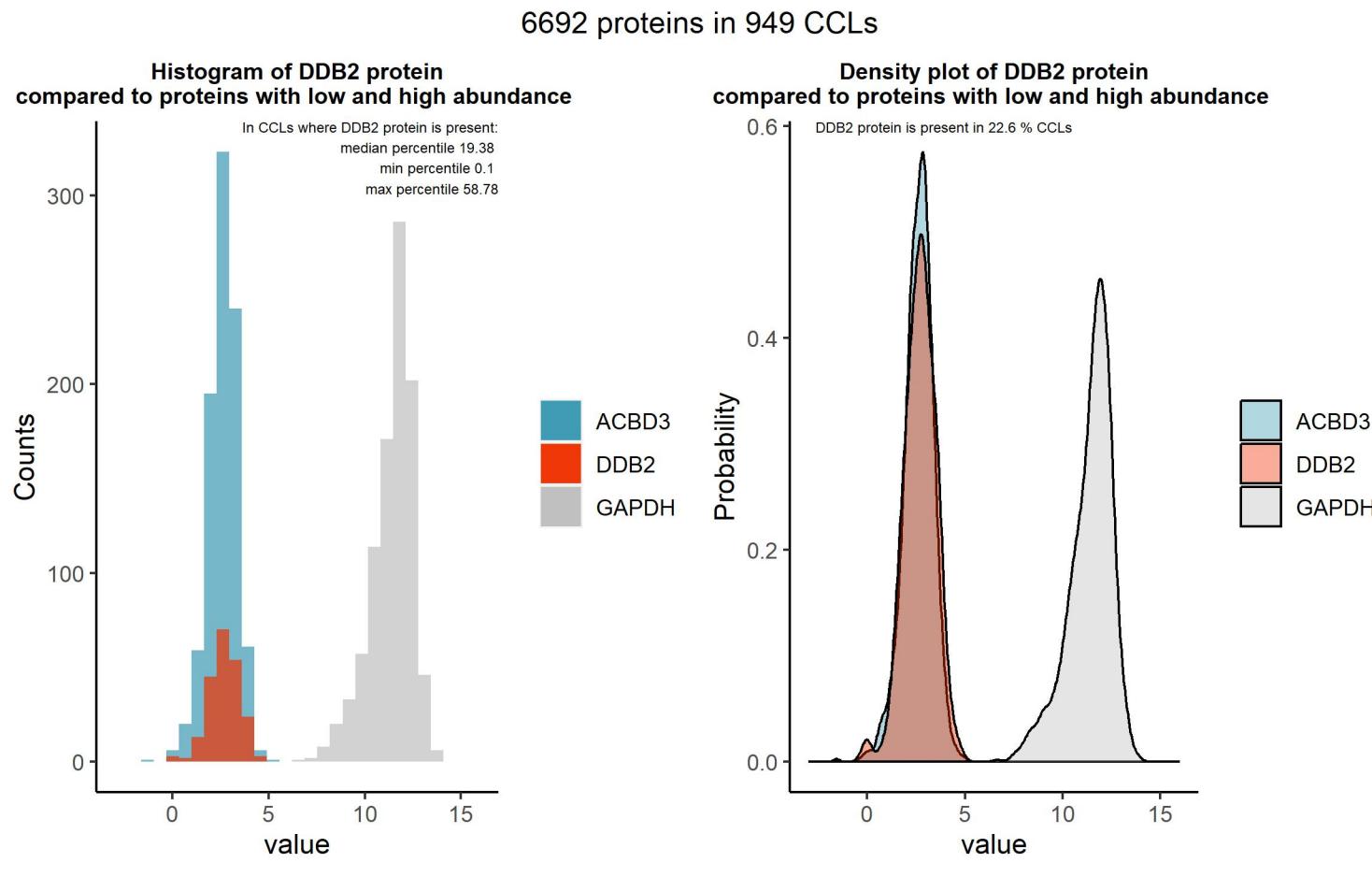


# DDB2

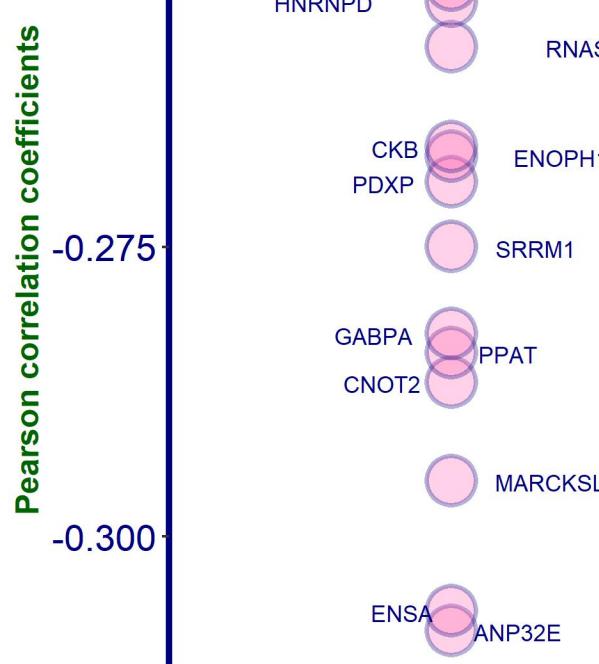
Protein name: DDB2 ; UNIPROT: Q92466 ; Gene name: damage specific DNA binding protein 2

Ligandable: Yes ; Ligandable\_by\_Chem: NA ; Is\_enzyme: NA (<https://cansar.ai/>)

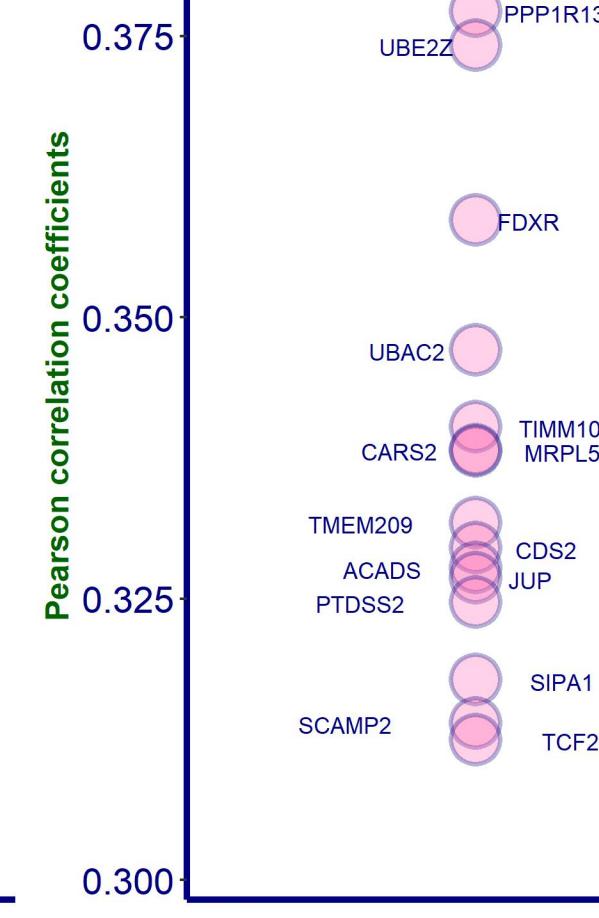
## Sanger Institute Protein Database 1 (DB1), protein presence is certain



### Top negative correlations of DDB2 protein, DB1

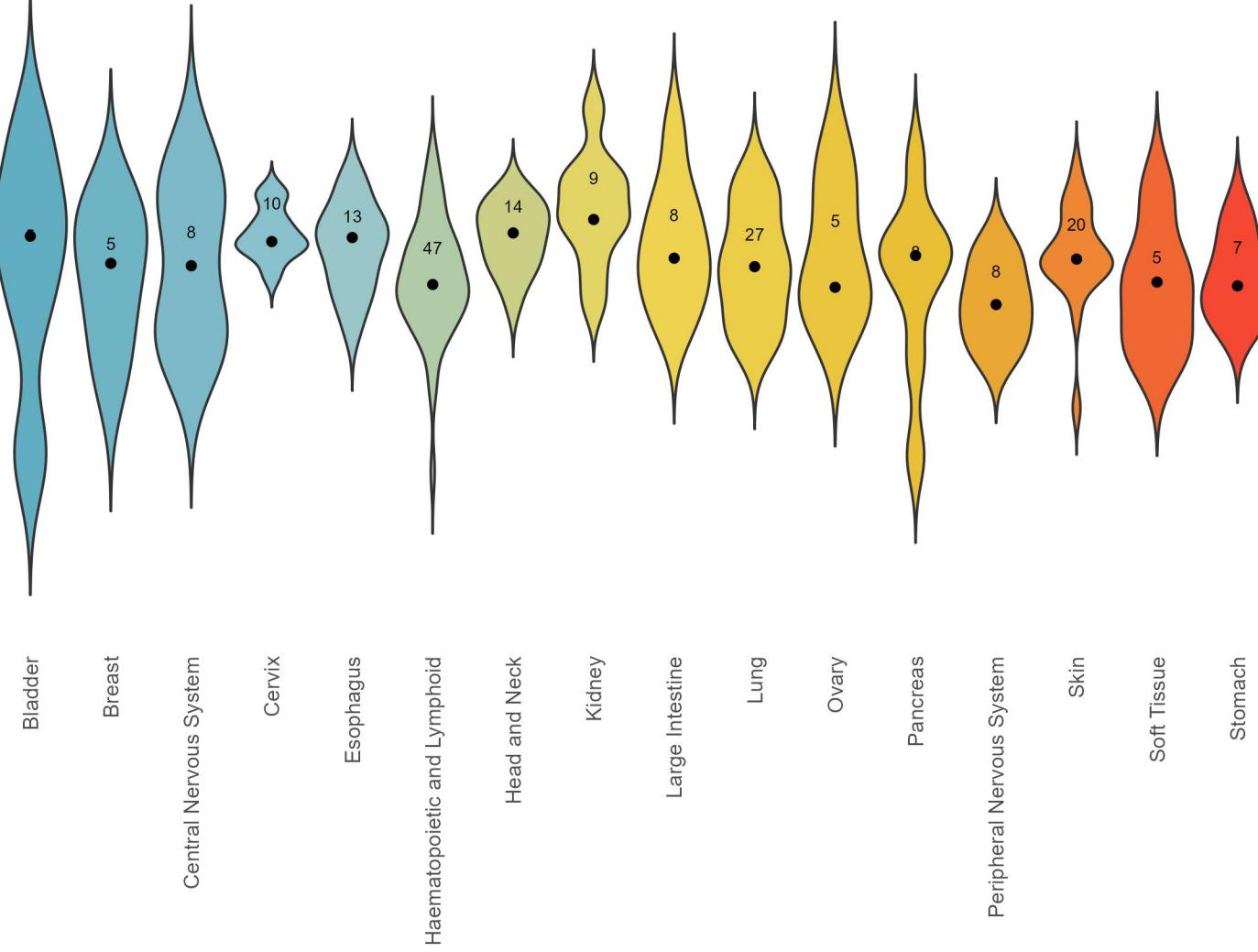


### Top positive correlations of DDB2 protein, DB1



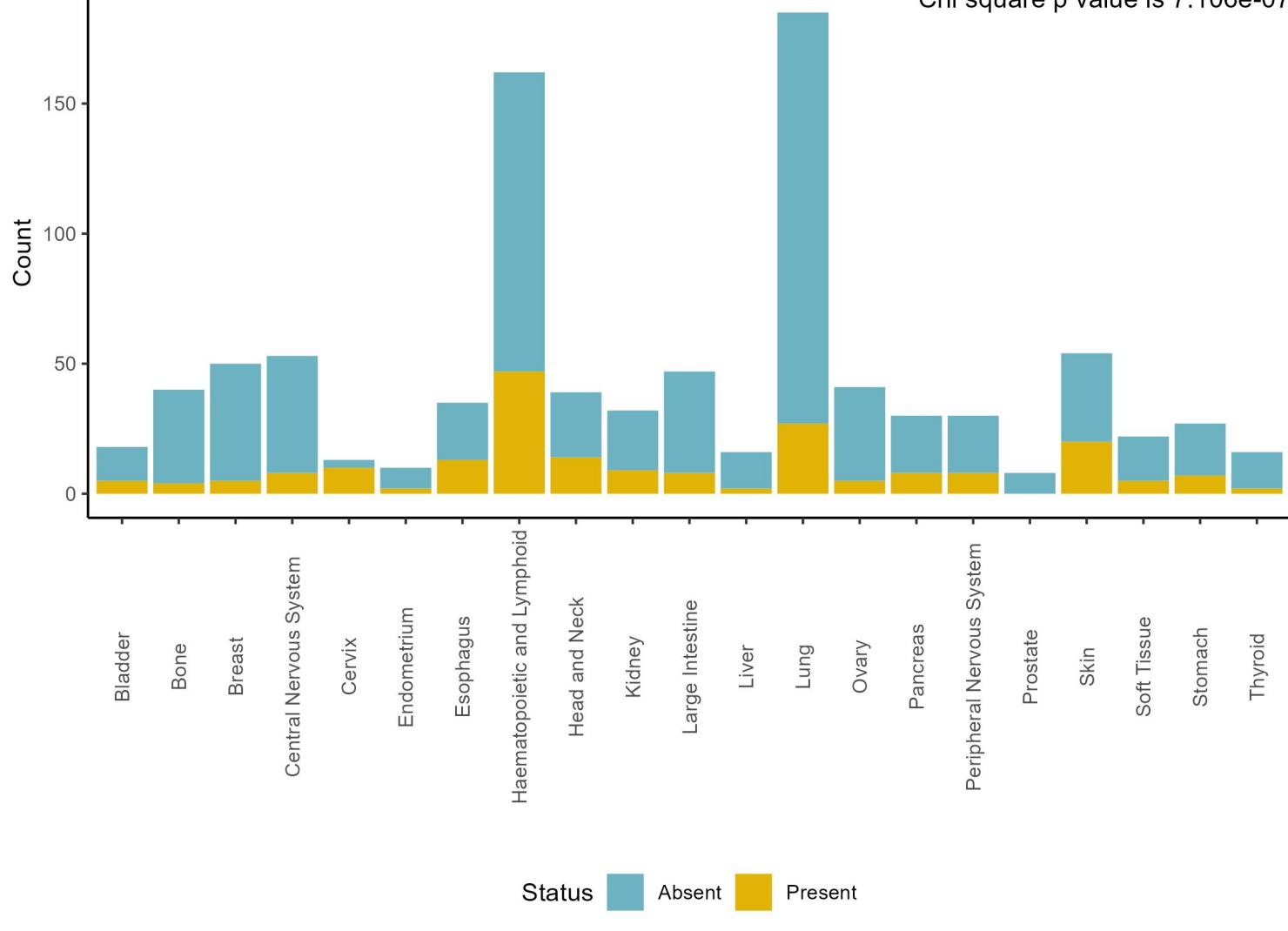
## Amount of DDB2 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 1.217e-01



## Present and absent DDB2 protein counts by tissue, DB1

Chi square p value is 7.106e-07

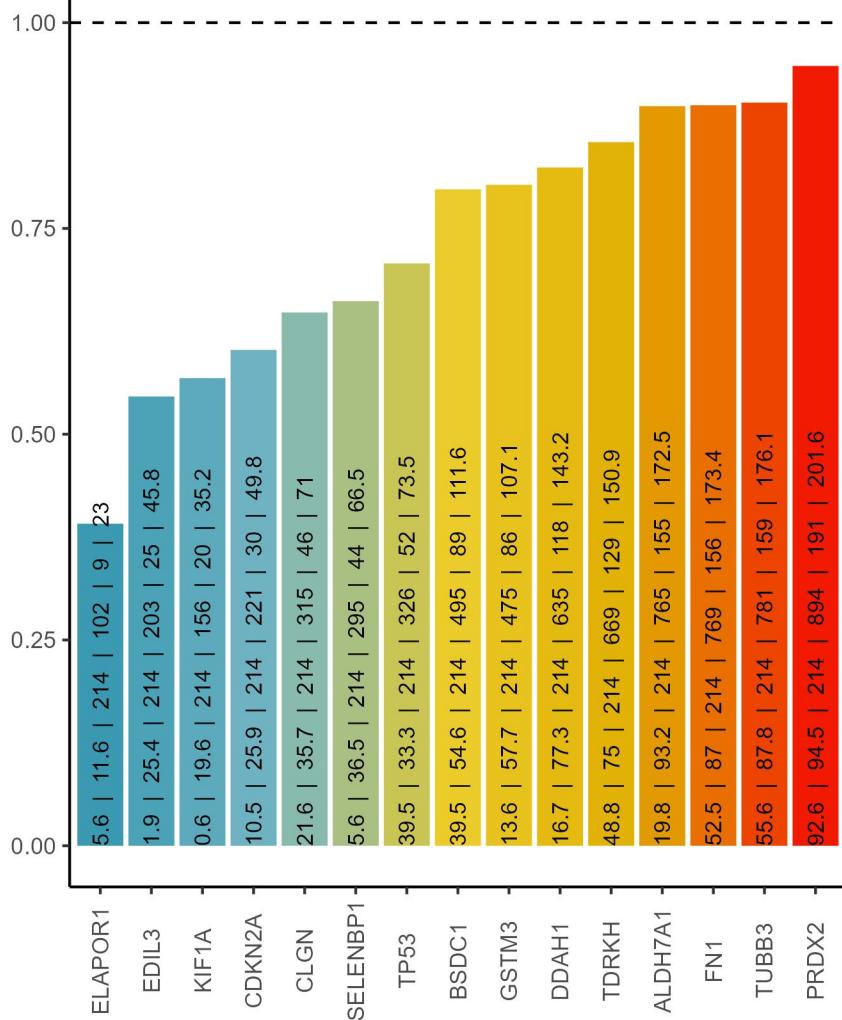


## Cooccurrence with DDB2 protein, DB1

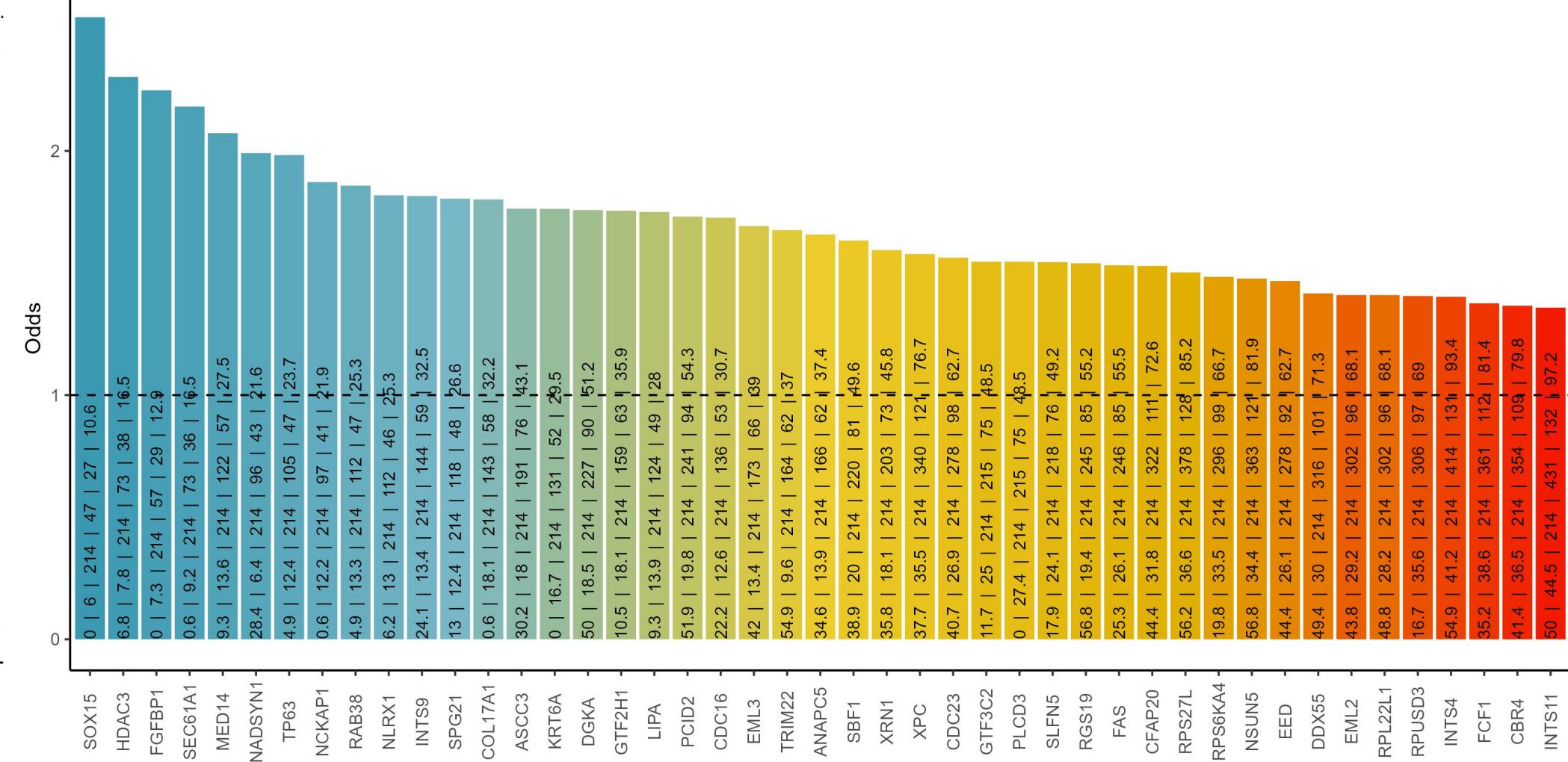
% of DDB2 in blood cancers: 29 ; % of DDB2 in solid cancers: 21.3

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of DDB2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

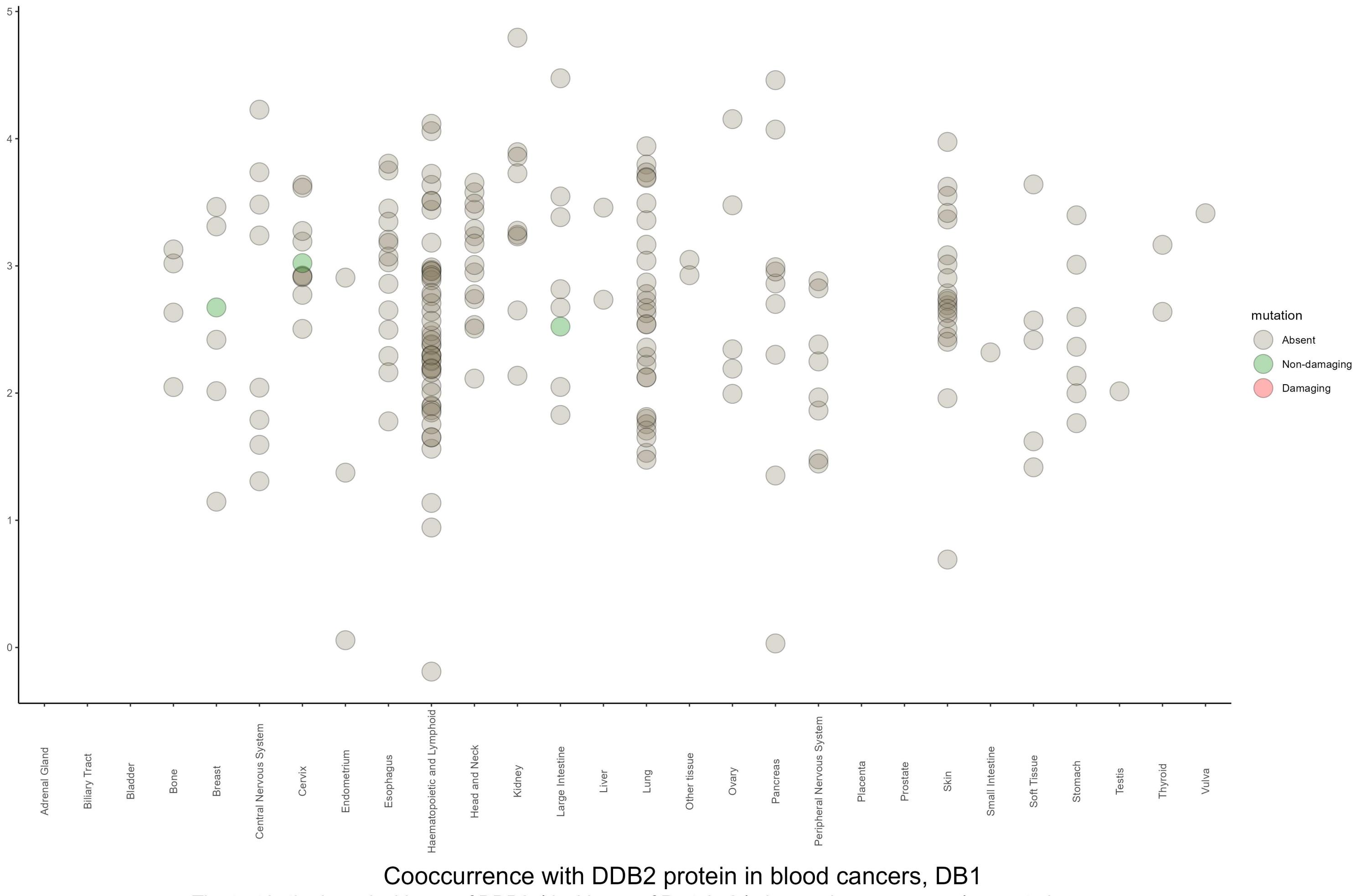
### Negative cooccurrence



### Positive cooccurrence

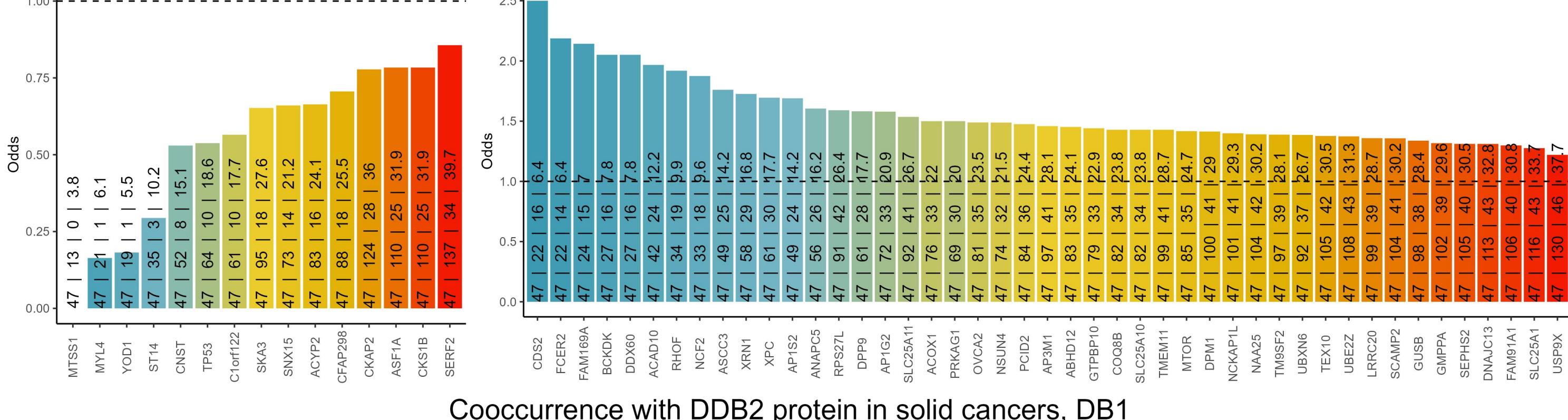


# Amount of DDB2 protein and mutation status by tissue, DB1



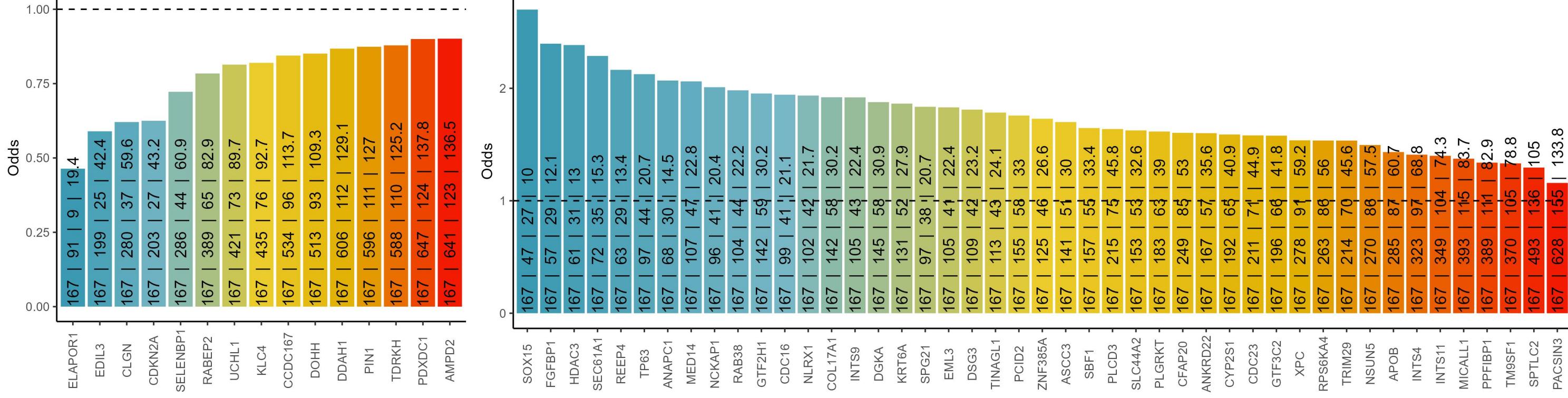
## Cooccurrence with DDB2 protein in blood cancers, DB1

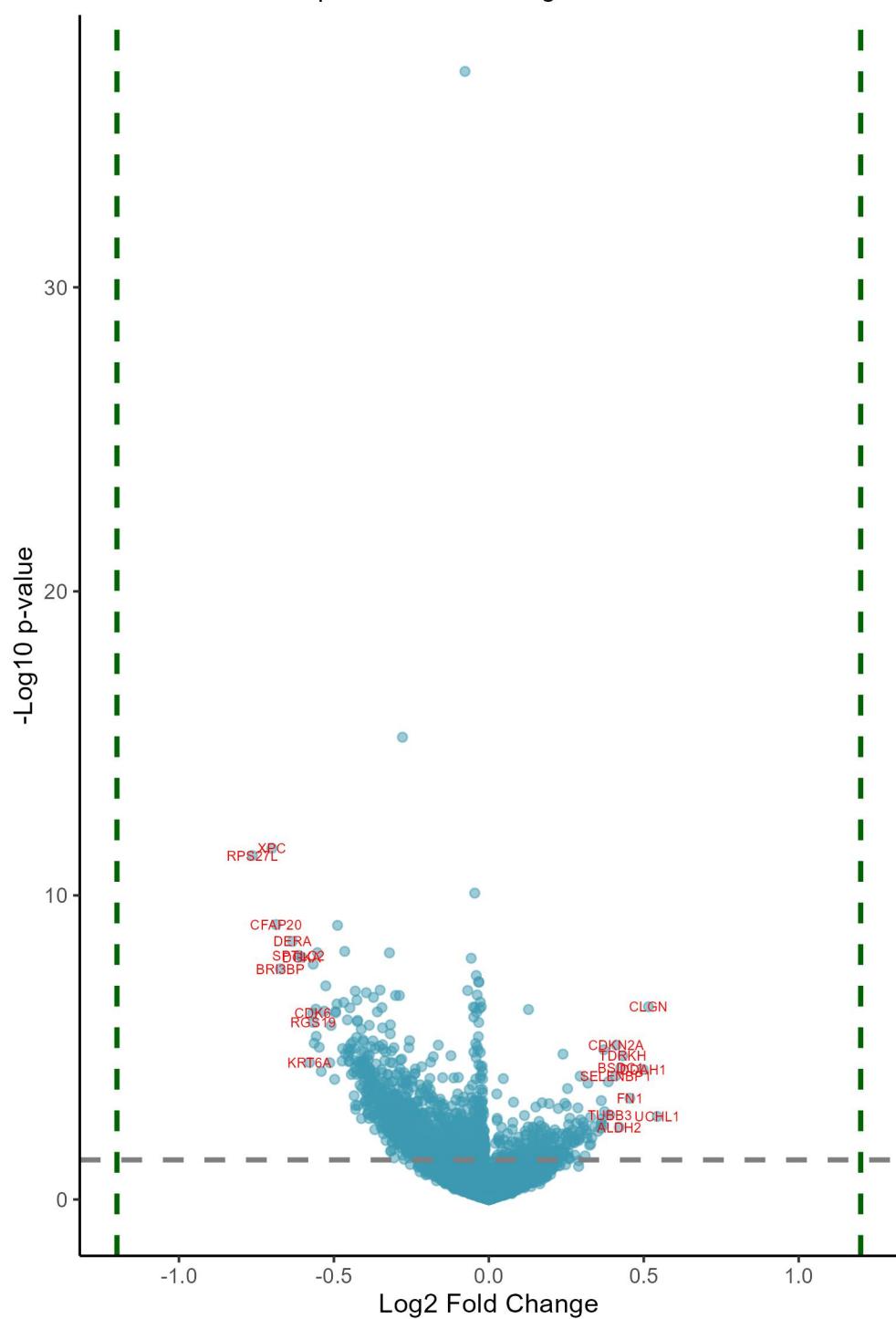
The text in the bars: incidence of DDB2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



## Cooccurrence with DDB2 protein in solid cancers, DB1

The text in the bars: incidence of DDB2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

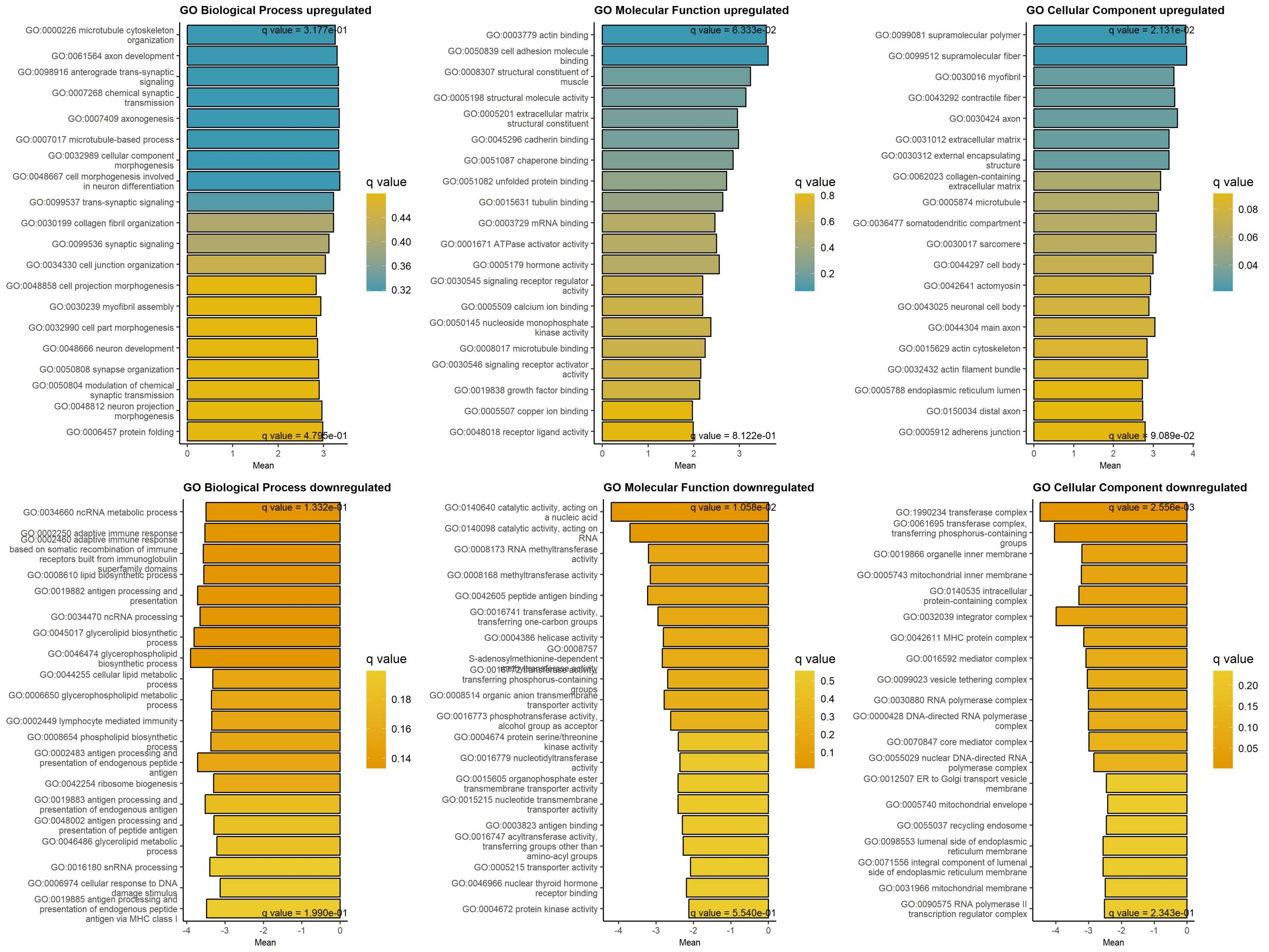




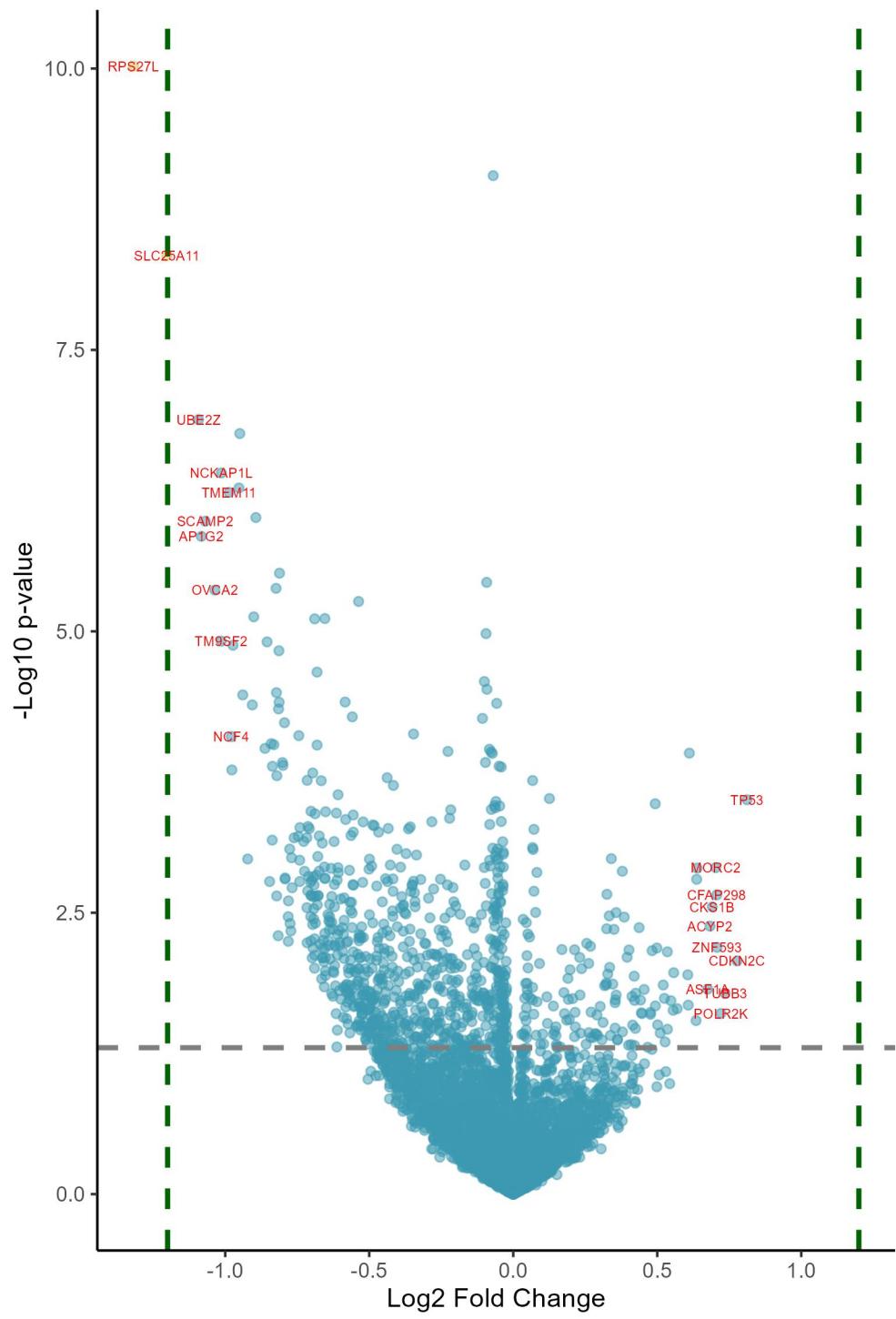
## Downregulated at low/absent DDB2 Upregulated at low/absent DDB2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.76	6.49e-09	RPS27L	ribosomal protein S27 like	0.54	2.74e-02	UCHL1	ubiquitin C-terminal hydrolase L1
-0.7	4.68e-09	XPC	XPC complex subunit, DNA damage rec	0.52	8.49e-05	CLGN	calmegin
-0.69	8.04e-07	CFAP20	cilia and flagella associated prote	0.5	2.56e-03	DDAH1	dimethylarginine dimethylaminohydro
-0.67	1.02e-05	BRI3BP	BRI3 binding protein	0.46	1.13e-02	FN1	fibronectin 1
-0.63	2.40e-06	DERA	deoxyribose-phosphate aldolase	0.43	1.24e-03	TDRKH	tudor and KH domain containing
-0.61	4.82e-06	SPTLC2	serine palmitoyltransferase long ch	0.43	2.36e-03	BSDC1	BSD domain containing 1
-0.6	5.10e-06	DGKA	diacylglycerol kinase alpha	0.42	4.63e-02	ALDH2	aldehyde dehydrogenase 2 family mem
-0.58	1.74e-03	KRT6A	keratin 6A	0.41	7.54e-04	CDKN2A	cyclin dependent kinase inhibitor 2
-0.57	1.04e-04	CDK6	cyclin dependent kinase 6	0.41	3.42e-03	SELENBP1	selenium binding protein 1
-0.57	1.85e-04	RGS19	regulator of G protein signaling 19	0.39	2.52e-02	TUBB3	tubulin beta 3 class III
-0.57	7.58e-06	MICALL1	MICAL like 1	0.39	4.60e-03	TP53	tumor protein p53
-0.56	7.00e-04	COL17A1	collagen type XVII alpha 1 chain	0.37	2.18e-02	GSTM3	glutathione S-transferase mu 3
-0.56	8.97e-05	TAOK3	TAO kinase 3	0.37	9.13e-04	EDIL3	EGF like repeats and discoidin doma
-0.56	4.72e-04	ATP5MF	ATP synthase membrane subunit f	0.37	4.23e-02	TMEM263	transmembrane protein 263
-0.55	4.30e-06	INTS11	integrator complex subunit 11	0.36	3.05e-02	ENAH	ENAH actin regulator
-0.55	8.40e-04	RPL22L1	ribosomal protein L22 like 1	0.36	1.31e-02	ATG9A	autophagy related 9A
-0.54	2.81e-03	RAB11B	RAB11B, member RAS oncogene family	0.36	3.74e-02	MYEF2	myelin expression factor 2
-0.53	9.90e-05	CD44	CD44 molecule (Indian blood group)	0.36	4.82e-02	CCDC167	coiled-coil domain containing 167
-0.53	2.99e-05	CDC23	cell division cycle 23	0.35	5.61e-02	TPM2	tropomyosin 2
-0.51	1.76e-03	TRIM29	tripartite motif containing 29	0.34	4.48e-02	AK1	adenylate kinase 1
-0.51	2.21e-04	FAS	Fas cell surface death receptor	0.33	7.72e-02	CFL2	cofilin 2
-0.5	4.07e-03	BST2	bone marrow stromal cell antigen 2	0.33	1.03e-01	MAP1B	microtubule associated protein 1B
-0.49	1.02e-04	TMEM33	transmembrane protein 33	0.33	2.82e-02	NOTCH2	notch receptor 2
-0.49	9.90e-05	RPS6KA4	ribosomal protein S6 kinase A4	0.33	1.08e-01	CALD1	caldesmon 1
-0.49	7.48e-05	AP3M1	adaptor related protein complex 3 s	0.32	4.94e-03	TSPY5L	TSPY like 5
-0.49	8.04e-07	SLC25A11	solute carrier family 25 member 11	0.32	6.30e-02	AKT1S1	AKT1 substrate 1
-0.47	1.85e-03	ACSS1	acyl-CoA synthetase short chain fam	0.32	7.84e-02	ALDH7A1	aldehyde dehydrogenase 7 family mem
-0.47	8.74e-04	ZNF148	zinc finger protein 148	0.31	5.40e-02	DDAH2	dimethylarginine dimethylaminohydro
-0.47	6.88e-05	NSUN5	NOP2/Sun RNA methyltransferase 5	0.31	1.78e-01	H1-0	H1.0 linker histone

## GAGE analysis on upregulated and downregulated proteins at low/absent DDB2 protein, DB1



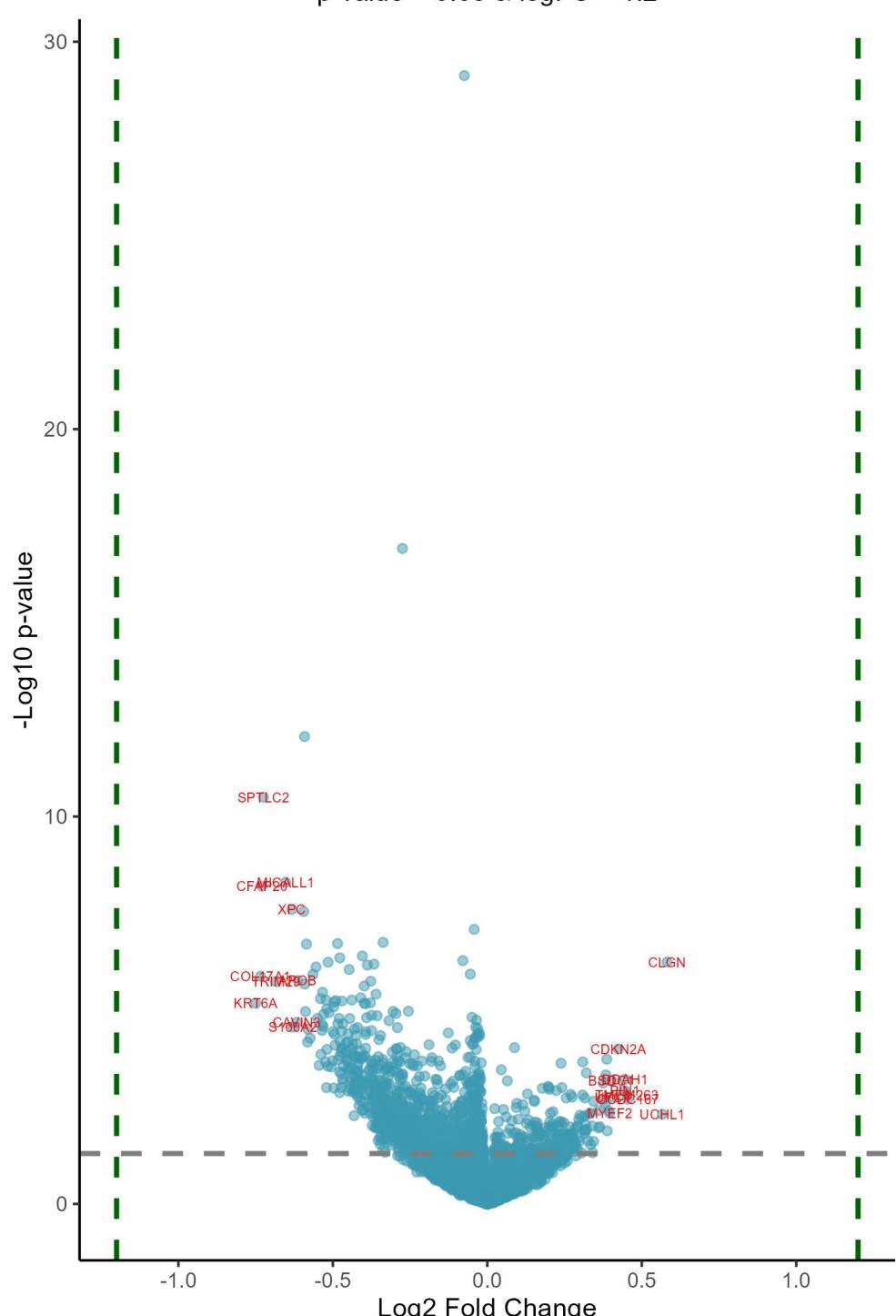
Differentially expressed proteins in blood cancers at absence/low amount of DDB2 , DB1  
p-value < 0.05 & logFC > 1.2



Downregulated in blood cancers at low/absent DDB2 Upregulated in blood cancers at low/absent DDB2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.32	3.18e-07	RPS27L	ribosomal protein S27 like	0.81	3.11e-02	TP53	tumor protein p53
-1.2	7.65e-06	SLC25A11	solute carrier family 25 member 11	0.78	1.42e-01	CDKN2C	cyclin dependent kinase inhibitor 2
-1.09	1.75e-04	UBE2Z	ubiquitin conjugating enzyme E2 Z	0.74	2.00e-01	TUBB3	tubulin beta 3 class III
-1.08	7.94e-04	AP1G2	adaptor related protein complex 1 s	0.72	2.42e-01	POLR2K	RNA polymerase II, I and III subunit
-1.07	6.36e-04	SCAMP2	secretory carrier membrane protein	0.71	1.25e-01	ZNF593	zinc finger protein 593
-1.04	1.79e-03	OVCA2	OVCA2 serine hydrolase domain conta	0.71	7.44e-02	CFAP298	cilia and flagella associated protein
-1.01	3.59e-03	TM9SF2	transmembrane 9 superfamily member	0.7	6.06e-02	MORC2	MORC family CW-type zinc finger 2
-1.01	3.72e-04	NCKAP1L	NCK associated protein 1 like	0.69	8.26e-02	CKS1B	CDC28 protein kinase regulatory sub
-0.99	4.31e-04	TMEM11	transmembrane protein 11	0.68	1.01e-01	ACYP2	acylphosphatase 2
-0.98	1.40e-02	NCF4	neutrophil cytosolic factor 4	0.67	1.93e-01	ASF1A	anti-silencing function 1A histone
-0.98	1.99e-02	BRI3BP	BRI3 binding protein	0.64	6.06e-02	SKA3	spindle and kinetochore associated
-0.97	3.69e-03	XPC	XPC complex subunit, DNA damage rec	0.64	6.61e-02	SNX15	sorting nexin 15
-0.95	4.31e-04	AP3M1	adaptor related protein complex 3 s	0.63	2.63e-01	IGF2BP1	insulin like growth factor 2 mRNA b
-0.95	1.94e-04	TEX10	testis expressed 10	0.61	1.61e-02	ST14	ST14 transmembrane serine protease
-0.94	8.14e-03	ABHD12	abhydrolase domain containing 12, I	0.61	2.20e-01	SERF2	small EDRK-rich factor 2
-0.92	5.66e-02	CD70	CD70 molecule	0.61	1.65e-01	UAP1	UDP-N-acetylglucosamine pyrophospho
-0.91	8.81e-03	TRAPPC4	trafficking protein particle comple	0.57	2.28e-01	GCSH	glycine cleavage system protein H
-0.9	2.58e-03	DPM1	dolichyl-phosphate mannosyltransfer	0.56	1.60e-01	PRKAR2B	protein kinase cAMP-dependent type
-0.89	6.36e-04	NAA25	N-alpha-acetyltransferase 25, NatB	0.56	2.33e-01	MRPS18C	mitochondrial ribosomal protein S18
-0.86	1.61e-02	SLC25A10	solute carrier family 25 member 10	0.55	2.08e-01	TSPY1L	TSPY like 1
-0.85	3.59e-03	SLC25A1	solute carrier family 25 member 1	0.54	4.84e-01	DDT	D-dopachrome tautomerase
-0.85	6.66e-02	DDX60	DExD/H-box helicase 60	0.54	2.89e-01	CDCA3	cell division cycle associated 3
-0.84	1.55e-02	LRRC20	leucine rich repeat containing 20	0.53	1.31e-01	KIF20A	kinesin family member 20A
-0.84	4.67e-02	ITGAL	integrin subunit alpha L	0.53	4.45e-01	TCL1A	TCL1 family AKT coactivator A
-0.84	1.91e-02	XRN1	5'-3' exoribonuclease 1	0.53	3.31e-01	CD81	CD81 molecule
-0.83	1.55e-02	ZMPSTE24	zinc metallopeptidase STE24	0.52	2.08e-01	TUBB2B	tubulin beta 2B class IIb
-0.82	1.79e-03	DERA	deoxyribose-phosphate aldolase	0.52	1.85e-01	CKAP2	cytoskeleton associated protein 2
-0.82	8.03e-03	MYO1G	myosin IG	0.51	3.01e-01	PCLAF	PCNA clamp associated factor
-0.82	7.44e-02	RPL22L1	ribosomal protein L22 like 1	0.51	4.55e-01	EPB41L2	erythrocyte membrane protein band 4

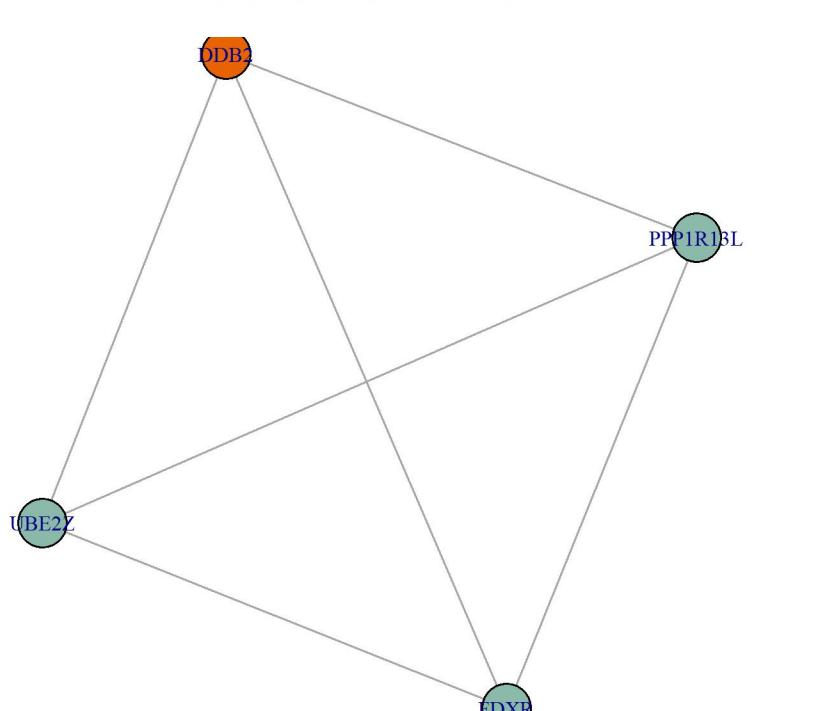
Differentially expressed proteins in solid cancers at absence/low amount of DDB2 , DB1  
p-value < 0.05 & logFC > 1.2



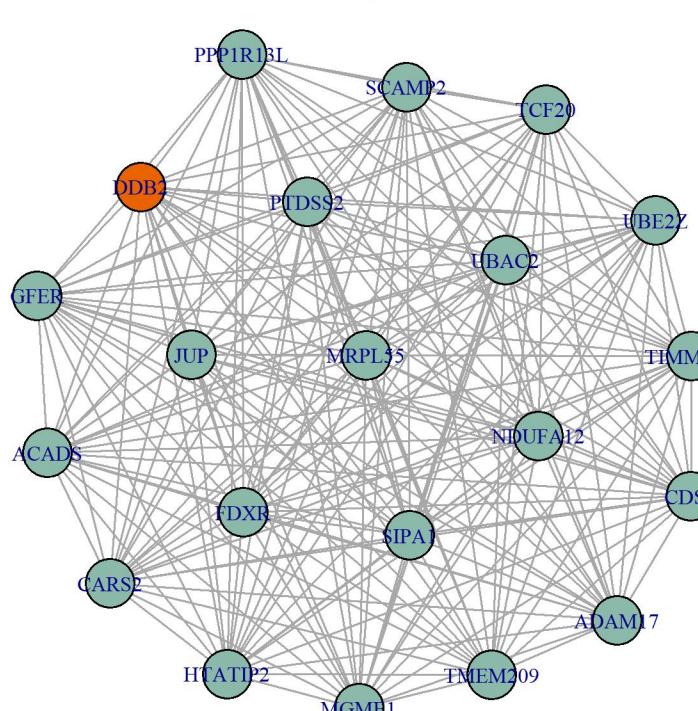
Downregulated in solid cancers at low/absent DDB2 Upregulated in solid cancers at low/absent DDB2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.75	1.05e-03	KRT6A	keratin 6A	0.58	2.13e-04	CLGN	calmegin
-0.73	3.51e-04	COL17A1	collagen type XVII alpha 1 chain	0.57	6.03e-02	UCHL1	ubiquitin C-terminal hydrolase L1
-0.73	5.94e-06	CFAP20	cilia and flagella associated protein	0.46	3.54e-02	CCDC167	coiled-coil domain containing 167
-0.72	4.20e-08	SPTLC2	serine palmitoyltransferase long ch	0.45	3.01e-02	TMEM263	transmembrane protein 263
-0.68	4.31e-04	TRIM29	tripartite motif containing 29	0.45	1.80e-02	DDAH1	dimethylarginine dimethylaminohydro
-0.65	5.51e-06	MICALL1	MICAL like 1	0.45	2.60e-02	PIN1	peptidylprolyl cis/trans isomerase,
-0.63	2.07e-05	XPC	XPC complex subunit, DNA damage rec	0.42	5.94e-03	CDKN2A	cyclin dependent kinase inhibitor 2
-0.63	2.70e-03	S100A2	S100 calcium binding protein A2	0.41	3.24e-02	UFC1	ubiquitin-fold modifier conjugating
-0.62	2.23e-03	CAVIN3	caveolae associated protein 3	0.4	1.85e-02	BSDC1	BSD domain containing 1
-0.61	4.31e-04	APOB	apolipoprotein B	0.4	5.87e-02	MYEF2	myelin expression factor 2
-0.59	2.09e-05	INTS11	integrator complex subunit 11	0.39	5.37e-02	FN1	fibronectin 1
-0.59	1.43e-09	PACSIN3	protein kinase C and casein kinase	0.39	1.07e-01	ANXA6	annexin A6
-0.59	4.83e-04	RPS27L	ribosomal protein S27 like	0.39	8.75e-03	EDIL3	EGF like repeats and discoidin doma
-0.59	1.50e-03	ATP5MF	ATP synthase membrane subunit f	0.38	1.50e-02	RABEP2	rabaptin, RAB GTPase binding effect
-0.59	1.00e-04	RPS6KA4	ribosomal protein S6 kinase A4	0.38	4.01e-02	SELENBP1	selenium binding protein 1
-0.58	4.65e-03	KRT13	keratin 13	0.38	3.58e-02	KLC4	kinesin light chain 4
-0.58	2.83e-03	BRI3BP	BRI3 binding protein	0.37	2.01e-02	TDRKH	tudor and KH domain containing
-0.57	3.91e-03	SERPINB5	serpin family B member 5	0.36	9.42e-02	ENO2	enolase 2
-0.56	3.31e-04	PPFIBP1	PPFIA binding protein 1	0.36	9.76e-02	UBE2V2	ubiquitin conjugating enzyme E2 V2
-0.55	2.42e-04	CD44	CD44 molecule (Indian blood group)	0.36	5.35e-02	PDXDC1	pyridoxal dependent decarboxylase d
-0.55	1.87e-03	TP63	tumor protein p63	0.34	3.74e-02	DOHH	deoxyhypusine hydroxylase
-0.54	1.06e-02	KRT5	keratin 5	0.34	1.55e-01	MAP1B	microtubule associated protein 1B
-0.54	9.80e-04	FAM83H	family with sequence similarity 83	0.34	2.28e-01	TMSB10	thymosin beta 10
-0.54	7.52e-03	ALDH3A1	aldehyde dehydrogenase 3 family mem	0.34	9.25e-02	GSTM3	glutathione S-transferase mu 3
-0.53	3.01e-03	PLGRKT	plasminogen receptor with a C-termini	0.33	1.75e-01	VTN	vitronectin
-0.53	2.43e-03	CDK6	cyclin dependent kinase 6	0.33	5.87e-02	TBCC	tubulin folding cofactor C
-0.53	7.38e-04	DGKA	diacylglycerol kinase alpha	0.33	5.92e-02	AMPD2	adenosine monophosphate deaminase 2
-0.53	2.70e-03	MAN2A1	mannosidase alpha class 2A member 1	0.33	1.51e-01	TPM2	tropomyosin 2
-0.53	1.65e-03	DERA	deoxyribose-phosphate aldolase	0.32	1.03e-01	MCRIP1	MAPK regulated corepressor interact

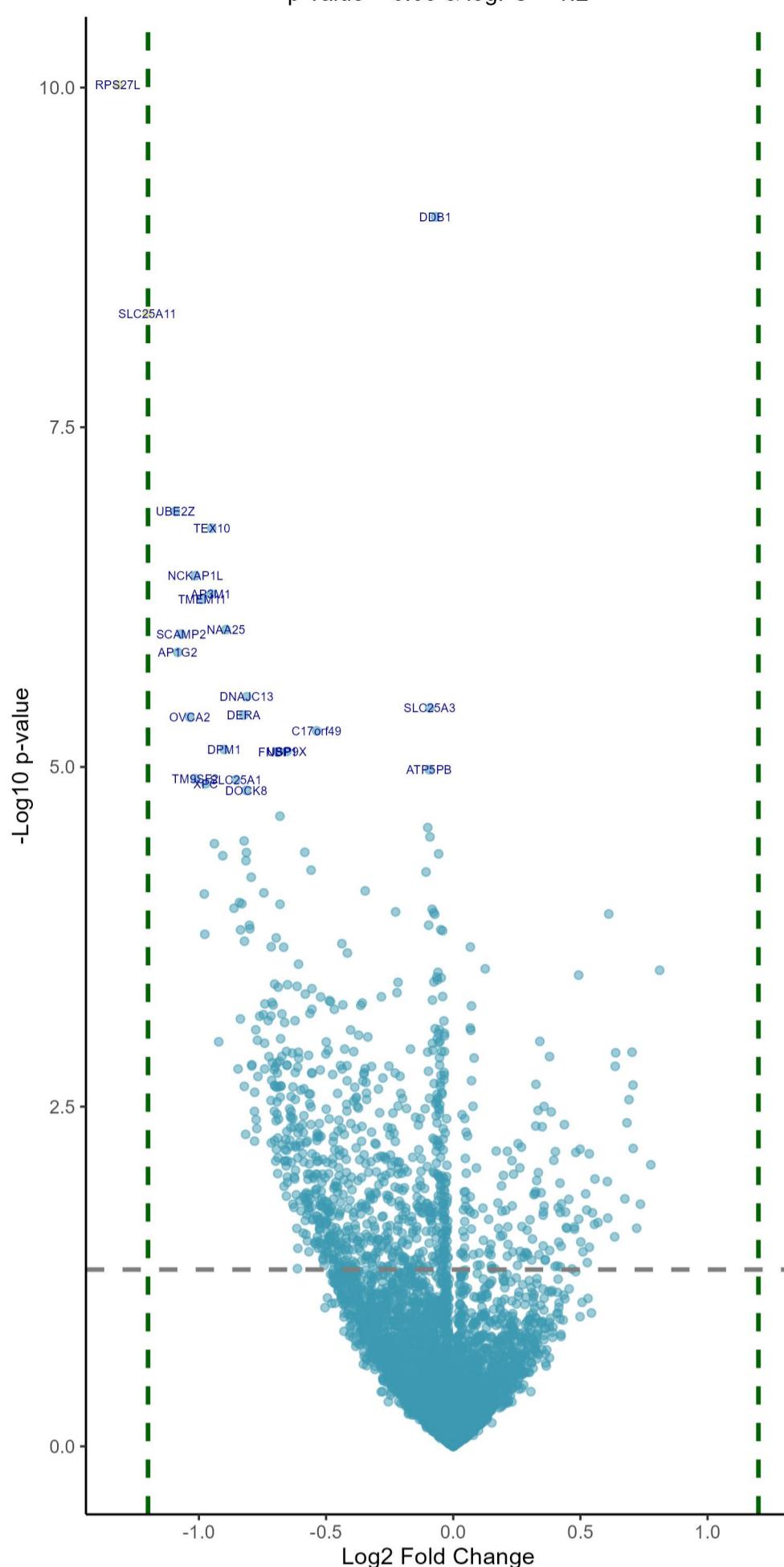
DDB2 network, DB1, all Pearson r > 0.35



DDB2 network, DB1, all Pearson r > 0.3



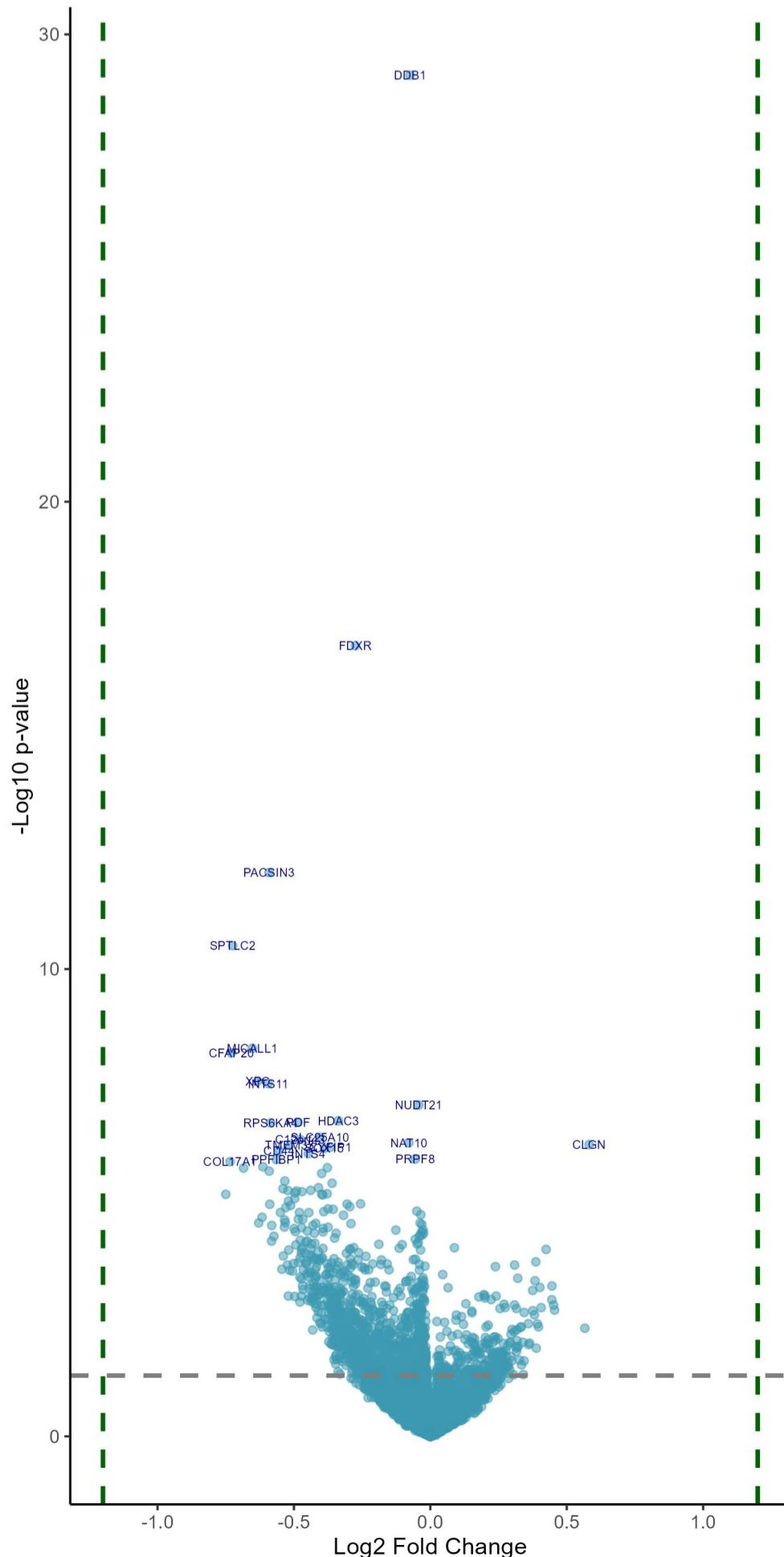
Differentially expressed proteins in blood cancers at absence/low amount of DDB2 , DB1  
p-value < 0.05 & logFC > 1.2



Sorted by p values!  
Downregulated in blood cancers at low/absent DDB2      Upregulated in blood cancers at low/absent DDB2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.32	3.18e-07	RPS27L	ribosomal protein S27 like	0.61	1.61e-02	ST14	ST14 transmembrane serine protease
-0.07	1.98e-06	DDB1	damage specific DNA binding protein	0.07	2.24e-02	POLR1C	RNA polymerase I and III subunit C
-1.2	7.65e-06	SLC25A11	solute carrier family 25 member 11	0.13	3.08e-02	OTUD6B	OTU deubiquitinase 6B
-1.09	1.75e-04	UBE2Z	ubiquitin conjugating enzyme E2 Z	0.81	3.11e-02	TP53	tumor protein p53
-0.95	1.94e-04	TEX10	testis expressed 10	0.49	3.28e-02	MYL4	myosin light chain 4
-1.01	3.72e-04	NCKAP1L	NCK associated protein 1 like	0.07	4.06e-02	EIF5	eukaryotic translation initiation f
-0.95	4.31e-04	AP3M1	adaptor related protein complex 3 s	0.07	5.15e-02	SUPT5H	SPT5 homolog, DSIF elongation facto
-0.99	4.31e-04	TMEM11	transmembrane protein 11	0.07	5.15e-02	EIF3J	eukaryotic translation initiation f
-0.89	6.36e-04	NAA25	N-alpha-acetyltransferase 25, NatB	0.34	5.66e-02	FHL2	four and a half LIM domains 2
-1.07	6.36e-04	SCAMP2	secretory carrier membrane protein	0.7	6.06e-02	MORC2	MORC family CW-type zinc finger 2
-1.08	7.94e-04	AP1G2	adaptor related protein complex 1 s	0.64	6.06e-02	SKA3	spindle and kinetochore associated
-0.81	1.56e-03	DNAJC13	DnaJ heat shock protein family (Hsp	0.38	6.22e-02	YOD1	YOD1 deubiquitinase
-0.09	1.74e-03	SLC25A3	solute carrier family 25 member 3	0.08	6.26e-02	HYPK	huntingtin interacting protein K
-0.82	1.79e-03	DERA	deoxyribose-phosphate aldolase	0.64	6.61e-02	SNX15	sorting nexin 15
-1.04	1.79e-03	OVCA2	OVCA2 serine hydrolase domain conta	0.07	7.21e-02	TXNL1	thioredoxin like 1
-0.54	2.12e-03	C17orf49	chromosome 17 open reading frame 49	0.33	7.44e-02	MTSS1	MTSS I-BAR domain containing 1
-0.9	2.58e-03	DPM1	dolichyl-phosphate mannosyltransfer	0.71	7.44e-02	CFAP298	cilia and flagella associated prote
-0.65	2.58e-03	USP9X	ubiquitin specific peptidase 9 X-li	0.69	8.26e-02	CKS1B	CDC28 protein kinase regulatory sub
-0.69	2.58e-03	FNBP1	formin binding protein 1	0.08	8.77e-02	NAA10	N-alpha-acetyltransferase 10, NatA
-0.09	3.32e-03	ATP5PB	ATP synthase peripheral stalk-membr	0.36	8.77e-02	HMGCR	3-hydroxy-3-methylglutaryl-CoA redu
-1.01	3.59e-03	TM9SF2	transmembrane 9 superfamily member	0.33	9.04e-02	P4HA2	prolyl 4-hydroxylase subunit alpha
-0.85	3.59e-03	SLC25A1	solute carrier family 25 member 1	0.39	9.08e-02	PWWP2A	PWWP domain containing 2A
-0.97	3.69e-03	XPC	XPC complex subunit, DNA damage rec	0.03	9.33e-02	CDC5L	cell division cycle 5 like
-0.81	3.96e-03	DOCK8	dedicator of cytokinesis 8	0.05	9.65e-02	SRRM2	serine/arginine repetitive matrix 2
-0.68	5.89e-03	SLC25A12	solute carrier family 25 member 12	0.68	1.01e-01	ACYP2	acylphosphatase 2
-0.1	6.88e-03	ACTBL2	actin beta like 2	0.44	1.02e-01	CNST	consortin, connexin sorting protein
-0.09	7.77e-03	PAFAH1B1	platelet activating factor acetylhy	0.32	1.04e-01	FKBP7	FKBP prolyl isomerase 7
-0.82	8.03e-03	MYO1G	myosin IG	0.35	1.04e-01	PRTFDC1	phosphoribosyl transferase domain c
-0.94	8.14e-03	ABHD12	abhydrolase domain containing 12, I	0.05	1.10e-01	PRDX6	peroxiredoxin 6
-0.58	8.79e-03	ILK	integrin linked kinase	0.06	1.13e-01	PRRC2C	proline rich coiled-coil 2C
-0.81	8.79e-03	UBXN6	UBX domain protein 6	0.26	1.19e-01	DEPTOR	DEP domain containing MTOR interact
-0.06	8.79e-03	RPL18	ribosomal protein L18	0.27	1.23e-01	DMTN	dematin actin binding protein
-0.91	8.81e-03	TRAPPC4	trafficking protein particle comple	0.71	1.25e-01	ZNF593	zinc finger protein 593
-0.81	9.30e-03	ACAD10	acyl-CoA dehydrogenase family membe	0.5	1.26e-01	STEEP1	STING1 ER exit protein 1
-0.56	1.06e-02	AP1M1	adaptor related protein complex 1 s	0.17	1.27e-01	PFDN4	prefoldin subunit 4
-0.11	1.07e-02	ARHGAP1	Rho GTPase activating protein 1	0.21	1.27e-01	PPID	peptidylprolyl isomerase D
-0.79	1.13e-02	NMI	N-myc and STAT interactor	0.4	1.28e-01	EPPK1	epiplakin 1
-0.35	1.39e-02	PFKL	phosphofructokinase, liver type	0.48	1.29e-01	ABLIM1	actin binding LIM protein 1
0.74	1.40e-02	EMO1A1	family with sequence similarity 91	0.53	1.31e-01	KIF20A	kinesin family member 20A

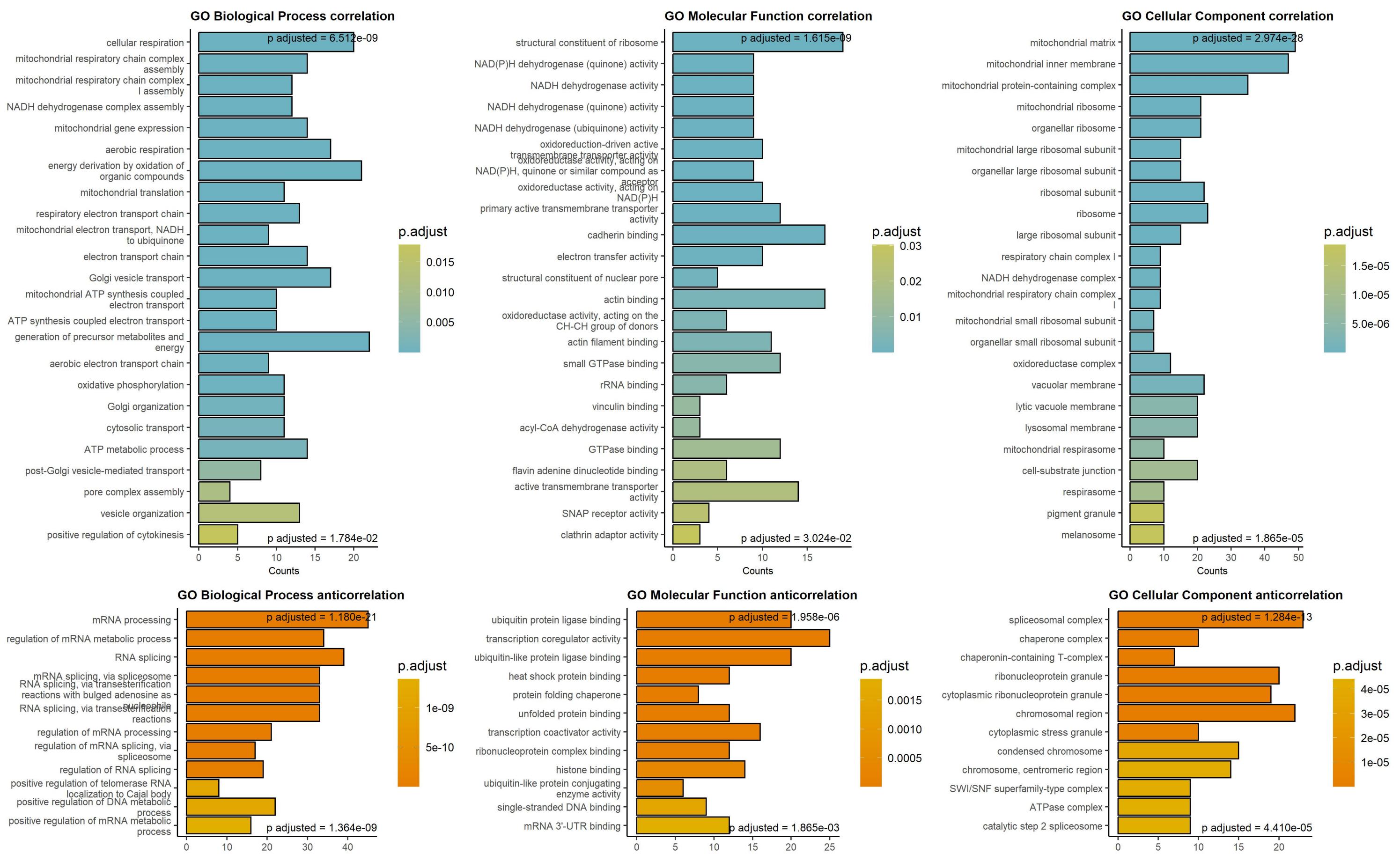
Differentially expressed proteins in solid cancers at absence/low amount of DDB2 , DB1  
p-value < 0.05 & logFC > 1.2



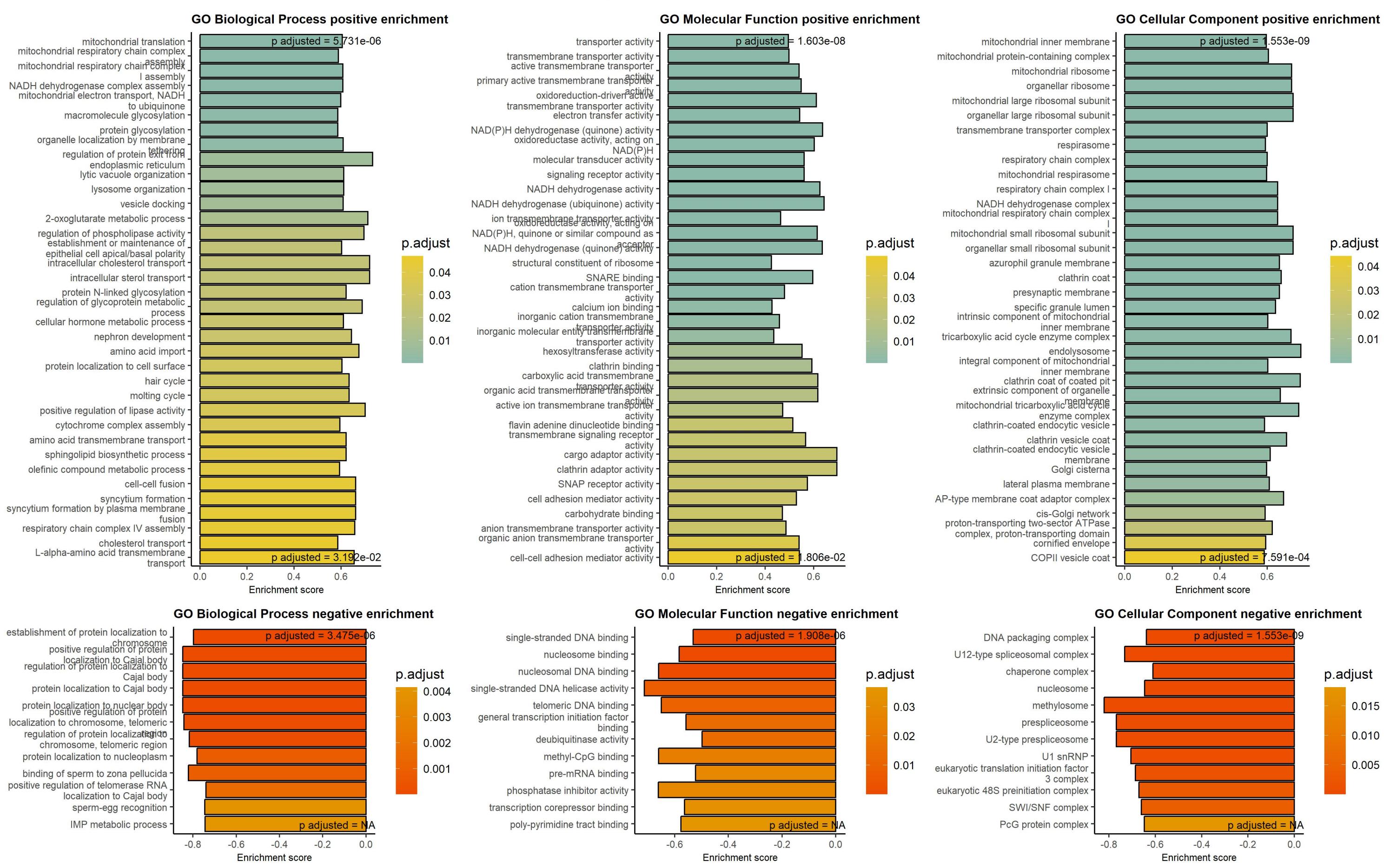
Sorted by p values!  
Downregulated in solid cancers at low/absent DDB2      Upregulated in solid cancers at low/absent DDB2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.07	2.49e-26	DDB1	damage specific DNA binding protein	0.58	2.13e-04	CLGN	calmegin
-0.27	2.66e-14	FDXR	ferredoxin reductase	0.09	5.78e-03	MIA3	MIA SH3 domain ER export factor 3
-0.59	1.43e-09	PACSIN3	protein kinase C and casein kinase	0.42	5.94e-03	CDKN2A	cyclin dependent kinase inhibitor 2
-0.72	4.20e-08	SPTLC2	serine palmitoyltransferase long ch	0.39	8.75e-03	EDIL3	EGF like repeats and discoidin doma
-0.65	5.51e-06	MICALL1	MICAL like 1	0.31	9.20e-03	CRABP1	cellular retinoic acid binding prot
-0.73	5.94e-06	CFAP20	cilia and flagella associated prote	0.24	9.76e-03	ELAPOR1	endosome-lysosome associated apopto
-0.63	2.07e-05	XPC	XPC complex subunit, DNA damage rec	0.05	1.23e-02	NSF	N-ethylmaleimide sensitive factor,
-0.59	2.09e-05	INTS11	integrator complex subunit 11	0.32	1.39e-02	KIF1A	kinesin family member 1A
-0.04	5.41e-05	NUDT21	nudix hydrolase 21	0.38	1.50e-02	RABEP2	rabaptin, RAB GTPase binding effect
-0.34	1.00e-04	HDAC3	histone deacetylase 3	0.45	1.80e-02	DDAH1	dimethylarginine dimethylaminohydro
-0.48	1.00e-04	PDF	peptide deformylase, mitochondrial	0.4	1.85e-02	BSDC1	BSD domain containing 1
-0.59	1.00e-04	RPS6KA4	ribosomal protein S6 kinase A4	0.06	1.87e-02	PGRMC1	progesterone receptor membrane comp
-0.4	1.89e-04	SLC25A10	solute carrier family 25 member 10	0.37	2.01e-02	TDRKH	tudor and KH domain containing
-0.48	1.97e-04	C12orf43	chromosome 12 open reading frame 43	0.2	2.25e-02	PCP4	Purkinje cell protein 4
-0.08	2.13e-04	NAT10	N-acetyltransferase 10	0.2	2.35e-02	PROX1	prospero homeobox 1
-0.52	2.13e-04	TMEM33	transmembrane protein 33	0.24	2.35e-02	FAM117B	family with sequence similarity 117
-0.37	2.27e-04	CYFIP1	cytoplasmic FMR1 interacting protei	0.18	2.40e-02	BGN	biglycan
-0.39	2.27e-04	SOX15	SRY-box transcription factor 15	0.2	2.49e-02	FILIP1L	filamin A interacting protein 1 lik
-0.55	2.42e-04	CD44	CD44 molecule (Indian blood group)	0.22	2.60e-02	BNIP3	BCL2 interacting protein 3
-0.45	2.69e-04	INTS4	integrator complex subunit 4	0.45	2.60e-02	PIN1	peptidylprolyl cis/trans isomerase,
-0.06	3.31e-04	PRPF8	pre-mRNA processing factor 8	0.13	2.92e-02	KMT2B	lysine methyltransferase 2B
-0.56	3.31e-04	PPFIBP1	PPFIA binding protein 1	0.27	2.96e-02	AKAP8L	A-kinase anchoring protein 8 like
-0.73	3.51e-04	COL17A1	collagen type XVII alpha 1 chain	0.31	3.01e-02	COL1A1	collagen type I alpha 1 chain
-0.61	4.31e-04	APOB	apolipoprotein B	0.45	3.01e-02	TMEM263	transmembrane protein 263
-0.38	4.31e-04	SFXN3	sideroflexin 3	0.27	3.23e-02	C19orf47	chromosome 19 open reading frame 47
-0.68	4.31e-04	TRIM29	tripartite motif containing 29	0.41	3.24e-02	UFC1	ubiquitin-fold modifier conjugating
-0.59	4.83e-04	RPS27L	ribosomal protein S27 like	0.26	3.35e-02	CLDN3	claudin 3
-0.4	5.25e-04	MRPL10	mitochondrial ribosomal protein L10	0.32	3.35e-02	TSPYL5	TSPY like 5
-0.53	7.38e-04	DGKA	diacylglycerol kinase alpha	0.46	3.54e-02	CCDC167	coiled-coil domain containing 167
-0.36	7.97e-04	MED14	mediator complex subunit 14	0.38	3.58e-02	KLC4	kinesin light chain 4
-0.41	9.60e-04	SEC11A	SEC11 homolog A, signal peptidase c	0.15	3.63e-02	NCALD	neurocalcin delta
-0.54	9.80e-04	FAM83H	family with sequence similarity 83	0.34	3.74e-02	DOHH	deoxyhypusine hydroxylase
-0.44	1.01e-03	PRORP	protein only RNase P catalytic subu</				

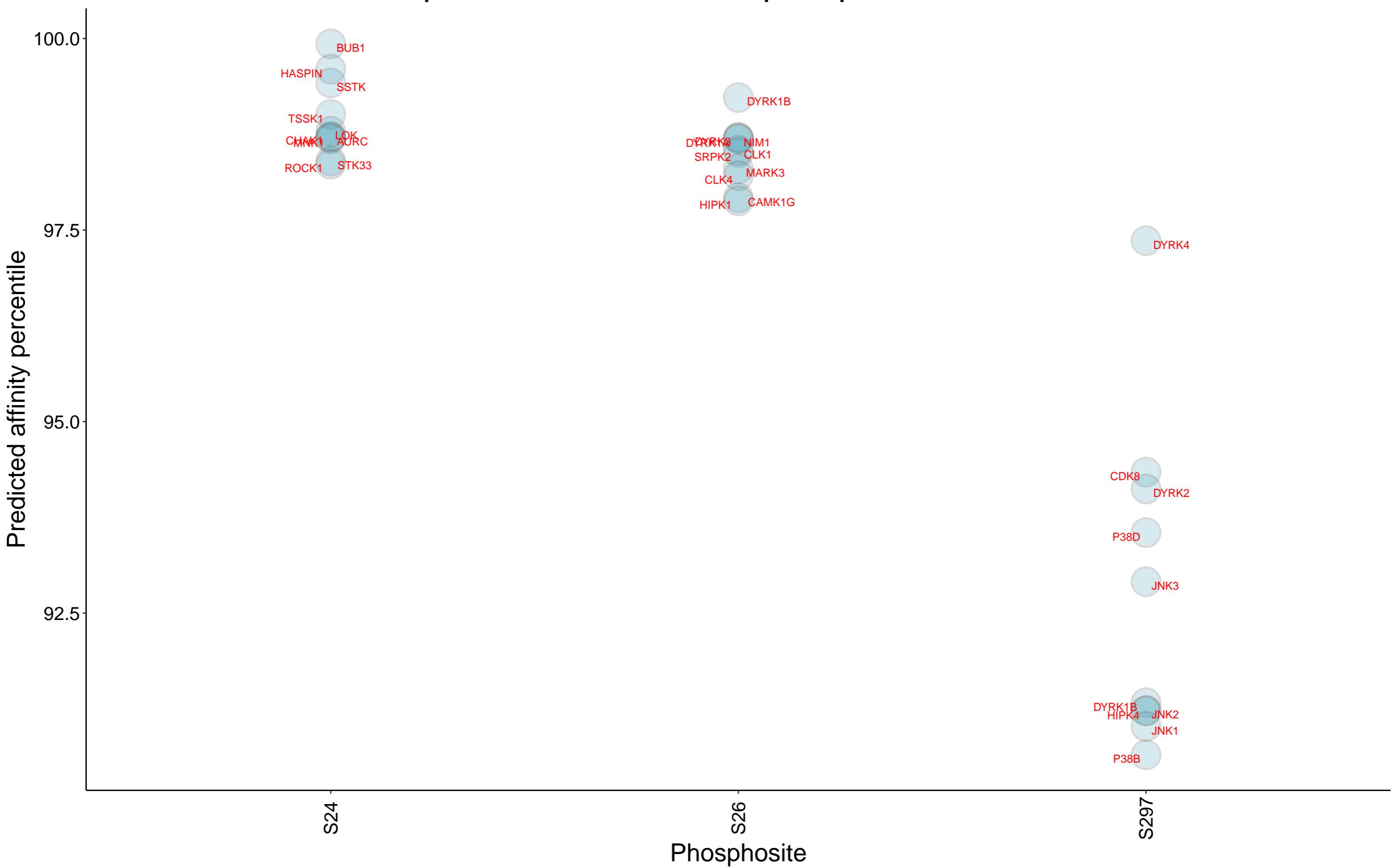
# Top 250 correlation coefficients overrepresentation, DDB2 protein, DB1



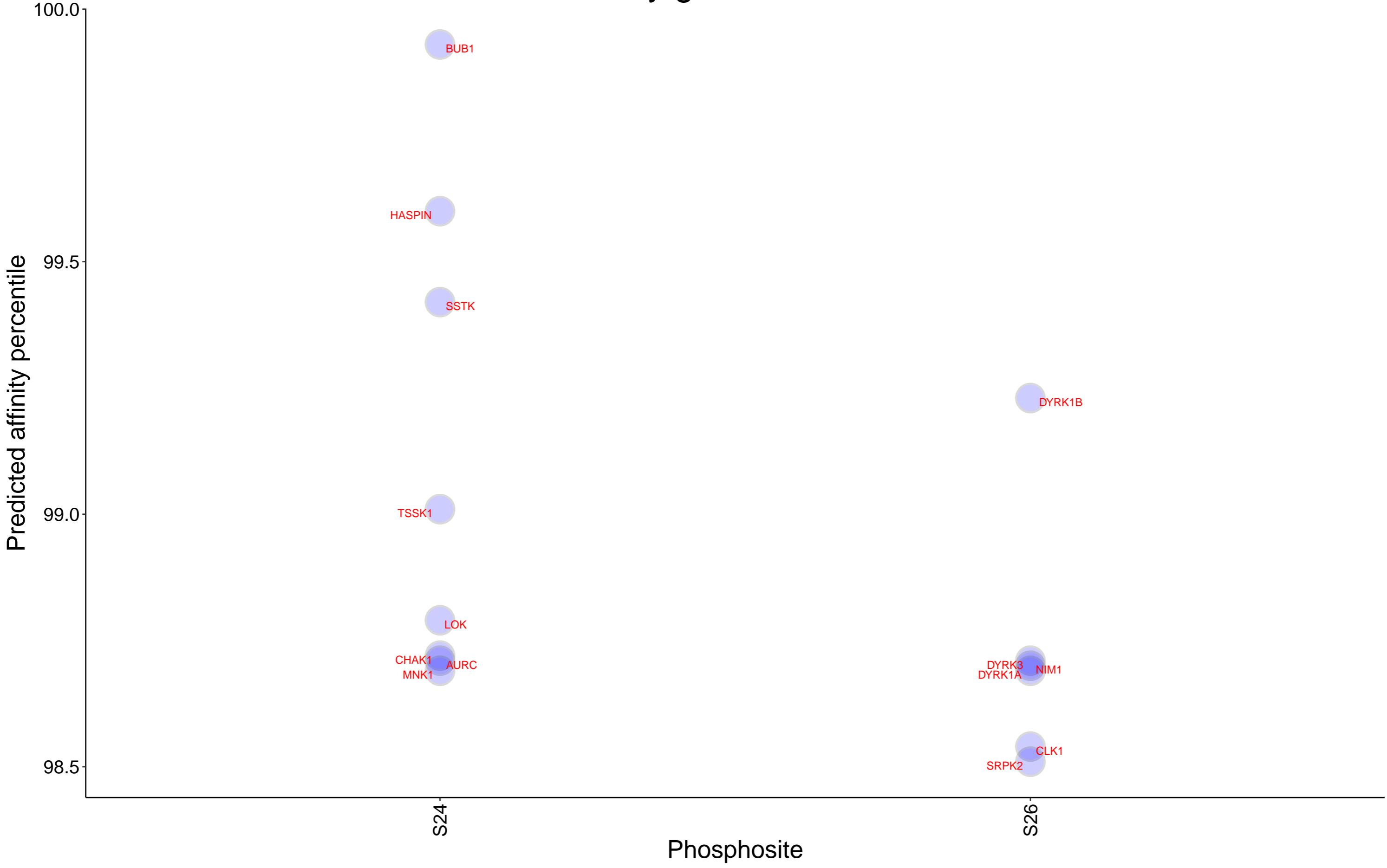
## Gene Set Enrichment analysis on protein correlation coefficients, DDB2 protein, DB1



# Top 10 kinases for each phosphosite in DDB2



Kinases with affinity greater than 98.5% to DDB2



# Top 15 positive correlation coefficients for DDB2 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

