

Cellular heterogeneity in the 16HBE14o- airway epithelial line impacts biological readouts

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Data Supplement

Figure Legends

Figure S1: CFTR protein analysis of 16HBE14o- CFTR^{high} and CFTR^{low} clones.

Figure S2: Open chromatin profiles of individual CFTR^{high} and CFTR^{low} clones.

Table S1: Oligonucleotides

Table S2: DEGs of CFTR-high vs CFTR-low with a fold change ≥ 1.5 or ≤ -1.5 , an adjusted p-value ≤ 0.01 , and a basemean >30

Table S3: DAVID GO term analysis for CFTR-high DEGs, p-value ≤ 0.01

Table S4: DAVID GO term analysis for CFTR-low DEGs, p-value ≤ 0.01

Supplementary Figure Legends

Figure S1: CFTR analysis of 16HBE14o⁻ CFTR^{high} and CFTR^{low} clones. Representative western blot showing CFTR protein levels in 16HBE14o⁻ cells, and 12 clones and β -tubulin loading control with the 4 chosen for subsequent analyses shown in brown (CFTR^{high}) or blue (CFTR^{low}).

Figure S2: Open chromatin profiles of individual CFTR^{high} and CFTR^{low} clones. Open chromatin mapping of 16HBE14o⁻ CFTR^{high} (clones 4 and 7, brown) and CFTR^{low} (clones 3 and 12, blue) cells, mapped to the hg19 genome build. Clonal cells were collected from two non-sequential passages. Sites where chromatin is more open in CFTR^{high} or CFTR^{low} clones are marked by arrows. At the top for comparison are shown Calu3 ATAC-seq and RNA-polII ChIP-seq (in dark grey) and 16HBE14o⁻ WT ATAC-seq RNA-polII ChIP-seq (in black) (GSE132808).

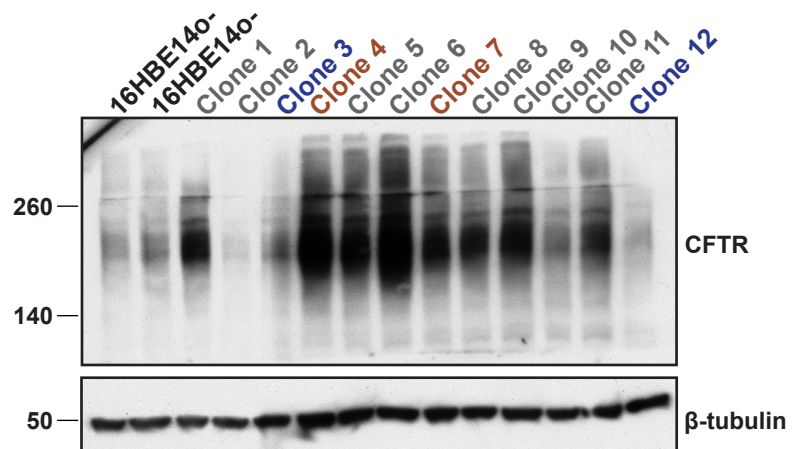


Figure S1

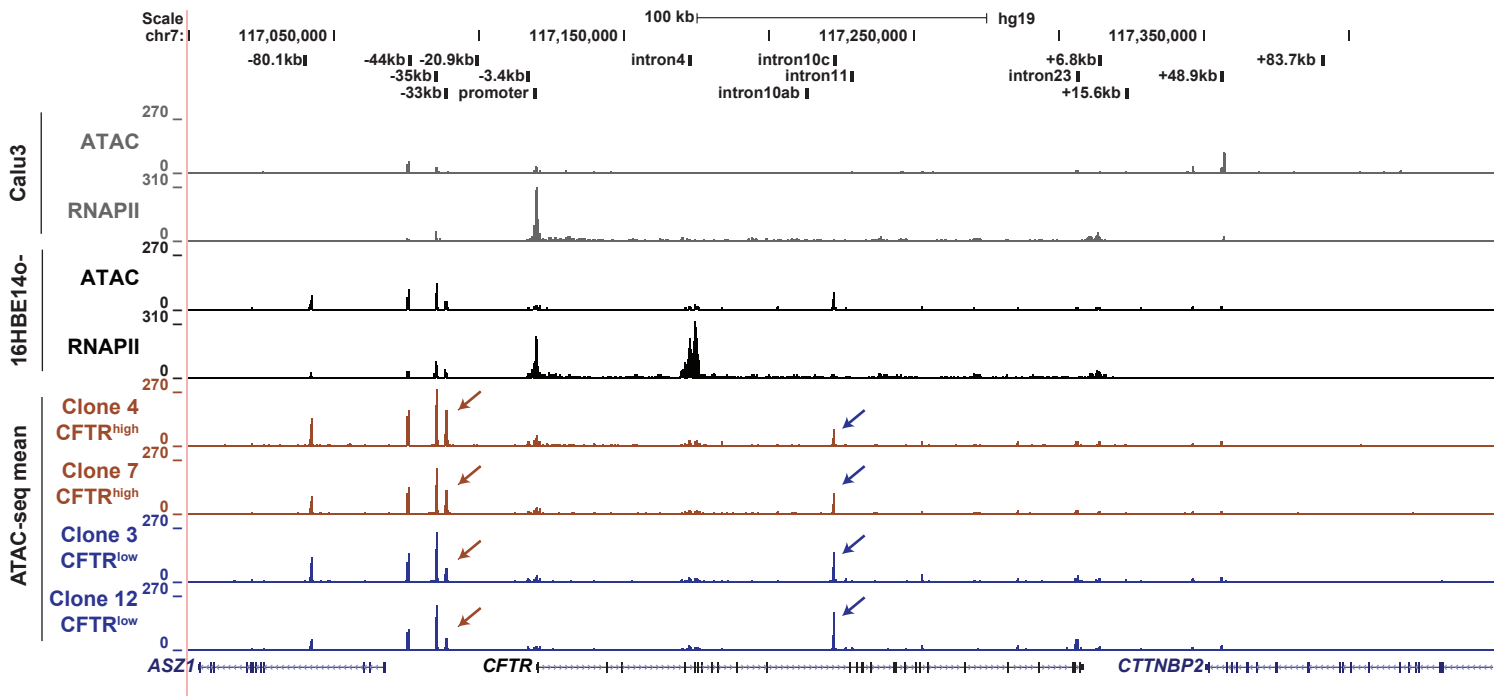


Figure S2

Table S1: Oligonucleotides

TaqMan Assay		
Gene	Sequence (5'>3')	
CFTR	AGCTGTCAAGCCGTGTTCTAGATA ATGAGGAGTGCCACTTGCAAA /56-FAM/CACACGAAA/ZEN/TGTGCCAATGCAAGTCCTT/3IABkFQ/ AAGTGGATCGAGACATGTAAG	
B2M	GCAAGCAAGCAGAATTGGA /56-JOEN/TCATGGAGG/ZEN/TTGAAGATGCCGCA/3IABkFQ/	

4C-seq		
Viewpoint (enzyme combo.)	Reading Primer (5'>3')	Non-reading Primer (5'>3')
DHS -20.9 kb (NlaIII/DpnII)	tacacgacgctcttccgatctTTAACAAAGTTTAGGTAAATGACCA	actggagttcagacgtgtgctcttccgatctCAAAGTGAGCTATTTGTTTTCTC
DHS +48.9 kb (NlaIII/DpnII)	tacacgacgctcttccgatctTACACGACGCTCTCCGATCT	actggagttcagacgtgtgctcttccgatctGAGTGAGCTTGAAGCCATG