

EYA1

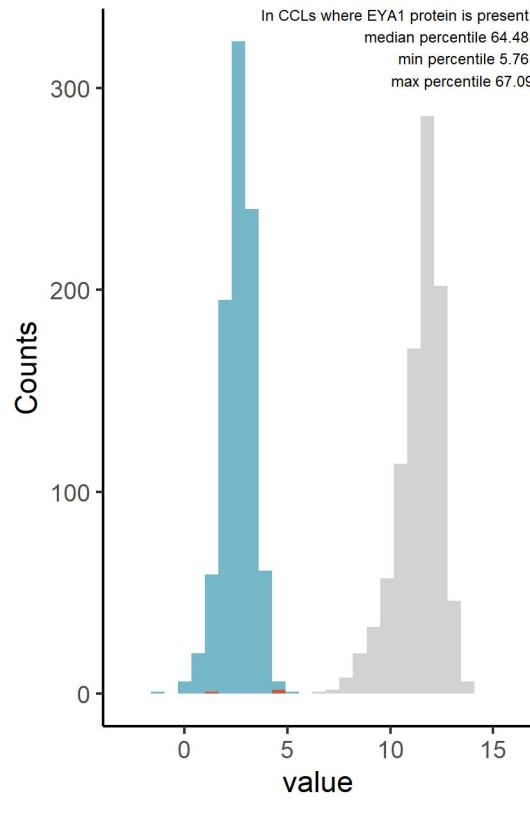
Protein name: EYA1 ; UNIPROT: Q99502 ; Gene name: EYA transcriptional coactivator and phosphatase 1

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

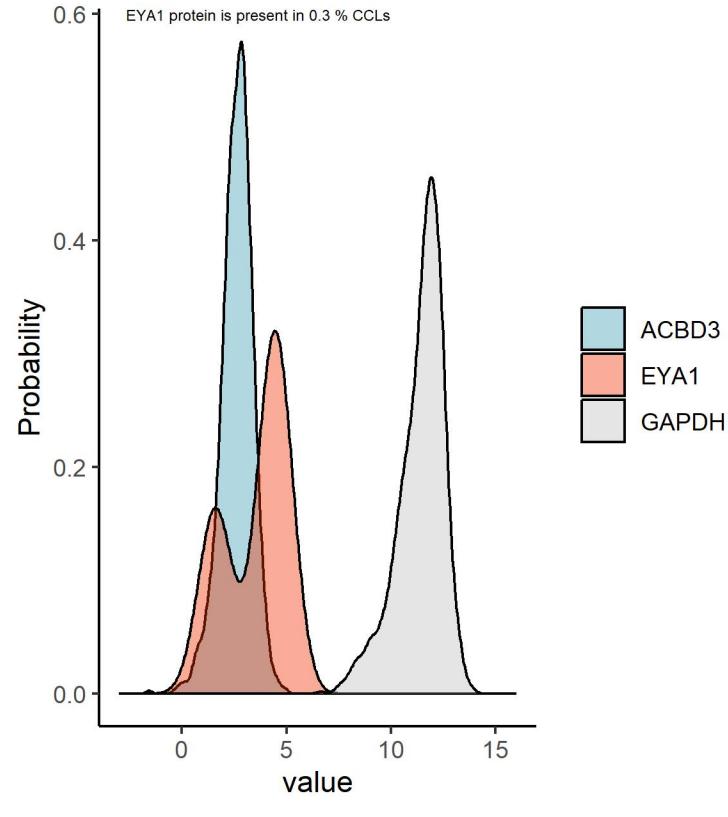
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

Histogram of EYA1 protein compared to proteins with low and high abundance



Density plot of EYA1 protein compared to proteins with low and high abundance



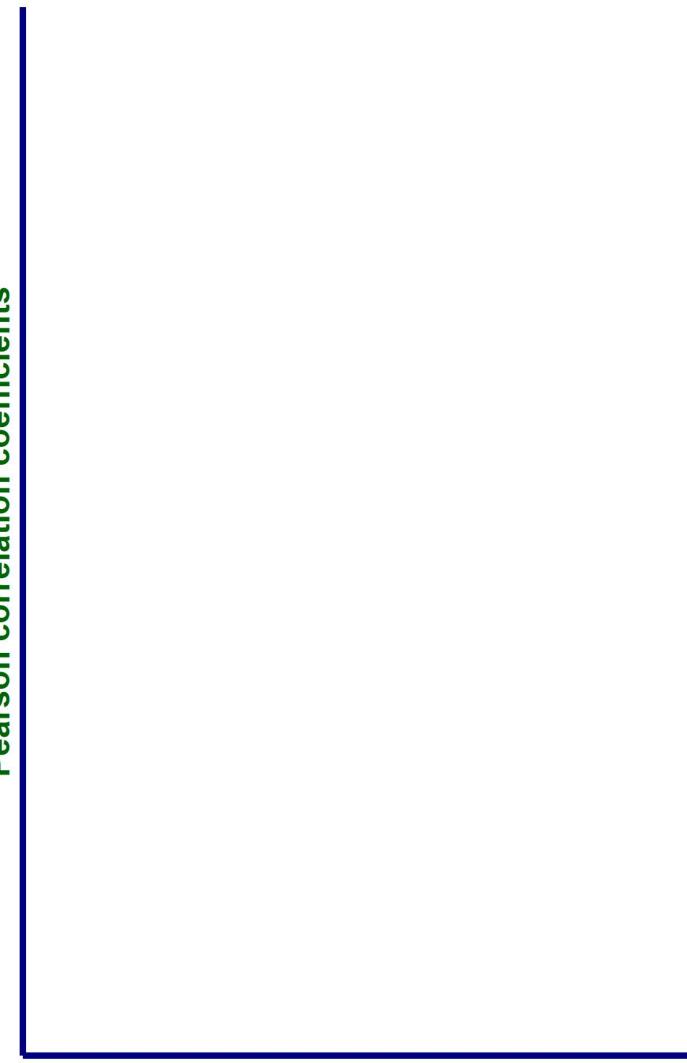
Top negative correlations of EYA1 protein, DB1

Pearson correlation coefficients



Top positive correlations of EYA1 protein, DB1

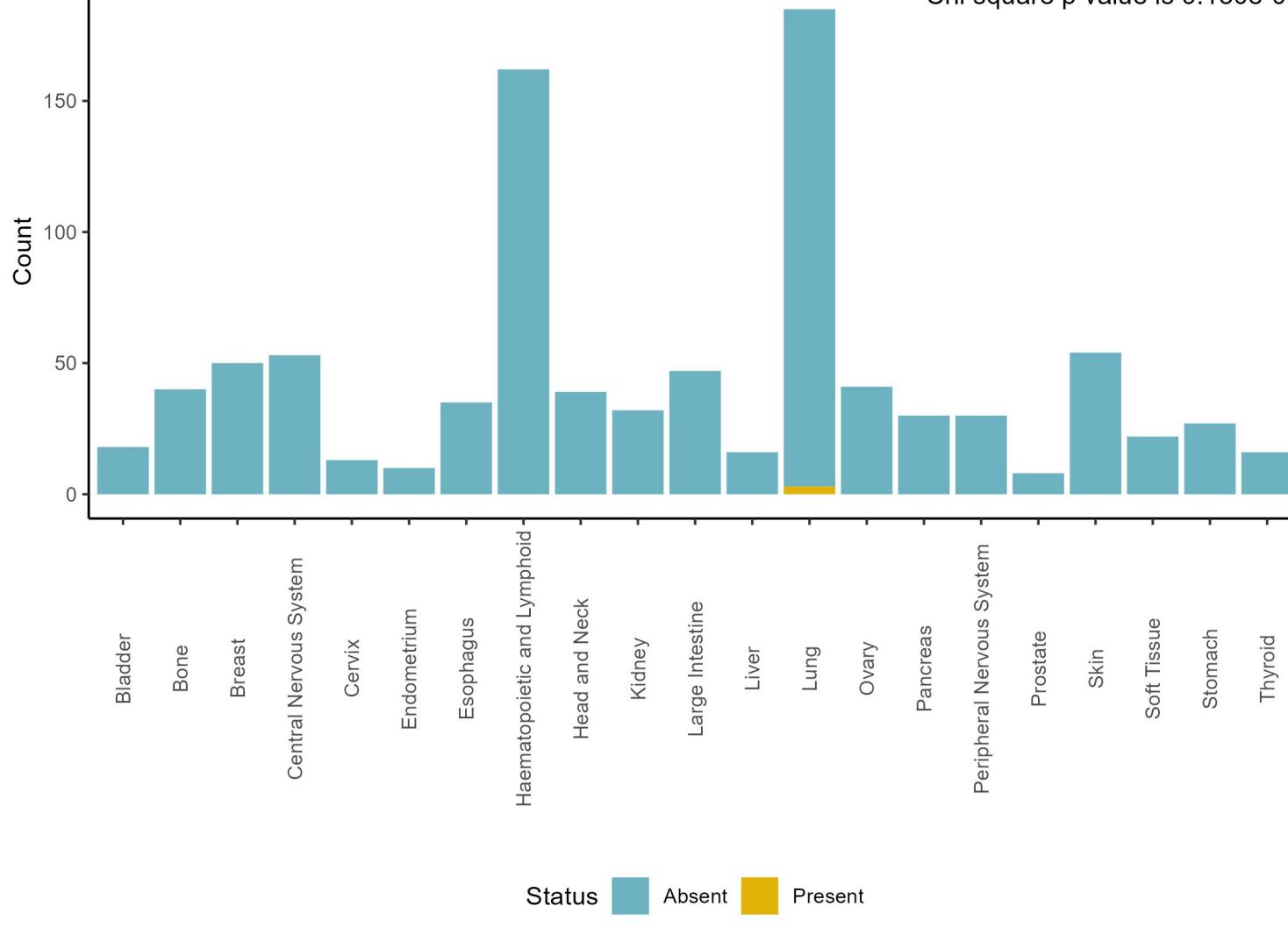
Pearson correlation coefficients



Amount of EYA1 protein, number of CCLs where it is present by tissue, DB1

Present and absent EYA1 protein counts by tissue, DB1

Chi square p value is 9.130e-01

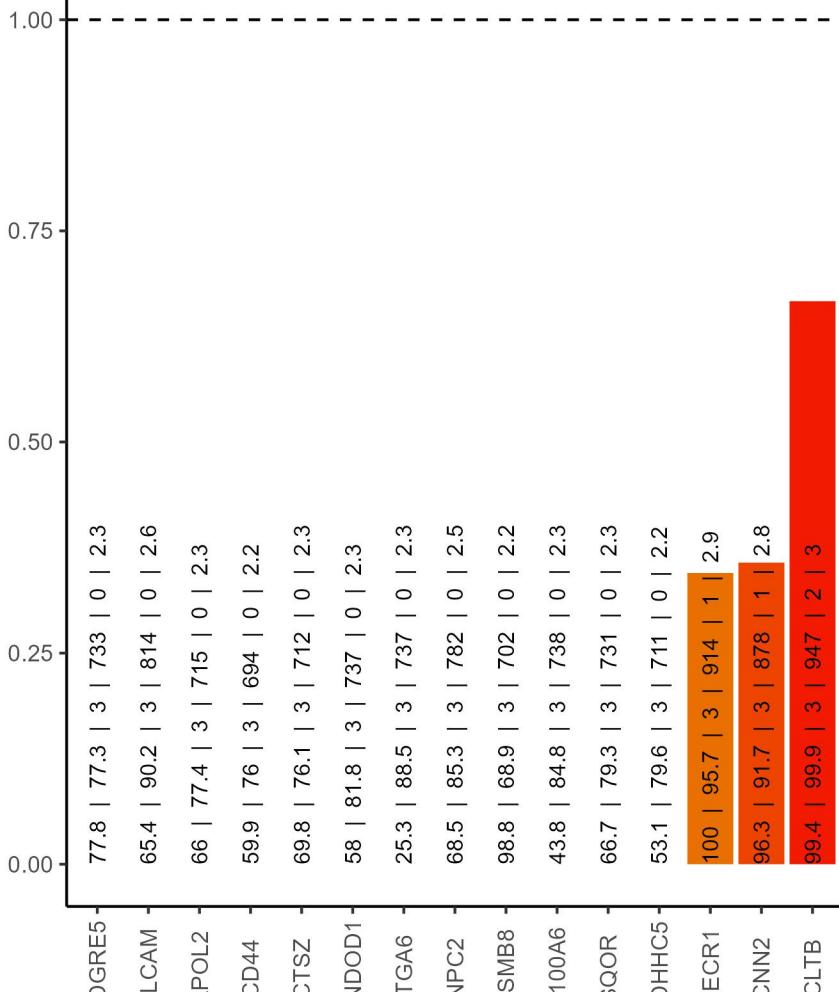


Cooccurrence with EYA1 protein, DB1

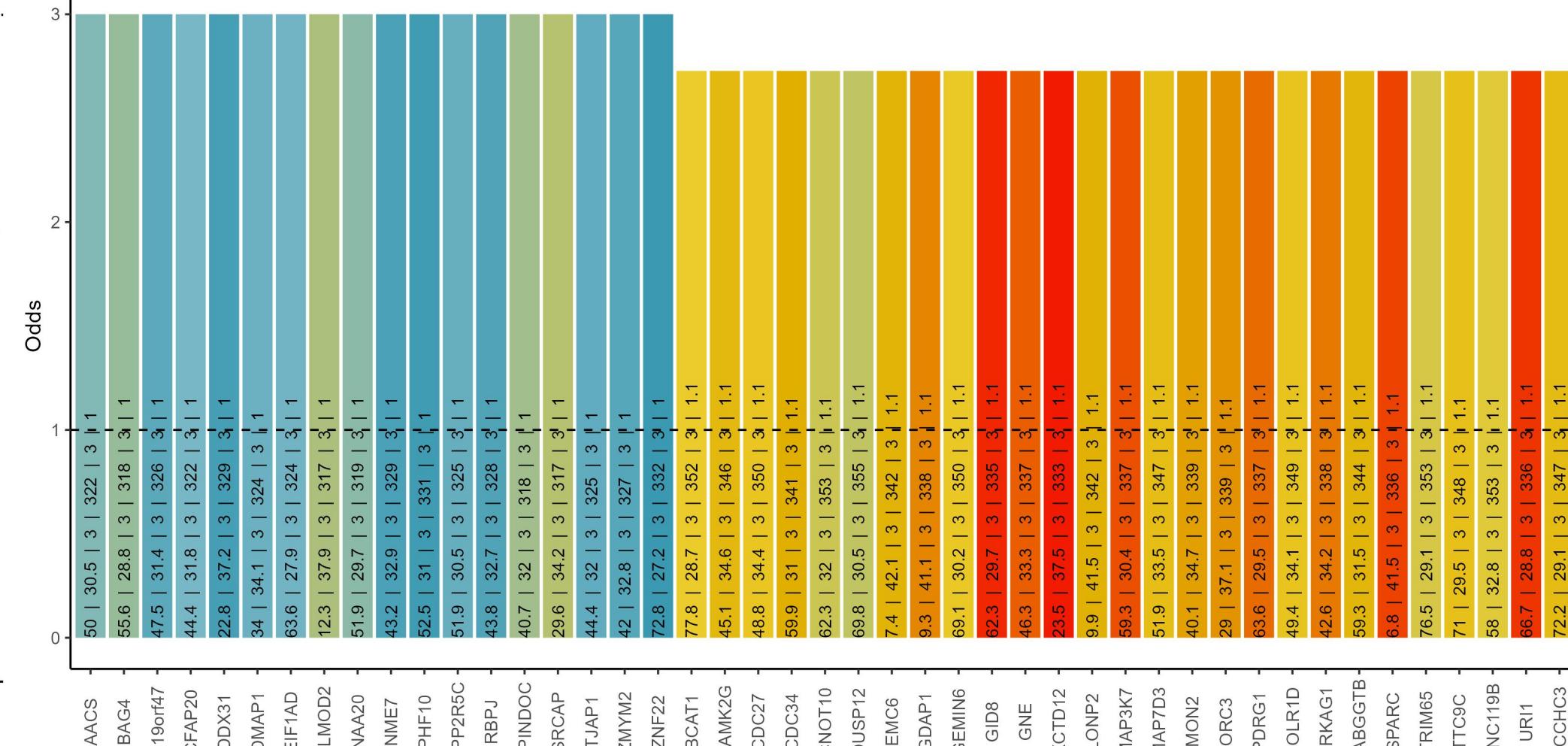
% of EYA1 in blood cancers: 0 ; % of EYA1 in solid cancers: 0.4

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of EYA1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

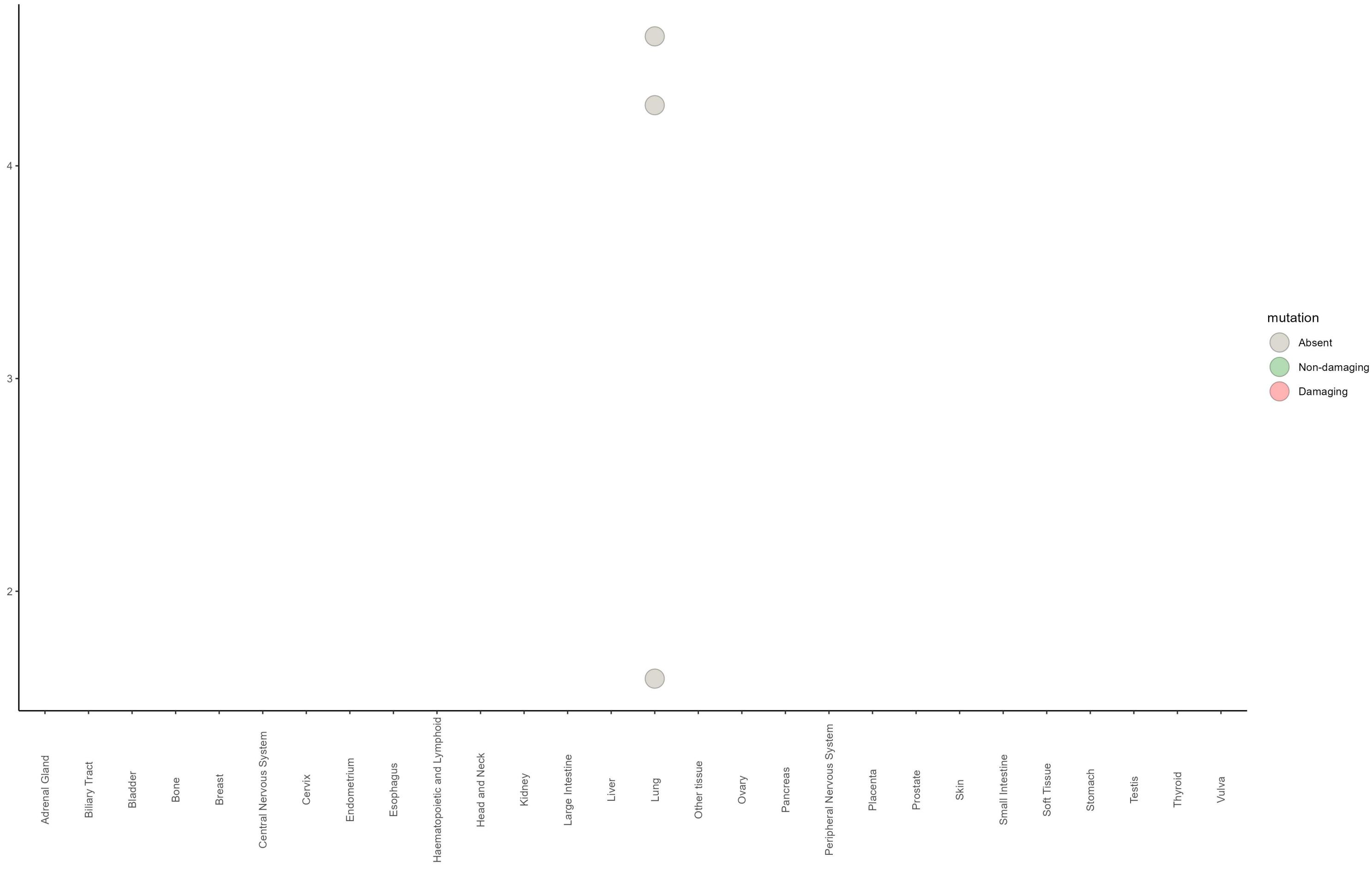
Negative cooccurrence



Positive cooccurrence

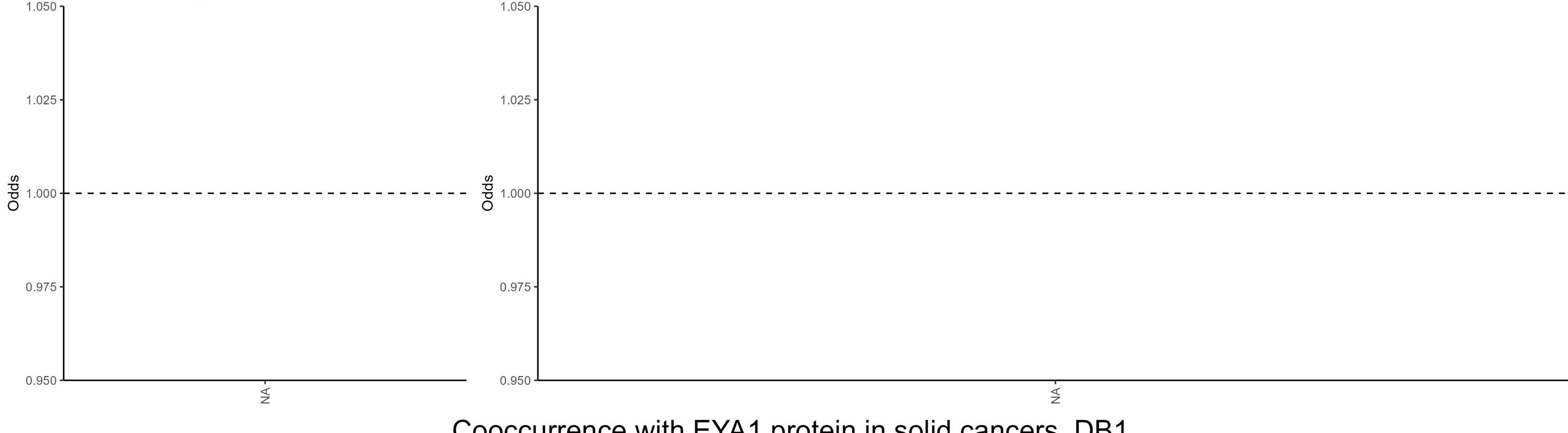


Amount of EYA1 protein and mutation status by tissue, DB1



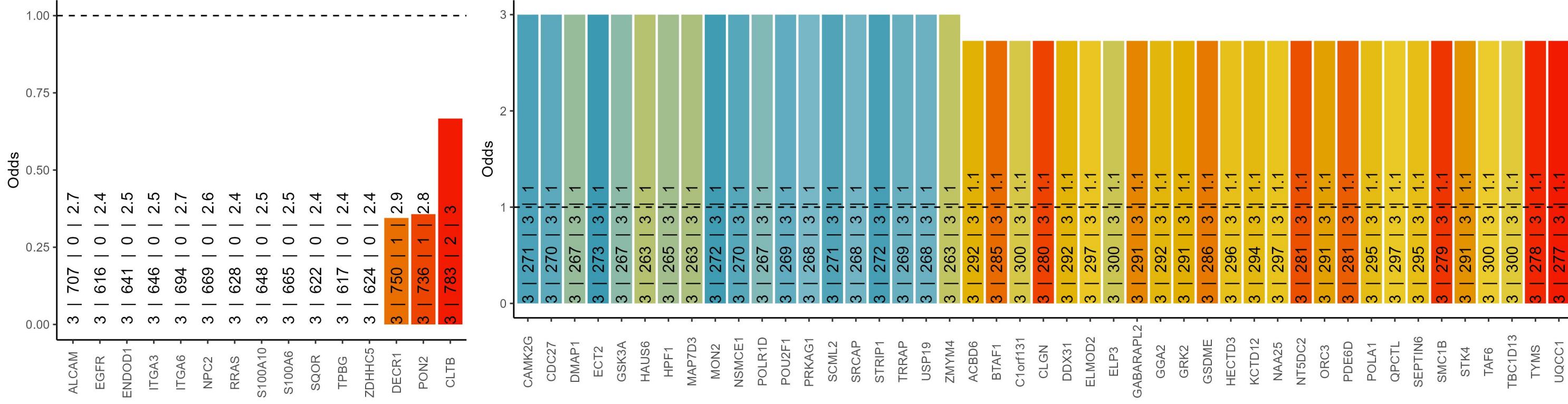
Cooccurrence with EYA1 protein in blood cancers, DB1

The text in the bars: incidence of EYA1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

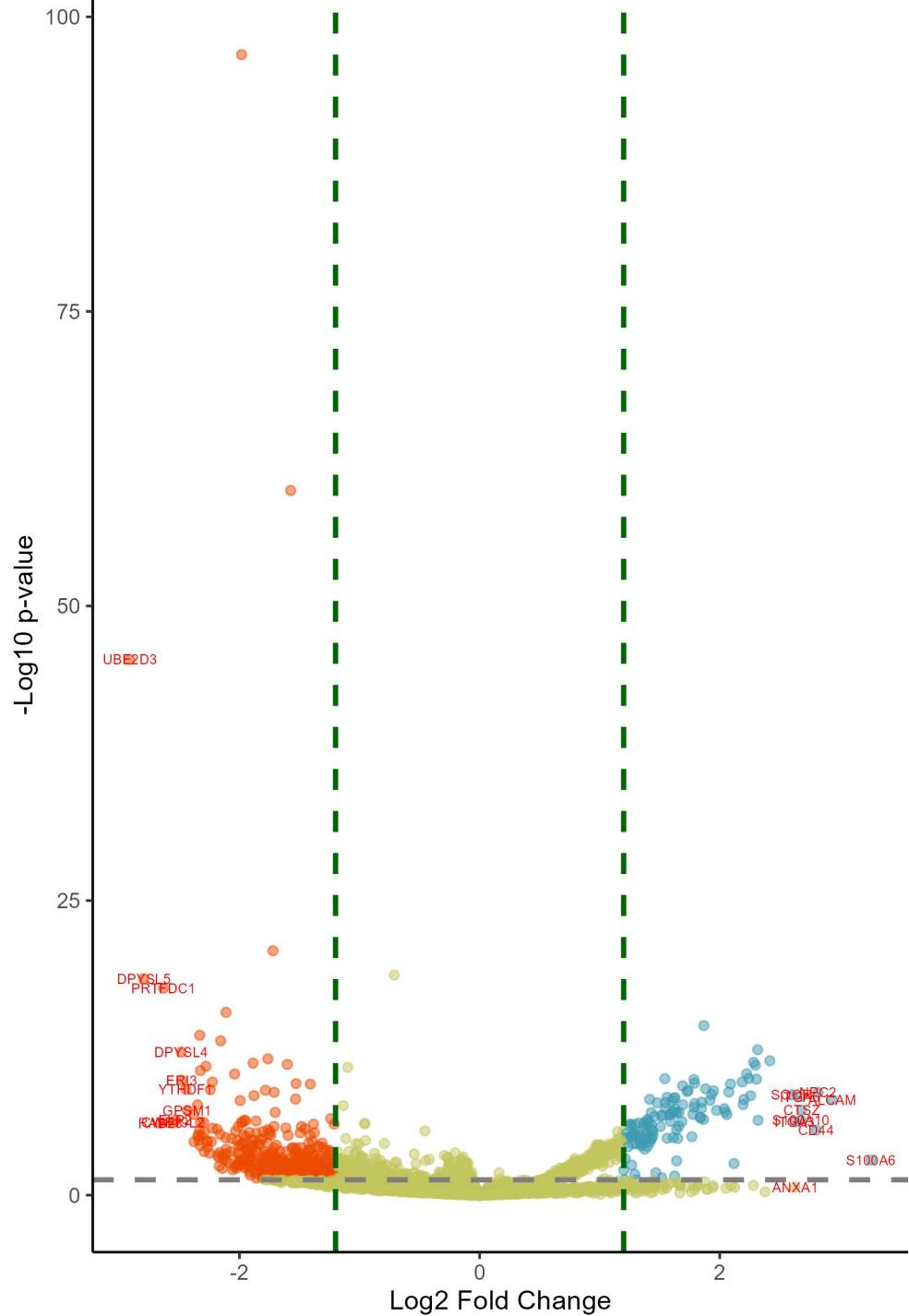


Cooccurrence with EYA1 protein in solid cancers, DB1

The text in the bars: incidence of EYA1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



p-value < 0.05 & logFC > 1.2

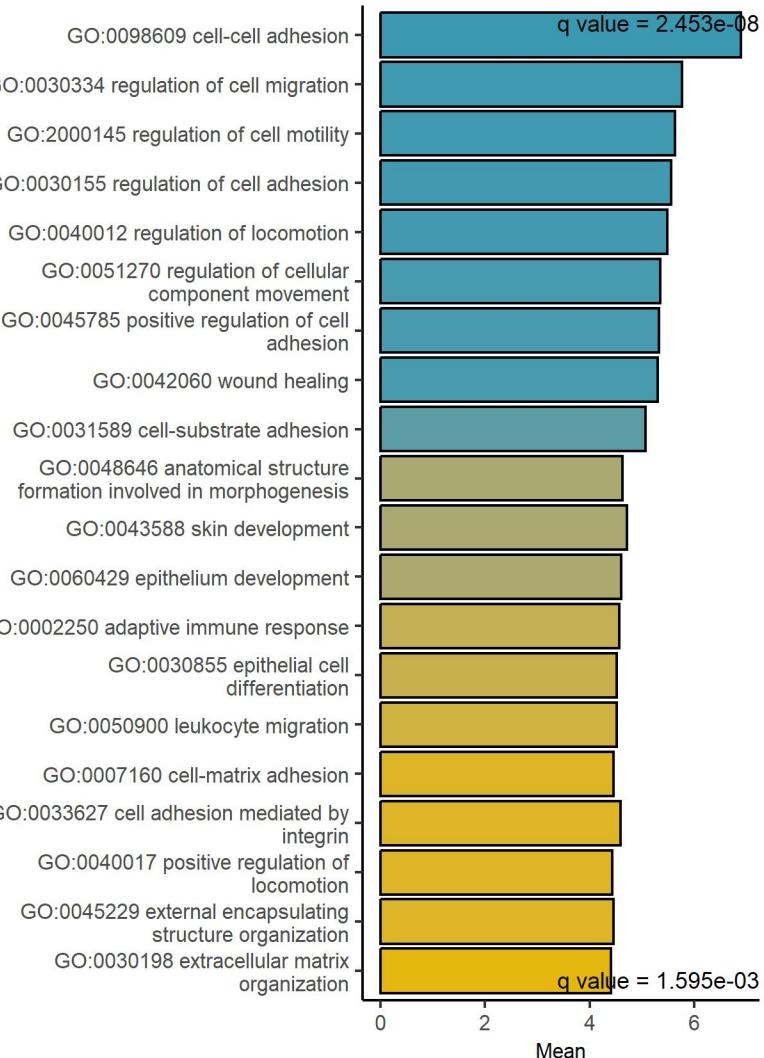


Downregulated at low/absent EYA1 Upregulated at low/absent EYA1

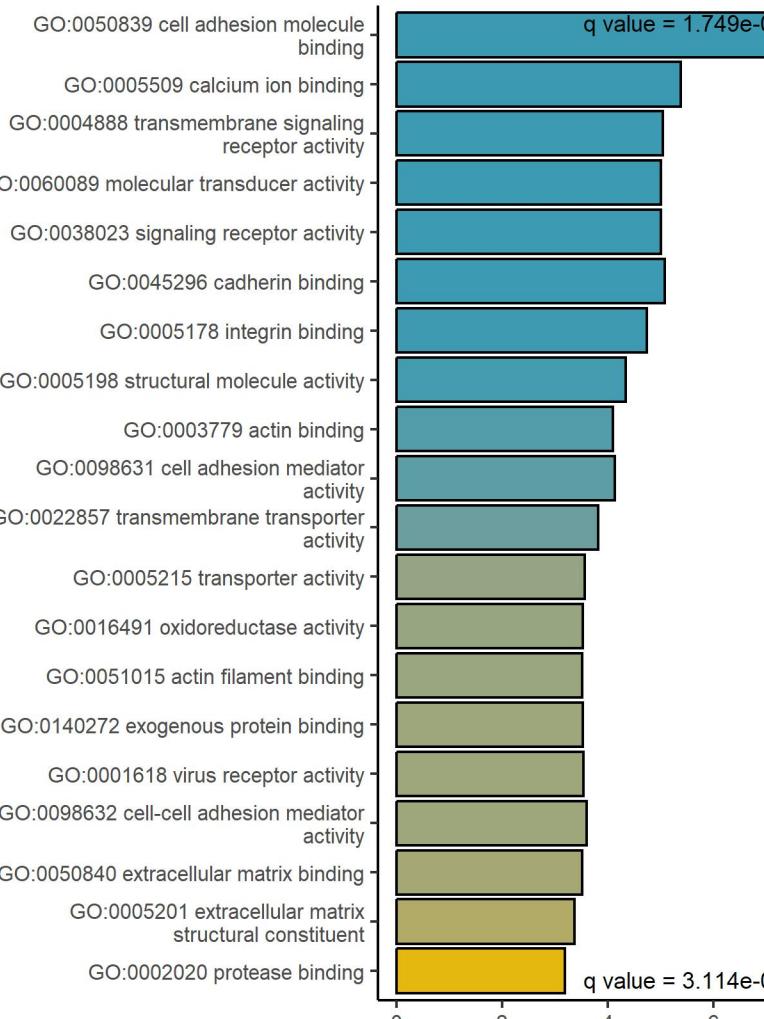
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.91	5.79e-43	UBE2D3	ubiquitin conjugating enzyme E2 D3	3.26	1.74e-02	S100A6	S100 calcium binding protein A6
-2.8	4.08e-16	DPYSL5	dihydropyrimidinase like 5	2.94	9.02e-07	ALCAM	activated leukocyte cell adhesion m
-2.66	4.25e-05	RAB28	RAB28, member RAS oncogene family	2.82	2.73e-07	NPC2	NPC intracellular cholesterol trans
-2.63	2.26e-15	PRTFDC1	phosphoribosyl transferase domain c	2.8	1.41e-04	CD44	CD44 molecule (Indian blood group)
-2.55	4.11e-05	CWF19L2	CWF19 like cell cycle control facto	2.68	5.22e-06	CTSZ	cathepsin Z
-2.54	2.82e-05	ELP2	elongator acetyltransferase complex	2.68	2.84e-05	S100A10	S100 calcium binding protein A10
-2.49	3.51e-10	DPYSL4	dihydropyrimidinase like 4	2.67	5.64e-07	ITGA6	integrin subunit alpha 6
-2.48	4.01e-08	ERI3	ERI1 exoribonuclease family member	2.63	5.99e-01	ANXA1	annexin A1
-2.45	1.75e-07	YTHDF1	YTH N6-methyladenosine RNA binding	2.63	3.62e-05	ITGA3	integrin subunit alpha 3
-2.44	5.36e-06	GPSM1	G protein signaling modulator 1	2.6	4.10e-07	SQOR	sulfide quinone oxidoreductase
-2.38	1.06e-05	JMD6	jumonji domain containing 6, argini	2.42	1.63e-09	ENDOD1	endonuclease domain containing 1
-2.38	9.73e-04	PCBP4	poly(rC) binding protein 4	2.38	8.61e-01	LGALS1	galectin 1
-2.35	2.09e-06	RAB6B	RAB6B, member RAS oncogene family	2.32	2.84e-05	CAVIN1	caveolae associated protein 1
-2.35	3.80e-04	CBX2	chromobox 2	2.32	2.33e-10	ADGRE5	adhesion G protein-coupled receptor
-2.34	3.15e-04	WAC	WW domain containing adaptor with c	2.31	3.43e-08	GLRX	glutaredoxin
-2.34	7.23e-04	KCTD15	potassium channel tetramerization d	2.3	3.09e-09	PSMB8	proteasome 20S subunit beta 8
-2.33	1.38e-04	GINS1	GINS complex subunit 1	2.28	2.11e-09	APOL2	apolipoprotein L2
-2.33	1.64e-11	CELF2	CUGBP Elav-like family member 2	2.28	5.04e-01	DECRI	2,4-dienoyl-CoA reductase 1
-2.33	1.82e-03	NFIB	nuclear factor I B	2.26	4.79e-07	DSG2	desmoglein 2
-2.33	3.84e-05	C9orf64	chromosome 9 open reading frame 64	2.24	3.15e-08	IFI16	interferon gamma inducible protein
-2.33	7.83e-09	SARM1	sterile alpha and TIR motif contain	2.22	1.38e-08	TAP1	transporter 1, ATP binding cassette
-2.32	3.78e-04	DPH5	diphthamide biosynthesis 5	2.2	8.78e-07	EGFR	epidermal growth factor receptor
-2.3	3.92e-05	DCAF16	DDB1 and CUL4 associated factor 16	2.2	2.04e-06	VAMP8	vesicle associated membrane protein
-2.29	4.74e-03	ZNF462	zinc finger protein 462	2.19	5.24e-08	RRAS	RAS related
-2.29	1.89e-04	WDR54	WD repeat domain 54	2.12	6.11e-01	NCEH1	neutral cholesterol ester hydrolase
-2.28	3.69e-09	GTF2E1	general transcription factor IIIE su	2.12	2.80e-02	HLA-B	major histocompatibility complex, c
-2.27	9.46e-04	ACTR1B	actin related protein 1B	2.1	5.18e-01	ANXA4	annexin A4
-2.27	8.55e-04	ARID3B	AT-rich interaction domain 3B	2.09	6.96e-08	TPBG	trophoblast glycoprotein
-2.27	2.28e-03	MEX3A	mex-3 RNA binding family member A	2.08	2.63e-07	ADAM9	ADAM metallopeptidase domain 9

GAGE analysis on upregulated and downregulated proteins at low/absent EYA1 protein, DB1

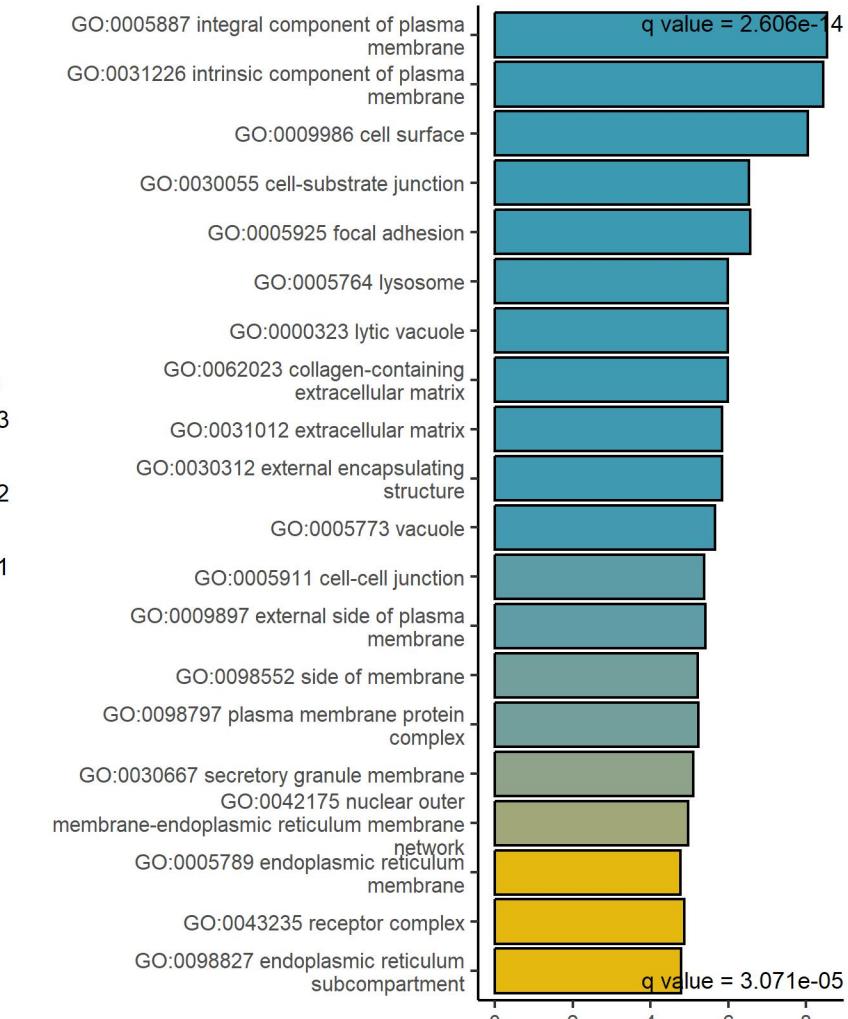
GO Biological Process upregulated



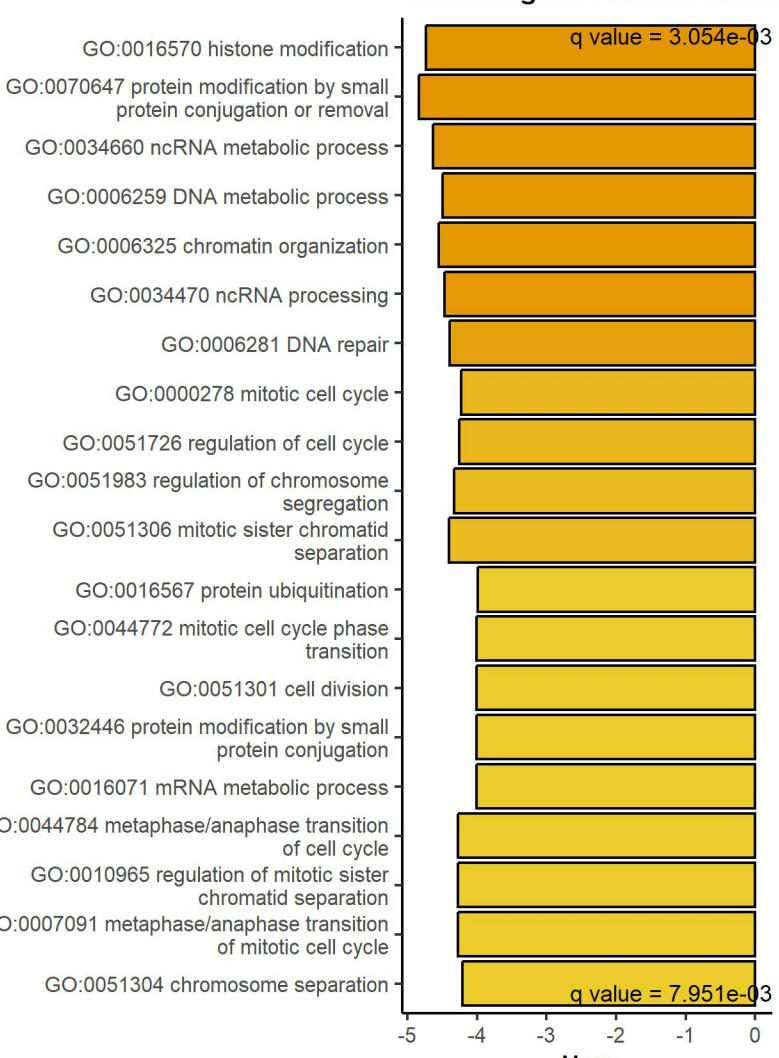
GO Molecular Function upregulated



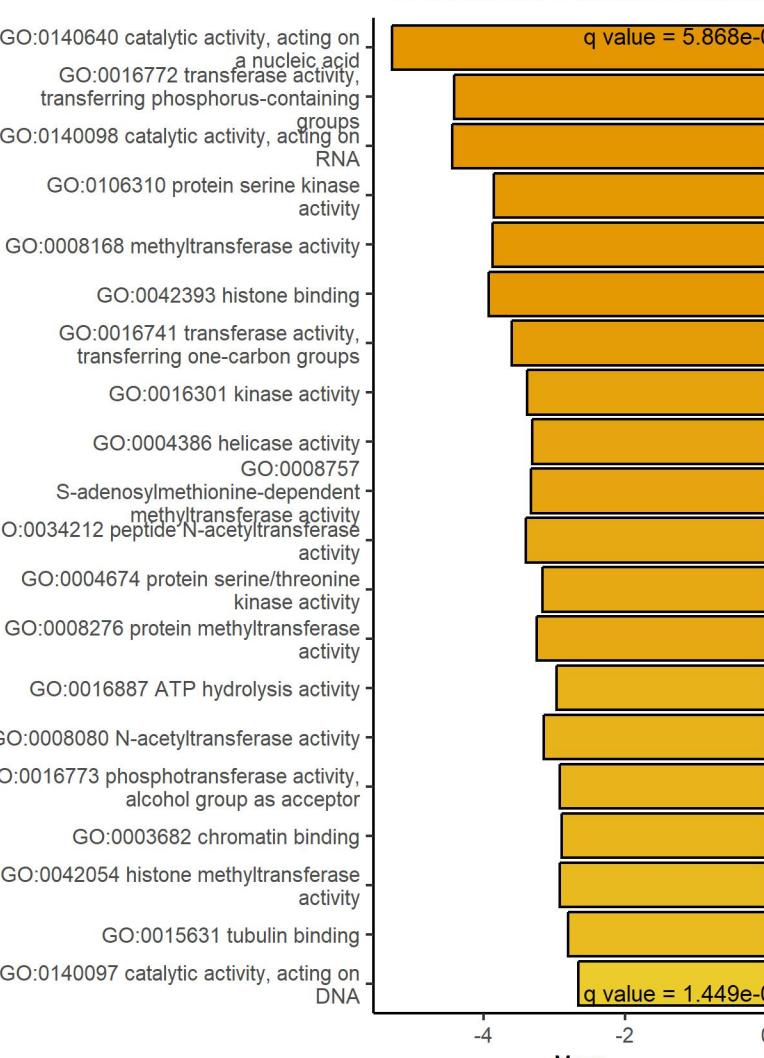
GO Cellular Component upregulated

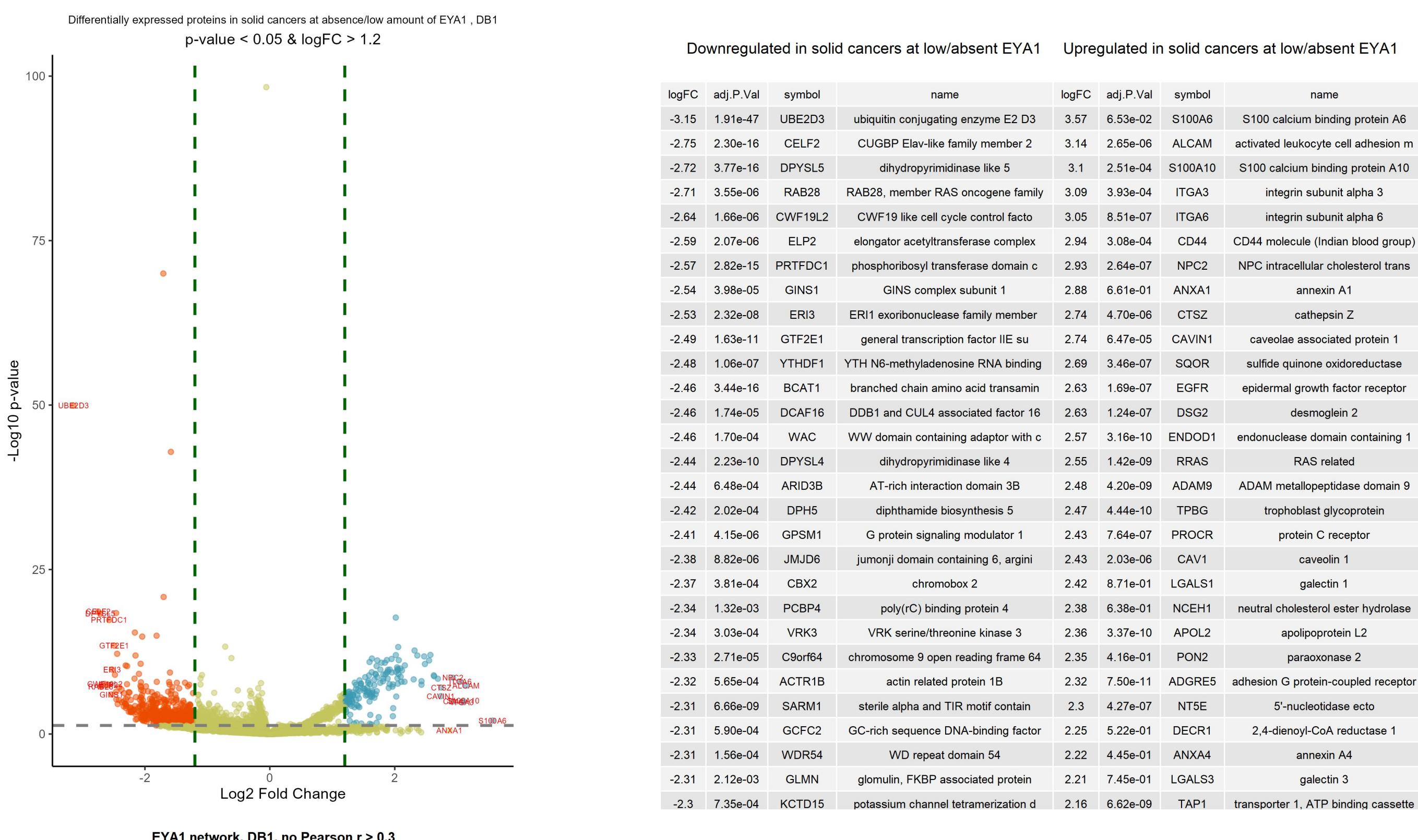


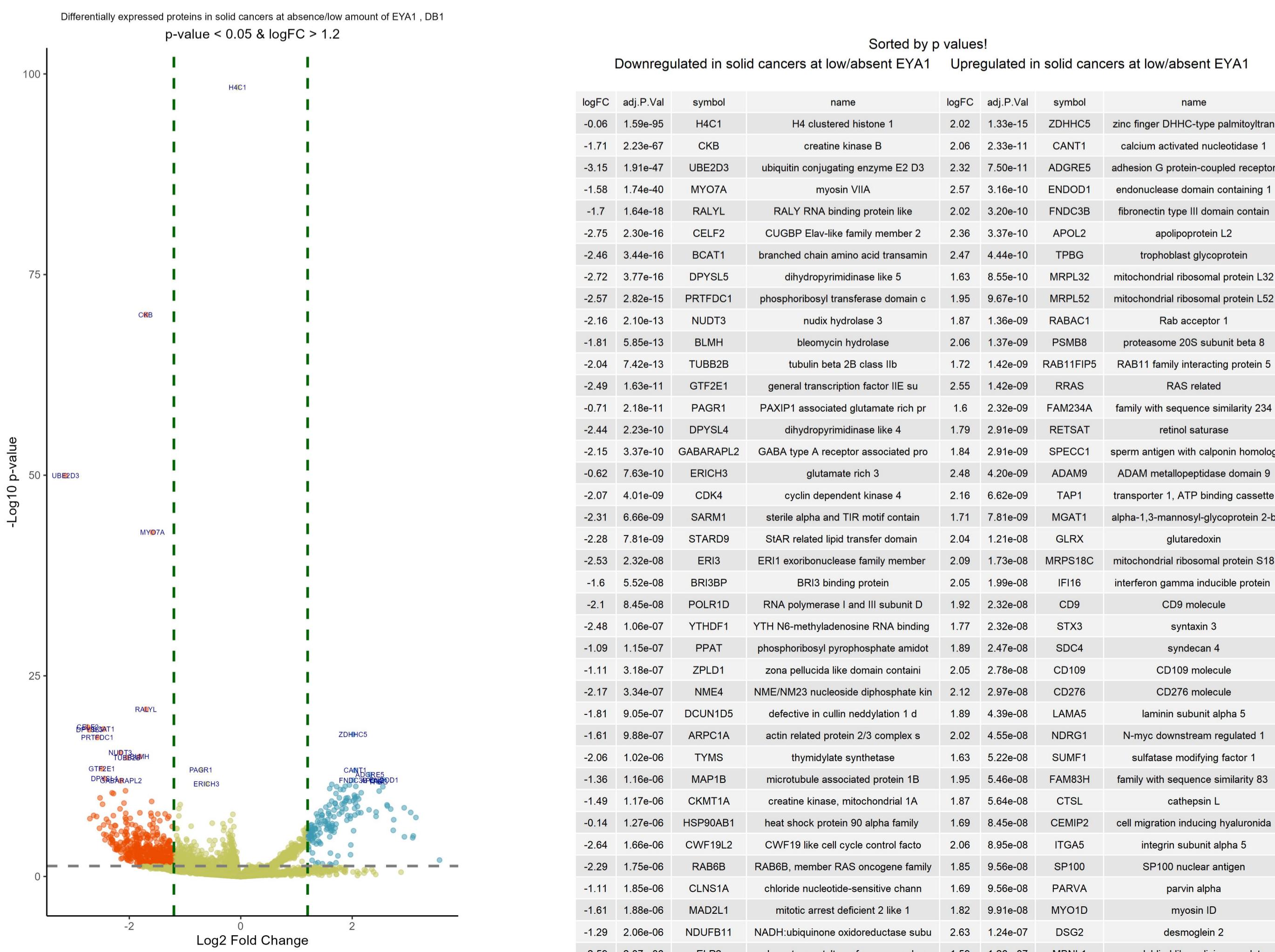
GO Biological Process downregulated



GO Molecular Function downregulated



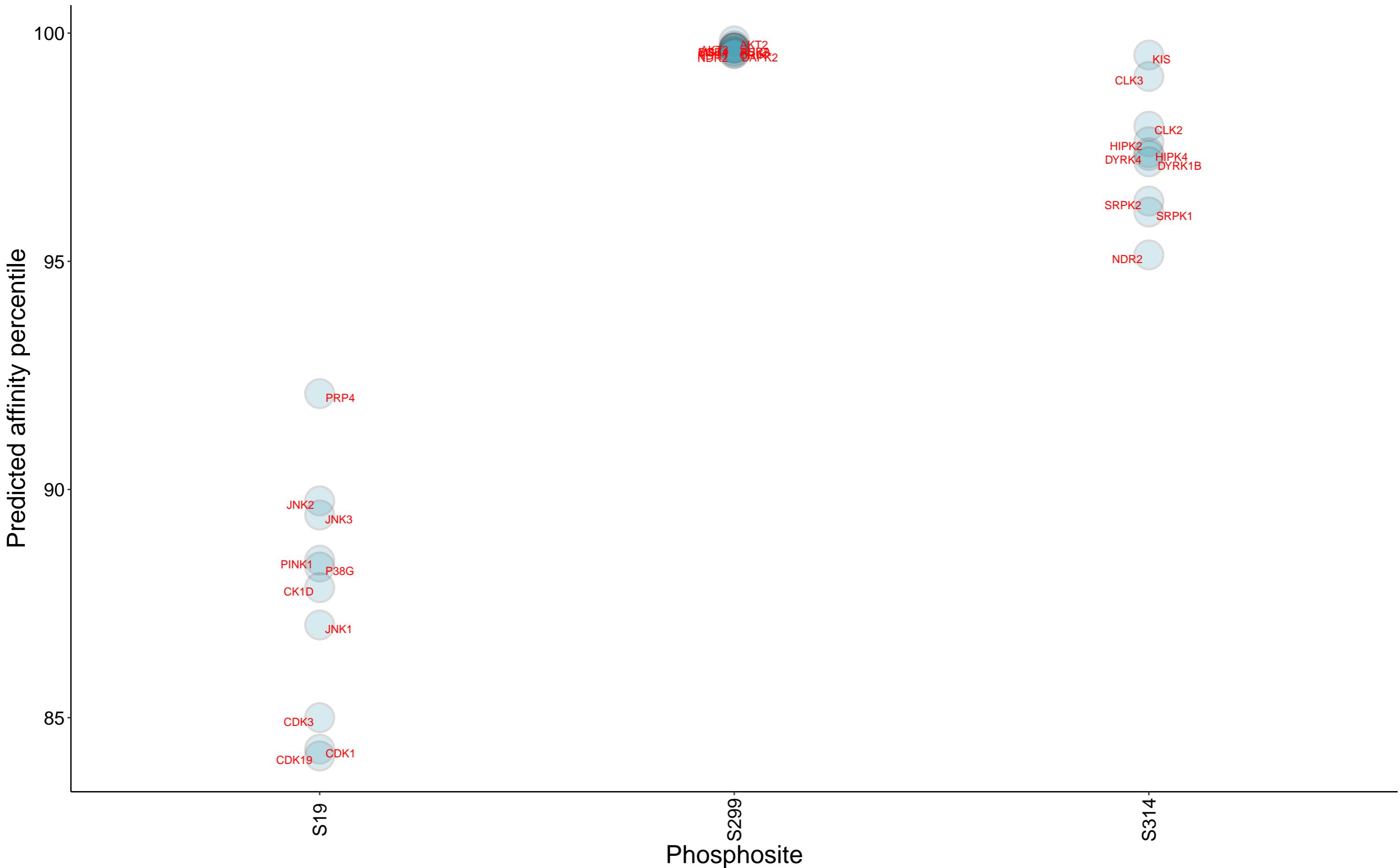




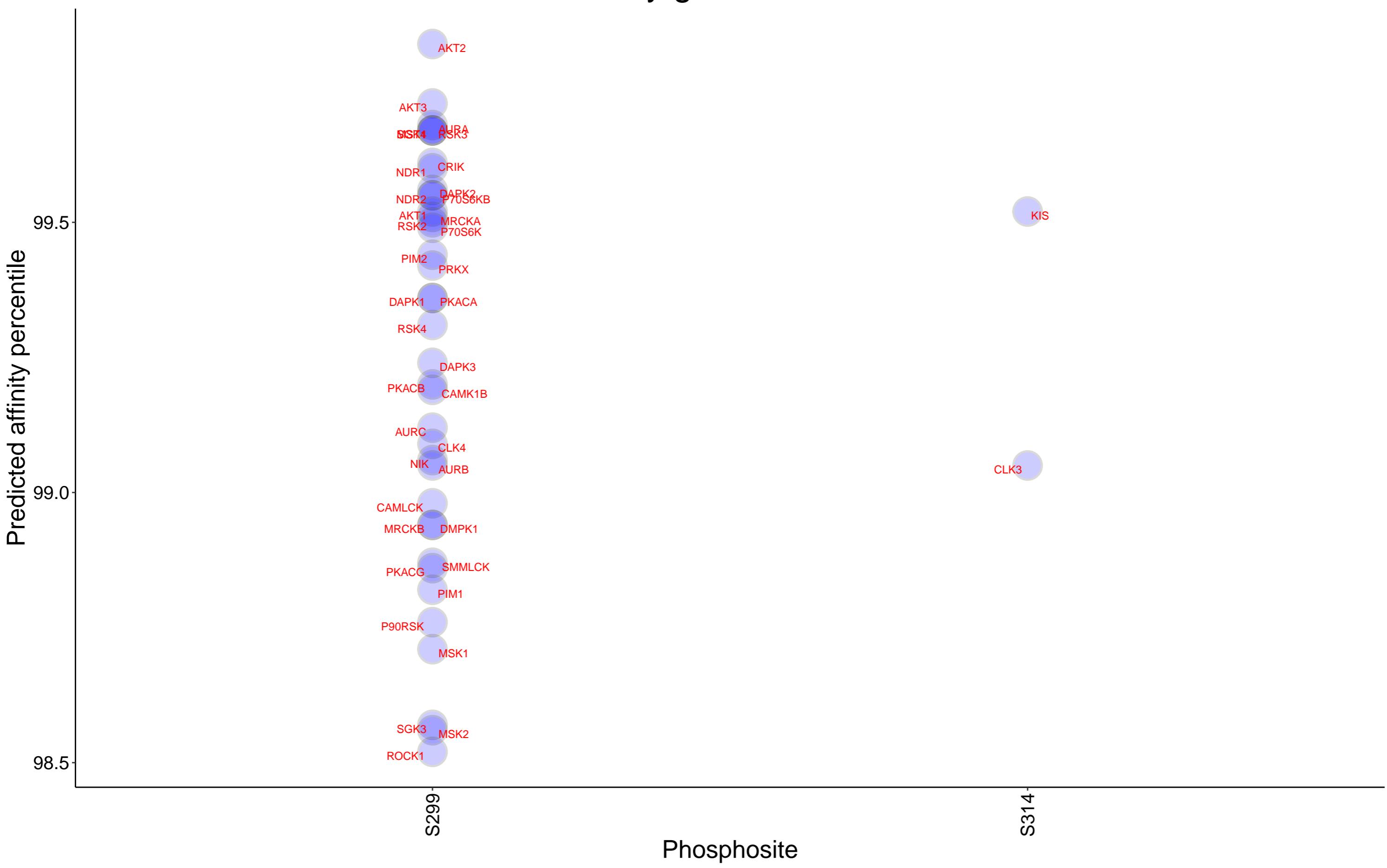
Insufficient number of paired observations in DB1 for EYA1

Insufficient number of paired observations in DB1 for EYA1

Top 10 kinases for each phosphosite in EYA1



Kinases with affinity greater than 98.5% to EYA1



No sufficient paired observations in DB1 for EYA1