Qualimap Report: BAM QC

QualiMap

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Input data and parameters

QualiMap command line

```
qualimap bamqc
/scratch/biol726315/BIOL7263_Genomics/sequencing_data/ecoli/mapping_to_reference/ecoli_mapped_namesort_fixmate_sort_markdup.bam
-gff /scratch/biol726315/BIOL7263_Genomics/reference_sequences/ecoli/GCF_000005845.2_ASM584v2_genomic.g
```

Alignment

Command line:	bwa mem -t 4 /scratch/biol726315/BIOL7263_Genomics/reference_sequences/ecoli/GCF_000005845.2_ASM584v2_genc /scratch/biol726315/BIOL7263_Genomics/sequencing_data/ecoli/trimmed_reads_val_1.fq.gz /scratch/biol726315/BIOL7263_Genomics/sequencing_data/ecoli/trimmed_reads_val_2.fq.gz /scratch/biol726315/BIOL7263_Genomics/sequencing_data/ecoli/mapping_to_reference/ecoli_map
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Thu Sep 12 16:19:50 CDT 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/scratch/biol726315/BIOL7263_Genomics/sequencing_data/ecoli/mapping_to_reference/ecoli_map

GFF region

Library protocol:	non-strand-specific
Outside statistics:	no
GFF file:	/scratch/biol726315/BIOL7263_Genomics/reference_sequences/ecoli/GCF_000005845.2_ASM584v2_genomic.gff

Summary

Globals

Reference size	4,641,652
Number of reads	5,645,078
Mapped reads	5,531,224 / 97.98%
Unmapped reads	113,854 / 2.02%

Mapped paired reads	5,531,224 / 97.98%
Mapped reads, first in pair	2,765,650 / 48.99%
Mapped reads, second in pair	2,765,574 / 48.99%
Mapped reads, both in pair	5,531,155 / 97.98%
Mapped reads, singletons	69 / 0%
Secondary alignments	0
Supplementary alignments	4,516 / 0.08%
Read min/max/mean length	30 / 150 / 140.51
Clipped reads	21,606 / 0.38%

Globals (inside of regions)

Regions size/percentage of reference	4,641,652 / 100%
Mapped reads	5,531,224 / 97.98%
Mapped reads, only first in pair	2,765,650 / 48.99%
Mapped reads, only second in pair	2,765,574 / 48.99%
Mapped reads, both in pair	5,531,155 / 97.98%
Mapped reads, singletons	69 / 0%
Correct strand reads	0 / 0%
Clipped reads	21,606 / 0.38%
Duplicated reads (estimated)	3,567,597 / 64.5%
Duplication rate	58.1%

ACGT Content (inside of regions)

Number/percentage of A's	191,792,757 / 24.7%
Number/percentage of C's	197,027,587 / 25.37%
Number/percentage of T's	191,464,451 / 24.65%
Number/percentage of G's	196,356,779 / 25.28%
Number/percentage of N's	8,923 / 0%
GC Percentage	50.65%

Coverage (inside of regions)

Mean	167.3237
Standard Deviation	45.7799

Mapping Quality (inside of regions)

Mean Mapping Quality	58.9

Insert size (inside of regions)

Mean	2,941.96

Standard Deviation	88,535.83
P25/Median/P75	150 / 219 / 337

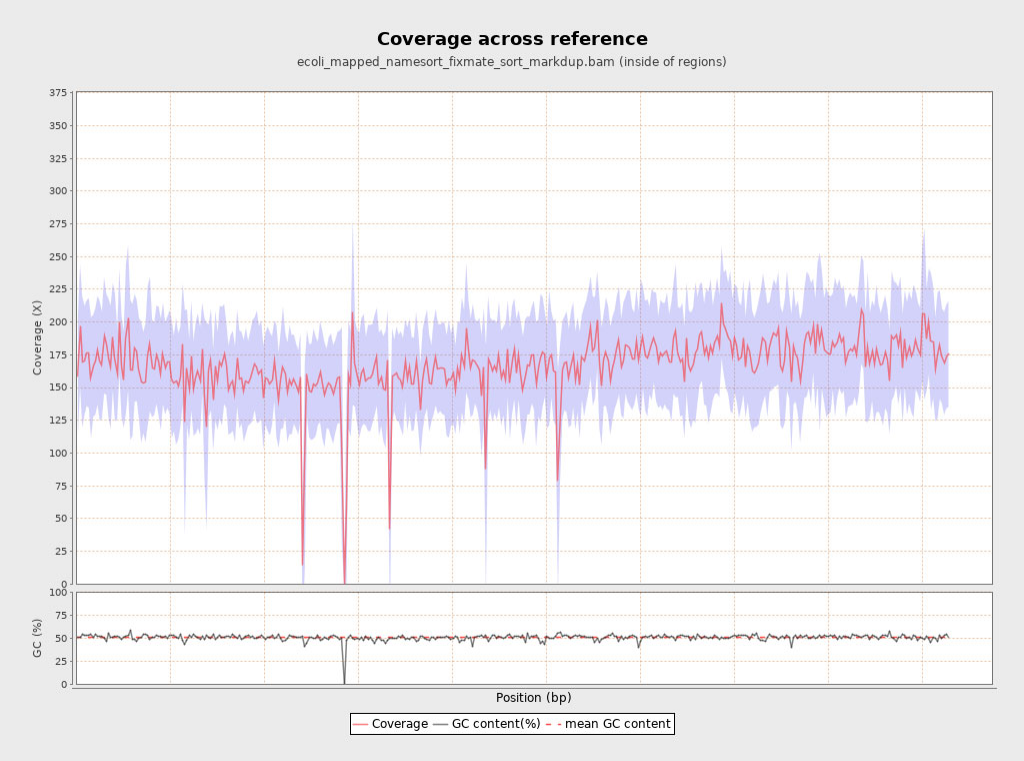
Mismatches and indels (inside of regions)

General error rate	0.08%
Mismatches	629,846
Insertions	1,188
Mapped reads with at least one insertion	0.02%
Deletions	5,439
Mapped reads with at least one deletion	0.1%
Homopolymer indels	64.64%

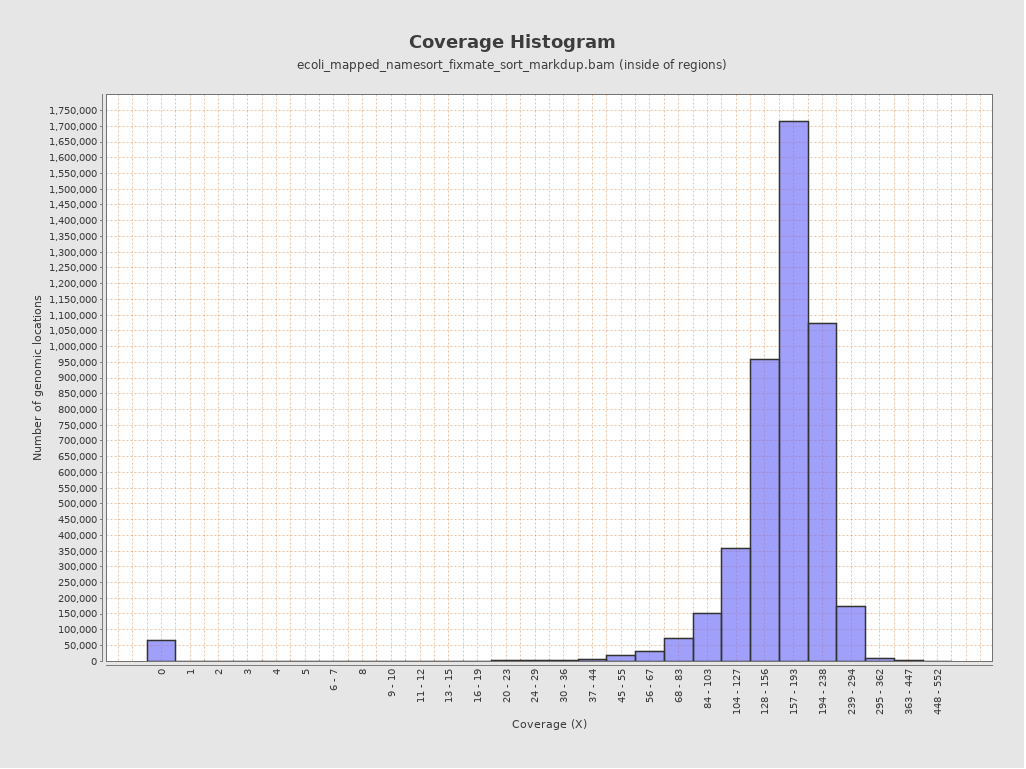
Chromosome stats (inside of regions)

Name	Length	Mapped bases	Mean coverage	Standard deviation
NC_000913.3	4641652	776658266	167.3237	45.7799

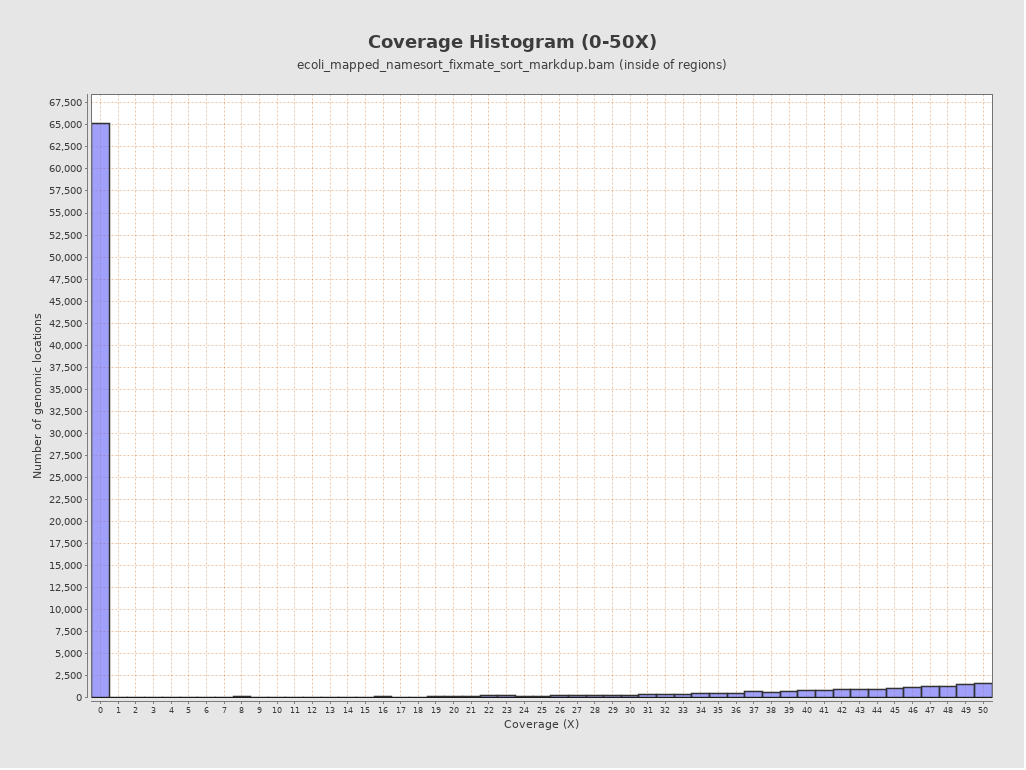
Coverage across reference



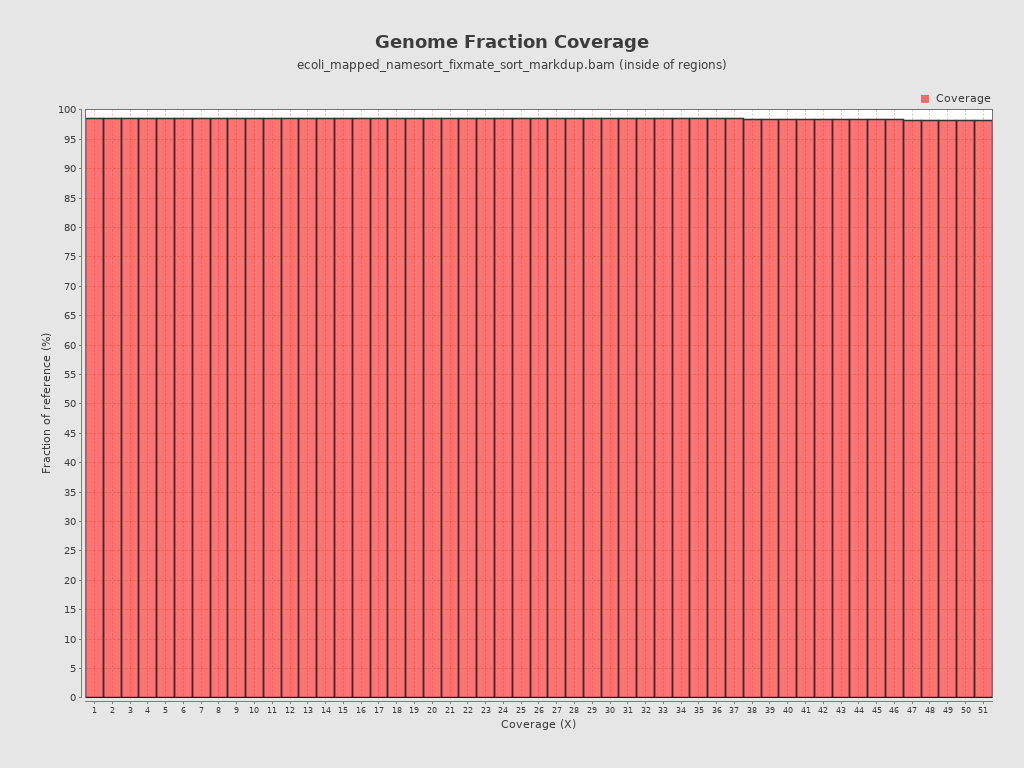
Coverage Histogram



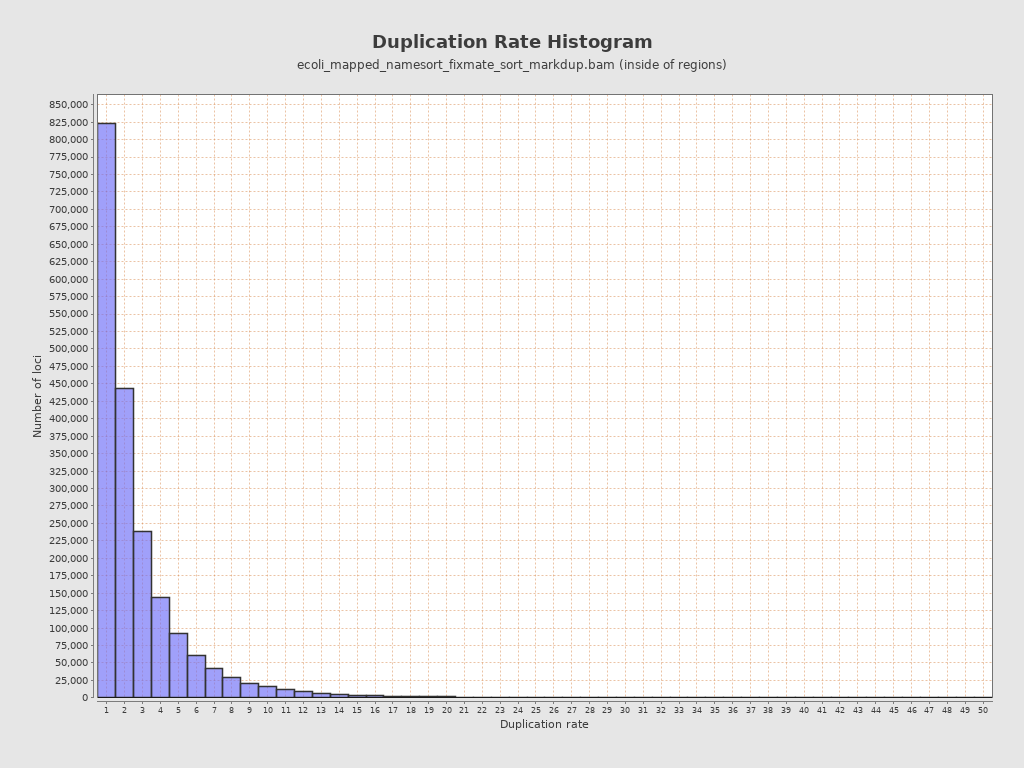
Coverage Histogram (0-50X)



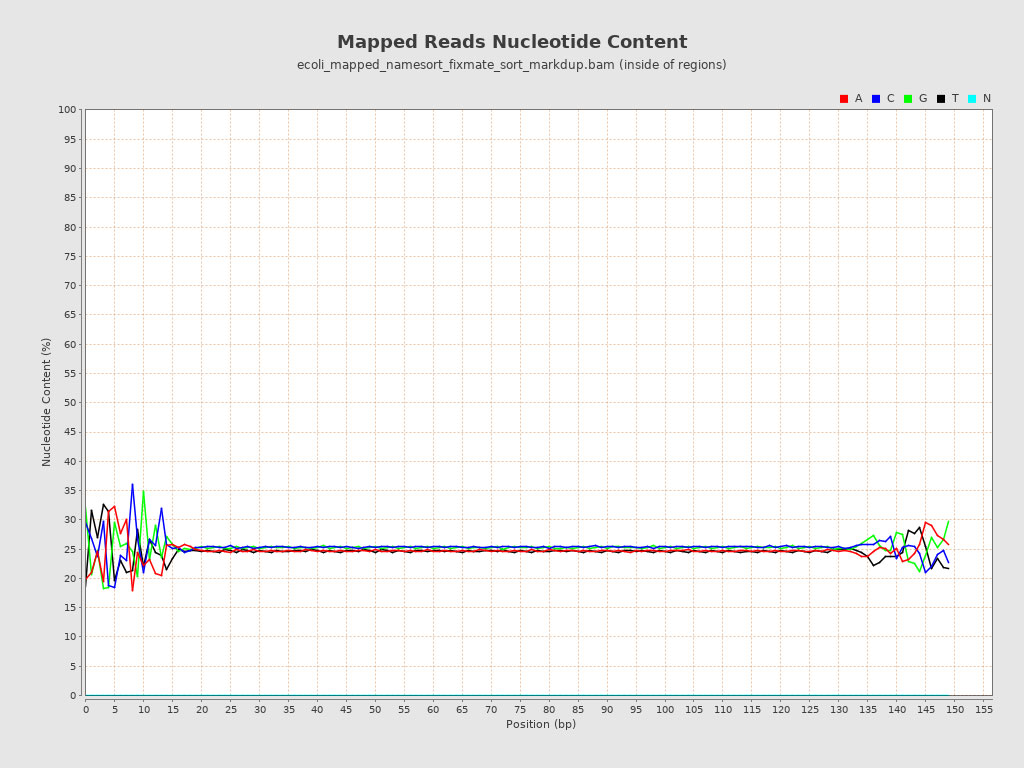
Genome Fraction Coverage



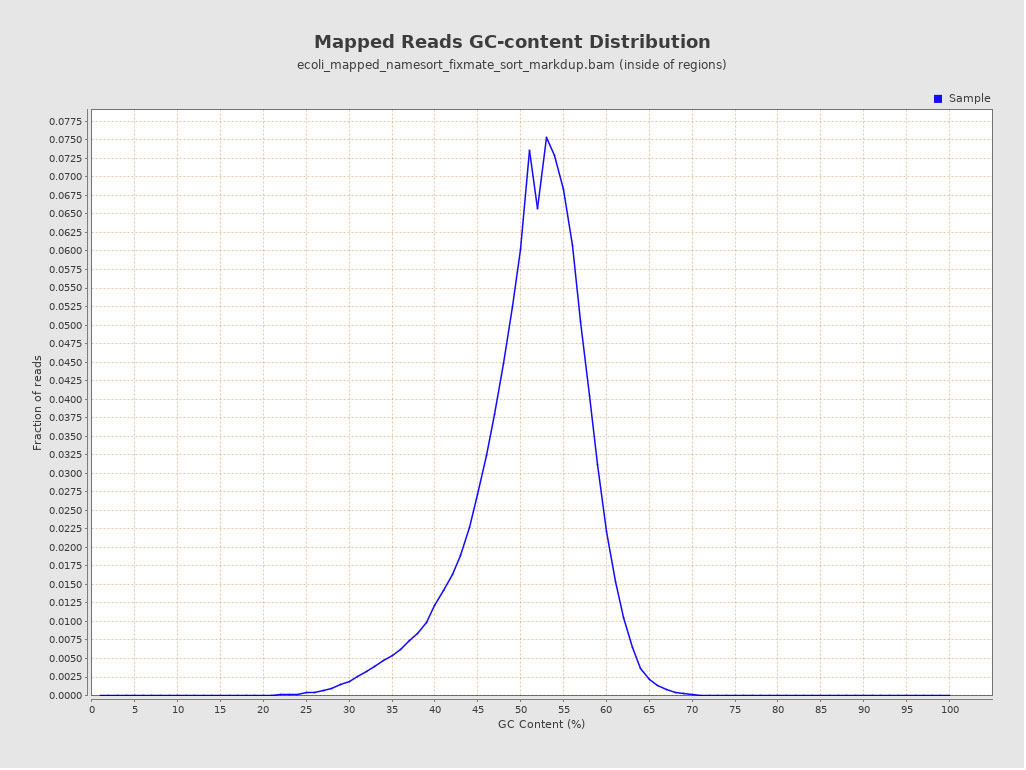
Duplication Rate Histogram



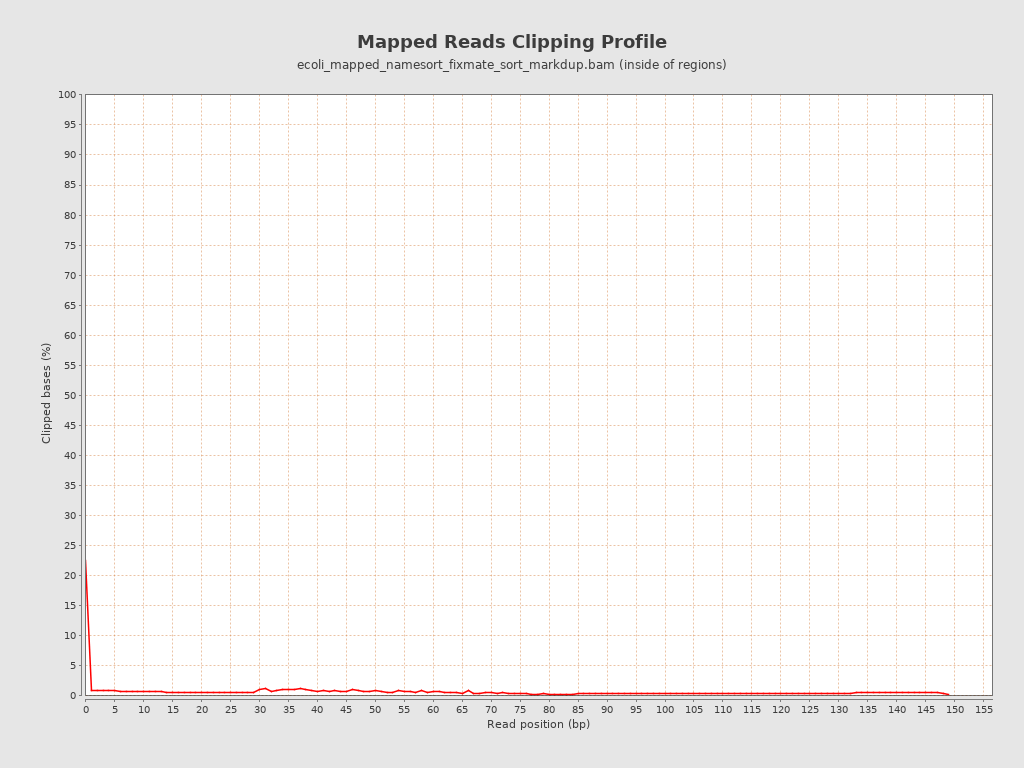
Mapped Reads Nucleotide Content



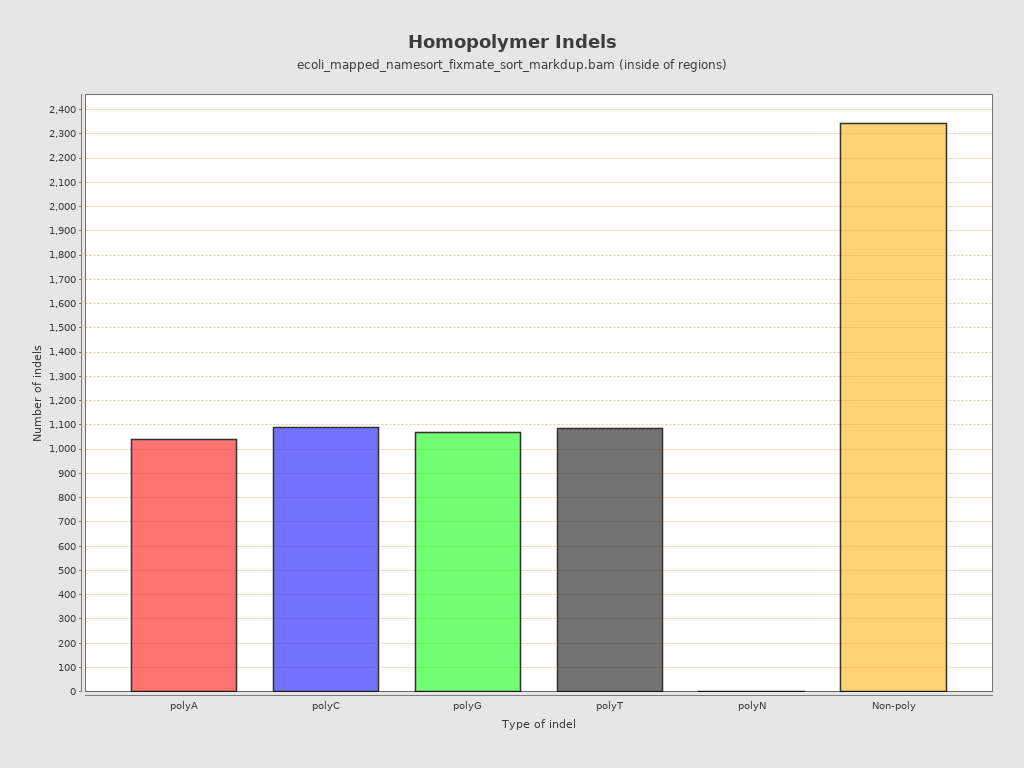
Mapped Reads GC-content Distribution



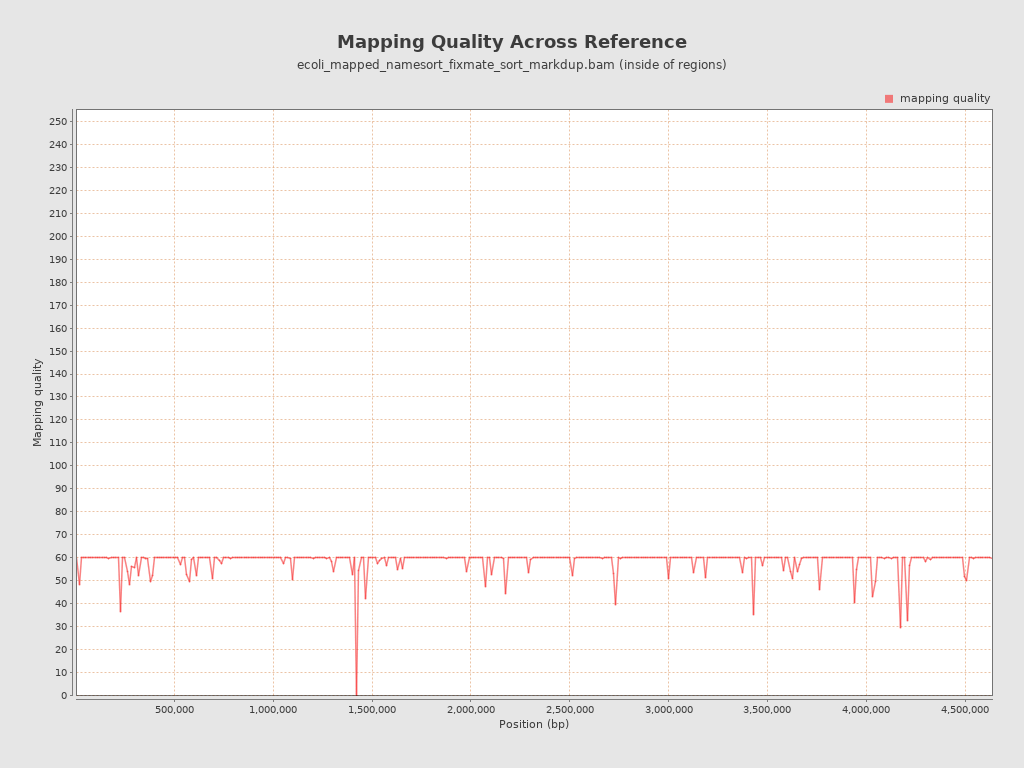
Mapped Reads Clipping Profile



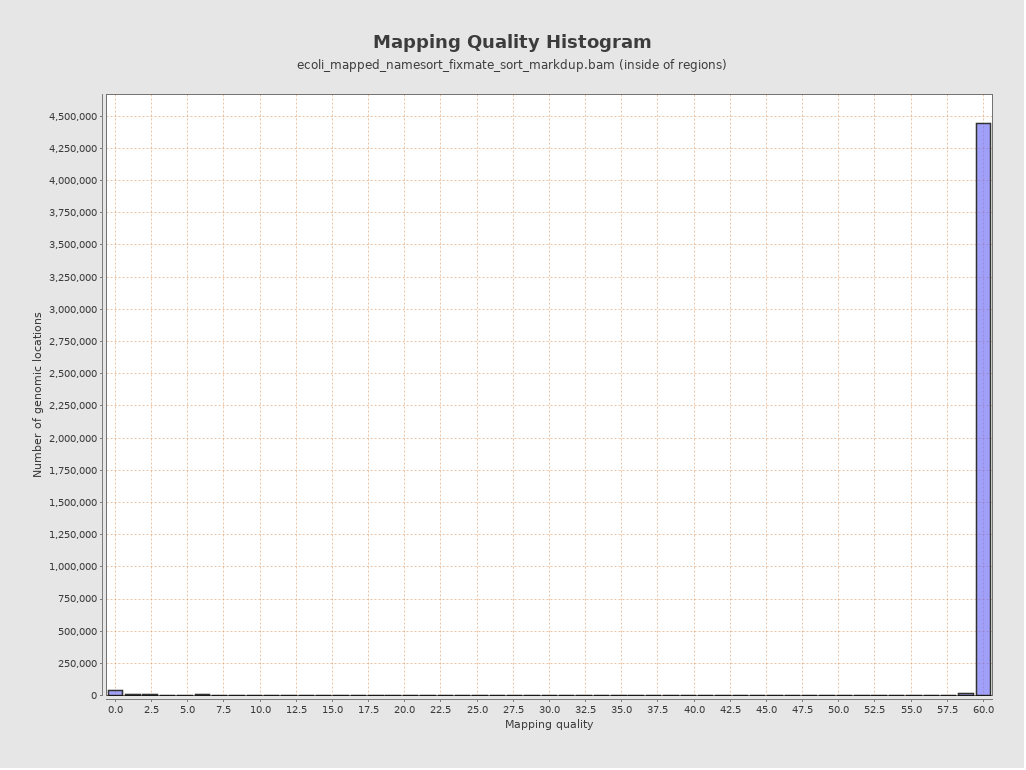
Homopolymer Indels



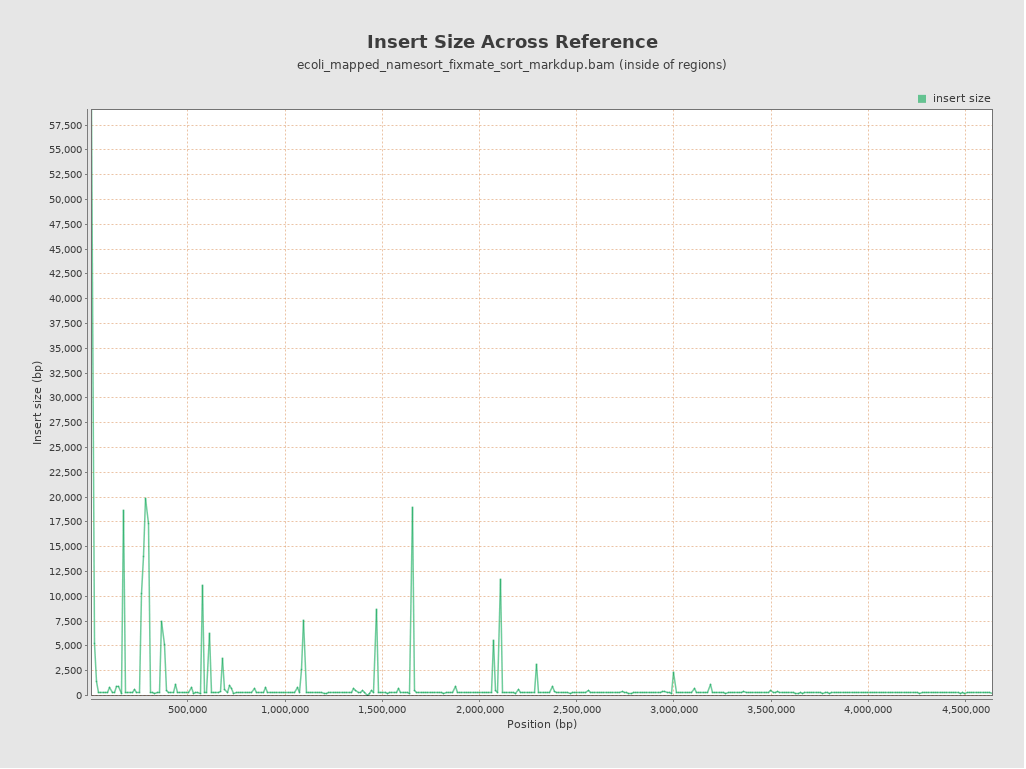
Mapping Quality Across Reference



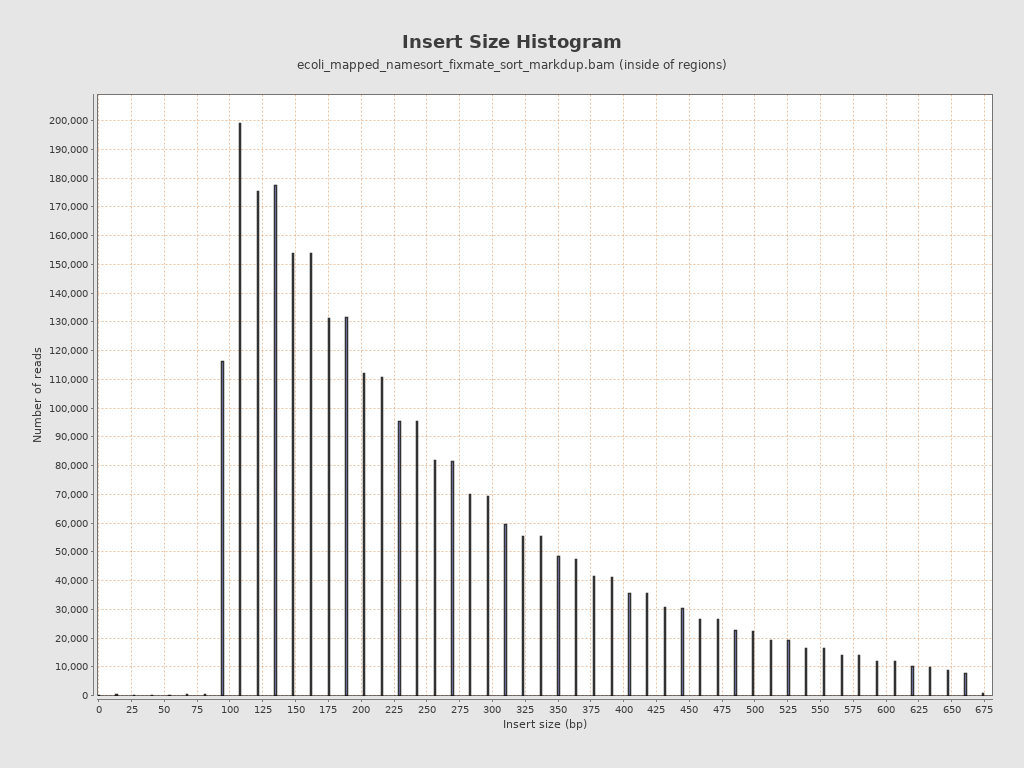
Mapping Quality Histogram



Insert Size Across Reference



Insert Size Histogram



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