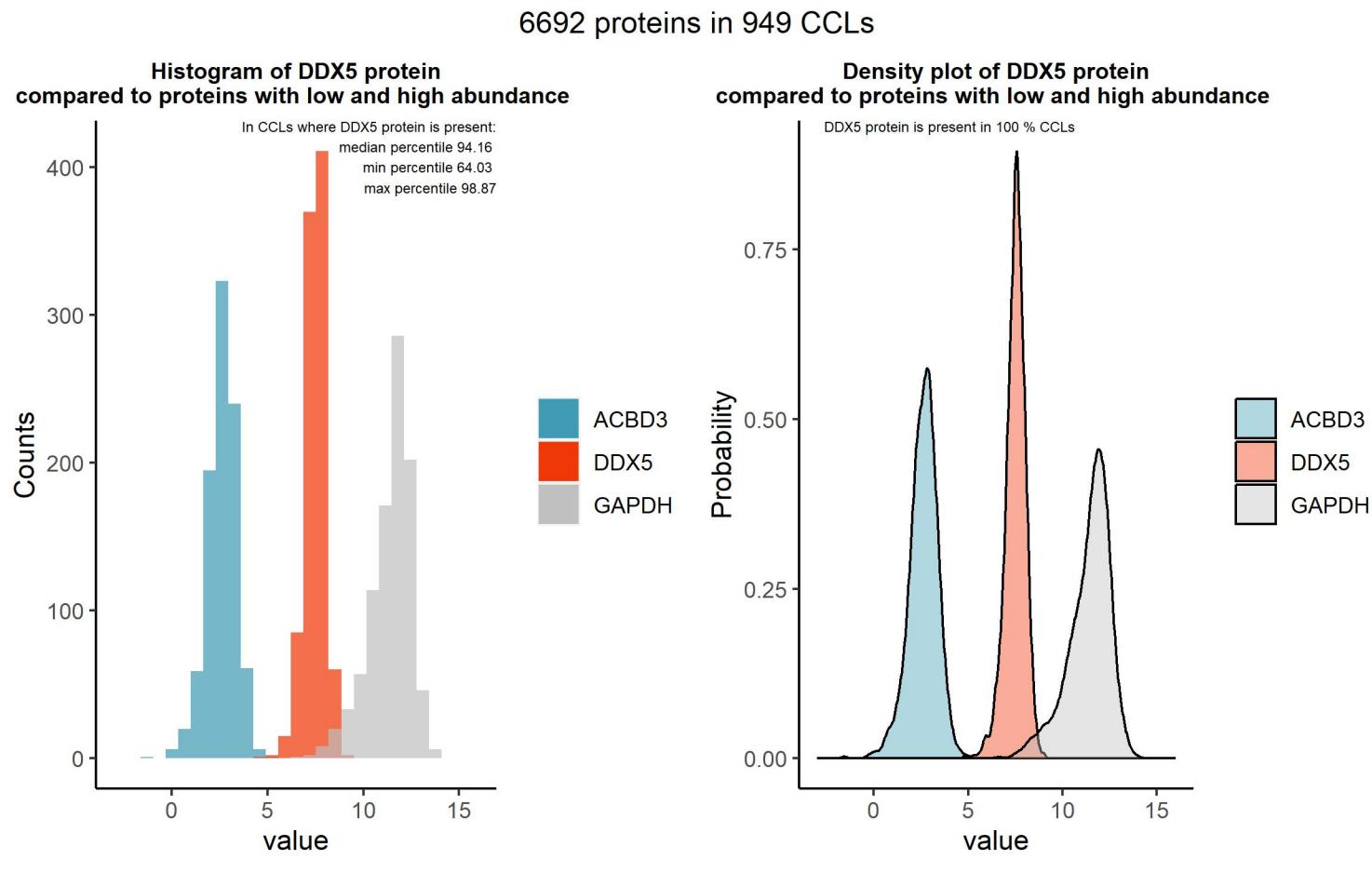


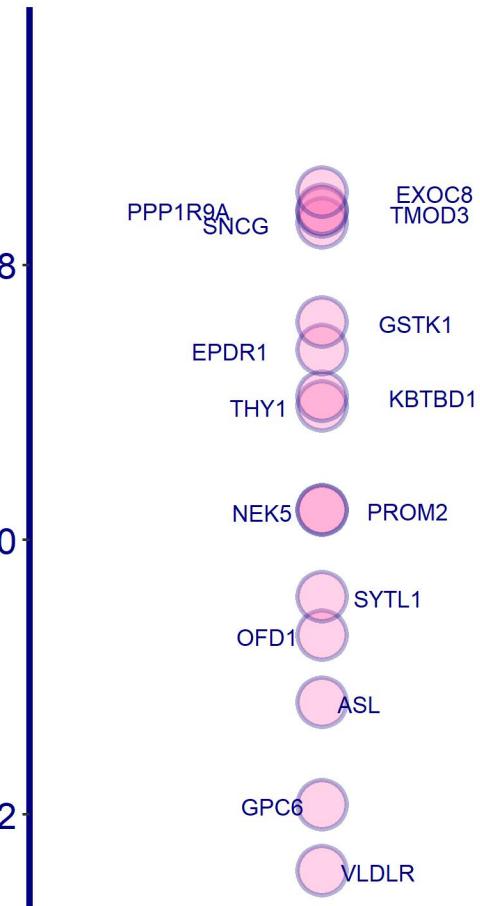
DDX5

Protein name: DDX5 ; UNIPROT: P17844 ; Gene name: DEAD-box helicase 5
 Ligandable: NA ; Ligandable_by_Chem: Yes ; Is_enzyme: Yes (<https://cansar.ai/>)

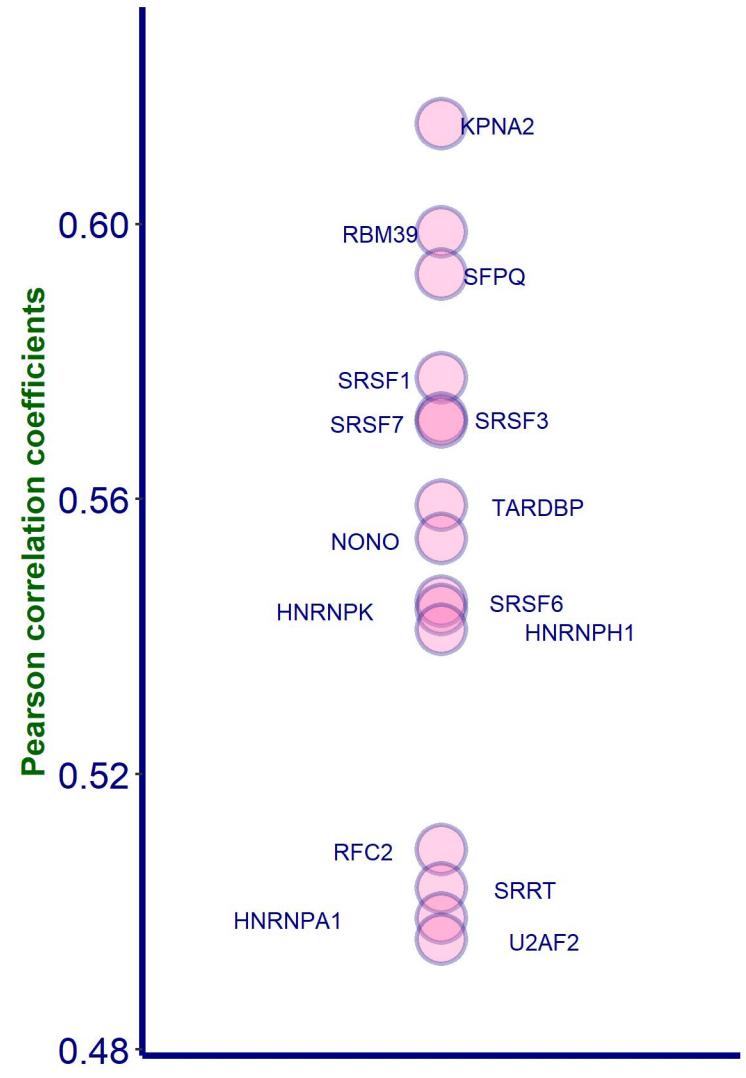
Sanger Institute Protein Database 1 (DB1), protein presence is certain



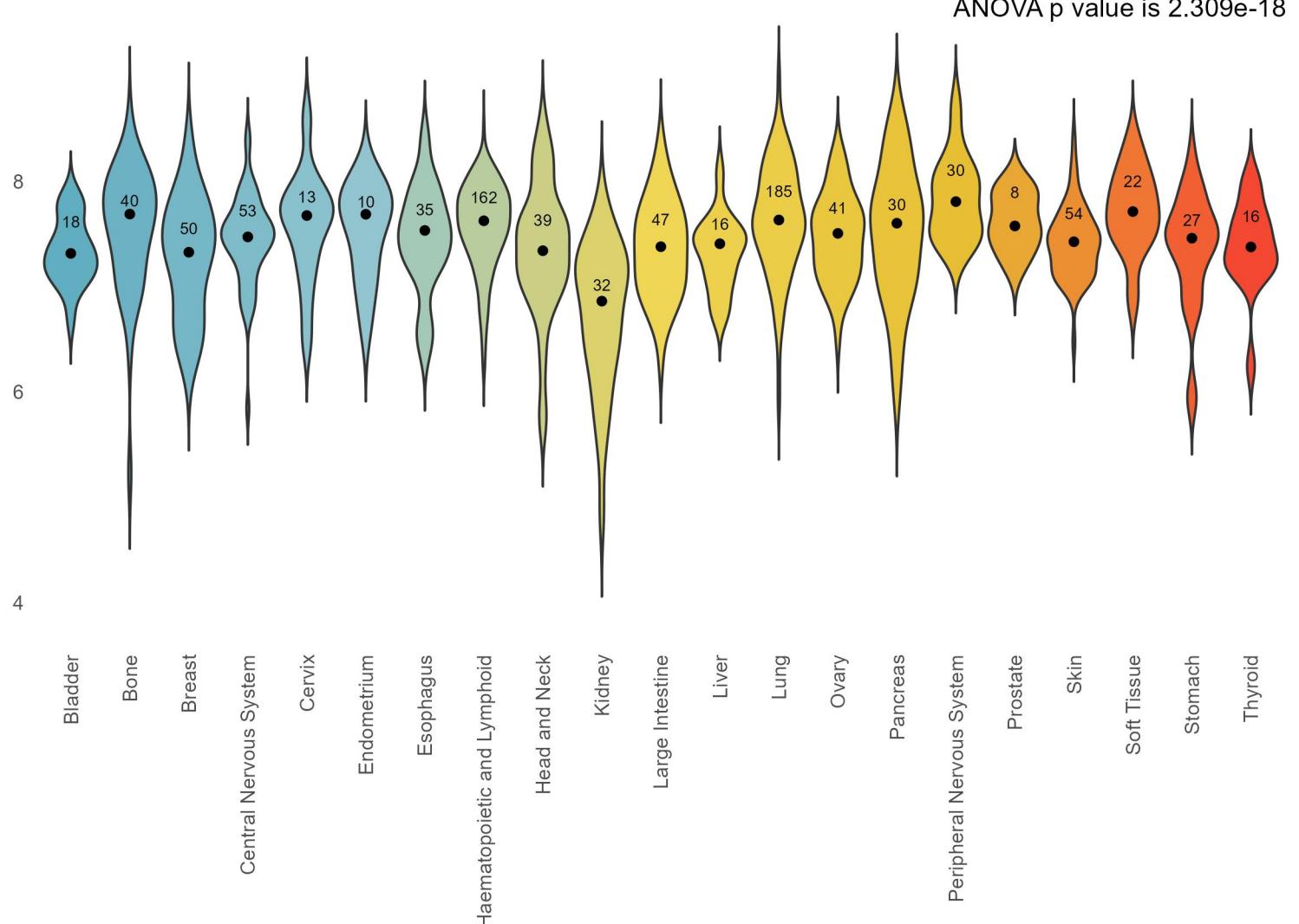
Top negative correlations of DDX5 protein, DB1



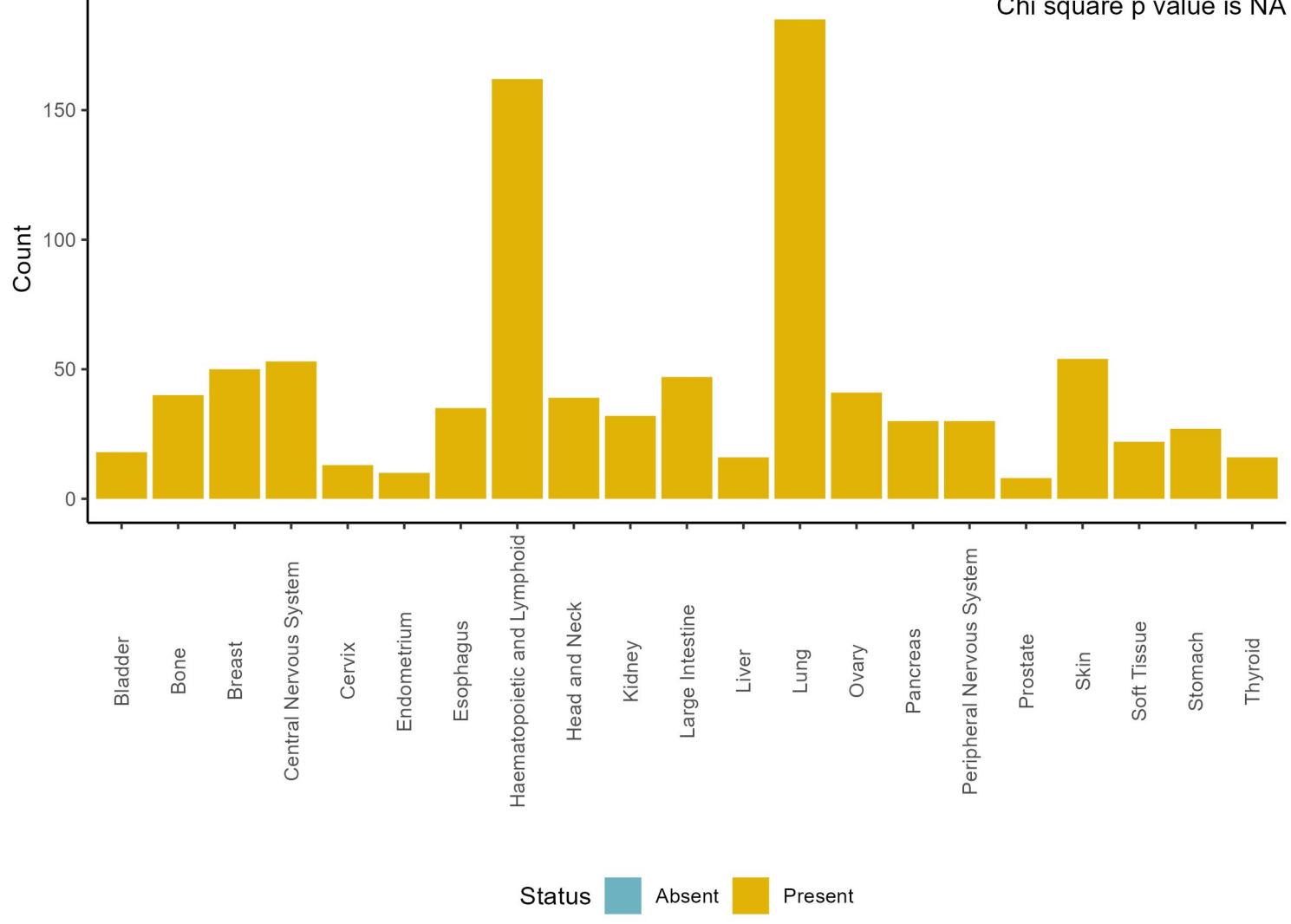
Top positive correlations of DDX5 protein, DB1



Amount of DDX5 protein, number of CCLs where it is present by tissue, DB1



Present and absent DDX5 protein counts by tissue, DB1

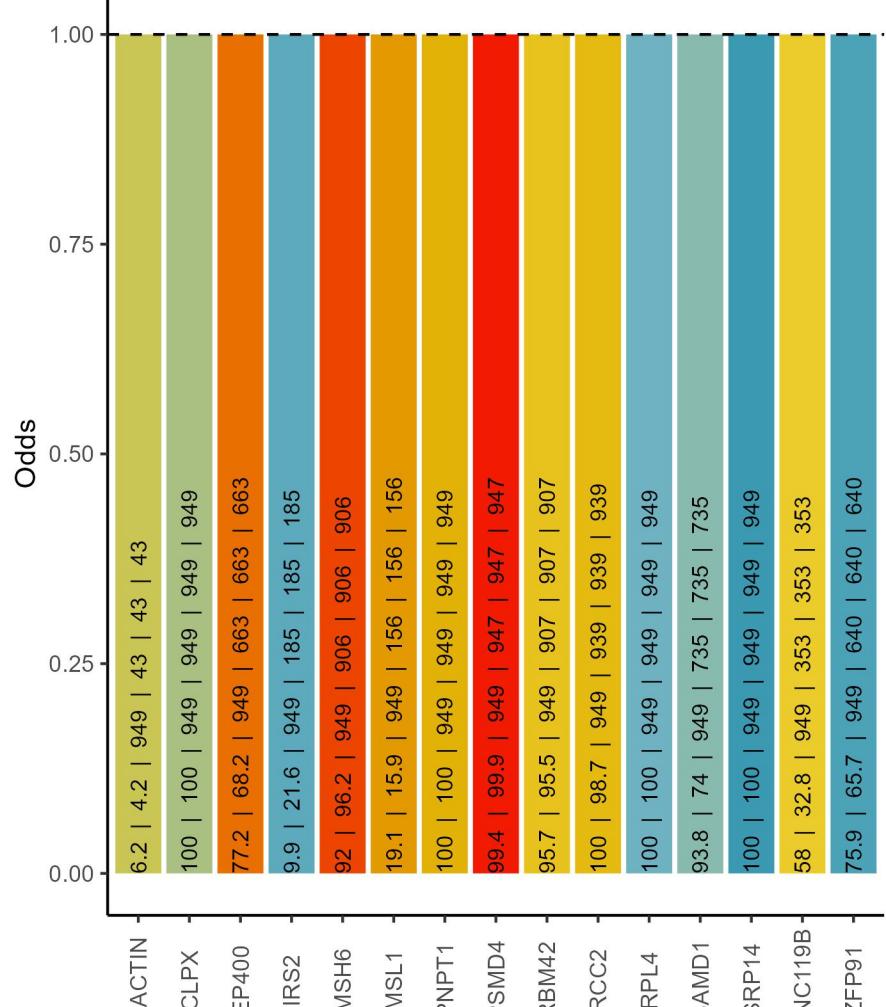


Cooccurrence with DDX5 protein, DB1

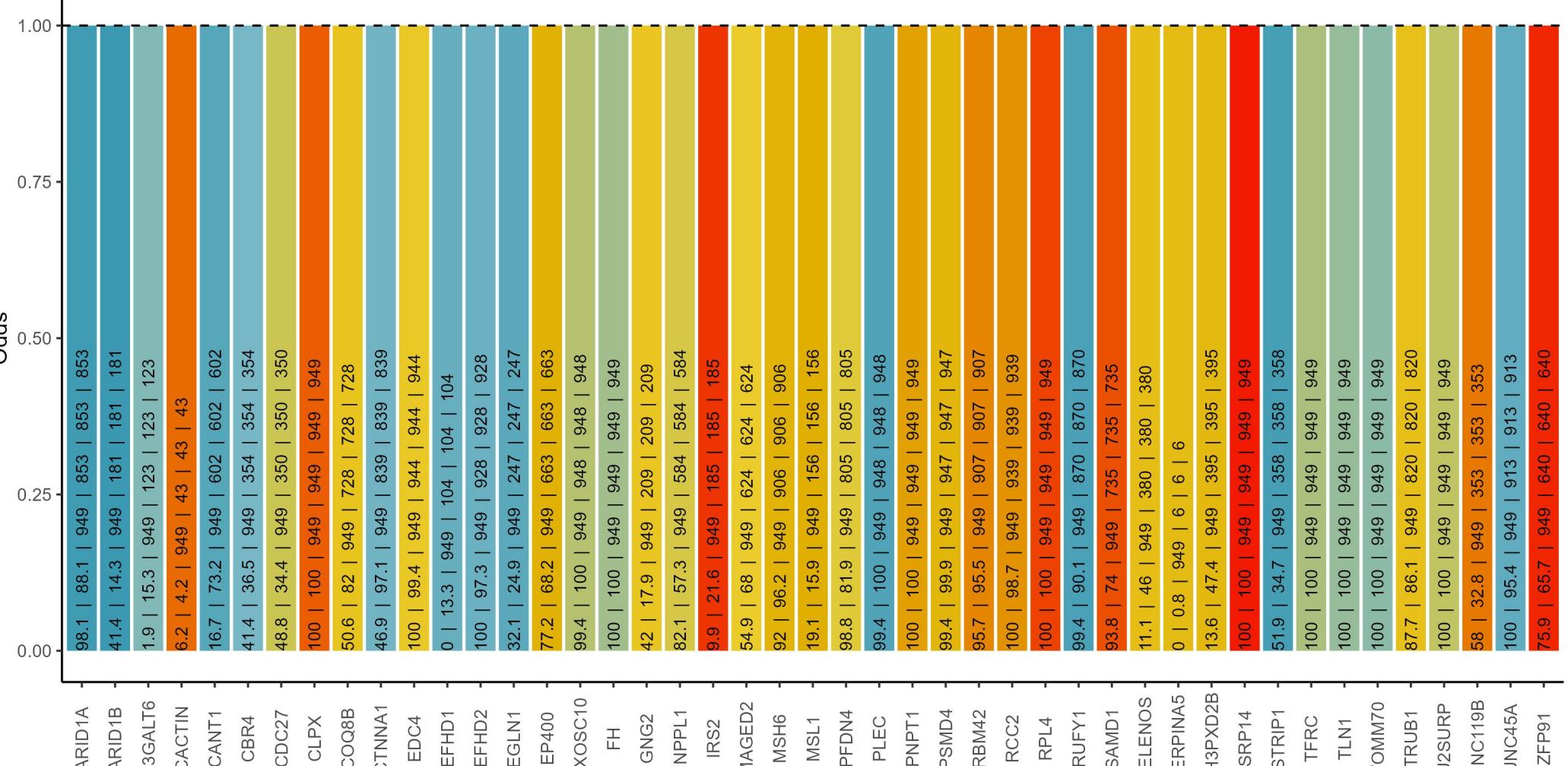
% of DDX5 in blood cancers: 100 ; % of DDX5 in solid cancers: 100

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of DDX5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

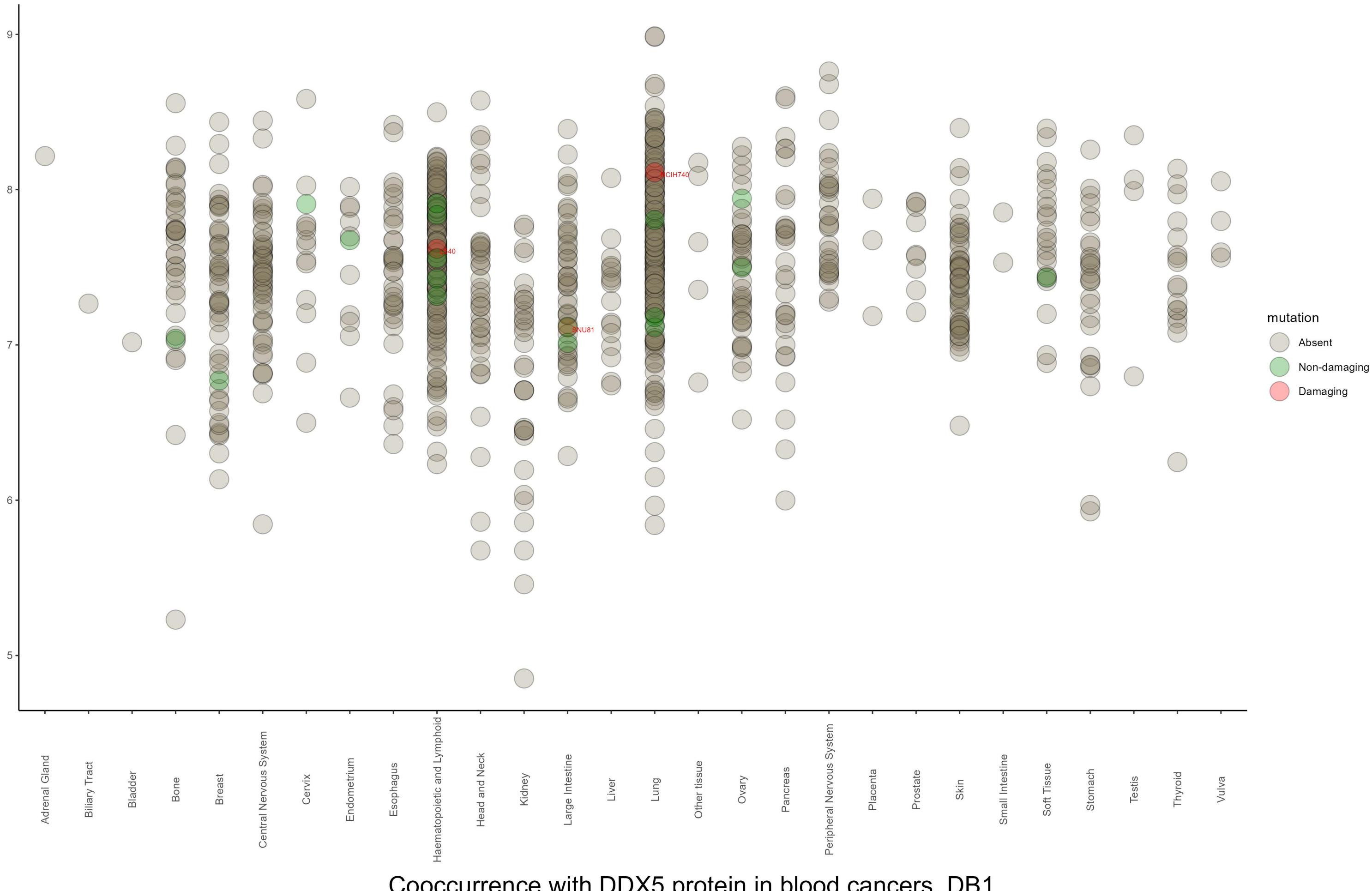
Negative cooccurrence



Positive cooccurrence



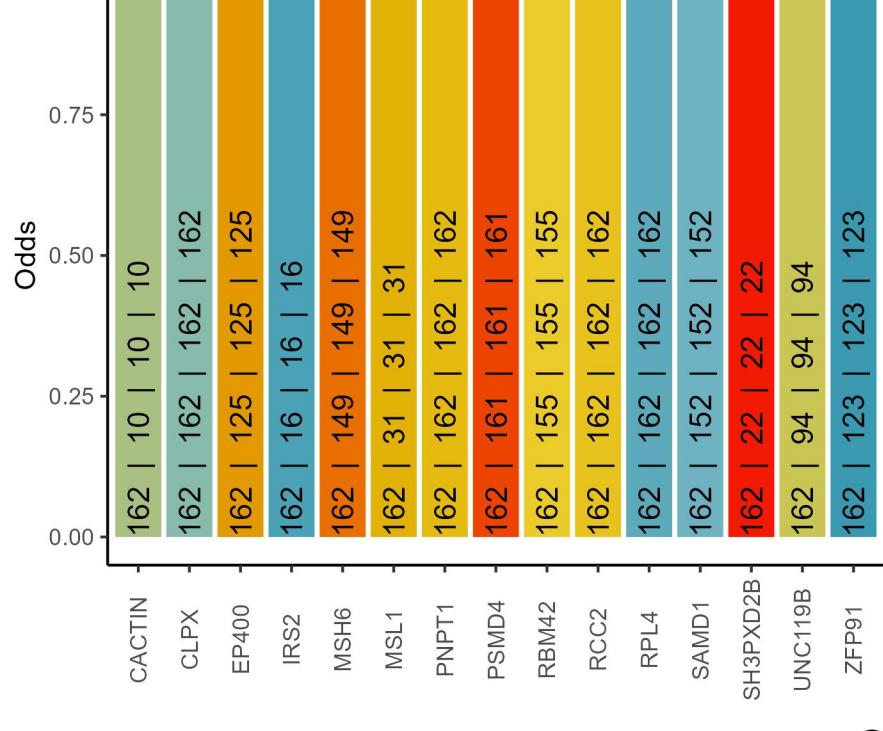
Amount of DDX5 protein and mutation status by tissue, DB1



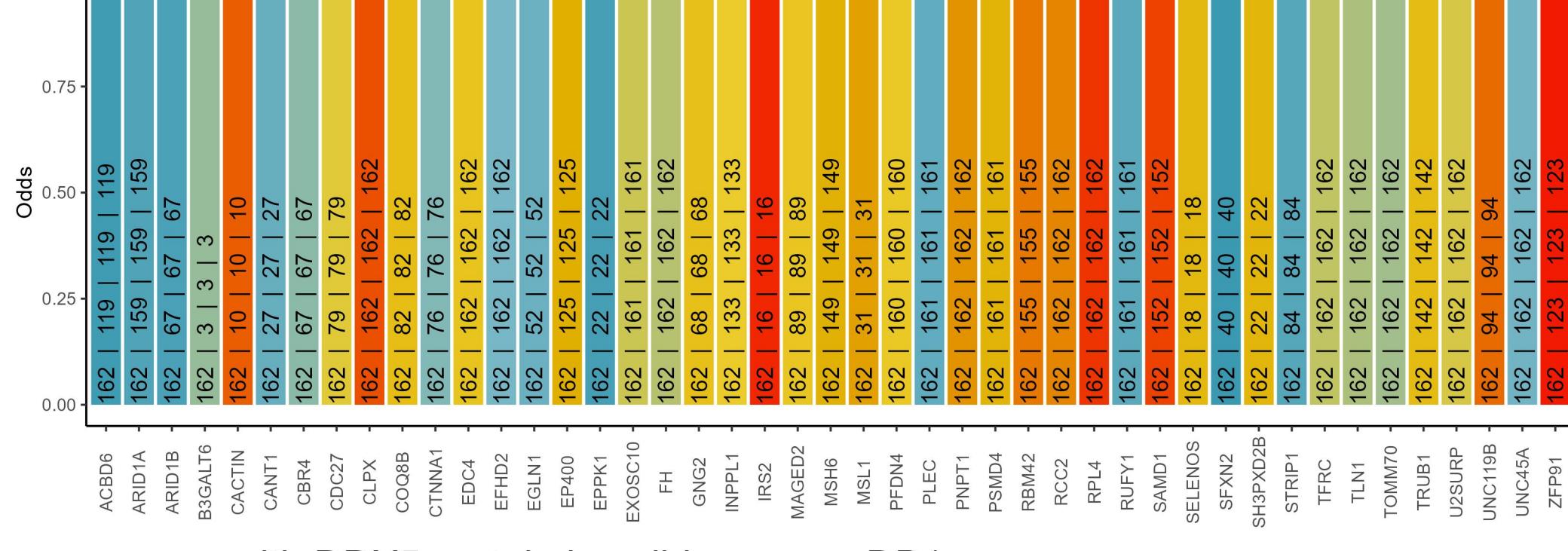
Cooccurrence with DDX5 protein in blood cancers, DB1

The text in the bars: incidence of DDX5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



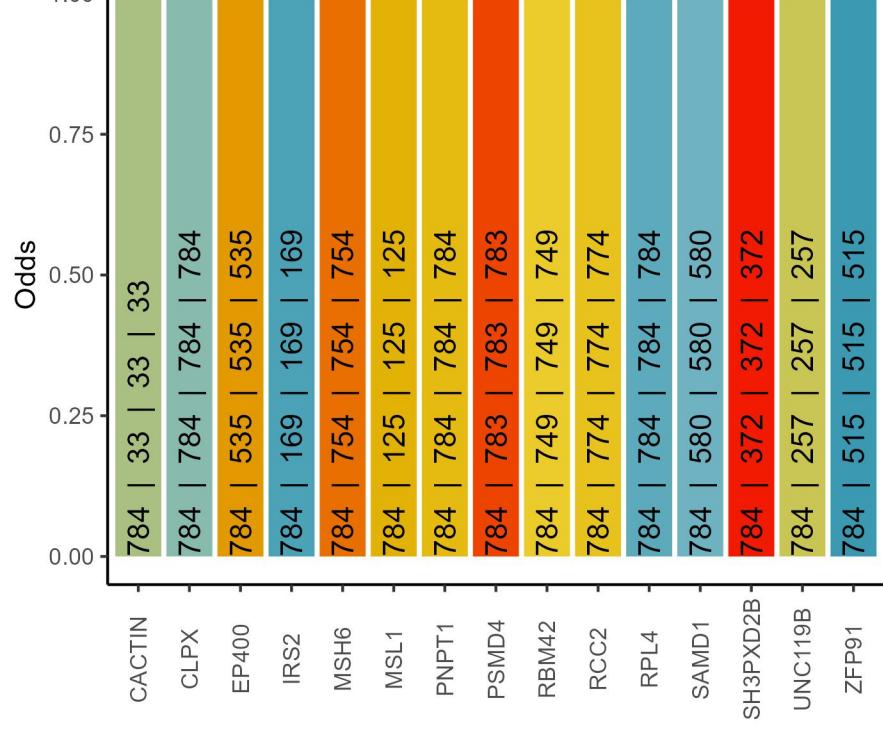
Positive cooccurrence



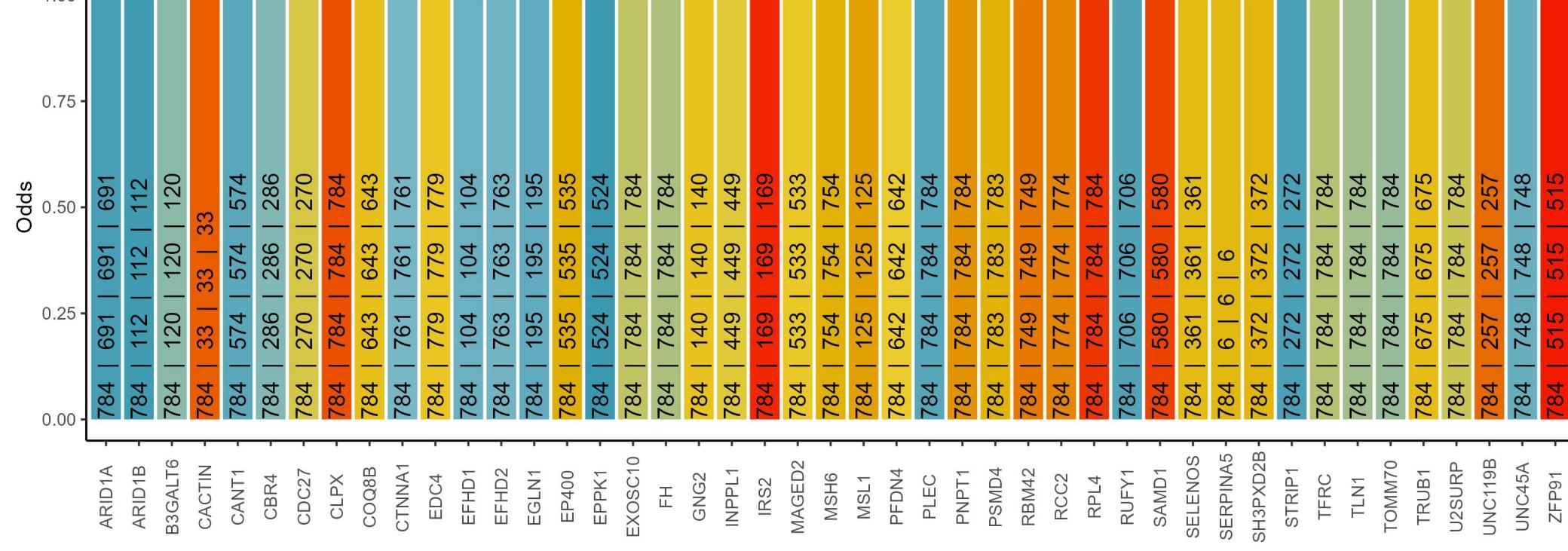
Cooccurrence with DDX5 protein in solid cancers, DB1

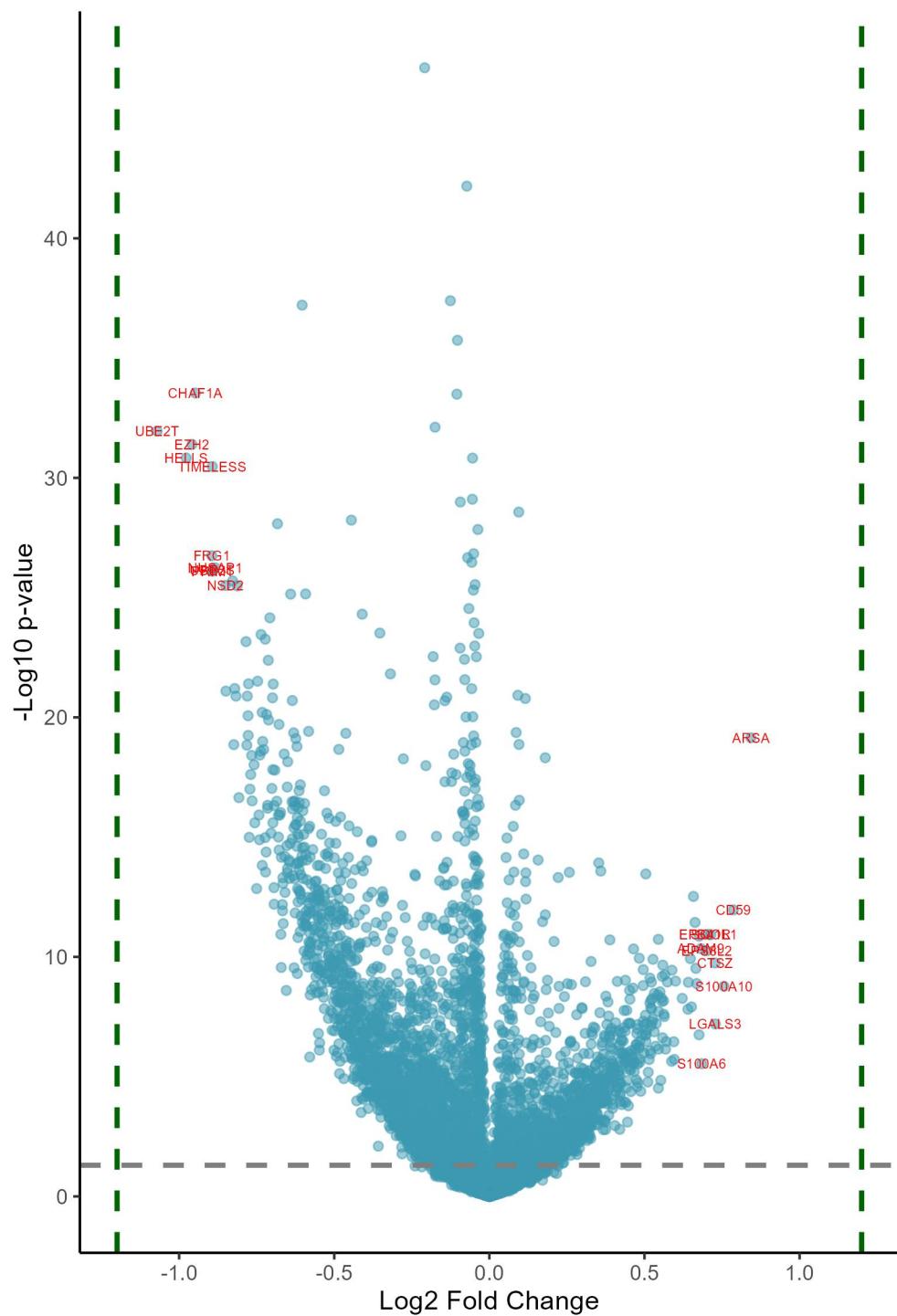
The text in the bars: incidence of DDX5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



Positive cooccurrence

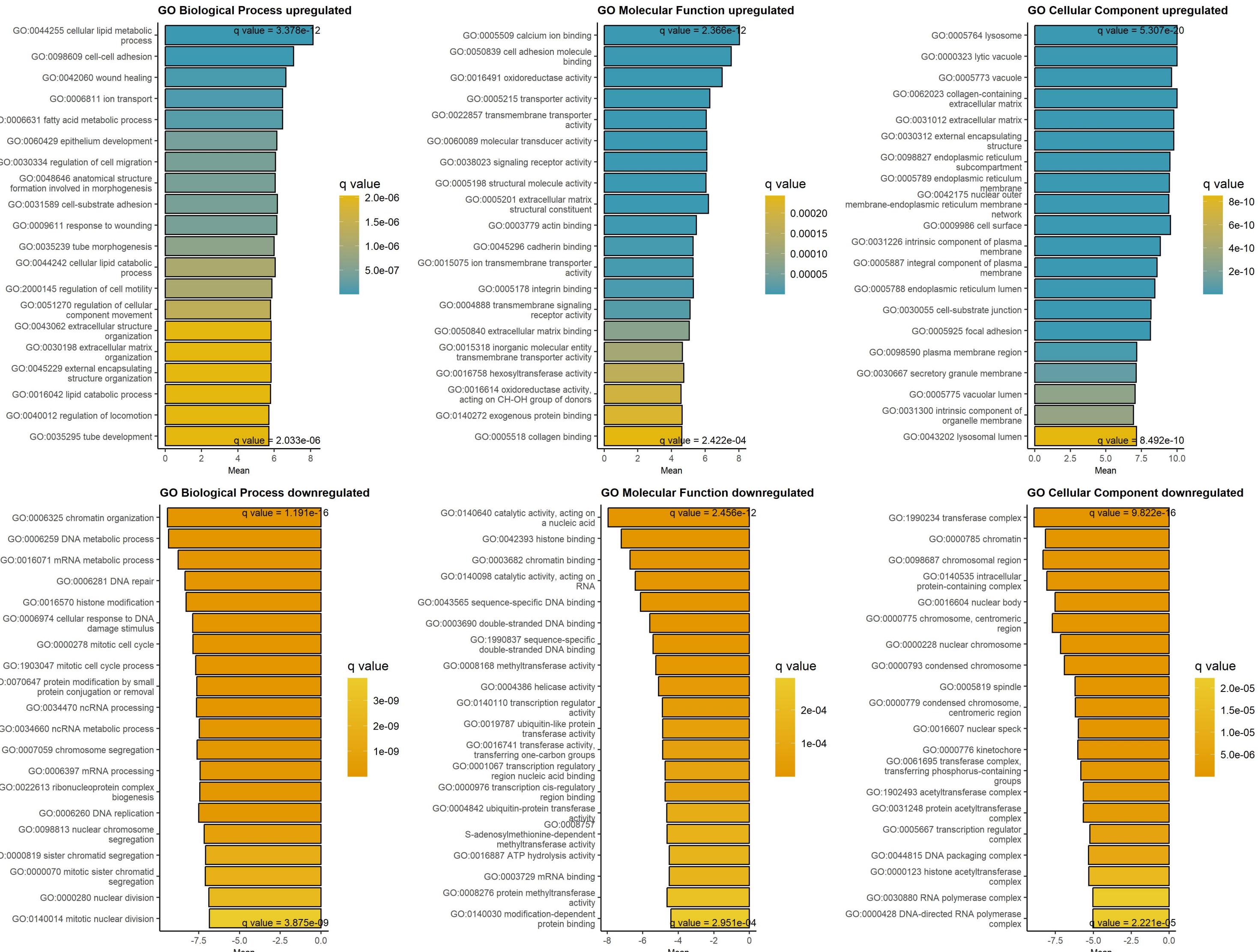




Downregulated at low/absent DDX5 Upregulated at low/absent DDX5

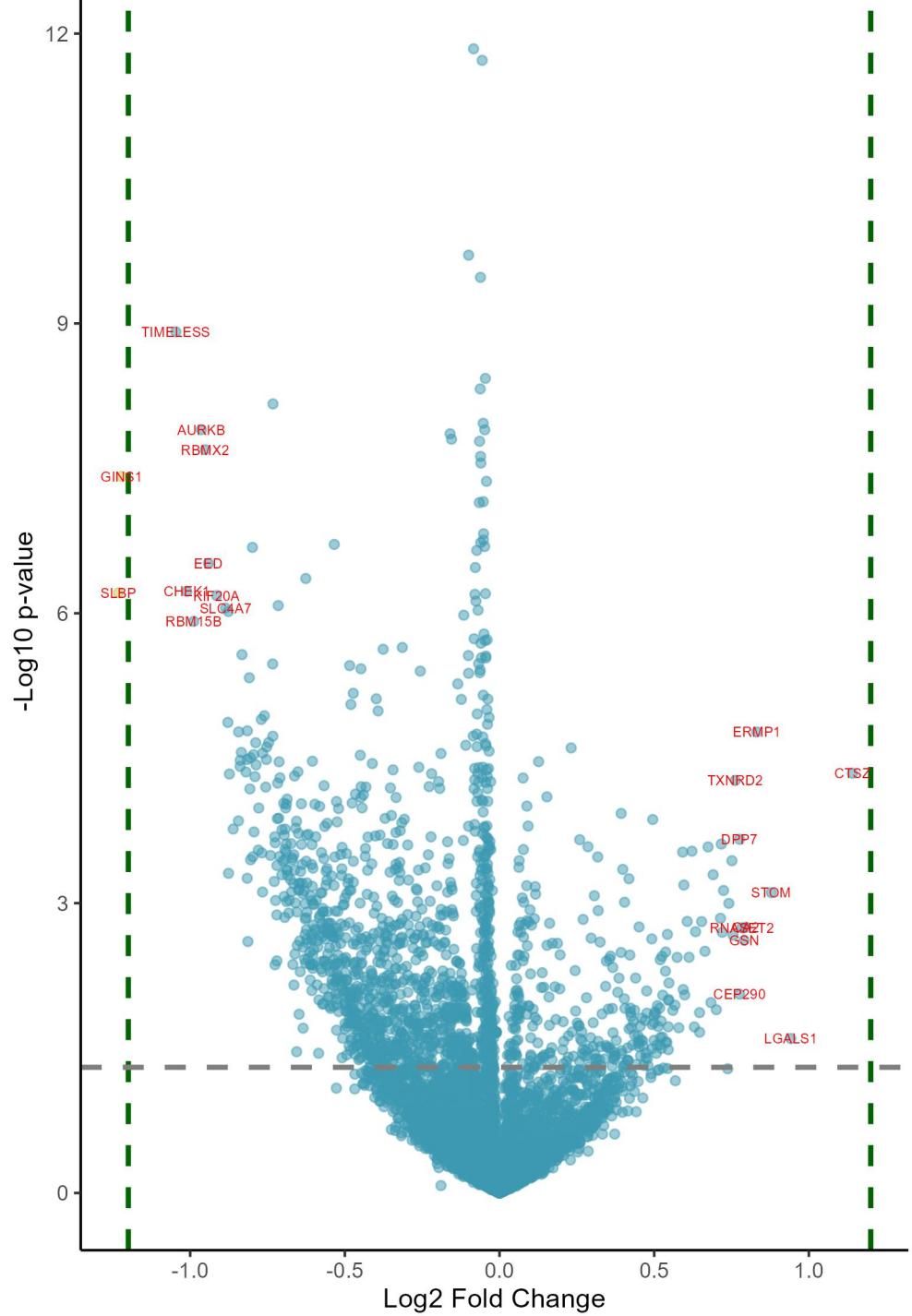
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.07	7.44e-30	UBE2T	ubiquitin conjugating enzyme E2 T	0.84	5.84e-18	ARSA	arylsulfatase A
-0.98	7.67e-29	HELLS	helicase, lymphoid specific	0.79	2.14e-11	CD59	CD59 molecule (CD59 blood group)
-0.96	2.43e-29	EZH2	enhancer of zeste 2 polycomb repres	0.76	1.66e-08	S100A10	S100 calcium binding protein A10
-0.95	2.67e-31	CHAF1A	chromatin assembly factor 1 subunit	0.73	4.42e-07	LGALS3	galectin 3
-0.89	5.41e-25	FRG1	FSHD region gene 1	0.73	2.22e-09	CTSZ	cathepsin Z
-0.89	1.79e-24	UBE2S	ubiquitin conjugating enzyme E2 S	0.71	1.82e-10	SQOR	sulfide quinone oxidoreductase
-0.89	1.59e-28	TIMELESS	timeless circadian regulator	0.71	1.77e-10	EPB41L1	erythrocyte membrane protein band 4
-0.89	1.97e-24	PRIM1	DNA primase subunit 1	0.7	7.58e-10	EPS8L2	EPS8 like 2
-0.88	1.52e-24	NUSAP1	nucleolar and spindle associated pr	0.68	1.40e-05	S100A6	S100 calcium binding protein A6
-0.85	6.84e-24	NSD2	nuclear receptor binding SET domain	0.68	6.27e-10	ADAM9	ADAM metallopeptidase domain 9
-0.85	9.18e-20	WDHD1	WD repeat and HMG-box DNA binding p	0.68	2.08e-10	RRAS	RAS related
-0.83	4.78e-24	AURKB	aurora kinase B	0.68	1.13e-06	CAVIN1	caveolae associated protein 1
-0.82	1.05e-17	BRD2	bromodomain containing 2	0.67	1.33e-08	RHOC	ras homolog family member C
-0.82	7.39e-20	KIF2C	kinesin family member 2C	0.67	3.57e-09	IGFBP7	insulin like growth factor binding
-0.82	1.42e-19	YRDC	yrdC N6-threonylcarbamoyltransferas	0.66	6.20e-11	BET1	Bet1 golgi vesicular membra traff
-0.81	6.91e-24	PRIM2	DNA primase subunit 2	0.66	6.58e-12	TRIOBP	TRIO and F-actin binding protein
-0.81	1.19e-15	PCLAF	PCNA clamp associated factor	0.65	9.85e-08	S100A16	S100 calcium binding protein A16
-0.78	1.06e-21	RRM2	ribonucleotide reductase regulatory	0.65	1.53e-09	SLC12A9	solute carrier family 12 member 9
-0.78	1.08e-17	NDC80	NDC80 kinetochore complex component	0.64	1.20e-08	NCEH1	neutral cholesterol ester hydrolase
-0.78	1.42e-19	GNL3L	G protein nucleolar 3 like	0.64	1.21e-07	NT5E	5'-nucleotidase ecto
-0.78	8.12e-19	UCK2	uridine-cytidine kinase 2	0.62	4.65e-08	STOM	stomatin
-0.78	4.78e-18	UBE2C	ubiquitin conjugating enzyme E2 C	0.6	1.09e-08	EPHX1	epoxide hydrolase 1
-0.78	4.89e-20	PCF11	PCF11 cleavage and polyadenylation	0.6	9.67e-06	ITGA3	integrin subunit alpha 3
-0.77	3.67e-14	PSME3IP1	proteasome activator subunit 3 inte	0.59	2.07e-06	GPRC5A	G protein-coupled receptor class C
-0.77	5.40e-16	DAXX	death domain associated protein	0.59	4.15e-09	SERPINE2	serpin family E member 2
-0.77	1.47e-16	CCNB1	cyclin B1	0.59	1.14e-05	CD44	CD44 molecule (Indian blood group)
-0.77	2.63e-17	POLA2	DNA polymerase alpha 2, accessory s	0.57	1.17e-08	MVP	major vault protein
-0.76	1.57e-15	ZNF593	zinc finger protein 593	0.57	2.04e-06	CAVIN3	caveolae associated protein 3
-0.76	6.13e-17	SSU72	SSU72 homolog, RNA polymerase II CT	0.57	3.91e-06	TGM2	transglutaminase 2

GAGE analysis on upregulated and downregulated proteins at low/absent DDX5 protein, DB1



Differentially expressed proteins in blood cancers at absence/low amount of DDX5 , DB1

p-value < 0.05 & logFC > 1.2

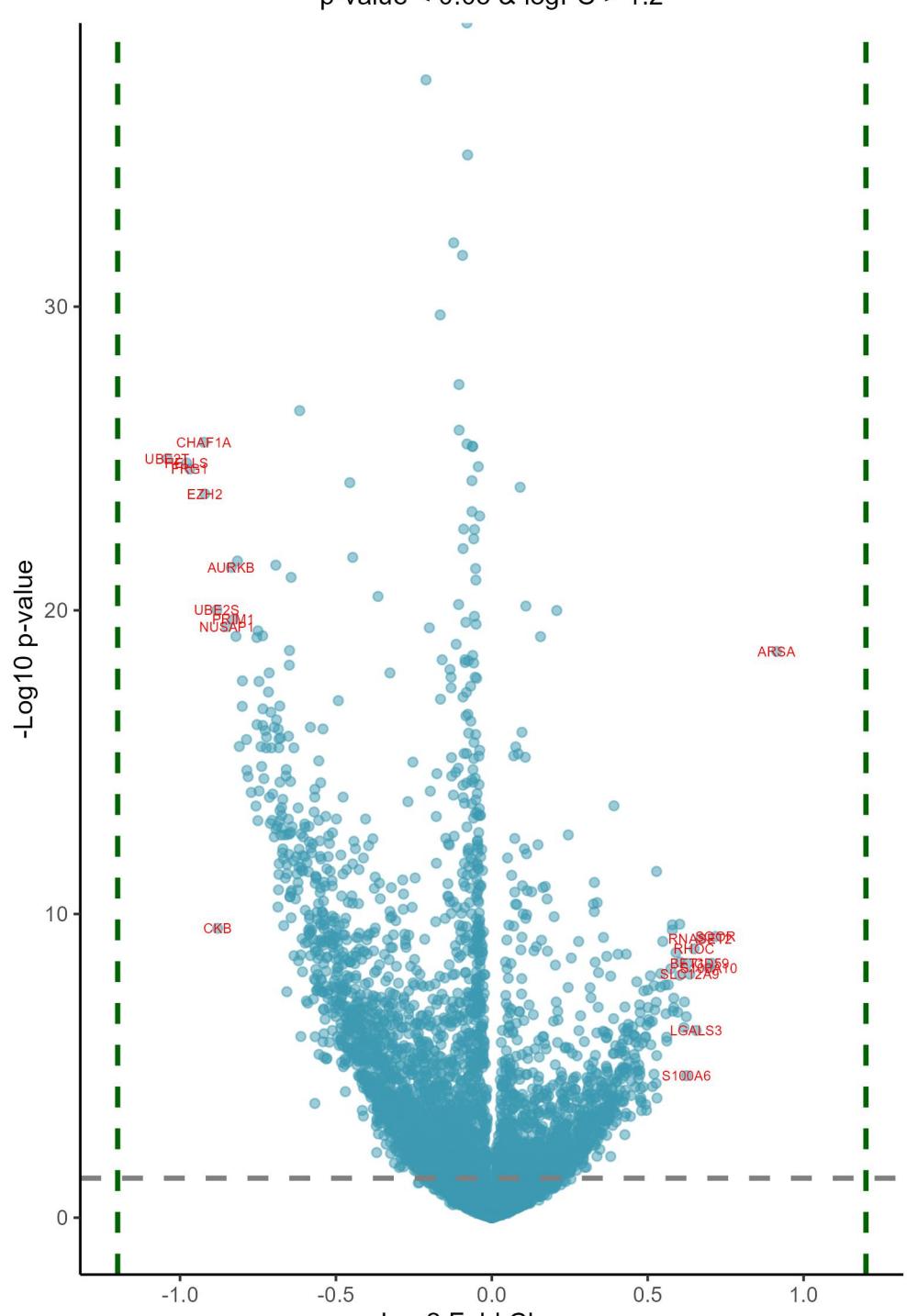


Downregulated in blood cancers at low/absent DDX5 Upregulated in blood cancers at low/absent DDX5

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.23	1.17e-04	SLBP	stem-loop binding protein	1.14	2.47e-03	CTSZ	cathepsin Z
-1.22	1.34e-05	GINS1	GINS complex subunit 1	0.94	9.47e-02	LGALS1	galectin 1
-1.05	1.35e-06	TIMELESS	timeless circadian regulator	0.88	1.45e-02	STOM	stomatin
-1.01	1.17e-04	CHEK1	checkpoint kinase 1	0.83	1.36e-03	ERMP1	endoplasmic reticulum metallopeptid
-0.99	1.83e-04	RBM15B	RNA binding motif protein 15B	0.8	2.48e-02	CA2	carbonic anhydrase 2
-0.96	6.99e-06	AURKB	aurora kinase B	0.79	2.95e-02	GSN	gelsolin
-0.95	8.43e-06	RBMX2	RNA binding motif protein X-linked	0.78	2.49e-02	RNASET2	ribonuclease T2
-0.94	6.75e-05	EED	embryonic ectoderm development	0.78	6.92e-02	CEP290	centrosomal protein 290
-0.91	1.18e-04	KIF20A	kinesin family member 20A	0.78	6.82e-03	DPP7	dipeptidyl peptidase 7
-0.89	1.47e-04	SLC4A7	solute carrier family 4 member 7	0.76	2.70e-03	TXNRD2	thioredoxin reductase 2
-0.88	1.13e-03	RPF1	ribosome production factor 1 homolo	0.76	2.74e-02	CAPN2	calpain 2
-0.88	1.52e-04	PDE6D	phosphodiesterase 6D	0.75	9.05e-03	DUSP23	dual specificity phosphatase 23
-0.88	1.07e-02	GABARAPL2	GABA type A receptor associated pro	0.74	1.72e-02	PYGL	glycogen phosphorylase L
-0.87	2.47e-03	XRCC4	X-ray repair cross complementing 4	0.74	1.59e-01	S100A4	S100 calcium binding protein A4
-0.86	5.90e-03	MAGED2	MAGE family member D2	0.72	1.40e-02	SNTB1	syntrophin beta 1
-0.84	5.23e-03	LEF1	lymphoid enhancer binding factor 1	0.72	2.65e-02	CTSG	cathepsin G
-0.84	1.36e-03	RNF138	ring finger protein 138	0.72	7.32e-03	LYN	LYN proto-oncogene, Src family tyro
-0.84	2.30e-03	ZAP70	zeta chain of T cell receptor assoc	0.71	2.19e-02	SPART	spartin
-0.84	2.11e-03	SNRNP27	small nuclear ribonucleoprotein U4/U	0.7	8.39e-02	ANXA1	annexin A1
-0.83	1.89e-03	CIP2A	cellular inhibitor of PP2A	0.69	1.10e-02	PRNT3	proteinase 3
-0.83	3.41e-04	UBE2C	ubiquitin conjugating enzyme E2 C	0.68	7.88e-02	IGF2BP2	insulin like growth factor 2 mRNA b
-0.82	2.43e-03	RAD18	RAD18 E3 ubiquitin protein ligase	0.67	7.57e-03	ANPEP	alanyl aminopeptidase, membrane
-0.82	1.18e-02	BLM	BLM RecQ like helicase	0.66	3.50e-02	LYZ	lysozyme
-0.82	2.09e-03	NOL9	nucleolar protein 9	0.65	2.30e-02	DTD1	D-aminoacyl-tRNA deacylase 1
-0.82	1.35e-03	CASP2	caspase 2	0.65	8.39e-02	PLP2	proteolipid protein 2
-0.81	3.00e-02	SEPTIN1	septin 1	0.65	8.39e-02	PTMS	parathymosin
-0.81	4.75e-04	MRFAP1	Morf4 family associated protein 1	0.63	2.64e-02	COQ8A	coenzyme Q8A
-0.81	2.97e-03	BRD2	bromodomain containing 2	0.63	8.39e-02	H1-0	H1.0 linker histone
-0.81	2.04e-03	CCNB2	cyclin B2	0.62	8.07e-03	ALG5	ALG5 dolichyl-phosphate beta-glucos

Differentially expressed proteins in solid cancers at absence/low amount of DDX5 , DB1

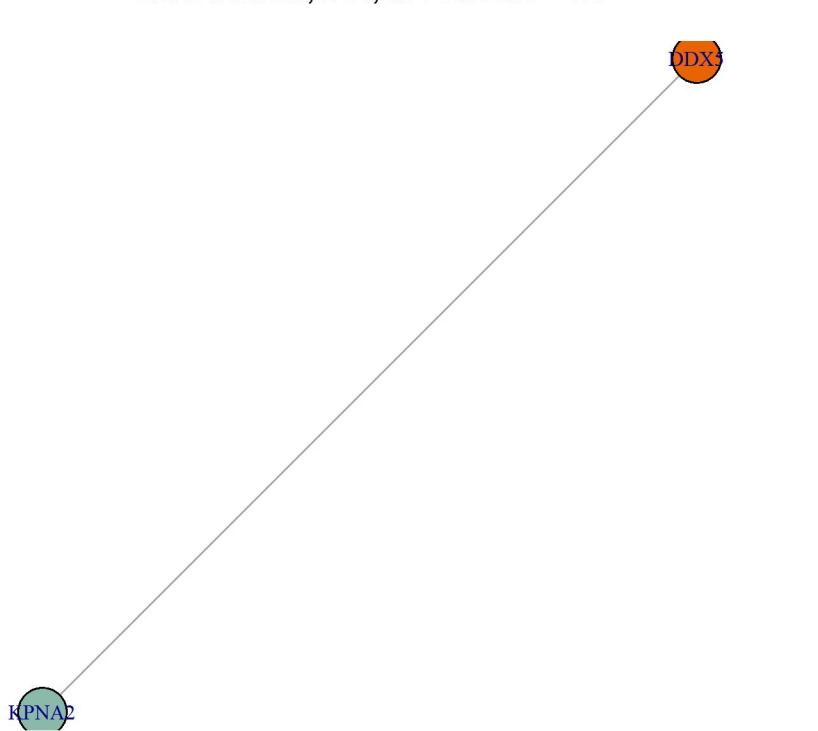
p-value < 0.05 & logFC > 1.2



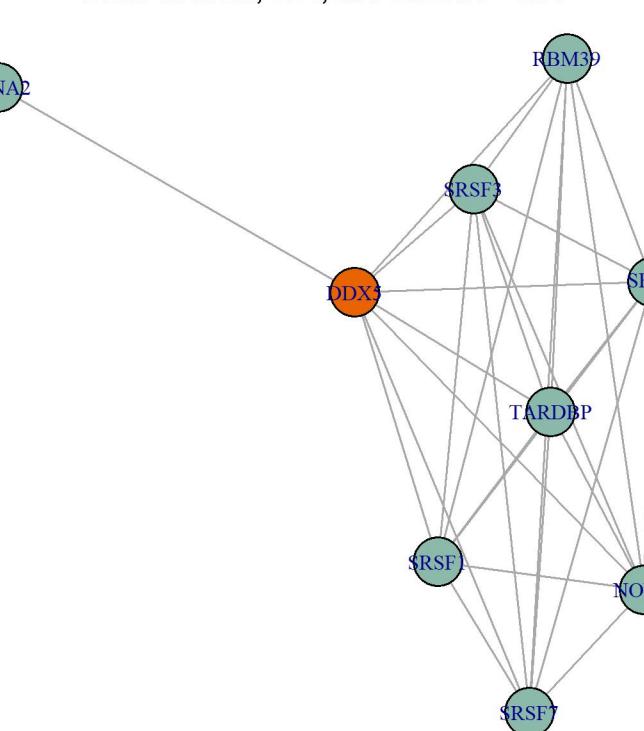
Downregulated in solid cancers at low/absent DDX5 Upregulated in solid cancers at low/absent DDX5

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.04	4.47e-23	UBE2T	ubiquitin conjugating enzyme E2 T	0.91	2.79e-17	ARSA	arylsulfatase A
-0.98	5.84e-23	HELLS	helicase, lymphoid specific	0.72	8.60e-09	SQOR	sulfide quinone oxidoreductase
-0.97	8.19e-23	FRG1	FSHD region gene 1	0.71	5.21e-08	CD59	CD59 molecule (CD59 blood group)
-0.92	1.77e-23	CHAF1A	chromatin assembly factor 1 subunit	0.7	7.30e-08	S100A10	S100 calcium binding protein A10
-0.92	4.42e-22	EZH2	enhancer of zeste 2 polycomb repres	0.67	9.99e-09	RNASET2	ribonuclease T2
-0.88	1.66e-18	UBE2S	ubiquitin conjugating enzyme E2 S	0.66	5.00e-06	LGALS3	galectin 3
-0.88	5.00e-09	CKB	creatine kinase B	0.65	1.95e-08	RHOC	ras homolog family member C
-0.85	5.08e-18	NUSAP1	nucleolar and spindle associated pr	0.64	1.12e-07	SLC12A9	solute carrier family 12 member 9
-0.84	7.96e-20	AURKB	aurora kinase B	0.63	5.27e-08	BET1	Bet1 golgi vesicular membrane traff
-0.83	3.18e-18	PRIM1	DNA primase subunit 1	0.62	1.06e-04	S100A6	S100 calcium binding protein A6
-0.82	9.77e-18	NSD2	nuclear receptor binding SET domain	0.62	1.97e-06	IGFBP7	insulin like growth factor binding
-0.82	5.28e-20	MDN1	midasin AAA ATPase 1	0.62	7.46e-07	EPS8L2	EPS8 like 2
-0.81	2.00e-14	WDHD1	WD repeat and HMG-box DNA binding p	0.62	4.09e-06	CTS2	cathepsin Z
-0.8	1.24e-15	ZNF280C	zinc finger protein 280C	0.6	4.73e-08	ADAM9	ADAM metallopeptidase domain 9
-0.8	2.06e-16	GNL3L	G protein nucleolar 3 like	0.6	1.21e-07	FAM114A1	family with sequence similarity 114
-0.79	1.21e-14	KIF2C	kinesin family member 2C	0.6	3.81e-09	MVP	major vault protein
-0.79	1.00e-13	DAXX	death domain associated protein	0.6	1.46e-06	EPB41L1	erythrocyte membrane protein band 4
-0.78	1.56e-13	ZNF593	zinc finger protein 593	0.59	2.49e-08	RRAS	RAS related
-0.77	4.65e-13	RPF1	ribosome production factor 1 homolo	0.58	1.08e-06	PAPSS2	3'-phosphoadenosine 5'-phosphosulfa
-0.76	1.19e-12	GRPEL2	GrpE like 2, mitochondrial	0.58	5.75e-07	SP100	SP100 nuclear antigen
-0.75	1.02e-17	PRIM2	DNA primase subunit 2	0.58	1.37e-06	NDRG1	N-myc downstream regulated 1
-0.75	4.56e-15	CDCA5	cell division cycle associated 5	0.58	3.96e-09	TRIOBP	TRIO and F-actin binding protein
-0.75	3.18e-12	BRD2	bromodomain containing 2	0.58	5.63e-09	CPQ	carboxypeptidase Q
-0.75	6.71e-18	SUZ12	SUZ12 polycomb repressive complex 2	0.57	7.66e-08	NCEH1	neutral cholesterol ester hydrolase
-0.75	2.12e-16	ANAPC7	anaphase promoting complex subunit	0.57	2.34e-07	RBPMS	RNA binding protein, mRNA processin
-0.75	4.22e-13	CCNB1	cyclin B1	0.56	1.03e-05	S100A16	S100 calcium binding protein A16
-0.74	2.00e-14	HAT1	histone acetyltransferase 1	0.56	7.81e-06	STOM	stomatin
-0.74	7.73e-14	MORF4L1	mortality factor 4 like 1	0.56	1.62e-06	SERPINE2	serpin family E member 2
-0.74	9.56e-18	INCENP	inner centromere protein	0.56	2.39e-07	APOL2	apolipoprotein L2

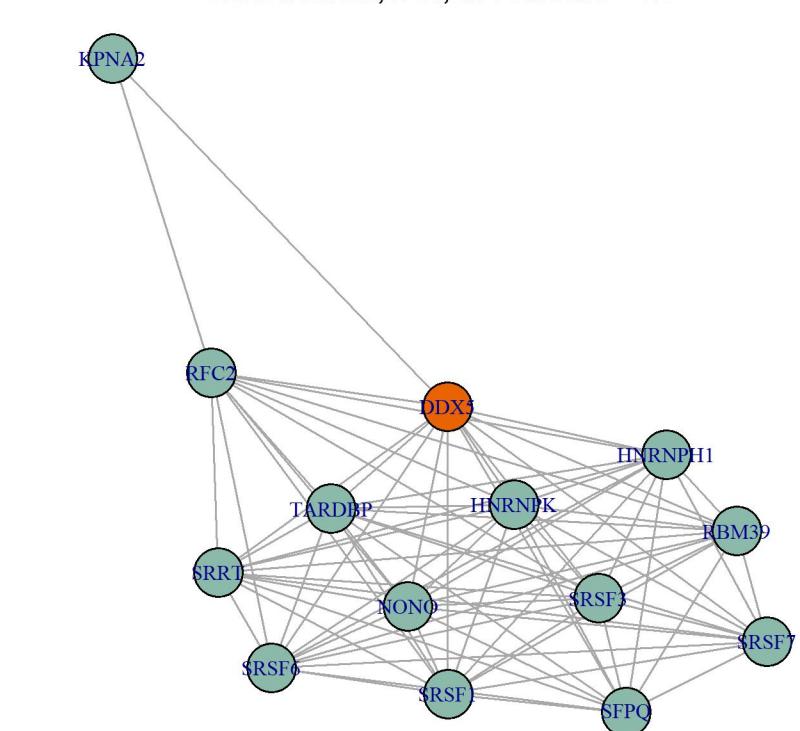
DDX5 network, DB1, all Pearson r > 0.6



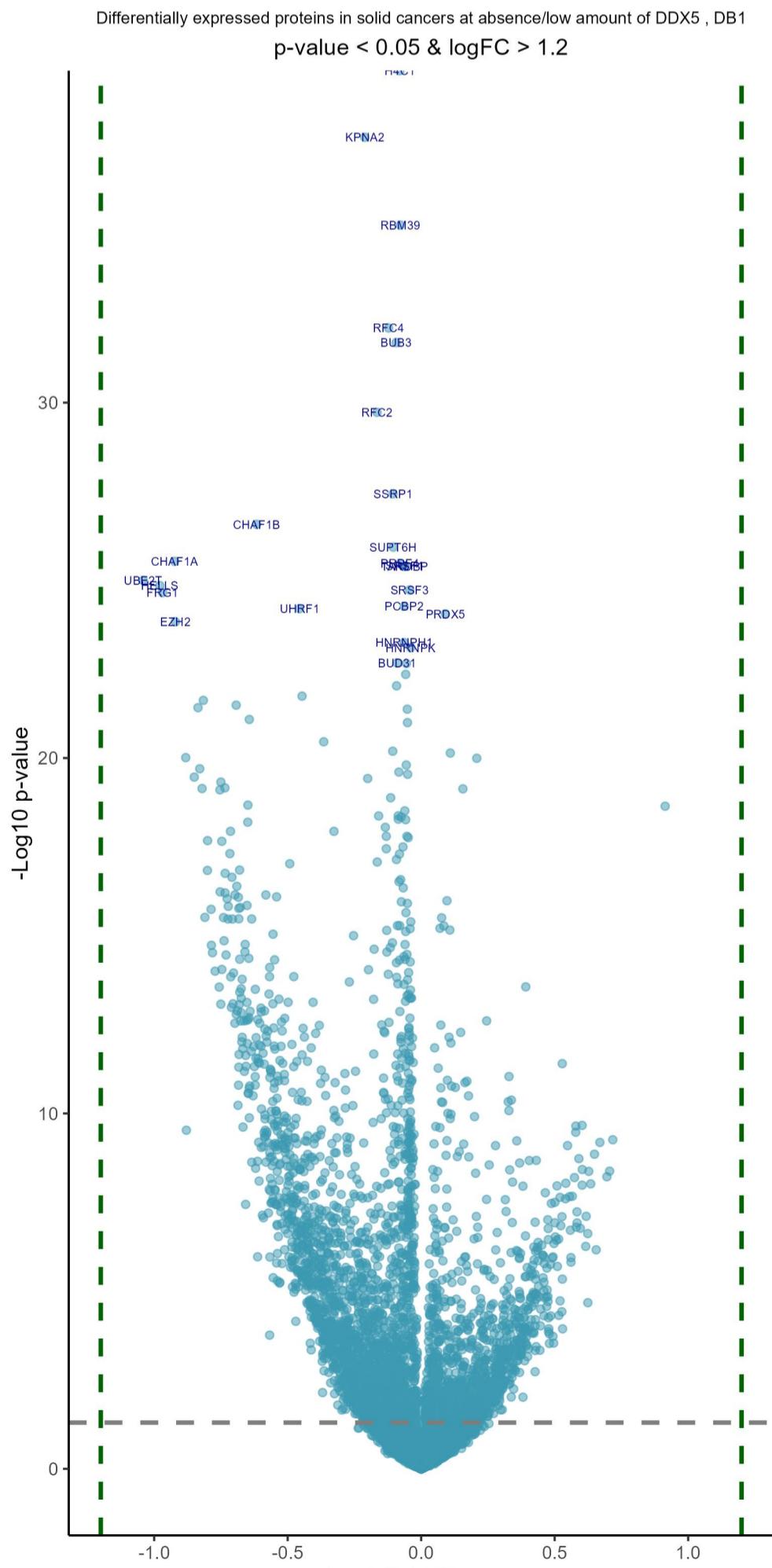
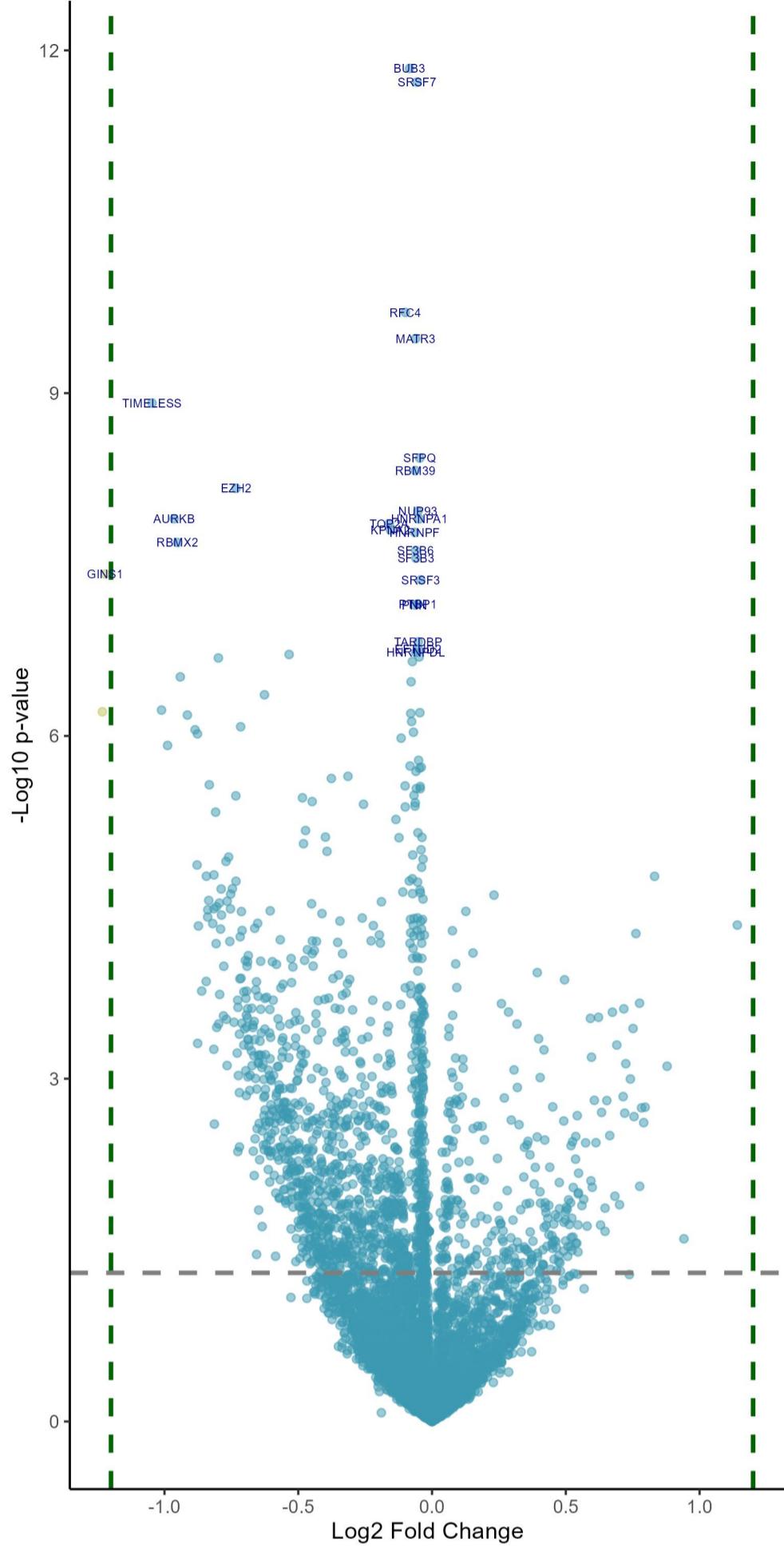
DDX5 network, DB1, all Pearson r > 0.55



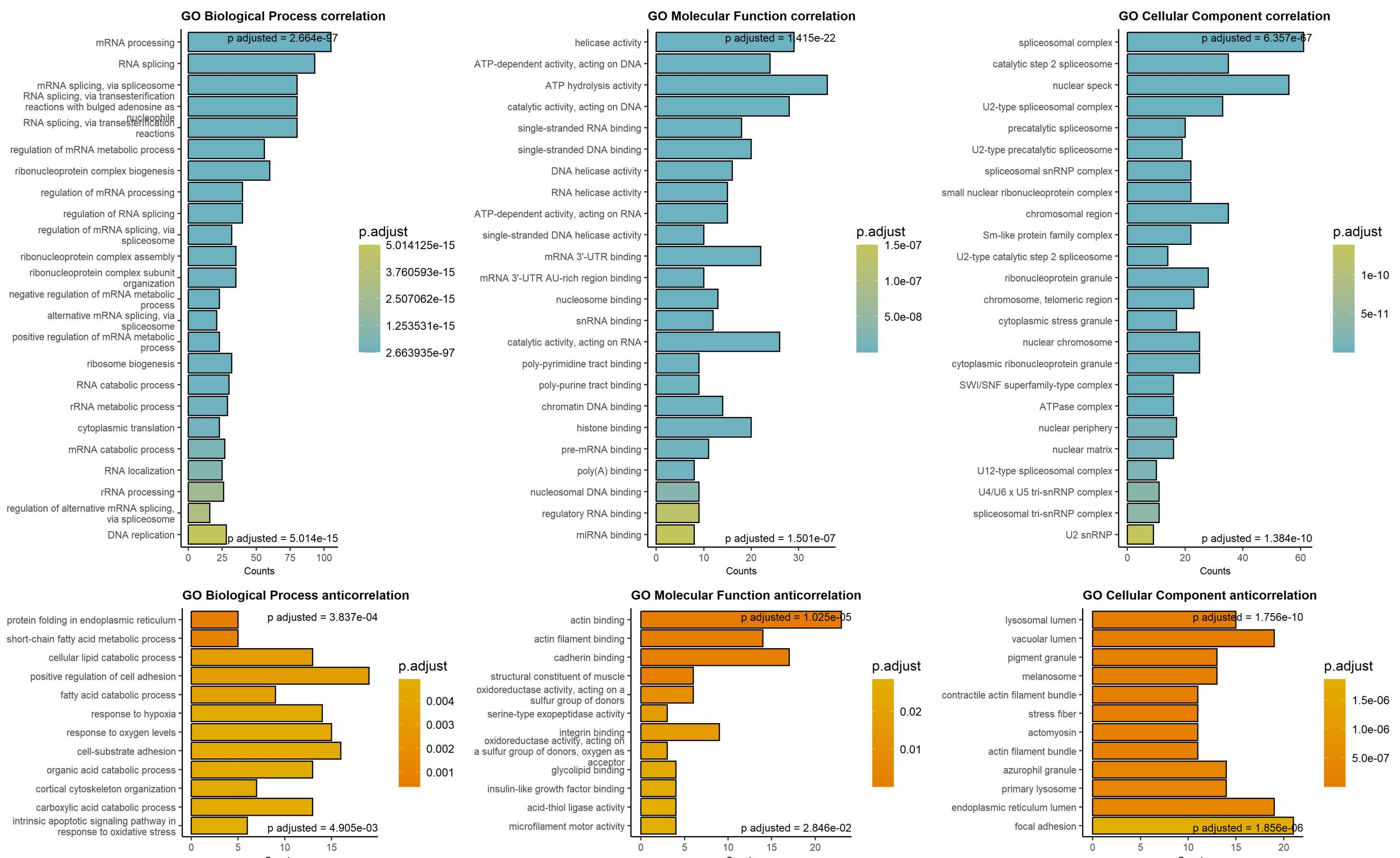
DDX5 network, DB1, all Pearson r > 0.5



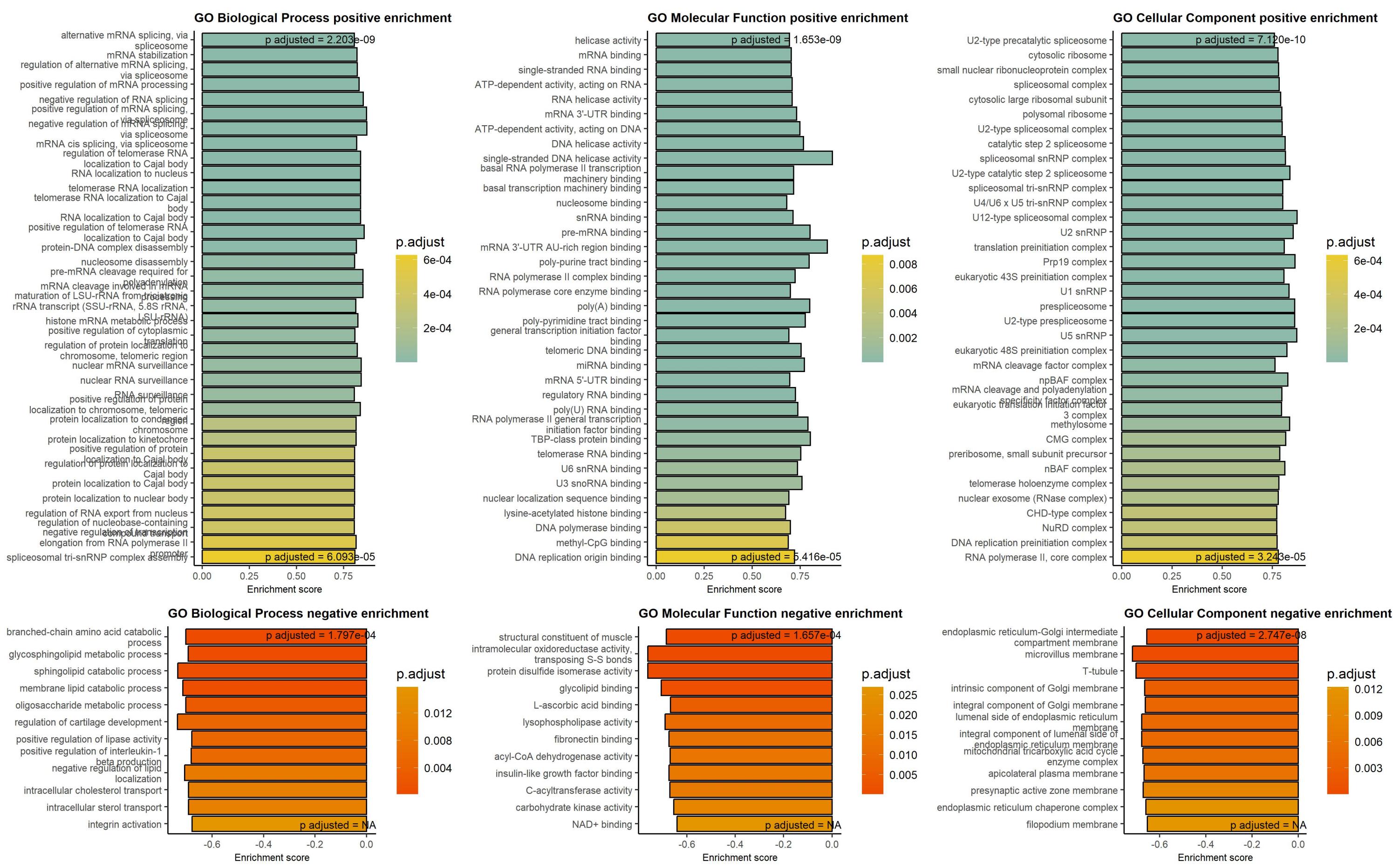
Differentially expressed proteins in blood cancers at absence/low amount of DDX5 , DB1
p-value < 0.05 & logFC > 1.2

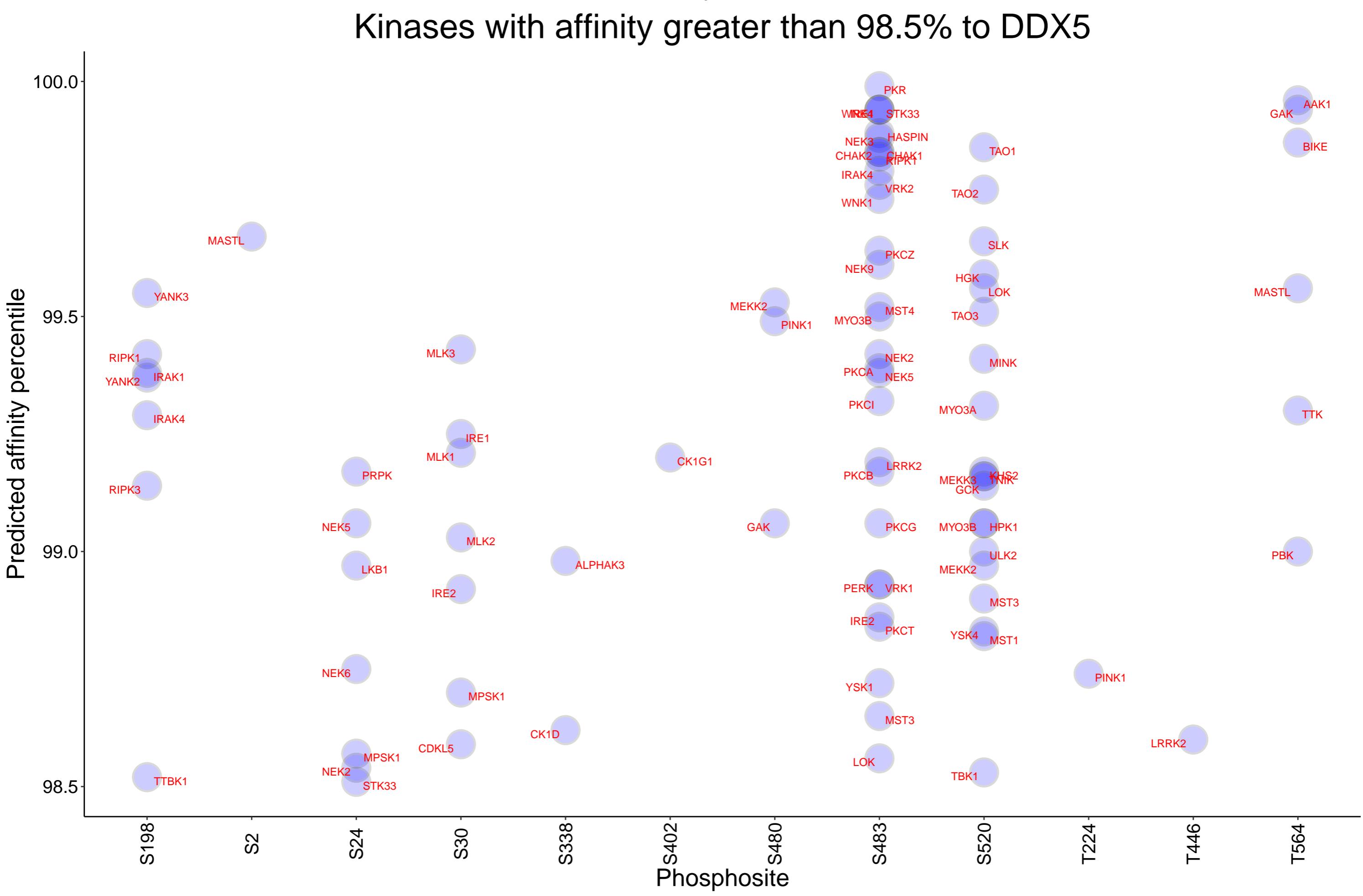
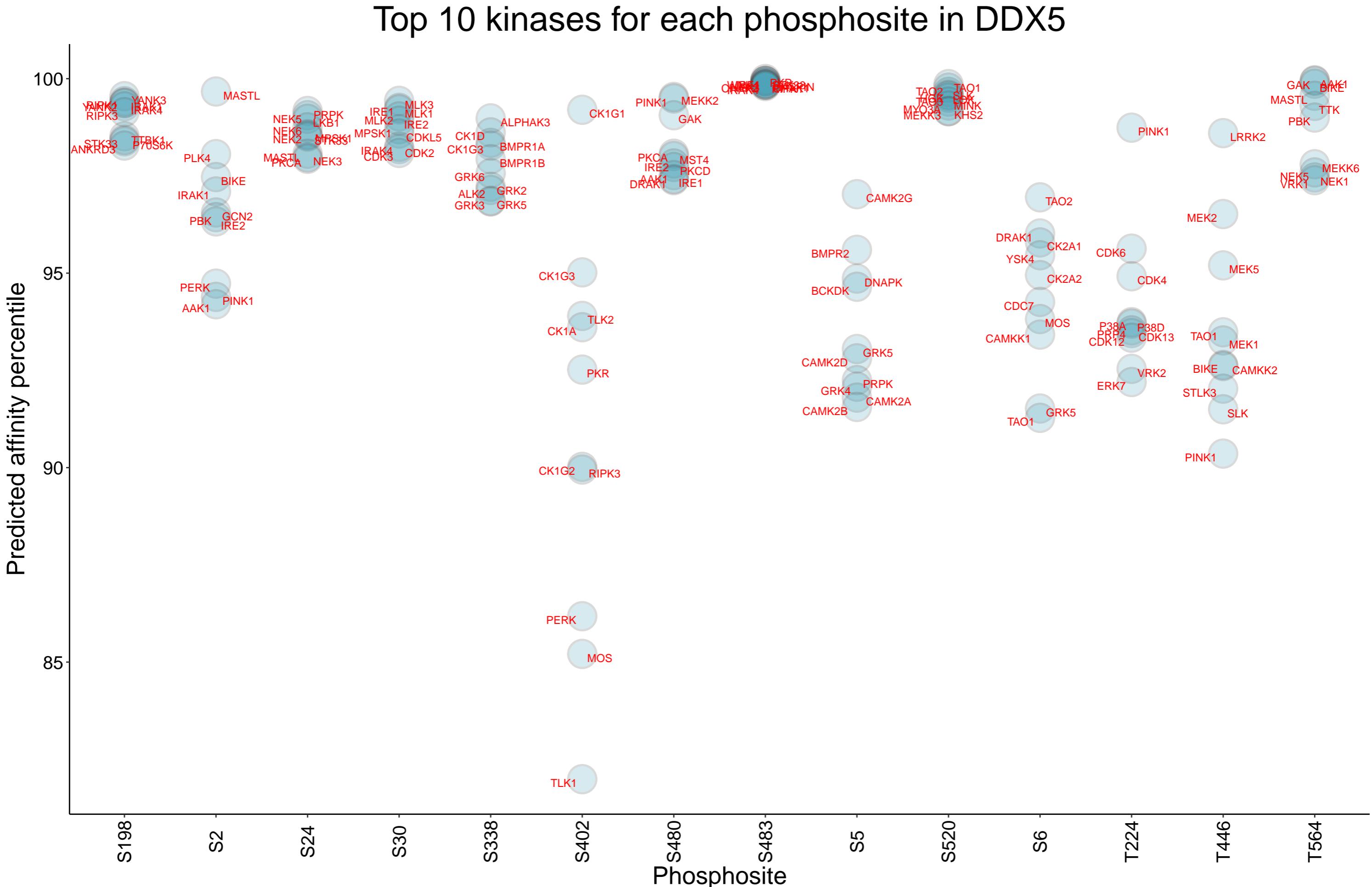


Top 250 correlation coefficients overrepresentation, DDX5 protein, DB1



Gene Set Enrichment analysis on protein correlation coefficients, DDX5 protein, DB1





Top 15 positive correlation coefficients for DDX5 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

