



Figure S1. Plots of differentially methylated regions (DMRs) in offspring mouse hearts. (A-B) Volcano plots depicting DMRs (1000 base pair segments of the genome) in males and females. Regions with FDR < 0.05 and at least 10% absolute change in DNA methylation were considered significant. (C-D) Annotation summary plots depicting the total number of CpGs tested in pink, hypermethylated DMRs in green, and hypomethylated DMRs in blue for each genomic annotation using the R annotatr package for males (C) and females (D).