

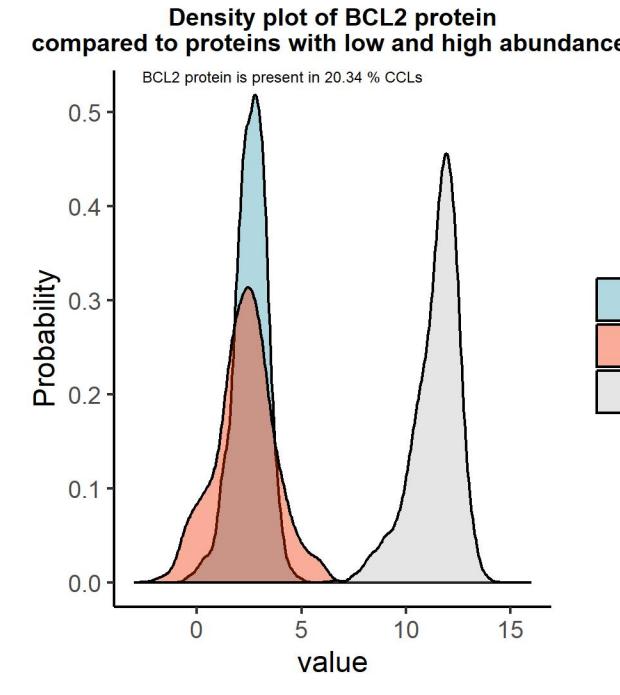
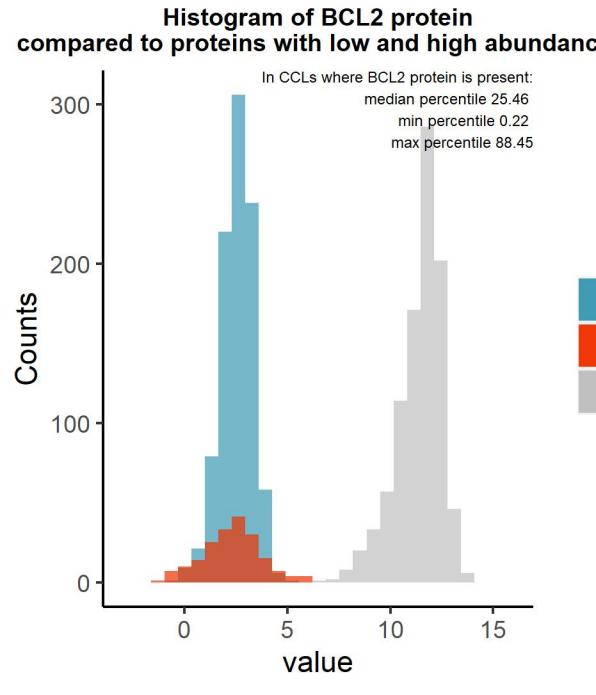
BCL2

Protein name: BCL2 ; UNIPROT: P10415 ; Gene name: BCL2 apoptosis regulator

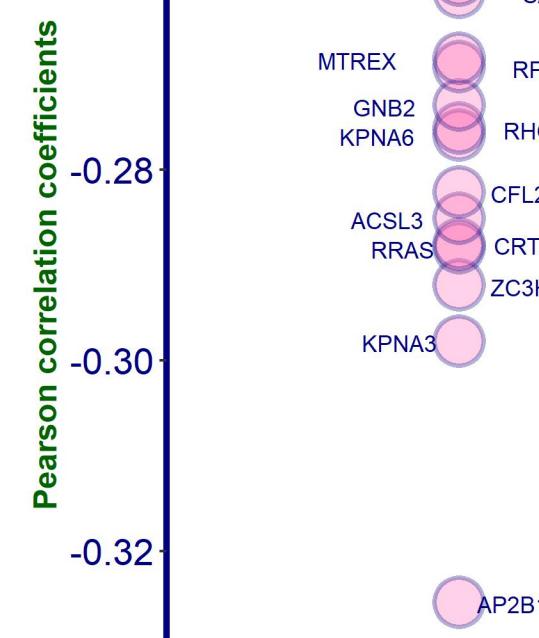
Ligandable: Yes ; Ligandable_by_Chem: Yes ; Is_enzyme: NA (<https://cansar.ai/>)

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

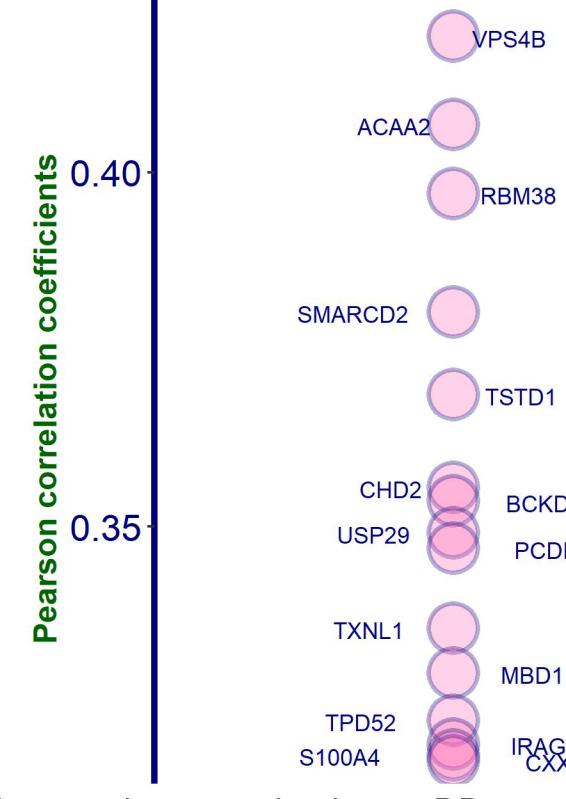
8498 proteins in same 949 CCLs



Negative correlations of BCL2 protein, DB2

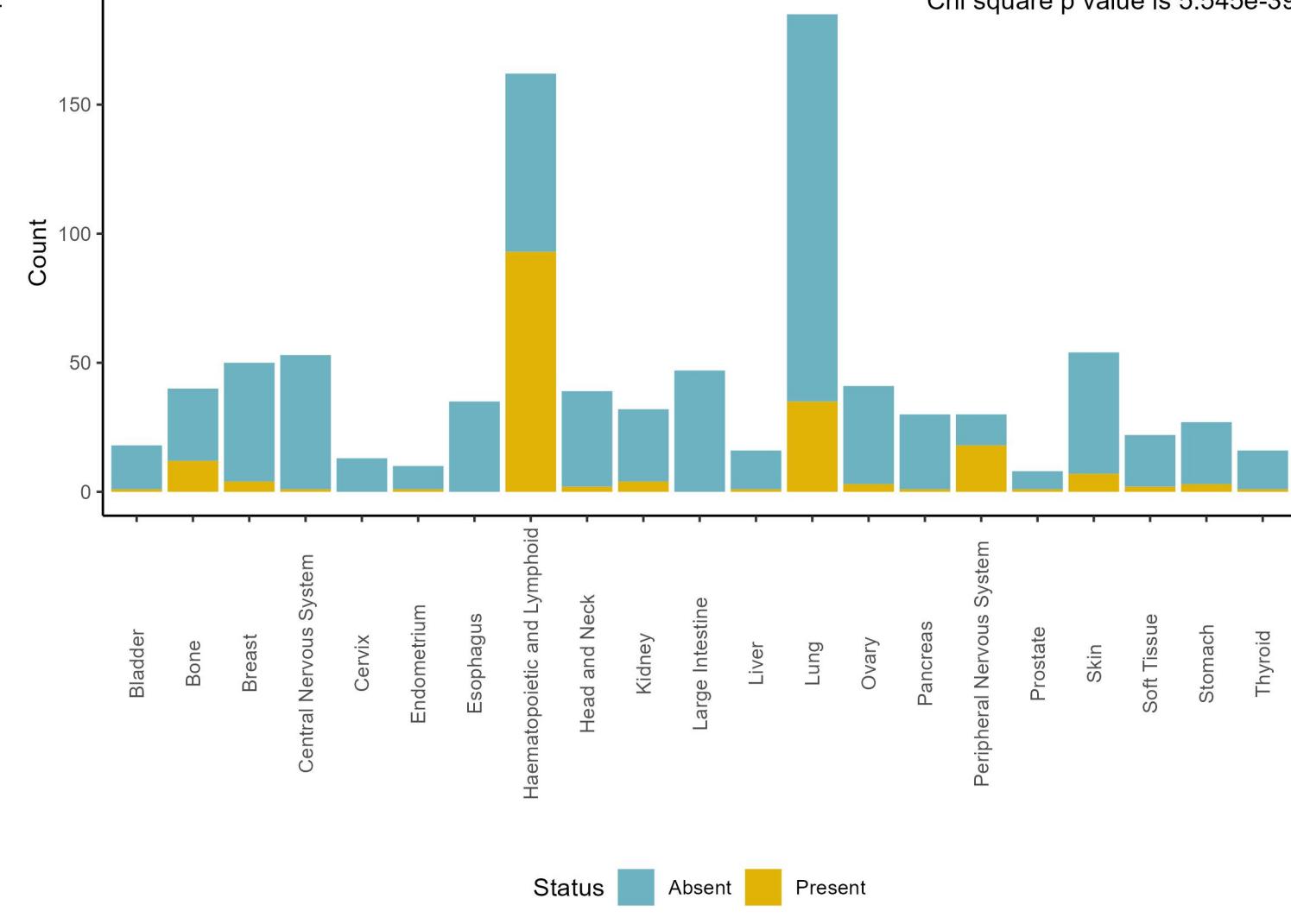
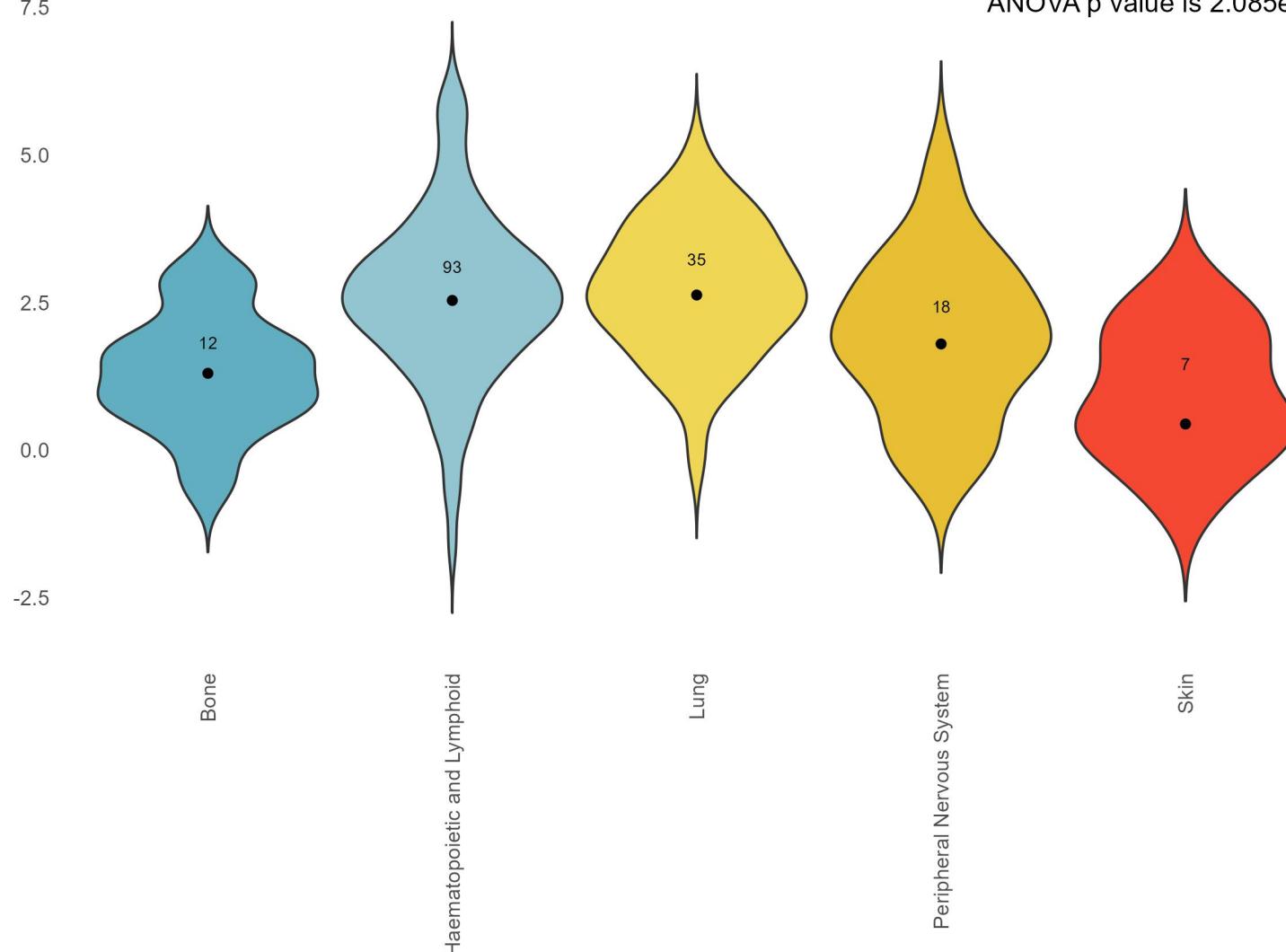


Positive correlations of BCL2 protein, DB2



Amount of BCL2 protein, number of CCLs where it is present by tissue, DB2

ANOVA p value is 2.085e-04

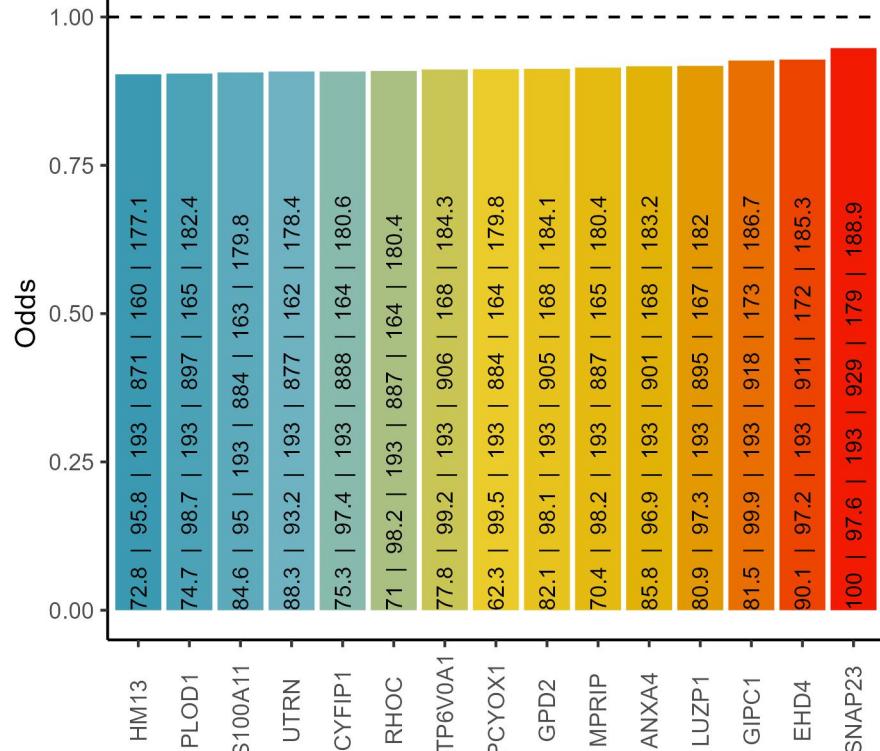


Cooccurrence with BCL2 protein, DB2

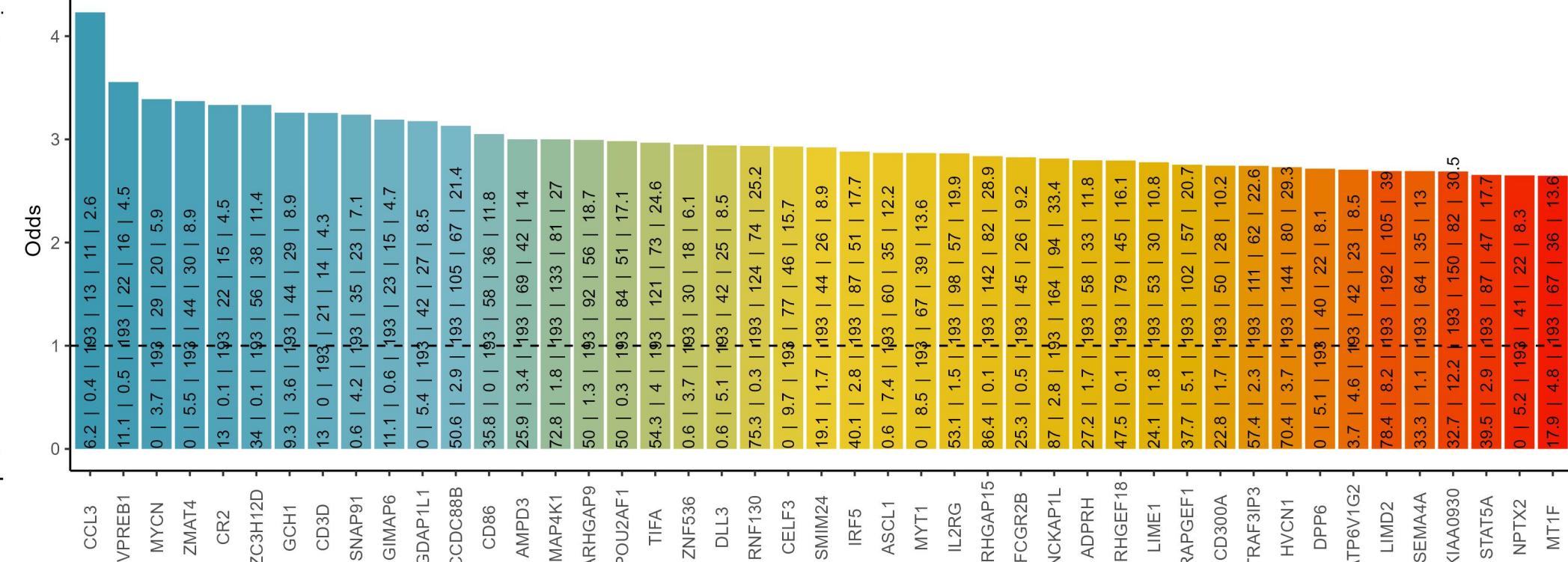
% of BCL2 in blood cancers: 57.4 ; % of BCL2 in solid cancers: 12.5

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of BCL2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

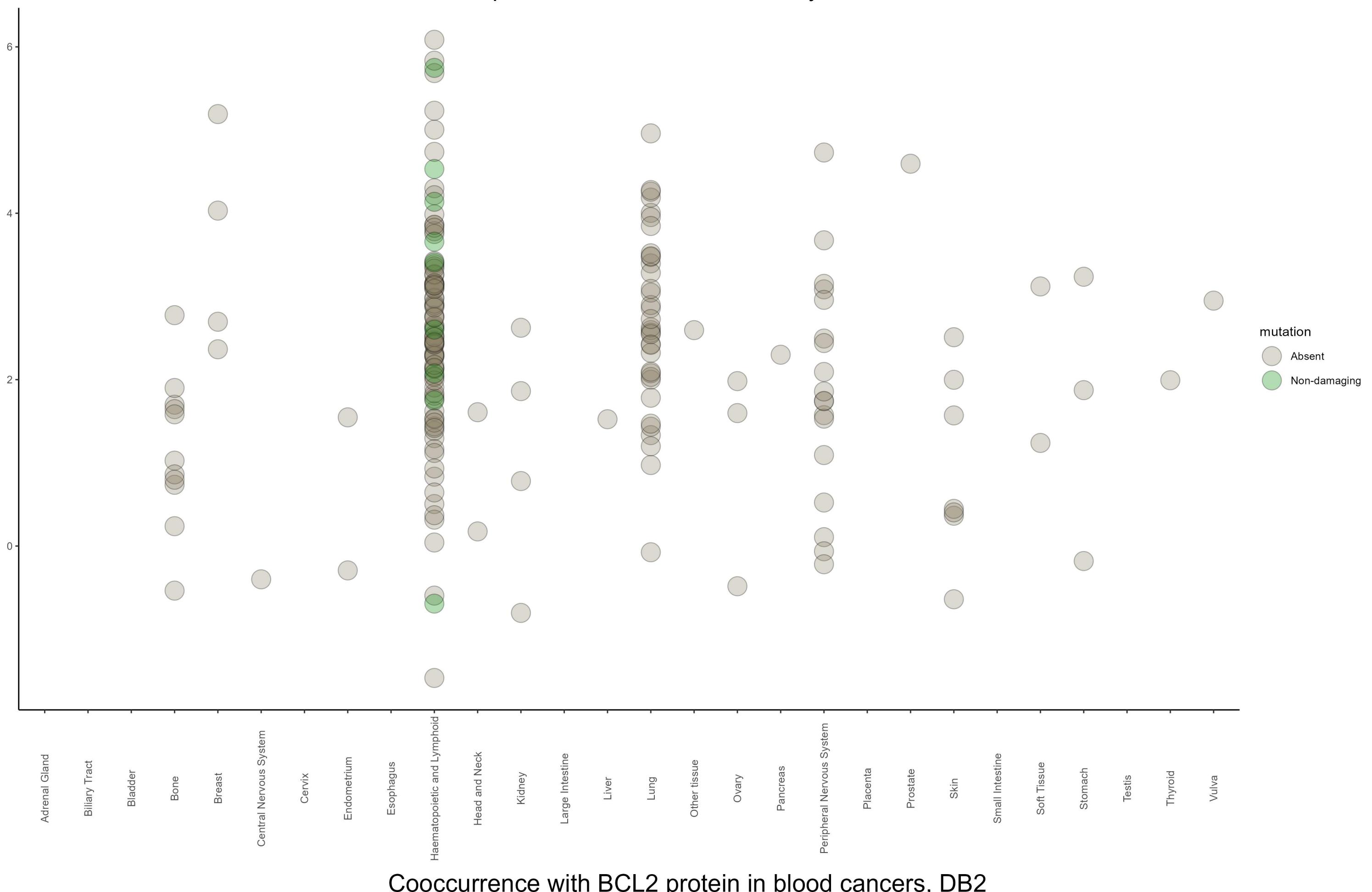
Negative cooccurrence



Positive cooccurrence

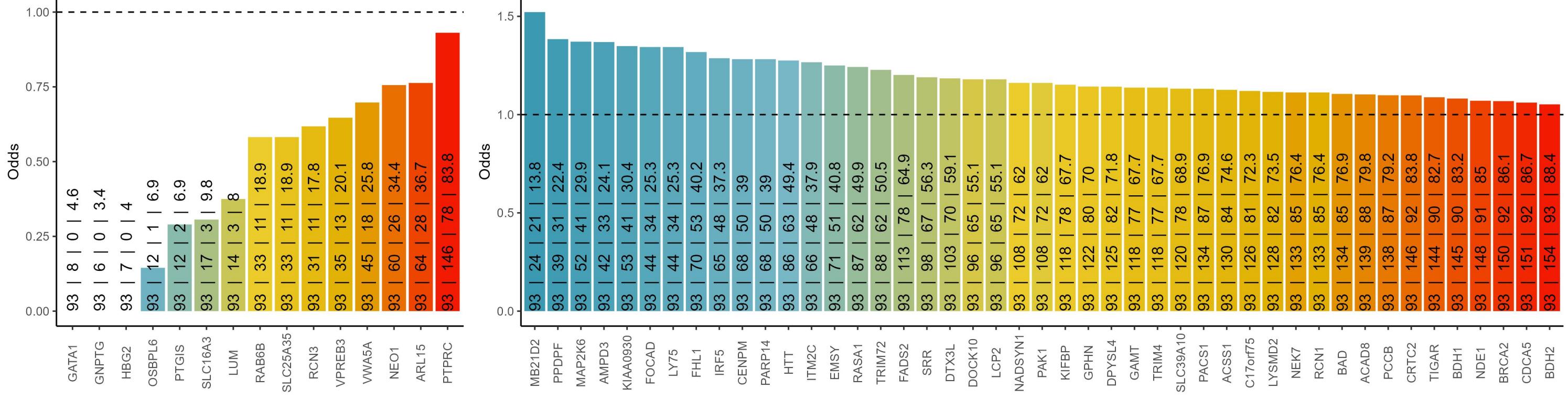


Amount of BCL2 protein and mutation status by tissue, DB2



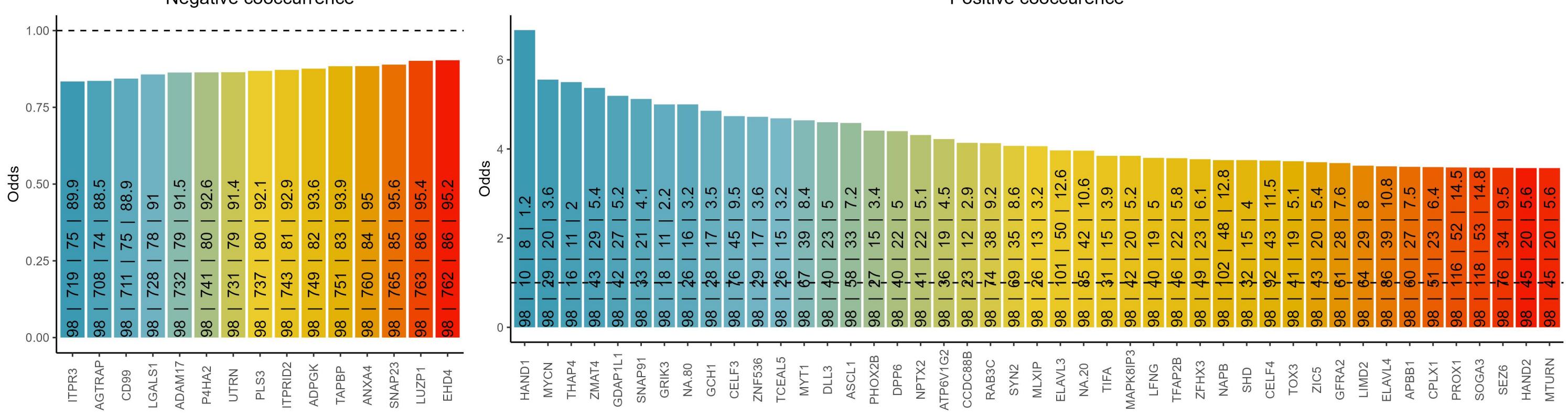
Cooccurrence with BCL2 protein in blood cancers, DB2

The text in the bars: incidence of BCL2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



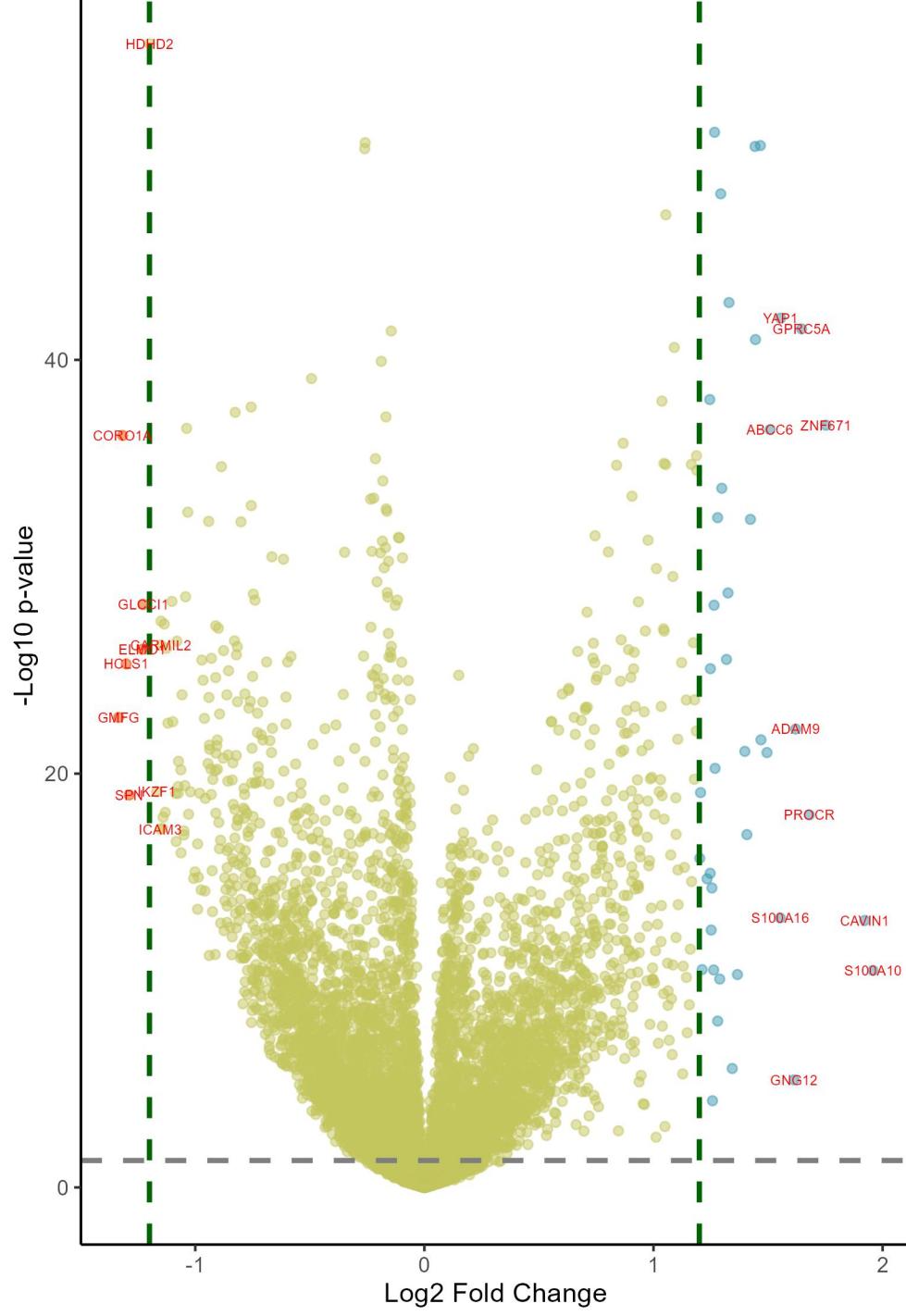
Cooccurrence with BCL2 protein in solid cancers, DB2

The text in the bars: incidence of BCL2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



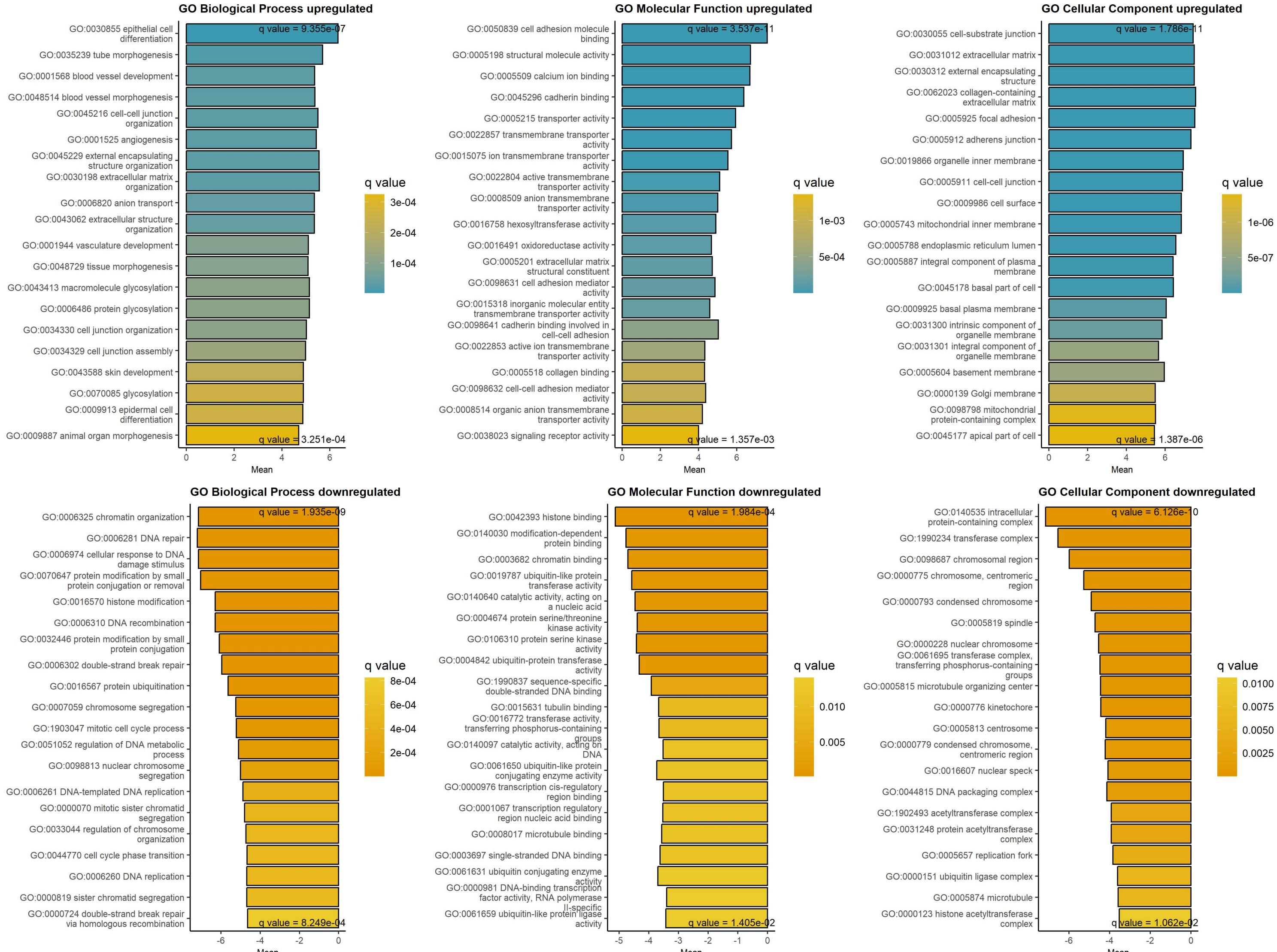
Downregulated at low/absent BCL2

Upregulated at low/absent BCL2



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.33	9.27e-22	GMFG	glia maturation factor gamma	1.96	2.38e-10	S100A10	S100 calcium binding protein A10
-1.32	1.45e-34	CORO1A	coronin 1A	1.92	1.34e-12	CAVIN1	caveolae associated protein 1
-1.3	3.51e-24	HCLS1	hematopoietic cell-specific Lyn sub	1.75	5.25e-35	ZNF671	zinc finger protein 671
-1.29	3.14e-18	SPN	sialophorin	1.68	2.47e-17	PROCR	protein C receptor
-1.23	8.30e-25	ELMO1	engulfment and cell motility 1	1.65	2.22e-39	GPRC5A	G protein-coupled receptor class C
-1.23	7.27e-27	GLCCI1	glucocorticoid induced 1	1.62	3.13e-21	ADAM9	ADAM metallopeptidase domain 9
-1.2	2.17e-52	HDHD2	haloacid dehalogenase like hydrolas	1.61	1.85e-05	GNG12	G protein subunit gamma 12
-1.17	2.24e-18	IKZF1	IKAROS family zinc finger 1	1.55	7.28e-40	YAP1	Yes1 associated transcriptional reg
-1.15	1.10e-16	ICAM3	intercellular adhesion molecule 3	1.55	1.02e-12	S100A16	S100 calcium binding protein A16
-1.15	5.35e-25	CARMIL2	capping protein regulator and myosi	1.51	7.81e-35	ABCC6	ATP binding cassette subfamily C me
-1.15	4.46e-26	FERMT3	FERM domain containing kindlin 3	1.5	3.68e-20	GPX8	glutathione peroxidase 8 (putative)
-1.14	1.00e-16	MZB1	marginal zone B and B1 cell specifi	1.47	9.76e-21	FHL2	four and a half LIM domains 2
-1.14	3.14e-17	LSP1	lymphocyte specific protein 1	1.47	6.71e-48	CACUL1	CDK2 associated cullin domain 1
-1.14	6.09e-26	CD300E	CD300e molecule	1.45	6.22e-39	CAVIN3	caveolae associated protein 3
-1.13	1.93e-17	RCSD1	RCSD domain containing 1	1.44	6.71e-48	CDC42EP1	CDC42 effector protein 1
-1.13	7.51e-25	WIPF1	WAS/WASL interacting protein family	1.42	9.28e-31	SDC4	syndecan 4
-1.12	1.70e-21	GNG2	G protein subunit gamma 2	1.41	1.88e-16	EPHA2	EPH receptor A2
-1.1	5.33e-27	BCL7A	BAF chromatin remodeling complex su	1.4	3.26e-20	ATP2B2	ATPase plasma membrane Ca ²⁺ transpo
-1.1	1.46e-21	KCNAB2	potassium voltage-gated channel sub	1.37	3.63e-10	CAV1	caveolin 1
-1.08	2.69e-18	FGD3	FYVE, RhoGEF and PH domain containi	1.34	5.66e-06	ITGA3	integrin subunit alpha 3
-1.08	3.80e-16	SASH3	SAM and SH3 domain containing 3	1.33	1.42e-40	F3	coagulation factor III, tissue fact
-1.08	3.63e-25	PIK3R1	phosphoinositide-3-kinase regulator	1.33	2.27e-27	RAB32	RAB32, member RAS oncogene family
-1.07	2.66e-18	ARHGAP45	Rho GTPase activating protein 45	1.32	2.27e-24	CTSL	cathepsin L
-1.07	1.33e-18	VAV1	vav guanine nucleotide exchange fac	1.3	3.62e-32	IL18	interleukin 18
-1.07	9.34e-20	TCF3	transcription factor 3	1.29	9.82e-46	UACA	uveal autoantigen with coiled-coil
-1.06	2.29e-19	CELF2	CUGBP Elav-like family member 2	1.29	5.77e-10	EGFR	epidermal growth factor receptor
-1.06	1.25e-15	TEX11	testis expressed 11	1.28	4.31e-08	FKBP9	FKBP prolyl isomerase 9
-1.06	8.90e-23	CUEDC2	CUE domain containing 2	1.28	7.86e-31	AXL	AXL receptor tyrosine kinase
-1.05	1.30e-16	INPP5D	inositol polyphosphate-5-phosphatas	1.27	1.97e-19	PRNP	prion protein

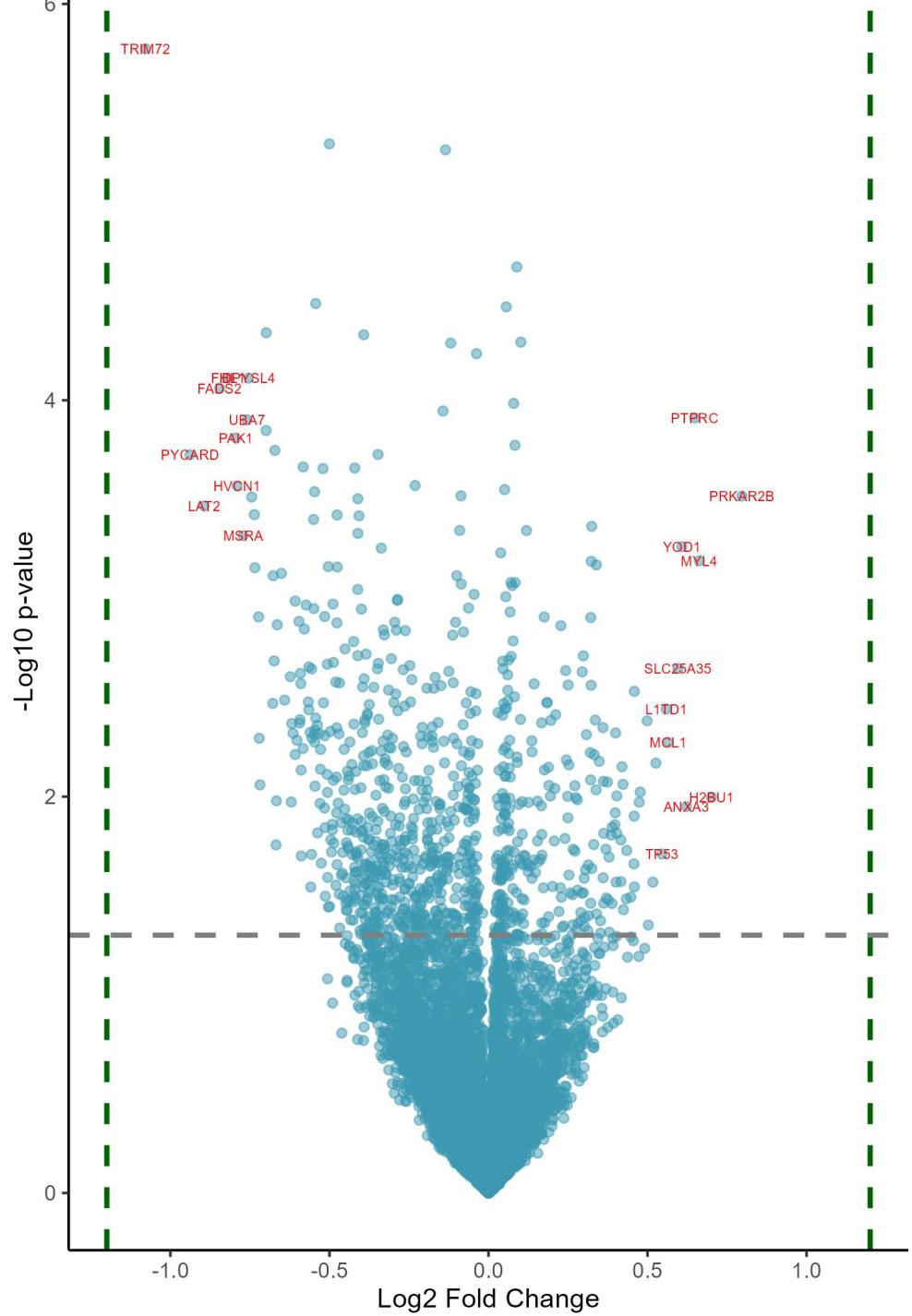
GAGE analysis on upregulated and downregulated proteins at low/absent BCL2 protein, DB2



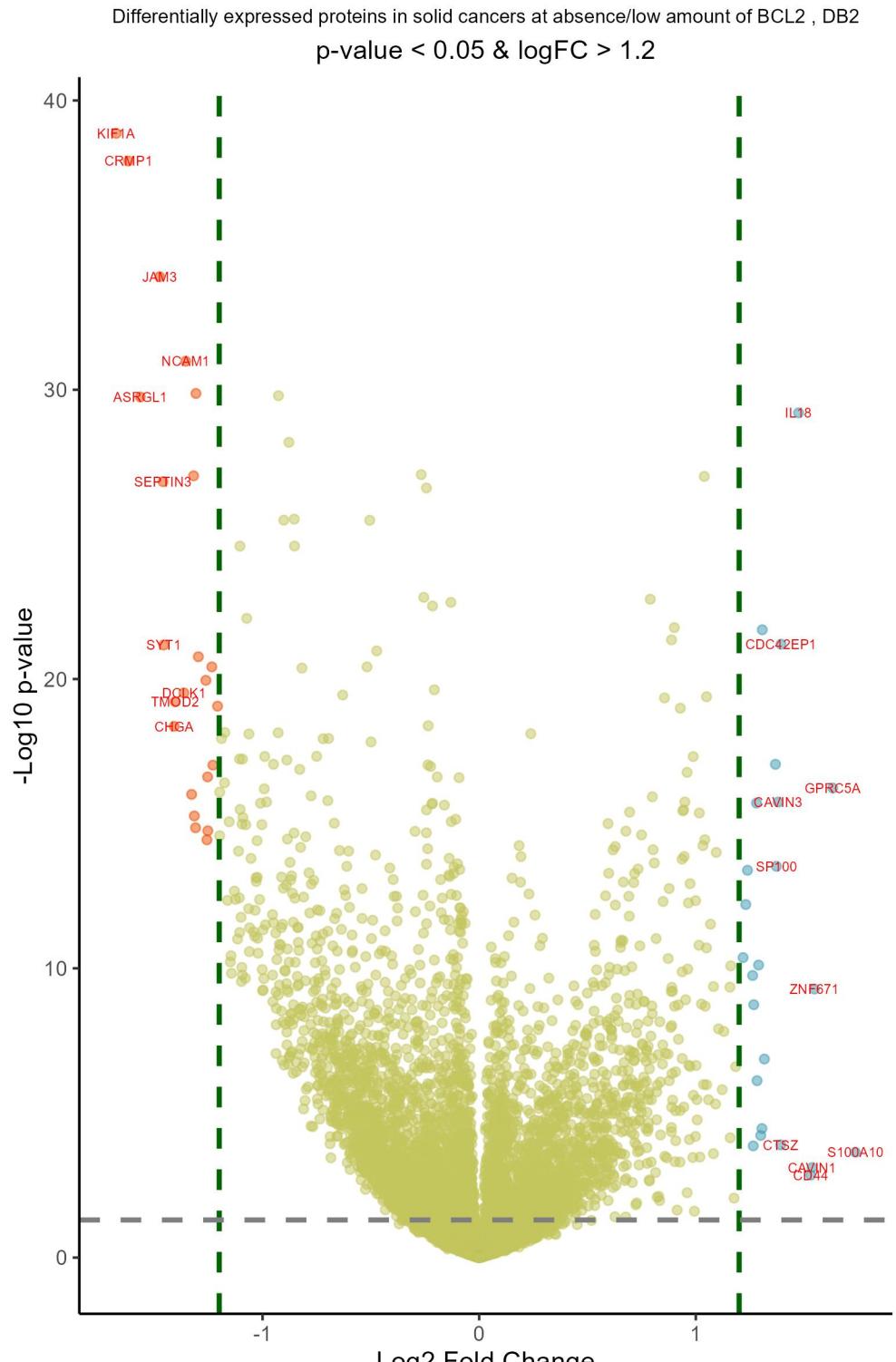
Differentially expressed proteins in blood cancers at absence/low amount of BCL2 , DB2

p-value < 0.05 & logFC > 1.2

Downregulated in blood cancers at low/absent BCL2 Upregulated in blood cancers at low/absent BCL2

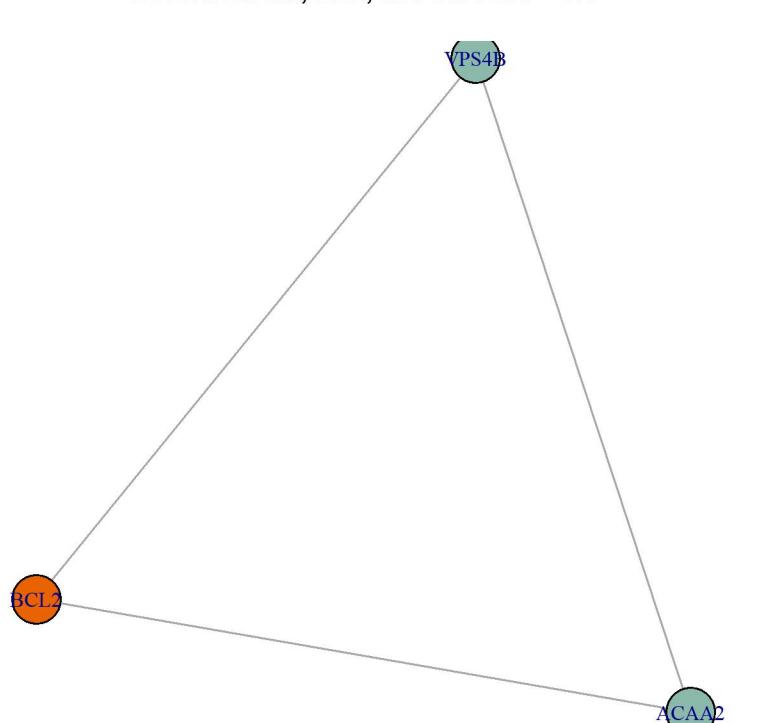


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.08	7.05e-03	TRIM72	tripartite motif containing 72	0.8	7.30e-02	PRKAR2B	protein kinase cAMP-dependent type
-0.94	6.31e-02	PYCARD	PYD and CARD domain containing	0.7	2.64e-01	H2BU1	H2B.U histone 1
-0.89	7.72e-02	LAT2	linker for activation of T cells fa	0.66	1.06e-01	MYL4	myosin light chain 4
-0.85	4.86e-02	FADS2	fatty acid desaturase 2	0.65	5.53e-02	PTPRC	protein tyrosine phosphatase recept
-0.82	4.62e-02	FHL1	four and a half LIM domains 1	0.62	2.69e-01	ANXA3	annexin A3
-0.79	6.17e-02	PAK1	p21 (RAC1) activated kinase 1	0.61	9.71e-02	YOD1	YOD1 deubiquitinase
-0.79	7.30e-02	HVCN1	hydrogen voltage gated channel 1	0.6	1.71e-01	SLC25A35	solute carrier family 25 member 35
-0.77	8.76e-02	MSRA	methionine sulfoxide reductase A	0.56	2.08e-01	MCL1	MCL1 apoptosis regulator, BCL2 fami
-0.76	5.53e-02	UBA7	ubiquitin like modifier activating	0.56	1.94e-01	L1TD1	LINE1 type transposase domain conta
-0.75	4.62e-02	DPYSL4	dihydropyrimidinase like 4	0.55	3.31e-01	TP53	tumor protein p53
-0.74	7.30e-02	EVI2B	ecotropic viral integration site 2B	0.53	2.29e-01	BCL2L1	BCL2 like 1
-0.74	8.00e-02	RASA1	RAS p21 protein activator 1	0.52	3.52e-01	CDS1	CDP-diacylglycerol synthase 1
-0.73	1.06e-01	RNF103	ring finger protein 103	0.5	4.28e-01	KRT19	keratin 19
-0.72	1.34e-01	GPX7	glutathione peroxidase 7	0.5	2.00e-01	ENPP4	ectonucleotide pyrophosphatase/phos
-0.72	2.08e-01	ASS1	argininosuccinate synthase 1	0.49	4.68e-01	KRT13	keratin 13
-0.72	2.51e-01	HLA-DRB5	major histocompatibility complex, c	0.48	2.57e-01	PKLR	pyruvate kinase L/R
-0.7	5.94e-02	SORBS3	sorbin and SH3 domain containing 3	0.47	2.64e-01	ERCC3	ERCC excision repair 3, TFIIH core
-0.7	3.91e-02	CLN6	CLN6 transmembrane ER protein	0.47	4.83e-01	MAGEA4	MAGE family member A4
-0.68	1.88e-01	ITGB7	integrin subunit beta 7	0.46	3.64e-01	HBB	hemoglobin subunit beta
-0.68	1.11e-01	DOCK10	dedicator of cytokinesis 10	0.46	1.81e-01	OXLD1	oxidoreductase like domain containi
-0.67	1.70e-01	CASP1	caspase 1	0.46	2.81e-01	FTSJ1	FtsJ RNA 2'-O-methyltransferase 1
-0.67	6.31e-02	HTT	huntingtin	0.46	3.35e-01	C17orf80	chromosome 17 open reading frame 80
-0.67	3.21e-01	CD44	CD44 molecule (Indian blood group)	0.46	4.51e-01	GRAMD1C	GRAM domain containing 1C
-0.67	2.64e-01	QPRT	quinolinate phosphoribosyltransfера	0.45	3.80e-01	ETS1	ETS proto-oncogene 1, transcription
-0.66	1.37e-01	TP53I3	tumor protein p53 inducible protein	0.45	4.46e-01	TNFRSF8	TNF receptor superfamily member 8
-0.65	1.11e-01	LMF2	lipase maturation factor 2	0.44	4.83e-01	GNG12	G protein subunit gamma 12
-0.64	1.88e-01	BRINP1	BMP/retinoic acid inducible neural	0.43	3.30e-01	RAB32	RAB32, member RAS oncogene family
-0.62	1.76e-01	TRIP6	thyroid hormone receptor interactor	0.43	3.82e-01	CD84	CD84 molecule
-0.62	2.64e-01	NAPRT	nicotinate phosphoribosyltransfера	0.42	4.07e-01	TUBB2A	tubulin beta 2A class IIa



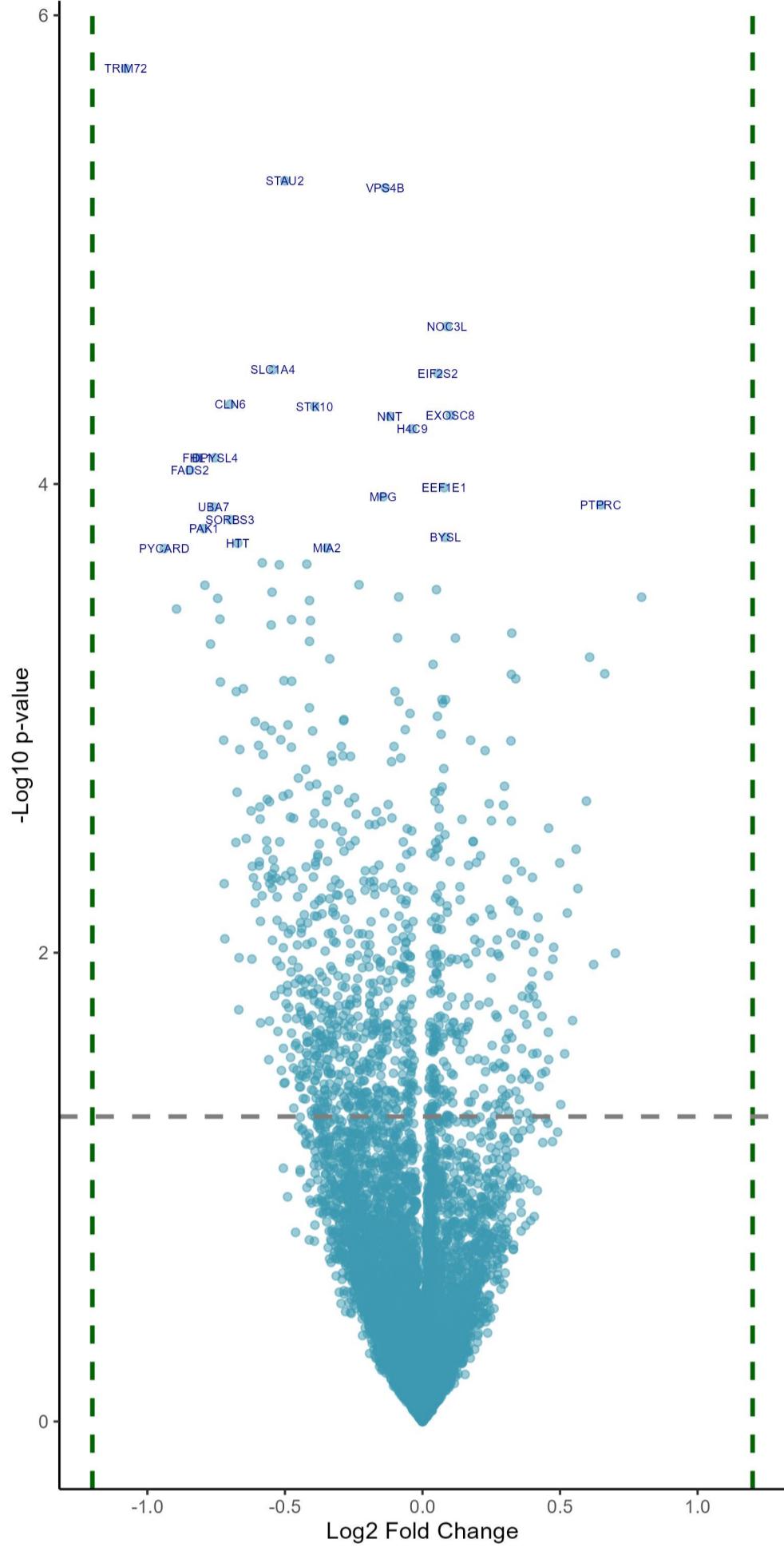
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.68	5.73e-36	KIF1A	kinesin family member 1A	1.74	9.84e-04	S100A10	S100 calcium binding protein A10
-1.62	3.45e-35	CRMP1	collapsin response mediator protein	1.63	6.80e-15	GPRC5A	G protein-coupled receptor class C
-1.56	1.86e-27	ASRGL1	asparaginase and isoaspartyl peptid	1.55	1.15e-08	ZNF671	zinc finger protein 671
-1.48	2.58e-31	JAM3	junctional adhesion molecule 3	1.54	2.83e-03	CAVIN1	caveolae associated protein 1
-1.46	9.00e-25	SEPTIN3	septin 3	1.53	4.73e-03	CD44	CD44 molecule (Indian blood group)
-1.46	1.86e-19	SYT1	synaptotagmin 1	1.47	5.84e-27	IL18	interleukin 18
-1.41	7.85e-17	CHGA	chromogranin A	1.39	1.80e-19	CDC42EP1	CDC42 effector protein 1
-1.4	1.21e-17	TMOD2	tropomodulin 2	1.39	5.94e-04	CTSZ	cathepsin Z
-1.36	6.66e-18	DCLK1	doublecortin like kinase 1	1.38	1.84e-14	CAVIN3	caveolae associated protein 3
-1.35	1.73e-28	NCAM1	neural cell adhesion molecule 1	1.37	1.81e-12	SP100	SP100 nuclear antigen
-1.33	1.08e-14	LIN7A	lin-7 homolog A, crumbs cell polari	1.37	1.19e-15	YAP1	Yes1 associated transcriptional reg
-1.32	6.35e-25	PRR36	proline rich 36	1.32	1.55e-06	EPHA2	EPH receptor A2
-1.31	4.86e-14	ELAVL3	ELAV like RNA binding protein 3	1.31	6.14e-20	F3	coagulation factor III, tissue fact
-1.31	1.12e-13	GNG4	G protein subunit gamma 4	1.31	1.90e-04	PROCR	protein C receptor
-1.31	1.86e-27	BCL7A	BAF chromatin remodeling complex su	1.3	3.10e-04	S100A16	S100 calcium binding protein A16
-1.3	4.43e-19	ZNF516	zinc finger protein 516	1.29	2.09e-09	ADGRE5	adhesion G protein-coupled receptor
-1.26	2.58e-18	RUFY3	RUN and FYVE domain containing 3	1.28	7.02e-06	HLA-B	major histocompatibility complex, c
-1.26	2.65e-13	PROX1	prospero homeobox 1	1.28	1.97e-14	CACUL1	CDK2 associated cullin domain 1
-1.25	2.94e-15	LYSMD1	LysM domain containing 1	1.27	3.47e-08	ABCC6	ATP binding cassette subfamily C me
-1.25	1.42e-13	MLLT11	MLLT11 transcription factor 7 cofac	1.27	6.36e-04	CAV1	caveolin 1
-1.23	9.36e-19	DPYSL5	dihydropyrimidinase like 5	1.26	4.42e-09	TAP1	transporter 1, ATP binding cassette
-1.23	1.24e-15	PIMREG	PICALM interacting mitotic regulato	1.24	2.39e-12	AXL	AXL receptor tyrosine kinase
-1.21	1.68e-17	ADD2	adducin 2	1.23	2.73e-11	MET	MET proto-oncogene, receptor tyrosi
-1.2	1.98e-13	CPE	carboxypeptidase E	1.22	1.21e-09	SDC4	syndecan 4
-1.2	9.17e-15	CBX2	chromobox 2	1.18	2.62e-06	ADAM9	ADAM metallopeptidase domain 9
-1.19	1.83e-16	GNAO1	G protein subunit alpha o1	1.18	2.23e-02	LGALS3	galectin 3
-1.18	4.57e-15	MAPT	microtubule associated protein tau	1.16	2.23e-09	RAB32	RAB32, member RAS oncogene family
-1.17	1.25e-16	UCHL1	ubiquitin C-terminal hydrolase L1	1.16	3.64e-04	NT5E	5'-nucleotidase ecto
-1.16	1.99e-11	GLCCI1	glucocorticoid induced 1	1.16	9.98e-09	KRT80	keratin 80

BCL2 network, DB2, all Pearson r > 0.4



Differentially expressed proteins in blood cancers at absence/low amount of BCL2 , DB2

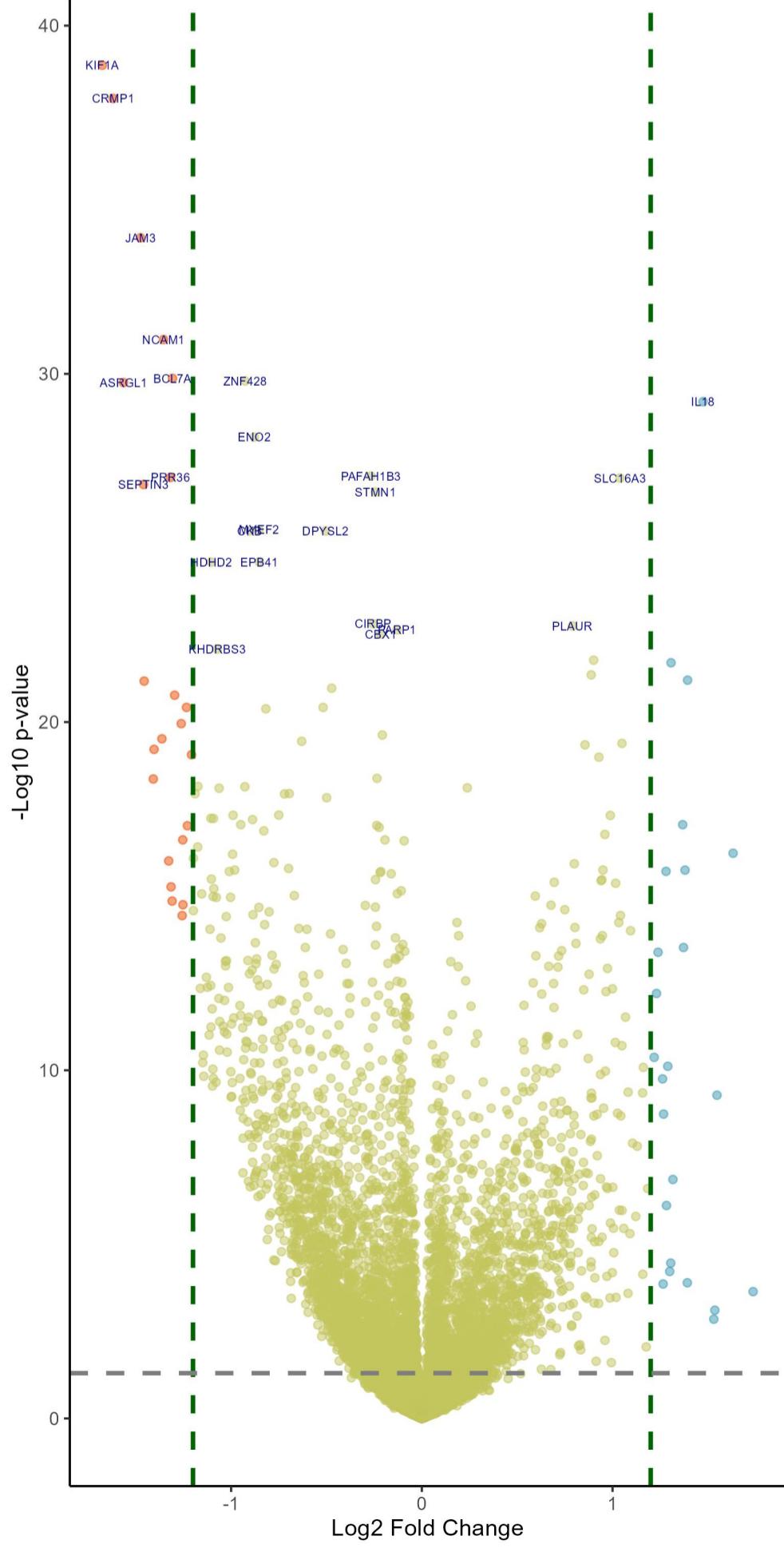
p-value < 0.05 & logFC > 1.2



Sorted by p values!

Downregulated in blood cancers at low/absent BCL2 Upregulated in blood cancers at low/absent BCL2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.08	7.05e-03	TRIM72	tripartite motif containing 72	0.09	3.55e-02	NOC3L	NOC3 like DNA replication regulator
-0.5	1.14e-02	STAU2	staufen double-stranded RNA binding	0.06	3.91e-02	EIF2S2	eukaryotic translation initiation f
-0.14	1.14e-02	VPS4B	vacuolar protein sorting 4 homolog	0.1	3.91e-02	EXOSC8	exosome component 8
-0.54	3.91e-02	SLC1A4	solute carrier family 1 member 4	0.08	5.42e-02	EEF1E1	eukaryotic translation elongation f
-0.7	3.91e-02	CLN6	CLN6 transmembrane ER protein	0.65	5.53e-02	PTPRC	protein tyrosine phosphatase recept
-0.39	3.91e-02	STK10	serine/threonine kinase 10	0.08	6.31e-02	BYSL	bystin like
-0.12	3.91e-02	NNT	nicotinamide nucleotide transhydrog	0.05	7.30e-02	EIF6	eukaryotic translation initiation f
-0.04	4.06e-02	H4C9	H4 clustered histone 9	0.8	7.30e-02	PRKAR2B	protein kinase cAMP-dependent type
-0.75	4.62e-02	DPYSL4	dihydropyrimidinase like 4	0.32	8.62e-02	PTGIS	prostaglandin I2 synthase
-0.82	4.62e-02	FHL1	four and a half LIM domains 1	0.12	8.64e-02	SLX9	SLX9 ribosome biogenesis factor
-0.85	4.86e-02	FADS2	fatty acid desaturase 2	0.61	9.71e-02	YOD1	YOD1 deubiquitinase
-0.14	5.53e-02	MPG	N-methylpurine DNA glycosylase	0.04	1.00e-01	RANBP2	RAN binding protein 2
-0.76	5.53e-02	UBA7	ubiquitin like modifier activating	0.66	1.06e-01	MYL4	myosin light chain 4
-0.7	5.94e-02	SORBS3	sorbin and SH3 domain containing 3	0.32	1.06e-01	CT47A11	cancer/testis antigen family 47 mem
-0.79	6.17e-02	PAK1	p21 (RAC1) activated kinase 1	0.34	1.06e-01	EXO1	exonuclease 1
-0.67	6.31e-02	HTT	huntingtin	0.07	1.16e-01	WDR43	WD repeat domain 43
-0.35	6.31e-02	MIA2	MIA SH3 domain ER export factor 2	0.08	1.16e-01	IPO4	importin 4
-0.94	6.31e-02	PYCARD	PYD and CARD domain containing	0.07	1.16e-01	EXOSC7	exosome component 7
-0.58	6.60e-02	PCCB	propionyl-CoA carboxylase subunit b	0.05	1.26e-01	DNAJC7	DnaJ heat shock protein family (Hsp)
-0.42	6.60e-02	GYS1	glycogen synthase 1	0.07	1.32e-01	EXOSC4	exosome component 4
-0.52	6.60e-02	ACAD8	acyl-CoA dehydrogenase family membe	0.18	1.34e-01	FAM89A	family with sequence similarity 89
-0.23	7.30e-02	DPYSL2	dihydropyrimidinase like 2	0.32	1.34e-01	HBG2	hemoglobin subunit gamma 2
-0.79	7.30e-02	HVCN1	hydrogen voltage gated channel 1	0.23	1.37e-01	IFRD1	interferon related developmental re
-0.55	7.30e-02	BDH1	3-hydroxybutyrate dehydrogenase 1	0.08	1.48e-01	LYAR	Ly1 antibody reactive
-0.09	7.30e-02	OPA1	OPA1 mitochondrial dynamin like GTP	0.3	1.67e-01	GDPD1	glycerophosphodiester phosphodieste
-0.74	7.30e-02	EVI2B	ecotropic viral integration site 2B	0.07	1.67e-01	MYBBP1A	MYB binding protein 1a
-0.41	7.30e-02	ZNRF2	zinc and ring finger 2	0.06	1.70e-01	WDR36	WD repeat domain 36
-0.89	7.72e-02	LAT2	linker for activation of T cells fa	0.04	1.70e-01	PRPF3	pre-mRNA processing factor 3
-0.74	8.00e-02	RASA1	RAS p21 protein activator 1	0.6	1.71e-01	SLC25A35	solute carrier family 25 member 35
-0.48	8.00e-02	VPREB1	V-set pre-B cell surrogate light ch	0.05	1.71e-01	BAG6	BAG cochaperone 6
-0.41	8.00e-02	PM20D2	peptidase M20 domain containing 2	0.24	1.71e-01	FAF1	Fas associated factor 1
-0.55	8.15e-02	NR3C1	nuclear receptor subfamily 3 group	0.29	1.71e-01	MDN1	midasin AAA ATPase 1
-0.09	8.64e-02	ARHGAP1	Rho GTPase activating protein 1	0.06	1.74e-01	NUP54	nucleoporin 54
-0.41	8.72e-02	TOR3A	torsin family 3 member A	0.14	1.79e-01	PPIL4	peptidylprolyl isomerase like 4
-0.77	8.76e-02	MSRA	methionine sulfoxide reductase A	0.25	1.79e-01	REXO2	RNA exonuclease 2
-0.34	9.71e-02	HMGCL	3-hydroxy-3-methylglutaryl-CoA lyas	0.32	1.79e-01	ABCC3	ATP binding cassette subfamily C me
-0.5	1.06e-01	PACS1	phosphofuran acidic cluster sorting	0.06	1.80e-01	PCMT1	protein-L-isoaspartate (D-aspartate)
-0.48	1.06e-01	MEF2D	myocyte enhancer factor 2D	0.46	1.81e-01	OXLD1	oxidoreductase like domain containi
0.73	1.06e-01	RNE103	ring finger protein 103	0.08	1.87e-01	IDT1	junior microtubule associated home

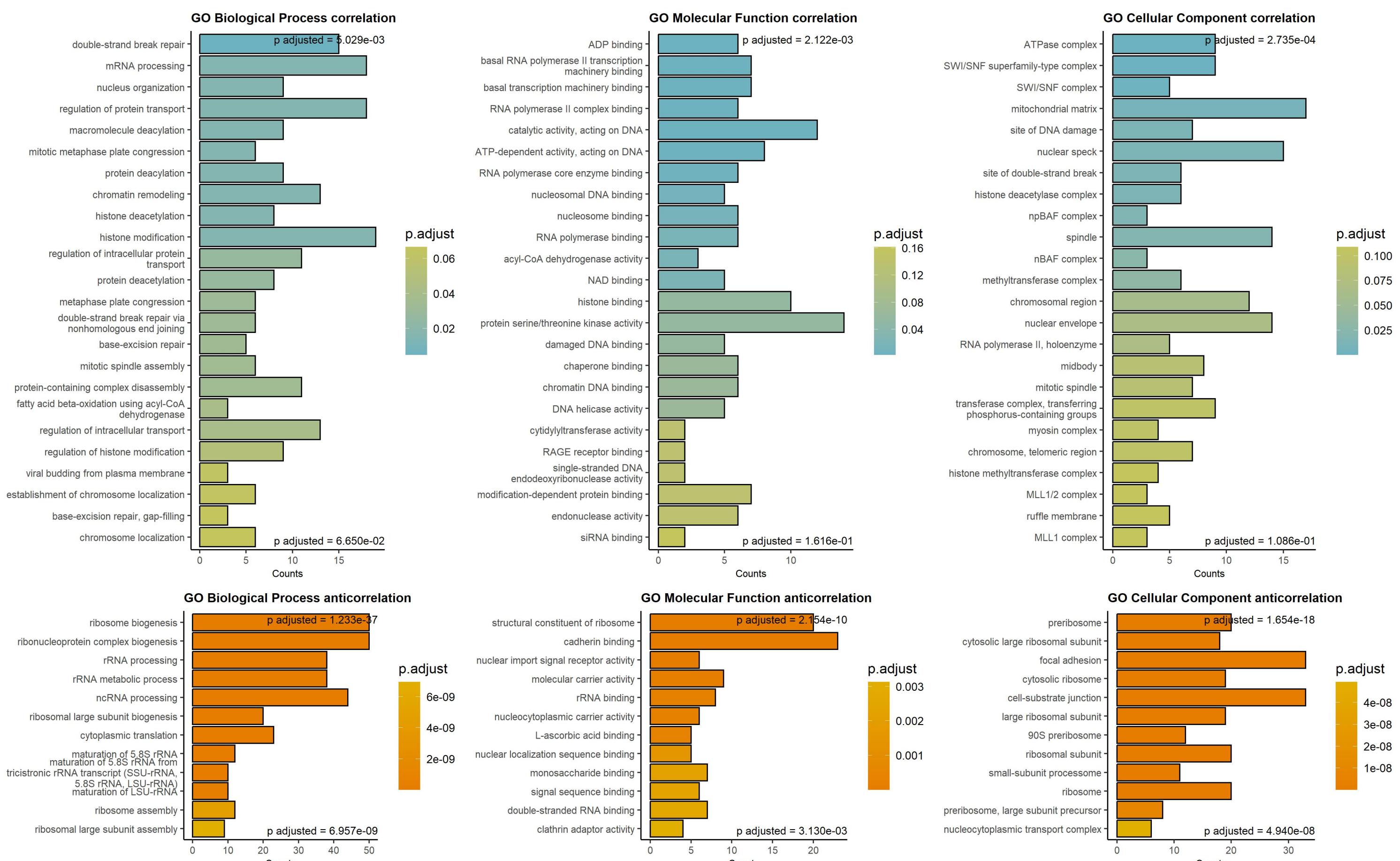
Differentially expressed proteins in solid cancers at absence/low amount of BCL2 , DB2
p-value < 0.05 & logFC > 1.2

Sorted by p values!

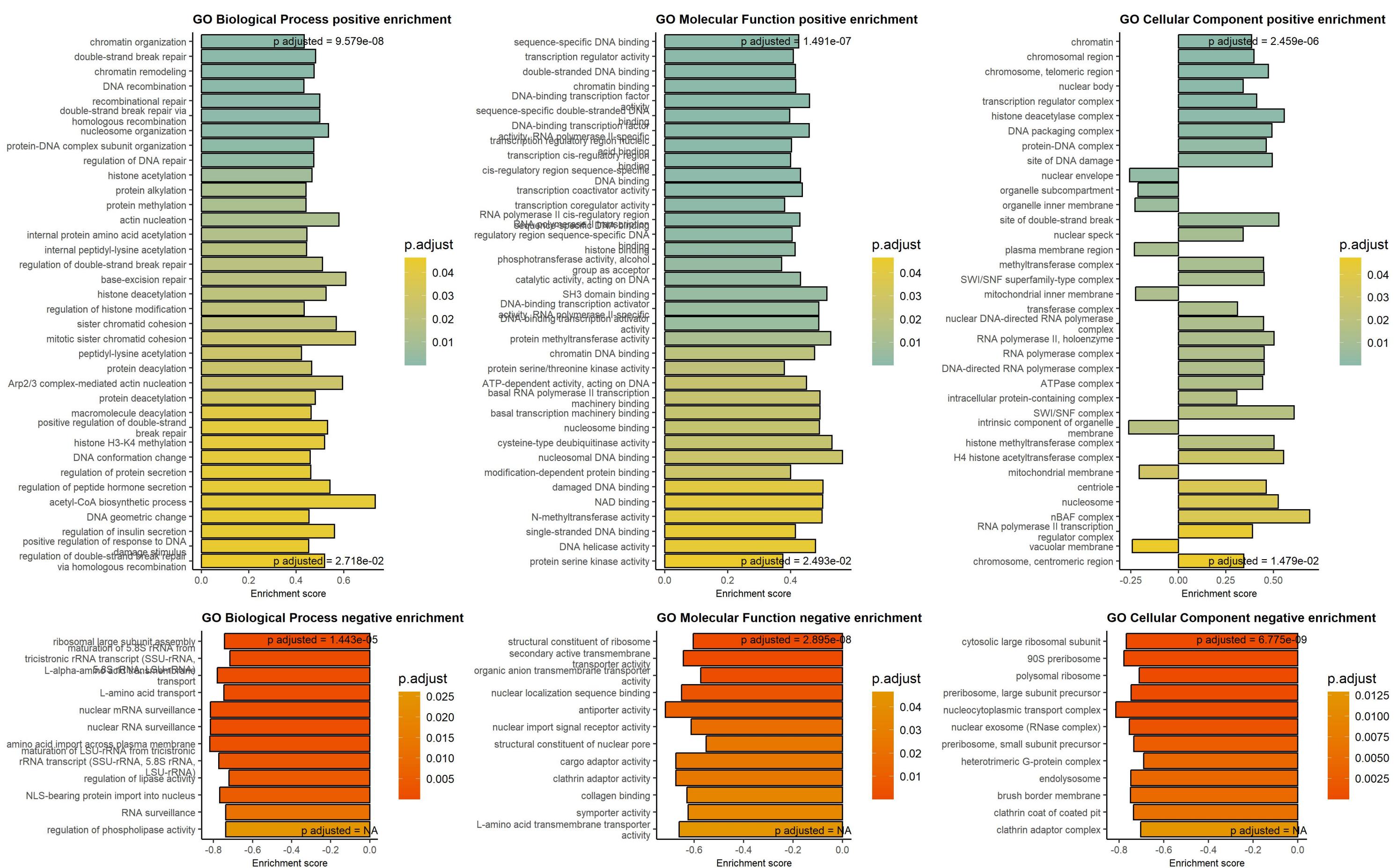
Downregulated in solid cancers at low/absent BCL2 Upregulated in solid cancers at low/absent BCL2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.68	5.73e-36	KIF1A	kinesin family member 1A	1.47	5.84e-27	IL18	interleukin 18
-1.62	3.45e-35	CRMP1	collapsin response mediator protein	1.04	6.35e-25	SLC16A3	solute carrier family 16 member 3
-1.48	2.58e-31	JAM3	junctional adhesion molecule 3	0.79	6.62e-21	PLAUR	plasminogen activator, urokinase re
-1.35	1.73e-28	NCAM1	neural cell adhesion molecule 1	0.9	5.38e-20	RHOF	ras homolog family member F, filopo
-1.31	1.86e-27	BCL7A	BAF chromatin remodeling complex su	1.31	6.14e-20	F3	coagulation factor III, tissue fact
-0.93	1.86e-27	ZNF428	zinc finger protein 428	0.89	1.32e-19	TOR4A	torsin family 4 member A
-1.56	1.86e-27	ASRGL1	asparaginase and isoaspartyl peptid	1.39	1.80e-19	CDC42EP1	CDC42 effector protein 1
-0.88	5.48e-26	ENO2	enolase 2	1.05	8.56e-18	FOSL1	FOS like 1, AP-1 transcription fact
-0.27	6.35e-25	PAFAH1B3	platelet activating factor acetylhy	0.86	9.18e-18	RHOXF1	Rho homeobox family member 1
-1.32	6.35e-25	PRR36	proline rich 36	0.93	1.94e-17	ALDH3B1	aldehyde dehydrogenase 3 family mem
-1.46	9.00e-25	SEPTIN3	septin 3	0.24	1.32e-16	TMOD3	tropomodulin 3
-0.24	1.39e-24	STMN1	stathmin 1	0.99	7.04e-16	TRIM16	tripartite motif containing 16
-0.85	1.51e-23	MYEF2	myelin expression factor 2	1.37	1.19e-15	YAP1	Yes1 associated transcriptional reg
-0.9	1.51e-23	CKB	creatine kinase B	0.96	2.10e-15	MYO1E	myosin IE
-0.51	1.51e-23	DPYSL2	dihydropyrimidinase like 2	1.63	6.80e-15	GPRC5A	G protein-coupled receptor class C
-0.85	1.07e-22	EPB41	erythrocyte membrane protein band 4	0.8	1.28e-14	LCN2	lipocalin 2
-1.1	1.07e-22	HDHD2	haloacid dehalogenase like hydrolas	0.95	1.84e-14	CCN1	cellular communication network fact
-0.26	5.97e-21	CIRBP	cold inducible RNA binding protein	1.38	1.84e-14	CAVIN3	caveolae associated protein 3
-0.13	8.14e-21	PARP1	poly(ADP-ribose) polymerase 1	1.28	1.97e-14	CACUL1	CDK2 associated culin domain 1
-0.22	1.04e-20	CBX1	chromobox 1	0.94	3.17e-14	CCDC9B	coiled-coil domain containing 9B
-1.07	2.67e-20	KHDRBS3	KH RNA binding domain containing, s	0.94	3.34e-14	PSMB10	proteasome 20S subunit beta 10
-1.46	1.86e-19	SYT1	synaptotagmin 1	0.69	3.67e-14	RHOD	ras homolog family member D
-0.47	2.88e-19	TUBB3	tubulin beta 3 class III	1.02	3.88e-14	IFI35	interferon induced protein 35
-1.3	4.43e-19	ZNF516	zinc finger protein 516	0.59	8.42e-14	KCNN4	potassium calcium-activated channel
-1.23	9.36e-19	DPYSL5	dihydropyrimidinase like 5	0.68	1.45e-13	GALNT5	polypeptide N-acetylgalactosaminylt
-0.52	9.36e-19	TUBB2B	tubulin beta 2B class IIb	0.75	1.88e-13	MICAL2	microtubule associated monooxygenas
-0.82	9.96e-19	ZNF24	zinc finger protein 24	1.04	2.65e-13	RBMS2	RNA binding motif single stranded i
-1.26	2.58e-18	RUFY3	RUN and FYVE domain containing 3	1.03	4.11e-13	PTGES	prostaglandin E synthase
-0.21	5.33e-18	HMGB2	high mobility group box 2	0.18	4.11e-13	IQGAP1	IQ motif containing GTPase activati
-1.36	6.66e-18	DCLK1	doublecortin like kinase 1	0.63	4.38e-13	MYADM	myeloid associated differentiation
-0.63	7.65e-18	ZMAT4	zinc finger matrin-type 4	0.8	5.48e-13	NMI	N-myc and STAT interactor
-1.4	1.21e-17	TMOD2	tropomodulin 2	0.62	5.50e-13	FOSL2	FOS like 2, AP-1 transcription fact
-1.21	1.68e-17	ADD2	adducin 2	1.09	6.53e-13	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-b
-0.24							

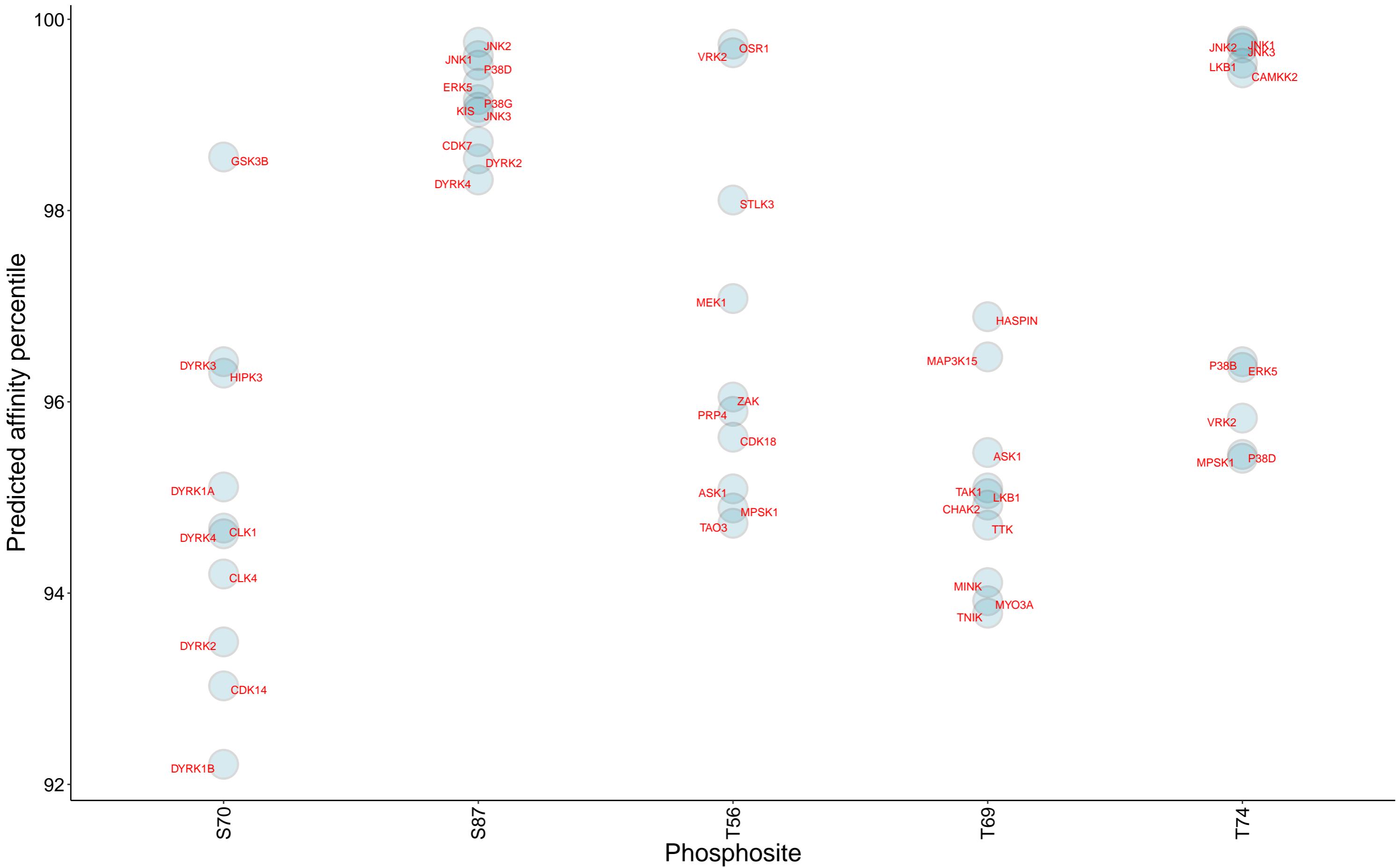
Top 250 correlation coefficients overrepresentation, BCL2 protein, DB2



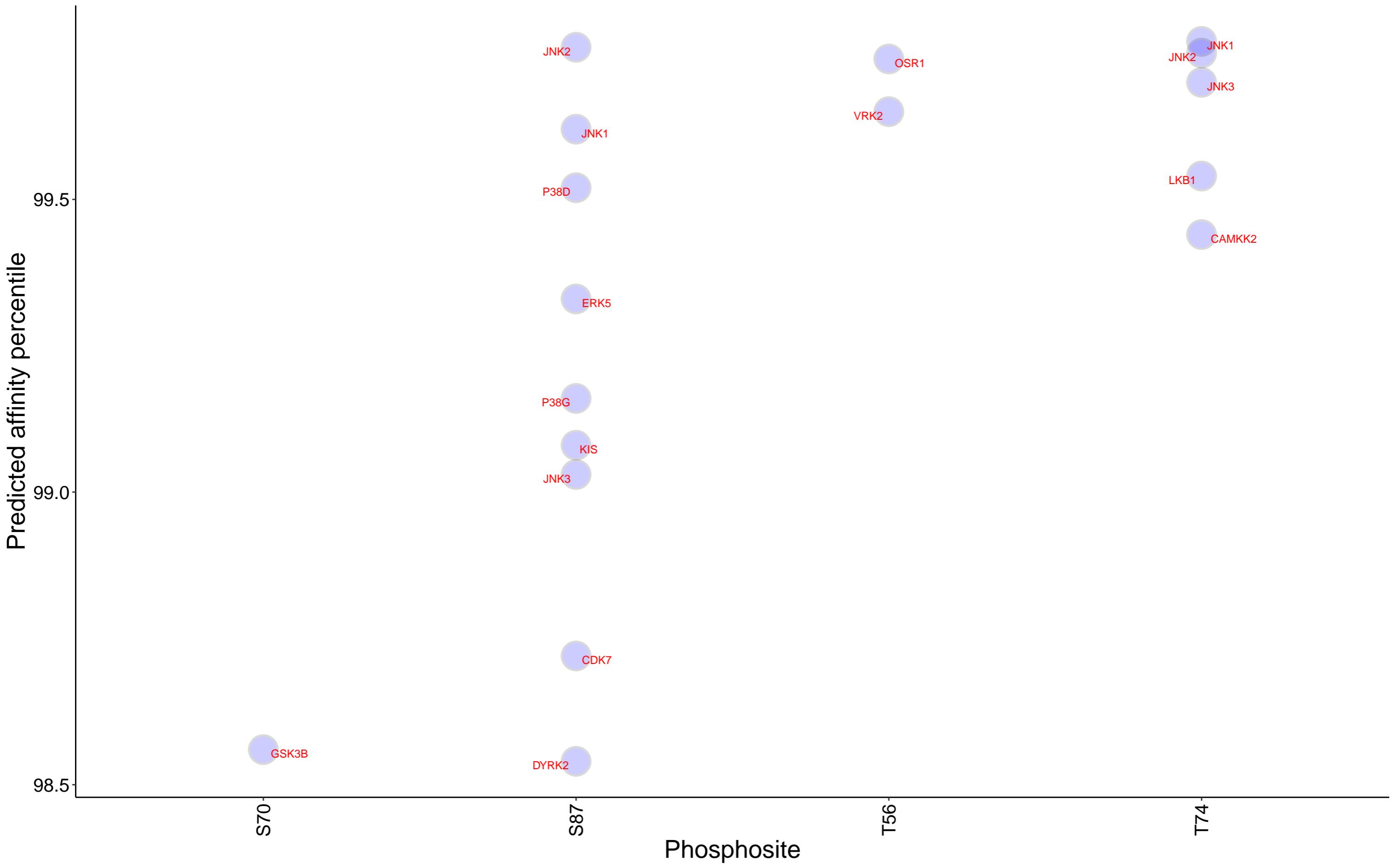
Gene Set Enrichment analysis on protein correlation coefficients, BCL2 protein, DB2



Top 10 kinases for each phosphosite in BCL2



Kinases with affinity greater than 98.5% to BCL2



Top 15 positive correlation coefficients for BCL2 protein by tissue, DB2

Beware of false positives in tissues with small number of samples

