

BCL2L11

Protein name: B2L11 ;

UNIPROT: O43521 ;

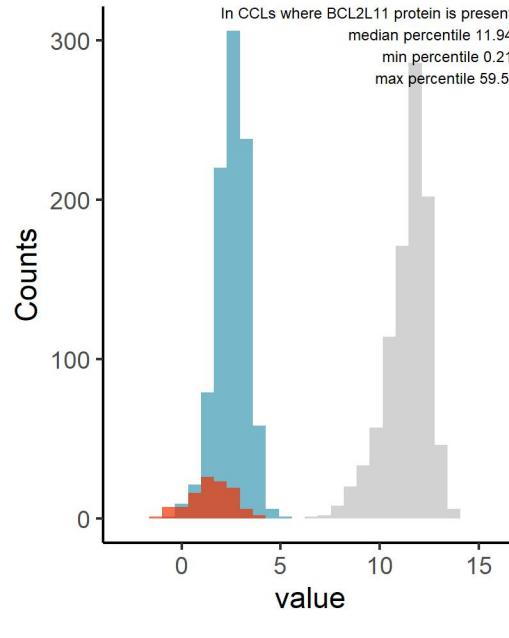
Gene name: BCL2 like 11

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

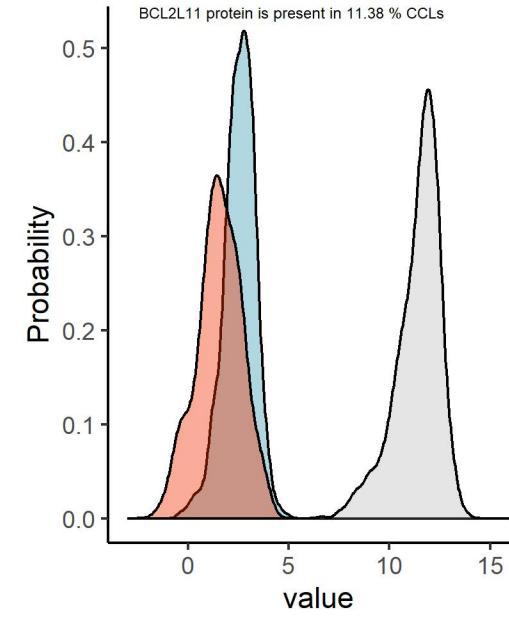
Sanger Institute Protein Database 2 (DB2), protein presence is less certain

8498 proteins in same 949 CCLs

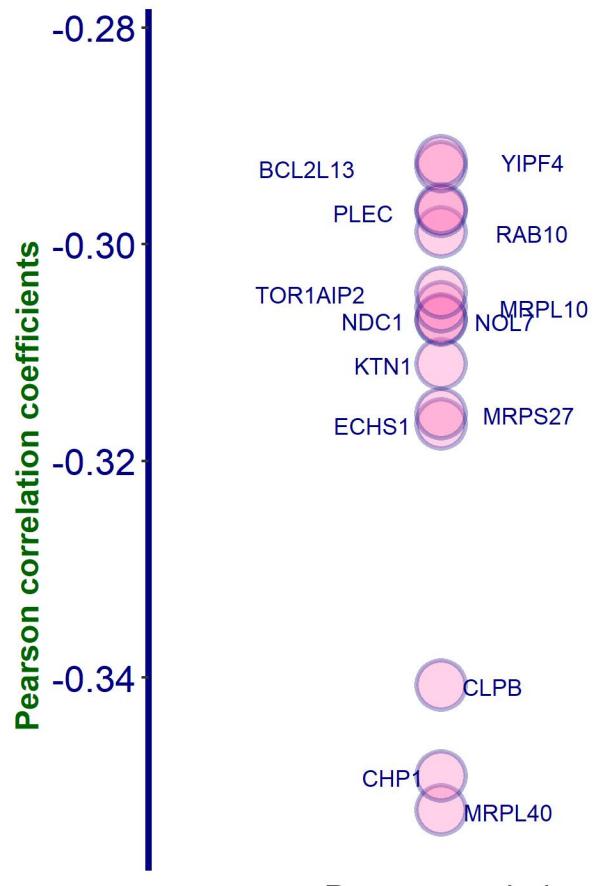
Histogram of BCL2L11 protein compared to proteins with low and high abundance



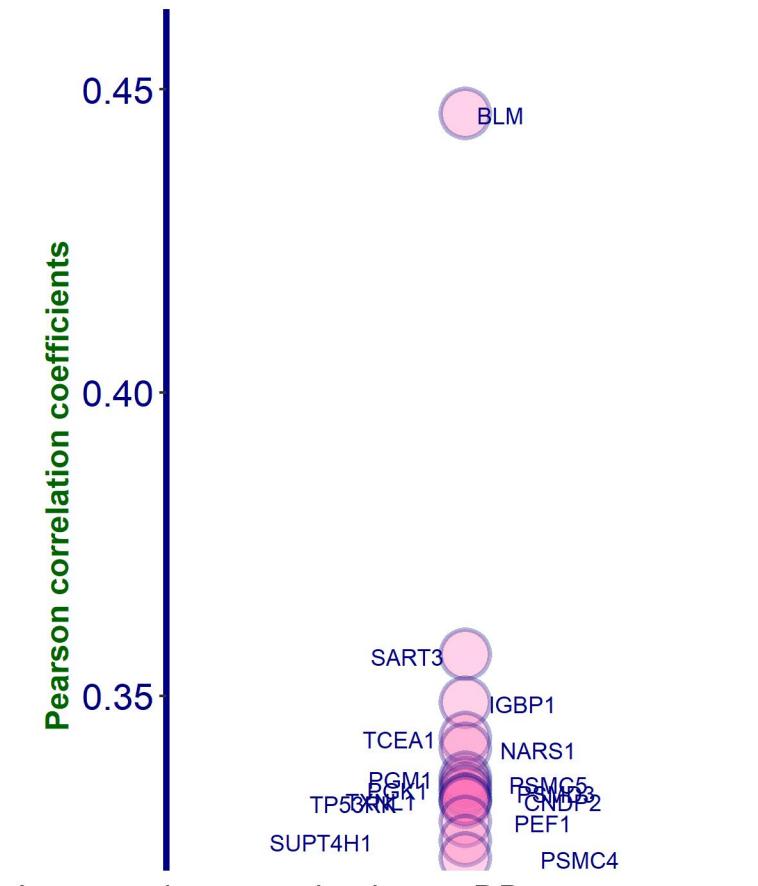
Density plot of BCL2L11 protein compared to proteins with low and high abundance



Negative correlations of BCL2L11 protein, DB2

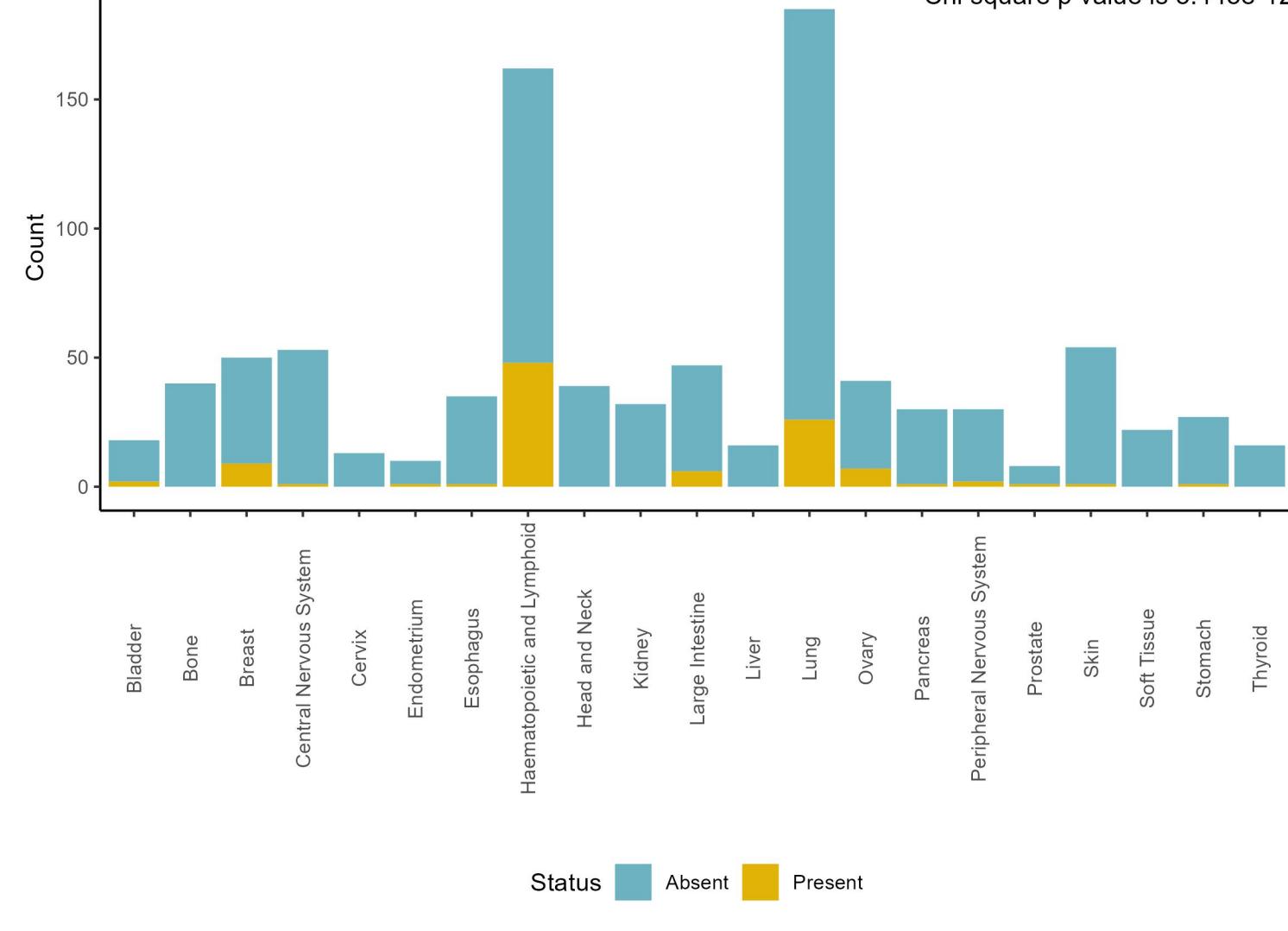
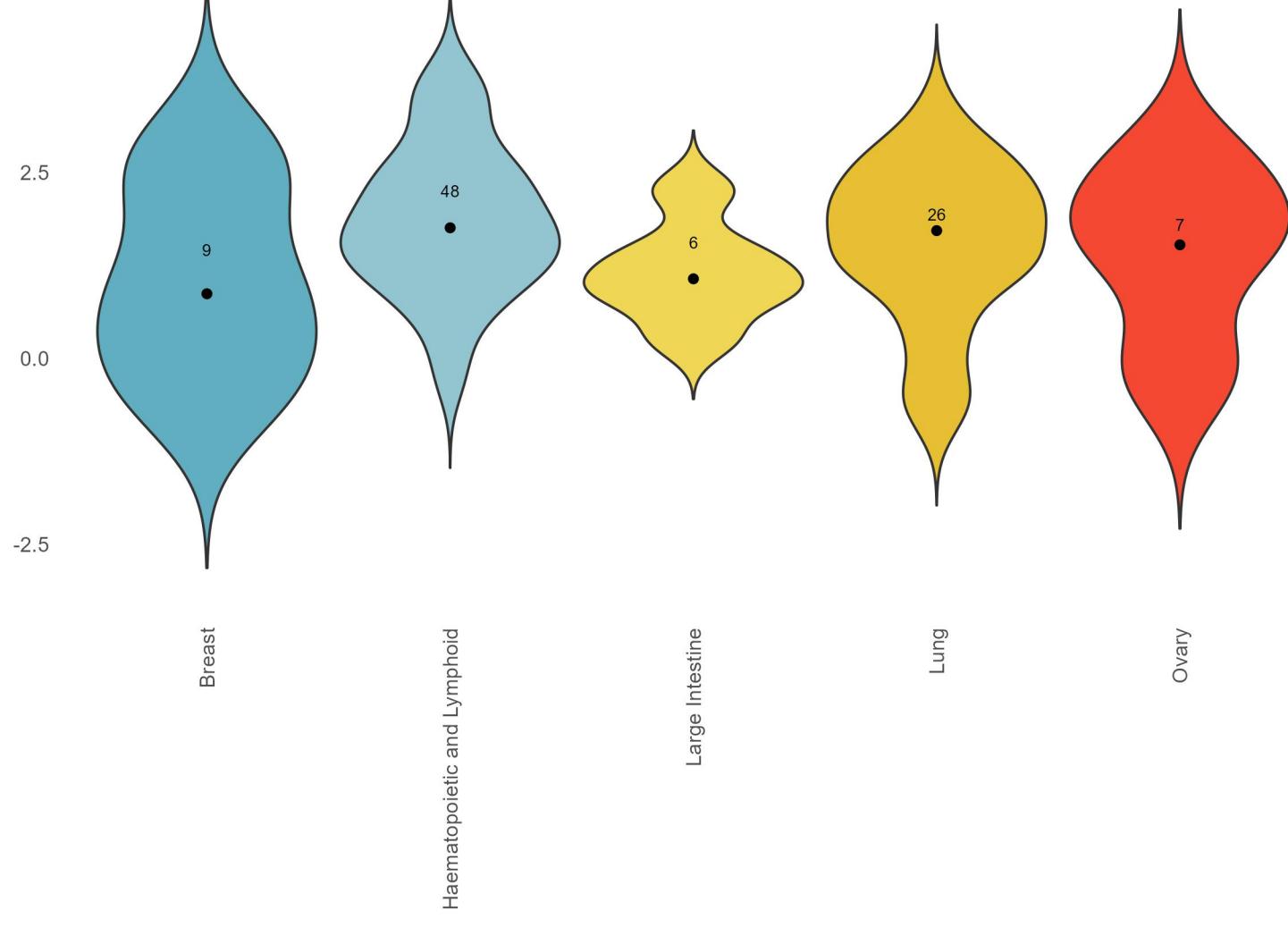


Positive correlations of BCL2L11 protein, DB2



Amount of BCL2L11 protein, number of CCLs where it is present by tissue, DB2

ANOVA p value is 2.066e-01

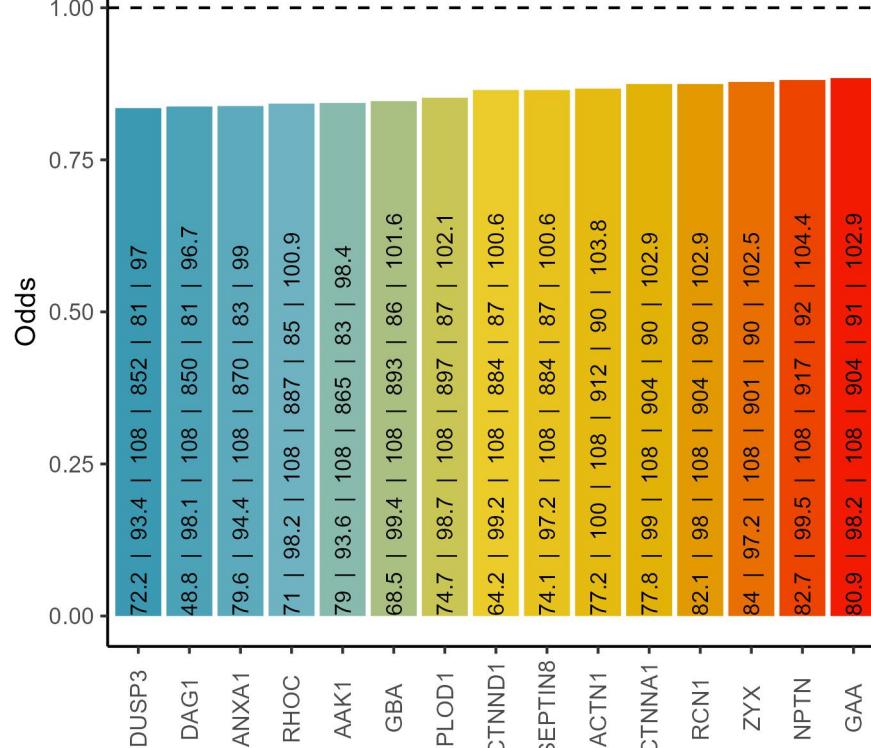


Cooccurrence with BCL2L11 protein, DB2

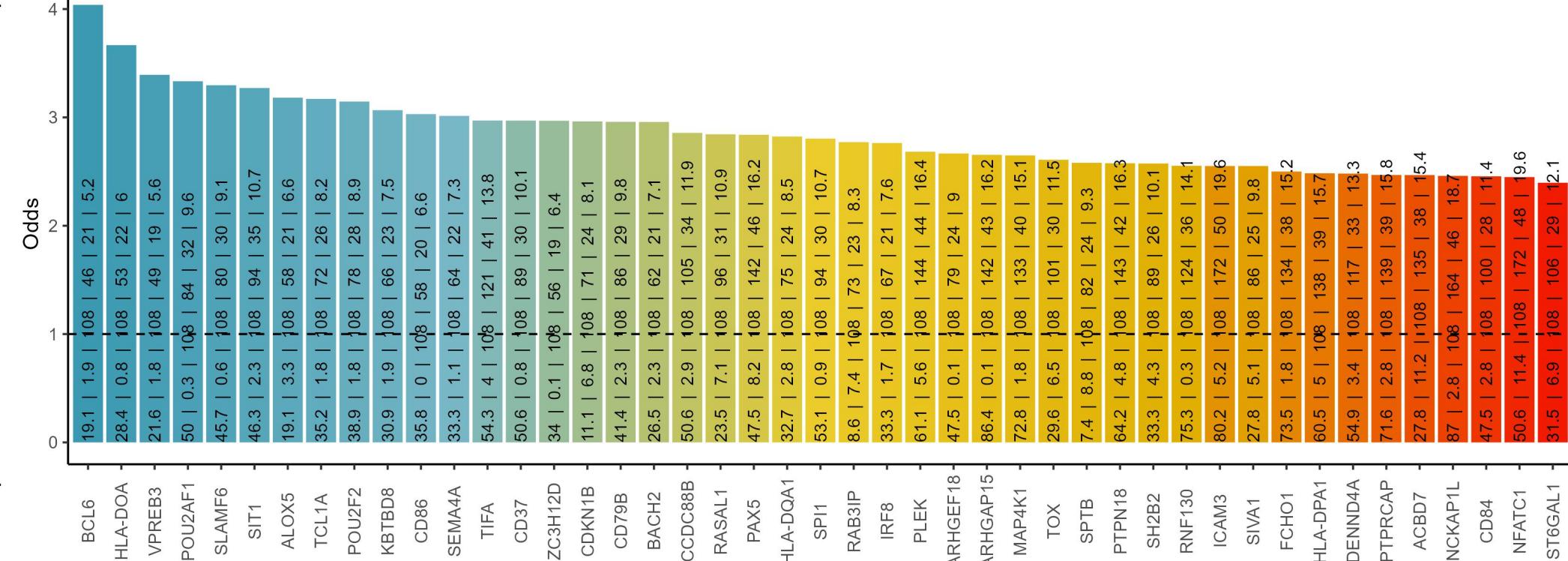
% of BCL2L11 in blood cancers: 29.6 ; % of BCL2L11 in solid cancers: 7.5

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of BCL2L11 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

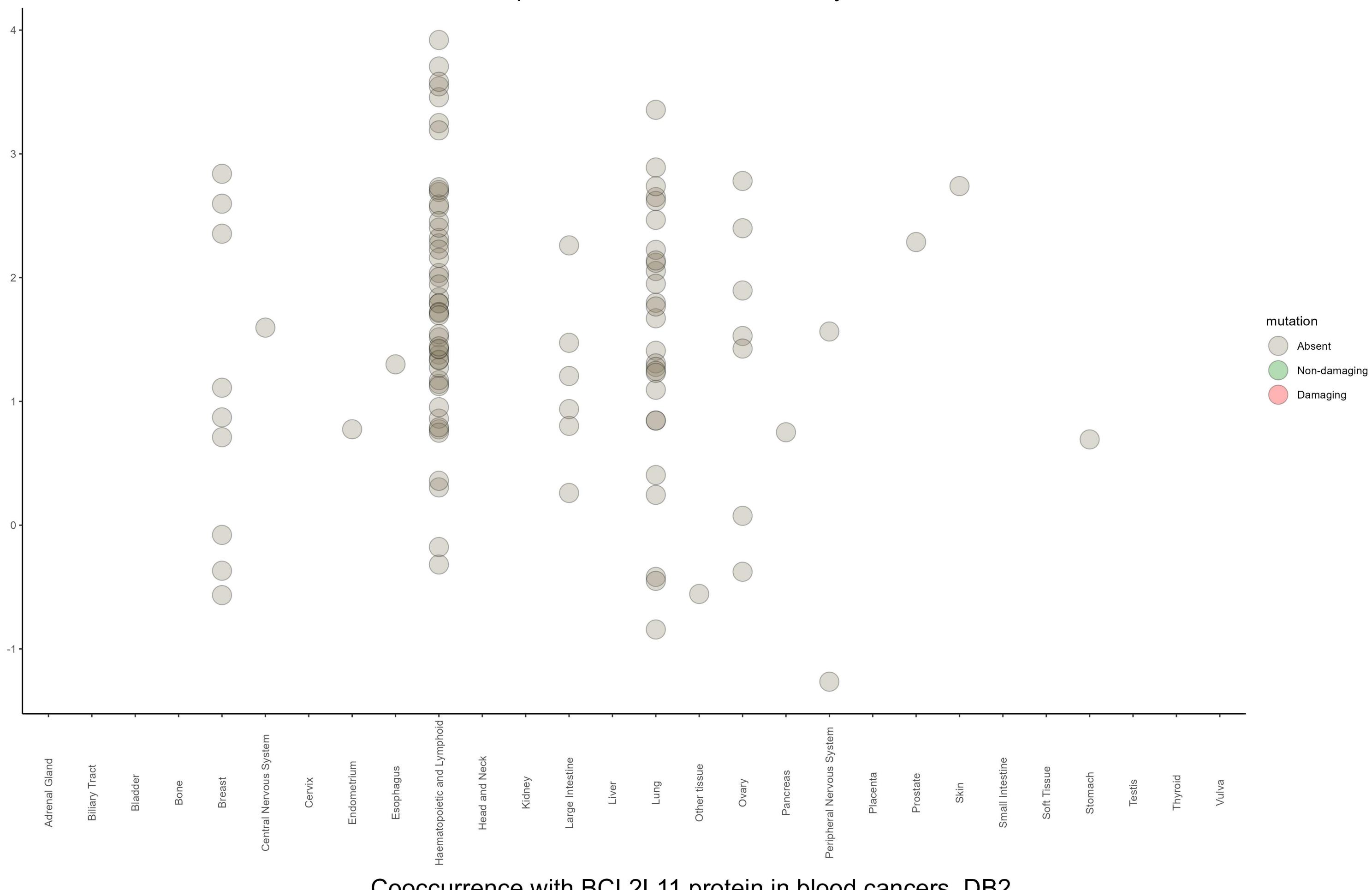
Negative cooccurrence



Positive cooccurrence

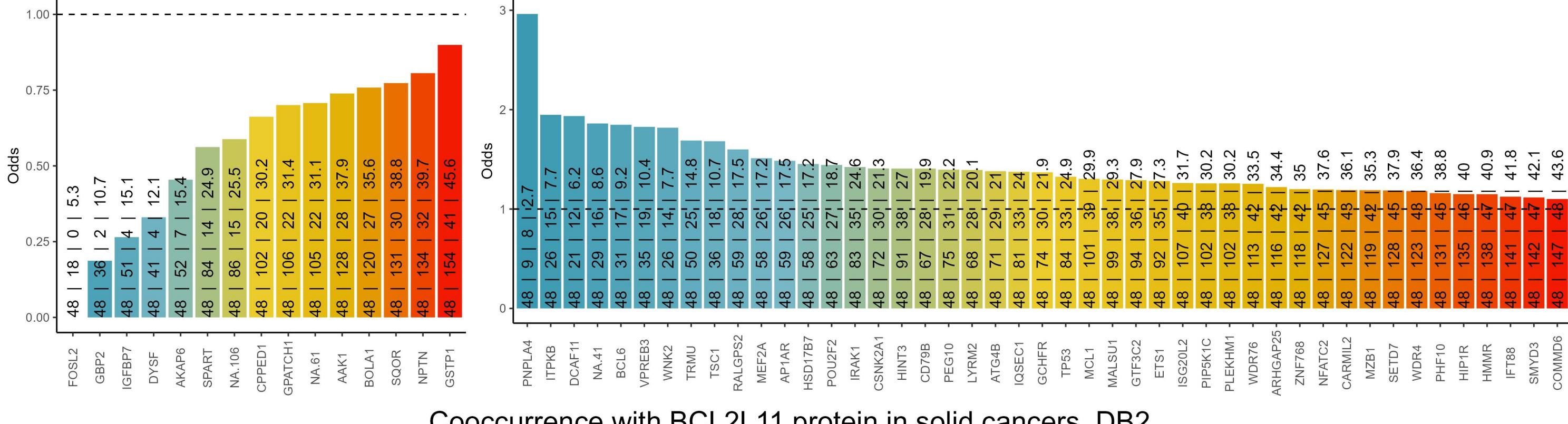


Amount of BCL2L11 protein and mutation status by tissue, DB2



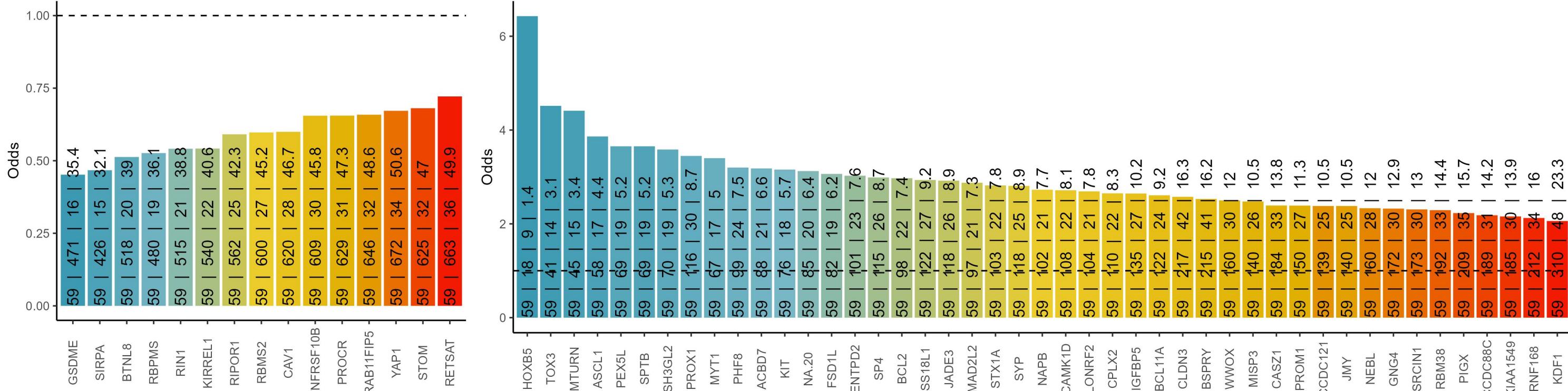
Cooccurrence with BCL2L11 protein in blood cancers, DB2

The text in the bars: incidence of BCL2L11 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

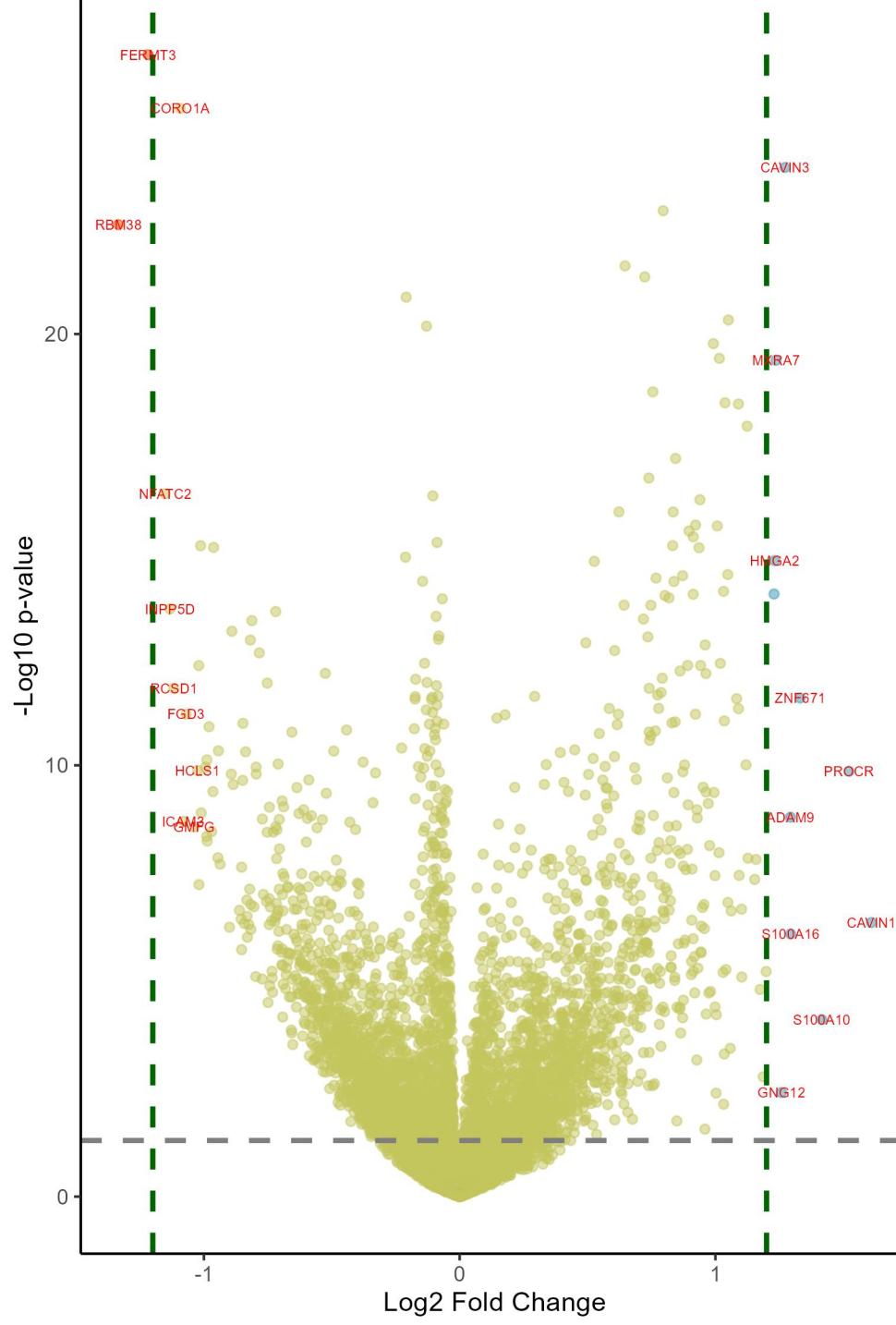


Cooccurrence with BCL2L11 protein in solid cancers, DB2

The text in the bars: incidence of BCL2L11 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

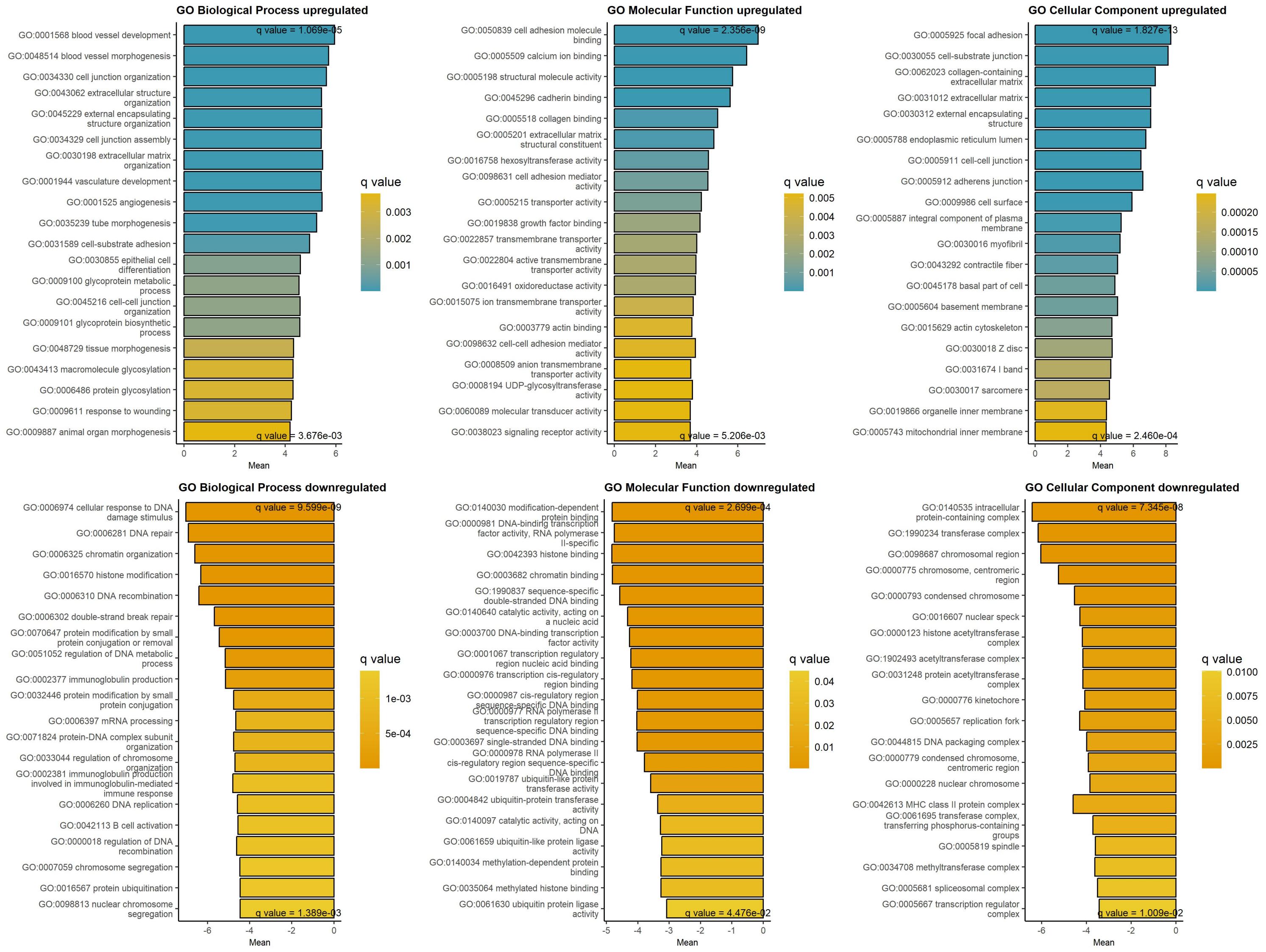


Downregulated at low/absent BCL2L11 Upregulated at low/absent BCL2L11

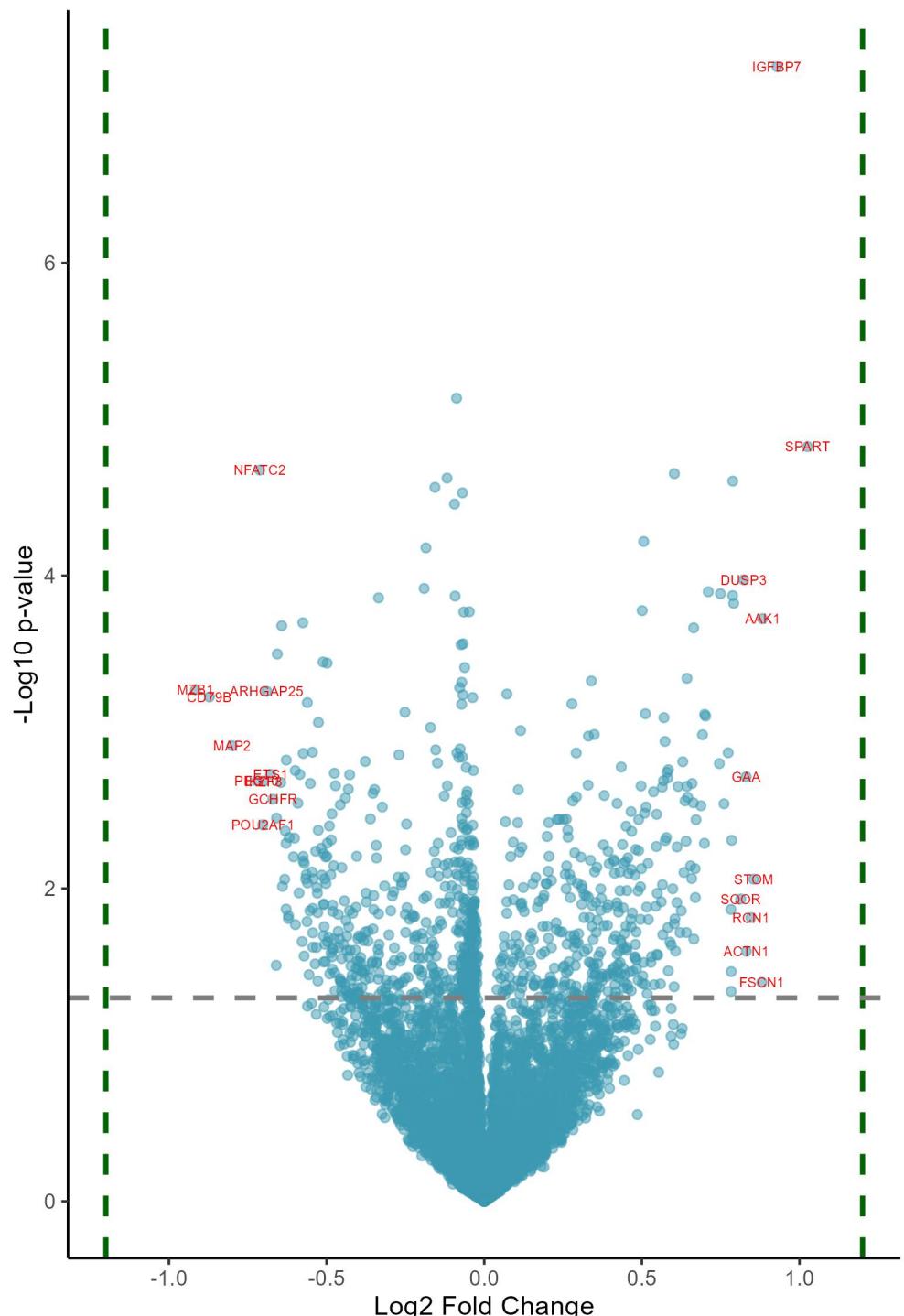


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.33	4.04e-20	RBM38	RNA binding motif protein 38	1.61	8.15e-06	CAVIN1	caveolae associated protein 1
-1.22	1.40e-23	FERMT3	FERM domain containing kindlin 3	1.52	7.89e-09	PROCR	protein C receptor
-1.15	2.00e-14	NFATC2	nuclear factor of activated T cells	1.42	5.86e-04	S100A10	S100 calcium binding protein A10
-1.13	3.88e-12	INPP5D	inositol polyphosphate-5-phosphatas	1.33	2.67e-10	ZNF671	zinc finger protein 671
-1.12	1.74e-10	RCSD1	RCSD domain containing 1	1.29	1.36e-05	S100A16	S100 calcium binding protein A16
-1.09	1.63e-22	CORO1A	coronin 1A	1.29	6.59e-08	ADAM9	ADAM metallopeptidase domain 9
-1.08	7.88e-08	ICAM3	intercellular adhesion molecule 3	1.27	2.87e-21	CAVIN3	caveolae associated protein 3
-1.07	5.59e-10	FGD3	FYVE, RhoGEF and PH domain containi	1.26	1.38e-02	GNG12	G protein subunit gamma 12
-1.04	1.02e-07	GMFG	glia maturation factor gamma	1.24	2.42e-17	MXRA7	matrix remodeling associated 7
-1.02	7.62e-09	HCLS1	hematopoietic cell-specific Lyn sub	1.23	4.17e-13	HMGA2	high mobility group AT-hook 2
-1.02	5.90e-11	GLCCI1	glucocorticoid induced 1	1.23	2.01e-12	CTSL	cathepsin L
-1.02	1.46e-06	SPN	sialophorin	1.2	7.09e-05	CAV1	caveolin 1
-1.01	2.11e-13	BAG1	BAG cochaperone 1	1.19	6.97e-03	CD44	CD44 molecule (Indian blood group)
-1.01	5.36e-08	MZB1	marginal zone B and B1 cell specifi	1.17	1.58e-04	FAM184B	family with sequence similarity 184
-0.99	6.53e-09	BCL2	BCL2 apoptosis regulator	1.16	4.63e-07	GPX8	glutathione peroxidase 8 (putative)
-0.99	1.56e-07	IL16	interleukin 16	1.15	1.16e-06	RRAS	RAS related
-0.99	4.73e-09	SYK	spleen associated tyrosine kinase	1.13	4.41e-07	FHL2	four and a half LIM domains 2
-0.99	2.00e-07	IKZF1	IKAROS family zinc finger 1	1.12	6.36e-16	AXL	AXL receptor tyrosine kinase
-0.98	9.79e-10	CD74	CD74 molecule	1.12	5.93e-09	NPHS1	NPHS1 adhesion molecule, nephrin
-0.97	1.25e-07	PAX5	paired box 5	1.1	9.15e-05	NECTIN2	nectin cell adhesion molecule 2
-0.96	1.99e-08	IRF4	interferon regulatory factor 4	1.1	4.50e-06	EPHA2	EPH receptor A2
-0.96	2.22e-13	BCL7A	BAF chromatin remodeling complex su	1.09	9.76e-07	MMP14	matrix metallopeptidase 14
-0.95	4.32e-07	LSP1	lymphocyte specific protein 1	1.09	2.06e-16	RAB11FIP5	RAB11 family interacting protein 5
-0.94	3.10e-09	PLCG2	phospholipase C gamma 2	1.09	4.38e-10	YAP1	Yes1 associated transcriptional reg
-0.94	5.82e-07	ARHGAP25	Rho GTPase activating protein 25	1.08	2.74e-10	RAB32	RAB32, member RAS oncogene family
-0.9	9.99e-06	PTPRCAP	protein tyrosine phosphatase recept	1.06	4.83e-06	ITGAS	integrin subunit alpha 5
-0.89	8.85e-09	CYFIP2	cytoplasmic FMR1 interacting protei	1.06	2.06e-03	BTNL8	butyrophilin like 8
-0.89	1.16e-11	TSTD1	thiosulfate sulfurtransferase like	1.05	3.95e-18	ITK	IL2 inducible T cell kinase
-0.89	1.45e-08	CARMIL2	capping protein regulator and myosi	1.05	3.30e-06	PCLO	piccolo presynaptic cytomatrix prot

GAGE analysis on upregulated and downregulated proteins at low/absent BCL2L11 protein, DB2

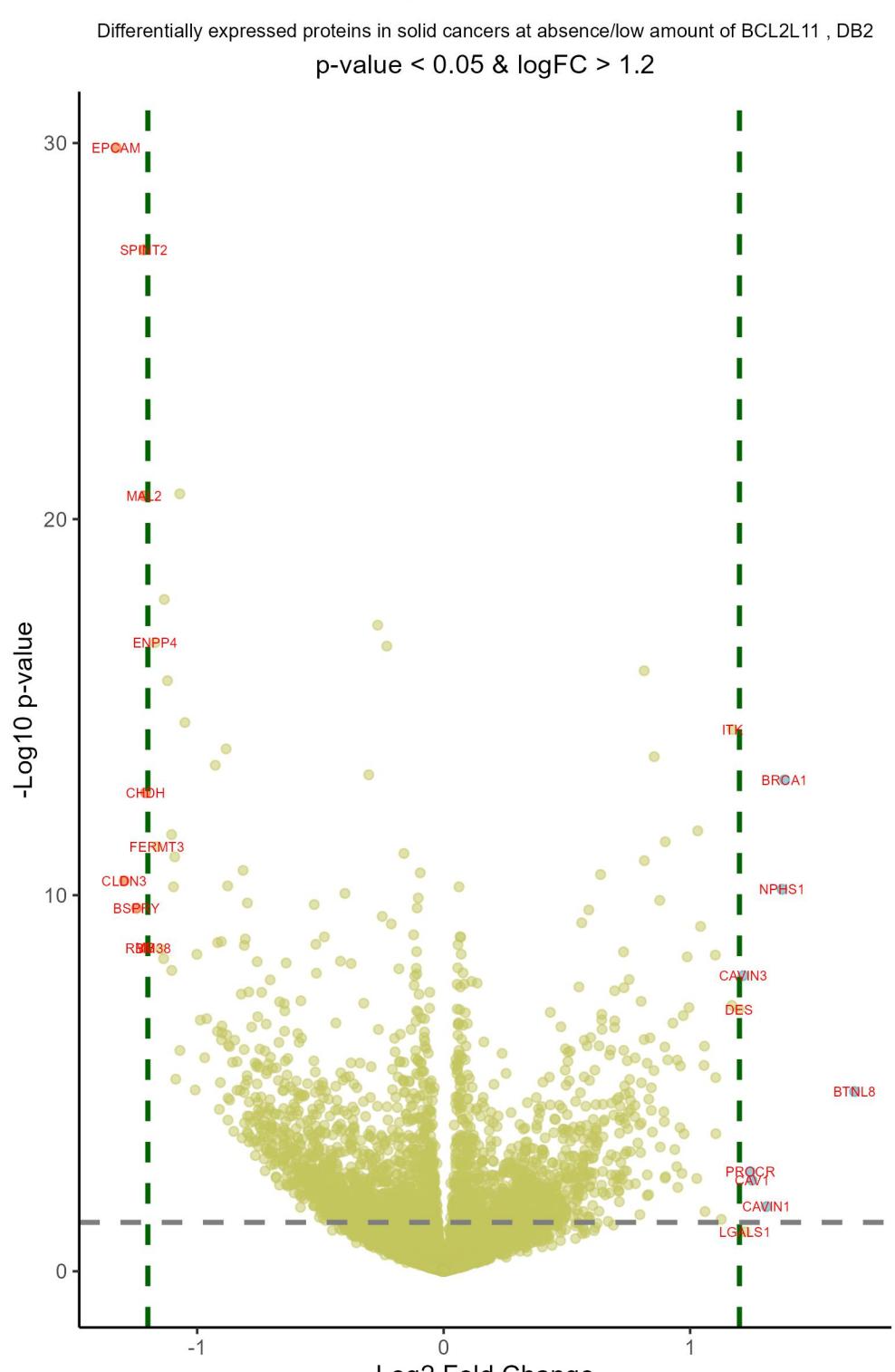


p-value < 0.05 & logFC > 1.2



Downregulated in blood cancers at low/absent BCL2L11 Upregulated in blood cancers at low/absent BCL2L11

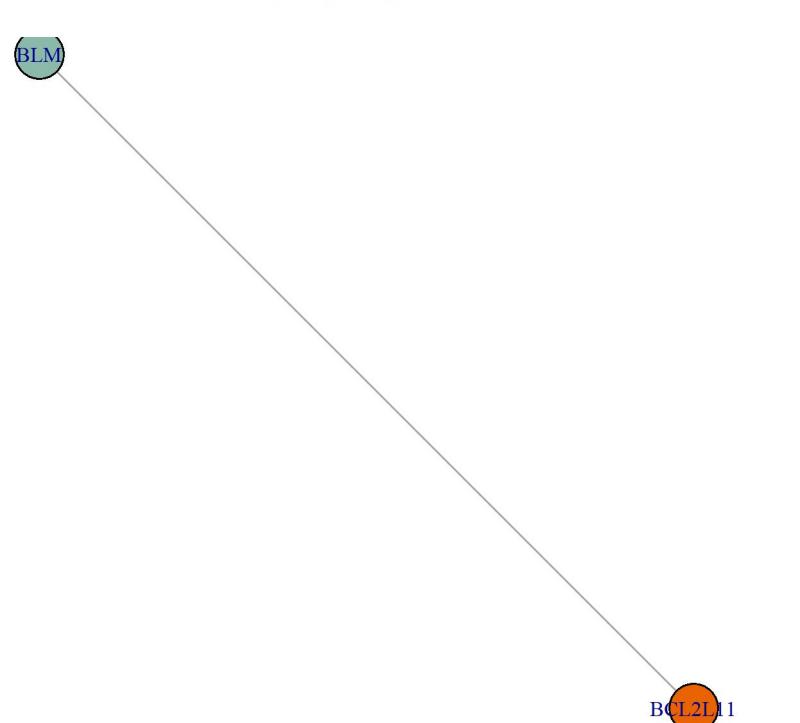
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.92	1.14e-01	MZB1	marginal zone B and B1 cell specific	1.03	2.47e-02	SPART	spartin
-0.87	1.14e-01	CD79B	CD79b molecule	0.93	2.33e-04	IGFBP7	insulin like growth factor binding
-0.8	1.70e-01	MAP2	microtubule associated protein 2	0.88	6.30e-02	AAK1	AP2 associated kinase 1
-0.72	1.88e-01	PEG10	paternally expressed 10	0.88	4.05e-01	FSCN1	fascin actin-bundling protein 1
-0.71	2.47e-02	NFATC2	nuclear factor of activated T cells	0.85	2.77e-01	STOM	stomatin
-0.7	2.24e-01	POU2AF1	POU class 2 homeobox associating fa	0.85	3.27e-01	RCN1	reticulocalbin 1
-0.7	1.88e-01	IKZF3	IKAROS family zinc finger 3	0.83	3.85e-01	ACTN1	actinin alpha 1
-0.69	1.14e-01	ARHGAP25	Rho GTPase activating protein 25	0.83	1.88e-01	GAA	alpha glucosidase
-0.68	1.84e-01	ETS1	ETS proto-oncogene 1, transcription	0.82	5.79e-02	DUSP3	dual specificity phosphatase 3
-0.67	1.97e-01	GCHFR	GTP cyclohydrolase I feedback regul	0.81	3.08e-01	SQOR	sulfide quinone oxidoreductase
-0.66	4.05e-01	TCL1A	TCL1 family AKT coactivator A	0.79	5.94e-02	LYZ	lysozyme
-0.66	2.17e-01	SEPTIN1	septin 1	0.79	2.47e-02	CPPED1	calcineurin like phosphoesterase do
-0.66	8.54e-02	WDR76	WD repeat domain 76	0.79	5.79e-02	TIMP1	TIMP metallopeptidase inhibitor 1
-0.65	1.88e-01	IRF4	interferon regulatory factor 4	0.79	2.45e-01	HPDL	4-hydroxyphenylpyruvate dioxygenase
-0.64	6.43e-02	CARMIL2	capping protein regulator and myosi	0.78	4.05e-01	CD44	CD44 molecule (Indian blood group)
-0.64	2.86e-01	SIT1	signaling threshold regulating tran	0.78	4.05e-01	TMEM70	transmembrane protein 70
-0.63	2.77e-01	GRM5	glutamate metabotropic receptor 5	0.78	3.15e-01	SPESP1	sperm equatorial segment protein 1
-0.63	2.31e-01	PIP5K1C	phosphatidylinositol-4-phosphate 5-	0.77	1.71e-01	PAK1	p21 (RAC1) activated kinase 1
-0.63	2.45e-01	POU2F2	POU class 2 homeobox 2	0.76	1.97e-01	PRKCB	protein kinase C beta
-0.63	3.15e-01	PAX5	paired box 5	0.75	5.79e-02	CST7	cystatin F
-0.63	1.77e-01	CEP97	centrosomal protein 97	0.75	1.77e-01	STING1	stimulator of interferon response c
-0.62	3.31e-01	MUC5B	mucin 5B, oligomeric mucus/gel-form	0.71	5.79e-02	S100A16	S100 calcium binding protein A16
-0.62	3.23e-01	VPREB3	V-set pre-B cell surrogate light ch	0.7	1.29e-01	AKAP6	A-kinase anchoring protein 6
-0.62	2.45e-01	EEDP1	endonuclease/exonuclease/phosphatas	0.7	1.29e-01	CLEC11A	C-type lectin domain containing 11A
-0.61	2.58e-01	ATP1A3	ATPase Na+/K+ transporting subunit	0.7	2.45e-01	BOLA1	bola family member 1
-0.6	2.45e-01	MCL1	MCL1 apoptosis regulator, BCL2 fami	0.69	1.52e-01	RASGRP2	RAS guanyl releasing protein 2
-0.6	1.84e-01	ISG20L2	interferon stimulated exonuclease g	0.69	1.99e-01	SEPTIN8	septin 8
-0.6	3.43e-01	IL27RA	interleukin 27 receptor subunit alp	0.67	2.17e-01	ADGRE5	adhesion G protein-coupled receptor
-0.59	1.97e-01	BCL6	BCL6 transcription repressor	0.67	3.06e-01	CGAS	cyclic GMP-AMP synthase



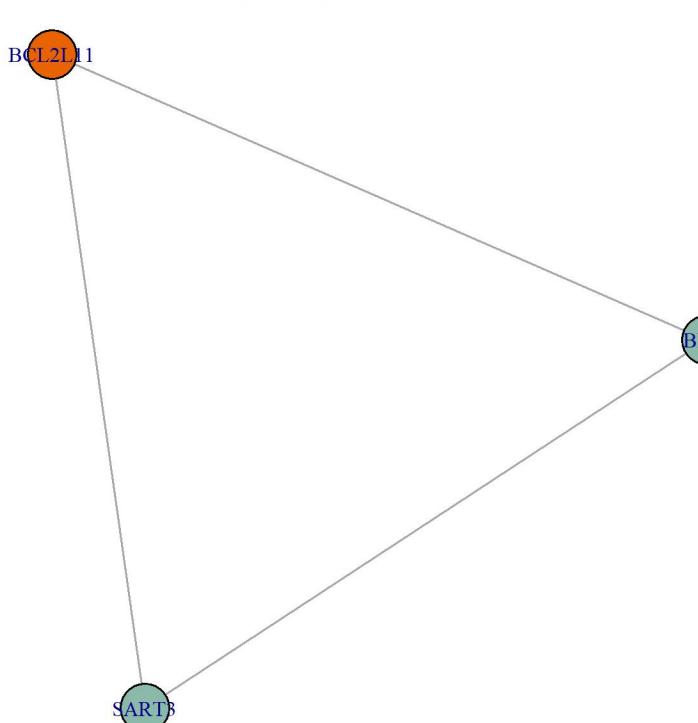
Downregulated in solid cancers at low/absent BCL2L11 Upregulated in solid cancers at low/absent BCL2L11

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.33	5.58e-27	EPCAM	epithelial cell adhesion molecule	1.67	4.55e-04	BTNL8	butyrophilin like 8
-1.3	1.16e-08	CLDN3	claudin 3	1.38	3.97e-11	BRCA1	BRCA1 DNA repair associated
-1.25	4.52e-08	BSPRY	B-box and SPRY domain containing	1.37	1.71e-08	NPHS1	NPHS1 adhesion molecule, nephrin
-1.22	1.92e-24	SPINT2	serine peptidase inhibitor, Kunitz	1.31	8.53e-02	CAVIN1	caveolae associated protein 1
-1.21	4.05e-18	MAL2	mal, T cell differentiation protein	1.25	2.72e-02	CAV1	caveolin 1
-1.21	3.68e-07	MB	myoglobin	1.24	1.89e-02	PROCR	protein C receptor
-1.21	8.25e-11	CHDH	choline dehydrogenase	1.22	2.42e-01	LGALS1	galectin 1
-1.2	3.68e-07	RBM38	RNA binding motif protein 38	1.22	1.47e-06	CAVIN3	caveolae associated protein 3
-1.17	2.02e-14	ENPP4	ectonucleotide pyrophosphatase/phos	1.2	8.74e-06	DES	desmin
-1.16	1.84e-09	FERMT3	FERM domain containing kindlin 3	1.17	2.54e-12	ITK	IL2 inducible T cell kinase
-1.15	3.82e-07	CPE	carboxypeptidase E	1.17	7.07e-06	SPESP1	sperm equatorial segment protein 1
-1.14	6.17e-07	CDKN2A	cyclin dependent kinase inhibitor 2	1.13	1.46e-01	CD44	CD44 molecule (Indian blood group)
-1.13	1.90e-15	TSTD1	thiosulfate sulfurtransferase like	1.1	3.29e-03	ITGA5	integrin subunit alpha 5
-1.12	1.50e-13	ESRP1	epithelial splicing regulatory prot	1.1	2.37e-04	NNMT	nicotinamide N-methyltransferase
-1.1	9.72e-10	ST14	ST14 transmembrane serine protease	1.1	5.10e-07	SIRPA	signal regulatory protein alpha
-1.1	1.13e-06	KIF1A	kinesin family member 1A	1.06	1.04e-01	S100A10	S100 calcium binding protein A10
-1.1	1.52e-08	KDF1	keratinocyte differentiation factor	1.06	5.29e-05	AXL	AXL receptor tyrosine kinase
-1.09	3.19e-09	PHF20L1	PHD finger protein 20 like 1	1.06	1.29e-04	MXRA7	matrix remodeling associated 7
-1.09	2.57e-04	IGFBP5	insulin like growth factor binding	1.04	1.23e-07	NEXN	nexilin F-actin binding protein
-1.07	4.05e-18	SPINT1	serine peptidase inhibitor, Kunitz	1.03	8.11e-10	GSDME	gasdermin E
-1.07	6.45e-05	PROX1	prospero homeobox 1	1.03	2.54e-02	STOM	stomatin
-1.05	1.78e-12	CDH1	cadherin 1	1	7.96e-06	DNAH8	dynein axonemal heavy chain 8
-1.01	4.26e-04	SCGN	secretogogin, EF-hand calcium bindi	0.99	5.61e-07	RAB31	RAB31, member RAS oncogene family
-1	4.95e-07	SIGIRR	single Ig and TIR domain containing	0.98	3.32e-03	HMGA2	high mobility group AT-hook 2
-0.99	1.47e-05	MAPK13	mitogen-activated protein kinase 13	0.97	1.18e-05	MRC2	mannose receptor C type 2
-0.97	9.41e-05	PIGX	phosphatidylinositol glycan anchor	0.97	2.05e-02	ZNF671	zinc finger protein 671
-0.96	1.37e-05	STARD10	StAR related lipid transfer domain	0.96	1.33e-04	PARVB	parvin beta
-0.93	1.83e-11	DYNLL2	dynein light chain LC8-type 2	0.96	2.50e-03	PAPSS2	3'-phosphoadenosine 5'-phosphosulfa
-0.92	2.53e-05	AP1M2	adaptor related protein complex 1 s	0.95	3.78e-02	MYO5C	myosin VC

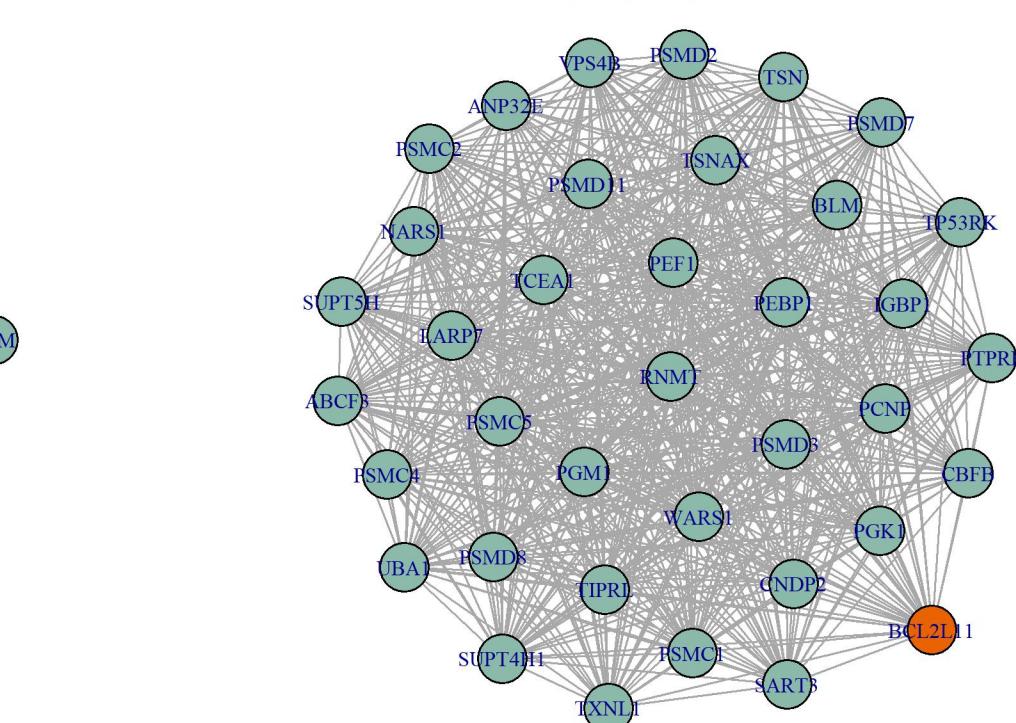
BCL2L11 network, DB2, all Pearson r > 0.4



BCL2L11 network, DB2, all Pearson r > 0.35

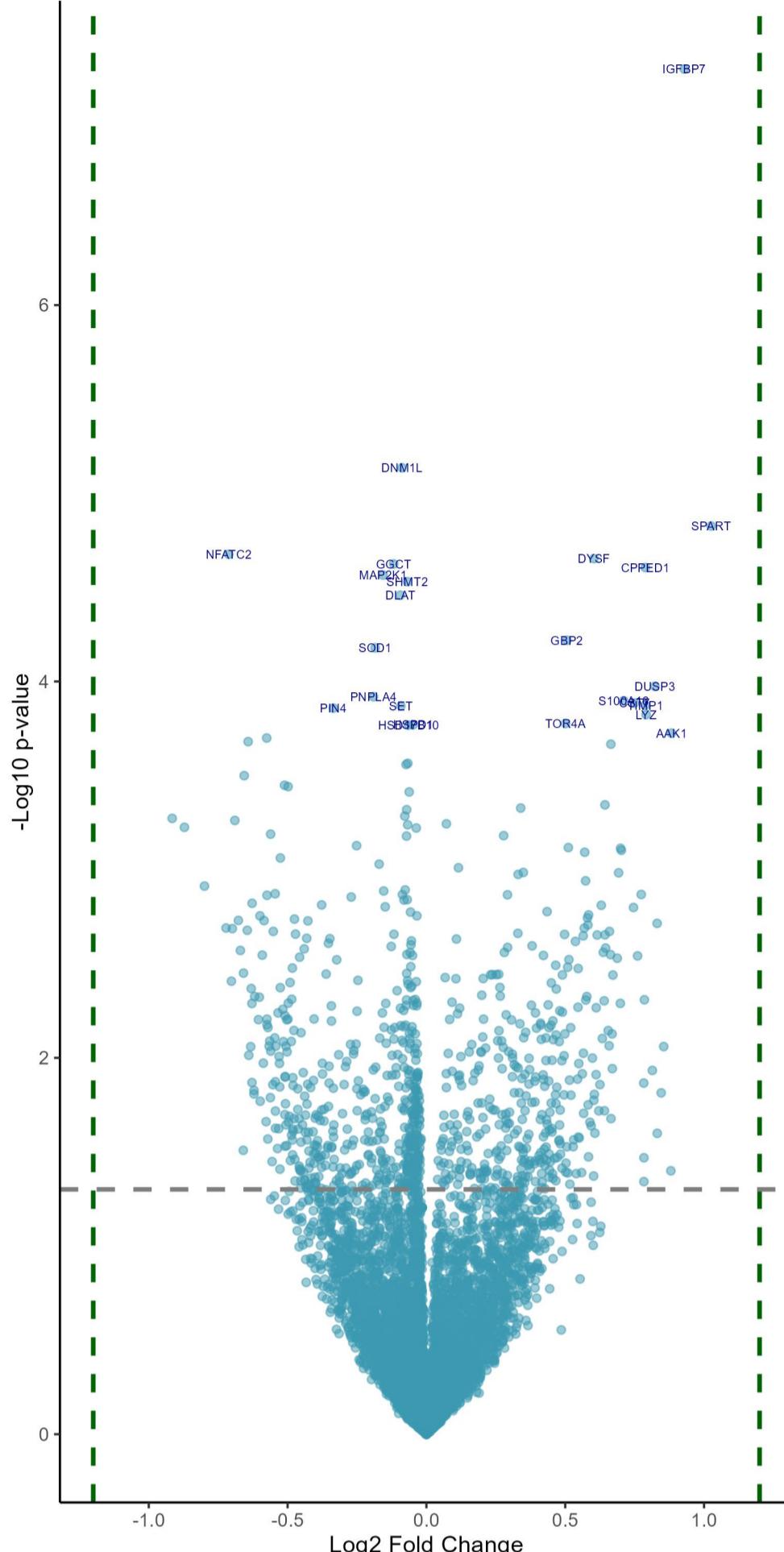


BCL2L11 network, DB2, all Pearson r > 0.3

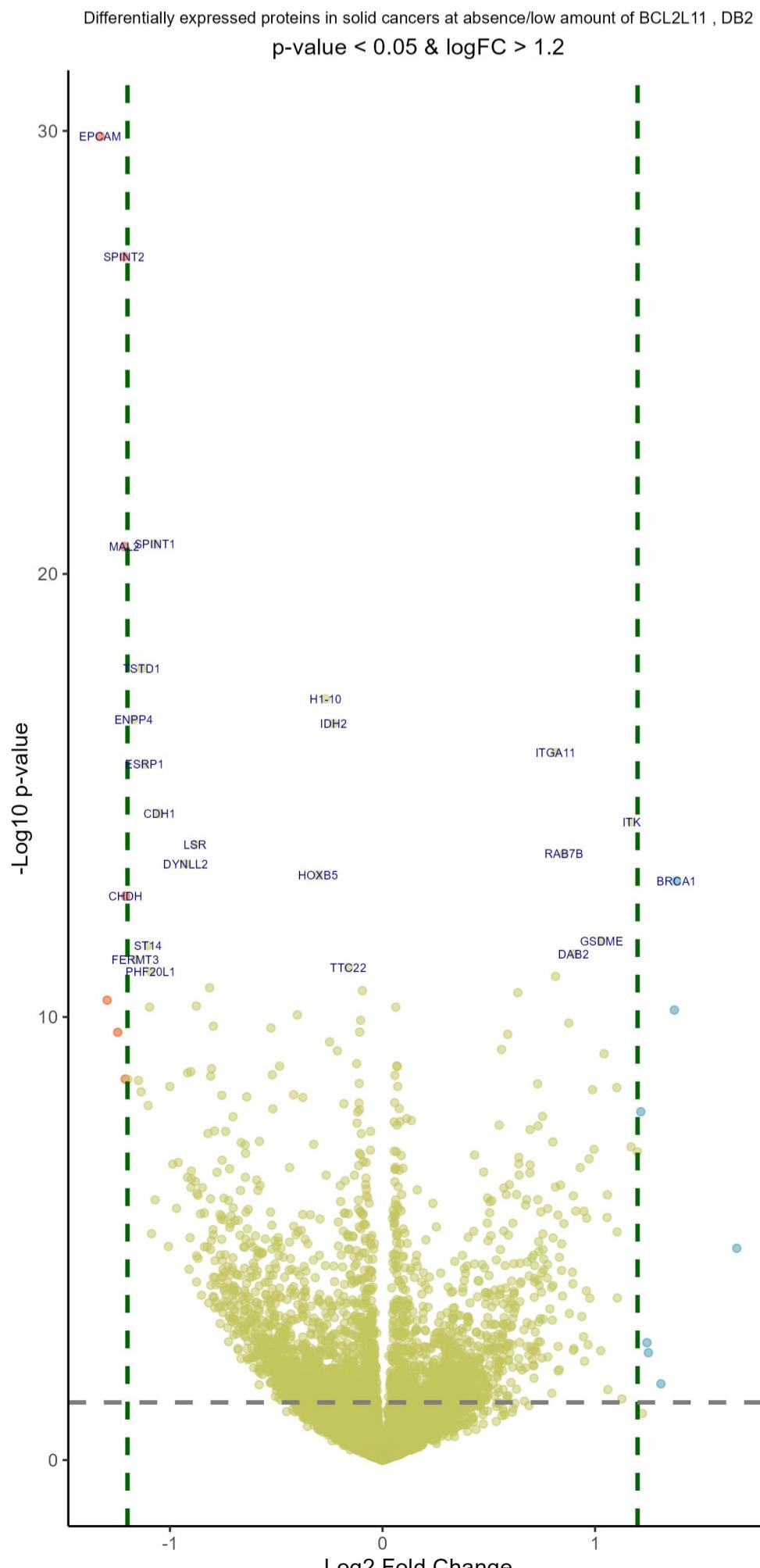


Sorted by p values!

Downregulated in blood cancers at low/absent BCL2L11 Upregulated in blood cancers at low/absent BCL2L11

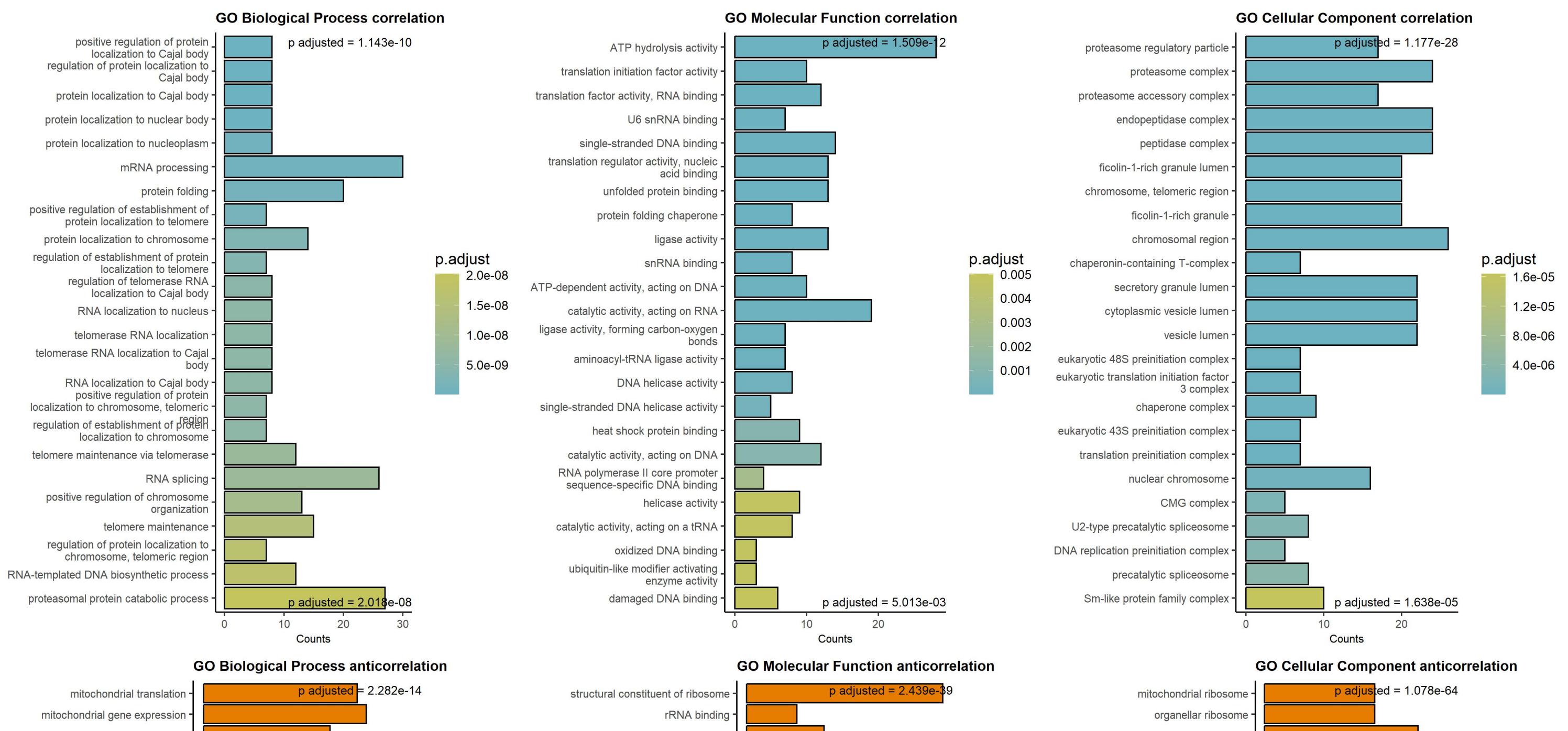


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.09	2.04e-02	DNM1L	dynamin 1 like	0.93	2.33e-04	IGFBP7	insulin like growth factor binding
-0.71	2.47e-02	NFATC2	nuclear factor of activated T cells	1.03	2.47e-02	SPART	spartin
-0.12	2.47e-02	GGCT	gamma-glutamylcyclotransferase	0.6	2.47e-02	DYSF	dysferlin
-0.16	2.47e-02	MAP2K1	mitogen-activated protein kinase ki	0.79	2.47e-02	CPPED1	calcineurin like phosphoesterase do
-0.07	2.47e-02	SHMT2	serine hydroxymethyltransferase 2	0.51	4.21e-02	GBP2	guanylate binding protein 2
-0.09	2.65e-02	DLAT	dihydrolipoamide S-acetyltransferas	0.82	5.79e-02	DUSP3	dual specificity phosphatase 3
-0.18	4.27e-02	SOD1	superoxide dismutase 1	0.71	5.79e-02	S100A16	S100 calcium binding protein A16
-0.19	5.79e-02	PNPLA4	patatin like phospholipase domain c	0.75	5.79e-02	CST7	cystatin F
-0.09	5.79e-02	SET	SET nuclear proto-oncogene	0.79	5.79e-02	TIMP1	TIMP metallopeptidase inhibitor 1
-0.34	5.79e-02	PIN4	peptidylprolyl cis/trans isomerase,	0.79	5.94e-02	LYZ	lysozyme
-0.05	5.94e-02	HSPD1	heat shock protein family D (Hsp60)	0.5	5.94e-02	TOR4A	torsin family 4 member A
-0.06	5.94e-02	HSD17B10	hydroxysteroid 17-beta dehydrogenas	0.88	6.30e-02	AAK1	AP2 associated kinase 1
-0.58	6.43e-02	MSI2	musashi RNA binding protein 2	0.66	6.43e-02	MNDA	myeloid cell nuclear differentiatio
-0.64	6.43e-02	CARMIL2	capping protein regulator and myosi	0.64	1.08e-01	RILPL2	Rab interacting lysosomal protein I
-0.07	7.70e-02	USP5	ubiquitin specific peptidase 5	0.34	1.09e-01	ASB9	ankyrin repeat and SOCS box contain
-0.07	7.70e-02	GARS1	glycyl-tRNA synthetase 1	0.07	1.14e-01	TARS1	threonyl-tRNA synthetase 1
-0.66	8.54e-02	WDR76	WD repeat domain 76	0.28	1.18e-01	CORO1C	coronin 1C
-0.51	9.17e-02	IFT88	intraflagellar transport 88	0.51	1.29e-01	GRB10	growth factor receptor bound protei
-0.5	9.17e-02	IGSF8	immunoglobulin superfamily member 8	0.7	1.29e-01	CLEC11A	C-type lectin domain containing 11A
-0.06	9.51e-02	SSBP1	single stranded DNA binding protein	0.7	1.29e-01	AKAP6	A-kinase anchoring protein 6
-0.07	1.09e-01	TOP1	DNA topoisomerase I	0.57	1.30e-01	STX11	syntaxin 11
-0.08	1.14e-01	GOT2	glutamic-oxaloacetic transaminase 2	0.12	1.49e-01	RNH1	ribonuclease/angiogenin inhibitor 1
-0.92	1.14e-01	MZB1	marginal zone B and B1 cell specifi	0.35	1.52e-01	SIGLEC12	sialic acid binding Ig like lectin
-0.69	1.14e-01	ARHGAP25	Rho GTPase activating protein 25	0.69	1.52e-01	RASGRP2	RAS guanyl releasing protein 2
-0.07	1.14e-01	SRP14	signal recognition particle 14	0.33	1.53e-01	NID2	nidogen 2
-0.87	1.14e-01	CD79B	CD79b molecule	0.57	1.63e-01	NCF2	neutrophil cytosolic factor 2
-0.04	1.14e-01	HSPE1	heat shock protein family E (Hsp10)	0.77	1.71e-01	PAK1	p21 (RAC1) activated kinase 1
-0.56	1.18e-01	SETD7	SET domain containing 7, histone ly	0.29	1.71e-01	FOSL2	FOS like 2, AP-1 transcription fact
-0.07	1.18e-01	TXNL1	thioredoxin like 1	0.63	1.77e-01	LPCAT2	lysophosphatidylcholine acyltransfe
-0.25	1.29e-01	TRIM9	tripartite motif containing 9	0.75	1.77e-01	STING1	stimulator of interferon response c
-0.53	1.37e-01	HIP1R	huntingtin interacting protein 1 re	0.43	1.83e-01	DRD2	dopamine receptor D2
-0.17	1.45e-01	RPAP3	RNA polymerase II associated protei	0.58	1.84e-01	TCIRG1	T cell immune regulator 1, ATPase H
-0.8	1.70e-01	MAP2	microtubule associated protein 2	0.58	1.84e-01	CALCOCO2	calcium binding and coiled-coil dom
-0.08	1.71e-01	NAA10	N-alpha-acetyltransferase 10, NatA	0.83	1.88e-01	GAA	alpha glucosidase
-0.15	1.71e-01	RBFOX2	RNA binding fox-1 homolog 2	0.58	1.88e-01	KSR1	kinase suppressor of ras 1
-0.54	1.71e-01	KCNH1	potassium voltage-gated channel sub	0.57	1.88e-01	KBTBD11	kelch repeat and BTB domain contain
-0.09	1.71e-01	SEC62	SEC62 homolog, preprotein transloca	0.66	1.88e-01	NMI	N-myc and STAT interactor
-0.57	1.71e-01	HMCES	5-hydroxymethylcytosine binding, ES	0.33	1.88e-01	CEBPD	CCAAT enhancer binding protein delt
0.27	1.72e-01	PTDSD71	protein tyrosine phosphatase recent	0.5	1.88e-01	HEYIM1	HEYIM1 D TEEh complex subunit 1

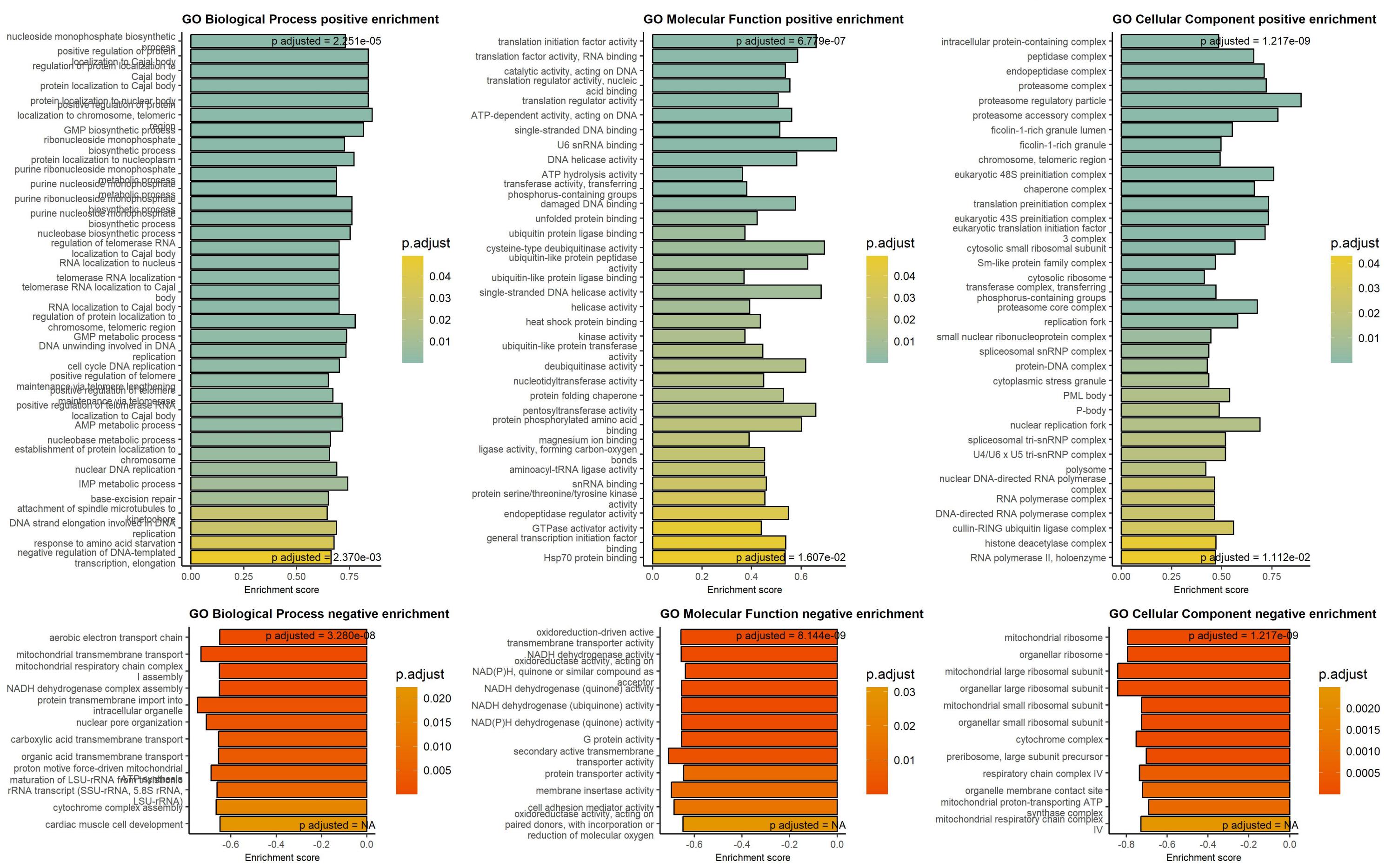


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.33	5.58e-27	EPCAM	epithelial cell adhesion molecule	0.81	8.99e-14	ITGA11	integrin subunit alpha 11
-1.22	1.92e-24	SPINT2	serine peptidase inhibitor, Kunitz	1.17	2.54e-12	ITK	IL2 inducible T cell kinase
-1.07	4.05e-18	SPINT1	serine peptidase inhibitor, Kunitz	0.85	1.15e-11	RAB7B	RAB7B, member RAS oncogene family
-1.21	4.05e-18	MAL2	mal, T cell differentiation protein	1.38	3.97e-11	BRCA1	BRCA1 DNA repair associated
-1.13	1.90e-15	TSTD1	thiosulfate sulfurtransferase like	1.03	8.11e-10	GSDME	gasdermin E
-0.27	7.87e-15	H1-10	H1.10 linker histone	0.9	1.44e-09	DAB2	DAB adaptor protein 2
-1.17	2.02e-14	ENPP4	ectonucleotide pyrophosphatase/phos	0.81	3.88e-09	ARHGAP18	Rho GTPase activating protein 18
-0.23	2.21e-14	IDH2	isocitrate dehydrogenase (NADP(+))	0.64	8.13e-09	ZFP36L1	ZFP36 ring finger protein like 1
-1.12	1.50e-13	ESRP1	epithelial splicing regulatory prot	0.06	1.52e-08	RPL31	ribosomal protein L31
-1.05	1.78e-12	CDH1	cadherin 1	1.37	1.71e-08	NPHS1	NPHS1 adhesion molecule, nephrin
-0.88	7.68e-12	LSR	lipolysis stimulated lipoprotein re	0.88	3.10e-08	SERPINE1	serpin family E member 1
-0.93	1.83e-11	DYNLL2	dynein light chain LC8-type 2	0.59	4.92e-08	FOSL2	FOS like 2, AP-1 transcription fact
-0.3	3.09e-11	HOXB5	homeobox B5	0.56	1.03e-07	FMNL3	formin like 3
-1.21	8.25e-11	CHDH	choline dehydrogenase	1.04	1.23e-07	NEXN	nexilin F-actin binding protein
-1.	9.72e-10	ST14	ST14 transmembrane serine protease	0.07	2.19e-07	RPL23A	ribosomal protein L23a
-1.16	1.84e-09	FERMT3	FERM domain containing kindlin 3	0.07	2.19e-07	RPL10A	ribosomal protein L10a
-0.16	2.71e-09	TTC22	tetratricopeptide repeat domain 22	0.06	3.15e-07	RPL12	ribosomal protein L12
-1.09	3.19e-09	PHF20L1	PHD finger protein 20 like 1	0.73	4.40e-07	MSRB3	methionine sulfoxide reductase B3
-0.81	6.77e-09	CGN	cingulin	0.07	4.95e-07	RPL5	ribosomal protein L5
-0.1	7.59e-09	SMC1A	structural maintenance of chromosom	1.1	5.10e-07	SIRPA	signal regulatory protein alpha
-1.3	1.16e-08	CLDN3	claudin 3	0.99	5.61e-07	RAB31	RAB31, member RAS oncogene family
-0.88	1.52e-08	FAM241B	family with sequence similarity 241	0.06	1.01e-06	RPL13	ribosomal protein L13
-1.1	1.52e-08	KDF1	keratinocyte differentiation factor	0.08	1.30e-06	RPS19	ribosomal protein S19
-0.4	2.14e-08	C8orf82	chromosome 8 open reading frame 82	1.22	1.47e-06	CAVIN3	caveolae associated protein 3
-0.1	2.75e-08	SMC3	structural maintenance of chromosom	0.75	1.83e-06	ITPRIP	inositol 1,4,5-trisphosphate recept
-0.8	3.54e-08	CKMT1B	creatine kinase, mitochondrial 1B	0.11	2.00e-06	EEF1D	eukaryotic translation elongation f
-0.53	3.79e-08	COQ6	coenzyme Q6, monooxygenase	0.14	2.19e-06	RPS26	ribosomal protein S26
-0.11	4.52e-08	RAD21	RAD21 cohesin complex component	0.08	2.29e-06	RPS8	ribosomal protein S8
-1.25	4.52e-08	BSPRY	B-box and SPRY domain containing	0.05	2.30e-06	RPS7	ribosomal protein S7

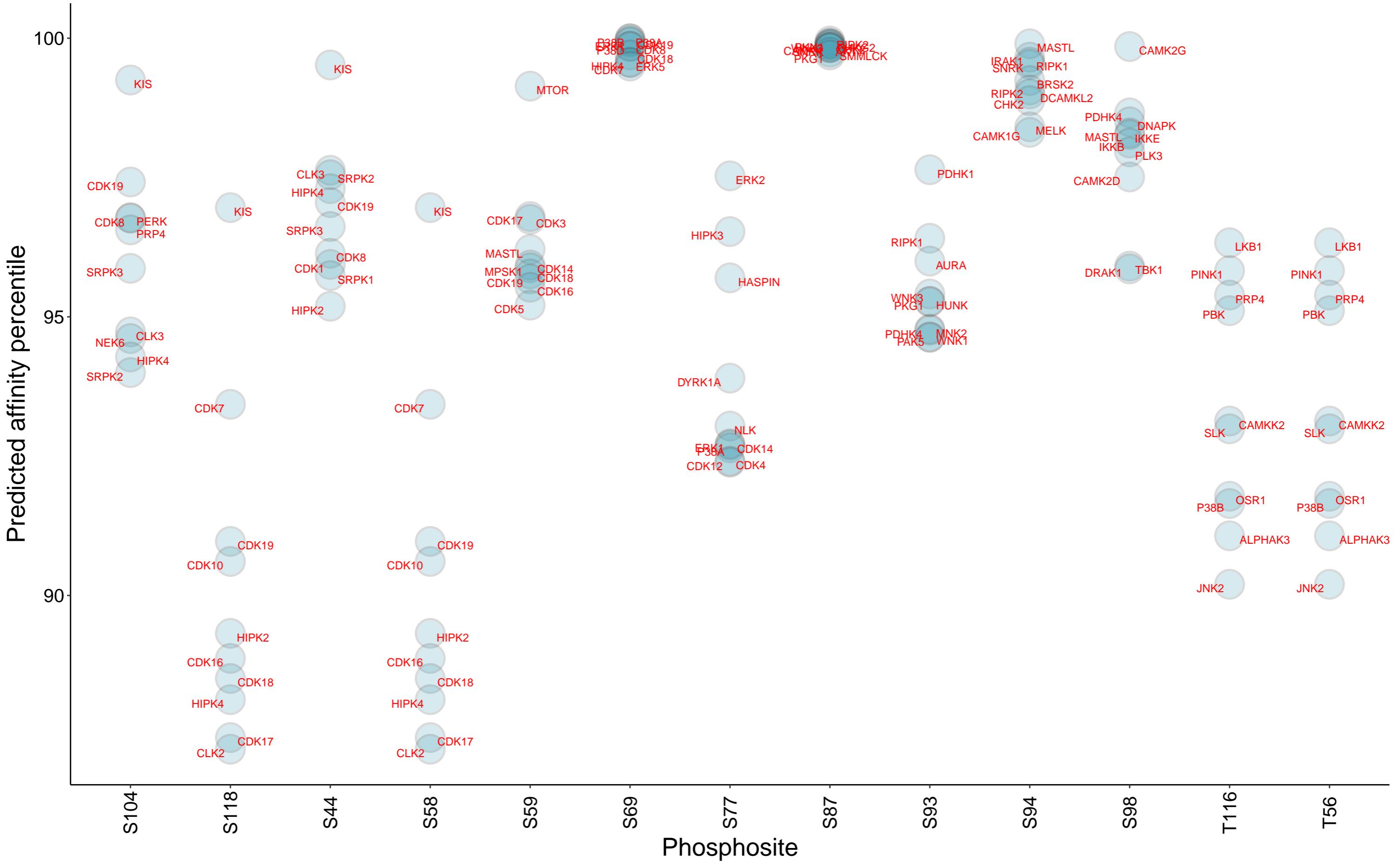
Top 250 correlation coefficients overrepresentation, BCL2L11 protein, DB2



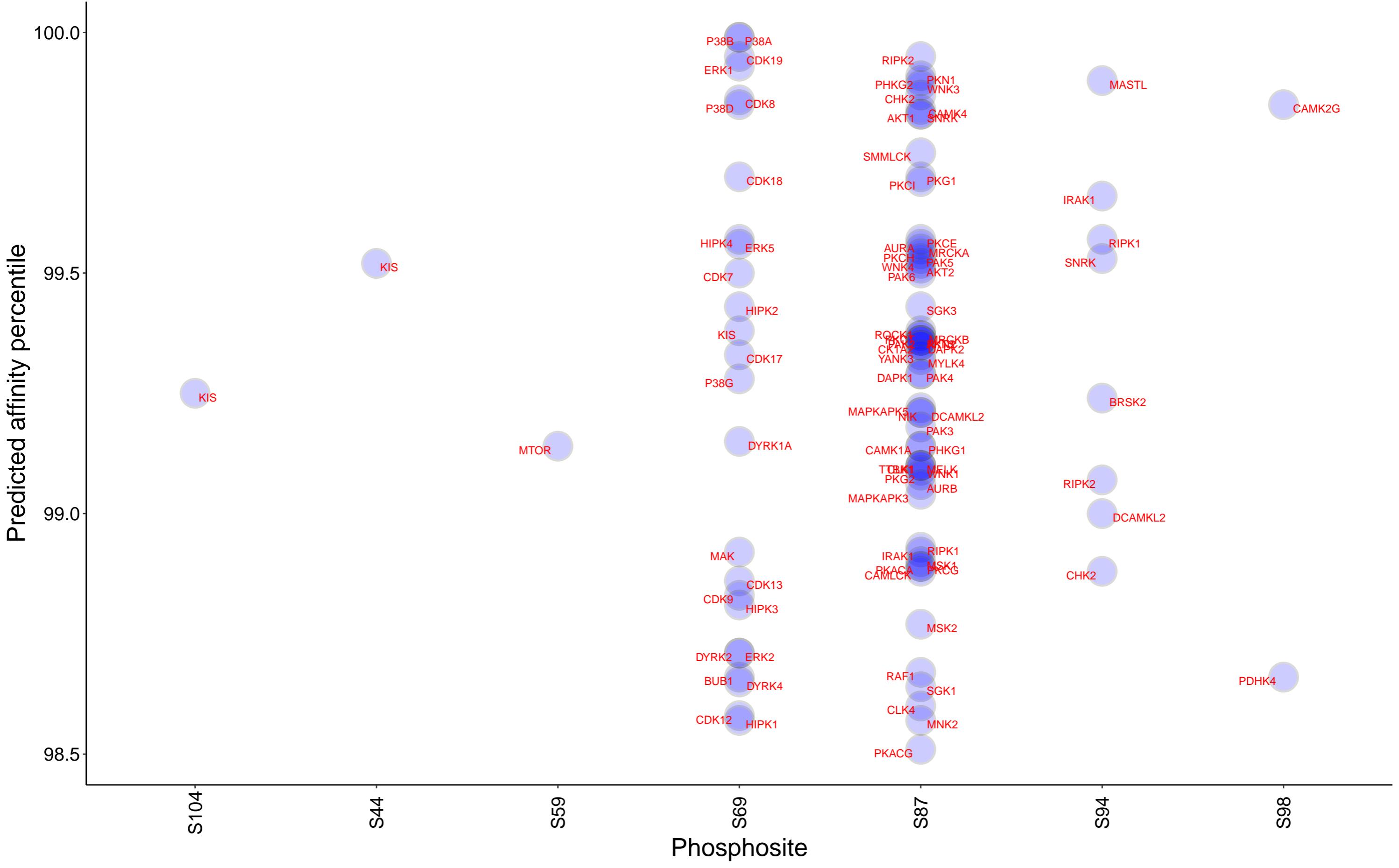
Gene Set Enrichment analysis on protein correlation coefficients, BCL2L11 protein, DB2



Top 10 kinases for each phosphosite in BCL2L11



Kinases with affinity greater than 98.5% to BCL2L11



No sufficient number of paired observations in DB2 for BCL2L11