

# EIF2AK4

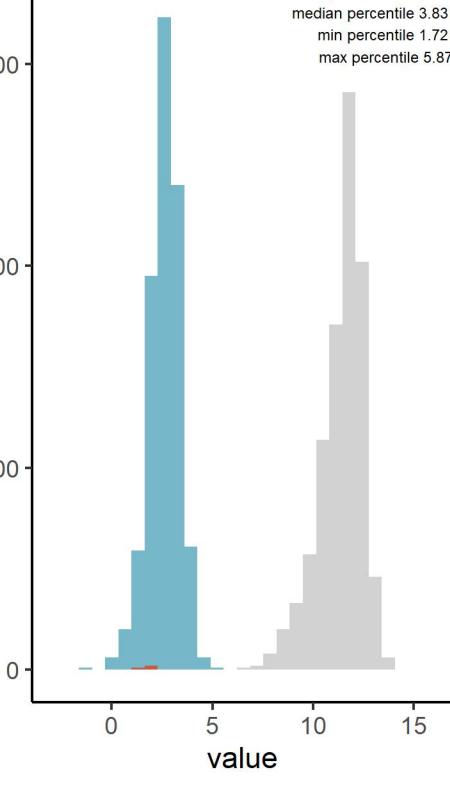
Protein name: E2AK4 ; UNIPROT: Q9P2K8 ; Gene name: eukaryotic translation initiation factor 2 alpha kinase 4

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

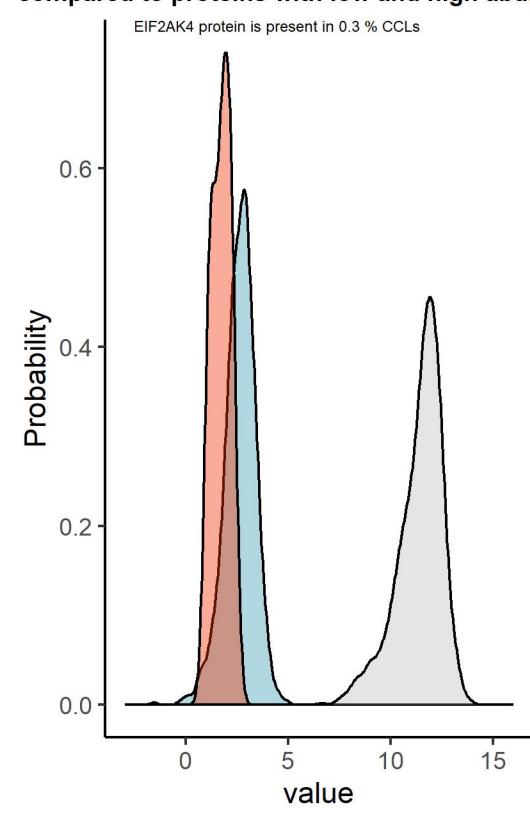
## Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

Histogram of EIF2AK4 protein compared to proteins with low and high abundance



Density plot of EIF2AK4 protein compared to proteins with low and high abundance



Top negative correlations of EIF2AK4 protein, DB1

Pearson correlation coefficients

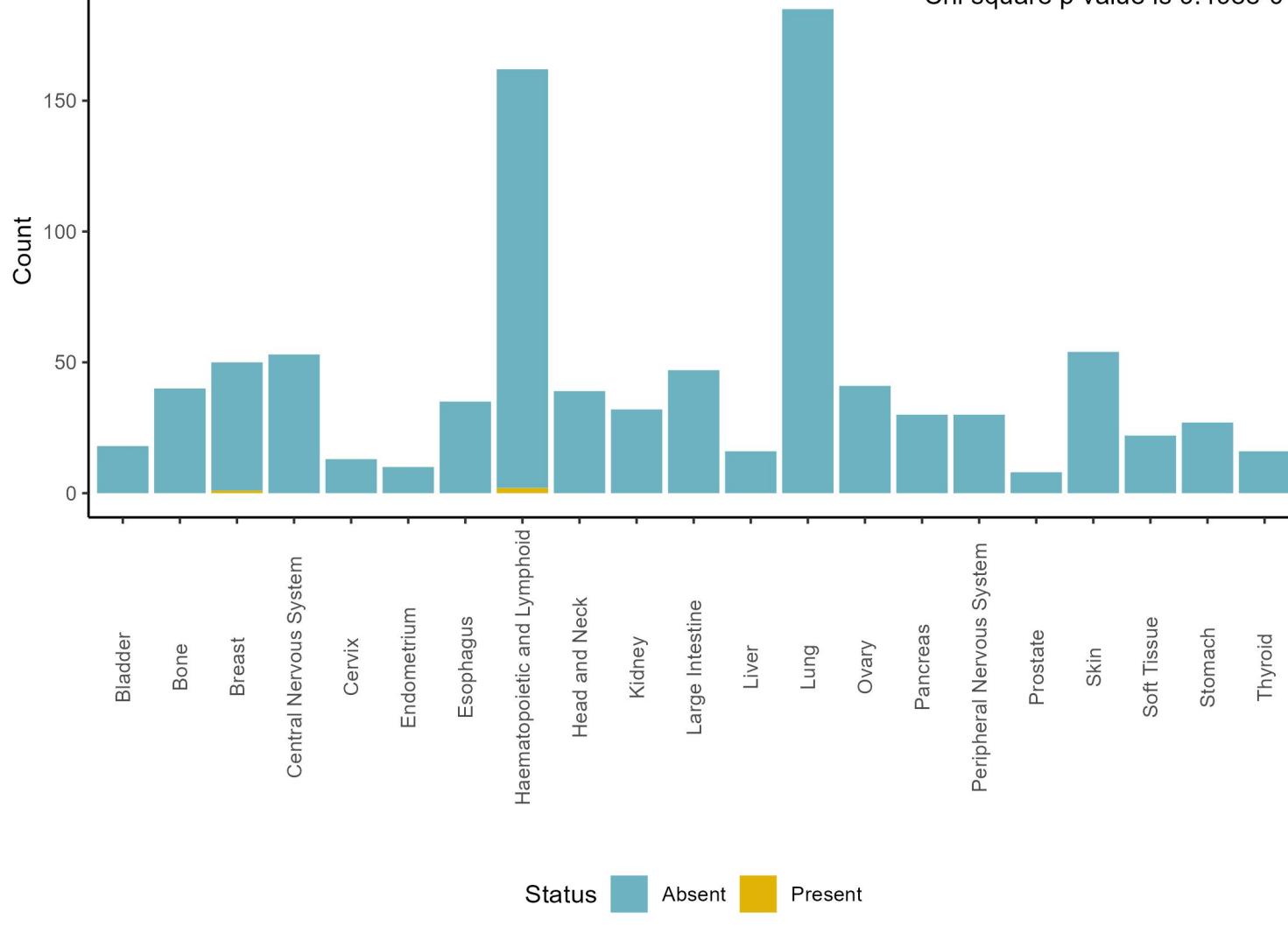
Top positive correlations of EIF2AK4 protein, DB1

Pearson correlation coefficients

Amount of EIF2AK4 protein, number of CCLs where it is present by tissue, DB1

Present and absent EIF2AK4 protein counts by tissue, DB1

Chi square p value is 9.498e-01

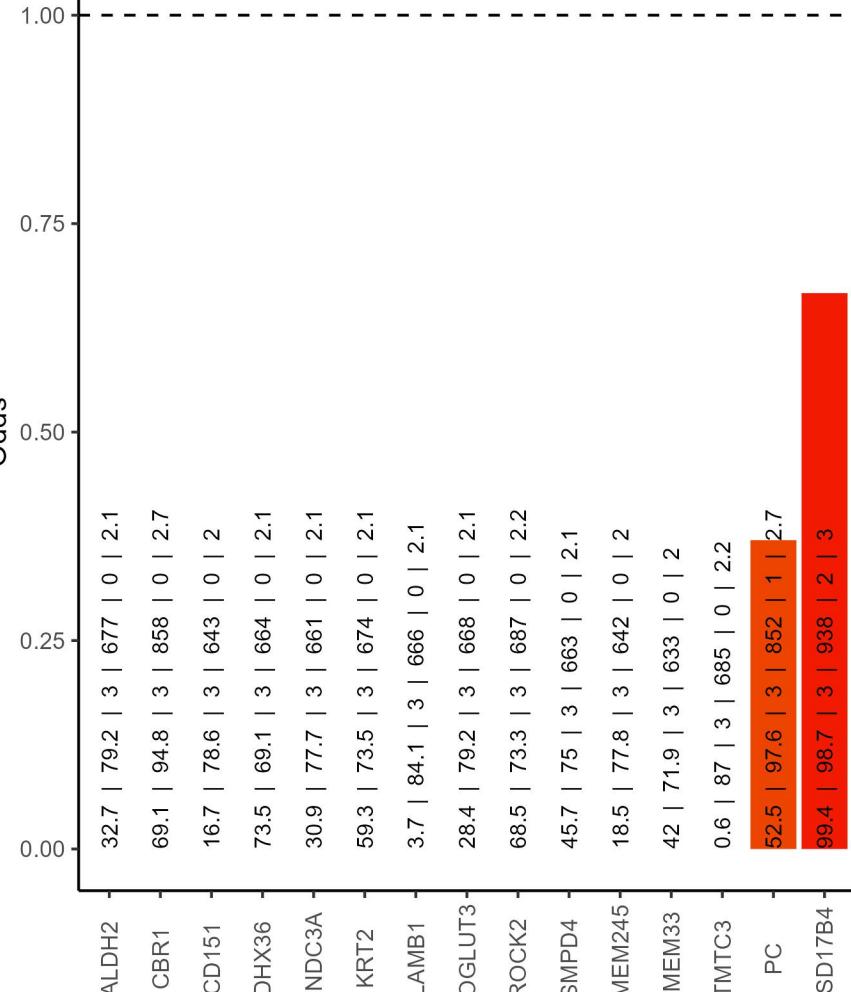


## Cooccurrence with EIF2AK4 protein, DB1

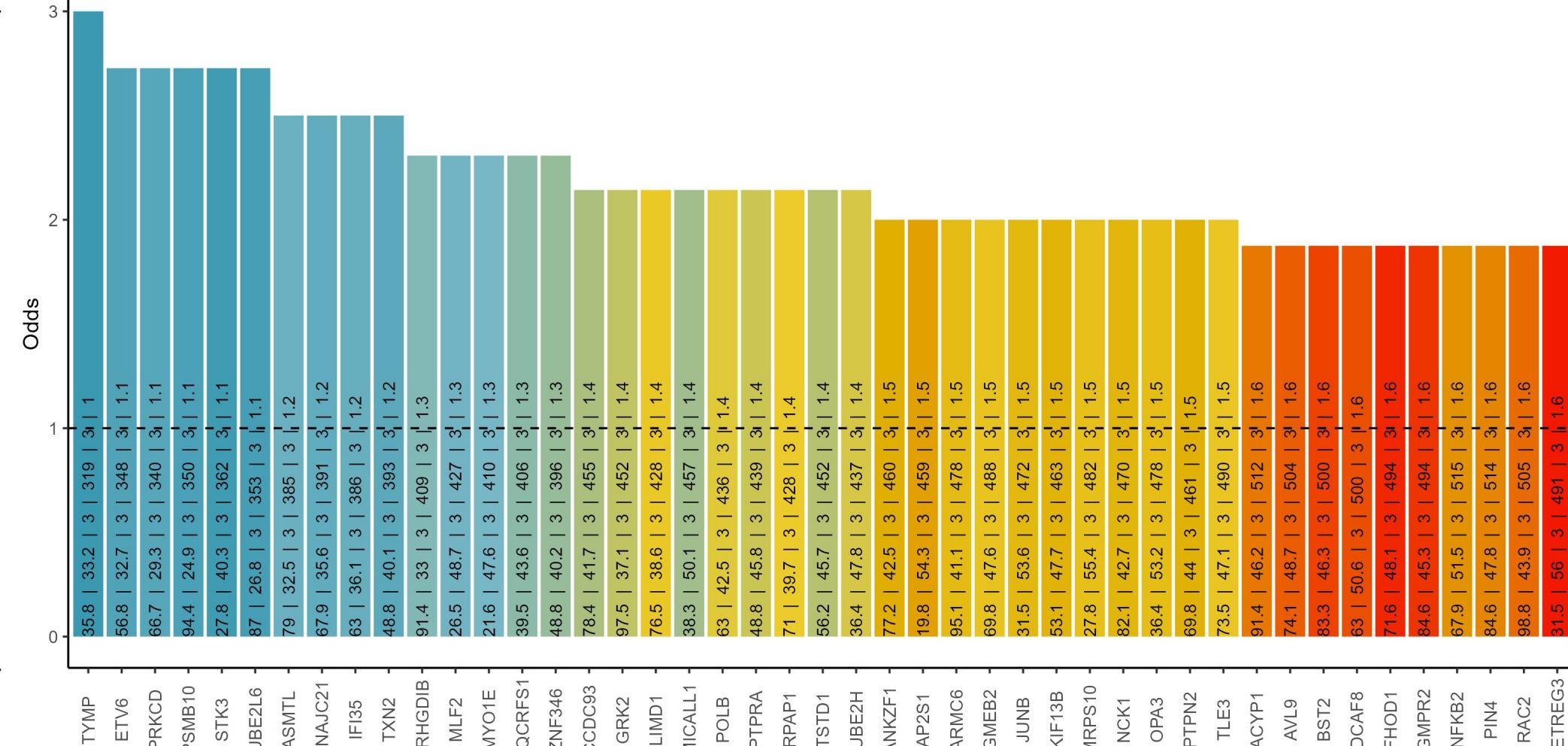
% of EIF2AK4 in blood cancers: 1.2 ; % of EIF2AK4 in solid cancers: 0.1

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of EIF2AK4 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

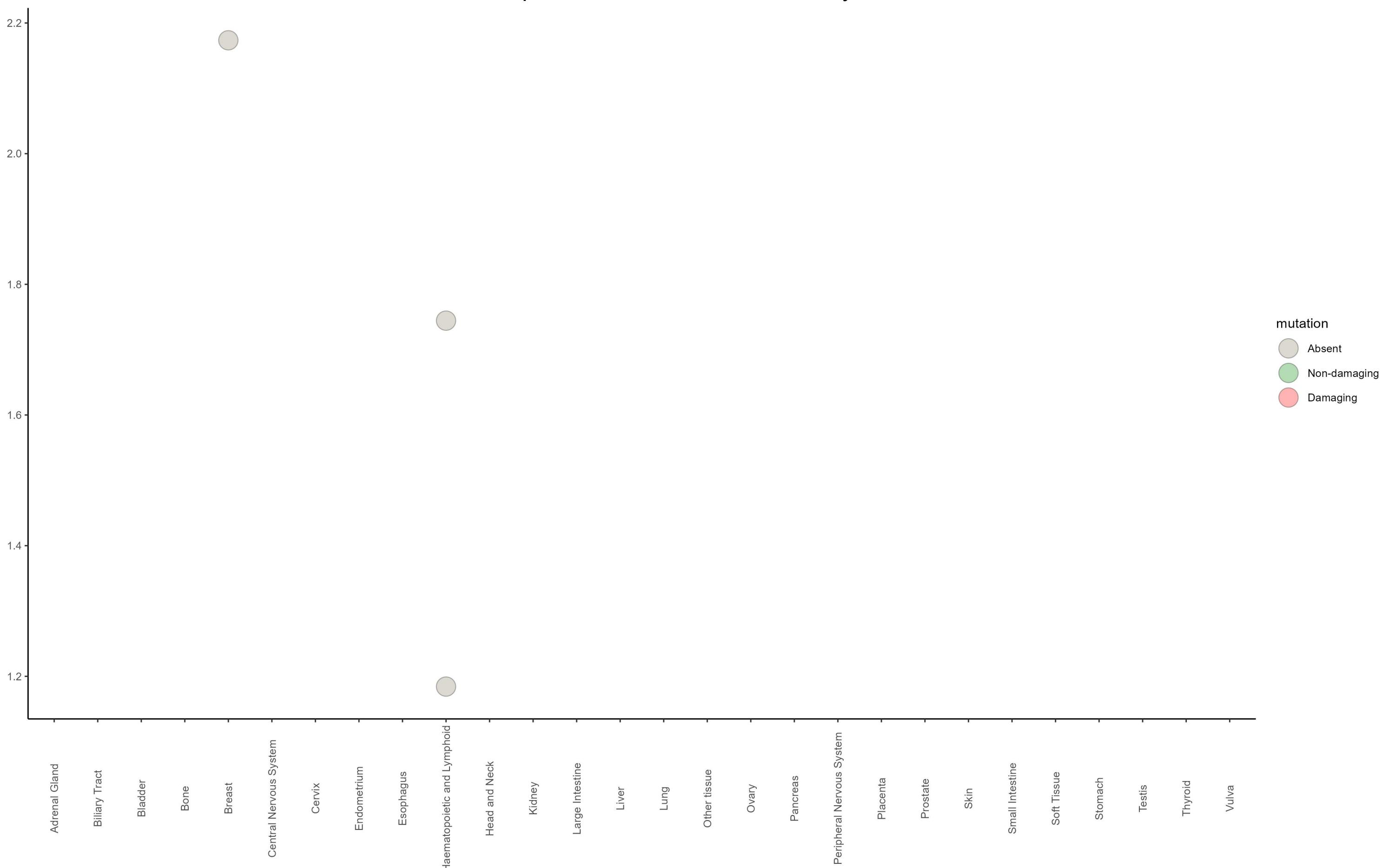
Negative cooccurrence



Positive cooccurrence

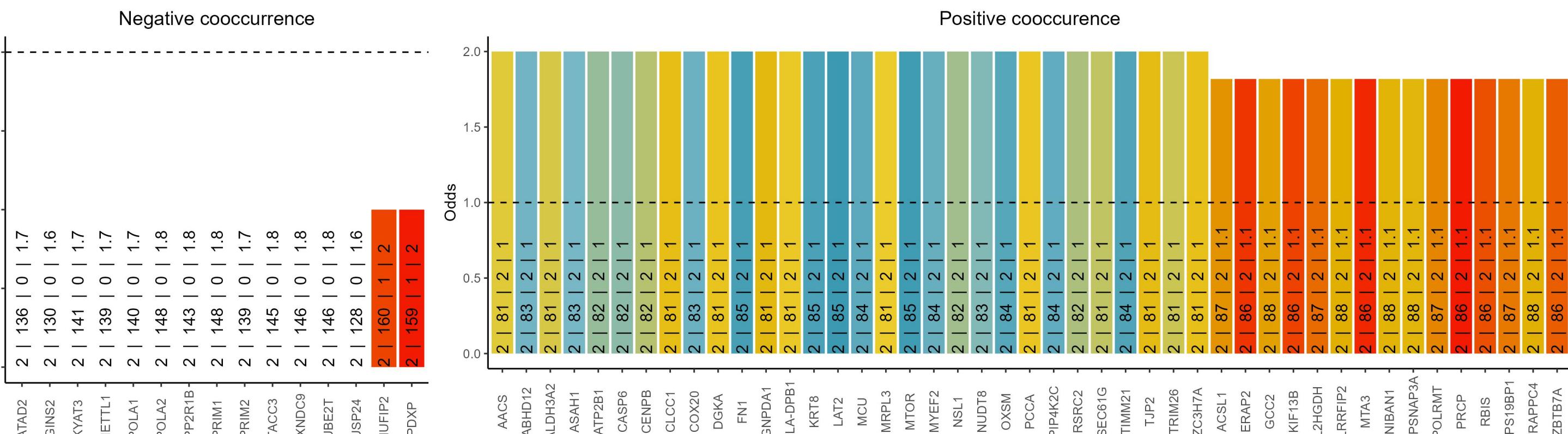


# Amount of EIF2AK4 protein and mutation status by tissue, DB1



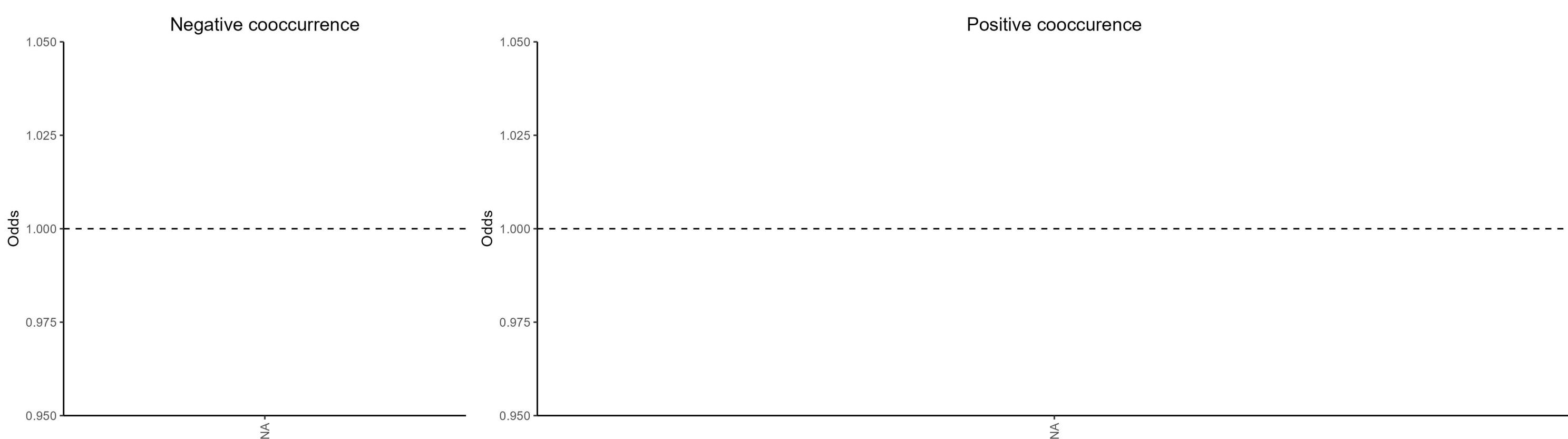
## Cooccurrence with EIF2AK4 protein in blood cancers, DB1

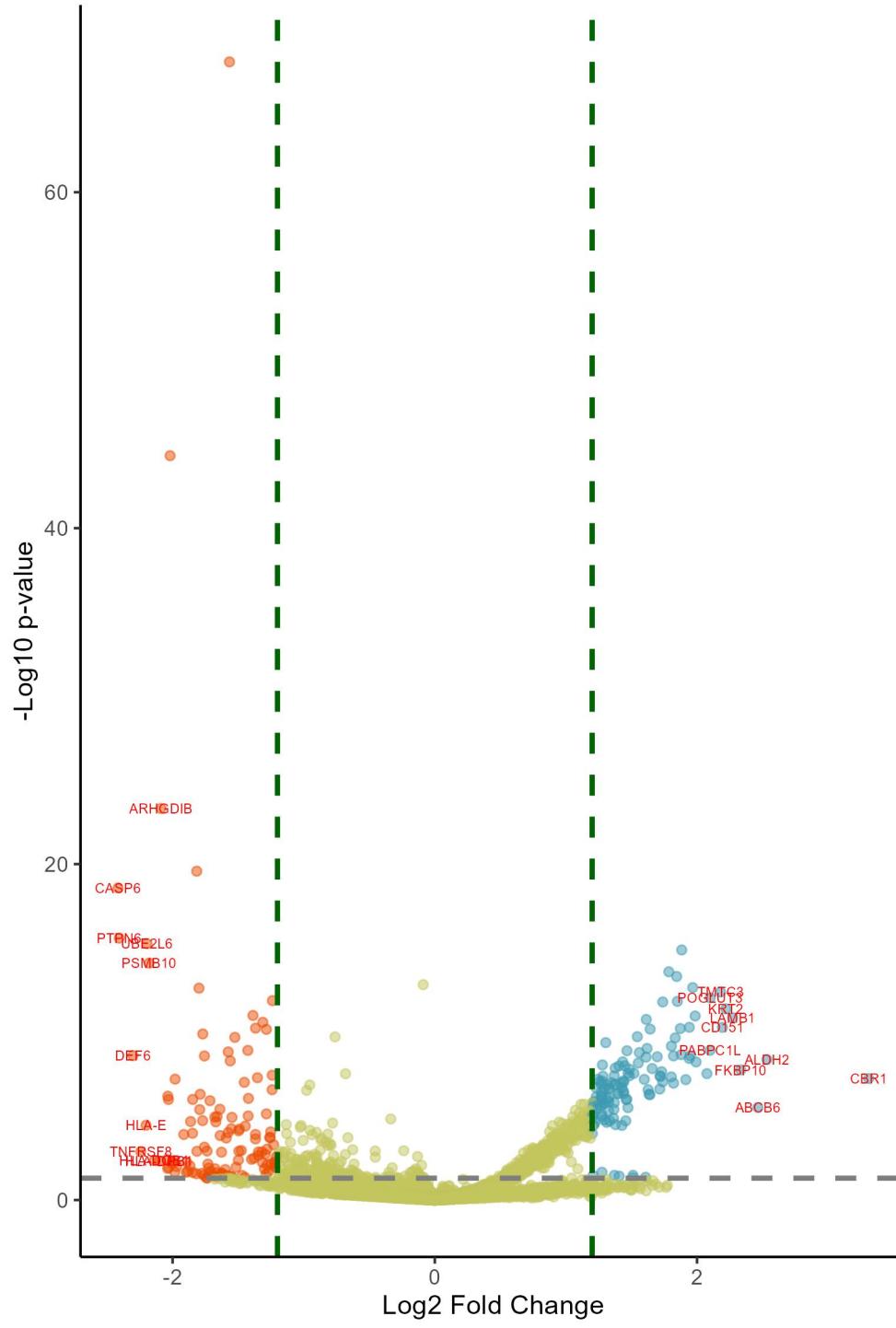
The text in the bars: incidence of EIF2AK4 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



## Cooccurrence with EIF2AK4 protein in solid cancers, DB1

The text in the bars: incidence of EIF2AK4 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

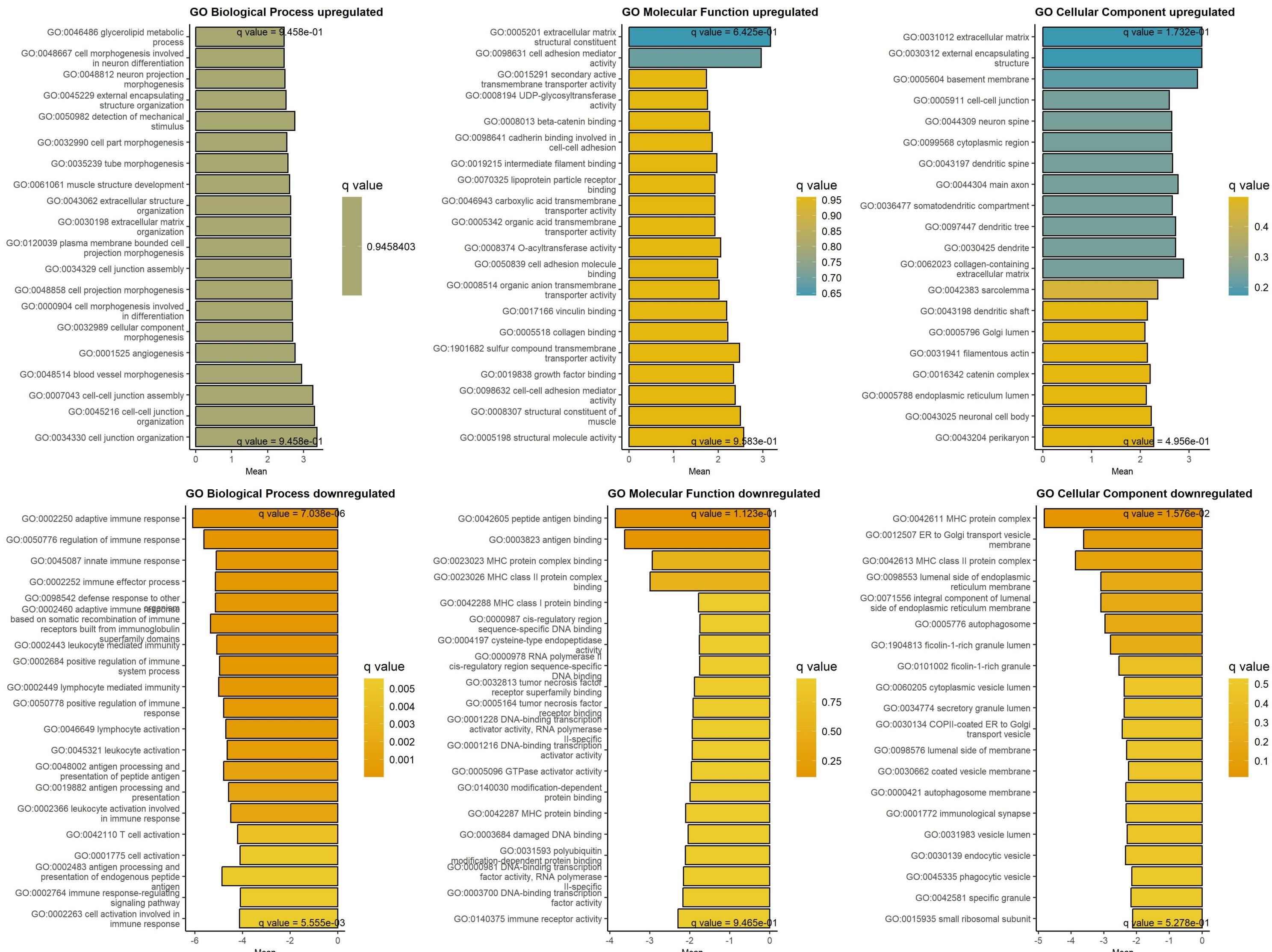




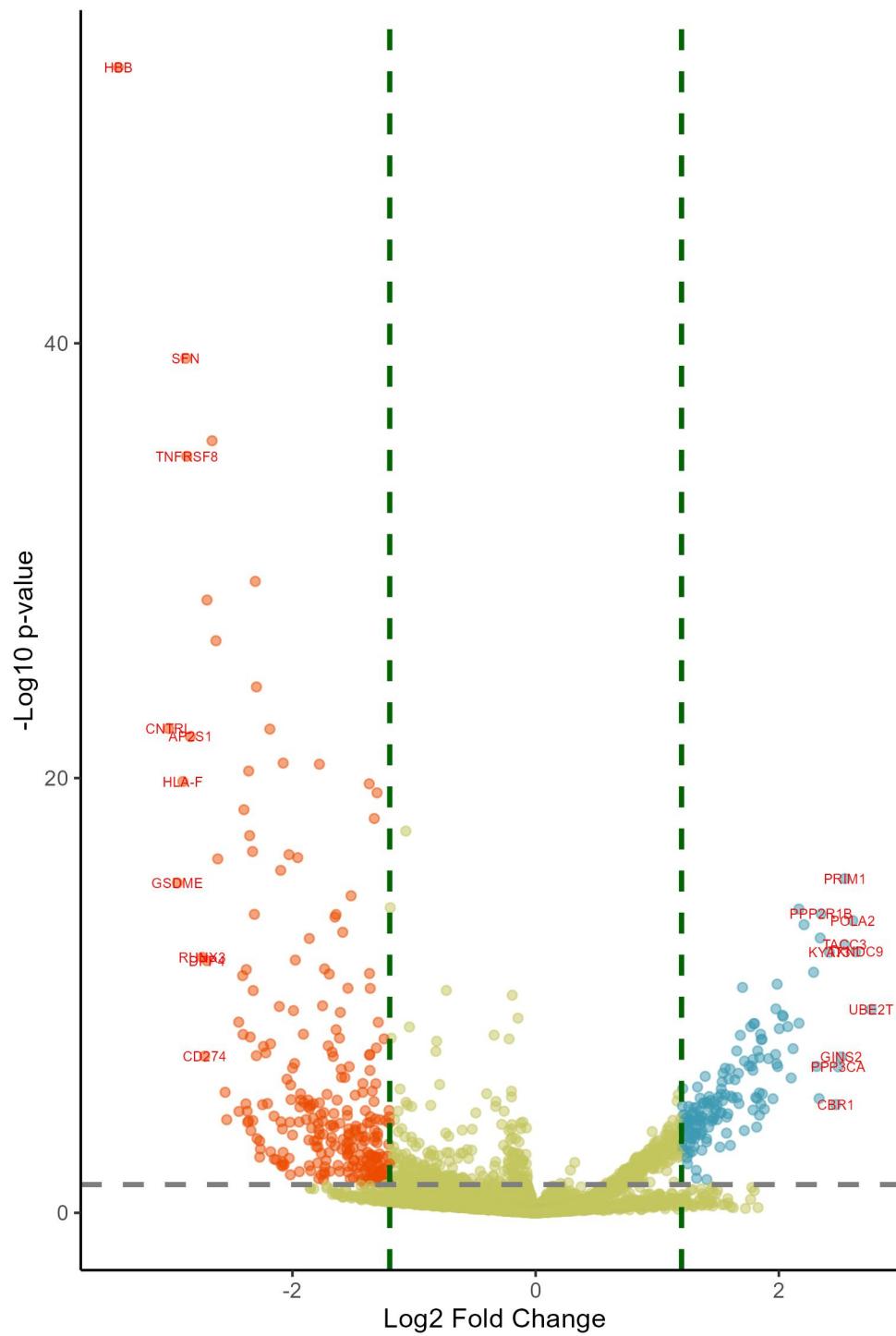
## Downregulated at low/absent EIF2AK4 Upregulated at low/absent EIF2AK4

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.42	2.91e-16	CASP6	caspase 6	3.31	4.94e-06	CBR1	carbonyl reductase 1
-2.41	2.43e-13	PTPN6	protein tyrosine phosphatase non-receptor type 6	2.53	5.28e-07	ALDH2	aldehyde dehydrogenase 2 family member 2
-2.3	3.52e-07	DEF6	DEF6 guanine nucleotide exchange factor	2.46	1.47e-04	ABC6	ATP binding cassette subfamily B member 6
-2.24	2.61e-02	TNFRSF8	TNF receptor superfamily member 8	2.33	1.85e-06	FKBP10	FKBP prolyl isomerase 10
-2.2	1.20e-03	HLA-E	major histocompatibility complex, class I, E	2.27	3.89e-09	LAMB1	laminin subunit beta 1
-2.2	4.52e-13	UBE2L6	ubiquitin conjugating enzyme E2 L6	2.22	1.32e-09	KRT2	keratin 2
-2.18	5.22e-12	PSMB10	proteasome 20S subunit beta 10	2.19	1.25e-08	CD151	CD151 molecule (Raph blood group)
-2.14	6.78e-02	HLA-DQB1	major histocompatibility complex, class II, DQB1	2.18	1.73e-10	TMTC3	transmembrane O-mannosyltransferase 3
-2.1	7.12e-02	HLA-DPB1	major histocompatibility complex, class II, DPB1	2.1	3.60e-10	POGLUT3	protein O-glucosyltransferase 3
-2.09	8.17e-21	ARHGDIB	Rho GDP dissociation inhibitor beta	2.1	1.95e-07	PABPC1L	poly(A) binding protein cytoplasmic 1-like
-2.04	6.01e-02	ICAM3	intercellular adhesion molecule 3	2.08	2.87e-06	PROCR	protein C receptor
-2.04	1.57e-01	CNTRL	centriolin	1.99	7.05e-07	MAP1B	microtubule associated protein 1B
-2.04	3.79e-05	TRIM21	tripartite motif containing 21	1.99	3.20e-09	TMEM33	transmembrane protein 33
-2.03	5.59e-05	SEPHS2	selenophosphate synthetase 2	1.97	1.07e-10	FNDC3A	fibronectin type III domain contain
-2.03	1.40e-01	HLA-DPA1	major histocompatibility complex, class I, DPA1	1.95	3.52e-07	ITGA5	integrin subunit alpha 5
-2.02	1.08e-41	BST2	bone marrow stromal cell antigen 2	1.94	1.25e-08	HM13	histocompatibility minor 13
-2.01	8.98e-02	HBB	hemoglobin subunit beta	1.94	4.71e-07	EPHA2	EPH receptor A2
-2	6.84e-02	MYO1G	myosin IG	1.91	5.46e-06	MACROH2A2	macroH2A.2 histone
-1.99	8.56e-02	RUNX3	RUNX family transcription factor 3	1.88	9.57e-13	ROCK2	Rho associated coiled-coil contain
-1.98	2.25e-01	HLA-DRB1	major histocompatibility complex, class II, DRB1	1.88	3.18e-07	TSPY1L	TSPY like 1
-1.98	5.29e-06	ETV6	ETS variant transcription factor 6	1.87	1.37e-08	ARL1	ADP ribosylation factor like GTPase
-1.97	1.28e-01	IRF4	interferon regulatory factor 4	1.85	5.24e-10	TMEM245	transmembrane protein 245
-1.91	3.55e-03	CCDC71L	coiled-coil domain containing 71 like	1.84	2.71e-11	SMPD4	sphingomyelin phosphodiesterase 4
-1.9	2.30e-01	SPN	sialophorin	1.83	3.98e-08	SMARCA1	SWI/SNF related, matrix associated, chromatin rearranger 1A
-1.89	7.87e-02	IRF5	interferon regulatory factor 5	1.82	8.05e-06	DPYSL3	dihydropyrimidinase like 3
-1.88	2.07e-01	SELPLG	selectin P ligand	1.82	3.52e-07	PIGT	phosphatidylinositol glycan anchor biosynthesis class P
-1.87	1.19e-01	PTPRC	protein tyrosine phosphatase receptor type C	1.8	1.17e-07	HDGFL3	HDGF like 3
-1.86	8.02e-04	PRKCD	protein kinase C delta	1.8	4.03e-06	MMP14	matrix metallopeptidase 14
-1.85	3.13e-03	TYMP	thymidine phosphorylase	1.78	1.57e-11	DHX36	DEAH-box helicase 36

## GAGE analysis on upregulated and downregulated proteins at low/absent EIF2AK4 protein, DB1

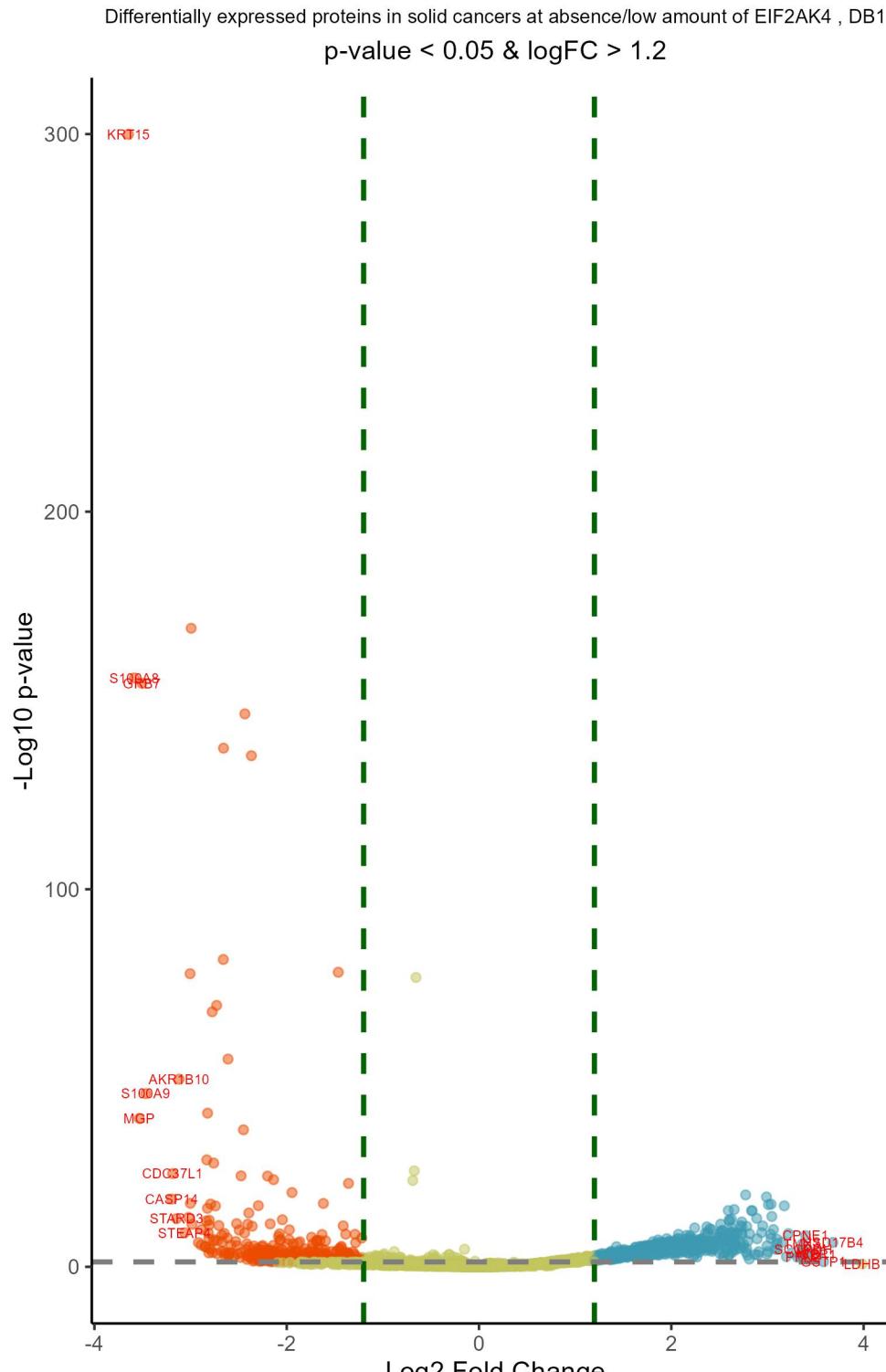


p-value &lt; 0.05 &amp; logFC &gt; 1.2



Downregulated in blood cancers at low/absent EIF2AK4 Upregulated in blood cancers at low/absent EIF2AK4

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-3.43	6.76e-50	HBB	hemoglobin subunit beta	2.76	4.58e-08	UBE2T	ubiquitin conjugating enzyme E2 T
-3.02	3.38e-20	CNTRL	centriolin	2.63	1.53e-10	TXNDC9	thioredoxin domain containing 9
-2.95	1.53e-13	GSDME	gasdermin E	2.61	6.50e-12	POLA2	DNA polymerase alpha 2, accessory s
-2.9	6.01e-18	HLA-F	major histocompatibility complex, c	2.54	9.98e-14	PRIM1	DNA primase subunit 1
-2.88	1.09e-36	SFN	stratifin	2.54	7.32e-11	TACC3	transforming acidic coiled-coil con
-2.87	2.10e-32	TNFRSF8	TNF receptor superfamily member 8	2.51	4.08e-06	GINS2	GINS complex subunit 2
-2.84	6.84e-20	AP2S1	adaptor related protein complex 2 s	2.49	1.05e-05	PPP3CA	protein phosphatase 3 catalytic sub
-2.74	2.60e-10	RUNX3	RUNX family transcription factor 3	2.47	3.62e-04	CBR1	carbonyl reductase 1
-2.72	3.87e-06	CD274	CD274 molecule	2.42	1.56e-10	KYAT3	kynurenine aminotransferase 3
-2.7	3.59e-10	DPP4	dipeptidyl peptidase 4	2.35	3.56e-12	PPP2R1B	protein phosphatase 2 scaffold subu
-2.7	6.13e-26	MX1	MX dynamin like GTPase 1	2.34	3.80e-11	POLA1	DNA polymerase alpha 1, catalytic s
-2.66	5.07e-33	CEP290	centrosomal protein 290	2.33	2.20e-04	PABPC1L	poly(A) binding protein cytoplasmic
-2.63	4.01e-24	JUNB	JunB proto-oncogene, AP-1 transcrip	2.31	1.04e-05	MSI2	musashi RNA binding protein 2
-2.61	1.34e-14	FAS	Fas cell surface death receptor	2.29	1.14e-09	ATAD2	ATPase family AAA domain containing
-2.55	1.27e-04	OASL	2'-5'-oligoadenylate synthetase lik	2.21	9.73e-12	METTL1	methyltransferase 1, tRNA methylgu
-2.54	1.37e-03	COL1A2	collagen type I alpha 2 chain	2.17	1.75e-07	RB1	RB transcriptional corepressor 1
-2.44	1.60e-07	IRF5	interferon regulatory factor 5	2.17	2.20e-12	PRIM2	DNA primase subunit 2
-2.44	6.56e-04	TNFRSF10B	TNF receptor superfamily member 10b	2.12	1.92e-06	VAV1	vav guanine nucleotide exchange fac
-2.41	1.55e-09	GATM	glycine amidinotransferase	2.1	3.12e-05	ASF1A	anti-silencing function 1A histone
-2.41	5.06e-07	PARVB	parvin beta	2.07	2.40e-07	DLGAP5	DLG associated protein 5
-2.4	9.98e-17	RHOC	ras homolog family member C	2.04	9.09e-08	POLR2G	RNA polymerase II subunit G
-2.38	3.38e-04	MX2	MX dynamin like GTPase 2	2.03	8.06e-08	CKAP2	cytoskeleton associated protein 2
-2.38	8.73e-10	TRPV2	transient receptor potential cation	2	2.87e-07	RABEPK	Rab9 effector protein with kelch mo
-2.37	6.46e-04	TMOD1	tropomodulin 1	1.99	1.05e-05	USP13	ubiquitin specific peptidase 13
-2.37	1.67e-03	PHKA2	phosphorylase kinase regulatory sub	1.99	3.74e-09	USP24	ubiquitin specific peptidase 24
-2.36	2.10e-18	RAB11B	RAB11B, member RAS oncogene family	1.98	8.10e-06	HIRIP3	HIRA interacting protein 3
-2.36	1.51e-03	ADGB	androglobin	1.98	4.39e-08	TDP2	tyrosyl-DNA phosphodiesterase 2
-2.35	1.34e-15	PFN2	profilin 2	1.97	3.31e-06	CIP2A	cellular inhibitor of PP2A
-2.35	6.41e-07	MLF2	myeloid leukemia factor 2	1.95	2.23e-04	CDKN2C	cyclin dependent kinase inhibitor 2

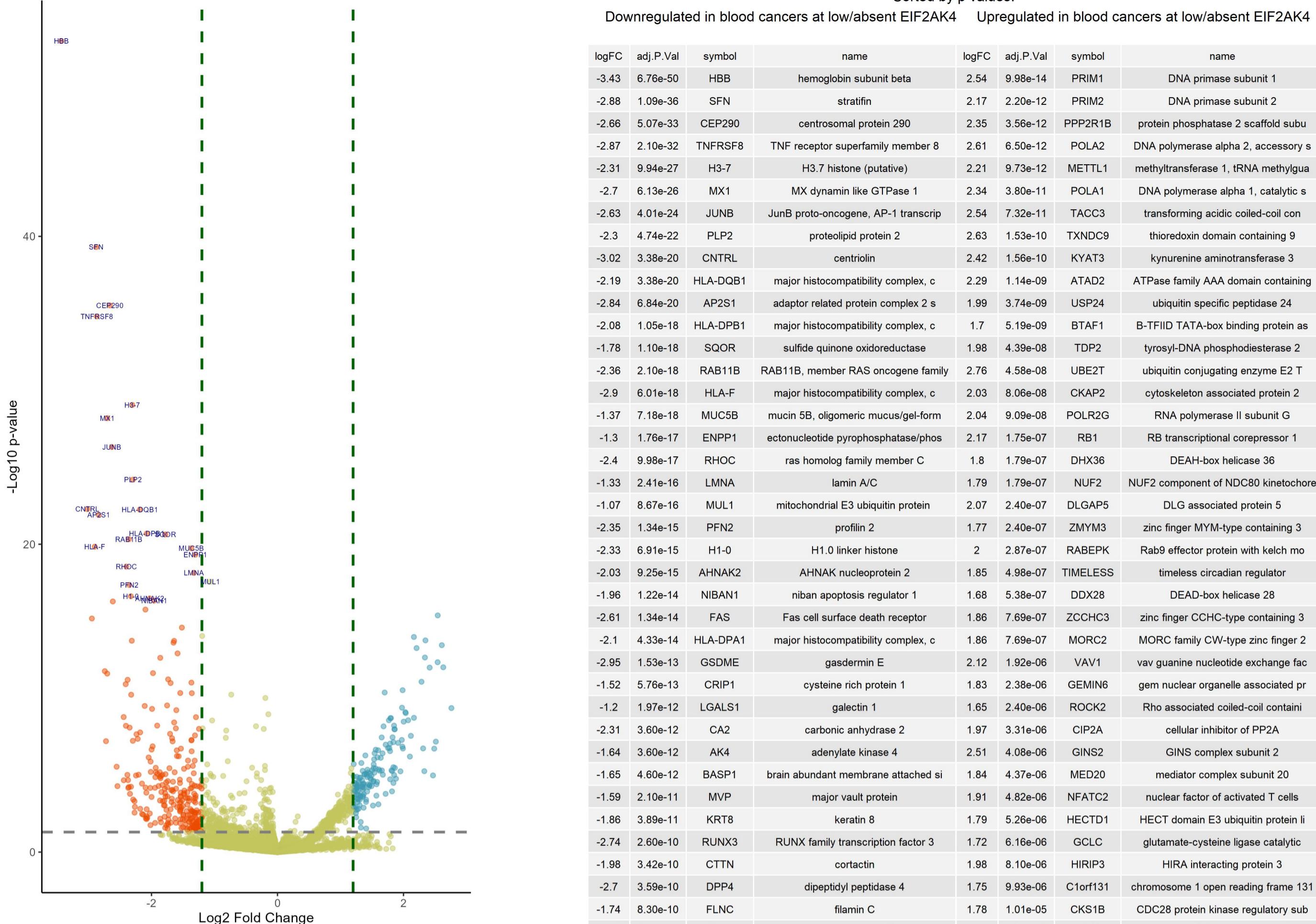
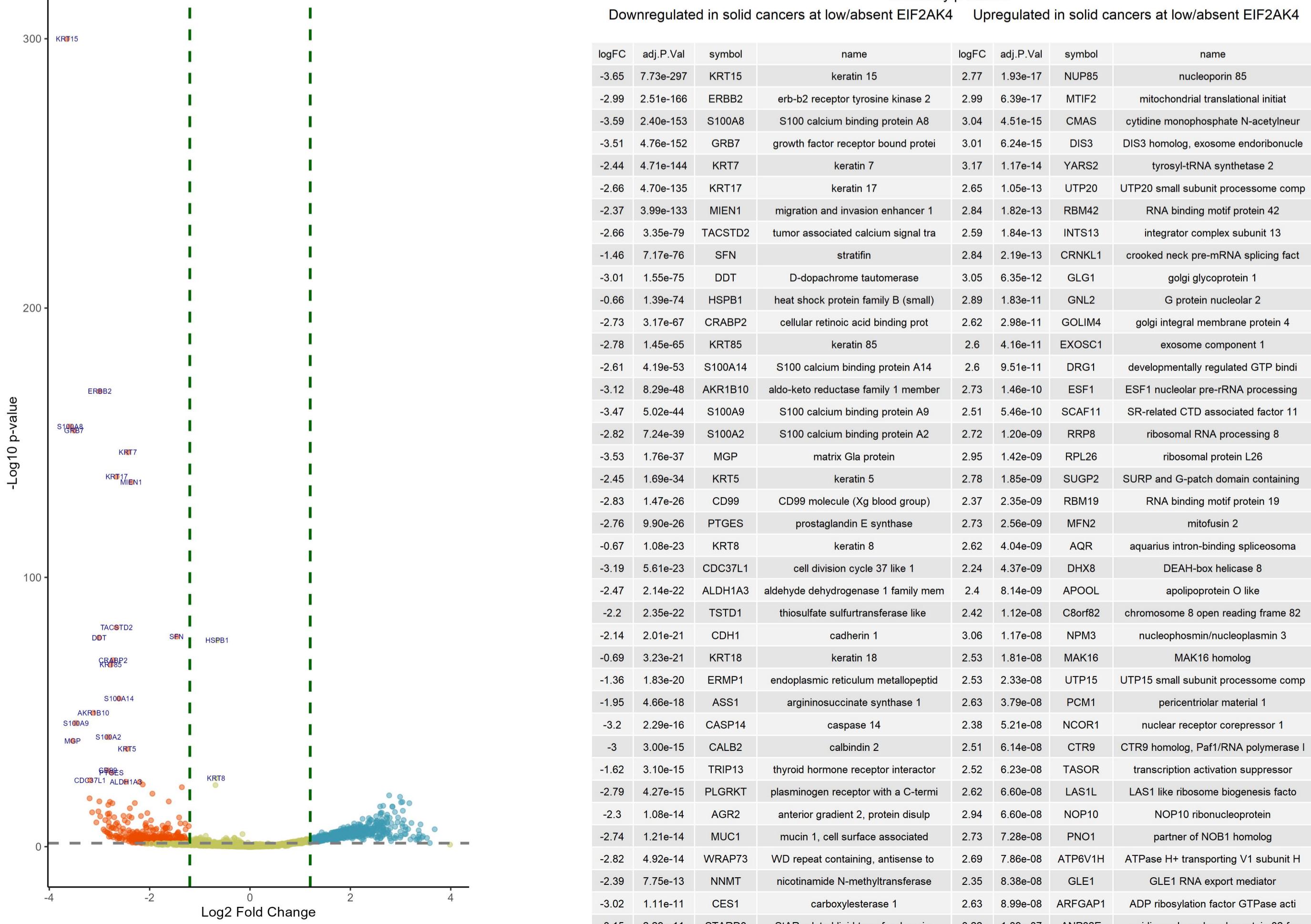


Downregulated in solid cancers at low/absent EIF2AK4 Upregulated in solid cancers at low/absent EIF2AK4

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-3.65	7.73e-297	KRT15	keratin 15	3.98	5.05e-01	LDHB	lactate dehydrogenase B
-3.59	2.40e-153	S100A8	S100 calcium binding protein A8	3.68	1.22e-05	HSD17B4	hydroxysteroid 17-beta dehydrogenas
-3.53	1.76e-37	MGP	matrix Gla protein	3.58	1.94e-01	GSTP1	glutathione S-transferase pi 1
-3.51	4.76e-152	GRB7	growth factor receptor bound protei	3.53	5.84e-03	CBR1	carbonyl reductase 1
-3.47	5.02e-44	S100A9	S100 calcium binding protein A9	3.44	1.73e-03	NNT	nicotinamide nucleotide transhydrol
-3.2	2.29e-16	CASP14	caspase 14	3.43	4.35e-03	IVD	isovaleryl-CoA dehydrogenase
-3.19	5.61e-23	CDC37L1	cell division cycle 37 like 1	3.4	3.15e-07	CPNE1	copine 1
-3.15	2.29e-11	STARD3	StAR related lipid transfer domain	3.38	4.35e-04	SCCPDH	saccharopine dehydrogenase (putativ
-3.12	8.29e-48	AKR1B10	aldo-keto reductase family 1 member	3.37	1.90e-02	PFN2	profilin 2
-3.06	7.21e-08	STEAP4	STEAP4 metalloreductase	3.36	2.69e-05	TMX3	thioredoxin related transmembrane p
-3.02	1.11e-11	CES1	carboxylesterase 1	3.35	2.77e-03	DPYSL2	dihydropyrimidinase like 2
-3.01	1.55e-75	DDT	D-dopachrome tautomerase	3.34	1.40e-02	ACAA2	acetyl-CoA acyltransferase 2
-3	3.00e-15	CALB2	calbindin 2	3.31	2.16e-02	AKR1B1	aldo-keto reductase family 1 member
-2.99	2.51e-166	ERBB2	erb-b2 receptor tyrosine kinase 2	3.25	2.39e-03	IGF2BP3	insulin like growth factor 2 mRNA b
-2.99	5.82e-10	EFHD1	EF-hand domain family member D1	3.22	1.09e-07	ANP32E	acidic nuclear phosphoprotein 32 fa
-2.92	1.32e-05	PSTPIP2	proline-serine-threonine phosphatas	3.2	1.63e-02	TMED5	transmembrane p24 trafficking prote
-2.89	4.48e-05	HPGD	15-hydroxyprostaglandin dehydrogena	3.17	1.17e-14	YARS2	tyrosyl-tRNA synthetase 2
-2.89	1.18e-08	CEACAM6	CEA cell adhesion molecule 6	3.15	1.08e-05	UQCC2	ubiquinol-cytochrome c reductase co
-2.85	1.04e-04	AMOT	angiomotin	3.1	3.85e-04	OXCT1	3-oxoacid CoA-transferase 1
-2.84	1.13e-04	PADI2	peptidyl arginine deiminase 2	3.1	1.99e-05	ESD	esterase D
-2.84	8.19e-11	SNCG	synuclein gamma	3.1	2.44e-06	RAB35	RAB35, member RAS oncogene family
-2.83	1.47e-26	CD99	CD99 molecule (Xg blood group)	3.08	3.82e-04	MRPL21	mitochondrial ribosomal protein L21
-2.82	4.92e-14	WRAP73	WD repeat containing, antisense to	3.06	1.17e-08	NPM3	nucleophosmin/nucleoplasmmin 3
-2.82	7.24e-39	S100A2	S100 calcium binding protein A2	3.05	6.35e-12	GLG1	golgi glycoprotein 1
-2.81	7.86e-08	KRT75	keratin 75	3.04	1.64e-06	LAMTOR3	late endosomal/lysosomal adaptor, M
-2.81	2.51e-04	CP	ceruloplasmin	3.04	4.51e-15	CMAS	cytidine monophosphate N-acetyleneur
-2.81	2.42e-03	HLA-DRB1	major histocompatibility complex, c	3.03	1.49e-07	ABHD12	abhydrolase domain containing 12, I
-2.81	1.62e-06	OXR1	oxidation resistance 1	3.01	6.24e-15	DIS3	DIS3 homolog, exosome endoribonucle
-2.81	9.20e-10	PROM2	prominin 2	3	1.32e-03	ARF4	ADP ribosylation factor 4

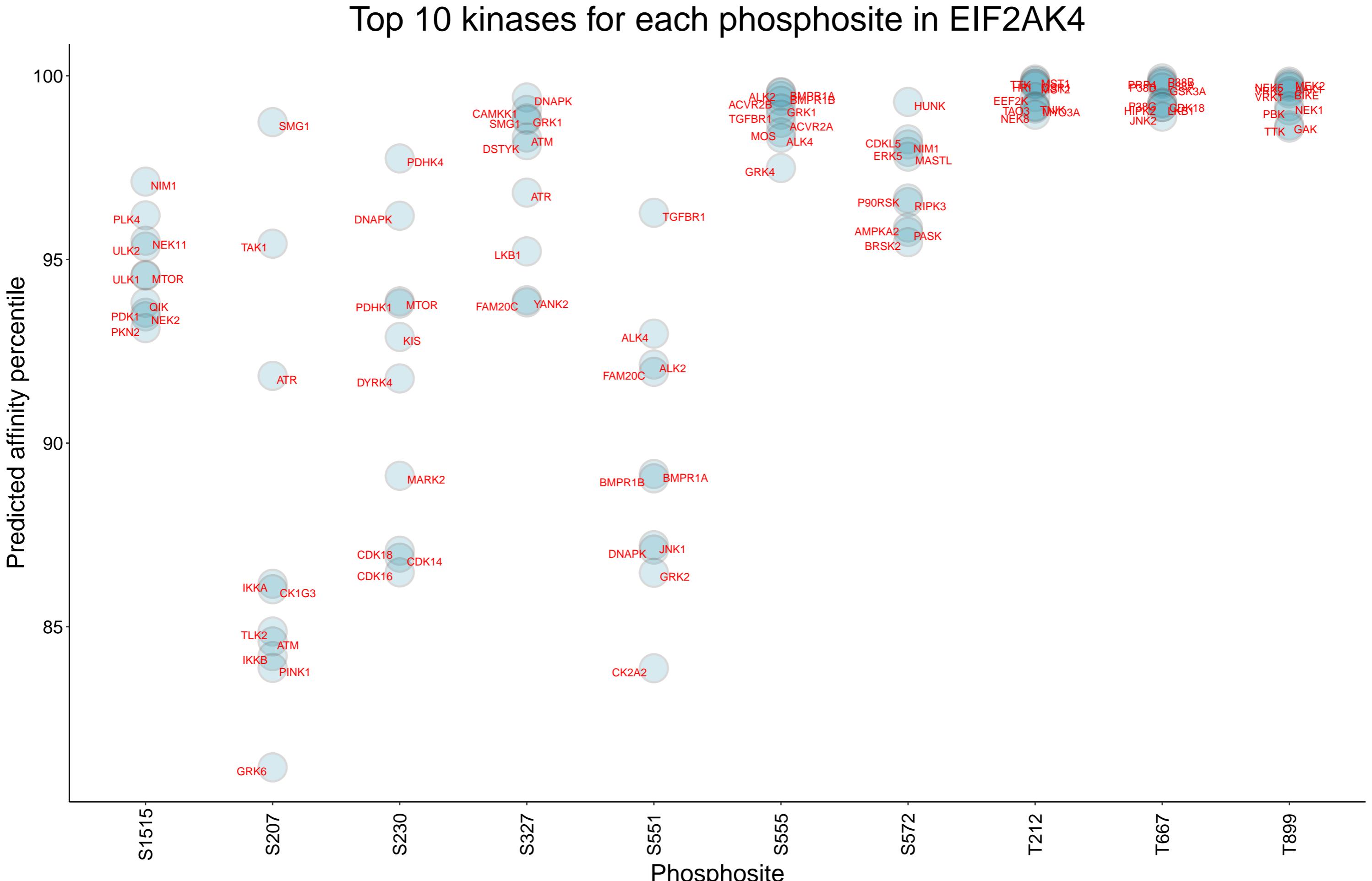
EIF2AK4 network, DB1, no Pearson r &gt; 0.3

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

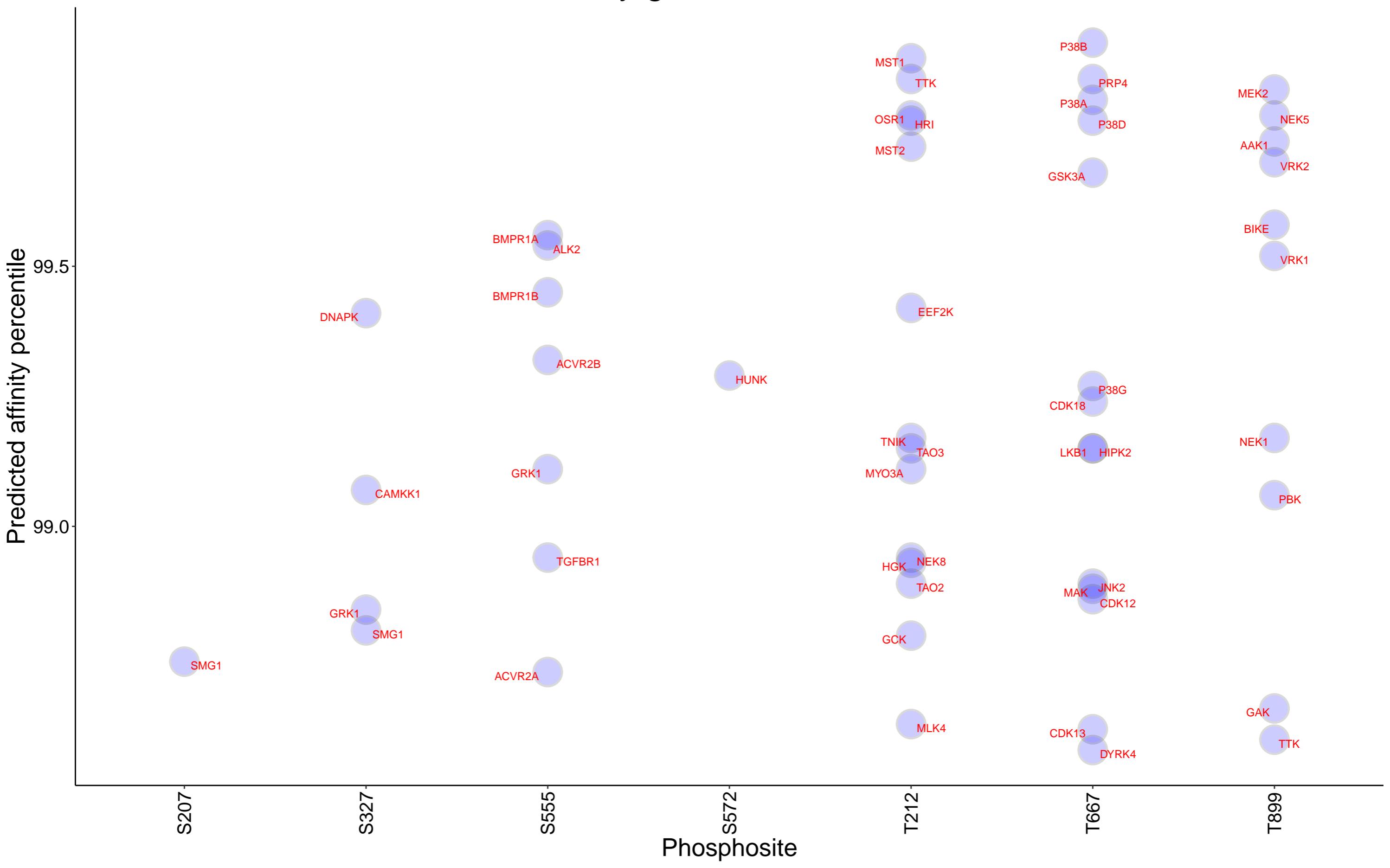
Differentially expressed proteins in solid cancers at absence/low amount of EIF2AK4 , DB1  
p-value < 0.05 & logFC > 1.2

Insufficient number of paired observations in DB1 for EIF2AK4

Insufficient number of paired observations in DB1 for EIF2AK4



## Kinases with affinity greater than 98.5% to EIF2AK4



No sufficient paired observations in DB1 for EIF2AK4