

# FEN1

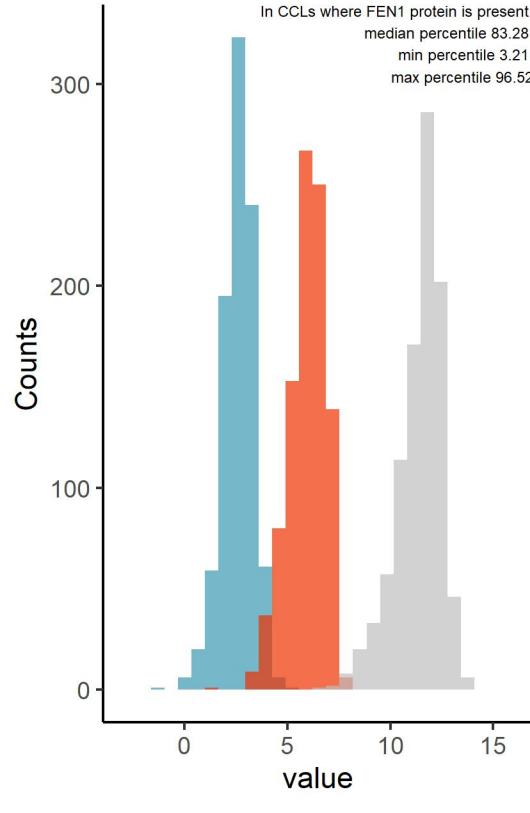
Protein name: FEN1 ; UNIPROT: P39748 ; Gene name: flap structure-specific endonuclease 1

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

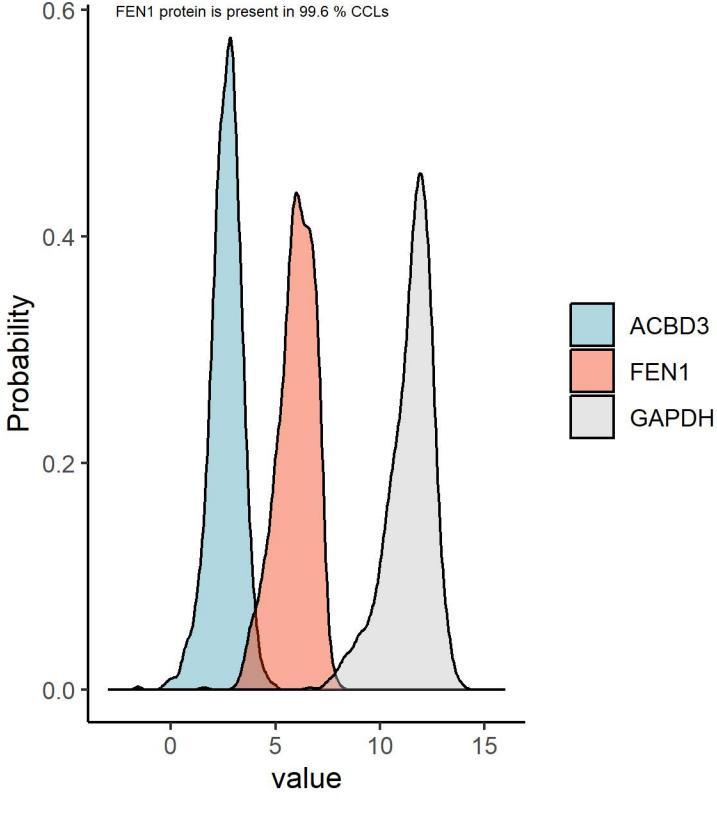
## Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

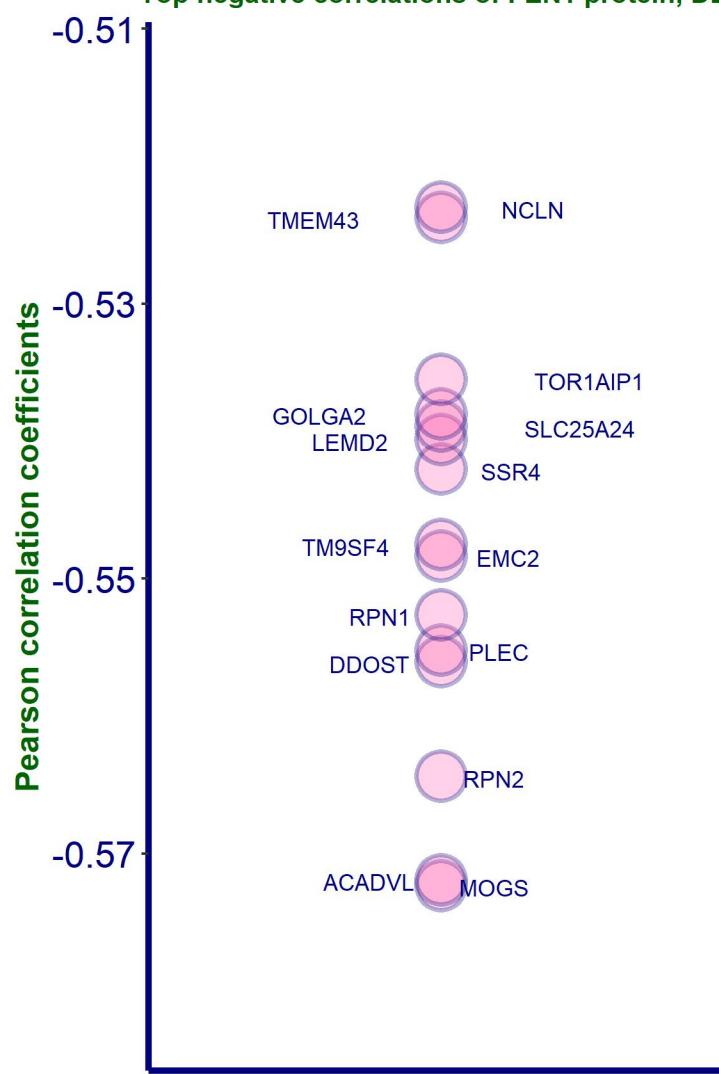
Histogram of FEN1 protein compared to proteins with low and high abundance



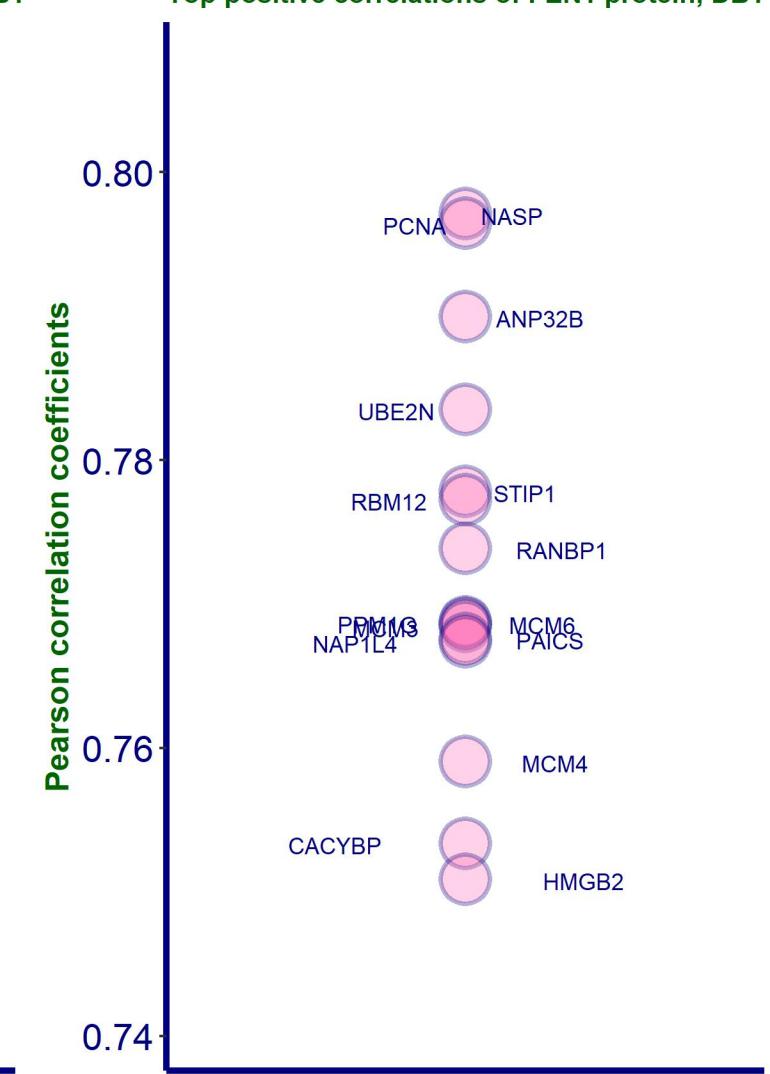
Density plot of FEN1 protein compared to proteins with low and high abundance



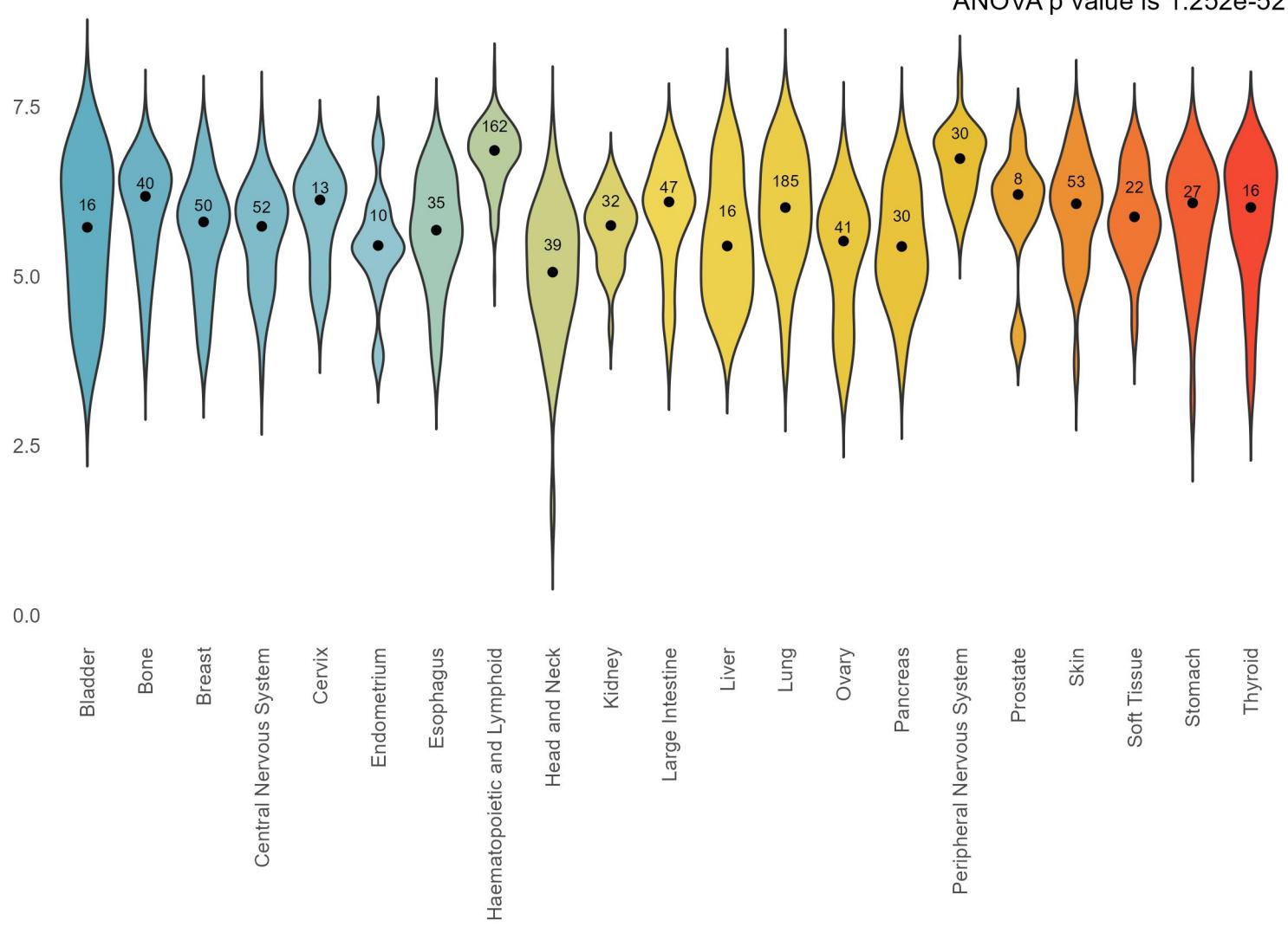
Top negative correlations of FEN1 protein, DB1



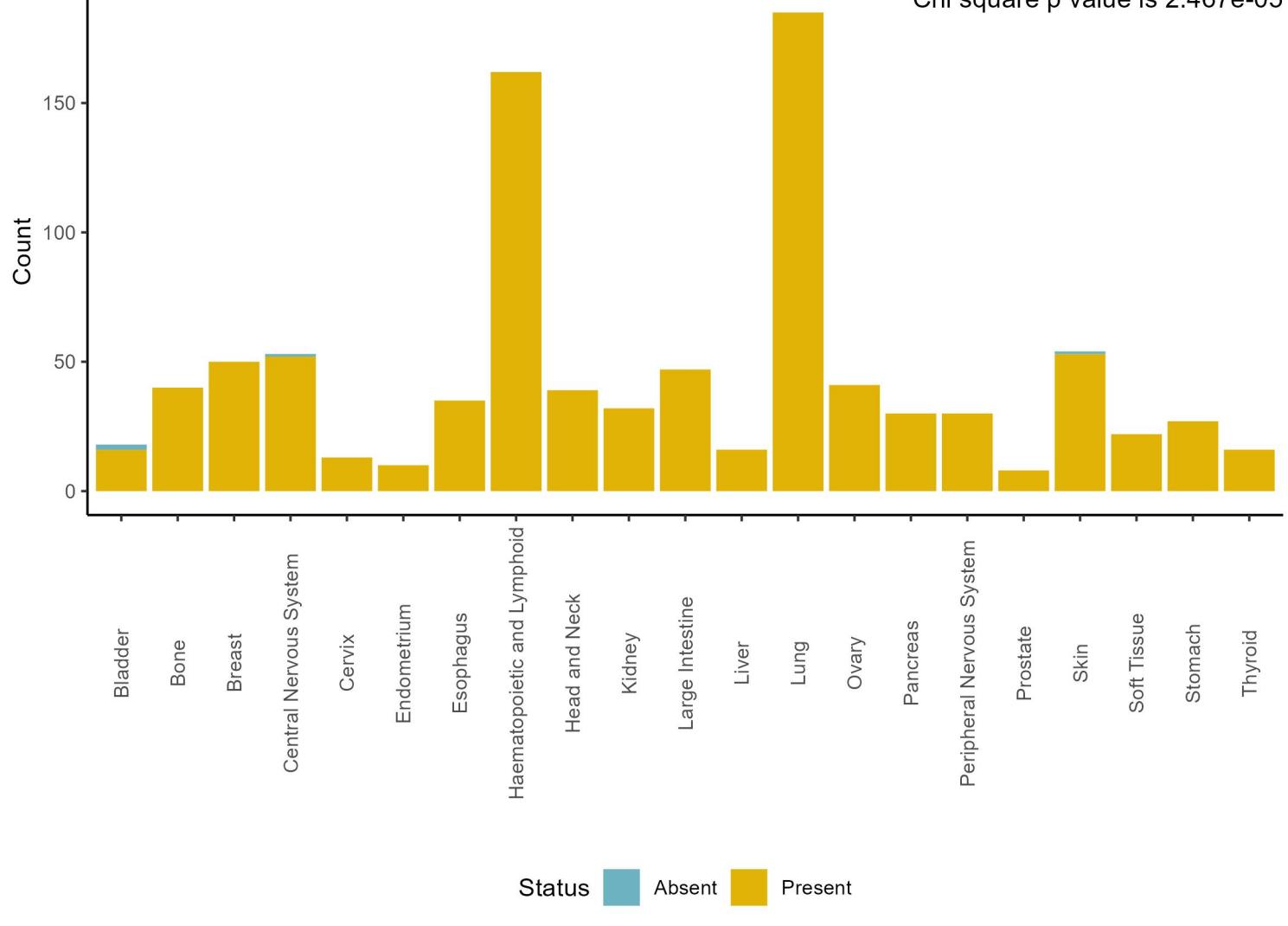
Top positive correlations of FEN1 protein, DB1



Amount of FEN1 protein, number of CCLs where it is present by tissue, DB1



Present and absent FEN1 protein counts by tissue, DB1

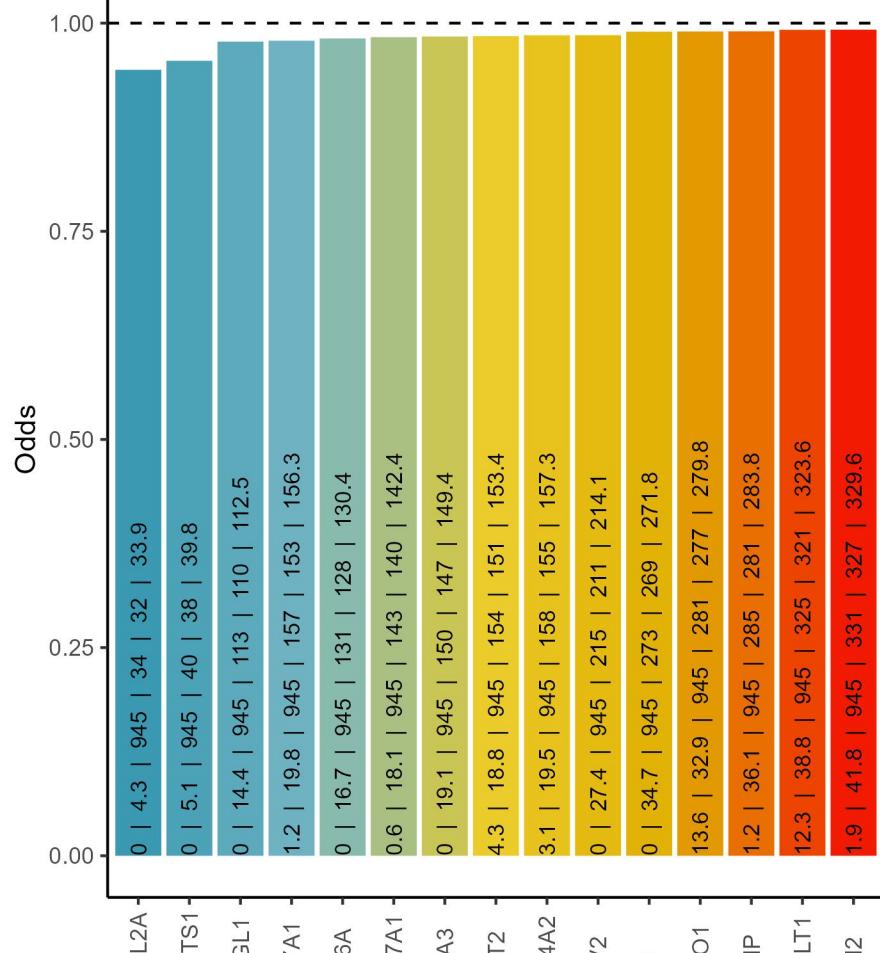


Cooccurrence with FEN1 protein, DB1

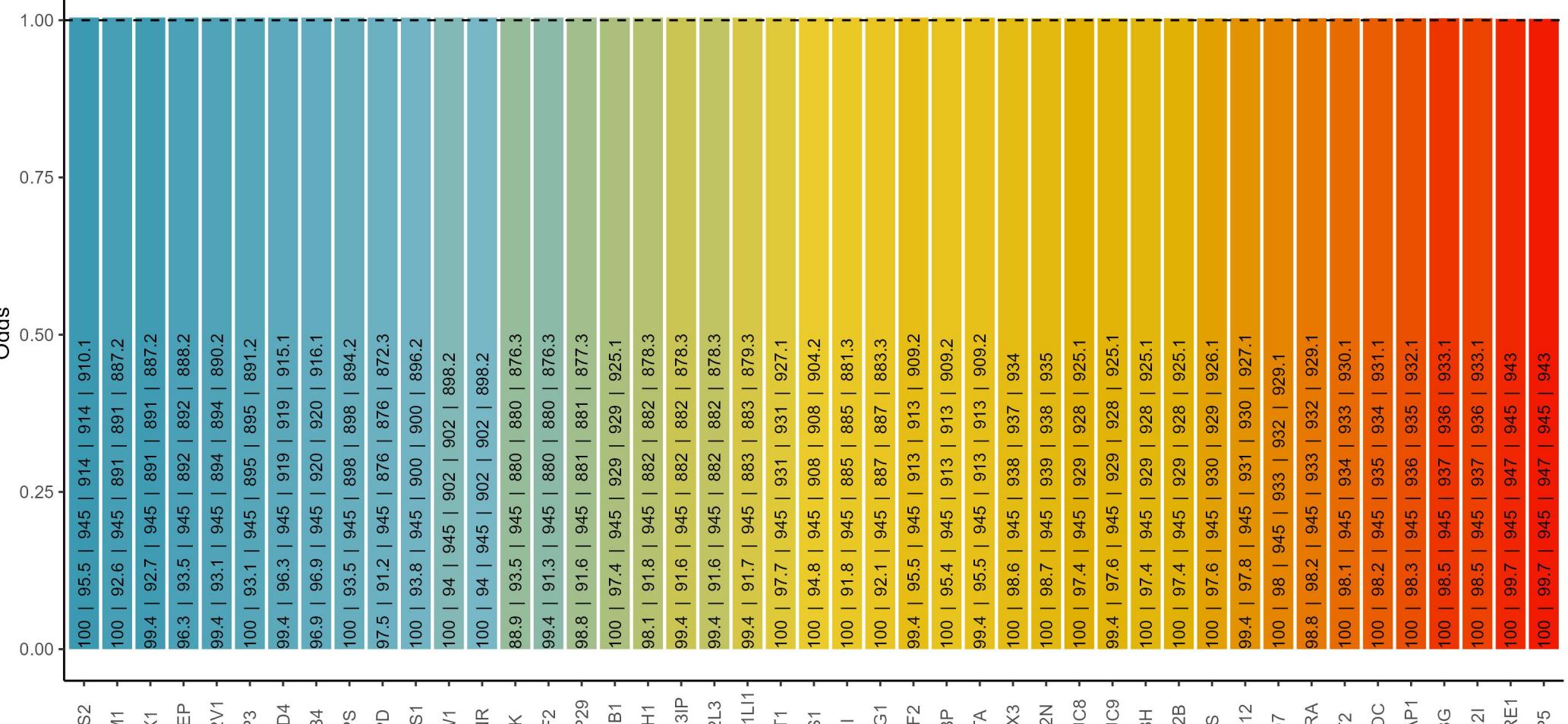
% of FEN1 in blood cancers: 100 ; % of FEN1 in solid cancers: 99.5

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of FEN1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

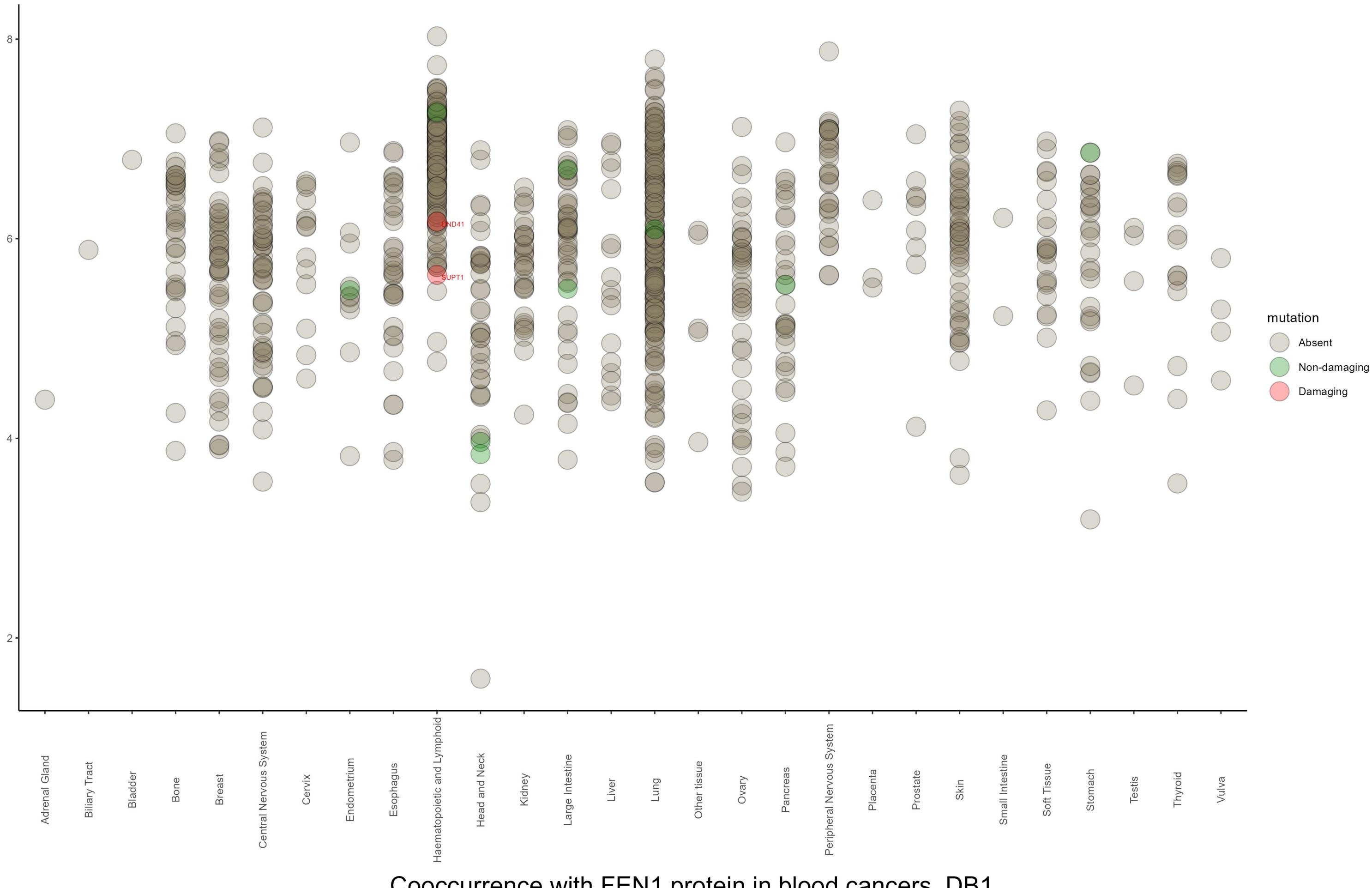
Negative cooccurrence



Positive cooccurrence



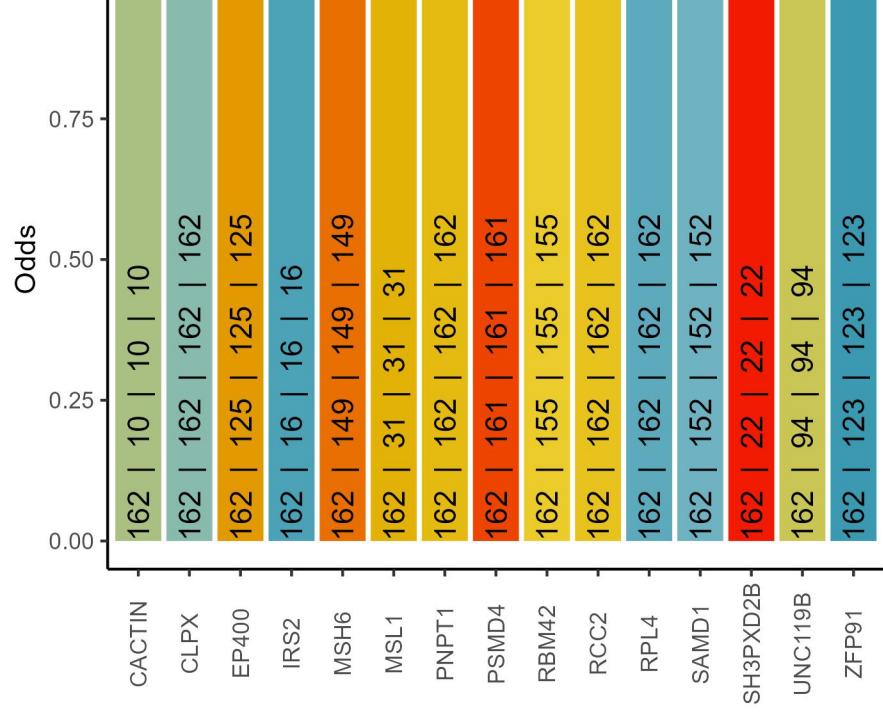
# Amount of FEN1 protein and mutation status by tissue, DB1



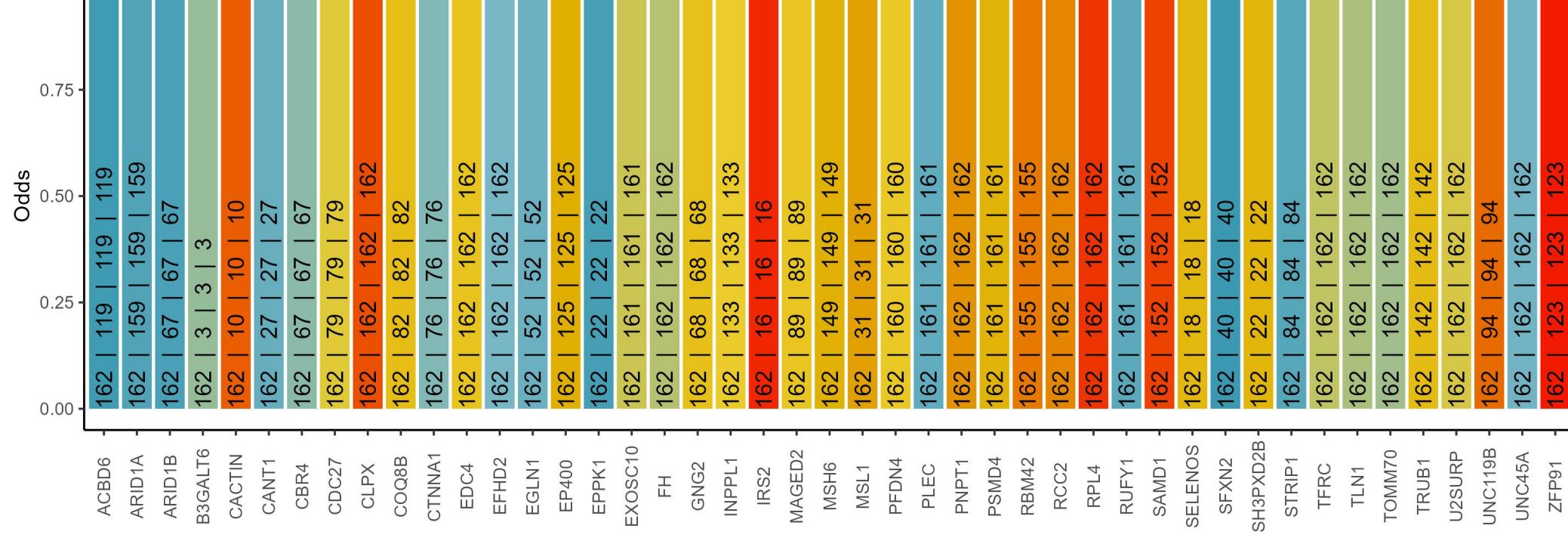
## Cooccurrence with FEN1 protein in blood cancers, DB1

The text in the bars: incidence of FEN1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



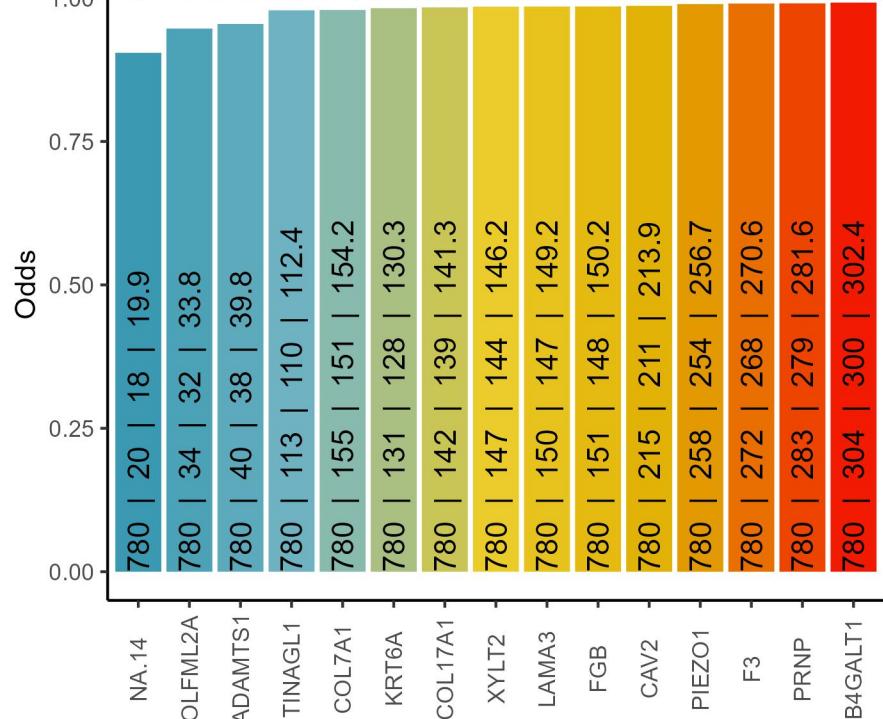
Positive cooccurrence



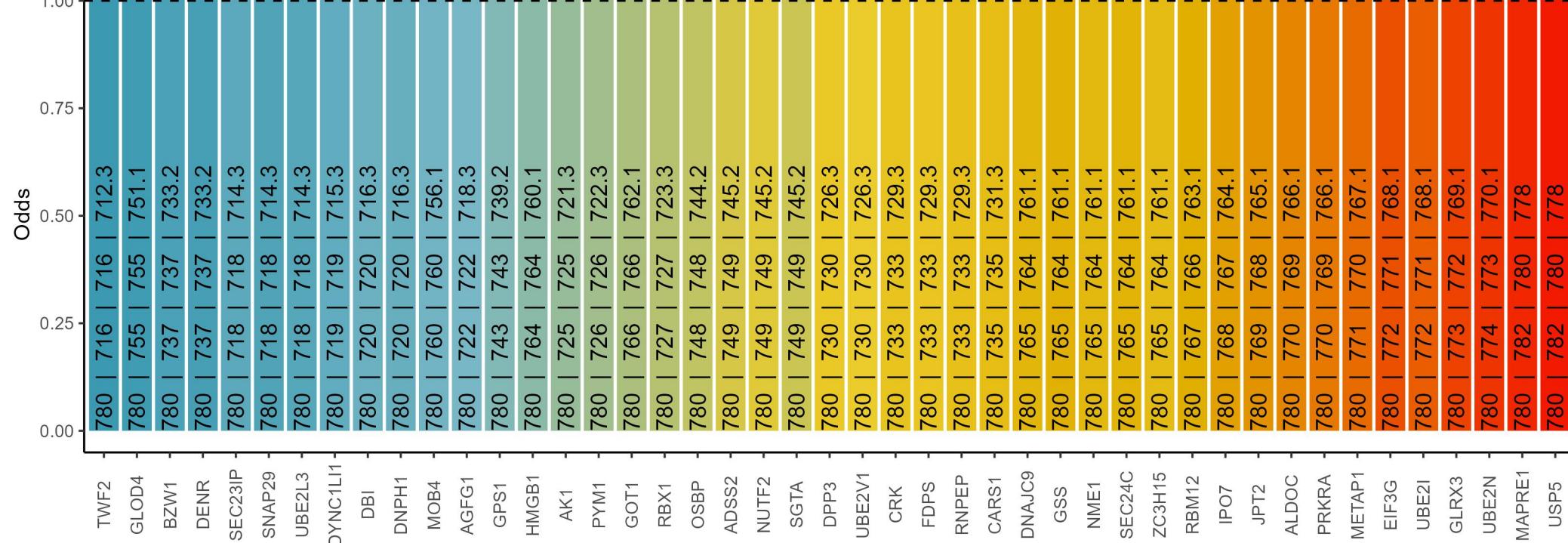
## Cooccurrence with FEN1 protein in solid cancers, DB1

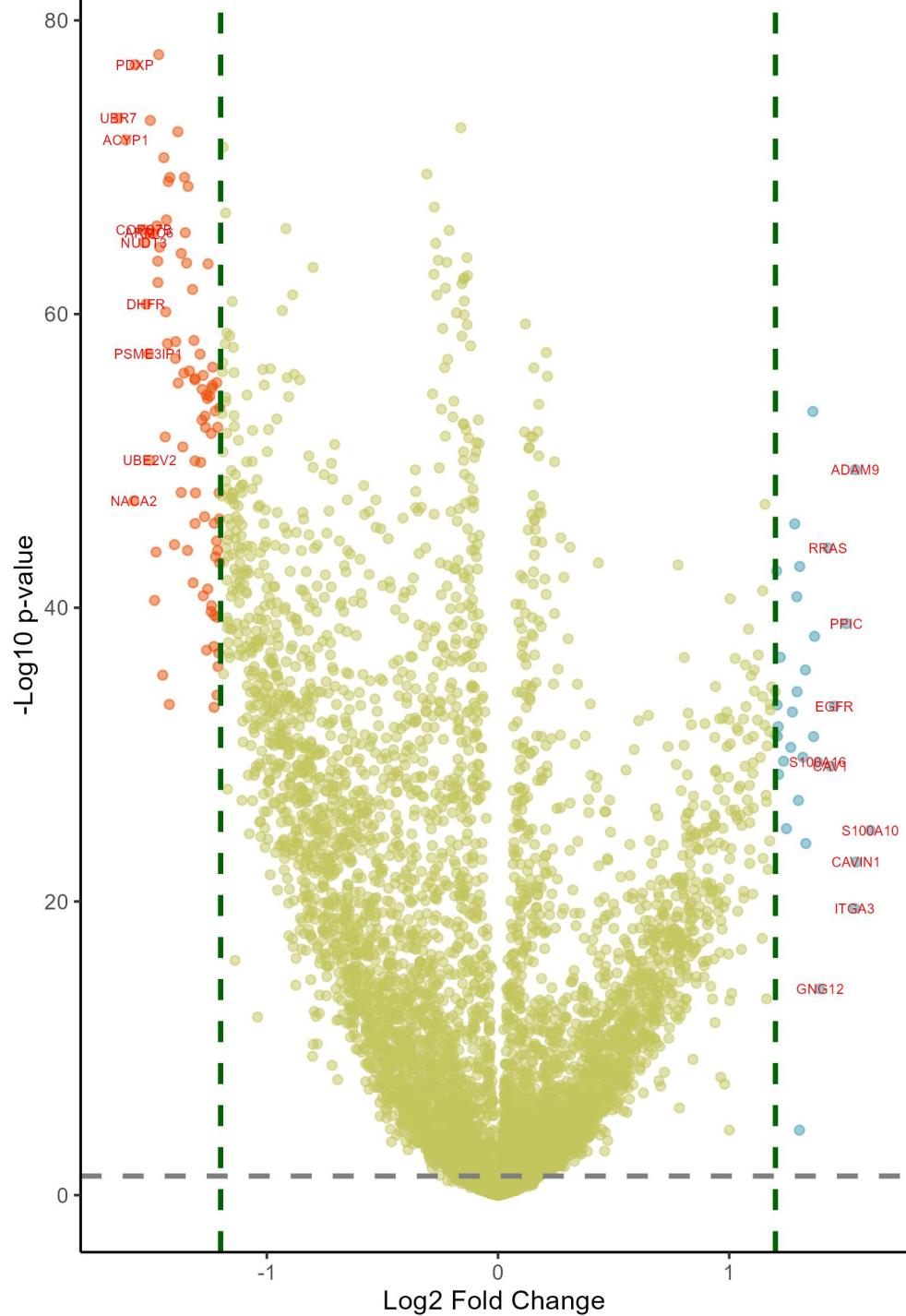
The text in the bars: incidence of FEN1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



Positive cooccurrence

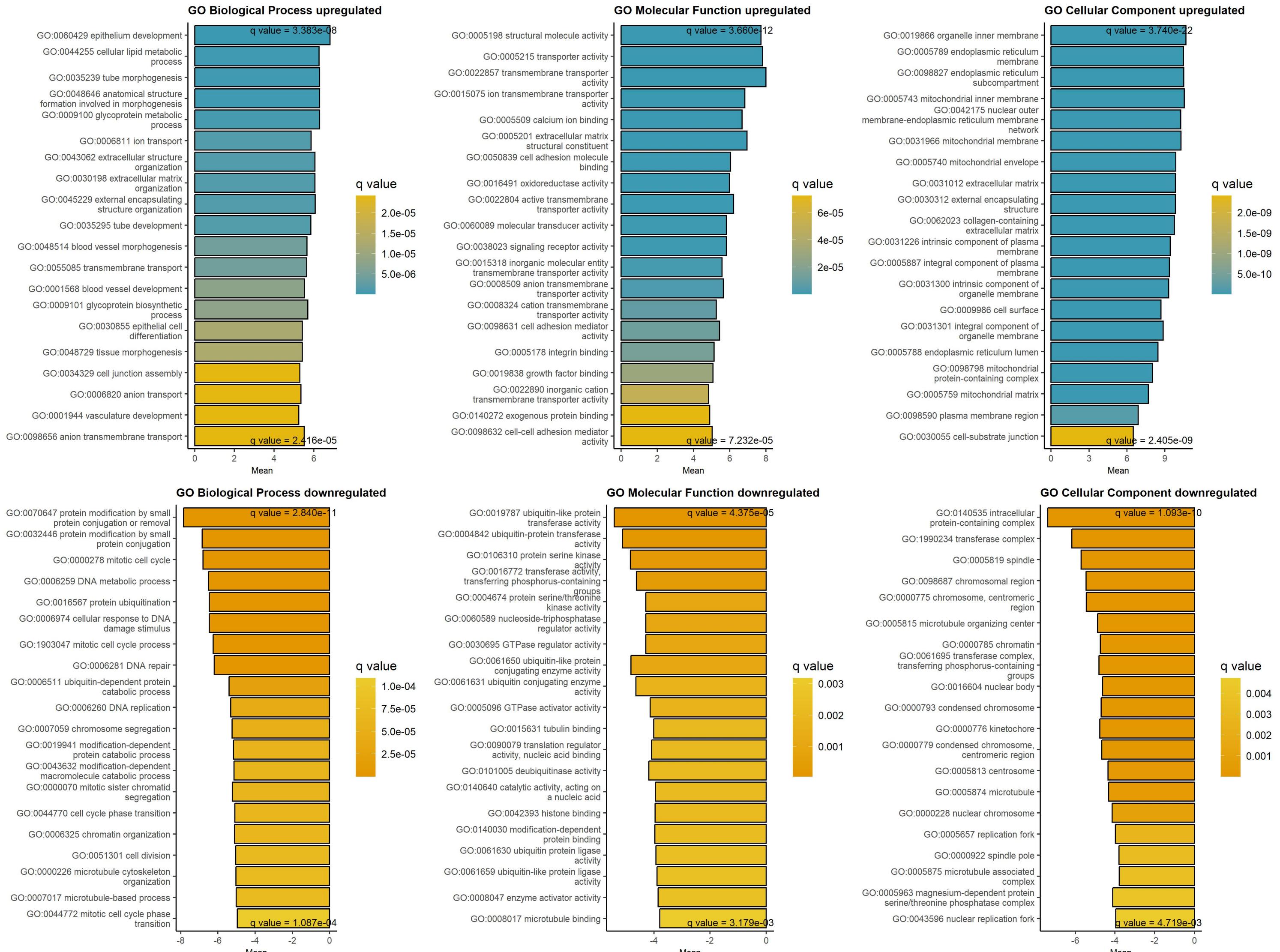


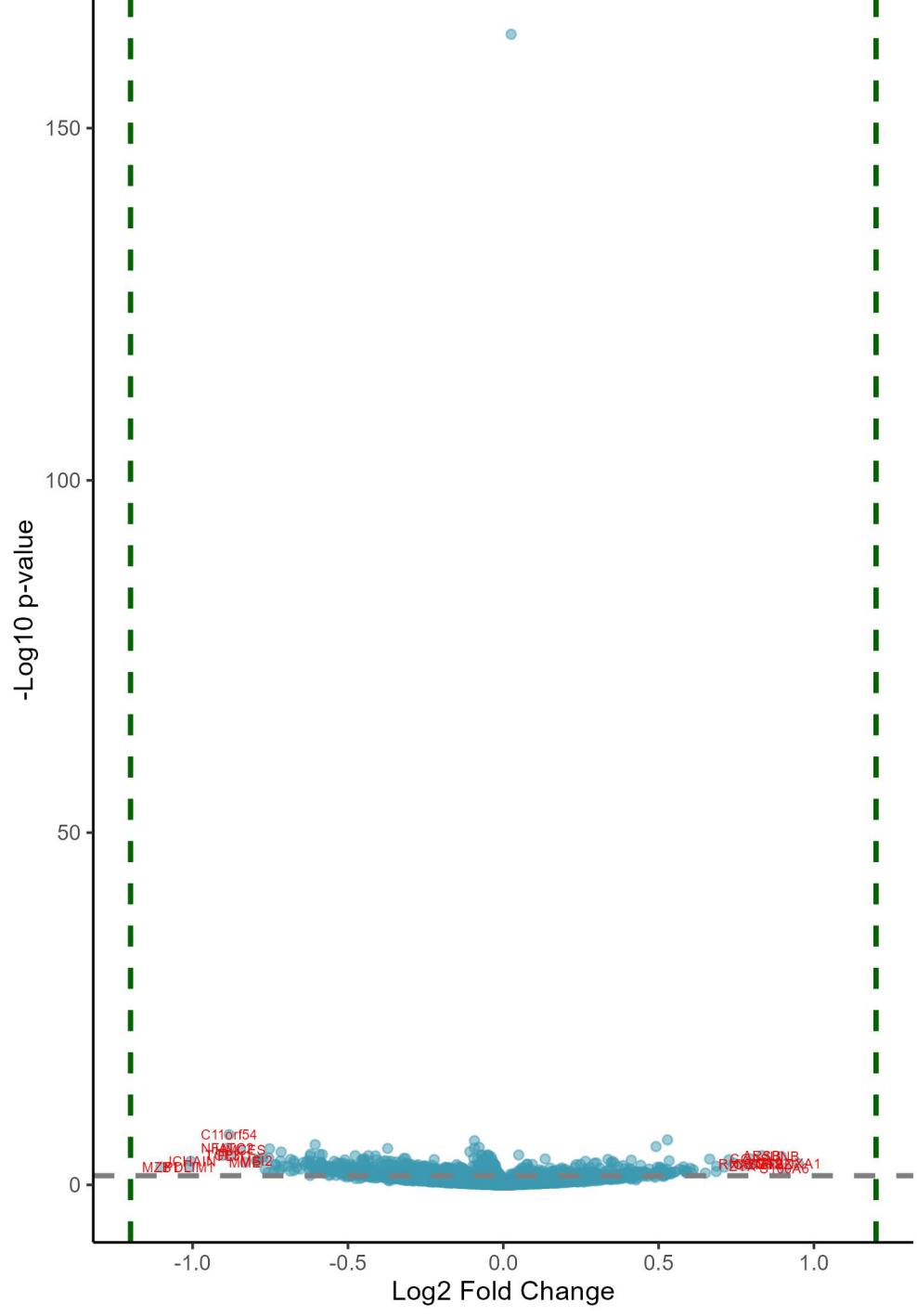


## Downregulated at low/absent FEN1 Upregulated at low/absent FEN1

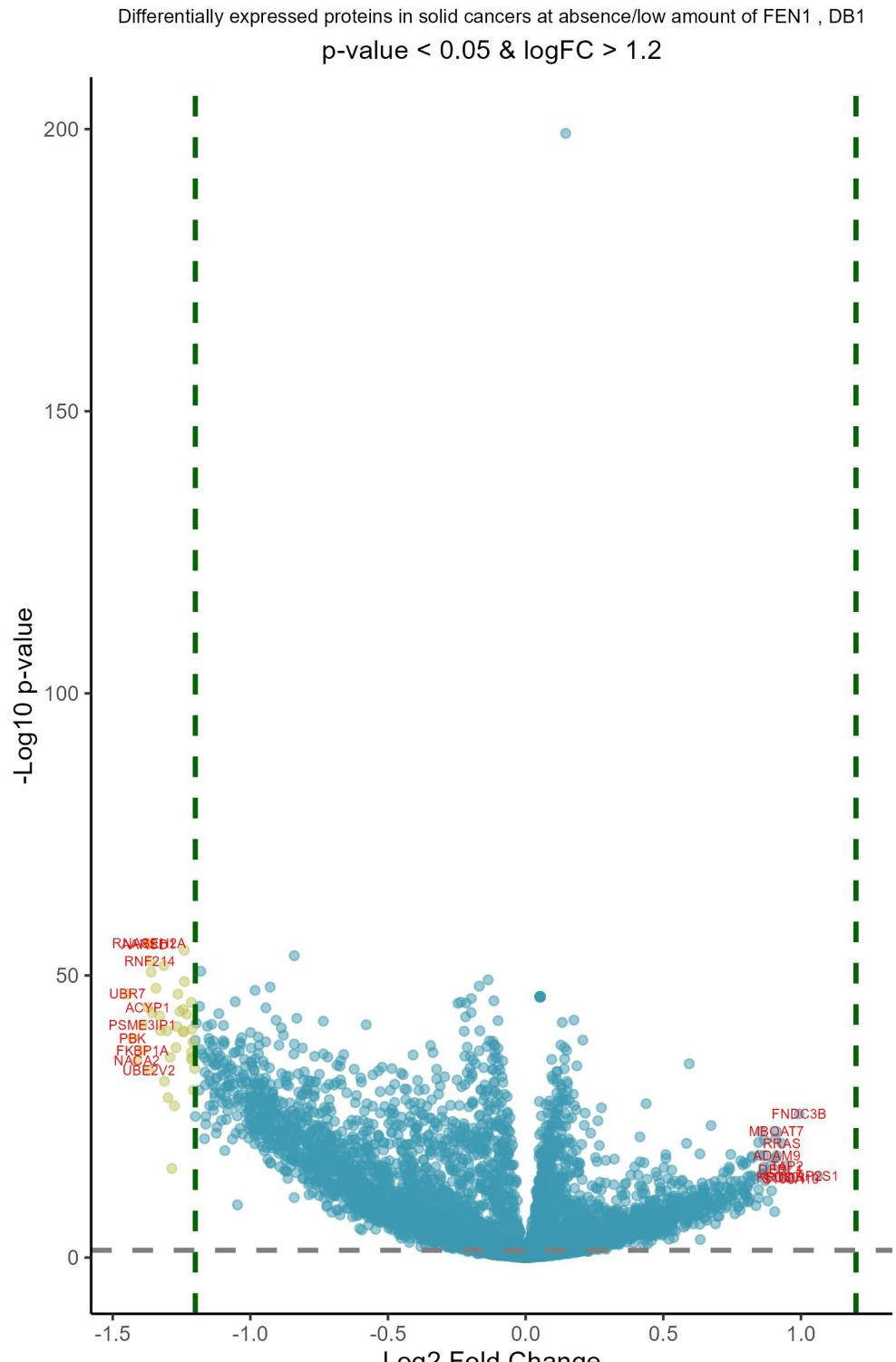
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.64	7.58e-71	UBR7	ubiquitin protein ligase E3 compone	1.61	8.05e-25	S100A10	S100 calcium binding protein A10
-1.61	1.15e-69	ACYP1	acylphosphatase 1	1.55	1.01e-22	CAVIN1	caveolae associated protein 1
-1.58	1.83e-46	NACA2	nascent polypeptide associated comp	1.55	1.68e-48	ADAM9	ADAM metallopeptidase domain 9
-1.57	2.32e-74	PDXP	pyridoxal phosphatase	1.54	1.24e-19	ITGA3	integrin subunit alpha 3
-1.53	5.67e-64	COPS7B	COP9 signalosome subunit 7B	1.51	1.93e-38	PPIC	peptidylprolyl isomerase C
-1.53	3.42e-63	NUDT3	nudix hydrolase 3	1.45	5.19e-33	EGFR	epidermal growth factor receptor
-1.52	2.86e-59	DHFR	dihydrofolate reductase	1.44	4.68e-29	CAV1	caveolin 1
-1.51	4.93e-56	PSME3IP1	proteasome activator subunit 3 inte	1.43	2.18e-43	RRAS	RAS related
-1.51	7.98e-64	ARMC6	armadillo repeat containing 6	1.39	2.78e-14	GNG12	G protein subunit gamma 12
-1.51	4.17e-49	UBE2V2	ubiquitin conjugating enzyme E2 V2	1.38	2.53e-29	S100A16	S100 calcium binding protein A16
-1.5	8.64e-71	RNASEH2B	ribonuclease H2 subunit B	1.37	1.32e-37	EPHA2	EPH receptor A2
-1.5	8.51e-64	HDHD2	haloacid dehalogenase like hydrolas	1.37	5.18e-31	NT5E	5'-nucleotidase ecto
-1.49	5.81e-40	BLMH	bleomycin hydrolase	1.36	2.70e-52	FNDC3B	fibronectin type III domain contain
-1.48	3.89e-43	CORO1A	coronin 1A	1.33	5.99e-24	MYOF	myoferlin
-1.48	3.47e-64	GRK2	G protein-coupled receptor kinase 2	1.33	2.16e-35	GPX8	glutathione peroxidase 8 (putative)
-1.47	5.17e-62	DCK	deoxycytidine kinase	1.32	1.20e-29	ITGB4	integrin subunit beta 4
-1.47	1.15e-60	UBE2T	ubiquitin conjugating enzyme E2 T	1.31	3.47e-42	SDC4	syndecan 4
-1.47	7.16e-75	RNASEH2A	ribonuclease H2 subunit A	1.3	6.18e-05	KRT18	keratin 18
-1.46	6.66e-63	SAAL1	serum amyloid A like 1	1.3	8.32e-27	ITGA2	integrin subunit alpha 2
-1.45	4.76e-35	ABRACL	ABRA C-terminal like	1.29	5.89e-34	P4HA2	prolyl 4-hydroxylase subunit alpha
-1.45	1.49e-68	ARPP19	cAMP regulated phosphoprotein 19	1.29	3.31e-40	MBOAT7	membrane bound O-acyltransferase do
-1.44	1.20e-50	C11orf54	chromosome 11 open reading frame 54	1.28	5.69e-45	AGRN	agrin
-1.44	9.25e-59	PRPSAP2	phosphoribosyl pyrophosphate synthetase	1.27	1.23e-32	BCAM	basal cell adhesion molecule (Luthe)
-1.43	1.43e-64	KIAA1143	KIAA1143	1.27	2.63e-30	PPL	periplakin
-1.43	1.11e-56	APIP	APAF1 interacting protein	1.25	6.20e-25	AP2S1	adaptor related protein complex 2 s
-1.43	4.54e-67	POLA2	DNA polymerase alpha 2, accessory s	1.24	2.18e-29	THBS1	thrombospondin 1
-1.42	3.97e-33	ZNF706	zinc finger protein 706	1.22	3.17e-36	ITGAV	integrin subunit alpha V
-1.42	2.54e-67	LIG1	DNA ligase 1	1.21	1.62e-28	MMP14	matrix metallopeptidase 14
-1.4	1.33e-43	PBK	PDZ binding kinase	1.21	1.15e-31	EPHX1	epoxide hydrolase 1

## GAGE analysis on upregulated and downregulated proteins at low/absent FEN1 protein, DB1





logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.1	9.77e-02	MZB1	marginal zone B and B1 cell specific	0.95	5.53e-02	ANXA1	annexin A1
-1.01	9.77e-02	PDLIM1	PDZ and LIM domain 1	0.9	1.11e-01	S100A6	S100 calcium binding protein A6
-1.01	4.09e-02	JCHAIN	joining chain of multimeric IgA and	0.89	1.84e-02	JUNB	JunB proto-oncogene, AP-1 transcrip
-0.9	1.63e-02	TCF3	transcription factor 3	0.87	6.37e-02	CTSZ	cathepsin Z
-0.89	4.09e-03	NFATC2	nuclear factor of activated T cells	0.85	5.37e-02	CA2	carbonic anhydrase 2
-0.88	1.66e-04	C11orf54	chromosome 11 open reading frame 54	0.83	1.63e-02	ARSB	arylsulfatase B
-0.88	1.63e-02	FLI1	Fli-1 proto-oncogene, ETS transcript	0.8	6.48e-02	CSTA	cystatin A
-0.85	6.05e-03	HMCES	5-hydroxymethylcytosine binding, ES	0.8	6.35e-02	RNASET2	ribonuclease T2
-0.83	5.05e-02	MME	membrane metalloendopeptidase	0.79	2.94e-02	CGAS	cyclic GMP-AMP synthase
-0.79	3.95e-02	MSI2	musashi RNA binding protein 2	0.77	8.40e-02	ZYX	zyxin
-0.79	3.44e-02	LZTFL1	leucine zipper transcription factor	0.74	5.37e-02	PLBD2	phospholipase B domain containing 2
-0.79	3.95e-02	DCAF16	DDB1 and CUL4 associated factor 16	0.73	3.44e-02	MNDA	myeloid cell nuclear differentiatio
-0.77	2.76e-02	CHEK1	checkpoint kinase 1	0.71	1.00e-01	RHOC	ras homolog family member C
-0.77	1.32e-01	UBE2D3	ubiquitin conjugating enzyme E2 D3	0.69	8.71e-02	SPART	spartin
-0.76	2.20e-01	UCHL1	ubiquitin C-terminal hydrolase L1	0.69	1.90e-01	FLNC	filamin C
-0.75	2.90e-02	ZFP91	ZFP91 zinc finger protein, atypical	0.66	3.18e-02	LRPAP1	LDL receptor related protein associ
-0.75	4.09e-03	EIF1AD	eukaryotic translation initiation f	0.65	2.32e-01	LMNA	lamin A/C
-0.74	1.62e-01	TCL1A	TCL1 family AKT coactivator A	0.61	1.43e-01	TNFRSF8	TNF receptor superfamily member 8
-0.73	7.29e-02	MGMT	O-6-methylguanine-DNA methyltransfe	0.61	2.25e-01	PLEK	pleckstrin
-0.73	6.90e-02	KIF15	kinesin family member 15	0.6	1.13e-01	MYO1F	myosin IF
-0.72	1.79e-01	TSTD1	thiosulfate sulfurtransferase like	0.59	1.70e-01	TYMP	thymidine phosphorylase
-0.72	1.41e-01	SEPTIN1	septin 1	0.59	2.24e-01	SQOR	sulfide quinone oxidoreductase
-0.72	3.95e-02	HDAC7	histone deacetylase 7	0.59	1.95e-01	ZMPSTE24	zinc metallopeptidase STE24
-0.72	9.60e-03	WDRT6	WD repeat domain 76	0.59	1.80e-01	PTPRC	protein tyrosine phosphatase recept
-0.71	8.74e-02	TMEM263	transmembrane protein 263	0.58	1.45e-01	SEPTIN8	septin 8
-0.69	8.67e-02	TUBB4A	tubulin beta 4A class IVa	0.58	9.46e-02	SLC29A1	solute carrier family 29 member 1 (
-0.69	1.79e-01	RAB11B	RAB11B, member RAS oncogene family	0.57	1.32e-01	TIMMD1	translocase of inner mitochondrial
-0.68	3.24e-02	TRPT1	tRNA phosphotransferase 1	0.55	1.93e-01	GAA	alpha glucosidase
-0.67	3.95e-02	SYVN1	synoviolin 1	0.55	2.01e-01	PYGL	glycogen phosphorylase L



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.45	3.96e-45	UBR7	ubiquitin protein ligase E3 compone	1.06	1.76e-14	AP2S1	adaptor related protein complex 2 s
-1.43	5.69e-38	PBK	PDZ binding kinase	0.99	4.27e-25	FNDC3B	fibronectin type III domain contain
-1.41	3.84e-34	NACA2	nascent polypeptide associated comp	0.96	4.94e-14	S100A10	S100 calcium binding protein A10
-1.39	3.41e-40	PSME3IP1	proteasome activator subunit 3 inte	0.95	2.89e-16	TAP2	transporter 2, ATP binding cassette
-1.39	7.22e-36	FKBP1A	FKBP prolyl isomerase 1A	0.94	2.69e-14	SQOR	sulfide quinone oxidoreductase
-1.37	2.99e-43	ACYP1	acylphosphatase 1	0.93	4.51e-20	RRAS	RAS related
-1.37	4.59e-53	AARSD1	alanyl-tRNA synthetase domain conta	0.93	1.34e-15	DERL1	derlin 1
-1.37	1.79e-32	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.92	2.70e-14	KRT80	keratin 80
-1.37	4.49e-53	RNASEH2A	ribonuclease H2 subunit A	0.91	5.31e-18	ADAM9	ADAM metallopeptidase domain 9
-1.37	2.50e-50	RNF214	ring finger protein 214	0.91	3.97e-22	MBOAT7	membrane bound O-acyltransferase do
-1.36	1.62e-48	DCK	deoxycytidine kinase	0.91	6.41e-21	RABAC1	Rab acceptor 1
-1.36	2.47e-42	UBE2T	ubiquitin conjugating enzyme E2 T	0.91	1.56e-17	SDC4	syndecan 4
-1.34	7.95e-46	PDXP	pyridoxal phosphatase	0.9	2.02e-08	CAVIN1	caveolae associated protein 1
-1.33	8.38e-42	SAAL1	serum amyloid A like 1	0.89	5.55e-12	TACSTD2	tumor associated calcium signal tra
-1.33	2.92e-39	RNASEH2C	ribonuclease H2 subunit C	0.89	2.63e-16	LRP10	LDL receptor related protein 10
-1.31	1.47e-49	GINS4	GINS complex subunit 4	0.88	3.03e-10	CAV1	caveolin 1
-1.31	1.25e-30	CLNS1A	chloride nucleotide-sensitive chann	0.87	1.06e-13	F3	coagulation factor III, tissue fact
-1.3	2.99e-39	DHFR	dihydrofolate reductase	0.87	1.28e-20	MGAT2	alpha-1,6-mannosyl-glycoprotein 2-b
-1.3	7.44e-28	BLMH	bleomycin hydrolase	0.87	5.66e-15	UXS1	UDP-glucuronate decarboxylase 1
-1.29	1.03e-34	C11orf54	chromosome 11 open reading frame 54	0.86	5.18e-18	ERGIC2	ERGIC and golgi 2
-1.29	8.45e-16	NME2	NME/NM23 nucleoside diphosphate kin	0.86	5.11e-16	MYOF	myoferlin
-1.28	1.72e-26	ABRACL	ABRA C-terminal like	0.86	6.73e-15	TAP1	transporter 1, ATP binding cassette
-1.27	2.52e-36	RPE	ribulose-5-phosphate-3-epimerase	0.85	4.17e-22	MAGT1	magnesium transporter 1
-1.27	5.67e-40	ARMC6	armadillo repeat containing 6	0.85	4.69e-18	GGCX	gamma-glutamyl carboxylase
-1.26	3.96e-45	GINS3	GINS complex subunit 3	0.85	3.64e-12	THBS1	thrombospondin 1
-1.26	1.48e-42	LIG1	DNA ligase 1	0.85	3.03e-20	LAMA3	laminin subunit alpha 3
-1.24	6.31e-43	POLA2	DNA polymerase alpha 2, accessory s	0.85	9.38e-11	CTSZ	cathepsin Z
-1.24	3.54e-39	TKFC	triokinase and FMN cyclase	0.84	1.92e-09	KRT17	keratin 17
-1.24	5.31e-39	PPP1R14B	protein phosphatase 1 regulatory in	0.83	5.68e-14	PIGT	phosphatidylinositol glycan anchor

FEN1 network, DB1, all Pearson r &gt; 0.75

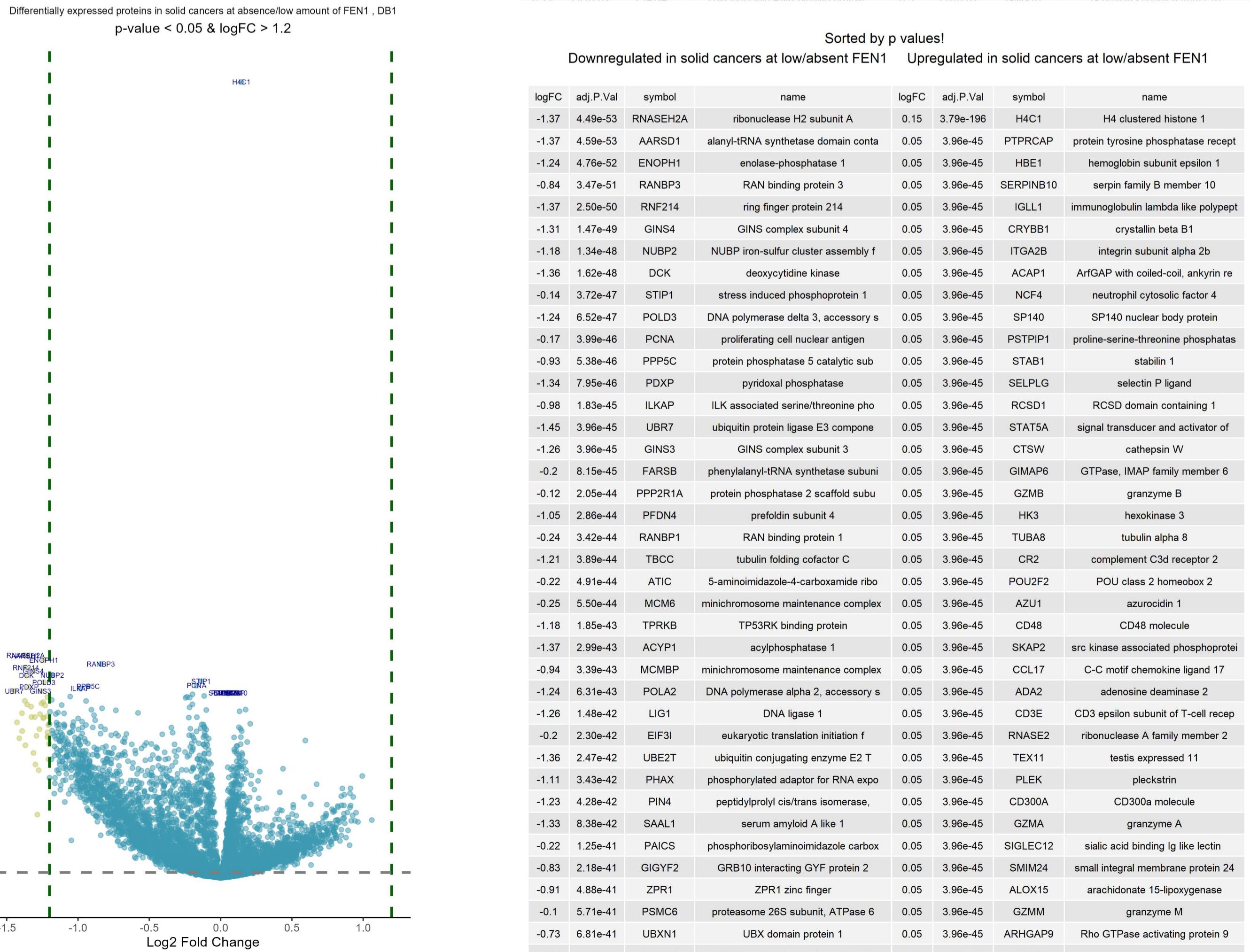
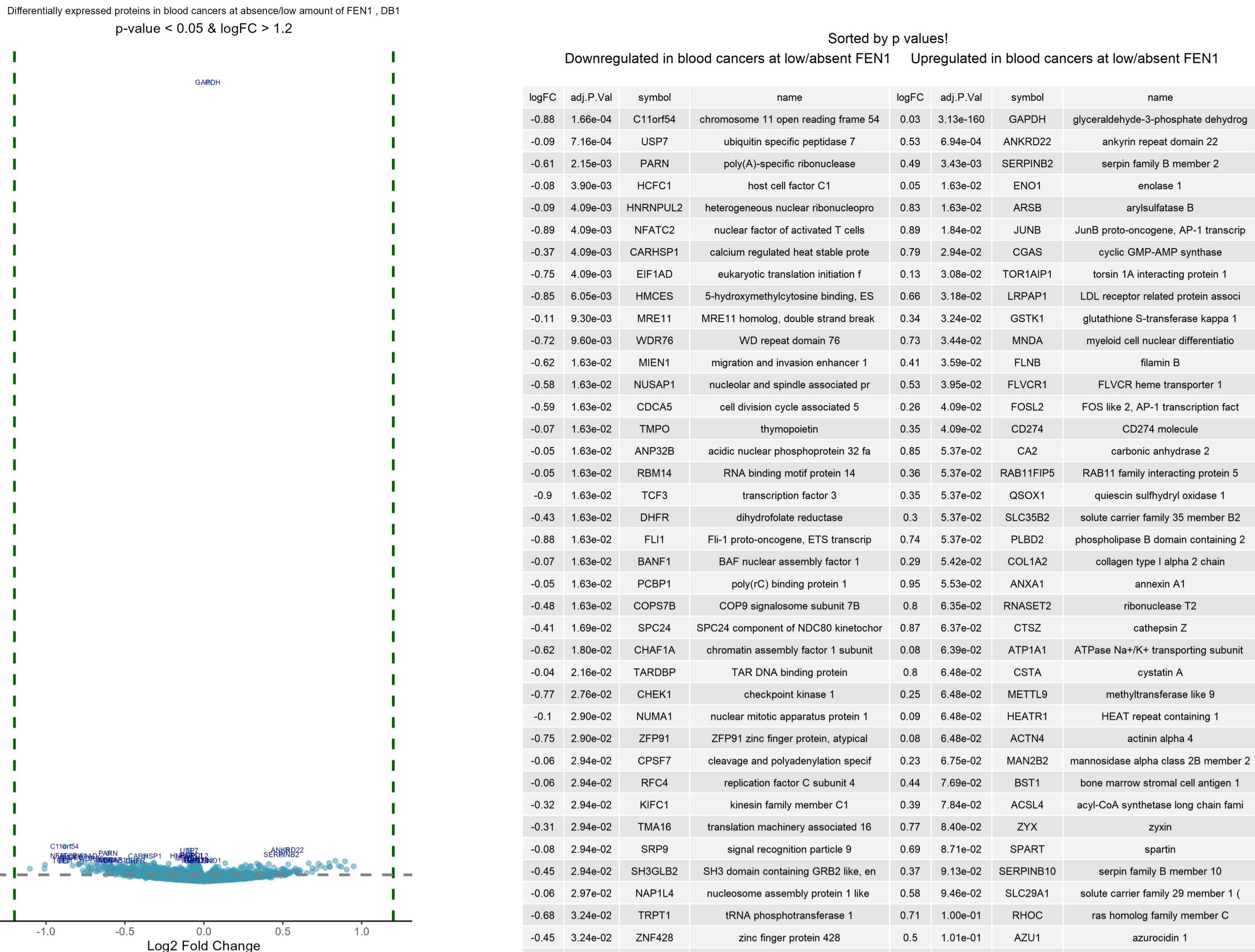


FEN1 network, DB1, all Pearson r &gt; 0.7

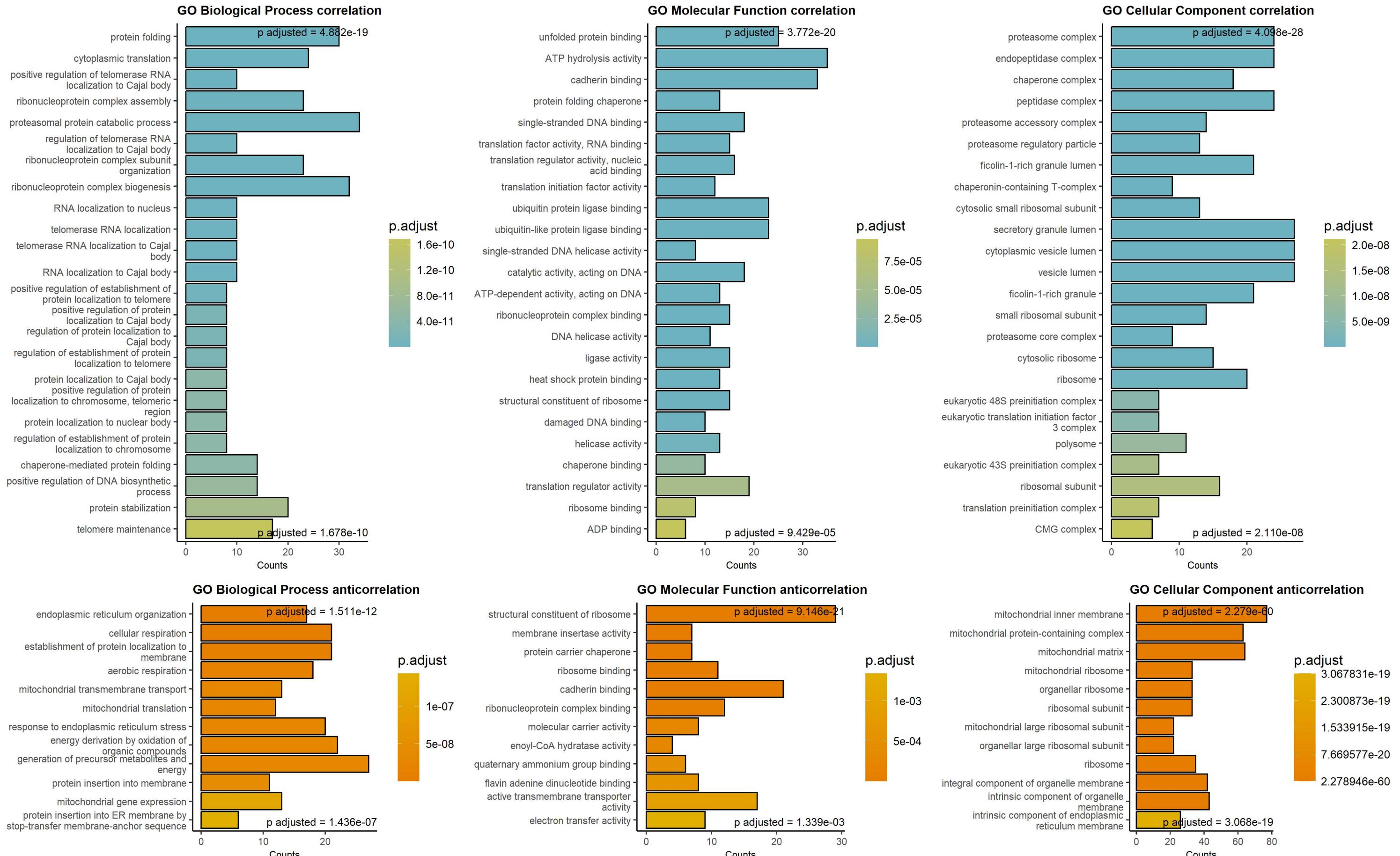


FEN1 network, DB1, all Pearson r &gt; 0.65

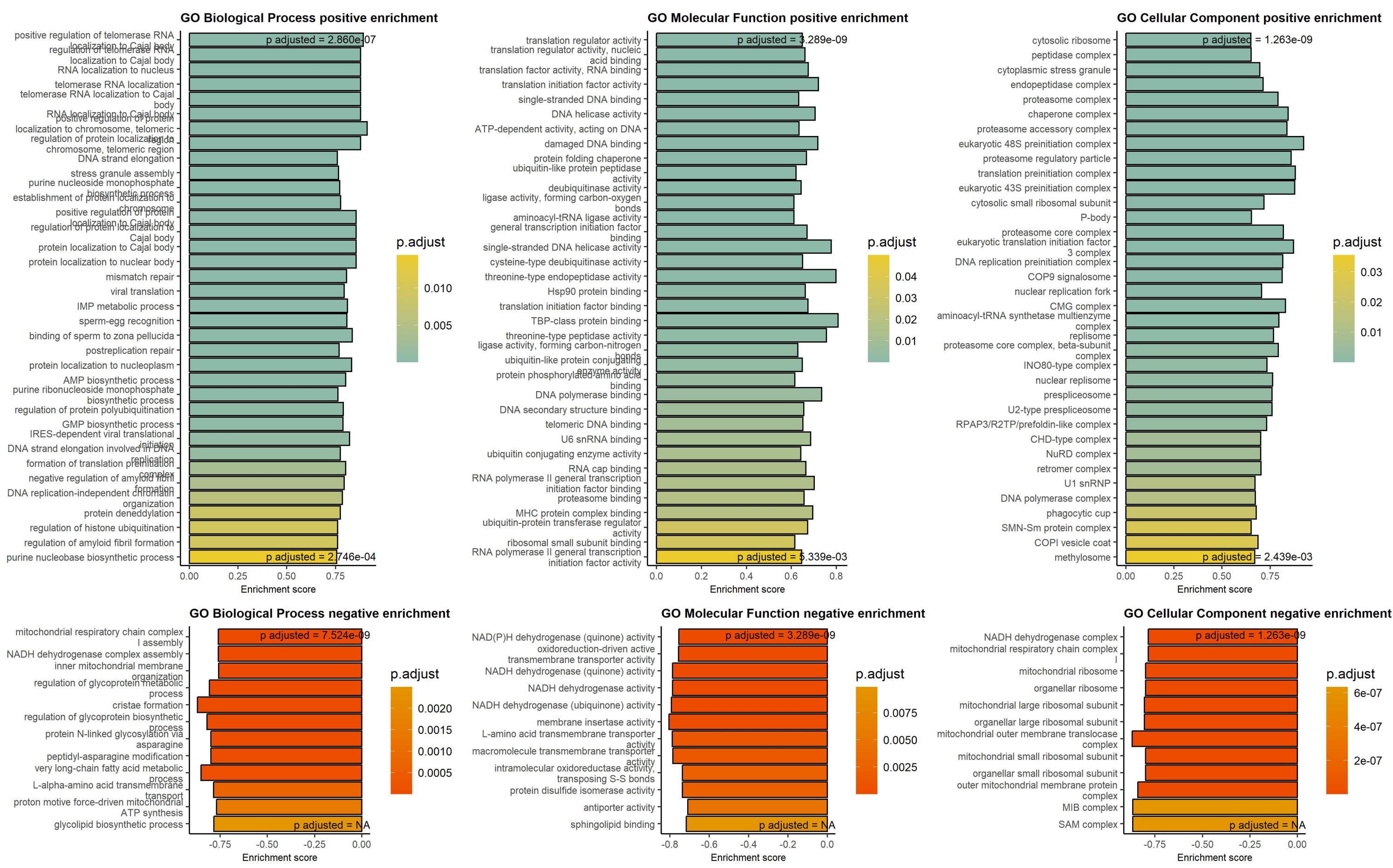




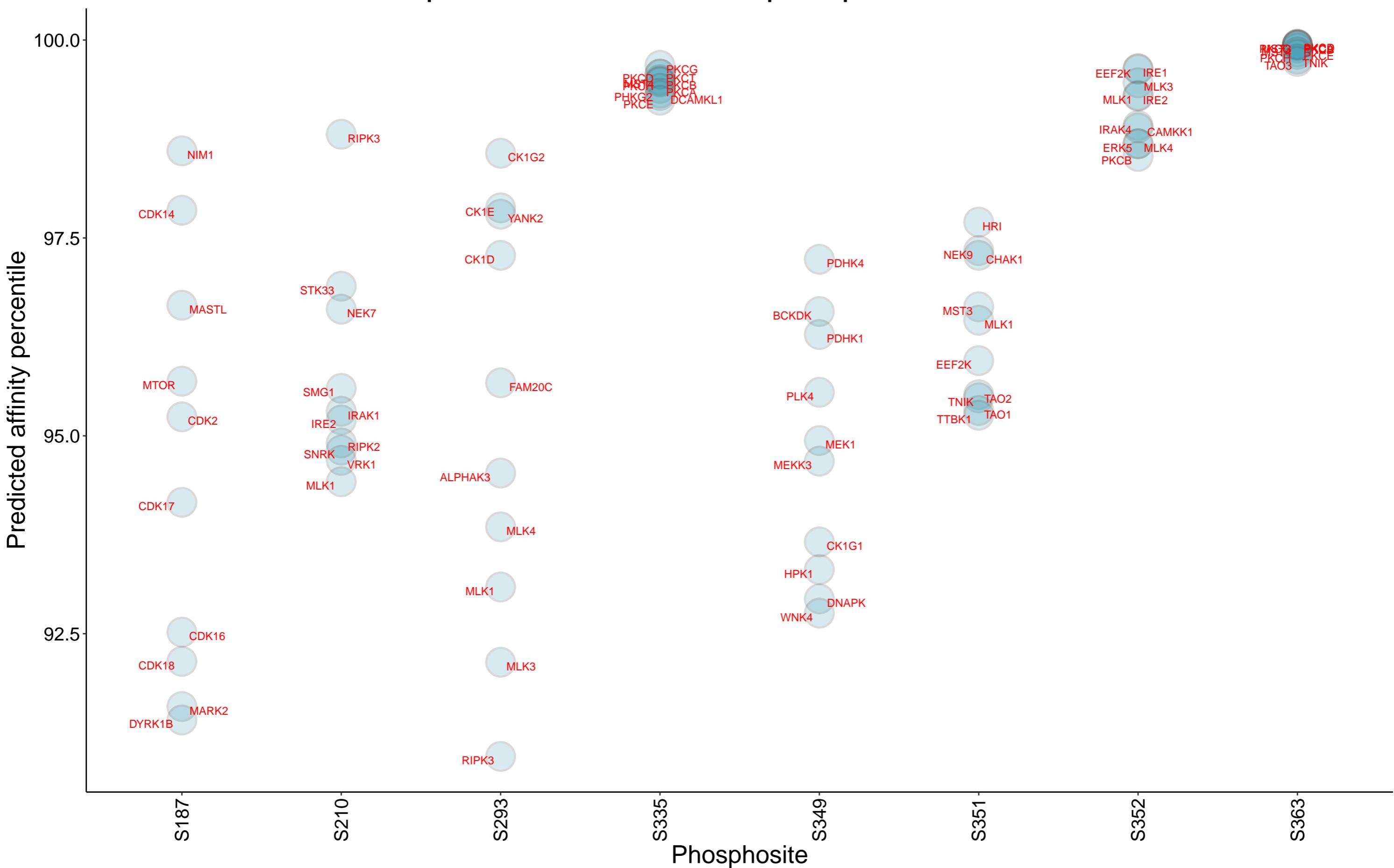
# Top 250 correlation coefficients overrepresentation, FEN1 protein, DB1



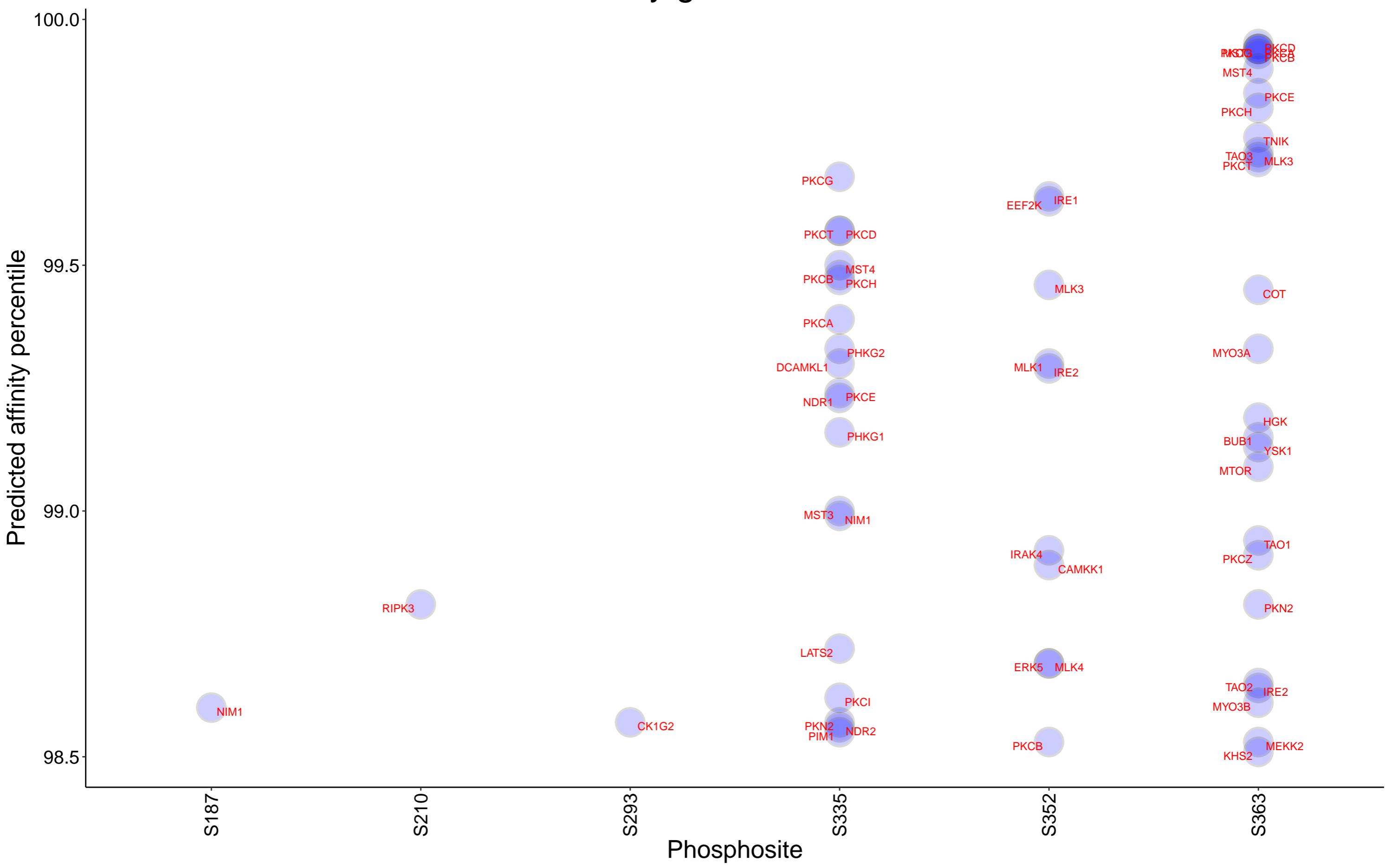
## Gene Set Enrichment analysis on protein correlation coefficients, FEN1 protein, DB1



# Top 10 kinases for each phosphosite in FEN1



Kinases with affinity greater than 98.5% to FEN1



## Top 15 positive correlation coefficients for FEN1 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

