

Table 1. 1219 down-regulated probes in livers of human patients with NAFLD/NASH.

Table 2. 219 potential target genes of miR-21.

Table 3. Thirteen down-regulated genes in livers of human NAFLD/NASH that have binding motifs for miR-21.

Table 4. RT-PCR primers used in this study

Table 5. miRNAs that are highly expressed in hepatocytes. Highly-expressed miRNAs were identified by comparing miRNA profiles of livers between wild-type and *Dicer1* knockout mice. Internal control is U6 nuclear small RNA and U6 was measured five times in each sample. The average Ct value of U6: WT1: 16.998; WT2: 17.58; DKO1: 16.150; and DKO2: 15.452. WT: Wild type; and DKO: *Dicer1* knockout.

Table 6. Comparison of mice treated with miR-21-ASO and miR-21-MM-ASO for four weeks. Data represent mean \pm SD. Mann-Whitney was used for statistical analysis.

Table 7. Comparison of mice treated with miR-21-ASO and miR-21-MM-ASO for eight weeks. Data represent mean \pm SD. Mann-Whitney was used for statistical analysis. * $p < 0.05$.

Table 8. Comparison of serum chemistry of mice treated with miR-21-ASO and miR-21-MM-ASO. Data represent mean \pm SD. Mann-Whitney was used for statistical analysis. * $p < 0.05$.