

EPHA2

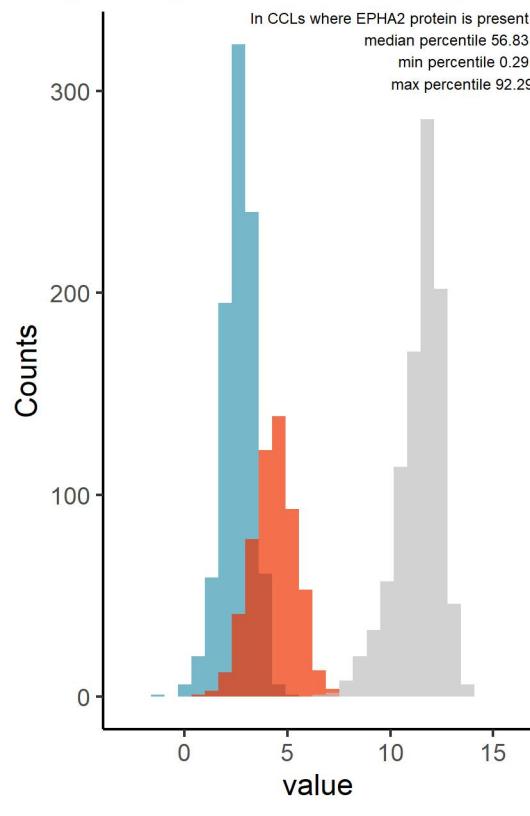
Protein name: EPHA2 ; UNIPROT: P29317 ; Gene name: EPH receptor A2

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

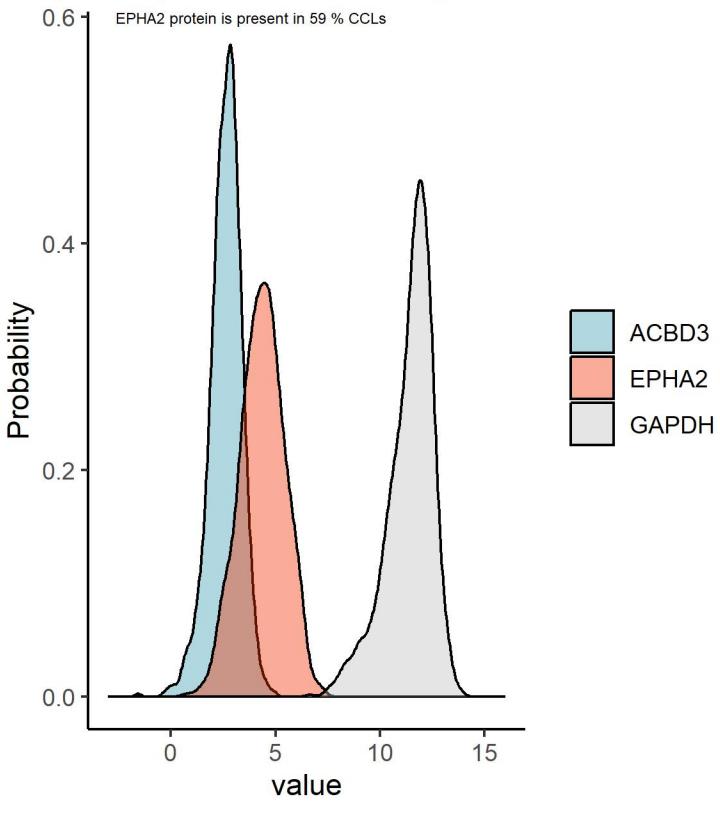
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

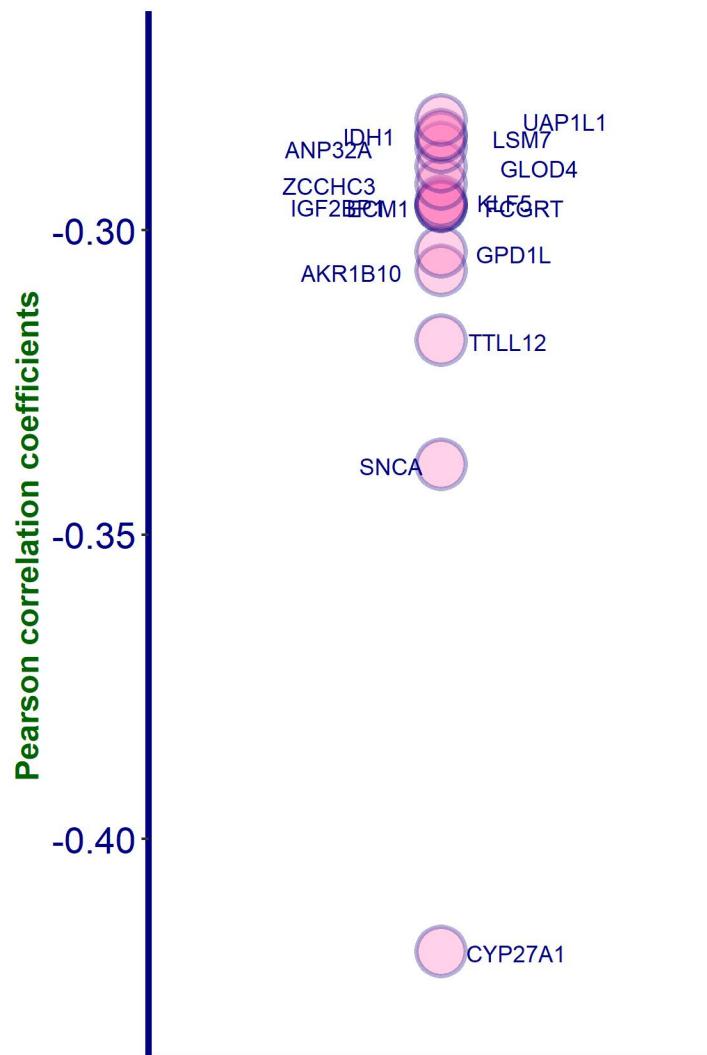
Histogram of EPHA2 protein compared to proteins with low and high abundance



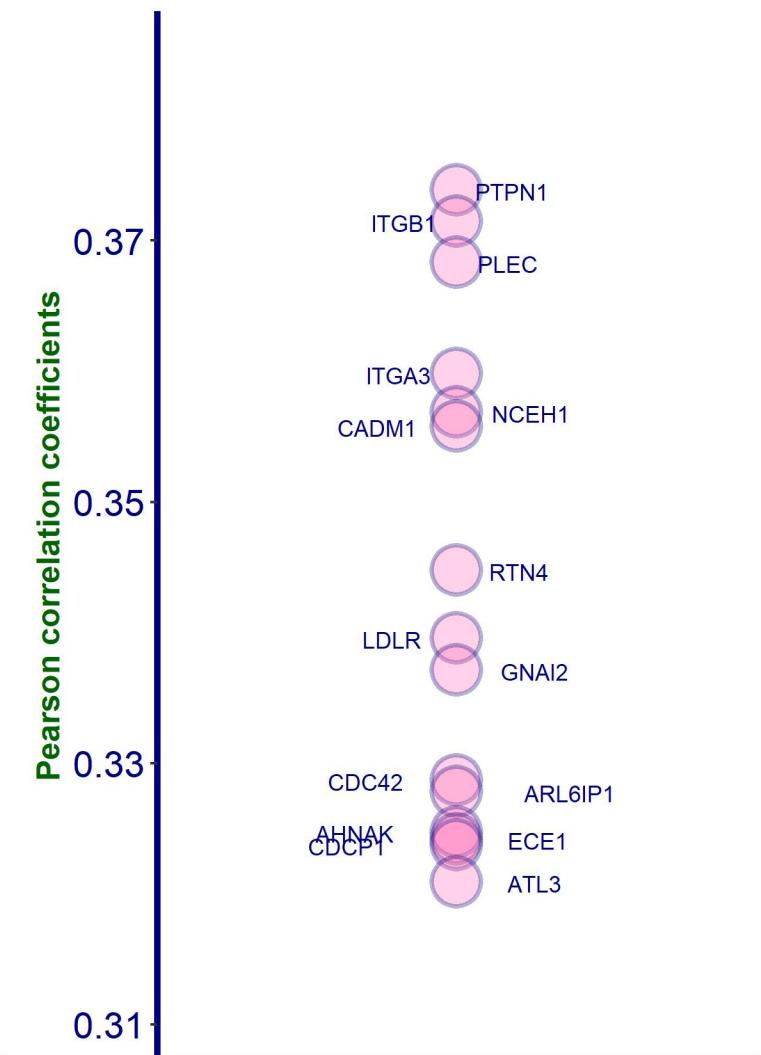
Density plot of EPHA2 protein compared to proteins with low and high abundance



Top negative correlations of EPHA2 protein, DB1

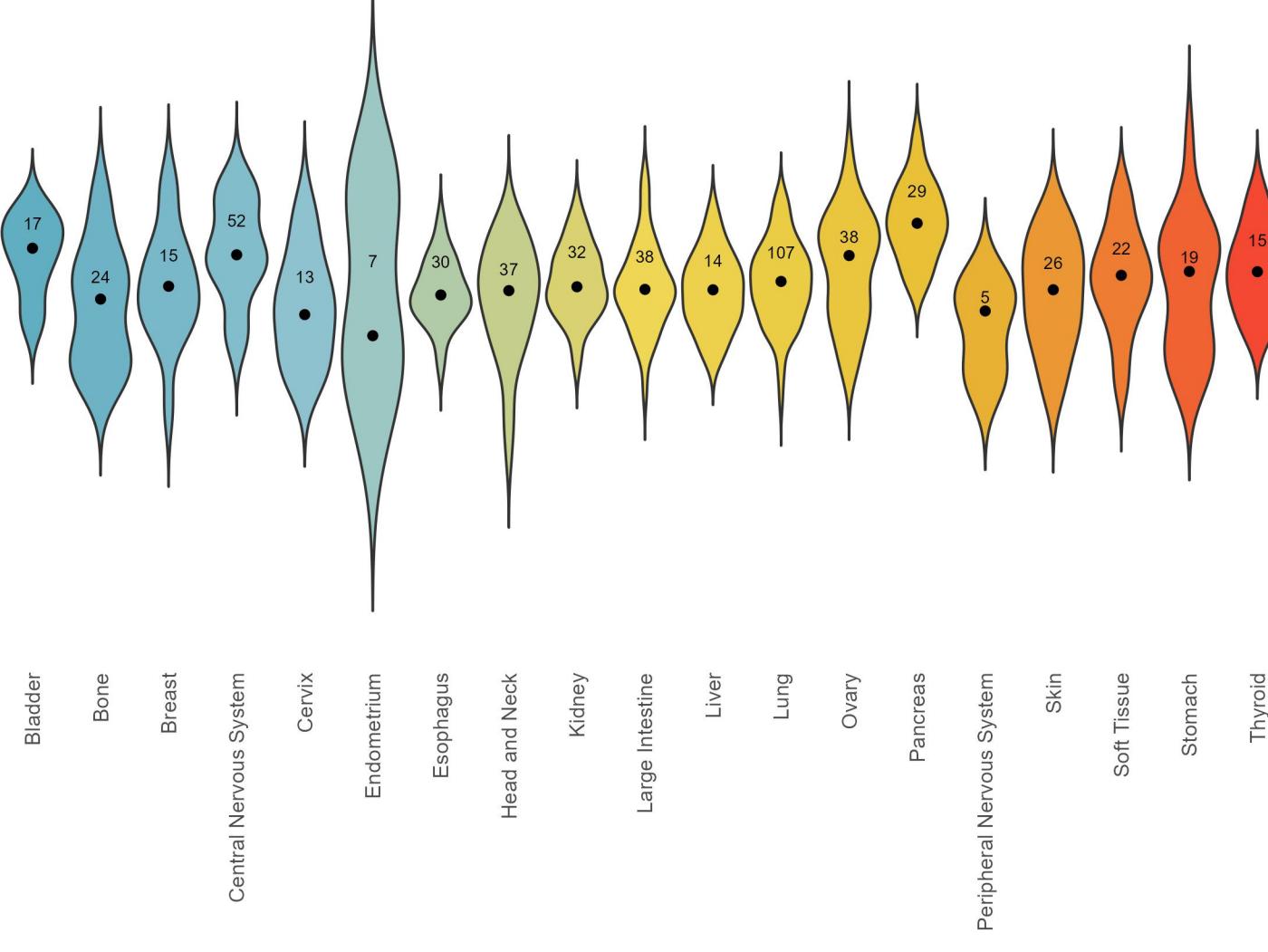


Top positive correlations of EPHA2 protein, DB1



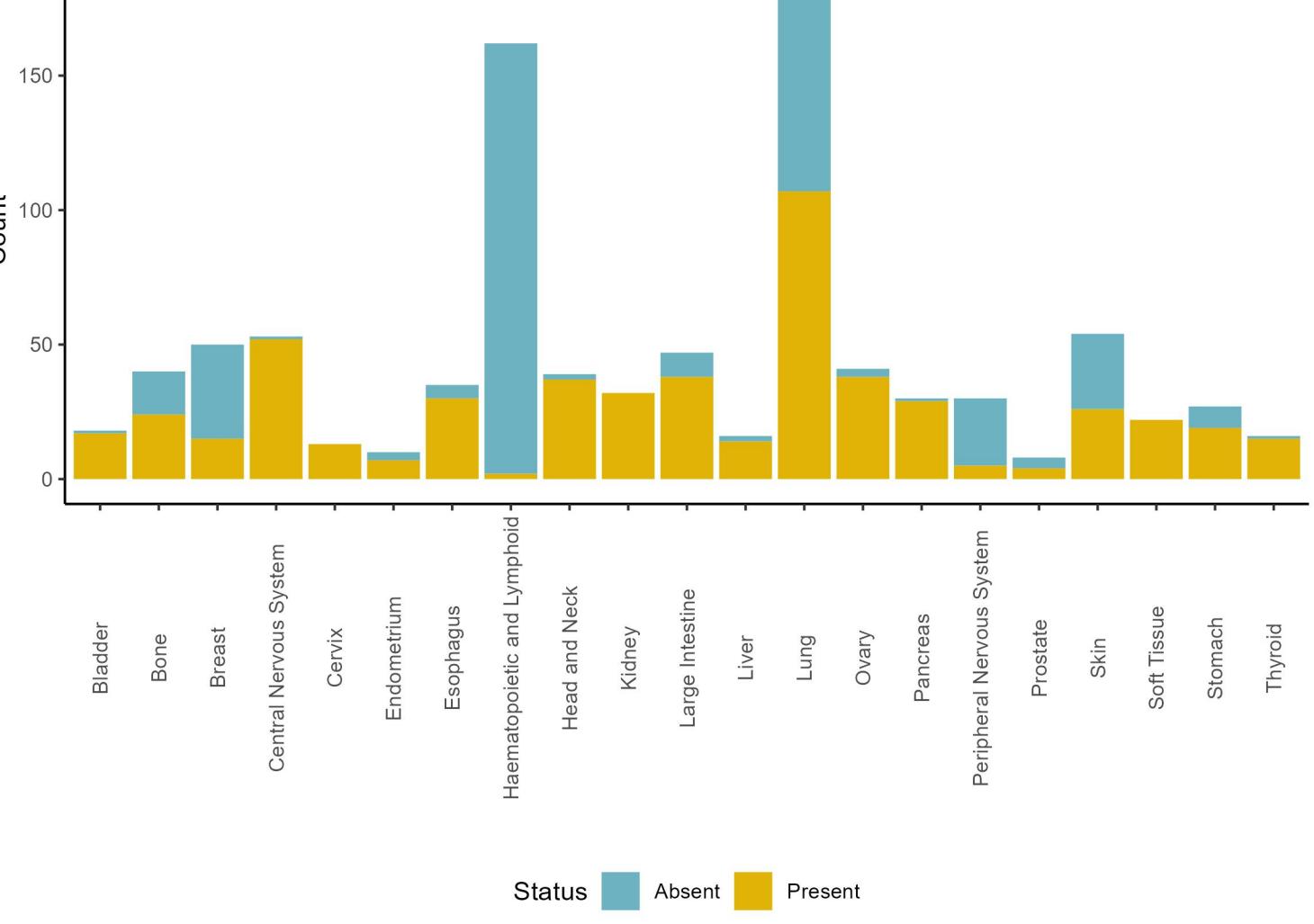
Amount of EPHA2 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 1.056e-12



Present and absent EPHA2 protein counts by tissue, DB1

Chi square p value is 2.779e-82

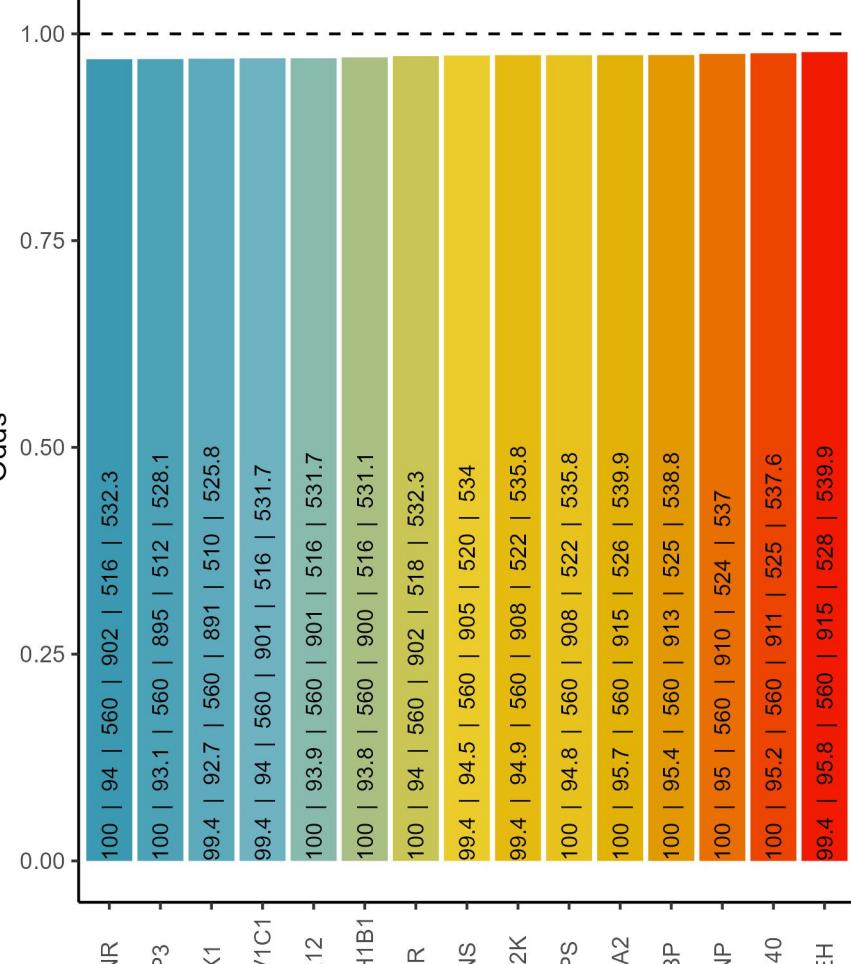


Cooccurrence with EPHA2 protein, DB1

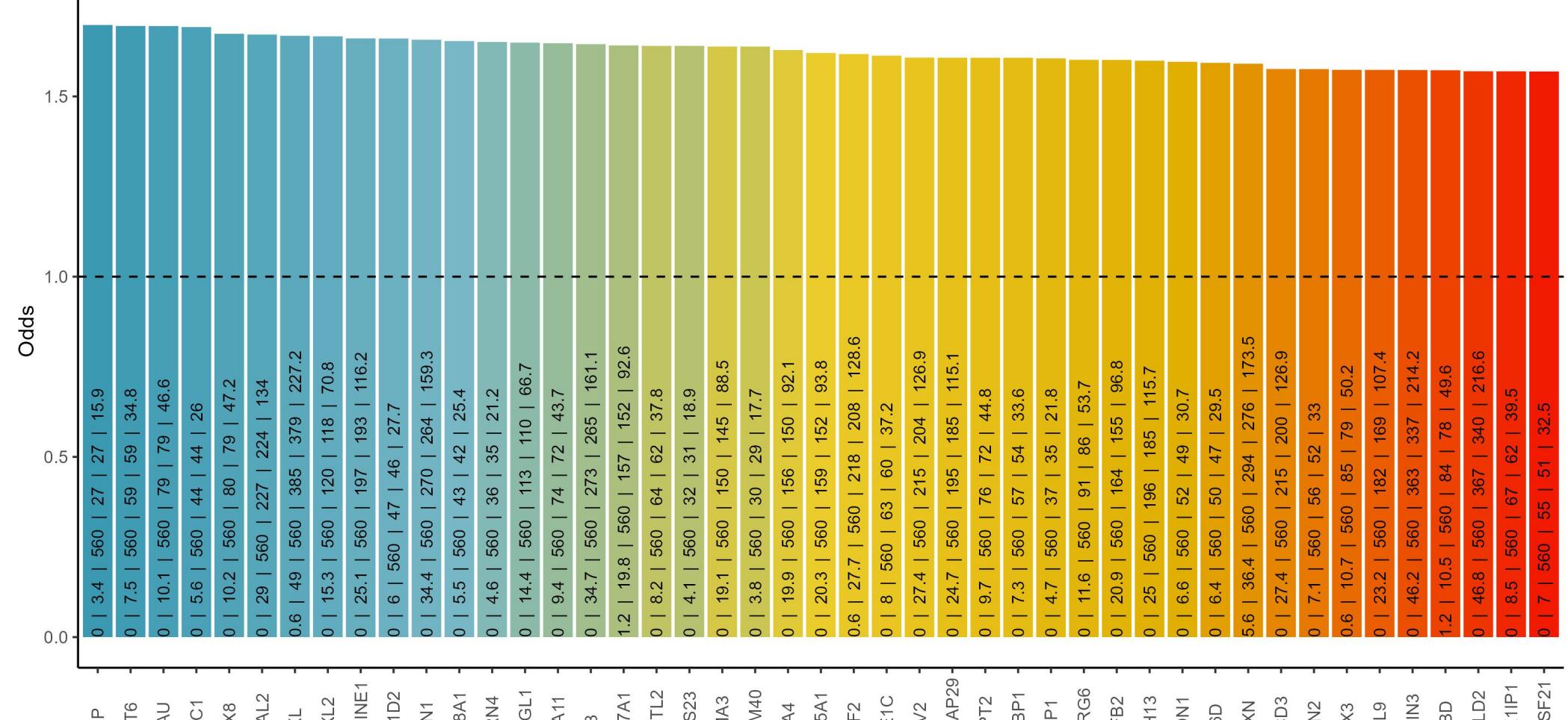
% of EPHA2 in blood cancers: 1.2 ; % of EPHA2 in solid cancers: 71

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of EPHA2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

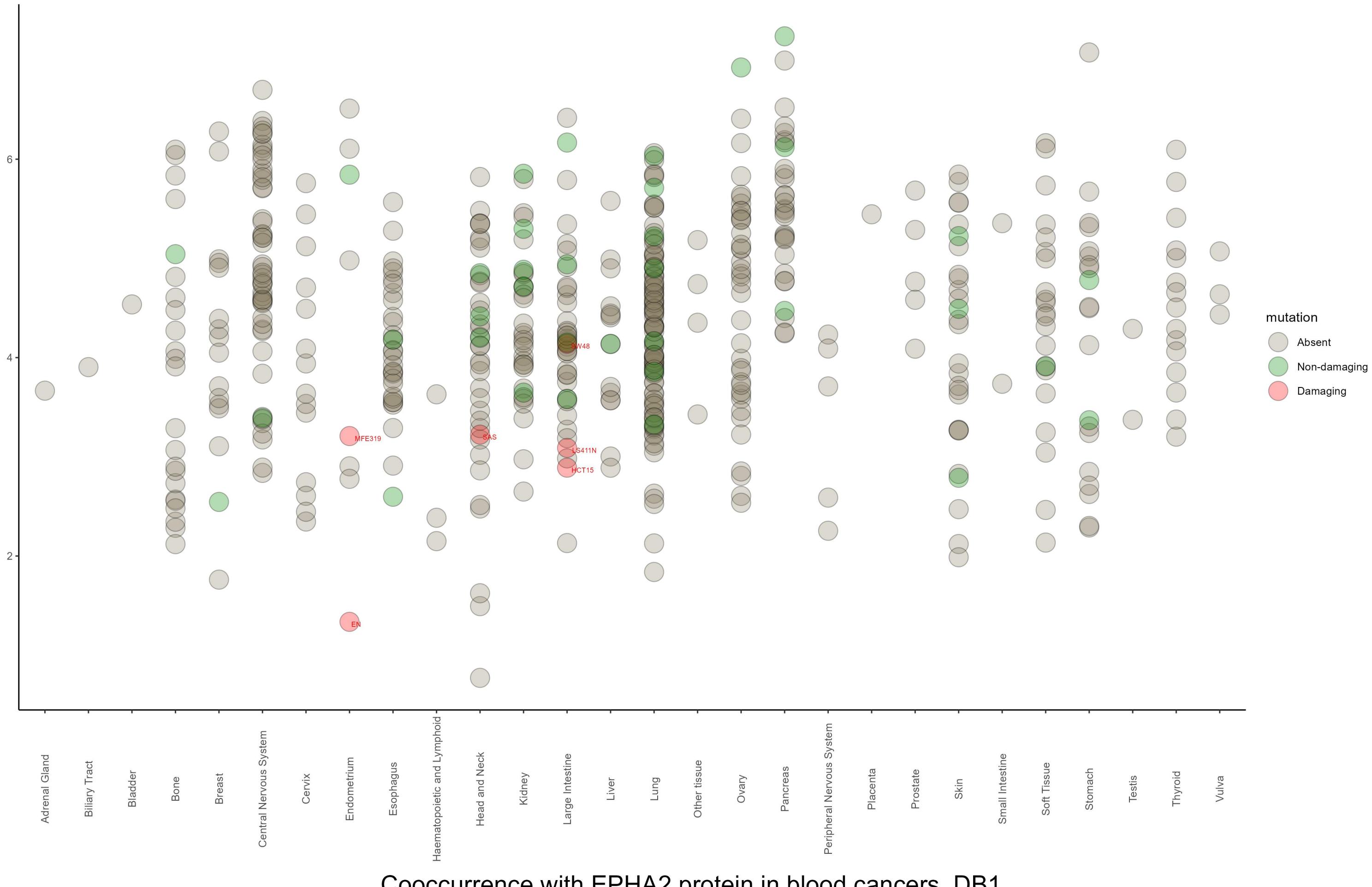
Negative cooccurrence



Positive cooccurrence

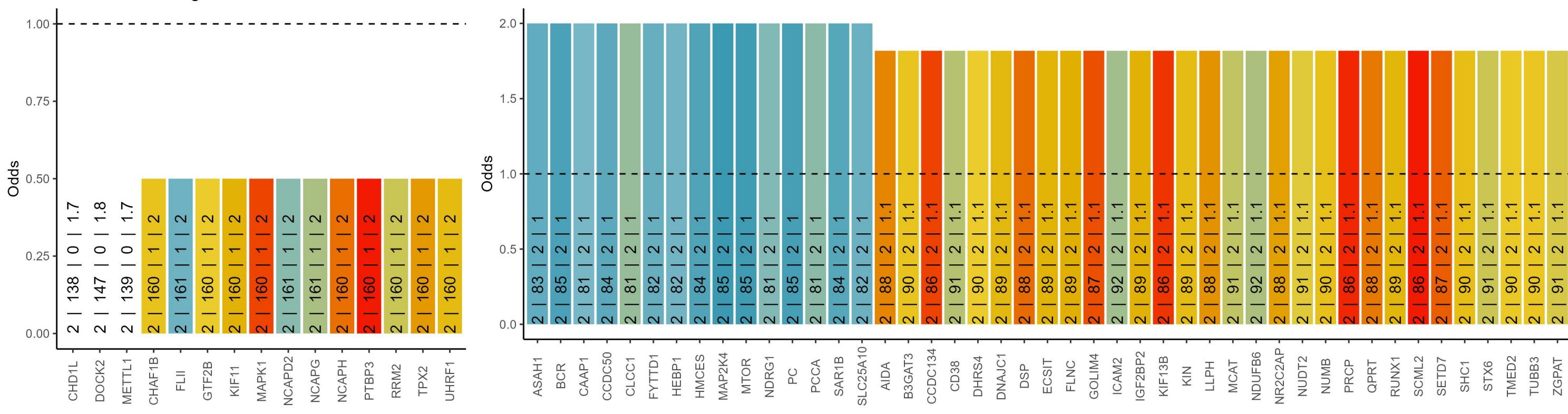


Amount of EPHA2 protein and mutation status by tissue, DB1

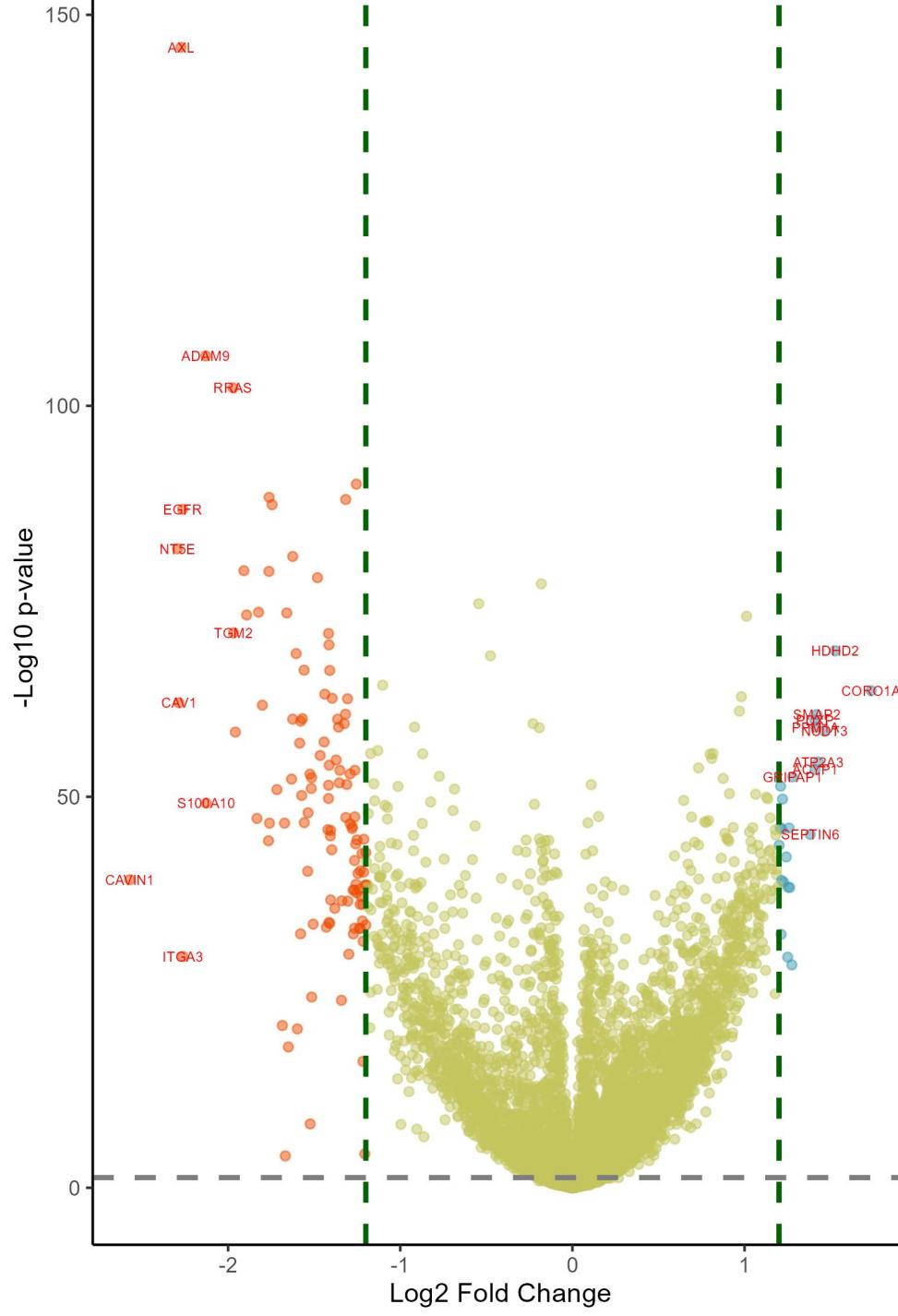


Cooccurrence with EPHA2 protein in blood cancers, DB1

The text in the bars: incidence of EPHA2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

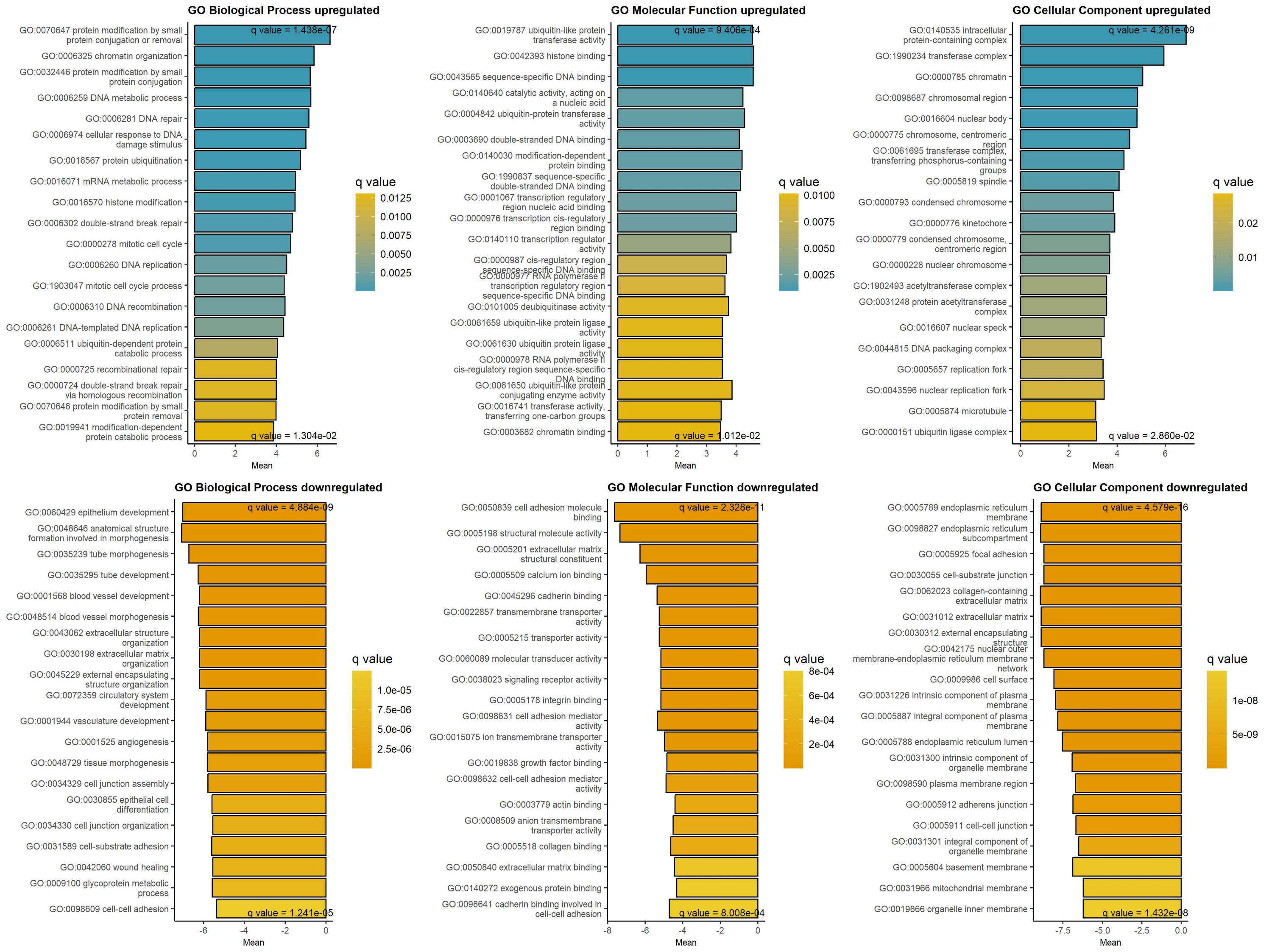


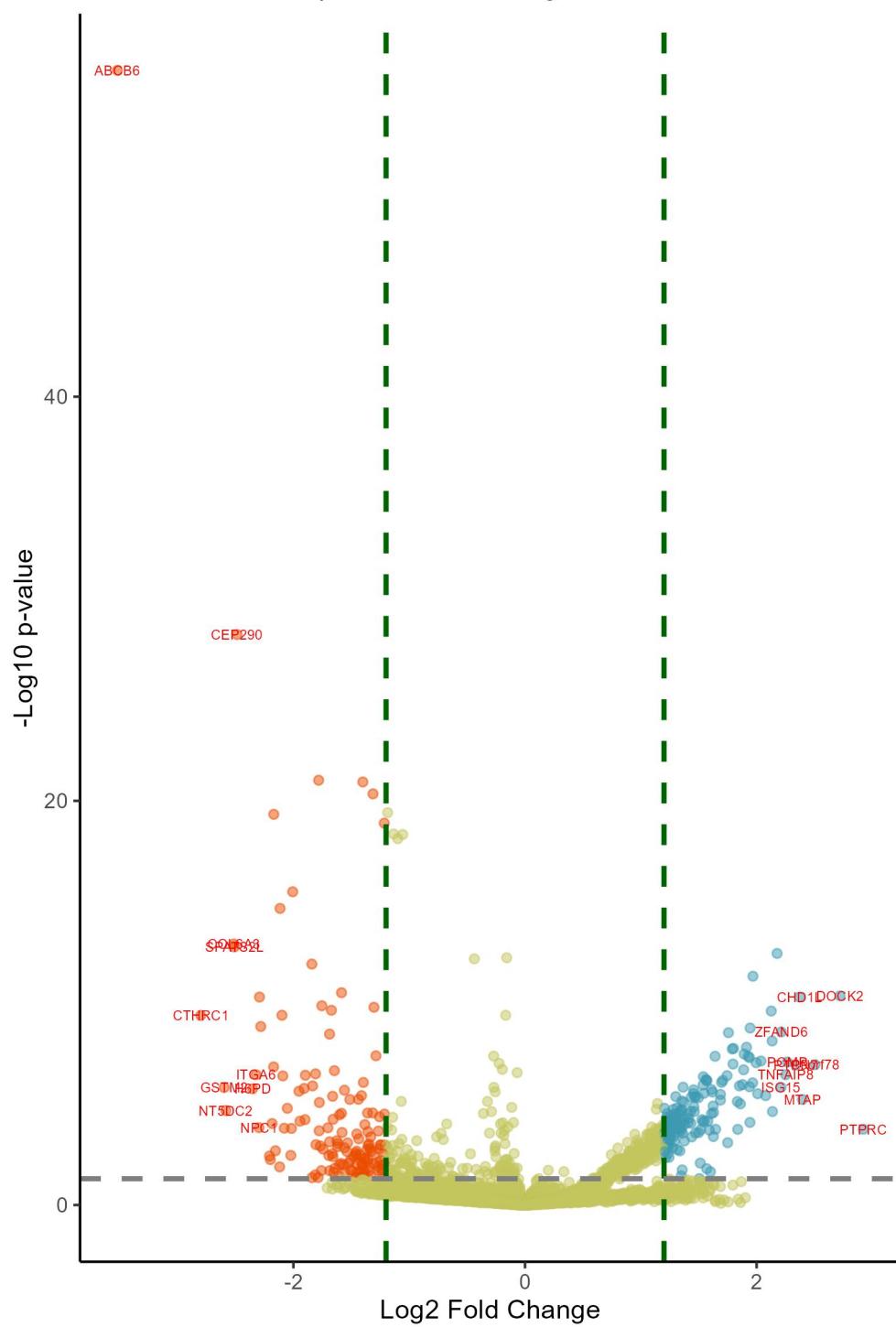
Downregulated at low/absent EPHA2 Upregulated at low/absent EPHA2



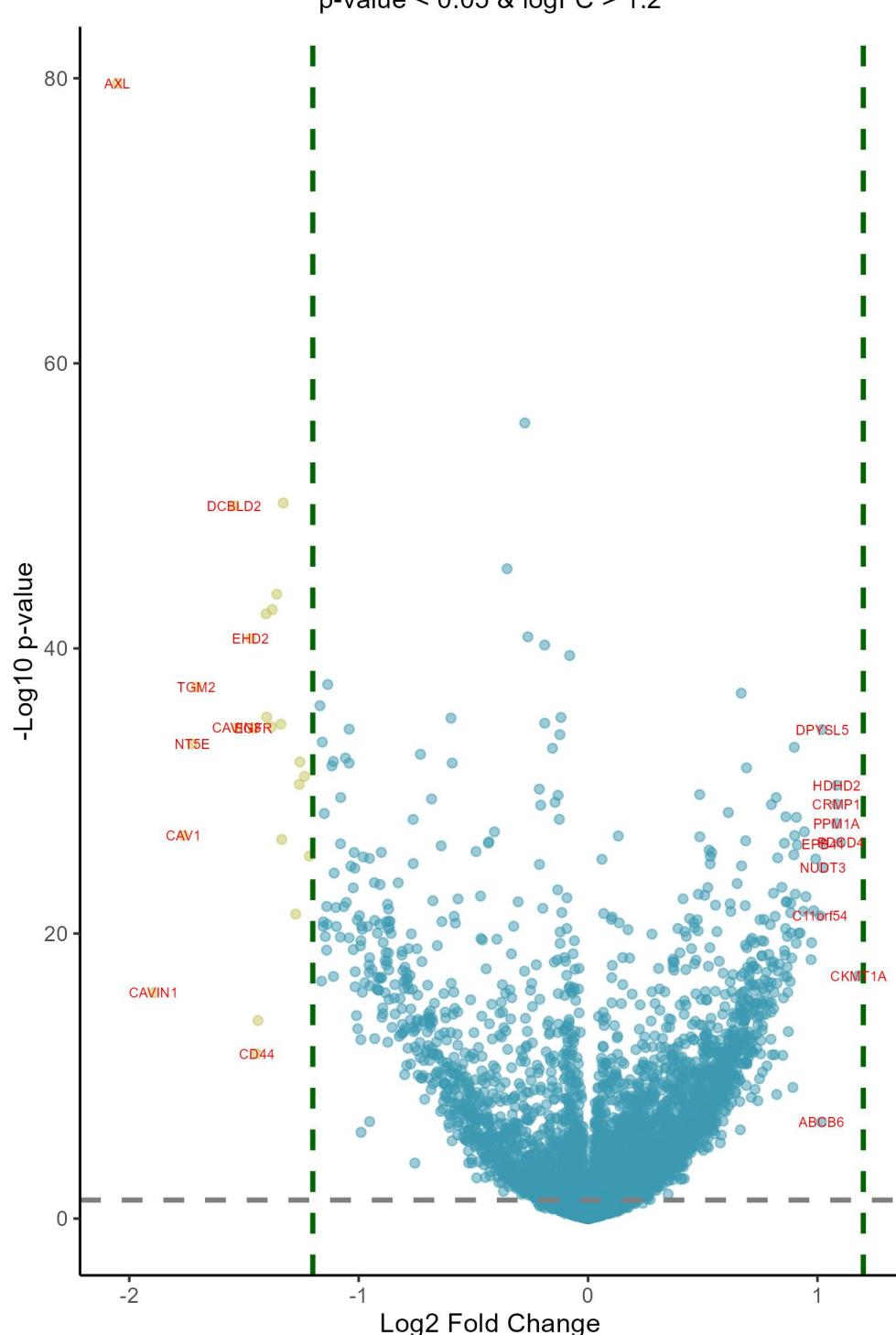
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.57	1.20e-38	CAVIN1	caveolae associated protein 1	1.74	6.11e-62	CORO1A	coronin 1A
-2.29	1.29e-79	NT5E	5'-nucleotidase ecto	1.53	5.93e-67	HDHD2	haloacid dehalogenase like hydrolas
-2.29	1.81e-60	CAV1	caveolin 1	1.46	5.10e-57	NUDT3	nudix hydrolase 3
-2.27	4.68e-143	AXL	AXL receptor tyrosine kinase	1.43	3.85e-53	ATP2A3	ATPase sarcoplasmic/endoplasmic ret
-2.26	1.28e-84	EGFR	epidermal growth factor receptor	1.42	5.07e-59	SMAP2	small ArfGAP2
-2.26	3.27e-29	ITGA3	integrin subunit alpha 3	1.41	1.73e-57	PPM1A	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe
-2.13	9.07e-104	ADAM9	ADAM metallopeptidase domain 9	1.41	3.43e-52	ACYP1	acylphosphatase 1
-2.13	4.42e-48	S100A10	S100 calcium binding protein A10	1.41	2.52e-58	PDXP	pyridoxal phosphatase
-1.97	8.56e-100	RRAS	RAS related	1.38	3.21e-44	SEPTIN6	septin 6
-1.97	3.42e-69	TGM2	transglutaminase 2	1.28	2.66e-51	GRIPAP1	GRIP1 associated protein 1
-1.96	6.77e-57	S100A16	S100 calcium binding protein A16	1.27	3.53e-28	ABRACL	ABRA C-terminal like
-1.91	6.77e-77	CAVIN3	caveolae associated protein 3	1.26	1.08e-37	PDCD4	programmed cell death 4
-1.89	1.97e-71	GPX8	glutathione peroxidase 8 (putative)	1.26	5.32e-45	GRK2	G protein-coupled receptor kinase 2
-1.83	3.66e-46	PROCR	protein C receptor	1.25	9.84e-38	C11orf54	chromosome 11 open reading frame 54
-1.82	9.77e-72	FHL2	four and a half LIM domains 2	1.25	4.01e-29	BLMH	bleomycin hydrolase
-1.8	3.55e-60	GPRC5A	G protein-coupled receptor class C	1.24	1.92e-41	SNRNP27	small nuclear ribonucleoprotein U4/U6
-1.77	1.93e-43	ITGA2	integrin subunit alpha 2	1.23	2.42e-38	UBR7	ubiquitin protein ligase E3 compone
-1.76	7.70e-77	EHD2	EH domain containing 2	1.22	1.42e-48	RNF113A	ring finger protein 113A
-1.76	5.56e-86	DCBLD2	discoidin, CUB and LCCL domain cont	1.22	1.46e-38	COPS7B	COP9 signalosome subunit 7B
-1.76	1.35e-45	MYOF	myoferlin	1.21	7.36e-45	RNASEH2B	ribonuclease H2 subunit B
-1.75	3.69e-85	MET	MET proto-oncogene, receptor tyrosi	1.21	6.44e-32	UBE2V2	ubiquitin conjugating enzyme E2 V2
-1.72	9.40e-50	PPIC	peptidylprolyl isomerase C	1.21	3.64e-50	POU2F1	POU class 2 homeobox 1
-1.69	1.16e-20	GNG12	G protein subunit gamma 12	1.21	4.58e-45	CCDC43	coiled-coil domain containing 43
-1.67	1.35e-45	ITGB4	integrin subunit beta 4	1.2	6.92e-43	EPB41	erythrocyte membrane protein band 4
-1.67	1.46e-04	KRT18	keratin 18	1.2	7.41e-38	CORO7	coronin 7
-1.66	1.15e-71	SDC4	syndecan 4	1.19	2.41e-41	TP53RK	TP53 regulating kinase
-1.65	5.13e-18	CD44	CD44 molecule (Indian blood group)	1.19	3.04e-39	PPM1B	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe
-1.63	4.81e-51	MMP14	matrix metallopeptidase 14	1.19	6.88e-40	MAPRE2	microtubule associated protein RP/E
-1.62	1.92e-58	RRAS2	RAS related 2	1.18	3.90e-44	ARPP19	cAMP regulated phosphoprotein 19

GAGE analysis on upregulated and downregulated proteins at low/absent EPHA2 protein, DB1





Differentially expressed proteins in solid cancers at absence/low amount of EPHA2 , DB1
p-value < 0.05 & logFC > 1.2



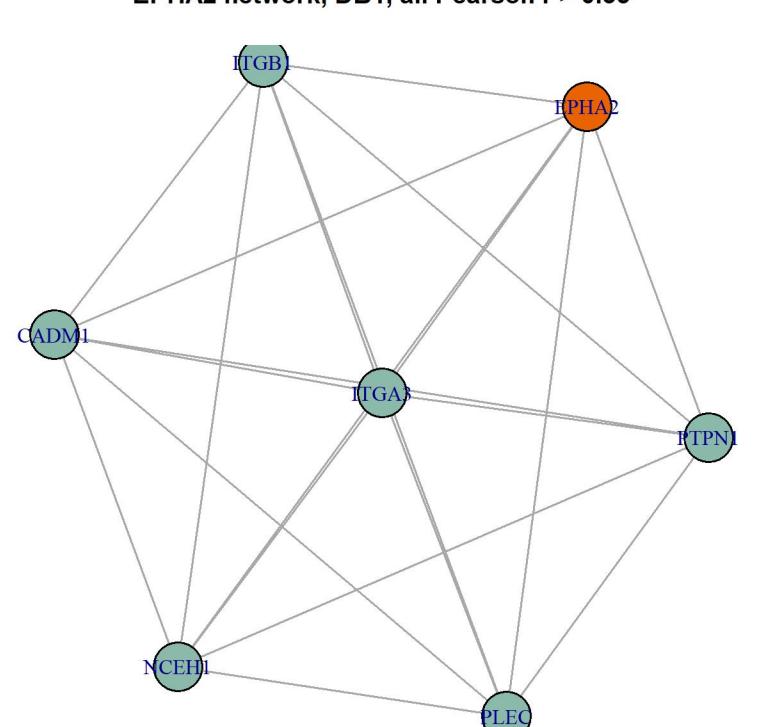
Downregulated in blood cancers at low/absent EPHA2 Upregulated in blood cancers at low/absent EPHA2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-3.52	2.37e-53	ABCB6	ATP binding cassette subfamily B me	2.92	6.00e-03	PTPRC	protein tyrosine phosphatase recept
-2.8	8.66e-08	CTHRC1	collagen triple helix repeat contai	2.72	1.30e-08	DOCK2	dedicator of cytokinesis 2
-2.6	1.25e-04	GSTM2	glutathione S-transferase mu 2	2.5	1.42e-05	C9orf78	chromosome 9 open reading frame 78
-2.58	1.12e-03	NT5DC2	5'-nucleotidase domain containing 2	2.4	3.78e-04	MTAP	methylthioadenosine phosphorylase
-2.51	5.40e-11	COL6A3	collagen type VI alpha 3 chain	2.37	1.36e-08	CHD1L	chromodomain helicase DNA binding p
-2.51	7.00e-11	SPATS2L	spermatogenesis associated serine r	2.34	1.47e-05	PTPN7	protein tyrosine phosphatase non-re
-2.49	1.30e-25	CEP290	centrosomal protein 290	2.26	1.14e-05	POMP	proteasome maturation protein
-2.35	1.40e-04	H6PD	hexose-6-phosphate dehydrogenase/gl	2.25	3.84e-05	TNFAIP8	TNF alpha induced protein 8
-2.32	3.84e-05	ITGA6	integrin subunit alpha 6	2.21	5.19e-07	ZFAND6	zinc finger AN1-type containing 6
-2.3	5.29e-03	NPC1	NPC intracellular cholesterol trans	2.21	1.24e-04	ISG15	ISG15 ubiquitin like modifier
-2.29	1.36e-08	GCSH	glycine cleavage system protein H	2.18	1.39e-10	METTL1	methyltransferase 1, tRNA methylgua
-2.28	2.96e-07	FHL1	four and a half LIM domains 1	2.14	1.22e-03	BASP1	brain abundant membrane attached si
-2.21	6.98e-02	MAN1A1	mannosidase alpha class 1A member 1	2.13	1.33e-06	BCKDHB	branched chain keto acid dehydrogen
-2.2	9.53e-02	TPBG	trophoblast glycoprotein	2.13	5.76e-08	CUTC	cutC copper transporter
-2.18	3.66e-03	ENAH	ENAH actin regulator	2.08	2.68e-04	COMMD8	COMM domain containing 8
-2.17	1.77e-05	ITPK1	inositol-tetrakisphosphate 1-kinase	2.04	1.04e-05	AVEN	apoptosis and caspase activation in
-2.17	3.85e-17	NDUFB11	NADH:ubiquinone oxidoreductase subu	2.01	2.23e-04	C1D	C1D nuclear receptor corepressor
-2.16	4.36e-02	CT47A11	cancer/testis antigen family 47 mem	2	1.21e-05	ABT1	activator of basal transcription 1
-2.12	1.79e-01	HMG2A2	high mobility group AT-hook 2	1.97	1.51e-09	SGF29	SAGA complex associated factor 29
-2.12	9.99e-13	PLP2	proteolipid protein 2	1.97	8.16e-05	TRMT61A	tRNA methyltransferase 61A
-2.1	8.66e-08	ATP5MF	ATP synthase membrane subunit f	1.94	3.42e-07	GTF3C4	general transcription factor IIIC s
-2.09	4.17e-05	GPT2	glutamic-pyruvic transaminase 2	1.94	3.31e-03	ANXA1	annexin A1
-2.08	5.55e-03	ALG13	ALG13 UDP-N-acetylglucosaminyltrans	1.94	1.20e-04	TMED1	transmembrane p24 trafficking prote
-2.05	9.07e-04	EGLN1	egl-9 family hypoxia inducible fact	1.94	7.23e-06	TLE3	TLE family member 3, transcriptiona
-2.02	6.60e-02	SCRN2	seccernin 2	1.93	6.31e-06	CHD8	chromodomain helicase DNA binding p
-2.02	5.61e-03	THNSL1	threonine synthase like 1	1.91	2.66e-06	NMD3	NMD3 ribosome export adaptor
-2.01	1.61e-13	UBE2D3	ubiquitin conjugating enzyme E2 D3	1.9	1.00e+00	CDV3	CDV3 homolog
-1.95	1.77e-04	UQCRRFS1	ubiquinol-cytochrome c reductase, R	1.89	5.35e-06	STAT6	signal transducer and activator of
-1.94	2.98e-03	AHCYL1	adenosylhomocysteinase like 1	1.89	2.36e-05	EARS2	glutamyl-tRNA synthetase 2, mitocho

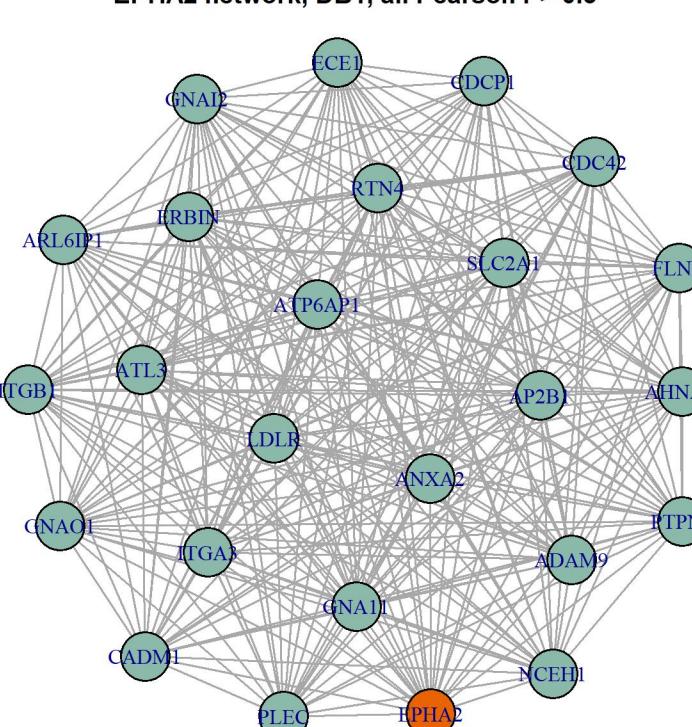
Downregulated in solid cancers at low/absent EPHA2 Upregulated in solid cancers at low/absent EPHA2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.05	7.63e-77	AXL	AXL receptor tyrosine kinase	1.18	2.19e-16	CKMT1A	creatine kinase, mitochondrial 1A
-1.9	2.72e-15	CAVIN1	caveolae associated protein 1	1.1	3.71e-25	PDCD4	programmed cell death 4
-1.76	1.39e-25	CAV1	caveolin 1	1.08	6.20e-29	HDHD2	haloacid dehalogenase like hydrolas
-1.72	1.11e-31	NT5E	5'-nucleotidase ecto	1.08	1.10e-27	CRMP1	collapsin response mediator protein
-1.71	2.34e-35	TGM2	transglutaminase 2	1.08	2.13e-26	PPM1A	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe
-1.54	1.33e-47	DCBLD2	discoidin, CUB and CCRL domain cont	1.03	4.76e-25	EPB41	erythrocyte membrane protein band 4
-1.53	1.03e-32	CAVIN3	caveolae associated protein 3	1.02	1.64e-23	NUDT3	nudix hydrolase 3
-1.47	1.21e-38	EHD2	EH domain containing 2	1.02	1.23e-32	DPYSL5	dihydropyrimidinase like 5
-1.46	1.06e-32	EGFR	epidermal growth factor receptor	1.02	7.64e-07	ABCB6	ATP binding cassette subfamily B me
-1.44	2.79e-11	CD44	CD44 molecule (Indian blood group)	1.01	2.73e-20	C11orf54	chromosome 11 open reading frame 54
-1.44	1.86e-13	ITGA3	integrin subunit alpha 3	0.99	4.48e-24	TKFC	triokinase and FMN cyclase
-1.4	2.80e-40	MET	MET proto-oncogene, receptor tyrosi	0.98	1.29e-20	ACYP1	acylphosphatase 1
-1.4	2.42e-33	RAC2	Rac family small GTPase 2	0.97	1.46e-18	MSI2	musashi RNA binding protein 2
-1.38	9.30e-33	F3	coagulation factor III, tissue fact	0.97	1.96e-17	UBE2V2	ubiquitin conjugating enzyme E2 V2
-1.38	1.58e-40	ADAM9	ADAM metallopeptidase domain 9	0.95	1.55e-21	PDXP	pyridoxal phosphatase
-1.36	1.49e-41	CCN1	cellular communication network fact	0.94	7.82e-26	KIF1A	kinesin family member 1A
-1.34	6.28e-33	FHL2	four and a half LIM domains 2	0.94	1.39e-20	SHTN1	shootin 1
-1.34	2.53e-25	S100A10	S100 calcium binding protein A10	0.93	3.43e-19	BOLA1	bolA family member 1
-1.33	1.05e-47	RRAS	RAS related	0.92	3.50e-19	GPD1L	glycerol-3-phosphate dehydrogenase
-1.27	2.12e-20	GPRC5A	G protein-coupled receptor class C	0.91	5.46e-25	TLE3	TLE family member 3, transcriptiona
-1.26	5.47e-29	RRAS2	RAS related 2	0.91	8.30e-27	TRIM24	tripartite motif containing 24
-1.26	1.71e-30	SP100	SP100 nuclear antigen	0.91	1.59e-18	PPM1B	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe
-1.24	1.53e-29	NEXN	nexilin F-actin binding protein	0.9	1.08e-21	GRIPAP1	GRIP1 associated protein 1
-1.21	2.97e-24	GPX8	glutathione peroxidase 8 (putative)	0.9	1.40e-25	BLOC1S1	biogenesis of lysosomal organelles
-1.17	4.08e-34	FNDC3B	fibronectin type III domain contain	0.9	1.84e-31	MAPT	microtubule associated protein tau
-1.16	4.90e-16	PROCR	protein C receptor	0.9	2.43e-24	POU2F1	POU class 2 homeobox 1
-1.16	8.55e-32	MYOF	myoferlin	0.89	4.21e-09	CKB	creatinine kinase B
-1.15	1.28e-19	S100A16	S100 calcium binding protein A16	0.89	1.54e-17	ENSA	endosulfine alpha
-1.15	6.61e-20	THBS1	thrombospondin 1	0.88	3.42e-19	COQ8A	coenzyme Q8A

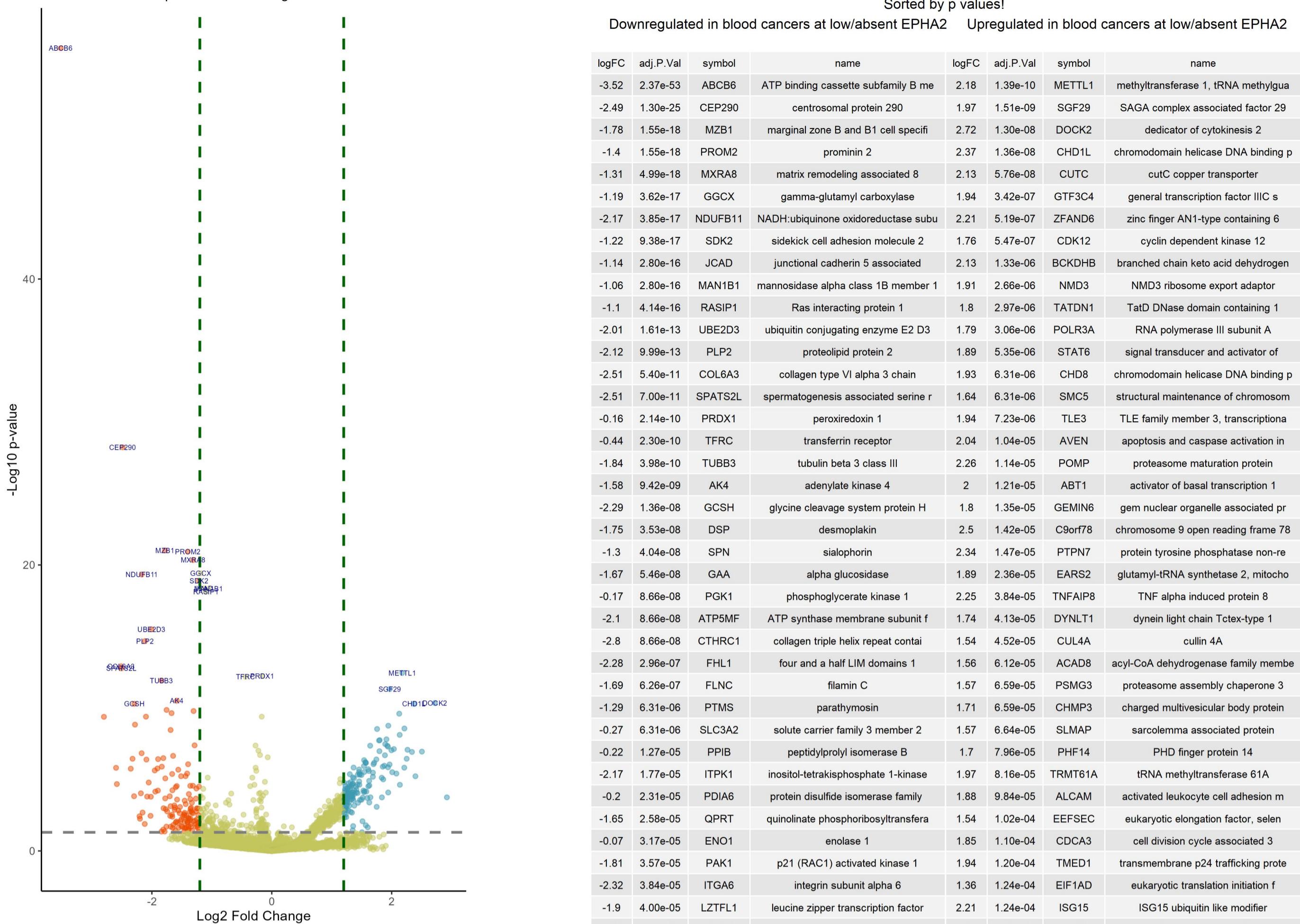
EPHA2 network, DB1, all Pearson r > 0.35



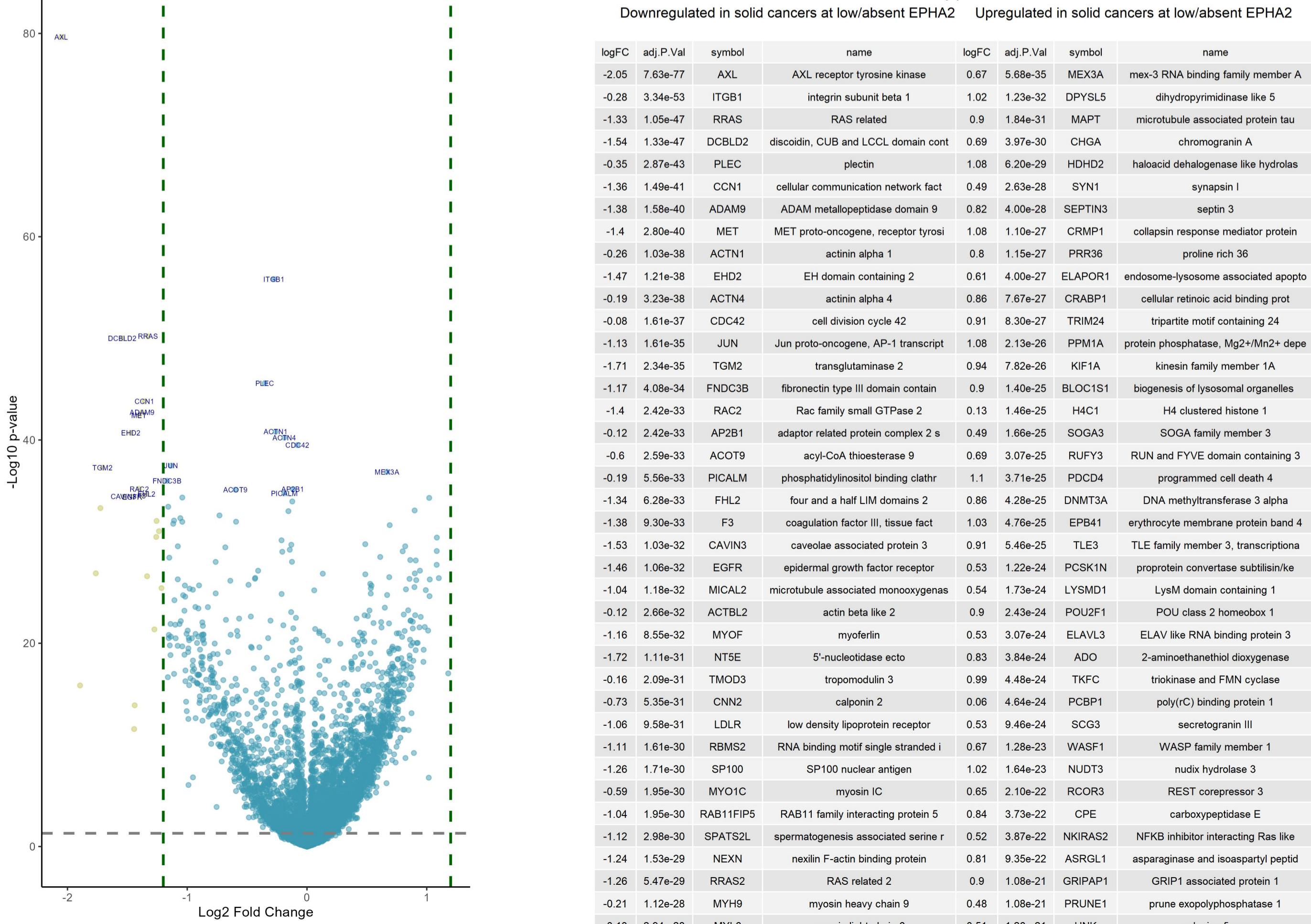
EPHA2 network, DB1, all Pearson r > 0.3



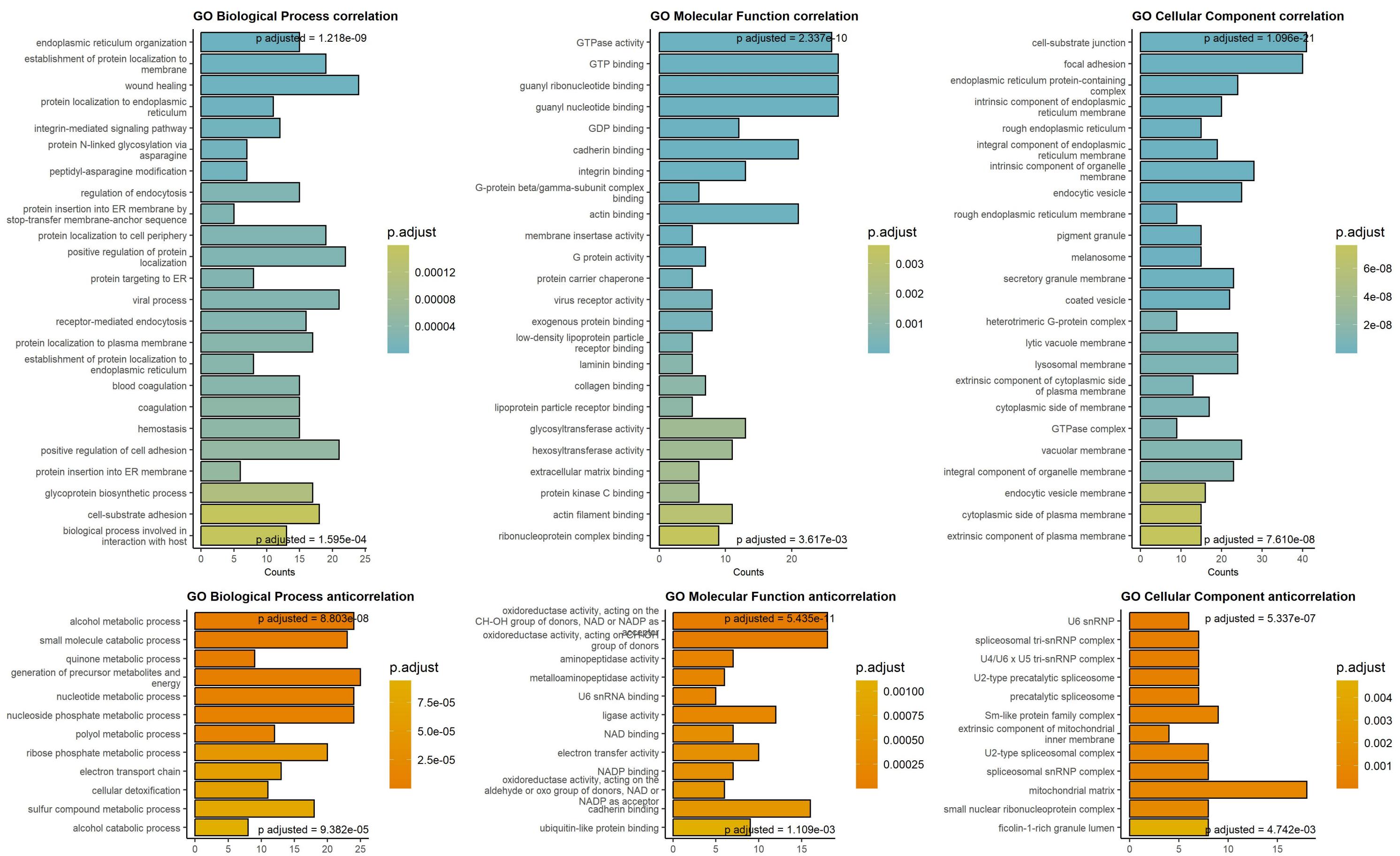
Differentially expressed proteins in blood cancers at absence/low amount of EPHA2 , DB1
p-value < 0.05 & logFC > 1.2



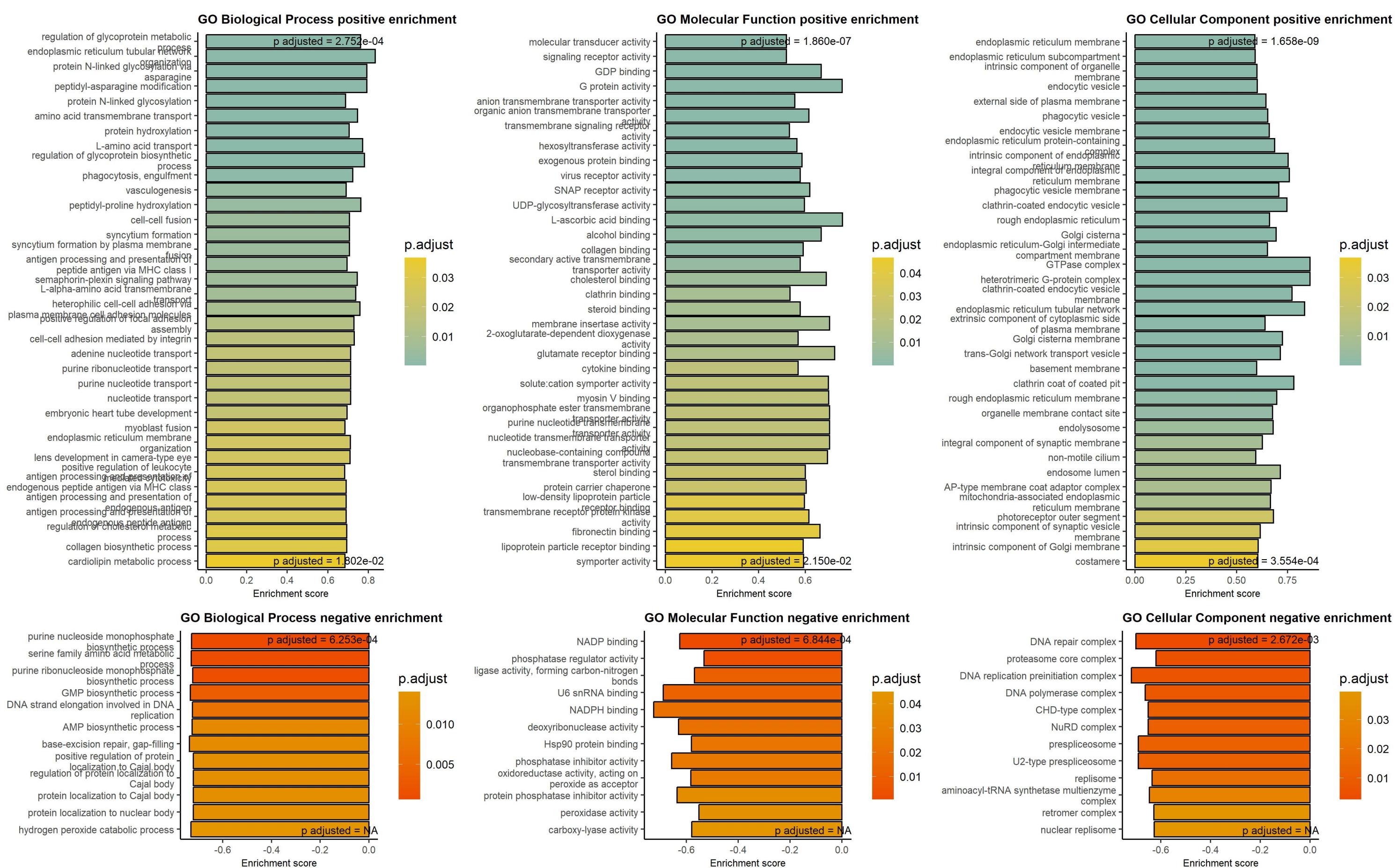
Differentially expressed proteins in solid cancers at absence/low amount of EPHA2 , DB1
p-value < 0.05 & logFC > 1.2



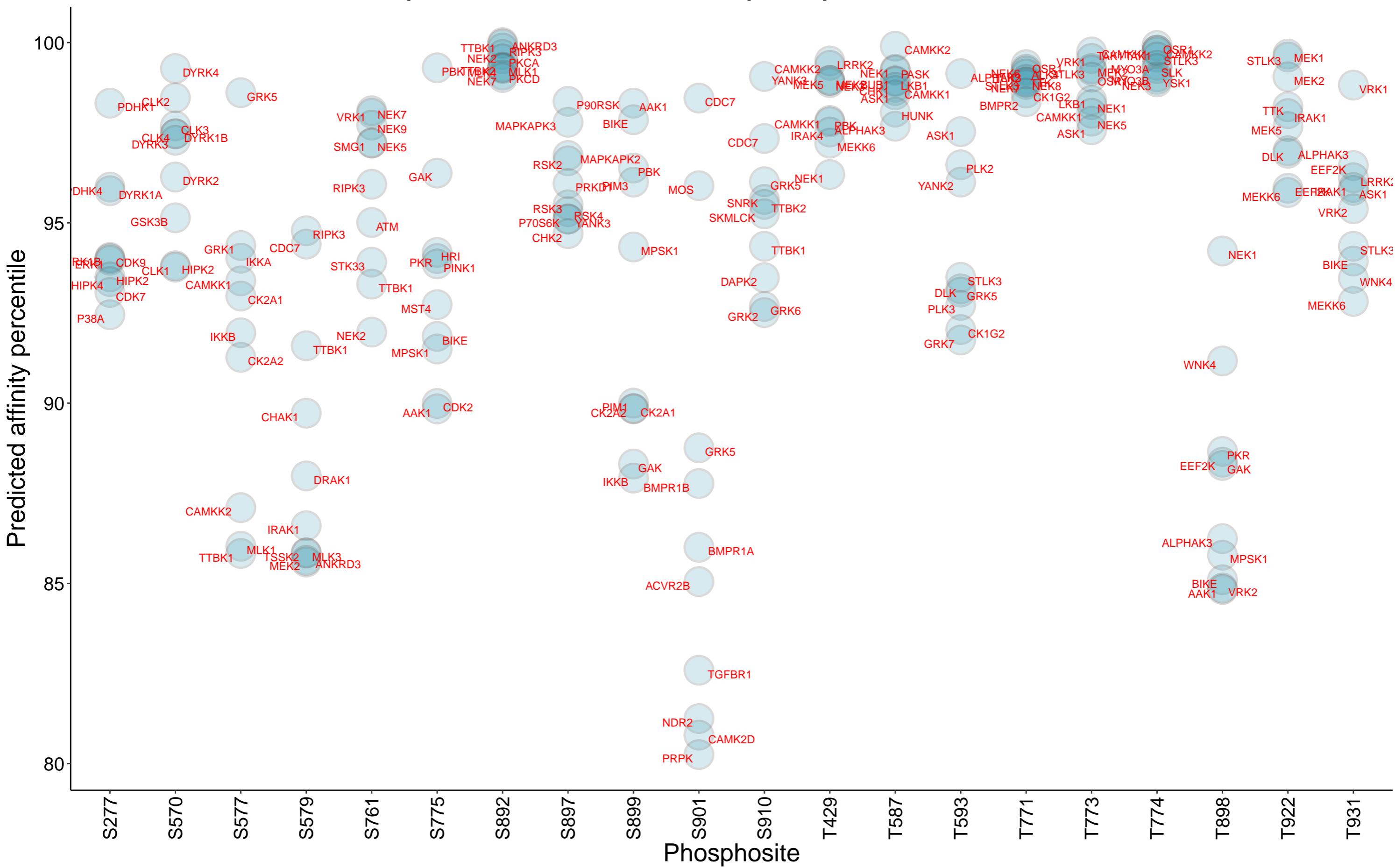
Top 250 correlation coefficients overrepresentation, EPHA2 protein, DB1



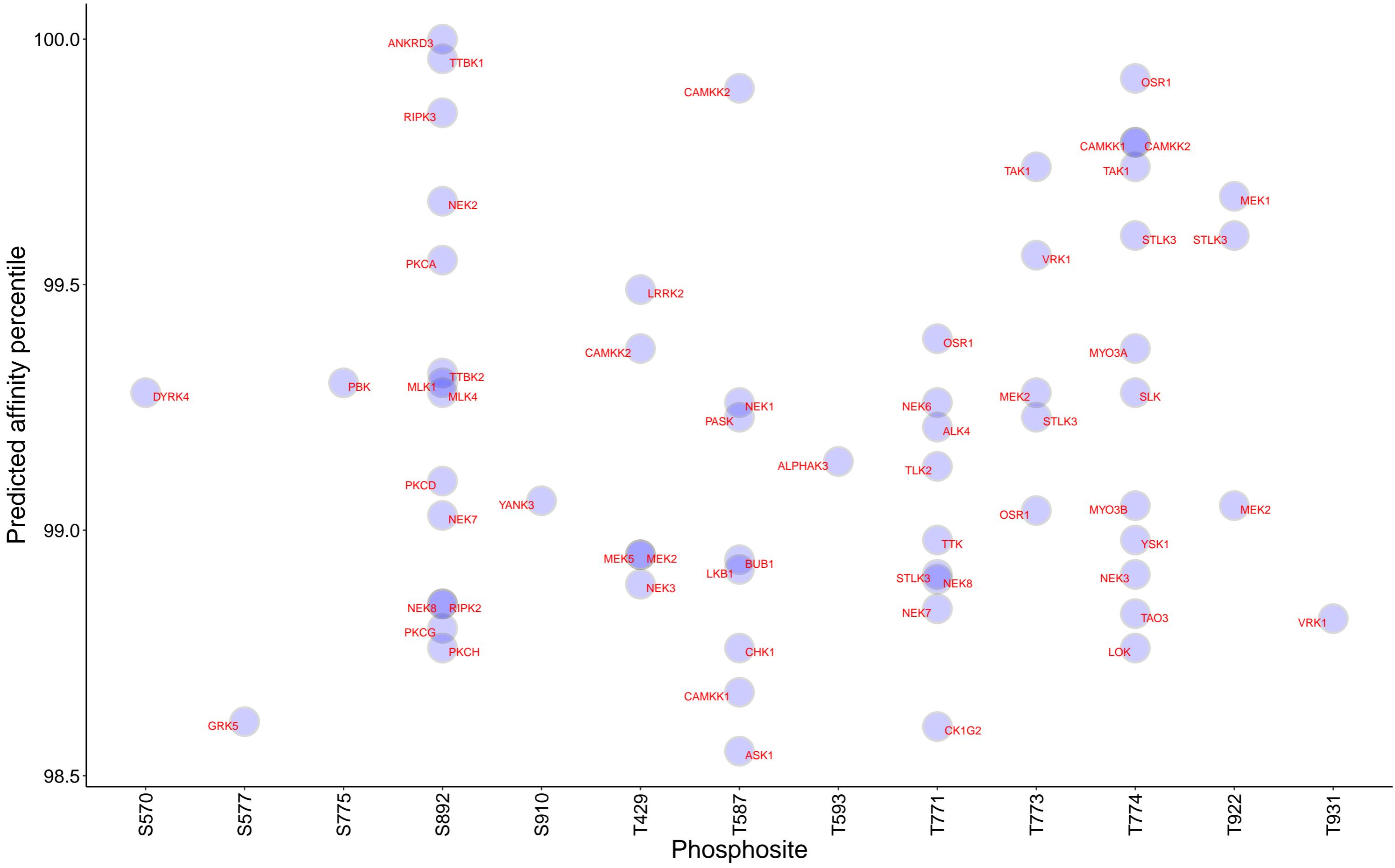
Gene Set Enrichment analysis on protein correlation coefficients, EPHA2 protein, DB1



Top 10 kinases for each phosphosite in EPHA2



Kinases with affinity greater than 98.5% to EPHA2



Top 15 positive correlation coefficients for EPHA2 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

