

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2019/10/20 21:24:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /home/anna/ib/raki/Eve1.1.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 21:20:43 MSK 2019
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/anna/ib/raki/Eve1.1.sam.bam_sorted.bam

2. Summary

2.1. Globals

Reference size	1 533
Number of reads	174 806
Mapped reads	174 806 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	174 806 / 100%
Mapped reads, first in pair	88 009 / 50,35%
Mapped reads, second in pair	86 797 / 49,65%
Mapped reads, both in pair	172 816 / 98,86%
Mapped reads, singletons	1 990 / 1,14%
Read min/max/mean length	101 / 101 / 101
Duplicated reads (estimated)	173 444 / 99,22%
Duplication rate	93,1%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	4 490 311 / 25,47%
Number/percentage of C's	3 311 719 / 18,79%
Number/percentage of T's	6 350 386 / 36,03%
Number/percentage of G's	3 474 854 / 19,71%
Number/percentage of N's	849 / 0%
GC Percentage	38,5%

2.3. Coverage

Mean	11 500,6223
Standard Deviation	9 172,7691

2.4. Mapping Quality

Mean Mapping Quality	40,21
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2.5. Insert size

Mean	185,82
Standard Deviation	71,3
P25/Median/P75	132 / 169 / 215

2.6. Mismatches and indels

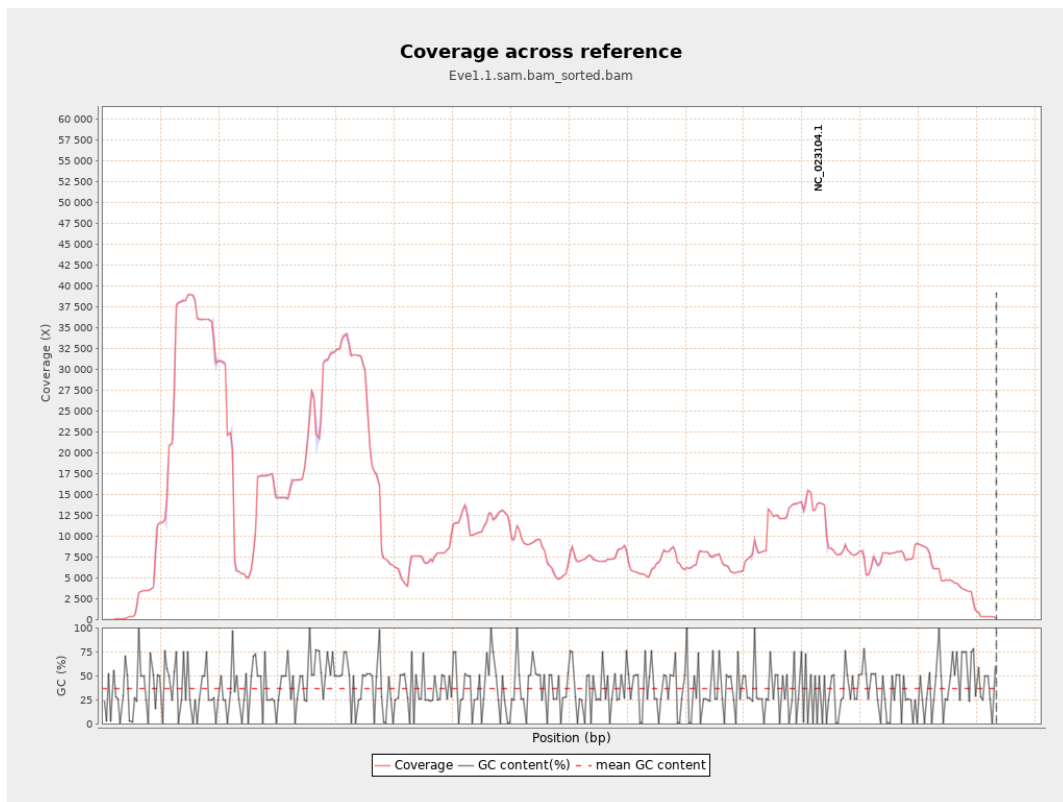
General error rate	1,06%
Mismatches	159 619
Insertions	7 010
Mapped reads with at least one insertion	3,46%
Deletions	1 918
Mapped reads with at least one deletion	1,09%
Homopolymer indels	21,53%

2.7. Chromosome stats

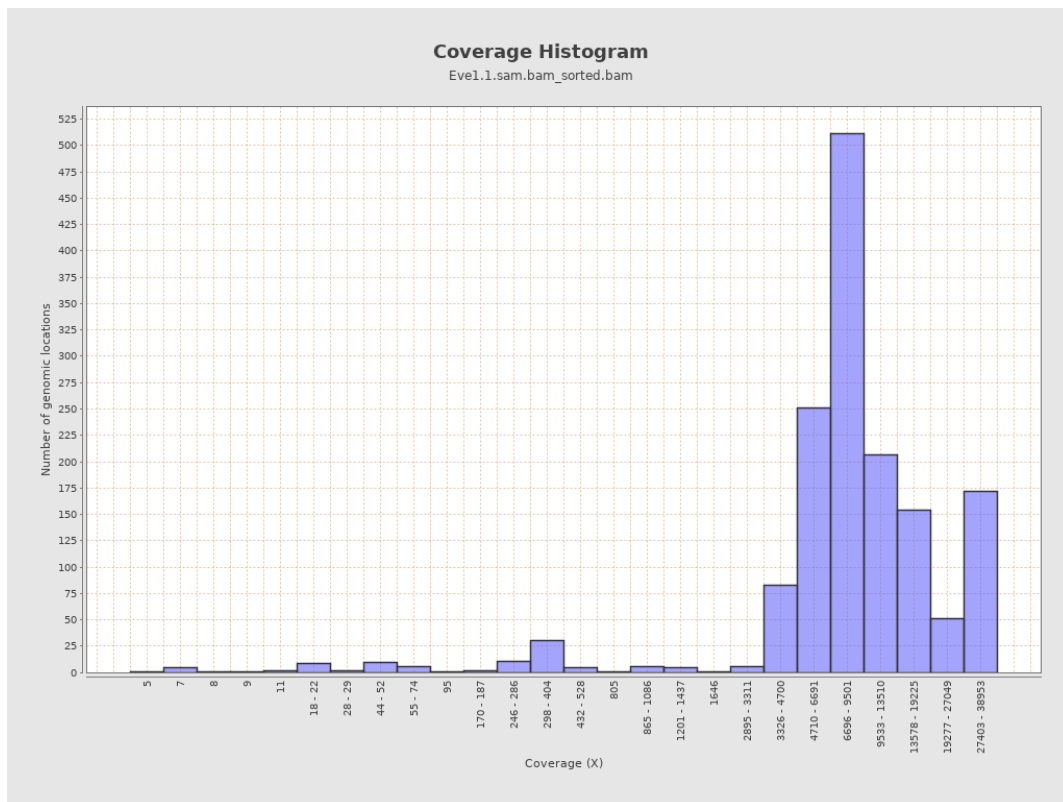
Name	Length	Mapped bases	Mean coverage	Standard deviation

NC_023104.1	1533	17630454	11 500,6223	9 172,7691
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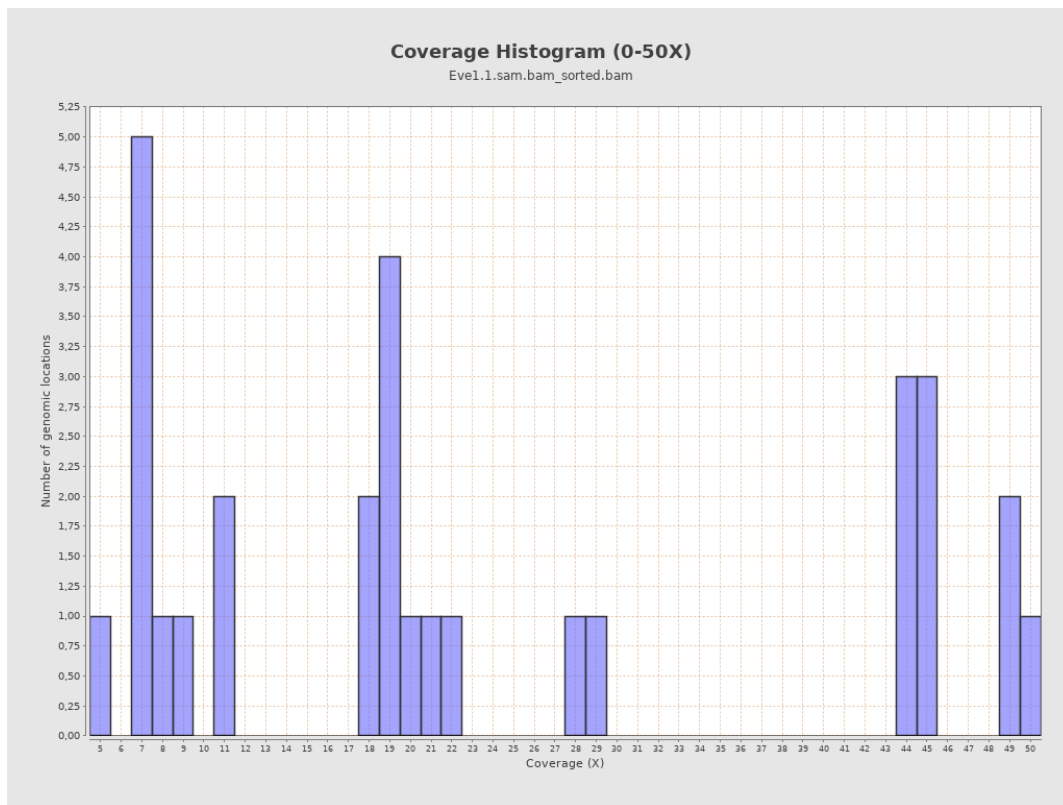
3. Results : Coverage across reference



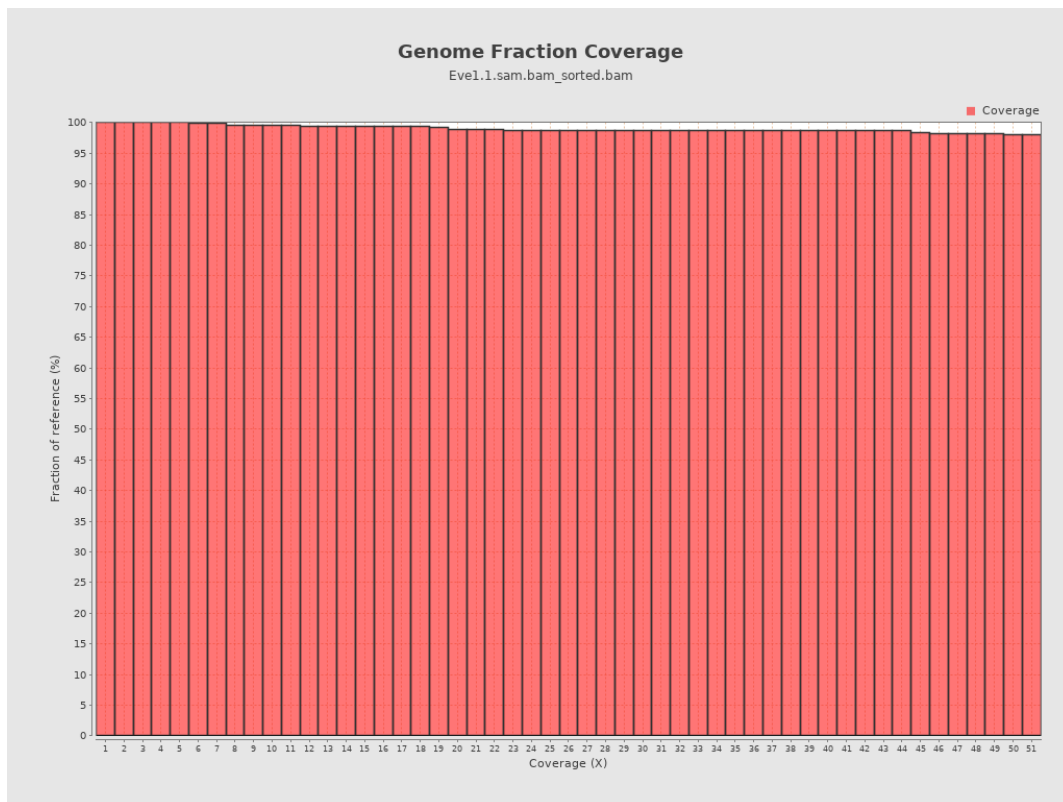
4. Results : Coverage Histogram



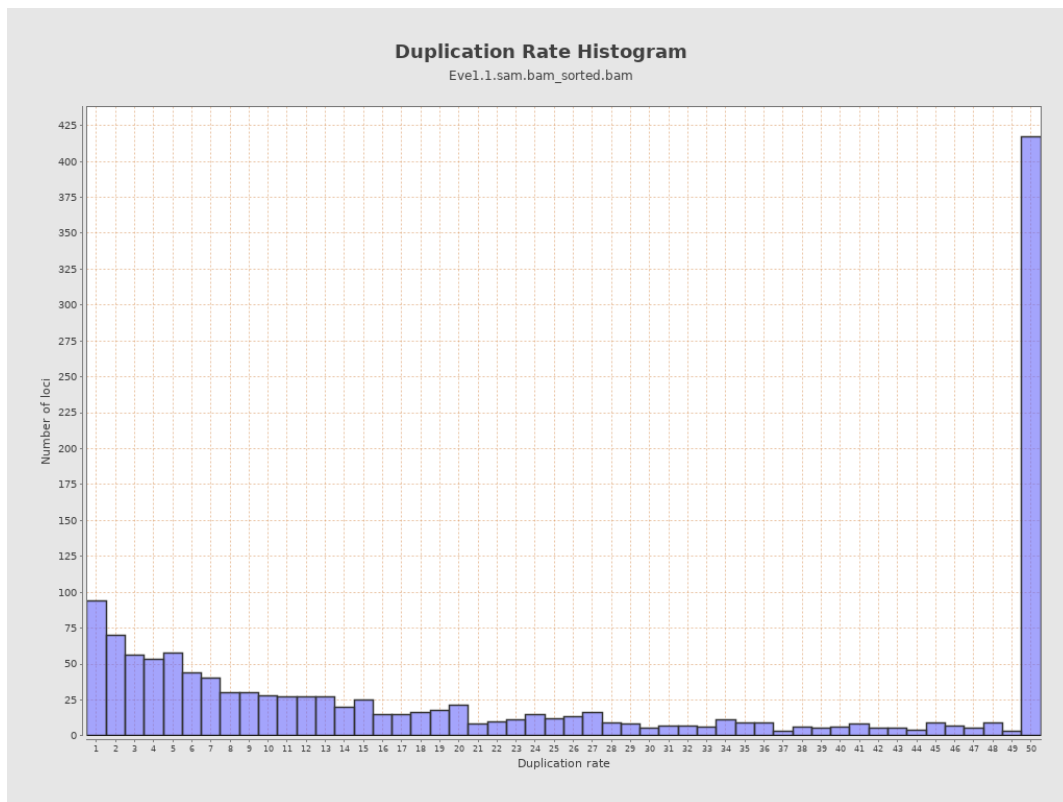
5. Results : Coverage Histogram (0-50X)



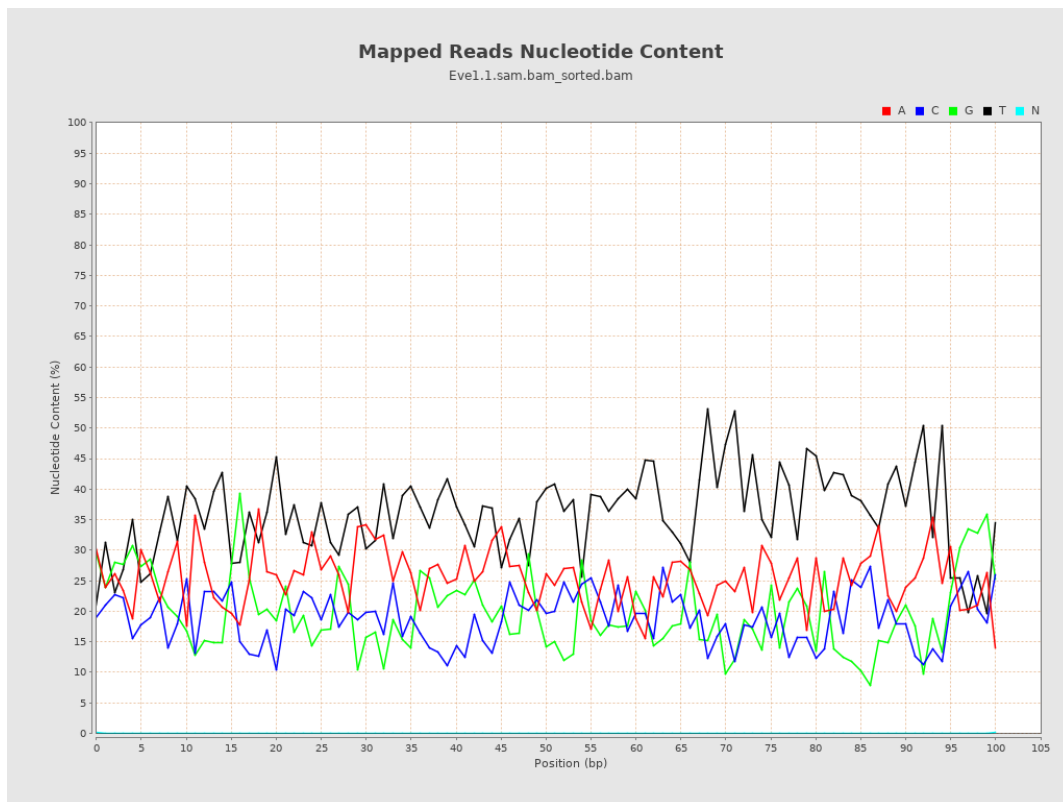
6. Results : Genome Fraction Coverage



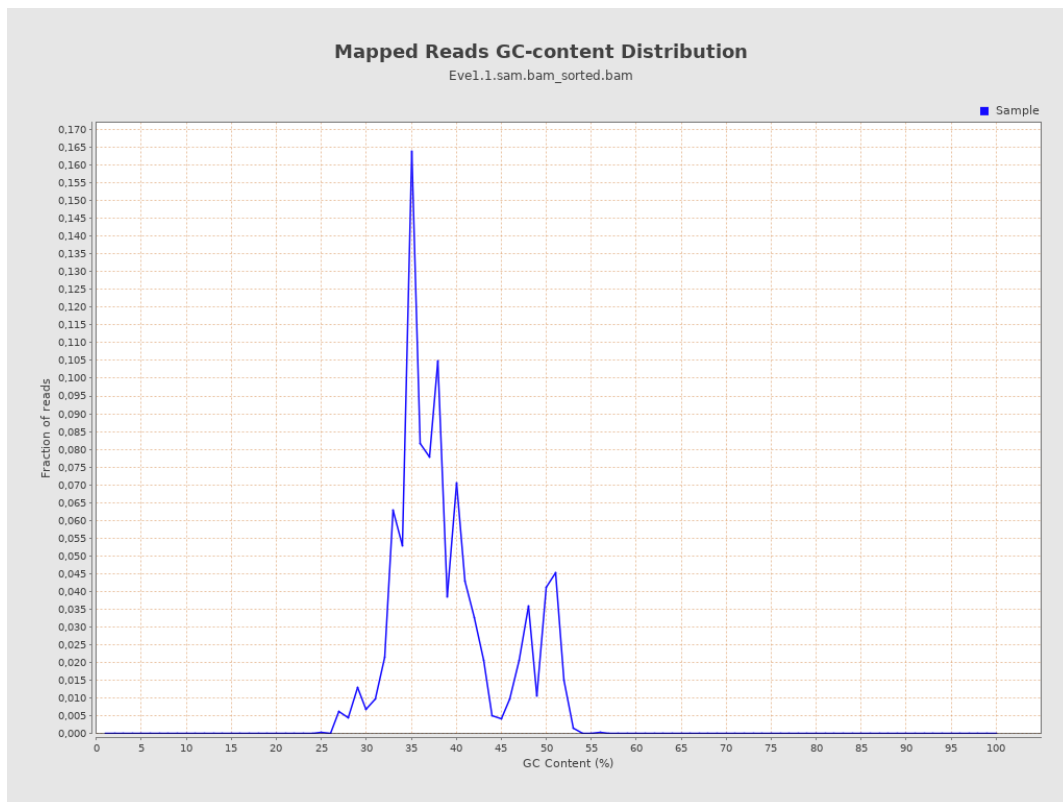
7. Results : Duplication Rate Histogram



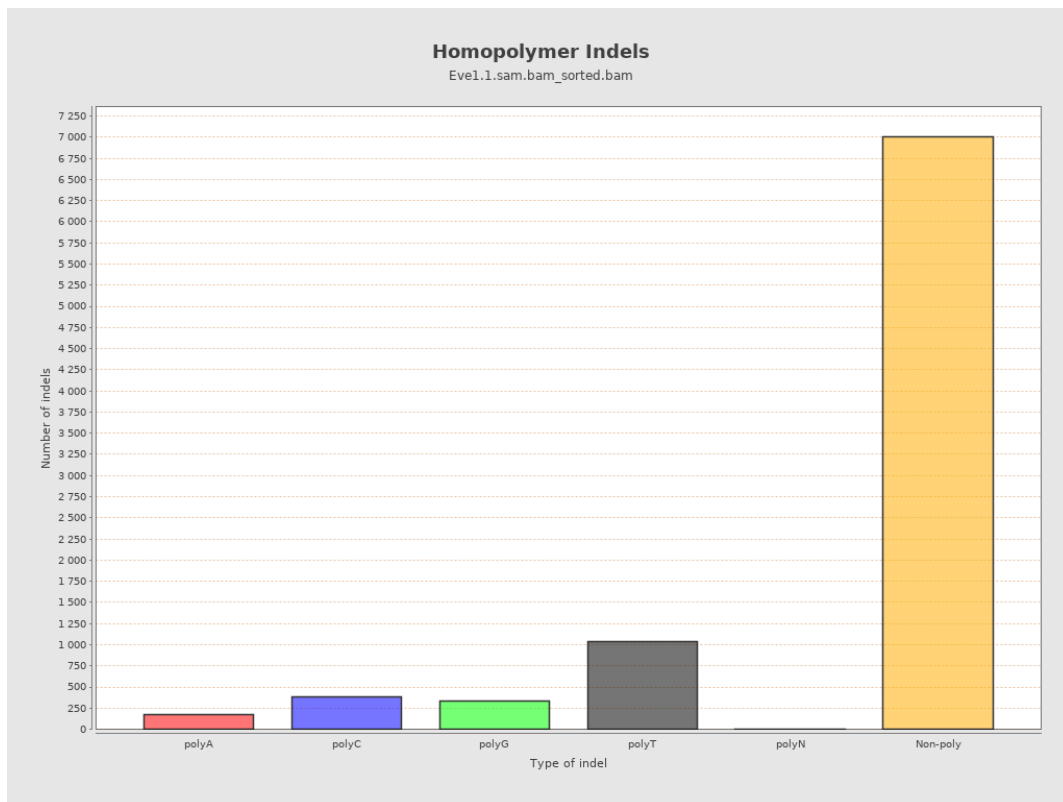
8. Results : Mapped Reads Nucleotide Content



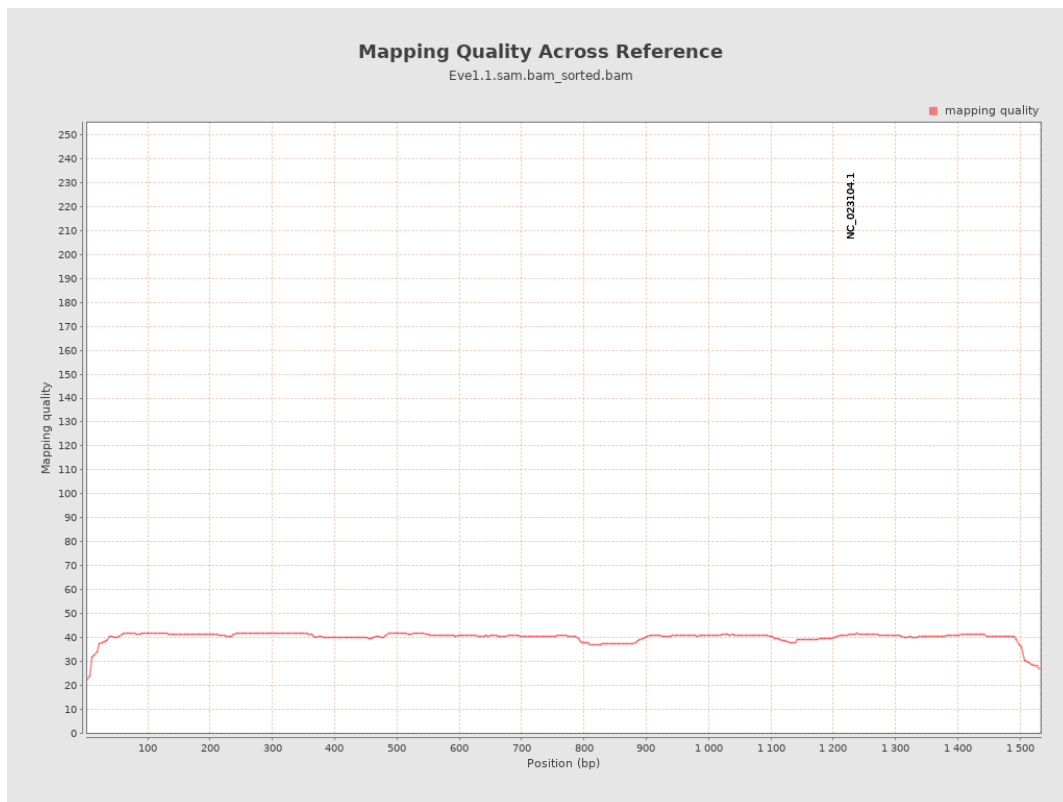
9. Results : Mapped Reads GC-content Distribution



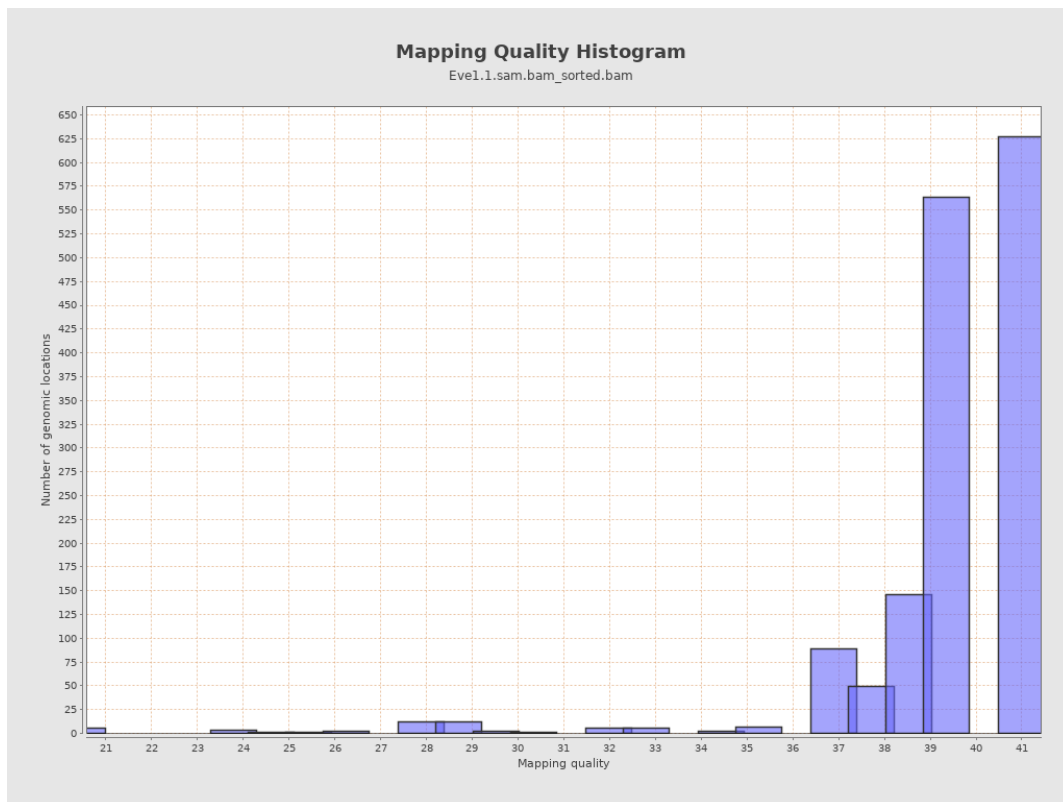
10. Results : Homopolymer Indels



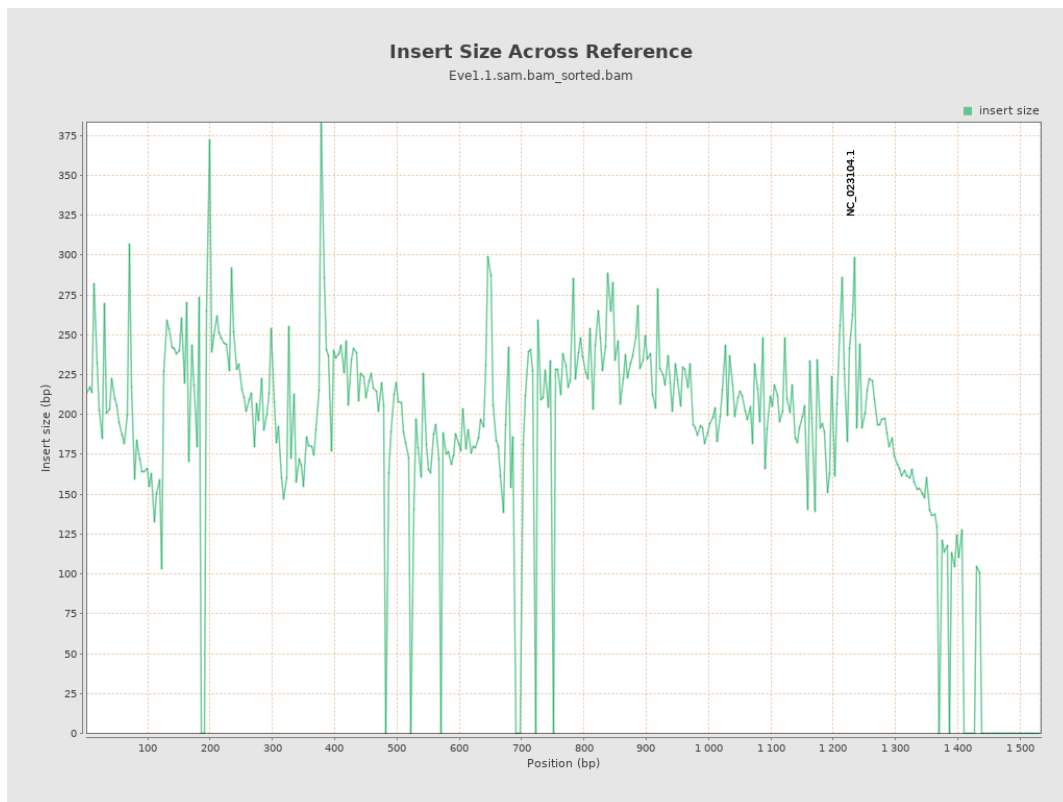
11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram



13. Results : Insert Size Across Reference



14. Results : Insert Size Histogram

