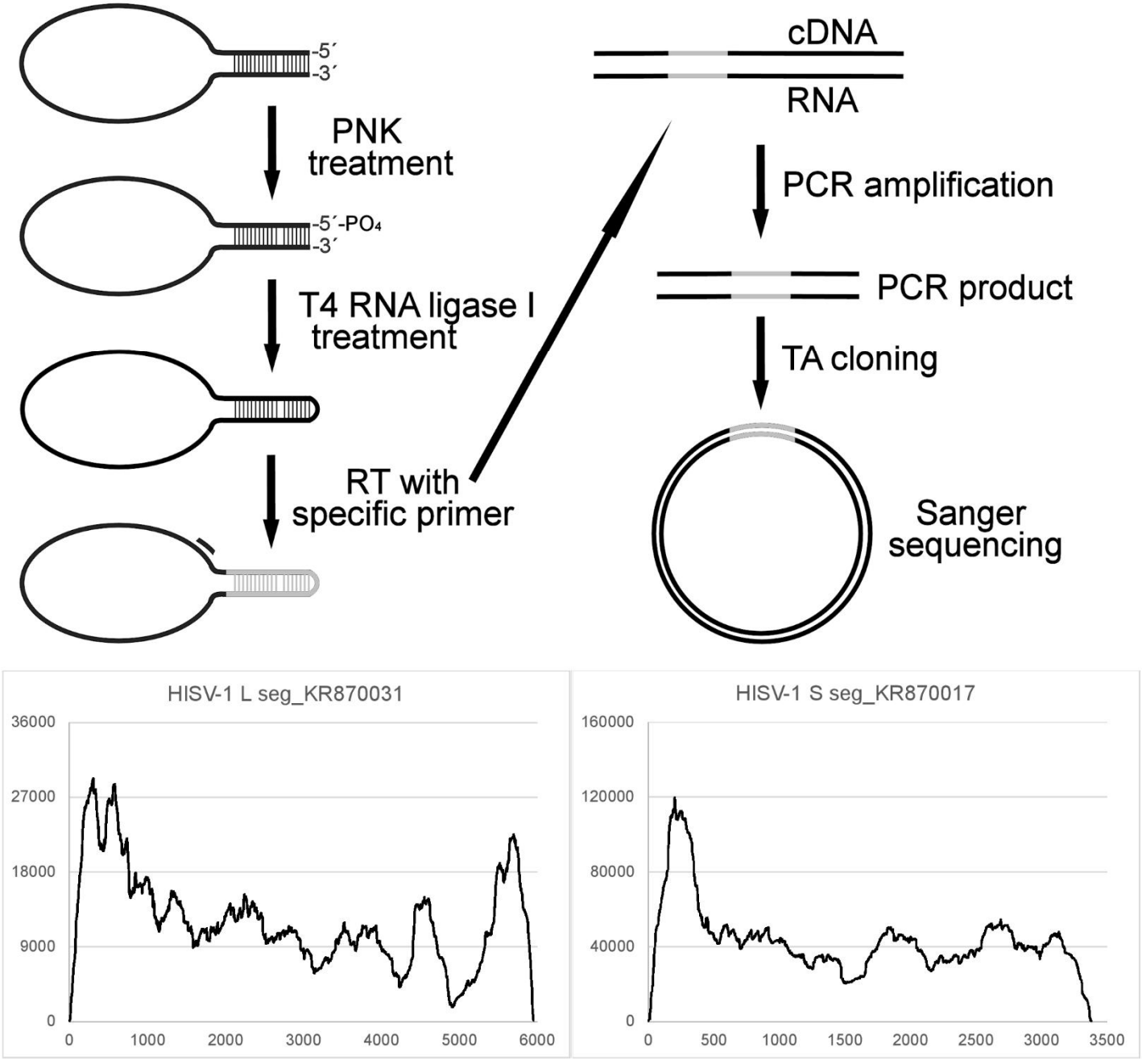

Supplementary figure 2. Schematic illustration of the sequencing strategy for HISV-1 genome ends. The viral RNA isolated from cell culture supernatant was treated with polynucleotide kinase (PNK) to ascertain the phosphorylation of 5 ´ end before treatment with T4 RNA ligase I. The ligated RNA was transcribed to cDNA using primer specific for either S or L segment, after which the genome ends were PCR amplified. The PCR products were cloned into a plasmid, and individual clones were Sanger sequenced. The coverage at which HISV-1 L and S segments were sequenced by NGS are shown below. The coverage was obtained by aligning reads to full length S and L segment of HISV-1 by using Bowtie2 in Unipro UGENE v.1.25.0.