

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.0

2016/05/19 11:52:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam  
/export/home/amirh/novoalign_testing/outputBAM/p20sorted.bam -c -nw 400  
-hm 3
```

1.2. Alignment

BAM file:	/export/home/amirh/novoalign_testing/outputBAM/p20sorted.bam
Program:	novoalign (V3.02.12)
Size of a homopolymer:	3
Number of windows:	400
Analysis date:	Thu May 19 09:11:48 MYT 2016
Draw chromosome limits:	yes

2. Summary

2.1. Globals

Reference size	119,667,750
Number of reads	11,947,007
Mapped reads	8,962,386 / 75.02%
Unmapped reads	2,984,621 / 24.98%
Paired reads	0 / 0%
Read min/max/mean length	100 / 100 / 100
Clipped reads	134,913 / 1.13%
Duplication rate	3.85%

2.2. ACGT Content

Number/percentage of A's	286,687,629 / 31.99%
Number/percentage of C's	161,472,547 / 18.02%
Number/percentage of T's	286,402,829 / 31.96%
Number/percentage of G's	161,481,690 / 18.02%
Number/percentage of N's	0 / 0%
GC Percentage	36.04%

2.3. Coverage

Mean	7.49
Standard Deviation	3.07

2.4. Mapping Quality

Mean Mapping Quality	68.77
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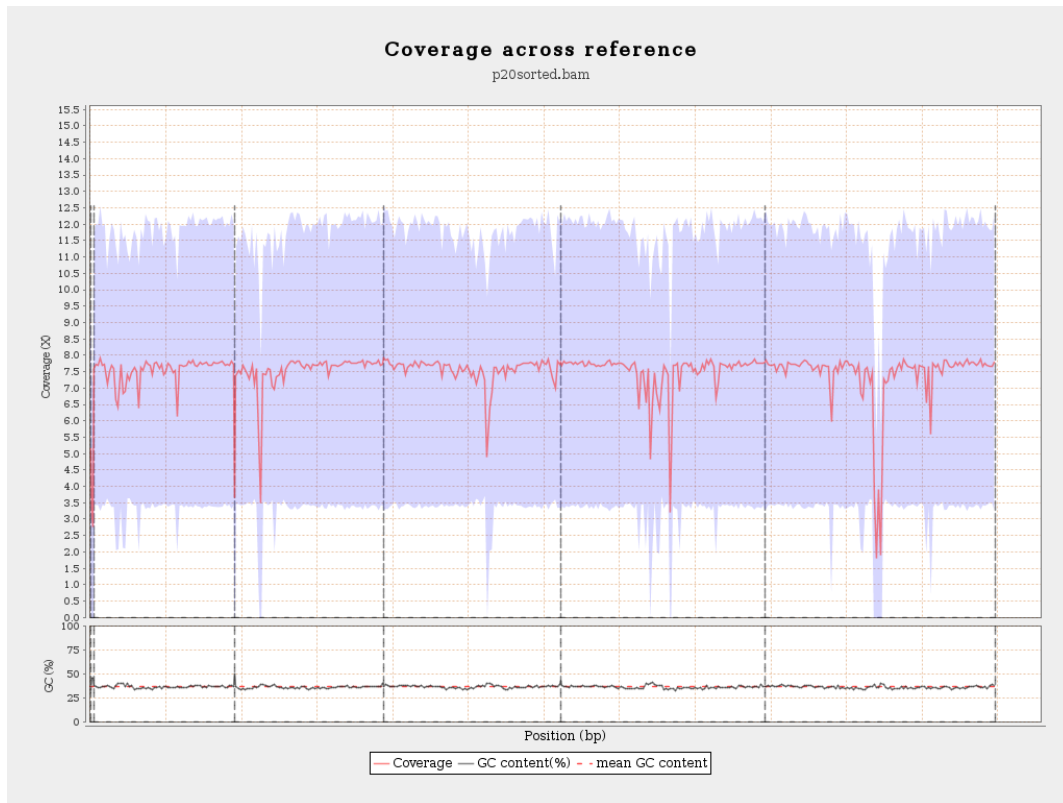
2.5. Mismatches and indels

General error rate	0.38%
Mismatches	3,414,251

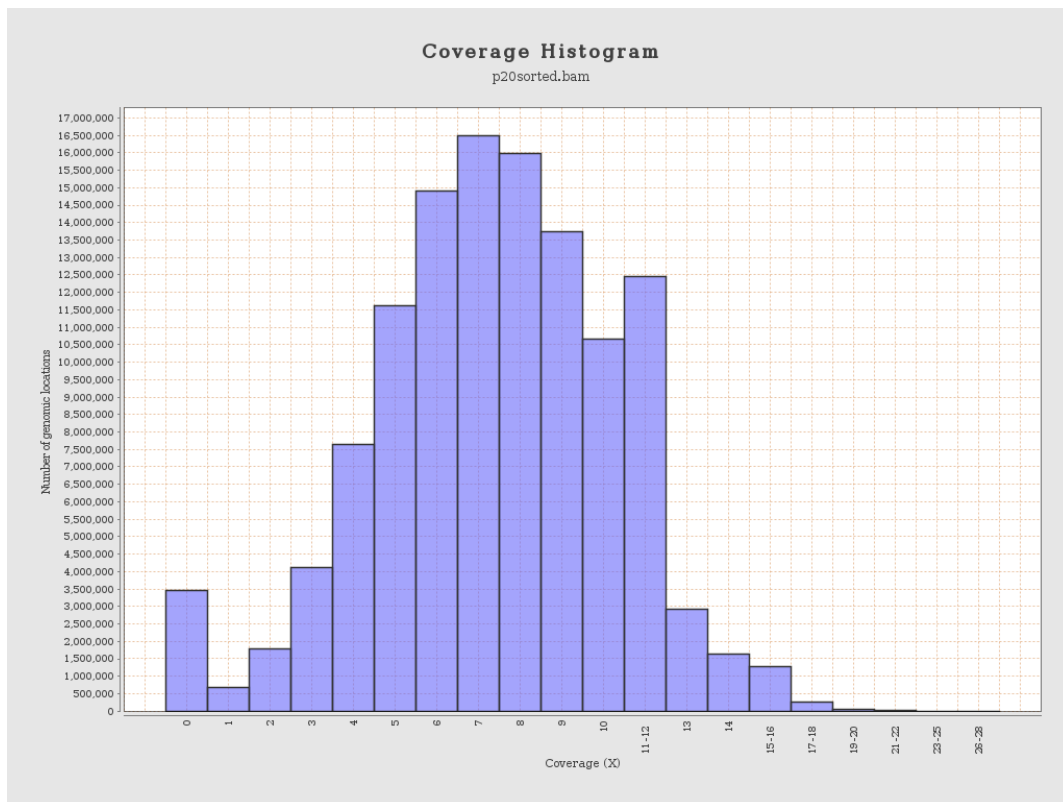
2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
Pt	154478	793031	5.13	4.32
Mt	366924	1076160	2.93	3.93
4	18585056	140430424	7.56	2.99
2	19698289	148366566	7.53	3.03
3	23459830	177569913	7.57	2.98
5	26975502	202730232	7.52	3.05
1	30427671	225078514	7.4	3.16

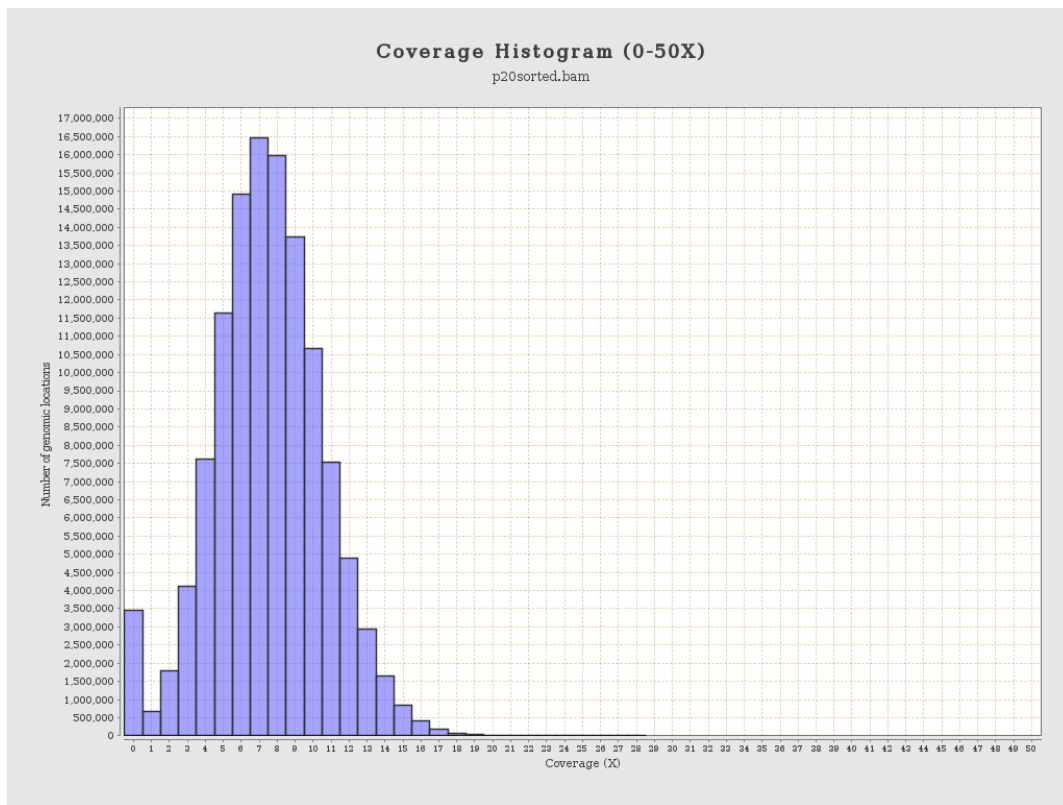
3. Results : Coverage across reference



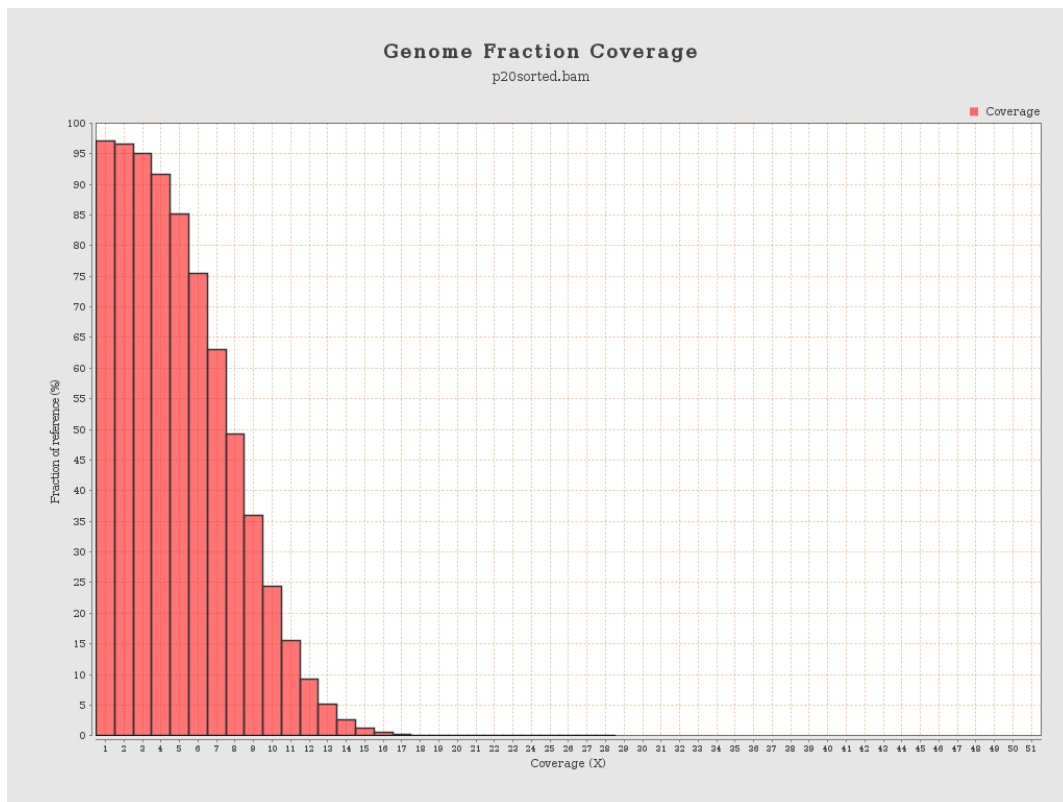
4. Results : Coverage Histogram



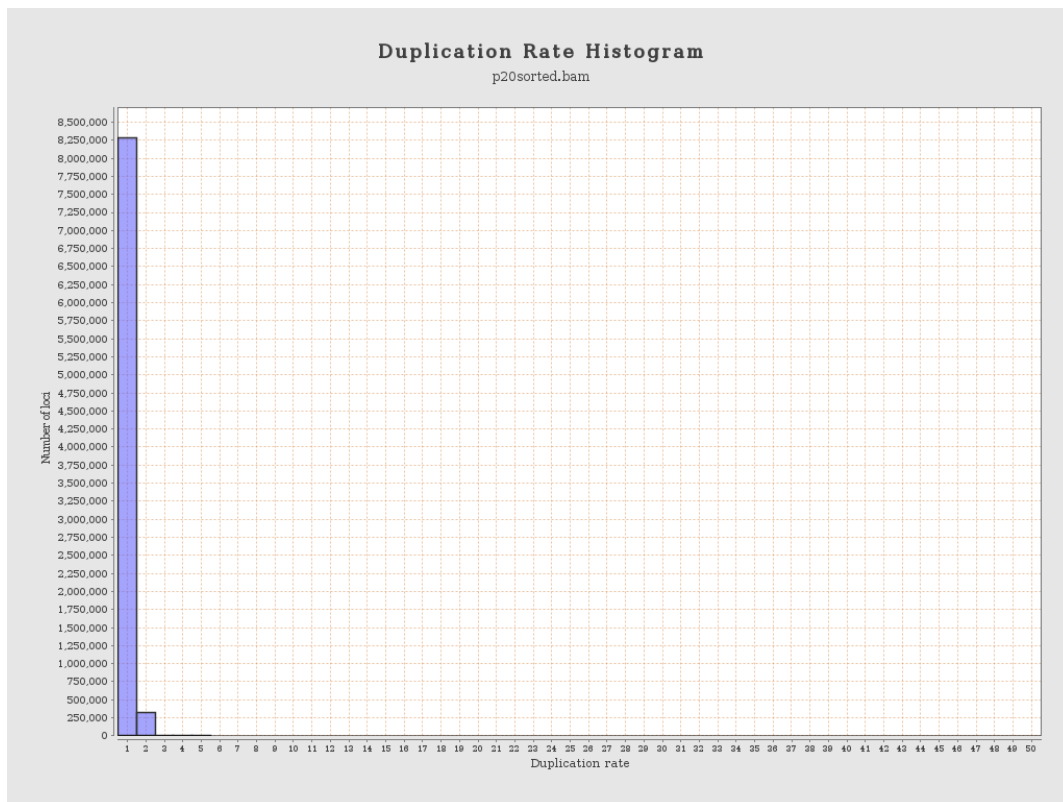
5. Results : Coverage Histogram (0-50X)



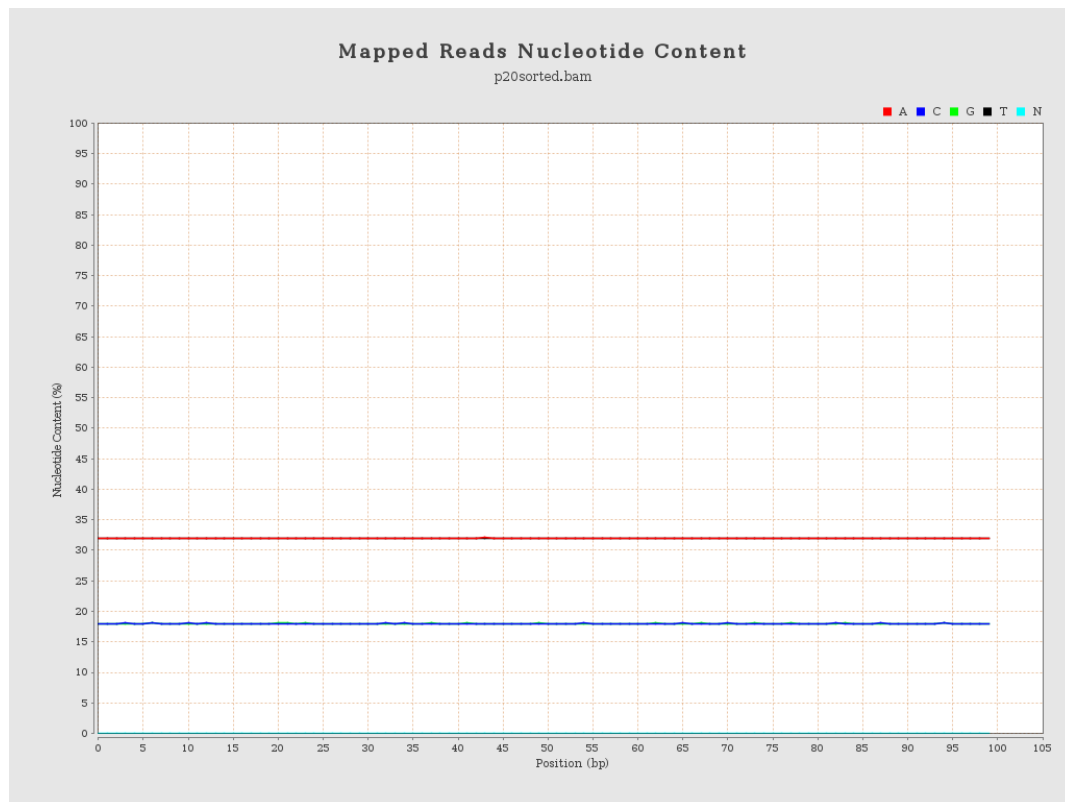
6. Results : Genome Fraction Coverage



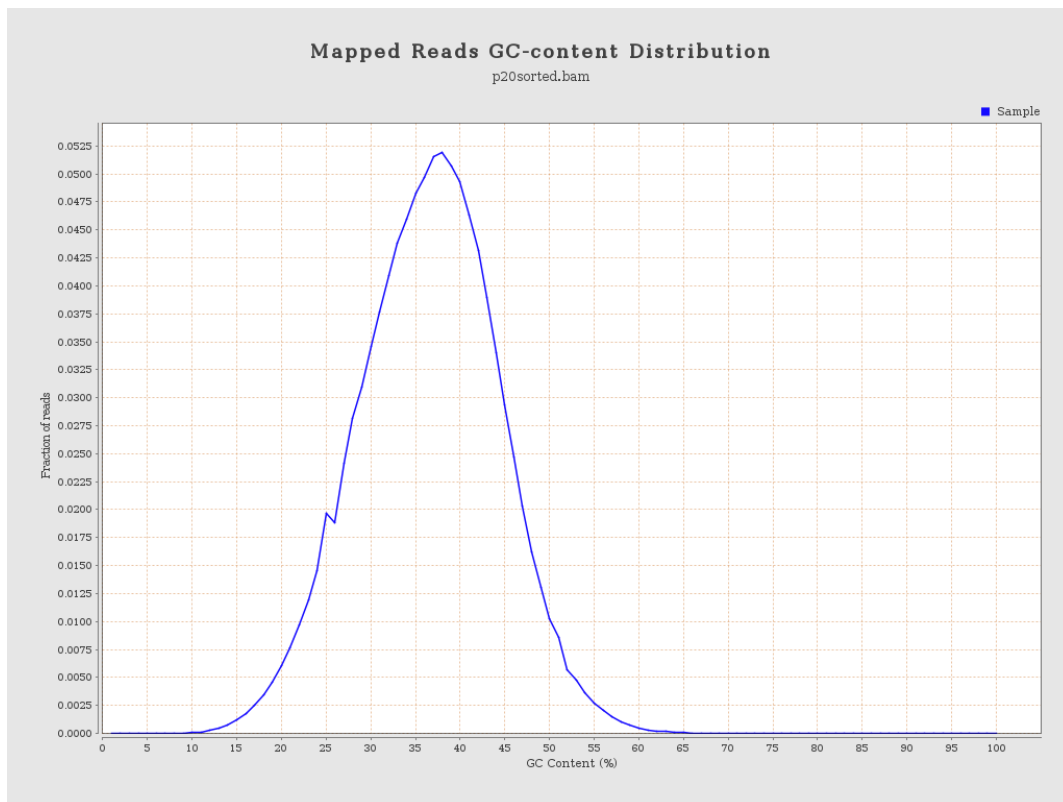
7. Results : Duplication Rate Histogram



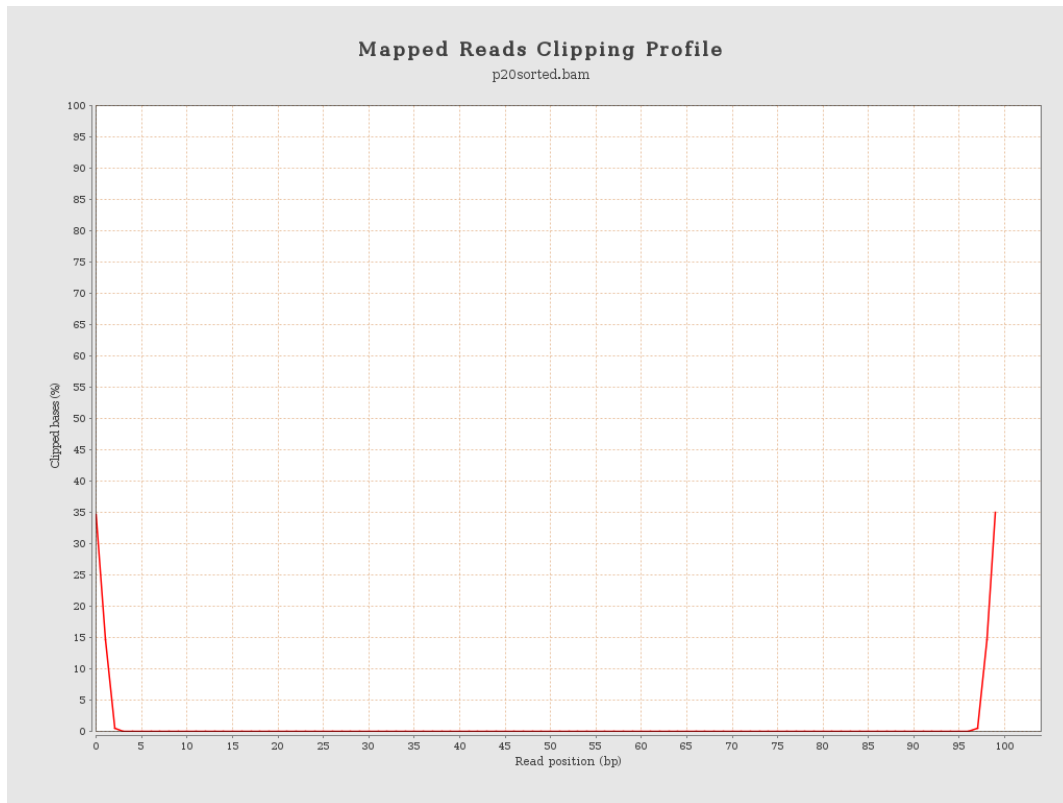
8. Results : Mapped Reads Nucleotide Content



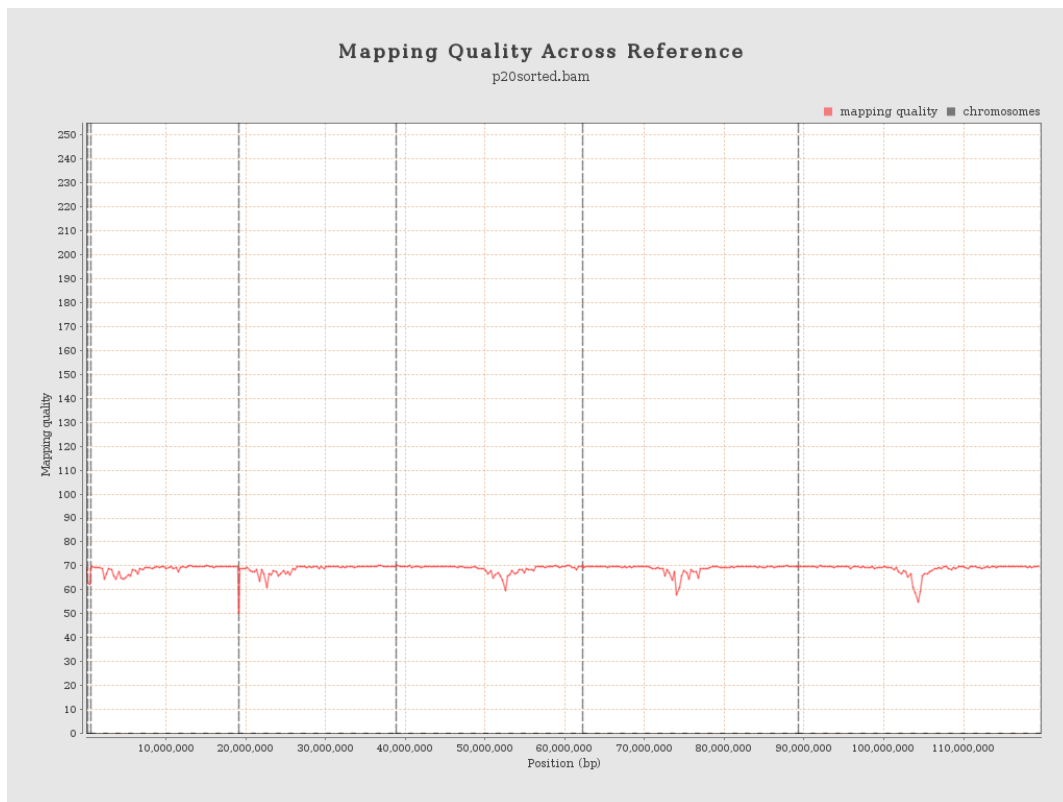
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

