Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.0-dev
2014/08/26 14:52:42

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
Analysis date:	Tue Aug 26 14:52:41 CEST 2014
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%
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	24.97

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	36.46
II	15279324	457196800	29.92	9.01
III	13783682	417175000	30.27	9.71
IV	17493784	546120800	31.22	10.35
V	20924143	635772800	30.38	18.79
X	17718854	554131800	31.27	8.62
MtDNA	13794	19987200	1,448.98	339.75

3. Results : Coverage across reference

Coverage across reference
ERR089819.bam

4. Results : Coverage Histogram
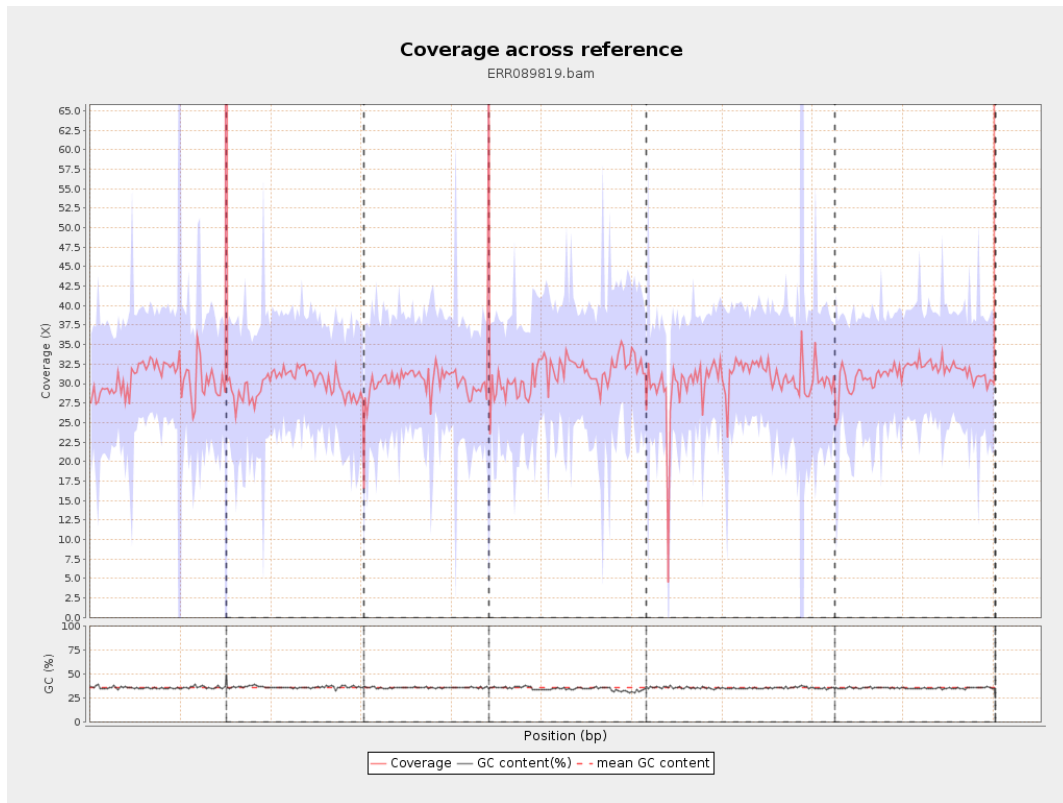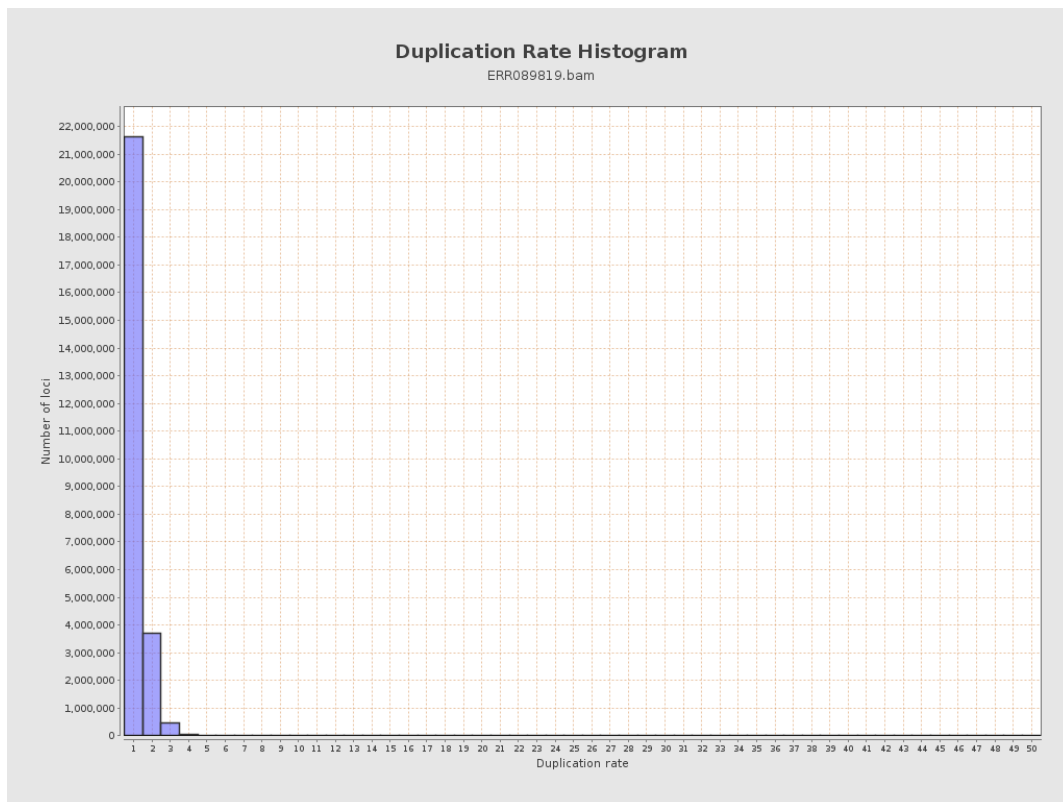

Coverage Histogram
ERR089819.bam
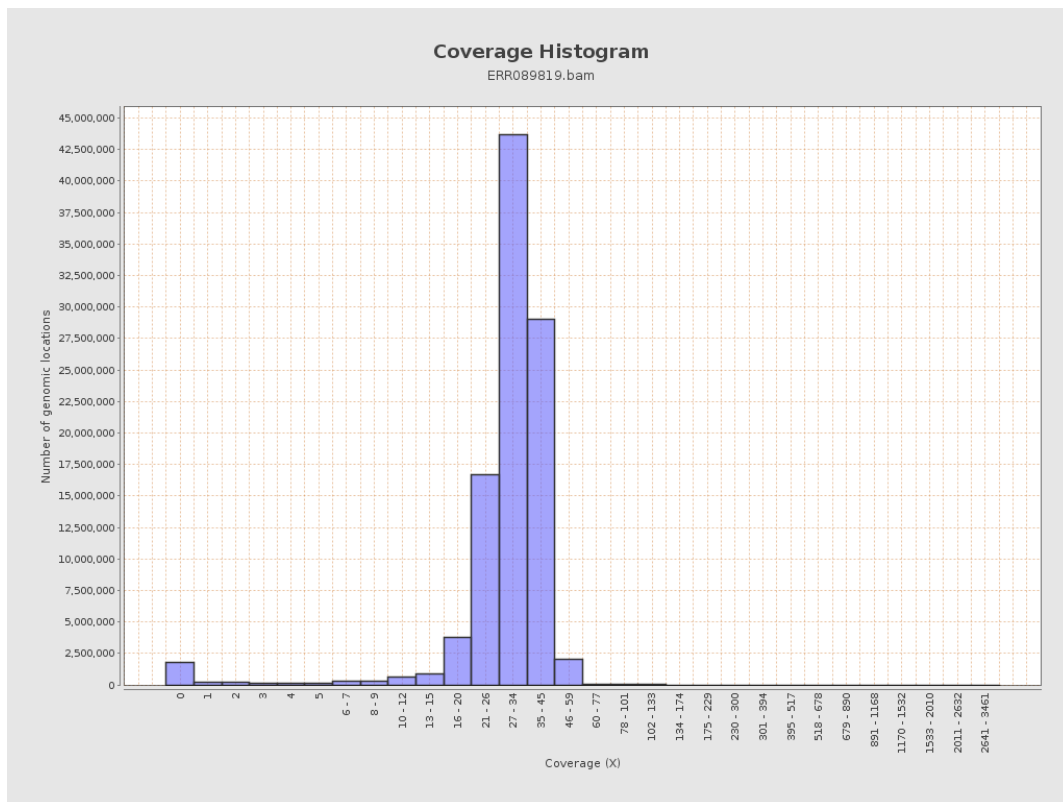
5. Results : Coverage Histogram (0-50X)
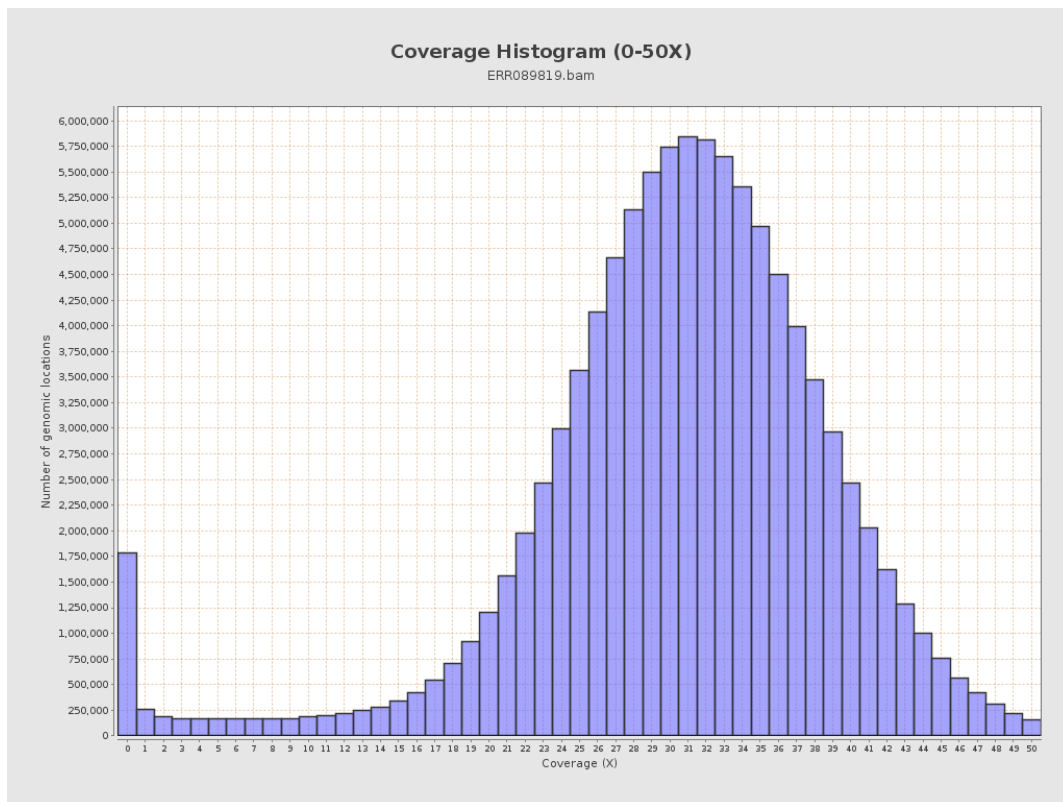
6. Results : Genome Fraction Coverage
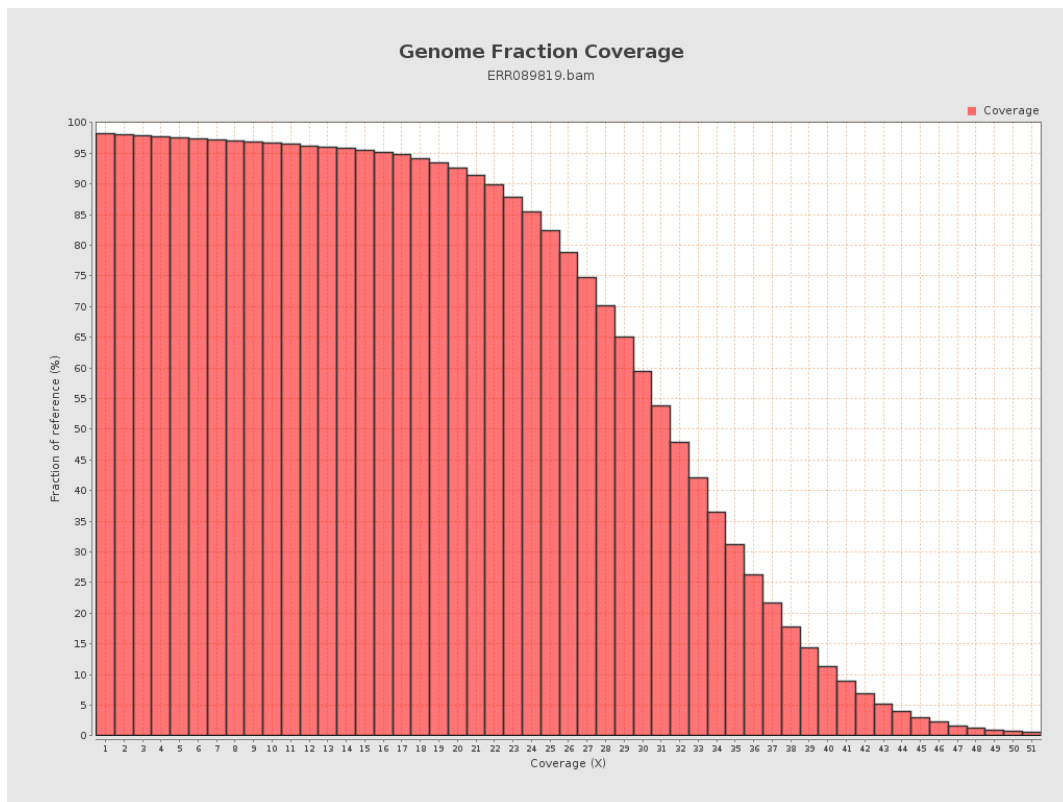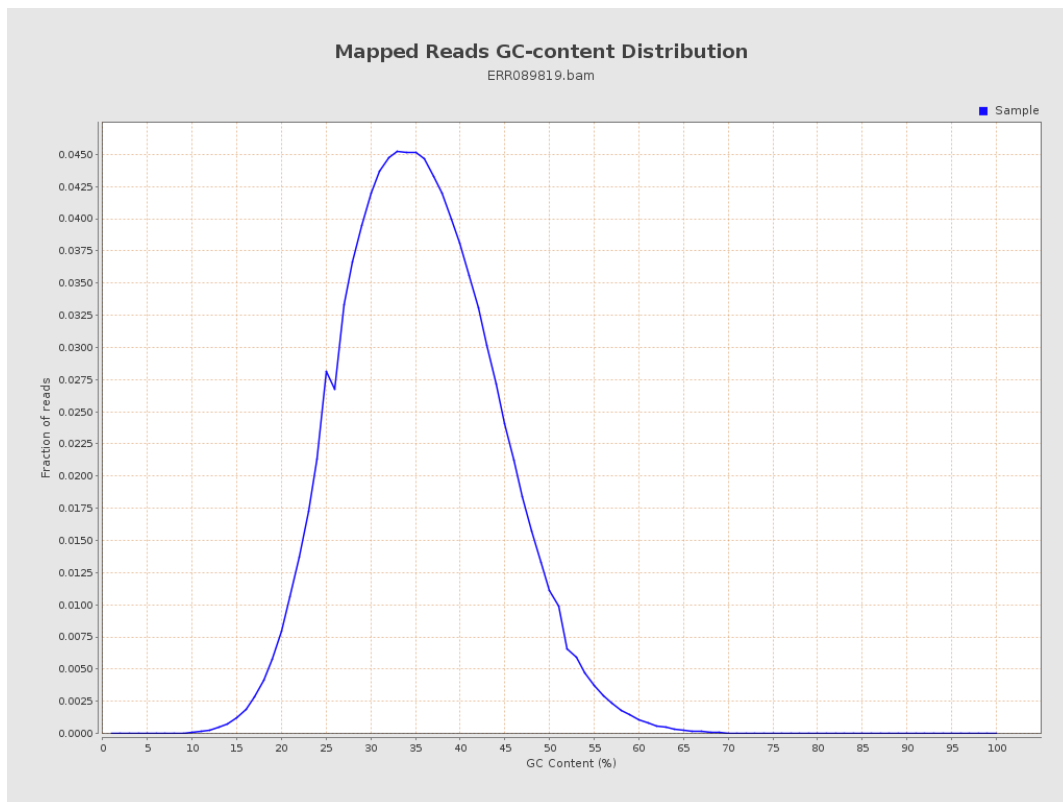
7. Results : Duplication Rate Histogram

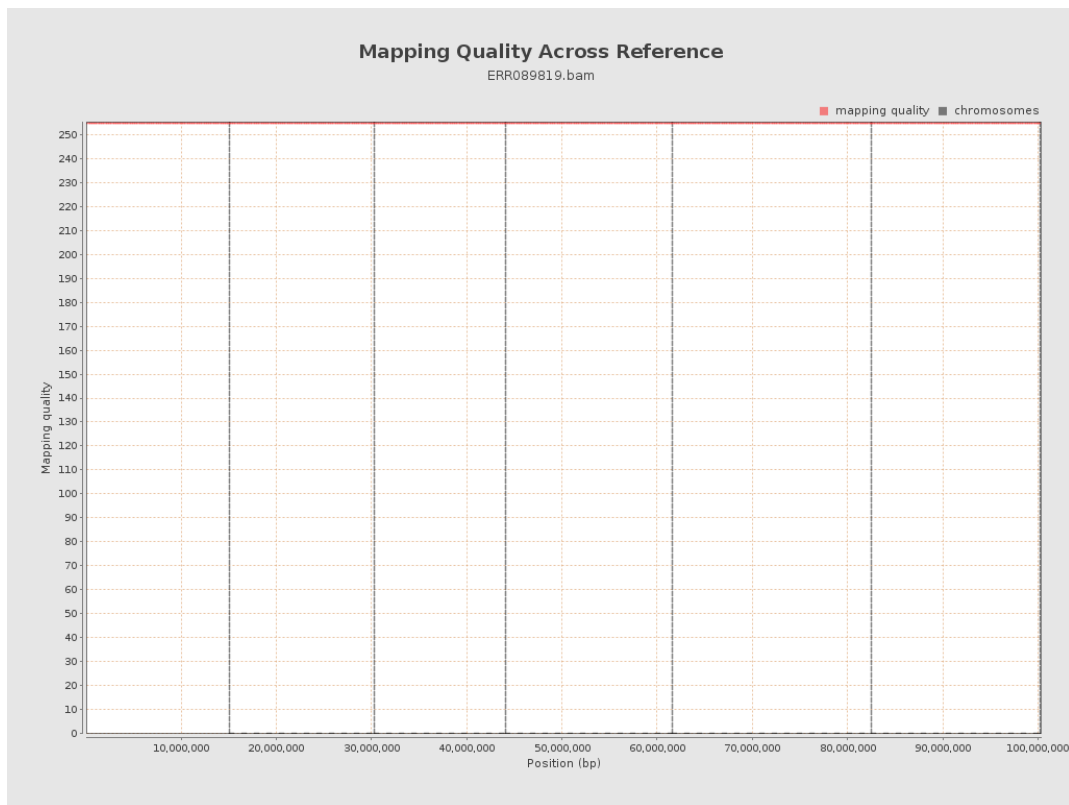**Duplication Rate Histogram**
ERR089819.bam

8. Results : Mapped Reads Nucleotide Content
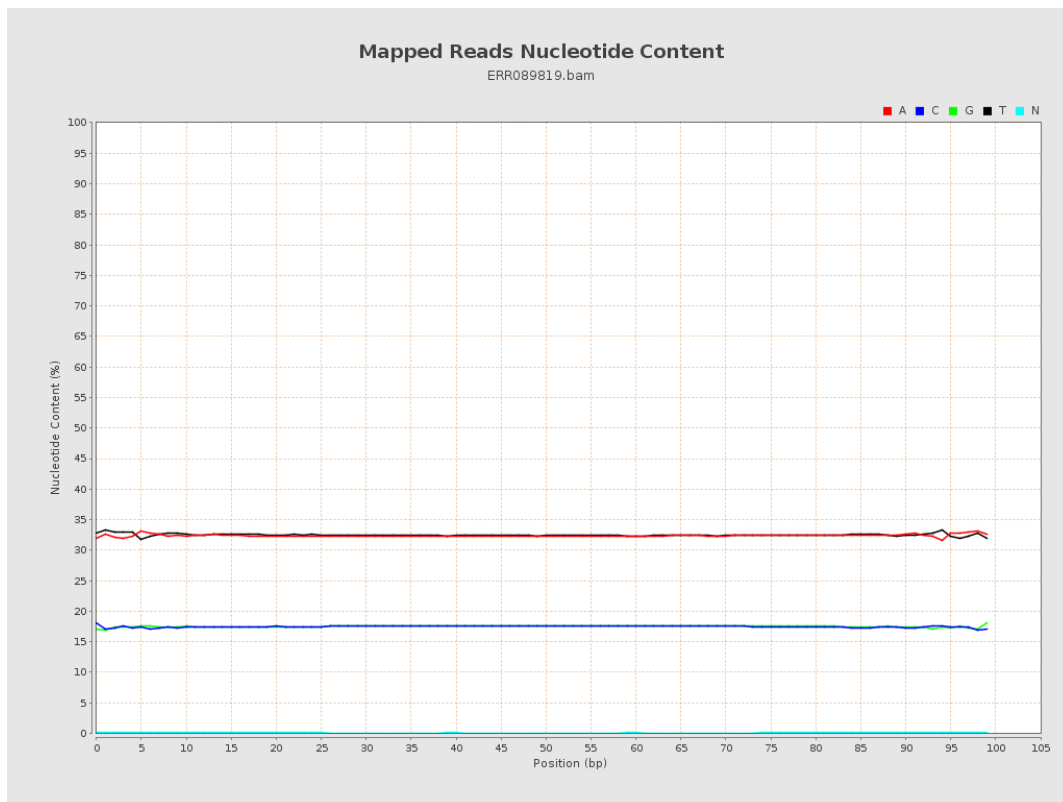
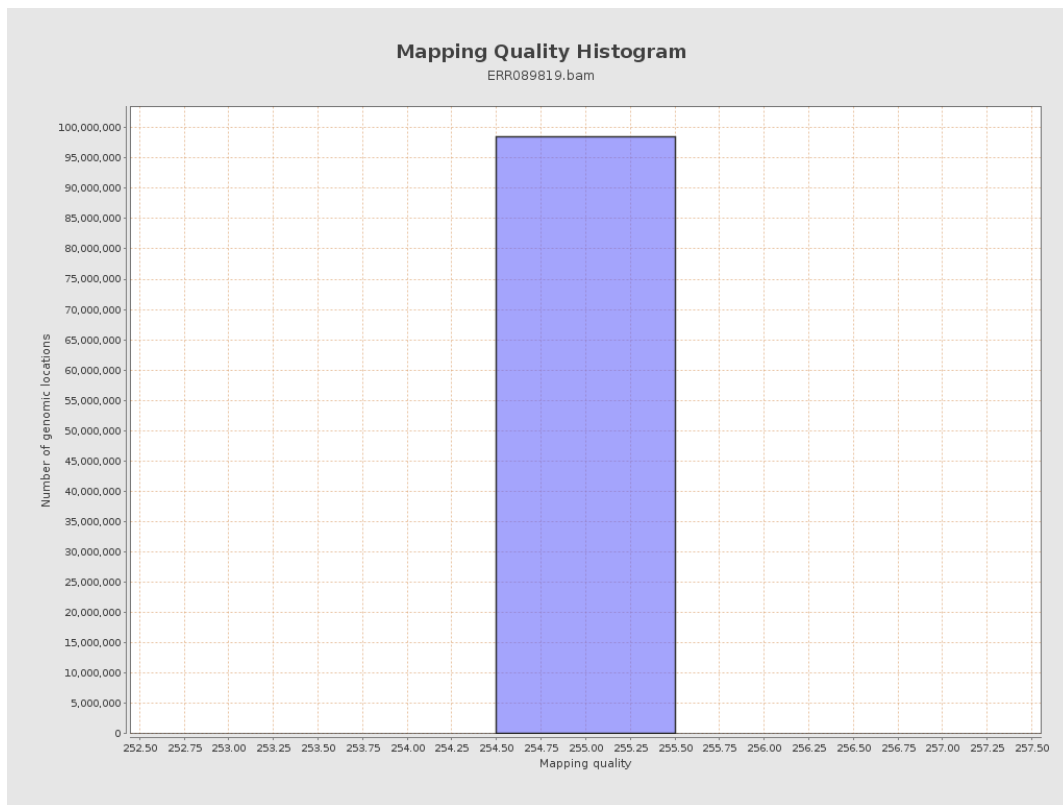# 9. Results : Mapped Reads GC-content Distribution

10. Results : Mapping Quality Across Reference

11. Results : Mapping Quality Histogram

Mapping Quality Histogram
ERR089819.bam

12. Results : Insert Size Across Reference

Insert Size Across Reference
ERR089819.bam
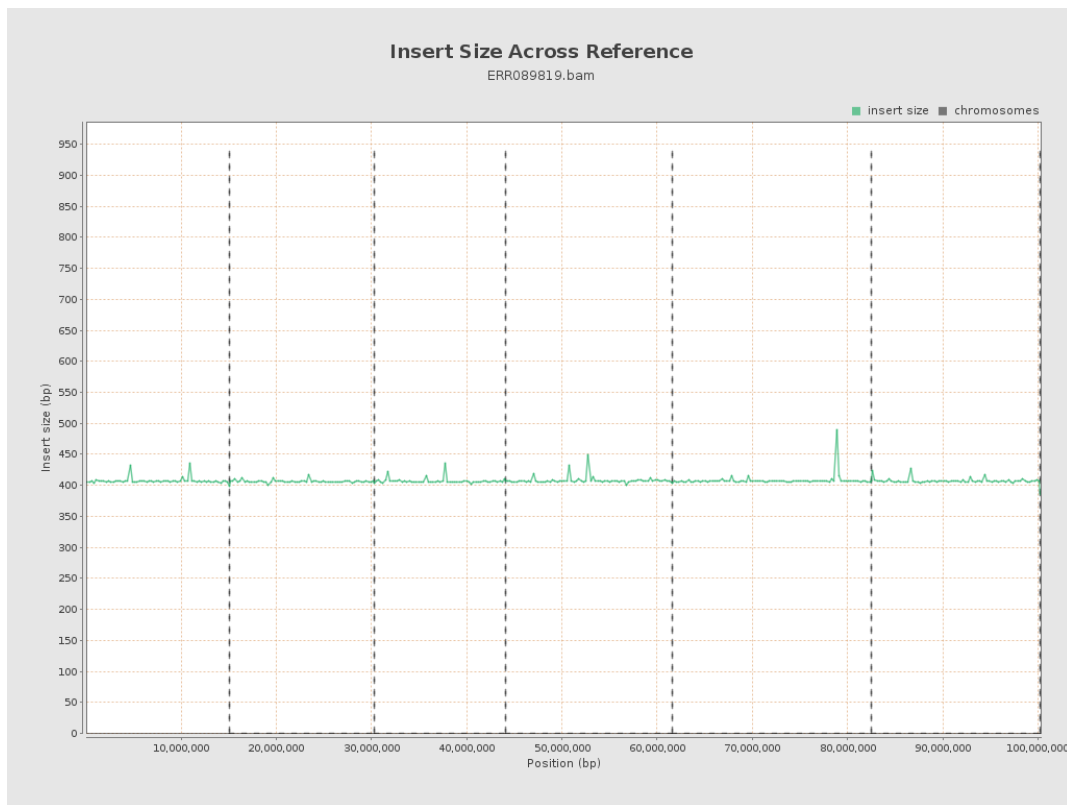
13. Results : Insert Size Histogram