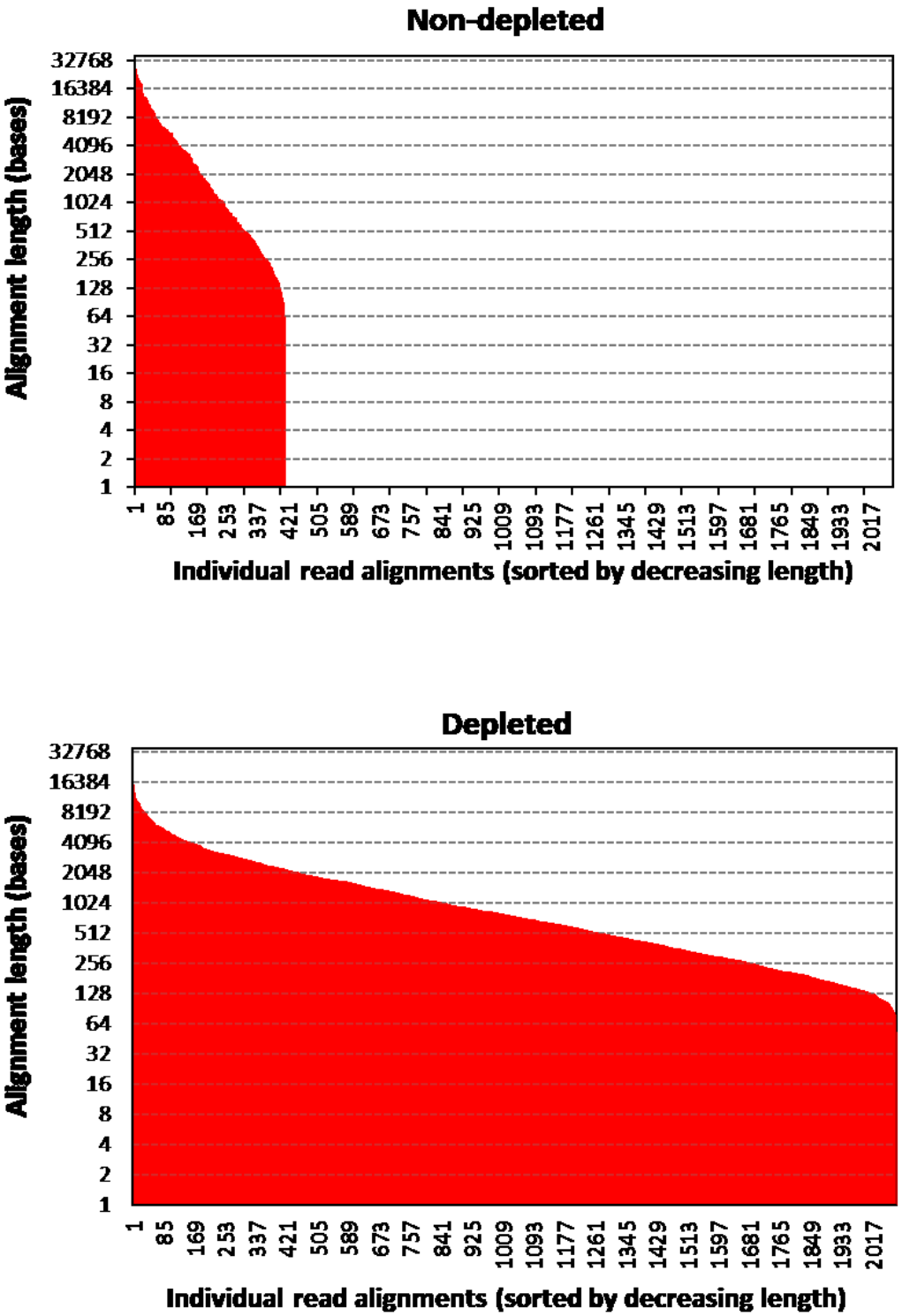

Figure S2. Read lengths of depleted vs. undepleted alignments to the BoHV-1 genome of sequence from undepleted and depleted (bead-beating and nuclease treatment prior to nucleic acid extraction) libraries generated from a nasal swab from a calf infected with BoHV-1. PCR-free tagmented libraries were 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 Fastq Custom Alignment workflow which employs minimap2. Graphs were created in Microsoft Excel and Microsoft PowerPoint in Microsoft Office Professional Plus 2016.