

**Figure S1**

Hierarchical Cluster analysis of genotype significant genes from cardiac mRNA microarray results. mRNA expression patterns were established for cardiac tissue from both male and female, ER -/- and wild type mice. HCL analysis was performed on intensity data using partek genomic suites for the significant gene list. FDR (0.05) corrected genes with a p value of 0.05 or less were considered significant.