

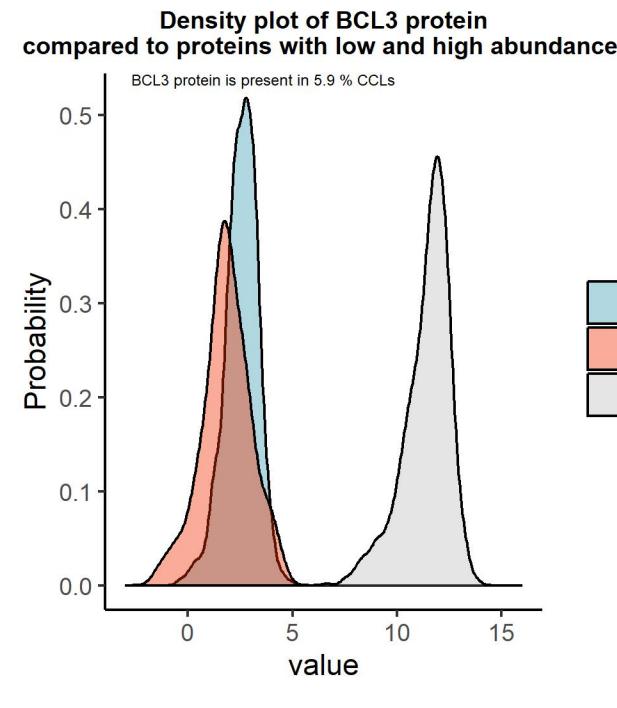
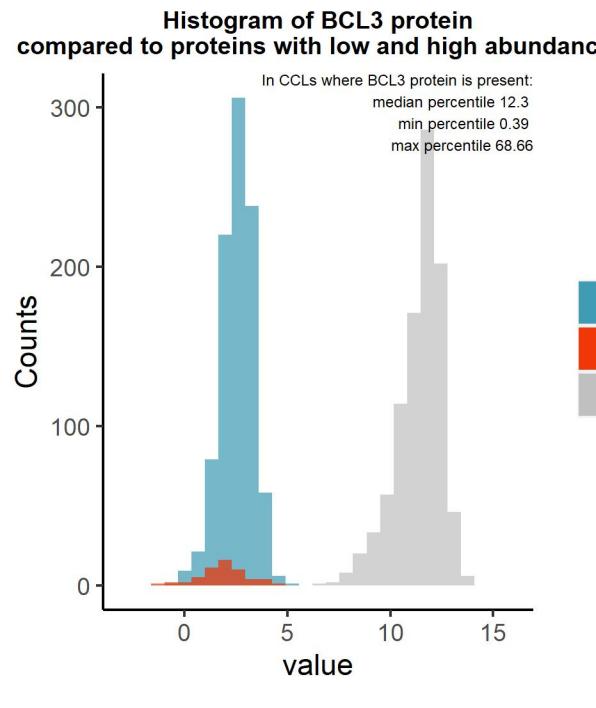
BCL3

Protein name: BCL3 ; UNIPROT: P20749 ; Gene name: BCL3 transcription coactivator

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

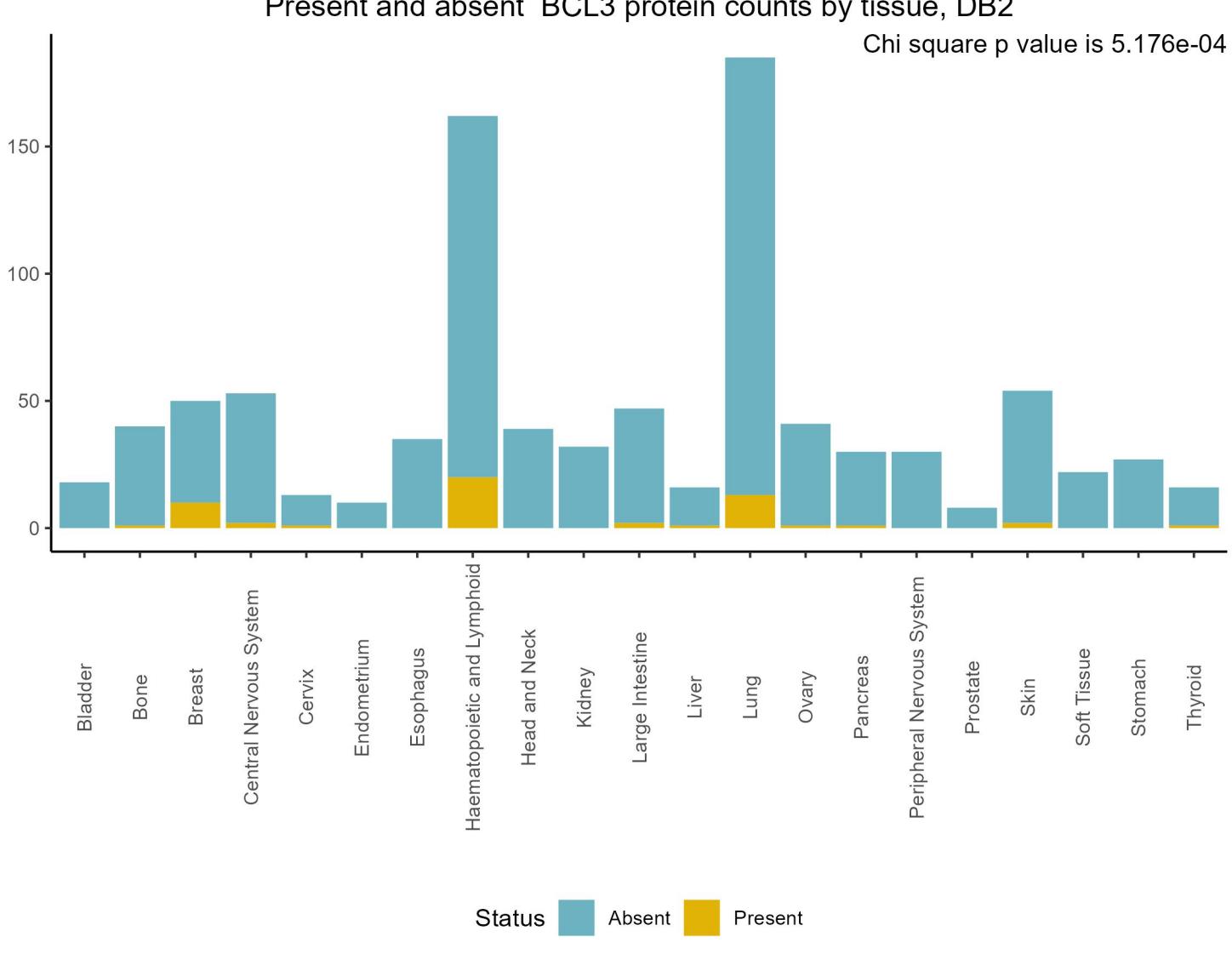
Sanger Institute Protein Database 2 (DB2), protein presence is less certain

8498 proteins in same 949 CCLs



Negative correlations of BCL3 protein, DB2

Pearson correlation coefficients

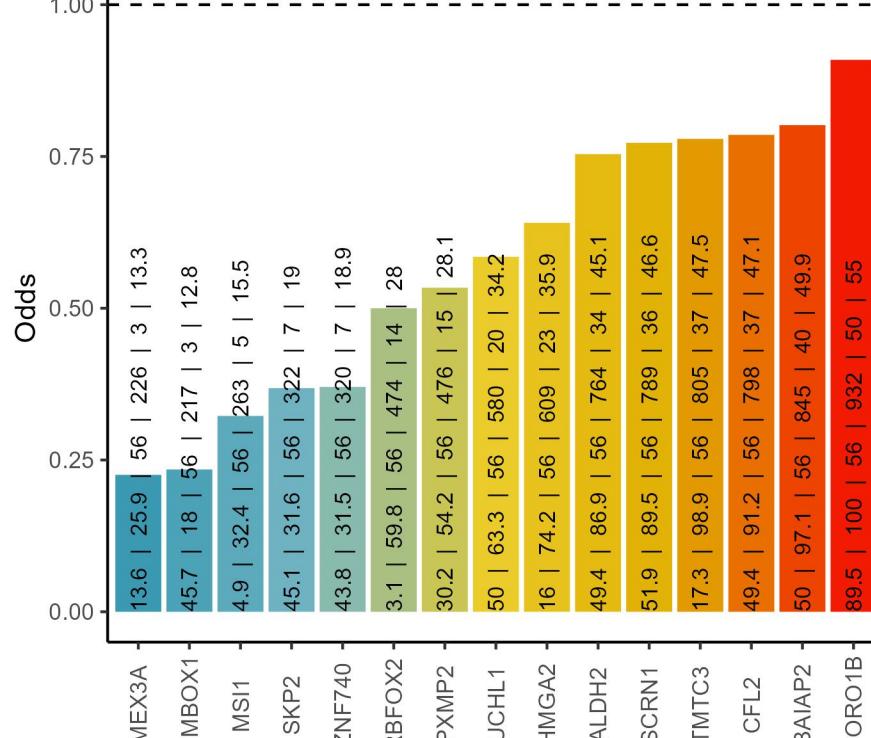


Cooccurrence with BCL3 protein, DB2

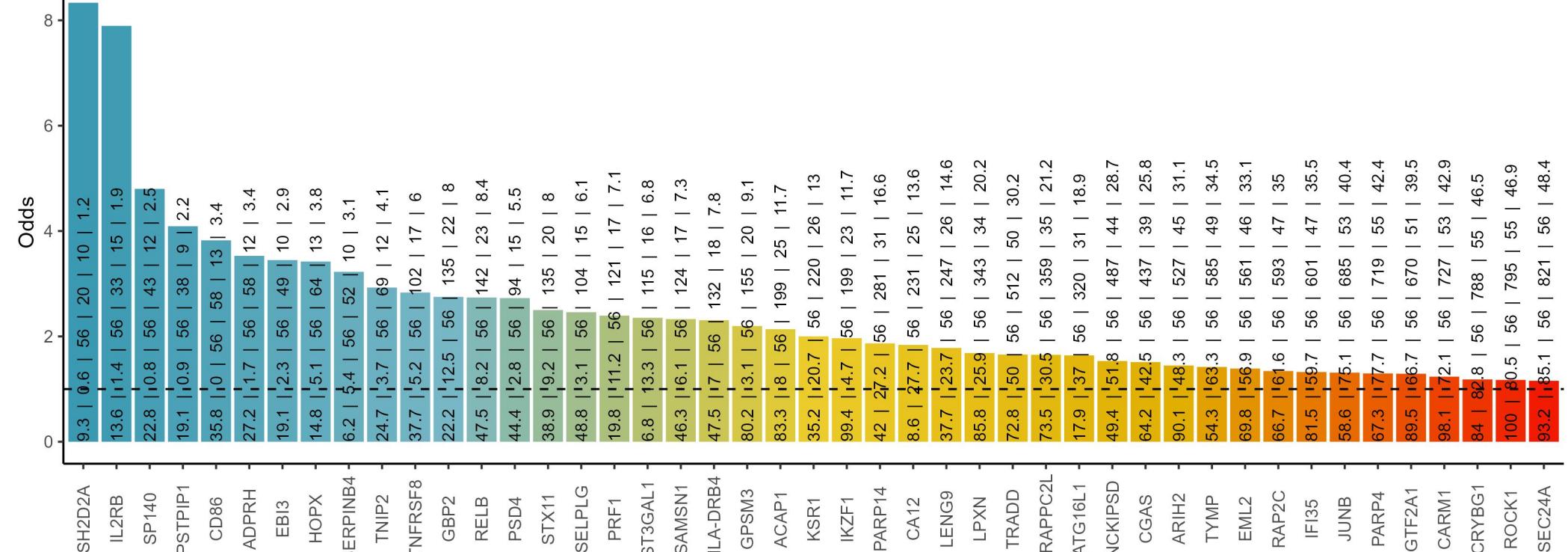
% of BCL3 in blood cancers: 12.3 ; % of BCL3 in solid cancers: 4.6

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of BCL3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

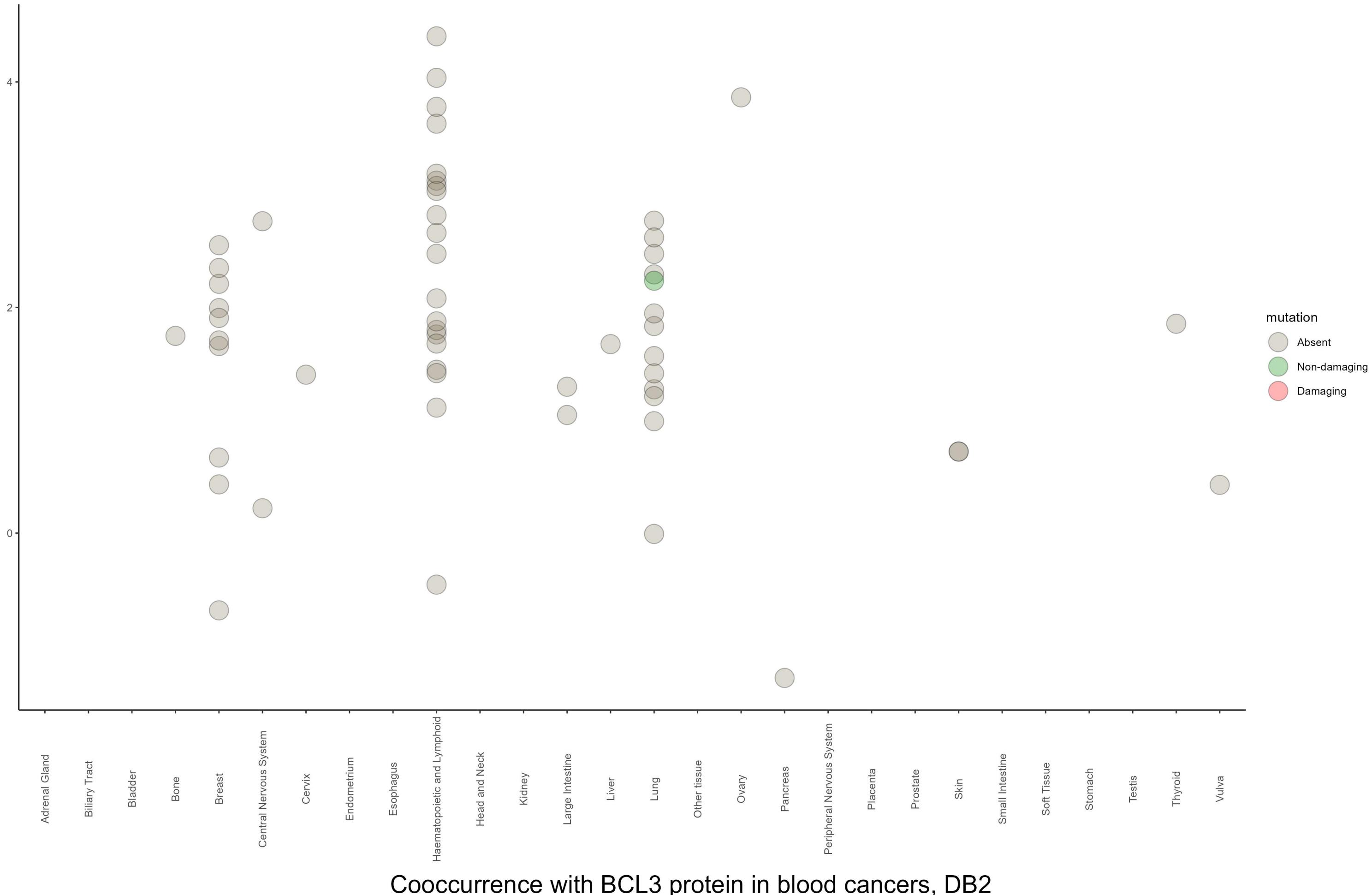
Negative cooccurrence

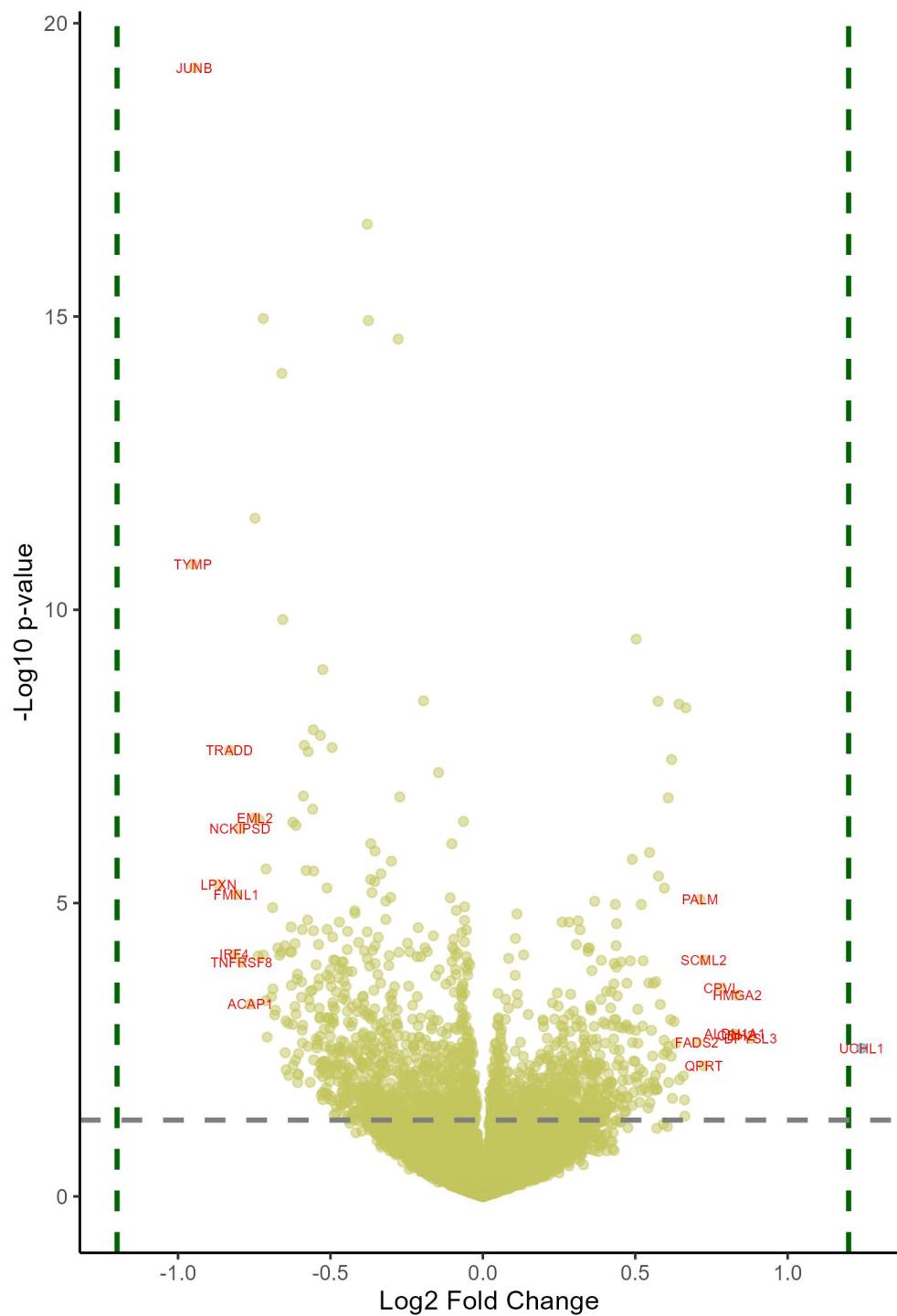


Positive cooccurrence



Amount of BCL3 protein and mutation status by tissue, DB2



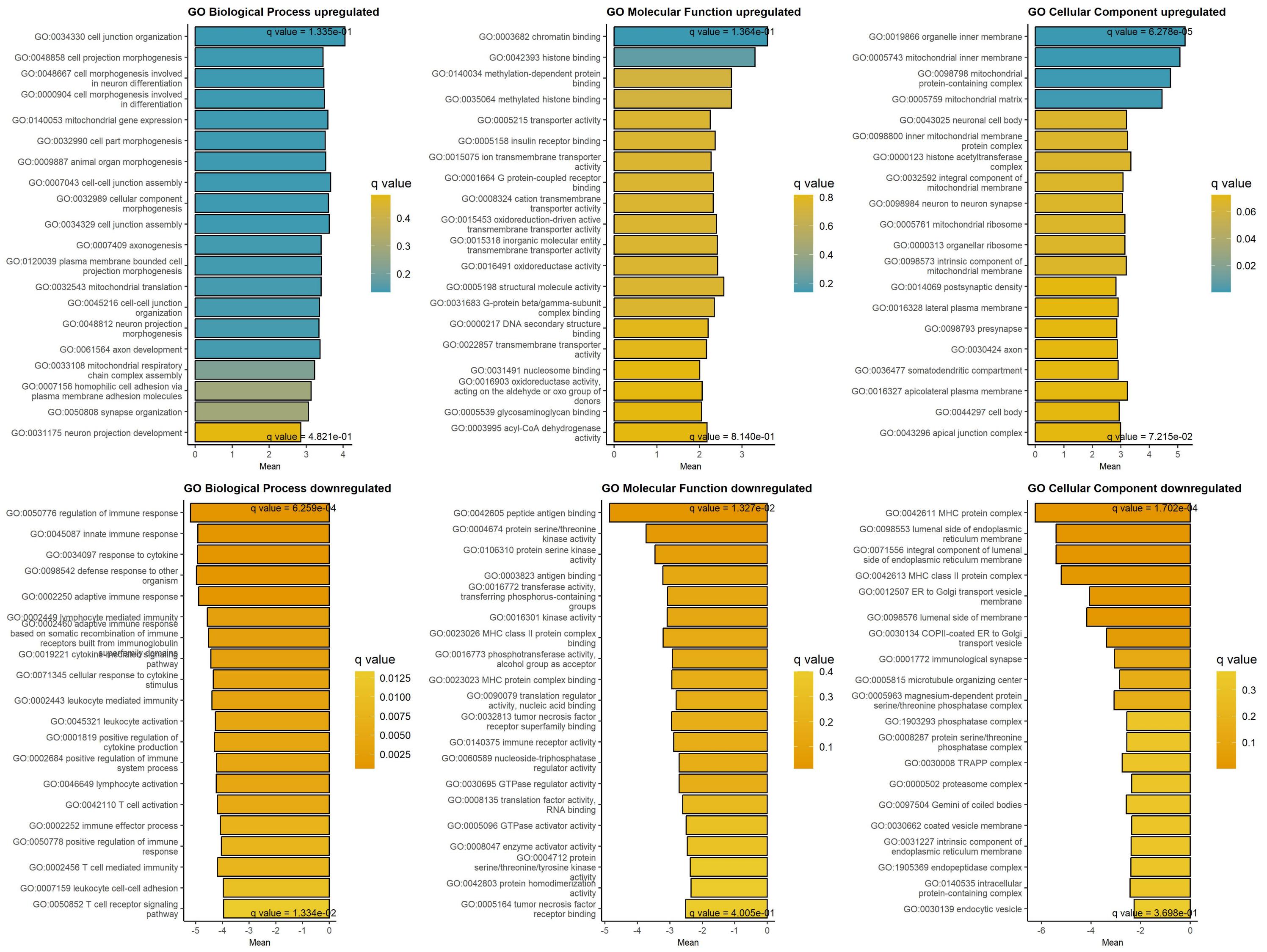


Downregulated at low/absent BCL3

Upregulated at low/absent BCL3

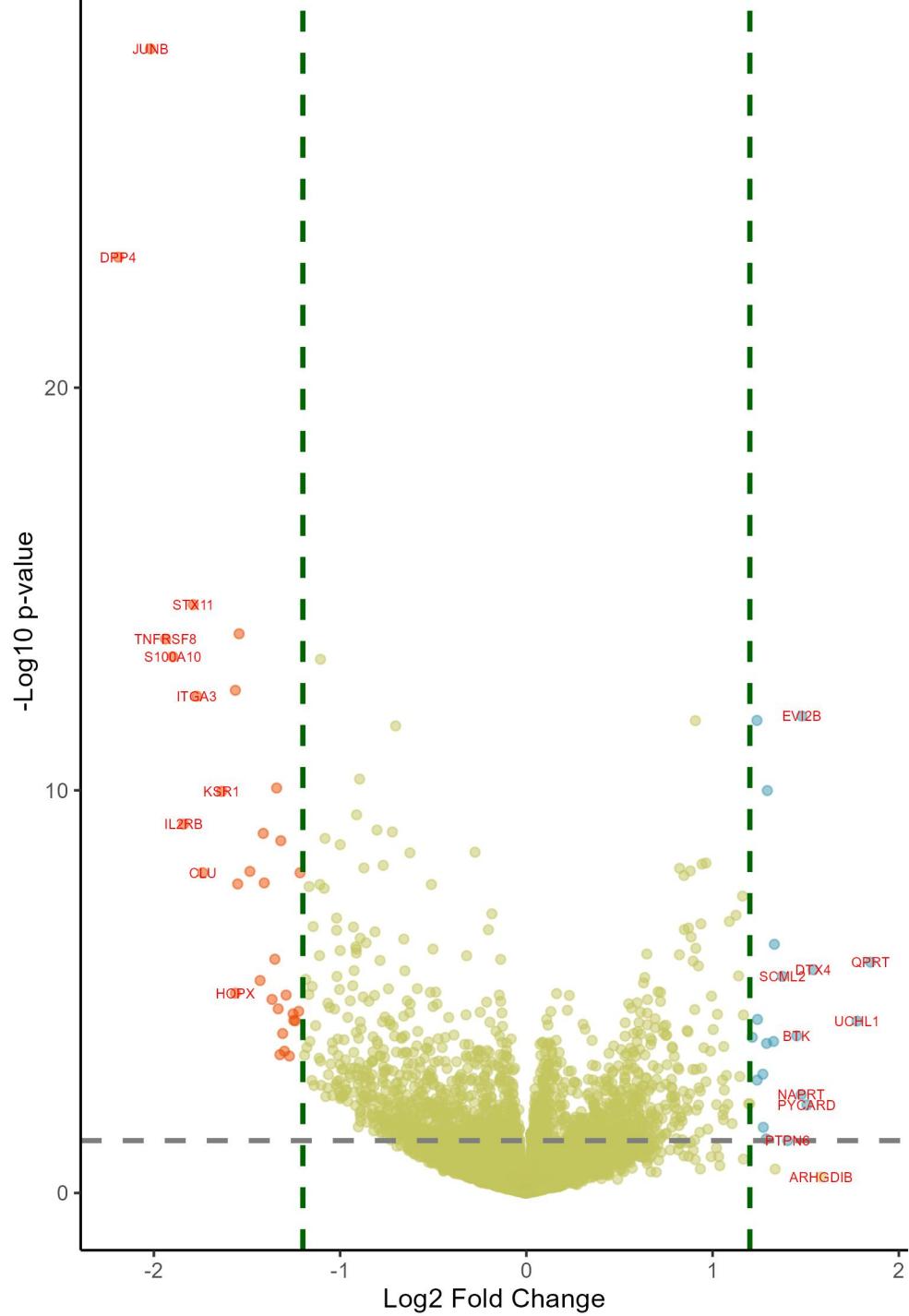
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.95	1.55e-08	TYMP	thymidine phosphorylase	1.24	5.70e-02	UCHL1	ubiquitin C-terminal hydrolase L1
-0.95	2.40e-16	JUNB	JunB proto-oncogene, AP-1 transcript	0.88	4.60e-02	DPYSL3	dihydropyrimidinase like 3
-0.87	8.38e-04	LPXN	leupaxin	0.84	1.54e-02	HMGAA2	high mobility group AT-hook 2
-0.83	9.90e-06	TRADD	TNFRSF1A associated via death domain	0.83	4.25e-02	CDH2	cadherin 2
-0.82	5.47e-03	IRF4	interferon regulatory factor 4	0.83	4.08e-02	ALDH1A1	aldehyde dehydrogenase 1 family member
-0.81	1.15e-03	FMNL1	formin like 1	0.78	1.28e-02	CPVL	carboxypeptidase vitellogenin like
-0.8	1.33e-04	NCKIPSD	NCK interacting protein with SH3 domain	0.73	6.10e-03	SCML2	Scm polycomb group protein like 2
-0.79	6.21e-03	TNFRSF8	TNF receptor superfamily member 8	0.72	8.41e-02	QPRT	quinolinate phosphoribosyltransferase
-0.76	1.95e-02	ACAP1	ArfGAP with coiled-coil, ankyrin repeat	0.71	1.31e-03	PALM	paralemmin
-0.75	1.01e-04	EML2	EMAP like 2	0.7	5.04e-02	FADS2	fatty acid desaturase 2
-0.75	2.89e-09	IL2RB	interleukin 2 receptor subunit beta	0.67	2.45e-06	IRS2	insulin receptor substrate 2
-0.74	5.51e-03	MAPKAPK2	MAPK activated protein kinase 2	0.66	2.29e-01	ALDH2	aldehyde dehydrogenase 2 family member
-0.73	1.06e-04	IFI35	interferon induced protein 35	0.66	1.70e-01	PTK7	protein tyrosine kinase 7 (inactive)
-0.72	1.96e-12	SQOR	sulfide quinone oxidoreductase	0.66	1.04e-01	CABP7	calcium binding protein 7
-0.72	5.47e-03	CGAS	cyclic GMP-AMP synthase	0.64	1.13e-01	CFL2	cofilin 2
-0.71	1.77e-02	HSPA6	heat shock protein family A (Hsp70)	0.64	2.27e-06	PXMP2	peroxisomal membrane protein 2
-0.71	5.35e-04	UBE2L6	ubiquitin conjugating enzyme E2 L6	0.63	5.19e-02	SORT1	sortilin 1
-0.71	4.44e-02	IKZF1	IKAROS family zinc finger 1	0.63	3.01e-02	ABI2	abl interactor 2
-0.69	1.58e-02	MYO1G	myosin IG	0.62	1.66e-01	CNN3	calponin 3
-0.69	1.64e-03	PKLR	pyruvate kinase L/R	0.62	1.30e-05	MSI1	musashi RNA binding protein 1
-0.69	1.30e-02	ALK	ALK receptor tyrosine kinase	0.62	6.87e-02	BAIAP2	BAR/IMD domain containing adaptor protein
-0.68	2.61e-02	CD74	CD74 molecule	0.62	2.88e-02	CADM4	cell adhesion molecule 4
-0.68	2.28e-02	DPP4	dipeptidyl peptidase 4	0.61	1.20e-01	SCRN1	secernin 1
-0.67	4.80e-03	SHKBP1	SH3KBP1 binding protein 1	0.61	5.48e-02	RAB34	RAB34, member RAS oncogene family
-0.67	5.49e-03	GBP2	guanylate binding protein 2	0.61	4.97e-05	CDCA7L	cell division cycle associated 7 li
-0.66	5.10e-03	RELB	RELB proto-oncogene, NF- κ B subunit	0.61	2.80e-01	FKBP10	FKBP prolyl isomerase 10
-0.66	1.12e-11	TAP1	transporter 1, ATP binding cassette	0.6	6.18e-02	TMTC3	transmembrane O-mannosyltransferase
-0.66	1.22e-07	TAP2	transporter 2, ATP binding cassette	0.6	9.30e-04	GPSM1	G protein signaling modulator 1
-0.65	4.60e-03	BST2	bone marrow stromal cell antigen 2	0.59	4.78e-02	RHOB	ras homolog family member B

GAGE analysis on upregulated and downregulated proteins at low/absent BCL3 protein, DB2

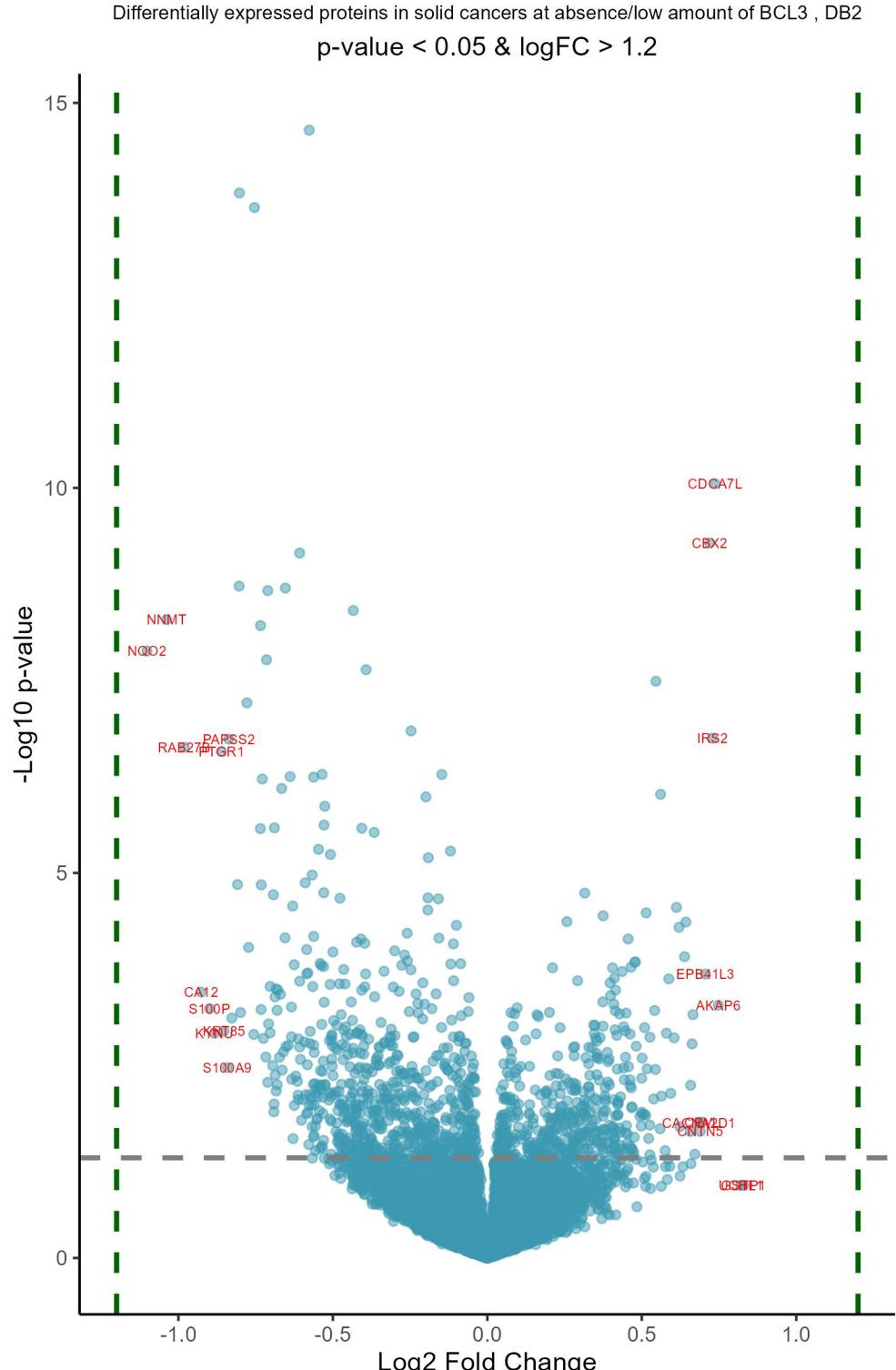


p-value < 0.05 & logFC > 1.2

Downregulated in blood cancers at low/absent BCL3 Upregulated in blood cancers at low/absent BCL3



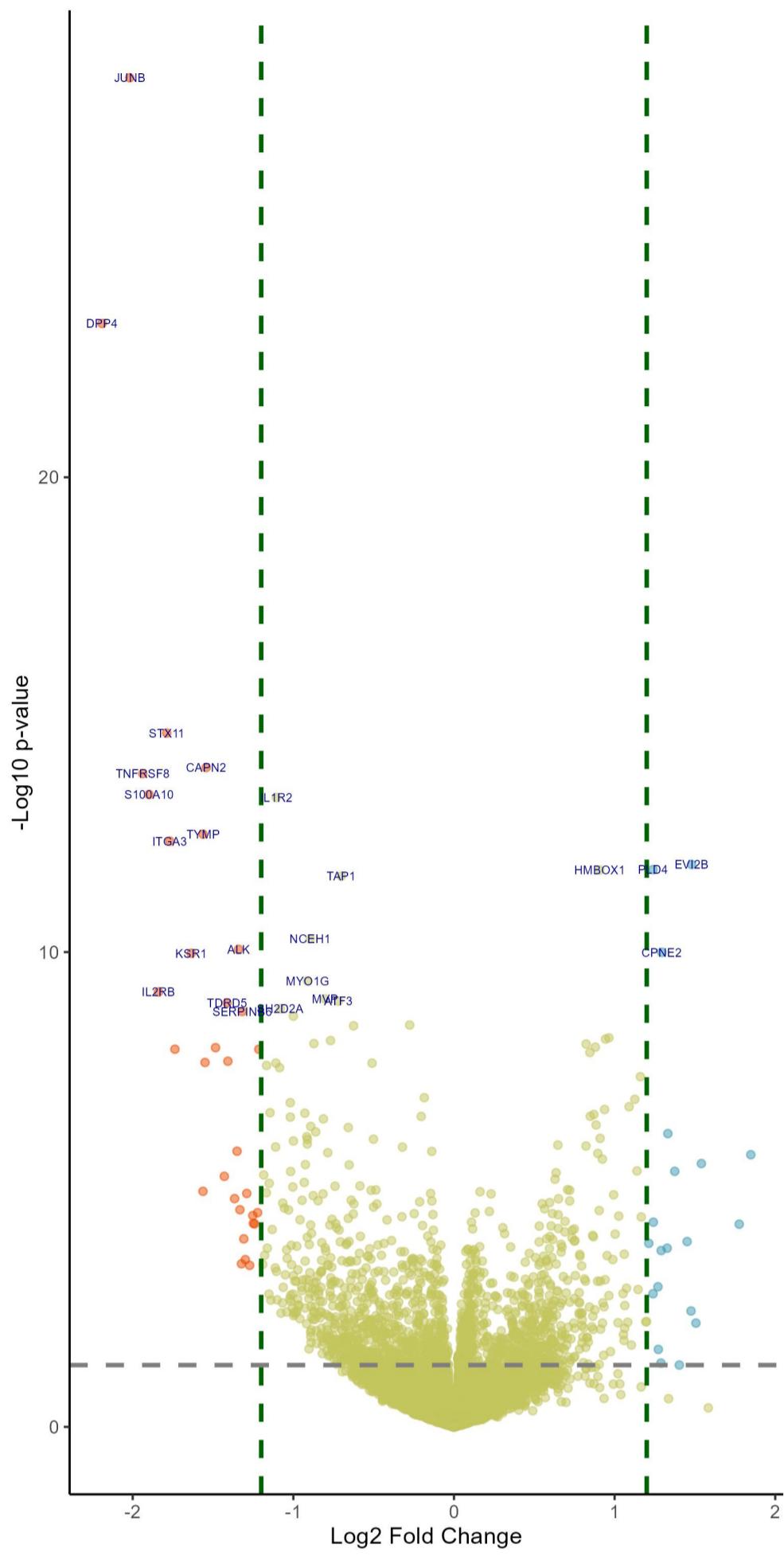
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.19	1.61e-20	DPP4	dipeptidyl peptidase 4	1.85	2.01e-04	QPRT	quinolinate phosphoribosyltransferase
-2.02	1.61e-25	JUNB	JunB proto-oncogene, AP-1 transcript	1.78	3.04e-03	UCHL1	ubiquitin C-terminal hydrolase L1
-1.94	2.44e-11	TNFRSF8	TNF receptor superfamily member 8	1.58	6.55e-01	ARHGDIB	Rho GDP dissociation inhibitor beta
-1.9	5.73e-11	S100A10	S100 calcium binding protein A10	1.54	3.01e-04	DTX4	deltex E3 ubiquitin ligase 4
-1.84	2.90e-07	IL2RB	interleukin 2 receptor subunit beta	1.51	7.86e-02	PYCARD	PYD and CARD domain containing
-1.79	5.10e-12	STX11	syntaxin 11	1.48	1.09e-09	EVI2B	ecotropic viral integration site 2B
-1.77	3.85e-10	ITGA3	integrin subunit alpha 3	1.48	5.45e-02	NAPRT	nicotinate phosphoribosyltransferase
-1.74	2.52e-06	CLU	clusterin	1.45	5.78e-03	BTK	Bruton tyrosine kinase
-1.64	4.93e-08	KSR1	kinase suppressor of ras 1	1.4	2.26e-01	PTPN6	protein tyrosine phosphatase non-receptor type 6
-1.56	9.34e-04	HOPX	HOP homeobox	1.37	4.17e-04	SCML2	Scm polycomb group protein like 2
-1.56	3.05e-10	TYMP	thymidine phosphorylase	1.34	5.47e-01	SPN	sialophorin
-1.55	4.34e-06	LGALS3	galectin 3	1.33	8.99e-05	PRKCB	protein kinase C beta
-1.54	2.17e-11	CAPN2	calpain 2	1.33	7.18e-03	FLI1	Fli-1 proto-oncogene, ETS transcription factor
-1.48	2.46e-06	HMOX1	heme oxygenase 1	1.29	4.93e-08	CPNE2	copine 2
-1.43	5.08e-04	ECHDC2	enoyl-CoA hydratase domain containing 2	1.29	7.70e-03	SYK	spleen associated tyrosine kinase
-1.41	4.26e-07	TDRD5	tudor domain containing 5	1.29	2.13e-01	RCSD1	RCSD domain containing 1
-1.41	4.27e-06	TIMP1	TIMP metallopeptidase inhibitor 1	1.27	1.71e-01	BCL7A	BAF chromatin remodeling complex subunit 7
-1.37	1.22e-03	HABP4	hyaluronan binding protein 4	1.27	2.52e-02	FADS2	fatty acid desaturase 2
-1.35	1.78e-04	RUNX3	RUNX family transcription factor 3	1.24	2.84e-03	CUEDC2	CUE domain containing 2
-1.34	4.58e-08	ALK	ALK receptor tyrosine kinase	1.24	3.11e-02	JCHAIN	joining chain of multimeric IgA and IgM
-1.33	1.82e-03	GBP2	guanylate binding protein 2	1.24	1.20e-09	PLD4	phospholipase D family member 4
-1.32	1.18e-02	PRF1	perforin 1	1.21	6.09e-03	SCRN1	secernin 1
-1.32	5.97e-07	SERPINB6	serpin family B member 6	1.2	7.57e-02	PTK2B	protein tyrosine kinase 2 beta
-1.31	5.24e-03	ASCL3	achaete-scute family bHLH transcript	1.19	7.62e-02	DOK3	docking protein 3
-1.3	1.04e-02	GZMB	granzyme B	1.17	2.31e-03	ALDH2	aldehyde dehydrogenase 2 family member 2
-1.29	9.96e-04	NPHS1	NPHS1 adhesion molecule, nephrin	1.17	4.22e-01	COTL1	coactosin like F-actin binding protein
-1.27	1.23e-02	SERPINA1	serpin family A member 1	1.16	7.84e-06	GNG7	G protein subunit gamma 7
-1.25	2.22e-03	H2BU1	H2B.U histone 1	1.15	2.75e-02	HVCN1	hydrogen voltage gated channel 1
-1.25	2.98e-03	CD274	CD274 molecule	1.14	4.14e-04	SYTL1	synaptotagmin like 1



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.1	7.83e-06	NQO2	N-ribosyldihydronicotinamide:quinon	0.83	4.71e-01	GSTP1	glutathione S-transferase pi 1
-1.04	3.57e-06	NNMT	nicotinamide N-methyltransferase	0.82	4.70e-01	UCHL1	ubiquitin C-terminal hydrolase L1
-0.98	8.84e-05	RAB27B	RAB27B, member RAS oncogene family	0.75	3.35e-02	AKAP6	A-kinase anchoring protein 6
-0.93	2.55e-02	CA12	carbonic anhydrase 12	0.74	1.47e-07	CDCA7L	cell division cycle associated 7 li
-0.9	3.61e-02	S100P	S100 calcium binding protein P	0.73	7.28e-05	IRS2	insulin receptor substrate 2
-0.88	5.57e-02	KYNU	kynureninase	0.72	7.23e-07	CBX2	chromobox 2
-0.86	9.68e-05	PTGR1	prostaglandin reductase 1	0.71	1.79e-02	EPB41L3	erythrocyte membrane protein band 4
-0.85	5.37e-02	KRT85	keratin 85	0.7	2.13e-01	CPVL	carboxypeptidase vitellogenin like
-0.84	9.12e-02	S100A9	S100 calcium binding protein A9	0.69	2.47e-01	CNTN5	contactin 5
-0.84	7.28e-05	PAPSS2	3'-phosphoadenosine 5'-phosphosulfa	0.68	2.14e-01	CACNA2D1	calcium voltage-gated channel auxil
-0.83	4.19e-02	HSPA6	heat shock protein family A (Hsp70)	0.67	3.37e-01	UCP1	uncoupling protein 1
-0.81	2.65e-03	TPD52L1	TPD52 like 1	0.67	3.86e-02	WDR76	WD repeat domain 76
-0.8	1.80e-06	EHD2	EH domain containing 2	0.66	6.19e-02	CCDC59	coiled-coil domain containing 59
-0.8	4.12e-11	CAPG	capping actin protein, gelsolin lik	0.66	3.78e-01	CABP7	calcium binding protein 7
-0.8	3.81e-02	MLPH	melanophilin	0.66	1.21e-01	JAM3	junctional adhesion molecule 3
-0.78	2.87e-05	MGST1	microsomal glutathione S-transferas	0.66	2.47e-01	ATP1A3	ATPase Na+/K+ transporting subunit
-0.77	1.11e-02	NCKIPSD	NCK interacting protein with SH3 do	0.64	6.25e-03	TSPYL5	TSPY like 5
-0.76	5.57e-02	CPM	carboxypeptidase M	0.64	1.36e-02	GPSM1	G protein signaling modulator 1
-0.75	4.78e-11	SQOR	sulfide quinone oxidoreductase	0.63	3.86e-01	CDH2	cadherin 2
-0.73	6.17e-04	TGM2	transglutaminase 2	0.62	4.26e-01	DPYSL3	dihydropyrimidinase like 3
-0.73	3.95e-06	HERC1	HECT and RLD domain containing E3 u	0.62	2.31e-01	MELTF	melanotransferrin
-0.73	3.67e-02	S100A4	S100 calcium binding protein A4	0.62	7.07e-03	MSI1	musashi RNA binding protein 1
-0.73	2.65e-03	SH3KBP1	SH3 domain containing kinase bindin	0.61	4.42e-03	PXMP2	peroxisomal membrane protein 2
-0.73	1.80e-04	KRT7	keratin 7	0.6	5.65e-02	GGA2	golgi associated, gamma adaptin ear
-0.72	5.68e-02	SHQ1	SHQ1, H/ACA ribonucleoprotein assem	0.59	1.38e-01	MAZ	MYC associated zinc finger protein
-0.72	7.69e-02	PLAUR	plasminogen activator, urokinase re	0.59	3.85e-01	FAM186A	family with sequence similarity 186
-0.71	9.51e-06	DAGLB	diacylglycerol lipase beta	0.59	2.03e-02	DDB2	damage specific DNA binding protein
-0.71	1.17e-01	KLC3	kinesin light chain 3	0.59	3.57e-01	DOCK9	dedicator of cytokinesis 9
-0.71	1.80e-06	FAM114A1	family with sequence similarity 114	0.58	4.36e-01	ALDH1A1	aldehyde dehydrogenase 1 family mem

BCL3 network, DB2, no Pearson r > 0.3

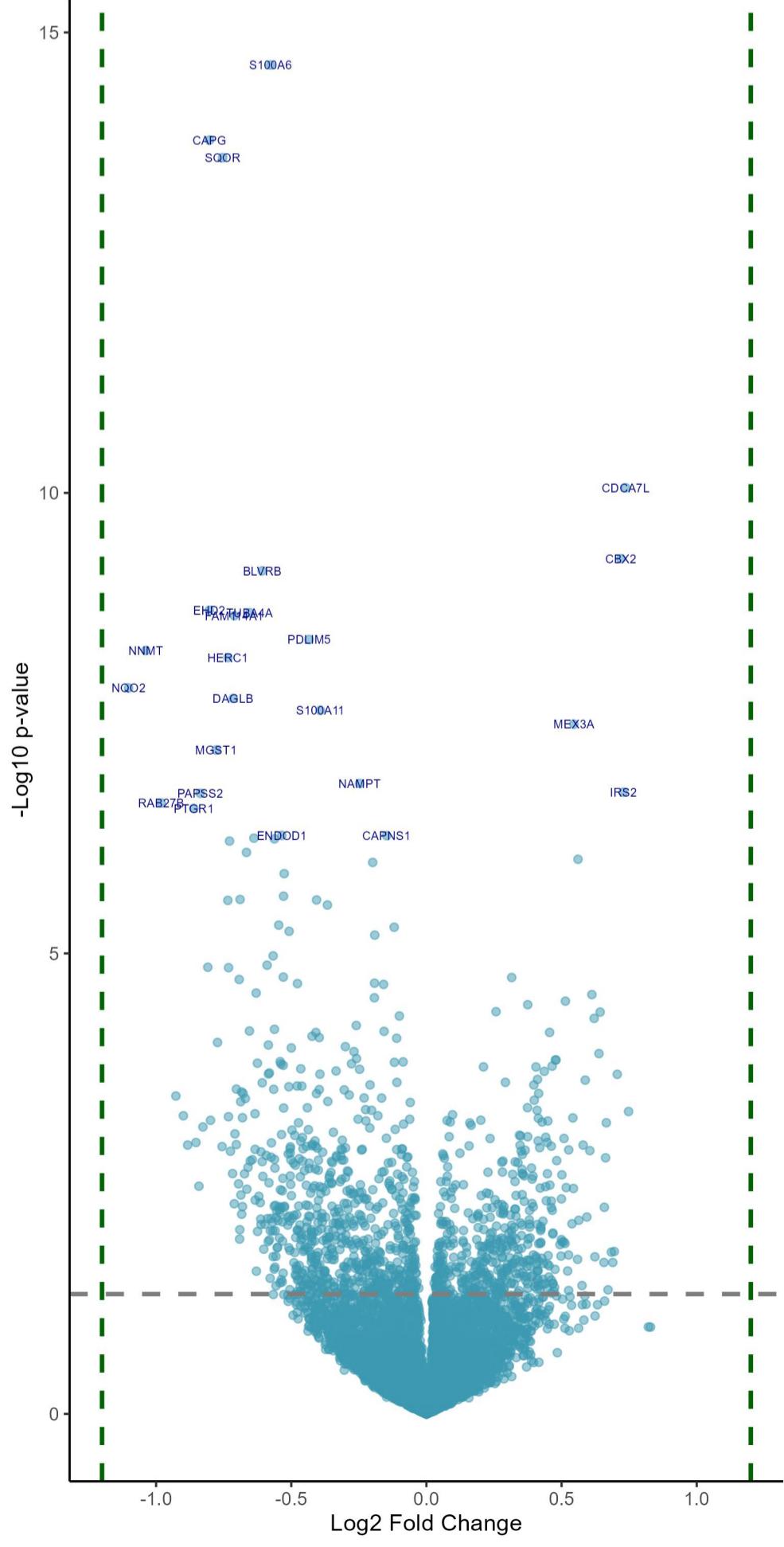
Differentially expressed proteins in blood cancers at absence/low amount of BCL3 , DB2
p-value < 0.05 & logFC > 1.2



Sorted by p values!
Downregulated in blood cancers at low/absent BCL3 Upregulated in blood cancers at low/absent BCL3

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.02	1.61e-25	JUNB	JunB proto-oncogene, AP-1 transcript	1.48	1.09e-09	EVI2B	ecotropic viral integration site 2B
-2.19	1.61e-20	DPP4	dipeptidyl peptidase 4	1.24	1.20e-09	PLD4	phospholipase D family member 4
-1.79	5.10e-12	STX11	syntaxin 11	0.91	1.20e-09	HMBOX1	homeobox containing 1
-1.54	2.17e-11	CAPN2	calpain 2	1.29	4.93e-08	CPNE2	copine 2
-1.94	2.44e-11	TNFRSF8	TNF receptor superfamily member 8	0.96	1.85e-06	SKP2	S-phase kinase associated protein 2
-1.9	5.73e-11	S100A10	S100 calcium binding protein A10	0.94	1.89e-06	CA8	carbonic anhydrase 8
-1.11	5.83e-11	IL1R2	interleukin 1 receptor type 2	0.82	2.19e-06	UBASH3B	ubiquitin associated and SH3 domain
-1.56	3.05e-10	TYMP	thymidine phosphorylase	0.88	2.46e-06	PATZ1	POZ/BTB and AT hook containing zinc
-1.77	3.85e-10	ITGA3	integrin subunit alpha 3	0.85	2.87e-06	KANK2	KN motif and ankyrin repeat domains
-0.7	1.50e-09	TAP1	transporter 1, ATP binding cassette	1.16	7.84e-06	GNG7	G protein subunit gamma 7
-0.9	2.93e-08	NCEH1	neutral cholesterol ester hydrolase	1.13	2.25e-05	SPI1	Spi-1 proto-oncogene
-1.34	4.58e-08	ALK	ALK receptor tyrosine kinase	1.09	3.08e-05	SSBP2	single stranded DNA binding protein
-1.64	4.93e-08	KSR1	kinase suppressor of ras 1	0.94	3.47e-05	MGST1	microsomal glutathione S-transferase
-0.91	1.78e-07	MYO1G	myosin IG	0.87	4.15e-05	ID3	inhibitor of DNA binding 3, HLH pro
-1.84	2.90e-07	IL2RB	interleukin 2 receptor subunit beta	0.85	4.40e-05	PLA2G15	phospholipase A2 group XV
-0.8	3.86e-07	MVP	major vault protein	0.88	6.32e-05	IGLL1	immunoglobulin lambda like polypept
-0.72	4.11e-07	ATF3	activating transcription factor 3	1.33	8.99e-05	PRKCB	protein kinase C beta
-1.41	4.26e-07	TDRD5	tudor domain containing 5	0.91	1.10e-04	ARHGEF18	Rho/Rac guanine nucleotide exchange
-1.08	5.45e-07	SH2D2A	SH2 domain containing 2A	0.65	1.41e-04	ZNF516	zinc finger protein 516
-1.32	5.97e-07	SERPINB6	serpin family B member 6	0.82	1.45e-04	MNDA	myeloid cell nuclear differentiatio
-1	7.19e-07	ACSL1	acyl-CoA synthetase long chain fami	0.9	1.91e-04	DNMBP	dynamin binding protein
-0.28	1.07e-06	NAMPT	nicotinamide phosphoribosyltransfer	1.85	2.01e-04	QPRT	quinolinate phosphoribosyltransfера
-0.63	1.07e-06	ANXA2	annexin A2	0.92	2.46e-04	CLEC11A	C-type lectin domain containing 11A
-0.77	1.97e-06	TAP2	transporter 2, ATP binding cassette	1.54	3.01e-04	DTX4	deltex E3 ubiquitin ligase 4
-0.87	2.19e-06	RNF213	ring finger protein 213	1.14	4.14e-04	SYTL1	synaptotagmin like 1
-1.48	2.46e-06	HMOX1	heme oxygenase 1	1.37	4.17e-04	SCML2	Scm polycomb group protein like 2
-1.74	2.52e-06	CLU	clusterin	0.64	4.38e-04	RB1CC1	RB1 inducible coiled-coil 1
-1.22	2.52e-06	FLVCR1	FLVCR heme transporter 1	0.63	5.77e-04	MILR1	mast cell immunoglobulin like recep
-1.41	4.27e-06	TIMP1	TIMP metallopeptidase inhibitor 1	0.71	8.97e-04	CD33	CD33 molecule
-1.55	4.34e-06	LGALS3	galectin 3	0.72	8.97e-04	VPREB3	V-set pre-B cell surrogate light ch
-1.11	4.34e-06	TDRKH	tudor and KH domain containing	0.16	9.45e-04	RCC2	regulator of chromosome condensatio
-0.51	4.34e-06	ROR2	receptor tyrosine kinase like orpha	0.23	9.98e-04	TPP2	tripeptidyl peptidase 2
-1.17	4.76e-06	SRXN1	sulfiredoxin 1	0.99	1.03e-03	SETMAR	SET domain and mariner transposase
-1.09	5.17e-06	PARP4	poly(ADP-ribose) polymerase family	0.65	1.22e-03	GRB10	growth factor receptor bound protei
-0.19	2.12e-05	FAF2	Fas associated factor family member	0.72	1.29e-03	CHTF18	chromosome transmission fidelity fa
-1.02	2.59e-05	TXNDC15	thioredoxin domain containing 15	0.6	1.37e-03	TOR4A	torsin family 4 member A
-1.14	3.96e-05	HSPG2	heparan sulfate proteoglycan 2	0.55	1.42e-03	ZNF8	zinc finger protein 8
-0.93	3.98e-05	SERPINB1	serpin family B member 1	0.56	1.75e-03	SMAD1	SMAD family member 1
0.2	4.10e-05	POB	cytochrome P450 oxidoreductase	0.9	1.86e-03	CFL2	cofilin 2

Differentially expressed proteins in solid cancers at absence/low amount of BCL3 , DB2
p-value < 0.05 & logFC > 1.2

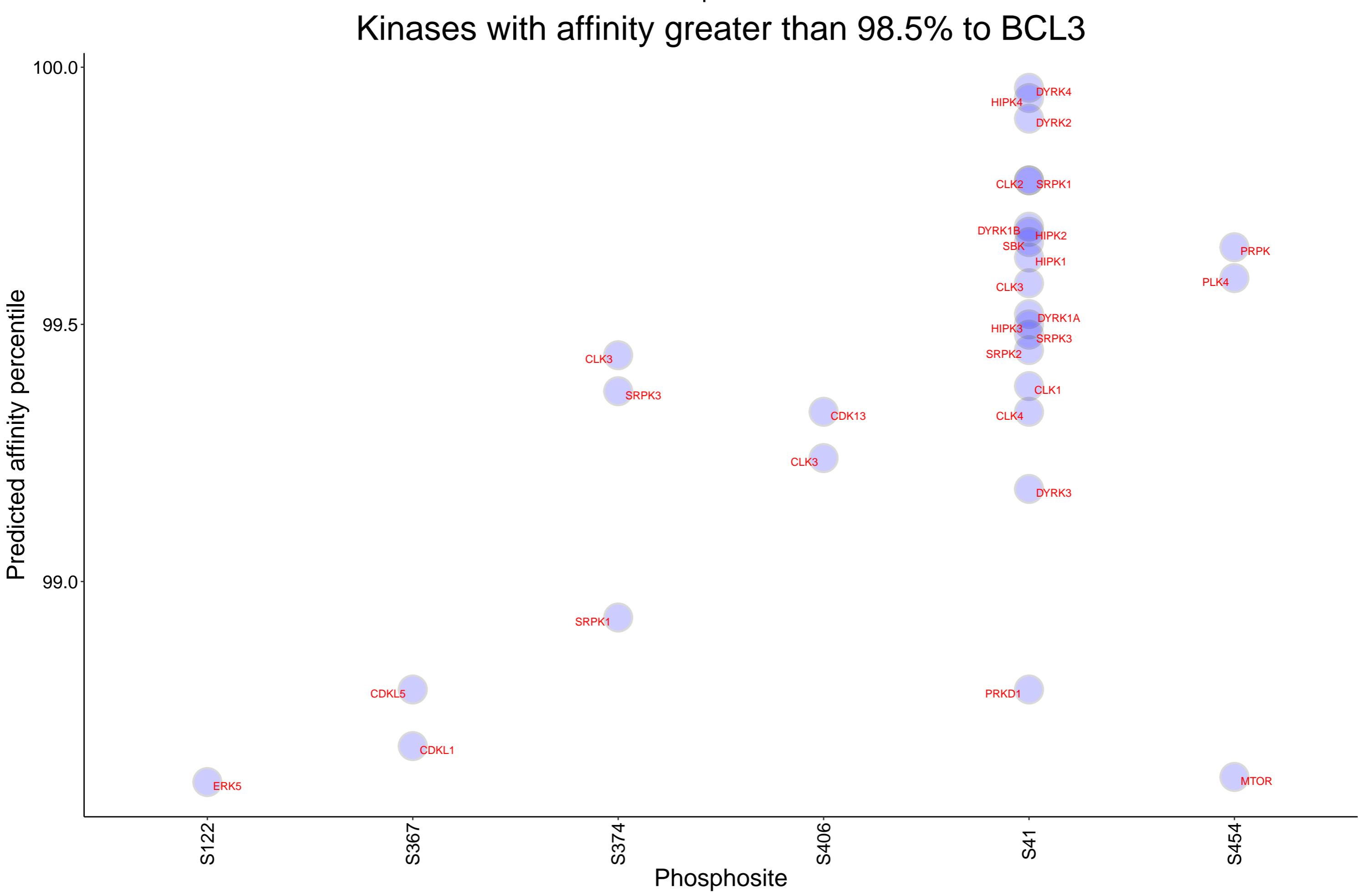
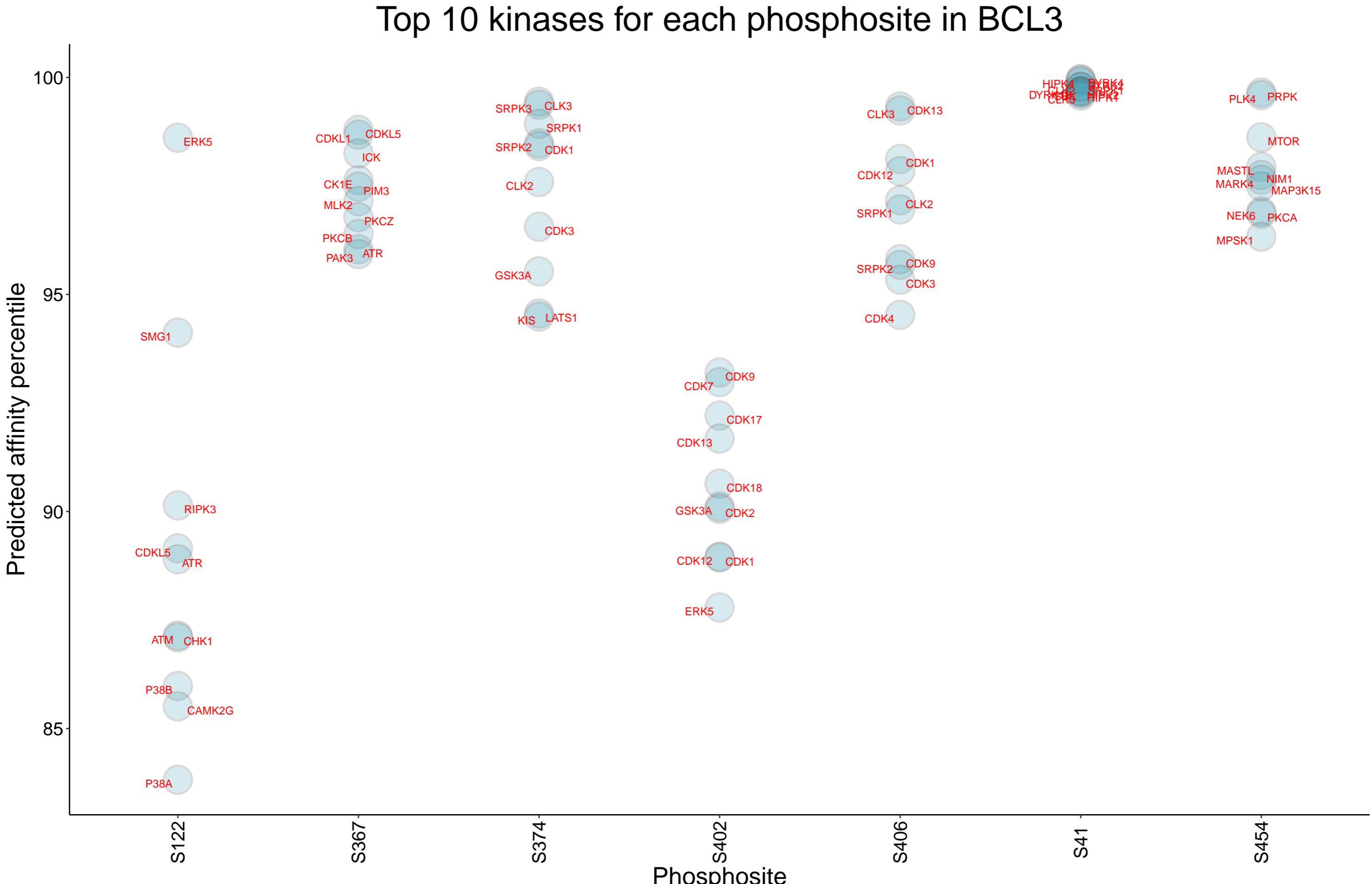


Sorted by p values!
Downregulated in solid cancers at low/absent BCL3 Upregulated in solid cancers at low/absent BCL3

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.58	9.44e-12	S100A6	S100 calcium binding protein A6	0.74	1.47e-07	CDCA7L	cell division cycle associated 7 li
-0.8	4.12e-11	CAPG	capping actin protein, gelsolin lik	0.72	7.23e-07	CBX2	chromobox 2
-0.75	4.78e-11	SQOR	sulfide quinone oxidoreductase	0.55	1.59e-05	MEX3A	mex-3 RNA binding family member A
-0.61	8.37e-07	BLVRB	biliverdin reductase B	0.73	7.28e-05	IRS2	insulin receptor substrate 2
-0.8	1.80e-06	EHD2	EH domain containing 2	0.56	2.65e-04	CDC16	cell division cycle 16
-0.65	1.80e-06	TUBA4A	tubulin alpha 4a	0.32	3.25e-03	SMUG1	single-strand-selective monofunctio
-0.71	1.80e-06	FAM114A1	family with sequence similarity 114	0.61	4.42e-03	PXMP2	peroxisomal membrane protein 2
-0.43	2.97e-06	PDLIM5	PDZ and LIM domain 5	0.51	5.01e-03	SV2A	synaptic vesicle glycoprotein 2A
-1.04	3.57e-06	NNMT	nicotinamide N-methyltransferase	0.37	5.38e-03	PHC1	polyhomeotic homolog 1
-0.73	3.95e-06	HERC1	HECT and RLD domain containing E3 u	0.26	6.25e-03	IPO5	importin 5
-1.1	7.83e-06	NQO2	N-ribosylidihydronicotinamide:quinon	0.64	6.25e-03	TSPYL5	TSPY like 5
-0.71	9.51e-06	DAGLB	diacylglycerol lipase beta	0.62	7.07e-03	MSI1	musashi RNA binding protein 1
-0.39	1.20e-05	S100A11	S100 calcium binding protein A11	0.46	9.14e-03	ZNF48	zinc finger protein 48
-0.78	2.87e-05	MGST1	microsomal glutathione S-transferas	0.64	1.36e-02	GPSM1	G protein signaling modulator 1
-0.25	6.29e-05	NAMPT	nicotinamide phosphoribosyltransfer	0.48	1.54e-02	CRB2	crumbs cell polarity complex compon
-0.84	7.28e-05	PAPSS2	3'-phosphoadenosine 5'-phosphosulfa	0.48	1.54e-02	SKP2	S-phase kinase associated protein 2
-0.98	8.84e-05	RAB27B	RAB27B, member RAS oncogene family	0.47	1.62e-02	TCF3	transcription factor 3
-0.86	9.68e-05	PTGR1	prostaglandin reductase 1	0.21	1.62e-02	UTP3	UTP3 small subunit processome compo
-0.53	1.76e-04	ENDOD1	endonuclease domain containing 1	0.41	1.62e-02	PROX1	prospero homeobox 1
-0.15	1.76e-04	CAPNS1	calpain small subunit 1	0.44	1.73e-02	PMEL	premelanosome protein
-0.64	1.77e-04	PPP1R13L	protein phosphatase 1 regulatory su	0.71	1.79e-02	EPB41L3	erythrocyte membrane protein band 4
-0.56	1.77e-04	S100A10	S100 calcium binding protein A10	0.41	2.01e-02	USP42	ubiquitin specific peptidase 42
-0.73	1.80e-04	KRT7	keratin 7	0.59	2.03e-02	DDB2	damage specific DNA binding protein
-0.67	2.31e-04	NOL3	nucleolar protein 3	0.29	2.10e-02	FAM120B	family with sequence similarity 120
-0.2	2.77e-04	VASP	vasodilator stimulated phosphoprote	0.4	2.18e-02	SYT5	synaptotagmin 5
-0.53	3.56e-04	SEC24A	SEC24 homolog A, COPII coat complex	0.42	2.44e-02	CARMIL2	capping protein regulator and myosi
-0.53	6.06e-04	LGALS3	galectin 3	0.4	2.73e-02	PPT2	palmitoyl-protein thioesterase 2
-0.69	6.17e-04	PCLO	piccolo presynaptic cytomatrix prot	0.37	3.17e-02	SOX2	SRY-box transcription factor 2
-0.41	6.17e-04	FAM177A1	family with sequence similarity 177	0.41	3.28e-02	CHEK1	checkpoint kinase 1
-0.73	6.17e-04	TGM2	transglutaminase 2	0.75	3.35e-02	AKAP6	A-kinase anchoring protein 6
-0.37	6.73e-04	ZYX	zyxin	0.1			

Insufficient number of paired observations in DB2 for BCL3

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