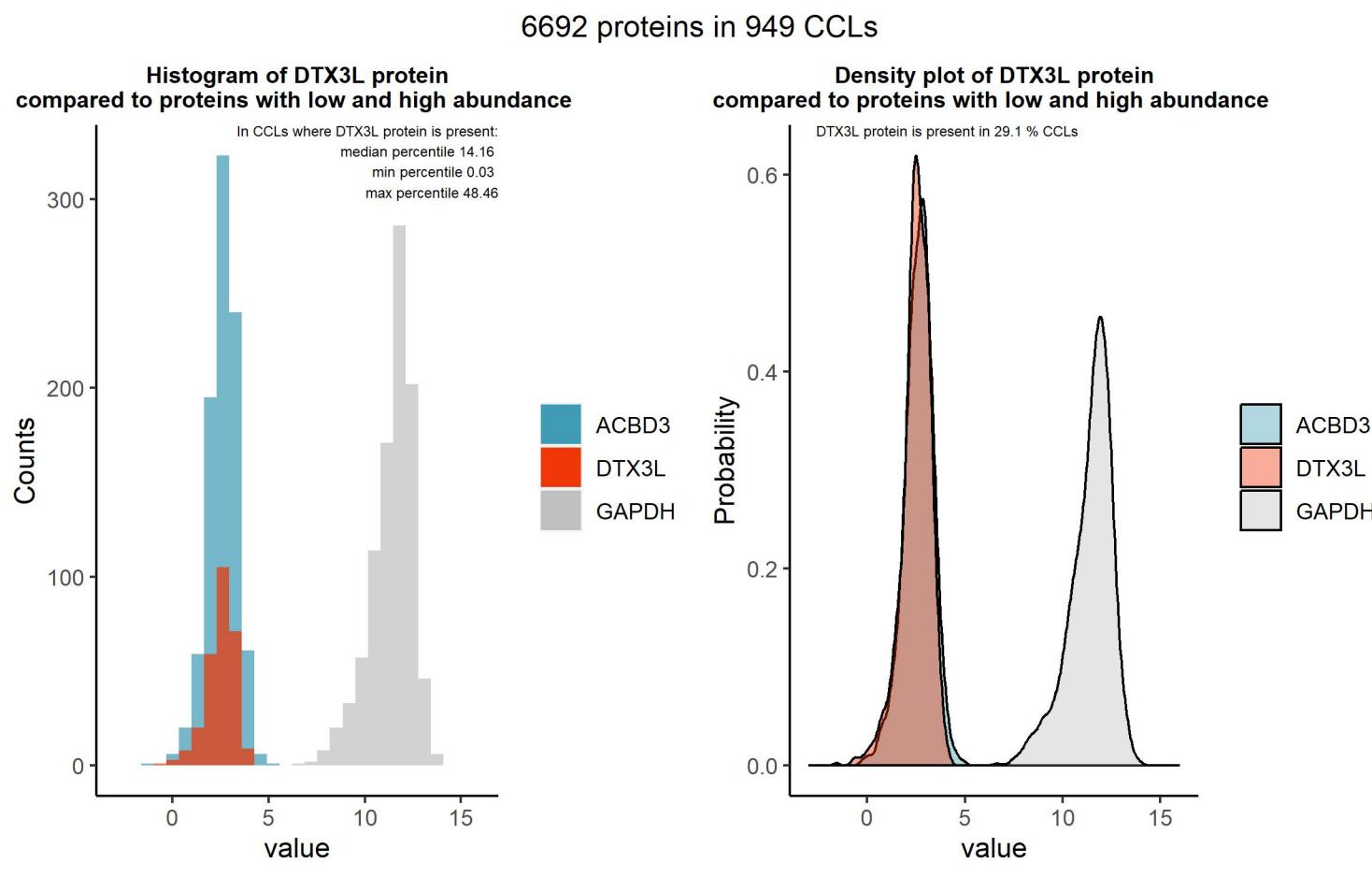


DTX3L

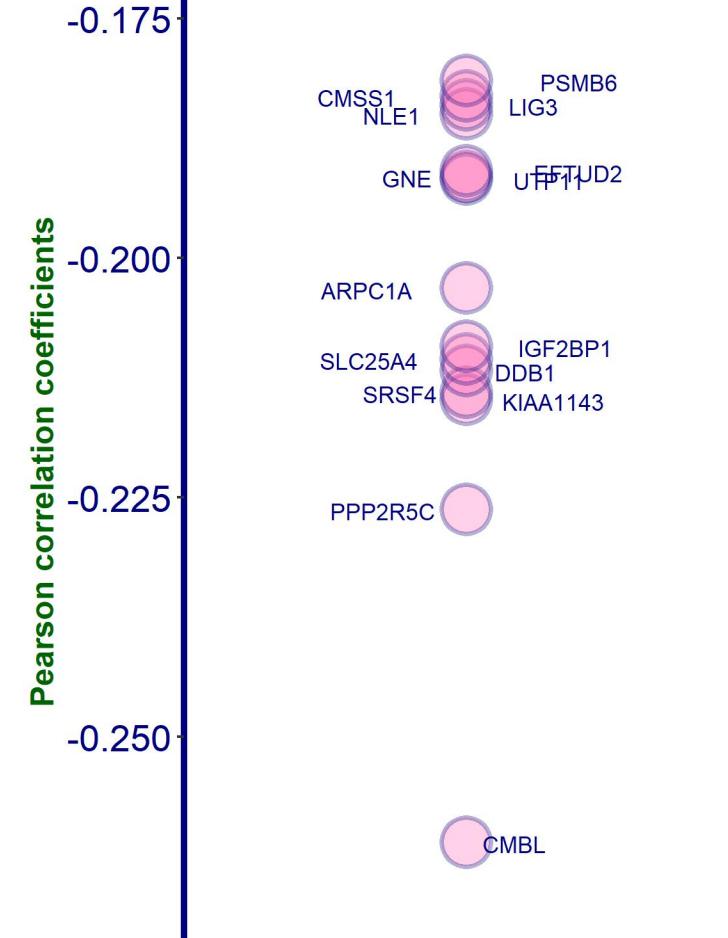
Protein name: DTX3L ; UNIPROT: Q8TDB6 ; Gene name: deltex E3 ubiquitin ligase 3L

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

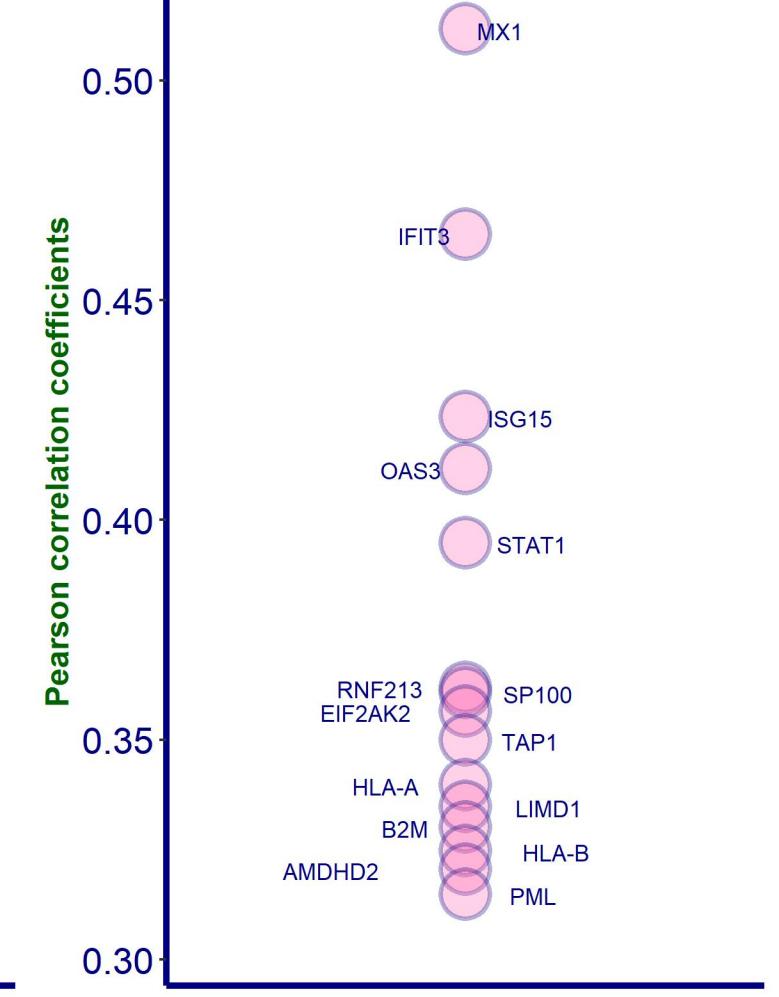
Sanger Institute Protein Database 1 (DB1), protein presence is certain



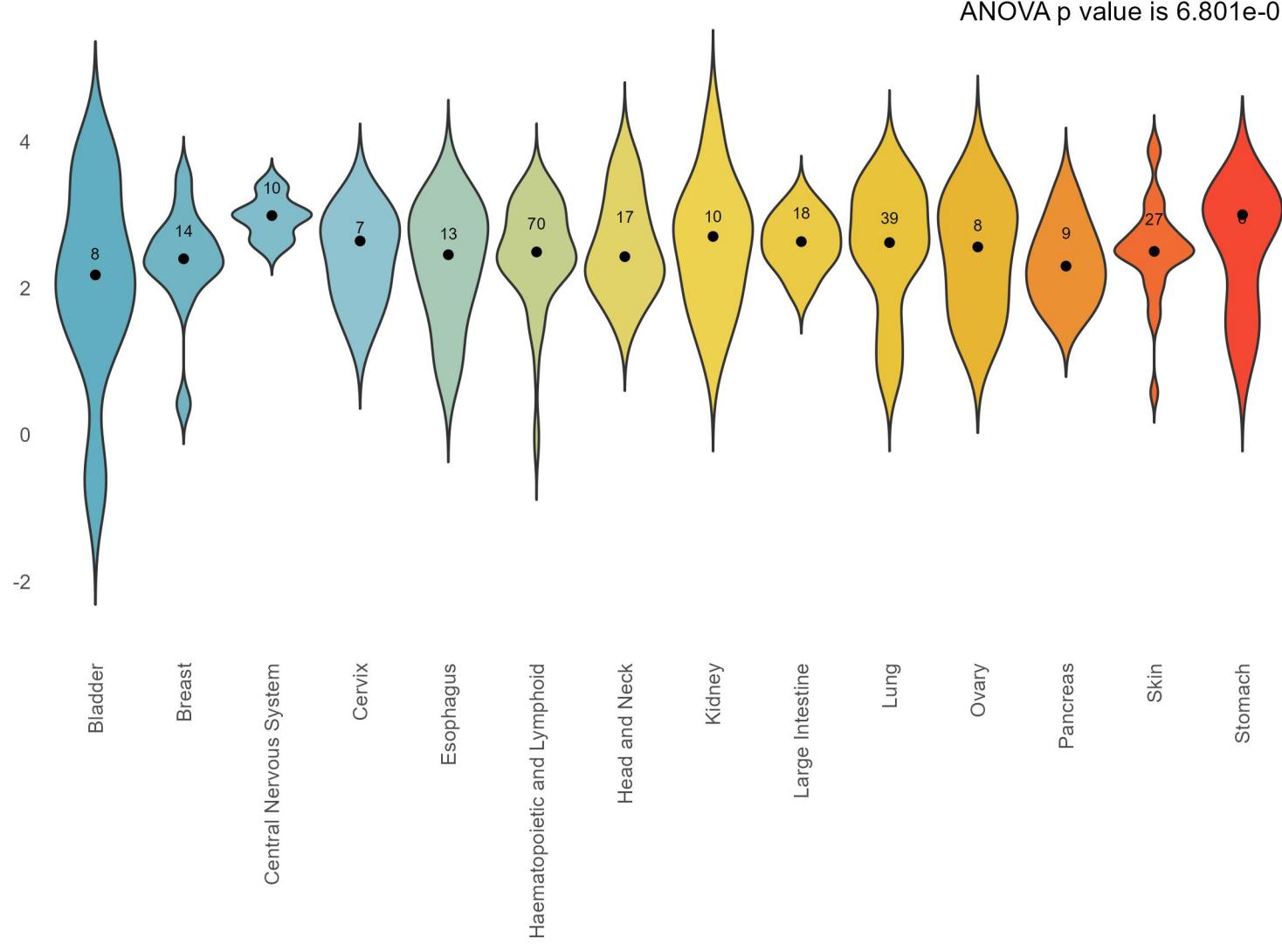
Top negative correlations of DTX3L protein, DB



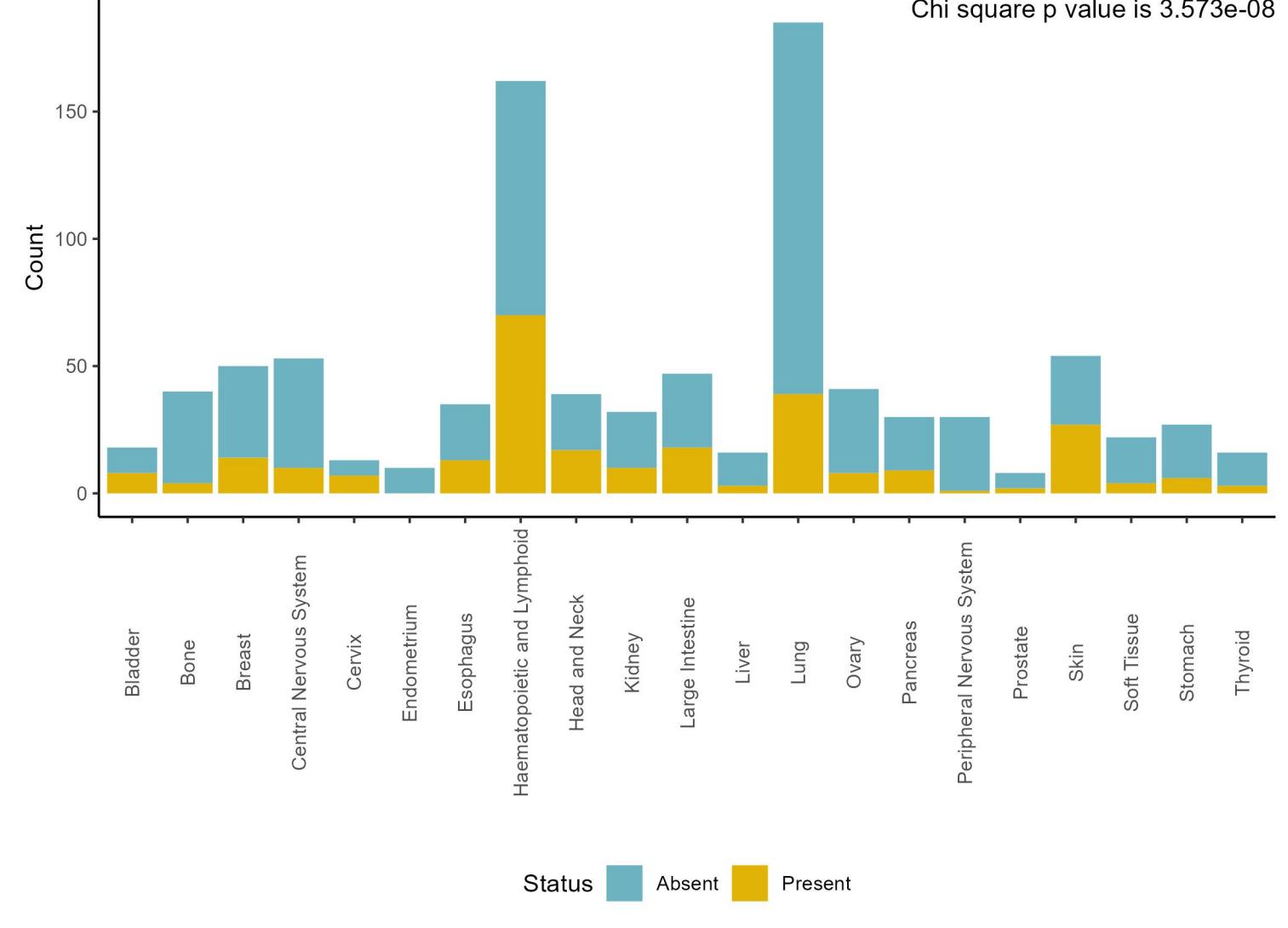
Top positive correlations of DTX3L protein, DB1



Amount of DTX3L protein, number of CCLs where it is present by tissue, DB1



Present and absent DTX3L protein counts by tissue, DB1

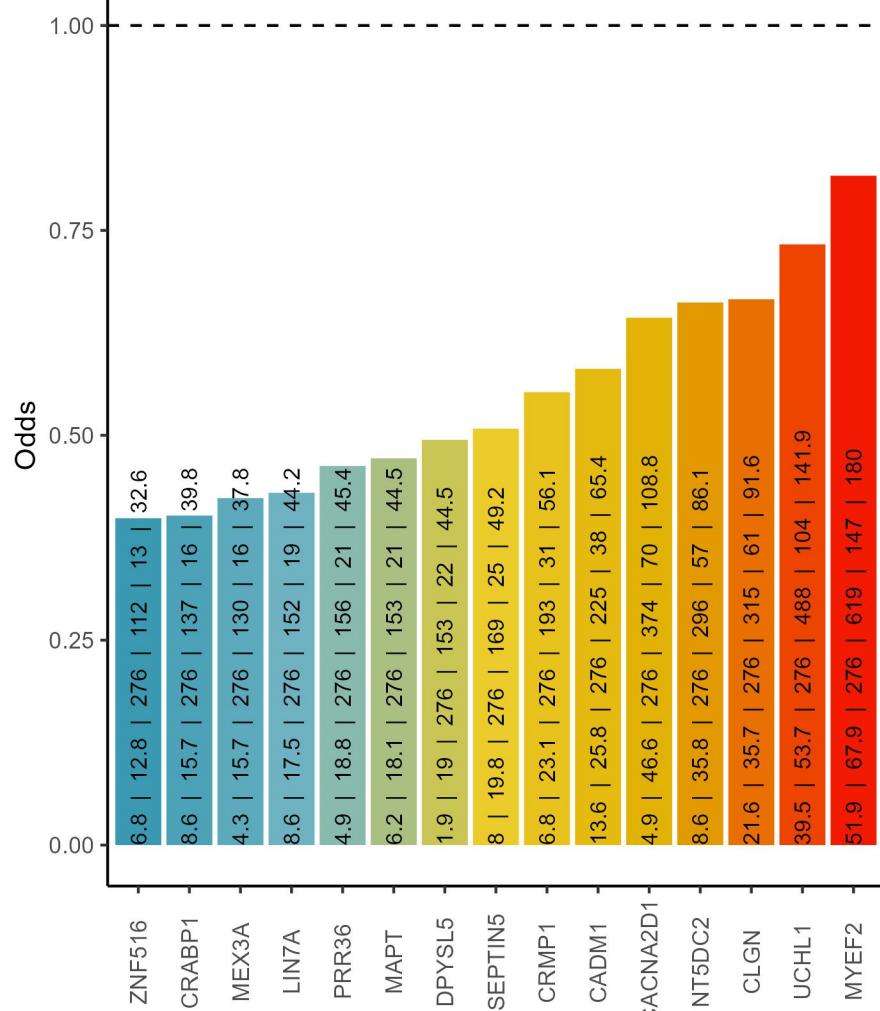


Cooccurrence with DTX3L protein, DB1

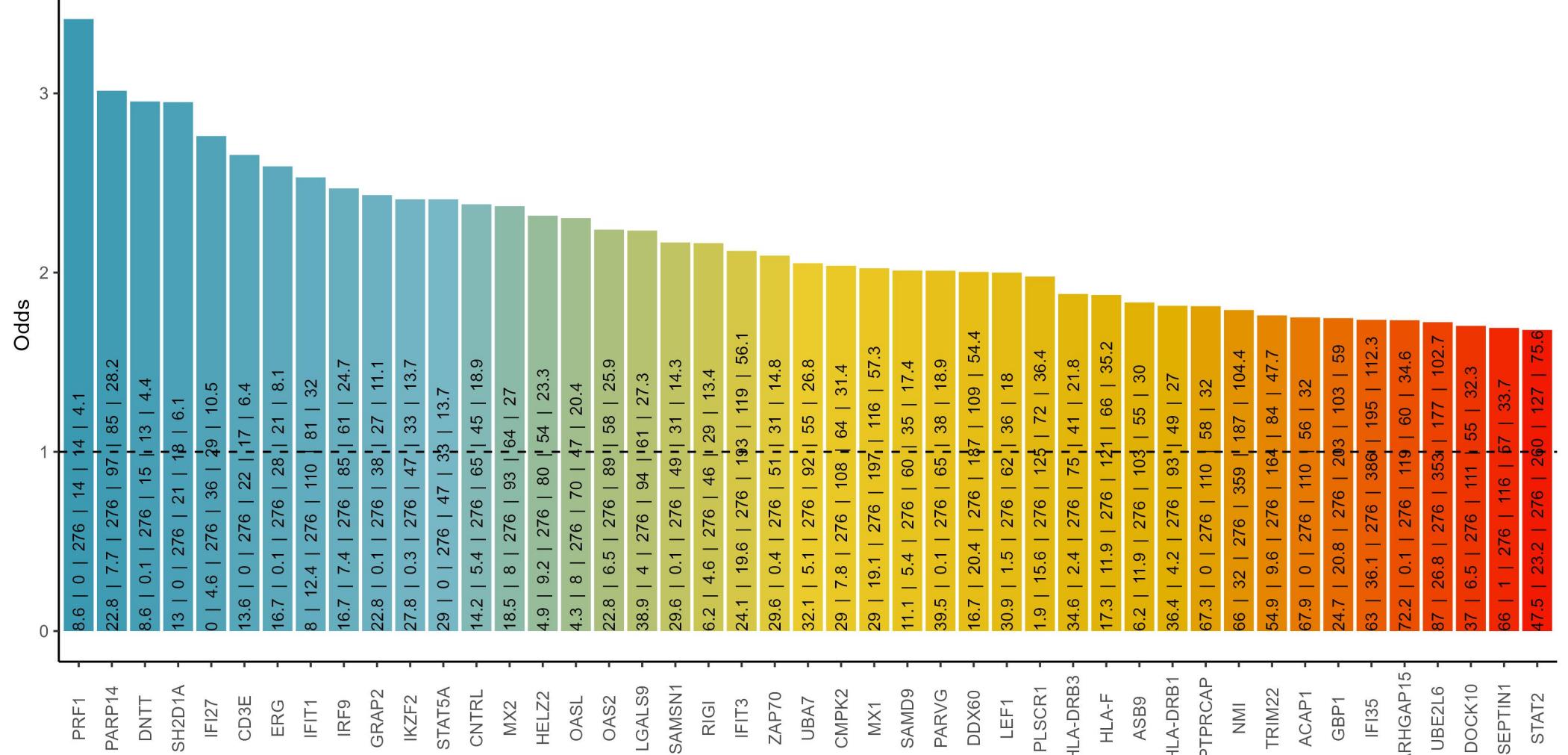
% of DTX3L in blood cancers: 43.2 ; % of DTX3L in solid cancers: 26.3

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of DTX3L | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

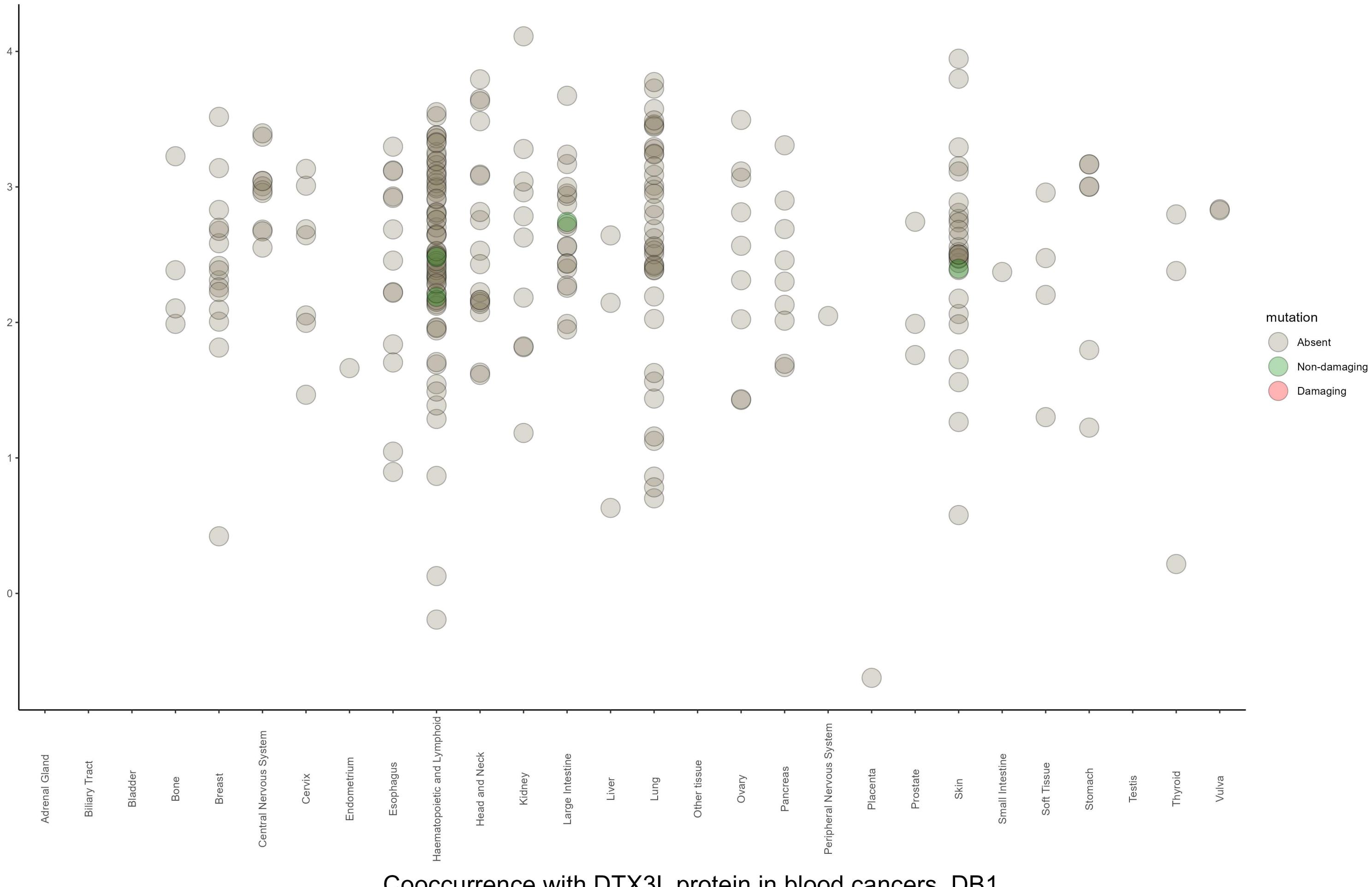
Negative cooccurrence



Positive cooccurrence

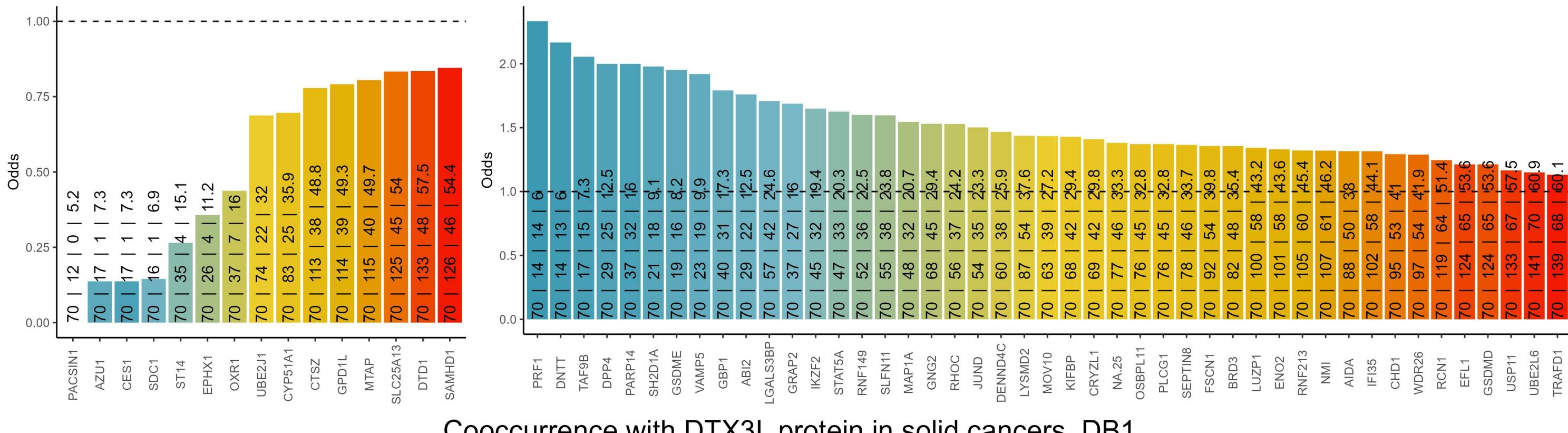


Amount of DTX3L protein and mutation status by tissue, DB1



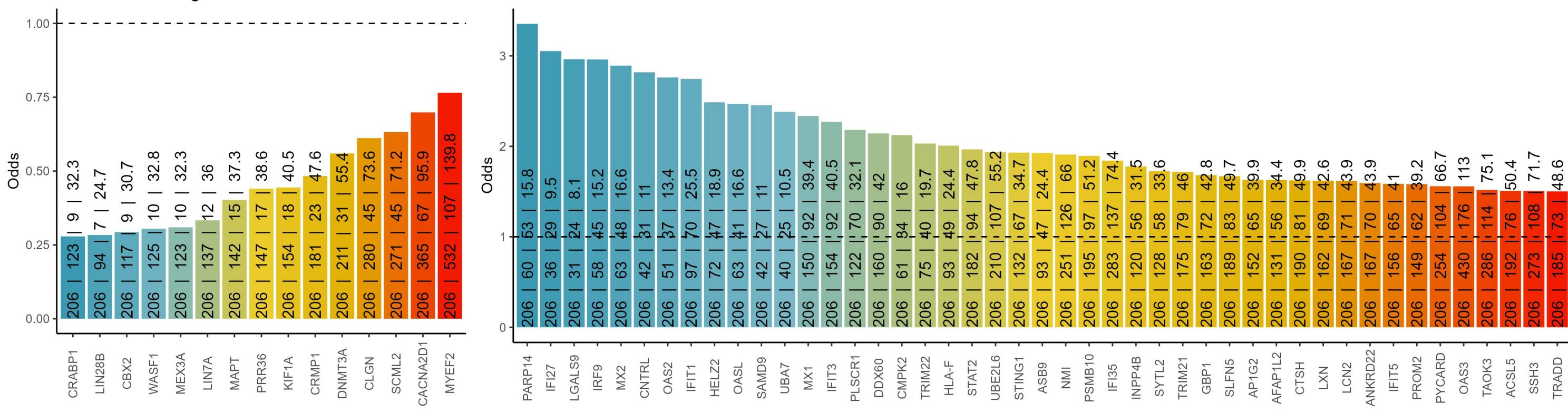
Cooccurrence with DTX3L protein in blood cancers, DB1

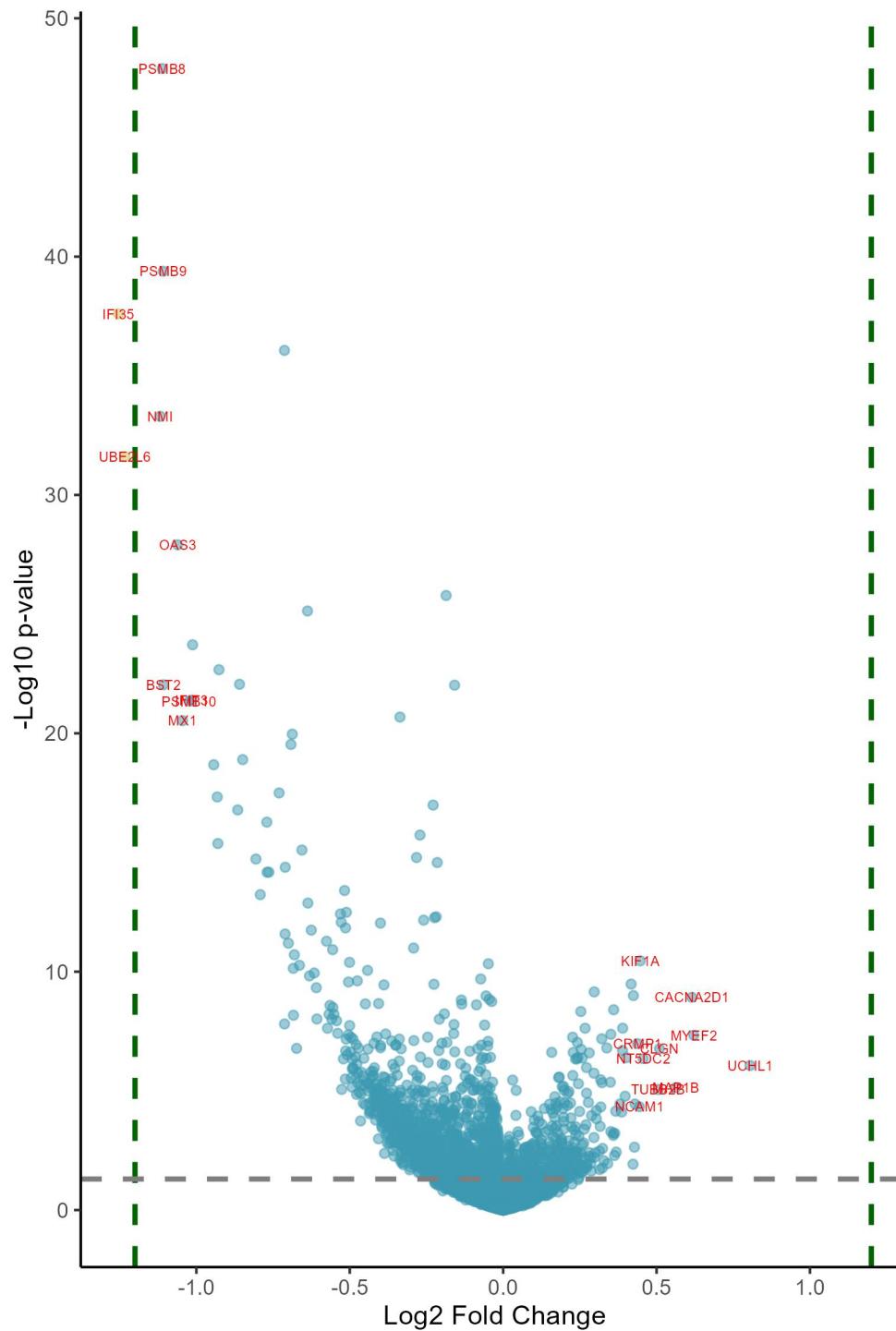
The text in the bars: incidence of DTX3L | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Cooccurrence with DTX3L protein in solid cancers, DB1

The text in the bars: incidence of DTX3L | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

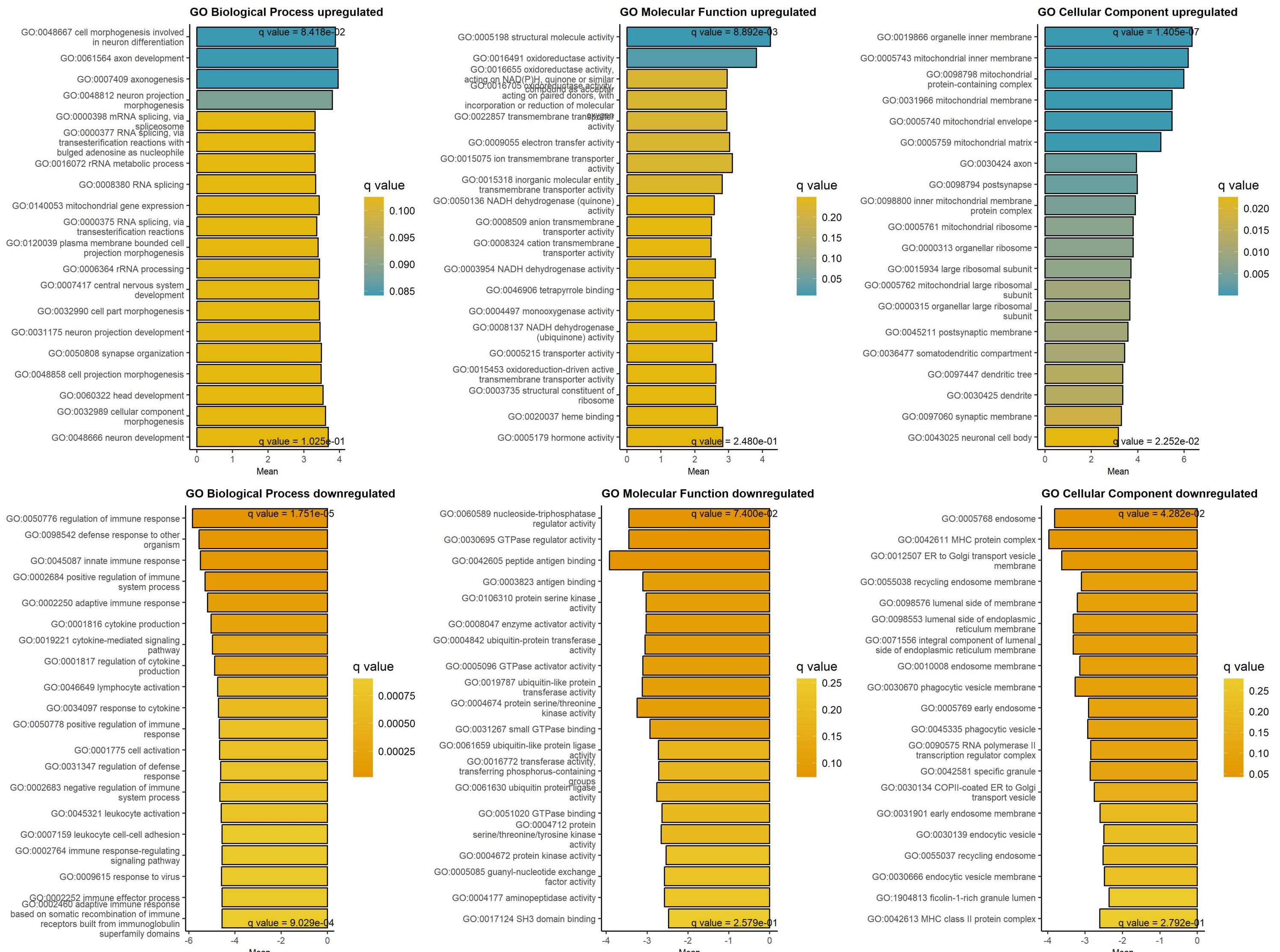




Downregulated at low/absent DTX3L Upregulated at low/absent DTX3L

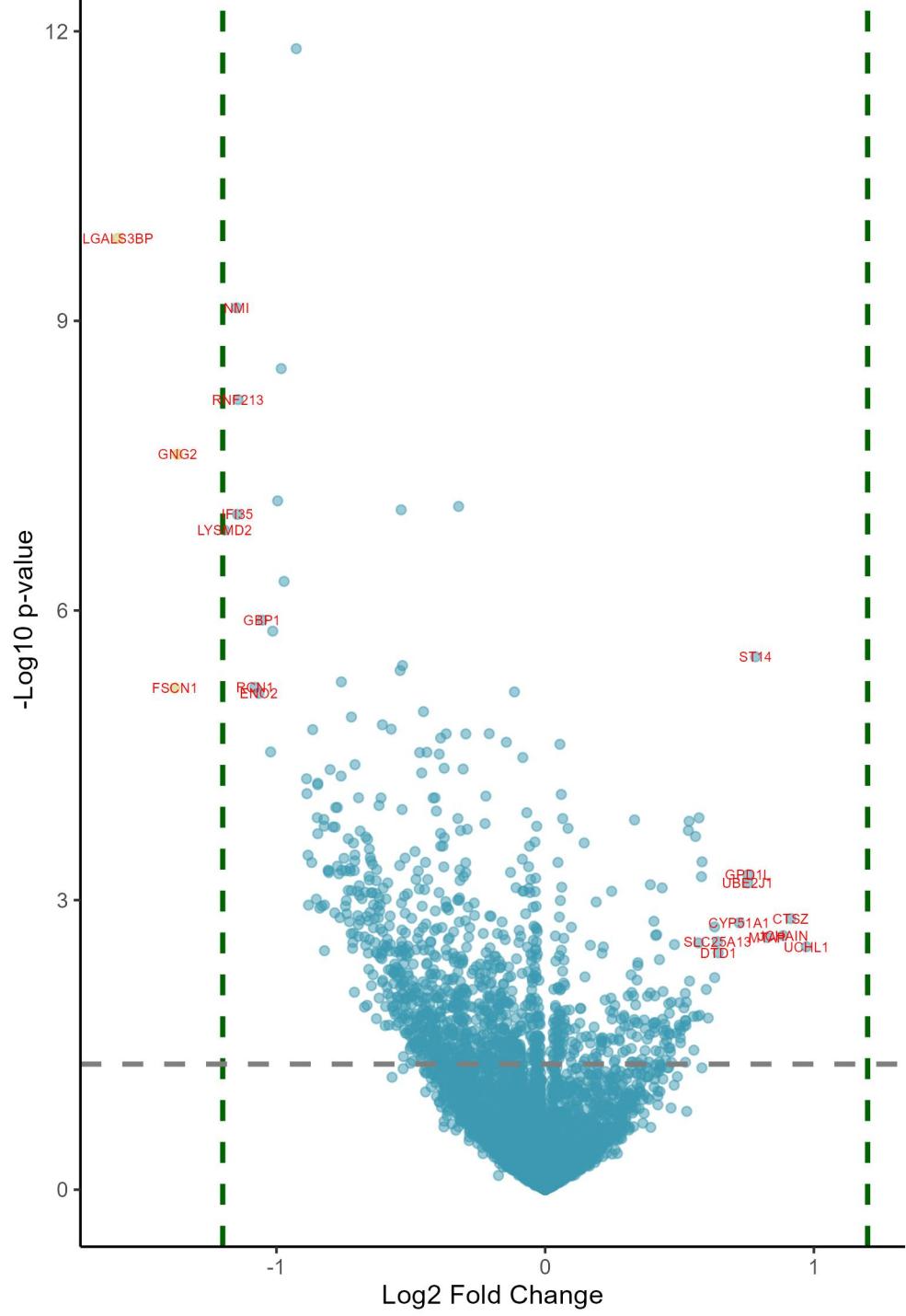
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.25	4.21e-35	IFI35	interferon induced protein 35	0.8	3.37e-05	UCHL1	ubiquitin C-terminal hydrolase L1
-1.23	2.30e-29	UBE2L6	ubiquitin conjugating enzyme E2 L6	0.62	2.89e-06	MYEF2	myelin expression factor 2
-1.12	5.53e-31	NMI	N-myc and STAT interactor	0.62	1.07e-07	CACNA2D1	calcium voltage-gated channel auxil
-1.11	4.27e-45	PSMB8	proteasome 20S subunit beta 8	0.56	2.04e-04	MAP1B	microtubule associated protein 1B
-1.11	9.14e-37	PSMB9	proteasome 20S subunit beta 9	0.51	8.38e-06	CLGN	calmegin
-1.11	4.24e-20	BST2	bone marrow stromal cell antigen 2	0.5	2.37e-04	TUBB2B	tubulin beta 2B class IIb
-1.06	1.02e-25	OAS3	2'-5'-oligoadenylate synthetase 3	0.46	1.87e-05	NT5DC2	5'-nucleotidase domain containing 2
-1.05	1.02e-18	MX1	MX dynamin like GTPase 1	0.45	4.17e-09	KIF1A	kinesin family member 1A
-1.02	1.75e-19	PSMB10	proteasome 20S subunit beta 10	0.44	8.71e-04	NCAM1	neural cell adhesion molecule 1
-1.02	1.67e-19	IFIT3	interferon induced protein with tet	0.44	5.66e-06	CRMP1	collapsin response mediator protein
-1.01	1.17e-21	ISG15	ISG15 ubiquitin like modifier	0.43	7.13e-04	INA	internexin neuronal intermediate fi
-0.94	6.00e-17	GSDMD	gasdermin D	0.43	1.81e-02	CKB	creatine kinase B
-0.93	1.24e-15	ICAM1	intercellular adhesion molecule 1	0.42	9.31e-08	LIN7A	lin-7 homolog A, crumbs cell polari
-0.93	9.30e-14	DDX60	DExD/H-box helicase 60	0.42	5.82e-02	ABCB6	ATP binding cassette subfamily B me
-0.93	1.19e-20	SP100	SP100 nuclear antigen	0.42	3.30e-08	CRABP1	cellular retinoic acid binding prot
-0.87	4.03e-15	TAP2	transporter 2, ATP binding cassette	0.4	1.74e-05	KIF5C	kinesin family member 5C
-0.86	4.24e-20	TAP1	transporter 1, ATP binding cassette	0.4	3.91e-04	MAP2	microtubule associated protein 2
-0.85	3.82e-17	HLA-B	major histocompatibility complex, c	0.39	1.57e-06	DPYSL5	dihydropyrimidinase like 5
-0.81	3.78e-13	TAOK3	TAO kinase 3	0.39	9.65e-06	CADM1	cell adhesion molecule 1
-0.79	1.00e-11	PYCARD	PYD and CARD domain containing	0.39	1.27e-03	THY1	Thy-1 cell surface antigen
-0.77	1.27e-14	IFI16	interferon gamma inducible protein	0.38	7.12e-04	PALM	paralemmin
-0.77	1.21e-12	STAT2	signal transducer and activator of	0.37	2.54e-02	DPYSL3	dihydropyrimidinase like 3
-0.76	1.21e-12	TRIM21	tripartite motif containing 21	0.37	1.19e-03	SCML2	Scm polycomb group protein like 2
-0.73	8.77e-16	IFIT1	interferon induced protein with tet	0.36	6.49e-03	MXRA7	matrix remodeling associated 7
-0.71	1.14e-33	PARP14	poly(ADP-ribose) polymerase family	0.36	3.17e-02	ALDH2	aldehyde dehydrogenase 2 family mem
-0.71	1.10e-06	ARHGDI	Rho GDP dissociation inhibitor beta	0.36	3.14e-07	SEPTIN5	septin 5
-0.71	3.49e-10	SERPINB1	serpin family B member 1	0.36	7.65e-03	SMARCA1	SWI/SNF related, matrix associated,
-0.71	7.90e-13	RNF213	ring finger protein 213	0.36	6.53e-03	P3H3	prolyl 3-hydroxylase 3
-0.7	8.14e-10	CAPG	capping actin protein, gelsolin lik	0.35	2.68e-06	MAPT	microtubule associated protein tau

GAGE analysis on upregulated and downregulated proteins at low/absent DTX3L protein, DB1



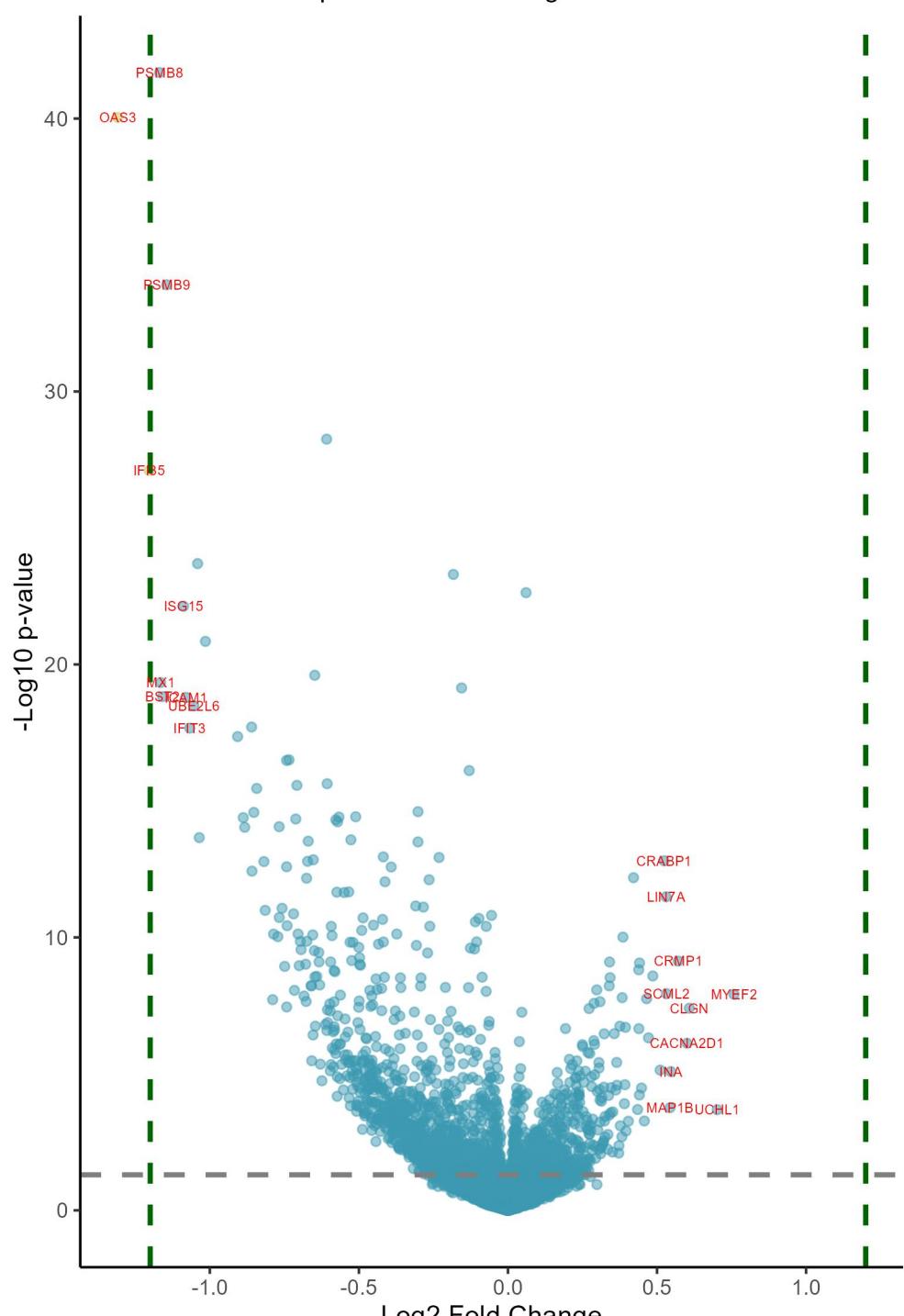
Differentially expressed proteins in blood cancers at absence/low amount of DTX3L , DB1

p-value < 0.05 & logFC > 1.2



Downregulated in blood cancers at low/absent DTX3L Upregulated in blood cancers at low/absent DTX3L

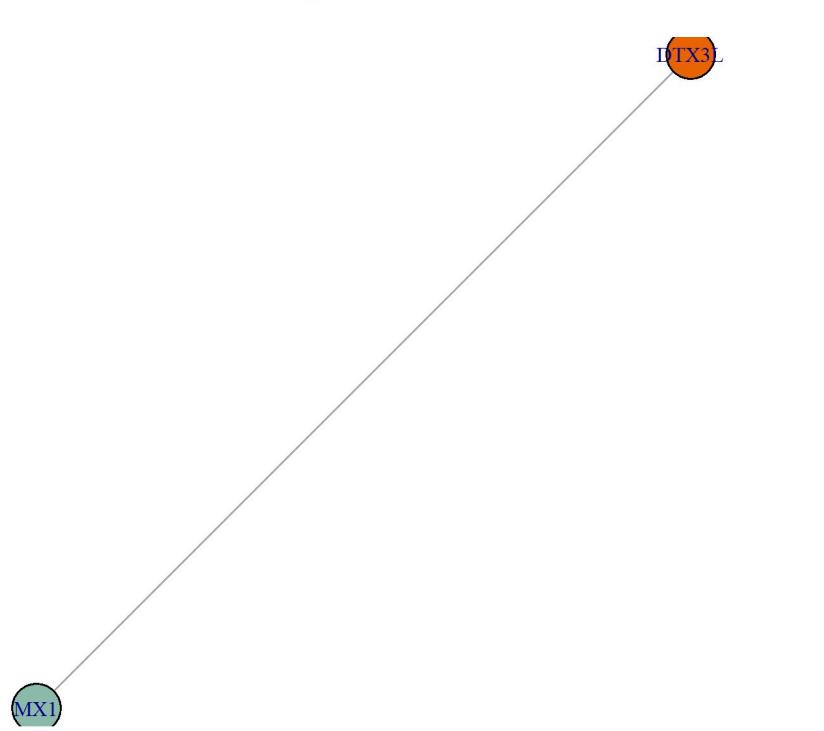
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.59	3.09e-07	LGALS3BP	galectin 3 binding protein	0.97	7.20e-02	UCHL1	ubiquitin C-terminal hydrolase L1
-1.38	2.02e-03	FSCN1	fascin actin-bundling protein 1	0.91	4.92e-02	CTSZ	cathepsin Z
-1.37	2.29e-05	GNG2	G protein subunit gamma 2	0.89	6.25e-02	JCHAIN	joining chain of multimeric IgA and
-1.19	8.15e-05	LYSMD2	LysM domain containing 2	0.83	6.38e-02	MTAP	methylthioadenosine phosphorylase
-1.15	1.22e-06	NMI	N-myc and STAT interactor	0.78	1.26e-03	ST14	ST14 transmembrane serine protease
-1.15	6.11e-05	IFI35	interferon induced protein 35	0.75	2.89e-02	GPD1L	glycerol-3-phosphate dehydrogenase
-1.14	7.24e-06	RNF213	ring finger protein 213	0.75	3.21e-02	UBE2J1	ubiquitin conjugating enzyme E2 J1
-1.08	2.02e-03	RCN1	reticulocalbin 1	0.72	5.24e-02	CYP51A1	cytochrome P450 family 51 subfamily
-1.07	2.09e-03	ENO2	enolase 2	0.64	7.65e-02	DTD1	D-aminoacyl-tRNA deacylase 1
-1.05	5.98e-04	GBP1	guanylate binding protein 1	0.64	6.76e-02	SLC25A13	solute carrier family 25 member 13
-1.02	5.33e-03	RHOC	ras homolog family member C	0.63	1.07e-01	SAMHD1	SAM and HD domain containing deoxyn
-1.01	7.25e-04	GSDMD	gasdermin D	0.63	5.63e-02	DUSP23	dual specificity phosphatase 23
-1	6.03e-05	DPP4	dipeptidyl peptidase 4	0.61	1.73e-01	IKZF3	IKAROS family zinc finger 3
-0.98	4.15e-06	PARP14	poly(ADP-ribose) polymerase family	0.6	1.26e-01	ALG1	ALG1 chitobiosyldiphosphodolichol b
-0.97	2.55e-04	LUZP1	leucine zipper protein 1	0.58	2.58e-02	OXR1	oxidation resistance 1
-0.93	5.03e-09	UBE2L6	ubiquitin conjugating enzyme E2 L6	0.58	2.99e-01	NDUFB11	NADH:ubiquinone oxidoreductase subu
-0.89	8.00e-03	GNPNAT1	glucosamine-phosphate N-acetyltrans	0.58	2.95e-02	EDEM3	ER degradation enhancing alpha-mann
-0.89	1.06e-02	SYNJ2BP	synaptotagmin 2 binding protein	0.58	1.69e-01	PLCG2	phospholipase C gamma 2
-0.88	2.40e-02	CLIP2	CAP-Gly domain containing linker pr	0.57	1.46e-02	EPHX1	epoxide hydrolase 1
-0.88	4.16e-02	CASP6	caspase 6	0.57	6.81e-02	PRTN3	proteinase 3
-0.87	2.58e-02	SAMSN1	SAM domain, SH3 domain and nuclear	0.57	1.71e-01	SYK	spleen associated tyrosine kinase
-0.87	4.07e-03	SLFN11	schlafin family member 11	0.56	1.80e-02	AZU1	azurocidin 1
-0.85	3.87e-02	CD99	CD99 molecule (Xg blood group)	0.55	2.45e-01	ITGAL	integrin subunit alpha L
-0.85	1.46e-02	BRD3	bromodomain containing 3	0.55	1.71e-01	ATP6V0A1	ATPase H ⁺ transporting V0 subunit a
-0.85	8.84e-03	VAMP5	vesicle associated membrane protein	0.54	1.11e-01	GPAA1	glycosylphosphatidylinositol anchor
-0.85	8.70e-03	RNF149	ring finger protein 149	0.54	1.49e-02	CES1	carboxylesterase 1
-0.85	1.71e-02	ETV6	ETS variant transcription factor 6	0.53	1.64e-02	SDC1	syndecan 1
-0.84	4.24e-02	PTPRCAP	protein tyrosine phosphatase recept	0.53	4.86e-01	XPNPEP3	X-prolyl aminopeptidase 3
-0.83	4.19e-02	DPYD	dihydropyrimidine dehydrogenase	0.53	1.46e-01	LYN	LYN proto-oncogene, Src family tyro

Differentially expressed proteins in solid cancers at absence/low amount of DTX3L , DB1
p-value < 0.05 & logFC > 1.2

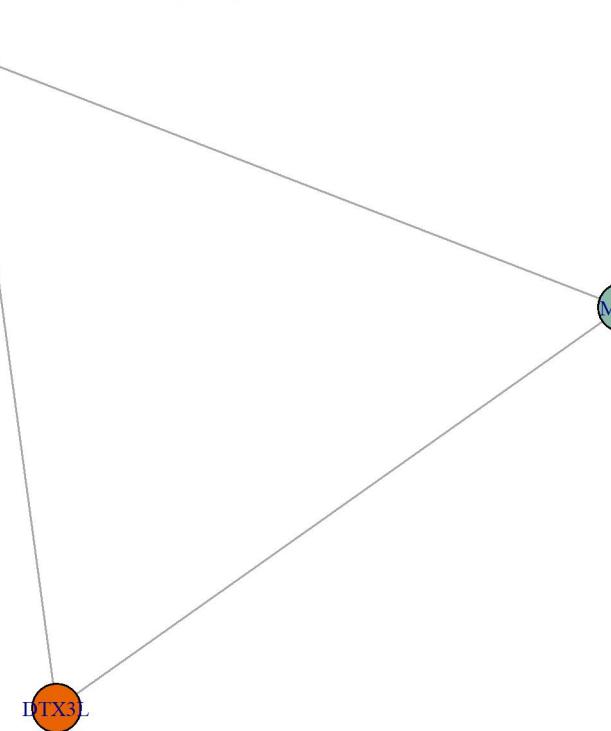
Downregulated in solid cancers at low/absent DTX3L Upregulated in solid cancers at low/absent DTX3L

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.31	2.01e-37	OAS3	2'-5'-oligoadenylate synthetase 3	0.76	5.98e-07	MYEF2	myelin expression factor 2
-1.2	8.63e-25	IFI35	interferon induced protein 35	0.7	2.54e-03	UCHL1	ubiquitin C-terminal hydrolase L1
-1.17	6.87e-39	PSMB8	proteasome 20S subunit beta 8	0.61	1.71e-06	CLGN	calmegin
-1.17	2.35e-17	MX1	MX dynamin like GTPase 1	0.6	2.45e-05	CACNA2D1	calcium voltage-gated channel auxil
-1.16	6.67e-17	BST2	bone marrow stromal cell antigen 2	0.57	4.95e-08	CRMP1	collapsin response mediator protein
-1.14	2.05e-31	PSMB9	proteasome 20S subunit beta 9	0.55	1.87e-04	INA	internexin neuronal intermediate fi
-1.09	4.92e-20	ISG15	ISG15 ubiquitin like modifier	0.54	2.22e-03	MAP1B	microtubule associated protein 1B
-1.08	6.71e-17	ICAM1	intercellular adhesion molecule 1	0.53	5.67e-07	SCML2	Scm polycomb group protein like 2
-1.07	7.53e-16	IFIT3	interferon induced protein with tet	0.53	3.81e-10	LIN7A	lin-7 homolog A, crumbs cell polari
-1.05	1.29e-16	UBE2L6	ubiquitin conjugating enzyme E2 L6	0.52	2.37e-11	CRABP1	cellular retinoic acid binding prot
-1.04	1.92e-21	SP100	SP100 nuclear antigen	0.51	1.71e-04	F5	coagulation factor V
-1.04	3.98e-12	DDX60	DExD/H-box helicase 60	0.49	1.53e-07	KIF1A	kinesin family member 1A
-1.01	8.63e-19	NMI	N-myc and STAT interactor	0.47	1.59e-05	MAP1A	microtubule associated protein 1A
-0.91	1.46e-15	HLA-B	major histocompatibility complex, c	0.46	8.32e-07	DPYSL5	dihydropyrimidinase like 5
-0.89	8.79e-13	TAP2	transporter 2, ATP binding cassette	0.46	5.50e-03	TUBB2B	tubulin beta 2B class IIb
-0.88	1.71e-12	STAT2	signal transducer and activator of	0.45	6.00e-04	PALM	paramelemin
-0.86	7.25e-16	TAP1	transporter 1, ATP binding cassette	0.44	5.60e-08	MAPT	microtubule associated protein tau
-0.86	5.07e-11	PSMB10	proteasome 20S subunit beta 10	0.44	9.64e-04	NT5DC2	5'-nucleotidase domain containing 2
-0.85	6.24e-13	LGALS3	galectin 3	0.44	8.20e-06	DPYSL4	dihydropyrimidinase like 4
-0.84	8.90e-14	IFIT1	interferon induced protein with tet	0.44	9.38e-08	DNMT3A	DNA methyltransferase 3 alpha
-0.82	2.41e-11	CD44	CD44 molecule (Indian blood group)	0.43	2.52e-03	THY1	Thy-1 cell surface antigen
-0.81	1.11e-09	ANXA3	annexin A3	0.42	8.65e-11	WASF1	WASP family member 1
-0.79	8.94e-07	TACSTD2	tumor associated calcium signal tra	0.4	5.57e-03	FADS1	fatty acid desaturase 1
-0.79	6.55e-09	GSDMD	gasdermin D	0.4	1.06e-02	FADS2	fatty acid desaturase 2
-0.77	7.78e-09	CAVIN1	caveolae associated protein 1	0.39	7.42e-06	SYT1	synaptotagmin 1
-0.77	1.67e-12	FHL2	four and a half LIM domains 2	0.39	4.73e-04	KIF5C	kinesin family member 5C
-0.77	1.94e-09	PYCARD	PYD and CARD domain containing	0.39	1.74e-03	CORO1A	coronin 1A
-0.76	9.50e-10	SERPINB1	serpin family B member 1	0.39	8.02e-09	CBX2	chromobox 2
-0.75	7.10e-08	PLSCR1	phospholipid scramblase 1	0.38	7.66e-07	PRR36	proline rich 36

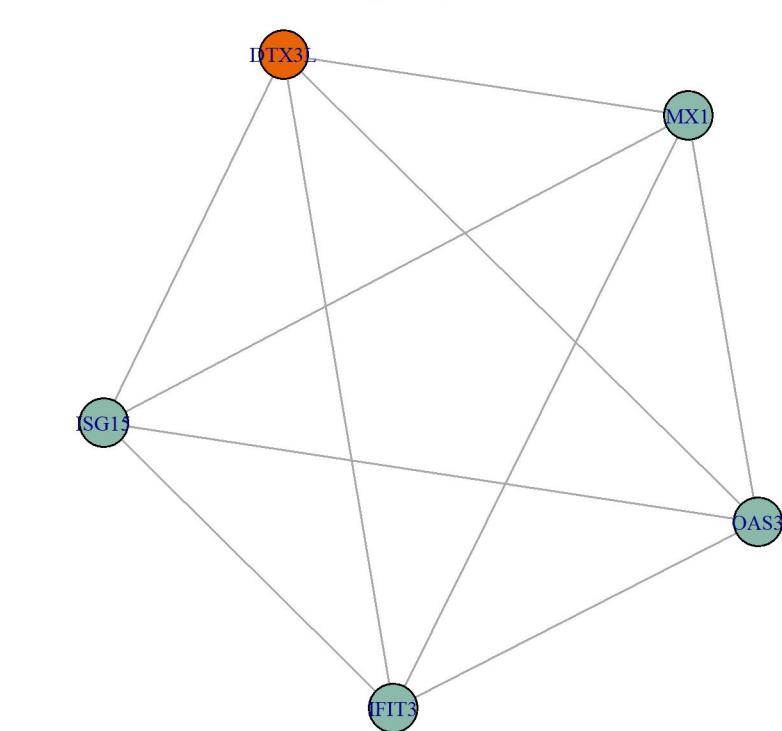
DTX3L network, DB1, all Pearson r > 0.5

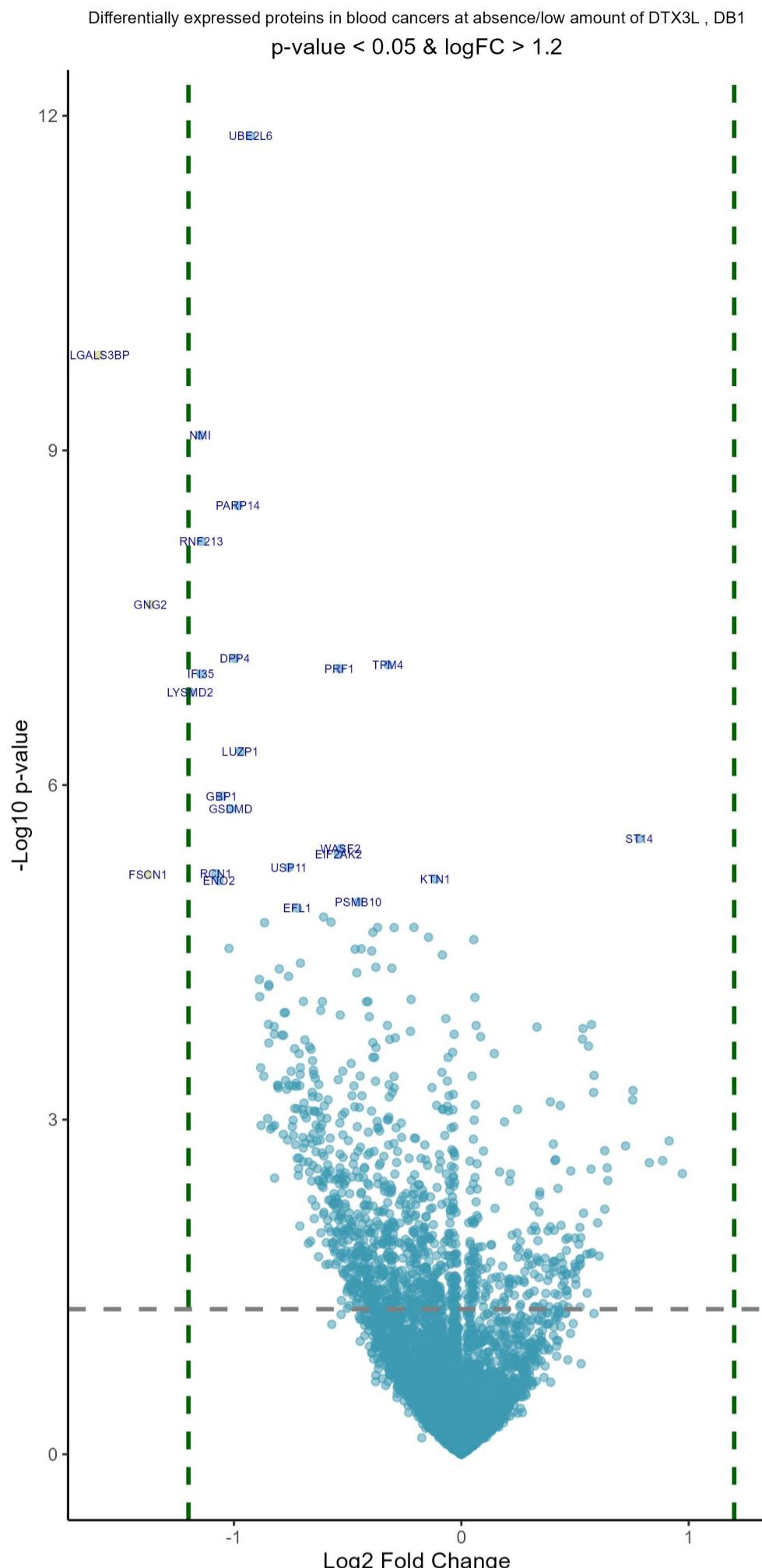


DTX3L network, DB1, all Pearson r > 0.45

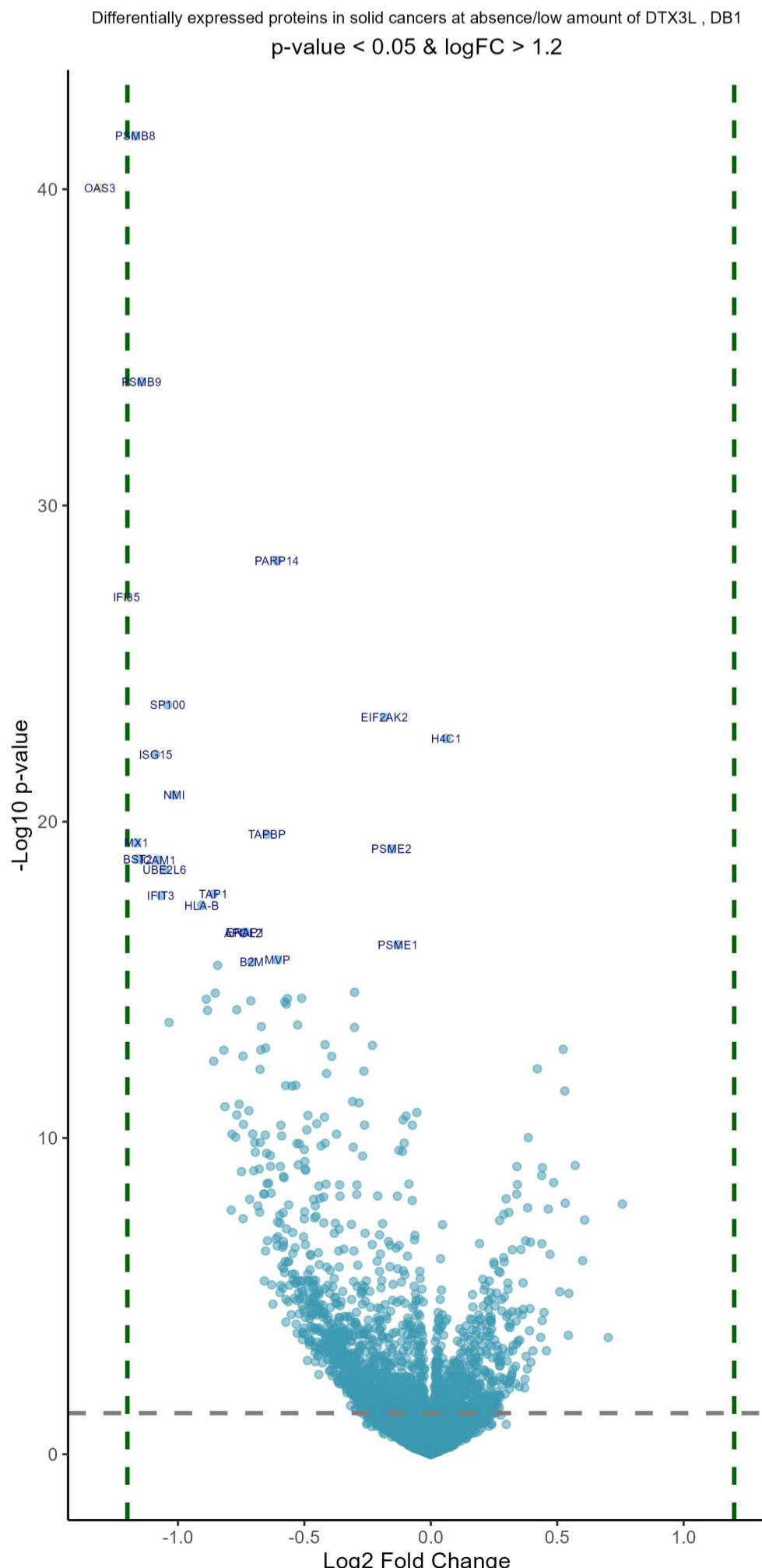


DTX3L network, DB1, all Pearson r > 0.4



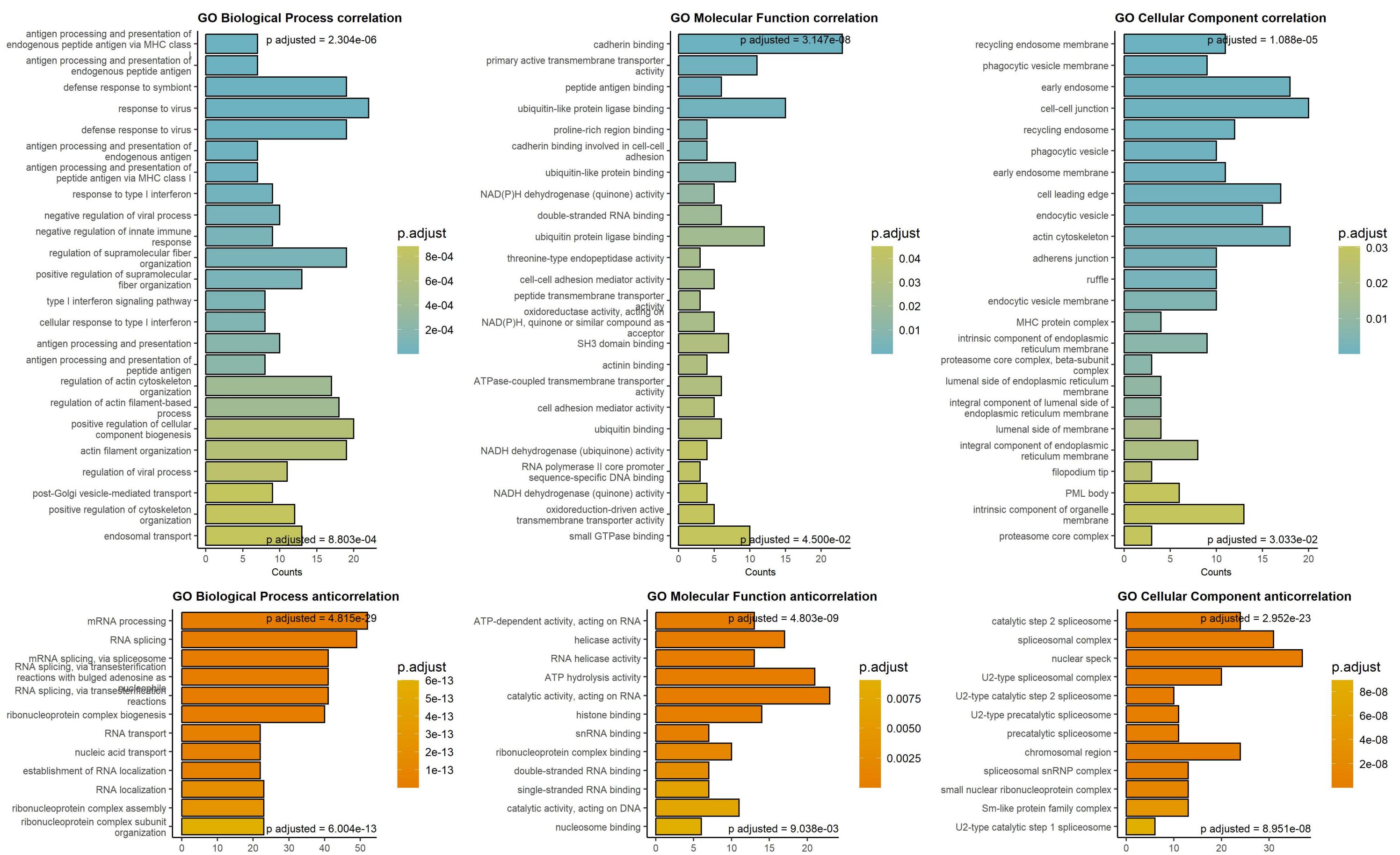


Sorted by p values!							
Downregulated in blood cancers at low/absent DTX3L				Upregulated in blood cancers at low/absent DTX3L			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.93	5.03e-09	UBE2L6	ubiquitin conjugating enzyme E2 L6	0.78	1.26e-03	ST14	ST14 transmembrane serine protease
-1.59	3.09e-07	LGALS3BP	galectin 3 binding protein	0.05	4.76e-03	FARSA	phenylalanyl-tRNA synthetase subunit
-1.15	1.22e-06	NMI	N-myc and STAT interactor	0.06	1.06e-02	TKT	transketolase
-0.98	4.15e-06	PARP14	Poly(ADP-ribose) polymerase family	0.57	1.46e-02	EPHX1	epoxide hydrolase 1
-1.14	7.24e-06	RNF213	ring finger protein 213	0.07	1.46e-02	SRM	spermidine synthase
-1.37	2.29e-05	GNG2	G protein subunit gamma 2	0.33	1.47e-02	PACSIN1	protein kinase C and casein kinase
-1	6.03e-05	DPP4	dipeptidyl peptidase 4	0.54	1.49e-02	CES1	carboxylesterase 1
-0.32	6.03e-05	TPM4	tropomyosin 4	0.09	1.62e-02	CLPP	caseinolytic mitochondrial matrix protein p
-0.54	6.03e-05	PRF1	perforin 1	0.53	1.64e-02	SDC1	syndecan 1
-1.15	6.11e-05	IFI35	interferon induced protein 35	0.56	1.80e-02	AZU1	azurocidin 1
-1.19	8.15e-05	LYSMD2	LysM domain containing 2	0.15	1.94e-02	MYDGF	myeloid derived growth factor
-0.97	2.55e-04	LUZP1	leucine zipper protein 1	0.58	2.58e-02	OXR1	oxidation resistance 1
-1.05	5.98e-04	GBP1	guanylate binding protein 1	0.05	2.58e-02	ATP5F1D	ATP synthase F1 subunit delta
-1.01	7.25e-04	GSDMD	gasdermin D	0.75	2.89e-02	GPD1L	glycerol-3-phosphate dehydrogenase
-0.53	1.45e-03	WASF2	WASP family member 2	0.58	2.95e-02	EDEM3	ER degradation enhancing alpha-man
-0.54	1.55e-03	EIF2AK2	eukaryotic translation initiation factor 2A kinase 2	0.75	3.21e-02	UBE2J1	ubiquitin conjugating enzyme E2 J1
-0.76	1.92e-03	USP11	ubiquitin specific peptidase 11	0.39	3.31e-02	CEBPA	CCAAT enhancer binding protein alpha
-1.08	2.02e-03	RCN1	reticulocalbin 1	0.06	3.47e-02	MYCBP	MYC binding protein
-1.38	2.02e-03	FSCN1	fascin actin-bundling protein 1	0.44	3.47e-02	BST1	bone marrow stromal cell antigen 1
-0.11	2.09e-03	KTN1	kinectin 1	0.25	3.52e-02	TXNDC5	thioredoxin domain containing 5
-1.07	2.09e-03	ENO2	enolase 2	0.06	3.91e-02	CS	citrate synthase
-0.45	3.09e-03	PSMB10	proteasome 20S subunit beta 10	0.19	4.00e-02	SOD1	superoxide dismutase 1
-0.72	3.38e-03	EFL1	elongation factor like GTPase 1	0.05	4.86e-02	SND1	staphylococcal nuclease and tudor domain containing 1
-0.61	3.90e-03	RNF181	ring finger protein 181	0.91	4.92e-02	CTSZ	cathepsin Z
-0.57	4.07e-03	TRAFD1	TRAF-type zinc finger domain containing 1	0.4	5.15e-02	SPECC1L	sperm antigen with calponin homolog
-0.87	4.07e-03	SLFN11	schlafin family member 11	0.72	5.24e-02	CYP51A1	cytochrome P450 family 51 subfamily A member 1
-0.21	4.07e-03	MACF1	microtubule actin crosslinking factor 1	0.63	5.63e-02	DUSP23	dual specificity phosphatase 23
-0.37	4.07e-03	STAT1	signal transducer and activator of transcription 1	0.1	5.63e-02	P4HB	prolyl 4-hydroxylase subunit beta
-0.3	4.07e-03	ZNF48	zinc finger protein 48	0.41	6.19e-02	CEND1	cell cycle exit and neuronal differentiation
-0.39	4.35e-03	TRIP12	thyroid hormone receptor interactor 1	0.41	6.25e-02	MAGEC1	MAGE family member C1
-0.14	4.67e-03	CD47	CD47 molecule	0.89	6.25e-02	JCHAIN	joining chain of multimeric IgA and IgM
-1.02	5.33e-03	RHOC	ras homolog family member C	0.04	6.28e-02	MDH2	malate dehydrogenase 2
-0.44	5.33e-03	ALK	ALK receptor tyrosine kinase	0.83	6.38e-02	MTAP	methylthioadenosine phosphorylase
-0.47	5.33e-03	BRK1	BRICK1 subunit of SCAR/WAVE actin nucleating complex	0.07	6.46e-02	PPIB	peptidylprolyl isomerase B
-0.39	5.38e-03	TAPBP	TAP binding protein	0.64	6.76e-02	SLC25A13	solute carrier family 25 member 13
-0.08	5.68e-03	PSME2	proteasome activator subunit 2	0.57	6.81e-02	PRTN3	proteinase inhibitor 3
-0.71	6.57e-03	C12orf57	chromosome 12 open reading frame 57	0.48	7.03e-02	SH2B2	SH2B adaptor protein 2
-0.38	6.88e-03	OGA	O-GlcNAcase	0.17	7.06e-02	MAN2B1	mannosidase alpha class 2B member
-0.31	6.88e-03	GRB5	guanine nucleotide binding protein G (rho) 5	0.97	7.20e-02	UCHL1	ubiquitin C-terminal hydrolase L1

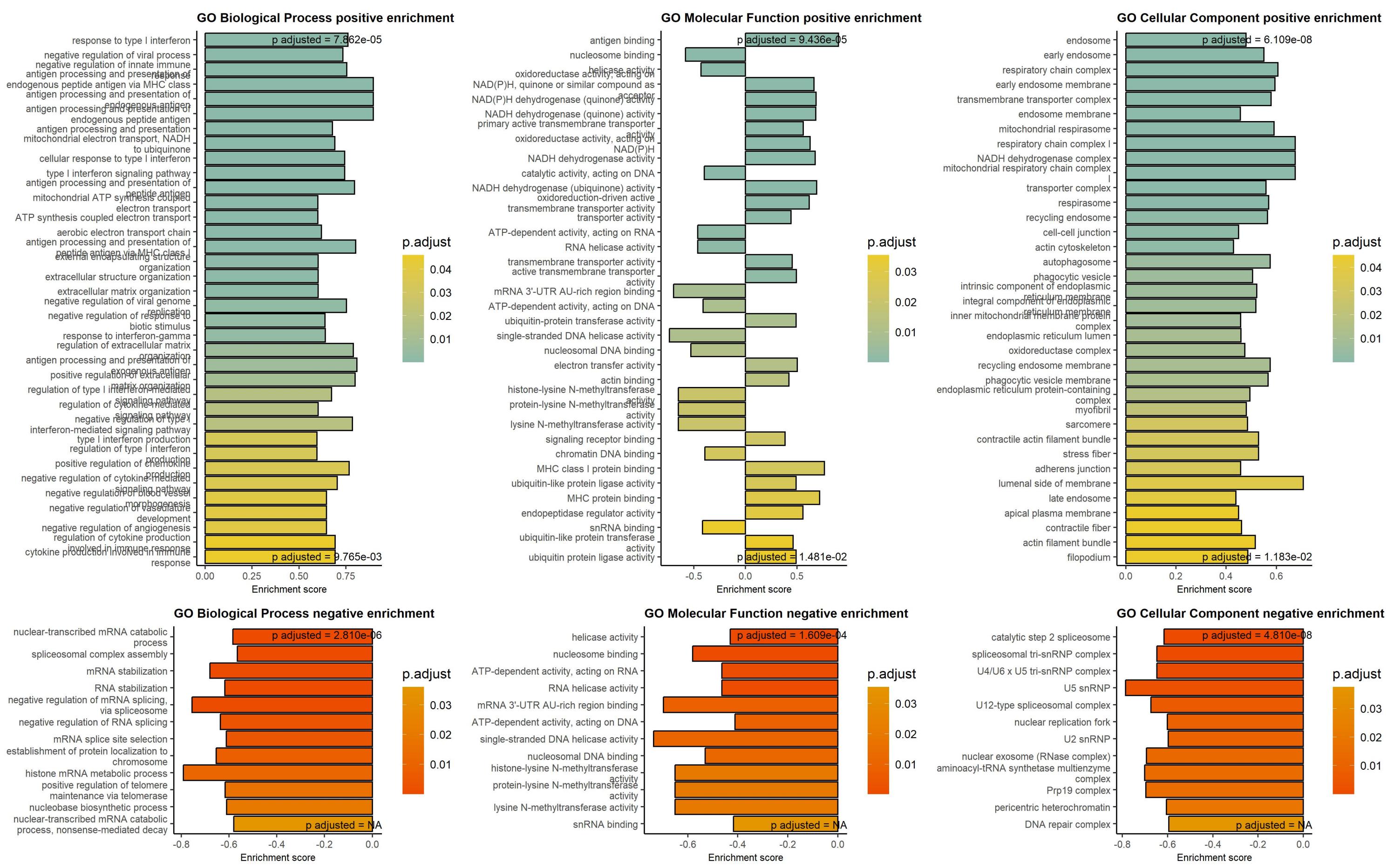


Sorted by p values!							
Downregulated in solid cancers at low/absent DTX3L				Upregulated in solid cancers at low/absent DTX3L			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.17	6.87e-39	PSMB8	proteasome 20S subunit beta 8	0.06	1.73e-20	H4C1	H4 clustered histone 1
-0.31	2.01e-37	OAS3	2'-5'-oligoadenylate synthetase 3	0.52	2.37e-11	CRABP1	cellular retinoic acid binding prot
-0.14	2.05e-31	PSMB9	proteasome 20S subunit beta 9	0.42	8.65e-11	WASF1	WASP family member 1
-0.61	7.41e-26	PARP14	Poly(ADP-ribose) polymerase family	0.53	3.81e-10	LIN7A	lin-7 homolog A, crumbs cell polarity
-0.12	8.63e-25	IFI35	interferon induced protein 35	0.39	8.02e-09	CBX2	chromobox 2
-0.04	1.92e-21	SP100	SP100 nuclear antigen	0.57	4.95e-08	CRMP1	collapsin response mediator protein
-0.18	4.19e-21	EIF2AK2	eukaryotic translation initiation f	0.34	5.20e-08	MEX3A	mex-3 RNA binding family member A
-0.09	4.92e-20	ISG15	ISG15 ubiquitin like modifier	0.44	5.60e-08	MAPT	microtubule associated protein tau
-0.01	8.63e-19	NMI	N-myc and STAT interactor	0.44	9.38e-08	DNMT3A	DNA methyltransferase 3 alpha
-0.65	1.38e-17	TAPBP	TAP binding protein	0.49	1.53e-07	KIF1A	kinesin family member 1A
-0.17	2.35e-17	MX1	MX dynamin like GTPase 1	0.34	1.69e-07	CPLX2	complexin 2
-0.16	3.45e-17	PSME2	proteasome activator subunit 2	0.34	3.21e-07	LIN28B	lin-28 homolog B
-0.16	6.67e-17	BST2	bone marrow stromal cell antigen 2	0.3	4.24e-07	DCX	doublecortin
-0.08	6.71e-17	ICAM1	intercellular adhesion molecule 1	0.53	5.67e-07	SCML2	Scm polycomb group protein like 2
-0.05	1.29e-16	UBE2L6	ubiquitin conjugating enzyme E2 L6	0.76	5.98e-07	MYEF2	myelin expression factor 2
-0.86	7.25e-16	TAP1	transporter 1, ATP binding cassette	0.38	7.66e-07	PRR36	proline rich 36
-0.07	7.53e-16	IFIT3	interferon induced protein with tet	0.46	8.32e-07	DPYSL5	dihydropyrimidinase like 5
-0.91	1.46e-15	HLA-B	major histocompatibility complex, c	0.31	1.04e-06	GAP43	growth associated protein 43
-0.73	9.91e-15	ERAP1	endoplasmic reticulum aminopeptidas	0.29	1.18e-06	NCAM2	neural cell adhesion molecule 2
-0.74	9.93e-15	APOL2	apolipoprotein L2	0.61	1.71e-06	CLGN	calmegin
-0.13	2.23e-14	PSME1	proteasome activator subunit 1	0.27	1.75e-06	SOGA3	SOGA family member 3
-0.61	6.50e-14	MVP	major vault protein	0.05	2.28e-06	SAFB	scaffold attachment factor B
-0.71	7.16e-14	B2M	beta-2-microglobulin	0.38	6.85e-06	SEPTIN5	septin 5
-0.84	8.90e-14	IFIT1	interferon induced protein with tet	0.39	7.42e-06	SYT1	synaptotagmin 1
-0.3	6.10e-13	STAT1	signal transducer and activator of	0.19	8.19e-06	RCOR2	REST corepressor 2
-0.85	6.24e-13	LGALS3	galectin 3	0.44	8.20e-06	DPYSL4	dihydropyrimidinase like 4
-0.51	8.65e-13	LGALS3BP	galectin 3 binding protein	0.36	1.17e-05	TCF12	transcription factor 12
-0.57	8.65e-13	NCEH1	neutral cholesterol ester hydrolase	0.32	1.18e-05	CHD7	chromodomain helicase DNA binding protein 7
-0.89	8.79e-13	TAP2	transporter 2, ATP binding cassette	0.47	1.59e-05	MAP1A	microtubule associated protein 1A
-0.71	9.57e-13	S100A10	S100 calcium binding protein A10	0.29	1.99e-05	SNAP25	synaptosome associated protein 25
-0.58	9.95e-13	MYOF	myoferlin	0.04	2.14e-05	HNRNPH1	heterogeneous nuclear ribonucleoprotein H
-0.57	1.14e-12	ITPRID2	ITPR interacting domain containing	0.6	2.45e-05	CACNA2D1	calcium voltage-gated channel auxiliary subunit 2D
-0.77	1.67e-12	FHL2	four and a half LIM domains 2	0.29	2.63e-05	PHF20L1	PHD finger protein 20 like 1
-0.88	1.71e-12	STAT2	signal transducer and activator of	0.25	2.68e-05	NOVA2	NOVA alternative splicing regulator
-0.04	3.98e-12	DDX60	DExD/H-box helicase 60	0.25	3.12e-05	ZNF516	zinc finger protein 516
-0.53	4.66e-12	IRF9	interferon regulatory factor 9	0.27	4.82e-05	PRPH	peripherin
-0.67	5.09e-12	MX2	MX dynamin like GTPase 2	0.27	5.23e-05	NR0B1	nuclear receptor subfamily 0 group 2 member 1
-0.3	5.29e-12	IFI27	interferon alpha inducible protein	0.21	8.30e-05	MLLT11	MLLT11 transcription factor 7 cofactor

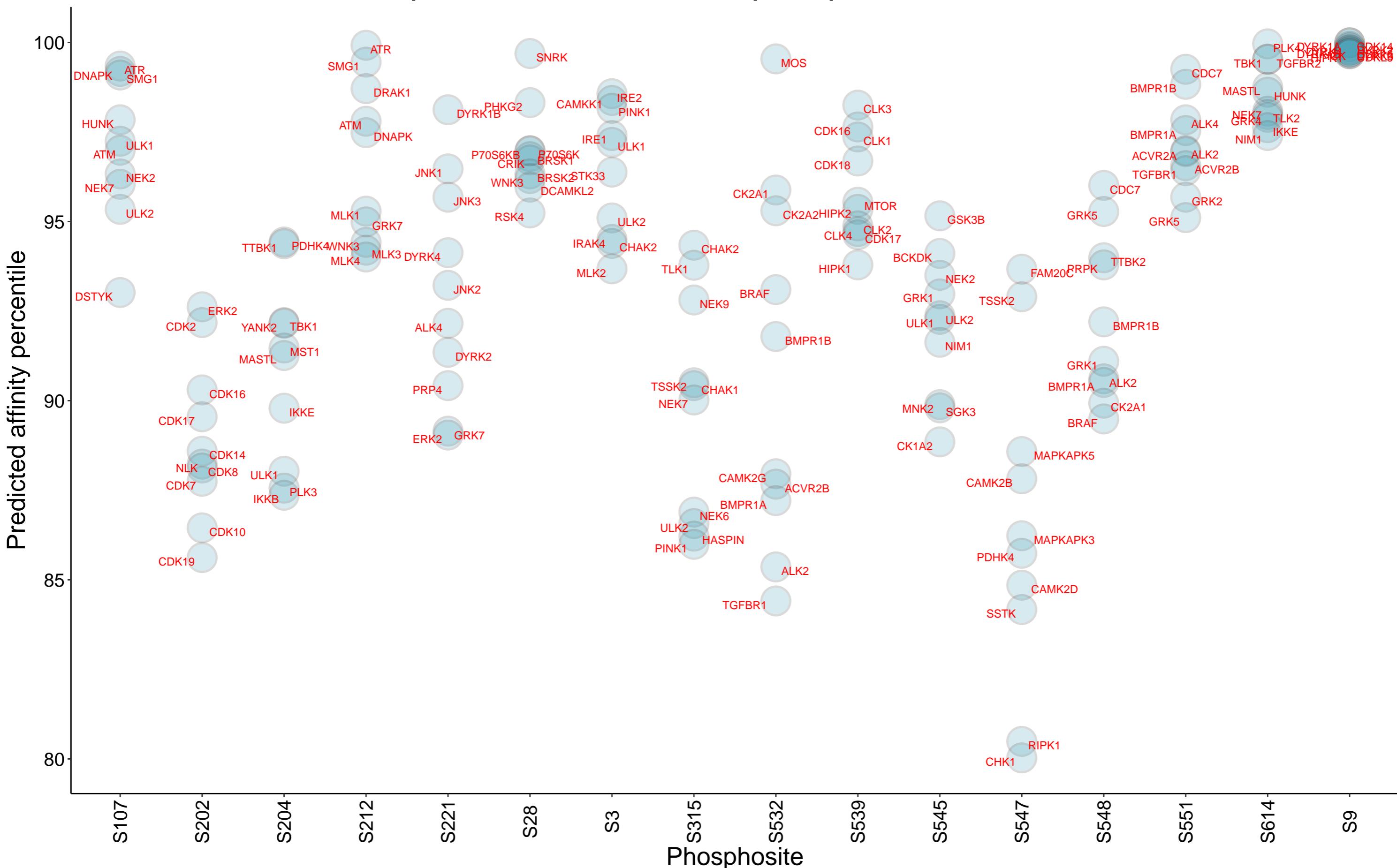
Top 250 correlation coefficients overrepresentation, DTX3L protein, DB1



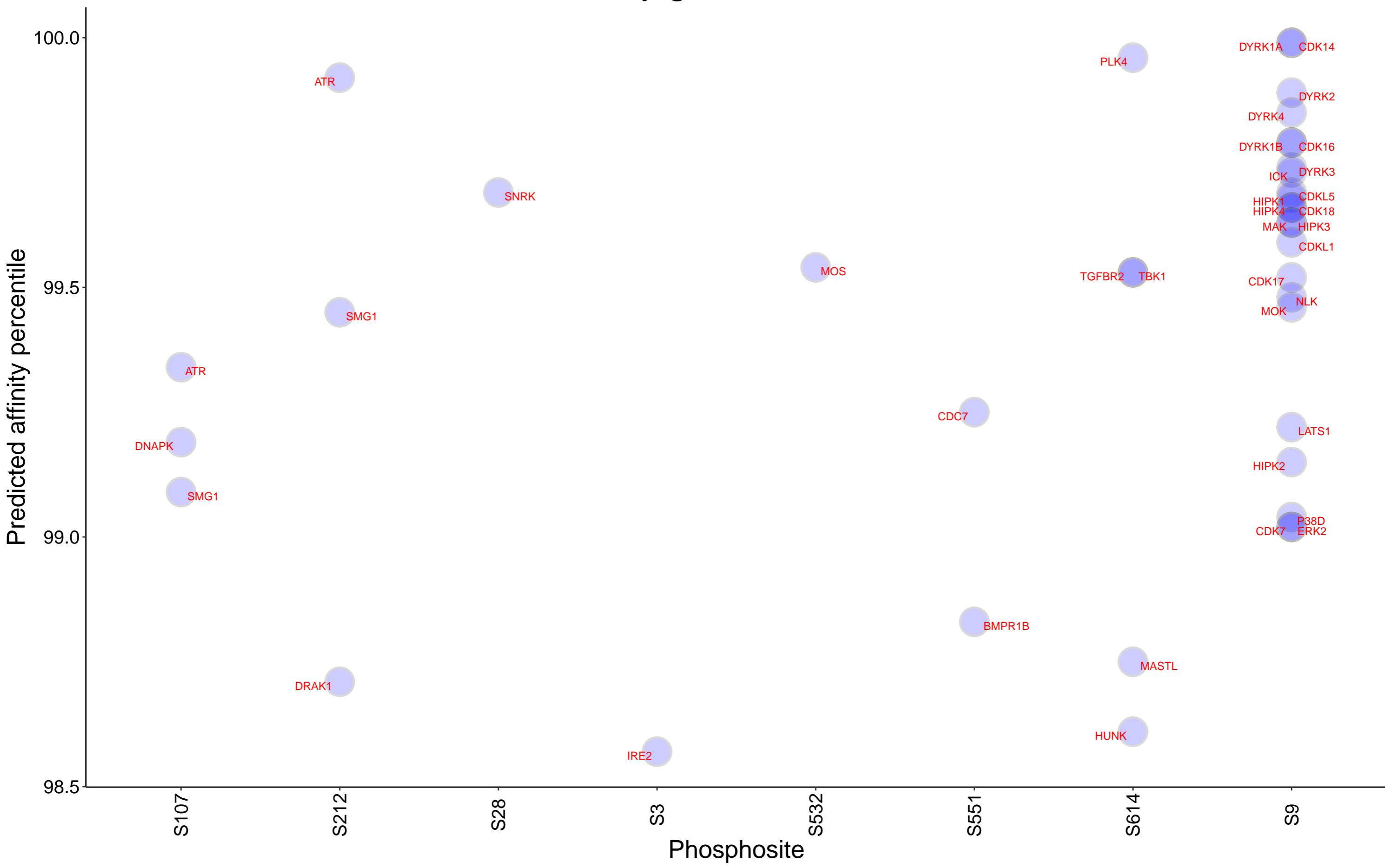
Gene Set Enrichment analysis on protein correlation coefficients, DTX3L protein, DB1



Top 10 kinases for each phosphosite in DTX3L



Kinases with affinity greater than 98.5% to DTX3L



Top 15 positive correlation coefficients for DTX3L protein by tissue, DB1

Beware of false positives in tissues with small number of samples

