

Supplementary Dataset 2

Proviral sequences generated as part of the study using the `medaka_consensus` program (<https://nanoporetech.github.io/medaka/index.html>) with manual correction guided by mapping reads to consensus and inspection in IGV

pBLV344

Bos-1053_BLV_consensus

Bos-1439_BLV_consensus

HIV_U1_CHRX

HIV_U1_CHR2

02006_consensus, consensus sequence of the proviruses from patient 02006

02006_chr10_sc, sequence of the provirus with ID chr10:41845251-42110306*

02006_cen, sequence of the provirus with ID chr13:16283554-17732159*

BosT_ERV_chr11_APOB

*these two consensus sequences were generated using a limited number of Nanopore reads and as a consequence there is a higher chance that they may contain errors.

>pBLV344 8721 bp

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>02006_consensus (9737 bp) Consensus sequence of the proviruses from patient 02006

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GGCCTACGTAAGTGGTGCAAACCTTCTTGTCTTGAAGTTTTATTGGTCTCCCGCGTAAACCAAGCTAC
TCAGCTTCTTTTCTCCACTGAAA

TTTCCTACTGAGCTATCCTCATTCTATTGTTCTCTATATCCCTAATTAGCATATAAATAGTCGCCGAC
GCCGTCTCCCCTTCGAATACCC

TGGATCAGCCGGGGCTGGTCCTCGGCA