

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2019/10/24 23:47:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /home/anna//alignment_sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	bwa mem GCF_000005845.2_ASM584v2_genomic.fna out51.fq out53r.fq
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 24 23:46:50 MSK 2019
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/anna//alignment_sorted.bam

2. Summary

2.1. Globals

Reference size	4 641 652
Number of reads	847 778
Mapped reads	846 529 / 99,85%
Supplementary alignments	208 / 0,02%
Unmapped reads	1 249 / 0,15%
Mapped paired reads	846 529 / 99,85%
Mapped reads, first in pair	423 252 / 49,92%
Mapped reads, second in pair	423 277 / 49,93%
Mapped reads, both in pair	845 508 / 99,73%
Mapped reads, singletons	1 021 / 0,12%
Read min/max/mean length	20 / 101 / 89,71
Duplicated reads (estimated)	152 590 / 18%
Duplication rate	17,04%
Clipped reads	44 720 / 5,27%

2.2. ACGT Content

Number/percentage of A's	18 744 201 / 24,97%
Number/percentage of C's	18 821 351 / 25,07%
Number/percentage of T's	18 706 420 / 24,92%
Number/percentage of G's	18 791 843 / 25,03%
Number/percentage of N's	13 372 / 0,02%
GC Percentage	50,11%

2.3. Coverage

Mean	16,1749
Standard Deviation	5,5847

2.4. Mapping Quality

Mean Mapping Quality	58,85
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2.5. Insert size

Mean	488,46
Standard Deviation	33 333,02
P25/Median/P75	144 / 183 / 229

2.6. Mismatches and indels

General error rate	0,14%
Mismatches	106 415
Insertions	1 072
Mapped reads with at least one insertion	0,13%
Deletions	846
Mapped reads with at least one deletion	0,1%
Homopolymer indels	50,78%

2.7. Chromosome stats

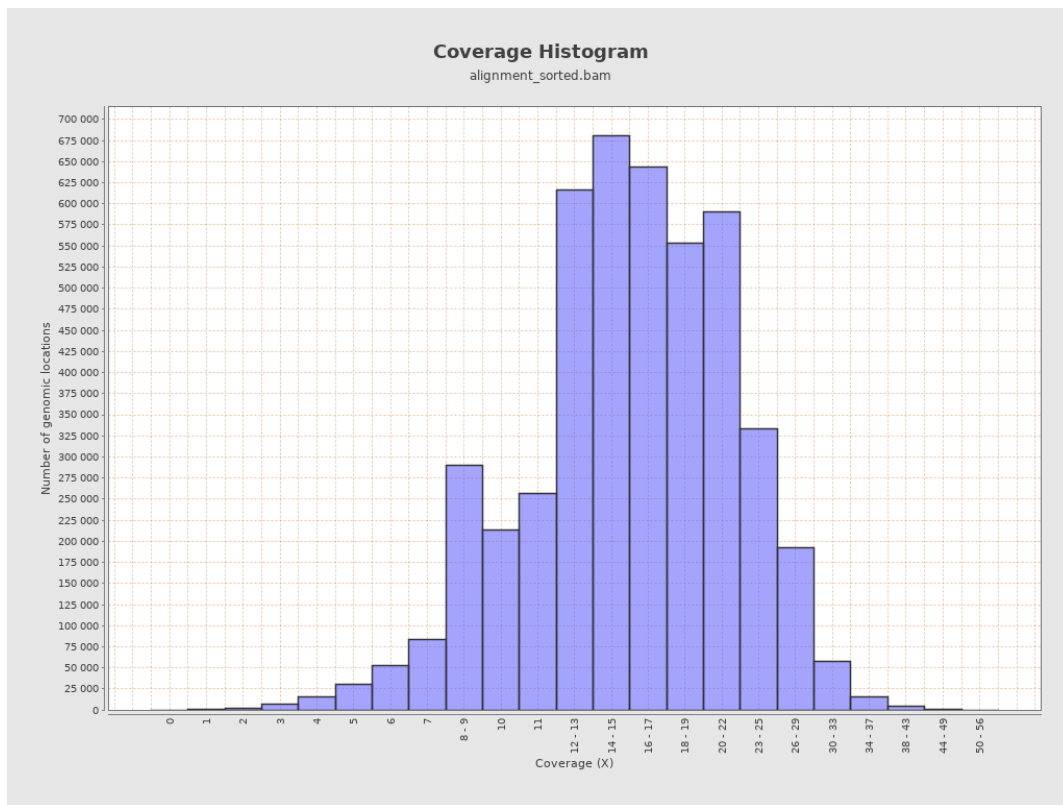
Name	Length	Mapped bases	Mean coverage	Standard deviation

NC_000913.3	4641652	75078172	16,1749	5,5847
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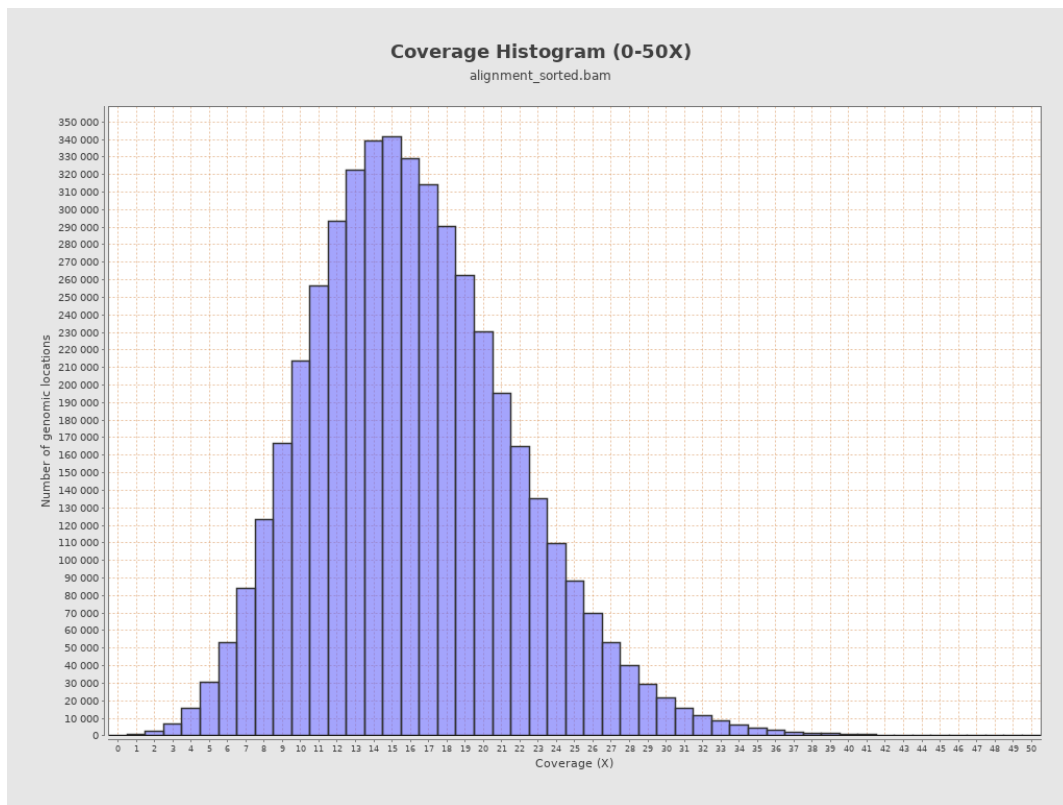
3. Results : Coverage across reference



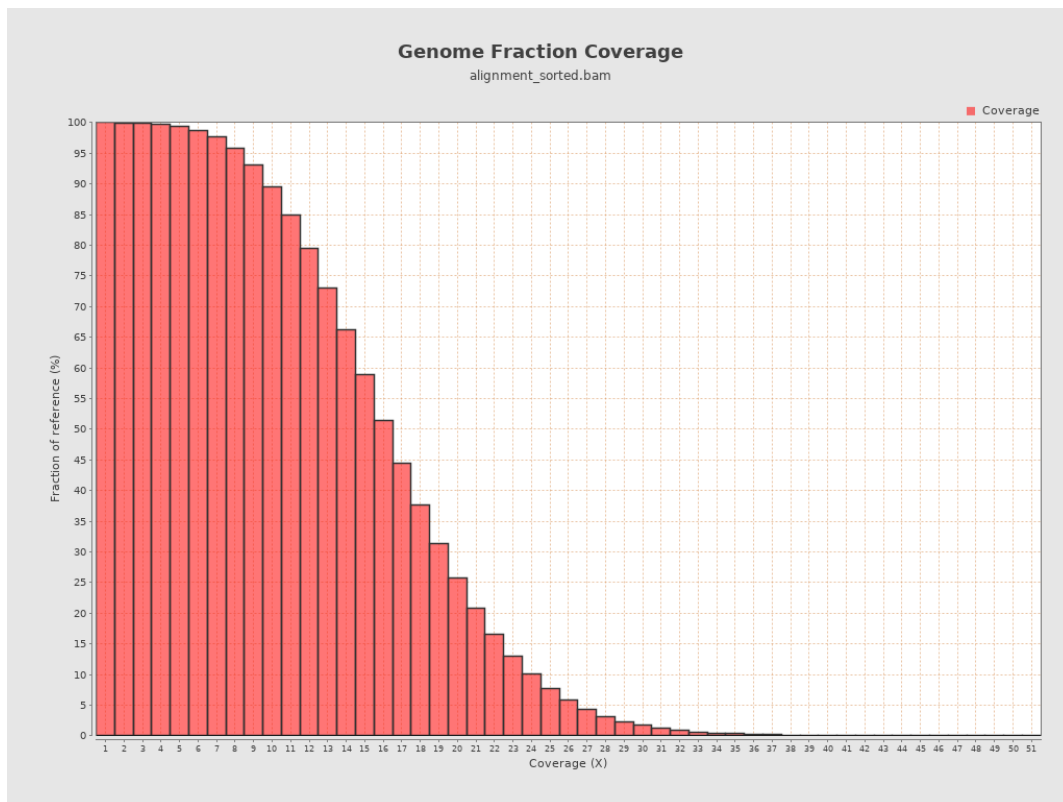
4. Results : Coverage Histogram



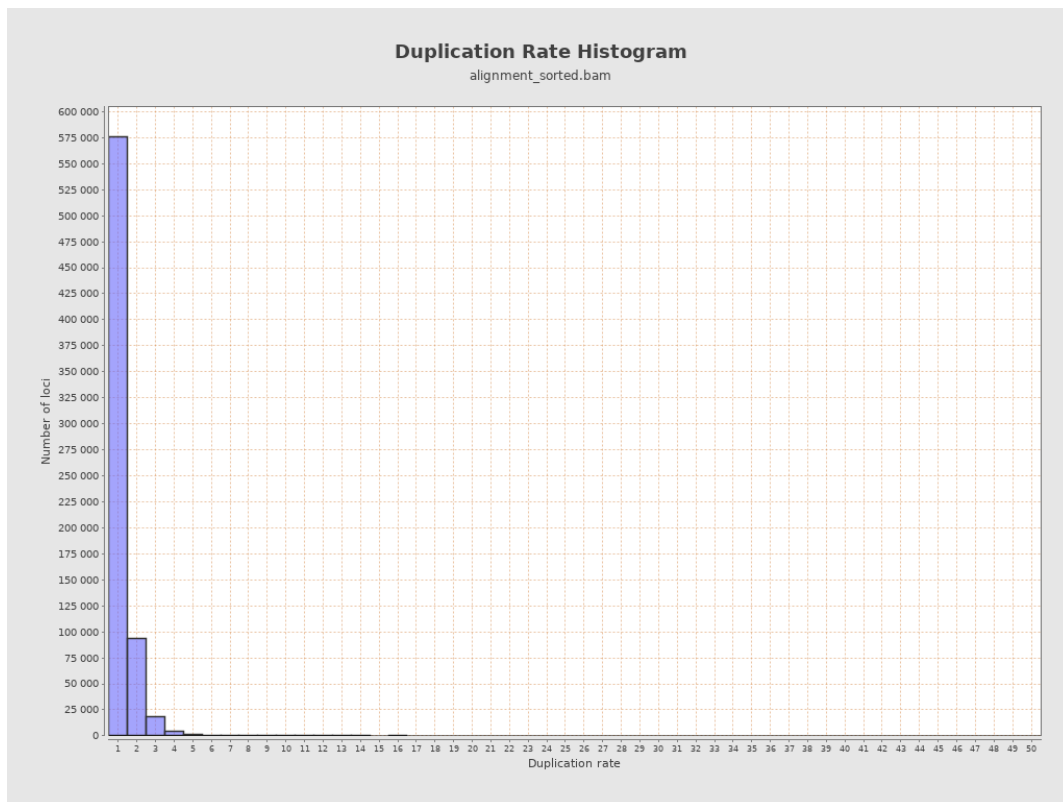
5. Results : Coverage Histogram (0-50X)



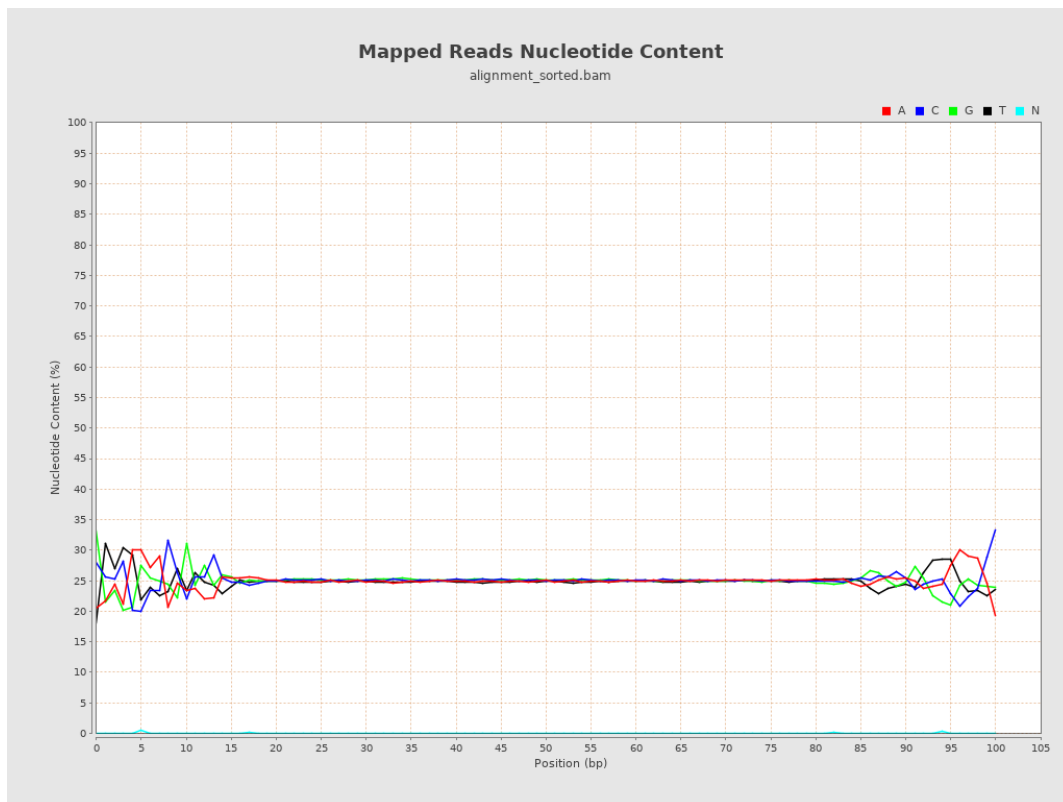
6. Results : Genome Fraction Coverage



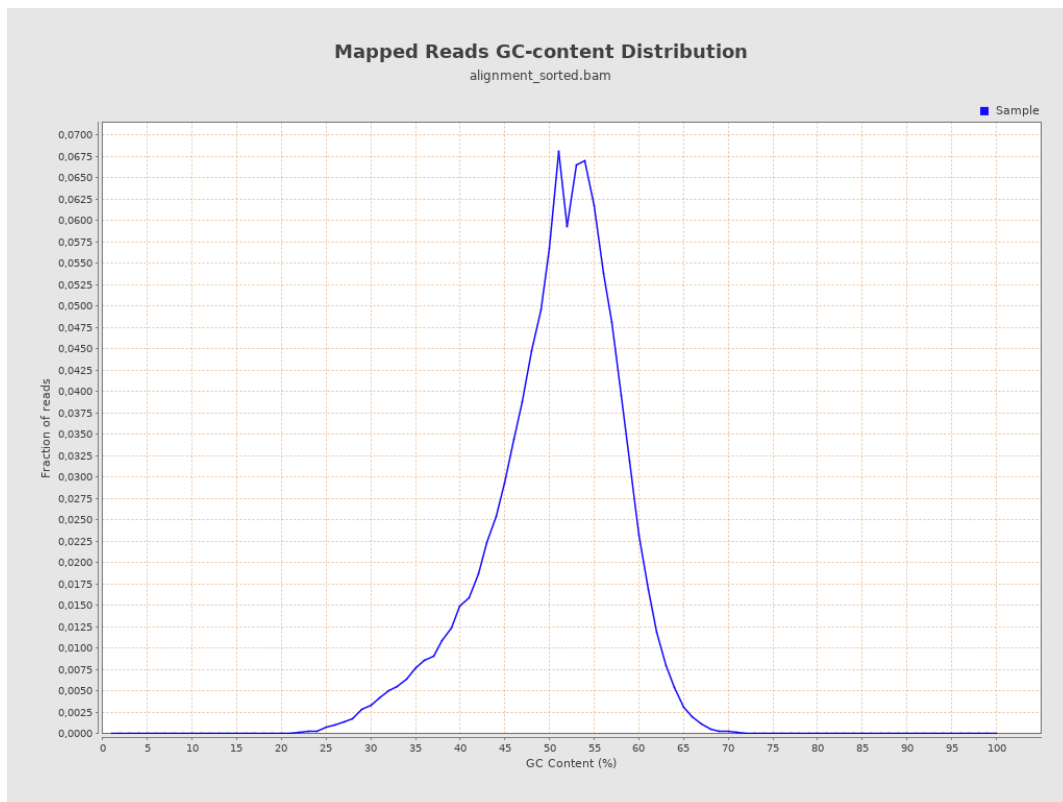
7. Results : Duplication Rate Histogram



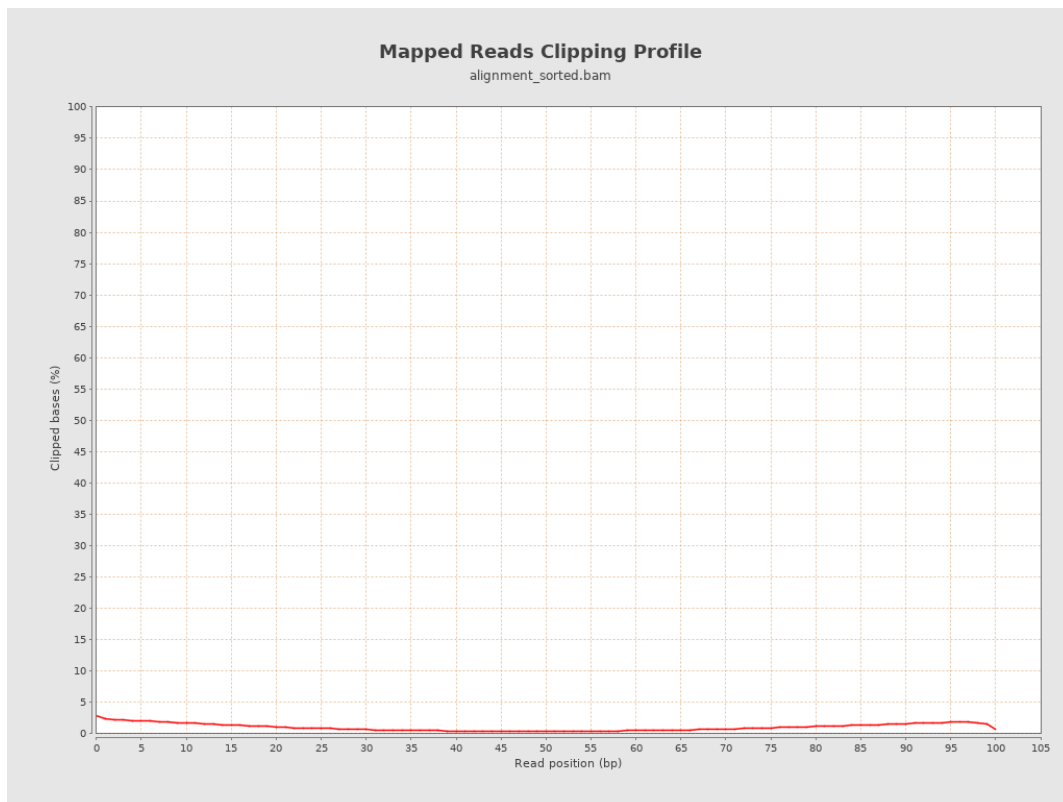
8. Results : Mapped Reads Nucleotide Content



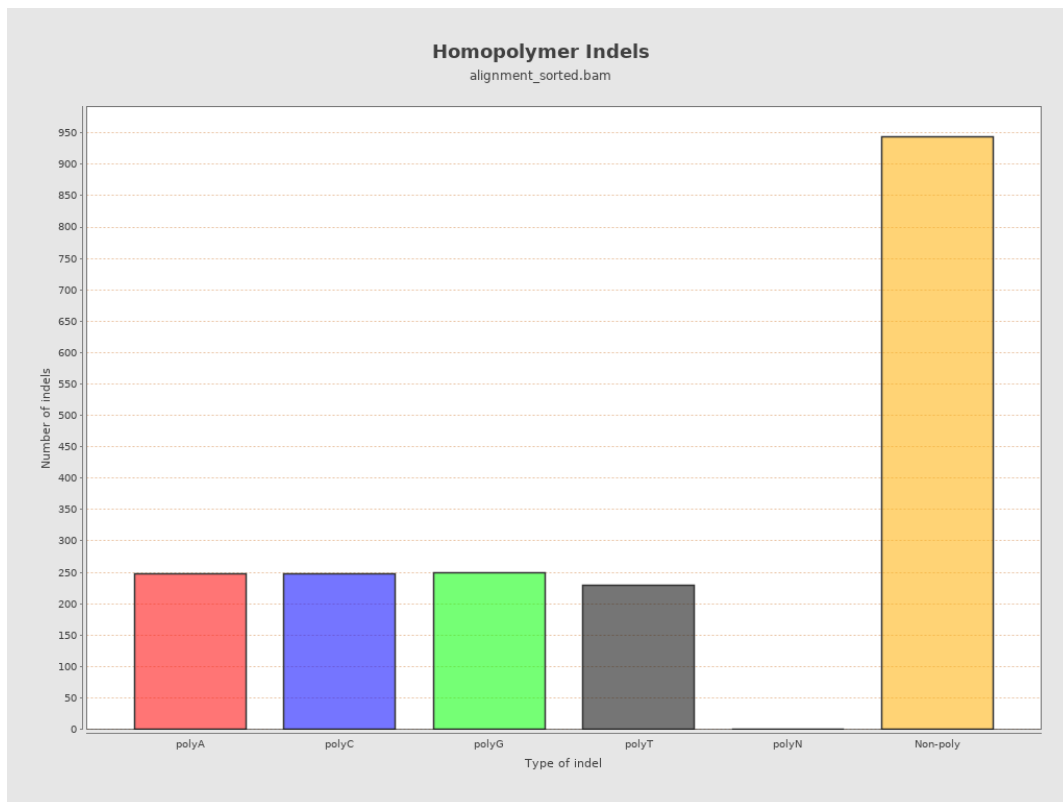
9. Results : Mapped Reads GC-content Distribution



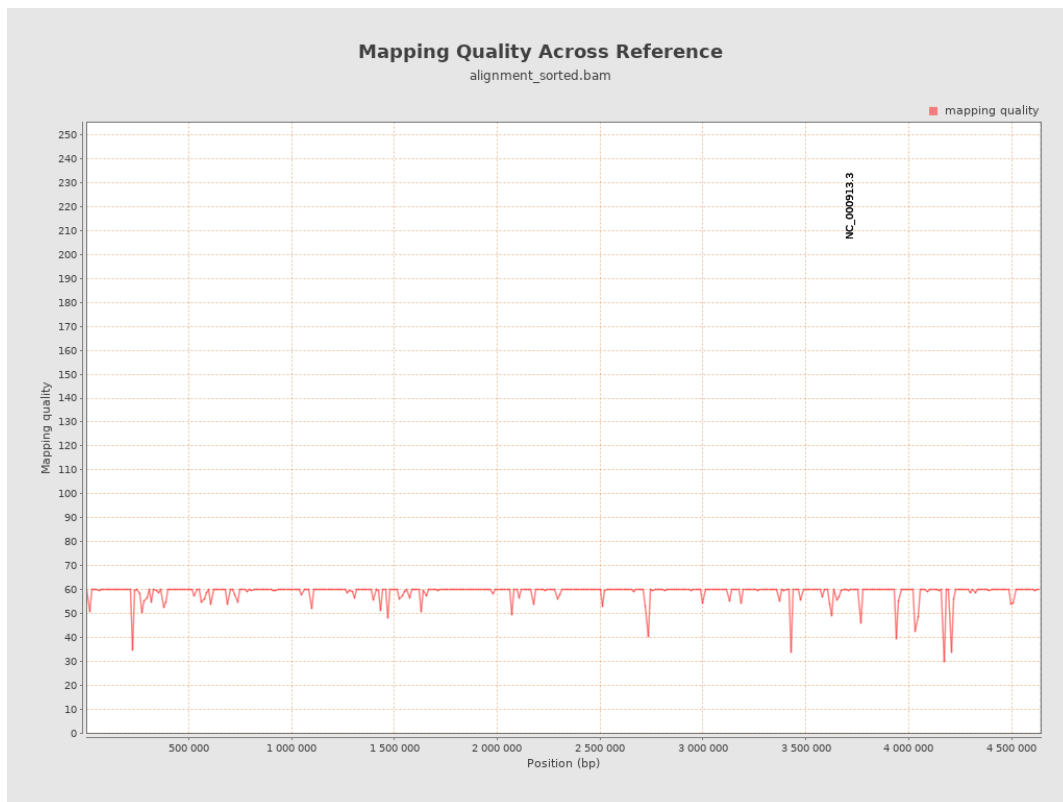
10. Results : Mapped Reads Clipping Profile



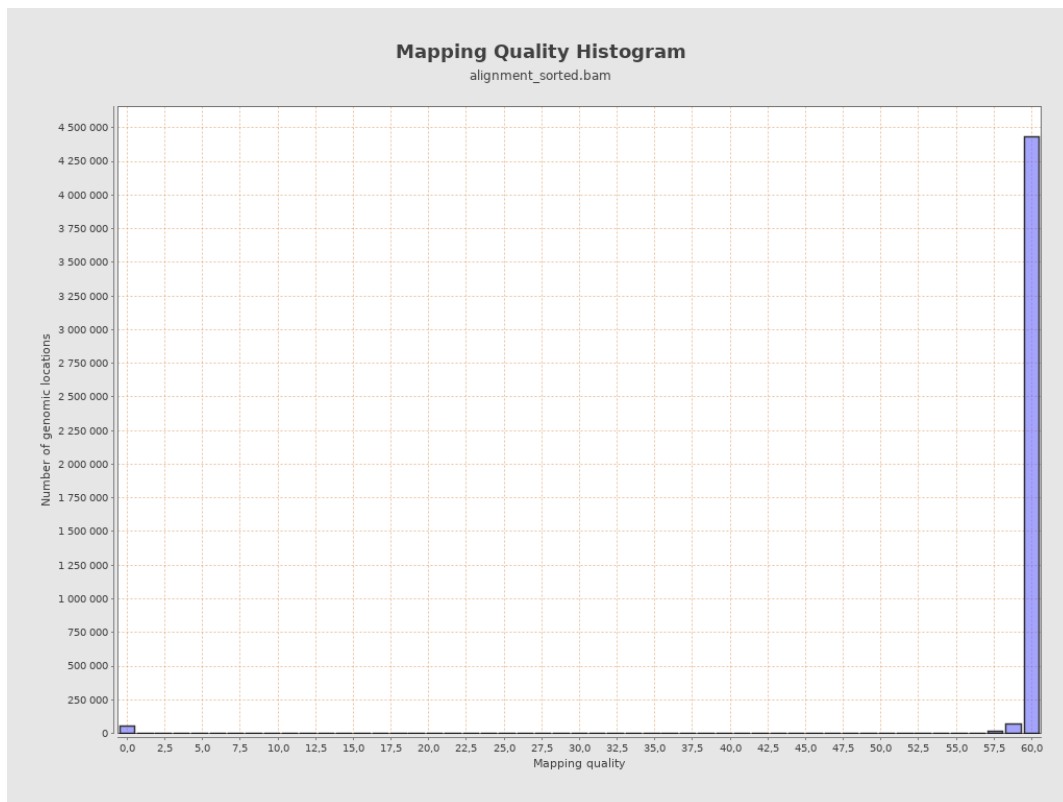
11. Results : Homopolymer Indels



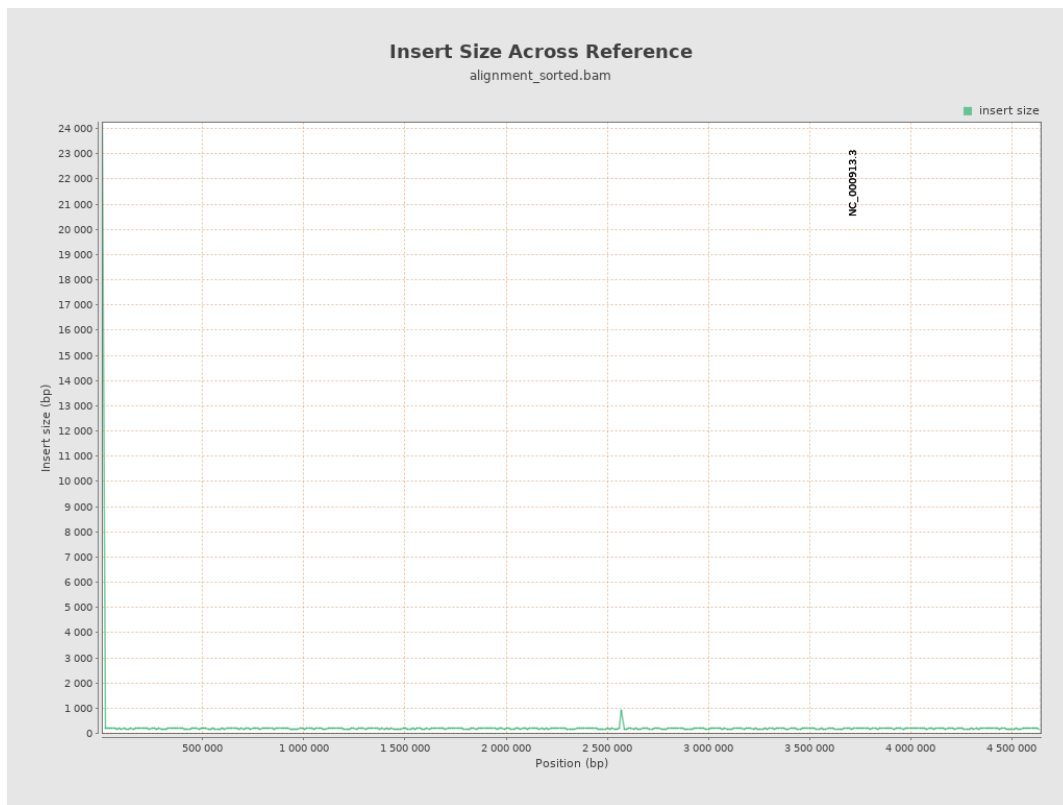
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

