Figure S1. Workflow of the identification of differentially methylated regions using array analyses of 4 cases of thoracic aortic dissection and 4 healthy controls. FDR, false discovery rate; chr, chromosome; SNP, single nucleotide polymorphism.

Illumina Infinium Methylation EPIC BeadChip

Remove probes
Detection P value>0.01
SNP probes
Bead count<3 in 5% samples
Located in chr X and chr Y

49983 probes remained
Normalization

Limmaempirical Bayes method and
Benjamini&Hochberg method,FDR<0.05