

CDC6

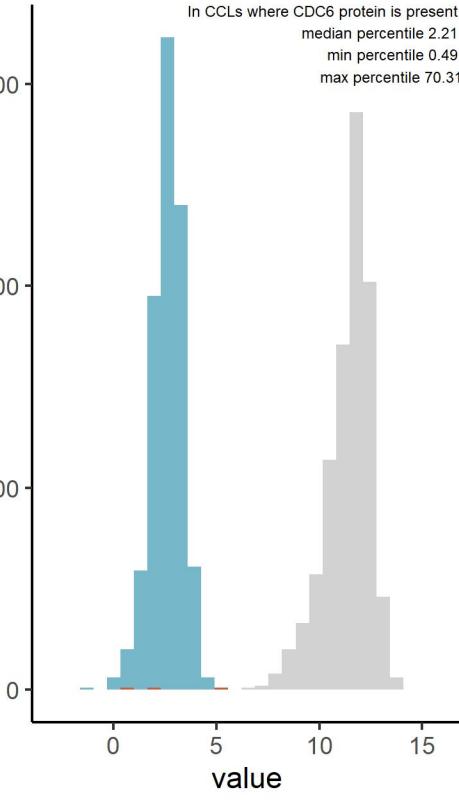
Protein name: CDC6 ; UNIPROT: Q99741 ; Gene name: cell division cycle 6

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

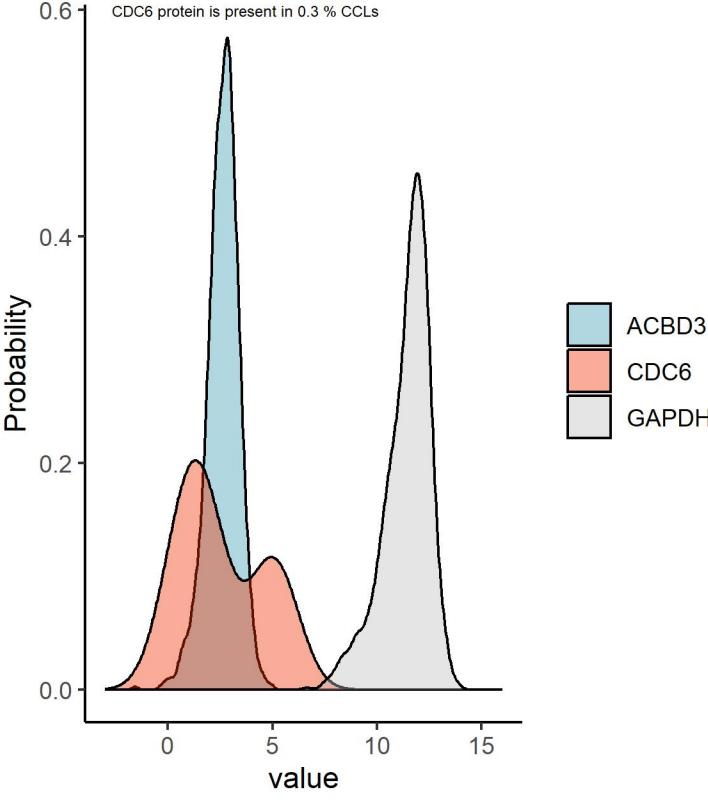
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

Histogram of CDC6 protein compared to proteins with low and high abundance



Density plot of CDC6 protein compared to proteins with low and high abundance



Top negative correlations of CDC6 protein, DB1

Pearson correlation coefficients

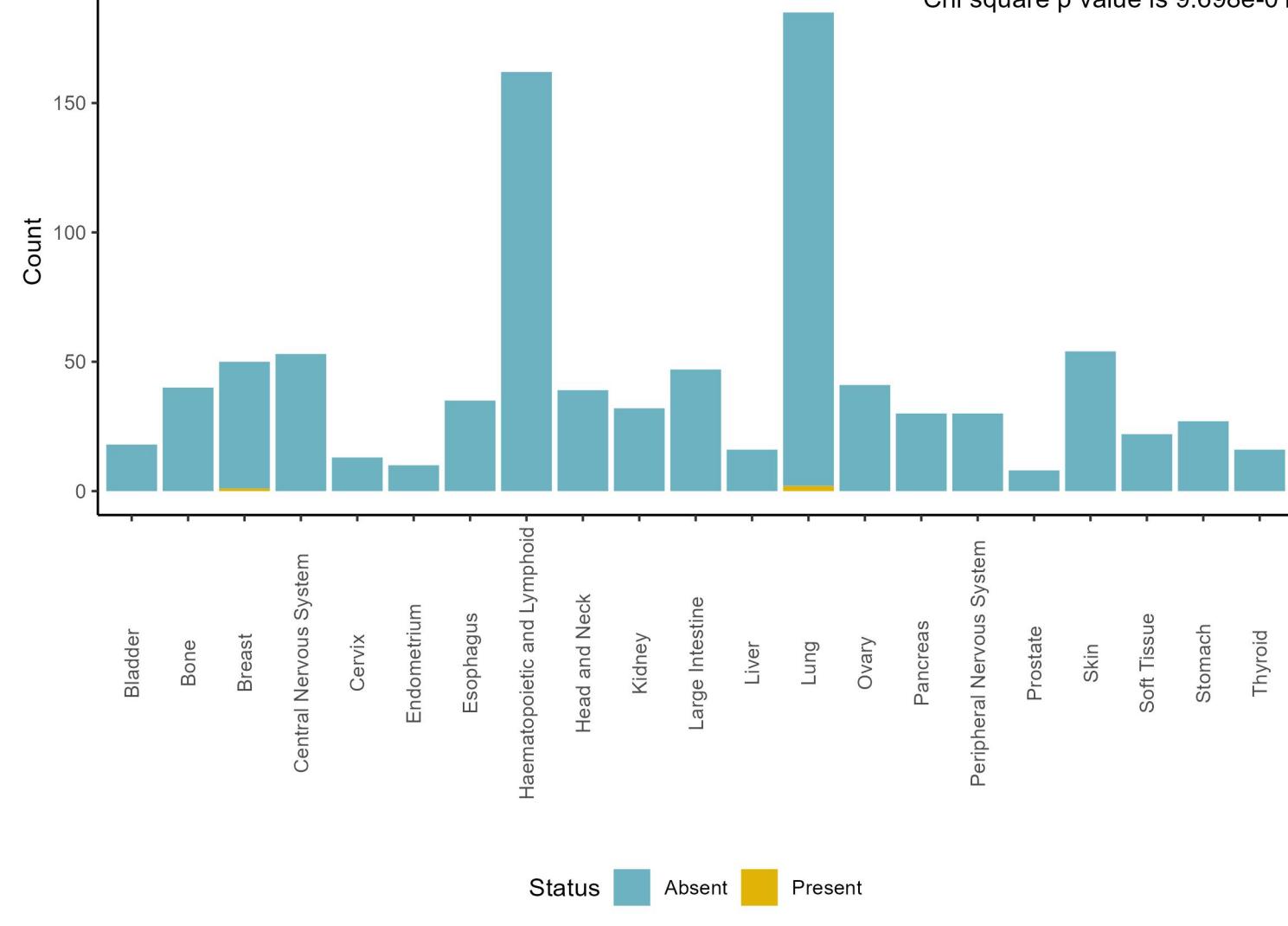
Top positive correlations of CDC6 protein, DB1

Pearson correlation coefficients

Amount of CDC6 protein, number of CCLs where it is present by tissue, DB1

Present and absent CDC6 protein counts by tissue, DB1

Chi square p value is 9.698e-01

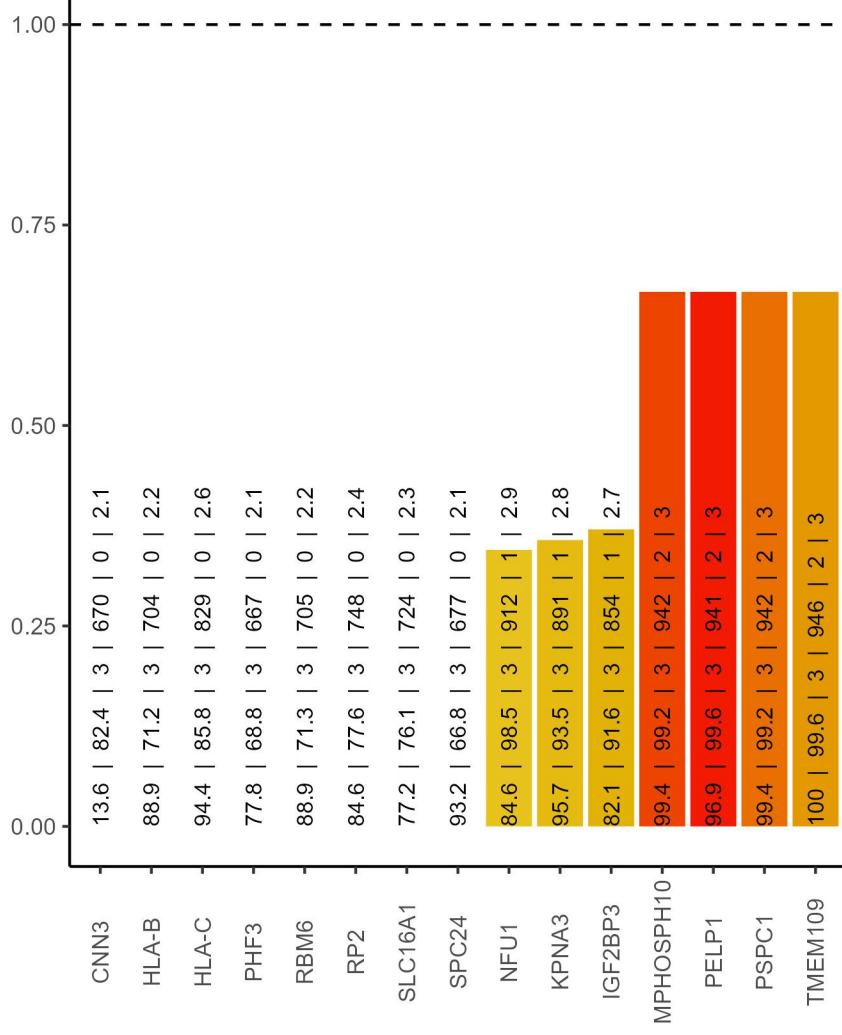


Cooccurrence with CDC6 protein, DB1

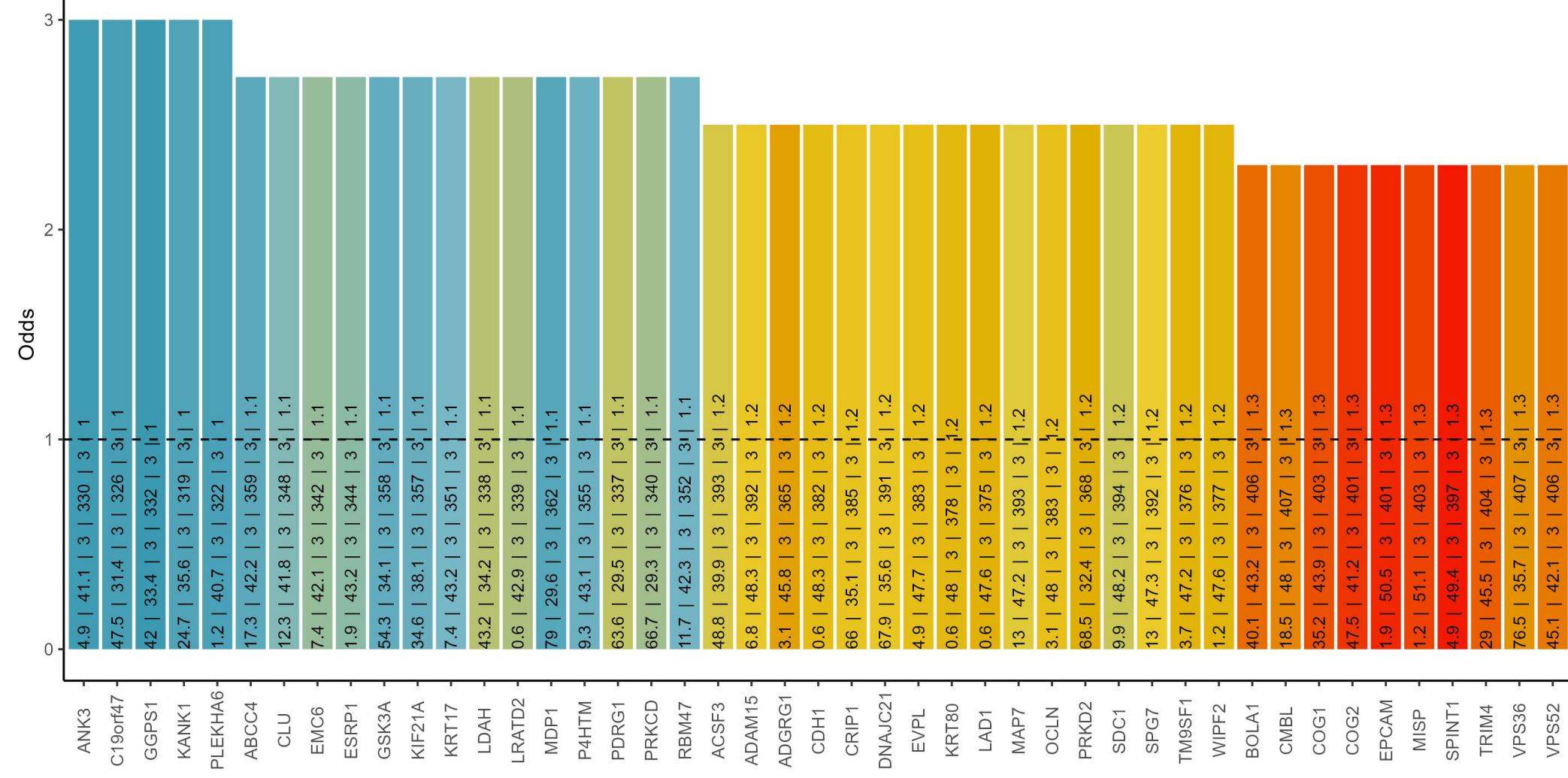
% of CDC6 in blood cancers: 0 ; % of CDC6 in solid cancers: 0.4

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CDC6 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

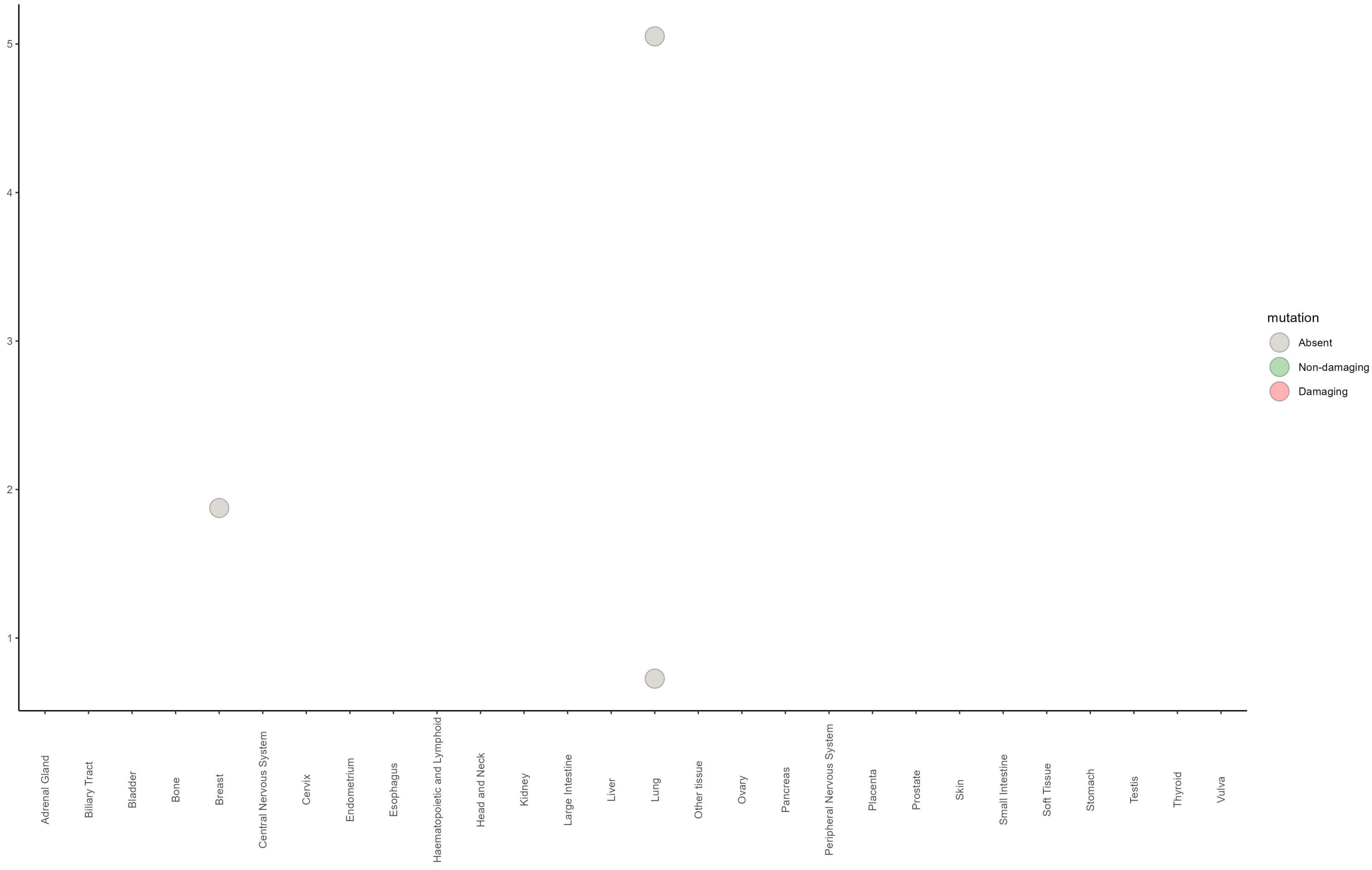
Negative cooccurrence



Positive cooccurrence

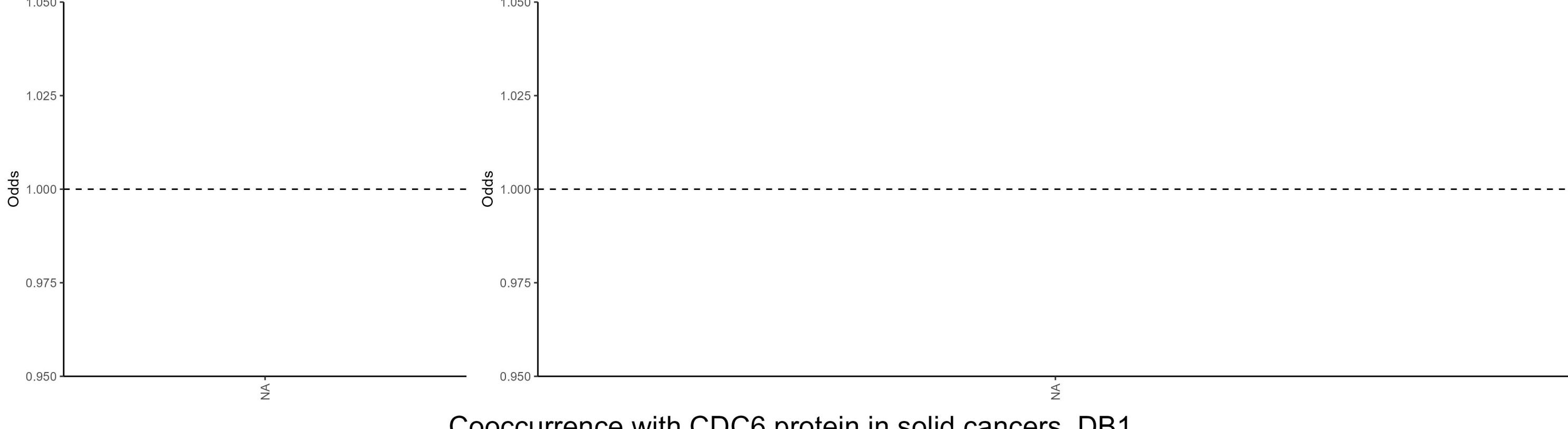


Amount of CDC6 protein and mutation status by tissue, DB1



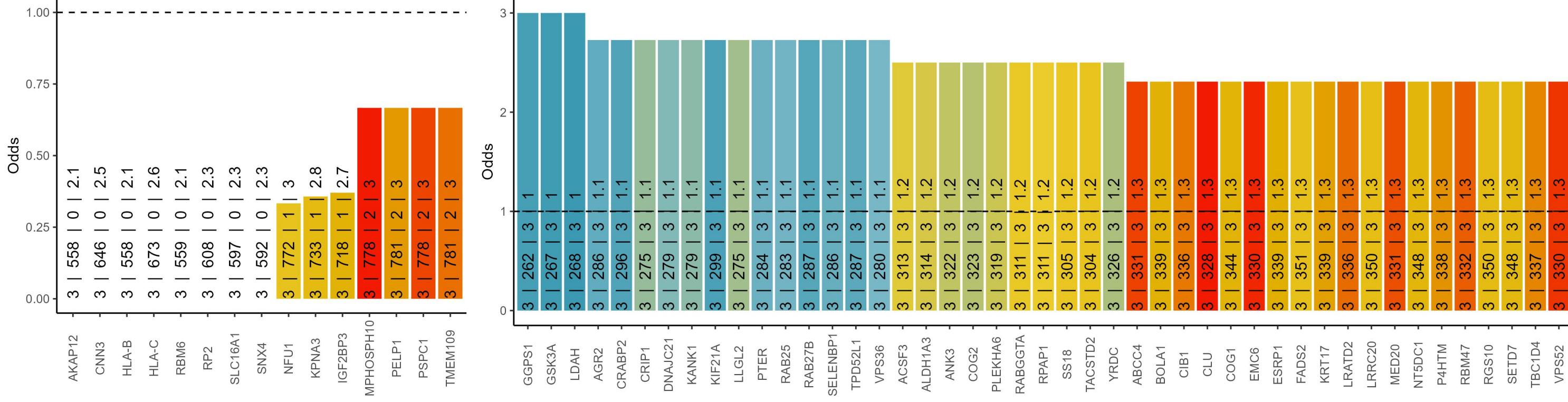
Cooccurrence with CDC6 protein in blood cancers, DB1

The text in the bars: incidence of CDC6 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



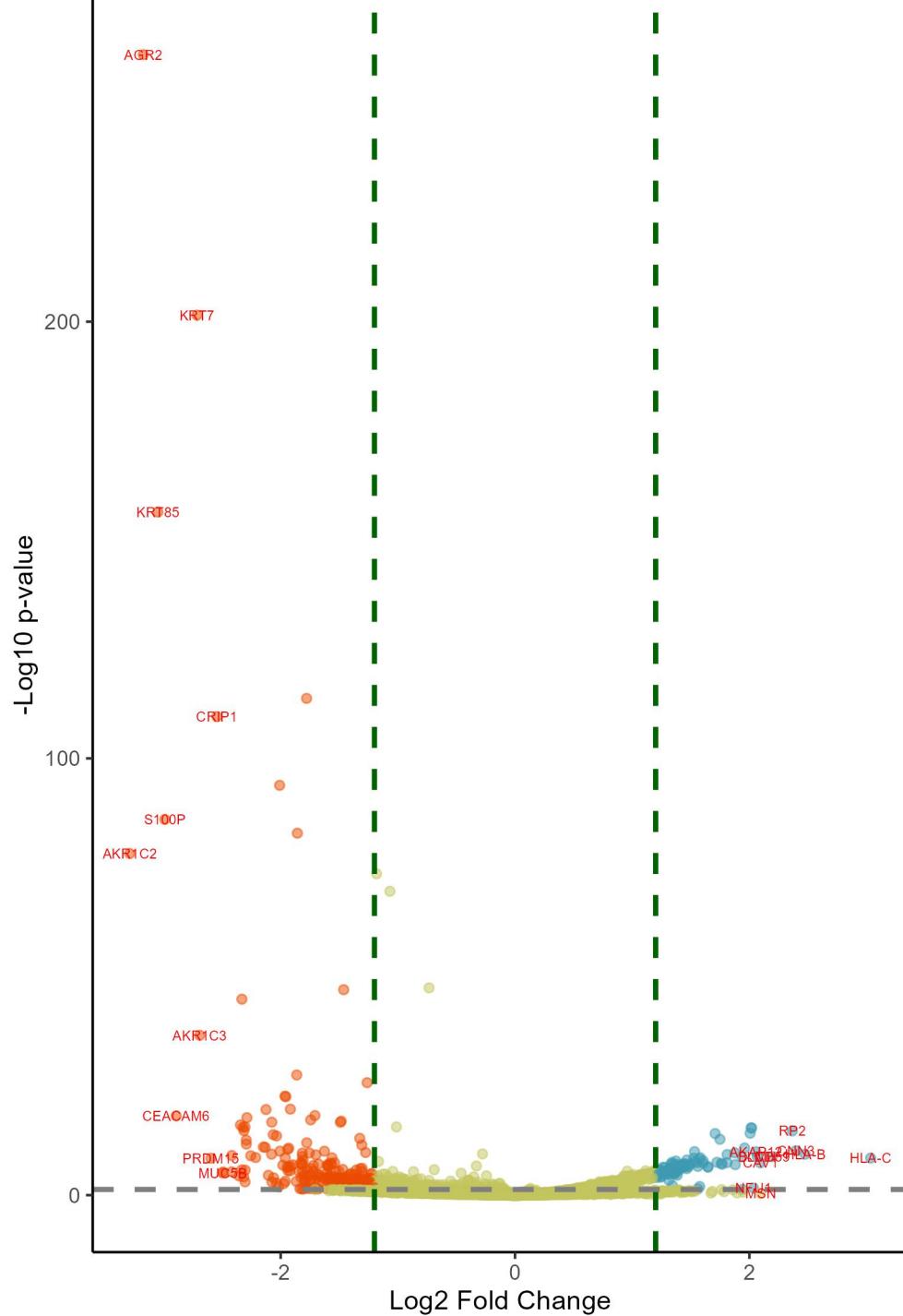
Cooccurrence with CDC6 protein in solid cancers, DB1

The text in the bars: incidence of CDC6 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



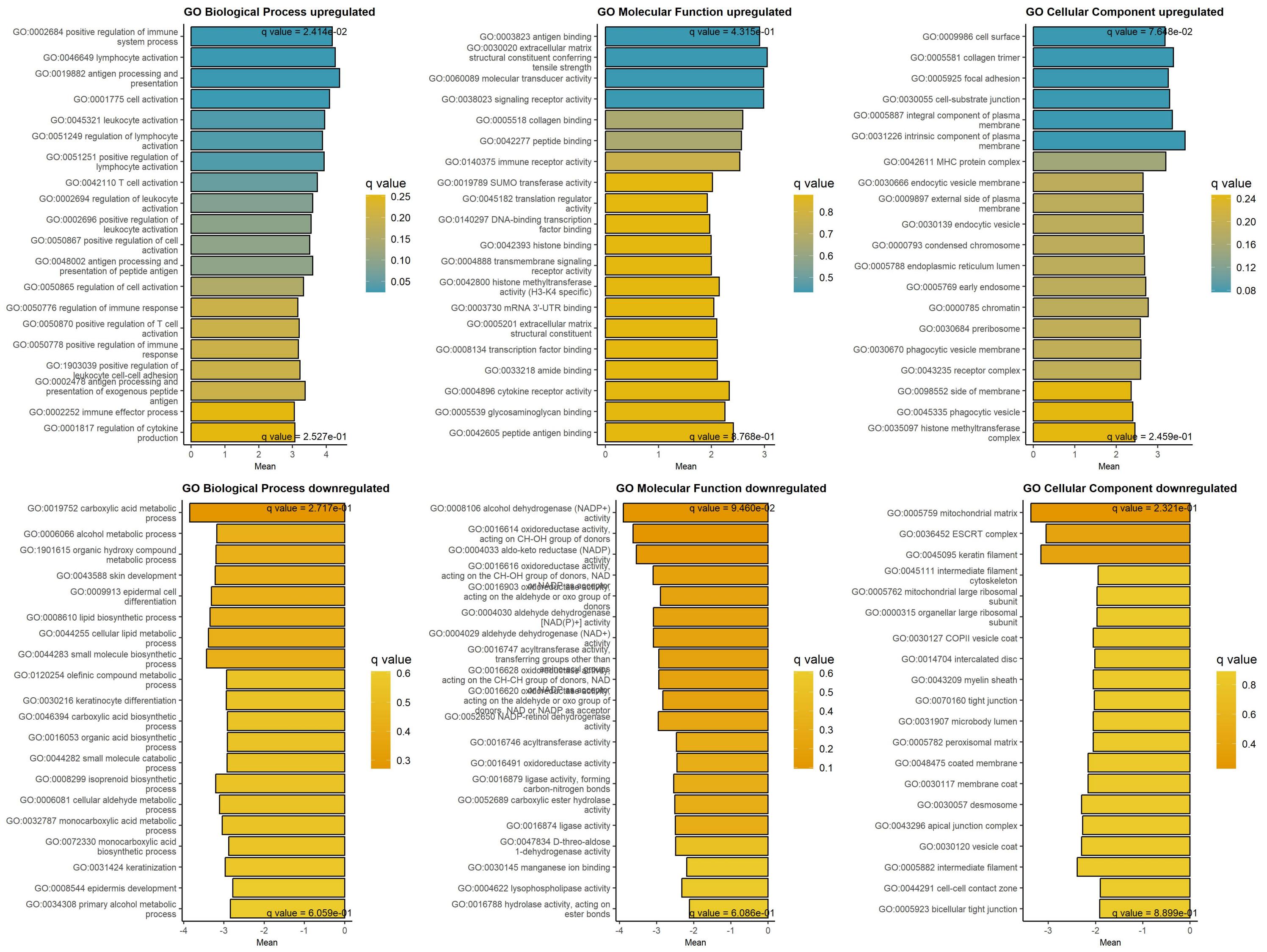
p-value < 0.05 & logFC > 1.2

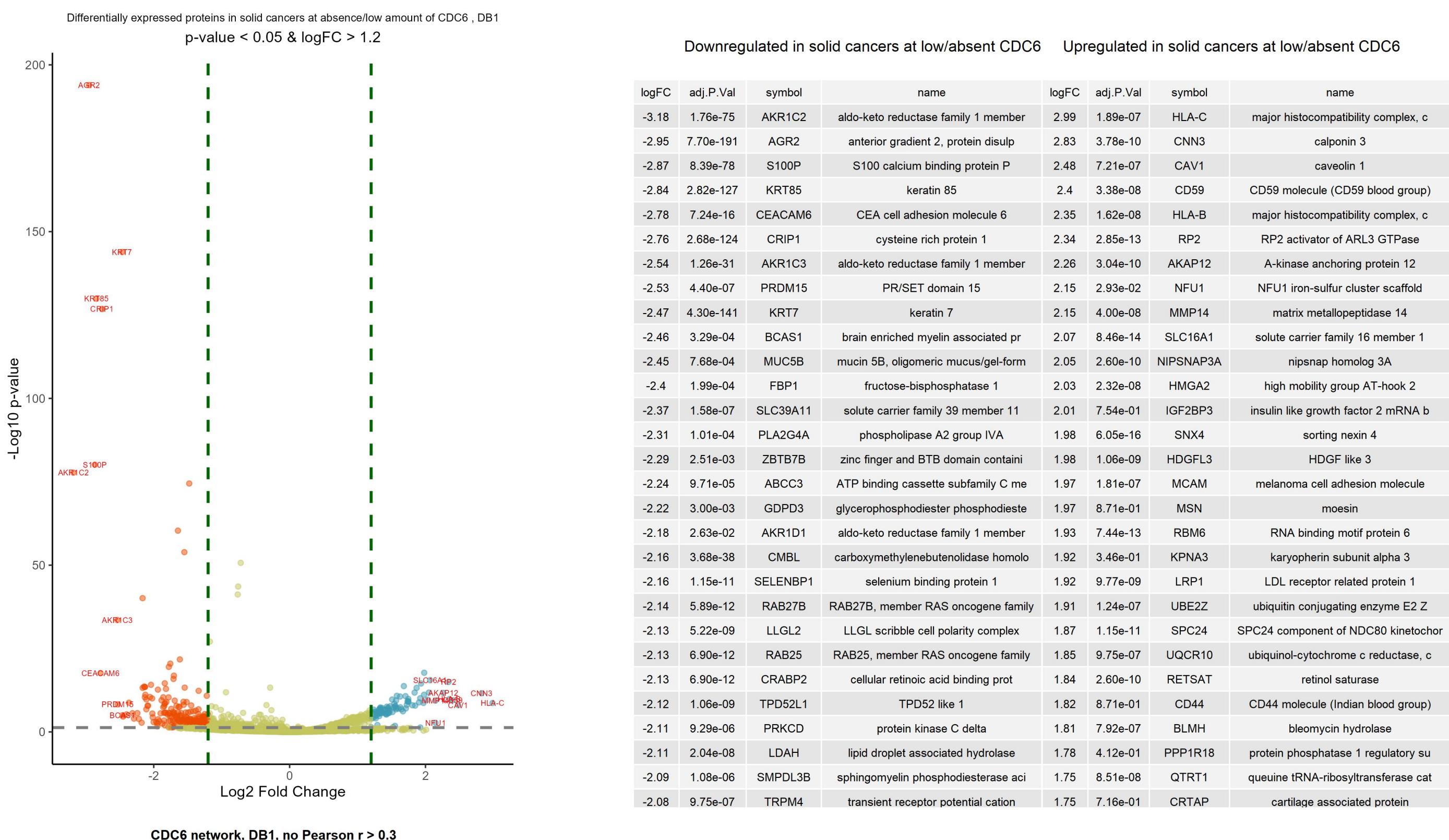
Downregulated at low/absent CDC6 Upregulated at low/absent CDC6

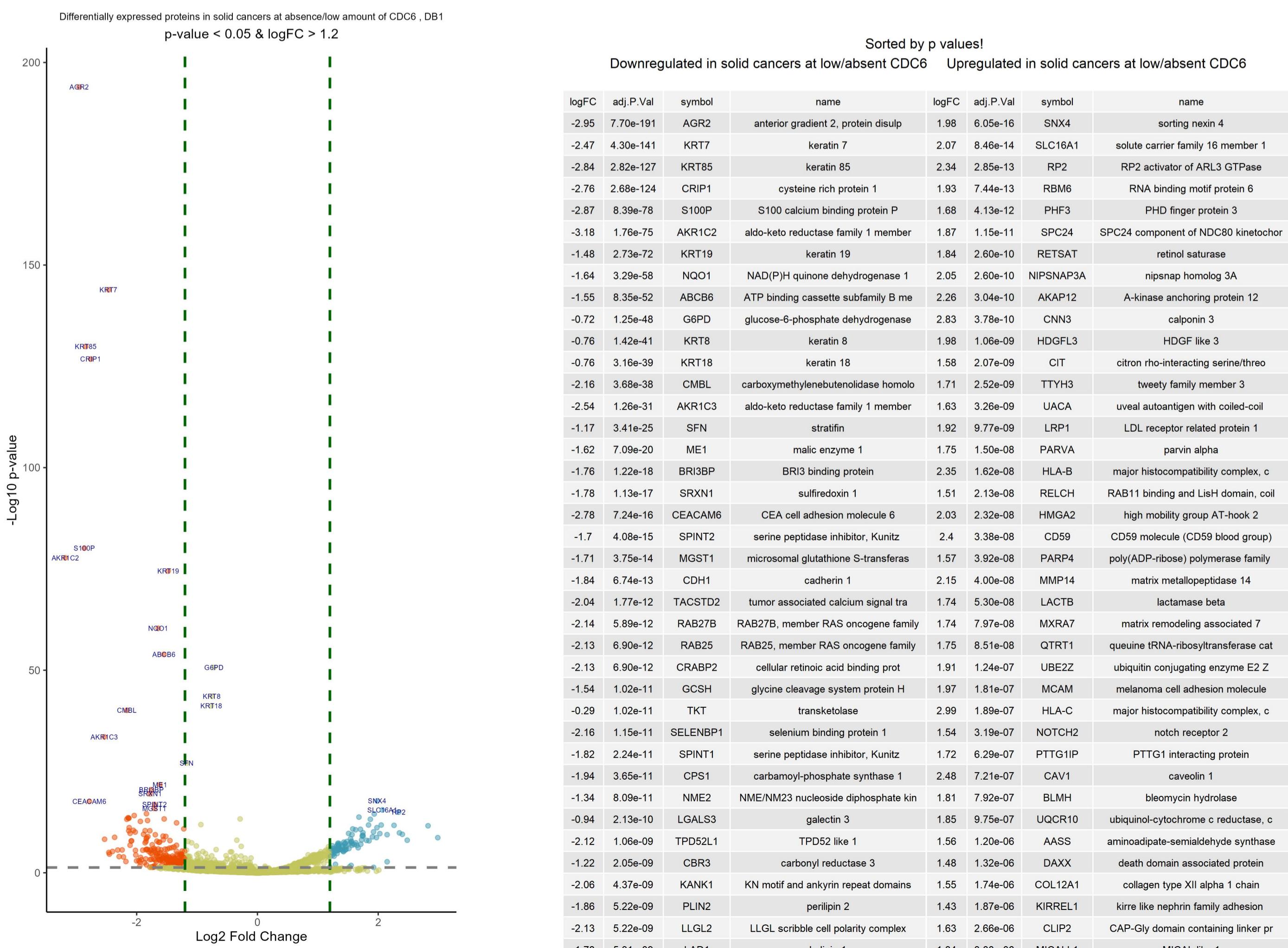


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-3.29	3.99e-76	AKR1C2	aldo-keto reductase family 1 member	3.03	2.80e-07	HLA-C	major histocompatibility complex, c
-3.17	4.82e-258	AGR2	anterior gradient 2, protein disulf	2.48	4.33e-08	HLA-B	major histocompatibility complex, c
-3.05	6.37e-154	KRT5	keratin 5	2.4	8.84e-09	CNN3	calponin 3
-2.99	7.84e-84	S100P	S100 calcium binding protein P	2.37	3.59e-13	RP2	RP2 activator of ARL3 GTPase
-2.89	1.90e-16	CEACAM6	CEA cell adhesion molecule 6	2.19	1.43e-07	CD59	CD59 molecule (CD59 blood group)
-2.71	1.09e-198	KRT7	keratin 7	2.1	8.88e-01	MSN	moesin
-2.69	1.05e-34	AKR1C3	aldo-keto reductase family 1 member	2.09	2.91e-06	CAV1	caveolin 1
-2.6	3.06e-07	PRDM15	PR/SET domain 15	2.07	1.41e-07	BLMH	bleomycin hydrolase
-2.54	3.03e-107	CRIP1	cysteine rich protein 1	2.06	1.38e-08	AKAP12	A-kinase anchoring protein 12
-2.49	3.27e-04	MUC5B	mucin 5B, oligomeric mucus/gel-form	2.04	2.09e-01	NFU1	NFU1 iron-sulfur cluster scaffold
-2.49	2.02e-04	BCAS1	brain enriched myelin associated pr	2.02	8.71e-14	SLC16A1	solute carrier family 16 member 1
-2.42	8.32e-08	SLC39A11	solute carrier family 39 member 11	2.02	7.18e-14	RBM6	RNA binding motif protein 6
-2.42	1.82e-04	FBP1	fructose-bisphosphatase 1	2.01	1.20e-12	SPC24	SPC24 component of NDC80 kinetochor
-2.35	1.20e-03	ZBTB7B	zinc finger and BTB domain containi	1.96	2.09e-09	NIPSNAP3A	nipsnap homolog 3A
-2.34	1.88e-14	RAB25	RAB25, member RAS oncogene family	1.95	7.53e-01	IGF2BP3	insulin like growth factor 2 mRNA b
-2.33	7.71e-05	ABCC3	ATP binding cassette subfamily C me	1.94	3.38e-01	KPNAA3	karyopherin subunit alpha 3
-2.33	6.04e-43	CMBL	carboxymethylenebutenolidase homolo	1.94	1.66e-07	UBE2Z	ubiquitin conjugating enzyme E2 Z
-2.32	6.33e-14	RAB27B	RAB27B, member RAS oncogene family	1.89	8.75e-01	FABP5	fatty acid binding protein 5
-2.32	1.85e-03	GDPD3	glycerophosphodiester phosphodieste	1.88	6.61e-06	RAC2	Rac family small GTPase 2
-2.31	3.25e-13	SELENBP1	selenium binding protein 1	1.88	2.35e-08	QTRT1	queuine tRNA-ribosyltransferase cat
-2.3	5.19e-14	CRABP2	cellular retinoic acid binding prot	1.86	3.80e-01	PPP1R18	protein phosphatase 1 regulatory su
-2.3	1.53e-02	AKR1D1	aldo-keto reductase family 1 member	1.81	5.04e-08	HDGFL3	HDGF like 3
-2.3	8.70e-05	PLA2G4A	phospholipase A2 group IVA	1.81	2.69e-06	MMP14	matrix metallopeptidase 14
-2.29	3.71e-11	TPD52L1	TPD52 like 1	1.78	6.72e-01	B2M	beta-2-microglobulin
-2.29	2.94e-10	LLGL2	LLGL scribble cell polarity complex	1.77	5.44e-06	NACA2	nascent polypeptide associated comp
-2.29	4.97e-16	TACSTD2	tumor associated calcium signal tra	1.76	3.59e-01	ACSL4	acyl-CoA synthetase long chain fami
-2.26	9.29e-08	TRPM4	transient receptor potential cation	1.76	3.64e-06	MCAM	melanoma cell adhesion molecule
-2.21	2.23e-07	SMPDL3B	sphingomyelin phosphodiesterase aci	1.75	2.52e-11	SNX4	sorting nexin 4
-2.15	1.33e-09	CLU	clusterin	1.72	2.34e-06	HMGA2	high mobility group AT-hook 2

GAGE analysis on upregulated and downregulated proteins at low/absent CDC6 protein, DB1



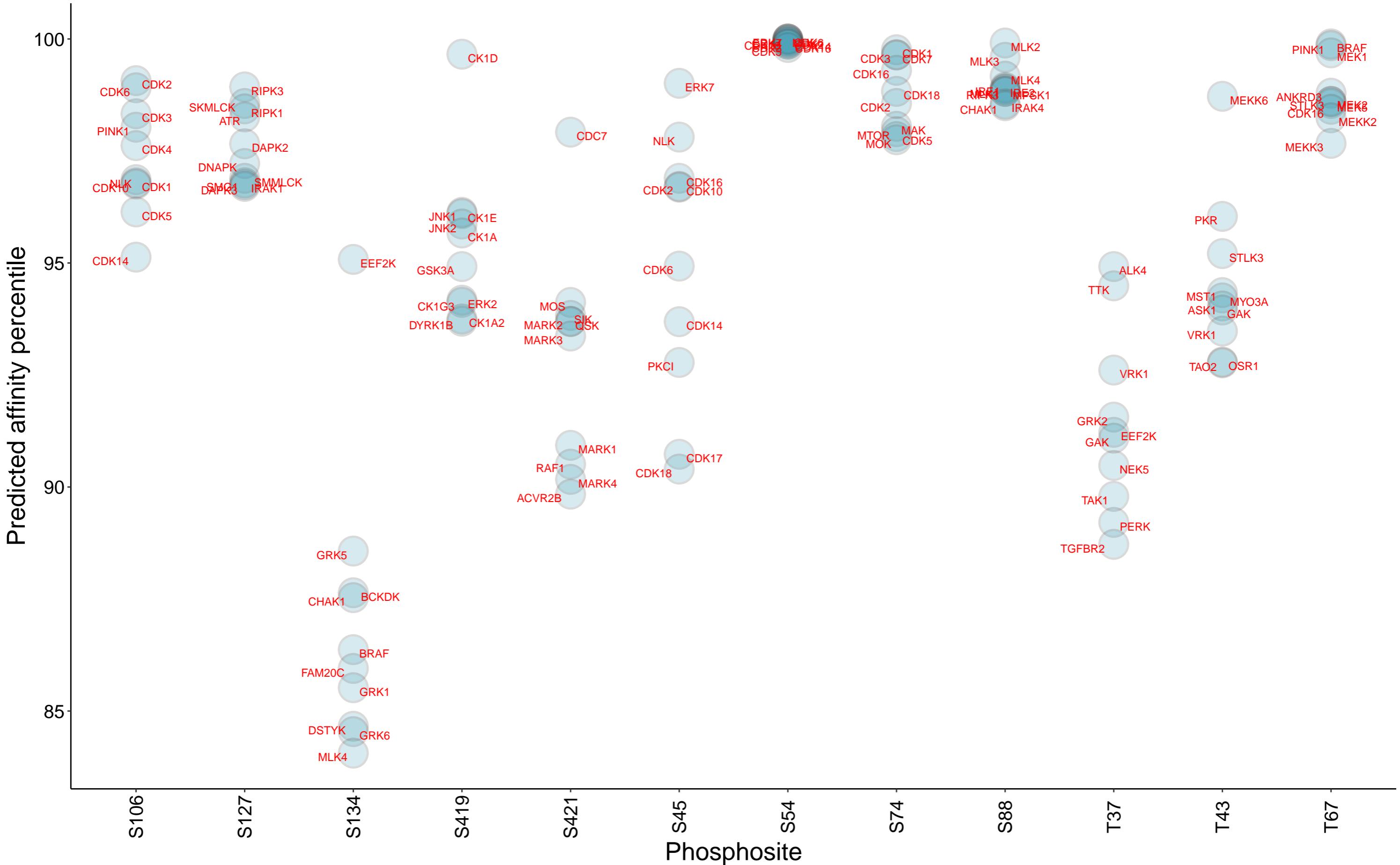




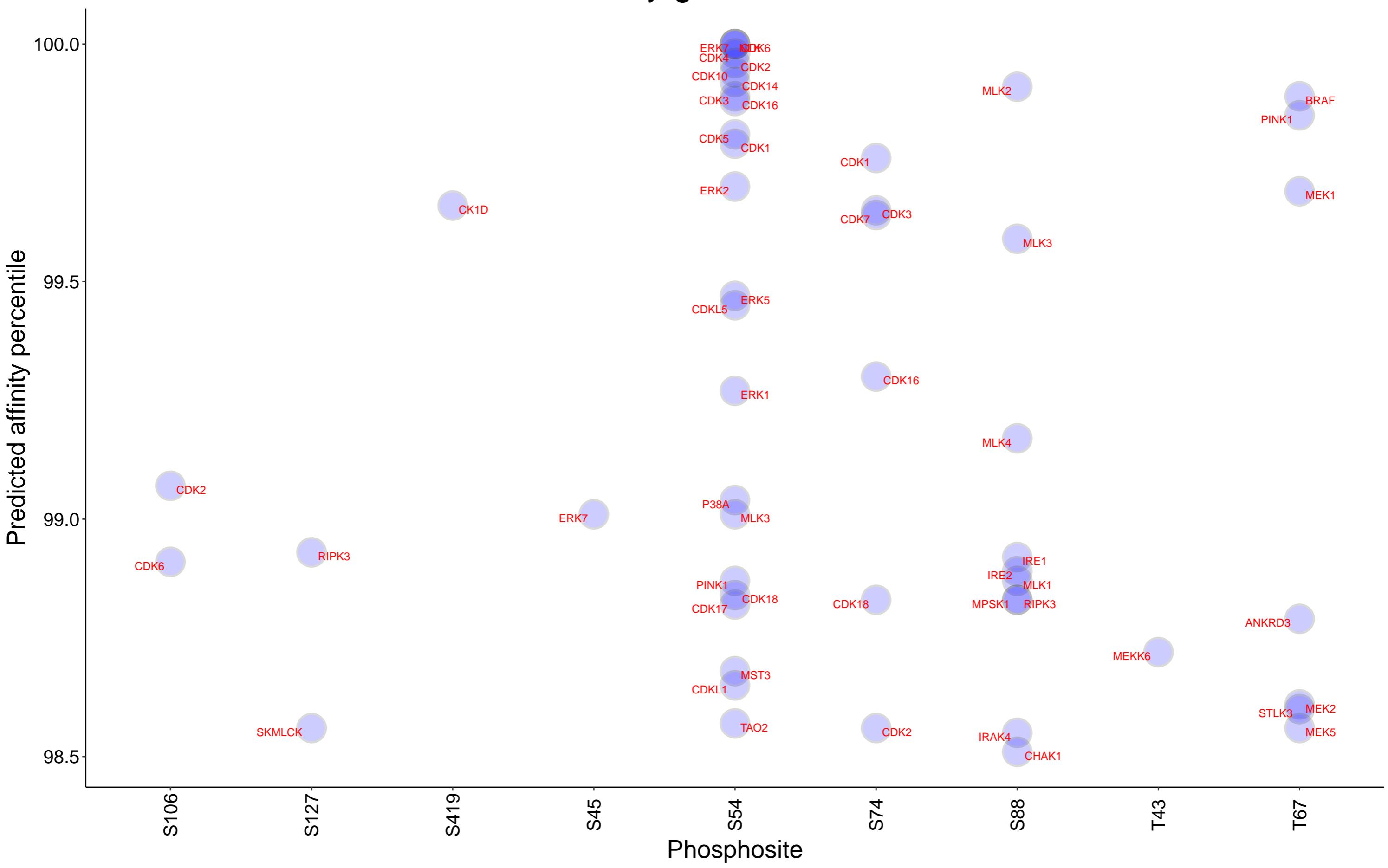
Insufficient number of paired observations in DB1 for CDC6

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Top 10 kinases for each phosphosite in CDC6



Kinases with affinity greater than 98.5% to CDC6



No sufficient paired observations in DB1 for CDC6