

BLM

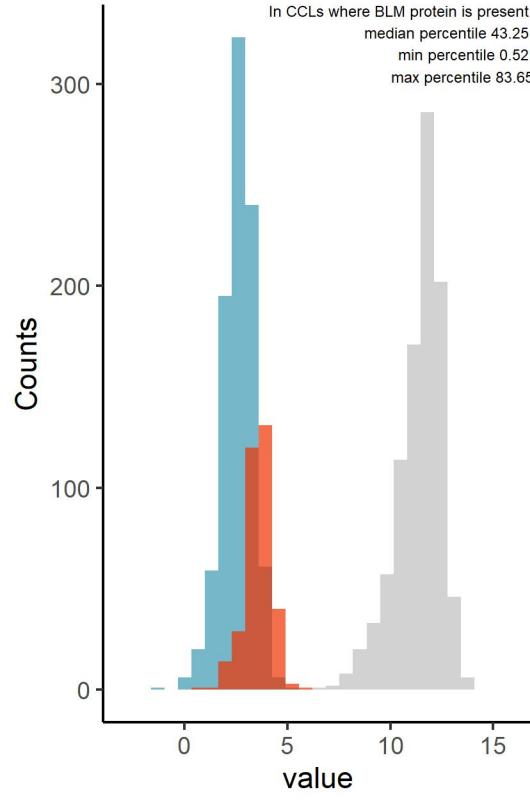
Protein name: BLM ; UNIPROT: P54132 ; Gene name: BLM RecQ like helicase

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

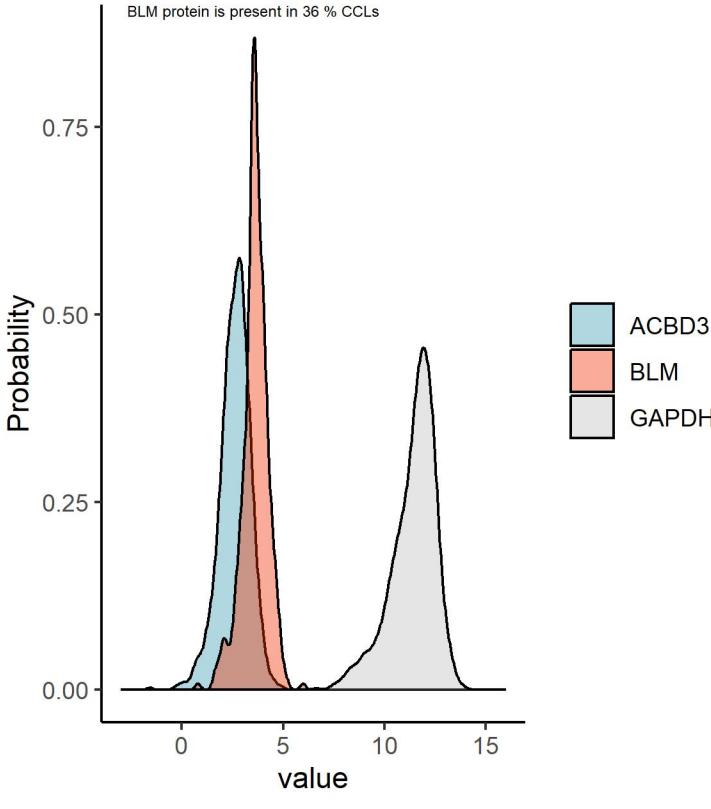
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

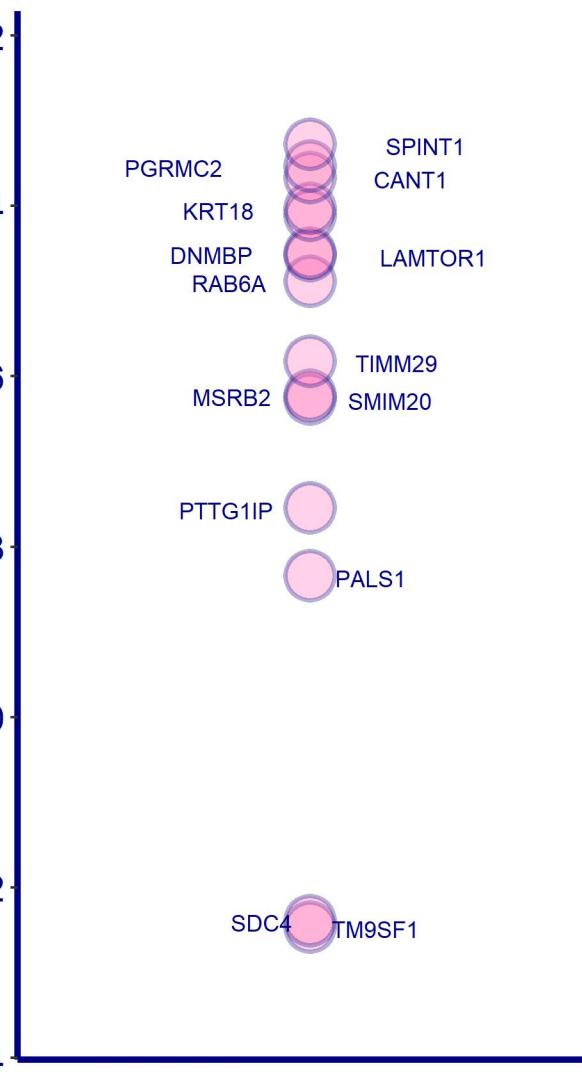
Histogram of BLM protein compared to proteins with low and high abundance



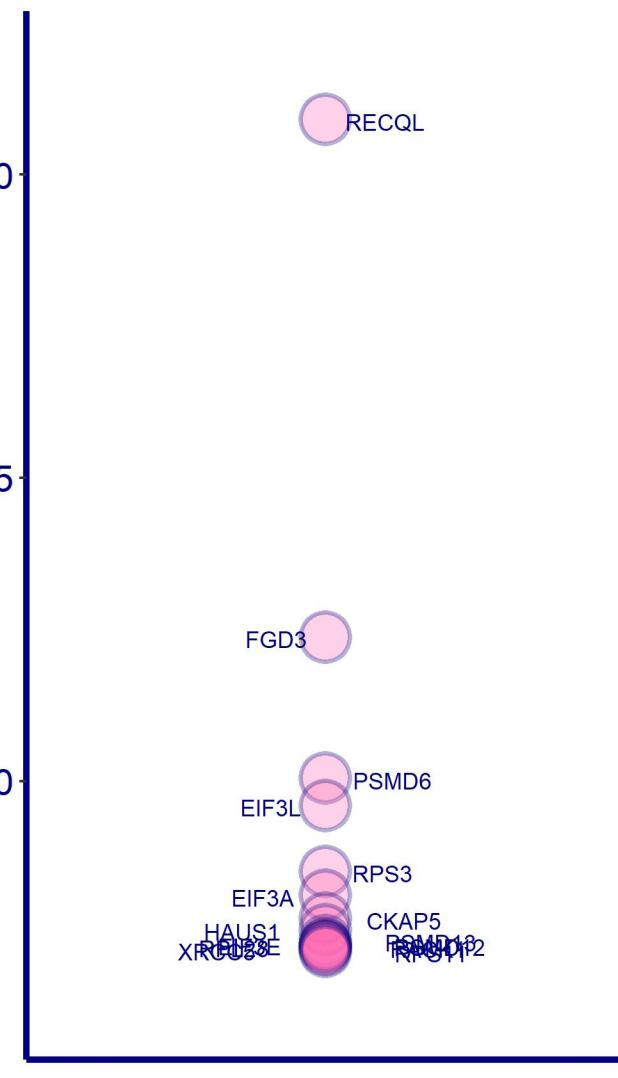
Density plot of BLM protein compared to proteins with low and high abundance



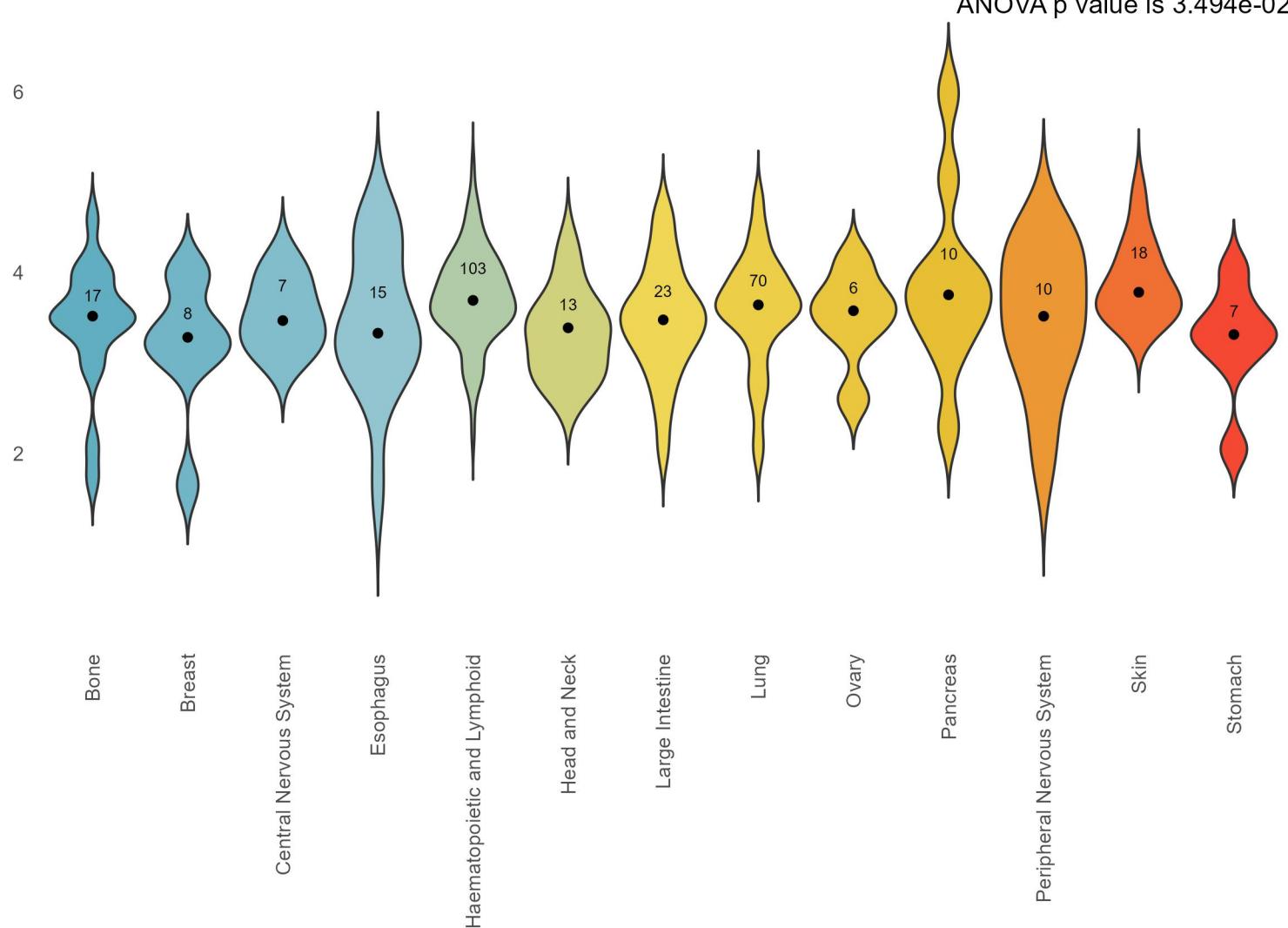
Top negative correlations of BLM protein, DB1



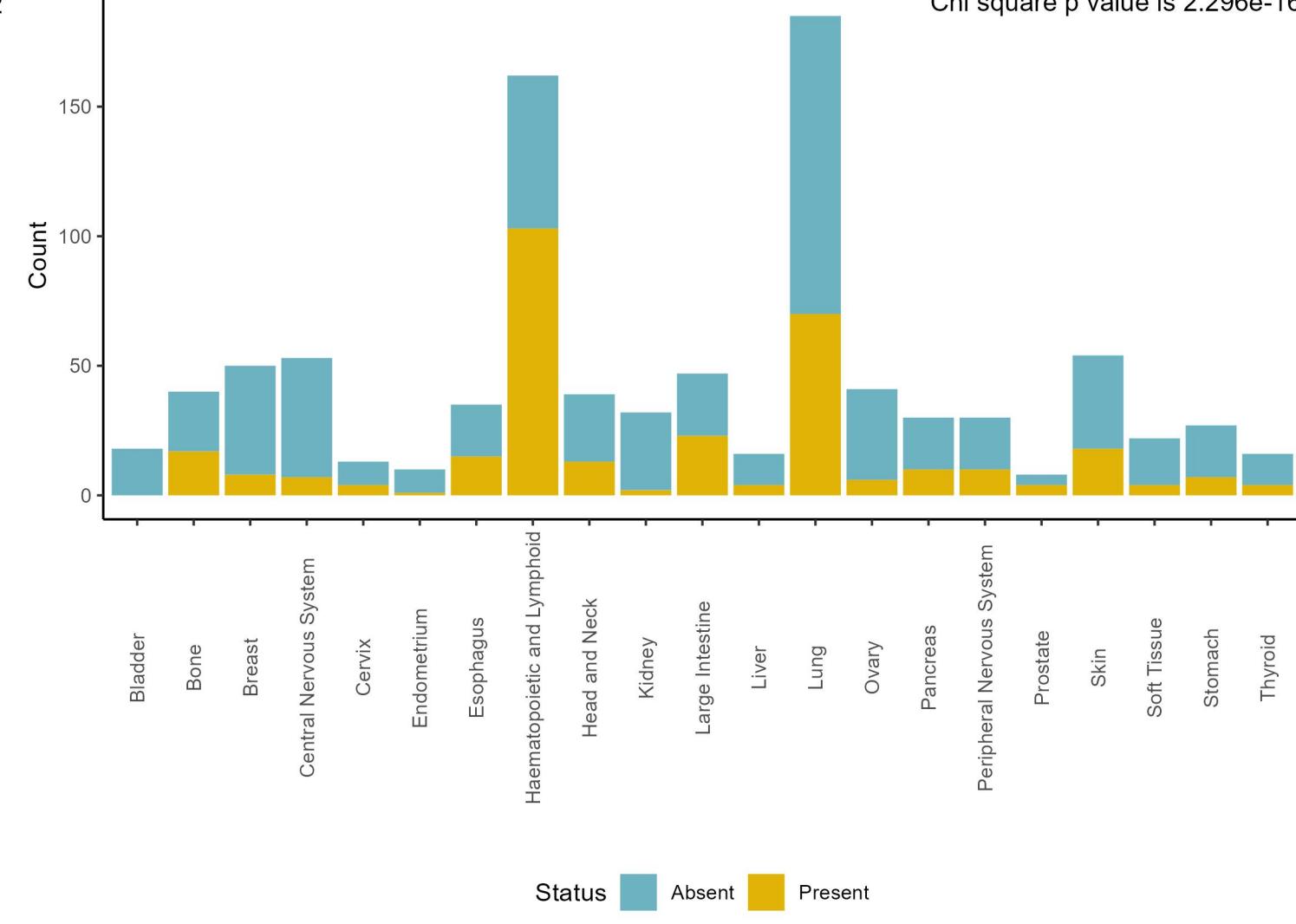
Top positive correlations of BLM protein, DB1



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



Present and absent BLM protein counts by tissue, DB1

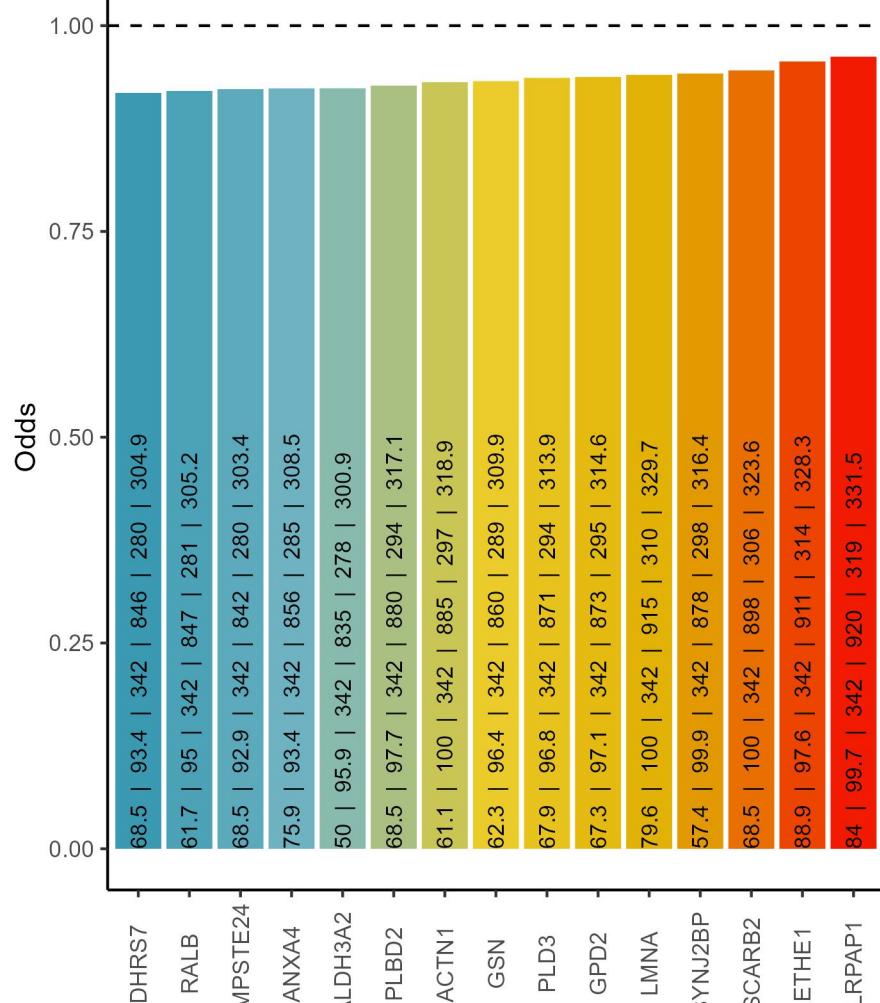


Cooccurrence with BLM protein, DB1

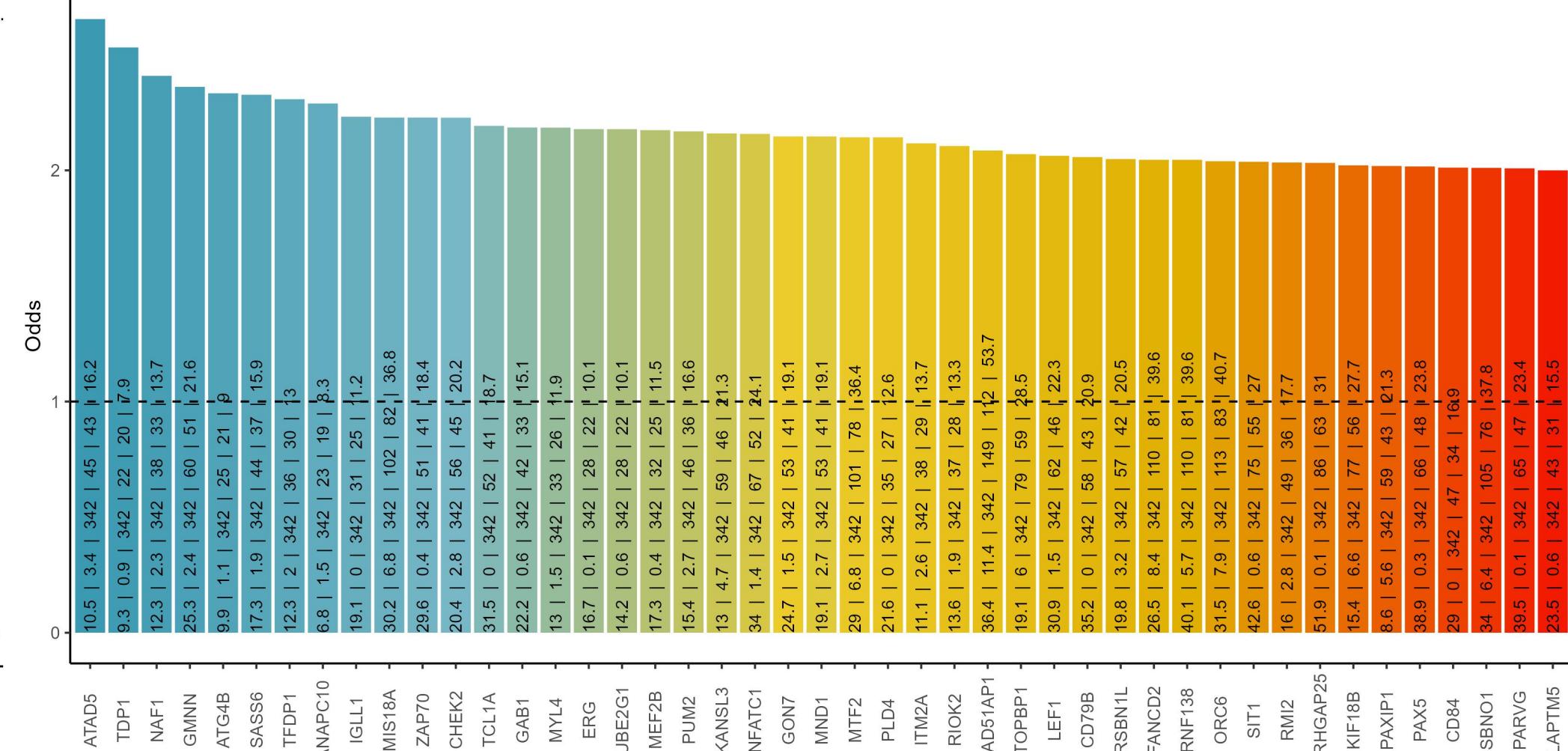
% of BLM in blood cancers: 63.6 ; % of BLM in solid cancers: 30.2

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

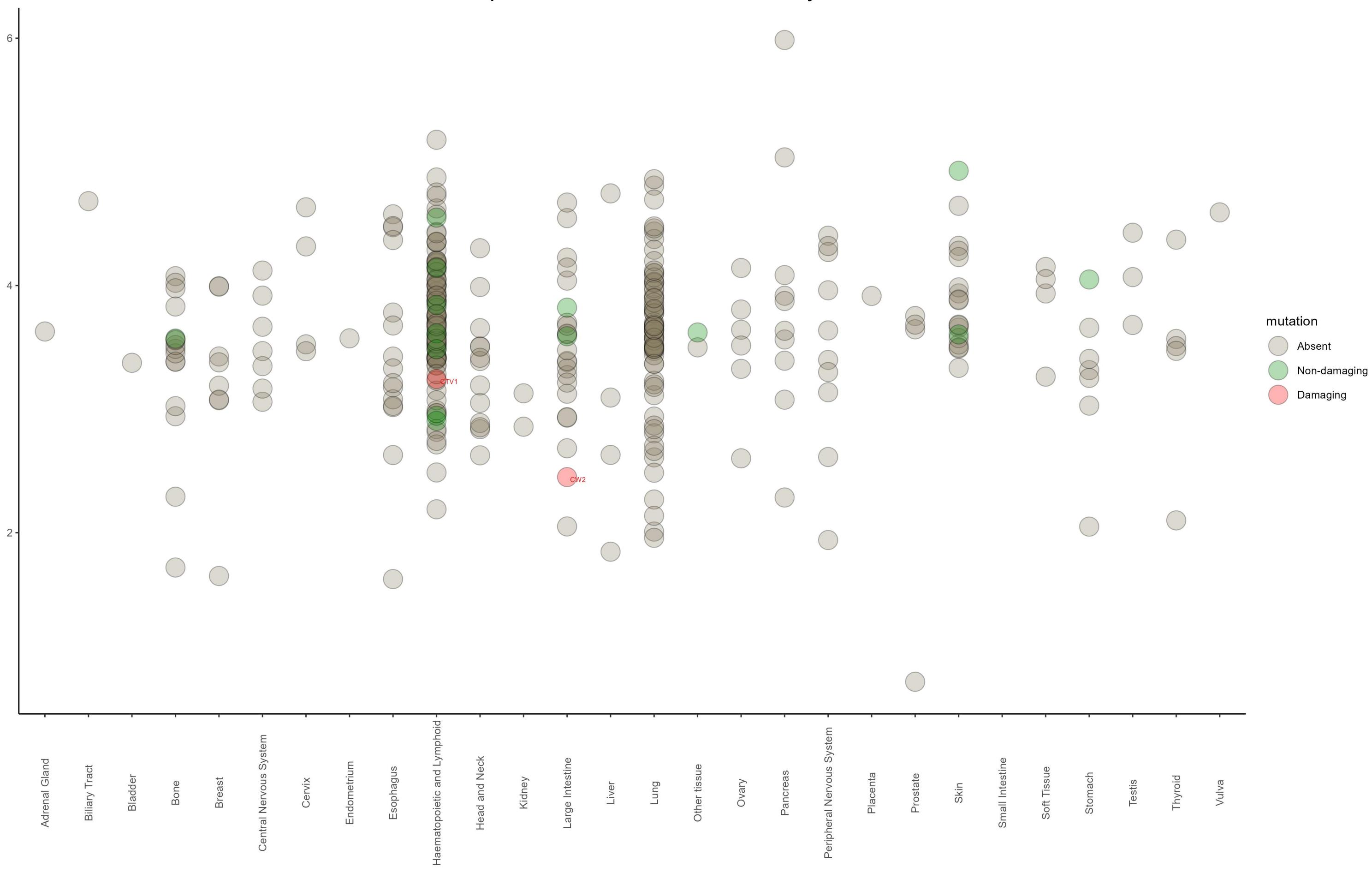
Negative cooccurrence



Positive cooccurrence



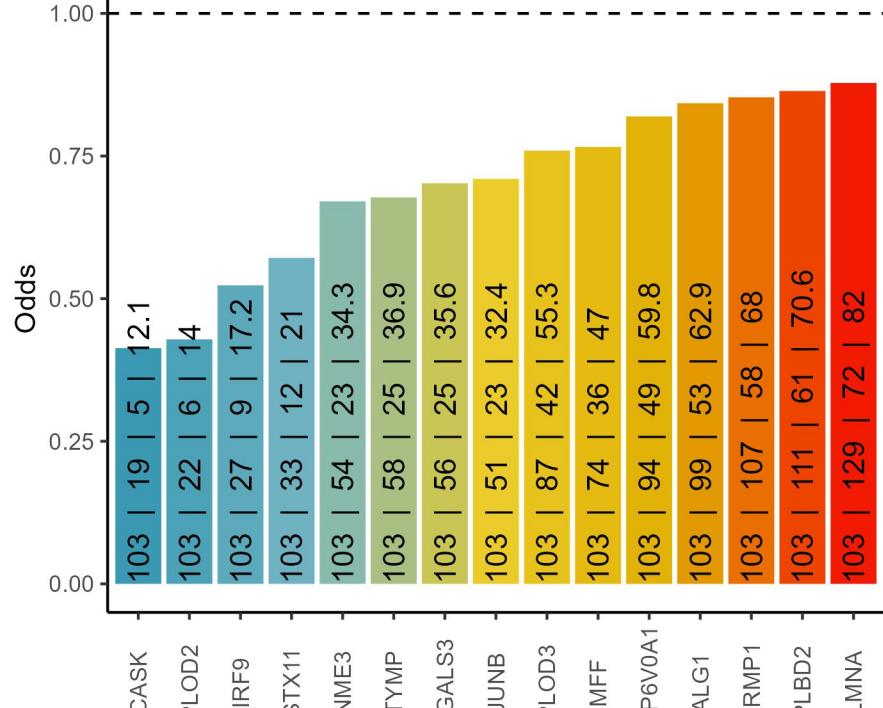
Amount of BLM protein and mutation status by tissue, DB1



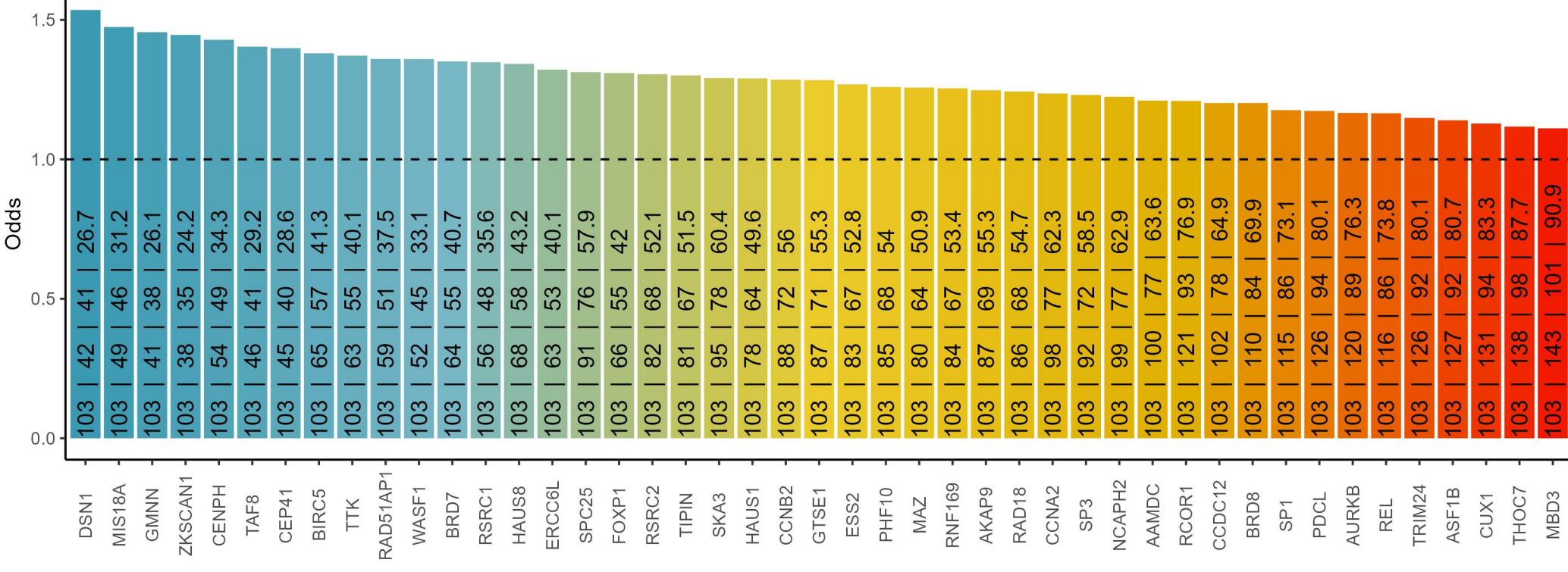
Cooccurrence with BLM protein in blood cancers, DB1

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

Negative cooccurrence



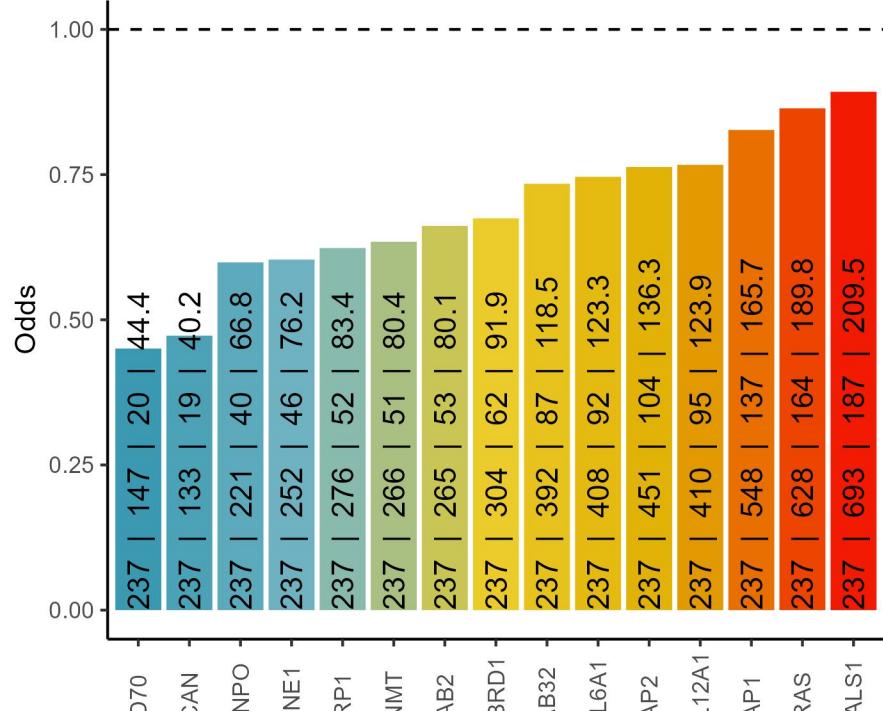
Positive cooccurrence



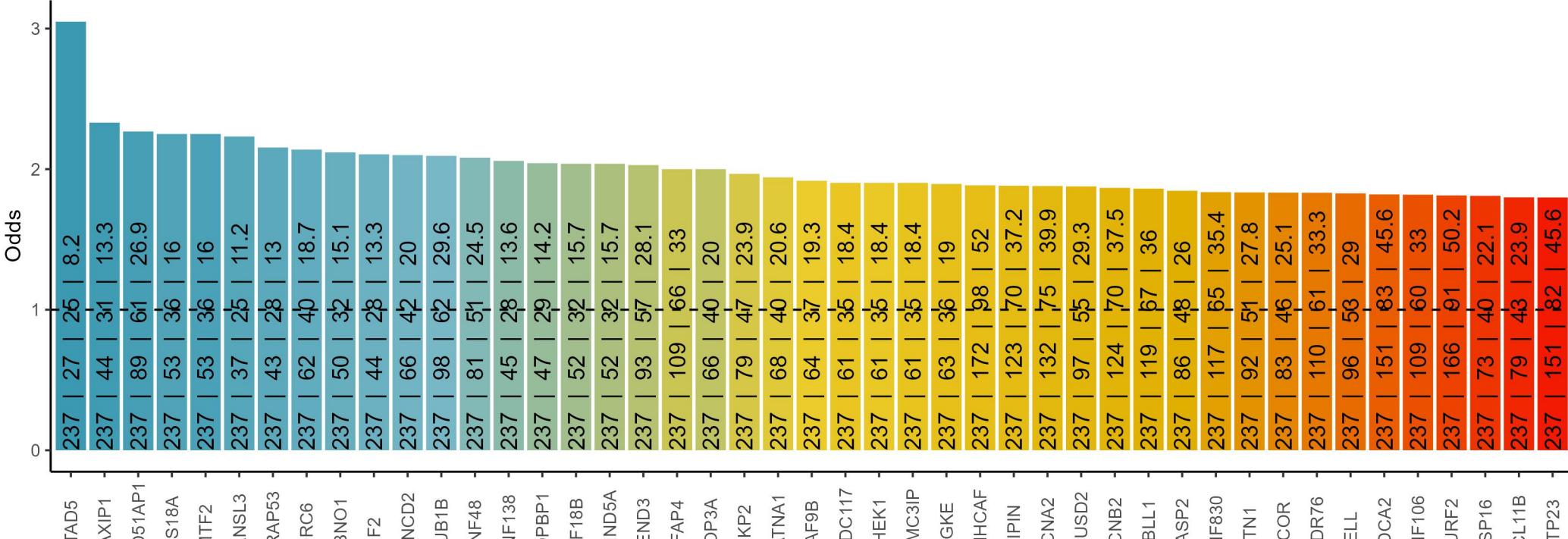
Cooccurrence with BLM protein in solid cancers, DB1

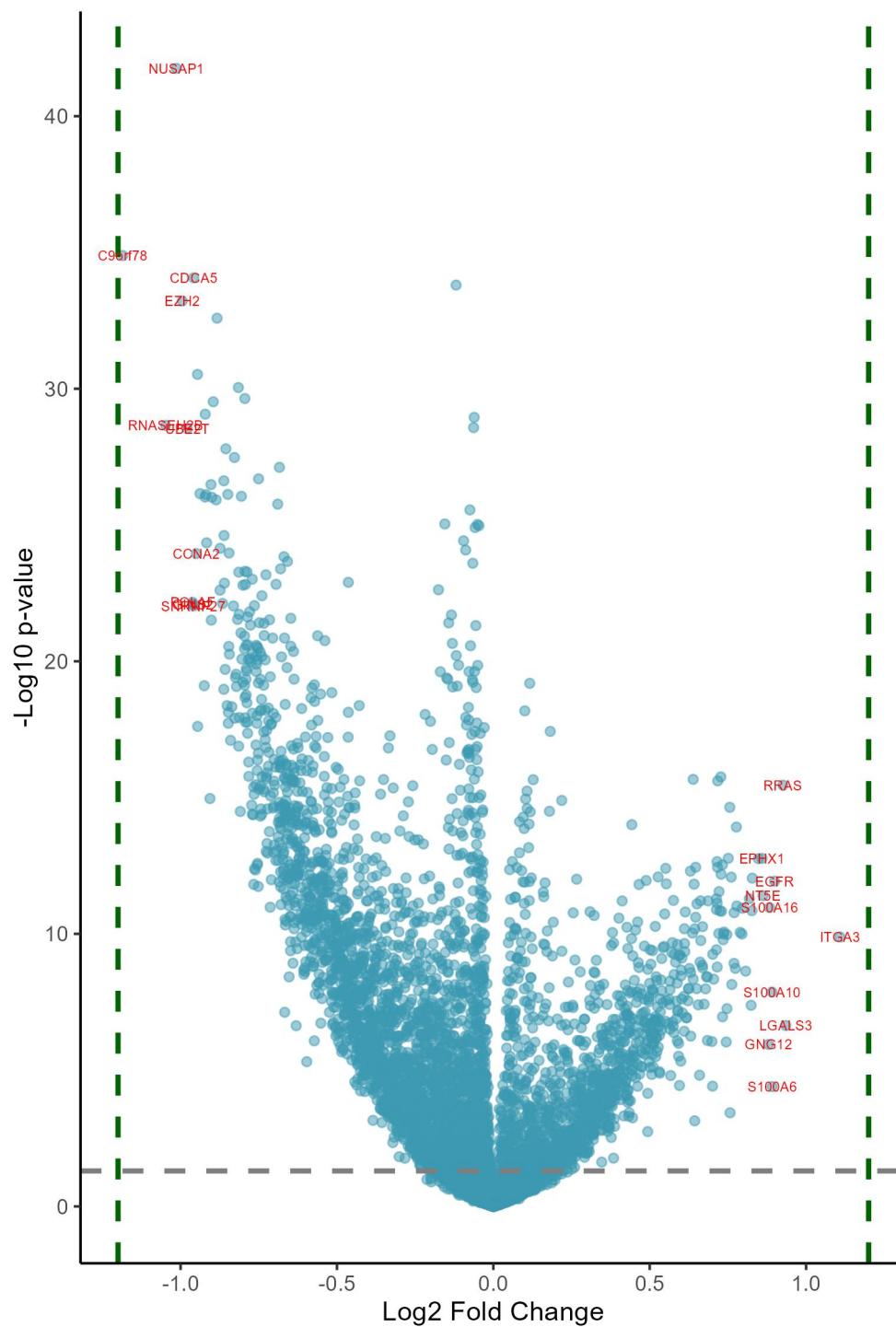
The text in the bars: incidence of BLM | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



Positive cooccurrence

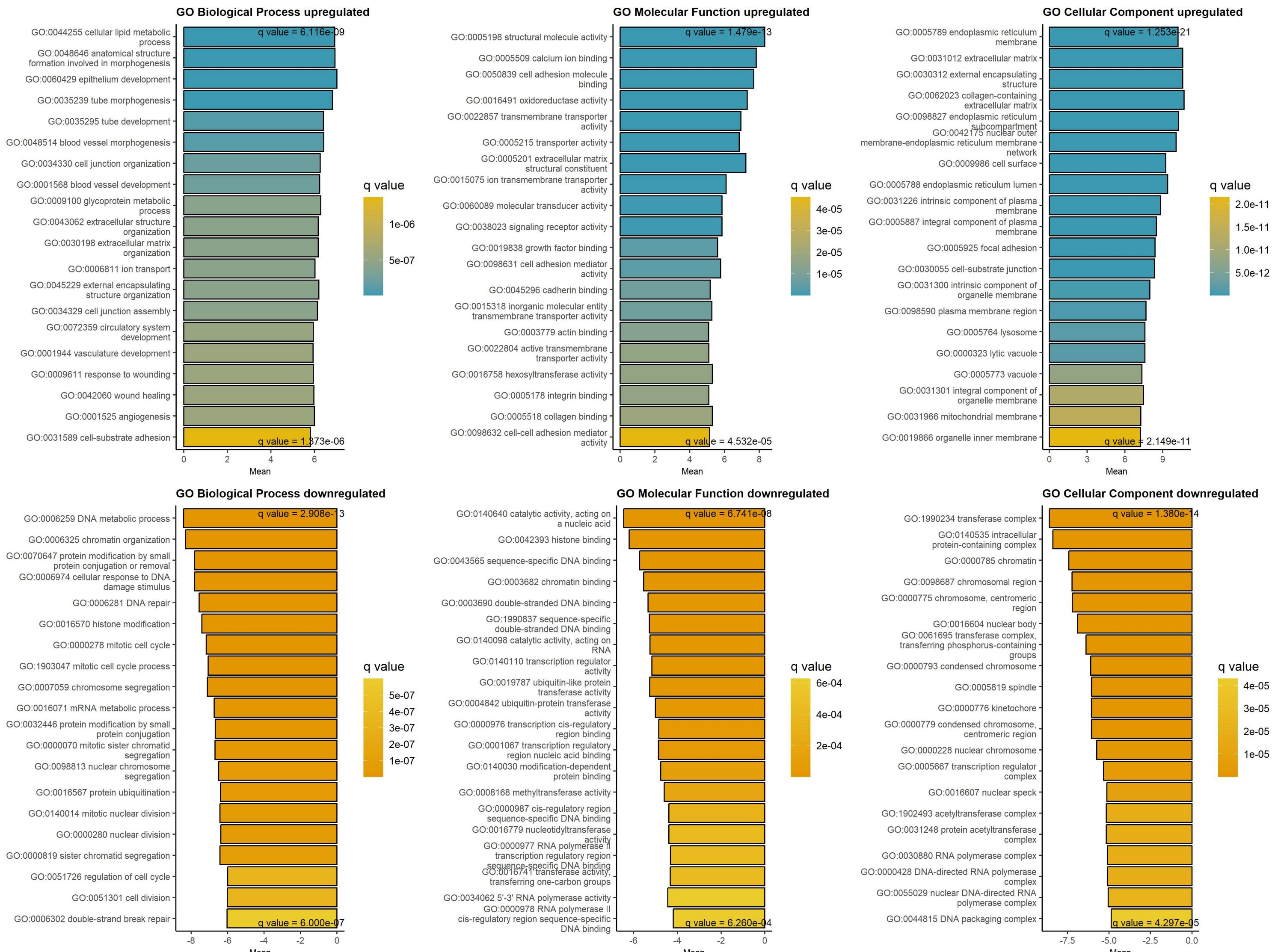


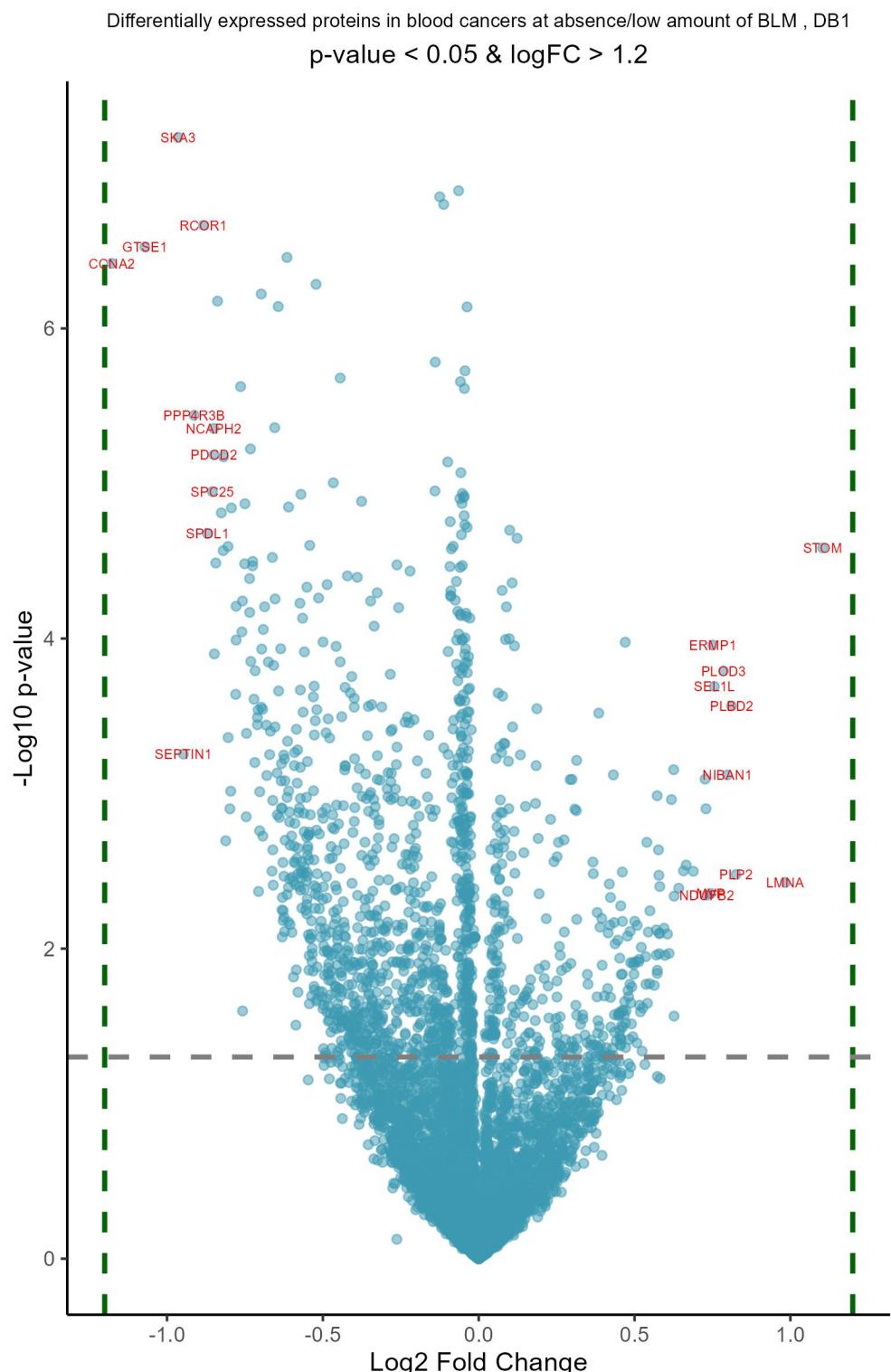


Downregulated at low/absent BLM Upregulated at low/absent BLM

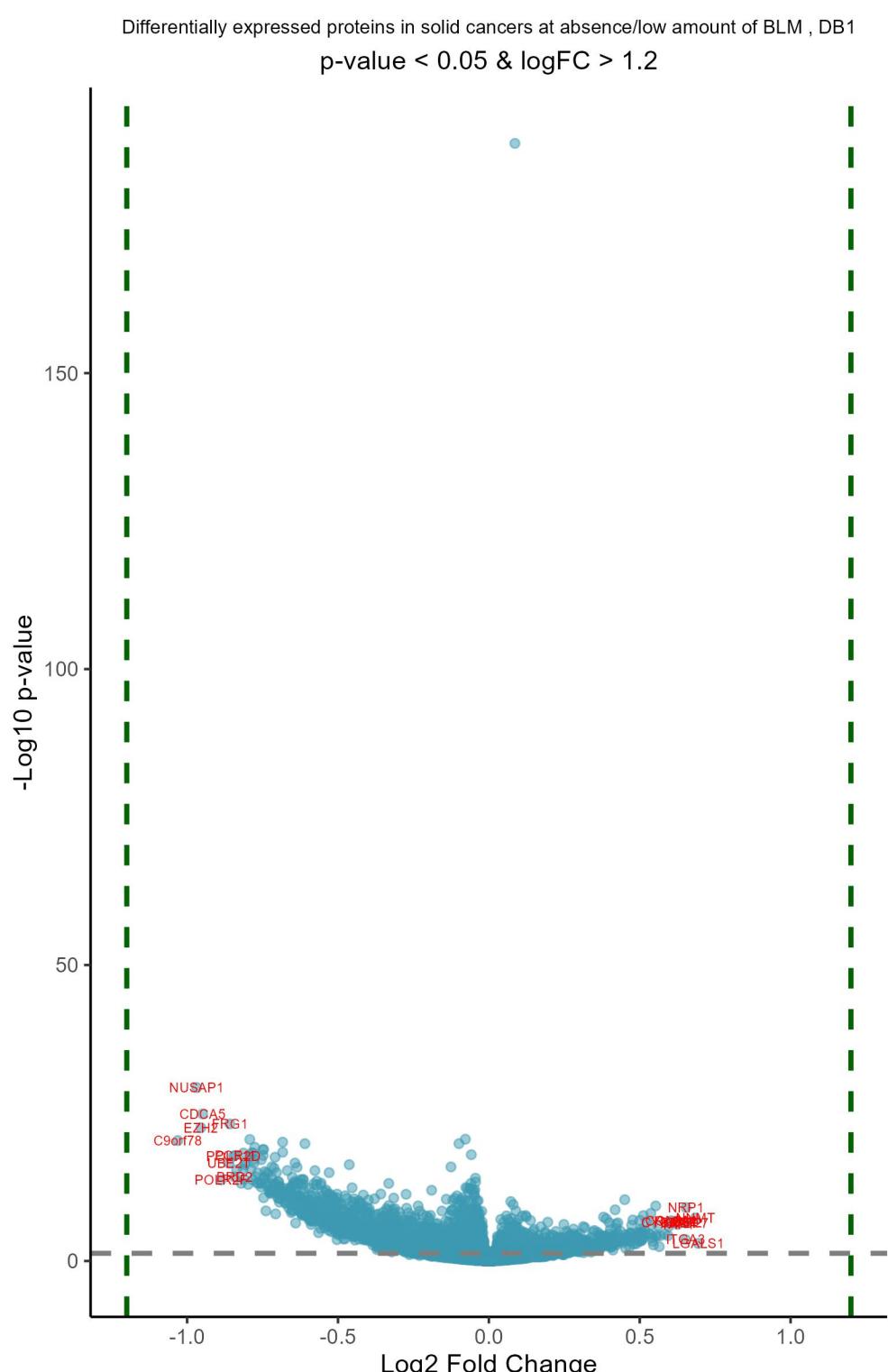
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.19	2.88e-32	C9orf78	chromosome 9 open reading frame 78	1.11	9.68e-10	ITGA3	integrin subunit alpha 3
-1.05	1.05e-26	RNASEH2B	ribonuclease H2 subunit B	0.94	9.20e-07	LGALS3	galectin 3
-1.01	5.84e-39	NUSAP1	nucleolar and spindle associated pr	0.93	8.21e-15	RRAS	RAS related
-0.99	6.64e-31	EZH2	enhancer of zeste 2 polycomb repres	0.9	1.32e-11	EGFR	epidermal growth factor receptor
-0.98	1.20e-26	UBE2T	ubiquitin conjugating enzyme E2 T	0.89	1.08e-04	S100A6	S100 calcium binding protein A6
-0.96	7.59e-21	PCLAF	PCNA clamp associated factor	0.89	6.81e-08	S100A10	S100 calcium binding protein A10
-0.96	8.61e-21	GINS2	GINS complex subunit 2	0.88	1.02e-10	S100A16	S100 calcium binding protein A16
-0.96	9.55e-21	SNRNP27	small nuclear ribonucleoprotein U4/	0.88	3.97e-06	GNG12	G protein subunit gamma 12
-0.96	1.41e-31	CDCA5	cell division cycle associated 5	0.86	4.06e-11	NT5E	5'-nucleotidase ecto
-0.95	1.77e-22	CCNA2	cyclin A2	0.86	2.34e-12	EPHX1	epoxide hydrolase 1
-0.95	2.47e-28	PCF11	PCF11 cleavage and polyadenylation	0.85	2.38e-12	ADAM9	ADAM metallopeptidase domain 9
-0.95	8.71e-17	NACA2	nascent polypeptide associated comp	0.83	1.04e-11	PLOD2	procollagen-lysine,2-oxoglutarate 5
-0.94	2.03e-24	DUS3L	dihydrouridine synthase 3 like	0.83	1.30e-10	PPIC	peptidylprolyl isomerase C
-0.92	3.81e-18	POLR2F	RNA polymerase II, I and III subuni	0.82	1.91e-07	CAVIN1	caveolae associated protein 1
-0.92	2.29e-24	POLA2	DNA polymerase alpha 2, accessory s	0.82	5.16e-11	ITGAV	integrin subunit alpha V
-0.92	4.77e-27	UPF3B	UPF3B regulator of nonsense mediate	0.81	1.35e-08	RHOC	ras homolog family member C
-0.92	2.03e-24	CKAP2	cytoskeleton associated protein 2	0.8	1.06e-10	P4HA2	prolyl 4-hydroxylase subunit alpha
-0.92	7.88e-23	RPIA	ribose 5-phosphate isomerase A	0.79	7.69e-10	CD59	CD59 molecule (CD59 blood group)
-0.91	2.28e-14	CORO1A	coronin 1A	0.79	6.83e-10	CALD1	caldesmon 1
-0.9	9.93e-25	TIMELESS	timeless circadian regulator	0.78	8.94e-11	EPS8L2	EPS8 like 2
-0.9	2.82e-20	BRD2	bromodomain containing 2	0.78	1.95e-13	NNMT	nicotinamide N-methyltransferase
-0.9	2.29e-24	RNASEH2C	ribonuclease H2 subunit C	0.77	1.10e-08	FKBP9	FKBP prolyl isomerase 9
-0.9	1.82e-27	KIF2C	kinesin family member 2C	0.77	1.51e-10	GPX8	glutathione peroxidase 8 (putative)
-0.89	2.74e-24	POLR2D	RNA polymerase II subunit D	0.77	7.48e-09	ITGA2	integrin subunit alpha 2
-0.88	2.45e-30	FRG1	FSHD region gene 1	0.76	3.79e-08	CAV1	caveolin 1
-0.87	2.82e-21	CKS1B	CDC28 protein kinase regulatory sub	0.76	9.69e-12	GPC1	glycan 1
-0.87	1.22e-22	WDHD1	WD repeat and HMG-box DNA binding p	0.76	8.35e-04	KRT18	keratin 18
-0.87	8.23e-21	TACC3	transforming acidic coiled-coil con	0.76	4.51e-14	COL6A1	collagen type VI alpha 1 chain
-0.86	4.95e-18	SLBP	stem-loop binding protein	0.75	2.33e-12	SDC4	syndecan 4

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

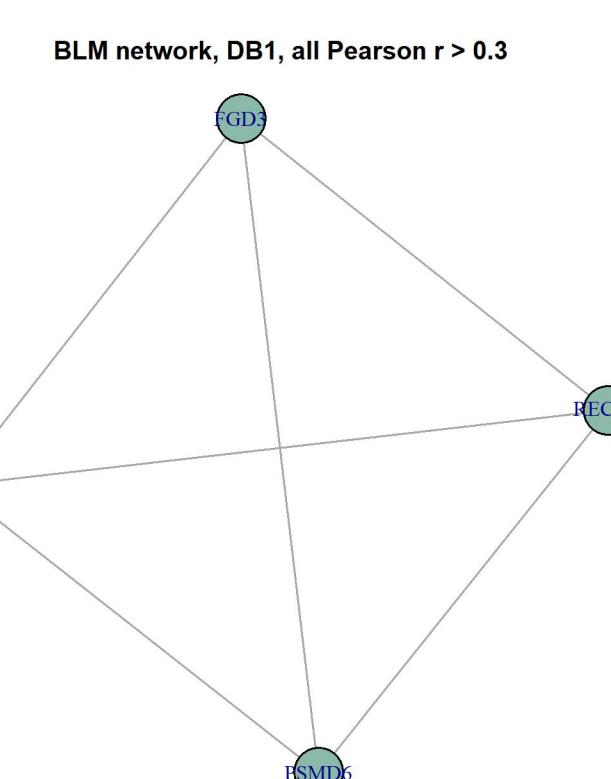
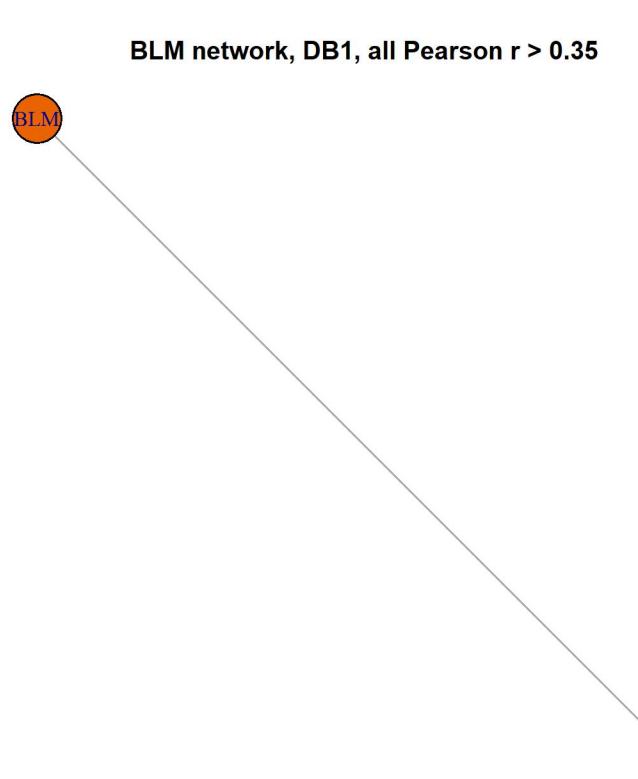
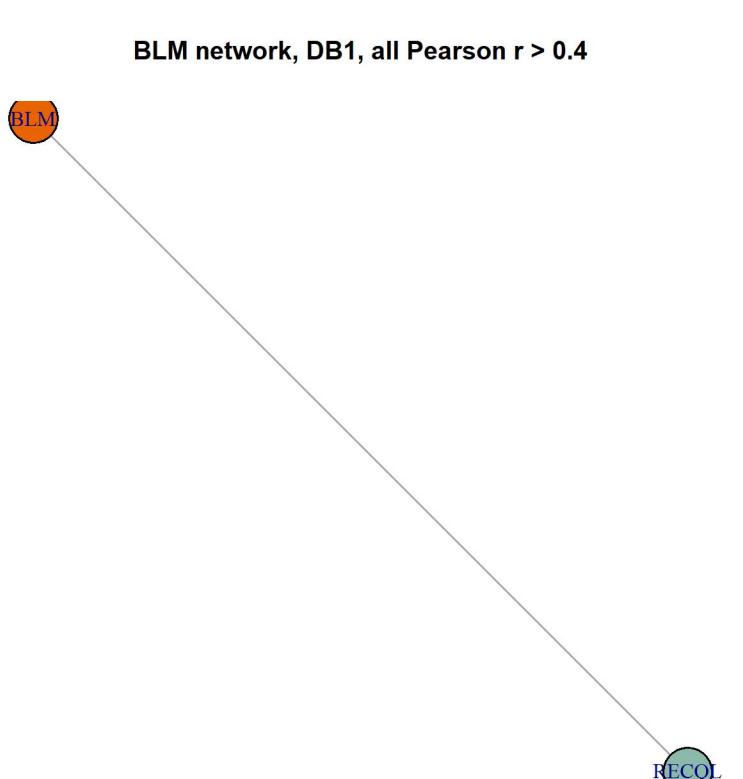




logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.18	2.81e-04	CCNA2	cyclin A2	1.1	3.19e-03	STOM	stomatin
-1.07	2.81e-04	GTSE1	G2 and S-phase expressed 1	0.98	4.54e-02	LMNA	lamin A/C
-0.96	1.95e-04	SKA3	spindle and kinetochore associated	0.83	4.54e-02	PLP2	proteolipid protein 2
-0.95	1.71e-02	SEPTIN1	septin 1	0.81	1.14e-02	PLBD2	phospholipase B domain containing 2
-0.91	1.15e-03	PPP4R3B	protein phosphatase 4 regulatory su	0.8	1.97e-02	NIBAN1	niban apoptosis regulator 1
-0.88	2.40e-04	RCOR1	REST corepressor 1	0.79	8.22e-03	PLOD3	procollagen-lysine,2-oxoglutarate 5
-0.87	2.91e-03	SPDL1	spindle apparatus coiled-coil prote	0.76	9.81e-03	SEL1L	SEL1L adaptor subunit of ERAD E3 ub
-0.85	2.30e-03	SPC25	SPC25 component of NDC80 kinetochor	0.75	6.66e-03	ERMP1	endoplasmic reticulum metallopeptid
-0.85	1.28e-03	NCAPH2	non-SMC condensin II complex subuni	0.74	4.54e-02	MVP	major vault protein
-0.85	1.72e-03	PDCD2	programmed cell death 2	0.73	4.54e-02	NDUFB2	NADH:ubiquinone oxidoreductase subu
-0.85	7.06e-03	CEP43	centrosomal protein 43	0.73	2.60e-02	CLCC1	chloride channel CLIC like 1
-0.84	3.56e-03	ZAP70	zeta chain of T cell receptor assoc	0.73	2.05e-02	DNAJC1	DnaJ heat shock protein family (Hsp
-0.84	3.45e-04	DSN1	DSN1 component of MIS12 kinetochore	0.69	4.45e-02	PLD3	phospholipase D family member 3
-0.83	2.45e-03	CCDC12	coiled-coil domain containing 12	0.67	4.16e-02	ATP6V0A1	ATPase H+ transporting V0 subunit a
-0.82	3.22e-03	RNF138	ring finger protein 138	0.66	4.45e-02	TRIP10	thyroid hormone receptor interactor
-0.82	1.72e-03	DLGAP5	DLG associated protein 5	0.64	4.54e-02	SSR3	signal sequence receptor subunit 3
-0.81	3.36e-02	DBN1	drebrin 1	0.63	4.54e-02	TMUB1	transmembrane and ubiquitin like do
-0.8	3.19e-03	MIS18A	MIS18 kinetochore protein A	0.63	1.09e-01	LGALS3	galectin 3
-0.8	1.44e-02	KIF15	kinesin family member 15	0.63	1.92e-02	TRADD	TNFRSF1A associated via death domai
-0.8	2.60e-02	SLBP	stem-loop binding protein	0.62	2.43e-02	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-b
-0.8	2.31e-02	INTS7	integrator complex subunit 7	0.61	5.49e-02	CD59	CD59 molecule (CD59 blood group)
-0.79	2.33e-03	CIT	citron rho-interacting serine/threo	0.61	4.54e-02	TYMP	thymidine phosphorylase
-0.78	1.04e-02	MAP1A	microtubule associated protein 1A	0.6	5.61e-02	MECR	mitochondrial trans-2-enoyl-CoA red
-0.78	4.77e-03	BRD7	bromodomain containing 7	0.59	4.54e-02	ALG1	ALG1 chitobiosyldiphospholichol b
-0.78	6.38e-03	PITPNA	phosphatidylinositol transfer prote	0.58	2.03e-01	SFN	stratifin
-0.76	8.11e-04	NCAPD3	non-SMC condensin II complex subuni	0.58	4.54e-02	DUSP3	dual specificity phosphatase 3
-0.76	6.08e-03	CCNB2	cyclin B2	0.58	4.54e-02	TMEM205	transmembrane protein 205
-0.76	4.59e-03	CHD8	chromodomain helicase DNA binding p	0.58	4.54e-02	ALB	albumin
-0.76	1.04e-01	H3-7	H3.7 histone (putative)	0.58	5.50e-02	MICOS13	mitochondrial contact site and cris

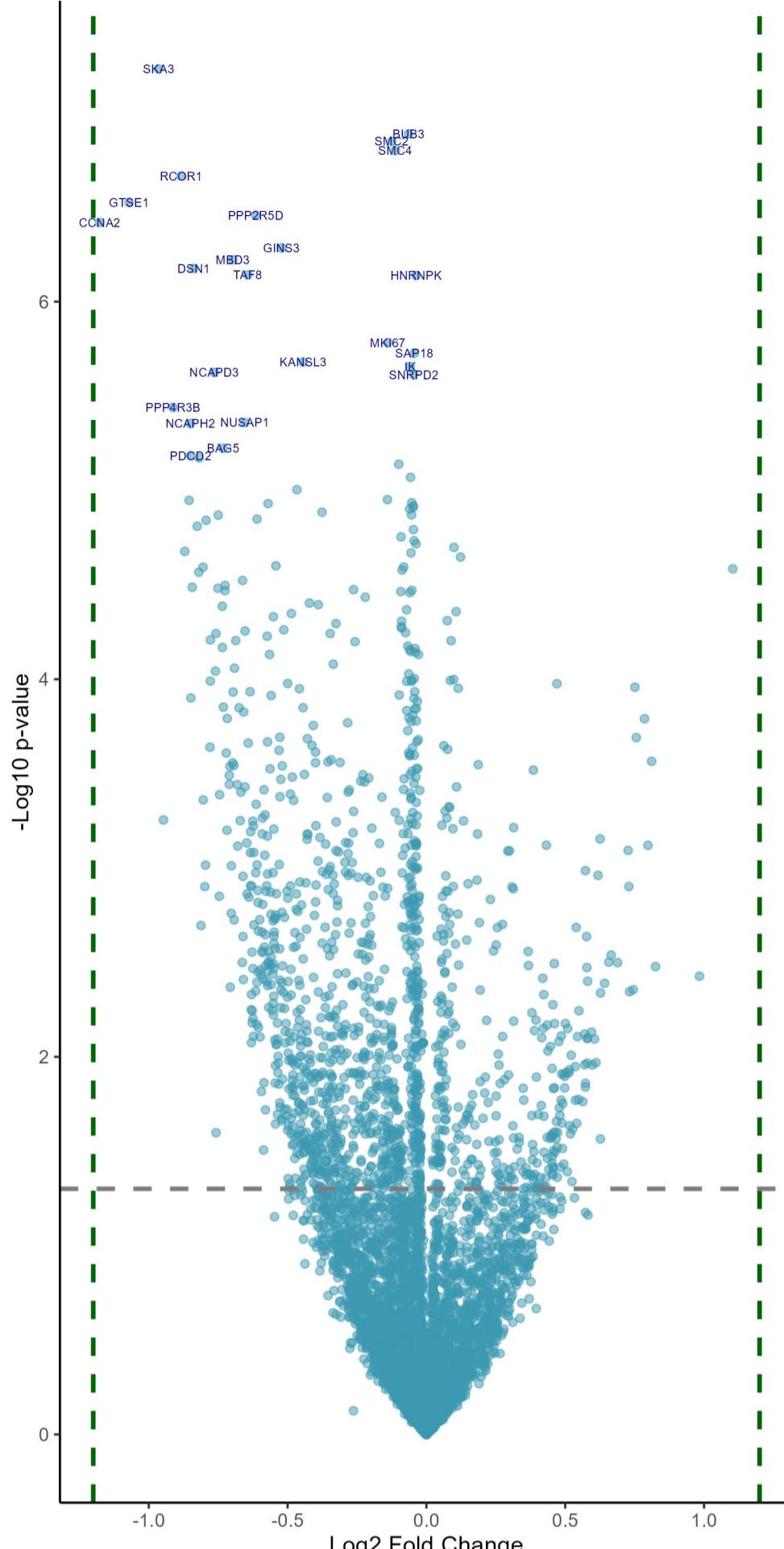


Downregulated in solid cancers at low/absent BLM				Upregulated in solid cancers at low/absent BLM			
	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
	3.26e-18	C9orf78	chromosome 9 open reading frame 78	0.69	3.87e-03	LGALS1	galectin 1
	1.10e-26	NUSAP1	nucleolar and spindle associated pr	0.68	7.80e-07	NNMT	nicotinamide N-methyltransferase
	3.38e-20	EZH2	enhancer of zeste 2 polycomb repres	0.65	3.64e-06	TAP2	transporter 2, ATP binding cassette
	2.33e-22	CDCA5	cell division cycle associated 5	0.65	2.34e-08	NRP1	neuropilin 1
	2.14e-12	POLR2F	RNA polymerase II, I and III subuni	0.65	9.98e-04	ITGA3	integrin subunit alpha 3
	6.59e-15	UBE2T	ubiquitin conjugating enzyme E2 T	0.65	3.94e-06	IGFBP7	insulin like growth factor binding
	9.29e-21	FRG1	FSHD region gene 1	0.63	6.58e-06	TAP1	transporter 1, ATP binding cassette
	5.60e-16	POLR2D	RNA polymerase II subunit D	0.62	2.60e-06	RAB32	RAB32, member RAS oncogene family
	8.76e-13	BRD2	bromodomain containing 2	0.6	1.96e-06	COL6A1	collagen type VI alpha 1 chain
	4.42e-16	PCF11	PCF11 cleavage and polyadenylation	0.6	3.23e-06	CYBRD1	cytochrome b reductase 1
	6.05e-14	MRGBP	MRG domain binding protein	0.6	1.32e-05	RRAS	RAS related
	6.70e-12	C1D	C1D nuclear receptor corepressor	0.59	2.89e-04	NT5E	5'-nucleotidase ecto
	4.78e-14	WDHD1	WD repeat and HMG-box DNA binding p	0.58	1.63e-04	HLA-B	major histocompatibility complex, c
	2.00e-16	KIF2C	kinesin family member 2C	0.57	2.87e-04	BST2	bone marrow stromal cell antigen 2
	1.75e-12	BUD23	BUD23 rRNA methyltransferase and ri	0.56	1.12e-02	S100A6	S100 calcium binding protein A6
	1.19e-14	FANCI	FA complementation group I	0.56	9.52e-06	COL12A1	collagen type XII alpha 1 chain
	5.99e-15	UPF3B	UPF3B regulator of nonsense mediate	0.56	3.51e-04	RHOC	ras homolog family member C
	9.26e-12	CDCA3	cell division cycle associated 3	0.55	2.40e-04	THBS1	thrombospondin 1
	2.44e-18	PRC1	protein regulator of cytokinesis 1	0.55	1.31e-08	CD70	CD70 molecule
	6.06e-16	CDK12	cyclin dependent kinase 12	0.55	6.47e-03	CD44	CD44 molecule (Indian blood group)
	5.84e-14	HELLS	helicase, lymphoid specific	0.54	1.89e-03	CTSZ	cathepsin Z
	2.00e-16	POLR2L	RNA polymerase II, I and III subuni	0.54	6.21e-04	CD59	CD59 molecule (CD59 blood group)
	2.19e-12	RPF1	ribosome production factor 1 homolo	0.54	8.38e-06	P3H2	prolyl 3-hydroxylase 2
	2.00e-16	UBE2S	ubiquitin conjugating enzyme E2 S	0.54	1.60e-07	SYNE1	spectrin repeat containing nuclear
	1.83e-15	CHAF1A	chromatin assembly factor 1 subunit	0.54	2.22e-04	AXL	AXL receptor tyrosine kinase
	6.08e-15	ORC2	origin recognition complex subunit	0.53	1.57e-04	MVP	major vault protein
	3.11e-17	TFIP11	tuftelin interacting protein 11	0.52	2.65e-06	RAB11FIP5	RAB11 family interacting protein 5
	8.44e-13	CKAP2	cytoskeleton associated protein 2	0.52	1.90e-04	EHD2	EH domain containing 2
	6.50e-12	BP1A	ribose 5-phosphate isomerase A	0.52	5.97e-05	CBAT	carnitine O-acetyltransferase



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

p-value < 0.05 & logFC > 1.2



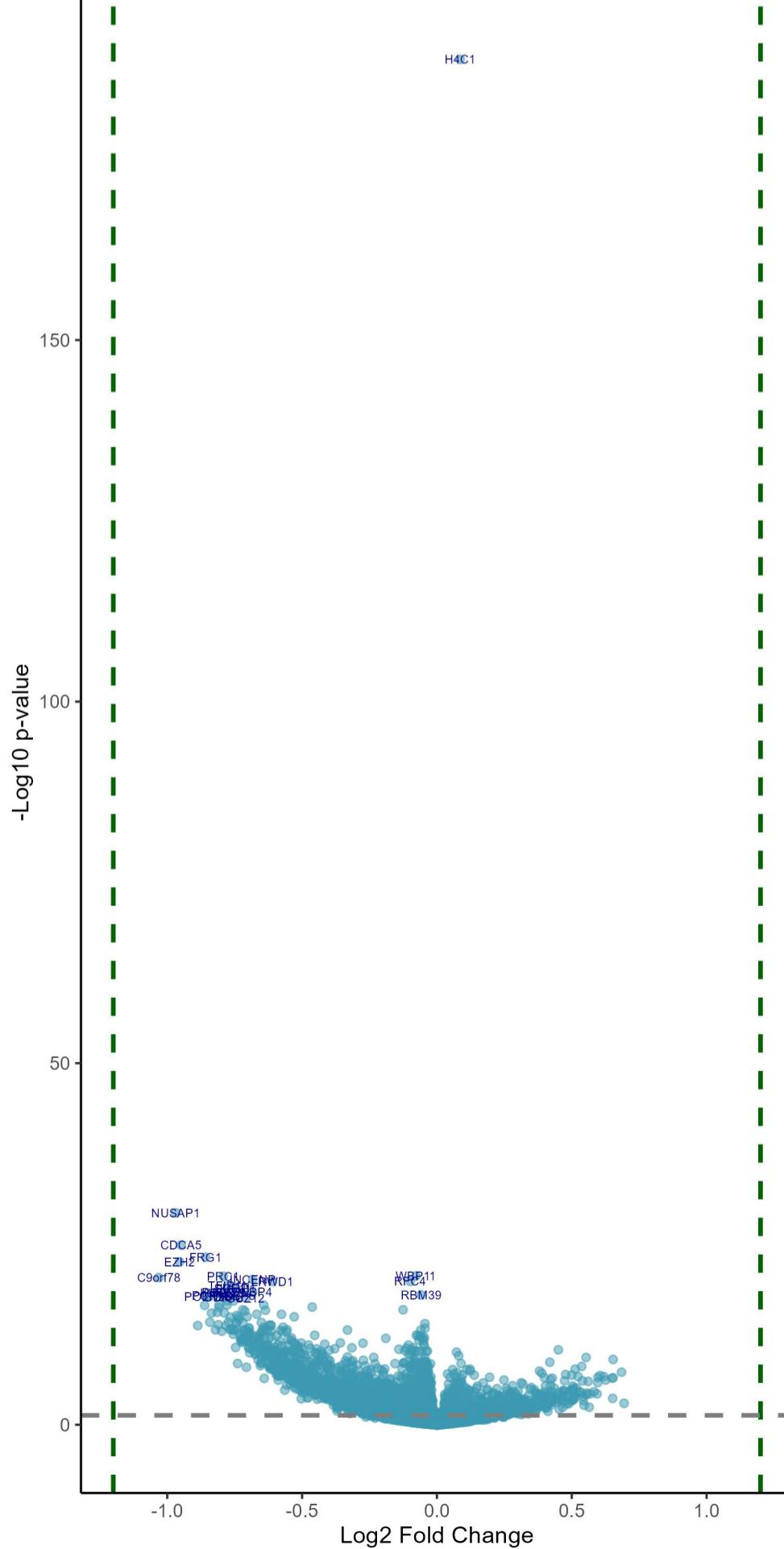
Sorted by p values!

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

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.96	1.95e-04	SKA3	spindle and kinetochore associated	0.1	2.83e-03	ATP2A2	ATPase sarcoplasmic/endoplasmic ret
-0.06	2.11e-04	BUB3	BUB3 mitotic checkpoint protein	0.12	3.00e-03	SRPRB	SRP receptor subunit beta
-0.12	2.11e-04	SMC2	structural maintenance of chromosom	1.1	3.19e-03	STOM	stomatin
-0.11	2.11e-04	SMC4	structural maintenance of chromosom	0.11	4.10e-03	MRPL38	mitochondrial ribosomal protein L38
-0.88	2.40e-04	RCOR1	REST corepressor 1	0.08	4.37e-03	PDIA6	protein disulfide isomerase family
-1.07	2.81e-04	GTSE1	G2 and S-phase expressed 1	0.09	4.77e-03	MRPL13	mitochondrial ribosomal protein L13
-0.62	2.81e-04	PPP2R5D	protein phosphatase 2 regulatory su	0.1	6.38e-03	MRPL45	mitochondrial ribosomal protein L45
-1.18	2.81e-04	CCNA2	cyclin A2	0.09	6.38e-03	HDLBP	high density lipoprotein binding pr
-0.52	3.45e-04	GINS3	GINS complex subunit 3	0.47	6.44e-03	CASK	calcium/calmodulin dependent serine
-0.7	3.45e-04	MBD3	methyl-CpG binding domain protein 3	0.75	6.66e-03	ERMP1	endoplasmic reticulum metallopeptid
-0.84	3.45e-04	DSN1	DSN1 component of MIS12 kinetochore	0.11	6.67e-03	PRDX4	peroxiredoxin 4
-0.64	3.45e-04	TAF8	TATA-box binding protein associated	0.79	8.22e-03	PLOD3	procollagen-lysine,2-oxoglutarate 5
-0.04	3.45e-04	HNRNPK	heterogeneous nuclear ribonucleopro	0.76	9.81e-03	SEL1L	SEL1L adaptor subunit of ERAD E3 ub
-0.14	7.31e-04	MKI67	marker of proliferation Ki-67	0.06	1.03e-02	OCIAD1	OCIA domain containing 1
-0.04	7.80e-04	SAP18	Sin3A associated protein 18	0.08	1.06e-02	HADHB	hydroxyacyl-CoA dehydrogenase triflu
-0.44	8.11e-04	KANSL3	KAT8 regulatory NSL complex subunit	0.81	1.14e-02	PLBD2	phospholipase B domain containing 2
-0.06	8.11e-04	IK	IK cytokine	0.19	1.16e-02	SPCS2	signal peptidase complex subunit 2
-0.76	8.11e-04	NCAPD3	non-SMC condensin II complex subuni	0.39	1.19e-02	SEC11C	SEC11 homolog C, signal peptidase c
-0.05	8.11e-04	SNRPD2	small nuclear ribonucleoprotein D2	0.11	1.33e-02	SSR4	signal sequence receptor subunit 4
-0.91	1.15e-03	PPP4R3B	protein phosphatase 4 regulatory su	0.08	1.53e-02	DNAJA3	Dnaj heat shock protein family (Hsp
-0.65	1.28e-03	NUSAP1	nucleolar and spindle associated pr	0.08	1.54e-02	GFM1	G elongation factor mitochondrial 1
-0.85	1.28e-03	NCAPH2	non-SMC condensin II complex subuni	0.07	1.60e-02	USO1	USO1 vesicle transport factor
-0.73	1.66e-03	BAG5	BAG cochaperone 5	0.07	1.69e-02	HADHA	hydroxyacyl-CoA dehydrogenase triflu
-0.85	1.72e-03	PDCD2	programmed cell death 2	0.13	1.71e-02	MYDGF	myeloid derived growth factor
-0.82	1.72e-03	DLGAP5	DLG associated protein 5	0.06	1.75e-02	TIMM44	translocase of inner mitochondrial
-0.1	1.79e-03	DUT	deoxyuridine triphosphatase	0.31	1.78e-02	COLGALT1	collagen beta(1-O)galactosyltransfe
-0.06	2.02e-03	ANP32B	acidic nuclear phosphoprotein 32 fa	0.1	1.79e-02	LMAN2	lectin, mannose binding 2
-0.47	2.27e-03	KIF2C	kinesin family member 2C	0.18	1.84e-02	POP1	POP1 homolog, ribonuclease P/MRP su
-0.14	2.30e-03	GATA2A	GATA zinc finger domain containing	0.63	1.92e-02	TRADD	TNFRSF1A associated via death domai
-0.85	2.30e-03	SPC25	SPC25 component of NDC80 kinetochor	0.43	1.97e-02	SRPRA	SRP receptor subunit alpha
-0.05	2.30e-03	CHD4	chromodomain helicase DNA binding p	0.8	1.97e-02	NIBAN1	niban apoptosis regulator 1
-0.57	2.30e-03	PSMC3IP	PSMC3 interacting protein	0.73	2.05e-02	DNAJC1	Dnaj heat shock protein family (Hsp
-0.05	2.30e-03	SF3A3	splicing factor 3a subunit 3	0.3	2.05e-02	STAT1	signal transducer and activator of
-0.05	2.30e-03	SF1	splicing factor 1	0.29	2.05e-02	ABCF3	ATP binding cassette subfamily F me
-0.06	2.30e-03	CBX3	chromobox 3	0.57	2.39e-02	NDUFAF7	NADH:ubiquinone oxidoreductase comp
-0.38	2.30e-03	NUDT1	nudix hydrolase 1	0.62	2.43e-02	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-b
-0.05	2.30e-03	PNN	pinin, desmosome associated protein	0.07	2.44e-02	UFL1	UFM1 specific ligase 1
-0.75	2.30e-03	PDCL	phosducin like	0.18	2.52e-02	NOL6	nucleolar protein 6
0.61	2.33e-03	CDCA7	cell division cycle associated 7	0.15	2.60e-02	EMC2	ER membrane protein complex subunit

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

p-value < 0.05 & logFC > 1.2

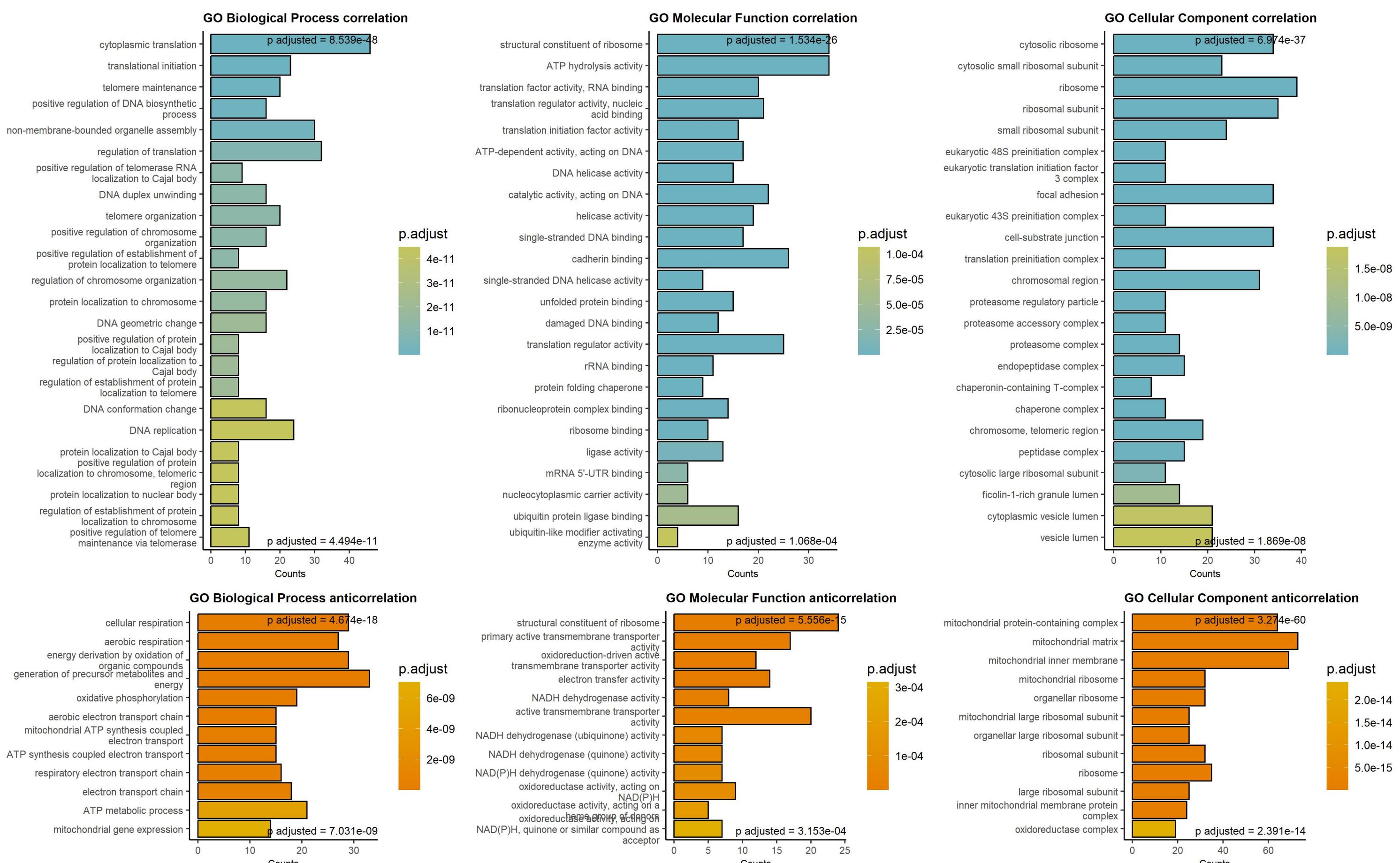


Sorted by p values!

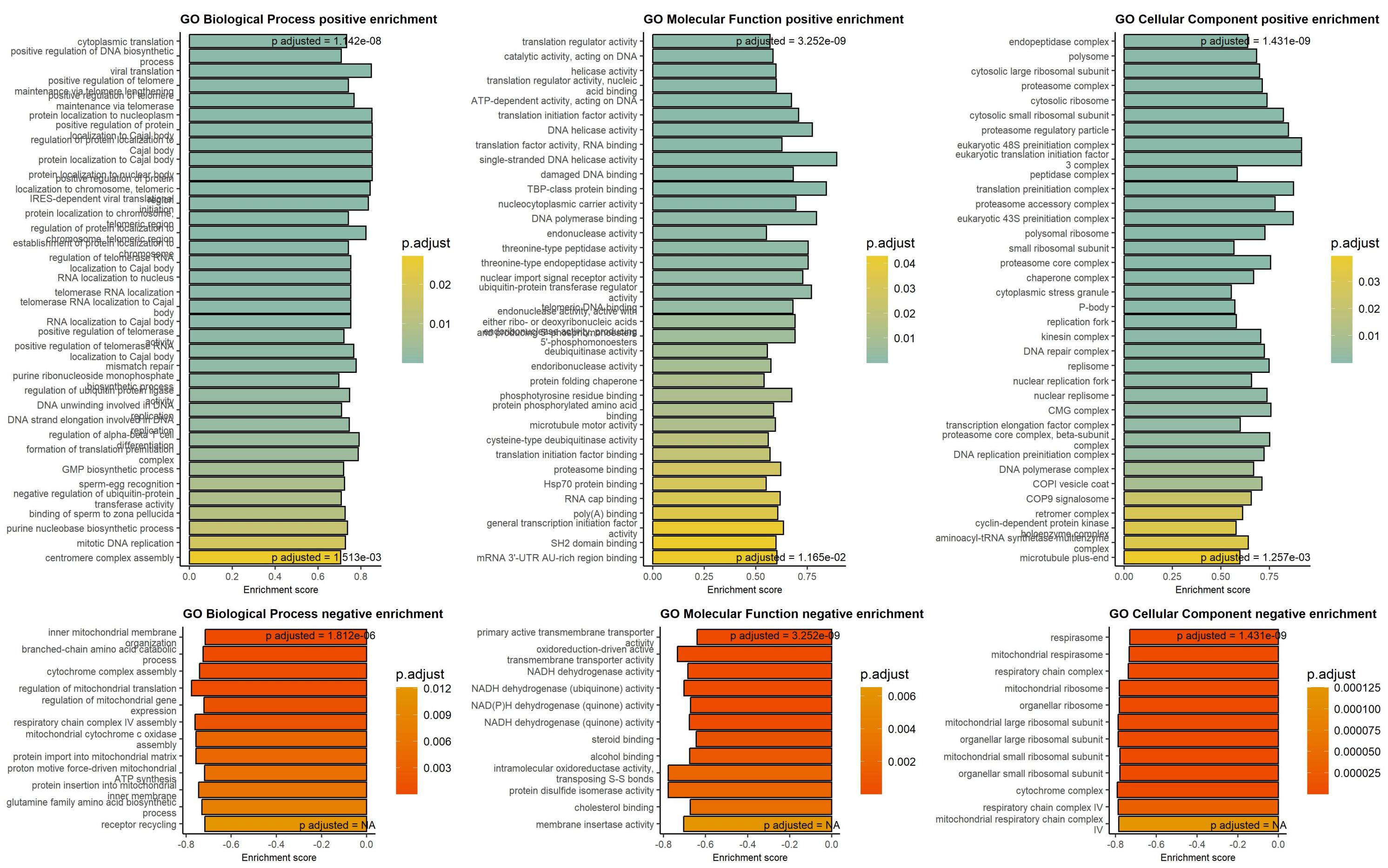
Downregulated in solid cancers at low/absent BLM Upregulated in solid cancers at low/absent BLM

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.97	1.10e-26	NUSAP1	nucleolar and spindle associated pr	0.09	5.12e-186	H4C1	H4 clustered histone 1
-0.95	2.33e-22	CDCA5	cell division cycle associated 5	0.45	1.69e-09	LOXL2	lysyl oxidase like 2
-0.86	9.29e-21	FRG1	FSHD region gene 1	0.07	3.06e-09	AP2B1	adaptor related protein complex 2 s
-0.95	3.38e-20	EZH2	enhancer of zeste 2 polycomb repres	0.08	8.31e-09	PGRMC2	progesterone receptor membrane comp
-0.08	2.44e-18	WBP11	WW domain binding protein 11	0.55	1.31e-08	CD70	CD70 molecule
-0.79	2.44e-18	PRC1	protein regulator of cytokinesis 1	0.65	2.34e-08	NRP1	neuropilin 1
-1.03	3.26e-18	C9orf78	chromosome 9 open reading frame 78	0.42	5.09e-08	VCAN	versican
-0.68	5.48e-18	INCENP	inner centromere protein	0.09	7.20e-08	AP2A1	adaptor related protein complex 2 s
-0.1	8.39e-18	RFC4	replication factor C subunit 4	0.54	1.60e-07	SYNE1	spectrin repeat containing nuclear
-0.61	8.39e-18	LRWD1	leucine rich repeats and WD repeat	0.12	3.36e-07	PITRM1	pitrilysin metallopeptidase 1
-0.78	3.11e-17	TFIP11	tufetin interacting protein 11	0.51	3.43e-07	SYNPO	synaptopodin
-0.75	6.55e-17	KIF11	kinesin family member 11	0.06	3.79e-07	P4HB	prolyl 4-hydroxylase subunit beta
-0.75	6.55e-17	SUGP1	SURP and G-patch domain containing	0.11	3.87e-07	CYB5R3	cytochrome b5 reductase 3
-0.68	1.77e-16	FNBP4	formin binding protein 4	0.12	5.67e-07	ITGB1	integrin subunit beta 1
-0.79	2.00e-16	POLR2L	RNA polymerase II, I and III subuni	0.38	5.71e-07	PLXDC2	plexin domain containing 2
-0.81	2.00e-16	KIF2C	kinesin family member 2C	0.68	7.80e-07	NNMT	nicotinamide N-methyltransferase
-0.78	2.00e-16	UBE2S	ubiquitin conjugating enzyme E2 S	0.07	8.75e-07	MYL6	myosin light chain 6
-0.06	3.69e-16	RBM39	RNA binding motif protein 39	0.39	1.04e-06	MOXD1	monooxygenase DBH like 1
-0.84	4.42e-16	PCF11	PCF11 cleavage and polyadenylation	0.04	1.27e-06	CLTC	clathrin heavy chain
-0.75	4.42e-16	RBBP6	RB binding protein 6, ubiquitin lig	0.06	1.32e-06	ACTBL2	actin beta like 2
-0.85	5.60e-16	POLR2D	RNA polymerase II subunit D	0.48	1.52e-06	CPQ	carboxypeptidase Q
-0.79	6.06e-16	CDK12	cyclin dependent kinase 12	0.1	1.61e-06	PICALM	phosphatidylinositol binding clathr
-0.71	7.71e-16	SUZ12	SUZ12 polycomb repressive complex 2	0.5	1.73e-06	DAB2	DAB adaptor protein 2
-0.78	1.83e-15	CHAF1A	chromatin assembly factor 1 subunit	0.14	1.76e-06	HIBADH	3-hydroxyisobutyrate dehydrogenase
-0.75	1.88e-15	POLE3	DNA polymerase epsilon 3, accessory	0.6	1.96e-06	COL6A1	collagen type VI alpha 1 chain
-0.81	5.99e-15	UPF3B	UPF3B regulator of nonsense mediate	0.62	2.60e-06	RAB32	RAB32, member RAS oncogene family
-0.78	6.08e-15	ORC2	origin recognition complex subunit	0.52	2.65e-06	RAB11FIP5	RAB11 family interacting protein 5
-0.64	6.26e-15	GTF2B	general transcription factor IIB	0.07	3.07e-06	MYDGF	myeloid derived growth factor
-0.86	6.59e-15	UBE2T	ubiquitin conjugating enzyme E2 T	0.2	3.16e-06	HEXB	hexosaminidase subunit beta
-0.46	1.11e-14	CHAF1B	chromatin assembly factor 1 subunit	0.6	3.23e-06	CYBRD1	cytochrome b reductase 1
-0.81	1.19e-14	FANCI	FA complementation group I	0.05	3.24e-06	ARPC4	actin related protein 2/3 complex s
-0.72	2.40e-14	SAP130	Sin3A associated protein 130	0.65	3.64e-06	TAP2	transporter 2, ATP binding cassette
-0.13	2.40e-14	RFC2	replication factor C subunit 2	0.4	3.66e-06	LOX	

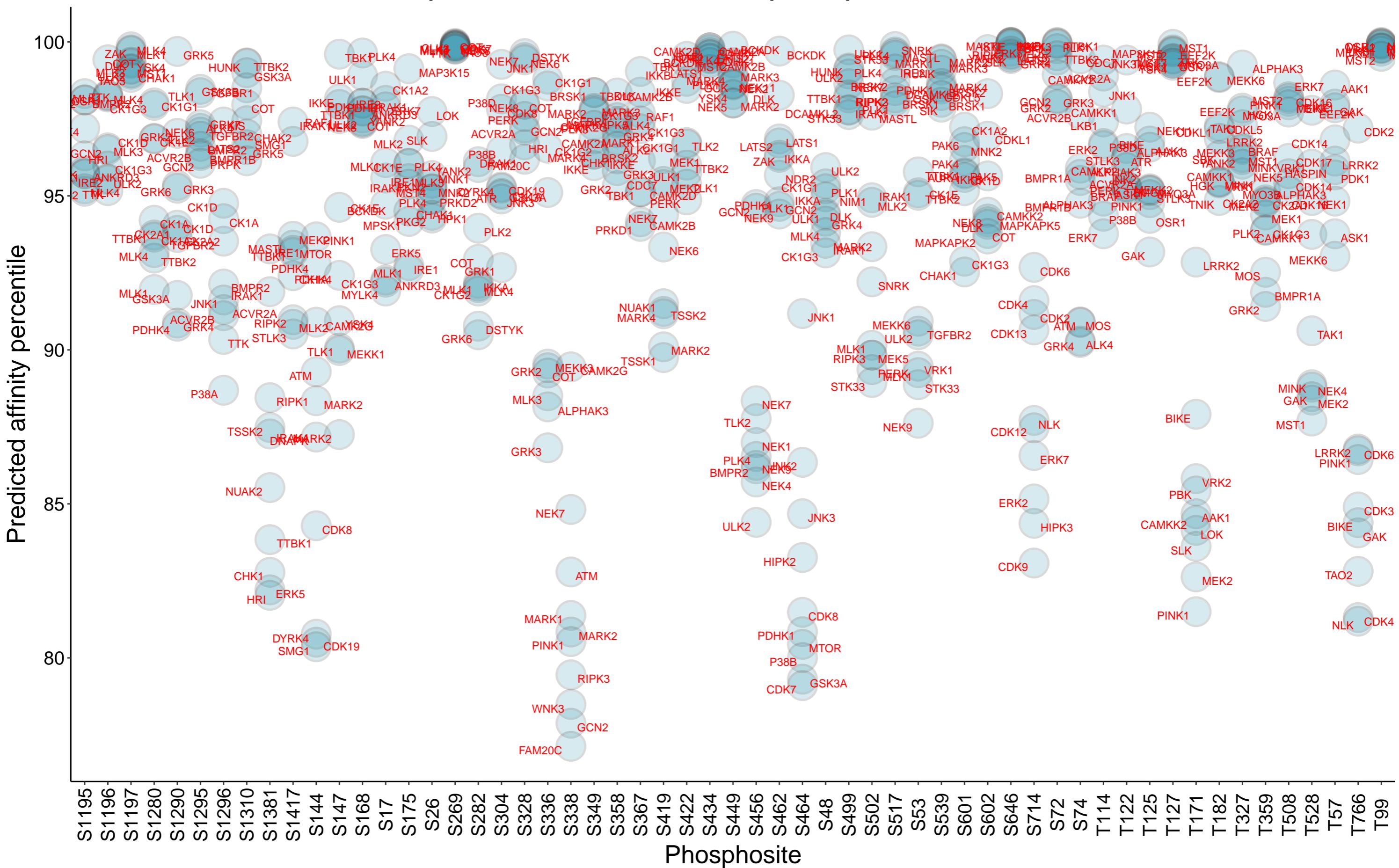
Top 250 correlation coefficients overrepresentation, BLM protein, DB1



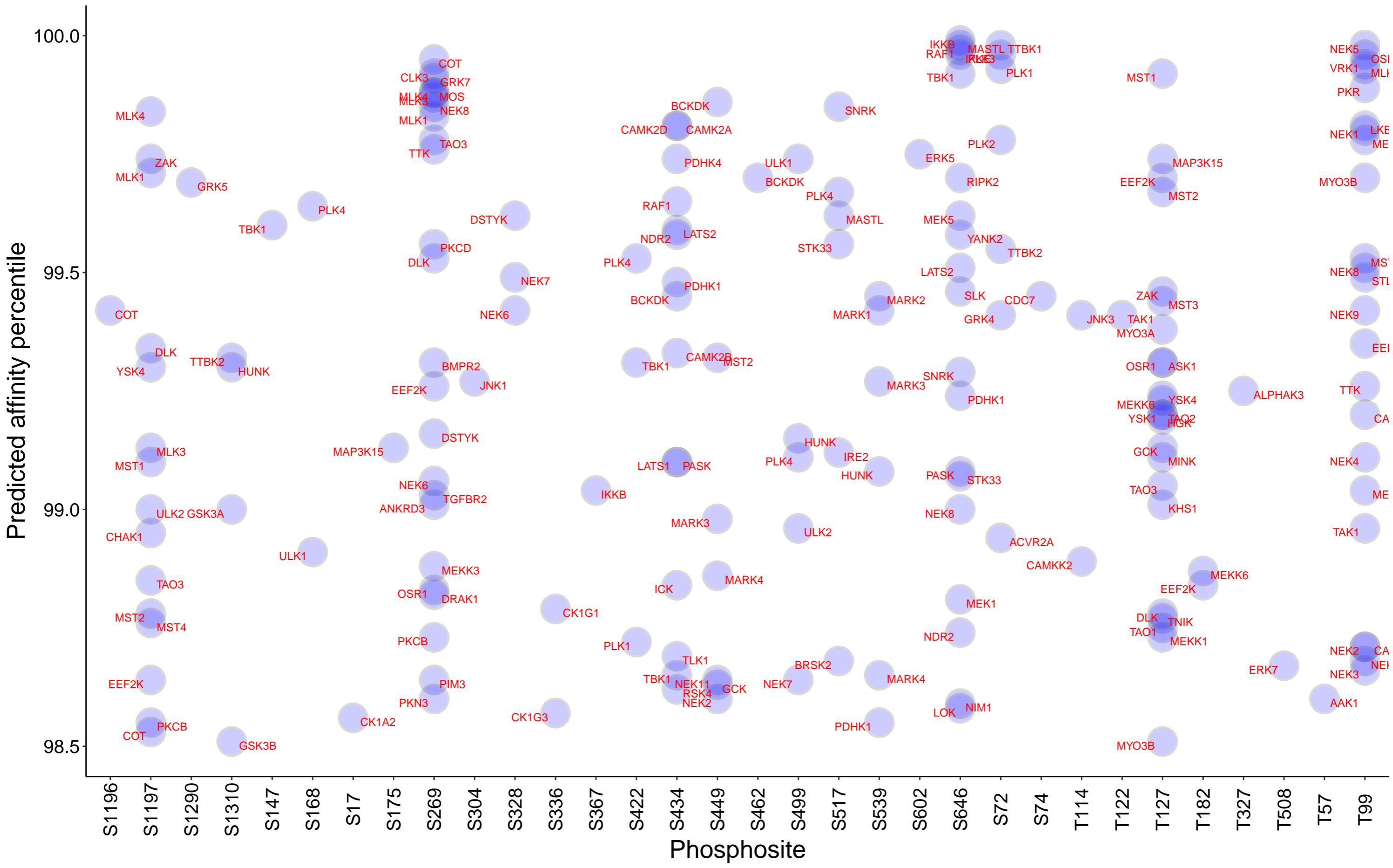
Gene Set Enrichment analysis on protein correlation coefficients, BLM protein, DB1



Top 10 kinases for each phosphosite in BLM

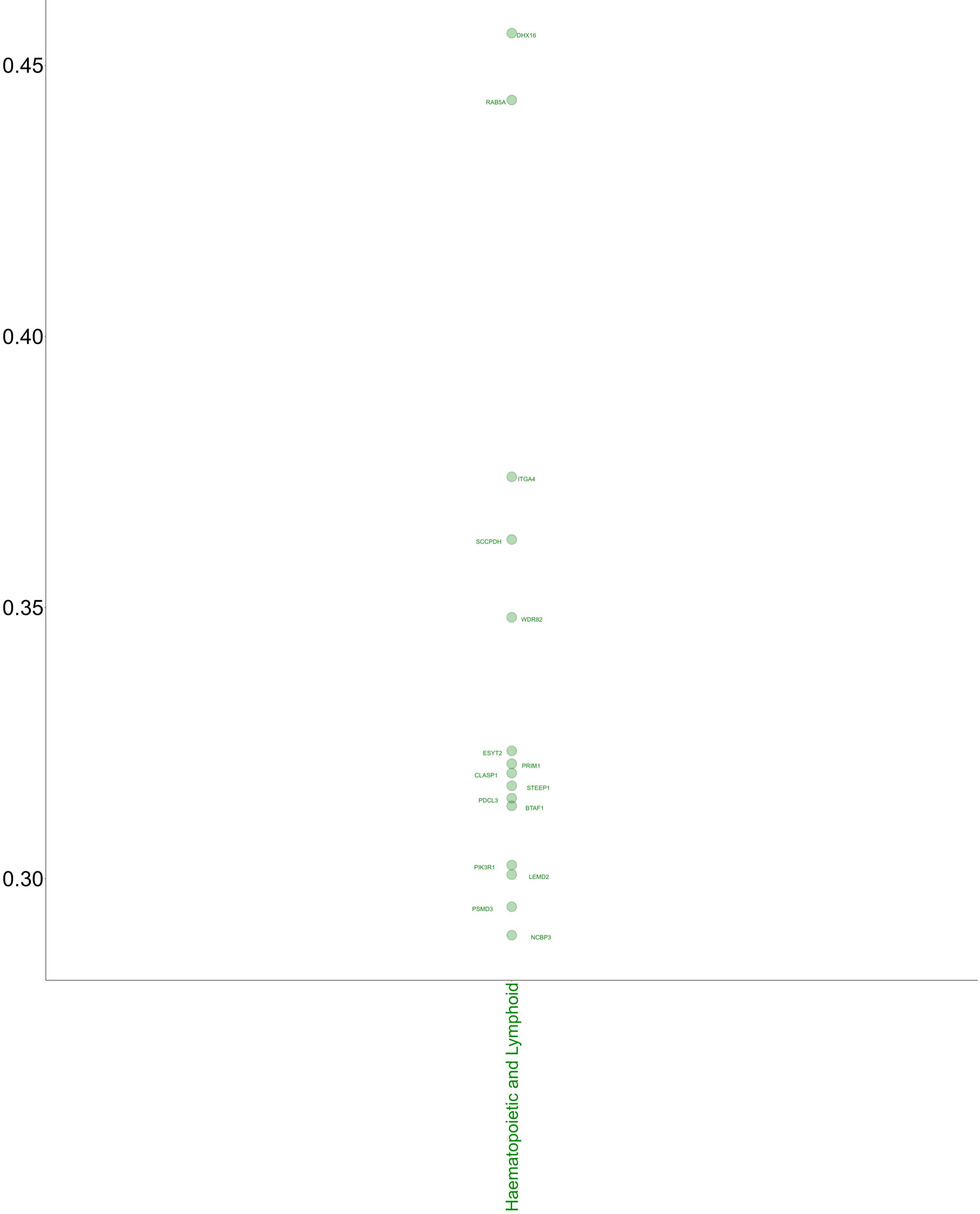


Kinases with affinity greater than 98.5% to BLM



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

Beware of false positives in tissues with small number of samples



Haematopoietic and Lymphoid