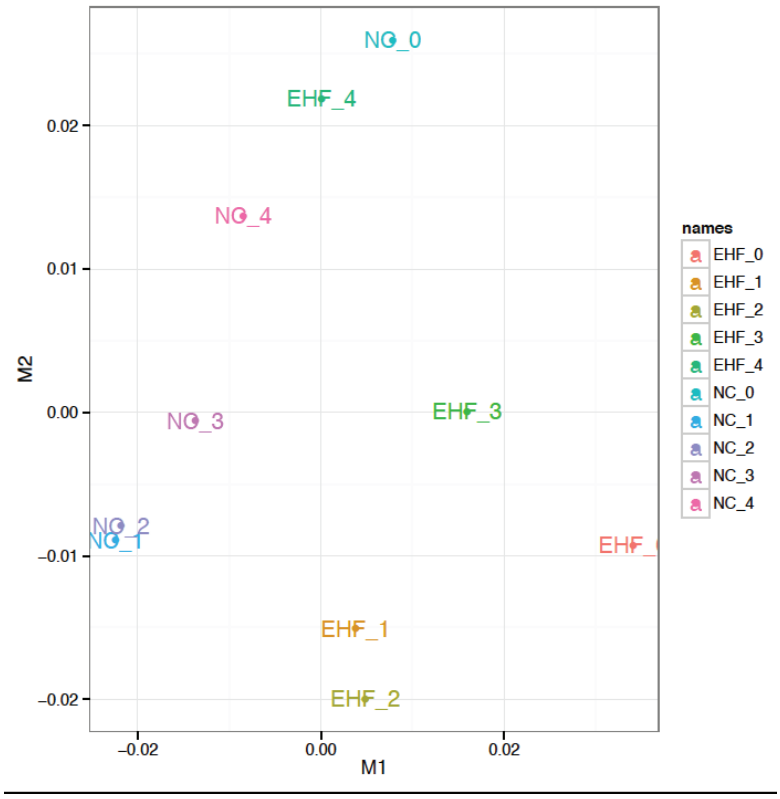

Figure S1. Multi-dimensional scaling (MDS) plot of RNA-seq samples. MDS of individual negative control (NC_0-NC_4) and EHF depleted (EHF_0-EHF_4) samples based on Fragments Per Kilobase of transcript per Million mapped reads (FPKM) values. Whole transcriptome expression values in FPKM at gene level were used to compare similarity among the samples through dimension reduction analysis.

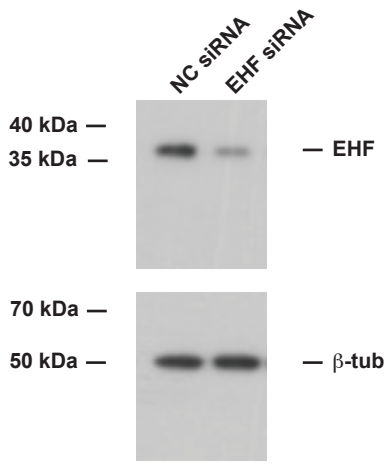

Figure S2. Depletion of EHF in primary HBE cells for RT-qPCR. siRNA depletion of EHF in undifferentiated HBE cells was measured by western blot with β-tubulin as a loading control.

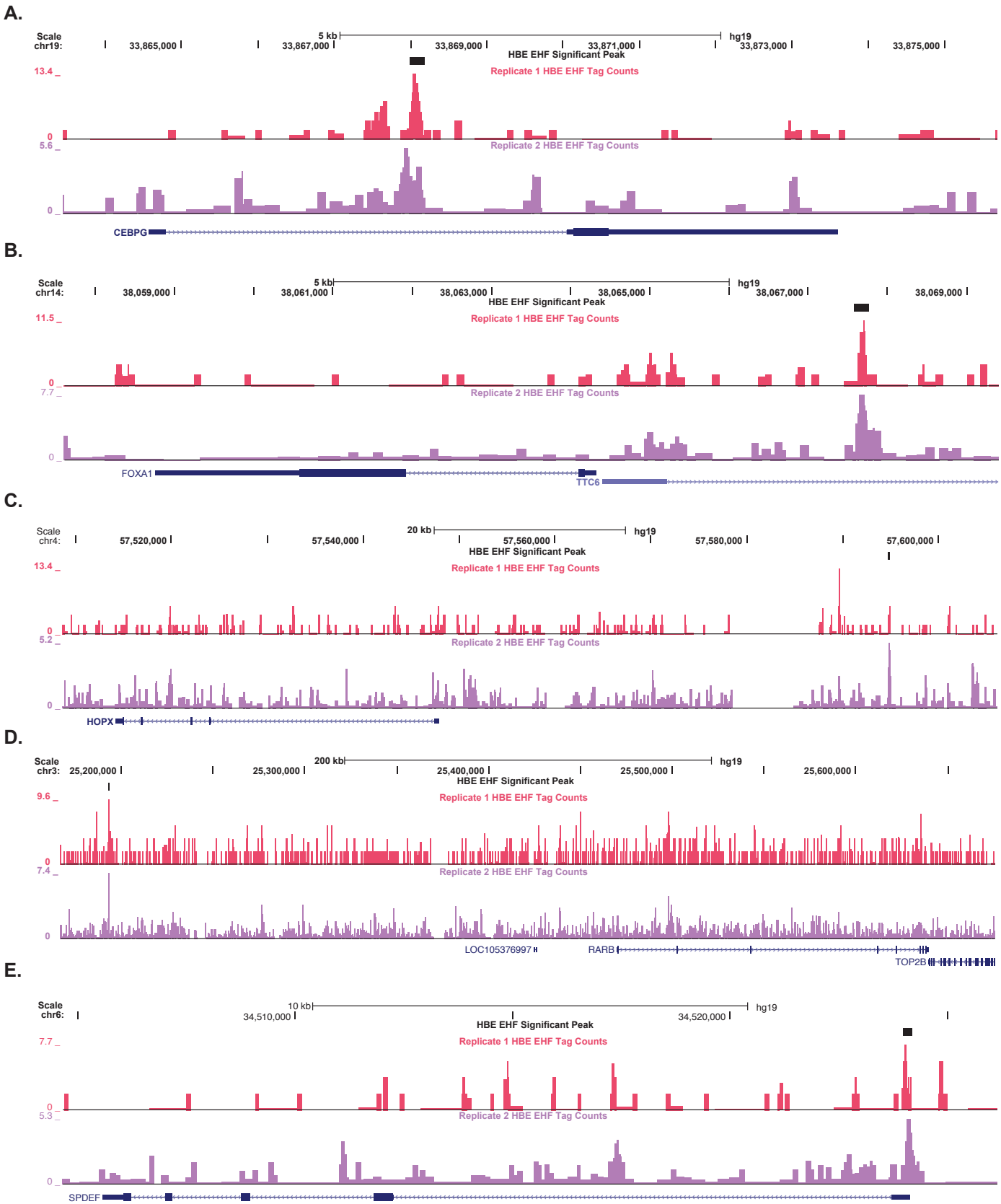

Figure S3. Visualization of EHF ChIP-seq replicates. In each panel, Genome Browser tracks show EHF peaks identified by IDR in HBE cells at the top (black), below are the EHF ChIP-seq tag counts for replicate 1 (red) and replicate 2 (purple) and the gene (blue) for A) CEPBG, B) FOXA1, C) HOPX, D) RARB, and E) SPDEF.

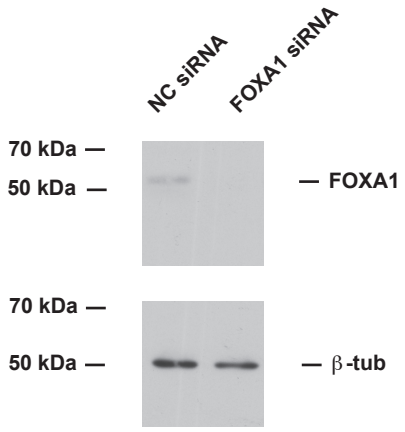

Figure S4. Depletion of FOXA1 in primary HBE cells for RT-qPCR. siRNA depletion of FOXA1 in undifferentiated HBE cells was measured by western blot with β-tubulin as a loading control.

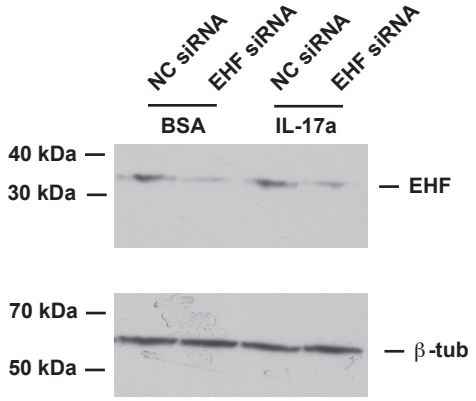

Figure S5. Depletion of EHF in Calu-3 cells treated with IL-17a. siRNA depletion of EHF in Calu-3 cells treated with vehicle (BSA) or IL-17a was measured by western blot with β-tubulin as a loading control.

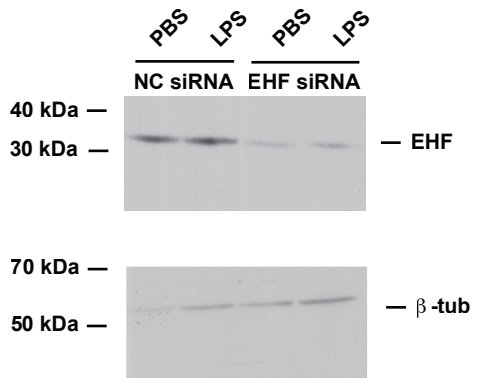

Figure S6. Depletion of EHF in Calu-3 cells treated with lipopolysaccharide (LPS). siRNA depletion of EHF in Calu-3 cells treated with vehicle (PBS) or LPS was measured by western blot with β-tubulin as a loading control.