

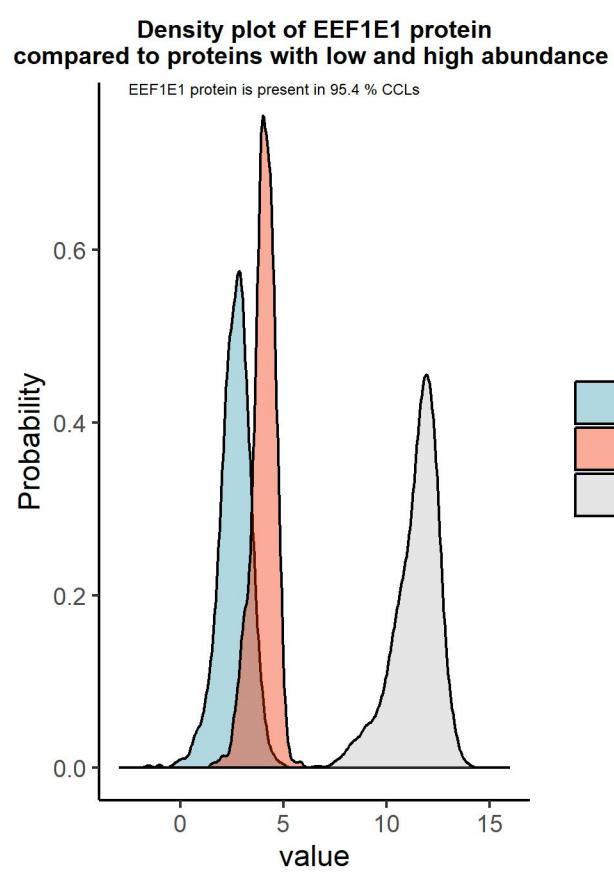
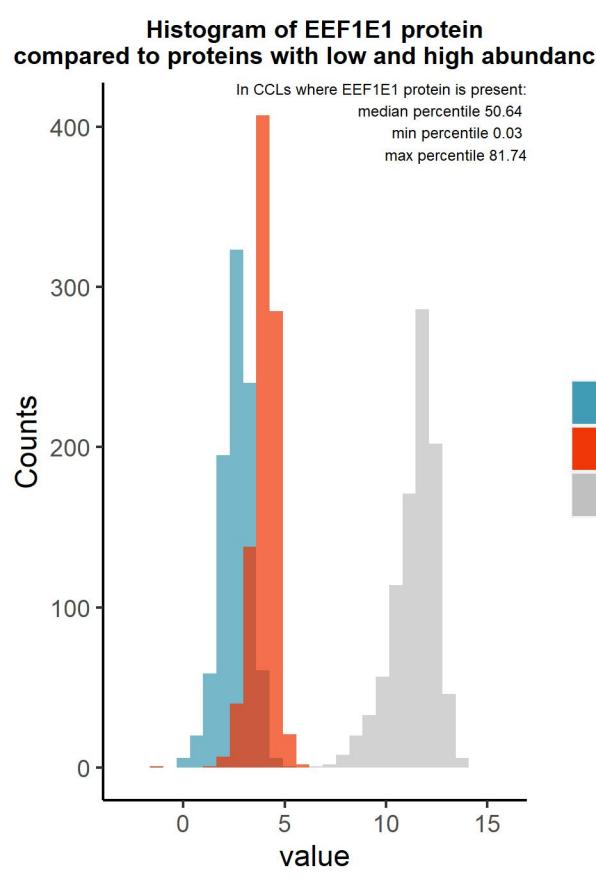
EEF1E1

Protein name: MCA3 ; UNIPROT: O43324 ; Gene name: eukaryotic translation elongation factor 1 epsilon 1

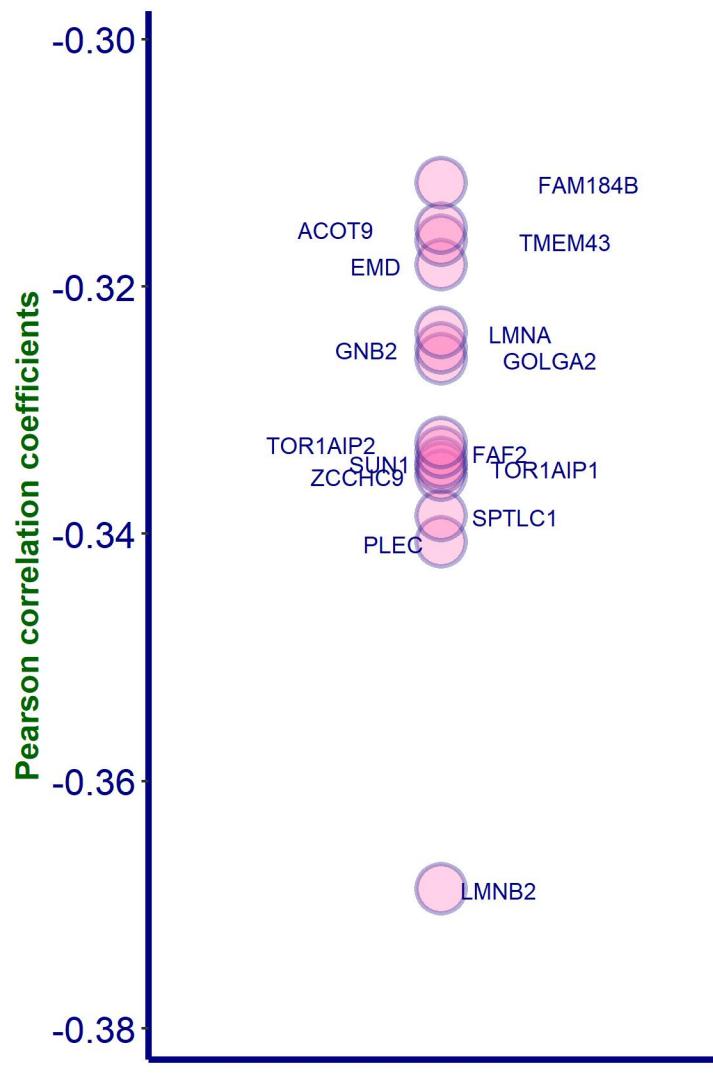
Ligandable: Yes ; Ligandable_by_Chem: NA ; Is_enzyme: NA (<https://cansar.ai/>)

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

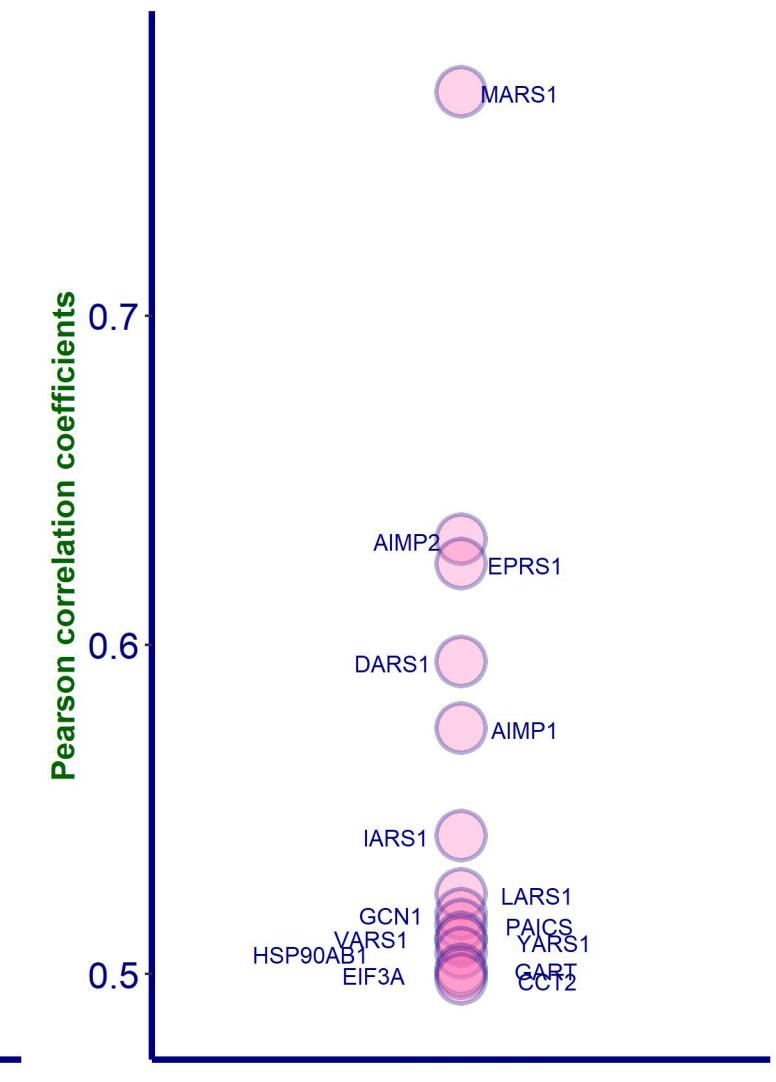
6692 proteins in 949 CCLs



Top negative correlations of EEF1E1 protein, DB1

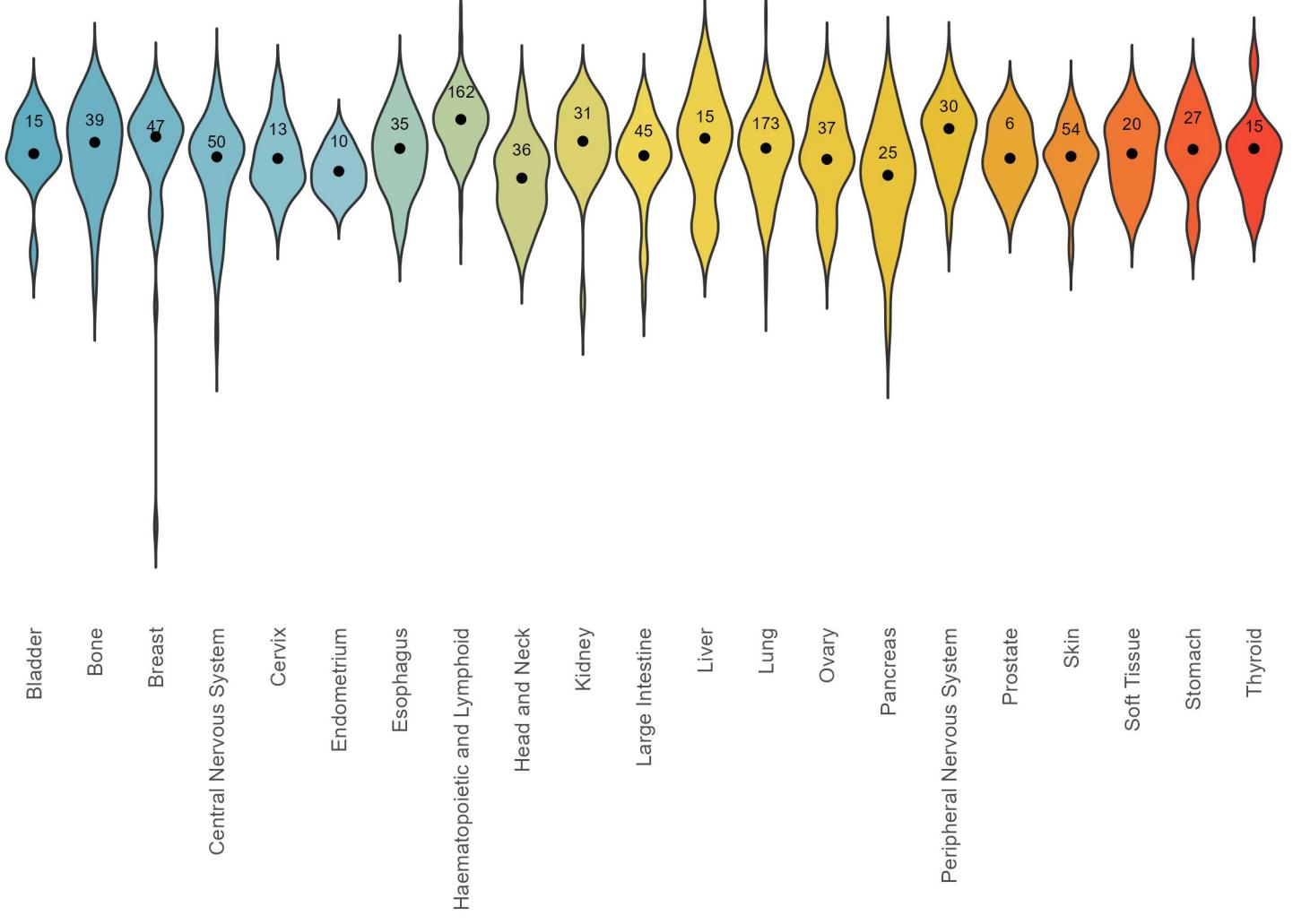


Top positive correlations of EEF1E1 protein, DB1



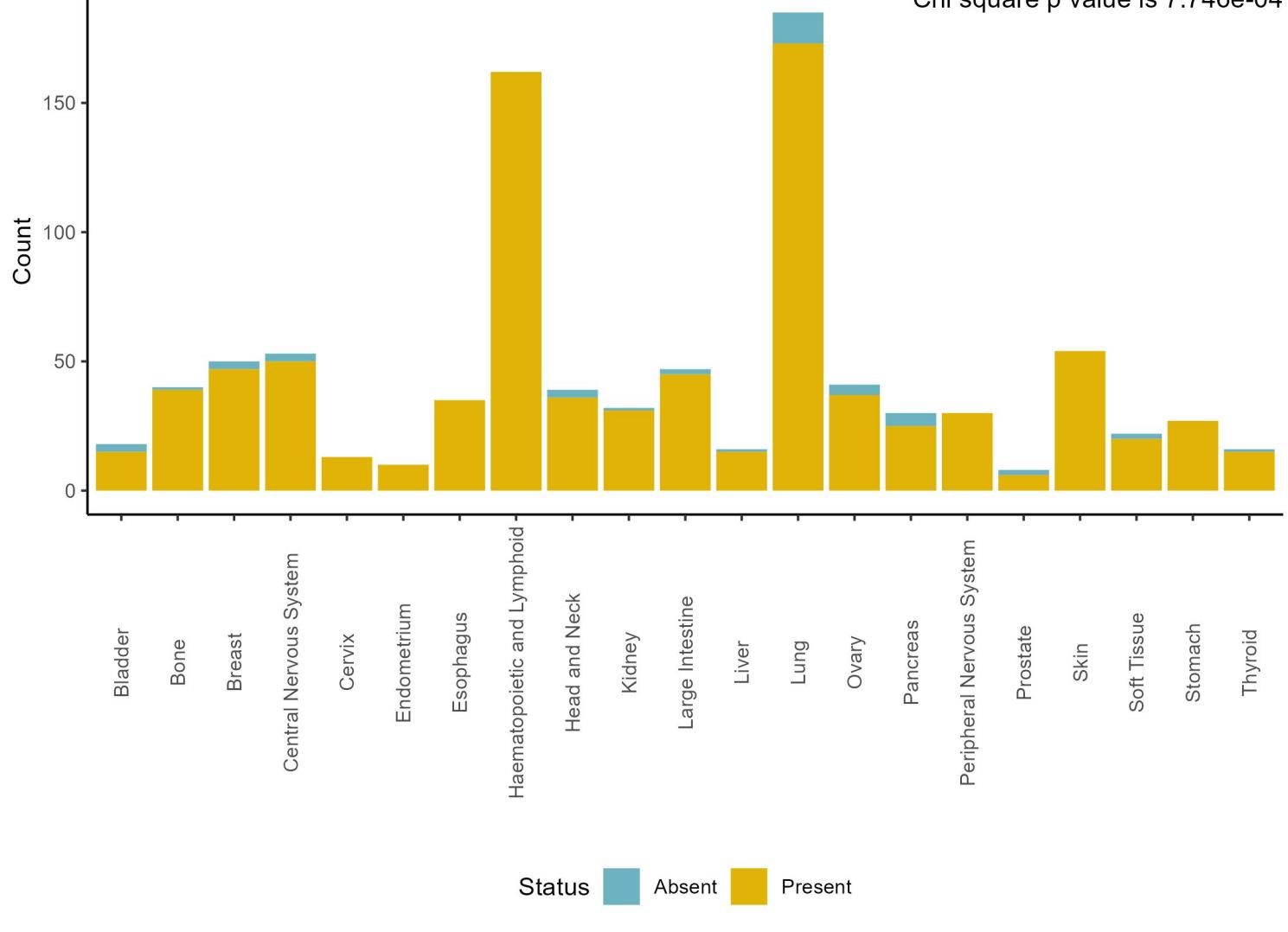
Amount of EEF1E1 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 6.812e-18



Present and absent EEF1E1 protein counts by tissue, DB1

Chi square p value is 7.746e-04

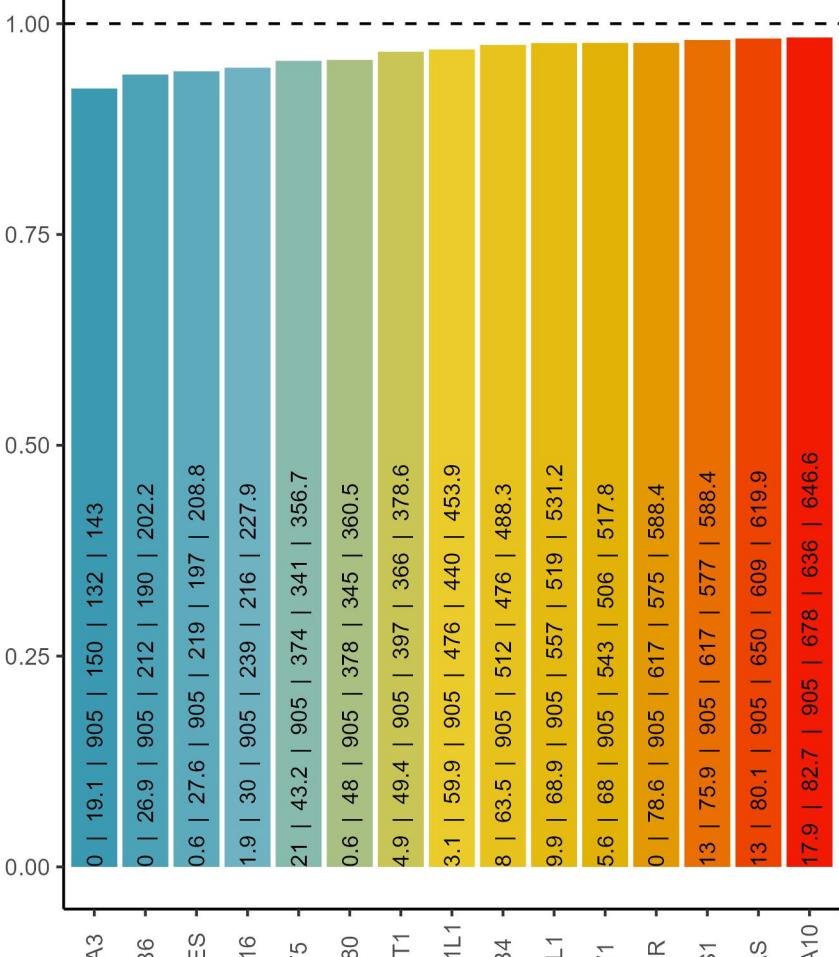


Cooccurrence with EEF1E1 protein, DB1

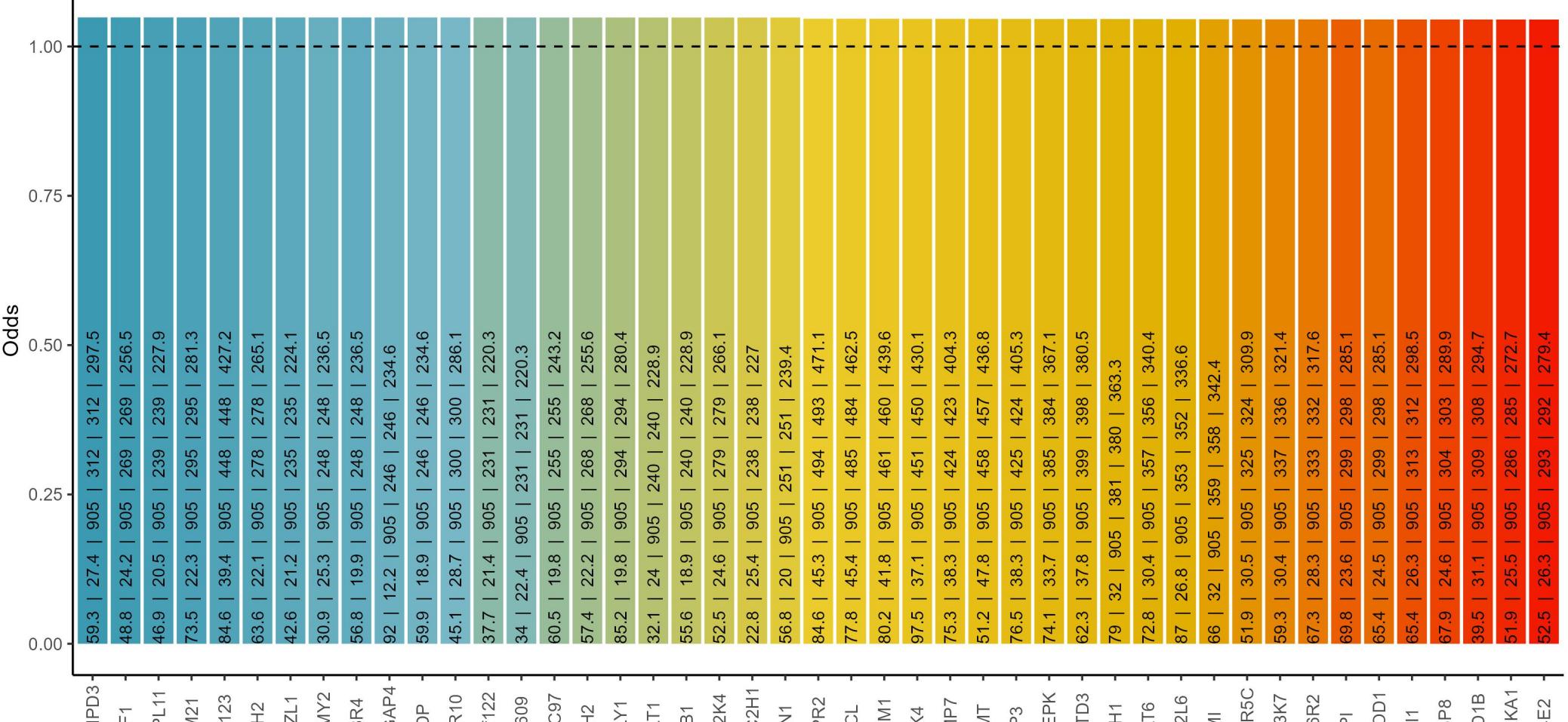
% of EEF1E1 in blood cancers: 100 ; % of EEF1E1 in solid cancers: 94.4

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of EEF1E1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

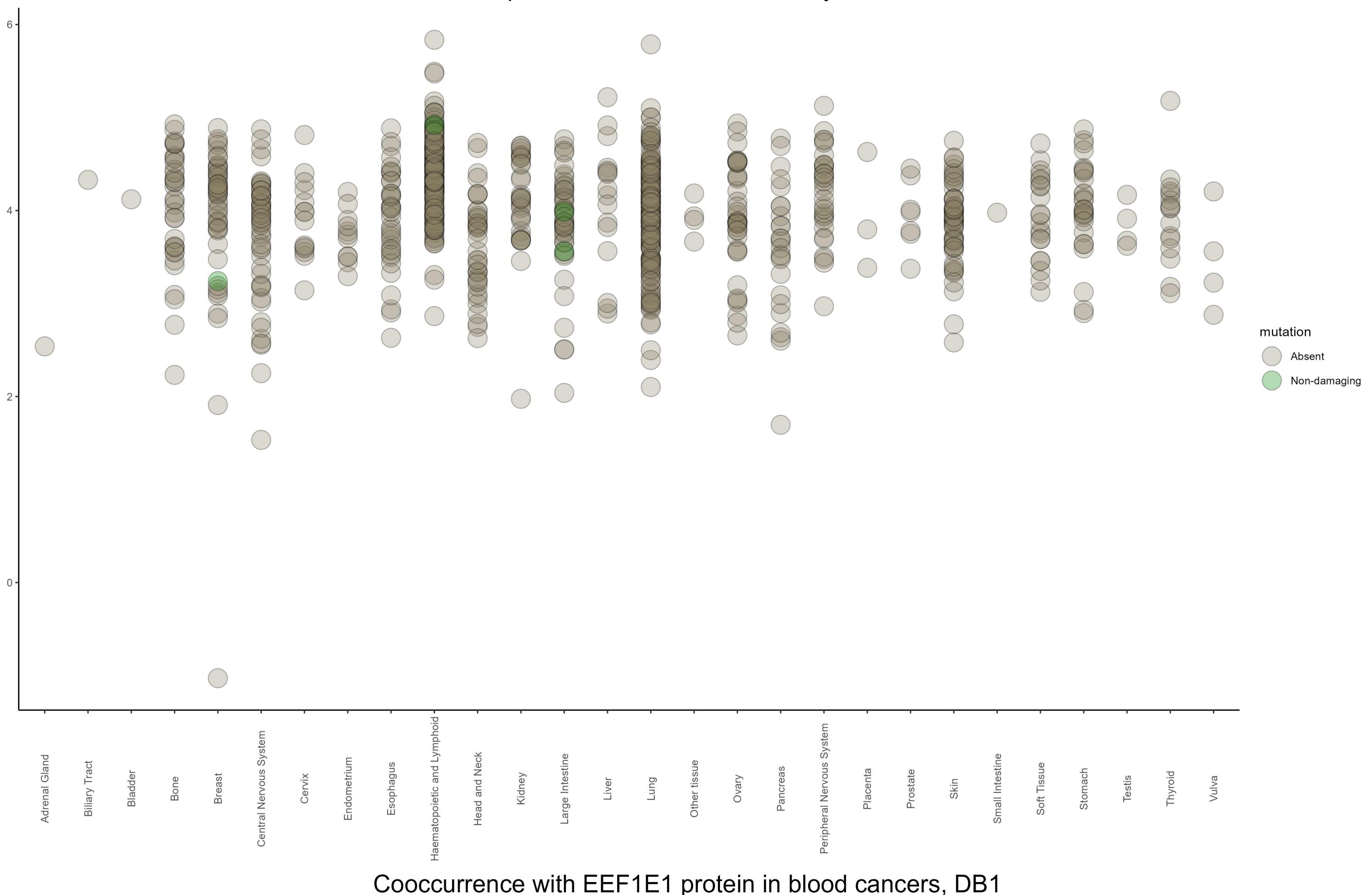
Negative cooccurrence



Positive cooccurrence



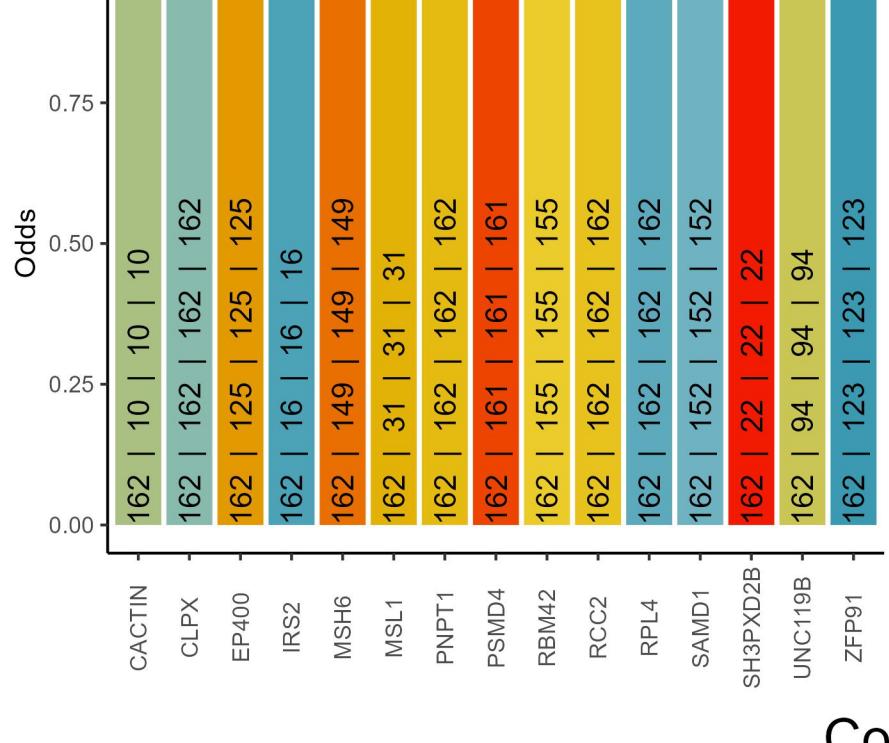
Amount of EEF1E1 protein and mutation status by tissue, DB1



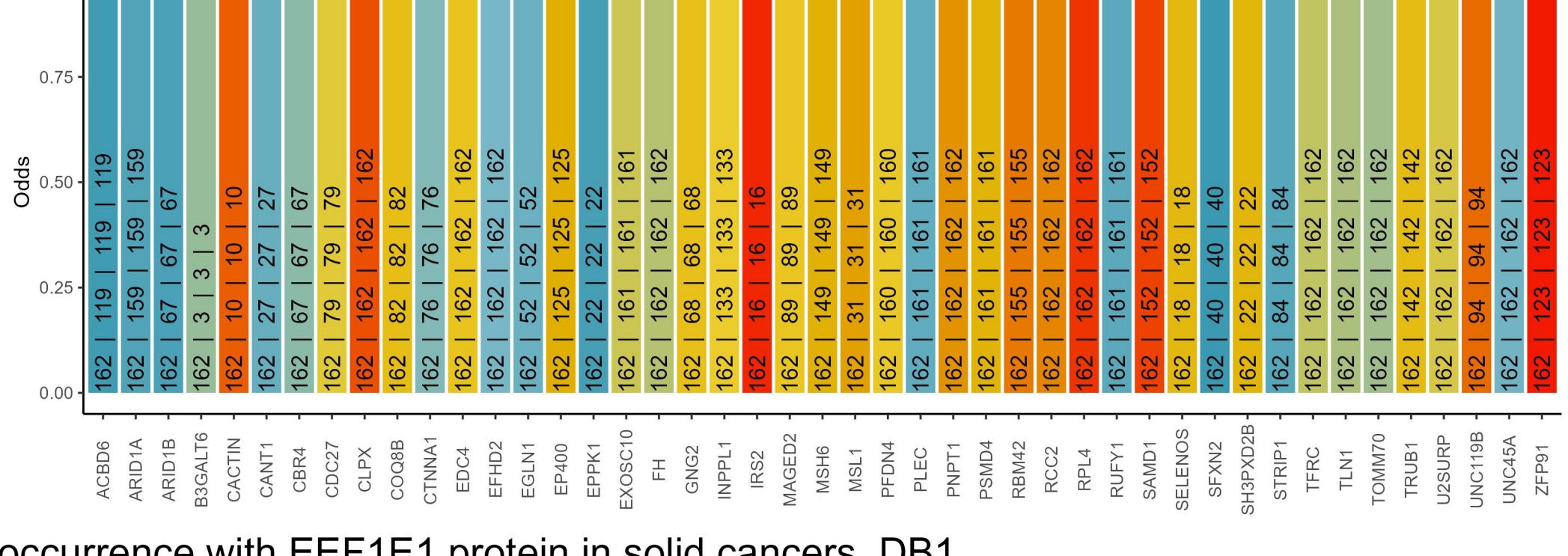
Cooccurrence with EEF1E1 protein in blood cancers, DB1

The text in the bars: incidence of EEF1E1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



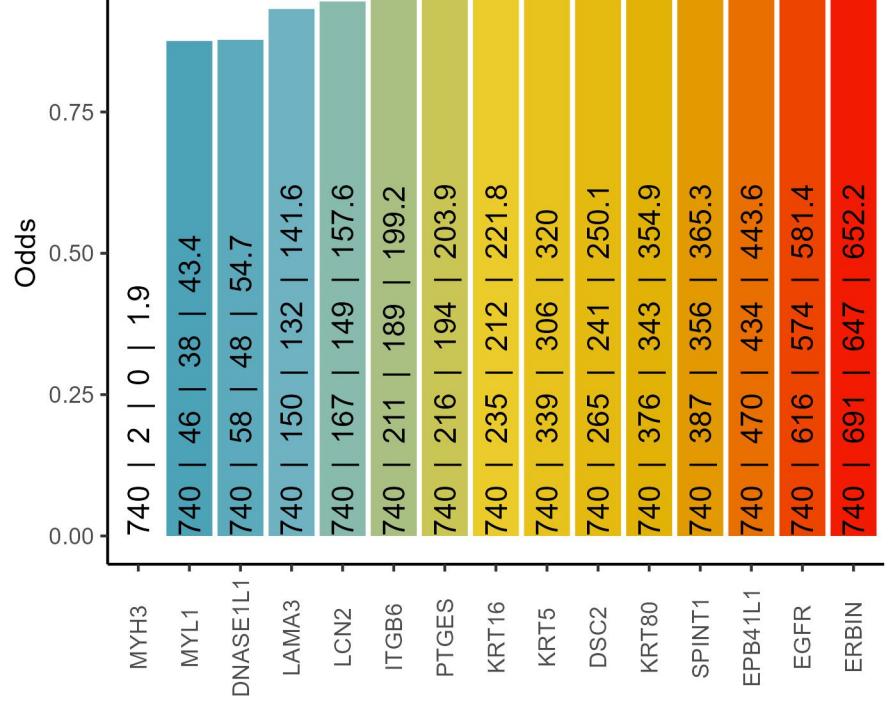
Positive cooccurrence



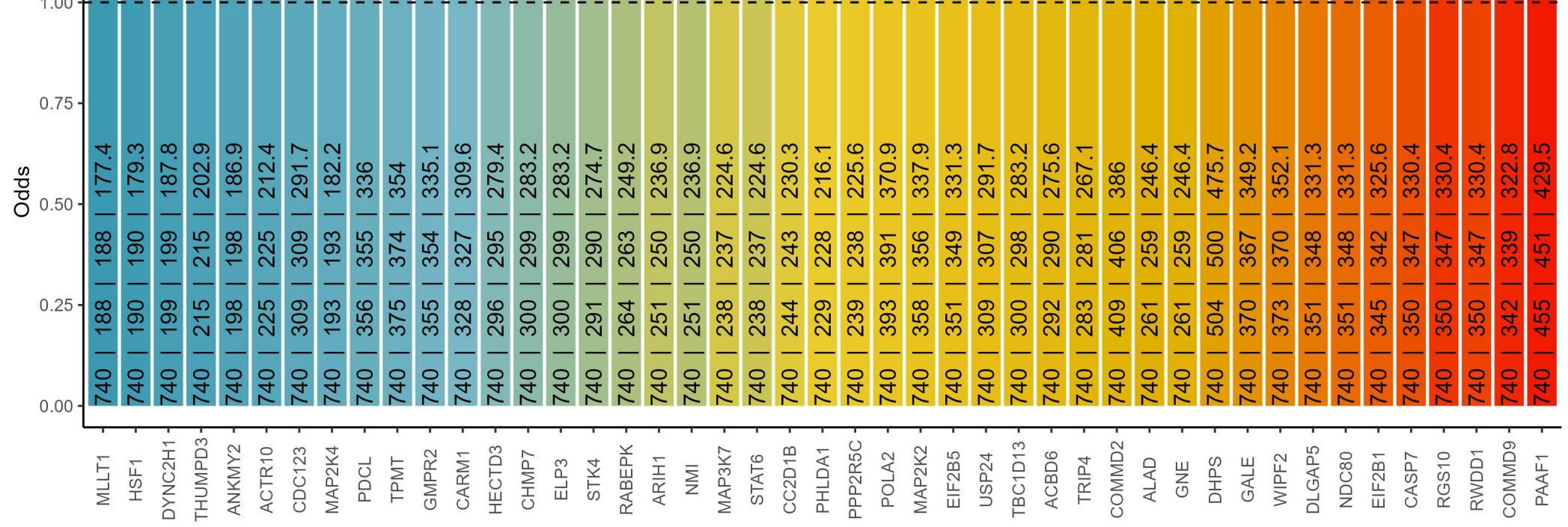
Cooccurrence with EEF1E1 protein in solid cancers, DB1

The text in the bars: incidence of EEF1E1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

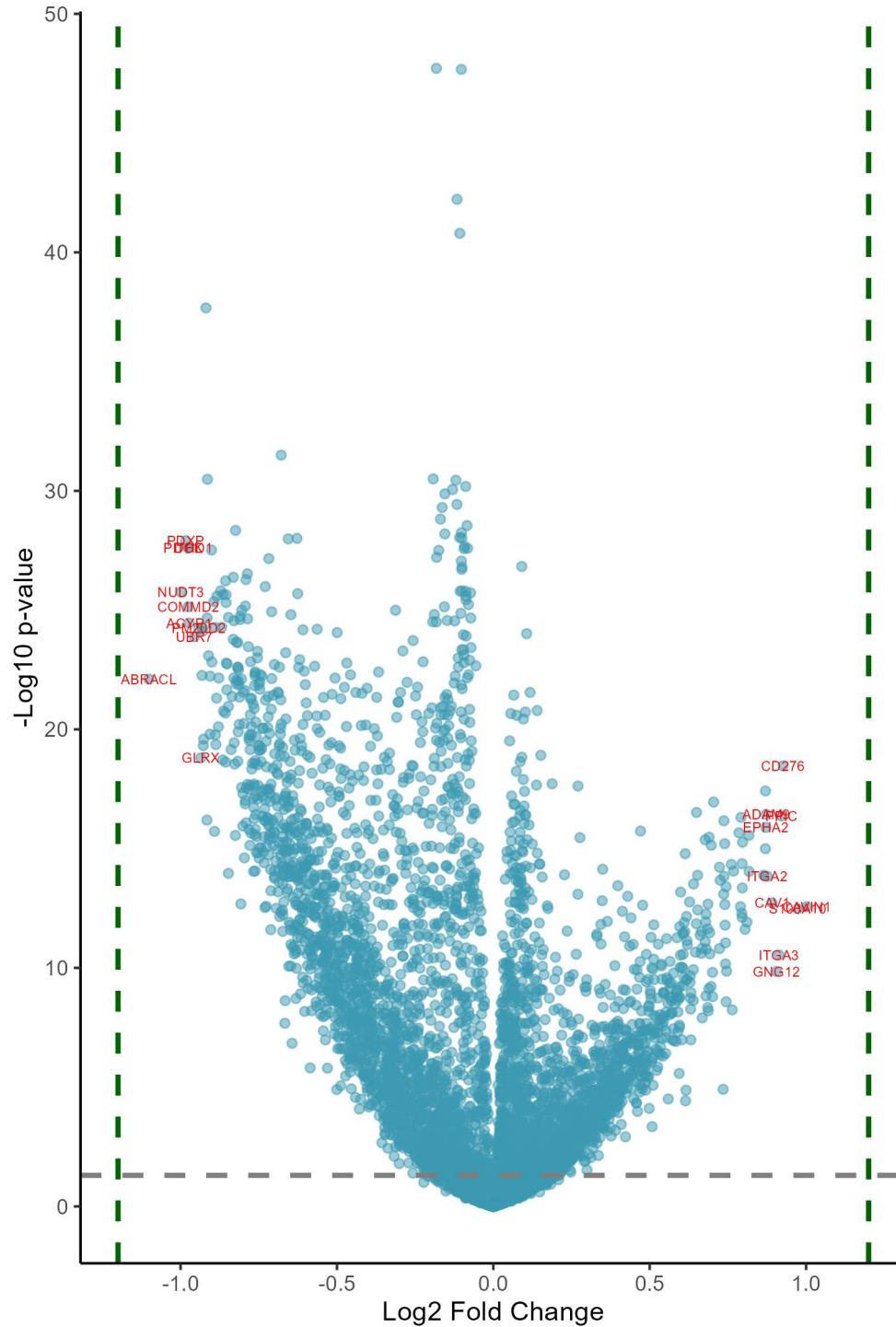
Negative cooccurrence



Positive cooccurrence



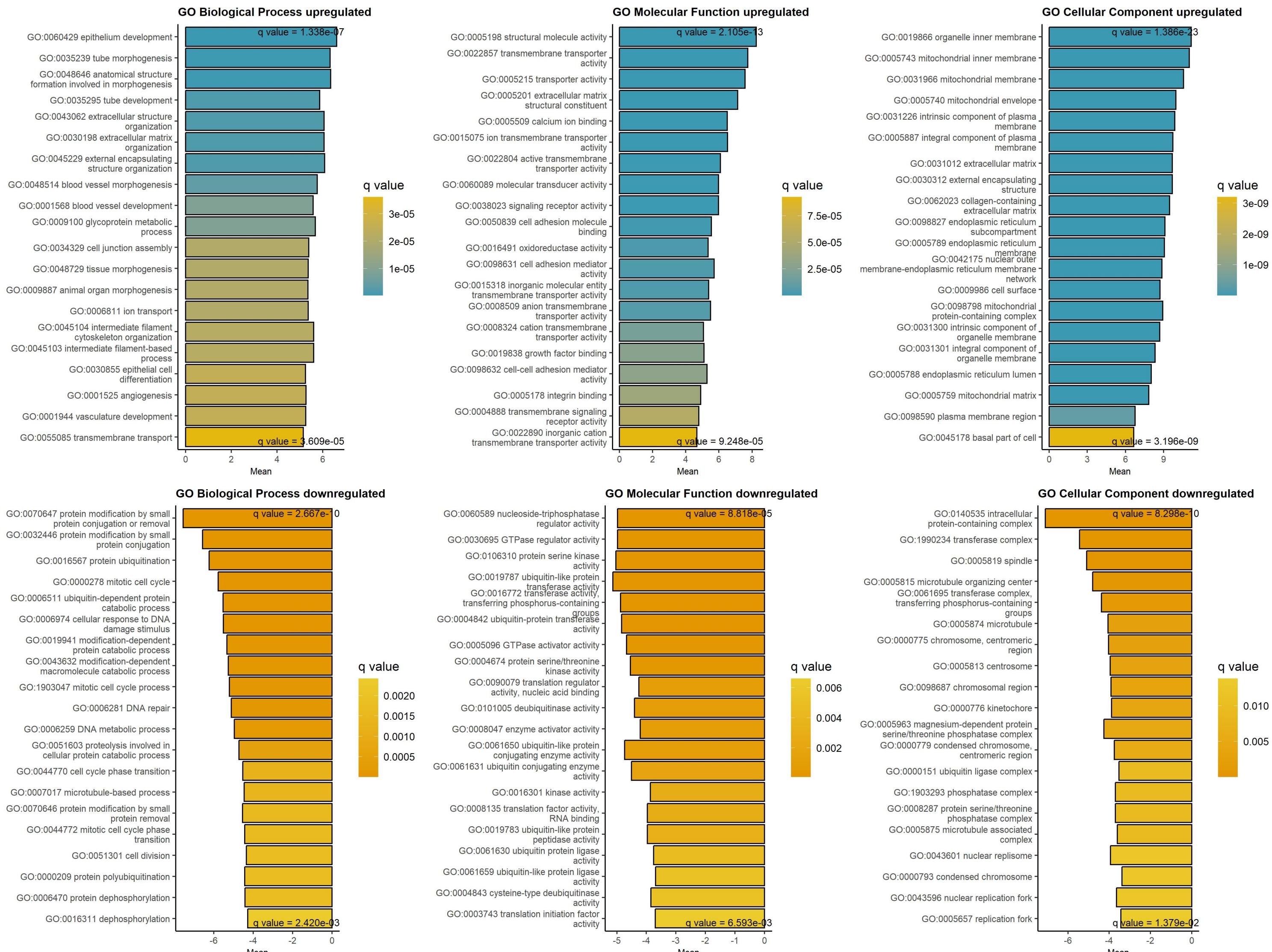
p-value < 0.05 & logFC > 1.2

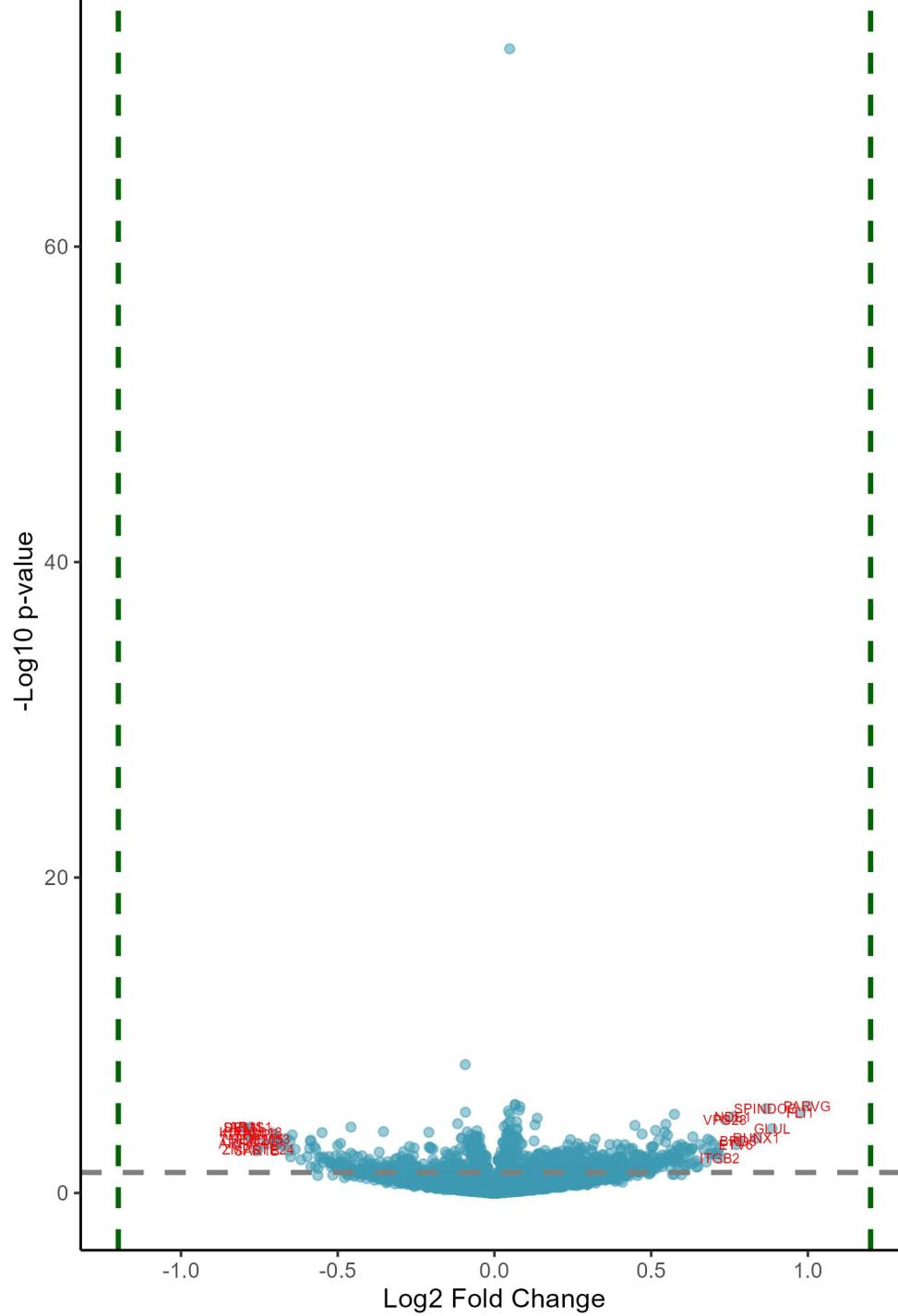


Downregulated at low/absent EEF1E1 Upregulated at low/absent EEF1E1

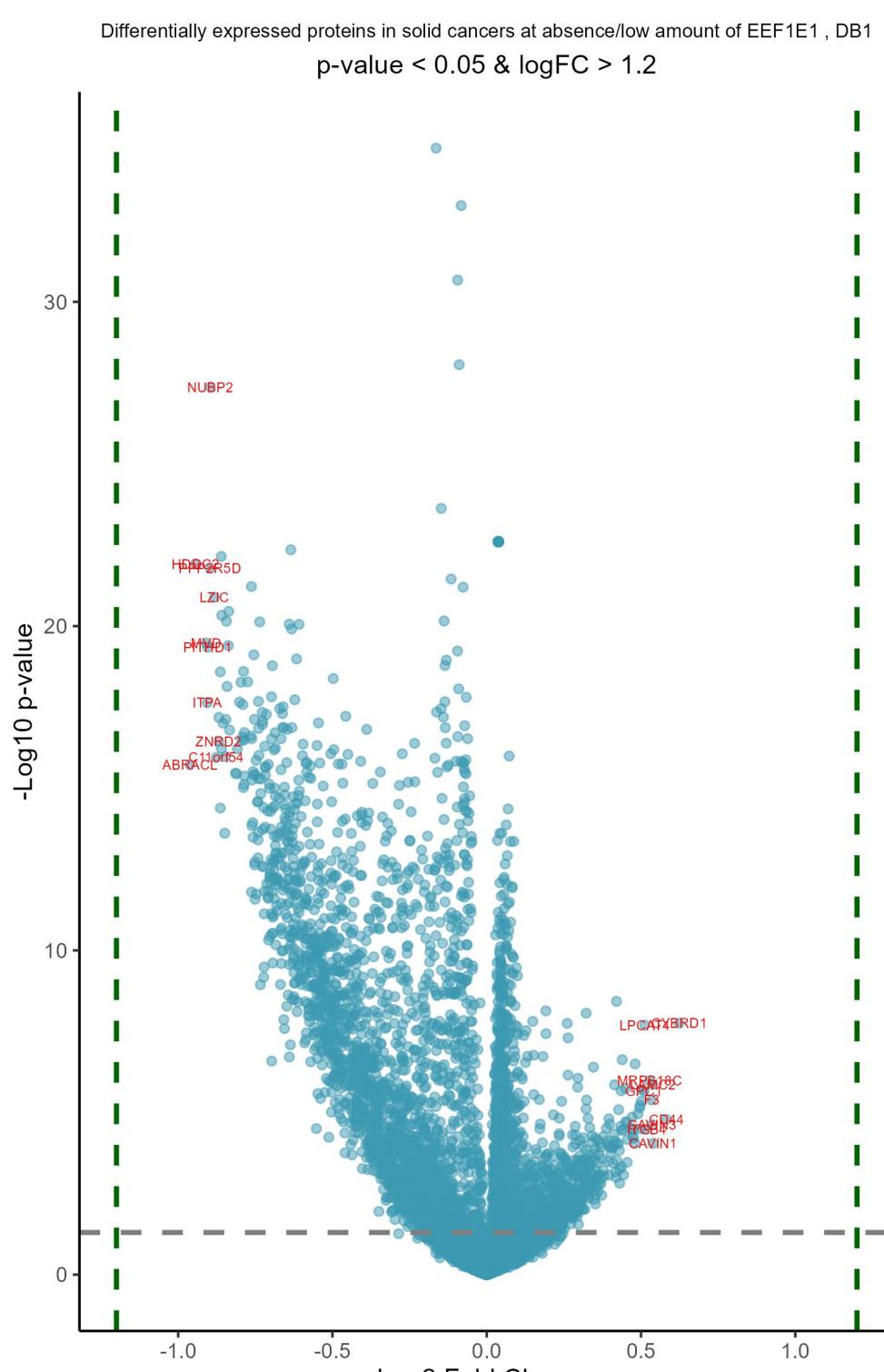
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.1	3.66e-21	ABRACL	ABRA C-terminal like	1	2.00e-12	CAVIN1	caveolae associated protein 1
-1	2.41e-24	NUDT3	nudix hydrolase 3	0.97	2.43e-12	S100A10	S100 calcium binding protein A10
-0.98	3.26e-26	PDXP	pyridoxal phosphatase	0.93	6.91e-18	CD276	CD276 molecule
-0.98	5.83e-26	PITHD1	PITH domain containing 1	0.92	6.04e-16	PPIC	peptidylprolyl isomerase C
-0.98	7.92e-24	COMMD2	COMM domain containing 2	0.91	1.61e-10	ITGA3	integrin subunit alpha 3
-0.97	5.83e-26	DCK	deoxycytidine kinase	0.9	7.22e-10	GNG12	G protein subunit gamma 12
-0.97	2.93e-23	ACYP1	acylphosphatase 1	0.89	1.43e-12	CAV1	caveolin 1
-0.96	9.52e-23	UBR7	ubiquitin protein ligase E3 compone	0.88	1.30e-13	ITGA2	integrin subunit alpha 2
-0.94	4.60e-23	PM20D2	peptidase M20 domain containing 2	0.87	5.22e-16	ADAM9	ADAM metallopeptidase domain 9
-0.94	3.43e-18	GLRX	glutaredoxin	0.87	1.68e-15	EPHA2	EPH receptor A2
-0.93	2.76e-21	PPP6R1	protein phosphatase 6 regulatory su	0.87	6.49e-17	GPC1	glycan 1
-0.93	4.32e-23	MVD	mevalonate diphosphate decarboxylas	0.87	1.12e-14	MMP14	matrix metallopeptidase 14
-0.93	5.93e-23	GRK2	G protein-coupled receptor kinase 2	0.86	1.18e-13	EGFR	epidermal growth factor receptor
-0.93	1.15e-18	GMDS	GDP-mannose 4,6-dehydratase	0.82	8.48e-14	GPX8	glutathione peroxidase 8 (putative)
-0.93	6.55e-19	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.82	3.36e-15	RRAS	RAS related
-0.92	2.36e-35	NUBP2	NUBP iron-sulfur cluster assembly f	0.81	8.28e-12	NT5E	5'-nucleotidase ecto
-0.92	8.66e-16	CORO1A	coronin 1A	0.8	1.56e-11	ITGB4	integrin subunit beta 4
-0.91	2.01e-23	HDDC2	HD domain containing 2	0.8	6.27e-15	CTNNB1	catenin beta 1
-0.91	2.39e-28	CASP3	caspase 3	0.8	3.70e-13	BCAM	basal cell adhesion molecule (Luthe
-0.91	5.24e-22	PRPSAP2	phosphoribosyl pyrophosphate synthetase	0.8	5.26e-12	CAVIN3	caveolae associated protein 3
-0.91	4.25e-19	C11orf54	chromosome 11 open reading frame 54	0.8	4.32e-14	CD109	CD109 molecule
-0.91	2.85e-21	ITPA	inosine triphosphatase	0.79	3.61e-12	DSG2	desmoglein 2
-0.9	6.47e-26	RNF114	ring finger protein 114	0.79	6.83e-16	ITGAV	integrin subunit alpha V
-0.9	9.01e-22	UBA5	ubiquitin like modifier activating	0.79	2.00e-12	ITGA6	integrin subunit alpha 6
-0.89	5.25e-24	LIG1	DNA ligase 1	0.79	2.67e-15	NECTIN2	nectin cell adhesion molecule 2
-0.89	2.38e-15	BLMH	bleomycin hydrolase	0.77	8.23e-14	FKBP9	FKBP prolyl isomerase 9
-0.89	4.32e-23	EIF2B1	eukaryotic translation initiation f	0.76	2.35e-08	CD44	CD44 molecule (Indian blood group)
-0.89	4.46e-19	DHFR	dihydrofolate reductase	0.76	4.57e-14	SDC4	syndecan 4
-0.89	1.05e-18	PRPS1	phosphoribosyl pyrophosphate synthetase	0.75	7.00e-10	GPRC5A	G protein-coupled receptor class C

GAGE analysis on upregulated and downregulated proteins at low/absent EEF1E1 protein, DB1



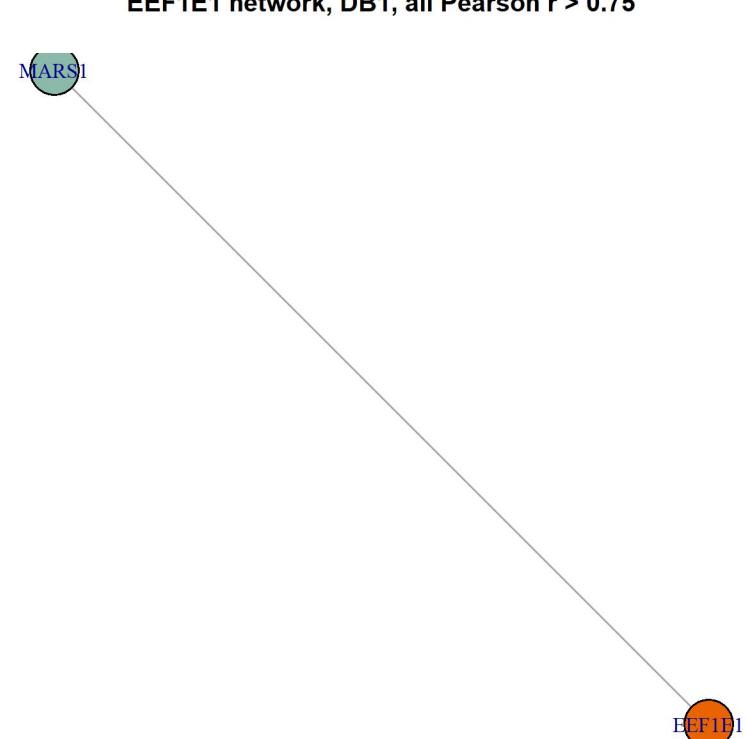


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.82	4.57e-02	ARF4	ADP ribosylation factor 4	1	3.19e-03	PARVG	parvin gamma
-0.8	1.63e-02	DPM1	dolichyl-phosphate mannosyltransfer	0.98	4.65e-03	FLI1	Fli-1 proto-oncogene, ETS transcrip
-0.8	1.67e-02	SEL1L	SEL1L adaptor subunit of ERAD E3 ub	0.89	1.77e-02	GLUL	glutamate-ammonia ligase
-0.78	1.63e-02	AP1S1	adaptor related protein complex 1 s	0.87	3.71e-03	SPINDOC	spindlin interactor and repressor o
-0.78	2.79e-02	GTPBP3	GTP binding protein 3, mitochondria	0.84	3.27e-02	RUNX1	RUNX family transcription factor 1
-0.78	2.35e-02	KIAA2013	KIAA2013	0.78	3.60e-02	BRD3	bromodomain containing 3
-0.77	3.29e-02	TMEM205	transmembrane protein 205	0.77	4.69e-02	ETV6	ETS variant transcription factor 6
-0.76	5.81e-02	SAR1B	secretion associated Ras related GT	0.76	6.65e-03	NDE1	nudE neurodevelopment protein 1
-0.75	5.81e-02	ZMPSTE24	zinc metallopeptidase STE24	0.74	8.83e-03	VPS28	VPS28 subunit of ESCRT-I
-0.74	3.29e-02	TMEM33	transmembrane protein 33	0.72	5.81e-02	ITGB2	integrin subunit beta 2
-0.73	4.69e-02	TRAPPC4	trafficking protein particle comple	0.72	5.81e-02	CELF2	CUGBP Elav-like family member 2
-0.7	3.29e-02	DNAJC10	DnaJ heat shock protein family (Hsp	0.71	5.81e-02	MPP1	MAGUK p55 scaffold protein 1
-0.7	2.60e-02	MGAT2	alpha-1,6-mannosyl-glycoprotein 2-b	0.71	5.81e-02	RCN1	reticulocalbin 1
-0.7	4.33e-02	ASNS	asparagine synthetase (glutamine-hy	0.7	4.65e-02	LANCL1	LanC like 1
-0.7	3.02e-02	CDC23	cell division cycle 23	0.7	5.81e-02	LYSMD2	LysM domain containing 2
-0.69	4.69e-02	CTH	cystathione gamma-lyase	0.69	5.81e-02	SASH3	SAM and SH3 domain containing 3
-0.68	4.57e-02	GYS1	glycogen synthase 1	0.69	3.57e-02	CMPK2	cytidine/uridine monophosphate kina
-0.67	5.27e-02	SEC11A	SEC11 homolog A, signal peptidase c	0.69	5.81e-02	ACSS1	acyl-CoA synthetase short chain fam
-0.66	3.27e-02	FASTKD5	FAST kinase domains 5	0.68	3.29e-02	CENPX	centromere protein X
-0.65	5.81e-02	PAK1IP1	PAK1 interacting protein 1	0.68	7.25e-02	ACTN1	actinin alpha 1
-0.65	3.57e-02	RSL24D1	ribosomal L24 domain containing 1	0.67	5.81e-02	UTRN	utrophin
-0.65	5.81e-02	FTL	ferritin light chain	0.66	4.69e-02	ARID1B	AT-rich interaction domain 1B
-0.65	2.79e-02	URB1	URB1 ribosome biogenesis homolog	0.65	1.21e-01	CAPG	capping actin protein, gelsolin lik
-0.64	5.81e-02	CSNK1A1	casein kinase 1 alpha 1	0.64	1.27e-01	ITGB5	integrin subunit beta 5
-0.62	5.81e-02	SYNGR2	synaptogyrin 2	0.64	6.15e-02	CLIP2	CAP-Gly domain containing linker pr
-0.6	5.81e-02	DAD1	defender against cell death 1	0.64	7.62e-02	PTPN6	protein tyrosine phosphatase non-re
-0.59	5.81e-02	RPF2	ribosome production factor 2 homolo	0.63	3.02e-02	GIT2	GIT ArfGAP 2
-0.59	3.62e-02	WDR75	WD repeat domain 75	0.63	5.81e-02	ARHGEF6	Rac/Cdc42 guanine nucleotide exchan
-0.59	3.45e-02	ITIH2	inter-alpha-trypsin inhibitor heavy	0.63	5.81e-02	CHMP3	charged multivesicular body protein

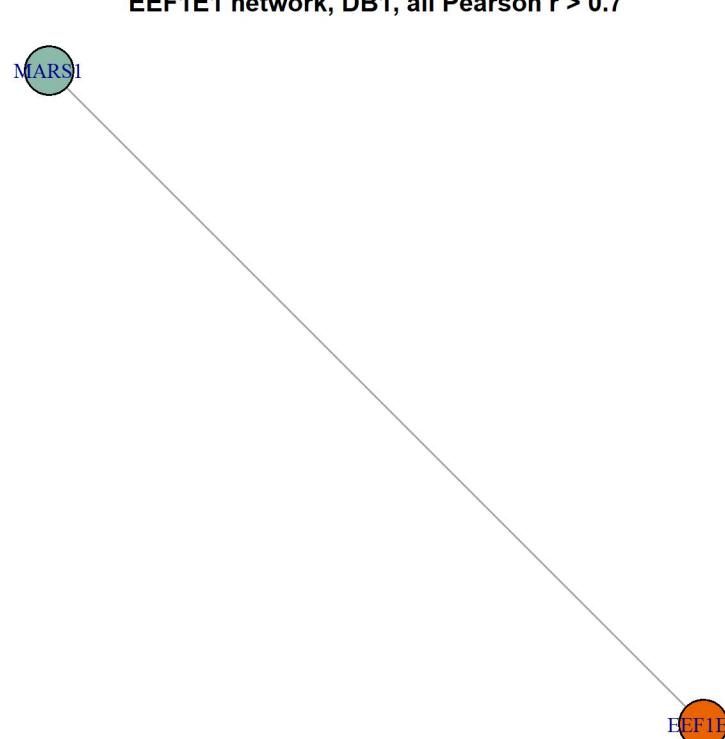


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.96	6.26e-15	ABRACL	ABRA C-terminal like	0.62	1.10e-07	CYBRD1	cytochrome b reductase 1
-0.94	9.01e-21	HDDC2	HD domain containing 2	0.58	6.06e-05	CD44	CD44 molecule (Indian blood group)
-0.91	2.12e-18	MVD	mevalonate diphosphate decarboxylas	0.54	2.92e-04	CAVIN1	caveolae associated protein 1
-0.91	1.21e-16	ITPA	inosine triphosphatase	0.54	6.14e-06	LAMC2	laminin subunit gamma 2
-0.91	2.80e-18	PITHD1	PITH domain containing 1	0.54	8.71e-05	CAVIN3	caveolae associated protein 3
-0.9	1.18e-20	PPP2R5D	protein phosphatase 2 regulatory su	0.53	1.69e-05	F3	coagulation factor III, tissue fact
-0.9	4.74e-25	NUBP2	NUBP iron-sulfur cluster assembly f	0.53	4.69e-06	MRPS18C	mitochondrial ribosomal protein S18
-0.88	9.04e-20	LZIC	leucine zipper and CTNNBIP1 domain	0.52	1.16e-04	ITGB4	integrin subunit beta 4
-0.88	4.10e-15	C11orf54	chromosome 11 open reading frame 54	0.51	1.25e-07	LPCAT4	lysophosphatidylcholine acyltransfe
-0.87	1.44e-15	ZNRD2	zinc ribbon domain containing 2	0.51	9.54e-06	GPC1	glycan 1
-0.87	3.17e-16	COMM2	COMM domain containing 2	0.5	8.45e-06	COL12A1	collagen type XII alpha 1 chain
-0.86	1.50e-17	PDXP	pyridoxal phosphatase	0.5	1.85e-05	CD109	CD109 molecule
-0.86	1.04e-13	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.5	1.13e-04	UQCRC10	ubiquinol-cytochrome c reductase, c
-0.86	5.29e-21	CASP3	caspase 3	0.5	2.41e-05	UXS1	UDP-glucuronate decarboxylase 1
-0.86	2.33e-15	UBR7	ubiquitin protein ligase E3 compone	0.5	2.82e-05	CD276	CD276 molecule
-0.86	3.19e-19	RNF114	ring finger protein 114	0.49	4.23e-05	BCAM	basal cell adhesion molecule (Luthe
-0.85	4.60e-16	NUDT3	nudix hydrolase 3	0.48	1.58e-06	LAMA3	laminin subunit alpha 3
-0.85	5.26e-13	GMDS	GDP-mannose 4,6-dehydratase	0.48	2.92e-04	SDC1	syndecan 1
-0.85	3.88e-15	ACYP1	acylphosphatase 1	0.48	2.07e-04	AXL	AXL receptor tyrosine kinase
-0.85	3.61e-16	TPMT	thiopurine S-methyltransferase	0.48	1.20e-04	DERL1	derlin 1
-0.84	4.74e-19	NT5DC1	5'-nucleotidase domain containing 1	0.47	1.84e-04	MMP14	matrix metallopeptidase 14
-0.84	4.10e-17	TKFC	trioquinase and FMN cyclase	0.47	5.26e-05	MFGE8	milk fat globule EGF and factor V/V
-0.84	2.52e-18	AARSD1	alanyl-tRNA synthetase domain conta	0.47	1.11e-04	S100A10	S100 calcium binding protein A10
-0.84	2.43e-19	TBCC	tubulin folding cofactor C	0.46	2.27e-04	KRT6A	keratin 6A
-0.83	7.00e-16	CFDP1	craniofacial development protein 1	0.46	9.96e-04	CAV1	caveolin 1
-0.81	1.08e-14	PDCL3	phosducin like 3	0.45	7.31e-05	PPIC	peptidylprolyl isomerase C
-0.81	1.12e-14	PPM1A	protein phosphatase, Mg2+/Mn2+ depe	0.45	7.14e-05	KRT16	keratin 16
-0.81	2.35e-15	VPS25	vacuolar protein sorting 25 homolog	0.45	7.90e-06	ALDH3B1	aldehyde dehydrogenase 3 family mem
-0.8	1.18e-16	ADI1	acireductone dioxygenase 1	0.44	2.25e-03	GPRC5A	G protein-coupled receptor class C

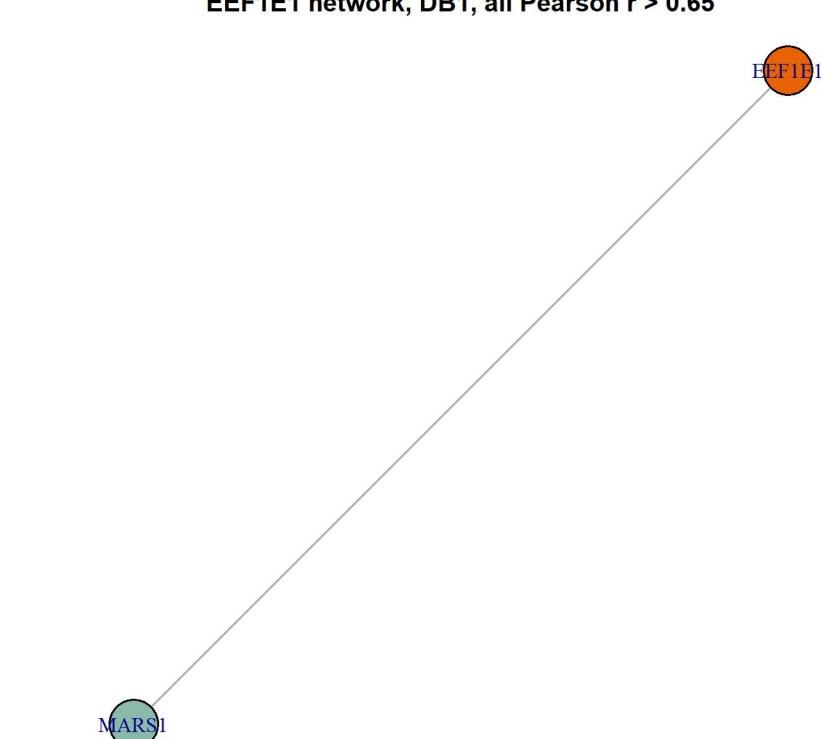
EEF1E1 network, DB1, all Pearson r > 0.75

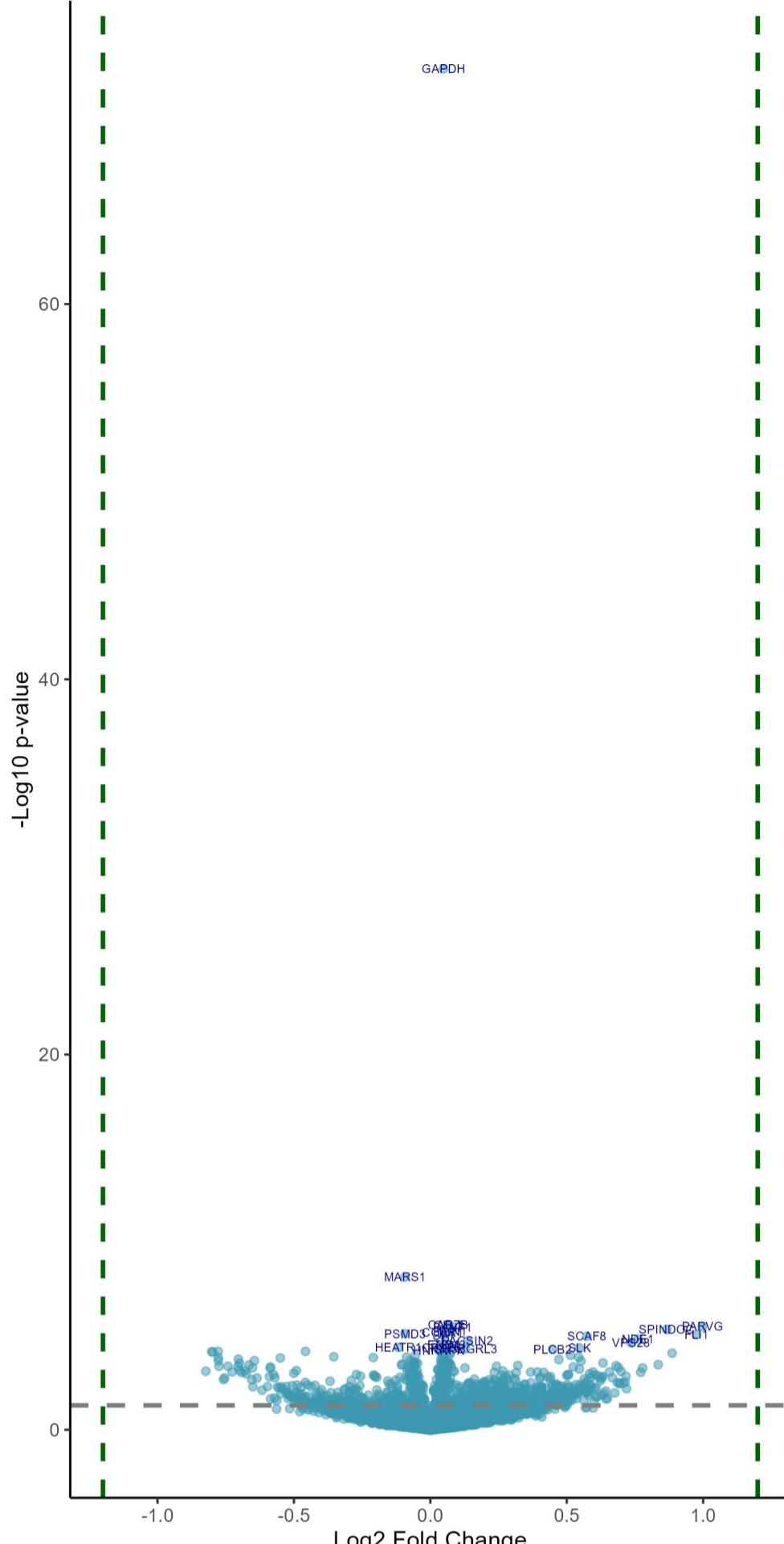


EEF1E1 network, DB1, all Pearson r > 0.7



EEF1E1 network, DB1, all Pearson r > 0.65

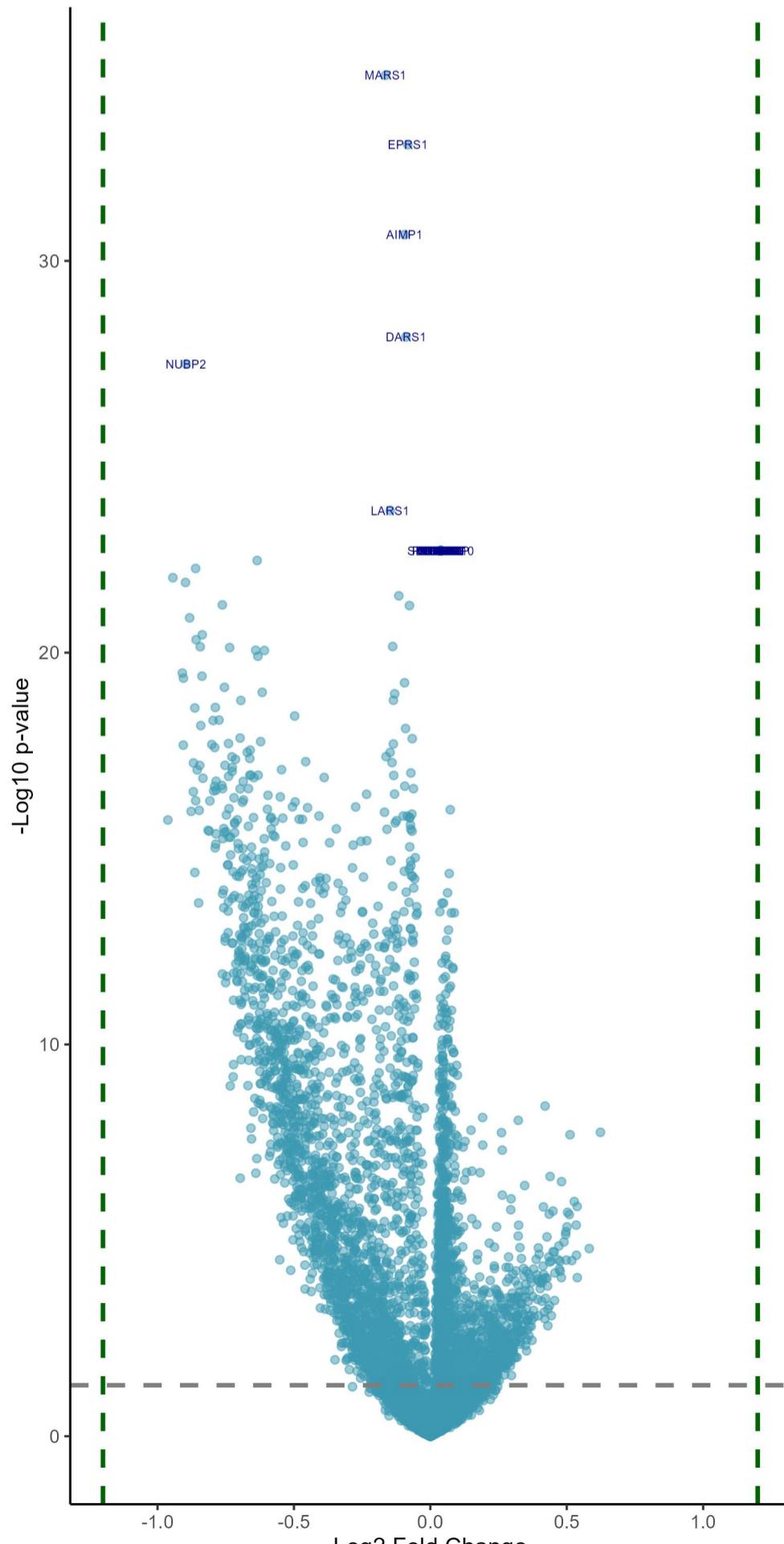




Sorted by p values!

Downregulated in blood cancers at low/absent EEF1E1 Upregulated in blood cancers at low/absent EEF1E1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.09	1.60e-05	MARS1	methionyl-tRNA synthetase 1	0.05	1.91e-69	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
-0.09	4.58e-03	PSMD3	proteasome 26S subunit, non-ATPase	0.07	3.19e-03	CAPZB	capping actin protein of muscle Z-line
-0.12	1.33e-02	HEATR1	HEAT repeat containing 1	0.07	3.19e-03	CFL1	cofilin 1
-0.78	1.63e-02	AP1S1	adaptor related protein complex 1 subunit	1	3.19e-03	PARVG	parvin gamma
-0.46	1.63e-02	ANKRD22	ankyrin repeat domain 22	0.08	3.19e-03	BANF1	BAF nuclear assembly factor 1
-0.8	1.63e-02	DPM1	dolichyl-phosphate mannose transferase	0.87	3.71e-03	SPINDOC	spindlin interactor and repressor of
-0.8	1.67e-02	SEL1L	SEL1L adaptor subunit of ERAD E3 ubiquitin ligase	0.08	4.14e-03	TLN1	talin 1
-0.06	2.15e-02	COPB2	COP1 coat complex subunit beta 2	0.04	4.16e-03	CCAR1	cell division cycle and apoptosis regulator
-0.35	2.30e-02	TMEM167A	transmembrane protein 167A	0.98	4.65e-03	FLI1	Fli-1 proto-oncogene, ETS transcription factor
-0.09	2.31e-02	GCN1	GCN1 activator of EIF2AK4	0.05	4.87e-03	SF1	splicing factor 1
-0.21	2.34e-02	NOL6	nucleolar protein 6	0.57	4.87e-03	SCAF8	SR-related CTD associated factor 8
-0.78	2.35e-02	KIAA2013	KIAA2013	0.76	6.65e-03	NDE1	nudE neurodevelopment protein 1
-0.55	2.35e-02	CDC16	cell division cycle 16	0.14	7.52e-03	PACSIN2	protein kinase C and casein kinase
-0.7	2.60e-02	MGAT2	alpha-1,6-mannosyl-glycoprotein 2-beta-1,6-N-acetylglucosaminyltransferase	0.74	8.83e-03	VPS28	VPS28 subunit of ESCRT-I
-0.07	2.79e-02	ABCE1	ATP binding cassette subfamily E member	0.05	1.05e-02	ENO1	enolase 1
-0.78	2.79e-02	GTPBP3	GTP binding protein 3, mitochondria	0.07	1.05e-02	TPM3	tropomyosin 3
-0.65	2.79e-02	URB1	URB1 ribosome biogenesis homolog	0.04	1.33e-02	CPSF6	cleavage and polyadenylation specific
-0.06	2.89e-02	PSMD6	proteasome 26S subunit, non-ATPase	0.55	1.33e-02	SLK	STE20 like kinase
-0.06	3.02e-02	QARS1	glutaminyl-tRNA synthetase 1	0.13	1.39e-02	SH3BGRL3	SH3 domain binding glutamate rich protein
-0.05	3.02e-02	EIF3B	eukaryotic translation initiation factor 3 subunit B	0.45	1.44e-02	PLCB2	phospholipase C beta 2
-0.7	3.02e-02	CDC23	cell division cycle 23	0.03	1.60e-02	HNRNPK	heterogeneous nuclear ribonucleoprotein
-0.05	3.02e-02	PSMD8	proteasome 26S subunit, non-ATPase	0.89	1.77e-02	GLUL	glutamate-ammonia ligase
-0.06	3.05e-02	TIMM44	translocase of inner mitochondrial membrane	0.07	1.77e-02	MYL6	myosin light chain 6
-0.1	3.19e-02	PPAT	phosphoribosyl pyrophosphate amidotransferase	0.07	2.09e-02	CAPZA1	capping actin protein of muscle Z-line
-0.66	3.27e-02	FASTKD5	FAST kinase domains 5	0.05	2.09e-02	SNRPF	small nuclear ribonucleoprotein polypeptide
-0.11	3.27e-02	RPL13A	ribosomal protein L13a	0.51	2.09e-02	WASF2	WASP family member 2
-0.06	3.29e-02	COPB1	COP1 coat complex subunit beta 1	0.05	2.15e-02	ZNF207	zinc finger protein 207
-0.7	3.29e-02	DNAJC10	DnaJ heat shock protein family (Hsp40) member	0.54	2.31e-02	INPP5D	inositol polyphosphate-5-phosphatase
-0.08	3.29e-02	MYBBP1A	MYB binding protein 1a	0.04	2.43e-02	SF3B2	splicing factor 3b subunit 2
-0.77	3.29e-02	TMEM205	transmembrane protein 205	0.47	2.68e-02	PAPOLA	poly(A) polymerase alpha
-0.74	3.29e-02	TMEM33	transmembrane protein 33	0.05	2.73e-02	PHF5A	PHD finger protein 5A
-0.59	3.45e-02	ITIH2	inter-alpha-trypsin inhibitor heavy chain 2	0.05	2.79e-02	YWHAZ	tyrosine 3-monooxygenase/tryptophan oxygenase
-0.08	3.55e-02	UTP4	UTP4 small subunit processome component	0.55	2.80e-02	C17orf49	chromosome 17 open reading frame 49
-0.07	3.57e-02	LONP1	lon peptidase 1, mitochondrial	0.04	2.80e-02	NONO	non-POU domain containing octamer binding protein
-0.65	3.57e-02	RSL24D1	ribosomal L24 domain containing 1	0.06	2.82e-02	RAD23B	RAD23 homolog B, nucleotide excising enzyme
-0.59	3.62e-02	WDR75	WD repeat domain 75	0.05	2.82e-02	PCBP1	poly(rC) binding protein 1
-0.06	3.87e-02	RPL3	ribosomal protein L3	0.06	3.02e-02	SMC3	structural maintenance of chromosomes 3
-0.7	4.33e-02	ASNS	asparagine synthetase (glutamine-hydrolysing)	0.63	3.02e-02	GIT2	GIT ArfGAP 2
0.05	4.51e-02	DAD51	arginyl tRNA synthetase 1	0.07	3.02e-02	E11S	E11S DNA binding protein

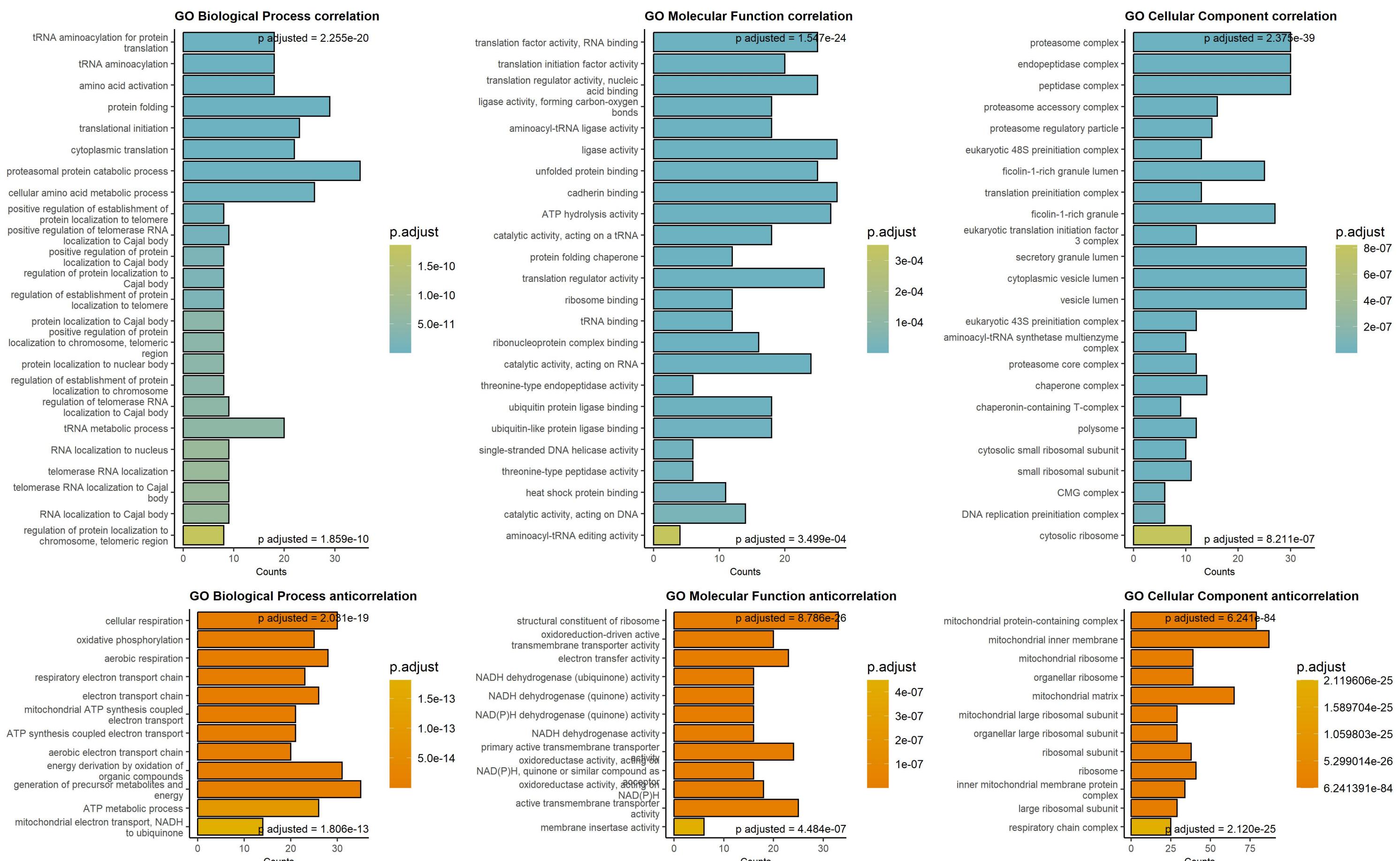


Sorted by p values!

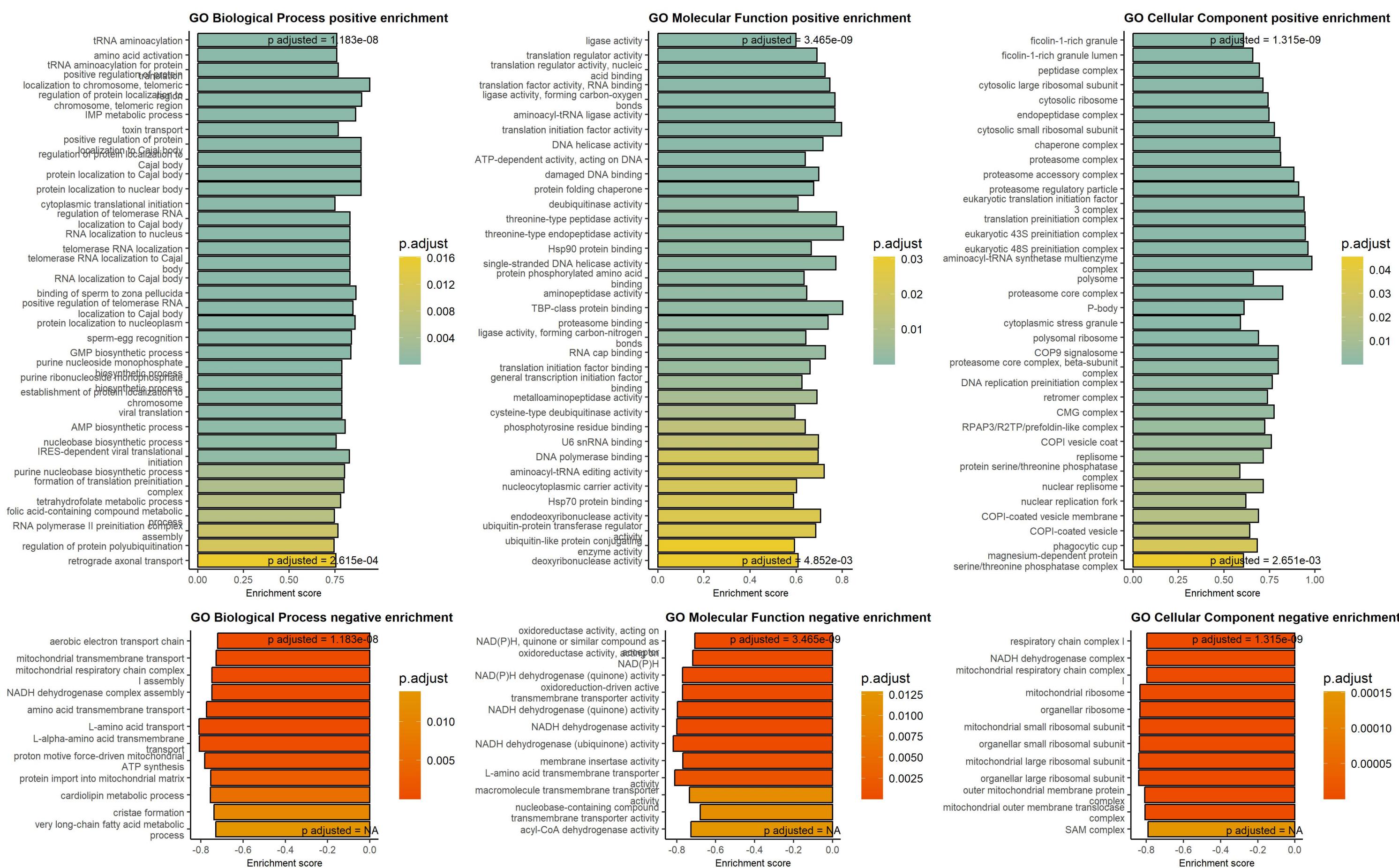
Downregulated in solid cancers at low/absent EEF1E1 Upregulated in solid cancers at low/absent EEF1E1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.16	6.07e-32	MARS1	methionyl-tRNA synthetase 1	0.04	1.91e-21	PTPRCAP	protein tyrosine phosphatase receptor type C
-0.08	2.39e-30	EPSS1	glutamyl-prolyl-tRNA synthetase 1	0.04	1.91e-21	HBE1	hemoglobin subunit epsilon 1
-0.09	3.55e-28	AIM1P1	aminoacyl tRNA synthetase complex I	0.04	1.91e-21	SERPINB10	serpin family B member 10
-0.09	1.16e-25	DARS1	aspartyl-tRNA synthetase 1	0.04	1.91e-21	IGLL1	immunoglobulin lambda like polypeptide 1
-0.9	4.74e-25	NUBP2	NUBP iron-sulfur cluster assembly f	0.04	1.91e-21	CRYBB1	crystallin beta B1
-0.15	1.91e-21	LARS1	leucyl-tRNA synthetase 1	0.04	1.91e-21	ITGA2B	integrin subunit alpha 2b
-0.63	3.35e-21	AASDHPPPT	amino adipate-semialdehyde dehydrogenase	0.04	1.91e-21	ACAP1	ArfGAP with coiled-coil, ankyrin repeat and PH-like domains
-0.86	5.29e-21	CASP3	caspase 3	0.04	1.91e-21	NCF4	neutrophil cytosolic factor 4
-0.94	9.01e-21	HDDC2	HD domain containing 2	0.04	1.91e-21	SP140	SP140 nuclear body protein
-0.9	1.18e-20	PPP2R5D	protein phosphatase 2 regulatory subunit B	0.04	1.91e-21	PSTPIP1	proline-serine-threonine phosphatase
-0.12	2.56e-20	IARS1	isoleucyl-tRNA synthetase 1	0.04	1.91e-21	STAB1	stabin 1
-0.76	4.30e-20	PFDN4	prefoldin subunit 4	0.04	1.91e-21	SEPLIG	selectin P ligand
-0.08	4.44e-20	RARS1	arginyl-tRNA synthetase 1	0.04	1.91e-21	RCSD1	RCSD domain containing 1
-0.88	9.04e-20	LZIC	leucine zipper and CTNNBIP1 domain	0.04	1.91e-21	STAT5A	signal transducer and activator of transcription 5A
-0.84	2.43e-19	TBCC	tubulin folding cofactor C	0.04	1.91e-21	CTSW	cathepsin W
-0.86	3.19e-19	RNF114	ring finger protein 114	0.04	1.91e-21	GIMAP6	GTPase, IMAP family member 6
-0.14	4.72e-19	AIMP2	aminoacyl tRNA synthetase complex I	0.04	1.91e-21	GZMB	granzyme B
-0.84	4.74e-19	NT5DC1	5'-nucleotidase domain containing 1	0.04	1.91e-21	HK3	hexokinase 3
-0.74	4.93e-19	RANBP9	RAN binding protein 9	0.04	1.91e-21	TUBA8	tubulin alpha 8
-0.64	5.72e-19	PPP5C	protein phosphatase 5 catalytic subunit	0.04	1.91e-21	CR2	complement C3d receptor 2
-0.61	5.74e-19	AKR7A2	aldo-keto reductase family 7 member	0.04	1.91e-21	POU2F2	POU class 2 homeobox 2
-0.63	7.95e-19	GNL1	G protein nucleolar 1 (putative)	0.04	1.91e-21	AZU1	azurocidin 1
-0.91	2.12e-18	MVD	mevalonate diphosphate decarboxylase	0.04	1.91e-21	CD48	CD48 molecule
-0.84	2.52e-18	AARSD1	alanyl-tRNA synthetase domain containing 1	0.04	1.91e-21	SKAP2	src kinase associated phosphoprotein
-0.91	2.80e-18	PITHD1	PITH domain containing 1	0.04	1.91e-21	CCL17	C-C motif chemokine ligand

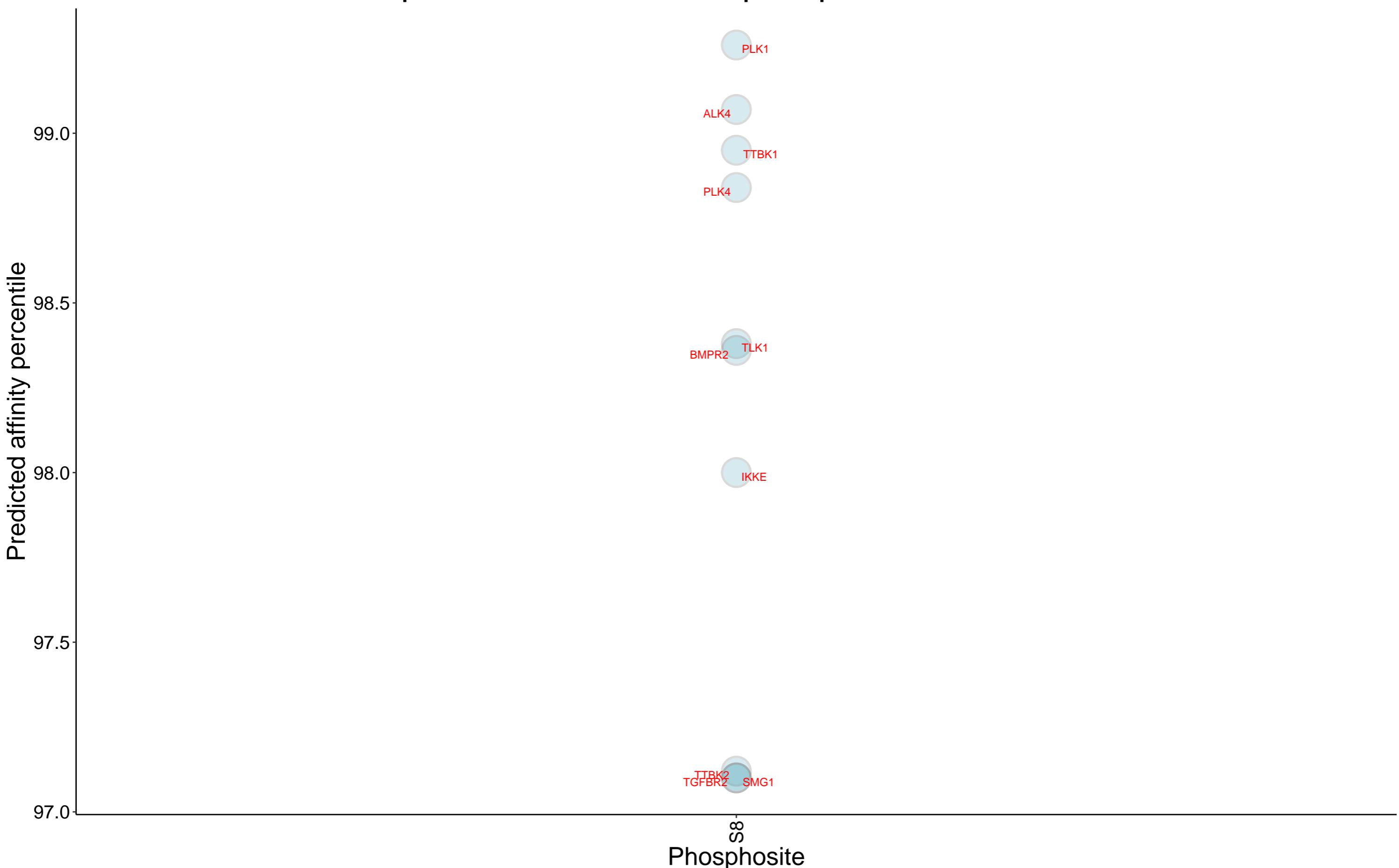
Top 250 correlation coefficients overrepresentation, EEF1E1 protein, DB1



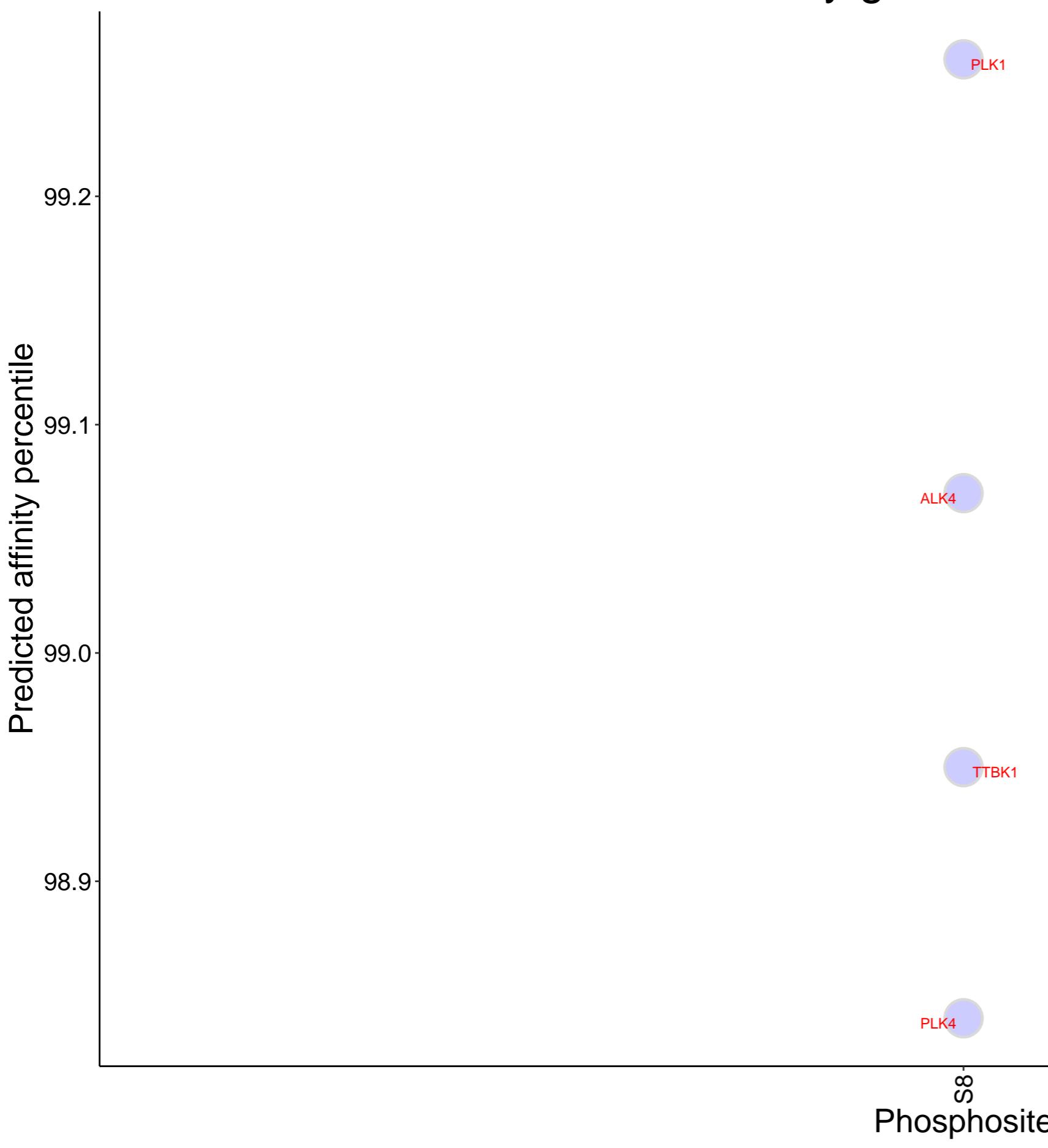
Gene Set Enrichment analysis on protein correlation coefficients, EEF1E1 protein, DB1



Top 10 kinases for each phosphosite in EEF1E1



Kinases with affinity greater than 98.5% to EEF1E1



Top 15 positive correlation coefficients for EEF1E1 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

