

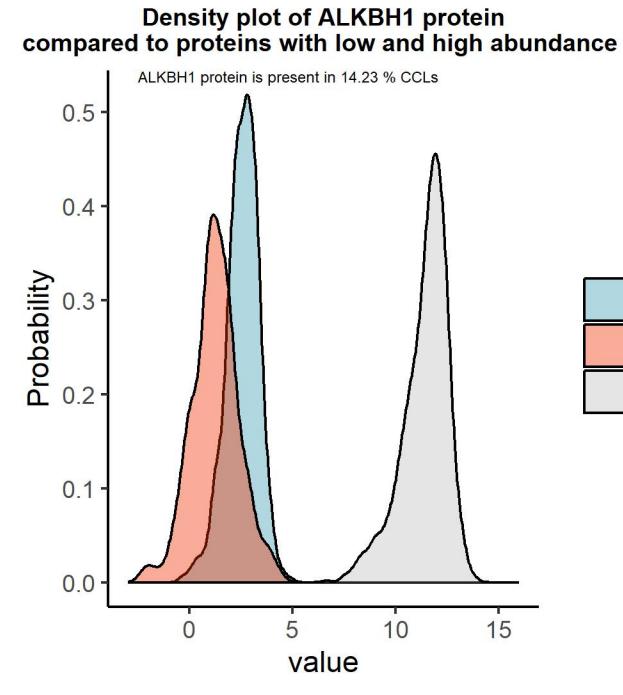
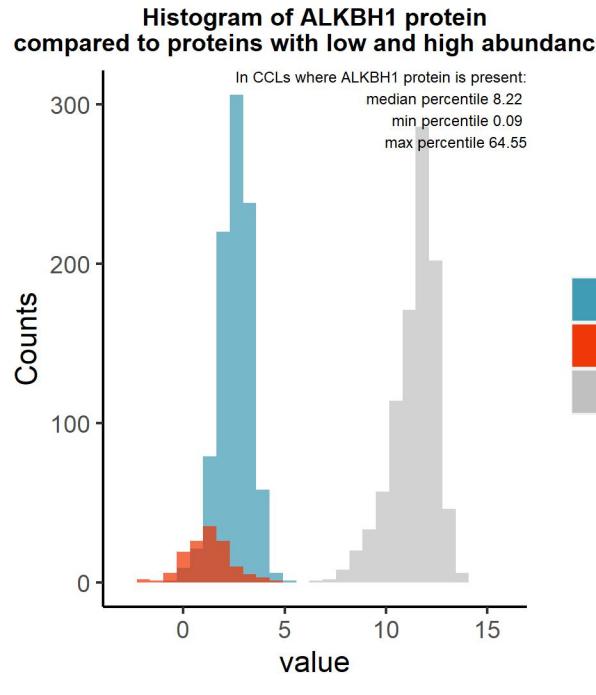
ALKBH1

Protein name: ALKBH1 ; UNIPROT: Q13686 ; Gene name: alkB homolog 1, histone H2A dioxygenase

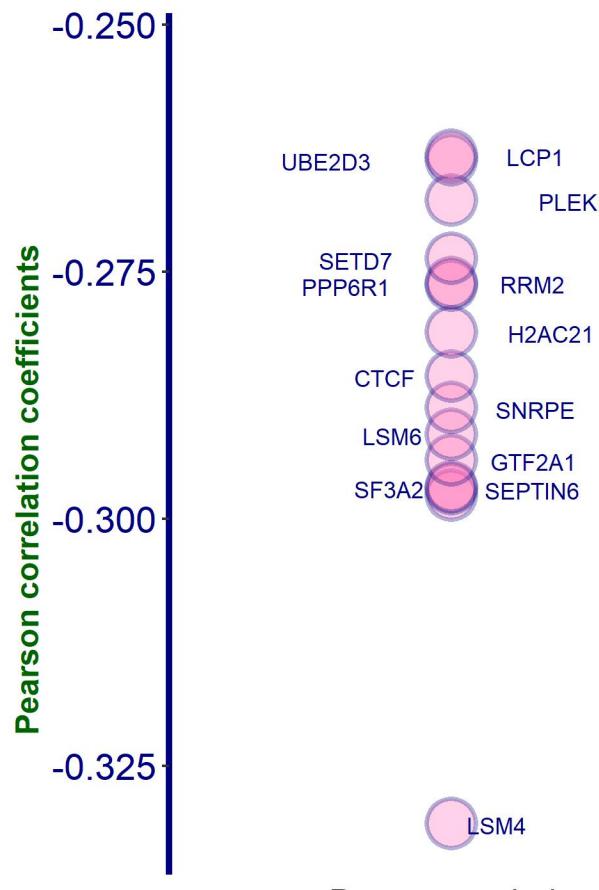
Ligandable: Yes ; Ligandable_by_Chem: NA ; Is_enzyme: Yes (<https://cansar.ai/>)

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

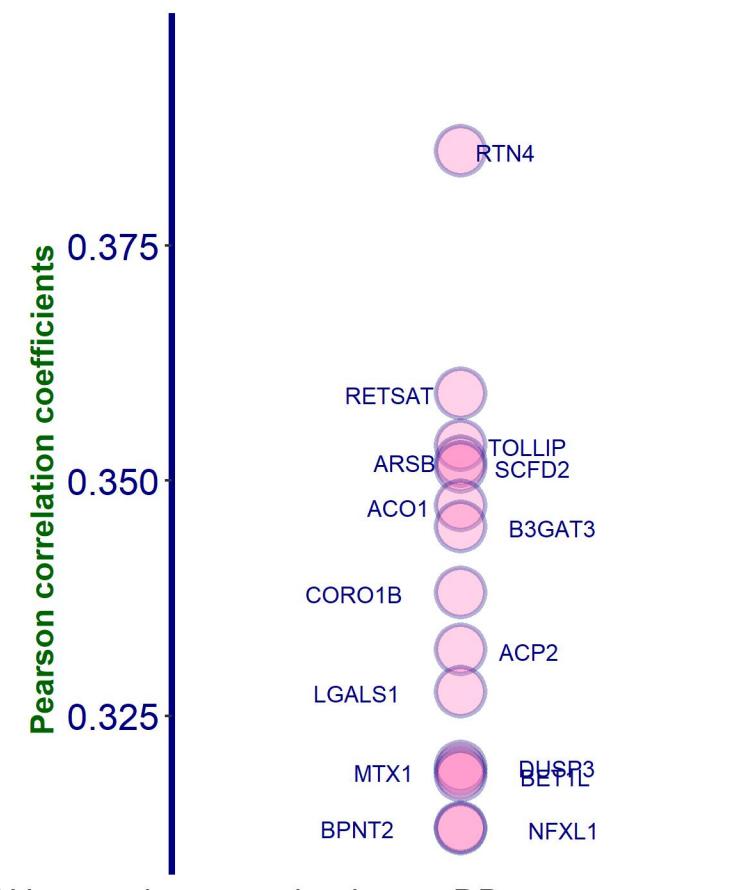
8498 proteins in same 949 CCLs



Negative correlations of ALKBH1 protein, DB2

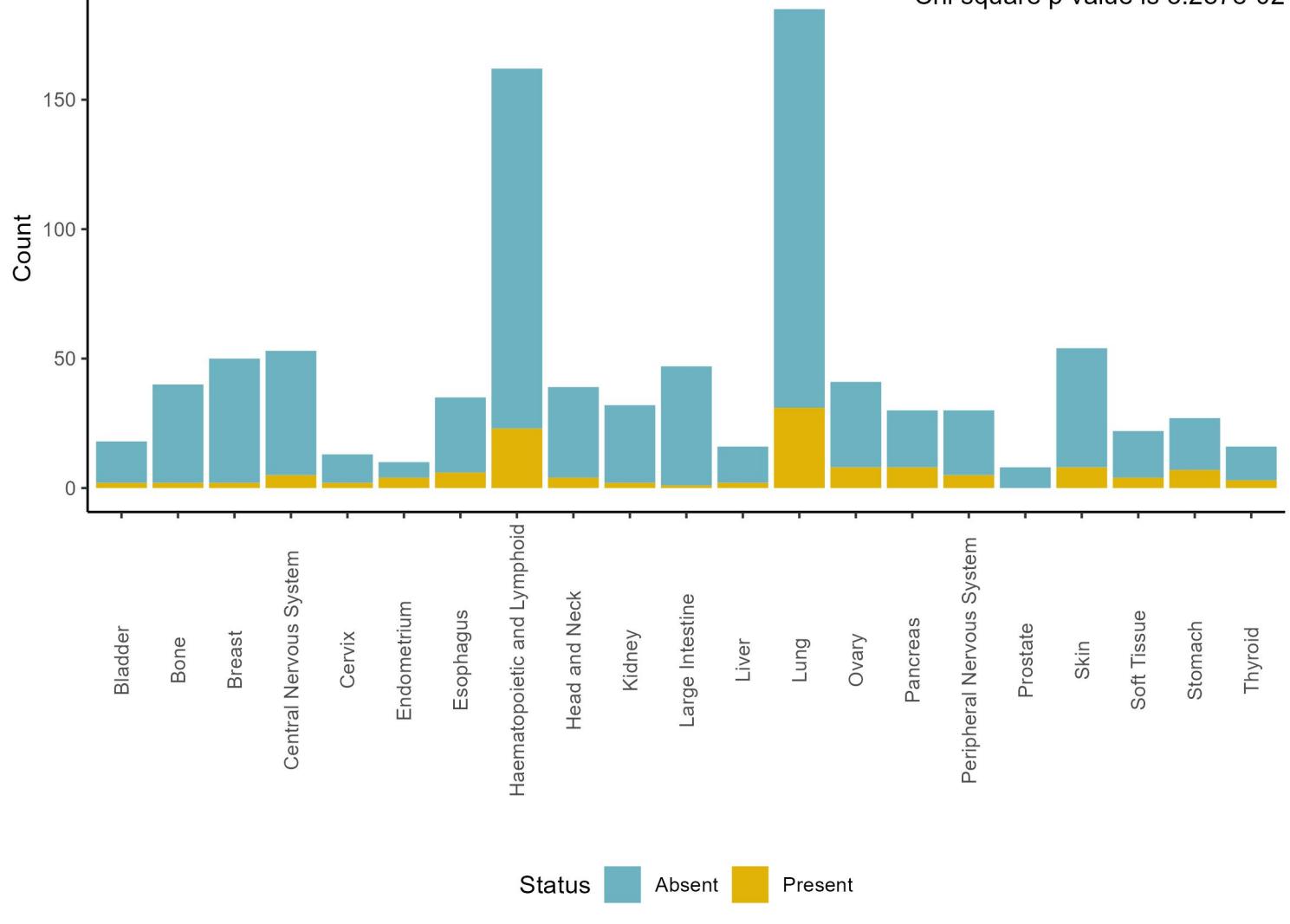
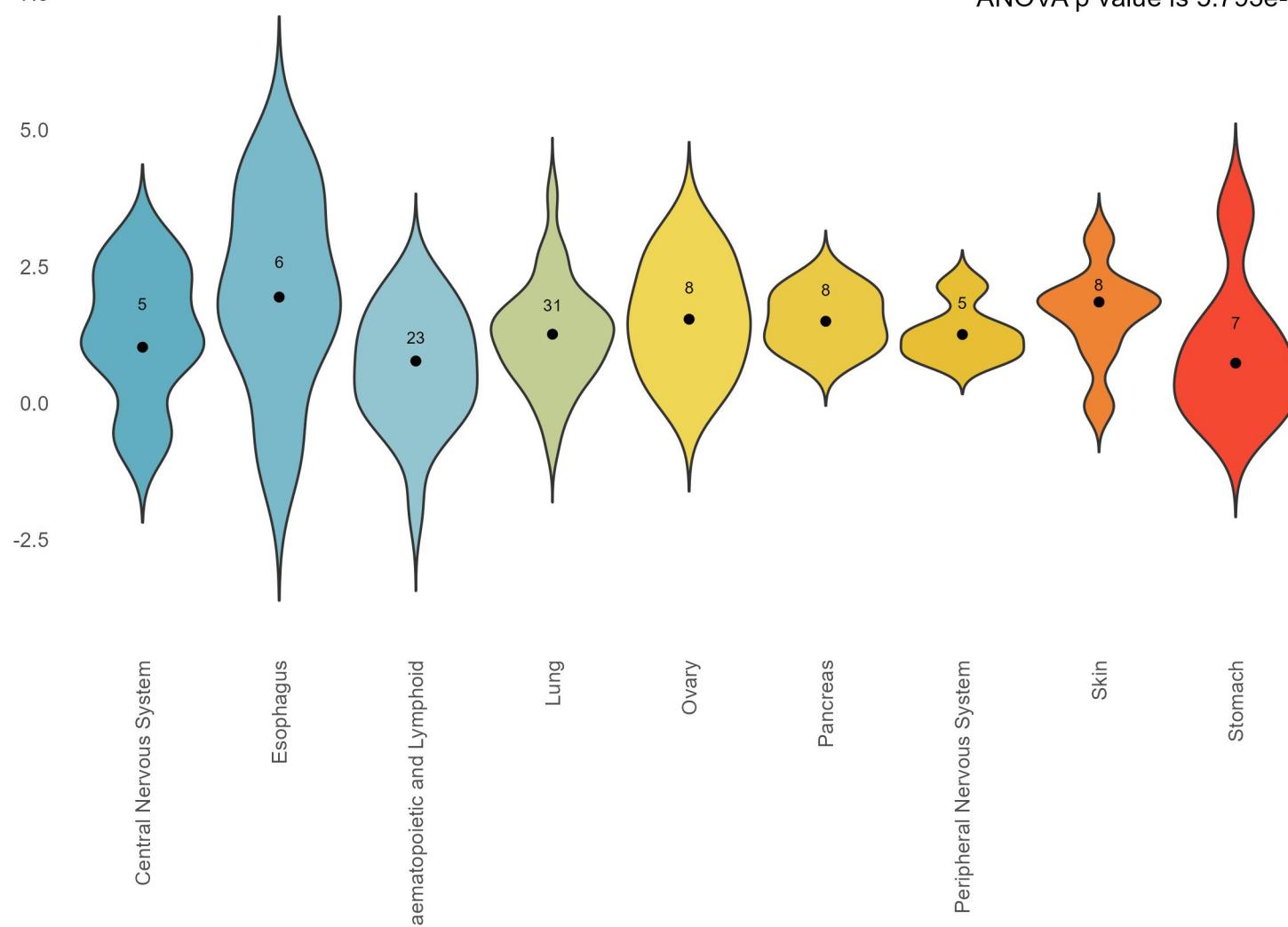


Positive correlations of ALKBH1 protein, DB2



Amount of ALKBH1 protein, number of CCLs where it is present by tissue, DB2

ANOVA p value is 5.793e-02

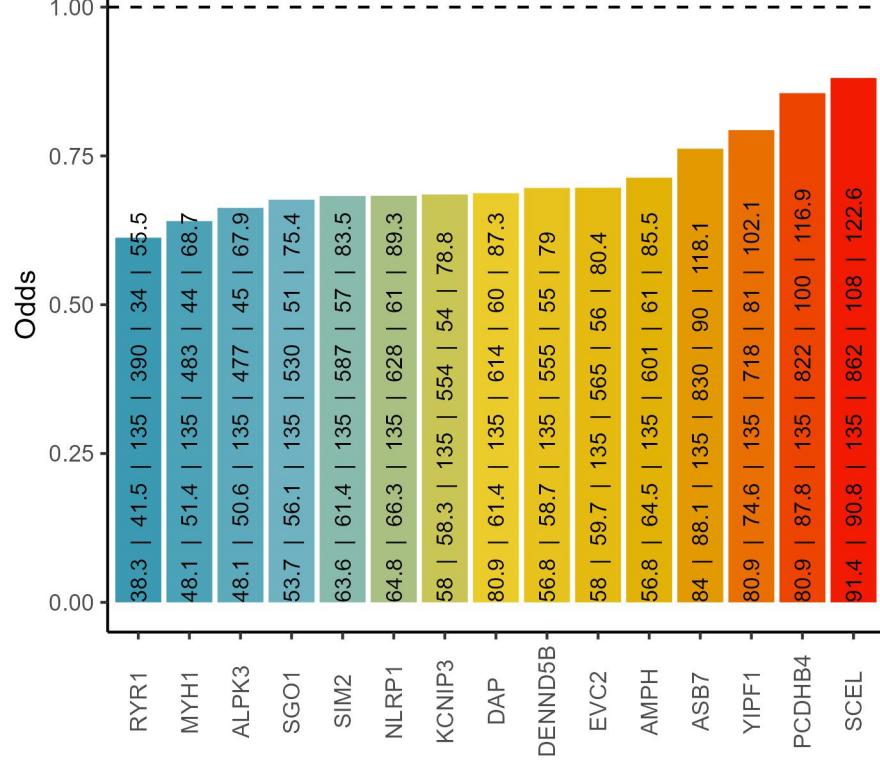


Cooccurrence with ALKBH1 protein, DB2

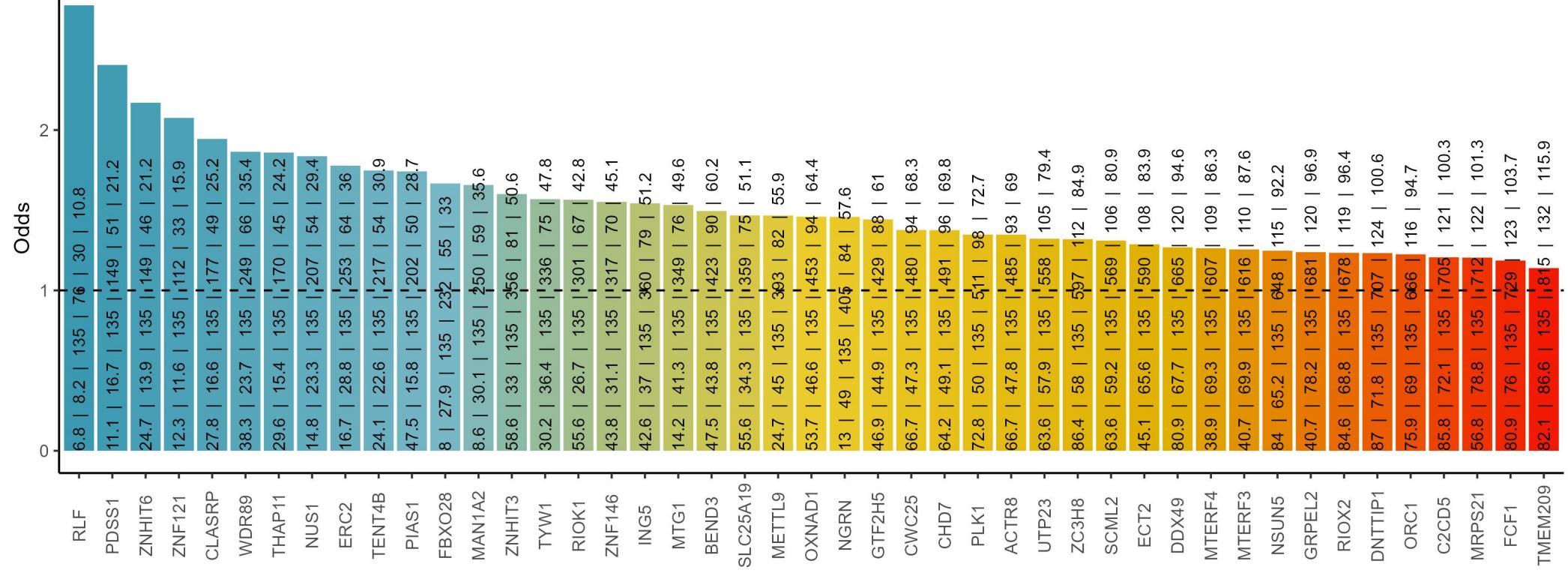
% of ALKBH1 in blood cancers: 14.2 ; % of ALKBH1 in solid cancers: 14.2

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ALKBH1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

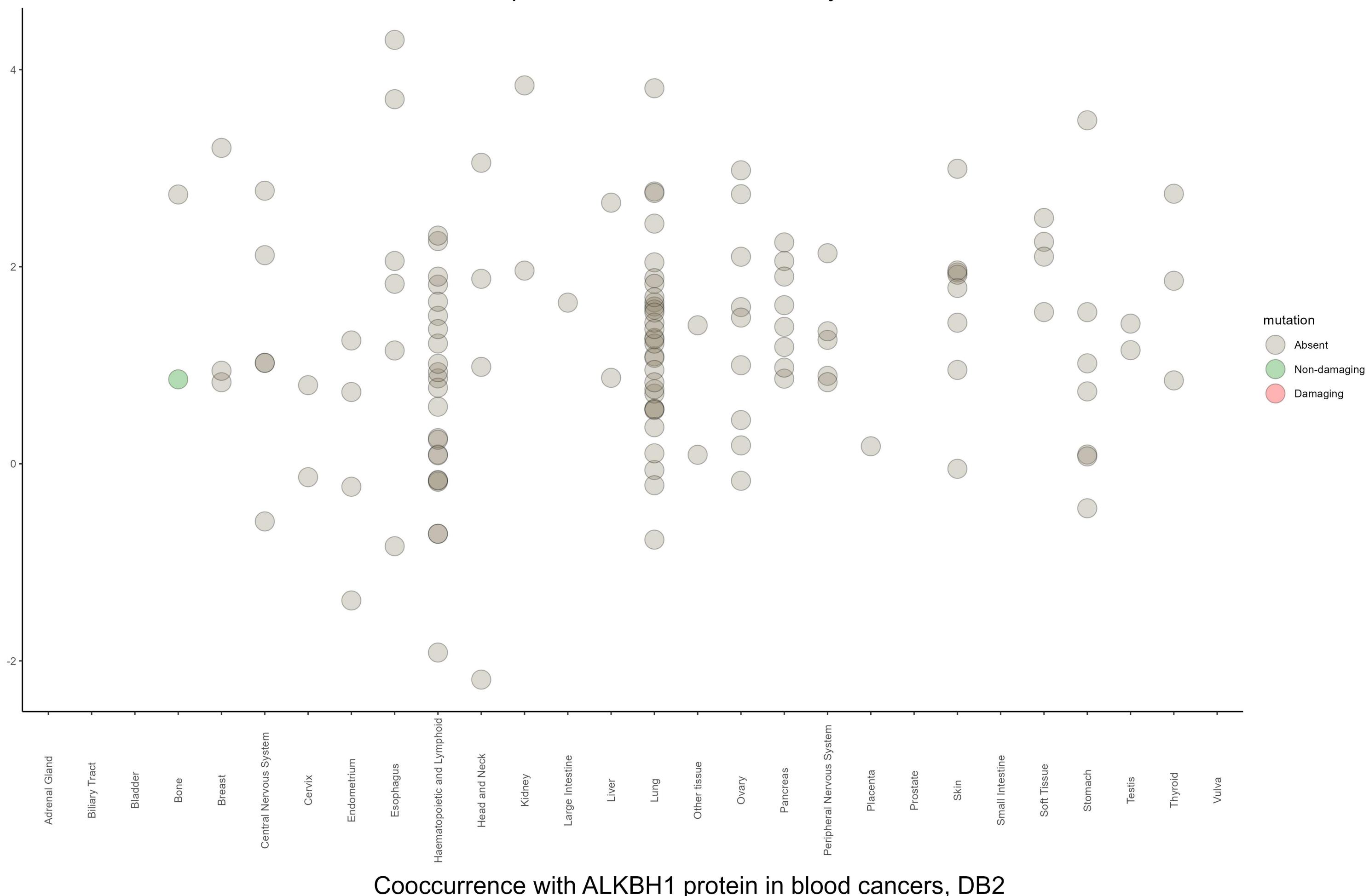
Negative cooccurrence



Positive cooccurrence

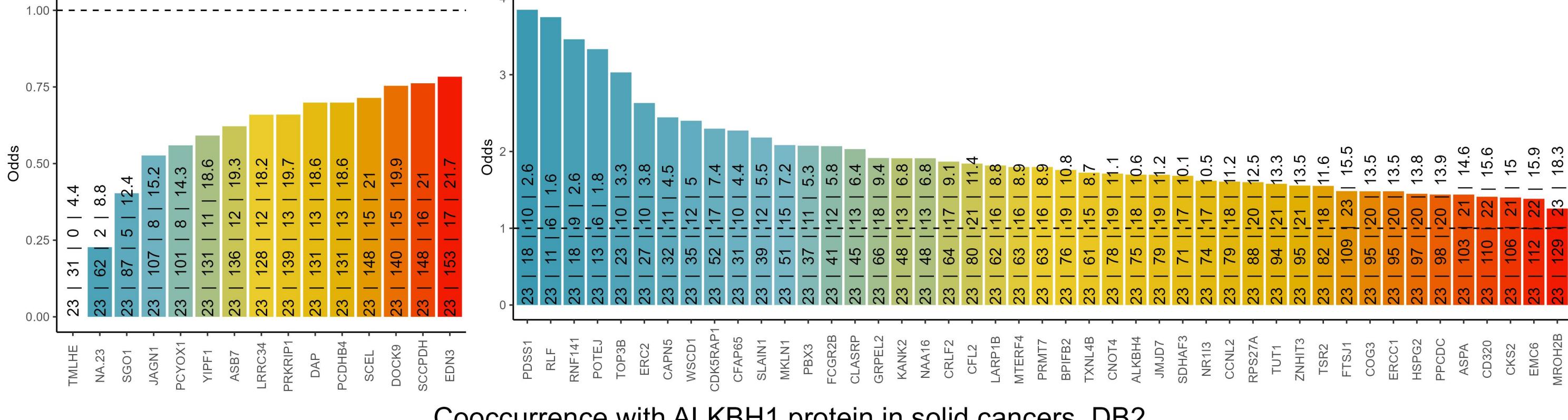


Amount of ALKBH1 protein and mutation status by tissue, DB2



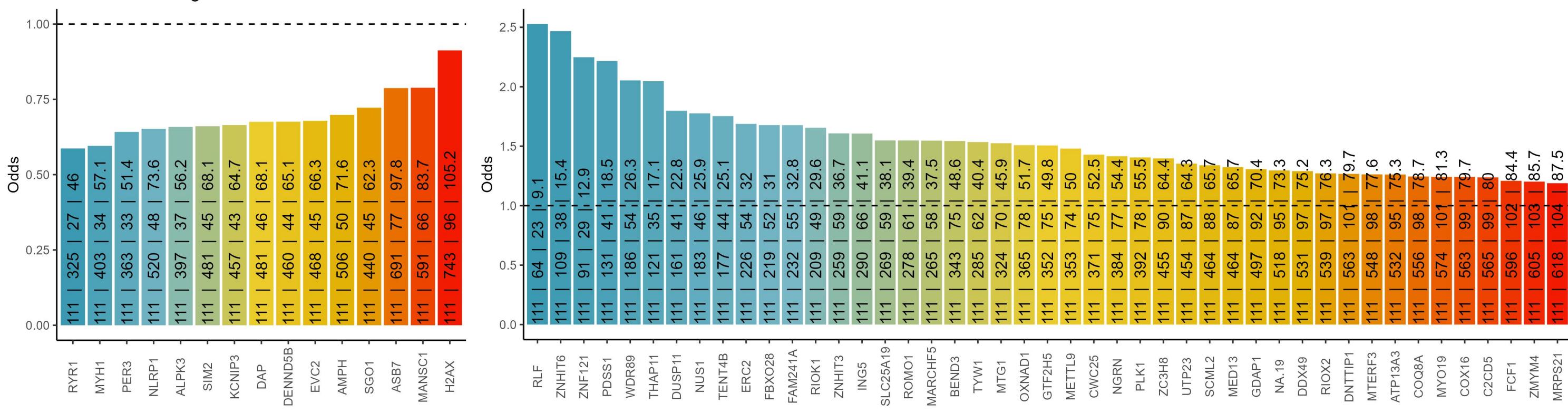
Cooccurrence with ALKBH1 protein in blood cancers, DB2

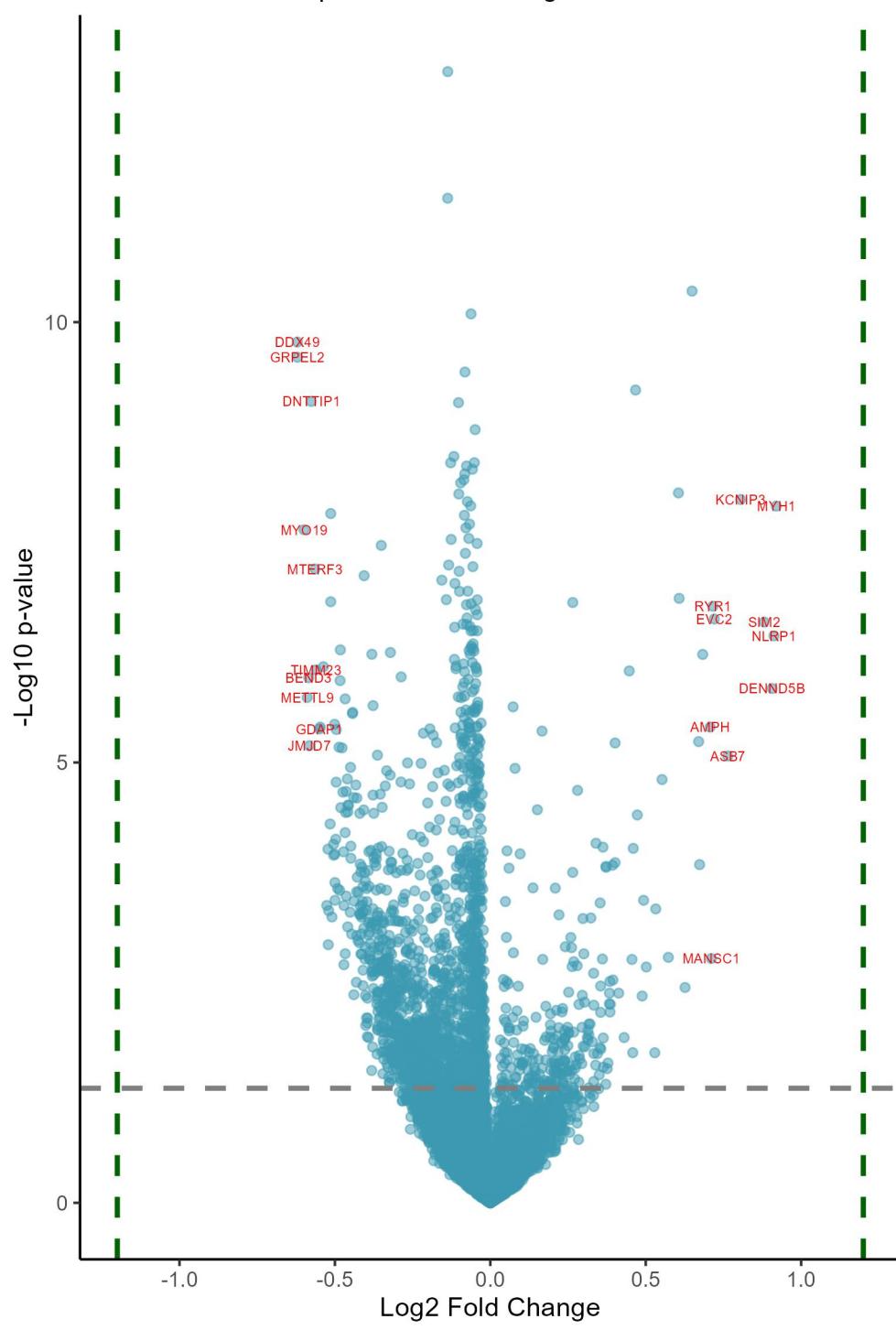
The text in the bars: incidence of ALKBH1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Cooccurrence with ALKBH1 protein in solid cancers, DB2

The text in the bars: incidence of ALKBH1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

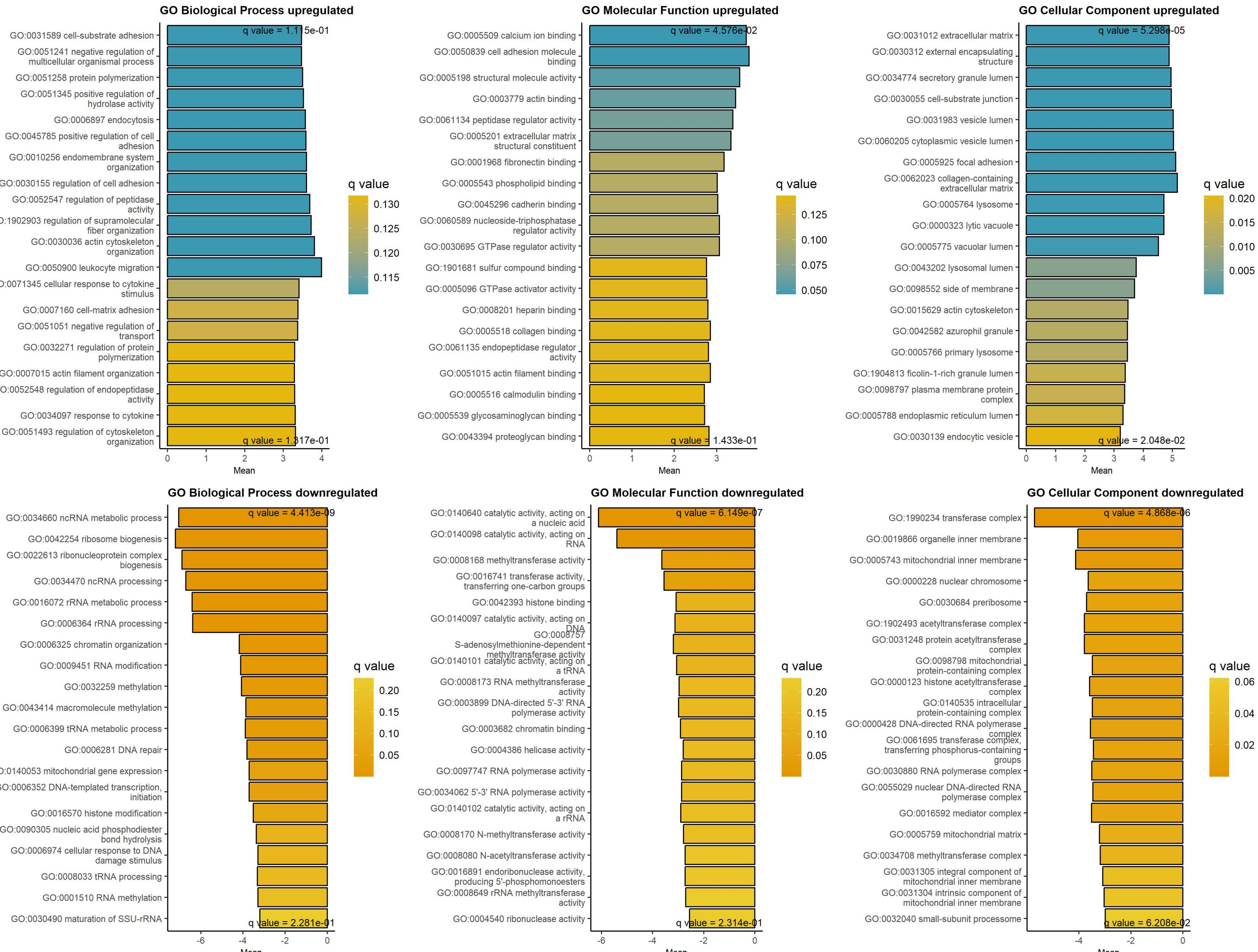




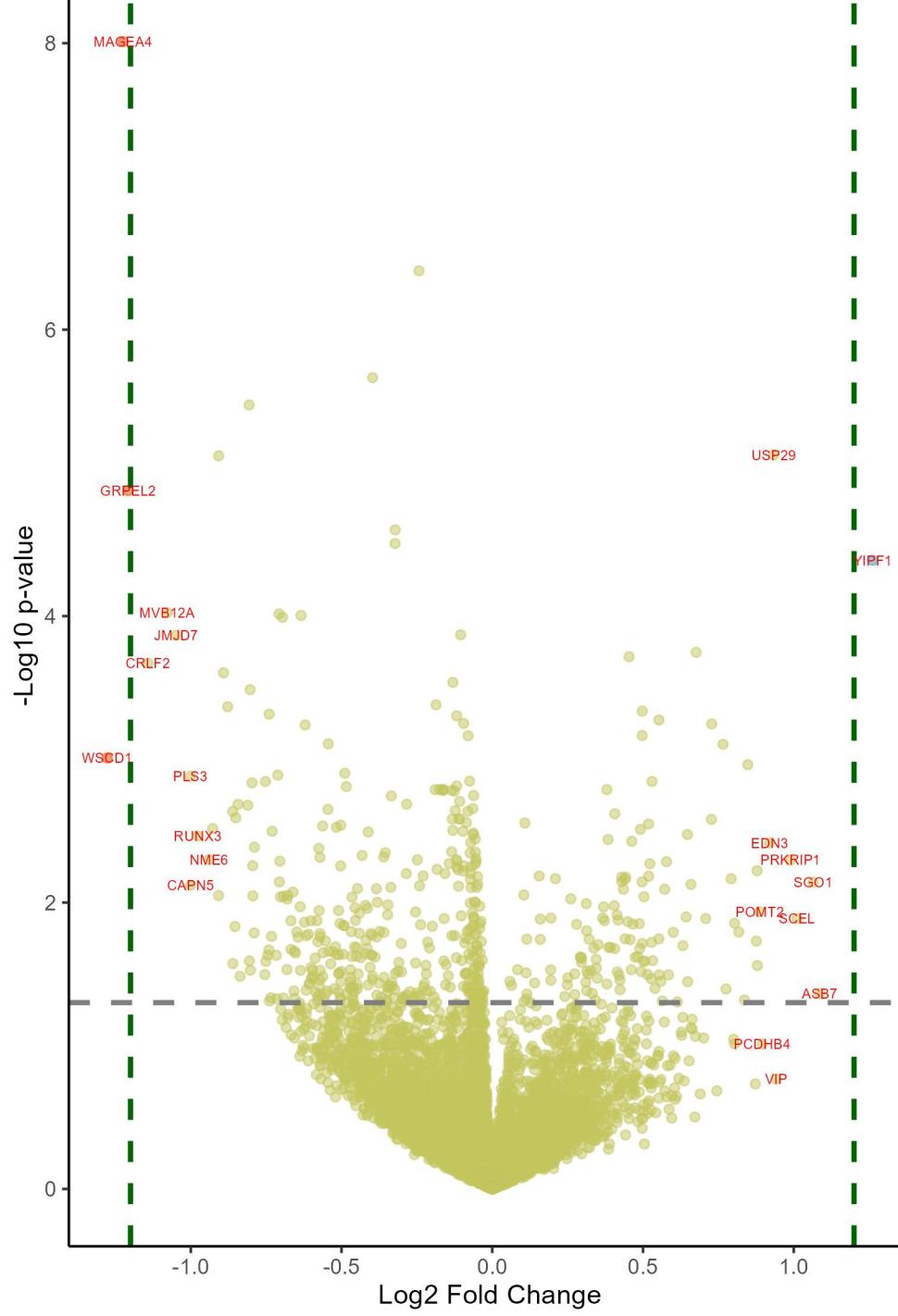
Downregulated at low/absent ALKBH1 Upregulated at low/absent ALKBH1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.62	2.34e-07	DDX49	DEAD-box helicase 49	0.92	3.94e-06	MYH1	myosin heavy chain 1
-0.62	3.00e-07	GRPEL2	GrpE like 2, mitochondrial	0.91	4.62e-05	NLRP1	NLR family pyrin domain containing
-0.6	6.15e-06	MYO19	myosin XIX	0.91	1.25e-04	DENND5B	DENN domain containing 5B
-0.59	1.49e-04	METTL9	methyltransferase like 9	0.88	3.67e-05	SIM2	SIM bHLH transcription factor 2
-0.58	1.00e-04	BEND3	BEN domain containing 3	0.8	3.75e-06	KCNIP3	potassium voltage-gated channel int
-0.58	3.51e-04	JMJD7	jumonji domain containing 7	0.76	4.30e-04	ASB7	ankyrin repeat and SOCS box contain
-0.58	6.24e-07	DNTTIP1	deoxyribonucleotidyltransferase termina	0.72	3.45e-05	EVC2	EvC ciliary complex subunit 2
-0.56	1.36e-05	MTERF3	mitochondrial transcription termina	0.72	2.66e-05	RYR1	ryanodine receptor 1
-0.56	8.64e-05	TIMM23	translocase of inner mitochondrial	0.71	2.28e-02	MANSC1	MANSC domain containing 1
-0.55	2.62e-04	GDAP1	ganglioside induced differentiation	0.71	2.59e-04	AMPH	amphiphysin
-0.55	2.59e-04	MTG1	mitochondrial ribosome associated G	0.68	6.44e-05	PER3	period circadian regulator 3
-0.54	8.26e-05	ZC3H8	zinc finger CCCH-type containing 8	0.67	3.78e-03	SGO1	shugoshin 1
-0.53	8.26e-03	MAST4	microtubule associated serine/threo	0.67	3.27e-04	LRRC34	leucine rich repeat containing 34
-0.52	2.92e-03	CDS1	CDP-diacylglycerol synthase 1	0.65	9.29e-08	DAP	death associated protein
-0.52	1.76e-02	SCGN	secretagogin, EF-hand calcium bindi	0.63	3.87e-02	TMEM70	transmembrane protein 70
-0.52	9.11e-03	CCSER1	coiled-coil serine rich protein 1	0.61	2.48e-05	YIPF1	Yip1 domain family member 1
-0.52	1.67e-03	SLC25A19	solute carrier family 25 member 19	0.61	3.40e-06	FGF11	fibroblast growth factor 11
-0.51	4.62e-06	FCF1	FCF1 rRNA-processing protein	0.57	2.24e-02	WRAP73	WD repeat containing, antisense to
-0.51	2.55e-05	SINHCAF	SIN3-HDAC complex associated factor	0.55	6.75e-04	PRKRIP1	PRKR interacting protein 1
-0.51	1.03e-02	DPYSL5	dihydropyrimidinase like 5	0.53	8.84e-03	PCDHB4	protocadherin beta 4
-0.5	2.67e-03	OGDHL	oxoglutarate dehydrogenase L	0.53	1.21e-01	IQCA1	IQ motif containing with AAA domain
-0.5	3.21e-03	ZBTB32	zinc finger and BTB domain containi	0.5	2.67e-02	ZNF296	zinc finger protein 296
-0.5	2.50e-04	GRAMD1C	GRAM domain containing 1C	0.49	7.53e-03	APBB1IP	amyloid beta precursor protein bind
-0.5	3.17e-03	ING5	inhibitor of growth family member 5	0.49	4.46e-02	ZC3H6	zinc finger CCCH-type containing 6
-0.5	5.29e-03	ROMO1	reactive oxygen species modulator 1	0.47	1.34e-03	SCEL	scillin
-0.5	7.53e-03	NLRP2	NLR family pyrin domain containing	0.47	5.49e-07	ALPK3	alpha kinase 3
-0.5	2.38e-03	DCAF16	DDB1 and CUL4 associated factor 16	0.46	2.87e-03	FBXO30	F-box protein 30
-0.5	7.07e-04	ATP13A3	ATPase 13A3	0.46	1.21e-01	KRT73	keratin 73
-0.5	2.63e-04	WDR89	WD repeat domain 89	0.46	2.29e-02	GPATCH3	G-patch domain containing 3

GAGE analysis on upregulated and downregulated proteins at low/absent ALKBH1 protein, DB2

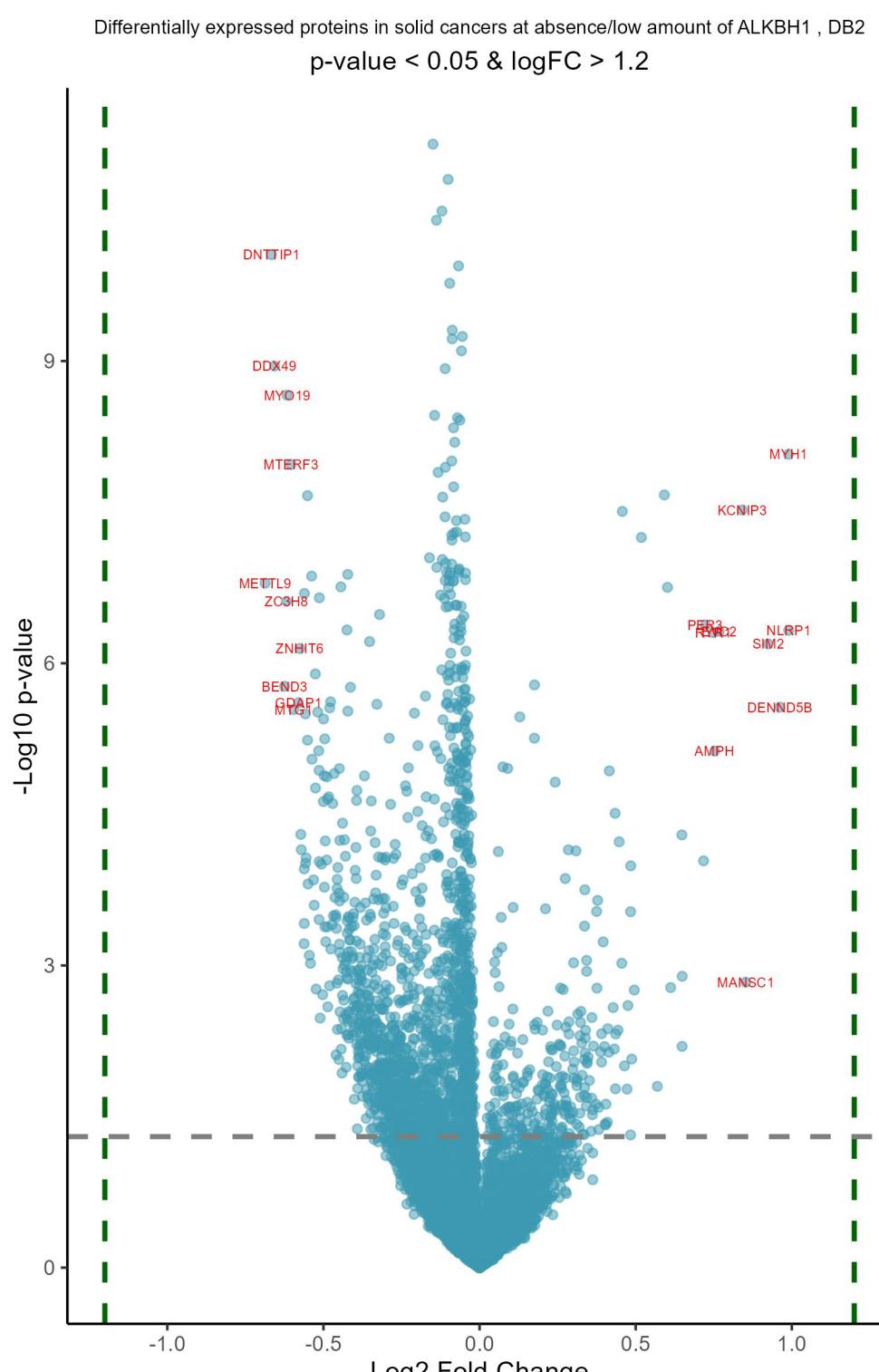


p-value < 0.05 & logFC > 1.2



Downregulated in blood cancers at low/absent ALKBH1 Upregulated in blood cancers at low/absent ALKBH1

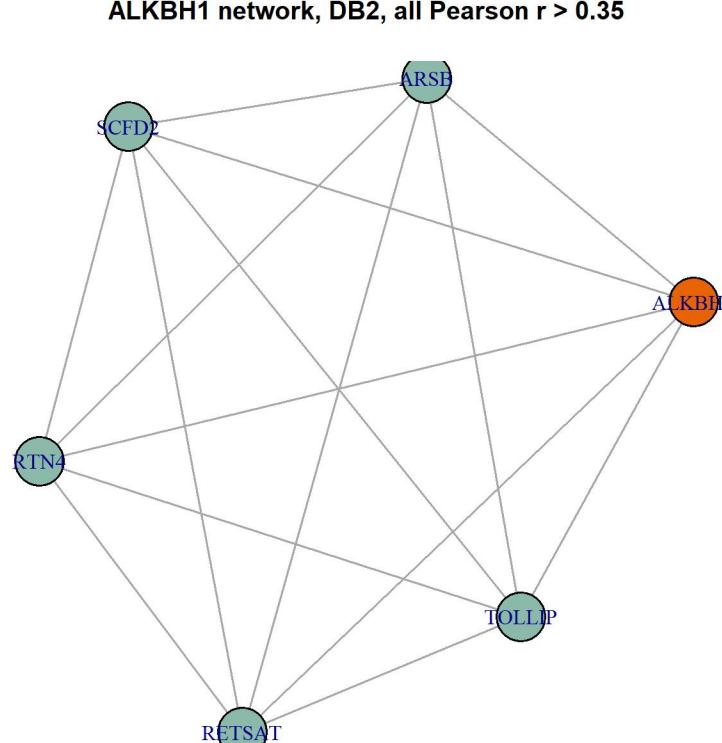
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.28	2.21e-01	WSCD1	WSC domain containing 1	1.26	3.10e-02	YIPF1	Yip1 domain family member 1
-1.22	4.07e-05	MAGEA4	MAGE family member A4	1.09	8.01e-01	ASB7	ankyrin repeat and SOCS box contain
-1.21	1.39e-02	GRPEL2	GrpE like 2, mitochondrial	1.06	4.31e-01	SGO1	shugoshin 1
-1.14	8.90e-02	CRLF2	cytokine receptor like factor 2	1.01	5.60e-01	SCEL	scillin
-1.08	5.68e-02	MVB12A	multivesicular body subunit 12A	0.99	3.92e-01	PRKRIP1	PRKR interacting protein 1
-1.05	6.68e-02	JMJD7	jumonji domain containing 7	0.94	9.50e-01	VIP	vasoactive intestinal peptide
-1	2.54e-01	PLS3	plastin 3	0.93	9.08e-03	USP29	ubiquitin specific peptidase 29
-1	4.43e-01	CAPN5	calpain 5	0.92	3.44e-01	EDN3	endothelin 3
-0.98	3.26e-01	RUNX3	RUNX family transcription factor 3	0.9	9.22e-01	PCDHB4	protocadherin beta 4
-0.94	3.92e-01	NME6	NME/NM23 nucleoside diphosphate kin	0.89	5.41e-01	POMT2	protein O-mannosyltransferase 2
-0.93	3.20e-01	TXNL4B	thioredoxin like 4B	0.88	7.08e-01	STK39	serine/threonine kinase 39
-0.91	4.76e-01	HLA-DRB3	major histocompatibility complex, c	0.88	4.11e-01	TNFAIP8L3	TNF alpha induced protein 8 like 3
-0.91	9.08e-03	CD151	CD151 molecule (Raph blood group)	0.88	6.17e-01	FBXO30	F-box protein 30
-0.89	9.92e-02	FANCD2	FA complementation group D2	0.87	9.50e-01	IQCA1	IQ motif containing with AAA domain
-0.88	1.44e-01	TUT1	terminal uridylyl transferase 1, U6	0.85	2.40e-01	DAP	death associated protein
-0.86	2.93e-01	BPIFB2	BPI fold containing family B member	0.84	8.18e-01	LRRC34	leucine rich repeat containing 34
-0.86	6.97e-01	FCGR2B	Fc gamma receptor IIb	0.82	5.99e-01	ZNF296	zinc finger protein 296
-0.85	5.71e-01	NQO2	N-ribosylhydronicotinamide:quinon	0.8	5.67e-01	ITGA3	integrin subunit alpha 3
-0.85	3.05e-01	DOK1	docking protein 1	0.8	9.22e-01	ALMS1	ALMS1 centrosome and basal body ass
-0.84	2.87e-01	ANKS1B	ankyrin repeat and sterile alpha mo	0.8	9.22e-01	ASS1	argininosuccinate synthase 1
-0.84	7.44e-01	FCGBP	Fc gamma binding protein	0.79	4.24e-01	ZNF101	zinc finger protein 101
-0.81	2.87e-01	ITGA6	integrin subunit alpha 6	0.78	7.92e-01	MTCH1	mitochondrial carrier 1
-0.81	5.61e-03	MINPP1	multiple inositol-polyphosphate pho	0.77	1.82e-01	JAGN1	jagunal homolog 1
-0.81	6.84e-01	PBX3	PBX homeobox 3	0.74	9.50e-01	H1-0	H1.0 linker histone
-0.8	1.19e-01	CD320	CD320 molecule	0.73	1.50e-01	PTPN18	protein tyrosine phosphatase non-re
-0.8	7.30e-01	COLGALT2	collagen beta(1-O)galactosyltransfe	0.73	3.05e-01	SERPINB8	serpin family B member 8
-0.8	2.54e-01	TARBP2	TARBP2 subunit of RISC loading comp	0.71	5.60e-01	MSRB2	methionine sulfoxide reductase B2
-0.79	3.97e-01	TSR2	TSR2 ribosome maturation factor	0.7	9.22e-01	IAH1	isoamyl acetate hydrolyzing esteras
-0.79	4.76e-01	PEX3	peroxisomal biogenesis factor 3	0.69	9.50e-01	CSPG4	chondroitin sulfate proteoglycan 4



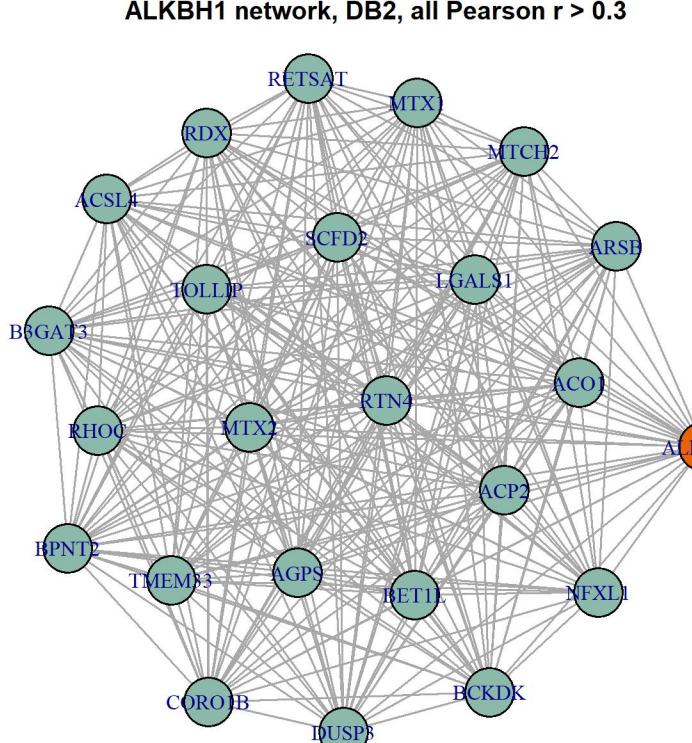
Downregulated in solid cancers at low/absent ALKBH1 Upregulated in solid cancers at low/absent ALKBH1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.69	2.24e-05	METTL9	methyltransferase like 9	0.99	4.74e-05	NLRP1	NLR family pyrin domain containing
-0.67	1.22e-07	DNNTIP1	deoxyribonucleotidyltransferase termina	0.99	3.35e-06	MYH1	myosin heavy chain 1
-0.66	7.11e-07	DDX49	DEAD-box helicase 49	0.96	1.78e-04	DENND5B	DENN domain containing 5B
-0.62	1.30e-04	BEND3	BEN domain containing 3	0.92	5.91e-05	SIM2	SIM bHLH transcription factor 2
-0.62	2.95e-05	ZC3H8	zinc finger CCCH-type containing 8	0.85	2.09e-02	MANSC1	MANSC domain containing 1
-0.62	1.22e-06	MYO19	myosin XIX	0.84	8.39e-06	KCNIP3	potassium voltage-gated channel int
-0.6	3.86e-06	MTERF3	mitochondrial transcription termina	0.77	4.75e-05	EVC2	EvC ciliary complex subunit 2
-0.6	1.83e-04	MTG1	mitochondrial ribosome associated G	0.75	3.79e-04	AMPH	amphiphysin
-0.58	1.67e-04	GDAP1	ganglioside induced differentiation	0.75	4.82e-05	RYR1	ryanodine receptor 1
-0.58	6.49e-05	ZNHIT6	zinc finger HIT-type containing 6	0.72	4.41e-05	PER3	period circadian regulator 3
-0.57	1.65e-03	ZBTB32	zinc finger and BTB domain containi	0.72	2.57e-03	ASB7	ankyrin repeat and SOCS box contain
-0.57	2.16e-03	CDKL5	cyclin dependent kinase like 5	0.65	1.90e-02	WRAP73	WD repeat containing, antisense to
-0.56	1.11e-02	CCSER1	coiled-coil serine rich protein 1	0.65	5.62e-02	TMEM70	transmembrane protein 70
-0.56	3.00e-03	ROMO1	reactive oxygen species modulator 1	0.65	1.66e-03	LRRC34	leucine rich repeat containing 34
-0.56	7.90e-03	DPYSL5	dihydropyrimidinase like 5	0.61	2.26e-02	SGO1	shugoshin 1
-0.56	2.65e-05	SINHCAF	SIN3-HDAC complex associated factor	0.6	2.36e-05	FGF11	fibroblast growth factor 11
-0.56	1.94e-04	TIMM23	translocase of inner mitochondrial	0.59	6.46e-06	DAP	death associated protein
-0.56	2.67e-03	SLC25A19	solute carrier family 25 member 19	0.57	1.03e-01	KRT73	keratin 73
-0.56	2.46e-03	ING5	inhibitor of growth family member 5	0.52	1.21e-05	CALHM2	calcium homeostasis modulator famil
-0.55	3.11e-04	INTS2	integrator complex subunit 2	0.5	2.35e-02	GPATCH3	G-patch domain containing 3
-0.55	6.46e-06	FCF1	FCF1 rRNA-processing protein	0.49	6.85e-02	ZC3H6	zinc finger CCCH-type containing 6
-0.55	3.96e-03	CDS1	CDP-diacylglycerol synthase 1	0.48	2.82e-03	YIPF1	Yip1 domain family member 1
-0.55	1.35e-02	MAST4	microtubule associated serine/threo	0.48	6.40e-03	APBB1IP	amyloid beta precursor protein bind
-0.54	1.52e-02	UVRAG	UV radiation resistance associated	0.48	2.07e-01	IQCA1	IQ motif containing with AAA domain
-0.54	2.11e-05	INTS5	integrator complex subunit 5	0.48	3.01e-02	PCDHB4	protocadherin beta 4
-0.54	4.34e-04	UTP23	UTP23 small subunit processome comp	0.47	1.06e-01	ITGB6	integrin subunit beta 6
-0.53	3.67e-03	DCAF16	DDB1 and CUL4 associated factor 16	0.46	7.61e-02	ZNF296	zinc finger protein 296
-0.53	5.74e-03	ORC6	origin recognition complex subunit	0.46	8.39e-06	ALPK3	alpha kinase 3
-0.53	1.04e-04	C2CD5	C2 calcium dependent domain contain	0.46	1.52e-02	PRKRIP1	PRKR interacting protein 1

ALKBH1 network, DB2, all Pearson r > 0.35

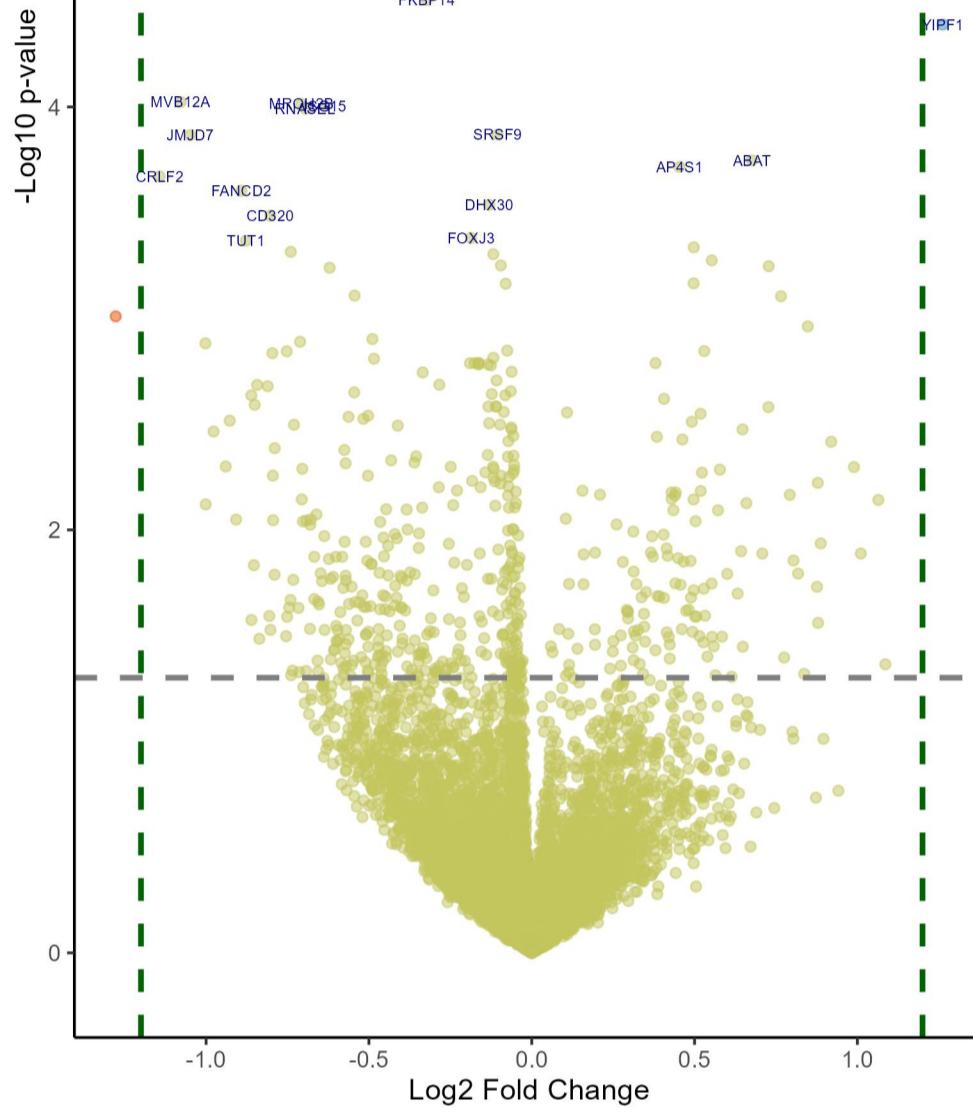


ALKBH1 network, DB2, all Pearson r > 0.3



Sorted by p values!

Downregulated in blood cancers at low/absent ALKBH1 Upregulated in blood cancers at low/absent ALKBH1

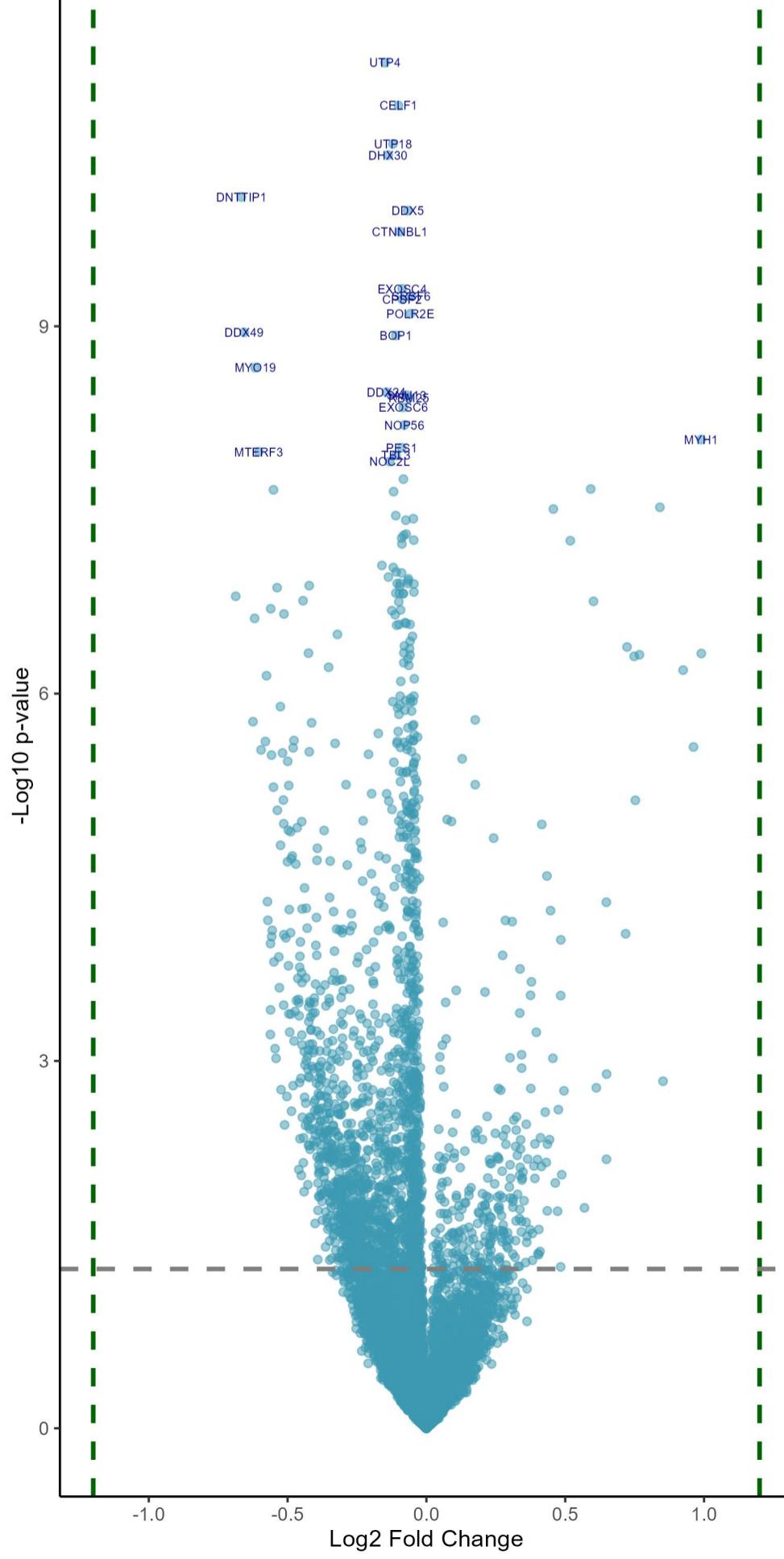


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.22	4.07e-05	MAGEA4	MAGE family member A4	0.93	9.08e-03	USP29	ubiquitin specific peptidase 29
-0.24	1.08e-03	TANGO6	transport and golgi organization 6	1.26	3.10e-02	YIPF1	Yip1 domain family member 1
-0.4	4.52e-03	PDZK1IP1	PDZK1 interacting protein 1	0.68	8.31e-02	ABAT	4-aminobutyrate aminotransferase
-0.81	5.61e-03	MINPP1	multiple inositol-polyphosphate pho	0.45	8.46e-02	AP4S1	adaptor related protein complex 4 s
-0.91	9.08e-03	CD151	CD151 molecule (Raph blood group)	0.5	1.48e-01	MIS12	MIS12 kinetochore complex component
-1.21	1.39e-02	GRPEL2	GrpE like 2, mitochondrial	0.55	1.50e-01	MBD4	methyl-CpG binding domain 4, DNA gl
-0.32	2.32e-02	MAGEA9	MAGE family member A9	0.73	1.50e-01	PTPN18	protein tyrosine phosphatase non-re
-0.32	2.61e-02	FKBP14	FKBP prolyl isomerase 14	0.5	1.69e-01	THBS2	thrombospondin 2
-1.08	5.68e-02	MVB12A	multivesicular body subunit 12A	0.77	1.82e-01	JAGN1	jagunal homolog 1
-0.71	5.68e-02	MROH2B	maestro heat like repeat family mem	0.85	2.40e-01	DAP	death associated protein
-0.63	5.68e-02	ISG15	ISG15 ubiquitin like modifier	0.53	2.54e-01	IRS2	insulin receptor substrate 2
-0.7	5.68e-02	RNASEL	ribonuclease L	0.38	2.54e-01	SRSF2	serine and arginine rich splicing f
-0.1	6.68e-02	SRSF9	serine and arginine rich splicing f	0.41	3.00e-01	TMLHE	trimethyllysine hydroxylase, epsilo
-1.05	6.68e-02	JMD7	jumonji domain containing 7	0.73	3.05e-01	SERPINB8	serpin family B member 8
-1.14	8.90e-02	CRLF2	cytokine receptor like factor 2	0.11	3.15e-01	RBX1	ring-box 1
-0.89	9.92e-02	FANCD2	FA complementation group D2	0.52	3.15e-01	ALPK3	alpha kinase 3
-0.13	1.10e-01	DHX30	DEHx-box helicase 30	0.49	3.20e-01	ANKRD22	ankyrin repeat domain 22
-0.8	1.19e-01	CD320	CD320 molecule	0.65	3.22e-01	COL17A1	collagen type XVII alpha 1 chain
-0.19	1.44e-01	FOXJ3	forkhead box J3	0.38	3.37e-01	FNIP2	folliculin interacting protein 2
-0.88	1.44e-01	TUT1	terminal uridylyl transferase 1, U6	0.46	3.43e-01	GIMAP7	GTPase, IMAP family member 7
-0.74	1.48e-01	TUBB8	tubulin beta 8 class VIII	0.92	3.44e-01	EDN3	endothelin 3
-0.12	1.48e-01	EIF3M	eukaryotic translation initiation f	0.99	3.92e-01	PRKRIP1	PRKR interacting protein 1
-0.09	1.50e-01	CIAO1	cytosolic iron-sulfur assembly comp	0.58	3.92e-01	CRYAB	crystallin alpha B
-0.62	1.50e-01	SPRYD4	SPRY domain containing 4	0.52	3.96e-01	PLSCR3	phospholipid scramblase 3
-0.08	1.69e-01	NUDC	nuclear distribution C, dynein comp	0.88	4.11e-01	TNFAIP8L3	TNF alpha induced protein 8 like 3
-0.54	1.82e-01	DCAF16	DDB1 and CUL4 associated factor 16	0.16	4.22e-01	ME2	malic enzyme 2
-1.28	2.21e-01	WSCD1	WSC domain containing 1	0.52	4.22e-01	QSOX1	quiescin sulfhydryl oxidase 1
-0.49	2.54e-01	EI24	EI24 autophagy associated transmemb	0.43	4.22e-01	CDH1	cadherin 1
-0.71	2.54e-01	TJP2	tight junction protein 2	0.44	4.22e-01	CAMSAP3	calmodulin regulated spectrin assoc
-1	2.54e-01	PLS3	plastin 3	0.21	4.24e-01	CLTB	clathrin light chain B
-0.08	2.54e-01	CLPX	caseinolytic mitochondrial matrix p	0.79	4.24e-01	ZNF101	zinc finger protein 101
-0.75	2.54e-01	FTSJ1	FtsJ RNA 2'-O-methyltransferase 1	0.44	4.24e-01	KRT80	keratin 80
-0.8	2.54e-01	TARBP2	TARBP2 subunit of RISC loading comp	0.43	4.31e-01	RPP40	ribonuclease P/MRP subunit p40
-0.12	2.54e-01	HSPBP1	HSPA (Hsp70) binding protein 1	0.5	4.31e-01	KYAT1	kynurenine aminotransferase 1
-0.48	2.54e-01	INPP5F	inositol polyphosphate-5-phosphatas	1.06	4.31e-01	SGO1	shugoshin 1
-0.18	2.54e-01	LRRC4B	leucine rich repeat containing 4B	0.66	4.41e-01	FGF11	fibroblast growth factor 11
-0.16	2.54e-01	MLIP	muscular LMNA interacting protein	0.43	4.44e-01	AGO4	argonaute RISC component 4
-0.16	2.54e-01	FAM151A	family with sequence similarity 151	0.57	4.44e-01	CDC26	cell division cycle 26
0.19	2.54e-01	OTY2	orthodontic homeobox ?	0.1	4.76e-01	PTMA	prothymosin alba

Differentially expressed proteins in solid cancers at absence/low amount of ALKBH1 , DB2
p-value < 0.05 & logFC > 1.2

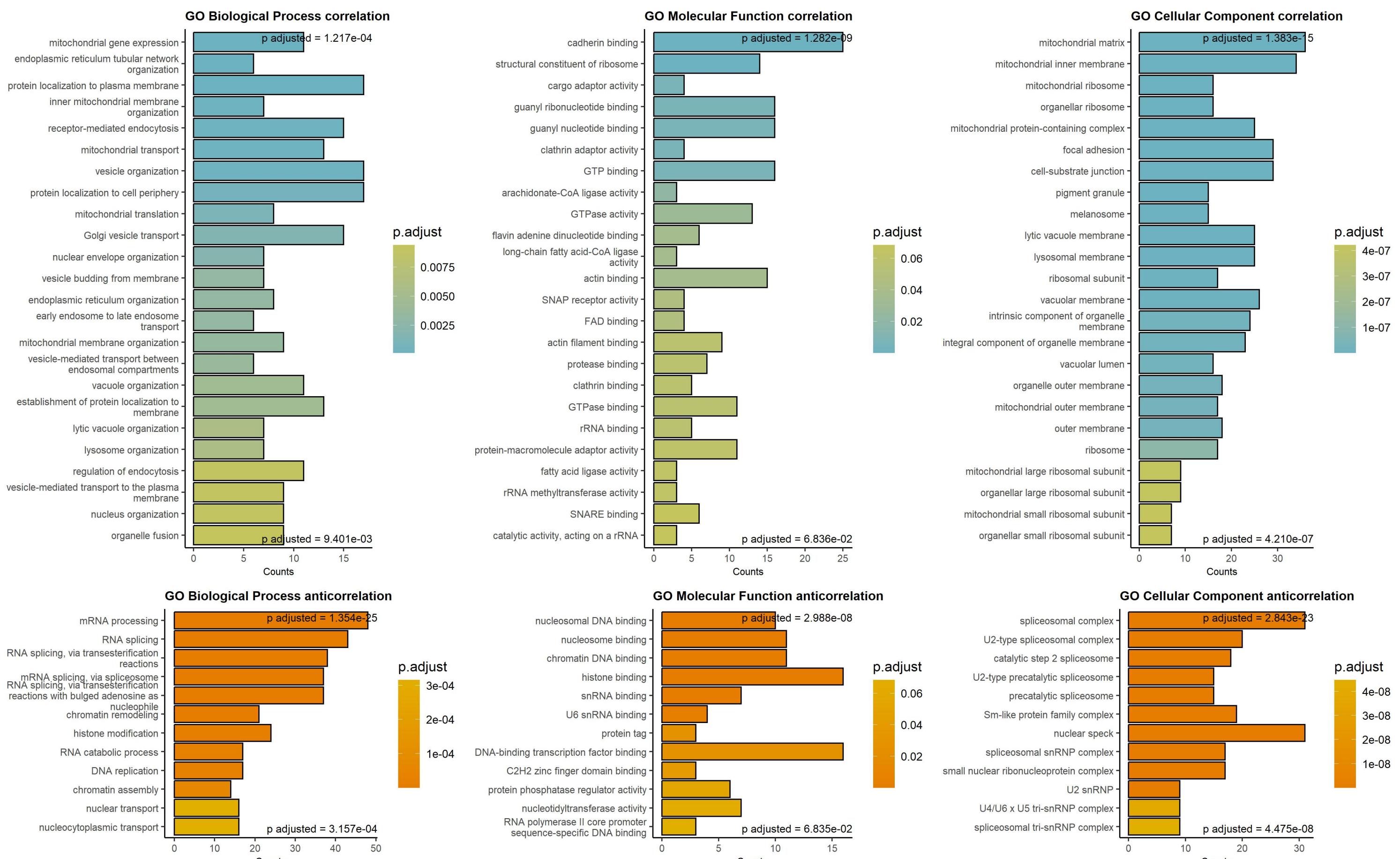
Sorted by p values!

Downregulated in solid cancers at low/absent ALKBH1 Upregulated in solid cancers at low/absent ALKBH1

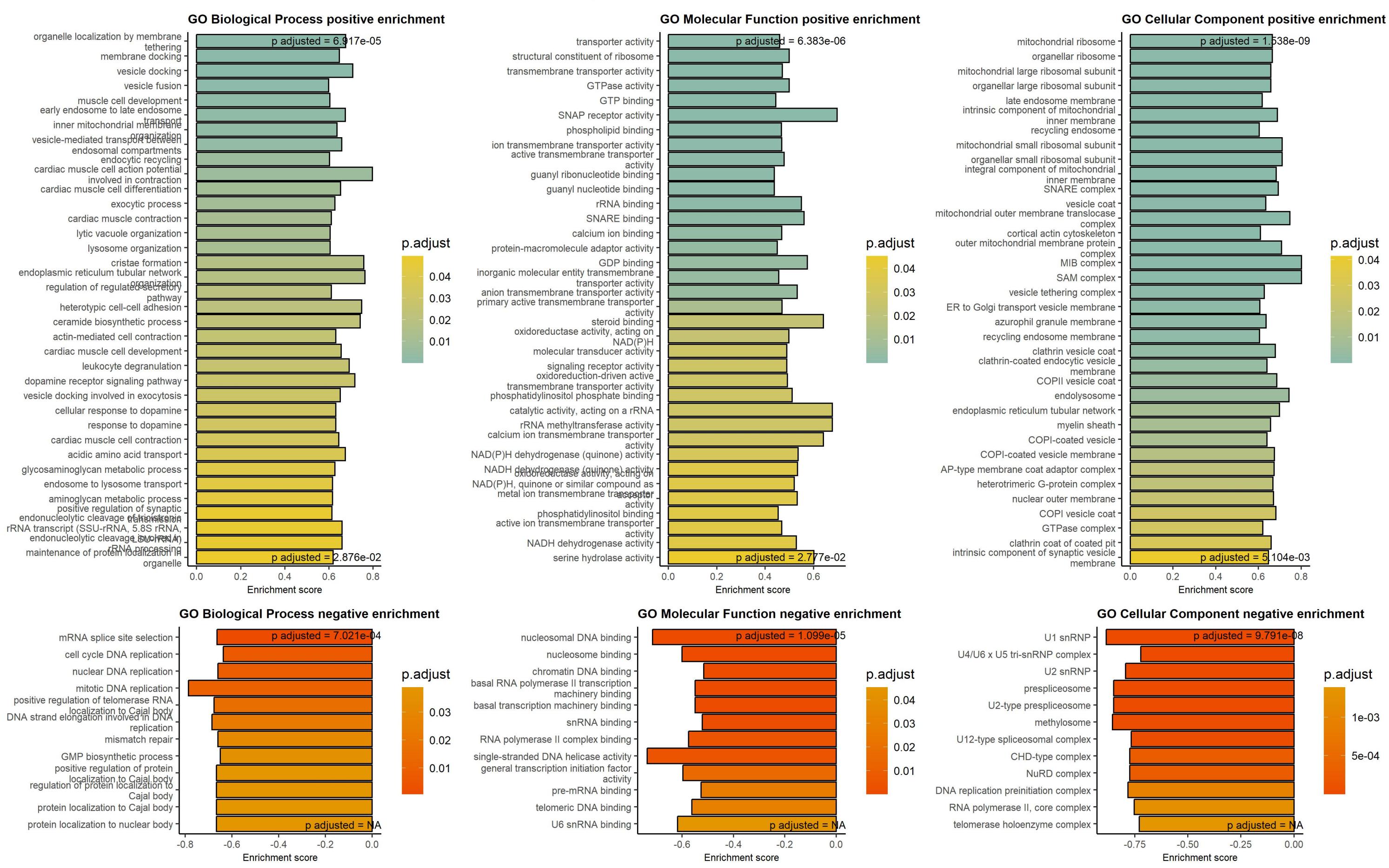


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.15	2.94e-08	UTP4	UTP4 small subunit processome compo	0.99	3.35e-06	MYH1	myosin heavy chain 1
-0.1	4.39e-08	CELF1	CUGBP Elav-like family member 1	0.59	6.46e-06	DAP	death associated protein
-0.12	6.69e-08	UTP18	UTP18 small subunit processome comp	0.84	8.39e-06	KCNIP3	potassium voltage-gated channel int
-0.14	6.69e-08	DHX30	DEHx-box helicase 30	0.46	8.39e-06	ALPK3	alpha kinase 3
-0.67	1.22e-07	DNTTIP1	dexoxynucleotidyltransferase termina	0.52	1.21e-05	CALHM2	calcium homeostasis modulator famil
-0.07	1.36e-07	DDX5	DEAD-box helicase 5	0.6	2.36e-05	FGF11	fibroblast growth factor 11
-0.1	1.77e-07	CTNNBL1	catenin beta like 1	0.72	4.41e-05	PER3	period circadian regulator 3
-0.09	4.58e-07	EXOSC4	exosome component 4	0.99	4.74e-05	NLRP1	NLR family pyrin domain containing
-0.06	4.58e-07	SRSF6	serine and arginine rich splicing f	0.77	4.75e-05	EVC2	EvC ciliary complex subunit 2
-0.09	4.58e-07	CPSF2	cleavage and polyadenylation specif	0.75	4.82e-05	RYR1	ryanodine receptor 1
-0.06	5.51e-07	POLR2E	RNA polymerase II, I and III subuni	0.92	5.91e-05	SIM2	SIM bHLH transcription factor 2
-0.66	7.11e-07	DDX49	DEAD-box helicase 49	0.18	1.27e-04	SETX	senataxin
-0.11	7.11e-07	BOP1	BOP1 ribosomal biogenesis factor	0.96	1.78e-04	DENND5B	DENN domain containing 5B
-0.62	1.22e-06	MYO19	myosin XIX	0.13	2.05e-04	TNKS1BP1	tankyrase 1 binding protein 1
-0.14	1.80e-06	DDX24	DEAD-box helicase 24	0.18	3.01e-04	TOM1	target of myb1 membrane trafficking
-0.07	1.80e-06	SNU13	small nuclear ribonucleoprotein 13	0.75	3.79e-04	AMPH	amphiphysin
-0.06	1.80e-06	RBM25	RNA binding motif protein 25	0.07	4.91e-04	CLIP1	CAP-Gly domain containing linker pr
-0.08	2.02e-06	EXOSC6	exosome component 6	0.09	4.99e-04	MYL6	myosin light chain 6
-0.08	2.68e-06	NOP56	NOP56 ribonucleoprotein	0.42	5.15e-04	PLXDC2	plexin domain containing 2
-0.09	3.73e-06	PES1	pescadillo ribosomal biogenesis fac	0.24	6.21e-04	SRSF2	serine and arginine rich splicing f
-0.6	3.86e-06	MTERF3	mitochondrial transcription termina	0.43	1.10e-03	THSD7A	thrombospondin type 1 domain contai
-0.11	3.95e-06	TBL3	transducin beta like 3	0.65	1.66e-03	LRRC34	leucine rich repeat containing 34
-0.13	4.26e-06	NOC2L	NOC2 like nucleolar associated tran	0.45	1.87e-03	DNAJB2	DnaJ heat shock protein family (Hsp
-0.08	5.70e-06	TIAL1	TIA1 cytotoxic granule associated R	0.28	2.16e-03	WDR27	WD repeat domain 27
-0.55	6.46e-06	FCF1	FCF1 rRNA-processing protein	0.31	2.20e-03	SPPL2A	signal peptide peptidase like 2A
-0.12	6.46e-06	DDX56	DEAD-box helicase 56	0.06	2.23e-03	TPM3	tropomyosin 3
-0.11	9.20e-06	RRP15	ribosomal RNA processing 15 homolog	0.72	2.57e-03	ASB7	ankyrin repeat and SOCS box contain
-0.05	9.43e-06	RUVBL2	RuvB like AAA ATPase 2	0.48	2.82e-03	YIPF1	Yip1 domain family member 1
-0.07	9.43e-06	NOP58	NOP58 ribonucleoprotein	0.27	3.61e-03	SYNC	syncolin, intermediate filament pr
-0.07	1.18e-05	CPSF3	cleavage and polyadenylation specif	0.34	4.37e-03	PDE4DIP	phosphodiesterase 4D interacting pr
-0.08	1.18e-05	RFC4	replication factor C subunit 4	0.38	5.25e-03	DCD	dermcidin
-0.09	1.21e-05	PPHLN1	periphilin 1	0.11	5.94e-03	MYH9	myosin heavy chain 9
-0							

Top 250 correlation coefficients overrepresentation, ALKBH1 protein, DB2



Gene Set Enrichment analysis on protein correlation coefficients, ALKBH1 protein, DB2



No information on Ser/Thr kinase phosphorylation sites for ALKBH1

No information on Ser/Thr kinase phosphorylation sites for ALKBH1

No sufficient number of paired observations in DB2 for ALKBH1