



Input data and parameters

QualiMap command line

```
qualimap bamqc -bam bowtie2_ecoli_sorted.bam -nw 400 -hm 3
```

Alignment

Command line:	"/home/*****/miniconda3/envs/bowtie2/bin/bowtie2-align-s --wrapper basic-0 -x Ecoli_ref_index -S bowtie2_ecoli_output.sam -1 SRR33285751_1_paired.fastq -2 SRR33285751_2_paired.fastq"
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bowtie2 (2.5.4)
Analysis date:	Wed May 14 16:04:45 UTC 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	bowtie2_ecoli_sorted.bam

Summary

Globals

Reference size	4,641,652
Number of reads	3,858,312
Mapped reads	3,822,573 / 99.07%
Unmapped reads	35,739 / 0.93%
Mapped paired reads	3,822,573 / 99.07%
Mapped reads, first in pair	1,919,900 / 49.76%
Mapped reads, second in pair	1,902,673 / 49.31%
Mapped reads, both in pair	3,803,136 / 98.57%
Mapped reads, singletons	19,437 / 0.5%
Secondary alignments	0
Read min/max/mean length	36 / 151 / 145.83
Duplicated reads (estimated)	2,350,833 / 60.93%
Duplication rate	55.02%
Clipped reads	0 / 0%

ACGT Content

Number/percentage of A's	136,665,031 / 24.48%
Number/percentage of C's	142,674,797 / 25.56%
Number/percentage of T's	136,474,777 / 24.45%
Number/percentage of G's	142,418,914 / 25.51%
Number/percentage of N's	19,775 / 0%
GC Percentage	51.07%

Coverage

Mean	120.2711
Standard Deviation	22.9004

Mapping Quality

Mean Mapping Quality 40.97

Insert size

Mean 502.68
Standard Deviation 26,186.71
P25/Median/P75 249 / 327 / 426

Mismatches and indels

General error rate 0.31%
Mismatches 1,491,045
Insertions 23,315
Mapped reads with at least one insertion 0.58%
Deletions 2,018
Mapped reads with at least one deletion 0.05%
Homopolymer indels 56.79%

Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
NC_000913.3	4641652	558256414	120.2711	22.9004

Coverage across reference



Coverage Histogram



Coverage Histogram (0-50X)



Genome Fraction Coverage



Duplication Rate Histogram



Mapped Reads Nucleotide Content



Mapped Reads GC-content Distribution



Homopolymer Indels



Mapping Quality Across Reference



Mapping Quality Histogram



Insert Size Across Reference



Insert Size Histogram



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