Description of Additional Supplementary Files

File Name: Supplementary Data 1
Description: List of rtQTLs Identified in This Study. The fastQTL package was used to calculate p-values for rtQTLs. The presented p-values were uncorrected for multiple testing. Correction for multiple testing was used when identifying significant associations (see Methods for details).

File Name: Supplementary Data 2
Description: Fine-mapped Genetic Variants of hESC rtQTLs by CAVIAR.

File Name: Supplementary Data 3
Description: Histone modifications associated with each hESC rtQTL.

File Name: Supplementary Data 4
Description: Locations of Histone modification Sites in hESCs.

File Name: Supplementary Data 5
Description: Locations of Replication Timing Peaks in hESCs.

File Name: Supplementary Data 6
Description: Locations of Histone modification Sites in iPSCs.

File Name: Supplementary Data 7
Description: Locations of Replication Timing Peaks in iPSCs.