

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2019/10/20 23:56:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam  
/home/anna/ib/raki/Eve100Vfast.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 23:52:46 MSK 2019
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/anna/ib/raki/Eve100Vfast.sam. bam_sorted.bam

2. Summary

2.1. Globals

Reference size	1 734
Number of reads	183 315
Mapped reads	183 315 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	183 315 / 100%
Mapped reads, first in pair	94 011 / 51,28%
Mapped reads, second in pair	89 304 / 48,72%
Mapped reads, both in pair	178 474 / 97,36%
Mapped reads, singletons	4 841 / 2,64%
Read min/max/mean length	101 / 101 / 101
Duplicated reads (estimated)	181 813 / 99,18%
Duplication rate	93,08%
Clipped reads	50 365 / 27,47%

2.2. ACGT Content

Number/percentage of A's	4 617 384 / 25,54%
Number/percentage of C's	3 402 069 / 18,82%
Number/percentage of T's	6 514 462 / 36,03%
Number/percentage of G's	3 546 562 / 19,62%
Number/percentage of N's	259 / 0%
GC Percentage	38,43%

2.3. Coverage

Mean	10 427,8945
Standard Deviation	9 239,6633

2.4. Mapping Quality

Mean Mapping Quality	43,03
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2.5. Insert size

Mean	184,63
Standard Deviation	71,05
P25/Median/P75	130 / 167 / 214

2.6. Mismatches and indels

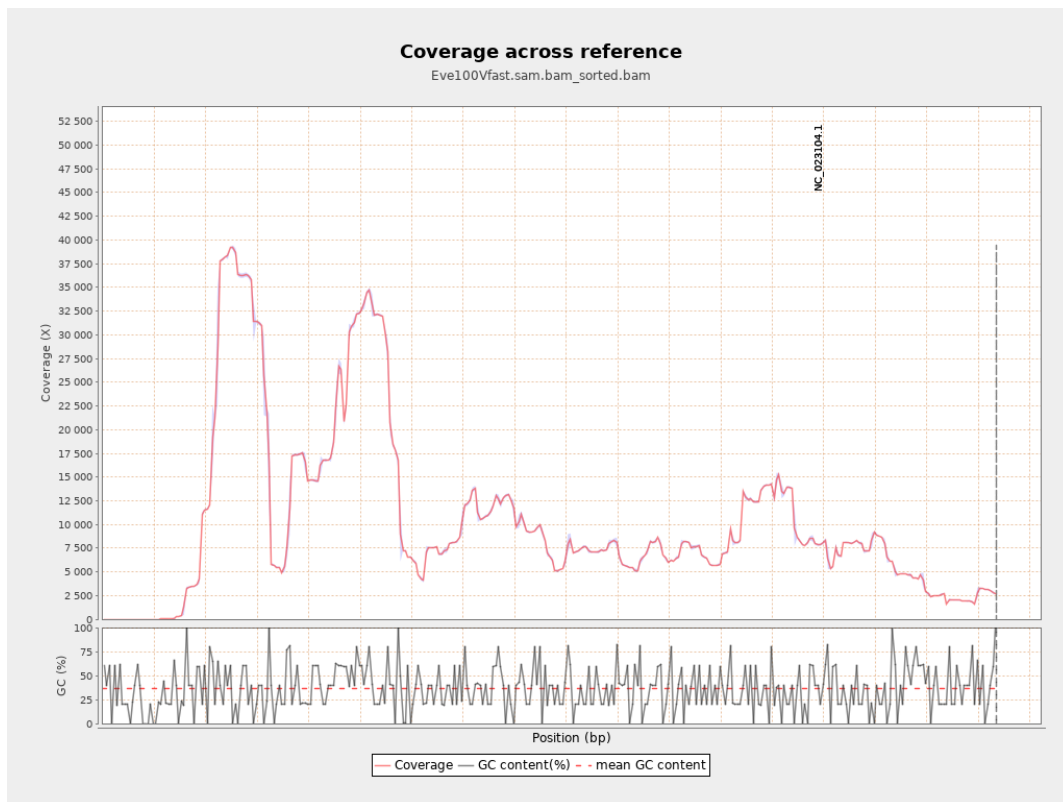
General error rate	0,53%
Mismatches	95 152
Insertions	1 017
Mapped reads with at least one insertion	0,53%
Deletions	1 179
Mapped reads with at least one deletion	0,63%
Homopolymer indels	65,89%

2.7. Chromosome stats

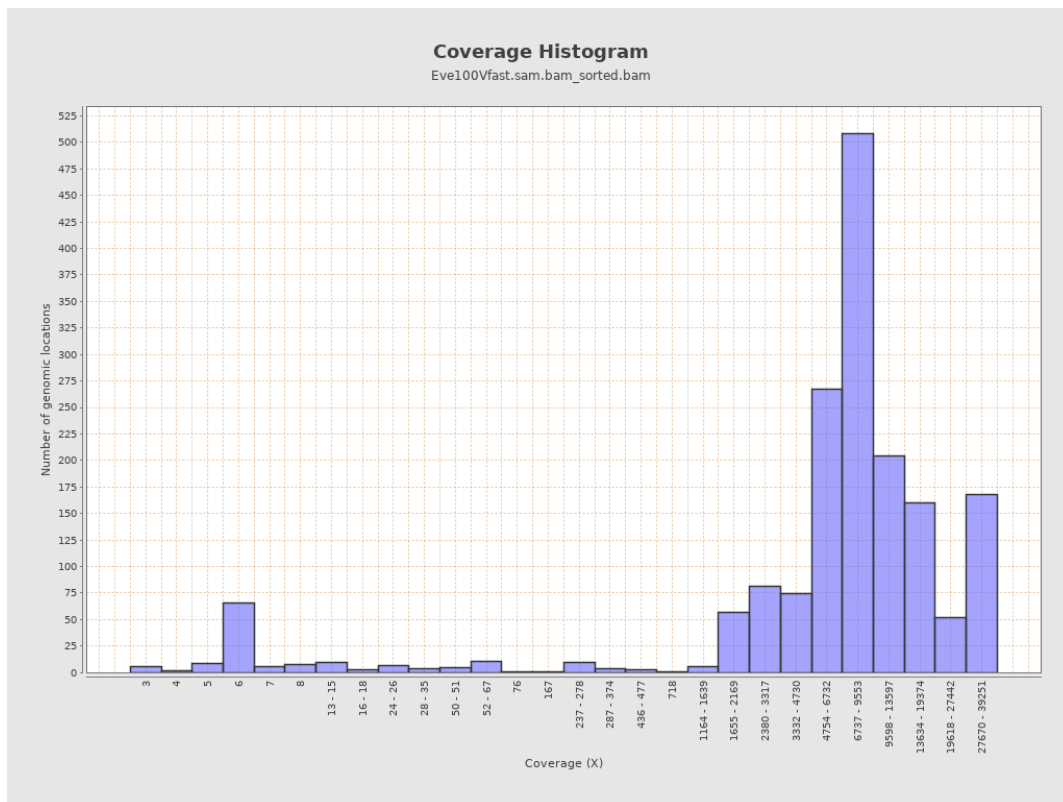
Name	Length	Mapped bases	Mean coverage	Standard deviation

NC_023104.1	1734	18081969	10 427,8945	9 239,6633
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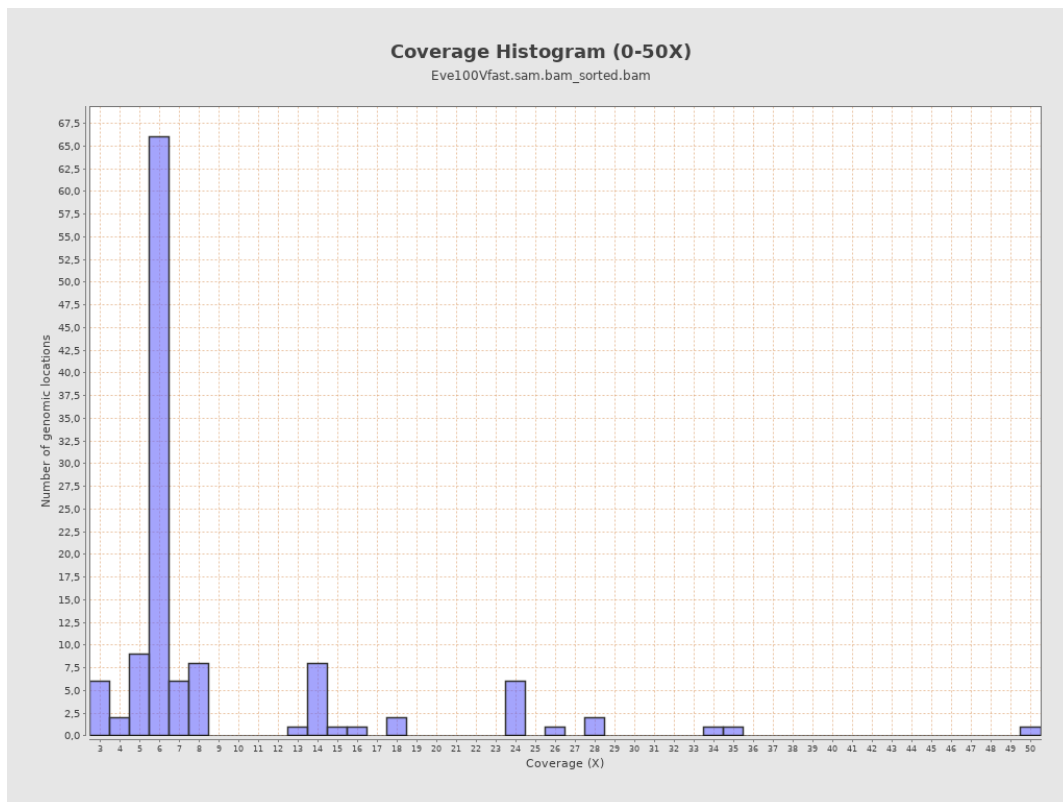
3. Results : Coverage across reference



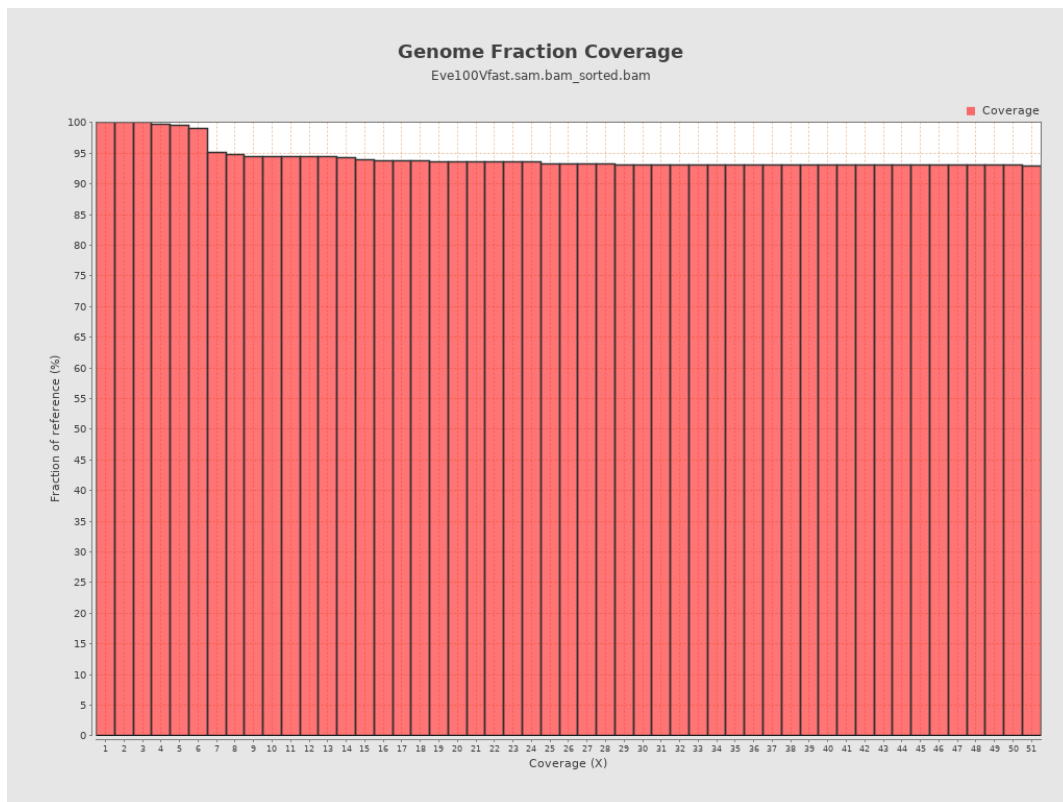
4. Results : Coverage Histogram



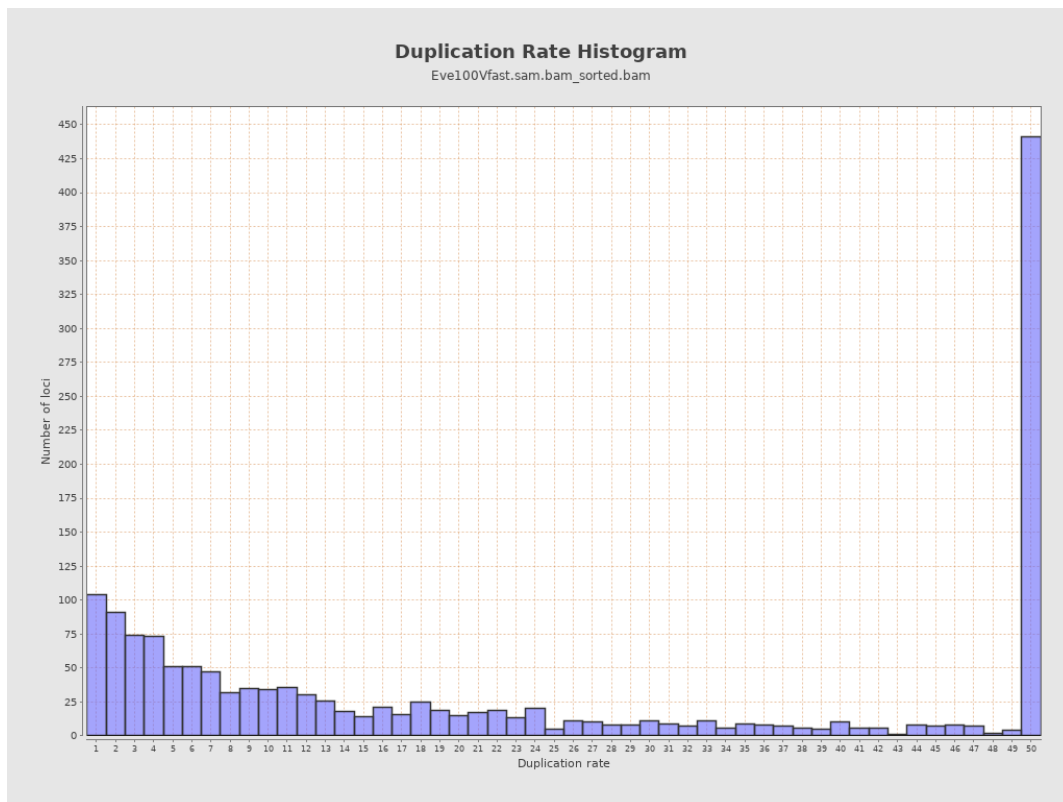
5. Results : Coverage Histogram (0-50X)



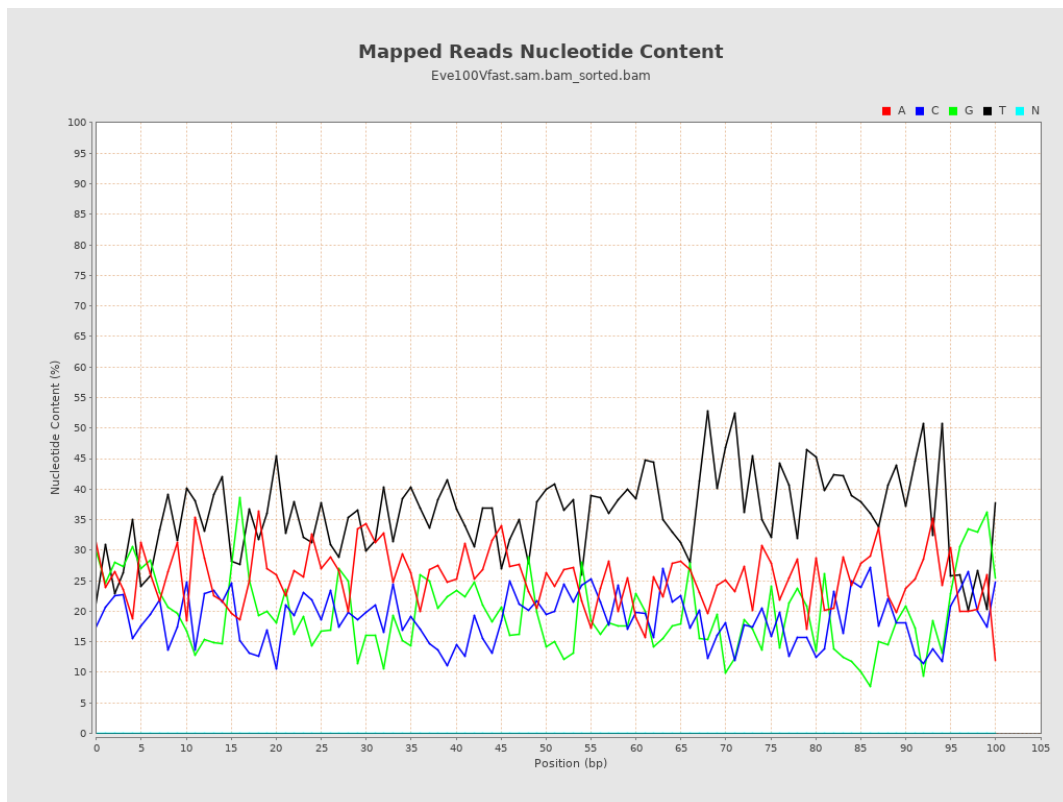
6. Results : Genome Fraction Coverage



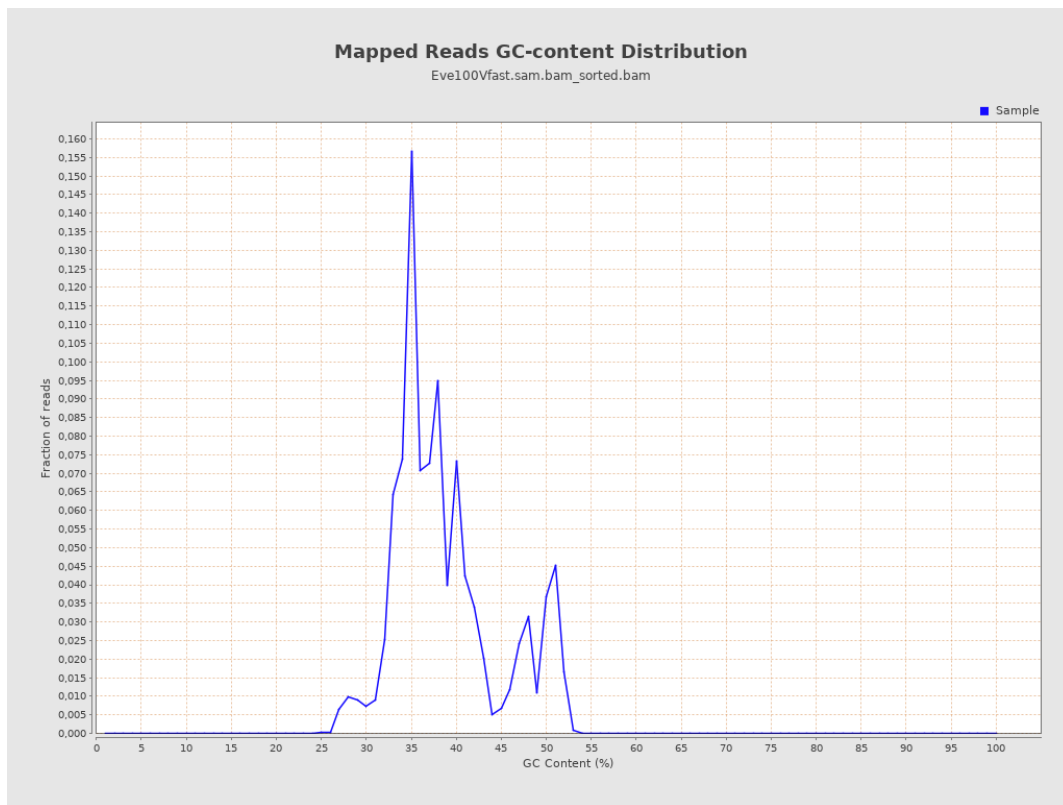
7. Results : Duplication Rate Histogram



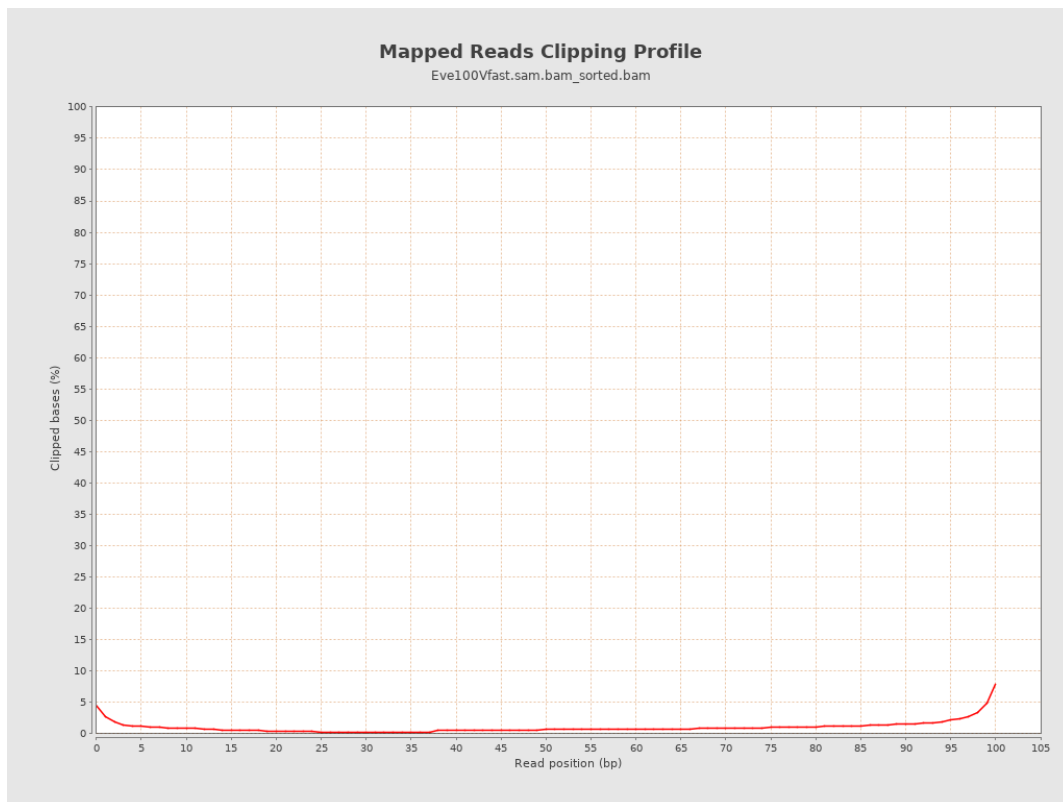
8. Results : Mapped Reads Nucleotide Content



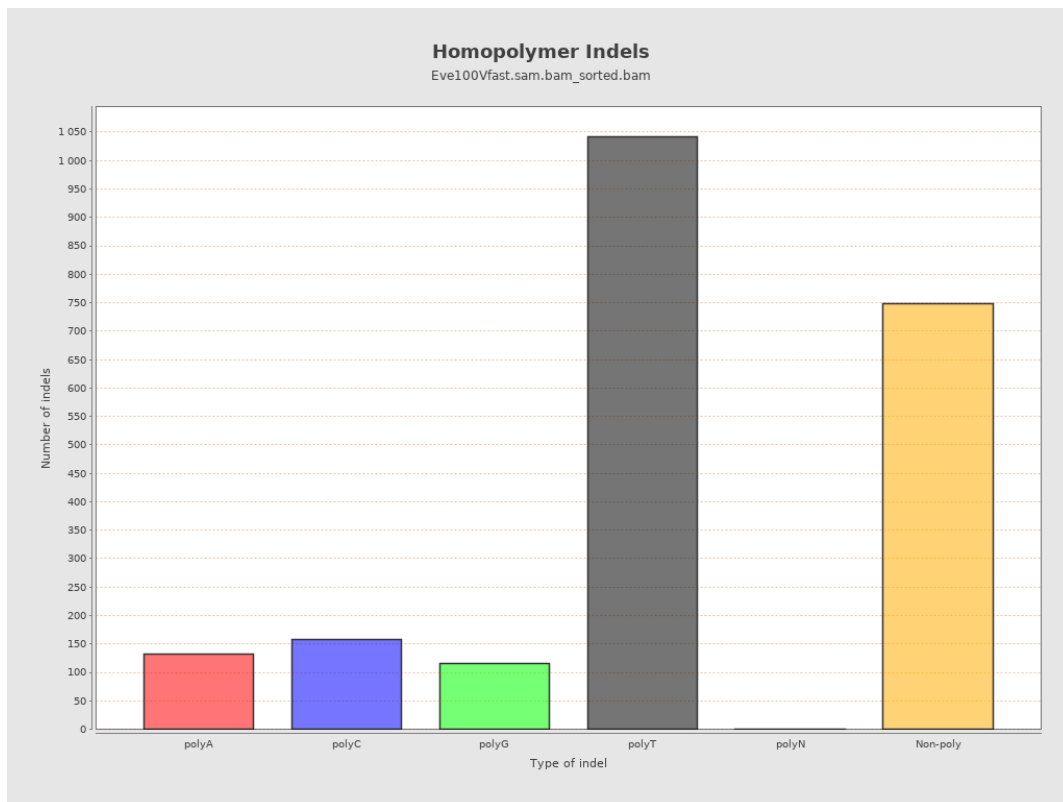
9. Results : Mapped Reads GC-content Distribution



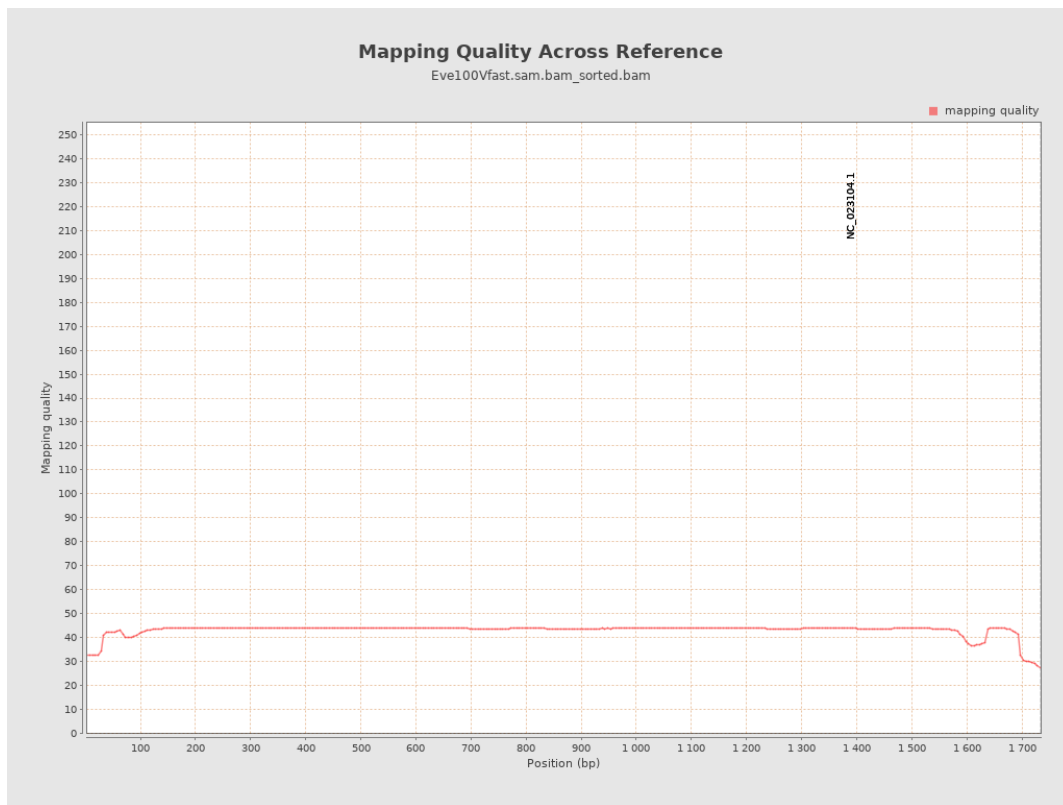
10. Results : Mapped Reads Clipping Profile



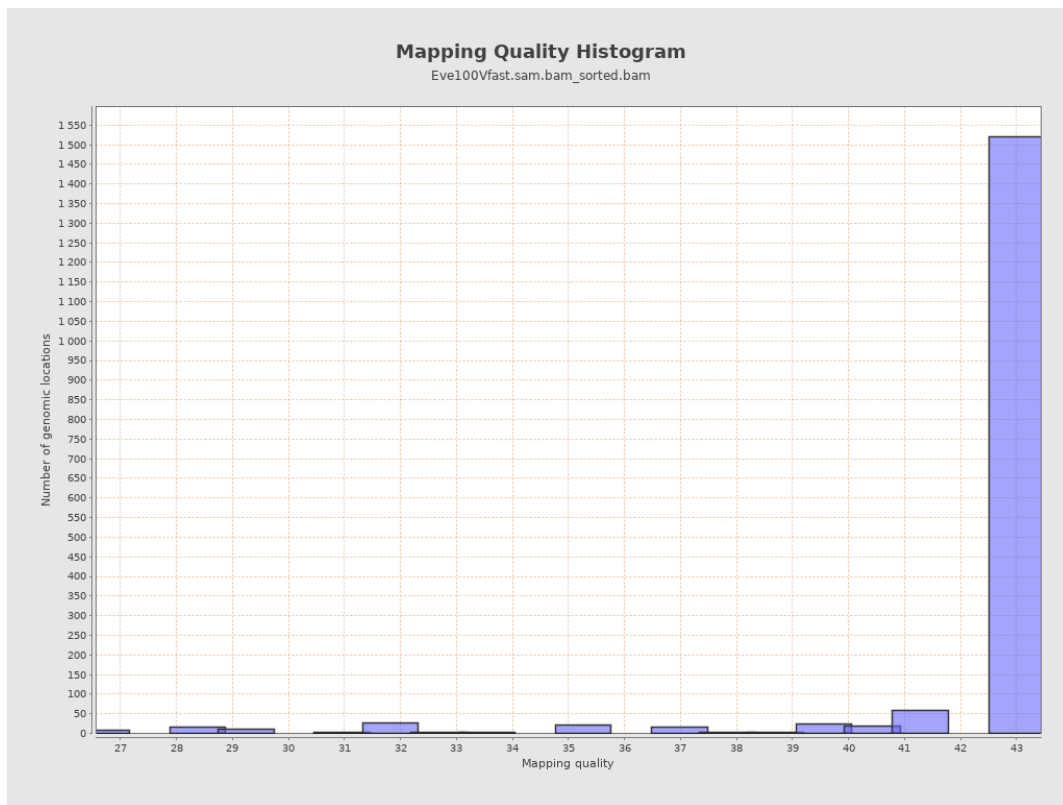
11. Results : Homopolymer Indels



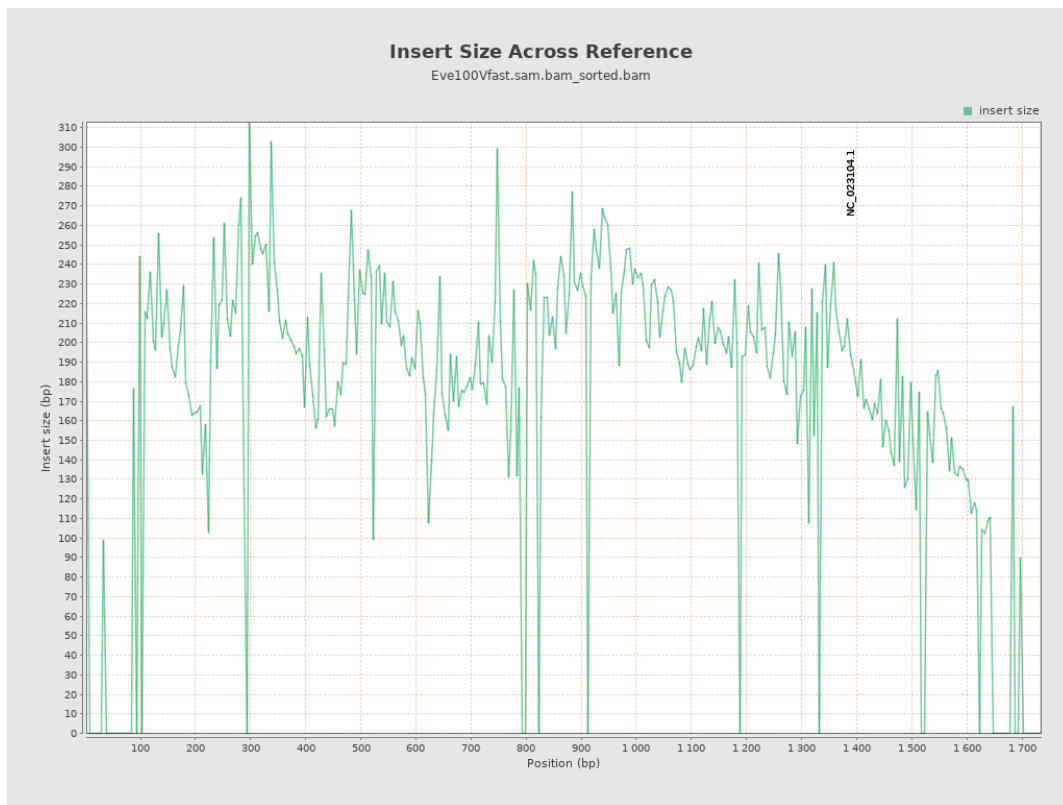
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

