Spontaneous HTLV-1 transcription and epigenetic changes around the pX region are CTCF-independent.

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Supplementary material

Supplementary Figure 1  Histone modifications in HTLV-1 provirus
(a) Histone modifications in each of the Tax+ and Tax− populations from an HTLV-1-infected T cell clone (TBX4B). The provirus loci examined by qPCR on the horizontal axis correspond to the ones shown in Figure 4a. (b) Histone modifications in each of the Tax+ and Tax− populations from an HTLV-1-infected T cell clone (11.65). The horizontal axis indicates the nucleotide position in the full-length HTLV-1 provirus (J02029), and the vertical axis the read depth (arbitrary units). The reads that aligned within the LTRs are indicated in grey. The bars on the horizontal axis indicates the LTRs.