Supplementary Fig. S1. Quality Assessment of MeRIP-seq and RNA-seq Data. **a**, Pearson correlation analysis of input and immunoprecipitation (IP) reads of the genomic bin regions identified from MeRIP-seq. **b**, Principal component analysis (PCA) dimensionality reduction and clustering illustrate the degree of variation among samples, with the X-axis representing principal component 1 (PC1) and the Y-axis representing principal component 2 (PC2). **c-d**, Correlation of gene expression among the three biological replicates within each SVF (**c**) and WAT (**d**) group. Correlation was assessed using Pearson's method.