

DDB1

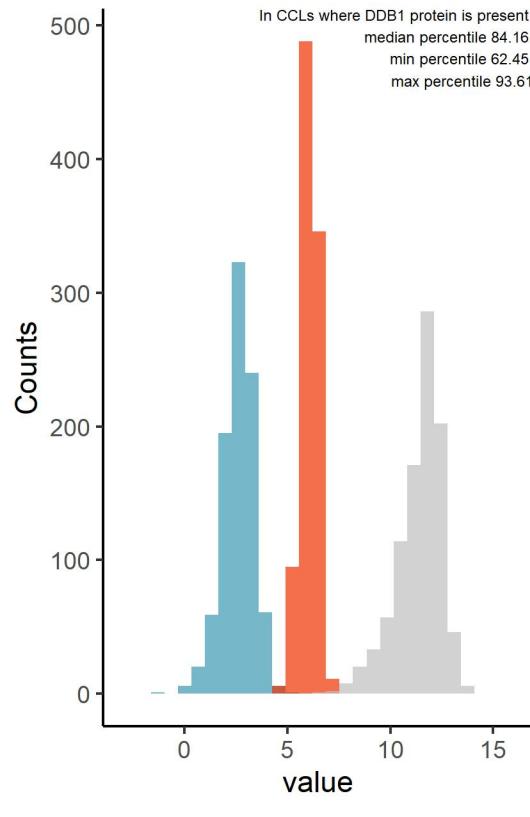
Protein name: DDB1 ; UNIPROT: Q16531 ; Gene name: damage specific DNA binding protein 1

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

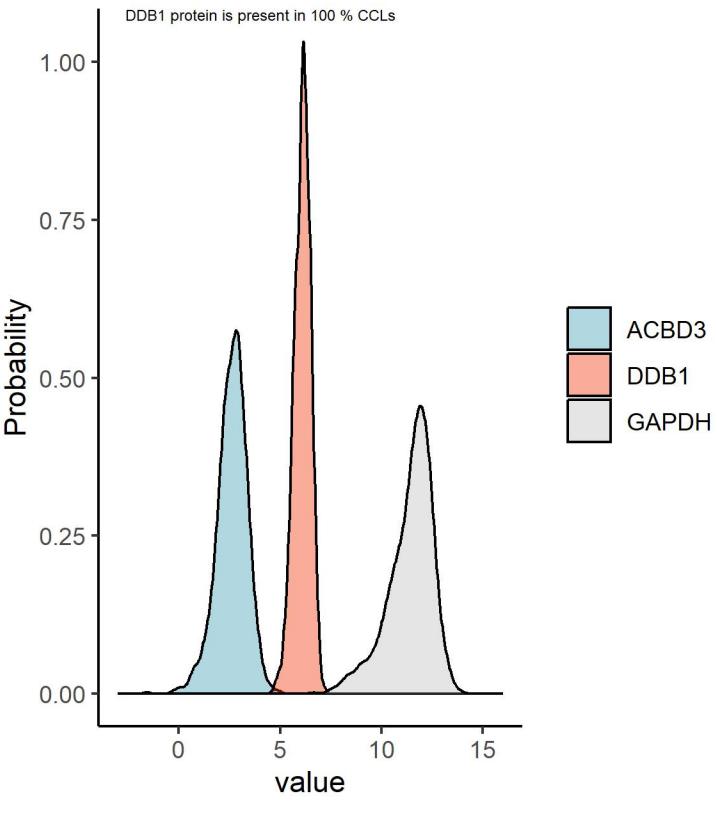
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

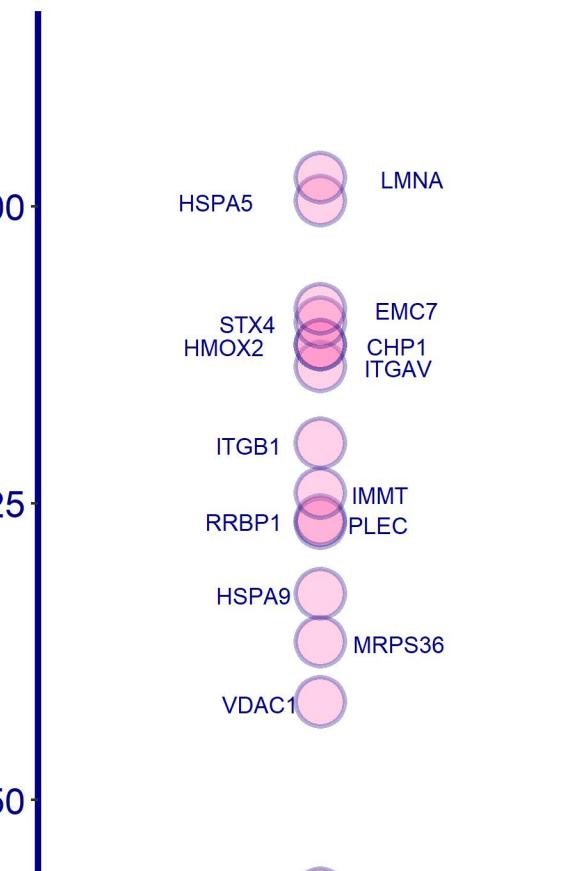
Histogram of DDB1 protein compared to proteins with low and high abundance



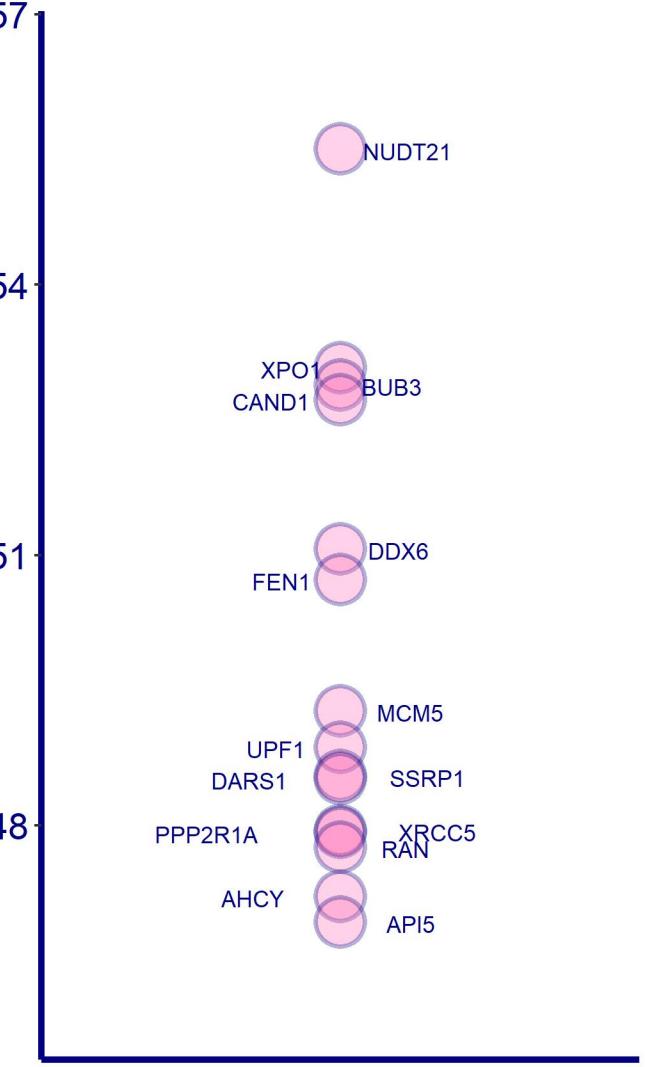
Density plot of DDB1 protein compared to proteins with low and high abundance



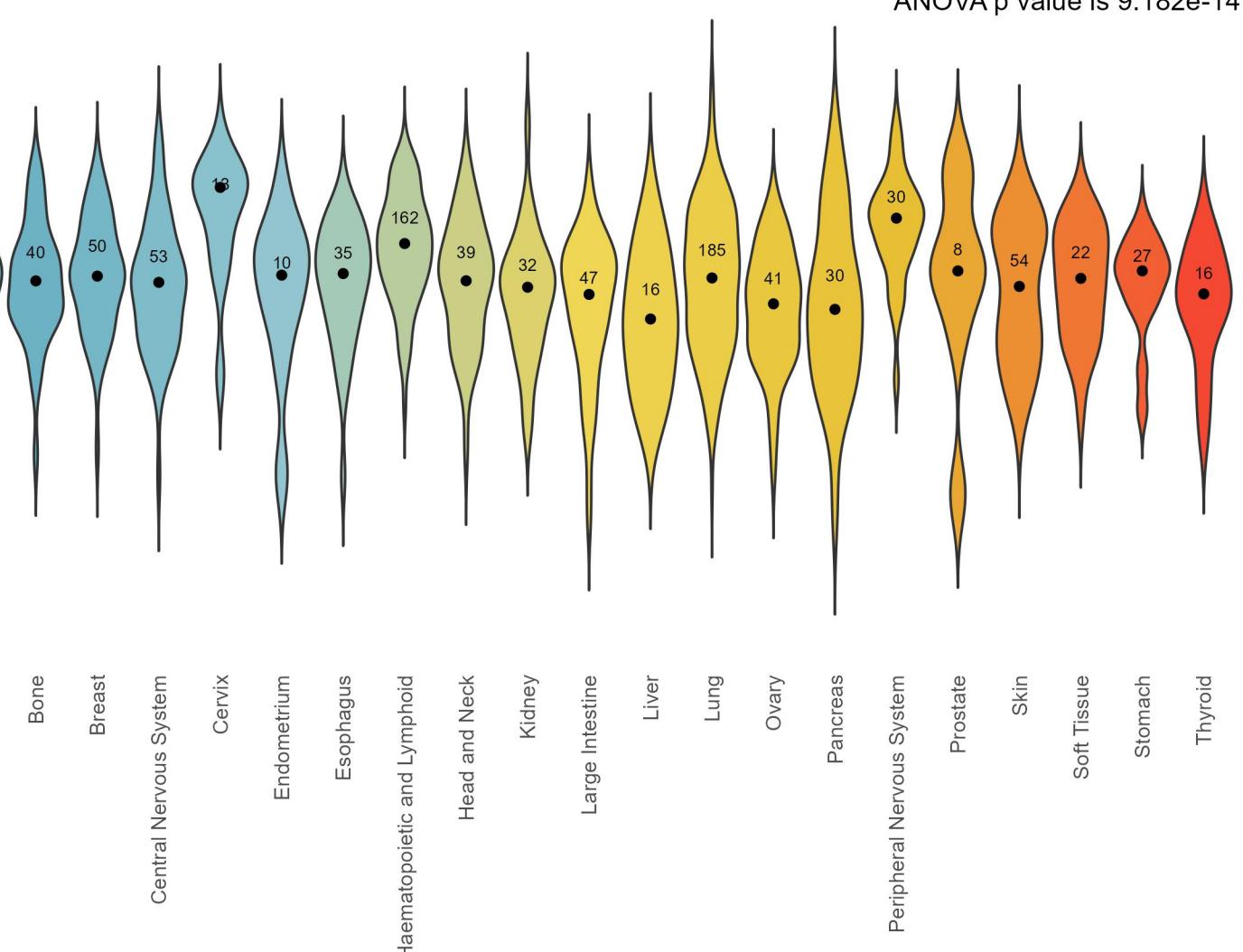
Top negative correlations of DDB1 protein, DB1



Top positive correlations of DDB1 protein, DB1

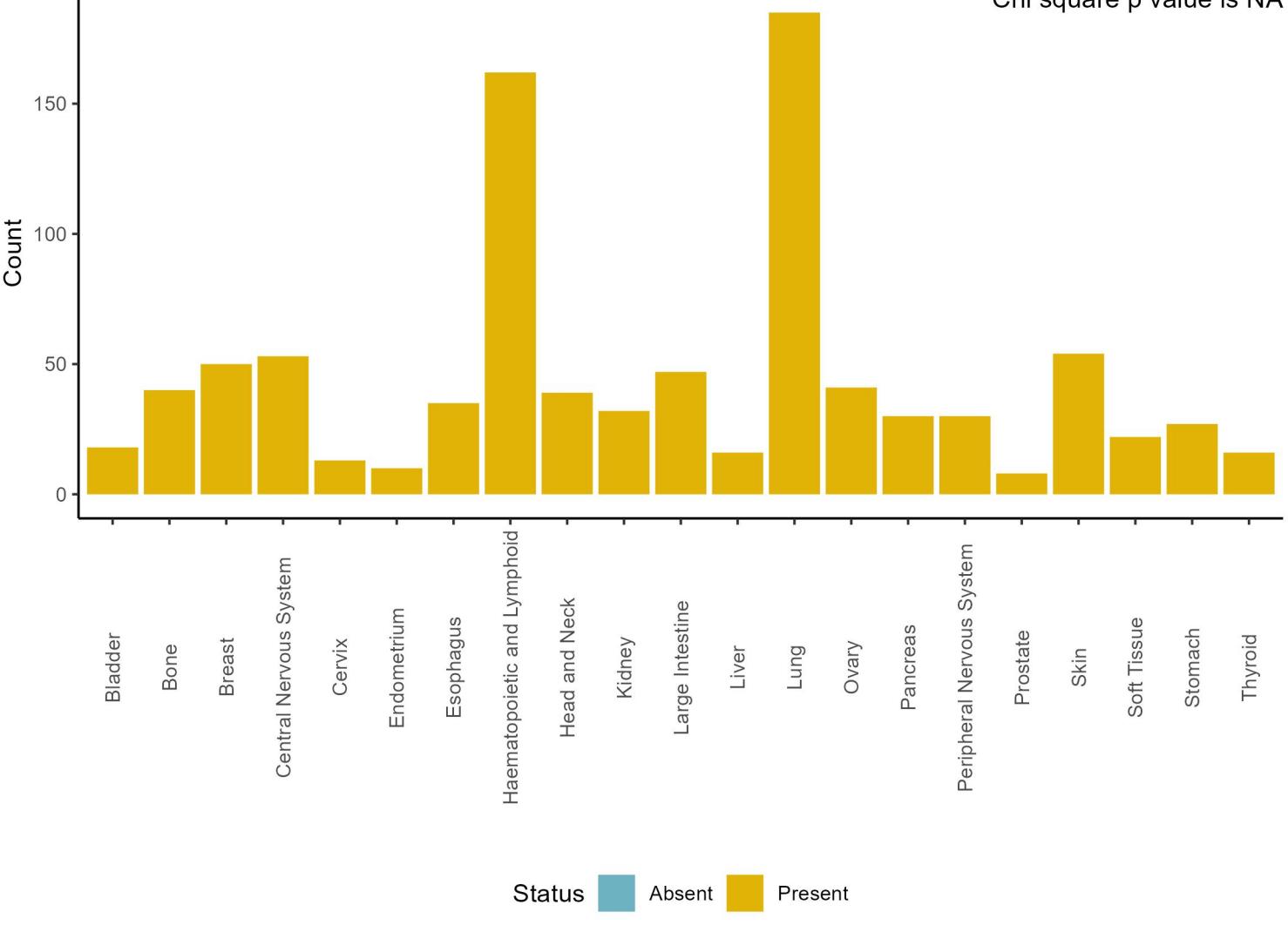


Amount of DDB1 protein, number of CCLs where it is present by tissue, DB1



ANOVA p value is 9.182e-14

Present and absent DDB1 protein counts by tissue, DB1

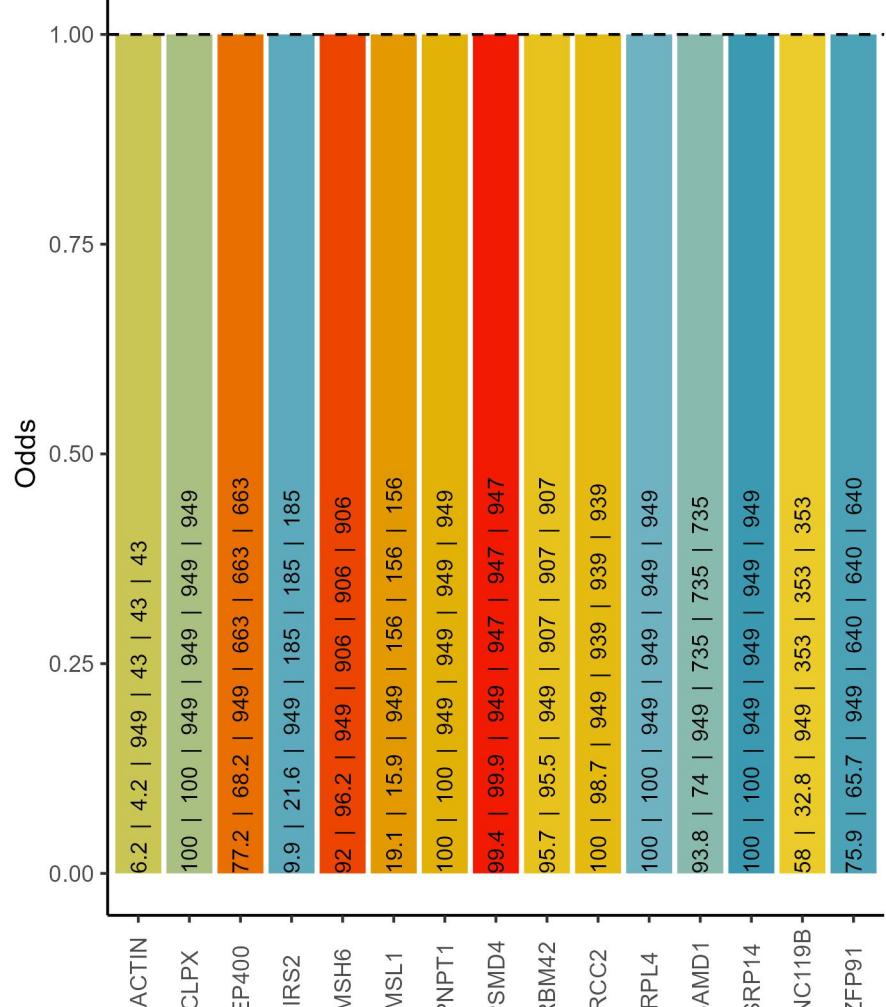


Cooccurrence with DDB1 protein, DB1

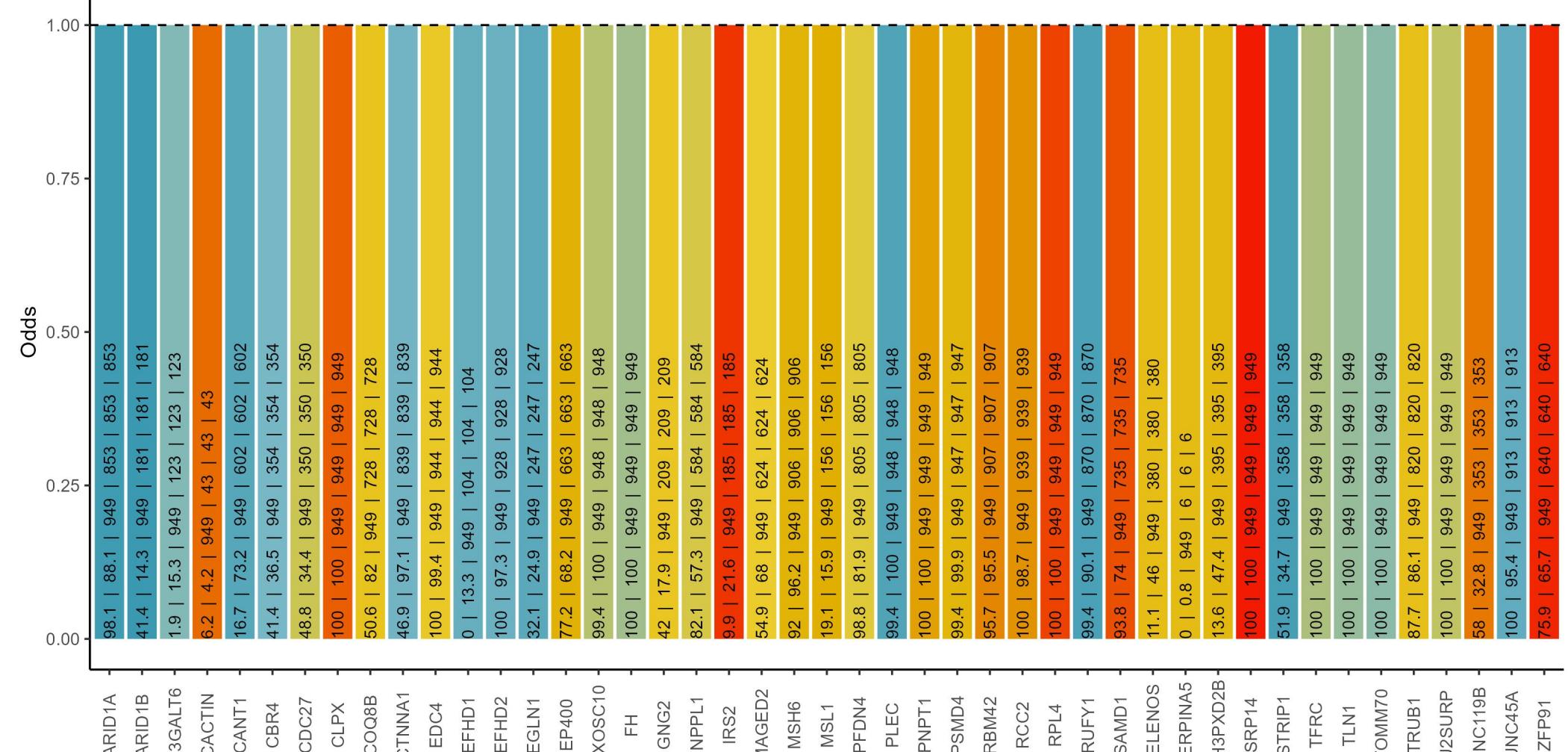
% of DDB1 in blood cancers: 100 ; % of DDB1 in solid cancers: 100

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of DDB1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

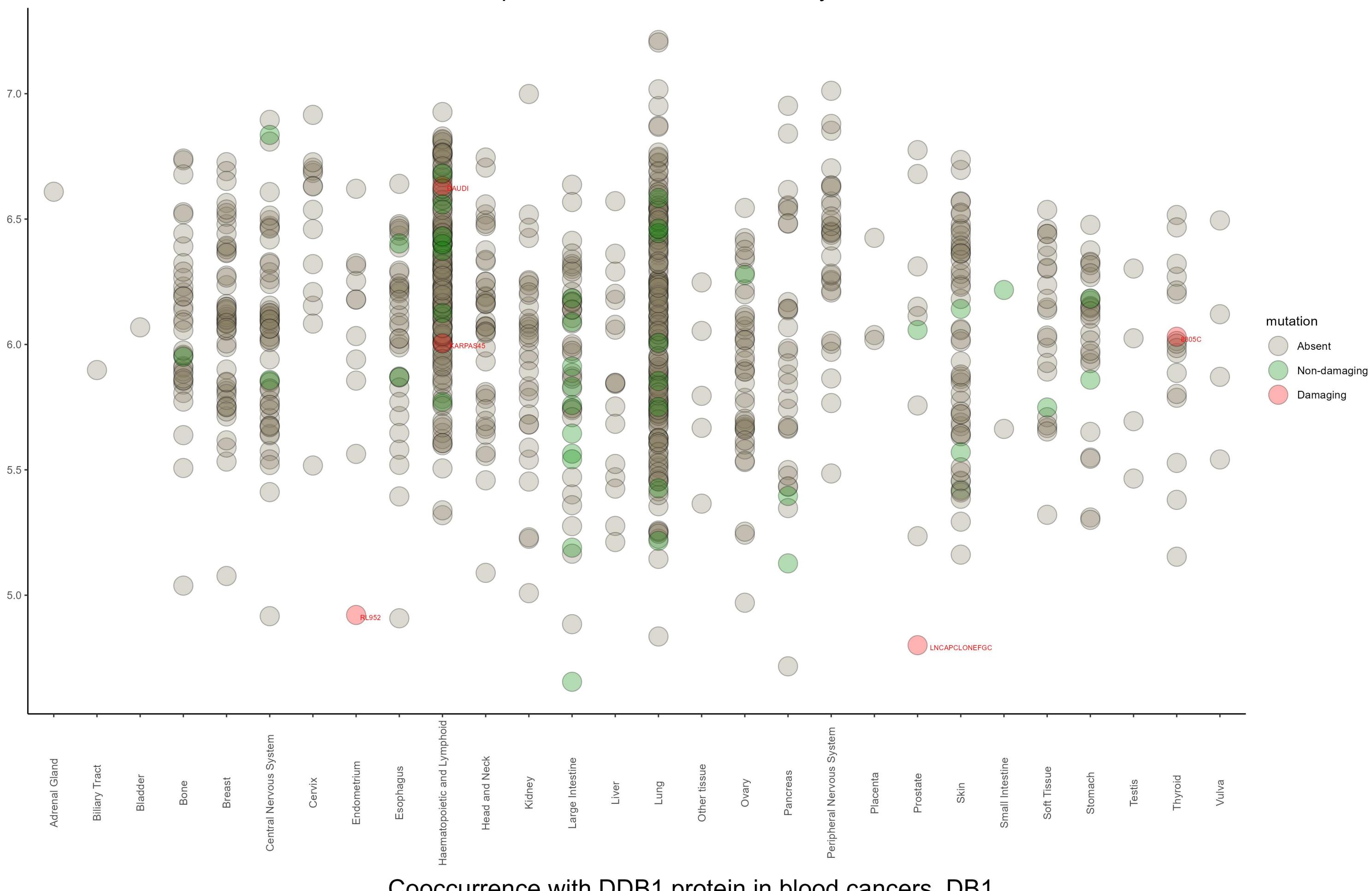
Negative cooccurrence



Positive cooccurrence



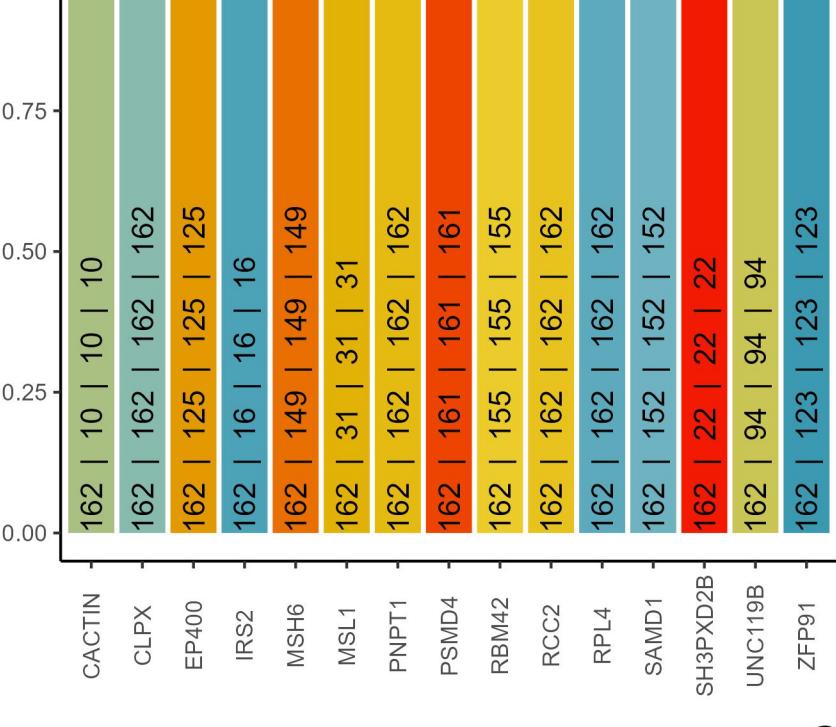
Amount of DDB1 protein and mutation status by tissue, DB1



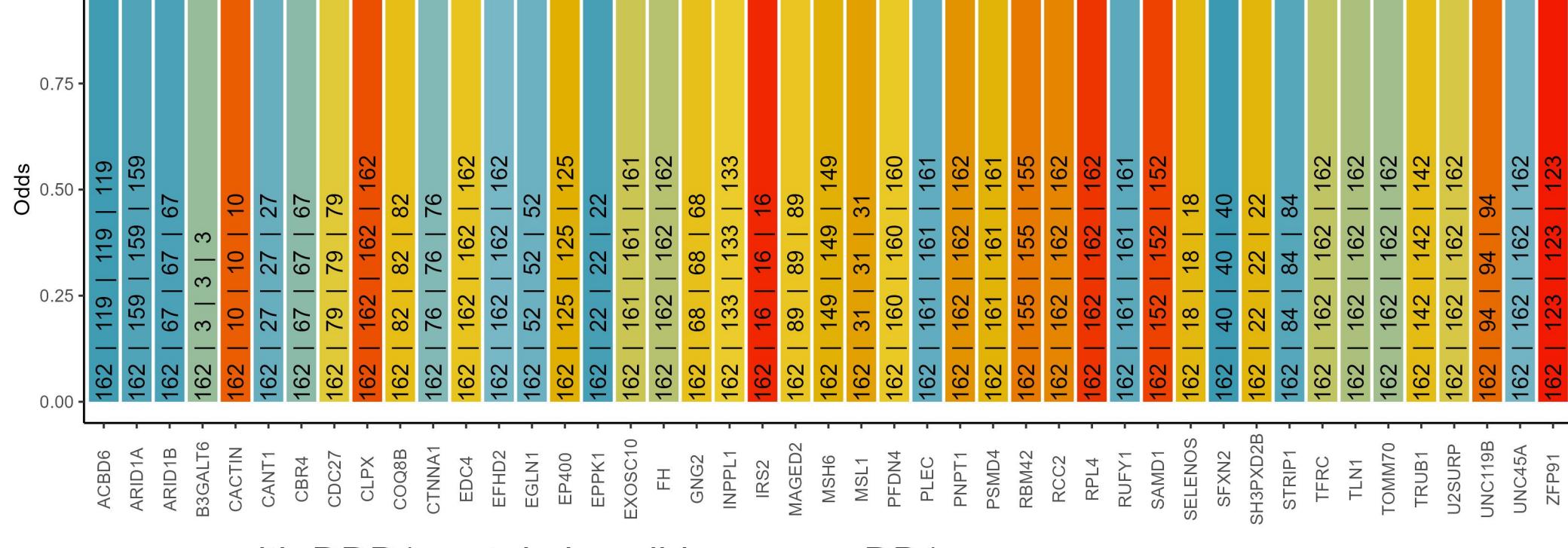
Cooccurrence with DDB1 protein in blood cancers, DB1

The text in the bars: incidence of DDB1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



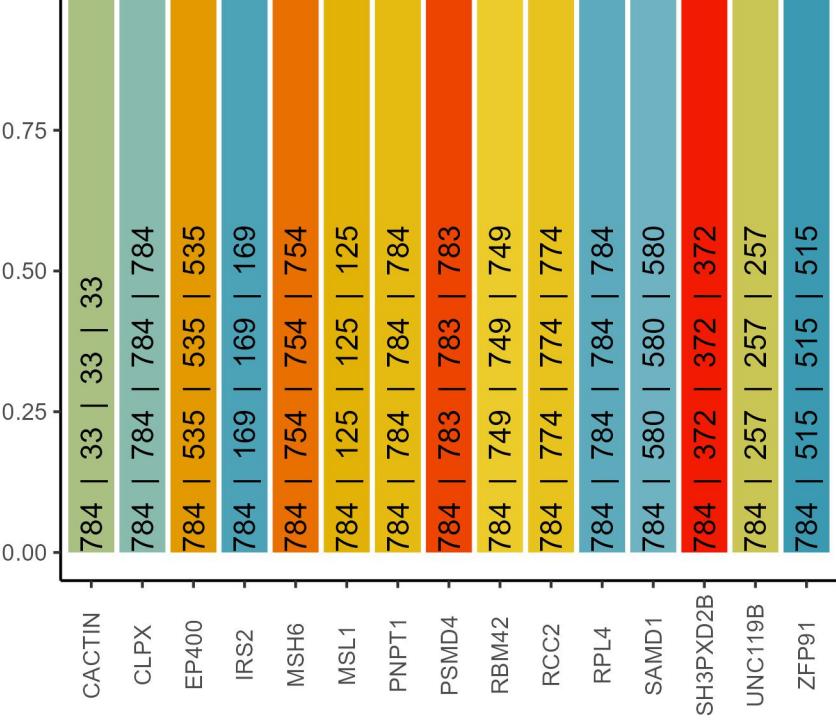
Positive cooccurrence



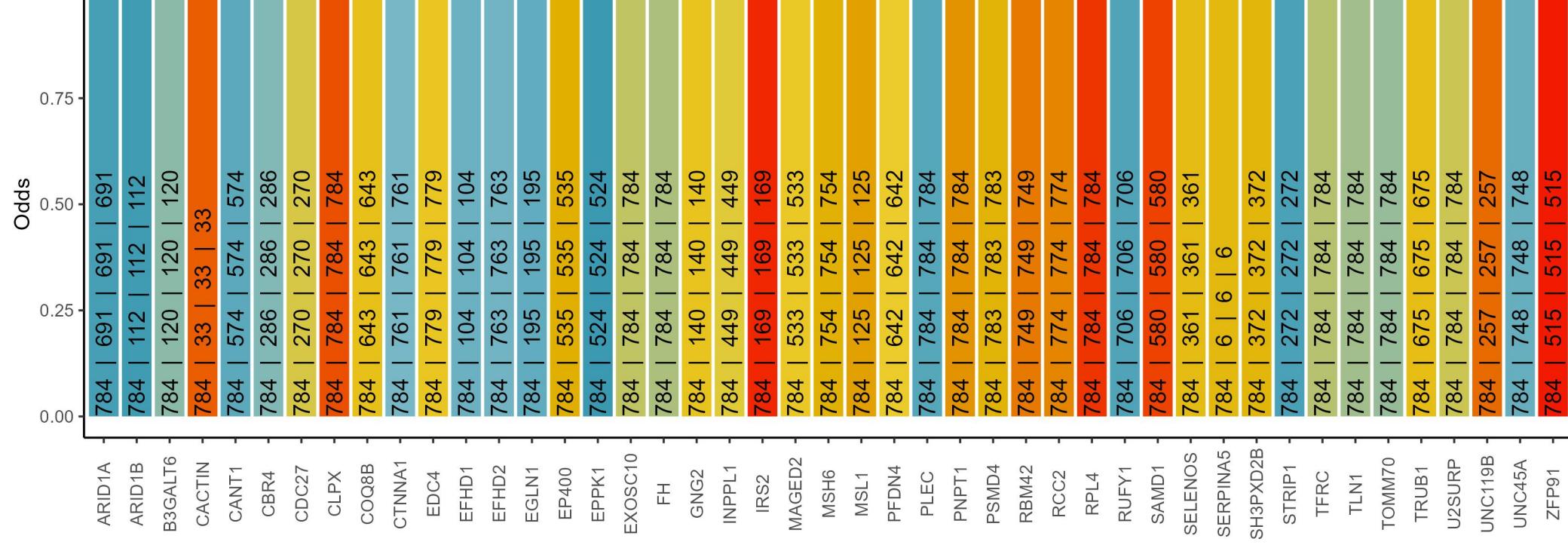
Cooccurrence with DDB1 protein in solid cancers, DB1

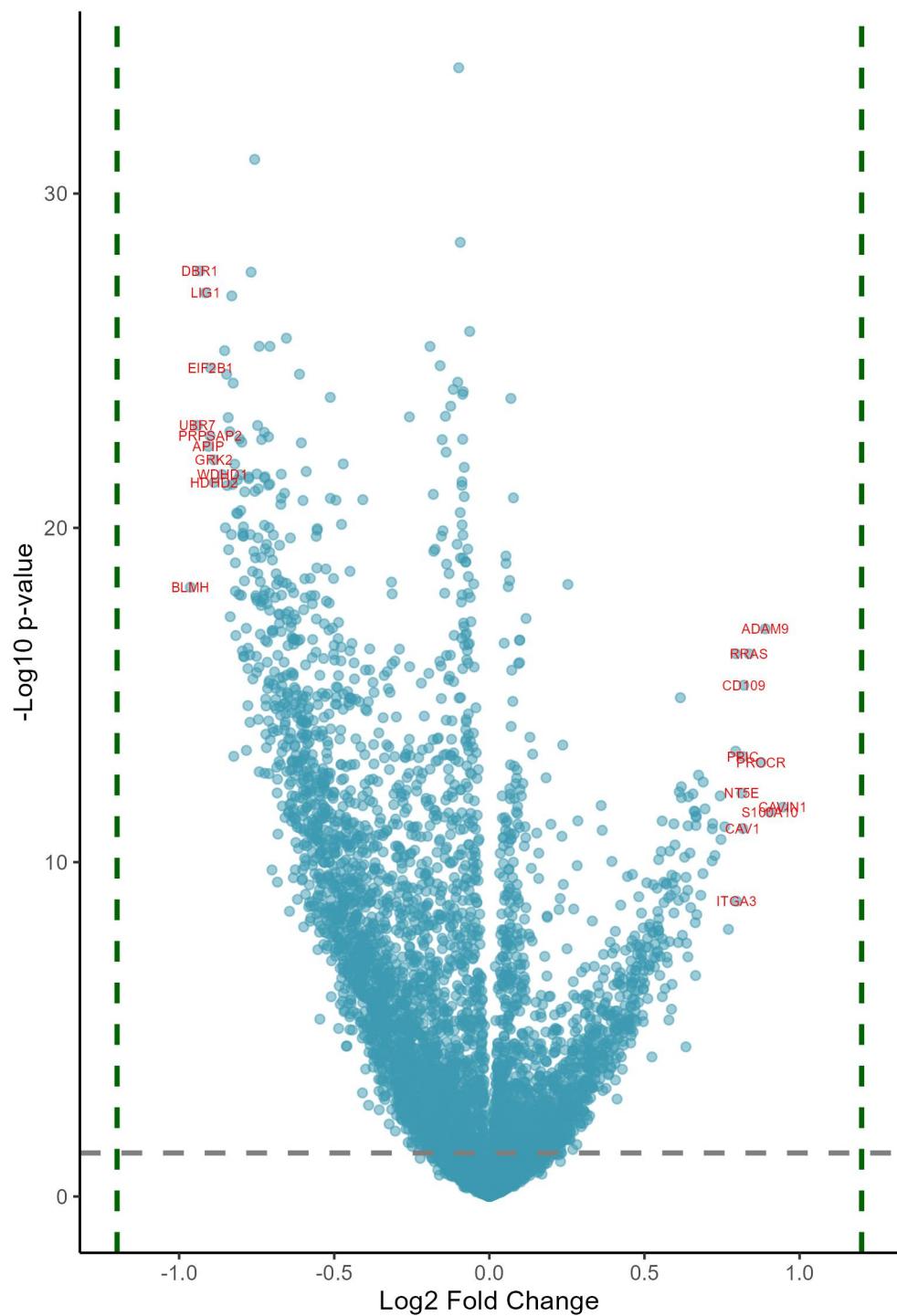
The text in the bars: incidence of DDB1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



Positive cooccurrence





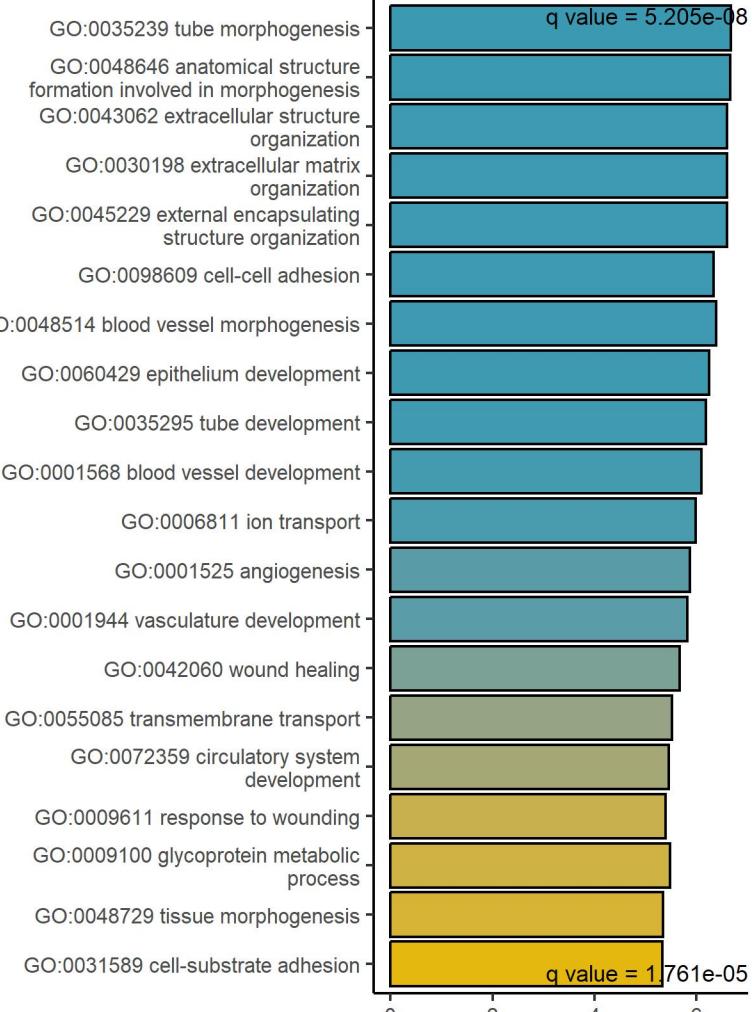
Downregulated at low/absent DDB1

Upregulated at low/absent DDB1

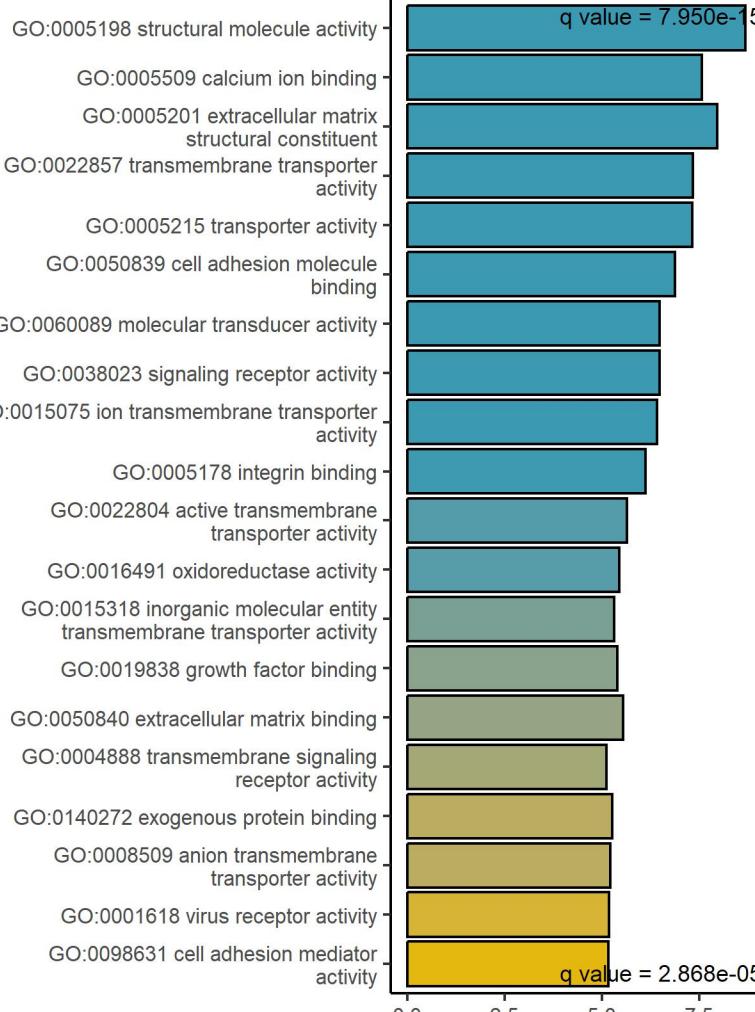
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.96	2.73e-17	BLMH	bleomycin hydrolase	0.95	2.33e-11	CAVIN1	caveolae associated protein 1
-0.94	1.86e-21	UBR7	ubiquitin protein ligase E3 compone	0.9	3.16e-11	S100A10	S100 calcium binding protein A10
-0.93	2.48e-25	DBR1	debranching RNA lariats 1	0.89	3.53e-16	ADAM9	ADAM metallopeptidase domain 9
-0.92	8.84e-25	LIG1	DNA ligase 1	0.88	1.42e-12	PROCR	protein C receptor
-0.91	5.80e-21	APIP	APAF1 interacting protein	0.84	1.63e-15	RRAS	RAS related
-0.9	3.45e-21	PRPSAP2	phosphoribosyl pyrophosphate synthetase	0.82	1.15e-14	CD109	CD109 molecule
-0.9	6.86e-23	EIF2B1	eukaryotic translation initiation factor 2	0.82	8.73e-11	CAV1	caveolin 1
-0.89	1.40e-20	GRK2	G protein-coupled receptor kinase 2	0.82	9.86e-13	PPIC	peptidylprolyl isomerase C
-0.89	4.96e-20	HDHD2	haloacid dehalogenase like hydrolases	0.81	9.65e-12	NT5E	5'-nucleotidase ecto
-0.86	3.30e-20	WDHD1	WD repeat and HMG-box DNA binding protein	0.8	8.74e-09	ITGA3	integrin subunit alpha 3
-0.85	2.37e-23	CMTR1	cap methyltransferase 1	0.79	1.62e-15	NECTIN2	nectin cell adhesion molecule 2
-0.85	7.61e-19	SHMT1	serine hydroxymethyltransferase 1	0.79	7.12e-13	EPHA2	EPH receptor A2
-0.85	9.39e-23	HAT1	histone acetyltransferase 1	0.77	5.23e-08	GNG12	G protein subunit gamma 12
-0.85	5.62e-20	RNASEH2B	ribonuclease H2 subunit B	0.76	7.77e-11	RHOC	ras homolog family member C
-0.84	1.15e-21	PPP4C	protein phosphatase 4 catalytic subunit	0.75	1.71e-10	MYOF	myoferlin
-0.84	2.77e-18	PM20D2	peptidase M20 domain containing 2	0.74	1.14e-11	ITGA5	integrin subunit alpha 5
-0.84	2.76e-21	PRIM1	DNA primase subunit 1	0.73	4.72e-10	ITGA2	integrin subunit alpha 2
-0.84	1.66e-16	PSME3IP1	proteasome activator subunit 3 interactor	0.72	6.47e-11	AXL	AXL receptor tyrosine kinase
-0.83	1.13e-18	PDXP	pyridoxal phosphatase	0.72	8.87e-11	GPX8	glutathione peroxidase 8 (putative)
-0.83	9.57e-25	PPP6C	protein phosphatase 6 catalytic subunit	0.72	6.74e-10	EGFR	epidermal growth factor receptor
-0.83	5.48e-20	TKFC	triokinase and FMN cyclase	0.7	2.59e-11	CD151	CD151 molecule (Raph blood group)
-0.83	1.55e-22	RABGGTA	Rab geranylgeranyltransferase subunit	0.69	4.82e-12	MBOAT7	membrane bound O-acyltransferase domain
-0.82	9.74e-13	CORO1A	coronin 1A	0.69	1.53e-09	NCEH1	neutral cholesterol ester hydrolase
-0.82	1.79e-20	EIF2B5	eukaryotic translation initiation factor 2B subunit 5	0.68	6.03e-09	CAVIN3	caveolae associated protein 3
-0.82	6.16e-18	PPM1A	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent	0.67	3.14e-12	HSPG2	heparan sulfate proteoglycan 2
-0.82	3.52e-17	HMGCS1	3-hydroxy-3-methylglutaryl-CoA lyase	0.67	2.05e-08	S100A16	S100 calcium binding protein A16
-0.82	5.33e-16	DHFR	dihydrofolate reductase	0.67	4.01e-11	MET	MET proto-oncogene, receptor tyrosine kinase
-0.81	3.00e-19	UBXN7	UBX domain protein 7	0.67	4.40e-11	CYBRD1	cytochrome b reductase 1
-0.81	4.23e-20	EIPR1	EARP complex and GARP complex interactor	0.67	7.22e-11	SDC4	syndecan 4

GAGE analysis on upregulated and downregulated proteins at low/absent DDB1 protein, DB1

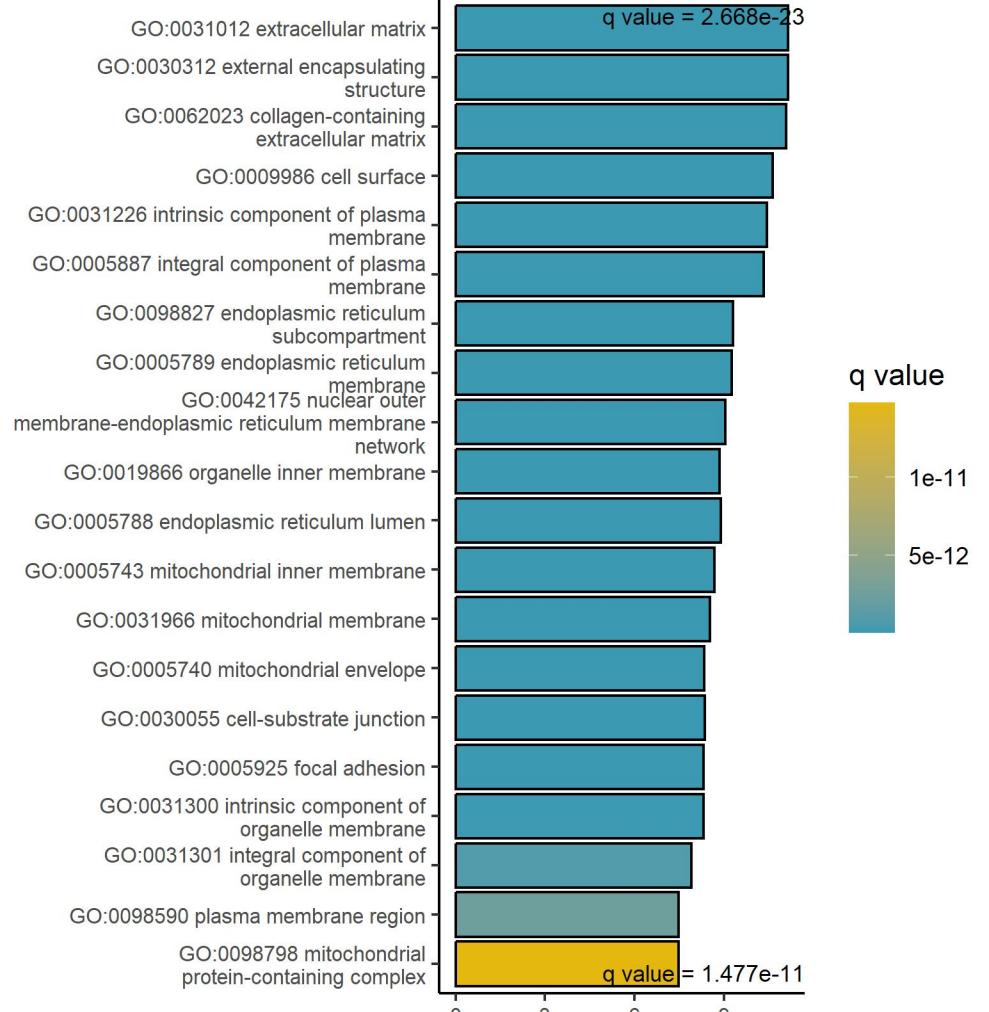
GO Biological Process upregulated



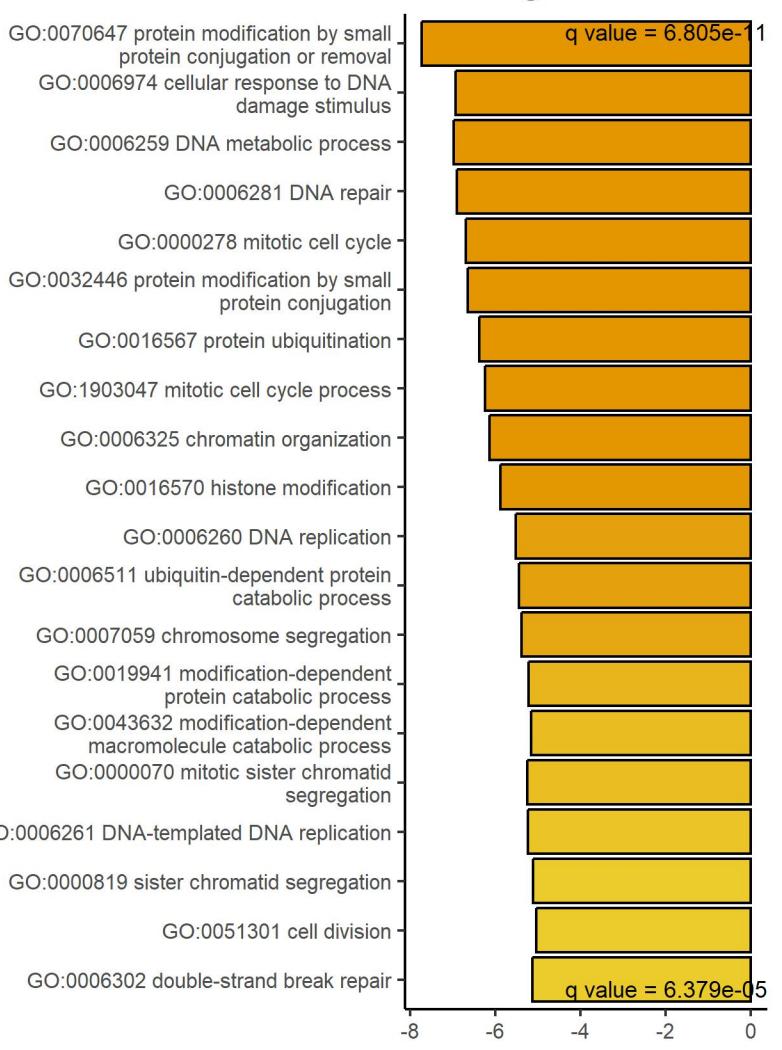
GO Molecular Function upregulated



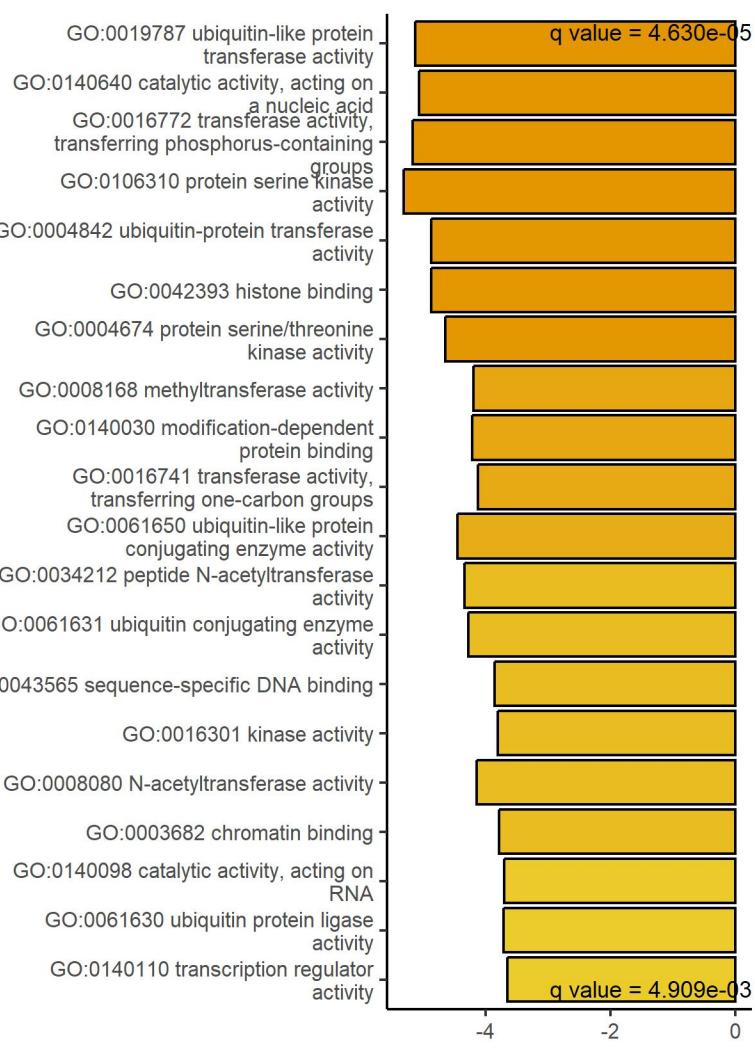
GO Cellular Component upregulated



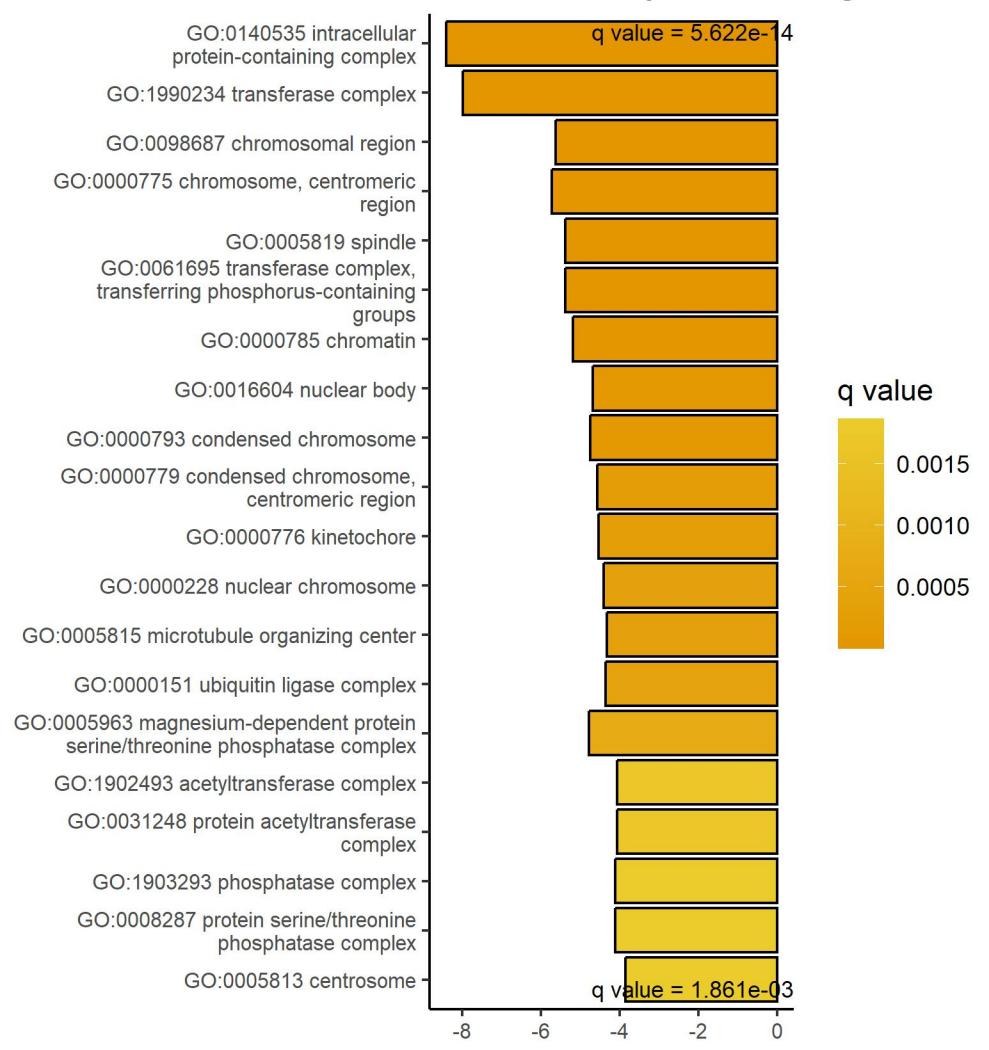
GO Biological Process downregulated

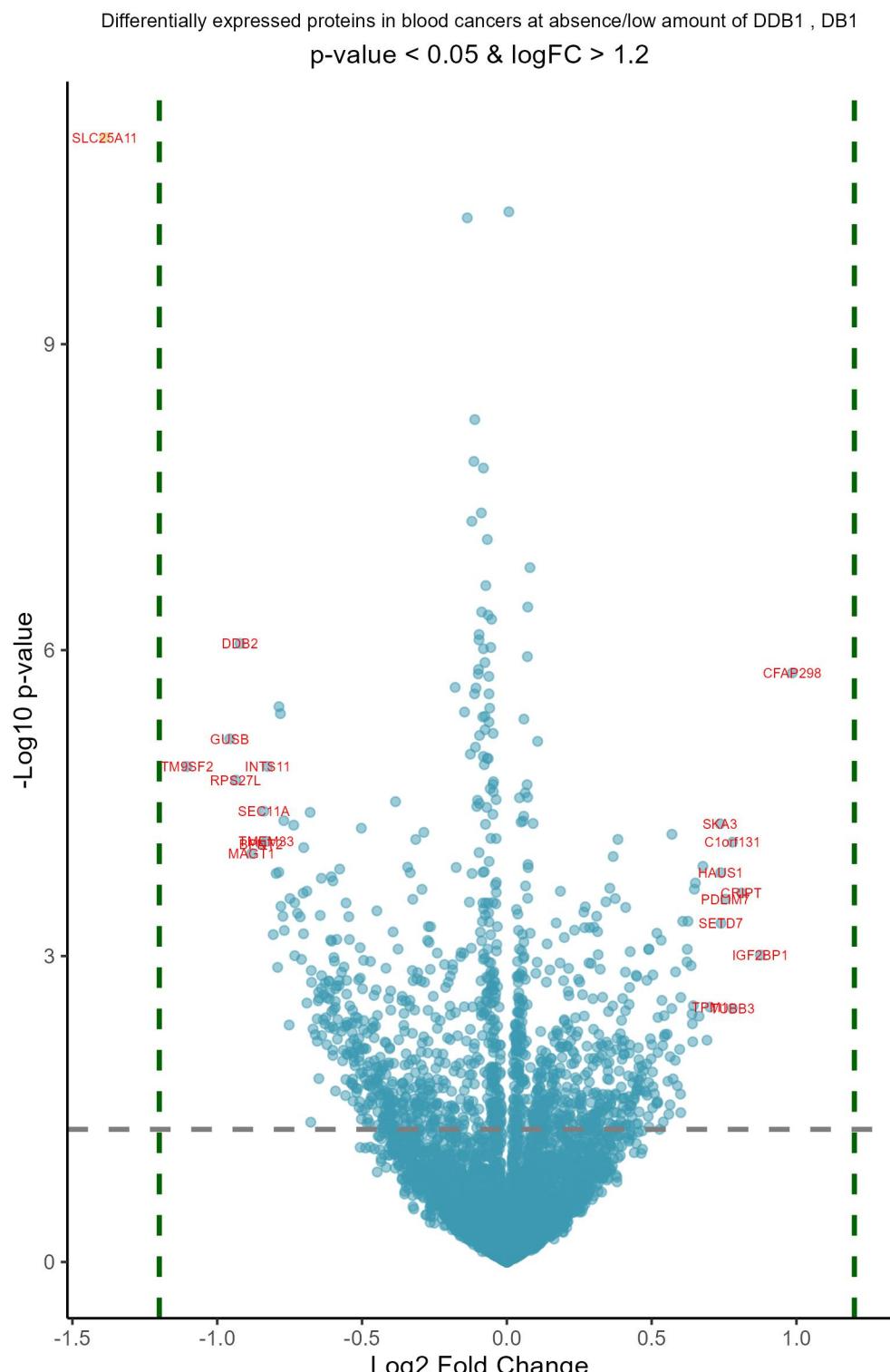


GO Molecular Function downregulated

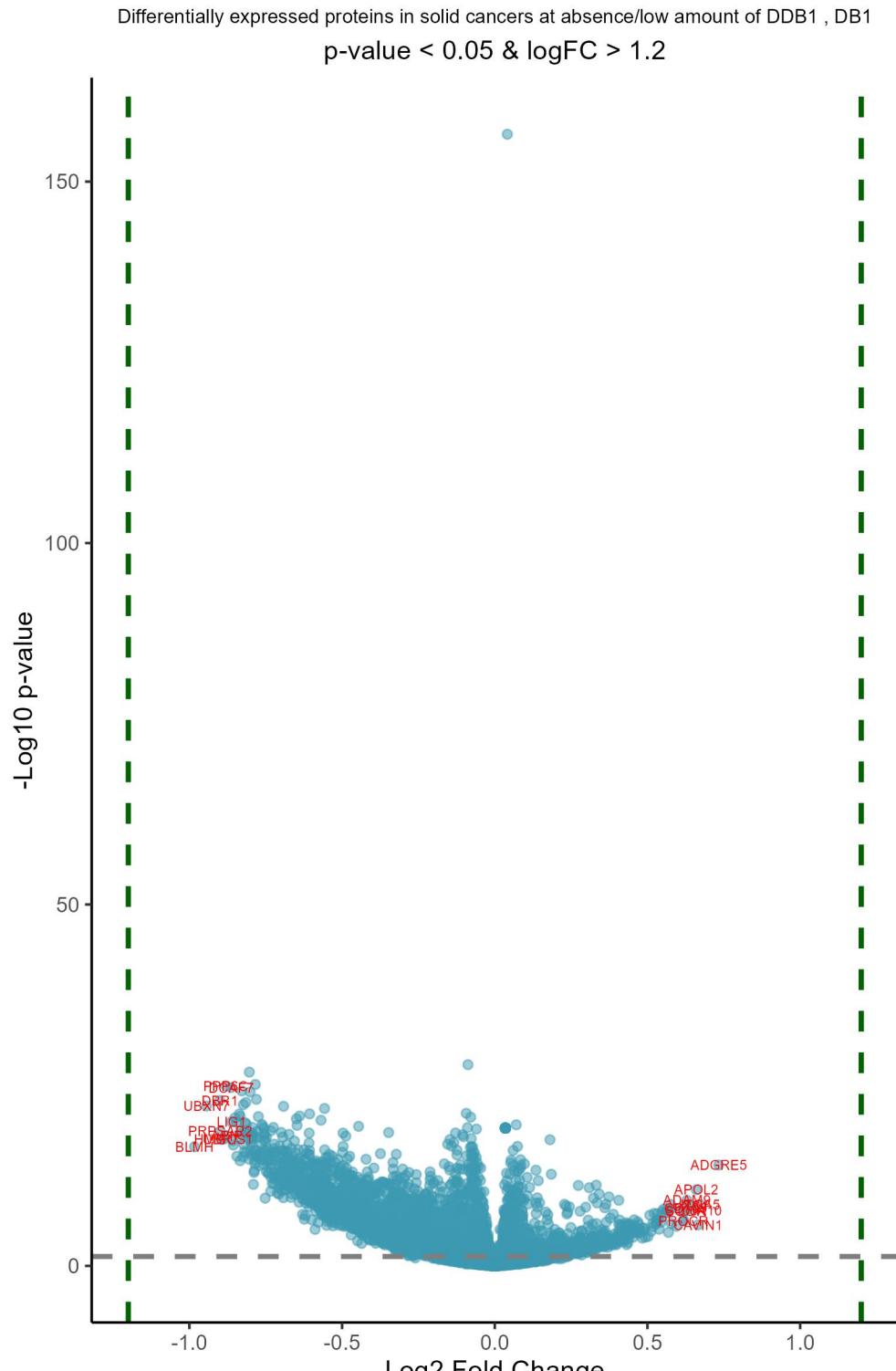


GO Cellular Component downregulated

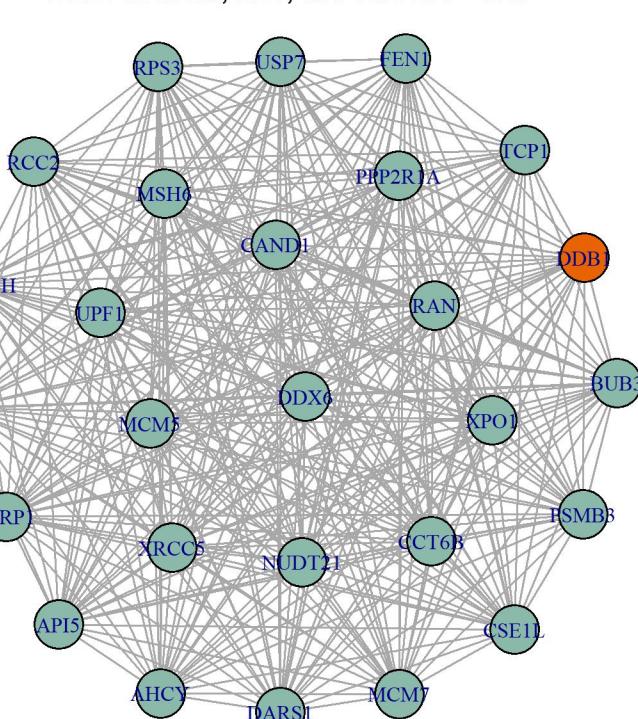
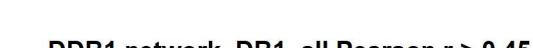
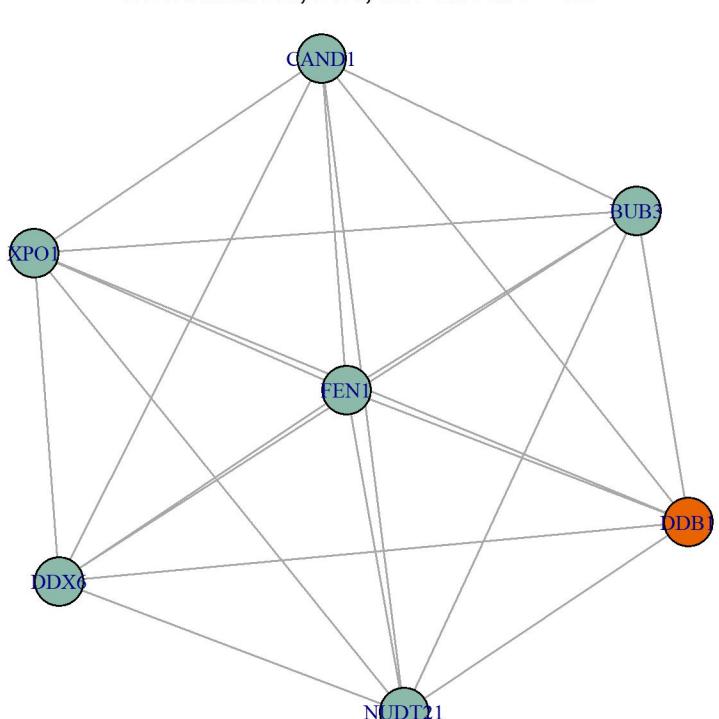




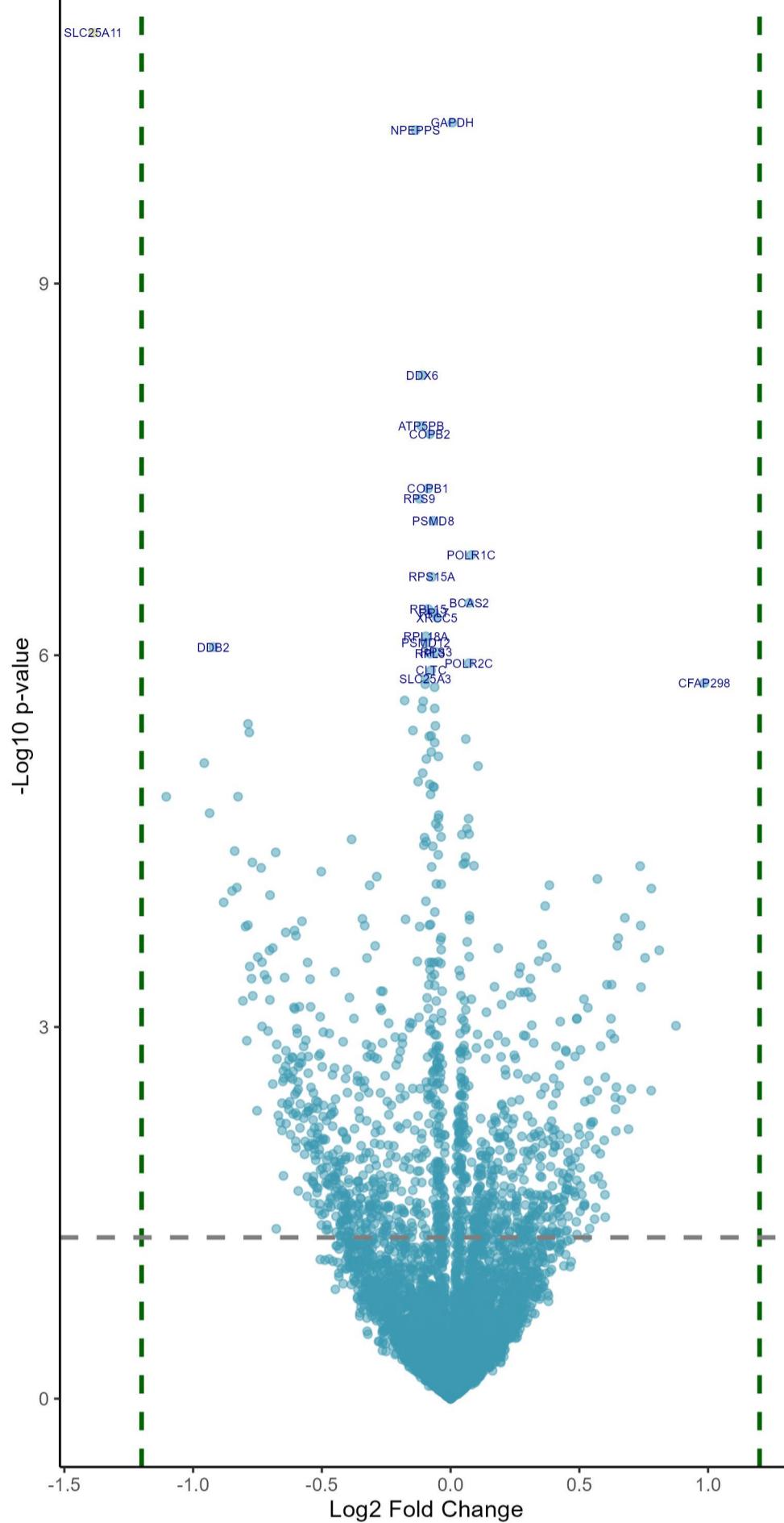
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.39	3.14e-08	SLC25A11	solute carrier family 25 member 11	0.99	4.38e-04	CFAP298	cilia and flagella associated prote
-1.1	1.77e-03	TM9SF2	transmembrane 9 superfamily member	0.88	3.19e-02	IGF2BP1	insulin like growth factor 2 mRNA b
-0.96	1.15e-03	GUSB	glucuronidase beta	0.81	1.33e-02	CRIP1	CXXC repeat containing interactor o
-0.94	2.36e-03	RPS27L	ribosomal protein S27 like	0.78	5.83e-03	C1orf131	chromosome 1 open reading frame 131
-0.92	3.01e-04	DDB2	damage specific DNA binding protein	0.78	6.11e-02	TUBB3	tubulin beta 3 class III
-0.88	7.21e-03	MAGT1	magnesium transporter 1	0.76	1.46e-02	PDLIM7	PDZ and LIM domain 7
-0.85	6.03e-03	BPNT2	3'(2'), 5'-bisphosphate nucleotidas	0.74	2.02e-02	SETD7	SET domain containing 7, histone ly
-0.84	3.72e-03	SEC11A	SEC11 homolog A, signal peptidase c	0.74	9.72e-03	HAUS1	HAUS augmin like complex subunit 1
-0.83	5.80e-03	TMEM33	transmembrane protein 33	0.74	4.40e-03	SKA3	spindle and kinetochore associated
-0.83	1.77e-03	INTS11	integrator complex subunit 11	0.7	5.97e-02	TPM1	tropomyosin 1
-0.81	2.35e-02	GLB1	galactosidase beta 1	0.69	9.25e-02	VPS37C	VPS37C subunit of ESCRT-I
-0.8	9.72e-03	DAD1	defender against cell death 1	0.68	9.21e-03	PDCL	phosducin like
-0.79	3.76e-02	SAR1B	secretion associated Ras related GT	0.66	6.75e-02	TP53	tumor protein p53
-0.79	9.72e-03	SLC25A10	solute carrier family 25 member 10	0.65	1.15e-02	CKAP2	cytoskeleton associated protein 2
-0.79	7.44e-04	DPP9	dipeptidyl peptidase 9	0.65	1.27e-02	RCOR1	REST corepressor 1
-0.78	7.97e-04	IER3IP1	immediate early response 3 interact	0.64	5.91e-02	ACYP2	acylphosphatase 2
-0.78	1.59e-02	OVCA2	OVCA2 serine hydrolase domain conta	0.64	9.42e-02	CD81	CD81 molecule
-0.77	1.82e-02	ABHD12	abhydrolase domain containing 12, I	0.64	7.54e-02	TUBB2B	tubulin beta 2B class IIb
-0.77	4.32e-03	SHMT1	serine hydroxymethyltransferase 1	0.64	6.57e-02	PTK2	protein tyrosine kinase 2
-0.77	2.25e-02	SLC25A1	solute carrier family 25 member 1	0.64	3.65e-02	BLOC1S5	biogenesis of lysosomal organelles
-0.75	7.66e-02	BLVRA	biliverdin reductase A	0.63	1.98e-02	MRFAP1	Morf4 family associated protein 1
-0.75	1.46e-02	STAG1	stromal antigen 1	0.62	2.94e-02	NECTIN2	nectin cell adhesion molecule 2
-0.74	4.43e-03	TEX10	testis expressed 10	0.62	3.49e-02	NCOA7	nuclear receptor coactivator 7
-0.73	3.21e-02	PEX11B	peroxisomal biogenesis factor 11 be	0.61	1.98e-02	GON7	GON7 subunit of KEOPS complex
-0.73	1.50e-02	TMEM11	transmembrane protein 11	0.6	5.39e-02	SDE2	SDE2 telomere maintenance homolog
-0.72	1.75e-02	ARL1	ADP ribosylation factor like GTPase	0.6	2.21e-01	TCL1A	TCL1 family AKT coactivator A
-0.71	1.82e-02	CSNK1A1	casein kinase 1 alpha 1	0.6	1.80e-01	POLR2K	RNA polymerase II, I and III subuni
-0.71	3.38e-02	ALDH3A2	aldehyde dehydrogenase 3 family mem	0.6	1.02e-01	CHMP5	charged multivesicular body protein
-0.7	1.33e-02	BCAT2	branched chain amino acid transamin	0.59	1.62e-01	GCSH	glycine cleavage system protein H



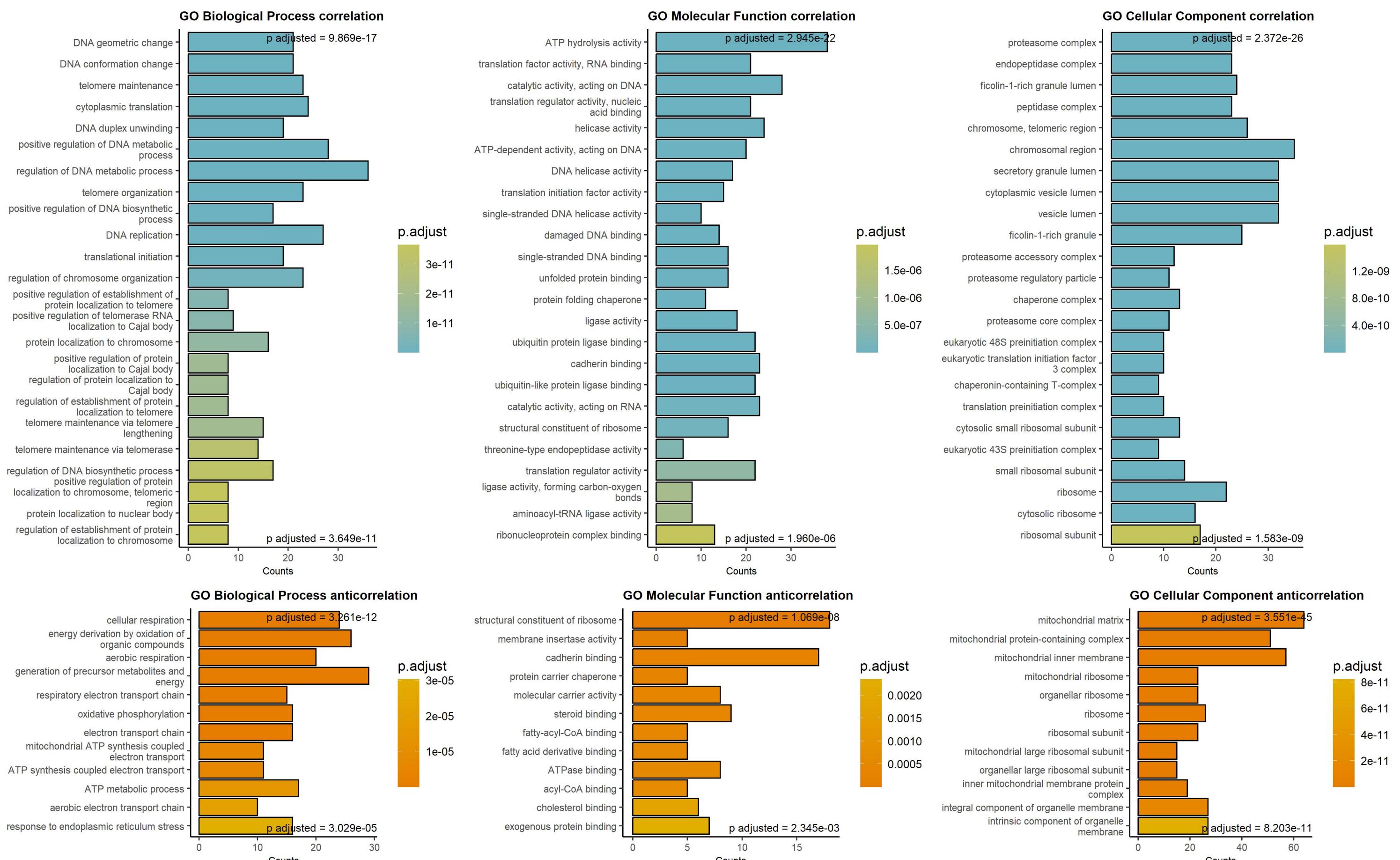
Downregulated in solid cancers at low/absent DDB1				Upregulated in solid cancers at low/absent DDB1			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.98	1.26e-15	BLMH	bleomycin hydrolase	0.73	2.53e-13	ADGRE5	adhesion G protein-coupled receptor
-0.94	3.70e-20	UBXN7	UBX domain protein 7	0.67	2.20e-08	ITGA5	integrin subunit alpha 5
-0.9	8.01e-21	DBR1	debranching RNA lariats 1	0.67	8.44e-06	CAVIN1	caveolae associated protein 1
-0.9	1.27e-17	PRPSAP2	phosphoribosyl pyrophosphate synthetase	0.66	3.16e-10	APOL2	apolipoprotein L2
-0.9	1.37e-16	UBR7	ubiquitin protein ligase E3 component	0.65	1.18e-07	S100A10	S100 calcium binding protein A10
-0.89	1.29e-16	HMGCS1	3-hydroxy-3-methylglutaryl-CoA synthetase	0.64	3.05e-08	UXS1	UDP-glucuronate decarboxylase 1
-0.88	1.36e-22	PPP6C	protein phosphatase 6 catalytic subunit	0.63	6.38e-09	ADAM9	ADAM metallopeptidase domain 9
-0.88	4.43e-17	APIP	APAF1 interacting protein	0.63	6.05e-08	CD109	CD109 molecule
-0.86	2.01e-22	DCAF7	DDB1 and CUL4 associated factor 7	0.62	1.46e-07	SQOR	sulfide quinone oxidoreductase
-0.86	2.84e-18	LIG1	DNA ligase 1	0.62	2.82e-06	PROCR	protein C receptor
-0.86	2.09e-16	CDK4	cyclin dependent kinase 4	0.62	2.08e-06	NT5E	5'-nucleotidase ecto
-0.86	7.38e-16	SHMT1	serine hydroxymethyltransferase 1	0.6	1.12e-07	SP100	SP100 nuclear antigen
-0.85	9.28e-19	HAT1	histone acetyltransferase 1	0.59	1.27e-05	CAV1	caveolin 1
-0.85	3.31e-18	CMTR1	cap methyltransferase 1	0.58	5.59e-06	CTSZ	cathepsin Z
-0.84	1.99e-14	LANCL1	LanC like 1	0.58	2.14e-08	RRAS	RAS related
-0.84	3.36e-19	PTPA	protein phosphatase 2 phosphatase alpha	0.58	7.55e-08	HSPG2	heparan sulfate proteoglycan 2
-0.83	8.15e-17	TKFC	triokinase and FMN cyclase	0.57	7.86e-05	CD44	CD44 molecule (Indian blood group)
-0.83	6.58e-19	PDE6D	phosphodiesterase 6D	0.57	2.11e-07	DPP4	dipeptidyl peptidase 4
-0.83	7.36e-14	PSME3IP1	proteasome activator subunit 3 interactor	0.56	9.20e-08	ITGB5	integrin subunit beta 5
-0.83	9.24e-18	POLA2	DNA polymerase alpha 2, accessory subunit	0.56	2.59e-07	RHOC	ras homolog family member C
-0.83	5.10e-22	PREP	prolyl endopeptidase	0.55	8.70e-08	KIRREL1	kirre like nephrin family adhesion
-0.83	2.20e-17	PPP1R14B	protein phosphatase 1 regulatory subunit 14B	0.55	2.07e-07	CD58	CD58 molecule
-0.82	2.41e-14	PPP2CA	protein phosphatase 2 catalytic subunit	0.54	3.97e-06	CYBRD1	cytochrome b reductase 1
-0.82	2.54e-20	IPO9	importin 9	0.54	3.02e-05	LGALS3	galectin 3
-0.82	5.69e-16	EIF4A2	eukaryotic translation initiation factor 4A2	0.54	2.02e-06	TAP1	transporter 1, ATP binding cassette
-0.82	5.03e-15	PPM1A	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent	0.53	1.57e-06	LACTB	lactamase beta
-0.82	3.69e-18	TLE5	TLE family member 5, transcriptional regulator	0.53	3.26e-07	NCEH1	neutral cholesterol ester hydrolase
-0.82	1.33e-20	XPO5	exportin 5	0.53	6.34e-06	RAB32	RAB32, member RAS oncogene family



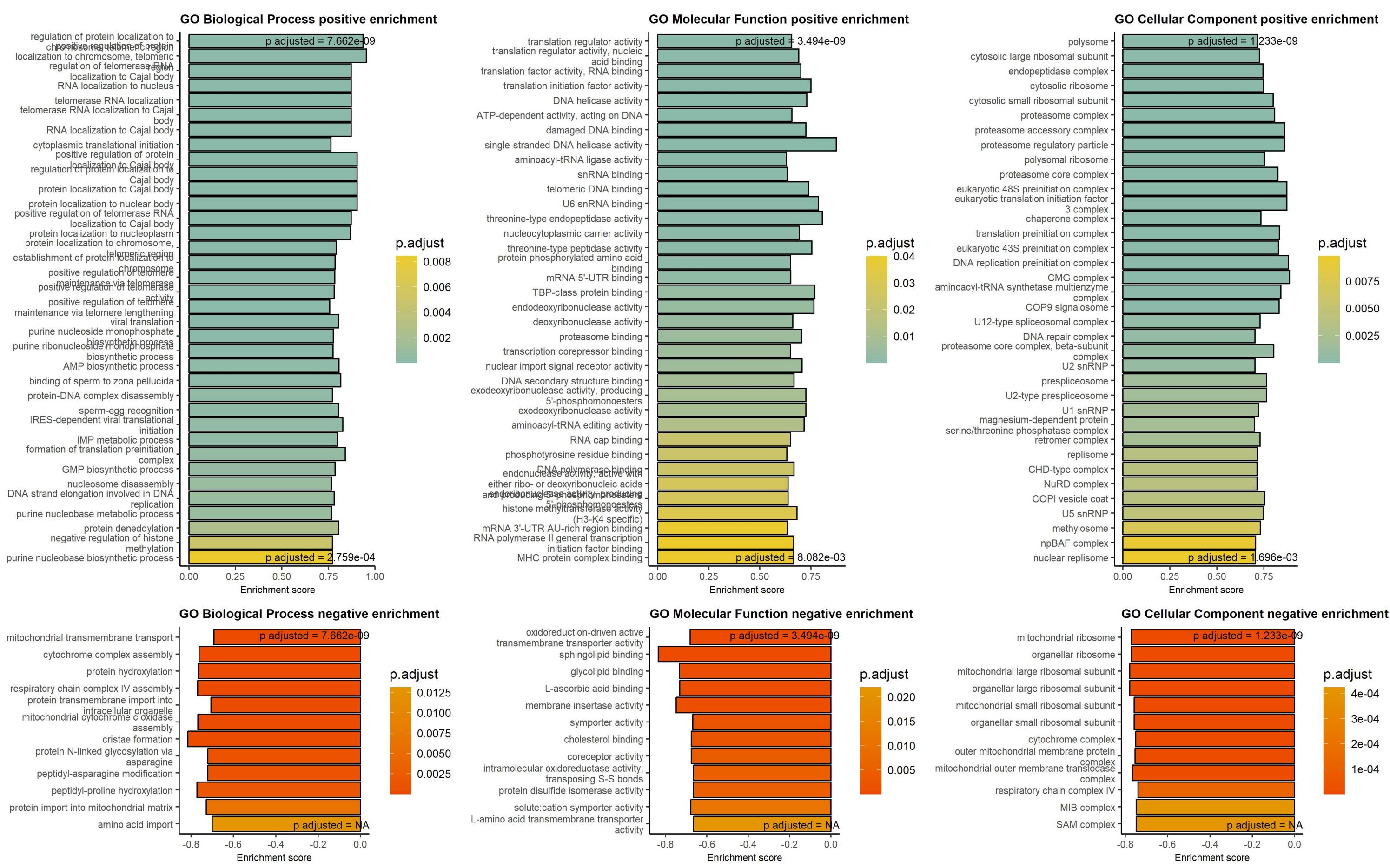
Sorted by p values!
 Downregulated in blood cancers at low/absent DDB1 Upregulated in blood cancers at low/absent DDB1



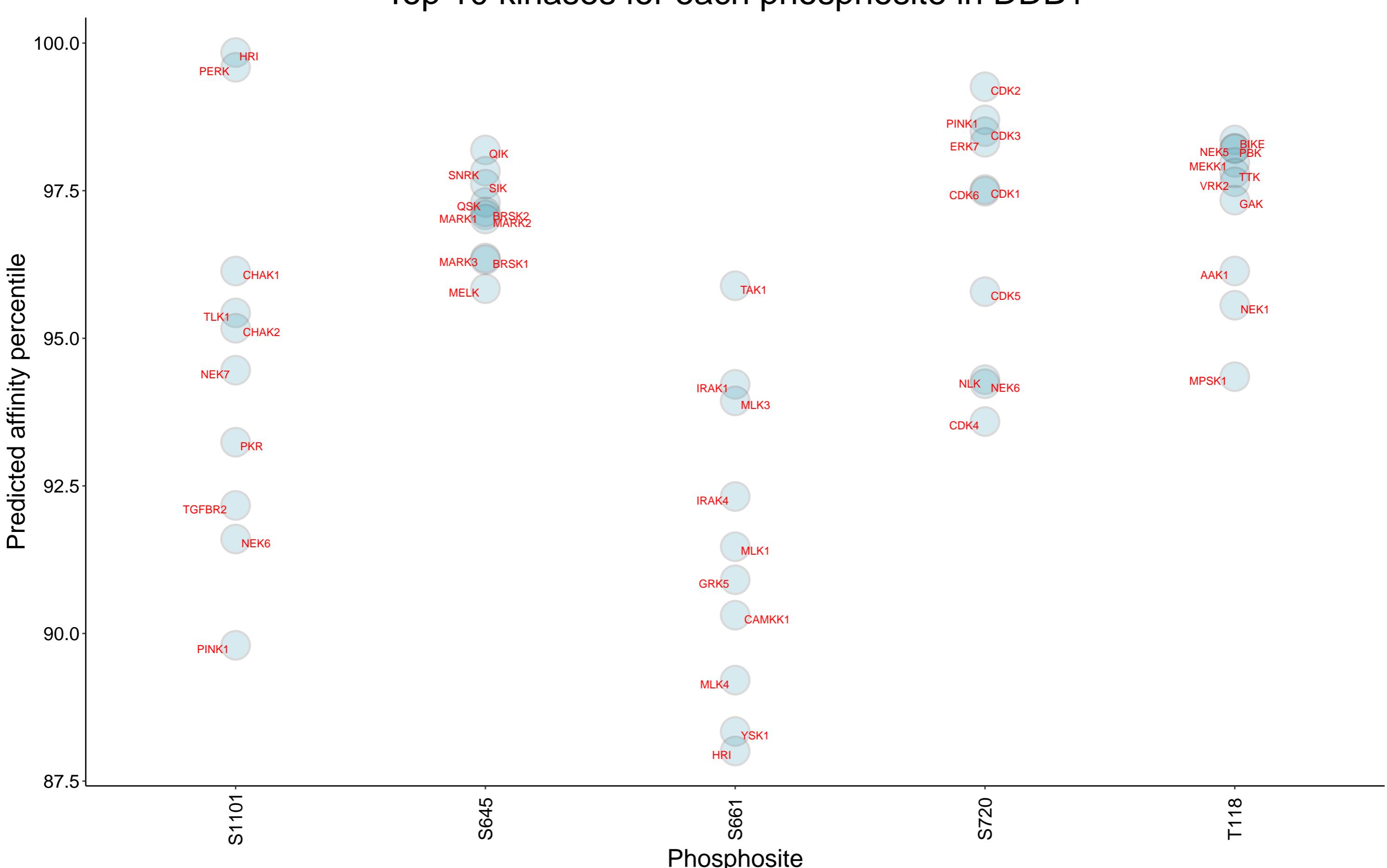
Top 250 correlation coefficients overrepresentation, DDB1 protein, DB1



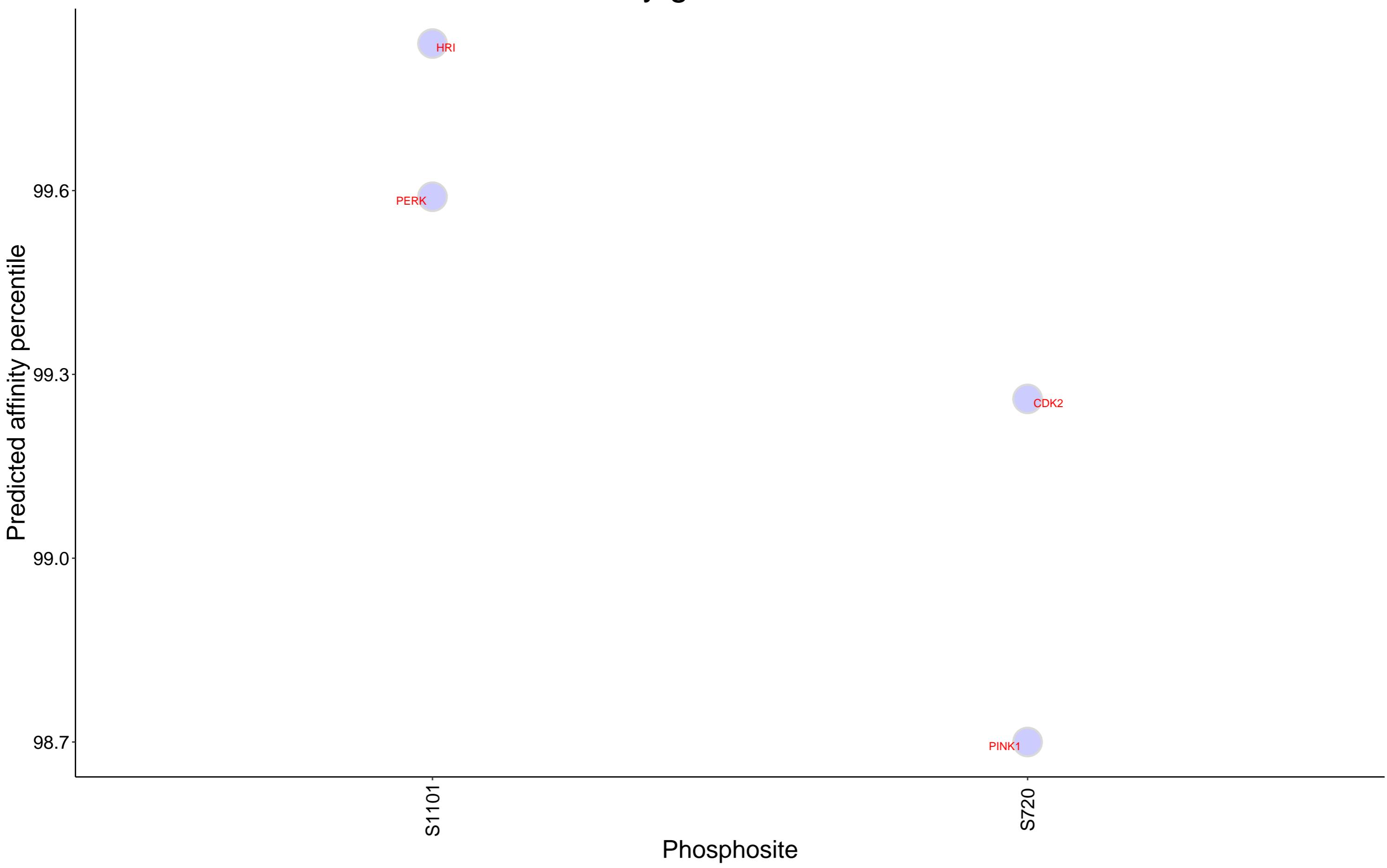
Gene Set Enrichment analysis on protein correlation coefficients, DDB1 protein, DB1



Top 10 kinases for each phosphosite in DDB1



Kinases with affinity greater than 98.5% to DDB1



Top 15 positive correlation coefficients for DDB1 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

