Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.0
2016/05/19 11:53:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/export/home/amirh/novoalign_testing/outputBAM/p10sorted.bam -c -nw 400
-hm 3
```

1.2. Alignment

BAM file:	/export/home/amirh/novoalign_testing /outputBAM/p10sorted.bam
Program:	novoalign (V3.02.12)
Size of a homopolymer:	3
Number of windows:	400
Analysis date:	Thu May 19 08:50:45 MYT 2016
Draw chromosome limits:	yes

2. Summary

2.1. Globals

Reference size	119,667,750
Number of reads	11,947,007
Mapped reads	5,492,123 / 45.97%
Unmapped reads	6,454,884 / 54.03%
Paired reads	0 / 0%
Read min/max/mean length	100 / 100 / 100
Clipped reads	7,872 / 0.07%
Duplication rate	2.38%

2.2. ACGT Content

Number/percentage of A's	175,927,603 / 32.03%
Number/percentage of C's	98,764,260 / 17.98%
Number/percentage of T's	175,719,306 / 32%
Number/percentage of G's	98,793,115 / 17.99%
Number/percentage of N's	0 / 0%
GC Percentage	35.97%

2.3. Coverage

Mean	4.59
Standard Deviation	2.31

2.4. Mapping Quality

Mean Mapping Quality	68.68

2.5. Mismatches and indels

General error rate	0.01%
Mismatches	62,176

2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
Pt	154478	486492	3.15	2.87
Mt	366924	670191	1.83	2.58
4	18585056	86096313	4.63	2.27
2	19698289	90941622	4.62	2.29
3	23459830	108875170	4.64	2.27
5	26975502	124310977	4.61	2.3
1	30427671	137823577	4.53	2.35

3. Results : Coverage across reference

4. Results : Coverage Histogram

Coverage Histogram
p10sorted.bam
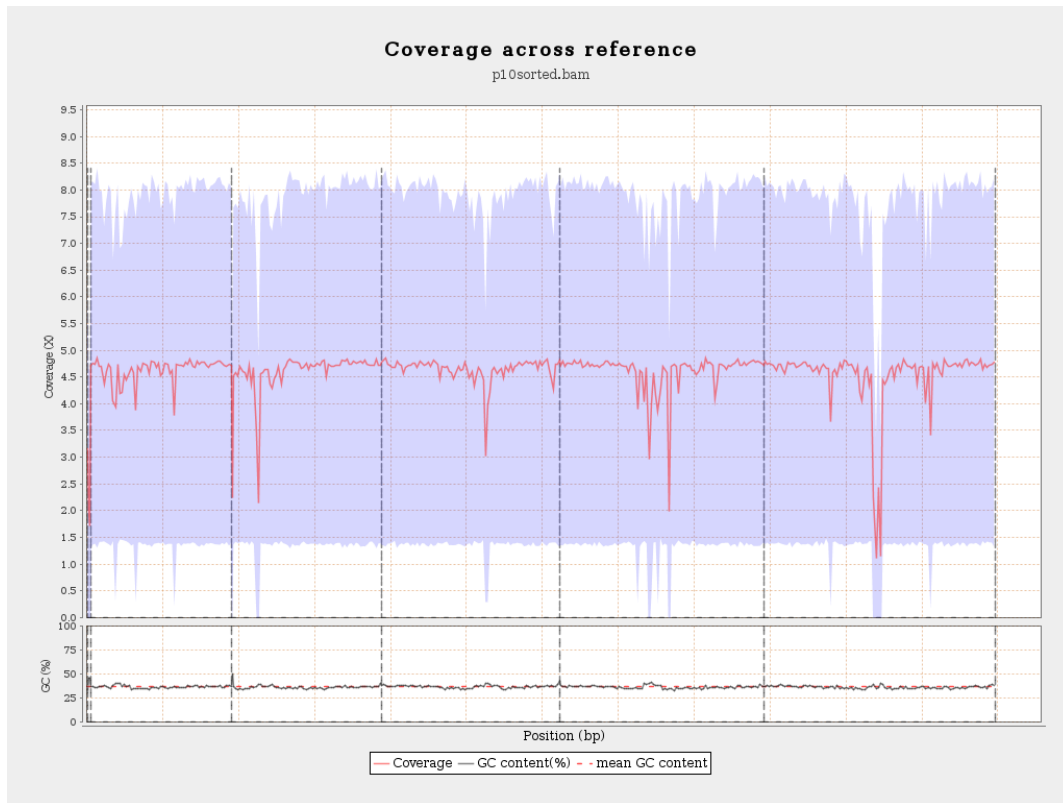
5. Results : Coverage Histogram (0-50X)
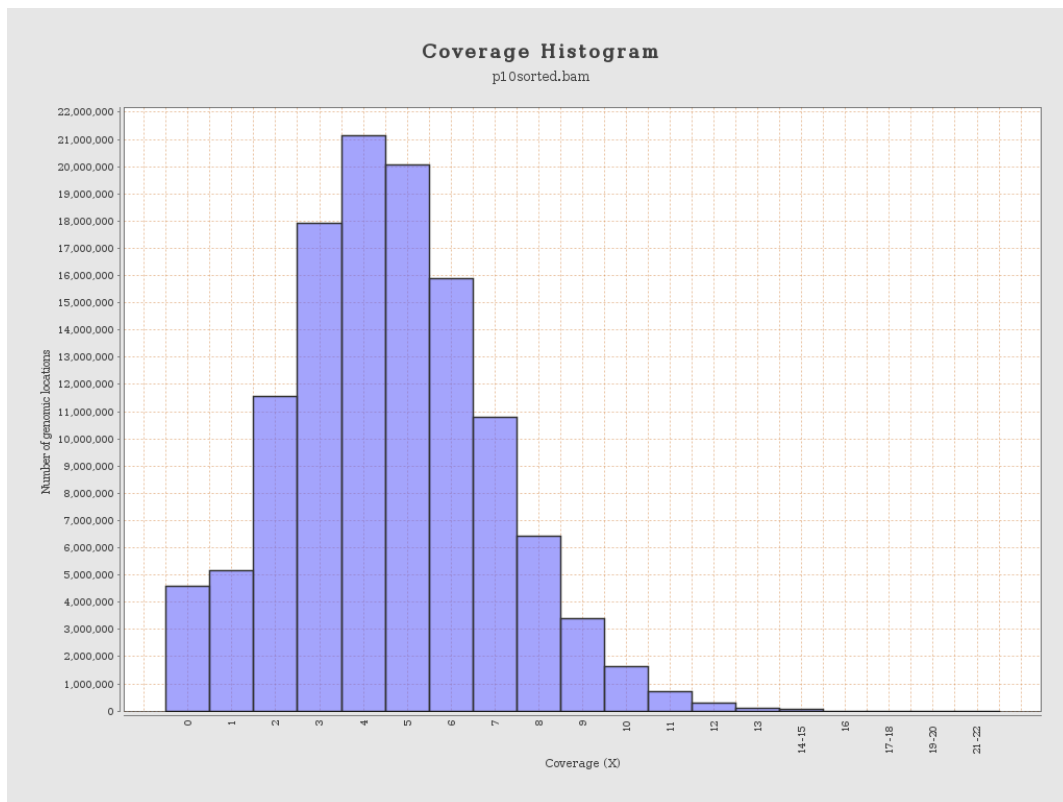
Coverage Histogram (0-50X)
p10sorted.bam
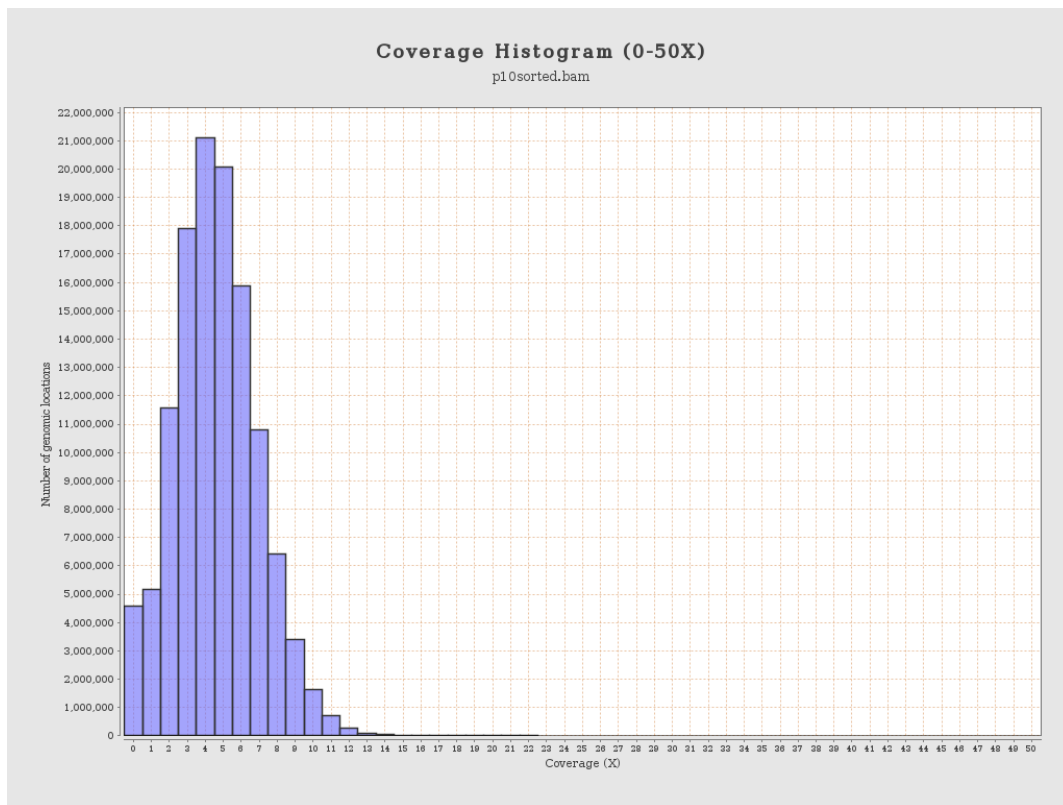
6. Results : Genome Fraction Coverage
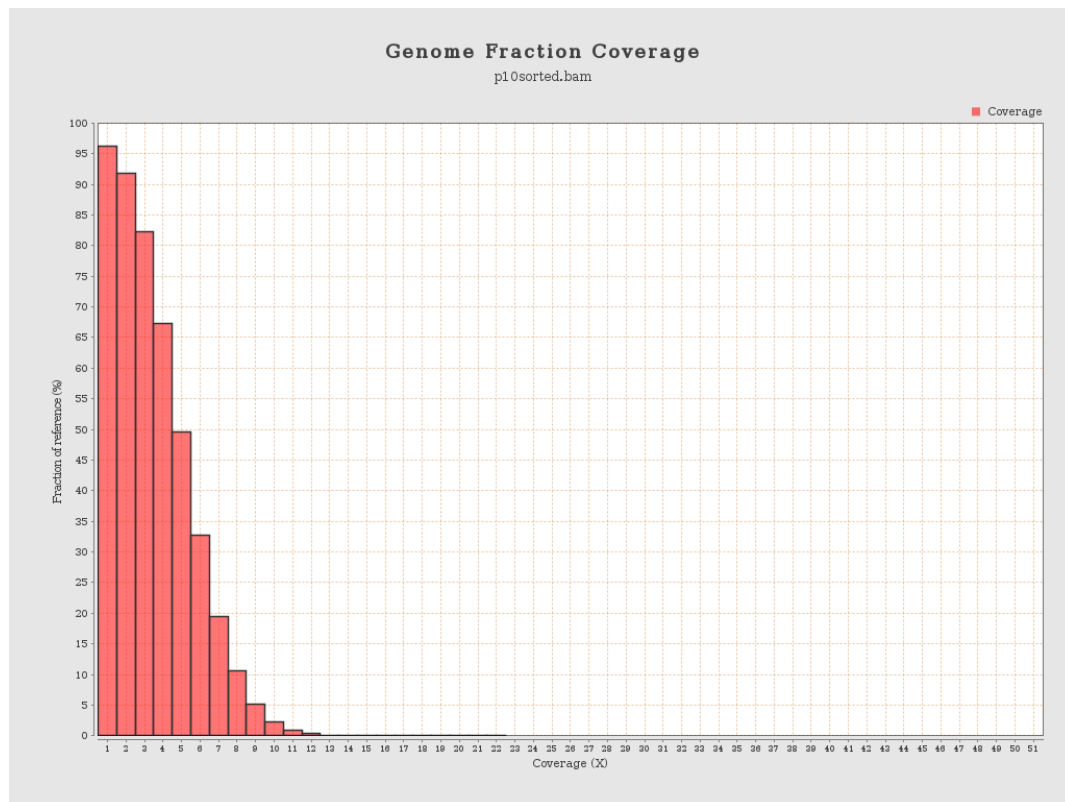
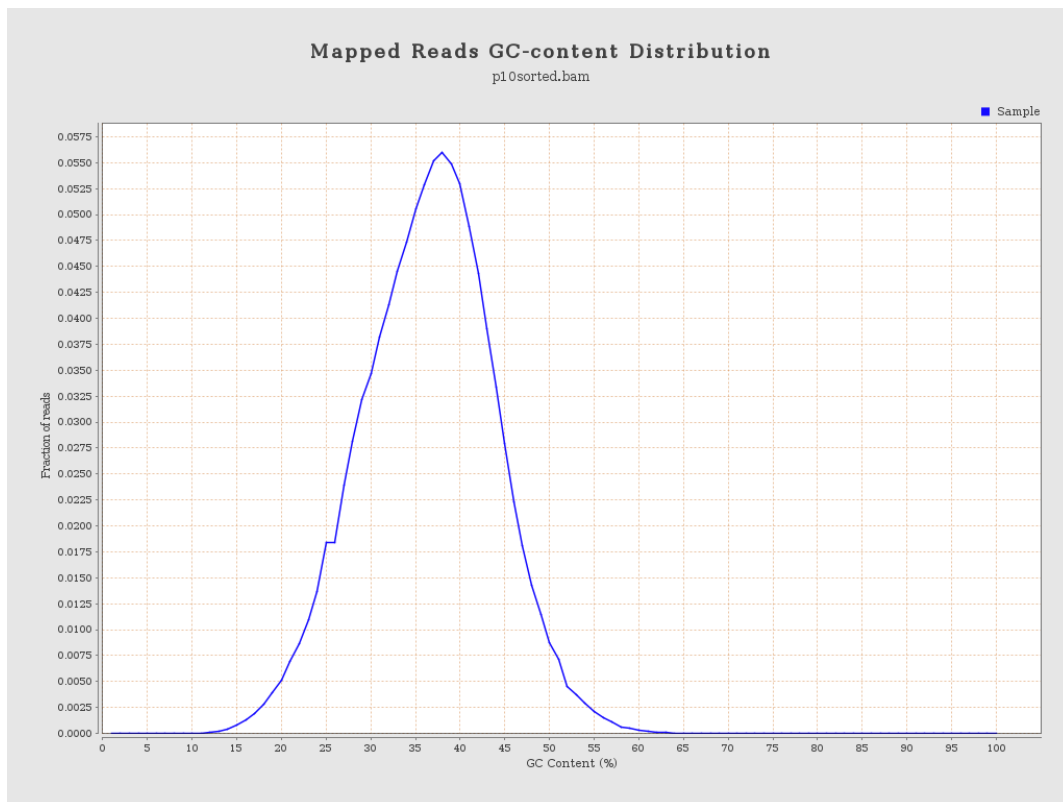# 7. Results : Duplication Rate Histogram
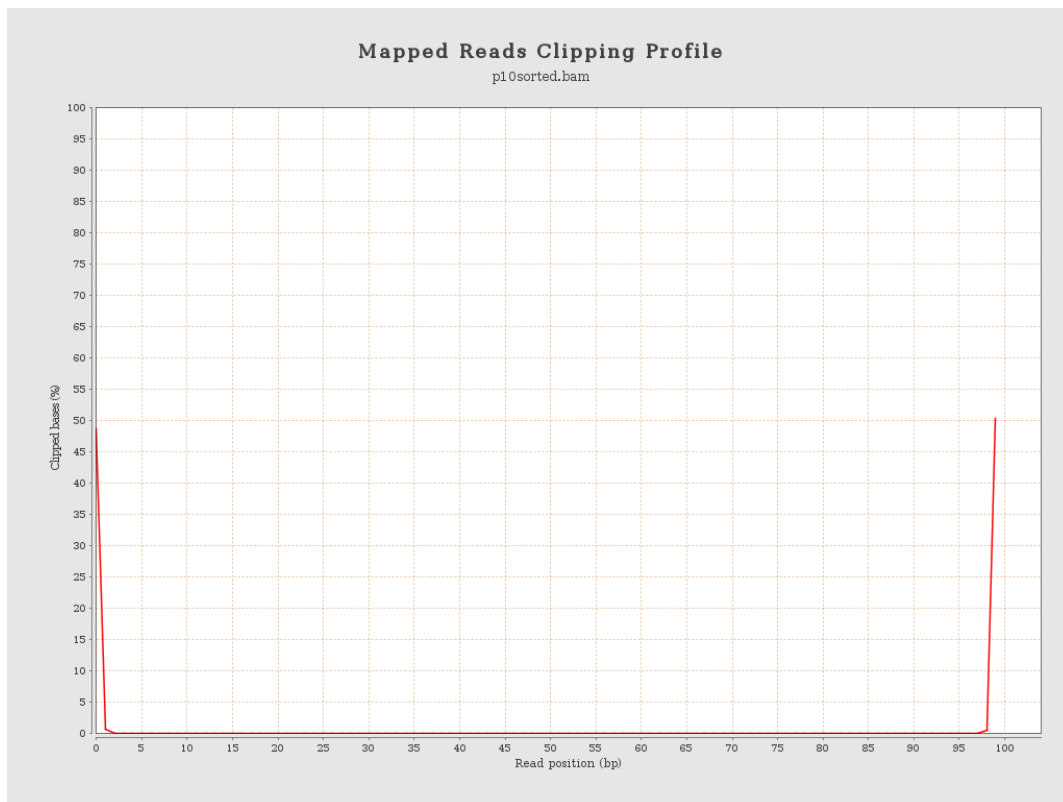

Duplication Rate Histogram
p10sorted.bam
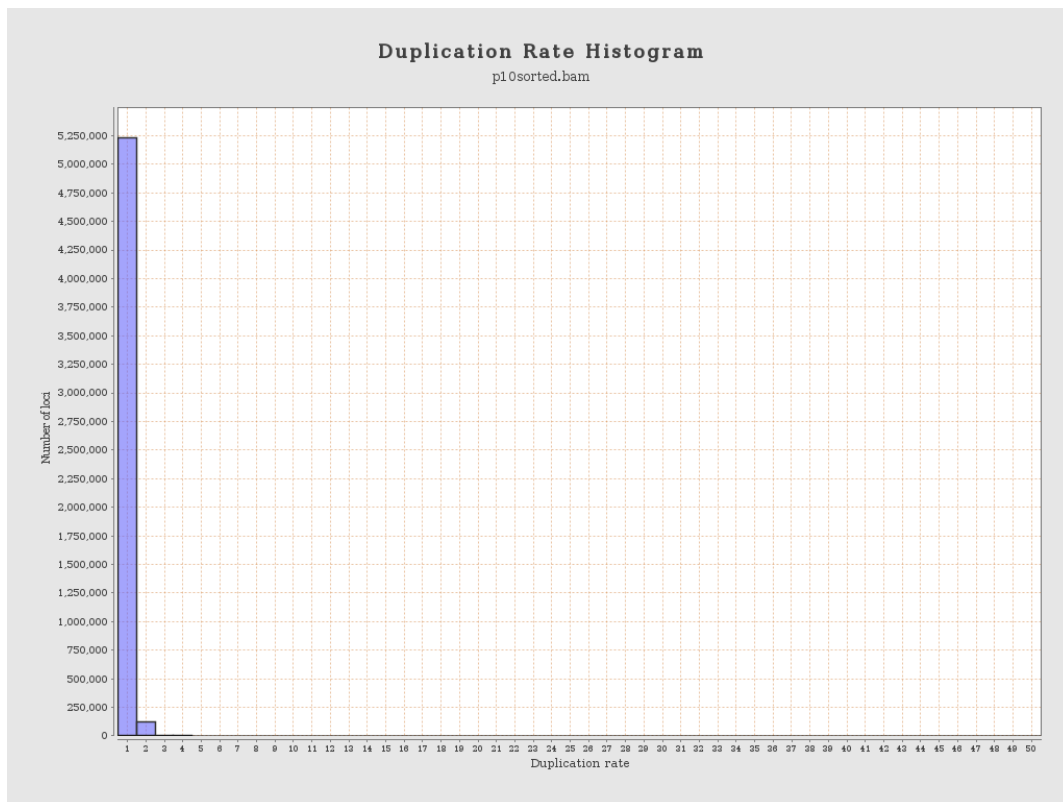
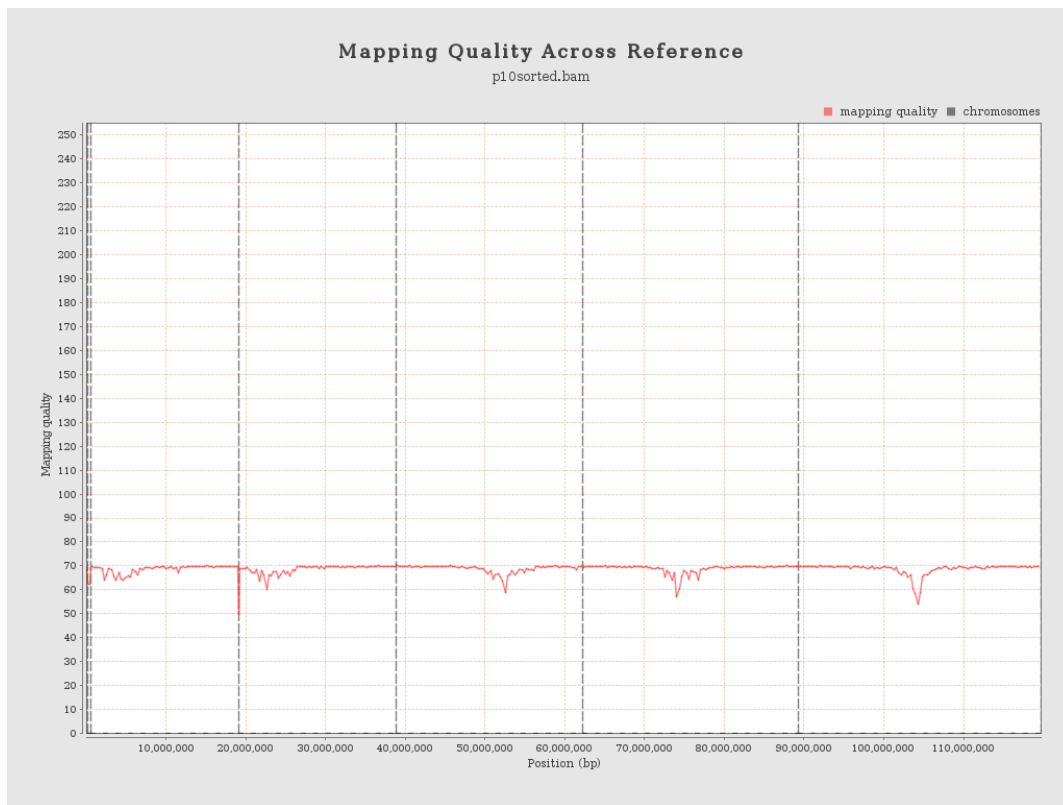# 8. Results : Mapped Reads Nucleotide Content
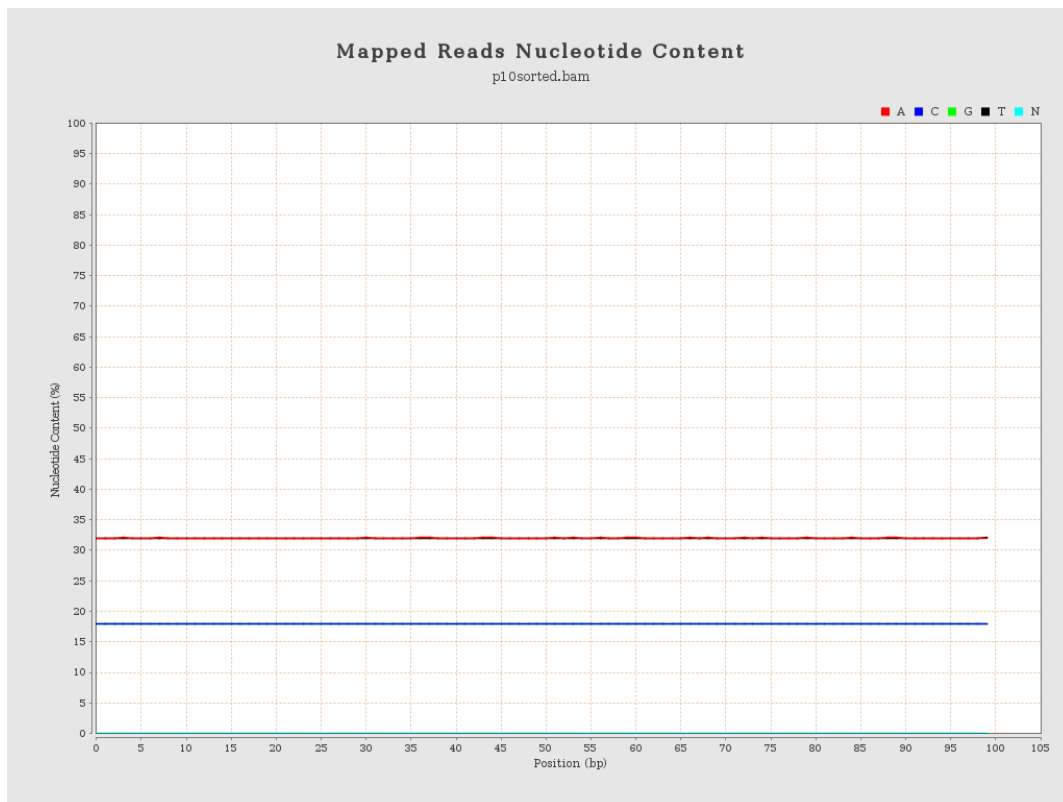
9. Results : Mapped Reads GC-content Distribution

10. Results : Mapped Reads Clipping Profile

11. Results : Mapping Quality Across Reference

12. Results : Mapping Quality Histogram

Mapping Quality Histogram
p10sorted.bam