

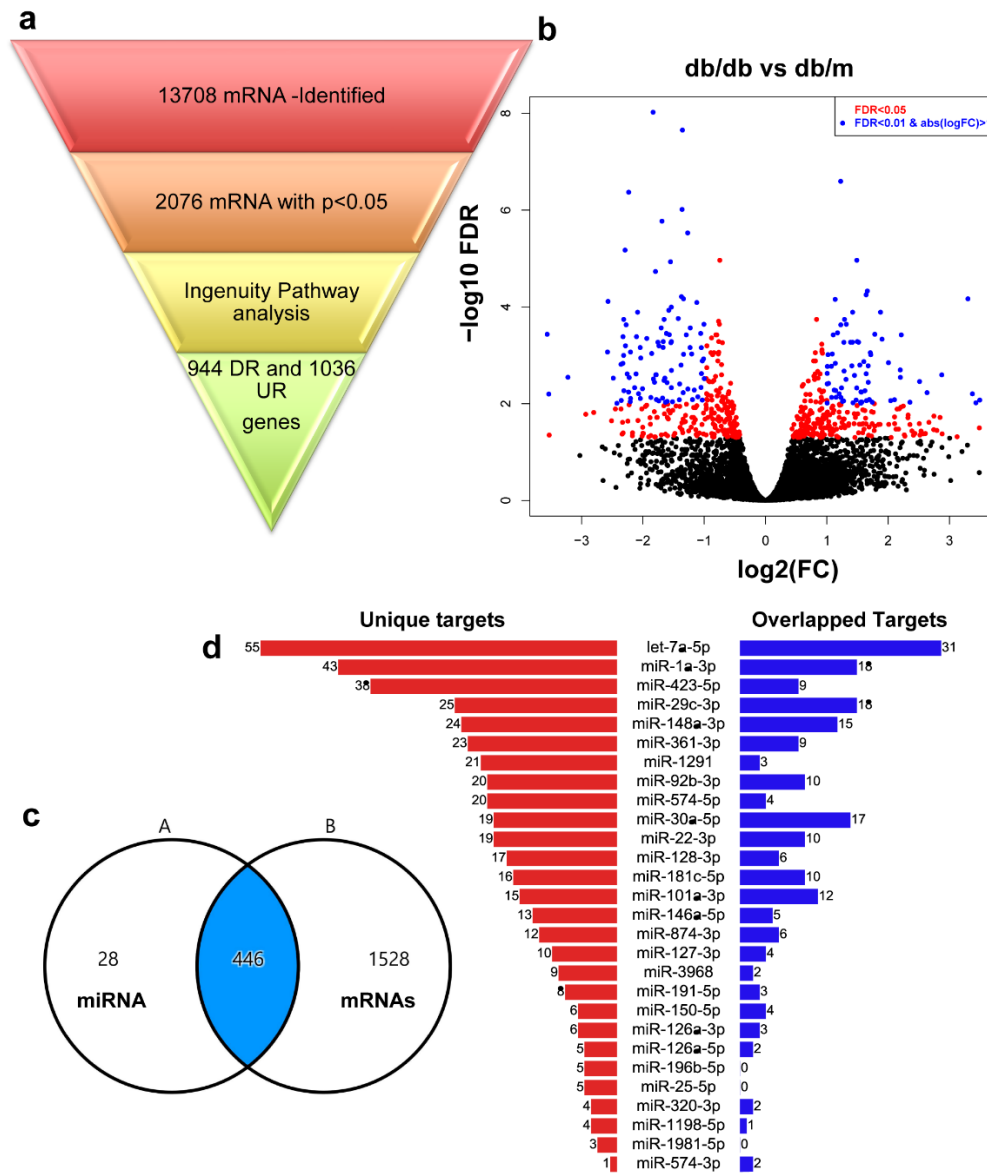


Fig S1. Sequencing data analysis of HSCs in db/db mice. (a,b) mRNA analysis: The raw sequencing data for mRNA was subjected to various analyses. We found 13708 mRNAs, out of which 2076 were statistically significant. **(a)** The schematic presentation of the steps followed for the data analysis for mRNAs. **(b)** The volcano plot represents all the differentially expressed mRNAs in db/db mice; red dots represent mRNAs with a false discovery rate (FDR) of less than 0.05 [or $-\log_{10} \text{FDR} < 1.3$] and blue dots represent mRNAs with a log fold change of more than 1 and a FDR of less than 0.01 [or $-\log_{10} \text{FDR} < 2.0$].

(c,d) miRNA analysis: The top 35 (significant or $p < 0.05$) miRNAs were subjected to microRNA filter analysis on IPA software and were overlaid with the mRNA targets found in our sequencing data. **(c)** Venn diagram

depicting 446 common mRNAs between miRNAs and mRNAs obtained from the sequencing data. **(d)** The microRNA target filter also showed that individual miRNA has some unique mRNA targets, and some mRNA targets were common among multiple miRNAs.