

Qualimap Report: BAM QC

Input data and parameters

QualiMap command line

qualimap bamqc -bam bowtie2 ecoli sorted.bam -nw 400 -hm 3

Alignment

"/home/******/miniconda3/envs/bowtie2/bin/bowtie2-align-s --wrapper basic-0 -x Ecoli ref index -S Command line:

bowtie2_ecoli_output.sam -1 SRR33285751_1_paired.fastq -2 SRR33285751_2_paired.fastq"

Draw chromosome

limits:

Analyze

overlapping paired- no

end reads:

Program: bowtie2 (2.5.4)

Analysis date: Wed May 14 16:04:45 UTC 2025

Size of a

3 homopolymer:

Skip duplicate

no alignments:

Number of

400 windows:

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

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

Insert size

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

Mismatches and indels

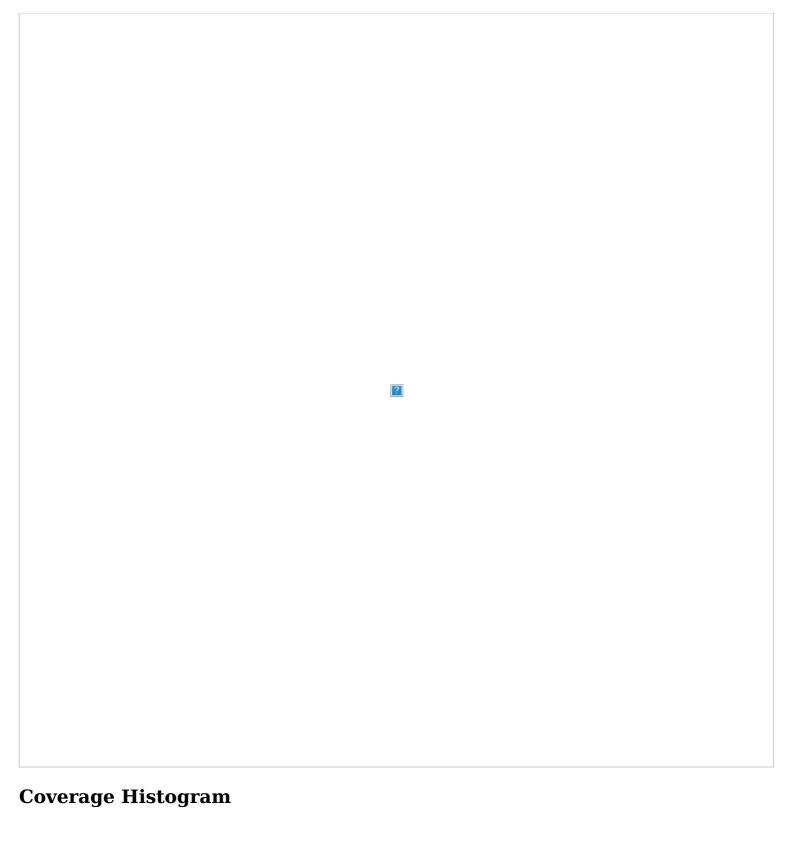
General error rate0.31%Mismatches1,491,045Insertions23,315Mapped reads with at least one insertion0.58%Deletions2,018Mapped reads with at least one deletion0.05%Homopolymer indels56.79%

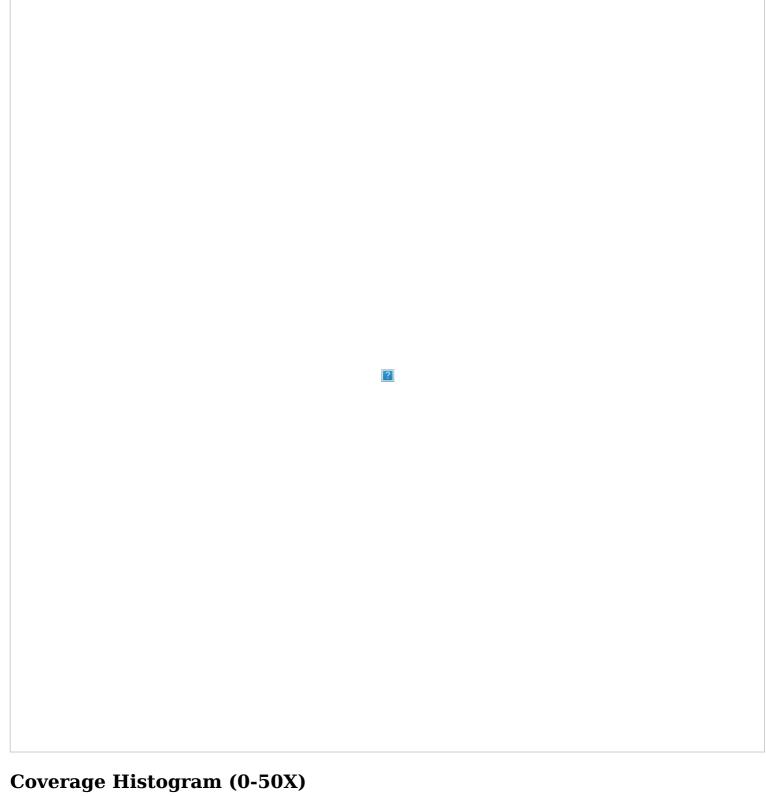
Chromosome stats

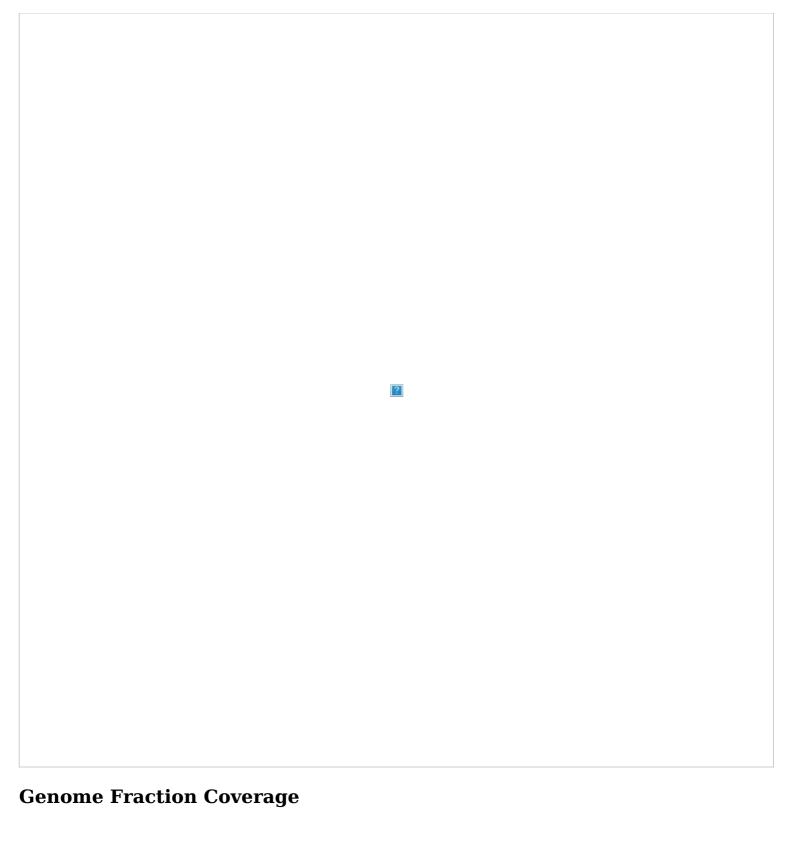
Name Length Mapped bases Mean coverage Standard deviation

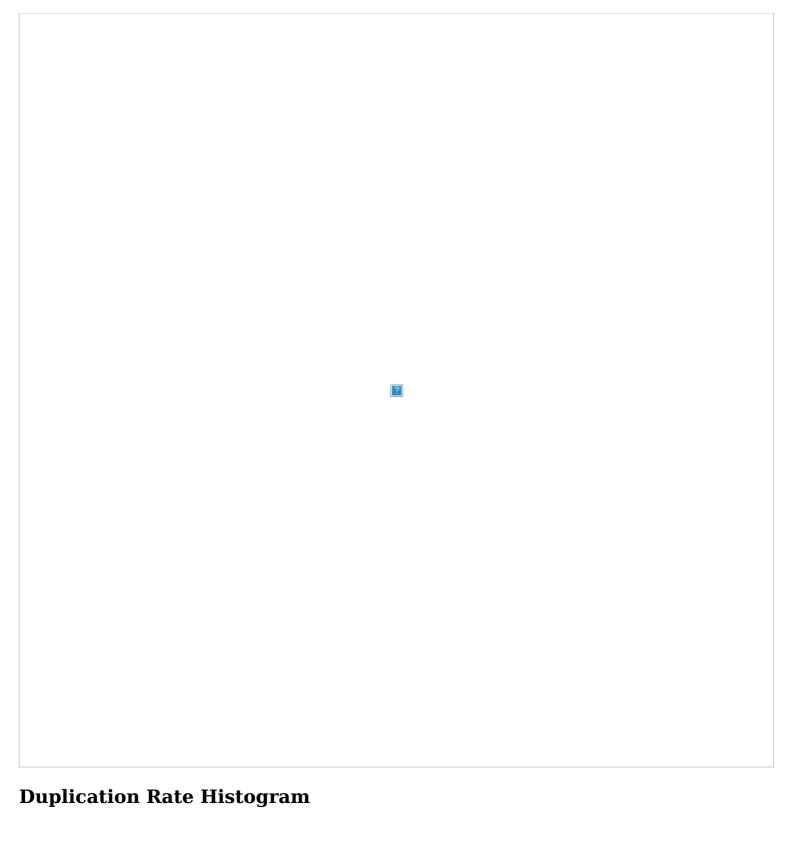
NC_000913.3 4641652 558256414 120.2711 22.9004

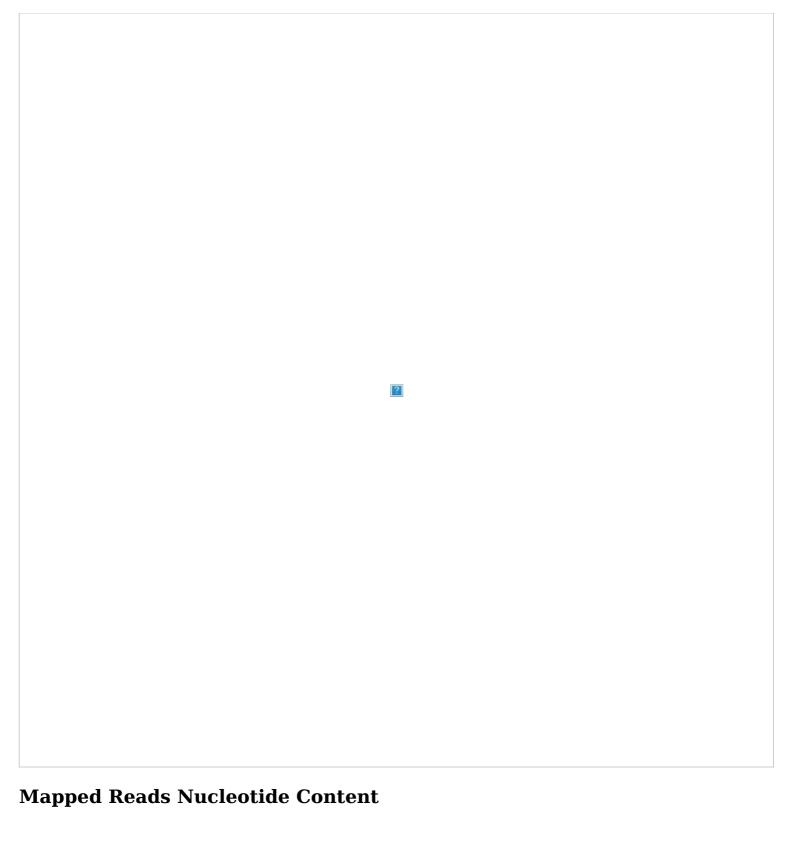
Coverage across reference

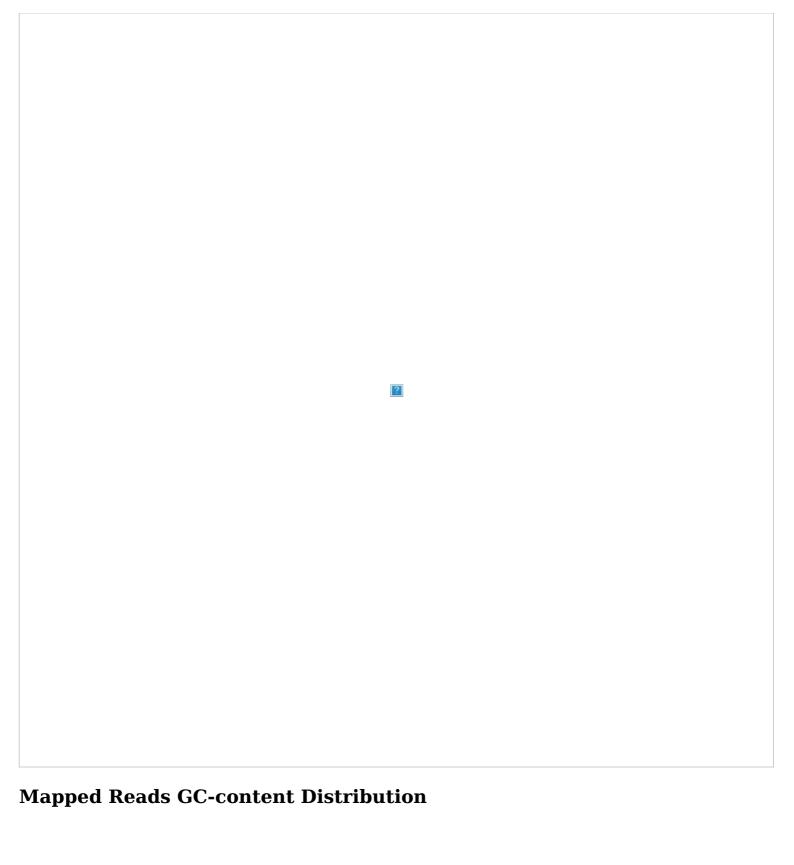


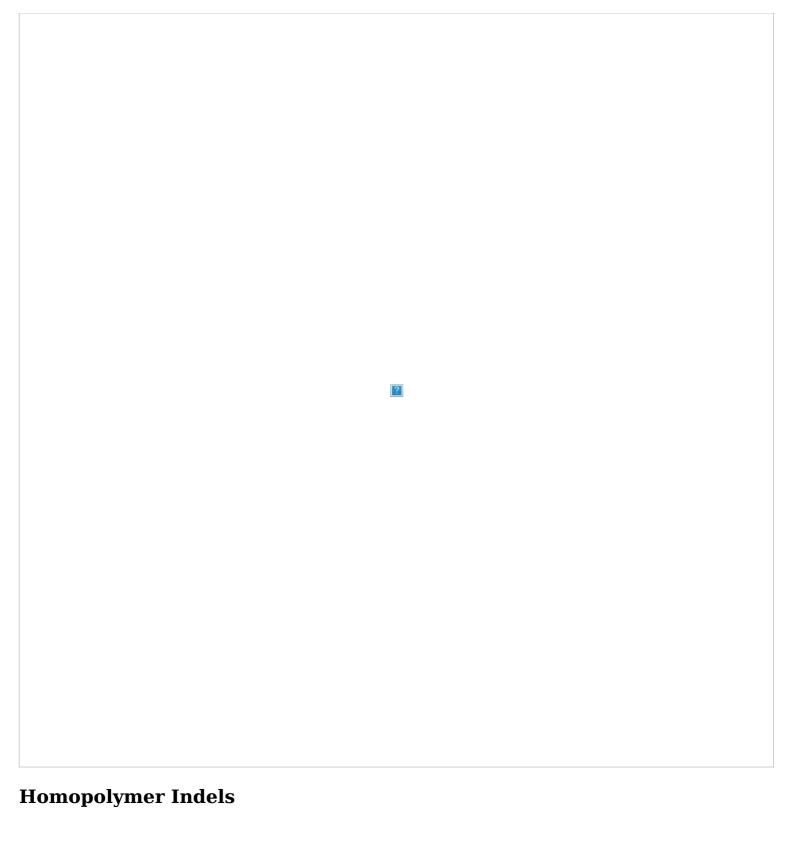




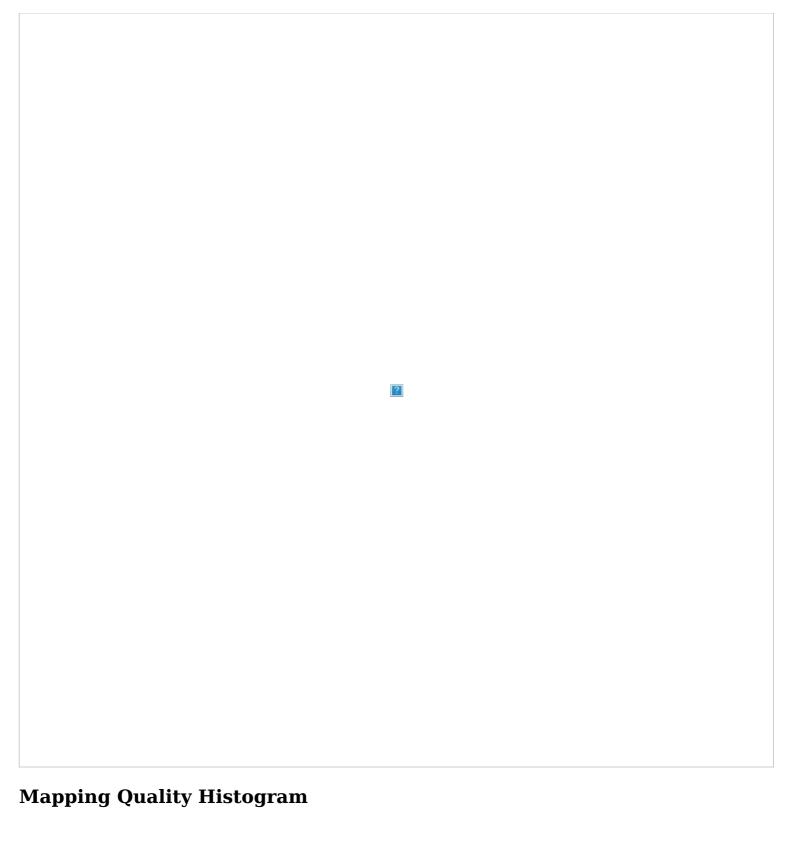


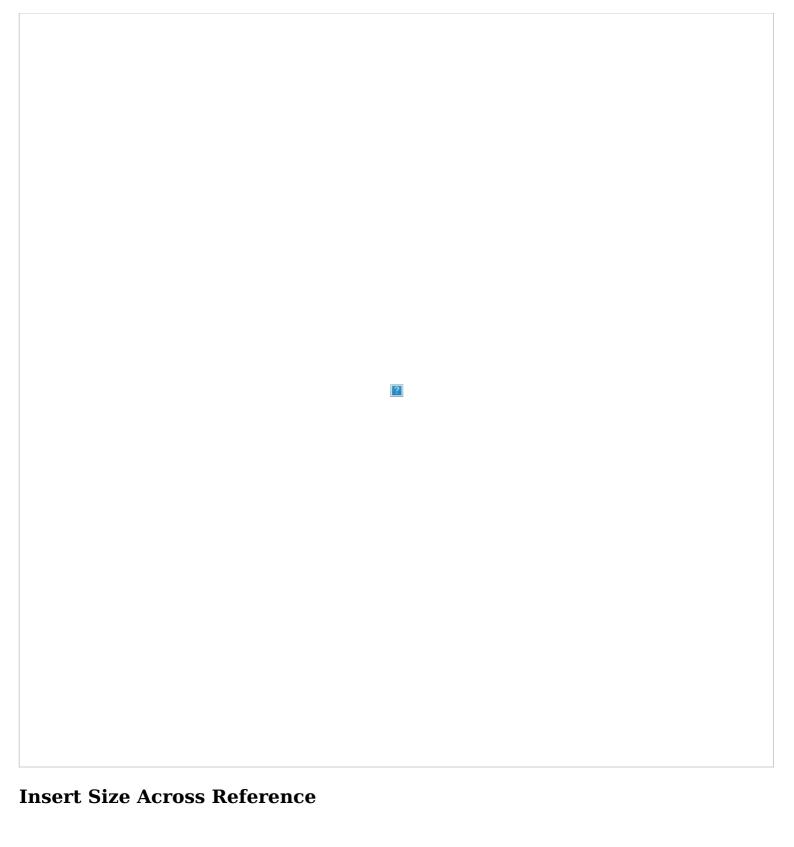


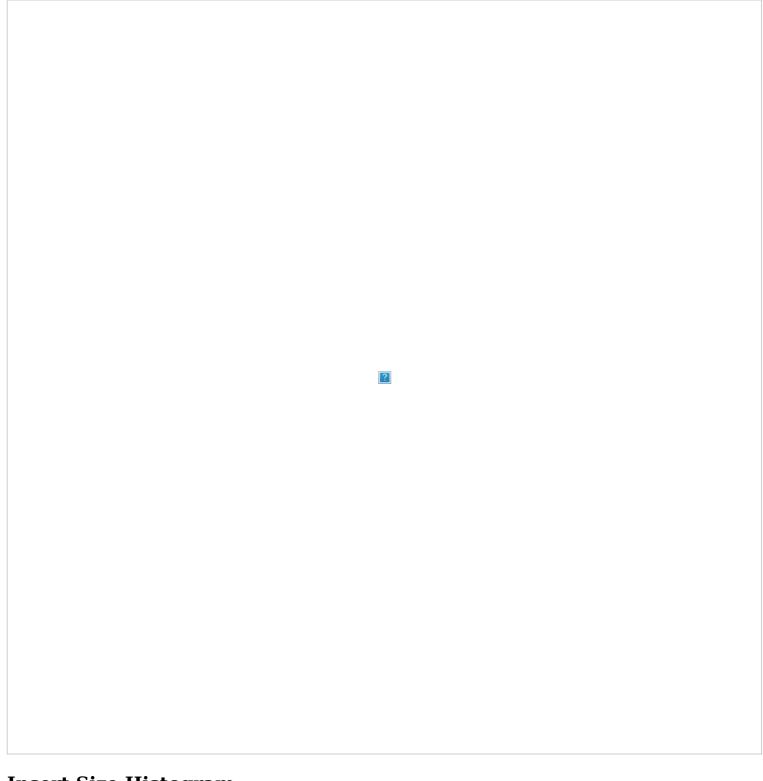




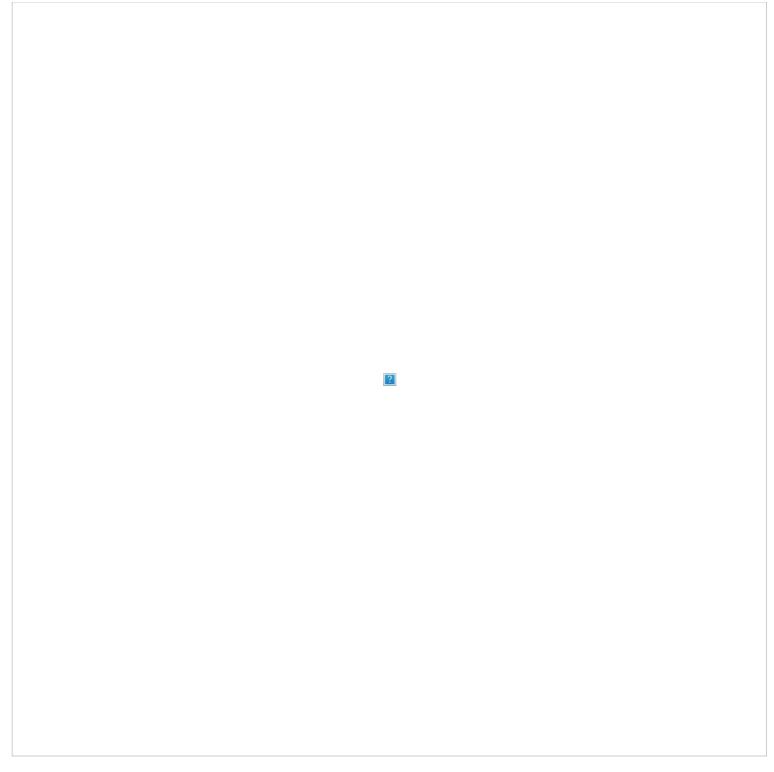








Insert Size Histogram



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2025/05/14 16:04:45

Generated by QualiMap v.2.2.2-dev