

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.0*

*2016/05/19 11:50:55*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam  
/export/home/amirh/novoalign_testing/outputBAM/p50sorted.bam -c -nw 400  
-hm 3
```

## 1.2. Alignment

BAM file:	/export/home/amirh/novoalign_testing/outputBAM/p50sorted.bam
Program:	novoalign (V3.02.12)
Size of a homopolymer:	3
Number of windows:	400
Analysis date:	Thu May 19 09:19:09 MYT 2016
Draw chromosome limits:	yes

## 2. Summary

### 2.1. Globals

Reference size	119,667,750
Number of reads	11,947,007
Mapped reads	11,337,187 / 94.9%
Unmapped reads	609,820 / 5.1%
Paired reads	0 / 0%
Read min/max/mean length	100 / 100 / 100
Clipped reads	352,179 / 2.95%
Duplication rate	4.85%

### 2.2. ACGT Content

Number/percentage of A's	362,216,343 / 31.97%
Number/percentage of C's	204,521,256 / 18.05%
Number/percentage of T's	361,868,975 / 31.94%
Number/percentage of G's	204,528,594 / 18.05%
Number/percentage of N's	0 / 0%
GC Percentage	36.1%

### 2.3. Coverage

Mean	9.47
Standard Deviation	3.54

### 2.4. Mapping Quality

Mean Mapping Quality	68.64
----------------------	-------

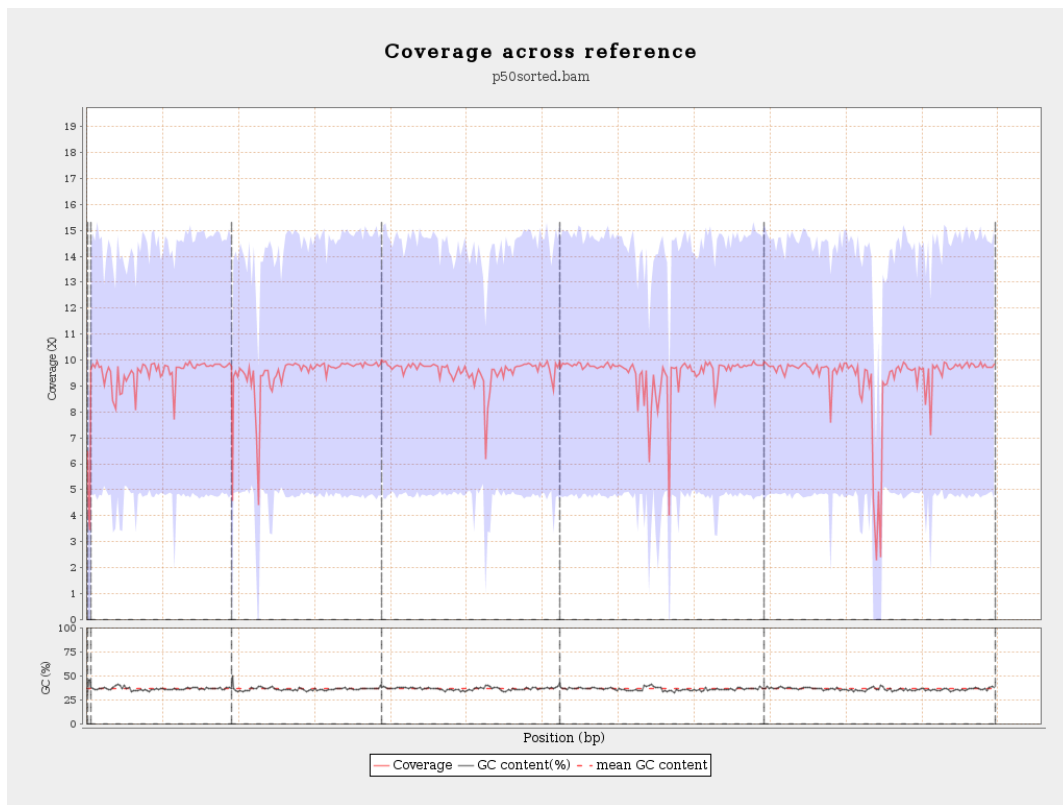
## 2.5. Mismatches and indels

General error rate	0.68%
Mismatches	7,685,760
Insertions	184
Deletions	264
Homopolymer indels	32.81%

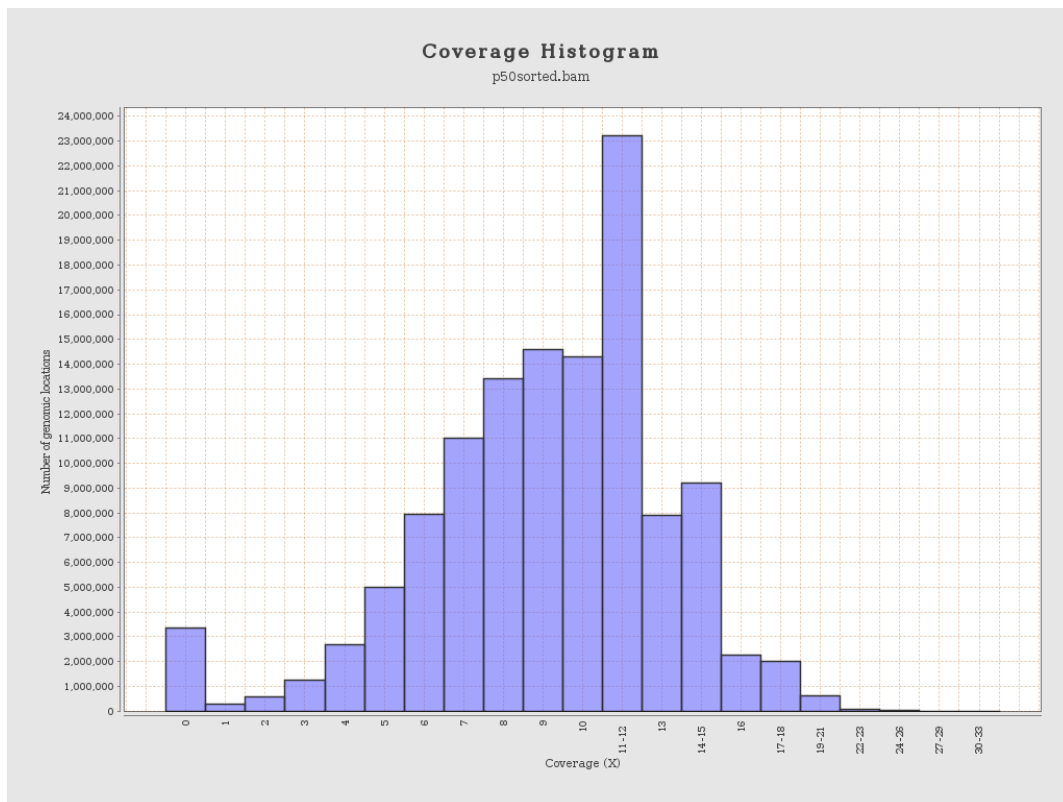
## 2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
Pt	154478	999608	6.47	5.28
Mt	366924	1349411	3.68	4.83
4	18585056	177593555	9.56	3.44
2	19698289	187575935	9.52	3.48
3	23459830	224655970	9.58	3.42
5	26975502	256354974	9.5	3.51
1	30427671	284606318	9.35	3.68

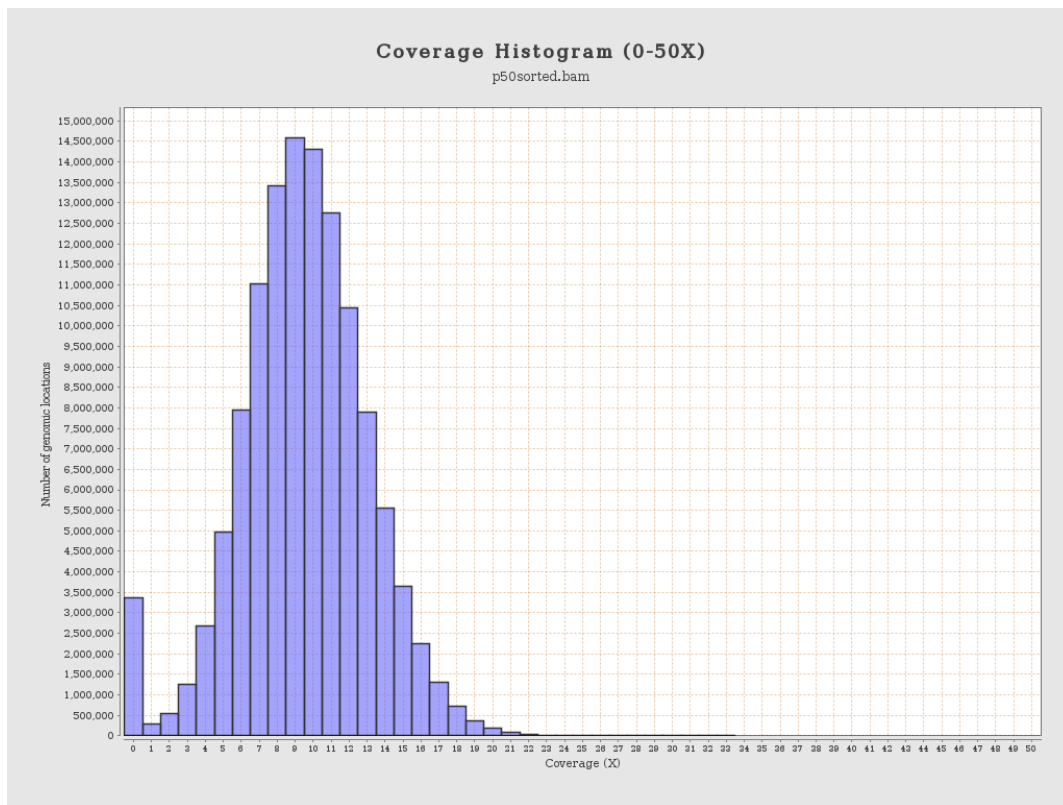
### 3. Results : Coverage across reference



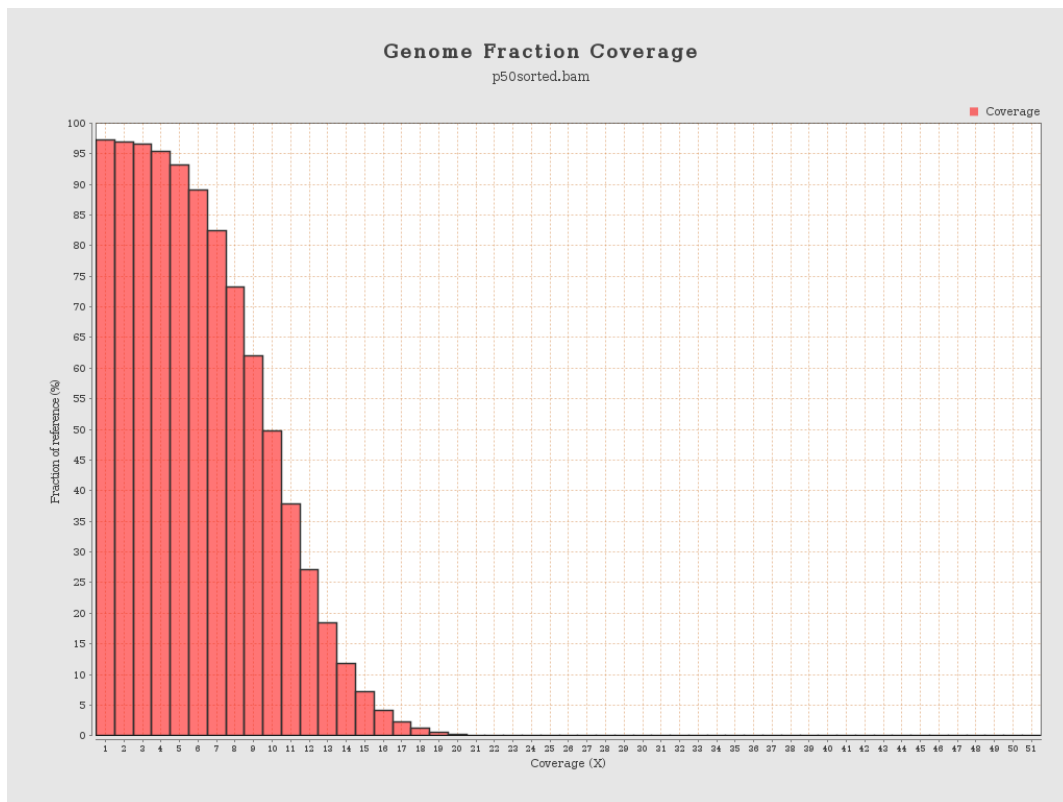
## 4. Results : Coverage Histogram



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

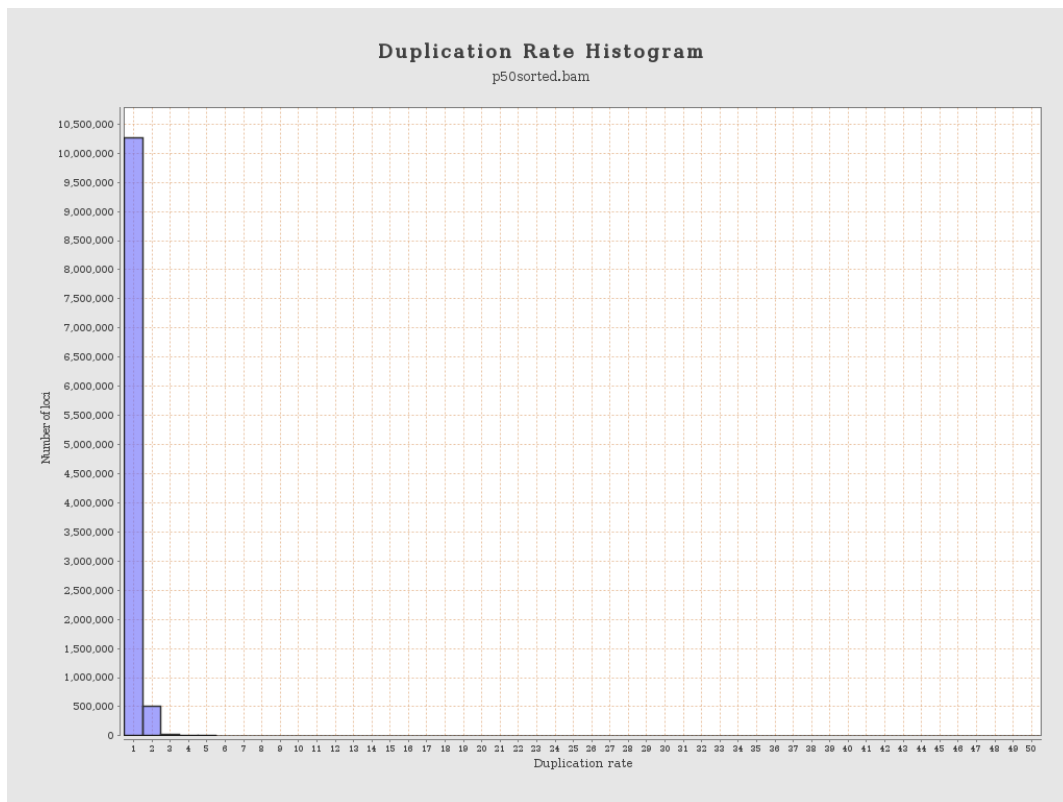


## 6. Results : Genome Fraction Coverage

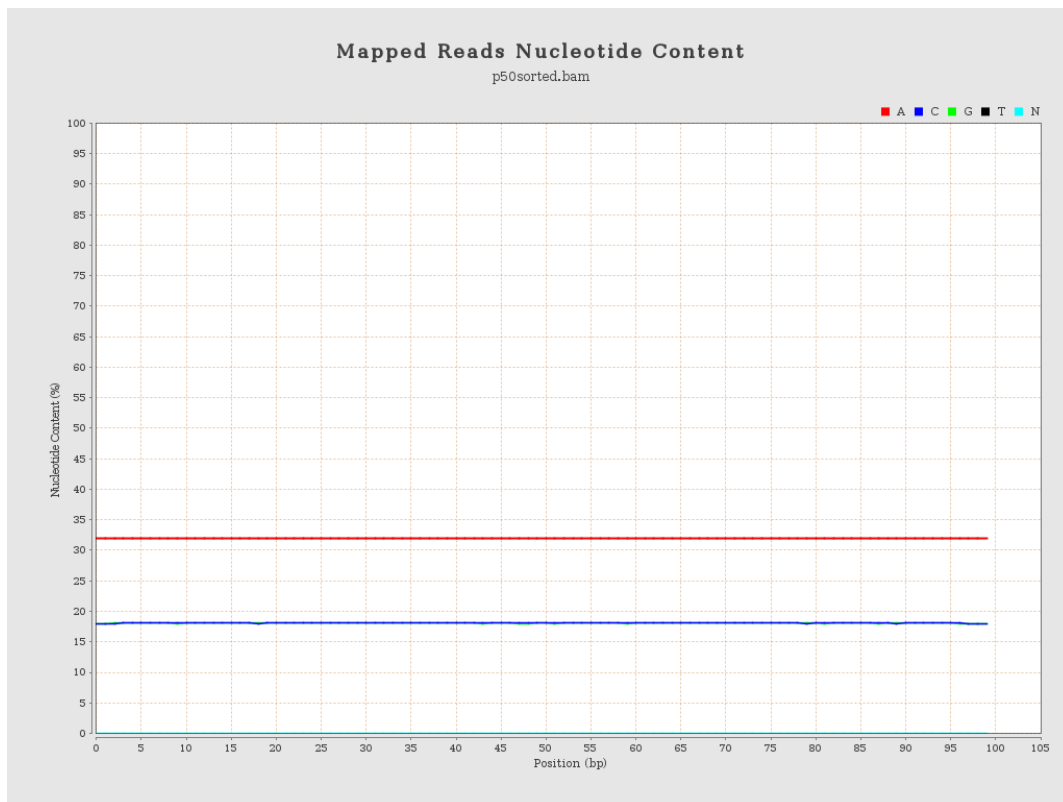




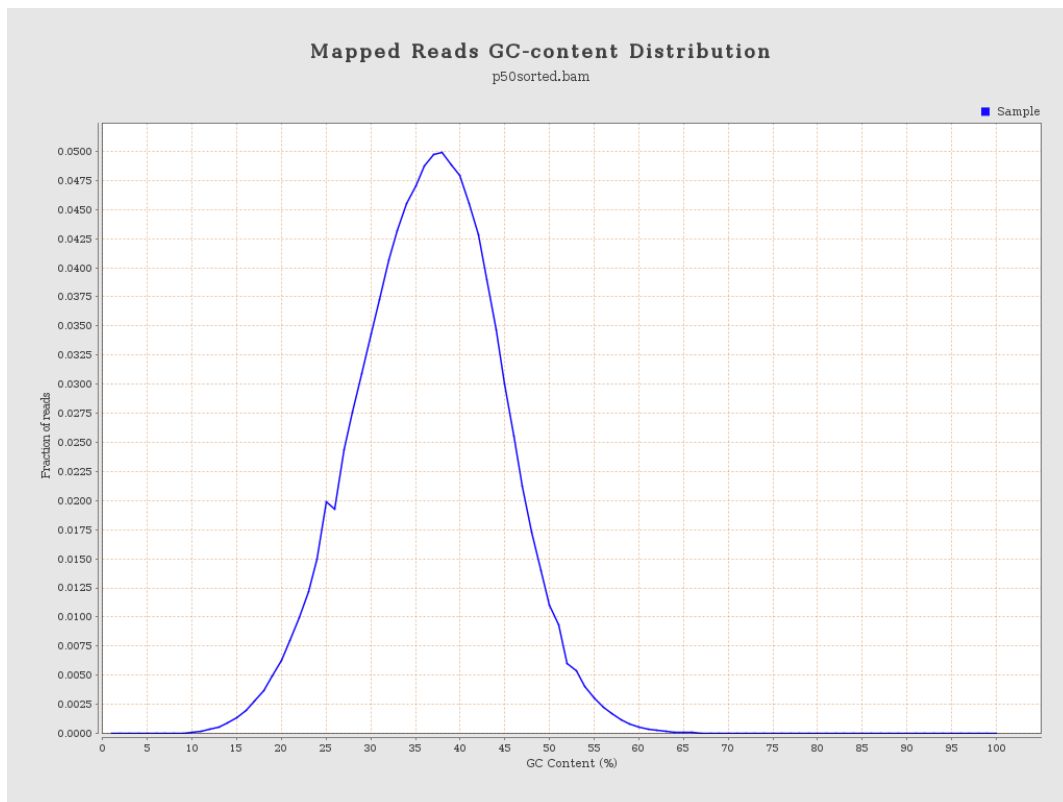
## 7. Results : Duplication Rate Histogram



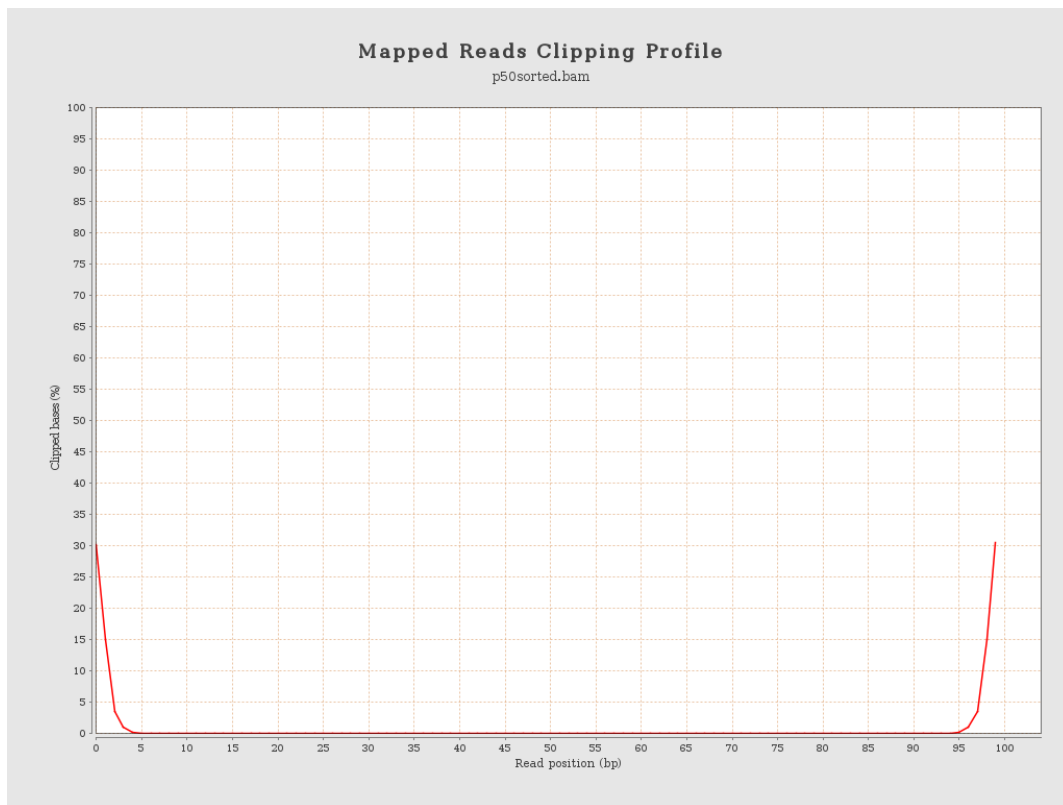
## 8. Results : Mapped Reads Nucleotide Content



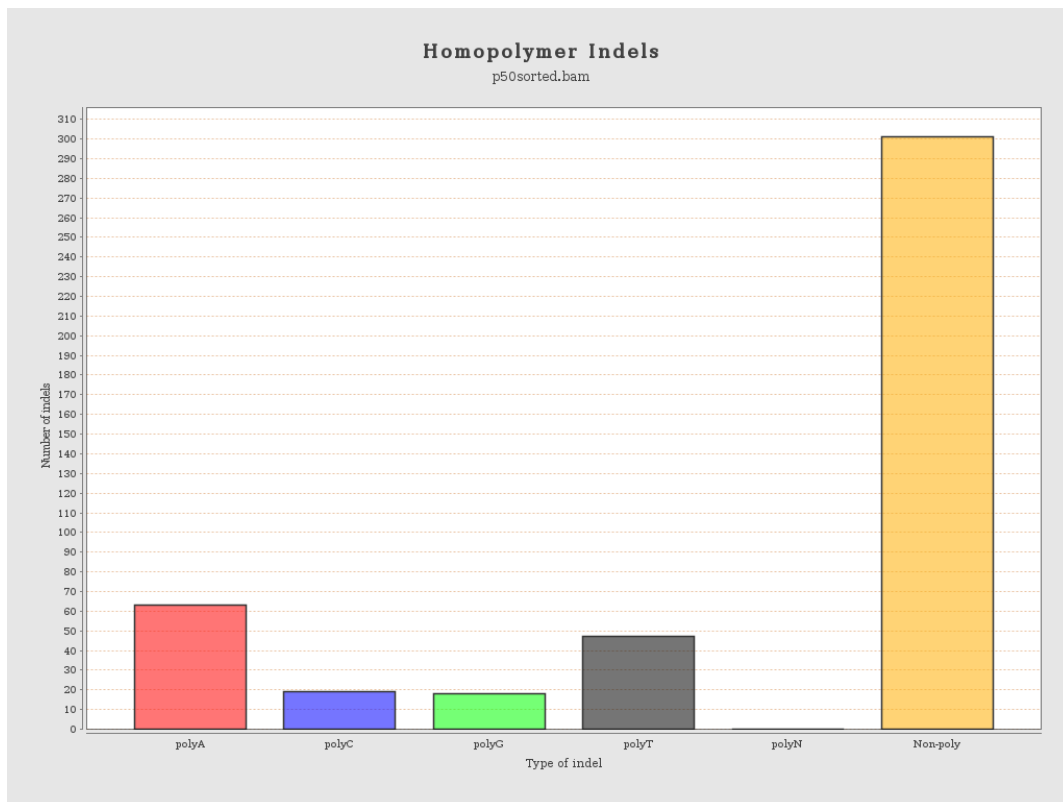
## 9. Results : Mapped Reads GC-content Distribution



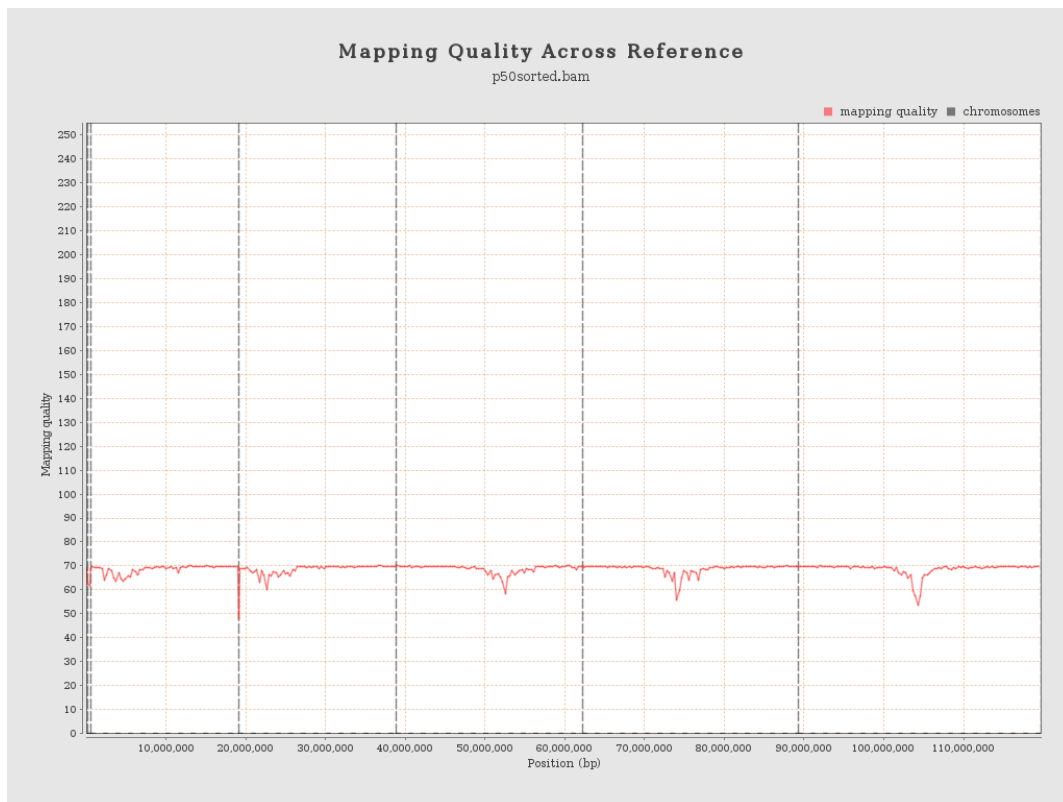
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

