Novel 1.5hr hybridization step for preparation of enriched libraries in a single day

Contrasting GC %GC sequence content.

We present an accelerated transposase transposase system. Fragmentations were amplified with Herculase II DNA polymerase and sequenced on the MiSeq platform. Picard analysis%GC demonstrates that SureSelectXT exhibits superior coverage compared to a competing transposase-based system, providing better coverage of AT-rich regions and substantially improving whole-genome sequencing of bacterial species with low %GC sequence content.

Methods & Results

50ng samples of bacterial DNAs from three genomes of divergent GC content were fragmented and tagged by the SureSelectXT transposase system. Fragmentations were amplified with Herculase II DNA polymerase and sequenced on the MiSeq platform. Picard analysis%GC demonstrates that SureSelectXT (%GC) exhibits superior coverage compared to a competing transposase-based system (%GC), providing better coverage of AT-rich regions and substantially improving whole-genome sequencing of bacterial species with low %GC sequence content.

Conclusions

We present a fast and simple library prep method that integrates seamlessly with the SureSelectXT target enrichment workflow.

References