

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.1.1

2015/09/02 09:37:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam  
/data/qualimap_release_data/alignments/ERR089819.bam -c -nw 400 -hm 3
```

1.2. Alignment

| | |
|-----------------------------|--|
| BAM file: | /data/qualimap_release_data/alignments/ERR089819.bam |
| Program: | Bowtie (0.12.7) |
| Size of a homopolymer: | 3 |
| Number of windows: | 400 |
| Skip duplicated alignments: | no |
| Analysis date: | Wed Sep 02 09:37:28 CEST 2015 |
| Draw chromosome limits: | yes |

2. Summary

2.1. Globals

| | |
|-----------------------------------|---------------------|
| Reference size | 100,286,002 |
| Number of reads | 35,576,180 |
| Mapped reads | 30,983,200 / 87.09% |
| Unmapped reads | 4,592,980 / 12.91% |
| Paired reads | 30,983,200 / 87.09% |
| Mapped reads, only first in pair | 15,491,600 / 43.54% |
| Mapped reads, only second in pair | 15,491,600 / 43.54% |
| Mapped reads, both in pair | 30,983,200 / 87.09% |
| Mapped reads, singletons | 0 / 0% |
| Read min/max/mean length | 100 / 100 / 100 |
| Clipped reads | 0 / 0% |
| Duplicated reads (estimated) | 5,125,380 / 14.41% |
| Duplication rate | 16.39% |

2.2. ACGT Content

| | |
|--------------------------|------------------------|
| Number/percentage of A's | 1,003,585,776 / 32.43% |
| Number/percentage of C's | 541,692,060 / 17.5% |
| Number/percentage of T's | 1,006,351,599 / 32.52% |
| Number/percentage of G's | 543,136,344 / 17.55% |
| Number/percentage of N's | 0 / 0% |
| GC Percentage | 35.05% |

2.3. Coverage

| | |
|--------------------|-------|
| Mean | 30.89 |
| Standard Deviation | 25.01 |

2.4. Mapping Quality

| | |
|----------------------|--------|
| Mean Mapping Quality | 254.71 |
|----------------------|--------|

2.5. Insert size

| | |
|--------------------|-----------------|
| Mean | 407.69 |
| Standard Deviation | 92.69 |
| P25/Median/P75 | 342 / 400 / 469 |

2.6. Mismatches and indels

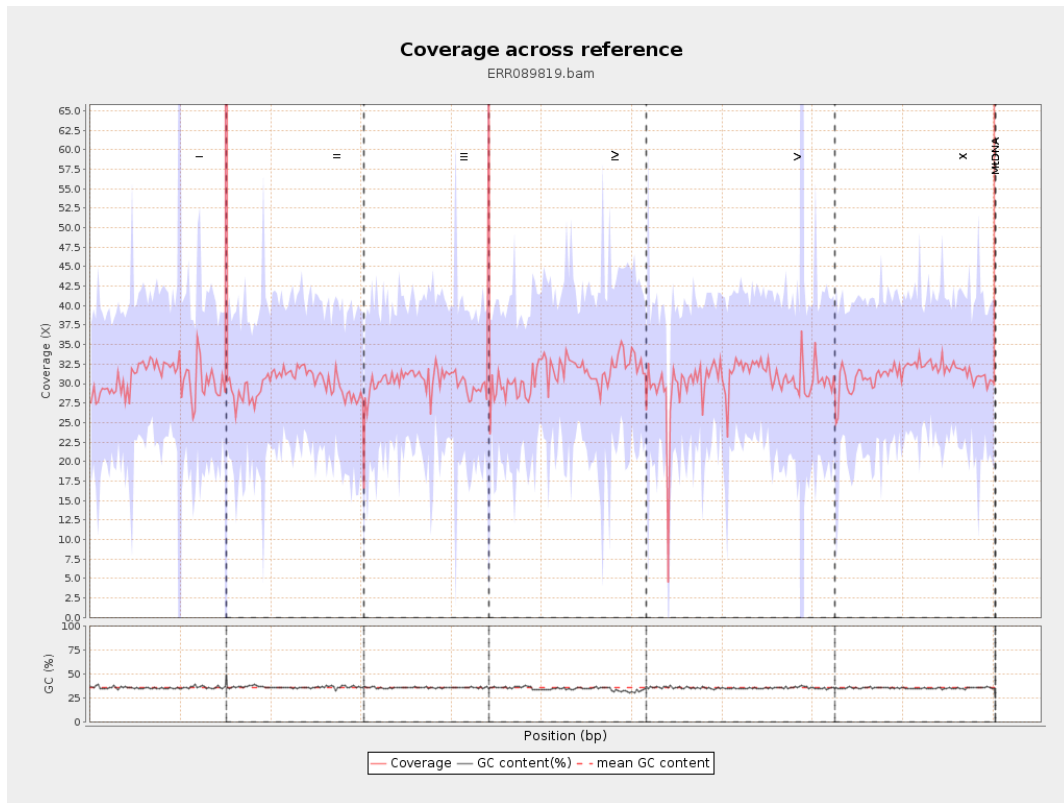
| | |
|--------------------|-----------|
| General error rate | 0.22% |
| Mismatches | 6,868,749 |

2.7. Chromosome stats

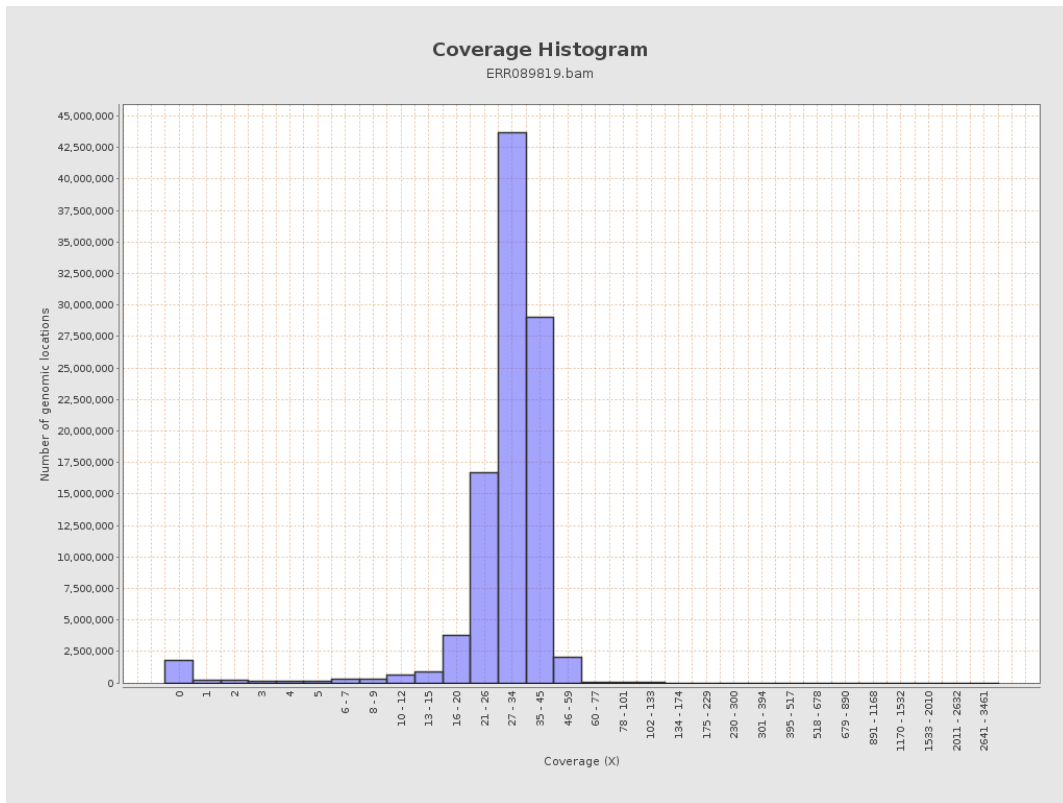
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|------|----------|--------------|---------------|--------------------|
| I | 15072421 | 467935600 | 31.05 | 36.49 |
| II | 15279324 | 457196800 | 29.92 | 9.13 |
| III | 13783682 | 417175000 | 30.27 | 9.81 |
| IV | 17493784 | 546120800 | 31.22 | 10.46 |
| V | 20924143 | 635772800 | 30.38 | 18.85 |
| X | 17718854 | 554131800 | 31.27 | 8.75 |
| | | | | |

| | | | | |
|-------|-------|----------|----------|--------|
| MtDNA | 13794 | 19987200 | 1,448.98 | 346.72 |
|-------|-------|----------|----------|--------|

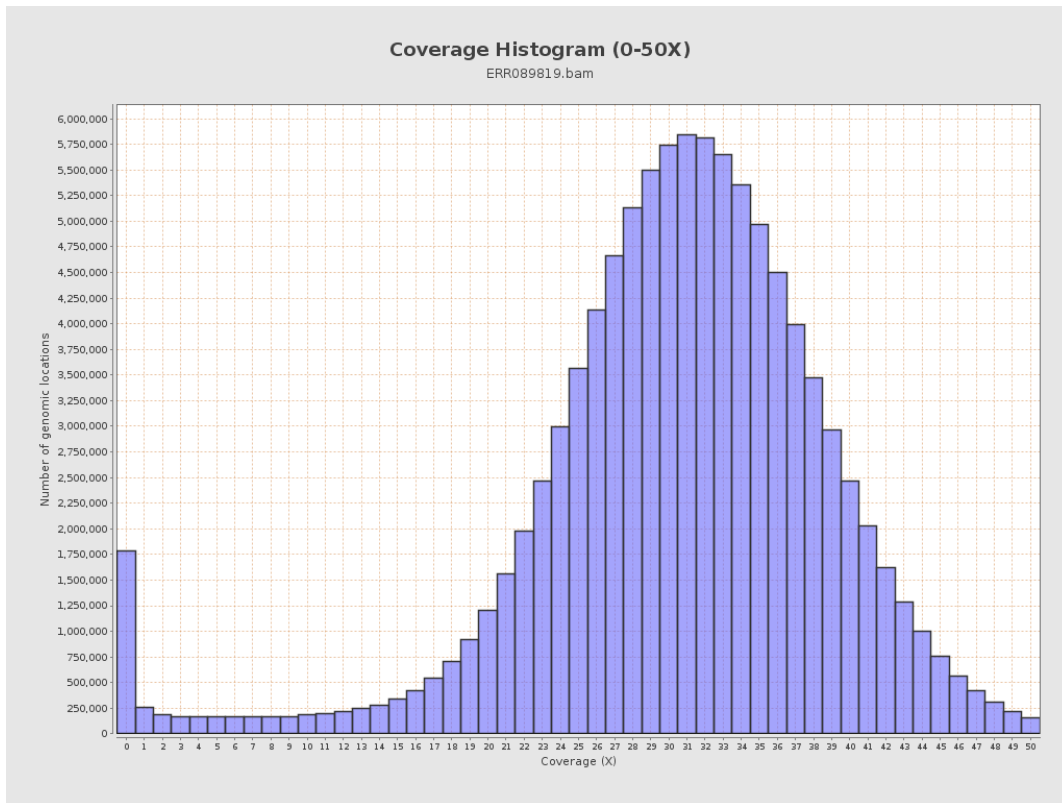
3. Results : Coverage across reference



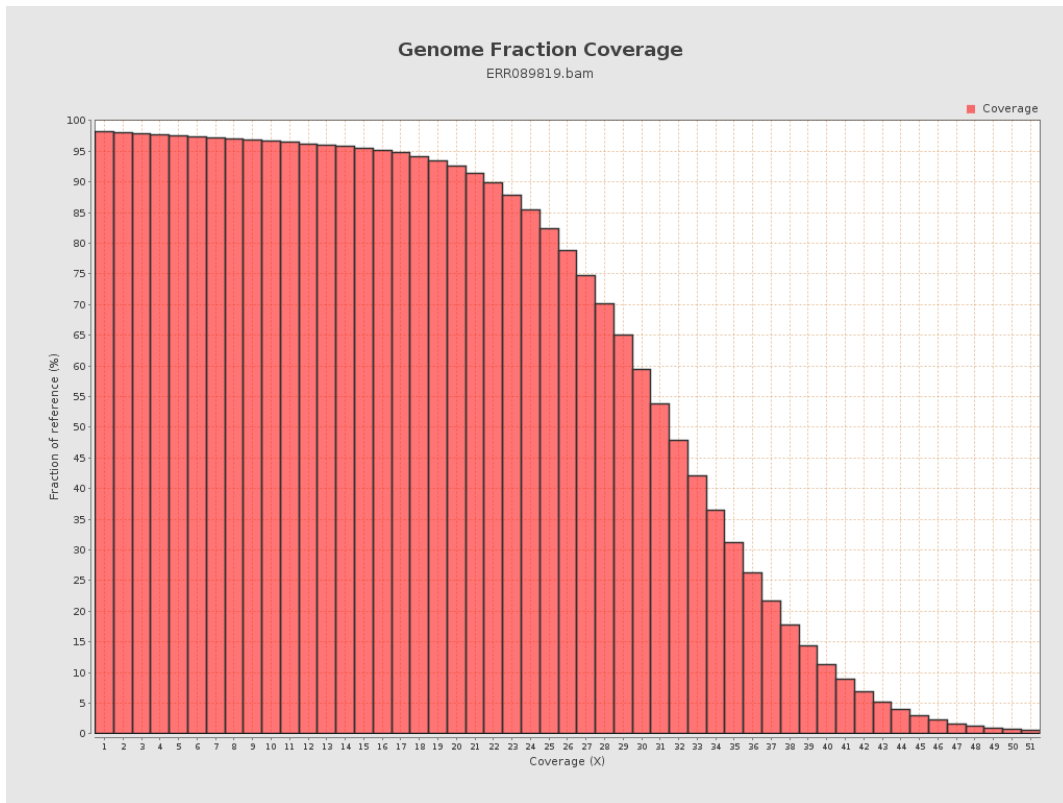
4. Results : Coverage Histogram



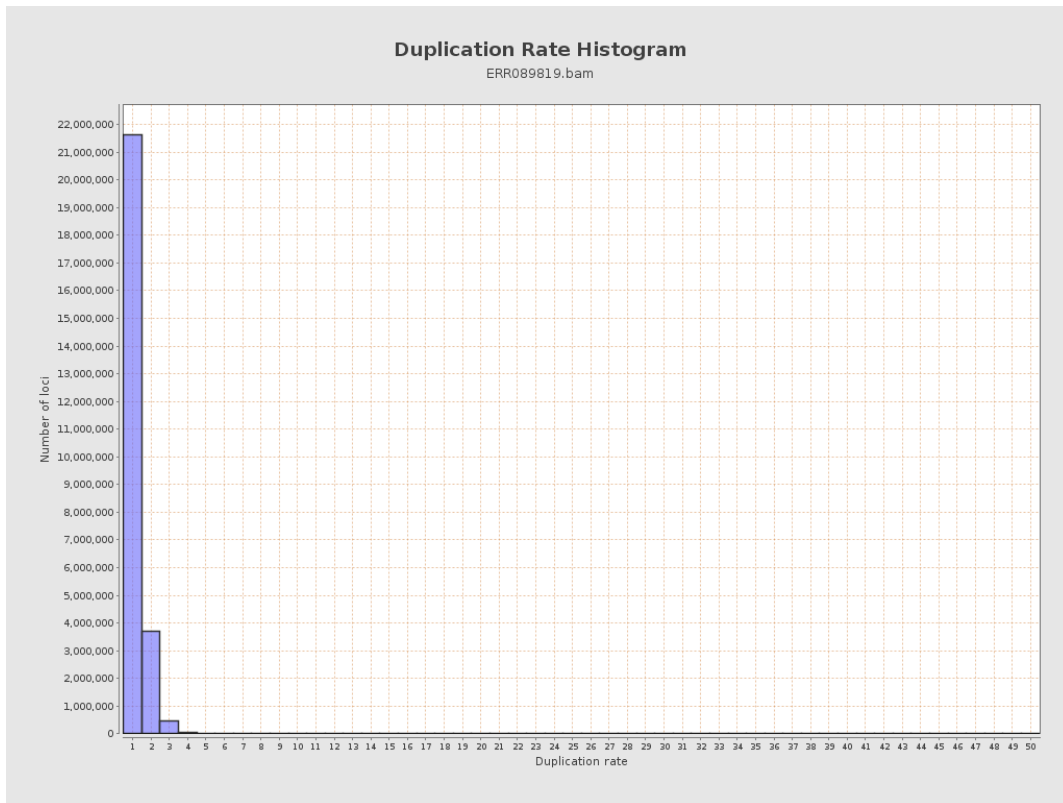
5. Results : Coverage Histogram (0-50X)



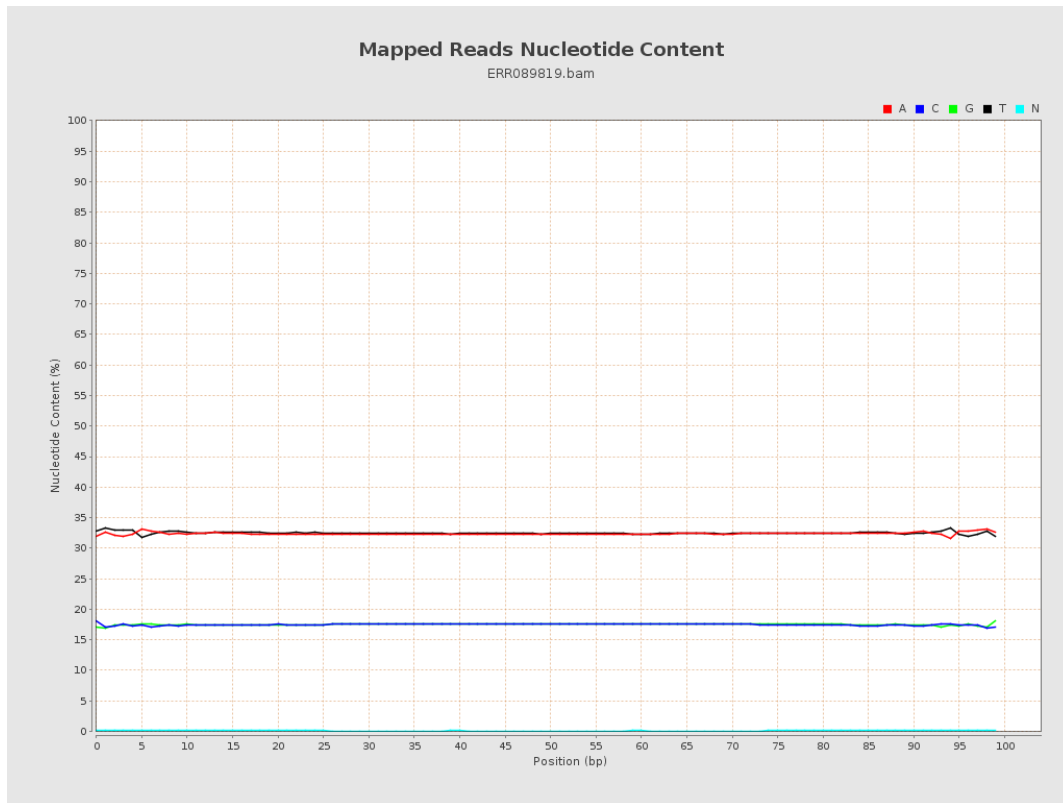
6. Results : Genome Fraction Coverage



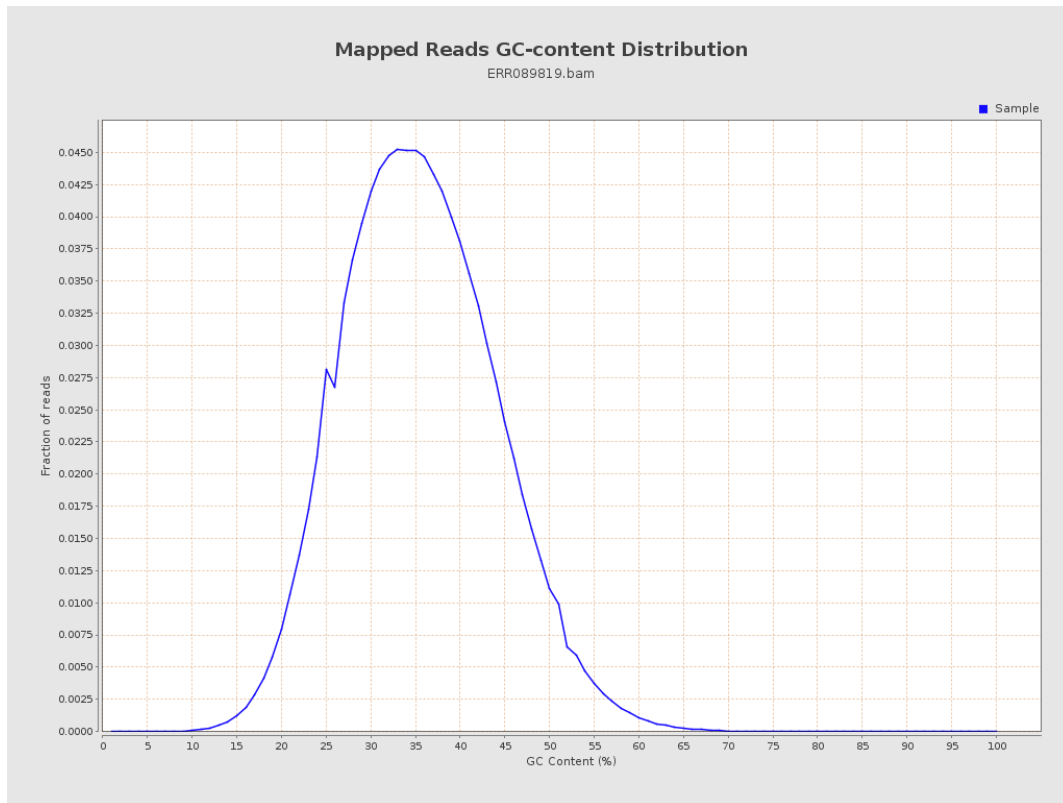
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content



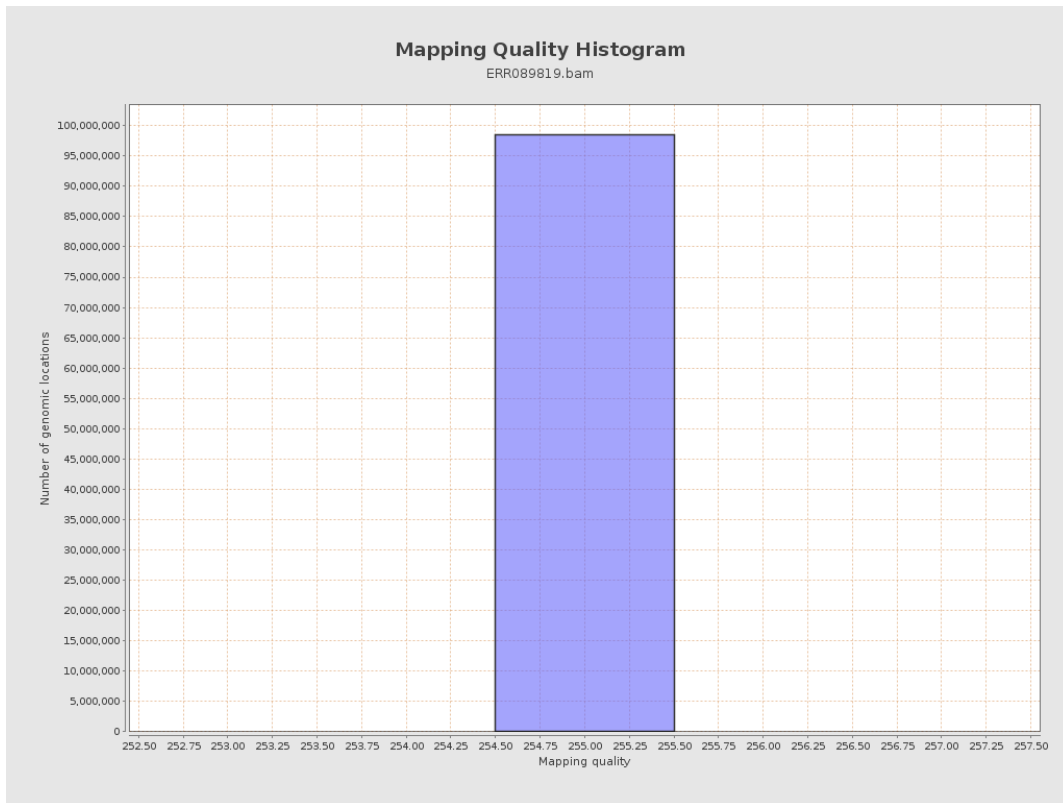
9. Results : Mapped Reads GC-content Distribution



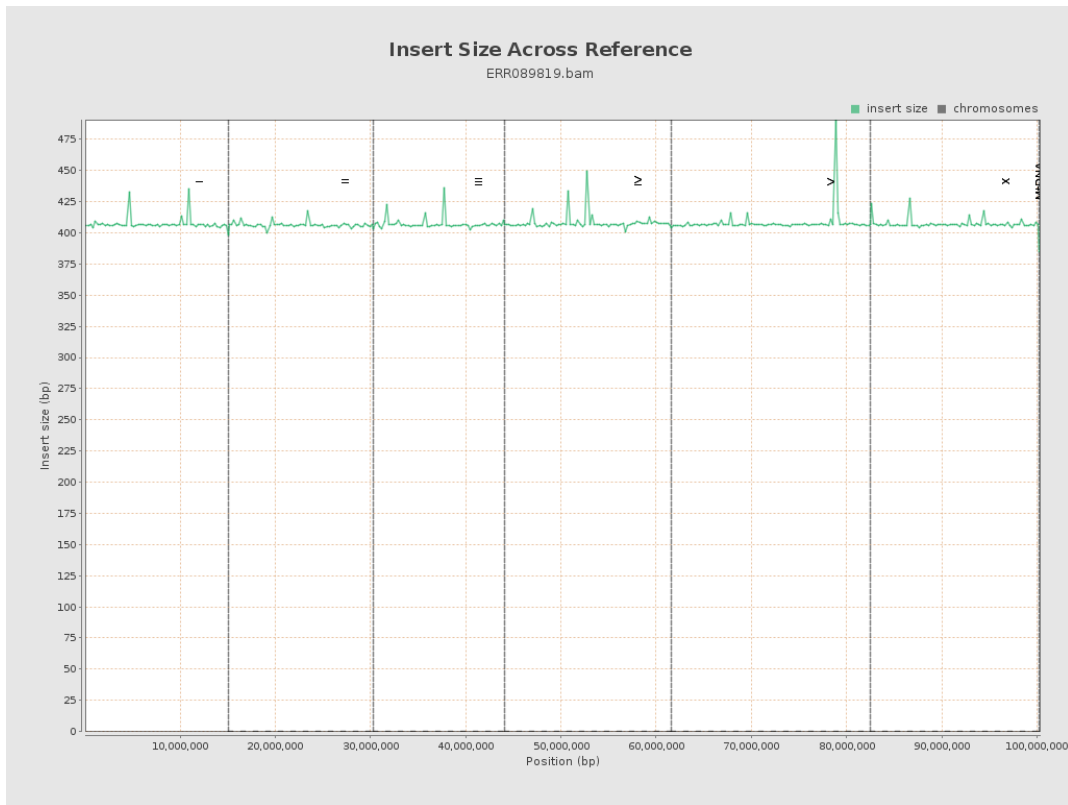
10. Results : Mapping Quality Across Reference



11. Results : Mapping Quality Histogram



12. Results : Insert Size Across Reference



13. Results : Insert Size Histogram

