Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2019/10/20 21:27:24

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam /home/anna/ib/raki/Eve1trim.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 21:25:09 MSK 2019
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/anna/ib/raki/Eve1trim.sam.bam_sorted.bam

2. Summary

2.1. Globals

Reference size	1 533
Number of reads	88 016
Mapped reads	88 016 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	88 016 / 100%
Mapped reads, first in pair	88 016 / 100%
Mapped reads, second in pair	0 / 0%
Mapped reads, both in pair	0 / 0%
Mapped reads, singletons	88 016 / 100%
Read min/max/mean length	20 / 101 / 100,19
Duplicated reads (estimated)	86 762 / 98,58%
Duplication rate	88,76%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	2 326 622 / 26,42%
Number/percentage of C's	1 627 896 / 18,49%
Number/percentage of T's	3 136 320 / 35,62%
Number/percentage of G's	1 714 427 / 19,47%
Number/percentage of N's	50 / 0%
GC Percentage	37,96%

2.3. Coverage

Mean	5 744,407
Standard Deviation	5 070,7121

2.4. Mapping Quality

Mean Mapping Quality	40,03

2.5. Mismatches and indels

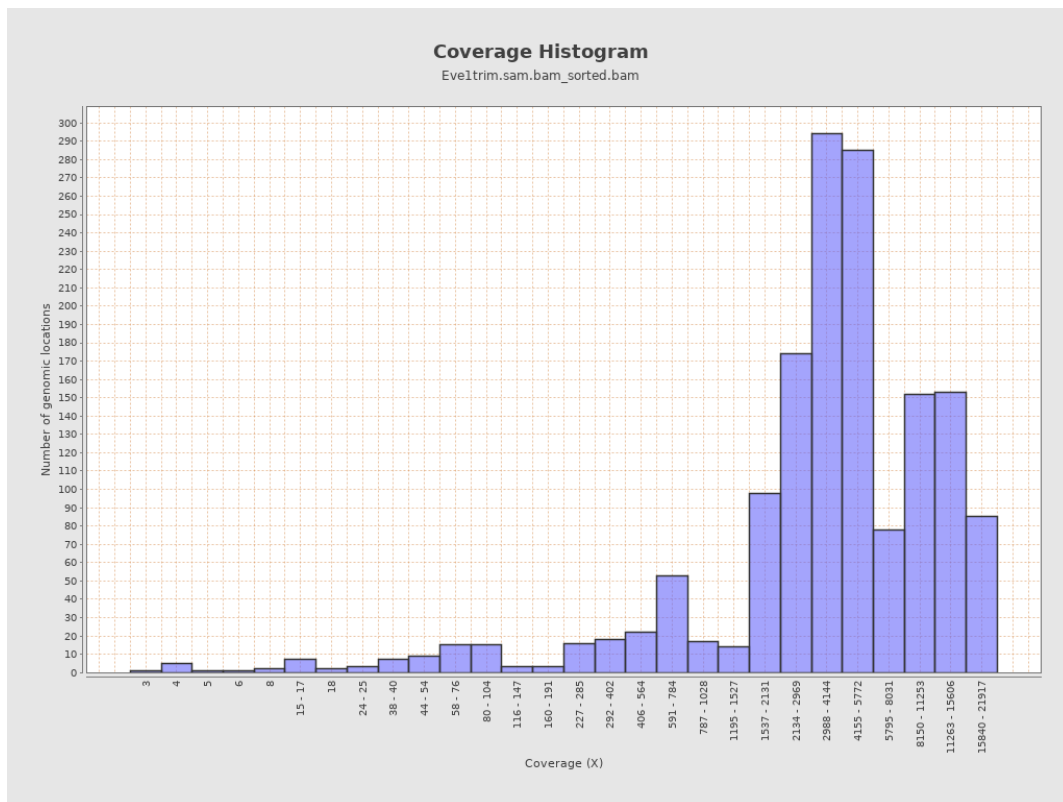|	
General error rate	0,85%
Mismatches	61 699
Insertions	3 334
Mapped reads with at least one insertion	3,22%
Deletions	744
Mapped reads with at least one deletion	0,83%
Homopolymer indels	19,35%

2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
NC_023104.1	1533	8806176	5 744,407	5 070,7121

3. Results : Coverage across reference

Coverage across reference
Eve1trim.sam.bam_sorted.bam

4. Results : Coverage Histogram

Coverage Histogram
Eve1trim.sam.bam_sorted.bam

5. Results : Coverage Histogram (0-50X)
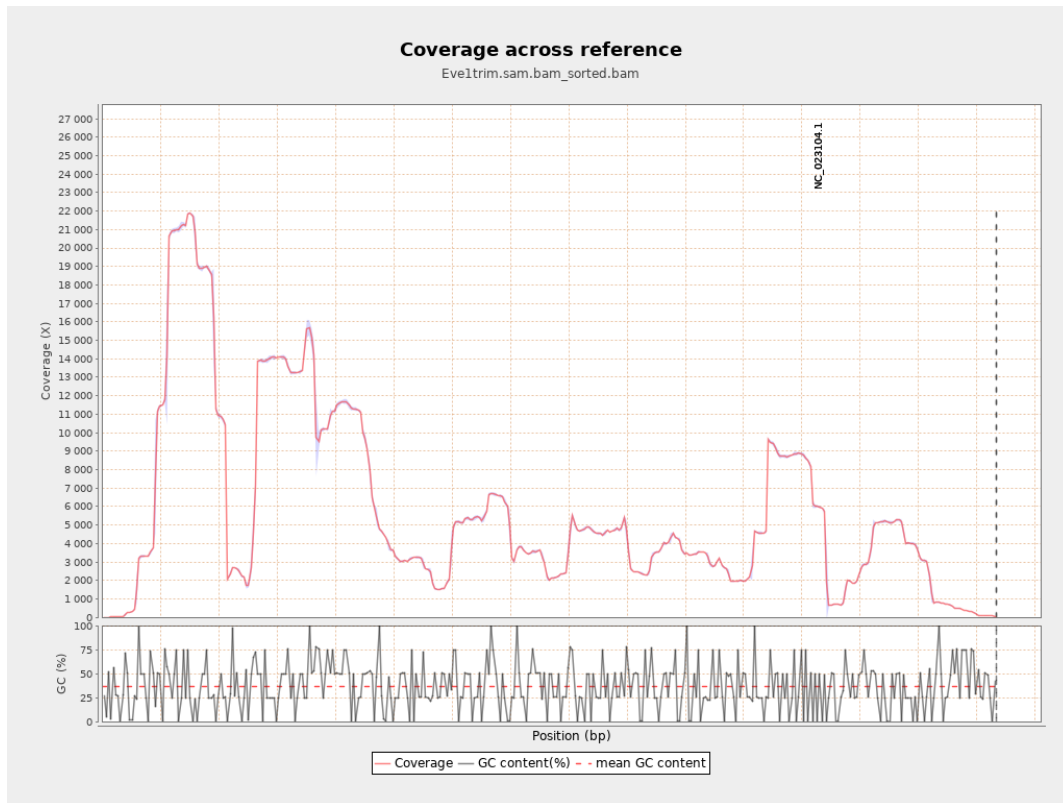
Coverage Histogram (0-50X)
Eve1trim.sam.bam_sorted.bam
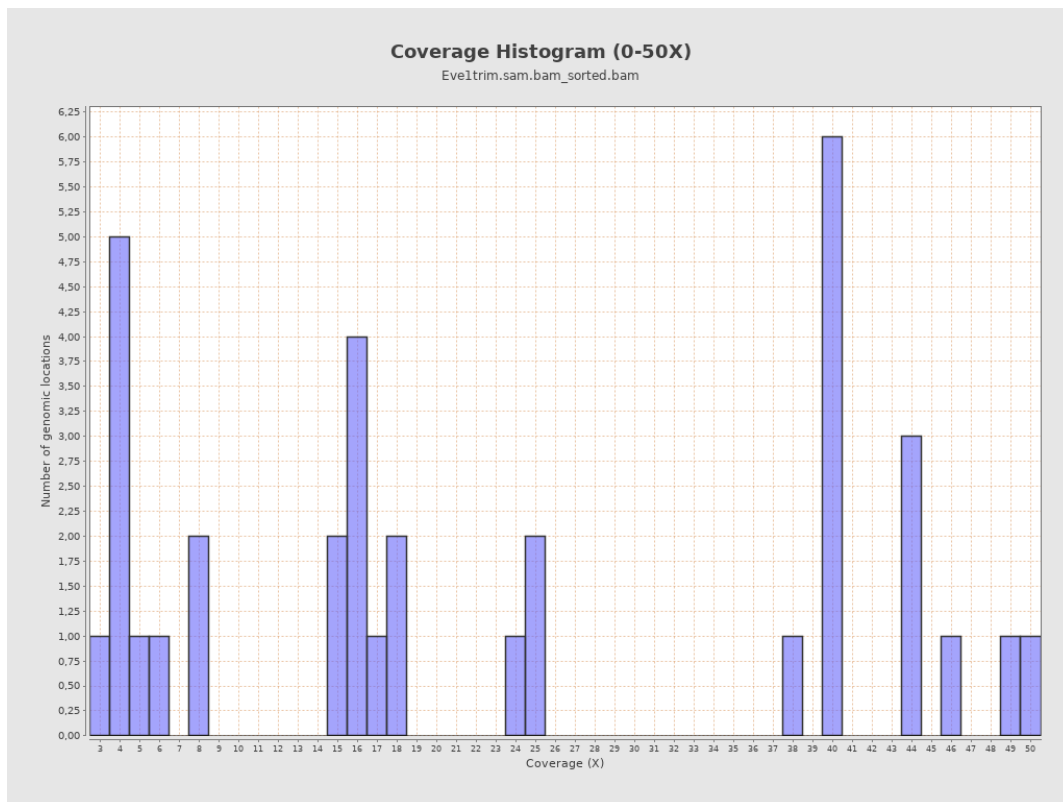
6. Results : Genome Fraction Coverage
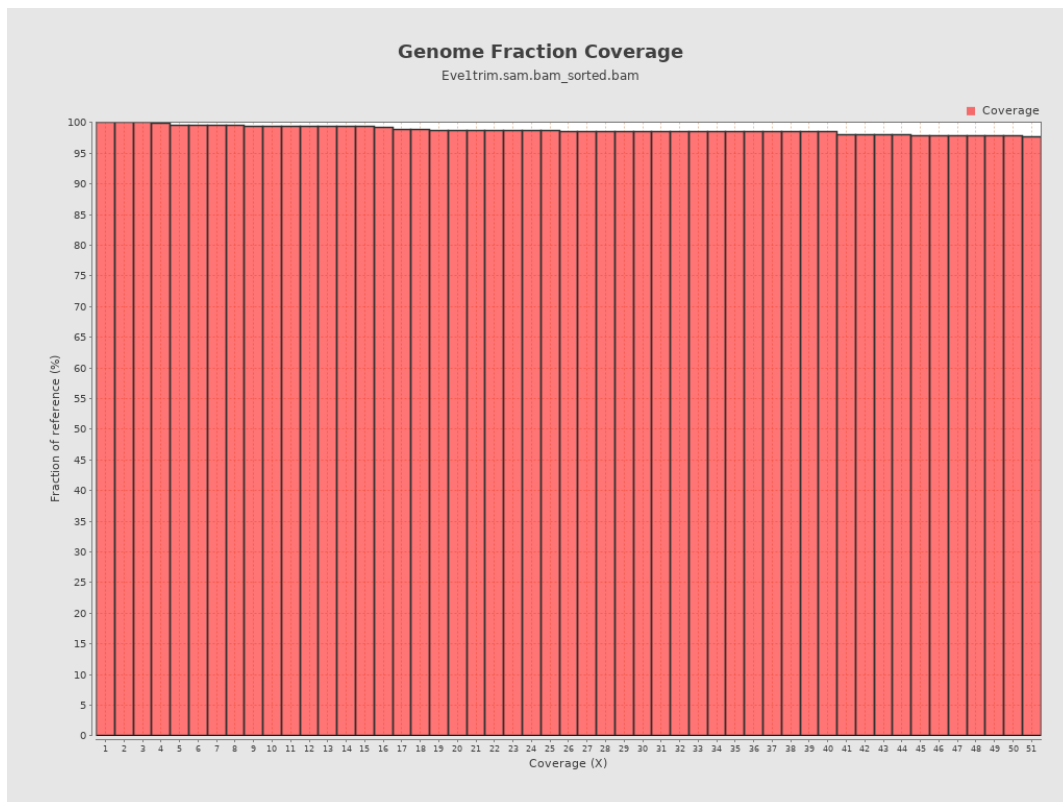
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
Eve1trim.sam.bam_sorted.bam

8. Results : Mapped Reads Nucleotide Content
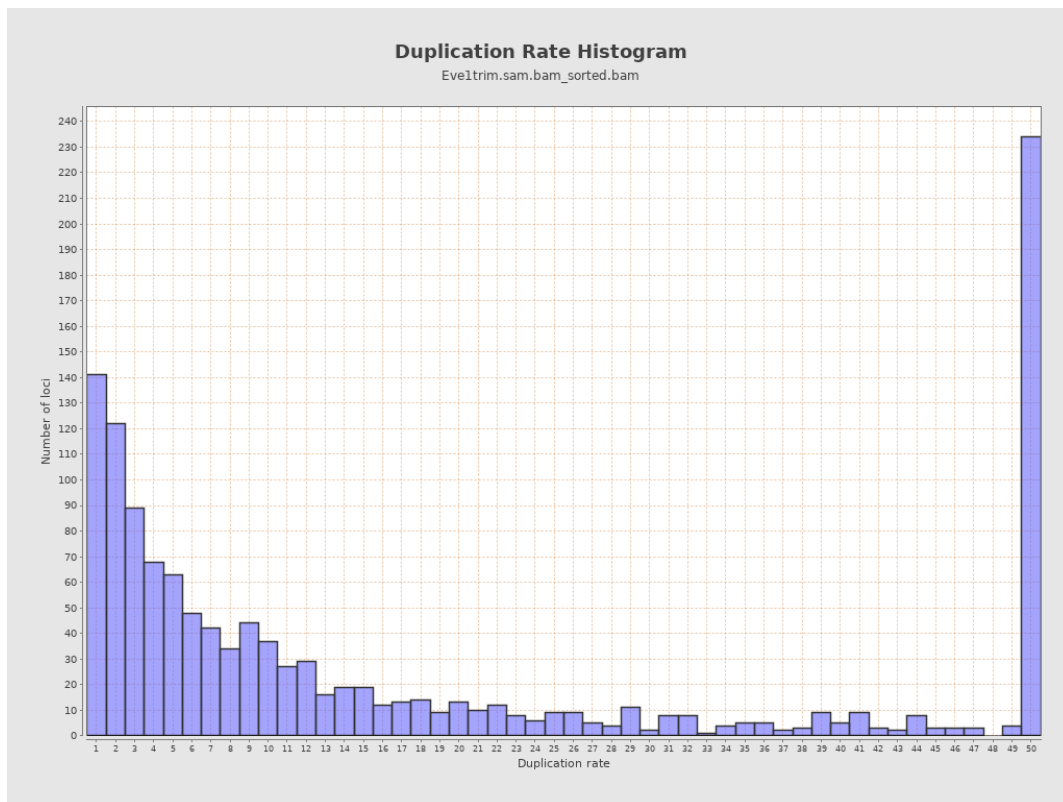
Mapped Reads Nucleotide Content
Eve1trim.sam.bam_sorted.bam
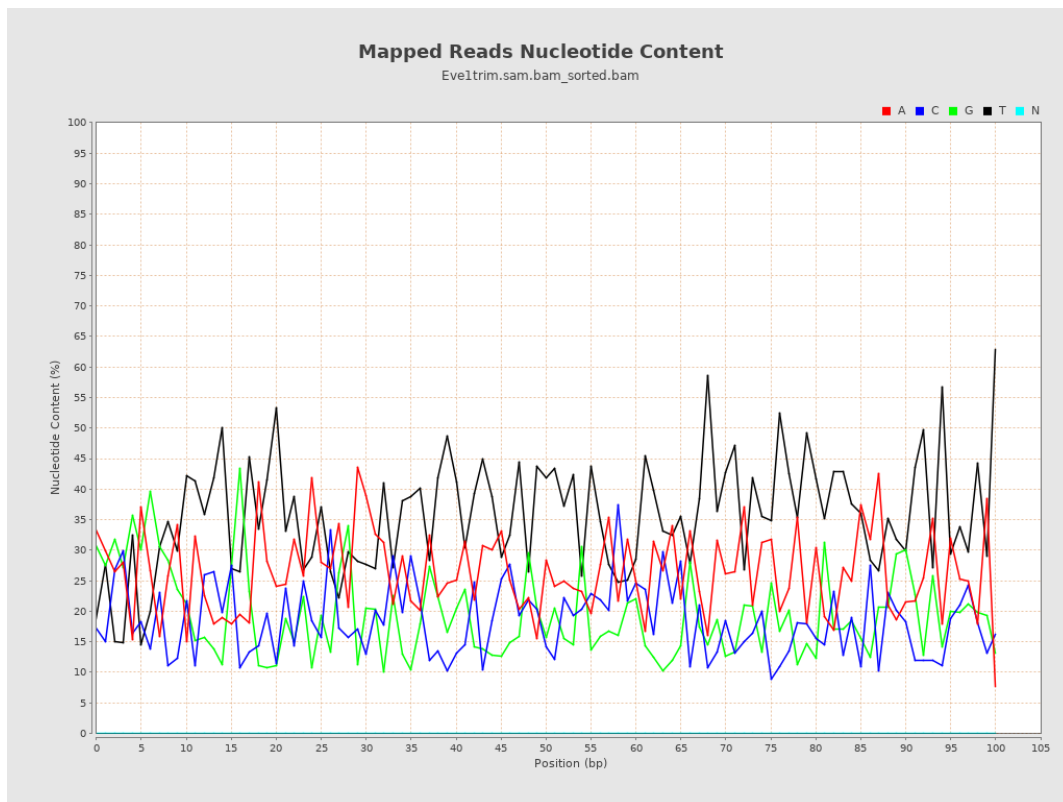
9. Results : Mapped Reads GC-content Distribution
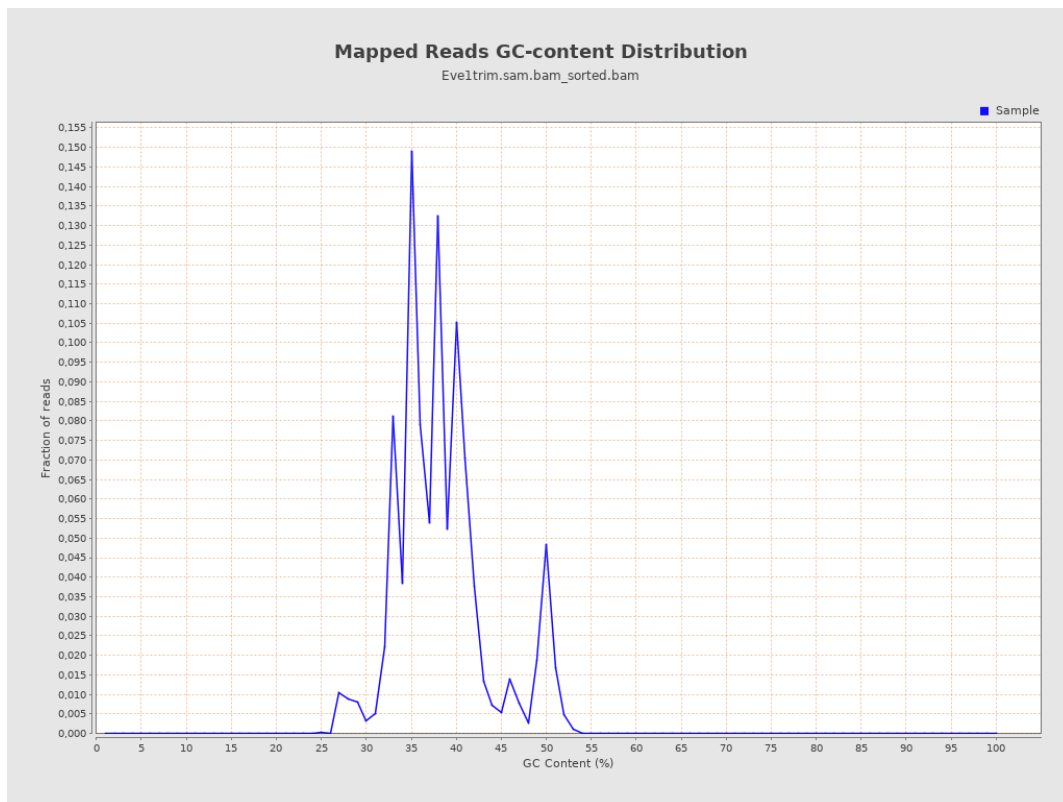
10. Results : Homopolymer Indels

Homopolymer Indels
Eve1trim.sam.bam_sorted.bam

11. Results : Mapping Quality Across Reference
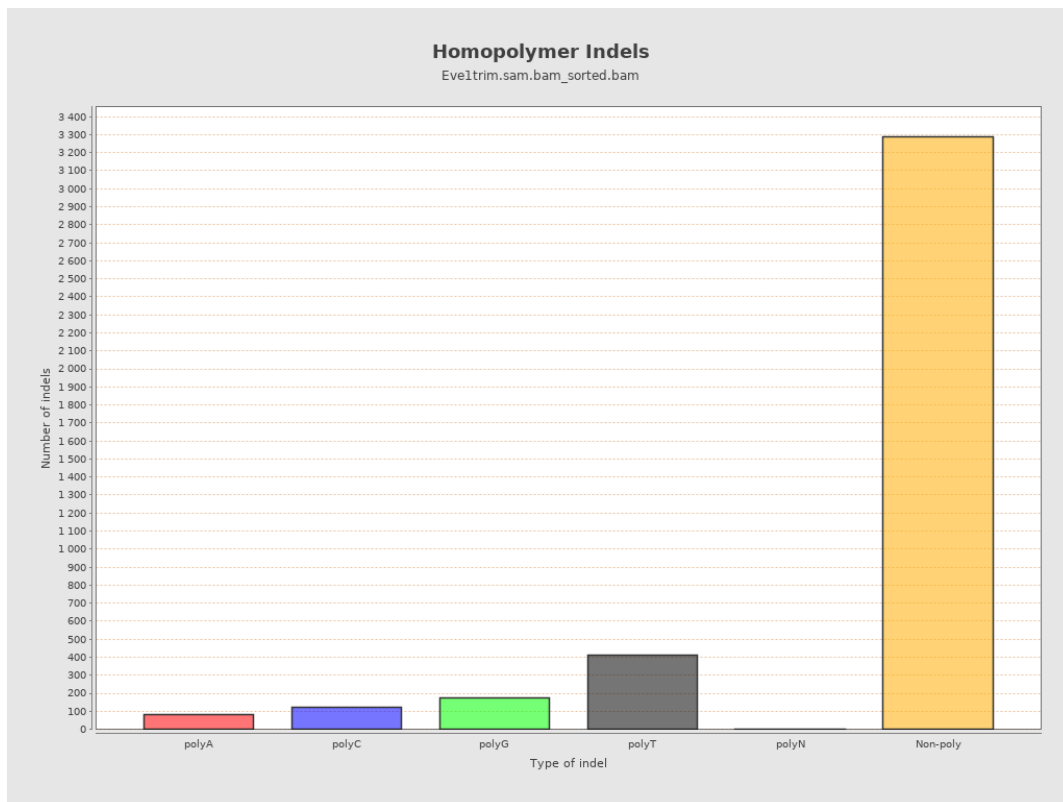
Mapping Quality Across Reference
Eve1trim.sam.bam_sorted.bam
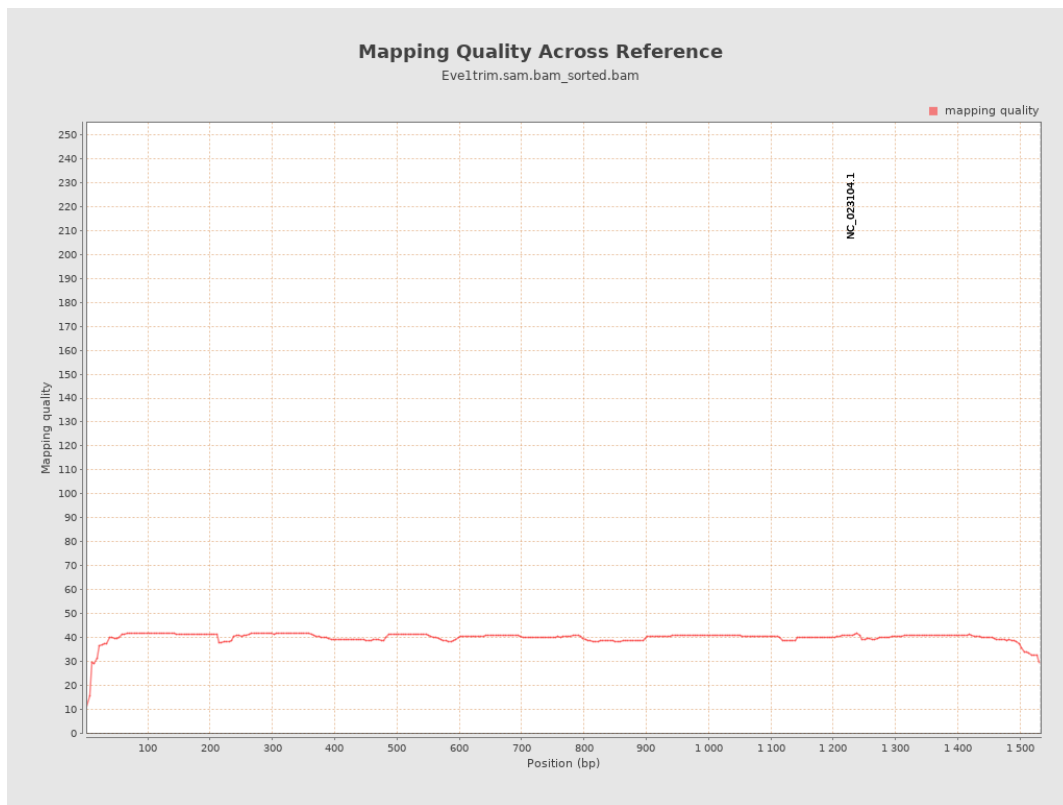
12. Results : Mapping Quality Histogram