Figure S12. Comparison of MCTA-Seq and RRBS.

(A) The MePM values of the CGCGCGG sequence with different methylation levels determined by RRBS of the sample samples are shown. The results of two biological liver tissue sample o replicates are shown. The error bars represent means ± s.d. **(B)** The absolute methylation level of a CGI was estimated for the MCTA-Seq data by means of the linear relationship between the MePM value and the dilution ratio of the methylated DNA, and the results of two biological replicates are shown. **(C)** The methylation levels determined by RRBS of

two biological replicates are shown. **(D)** Comparison between the MCTA-Seq and RRBS results for biological replicate 1. A total of 4,155 CGIs having high correlation ($r > 0.9$) between the MePM value and the dilution ratio of the methylated DNA and more than 10 detected CpGs in both RRBS data were selected for **(B-D)**. Note that the methylation level assessed by MCTA-Seq was generally lower than that determined by RRBS.