

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2019/11/03 23:44:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /home/anna/ib/Project2/roommate_sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

| | |
|---------------------------------------|--|
| Command line: | bwa mem refer.fasta SRR1705851.fastq |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Nov 03 23:44:19 MSK 2019 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | /home/anna/ib/Project2/roommate_sorted.bam |

2. Summary

2.1. Globals

| | |
|------------------------------|-------------------|
| Reference size | 1 665 |
| Number of reads | 361 349 |
| Mapped reads | 361 116 / 99,94% |
| Supplementary alignments | 3 084 / 0,85% |
| Unmapped reads | 233 / 0,06% |
| Mapped paired reads | 0 / 0% |
| Read min/max/mean length | 30 / 151 / 146,36 |
| Duplicated reads (estimated) | 359 516 / 99,49% |
| Duplication rate | 98,19% |
| Clipped reads | 27 903 / 7,72% |

2.2. ACGT Content

| | |
|--------------------------|---------------------|
| Number/percentage of A's | 17 971 753 / 34,58% |
| Number/percentage of C's | 10 366 262 / 19,95% |
| Number/percentage of T's | 12 095 861 / 23,28% |
| Number/percentage of G's | 11 533 867 / 22,19% |
| Number/percentage of N's | 1 440 / 0% |
| GC Percentage | 42,14% |

2.3. Coverage

| | |
|--------------------|-------------|
| Mean | 31 218,1195 |
| Standard Deviation | 7 853,546 |

2.4. Mapping Quality

| | |
|----------------------|-------|
| Mean Mapping Quality | 59,98 |
|----------------------|-------|

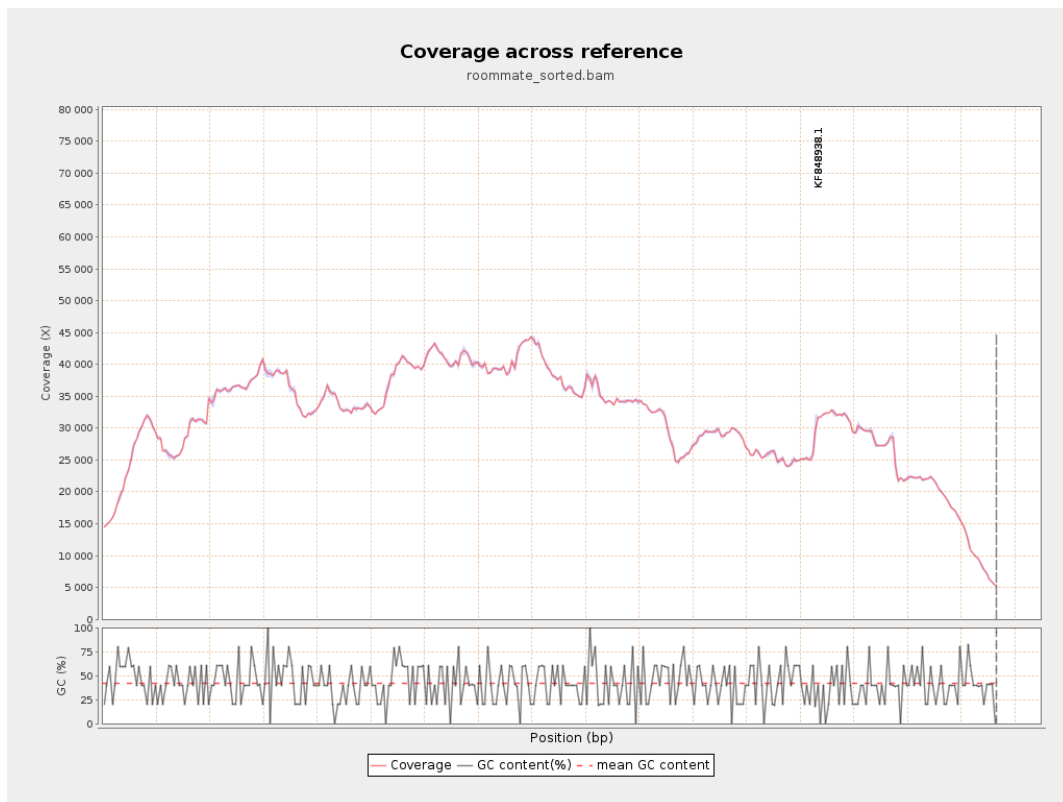
2.5. Mismatches and indels

| | |
|--|---------|
| General error rate | 0,43% |
| Mismatches | 221 489 |
| Insertions | 193 |
| Mapped reads with at least one insertion | 0,05% |
| Deletions | 2 230 |
| Mapped reads with at least one deletion | 0,61% |
| Homopolymer indels | 32,56% |

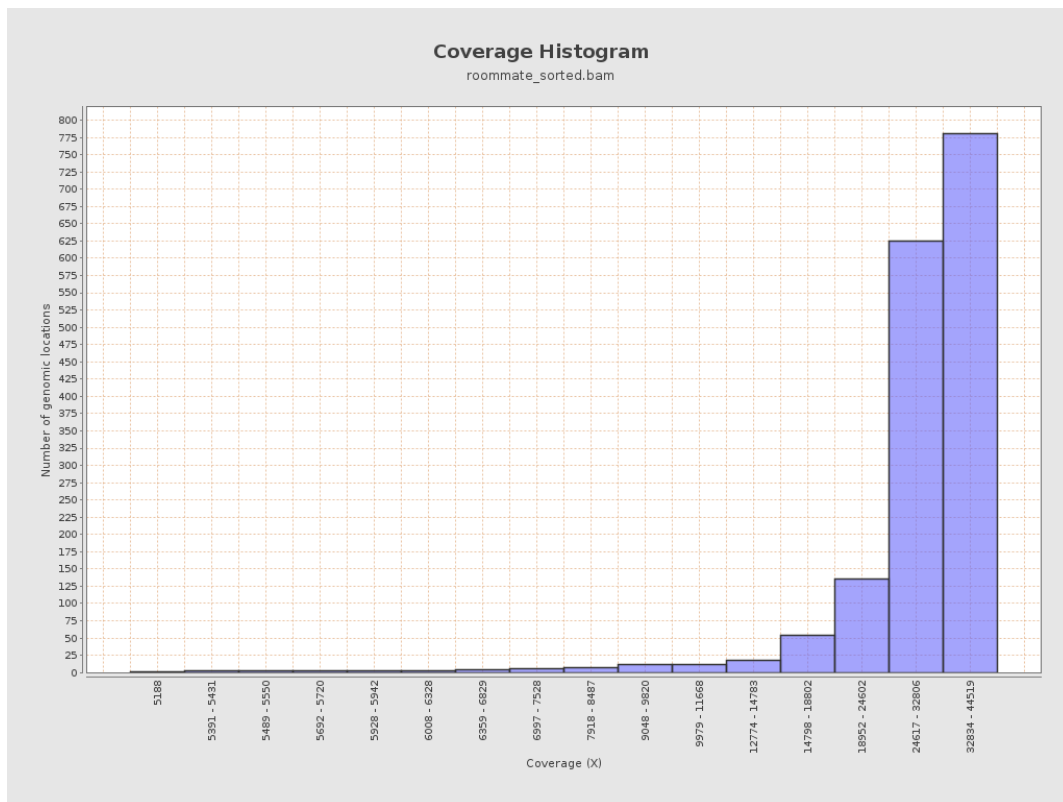
2.6. Chromosome stats

| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|------------|--------|--------------|---------------|--------------------|
| KF848938.1 | 1665 | 51978169 | 31 218,1195 | 7 853,546 |

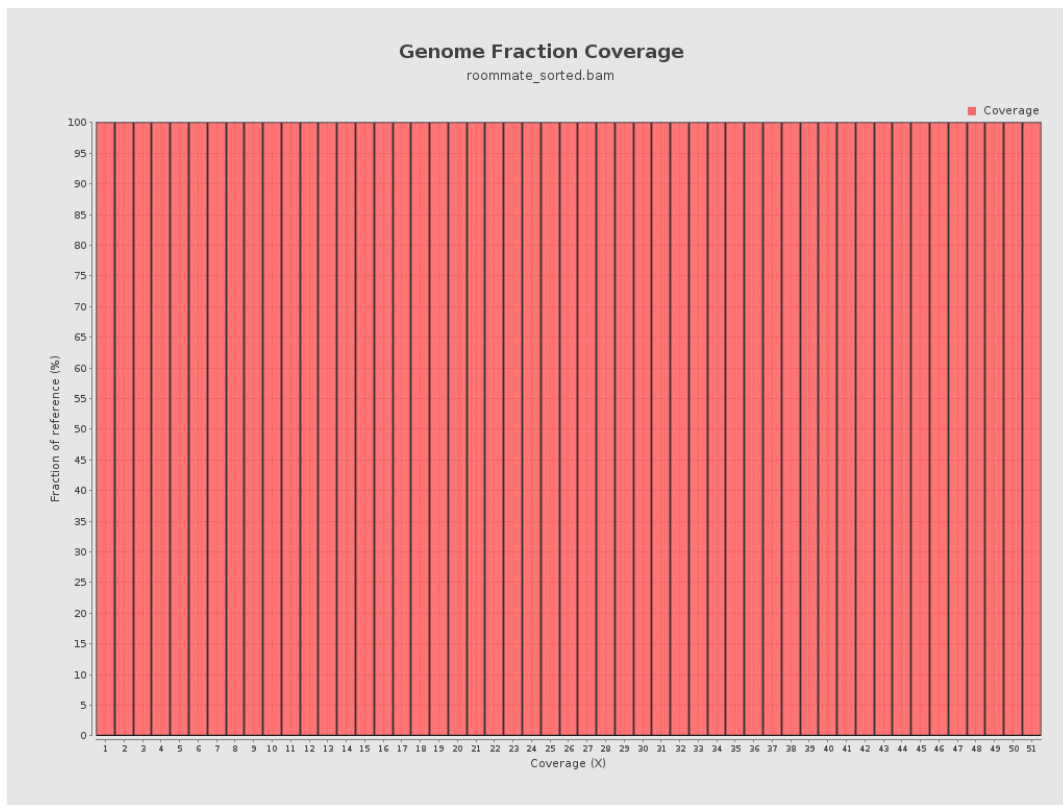
3. Results : Coverage across reference



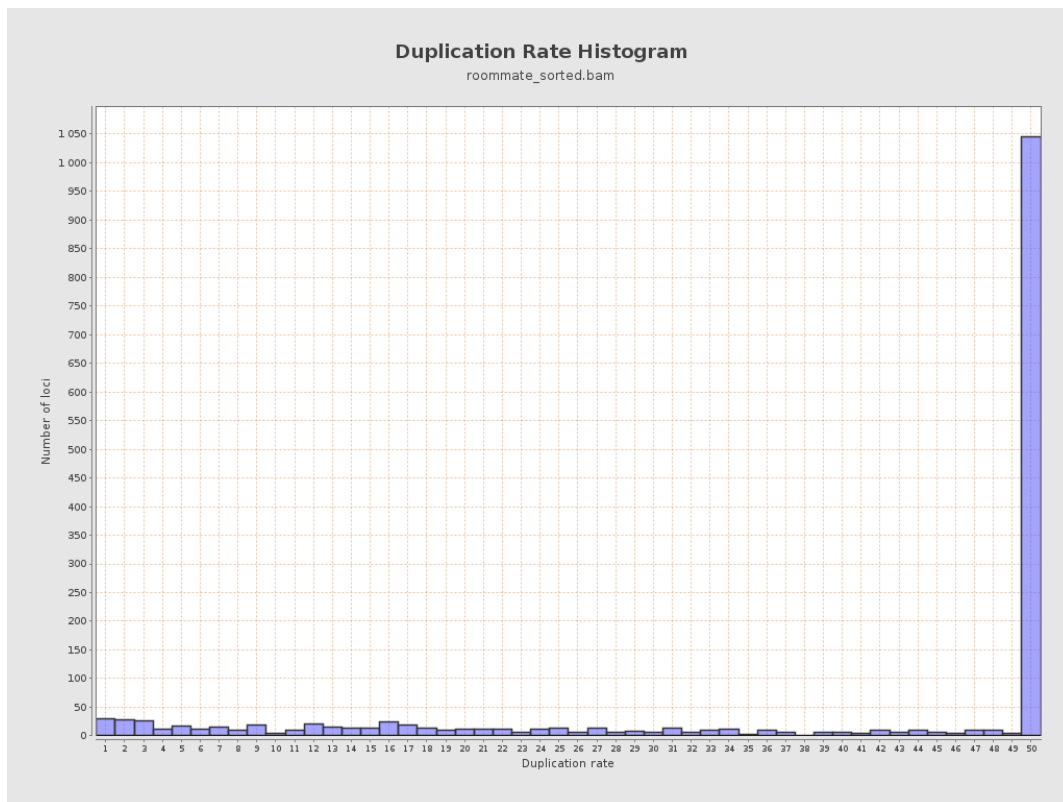
4. Results : Coverage Histogram



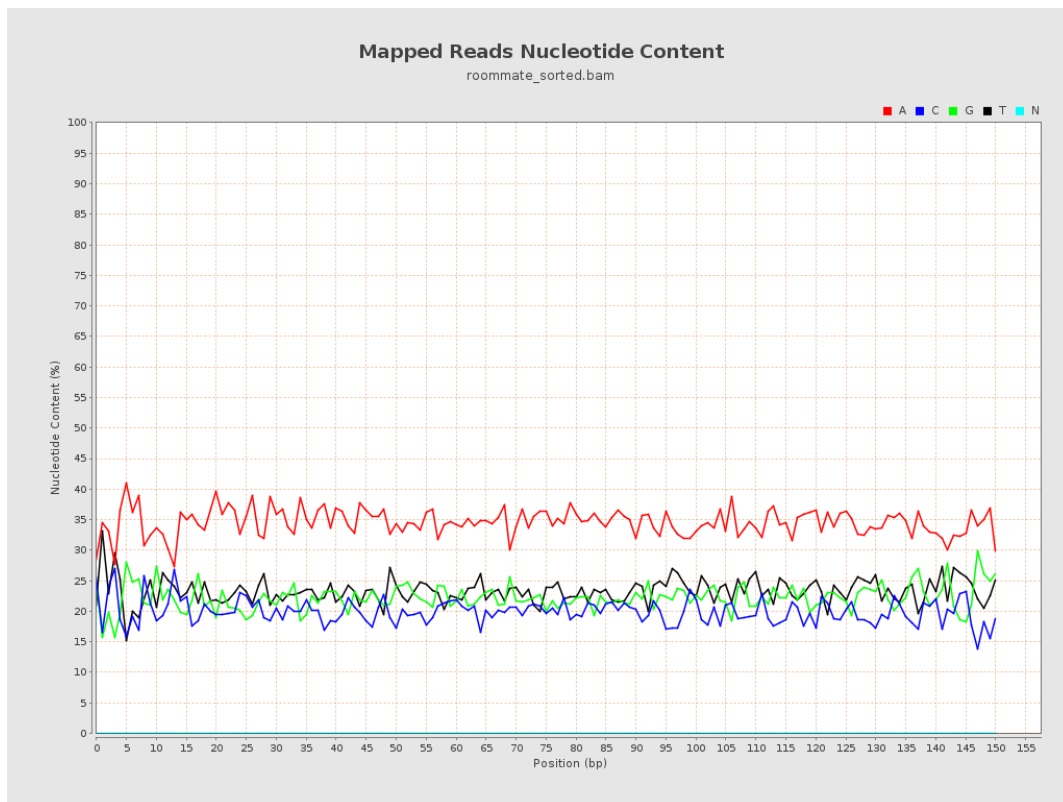
5. Results : Genome Fraction Coverage



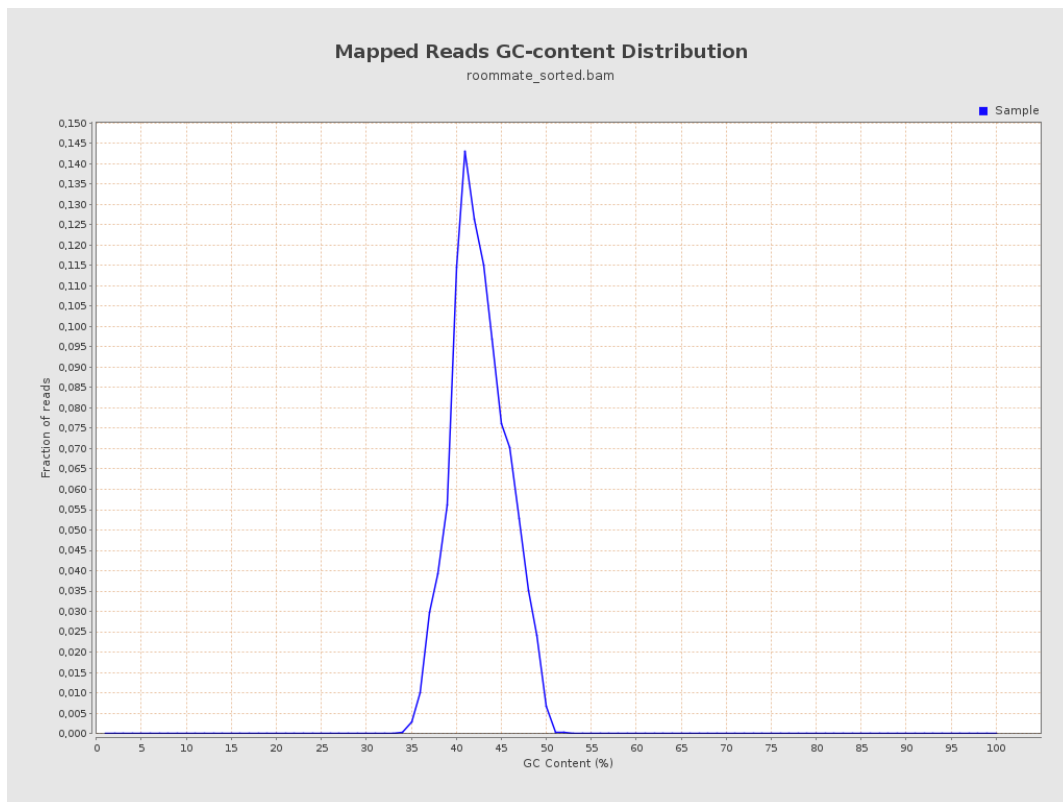
6. Results : Duplication Rate Histogram



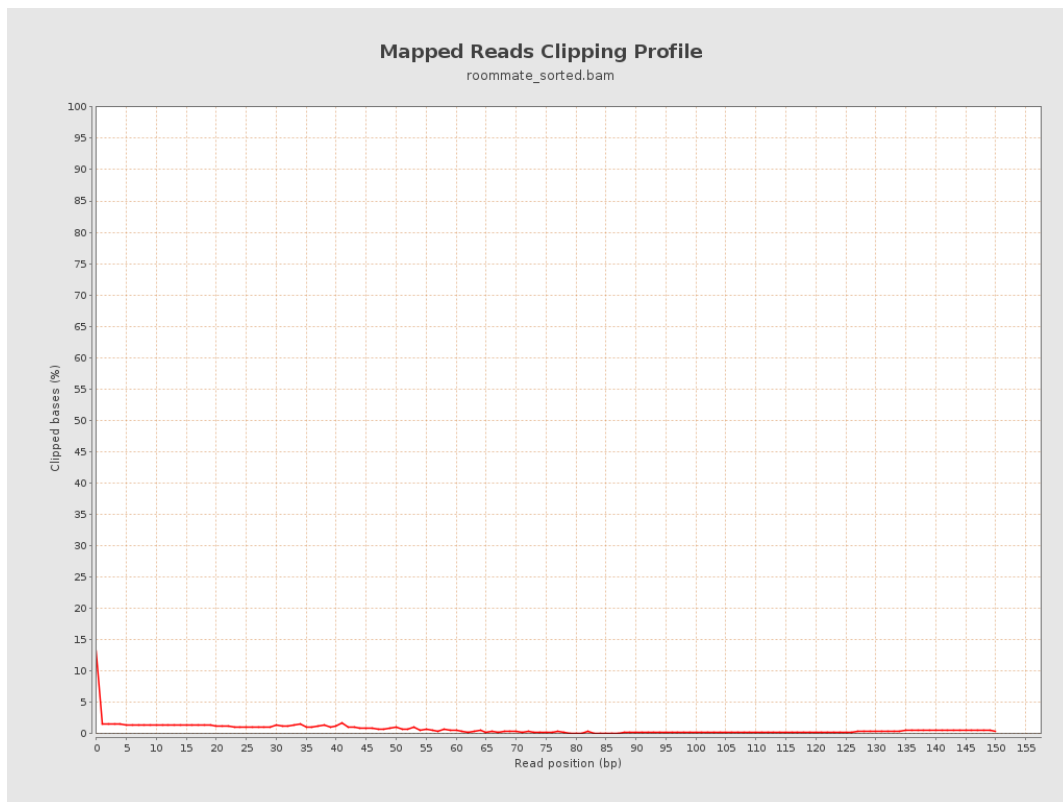
7. Results : Mapped Reads Nucleotide Content



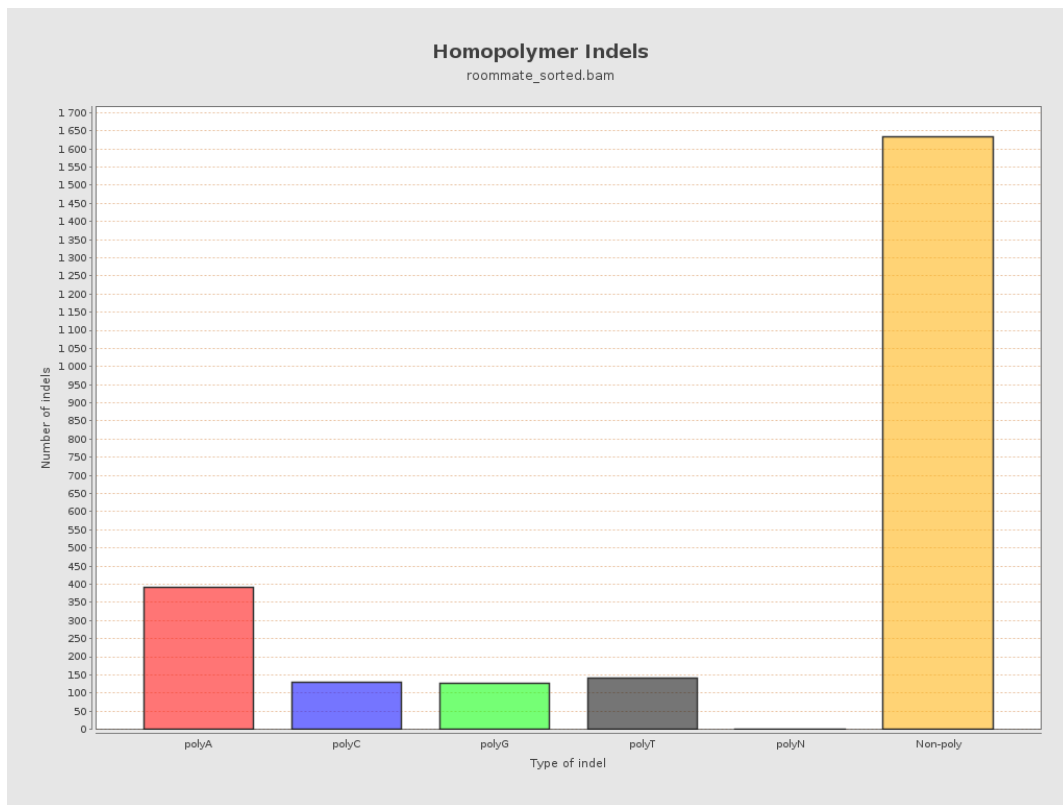
8. Results : Mapped Reads GC-content Distribution



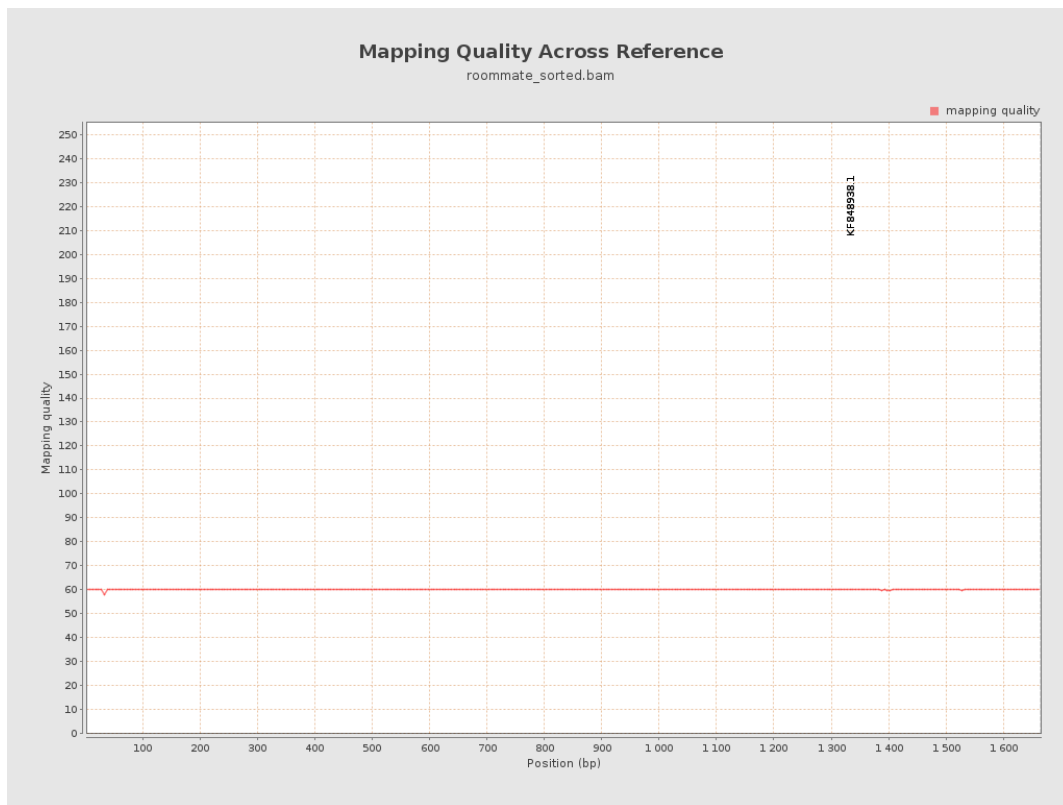
9. Results : Mapped Reads Clipping Profile



10. Results : Homopolymer Indels



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

