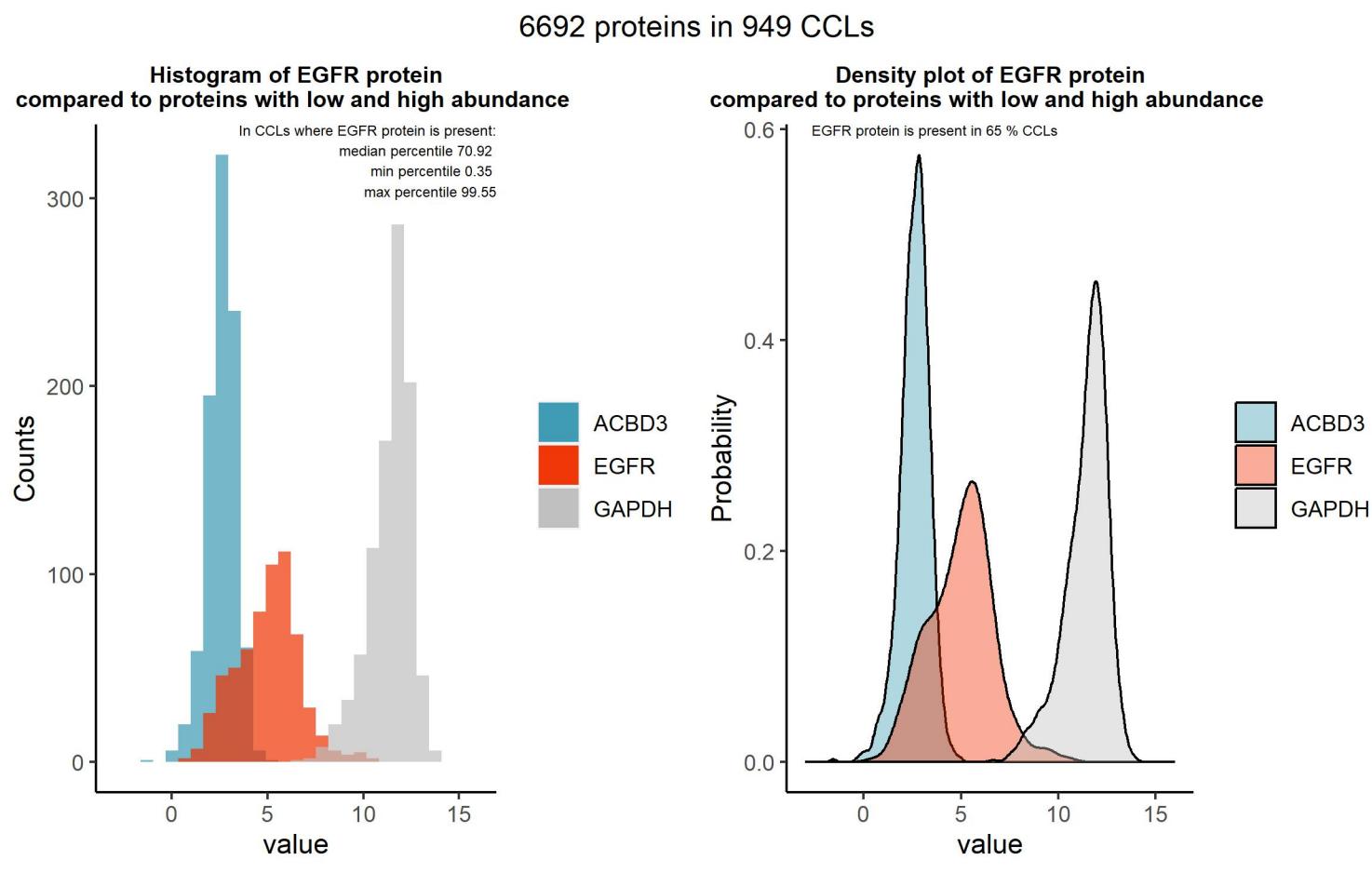


EGFR

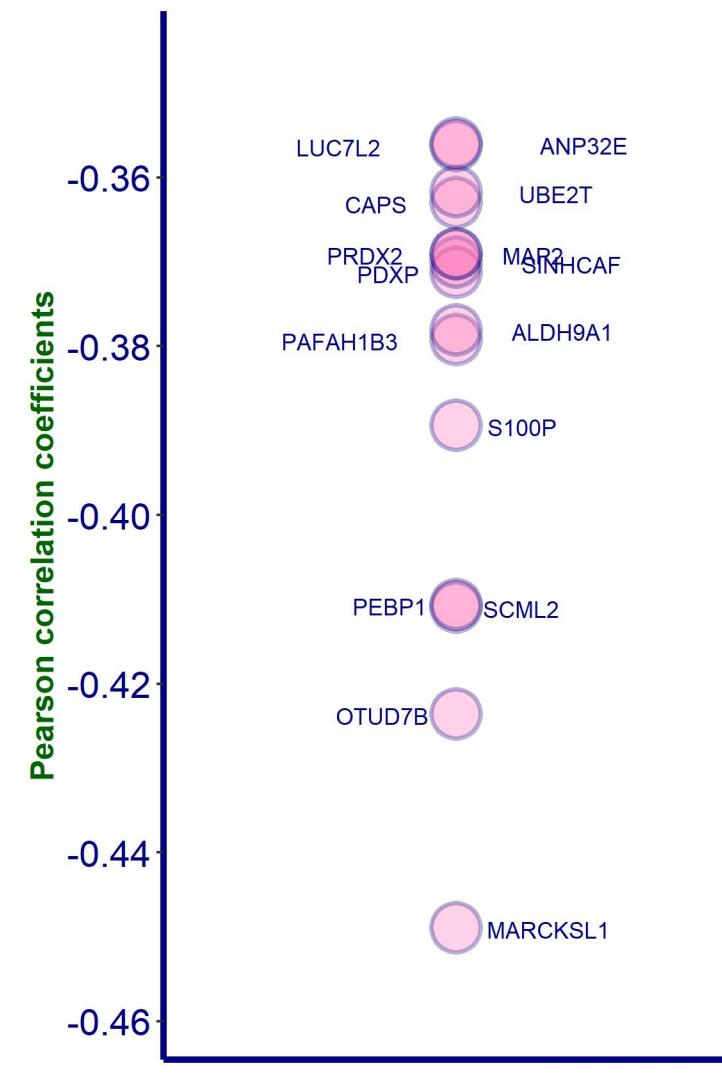
Protein name: EGFR ; UNIPROT: P00533 ; Gene name: epidermal growth factor receptor

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

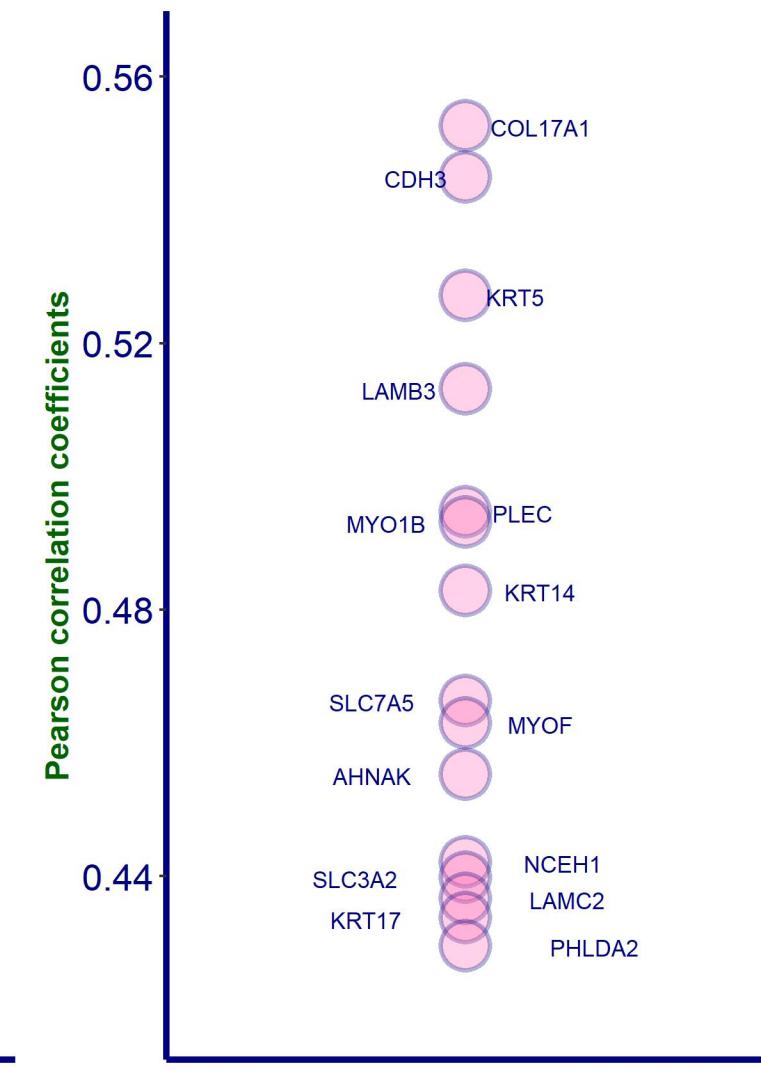
Sanger Institute Protein Database 1 (DB1), protein presence is certain



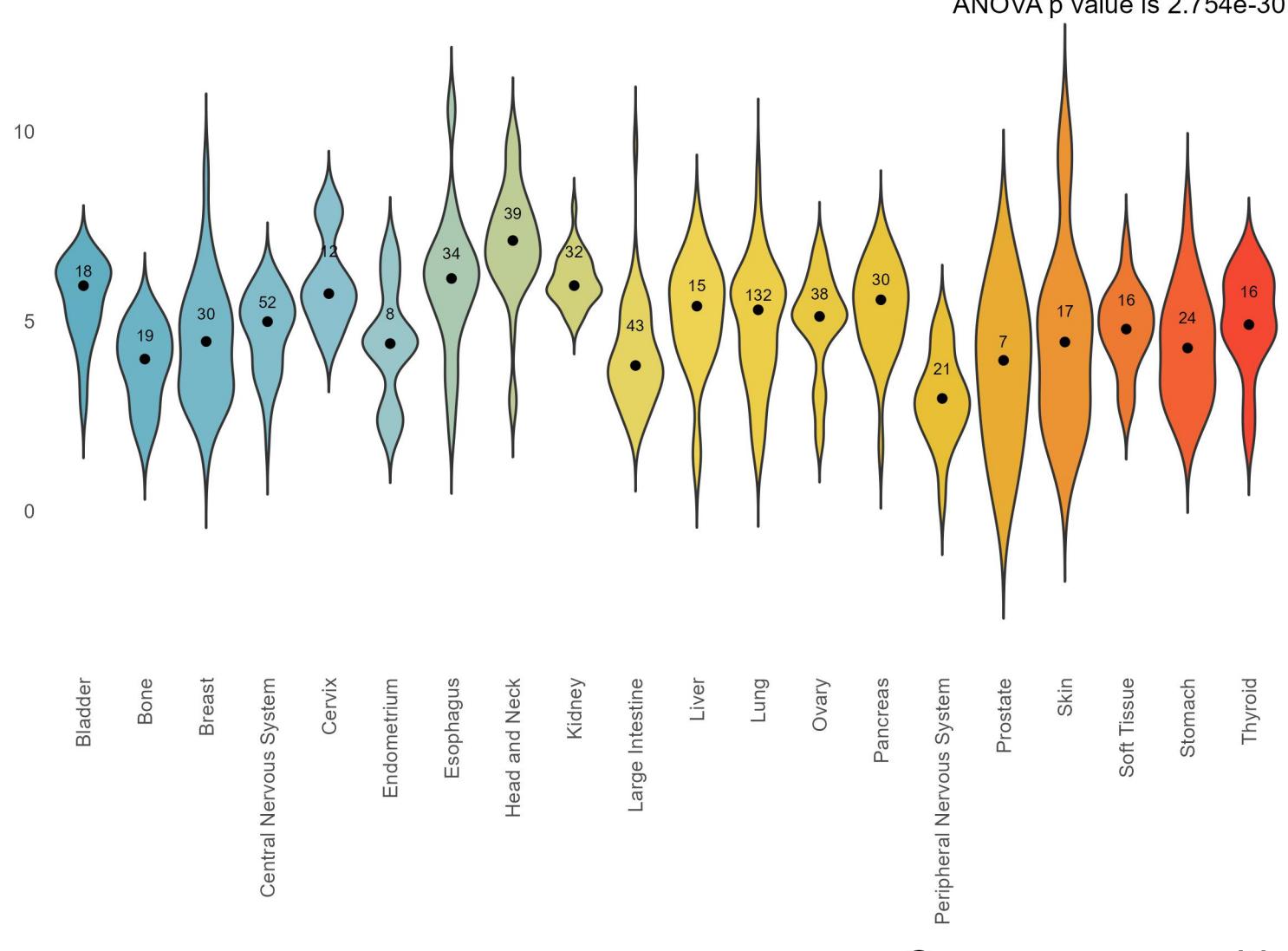
Top negative correlations of EGFR protein, DB1



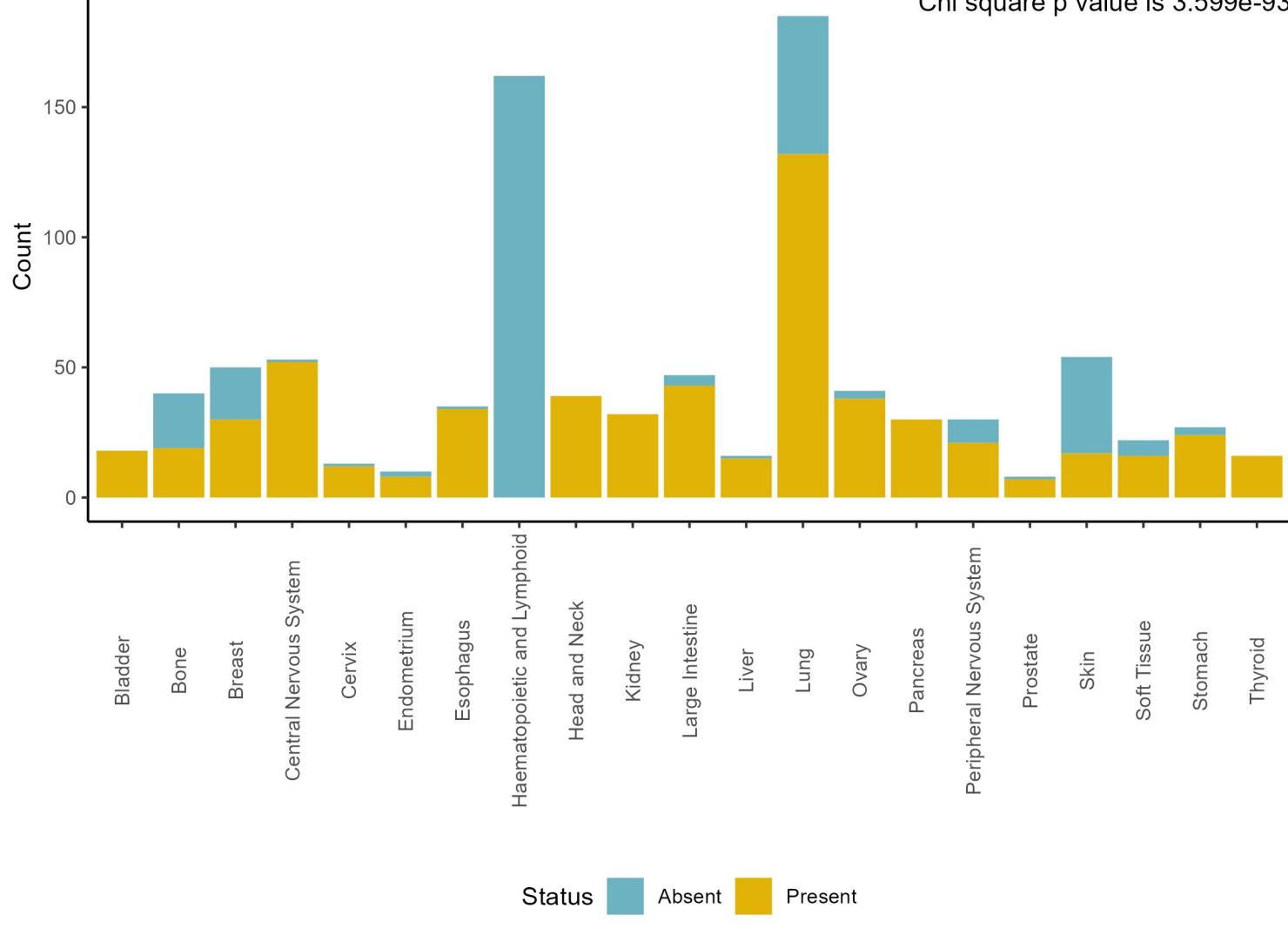
Top positive correlations of EGFR protein, DB1



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



Present and absent EGFR protein counts by tissue, DB1

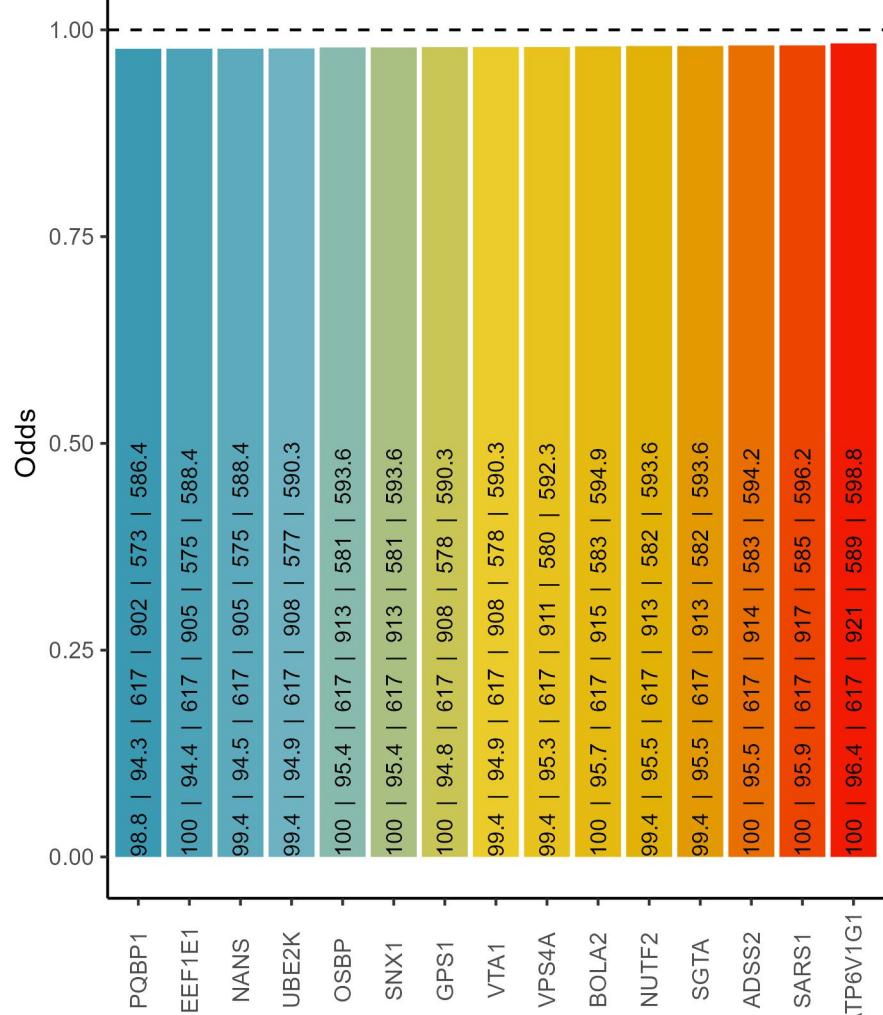


Cooccurrence with EGFR protein, DB1

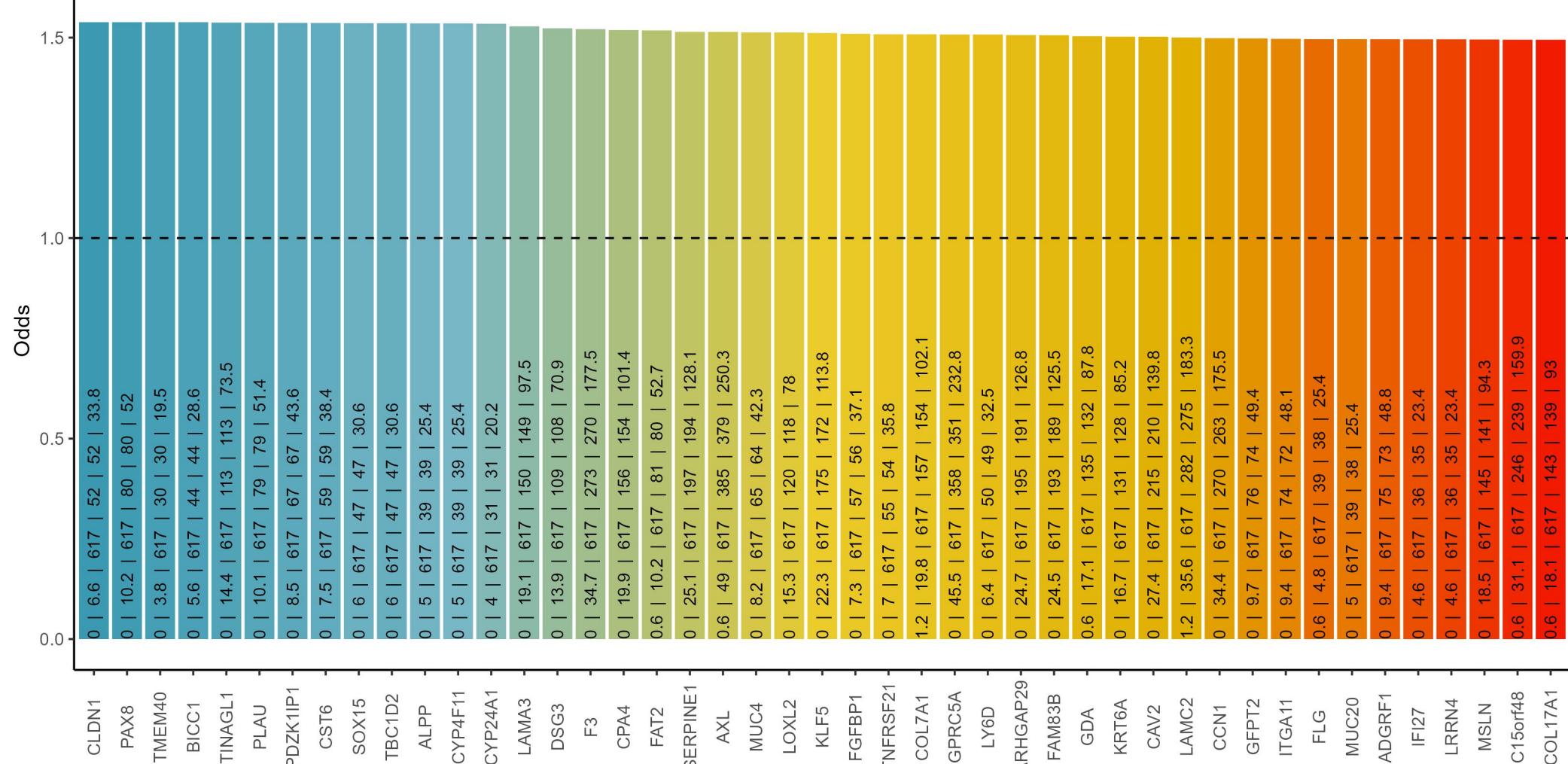
% of EGFR in blood cancers: 0 ; % of EGFR in solid cancers: 78.6

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

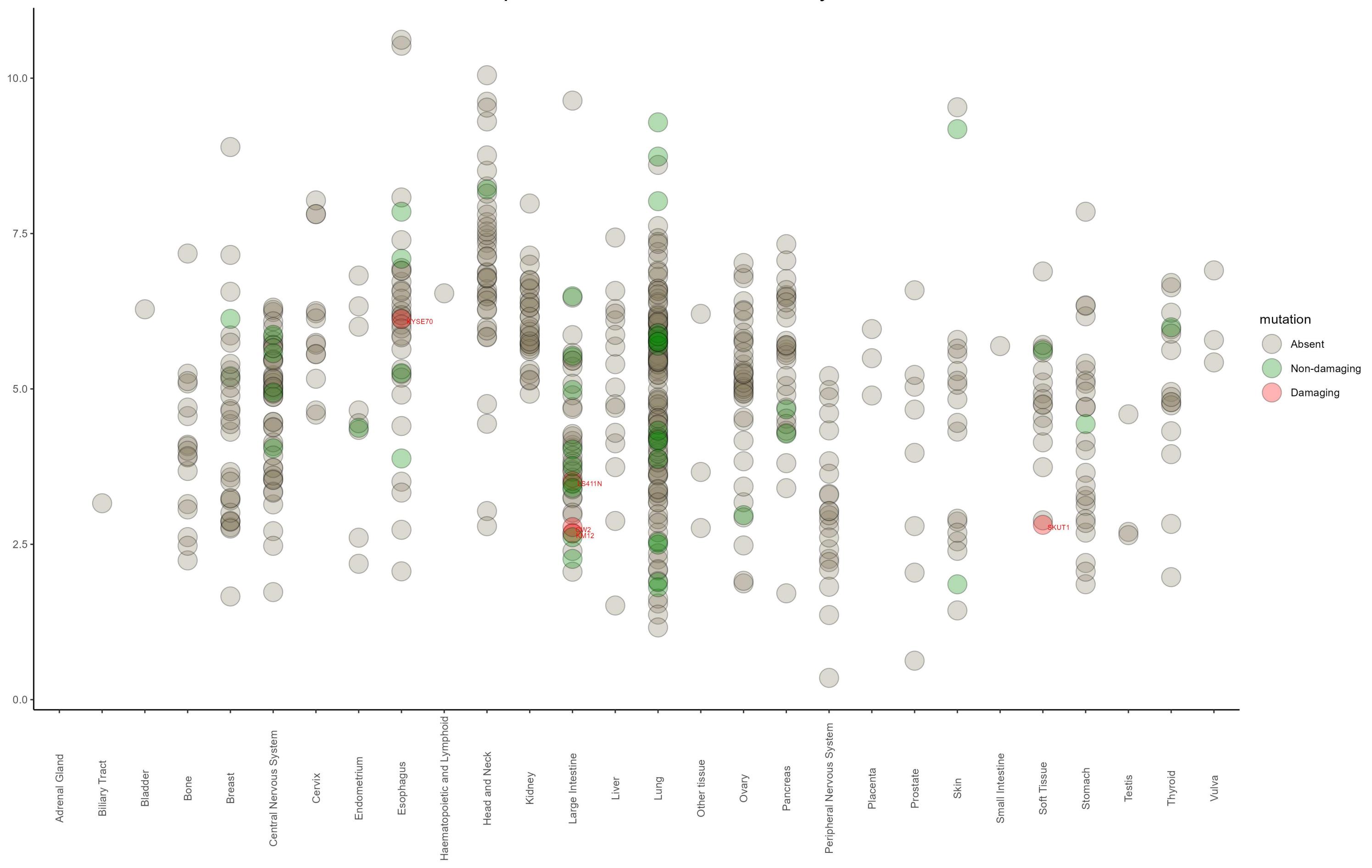
Negative cooccurrence



Positive cooccurrence

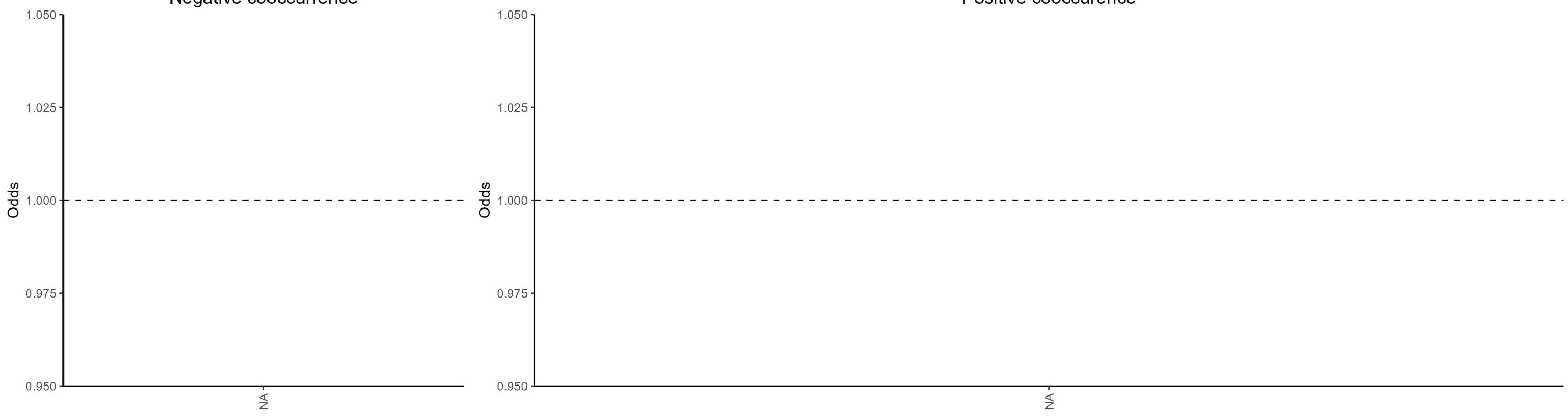


Amount of EGFR protein and mutation status by tissue, DB1



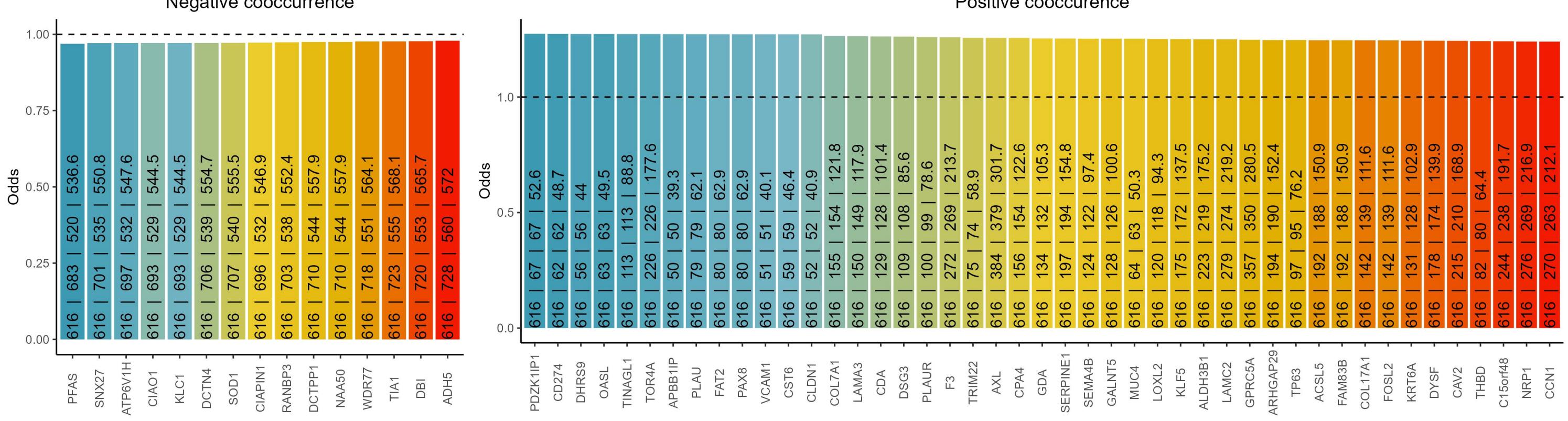
Cooccurrence with EGFR protein in blood cancers, DB1

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



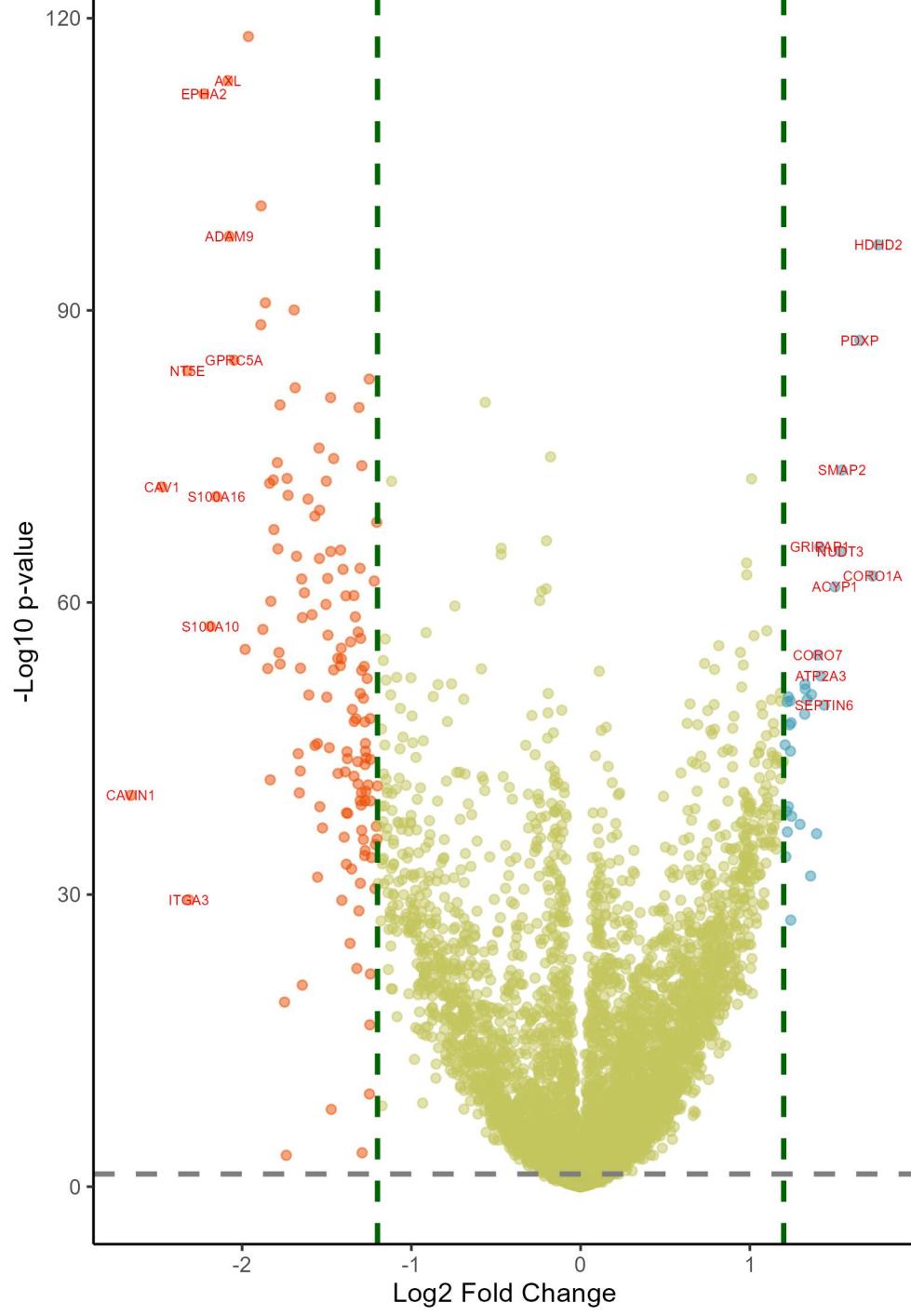
Cooccurrence with EGFR protein in solid cancers, DB1

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



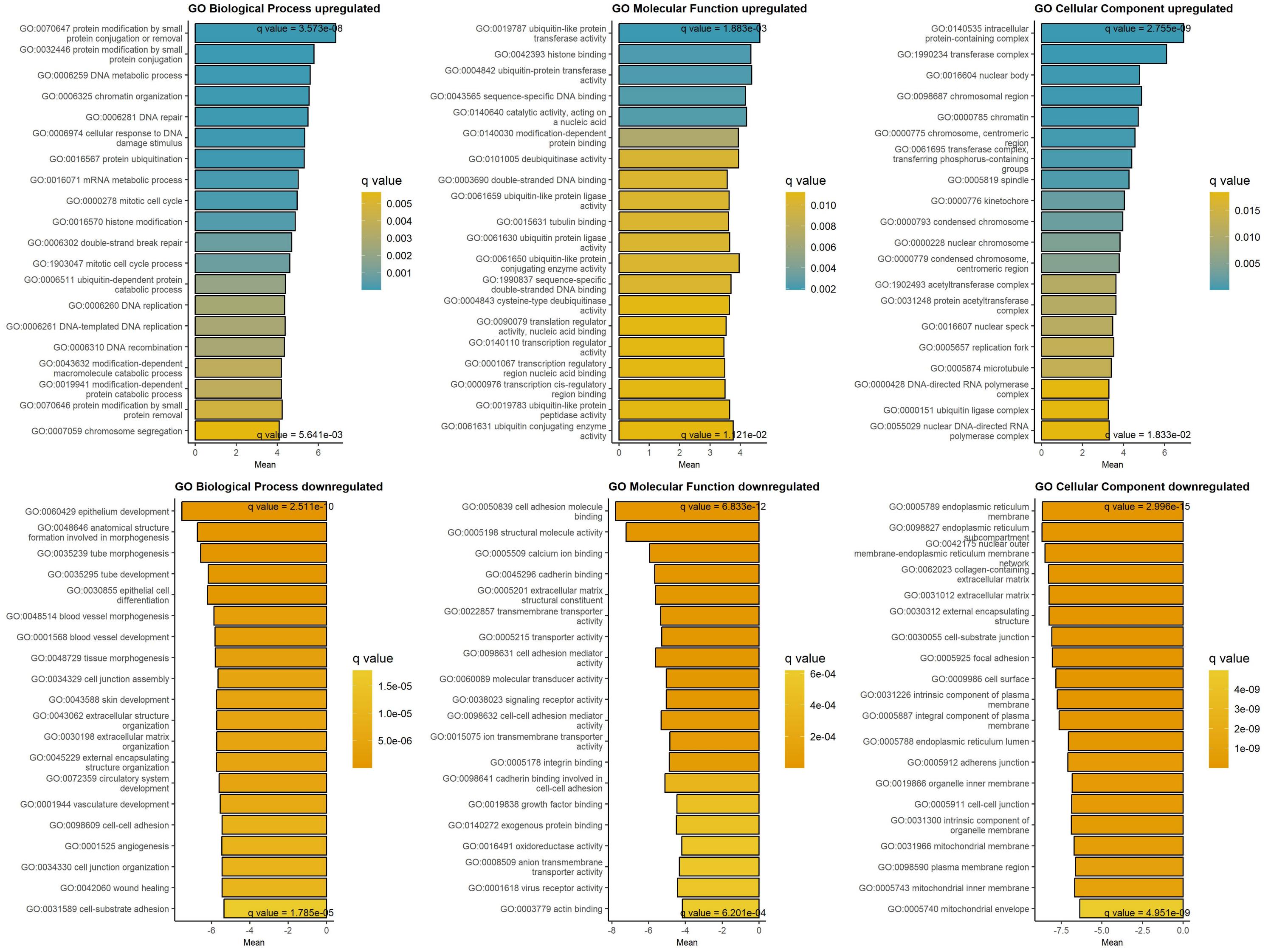
p-value < 0.05 & logFC > 1.2

Downregulated at low/absent EGFR Upregulated at low/absent EGFR



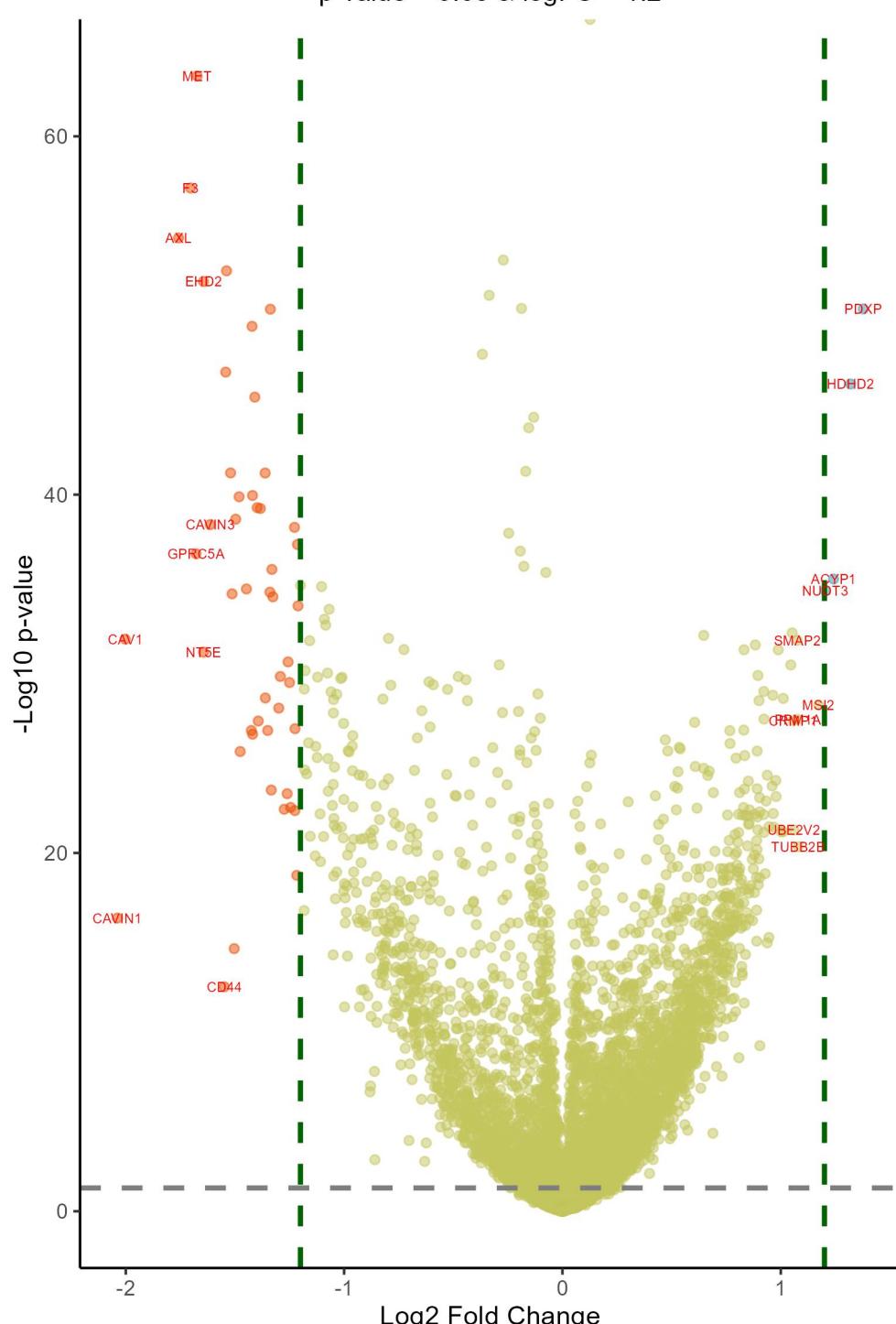
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.66	1.65e-39	CAVIN1	caveolae associated protein 1	1.76	1.78e-94	HDHD2	haloacid dehalogenase like hydrolase
-2.47	2.83e-70	CAV1	caveolin 1	1.73	2.31e-61	CORO1A	coronin 1A
-2.32	8.08e-82	NT5E	5'-nucleotidase ecto	1.65	7.19e-85	PDXP	pyridoxal phosphatase
-2.31	3.77e-29	ITGA3	integrin subunit alpha 3	1.54	6.72e-72	SMAP2	small ArfGAP2
-2.23	9.63e-110	EPHA2	EPH receptor A2	1.54	8.43e-64	NUDT3	nudix hydrolase 3
-2.19	2.66e-56	S100A10	S100 calcium binding protein A10	1.5	2.85e-60	ACYP1	acylphosphatase 1
-2.15	2.60e-69	S100A16	S100 calcium binding protein A16	1.44	1.78e-48	SEPTIN6	septin 6
-2.08	5.64e-111	AXL	AXL receptor tyrosine kinase	1.42	2.33e-51	ATP2A3	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporting 2A
-2.08	2.73e-95	ADAM9	ADAM metallopeptidase domain 9	1.41	3.26e-64	GRIPAP1	GRIP1 associated protein 1
-2.05	7.36e-83	GPRC5A	G protein-coupled receptor class C	1.4	1.93e-53	CORO7	coronin 7
-1.98	5.35e-54	ITGA2	integrin subunit alpha 2	1.39	1.03e-35	BLMH	bleomycin hydrolase
-1.96	2.48e-115	MET	MET proto-oncogene, receptor tyrosine kinase	1.36	1.70e-49	COPS7B	COP9 signalosome subunit 7B
-1.89	2.00e-86	RRAS	RAS related	1.36	1.60e-31	ABRACL	ABRA C-terminal like
-1.89	2.50e-98	SDC4	syndecan 4	1.34	5.22e-49	ARMC6	armadillo repeat containing 6
-1.88	5.38e-56	ITGB4	integrin subunit beta 4	1.33	4.85e-50	PPM1A	protein phosphatase, Mg2+/Mn2+ dependent 1A
-1.86	1.41e-88	EHD2	EH domain containing 2	1.33	1.55e-50	GRK2	G protein-coupled receptor kinase 2
-1.85	4.23e-52	MYOF	myoferlin	1.32	1.43e-47	SNRNP27	small nuclear ribonucleoprotein U4/U6-S5
-1.84	1.22e-70	CAVIN3	caveolae associated protein 3	1.3	1.22e-36	UBE2V2	ubiquitin conjugating enzyme E2 V2
-1.83	4.84e-41	GNG12	G protein subunit gamma 12	1.25	1.88e-37	MSI2	musashi RNA binding protein 2
-1.83	7.72e-59	TGM2	transglutaminase 2	1.24	1.02e-46	RABEP1	rabaptin, RAB GTPase binding effect
-1.82	6.19e-71	FHL2	four and a half LIM domains 2	1.24	4.02e-27	ZNF706	zinc finger protein 706
-1.81	5.59e-66	EPS8L2	EPS8 like 2	1.24	6.97e-44	MAPRE2	microtubule associated protein RP/E
-1.79	1.27e-72	RRAS2	RAS related 2	1.24	6.68e-49	ARPP19	cAMP regulated phosphoprotein 19
-1.79	4.86e-64	GPX8	glutathione peroxidase 8 (putative)	1.23	1.62e-46	KIAA1143	KIAA1143
-1.78	1.09e-53	PPIC	peptidylprolyl isomerase C	1.23	2.17e-38	PPP6R1	protein phosphatase 6 regulatory subunit 1
-1.78	1.92e-78	CDCP1	CUB domain containing protein 1	1.23	2.77e-49	RNF113A	ring finger protein 113A
-1.78	1.54e-52	ANXA3	annexin A3	1.22	6.80e-36	C11orf54	chromosome 11 open reading frame 54
-1.75	5.42e-19	CD44	CD44 molecule (Indian blood group)	1.22	8.49e-49	ARHGEF7	Rho guanine nucleotide exchange factor 7
-1.74	9.23e-04	KRT18	keratin 18	1.22	6.40e-38	UBR7	ubiquitin protein ligase E3 component

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



Differentially expressed proteins in solid cancers at absence/low amount of EGFR , DB1

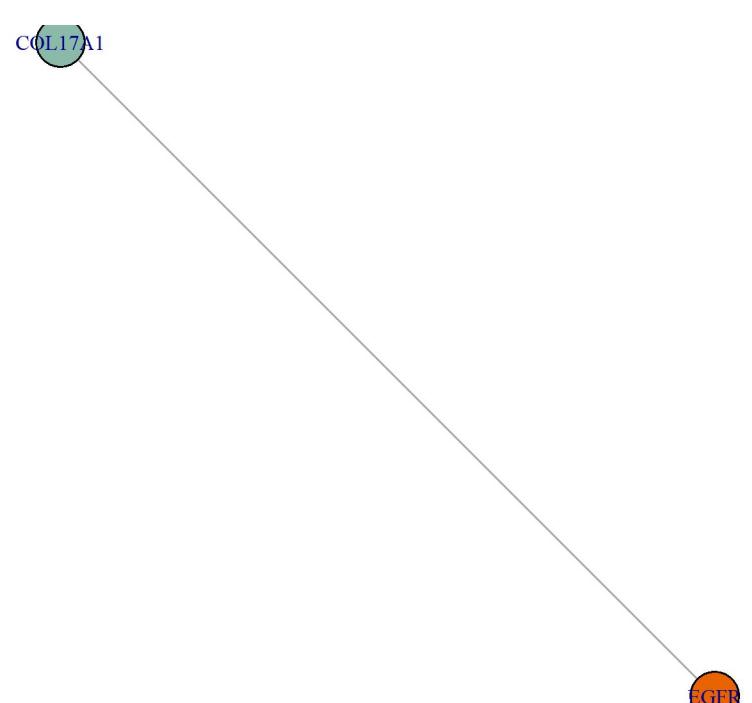
p-value < 0.05 & logFC > 1.2



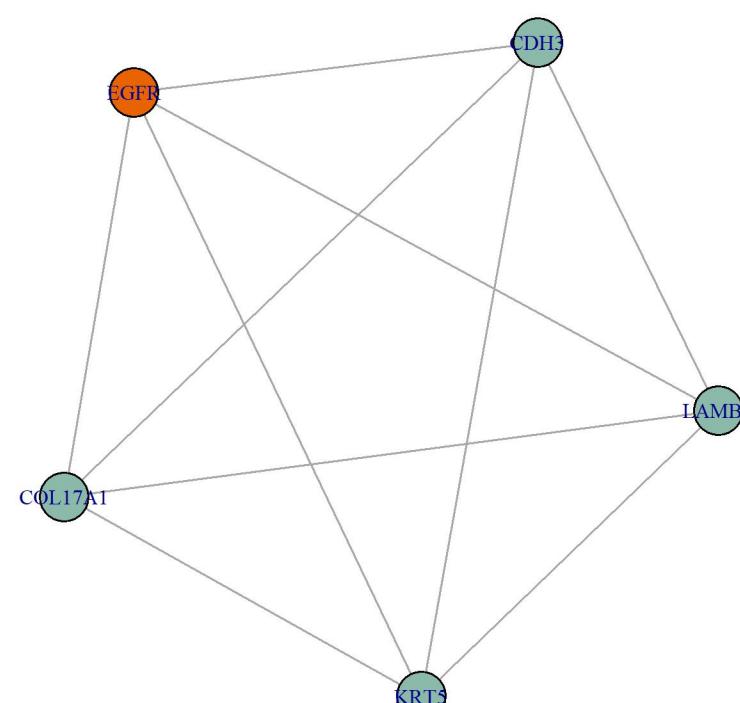
Downregulated in solid cancers at low/absent EGFR Upregulated in solid cancers at low/absent EGFR

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.04	6.15e-16	CAVIN1	caveolae associated protein 1	1.38	2.47e-48	PDXP	pyridoxal phosphatase
-2	1.49e-30	CAV1	caveolin 1	1.32	2.78e-44	HDHD2	haloacid dehalogenase like hydrolase
-1.76	6.20e-52	AXL	AXL receptor tyrosine kinase	1.24	9.18e-34	ACYP1	acylphosphatase 1
-1.7	1.27e-54	F3	coagulation factor III, tissue fact	1.2	3.69e-33	NUDT3	nudix hydrolase 3
-1.68	4.03e-35	GPRC5A	G protein-coupled receptor class C	1.17	4.07e-27	MSI2	musashi RNA binding protein 2
-1.67	9.58e-61	MET	MET proto-oncogene, receptor tyrosi	1.08	1.13e-19	TUBB2B	tubulin beta 2B class IIb
-1.64	1.05e-49	EHD2	EH domain containing 2	1.08	2.43e-26	PPM1A	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe
-1.64	6.99e-30	NT5E	5'-nucleotidase ecto	1.08	1.71e-30	SMAP2	small ArfGAP2
-1.61	1.12e-36	CAVIN3	caveolae associated protein 3	1.06	1.50e-20	UBE2V2	ubiquitin conjugating enzyme E2 V2
-1.55	2.43e-12	CD44	CD44 molecule (Indian blood group)	1.06	2.80e-26	CRMP1	collapsin response mediator protein
-1.54	6.41e-45	RRAS2	RAS related 2	1.05	7.14e-31	ZNF428	zinc finger protein 428
-1.54	3.06e-50	SDC4	syndecan 4	1.05	3.44e-29	SCML2	Scm polycomb group protein like 2
-1.52	1.88e-39	EPHA2	EPH receptor A2	1.01	1.87e-27	GRIPAP1	GRIP1 associated protein 1
-1.51	5.31e-33	THBS1	thrombospondin 1	1.01	1.86e-20	C11orf54	chromosome 11 open reading frame 54
-1.5	2.41e-14	ITGA3	integrin subunit alpha 3	1	1.85e-20	SELENBP1	selenium binding protein 1
-1.5	5.78e-37	KRT80	keratin 80	0.99	5.22e-30	KIF1A	kinesin family member 1A
-1.48	3.64e-38	RAC2	Rac family small GTPase 2	0.98	2.71e-22	CORO7	coronin 7
-1.48	1.15e-24	ITGB4	integrin subunit beta 4	0.98	3.92e-23	ZNF24	zinc finger protein 24
-1.45	3.06e-33	EPS8L2	EPS8 like 2	0.97	1.06e-20	ENSA	endosulfine alpha
-1.42	9.16e-26	TGM2	transglutaminase 2	0.97	2.13e-21	GPD1L	glycerol-3-phosphate dehydrogenase
-1.42	2.06e-47	TNFAIP2	TNF alpha induced protein 2	0.96	1.28e-27	DPYSL5	dihydropyrimidinase like 5
-1.42	3.21e-38	LAMB3	laminin subunit beta 3	0.96	7.64e-23	RPRD1A	regulation of nuclear pre-mRNA doma
-1.42	1.43e-25	ANXA3	annexin A3	0.95	1.01e-20	COPS7B	COP9 signalosome subunit 7B
-1.41	1.41e-43	P3H2	prolyl 3-hydroxylase 2	0.95	6.18e-15	BLMH	bleomycin hydrolase
-1.4	1.42e-37	LAMC2	laminin subunit gamma 2	0.94	2.04e-23	NECAP1	NECAP endocytosis associated 1
-1.39	2.90e-26	HLA-B	major histocompatibility complex, c	0.94	1.21e-14	ABRACL	ABRA C-terminal like
-1.38	1.51e-37	SP100	SP100 nuclear antigen	0.93	4.70e-22	CGGBP1	CGG triplet repeat binding protein
-1.36	1.88e-39	ADAM9	ADAM metallopeptidase domain 9	0.93	2.99e-18	UBR7	ubiquitin protein ligase E3 compone
-1.36	1.79e-27	S100A10	S100 calcium binding protein A10	0.92	2.34e-26	IRF2BP1	interferon regulatory factor 2 bind

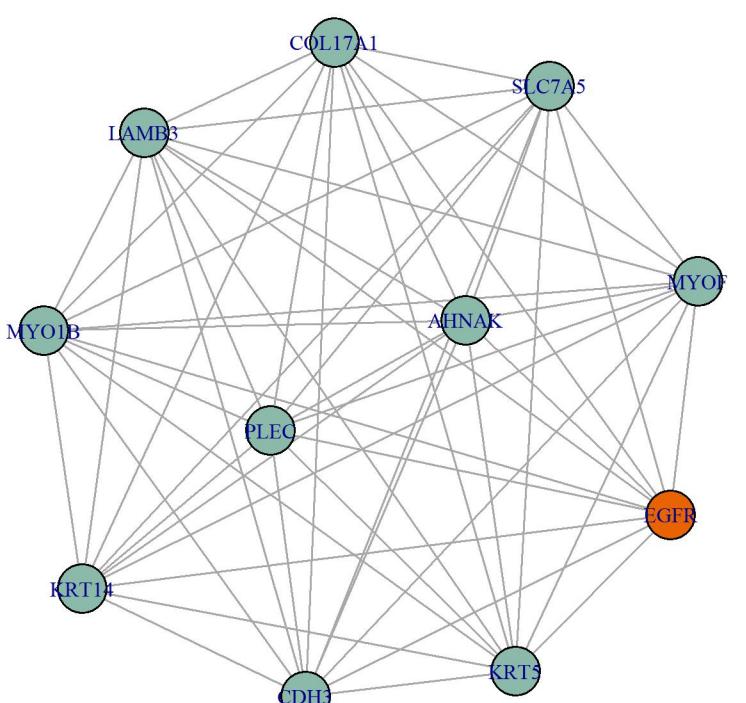
EGFR network, DB1, all Pearson r > 0.55

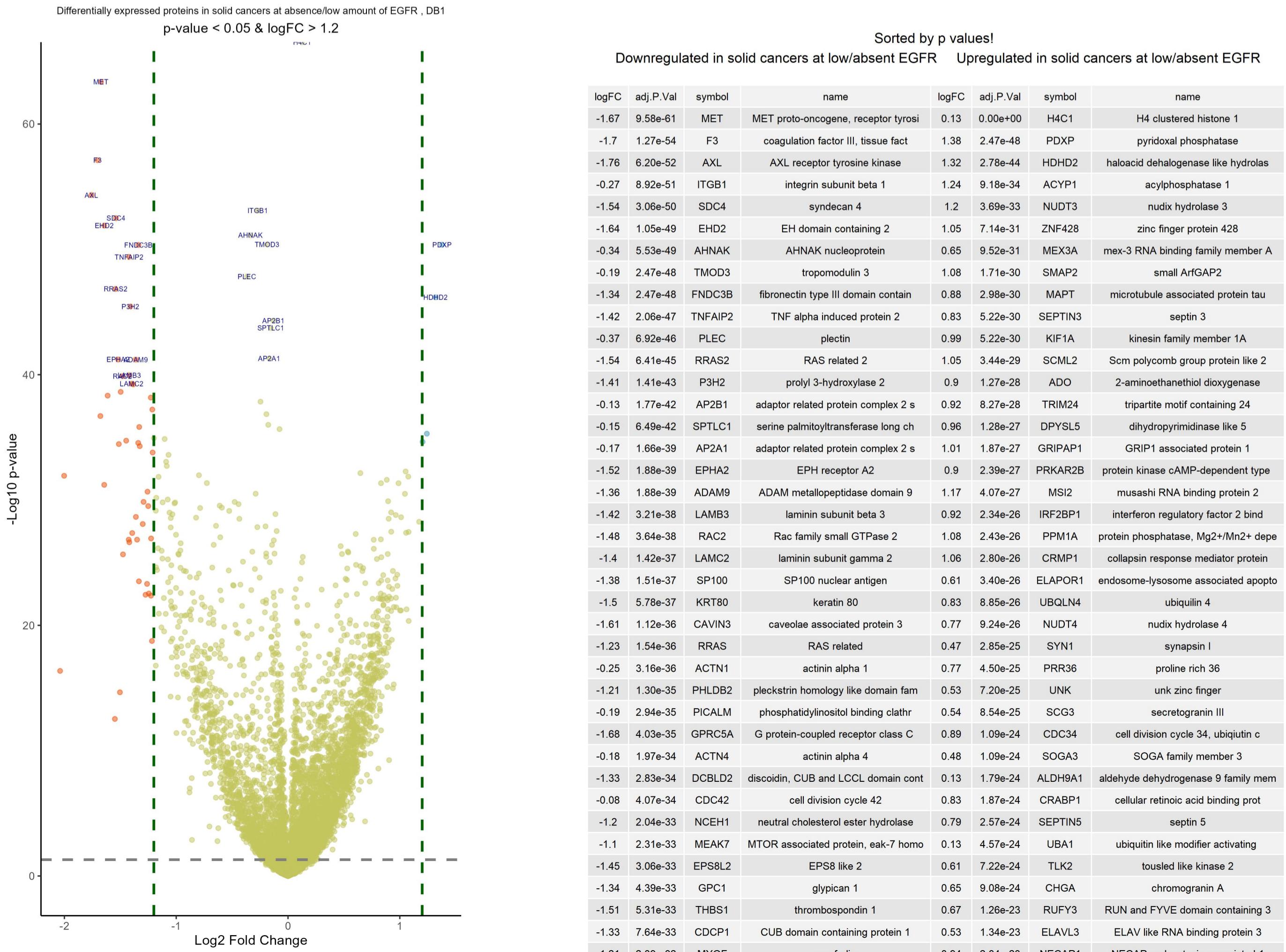


EGFR network, DB1, all Pearson r > 0.5

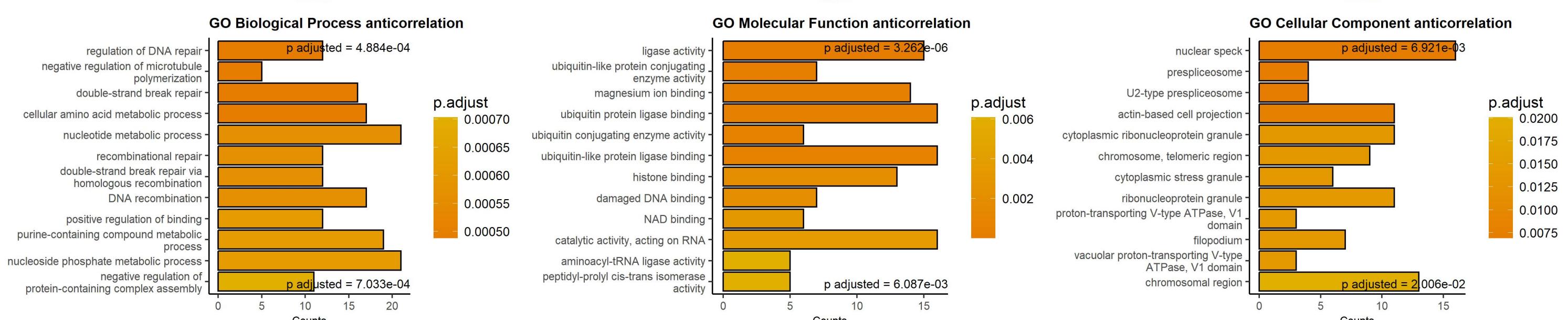
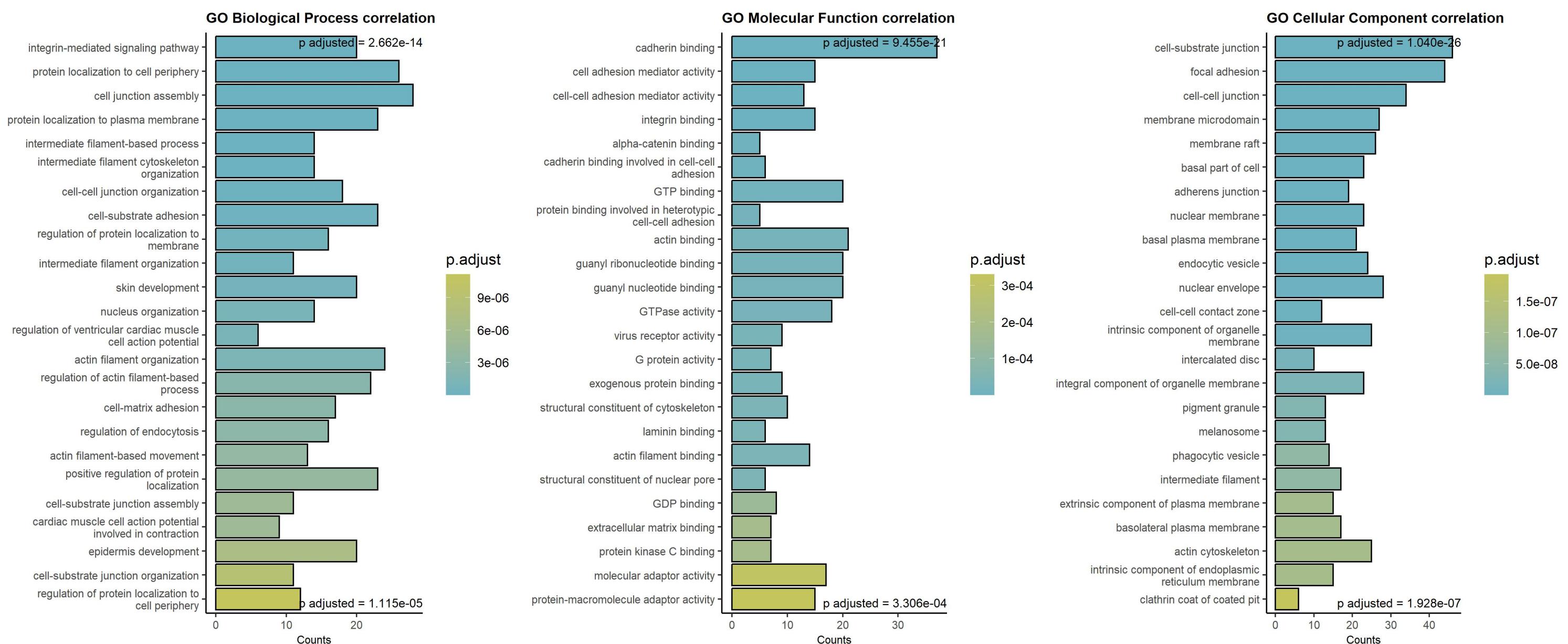


EGFR network, DB1, all Pearson r > 0.45

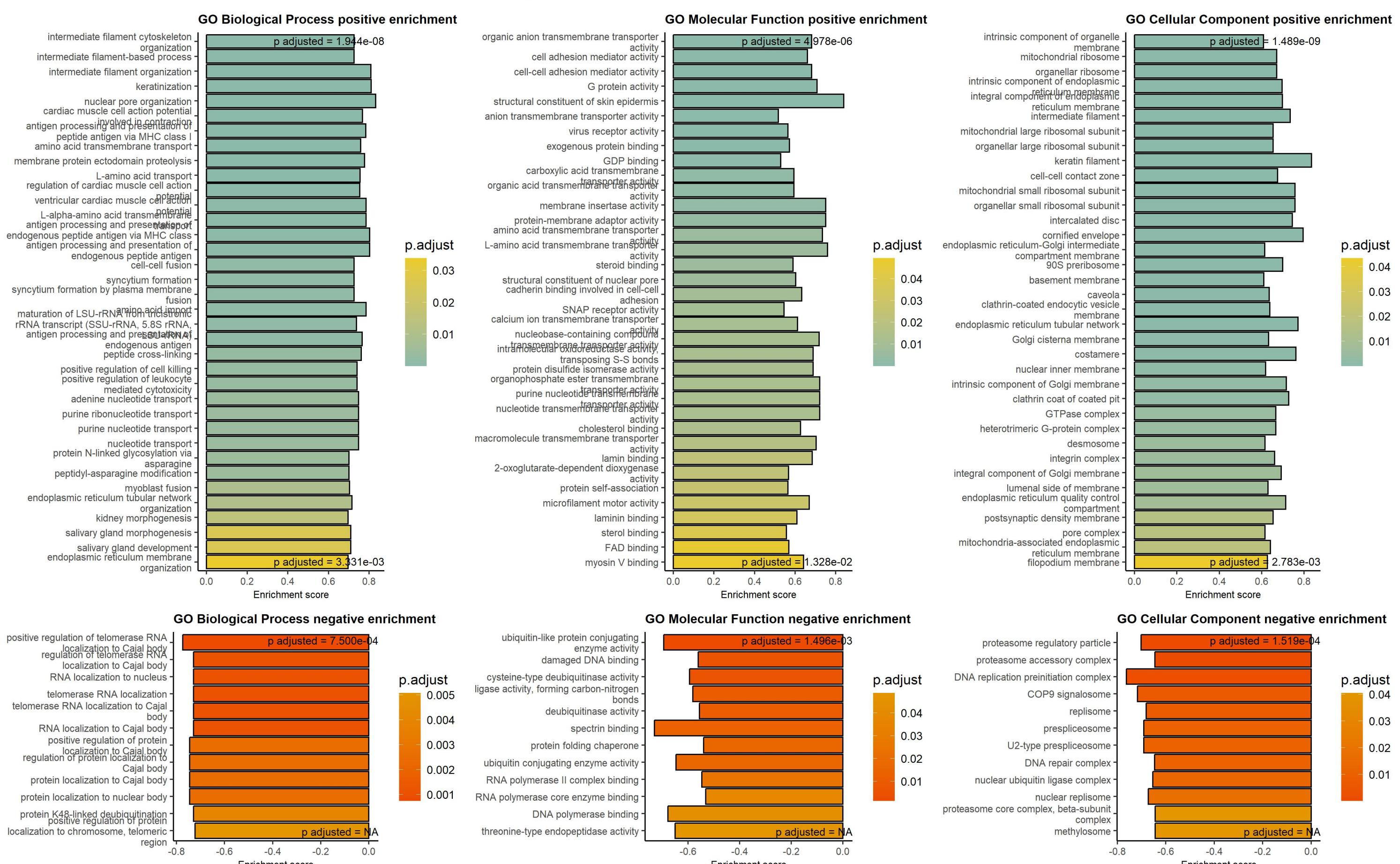




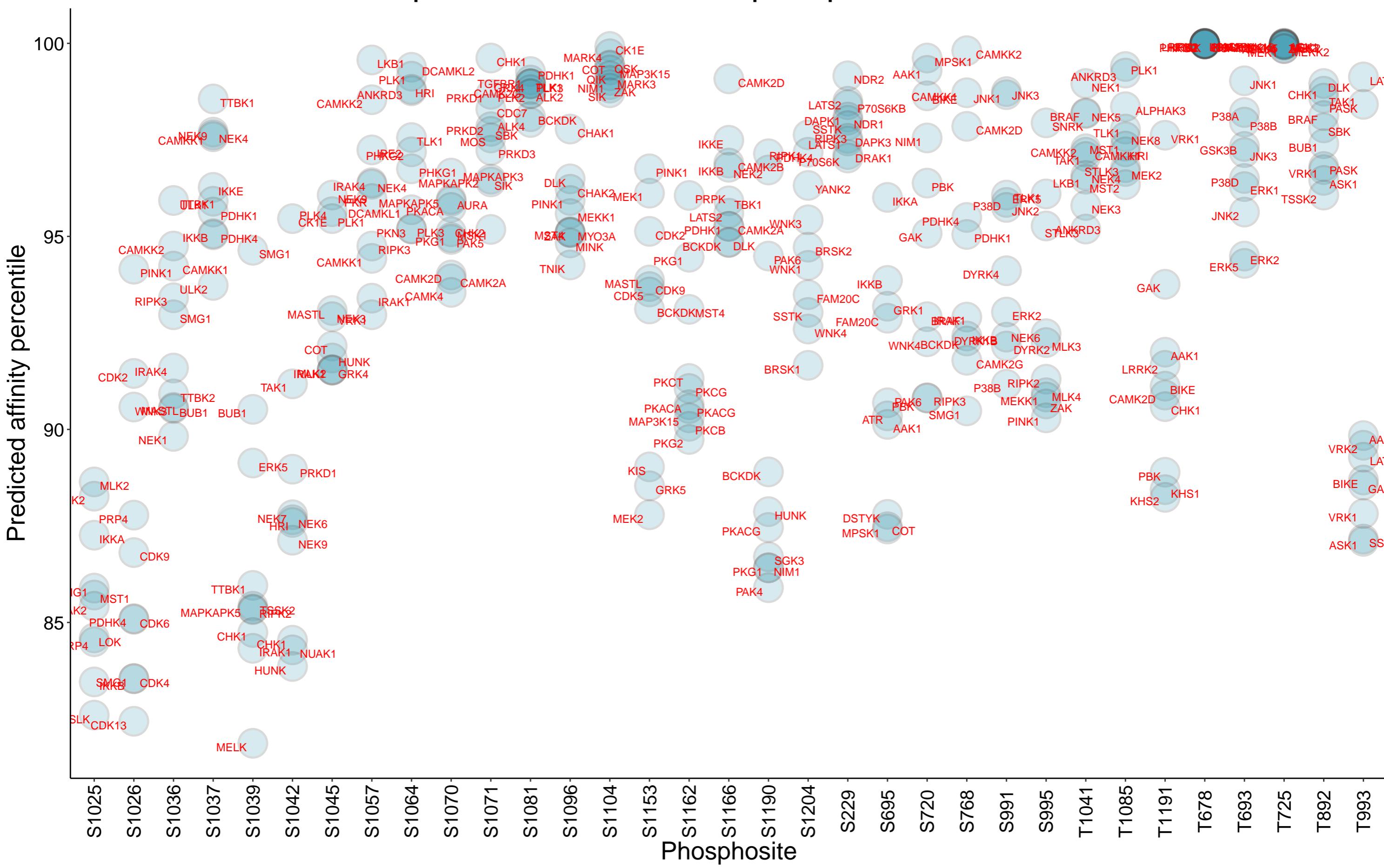
Top 250 correlation coefficients overrepresentation, EGFR protein, DB1



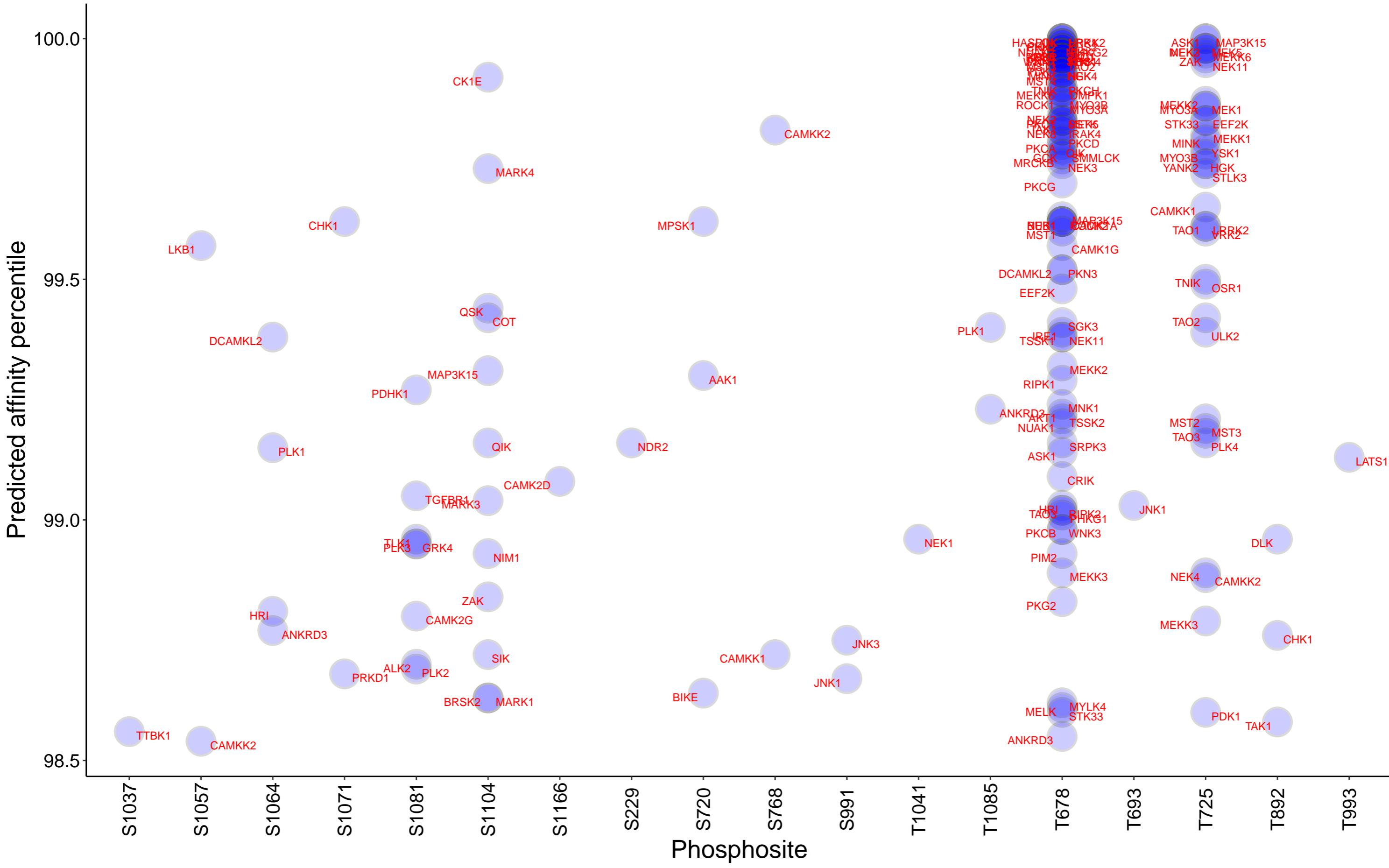
Gene Set Enrichment analysis on protein correlation coefficients, EGFR protein, DB1



Top 10 kinases for each phosphosite in EGFR



Kinases with affinity greater than 98.5% to EGFR



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

Beware of false positives in tissues with small number of samples

