Supplemental Table 1 List of miRNA-specific stem-loop primers.

Name	Context sequence
hsa-miR-101 mmu- miR-101	UACAGUACUGUGAUAACUGAA
hsa-miR-335 mmu-miR-335	UCAAGAGCAAUAACGAAAAAUGU
hsa-miR-375 mmu-miR-375	UUUGUUCGUUCGGCUCGCGUGA
hsa-miR-802	CAGUAACAAAGAUUCAUCCUUGU
mmu-miR-802	UCAGUAACAAAGAUUCAUCCUU
cel-miR-39	UCACCGGGUGUAAAUCAGCUUG
snoRNA202	GCTGTACTGACTTGATGAAAGTACTTTTGAACCCTTTTCCATCTGATG
snoRNA234	CTTTTGGAACTGAATCTAAGTGATTTAACAAAAATTCGTCACTACCACTGAGA

Supplemental Table 2 Read number of sequences mapped to known RNAs, and repeats in the serum, liver and epididymal white adipose tissue (WAT) in the male C57BL/6J mice fed with standard (STD) and high fat-high sucrose (HFHS) chow.

Type	Serum under HFHS chow	Liver under HFHS chow	WAT under HFHS chow	Serum under STD chow	Liver under STD chow	WAT under STD chow
DNA	881	14,089	18,812	2,422	14,214	6,868
LINE	41,225	161,270	137,254	48,587	161,016	91,583
LTR	85,528	104,337	66,095	115,044	87,517	55,731
Low_complexity	13,420	16,389	5,530	10,528	11,296	10,016
Other	184	695	363	242	751	250
RC	4	5	1	0	5	2
RNA	726	2,122	1,072	1,158	1,779	772
SINE	58,571	172,997	171,624	63,230	134,945	121,275
Satellite	3,981	1,428	1,146	6,340	1,170	638
Simple repeat	14,692	22,714	11,438	11,982	16,887	14,924
Unknown	2,047,718	2,637,993	1,332,191	2,540,522	3,659,461	956,616
piRNA	31,483	428,362	344,570	35,402	620,659	293,636
rRNA	818,222	3,099,368	1,821,839	1,032,694	2,590,623	1,051,961
scRNA	18,112	194,761	250,997	20,365	128,956	150,953
snRNA	48,680	183,718	189,522	59,045	163,697	105,356
snoRNA	9,196	895,973	847,431	18,846	1,043,369	538,026
srpRNA	46,933	25,950	21,105	62,396	15,985	6,999
tRNA	15,489,886	2,056,834	2,946,587	14,909,133	1,472,227	3,529,482
mRNA	30,525	313,434	167,544	37,470	385,998	105,719
miRNA	4,530,125	14,694,007	20,241,985	5,643,061	15,412,361	17,267,017
Total	23,290,092	25,026,446	28,577,106	24,618,467	25,922,916	24,307,824
Mapped reads	21,198,758	23,771,767	27,560,090	22,083,910	24,840,095	23,475,703

Sequences are clustered based on overlapping mapping coordinates and intersection with known miRNAs, snoRNAs, piRNA clusters and repeats. LINE, long interspersed repetitive elements; LTR, long terminal repeat; SINE, short interspersed repetitive elements, piRNA, piwi-interacting RNA; RC, rolling circle; rRNA, ribosomal RNA; scRNA, small cytoplasmic RNA; snRNA, small nuclear RNA; snoRNA, small nucleolar RNA; srpRNA, signal recognition particle RNA; tRNA, transfer RNA; mRNA, messenger RNA; miRNA, micro RNA.

Supplemental Table 3 RPM (reads per million mapped reads) of sequences mapped to known RNAs, and repeats in the serum, liver and epididymal white adipose tissue (WAT) in the male C57BL/6J mice fed with standard (STD) and high fat-high sucrose (HFHS) chow.

Type	Serum under HFHS chow	Liver under HFHS chow	WAT under HFHS chow	Serum under STD chow	Liver under STD chow	WAT under STD chow
DNA	42	593	683	110	572	293
LINE	1,945	6,784	4,980	2,200	6,482	3,901
LTR	4,035	4,389	2,398	5,209	3,523	2,374
Low_complexity	633	689	201	477	455	427
Other	9	29	13	11	30	11
RC	0	0	0	0	0	0
RNA	34	89	39	52	72	33
SINE	2,763	7,277	6,227	2,863	5,433	5,166
Satellite	188	60	42	287	47	27
Simple_repeat	693	956	415	543	680	636
Unknown	96,596	110,972	48,338	115,040	147,321	40,749
piRNA	1,485	18,020	12,502	1,603	24,986	12,508
rRNA	38,598	130,380	66,104	46,762	104,292	44,811
scRNA	854	8,193	9,107	922	5,191	6,430
snRNA	2,296	7,728	6,877	2,674	6,590	4,488
snoRNA	434	37,691	30,748	853	42,003	22,918
srpRNA	2,214	1,092	766	2,825	644	298
tRNA	730,698	86,524	106,915	675,113	59,268	150,346
mRNA	1,440	13,185	6,079	1,697	15,539	4,503
miRNA	213,698	618,129	734,467	255,528	620,463	735,527
Total	1,098,654	1,052,780	1,036,902	1,114,769	1,043,592	1,035,446

Sequences are clustered based on overlapping mapping coordinates and intersection with known miRNAs, snoRNAs, piRNA clusters and repeats. LINE, long interspersed repetitive elements; LTR, long terminal repeat; SINE, short interspersed repetitive elements, piRNA, piwi-interacting RNA; RC, rolling circle; rRNA, ribosomal RNA; scRNA, small cytoplasmic RNA; snRNA, small nuclear RNA; snoRNA, small nucleolar RNA; srpRNA, signal recognition particle RNA; tRNA, transfer RNA; mRNA, messenger RNA; miRNA, micro RNA.

Supplemental Table 4 Read number of sequences mapped to known micro RNAs (miRNAs) upregulated in the serum, liver and epididymal white adipose tissue (WAT) in the male C57BL/6J mice fed with high fat-high sucrose (HFHS) chow versus the mice fed with standard chow (STD) chow.

miRBase	HFHS			STD			HFHS/STD ratio		
	Serum	Liver	WAT	Serum	Liver	WAT	Serum	Liver	WAT
Mmu-miR-101	1894	215325	19259	1459	154713	18731	1.2	1.3	1.0
Mmu-miR-335	137	2673	110365	54	1504	8778	2.5	1.7	12
Mmu-miR-375	8270	137	12	4163	133	6	1.9	1.0	2.0
Mmu-miR-802	167	33519	25	64	7020	5	2.6	4.7	5.0

Supplemental Table 5 Multiple linear regression analysis using $\log_{10}$miR-101 as the dependent variable

Independent variables	Unstandardized coefficient		Standardized coefficients	t value	P value	Model R
	B	Standard Error	Beta			
Forced entry						
Age (year)	0.018	0.012	0.125	1.478	0.142	0.350
HbA1c (%)	0.430	0.179	0.227	2.408	0.017	
PG (mmol/L)	0.037	0.064	0.054	0.583	0.561	
BMI (kg/m^2)	0.058	0.037	0.129	1.546	0.124	
Stepwise regression analysis						
HbA1c	0.579	0.153	0.306	3.787	2.26×10^{-4}	0.306

Supplemental Table 6 Multiple linear regression analysis using $\log_{10}$miR-802 as the
dependent variable

Independent variables	Unstandardized coefficient		Standardized coefficients	t value	P value	Model R
	B	Standard Error	Beta			
Forced entry						
Age (year)	5.39×10^{-3}	7.30×10^{-3}	0.056	0.738	0.462	0.387
eGFR (mL/s)	-0.772	0.297	-0.197	-2.601	0.010	
TG (mmol/L)	0.203	0.144	0.117	1.411	0.160	
HDL-C (mmol/L)	-0.388	0.230	-0.135	-1.688	0.093	
HbA1c (%)	0.229	0.107	0.183	2.136	0.034	
PG (mmol/L)	5.07×10^{-3}	0.038	0.011	0.133	0.894	
Stepwise regression analysis						
eGFR (mL/s)	-0.920	0.281	-0.235	-3.281	0.001	0.363
HbA1c (%)	0.266	0.088	0.214	3.013	0.003	
HDL-C (mmol/L)	-0.535	0.206	-0.186	-2.604	0.010	