# Qualimap Analysis Results

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

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/export/home/amirh/novoalign_testing/outputBAM/p30sorted.bam -c -nw 400
-hm 3
```

## 1.2. Alignment

| | |
|---|---|
| BAM file: | /export/home/amirh/novoalign_testing /outputBAM/p30sorted.bam |
| Program: | novoalign (V3.02.12) |
| Size of a homopolymer: | 3 |
| Number of windows: | 400 |
| Analysis date: | Thu May 19 09:16:15 MYT 2016 |
| Draw chromosome limits: | yes |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 119,667,750 |
| Number of reads | 11,947,007 |
| Mapped reads | 10,345,426 / 86.59% |
| Unmapped reads | 1,601,581 / 13.41% |
| Paired reads | 0 / 0% |
| Read min/max/mean length | 100 / 100 / 100 |
| Clipped reads | 237,266 / 1.99% |
| Duplication rate | 4.43% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 330,701,633 / 31.98% |
| Number/percentage of C's | 186,532,386 / 18.04% |
| Number/percentage of T's | 330,402,822 / 31.95% |
| Number/percentage of G's | 186,544,450 / 18.04% |
| Number/percentage of N's | 0 / 0% |
| GC Percentage | 36.07% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 8.64 |
| Standard Deviation | 3.35 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 68.75 |

## 2.5. Mismatches and indels

| | |
|---|---|
| General error rate | 0.55% |
| Mismatches | 5,677,185 |

## 2.6. Chromosome stats

| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| Pt | 154478 | 910388 | 5.89 | 4.86 |
| Mt | 366924 | 1227569 | 3.35 | 4.43 |
| 4 | 18585056 | 162077873 | 8.72 | 3.25 |
| 2 | 19698289 | 171205271 | 8.69 | 3.29 |
| 3 | 23459830 | 204997378 | 8.74 | 3.24 |
| 5 | 26975502 | 233996739 | 8.67 | 3.32 |
| 1 | 30427671 | 259766293 | 8.54 | 3.46 |

# 3. Results : Coverage across reference



Coverage across reference
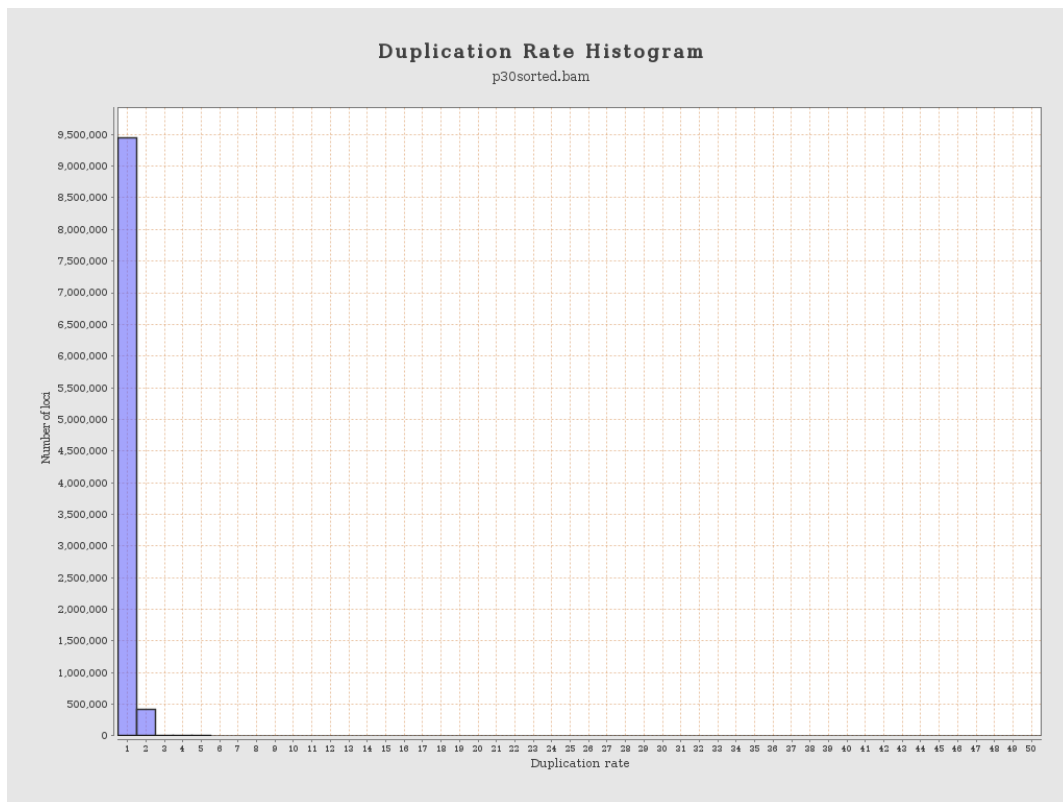p30sorted.bam

# 4. Results : Coverage Histogram



Coverage Histogram
p30sorted.bam
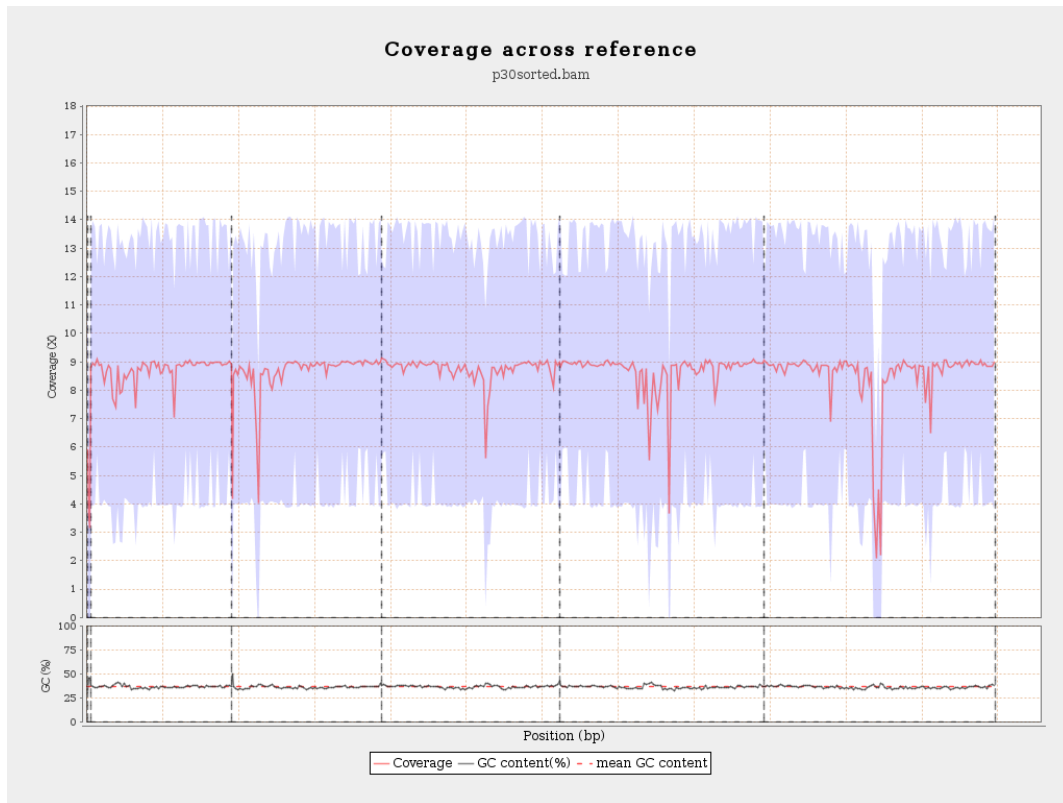
# 5. Results : Coverage Histogram (0-50X)
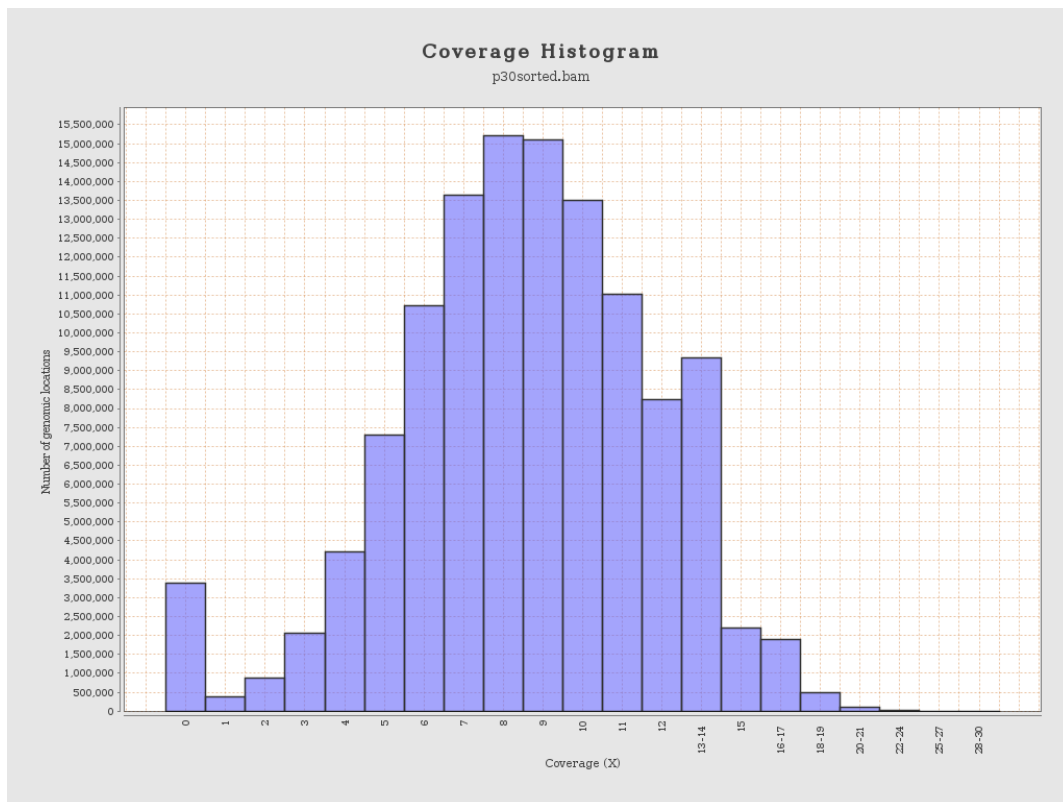


**Coverage Histogram (0-50X)**
p30sorted.bam
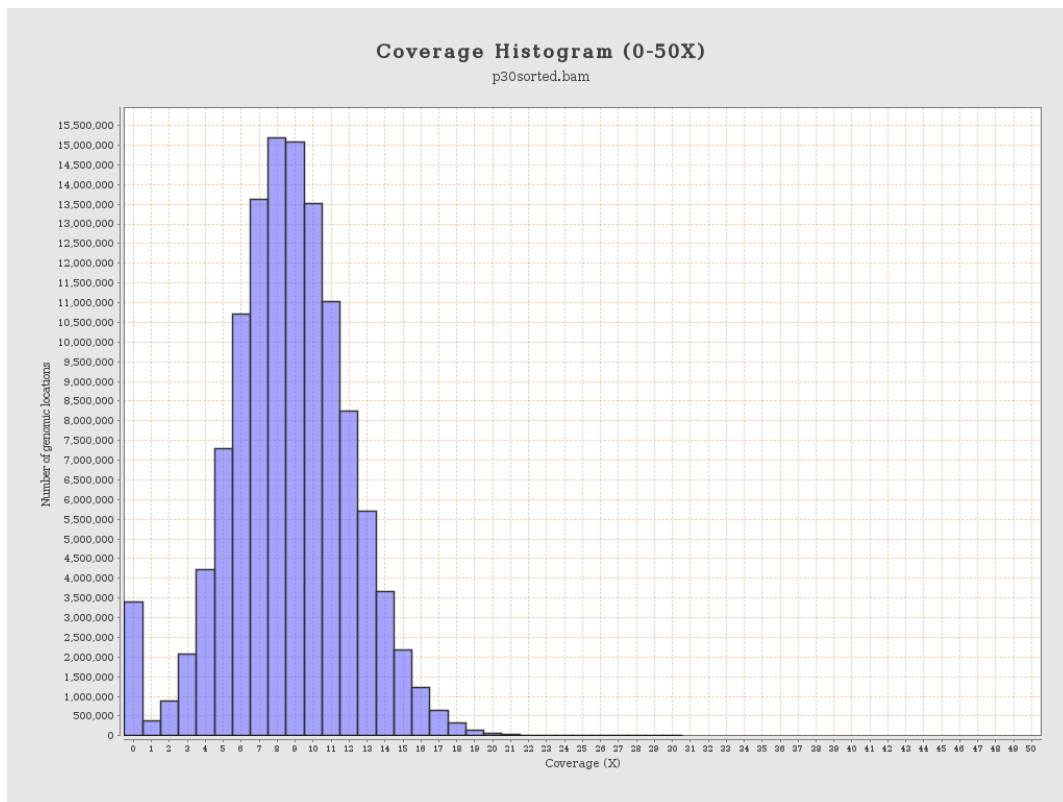
# 6. Results : Genome Fraction Coverage
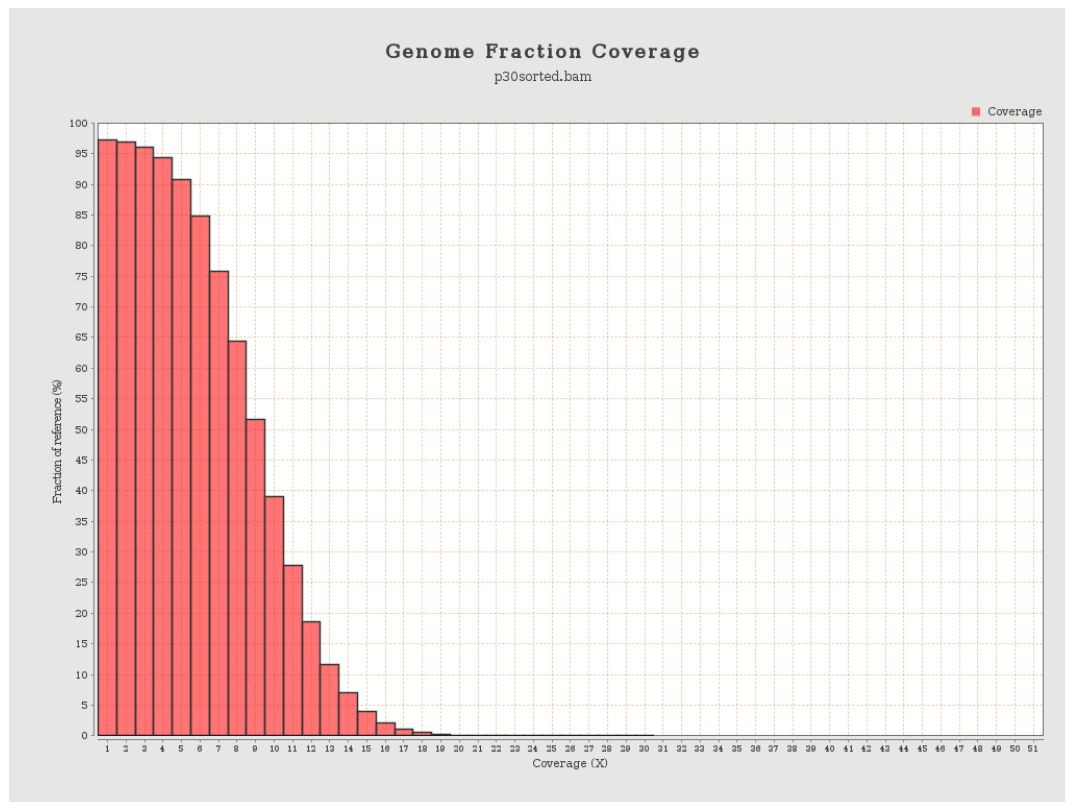
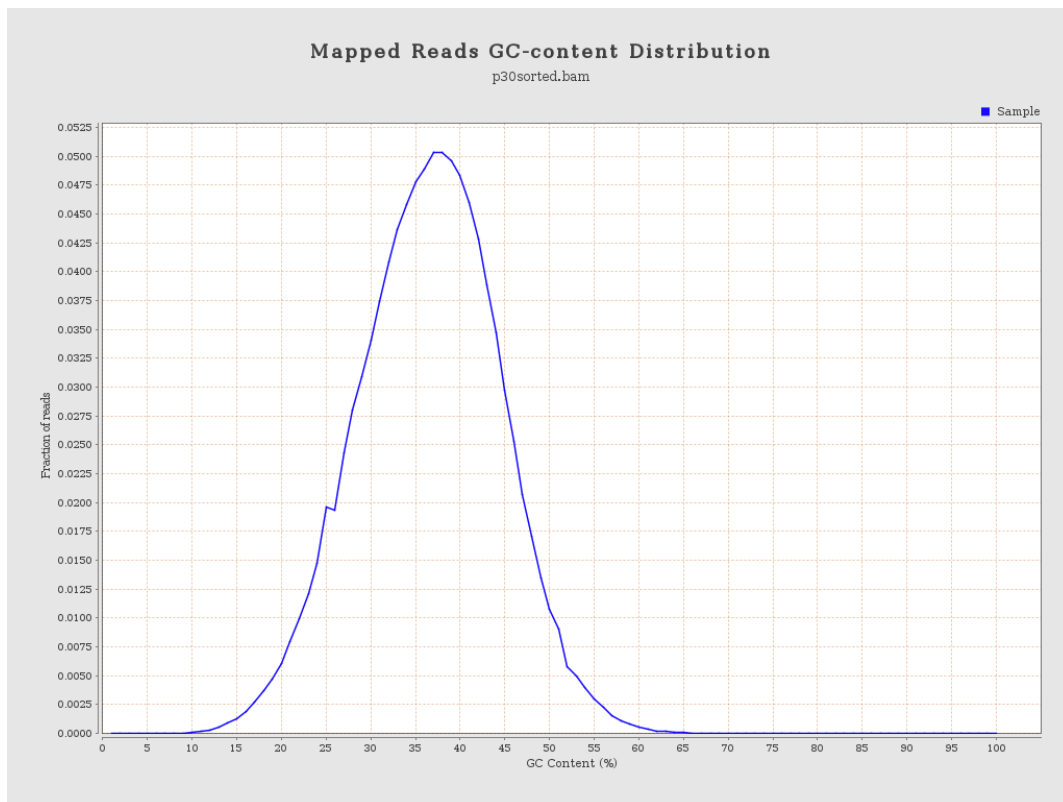# 7. Results : Duplication Rate Histogram
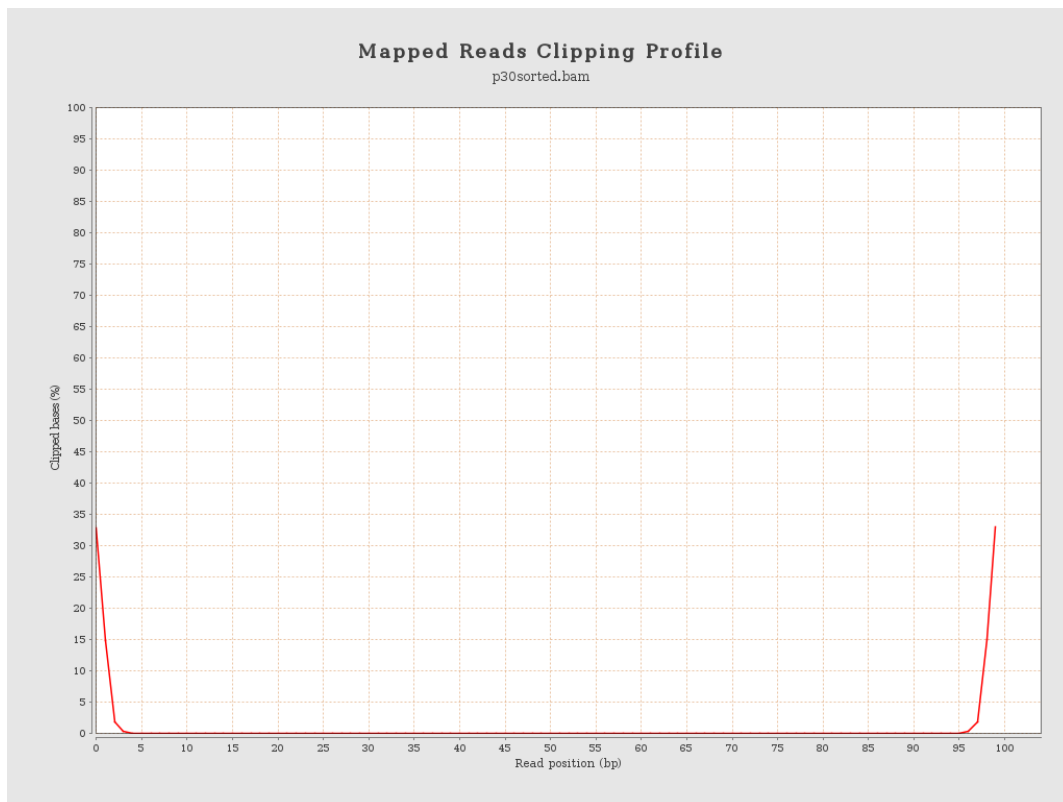


Duplication Rate Histogram
p30sorted.bam

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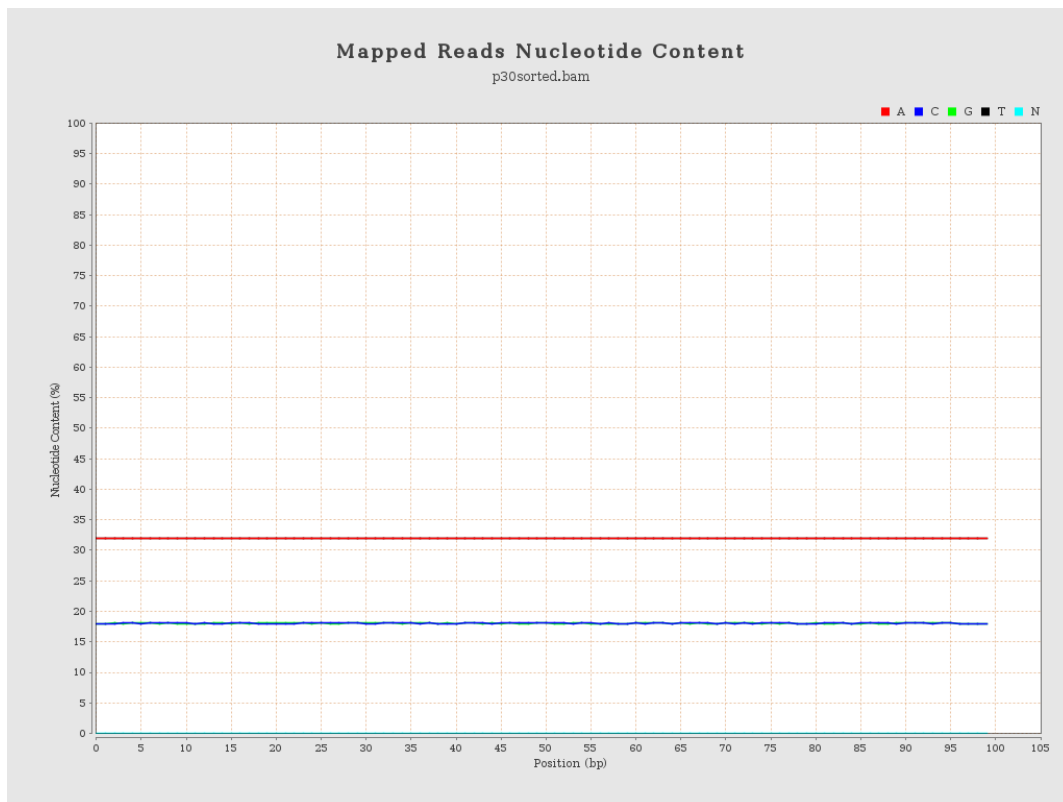
# 9. Results : Mapped Reads GC-content Distribution

# 10. Results : Mapped Reads Clipping Profile



Mapped Reads Clipping Profile
p30sorted.bam

# 11. Results : Mapping Quality Across Reference
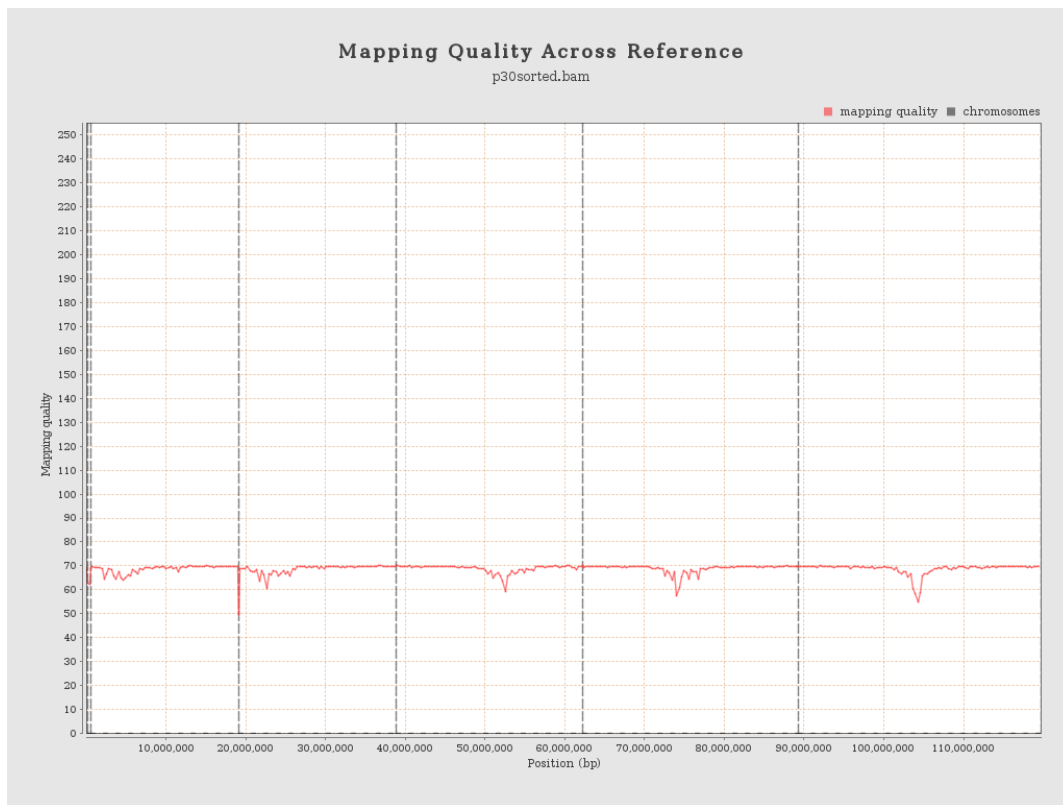
# 12. Results : Mapping Quality Histogram