Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2019/10/20 22:04:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /home/anna/ib/raki/Eve100.sam.bam_sorted.bam -c -
nw 400 -hm 3
```

1.2. Alignment

Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bowtie2 (2.1.0)
Analysis date:	Sun Oct 20 22:03:15 MSK 2019
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/anna/ib/raki/Eve100.sam.bam_sorted.bam

2. Summary

2.1. Globals

Reference size	1 734
Number of reads	176 894
Mapped reads	176 894 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	176 894 / 100%
Mapped reads, first in pair	89 365 / 50,52%
Mapped reads, second in pair	87 529 / 49,48%
Mapped reads, both in pair	174 274 / 98,52%
Mapped reads, singletons	2 620 / 1,48%
Read min/max/mean length	101 / 101 / 101
Duplicated reads (estimated)	175 427 / 99,17%
Duplication rate	92,23%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	4 552 992 / 25,53%
Number/percentage of C's	3 356 247 / 18,82%
Number/percentage of T's	6 413 834 / 35,96%
Number/percentage of G's	3 512 503 / 19,69%
Number/percentage of N's	857 / 0%
GC Percentage	38,51%

2.3. Coverage

Mean	10 287,6505
Standard Deviation	9 258,7585

2.4. Mapping Quality

Mean Mapping Quality	39,24

2.5. Insert size

Mean	185,88
Standard Deviation	71,41
P25/Median/P75	132 / 169 / 216

2.6. Mismatches and indels

General error rate	1,08%
Mismatches	162 767
Insertions	7 471
Mapped reads with at least one insertion	3,67%
Deletions	1 929
Mapped reads with at least one deletion	1,08%
Homopolymer indels	22,46%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

NC_023104.1	1734	17838786	10 287,6505	9 258,7585

3. Results : Coverage across reference

Coverage across reference
Eve100.sam.bam_sorted.bam
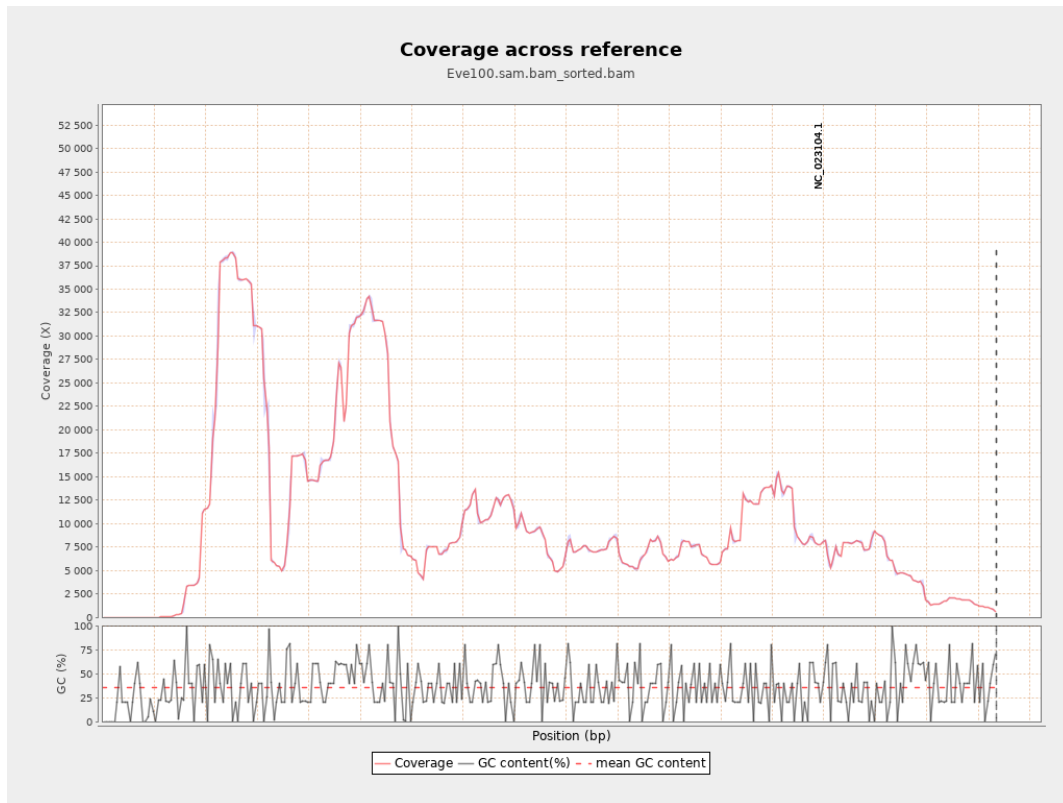
4. Results : Coverage Histogram

5. Results : Coverage Histogram (0-50X)
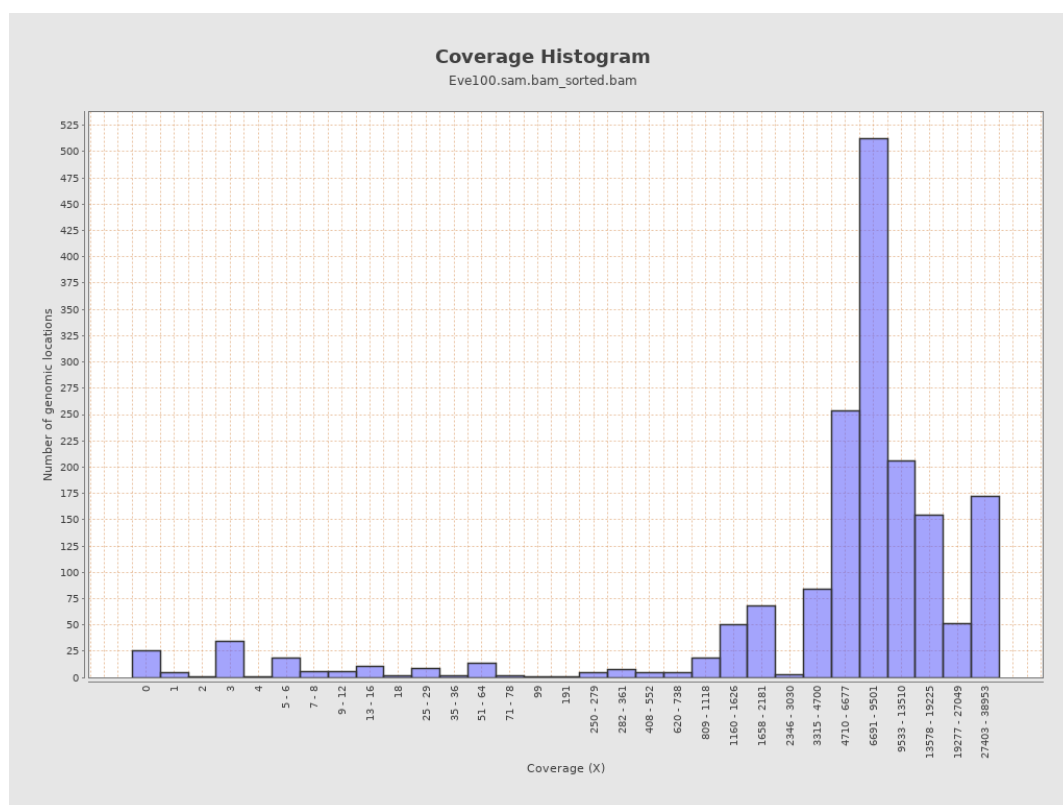
Coverage Histogram (0-50X)
Eve100.sam.bam_sorted.bam
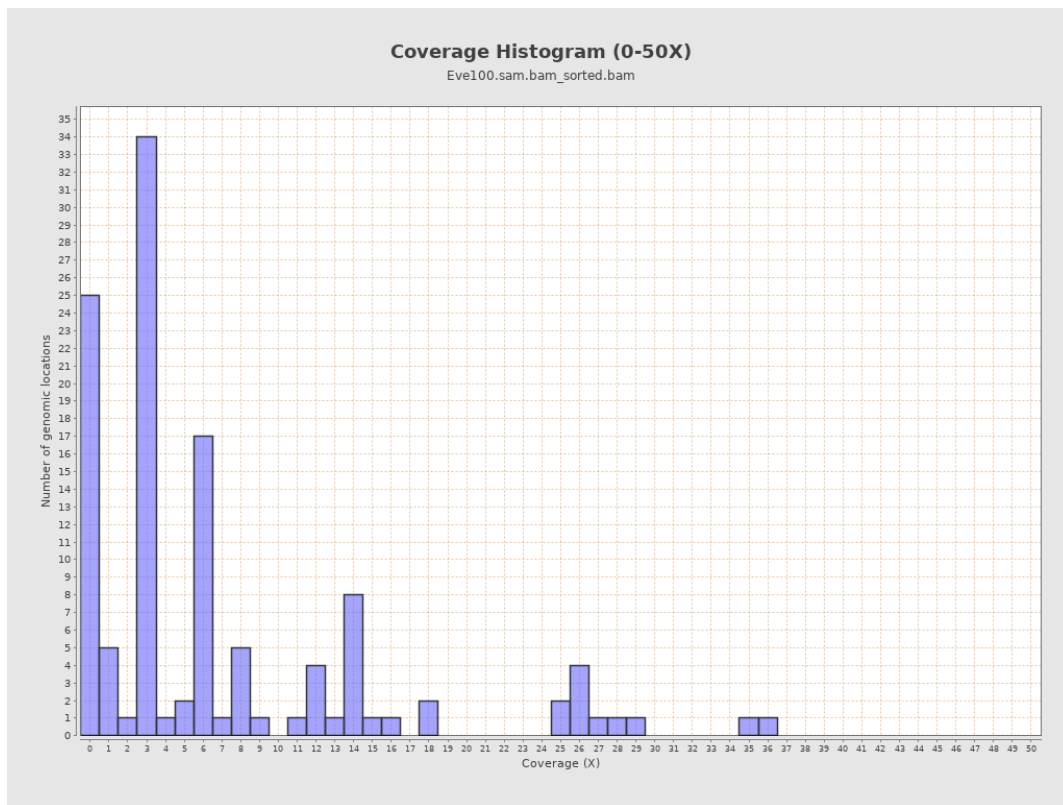
6. Results : Genome Fraction Coverage
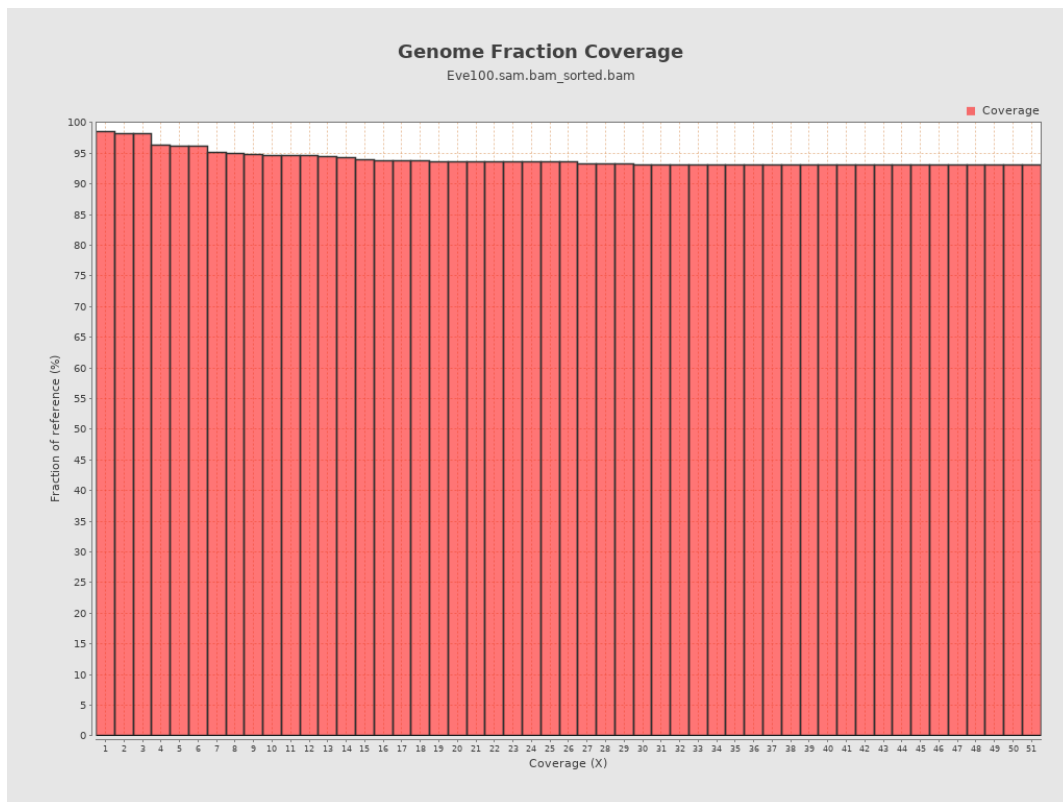
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
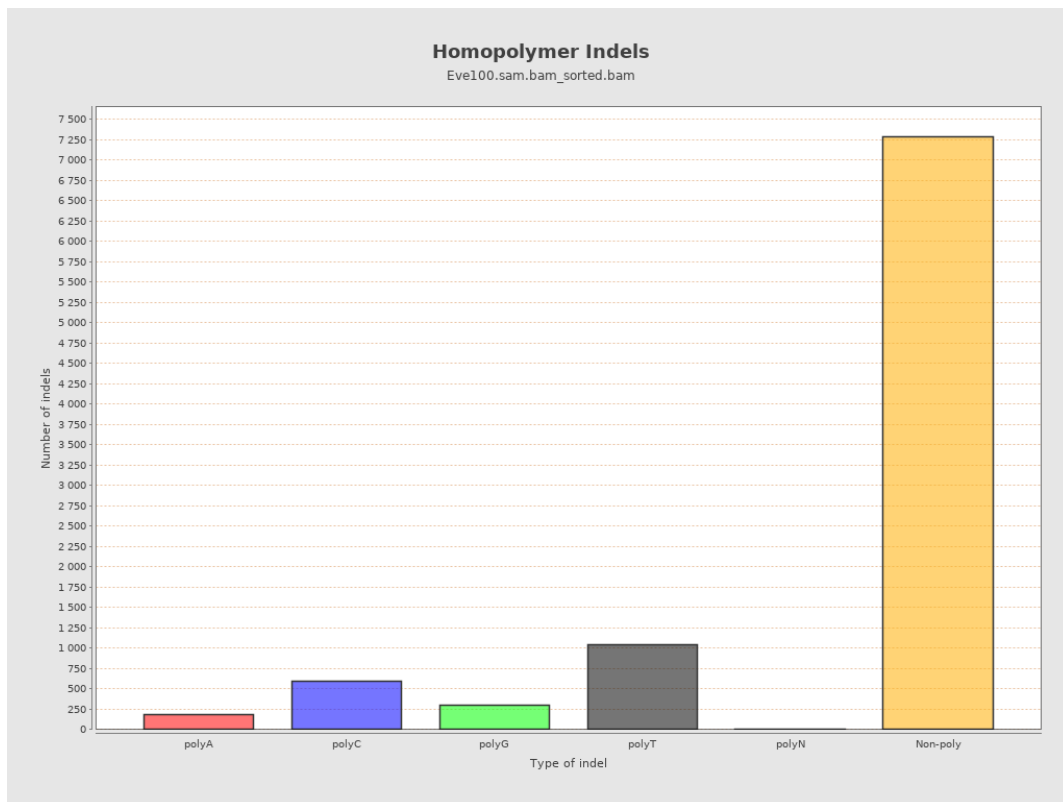Eve100.sam.bam_sorted.bam
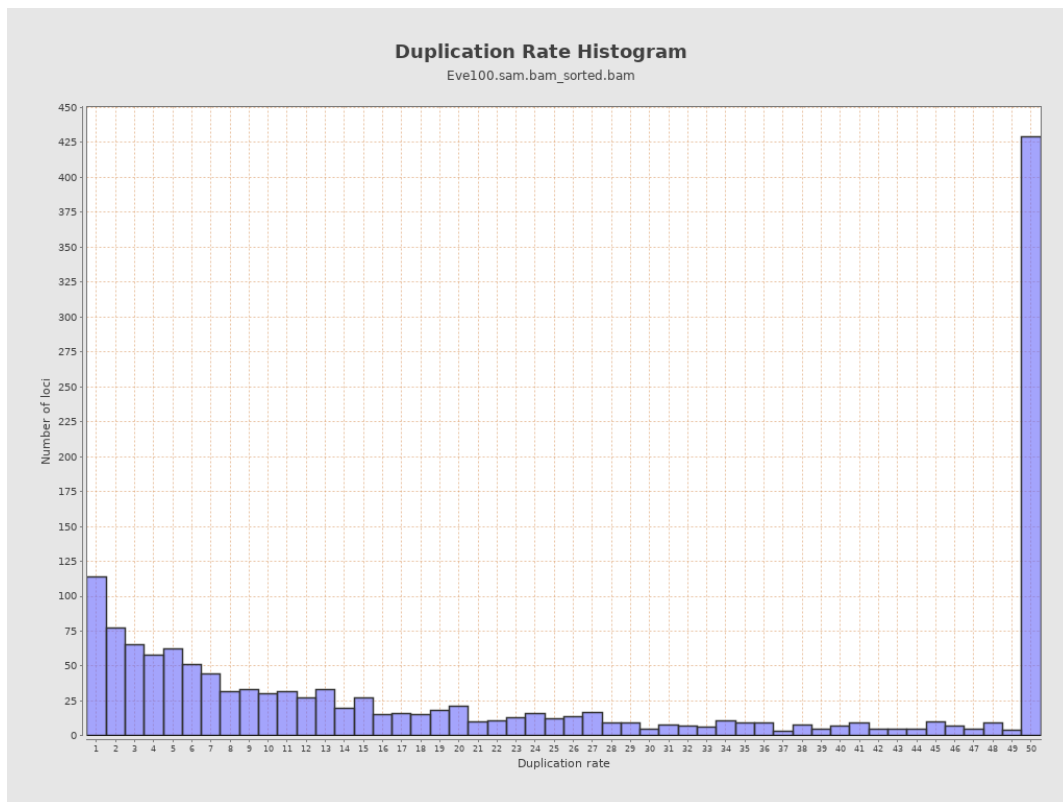
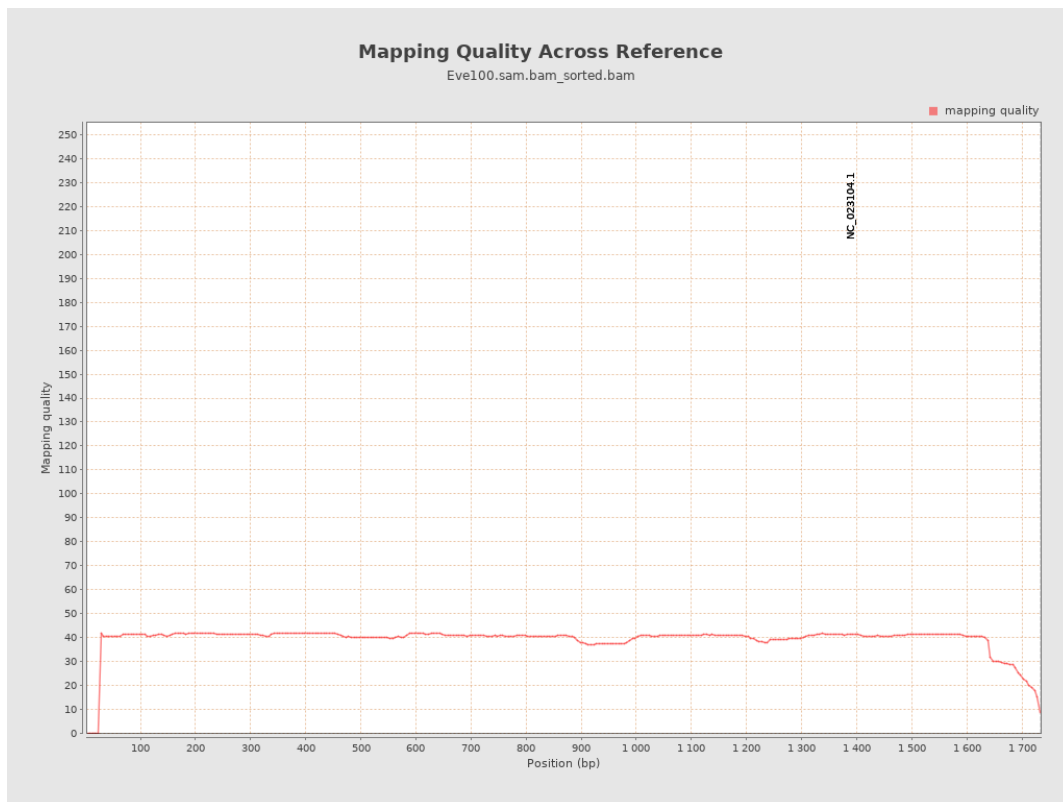# 8. Results : Mapped Reads Nucleotide Content
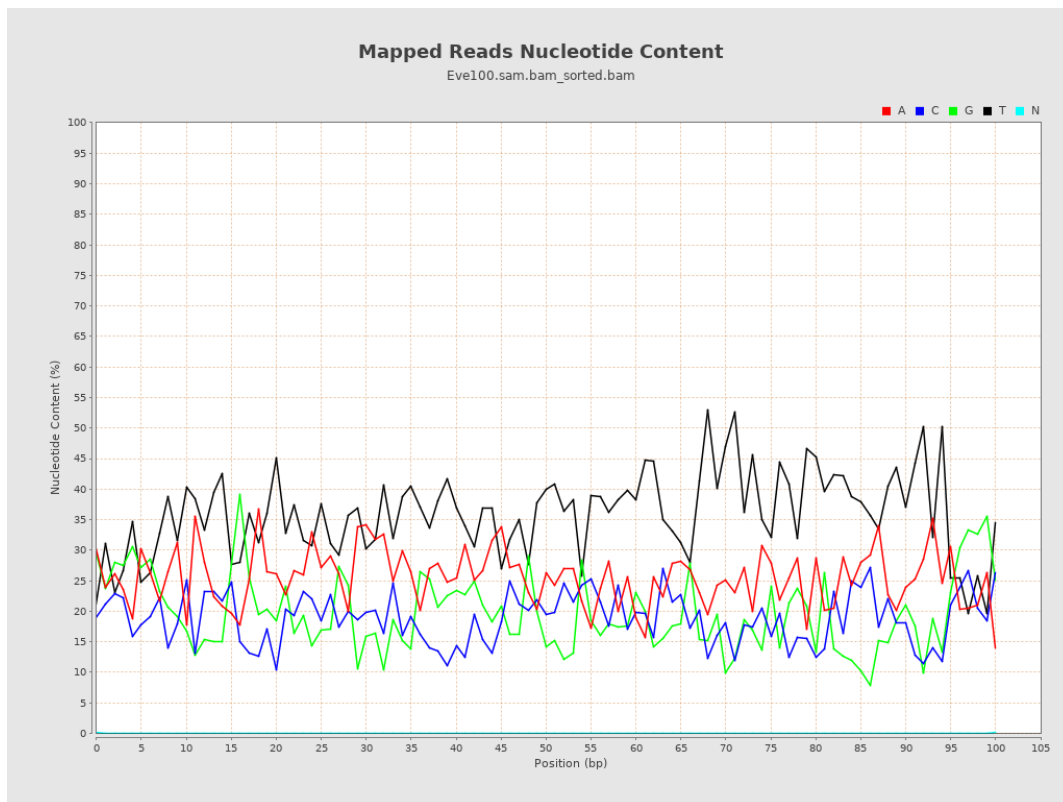
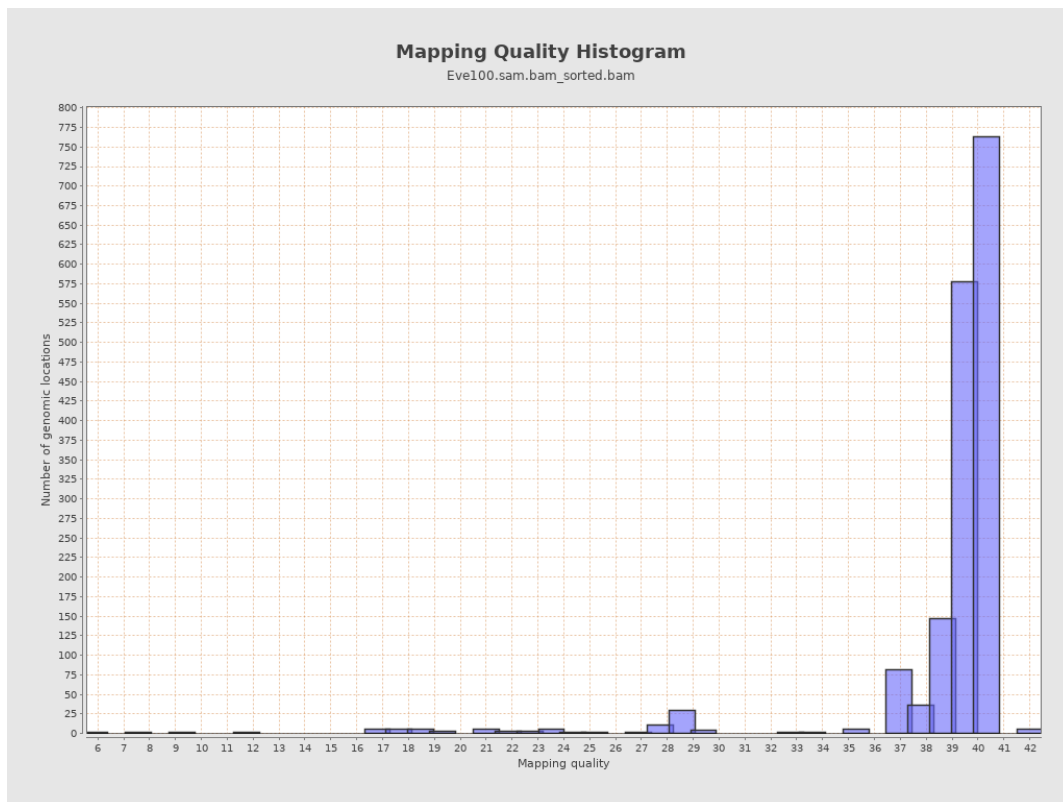# 9. Results : Mapped Reads GC-content Distribution
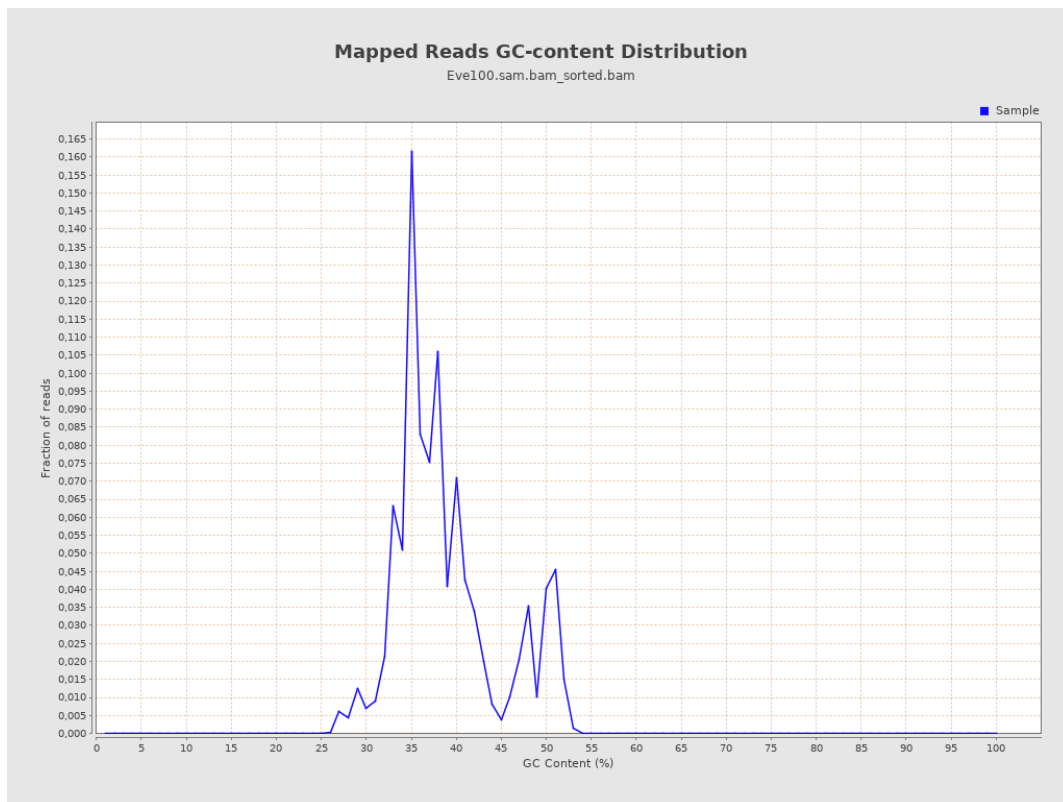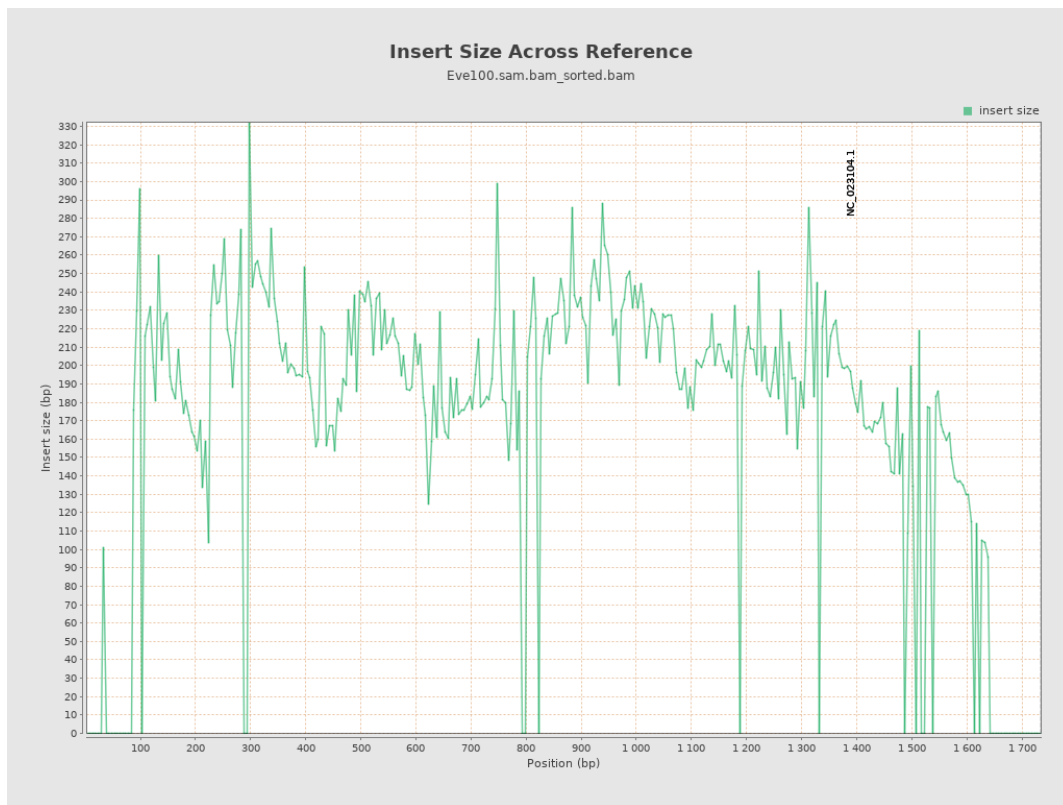
10. Results : Homopolymer Indels

11. Results : Mapping Quality Across Reference

12. Results : Mapping Quality Histogram

13. Results : Insert Size Across Reference

Insert Size Across Reference
Eve100.sam.bam_sorted.bam

14. Results : Insert Size Histogram