

DHX9

Protein name: DHX9 ;

UNIPROT: Q08211 ;

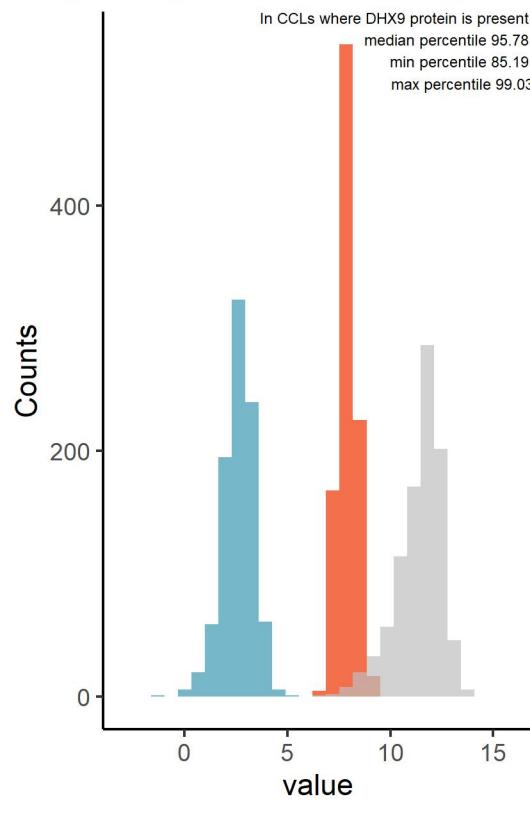
Gene name: DExH-box helicase 9

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

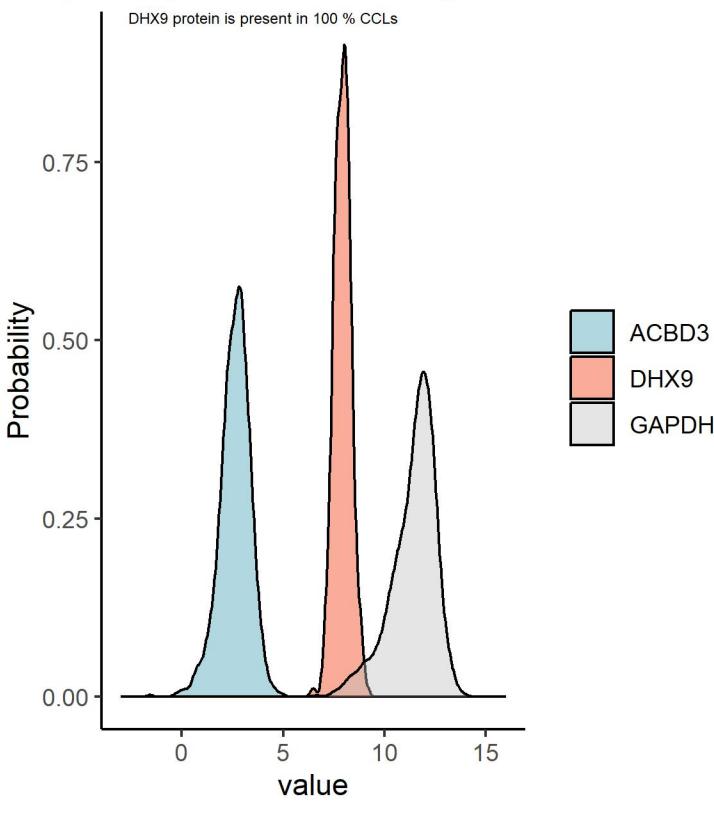
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

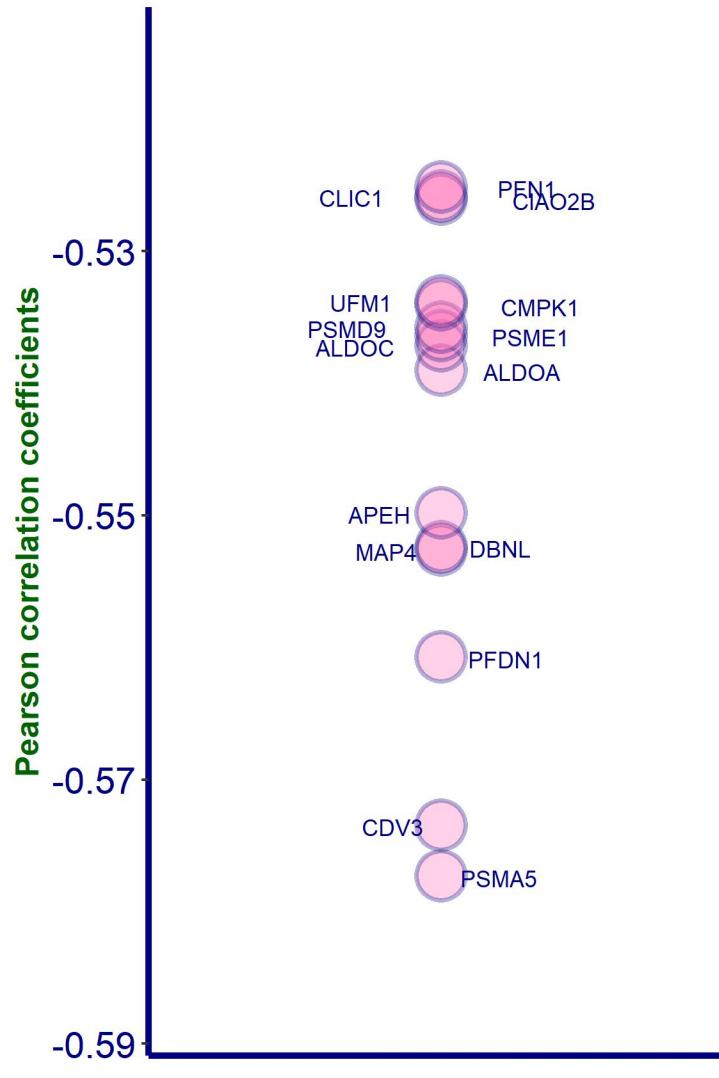
Histogram of DHX9 protein compared to proteins with low and high abundance



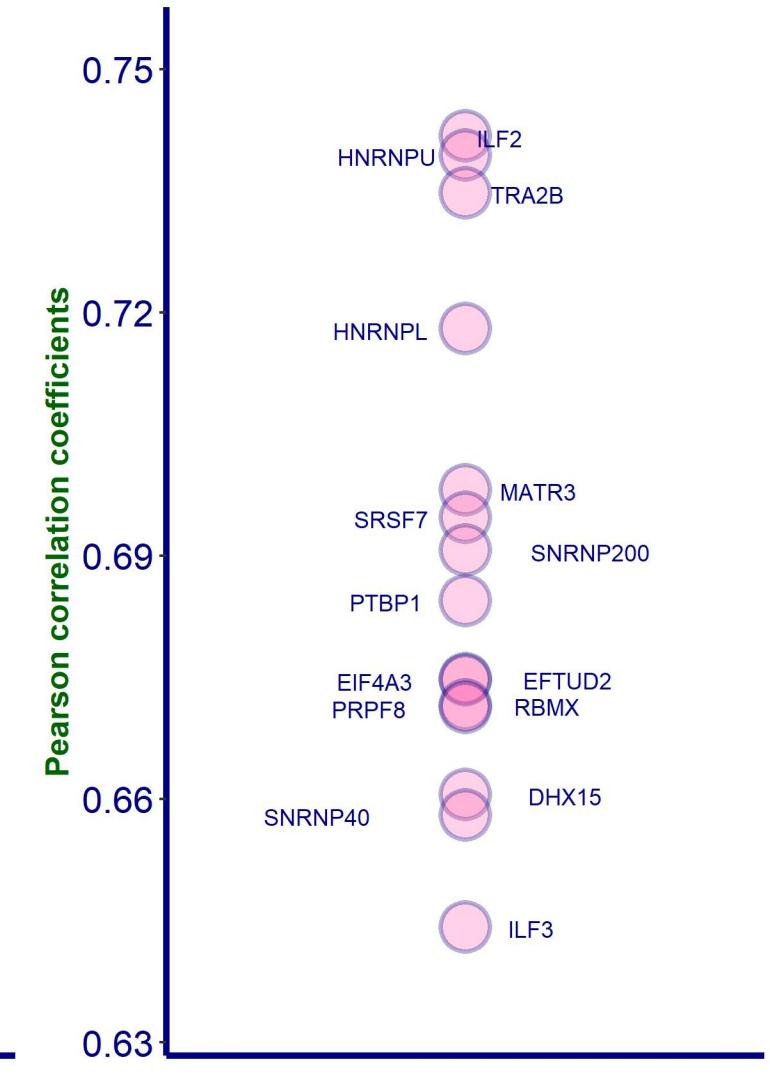
Density plot of DHX9 protein compared to proteins with low and high abundance



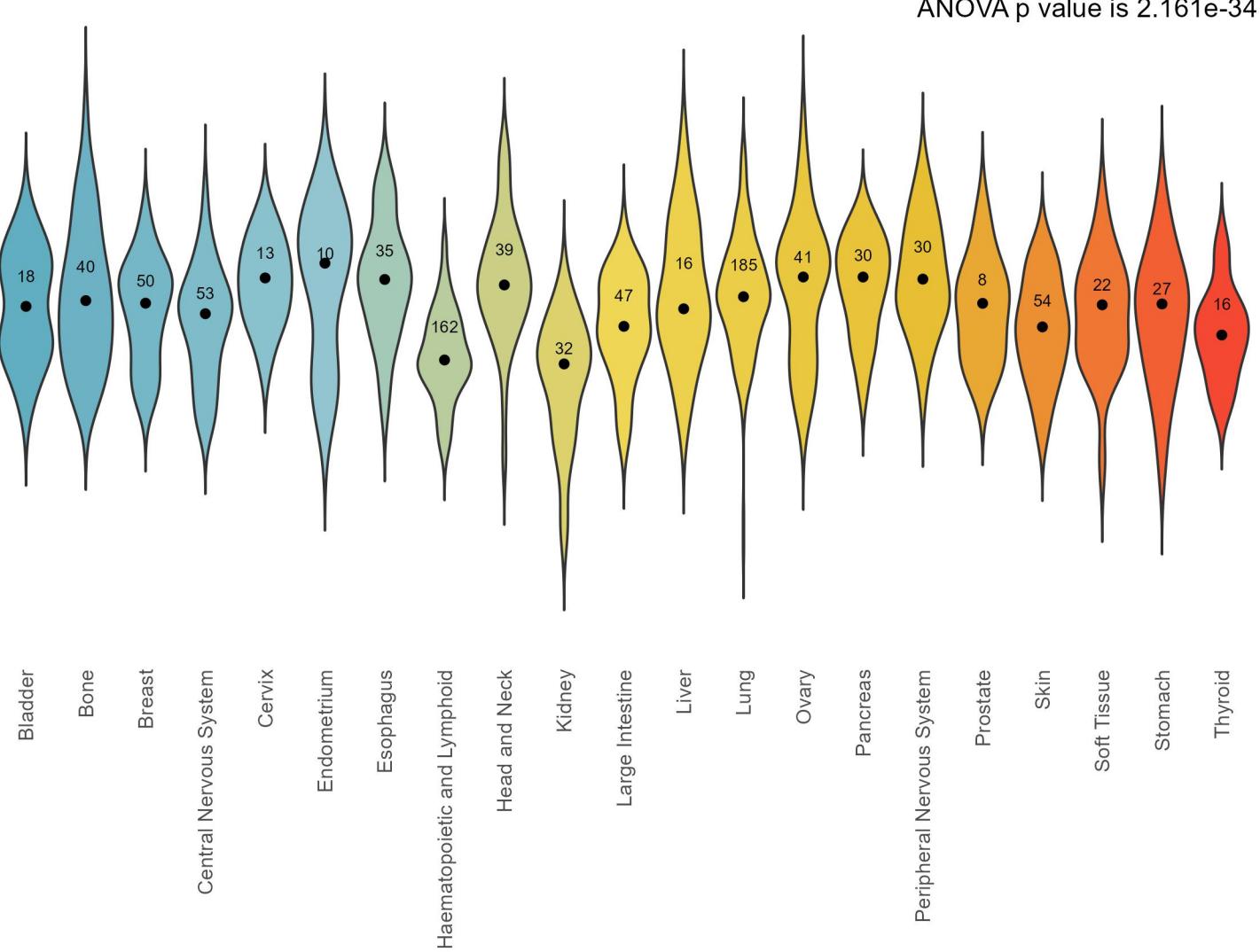
Top negative correlations of DHX9 protein, DB1



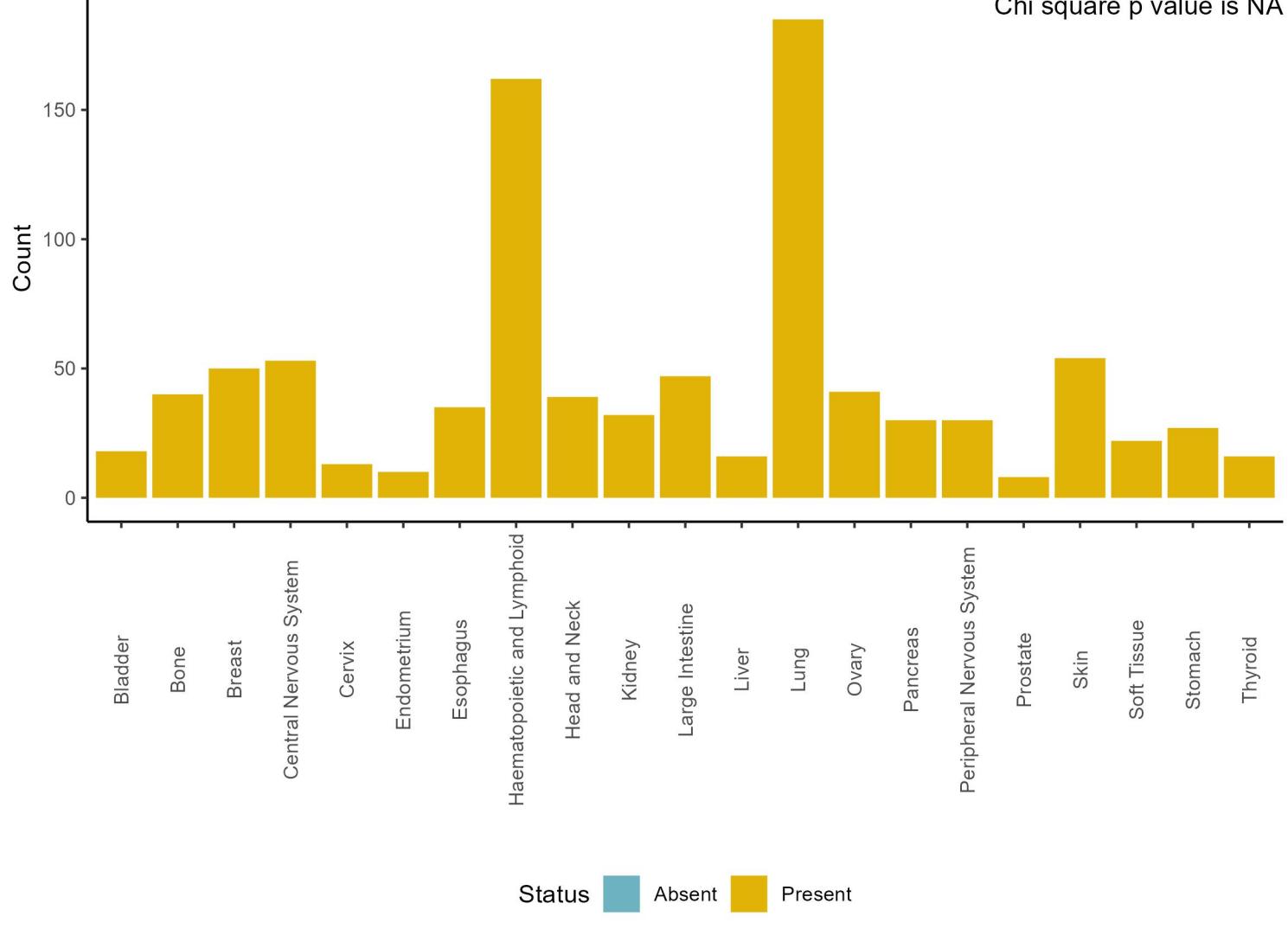
Top positive correlations of DHX9 protein, DB1



Amount of DHX9 protein, number of CCLs where it is present by tissue, DB1



Present and absent DHX9 protein counts by tissue, DB1

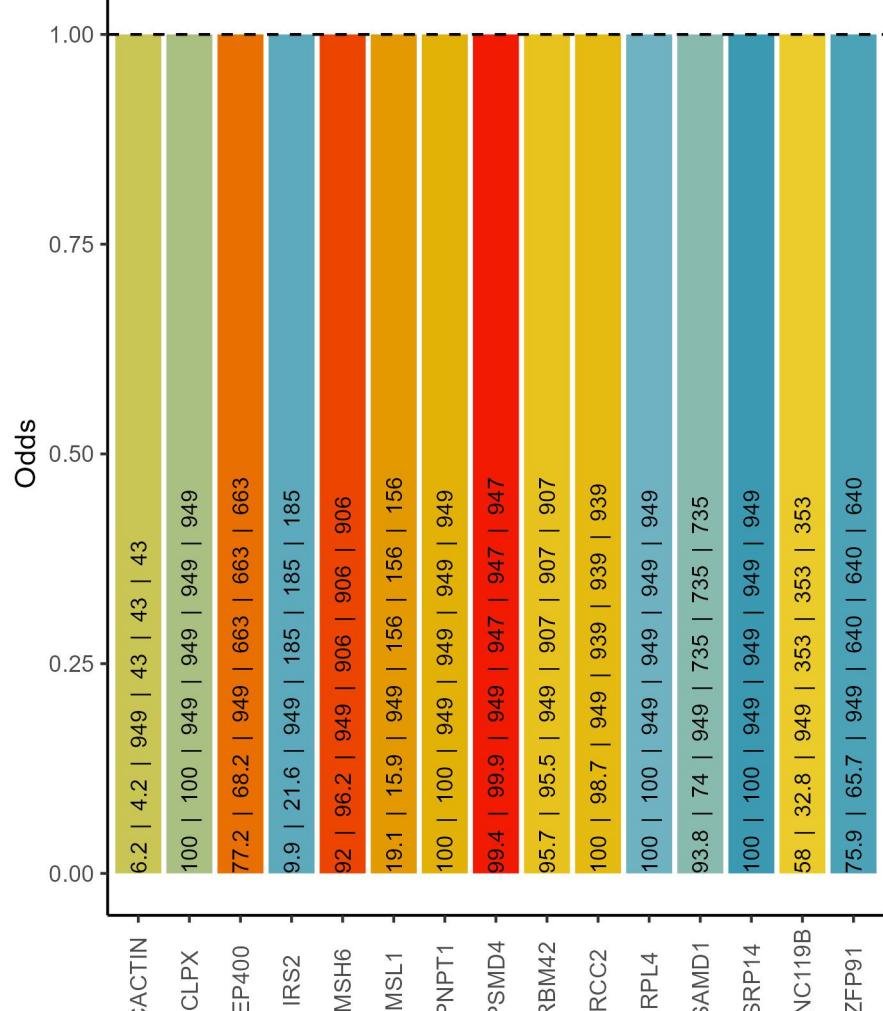


Cooccurrence with DHX9 protein, DB1

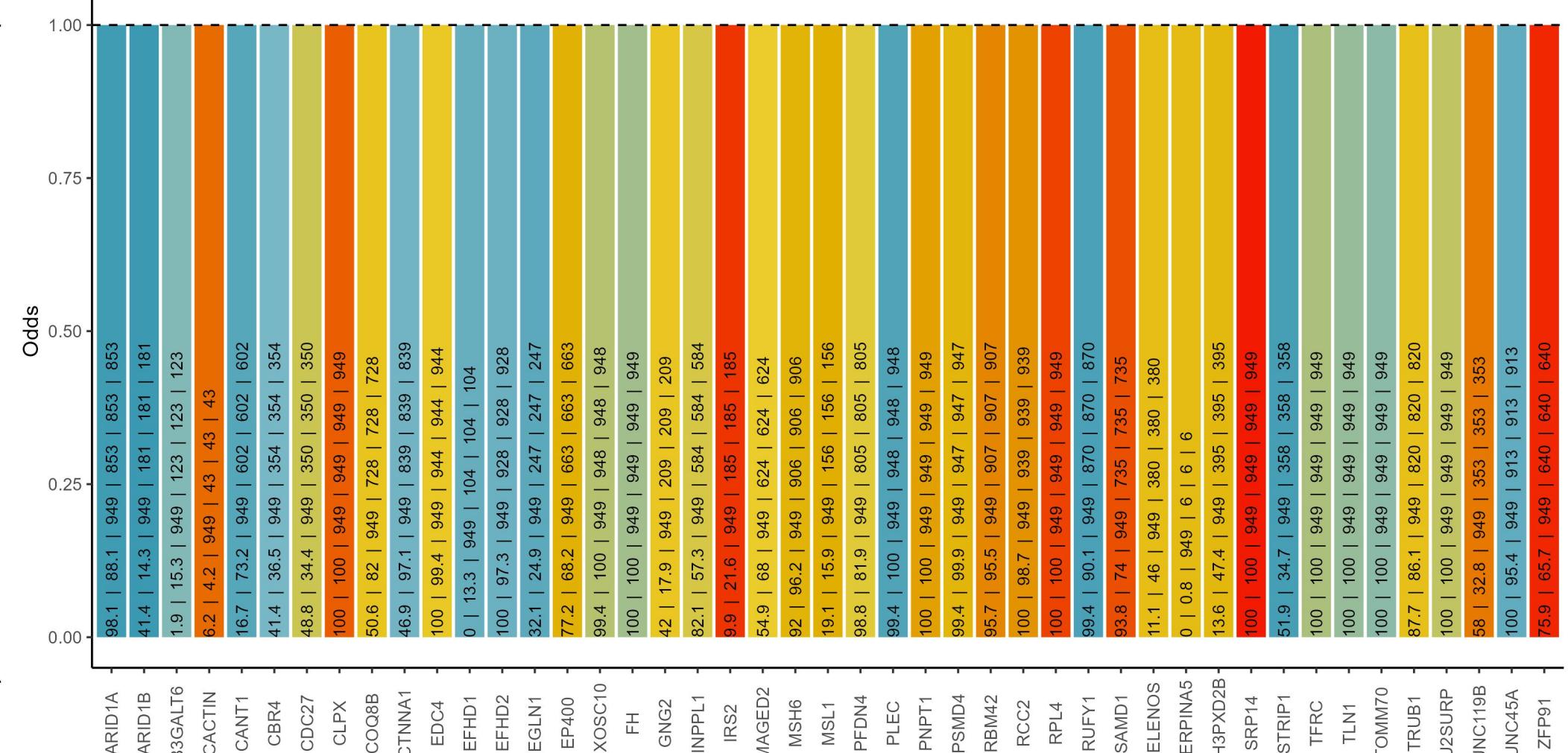
% of DHX9 in blood cancers: 100 ; % of DHX9 in solid cancers: 100

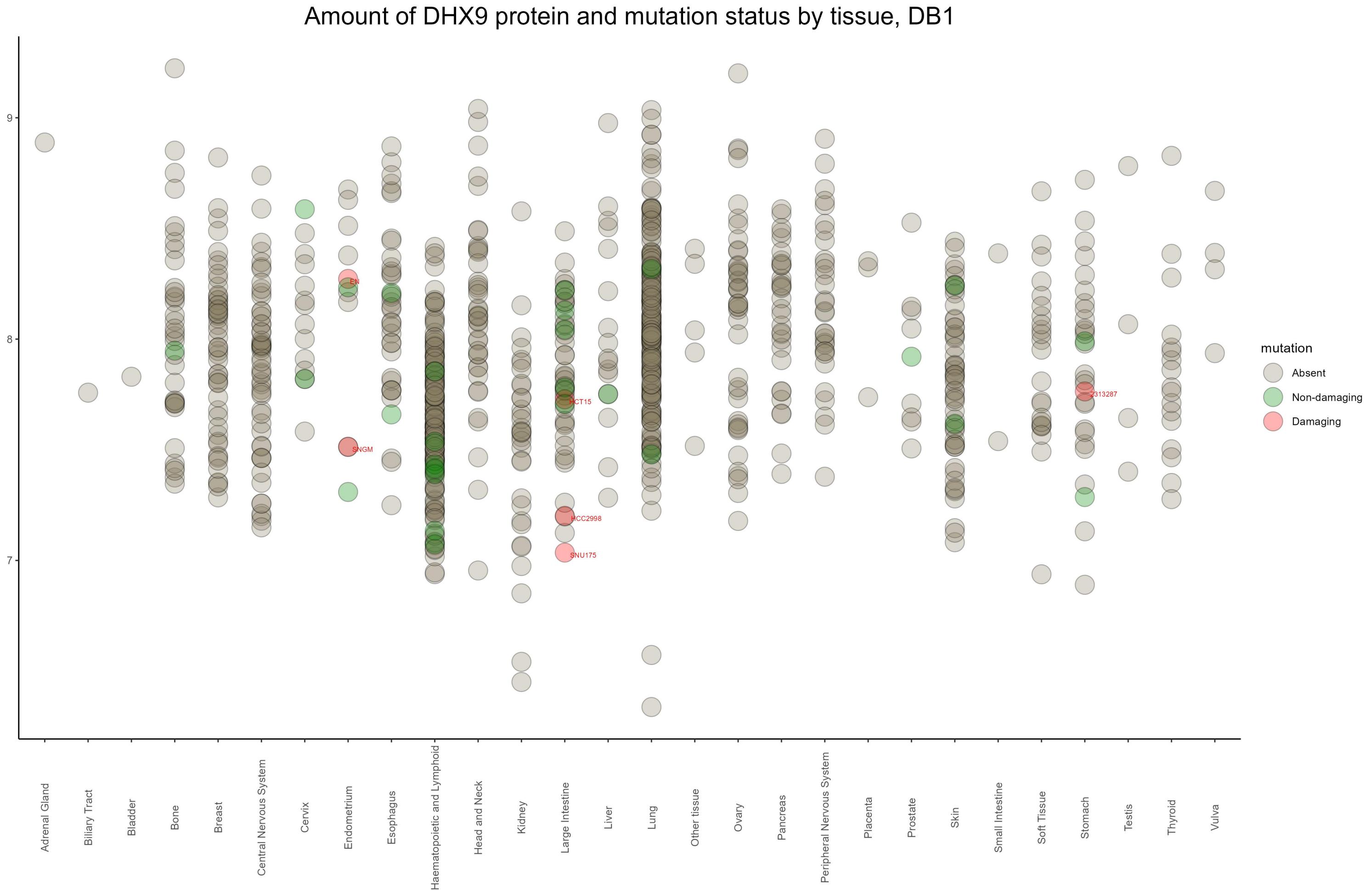
Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of DHX9 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



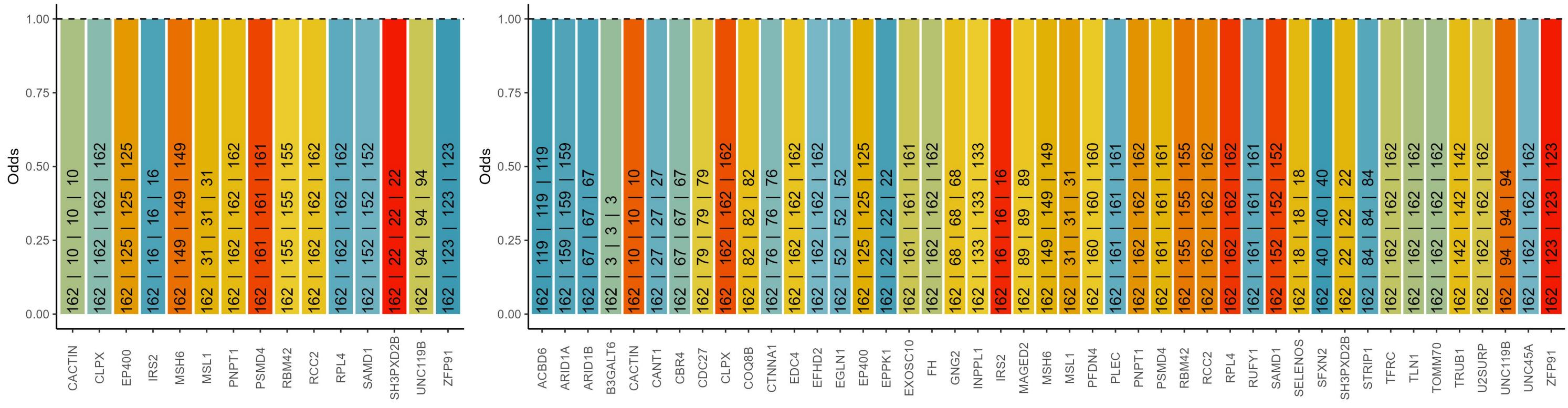
Positive cooccurrence





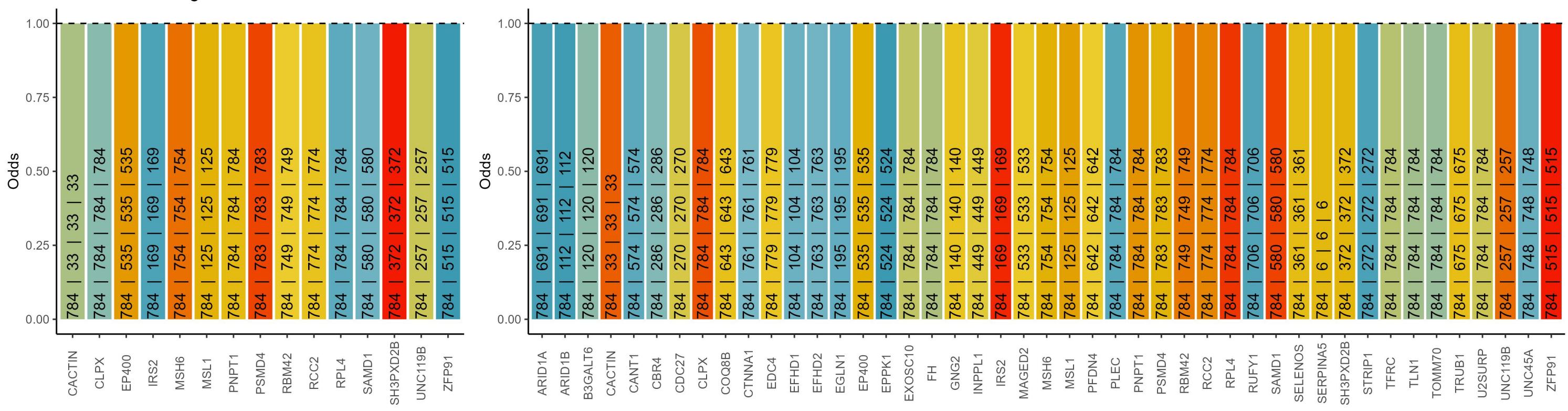
cooccurrence with DHX9 protein in blood cancers; DHX9 incidence of DHX9 | incidence of Protein 2 | observed cooccurrence | e

Positive cooccurrence

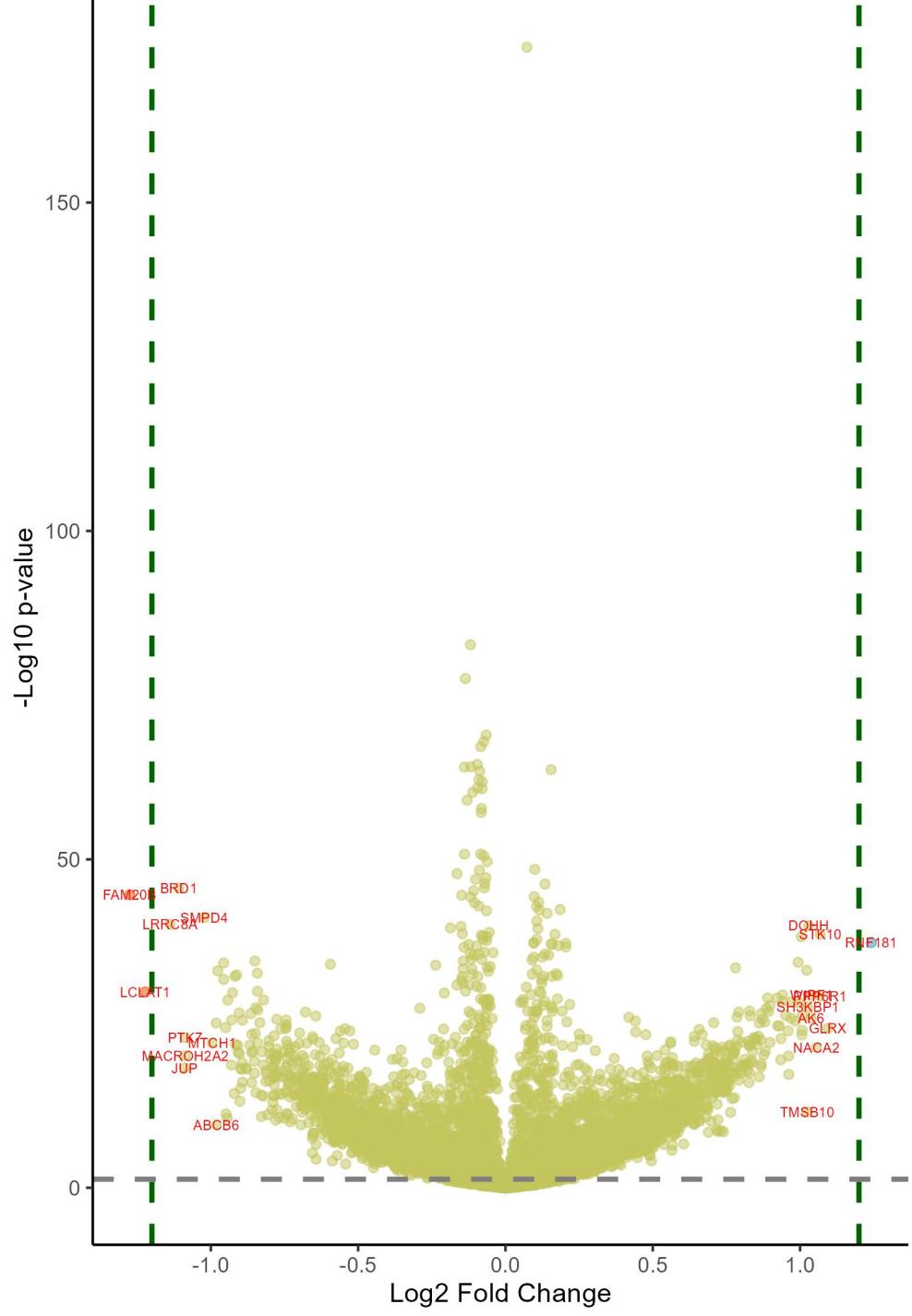


Cooccurrence with DHX9 protein in solid cancers, BBT incidence of DHX9 | incidence of Protein 2 | observed cooccurrence |

The text in the belief instances of DTYPE | instances of PISTON_E | observed cooccurrence | expected cooccurrence

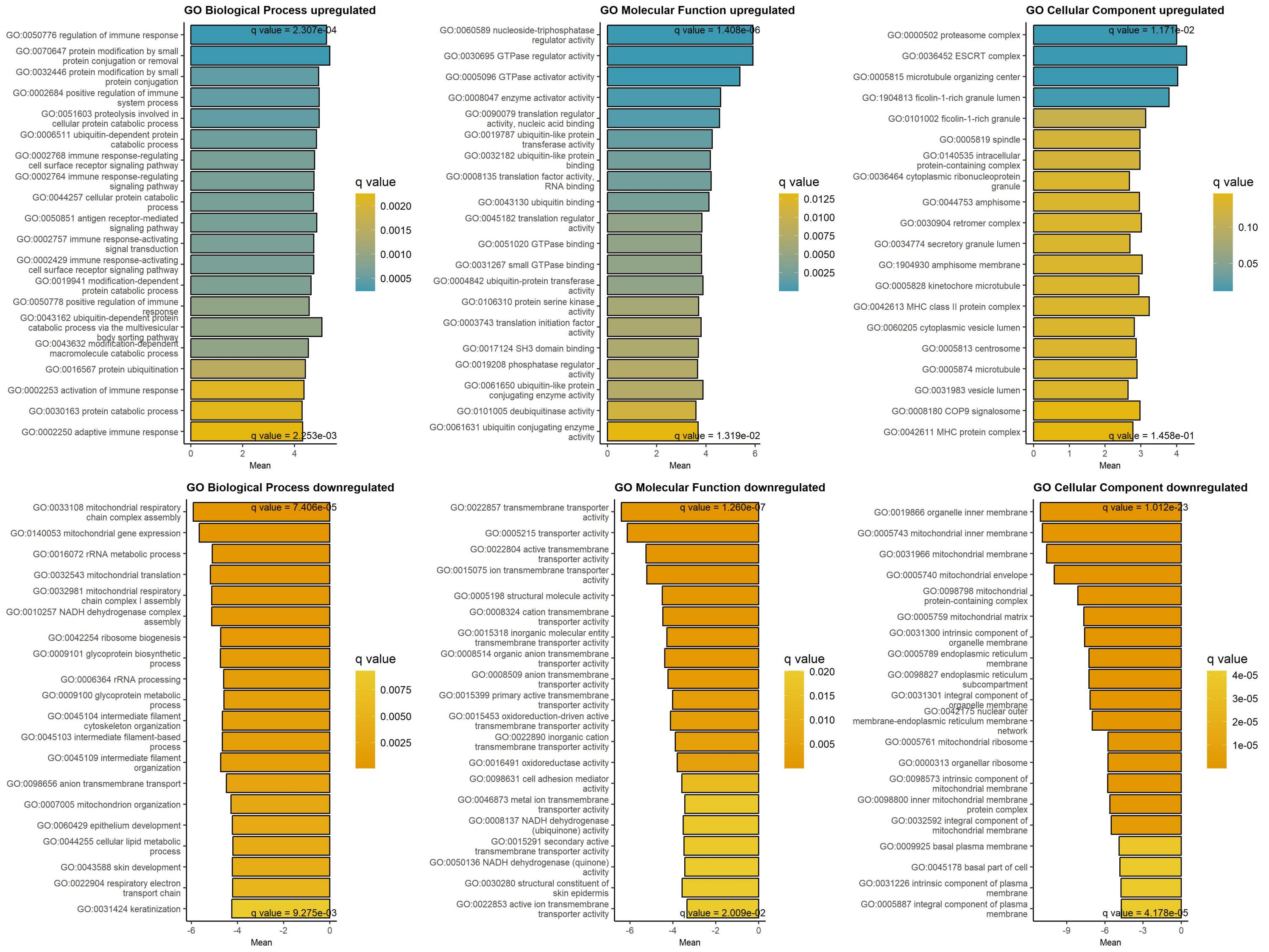


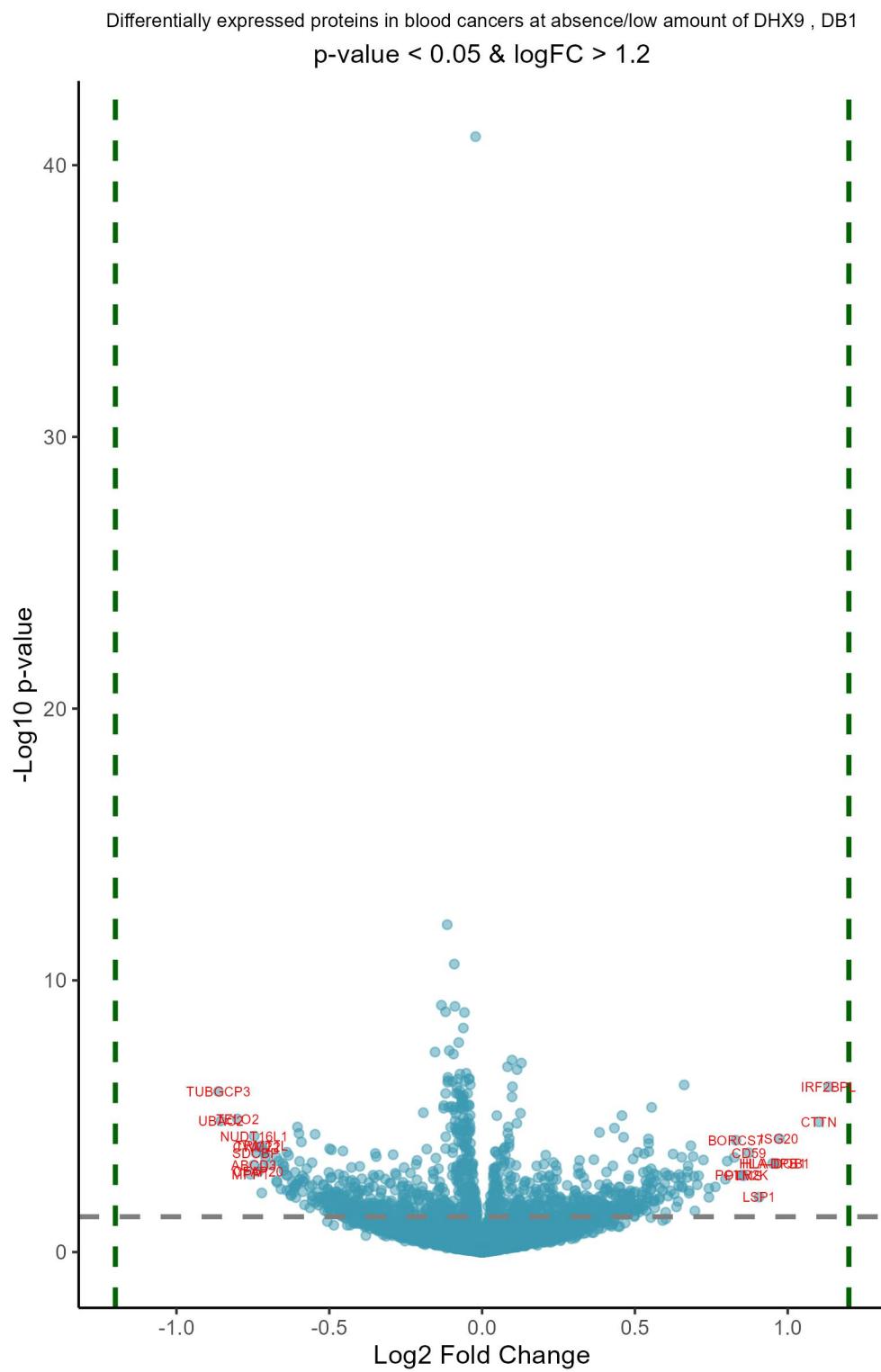
Downregulated at low/absent DHX9 Upregulated at low/absent DHX9



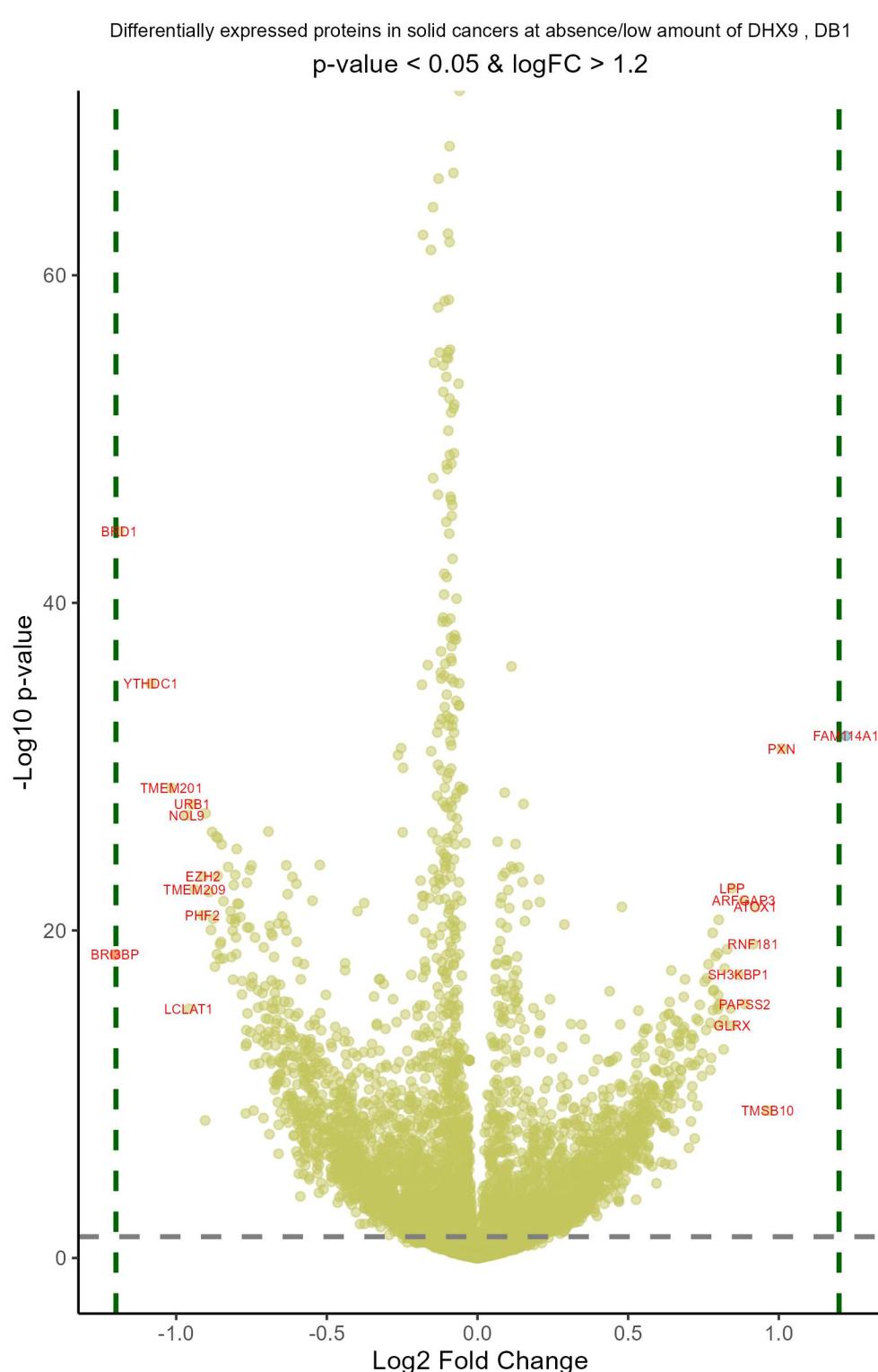
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.27	4.63e-43	FAM20B	FAM20B glycosaminoglycan xylosylkin	1.24	4.73e-36	RNF181	ring finger protein 181
-1.22	8.02e-29	LCLAT1	lysocardiolipin acyltransferase 1	1.09	1.61e-23	GLRX	glutaredoxin
-1.14	1.05e-38	LRRC8A	leucine rich repeat containing 8 VR	1.07	2.93e-37	STK10	serine/threonine kinase 10
-1.11	4.87e-44	BRD1	bromodomain containing 1	1.07	3.30e-28	PPP6R1	protein phosphatase 6 regulatory su
-1.09	7.85e-18	JUP	junction plakoglobin	1.06	8.90e-21	NACA2	nascent polypeptide associated comp
-1.09	3.62e-22	PTK7	protein tyrosine kinase 7 (inactive)	1.04	2.46e-28	WIPF1	WAS/WASL interacting protein family
-1.09	1.36e-19	MACROH2A2	macroH2A.2 histone	1.04	5.15e-25	AK6	adenylate kinase 6
-1.02	1.12e-39	SMPD4	sphingomyelin phosphodiesterase 4	1.03	1.58e-38	DOHH	deoxyhypusine hydroxylase
-1	1.99e-21	MTCH1	mitochondrial carrier 1	1.03	1.22e-26	SH3KBP1	SH3 domain containing kinase bindin
-0.98	1.03e-09	ABCB6	ATP binding cassette subfamily B me	1.02	1.45e-11	TMSB10	thymosin beta 10
-0.98	2.65e-24	PRXL2A	peroxiredoxin like 2A	1.02	5.11e-32	ATOX1	antioxidant 1 copper chaperone
-0.98	6.27e-32	NOL9	nucleolar protein 9	1.01	1.89e-25	RPE	ribulose-5-phosphate-3-epimerase
-0.96	4.32e-33	TMEM201	transmembrane protein 201	1.01	3.15e-23	FKBP1A	FKBP prolyl isomerase 1A
-0.96	1.11e-30	YTHDC1	YTH domain containing 1	1.01	1.41e-22	UBE2V2	ubiquitin conjugating enzyme E2 V2
-0.95	1.23e-23	SURF1	SURF1 cytochrome c oxidase assembly	1	6.24e-37	SRA1	steroid receptor RNA activator 1
-0.95	2.73e-11	NDUFB11	NADH:ubiquinone oxidoreductase subu	1	3.03e-27	UBA5	ubiquitin like modifier activating
-0.94	1.11e-10	H1-0	H1.0 linker histone	0.99	3.51e-33	LIMD1	LIM domain containing 1
-0.94	1.25e-27	PHF2	PHD finger protein 2	0.98	1.35e-24	PSMB10	proteasome 20S subunit beta 10
-0.93	2.89e-18	CD276	CD276 molecule	0.97	1.83e-27	NECAP2	NECAP endocytosis associated 2
-0.93	9.91e-25	TMTC3	transmembrane O-mannosyltransferase	0.97	5.63e-25	ADA	adenosine deaminase
-0.93	1.04e-28	MFN1	mitofusin 1	0.96	6.21e-17	ABRACL	ABRA C-terminal like
-0.92	3.37e-14	CKMT1A	creatine kinase, mitochondrial 1A	0.96	1.47e-19	SH3BGR	SH3 domain binding glutamate rich p
-0.92	3.82e-31	L2HGDH	L-2-hydroxyglutarate dehydrogenase	0.96	3.60e-23	UBE2L6	ubiquitin conjugating enzyme E2 L6
-0.92	3.55e-21	ATRN	actin	0.95	2.25e-25	CZIB	CXXC motif containing zinc binding
-0.91	2.45e-31	URB1	URB1 ribosome biogenesis homolog	0.94	1.91e-27	BCL10	BCL10 immune signaling adaptor
-0.91	4.15e-21	ATP6AP2	ATPase H ⁺ transporting accessory pr	0.94	2.24e-28	RABEP2	rabaptin, RAB GTPase binding effect
-0.91	4.14e-20	SLC25A4	solute carrier family 25 member 4	0.94	4.93e-22	ABHD14B	abhydrolase domain containing 14B
-0.9	8.85e-26	FASTKD2	FAST kinase domains 2	0.93	5.17e-19	GBE1	1,4-alpha-glucan branching enzyme 1
-0.9	7.30e-20	GNA11	G protein subunit alpha 11	0.93	7.00e-24	COMMD8	COMM domain containing 8

GAGE analysis on upregulated and downregulated proteins at low/absent DHX9 protein, DB1



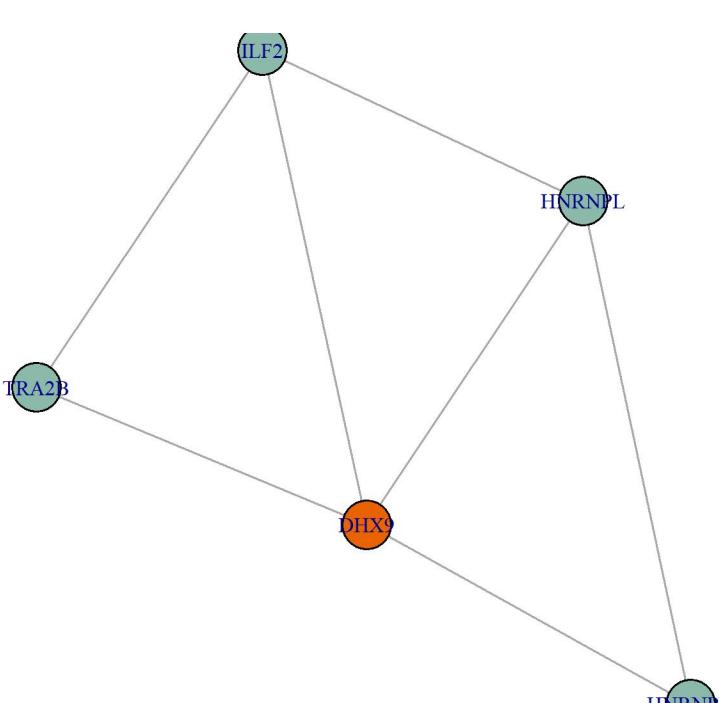


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.86	2.40e-04	TUBGCP3	tubulin gamma complex associated pr	1.13	1.74e-04	IRF2BPL	interferon regulatory factor 2 bind
-0.85	1.39e-03	UBAC2	UBA domain containing 2	1.1	1.49e-03	CTTN	cortactin
-0.8	1.21e-03	TELO2	telomere maintenance 2	0.97	4.19e-03	ISG20	interferon stimulated exonuclease g
-0.76	3.60e-02	MPP1	MAGUK p55 scaffold protein 1	0.96	1.95e-02	HLA-DQB1	major histocompatibility complex, c
-0.75	2.15e-02	ABCD3	ATP binding cassette subfamily D me	0.95	1.94e-02	HLA-DPB1	major histocompatibility complex, c
-0.75	3.54e-03	NUDT16L1	nudix hydrolase 16 like 1	0.91	1.16e-01	LSP1	lymphocyte specific protein 1
-0.74	1.02e-02	SDCBP	syndecan binding protein	0.87	1.01e-02	CD59	CD59 molecule (CD59 blood group)
-0.74	7.09e-03	CWC22	CWC22 spliceosome associated protei	0.86	3.78e-02	PTMS	parathymosin
-0.73	3.10e-02	CFAP20	cilia and flagella associated prote	0.85	3.73e-02	POLR2K	RNA polymerase II, I and III subuni
-0.72	6.68e-03	TRMT1L	tRNA methyltransferase 1 like	0.83	4.64e-03	BORCS7	BLOC-1 related complex subunit 7
-0.72	9.37e-02	PTPRF	protein tyrosine phosphatase recept	0.83	1.33e-02	JUNB	JunB proto-oncogene, AP-1 transcrip
-0.72	2.41e-02	HS2ST1	heparan sulfate 2-O-sulfotransferas	0.8	1.70e-02	GLCCI1	glucocorticoid induced 1
-0.72	8.83e-03	INTS11	integrator complex subunit 11	0.8	4.64e-02	HLA-DPA1	major histocompatibility complex, c
-0.71	1.02e-02	RBPJ	recombination signal binding protei	0.76	7.17e-02	IRF4	interferon regulatory factor 4
-0.71	1.31e-02	MLLT1	MLLT1 super elongation complex subu	0.74	1.17e-01	HLA-DRB1	major histocompatibility complex, c
-0.69	2.11e-02	PXK	PX domain containing serine/threoni	0.74	7.59e-02	HLA-DRB3	major histocompatibility complex, c
-0.67	1.31e-02	GEMIN4	gem nuclear organelle associated pr	0.72	1.58e-02	MYO1C	myosin IC
-0.67	5.05e-02	GPX7	glutathione peroxidase 7	0.71	3.77e-02	SS18	SS18 subunit of BAF chromatin remod
-0.67	5.55e-02	CTBP2	C-terminal binding protein 2	0.7	6.34e-02	CD40	CD40 molecule
-0.66	1.70e-02	VRK3	VRK serine/threonine kinase 3	0.7	2.14e-01	CRIP1	cysteine rich protein 1
-0.66	7.85e-02	CORO1B	coronin 1B	0.69	3.89e-02	SELPLG	selectin P ligand
-0.65	2.00e-02	SLFN11	schlafen family member 11	0.69	1.28e-02	TRMT5	tRNA methyltransferase 5
-0.65	2.96e-02	VPS36	vacuolar protein sorting 36 homolog	0.68	6.72e-03	GGA1	golgi associated, gamma adaptin ear
-0.65	2.22e-02	CCT6B	chaperonin containing TCP1 subunit	0.68	9.58e-02	ICAM1	intercellular adhesion molecule 1
-0.64	3.65e-02	VAV1	vav guanine nucleotide exchange fac	0.68	8.52e-02	IKZF3	IKAROS family zinc finger 3
-0.64	8.34e-02	LYZ	lysozyme	0.67	2.20e-02	MBNL1	muscleblind like splicing regulator
-0.64	9.87e-03	LRRC57	leucine rich repeat containing 57	0.67	3.10e-02	SVIP	small VCP interacting protein
-0.64	3.77e-02	OAT	ornithine aminotransferase	0.67	4.20e-02	RGS14	regulator of G protein signaling 14
-0.63	1.18e-02	WDR76	WD repeat domain 76	0.66	1.62e-04	CARMIL1	capping protein regulator and myosi

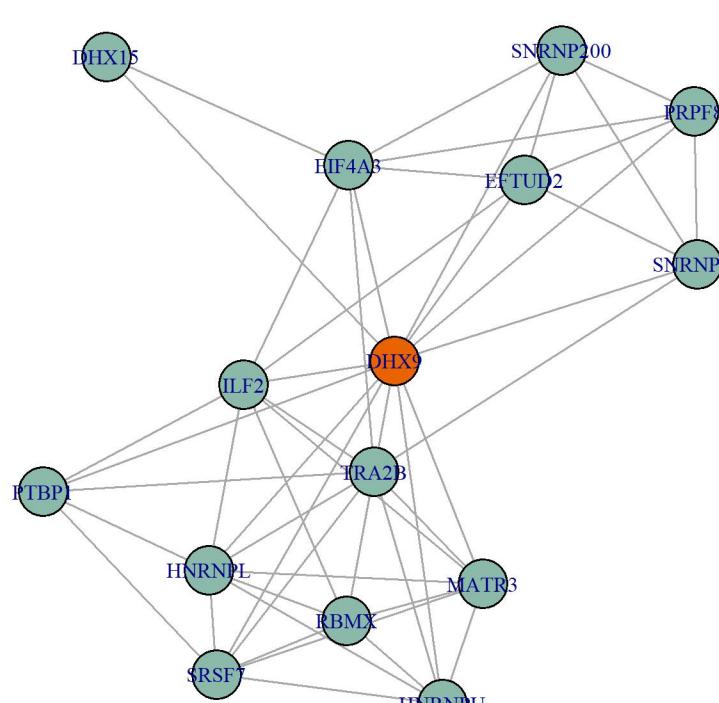


Downregulated in solid cancers at low/absent DHX9				Upregulated in solid cancers at low/absent DHX9			
FC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
2	7.76e-18	BRI3BP	BRI3 binding protein	1.22	1.04e-30	FAM114A1	family with sequence similarity 114
19	6.94e-43	BRD1	bromodomain containing 1	1.01	6.05e-30	PXN	paxillin
8	8.22e-34	YTHDC1	YTH domain containing 1	0.96	6.65e-09	TMSB10	thymosin beta 10
2	1.33e-27	TMEM201	transmembrane protein 201	0.92	1.26e-20	ATOX1	antioxidant 1 copper chaperone
6	5.39e-26	NOL9	nucleolar protein 9	0.91	1.84e-18	RNF181	ring finger protein 181
6	1.09e-14	LCLAT1	lysocardiolipin acyltransferase 1	0.89	5.88e-15	PAPSS2	3'-phosphoadenosine 5'-phosphosulfatase
5	1.20e-26	URB1	URB1 ribosome biogenesis homolog	0.88	5.20e-21	ARFGAP3	ADP ribosylation factor GTPase activating protein 3
4	1.20e-21	TMEM209	transmembrane protein 209	0.87	1.15e-16	SH3KBP1	SH3 domain containing kinase binding protein 1
1	3.83e-20	PHF2	PHD finger protein 2	0.85	1.01e-13	GLRX	glutaredoxin
1	2.10e-22	EZH2	enhancer of zeste 2 polycomb repressor complex 2 subunit	0.84	1.03e-21	LPP	LIM domain containing preferred target 1
9	2.36e-08	NDUFB11	NADH:ubiquinone oxidoreductase subunit 11	0.84	1.05e-14	ACY1	aminoacylase 1
9	4.13e-26	TRRAP	transformation/transcription domain containing 1	0.83	3.76e-18	STAM2	signal transducing adaptor molecule 2
9	1.68e-21	NOL8	nucleolar protein 8	0.82	4.95e-17	DCTD	dCMP deaminase
8	2.69e-19	SRCAP	Snf2 related CREBBP activator protein	0.82	4.80e-14	FAH	fumarylacetoacetate hydrolase
8	5.39e-25	KAT7	lysine acetyltransferase 7	0.82	2.32e-12	GBE1	1,4-alpha-glucan branching enzyme 1
8	6.32e-20	MEAF6	MYST/Esa1 associated factor 6	0.8	5.69e-15	GALE	UDP-galactose-4-epimerase
7	3.84e-17	RPF1	ribosome production factor 1 homolog	0.8	7.06e-20	SRA1	steroid receptor RNA activator 1
7	9.91e-25	ATAD2	ATPase family AAA domain containing 2	0.8	7.60e-15	CZIB	CXXC motif containing zinc binding protein
6	7.33e-18	FAM20B	FAM20B glycosaminoglycan xylosylkinase	0.8	9.72e-14	RPE	ribulose-5-phosphate-3-epimerase
6	1.98e-22	THOC5	THO complex 5	0.8	1.76e-15	NECAP2	NECAP endocytosis associated 2
6	1.22e-24	SMC6	structural maintenance of chromosomes 6	0.8	6.42e-18	HOOK3	hook microtubule tethering protein
5	1.35e-17	EMC6	ER membrane protein complex subunit	0.8	1.14e-14	AKT1S1	AKT1 substrate 1
5	1.84e-18	ZNF280C	zinc finger protein 280C	0.79	9.33e-18	AAK1	AP2 associated kinase 1
5	1.35e-18	LRRC8A	leucine rich repeat containing 8 VR	0.78	8.80e-16	PDLIM2	PDZ and LIM domain 2
5	2.76e-24	RBMX2	RNA binding motif protein X-linked	0.78	1.01e-15	PARP4	Poly(ADP-ribose) polymerase family member 4
4	1.29e-17	SUDS3	SDS3 homolog, SIN3A corepressor complex	0.78	1.28e-14	OPTN	optineurin
4	5.72e-21	AURKB	aurora kinase B	0.78	4.03e-19	LIMD1	LIM domain containing 1
3	6.08e-23	DDX31	DEAD-box helicase 31	0.78	7.10e-12	FKBP1A	FKBP prolyl isomerase 1A
2	2.19e-20	BUD13	BUD13 homolog	0.77	3.05e-11	RHOC	ras homolog family member C

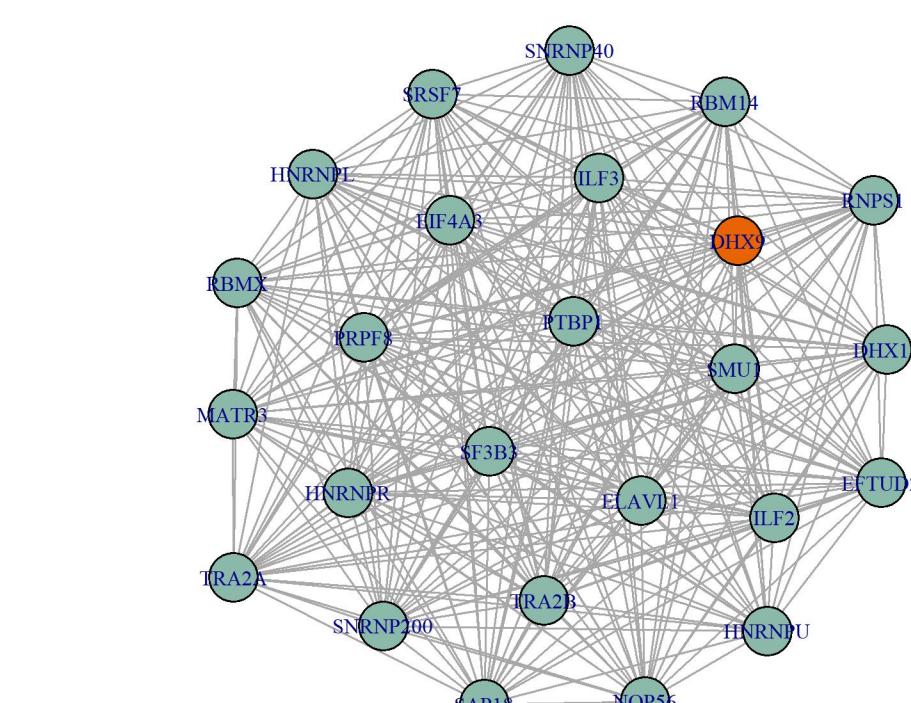
DHX9 network, DB1, all Pearson $r > 0.7$

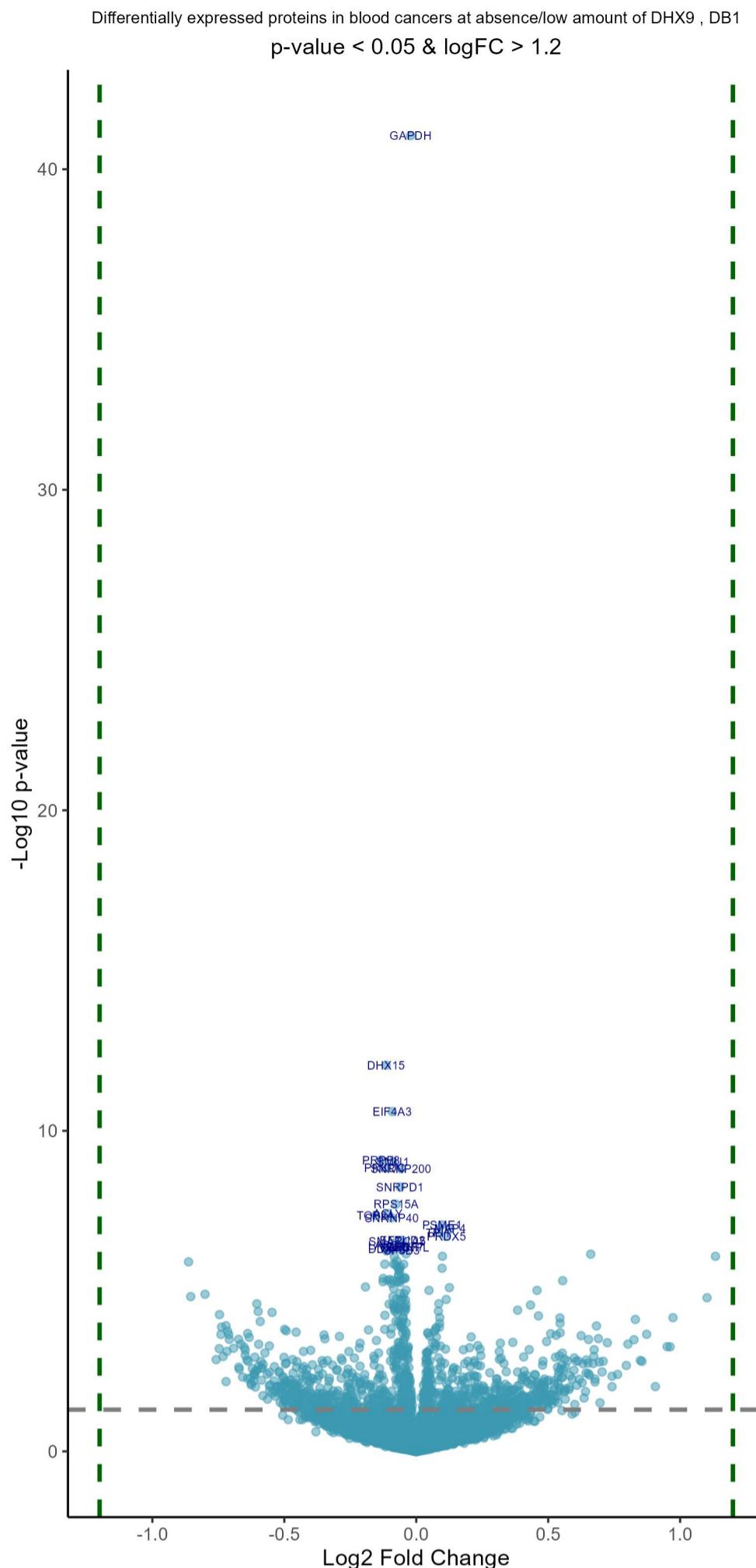


DHX9 network, DB1, all Pearson r > 0.65

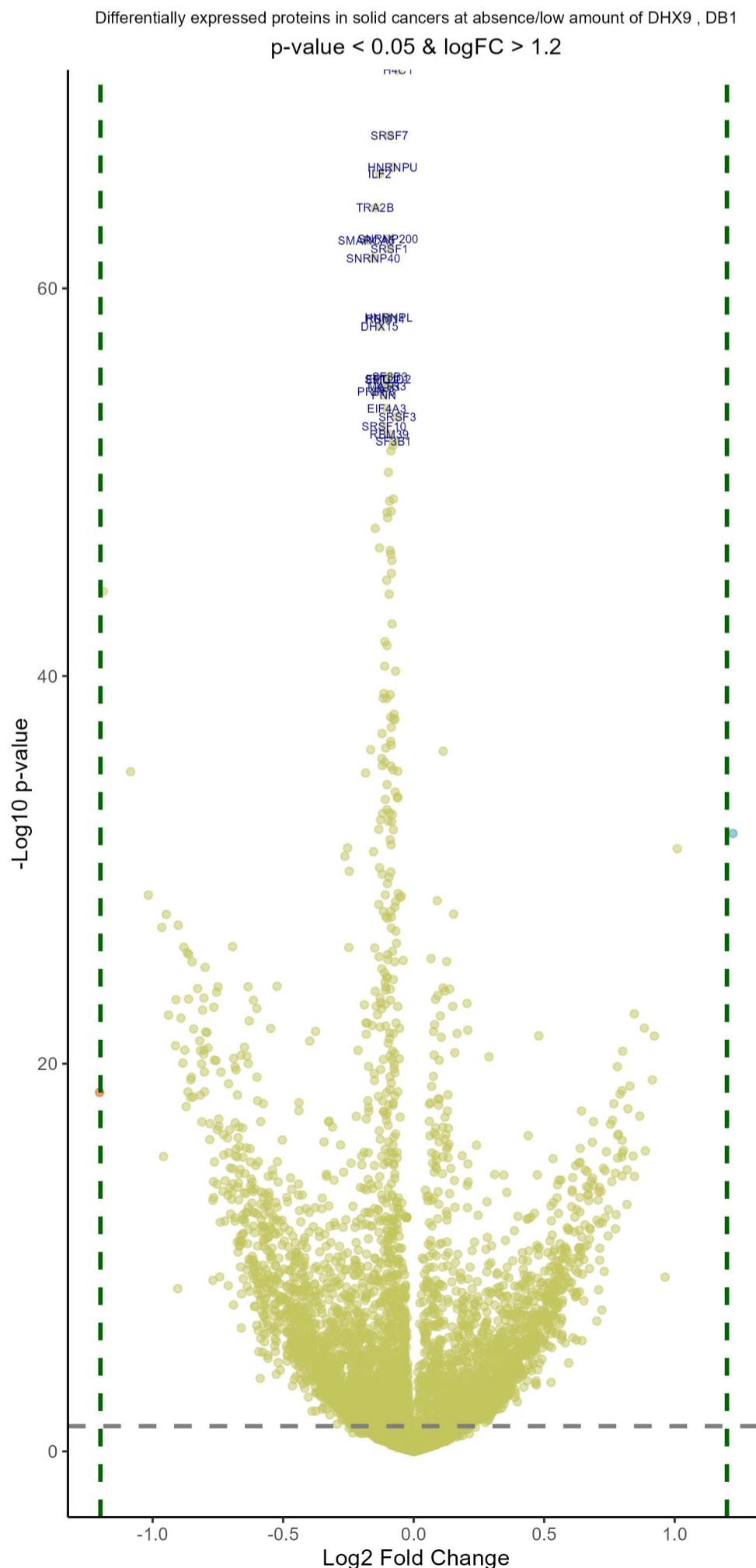


DHX9 network, DB1, all Pearson $r > 0.6$



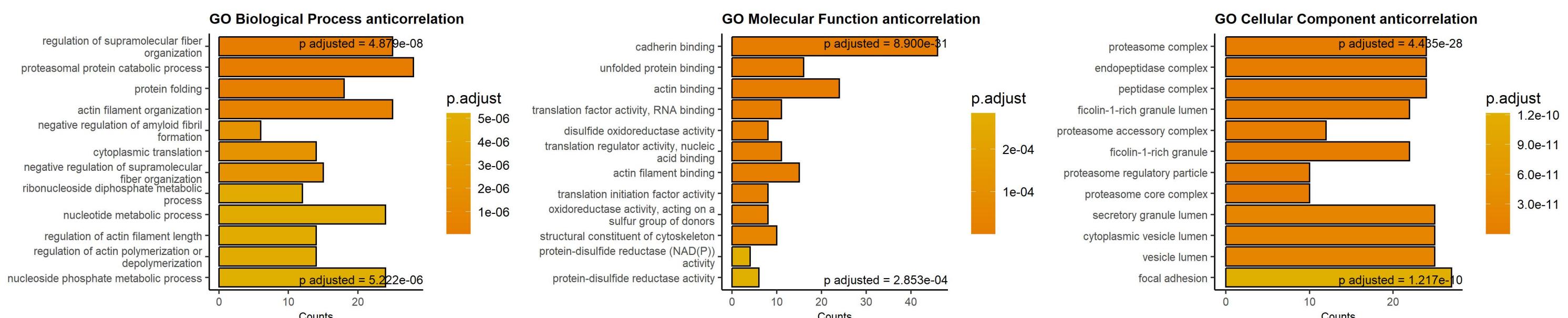
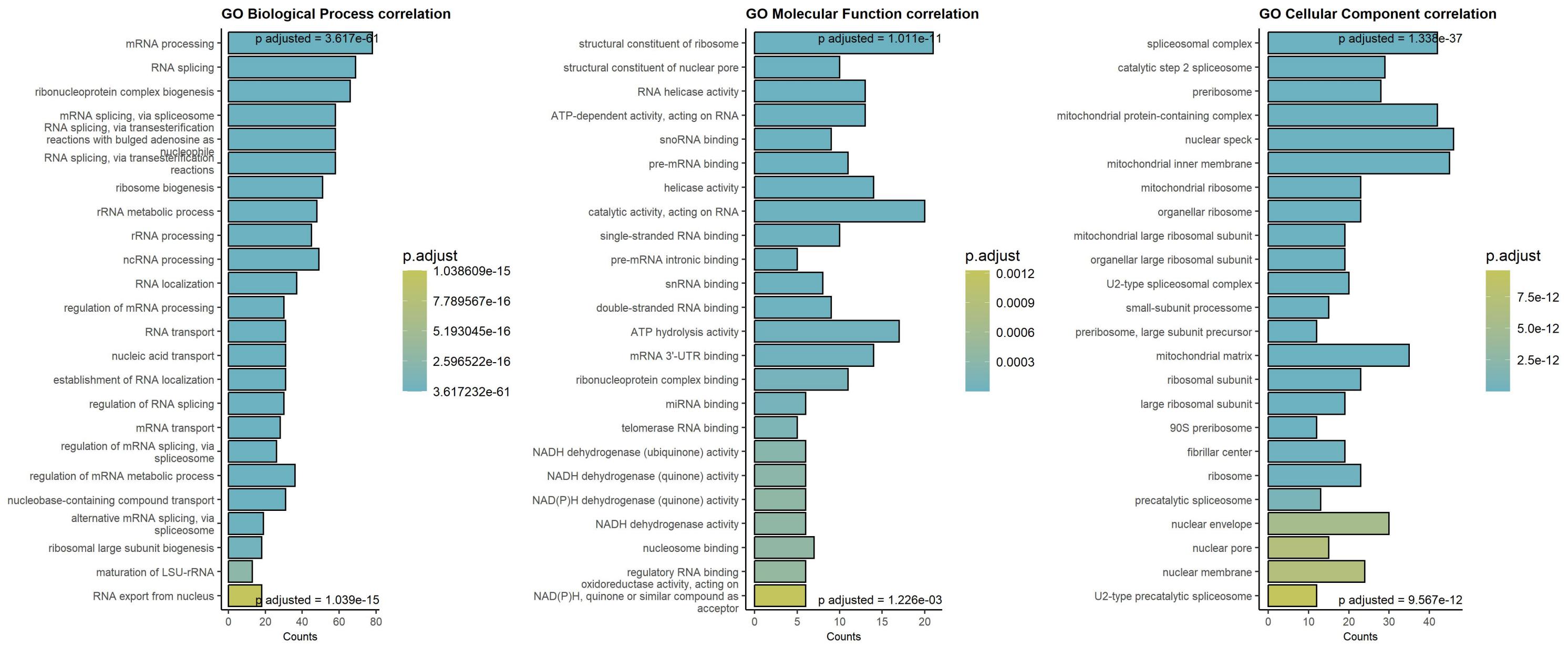


Sorted by p values!							
Downregulated in blood cancers at low/absent DHX9				Upregulated in blood cancers at low/absent DHX9			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.02	5.94e-38	GAPDH	glyceraldehyde-3-phosphate dehydrog	0.1	4.10e-05	PSME1	proteasome activator subunit 1
-0.11	1.99e-09	DHX15	DEAH-box helicase 15	0.13	4.91e-05	MAP4	microtubule associated protein 4
-0.09	4.18e-08	EIF4A3	eukaryotic translation initiation f	0.08	6.29e-05	TPI1	triosephosphate isomerase 1
-0.13	1.01e-06	PRPF8	pre-mRNA processing factor 8	0.11	7.54e-05	PRDX5	peroxiredoxin 5
-0.09	1.01e-06	SMU1	SMU1 DNA replication regulator and	0.66	1.62e-04	CARMIL1	capping protein regulator and myosi
-0.12	1.26e-06	PRKDC	protein kinase, DNA-activated, cata	0.1	1.74e-04	PSMD9	proteasome 26S subunit, non-ATPase
-0.06	1.26e-06	SNRNP200	small nuclear ribonucleoprotein U5	1.13	1.74e-04	IRF2BPL	interferon regulatory factor 2 bind
-0.06	4.20e-06	SNRPD1	small nuclear ribonucleoprotein D1	0.1	3.12e-04	PSME2	proteasome activator subunit 2
-0.08	1.29e-05	RPS15A	ribosomal protein S15a	0.55	5.72e-04	PPM1A	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe
-0.11	2.32e-05	ACLY	ATP citrate lyase	0.13	8.36e-04	CNPY2	canopy FGF signaling regulator 2
-0.15	2.42e-05	TOP2A	DNA topoisomerase II alpha	0.05	9.58e-04	PSMA5	proteasome 20S subunit alpha 5
-0.09	2.64e-05	SNRNP40	small nuclear ribonucleoprotein U5	0.46	9.58e-04	TIMM9	translocase of inner mitochondrial
-0.05	9.68e-05	EFTUD2	elongation factor Tu GTP binding do	1.1	1.49e-03	CTTN	cortactin
-0.07	9.86e-05	SMARCA5	SWI/SNF related, matrix associated,	0.11	1.61e-03	FKBP2	FKBP prolyl isomerase 2
-0.11	1.24e-04	LARS1	leucyl-tRNA synthetase 1	0.09	2.07e-03	FKBP3	FKBP prolyl isomerase 3
-0.04	1.26e-04	SRSF7	serine and arginine rich splicing f	0.43	2.16e-03	ACTL8	actin like 8
-0.08	1.26e-04	CLTC	clathrin heavy chain	0.38	2.76e-03	HMBS	hydroxymethylbilane synthase
-0.04	1.26e-04	HNRNPL	heterogeneous nuclear ribonucleopro	0.08	2.89e-03	CCDC124	coiled-coil domain containing 124
-0.11	1.32e-04	DDX18	DEAD-box helicase 18	0.46	3.79e-03	ARFGAP1	ADP ribosylation factor GTPase acti
-0.06	1.37e-04	SF3B3	splicing factor 3b subunit 3	0.09	4.19e-03	TXN	thioredoxin
-0.1	1.37e-04	DDX6	DEAD-box helicase 6	0.97	4.19e-03	ISG20	interferon stimulated exonuclease g
-0.11	1.38e-04	NUP155	nucleoporin 155	0.54	4.22e-03	GRIPAP1	GRIP1 associated protein 1
-0.04	1.62e-04	HNRNPU	heterogeneous nuclear ribonucleopro	0.83	4.64e-03	BORCS7	BLOC-1 related complex subunit 7
-0.08	1.74e-04	RPL15	ribosomal protein L15	0.54	5.71e-03	CRK	CRK proto-oncogene, adaptor protein
-0.07	2.31e-04	RPL27	ribosomal protein L27	0.09	5.71e-03	PDAP1	PDGFA associated protein 1
-0.86	2.40e-04	TUBGCP3	tubulin gamma complex associated pr	0.68	6.72e-03	GGA1	golgi associated, gamma adaptin ear
-0.09	2.56e-04	XPO1	exportin 1	0.09	7.16e-03	NSFL1C	NSFL1 cofactor
-0.12	2.56e-04	MACROH2A1	macroH2A.1 histone	0.08	7.24e-03	LSM3	LSM3 homolog, U6 small nuclear RNA
-0.05	2.56e-04	PTBP1	polypyrimidine tract binding protei	0.07	7.97e-03	BOLA2	bola family member 2
-0.08	2.56e-04	NAT10	N-acetyltransferase 10	0.07	8.84e-03	DCTN2	dynactin subunit 2
-0.06	2.88e-04	RPL4	ribosomal protein L4	0.04	9.49e-03	EIF4B	eukaryotic translation initiation f
-0.07	2.88e-04	TNPO1	transportin 1	0.55	9.49e-03	FAM234A	family with sequence similarity 234
-0.06	3.12e-04	RPS16	ribosomal protein S16	0.04	9.87e-03	ENO1	enolase 1
-0.07	3.36e-04	NUP133	nucleoporin 133	0.51	9.87e-03	TSSC4	tumor suppressing subtransferable c
-0.06	3.72e-04	RPL18	ribosomal protein L18	0.87	1.01e-02	CD59	CD59 molecule (CD59 blood group)
-0.07	4.57e-04	RPL28	ribosomal protein L28	0.53	1.06e-02	CGN	cingulin
-0.07	4.84e-04	MTREX	Mtr4 exosome RNA helicase	0.62	1.08e-02	NCOR2	nuclear receptor corepressor 2
-0.04	5.35e-04	SRSF1	serine and arginine rich splicing f	0.05	1.12e-02	COX5B	cytochrome c oxidase subunit 5B
-0.13	5.49e-04	PABPC	PABPC member PABP oncogenic family	0.08	1.16e-02	NUDT5	nudin hydroxylase 5

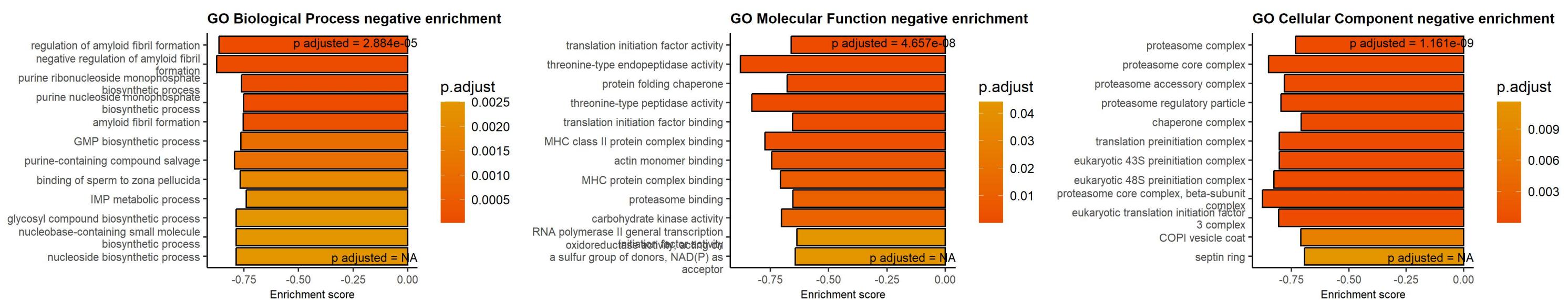
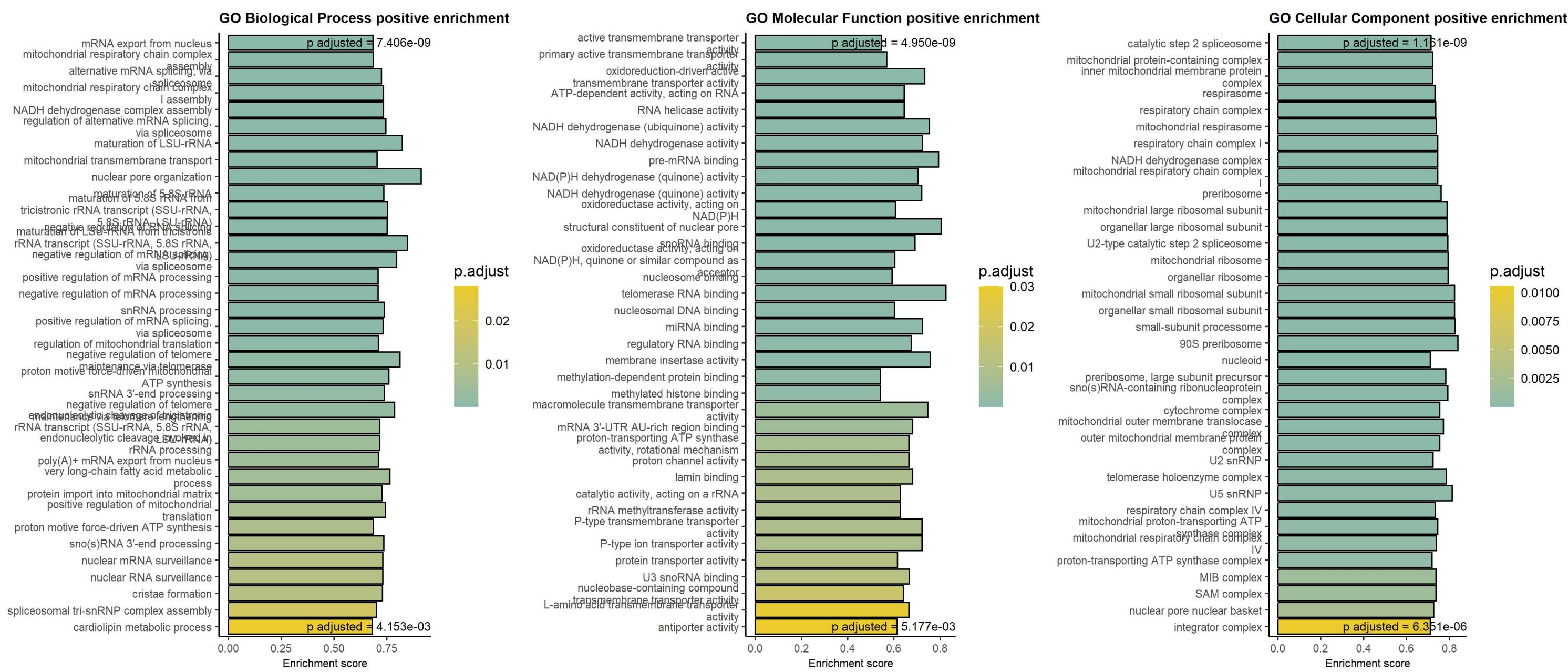


Sorted by p values!							
Downregulated in solid cancers at low/absent DHX9				Upregulated in solid cancers at low/absent DHX9			
C	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
6	0.00e+00	H4C1	H4 clustered histone 1	0.11	8.14e-35	PSMA5	proteasome 20S subunit alpha 5
9	2.93e-65	SRSF7	serine and arginine rich splicing f	1.22	1.04e-30	FAM114A1	family with sequence similarity 114
3	9.45e-64	HNRNPU	heterogeneous nuclear ribonucleoprotein U5	1.01	6.05e-30	PXN	paxillin
3	1.67e-63	ILF2	interleukin enhancer binding factor	0.09	2.52e-27	EEF1D	eukaryotic translation elongation f
5	7.75e-62	TRA2B	transformer 2 beta homolog	0.15	1.16e-26	CLIC1	chloride intracellular channel 1
	2.69e-60	SNRNP200	small nuclear ribonucleoprotein U5	0.07	1.97e-24	PSMA1	proteasome 20S subunit alpha 1
3	2.87e-60	SMARCA5	SWI/SNF related, matrix associated, chromatin rearranger and histone deacetylase complex subunit 5	0.13	2.69e-24	ALDOA	aldolase, fructose-bisphosphate A
9	6.88e-60	SRSF1	serine and arginine rich splicing f	0.11	5.73e-23	PFN1	profilin 1
5	1.88e-59	SNRNP40	small nuclear ribonucleoprotein U5	0.14	6.36e-23	PDCD6IP	programmed cell death 6 interacting protein
	1.89e-56	HNRNPL	heterogeneous nuclear ribonucleoprotein L	0.12	7.97e-23	MYL6	myosin light chain 6
1	2.10e-56	RBM14	RNA binding motif protein 14	0.09	1.30e-22	PSMA6	proteasome 20S subunit alpha 6
3	4.69e-56	DHX15	DEAH-box helicase 15	0.08	2.04e-22	AIMP1	aminoacyl tRNA synthetase complex I
9	1.66e-53	SF3B3	splicing factor 3b subunit 3	0.2	3.18e-22	LASP1	LIM and SH3 protein 1
	2.12e-53	EFTUD2	elongation factor Tu GTP binding domain	0.15	4.42e-22	CAP1	cyclase associated actin cytoskeleton-associated protein
3	2.17e-53	SMU1	SMU1 DNA replication regulator and telomerase component	0.84	1.03e-21	LPP	LIM domain containing preferred target of p53
	4.32e-53	MATR3	matrin 3	0.1	1.30e-21	ARCN1	archain 1
	4.38e-53	ILF3	interleukin enhancer binding factor	0.08	3.53e-21	PSMA2	proteasome 20S subunit alpha 2
4	7.43e-53	PRPF8	pre-mRNA processing factor 8	0.88	5.20e-21	ARFGAP3	ADP ribosylation factor GTPase activating protein 3
1	1.07e-52	PNN	pinin, desmosome associated protein	0.21	6.54e-21	VCL	vinculin
	5.04e-52	EIF4A3	eukaryotic translation initiation f	0.08	7.63e-21	PSMC4	proteasome 26S subunit, ATPase 4
6	1.27e-51	SRSF3	serine and arginine rich splicing f	0.17	9.37e-21	TLN1	talin 1
1	3.81e-51	SRSF10	serine and arginine rich splicing f	0.48	1.23e-20	PLIN3	perilipin 3
9	9.18e-51	RBM39	RNA binding motif protein 39	0.92	1.26e-20	ATOX1	antioxidant 1 copper chaperone for superoxide dismutase
3	2.06e-50	SF3B1	splicing factor 3b subunit 1	0.11	1.44e-20	TPD52L2	TPD52 like 2
3	3.29e-50	SFPQ	splicing factor proline and glutami	0.8	7.06e-20	SRA1	steroid receptor RNA activator 1
9	5.94e-50	PTBP1	polypyrimidine tract binding protei	0.16	8.44e-20	DCTN2	dynactin subunit 2
	7.38e-49	RBMX	RNA binding motif protein X-linked	0.08	1.09e-19	EEF1B2	eukaryotic translation elongation f
3	1.68e-47	SRRT	serrate, RNA effector molecule	0.29	1.32e-19	MAP4	microtubule associated protein 4
9	2.07e-47	ELAVL1	ELAV like RNA binding protein 1	0.1	1.93e-19	PSMA3	proteasome 20S subunit alpha 3
9	6.73e-47	U2SURP	U2 snRNP associated SURP domain con	0.78	4.03e-19	LIMD1	LIM domain containing 1
	7.58e-47	PRPF40A	pre-mRNA processing factor 40 homol	0.08	1.24e-18	PSMC5	proteasome 26S subunit, ATPase 5
1	1.37e-46	HNRNPR	heterogeneous nuclear ribonucleoprotein R	0.91	1.84e-18	RNF181	ring finger protein 181
5	4.74e-46	DKC1	dyskerin pseudouridine synthase 1	0.83	3.76e-18	STAM2	signal transducing adaptor molecule 2
3	4.69e-45	NOP56	NOP56 ribonucleoprotein	0.07	3.89e-18	PSMC2	proteasome 26S subunit, ATPase 2
9	6.16e-45	SNRPA1	small nuclear ribonucleoprotein pol	0.8	6.42e-18	HOOK3	hook microtubule tethering protein
9	9.16e-45	SAP18	Sin3A associated protein 18	0.79	9.33e-18	AAK1	AP2 associated kinase 1
3	1.92e-44	PRPF19	pre-mRNA processing factor 19	0.13	1.01e-17	TUBB4B	tubulin beta 4B class IVb
9	8.52e-44	SF3B6	splicing factor 3b subunit 6	0.09	1.60e-17	CTTN	cortactin
1	1.00e-43	PRPF4	RNA processing factor 4	0.1	1.25e-17	CEP1	CEP152

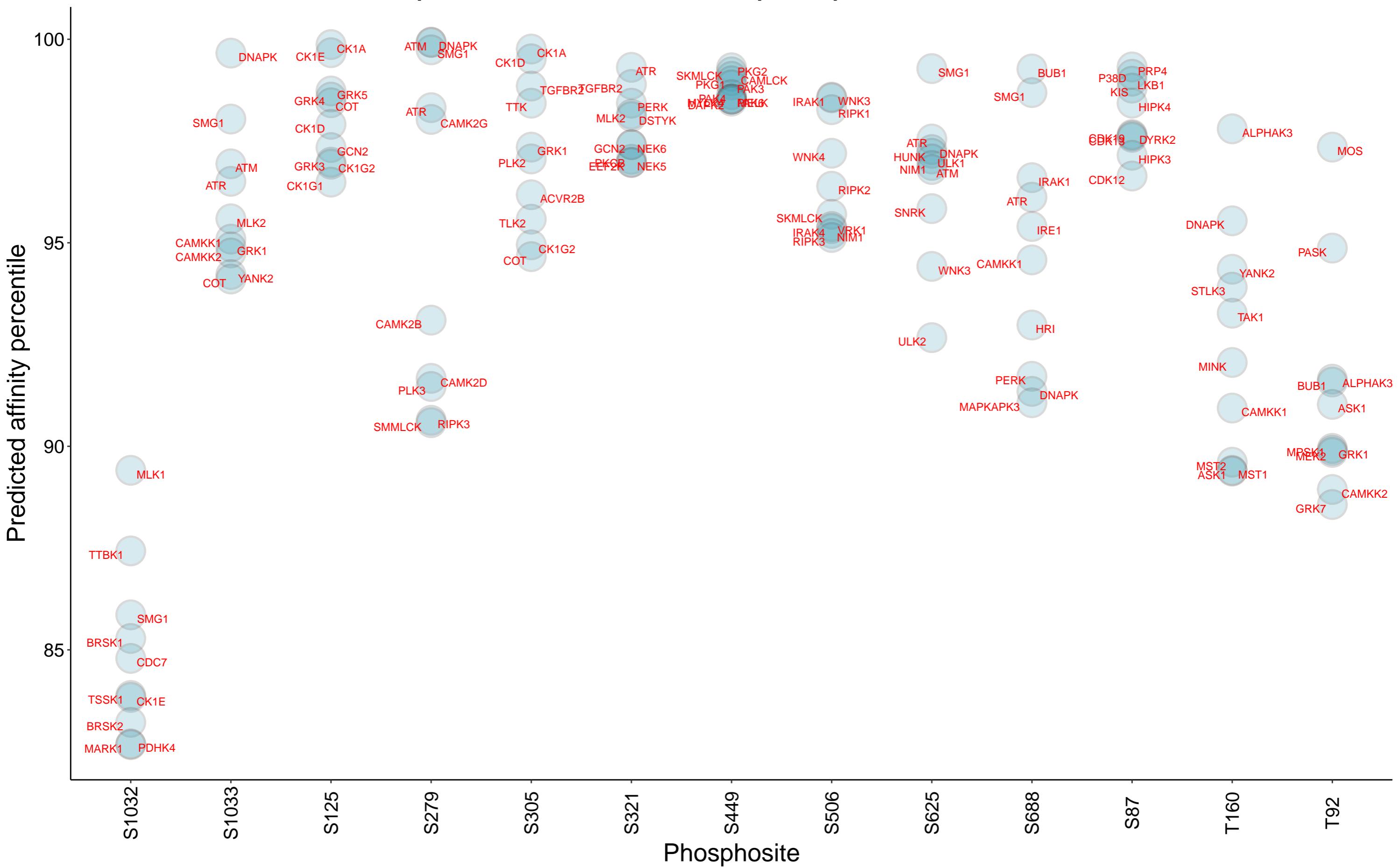
Top 250 correlation coefficients overrepresentation, DHX9 protein, DB1



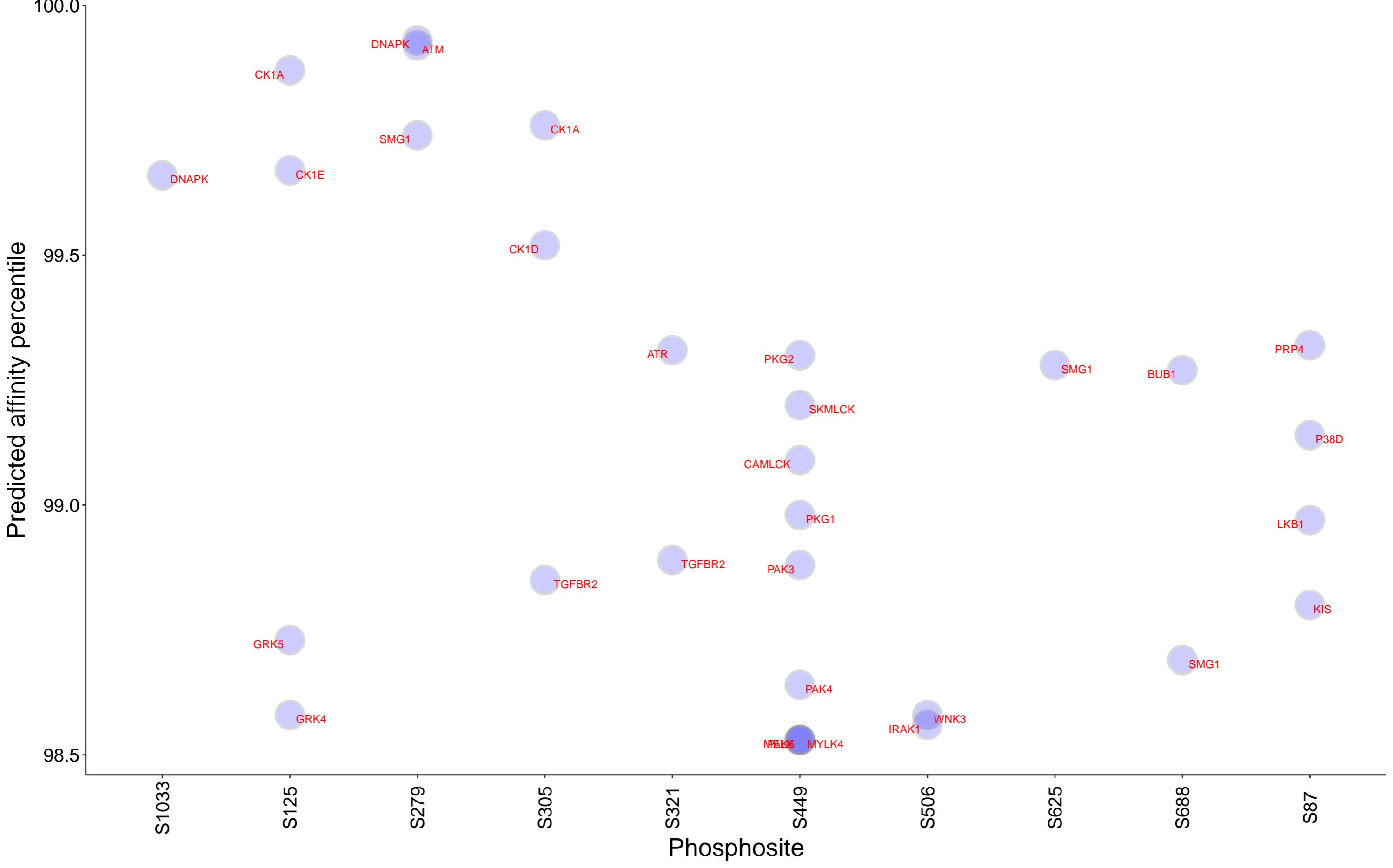
Gene Set Enrichment analysis on protein correlation coefficients, DHX9 protein, DB1



Top 10 kinases for each phosphosite in DHX9



Kinases with affinity greater than 98.5% to DHX9



Top 15 positive correlation coefficients for DHX9 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

