











Supplemental file F2. qPCR validation of microarray results – complete results.

The left panels show DNA methylation and gene expression microarray results represented by red bars and black markers, respectively; DNA methylation is expressed as MeDIP enrichment and gene expression levels as normalized microarray signals. The black markers preceding that of neonatal d1 represent gene expression levels in embryonic hearts E16, E18, E19, E20.

The middle panels present DNA methylation levels estimated with Methylation Dependent Restriction Digestion followed by qPCR (MDRE-qPCR) where the methylation levels correspond to the amounts of DNA undigested by CpG methylation dependent McrBC enzyme (1-(McrBC/Input).

The right panels demonstrate transcript levels determined with qPCR as the ratios to the reference transcript of the Tbp gene (TATA binding protein gene).

The microarray results were determined for pooled samples of 3 mice.

The qPCR results represent average values obtained for three individuals for each developmental time-point.

The statistical significance has been determined with two-tailed heteroscedastic Student's t-test.