Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.0
2016/05/19 11:53:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/export/home/amirh/novoalign_testing/outputBAM/p100sorted.bam -c -nw
400 -hm 3
```

1.2. Alignment

BAM file:	/export/home/amirh/novoalign_testing /outputBAM/p100sorted.bam
Program:	novoalign (V3.02.12)
Size of a homopolymer:	3
Number of windows:	400
Analysis date:	Thu May 19 08:48:08 MYT 2016
Draw chromosome limits:	yes

2. Summary

2.1. Globals

Reference size	119,667,750
Number of reads	11,947,007
Mapped reads	11,503,018 / 96.28%
Unmapped reads	443,989 / 3.72%
Paired reads	0 / 0%
Read min/max/mean length	100 / 100 / 100
Clipped reads	382,884 / 3.2%
Duplication rate	4.92%

2.2. ACGT Content

Number/percentage of A's	367,458,806 / 31.96%
Number/percentage of C's	207,539,808 / 18.05%
Number/percentage of T's	367,106,301 / 31.93%
Number/percentage of G's	207,547,394 / 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

2.5. Mismatches and indels

General error rate	0.71%
Mismatches	8,208,962
Insertions	424
Deletions	626
Homopolymer indels	33.33%

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	180198310	9.7	3.46
2	19698289	190295757	9.66	3.51
3	23459830	227918850	9.72	3.45
5	26975502	260083605	9.64	3.54
1	30427671	288770647	9.49	3.71

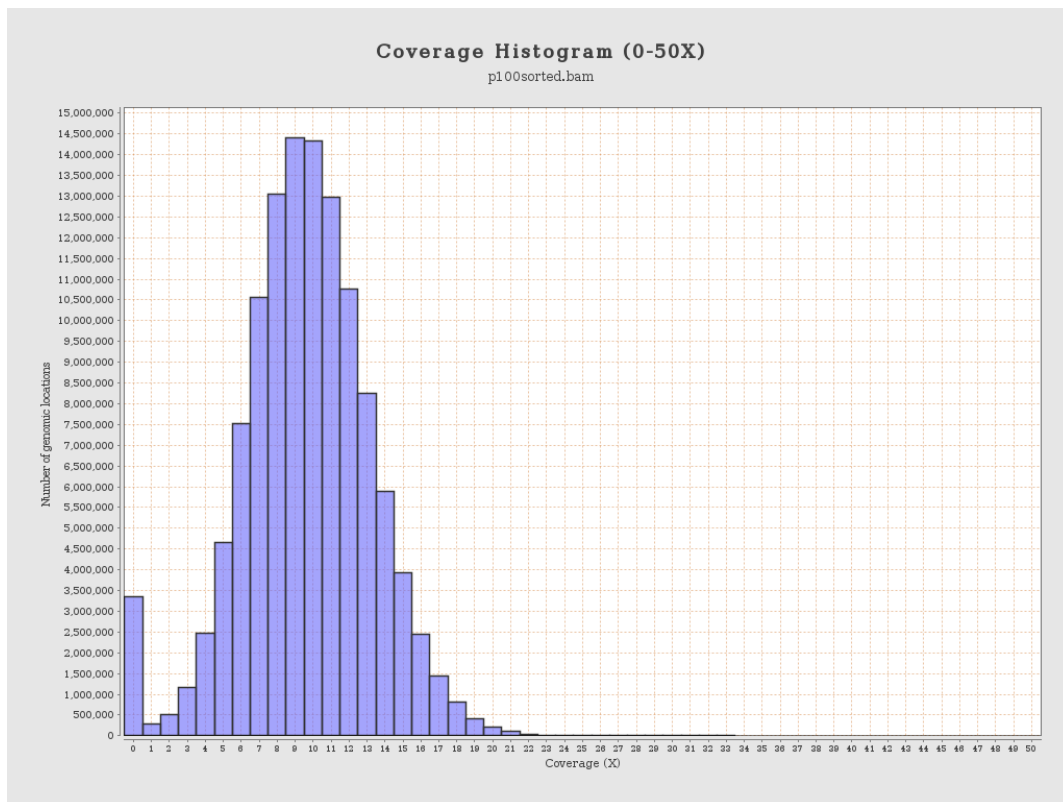# 3. Results : Coverage across reference

4. Results : Coverage Histogram

Coverage Histogram
p100sorted.bam
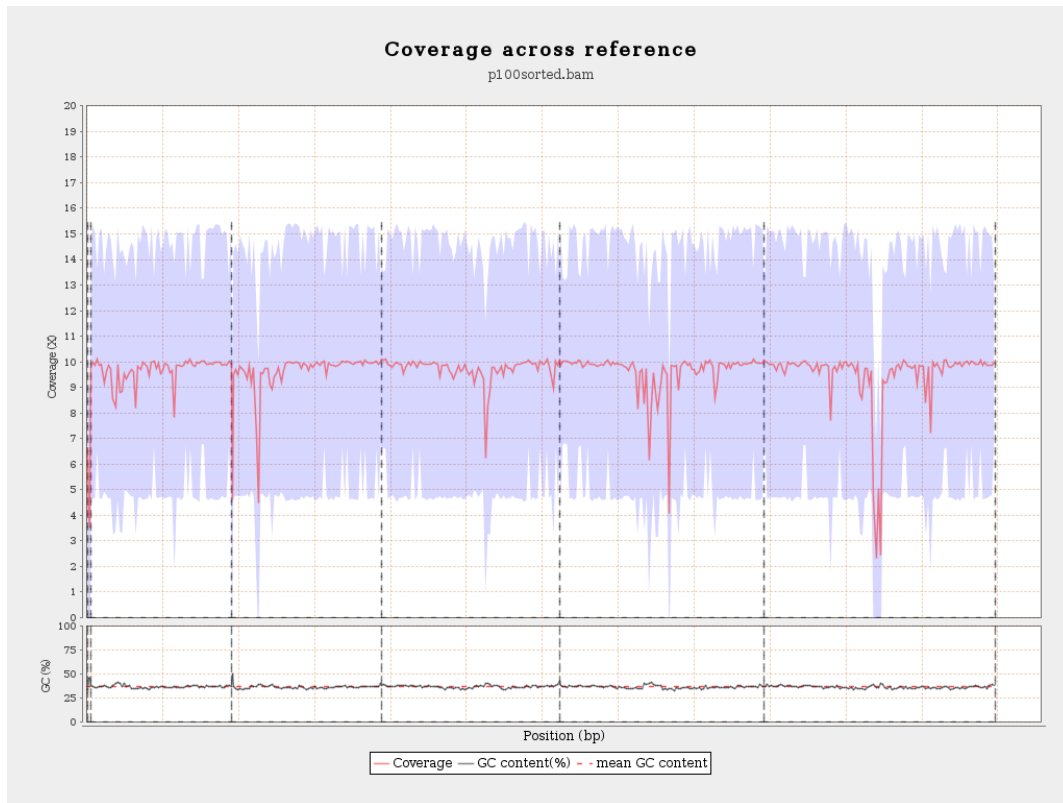
5. Results : Coverage Histogram (0-50X)
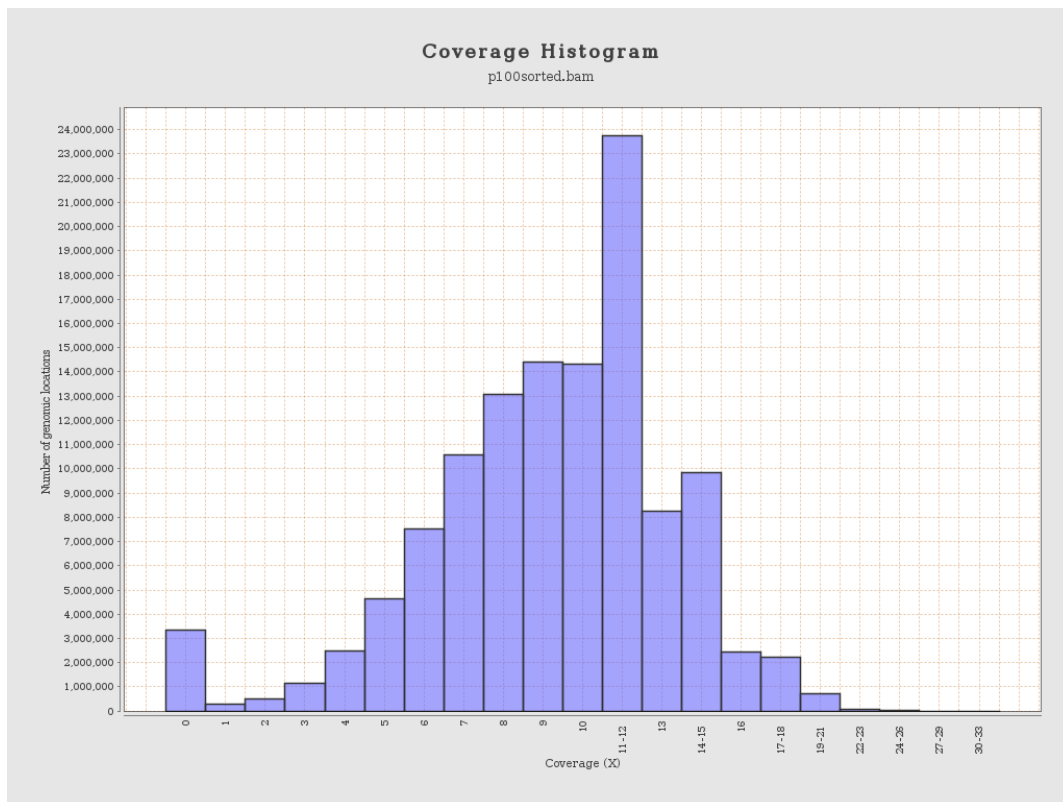
Coverage Histogram (0-50X)
p100sorted.bam

6. Results : Genome Fraction Coverage

Genome Fraction Coverage
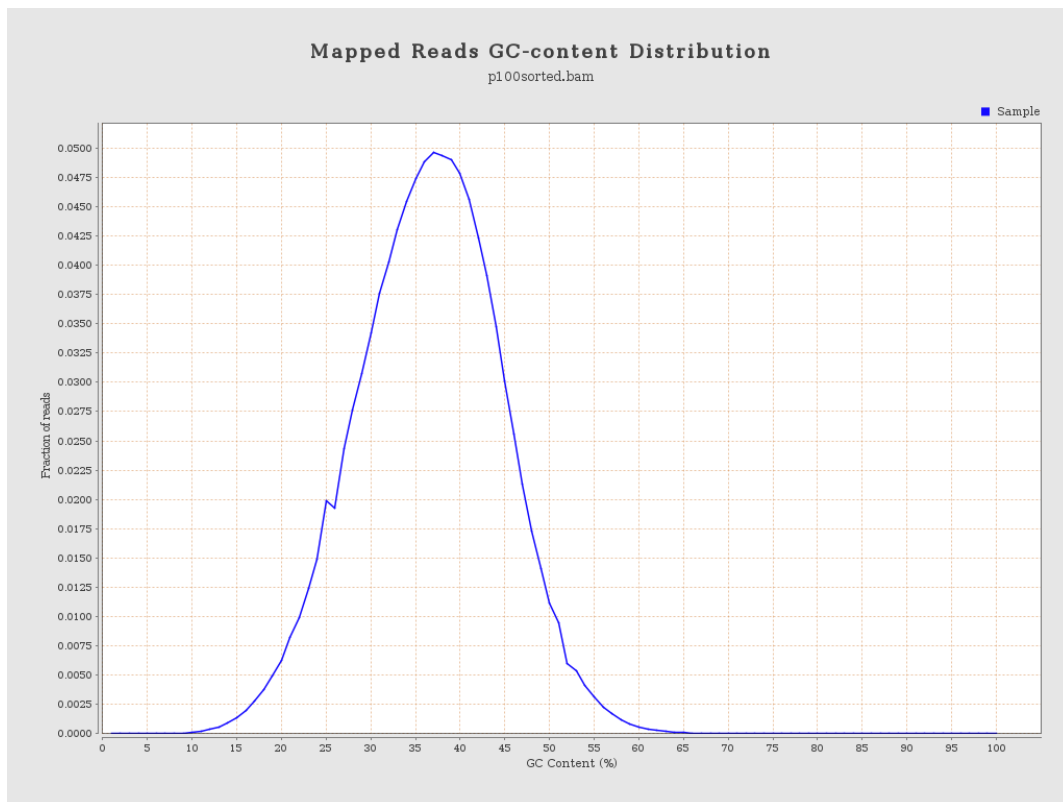p100sorted.bam
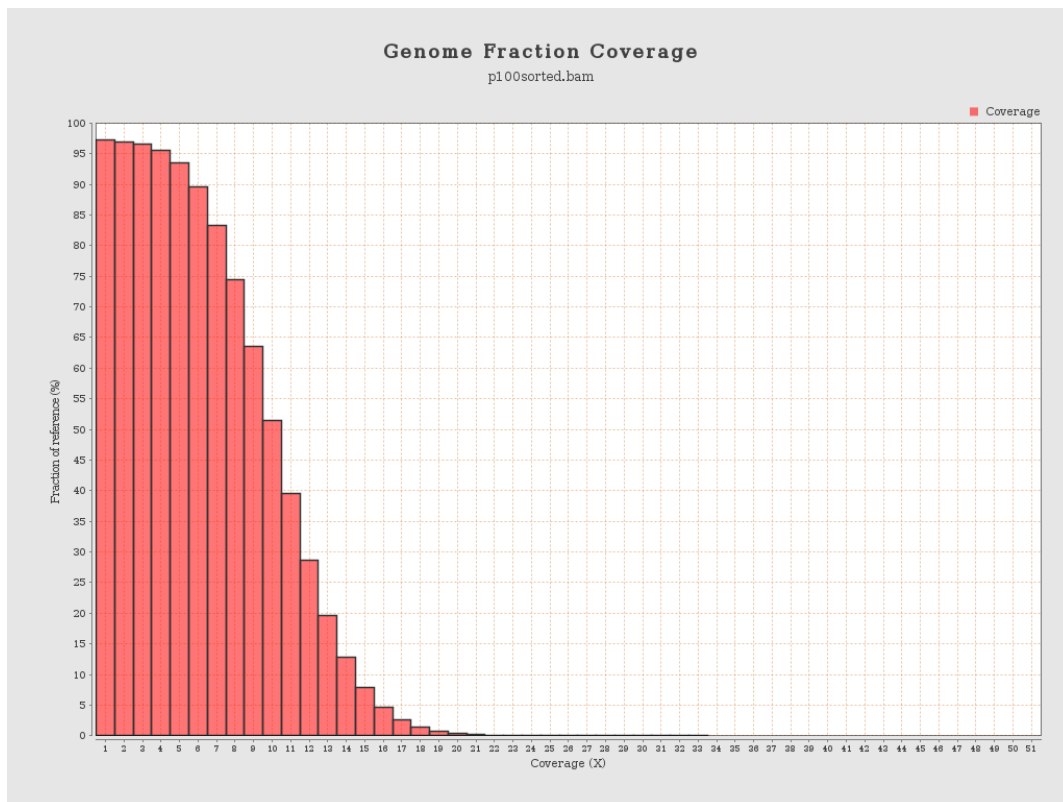
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
p100sorted.bam
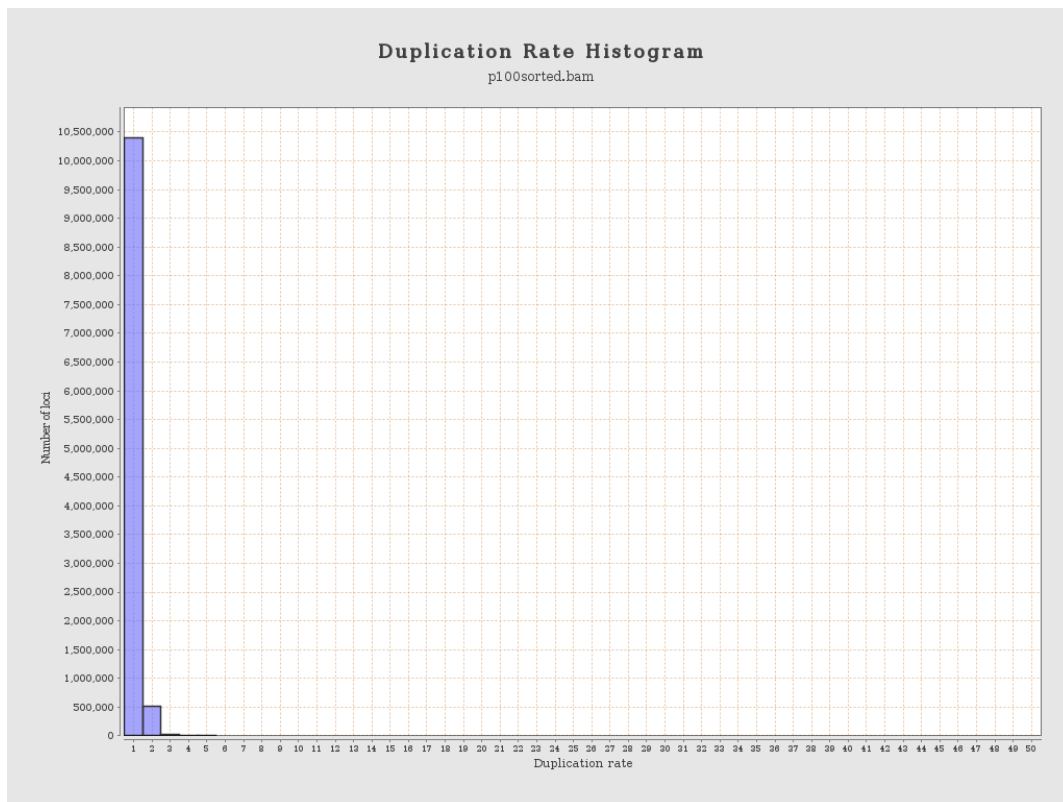
8. Results : Mapped Reads Nucleotide Content

9. Results : Mapped Reads GC-content Distribution
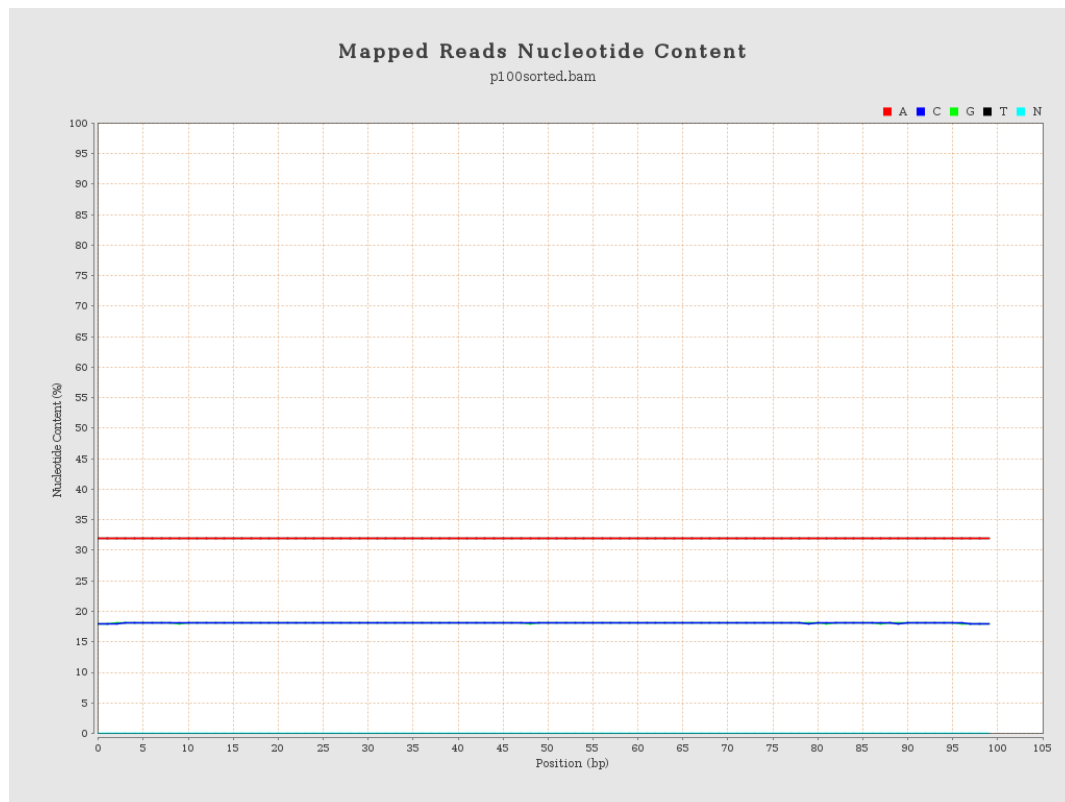
Mapped Reads GC-content Distribution
p100sorted.bam

10. Results : Mapped Reads Clipping Profile
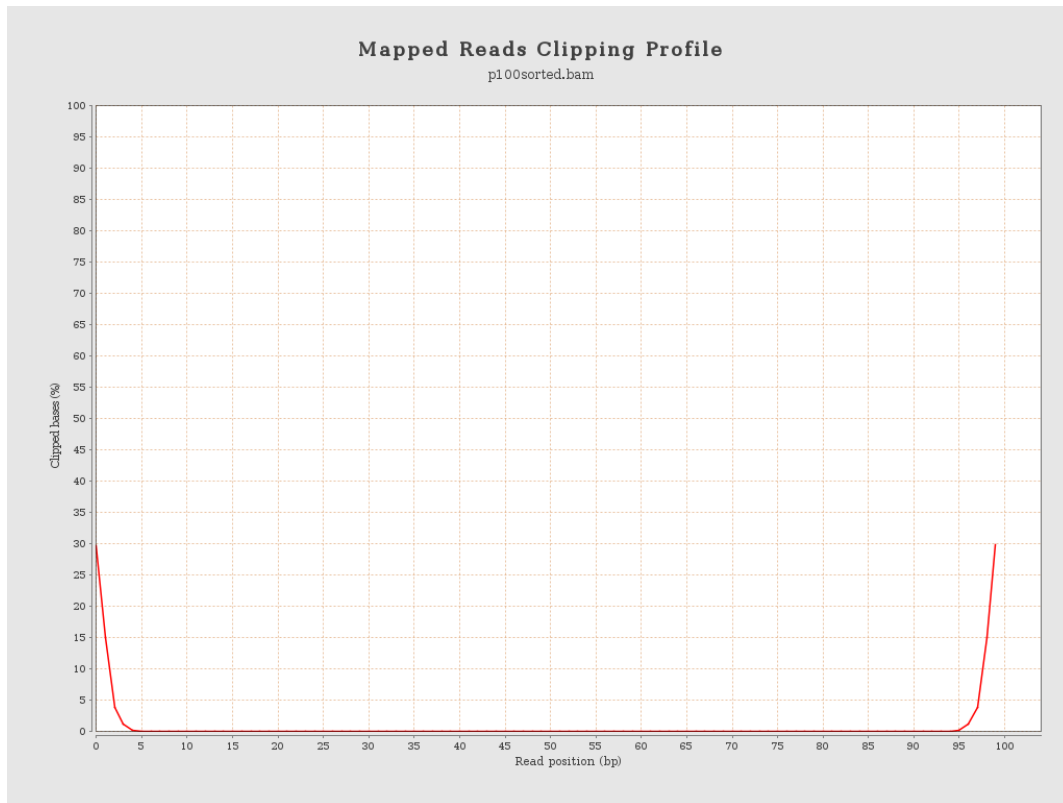
11. Results : Homopolymer Indels

Homopolymer Indels
p100sorted.bam
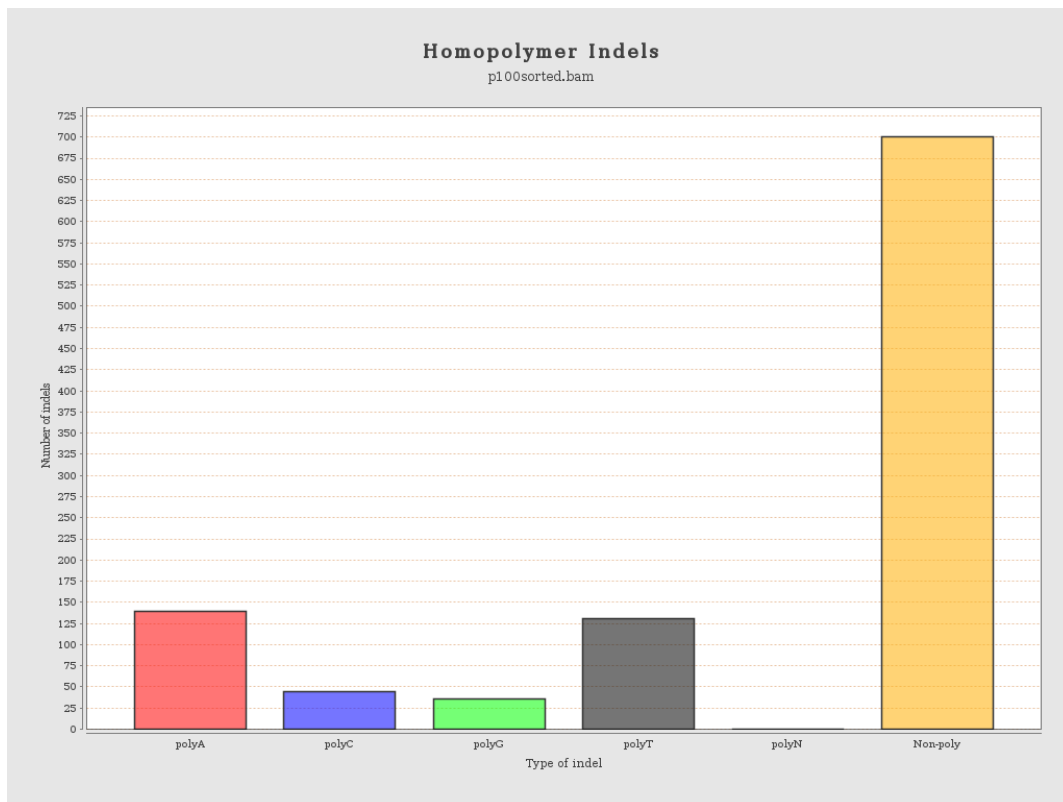
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
p100sorted.bam