Supplementary Table 1. Fold change of miR-33 heptamer-matched genes in the liver after 4 weeks of treatment

Gene id	Gene Title	Fold Change	P-Value
ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	1.46	0.0041
RGS5	regulator of G-protein signaling 5	1.36	0.0297
SLC22A23	solute carrier family 22, member 23	1.29	0.0069
C1orf158	chromosome 1 open reading frame 158	1.28	0.0044
PIN4	(peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)	1.27	0.0006
FLT1	fms-related tyrosine kinase 1 (VEGF/vascular permeability factor receptor)	1.26	0.0085
CLEC10A	C-type lectin domain family 10, member A	1.26	0.0023
STS	steroid sulfatase (microsomal), isozyme S	1.26	0.0047
IRAK3	interleukin-1 receptor-associated kinase 3	1.23	0.0166
EFNA5	ephrin-A5	1.23	0.0350
PAX5	paired box 5	1.21	0.0179
ABAT	4-aminobutyrate aminotransferase	1.21	0.0393
ATP2B2	ATPase, Ca++ transporting, plasma membrane 2	1.21	0.0295
ZNF300	zinc finger protein 300	1.21	0.0110
THSD4	thrombospondin, type I, domain containing 4	1.20	0.0246
TMEM133	transmembrane protein 133	1.20	0.0431
SCN1A	sodium channel, voltage-gated, type I, alpha subunit	1.20	0.0460
COLQ	collagen-like tail subunit of asymmetric acetylcholinesterase	1.20	0.0159
SIRPG	signal-regulatory protein gamma	1.20	0.0145
CRHR2	corticotropin releasing hormone receptor 2	1.19	0.0276
CNPY1	canopy 1 homolog (zebrafish)	1.19	0.0024
LPCAT2	lysophosphatidylcholine acyltransferase 2	1.19	0.0167
NTRK2	neurotrophic tyrosine kinase, receptor, type 2	1.19	0.0041
RCN1	reticulocalbin 1, EF-hand calcium binding domain	1.19	0.0228
GOPC	golgi-associated PDZ and coiled-coil motif containing	1.18	0.0330
FAM81A	family with sequence similarity 81, member A	1.18	0.0253
S100A7A	S100 calcium binding protein A7A	1.17	0.0125
PURB	purine-rich element binding protein B	1.17	0.0313
RTKN2	rhotekin 2	1.17	0.0036
SLC26A1	solute carrier family 26 (sulfate transporter), member 1	1.17	0.0155
CRY2	cryptochrome 2 (photolyase-like)	1.17	0.0054
DPPA4	developmental pluripotency associated 4	1.17	0.0370
SPDYE1	speedy homolog E1 (Xenopus laevis)	1.17	0.0216
OPN4	opsin 4	1.16	0.0398
C19orf25	chromosome 19 open reading frame 25	1.16	0.0358
SERPINA9	serpin peptidase inhibitor, clade A (α1 antiproteinase, antitrypsin), member 9	1.15	0.0340
KCNH8	potassium voltage-gated channel, subfamily H (eag-related), member 8	1.15	0.0129
TNFRSF11A	TNF receptor superfamily, member 11a, NFKB activator	1.15	0.0221
VTCN1	V-set domain containing T cell activation inhibitor 1	1.15	0.0394
ZFAT	zinc finger and AT hook domain containing	1.15	0.0298
CDRT4	CMT1A duplicated region transcript 4	1.15	0.0447
C16orf57	chromosome 16 open reading frame 57	1.15	0.0114
DIRAS2	DIRAS family, GTP-binding RAS-like 2	1.15	0.0108

Fold change of miR-33 heptamer matched target genes in livers of anti-miR-33 vs control anti-miR treated monkeys (n=6) with an uncorrected p value of <0.05.

Supplementary Table 2. Fold change of miR-33 heptamer-matched genes in the liver after 12 weeks of treatment

Gene id	Gene Title	Fold Change	P-Value
FETUB	fetuin B	1.57	0.0058
HADHB	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratas	1.43	0.0173
ATP2B2	ATPase, Ca++ transporting, plasma membrane 2	1.37	0.0011
PIN4	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)	1.33	0.0001
SLC35A3	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter	1.33	0.0418
CROT	carnitine O-octanoyltransferase	1.27	0.0079
SCRN3	secernin 3	1.24	0.0448
SLC20A2	solute carrier family 20 (phosphate transporter), member 2	1.24	0.0201
LMBR1	limb region 1 homolog (mouse)	1.21	0.0296
C10orf31	chromosome 10 open reading frame 31	1.19	0.0196
BCL10	B-cell CLL/lymphoma 10	1.18	0.0349
KLHL3	kelch-like 3 (Drosophila)	1.18	0.0060
IRF6	interferon regulatory factor 6	1.18	0.0209
B3GNT7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	1.17	0.0235
PRIMA1	proline rich membrane anchor 1	1.17	0.0482
IRAK2	interleukin-1 receptor-associated kinase 2	1.17	0.0206
FGA	fibrinogen alpha chain	1.16	0.0452
BACH1	BTB and CNC homology 1, basic leucine zipper transcription factor 1	1.16	0.0075
CPD	carboxypeptidase D	1.15	0.0373
ZNF347	zinc finger protein 347	1.15	0.0475

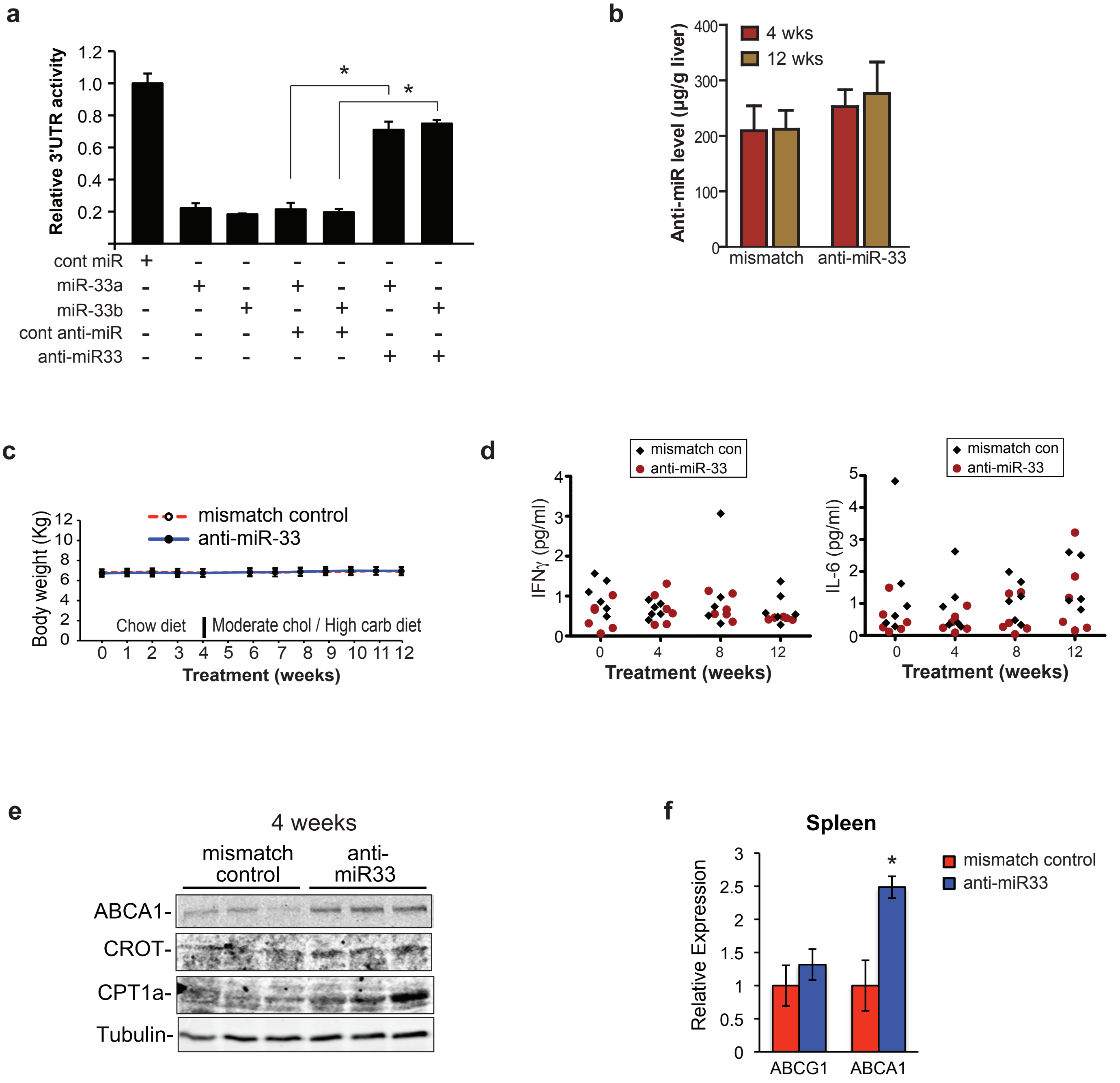
Fold change of miR-33 heptamer matched target genes in livers of anti-miR-33 vs control anti-miR treated monkeys (n=6) with an uncorrected p value of <0.05.

Supplemental Table 3. Composition of semisynthetic diet

Ingredient	g/100 g dry weight
Oleic Blend	4.0000
Fish Oil	0.2000
Casein, USP	8.0000
Lactalbumin	4.0000
Fructose	20.0000
Sucrose	20.0000
Applesauce, sweetened	4.5000
Wheat Flour, self-rising	22.2050
Crystalline Cholesterol	0.0640
Sitosterol	0.0068
Alphacel	9.5000
Vitamin Mixture	2.5000
Hegsted Salt Mixture	5.0000
Tenox 20A	0.0080
MTS-50	0.0122
Vit E 5-67	0.0040
TOTAL	100.0

Macronutrient	Calories (%)
Fat	12
Carbohydrate	71
Protein	17

Supplementary Figure 1. Rayner et al.



SFig 1. Silencing of miR-33a/b in non-human primates. (a) Relative activity of a luciferase reporter construct fused to the 3’UTR of human ABCA1 in HEK293 cells overexpressing miR-33a or miR-33b (1.7-3.5 x 105 copies/ng RNA) in the presence of anti-miR-33 or control mismatch oligonucleotide. Data are expressed as mean % 3’UTR activity of control miR ± s.e.m and are representative of 3 experiments.(b) Hepatic levels of anti-miR-33 or mismatch control as measured by ion-pairing HPLC-ES/MS following 4 weeks and 12 weeks of treatment. (c) Body weight of anti-miR33 or mismatch control oligonucleotide treated African green monkeys (n=6 per group). (d) Plasma levels of IL-6 and IFNγ at baseline and after 4, 8 and 12 weeks of treatment. (e) Western blot for ABCA1, Cpt1a and CROT in liver samples following 4 weeks of anti-miR treatment. (f) QRT-PCR analysis of ABCA1 and ABCG1 mRNA levels in the spleen following 12 weeks of anti-miR treatment. Data in d and f are the mean ± SEM. *P ≤ 0.05.

Supplementary Figure 2.

Abca1 3'-UTR

binding site 1:134-140

```
        3'-ACGUUACGUUGUCGUUACGUG-5'   hsa-miR-33b
           | |          |||||||
Hsa  5'-CUGUACUGAUACUAUUCAAUGCAAUGCAAUUCAAUGCAAUGA-3'
Ptr  5'-CUGUACUGAUACUAUUCAAUGCAAUGCAAUUCAAUGCAAUGA-3'
Mml  5'--------------------------------------------3'
Mmu  5'-CUGUACUGACACUAUUCAAUGCAAUGCACUUCAAUGCAACGA-3'
```

```
        3'-ACGUUACGUUGAUGUUACGUG-5'   hsa-miR-33a
           | |        | |||||||
Hsa  5'-CUGUACUGAUACUAUUCAAUGCAAUGCAAUUCAAUGCAAUGA-3'
Ptr  5'-CUGUACUGAUACUAUUCAAUGCAAUGCAAUUCAAUGCAAUGA-3'
Mml  5'--------------------------------------------3'
Mmu  5'-CUGUACUGACACUAUUCAAUGCAAUGCACUUCAAUGCAACGA-3'
```

binding site 2:139-145

```
             3'-ACGUUACGUUGUCGUUACGUG-5'   hsa-miR-33b
                         |  ||||||||
Hsa  5'-CUGUACUGAUACUAUUCAAUGCAAUGCAAUUCAAUGCAAUGA-3'
Ptr  5'-CUGUACUGAUACUAUUCAAUGCAAUGCAAUUCAAUGCAAUGA-3'
Mml  5'--------------------------------------------3'
Mmu  5'-CUGUACUGACACUAUUCAAUGCAAUGCACUUCAAUGCAACGA-3'
```

```
             3'-ACGUUACGUUGAUGUUACGUG-5'   hsa-miR-33a
                         | | |||||||
Hsa  5'-CUGUACUGAUACUAUUCAAUGCAAUGCAAUUCAAUGCAAUGA-3'
Ptr  5'-CUGUACUGAUACUAUUCAAUGCAAUGCAAUUCAAUGCAAUGA-3'
Mml  5'--------------------------------------------3'
Mmu  5'-CUGUACUGACACUAUUCAAUGCAAUGCACUUCAAUGCAACGA-3'
```

binding site 3:149-155

```
                       3'-ACGUUACGUUGUCGUUACGUG-5'   hsa-miR-33b
                              |    |   |||||||
Hsa  5'-CUGUACUGAUACUAUUCAAUGCAAUGCAAUUCAAUGCAAUGA-3'
Ptr  5'-CUGUACUGAUACUAUUCAAUGCAAUGCAAUUCAAUGCAAUGA-3'
Mml  5'--------------------------------------------3'
Mmu  5'-CUGUACUGACACUAUUCAAUGCAAUGCACUUCAAUGCAACGA-3'
```

```
                       3'-ACGUUACGUUGAUGUUACGUG-5'   hsa-miR-33a
                              |    | | |||||||
Hsa  5'-CUGUACUGAUACUAUUCAAUGCAAUGCAAUUCAAUGCAAUGA-3'
Ptr  5'-CUGUACUGAUACUAUUCAAUGCAAUGCAAUUCAAUGCAAUGA-3'
Mml  5'--------------------------------------------3'
Mmu  5'-CUGUACUGACACUAUUCAAUGCAAUGCACUUCAAUGCAACGA-3'
```

Abcg1 3'-UTR

binding site 1:717-723

```
Hsa  5'-GCAGACAUU-----------UUUAAAAGCUAUACAAAAAAUUG-3'
Ptr  5'-GCAGACAUU-----------UUUUAAAGCUAUACAAAAAAUUG-3'
Mml  5'-GCAGAAAUU-----------UUUAAAAGCUAUACAAAACAUUG-3'
Mmu  5'-GCAGGGACUAACGCAACGCAAUGCAACGCAAUGCAGACAGUGC-3'
               | |    |  ||||||||
          3'-ACGUUACGUUGUCGUUACGUG-5'   hsa-miR-33b
```

```
Hsa  5'-GCAGACAUU-----------UUUAAAAGCUAUACAAAAAAUUG-3'
Ptr  5'-GCAGACAUU-----------UUUUAAAGCUAUACAAAAAAUUG-3'
Mml  5'-GCAGAAAUU-----------UUUAAAAGCUAUACAAAACAUUG-3'
Mmu  5'-GCAGGGACUAACGCAACGCAAUGCAACGCAAUGCAGACAGUGC-3'
               | |    |   |||||||
          3'-ACGUUACGUUGAUGUUACGUG-5'   hsa-miR-33b
```

binding site 2:727-733

```
Hsa  5'-GCAGACAUU-----------UUUAAAAGCUAUACAAAAAAUUG-3'
Ptr  5'-GCAGACAUU-----------UUUUAAAGCUAUACAAAAAAUUG-3'
Mml  5'-GCAGAAAUU-----------UUUAAAAGCUAUACAAAACAUUG-3'
Mmu  5'-GCAGGGACUAACGCAACGCAAUGCAACGCAAUGCAGACAGUGC-3'
                         | |    |  ||||||||
                    3'-ACGUUACGUUGUCGUUACGUG-5'   hsa-miR-33b
```

```
Hsa  5'-GCAGACAUU-----------UUUAAAAGCUAUACAAAAAAUUG-3'
Ptr  5'-GCAGACAUU-----------UUUUAAAGCUAUACAAAAAAUUG-3'
Mml  5'-GCAGAAAUU-----------UUUAAAAGCUAUACAAAACAUUG-3'
Mmu  5'-GCAGGGACUAACGCAACGCAAUGCAACGCAAUGCAGACAGUGC-3'
                         | |    |   |||||||
                    3'-ACGUUACGUUGAUGUUACGUG-5'   hsa-miR-33b
```

Crot 3'-UTR

binding site 1: 216-222

```
             3'-ACGUUACGUUGUCGUUACGUG-5'   hsa-miR-33b
                ||   ||||||  |||||||
Hsa  5'-AAGC-UCCUCUGAUGCAGCAGCAAUGCAAAUUAUGACAU-3'
Ptr  5'-AAGC-UCCUCUGAUGCAGCAGCAAUGCAAAUUAUGACAU-3'
Mml  5'-AAGUCUCCUGUGUUGCAACCACAAUGCAAAGUCAGAUAU-3'
Mmu  5'-AAGC-UCCUCUGAUGCAGCAGCAAUGCAAAUUAUGACAU-3'
```

```
             3'-ACGUUACGUUGAUGUUACGUG-5'   hsa-miR-33a
                ||   |||||| ||||||||
Hsa  5'-AAGC-UCCUCUGAUGCAGCAGCAAUGCAAAUUAUGACAU-3'
Ptr  5'-AAGC-UCCUCUGAUGCAGCAGCAAUGCAAAUUAUGACAU-3'
Mml  5'-AAGUCUCCUGUGUUGCAACCACAAUGCAAAGUCAGAUAU-3'
Mmu  5'-AAGC-UCCUCUGAUGCAGCAGCAAUGCAAAUUAUGACAU-3'
```

binding site 2: 292-298

```
              3'-ACGUUACGUUGUCGUUACGUG-5'   hsa-miR-33b
                     |      | |||||||
Hsa  5'-AAUCCAAAUCUACAAACUUUAACAAUGCAAGUCU-3'
Ptr  5'-AAUCCAAAUCUACAAACUUUAACAAUGCAAGUCU-3'
Mml  5'-AAUCCAAAUCUAUAAAUUUUAACAAUGCAAAUCU-3'
```

```
              3'-ACGUUACGUUGAUGUUACGUG-5'   hsa-miR-33a
                     |       ||||||||
Hsa  5'-AAUCCAAAUCUACAAACUUUAACAAUGCAAGUCU-3'
Ptr  5'-AAUCCAAAUCUACAAACUUUAACAAUGCAAGUCU-3'
Mml  5'-AAUCCAAAUCUAUAAAUUUUAACAAUGCAAAUCU-3'
```

Cpt1a 3'-UTR

binding site 1: 2499-2506

```
                 3'-ACGUUACGUUGUCGUUACGUG-5'   hsa-miR-33b
                               | ||| |||
Hsa  5'-AAUUGUUGCUCAUCAGUGCAGUUAUCAAUGCAAUUUUAUAU-3'
Ptr  5'-------------------------------------------3'
Mml  5'-------------------------------------------3'
Mmu  5'-AAUCACACCUCUCCUGAGCAGUUACCAAUGCAAUUUUUUAC-3'
```

```
                 3'-ACGUUACGUUGAUGUUACGUG-5'   hsa-miR-33a
                                 ||| |||
Hsa  5'-AAUUGUUGCUCAUCAGUGCAGUUAUCAAUGCAAUUUUAUAUUCCU-3'
Ptr  5'-----------------------------------------------3'
Mml  5'-----------------------------------------------3'
Mmu  5'-AAUCACACCUCUCCUGAGCAGUUACCAAUGCAAUUUUUUACUCCU-3'
```

Hadhb 3'-UTR

binding site 1: 61-67

```
              3'-ACGUUACGUUGUCGUUACGUG-5'   hsa-miR-33b
                  ||||||| |   ||| |||
Hsa  5'-CUCACACUAGGCAAUGCCAUUUCAAUGCAUUACUAAAUGACAUUUG-3'
Ptr  5'-CUCACACUAGGCAAUGCCAUUUCAAUGCAUUACUAAAUGACAUUUG-3'
Mml  5'------------------------------------------------3'
Mmu  5'-CUUGCACUGGGCAAUGCCAUUUCAAUGCACUACCAAGUGAUACCUG-3'
```

```
              3'-ACGUUACGUUGAUGUUACGUG-5'   hsa-miR-33a
                  ||||||| | | ||| |||
Hsa  5'-CUCACACUAGGCAAUGCCAUUUCAAUGCAUUACUAAAUGACA-3'
Ptr  5'-CUCACACUAGGCAAUGCCAUUUCAAUGCAUUACUAAAUGACA-3'
Mml  5'--------------------------------------------3'
Mmu  5'-CUUGCACUGGGCAAUGCCAUUUCAAUGCACUACCAAGUGAUA-3'
```

Supplementary Figure 2 (cont'd).

Prkaa1 3'-UTR

binding site 1: 115-121

```
       3'-ACGUUACGUUGUCGUUACGUG-5'    hsa-miR-33b
           ||         | ||||||
Hsa  5'-AGGGCUGGCGUUUUGGAAUGCAAUUUGCACAGG-3'
Ptr  5'-AGGGCUGGCGUUUUGGAAUGCAAUUUGCACAGG-3'
Mml  5'-AGGGCUGGCGUUUUGAAAUGCAAUUUGCACAGG-3'
Mmu  5'-AGGAUUGGCCUUUUGGAAUGCAGUUUGCACAGG-3'
```

```
       3'-ACGUUACGUUGAUGUUACGUG-5'    hsa-miR-33a
           ||        |  ||||||
Hsa  5'-AGGGCUGGCGUUUUGGAAUGCAAUUUGCACAGG-3'
Ptr  5'-AGGGCUGGCGUUUUGGAAUGCAAUUUGCACAGG-3'
Mml  5'-AGGGCUGGCGUUUUGAAAUGCAAUUUGCACAGG-3'
Mmu  5'-AGGAUUGGCCUUUUGGAAUGCAGUUUGCACAGG-3'
```

binding site 2: 2532-2538

```
        3'-ACGUUACGUUGUCGUUACGUG-5'    hsa-miR-33b
            |  |       ||||||||
Hsa  5'-AAGAGGUAA-GGGAGGCAAUGCAAAUGAUUUUUAA-3'
Ptr  5'-AAGAGAUAA-GGGAGGCAAUGCAAAUGAUUUUUAA-3'
Mml  5'-GGGAGGUAA-GGGAGGCAAUGCAAAUGAUUUUUAA-3'
Mmu  5'-AAAAUGUAAAGGGAGUCAAUGCAAAUGAUUUUUAA-3'
```

```
        3'-ACGUUACGUUGAUGUUACGUG-5'    hsa-miR-33a
            |  |        |||||||
Hsa  5'-AAGAGGUAA-GGGAGGCAAUGCAAAUGAUUUUUAA-3'
Ptr  5'-AAGAGAUAA-GGGAGGCAAUGCAAAUGAUUUUUAA-3'
Mml  5'-GGGAGGUAA-GGGAGGCAAUGCAAAUGAUUUUUAA-3'
Mmu  5'-AAAAUGUAAAGGGAGUCAAUGCAAAUGAUUUUUAA-3'
```

Sirt6 3'-UTR

binding site 1: 478-484

```
           3'-ACGUUACGUUGUCGUUACGUG-5'    hsa-miR-33b
                  |     |  |||||||
Hsa  5'-AGGCUUCUGGAAAAGUCCUCAAUGCAAUAAAAACAAUUU-3'
Ptr  5'-AGGCUUCUGGAAAAGUCCUCAAUGCAAUAAAAACAAUUU-3'
Mml  5'-AGGCUUCUGGAAAAGUCCUCAAUGCAAUAAAAA--AUUU-3'
Mmu  5'-----------------------------------------3'
```

```
           3'-ACGUUACGUUGAUGUUACGUG-5'    hsa-miR-33a
                  |     |  |||||||
Hsa  5'-AGGCUUCUGGAAAAGUCCUCAAUGCAAUAAAAACAAUUU-3'
Ptr  5'-AGGCUUCUGGAAAAGUCCUCAAUGCAAUAAAAACAAUUU-3'
Mml  5'-AGGCUUCUGGAAAAGUCCUCAAUGCAAUAAAAA--AUUU-3'
Mmu  5'-----------------------------------------3'
```

Irs2 3'-UTR

binding site 1: 1577-1583

```
    3'-ACGUUACGUUGUCGUUACGUG-5'    hsa-miR-33b
           ||  ||  ||||||||
Hsa  5'-UAUAUUUAAUGGCAAUGCAAAAGUCUUCCUGCUUCCGU-3'
Ptr  5'-UAUAUUUAAUGGCAAUGCAAAAGUCUUCCUGCUUCCGU-3'
Mml  5'-UAUAUUUAAUGGCAAUGCAAAAGUCUUCCUGCUUCCGU-3'
Mmu  5'-UAUAUUUAAUGGCAAUGCAGCAGUCUUCCUGCUUCCGU-3'
```

```
    3'-ACGUUACGUUGAUGUUACGUG-5'    hsa-miR-33a
           ||  ||   |||||||
Hsa  5'-UAUAUUUAAUGGCAAUGCAAAAGUCUUCCUGCUUCCGU-3'
Ptr  5'-UAUAUUUAAUGGCAAUGCAAAAGUCUUCCUGCUUCCGU-3'
Mml  5'-UAUAUUUAAUGGCAAUGCAAAAGUCUUCCUGCUUCCGU-3'
Mmu  5'-UAUAUUUAAUGGCAAUGCAGCAGUCUUCCUGCUUCCGU-3'
```

Sirt1 3'-UTR

binding site 1: 1518-1524

```
        3'-ACGUUACGUUGUCGUUACGUG-5'    hsa-miR-33b
           ||         |  ||||||
Hsa  5'-AUUUGGCUACACUAAAGAAUGCAGUAUAUUUAGUUUUCC-3'
Ptr  5'-AUUUGGCUACACUAAAGAAUGCAGUAUAUUUAGUUUUCC-3'
Mml  5'-AUUUGGCUACACUAAAGAAUGCAGUAUAUUUAGUUUUCC-3'
Mmu  5'-AUUUGGCUACACUAAAGAAUGCAGUAUAUUUAGUUUUCC-3'
```

```
        3'-ACGUUACGUUGAUGUUACGUG-5'    hsa-miR-33a
           ||          | ||||||
Hsa  5'-AUUUGGCUACACUAAAGAAUGCAGUAUAUUUAGUUUUCC-3'
Ptr  5'-AUUUGGCUACACUAAAGAAUGCAGUAUAUUUAGUUUUCC-3'
Mml  5'-AUUUGGCUACACUAAAGAAUGCAGUAUAUUUAGUUUUCC-3'
Mmu  5'-AUUUGGCUACACUAAAGAAUGCAGUAUAUUUAGUUUUCC-3'
```

NPC1 3'-UTR

binding site 1: 443-449

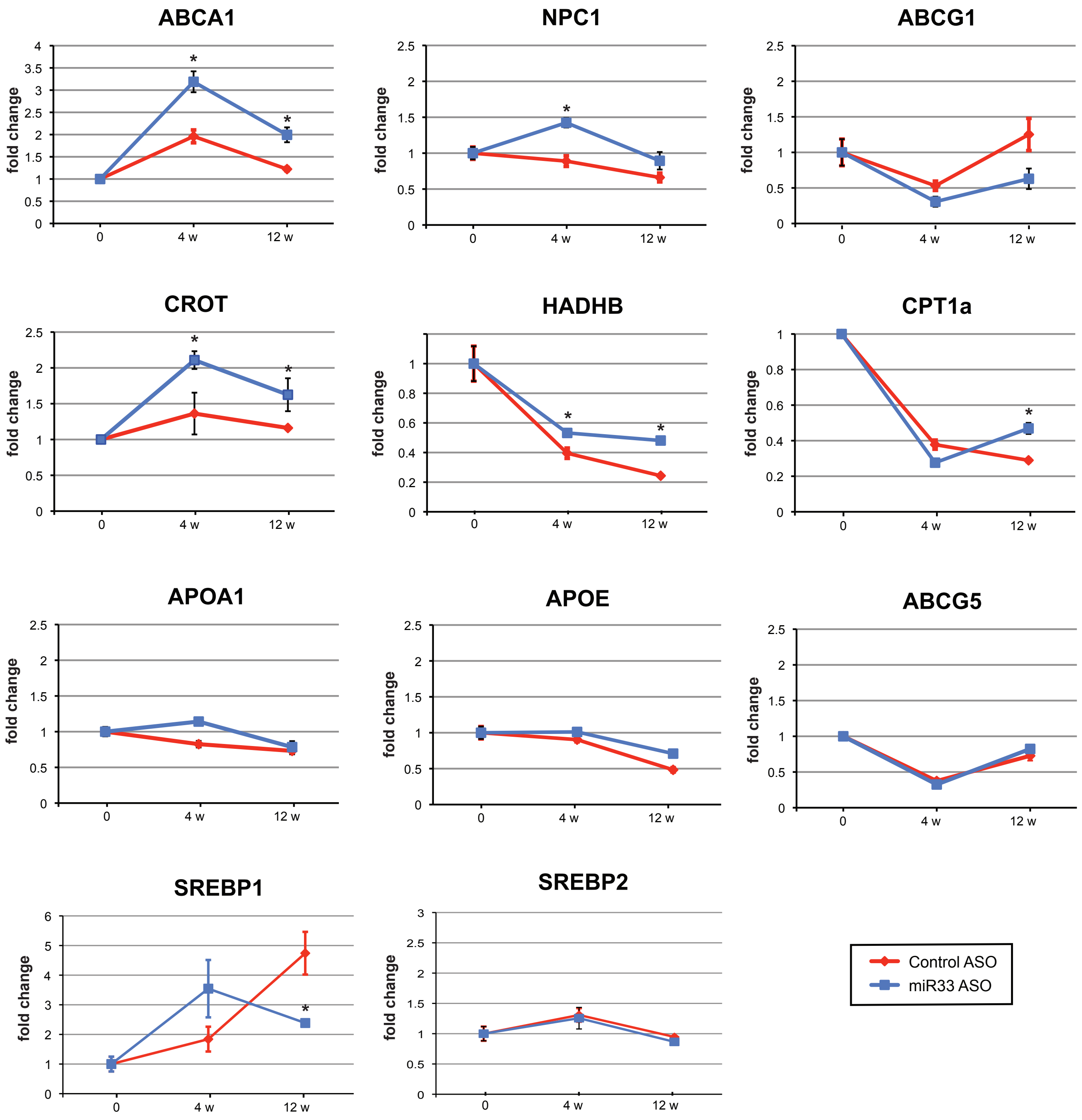
```
     3'-ACGUUACGUUGUCGUUACGUG-5'    hsa-miR-33b
        |  |  ||   |  ||||||
Hsa  5'-UAAAGAGCUUUAUUAAUGCAAUAAAUUAACUUUGUACAC-3'
Ptr  5'-UAAAGAGCUUUAUUAAUGCAAUAAAUUAACUUUGUACAC-3'
Mml  5'-UAAAGAGCUUUAUUAAUGCAAUAAAUUAACUUUGUACAC-3'
Mmu  5'-UAAAGAGCUUUAUUAAUGCAAUAAAUUAACUUUGUACA--3'
```

```
     3'-ACGUUACGUUGAUGUUACGUG-5'    hsa-miR-33b
        |  |  ||      ||||||
Hsa  5'-UAAAGAGCUUUAUUAAUGCAAUAAAUUAACUUUGUACAC-3'
Ptr  5'-UAAAGAGCUUUAUUAAUGCAAUAAAUUAACUUUGUACAC-3'
Mml  5'-UAAAGAGCUUUAUUAAUGCAAUAAAUUAACUUUGUACAC-3'
Mmu  5'-UAAAGAGCUUUAUUAAUGCAAUAAAUUAACUUUGUACA--3'
```

SFig 2. Predicted target sites of miR-33 in the 3'UTR of indicated genes.

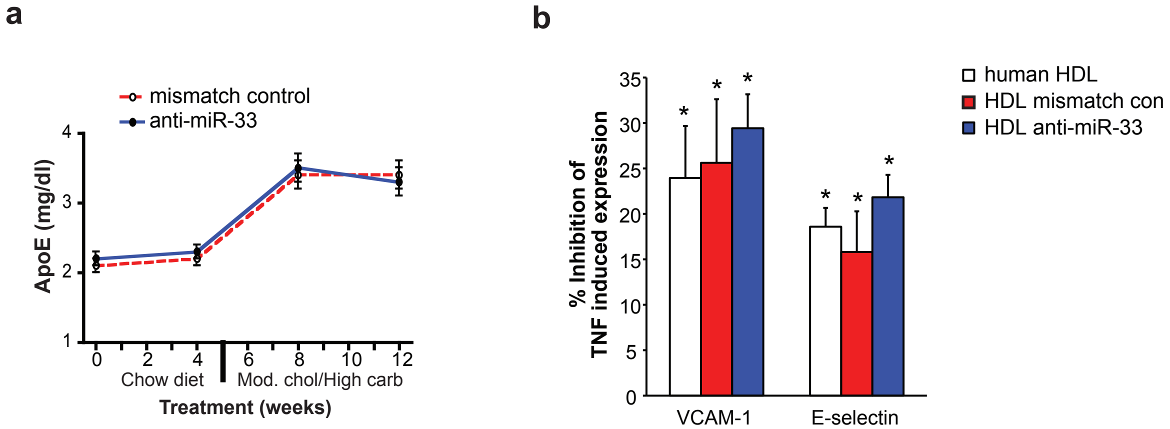
Predicted miR-33a/b binding sites in the indicated genes are shown by bolded sequence in the following species: Hsa=human; Ptr=chimpanzee; Mml=rhesus; Mmu=mouse.

Supplementary Fig 3. Rayner et al.



SFig 3. QRT-PCR analysis of hepatic mRNA expression at baseline (time 0), 4 or 12 weeks of anti-miR treatment. Data are the mean ± SEM. *P ≤ 0.05.

Supplementary Figure 4.



SFig 4. Characterization of plasma HDL. (a) Plasma apoE in anti-miR treated monkeys. *P ≤ 0.05. (b) Inhibition of TNFa-induced VCAM-1 and E-selectin on endothelial cells treated with human HDL (500 µg protein/ml), or equal volumes of PEG-isolated HDL from anti-miR treated monkeys. Data are the mean ± SD and are representative of 3 experiments. *P ≤ 0.05.