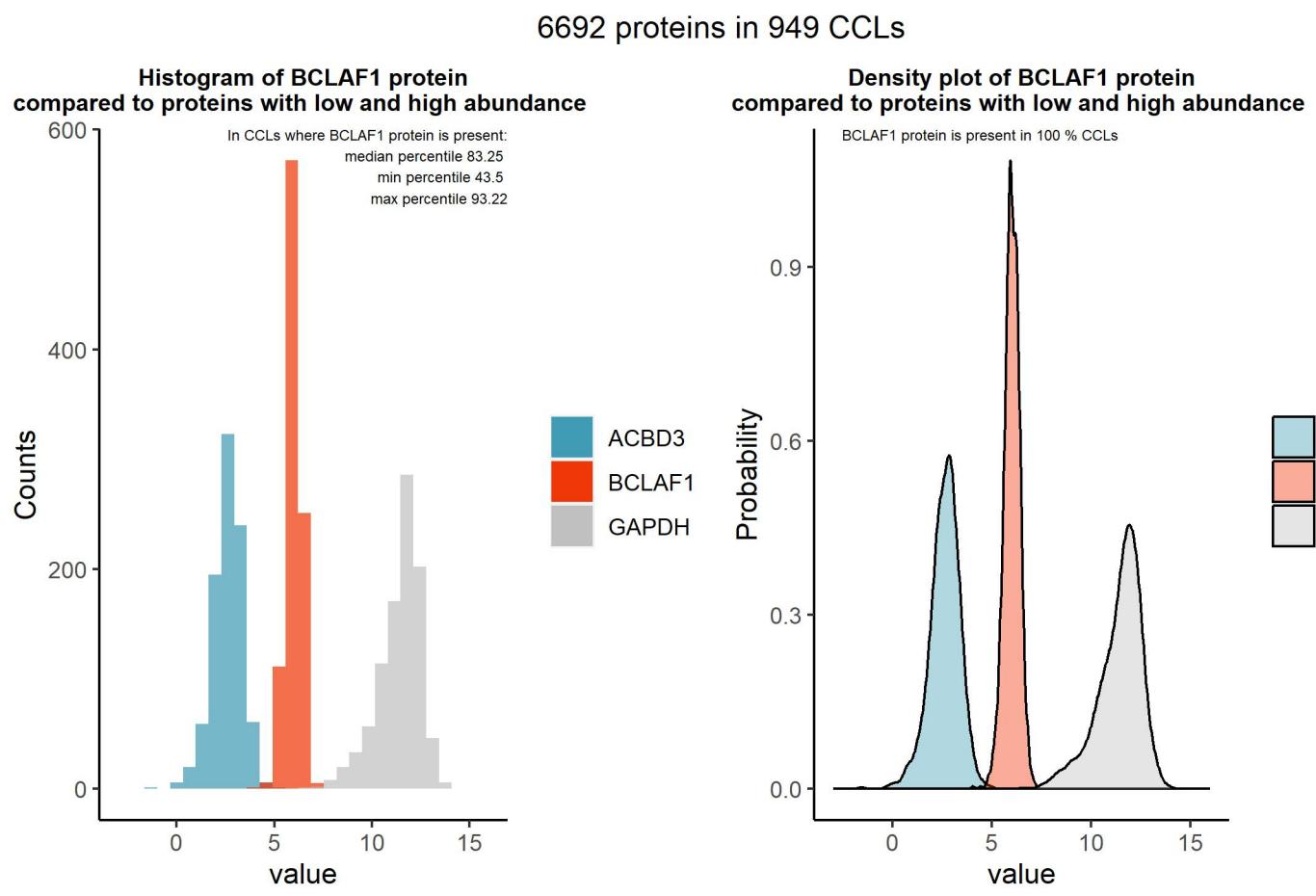


BCLAF1

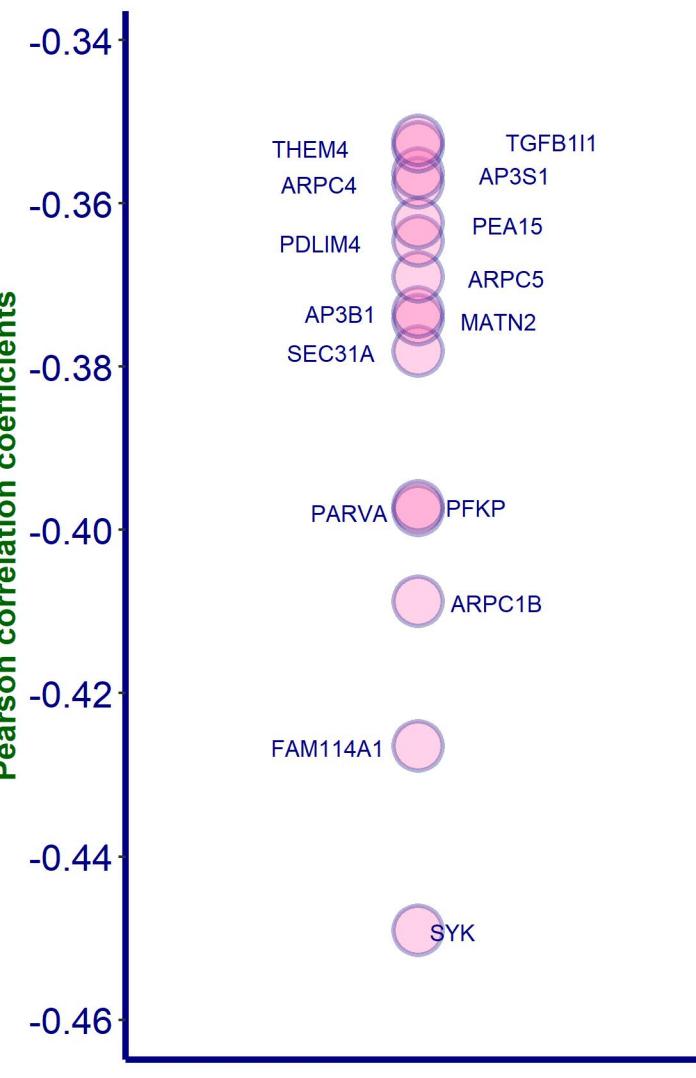
Protein name: BCLF1 ; UNIPROT: Q9NYF8 ; Gene name: BCL2 associated transcription factor 1

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

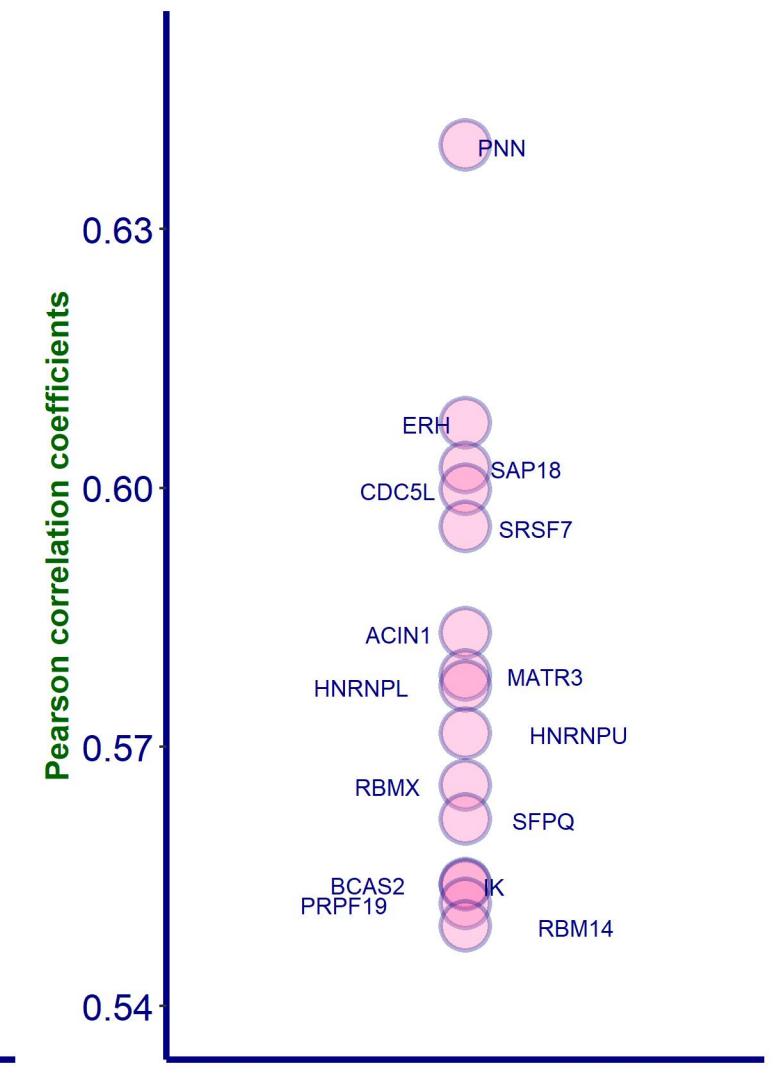
Sanger Institute Protein Database 1 (DB1), protein presence is certain



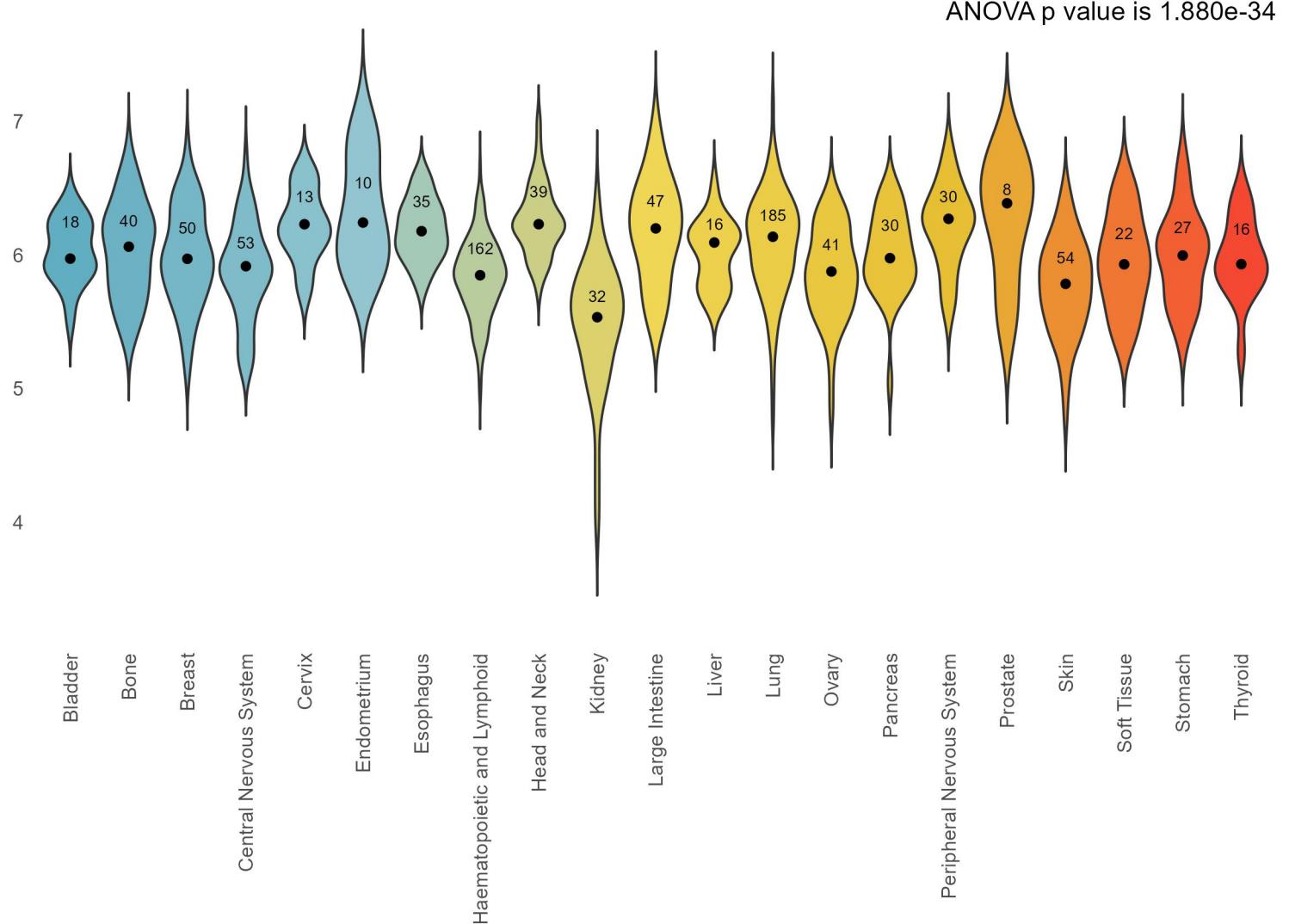
Top negative correlations of BCLAF1 protein, DB1



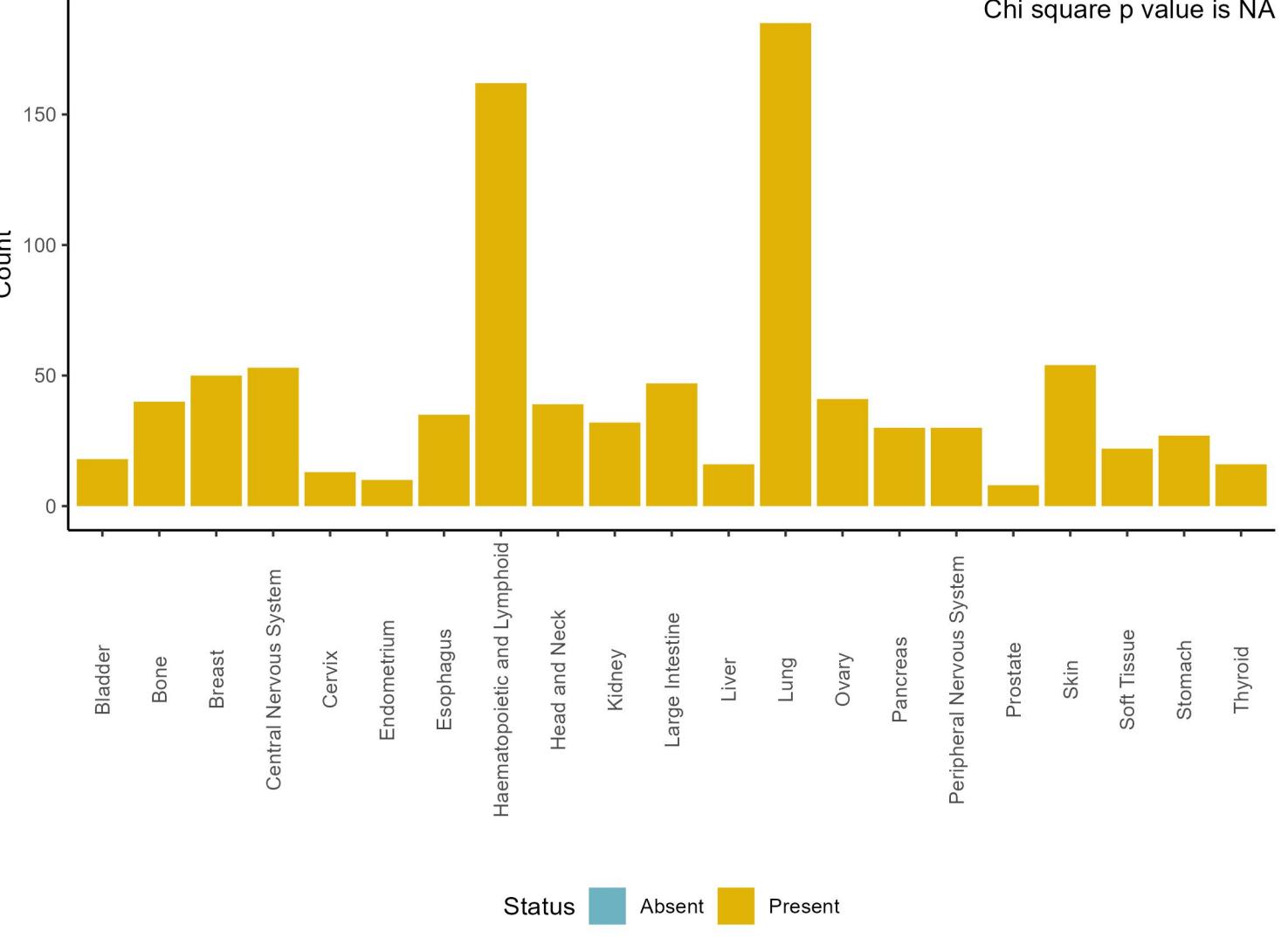
Top positive correlations of BCLAF1 protein, DB1



Amount of BCLAF1 protein, number of CCLs where it is present by tissue, DB1



Present and absent BCLAF1 protein counts by tissue, DB1

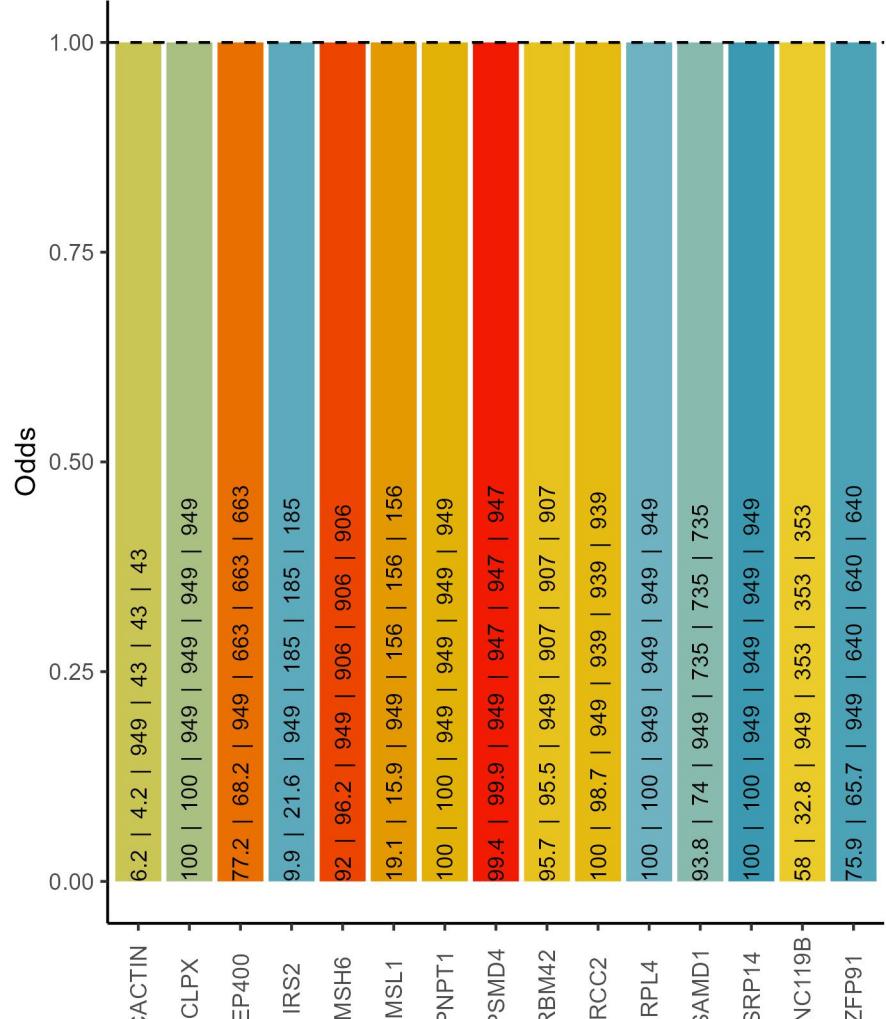


Cooccurrence with BCLAF1 protein, DB1

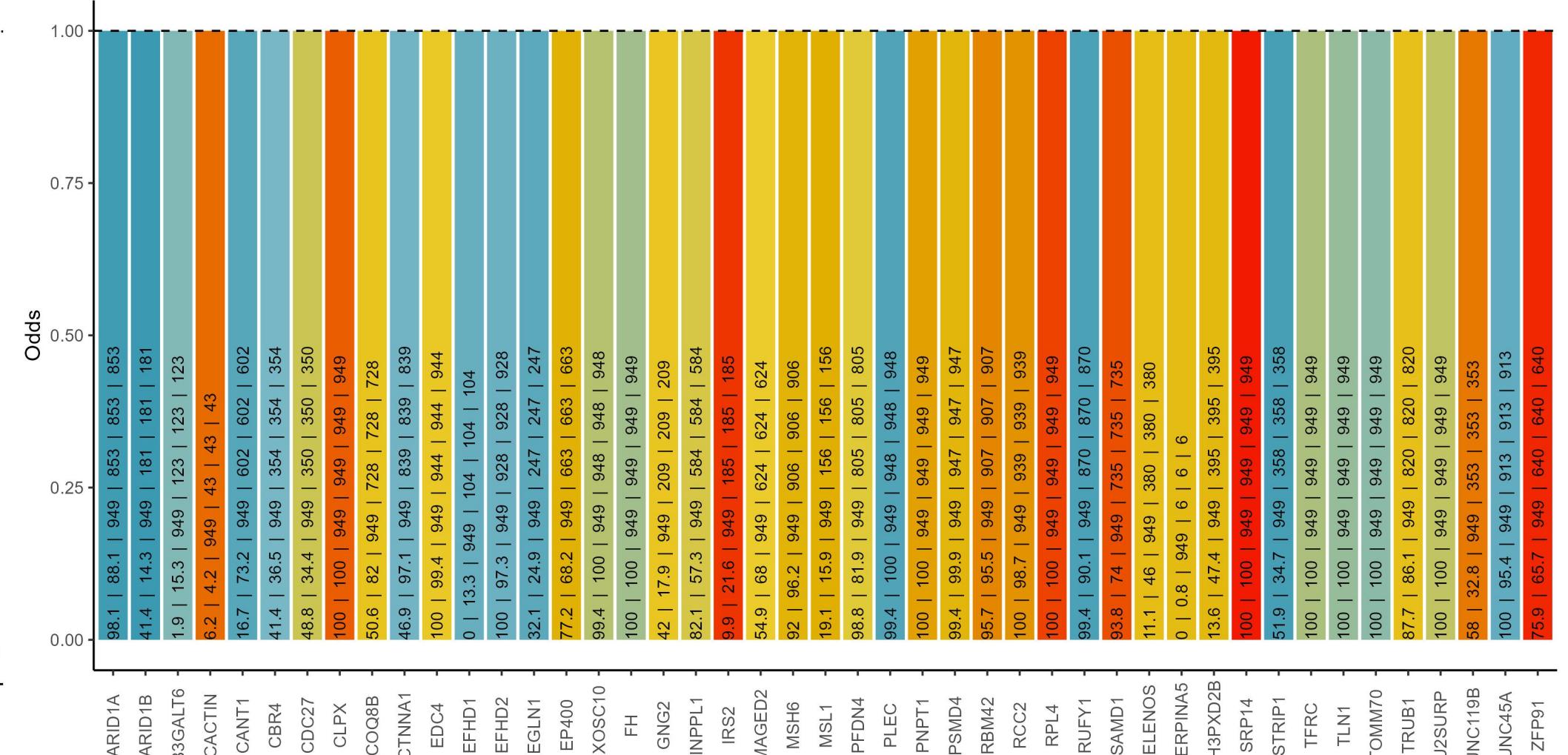
% of BCLAF1 in blood cancers: 100 ; % of BCLAF1 in solid cancers: 100

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of BCLAF1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

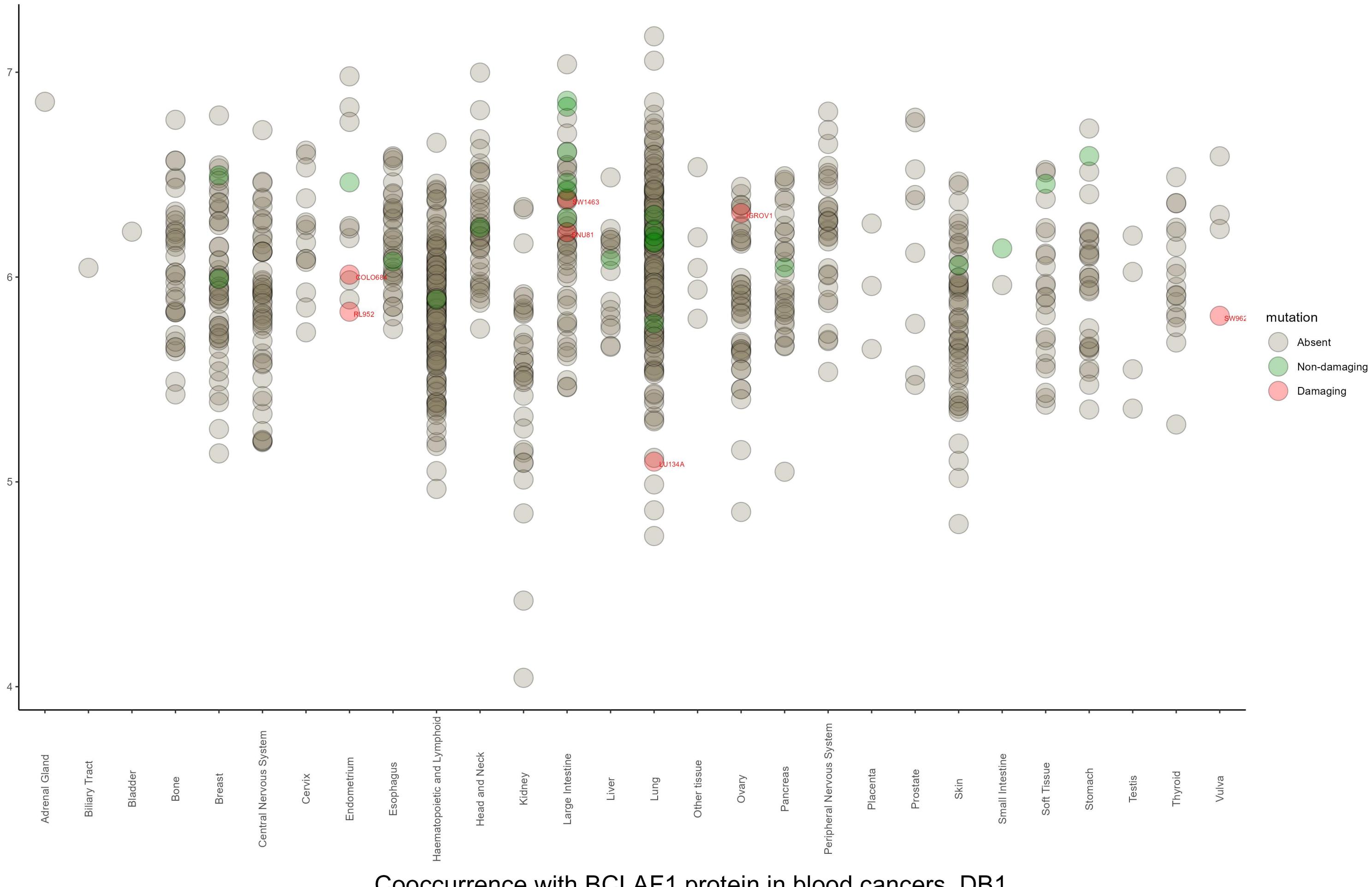
Negative cooccurrence



Positive cooccurrence



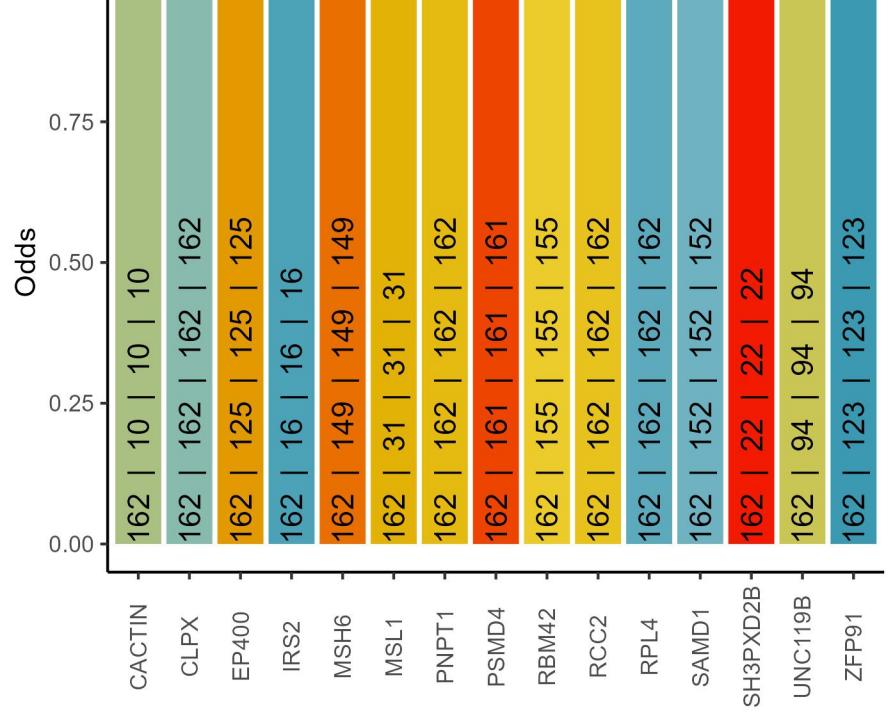
Amount of BCLAF1 protein and mutation status by tissue, DB1



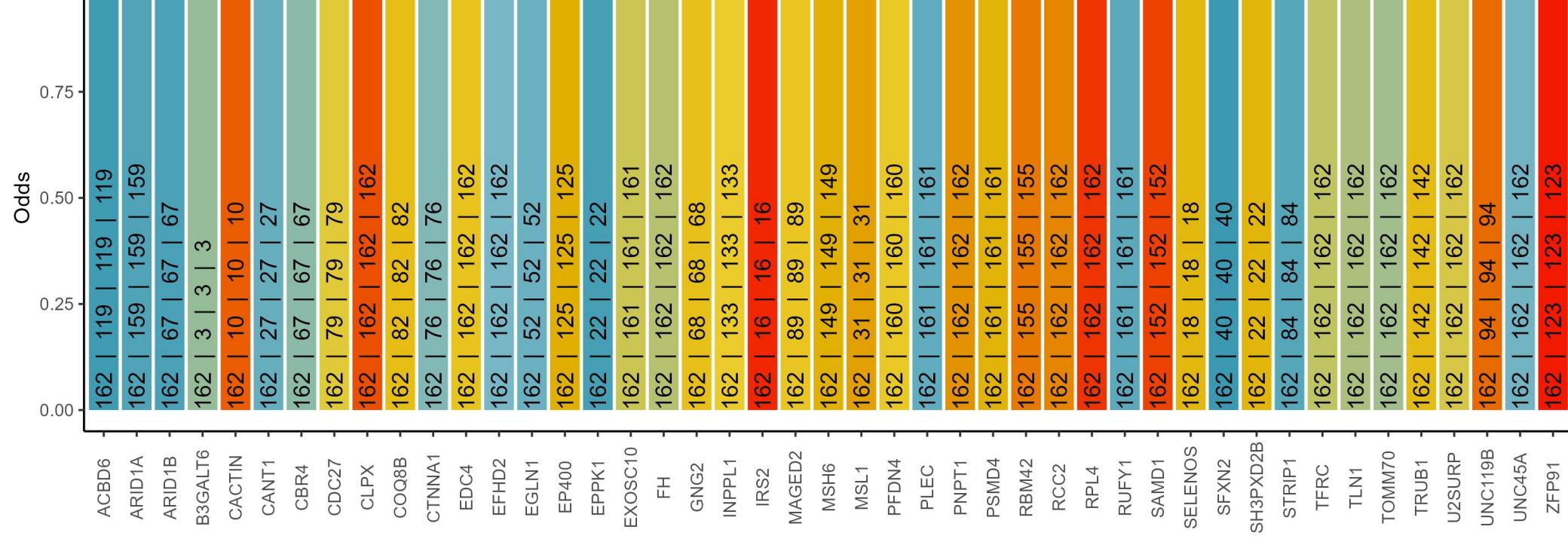
Cooccurrence with BCLAF1 protein in blood cancers, DB1

The text in the bars: incidence of BCLAF1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



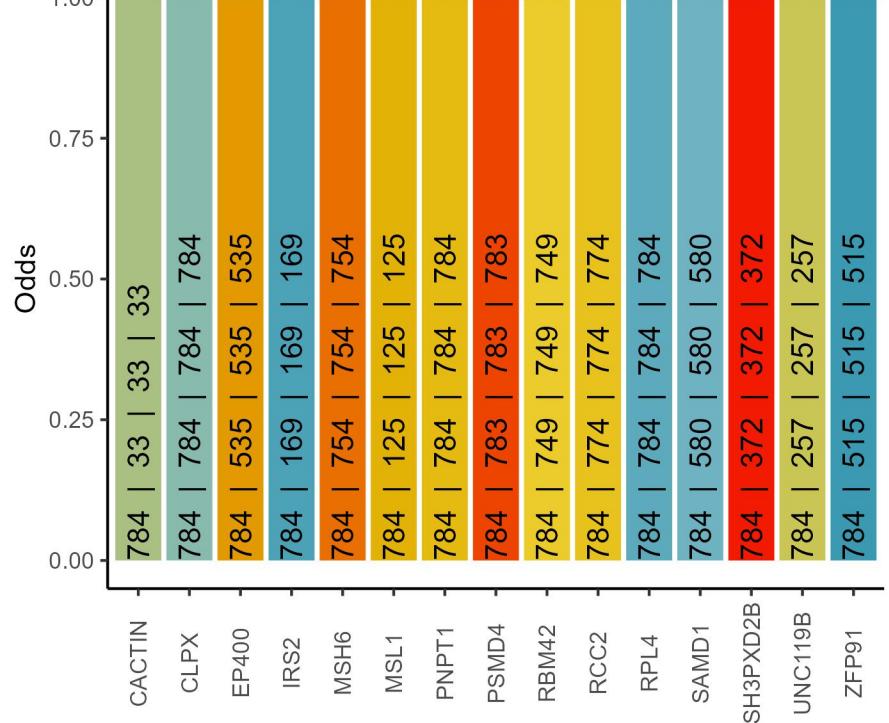
Positive cooccurrence



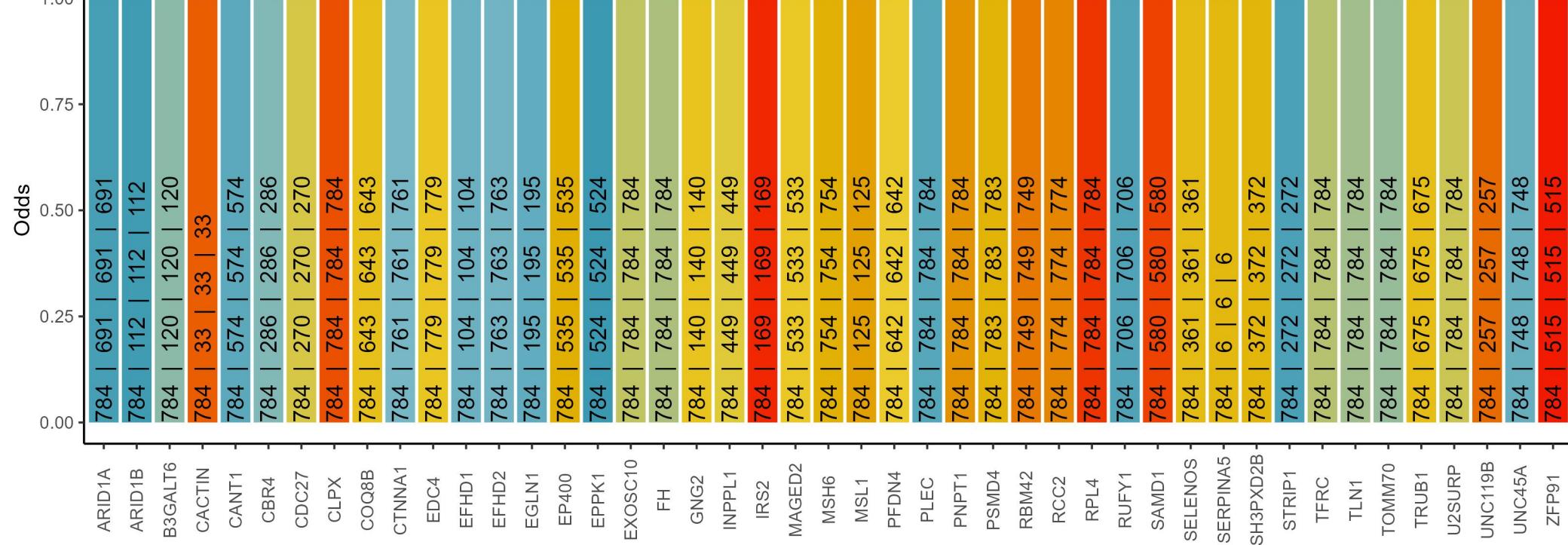
Cooccurrence with BCLAF1 protein in solid cancers, DB1

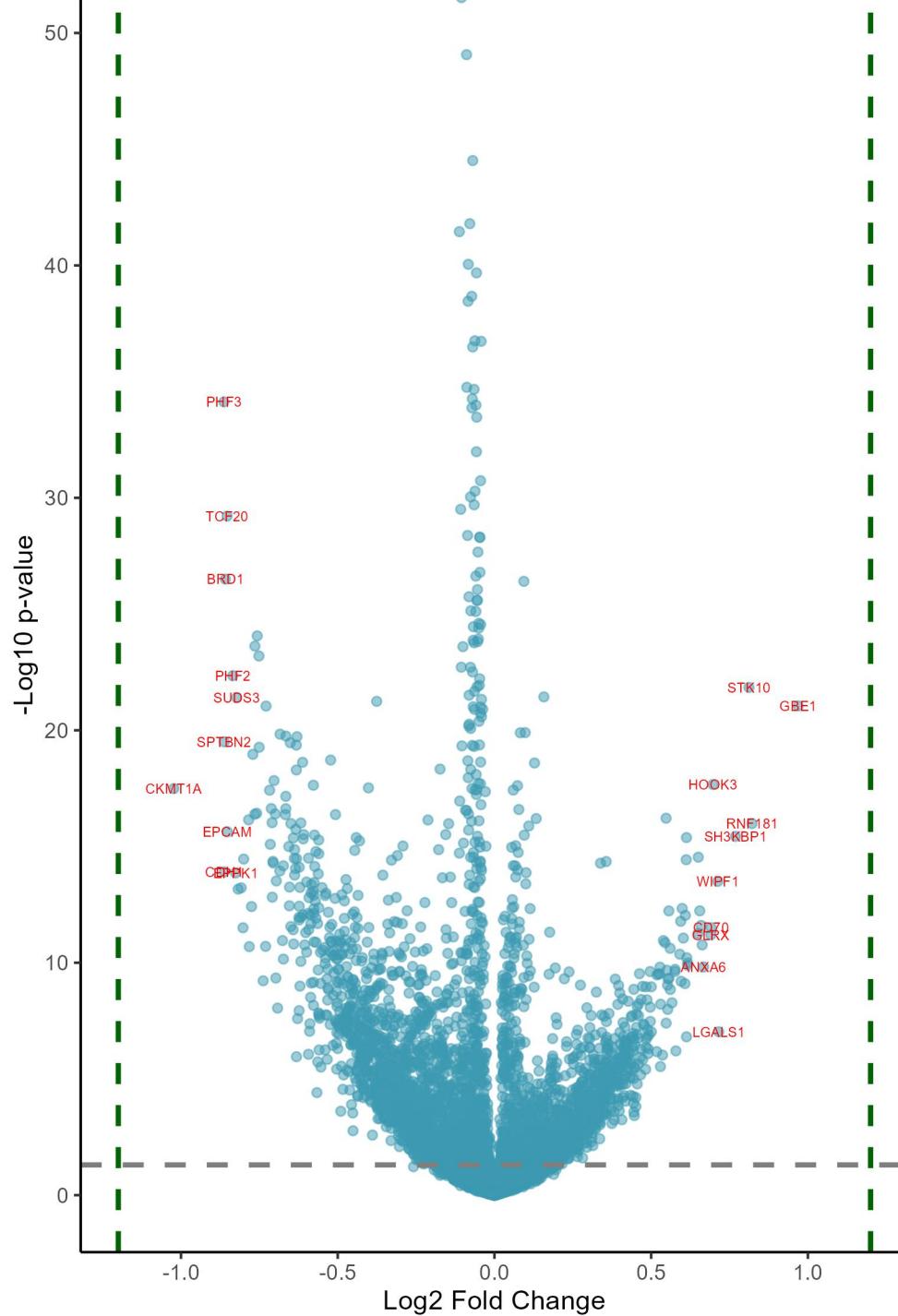
The text in the bars: incidence of BCLAF1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



Positive cooccurrence

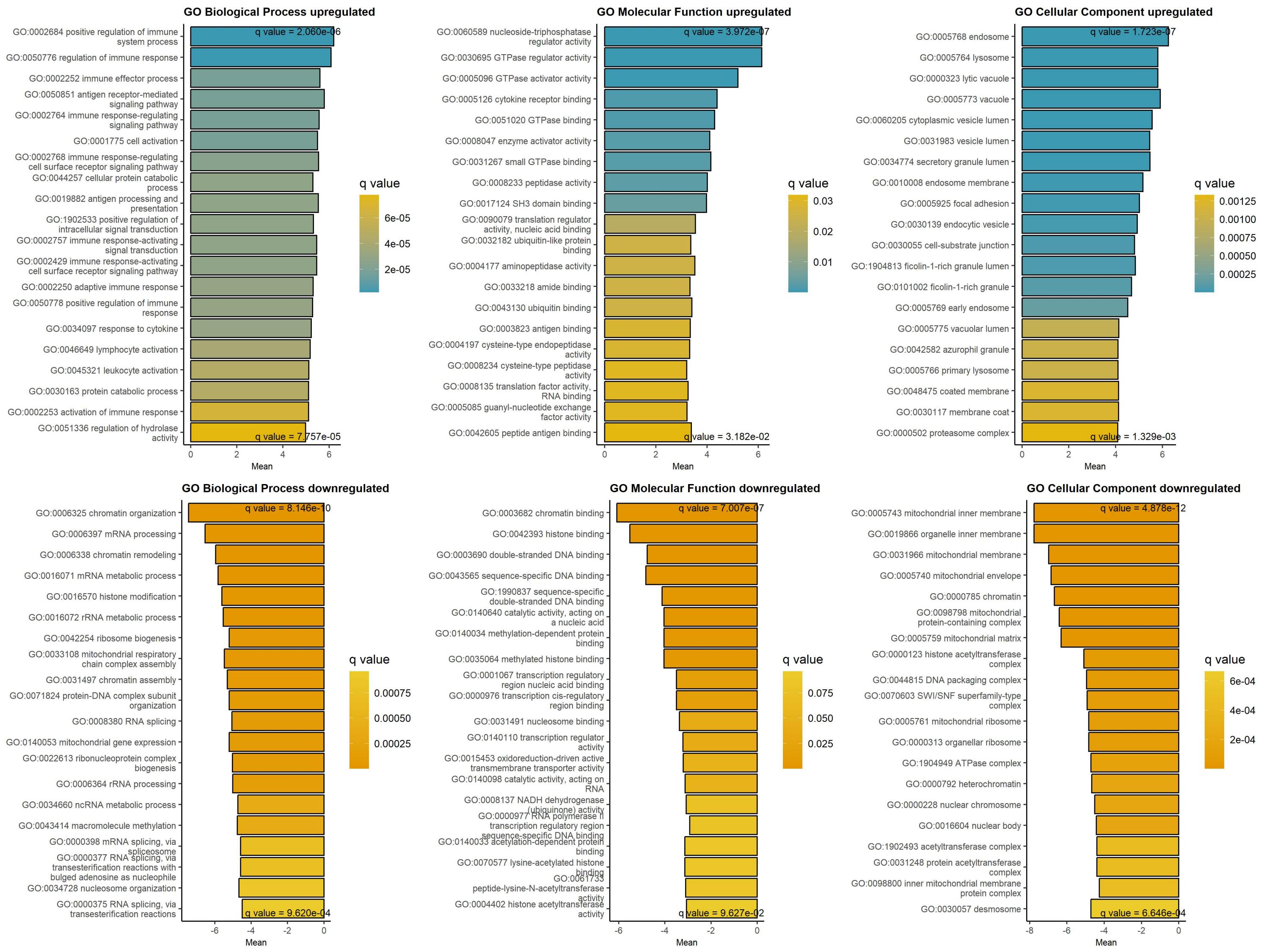




Downregulated at low/absent BCLAF1 Upregulated at low/absent BCLAF1

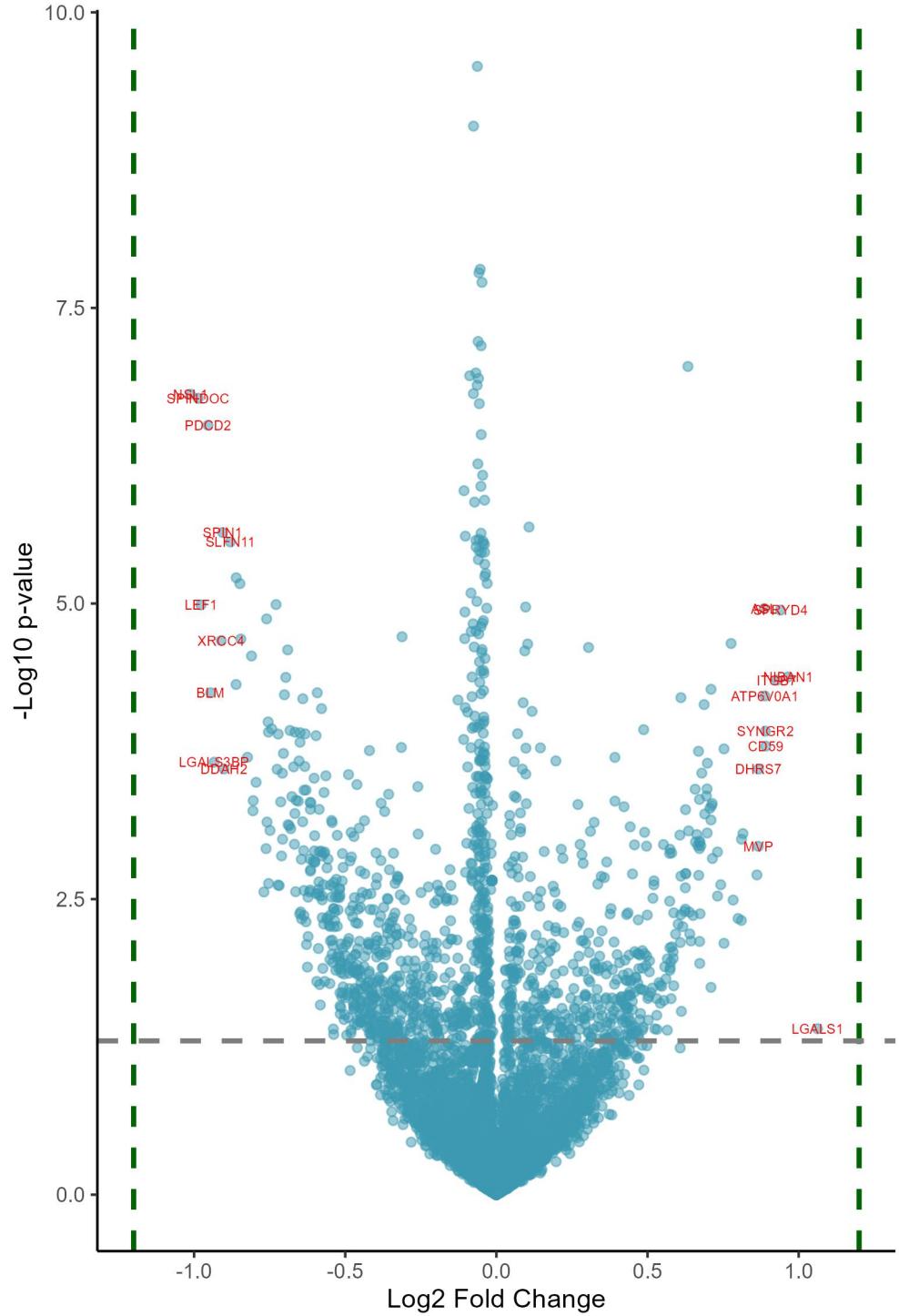
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.02	1.91e-16	CKMT1A	creatine kinase, mitochondrial 1A	0.97	8.75e-20	GBE1	1,4-alpha-glucan branching enzyme 1
-0.86	2.92e-32	PHF3	PHD finger protein 3	0.82	4.83e-15	RNF181	ring finger protein 181
-0.86	2.45e-18	SPTBN2	spectrin beta, non-erythrocytic 2	0.81	1.56e-20	STK10	serine/threonine kinase 10
-0.86	3.99e-13	CDH1	cadherin 1	0.77	1.60e-14	SH3KBP1	SH3 domain containing kinase bindin
-0.86	6.15e-25	BRD1	bromodomain containing 1	0.72	7.65e-07	LGALS1	galectin 1
-0.85	1.50e-27	TCF20	transcription factor 20	0.71	9.62e-13	WIPF1	WAS/WASL interacting protein family
-0.85	1.05e-14	EPCAM	epithelial cell adhesion molecule	0.7	1.34e-16	HOOK3	hook microtubule tethering protein
-0.83	5.23e-21	PHF2	PHD finger protein 2	0.69	6.73e-11	CD70	CD70 molecule
-0.83	4.39e-13	EPPK1	epiplakin 1	0.69	1.31e-10	GLRX	glutaredoxin
-0.82	4.00e-20	SUDS3	SDS3 homolog, SIN3A corepressor com	0.67	2.35e-09	ANXA6	annexin A6
-0.82	1.95e-12	SPINT2	serine peptidase inhibitor, Kunitz	0.66	3.18e-10	SH3BGR	SH3 domain binding glutamate rich p
-0.81	1.73e-12	LAD1	ladinin 1	0.66	5.53e-11	RFTN1	raftlin, lipid raft linker 1
-0.8	6.79e-11	MACROH2A2	macroH2A.2 histone	0.66	1.48e-11	FMNL1	formin like 1
-0.8	1.25e-13	CXADR	CXADR Ig-like cell adhesion molecu	0.65	1.06e-13	DAB2	DAB adaptor protein 2
-0.78	3.51e-15	ESRP1	epithelial splicing regulatory prot	0.65	1.14e-10	FAH	fumarylacetoacetate hydrolase
-0.78	3.72e-10	JUP	junction plakoglobin	0.62	1.60e-09	PMSB10	proteasome 20S subunit beta 10
-0.77	1.00e-11	SPINT1	serine peptidase inhibitor, Kunitz	0.62	2.01e-09	UBE2L6	ubiquitin conjugating enzyme E2 L6
-0.77	7.75e-18	ZNF280C	zinc finger protein 280C	0.61	9.94e-10	PIP4K2A	phosphatidylinositol-5-phosphate 4-
-0.76	2.10e-15	MAP7	microtubule associated protein 7	0.61	1.19e-06	BST2	bone marrow stromal cell antigen 2
-0.76	3.12e-22	KAT7	lysine acetyltransferase 7	0.61	1.78e-14	PLEKHO2	pleckstrin homology domain containi
-0.76	1.95e-15	CENPV	centromere protein V	0.61	1.33e-13	CASP8	caspase 8
-0.76	1.26e-22	RBMX2	RNA binding motif protein X-linked	0.61	2.19e-11	FHD1	formin homology 2 domain containing
-0.75	8.01e-22	KMT2A	lysine methyltransferase 2A	0.61	1.02e-08	PMSB9	proteasome 20S subunit beta 9
-0.75	3.89e-18	YTHDC1	YTH domain containing 1	0.6	1.75e-10	GYS1	glycogen synthase 1
-0.74	7.97e-09	BRI3BP	BRI3 binding protein	0.6	1.19e-11	TRIM21	tripartite motif containing 21
-0.73	3.65e-10	ASS1	argininosuccinate synthase 1	0.6	8.37e-09	SP100	SP100 nuclear antigen
-0.73	8.76e-20	BUD13	BUD13 homolog	0.59	3.81e-11	LPXN	leupaxin
-0.72	2.18e-16	MEAF6	MYST/Esa1 associated factor 6	0.59	7.23e-10	OPTN	optineurin
-0.72	3.30e-14	GRPEL2	GrpE like 2, mitochondrial	0.58	4.11e-06	RAC2	Rac family small GTPase 2

GAGE analysis on upregulated and downregulated proteins at low/absent BCLAF1 protein, DB1



Differentially expressed proteins in blood cancers at absence/low amount of BCLAF1 , DB1

p-value < 0.05 & logFC > 1.2

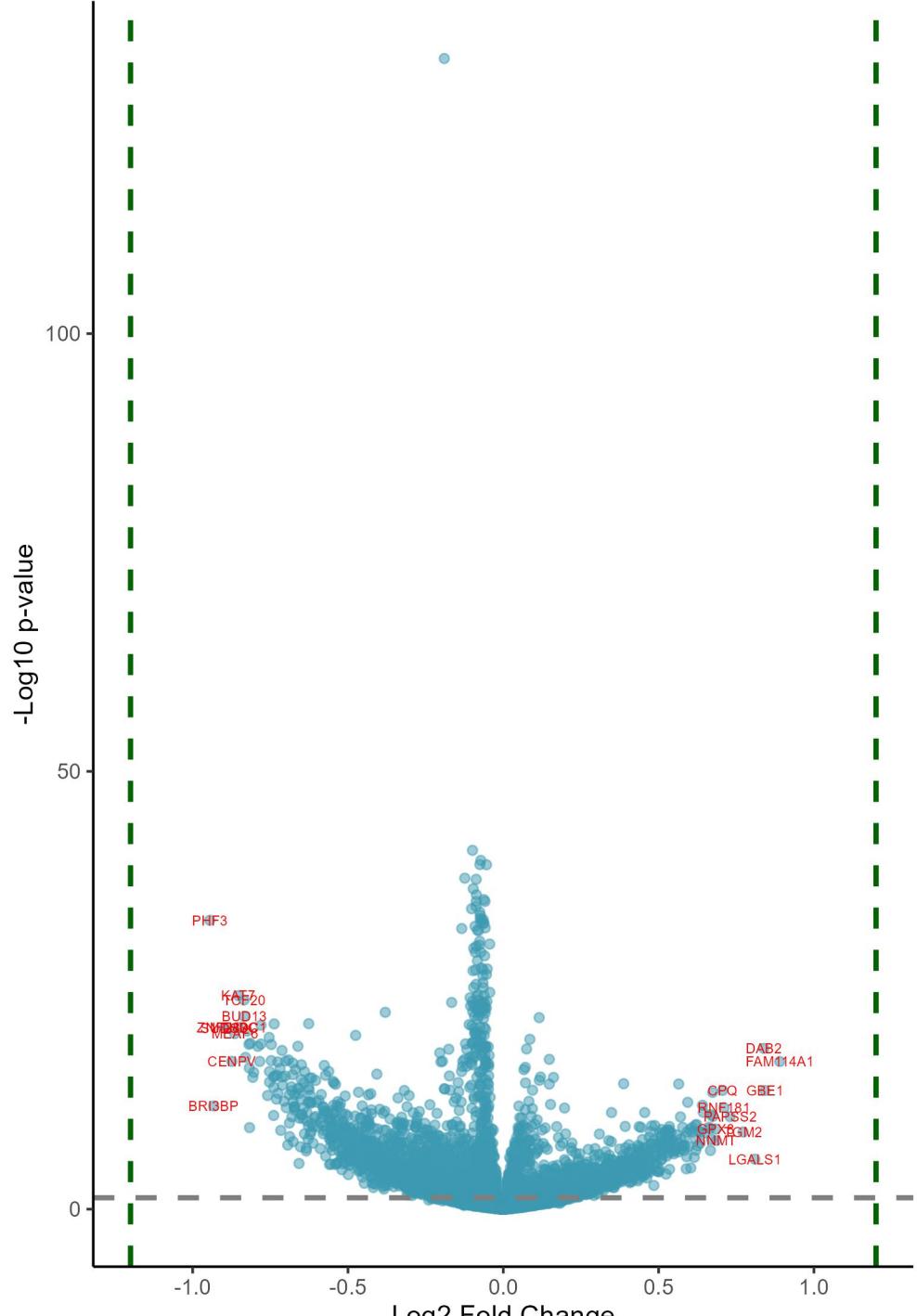


Downregulated in blood cancers at low/absent BCLAF1 Upregulated in blood cancers at low/absent BCLAF1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.01	7.53e-05	NSL1	NSL1 component of MIS12 kinetochore	1.06	1.46e-01	LGALS1	galectin 1
-0.99	7.64e-05	SPINDOC	spindlin interactor and repressor o	0.97	3.33e-03	NIBAN1	niban apoptosis regulator 1
-0.98	1.37e-03	LEF1	lymphoid enhancer binding factor 1	0.94	1.40e-03	SPRYD4	SPRY domain containing 4
-0.95	1.15e-04	PDCD2	programmed cell death 2	0.93	3.49e-03	ITGB7	integrin subunit beta 7
-0.95	4.16e-03	BLM	BLM RecQ like helicase	0.89	8.28e-03	CD59	CD59 molecule (CD59 blood group)
-0.93	9.55e-03	LGALS3BP	galectin 3 binding protein	0.89	6.81e-03	SYNGR2	synaptogyrin 2
-0.91	2.04e-03	XRCC4	X-ray repair cross complementing 4	0.89	4.28e-03	ATP6V0A1	ATPase H+ transporting V0 subunit a
-0.91	6.00e-04	SPIN1	spindlin 1	0.89	1.38e-03	ASL	argininosuccinate lyase
-0.9	1.04e-02	DDAH2	dimethylarginine dimethylaminohydro	0.87	1.04e-02	DHRS7	dehydrogenase/reductase 7
-0.88	6.00e-04	SLFN11	schlafen family member 11	0.87	1.61e-02	MVP	major vault protein
-0.86	3.70e-03	GTSE1	G2 and S-phase expressed 1	0.86	1.61e-02	CD48	CD48 molecule
-0.86	9.15e-04	CCDC12	coiled-coil domain containing 12	0.82	1.61e-02	CAPN2	calpain 2
-0.85	9.80e-04	MIS18A	MIS18 kinetochore protein A	0.81	1.61e-02	SAR1B	secretion associated Ras related GT
-0.85	2.01e-03	SDCBP	syndecan binding protein	0.81	3.05e-02	JCHAIN	joining chain of multimeric IgA and
-0.82	9.25e-03	CEP43	centrosomal protein 43	0.8	2.96e-02	LGALS3	galectin 3
-0.81	2.43e-03	KATNA1	kataman catalytic subunit A1	0.78	2.18e-02	CTSZ	cathepsin Z
-0.81	1.61e-02	RUNX1	RUNX family transcription factor 1	0.78	2.12e-03	MYO5A	myosin VA
-0.8	1.54e-02	ASF1A	anti-silencing function 1A histone	0.75	8.36e-03	TMED2	transmembrane p24 trafficking prote
-0.79	1.22e-02	FLI1	Fli-1 proto-oncogene, ETS transcript	0.75	4.36e-02	PLP2	proteolipid protein 2
-0.77	1.94e-02	DBN1	drebrin 1	0.74	1.73e-02	IKZF3	IKAROS family zinc finger 3
-0.76	1.61e-02	CCNA2	cyclin A2	0.73	2.07e-02	ISG20	interferon stimulated exonuclease g
-0.76	1.60e-03	RCOR1	REST corepressor 1	0.73	1.61e-02	TYMP	thymidine phosphorylase
-0.76	1.61e-02	CFAP20	cilia and flagella associated prote	0.71	1.61e-02	PLBD2	phospholipase B domain containing 2
-0.76	6.18e-03	CCNB2	cyclin B2	0.71	1.57e-02	MYO1C	myosin IC
-0.75	6.81e-03	ARHGEF6	Rac/Cdc42 guanine nucleotide exchan	0.71	1.60e-02	TMEM214	transmembrane protein 214
-0.75	1.69e-02	SLBP	stem-loop binding protein	0.71	4.02e-03	ALDH1L2	aldehyde dehydrogenase 1 family mem
-0.75	1.61e-02	BRD3	bromodomain containing 3	0.71	8.37e-02	LMNA	lamin A/C
-0.74	6.69e-03	YEATS4	YEATS domain containing 4	0.71	1.61e-02	DTD1	D-aminoacyl-tRNA deacylase 1
-0.73	1.37e-03	TTK	TTK protein kinase	0.71	1.61e-02	SIL1	SIL1 nucleotide exchange factor

Differentially expressed proteins in solid cancers at absence/low amount of BCLAF1 , DB1

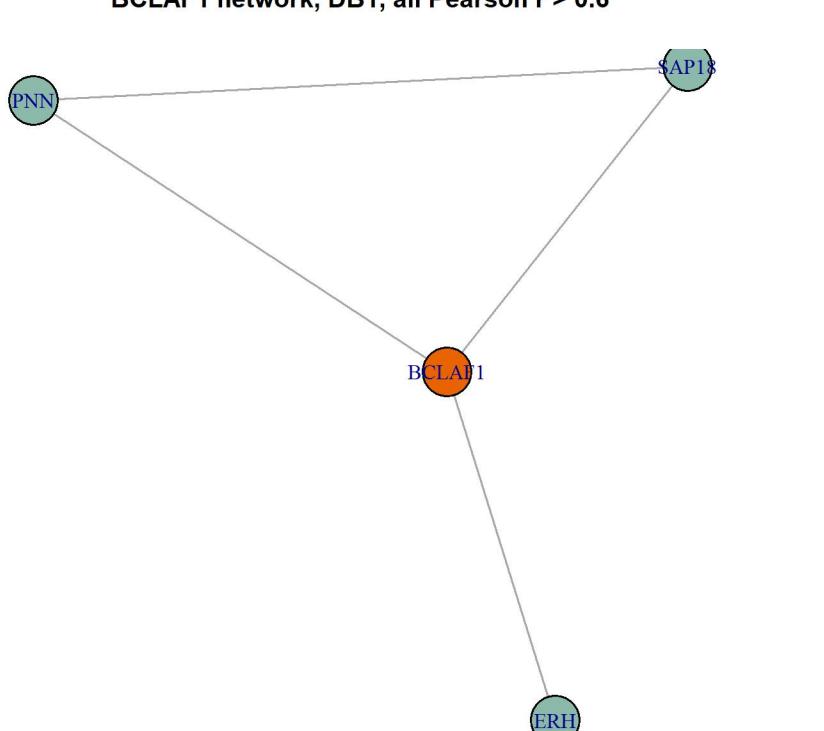
p-value < 0.05 & logFC > 1.2



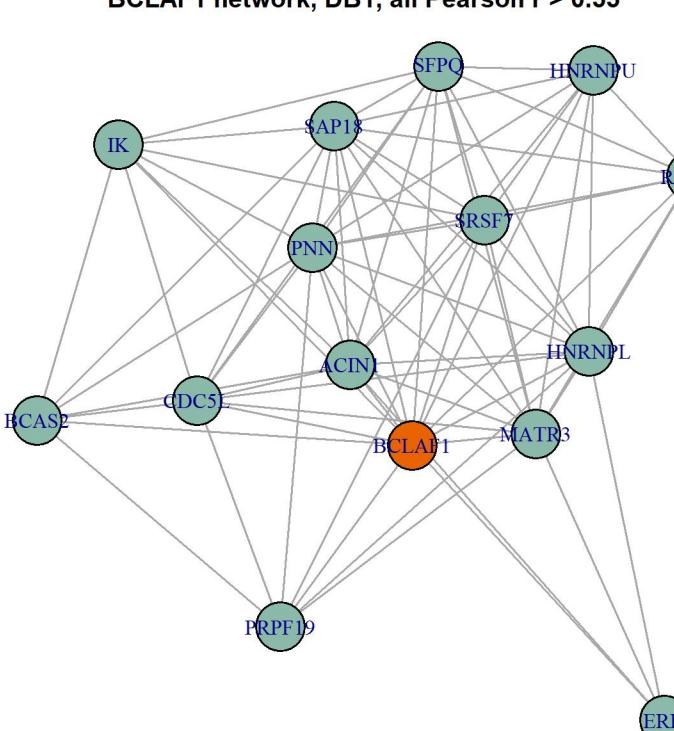
Downregulated in solid cancers at low/absent BCLAF1 Upregulated in solid cancers at low/absent BCLAF1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.94	3.21e-31	PHF3	PHD finger protein 3	0.89	5.82e-16	FAM114A1	family with sequence similarity 114
-0.93	3.72e-11	BRI3BP	BRI3 binding protein	0.84	7.85e-13	GBE1	1,4-alpha-glucan branching enzyme 1
-0.9	1.42e-19	SUDS3	SDS3 homolog, SIN3A corepressor com	0.84	2.23e-17	DAB2	DAB adaptor protein 2
-0.89	1.30e-19	ZNF280C	zinc finger protein 280C	0.81	1.25e-05	LGALS1	galectin 1
-0.87	5.69e-16	CENPV	centromere protein V	0.77	2.07e-08	TGM2	transglutaminase 2
-0.86	5.93e-19	MEAF6	MYST/Esa1 associated factor 6	0.73	5.12e-10	PAPSS2	3'-phosphoadenosine 5'-phosphosulfa
-0.85	5.21e-23	KAT7	lysine acetyltransferase 7	0.71	5.98e-11	RNF181	ring finger protein 181
-0.85	1.30e-19	YTHDC1	YTH domain containing 1	0.71	7.55e-13	CPQ	carboxypeptidase Q
-0.83	1.53e-22	TCF20	transcription factor 20	0.69	1.61e-07	NNMT	nicotinamide N-methyltransferase
-0.83	8.06e-21	BUD13	BUD13 homolog	0.68	1.01e-08	GPX8	glutathione peroxidase 8 (putative)
-0.83	2.13e-16	PHF2	PHD finger protein 2	0.67	4.88e-10	SH3KBP1	SH3 domain containing kinase bindin
-0.82	3.07e-19	BRD1	bromodomain containing 1	0.67	1.27e-12	HOOK3	hook microtubule tethering protein
-0.82	8.51e-18	NOL8	nucleolar protein 8	0.67	1.24e-07	SPARC	secreted protein acidic and cystein
-0.82	2.85e-15	MBD1	methyl-CpG binding domain protein 1	0.67	3.09e-10	GALE	UDP-galactose-4-epimerase
-0.82	7.29e-09	CKMT1A	creatine kinase, mitochondrial 1A	0.67	1.63e-06	CBR3	carbonyl reductase 3
-0.81	6.65e-18	CDCA5	cell division cycle associated 5	0.67	9.34e-09	SYNM	synemin
-0.81	2.96e-14	BRD2	bromodomain containing 2	0.66	6.65e-09	NRP1	neuropilin 1
-0.8	8.47e-15	BRD3	bromodomain containing 3	0.65	2.62e-08	RHOC	ras homolog family member C
-0.79	1.37e-17	CHAF1A	chromatin assembly factor 1 subunit	0.64	1.80e-10	PDLIM2	PDZ and LIM domain 2
-0.78	5.76e-16	SAMD1	sterile alpha motif domain contain	0.64	3.16e-11	ELMO2	engulfment and cell motility 2
-0.78	7.90e-18	ZMYM3	zinc finger MYM-type containing 3	0.64	1.89e-08	PTPRJ	protein tyrosine phosphatase recept
-0.78	7.32e-20	RBMX2	RNA binding motif protein X-linked	0.63	2.88e-07	ITGA5	integrin subunit alpha 5
-0.76	2.76e-12	MAP7	microtubule associated protein 7	0.63	1.71e-08	FAH	fumarylacetate hydrolase
-0.75	1.51e-18	SUZ12	SUZ12 polycomb repressive complex 2	0.63	5.42e-07	STOM	stomatin
-0.75	7.05e-15	UTP25	UTP25 small subunit processome comp	0.62	3.56e-09	OPTN	optineurin
-0.75	9.82e-14	SRCP	Snf2 related CREBBP activator prote	0.62	1.58e-06	S100A10	S100 calcium binding protein A10
-0.75	4.75e-16	RBM45	RNA binding motif protein 45	0.62	4.11e-09	CAP2	cyclase associated actin cytoskelet
-0.75	8.98e-18	ATAD2	ATPase family AAA domain containing	0.62	1.00e-07	GLRX	glutaredoxin
-0.74	2.79e-14	NSD3	nuclear receptor binding SET domain	0.61	8.14e-06	CAVIN3	caveolae associated protein 3

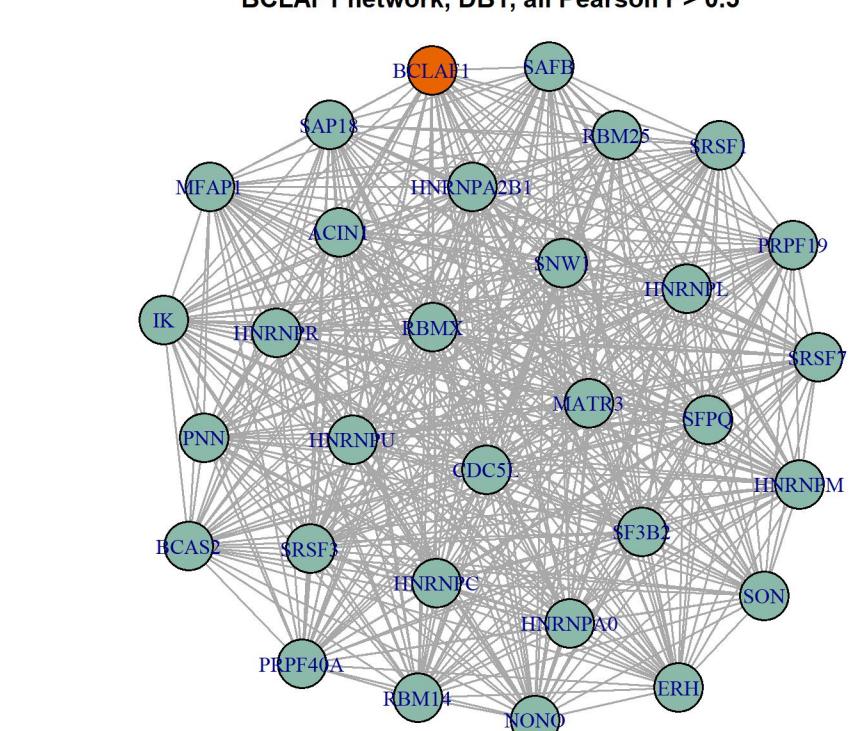
BCLAF1 network, DB1, all Pearson r > 0.6



BCLAF1 network, DB1, all Pearson r > 0.55

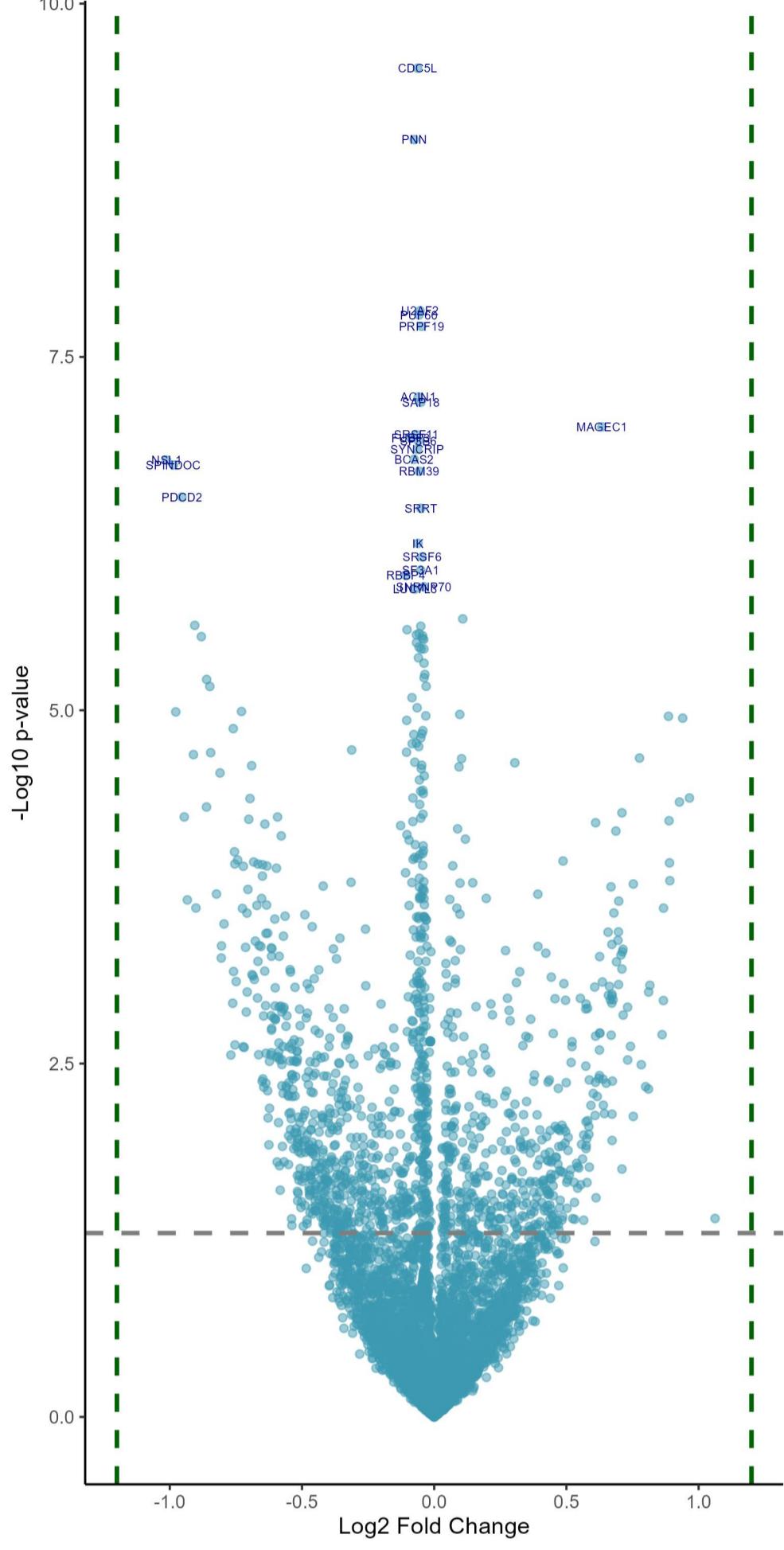


BCLAF1 network, DB1, all Pearson r > 0.5



Differentially expressed proteins in blood cancers at absence/low amount of BCLAF1, DB1

p-value < 0.05 & logFC > 1.2



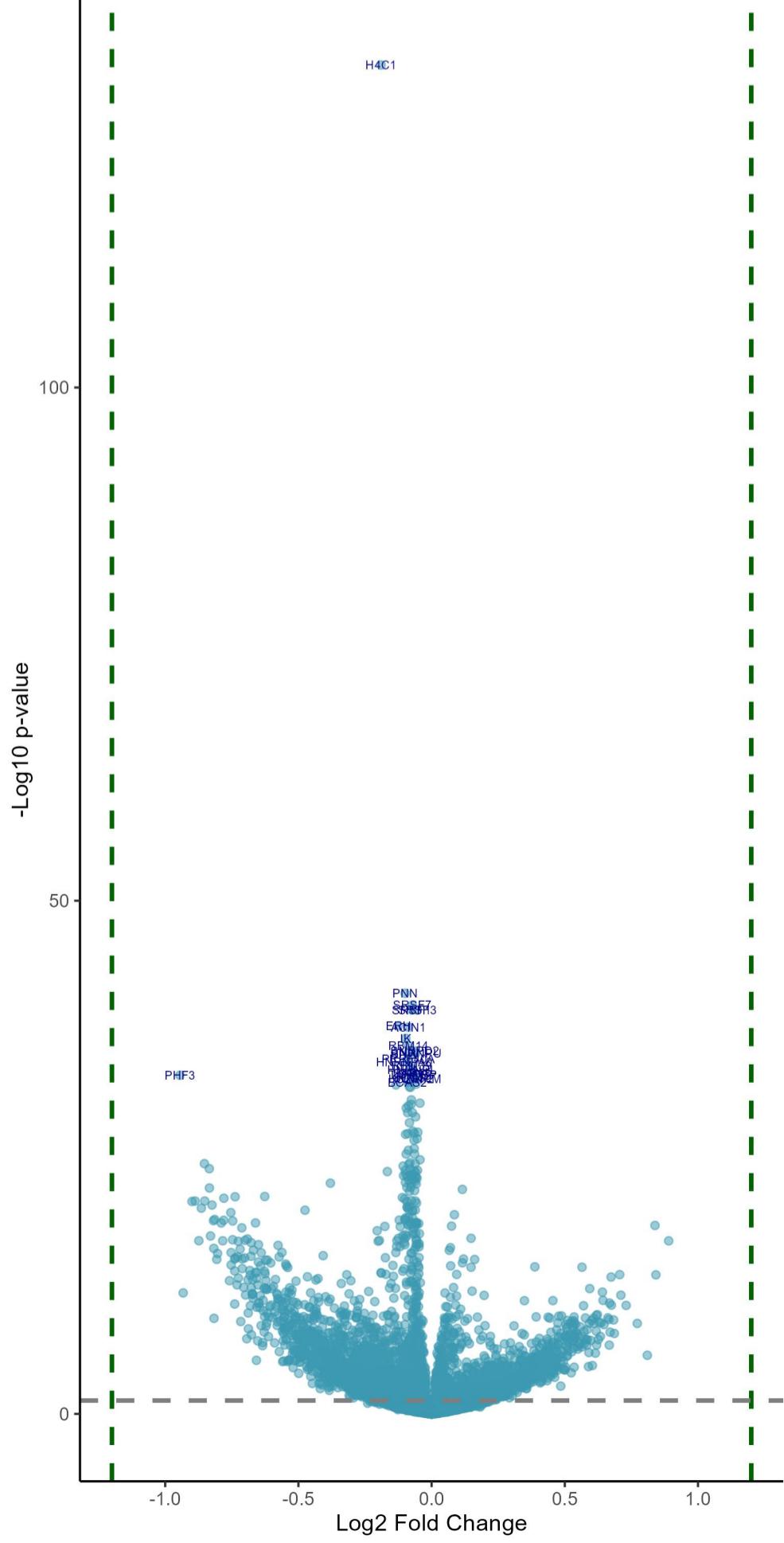
Sorted by p values!

Downregulated in blood cancers at low/absent BCLAF1 Upregulated in blood cancers at low/absent BCLAF1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.06	9.52e-07	CDC5L	cell division cycle 5 like	0.63	6.91e-05	MAGEC1	MAGE family member C1
-0.08	2.03e-06	PNN	pinin, desmosome associated protein	0.11	5.77e-04	PRDX5	peroxiredoxin 5
-0.05	2.12e-05	U2AF2	U2 small nuclear RNA auxiliary fact	0.1	1.38e-03	CLPP	caseinolytic mitochondrial matrix p
-0.06	2.12e-05	PUF60	poly(U) binding splicing factor 60	0.89	1.38e-03	ASL	argininosuccinate lyase
-0.05	2.13e-05	PRPF19	pre-mRNA processing factor 19	0.94	1.40e-03	SPRYD4	SPRY domain containing 4
-0.06	5.50e-05	ACIN1	apoptotic chromatin condensation in	0.78	2.12e-03	MYO5A	myosin VA
-0.05	5.50e-05	SAP18	Sin3A associated protein 18	0.1	2.12e-03	TMED10	transmembrane p24 trafficking prote
-0.07	6.91e-05	SRSF11	serine and arginine rich splicing f	0.3	2.20e-03	ATOX1	antioxidant 1 copper chaperone
-0.09	6.91e-05	FUBP3	far upstream element binding protei	0.09	2.26e-03	ACO2	acoritase 2
-0.06	6.91e-05	SF3B6	splicing factor 3b subunit 6	0.97	3.33e-03	NIBAN1	niban apoptosis regulator 1
-0.06	7.29e-05	SYNCRIP	synaptotagmin binding cytoplasmic R	0.93	3.49e-03	ITGB7	integrin subunit beta 7
-0.08	7.53e-05	BCAS2	BCAS2 pre-mRNA processing factor	0.71	4.02e-03	ALDH1L2	aldehyde dehydrogenase 1 family mem
-1.01	7.53e-05	NSL1	NSL1 component of MIS12 kinetochore	0.89	4.28e-03	ATP6V0A1	ATPase H+ transporting V0 subunit a
-0.99	7.64e-05	SPINDOC	spindlin interactor and repressor o	0.61	4.33e-03	SDC1	syndecan 1
-0.06	7.97e-05	RBM39	RNA binding motif protein 39	0.09	4.64e-03	HDLBP	high density lipoprotein binding pr
-0.95	1.15e-04	PDCD2	programmed cell death 2	0.69	4.76e-03	VARS2	valyl-tRNA synthetase 2, mitochondrion
-0.05	1.30e-04	SRRT	serrate, RNA effector molecule	0.12	5.27e-03	PRDX4	peroxiredoxin 4
-0.06	2.19e-04	IK	IK cytokine	0.49	6.74e-03	FAHD2A	fumarylacetate hydrolase domai
-0.05	2.60e-04	SRSF6	serine and arginine rich splicing f	0.89	6.81e-03	SYNGR2	synaptogyrin 2
-0.05	3.08e-04	SF3A1	splicing factor 3a subunit 1	0.07	6.81e-03	TMED9	transmembrane p24 trafficking prote
-0.11	3.21e-04	RBBP4	RB binding protein 4, chromatin rem	0.89	8.28e-03	CD59	CD59 molecule (CD59 blood group)
-0.04	3.69e-04	SNRNP70	small nuclear ribonucleoprotein U1	0.15	8.29e-03	MYDGF	myeloid derived growth factor
-0.07	3.69e-04	LUC7L3	LUC7 like 3 pre-mRNA splicing facto	0.1	8.29e-03	PDIA4	protein disulfide isomerase family
-0.91	6.00e-04	SPIN1	spindlin 1	0.75	8.36e-03	TMED2	transmembrane p24 trafficking prote
-0.05	6.00e-04	SNRPA1	small nuclear ribonucleoprotein pol	0.67	8.58e-03	MYO1E	myosin IE
-0.1	6.00e-04	IPO7	importin 7	0.39	9.25e-03	SEC11C	SEC11 homolog C, signal peptidase c
-0.06	6.00e-04	SON	SON DNA and RNA binding protein	0.2	9.49e-03	PMVK	phosphomevalonate kinase
-0.07	6.00e-04	MFAP1	microfibril associated protein 1	0.06	9.54e-03	SND1	staphylococcal nuclease and tudor d
-0.04	6.00e-04	SF3B1	splicing factor 3b subunit 1	0.7	9.67e-03	MYO1D	myosin ID
-0.88	6.00e-04	SLFN11	schlafen family member 11	0.87	1.04e-02	DHRS7	dehydrogenase/reductase 7
-0.04	6.00e-04	SRSF1	serine and arginine rich splicing f	0.09	1.04e-02	CYCS	cytochrome c, somatic
-0.04	6.00e-04	HNRNPL	heterogeneous nuclear ribonucleopro	0.68	1.10e-02	MGAT2	alpha-1,6-mannosyl-glycoprotein 2-b
-0.07	6.13e-04	SSRP1	structure specific recognition prot	0.1	1.12e-02	FKBP2	FKBP prolyl isomerase 2
-0.06	6.28e-04	BUB3	BUB3 mitotic checkpoint protein	0.7	1.34e-02	PLS3	plastin 3
-0.04	6.28e-04	SRSF3	serine and arginine rich splicing f	0.66	1.34e-02	TRADD	TNFRSF1A associated via death domai
-0.05	6.28e-04	SF3A3	splicing factor 3a subunit 3	0.06	1.45e-02	CS	citrate synthase
-0.06	7.07e-04	RBM8A	RNA binding motif protein 8A	0.69	1.45e-02	NME3	NME/NM23 nucleoside diphosphate kin
-0.04	7.54e-04	SRSF7	serine and arginine rich splicing f	0.07	1.48e-02	PDIA6	protein disulfide isomerase family
0.01	9.83e-04	HNRNPK	heterogeneous nuclear ribonucleoproteins	0.67	1.52e-02	DABP1	poly(ADP-ribose) polymerase family

Differentially expressed proteins in solid cancers at absence/low amount of BCLAF1, DB1

p-value < 0.05 & logFC > 1.2

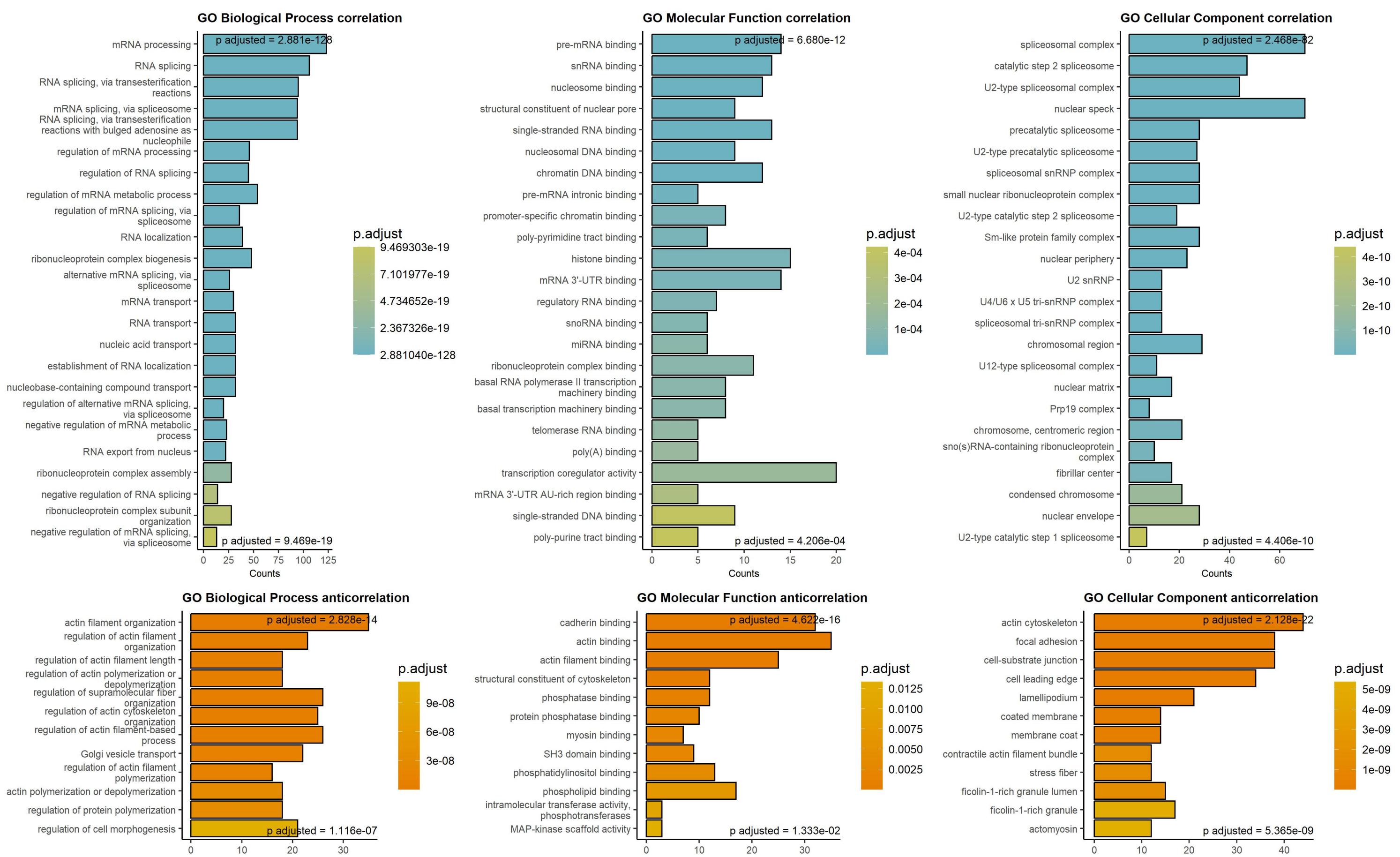


Sorted by p values!

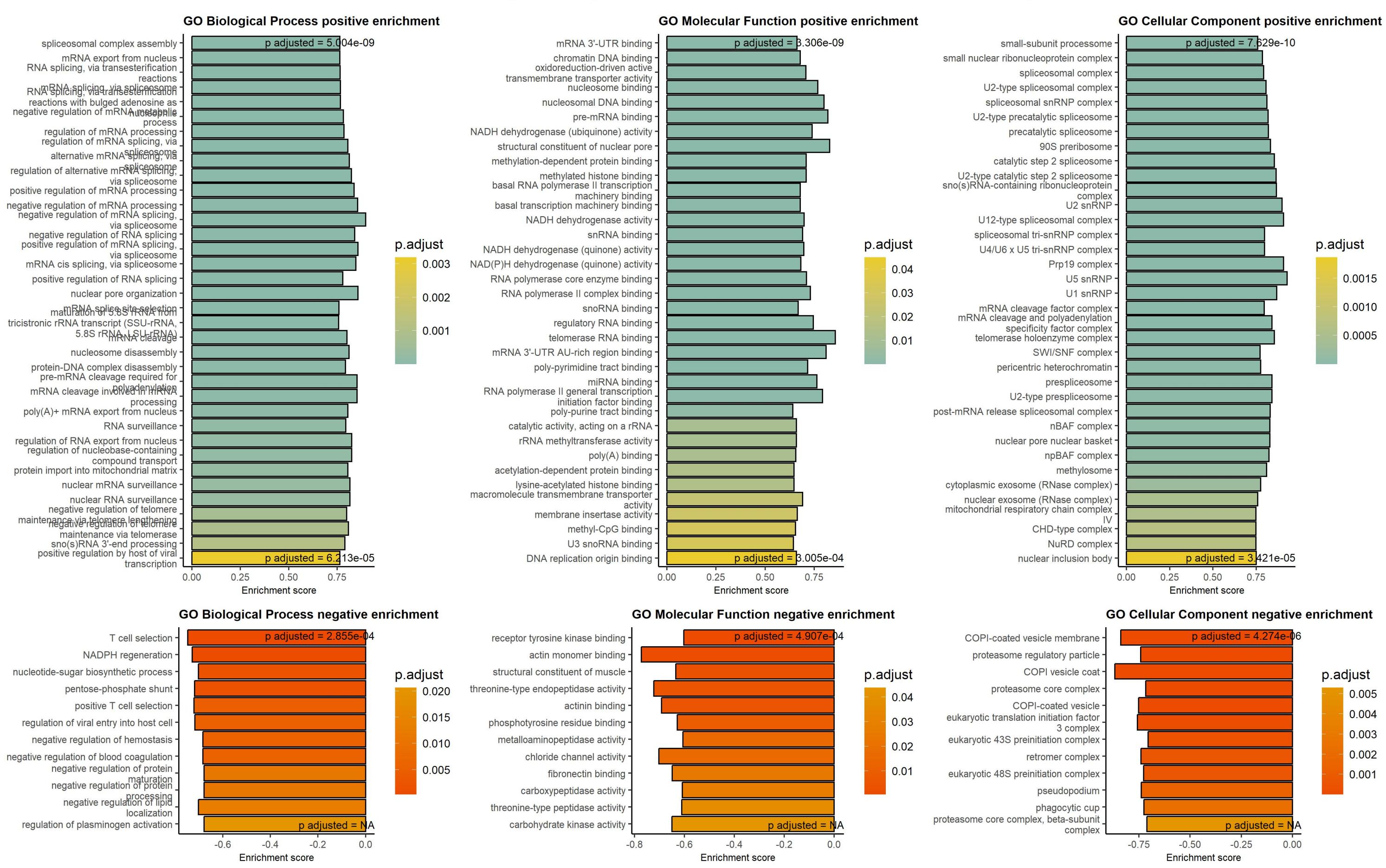
Downregulated in solid cancers at low/absent BCLAF1 Upregulated in solid cancers at low/absent BCLAF1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.19	2.52e-128	H4C1	H4 clustered histone 1	0.12	1.08e-20	MYL6	myosin light chain 6
-0.1	2.30e-38	PNN	pinin, desmosome associated protein	0.09	2.43e-18	TPM3	tropomyosin 3
-0.07	2.46e-37	SRSF7	serine and arginine rich splicing f	0.84	2.23e-17	DAB2	DAB adaptor protein 2
-0.08	5.06e-37	SRSF1	serine and arginine rich splicing f	0.07	2.55e-17	ARPC4	actin related protein 2/3 complex s
-0.05	5.06e-37	SRSF3	serine and arginine rich splicing f	0.15	3.55e-16	TLN1	talin 1
-0.12	1.48e-35	ERH	ERH mRNA splicing and mitosis facto	0.89	5.82e-16	FAM114A1	family with sequence similarity 114
-0.09	1.77e-35	ACIN1	apoptotic chromatin condensation in	0.07	2.44e-15	COPA	COPI coat complex subunit alpha
-0.1	1.88e-34	IK	IK cytokine	0.07	4.33e-15	EEF1D	eukaryotic translation elongation f
-0.09	8.44e-34	RBM14	RNA binding motif protein 14	0.12	2.77e-14	CAP1	cyclase associated actin cytoskelet
-0.06	2.64e-33	SNRPD2	small nuclear ribonucleoprotein D2	0.16	2.99e-14	ACTN1	actinin alpha 1
-0.09	3.66e-33	SNW1	SNW domain containing 1	0.12	6.21e-14	CALU	calumenin
-0.06	3.66e-33	HNRNPL	heterogeneous nuclear ribonucleopro	0.07	1.19e-13	PKM	pyruvate kinase M1/2
-0.09	1.23e-32	PRPF40A	pre-mRNA processing factor 40 homol	0.39	1.45e-13	PLIN3	perilipin 3
-0.1	2.16e-32	HNRNPA0	heterogeneous nuclear ribonucleoprotein	0.56	1.57e-13	RILPL1	Rab interacting lysosomal protein I
-0.08	4.85e-32	RBM39	RNA binding motif protein 39	0.15	1.58e-13	MYH9	myosin heavy chain 9
-0.07	1.15e-31	HNRNPL	heterogeneous nuclear ribonucleoprotein	0.09	7.31e-13	IQGAP1	IQ motif containing GTPase activati
-0.07	2.40e-31	SAP18	Sin3A associated protein 18	0.71	7.55e-13	CPQ	carboxypeptidase Q
-0.06	2.81e-31	SRRT	serrate, RNA effector molecule	0.84	7.85e-13	GBE1	1,4-alpha-glucan branching enzyme 1
-0.07	2.81e-31	TARDBP	TAR DNA binding protein	0.67	1.27e-12	HOOK3	hook microtubule tethering protein
-0.94	3.21e-31	PHF3	PHD finger protein 3	0.08	1.19e-11	ALDOA	aldolase, fructose-bisphosphate A
-0.07	5.51e-31	CDC5L	cell division cycle 5 like	0.59	1.48e-11	STK10	serine/threonine kinase 10
-0.06	6.21e-31	HNRNPM	heterogeneous nuclear				

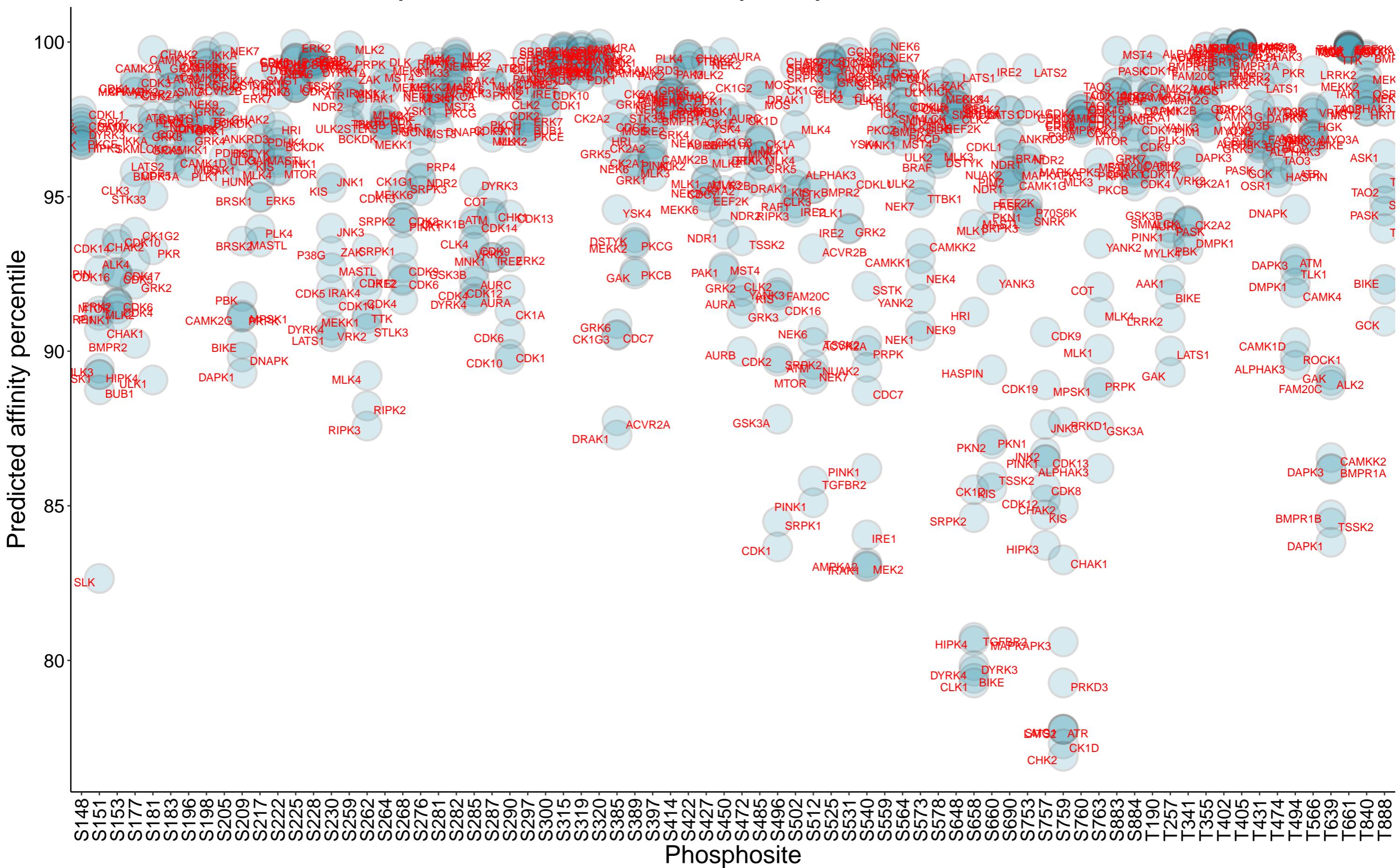
Top 250 correlation coefficients overrepresentation, BCLAF1 protein, DB1



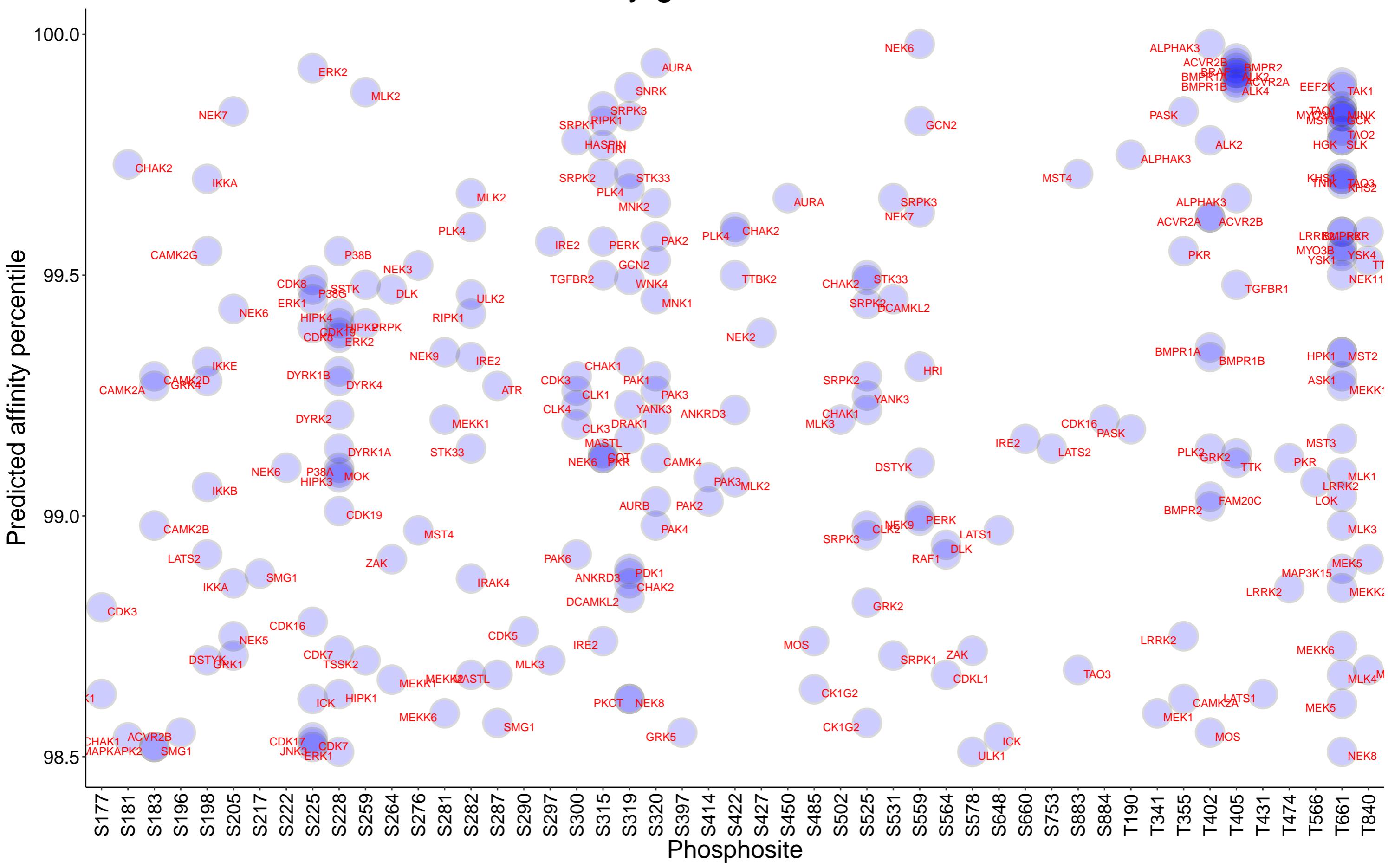
Gene Set Enrichment analysis on protein correlation coefficients, BCLAF1 protein, DB1



Top 10 kinases for each phosphosite in BCLAF1



Kinases with affinity greater than 98.5% to BCLAF1



Top 15 positive correlation coefficients for BCLAF1 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

