

Supplementary Table 1. Characteristics of primers used in RT-qPCR according to MIQE guidelines.

Gene Symbol	Accession		Sequence	Amplicon Length	Exons	[Primer]	Efficiency
<i>H4c17</i>	NM_001195421.1	Sense Antisense	CAAAGTGCTGCGCGATAAC A AGATGCGCTTCACTCCTCC TTGTGGAGAGTGTACACACC	83	1	0.2 µM	94%
<i>LOC100862456</i>	XM_006537451.3	Sense Antisense	G TCGAGCATCAAAAACCACC A GTAGGAGCCTCGACCTCTC	121	1	0.05 µM	92%
<i>Ccl19-ps2</i>	XM_006536385.3	Sense Antisense	A GGAAGGTCCAGAGAACCA GC	142	1	0.2 µM	94%
<i>Ctrb1</i>	NM_025583.2	Sense Antisense	CACCACCATGGCATTCTTT GCATCCTCTCCGTTGACGAT	126	1/2	0.075 µM	94%
<i>Cyp2b10</i>	NM_009999.4	Sense Antisense	ATGTTTAGTGGAGGAAGT CGG ATATTGGCCGTGATGCACT G	81	3/4	0.1 µM	103%
<i>Zfp969</i>	XM_017319408.2	Sense Antisense	ATGAAAGAGAAACCCTATG AATGC ACACCCCTGTATCCTCTTGA CTTCACTCAGGAAGAGTGG	112	1	0.2 µM	96%
<i>Zfp965</i>	NM_001242944.1	Sense Antisense	GC TGCCTTTGACTACGACTCTG A	243	2/4	0.1 µM	95%
<i>Ttn</i>	NM_011652.3	Sense Antisense	GCCACTGCTGTGGTAGAAG T CTTAGACCCGCCATCGTCTC AATGTCGATGGGGCGGATA	129	245/246	0.2 µM	98%
<i>Rbm14-rbm4</i>	NM_001290127.1	Sense Antisense	C CAGCTCATGACCGTGCCAT A TTGTTGAGCCAAGTCAGCG G	74	1	0.2 µM	106%
<i>Sec61g</i>	XM_003085302.1	Sense Antisense	GTGG TGATAGCAAATCCTATCGTT GTGG	120	1/2	0.05 µM	105%
<i>Rbm24</i>	NM_001081425.1	Sense Antisense	TGCAGCCAGGTTTTGCCTTT ATGTACGGTGTGGTGAAG CC TGGCCTTGGCTACAAGGAA G	166	2/4	0.2 µM	95%
<i>Tmem81</i>	NM_029025.3	Sense Antisense	G AATTGGCTCGGAAGGGTCT G	266	2	0.1 µM	93%
<i>Rnase2a</i>	NM_053113.2	Sense Antisense	GAGCCTATCCCCGATGTGA TG ATGACTGGCCGGAGTTGTG	218	2	0.1 µM	93%

<i>Sult2a2</i>	NM_009286.2	Sense Antisense	ACCTCCCATCTTCCCATCCA TCATGAGATAGATCGCCTT GG	73	2/3	0.1 µM	95%
<i>Ndufb4b</i>	XM_001478443.6	Sense Antisense	TGAAAATCCCGGGGAGTCA A CGGAGACACGTCATACTCG G	102	1	0.2 µM	94%
<i>Dmbt1</i>	NM_001347632.2	Sense Antisense	CACCACCAATCTCCTTTGTC AG GTCTCGTTGTCAGCCTGTTT GA	207	44/46	0.1 µM	99%
<i>Cyp2b13</i>	NM_007813.2	Sense Antisense	CTCATGCTGAGTCACTTCCC TCTT ACAGACCACAGAGTGTGAA GTTGG	52	9	0.1 µM	91%
<i>Prtn3</i>	NM_011178.2	Sense Antisense	CAATTACAACCCCGAGGAG AAC TTTAGCTGGAGGAGAAGCA CGT	51	3/4	0.1 µM	95%
<i>Amy2a5</i>	NM_001042711.2	Sense Antisense	TGCTTTCCCTCATTGGGTTC AATATCAACCCAGCGCCAC T	101	1	0.1 µM	93%
<i>Cyp2b9</i>	NM_010000.2	Sense Antisense	ACCAGATCTACTTCTTAGCC CGCT GAGAACAACAGTAGAAGG AAGGGTG	151	9	0.1 µM	104%
<i>Mup1</i>	NM_001163011.1	Sense Antisense	TAAGAACAAGCAAAGGGG CTGG TCAGTCCCAAACACAGCAG CA	127	1	0.1 µM	97%
<i>Apoa1</i>	NM_009692.4	Sense Antisense	GCTGAACCTGAATCTCCTG GAA ACTAACGGTTGAACCCAGA GTGTC	52	3/4	0.1 µM	-
<i>ApoE</i>	NM_009696.4	Sense Antisense	CTTGTTTCGGAAGGAGCTG ACT AGGCATCCTGTCAGCAATG TG	92	1/3	0.1 µM	-
<i>Tbp</i>	NM_013684.3	Sense Antisense	GTGAGTTGCTTGCTCTGTGC GCTGCGTTTTTGTGCAGAGT	359	8	0.2 µM	104%
<i>Pipb</i>	NM_011149	Sense Antisense	GGAGATGGCACAGGAGGA A GTAGTGCTTCAGCTTGAAGT TCTCAT	72	3/4	0.1 µM	103%

Supplementary Figure 1. PCR products obtained from hepatic RNA by RT-PCR. *Apoa1*-deficient mice do not express *Apoa1* and *ApoE*-deficient mice do not express *ApoE*. Lane 1, *Apoa1*-deficient mice; lane 2, *ApoE*-deficient mice and lane 3, negative control, no cDNA input. M, DNA ladder. PCR products were run into a 2% agarose gel and stained with ethidium bromide.

