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.