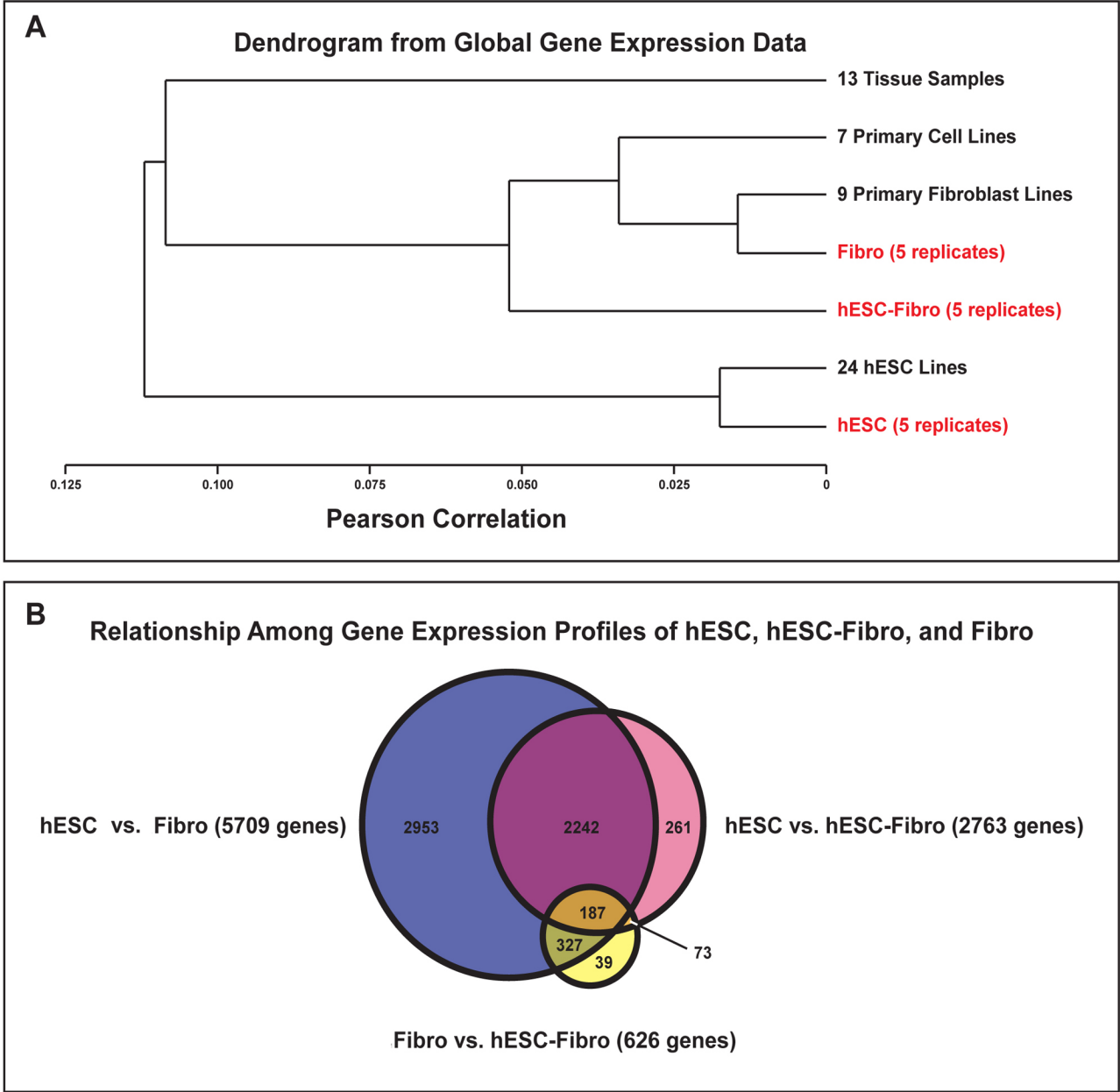
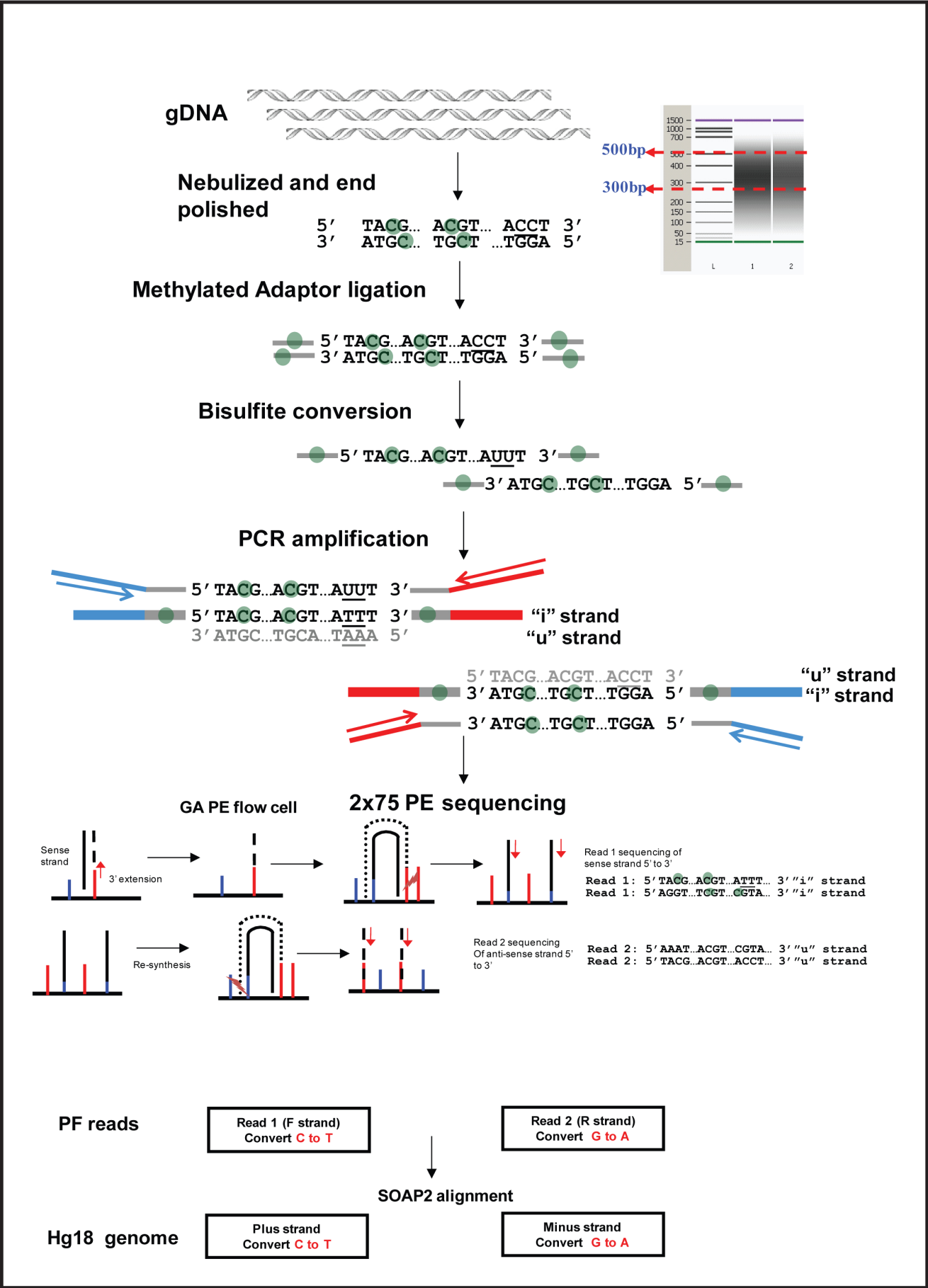


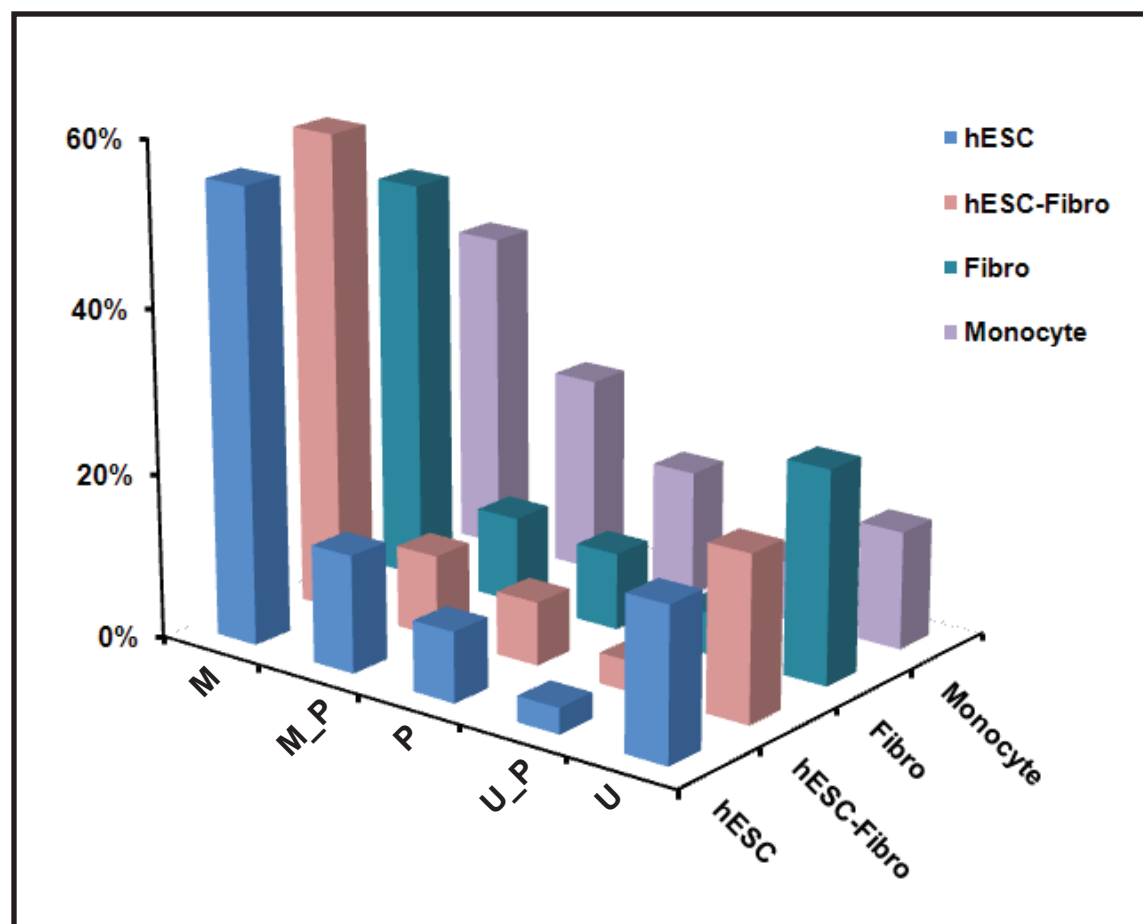
Supplementary Figure 1.



Supplementary Figure 2.

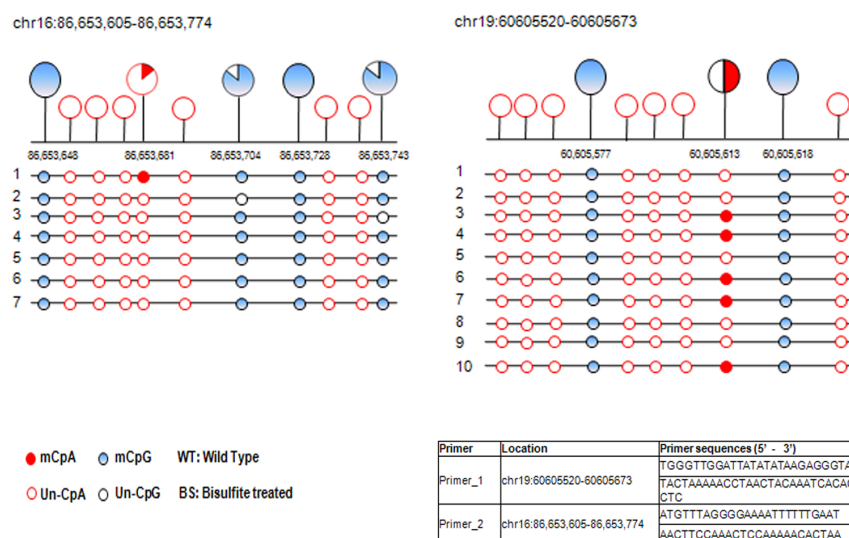


Supplementary Figure 3.

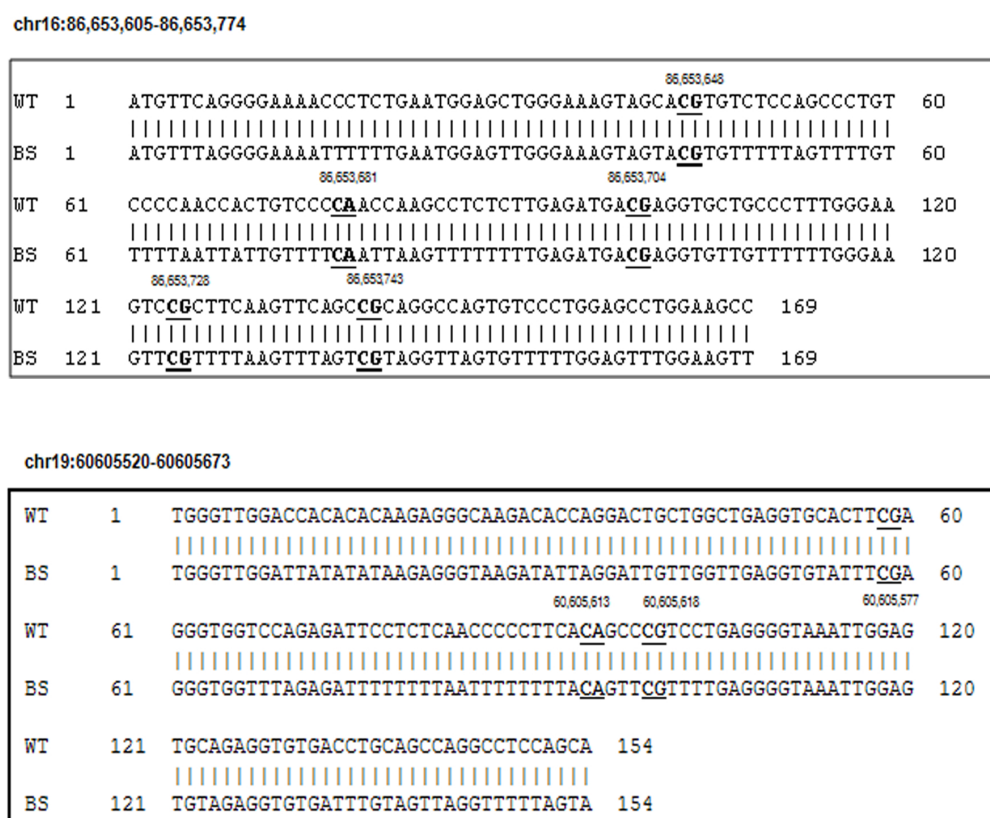


Supplementary Figure 4.

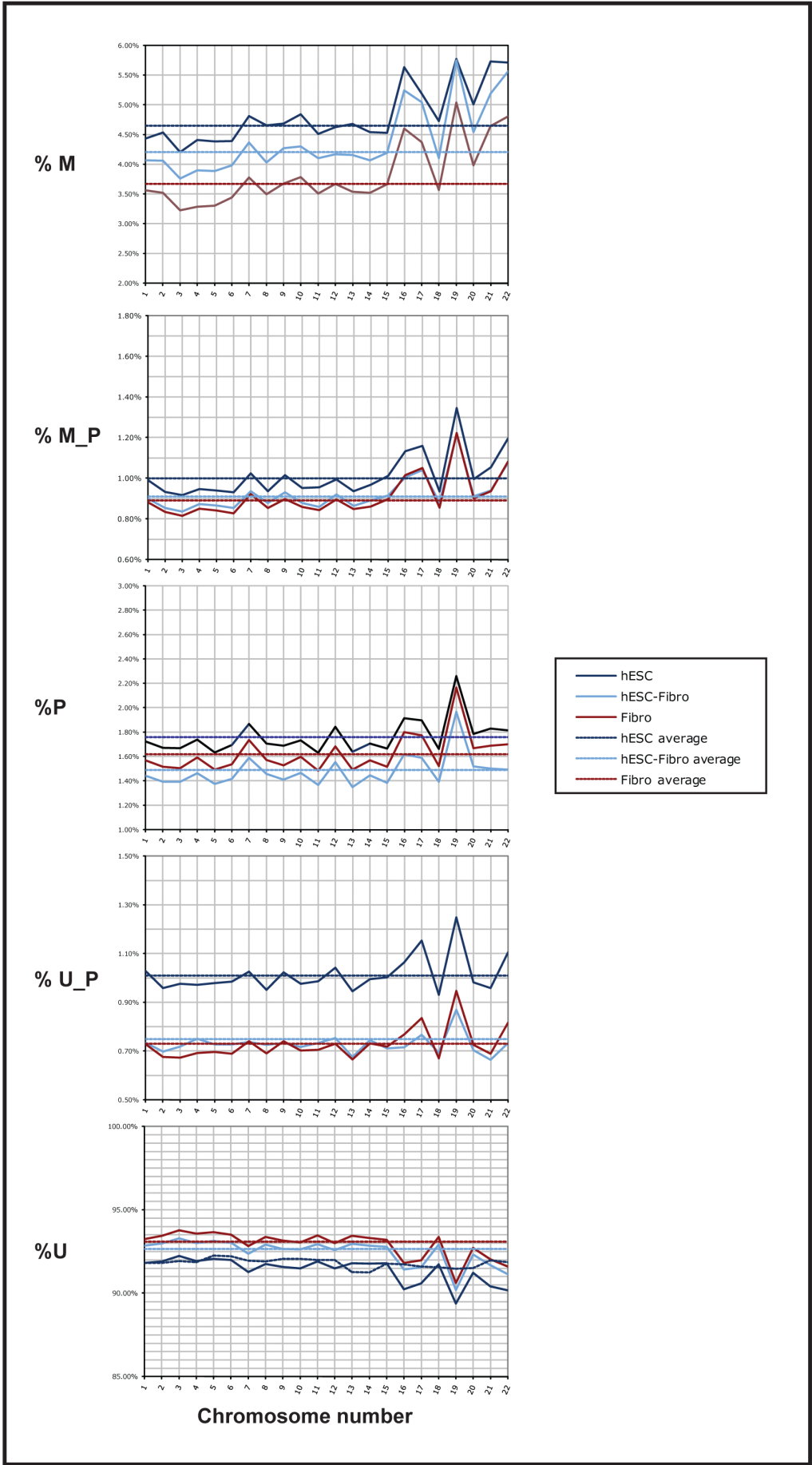
A



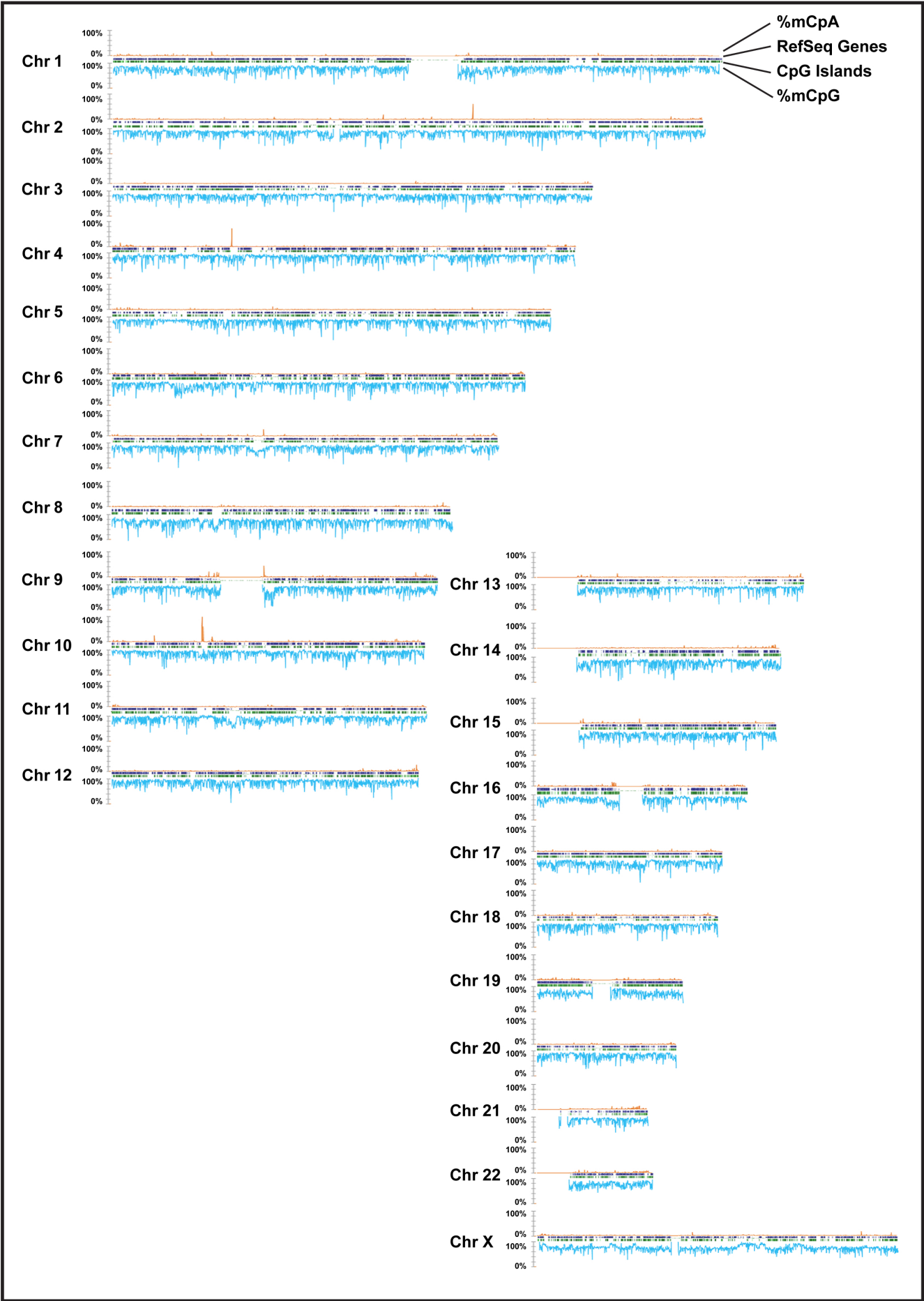
B



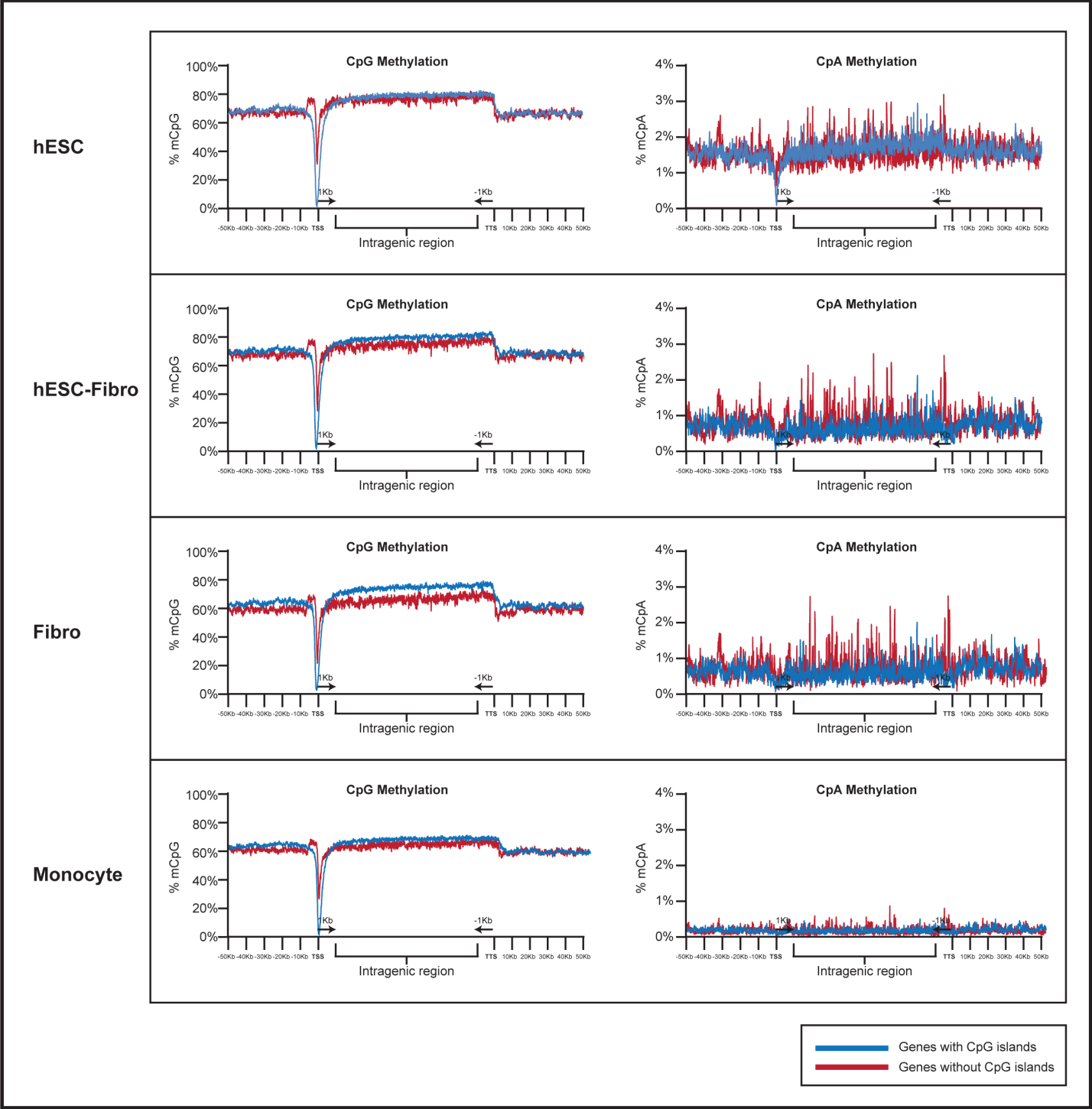
Supplementary Figure 5.



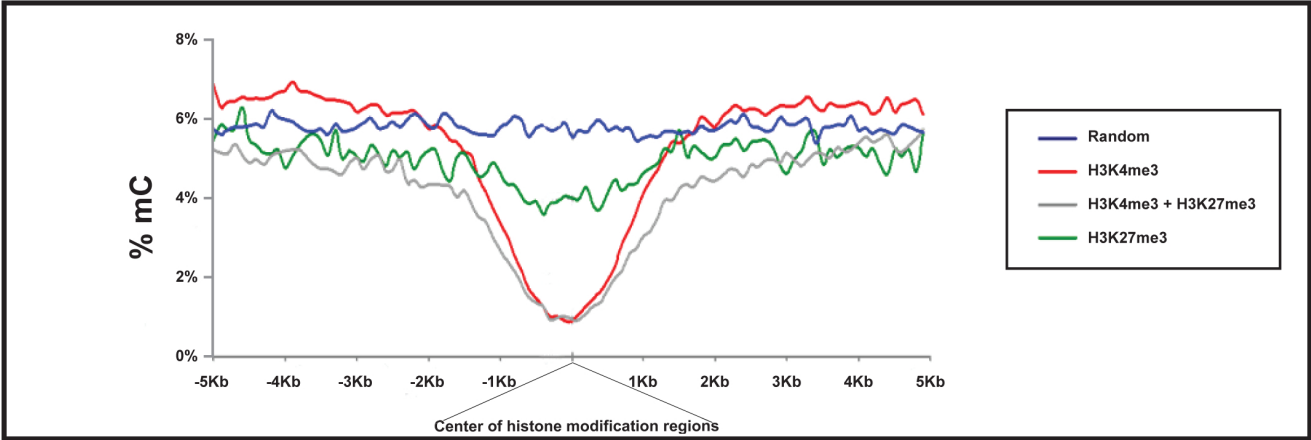
Supplementary Figure 6.



Supplementary Figure 7.



Supplementary Figure 8.



The figure displays two panels of genomic tracks, each showing H3K27me3 enrichment across four cell types (hESC, hESC-Fibro, Fibro, Monocyte) and a corresponding gene model.

Top Panel: chr12:84,192,784-84,225,074. The tracks show H3K27me3 enrichment for hESC, hESC-Fibro, Fibro, and Monocyte. A red box highlights a region of high enrichment in hESC and hESC-Fibro. The gene model below shows the ALX1 gene structure with a blue arrow indicating the transcription start site.

Bottom Panel: chr5:149,522,091,149,548,759. The tracks show H3K27me3 enrichment for hESC, hESC-Fibro, Fibro, and Monocyte. A red box highlights a region of high enrichment in hESC and hESC-Fibro. The gene model below shows the CDX1 gene structure with a blue arrow indicating the transcription start site.

