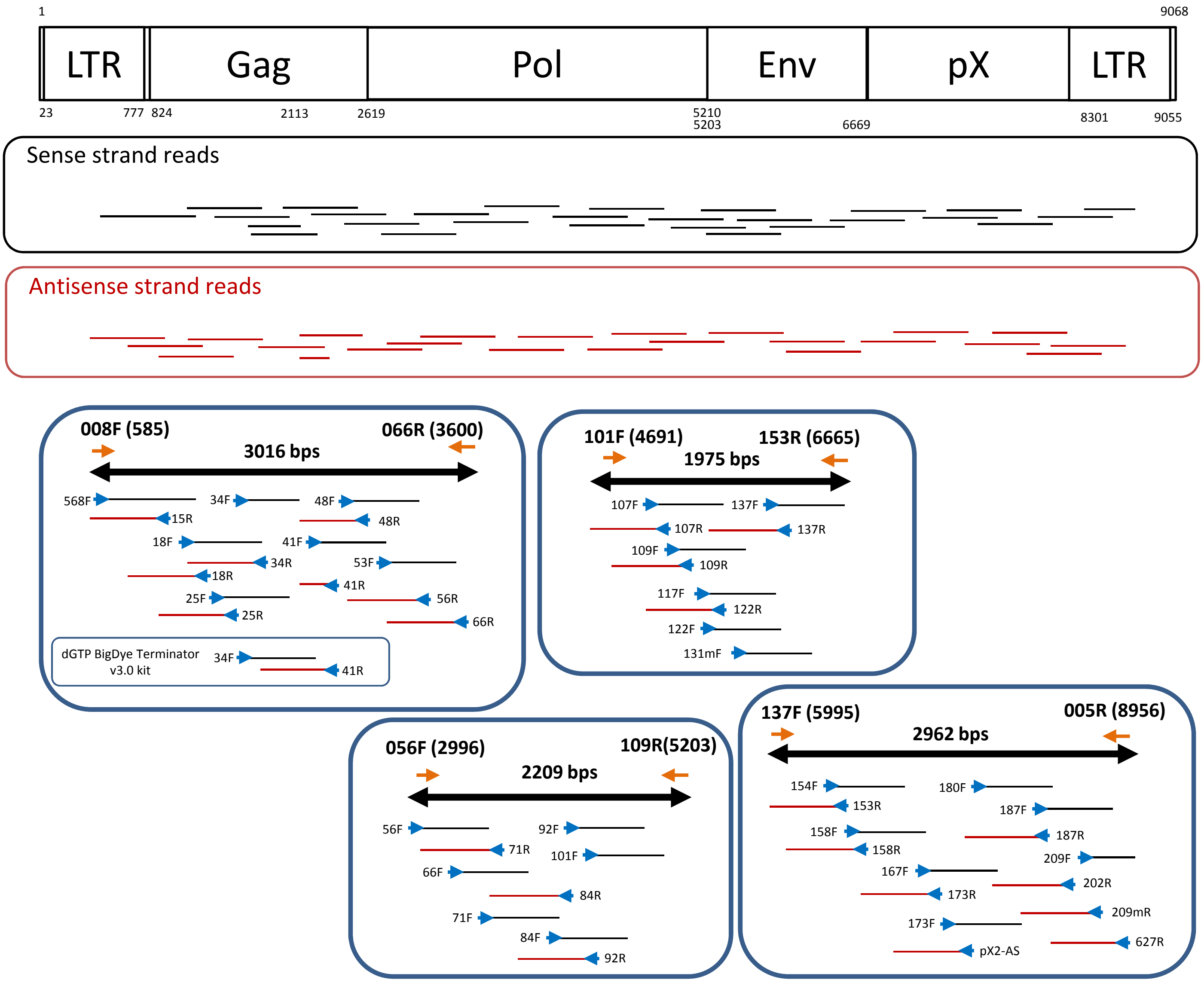
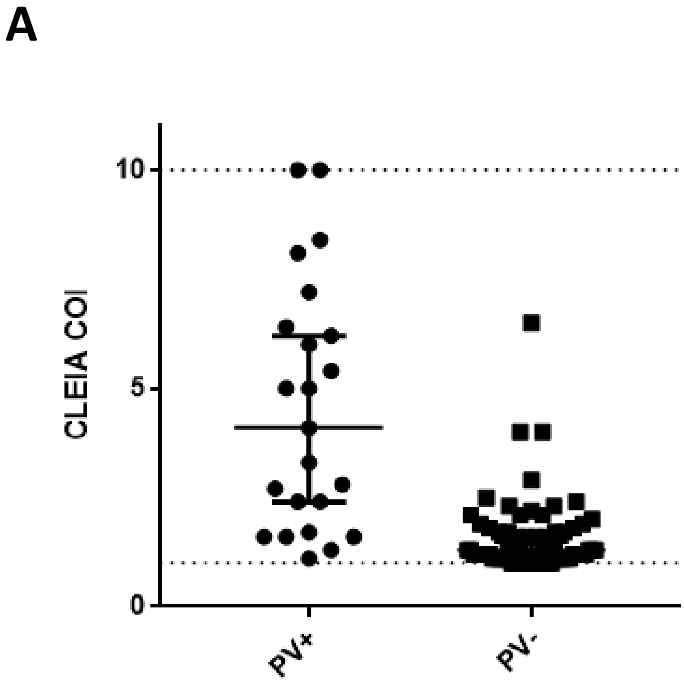


Supplemental Figure S1. Schematic of long PCR and sequencing for determination of the complete HTLV-1 proviral genome.

As described in the Materials and Methods and Supplemental Table S6, four long DNA fragments in the full HTLV-1 genome were amplified using primers indicated by orange arrows. Using the sequencing primers indicated by blue arrows (also listed in Supplemental Table S7), nucleotide sequences were read from both strands. Sequence tags in the sense orientation are indicated as black lines, and those in antisense orientations are indicated by red lines. The size of the line is set as ~600 bases in this figure. Nucleotide numbering is based on the ATK-1 prototypic sequence (Genbank: J02029).



Supplemental Figure S2. Correlation between the CLEIA cutoff index (COI) and HTLV-1 qPCR results.

CLEIA COIs at the initial screening test of PV+ and PV- blood donors were plotted. PV+: WB indeterminate samples that were provirus positive in HTLV-1 qPCR. PV-: WB indeterminate samples that were provirus negative in HTLV-1 qPCR.