Supplemental Material

Table S1. List of the primers for real-time qPCR assay used in this study.

miR-33a sense	GGCACTACTTCTGATCCTTC
miR-33a antisense (WT)	CAACTACAATGCACCACAGCTG
miR-33a antisense (KO)	TTGGGATCCAGAATTCGTGATTAA
miR-33b sense	GTACCCACTGGTAGAGCATATC
miR-33b antisense (WT)	CATCACTGAAGCACTGCATCTGC
miR-33b antisense (KI)	AAGTGGATCCAGAATTCGTGA

Table S2. List of the primers for mice genotyping used in this study.

	Sense	Antisense
Abca1	AACAGTTTGTGGCCCTTTTG	AGTTCCAGGCTGGGGTACTT
Abcg1	GATTGGGAATGAAGCCAAGA	CAGTAGGCCACAGGGAACAT
Abcg5	AAAACCTTACCCACGGTTCC	GTTACTCGCCTCAGCAGGAC
Abcg8	CCTGATCCGTCGTCAGATTT	CCATGGCCGTAGTAAAGGAA
Actb	GATCTGGCACCACACCTTCT	GGGGTGTTGAAGGTCTCAAA
ApoB	CTCCAAAGAGGCCAGTCAAG	GAGAGGCTTGCAAGTTGACC
ApoE	CAGAGCTCCCAAGTCACACA	CCCGTATCTCCTCTGTGCTC
CCR2	ATCTGCTCAACTTGGCCATC	CCCAAAGACCCACTCATTTG
Cpt1a	GATCTACAATTCCCCTCTGCTCT	TAGAGCCAGACCTTGAAGTAACG
Crot	TACTTTTACCACGGCCGAAC	GACGGTCAAATCCTTTTCCA
Cyp7a1	GAGCCCTGAAGCAATGAAAG	GCTGTCCGGATATTCAAGGA
F4/80	CCCAGCTTATGCCACCTGCA	GGAGCCATTCAAGACAAAGCC
Fasn	GGGTTCTAGCCAGCAGAGTCTA	TGAGATGTGGATACCACCAGAG
Hmgcr	CGTAACCCAAAGGGTCAAGA	GACCCAAGGAAACCTTAGCC
Hmgcs2	AGAAATCCCTGGCTCGGGTTG	AGCTTTAGACCCCTGAAGGC
Idol	CGAAGCATAAGGAGCTGGAG	CCTCACAGCATGCCACTCTA
IL-10	AAATAAGAGCAAGGCAGTGGAG	TCATTCATGGCCTTGTAGACAC
Il-1β	TCAGGCAGGCAGTATCACTCA	GGAAGGTCCACGGGAAAGAC
Il-6	ACCACGGCCTTCCCTACTTC	AGATTGTTTTCTGCAAGTGCATCA
Ldlr	ATTGGGTTGATTCCAAACTCC	ATTCACATCTGAACCCGTGAG
Lrp1	CTGAAGGCTCCCGAGTACCAG	GTAGGAGATTGTGCCCGTGT
MCP1	CTGGATCGGAACCAAATGAG	TGAGGTGGTTGTGGAAAAGG
Mvd	AAGCAGACGGGCAGTACAGT	CCTGGAGGTGTCATTGAGGT
Pcsk9	TCCATTGGGAAGTGGAAGAC	ACCTGCTCTGAAGGACCTGA
Scd1	GCGATACACTCTGGTGCTCA	CCCAGGGAAACCAGGATATT
Srebf1	TAGAGCATATCCCCCAGGTG	GGTACGGGCCACAAGAAGTA
Srebf2	GTGGAGCAGTCTCAACGTCA	TGGTAGGTCTCACCCAGGAG
TNFa	CCAGACCCTCACACTCAGATC	CACTTGGTGGTTTGCTACGAC

Figure S1. Liver miR transcriptome obtained from miR-33 KO mice and miR-33 WT mice.

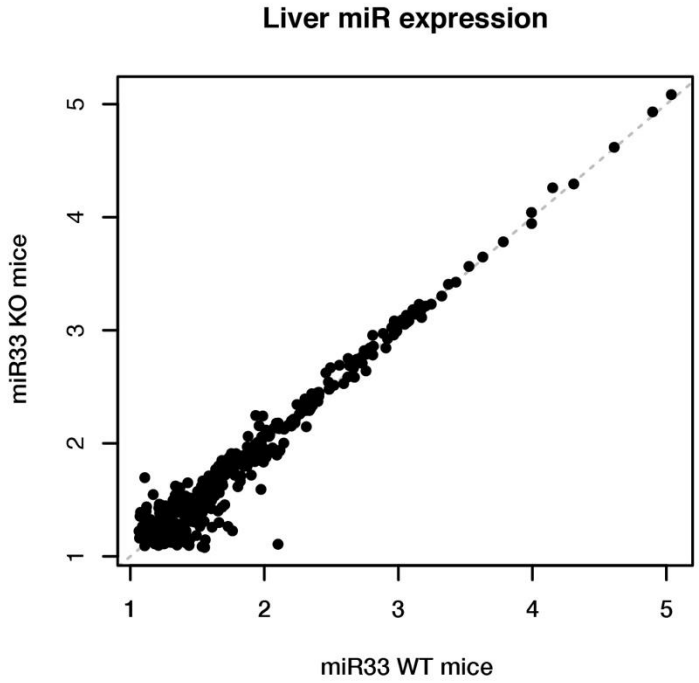
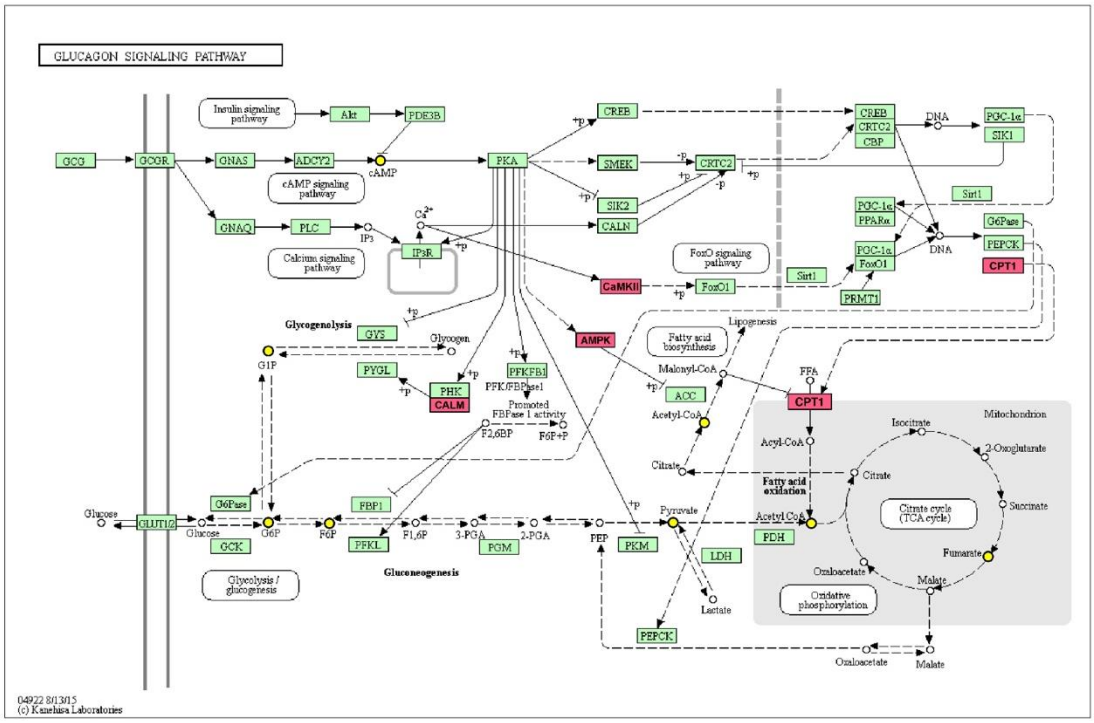
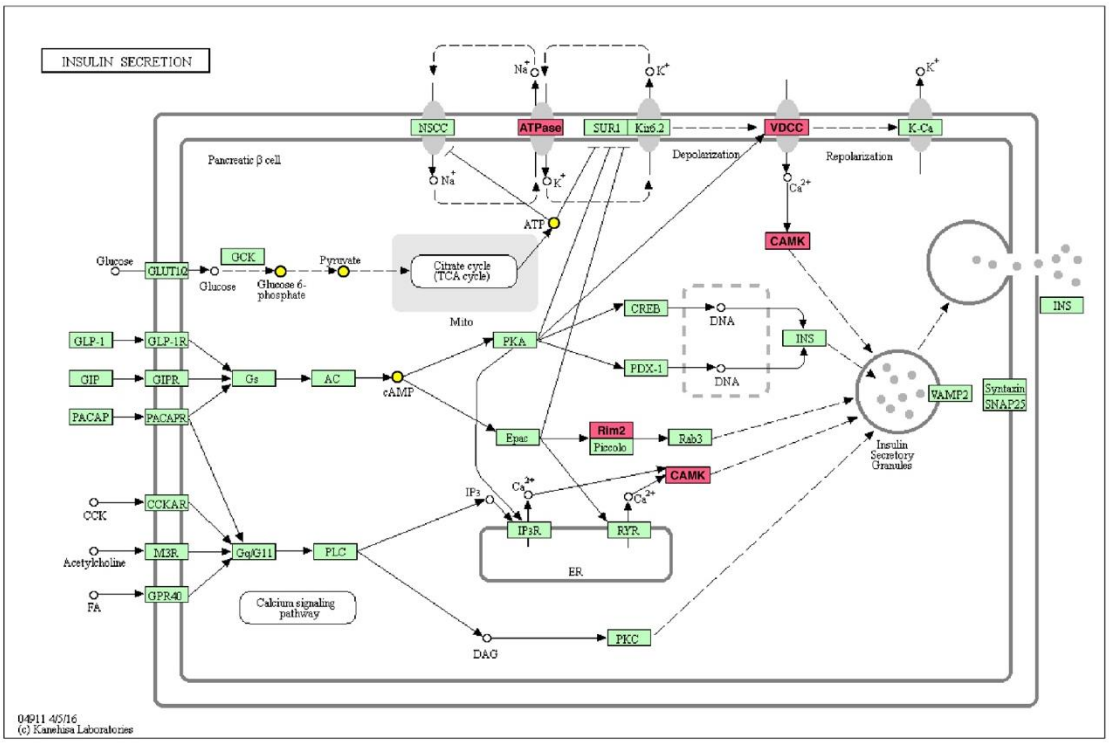


Figure S2. Dysregulated metabolite and miR-33 target genes on the KEGG pathways. (Glucagon signaling pathway).



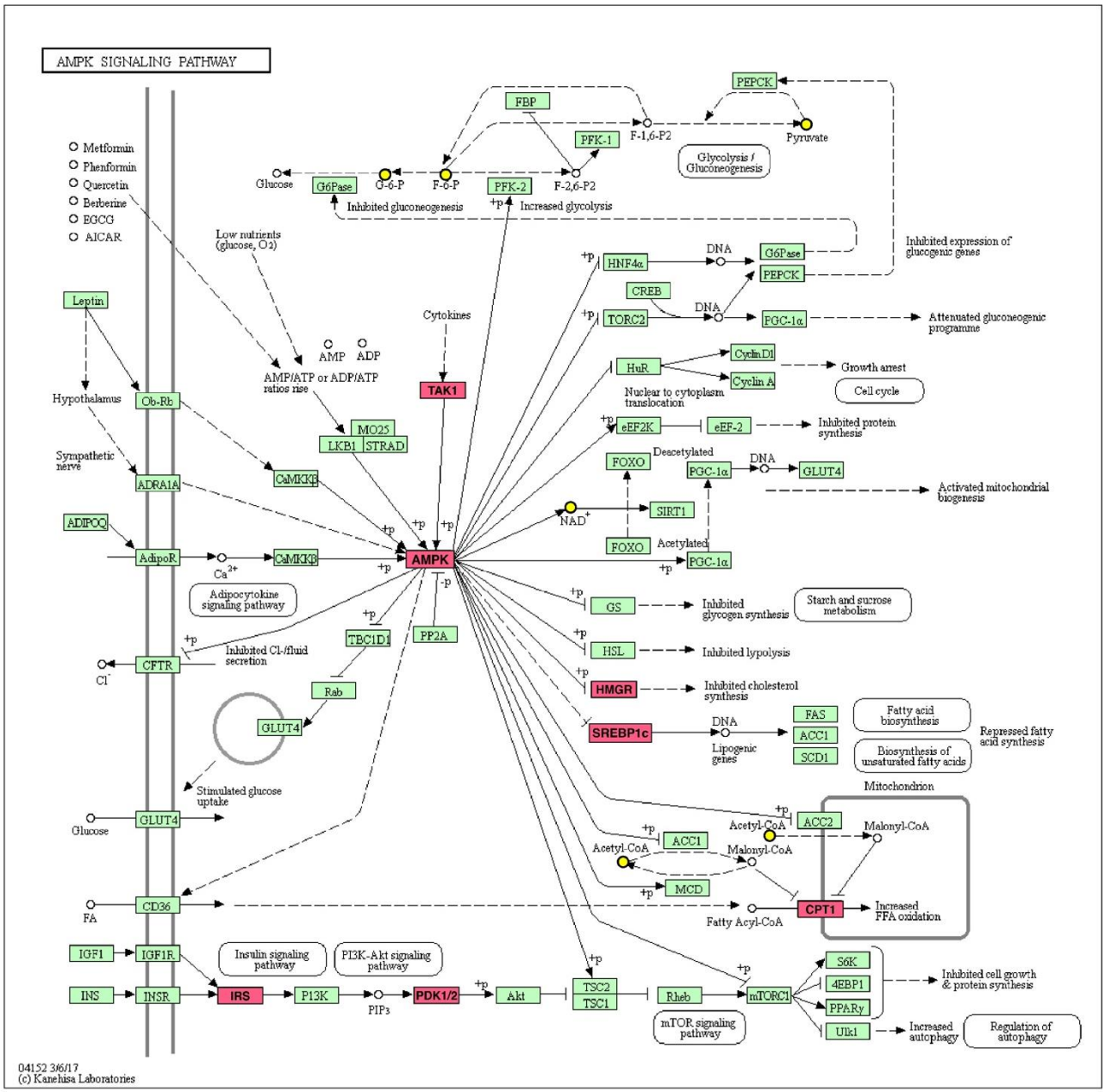
Yellow circles indicate dysregulated metabolites. Predicted miR-33 targets are highlighted in red.

Figure S3. Dysregulated metabolite and miR-33 target genes on the KEGG pathway (Insulin secretion pathway).



Yellow circles indicate dysregulated metabolites. Predicted miR-33 targets are highlighted in red.

Figure S4. Dysregulated metabolite and miR-33 target genes on the KEGG pathways (AMPK signaling pathway).



Yellow circles indicate dysregulated metabolites. Predicted miR-33 targets are highlighted in red.