*Bpi*I *Pci*I

5’ gcgatgtagaagacg**acatgt**tctttcctgcgttatcccctgattctgtggataaccgtattaccgcctttgagtgagctgataccgctcgccgc

agccgaacgaccgagcgcagcgagtcagtgagcgaggaagcggaagagcgcccaatacgcaaaccgcctctccccgcgcgttgg

ccgattcattaatccagctggcacgacaggtttcccgactggaaagcgggcagtgagcgcaacgcaattaatgtgagttacctcactcatt

aggcaccccaggctttacactttatgcttccggctcgtatgttgtgtggaattgtgagcggataacaatttcacacaggaaacagctatgacc

atgattacgaattaac *tcgagagatctgtcgacaaaatttttatcgatcacgagactagcctcgatcgaggtcaattcacgcgagttaataatt*

accagcgcgggccaaataaataatccgcgaggggcaggtgacgtttgcccagcgcgcgctggtaattattaacctcgcgaatattgattc

gaggccgcgattgccgcaatcgcgaggggcaggtgacctttgcccagcgcgcgttcgccccgccccggacggtatcgataagcttagg

agcttgggctgcaggtcgagggcactgggaggatgttgagtaagatggaaaactactgatgacccttgcagagacagagtattaggac

atgtttgaacaggggccgggcgatcagcaggtagctctagaggatccccgtctgtctgcacatttcgtagagcgagtgttccgatactctaa

tctccctaggcaaggttcatatttgtgtaggttacttattctccttttgttgactaagtcaataatcagaatcagcaggtttggagtcagcttggca

gggatcagcagcctgggttggaaggaggggtataaaagccccttcaccaggagaagccgtcacacagatccacaagctcctgccac

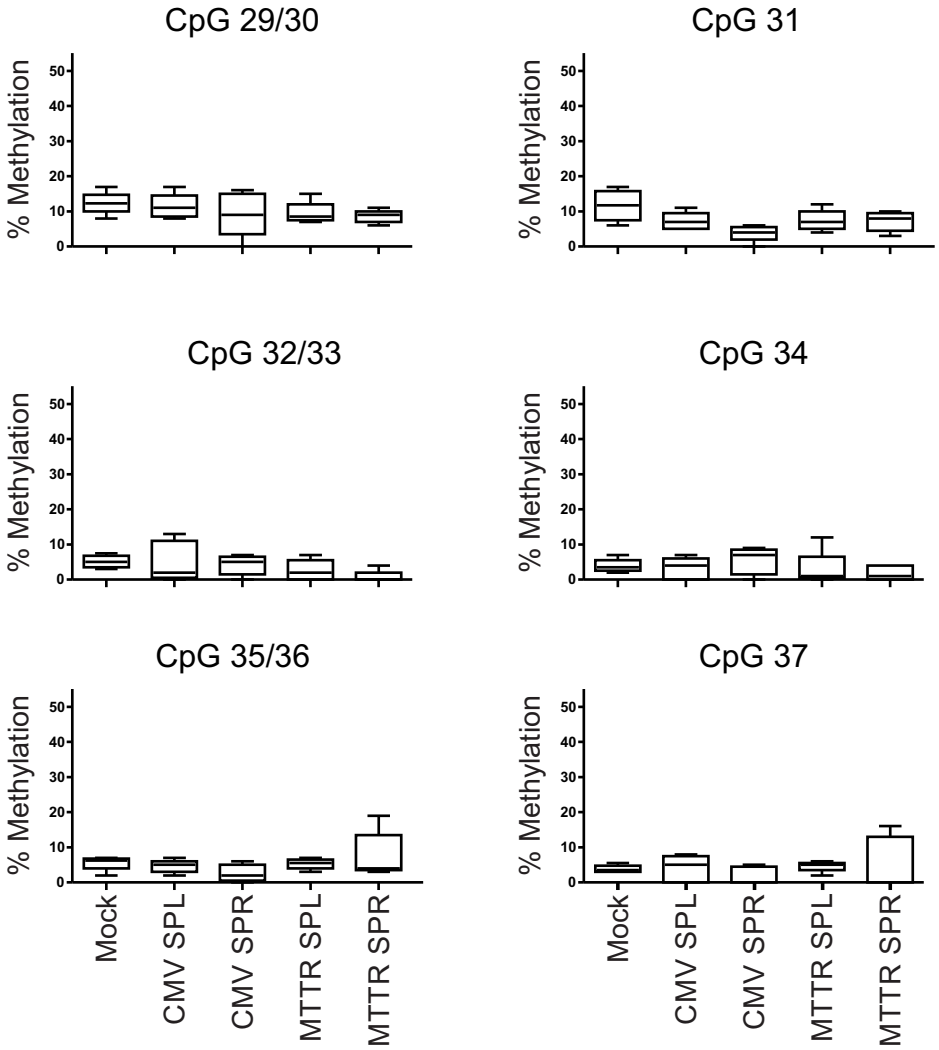
catggtgagctagcgatcagg cgcgccatagagtctatggcccacccccttggcttcgttagaacgcggctacaattaatacataaccttat

gtatcatacacatacgatttaggtgacactatagaataacatccactttgcctttctctccacaggtgtccactcccaggtccaactgcacctc

ggttctatcgattgaattgacatgtacccatacgatgtcccagactacgcgaatttta**gcggccgc**gtcttcatcatcgc 3’

*Not*I *Bpi*I

Supplementary Figure 1. Synthesized sequence encompassing the MTTR promoter. The MTTR promoter sequence, together with flanking regions containing *Bpi*I (underlined), *Pci*I (bold) and *Not*I (bold) restriction sites were synthesized. The essential MTTR promoter is indicated in italic font with grey shading. After digestion with *Bpi*I, sticky ends complementary to those of *Pci*I an *Not*I were generated to enable substitution of the CMV promoter with the MTTR promoter in SPL and SPR plasmids.



Supplementary Figure 2. Box and whiskers plot of the percentage methylation across CpG points 29 to 38 of HBV island II. Percentage methylation was determined by EpiTYPER MassARRAY on DNA extracted from mouse livers. An increase in the percentage methylation can be seen for MTTR-SPR at CpG positions 35/36 and 37. For CMV-SPL, CMV-SPR and MTTR-SPL, a 2-fold increase in methylation was measured at CpG positon 38.