Description of Additional Supplementary Files

Supplementary Data1

a. Mapping information for each replicate used in the RNA-seq analysis.
b. List of genes identified as Epi or PrE specific in single-cell RNAseq datasets, and genes identifies as up- and down-regulated during in vitro PrE differentiation.
c. Mapping and peak information for each replicate on which ATAC-seq was performed.
d. Mapping and peak information for replicates from CUT&RUN analysis.
e. Mapping and peak information for replicates from CUT&TAG analysis.
f. Mapping and peak information for replicates from ChIP-seq analysis.
g. Mapping information for HiC and Capture-C analysis.
h. List of biotinylated oligos used in Capture-C