

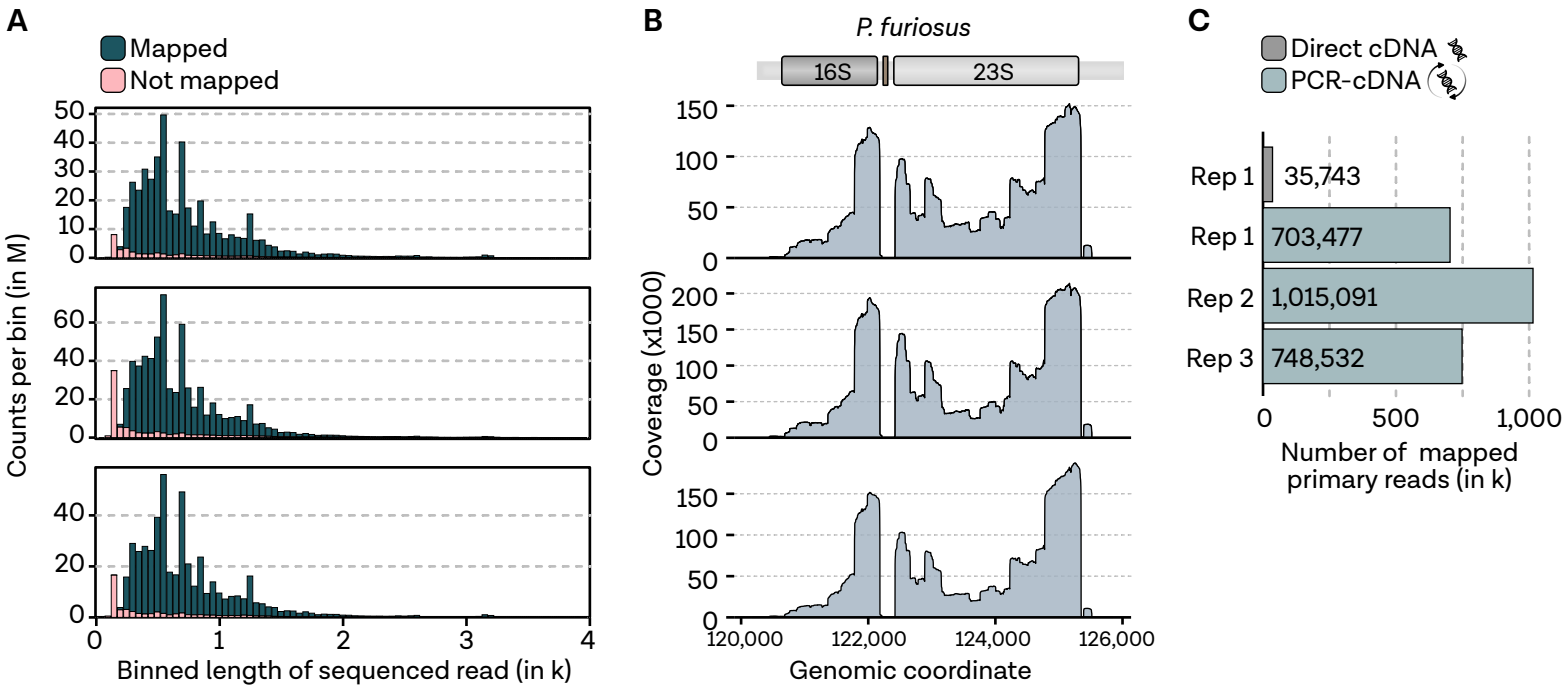


Fig. S10 | Nanopore-based PCR-cDNA sequencing of *P. furiosus*.

A, Distribution of sequenced read length (bin size 50 nt), stacked by alignment group (blue: full-length mapped reads; pink: not mapped). **B**, Coverage profiles of pychopper filtered full-length reads mapping to the rRNA region. **C**, Total number of primary mapped reads in direct cDNA (grey) and PCR-cDNA (blue) samples.