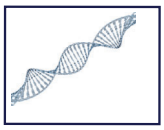
How to Improve
Your WGS DNA Library

Successful sequencing of entire genomes often requires deep sequencing, in order to detect rare single nucleotide variations (SNV), point mutations, and single nucleotide polymorphisms (SNP). The PCR-based and PCR-free Invitrogen™ Collibri™ PS DNA Library Prep Kits for Illumina™ systems provide even coverage of genomic regions for reduced biases.

Factors that impact GC coverage bias



DNA shearing

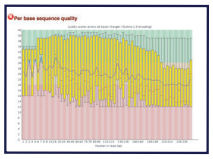
Ligation efficiency

PCR amplification (major source)

Why is GC coverage bias a problem?

- GC-poor and GC-rich sequences lead to uneven or no coverage of reads
- GC content is heterogeneous within genomes, but most assemblers assume uniform coverage
- GC effect can be hard to tell apart from true signal, as GC abundance is often correlated with functionality
- Genome assembly is hindered

What does GC coverage bias affect?

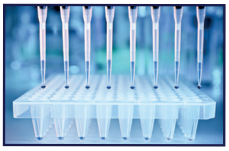


Sequencing data quality scores

Data interpretation

How to reduce GC coverage bias in WGS libraries

Improve PCR protocols to reduce amplification bias



- Optimzation of temperature ramp
- Increase duration of denaturation phase

Use novel PCR-based and PCR-free kits

- Invitrogen Collibri PCR-Free PS DNA Library Prep Kit for Illumina Systems
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