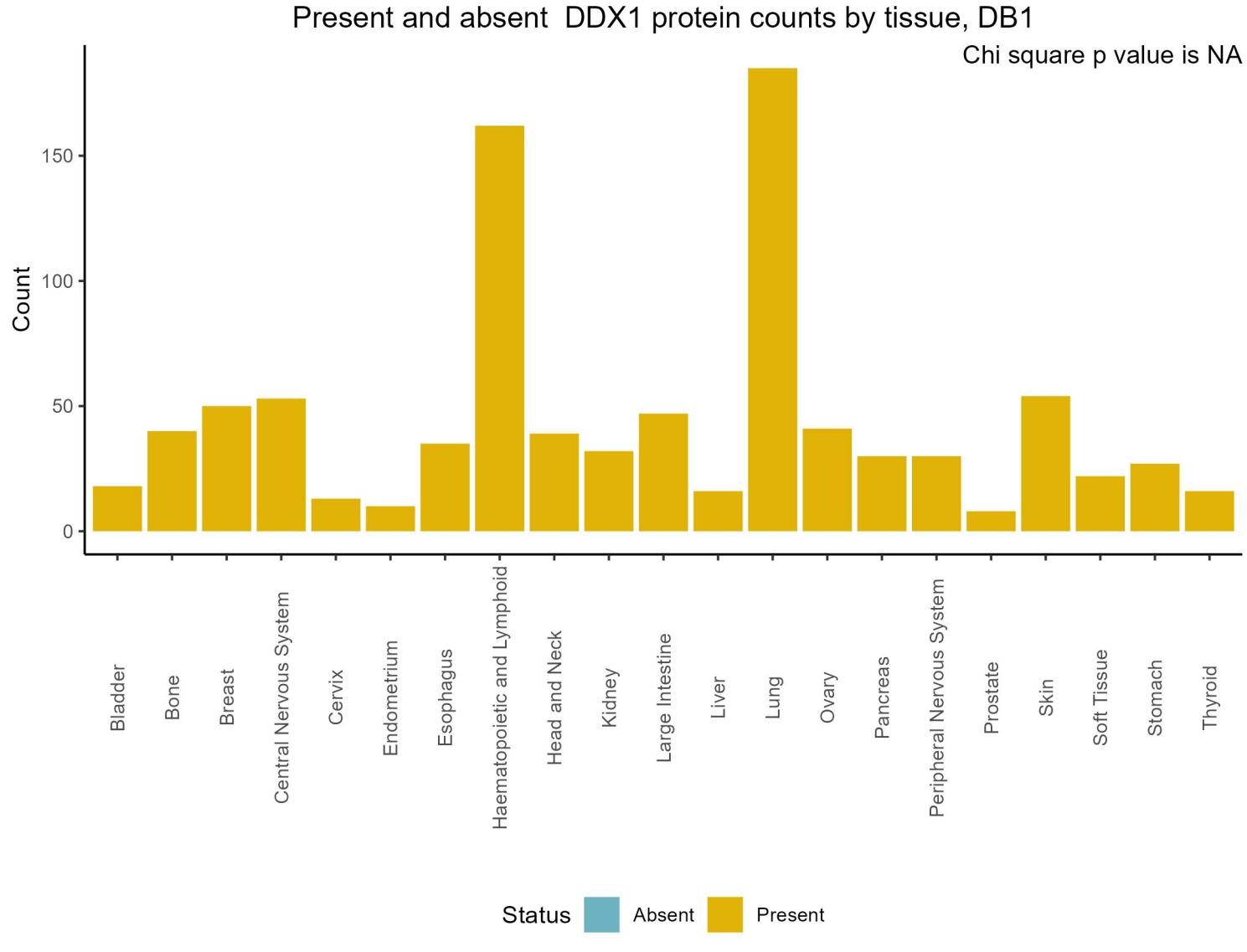
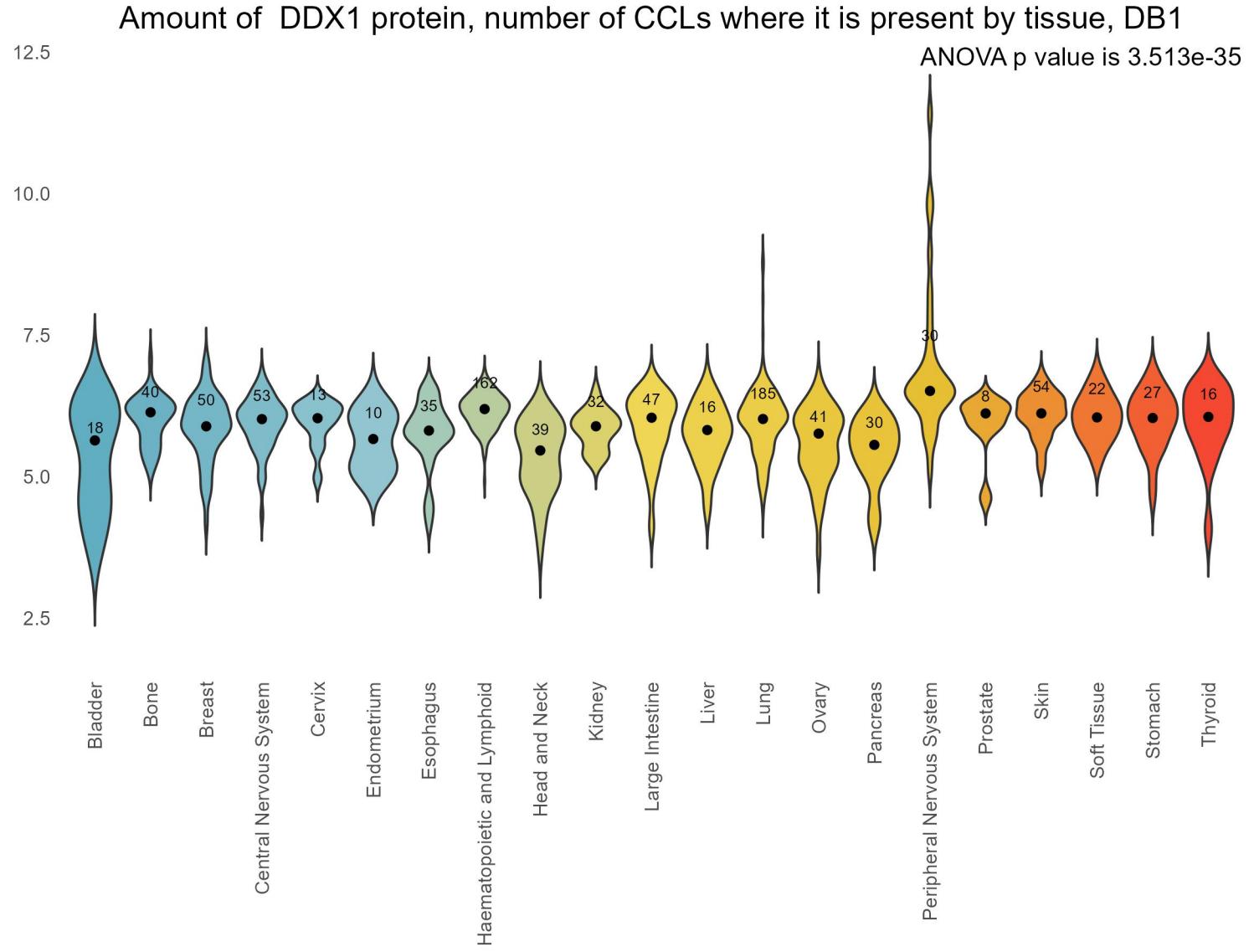
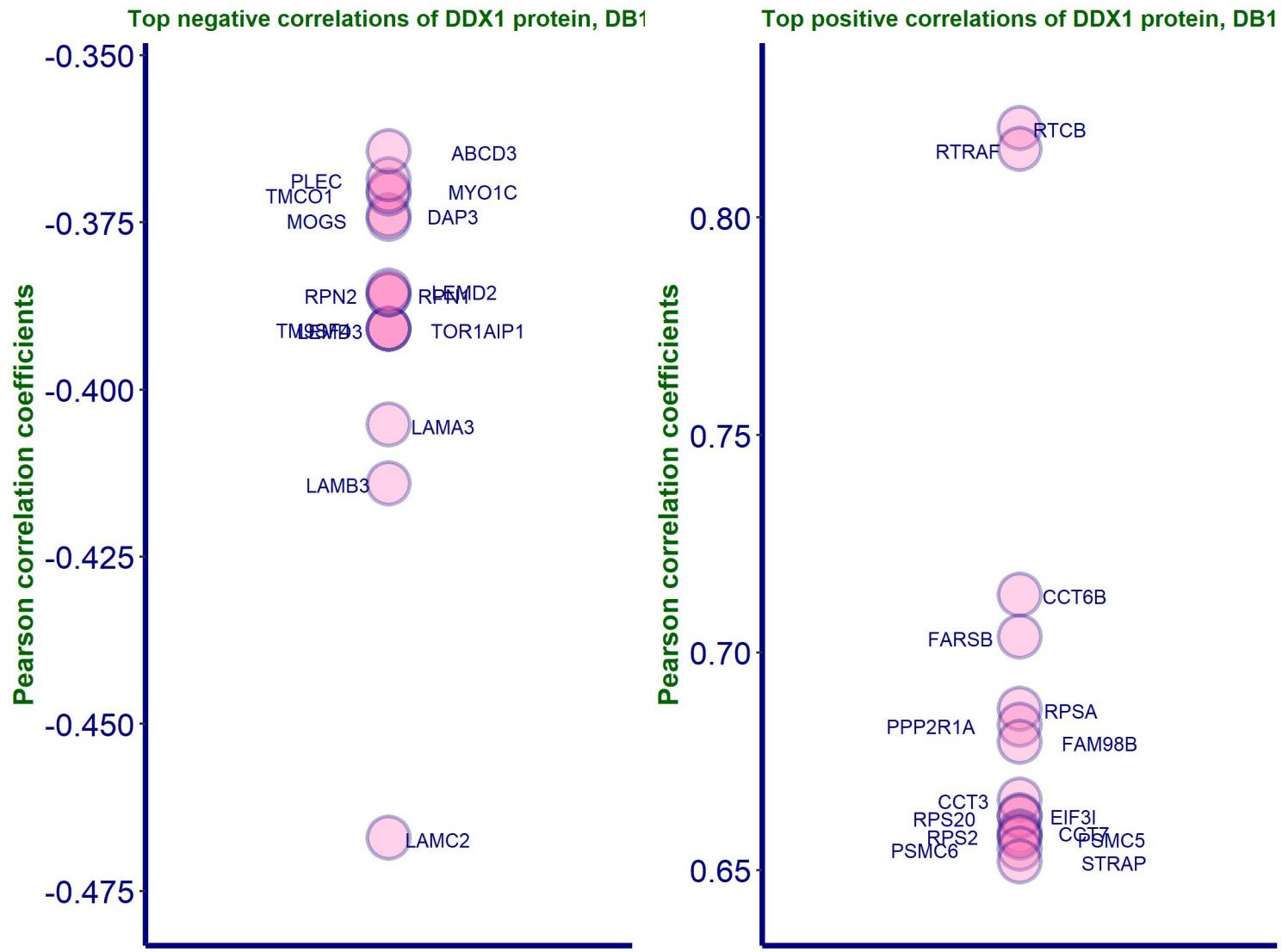
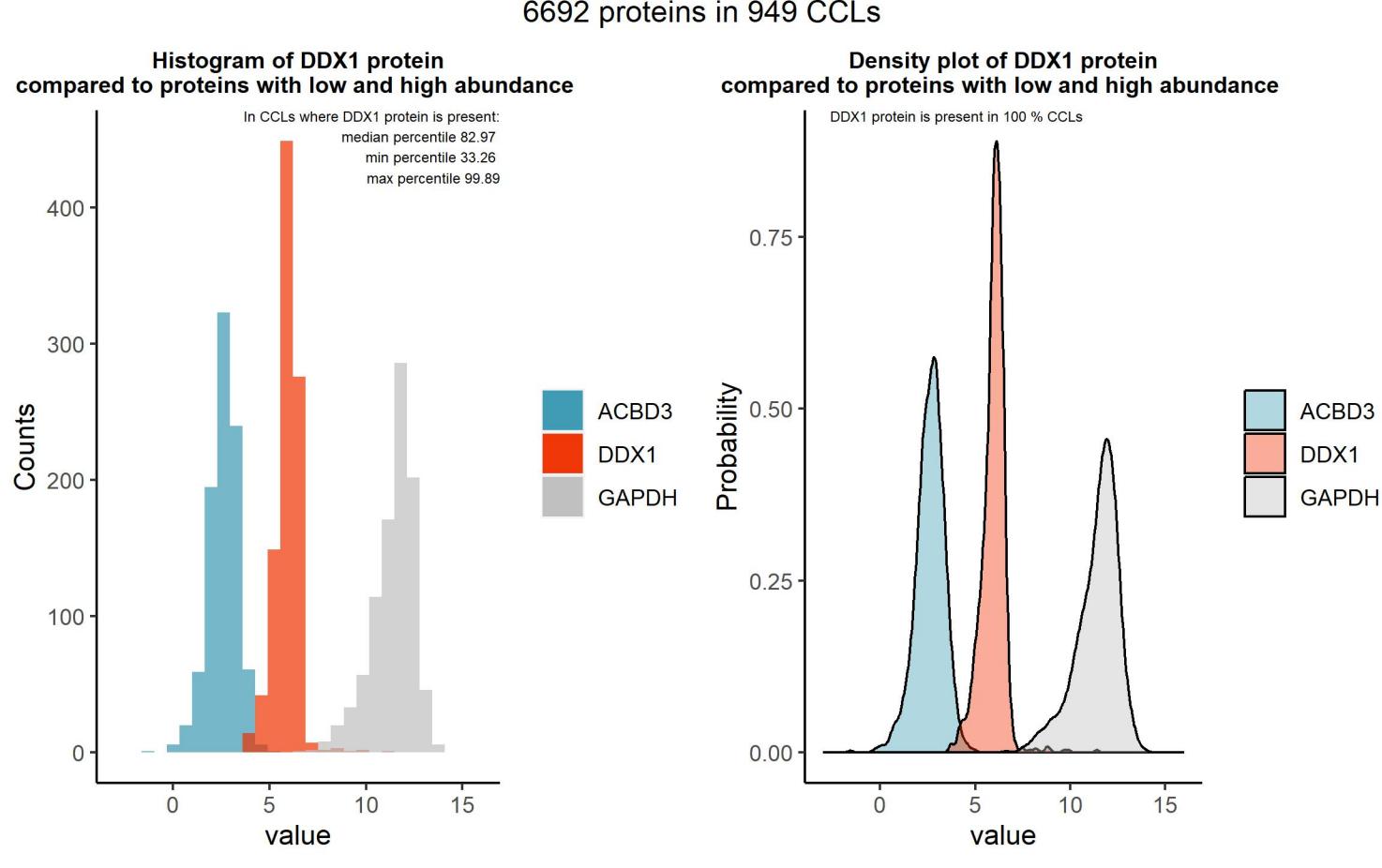


DDX1

Protein name: DDX1 ; UNIPROT: Q92499 ; Gene name: DEAD-box helicase 1
Ligandable: NA ; Ligandable_by_Chem: NA ; Is_enzyme: Yes (<https://cansar.ai/>)

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

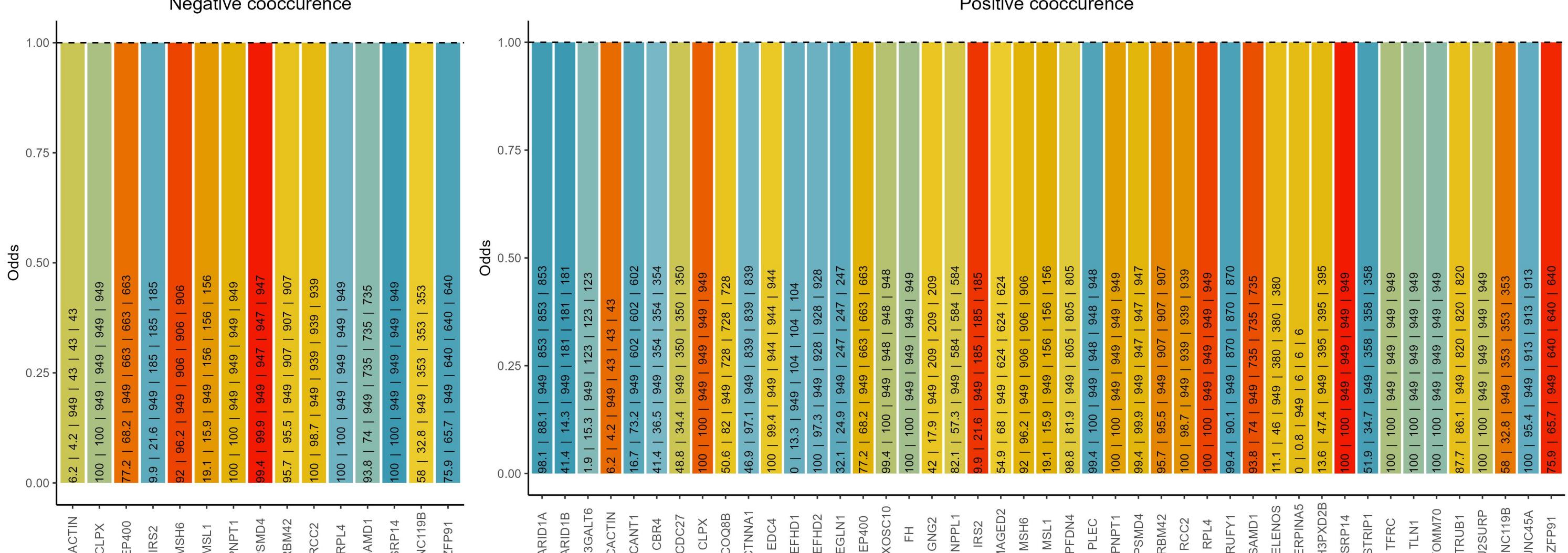


Cooccurrence with DDX1 protein, DB1

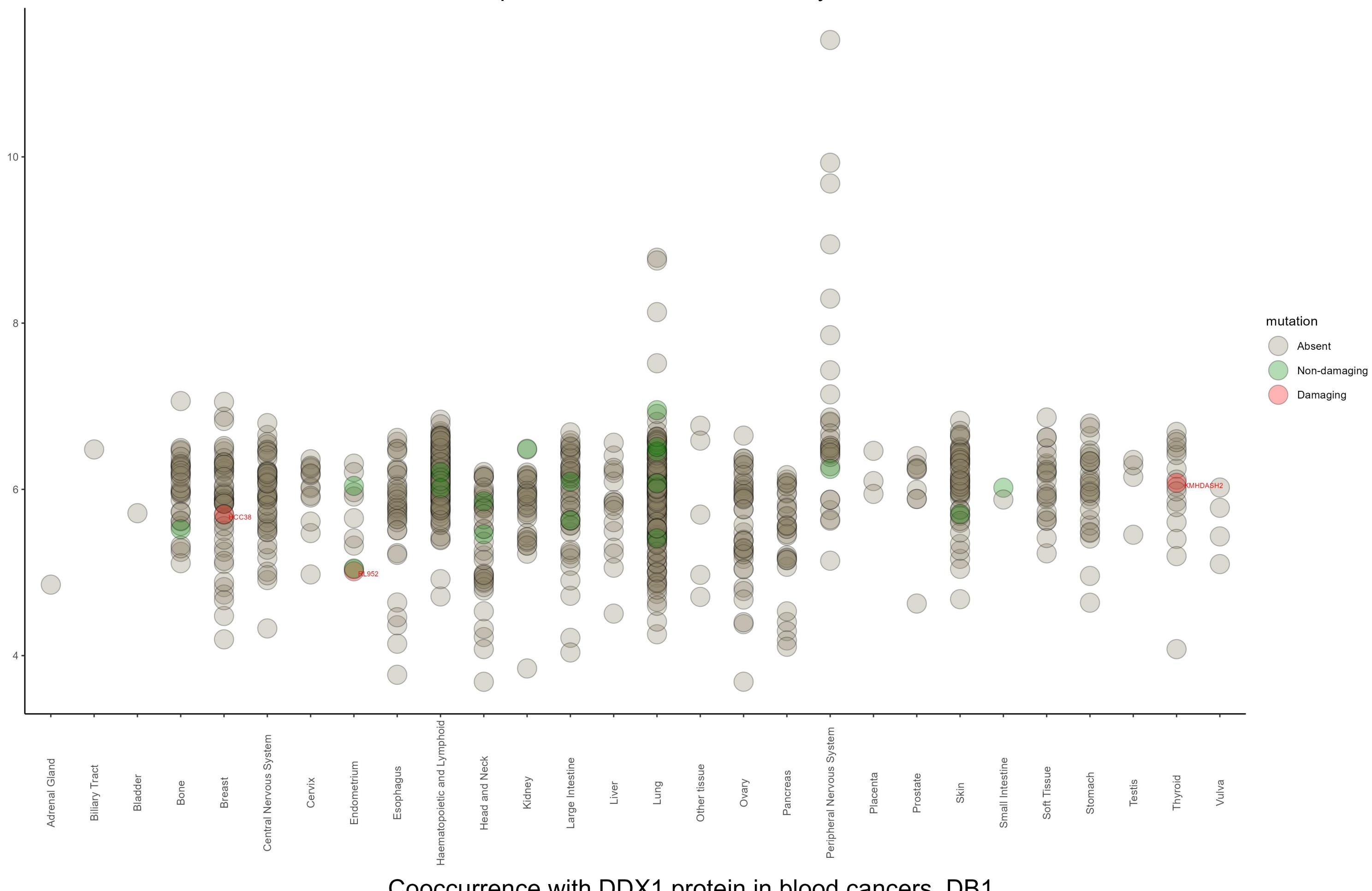
DDX1 in blood cancers: 100% of DDX1 in solid cancers

% of DDX1 in blood cancers. 100 , % of DDX1 in solid cancers. 100
of Protein 2 in solid cancers | incidence of DDX1 | incidence of Prote

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | Incidence of DDX1 | Incidence of Protein 2 | observed cooccurrence | expected cooccurrence

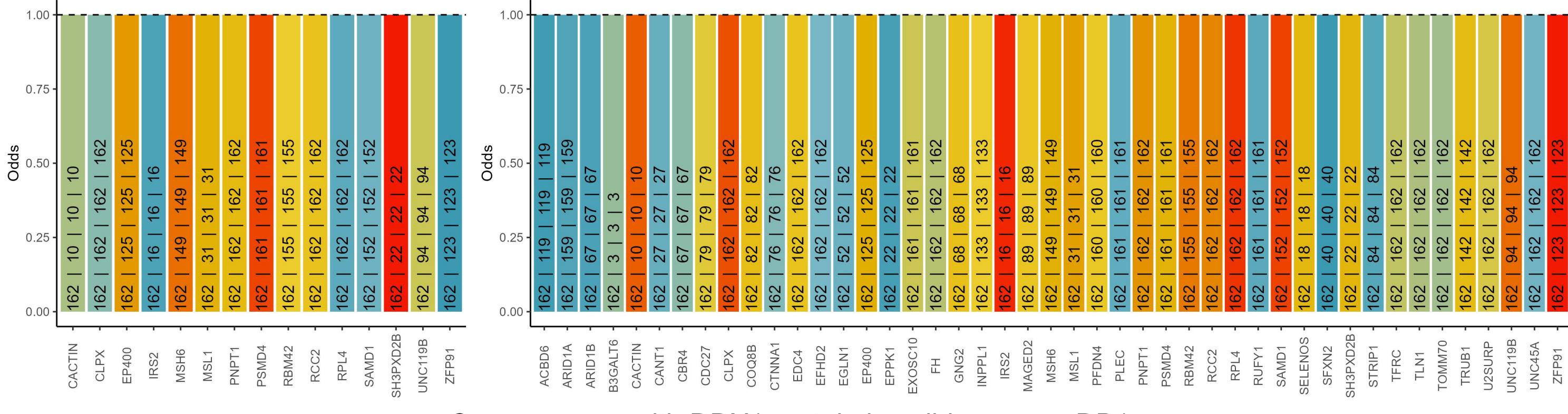


Amount of DDX1 protein and mutation status by tissue, DB1



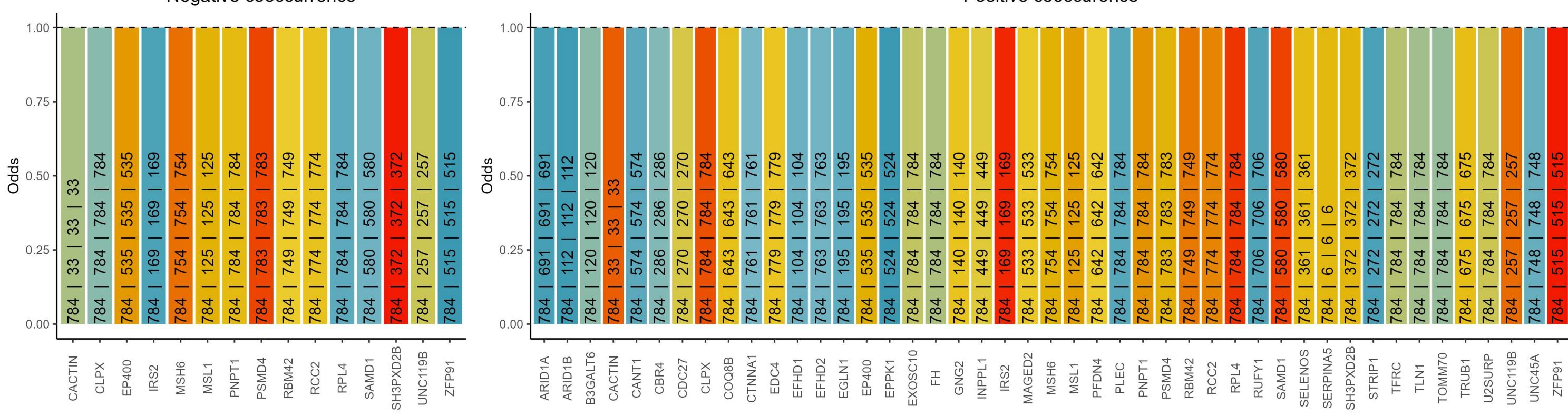
Cooccurrence with DDX1 protein in blood cancers, DB1

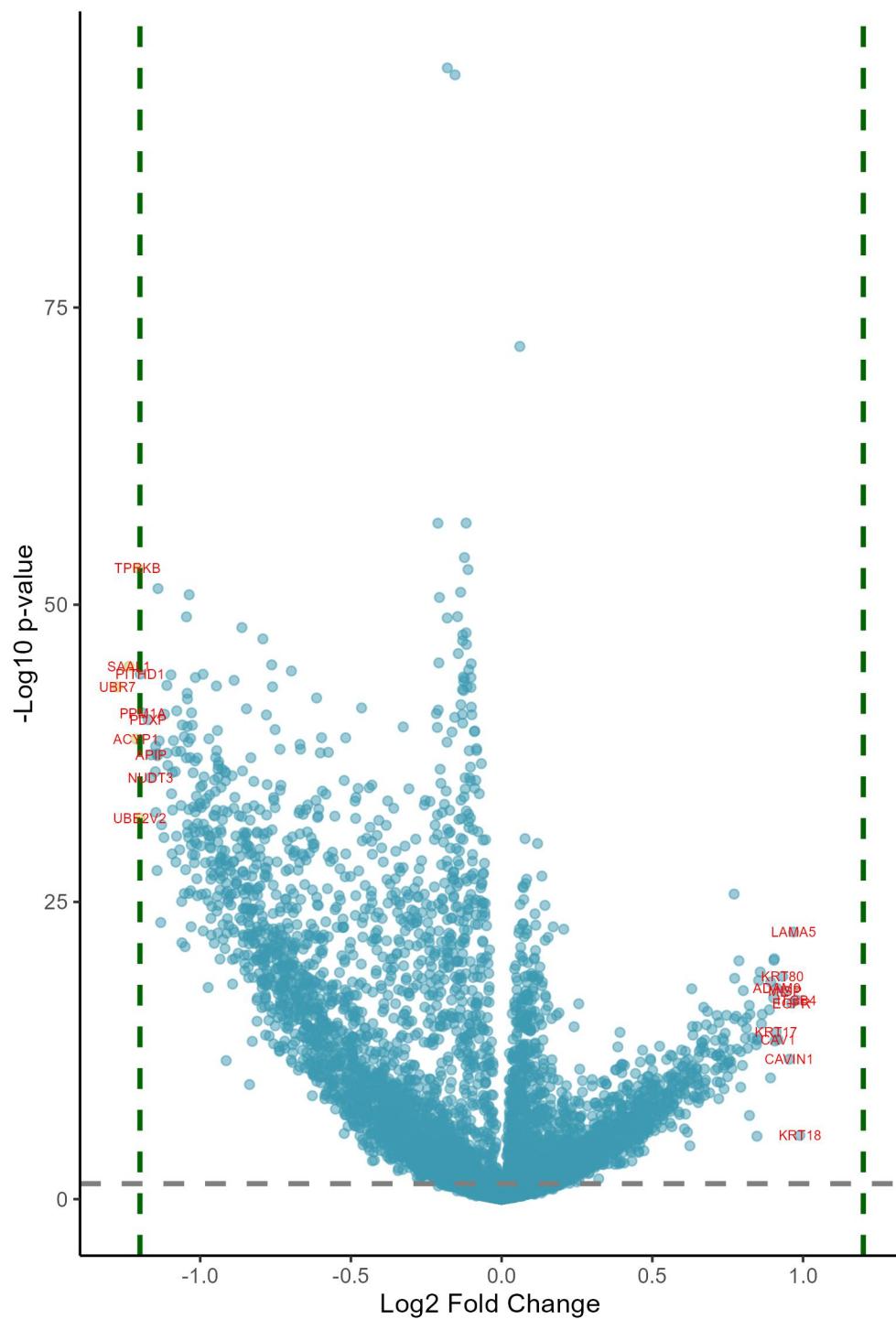
The text in the bars: incidence of DDX1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Cooccurrence with DDX1 protein in solid cancers, DB1

The text in the bars: incidence of DDX1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

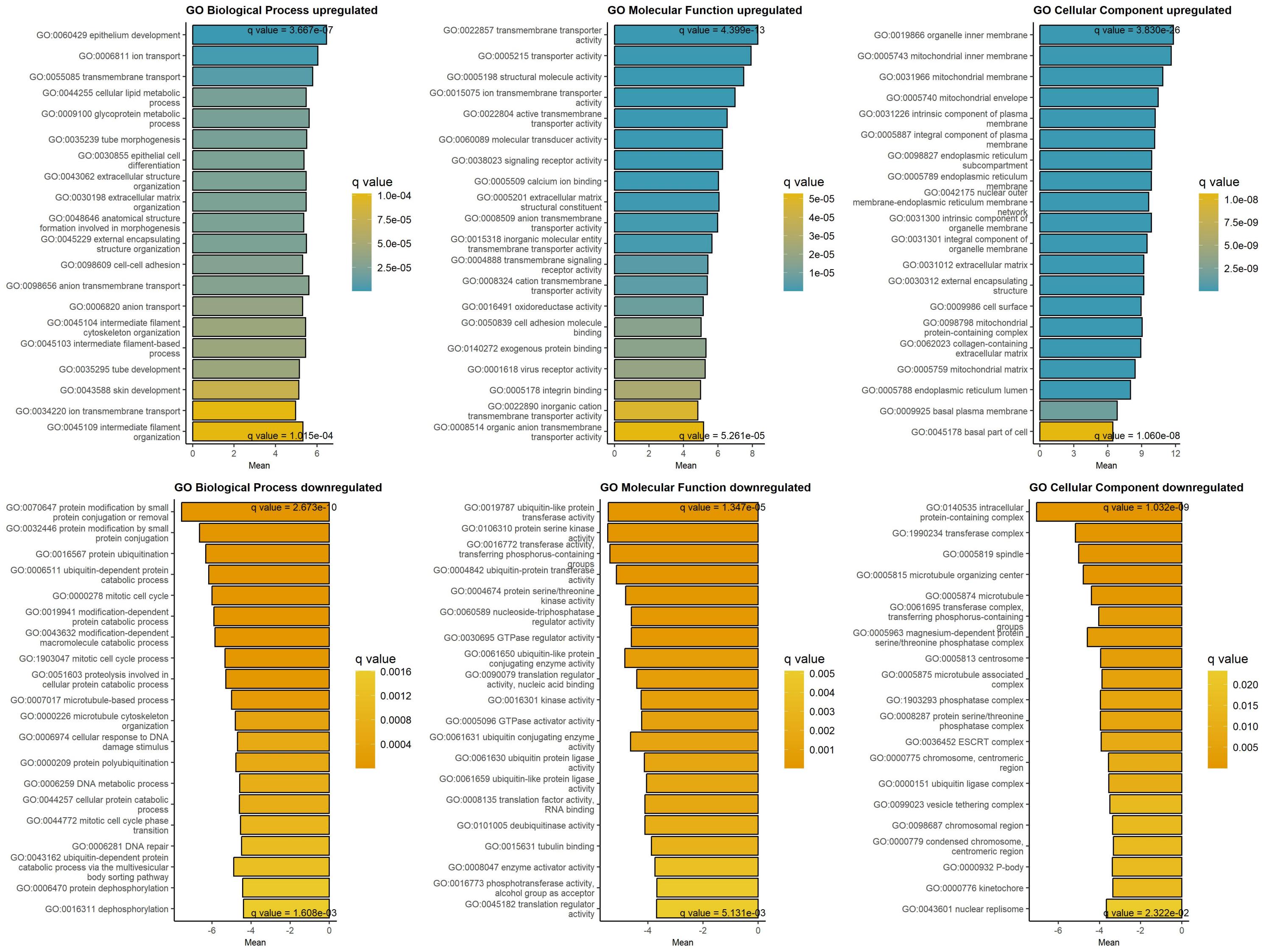


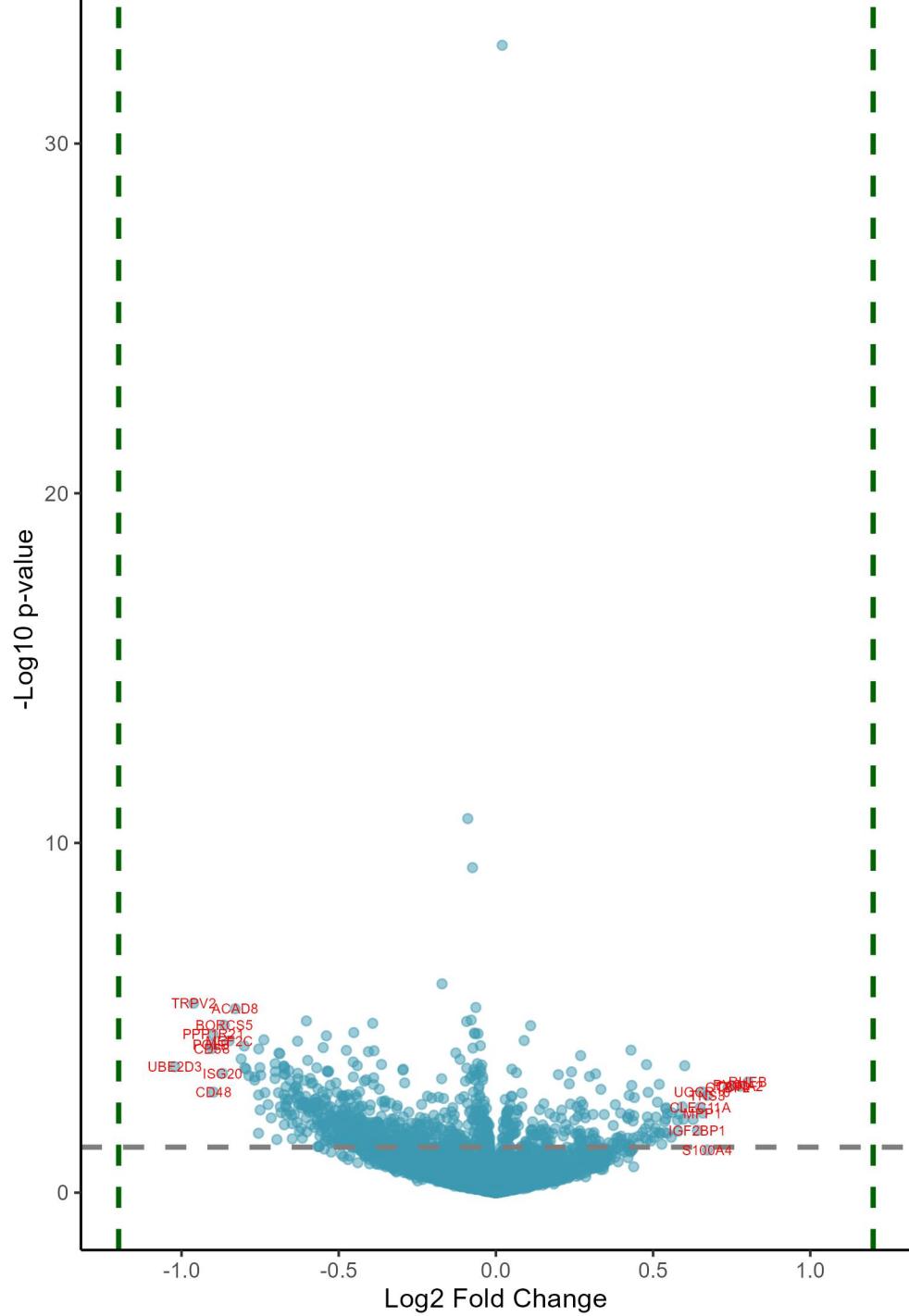


Downregulated at low/absent DDX1 Upregulated at low/absent DDX1

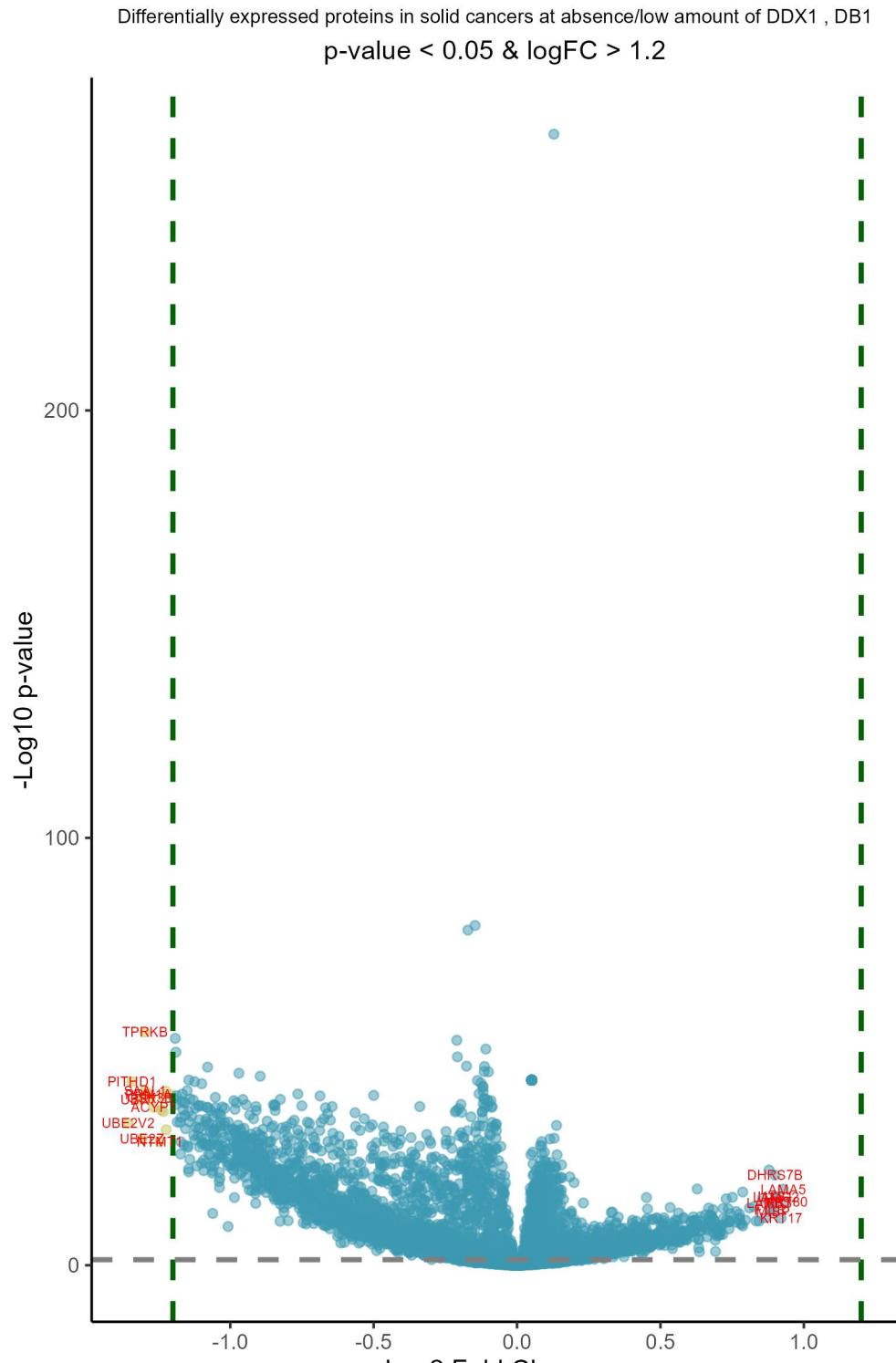
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-1.28	1.26e-41	UBR7	ubiquitin protein ligase E3 compone	0.99	1.04e-05	KRT18	keratin 18
-1.24	3.66e-43	SAAL1	serum amyloid A like 1	0.98	1.17e-16	ITGB4	integrin subunit beta 4
-1.21	1.61e-37	ACYP1	acylphosphatase 1	0.97	3.69e-22	LAMA5	laminin subunit alpha 5
-1.21	6.94e-51	TPRKB	TP53RK binding protein	0.96	2.08e-16	EGFR	epidermal growth factor receptor
-1.2	2.81e-31	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.95	7.53e-12	CAVIN1	caveolae associated protein 1
-1.2	1.50e-42	PITHD1	PITH domain containing 1	0.94	2.08e-17	MISP	mitotic spindle positioning
-1.19	1.51e-39	PPM1A	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe	0.93	1.42e-18	KRT80	keratin 80
-1.17	4.89e-39	PDXP	pyridoxal phosphatase	0.92	1.88e-13	CAV1	caveolin 1
-1.16	1.83e-34	NUDT3	nudix hydrolase 3	0.91	1.26e-17	ADAM9	ADAM metallopeptidase domain 9
-1.16	2.77e-36	APIP	APAF1 interacting protein	0.91	4.60e-14	KRT17	keratin 17
-1.15	6.15e-35	ARMC6	armadillo repeat containing 6	0.91	2.48e-13	JUP	junction plakoglobin
-1.15	6.12e-37	PDCL3	phosducin like 3	0.9	5.24e-20	LAMB3	laminin subunit beta 3
-1.15	1.03e-31	PSME3IP1	proteasome activator subunit 3 inte	0.9	6.99e-20	SDC4	syndecan 4
-1.14	4.19e-27	UBE2Z	ubiquitin conjugating enzyme E2 Z	0.9	7.68e-17	EPHA2	EPH receptor A2
-1.14	2.30e-36	SMAP2	small ArfGAP2	0.89	3.93e-18	RRAS	RAS related
-1.14	3.33e-36	UBA5	ubiquitin like modifier activating	0.89	2.47e-10	ITGA3	integrin subunit alpha 3
-1.14	2.91e-49	EIF2B2	eukaryotic translation initiation f	0.89	7.15e-16	UQCR10	ubiquinol-cytochrome c reductase, c
-1.14	2.24e-37	DCK	deoxyribonucleic kinase	0.86	1.67e-15	BCAM	basal cell adhesion molecule (Luthe
-1.13	6.32e-23	ABRACL	ABRA C-terminal like	0.86	9.84e-15	F11R	F11 receptor
-1.13	9.74e-31	PRPS1	phosphoribosyl pyrophosphate synthe	0.86	6.23e-19	LAMC2	laminin subunit gamma 2
-1.12	9.86e-30	C11orf54	chromosome 11 open reading frame 54	0.85	3.07e-18	UXS1	UDP-glucuronate decarboxylase 1
-1.12	1.84e-39	PDE6D	phosphodiesterase 6D	0.85	1.55e-13	CDH1	cadherin 1
-1.11	1.05e-41	PAAF1	proteasomal ATPase associated facto	0.85	2.10e-13	PKP3	plakophilin 3
-1.11	2.06e-36	MAP2K2	mitogen-activated protein kinase ki	0.85	1.20e-05	KRT8	keratin 8
-1.11	1.96e-35	TP53RK	TP53 regulating kinase	0.84	5.09e-13	ITGA2	integrin subunit alpha 2
-1.1	1.65e-42	MEMO1	mediator of cell motility 1	0.83	1.36e-13	SPINT2	serine peptidase inhibitor, Kunitz
-1.1	3.50e-33	GSK3B	glycogen synthase kinase 3 beta	0.82	1.63e-15	FAM83H	family with sequence similarity 83
-1.09	1.96e-28	NTMT1	N-terminal Xaa-Pro-Lys N-methyltran	0.82	2.62e-07	KRT19	keratin 19
-1.09	7.18e-35	CZIB	CXXC motif containing zinc binding	0.82	3.16e-16	F3	coagulation factor III, tissue fact

GAGE analysis on upregulated and downregulated proteins at low/absent DDX1 protein, DB1



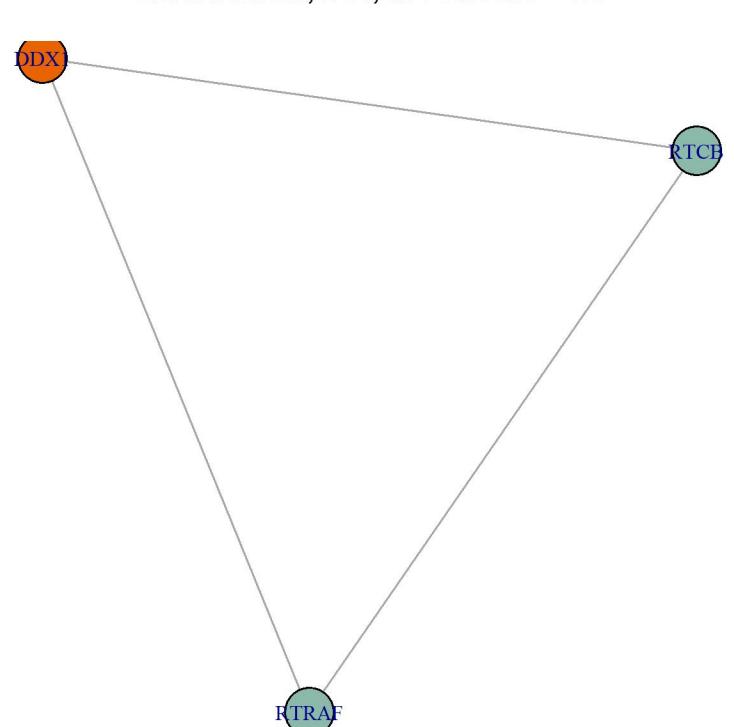


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-1.02	3.14e-02	UBE2D3	ubiquitin conjugating enzyme E2 D3	0.8	4.45e-02	RHEB	Ras homolog, mTORC1 binding
-0.96	4.25e-03	TRPV2	transient receptor potential cation	0.78	5.22e-02	CCNA2	cyclin A2
-0.91	1.56e-02	POLB	DNA polymerase beta	0.75	5.02e-02	PYGL	glycogen phosphorylase L
-0.9	1.67e-02	CD58	CD58 molecule	0.74	5.55e-02	CTBP2	C-terminal binding protein 2
-0.9	1.03e-02	PPP1R21	protein phosphatase 1 regulatory su	0.67	3.82e-01	S100A4	S100 calcium binding protein A4
-0.9	6.84e-02	CD48	CD48 molecule	0.67	7.71e-02	TNS3	tensin 3
-0.87	3.44e-02	ISG20	interferon stimulated exonuclease g	0.66	1.31e-01	MPP1	MAGUK p55 scaffold protein 1
-0.86	7.98e-03	BORCS5	BLOC-1 related complex subunit 5	0.66	6.77e-02	UQCR10	ubiquinol-cytochrome c reductase, c
-0.85	1.29e-02	MEF2C	myocyte enhancer factor 2C	0.65	1.10e-01	CLEC11A	C-type lectin domain containing 11A
-0.83	4.58e-03	ACAD8	acyl-CoA dehydrogenase family membe	0.64	2.20e-01	IGF2BP1	insulin like growth factor 2 mRNA b
-0.81	2.49e-02	IL4I1	interleukin 4 induced 1	0.63	1.57e-01	ITGA5	integrin subunit alpha 5
-0.8	1.58e-02	PLEKHO2	pleckstrin homology domain containi	0.6	3.11e-02	AZU1	azurocidin 1
-0.8	3.16e-02	RRAS2	RAS related 2	0.6	1.57e-01	LYZ	lysozyme
-0.79	3.16e-02	PAK1	p21 (RAC1) activated kinase 1	0.59	1.09e-01	PRTN3	proteinase 3
-0.79	3.63e-02	ARID3B	AT-rich interaction domain 3B	0.58	1.36e-01	COL6A3	collagen type VI alpha 3 chain
-0.77	4.11e-02	NUDT2	nudix hydrolase 2	0.58	2.24e-01	CSTA	cystatin A
-0.77	3.70e-02	CCDC90B	coiled-coil domain containing 90B	0.58	1.61e-01	ADD2	adducin 2
-0.76	2.36e-01	MZB1	marginal zone B and B1 cell specifi	0.56	1.29e-01	PPP4R3B	protein phosphatase 4 regulatory su
-0.75	7.66e-02	CD40	CD40 molecule	0.56	2.64e-01	ASS1	argininosuccinate synthase 1
-0.75	1.67e-02	PACS1	phosphofuran acidic cluster sorting	0.55	1.33e-01	C9orf78	chromosome 9 open reading frame 78
-0.75	3.16e-02	FAS	Fas cell surface death receptor	0.55	2.36e-01	CTSG	cathepsin G
-0.75	1.18e-01	POLR1D	RNA polymerase I and III subunit D	0.54	1.10e-01	CUX1	cut like homeobox 1
-0.75	3.55e-02	MON2	MON2 homolog, regulator of endosome	0.54	1.57e-01	ZEB2	zinc finger E-box binding homeobox
-0.74	1.29e-02	RRP7A	ribosomal RNA processing 7 homolog	0.54	1.14e-01	MIS18A	MIS18 kinetochore protein A
-0.73	6.88e-02	DST	dystonin	0.54	1.68e-01	PDLM7	PDZ and LIM domain 7
-0.72	1.03e-01	CLIP2	CAP-Gly domain containing linker pr	0.54	2.32e-01	GLUL	glutamate-ammonia ligase
-0.71	1.53e-01	BLVRA	biliverdin reductase A	0.53	3.26e-01	CA2	carbonic anhydrase 2
-0.7	3.92e-02	NT5C	5', 3'-nucleotidase, cytosolic	0.52	2.37e-01	CFAP20	cilia and flagella associated prote
-0.7	3.03e-02	FNDC3A	fibronectin type III domain contain	0.52	4.87e-02	SP3	Sp3 transcription factor

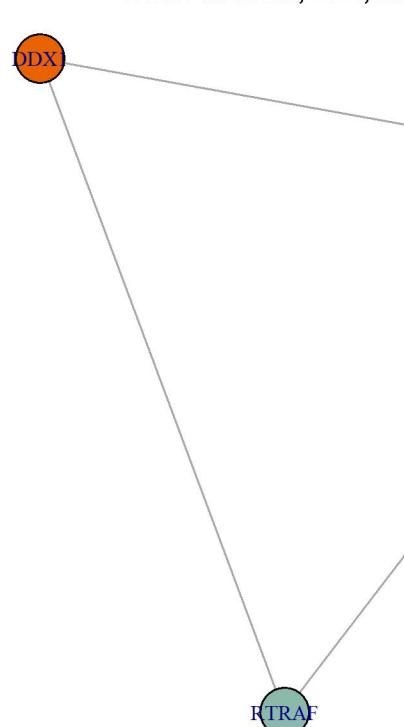


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.36	1.76e-32	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.94	6.71e-15	KRT80	keratin 80
-1.34	7.33e-42	PITHD1	PITH domain containing 1	0.93	1.18e-17	LAMA5	laminin subunit alpha 5
-1.32	9.88e-38	UBR7	ubiquitin protein ligase E3 compone	0.92	3.88e-11	KRT17	keratin 17
-1.31	5.16e-29	UBE2Z	ubiquitin conjugating enzyme E2 Z	0.9	6.96e-16	LAMC2	laminin subunit gamma 2
-1.3	3.65e-52	TPRKB	TP53RK binding protein	0.9	4.51e-16	UXS1	UDP-glucuronate decarboxylase 1
-1.3	9.74e-40	SAAL1	serum amyloid A like 1	0.9	1.49e-14	F3	coagulation factor III, tissue fact
-1.29	5.66e-39	PPM1A	protein phosphatase, Mg2+/Mn2+ depe	0.9	7.65e-21	DHRS7B	dehydrogenase/reductase 7B
-1.28	4.15e-38	GSK3B	glycogen synthase kinase 3 beta	0.89	1.36e-12	MISP	mitotic spindle positioning
-1.27	4.72e-36	ACYP1	acylphosphatase 1	0.88	4.90e-13	F11R	F11 receptor
-1.25	2.26e-28	NTMT1	N-terminal Xaa-Pro-Lys N-methyltran	0.88	1.37e-14	LAMB3	laminin subunit beta 3
-1.24	1.81e-35	PDCL3	phosducin like 3	0.88	5.48e-22	LAMA3	laminin subunit alpha 3
-1.23	2.19e-38	PDXP	pyridoxal phosphatase	0.87	3.12e-11	VAMP8	vesicle associated membrane protein
-1.23	4.27e-35	CZIB	CXXC motif containing zinc binding	0.86	1.20e-15	SDC4	syndecan 4
-1.23	1.09e-39	DCK	deoxycytidine kinase	0.84	1.79e-10	ITGB4	integrin subunit beta 4
-1.22	5.36e-31	PPP2CA	protein phosphatase 2 catalytic sub	0.83	1.70e-10	TACSTD2	tumor associated calcium signal tra
-1.2	8.67e-39	LZIC	leucine zipper and CTNNB1P1 domain	0.83	9.82e-14	SYNGR2	synaptogyrin 2
-1.2	5.06e-38	RNF214	ring finger protein 214	0.81	2.00e-13	TAP1	transporter 1, ATP binding cassette
-1.19	9.24e-51	NUBP2	NUBP iron-sulfur cluster assembly f	0.8	1.08e-10	UQCR10	ubiquinol-cytochrome c reductase, c
-1.19	1.17e-36	TAB1	TGF-beta activated kinase 1 (MAP3K7	0.79	2.20e-09	CDH1	cadherin 1
-1.19	1.03e-47	UBE3A	ubiquitin protein ligase E3A	0.79	4.90e-17	MRPS10	mitochondrial ribosomal protein S10
-1.19	1.20e-38	PHPT1	phosphohistidine phosphatase 1	0.78	9.46e-10	KRT5	keratin 5
-1.18	1.04e-32	APIP	APAF1 interacting protein	0.78	6.65e-10	SPINT2	serine peptidase inhibitor, Kunitz
-1.17	1.23e-32	UBA5	ubiquitin like modifier activating	0.78	3.47e-11	TAP2	transporter 2, ATP binding cassette
-1.17	1.45e-25	FKBP1A	FKBP prolyl isomerase 1A	0.78	4.61e-12	FAM83H	family with sequence similarity 83
-1.17	2.58e-28	PRPS1	phosphoribosyl pyrophosphate synthe	0.77	8.40e-11	SQOR	sulfide quinone oxidoreductase
-1.17	9.32e-34	ARMC6	armadillo repeat containing 6	0.76	1.22e-12	ITGB6	integrin subunit beta 6
-1.17	1.81e-37	AARSD1	alanyl-tRNA synthetase domain conta	0.76	3.39e-10	THBS1	thrombospondin 1
-1.17	5.42e-39	MEMO1	mediator of cell motility 1	0.75	7.68e-16	ADAM17	ADAM metallopeptidase domain 17
-1.16	1.59e-35	TP53RK	TP53 regulating kinase	0.74	3.30e-12	ADAM9	ADAM metallopeptidase domain 9

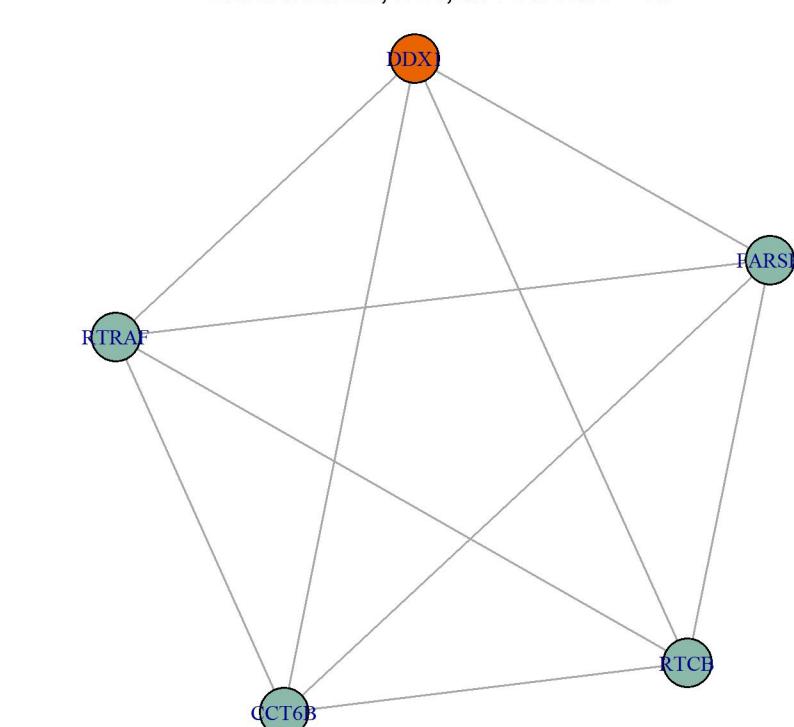
DDX1 network, DB1, all Pearson r > 0.8

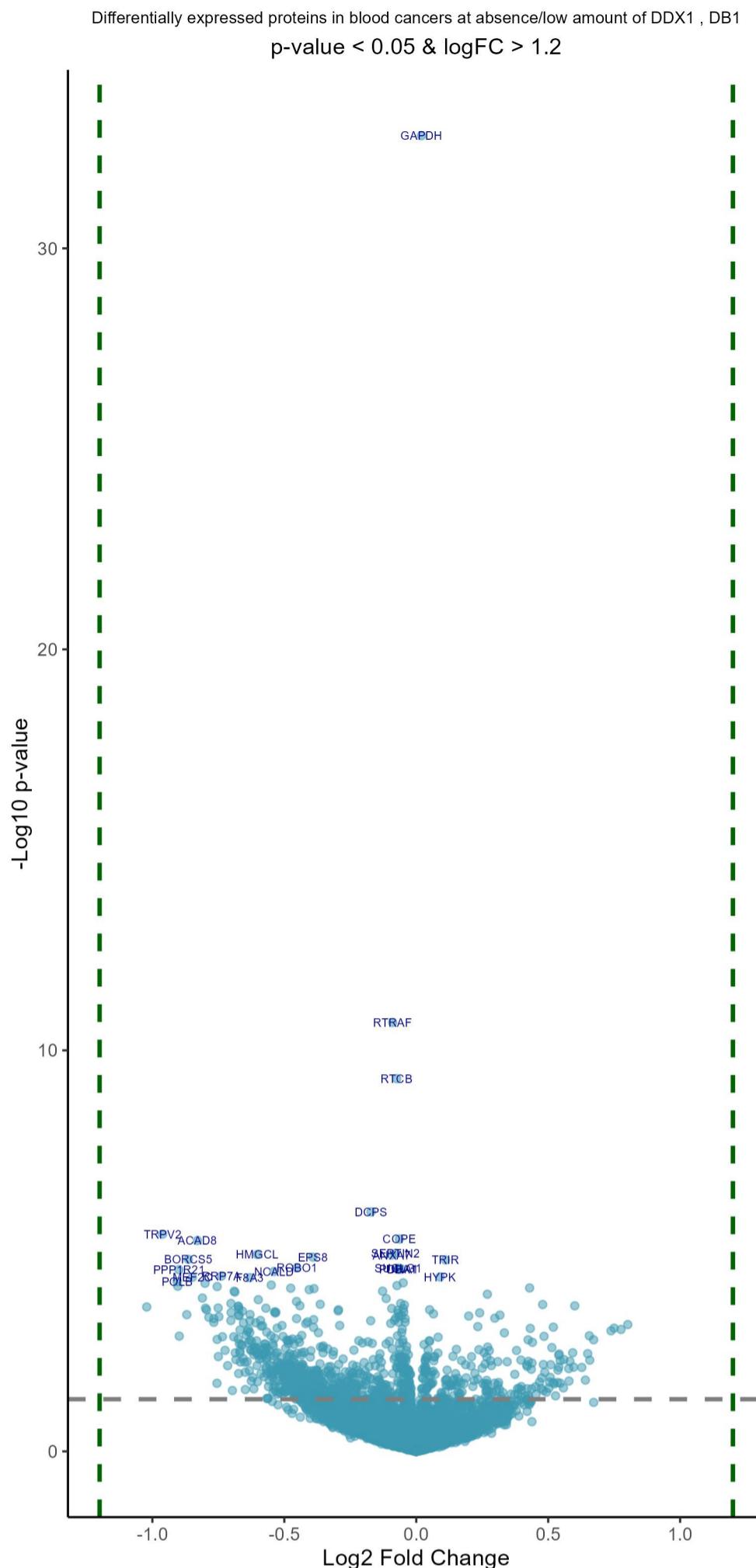


DDX1 network, DB1, all Pearson r > 0.75

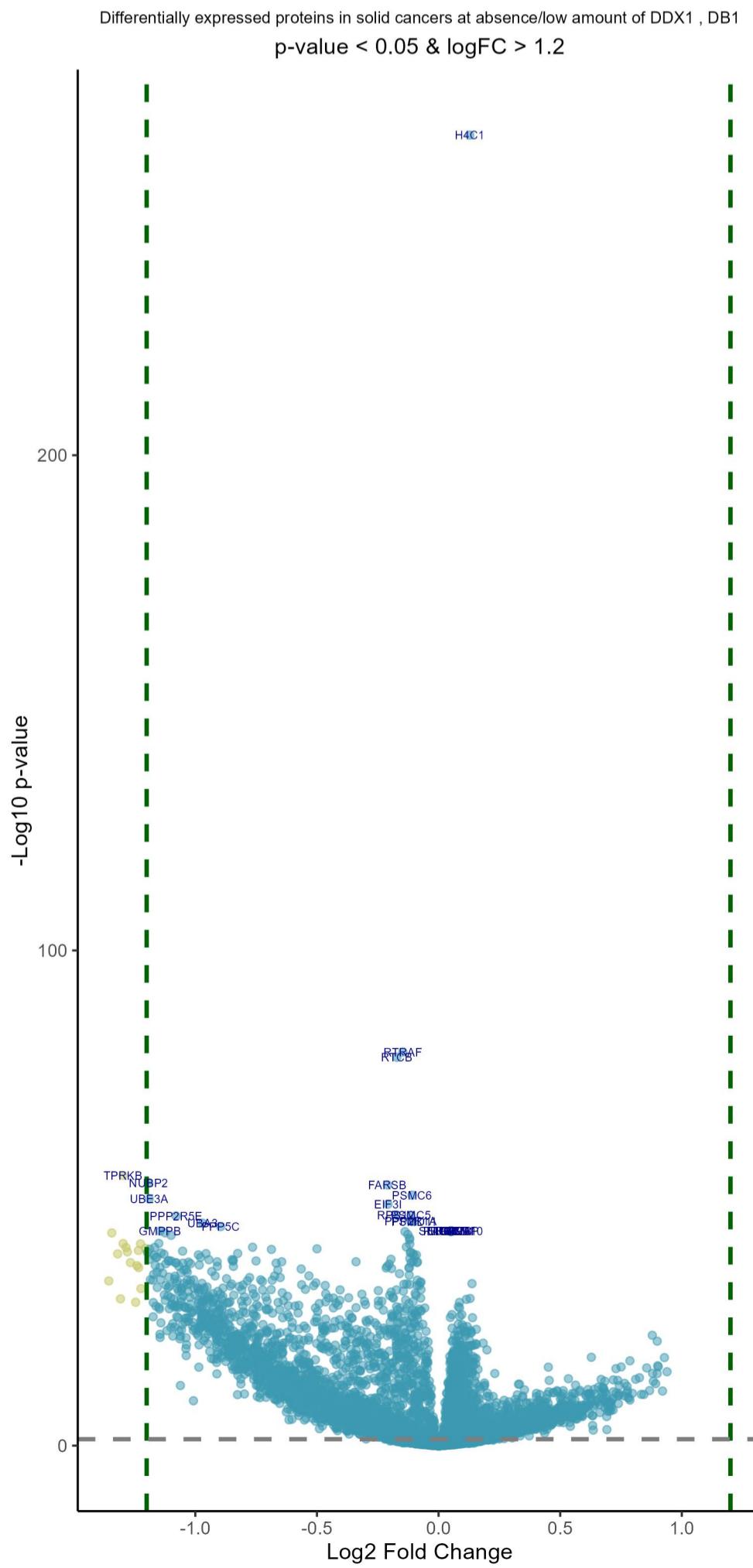


DDX1 network, DB1, all Pearson r > 0.7



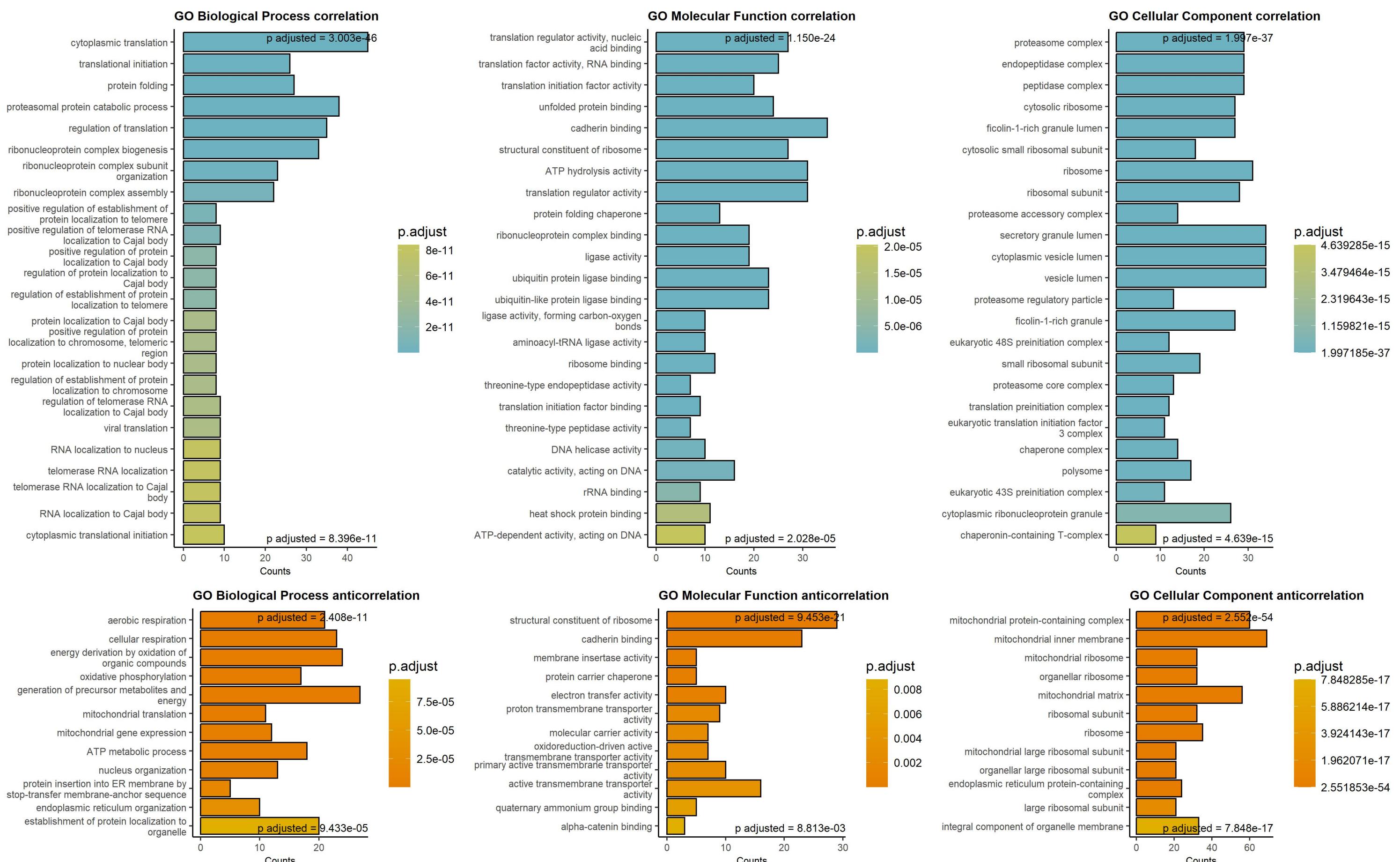


Sorted by p values!							
Downregulated in blood cancers at low/absent DDX1				Upregulated in blood cancers at low/absent DDX1			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.09	4.46e-08	RTRAF	RNA transcription, translation and	0.02	1.03e-29	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
-0.07	8.44e-07	RTCB	RNA 2',3'-cyclic phosphate and 5'-O	0.11	7.98e-03	TRIR	telomerase RNA component interacting protein
-0.17	1.42e-03	DCPS	decapping enzyme, scavenger	0.09	1.29e-02	HYPK	huntingtin interacting protein K
-0.19	4.25e-03	TRPV2	transient receptor potential cation	0.43	1.71e-02	NUCB2	nucleobindin 2
-0.06	4.58e-03	COPE	COPII coat complex subunit epsilon	0.27	2.06e-02	HMGN2	high mobility group nucleosomal binding protein 2
-0.83	4.58e-03	ACAD8	acyl-CoA dehydrogenase family member	0.48	3.09e-02	VAT1	vesicle amine transport 1
-0.08	7.69e-03	SEPTIN2	septin 2	0.6	3.11e-02	AZU1	azurocidin 1
-0.6	7.69e-03	HMGCL	3-hydroxy-3-methylglutaryl-CoA lyase	0.05	3.16e-02	EIF4A3	eukaryotic translation initiation factor 4A3
-0.09	7.69e-03	ANXA7	annexin A7	0.24	3.31e-02	KIF22	kinesin family member 22
-0.39	7.95e-03	EPS8	epidermal growth factor receptor partner	0.07	3.39e-02	WDR12	WD repeat domain 12
-0.86	7.98e-03	BORCS5	BLOC-1 related complex subunit 5	0.32	3.44e-02	PROCR	protein C receptor
-0.45	1.03e-02	ROBO1	roundabout guidance receptor 1	0.2	3.50e-02	PRRC2A	proline rich coiled-coil 2A
-0.07	1.03e-02	SUCLG1	succinate-CoA ligase GDP/ADP-formin	0.3	3.70e-02	MMP14	matrix metallopeptidase 14
-0.06	1.03e-02	UBA1	ubiquitin like modifier activating	0.8	4.45e-02	RHEB	Ras homolog, mTORC1 binding
-0.07	1.03e-02	PDHA1	pyruvate dehydrogenase E1 subunit alpha	0.23	4.77e-02	NOP9	NOP9 nucleolar protein
-0.9	1.03e-02	PPP1R21	protein phosphatase 1 regulatory subunit	0.52	4.87e-02	SP3	Sp3 transcription factor
-0.54	1.09e-02	NCALD	neurocalcin delta	0.75	5.02e-02	PYGL	glycogen phosphorylase L
-0.74	1.29e-02	RRP7A	ribosomal RNA processing 7 homolog	0.43	5.05e-02	BZW2	basic leucine zipper and W2 domains
-0.85	1.29e-02	MEF2C	myocyte enhancer factor 2C	0.78	5.22e-02	CCNA2	cyclin A2
-0.63	1.29e-02	F8A3	coagulation factor VIII associated	0.74	5.55e-02	CTBP2	C-terminal binding protein 2
-0.91	1.56e-02	POLB	DNA polymerase beta	0.33	5.94e-02	FCGR2T	Fc gamma receptor and transporter
-0.05	1.58e-02	CDC42	cell division cycle 42	0.66	6.77e-02	UQCR10	ubiquinol-cytochrome c reductase, complex II
-0.8	1.58e-02	PLEKHO2	pleckstrin homology domain containing	0.48	6.87e-02	PTPN12	protein tyrosine phosphatase non-receptor type 12
-0.55	1.67e-02	STX18	syntaxin 18	0.08	7.00e-02	UNC45A	unc-45 myosin chaperone A
-0.07	1.67e-02	TFAM	transcription factor A, mitochondrial	0.67	7.71e-02	TNS3	tensin 3
-0.9	1.67e-02	CD58	CD58 molecule	0.42	7.71e-02	PSMG1	proteasome assembly chaperone 1
-0.75	1.67e-02	PACS1	phosphofuranic acid cluster sorting	0.05	7.78e-02	TBCA	tubulin folding cofactor A
-0.48	1.71e-02	RAP2C	RAP2C, member of RAS oncogene family	0.05	7.84e-02	PFDN1	prefoldin subunit 1
-0.39	1.71e-02	DOK1	docking protein 1	0.44	8.15e-02	BST1	bone marrow stromal cell antigen 1
-0.41	1.76e-02	ADPRH	ADP-ribosylarginine hydrolase	0.03	8.44e-02	SF3B1	splicing factor 3b subunit 1
-0.13	1.82e-02	DECR1	2,4-dienoyl-CoA reductase 1	0.27	9.46e-02	UBE2S	ubiquitin conjugating enzyme E2 S
-0.69	1.82e-02	C11orf54	chromosome 11 open reading frame 54	0.51	9.56e-02	EPHX1	epoxide hydrolase 1
-0.69	1.87e-02	MVK	mevalonate kinase	0.15	1.01e-01	RUFY1	RUN and FYVE domain containing 1
-0.81	2.49e-02	IL4I1	interleukin 4 induced 1	0.24	1.01e-01	UHFR1	ubiquitin like with PHD and ring finger
-0.11	2.49e-02	AKR1A1	aldo-keto reductase family 1 member	0.04	1.02e-01	POLR2C	RNA polymerase II subunit C
-0.6	2.61e-02	IRF9	interferon regulatory factor 9	0.38	1.03e-01	CEBPA	CCAAT enhancer binding protein alpha
-0.45	2.82e-02	LYPLA2	lysophospholipase 2	0.28	1.03e-01	SERPINA1	serpin family A member 1
-0.06	3.03e-02	PDHB	pyruvate dehydrogenase E1 subunit b	0.26	1.09e-01	ABCD1	ATP binding cassette subfamily D member 1
-0.7	3.03e-02	ENDC3A	fibronectin type III domain containing	0.59	1.09e-01	PRTN3	proteinase 3

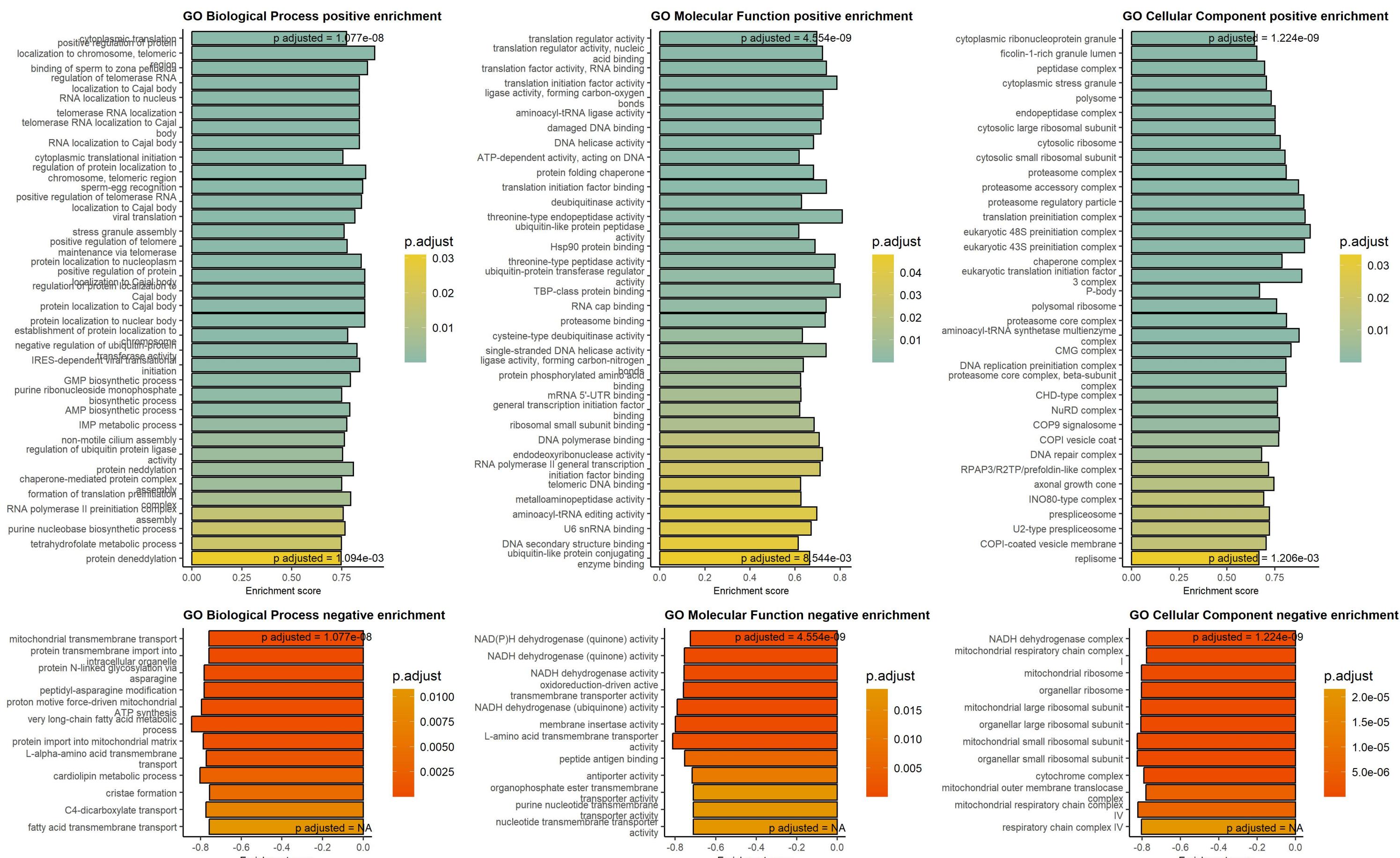


Sorted by p values!							
Downregulated in solid cancers at low/absent DDX1				Upregulated in solid cancers at low/absent DDX1			
FC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.15	7.13e-77	RTRAF	RNA transcription, translation and	0.13	1.52e-261	H4C1	H4 clustered histone 1
-1.17	6.29e-76	RTCB	RNA 2',3'-cyclic phosphate and 5'-O	0.05	3.27e-42	PTPRCAP	protein tyrosine phosphatase receptor
-1.3	3.65e-52	TPRKB	TP53RK binding protein	0.05	3.27e-42	HBE1	hemoglobin subunit epsilon 1
-1.19	9.24e-51	NUBP2	NUBP iron-sulfur cluster assembly f	0.05	3.27e-42	SERPINB10	serpin family B member 10
-1.21	2.12e-50	FARSB	phenylalanyl-tRNA synthetase subunit	0.05	3.27e-42	IGLL1	immunoglobulin lambda like polypep
-1.11	2.16e-48	PSMC6	proteasome 26S subunit, ATPase 6	0.05	3.27e-42	CRYBB1	crystallin beta B1
-1.19	1.03e-47	UBE3A	ubiquitin protein ligase E3A	0.05	3.27e-42	ITGA2B	integrin subunit alpha 2b
-1.21	1.16e-46	EIF3I	eukaryotic translation initiation f	0.05	3.27e-42	ACAP1	ArfGAP with coiled-coil, ankyrin re
-1.18	1.57e-44	RPS12	ribosomal protein S12	0.05	3.27e-42	NCF4	neutrophil cytosolic factor 4
-1.11	1.73e-44	PSMC5	proteasome 26S subunit, ATPase 5	0.05	3.27e-42	SP140	SP140 nuclear body protein
-1.08	2.20e-44	PPP2R5E	protein phosphatase 2 regulatory su	0.05	3.27e-42	PSTPIP1	proline-serine-threonine phosphatase
-1.11	2.24e-43	PPP2R1A	protein phosphatase 2 scaffold subu	0.05	3.27e-42	STAB1	stabilin 1
-1.1	2.51e-43	PSMD11	proteasome 26S subunit, non-ATPase	0.05	3.27e-42	SELPLG	selectin P ligand
-1.97	4.92e-43	UBA3	ubiquitin like modifier activating	0.05	3.27e-42	RCSD1	RCSD domain containing 1
-1.9	2.29e-42	PPP5C	protein phosphatase 5 catalytic sub	0.05	3.27e-42	STAT5A	signal transducer and activator of
-1.14	3.27e-42	GMPPB	GDP-mannose pyrophosphorylase B	0.05	3.27e-42	CTSW	cathepsin W
-1.14	4.01e-42	PSMD7	proteasome 26S subunit, non-ATPase	0.05	3.27e-42	GIMAP6	GTPase, IMAP family member 6
-1.12	7.13e-42	EIF2B2	eukaryotic translation initiation f	0.05	3.27e-42	GZMB	granzyme B
-1.34	7.33e-42	PITHD1	PITH domain containing 1	0.05	3.27e-42	HK3	hexokinase 3
-1.13	1.46e-41	PSMD1	proteasome 26S subunit, non-ATPase	0.05	3.27e-42	TUBA8	tubulin alpha 8
-1.1	2.20e-41	PIH1D1	PIH1 domain containing 1	0.05	3.27e-42	CR2	complement C3d receptor 2
-1.12	7.73e-41	CCT7	chaperonin containing TCP1 subunit	0.05	3.27e-42	POU2F2	POU class 2 homeobox 2
-1.12	1.58e-40	PSMD14	proteasome 26S subunit, non-ATPase	0.05	3.27e-42	AZU1	azurocidin 1
-1.15	8.92e-40	DOHH	deoxyhypusine hydroxylase	0.05	3.27e-42	CD48	CD48 molecule
-1.3	9.74e-40	SAAL1	serum amyloid A like 1	0.05	3.27e-42	SKAP2	src kinase associated phosphoprote
-1.23	1.09e-39	DCK	deoxycytidine kinase	0.05	3.27e-42	CCL17	C-C motif chemokine ligand 17
-1.12	1.22e-39	CCT3	chaperonin containing TCP1 subunit	0.05	3.27e-42	ADA2	adenosine deaminase 2
-1.13	4.54e-39	PSMA3	proteasome 20S subunit alpha 3	0.05	3.27e-42	CD3E	CD3 epsilon subunit of T-cell recep
-1.76	5.14e-39	EIF2B4	eukaryotic translation initiation f	0.05	3.27e-42	RNASE2	ribonuclease A family member 2
-1.17	5.42e-39	MEMO1	mediator of cell motility 1	0.05	3.27e-42	TEX11	testis expressed 11
-1.29	5.66e-39	PPM1A	protein phosphatase, Mg2+/Mn2+ depe	0.05	3.27e-42	PLEK	pleckstrin
-1.2	8.67e-39	LZIC	leucine zipper and CTNNBIP1 domain	0.05	3.27e-42	CD300A	CD300a molecule
-1.5	1.03e-38	FAM98B	family with sequence similarity 98	0.05	3.27e-42	GZMA	granzyme A
-1.19	1.20e-38	PHPT1	phosphohistidine phosphatase 1	0.05	3.27e-42	SIGLEC12	sialic acid binding Ig like lectin
-1.69	1.36e-38	NAA50	N-alpha-acetyltransferase 50, NatE	0.05	3.27e-42	SMIM24	small integral membrane protein 24
-1.23	2.19e-38	PDXP	pyridoxal phosphatase	0.05	3.27e-42	ALOX15	arachidonate 15-lipoxygenase
-1.05	2.93e-38	RAP1GDS1	Rap1 GTPase-GDP dissociation stimul	0.05	3.27e-42	GZMM	granzyme M
-1.28	4.15e-38	GSK3B	glycogen synthase kinase 3 beta	0.05	3.27e-42	ARHGAP9	Rho GTPase activating protein 9
-1.2	5.69e-38	RNF214	transmembrane protein 214	0.05	3.27e-42	NINJ2	neurofibromatosis 2

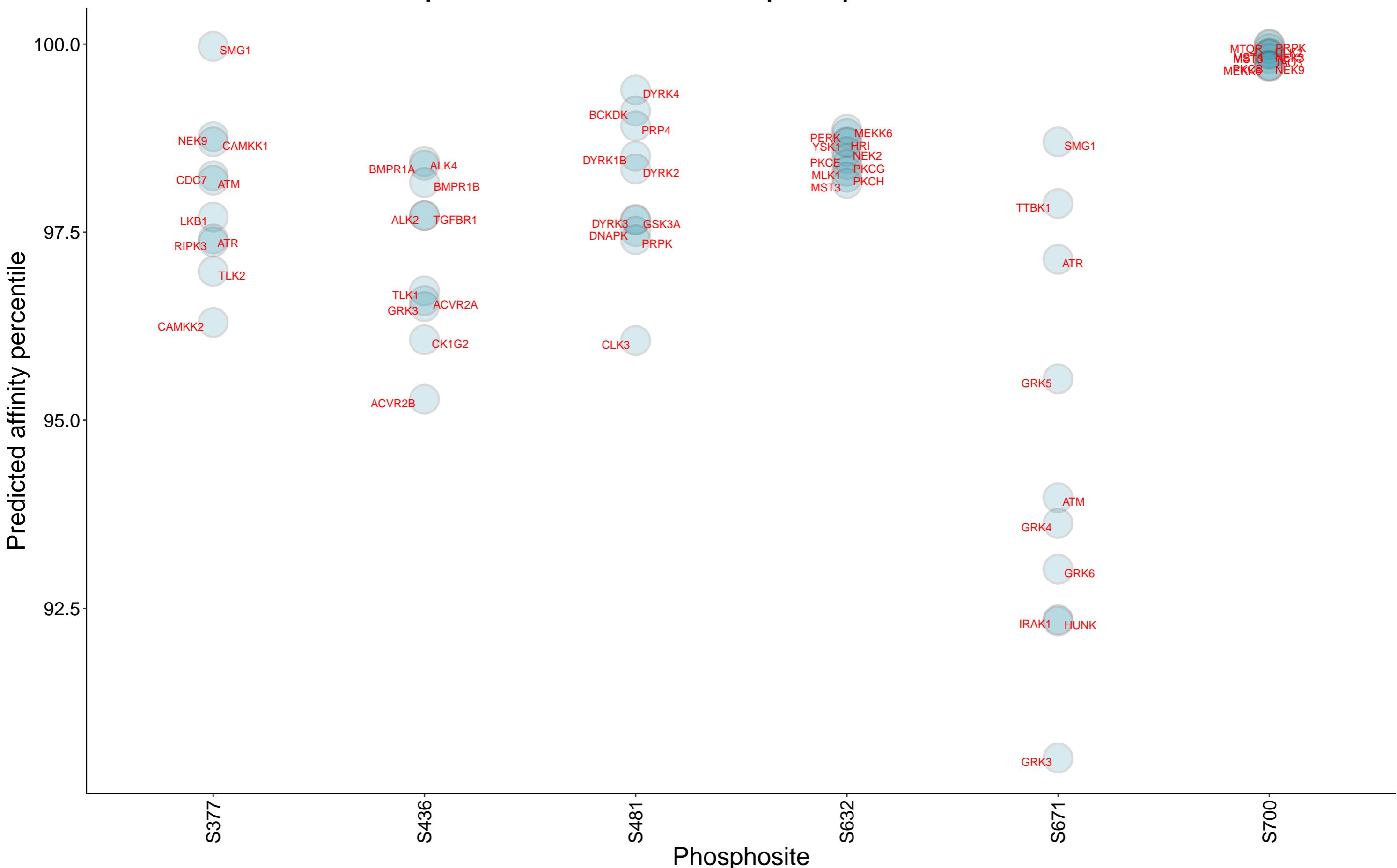
Top 250 correlation coefficients overrepresentation, DDX1 protein, DB1



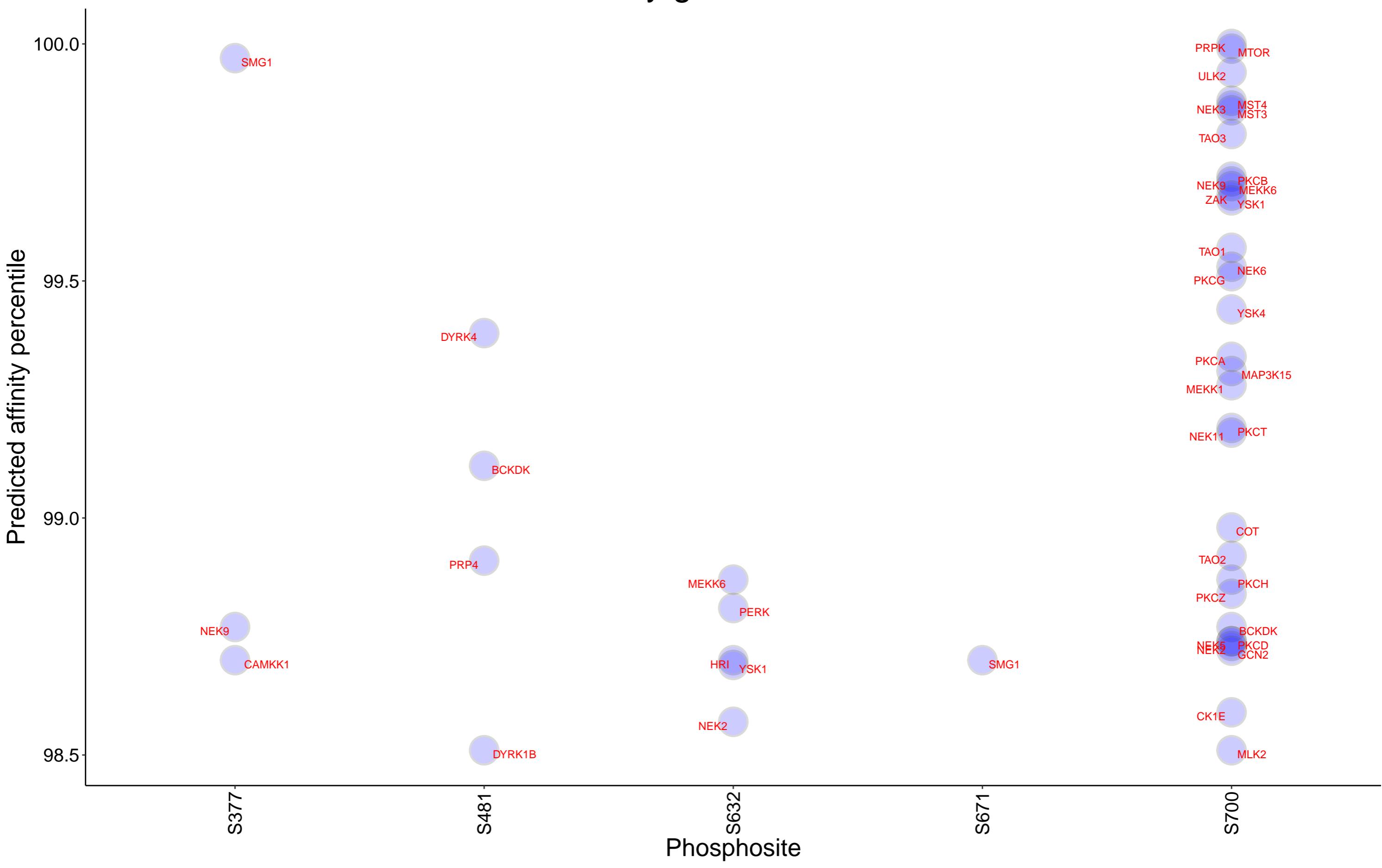
Gene Set Enrichment analysis on protein correlation coefficients, DDX1 protein, DB1



Top 10 kinases for each phosphosite in DDX1



Kinases with affinity greater than 98.5% to DDX1



Top 15 positive correlation coefficients for DDX1 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

