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

Miura M et al. *Wellcome Open Res* 2018

Supplementary material

**Supplementary Figure 2** DNA methylation in the 5′ LTR promoter in HTLV-1-infected clones

(a) Region amplified by PCR for bisulfite sequencing. The three Tax-responsive elements are indicated in red. (b) Schematic representation of DNA methylation. Each bar represents a PCR fragment that was cloned and sequenced. Open circles indicate unmethylated cytosine, and closed circles methylated cytosine. The numbers correspond to the positions shown in Figure 5a. The HTLV-1 T cell clone TBX4B does not have CpG at position 6, so this position is omitted.

(c) DNA methylation in the 5′ LTR promoter in mutated HTLV-1-infected clones that lack CTCF binding in the provirus.