



Figure S3. Visualization of chimeric reads mapped to the *E. coli* genome.

Long reads were mapped to the Ecoli.UMIGS genome assembly. After determining putative chimeric reads in each dataset, BAM files were filtered to retain only chimeric alignments. Mapped reads were visualized in IGV. The region shown here contains chimeric reads in four of five datasets (excluding PacBio HiFi). Reads outlined in blue were assigned the supplementary (chimeric) alignment SAM flag. Chimeric alignments often involve a single read mapping to opposite DNA strands in the same region (two alignments connected by red arrows) or a read mapping to two distinct regions in the *E. coli* genome (black arrow; second alignment not shown). There was no apparent evidence of supplementary alignments immediately adjacent to primary alignments representing erroneous chimera assignment.