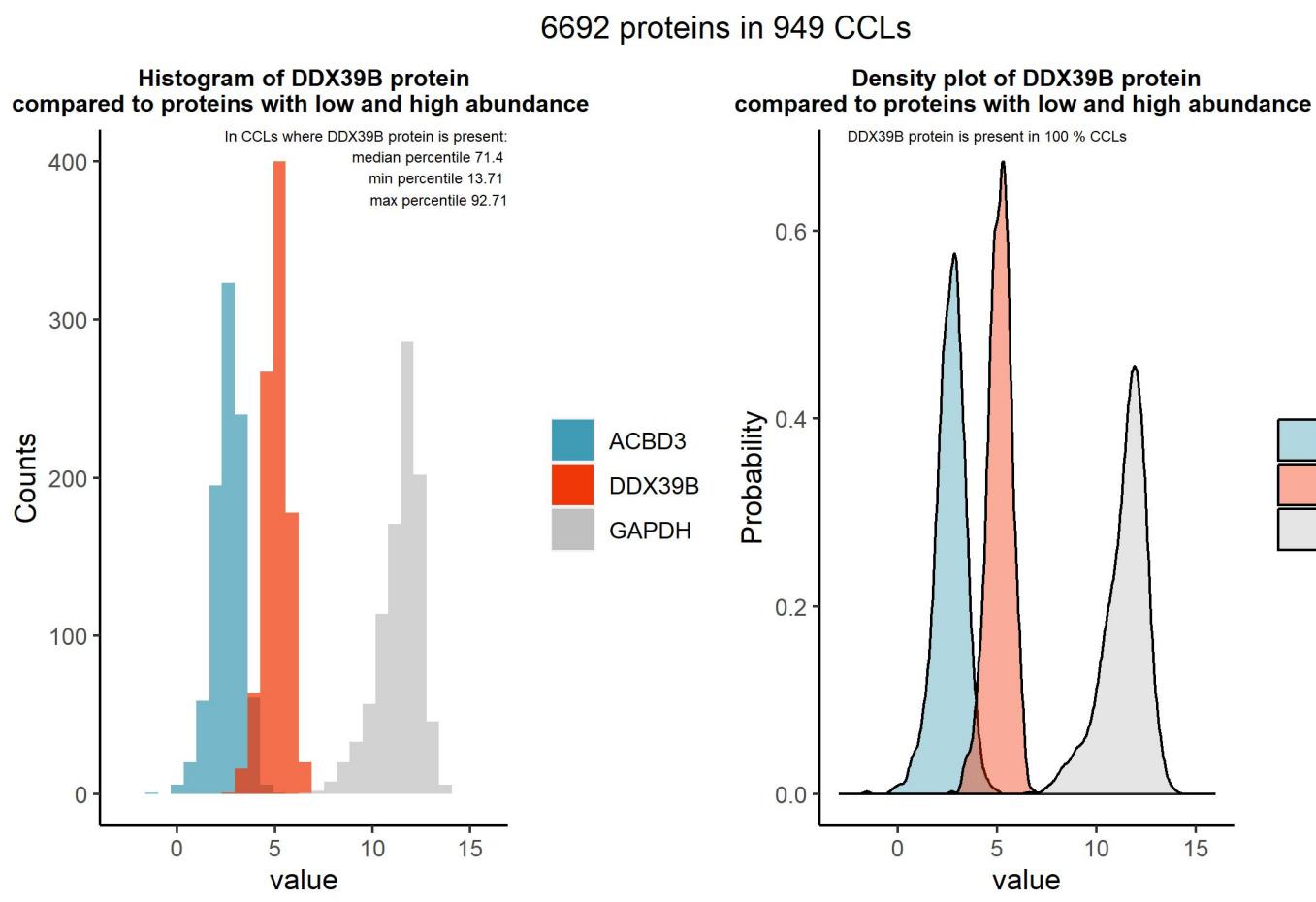


DDX39B

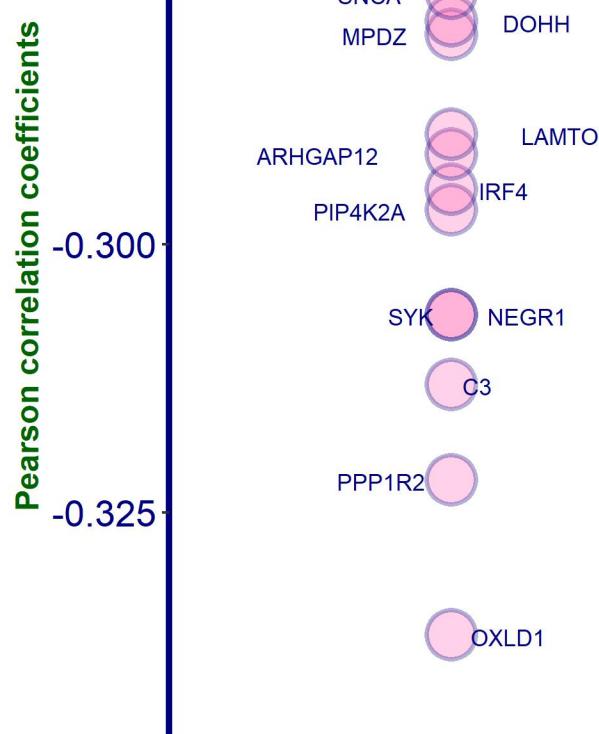
Protein name: DX39B ; UNIPROT: Q13838 ; Gene name: DExD-box helicase 39B

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

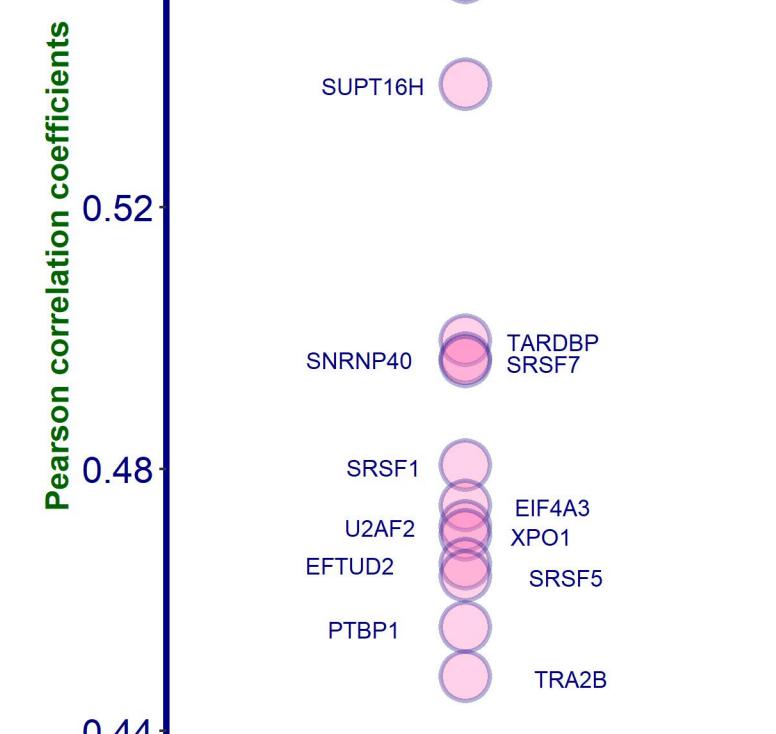
Sanger Institute Protein Database 1 (DB1), protein presence is certain



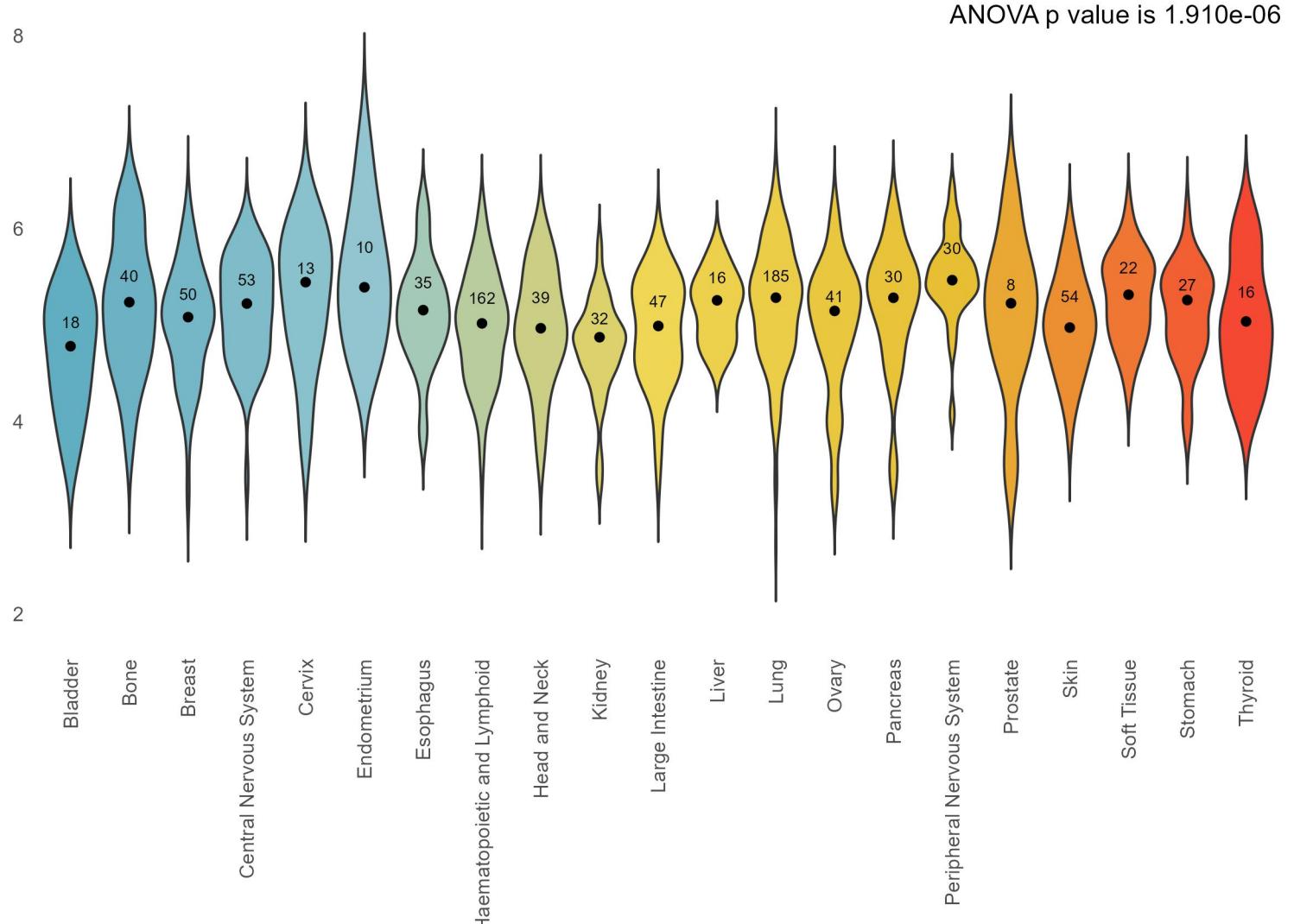
Top negative correlations of DDX39B protein, DE



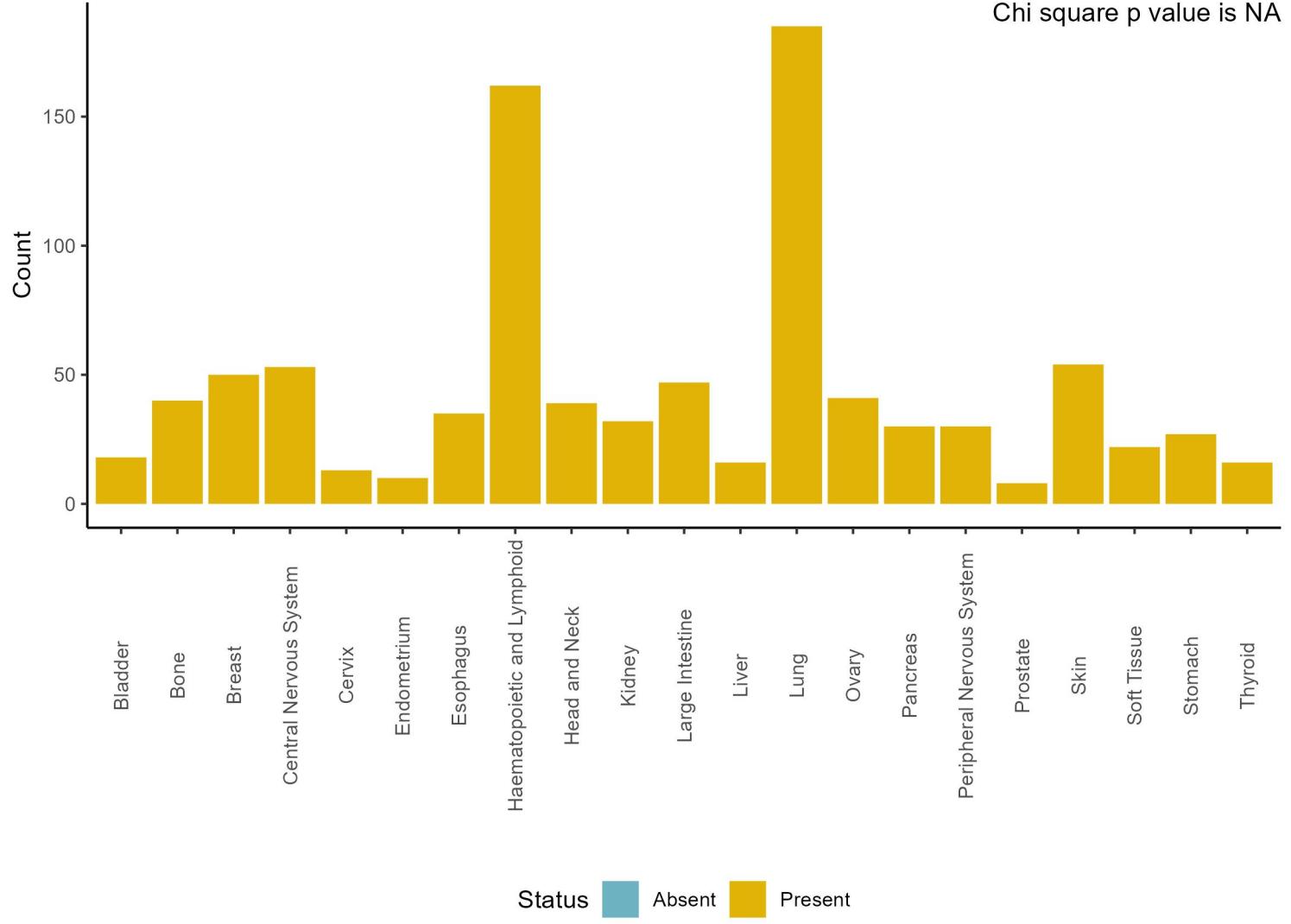
Top positive correlations of DDX39B protein, DB1



Amount of DDX39B protein, number of CCLs where it is present by tissue, DB1



Present and absent DDX39B protein counts by tissue, DB1

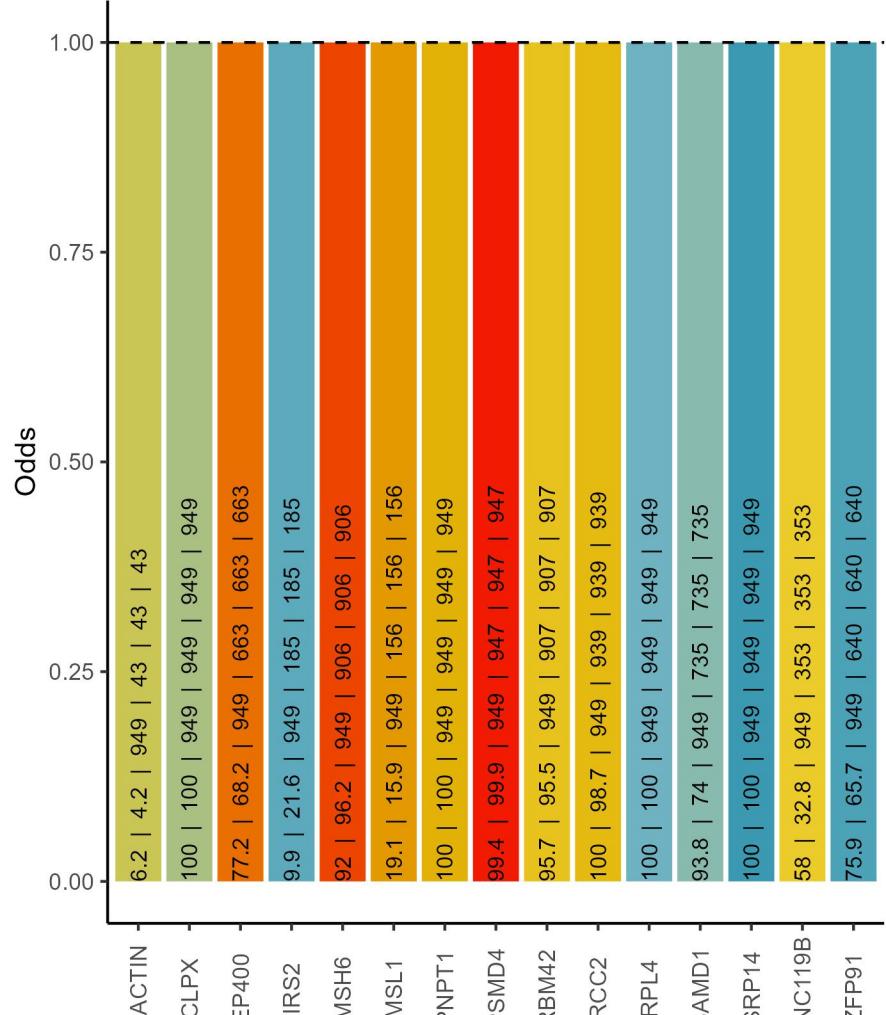


Cooccurrence with DDX39B protein, DB1

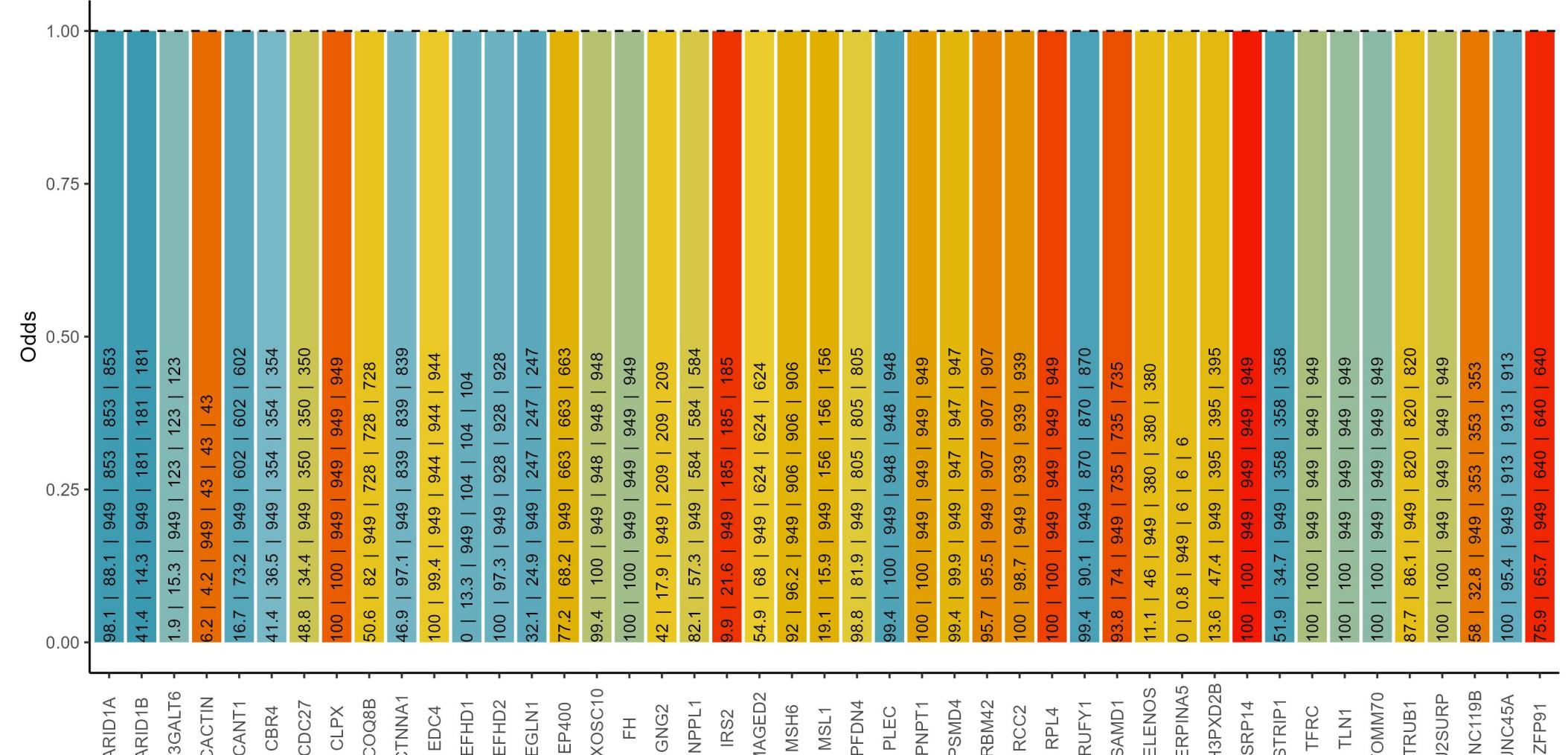
% of DDX39B in blood cancers: 100 ; % of DDX39B in solid cancers: 100

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of DDX39B | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



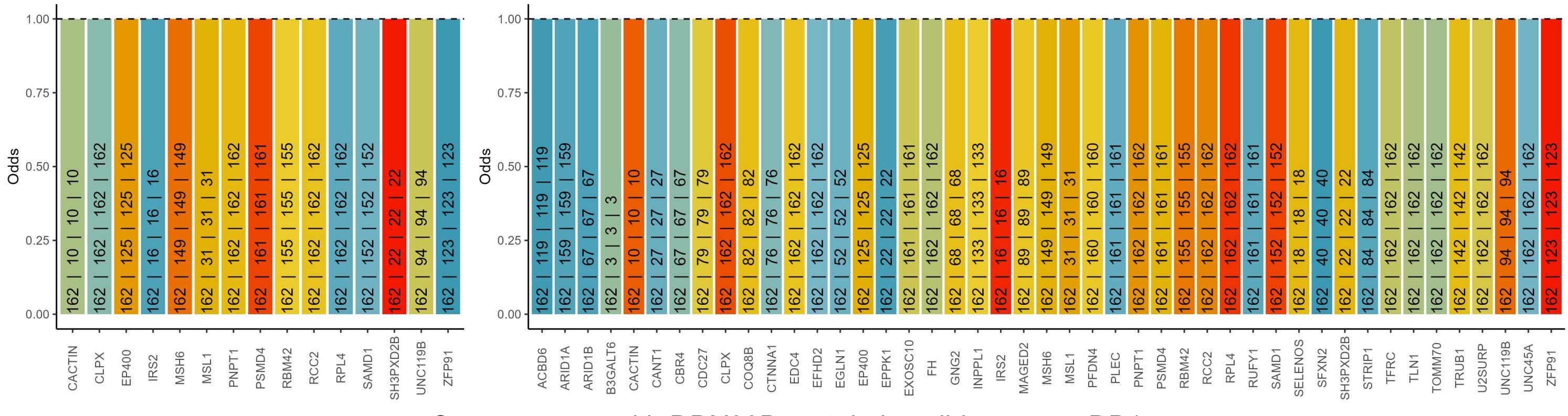
Positive cooccurrence





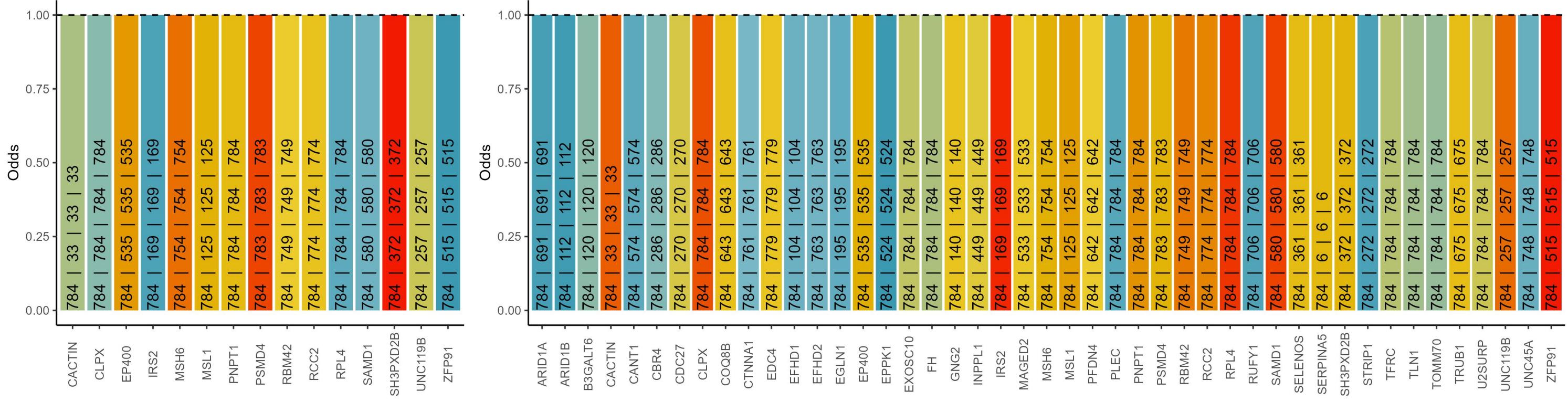
cooccurrence with DDX39B protein in breast cancer; DDX39B | incidence of DDX39B | incidence of Protein 2 | observed cooccurrence | evidence

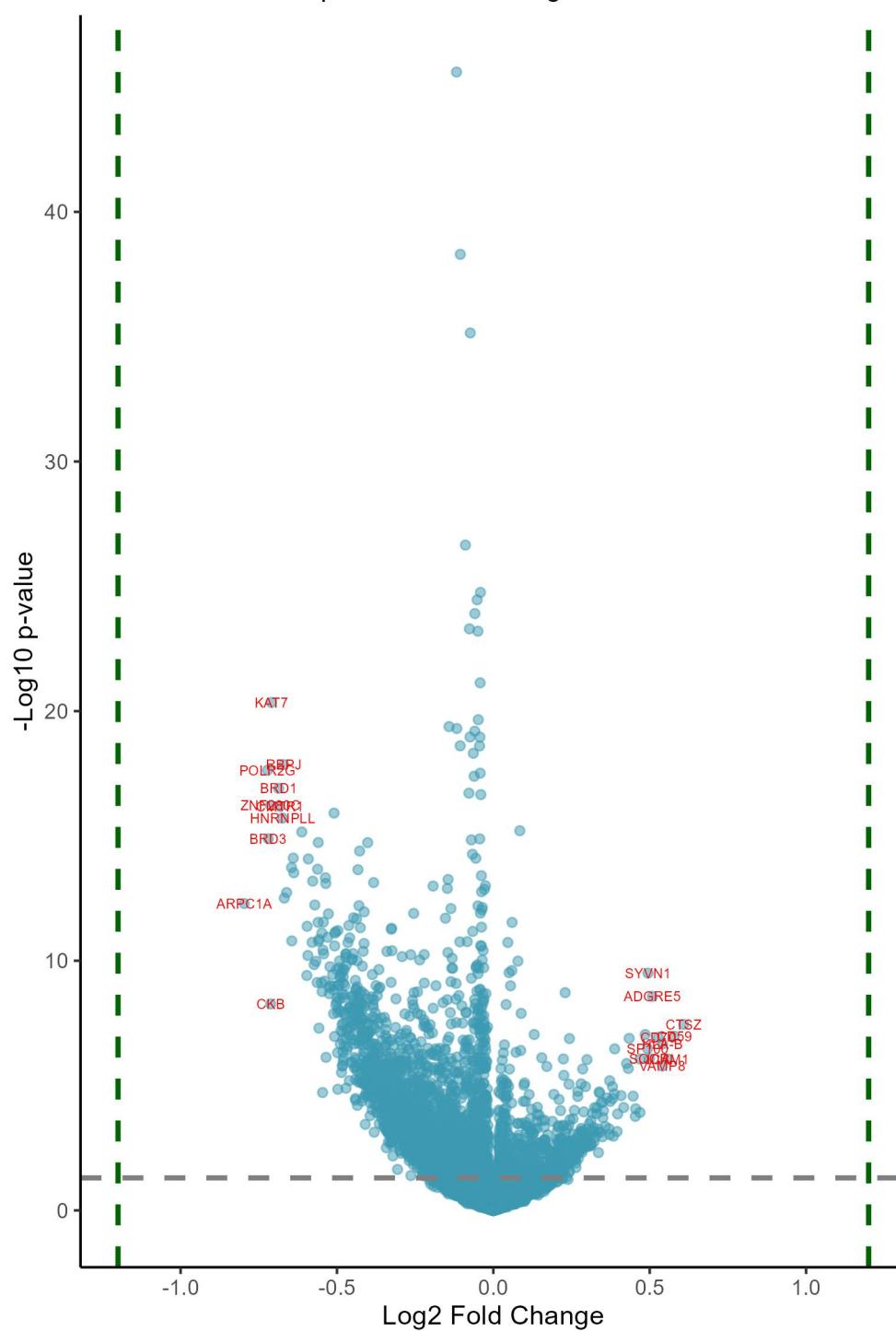
negative cooccurrence Positive cooccurrence



incidence of DDX39B | incidence of Protein 2 | observed cooccurrence | e

negative cooccurrence Positive cooccurrence

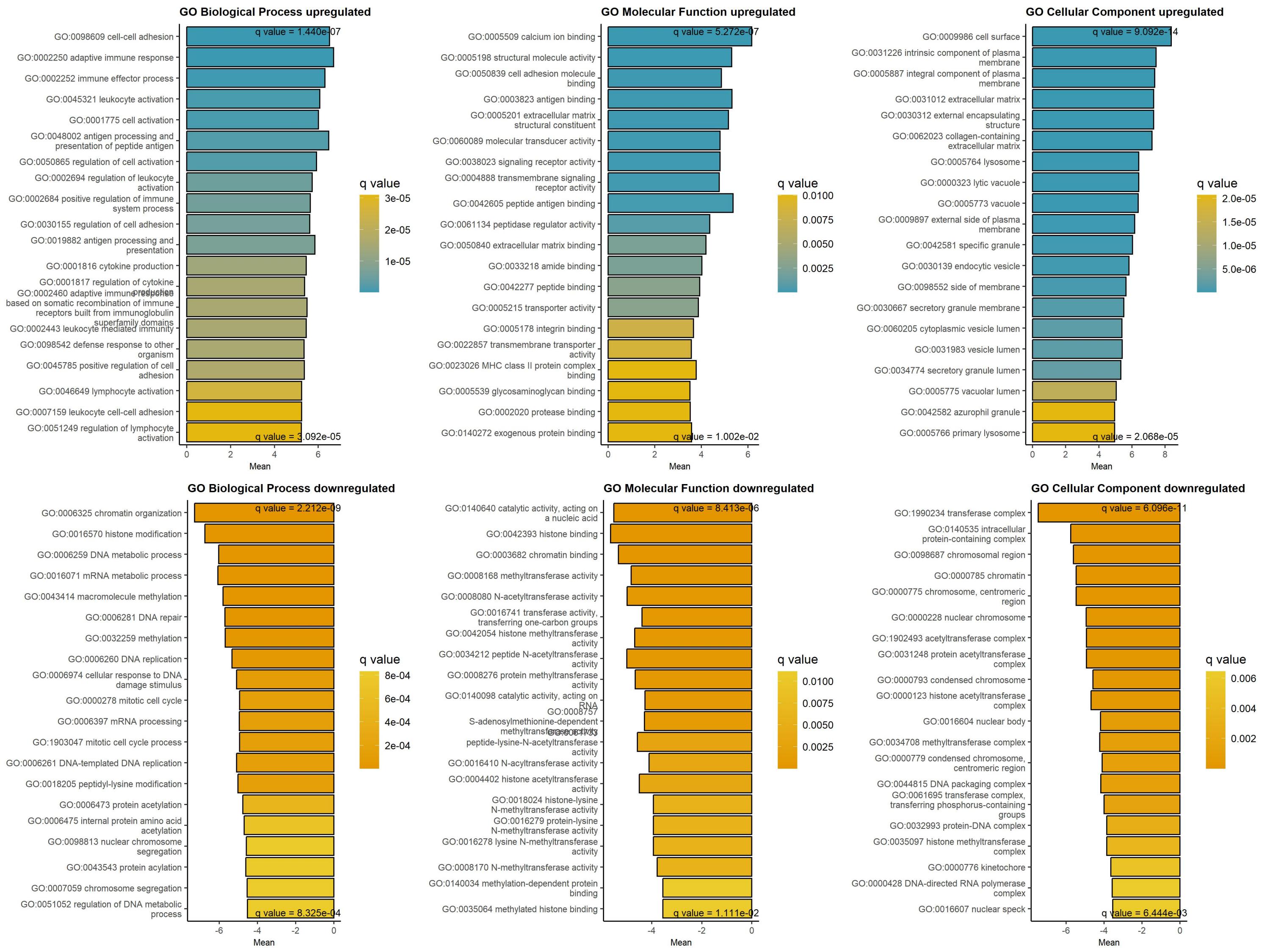


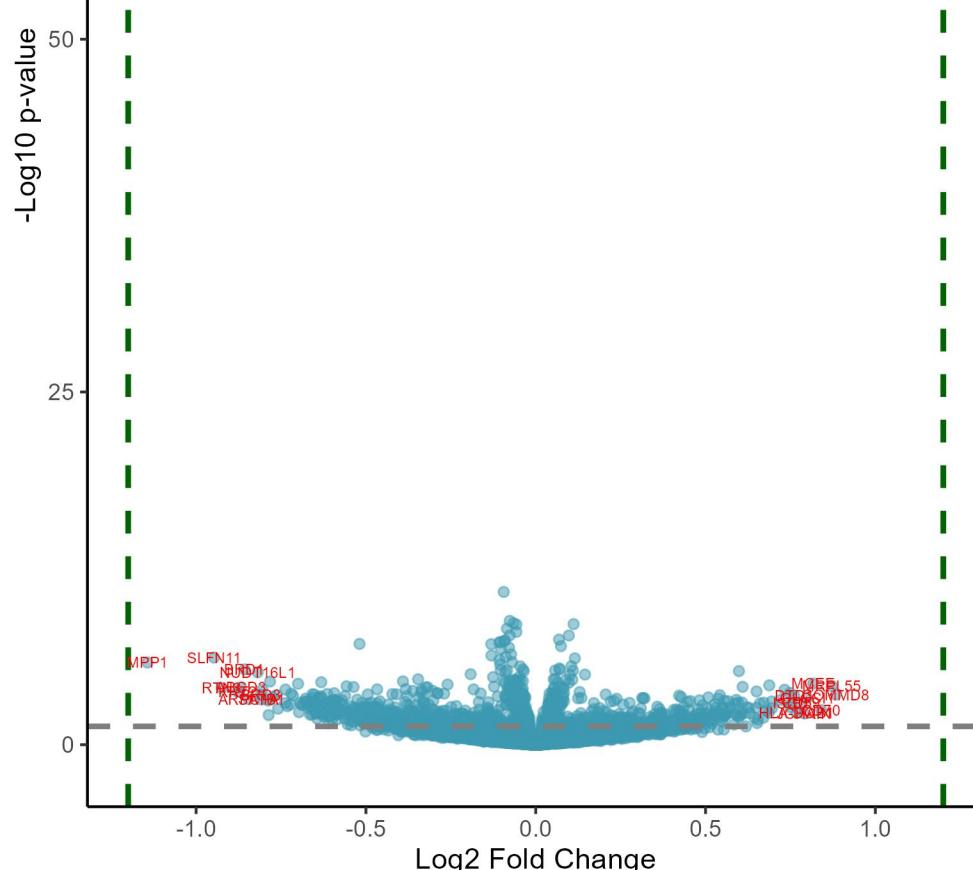


Downregulated at low/absent DDX39B Upregulated at low/absent DDX39B

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.8	5.49e-11	ARPC1A	actin related protein 2/3 complex s	0.61	7.86e-07	CTSZ	cathepsin Z
-0.72	6.77e-16	POLR2G	RNA polymerase II subunit G	0.58	1.97e-06	CD59	CD59 molecule (CD59 blood group)
-0.72	2.43e-13	BRD3	bromodomain containing 3	0.56	1.21e-05	ICAM1	intercellular adhesion molecule 1
-0.71	1.36e-14	ZNF280C	zinc finger protein 280C	0.54	3.62e-06	HLA-B	major histocompatibility complex, c
-0.71	1.61e-07	CKB	creatine kinase B	0.54	2.04e-05	VAMP8	vesicle associated membrane protein
-0.71	2.50e-18	KAT7	lysine acetyltransferase 7	0.53	2.16e-06	CD70	CD70 molecule
-0.69	3.18e-15	BRD1	bromodomain containing 1	0.51	8.92e-08	ADGRE5	adhesion G protein-coupled receptor
-0.68	1.46e-14	CMTTR1	cap methyltransferase 1	0.5	1.18e-05	SQOR	sulfide quinone oxidoreductase
-0.67	4.00e-14	HNRNPLL	heterogeneous nuclear ribonucleoprotein	0.49	1.42e-08	SYVN1	synoviolin 1
-0.67	4.20e-16	RBPJ	recombination signal binding protein	0.49	5.31e-06	SP100	SP100 nuclear antigen
-0.67	3.37e-11	BRD2	bromodomain containing 2	0.49	1.73e-06	MVP	major vault protein
-0.66	2.05e-11	PHC2	polyhomeotic homolog 2	0.47	1.21e-05	TAP1	transporter 1, ATP binding cassette
-0.65	2.74e-12	PPP4C	protein phosphatase 4 catalytic subunit	0.47	7.41e-04	LCP1	lymphocyte cytosolic protein 1
-0.64	1.15e-09	HDGFL3	HDGF like 3	0.45	5.57e-04	RAC2	Rac family small GTPase 2
-0.64	1.21e-12	YTHDC1	YTH domain containing 1	0.45	1.00e-03	LGALS3	galectin 3
-0.64	4.14e-12	PRPF38B	pre-mRNA processing factor 38B	0.45	2.06e-04	FKBP11	FKBP prolyl isomerase 11
-0.61	1.36e-13	ERI3	ERI1 exoribonuclease family member	0.43	2.36e-06	HLA-C	major histocompatibility complex, c
-0.6	1.72e-08	MAD2L1	mitotic arrest deficient 2 like 1	0.43	2.43e-05	APOL2	apolipoprotein L2
-0.6	3.47e-10	SUDS3	SDS3 homolog, SIN3A corepressor complex	0.43	1.67e-05	NFKB2	nuclear factor kappa B subunit 2
-0.59	3.53e-09	ABI2	abl interactor 2	0.42	5.02e-04	LGALS1	galectin 1
-0.59	1.27e-12	MDN1	midasin AAA ATPase 1	0.41	1.98e-04	PSMB9	proteasome 20S subunit beta 9
-0.58	1.26e-09	DBR1	debranching RNA lariats 1	0.4	8.30e-04	STOM	stomatin
-0.58	8.26e-12	CHD1	chromodomain helicase DNA binding protein	0.4	3.23e-03	BST2	bone marrow stromal cell antigen 2
-0.57	7.41e-09	CFAP20	cilia and flagella associated protein	0.39	5.39e-06	TAPBP	TAP binding protein
-0.57	6.17e-11	ZMYM3	zinc finger MYM-type containing 3	0.39	1.75e-04	SLC30A1	solute carrier family 30 member 1
-0.57	5.51e-09	CRMP1	collapsin response mediator protein	0.38	4.54e-03	CD44	CD44 molecule (Indian blood group)
-0.56	3.10e-08	TMEM33	transmembrane protein 33	0.38	2.50e-04	CD74	CD74 molecule
-0.56	3.11e-12	IPO8	importin 8	0.38	9.95e-05	B2M	beta-2-microglobulin
-0.56	2.48e-10	ZMYM4	zinc finger MYM-type containing 4	0.37	3.14e-04	PSMB8	proteasome 20S subunit beta 8

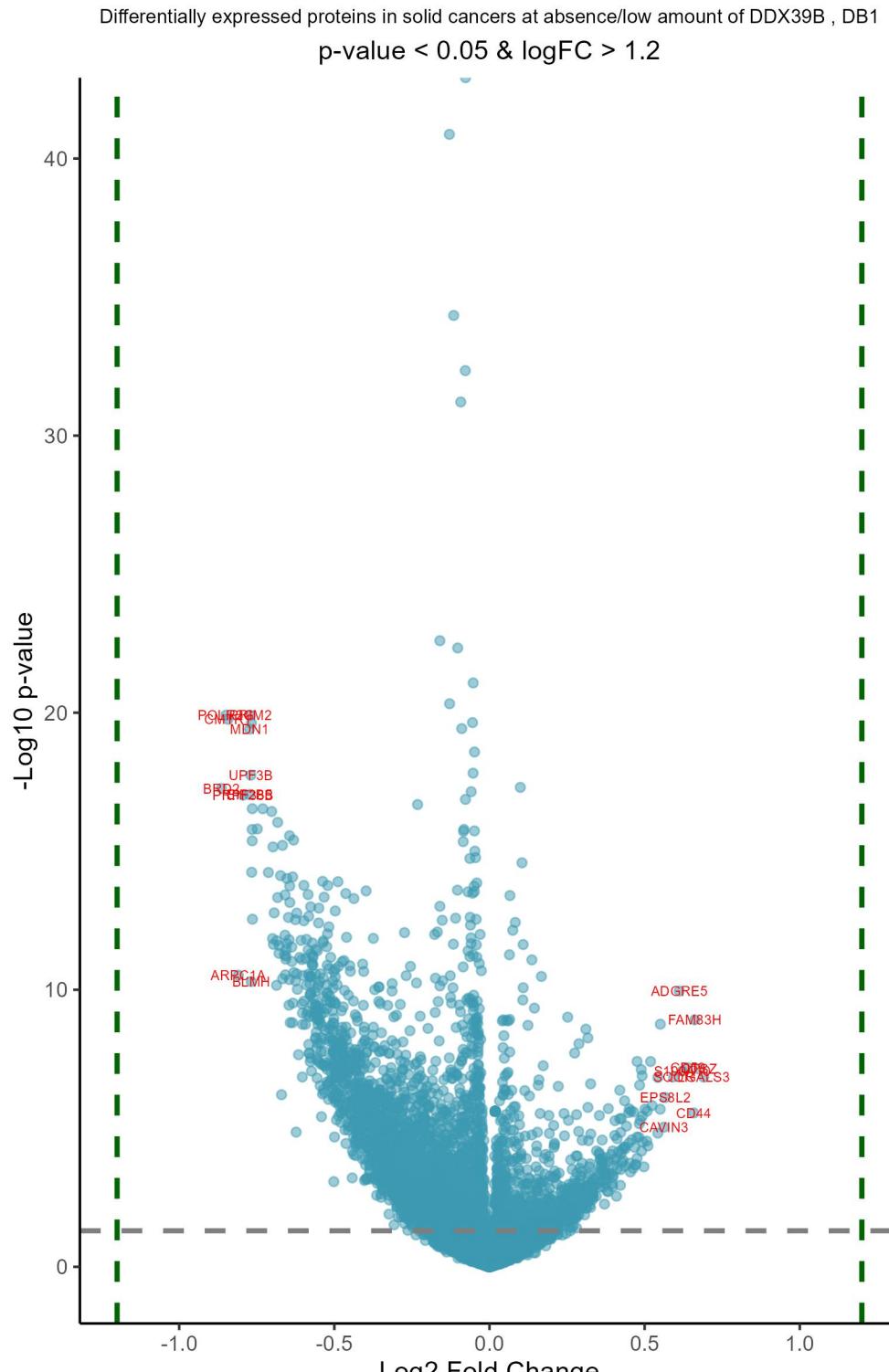
GAGE analysis on upregulated and downregulated proteins at low/absent DDX39B protein, DB1





Downregulated in blood cancers at low/absent DDX39B Upregulated in blood cancers at low/absent DDX39B

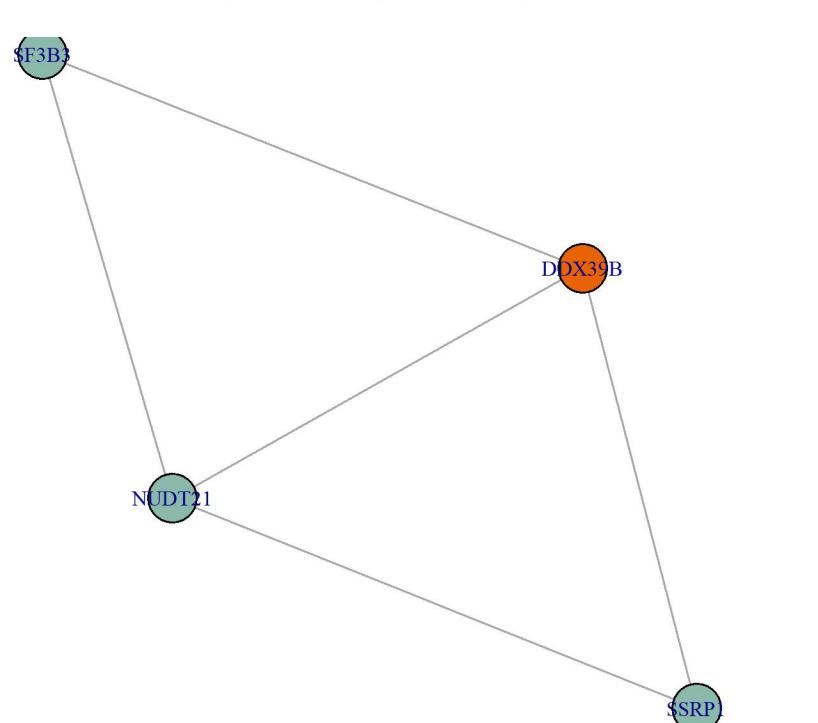
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.14	3.42e-04	MPP1	MAGUK p55 scaffold protein 1	0.88	1.39e-02	COMM8	COMM domain containing 8
-0.95	1.76e-04	SLFN11	schlafen family member 11	0.87	5.97e-03	MRPL55	mitochondrial ribosomal protein L55
-0.92	7.13e-03	RTN3	reticulon 3	0.84	6.28e-02	CD70	CD70 molecule
-0.88	1.13e-02	KRT2	keratin 2	0.82	4.35e-03	MCEE	methylmalonyl-CoA epimerase
-0.87	6.67e-03	ABCD3	ATP binding cassette subfamily D me	0.8	1.92e-02	GLCCI1	glucocorticoid induced 1
-0.86	8.69e-04	BRD1	bromodomain containing 1	0.79	8.57e-02	JCHAIN	joining chain of multimeric IgA and
-0.85	2.14e-02	ARPC1A	actin related protein 2/3 complex s	0.78	2.95e-02	CD59	CD59 molecule (CD59 blood group)
-0.82	1.12e-03	NUDT16L1	nudix hydrolase 16 like 1	0.77	8.42e-02	HLA-DQB1	major histocompatibility complex, c
-0.81	1.41e-02	BRD3	bromodomain containing 3	0.76	1.49e-02	DTD1	D-aminoacyl-tRNA deacetylase 1
-0.81	2.26e-02	SATB1	SATB homeobox 1	0.75	3.20e-02	ISCU	iron-sulfur cluster assembly enzyme
-0.81	8.39e-03	IGLL1	immunoglobulin lambda like polypept	0.75	4.78e-02	IKZF3	IKAROS family zinc finger 3
-0.79	2.53e-02	RUNX1	RUNX family transcription factor 1	0.75	1.26e-02	GOLM1	golgi membrane protein 1
-0.79	1.01e-01	FSCN1	fascin actin-bundling protein 1	0.73	8.39e-03	ASNS	asparagine synthetase (glutamine-hy
-0.78	3.46e-03	MOV10	Mov10 RISC complex RNA helicase	0.72	2.41e-02	AKT1S1	AKT1 substrate 1
-0.78	1.75e-02	GPX7	glutathione peroxidase 7	0.7	5.27e-02	ITGB7	integrin subunit beta 7
-0.76	1.44e-02	NCKAP1L	NCK associated protein 1 like	0.69	2.70e-02	SLC4A2	solute carrier family 4 member 2
-0.76	5.48e-02	LGALS3BP	galectin 3 binding protein	0.69	5.50e-03	ANKZF1	ankyrin repeat and zinc finger pept
-0.74	3.06e-02	MAGT1	magnesium transporter 1	0.69	8.29e-02	ISG20	interferon stimulated exonuclease g
-0.74	8.39e-03	PIK3R1	phosphoinositide-3-kinase regulator	0.68	6.69e-02	HSPA4L	heat shock protein family A (Hsp70)
-0.73	4.28e-02	ITGA5	integrin subunit alpha 5	0.67	2.99e-02	STAM	signal transducing adaptor molecule
-0.72	3.52e-02	LGALS9	galectin 9	0.67	1.27e-01	IGF2BP1	insulin like growth factor 2 mRNA b
-0.72	1.28e-02	KRT9	keratin 9	0.66	3.18e-02	CBR4	carbonyl reductase 4
-0.71	1.49e-02	ACSF2	acyl-CoA synthetase family member 2	0.65	1.52e-01	CD48	CD48 molecule
-0.7	4.37e-03	PCID2	PCI domain containing 2	0.65	2.05e-01	NME2	NME/NM23 nucleoside diphosphate kin
-0.7	7.92e-02	PLIN2	perilipin 2	0.65	1.07e-02	PAGE5	PAGE family member 5
-0.69	3.01e-02	PTK7	protein tyrosine kinase 7 (inactive	0.65	5.06e-02	PDK1	pyruvate dehydrogenase kinase 1
-0.69	3.57e-02	ELMO2	engulfment and cell motility 2	0.64	1.27e-01	MVP	major vault protein
-0.69	3.74e-02	PARVG	parvin gamma	0.63	8.43e-02	PPP1R2	protein phosphatase 1 regulatory in
-0.68	2.68e-02	ACOX1	acyl-CoA oxidase 1	0.63	5.06e-02	ASDURF	ASNSD1 upstream open reading frame



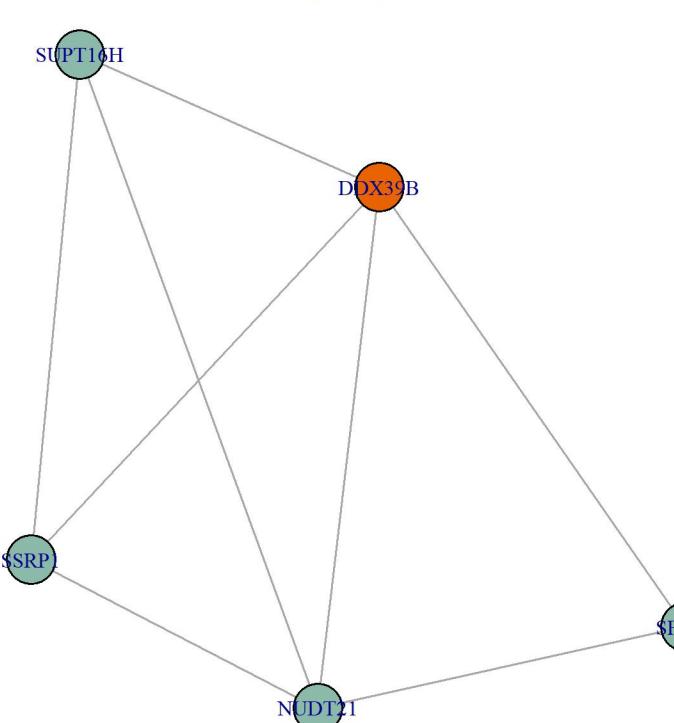
Downregulated in solid cancers at low/absent DDX39B Upregulated in solid cancers at low/absent DDX39B

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.86	1.64e-15	BRD2	bromodomain containing 2	0.69	1.73e-06	LGALS3	galectin 3
-0.85	6.87e-18	POLR2G	RNA polymerase II subunit G	0.68	9.76e-07	CTSZ	cathepsin Z
-0.84	8.83e-18	CMTR1	cap methyltransferase 1	0.66	2.85e-08	FAM83H	family with sequence similarity 83
-0.81	1.21e-09	ARPC1A	actin related protein 2/3 complex s	0.66	2.02e-05	CD44	CD44 molecule (Indian blood group)
-0.79	2.54e-15	PRPF38B	pre-mRNA processing factor 38B	0.64	8.98e-07	CD59	CD59 molecule (CD59 blood group)
-0.77	2.49e-15	EIF2B5	eukaryotic translation initiation f	0.62	1.13e-06	S100A10	S100 calcium binding protein A10
-0.77	1.53e-17	MDN1	midasin AAA ATPase 1	0.61	3.68e-09	ADGRE5	adhesion G protein-coupled receptor
-0.77	6.87e-18	PRIM2	DNA primase subunit 2	0.59	1.70e-06	SQOR	sulfide quinone oxidoreductase
-0.77	5.97e-16	UPF3B	UPF3B regulator of nonsense mediate	0.57	7.35e-06	EPS8L2	EPS8 like 2
-0.77	1.86e-09	BLMH	bleomycin hydrolase	0.56	5.62e-05	CAVIN3	caveolae associated protein 3
-0.77	1.05e-17	RBPJ	recombination signal binding protei	0.55	3.89e-08	MVP	major vault protein
-0.77	8.09e-13	BRD3	bromodomain containing 3	0.55	1.68e-05	HLA-B	major histocompatibility complex, c
-0.76	3.20e-14	EIF2B1	eukaryotic translation initiation f	0.54	1.76e-06	RHOC	ras homolog family member C
-0.76	7.18e-14	ZNF280C	zinc finger protein 280C	0.54	8.66e-05	VAMP8	vesicle associated membrane protein
-0.76	6.73e-15	HAT1	histone acetyltransferase 1	0.52	1.31e-05	CD109	CD109 molecule
-0.76	2.29e-11	MAD2L1	mitotic arrest deficient 2 like 1	0.52	5.72e-07	MYOF	myoferlin
-0.75	3.20e-14	PPP4C	protein phosphatase 4 catalytic sub	0.51	2.15e-04	ITGB4	integrin subunit beta 4
-0.73	6.73e-15	ZMYM3	zinc finger MYM-type containing 3	0.51	1.80e-05	SP100	SP100 nuclear antigen
-0.71	8.09e-13	EZH2	enhancer of zeste 2 polycomb repres	0.51	1.53e-04	IGFBP7	insulin like growth factor binding
-0.7	8.13e-15	KAT7	lysine acetyltransferase 7	0.5	1.67e-05	FAM114A1	family with sequence similarity 114
-0.7	9.38e-11	TRMT61A	tRNA methyltransferase 61A	0.5	9.75e-04	CAVIN1	caveolae associated protein 1
-0.7	1.11e-13	HNRNPLL	heterogeneous nuclear ribonucleoprotein	0.49	1.63e-04	KRT80	keratin 80
-0.7	1.37e-10	DAXX	death domain associated protein	0.49	2.53e-05	HSPB8	heat shock protein family B (small)
-0.69	1.47e-11	CWF19L1	CWF19 like cell cycle control facto	0.49	1.57e-06	KIAA1217	KIAA1217
-0.69	2.43e-09	PRMT3	protein arginine methyltransferase	0.49	3.12e-04	MISP	mitotic spindle positioning
-0.69	1.07e-10	PDXP	pyridoxal phosphatase	0.49	1.01e-06	RAB11FIP5	RAB11 family interacting protein 5
-0.68	4.52e-12	YTHDC1	YTH domain containing 1	0.49	3.38e-05	TAP1	transporter 1, ATP binding cassette
-0.68	1.95e-14	VIRMA	vir like m6A methyltransferase asso	0.48	3.09e-06	ENDOD1	endonuclease domain containing 1
-0.68	2.62e-10	PM20D2	peptidase M20 domain containing 2	0.48	4.38e-05	PPIC	peptidylprolyl isomerase C

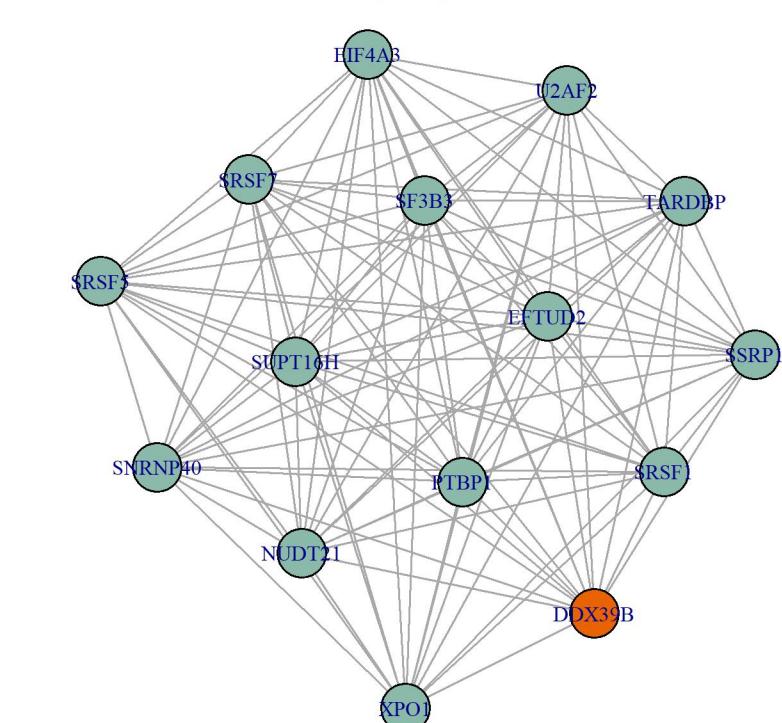
DDX39B network, DB1, all Pearson r > 0.55

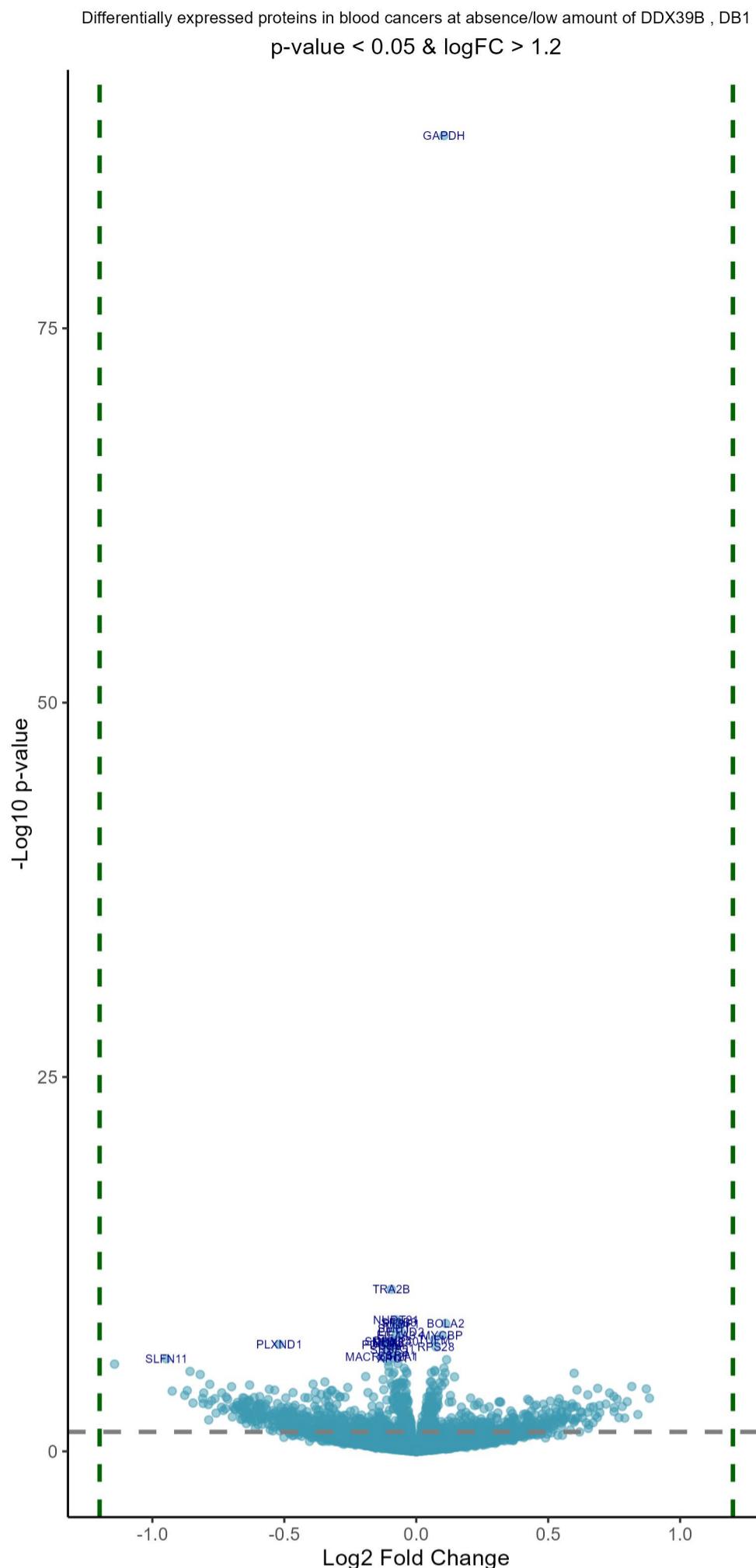


DDX39B network, DB1, all Pearson r > 0.5

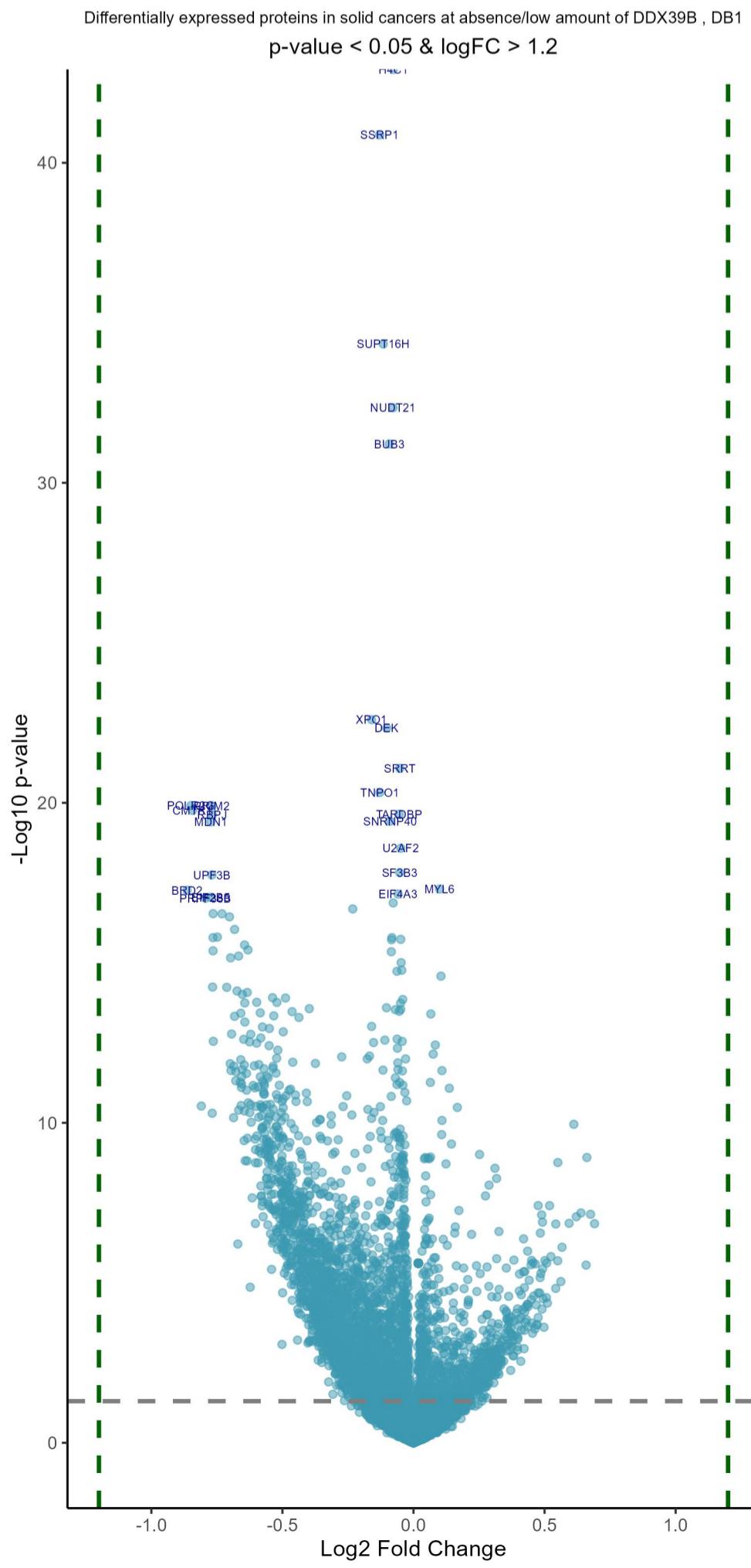


DDX39B network, DB1, all Pearson r > 0.45



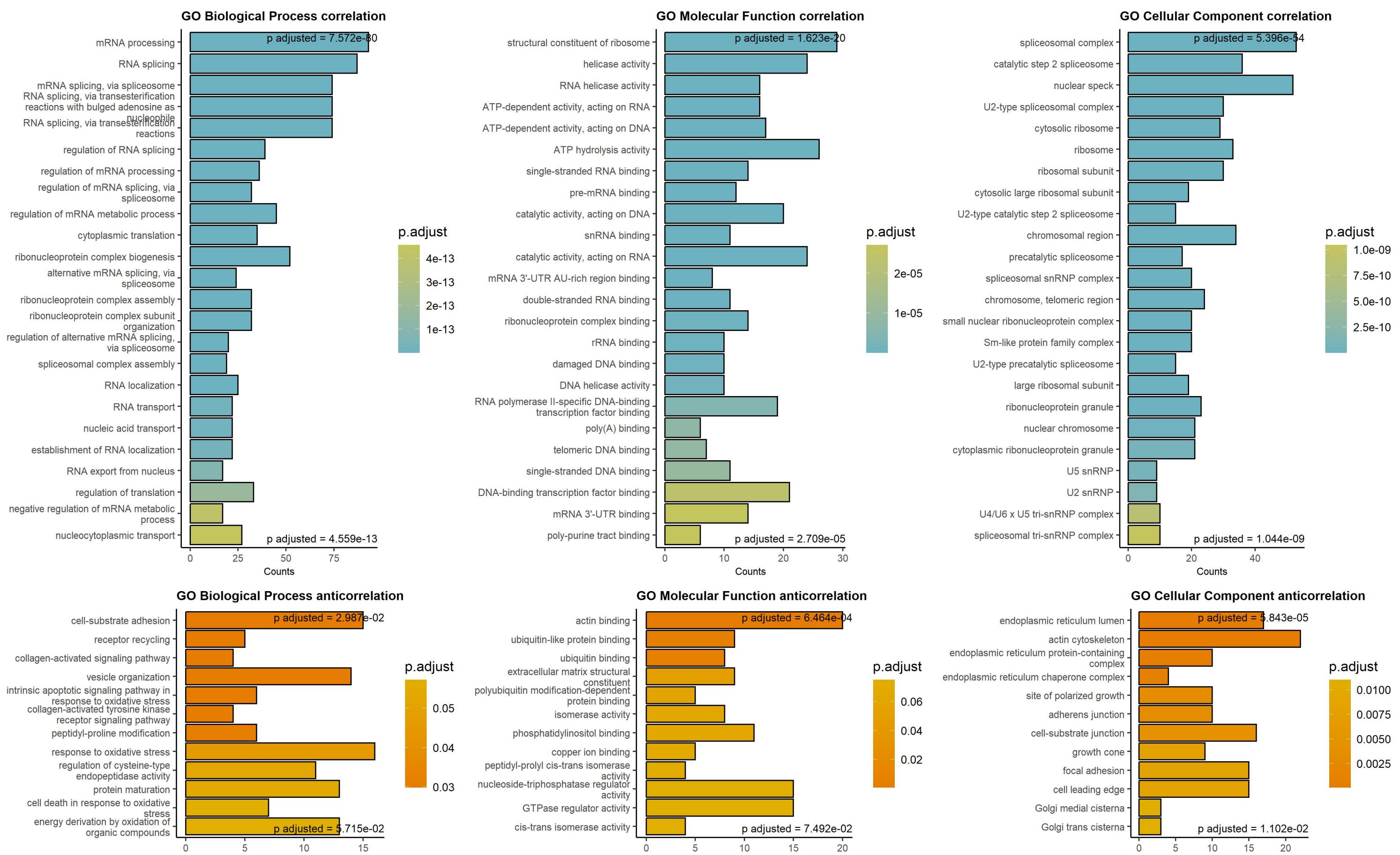


Sorted by p values!							
Downregulated in blood cancers at low/absent DDX39B				Upregulated in blood cancers at low/absent DDX39B			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.09	3.30e-08	TRA2B	transformer 2 beta homolog	0.11	8.99e-85	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
-0.08	2.77e-06	NUDT21	nudix hydrolase 21	0.11	2.90e-06	BOLA2	bola family member 2
-0.07	2.90e-06	SF3B3	splicing factor 3b subunit 3	0.1	1.10e-05	MYCBP	MYC binding protein
-0.06	2.90e-06	PTBP1	polypyrimidine tract binding protein	0.07	1.97e-05	TUFM	Tu translation elongation factor, m
-0.08	4.95e-06	SMU1	SMU1 DNA replication regulator and	0.07	3.61e-05	RPS28	ribosomal protein S28
-0.06	7.49e-06	EFTUD2	elongation factor Tu GTP binding do	0.12	1.93e-04	CYCS	cytochrome c, somatic
-0.08	1.10e-05	EIF4A3	eukaryotic translation initiation f	0.1	5.81e-04	PRDX5	peroxiredoxin 5
-0.09	2.05e-05	DHX15	DEAH-box helicase 15	0.07	7.90e-04	CDC37	cell division cycle 37, HSP90 cocha
-0.09	2.15e-05	SNRNP40	small nuclear ribonucleoprotein U5	0.07	8.89e-04	PFDN2	prefoldin subunit 2
-0.1	2.29e-05	DDX6	DEAD-box helicase 6	0.06	9.42e-04	FARSA	phenylalanyl-tRNA synthetase subunit
-0.11	2.29e-05	RCC2	regulator of chromosome condensatio	0.11	9.44e-04	MAP4	microtubule associated protein 4
-0.52	2.75e-05	PLXND1	plexin D1	0.6	9.65e-04	CADM1	cell adhesion molecule 1
-0.13	2.75e-05	PDCD6	programmed cell death 6	0.15	1.54e-03	NDUFS6	NADH:ubiquinone oxidoreductase subu
-0.08	4.32e-05	TNPO1	transportin 1	0.1	1.59e-03	PDAP1	PDGFA associated protein 1
-0.1	5.20e-05	SRSF5	serine and arginine rich splicing f	0.06	2.96e-03	VBP1	VHL binding protein 1
-0.07	1.20e-04	SSRP1	structure specific recognition prot	0.05	2.96e-03	ATP5F1D	ATP synthase F1 subunit delta
-0.13	1.37e-04	MACROH2A1	macroH2A.1 histone	0.11	3.08e-03	NDUFA2	NADH:ubiquinone oxidoreductase subu
-0.09	1.67e-04	XPO1	exportin 1	0.09	3.08e-03	LAP3	leucine aminopeptidase 3
-0.95	1.76e-04	SLFN11	schlafen family member 11	0.06	3.97e-03	PFDN5	prefoldin subunit 5
-0.11	2.43e-04	PRPF8	pre-mRNA processing factor 8	0.1	3.97e-03	TIMM13	translocase of inner mitochondrial
-0.07	3.34e-04	SUPT16H	SPT16 homolog, facilitates chromati	0.82	4.35e-03	MCEE	methylmalonyl-CoA epimerase
-1.14	3.42e-04	MPP1	MAGUK p55 scaffold protein 1	0.69	5.50e-03	ANKZF1	ankyrin repeat and zinc finger pept
-0.1	4.58e-04	CTBP1	C-terminal binding protein 1	0.87	5.97e-03	MRPL55	mitochondrial ribosomal protein L55
-0.05	5.81e-04	SNRNP200	small nuclear ribonucleoprotein U5	0.07	6.53e-03	PDCD5	programmed cell death 5
-0.04	8.69e-04	SRSF7	serine and arginine rich splicing f	0.61	6.55e-03	SDC1	syndecan 1
-0.86	8.69e-04	BRD1	bromodomain containing 1	0.05	6.67e-03	PFDN6	prefoldin subunit 6
-0.1	9.32e-04	WDR5	WD repeat domain 5	0.08	6.67e-03	NUDT5	nudix hydrolase 5
-0.08	9.42e-04	PPP1CA	protein phosphatase 1 catalytic sub	0.08	7.78e-03	CCDC124	coiled-coil domain containing 124
-0.04	9.65e-04	HNRNPU	heterogeneous nuclear ribonucleopro	0.05	7.78e-03	COX5B	cytochrome c oxidase subunit 5B
-0.09	1.11e-03	CTPS1	CTP synthase 1	0.73	8.39e-03	ASNS	asparagine synthetase (glutamine-hy
-0.82	1.12e-03	NUDT16L1	nudix hydrolase 16 like 1	0.65	1.07e-02	PAGE5	PAGE family member 5
-0.19	1.48e-03	TOP2B	DNA topoisomerase II beta	0.13	1.13e-02	UQCRH	ubiquinol-cytochrome c reductase hi
-0.05	2.10e-03	SF3B6	splicing factor 3b subunit 6	0.05	1.22e-02	SLIRP	SRA stem-loop interacting RNA bindi
-0.13	2.19e-03	TOP2A	DNA topoisomerase II alpha	0.75	1.26e-02	GOLM1	golgi membrane protein 1
-0.35	2.96e-03	RFC5	replication factor C subunit 5	0.08	1.26e-02	CLPP	caseinolytic mitochondrial matrix p
-0.07	3.08e-03	RBM22	RNA binding motif protein 22	0.05	1.28e-02	EIF3G	eukaryotic translation initiation f
-0.05	3.08e-03	DARS1	aspartyl-tRNA synthetase 1	0.04	1.28e-02	RPLP2	ribosomal protein lateral stalk sub
-0.06	3.08e-03	RPS15A	ribosomal protein S15a	0.06	1.32e-02	RAD23B	RAD23 homolog B, nucleotide excisio
-0.04	3.08e-03	IEF2	interleukin enhancer binding factor	0.21	1.38e-02	COX6B1	cytochrome c oxidase subunit 6B1

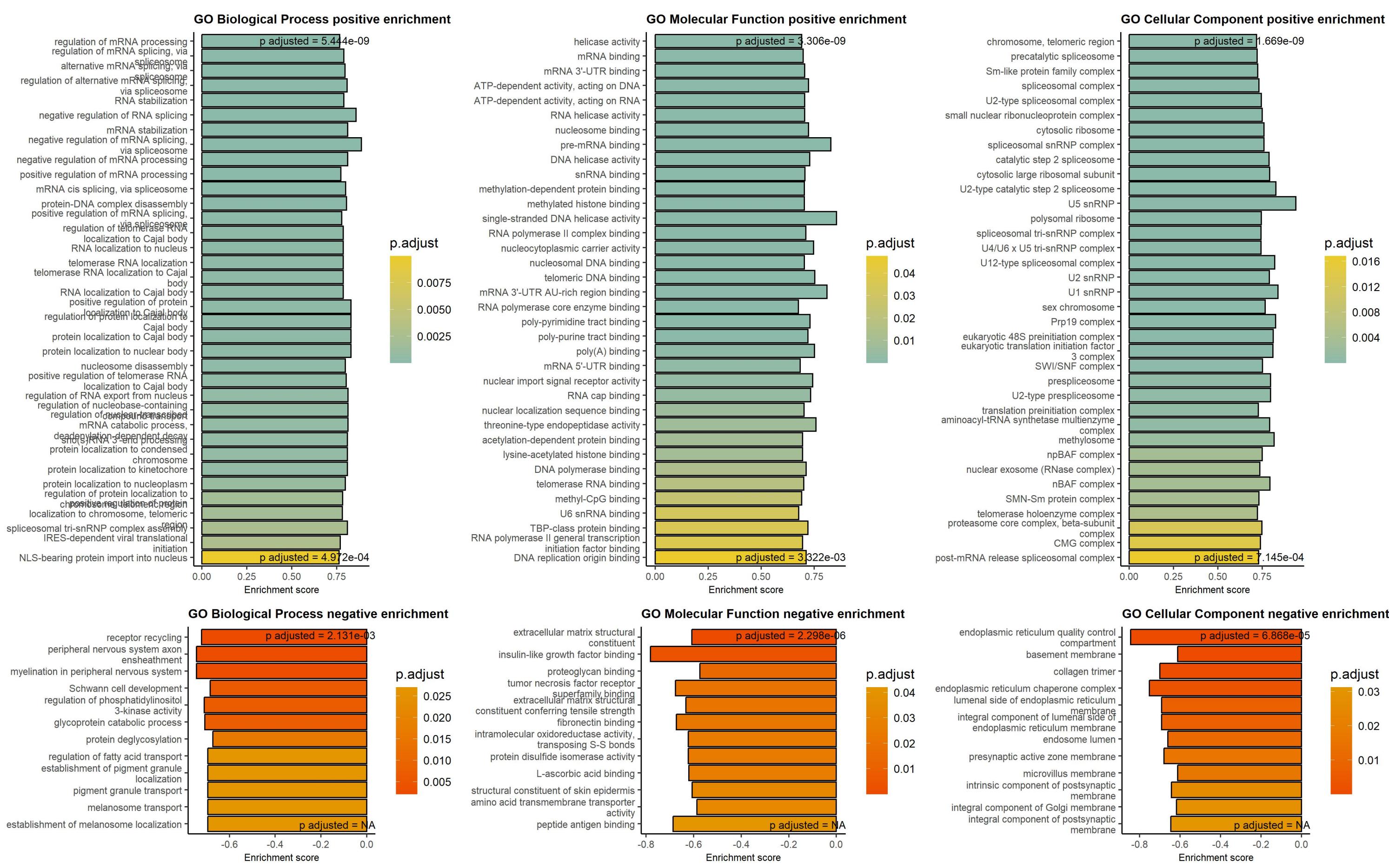


Sorted by p values!							
Downregulated in solid cancers at low/absent DDX39B				Upregulated in solid cancers at low/absent DDX39B			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.08	0.00e+00	H4C1	H4 clustered histone 1	0.1	1.57e-15	MYL6	myosin light chain 6
-0.13	2.96e-38	SSRP1	structure specific recognition prot	0.1	3.78e-13	TMOD3	tropomodulin 3
-0.12	7.64e-32	SUPT16H	SPT16 homolog, facilitates chromati	0.07	3.95e-12	P4HB	prolyl 4-hydroxylase subunit beta
-0.08	6.01e-30	NUDT21	nudix hydrolase 21	0.08	2.83e-11	MYDGF	myeloid derived growth factor
-0.09	6.77e-29	BUB3	BUB3 mitotic checkpoint protein	0.08	5.21e-11	CTTN	cortactin
-0.16	2.39e-20	XPO1	exportin 1	0.11	1.37e-10	CLTB	clathrin light chain B
-0.1	3.84e-20	DEK	DEK proto-oncogene	0.06	2.87e-10	TPM3	tropomyosin 3
-0.05	6.23e-19	SRRT	serrate, RNA effector molecule	0.14	4.01e-10	LMNA	lamin A/C
-0.13	3.16e-18	TNPO1	transportin 1	0.17	1.29e-09	PLEC	plectin
-0.85	6.87e-18	POLR2G	RNA polymerase II subunit G	0.11	2.89e-09	CTSD	cathepsin D
-0.77	6.87e-18	PRIM2	DNA primase subunit 2	0.61	3.68e-09	ADGRE5	adhesion G protein-coupled receptor
-0.84	8.83e-18	CMTR1	cap methyltransferase 1	0.11	7.16e-09	GOLGB1	golgin B1
-0.05	1.05e-17	TARDBP	TAR DNA binding protein	0.14	1.23e-08	RRBP1	ribosome binding protein 1
-0.77	1.05e-17	RBPJ	recombination signal binding protei	0.25	2.38e-08	SUCLG2	succinate-CoA ligase GDP-forming su
-0.09	1.53e-17	SNRNP40	small nuclear ribonucleoprotein U5	0.06	2.79e-08	SPTAN1	spectrin alpha, non-erythrocytic 1
-0.77	1.53e-17	MDN1	midasin AAA ATPase 1	0.04	2.85e-08	LRRC59	leucine rich repeat containing 59
-0.05	9.69e-17	U2AF2	U2 small nuclear RNA auxiliary fact	0.66	2.85e-08	FAM83H	family with sequence similarity 83
-0.05	5.33e-16	SF3B3	splicing factor 3b subunit 3	0.05	2.98e-08	PRDX5	peroxiredoxin 5
-0.77	5.97e-16	UPF3B	UPF3B regulator of nonsense mediate	0.06	3.08e-08	TMED9	transmembrane p24 trafficking prote
-0.86	1.64e-15	BRD2	bromodomain containing 2	0.04	3.08e-08	HSPA5	heat shock protein family A (Hsp70)
-0.06	2.05e-15	EIF4A3	eukaryotic translation initiation f	0.55	3.89e-08	MVP	major vault protein
-0.77	2.49e-15	EIF2B5	eukaryotic translation initiation f	0.12	4.20e-08	LRPAP1	LDL receptor related protein associ
-0.79	2.54e-15	PRPF38B	pre-mRNA processing factor 38B	0.31	5.54e-08	SQSTM1	sequestosome 1
-0.08	3.44e-15	TRA2B	transformer 2 beta homolog	0.05	9.02e-08	CANX	calnexin
-0.23	5.10e-15	RCC2	regulator of chromosome condensatio	0.32	1.06e-07	MYO1C	myosin IC
-0.76	6.73e-15	HAT1	histone acetyltransferase 1	0.29	1.62e-07	GSTK1	glutathione S-transferase kappa 1
-0.73	6.73e-15	ZMYM3	zinc finger MYM-type containing 3	0.04	2.17e-07	CHCHD3	coiled-coil-helix-coiled-coil-helix
-0.7	8.13e-15	KAT7	lysine acetyltransferase 7	0.07	2.93e-07	GOLGA2	golgin A2
-0.68	1.95e-14	VIRMA	vir like m6A methyltransferase asso	0.27	3.15e-07	STIM1	stromal interaction molecule 1
-0.75	3.20e-14	PPP4C	protein phosphatase 4 catalytic sub	0.05	4.52e-07	ERP29	endoplasmic reticulum protein 29
-0.08	3.20e-14	SUPT6H	SPT6 homolog, histone chaperone and	0.48	5.70e-07	SYVN1	synoviolin 1
-0.76	3.20e-14	EIF2B1	eukaryotic translation initiation f	0.52	5.72e-07	MYOF	myoferlin
-0.05	3.51e-14	SRSF1	serine and arginine rich splicing f	0.17	7.74e-07	CTSB	cathepsin B
-0.08	3.51e-14	CTNNBL1	catenin beta like 1	0.64	8.98e-07	CD59	CD59 molecule (CD59 blood group)
-0.64	4.98e-14	CNOT9	CCR4-NOT transcription complex subu	0.68	9.76e-07	CTSZ	cathepsin Z
-0.63	6.92e-14	IPO8	importin 8	0.49	1.01e-06	RAB11FIP5	RAB11 family interacting protein 5
-0.76	7.18e-14	ZNF280C	zinc finger protein 280C	0.62	1.13e-06	S100A10	S100 calcium binding protein A10
-0.08	7.49e-14	PARP1	poly(ADP-ribose) polymerase 1	0.06	1.23e-06	BCAP31	B cell receptor associated protein
-0.07	9.22e-14	YPCF5	YPCF5	0.06	1.23e-06	LAMTOR1	LAMP-associated membrane protein 1

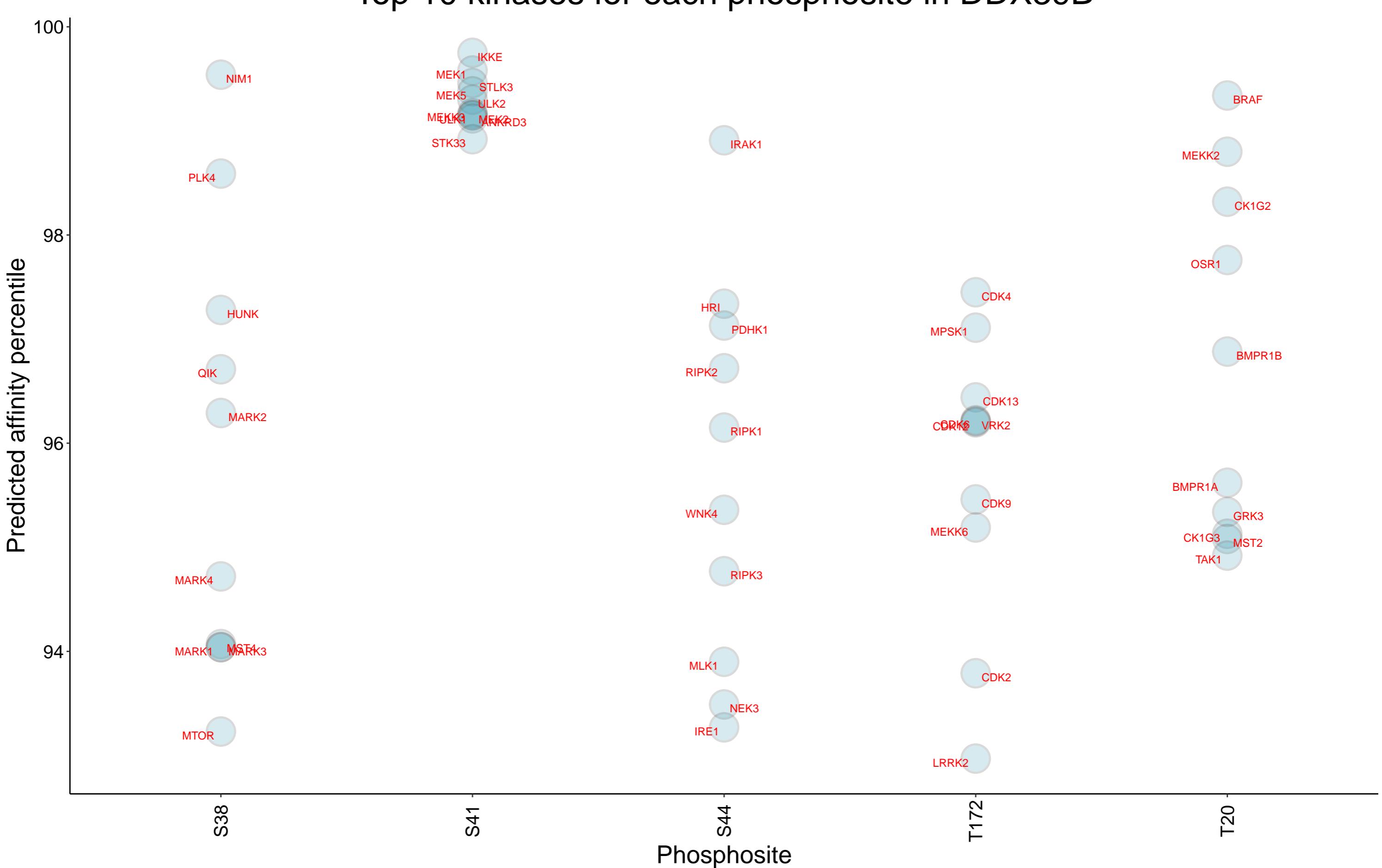
Top 250 correlation coefficients overrepresentation, DDX39B protein, DB1



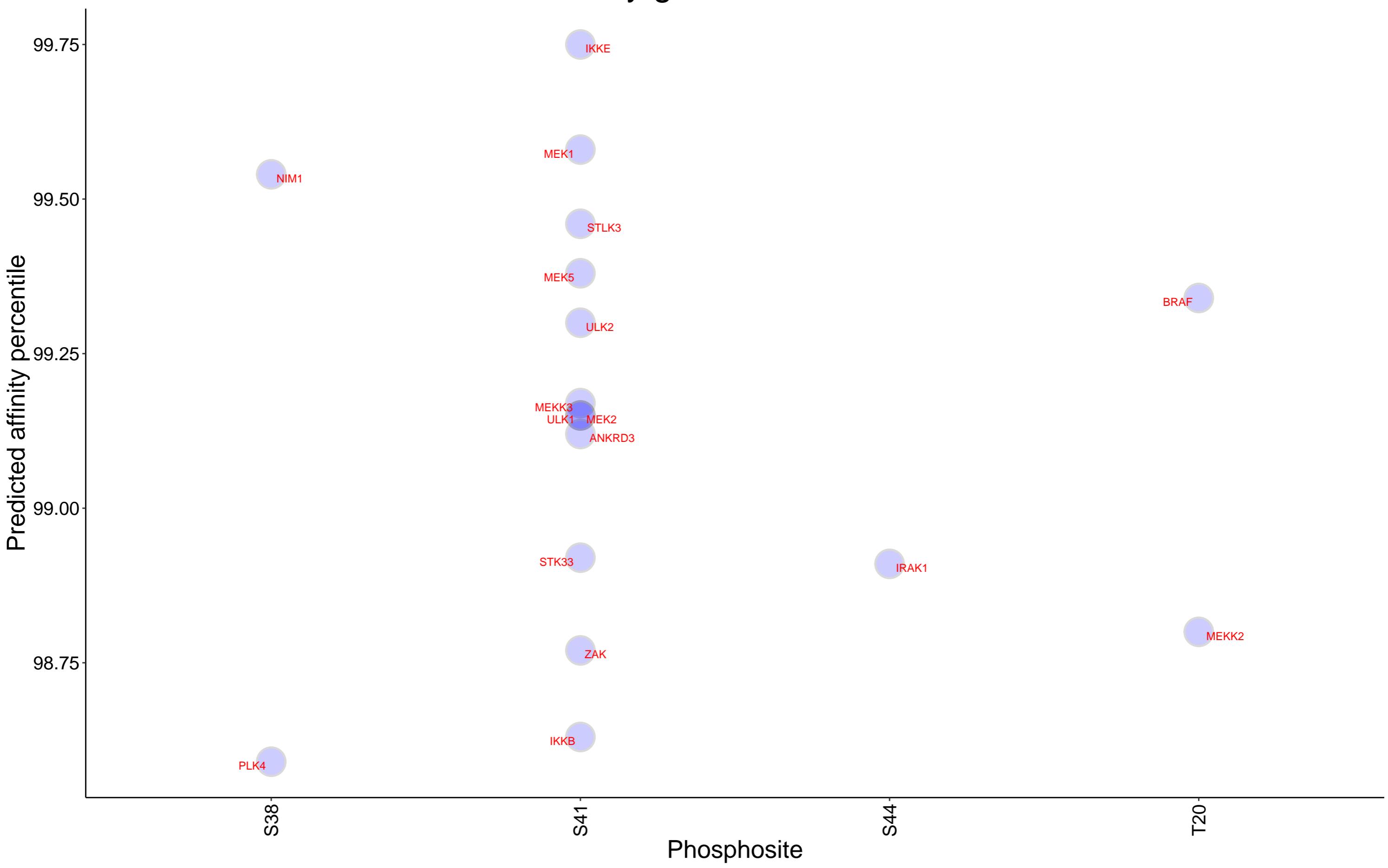
Gene Set Enrichment analysis on protein correlation coefficients, DDX39B protein, DB1



Top 10 kinases for each phosphosite in DDX39B



Kinases with affinity greater than 98.5% to DDX39B



Top 15 positive correlation coefficients for DDX39B protein by tissue, DB1

Beware of false positives in tissues with small number of samples

