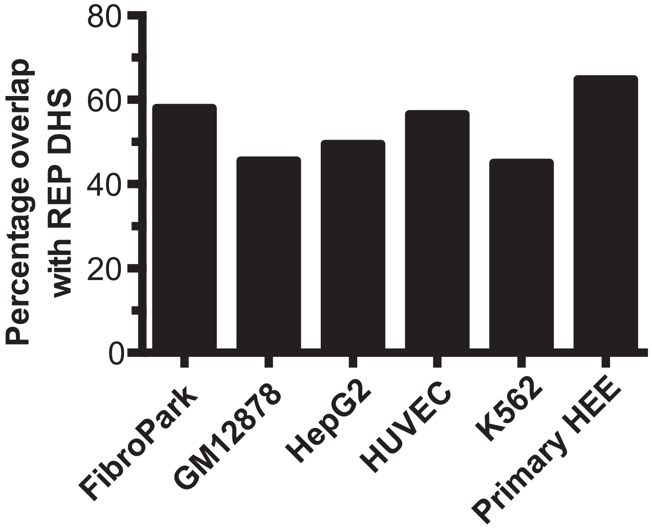
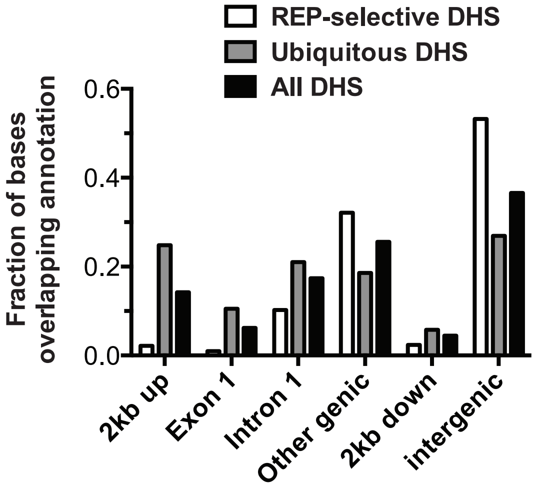
Supplemental Figure 1. Cell-type specificity of DNase I hypersensitive sites (DHS) in the immortalized HEE cell line, REP. The genomic overlap between REP DHS, the other five cell types and primary HEE cells. Percentage of REP DHS that overlap with the DHS from each of the five individual background cell types and primary HEE cells.

Supplemental Figure 2. REP-selective DHS are more frequent in either intronic or intergenic sequences rather than in promoters, where ubiquitous DHS predominate. Three categories of DHS (all DHS, HEE selective DHS, and ubiquitous DHS) were overlapped with different genomic regions to determine their distribution with respect to genes. Definition: 2 kb up, including 2 kb 50 to genes; other genic, all exons and introns of genes excluding the first; 2 kb down, including 2 kb 30 to genes; intergenic, all genomic sequence more than 2 kb from genes.

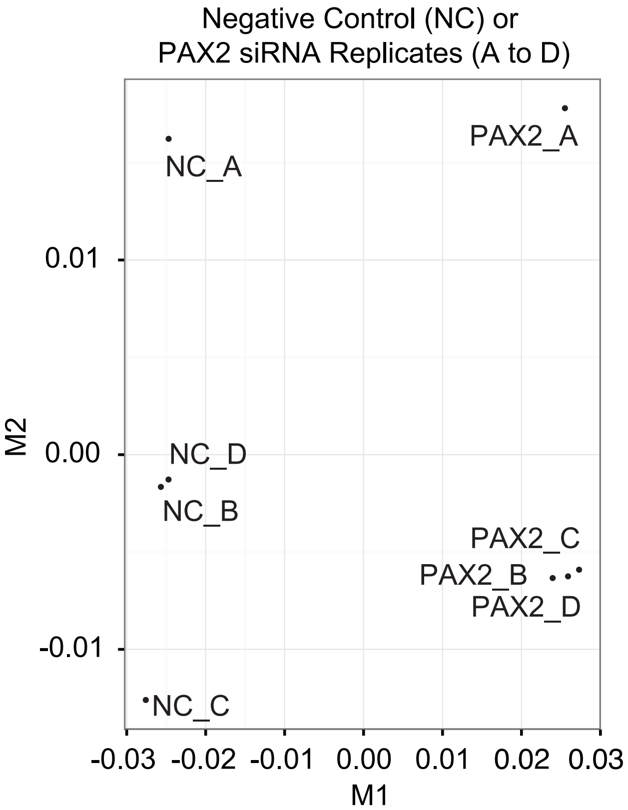
Supplemental Figure 3. RNA-seq quality control analysis. A MultiDimensional Scaling (MDS) plot to show that the PAX2- and negative control siRNA-treated samples clustered together respectively.



SUPPLEMENTARY FIGURE 1



SUPPLEMENTARY FIGURE 2



SUPPLEMENTARY FIGURE 3