Supplemental Information

Title: An Integrated Transcriptomics and Proteomics Analysis Implicates lncRNA MALAT1 in the Regulation of Lipid Metabolism

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Supplemental table S1. The siRNA sequences used for MALAT1 knockdown.

MALAT1	siMALAT1-1	GAGGTGTAAAGGGATTTAT
	siMALAT1-2	CACAGGGAAAGCGAGTGGTTGGTAA

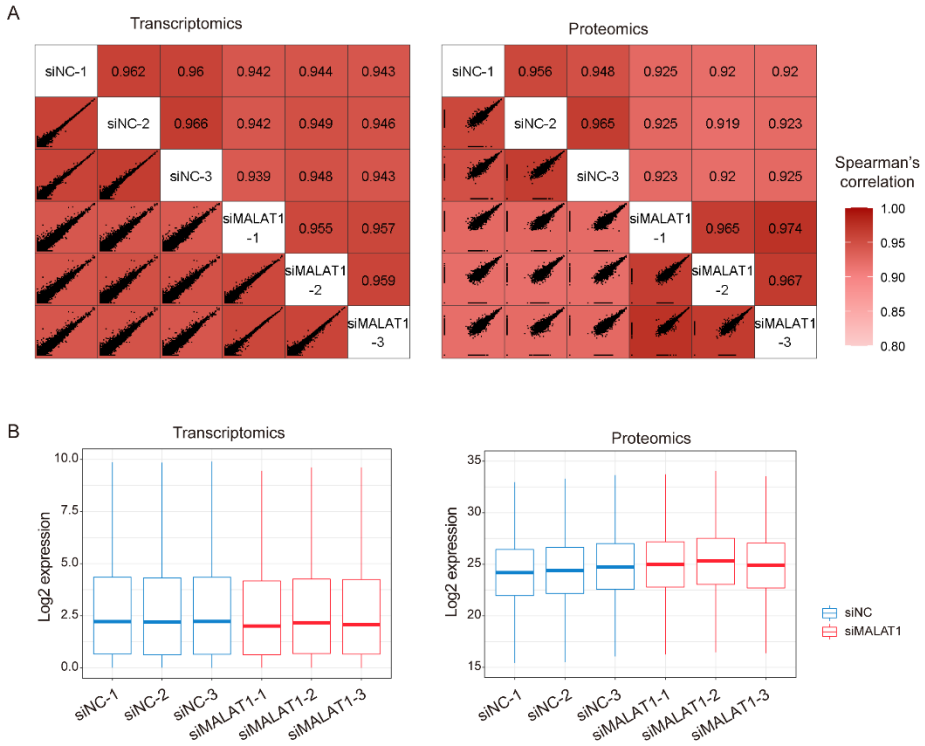
Supplemental table S2. List of the primer sequences used in the qRT-PCR experiments.

Primer name	**Sequence (5'–3')**
MALAT1 Forward	CTCCCCACAAGCAACTTCTC
MALAT1 Reverse	TTCAACCCACCAAAGACCTC
GAPDH Forward	TGCACCACCAACTGCTTAGC
GAPDH Reverse	GGCATGGACTGTGGTCATGAG
SCD Forward	TTCCCGACGTGGCTTTTTCT
SCD Reverse	AGCCAGGTTTGTAGTACCTCC
SREBF1 Forward	GTCTCAGTCCCCTGGTCTCT
SREBF1 Reverse	CCGGTTGATAGGCAGCTTCT
RAB14 Forward	ATTATTGGGGACATGGGAGTAGG
RAB14 Reverse	TAAATCGCTCCTGTCCTGCC
PRKAB1 Forward	GGGGGCGGAAAGGAAGTTTA
PRKAB1 Reverse	GCTGGTTACTATGGGCTCGG
PRKAG1 Forward	TCGCTGCTATGACCTGATTCC
PRKAG1 Reverse	GAGCCCTCAGCACCACAAAA
pre-SREBF1 Forward	TCTACAGGTAAGGGGGATGTGT
pre-SREBF1 Reverse	ACCTCTACTCACATCACAGCA
pre-SCD1 Forward	GCGTGATTAGAGAGCGGAGT
pre-SCD1 Reverse	GGTGGTGGTGGTATAGGAGC
pre-RAB14 Forward	ACCATGGCAACTGCACCATA
pre-RAB14 Reverse	CTCAGTCCTGAAGTGGTACTGT
pre-PRKAG1 Forward	AAAGGGATGGCGGGTTTCTG
pre-PRKAG1 Reverse	AACTGGAACTCACCTGGCAT
pre-PRKAB1 Forward	AACGGTGTTTCGATGGACGG
pre-PRKAB1 Reverse	ATATGTGAACACTCCCCAGGC

Supplemental table S3. List of the anti-sense probe sequences used for the isolation of MALAT1.

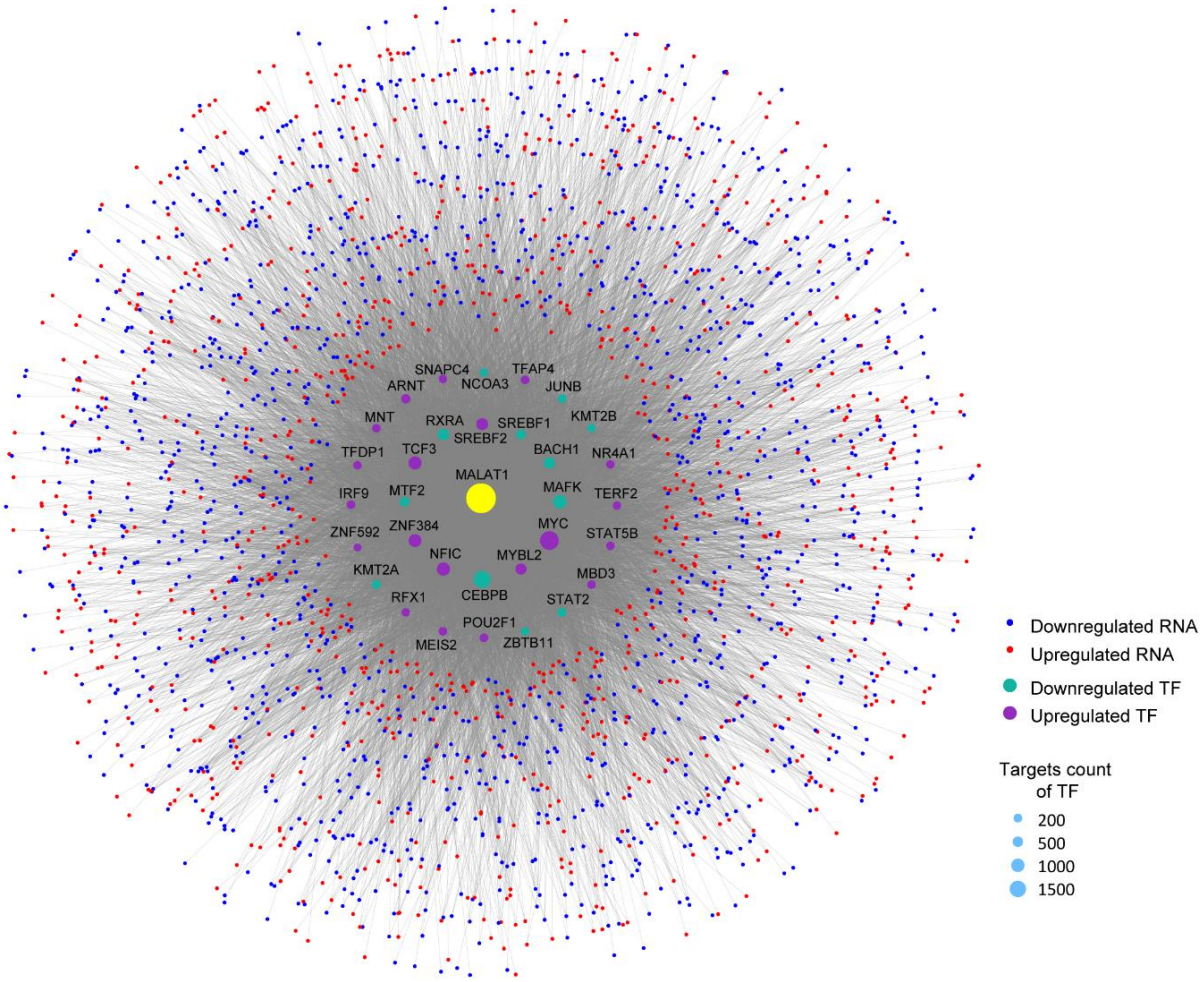
Probe name	**Sequence (5'–3')**
MALAT1-1	GCTTAAGAGGGCAGGAGAGGCCAGTTGCGGGGCCCCAGTCCTTTACAGAA
MALAT1-2	GTGTTCTCTTGAGGGACAGTAGGTATAGTTTACCACCTTTTGAAGGAAGA
MALAT1-3	ATCCTACCACTCCCAATTAATCTTTCCATTTTCGTCTGCGTTTAGTAAAT
MALAT1-4	CCTGGACTCTTTTCCTATCTTCACCACGAACTGCTGCTTGCTCGCTTGCT
MALAT1-5	GAGTAACTACCAGCCATTTCTCCAATGGACATCTCTTCCACAGACCTCAA
MALAT1-6	TCAGGATCATTAAGCCACTTCCTTTGCTCTGCAGTTTCTATAGTAGTTTT
MALAT1-7	ATTTAAGAACTCCACAGCTCTTAAAAATAAGCACTTATCCCTAACATGCA
MALAT1-8	ATGCAATTCAAAATCCTGAATGGCTTCATGAAGGATGAAATGCCTCTGCA
MALAT1-9	ATCTATTCAATACTATTGTCCCATAACTGATCTGACTTTGTATGTAAATA
MALAT1-10	TCAGCTTCCGCTAAGATGCTAGCTTGGCCAAGTCTGTTATGTTCACCTGA
LacZ-1	TTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATCCGTAATCATG
LacZ-2	AGTGGCAACATGGAAATCGCTGATTTGTGTAGTCGGTTTATGCAGCAACG
LacZ-3	AGTGCAGGAGCTCGTTATCGCTATGACGGAACAGGTATTCGCTGGTCACT

Supplemental Figure S1



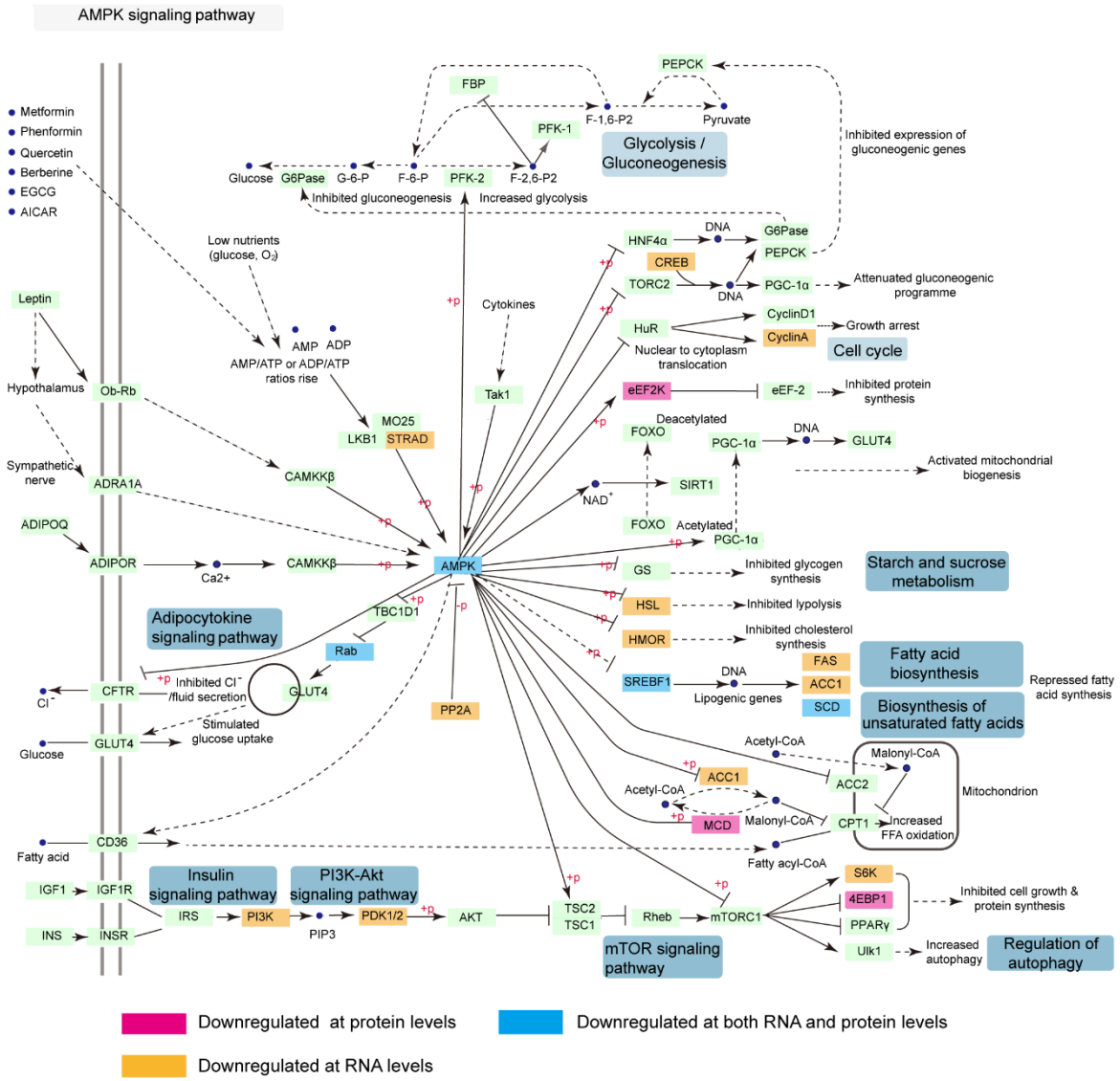
Supplemental Figure S1. Quality assessment of the transcriptome and proteome data. **A**, Scatter plots and Spearman's correlation coefficients of the transcriptome (left panel) and proteome (right panel) data. The top-right half of the panel represents the pairwise Spearman's correlation coefficients between samples, and the bottom-left half of the panel depicts the pairwise scatter plots from the same comparison. **B**, Boxplots showing the distribution of log2-transformed expression intensities from the transcriptome (left panel) and proteome data (right panel). In the box plots, the middle bars represent the median, and the boxes represent the interquartile range; bars extend to 1.5× the interquartile range.

Supplemental Figure S2



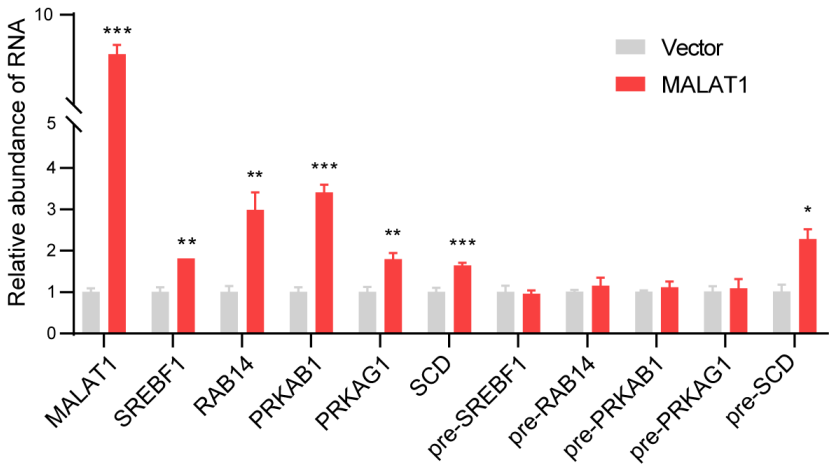
Supplemental Figure S2. The gene expression network potentially regulated by MALAT1. The regulatory information between TFs with altered expression and the target mRNAs was acquired from the ChEA3 ChIP-seq database (https://maayanlab.cloud/chea3/, ENCODE_ChIP-seq, Literature_ChIP-seq, ReMap_ChIP-seq). The node size of TFs in the network represent the numbers of its targets. The network was constructed by Cytoscape (version: 3.8.0).

Supplemental Figure S3



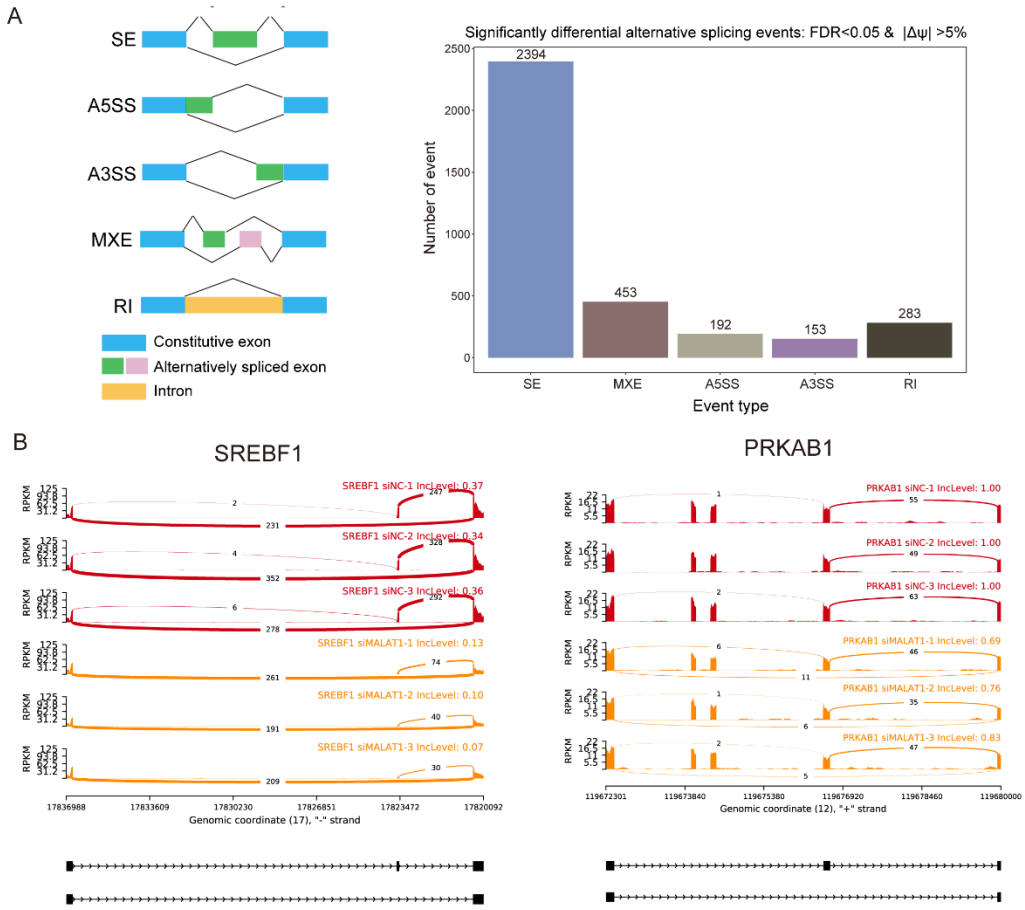
Supplemental Figure S3. The AMPK signaling pathway. Schematic diagram of the pathway was constructed from KEGG pathway database by using the KEGGscape (version: 0.9.0) application implemented in cytoscape (version: 3.8.1). Signaling molecules and enzymes with abundance changes at mRNA or protein levels induced by MALAT1 knockdown were indicated with different colors.

Supplemental Figure S4



Supplemental Figure S4. Overexpression of MALAT1 elevated the mRNA levels of genes in the AMPK signaling and lipid metabolism pathways. Relative quantification of the mRNAs and the corresponding pre-mRNAs was examined by qRT-PCR. Data represent mean ± s.d. of triplicate independent experiments (*$P < 0.05$, **$P < 0.01$, ***$P < 0.001$, by two-sided Student's *t*-test).

Supplemental Figure S5



Supplemental Figure S5. Differential analysis of alternative splicing using the transcriptomics data. **A**, bar plot showing the numbers of significantly changed alternative splicing events in siMALAT1 compared to siNC cells. rMATS was employed to analyze all major types of alternative splicing patterns, including: skipped exon (SE), mutually exclusive exons (MXE), alternative 5' splice site (A5SS), alternative 3' splice site (A3SS) and retained intron (RI). **B**, Sashimi plots showing the differential SE events of SREBF1 and PRKAB1.