

Supplemental Table 1. Differentially-expressed miRNAs in livers of ob/ob mice compared with that of C57BL/6 mice, segregated by gender.

miRNA	SAM score	Fold Change	<i>q</i> -value(%) ^a
Male ob/ob mice vs. male C57BL/6 mice			
Up-regulated			
mmu-miR-34a	4.52	3.23	0.00
mmu-miR-107	3.16	2.84	0.00
mmu-miR-15b	3.13	2.36	0.00
mmu-miR-31	2.98	2.41	0.00
mmu-miR-152	2.82	2.15	0.00
mmu-miR-103	2.76	2.26	0.00
mmu-miR-221	2.51	2.32	0.00
mmu-miR-222	2.22	2.86	0.00
mmu-miR-335-5p	1.94	2.08	0.00
Down-regulated			
mmu-miR-21	-3.38	0.25	0.00
mmu-miR-101	-2.87	0.20	0.00
mmu-miR-30e	-2.75	0.42	0.00
mmu-miR-451	-2.49	0.39	0.00
mmu-miR-29c	-2.43	0.37	0.00
mmu-miR-215	-2.27	0.43	0.00
mmu-miR-130b	-1.96	0.32	0.00
mmu-miR-1	-1.84	0.37	0.00
mmu-miR-19a	-1.61	0.47	0.00
mmu-miR-122 ^b	-1.29	0.61	0.00
Female ob/ob mice vs. female C57BL/6 mice			
Up-regulated			
mmu-miR-31	6.99	3.68	0.00
mmu-miR-193	6.15	3.75	0.00
mmu-miR-153	5.78	3.16	0.00
mmu-miR-26b	5.62	2.27	0.00
mmu-miR-34a	5.26	3.42	0.00
mmu-miR-103	4.77	2.67	0.00
mmu-miR-296-5p	4.62	3.63	0.00

mmu-miR-20a	4.47	2.11	0.00
mmu-miR-19a	4.34	2.86	0.00
mmu-miR-98	4.24	2.05	0.00
mmu-miR-126-3p	3.92	2.03	0.00
mmu-miR-106a	3.64	2.44	0.00
mmu-miR-194	3.52	2.67	0.00
mmu-miR-30d	3.28	2.18	0.00
mmu-miR-335-5p	3.17	3.35	0.00
mmu-let-7i	3.14	2.06	0.00
mmu-miR-203	2.98	2.10	0.00
mmu-miR-200a	2.96	3.03	0.00
mmu-miR-107	2.74	2.18	0.00
Down-regulated			
mmu-miR-125b-5p	-6.67	0.35	0.00
mmu-miR-100	-4.54	0.40	0.00
mmu-miR-191	-4.11	0.40	0.00
mmu-miR-23a	-2.95	0.49	0.00

^a *q*-value: false discovery rate, the expected percentage of genes identified by chance.

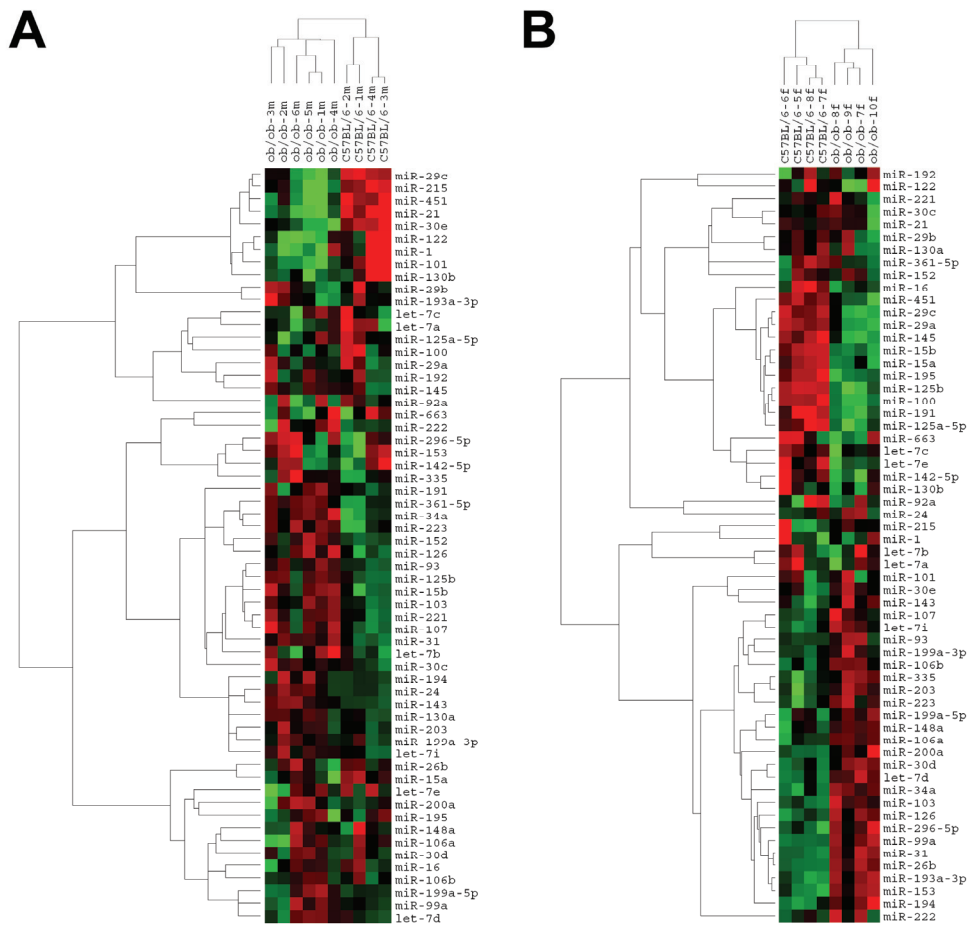
^b These miRNAs were not considered as significantly changed by SAM due to insufficient fold-change, but proved to be significantly changed by real-time qRT-PCR.

Supplemental Table 2. Differentially-expressed miRNAs in livers of STZ-induced diabetic mice compared with that of C57BL/6 mice and in livers of ob/ob mice compared with that of STZ-induced diabetic mice, segregated by gender.

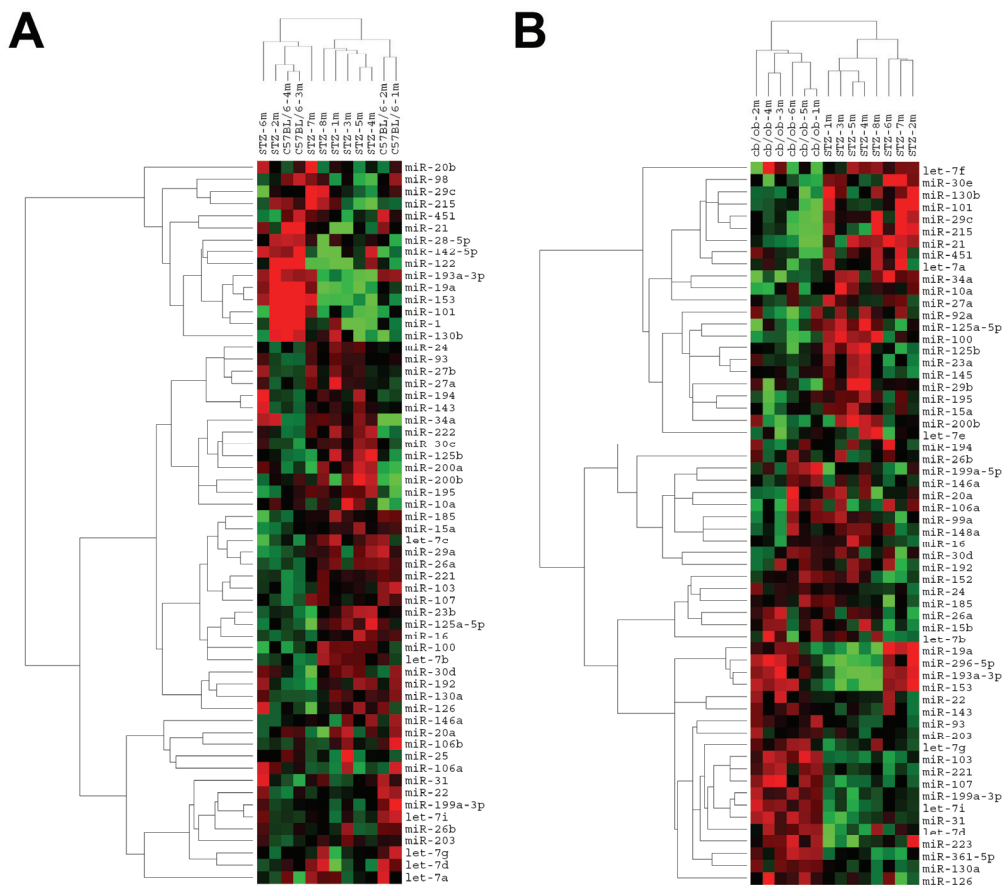
miRNA	SAM score	Fold Change	<i>q</i> -value(%) ^a
Male STZ-induced diabetic mice vs. male C57BL/6 mice			
Up-regulated			
mmu-miR-34a	6.20	5.93	0.00
mmu-miR-222	2.13	2.52	0.00
mmu-miR-200a	2.04	2.07	0.00
Down-regulated			
mmu-miR-451	-2.29	0.48	0.00
mmu-miR-122 ^b	-0.92	0.72	0.00
Male ob/ob mice vs. male STZ-induced diabetic mice			
Up-regulated			
mmu-miR-103	5.16	2.62	0.00
mmu-miR-107	3.99	2.84	0.00
mmu-miR-31	3.65	2.39	0.00
mmu-let-7i	3.54	2.01	0.00
mmu-miR-221	2.89	2.11	0.00
Down-regulated			
mmu-miR-100	-2.59	0.50	0.00
mmu-miR-29c	-2.41	0.41	0.00
mmu-miR-21	-2.36	0.46	0.00
mmu-miR-130b	-2.18	0.44	0.00
mmu-miR-215	-1.83	0.44	0.00
mmu-miR-101a	-1.75	0.43	0.00

^a *q*-value: false discovery rate, the expected percentage of genes identified by chance.

^b These miRNAs were not considered as significantly changed by SAM due to insufficient fold-change, but proved to be significantly changed by real-time qRT-PCR.



Supplemental Figure 1. Hierarchical cluster analysis of miRNAs in livers of ob/ob mice versus C57BL/6 mice, segregated by gender. Two-way (genes against samples) unsupervised hierarchical cluster of a set of 60 most varied miRNAs in livers of 6 male ob/ob mice and 4 male C57BL/6 mice (A) and in livers of 4 female ob/ob mice and 4 female C57BL/6 mice (B). Sample dendrograms generated by cluster analysis show clear separation of ob/ob mice samples from that of C57BL/6 mice based on the miRNA signature. Mean centered signal intensities of miRNA-expression are depicted by a log-transform (2 scale). Color areas indicate relative expression of each miRNA compared to the miRNA median expression (red, above; green, below; and black, close to the median value). m, male; f, female.



Supplemental Figure 2. Hierarchical cluster analysis of miRNAs in livers of STZ-induced diabetic mice versus C57BL/6 mice and in livers of ob/ob mice versus STZ-induced diabetic mice, segregated by gender. (A) Two-way (genes against samples) unsupervised hierarchical cluster of a set of 60 miRNAs with most variation in livers of STZ-induced diabetic mice and C57BL/6 mice. Sample dendrogram shows no clear separation between STZ samples and C57BL/6 samples based on the miRNA signature. 8 male STZ-induced diabetic mice and 4 male C57BL/6 mice are used. (B) Unsupervised hierarchical cluster of most altered miRNAs in livers of ob/ob mice and STZ-induced diabetic mice. Sample dendrogram generated by cluster analysis shows a clear separation of ob/ob mice samples from that of STZ-induced diabetic mice based on the miRNA signature. 6 male ob/ob mice and 8 male STZ-induced diabetic mice are used. Mean centered signal intensities of miRNA-expression are depicted by a log-transform (2 scale). Color areas indicate relative expression of each miRNA compared to the miRNA median expression (red, above; green, below; and black, close to the median value). m, male.