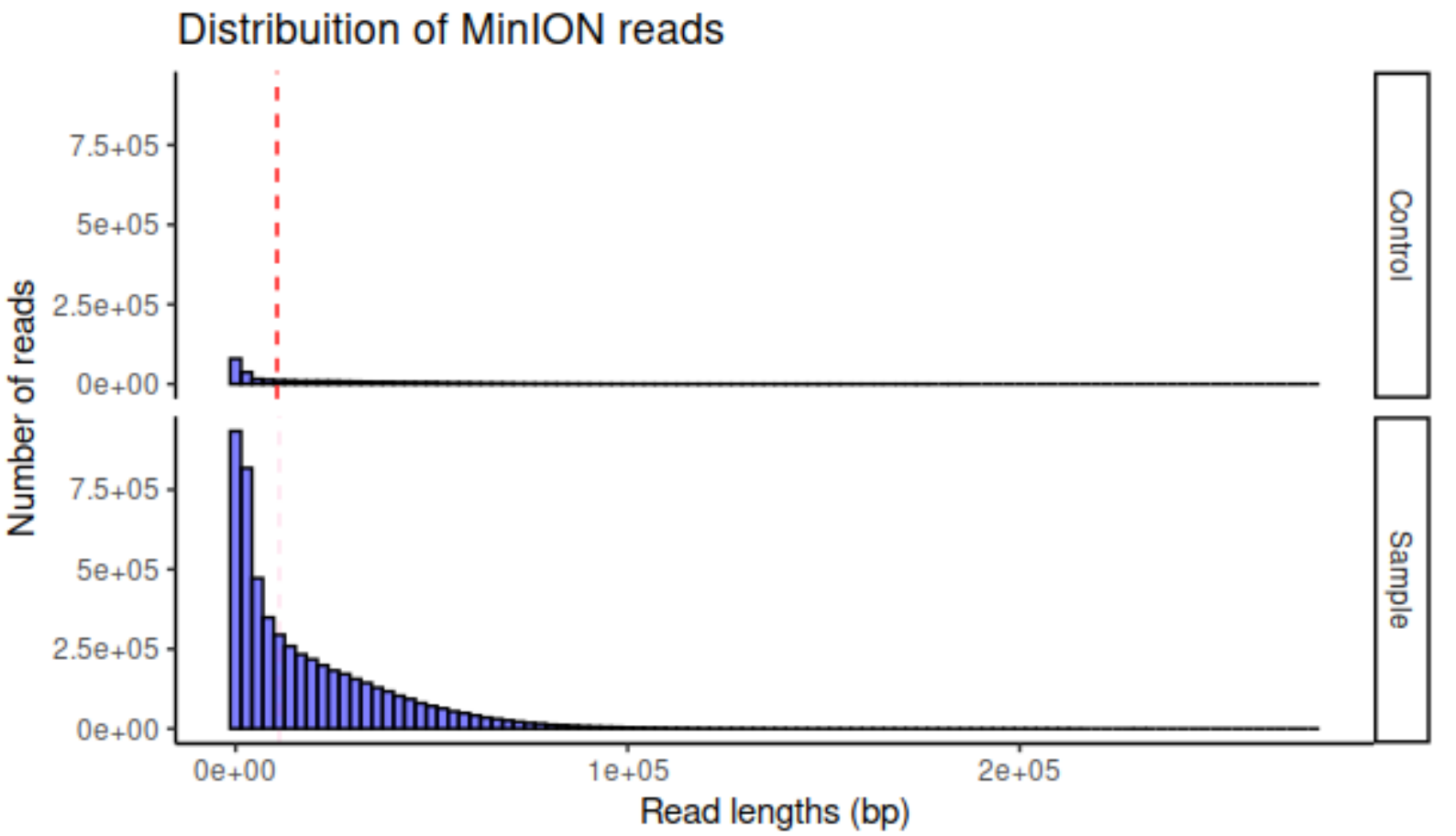
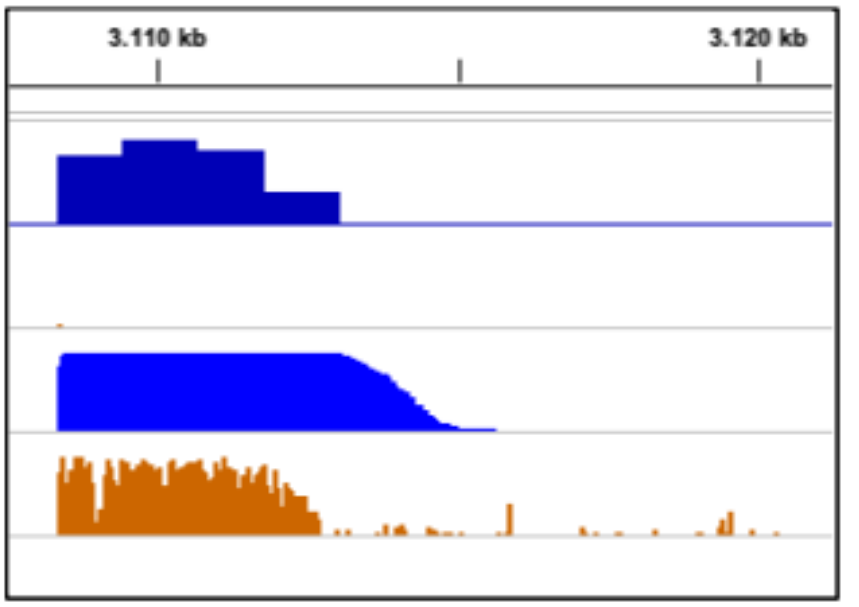
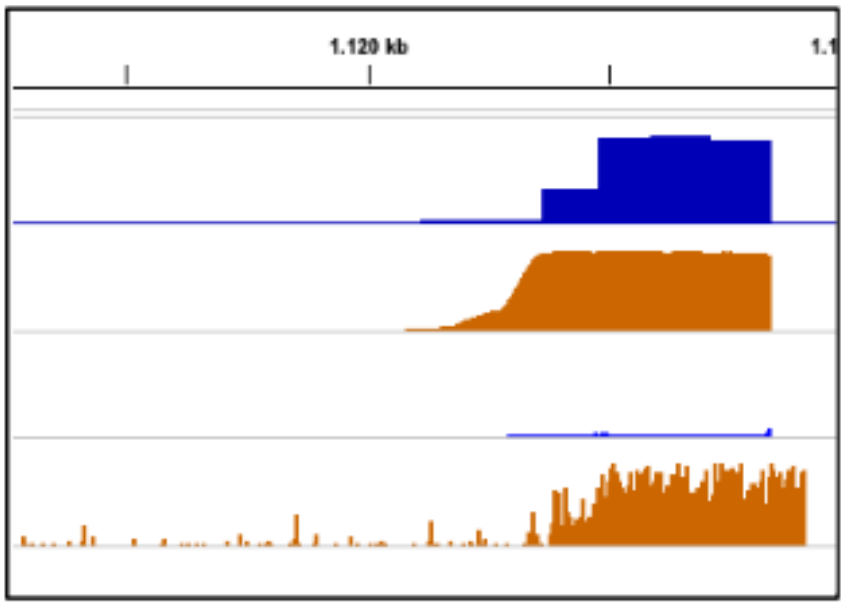


Fig. S1. Nanopore sequencing reads after base calling.

A) Rightward moving fork



B) Leftward moving fork



C) Bidirectional moving forks

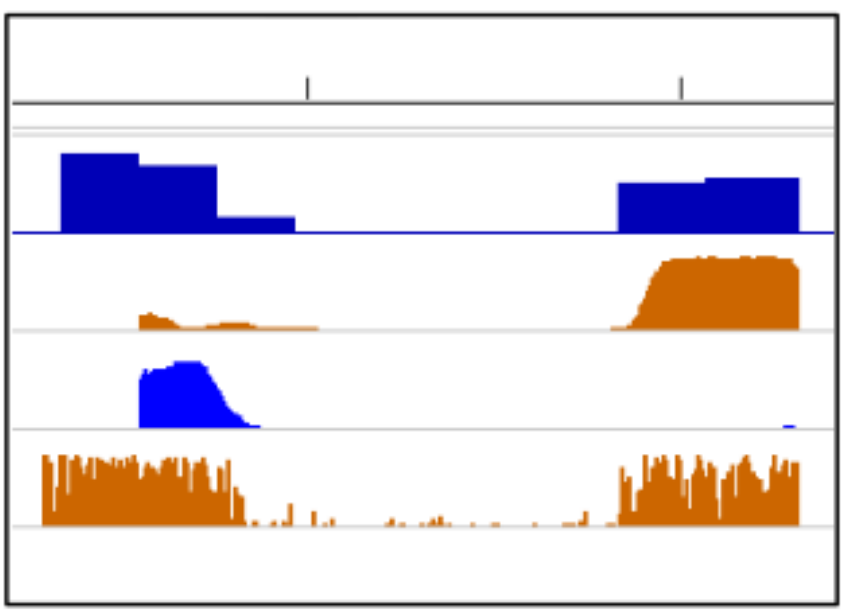


Fig. S2. Detection of BrdU-incorporated nanopore sequenced molecules and movement of replication forks analyzed by DNAscent. Bedgraphs visualized in IGV showing the probability of BrdU called at each thymidine position for three selected reads (**A-C)**. Each read is represented by a group of four tracks: profile of BrdU detection (upper track), probability of a leftward moving fork (upper-middle track), probability of a rightward moving fork (lower-middle track), probability of BrdU at each thymidine position (lower track) from DNAscent forksense.

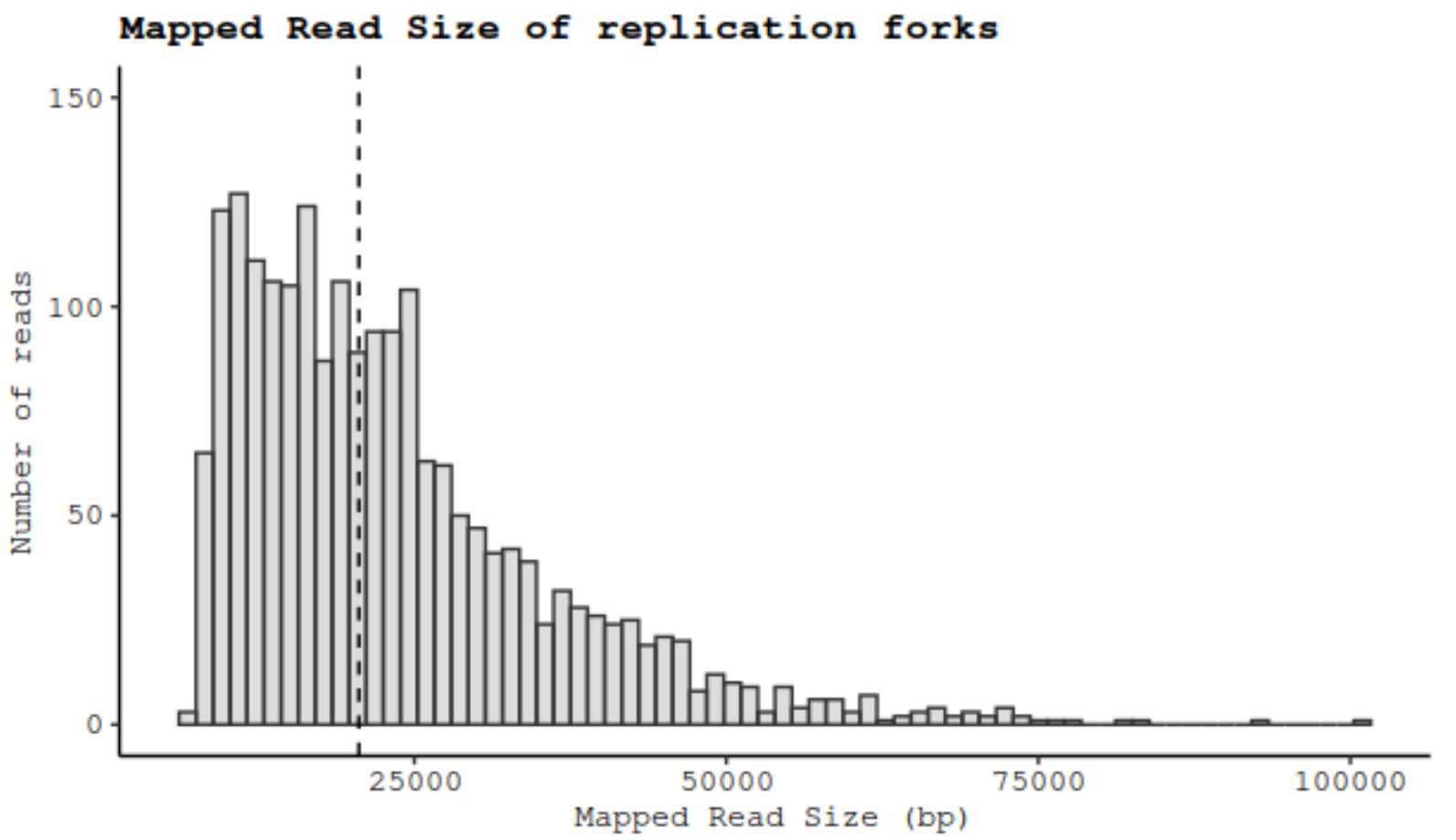


Fig. S3. Mapped read size of replication forks.

Table S1. BrdU positive reads analyzed by DNAscent. Regions containing fork direction were plotted and matched with the annotated genome to analyze replication fork and transcription directions and evaluate potential HoRT collisions.

Click here to download Table S1

Table S2. MinION sequencing data and DNAscent analysis summary.

Experiment	MinION runs	MinION reads	Estimated bases (Gb)	Average read length (bp)	Mapped read (%)	Positive BrdU molecules (probability ≥ 70%)	%Positive reads	Input DNA per run (ug)
Giardia intestinalis trophozoites negative control	1	29770	0,58	4220	91,23	9	0.09	5
Giardia intestinalis trophozoites BrdU 300uM a	1	90130	1,3	38110	94,94	286	0.32	5
Giardia intestinalis trophozoites BrdU 300uM b	2	455750	8,86	30460		3377	0.74	5