

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.0*

*2016/05/19 11:53:14*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam  
/export/home/amirh/novoalign_testing/outputBAM/p120sorted.bam -c -nw  
400 -hm 3
```

## 1.2. Alignment

BAM file:	/export/home/amirh/novoalign_testing/outputBAM/p120sorted.bam
Program:	novoalign (V3.02.12)
Size of a homopolymer:	3
Number of windows:	400
Analysis date:	Thu May 19 08:54:24 MYT 2016
Draw chromosome limits:	yes

## 2. Summary

### 2.1. Globals

Reference size	119,667,750
Number of reads	11,947,007
Mapped reads	11,503,439 / 96.29%
Unmapped reads	443,568 / 3.71%
Paired reads	0 / 0%
Read min/max/mean length	100 / 100 / 100
Clipped reads	383,011 / 3.21%
Duplication rate	4.92%

### 2.2. ACGT Content

Number/percentage of A's	367,471,977 / 31.96%
Number/percentage of C's	207,547,426 / 18.05%
Number/percentage of T's	367,119,540 / 31.93%
Number/percentage of G's	207,555,057 / 18.05%
Number/percentage of N's	0 / 0%
GC Percentage	36.11%

### 2.3. Coverage

Mean	9.61
Standard Deviation	3.58

### 2.4. Mapping Quality

Mean Mapping Quality	68.64
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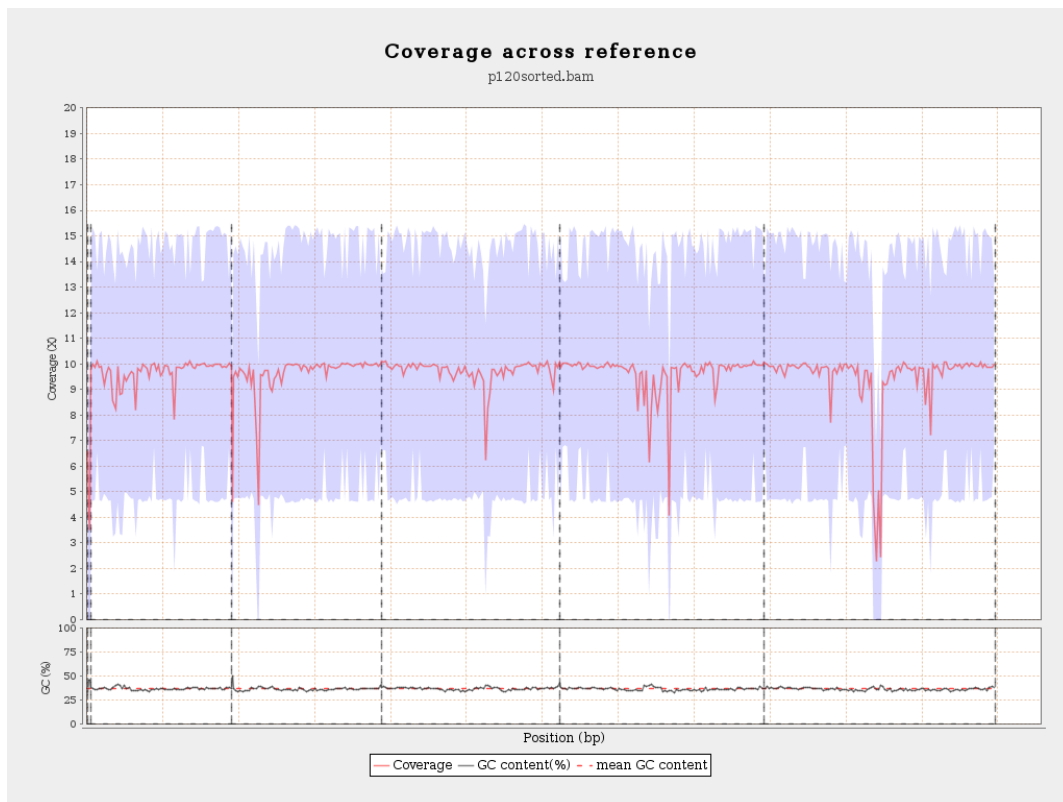
## 2.5. Mismatches and indels

General error rate	0.71%
Mismatches	8,211,044
Insertions	427
Deletions	631
Homopolymer indels	33.36%

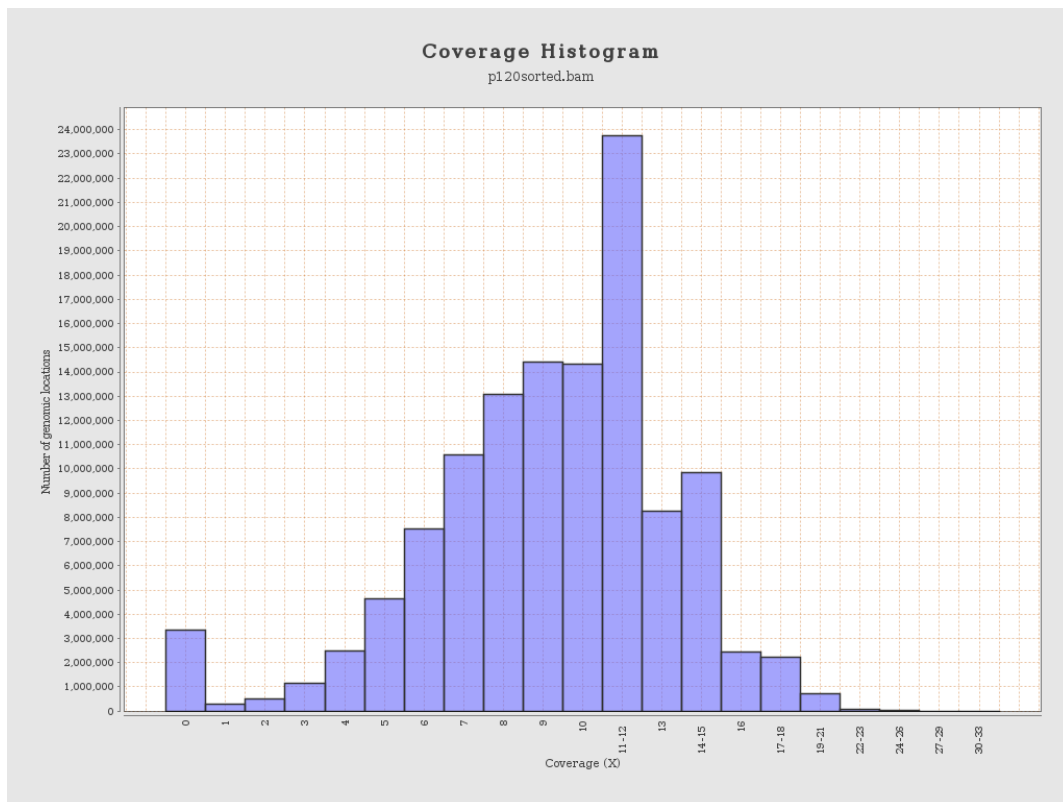
## 2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
Pt	154478	1014355	6.57	5.35
Mt	366924	1371937	3.74	4.9
4	18585056	180205771	9.7	3.46
2	19698289	190302799	9.66	3.51
3	23459830	227928262	9.72	3.45
5	26975502	260092506	9.64	3.54
1	30427671	288779577	9.49	3.71

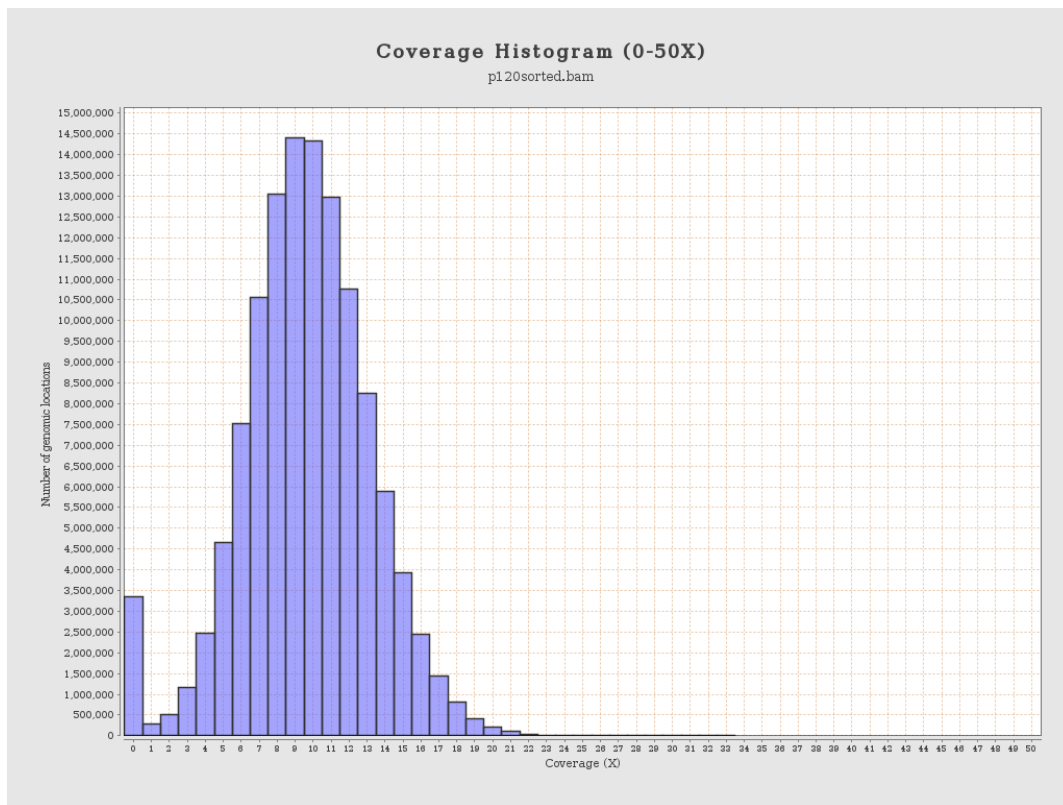
### 3. Results : Coverage across reference



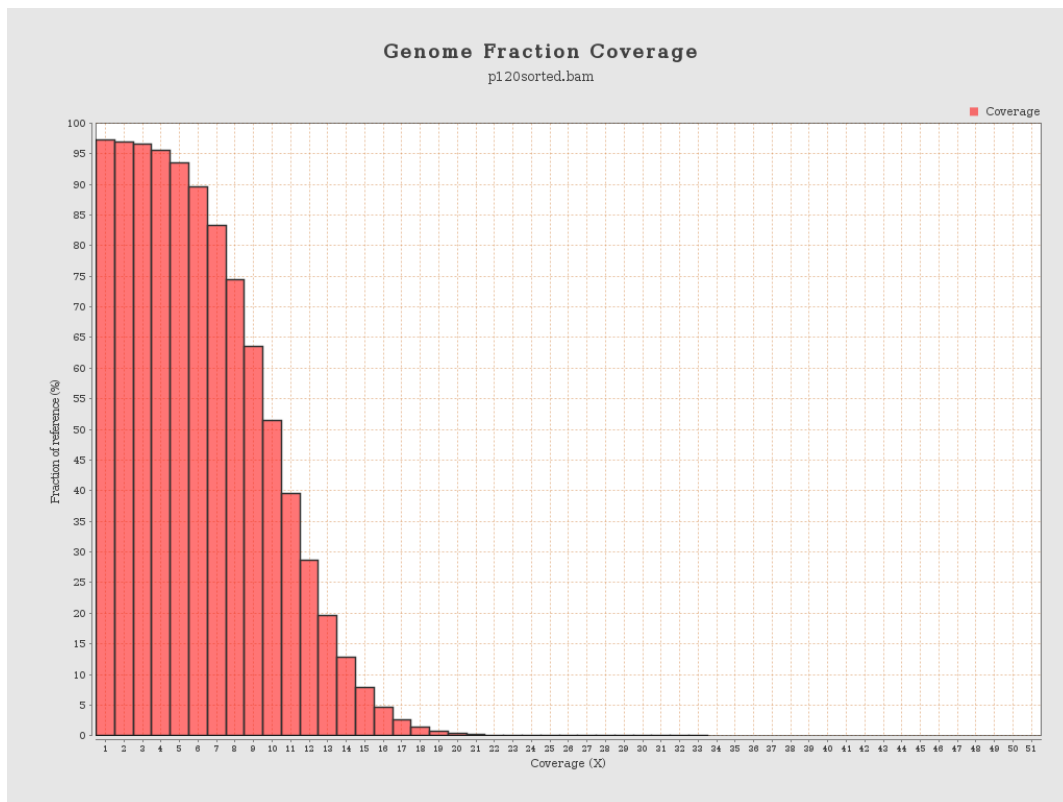
## 4. Results : Coverage Histogram



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

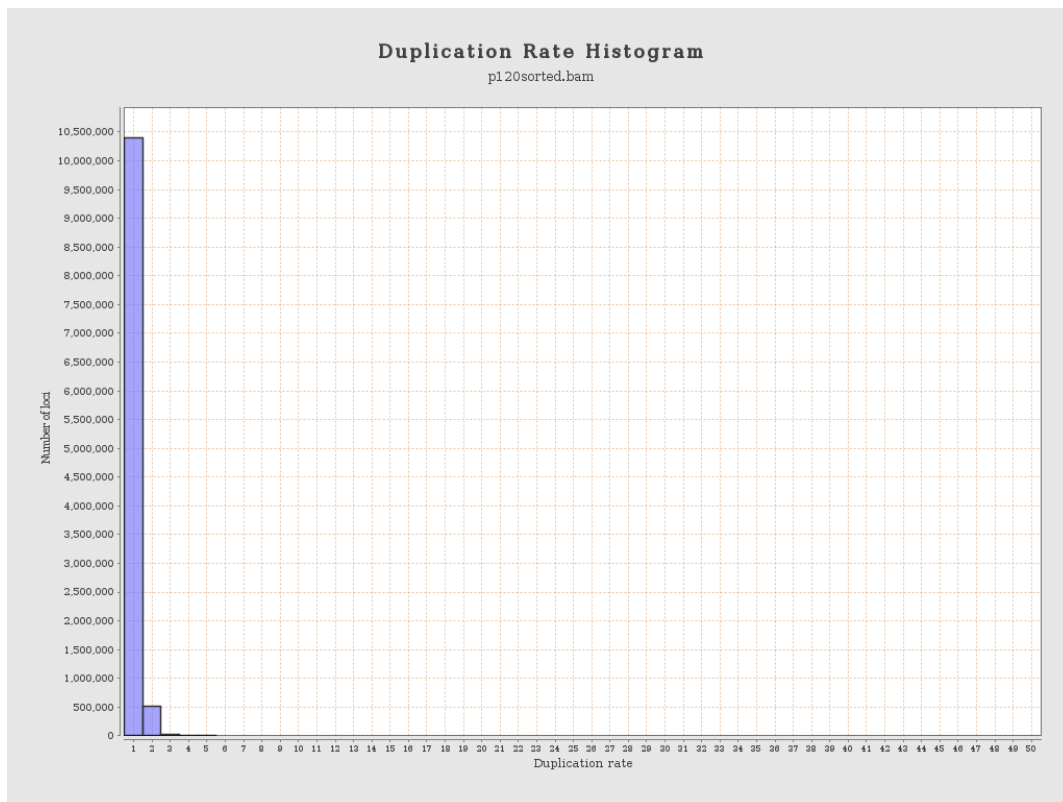


## 6. Results : Genome Fraction Coverage

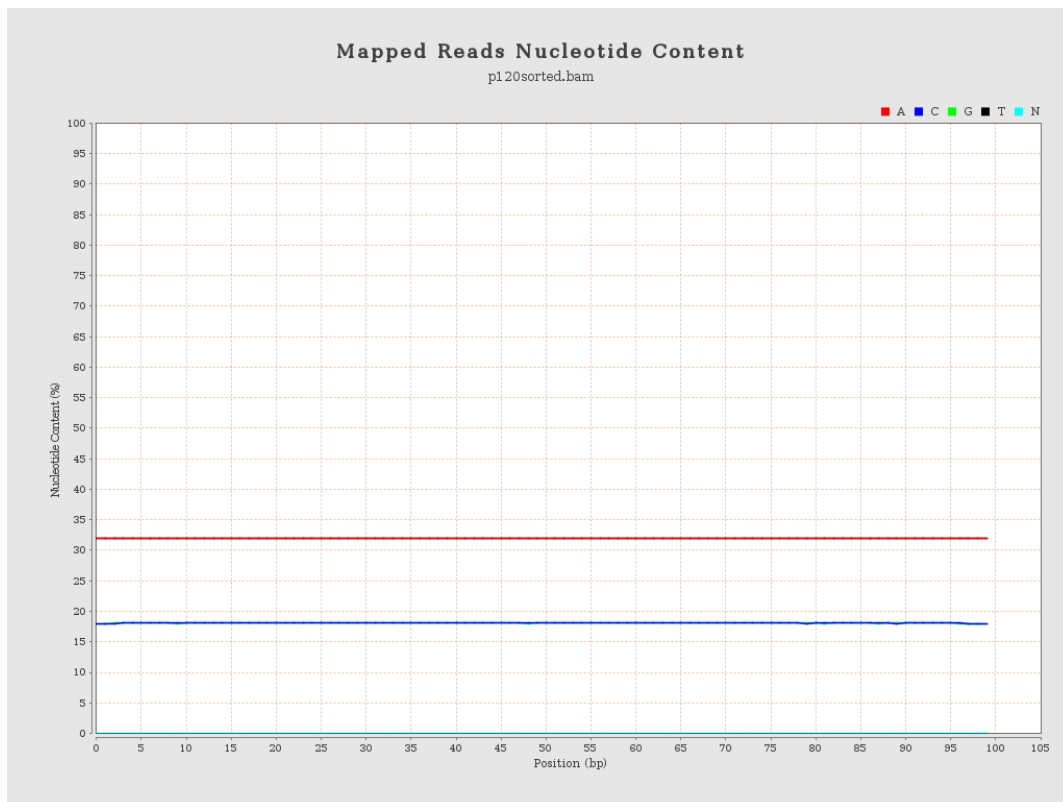




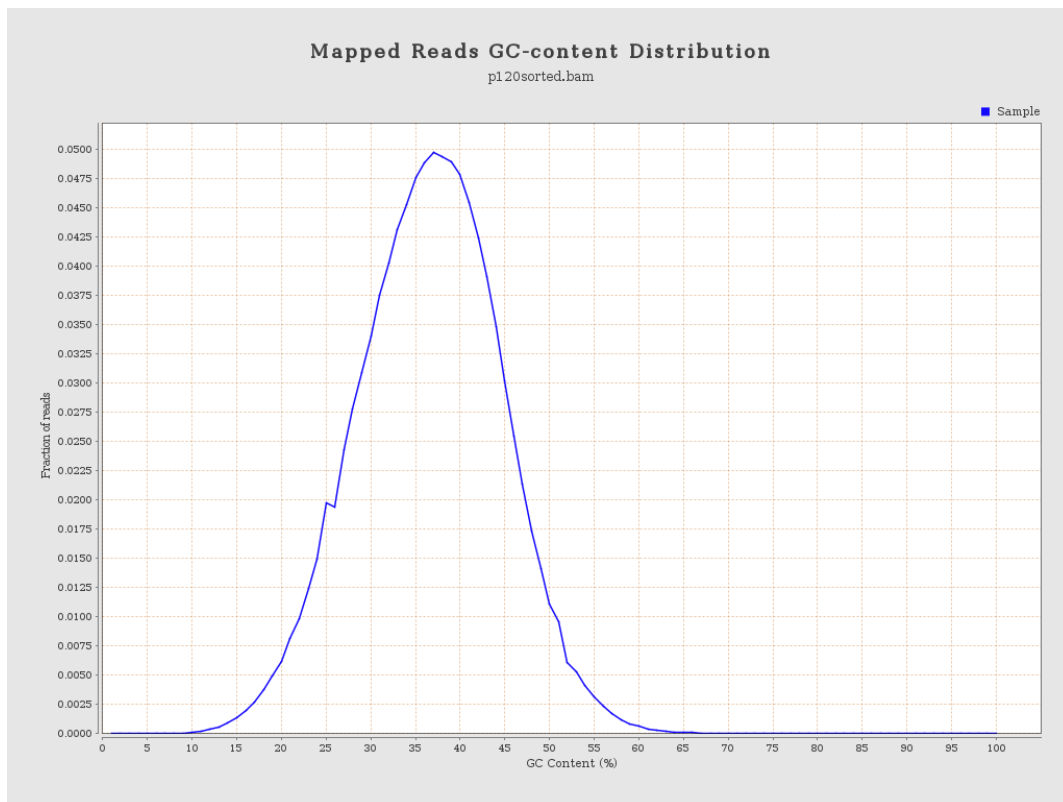
## 7. Results : Duplication Rate Histogram



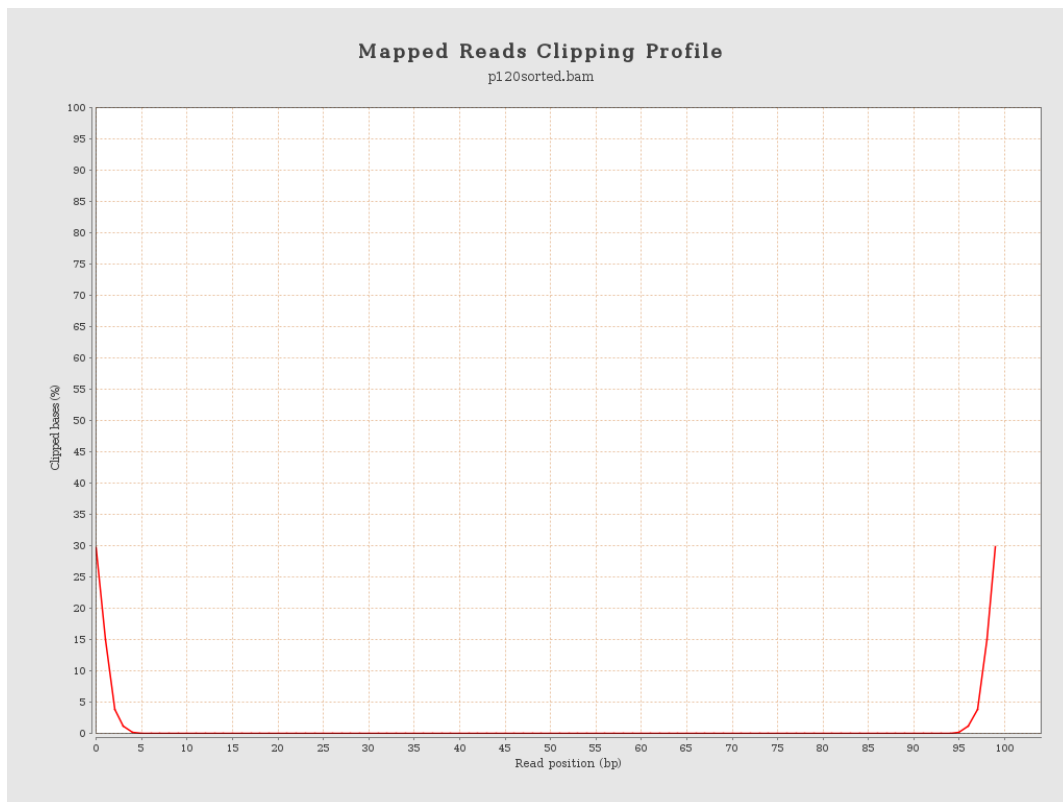
## 8. Results : Mapped Reads Nucleotide Content



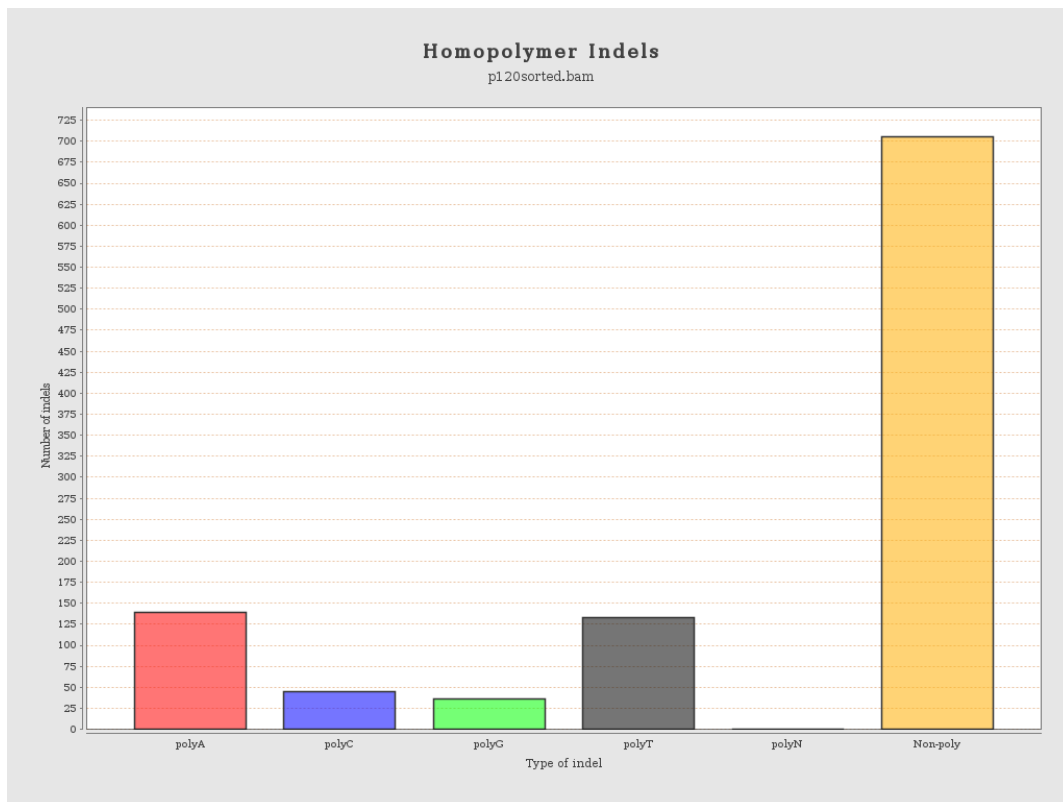
## 9. Results : Mapped Reads GC-content Distribution



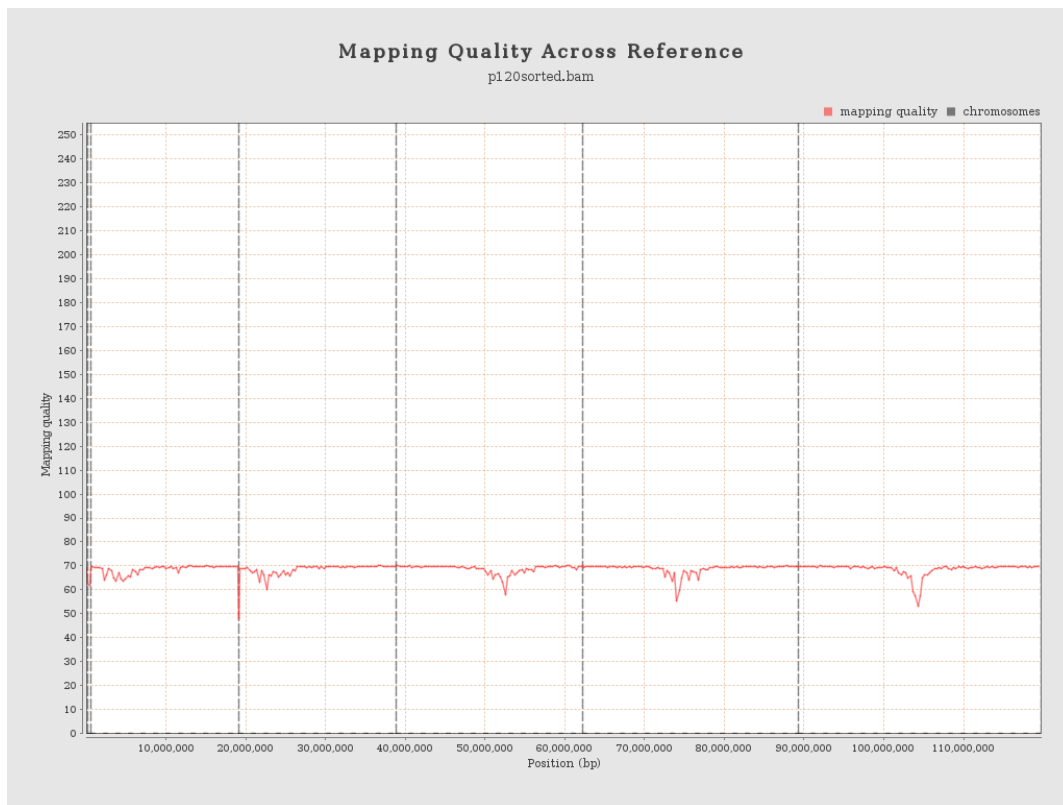
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

