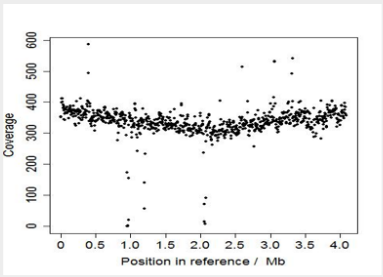
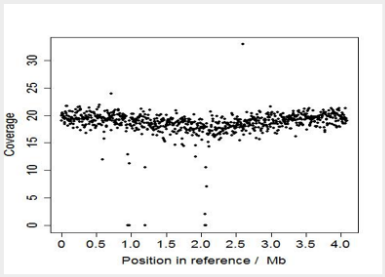
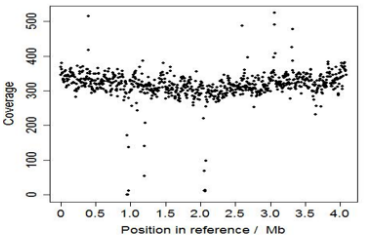
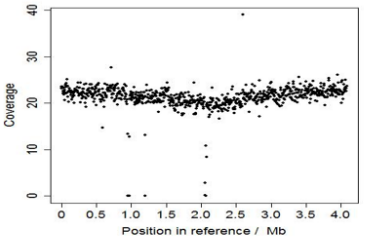
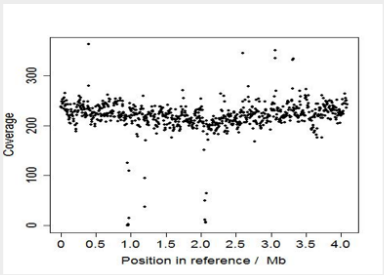
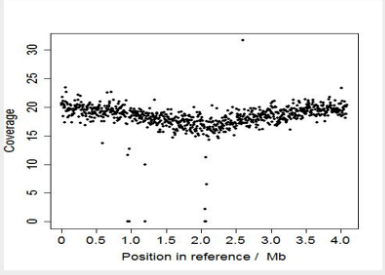
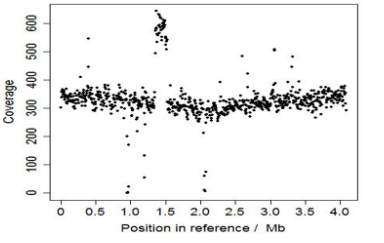
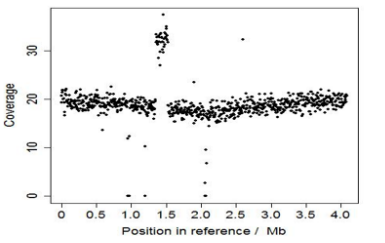
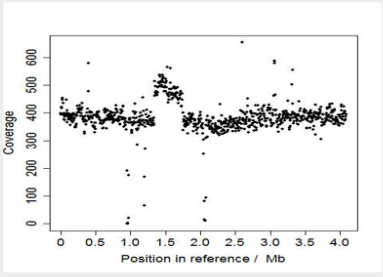
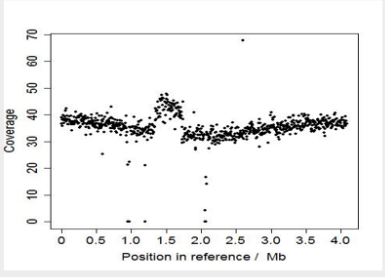
| Strain | Nanopore reads | Illumina reads |
|---|---|---|
| UK36 |  |  |
| UK38 |  |  |
| UK39 |  |  |
| UK48 |  |  |
| UK76 |  |  |

**Fig. S3: Alignment of nanopore reads to Tohama I reference sequence compared to alignment of Illumina reads to Tohama I reference sequence.** Raw reads from each sequencer were aligned to the reference using BWA MEM, followed by coverage calculation with samtools depth. The coverage abnormalities seen in UK48 and UK76 are present in both sets of reads, suggesting they are not the result of a quirk in sequencing method, or contamination.