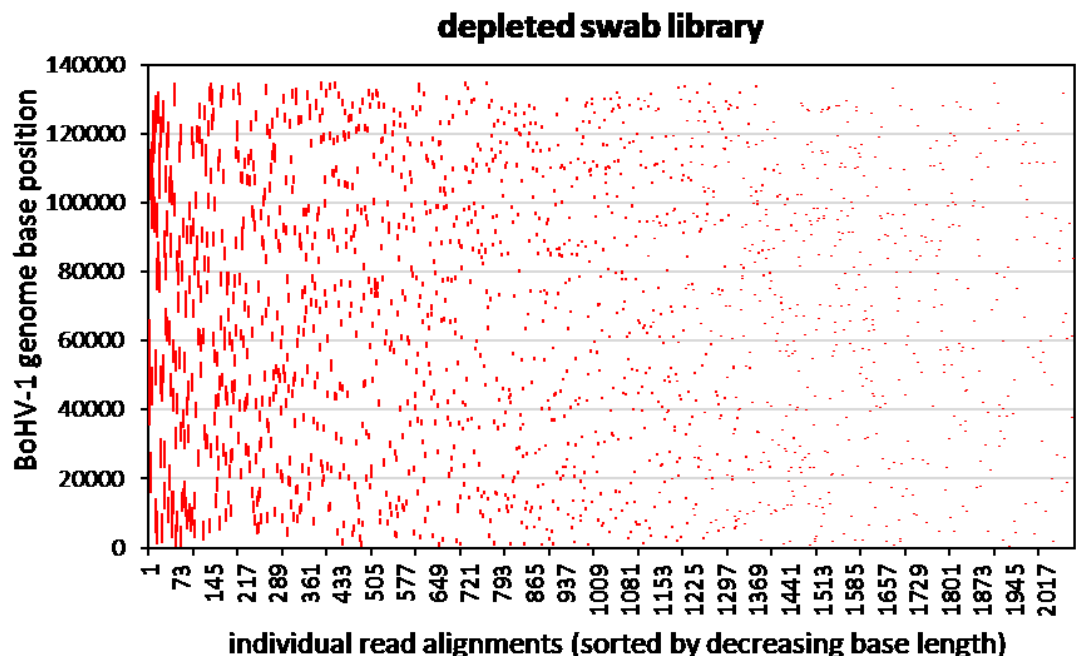


Average alignment length = 4,013. Number of aligned bases = 1,657,348. Number of aligned reads = 414.
Total bases sequenced = 1,800 Mb. % of total bases sequenced that aligned to BoHV-1 genome = 0.092%



Average alignment length = 1,443. Number of aligned bases = 3,003,635. Number of aligned reads = 2,082.
Total bases sequenced 85.7 Mb. % of total bases sequenced that aligned to BoHV-1 genome = 3.5%

Figure S1. Alignments to the BoHV-1 genome of sequence from undepleted and depleted (bead-beating and nuclease treatment prior to nucleic acid extraction) libraries generated from a nasal swab from a calf infected with BoHV-1. PCR-free tagged libraries were generated with the ONT Field Sequencing Kit and sequenced on a MinION R9 flowcell using rapid base calling. FASTQ files were aligned to the BoHV-1 genome sequence using the EPI2ME Custom Reference Aligner workflow which employs minimap2. Graphs were created in Microsoft Excel and Microsoft PowerPoint in Microsoft Office Professional Plus 2016.