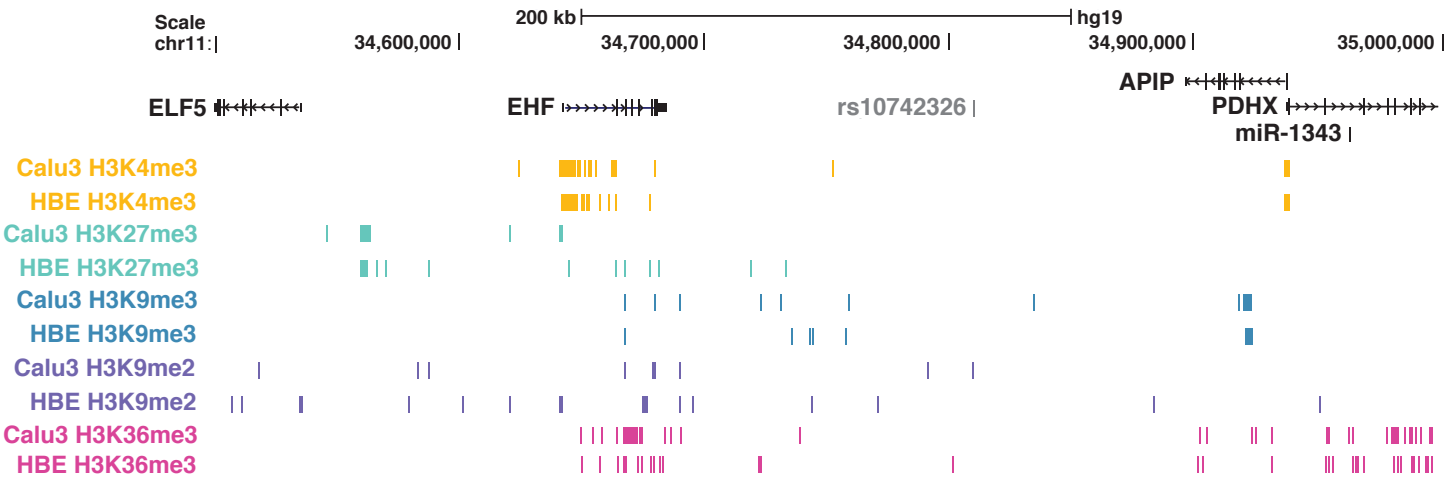
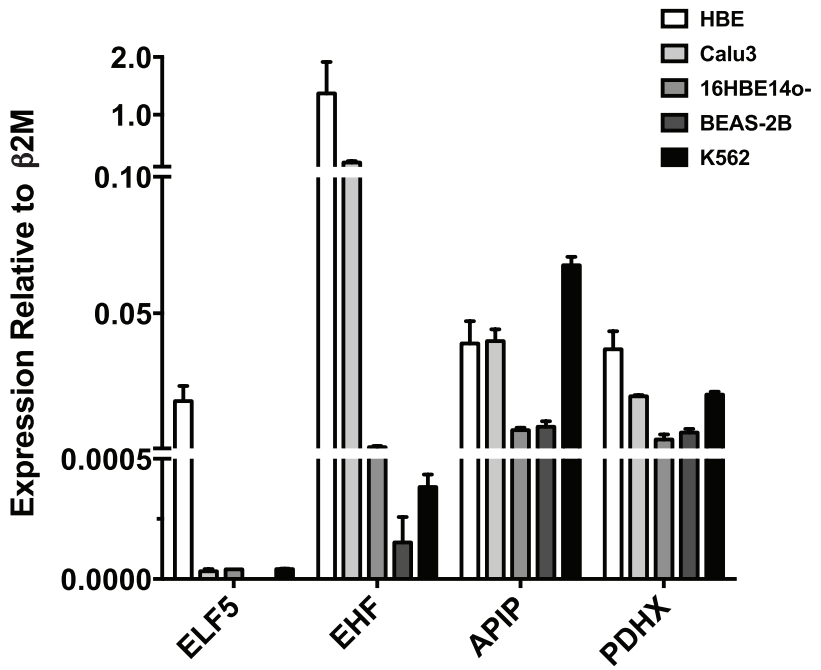
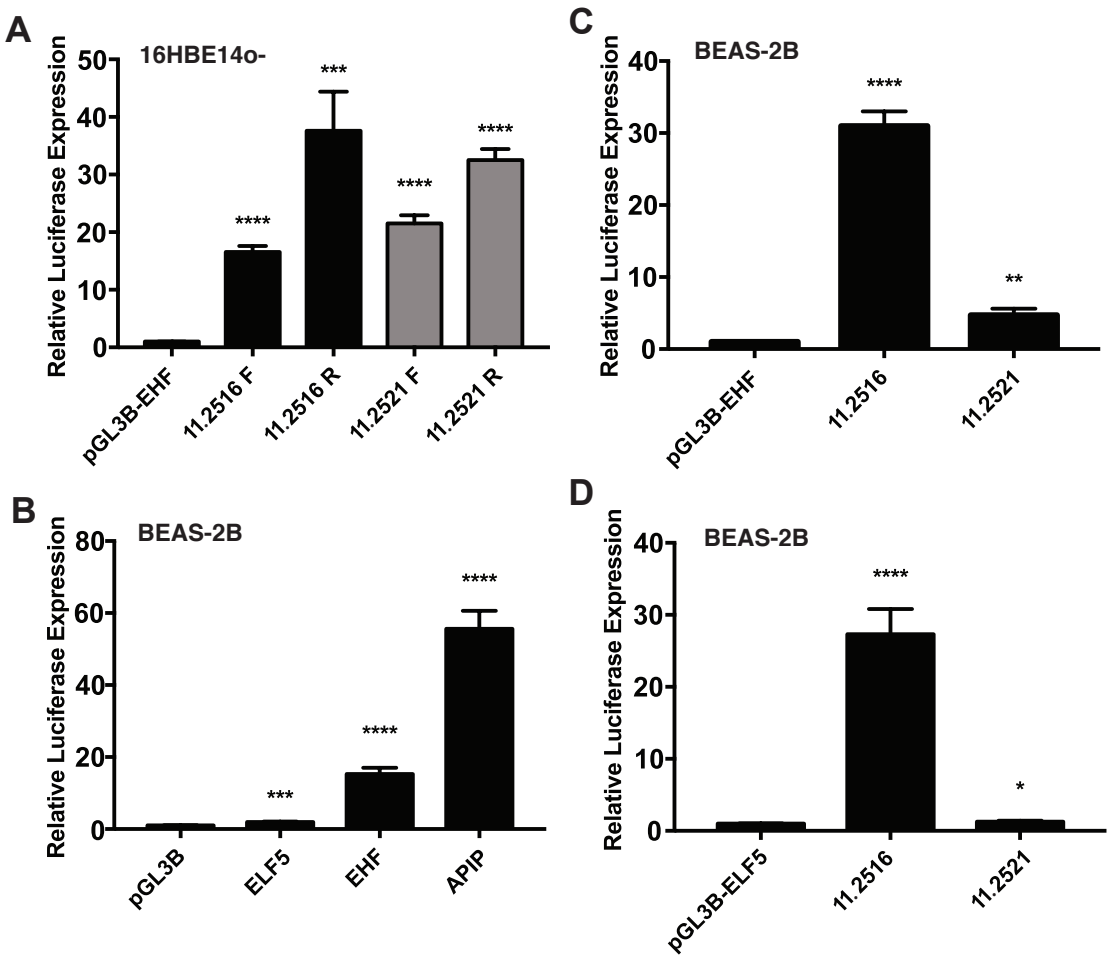


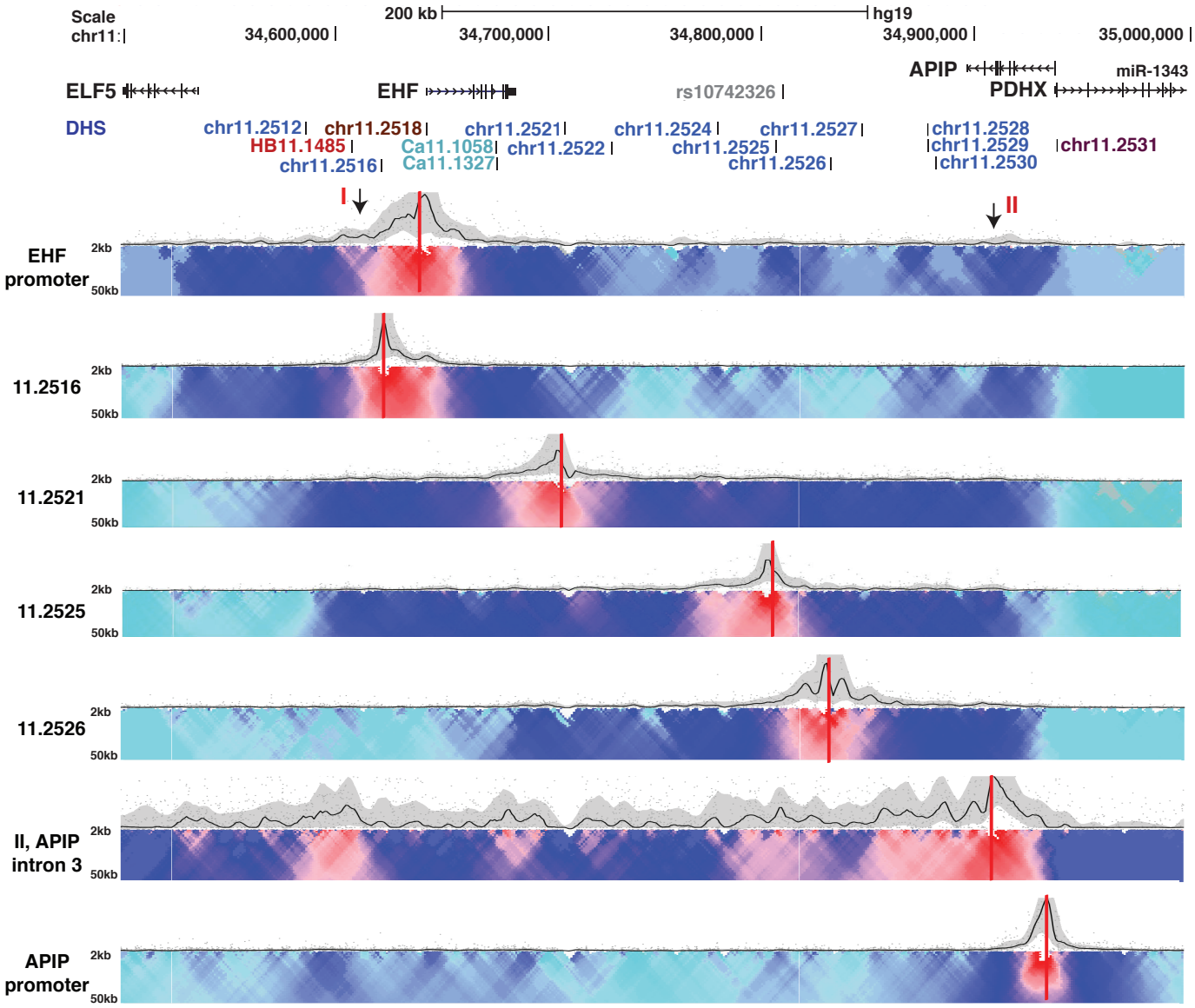
Suppl. Fig. 1. Histone modifications at 11p13 in Calu3 and HBE cells. A schematic at the top illustrates a 500kb window surrounding the highest p-value SNPs at 11p13 between *EHF* and *APIP*, with the most significant GWAS(I+II) SNP (rs10742326) shown in grey. ChIP-seq data are shown for a promoter-specific histone mark (H3K4me3, yellow), and negative histone marks (H3K27me3, aqua; H3K9me3, blue; H3K9me2, purple; H3K36me3, pink).



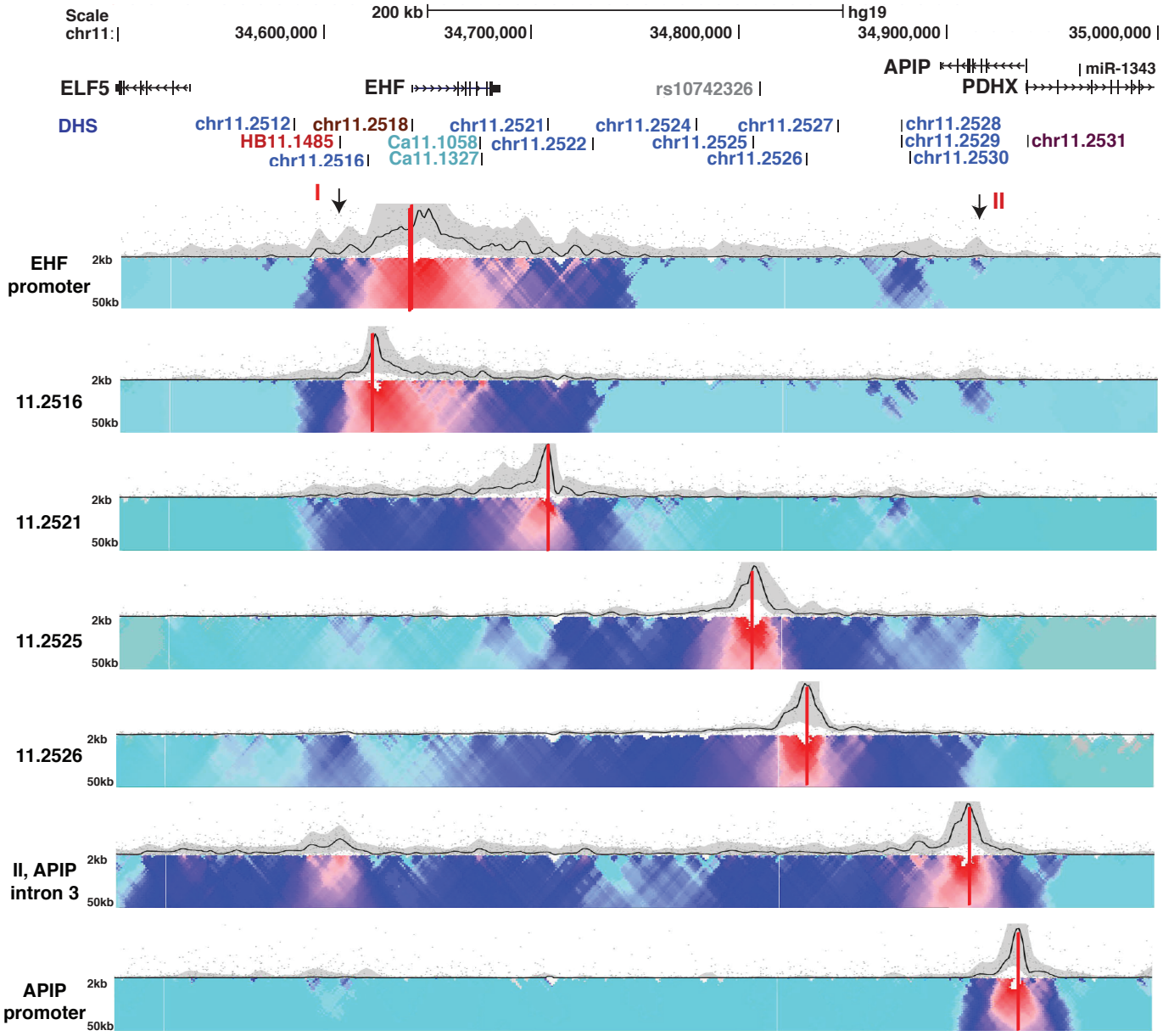
Suppl. Fig. 2. Relative expression levels of 11p13 genes in different cell types. The expression of *ELF5*, *EHF*, *APIP*, and *PDHX* was quantified using SYBR Green qPCR assays and analyzed relative to β-2-microglobulin (β2M) levels. Data are shown for primary HBE (white), Calu3 (light grey), 16HBE14o- (medium grey), BEAS-2B (dark grey), and K562 (black) cells. For HBE samples, three different donor codes were assayed twice each (n=3). For cell lines, n=2.



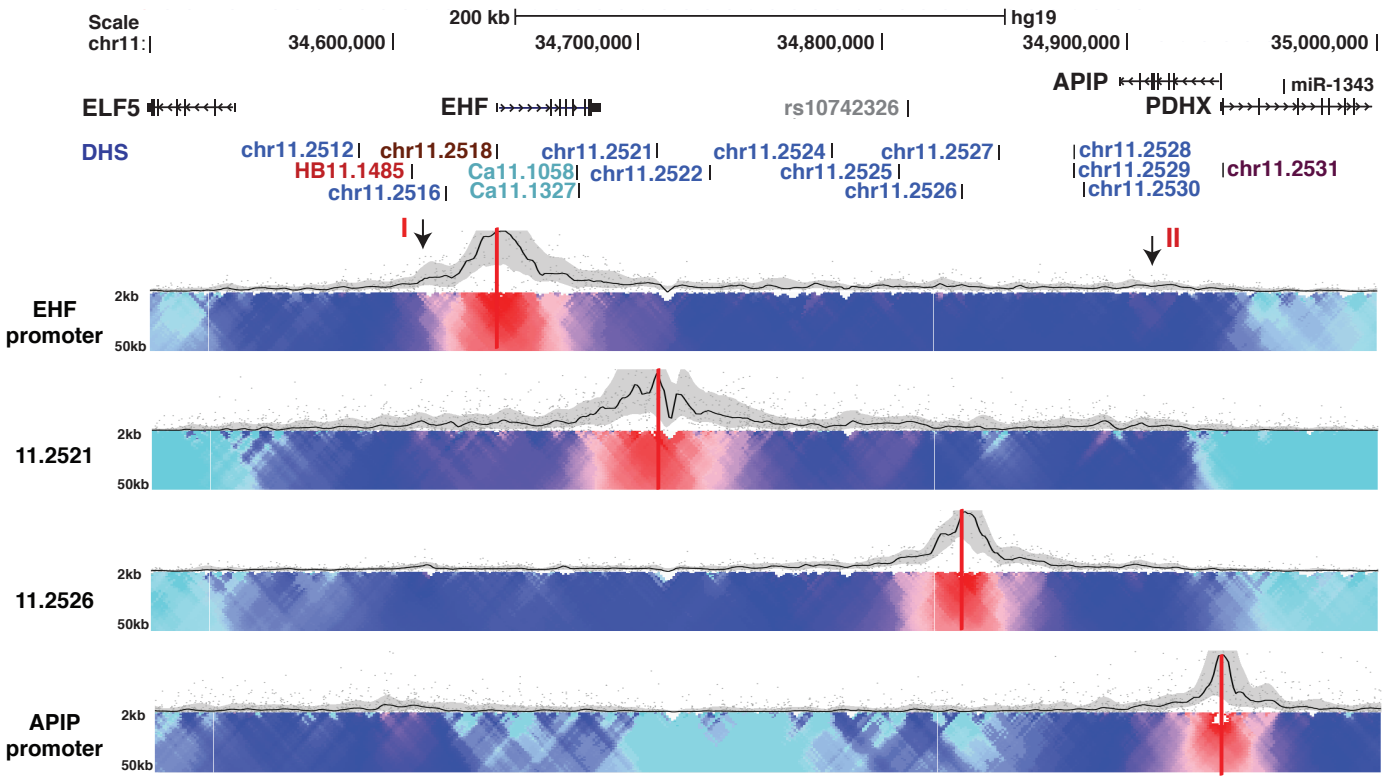
Suppl. Fig. 3. DHS 11.2516 and 11.1521 contain classical enhancer elements which function in several airway cell lines. A. The 11.2516 (black bars) and 11.2521 (grey bars) elements were cloned into the enhancer site of the pGL3B-*EHF* promoter vector in both the forward and reverse orientations. Constructs were transfected into 16HBE14o- cells along with a Renilla control vector and luciferase expression was measured 48 hours post-transfection. n=3. ****p<0.0001, ***p<0.001, **p<0.01, *p<0.05. Data show these enhancers are active in both orientations with respect to the promoter. B. The promoters for *EHF, ELF5,* and *APIP* were cloned into the pGL3B vector and transfected into BEAS-2B cells. Luciferase expression was measured as in (A). n=3. p-values as for (A). C. The 2516 and 2521 enhancers were cloned into the enhancer site of the pGL3B-*EHF* promoter construct and transfected into BEAS-2B cells as in (B). n=3. p-values as for (A). D. 11.2516 and 2521 inserted into the pGL3B-*ELF5* promoter construct; see (C).



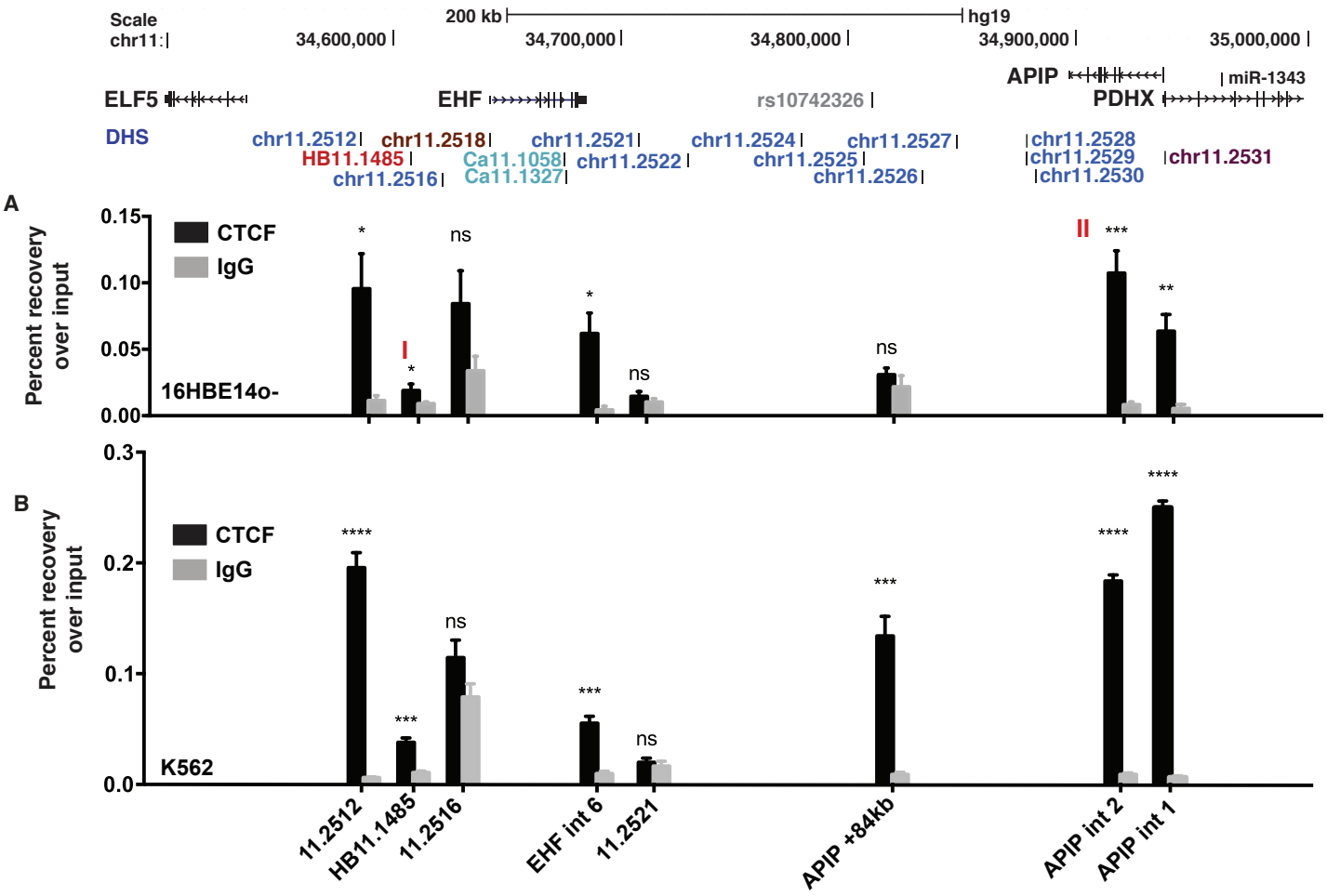
Suppl. Fig. 4. 4C-seq from multiple viewpoints reveals the 11p13 chromosome conformation in primary HBE cells. 4C-seq data tracks are as described in Figure 3. Viewpoints are at the *EHF* promoter, DHS 11.2516, 2521, 2525, 2526, *APIP* intron 3, and the *APIP* promoter. For all 4C data shown in Suppl. Figs. 4 - 6 each viewpoint was assayed twice in separate experiments to demonstrate reproducibility of interactions and one of them is shown.



Suppl. Fig. 5. 4C-seq from multiple viewpoints reveals the 11p13 chromosome conformation in 16HBE14o- cells. 4C-seq data tracks are as described in Figure 3. Viewpoints are at the *EHF* promoter, DHS 11.2516, 2521, 2525, 2526, *APIP* intron 3, and the *APIP* promoter.



Suppl. Fig. 6. 4C-seq from multiple viewpoints reveals the 11p13 chromosome conformation in in K562 cells. 4C-seq data tracks are as described in Figure 3. Viewpoints are at the *EHF* promoter, DHS 2521, 2526, and the *APIP* promoter.



Suppl. Fig. 7. CTCF enrichment across the 11p13 region in 16HBE14o- and K562 cells. A. ChIP-qPCR for CTCF occupancy in 16HBE14o- cells at DHS 11.2512 (EHF -55kb), HB11.1485 (I), DHS 2516, EHF intron 6, APIP +84kb, APIP intron 2 (II), and APIP intron 1 sites across the 11p13 region. Data are shown as percent recovery over input for CTCF (black bars) and IgG control (grey bars). n=3. ****p<0.0001, ***p<0.001, **p<0.01, *p<0.05. B. ChIP-qPCR for CTCF occupancy in K562 cells. Data are shown as in (A).

Region	Forward Primer	Reverse Primer
ELF5 Promoter	CG**GAGCTC**TGACAAGATAGGCCAGTGCCCA	CC**CTCGAG**CAGCACCAGCGTGCAGTGGAA
EHF Promoter	CG**GAGCTC**ACCTGCCCAGCTTCCAAGACCTT	CC**CTCGAG**GGGCACCACGGGTGTTATCAAG
APIP Promoter	**CTCGAG**AGCCCCACACCAGACCAGACC	**CTCGAG**ACACTTGCCCAGGAACGATCTCCA
DHS 11.2516	GCA**GTCGAC**AAAGGTCCTGTTCAACCTCTGG	GCA**GTCGAC**GTGGGCCTCTCCTTCATCTTTT
DHS 11.2521	**GGATCC**ACAAAGTGTCTCTCAATGAA	**GGATCC**CCCTGTGGTCTCCAATTGTA
DHS 11.2522	CG**GGATCC**AGTGAGGAAGCCAGCCAGGC	CG**GGATCC**AGACACCAGCTGGGGCAGCT
DHS 11.2524	CG**GGATCC**GCCTAGGAACAATAGGATGTACC	CG**GGATCC**GCACATCTTCACATCTCTGAACC
DHS 11.2525	**GGATCC**GGAACAGAGATGAGGTACTT	**GGATCC**GCAATTACCACACCTCTCAC
DHS 11.2526	GCA**GTCGAC**AAAGGTCCTGTTCAACCTCTGG	GCA**GTCGAC**GTGGGCCTCTCCTTCATCTTTT
DHS 11.2527	**GGATCC**CTTTCTCAGCAGCTTCTGGT	**GGATCC**TGAGACCACACTTGGCACCT
DHS 11.2528	CG**GGATCC**GGCGGTTCTGCTCCCTTGGG	CG**GGATCC**ACTGGAGACTGGGAAAGCTG
DHS 11.2529	GC**GGATCC**GGCGAGTCACTCTTCAGGTGCA	GC**GGATCC**TGGTGCTCCCTGGAGTTCTGT
DHS 11.2530	CG**GGATCC**TGCAAAAGACCAGAGTGCCCACT	CG**GGATCC**AAACAGCTGGGGAGGGAATGCT

Suppl. Table 1A: Primers used for cloning. Bold denotes restriction enzyme site used for cloning into pGL3B.

Region	Forward Primer	Reverse Primer
DHS 11.2512	GCTTCTATTCATTCACCCAACAC	GTAGTAGCCCTGCCACCAGA
HB11.1485 (I)	GATTTTCCGAAGCTGTGGAGG	CCACCATACGCAATCACAGG
DHS 11.2516	TCCTGTCTTGAAGCGACCAC	GGCTCAGGGGAGAAGCAAAT
EHF intron 6	CCCGTAAAGAAATGGCTCAC	AGGCCAAGGTCCTATCCAGT
DHS 11.2521	CTCAAGCCTGGAAAGCCTCA	GCTGCATCTACCCGAGAGTC
APIP +84 kb	CTGTCATGCAAAGAATCAGGTTT	TAAGAAACTGTCCAGCAGAGGTC
APIP intron 2 (II)	CTGTCATGCAAAGAATCAGGTTT	TAAGAAACTGTCCAGCAGAGGTC
APIP intron 1	CAAGCCAGGATGGTCTCAAT	TCCACTAGGTGGCACTGTTG
11p13 NC	TCCTTCCAGGTTTTGGCTCC	GCCCCAGATCAGGAGAGAGA
CFTR +48.9kb	GGCATCAGCCAGTCAAGGTT	AGCAGAGGGCAAAGTGGTACTT

Suppl. Table 1B: Primers used for ChIP-qPCR.

Gene	Forward Primer	Reverse Primer
ELF5	TGCTTGAAAACAAGTGGCATC	AGGGCTTCCGATTTAACCACC
EHF	GCAGCATGAGTTTGCAGGAG	GTGTGTGGACTGGAAACAGGT
APIP	GGCCACACTTCTCTTTCCAG	GCATGAGCCATTCTATCTTTGAGG
PDHX	GACATTTCAGTGGCTGTGGC	TCGATGCCAAACATCCCCAA
Beta-2-Microglobulin	CTCTCTCTTTCTGGCCTGGAG	TCTGCTGGATGACGTGAGTA

Suppl. Table 1C: Primers used to measure gene expression in SYBR Green qPCR assays.

Viewpoint	Reading Primer	Non-reading Primer
EHF Promoter	AATGATACGGCGACCACCGAACACTCTTT CCCTACACGACGCTCTTCCGATCTTTTAGT CCACCCTGCTTTGG	CAAGCAGAAGACGGCAT ACGATTAGGGCTCAGAG TACACGG
EHF Promoter (16HBE14o-)	AATGATACGGCGACCACCGAACACTCTTT CCCTACACGACGCTCTTCCGATCTATTATC TGTGAATTTCCTGCAT	CAAGCAGAAGACGGCAT ACGATTTAGTCCACCCT GCTTTGG
APIP Promoter	AATGATACGGCGACCACCGAACACTCTTT CCCTACACGACGCTCTTCCGATCTTGTTG GTTTGTGTAAATGACCGA	CAAGCAGAAGACGGCAT ACGATCCCCAAATTAGC AAAGACGAC
HB11.1485 (I)	AATGATACGGCGACCACCGAACACTCTTT CCCTACACGACGCTCTTCCGATCTCTTGG GGAGTAGCAAAAGAT	CAAGCAGAAGACGGCAT ACGATCCAAACCTCTATT TCCTCA
DHS 11.2516	AATGATACGGCGACCACCGAACACTCTTT CCCTACACGACGCTCTTCCGATCTCTCCC CAAATTAGCACCATG	CAAGCAGAAGACGGCAT ACGAAGGCAGCCTTCTT GCTTTCT
DHS 11.2521	AATGATACGGCGACCACCGAACACTCTTT CCCTACACGACGCTCTTCCGATCTTTTGTT CATTGAAGGACATCAT	CAAGCAGAAGACGGCAT ACGATTGTCTTGGTAATT TGTGAACC
DHS 11.2525	AATGATACGGCGACCACCGAACACTCTTT CCCTACACGACGCTCTTCCGATCTATGCC CCAAACAGTCCCATG	CAAGCAGAAGACGGCAT ACGAGGAGGTAAGGAA GGTAAGGG
DHS 11.2526	AATGATACGGCGACCACCGAACACTCTTT CCCTACACGACGCTCTTCCGATCTATGGT GGGTTTAAATAAATTACAGA	CAAGCAGAAGACGGCAT ACGAACTTGCAGGAAGC CAGATTG
APIP intron 3 (II)	AATGATACGGCGACCACCGAACACTCTTT CCCTACACGACGCTCTTCCGATCTCCCTC TATAAATAGCCTGAAGACATG	CAAGCAGAAGACGGCAT ACGAAACCCTTGAGAAA TTTAGATGGT

Suppl. Table 1D: Primers used for 4C-seq. Red denotes Illumina P5 adapter sequence and blue denotes Illumina P7 adapter sequence used for library generation.