Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.0
2016/05/19 11:51:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/export/home/amirh/novoalign_testing/outputBAM/p40sorted.bam -c -nw 400
-hm 3
```

1.2. Alignment

BAM file:	/export/home/amirh/novoalign_testing /outputBAM/p40sorted.bam
Program:	novoalign (V3.02.12)
Size of a homopolymer:	3
Number of windows:	400
Analysis date:	Thu May 19 09:17:42 MYT 2016
Draw chromosome limits:	yes

2. Summary

2.1. Globals

Reference size	119,667,750
Number of reads	11,947,007
Mapped reads	11,022,579 / 92.26%
Unmapped reads	924,428 / 7.74%
Paired reads	0 / 0%
Read min/max/mean length	100 / 100 / 100
Clipped reads	309,246 / 2.59%
Duplication rate	4.72%

2.2. ACGT Content

Number/percentage of A's	352,239,694 / 31.97%
Number/percentage of C's	198,807,434 / 18.04%
Number/percentage of T's	351,899,635 / 31.94%
Number/percentage of G's	198,813,566 / 18.05%
Number/percentage of N's	0 / 0%
GC Percentage	36.09%

2.3. Coverage

Mean	9.21
Standard Deviation	3.48

2.4. Mapping Quality

Mean Mapping Quality	68.65

2.5. Mismatches and indels

General error rate	0.63%
Mismatches	6,935,604

2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
Pt	154478	968684	6.27	5.13
Mt	366924	1308422	3.57	4.7
4	18585056	172690813	9.29	3.38
2	19698289	182404776	9.26	3.42
3	23459830	218421433	9.31	3.36
5	26975502	249268945	9.24	3.45
1	30427671	276697576	9.09	3.61

3. Results : Coverage across reference

Coverage across reference
p40sorted.bam
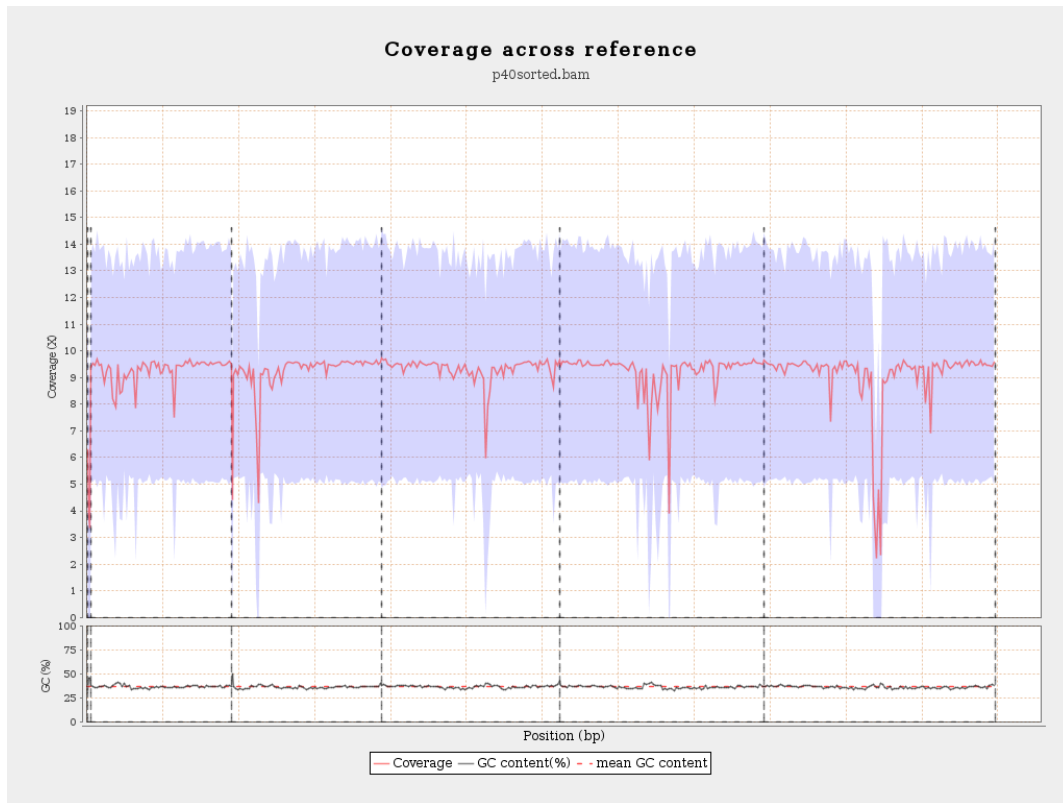
4. Results : Coverage Histogram

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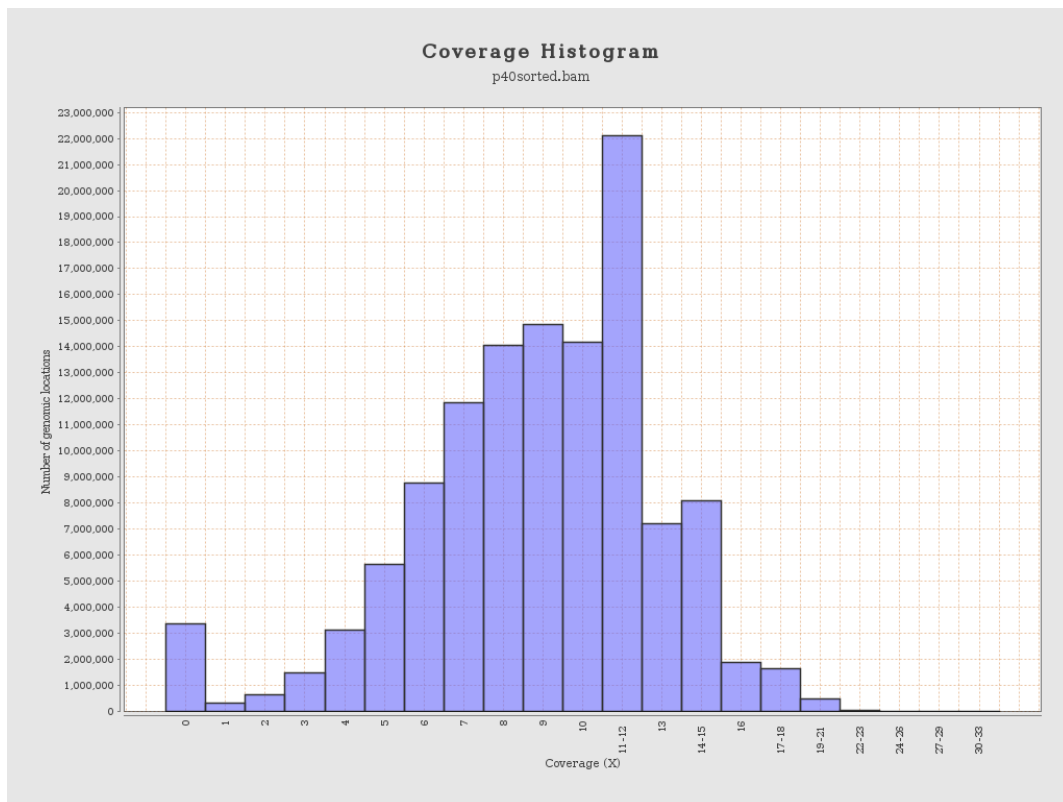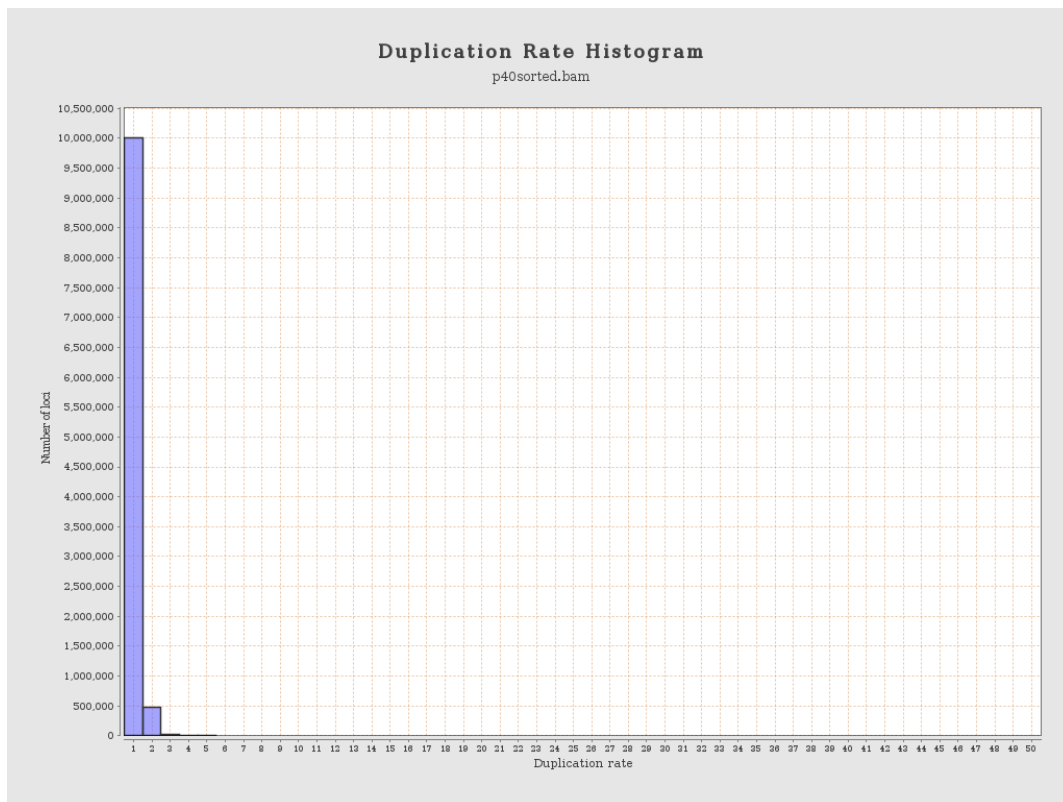

Coverage Histogram (0-50X)
p40sorted.bam
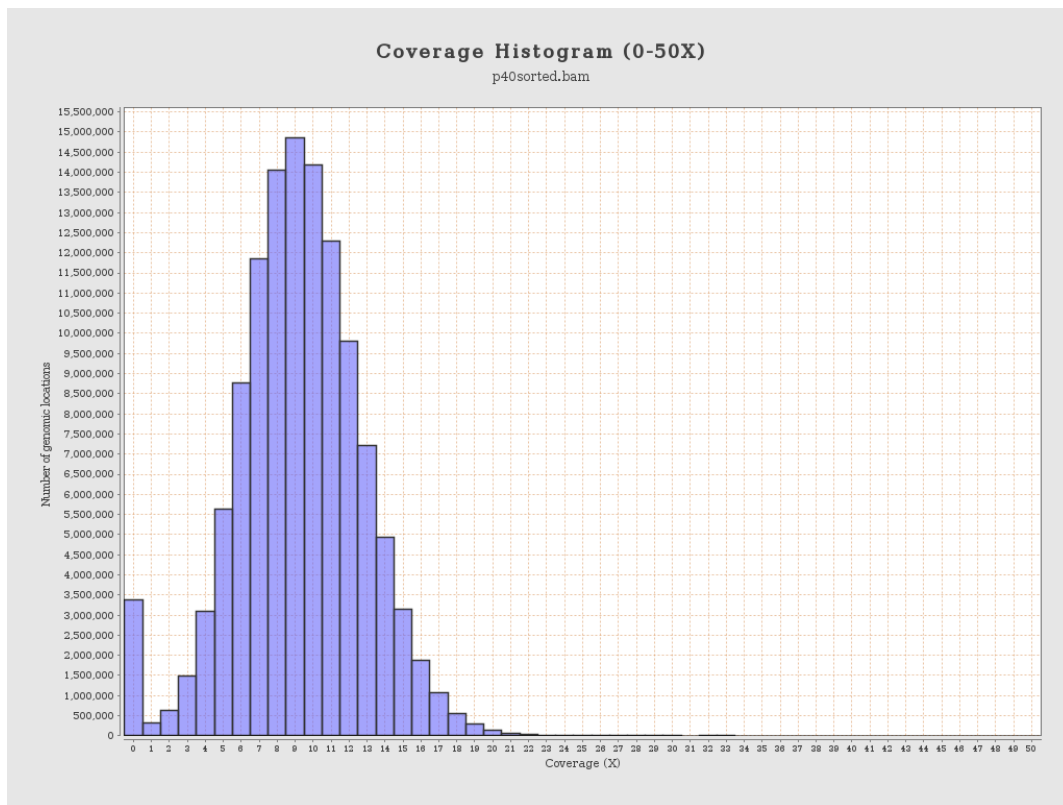
6. Results : Genome Fraction Coverage
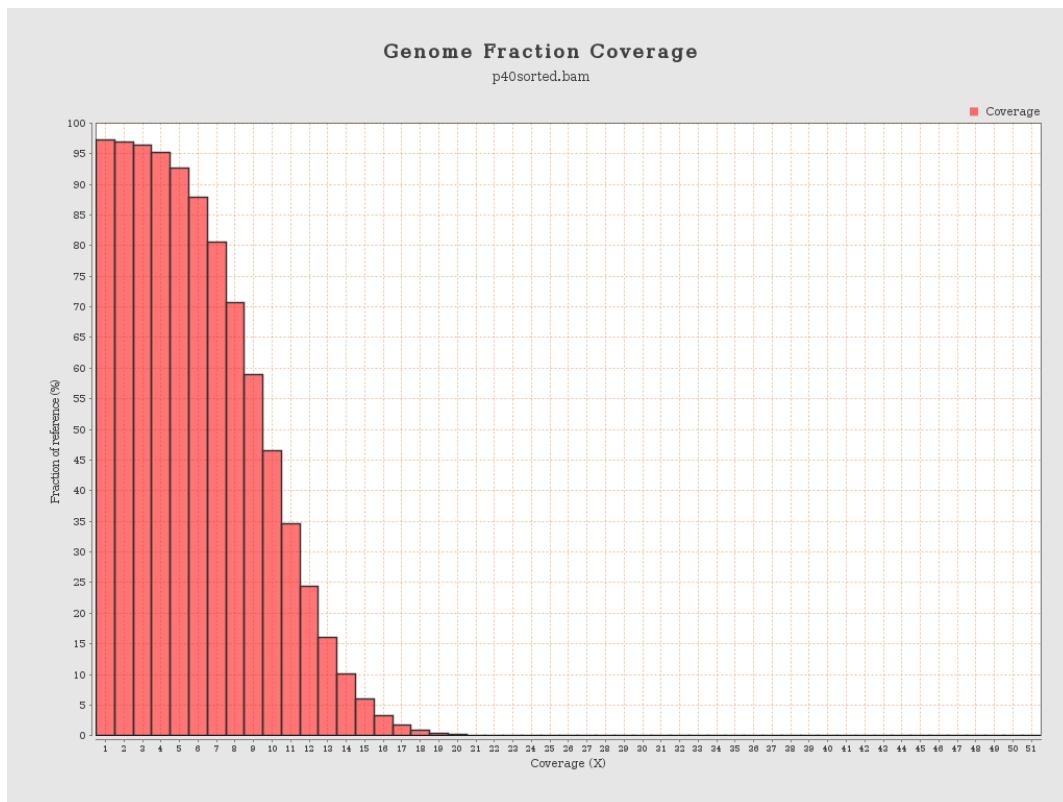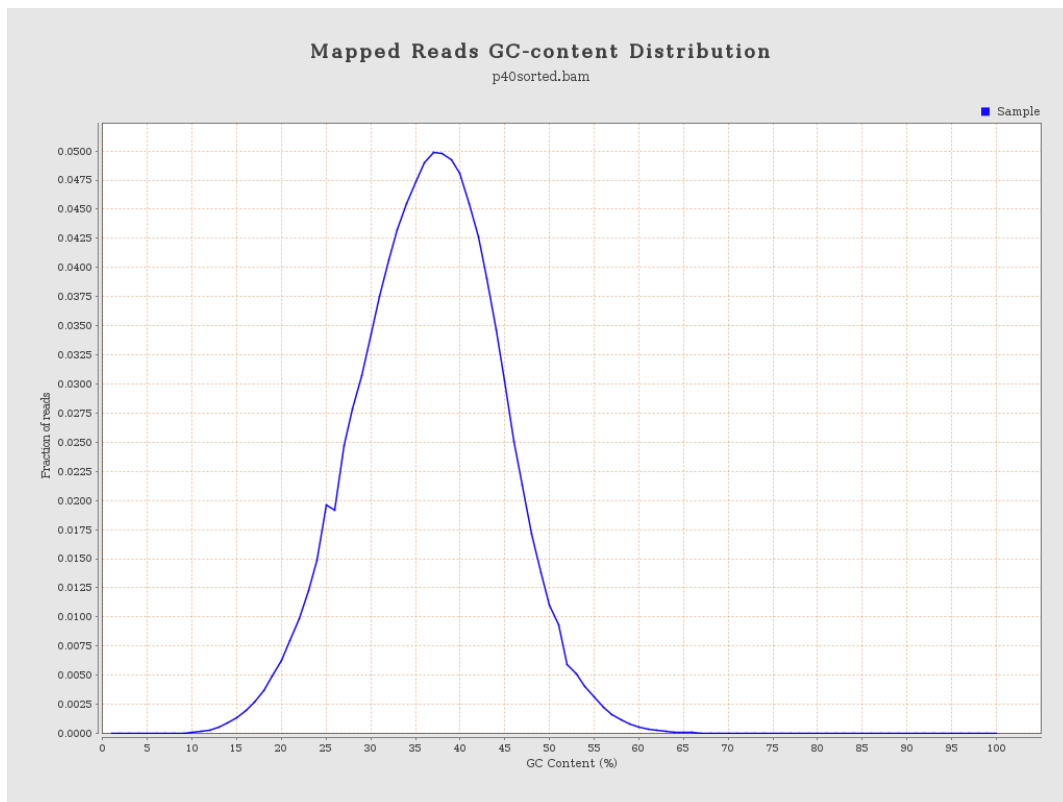
7. Results : Duplication Rate Histogram
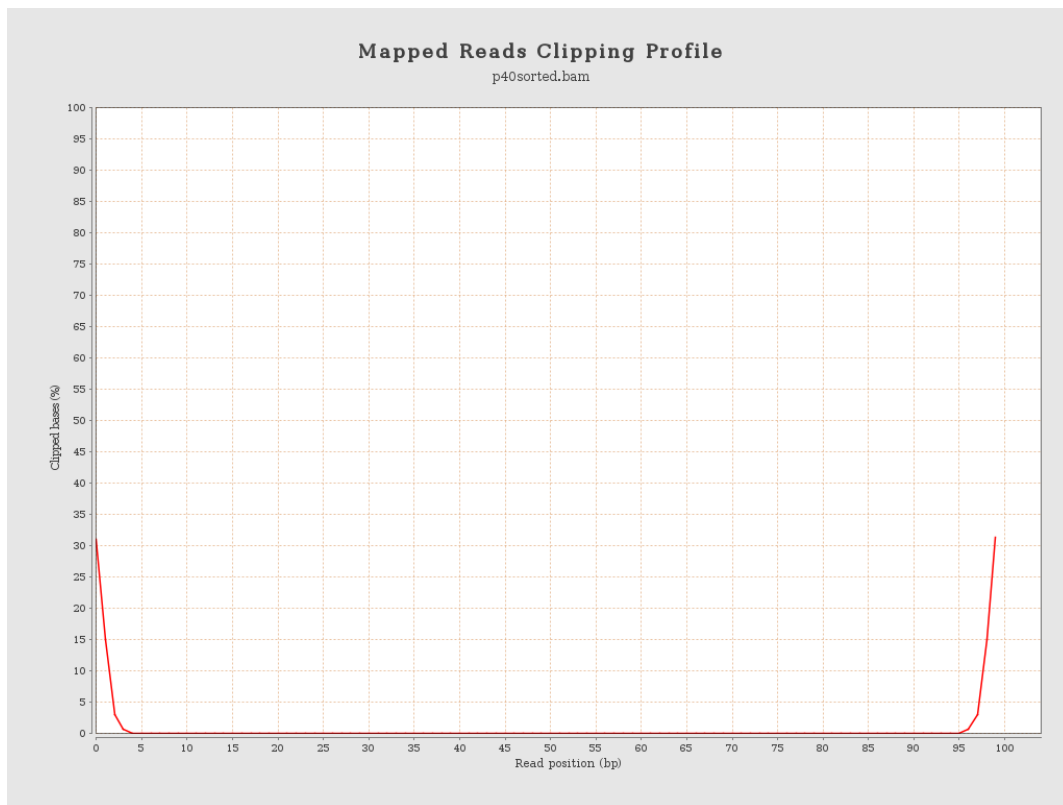

Duplication Rate Histogram
p40sorted.bam
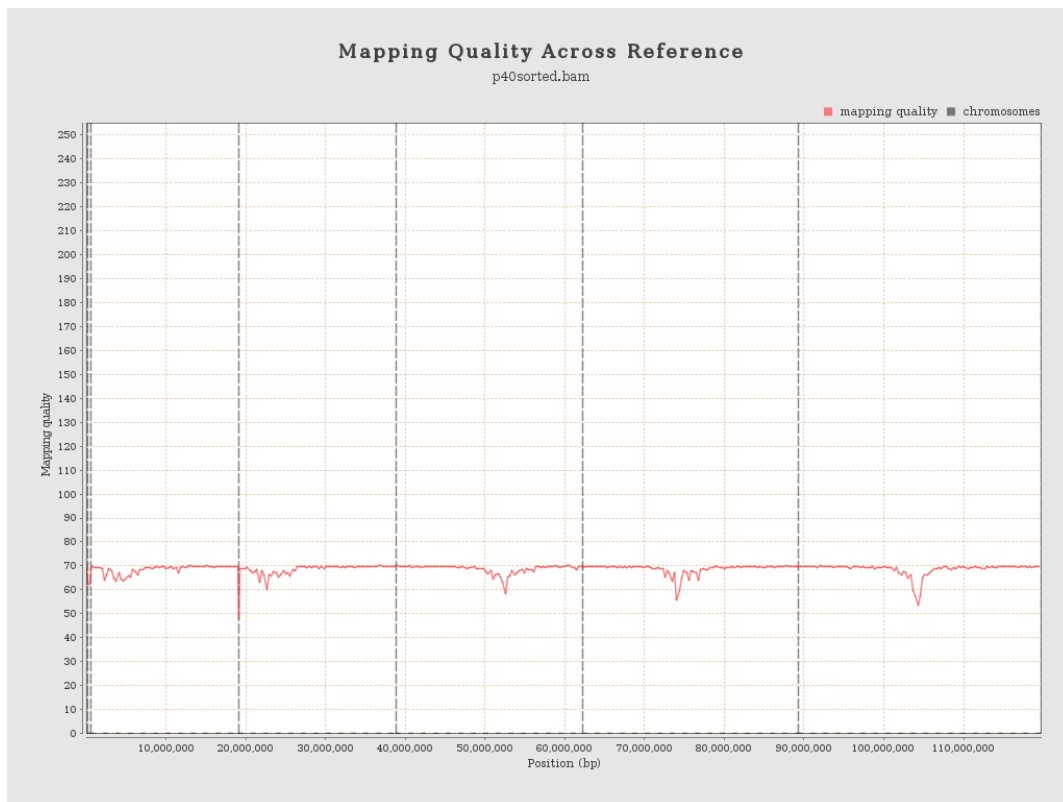
8. Results : Mapped Reads Nucleotide Content
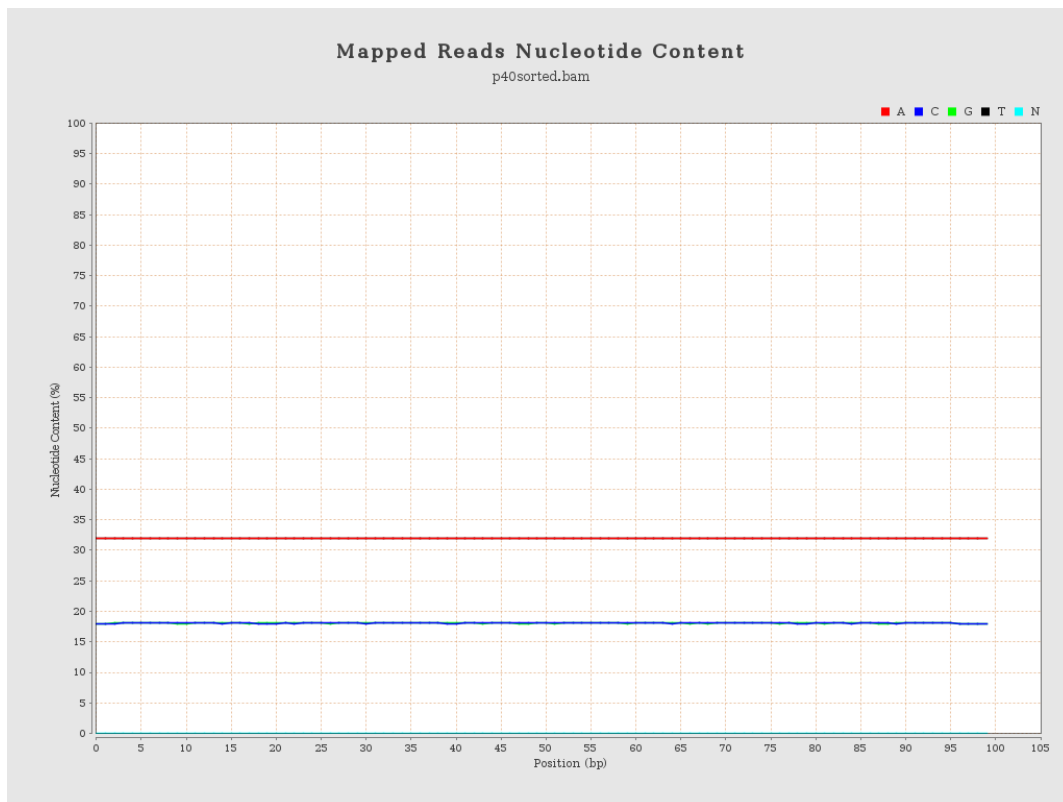
9. Results : Mapped Reads GC-content Distribution

10. Results : Mapped Reads Clipping Profile

11. Results : Mapping Quality Across Reference

Mapping Quality Across Reference
p40sorted.bam

12. Results : Mapping Quality Histogram

Mapping Quality Histogram
p40sorted.bam