

# FMN2

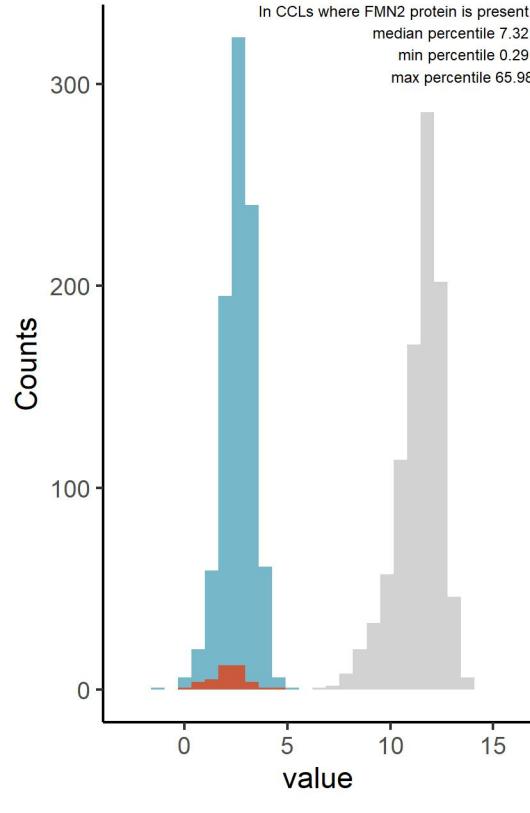
Protein name: FMN2 ; UNIPROT: Q9NZ56 ; Gene name: formin 2

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

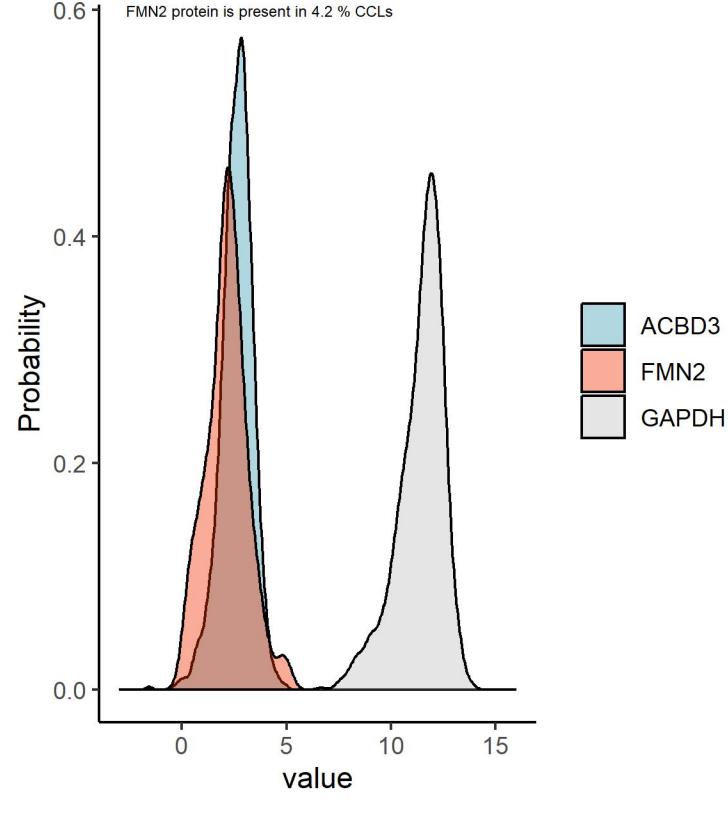
## Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

Histogram of FMN2 protein compared to proteins with low and high abundance



Density plot of FMN2 protein compared to proteins with low and high abundance



Top negative correlations of FMN2 protein, DB1

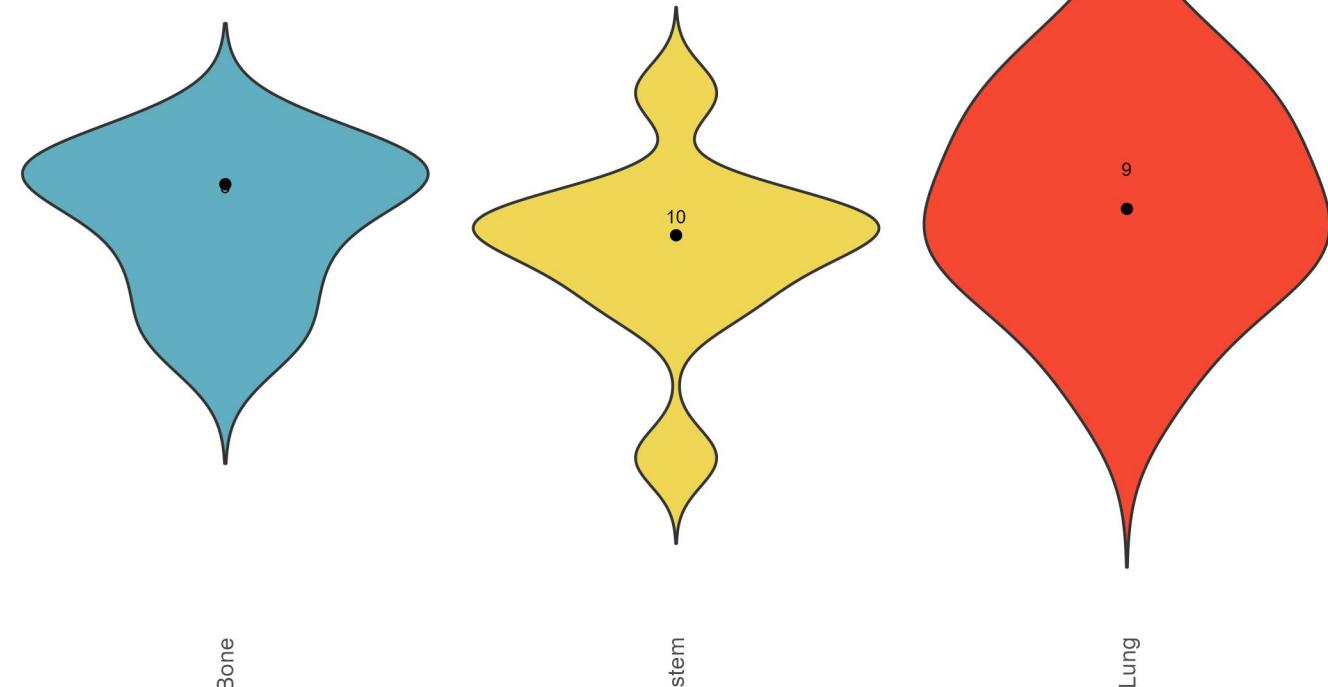
Pearson correlation coefficients

Top positive correlations of FMN2 protein, DB1

Pearson correlation coefficients

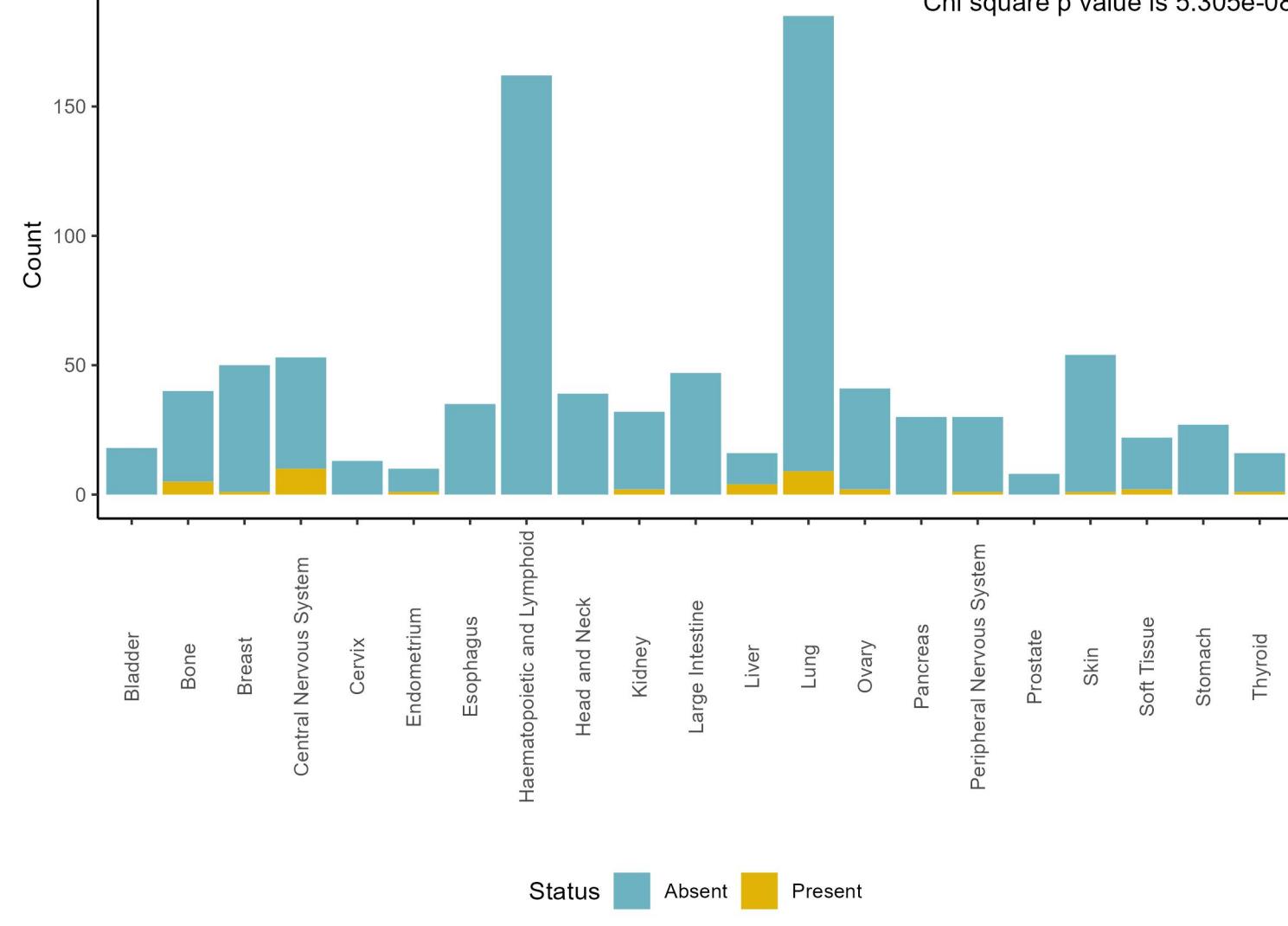
Amount of FMN2 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 1.132e-01



Present and absent FMN2 protein counts by tissue, DB1

Chi square p value is 5.305e-08

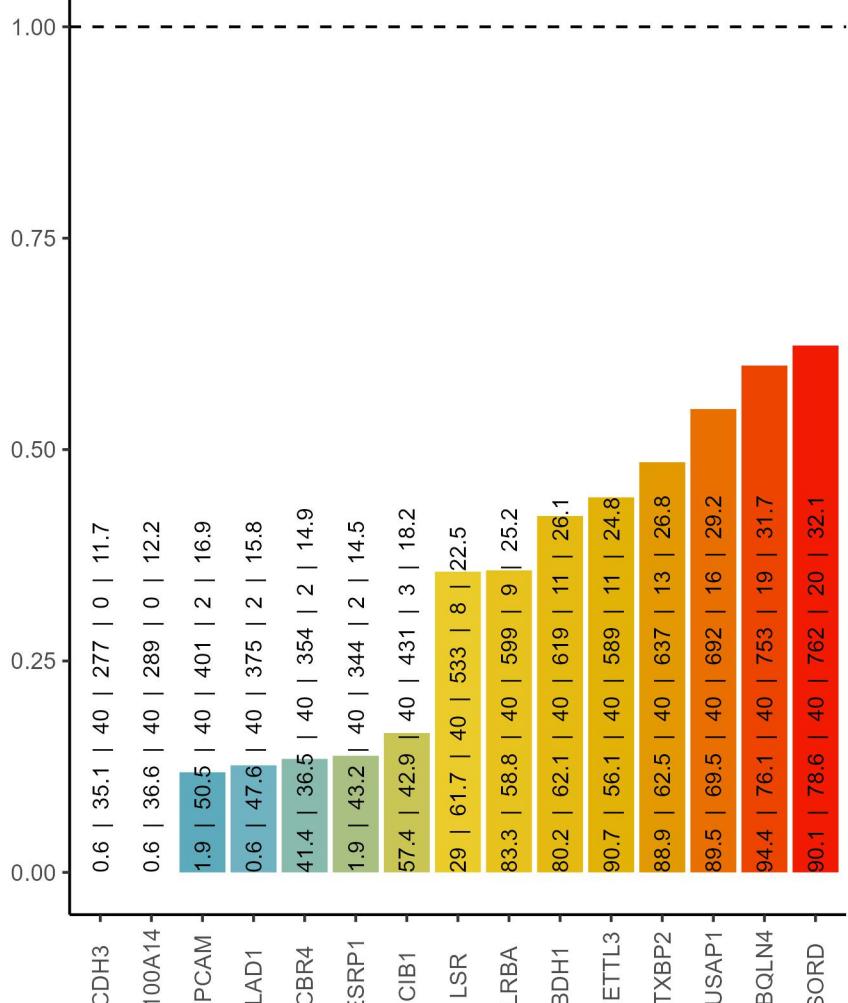


## Cooccurrence with FMN2 protein, DB1

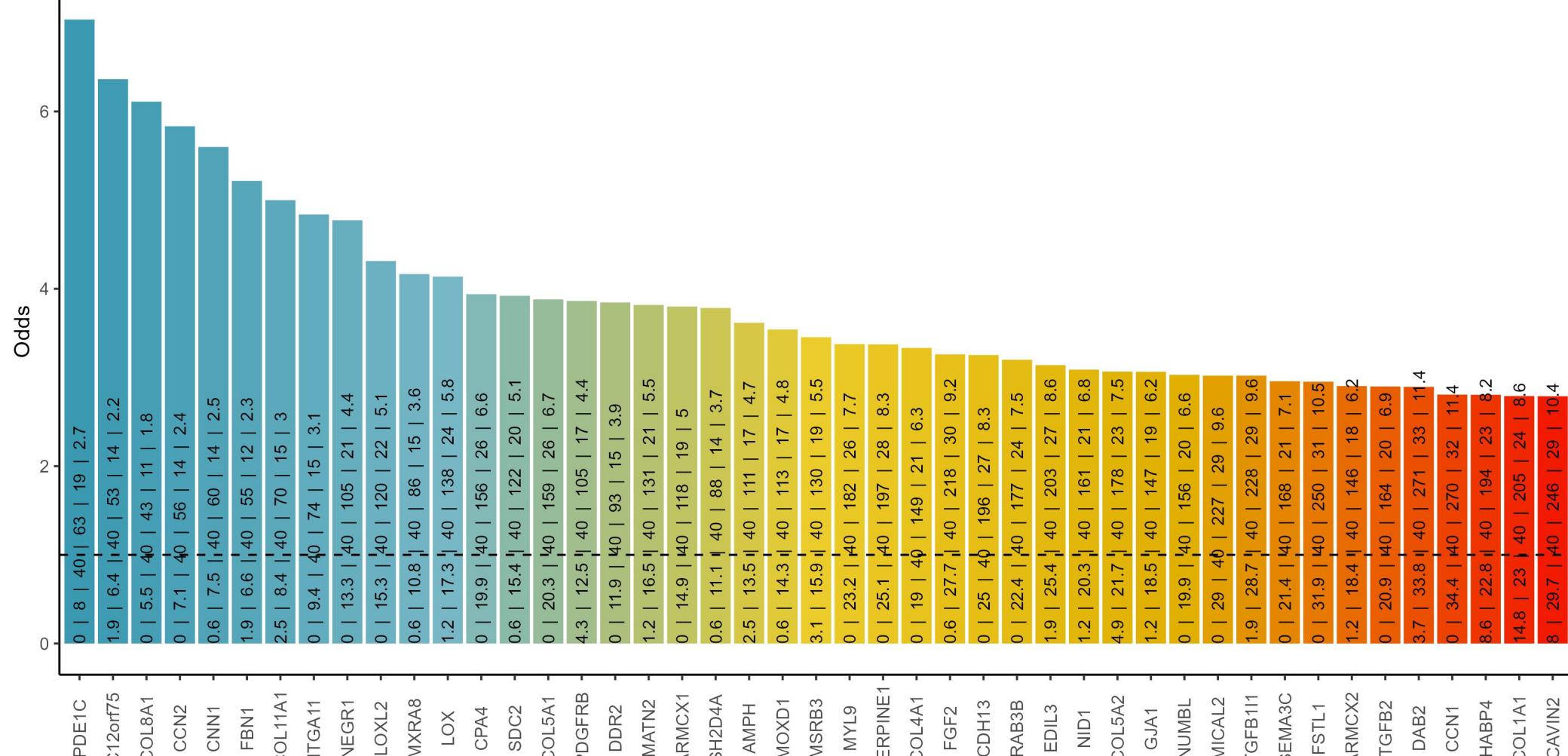
% of FMN2 in blood cancers: 0 ; % of FMN2 in solid cancers: 5.1

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of FMN2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

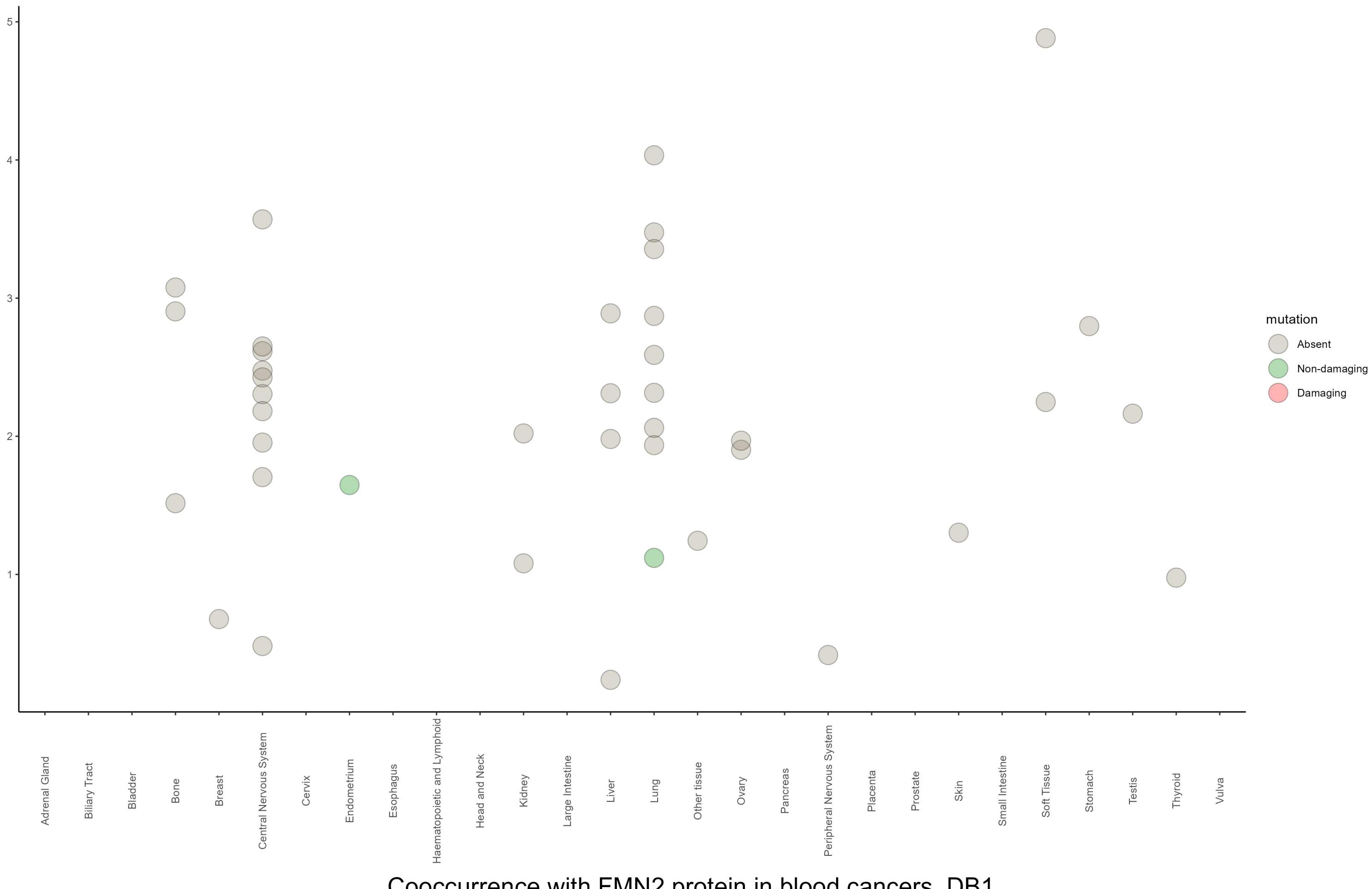
Negative cooccurrence



Positive cooccurrence

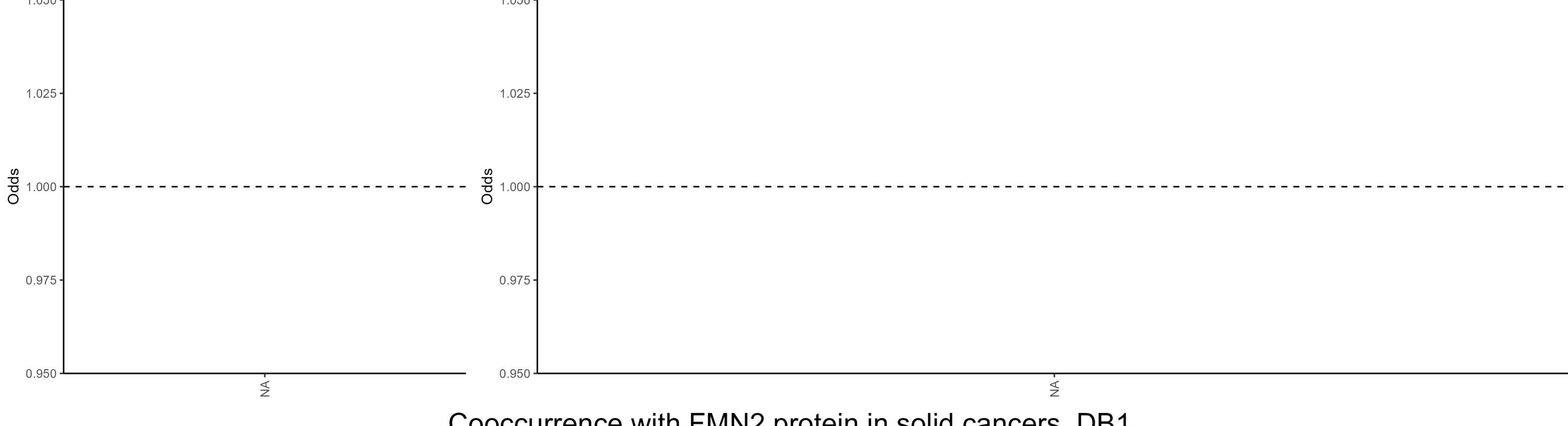


# Amount of FMN2 protein and mutation status by tissue, DB1



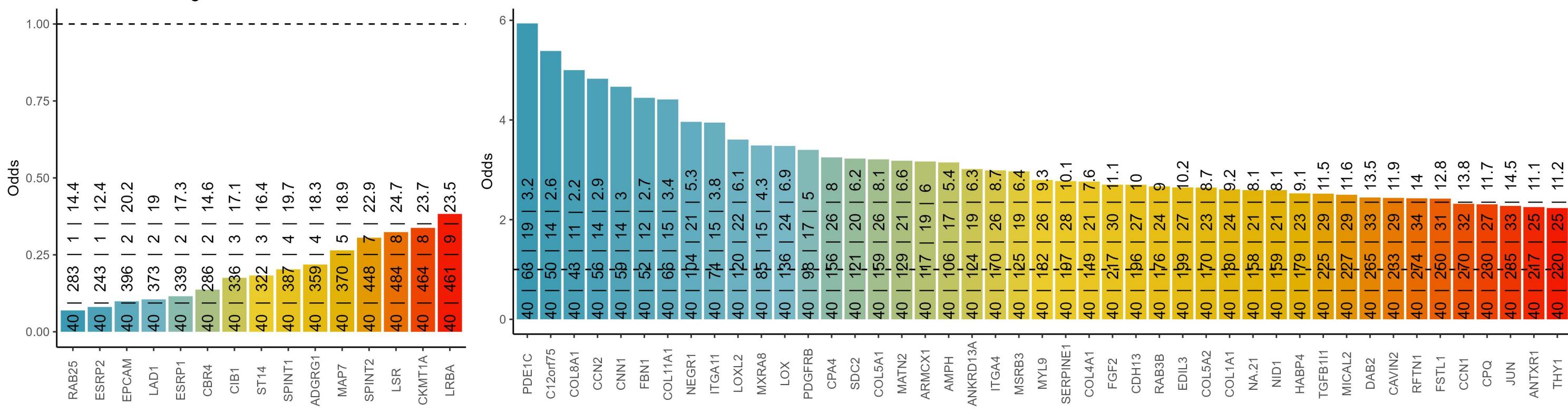
## Cooccurrence with FMN2 protein in blood cancers, DB1

The text in the bars: incidence of FMN2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

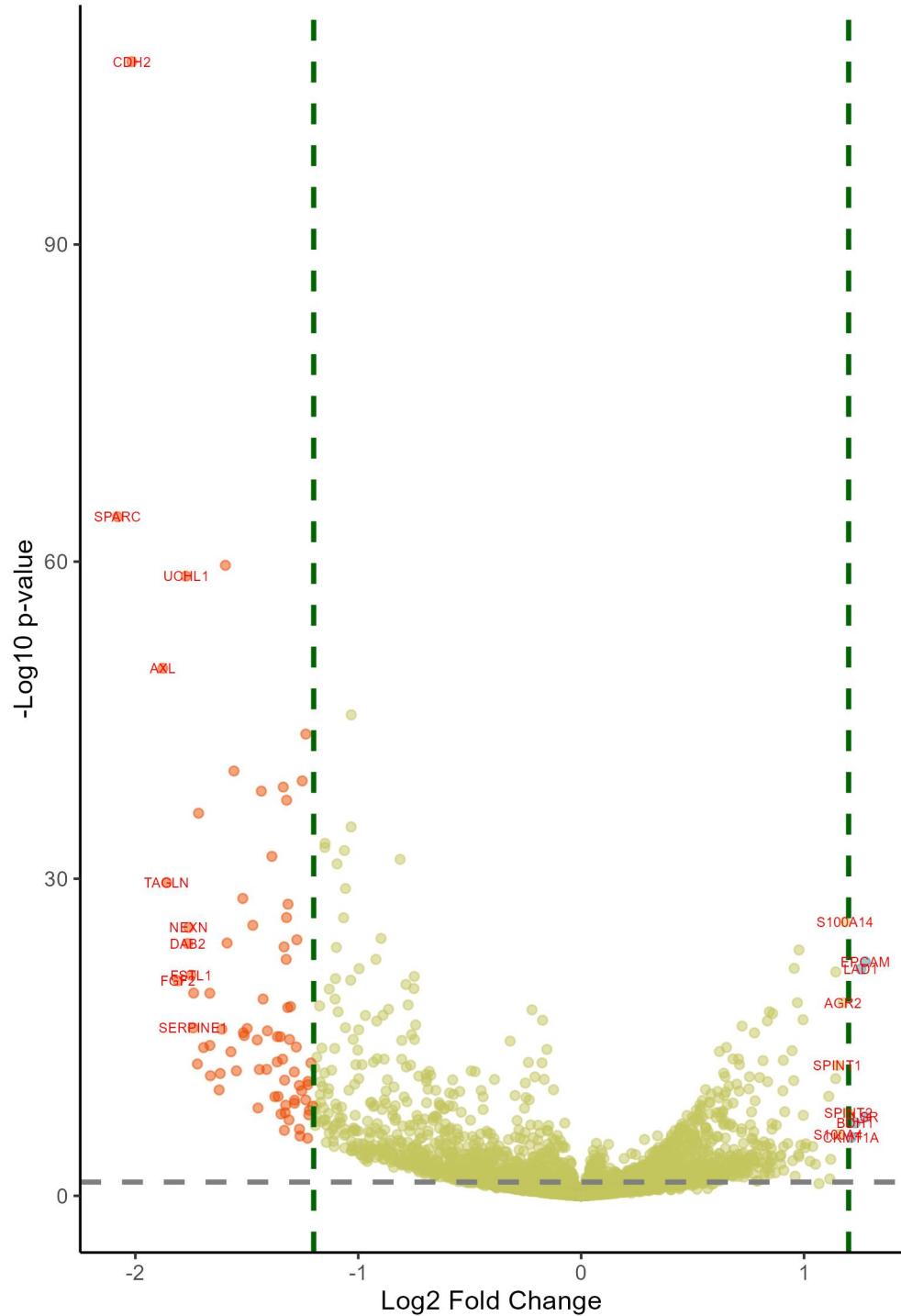


## Cooccurrence with FMN2 protein in solid cancers, DB1

The text in the bars: incidence of FMN2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



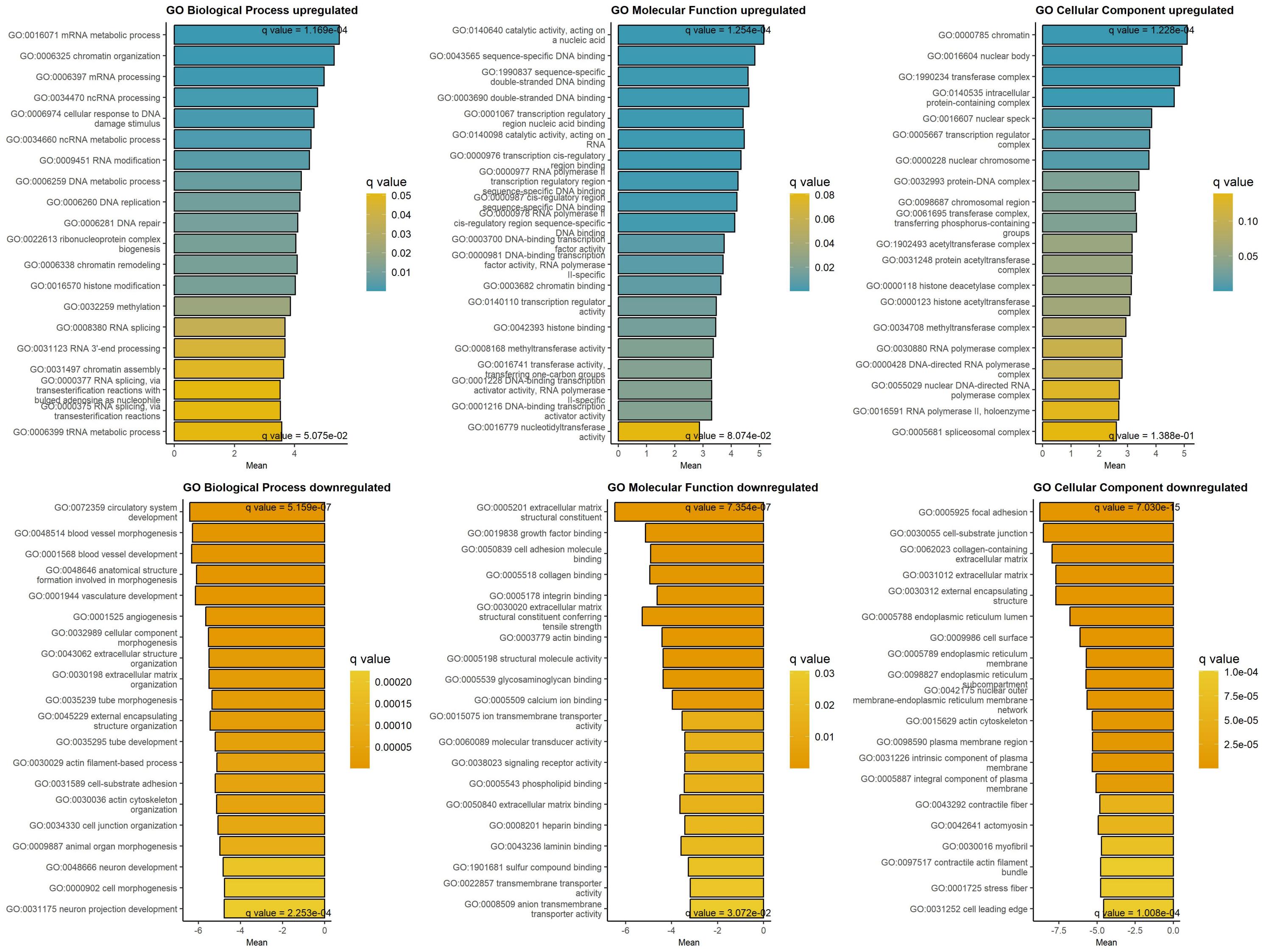
p-value &lt; 0.05 &amp; logFC &gt; 1.2

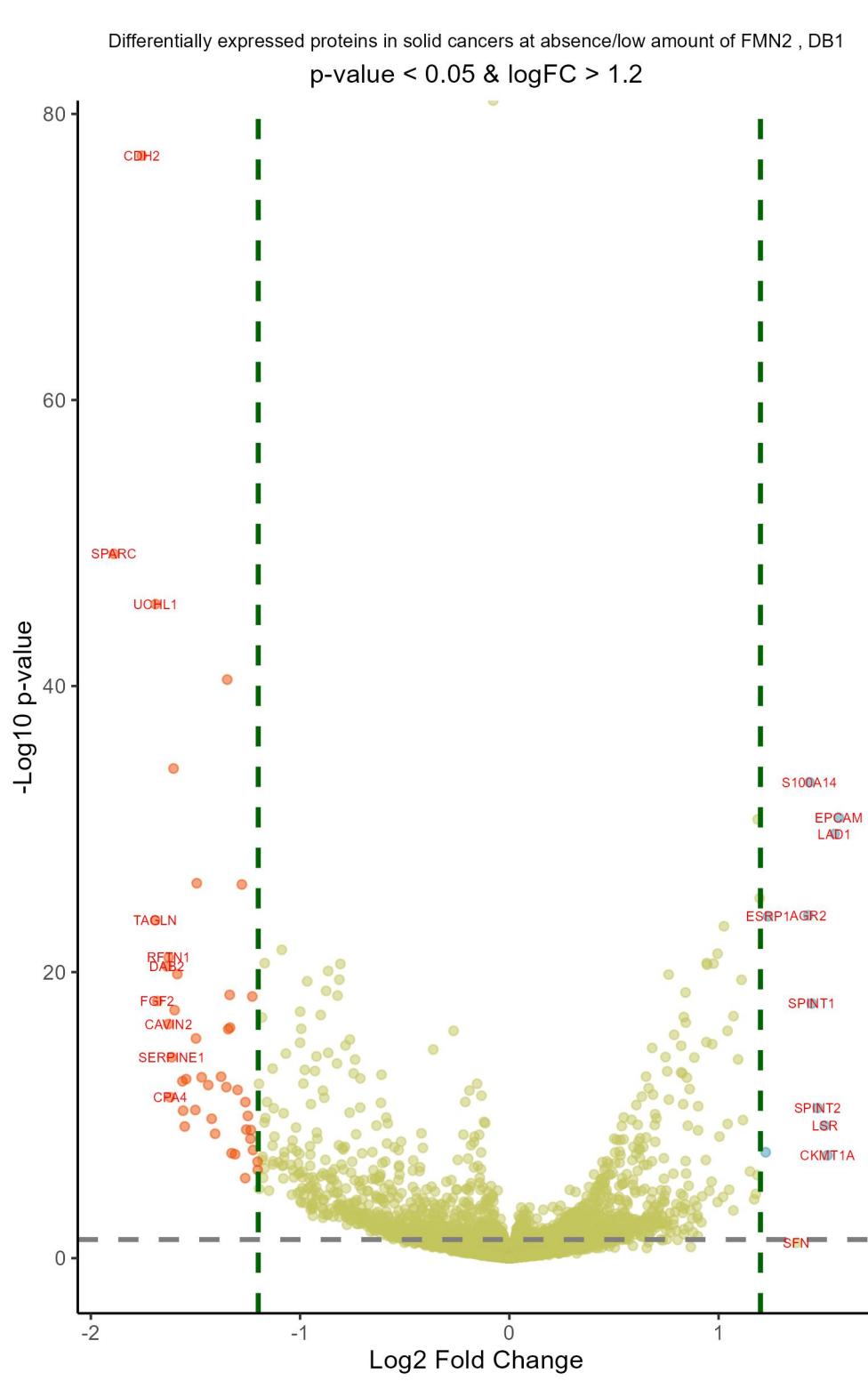


## Downregulated at low/absent FMN2 Upregulated at low/absent FMN2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.08	1.27e-61	SPARC	secreted protein acidic and cystein	1.28	8.65e-07	LSR	lipolysis stimulated lipoprotein re
-2.02	1.67e-104	CDH2	cadherin 2	1.27	1.18e-20	EPCAM	epithelial cell adhesion molecule
-1.88	1.36e-47	AXL	AXL receptor tyrosine kinase	1.25	5.35e-20	LAD1	ladinin 1
-1.86	7.01e-28	TAGLN	transgelin	1.23	2.81e-06	BDH1	3-hydroxybutyrate dehydrogenase 1
-1.81	6.10e-19	FGF2	fibroblast growth factor 2	1.21	4.93e-05	CKMT1A	creatine kinase, mitochondrial 1A
-1.77	3.15e-56	UCHL1	ubiquitin C-terminal hydrolase L1	1.2	3.73e-07	SPINT2	serine peptidase inhibitor, Kunitz
-1.77	2.60e-22	DAB2	DAB adaptor protein 2	1.18	2.88e-24	S100A14	S100 calcium binding protein A14
-1.76	8.98e-24	NEXN	nexilin F-actin binding protein	1.17	6.31e-17	AGR2	anterior gradient 2, protein disulp
-1.75	1.97e-19	FSTL1	follistatin like 1	1.15	2.93e-05	S100A4	S100 calcium binding protein A4
-1.74	1.14e-14	SERPINE1	serpin family E member 1	1.15	2.45e-11	SPINT1	serine peptidase inhibitor, Kunitz
-1.74	8.35e-18	CAVIN2	caveolae associated protein 2	1.14	9.94e-20	CIB1	calcium and integrin binding 1
-1.72	1.89e-11	CPA4	carboxypeptidase A4	1.14	3.70e-10	LRBA	LPS responsive beige-like anchor pr
-1.72	3.02e-34	EHD2	EH domain containing 2	1.12	3.23e-03	SORD	sorbitol dehydrogenase
-1.69	6.40e-13	CDH13	cadherin 13	1.12	9.74e-02	FABP5	fatty acid binding protein 5
-1.67	8.43e-18	CCN1	cellular communication network fact	1.11	1.36e-08	ELF1	E74 like ETS transcription factor 1
-1.67	4.20e-13	EDIL3	EGF like repeats and discoidin doma	1.07	2.06e-01	SFN	stratifin
-1.66	2.08e-10	COL5A1	collagen type V alpha 1 chain	1.05	7.98e-03	VAMP8	vesicle associated membrane protein
-1.62	3.71e-09	LOX	lysyl oxidase	1.04	2.84e-04	NAPRT	nicotinate phosphoribosyltransferas
-1.62	1.30e-10	MYL9	myosin light chain 9	1.03	4.60e-03	LYPLA2	lysophospholipase 2
-1.61	1.45e-14	NNMT	nicotinamide N-methyltransferase	1.01	1.70e-04	NUSAP1	nucleolar and spindle associated pr
-1.6	3.70e-57	MAP1B	microtubule associated protein 1B	1.01	3.60e-04	CIAO2A	cytosolic iron-sulfur assembly comp
-1.59	2.45e-22	PRAF2	PRA1 domain family member 2	1	6.31e-07	HPDL	4-hydroxyphenylpyruvate dioxygenase
-1.57	1.51e-12	TGFBI11	transforming growth factor beta 1 i	1	2.07e-15	ESRP1	epithelial splicing regulatory prot
-1.56	4.78e-38	TPM2	tropomyosin 2	0.99	2.24e-04	TKFC	triokinase and FMN cyclase
-1.55	7.68e-11	THY1	Thy-1 cell surface antigen	0.98	1.93e-03	PLS1	plastin 1
-1.52	2.05e-26	MXRA7	matrix remodeling associated 7	0.98	9.96e-22	CDH3	cadherin 3
-1.52	2.98e-14	CSPG4	chondroitin sulfate proteoglycan 4	0.97	1.32e-03	SCARB1	scavenger receptor class B member 1
-1.51	5.36e-14	JUN	Jun proto-oncogene, AP-1 transcript	0.97	6.23e-17	RAB25	RAB25, member RAS oncogene family
-1.5	1.27e-14	P3H2	prolyl 3-hydroxylase 2	0.96	6.35e-02	CHRAC1	chromatin accessibility complex sub

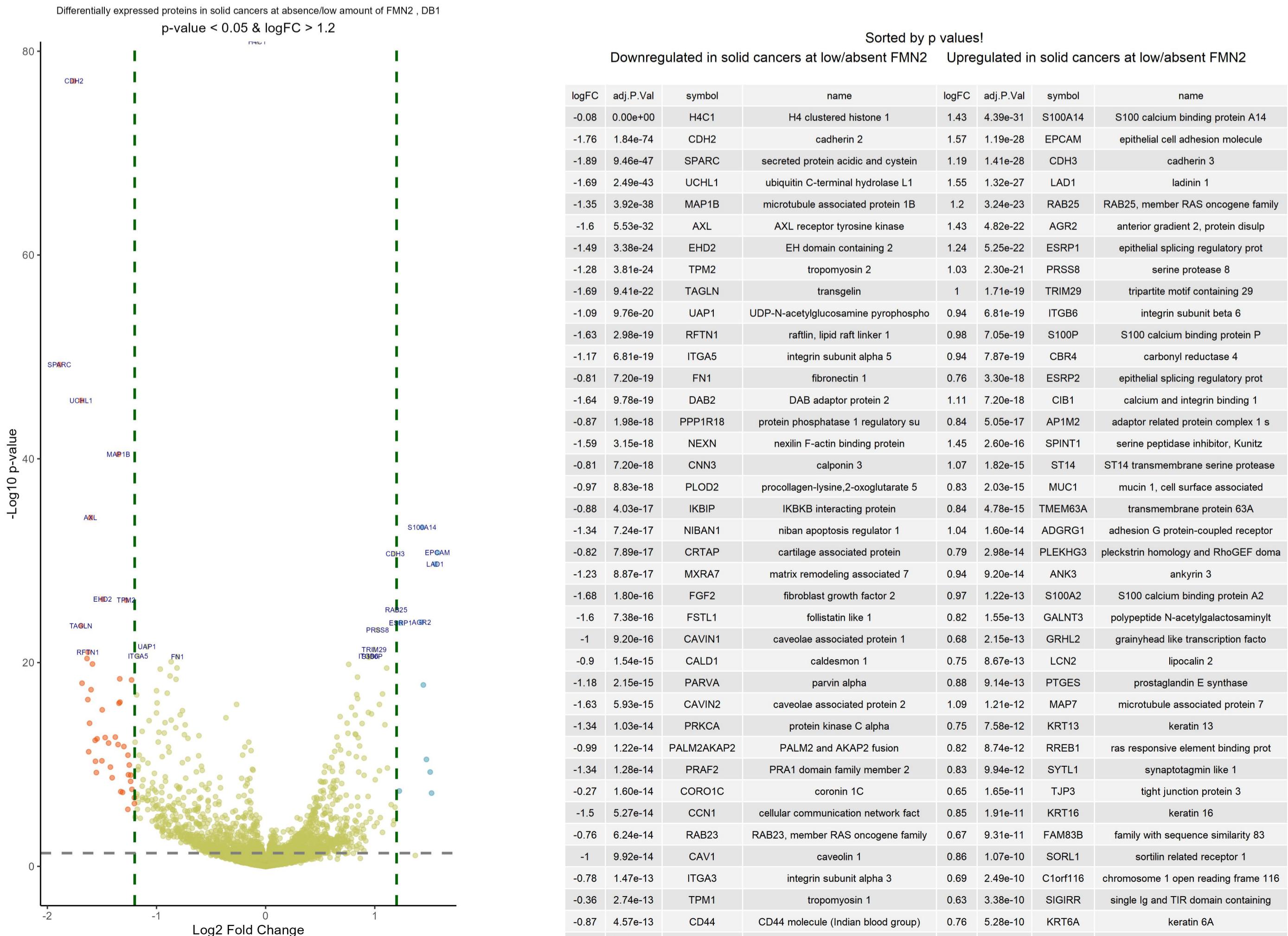
## GAGE analysis on upregulated and downregulated proteins at low/absent FMN2 protein, DB1





Downregulated in solid cancers at low/absent FMN2      Upregulated in solid cancers at low/absent FMN2

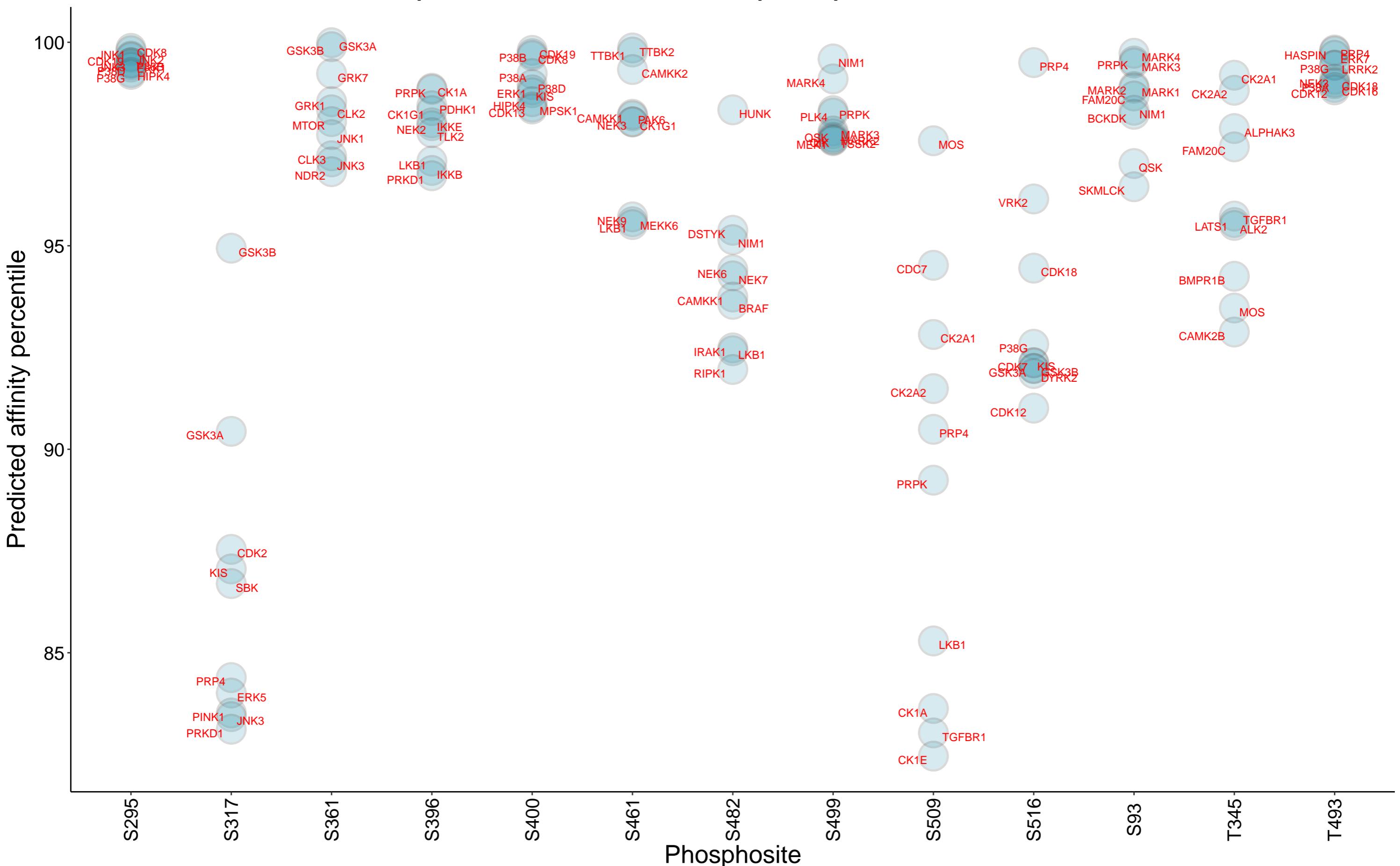
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.89	9.46e-47	SPARC	secreted protein acidic and cystein	1.57	1.19e-28	EPCAM	epithelial cell adhesion molecule
-1.76	1.84e-74	CDH2	cadherin 2	1.55	1.32e-27	LAD1	ladinin 1
-1.69	9.41e-22	TAGLN	transgelin	1.52	2.17e-06	CKMT1A	creatine kinase, mitochondrial 1A
-1.69	2.49e-43	UCHL1	ubiquitin C-terminal hydrolase L1	1.51	2.66e-08	LSR	lipolysis stimulated lipoprotein re
-1.68	1.80e-16	FGF2	fibroblast growth factor 2	1.47	1.87e-09	SPINT2	serine peptidase inhibitor, Kunitz
-1.64	9.78e-19	DAB2	DAB adaptor protein 2	1.45	2.60e-16	SPINT1	serine peptidase inhibitor, Kunitz
-1.63	5.93e-15	CAVIN2	caveolae associated protein 2	1.43	4.39e-31	S100A14	S100 calcium binding protein A14
-1.63	2.98e-19	RFTN1	raftlin, lipid raft linker 1	1.43	4.82e-22	AGR2	anterior gradient 2, protein disulp
-1.62	3.69e-10	CPA4	carboxypeptidase A4	1.37	2.88e-01	SFN	stratin
-1.61	8.77e-13	SERPINE1	serpin family E member 1	1.24	5.25e-22	ESRP1	epithelial splicing regulatory prot
-1.6	5.53e-32	AXL	AXL receptor tyrosine kinase	1.22	1.41e-06	CDH1	cadherin 1
-1.6	7.38e-16	FSTL1	follistatin like 1	1.2	3.24e-23	RAB25	RAB25, member RAS oncogene family
-1.59	3.15e-18	NEXN	nexilin F-actin binding protein	1.19	1.41e-28	CDH3	cadherin 3
-1.56	3.27e-11	CDH13	cadherin 13	1.19	3.92e-05	FAM83H	family with sequence similarity 83
-1.56	2.79e-09	COL5A1	collagen type V alpha 1 chain	1.18	5.73e-04	PKP3	plakophilin 3
-1.55	2.97e-08	LOX	lysyl oxidase	1.17	1.24e-03	EPPK1	epiplakin 1
-1.54	2.36e-11	EDIL3	EGF like repeats and discoidin doma	1.15	2.34e-05	BDH1	3-hydroxybutyrate dehydrogenase 1
-1.5	2.52e-09	MYL9	myosin light chain 9	1.12	1.16e-08	TACSTD2	tumor associated calcium signal tra
-1.5	5.27e-14	CCN1	cellular communication network fact	1.11	7.20e-18	CIB1	calcium and integrin binding 1
-1.49	3.38e-24	EHD2	EH domain containing 2	1.09	1.21e-12	MAP7	microtubule associated protein 7
-1.47	1.82e-11	TGFB1I1	transforming growth factor beta 1 i	1.07	1.82e-15	ST14	ST14 transmembrane serine protease
-1.44	5.75e-11	NNMT	nicotinamide N-methyltransferase	1.07	5.85e-03	SORD	sorbitol dehydrogenase
-1.42	9.57e-09	THY1	Thy-1 cell surface antigen	1.05	3.25e-04	NAPRT	nicotinate phosphoribosyltransferas
-1.41	9.12e-08	ITGA4	integrin subunit alpha 4	1.04	2.08e-08	LRBA	LPS responsive beige-like anchor pr
-1.38	1.67e-11	JUN	Jun proto-oncogene, AP-1 transcript	1.04	1.60e-14	ADGRG1	adhesion G protein-coupled receptor
-1.35	7.96e-11	CSPG4	chondroitin sulfate proteoglycan 4	1.03	2.30e-21	PRSS8	serine protease 8
-1.35	3.92e-38	MAP1B	microtubule associated protein 1B	1.02	8.96e-04	MISP	mitotic spindle positioning
-1.34	1.28e-14	PRAF2	PRA1 domain family member 2	1	1.39e-07	EVPL	envoplakin
-1.34	7.24e-17	NIBAN1	niban apoptosis regulator 1	1	1.71e-19	TRIM29	tripartite motif containing 29



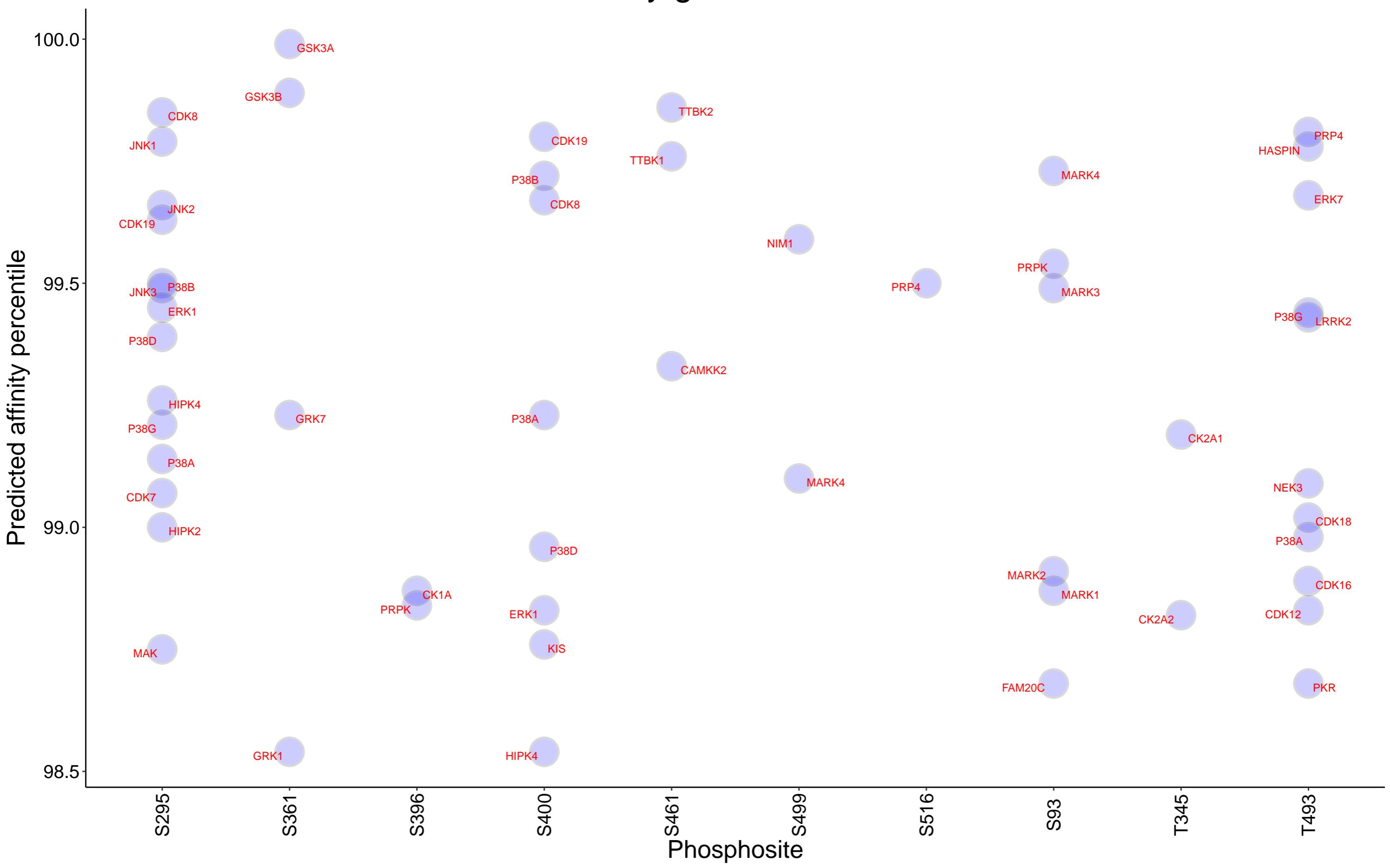
Insufficient number of paired observations in DB1 for FMN2

Insufficient number of paired observations in DB1 for FMN2

# Top 10 kinases for each phosphosite in FMN2



Kinases with affinity greater than 98.5% to FMN2



No sufficient paired observations in DB1 for FMN2