

CDCA5

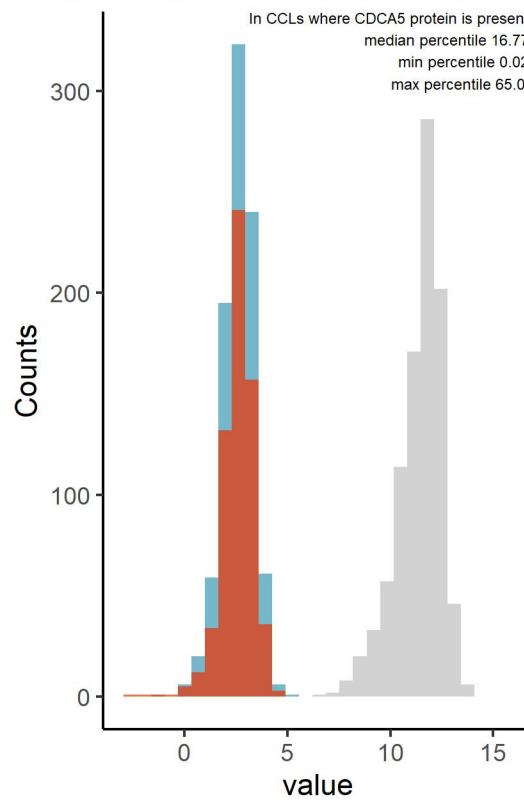
Protein name: CDCA5 ; UNIPROT: Q96FF9 ; Gene name: cell division cycle associated 5

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

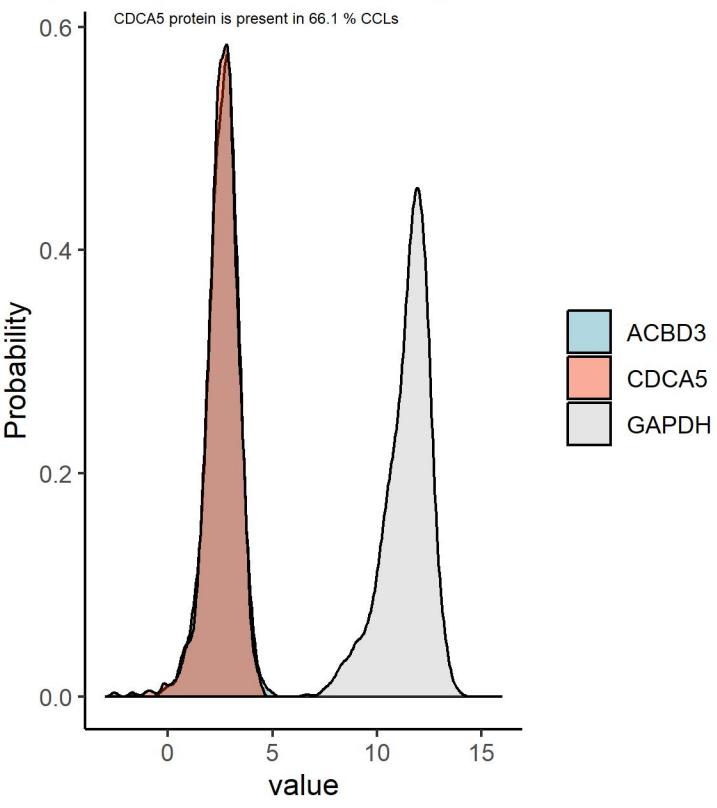
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

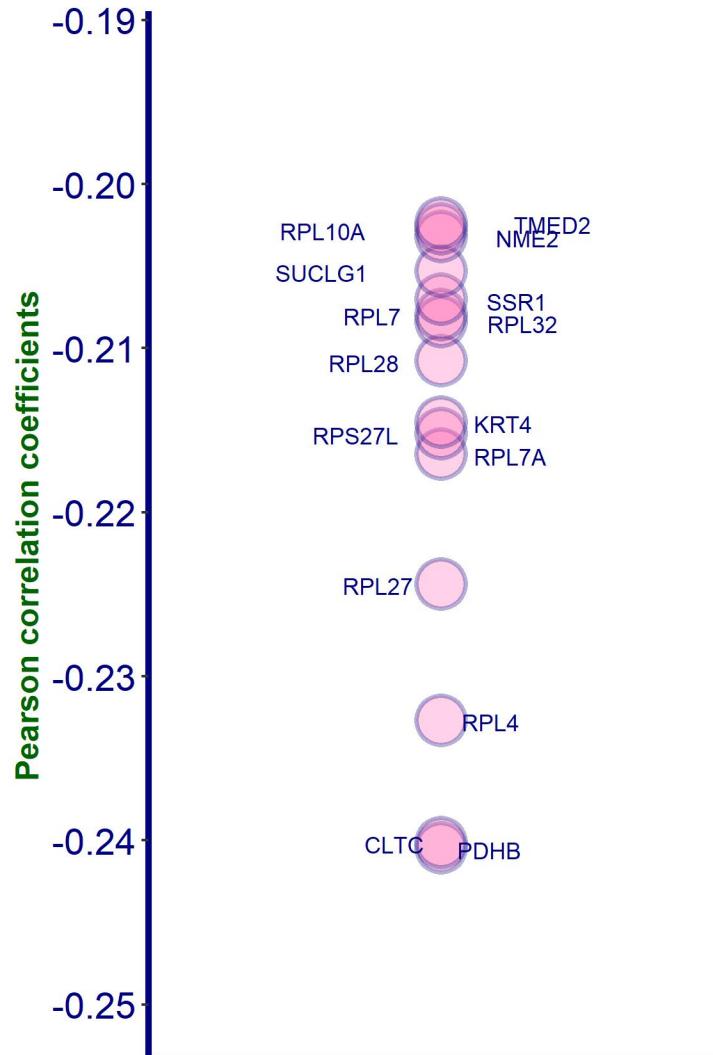
Histogram of CDCA5 protein compared to proteins with low and high abundance



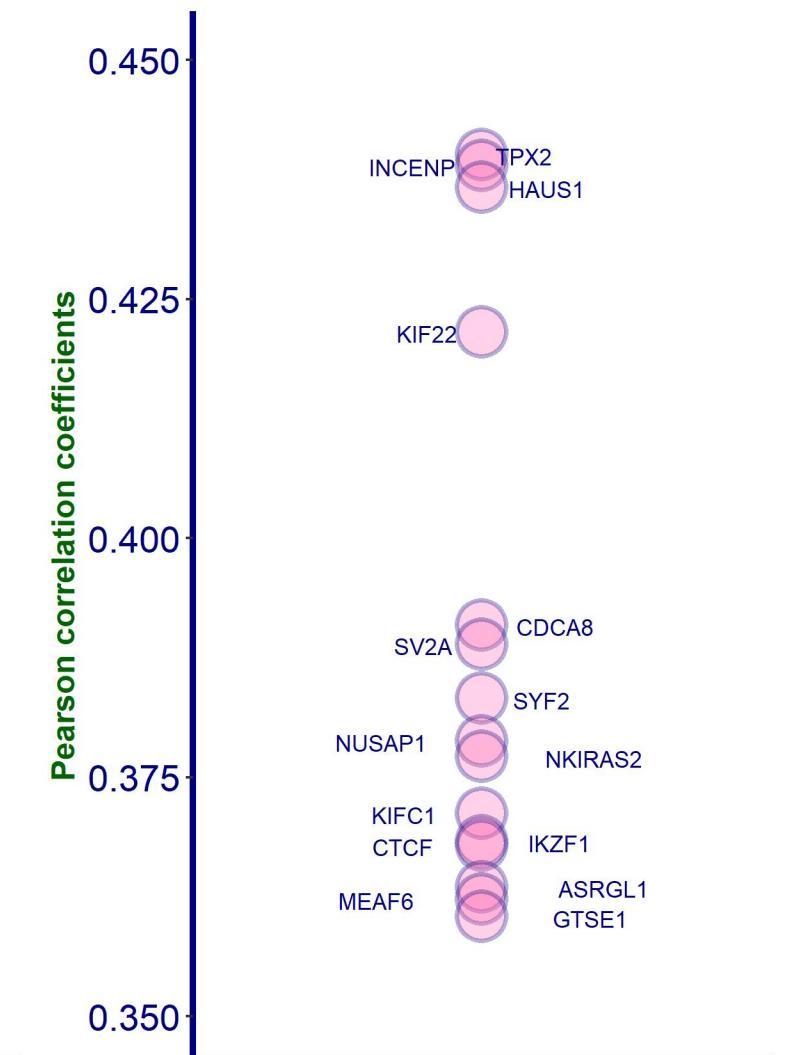
Density plot of CDCA5 protein compared to proteins with low and high abundance



Top negative correlations of CDCA5 protein, DB1

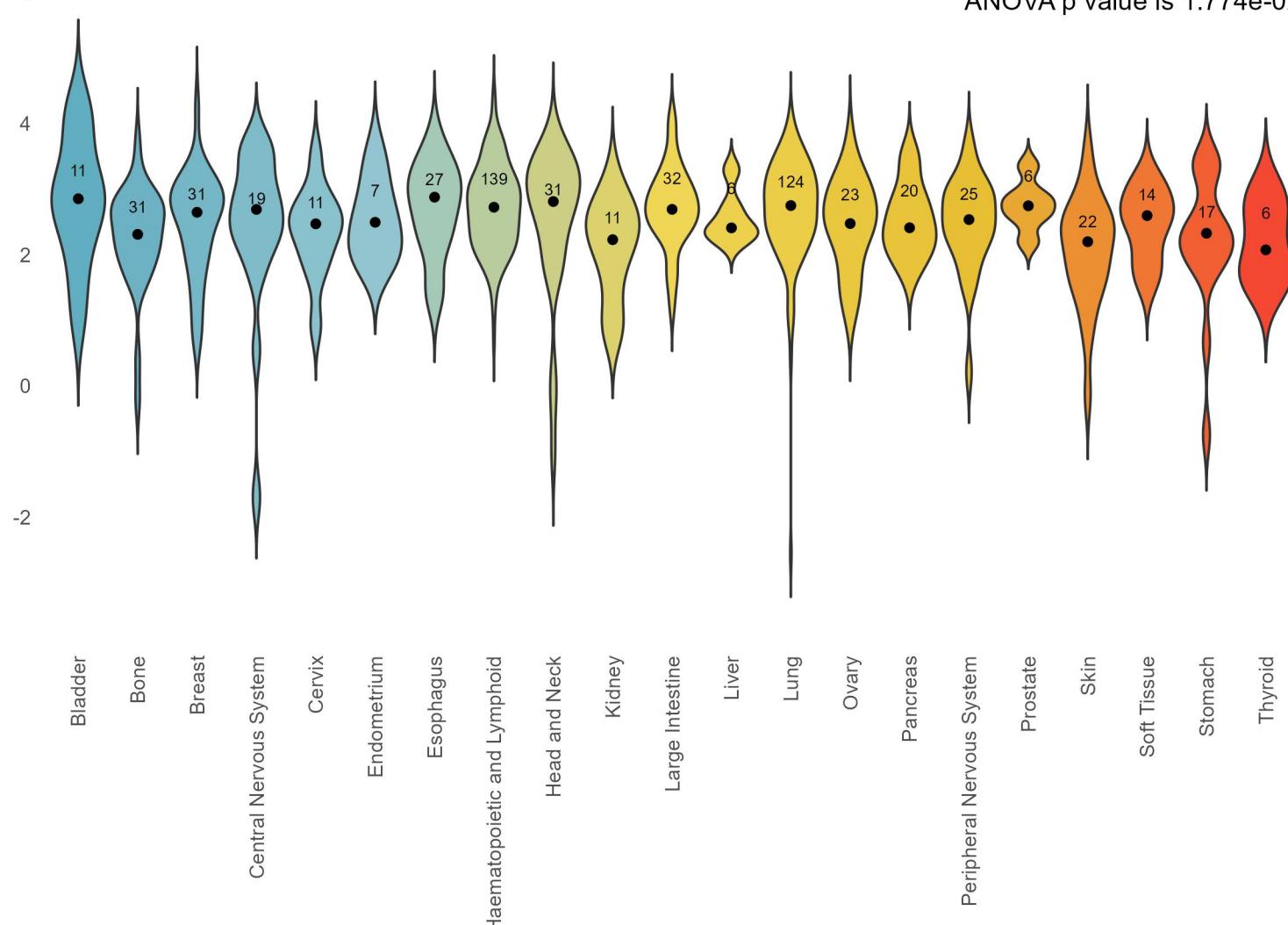


Top positive correlations of CDCA5 protein, DB1



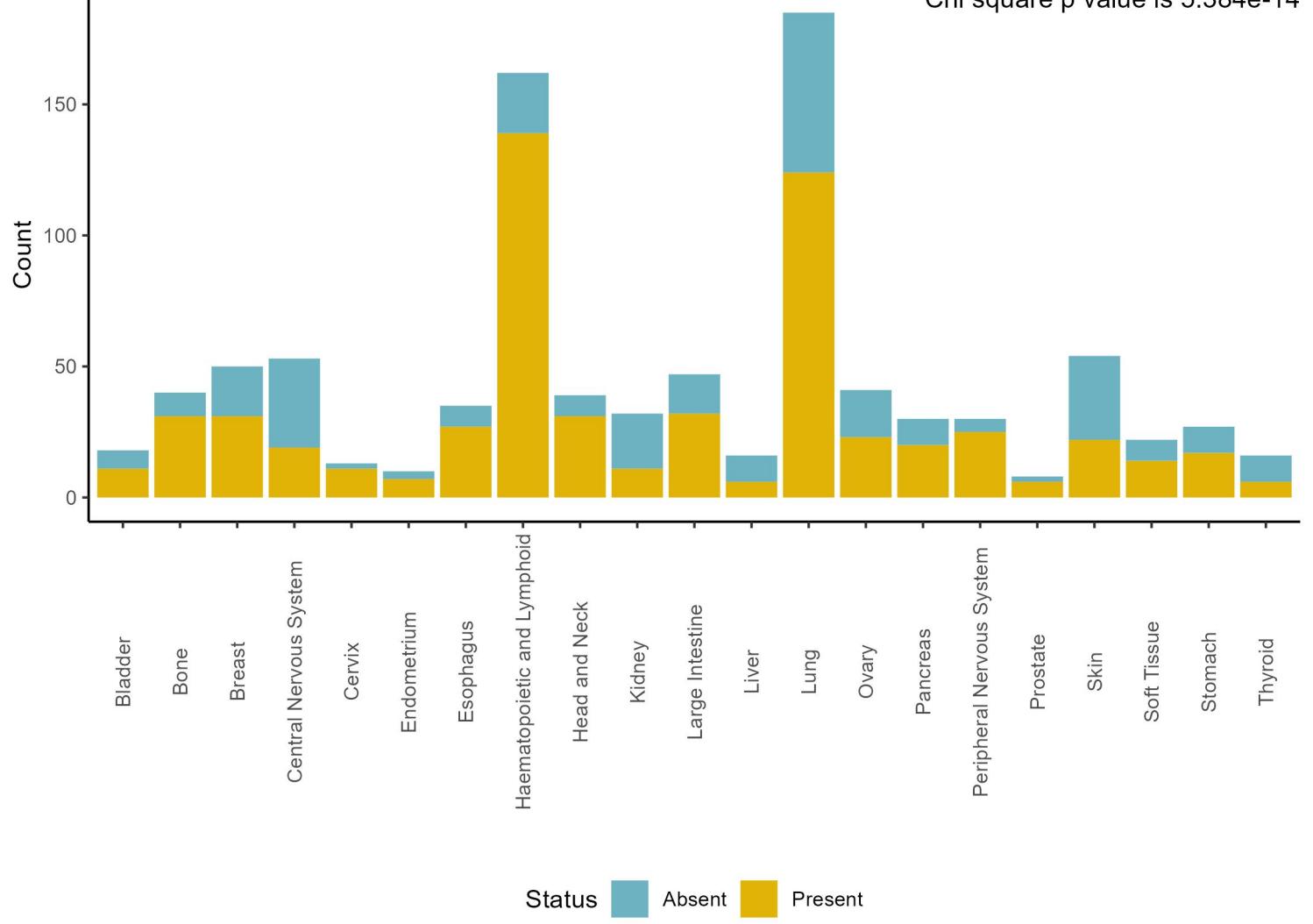
Amount of CDCA5 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 1.774e-02



Present and absent CDCA5 protein counts by tissue, DB1

Chi square p value is 5.384e-14

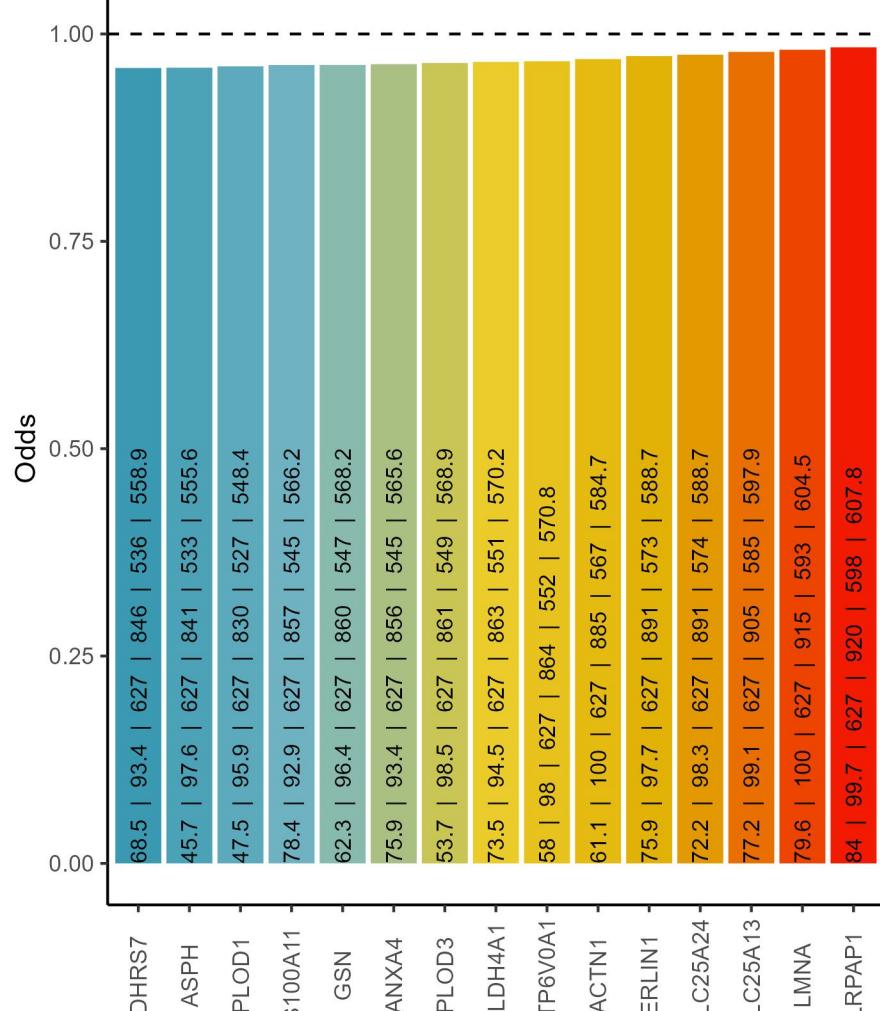


Cooccurrence with CDCA5 protein, DB1

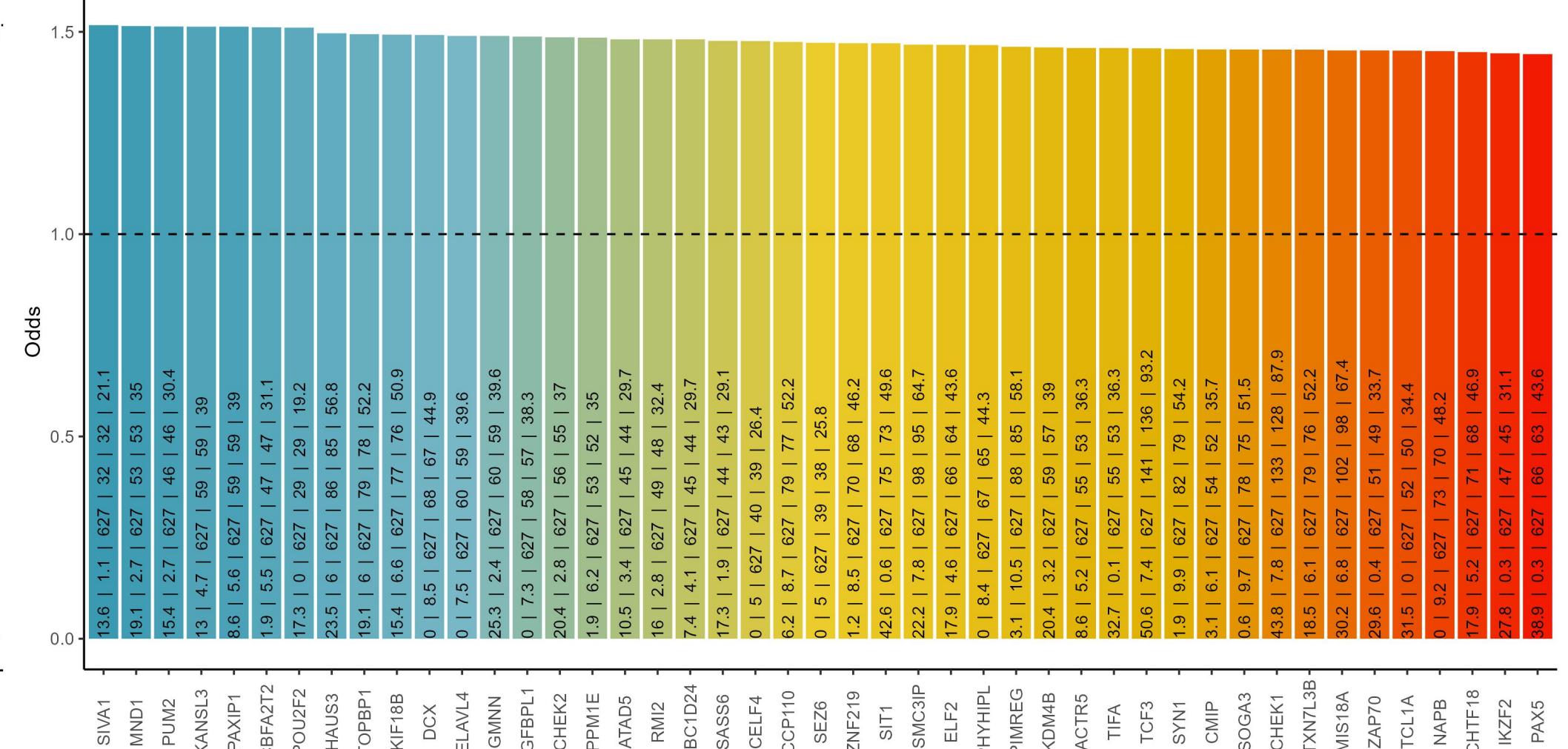
% of CDCA5 in blood cancers: 85.8 ; % of CDCA5 in solid cancers: 61.9

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CDCA5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

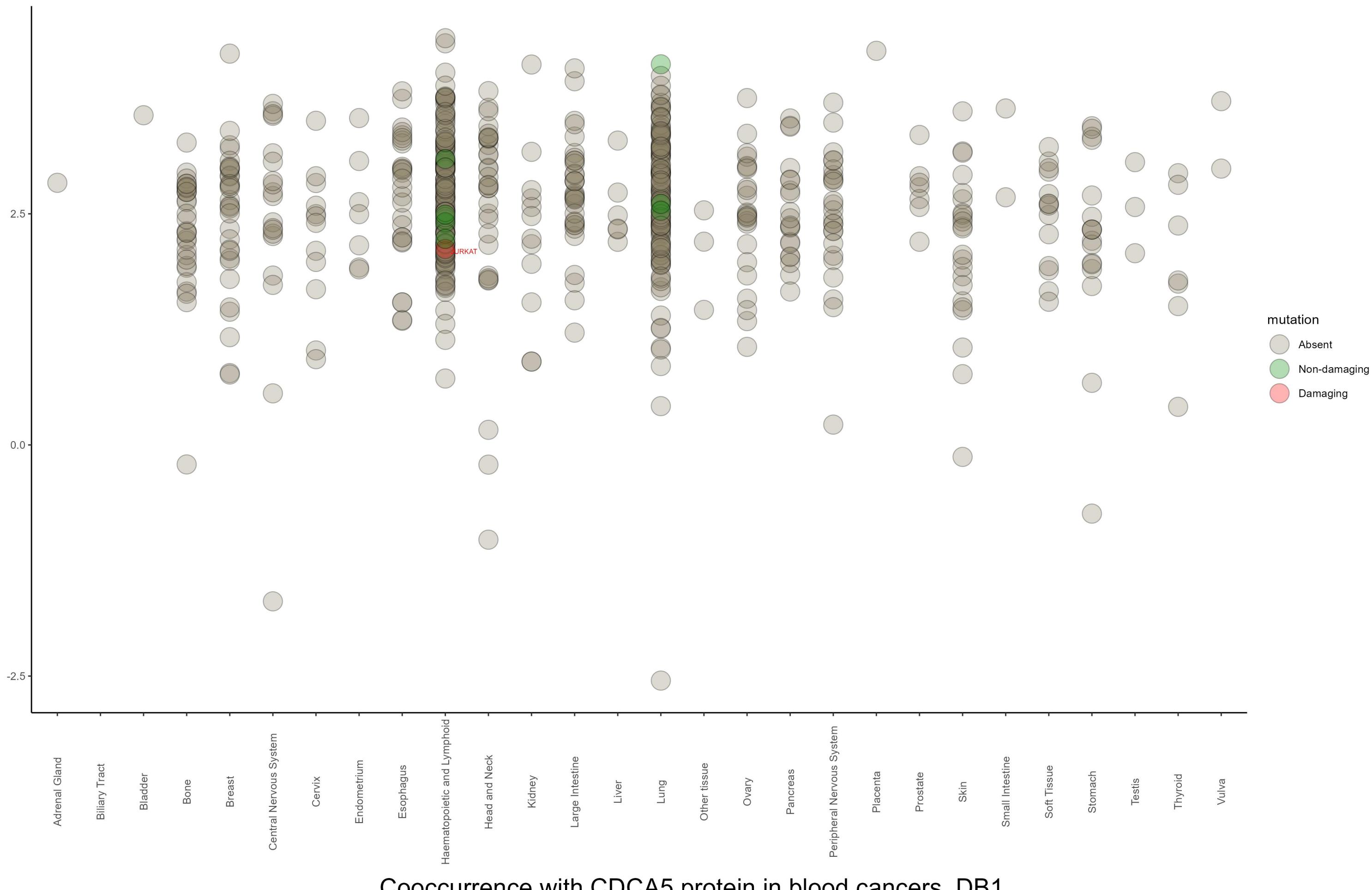
Negative cooccurrence



Positive cooccurrence

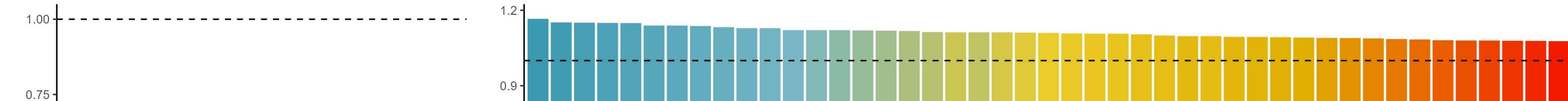


Amount of CDCA5 protein and mutation status by tissue, DB1



Cooccurrence with CDCA5 protein in blood cancers, DB1

The text in the bars: incidence of CDCA5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



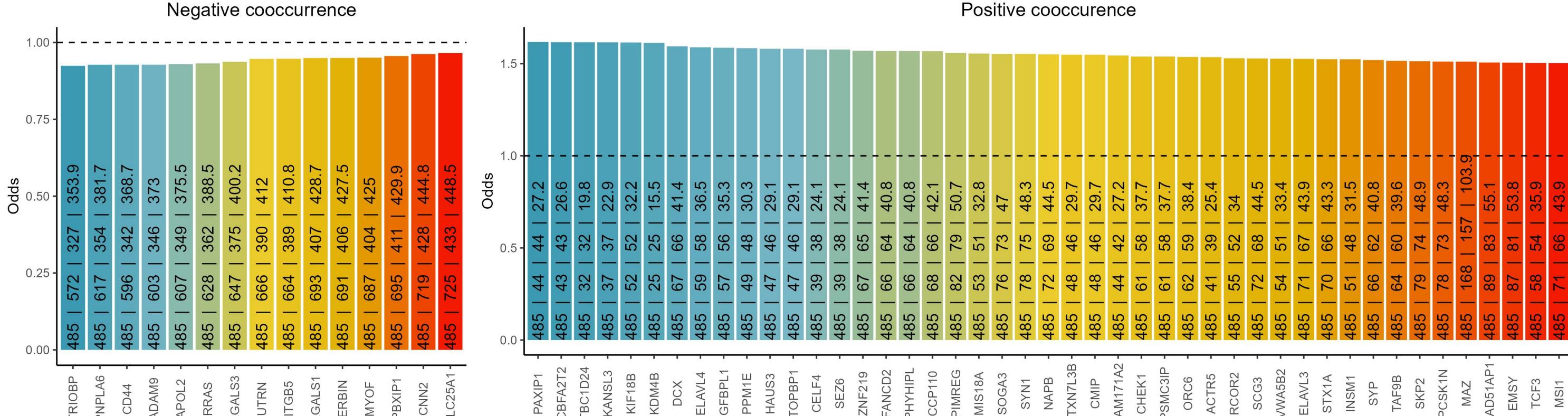
Cooccurrence with CDCA5 protein in solid cancers, DB1

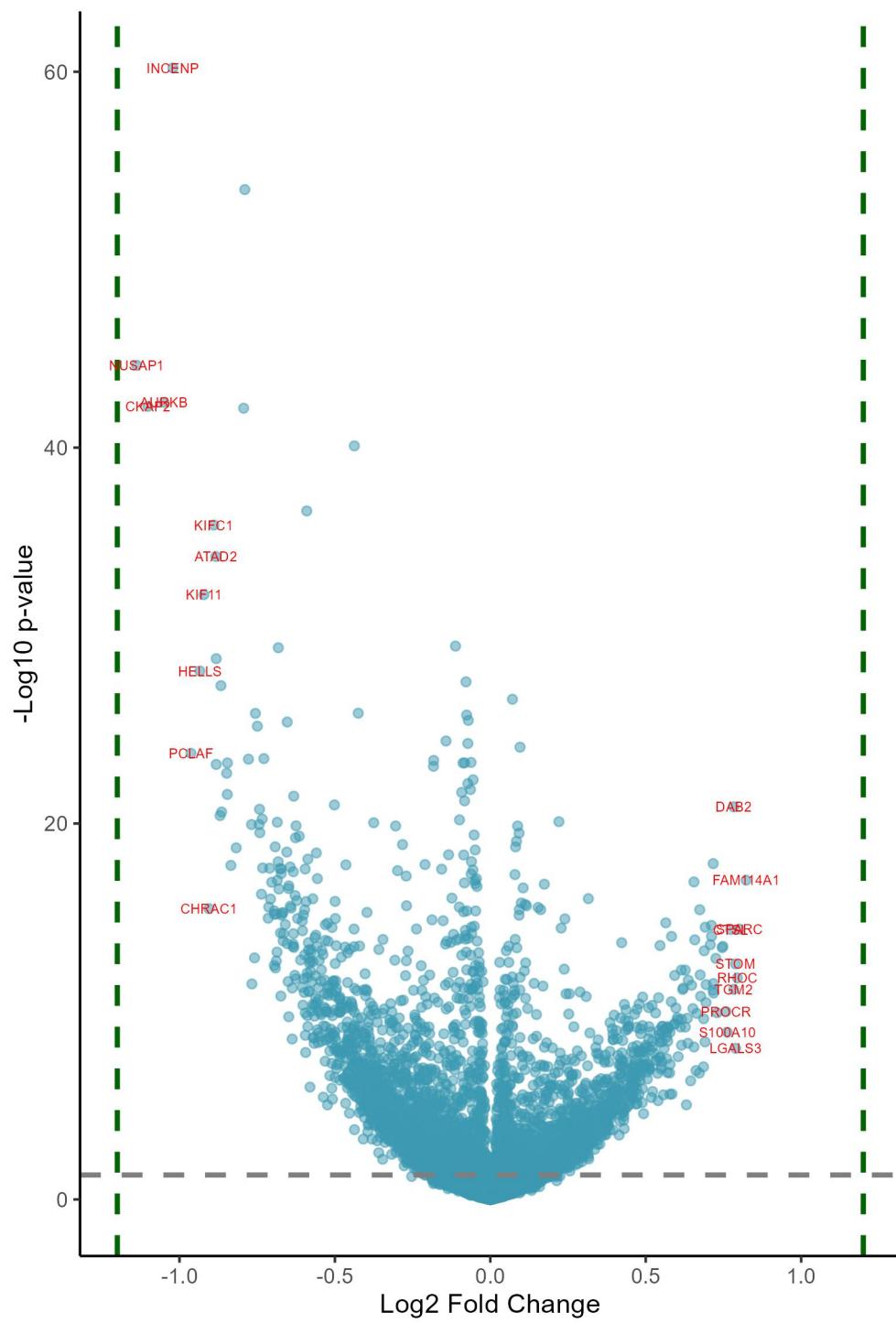
The text in the bars: incidence of CDCA5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Cooccurrence with CDCA5 protein in solid cancers, DB1

The text in the bars: incidence of CDCA5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

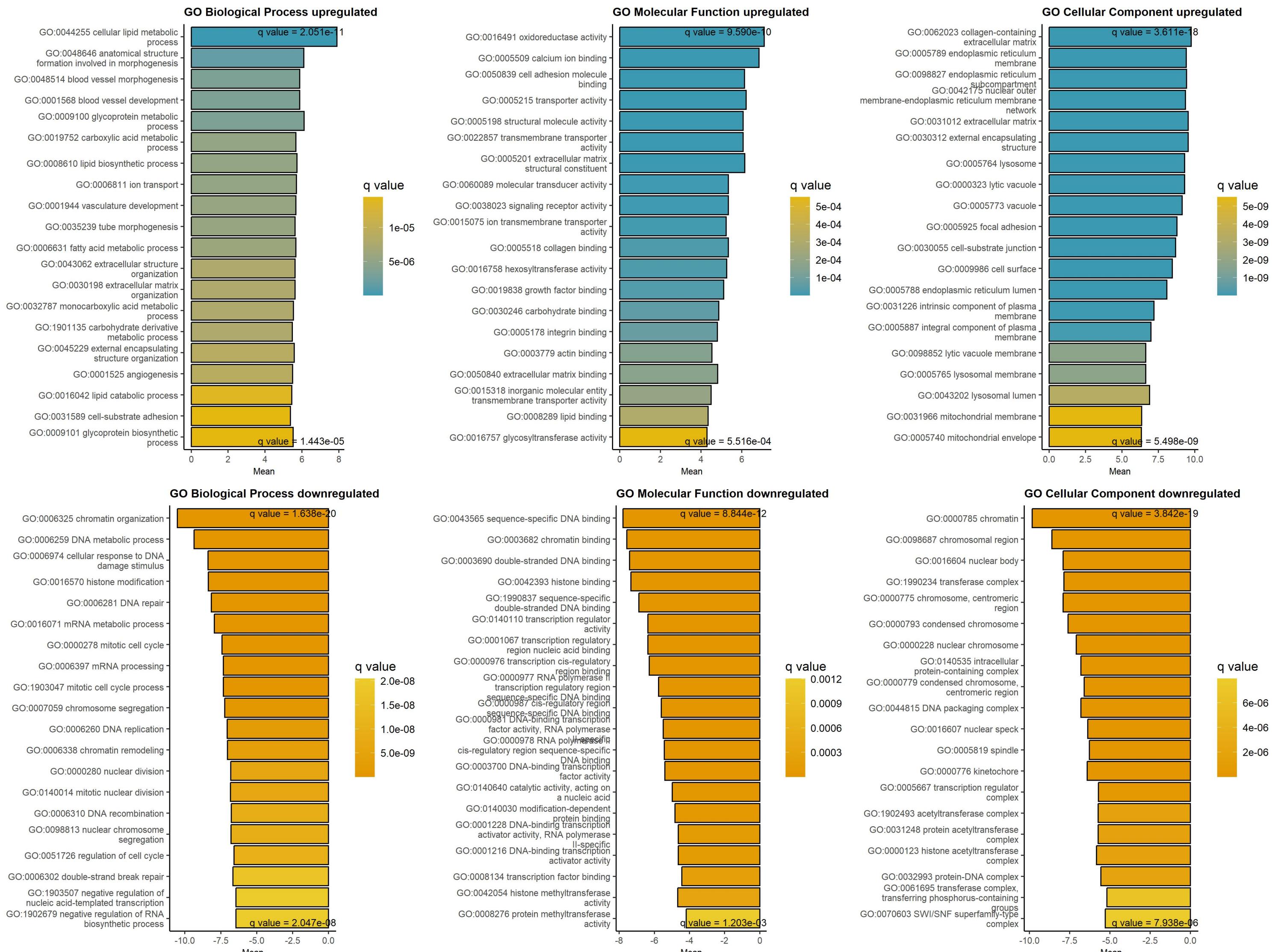




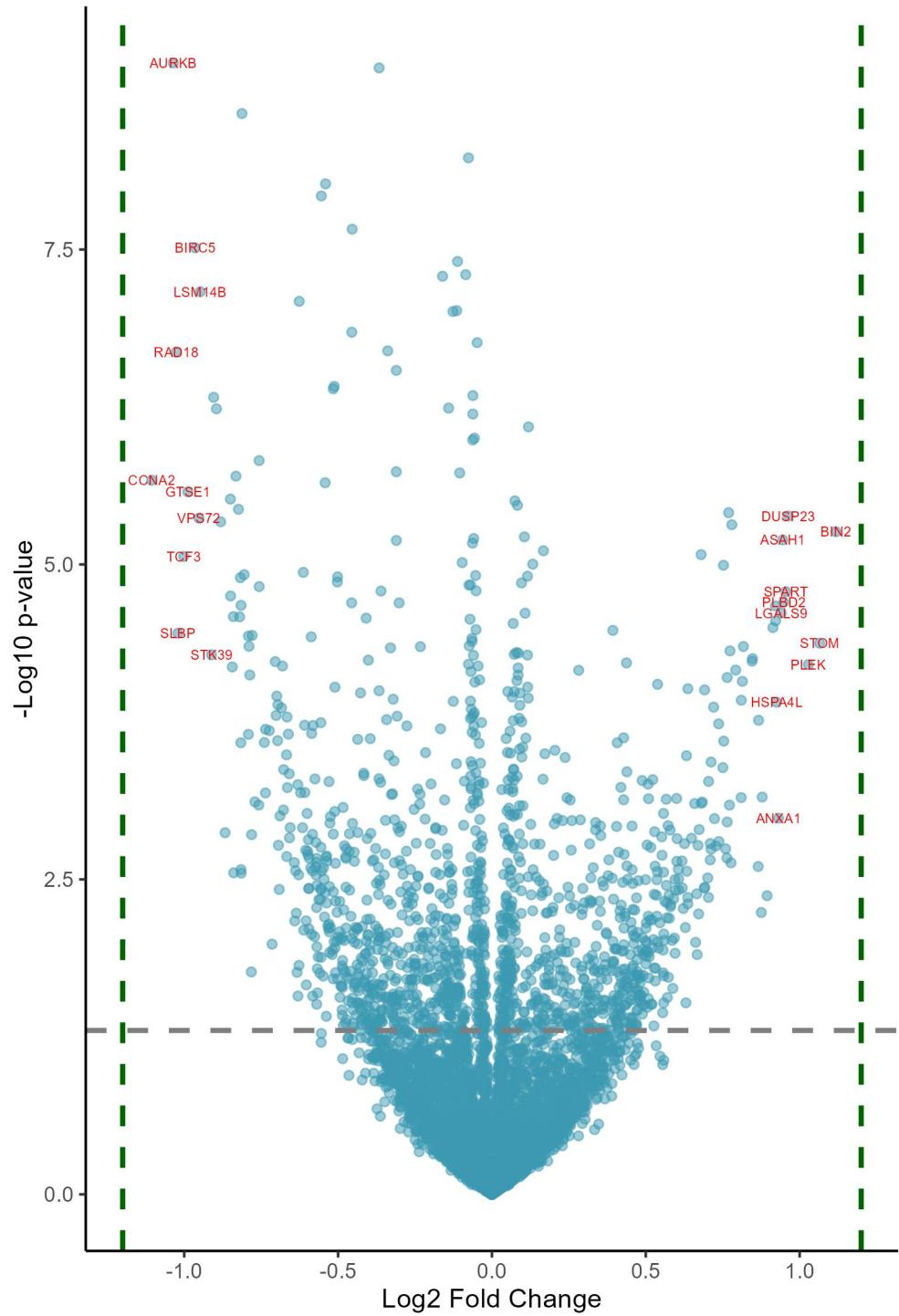
Downregulated at low/absent CDCA5 Upregulated at low/absent CDCA5

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.14	6.98e-42	NUSAP1	nucleolar and spindle associated pr	0.82	6.88e-16	FAM114A1	family with sequence similarity 114
-1.1	6.99e-40	CKAP2	cytoskeleton associated protein 2	0.8	1.65e-13	SPARC	secreted protein acidic and cystein
-1.05	5.19e-40	AURKB	aurora kinase B	0.79	3.97e-11	RHOC	ras homolog family member C
-1.02	2.09e-57	INCENP	inner centromere protein	0.79	9.21e-08	LGALS3	galectin 3
-0.96	4.21e-22	PCLAF	PCNA clamp associated factor	0.79	7.94e-12	STOM	stomatin
-0.93	3.19e-26	HELLS	helicase, lymphoid specific	0.78	1.80e-19	DAB2	DAB adaptor protein 2
-0.92	3.69e-30	KIF11	kinesin family member 11	0.78	1.38e-10	TGM2	transglutaminase 2
-0.91	1.72e-14	CHRAC1	chromatin accessibility complex sub	0.77	1.72e-13	CTSL	cathepsin L
-0.89	8.77e-34	KIFC1	kinesin family member C1	0.76	1.53e-08	S100A10	S100 calcium binding protein A10
-0.88	3.76e-32	ATAD2	ATPase family AAA domain containing	0.76	1.57e-09	PROCR	protein C receptor
-0.88	1.29e-21	CCNB1	cyclin B1	0.75	1.11e-12	NPC1	NPC intracellular cholesterol trans
-0.88	7.48e-27	CHAF1A	chromatin assembly factor 1 subunit	0.75	1.28e-12	LRP1	LDL receptor related protein 1
-0.87	4.91e-19	BLM	BLM RecQ like helicase	0.73	1.80e-09	NT5E	5'-nucleotidase ecto
-0.87	1.70e-25	SAMD1	sterile alpha motif domain containi	0.73	4.27e-12	RAB32	RAB32, member RAS oncogene family
-0.86	3.23e-19	UBE2T	ubiquitin conjugating enzyme E2 T	0.72	2.04e-10	GPX8	glutathione peroxidase 8 (putative)
-0.85	3.60e-21	KIF2C	kinesin family member 2C	0.72	7.30e-11	FHL2	four and a half LIM domains 2
-0.85	4.28e-20	KIAA1143	KIAA1143	0.72	1.13e-16	CPQ	carboxypeptidase Q
-0.85	1.11e-21	TACC3	transforming acidic coiled-coil con	0.72	1.51e-10	NNMT	nicotinamide N-methyltransferase
-0.83	1.36e-16	C9orf78	chromosome 9 open reading frame 78	0.71	3.72e-13	HSPG2	heparan sulfate proteoglycan 2
-0.82	1.84e-17	CDCA3	cell division cycle associated 3	0.71	1.10e-13	TRIOBP	TRIO and F-actin binding protein
-0.79	7.58e-40	CDCA8	cell division cycle associated 8	0.71	9.38e-13	ARSA	arylsulfatase A
-0.79	4.14e-51	KIF22	kinesin family member 22	0.69	8.24e-11	PLS3	plastin 3
-0.78	8.10e-22	MAZ	MYC associated zinc finger protein	0.69	5.84e-10	ITGA5	integrin subunit alpha 5
-0.77	1.30e-18	EZH2	enhancer of zeste 2 polycomb repres	0.69	1.35e-13	RBPMS	RNA binding protein, mRNA processin
-0.77	7.62e-11	CORO1A	coronin 1A	0.69	4.52e-08	ANXA1	annexin A1
-0.76	4.06e-12	H2AX	H2A.X variant histone	0.69	1.80e-12	FNDC3B	fibronectin type III domain contain
-0.76	4.37e-24	GTSE1	G2 and S-phase expressed 1	0.69	3.51e-09	MMP14	matrix metallopeptidase 14
-0.75	1.77e-23	EP400	E1A binding protein p400	0.69	7.06e-07	ITGA3	integrin subunit alpha 3
-0.74	1.30e-18	CCNA2	cyclin A2	0.68	2.92e-10	P4HA2	prolyl 4-hydroxylase subunit alpha

GAGE analysis on upregulated and downregulated proteins at low/absent CDCA5 protein, DB1

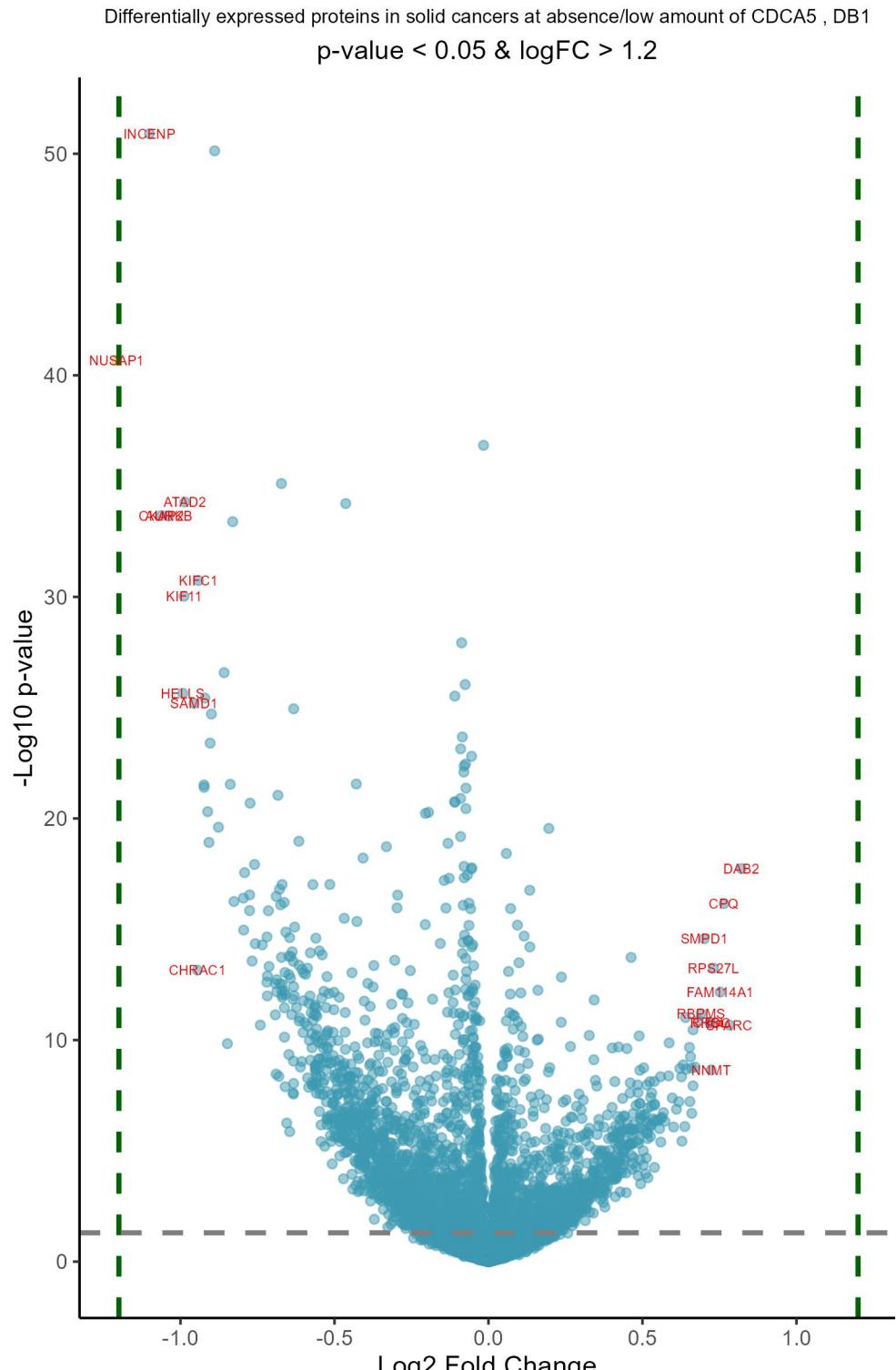


p-value < 0.05 & logFC > 1.2



Downregulated in blood cancers at low/absent CDCA5 Upregulated in blood cancers at low/absent CDCA5

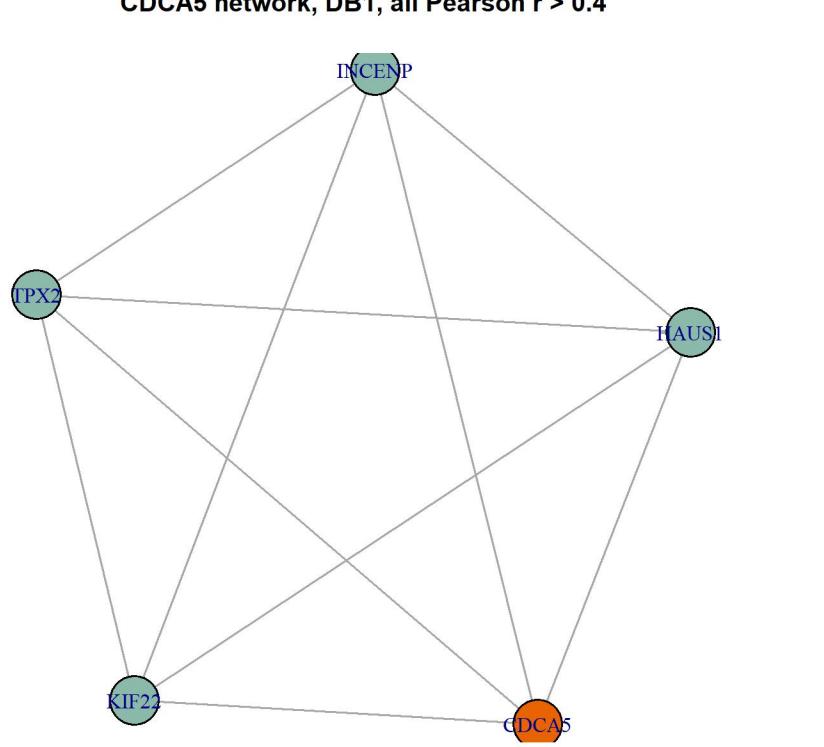
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.11	3.97e-04	CCNA2	cyclin A2	1.12	7.61e-04	BIN2	bridging integrator 2
-1.04	2.54e-06	AURKB	aurora kinase B	1.06	2.89e-03	STOM	stomatin
-1.03	6.84e-05	RAD18	RAD18 E3 ubiquitin protein ligase	1.03	3.57e-03	PLEK	pleckstrin
-1.02	2.57e-03	SLBP	stem-loop binding protein	0.96	6.23e-04	DUSP23	dual specificity phosphatase 23
-1	1.03e-03	TCF3	transcription factor 3	0.96	1.50e-03	SPART	spartin
-0.99	4.64e-04	GTSE1	G2 and S-phase expressed 1	0.95	1.74e-03	PLBD2	phospholipase B domain containing 2
-0.96	2.26e-05	BIRC5	baculoviral IAP repeat containing 5	0.94	8.24e-04	ASAHI	N-acylsphingosine amidohydrolase 1
-0.95	6.34e-04	VPS72	vacuolar protein sorting 72 homolog	0.94	2.00e-03	LGALS9	galectin 9
-0.95	3.50e-05	LSM14B	LSM family member 14B	0.93	2.34e-02	ANXA1	annexin A1
-0.91	3.21e-03	STK39	serine/threonine kinase 39	0.93	5.56e-03	HSPA4L	heat shock protein family A (Hsp70)
-0.9	1.25e-04	KIAA1143	KIAA1143	0.92	2.17e-03	ATP6VOA1	ATPase H ⁺ transporting V0 subunit a
-0.9	1.43e-04	SKA3	spindle and kinetochore associated	0.92	1.80e-03	LYZ	lysozyme
-0.88	6.63e-04	CCNB2	cyclin B2	0.91	2.39e-03	RPS27L	ribosomal protein S27 like
-0.87	2.72e-02	GNG5	G protein subunit gamma 5	0.89	5.27e-02	COTL1	coactosin like F-actin binding prot
-0.85	5.16e-04	CIT	citron rho-interacting serine/threono	0.88	1.82e-02	GSN	gelsolin
-0.85	1.60e-03	H2AX	H2A.X variant histone	0.88	6.40e-02	LMNA	lamin A/C
-0.84	3.64e-03	MAZ	MYC associated zinc finger protein	0.87	7.04e-03	PPCS	phosphopantethenoylcysteine synthet
-0.84	2.09e-03	HIP1R	huntingtin interacting protein 1 re	0.87	3.93e-02	CD44	CD44 molecule (Indian blood group)
-0.84	4.15e-02	TCL1A	TCL1 family AKT coactivator A	0.85	3.38e-03	PDIA5	protein disulfide isomerase family
-0.83	3.78e-04	CKAP2	cytoskeleton associated protein 2	0.85	3.47e-03	LPCAT2	lysophosphatidylcholine acyltransfe
-0.82	5.78e-04	NSD2	nuclear receptor binding SET domain	0.82	2.96e-03	MRPS30	mitochondrial ribosomal protein S30
-0.82	2.09e-03	CEP131	centrosomal protein 131	0.81	4.36e-03	LACTB	lactamase beta
-0.82	1.30e-03	RNF169	ring finger protein 169	0.81	5.48e-03	PRKCD	protein kinase C delta
-0.82	9.06e-03	LEF1	lymphoid enhancer binding factor 1	0.81	1.83e-02	TUBA1C	tubulin alpha 1c
-0.82	4.05e-02	SEPTIN1	septin 1	0.79	3.77e-03	MNDA	myeloid cell nuclear differentiatio
-0.82	1.80e-03	YEATS4	YEATS domain containing 4	0.78	6.85e-04	WASHC5	WASH complex subunit 5
-0.81	4.15e-02	TMEM123	transmembrane protein 123	0.78	3.75e-02	CA2	carbonic anhydrase 2
-0.81	4.38e-06	NUSAP1	nucleolar and spindle associated pr	0.77	3.13e-03	PRTN3	proteinase 3
-0.81	1.30e-03	DLGAP5	DLG associated protein 5	0.77	1.97e-02	PIGK	phosphatidylinositol glycan anchor



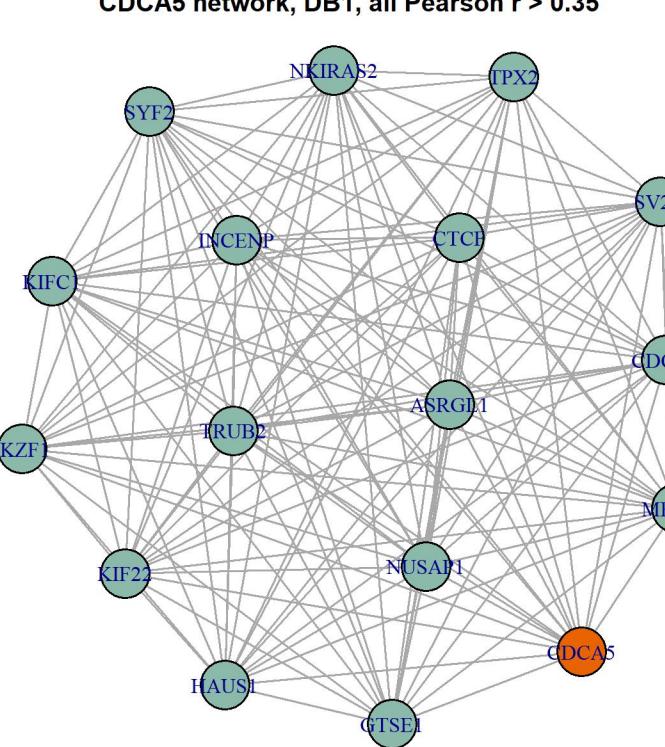
Downregulated in solid cancers at low/absent CDCA5 Upregulated in solid cancers at low/absent CDCA5

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.21	3.45e-38	NUSAP1	nucleolar and spindle associated pr	0.82	2.18e-16	DAB2	DAB adaptor protein 2
-1.1	4.18e-48	INCENP	inner centromere protein	0.78	5.91e-10	SPARC	secreted protein acidic and cystein
-1.06	1.50e-31	CKAP2	cytoskeleton associated protein 2	0.76	6.11e-15	CPQ	carboxypeptidase Q
-1.04	1.50e-31	AURKB	aurora kinase B	0.75	2.80e-11	FAM114A1	family with sequence similarity 114
-0.99	8.70e-24	HELLS	helicase, lymphoid specific	0.73	3.00e-12	RPS27L	ribosomal protein S27 like
-0.99	4.77e-28	KIF11	kinesin family member 11	0.72	3.88e-08	NNMT	nicotinamide N-methyltransferase
-0.99	4.97e-32	ATAD2	ATPase family AAA domain containing	0.72	4.79e-10	RHOC	ras homolog family member C
-0.96	2.10e-23	SAMD1	sterile alpha motif domain containi	0.72	4.54e-10	CTSL	cathepsin L
-0.95	3.64e-12	CHRAC1	chromatin accessibility complex sub	0.7	1.84e-13	SMPD1	sphingomyelin phosphodiesterase 1
-0.94	1.01e-28	KIFC1	kinesin family member C1	0.69	2.04e-10	RBPMS	RNA binding protein, mRNA processin
-0.92	6.34e-20	CCNB1	cyclin B1	0.68	3.85e-10	HSPG2	heparan sulfate proteoglycan 2
-0.92	7.90e-20	PCLAF	PCNA clamp associated factor	0.67	2.98e-08	GBE1	1,4-alpha-glucan branching enzyme 1
-0.92	1.29e-23	CHAF1A	chromatin assembly factor 1 subunit	0.66	9.39e-10	APOL2	apolipoprotein L2
-0.91	7.99e-19	BLM	BLM RecQ like helicase	0.66	1.65e-07	STOM	stomatin
-0.91	1.67e-17	UBE2T	ubiquitin conjugating enzyme E2 T	0.66	2.21e-06	TGM2	transglutaminase 2
-0.9	1.10e-21	C5orf24	chromosome 5 open reading frame 24	0.66	3.24e-08	RAB32	RAB32, member RAS oncogene family
-0.9	5.84e-23	PRC1	protein regulator of cytokinesis 1	0.66	1.16e-08	NPC1	NPC intracellular cholesterol trans
-0.89	1.64e-47	KIF22	kinesin family member 22	0.65	7.25e-07	IGFBP7	insulin like growth factor binding
-0.88	3.75e-18	KIF2C	kinesin family member 2C	0.65	4.83e-09	ARSA	arylsulfatase A
-0.86	1.16e-24	EP400	E1A binding protein p400	0.64	3.66e-08	LRP1	LDL receptor related protein 1
-0.85	3.40e-09	CKMT1A	creatine kinase, mitochondrial 1A	0.64	2.97e-10	PARP4	poly(ADP-ribose) polymerase family
-0.84	6.18e-20	CENPF	centromere protein F	0.64	7.06e-06	LGALS3	galectin 3
-0.83	2.44e-31	CDCA8	cell division cycle associated 8	0.63	2.45e-08	LACTB	lactamase beta
-0.83	5.16e-15	CDCA3	cell division cycle associated 3	0.63	2.67e-05	LGALS1	galectin 1
-0.8	3.68e-15	UBE2S	ubiquitin conjugating enzyme E2 S	0.63	7.29e-08	SERpine2	serpin family E member 2
-0.79	8.06e-14	WDHD1	WD repeat and HMG-box DNA binding p	0.62	3.38e-08	FAH	fumarylacetoacetate hydrolase
-0.79	3.19e-16	EZH2	enhancer of zeste 2 polycomb repres	0.62	7.36e-07	ITGA5	integrin subunit alpha 5
-0.78	1.16e-14	ZNF280C	zinc finger protein 280C	0.61	1.49e-06	S100A10	S100 calcium binding protein A10
-0.78	2.75e-15	NSD3	nuclear receptor binding SET domain	0.6	7.34e-06	NT5E	5'-nucleotidase ecto

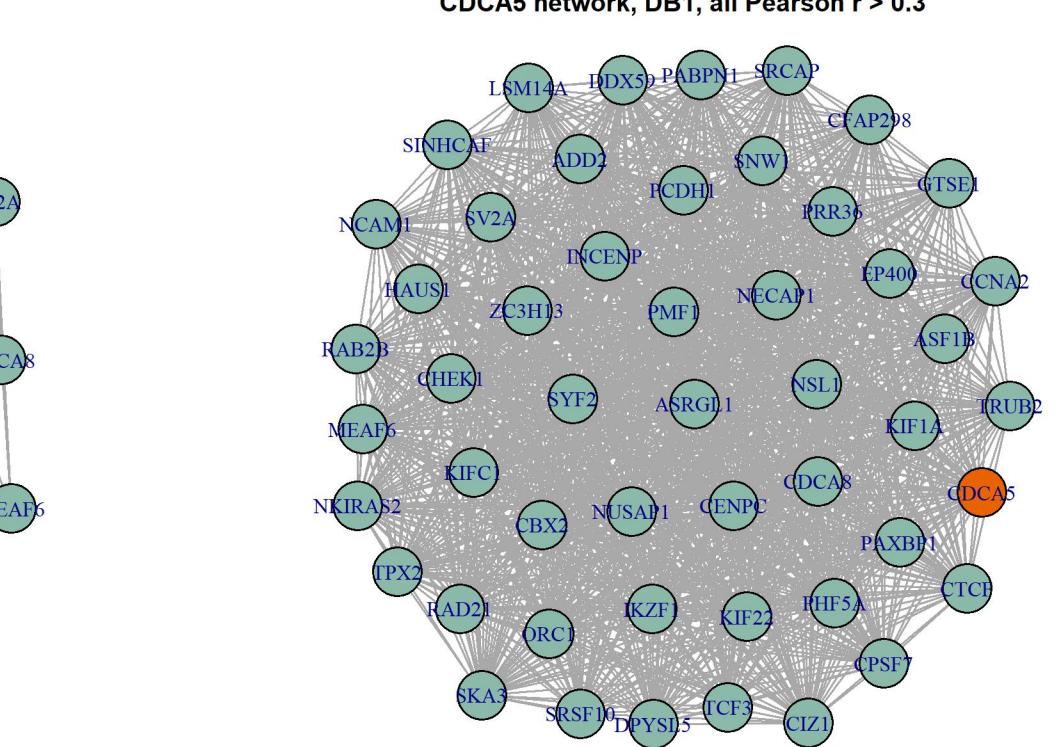
CDCA5 network, DB1, all Pearson r > 0.4

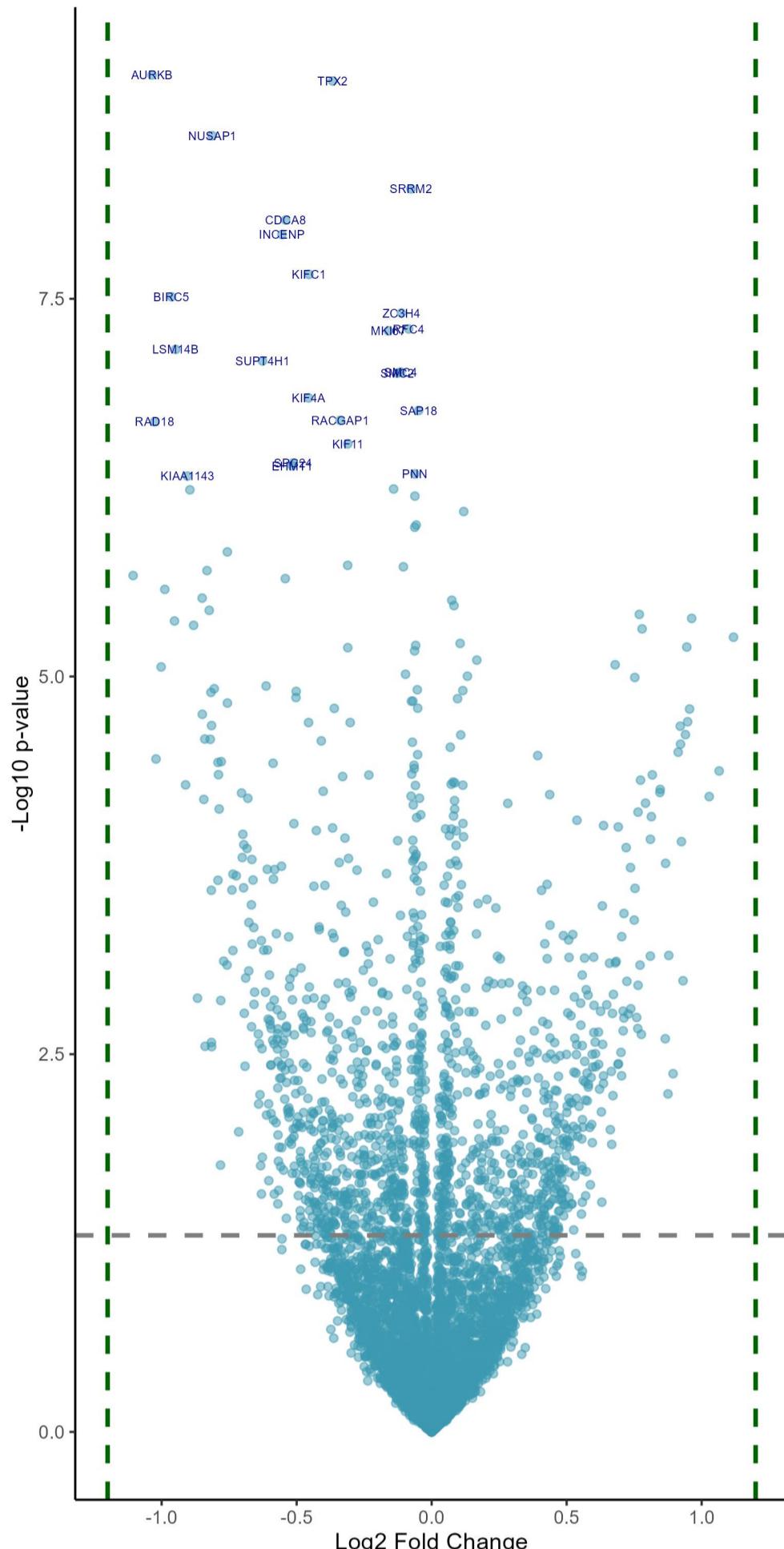


CDCA5 network, DB1, all Pearson r > 0.35



CDCA5 network, DB1, all Pearson r > 0.3

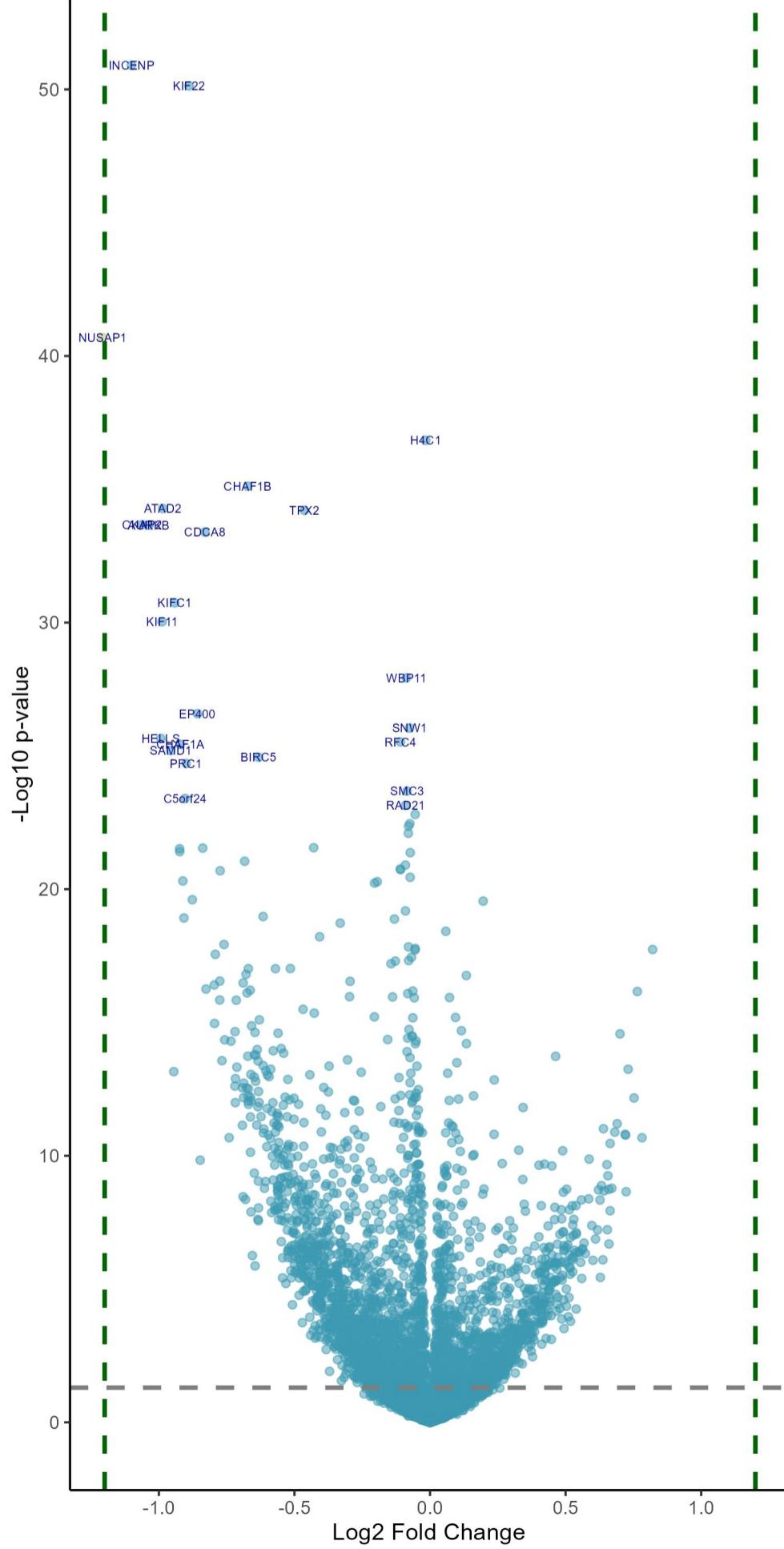




Sorted by p values!

Downregulated in blood cancers at low/absent CDCA5 Upregulated in blood cancers at low/absent CDCA5

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.04	2.54e-06	AURKB	aurora kinase B	0.12	1.86e-04	NDUFS2	NADH:ubiquinone oxidoreductase core
-0.37	2.54e-06	TPX2	TPX2 microtubule nucleation factor	0.07	5.20e-04	PDHB	pyruvate dehydrogenase E1 subunit b
-0.81	4.38e-06	NUSAP1	nucleolar and spindle associated pr	0.08	5.50e-04	CALR	calreticulin
-0.08	7.88e-06	SRRM2	serine/arginine repetitive matrix 2	0.77	6.00e-04	CD33	CD33 molecule
-0.54	1.05e-05	CDCA8	cell division cycle associated 8	0.96	6.23e-04	DUSP23	dual specificity phosphatase 23
-0.55	1.13e-05	INCENP	inner centromere protein	0.78	6.85e-04	WASH5	WASH complex subunit 5
-0.45	1.81e-05	KIFC1	kinesin family member C1	1.12	7.61e-04	BIN2	bridging integrator 2
-0.96	2.26e-05	BIRC5	baculoviral IAP repeat containing 5	0.11	8.20e-04	NDUFS1	NADH:ubiquinone oxidoreductase core
-0.11	2.61e-05	ZC3H4	zinc finger CCCH-type containing 4	0.94	8.24e-04	ASA1	N-acylsphingosine amidohydrolase 1
-0.09	2.85e-05	RFC4	replication factor C subunit 4	0.17	9.59e-04	IDH1	isocitrate dehydrogenase (NADP+)
-0.16	2.85e-05	MKI67	marker of proliferation Ki-67	0.68	1.01e-03	AZU1	azurocidin 1
-0.95	3.50e-05	LSM14B	LSM family member 14B	0.13	1.14e-03	NIT2	nitrilase family member 2
-0.63	3.87e-05	SUPT4H1	SPT4 homolog, DSIF elongation facto	0.75	1.14e-03	DNAJC13	DnaJ heat shock protein family (Hsp)
-0.11	4.08e-05	SMC4	structural maintenance of chromosom	0.12	1.30e-03	MRPL38	mitochondrial ribosomal protein L38
-0.13	4.08e-05	SMC2	structural maintenance of chromosom	0.1	1.39e-03	HDLBP	high density lipoprotein binding pr
-0.46	5.61e-05	KIF4A	kinesin family member 4A	0.96	1.50e-03	SPART	spartin
-0.05	6.41e-05	SAP18	Sin3A associated protein 18	0.95	1.74e-03	PLBD2	phospholipase B domain containing 2
-0.34	6.84e-05	RACGAP1	Rac GTPase activating protein 1	0.92	1.80e-03	LYZ	lysozyme
-1.03	6.84e-05	RAD18	RAD18 E3 ubiquitin protein ligase	0.94	2.00e-03	LGALS9	galectin 9
-0.31	9.13e-05	KIF11	kinesin family member 11	0.11	2.00e-03	BCAP31	B cell receptor associated protein
-0.51	1.17e-04	SPC24	SPC24 component of NDC80 kinetochor	0.92	2.17e-03	ATP6V0A1	ATPase H ⁺ transporting V0 subunit a
-0.52	1.17e-04	EHMT1	euchromatic histone lysine methyltr	0.07	2.25e-03	COPB1	COPI coat complex subunit beta 1
-0.06	1.25e-04	PNN	pinin, desmosome associated protein	0.91	2.39e-03	RPS27L	ribosomal protein S27 like
-0.9	1.25e-04	KIAA1143	KIAA1143	0.39	2.47e-03	VCL	vinculin
-0.14	1.43e-04	TOP2A	DNA topoisomerase II alpha	1.06	2.89e-03	STOM	stomatin
-0.9	1.43e-04	SKA3	spindle and kinetochore associated	0.82	2.96e-03	MRPS30	mitochondrial ribosomal protein S30
-0.06	1.52e-04	ATXN2L	ataxin 2 like	0.77	3.13e-03	PRTN3	proteinase 3
-0.06	2.20e-04	RBM14	RNA binding motif protein 14	0.08	3.20e-03	MRPL17	mitochondrial ribosomal protein L17
-0.06	2.21e-04	HNRNPH1	heterogeneous nuclear ribonucleop	0.09	3.20e-03	HADHB	hydroxyacyl-CoA dehydrogenase triflu
-0.76	3.11e-04	CHAF1A	chromatin assembly factor 1 subunit	0.07	3.21e-03	SRP68	signal recognition particle 68
-0.31	3.67e-04	KIF22	kinesin family member 22	0.12	3.21e-03	DDOST	dolichyl-diphosphooligosaccharide--
-0.1	3.67e-04	BAZ1B	bromodomain adjacent to zinc finger	0.85	3.38e-03	PDIA5	protein disulfide isomerase family
-0.83	3.78e-04	CKAP2	cytoskeleton associated protein 2	0.85	3.47e-03	LPCAT2	lysophosphatidylcholine acyltransfe
-1.11	3.97e-04	CCNA2	cyclin A2	0.44	3.53e-03	ERLIN2	ER lipid raft associated 2
-0.54	4.04e-04	GUK1	guanylate kinase 1	1.03	3.57e-03	PLEK	pleckstrin
-0.99	4.64e-04	GTSE1	G2 and S-phase expressed 1	0.08	3.67e-03	ARPC2	actin related protein 2/3 complex s
-0.85	5.16e-04	CIT	citron rho-interacting serine/threo	0.79	3.77e-03	MNDA	myeloid cell nuclear differentiatio
-0.82	5.78e-04	NSD2	nuclear receptor binding SET domain	0.28	3.77e-03	SLC38A10	solute carrier family 38 member 10
0.05	6.34e-04	VPS72	vesicular protein sorting 72 homolog	0.00	4.01e-03	HADHA	hydroxyacyl-CoA dehydrogenase triflu

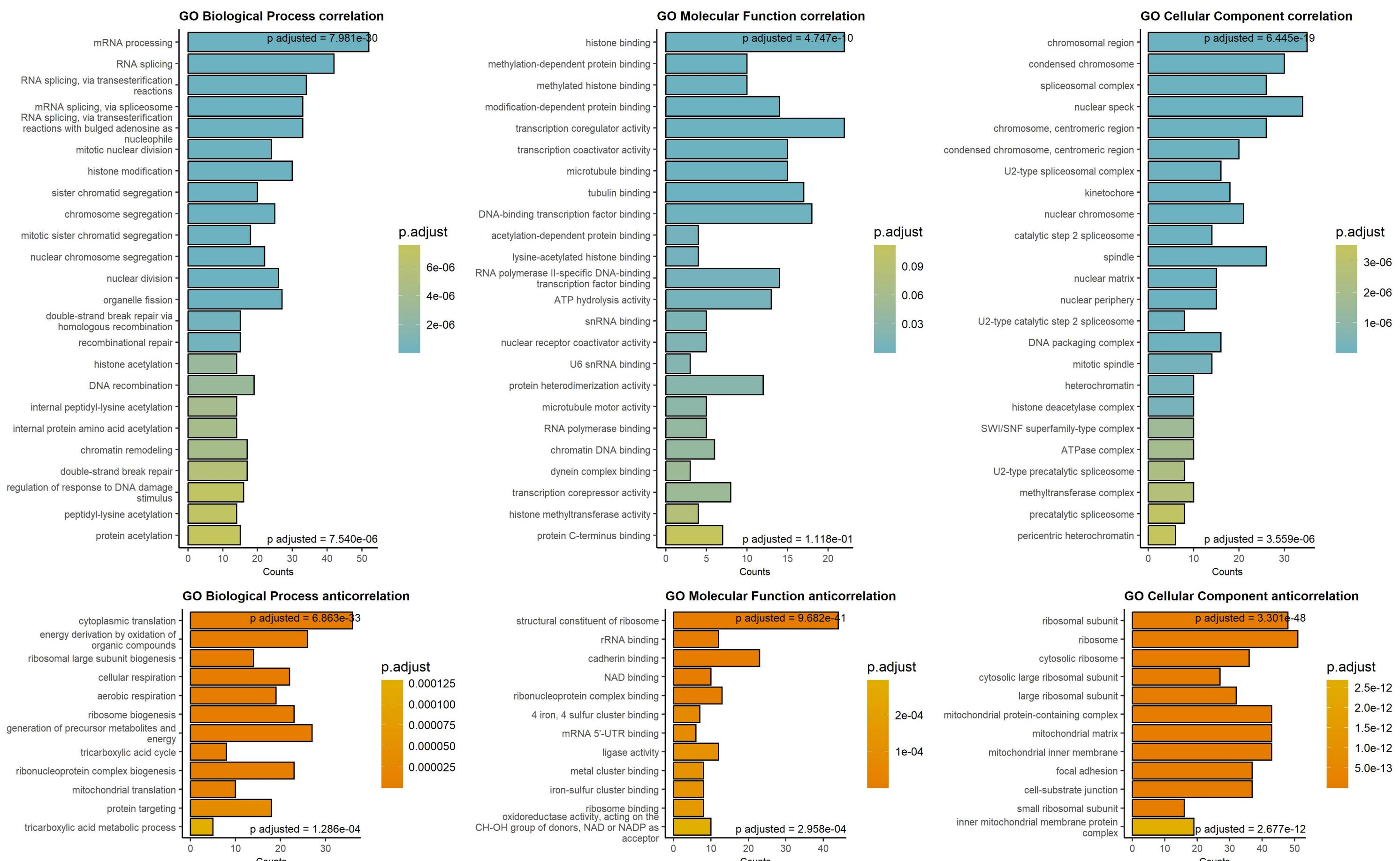


Sorted by p values!

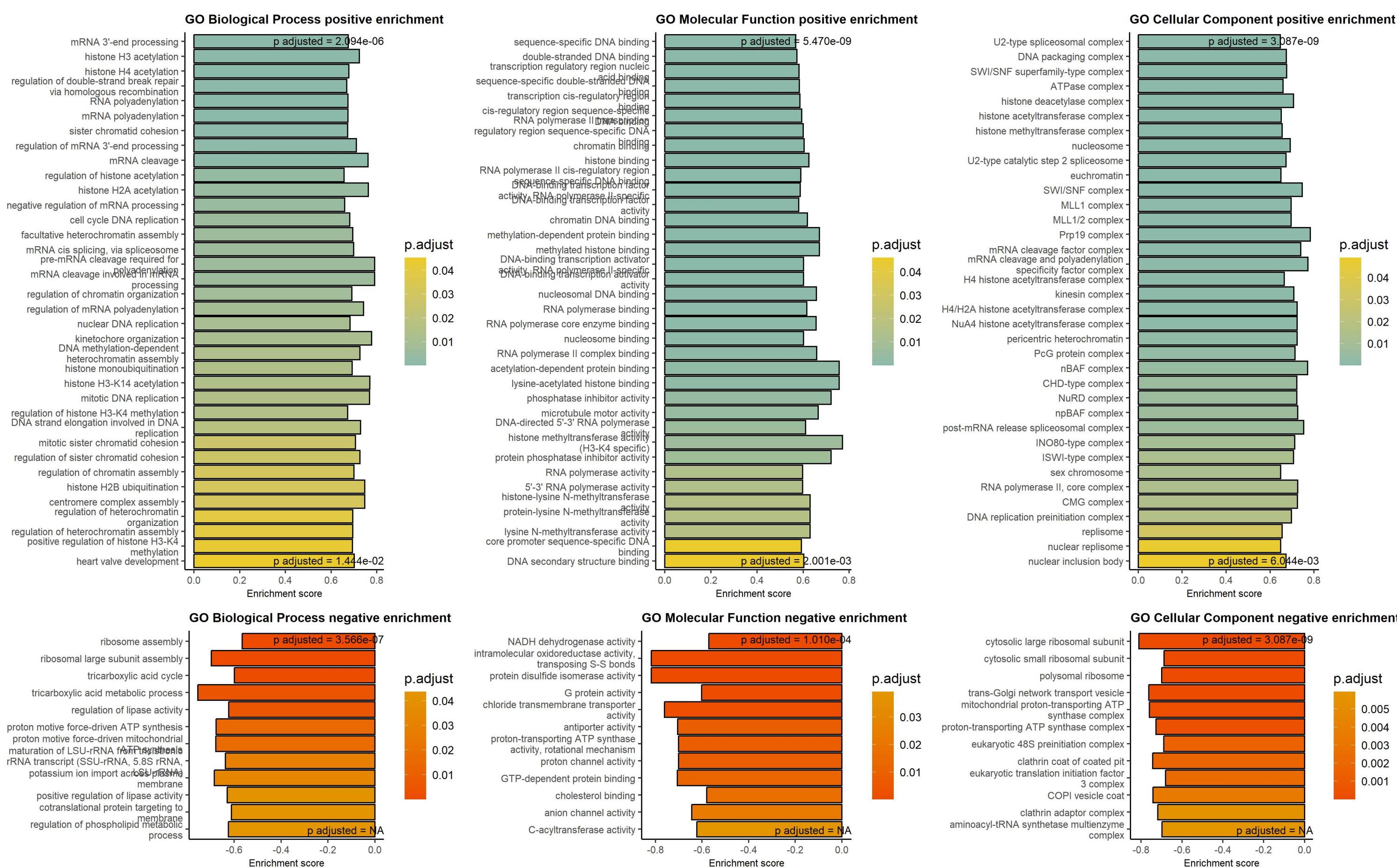
Downregulated in solid cancers at low/absent CDCA5 Upregulated in solid cancers at low/absent CDCA5

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.1	4.18e-48	INCENP	inner centromere protein	0.2	4.16e-18	RRBP1	ribosome binding protein 1
-0.89	1.64e-47	KIF22	kinesin family member 22	0.06	4.95e-17	CLTC	clathrin heavy chain
-1.21	3.45e-38	NUSAP1	nucleolar and spindle associated pr	0.82	2.18e-16	DAB2	DAB adaptor protein 2
-0.02	1.93e-34	H4C1	H4 clustered histone 1	0.13	1.73e-15	GNS	glucosamine (N-acetyl)-6-sulfatase
-0.67	8.49e-33	CHAF1B	chromatin assembly factor 1 subunit	0.76	6.11e-15	CPQ	carboxypeptidase Q
-0.99	4.97e-32	ATAD2	ATPase family AAA domain containing	0.07	9.67e-15	P4HB	prolyl 4-hydroxylase subunit beta
-0.46	5.11e-32	TPX2	TPX2 microtubule nucleation factor	0.09	4.97e-14	MYL6	myosin light chain 6
-1.06	1.50e-31	CKAP2	cytoskeleton associated protein 2	0.12	1.46e-13	CALU	calumenin
-1.04	1.50e-31	AURKB	aurora kinase B	0.7	1.84e-13	SMPD1	sphingomyelin phosphodiesterase 1
-0.83	2.44e-31	CDCA8	cell division cycle associated 8	0.13	3.94e-13	CTSD	cathepsin D
-0.94	1.01e-28	KIFC1	kinesin family member C1	0.46	1.08e-12	CTSA	cathepsin A
-0.99	4.77e-28	KIF11	kinesin family member 11	0.1	1.79e-12	AP2A1	adaptor related protein complex 2 s
-0.09	5.61e-26	WBP11	WW domain binding protein 11	0.73	3.00e-12	RPS27L	ribosomal protein S27 like
-0.86	1.16e-24	EP400	E1A binding protein p400	0.07	4.11e-12	VDAC1	voltage dependent anion channel 1
-0.08	3.76e-24	SNW1	SNW domain containing 1	0.24	6.80e-12	HEXB	hexosaminidase subunit beta
-0.99	8.70e-24	HELLS	helicase, lymphoid specific	0.16	2.42e-11	HIBADH	3-hydroxyisobutyrate dehydrogenase
-0.11	1.11e-23	RFC4	replication factor C subunit 4	0.75	2.80e-11	FAM114A1	family with sequence similarity 114
-0.92	1.29e-23	CHAF1A	chromatin assembly factor 1 subunit	0.1	3.02e-11	ACTN4	actinin alpha 4
-0.96	2.10e-23	SAMD1	sterile alpha motif domain containi	0.07	3.34e-11	TMED9	transmembrane p24 trafficking prote
-0.63	3.56e-23	BIRC5	baculoviral IAP repeat containing 5	0.34	5.67e-11	PLIN3	perilipin 3
-0.9	5.84e-23	PRC1	protein regulator of cytokinesis 1	0.07	1.94e-10	SSR1	signal sequence receptor subunit 1
-0.08	6.05e-22	SMC3	structural maintenance of chromosom	0.69	2.04e-10	RBPMS	RNA binding protein, mRNA processin
-0.9	1.10e-21	C5orf24	chromosome 5 open reading frame 24	0.08	2.31e-10	MYDGF	myeloid derived growth factor
-0.09	1.92e-21	RAD21	RAD21 cohesin complex component	0.08	2.57e-10	IQGAP1	IQ motif containing GTPase activati
-0.05	4.01e-21	SF1	splicing factor 1	0.64	2.97e-10	PARP4	poly(ADP-ribose) polymerase family
-0.07	8.60e-21	SMC1A	structural maintenance of chromosom	0.68	3.85e-10	HSPG2	heparan sulfate proteoglycan 2
-0.08	1.03e-20	TMPO	thymopoietin	0.06	4.01e-10	RAB1A	RAB1A, member RAS oncogene family
-0.43	6.17e-20	UHRF1	ubiquitin like with PHD and ring fi	0.72	4.54e-10	CTS1	cathepsin L
-0.84	6.18e-20	CENPF	centromere protein F	0.24	4.54e-10	CTSB	cathepsin B
-0.92	6.34e-20	CCNB1	cyclin B1	0.72	4.		

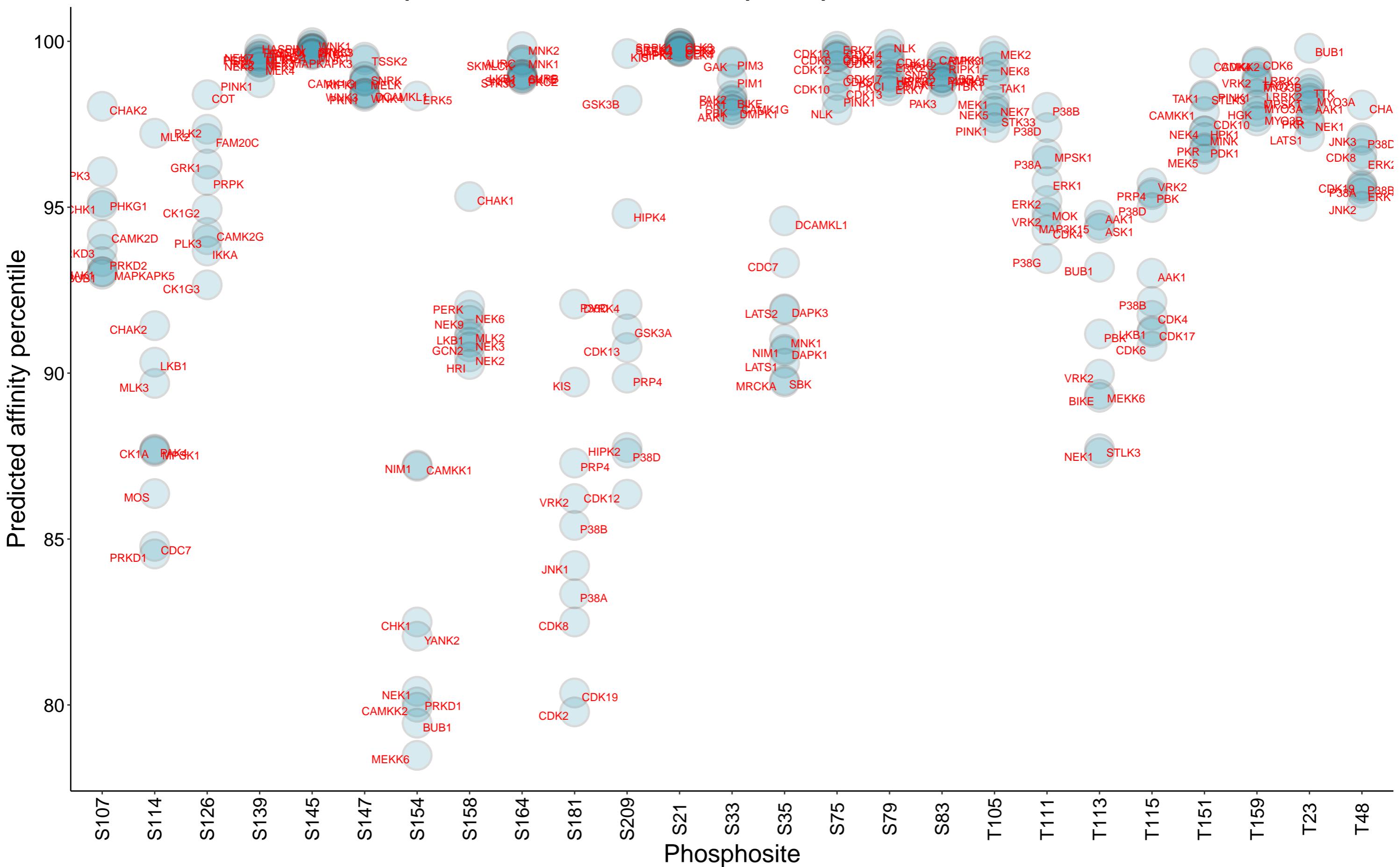
Top 250 correlation coefficients overrepresentation, CDCA5 protein, DB1



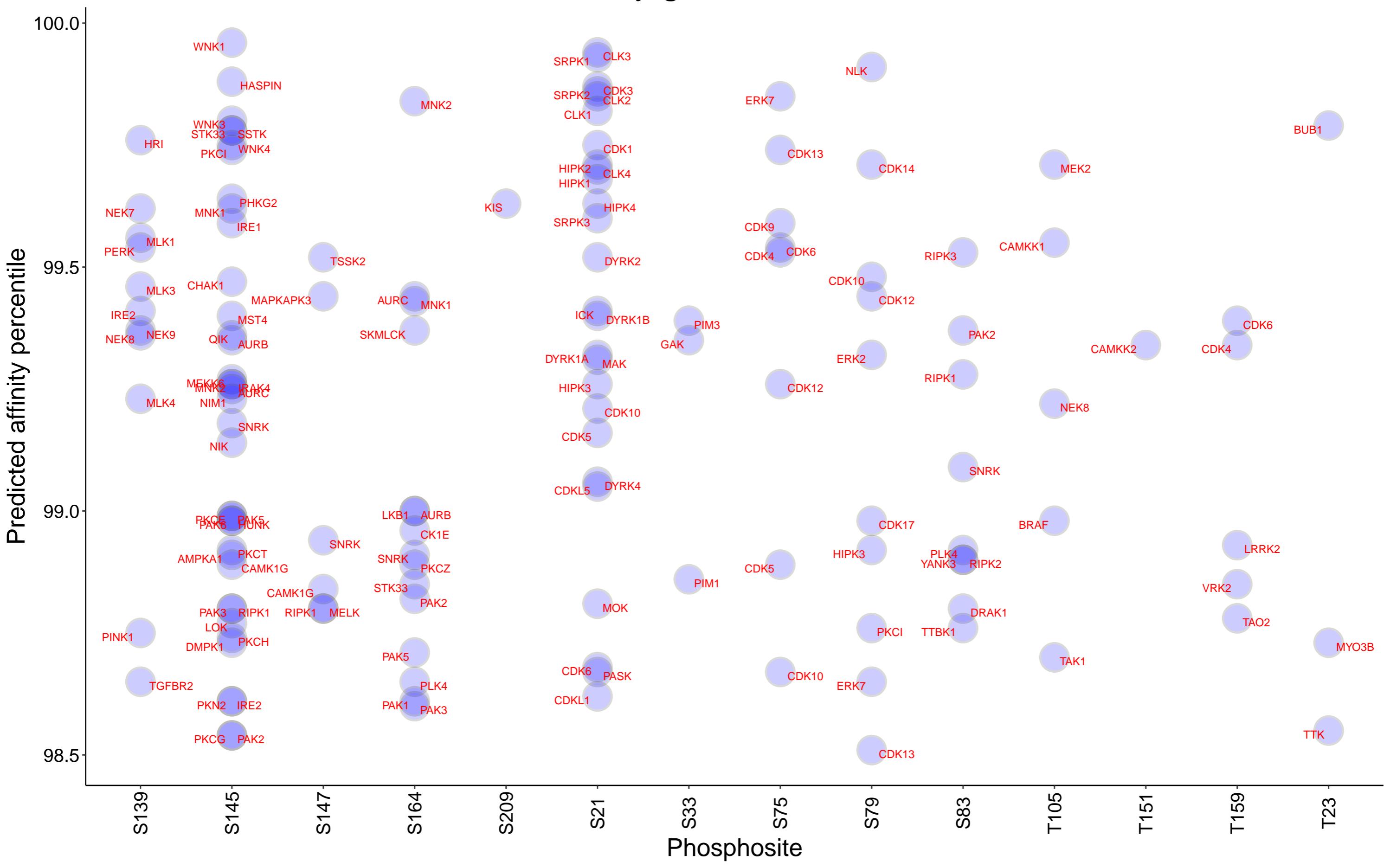
Gene Set Enrichment analysis on protein correlation coefficients, CDCA5 protein, DB1



Top 10 kinases for each phosphosite in CDCA5



Kinases with affinity greater than 98.5% to CDCA5



Top 15 positive correlation coefficients for CDCA5 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

