

EYA3

Protein name: EYA3 ;

UNIPROT: Q99504 ;

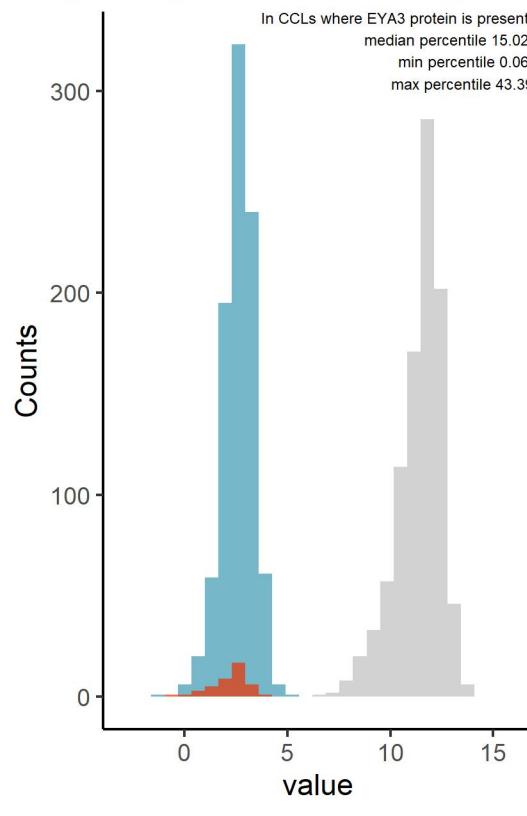
Gene name: EYA transcriptional coactivator and phosphatase 3

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

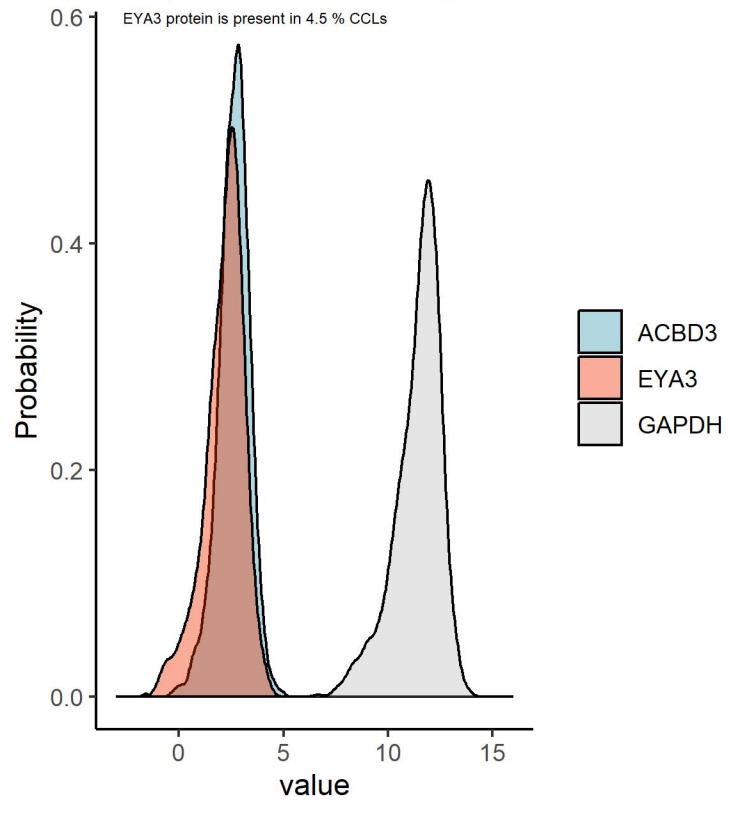
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

Histogram of EYA3 protein compared to proteins with low and high abundance



Density plot of EYA3 protein compared to proteins with low and high abundance



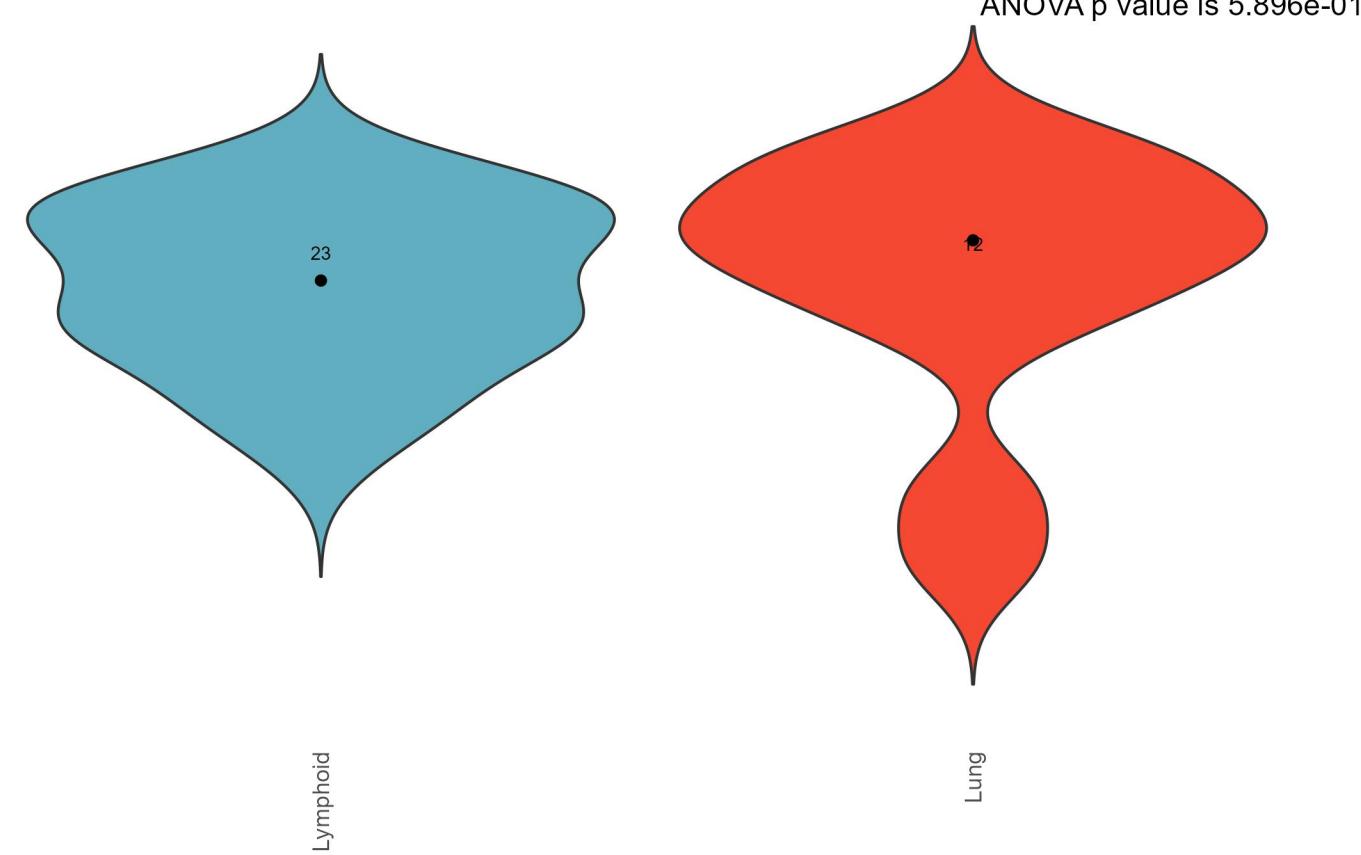
Top negative correlations of EYA3 protein, DB1

Pearson correlation coefficients

Top positive correlations of EYA3 protein, DB1

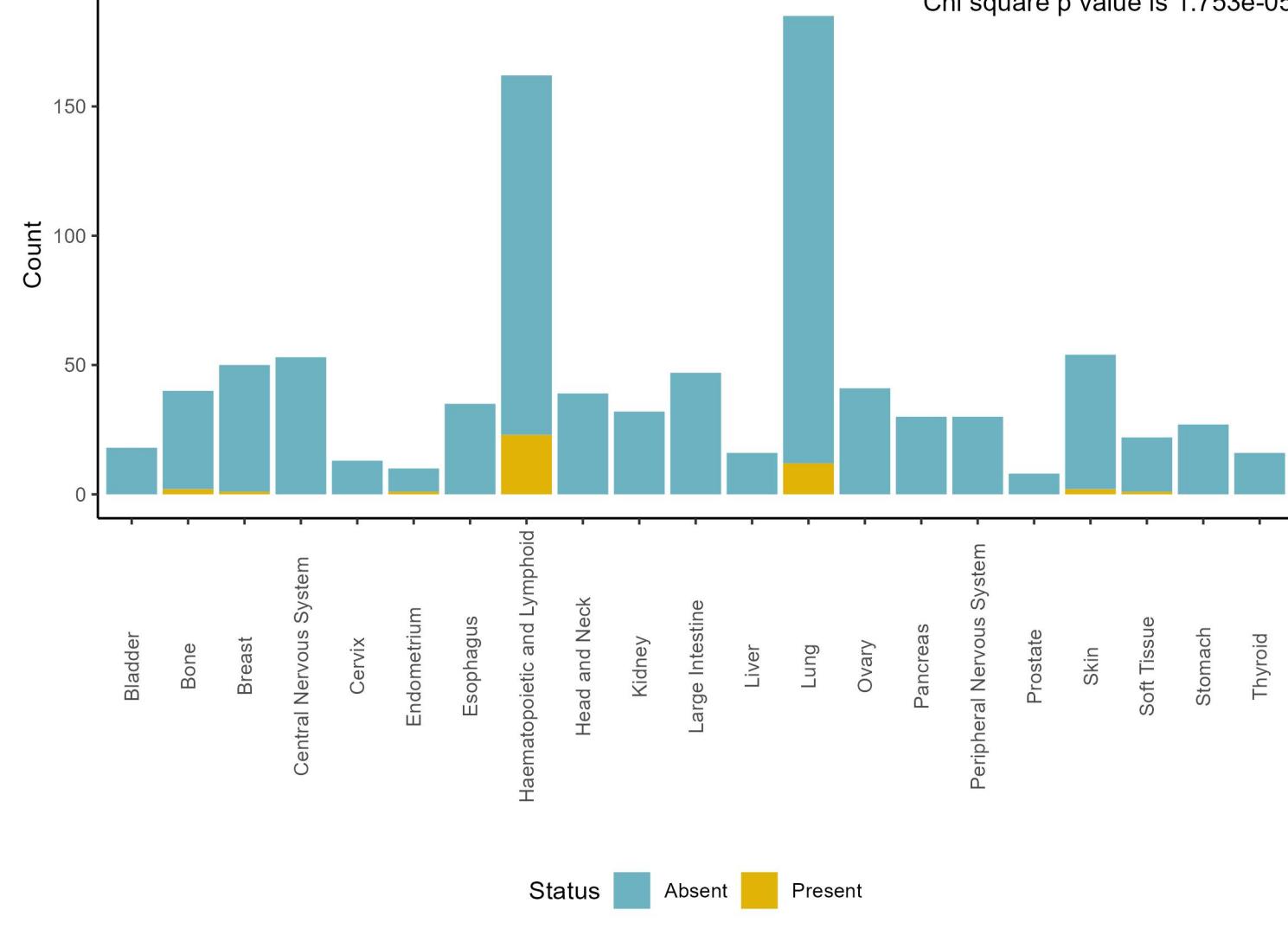
Pearson correlation coefficients

Amount of EYA3 protein, number of CCLs where it is present by tissue, DB1



Present and absent EYA3 protein counts by tissue, DB1

Chi square p value is 1.753e-05

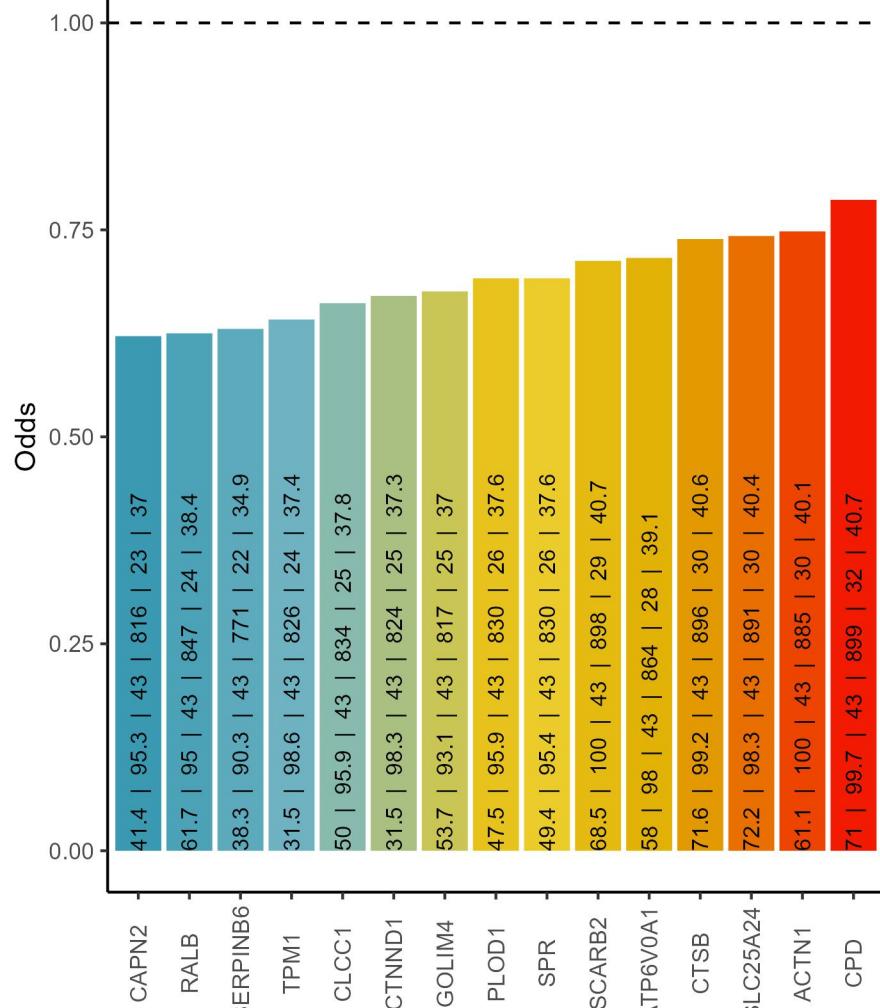


Cooccurrence with EYA3 protein, DB1

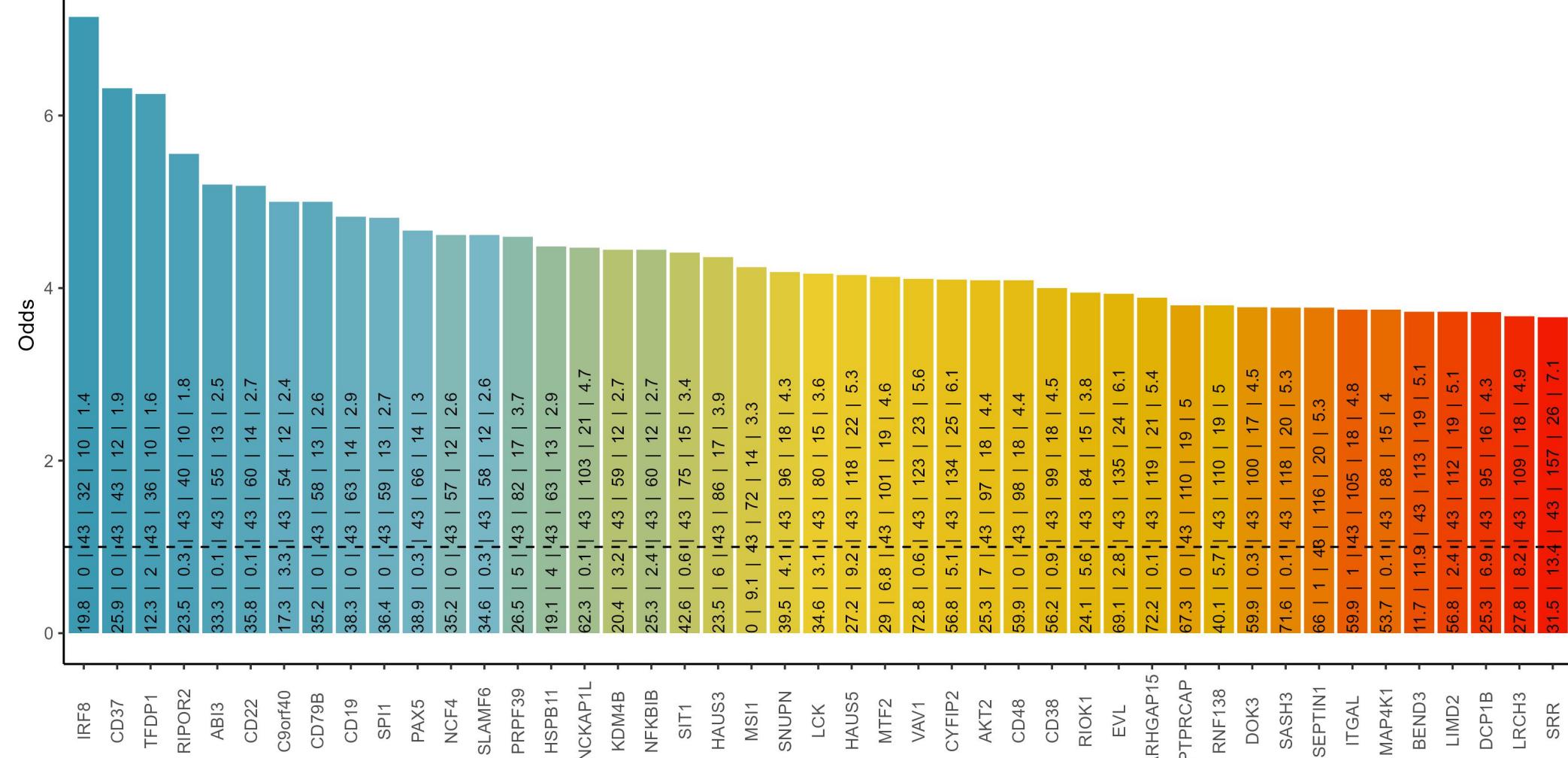
% of EYA3 in blood cancers: 14.2 ; % of EYA3 in solid cancers: 2.6

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of EYA3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

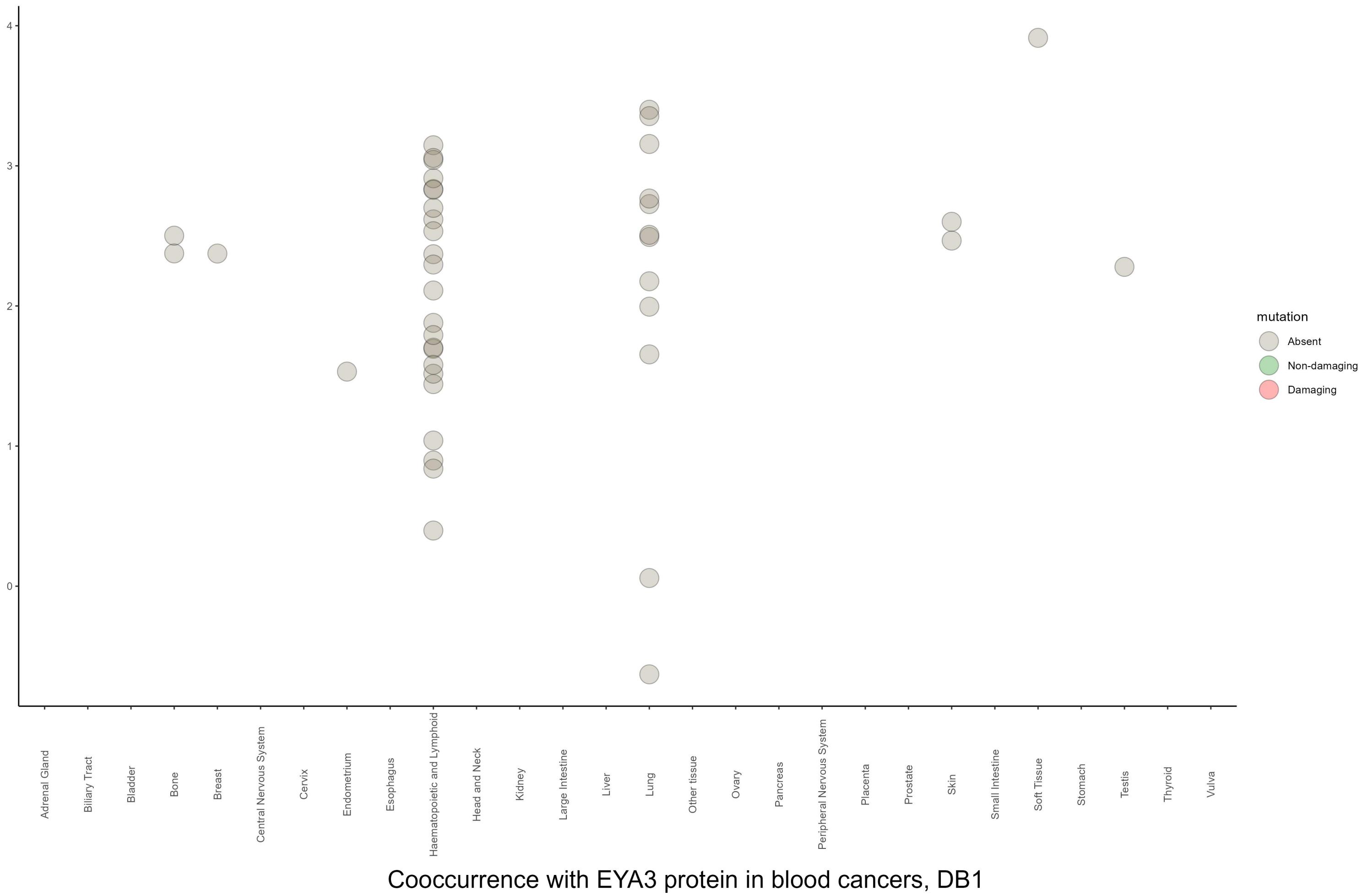
Negative cooccurrence



Positive cooccurrence

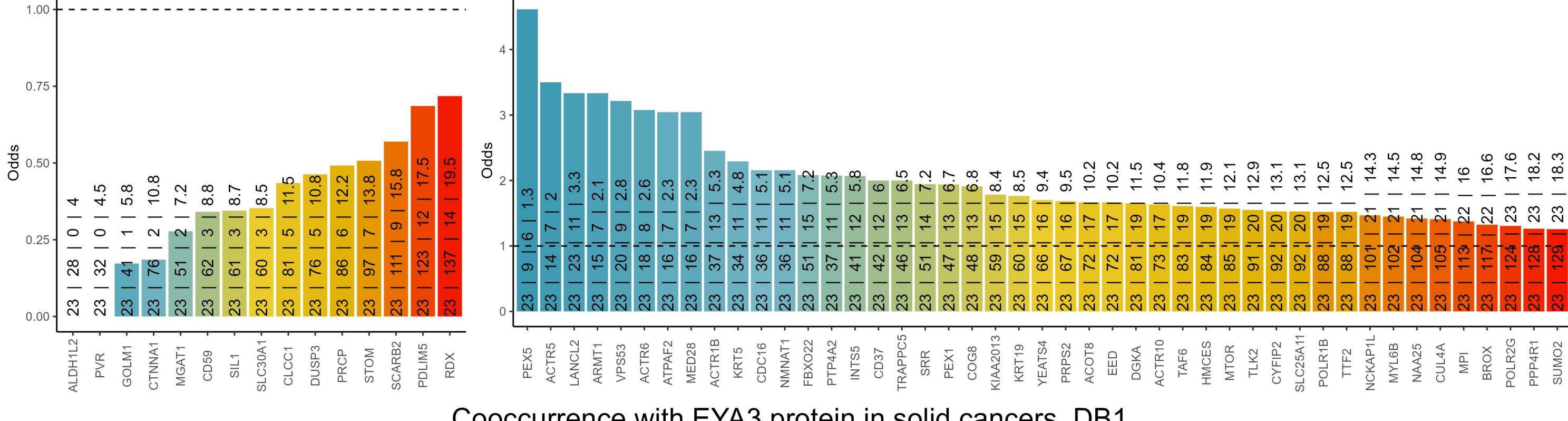


Amount of EYA3 protein and mutation status by tissue, DB1



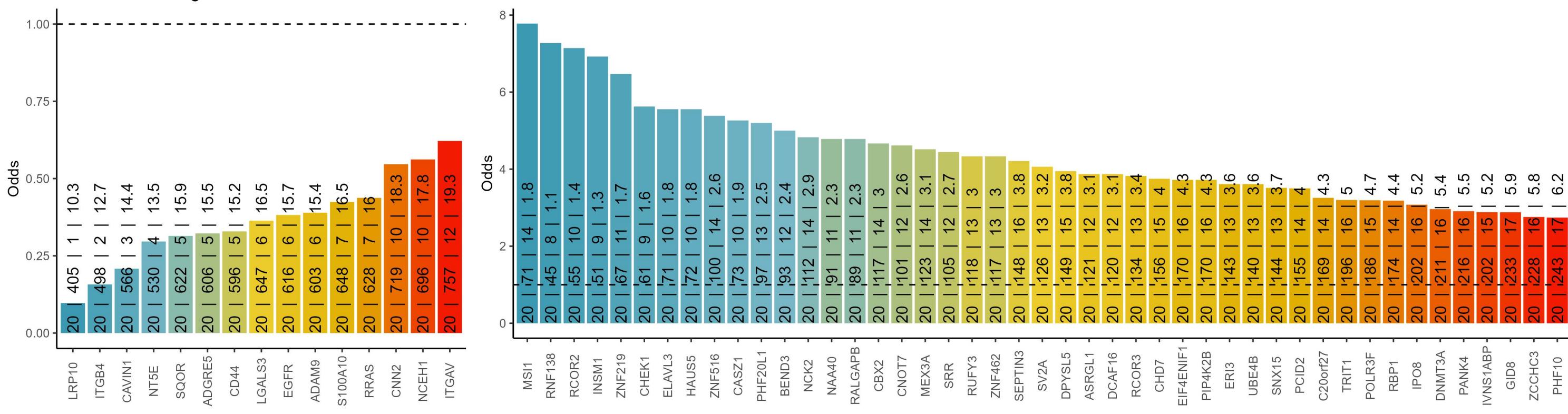
Cooccurrence with EYA3 protein in blood cancers, DB1

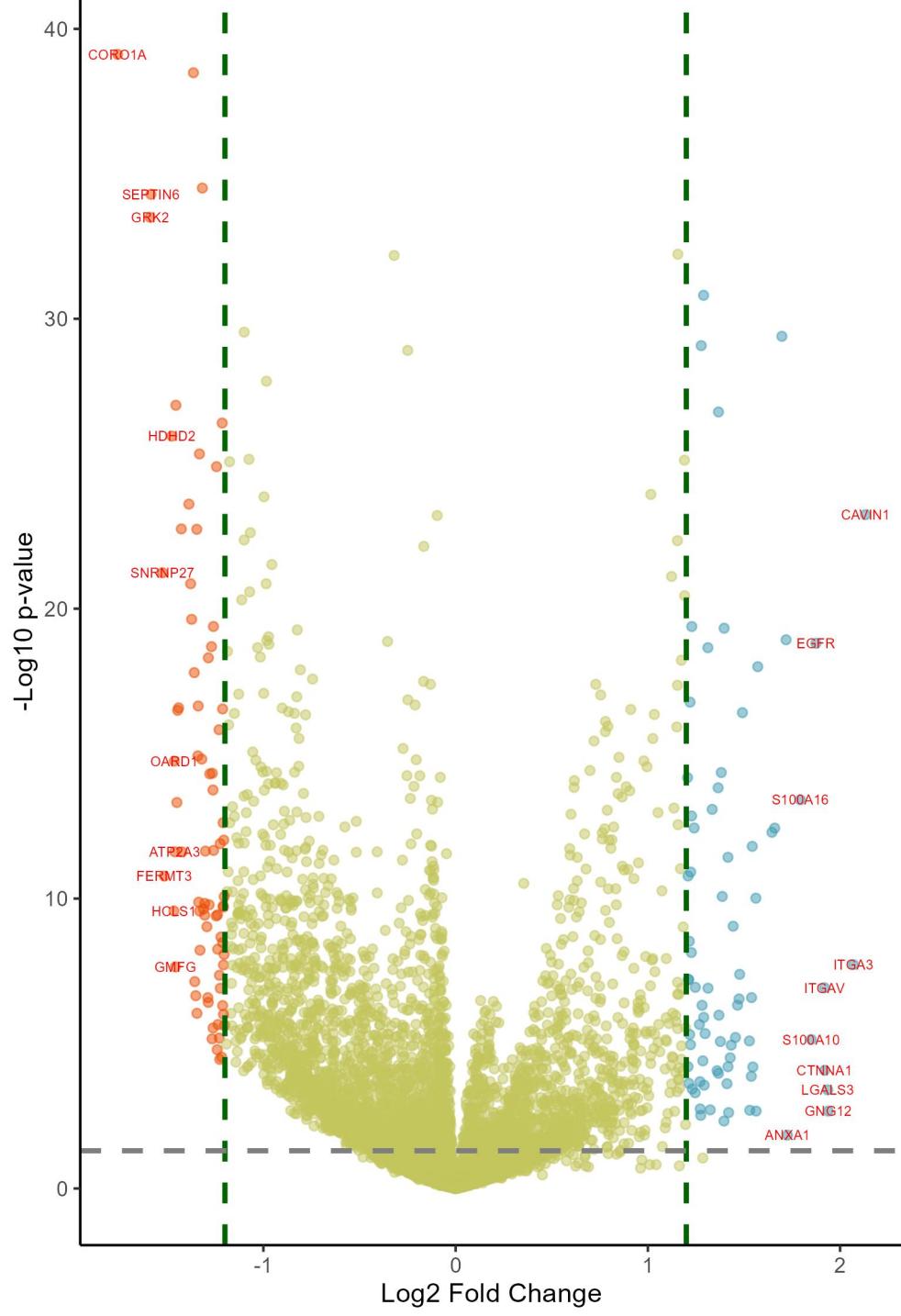
The text in the bars: incidence of EYA3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Cooccurrence with EYA3 protein in solid cancers, DB1

The text in the bars: incidence of EYA3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

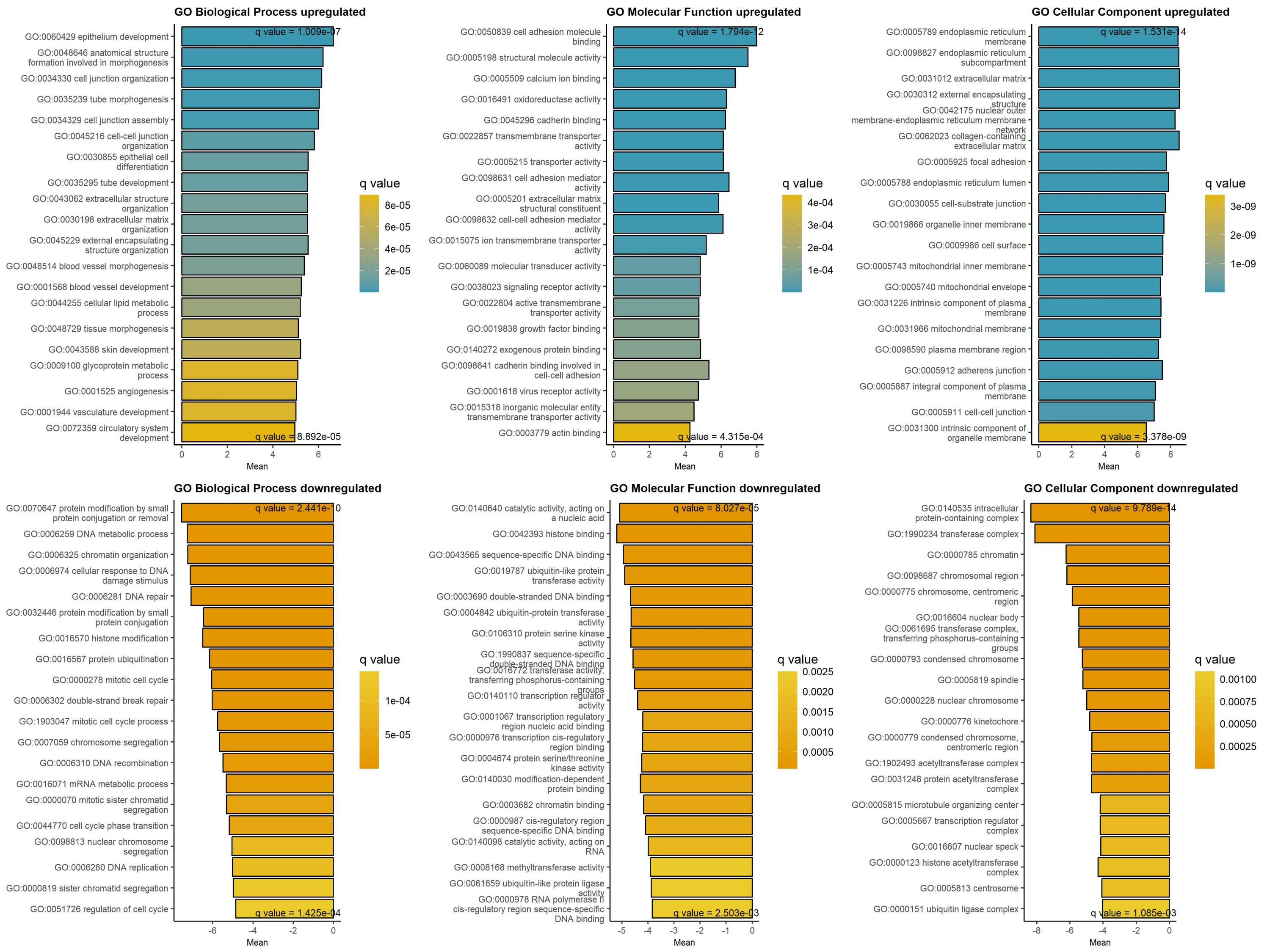


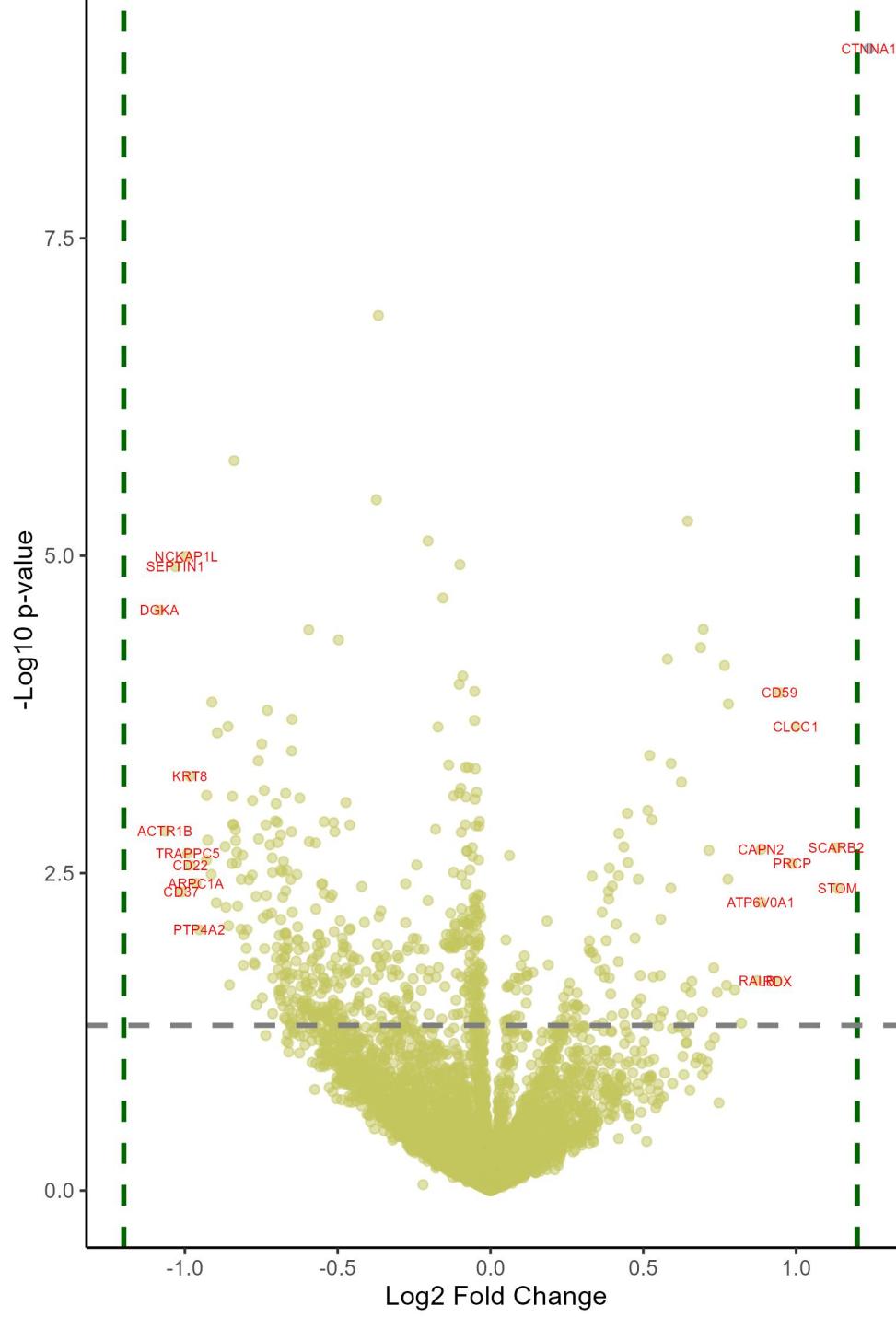


Downregulated at low/absent EYA3 Upregulated at low/absent EYA3

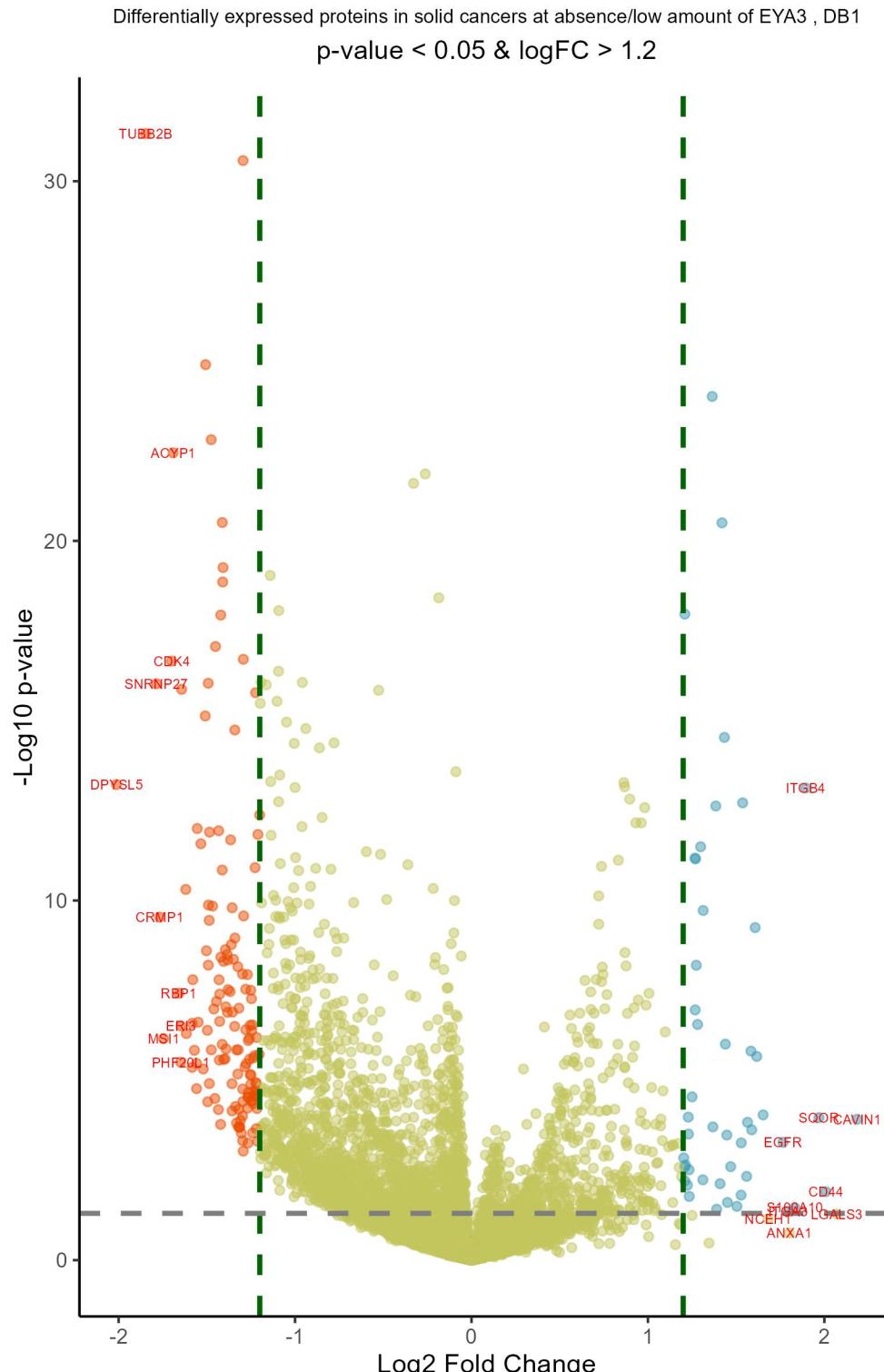
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.76	2.51e-36	CORO1A	coronin 1A	2.13	1.41e-21	CAVIN1	caveolae associated protein 1
-1.59	3.51e-31	GRK2	G protein-coupled receptor kinase 2	2.07	2.57e-07	ITGA3	integrin subunit alpha 3
-1.58	6.77e-32	SEPTIN6	septin 6	1.94	6.66e-03	GNG12	G protein subunit gamma 12
-1.52	1.06e-19	SNRNP27	small nuclear ribonucleoprotein U4/U6	1.94	1.57e-03	LGALS3	galectin 3
-1.52	4.65e-10	FERMT3	FERM domain containing kindlin 3	1.92	4.10e-04	CTNNAI	catenin alpha 1
-1.48	4.11e-24	HDHD2	haloacid dehalogenase like hydrolase	1.92	1.31e-06	ITGAV	integrin subunit alpha V
-1.47	5.37e-09	HCLS1	hematopoietic cell-specific Lyn sub	1.87	2.00e-17	EGFR	epidermal growth factor receptor
-1.46	1.14e-13	OARD1	O-acetyl-ADP-ribose deacetylase 1	1.85	4.87e-05	S100A10	S100 calcium binding protein A10
-1.46	7.89e-11	ATP2A3	ATPase sarcoplasmic/endoplasmic reticulum	1.79	1.82e-12	S100A16	S100 calcium binding protein A16
-1.46	2.99e-07	GMFG	glia maturation factor gamma	1.73	3.31e-02	ANXA1	annexin A1
-1.46	4.27e-25	ARMC6	armadillo repeat containing 6	1.72	1.61e-17	ADAM9	ADAM metallopeptidase domain 9
-1.45	2.21e-12	SSNA1	SS nuclear autoantigen 1	1.7	2.43e-27	ITGB4	integrin subunit beta 4
-1.45	2.64e-15	RNASEH2B	ribonuclease H2 subunit B	1.66	1.44e-11	CAV1	caveolin 1
-1.44	2.28e-15	MAPRE2	microtubule associated protein RP/E	1.65	1.98e-11	RRAS	RAS related
-1.43	4.04e-21	NUDT3	nudix hydrolase 3	1.57	1.09e-16	EPHA2	EPH receptor A2
-1.42	7.92e-11	CELF2	CUGBP Elav-like family member 2	1.56	6.62e-03	NCEH1	neutral cholesterol ester hydrolase
-1.39	6.34e-22	EIF2B1	eukaryotic translation initiation factor	1.56	2.27e-09	PROCR	protein C receptor
-1.38	2.36e-19	COPS7B	COP9 signalosome subunit 7B	1.55	3.26e-04	PVR	PVR cell adhesion molecule
-1.37	3.60e-18	SMAP2	small ArfGAP2	1.54	5.38e-11	NT5E	5'-nucleotidase ecto
-1.36	7.23e-36	BLMH	bleomycin hydrolase	1.54	2.66e-06	ITGA2	integrin subunit alpha 2
-1.36	1.70e-16	ARHGEF7	Rho guanine nucleotide exchange factor	1.54	6.22e-04	PON2	paraoxonase 2
-1.36	8.44e-07	EVL	Enah/Vasp-like	1.53	6.29e-03	CD44	CD44 molecule (Indian blood group)
-1.35	2.30e-06	PTPRC	protein tyrosine phosphatase receptor	1.53	5.40e-05	MYO1C	myosin IC
-1.35	4.04e-21	ACYP1	acylphosphatase 1	1.49	3.09e-15	EPS8L2	EPS8 like 2
-1.35	7.99e-06	SEPTIN1	septin 1	1.48	4.99e-07	PPIC	peptidylprolyl isomerase C
-1.34	7.96e-14	PDE6D	phosphodiesterase 6D	1.47	2.90e-06	DSG2	desmoglein 2
-1.34	1.99e-15	POLA1	DNA polymerase alpha 1, catalytic subunit	1.47	4.54e-06	P4HA2	prolyl 4-hydroxylase subunit alpha
-1.34	2.94e-09	ASF1A	anti-silencing function 1A histone	1.46	4.22e-05	NQO1	NAD(P)H quinone dehydrogenase 1
-1.33	1.61e-23	PDXP	pyridoxal phosphatase	1.44	1.60e-08	ITPRID2	ITPR interacting domain containing

GAGE analysis on upregulated and downregulated proteins at low/absent EYA3 protein, DB1



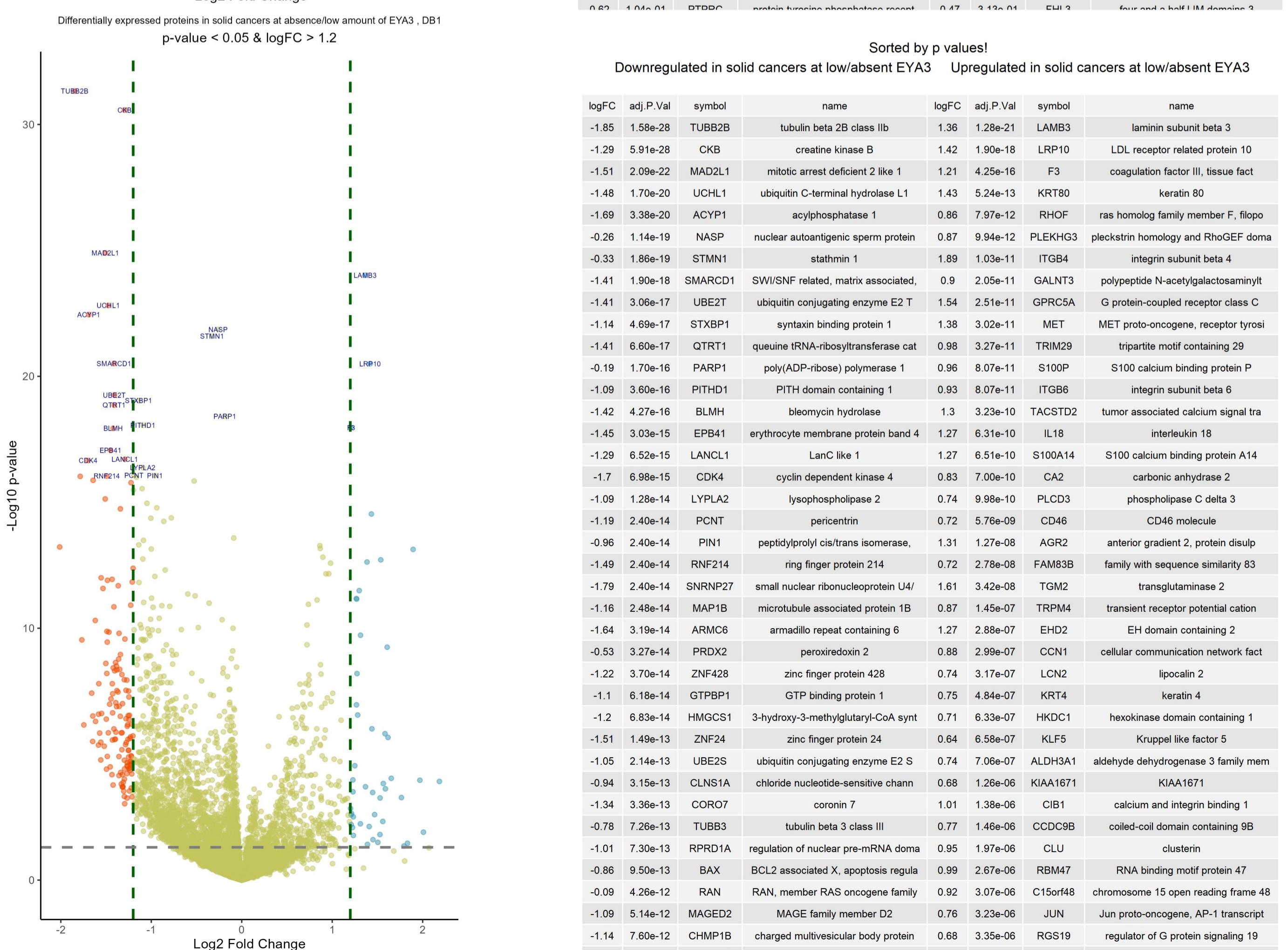
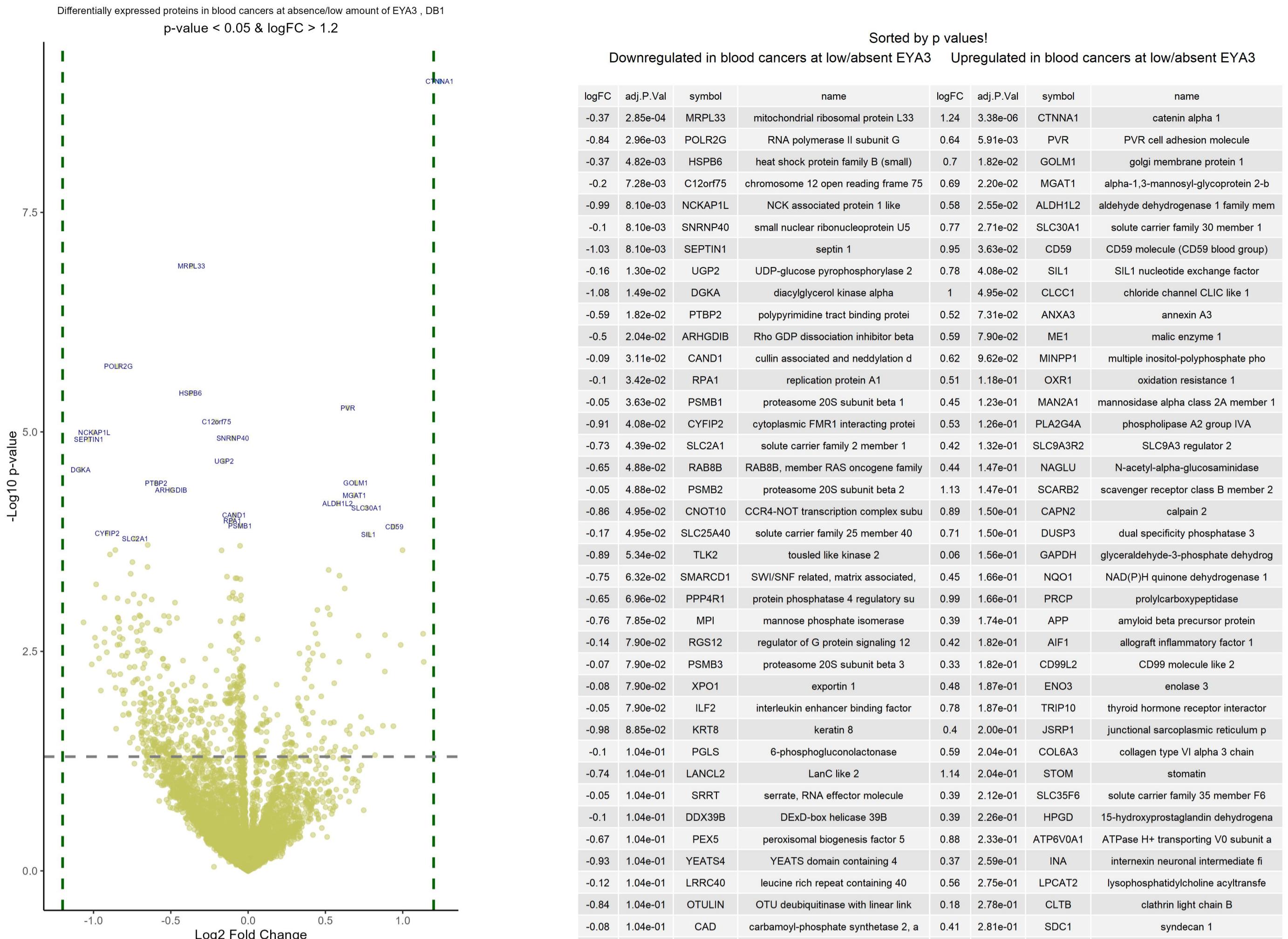


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.08	1.49e-02	DGKA	diacylglycerol kinase alpha	1.24	3.38e-06	CTNNNA1	catenin alpha 1
-1.06	1.30e-01	ACTR1B	actin related protein 1B	1.14	2.04e-01	STOM	stomatin
-1.03	8.10e-03	SEPTIN1	septin 1	1.13	1.47e-01	SCARB2	scavenger receptor class B member 2
-1.01	2.13e-01	CD37	CD37 molecule	1	4.95e-02	CLCC1	chloride channel CLIC like 1
-0.99	8.10e-03	NCKAP1L	NCK associated protein 1 like	0.99	1.66e-01	PRCP	prolylcarboxypeptidase
-0.99	1.53e-01	TRAPPC5	trafficking protein particle comple	0.95	3.63e-02	CD59	CD59 molecule (CD59 blood group)
-0.98	8.85e-02	KRT8	keratin 8	0.94	3.94e-01	RDX	radixin
-0.98	1.67e-01	CD22	CD22 molecule	0.89	1.50e-01	CAPN2	calpain 2
-0.96	1.95e-01	ARPC1A	actin related protein 2/3 complex s	0.88	2.33e-01	ATP6V0A1	ATPase H ⁺ transporting V0 subunit a
-0.95	2.95e-01	PTPRA2	protein tyrosine phosphatase 4A2	0.87	3.94e-01	RALB	RAS like proto-oncogene B
-0.93	1.63e-01	FBXO22	F-box protein 22	0.82	5.26e-01	NPC2	NPC intracellular cholesterol trans
-0.93	1.04e-01	YEATS4	YEATS domain containing 4	0.8	4.23e-01	PLBD2	phospholipase B domain containing 2
-0.93	1.42e-01	GSPT2	G1 to S phase transition 2	0.78	4.08e-02	SIL1	SIL1 nucleotide exchange factor
-0.91	1.82e-01	KRT19	keratin 19	0.78	1.87e-01	TRIP10	thyroid hormone receptor interactor
-0.91	4.08e-02	CYFIP2	cytoplasmic FMR1 interacting protei	0.77	4.08e-01	NIBAN1	niban apoptosis regulator 1
-0.9	2.34e-01	LCK	LCK proto-oncogene, Src family tyro	0.77	2.71e-02	SLC30A1	solute carrier family 30 member 1
-0.89	5.34e-02	TLK2	tousled like kinase 2	0.75	7.90e-01	ANXA2	annexin A2
-0.87	1.47e-01	ANAPC5	anaphase promoting complex subunit	0.74	4.30e-01	DNAJC3	DnaJ heat shock protein family (Hsp
-0.87	2.49e-01	PEX1	peroxisomal biogenesis factor 1	0.73	5.64e-01	PLP2	proteolipid protein 2
-0.86	4.95e-02	CNOT10	CCR4-NOT transcription complex subu	0.73	3.75e-01	PDLIM5	PDZ and LIM domain 5
-0.86	2.85e-01	PAX5	paired box 5	0.72	5.87e-01	HSPA4L	heat shock protein family A (Hsp70)
-0.85	4.08e-01	IGHM	immunoglobulin heavy constant mu	0.71	1.50e-01	DUSP3	dual specificity phosphatase 3
-0.85	1.66e-01	CD38	CD38 molecule	0.71	6.51e-01	ACTN1	actinin alpha 1
-0.84	1.04e-01	OTULIN	OTU deubiquitinase with linear link	0.71	6.80e-01	RCN1	reticulocalbin 1
-0.84	1.26e-01	SLC25A11	solute carrier family 25 member 11	0.7	1.82e-02	GOLM1	golgi membrane protein 1
-0.84	1.26e-01	MRPS14	mitochondrial ribosomal protein S14	0.69	6.99e-01	EPB41L2	erythrocyte membrane protein band 4
-0.84	2.96e-03	POLR2G	RNA polymerase II subunit G	0.69	5.04e-01	PCCB	propionyl-CoA carboxylase subunit b
-0.83	1.30e-01	POLR1B	RNA polymerase I subunit B	0.69	6.37e-01	DTD1	D-aminoacyl-tRNA deacylase 1
-0.83	1.42e-01	EED	embryonic ectoderm development	0.69	2.20e-02	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-b



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.01	8.79e-12	DPYSL5	dihydropyrimidinase like 5	2.18	1.20e-03	CAVIN1	caveolae associated protein 1
-1.85	1.58e-28	TUBB2B	tubulin beta 2B class IIb	2.07	1.41e-01	LGALS3	galectin 3
-1.79	2.40e-14	SNRNP27	small nuclear ribonucleoprotein U4/U	2.01	4.89e-02	CD44	CD44 molecule (Indian blood group)
-1.77	1.84e-08	CRMP1	collapsin response mediator protein	1.97	1.10e-03	SQOR	sulfide quinone oxidoreductase
-1.75	1.59e-05	MSI1	musashi RNA binding protein 1	1.89	1.03e-11	ITGB4	integrin subunit beta 4
-1.7	6.98e-15	CDK4	cyclin dependent kinase 4	1.83	1.05e-01	S100A10	S100 calcium binding protein A10
-1.69	3.38e-20	ACYP1	acylphosphatase 1	1.8	3.30e-01	ANXA1	annexin A1
-1.66	1.37e-06	RBP1	retinol binding protein 1	1.79	1.26e-01	ITGA3	integrin subunit alpha 3
-1.65	5.63e-05	PHF20L1	PHD finger protein 20 like 1	1.77	4.00e-03	EGFR	epidermal growth factor receptor
-1.65	8.12e-06	ERI3	ERI1 exoribonuclease family member	1.68	1.74e-01	NCEH1	neutral cholesterol ester hydrolase
-1.64	3.19e-14	ARMC6	armadillo repeat containing 6	1.65	9.57e-04	NT5E	5'-nucleotidase ecto
-1.62	3.90e-09	SPINDOC	spindlin interactor and repressor o	1.62	4.14e-05	ADGRE5	adhesion G protein-coupled receptor
-1.62	1.21e-05	SEPTIN3	septin 3	1.61	3.42e-08	TGM2	transglutaminase 2
-1.58	7.46e-05	CBX2	chromobox 2	1.59	2.06e-03	ADAM9	ADAM metallopeptidase domain 9
-1.58	7.08e-06	C20orf27	chromosome 20 open reading frame 27	1.58	3.03e-05	EPS8L2	EPS8 like 2
-1.58	6.33e-07	IPO8	importin 8	1.56	1.40e-03	HLA-B	major histocompatibility complex, c
-1.57	2.91e-05	GPX7	glutathione peroxidase 7	1.56	2.28e-02	S100A16	S100 calcium binding protein A16
-1.56	2.38e-04	ASRGL1	asparaginase and isoasparyl peptid	1.54	2.51e-11	GPRC5A	G protein-coupled receptor class C
-1.56	5.98e-05	KIF5C	kinesin family member 5C	1.53	4.11e-03	RRAS	RAS related
-1.55	1.12e-10	NUDT3	nudix hydrolase 3	1.53	5.78e-02	CTSZ	cathepsin Z
-1.55	6.73e-06	EIF4ENIF1	eukaryotic translation initiation f	1.5	9.93e-02	CNN2	calponin 2
-1.53	2.70e-10	SMAD4	SMAD family member 4	1.47	1.41e-02	ITGAV	integrin subunit alpha V
-1.52	8.11e-05	MEX3A	mex-3 RNA binding family member A	1.45	8.29e-02	MVP	major vault protein
-1.51	1.49e-13	ZNF24	zinc finger protein 24	1.45	2.70e-03	EPHA2	EPH receptor A2
-1.51	2.09e-22	MAD2L1	mitotic arrest deficient 2 like 1	1.44	2.11e-05	FAM83H	family with sequence similarity 83
-1.5	1.32e-07	ZMYM4	zinc finger MYM-type containing 4	1.43	5.24e-13	KRT80	keratin 80
-1.5	1.03e-05	TRIT1	tRNA isopentenyltransferase 1	1.42	1.90e-18	LRP10	LDL receptor related protein 10
-1.5	4.72e-04	ZNF462	zinc finger protein 462	1.41	3.28e-02	CAV1	caveolin 1
-1.49	2.40e-14	RNF214	ring finger protein 214	1.39	1.14e-01	RHOC	ras homolog family member C

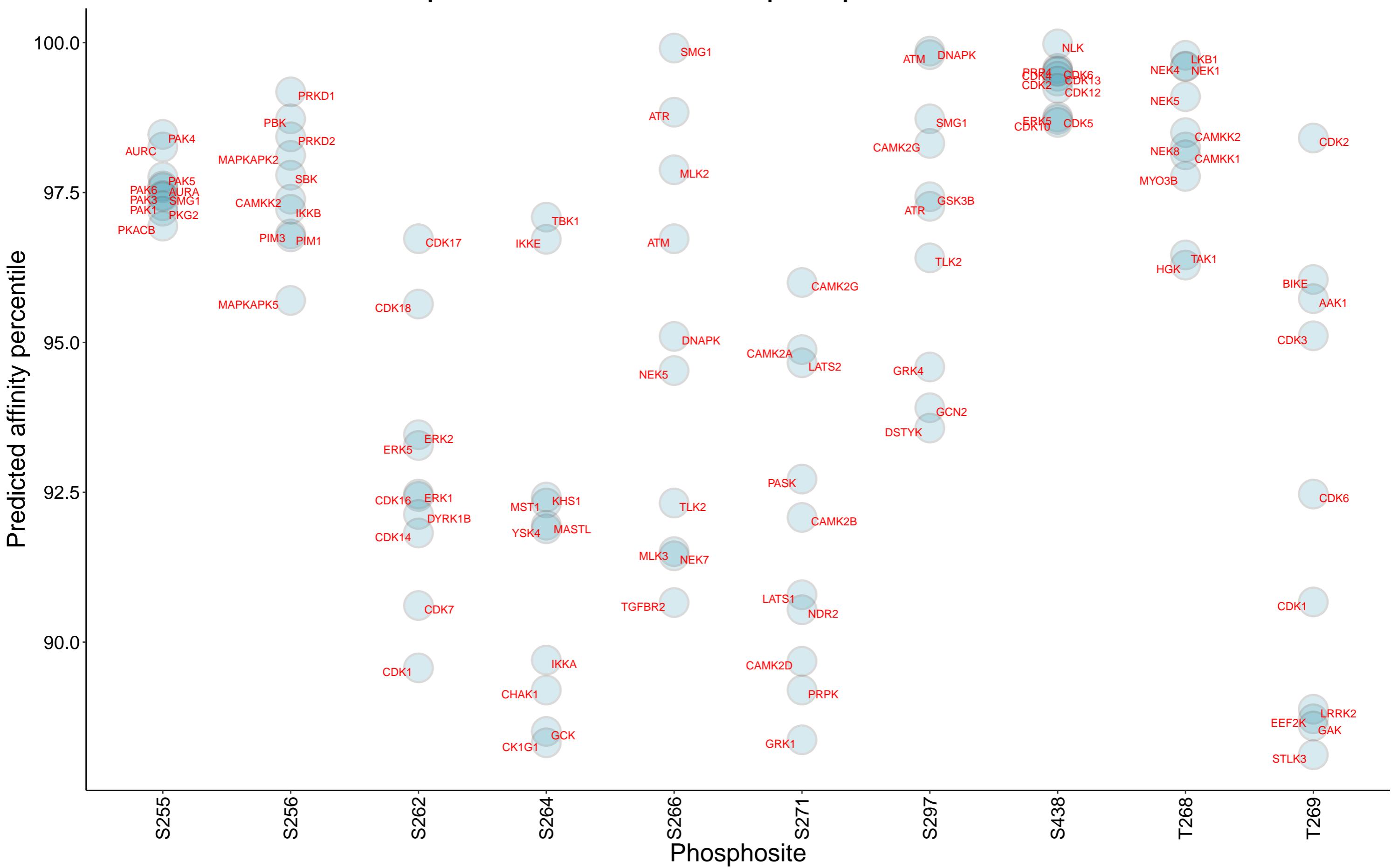
EYA3 network, DB1, no Pearson r > 0.3



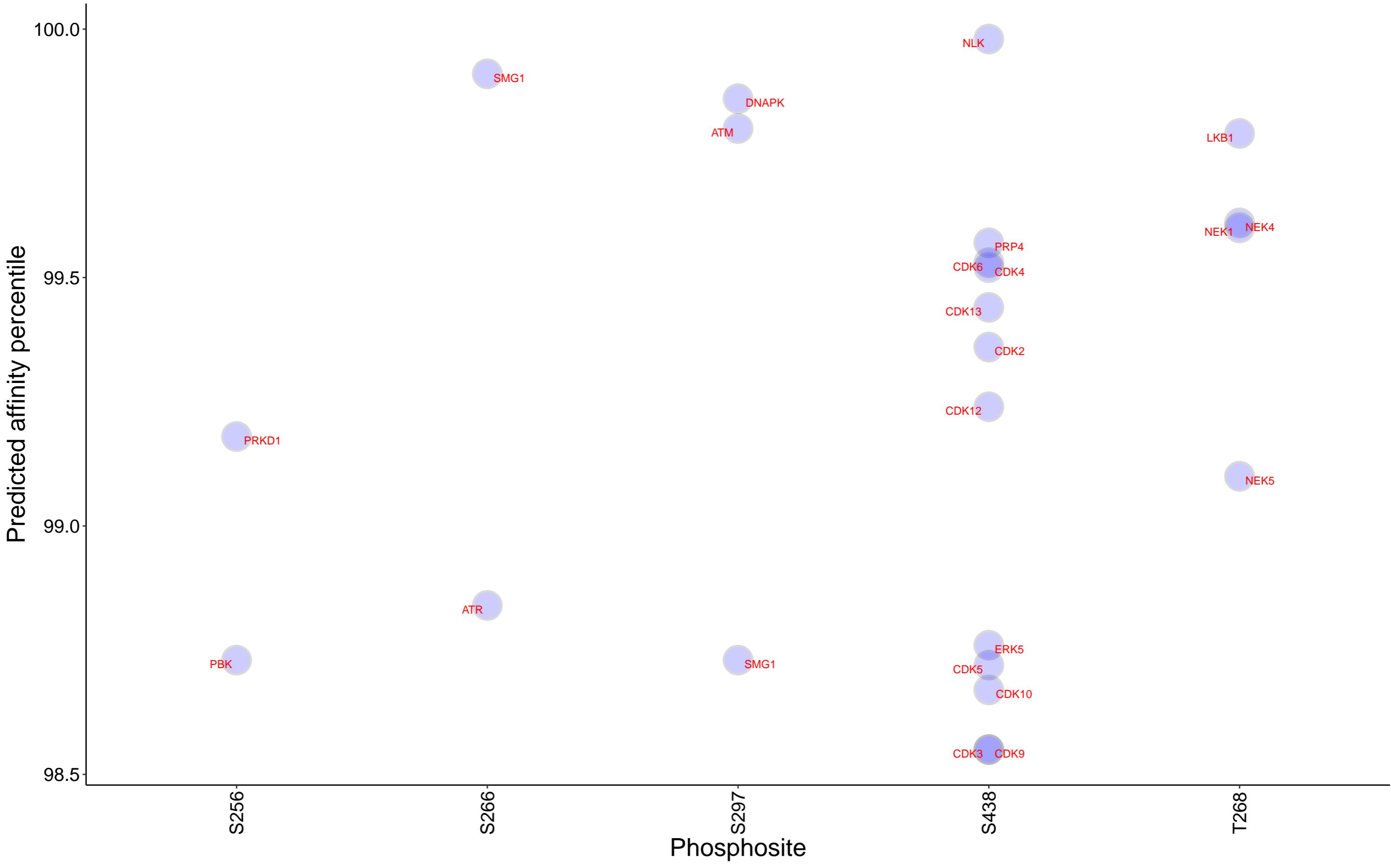
Insufficient number of paired observations in DB1 for EYA3

Insufficient number of paired observations in DB1 for EYA3

Top 10 kinases for each phosphosite in EYA3



Kinases with affinity greater than 98.5% to EYA3



No sufficient paired observations in DB1 for EYA3