Figure S4. Scatter plots of methylation percentages obtained by Sanger sequencing or Fluidigm and whole genome bisulphite sequencing (WGBS) in the SHR and BN inbred strains.

(A) Methylation data were obtained by Sanger sequencing (y-axis) and WGBS (x-axis) for 70 individual CpG dinucleotides in each of the Brown Norway (n=4) and the spontaneously hypertensive rat (n=4) strains.

(B) Methylation data were obtained by Fluidigm (y-axis) and WGBS (x-axis) for 131 individual CpG dinucleotides in each of the Brown Norway (n=4) and the spontaneously hypertensive rat (n=4) strains. Pearson's correlation coefficient and associated p value are given.

Figure S6