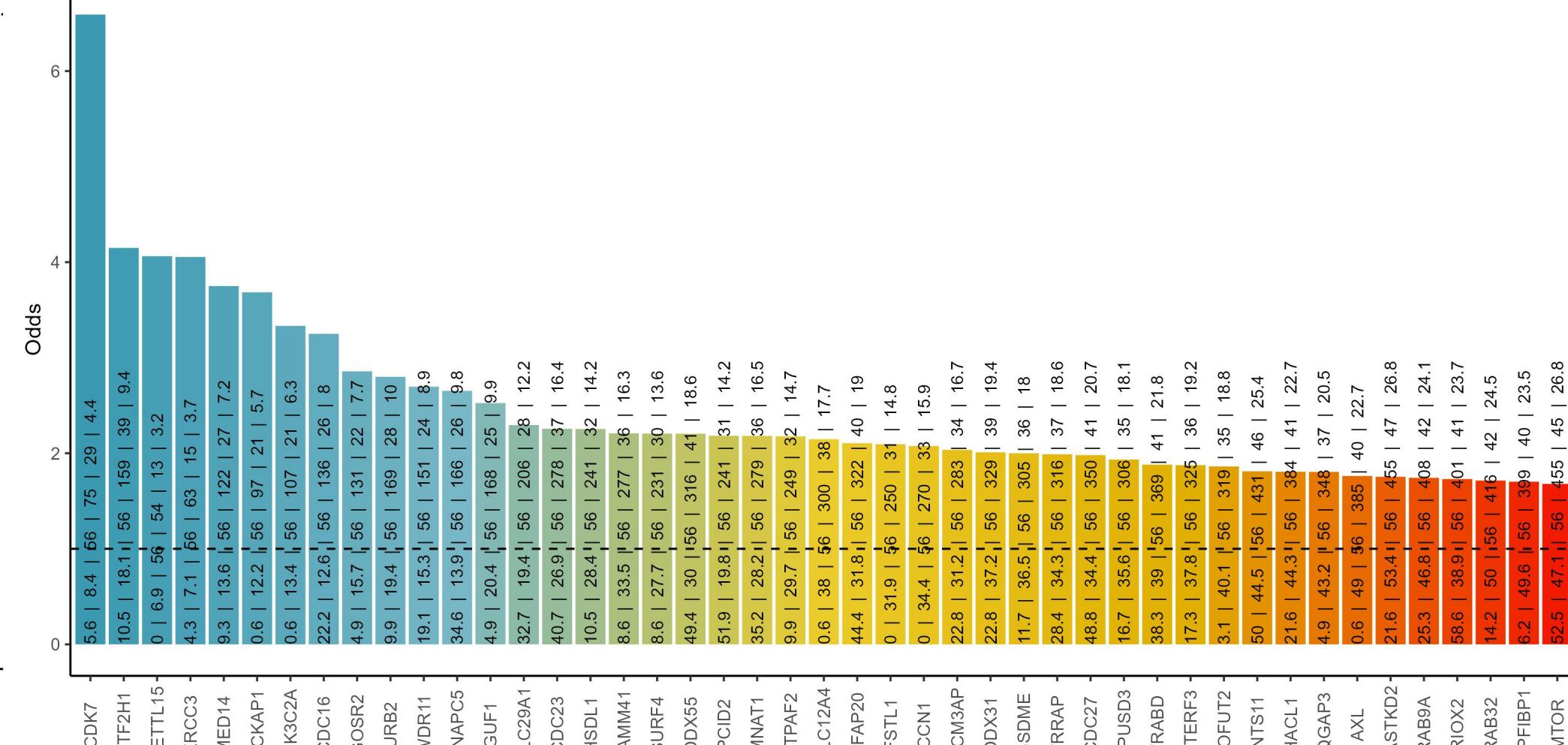
% of ERCC2 in blood cancers: 2.5 ; % of ERCC2 in solid cancers: 6.6

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ERCC2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

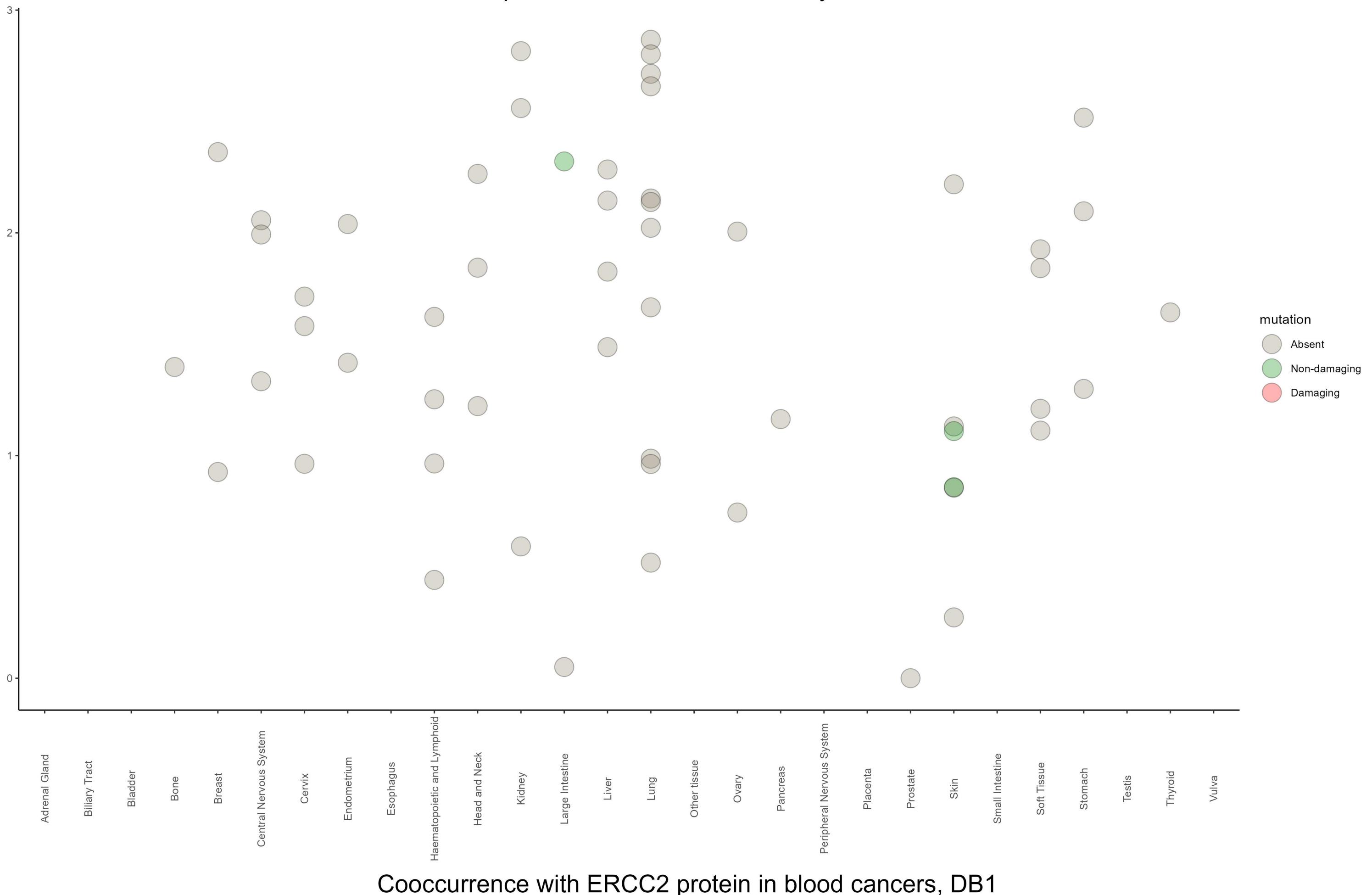
### Negative cooccurrence



### Positive cooccurrence

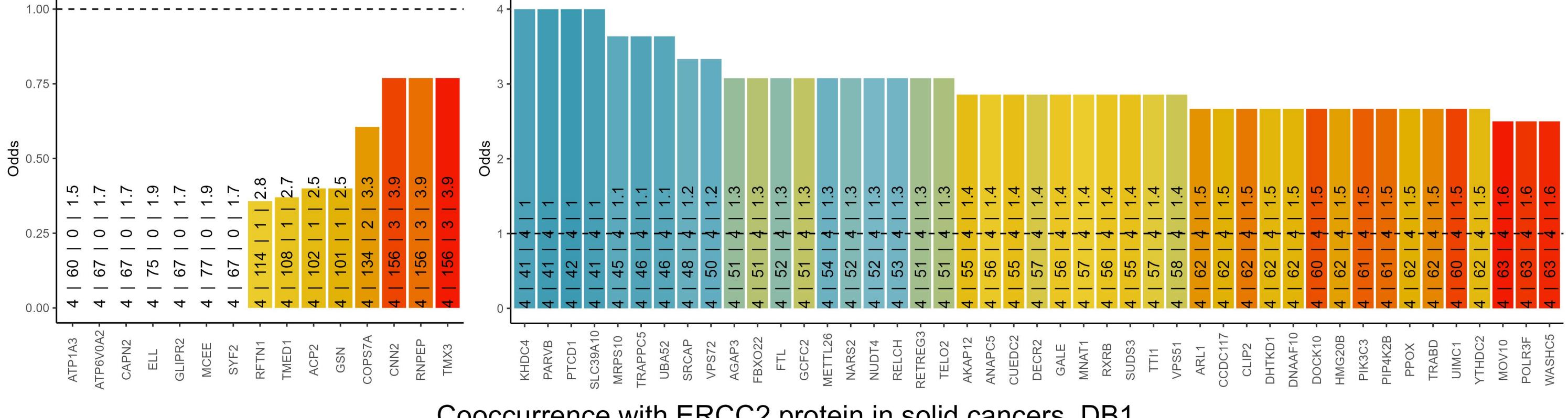


# Amount of ERCC2 protein and mutation status by tissue, DB1



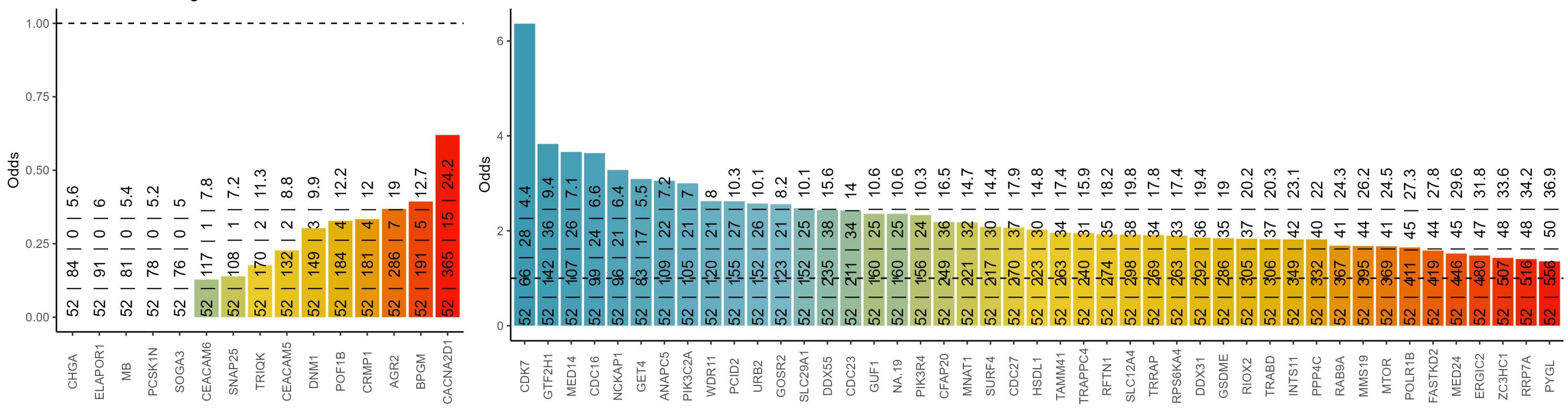
## Cooccurrence with ERCC2 protein in blood cancers, DB1

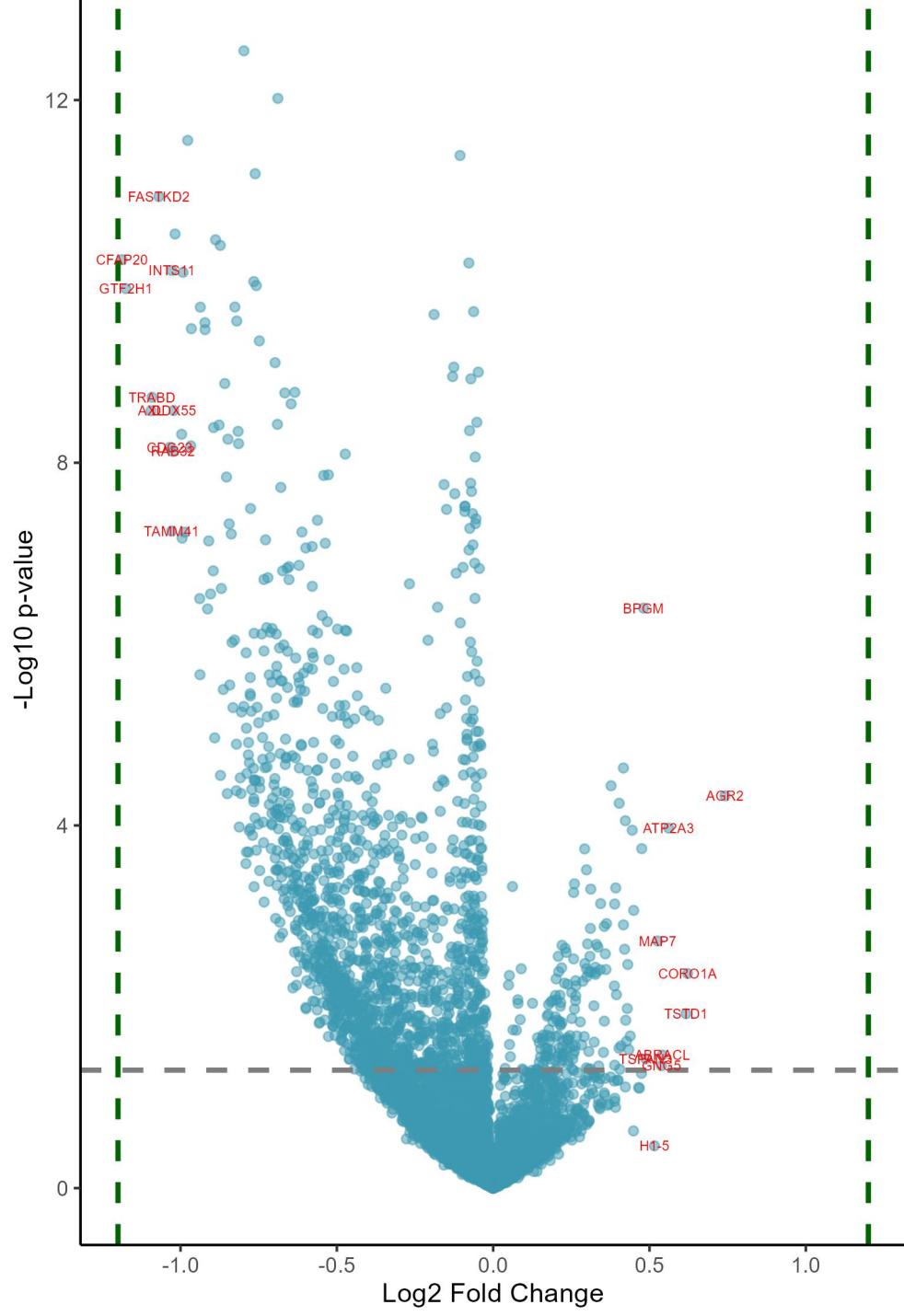
The text in the bars: incidence of ERCC2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



## Cooccurrence with ERCC2 protein in solid cancers, DB1

The text in the bars: incidence of ERCC2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

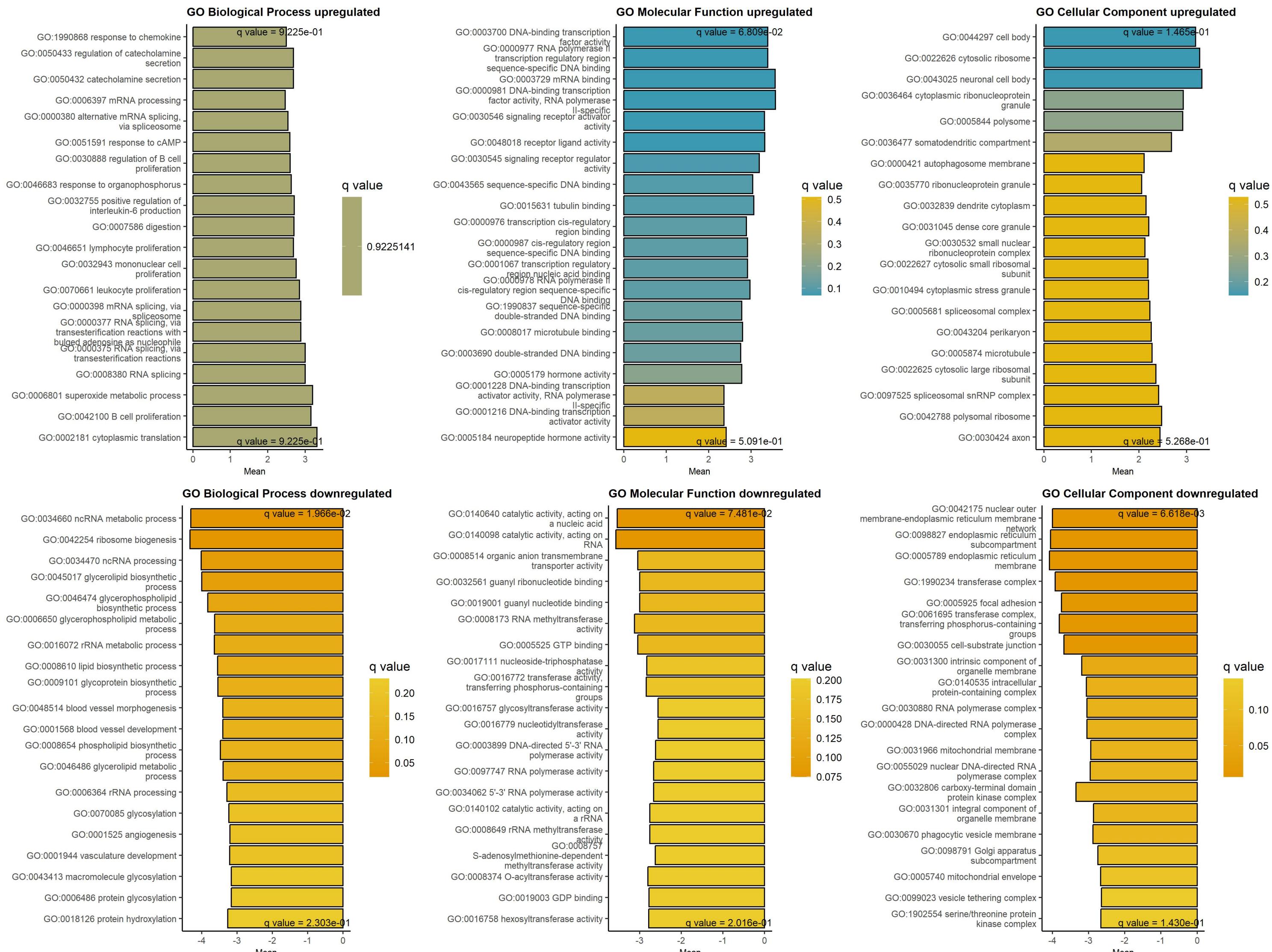




### Downregulated at low/absent ERCC2 Upregulated at low/absent ERCC2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.19	3.47e-08	CFAP20	cilia and flagella associated prote	0.74	1.12e-03	AGR2	anterior gradient 2, protein disul
-1.17	4.69e-08	GTF2H1	general transcription factor IIH su	0.62	3.25e-02	CORO1A	coronin 1A
-1.09	4.67e-07	AXL	AXL receptor tyrosine kinase	0.62	6.78e-02	TSTD1	thiosulfate sulfurtransferase like
-1.09	3.60e-07	TRABD	TraB domain containing	0.56	2.02e-03	ATP2A3	ATPase sarcoplasmic/endoplasmic ret
-1.07	1.10e-08	FASTKD2	FAST kinase domains 2	0.54	1.44e-01	ABRACL	ABRA C-terminal like
-1.03	9.17e-07	CDC23	cell division cycle 23	0.54	1.72e-01	GNG5	G protein subunit gamma 5
-1.03	5.24e-06	TAMM41	TAM41 mitochondrial translocator as	0.53	1.76e-02	MAP7	microtubule associated protein 7
-1.03	3.77e-08	INTS11	integrator complex subunit 11	0.52	5.94e-01	H1-5	H1.5 linker histone, cluster member
-1.02	9.96e-07	RAB32	RAB32, member RAS oncogene family	0.49	1.53e-01	TSPAN3	tetraspanin 3
-1.02	4.67e-07	DDX55	DEAD-box helicase 55	0.48	2.59e-05	BPGM	bisphosphoglycerate mutase
-1.02	2.49e-08	SAR1B	secretion associated Ras related GT	0.48	3.03e-03	CDKN2C	cyclin dependent kinase inhibitor 2
-1	7.18e-07	CDC27	cell division cycle 27	0.47	1.91e-01	CRIP1	cysteine rich protein 1
-0.99	5.93e-06	RAB11B	RAB11B, member RAS oncogene family	0.47	2.42e-01	S100A4	S100 calcium binding protein A4
-0.99	3.77e-08	POLR1B	RNA polymerase I subunit B	0.47	2.39e-01	H2AX	H2A.X variant histone
-0.99	5.24e-06	TGM2	transglutaminase 2	0.45	9.87e-03	PTPN6	protein tyrosine phosphatase non-re
-0.98	4.62e-09	GPX8	glutathione peroxidase 8 (putative)	0.45	4.80e-01	MIF	macrophage migration inhibitory fac
-0.97	9.02e-07	PARVA	parvin alpha	0.44	2.11e-03	CRMP1	collapsin response mediator protein
-0.97	9.05e-08	ERGIC2	ERGIC and golgi 2	0.44	1.03e-01	KLC4	kinesin light chain 4
-0.94	2.07e-05	SLC12A4	solute carrier family 12 member 4	0.43	1.31e-01	GCA	grancalcin
-0.94	1.02e-04	CCN1	cellular communication network fact	0.43	2.76e-02	S100P	S100 calcium binding protein P
-0.94	6.73e-08	CDK7	cyclin dependent kinase 7	0.43	6.13e-02	WIPF1	WAS/WASL interacting protein family
-0.92	8.24e-08	MTCH1	mitochondrial carrier 1	0.43	1.13e-01	CACNA2D1	calcium voltage-gated channel auxil
-0.92	9.05e-08	ICAM1	intercellular adhesion molecule 1	0.42	7.66e-02	SNTB1	syntrophin beta 1
-0.91	2.62e-05	SOAT1	sterol O-acyltransferase 1	0.42	1.79e-03	POF1B	POF1B actin binding protein
-0.91	6.21e-06	KDSR	3-ketodihydrophosphingosine reductase	0.42	2.37e-01	UBE2V2	ubiquitin conjugating enzyme E2 V2
-0.9	1.88e-05	RAB9A	RAB9A, member RAS oncogene family	0.42	2.06e-02	PYM1	PYM homolog 1, exon junction comple
-0.9	1.14e-05	DDX31	DEAD-box helicase 31	0.42	1.29e-02	MAPRE3	microtubule associated protein RP/E
-0.89	6.48e-07	CAV1	caveolin 1	0.42	6.47e-04	TRIQK	triple QxxK/R motif containing
-0.89	3.65e-04	FSTL1	follistatin like 1	0.41	1.23e-01	PAK1	p21 (RAC1) activated kinase 1

### GAGE analysis on upregulated and downregulated proteins at low/absent ERCC2 protein, DB1







Insufficient number of paired observations in DB1 for ERCC2

Insufficient number of paired observations in DB1 for ERCC2

No information on Ser/Thr kinase phosphorylation sites for ERCC2

No information on Ser/Thr kinase phosphorylation sites for ERCC2

No sufficient paired observations in DB1 for ERCC2