## SUPPLEMENTAL MATERIAL

**Figure S1:** Comparison of purine (R) versus pyrimidine (Y) 2' modifications in the absence of 5' phosphorylation of the guide strand. In vitro cell-based evaluation of mRNA knockdown (error bars represent standard deviation of 4 replicates). Unmodified ribose ("r") compared to 2'-deoxy ("d"), 2'-fluoro ("f") and 2'-methoxy ("m"). (**A**) ApoB (6981), (**B**) ApoB (9470), (**C**) ApoB (10127), (**D**) SSB (386), and (**E**) SSB (963) target sites evaluated. Single strands containing 2'F content exhibit the most pronounced mRNA knockdown of the various single strand modification patterns tested.

**Figure S2:** Comparison of purine (R) versus pyrimidine (Y) 2' modifications in the presence of 5' phosphorylation of the guide strand. In vitro cell-based evaluation of mRNA knockdown (error bars represent standard deviation of 4 replicates). Unmodified ribose ("r") compared to 2'-deoxy ("d"), 2'-fluoro ("f") and 2'-methoxy ("m"). (**A**) ApoB (6981), (**B**) ApoB (9470), (**C**) ApoB (10127), (**D**) SSB (386), and (**E**) SSB (963) target sites evaluated. Single strands containing 2'F content exhibit the most pronounced mRNA knockdown of the various single strand modification patterns tested.

**Figure S3:** Three abasic residues (3aba) at positions 1-3 of antisense strand decrease activity for both duplex and single strands. In vitro cell-based evaluation of mRNA knockdown (error bars represent standard deviation of 4 replicates). Unmodified ribose ("r") compared to 2'-deoxy ("d"), 2'-fluoro ("f") and 2'-methoxy ("m"). (**A**) ApoB (8786), (**B**) ApoB (6981), (**C**) ApoB (9470), (**D**) ApoB (10127), (**E**) SSB (386), and (**F**) SSB (963) target sites evaluated. All RNA oligos contain 5' phosphate (5'p).

Figure S1

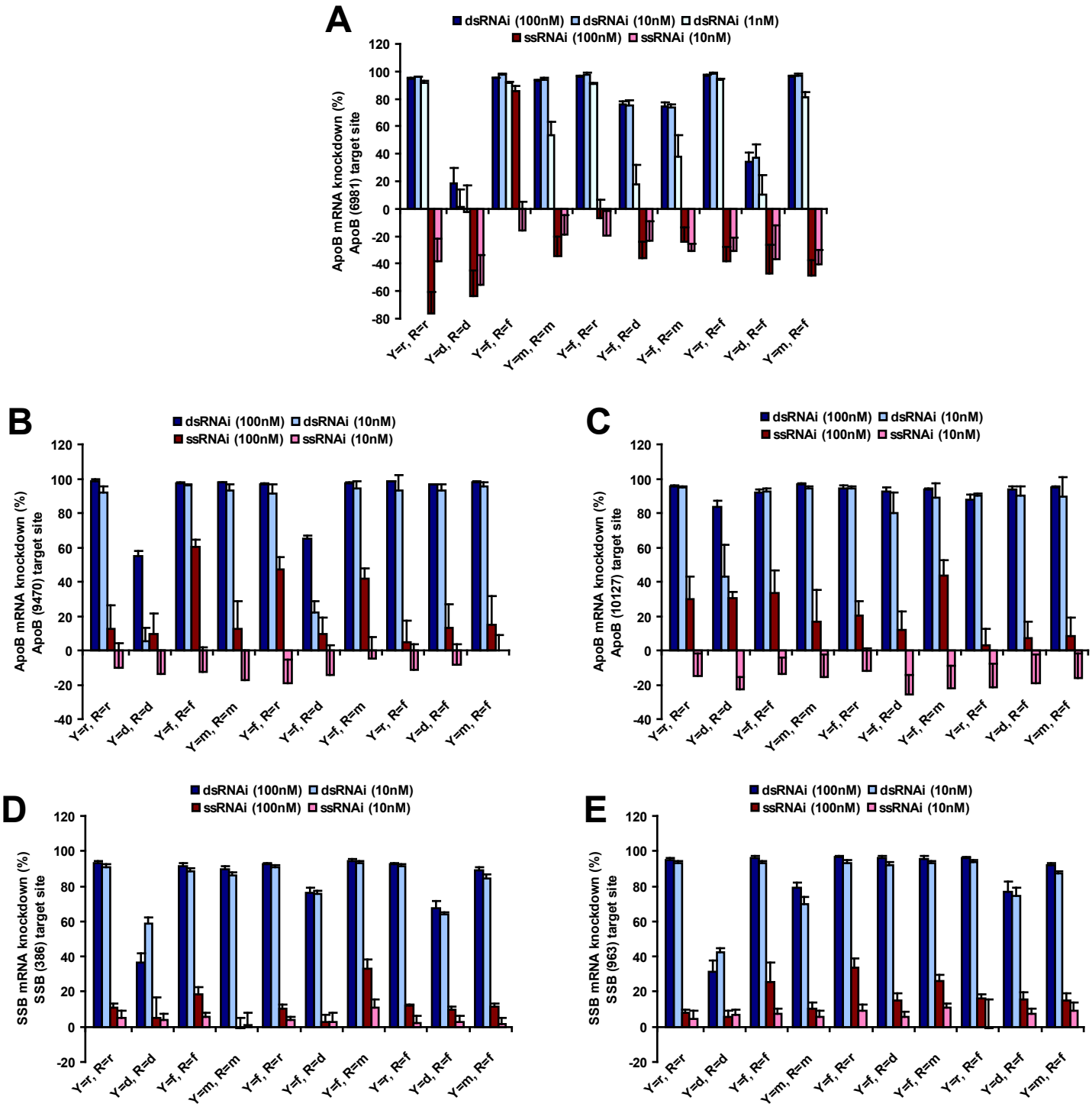
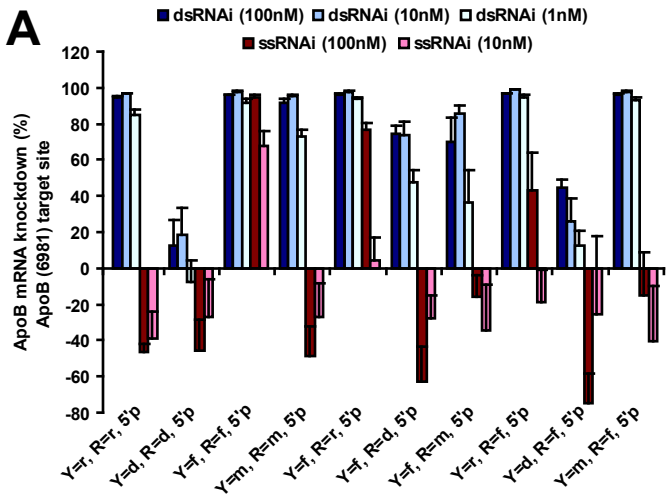
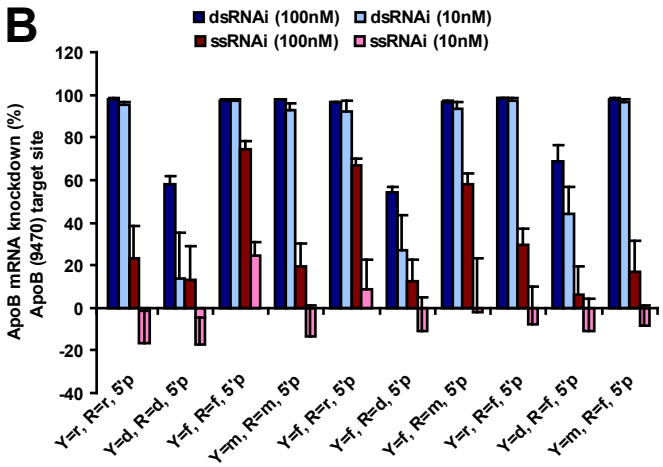
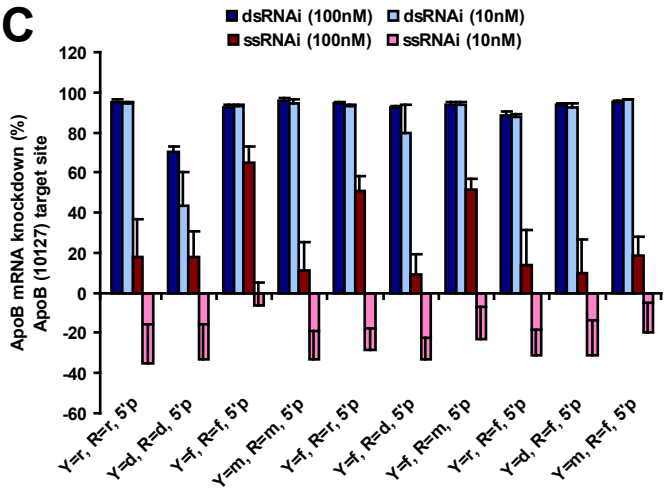
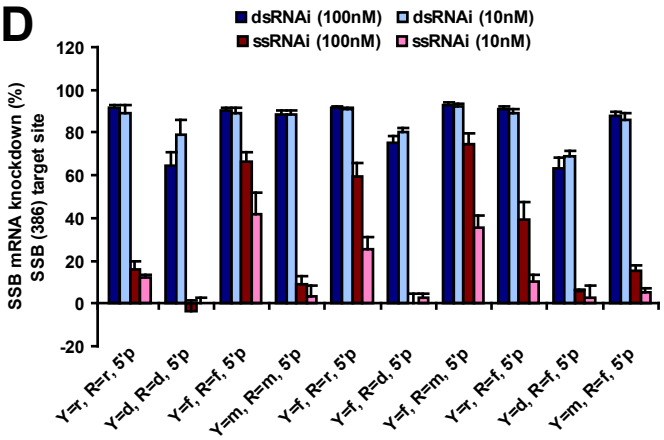

A
dsRNAi (100nM)
dsRNAi (10nM)
dsRNAi (1nM)
ssRNAi (100nM)
ssRNAi (10nM)
ApoB mRNA knockdown (%)
ApoB (6981) target site
B
ApoB (9470) target site
C
ApoB (10127) target site
D
SSB mRNA knockdown (%)
SSB (386) target site
E
SSB (963) target site
Y=r, R=r
Y=d, R=d
Y=f, R=f
Y=m, R=m
Y=f, R=r
Y=f, R=d
Y=f, R=m
Y=r, R=f
Y=d, R=f
Y=m, R=f

Figure S2


A
dsRNAi (100nM)
dsRNAi (10nM)
dsRNAi (1nM)
ssRNAi (100nM)
ssRNAi (10nM)
ApoB mRNA knockdown (%)
ApoB (6981) target site
Y=r, R=r, 5'p
Y=d, R=d, 5'p
Y=f, R=f, 5'p
Y=m, R=m, 5'p
Y=f, R=r, 5'p
Y=f, R=d, 5'p
Y=f, R=m, 5'p
Y=r, R=f, 5'p
Y=d, R=f, 5'p
Y=m, R=f, 5'p


B
dsRNAi (100nM)
dsRNAi (10nM)
ssRNAi (100nM)
ssRNAi (10nM)
ApoB mRNA knockdown (%)
ApoB (9470) target site
Y=r, R=r, 5'p
Y=d, R=d, 5'p
Y=f, R=f, 5'p
Y=m, R=m, 5'p
Y=f, R=r, 5'p
Y=f, R=d, 5'p
Y=f, R=m, 5'p
Y=r, R=f, 5'p
Y=d, R=f, 5'p
Y=m, R=f, 5'p


C
dsRNAi (100nM)
dsRNAi (10nM)
ssRNAi (100nM)
ssRNAi (10nM)
ApoB mRNA knockdown (%)
ApoB (10127) target site
Y=r, R=r, 5'p
Y=d, R=d, 5'p
Y=f, R=f, 5'p
Y=m, R=m, 5'p
Y=f, R=r, 5'p
Y=f, R=d, 5'p
Y=f, R=m, 5'p
Y=r, R=f, 5'p
Y=d, R=f, 5'p
Y=m, R=f, 5'p


D
dsRNAi (100nM)
dsRNAi (10nM)
ssRNAi (100nM)
ssRNAi (10nM)
SSB mRNA knockdown (%)
SSB (386) target site
Y=r, R=r, 5'p
Y=d, R=d, 5'p
Y=f, R=f, 5'p
Y=m, R=m, 5'p
Y=f, R=r, 5'p
Y=f, R=d, 5'p
Y=f, R=m, 5'p
Y=r, R=f, 5'p
Y=d, R=f, 5'p
Y=m, R=f, 5'p

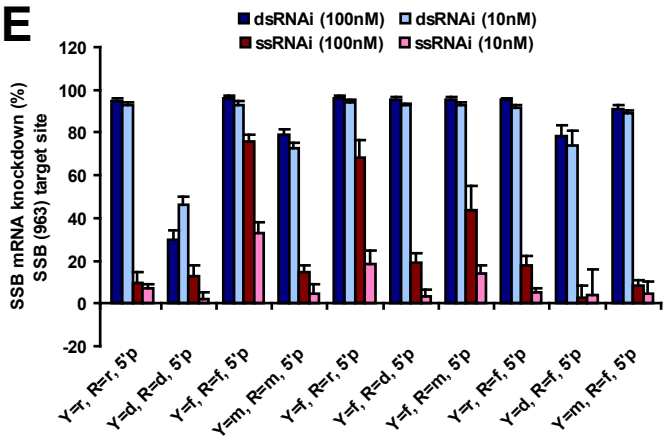

E
dsRNAi (100nM)
dsRNAi (10nM)
ssRNAi (100nM)
ssRNAi (10nM)
SSB mRNA knockdown (%)
SSB (963) target site
Y=r, R=r, 5'p
Y=d, R=d, 5'p
Y=f, R=f, 5'p
Y=m, R=m, 5'p
Y=f, R=r, 5'p
Y=f, R=d, 5'p
Y=f, R=m, 5'p
Y=r, R=f, 5'p
Y=d, R=f, 5'p
Y=m, R=f, 5'p

Figure S3

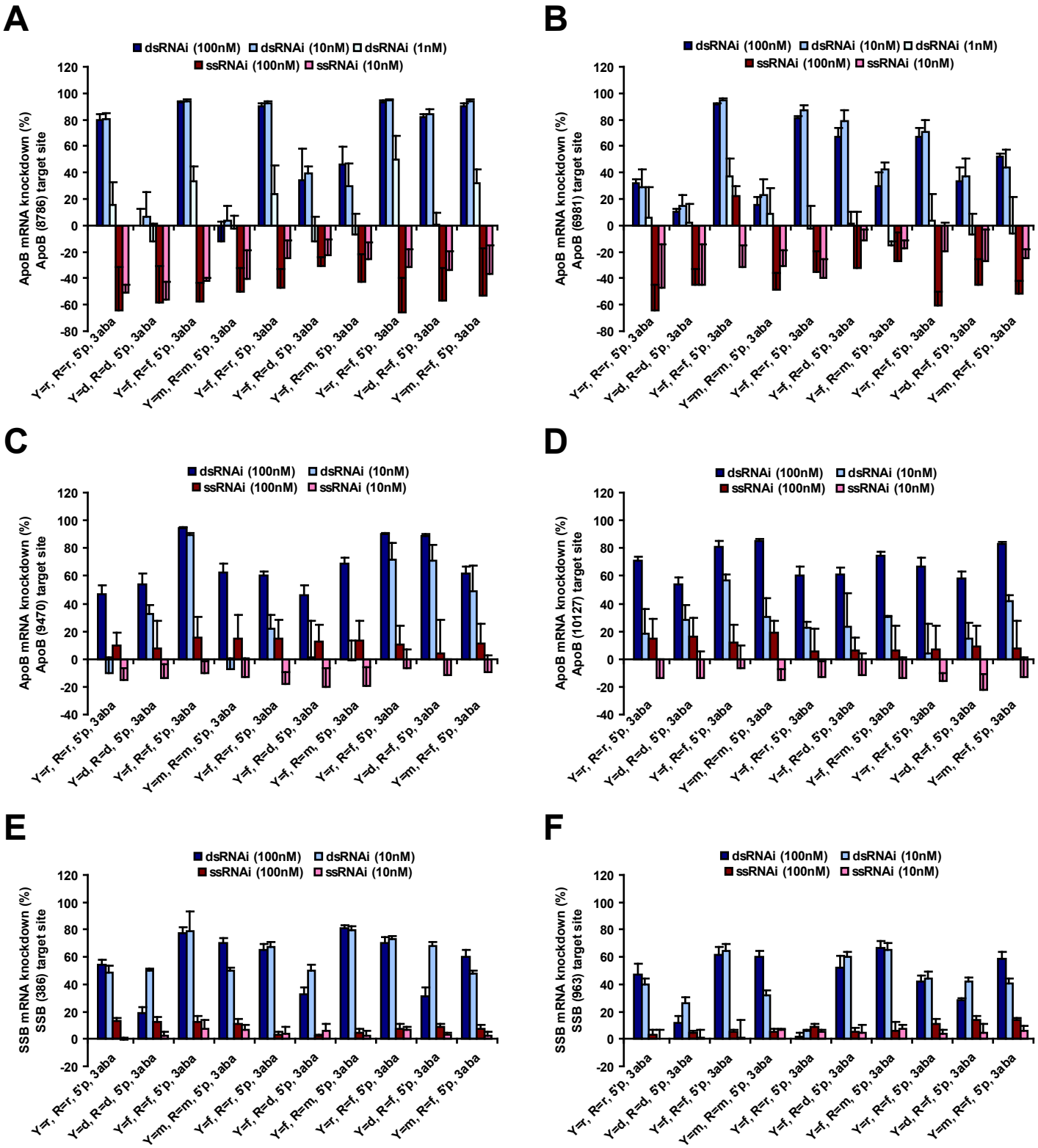

A
dsRNAi (100nM)
dsRNAi (10nM)
dsRNAi (1nM)
ssRNAi (100nM)
ssRNAi (10nM)
ApoB mRNA knockdown (%)
ApoB (8786) target site
B
ApoB (6981) target site
C
ApoB (9470) target site
D
ApoB (10127) target site
E
SSB mRNA knockdown (%)
SSB (386) target site
F
SSB (963) target site
Y=r, R=r, 5'p, 3aba
Y=d, R=d, 5'p, 3aba
Y=f, R=f, 5'p, 3aba
Y=m, R=m, 5'p, 3aba
Y=f, R=r, 5'p, 3aba
Y=f, R=d, 5'p, 3aba
Y=f, R=m, 5'p, 3aba
Y=r, R=f, 5'p, 3aba
Y=d, R=f, 5'p, 3aba
Y=m, R=f, 5'p, 3aba

**Table S1:** In vitro potency and mRNA knockdown (at 10nM) measured in the Hepa1-6 mouse hepatocyte derived cell line. Cells transfected with RNAi Max.

| | | In Vitro Efficacy (24 hrs) | | |
|---|---|---|---|---|
| target | mod type | EC50 (nM) | EC50 ($R^2$) | % KD (10nM) |
| ApoB(8786) | duplex (2'OH, 5'p) | 0.015 | 0.992 | 98 |
| ApoB(8786) | single (2'OH, 5'p) | na | na | 3 |
| ApoB(8786) | duplex (2'F, 5'p) | 0.015 | 0.999 | 97 |
| ApoB(8786) | single (2'F, 5'p) | 1.188 | 0.990 | 91 |
| ApoB(6981) | duplex (2'OH, 5'p) | 0.098 | 0.992 | 94 |
| ApoB(6981) | single (2'OH, 5'p) | na | na | 6 |
| ApoB(6981) | duplex (2'F, 5'p) | 0.042 | 0.997 | 97 |
| ApoB(6981) | single (2'F, 5'p) | 0.890 | 0.988 | 89 |

**Table S2:** In vivo knockdown measured in mouse livers. Percent knockdown, error (standard deviation), and number of mice per group (N) are shown.

| | | | | day 3 | | | day 2 | | | day 7 | | | day 14 | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| target | mod type | study | dose | KD (%) | KD (SD) | N | KD (%) | KD (SD) | N | KD (%) | KD (SD) | N | KD (%) | KD (SD) | N | guide strand |
| ApoB (8786) | duplex (2'OH, 5'p) | study 1 | 3mpk | 97 | 1 | 5 | | | | | | | | | | p;rU;rU;rA;rA;rG;rA;rG;rA;rA;rG;rC;rC;rU;rU;rA;rC;rU;rG;rG;mU;mU |
| ApoB (8786) | single (2'OH, 5'p) | study 1 | 3mpk | 14 | 4 | 5 | | | | | | | | | | p;rU;rU;rA;rA;rG;rA;rG;rA;rA;rG;rC;rC;rU;rU;rA;rC;rU;rG;rG;mU;mU |
| ApoB (8786) | duplex (2'F, 5'p) | study 1 | 3mpk | 98 | 1 | 5 | | | | | | | | | | p;fU;fU;fA;fA;fG;fA;fG;fA;fA;fG;fC;fC;fU;fU;fA;fC;fU;fG;fG;mU;mU |
| ApoB (8786) | single (2'F, 5'p) | study 1 | 3mpk | 74 | 6 | 5 | | | | | | | | | | p;fU;fU;fA;fA;fG;fA;fG;fA;fA;fG;fC;fC;fU;fU;fA;fC;fU;fG;fG;mU;mU |
| ApoB (6981) | duplex (2'OH, 5'p) | study 1 | 3mpk | 85 | 5 | 5 | | | | | | | | | | p;rU;rU;rG;rA;rU;rC;rU;rA;rA;rA;rU;rG;rC;rA;rU;rU;rG;rU;rG;mU;mU |
| ApoB (6981) | single (2'OH, 5'p) | study 1 | 3mpk | 6 | 12 | 5 | | | | | | | | | | p;rU;rU;rG;rA;rU;rC;rU;rA;rA;rA;rU;rG;rC;rA;rU;rU;rG;rU;rG;mU;mU |
| ApoB (6981) | duplex (2'F, 5'p) | study 1 | 3mpk | 97 | 0 | 5 | | | | | | | | | | p;fU;fU;fG;fA;fU;fC;fU;fA;fA;fA;fU;fG;fC;fA;fU;fU;fG;fU;fG;mU;mU |
| ApoB (6981) | single (2'F, 5'p) | study 1 | 3mpk | 61 | 6 | 5 | | | | | | | | | | p;fU;fU;fG;fA;fU;fC;fU;fA;fA;fA;fU;fG;fC;fA;fU;fU;fG;fU;fG;mU;mU |
| ApoB (8786) | duplex (2'F, 5'p) | study 2 | 6mpk | | | | 98 | 1 | 5 | 97 | 0 | 5 | 95 | 1 | 5 | p;fU;fU;fA;fA;fG;fA;fG;fA;fA;fG;fC;fC;fU;fU;fA;fC;fU;fG;fG;mU;mU |
| ApoB (8786) | single (2'F, 5'p) | study 2 | 6mpk | | | | 91 | 1 | 5 | 77 | 4 | 5 | 34 | 14 | 5 | p;fU;fU;fA;fA;fG;fA;fG;fA;fA;fG;fC;fC;fU;fU;fA;fC;fU;fG;fG;mU;mU |
| ApoB (6981) | duplex (2'F, 5'p) | study 2 | 6mpk | | | | 97 | 1 | 5 | 97 | 1 | 5 | 95 | 1 | 5 | p;fU;fU;fG;fA;fU;fC;fU;fA;fA;fA;fU;fG;fC;fA;fU;fU;fG;fU;fG;mU;mU |
| ApoB (6981) | single (2'F, 5'p) | study 2 | 6mpk | | | | 84 | 8 | 3 | 71 | 3 | 3 | 19 | 4 | 4 | p;fU;fU;fG;fA;fU;fC;fU;fA;fA;fA;fU;fG;fC;fA;fU;fU;fG;fU;fG;mU;mU |

**Table S3:** In vitro knockdown and sequence information for 180 guide strands used in this study. "ss" refers to single strand RNA, "ds" double strand siRNA, "Y" is short for pyrimidine, "R" is short for purine, "m" denotes 2'OMe, "f" denotes 2'F, "r" denotes 2'OH, and "d" denotes 2'H. 5' phosphorylation is noted as "5'p" or "p" and abasic incorporations are noted as "3aba" or "aba".

| siRNA ID | guide strand | mod pattern | ds 100nM %KD | ds 100nM STDEV | ds 10nM %KD | ds 10nM STDEV | ds 1nM %KD | ds 1nM STDEV | ss 100nM %KD | ss 100nM STDEV | ss 10nM %KD | ss 10nM STDEV |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| APOB8786-100 | p;rU;rU;rA;rA;rG;rA;rG;rA;rA;rG;rC;rC;rU;rU;rA;rC;rU;rG;rG;mU;mU | Y=r, R=r, 5'p | 96.95 | 0.33 | 98.52 | 0.39 | 95.53 | 0.48 | -3.23 | 14.39 | -44.59 | 20.35 |
| APOB8786-101 | p;dT;dT;dA;dA;dG;dA;dG;dA;dA;dG;dC;dC;dT;dT;dA;dC;dT;dG;dG;mU;mU | Y=d, R=d, 5'p | 12.00 | 19.89 | 21.62 | 12.36 | -5.25 | 27.05 | -38.09 | 14.03 | -30.37 | 18.07 |
| APOB8786-102 | p;fU;fU;fA;fA;fG;fA;fG;fA;fA;fG;fC;fC;fU;fU;fA;fC;fU;fG;fG;mU;mU | Y=f, R=f, 5'p | 96.82 | 0.35 | 97.96 | 0.85 | 94.11 | 2.83 | 89.67 | 3.62 | 57.52 | 5.45 |
| APOB8786-103 | p;mU;mU;mA;mA;mG;mA;mG;mA;mA;mG;mC;mC;mU;rU;mA;mC;mU;mG;mG;mU;mU | Y=m, R=m, 5'p | 88.15 | 2.46 | 85.84 | 1.58 | 63.65 | 9.05 | -43.61 | 18.39 | -33.00 | 9.42 |
| APOB8786-104 | p;fU;fU;rA;rA;rG;rA;rG;rA;rA;rG;fC;fC;fU;fU;rA;fC;fU;rG;rG;mU;mU | Y=f, R=r, 5'p | 97.14 | 0.37 | 98.81 | 0.33 | 96.20 | 0.76 | 86.64 | 1.63 | 20.37 | 11.26 |
| APOB8786-105 | p;fU;fU;dA;dA;dG;dA;dG;dA;dA;dG;fC;fC;fU;fU;dA;fC;fU;dG;dG;mU;mU | Y=f, R=d, 5'p | 80.80 | 2.35 | 84.59 | 2.95 | 59.21 | 2.33 | -2.17 | 12.63 | -46.47 | 6.76 |
| APOB8786-106 | p;fU;fU;mA;mA;mG;mA;mG;mA;mA;mG;fC;fC;fU;fU;mA;fC;fU;mG;mG;mU;mU | Y=f, R=m, 5'p | 96.65 | 0.66 | 97.87 | 0.52 | 91.67 | 2.78 | 78.23 | 1.86 | -23.06 | 20.39 |
| APOB8786-107 | p;rU;rU;fA;fA;fG;fA;fG;fA;fA;fG;rC;rC;rU;rU;fA;rC;rU;fG;fG;mU;mU | Y=r, R=f, 5'p | 96.85 | 0.64 | 98.40 | 0.34 | 95.88 | 1.03 | 42.58 | 7.19 | -11.69 | 3.86 |
| APOB8786-108 | p;dT;dT;fA;fA;fG;fA;fG;fA;fA;fG;dC;dC;dT;dT;fA;dC;dT;fG;fG;mU;mU | Y=d, R=f, 5'p | 95.64 | 0.84 | 96.21 | 0.74 | 90.11 | 1.07 | 27.73 | 14.05 | -37.63 | 4.94 |
| APOB8786-109 | p;mU;mU;fA;fA;fG;fA;fG;fA;fA;fG;mC;mC;mU;rU;fA;mC;mU;fG;fG;mU;mU | Y=m, R=f, 5'p | 94.35 | 0.44 | 96.74 | 0.52 | 83.28 | 4.22 | -42.64 | 11.66 | -33.81 | 4.11 |
| APOB8786-110 | rU;rU;rA;rA;rG;rA;rG;rA;rA;rG;rC;rC;rU;rU;rA;rC;rU;rG;rG;mU;mU | Y=r, R=r | 97.62 | 0.43 | 98.15 | 0.63 | 95.79 | 0.82 | -41.42 | 18.87 | -27.04 | 13.58 |
| APOB8786-111 | dT;dT;dA;dA;dG;dA;dG;dA;dA;dG;dC;dC;dT;dT;dA;dC;dT;dG;dG;mU;mU | Y=d, R=d | -2.86 | 24.82 | -8.26 | 10.52 | -19.36 | 14.94 | -40.26 | 22.41 | -31.18 | 16.28 |
| APOB8786-112 | fU;fU;fA;fA;fG;fA;fG;fA;fA;fG;fC;fC;fU;fU;fA;fC;fU;fG;fG;mU;mU | Y=f, R=f | 96.02 | 0.68 | 98.70 | 0.37 | 93.95 | 2.40 | 67.18 | 3.36 | -23.53 | 6.76 |
| APOB8786-113 | mU;mU;mA;mA;mG;mA;mG;mA;mA;mG;mC;mC;mU;rU;mA;mC;mU;mG;mG;mU;mU | Y=m, R=m | 84.92 | 2.88 | 88.17 | 1.09 | 52.87 | 16.66 | -45.50 | 17.28 | -38.75 | 7.11 |
| APOB8786-114 | fU;fU;rA;rA;rG;rA;rG;rA;rA;rG;fC;fC;fU;fU;rA;fC;fU;rG;rG;mU;mU | Y=f, R=r | 97.53 | 0.24 | 98.10 | 0.36 | 94.51 | 2.16 | 55.33 | 8.10 | -14.81 | 7.96 |
| APOB8786-115 | fU;fU;dA;dA;dG;dA;dG;dA;dA;dG;fC;fC;fU;fU;dA;fC;fU;dG;dG;mU;mU | Y=f, R=d | 91.55 | 0.67 | 84.66 | 5.38 | 33.98 | 17.01 | -40.63 | 16.80 | -31.43 | 14.64 |
| APOB8786-116 | fU;fU;mA;mA;mG;mA;mG;mA;mA;mG;fC;fC;fU;fU;mA;fC;fU;mG;mG;mU;mU | Y=f, R=m | 96.84 | 0.72 | 97.68 | 0.79 | 93.85 | 1.07 | 1.86 | 5.76 | -39.27 | 27.10 |
| APOB8786-117 | rU;rU;fA;fA;fG;fA;fG;fA;fA;fG;rC;rC;rU;rU;fA;rC;rU;fG;fG;mU;mU | Y=r, R=f | 97.16 | 0.62 | 98.31 | 0.91 | 94.65 | 0.14 | -16.59 | 8.12 | -26.54 | 13.26 |
| APOB8786-118 | dT;dT;fA;fA;fG;fA;fG;fA;fA;fG;dC;dC;dT;dT;fA;dC;dT;fG;fG;mU;mU | Y=d, R=f | 95.29 | 1.52 | 96.51 | 1.61 | 79.94 | 6.53 | -38.21 | 30.04 | -44.52 | 13.36 |
| APOB8786-119 | mU;mU;fA;fA;fG;fA;fG;fA;fA;fG;mC;mC;mU;rU;fA;mC;mU;fG;fG;mU;mU | Y=m, R=f | 94.21 | 0.57 | 95.94 | 0.97 | 70.29 | 3.15 | 1.51 | 7.68 | -52.04 | 16.63 |
| APOB8786-120 | p;aba;aba;aba;rA;rG;rA;rG;rA;rA;rG;rC;rC;rU;rU;rA;rC;rU;rG;rG;mU;mU | Y=r, R=r, 5'p, 3aba | 79.75 | 4.55 | 80.56 | 4.25 | 15.28 | 17.38 | -64.53 | 32.69 | -50.75 | 5.45 |
| APOB8786-121 | p;aba;aba;aba;dA;dG;dA;dG;dA;dA;dG;dC;dC;dT;dT;dA;dC;dT;dG;dG;mU;mU | Y=d, R=d, 5'p, 3aba | 0.11 | 12.58 | 6.69 | 18.40 | -11.96 | 13.05 | -58.55 | 27.92 | -56.16 | 13.80 |
| APOB8786-122 | p;aba;aba;aba;fA;fG;fA;fG;fA;fA;fG;fC;fC;fU;fU;fA;fC;fU;fG;fG;mU;mU | Y=f, R=f, 5'p, 3aba | 93.30 | 0.49 | 94.00 | 1.34 | 33.23 | 11.62 | -57.91 | 14.47 | -42.28 | 2.85 |
| APOB8786-123 | p;aba;aba;aba;mA;mG;mA;mG;mA;mA;mG;mC;mC;mU;rU;mA;mC;mU;mG;mG;mU;mU | Y=m, R=m, 5'p, 3aba | -12.21 | 15.10 | 3.41 | 11.38 | -2.70 | 10.18 | -50.47 | 18.11 | -40.41 | 21.29 |
| APOB8786-124 | p;aba;aba;aba;rA;rG;rA;rG;rA;rA;rG;fC;fC;fU;fU;rA;fC;fU;rG;rG;mU;mU | Y=f, R=r, 5'p, 3aba | 90.34 | 1.82 | 92.41 | 1.13 | 23.55 | 21.77 | -47.40 | 14.29 | -24.48 | 13.16 |
| APOB8786-125 | p;aba;aba;aba;dA;dG;dA;dG;dA;dA;dG;fC;fC;fU;fU;dA;fC;fU;dG;dG;mU;mU | Y=f, R=d, 5'p, 3aba | 34.45 | 23.77 | 39.34 | 5.36 | -11.72 | 18.34 | -30.55 | 6.24 | -22.56 | 12.01 |
| APOB8786-126 | p;aba;aba;aba;mA;mG;mA;mG;mA;mA;mG;fC;fC;fU;fU;mA;fC;fU;mG;mG;mU;mU | Y=f, R=m, 5'p, 3aba | 45.99 | 13.41 | 30.04 | 16.80 | -6.84 | 15.80 | -42.85 | 21.23 | -25.40 | 12.87 |
| APOB8786-127 | p;aba;aba;aba;fA;fG;fA;fG;fA;fA;fG;rC;rC;rU;rU;fA;rC;rU;fG;fG;mU;mU | Y=r, R=f, 5'p, 3aba | 93.10 | 1.43 | 94.57 | 0.77 | 50.20 | 17.71 | -65.93 | 26.43 | -31.12 | 13.37 |
| APOB8786-128 | p;aba;aba;aba;fA;fG;fA;fG;fA;fA;fG;dC;dC;dT;dT;fA;dC;dT;fG;fG;mU;mU | Y=d, R=f, 5'p, 3aba | 82.24 | 2.28 | 84.36 | 3.33 | 0.84 | 8.47 | -56.88 | 24.91 | -33.47 | 13.62 |
| APOB8786-129 | p;aba;aba;aba;fA;fG;fA;fG;fA;fA;fG;mC;mC;mU;rU;fA;mC;mU;fG;fG;mU;mU | Y=m, R=f, 5'p, 3aba | 90.40 | 2.00 | 93.68 | 1.62 | 32.22 | 10.39 | -52.96 | 35.85 | -36.61 | 21.60 |
| APOB6981-100 | p;rU;rU;rG;rA;rU;rC;rU;rA;rA;rA;rU;rG;rC;rA;rU;rU;rG;rU;rG;mU;mU | Y=r, R=r, 5'p | 94.66 | 0.53 | 96.51 | 0.71 | 84.89 | 2.70 | -46.35 | 4.64 | -38.63 | 14.32 |
| APOB6981-101 | p;dT;dT;dG;dA;dT;dC;dT;dA;dA;dA;dT;dG;dC;dA;dT;dT;dG;dT;dG;mU;mU | Y=d, R=d, 5'p | 12.26 | 14.63 | 18.58 | 14.75 | -7.98 | 12.16 | -45.72 | 17.13 | -26.91 | 20.88 |
| APOB6981-102 | p;fU;fU;fG;fA;fU;fC;fU;fA;fA;fA;fU;fG;fC;fA;fU;fU;fG;fU;fG;mU;mU | Y=f, R=f, 5'p | 96.00 | 0.41 | 97.59 | 0.81 | 91.77 | 1.75 | 94.55 | 1.23 | 68.06 | 7.93 |
| APOB6981-103 | p;mU;mU;mG;mA;mU;mC;mU;mA;mA;mA;mU;mG;mC;rA;mU;mU;mG;mU;mG;mU;mU | Y=m, R=m, 5'p | 91.97 | 1.61 | 95.14 | 0.97 | 72.68 | 3.67 | -48.93 | 16.66 | -27.35 | 18.92 |
| APOB6981-104 | p;fU;fU;rG;rA;fU;fC;fU;rA;rA;rA;fU;rG;fC;rA;fU;fU;rG;fU;rG;mU;mU | Y=f, R=r, 5'p | 95.94 | 1.26 | 97.85 | 0.50 | 93.55 | 1.44 | 76.64 | 4.16 | 4.57 | 12.65 |
| APOB6981-105 | p;fU;fU;dG;dA;fU;fC;fU;dA;dA;dA;fU;dG;fC;dA;fU;fU;dG;fU;dG;mU;mU | Y=f, R=d, 5'p | 74.77 | 4.19 | 73.48 | 7.63 | 47.36 | 6.89 | -62.65 | 19.09 | -28.10 | 13.32 |
| APOB6981-106 | p;fU;fU;mG;mA;fU;fC;fU;mA;mA;mA;fU;mG;fC;mA;fU;fU;mG;fU;mG;mU;mU | Y=f, R=m, 5'p | 69.79 | 13.41 | 85.47 | 4.38 | 36.56 | 17.48 | -15.78 | 12.05 | -34.58 | 25.28 |
| APOB6981-107 | p;rU;rU;fG;fA;rU;rC;rU;fA;fA;fA;rU;fG;rC;fA;rU;rU;fG;rU;fG;mU;mU | Y=r, R=f, 5'p | 96.63 | 0.39 | 98.76 | 0.28 | 94.51 | 1.59 | 42.99 | 20.74 | -18.65 | 17.97 |
| APOB6981-108 | p;dT;dT;fG;fA;dT;dC;dT;fA;fA;fA;dT;fG;dC;fA;dT;dT;fG;dT;fG;mU;mU | Y=d, R=f, 5'p | 44.66 | 4.44 | 26.18 | 12.35 | 12.19 | 8.23 | -74.59 | 16.51 | -25.81 | 43.55 |
| APOB6981-109 | p;mU;mU;fG;fA;mU;mC;mU;fA;fA;fA;mU;fG;mC;rA;mU;mU;fG;mU;fG;mU;mU | Y=m, R=f, 5'p | 96.35 | 0.80 | 97.42 | 0.88 | 92.88 | 1.44 | -15.43 | 24.50 | -40.66 | 30.83 |
| APOB6981-110 | rU;rU;rG;rA;rU;rC;rU;rA;rA;rA;rU;rG;rC;rA;rU;rU;rG;rU;rG;mU;mU | Y=r, R=r | 94.32 | 1.01 | 95.75 | 0.72 | 91.30 | 1.56 | -76.22 | 15.98 | -37.88 | 16.10 |
| APOB6981-111 | dT;dT;dG;dA;dT;dC;dT;dA;dA;dA;dT;dG;dC;dA;dT;dT;dG;dT;dG;mU;mU | Y=d, R=d | 18.38 | 11.02 | 1.58 | 12.54 | -2.15 | 19.28 | -63.81 | 19.20 | -55.34 | 21.95 |
| APOB6981-112 | fU;fU;fG;fA;fU;fC;fU;fA;fA;fA;fU;fG;fC;fA;fU;fU;fG;fU;fG;mU;mU | Y=f, R=f | 95.54 | 0.10 | 97.82 | 0.68 | 91.52 | 0.78 | 85.80 | 3.49 | -16.06 | 21.16 |
| APOB6981-113 | mU;mU;mG;mA;mU;mC;mU;mA;mA;mA;mU;mG;mC;rA;mU;mU;mG;mU;mG;mU;mU | Y=m, R=m | 93.25 | 0.80 | 94.03 | 1.32 | 53.66 | 9.53 | -34.73 | 14.55 | -18.49 | 13.67 |
| APOB6981-114 | fU;fU;rG;rA;fU;fC;fU;rA;rA;rA;fU;rG;fC;rA;fU;fU;rG;fU;rG;mU;mU | Y=f, R=r | 96.14 | 0.66 | 97.55 | 1.32 | 90.66 | 0.62 | -7.05 | 13.88 | -19.86 | 17.96 |
| APOB6981-115 | fU;fU;dG;dA;fU;fC;fU;dA;dA;dA;fU;dG;fC;dA;fU;fU;dG;fU;dG;mU;mU | Y=f, R=d | 76.22 | 2.26 | 75.25 | 3.68 | 17.73 | 14.12 | -35.66 | 11.69 | -23.54 | 14.66 |
| APOB6981-116 | fU;fU;mG;mA;fU;fC;fU;mA;mA;mA;fU;mG;fC;mA;fU;fU;mG;fU;mG;mU;mU | Y=f, R=m | 74.30 | 3.28 | 73.77 | 2.51 | 37.96 | 15.29 | -24.06 | 10.65 | -30.91 | 5.66 |
| APOB6981-117 | rU;rU;fG;fA;rU;rC;rU;fA;fA;fA;rU;fG;rC;fA;rU;rU;fG;rU;fG;mU;mU | Y=r, R=f | 97.07 | 0.29 | 98.54 | 0.53 | 94.03 | 0.87 | -38.37 | 10.65 | -30.75 | 9.96 |
| APOB6981-118 | dT;dT;fG;fA;dT;dC;dT;fA;fA;fA;dT;fG;dC;fA;dT;dT;fG;dT;fG;mU;mU | Y=d, R=f | 34.12 | 7.09 | 36.81 | 10.24 | 10.53 | 13.95 | -47.52 | 21.06 | -36.78 | 24.95 |
| APOB6981-119 | mU;mU;fG;fA;mU;mC;mU;fA;fA;fA;mU;fG;mC;rA;mU;mU;fG;mU;fG;mU;mU | Y=m, R=f | 95.77 | 0.85 | 96.92 | 1.22 | 81.50 | 3.26 | -48.42 | 11.29 | -40.54 | 10.39 |

| siRNA ID | guide strand | mod pattern | ds 100nM %KD | ds 100nM STDEV | ds 10nM %KD | ds 10nM STDEV | ds 1nM %KD | ds 1nM STDEV | ss 100nM %KD | ss 100nM STDEV | ss 10nM %KD | ss 10nM STDEV |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| APOB6981-120 | p;aba;aba;aba;rA;rU;rC;rU;rA;rA;rA;rU;rG;rC;rA;rU;rU;rG;rU;rG;mU;mU | Y=r, R=r, 5'p, 3aba | 32.12 | 2.98 | 28.67 | 13.91 | 5.63 | 23.56 | -64.64 | 19.45 | -47.43 | 32.99 |
| APOB6981-121 | p;aba;aba;aba;dA;dT;dC;dT;dA;dA;dA;dT;dG;dC;dA;dT;dT;dG;dT;dG;mU;mU | Y=d, R=d, 5'p, 3aba | 10.62 | 1.67 | 14.94 | 7.73 | 1.95 | 14.26 | -45.11 | 12.43 | -45.16 | 31.13 |
| APOB6981-122 | p;aba;aba;aba;fA;fU;fC;fU;fA;fA;fA;fU;fG;fC;fA;fU;fU;fG;fU;fG;mU;mU | Y=f, R=f, 5'p, 3aba | 91.54 | 0.81 | 94.42 | 1.63 | 37.24 | 13.67 | 22.06 | 7.96 | -31.59 | 16.20 |
| APOB6981-123 | p;aba;aba;aba;mA;mU;mC;mU;mA;mA;mA;mU;mG;mC;rA;mU;mU;mG;mU;mG;mU;mU | Y=m, R=m, 5'p, 3aba | 15.30 | 6.40 | 23.02 | 11.63 | 9.13 | 19.30 | -48.36 | 12.13 | -30.51 | 11.55 |
| APOB6981-124 | p;aba;aba;aba;rA;fU;fC;fU;rA;rA;rA;fU;rG;fC;rA;fU;fU;rG;fU;rG;mU;mU | Y=f, R=r, 5'p, 3aba | 81.01 | 1.80 | 87.30 | 3.65 | -2.20 | 17.16 | -35.39 | 15.60 | -39.53 | 13.78 |
| APOB6981-125 | p;aba;aba;aba;dA;fU;fC;fU;dA;dA;dA;fU;dG;fC;dA;fU;fU;dG;fU;dG;mU;mU | Y=f, R=d, 5'p, 3aba | 66.94 | 6.45 | 78.86 | 8.28 | 1.64 | 8.67 | -32.35 | 42.90 | -11.55 | 8.26 |
| APOB6981-126 | p;aba;aba;aba;mA;fU;fC;fU;mA;mA;mA;fU;mG;fC;mA;fU;fU;mG;fU;mG;mU;mU | Y=f, R=m, 5'p, 3aba | 29.77 | 10.56 | 42.73 | 5.01 | -14.76 | 2.84 | -26.67 | 21.06 | -17.25 | 5.86 |
| APOB6981-127 | p;aba;aba;aba;fA;rU;rC;rU;fA;fA;fA;rU;fG;rC;fA;rU;rU;fG;rU;fG;mU;mU | Y=r, R=f, 5'p, 3aba | 67.37 | 6.41 | 70.83 | 8.85 | 3.51 | 20.24 | -60.96 | 10.74 | -19.46 | 21.72 |
| APOB6981-128 | p;aba;aba;aba;fA;dT;dC;dT;fA;fA;fA;dT;fG;dC;fA;dT;dT;fG;dT;fG;mU;mU | Y=d, R=f, 5'p, 3aba | 33.35 | 10.67 | 37.16 | 13.53 | -6.97 | 15.98 | -44.61 | 19.30 | -26.85 | 23.42 |
| APOB6981-129 | p;aba;aba;aba;fA;mU;mC;mU;fA;fA;fA;mU;fG;mC;rA;mU;mU;fG;mU;fG;mU;mU | Y=m, R=f, 5'p, 3aba | 51.92 | 2.27 | 43.98 | 13.48 | -6.30 | 27.92 | -51.67 | 9.65 | -25.14 | 6.76 |
| APOB9470-100 | p;rA;rU;rU;rU;rC;rA;rG;rG;rA;rA;rU;rU;rG;rU;rU;rA;rA;rA;rG;mU;mU | Y=r, R=r, 5'p | 97.86 | 0.34 | 95.04 | 1.44 | | | 23.20 | 15.18 | -16.51 | 14.89 |
| APOB9470-101 | p;dA;dT;dT;dT;dC;dA;dG;dG;dA;dA;dT;dT;dG;dT;dT;dA;dA;dG;mU;mU | Y=d, R=d, 5'p | 57.97 | 3.94 | 13.91 | 21.19 | | | 13.26 | 15.75 | -17.44 | 12.56 |
| APOB9470-102 | p;fA;fU;fU;fU;fC;fA;fG;fG;fA;fA;fU;fU;fG;fU;fU;fA;fA;fA;fG;mU;mU | Y=f, R=f, 5'p | 97.54 | 0.50 | 97.21 | 0.53 | | | 74.64 | 3.89 | 24.63 | 5.91 |
| APOB9470-103 | p;mA;mU;mU;mU;mC;mA;mG;mG;mA;mA;mU;mU;mG;rU;mU;mA;mA;mA;mG;mU;mU | Y=m, R=m, 5'p | 97.78 | 0.30 | 92.56 | 3.36 | | | 19.38 | 10.67 | -13.48 | 14.29 |
| APOB9470-104 | p;rA;fU;fU;fU;fC;rA;rG;rG;rA;rA;fU;fU;rG;fU;fU;rA;rA;rA;rG;mU;mU | Y=f, R=r, 5'p | 96.62 | 0.20 | 91.90 | 5.11 | | | 66.70 | 3.53 | 8.71 | 13.62 |
| APOB9470-105 | p;dA;fU;fU;fU;fC;dA;dG;dG;dA;dA;fU;fU;dG;fU;fU;dA;dA;dA;dG;mU;mU | Y=f, R=d, 5'p | 54.35 | 2.18 | 27.13 | 16.37 | | | 12.20 | 10.48 | -10.96 | 16.05 |
| APOB9470-106 | p;mA;fU;fU;fU;fC;mA;mG;mG;mA;mA;fU;fU;mG;fU;fU;mA;mA;mA;mG;mU;mU | Y=f, R=m, 5'p | 96.81 | 0.36 | 93.72 | 2.99 | | | 57.79 | 5.18 | -2.13 | 25.30 |
| APOB9470-107 | p;fA;rU;rU;rU;rC;fA;fG;fG;fA;fA;rU;rU;fG;rU;rU;fA;fA;fA;fG;mU;mU | Y=r, R=f, 5'p | 98.23 | 0.26 | 97.50 | 0.94 | | | 29.40 | 7.98 | -7.94 | 17.91 |
| APOB9470-108 | p;fA;dT;dT;dT;dC;fA;fG;fG;fA;fA;dT;dT;fG;dT;dT;fA;fA;fA;fG;mU;mU | Y=d, R=f, 5'p | 69.03 | 7.11 | 44.02 | 12.55 | | | 5.91 | 13.65 | -10.65 | 14.85 |
| APOB9470-109 | p;fA;mU;mU;mU;mC;fA;fG;fG;fA;fA;mU;mU;fG;rU;mU;fA;fA;fA;fG;mU;mU | Y=m, R=f, 5'p | 97.99 | 0.31 | 96.89 | 1.12 | | | 17.08 | 14.11 | -8.66 | 10.05 |
| APOB9470-110 | rA;rU;rU;rU;rC;rA;rG;rG;rA;rA;rU;rU;rG;rU;rU;rA;rA;rA;rG;mU;mU | Y=r, R=r | 98.32 | 1.10 | 92.16 | 3.20 | | | 12.52 | 13.89 | -10.31 | 14.64 |
| APOB9470-111 | dA;dT;dT;dT;dC;dA;dG;dG;dA;dA;dT;dT;dG;dT;dT;dA;dA;dA;dG;mU;mU | Y=d, R=d | 54.79 | 3.20 | 5.13 | 7.76 | | | 9.68 | 11.90 | -13.82 | 13.96 |
| APOB9470-112 | fA;fU;fU;fU;fC;fA;fG;fG;fA;fA;fU;fU;fG;fU;fU;fA;fA;fA;fG;mU;mU | Y=f, R=f | 97.30 | 0.40 | 95.90 | 0.66 | | | 60.43 | 4.24 | -12.75 | 14.35 |
| APOB9470-113 | mA;mU;mU;mU;mC;mA;mG;mG;mA;mA;mU;mU;mG;rU;mU;mA;mA;mA;mG;mU;mU | Y=m, R=m | 97.63 | 0.38 | 93.06 | 3.94 | | | 12.33 | 16.15 | -17.37 | 17.54 |
| APOB9470-114 | rA;fU;fU;fU;fC;rA;rG;rG;rA;rA;fU;fU;rG;fU;fU;rA;rA;rA;rG;mU;mU | Y=f, R=r | 96.81 | 0.46 | 91.48 | 5.46 | | | 47.32 | 6.93 | -19.37 | 13.70 |
| APOB9470-115 | dA;fU;fU;fU;fC;dA;dG;dG;dA;dA;fU;fU;dG;fU;fU;dA;dA;dA;dG;mU;mU | Y=f, R=d | 64.82 | 2.23 | 22.31 | 6.50 | | | 9.78 | 9.40 | -14.28 | 17.31 |
| APOB9470-116 | mA;fU;fU;fU;fC;mA;mG;mG;mA;mA;fU;fU;mG;fU;fU;mA;mA;mA;mG;mU;mU | Y=f, R=m | 97.14 | 0.75 | 94.13 | 4.09 | | | 41.53 | 5.97 | -5.04 | 12.70 |
| APOB9470-117 | fA;rU;rU;rU;rC;fA;fG;fG;fA;fA;rU;rU;fG;rU;rU;fA;fA;fA;fG;mU;mU | Y=r, R=f | 98.43 | 0.09 | 93.10 | 8.97 | | | 4.96 | 12.37 | -11.38 | 14.84 |
| APOB9470-118 | fA;dT;dT;dT;dC;fA;fG;fG;fA;fA;dT;dT;fG;dT;dT;fA;fA;fA;fG;mU;mU | Y=d, R=f | 96.43 | 0.43 | 93.27 | 3.60 | | | 13.19 | 13.75 | -8.24 | 11.73 |
| APOB9470-119 | fA;mU;mU;mU;mC;fA;fG;fG;fA;fA;mU;mU;fG;rU;mU;fA;fA;fA;fG;mU;mU | Y=m, R=f | 97.78 | 0.57 | 95.36 | 2.46 | | | 14.99 | 16.61 | -0.16 | 9.21 |
| APOB9470-120 | p;aba;aba;aba;rU;rC;rA;rG;rG;rA;rA;rU;rU;rG;rU;rU;rA;rA;rA;rG;mU;mU | Y=r, R=r, 5'p, 3aba | 46.66 | 6.70 | -9.95 | 11.27 | | | 9.77 | 9.10 | -14.81 | 8.02 |
| APOB9470-121 | p;aba;aba;aba;dT;dC;dA;dG;dG;dA;dA;dT;dT;dG;dT;dT;dA;dA;dA;dG;mU;mU | Y=d, R=d, 5'p, 3aba | 53.94 | 7.54 | 32.68 | 6.48 | | | 7.86 | 20.02 | -13.64 | 9.79 |
| APOB9470-122 | p;aba;aba;aba;fU;fC;fA;fG;fG;fA;fA;fU;fU;fG;fU;fU;fA;fA;fA;fG;mU;mU | Y=f, R=f, 5'p, 3aba | 94.62 | 0.62 | 89.33 | 1.63 | | | 15.76 | 14.90 | -10.41 | 9.15 |
| APOB9470-123 | p;aba;aba;aba;mU;mC;mA;mG;mG;mA;mA;mU;mU;mG;rU;mU;mA;mA;mA;mG;mU;mU | Y=m, R=m, 5'p, 3aba | 62.30 | 6.72 | -7.57 | 8.43 | | | 15.02 | 16.90 | -13.25 | 13.96 |
| APOB9470-124 | p;aba;aba;aba;fU;fC;rA;rG;rG;rA;rA;fU;fU;rG;fU;fU;rA;rA;rA;rG;mU;mU | Y=f, R=r, 5'p, 3aba | 60.53 | 2.42 | 21.59 | 10.31 | | | 14.75 | 13.66 | -18.26 | 8.66 |
| APOB9470-125 | p;aba;aba;aba;fU;fC;dA;dG;dG;dA;dA;fU;fU;dG;fU;fU;dA;dA;dA;dG;mU;mU | Y=f, R=d, 5'p, 3aba | 45.70 | 7.21 | 1.51 | 25.94 | | | 12.48 | 12.41 | -20.20 | 13.95 |
| APOB9470-126 | p;aba;aba;aba;fU;fC;mA;mG;mG;mA;mA;fU;fU;mG;fU;fU;mA;mA;mA;mG;mU;mU | Y=f, R=m, 5'p, 3aba | 68.81 | 4.04 | -1.15 | 14.27 | | | 13.55 | 14.25 | -19.41 | 13.64 |
| APOB9470-127 | p;aba;aba;aba;rU;rC;fA;fG;fG;fA;fA;rU;rU;fG;rU;rU;fA;fA;fA;fG;mU;mU | Y=r, R=f, 5'p, 3aba | 90.42 | 0.51 | 71.62 | 11.77 | | | 10.79 | 12.86 | -6.23 | 13.00 |
| APOB9470-128 | p;aba;aba;aba;dT;dC;fA;fG;fG;fA;fA;dT;dT;fG;dT;dT;fA;fA;fA;fG;mU;mU | Y=d, R=f, 5'p, 3aba | 88.92 | 1.37 | 70.88 | 11.30 | | | 4.20 | 24.33 | -11.90 | 11.83 |
| APOB9470-129 | p;aba;aba;aba;mU;mC;fA;fG;fG;fA;fA;mU;mU;fG;rU;mU;fA;fA;fA;fG;mU;mU | Y=m, R=f, 5'p, 3aba | 61.59 | 4.77 | 49.21 | 18.11 | | | 11.43 | 14.13 | -9.39 | 11.86 |
| APOB10127-100 | p;rU;rU;rG;rG;rU;rA;rU;rU;rC;rA;rG;rU;rG;rU;rG;rA;rU;rG;rA;mU;mU | Y=r, R=r, 5'p | 95.33 | 0.93 | 94.24 | 1.05 | | | 18.03 | 18.83 | -34.85 | 19.52 |
| APOB10127-101 | p;dT;dT;dG;dG;dT;dA;dT;dT;dC;dA;dG;dT;dG;dT;dG;dA;dT;dG;dA;mU;mU | Y=d, R=d, 5'p | 70.29 | 2.63 | 43.28 | 16.75 | | | 18.05 | 12.70 | -33.21 | 17.48 |
| APOB10127-102 | p;fU;fU;fG;fG;fU;fA;fU;fU;fC;fA;fG;fU;fG;fU;fG;fA;fU;fG;fA;mU;mU | Y=f, R=f, 5'p | 92.19 | 1.28 | 93.32 | 0.56 | | | 65.11 | 7.63 | -6.08 | 11.02 |
| APOB10127-103 | p;mU;mU;mG;mG;mU;mA;mU;mU;mC;mA;mG;mU;mG;rU;mG;mA;mU;mG;mA;mU;mU | Y=m, R=m, 5'p | 95.91 | 1.00 | 94.42 | 2.28 | | | 11.25 | 13.89 | -33.15 | 13.97 |
| APOB10127-104 | p;fU;fU;rG;rG;fU;rA;fU;fU;fC;rA;rG;fU;rG;fU;rG;rA;fU;rG;rA;mU;mU | Y=f, R=r, 5'p | 94.30 | 1.04 | 93.00 | 0.59 | | | 50.53 | 7.64 | -28.69 | 11.20 |
| APOB10127-105 | p;fU;fU;dG;dG;fU;dA;fU;fU;fC;dA;dG;fU;dG;fU;dG;dA;fU;dG;dA;mU;mU | Y=f, R=d, 5'p | 92.16 | 0.97 | 79.47 | 14.02 | | | 8.92 | 10.16 | -33.21 | 10.58 |
| APOB10127-106 | p;fU;fU;mG;mG;fU;mA;fU;fU;fC;mA;mG;fU;mG;fU;mG;mA;fU;mG;mA;mU;mU | Y=f, R=m, 5'p | 93.62 | 1.28 | 93.87 | 1.56 | | | 51.65 | 5.09 | -22.83 | 15.89 |
| APOB10127-107 | p;rU;rU;fG;fG;rU;fA;rU;rU;rC;fA;fG;rU;fG;rU;fG;fA;rU;fG;fA;mU;mU | Y=r, R=f, 5'p | 88.23 | 2.21 | 87.46 | 1.54 | | | 13.93 | 17.10 | -31.29 | 12.96 |
| APOB10127-108 | p;dT;dT;fG;fG;dT;fA;dT;dT;dC;fA;fG;dT;fG;dT;fG;fA;dT;fG;fA;mU;mU | Y=d, R=f, 5'p | 93.60 | 0.87 | 92.38 | 1.82 | | | 10.08 | 16.25 | -31.09 | 17.53 |
| APOB10127-109 | p;mU;mU;fG;fG;mU;fA;mU;mU;mC;fA;fG;mU;fG;rU;fG;fA;mU;fG;fA;mU;mU | Y=m, R=f, 5'p | 95.29 | 0.79 | 96.28 | 0.36 | | | 18.63 | 9.30 | -19.70 | 14.46 |
| APOB10127-110 | rU;rU;rG;rG;rU;rA;rU;rU;rC;rA;rG;rU;rG;rU;rG;rA;rU;rG;rA;mU;mU | Y=r, R=r | 95.39 | 0.77 | 95.13 | 0.54 | | | 29.56 | 13.29 | -15.05 | 13.54 |
| APOB10127-111 | dT;dT;dG;dG;dT;dA;dT;dT;dC;dA;dG;dT;dG;dT;dG;dA;dT;dG;dA;mU;mU | Y=d, R=d | 83.65 | 3.29 | 43.07 | 18.29 | | | 30.65 | 3.41 | -22.56 | 6.95 |
| APOB10127-112 | fU;fU;fG;fG;fU;fA;fU;fU;fC;fA;fG;fU;fG;fU;fG;fA;fU;fG;fA;mU;mU | Y=f, R=f | 91.93 | 1.66 | 92.48 | 1.86 | | | 33.15 | 13.46 | -13.54 | 9.09 |
| APOB10127-113 | mU;mU;mG;mG;mU;mA;mU;mU;mC;mA;mG;mU;mG;rU;mG;mA;mU;mG;mA;mU;mU | Y=m, R=m | 96.57 | 0.59 | 94.55 | 0.77 | | | 16.98 | 18.00 | -15.25 | 13.03 |

| siRNA ID | guide strand | mod pattern | ds 100nM %KD | ds 100nM STDEV | ds 10nM %KD | ds 10nM STDEV | ds 1nM %KD | ds 1nM STDEV | ss 100nM %KD | ss 100nM STDEV | ss 10nM %KD | ss 10nM STDEV |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| APOB10127-114 | fU;fU;rG;rG;fU;rA;fU;fU;fC;rA;rG;fU;rG;fU;rG;rA;fU;rG;rA;mU;mU | Y=f, R=r | 94.33 | 1.52 | 94.45 | 0.92 | | | 20.20 | 8.43 | -11.89 | 13.29 |
| APOB10127-115 | fU;fU;dG;dG;fU;dA;fU;fU;fC;dA;dG;fU;dG;fU;dG;dA;fU;dG;dA;mU;mU | Y=f, R=d | 92.58 | 2.56 | 79.86 | 11.97 | | | 12.12 | 10.84 | -25.52 | 11.26 |
| APOB10127-116 | fU;fU;mG;mG;fU;mA;fU;fU;fC;mA;mG;fU;mG;fU;mG;mA;fU;mG;mA;mU;mU | Y=f, R=m | 93.59 | 0.89 | 89.04 | 8.19 | | | 43.72 | 8.64 | -22.31 | 13.08 |
| APOB10127-117 | rU;rU;fG;fG;rU;fA;rU;rU;rC;fA;fG;rU;fG;rU;fG;fA;rU;fG;fA;mU;mU | Y=r, R=f | 87.90 | 2.67 | 90.43 | 1.01 | | | 2.72 | 9.94 | -21.56 | 13.54 |
| APOB10127-118 | dT;dT;fG;fG;dT;fA;dT;dT;dC;fA;fG;dT;fG;dT;fG;fA;dT;fG;fA;mU;mU | Y=d, R=f | 93.97 | 1.27 | 90.36 | 5.45 | | | 6.94 | 9.85 | -18.83 | 16.49 |
| APOB10127-119 | mU;mU;fG;fG;mU;fA;mU;mU;mC;fA;fG;mU;fG;rU;fG;fA;mU;fG;fA;mU;mU | Y=m, R=f | 94.94 | 0.73 | 89.54 | 11.43 | | | 8.28 | 10.53 | -16.34 | 14.38 |
| APOB10127-120 | p;aba;aba;aba;rG;rU;rA;rU;rU;rC;rA;rG;rU;rG;rU;rG;rA;rU;rG;rA;mU;mU | Y=r, R=r, 5'p, 3aba | 70.58 | 2.86 | 18.48 | 17.45 | | | 14.50 | 14.64 | -13.66 | 13.33 |
| APOB10127-121 | p;aba;aba;aba;dG;dT;dA;dT;dT;dC;dA;dG;dT;dG;dT;dG;dA;dT;dG;dA;mU;mU | Y=d, R=d, 5'p, 3aba | 53.90 | 5.04 | 28.43 | 10.36 | | | 15.89 | 13.64 | -14.02 | 19.48 |
| APOB10127-122 | p;aba;aba;aba;fG;fU;fA;fU;fU;fC;fA;fG;fU;fG;fU;fG;fA;fU;fG;fA;mU;mU | Y=f, R=f, 5'p, 3aba | 81.11 | 4.19 | 56.38 | 4.28 | | | 11.99 | 12.75 | -6.68 | 16.24 |
| APOB10127-123 | p;aba;aba;aba;mG;mU;mA;mU;mU;mC;mA;mG;mU;mG;rU;mG;mA;mU;mG;mA;mU;mU | Y=m, R=m, 5'p, 3aba | 84.93 | 1.64 | 30.38 | 13.88 | | | 19.26 | 8.20 | -14.92 | 7.84 |
| APOB10127-124 | p;aba;aba;aba;rG;fU;rA;fU;fU;fC;rA;rG;fU;rG;fU;rG;rA;fU;rG;rA;mU;mU | Y=f, R=r, 5'p, 3aba | 59.99 | 6.67 | 22.46 | 4.33 | | | 5.86 | 15.91 | -12.94 | 11.34 |
| APOB10127-125 | p;aba;aba;aba;dG;fU;dA;fU;fU;fC;dA;dG;fU;dG;fU;dG;dA;fU;dG;dA;mU;mU | Y=f, R=d, 5'p, 3aba | 60.63 | 5.03 | 23.44 | 23.86 | | | 6.06 | 9.23 | -11.21 | 15.27 |
| APOB10127-126 | p;aba;aba;aba;mG;fU;mA;fU;fU;fC;mA;mG;fU;mG;fU;mG;mA;fU;mG;mA;mU;mU | Y=f, R=m, 5'p, 3aba | 74.71 | 2.31 | 30.20 | 0.55 | | | 5.87 | 17.86 | -13.71 | 14.67 |
| APOB10127-127 | p;aba;aba;aba;fG;rU;fA;rU;rU;rC;fA;fG;rU;fG;rU;fG;fA;rU;fG;fA;mU;mU | Y=r, R=f, 5'p, 3aba | 66.88 | 6.51 | 4.33 | 20.82 | | | 6.65 | 17.34 | -15.71 | 5.33 |
| APOB10127-128 | p;aba;aba;aba;fG;dT;fA;dT;dT;dC;fA;fG;dT;fG;dT;fG;fA;dT;fG;fA;mU;mU | Y=d, R=f, 5'p, 3aba | 58.32 | 4.80 | 14.87 | 11.04 | | | 8.83 | 15.45 | -22.23 | 11.24 |
| APOB10127-129 | p;aba;aba;aba;fG;mU;fA;mU;mU;mC;fA;fG;mU;fG;rU;fG;fA;mU;fG;fA;mU;mU | Y=m, R=f, 5'p, 3aba | 83.22 | 1.25 | 41.89 | 4.44 | | | 7.90 | 19.66 | -12.96 | 14.13 |
| SSB386-100 | p;rU;rU;rA;rC;rA;rU;rU;rA;rA;rG;rU;rC;rU;rG;rU;rU;rG;rU;mU;mU | Y=r, R=r, 5'p | 91.33 | 1.55 | 89.40 | 3.32 | | | 16.06 | 3.73 | 12.07 | 1.35 |
| SSB386-101 | p;dT;dT;dA;dC;dA;dT;dT;dA;dA;dA;dG;dT;dC;dT;dG;dT;dT;dG;dT;mU;mU | Y=d, R=d, 5'p | 64.30 | 6.34 | 78.74 | 7.43 | | | -3.62 | 5.06 | 0.19 | 2.67 |
| SSB386-102 | p;fU;fU;fA;fC;fA;fU;fU;fA;fA;fA;fG;fU;fC;fU;fG;fU;fU;fG;fU;mU;mU | Y=f, R=f, 5'p | 90.57 | 0.98 | 89.30 | 2.30 | | | 66.56 | 4.55 | 41.96 | 9.67 |
| SSB386-103 | p;mU;mU;mA;mC;mA;mU;mU;mA;mA;mA;mG;mU;mC;rU;mG;mU;mU;mG;mU;mU;mU | Y=m, R=m, 5'p | 88.27 | 1.93 | 88.19 | 1.91 | | | 9.07 | 3.44 | 3.32 | 5.24 |
| SSB386-104 | p;fU;fU;rA;fC;rA;fU;fU;rA;rA;rA;rG;fU;fC;fU;rG;fU;fU;rG;fU;mU;mU | Y=f, R=r, 5'p | 91.63 | 0.64 | 90.87 | 1.03 | | | 59.15 | 6.54 | 25.28 | 5.77 |
| SSB386-105 | p;fU;fU;dA;fC;dA;fU;fU;dA;dA;dA;dG;fU;fC;fU;dG;fU;fU;dG;fU;mU;mU | Y=f, R=d, 5'p | 74.93 | 3.51 | 80.03 | 2.23 | | | 0.05 | 4.34 | 2.46 | 2.26 |
| SSB386-106 | p;fU;fU;mA;fC;mA;fU;fU;mA;mA;mA;mG;fU;fC;fU;mG;fU;fU;mG;fU;mU;mU | Y=f, R=m, 5'p | 92.80 | 1.42 | 91.97 | 1.85 | | | 74.61 | 4.95 | 35.48 | 5.52 |
| SSB386-107 | p;rU;rU;fA;rC;fA;rU;rU;fA;fA;fA;fG;rU;rC;rU;fG;rU;rU;fG;rU;mU;mU | Y=r, R=f, 5'p | 91.20 | 1.32 | 89.06 | 1.74 | | | 39.30 | 8.44 | 10.12 | 3.10 |
| SSB386-108 | p;dT;dT;fA;dC;fA;dT;dT;fA;fA;fA;fG;dT;dC;dT;fG;dT;dT;fG;dT;mU;mU | Y=d, R=f, 5'p | 63.24 | 4.85 | 68.97 | 2.75 | | | 5.54 | 1.02 | 2.83 | 5.27 |
| SSB386-109 | p;mU;mU;fA;mC;fA;mU;mU;fA;fA;fA;fG;mU;mC;rU;fG;mU;mU;fG;mU;mU;mU | Y=m, R=f, 5'p | 87.66 | 2.03 | 85.88 | 3.19 | | | 15.53 | 2.19 | 5.20 | 1.67 |
| SSB386-110 | rU;rU;rA;rC;rA;rU;rU;rA;rA;rA;rG;rU;rC;rU;rG;rU;rU;rG;rU;mU;mU | Y=r, R=r | 92.95 | 1.34 | 90.57 | 2.29 | | | 11.16 | 1.95 | 5.22 | 4.04 |
| SSB386-111 | dT;dT;dA;dC;dA;dT;dT;dA;dA;dA;dG;dT;dC;dT;dG;dT;dT;dG;dT;mU;mU | Y=d, R=d | 36.37 | 5.22 | 58.60 | 3.37 | | | 5.18 | 11.54 | 3.94 | 3.27 |
| SSB386-112 | fU;fU;fA;fC;fA;fU;fU;fA;fA;fG;fU;fC;fU;fG;fU;fU;fG;fU;mU;mU | Y=f, R=f | 91.35 | 1.58 | 88.41 | 1.83 | | | 18.33 | 4.36 | 5.60 | 2.36 |
| SSB386-113 | mU;mU;mA;mC;mA;mU;mU;mA;mA;mA;mG;mU;mC;rU;mG;mU;mU;mG;mU;mU;mU | Y=m, R=m | 89.53 | 1.90 | 86.05 | 1.95 | | | -0.94 | 6.10 | 0.78 | 7.15 |
| SSB386-114 | fU;fU;rA;fC;rA;fU;fU;rA;rA;rA;rG;fU;fC;fU;rG;fU;fU;rG;fU;mU;mU | Y=f, R=r | 92.62 | 0.74 | 90.82 | 1.04 | | | 10.35 | 2.50 | 4.17 | 1.43 |
| SSB386-115 | fU;fU;dA;fC;dA;fU;fU;dA;dA;dA;dG;fU;fC;fU;dG;fU;fU;dG;fU;mU;mU | Y=f, R=d | 76.42 | 2.60 | 75.59 | 2.01 | | | 2.48 | 4.15 | 2.46 | 5.36 |
| SSB386-116 | fU;fU;mA;fC;mA;fU;fU;mA;mA;mA;mG;fU;fC;fU;mG;fU;fU;mG;fU;mU;mU | Y=f, R=m | 94.37 | 1.12 | 92.98 | 1.23 | | | 33.07 | 5.29 | 11.07 | 4.24 |
| SSB386-117 | rU;rU;fA;rC;fA;rU;rU;fA;fA;fA;fG;rU;rC;rU;fG;rU;rU;fG;rU;mU;mU | Y=r, R=f | 92.73 | 0.68 | 91.31 | 1.05 | | | 12.00 | 0.67 | 2.28 | 3.84 |
| SSB386-118 | dT;dT;fA;dC;fA;dT;dT;fA;fA;fA;fG;dT;dC;dT;fG;dT;dT;fG;dT;mU;mU | Y=d, R=f | 67.24 | 4.15 | 64.22 | 0.93 | | | 9.55 | 2.08 | 2.90 | 3.30 |
| SSB386-119 | mU;mU;fA;mC;fA;mU;mU;fA;fA;fA;fG;mU;mC;rU;fG;mU;mU;fG;mU;mU;mU | Y=m, R=f | 89.08 | 1.73 | 84.46 | 2.18 | | | 11.75 | 1.70 | 1.41 | 3.69 |
| SSB386-120 | p;aba;aba;aba;rC;rA;rU;rU;rA;rA;rA;rG;rU;rC;rU;rG;rU;rU;rG;rU;mU;mU | Y=r, R=r, 5'p, 3aba | 54.00 | 3.74 | 48.47 | 5.20 | | | 12.95 | 2.09 | -0.59 | 1.58 |
| SSB386-121 | p;aba;aba;aba;dC;dA;dT;dT;dA;dA;dA;dG;dT;dC;dT;dG;dT;dT;dG;dT;mU;mU | Y=d, R=d, 5'p, 3aba | 18.64 | 4.53 | 49.90 | 1.72 | | | 12.73 | 3.18 | 2.42 | 2.89 |
| SSB386-122 | p;aba;aba;aba;fC;fA;fU;fU;fA;fA;fA;fG;fU;fC;fU;fG;fU;fU;fG;fU;mU;mU | Y=f, R=f, 5'p, 3aba | 77.39 | 4.34 | 78.85 | 14.58 | | | 12.74 | 3.79 | 7.35 | 6.40 |
| SSB386-123 | p;aba;aba;aba;mC;mA;mU;mU;mA;mA;mA;mG;mU;mC;rU;mG;mU;mU;mG;mU;mU;mU | Y=m, R=m, 5'p, 3aba | 69.98 | 3.86 | 49.92 | 2.22 | | | 11.03 | 3.70 | 6.60 | 3.87 |
| SSB386-124 | p;aba;aba;aba;fC;rA;fU;fU;rA;rA;rA;rG;fU;fC;fU;rG;fU;fU;rG;fU;mU;mU | Y=f, R=r, 5'p, 3aba | 65.06 | 4.73 | 67.46 | 3.62 | | | 3.14 | 2.07 | 3.64 | 5.04 |
| SSB386-125 | p;aba;aba;aba;fC;dA;fU;fU;dA;dA;dA;dG;fU;fC;fU;dG;fU;fU;dG;fU;mU;mU | Y=f, R=d, 5'p, 3aba | 32.43 | 5.01 | 50.27 | 3.93 | | | 2.60 | 0.63 | 6.01 | 4.90 |
| SSB386-126 | p;aba;aba;aba;fC;mA;fU;fU;mA;mA;mA;mG;fU;fC;fU;mG;fU;fU;mG;fU;mU;mU | Y=f, R=m, 5'p, 3aba | 81.10 | 2.19 | 79.41 | 3.01 | | | 4.66 | 3.02 | 2.56 | 3.29 |
| SSB386-127 | p;aba;aba;aba;rC;fA;rU;rU;fA;fA;fA;fG;rU;rC;rU;fG;rU;rU;fG;rU;mU;mU | Y=r, R=f, 5'p, 3aba | 70.54 | 3.70 | 73.27 | 2.32 | | | 7.13 | 3.95 | 6.69 | 2.25 |
| SSB386-128 | p;aba;aba;aba;dC;fA;dT;dT;fA;fA;fA;fG;dT;dC;dT;fG;dT;dT;fG;dT;mU;mU | Y=d, R=f, 5'p, 3aba | 31.50 | 6.12 | 67.94 | 2.87 | | | 8.66 | 2.52 | 3.24 | 1.34 |
| SSB386-129 | p;aba;aba;aba;mC;fA;mU;mU;fA;fA;fA;fG;mU;mC;rU;fG;mU;mU;fG;mU;mU;mU | Y=m, R=f, 5'p, 3aba | 59.81 | 5.65 | 48.19 | 1.65 | | | 7.65 | 2.73 | 2.36 | 2.64 |
| SSB963-100 | p;rU;rU;rU;rU;rA;rU;rU;rU;rC;rA;rC;rC;rA;rU;rG;rA;rU;rU;rU;mU;mU | Y=r, R=r, 5'p | 95.08 | 0.83 | 93.09 | 1.16 | | | 9.65 | 5.27 | 7.05 | 1.96 |
| SSB963-101 | p;dT;dT;dT;dT;dA;dT;dT;dT;dC;dA;dC;dC;dA;dT;dG;dA;dT;dT;dT;mU;mU | Y=d, R=d, 5'p | 30.09 | 3.88 | 46.52 | 3.50 | | | 12.54 | 5.23 | 2.37 | 3.16 |
| SSB963-102 | p;fU;fU;fU;fU;fA;fU;fU;fU;fC;fA;fC;fC;fA;fU;fG;fA;fU;fU;fU;mU;mU | Y=f, R=f, 5'p | 95.82 | 1.30 | 92.80 | 1.73 | | | 75.81 | 3.30 | 32.82 | 5.51 |
| SSB963-103 | p;mU;mU;mU;mU;mA;mU;mU;mU;mC;mA;mC;mC;mA;rU;mG;mA;mU;mU;mU;mU;mU | Y=m, R=m, 5'p | 79.02 | 2.26 | 72.84 | 2.50 | | | 14.48 | 3.55 | 4.70 | 4.03 |
| SSB963-104 | p;fU;fU;fU;fU;rA;fU;fU;fU;fC;rA;fC;fC;rA;fU;rG;rA;fU;fU;fU;mU;mU | Y=f, R=r, 5'p | 96.20 | 1.38 | 94.18 | 1.24 | | | 68.54 | 8.20 | 18.68 | 6.28 |
| SSB963-105 | p;fU;fU;fU;fU;dA;fU;fU;fU;fC;dA;fC;fC;dA;fU;dG;dA;fU;fU;fU;mU;mU | Y=f, R=d, 5'p | 95.34 | 1.26 | 92.80 | 0.92 | | | 19.19 | 4.41 | 3.27 | 3.37 |
| SSB963-106 | p;fU;fU;fU;fU;mA;fU;fU;fU;fC;mA;fC;fC;mA;fU;mG;mA;fU;fU;fU;mU;mU | Y=f, R=m, 5'p | 95.54 | 1.25 | 92.98 | 1.03 | | | 43.84 | 11.28 | 13.88 | 4.00 |
| SSB963-107 | p;rU;rU;rU;rU;fA;rU;rU;rU;rC;fA;rC;rC;fA;rU;fG;fA;rU;rU;rU;mU;mU | Y=r, R=f, 5'p | 95.54 | 0.66 | 91.47 | 1.18 | | | 18.05 | 4.35 | 5.36 | 1.59 |

| siRNA ID | guide strand | mod pattern | ds 100nM %KD | ds 100nM STDEV | ds 10nM %KD | ds 10nM STDEV | ds 1nM %KD | ds 1nM STDEV | ss 100nM %KD | ss 100nM STDEV | ss 10nM %KD | ss 10nM STDEV |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SSB963-108 | p;dT;dT;dT;dT;fA;dT;dT;dT;dC;fA;dC;dC;fA;dT;fG;fA;dT;dT;dT;mU;mU | Y=d, R=f, 5'p | 78.67 | 4.68 | 73.80 | 7.24 | | | 2.75 | 5.67 | 3.88 | 12.33 |
| SSB963-109 | p;mU;mU;mU;mU;fA;mU;mU;mU;mC;fA;mC;mC;fA;rU;fG;fA;mU;mU;mU;mU;mU | Y=m, R=f, 5'p | 91.11 | 2.07 | 89.08 | 1.47 | | | 8.13 | 2.87 | 4.69 | 5.65 |
| SSB963-110 | rU;rU;rU;rU;rA;rU;rU;rU;rC;rA;rC;rC;rA;rU;rG;rA;rU;rU;rU;mU;mU | Y=r, R=r | 95.16 | 0.69 | 93.16 | 0.95 | | | 7.91 | 1.95 | 4.44 | 4.51 |
| SSB963-111 | dT;dT;dT;dT;dA;dT;dT;dT;dC;dA;dC;dC;dA;dT;dG;dA;dT;dT;dT;mU;mU | Y=d, R=d | 31.27 | 6.55 | 42.39 | 2.50 | | | 5.85 | 3.18 | 6.61 | 3.42 |
| SSB963-112 | fU;fU;fU;fU;fA;fU;fU;fU;fC;fA;fC;fC;fA;fU;fG;fA;fU;fU;fU;mU;mU | Y=f, R=f | 95.96 | 1.02 | 93.42 | 0.98 | | | 25.26 | 11.11 | 7.26 | 3.25 |
| SSB963-113 | mU;mU;mU;mU;mA;mU;mU;mU;mC;mA;mC;mC;mA;rU;mG;mA;mU;mU;mU;mU;mU | Y=m, R=m | 79.33 | 2.98 | 69.90 | 3.97 | | | 10.47 | 3.23 | 5.38 | 4.06 |
| SSB963-114 | fU;fU;fU;fU;rA;fU;fU;fU;fC;rA;fC;fC;rA;fU;rG;rA;fU;fU;fU;mU;mU | Y=f, R=r | 96.51 | 0.94 | 93.43 | 1.43 | | | 33.75 | 5.20 | 9.15 | 3.51 |
| SSB963-115 | fU;fU;fU;fU;dA;fU;fU;fU;fC;dA;fC;fC;dA;fU;dG;dA;fU;fU;fU;mU;mU | Y=f, R=d | 95.96 | 1.10 | 92.24 | 1.55 | | | 15.19 | 4.00 | 5.84 | 2.86 |
| SSB963-116 | fU;fU;fU;fU;mA;fU;fU;fU;fC;mA;fC;fC;mA;fU;mG;mA;fU;fU;fU;mU;mU | Y=f, R=m | 95.72 | 1.60 | 93.28 | 1.30 | | | 25.87 | 3.96 | 11.19 | 2.26 |
| SSB963-117 | rU;rU;rU;rU;fA;rU;rU;rU;rC;fA;rC;rC;fA;rU;fG;fA;rU;rU;rU;mU;mU | Y=r, R=f | 96.07 | 0.70 | 93.72 | 0.96 | | | 15.91 | 2.41 | -1.03 | 16.33 |
| SSB963-118 | dT;dT;dT;dT;fA;dT;dT;dT;dC;fA;dC;dC;fA;dT;fG;fA;dT;dT;dT;mU;mU | Y=d, R=f | 76.93 | 5.75 | 74.70 | 4.25 | | | 15.86 | 4.08 | 7.44 | 3.18 |
| SSB963-119 | mU;mU;mU;mU;fA;mU;mU;mU;mC;fA;mC;mC;fA;rU;fG;fA;mU;mU;mU;mU;mU | Y=m, R=f | 91.78 | 1.47 | 87.07 | 1.46 | | | 15.27 | 3.77 | 8.93 | 4.73 |
| SSB963-120 | p;aba;aba;aba;rU;rA;rU;rU;rU;rC;rA;rC;rC;rA;rU;rG;rA;rU;rU;rU;mU;mU | Y=r, R=r, 5'p, 3aba | 47.26 | 7.81 | 39.80 | 4.23 | | | 3.20 | 3.40 | 0.20 | 6.28 |
| SSB963-121 | p;aba;aba;aba;dT;dA;dT;dT;dT;dC;dA;dC;dC;dA;dT;dG;dA;dT;dT;dT;mU;mU | Y=d, R=d, 5'p, 3aba | 12.07 | 4.88 | 26.16 | 4.08 | | | 4.58 | 1.26 | 1.02 | 5.50 |
| SSB963-122 | p;aba;aba;aba;fU;fA;fU;fU;fU;fC;fA;fC;fC;fA;fU;fG;fA;fU;fU;fU;mU;mU | Y=f, R=f, 5'p, 3aba | 61.82 | 5.24 | 64.71 | 5.07 | | | 5.21 | 1.85 | 0.83 | 12.77 |
| SSB963-123 | p;aba;aba;aba;mU;mA;mU;mU;mU;mC;mA;mC;mC;mA;rU;mG;mA;mU;mU;mU;mU;mU | Y=m, R=m, 5'p, 3aba | 60.06 | 4.16 | 32.24 | 2.99 | | | 5.38 | 2.30 | 6.61 | 0.92 |
| SSB963-124 | p;aba;aba;aba;fU;rA;fU;fU;fU;fC;rA;fC;fC;rA;fU;rG;rA;fU;fU;fU;mU;mU | Y=f, R=r, 5'p, 3aba | 1.88 | 2.87 | 5.72 | 1.27 | | | 8.64 | 2.57 | 5.17 | 1.84 |
| SSB963-125 | p;aba;aba;aba;fU;dA;fU;fU;fU;fC;dA;fC;fC;dA;fU;dG;dA;fU;fU;fU;mU;mU | Y=f, R=d, 5'p, 3aba | 52.10 | 8.61 | 60.40 | 3.50 | | | 5.24 | 2.74 | 4.37 | 6.01 |
| SSB963-126 | p;aba;aba;aba;fU;mA;fU;fU;fU;fC;mA;fC;fC;mA;fU;mG;mA;fU;fU;fU;mU;mU | Y=f, R=m, 5'p, 3aba | 66.52 | 4.83 | 65.16 | 5.04 | | | 5.88 | 6.29 | 7.54 | 2.60 |
| SSB963-127 | p;aba;aba;aba;rU;fA;rU;rU;rU;rC;fA;rC;rC;fA;rU;fG;fA;rU;rU;rU;mU;mU | Y=r, R=f, 5'p, 3aba | 41.97 | 4.22 | 44.11 | 5.05 | | | 11.16 | 3.66 | 4.05 | 2.74 |
| SSB963-128 | p;aba;aba;aba;dT;fA;dT;dT;dT;dC;fA;dC;dC;fA;dT;fG;fA;dT;dT;dT;mU;mU | Y=d, R=f, 5'p, 3aba | 28.25 | 1.56 | 42.17 | 2.76 | | | 13.97 | 3.04 | 4.85 | 5.91 |
| SSB963-129 | p;aba;aba;aba;mU;fA;mU;mU;mU;mC;fA;mC;mC;fA;rU;fG;fA;mU;mU;mU;mU;mU | Y=m, R=f, 5'p, 3aba | 58.65 | 4.84 | 40.77 | 3.28 | | | 13.96 | 1.31 | 5.99 | 3.43 |

**Table S4:** Passenger strands used in this study.

| siRNA ID | passenger strand |
|---|---|
| APOB8786 | iB;rC;rC;rA;rG;rU;rA;rA;rG;rG;rC;rU;rU;rC;rU;rC;rU;rU;rA;rA;mU;mU;iB |
| APOB6981 | iB;rC;rA;rC;rA;rA;rU;rG;rC;rA;rU;rU;rU;rA;rG;rA;rU;rC;rA;rA;mU;mU;iB |
| APOB10127 | iB;rU;rC;rA;rU;rC;rA;rC;rA;rC;rU;rG;rA;rA;rU;rA;rC;rC;rA;rA;mU;mU;iB |
| APOB9470 | iB;rC;rU;rU;rU;rA;rA;rC;rA;rA;rU;rU;rC;rC;rU;rG;rA;rA;rA;rU;mU;mU;iB |
| SSB386 | iB;rA;rC;rA;rA;rC;rA;rG;rA;rC;rU;rU;rU;rA;rA;rU;rG;rU;rA;rA;mU;mU;iB |
| SSB963 | iB;rA;rA;rA;rU;rC;rA;rU;rG;rG;rU;rG;rA;rA;rA;rU;rA;rA;rA;rA;mU;mU;iB |

**Table S5:** DNA primers used for 5'RACE (see Figure 6).

| name | sequence | amplicon size* | ApoB site** |
|---|---|---|---|
| rev1 | GGCATTGTGCTCACCAGTCATTTCTGCCTT | 358 | 9153 |
| rev1n | GAGCAGTGCCCGACCATTGGCTGTT | 319 | 9114 |
| rev2 | CTCCGTGTAAGGCAAGTTAATTTCAGGAATTGTT | 712 | 9507 |
| rev2n | CCAGGTTGGCATCTCCATTCATTCCTATA | 659 | 9454 |
| GeneRacer5′ | CGACTGGAGCACGAGGACACTGA | | |
| GeneRacer5′ Nested | GGACACTGACATGGACTGAAGGAGTA | | |

** amplicon size calculated based on predicted cleavage site of ApoB (8786) siRNA*

*** site relative to NM009693*