Supplementary Table 1

MiRNA profiling results in islet, adipose tissue and liver collected from B6-lean, B6-ob/ob, BTBR-lean and BTBR-ob/ob mice.

Pancreatic islet, adipose tissue, and liver were harvested and miRNA measurements performed by LNA-based RT-PCR profiling. The miRNA abundance is shown as copy number/cell. Pools of RNA samples were used for the islet profiling, whereas 5 individuals were profiled for the adipose tissue and liver. MiRNAs are ordered by relative abundance, showing that miR-211 was the most abundant miRNA in all 3 tissues.

Supplementary Table 2

Taqman-based real time PCR measurement on 10 individual islet samples confirms majority of LNA-based profiling results for selected miRNAs.

MiRNA from the pooled islet samples which showed significant changes from LNA-based PCR profiling results were subsequently measured by Taqman-based PCR on 10 individual samples of B6-lean, B6-*ob/ob*, BTBR-lean and BTBR-*ob/ob* mice. MiRNA expression values are shown as ΔCT normalized to SnoRNA234 (a house-keeping, small nucleolar RNA molecule) ± standard deviation. Correlation shows the Pearson's correlation between the Taqman individual measurements and the LNA pooled measurements for the miRNAs selected. Expression profiles across the 4 experimental groups between Taqman and LNA PCR methods were highly correlated, except for

miR-214.

Supplementary Table 3

Genomic location and position of hepatic miR-eQTL for 21 miRNAs.

Twenty-one miRNAs which showed significant linkage in F2 liver are listed according to their LOD score. The genomic location and position of the QTL loci are provided. *Cis*-mapping miRNAs are indicated by *; all other miRNAs map in *trans*. # indicates the two miRNAs (let-7c and miR-16) that derive from more than one genomic location. As these both map in trans, we cannot distinguish which genomic position contributed to the QTL.