

BCL2L1

Protein name: B2CL1 ;

UNIPROT: Q07817 ;

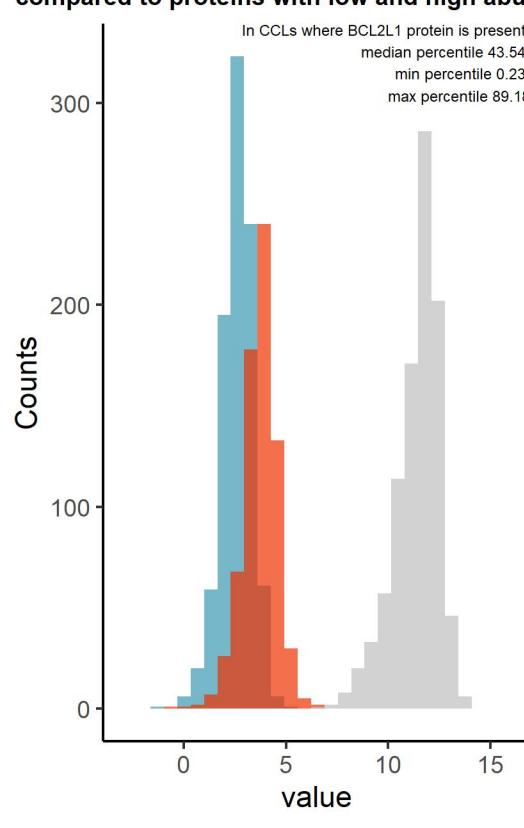
Gene name: BCL2 like 1

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

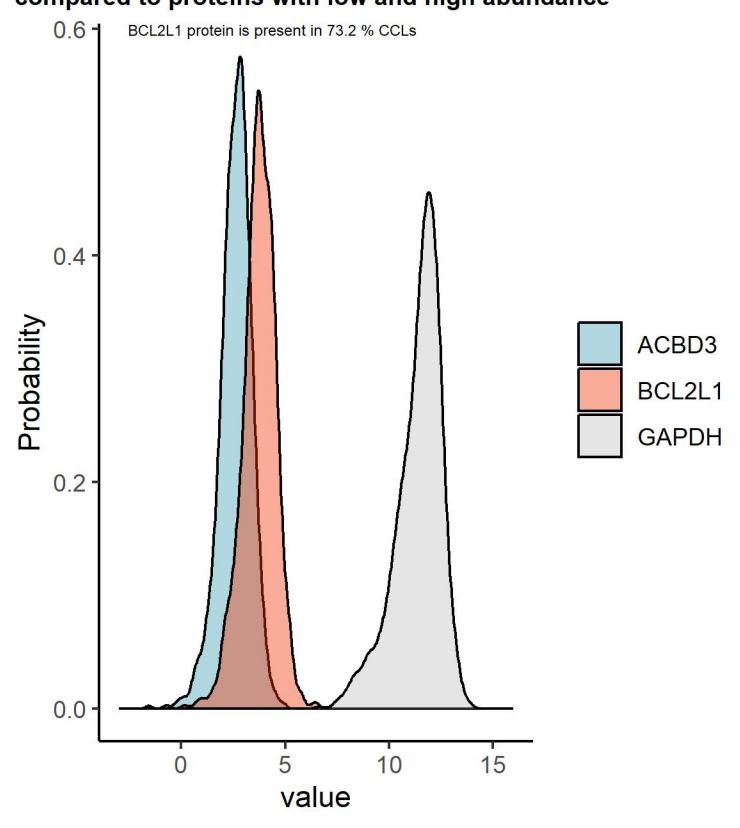
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

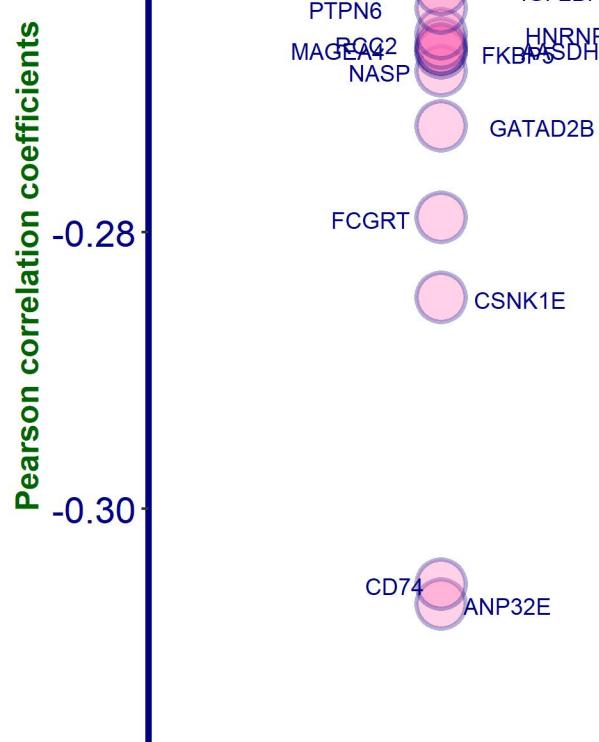
Histogram of BCL2L1 protein compared to proteins with low and high abundance



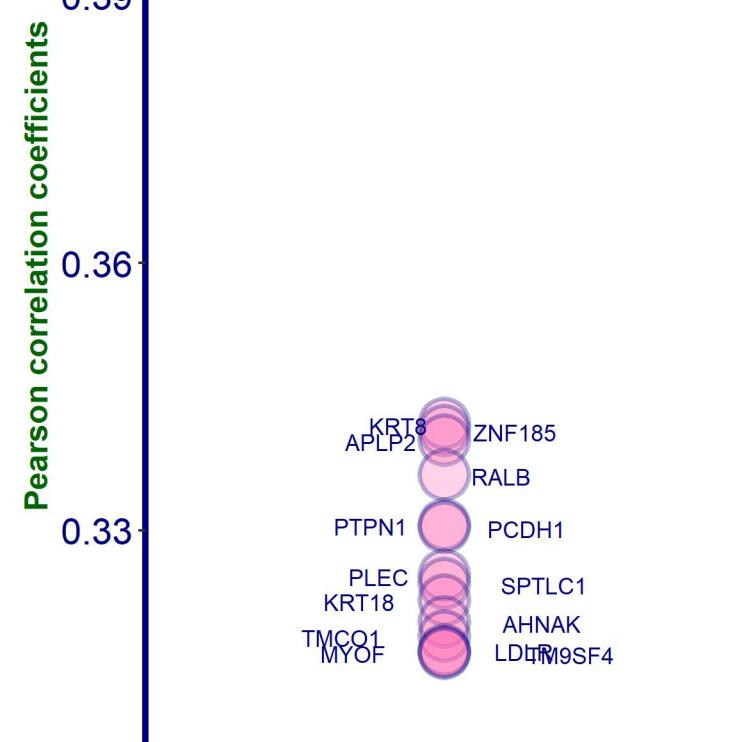
Density plot of BCL2L1 protein compared to proteins with low and high abundance



Top negative correlations of BCL2L1 protein, DB1

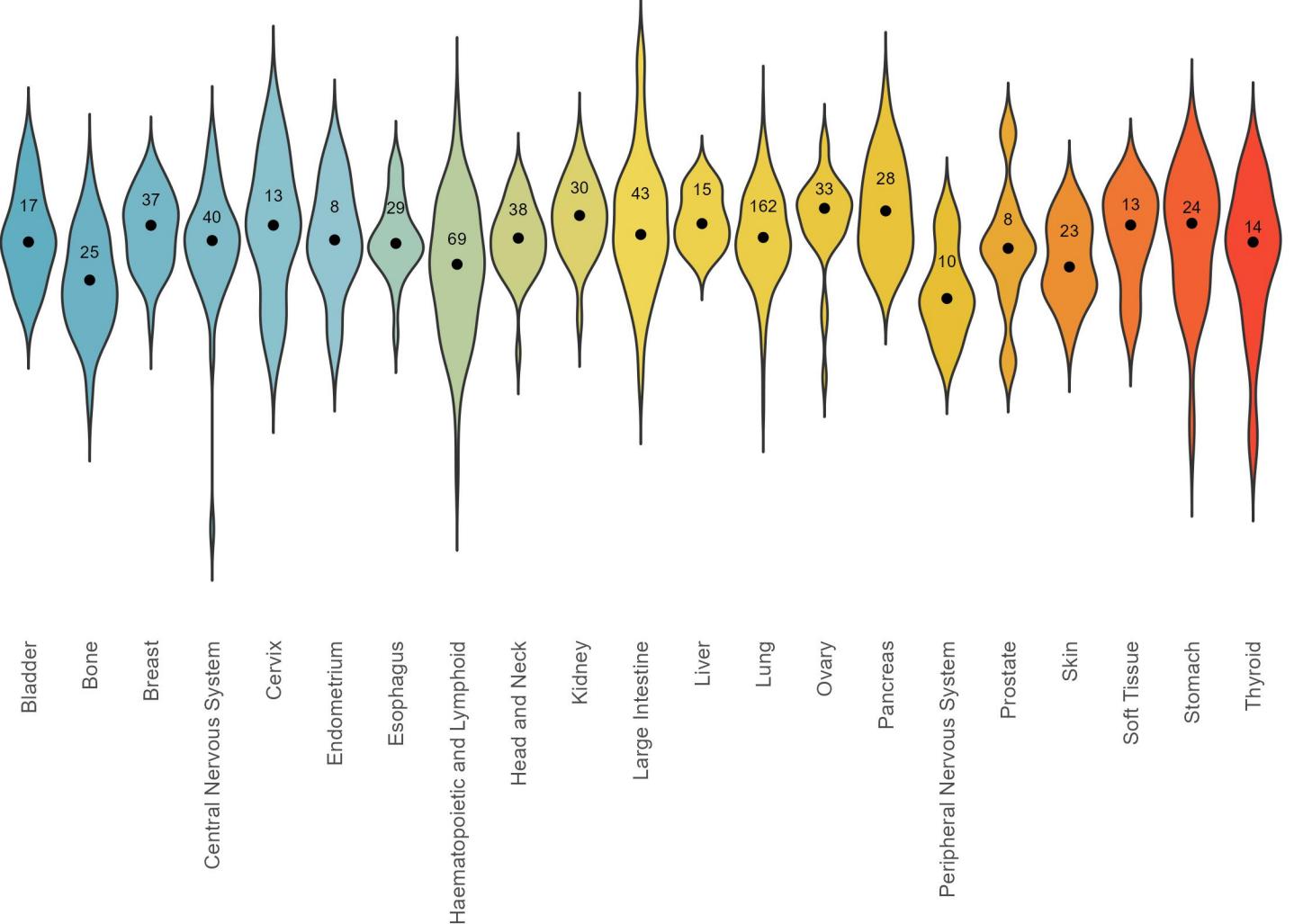


Top positive correlations of BCL2L1 protein, DB1



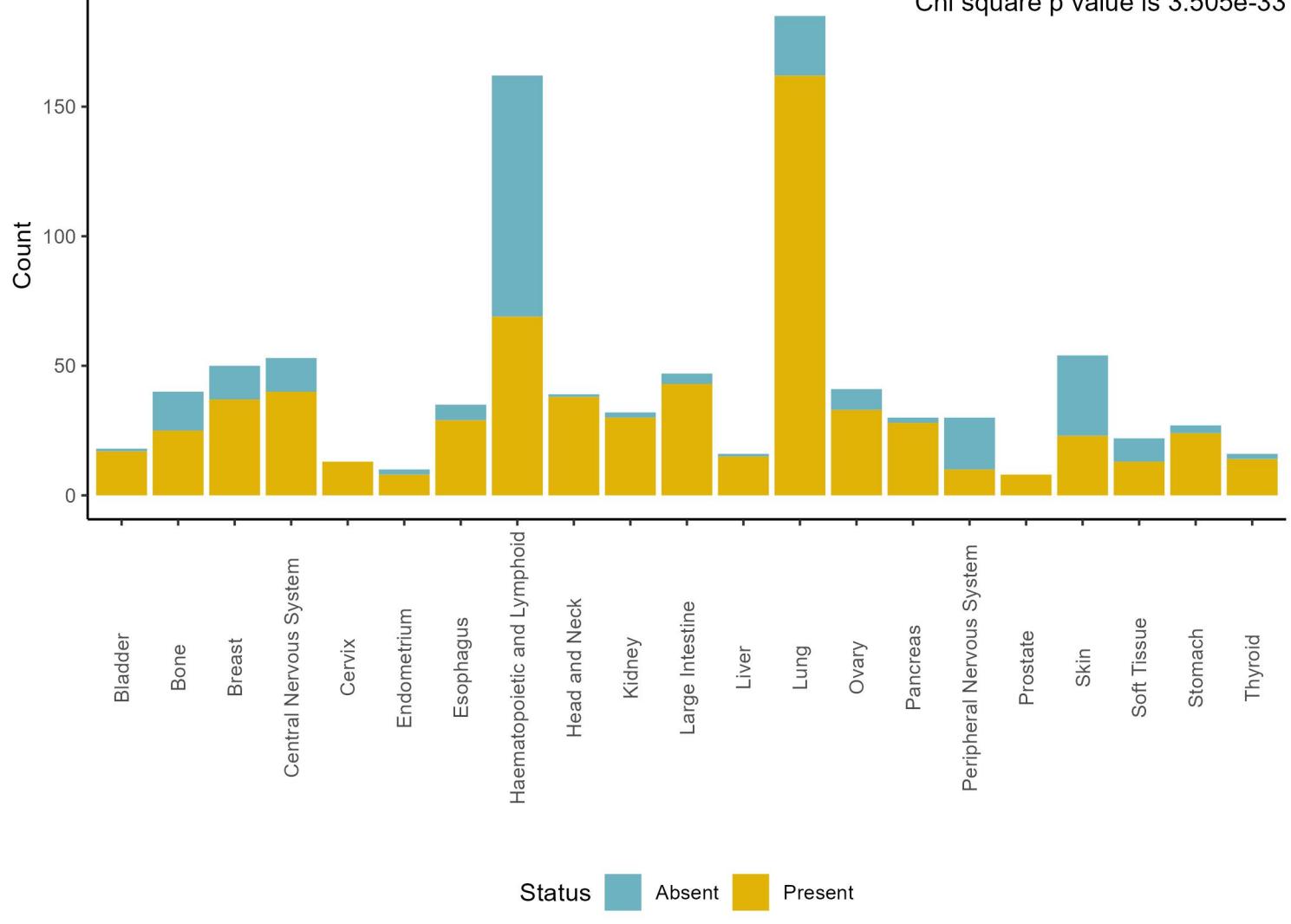
Amount of BCL2L1 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 2.026e-09



Present and absent BCL2L1 protein counts by tissue, DB1

Chi square p value is 3.505e-33

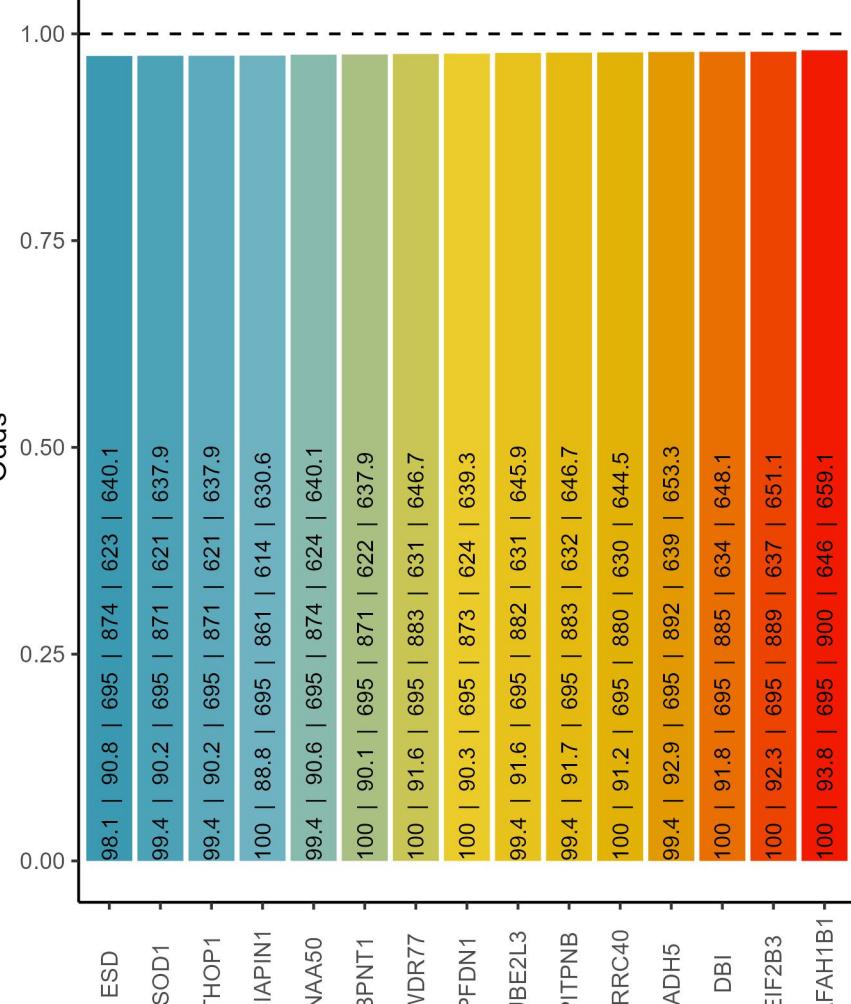


Cooccurrence with BCL2L1 protein, DB1

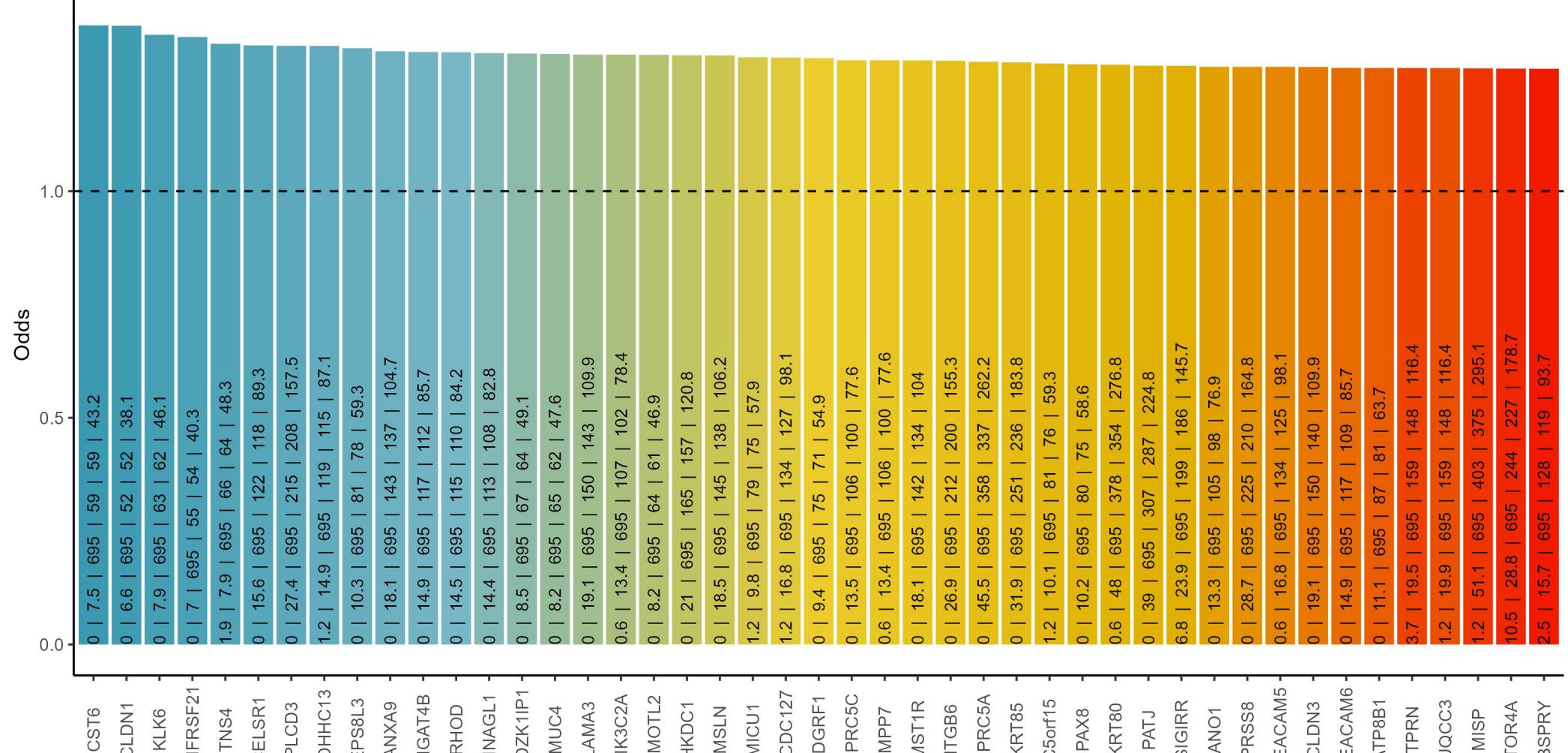
% of BCL2L1 in blood cancers: 42.6 ; % of BCL2L1 in solid cancers: 79.6

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of BCL2L1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

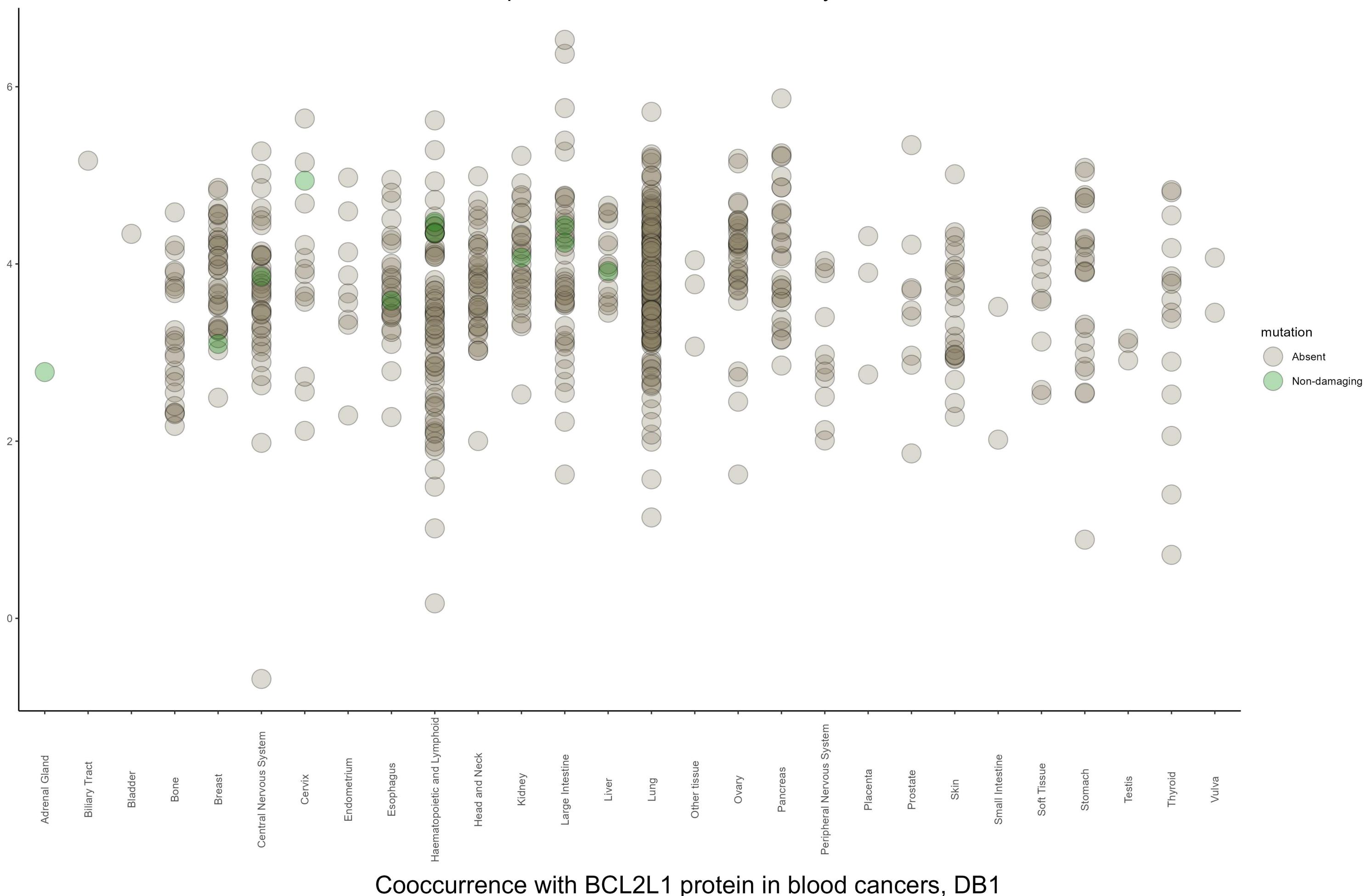
Negative cooccurrence



Positive cooccurrence

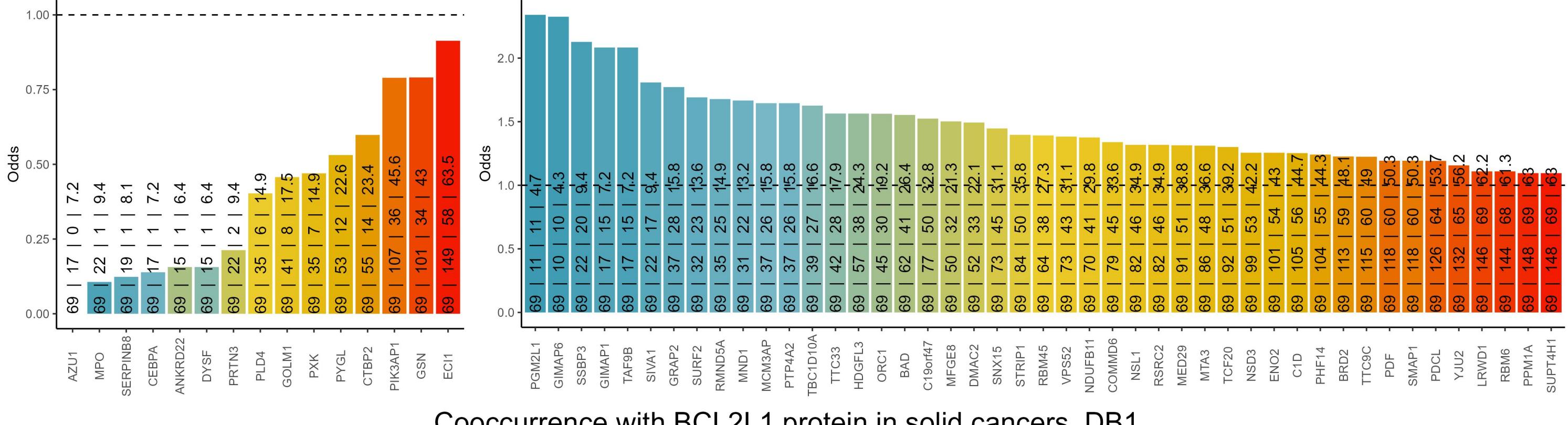


Amount of BCL2L1 protein and mutation status by tissue, DB1



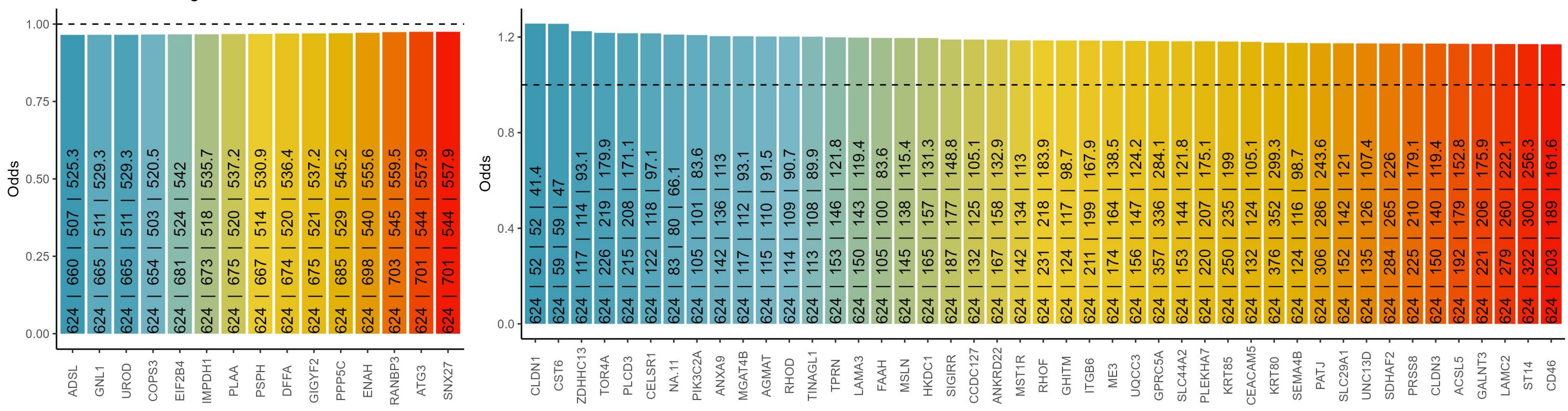
Cooccurrence with BCL2L1 protein in blood cancers, DB1

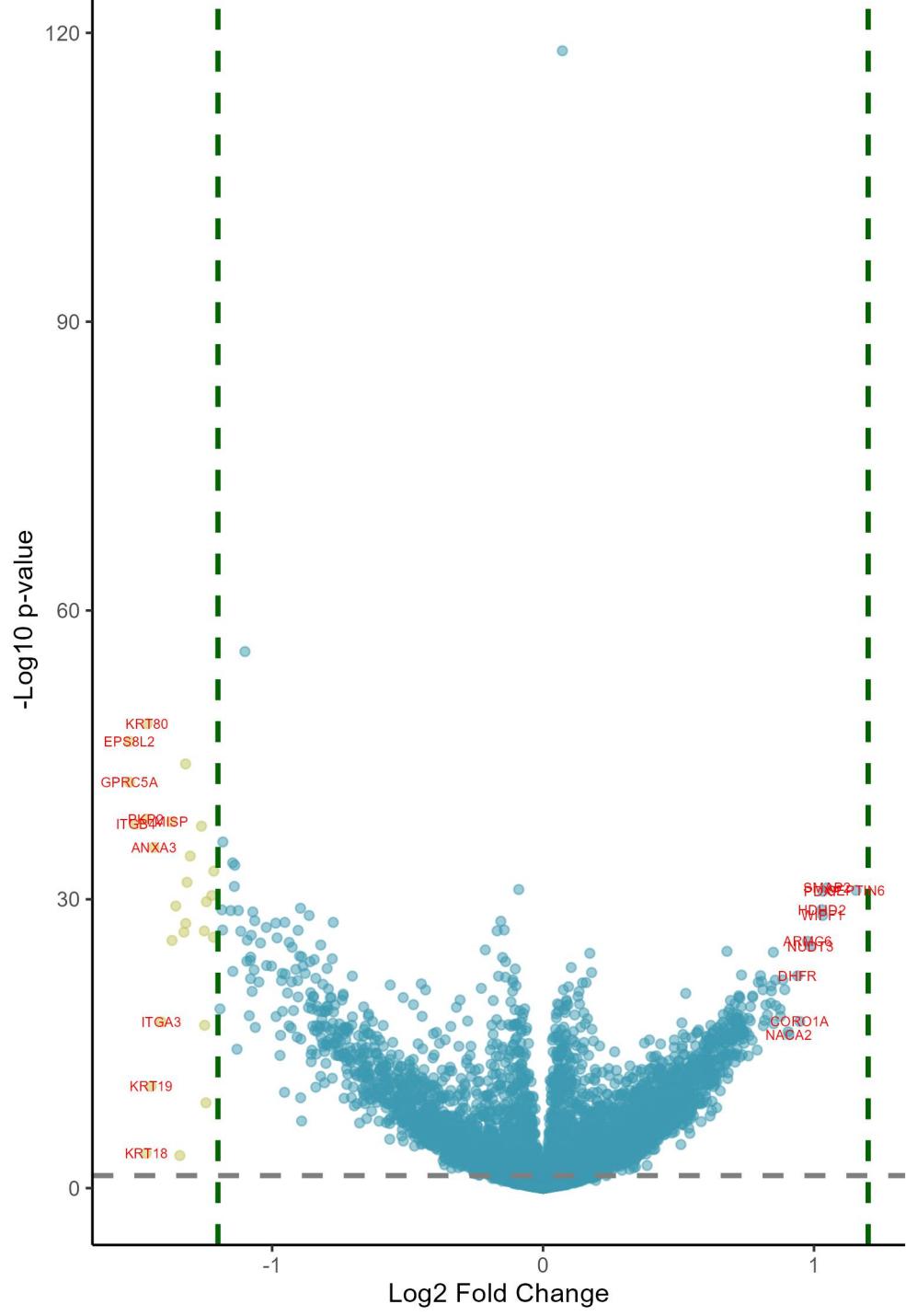
The text in the bars: incidence of BCL2L1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Cooccurrence with BCL2L1 protein in solid cancers, DB1

The text in the bars: incidence of BCL2L1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

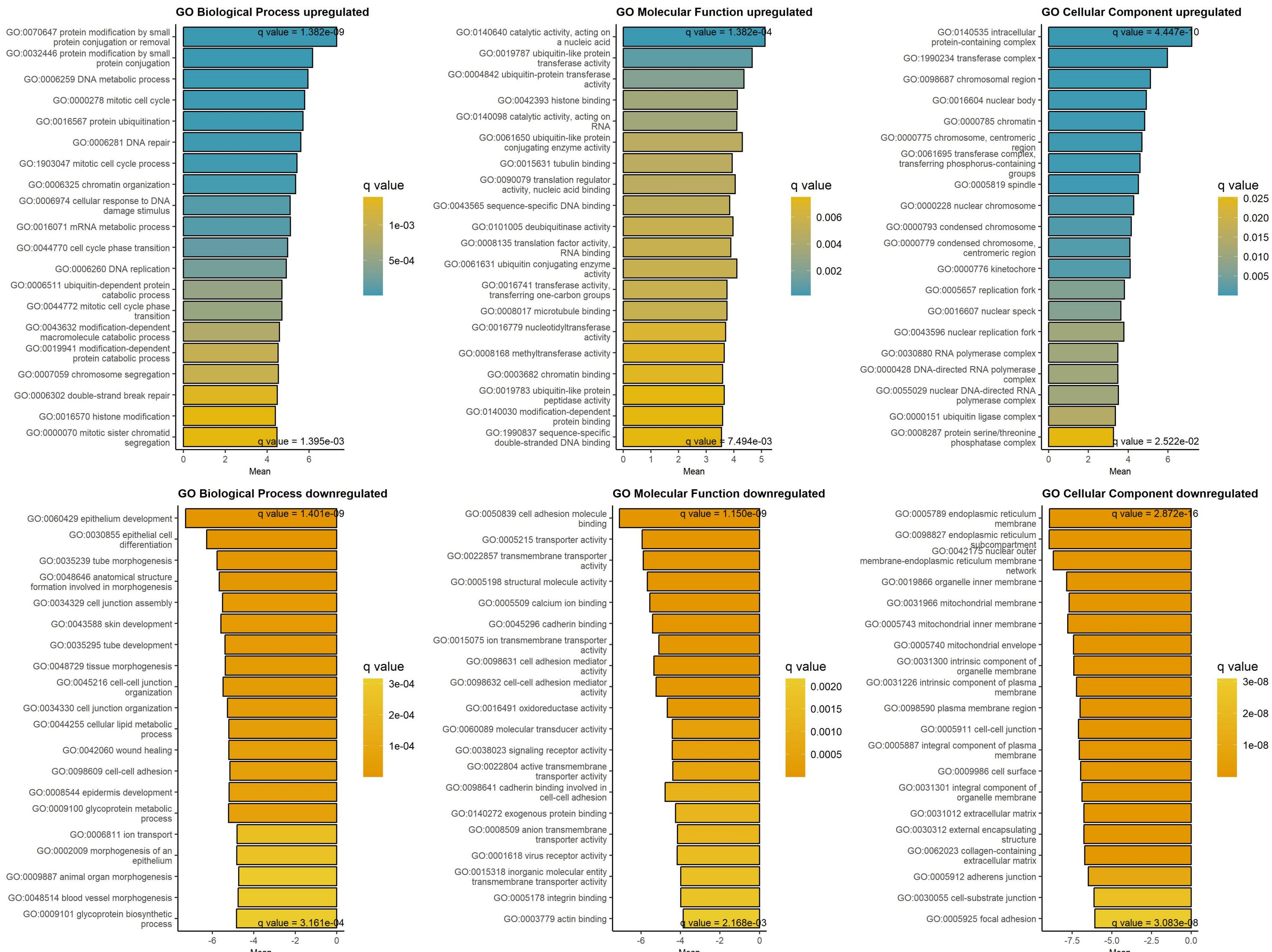




Downregulated at low/absent BCL2L1 Upregulated at low/absent BCL2L1

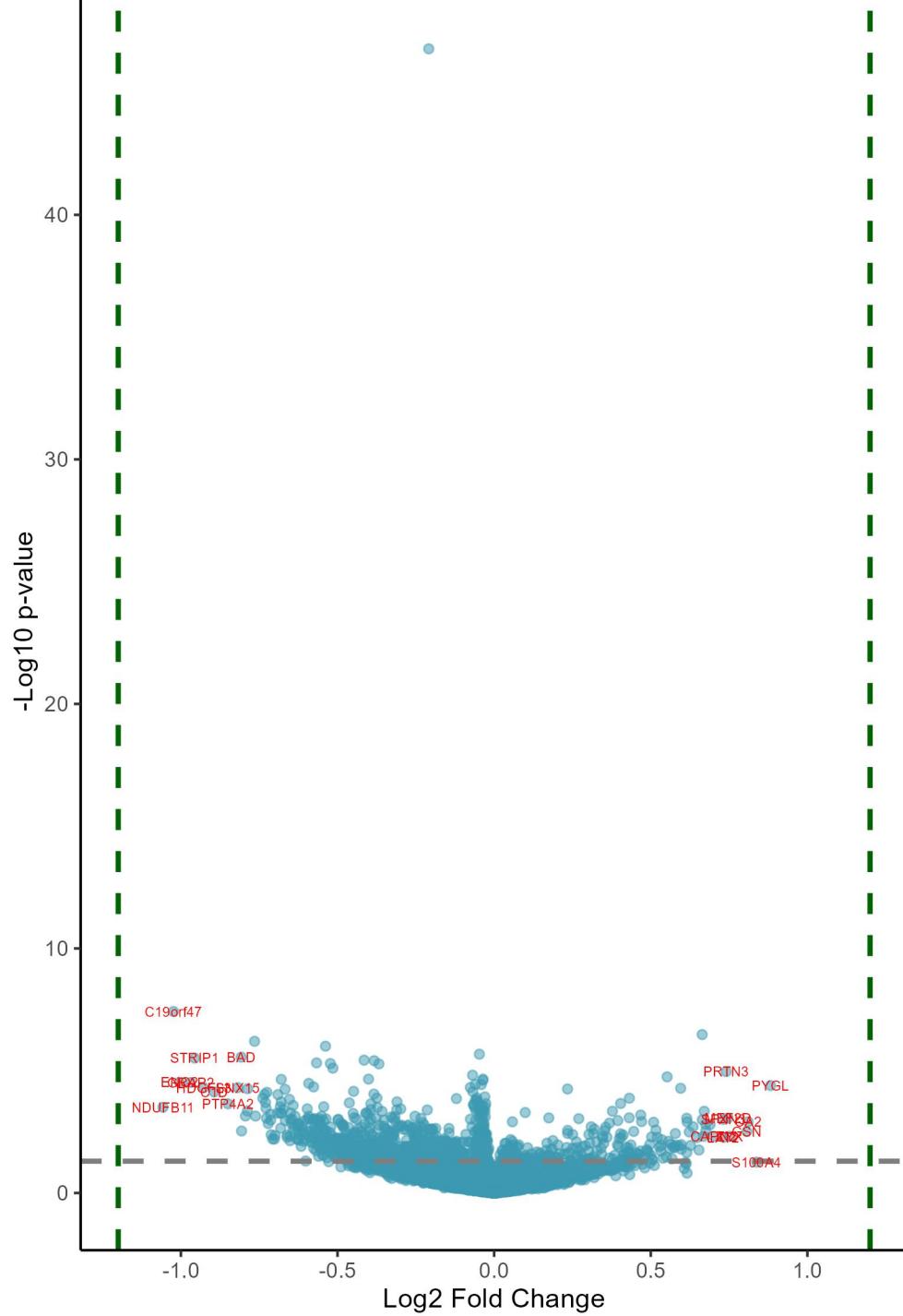
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.53	6.51e-40	GPRC5A	G protein-coupled receptor class C	1.16	3.52e-29	SEPTIN6	septin 6
-1.53	5.31e-44	EPS8L2	EPS8 like 2	1.05	2.14e-29	SMAP2	small ArfGAP2
-1.5	1.05e-35	ITGB4	integrin subunit beta 4	1.03	4.26e-29	PDXP	pyridoxal phosphatase
-1.47	3.84e-36	PKP2	plakophilin 2	1.03	9.38e-27	WIPF1	WAS/WASL interacting protein family
-1.46	5.30e-04	KRT18	keratin 18	1.03	2.85e-27	HDHD2	haloacid dehalogenase like hydrolase
-1.46	9.46e-46	KRT80	keratin 80	0.99	8.63e-24	NUDT3	nudix hydrolase 3
-1.45	1.86e-10	KRT19	keratin 19	0.98	2.88e-24	ARMC6	armadillo repeat containing 6
-1.44	2.04e-33	ANXA3	annexin A3	0.95	1.48e-16	CORO1A	coronin 1A
-1.41	1.69e-16	ITGA3	integrin subunit alpha 3	0.94	6.57e-21	DHFR	dihydrofolate reductase
-1.37	6.48e-36	MISP	mitotic spindle positioning	0.91	2.35e-15	NACA2	nascent polypeptide associated comp
-1.37	2.34e-24	JUP	junction plakoglobin	0.9	1.27e-15	BLMH	bleomycin hydrolase
-1.36	1.26e-27	EGFR	epidermal growth factor receptor	0.89	1.40e-19	ACYP1	acylphosphatase 1
-1.34	8.87e-04	KRT8	keratin 8	0.88	1.63e-20	UBE2T	ubiquitin conjugating enzyme E2 T
-1.33	3.63e-25	S100A16	S100 calcium binding protein A16	0.88	4.80e-17	UBE2V2	ubiquitin conjugating enzyme E2 V2
-1.32	9.73e-42	SDC4	syndecan 4	0.88	1.03e-17	AK6	adenylate kinase 6
-1.32	5.31e-26	ITGA2	integrin subunit alpha 2	0.86	4.71e-18	MAD2L1	mitotic arrest deficient 2 like 1
-1.31	6.35e-30	PKP3	plakophilin 3	0.86	1.70e-20	USP13	ubiquitin specific peptidase 13
-1.3	1.55e-32	EPHA2	EPH receptor A2	0.85	2.45e-16	PBK	PDZ binding kinase
-1.26	1.52e-35	CDCP1	CUB domain containing protein 1	0.85	3.37e-23	NUDT1	nudix hydrolase 1
-1.25	2.80e-25	DSG2	desmoglein 2	0.84	1.85e-19	TYMS	thymidylate synthetase
-1.25	3.36e-16	CAVIN1	caveolae associated protein 1	0.84	5.87e-20	HDDC2	HD domain containing 2
-1.24	7.23e-09	SFN	stratifin	0.84	2.72e-18	GINS2	GINS complex subunit 2
-1.24	4.73e-28	SPINT2	serine peptidase inhibitor, Kunitz	0.83	3.65e-17	UBR7	ubiquitin protein ligase E3 compone
-1.22	1.11e-28	BCAM	basal cell adhesion molecule (Luthe)	0.82	4.09e-18	PRPSAP2	phosphoribosyl pyrophosphate synthe
-1.22	1.18e-24	TGM2	transglutaminase 2	0.82	1.20e-16	COPS7B	COP9 signalosome subunit 7B
-1.22	4.66e-31	ZNF185	zinc finger protein 185 with LIM do	0.81	3.63e-16	C9orf78	chromosome 9 open reading frame 78
-1.19	9.56e-18	KRT7	keratin 7	0.81	1.41e-19	GTPBP1	GTP binding protein 1
-1.19	2.85e-27	ADAM9	ADAM metallopeptidase domain 9	0.81	2.23e-20	UCK2	uridine-cytidine kinase 2
-1.18	2.38e-25	PPL	periplakin	0.8	6.48e-21	RWDD4	RWD domain containing 4

GAGE analysis on upregulated and downregulated proteins at low/absent BCL2L1 protein, DB1

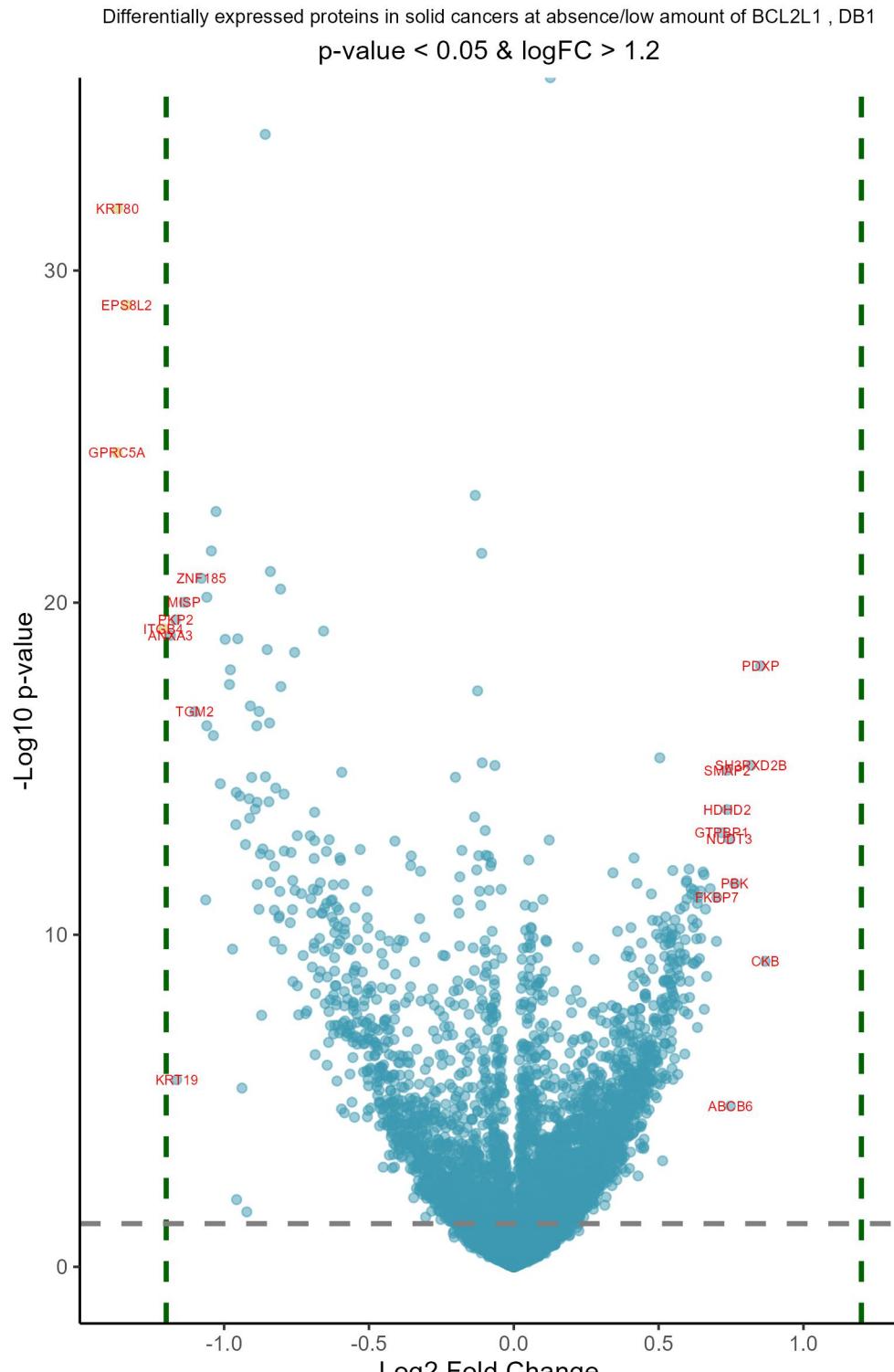


p-value < 0.05 & logFC > 1.2

Downregulated in blood cancers at low/absent BCL2L1 Upregulated in blood cancers at low/absent BCL2L1

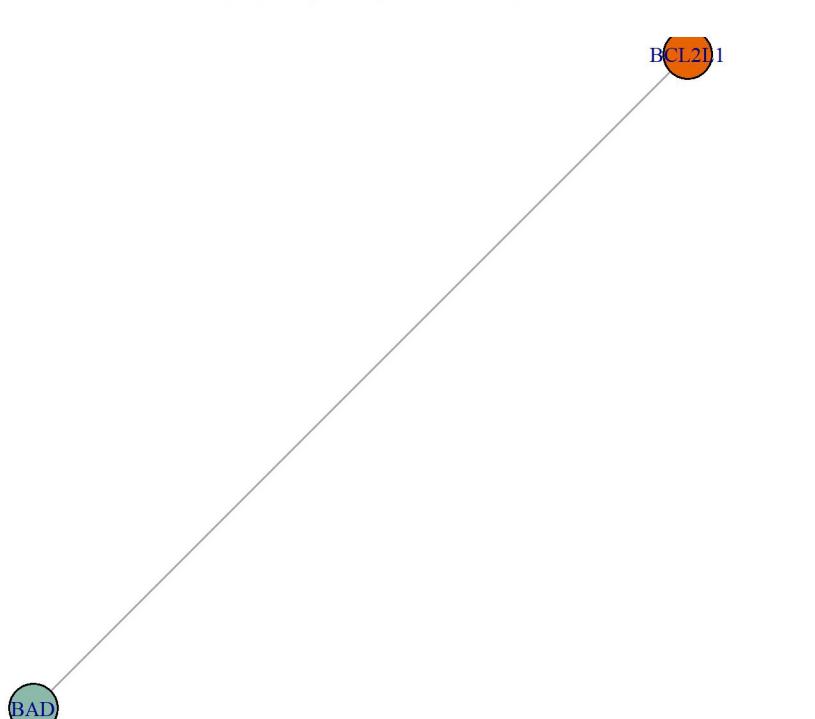


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.06	2.87e-02	NDUFB11	NADH:ubiquinone oxidoreductase subu	0.88	9.57e-03	PYGL	glycogen phosphorylase L
-1.02	8.38e-05	C19orf47	chromosome 19 open reading frame 47	0.84	2.89e-01	S100A4	S100 calcium binding protein A4
-1	8.40e-03	ENO2	enolase 2	0.81	5.22e-02	CA2	carbonic anhydrase 2
-0.97	8.40e-03	GRAP2	GRB2 related adaptor protein 2	0.81	8.25e-02	GSN	gelsolin
-0.96	2.23e-03	STRIP1	striatin interacting protein 1	0.75	1.01e-01	ZYX	zyxin
-0.93	1.02e-02	HDGFL3	HDGF like 3	0.75	4.61e-02	MEF2D	myocyte enhancer factor 2D
-0.89	1.24e-02	C1D	C1D nuclear receptor corepressor	0.74	4.53e-03	PRTN3	proteinase 3
-0.85	2.43e-02	PTP4A2	protein tyrosine phosphatase 4A2	0.73	4.66e-02	SFXN3	sideroflexin 3
-0.82	1.02e-02	SNX15	sorting nexin 15	0.73	1.05e-01	LAT2	linker for activation of T cells fa
-0.81	2.23e-03	BAD	BCL2 associated agonist of cell dea	0.7	1.00e-01	CAPN2	calpain 2
-0.81	7.99e-02	RAB11B	RAB11B, member RAS oncogene family	0.69	6.07e-02	CTBP2	C-terminal binding protein 2
-0.79	4.35e-02	NRAS	NRAS proto-oncogene, GTPase	0.68	7.99e-02	PIK3AP1	phosphoinositide-3-kinase adaptor p
-0.79	3.29e-02	ISCU	iron-sulfur cluster assembly enzyme	0.68	6.02e-02	CTSG	cathepsin G
-0.79	1.06e-02	BRD2	bromodomain containing 2	0.67	3.29e-02	GOLM1	golgi membrane protein 1
-0.76	8.33e-04	SSBP3	single stranded DNA binding protein	0.67	1.01e-01	TST	thiosulfate sulfurtransferase
-0.76	4.35e-02	ECE1	endothelin converting enzyme 1	0.66	4.73e-02	LYZ	lysozyme
-0.74	1.84e-02	FOXK2	forkhead box K2	0.66	5.52e-04	AZU1	azurocidin 1
-0.73	1.45e-02	TTC9C	tetratricopeptide repeat domain 9C	0.65	1.73e-01	CTSZ	cathepsin Z
-0.73	2.37e-02	PHF14	PHD finger protein 14	0.65	1.06e-01	GAA	alpha glucosidase
-0.73	3.06e-02	STAT5A	signal transducer and activator of	0.63	6.69e-02	PLD4	phospholipase D family member 4
-0.73	4.61e-02	MON2	MON2 homolog, regulator of endosome	0.63	1.45e-01	DOK3	docking protein 3
-0.73	1.27e-02	SMARCD1	SWI/SNF related, matrix associated,	0.62	8.39e-02	TNS3	tensin 3
-0.72	5.76e-02	RRAS2	RAS related 2	0.62	5.22e-02	S100A8	S100 calcium binding protein A8
-0.71	3.85e-02	MTA3	metastasis associated 1 family memb	0.62	3.76e-01	XPNPEP3	X-prolyl aminopeptidase 3
-0.71	4.77e-02	MFGE8	milk fat globule EGF and factor V/V	0.61	1.89e-01	STOM	stomatin
-0.71	9.34e-02	CLIP2	CAP-Gly domain containing linker pr	0.61	4.61e-02	PXK	PX domain containing serine/threoni
-0.71	1.13e-01	CTTN	cortactin	0.61	3.04e-01	CRIP1	cysteine rich protein 1
-0.7	1.13e-01	SEPTIN1	septin 1	0.61	2.95e-01	S100A6	S100 calcium binding protein A6
-0.7	9.76e-02	GSPT2	G1 to S phase transition 2	0.61	3.68e-01	LGALS1	galectin 1

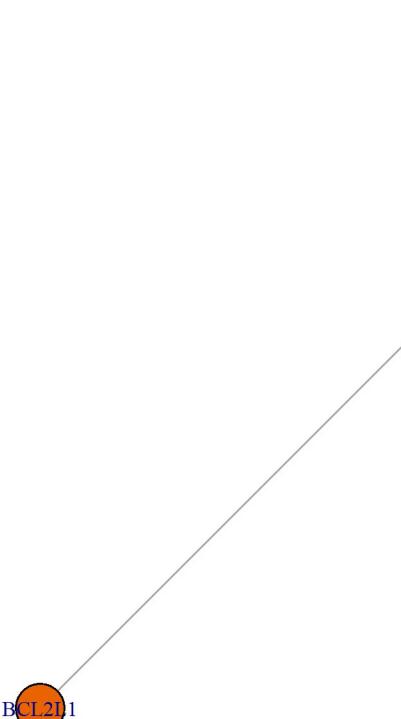


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.37	3.36e-22	GPRC5A	G protein-coupled receptor class C	0.87	1.64e-08	CKB	creatine kinase B
-1.37	2.27e-29	KRT80	keratin 80	0.85	2.23e-16	PDXP	pyridoxal phosphatase
-1.34	1.47e-26	EPS8L2	EPS8 like 2	0.82	1.37e-13	SH3PXD2B	SH3 and PX domains 2B
-1.21	2.42e-17	ITGB4	integrin subunit beta 4	0.76	1.84e-10	PBK	PDZ binding kinase
-1.19	3.39e-17	ANXA3	annexin A3	0.75	9.14e-05	ABCB6	ATP binding cassette subfamily B me
-1.17	1.37e-17	PKP2	plakophilin 2	0.74	1.37e-11	NUDT3	nudix hydrolase 3
-1.16	1.95e-05	KRT19	keratin 19	0.74	1.85e-13	SMAP2	small ArfGAP2
-1.14	4.33e-18	MISP	mitotic spindle positioning	0.74	2.09e-12	HDHD2	haloacid dehalogenase like hydrolas
-1.1	4.08e-15	TGM2	transglutaminase 2	0.72	9.37e-12	GTPBP1	GTP binding protein 1
-1.08	1.03e-18	ZNF185	zinc finger protein 185 with LIM do	0.7	4.07e-10	FKBP7	FKBP prolyl isomerase 7
-1.06	4.62e-10	KRT7	keratin 7	0.7	5.18e-09	UBE2V2	ubiquitin conjugating enzyme E2 V2
-1.06	9.95e-15	KRT85	keratin 85	0.68	2.50e-10	SEPTIN6	septin 6
-1.06	3.26e-18	IL18	interleukin 18	0.67	4.17e-08	TUBB4A	tubulin beta 4A class IVa
-1.04	2.05e-19	CDCP1	CUB domain containing protein 1	0.66	7.96e-10	ARMC6	armadillo repeat containing 6
-1.04	1.91e-14	PKP3	plakophilin 3	0.66	2.86e-07	TUBB2B	tubulin beta 2B class IIb
-1.03	1.50e-20	SDC4	syndecan 4	0.66	1.07e-10	YRDC	yrdC N6-threonylcarbamoyltransfers
-1.01	4.21e-13	VAMP8	vesicle associated membrane protein	0.65	9.14e-11	SCML2	Scm polycomb group protein like 2
-1	4.03e-17	LAMC2	laminin subunit gamma 2	0.65	4.45e-09	CRMP1	collapsin response mediator protein
-0.98	7.45e-16	EPHA2	EPH receptor A2	0.64	2.73e-10	UCK2	uridine-cytidine kinase 2
-0.98	2.80e-16	LAMB3	laminin subunit beta 3	0.64	1.41e-08	ACYP1	acylphosphatase 1
-0.97	8.00e-09	ITGA3	integrin subunit alpha 3	0.64	4.09e-10	NUDT1	nudix hydrolase 1
-0.96	5.56e-12	S100A16	S100 calcium binding protein A16	0.63	8.53e-07	BLMH	bleomycin hydrolase
-0.96	7.34e-13	SPINT2	serine peptidase inhibitor, Kunitz	0.63	5.71e-10	USP13	ubiquitin specific peptidase 13
-0.96	2.24e-02	KRT18	keratin 18	0.63	1.84e-09	SMAD4	SMAD family member 4
-0.95	4.03e-17	MET	MET proto-oncogene, receptor tyrosi	0.63	1.64e-08	DHFR	dihydrofolate reductase
-0.95	9.05e-13	EGFR	epidermal growth factor receptor	0.63	4.59e-09	PITHD1	PITH domain containing 1
-0.94	3.18e-05	SFN	stratin	0.62	1.92e-08	UBE2T	ubiquitin conjugating enzyme E2 T
-0.93	1.88e-11	TACSTD2	tumor associated calcium signal tra	0.62	2.67e-10	ZNF428	zinc finger protein 428
-0.92	4.61e-02	KRT8	keratin 8	0.62	2.37e-09	UBE2S	ubiquitin conjugating enzyme E2 S

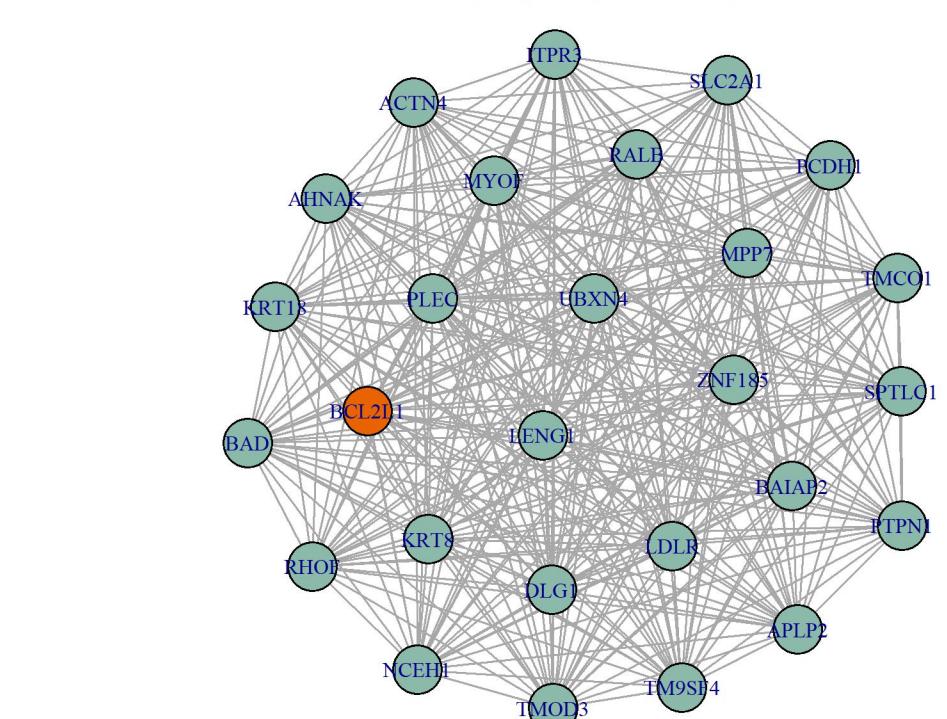
BCL2L1 network, DB1, all Pearson r > 0.4

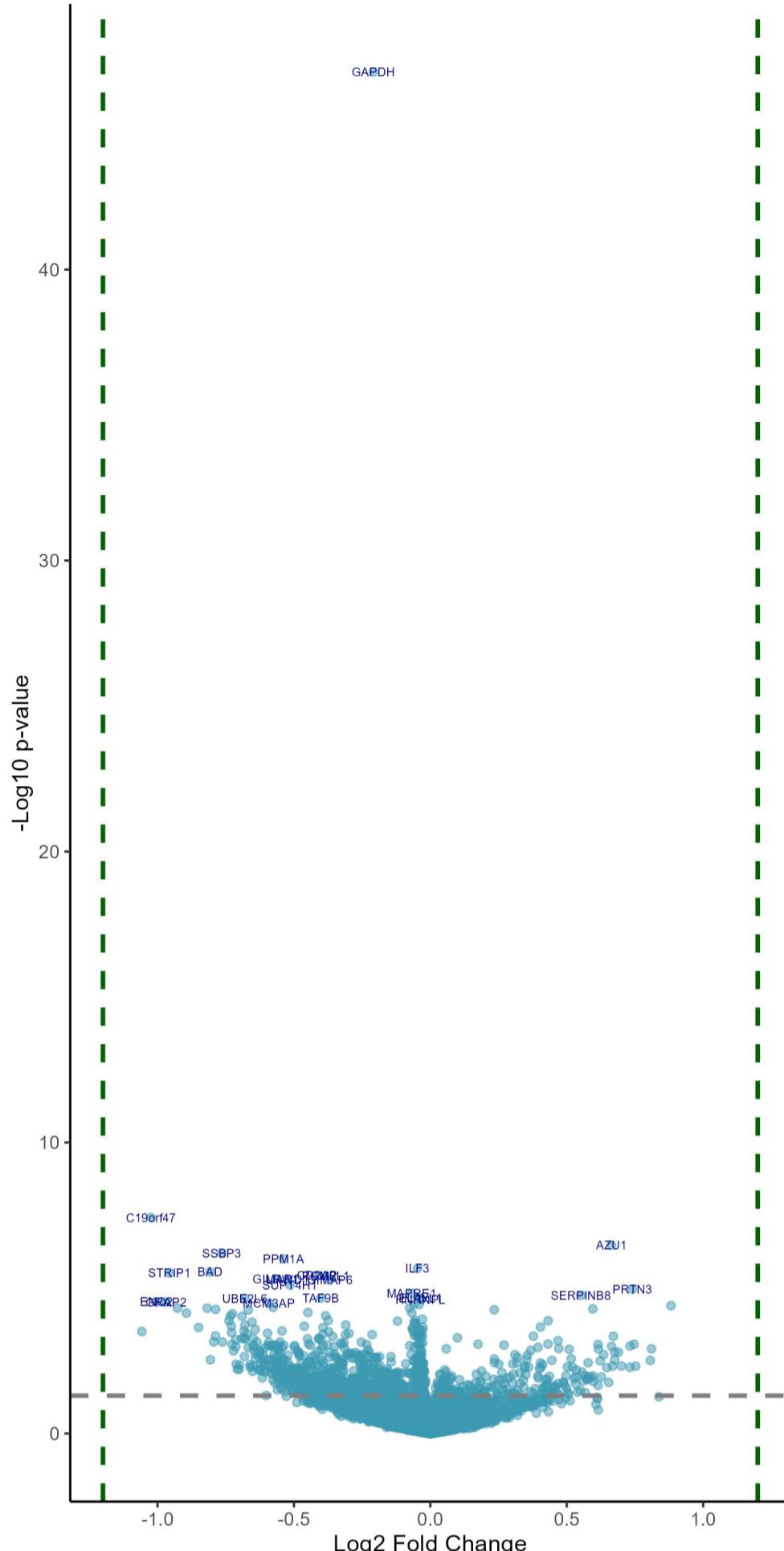


BCL2L1 network, DB1, all Pearson r > 0.35



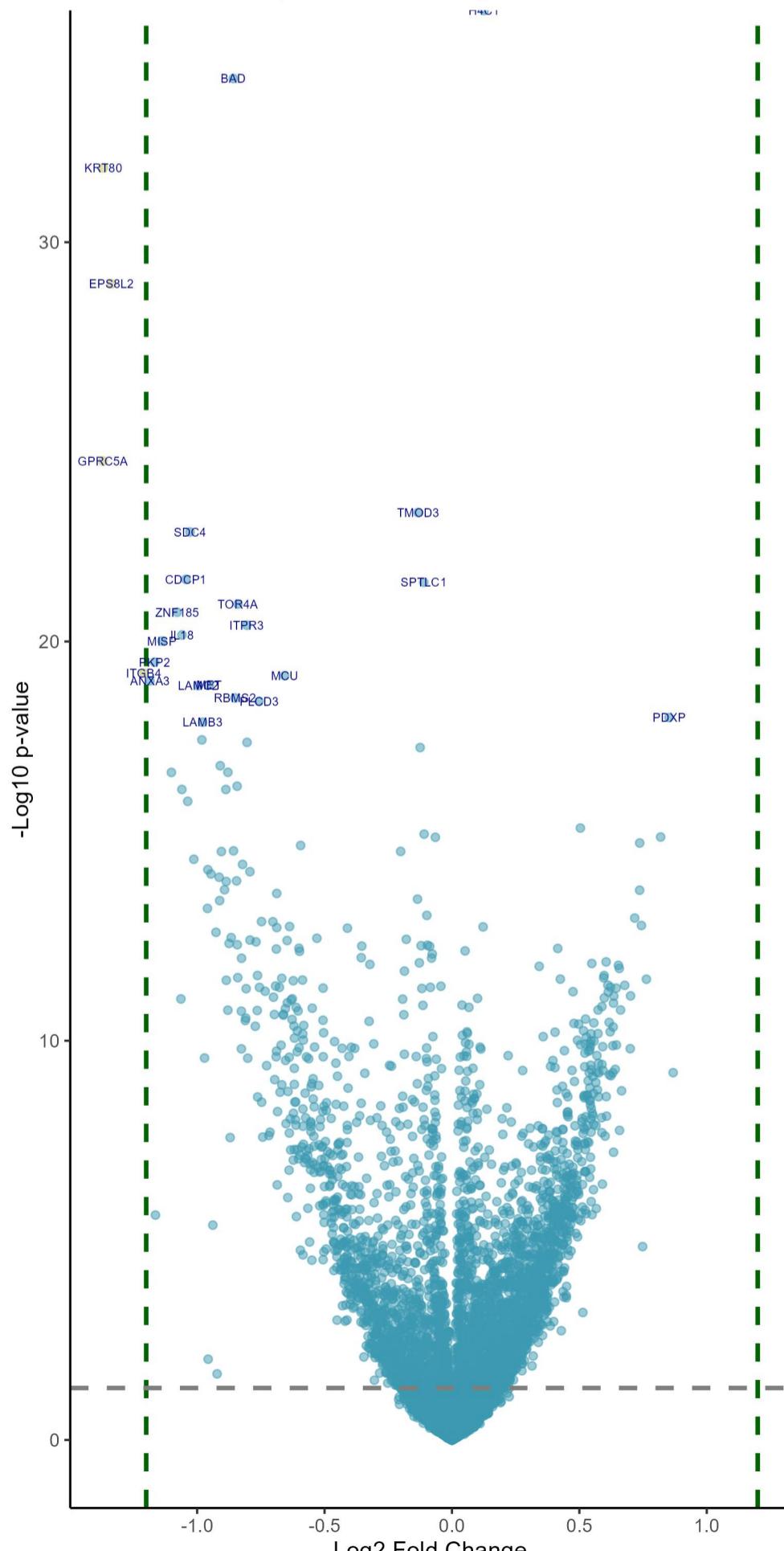
BCL2L1 network, DB1, all Pearson r > 0.3





Sorted by p values!
Downregulated in blood cancers at low/absent BCL2L1 Upregulated in blood cancers at low/absent BCL2L1

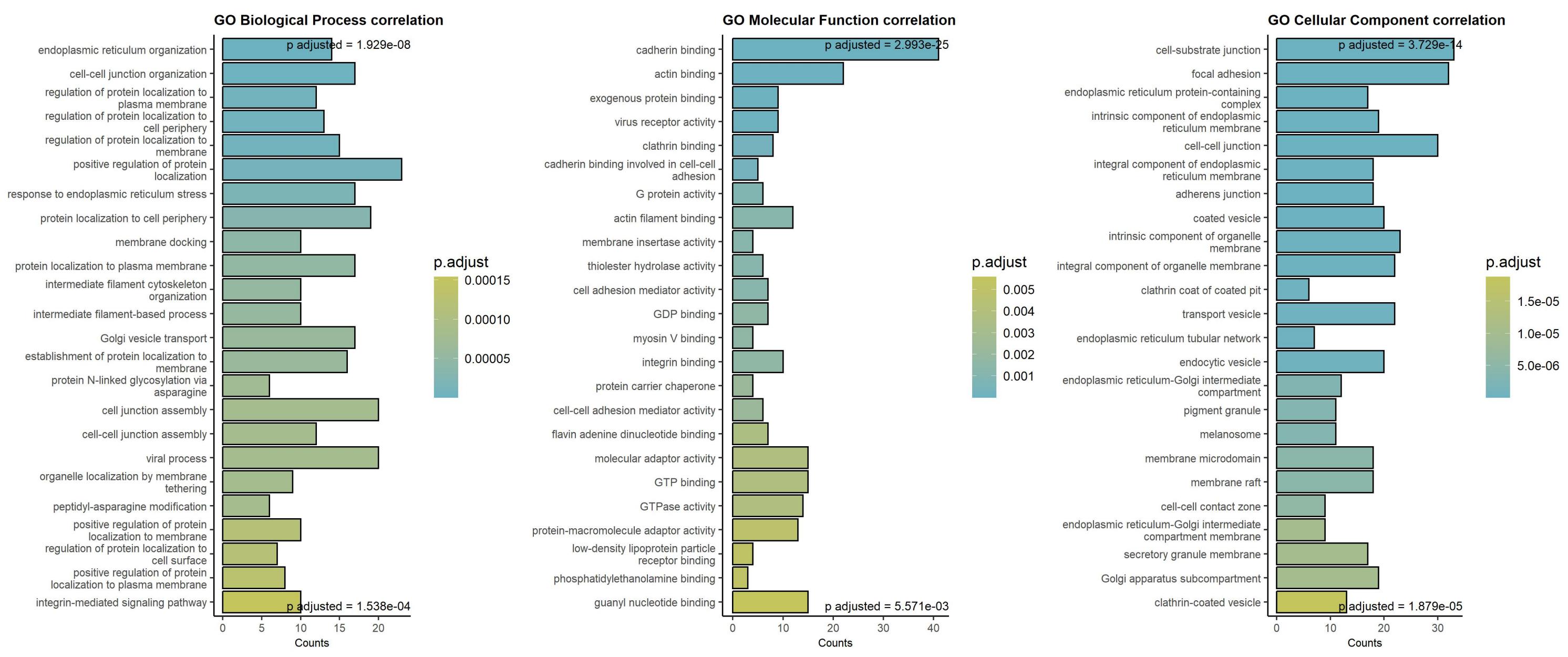
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.21	5.41e-44	GAPDH	glyceraldehyde-3-phosphate dehydrog	0.66	5.52e-04	AZU1	azurocidin 1
-1.02	8.38e-05	C19orf47	chromosome 19 open reading frame 47	0.74	4.53e-03	PRTN3	proteinase 3
-0.76	8.33e-04	SSBP3	single stranded DNA binding protein	0.55	6.58e-03	SERPINB8	serpin family B member 8
-0.54	1.10e-03	PPM1A	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe	0.88	9.57e-03	PYGL	glycogen phosphorylase L
-0.05	2.00e-03	ILF3	interleukin enhancer binding factor	0.6	1.05e-02	MPO	myeloperoxidase
-0.81	2.23e-03	BAD	BCL2 associated agonist of cell dea	0.23	1.06e-02	MAN2B1	mannosidase alpha class 2B member 1
-0.96	2.23e-03	STRIP1	striatin interacting protein 1	0.43	1.84e-02	CEBPA	CCAAT enhancer binding protein alph
-0.42	2.35e-03	CD2AP	CD2 associated protein	0.4	2.43e-02	ANKRD22	ankyrin repeat domain 22
-0.38	2.35e-03	PGM2L1	phosphoglucomutase 2 like 1	0.38	3.29e-02	DYSF	dystrofelin
-0.57	2.49e-03	GIMAP1	GTPase, IMAP family member 1	0.67	3.29e-02	GOLM1	golgi membrane protein 1
-0.52	2.49e-03	LRWD1	leucine rich repeats and WD repeat	0.1	3.58e-02	ACAT1	acetyl-CoA acetyltransferase 1
-0.37	2.49e-03	GIMAP6	GTPase, IMAP family member 6	0.47	4.10e-02	RCN3	reticulocalbin 3
-0.51	3.49e-03	SUPT4H1	SPT4 homolog, DSIF elongation facto	0.43	4.61e-02	BST1	bone marrow stromal cell antigen 1
-0.07	5.95e-03	MAPRE1	microtubule associated protein RP/E	0.17	4.61e-02	IMPDH1	inosine monophosphate dehydrogenase
-0.4	7.16e-03	TAF9B	TATA-box binding protein associated	0.75	4.61e-02	MEF2D	myocyte enhancer factor 2D
-0.04	7.16e-03	ELAVL1	ELAV like RNA binding protein 1	0.61	4.61e-02	PXK	PX domain containing serine/threoni
-0.68	7.16e-03	UBE2L6	ubiquitin conjugating enzyme E2 L6	0.27	4.61e-02	ABCD1	ATP binding cassette subfamily D me
-0.04	7.45e-03	HNRNPL	heterogeneous nuclear ribonucleopro	0.73	4.66e-02	SFXN3	sideroflexin 3
-1	8.40e-03	ENO2	enolase 2	0.66	4.73e-02	LYZ	lysozyme
-0.97	8.40e-03	GRAP2	GRB2 related adaptor protein 2	0.39	4.84e-02	CLCN7	chloride voltage-gated channel 7
-0.59	8.75e-03	MCM3AP	minichromosome maintenance complex	0.47	5.17e-02	ECI1	enoyl-CoA delta isomerase 1
-0.06	9.14e-03	PARK7	Parkinsonism associated deglycase	0.81	5.22e-02	CA2	carbonic anhydrase 2
-0.04	9.14e-03	SRRT	serrate, RNA effector molecule	0.06	5.22e-02	IARS1	isoleucyl-tRNA synthetase 1
-0.58	1.02e-02	PPM1B	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe	0.62	5.22e-02	S100A8	S100 calcium binding protein A8
-0.08	1.02e-02	ERH	ERH mRNA splicing and mitosis facto	0.51	5.33e-02	CERS2	ceramide synthase 2
-0.82	1.02e-02	SNX15	sorting nexin 15	0.37	5.70e-02	RAB44	RAB44, member RAS oncogene family
-0.93	1.02e-02	HDGFL3	HDGF like 3	0.68	6.02e-02	CTSG	cathepsin G
-0.79	1.06e-02	BRD2	bromodomain containing 2	0.69	6.07e-02	CTBP2	C-terminal binding protein 2
-0.67	1.06e-02	PDCL	phosducin like	0.63	6.69e-02	PLD4	phospholipase D family member 4
-0.45	1.24e-02	GUK1	guanylate kinase 1	0.31	6.69e-02	ALK	ALK receptor tyrosine kinase
-0.07	1.24e-02	HNRNPA0	heterogeneous nuclear ribonucleopro	0.36	6.76e-02	RNASE2	ribonuclease A family member 2
-0.89	1.24e-02	C1D	C1D nuclear receptor corepressor	0.32	7.36e-02	VCL	vinculin
-0.73	1.27e-02	SMARCD1	SWI/SNF related, matrix associated,	0.52	7.74e-02	KBTBD11	kelch repeat and BTB domain contain
-0.38	1.45e-02	SFSWAP	splicing factor SWAP	0.23	7.80e-02	NLN	neurolysin
-0.73	1.45e-02	TTC9C	tetratricopeptide repeat domain 9C	0.35	7.97e-02	FBP1	fructose-bisphosphatase 1
-0.69	1.46e-02	SMAP1	small ArfGAP 1	0.68	7.99e-02	PIK3AP1	phosphoinositide-3-kinase adaptor p
-0.03	1.77e-02	SRSF3	serine and arginine rich splicing f	0.45	8.25e-02	CES1	carboxylesterase 1
-0.06	1.84e-02	PTGES3	prostaglandin E synthase 3	0.81	8.25e-02	GSN	gelsolin
0.37	1.84e-02	ADP ribosylation factor like GTPase		0.62	8.39e-02	TNS3	tonin 3



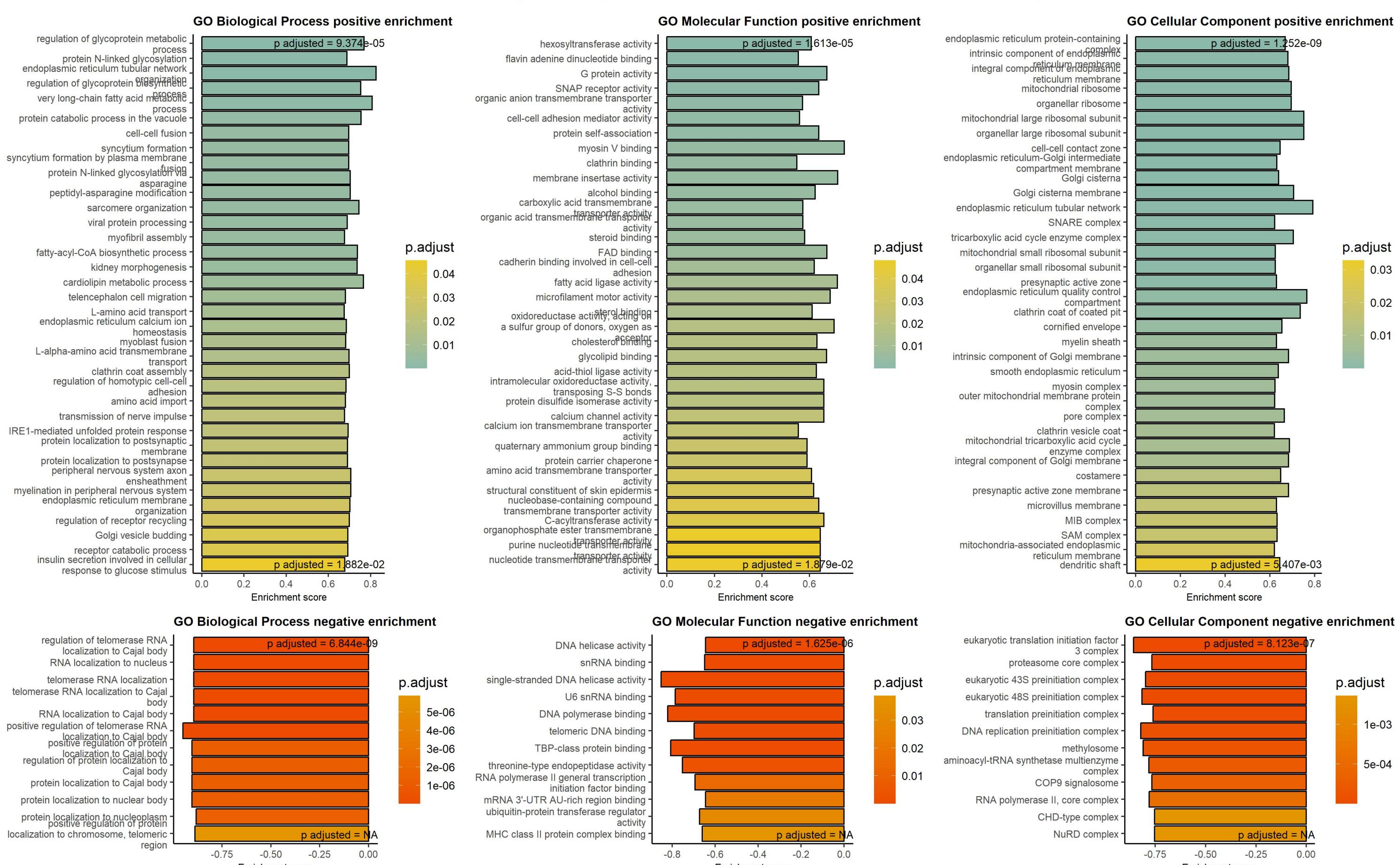
Sorted by p values!
Downregulated in solid cancers at low/absent BCL2L1 Upregulated in solid cancers at low/absent BCL2L1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.86	1.75e-31	BAD	BCL2 associated agonist of cell dea	0.13	0.00e+00	H4C1	H4 clustered histone 1
-1.37	2.27e-29	KRT80	keratin 80	0.85	2.23e-16	PDXP	pyridoxal phosphatase
-1.34	1.47e-26	EPS8L2	EPS8 like 2	0.5	8.71e-14	ZEB2	zinc finger E-box binding homeobox
-1.37	3.36e-22	GPRC5A	G protein-coupled receptor class C	0.82	1.37e-13	SH3PXD2B	SH3 and PX domains 2B
-0.13	5.59e-21	TMOD3	tropomodulin 3	0.74	1.85e-13	SMAP2	small ArfGAP2
-1.03	1.50e-20	SDC4	syndecan 4	0.74	2.09e-12	HDHD2	haloacid dehalogenase like hydrolas
-1.04	2.05e-19	CDCP1	CUB domain containing protein 1	0.72	9.37e-12	GTPBP1	GTP binding protein 1
-0.11	2.18e-19	SPTLC1	serine palmitoyltransferase long ch	0.74	1.37e-11	NUDT3	nudix hydrolase 3
-0.84	6.97e-19	TOR4A	torsin family 4 member A	0.12	1.44e-11	NASP	nuclear autoantigenic sperm protein
-1.08	1.03e-18	ZNF185	zinc finger protein 185 with LIM do	0.42	3.96e-11	PCBP4	poly(rC) binding protein 4
-0.81	2.00e-18	ITPR3	inositol 1,4,5-trisphosphate recept	0.05	4.45e-11	HSP90AB1	heat shock protein 90 alpha family
-1.06	3.26e-18	IL18	interleukin 18	0.61	7.83e-11	PHF23	PHD finger protein 23
-1.14	4.33e-18	MISP	mitotic spindle positioning	0.55	8.40e-11	HPF1	histone PARylation factor 1
-1.17	1.37e-17	PKP2	plakophilin 2	0.65	9.14e-11	SCML2	Scm polycomb group protein like 2
-1.21	2.42e-17	ITGB4	integrin subunit beta 4	0.34	9.58e-11	MAP2K6	mitogen-activated protein kinase ki
-0.66	2.65e-17	MCU	mitochondrial calcium uniporter	0.66	1.07e-10	YRDC	yrdC N6-threonylcarbamoyltransferas
-1.19	3.39e-17	ANXA3	annexin A3	0.6	1.56e-10	PAPOLA	poly(A) polymerase alpha
-0.95	4.03e-17	MET	MET proto-oncogene, receptor tyrosi	0.6	1.75e-10	YTHDF2	YTH N6-methyladenosine RNA binding
-1	4.03e-17	LAMC2	laminin subunit gamma 2	0.43	1.84e-10	GSTM2	glutathione S-transferase mu 2
-0.85	7.84e-17	RBMS2	RNA binding motif single stranded i	0.76	1.84e-10	PBK	PDZ binding kinase
-0.76	9.10e-17	PLCD3	phospholipase C delta 3	0.61	2.49e-10	AGAP3	ArfGAP with GTPase domain, ankyrin
-0.98	2.80e-16	LAMB3	laminin subunit beta 3	0.68	2.50e-10	SEPTIN6	septin 6
-0.98	7.45e-16	EPHA2	EPH receptor A2	0.62	2.67e-10	ZNF428	zinc finger protein 428
-0.8	8.29e-16	RHOF	ras homolog family member F, filopo	0.64	2.73e-10	UCK2	uridine-cytidine kinase 2
-0.12	1.08e-15	ACTN4	actinin alpha 4	0.47	3.25e-10	GNL1	G protein nucleolar 1 (putative)
-0.91	2.97e-15	EVPL	envoplakin	0.61	3.28e-10	DPYSL4	dihydropyrimidinase like 4
-0.88	4.08e-15	KIAA1522	KIAA1522	0.7	4.07e-10	FKBP7	FKBP prolyl isomerase 7
-1.1	4.08e-15	TGM2	transglutaminase 2	0.64	4.09e-10	NUDT1	nudix hydrolase 1
-0.84	8.74e-15	TNFAIP2	TNF alpha induced protein 2	0.6	4.46e-10	EIF4G3	eukaryotic translation initiation f
-1.06	9.95e-15	KRT85	keratin 85	0.1	4.55e-10	RBBP4	RB binding protein 4, chromatin rem
-0.89	9.95e-15	LAMA5	laminin				

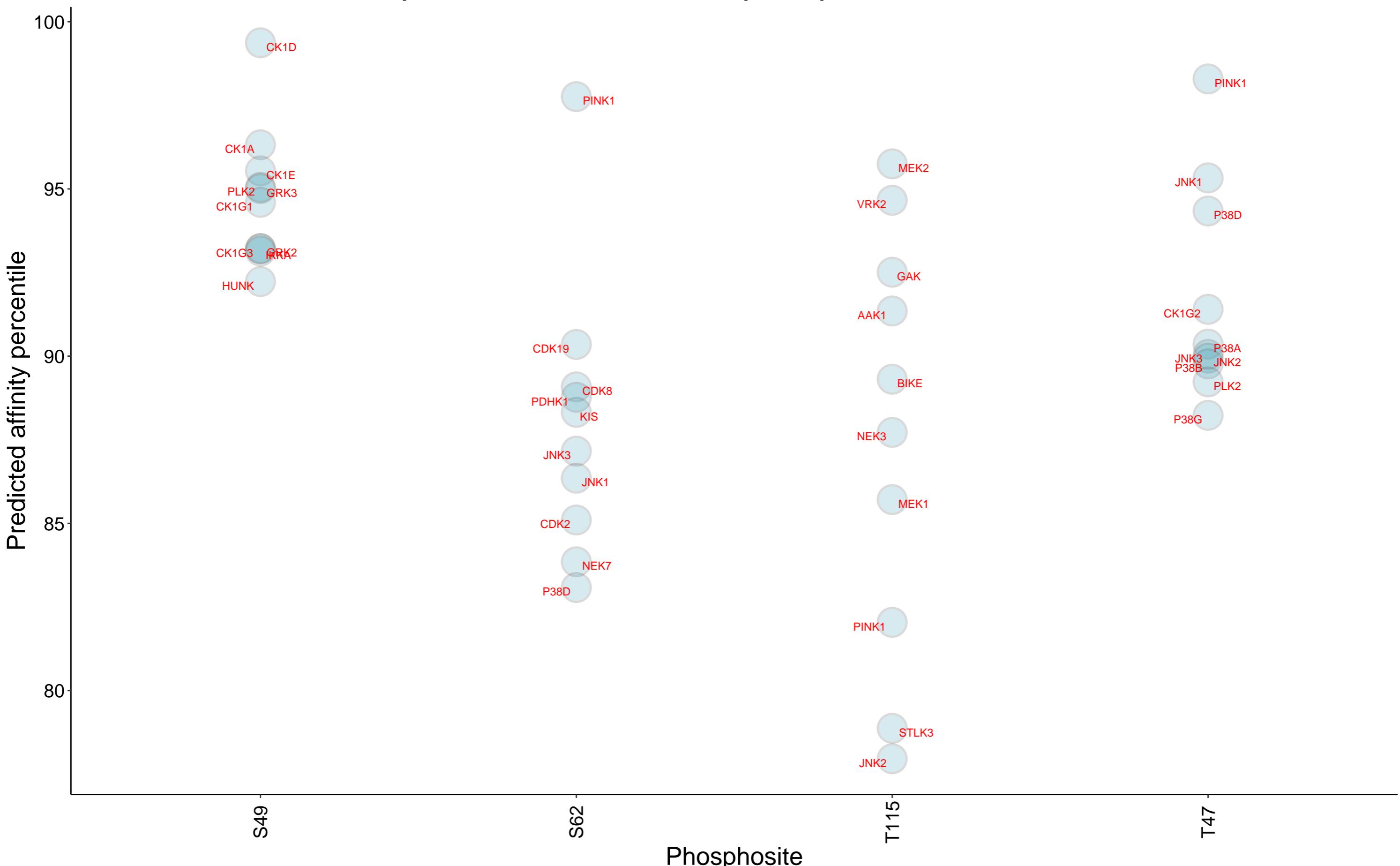
Top 250 correlation coefficients overrepresentation, BCL2L1 protein, DB1



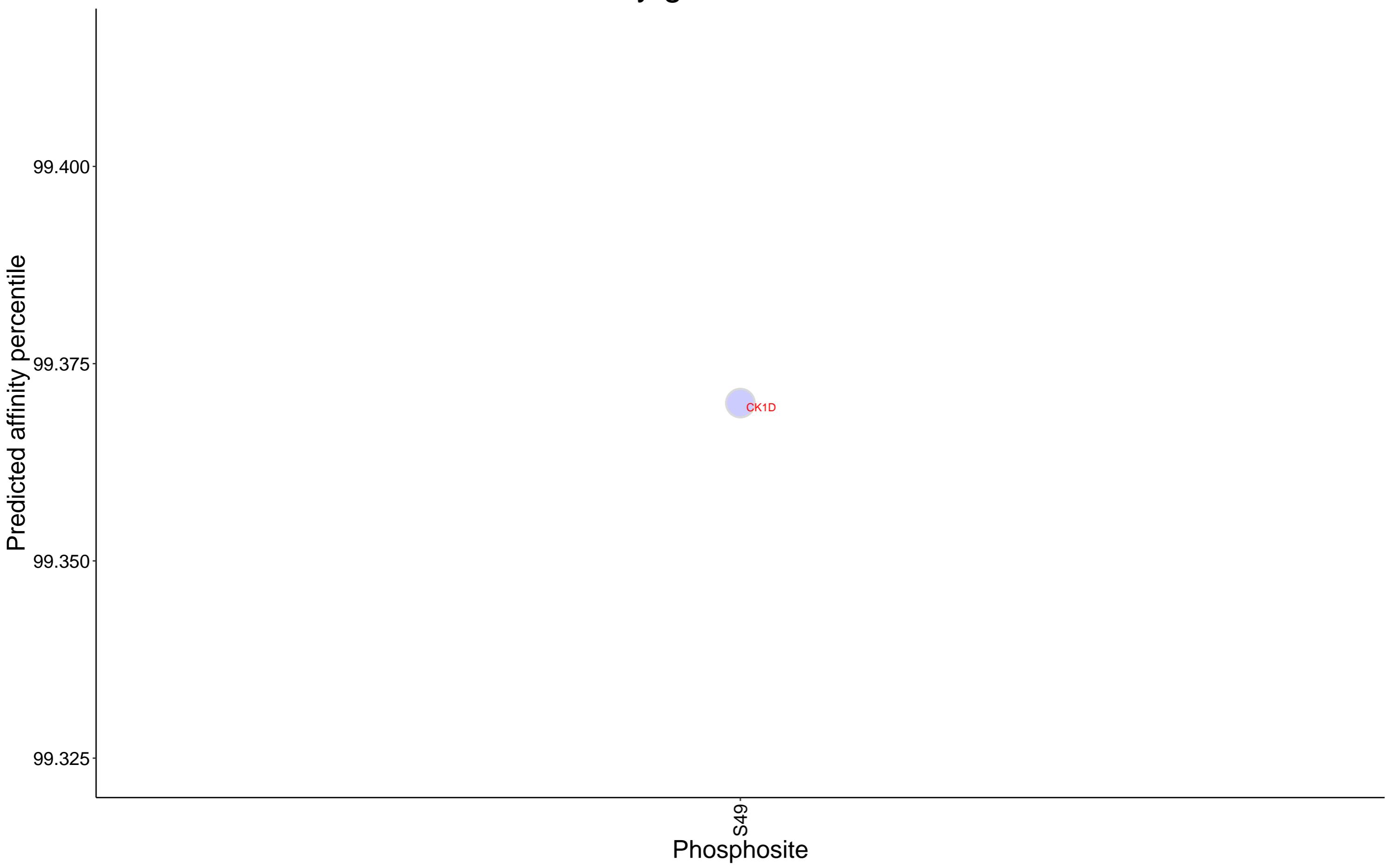
Gene Set Enrichment analysis on protein correlation coefficients, BCL2L1 protein, DB1



Top 10 kinases for each phosphosite in BCL2L1



Kinases with affinity greater than 98.5% to BCL2L1



Top 15 positive correlation coefficients for BCL2L1 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

