

CDC45

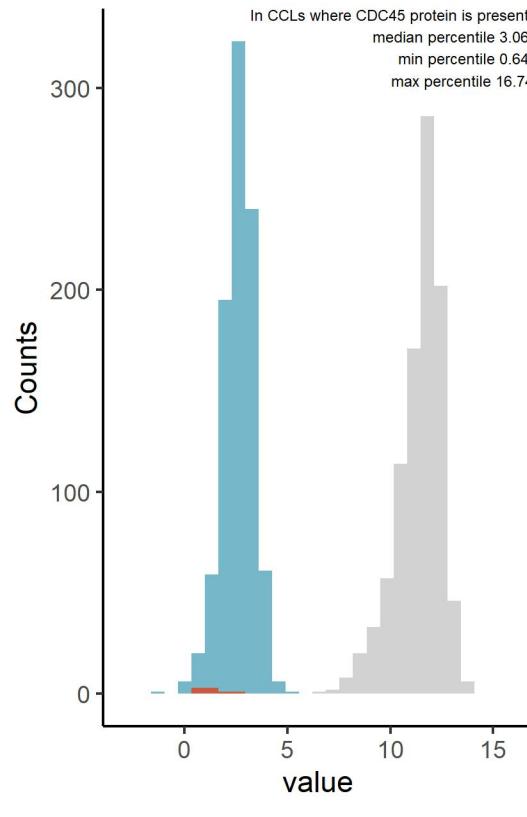
Protein name: CDC45 ; UNIPROT: O75419 ; Gene name: cell division cycle 45

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

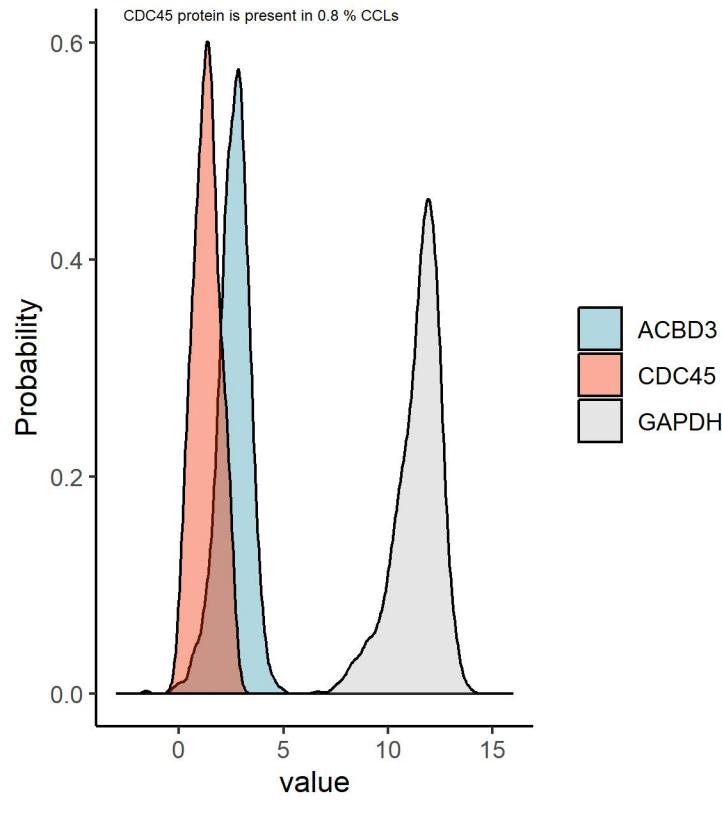
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

Histogram of CDC45 protein compared to proteins with low and high abundance



Density plot of CDC45 protein compared to proteins with low and high abundance



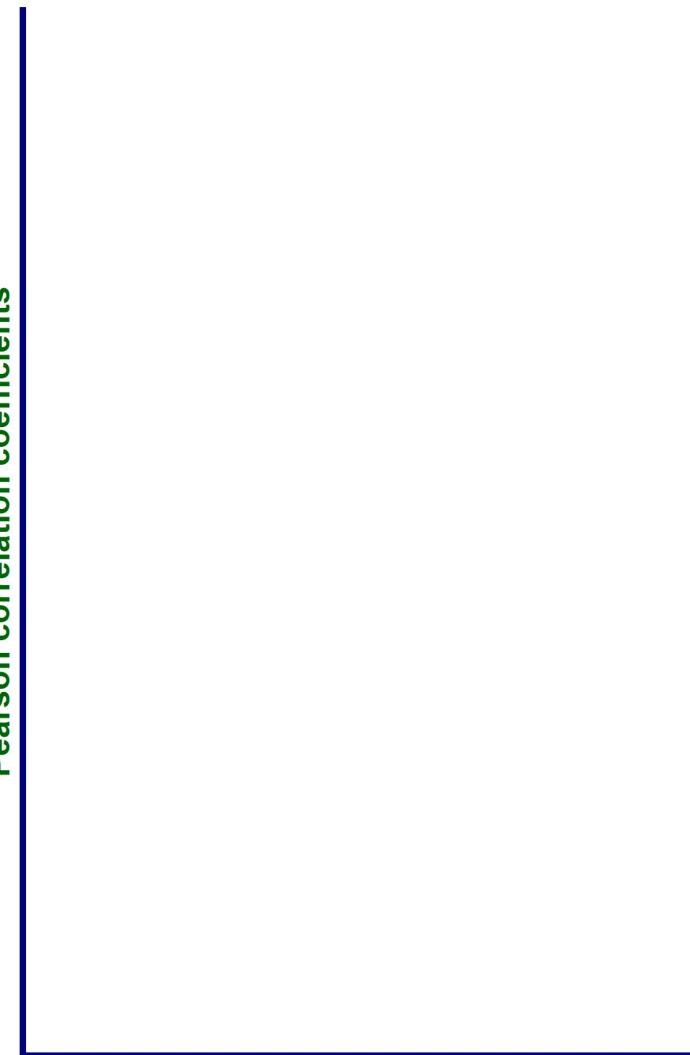
Top negative correlations of CDC45 protein, DB1

Pearson correlation coefficients



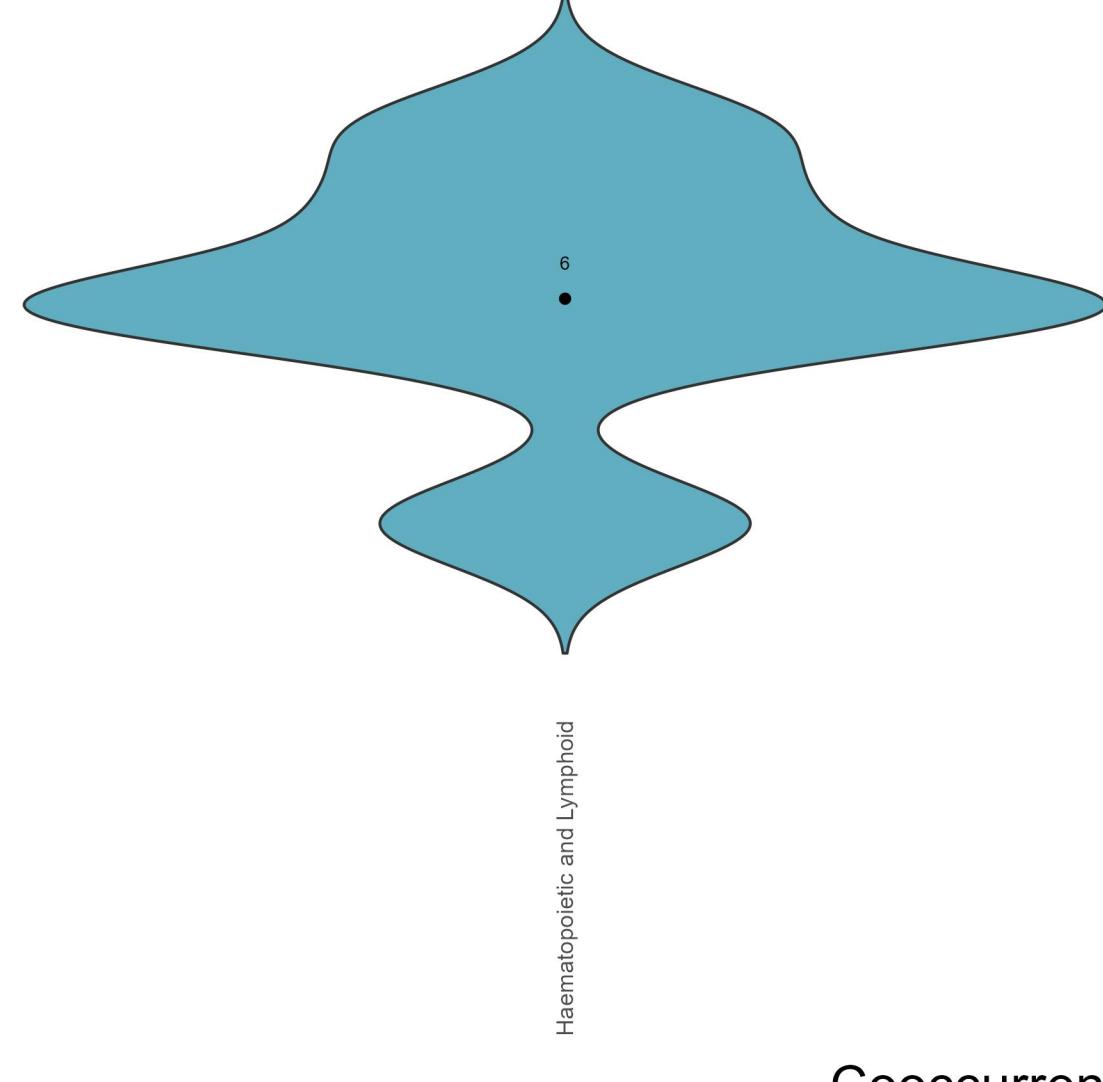
Top positive correlations of CDC45 protein, DB1

Pearson correlation coefficients



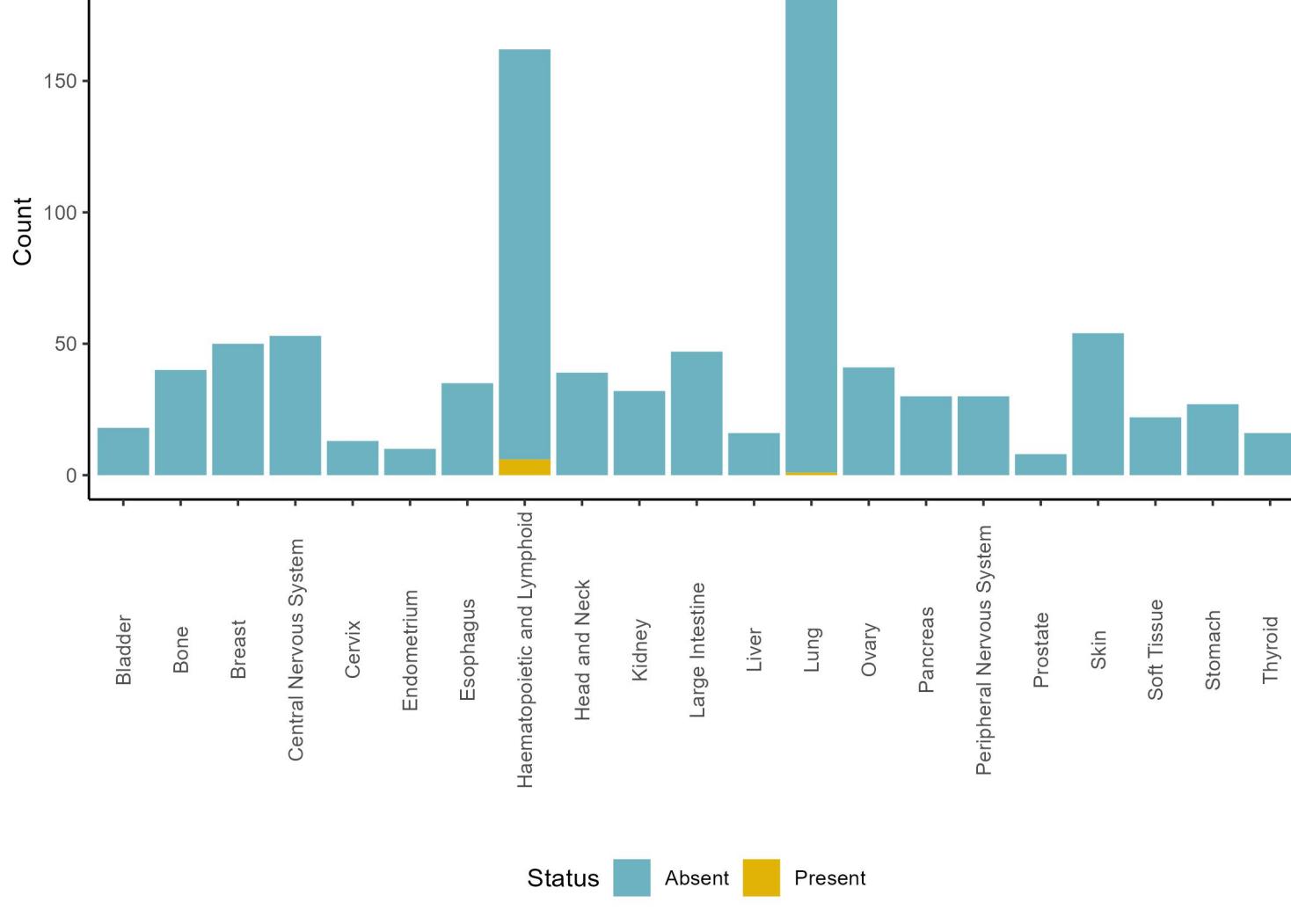
Amount of CDC45 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 5.004e-01



Present and absent CDC45 protein counts by tissue, DB1

Chi square p value is 2.718e-01

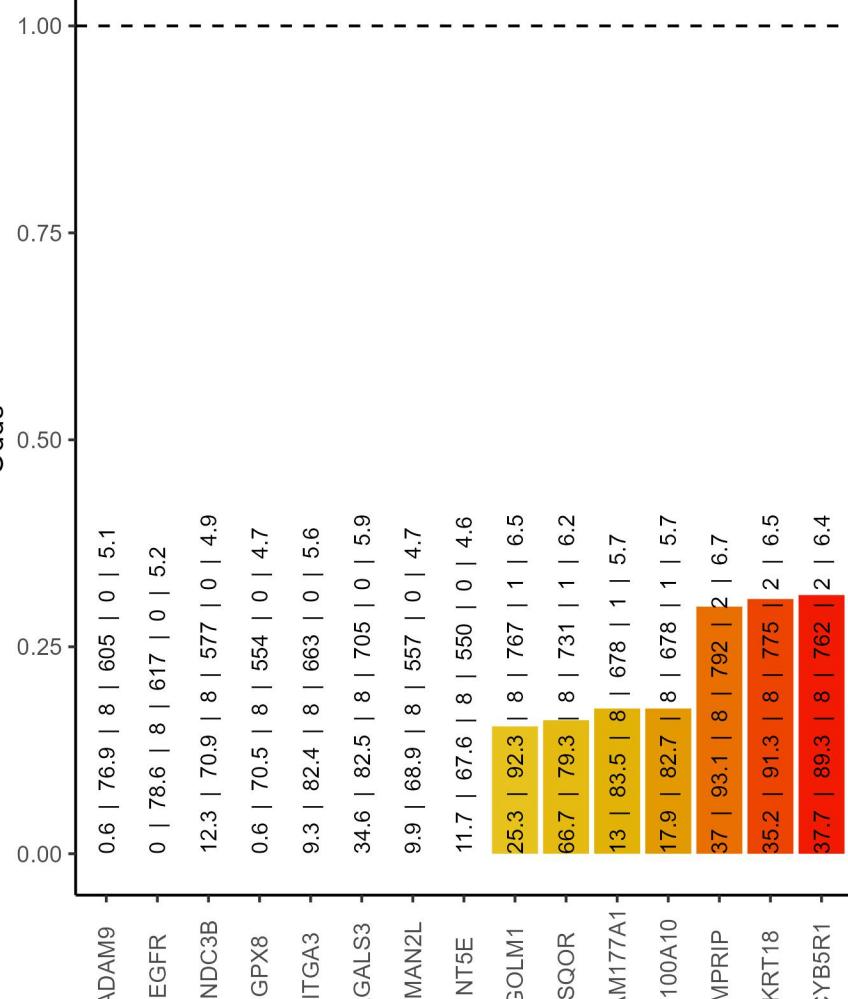


Cooccurrence with CDC45 protein, DB1

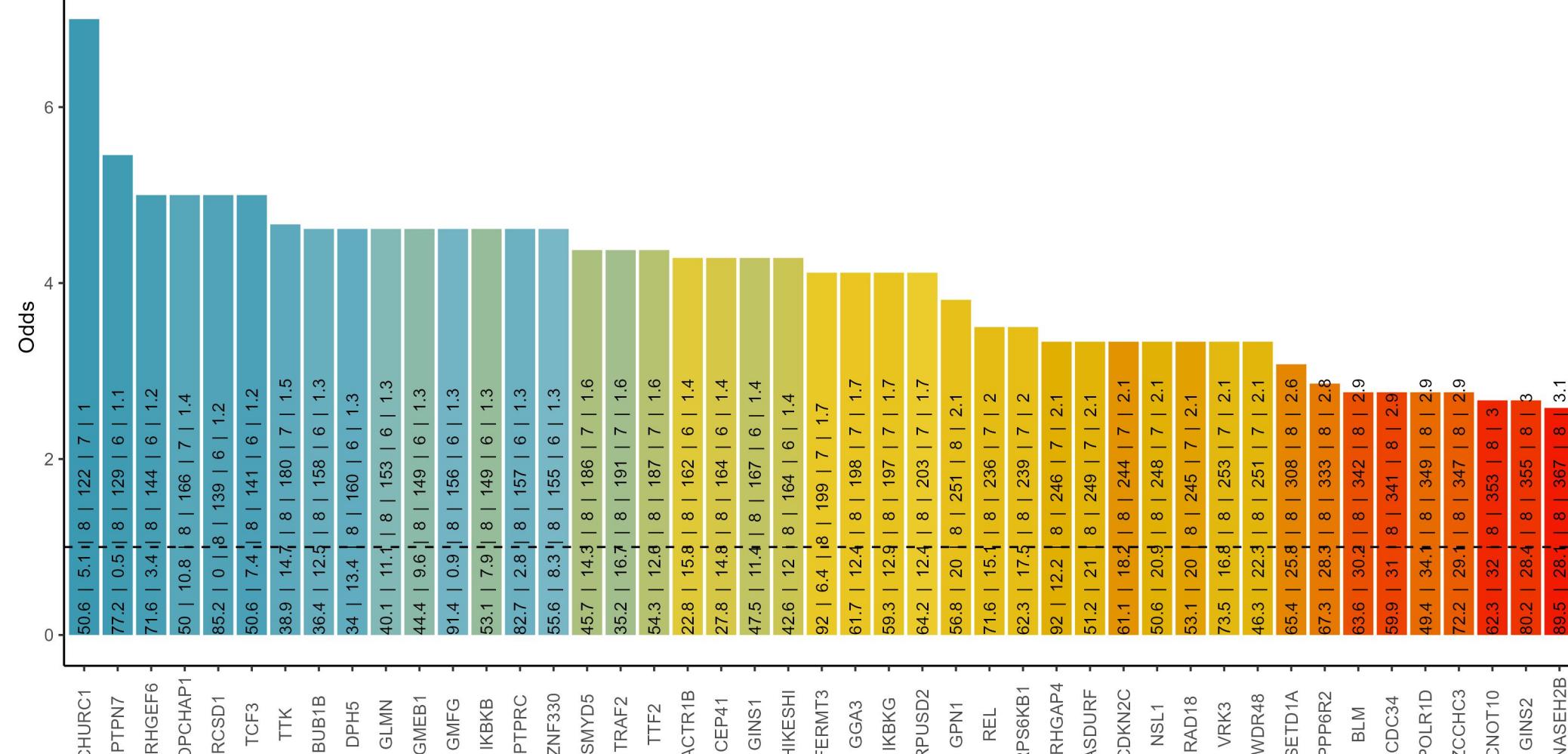
% of CDC45 in blood cancers: 3.7 ; % of CDC45 in solid cancers: 0.3

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CDC45 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

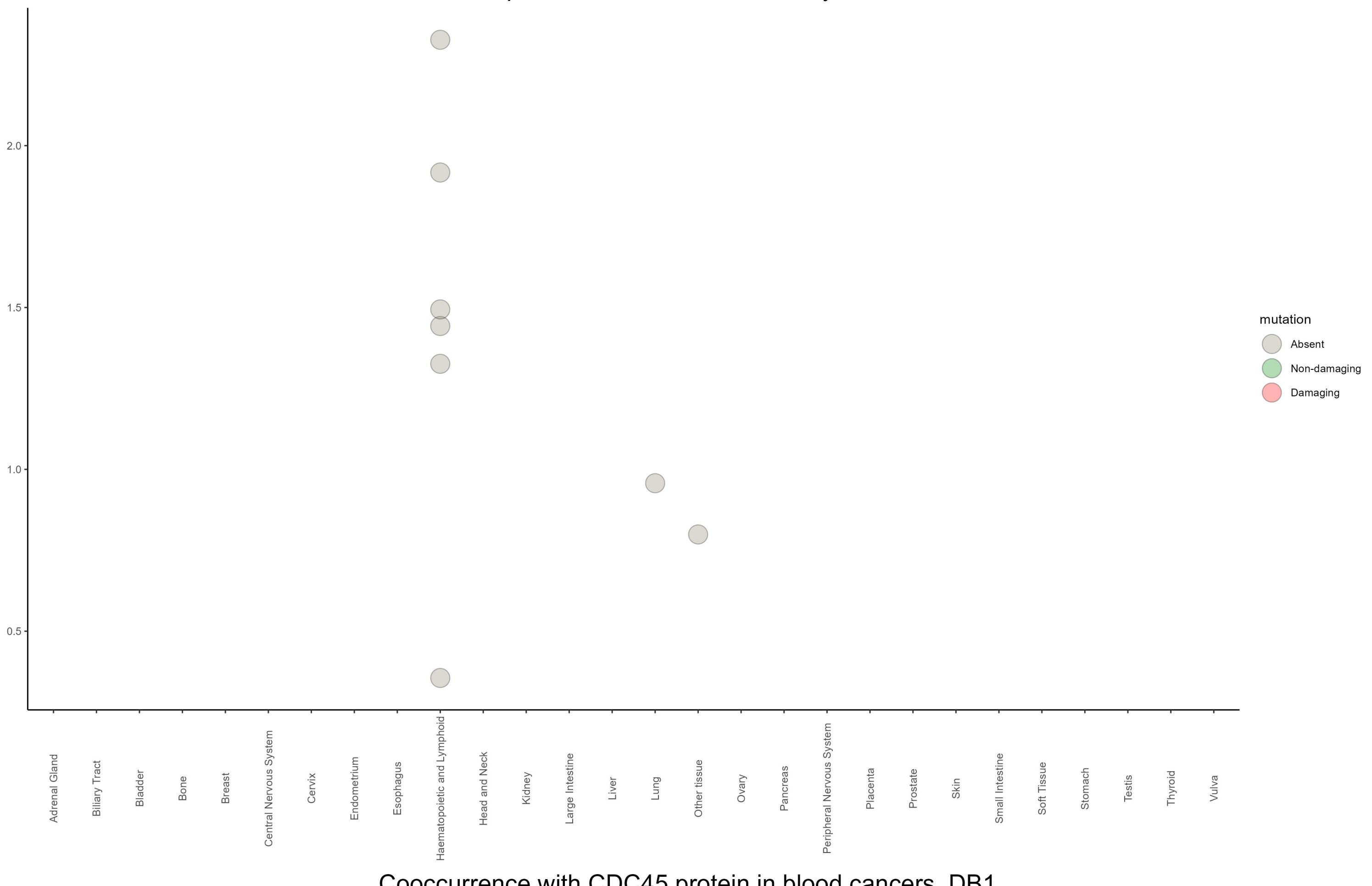
Negative cooccurrence



Positive cooccurrence



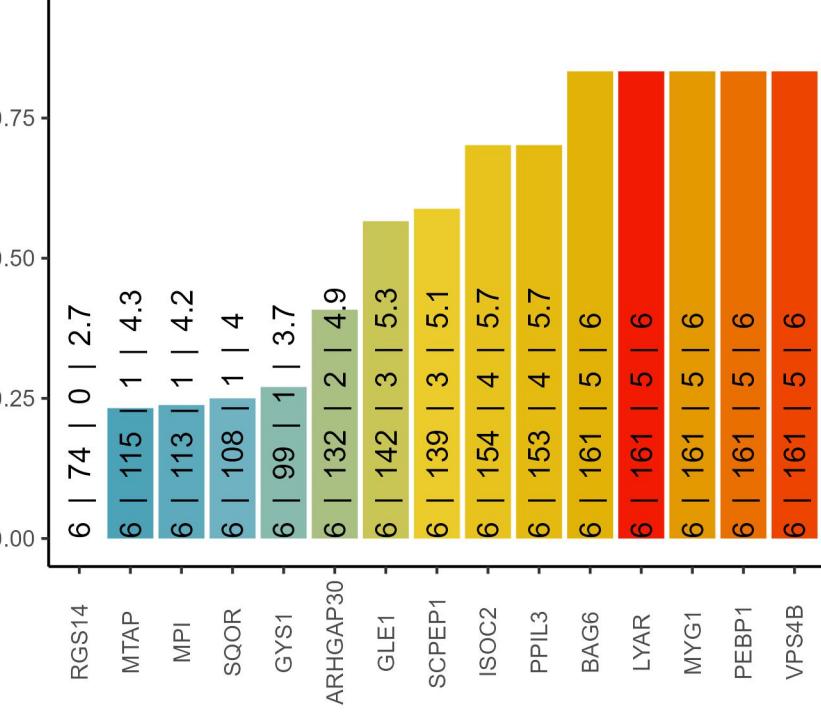
Amount of CDC45 protein and mutation status by tissue, DB1



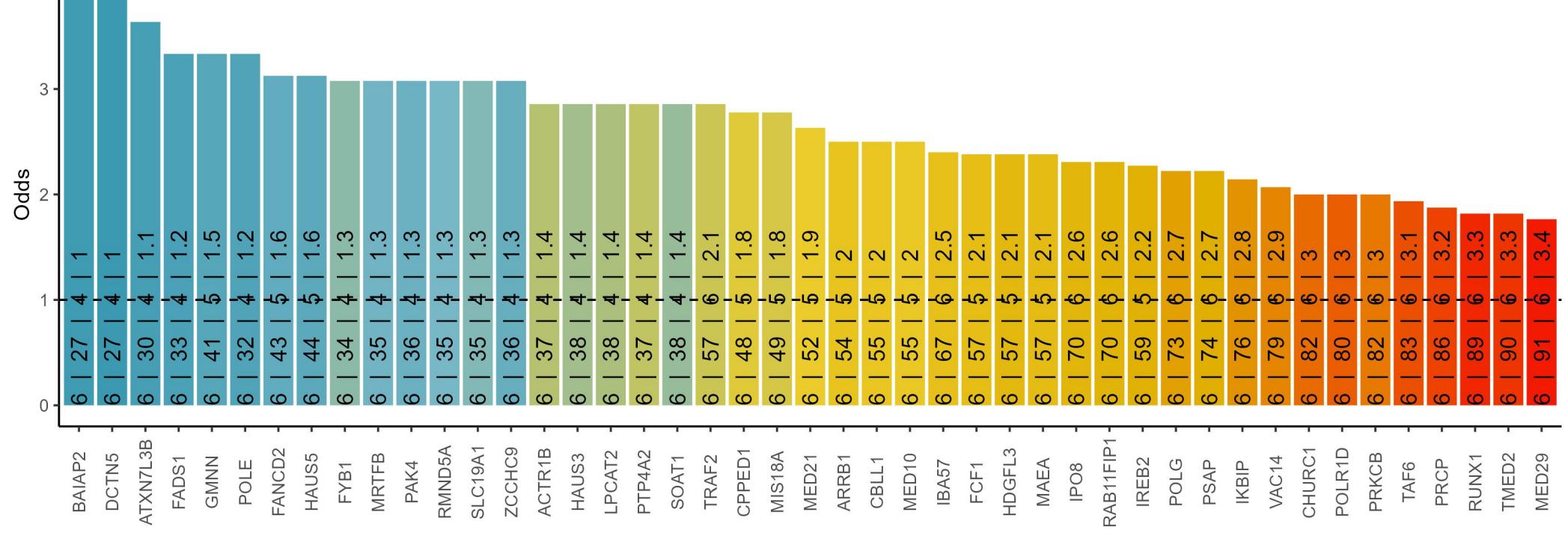
Cooccurrence with CDC45 protein in blood cancers, DB1

The text in the bars: incidence of CDC45 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



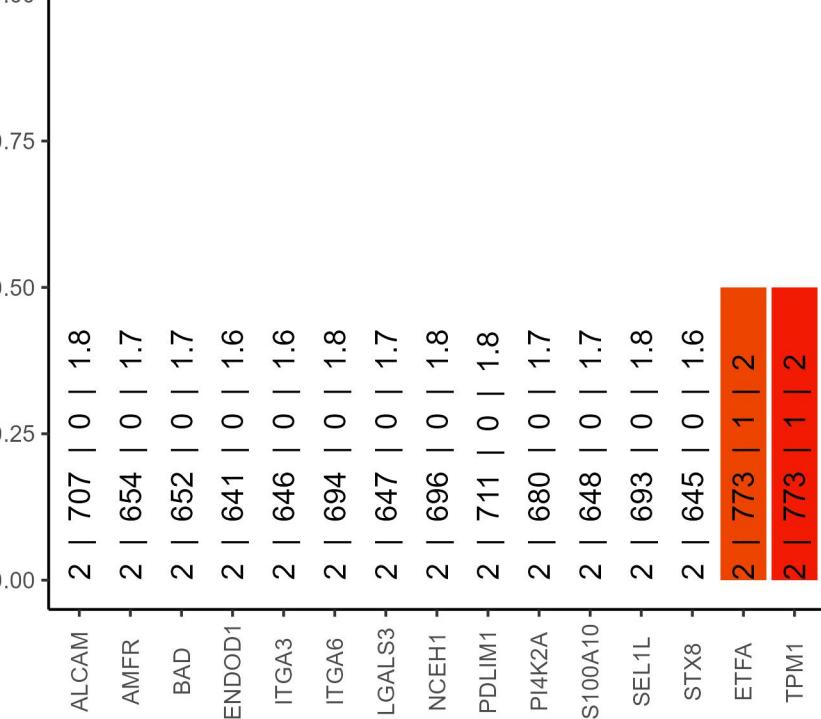
Positive cooccurrence



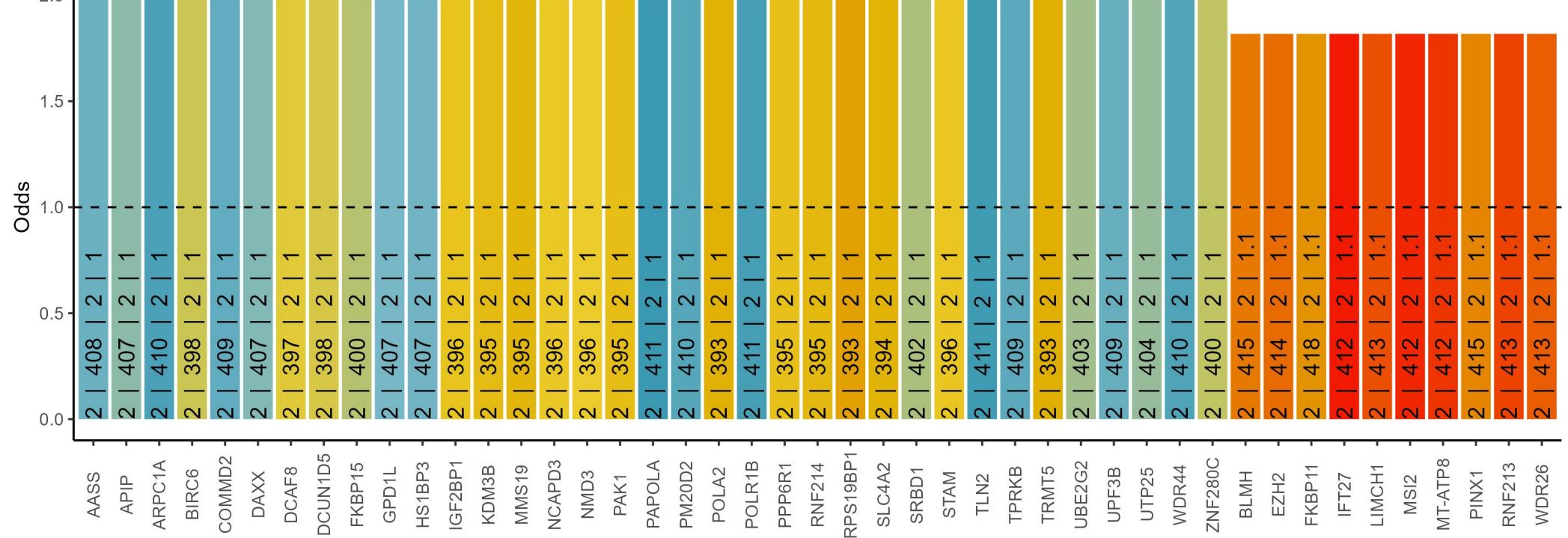
Cooccurrence with CDC45 protein in solid cancers, DB1

The text in the bars: incidence of CDC45 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

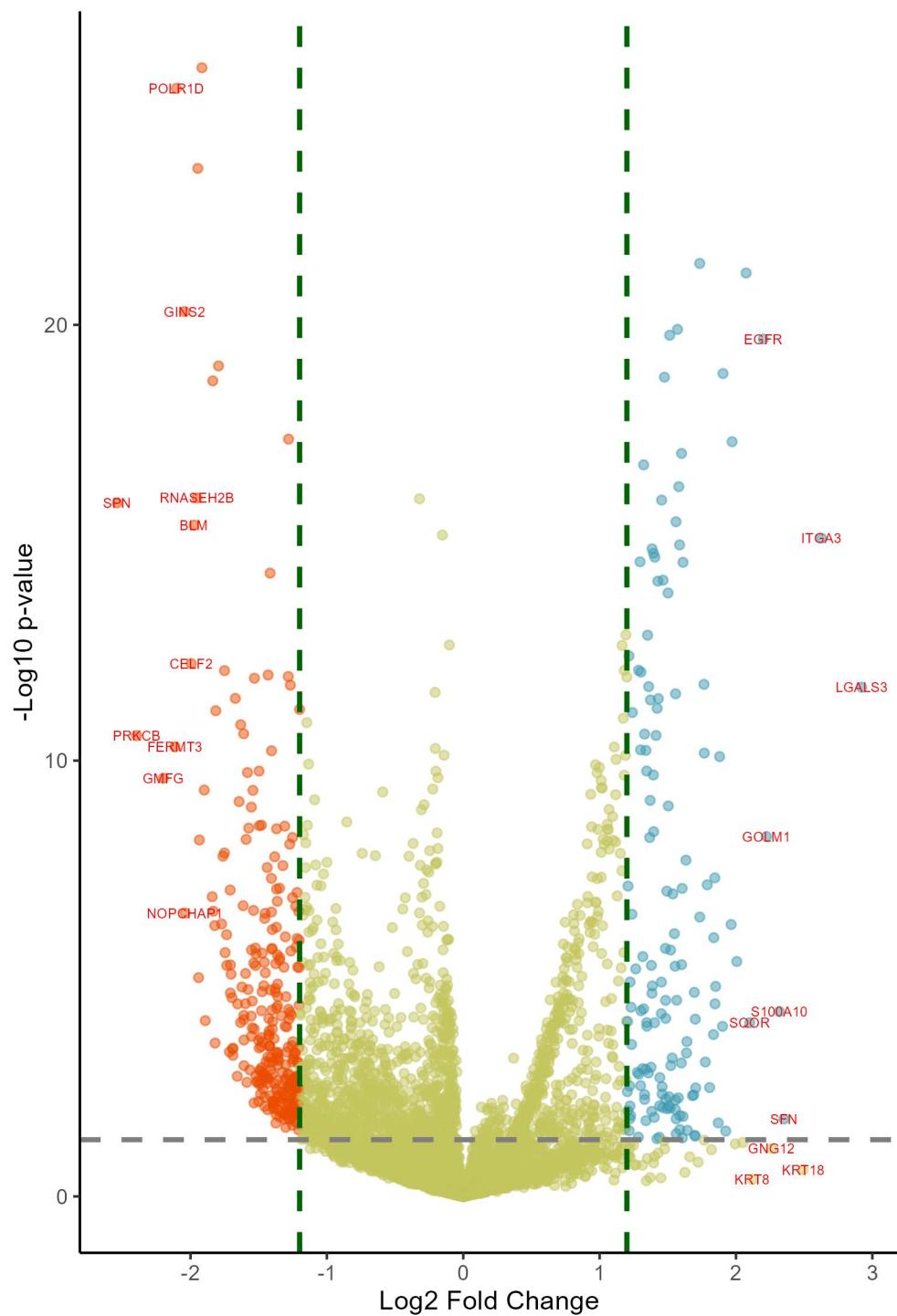
Negative cooccurrence



Positive cooccurrence



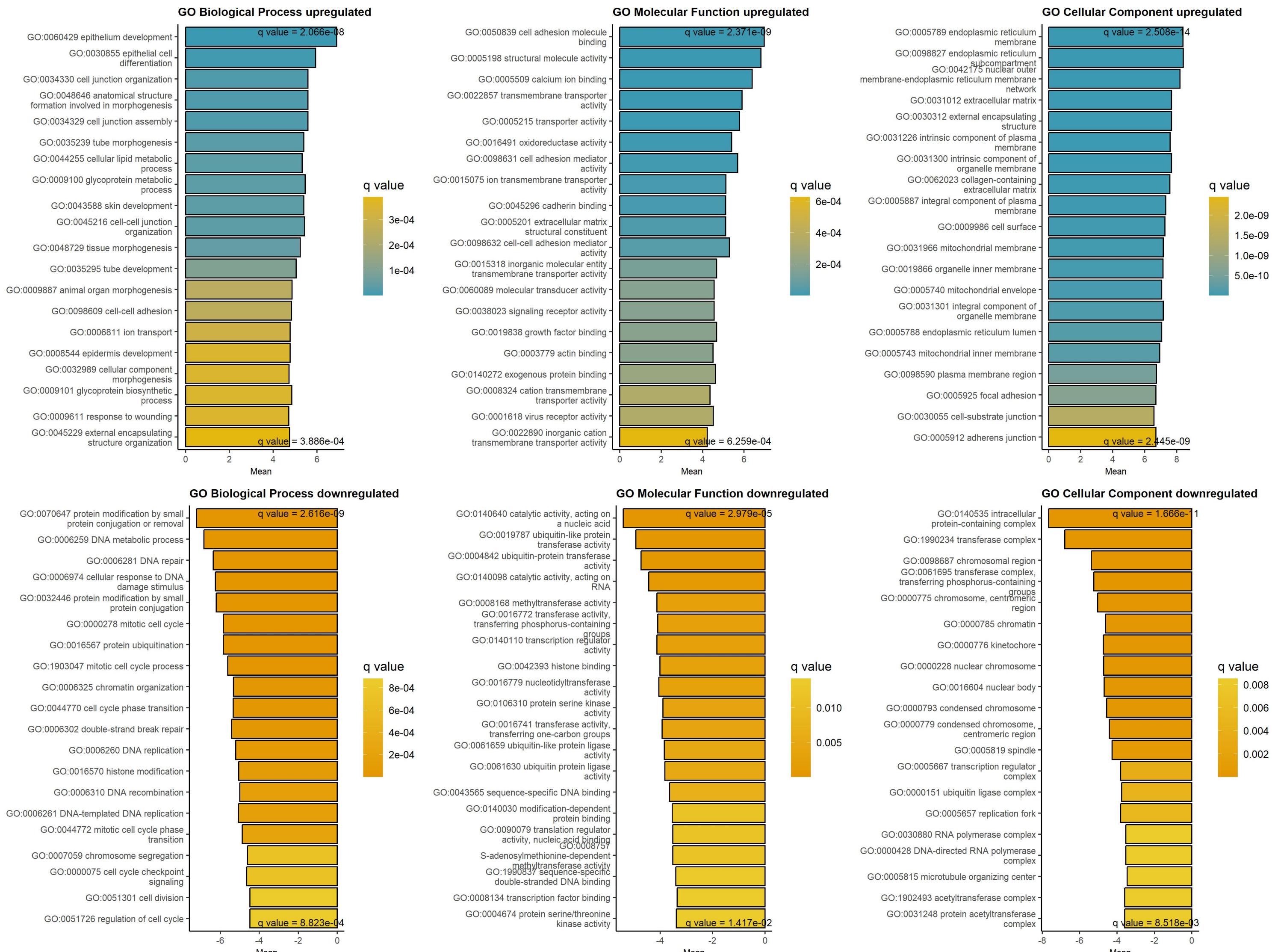
p-value < 0.05 & logFC > 1.2



Downregulated at low/absent CDC45 Upregulated at low/absent CDC45

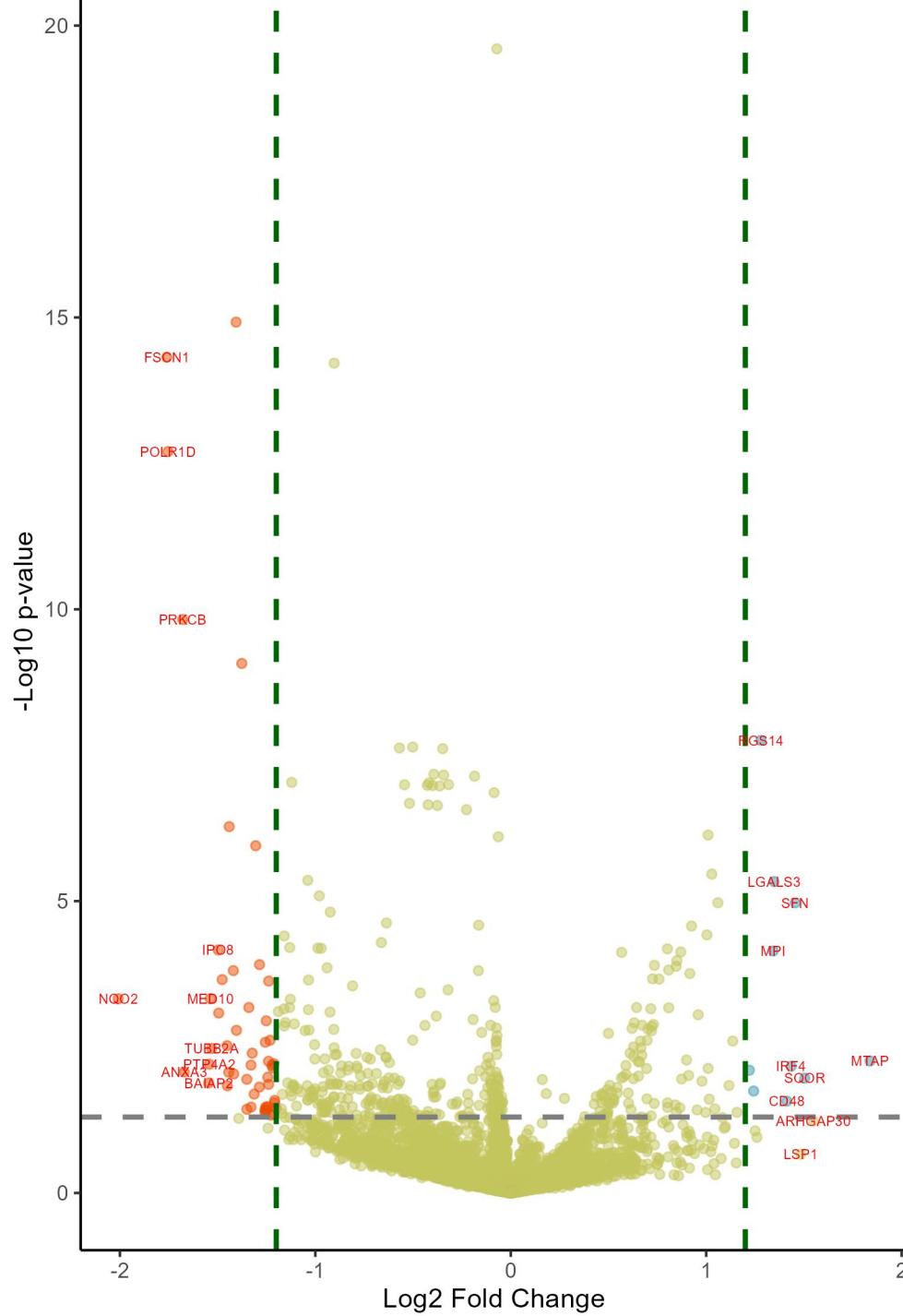
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.54	3.51e-14	SPN	sialophorin	2.92	2.51e-10	LGALS3	galectin 3
-2.4	2.49e-09	PRKCB	protein kinase C beta	2.63	1.93e-13	ITGA3	integrin subunit alpha 3
-2.2	1.79e-08	GMFG	glia maturation factor gamma	2.49	4.76e-01	KRT18	keratin 18
-2.11	4.42e-09	FERMT3	FERM domain containing kindlin 3	2.35	7.76e-02	SFN	stratifin
-2.1	8.29e-23	POLR1D	RNA polymerase I and III subunit D	2.32	8.71e-04	S100A10	S100 calcium binding protein A10
-2.04	4.70e-18	GINS2	GINS complex subunit 2	2.26	2.34e-01	GNG12	G protein subunit gamma 12
-2.04	9.93e-06	NOPCHAP1	NOP protein chaperone 1	2.22	2.87e-07	GOLM1	golgi membrane protein 1
-1.99	9.17e-11	CELF2	CUGBP Elav-like family member 2	2.2	1.41e-17	EGFR	epidermal growth factor receptor
-1.97	1.05e-13	BLM	BLM RecQ like helicase	2.12	6.41e-01	KRT8	keratin 8
-1.95	3.11e-14	RNASEH2B	ribonuclease H2 subunit B	2.1	1.36e-03	SQOR	sulfide quinone oxidoreductase
-1.95	4.28e-21	RNF181	ring finger protein 181	2.07	7.17e-19	ADAM9	ADAM metallopeptidase domain 9
-1.94	1.92e-04	PTPRC	protein tyrosine phosphatase recept	2.05	1.91e-01	NCEH1	neutral cholesterol ester hydrolase
-1.93	3.31e-07	GPN1	GPN-loop GTPase 1	2.01	9.18e-05	JUP	junction plakoglobin
-1.92	4.19e-23	ARHGDI	Rho GDP dissociation inhibitor beta	1.99	2.00e-01	KRT19	keratin 19
-1.9	3.19e-08	HMGN5	high mobility group nucleosome bind	1.97	2.00e-15	NT5E	5'-nucleotidase ecto
-1.89	1.27e-03	PTPN7	protein tyrosine phosphatase non-re	1.96	1.68e-05	DSG2	desmoglein 2
-1.84	4.72e-06	ASF1A	anti-silencing function 1A histone	1.92	1.23e-01	ALCAM	activated leukocyte cell adhesion m
-1.84	9.17e-17	PCLAF	PCNA clamp associated factor	1.9	7.26e-17	GPX8	glutathione peroxidase 8 (putative)
-1.83	9.22e-06	ARHGAP4	Rho GTPase activating protein 4	1.9	1.60e-03	MPPRIP	myosin phosphatase Rho interacting
-1.82	1.75e-05	CDKN2C	cyclin dependent kinase inhibitor 2	1.88	6.62e-09	SEC61G	SEC61 translocon subunit gamma
-1.82	3.38e-03	RCSD1	RCSD domain containing 1	1.87	8.90e-02	ITGAV	integrin subunit alpha V
-1.81	7.55e-10	PPIPK2	diphosphoinositol pentakisphosphate	1.85	2.83e-04	ITPR3	inositol 1,4,5-trisphosphate recept
-1.79	5.29e-17	SEPTIN6	septin 6	1.85	6.19e-04	S100A16	S100 calcium binding protein A16
-1.77	1.64e-05	CEP43	centrosomal protein 43	1.84	1.93e-06	PLOD2	procollagen-lysine,2-oxoglutarate 5
-1.76	6.90e-07	H3-7	H3.7 histone (putative)	1.84	3.08e-05	RRAS	RAS related
-1.75	1.24e-10	TYMS	thymidylate synthetase	1.84	2.31e-03	MYO1B	myosin IB
-1.75	6.00e-07	ZCCHC3	zinc finger CCHC-type containing 3	1.82	2.44e-01	FKBP9	FKBP prolyl isomerase 9
-1.75	6.14e-05	USP48	ubiquitin specific peptidase 48	1.81	2.22e-02	LMO7	LIM domain 7
-1.74	2.64e-05	SSNA1	SS nuclear autoantigen 1	1.79	2.72e-06	TPBG	trophoblast glycoprotein

GAGE analysis on upregulated and downregulated proteins at low/absent CDC45 protein, DB1

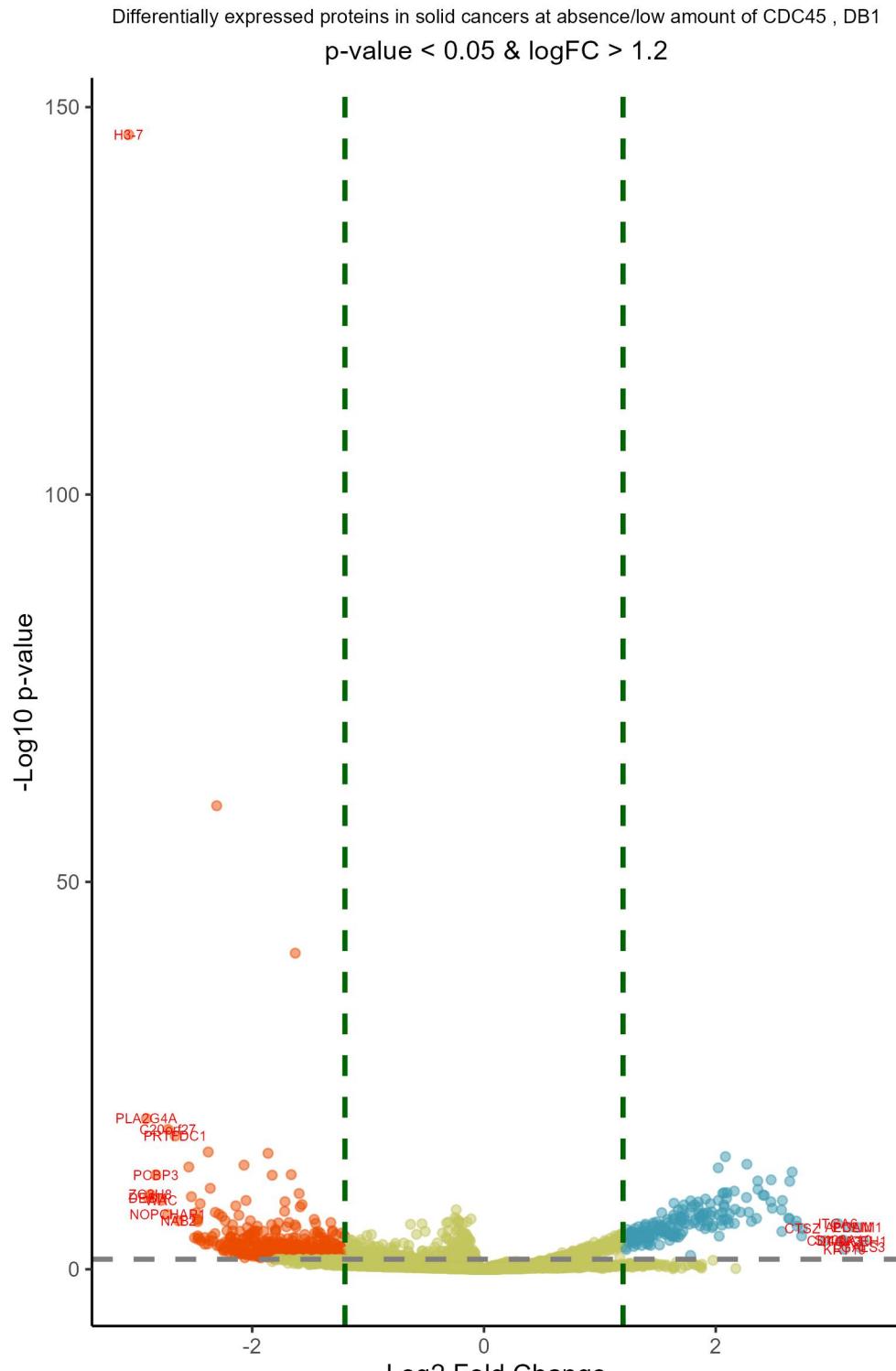


p-value < 0.05 & logFC > 1.2

Downregulated in blood cancers at low/absent CDC45 Upregulated in blood cancers at low/absent CDC45

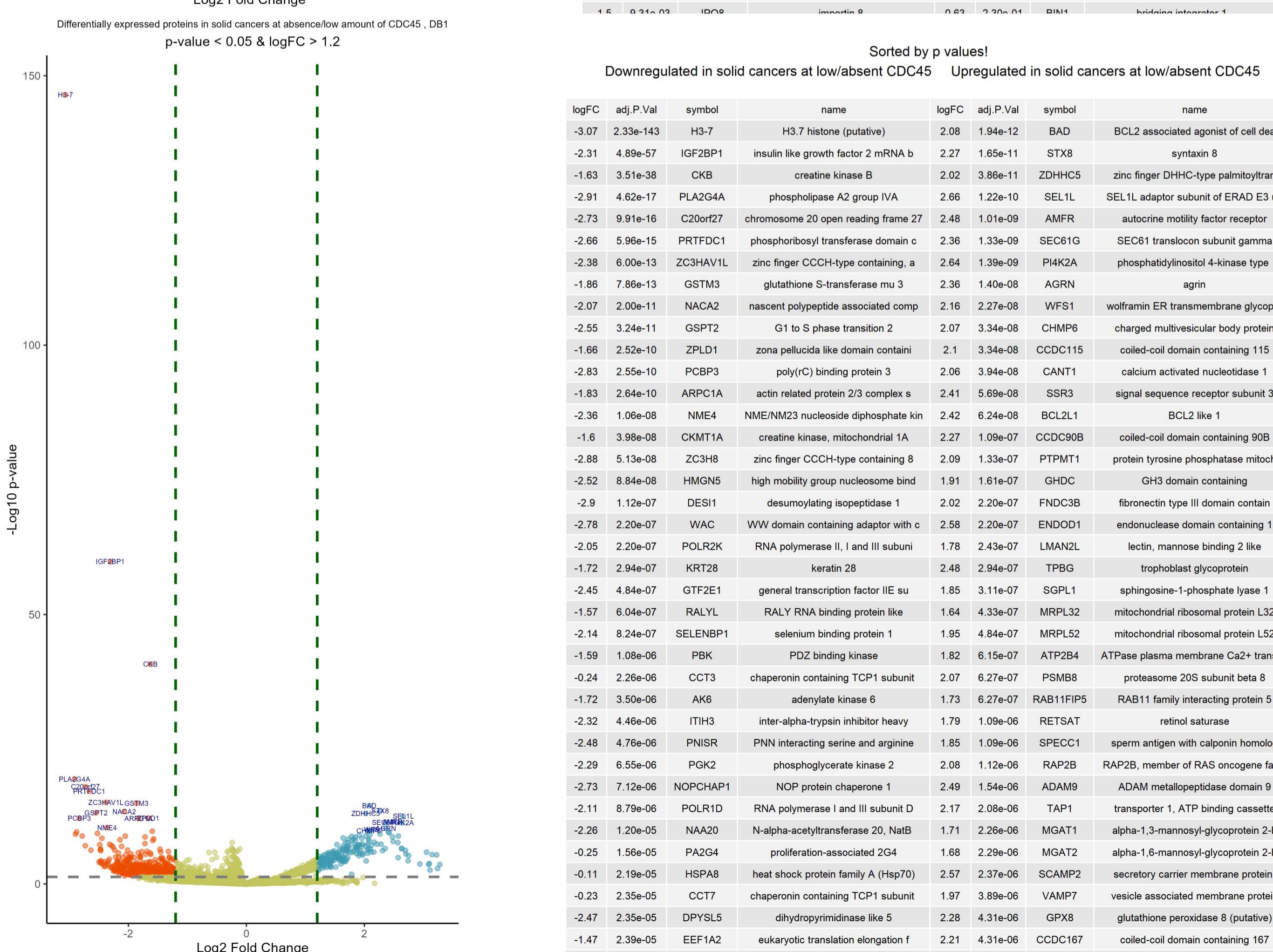
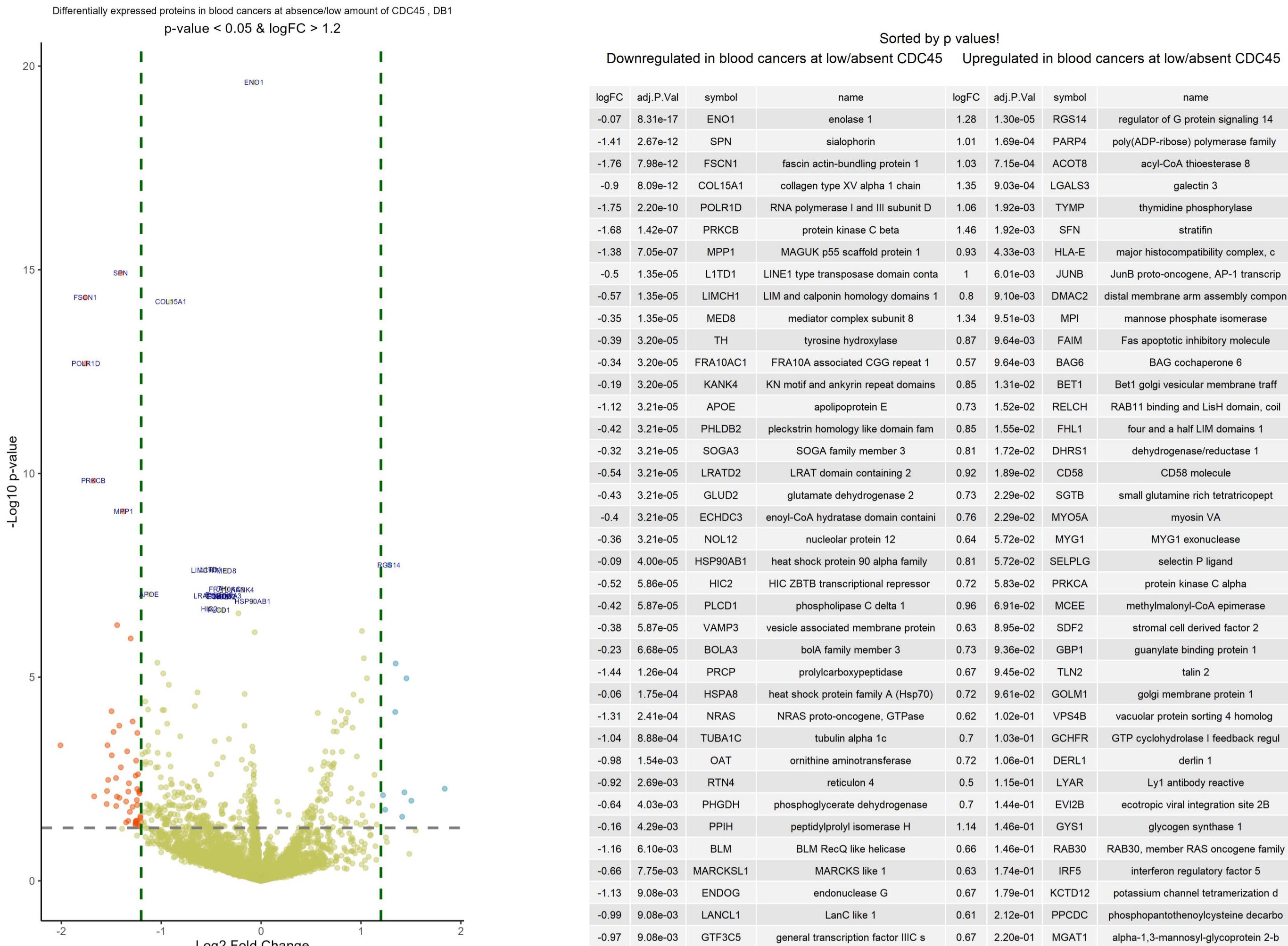


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.01	4.40e-02	NQO2	N-ribosyldihydronicotinamide:quinon	1.84	2.59e-01	MTAP	methylthioadenosine phosphorylase
-1.76	7.98e-12	FSCN1	fascin actin-bundling protein 1	1.55	6.21e-01	ARHGAP30	Rho GTPase activating protein 30
-1.75	2.20e-10	POLR1D	RNA polymerase I and III subunit D	1.5	3.88e-01	SQOR	sulfide quinone oxidoreductase
-1.68	1.42e-07	PRKCB	protein kinase C beta	1.48	7.72e-01	LSP1	lymphocyte specific protein 1
-1.67	3.37e-01	ANXA3	annexin A3	1.46	1.92e-03	SFN	stratifin
-1.55	4.35e-01	BAIAP2	BAR/IMD domain containing adaptor p	1.43	2.87e-01	IRF4	interferon regulatory factor 4
-1.54	2.80e-01	PTP4A2	protein tyrosine phosphatase 4A2	1.41	5.94e-01	CD48	CD48 molecule
-1.54	4.40e-02	MED10	mediator complex subunit 10	1.35	9.03e-04	LGALS3	galectin 3
-1.53	1.80e-01	TUBB2A	tubulin beta 2A class IIa	1.34	9.51e-03	MPI	mannose phosphate isomerase
-1.5	9.31e-03	IPO8	importin 8	1.28	1.30e-05	RGS14	regulator of G protein signaling 14
-1.49	6.55e-02	ARRB1	arrestin beta 1	1.26	6.21e-01	FKBP11	FKBP prolyl isomerase 11
-1.48	2.29e-02	IBA57	iron-sulfur cluster assembly factor	1.25	6.21e-01	SCPEP1	serine carboxypeptidase 1
-1.45	1.69e-01	MIS18A	MIS18 kinetochore protein A	1.24	4.92e-01	IKZF3	IKAROS family zinc finger 3
-1.45	4.36e-01	FADS1	fatty acid desaturase 1	1.22	3.21e-01	DST	dystonin
-1.44	3.38e-01	GMNN	geminin DNA replication inhibitor	1.16	6.21e-01	HLA-DPB1	major histocompatibility complex, c
-1.44	1.26e-04	PRCP	prolylcarboxypeptidase	1.15	8.63e-01	MZB1	marginal zone B and B1 cell specific
-1.42	1.72e-02	POLG	DNA polymerase gamma, catalytic sub	1.14	6.47e-01	FAM107B	family with sequence similarity 107
-1.42	3.51e-01	CD99	CD99 molecule (Xg blood group)	1.14	1.46e-01	GYS1	glycogen synthase 1
-1.41	2.67e-12	SPN	sialophorin	1.12	4.36e-01	GLE1	GLE1 RNA export mediator
-1.4	1.05e-01	TRAF2	TNF receptor associated factor 2	1.1	6.21e-01	KRT8	keratin 8
-1.39	6.21e-01	PLD2	phospholipase D2	1.09	6.21e-01	MEF2D	myocyte enhancer factor 2D
-1.38	7.05e-07	MPP1	MAGUK p55 scaffold protein 1	1.08	6.21e-01	HLA-DQB1	major histocompatibility complex, c
-1.35	3.95e-01	SAMSN1	SAM domain, SH3 domain and nuclear	1.08	8.13e-01	IRAG2	inositol 1,4,5-triphosphate receptor
-1.35	6.21e-01	ABCB6	ATP binding cassette subfamily B member	1.06	1.92e-03	TYMP	thymidine phosphorylase
-1.34	5.72e-02	PSAP	prosaposin	1.05	9.60e-01	AKR1B1	aldo-keto reductase family 1 member
-1.33	2.85e-01	LGALS3BP	galectin 3 binding protein	1.04	6.21e-01	NDUFB2	NADH:ubiquinone oxidoreductase subunit
-1.33	6.21e-01	ATXN7L3B	ataxin 7 like 3B	1.04	8.69e-01	CD74	CD74 molecule
-1.32	2.12e-01	IREB2	iron responsive element binding protein	1.04	6.21e-01	TKFC	triokinase and FMN cyclase
-1.31	5.20e-01	NDRG2	NDRG family member 2	1.03	6.82e-01	IL16	interleukin 16



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-3.07	2.33e-143	H3-7	H3.7 histone (putative)	3.28	4.53e-03	NCEH1	neutral cholesterol ester hydrolase
-2.91	4.62e-17	PLA2G4A	phospholipase A2 group IVA	3.24	1.81e-02	LGALS3	galectin 3
-2.9	1.12e-07	DESI1	desmoylating isopeptidase 1	3.22	1.63e-04	PDLIM1	PDZ and LIM domain 1
-2.88	5.13e-08	ZC3H8	zinc finger CCCH-type containing 8	3.15	1.49e-04	ALCAM	activated leukocyte cell adhesion molecule
-2.83	2.55e-10	PCBP3	poly(rC) binding protein 3	3.11	3.02e-02	KRT19	keratin 19
-2.78	2.20e-07	WAC	WW domain containing adaptor with caspase recruitment domain	3.1	3.41e-03	S100A10	S100 calcium binding protein A10
-2.73	7.12e-06	NOPCHAP1	NOP protein chaperone 1	3.09	4.57e-03	ITGA3	integrin subunit alpha 3
-2.73	9.91e-16	C20orf27	chromosome 20 open reading frame 27	3.05	6.12e-05	ITGA6	integrin subunit alpha 6
-2.66	5.96e-15	PRTFDC1	phosphoribosyl transferase domain containing 1	2.94	3.88e-03	CD44	CD44 molecule (Indian blood group)
-2.64	3.22e-05	NAB2	NGFL-A binding protein 2	2.75	2.19e-04	CTSZ	cathepsin Z
-2.55	3.24e-11	GSPT2	G1 to S phase transition 2	2.74	1.30e-03	CAVIN1	caveolae associated protein 1
-2.52	8.84e-08	HMGN5	high mobility group nucleosome binding protein 5	2.7	1.16e-04	JUP	junction plakophilin
-2.5	1.98e-03	CDC20	cell division cycle 20	2.69	3.38e-05	SQOR	sulfide quinone oxidoreductase
-2.48	4.76e-06	PNISR	PNN interacting serine and arginine rich protein	2.66	1.22e-10	SEL1L	SEL1L adaptor subunit of ERAD E3 ubiquitin ligase
-2.47	2.42e-05	ASF1A	anti-silencing function 1A histone	2.64	1.39e-09	PI4K2A	phosphatidylinositol 4-kinase type 2
-2.47	2.35e-05	DPYSL5	dihydropyrimidinase like 5	2.64	2.18e-05	EGFR	epidermal growth factor receptor
-2.47	3.94e-05	RAB1F	RAB interacting factor	2.63	1.76e-05	DSG2	desmoglein 2
-2.47	2.75e-03	POLE	DNA polymerase epsilon, catalytic subunit	2.58	2.20e-07	ENDOD1	endonuclease domain containing 1
-2.47	1.25e-03	EIF1AX	eukaryotic translation initiation factor 1A	2.57	4.45e-04	NQO1	NAD(P)H quinone dehydrogenase 1
-2.46	1.98e-03	DPH5	diphthamide biosynthesis 5	2.57	2.37e-06	SCAMP2	secretory carrier membrane protein
-2.45	4.84e-07	GTF2E1	general transcription factor IIIE subunit	2.49	1.54e-06	ADAM9	ADAM metallopeptidase domain 9
-2.44	4.01e-03	GLMN	glomulin, FKBP associated protein	2.48	1.01e-09	AMFR	autocrine motility factor receptor
-2.41	9.27e-03	SKP2	S-phase kinase associated protein 2	2.48	2.94e-07	TPBG	trophoblast glycoprotein
-2.41	1.86e-03	UBE2Q1	ubiquitin conjugating enzyme E2 Q1	2.42	6.24e-08	BCL2L1	BCL2 like 1
-2.38	8.71e-03	CKS2	CDC28 protein kinase regulatory subunit	2.41	5.69e-08	SSR3	signal sequence receptor subunit 3
-2.38	6.00e-13	ZC3HAV1L	zinc finger CCCH-type containing 1, a	2.36	1.40e-08	AGRIN	agrin
-2.37	3.88e-03	DCAF16	DDB1 and CUL4 associated factor 16	2.36	1.33e-09	SEC61G	SEC61 translocon subunit gamma
-2.36	1.06e-08	NME4	NME/NM23 nucleoside diphosphate kinase	2.35	1.96e-05	CD59	CD59 molecule (CD59 blood group)
-2.35	1.47e-03	ERI3	ERI3 exoribonuclease family member	2.31	3.79e-05	NT5E	5'-nucleotidase ecto

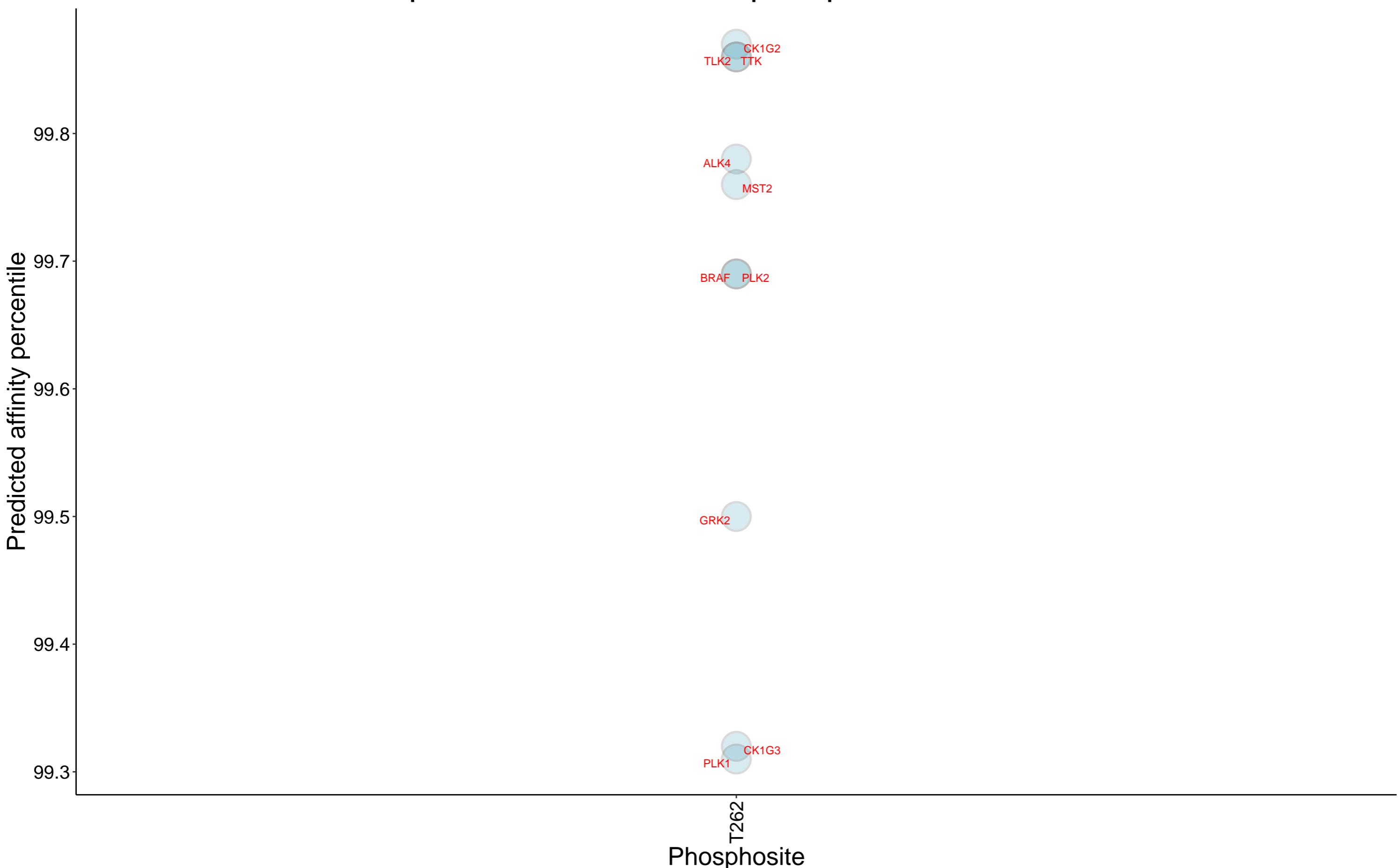
CDC45 network, DB1, no Pearson r > 0.3



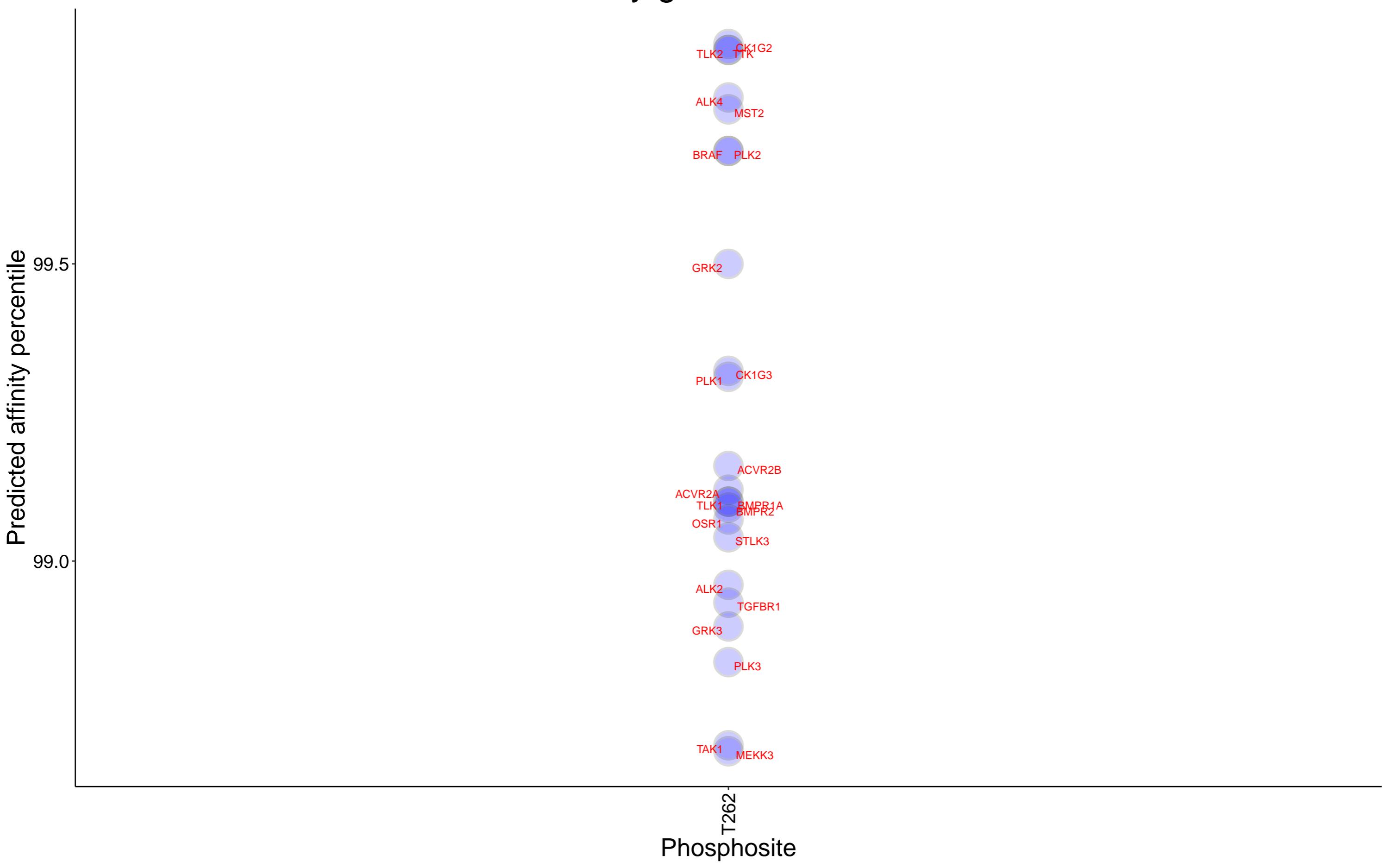
Insufficient number of paired observations in DB1 for CDC45

Insufficient number of paired observations in DB1 for CDC45

Top 10 kinases for each phosphosite in CDC45



Kinases with affinity greater than 98.5% to CDC45



No sufficient paired observations in DB1 for CDC45