

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.0

2016/05/19 11:50:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam  
/export/home/amirh/novoalign_testing/outputBAM/p60sorted.bam -c -nw 400  
-hm 3
```

1.2. Alignment

BAM file:	/export/home/amirh/novoalign_testing/outputBAM/p60sorted.bam
Program:	novoalign (V3.02.12)
Size of a homopolymer:	3
Number of windows:	400
Analysis date:	Thu May 19 09:20:43 MYT 2016
Draw chromosome limits:	yes

2. Summary

2.1. Globals

Reference size	119,667,750
Number of reads	11,947,007
Mapped reads	11,447,727 / 95.82%
Unmapped reads	499,280 / 4.18%
Paired reads	0 / 0%
Read min/max/mean length	100 / 100 / 100
Clipped reads	370,879 / 3.1%
Duplication rate	4.9%

2.2. ACGT Content

Number/percentage of A's	365,711,413 / 31.96%
Number/percentage of C's	206,533,517 / 18.05%
Number/percentage of T's	365,366,029 / 31.93%
Number/percentage of G's	206,539,471 / 18.05%
Number/percentage of N's	0 / 0%
GC Percentage	36.1%

2.3. Coverage

Mean	9.56
Standard Deviation	3.57

2.4. Mapping Quality

Mean Mapping Quality	68.64
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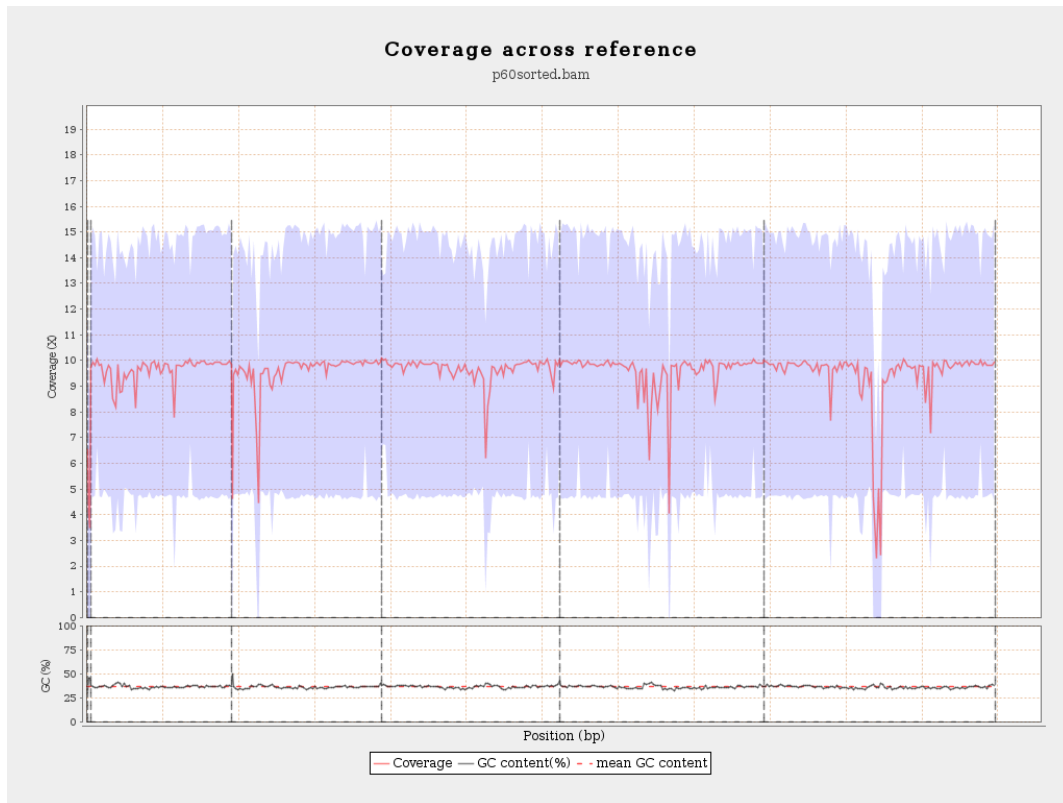
2.5. Mismatches and indels

General error rate	0.7%
Mismatches	8,014,623
Insertions	275
Deletions	404
Homopolymer indels	32.11%

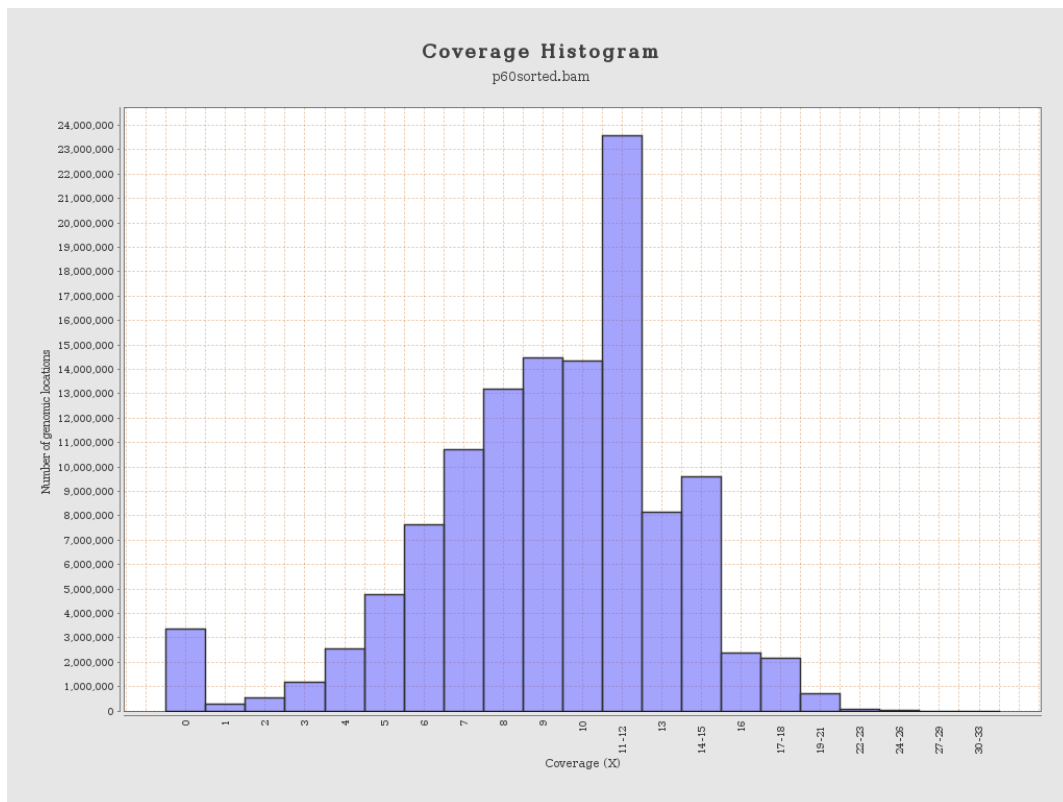
2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
Pt	154478	1009766	6.54	5.32
Mt	366924	1364273	3.72	4.88
4	18585056	179318967	9.65	3.45
2	19698289	189382946	9.61	3.5
3	23459830	226840988	9.67	3.44
5	26975502	258839915	9.6	3.53
1	30427671	287394369	9.45	3.7

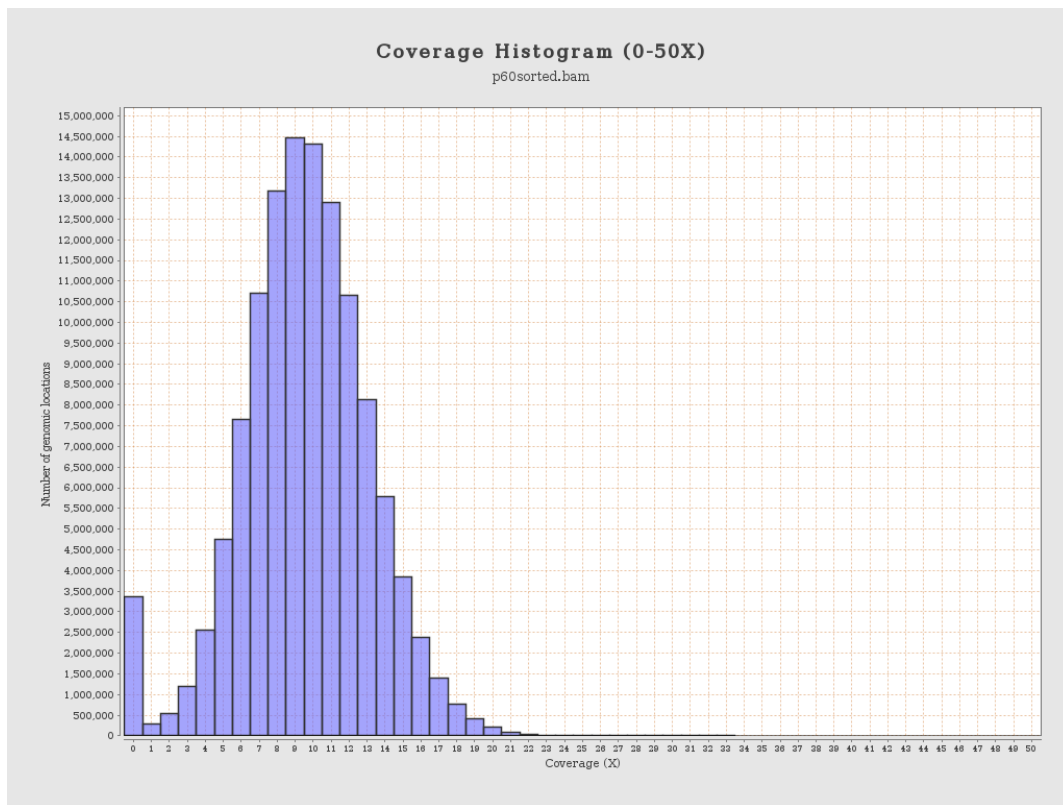
3. Results : Coverage across reference



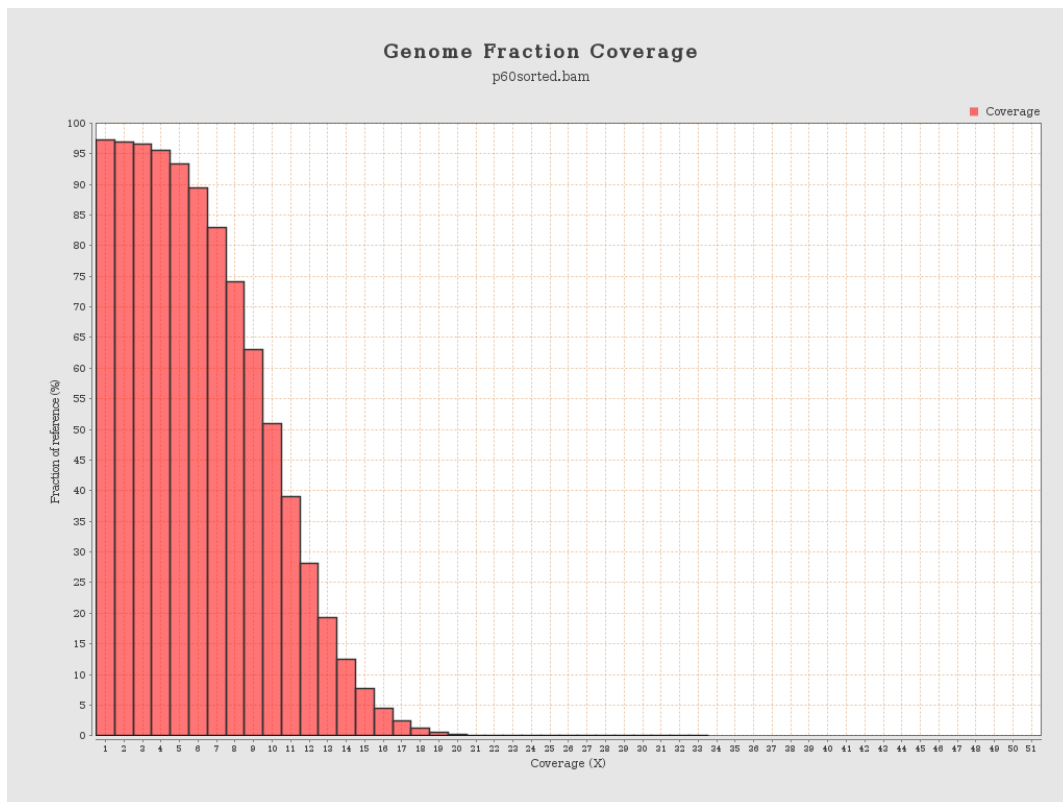
4. Results : Coverage Histogram



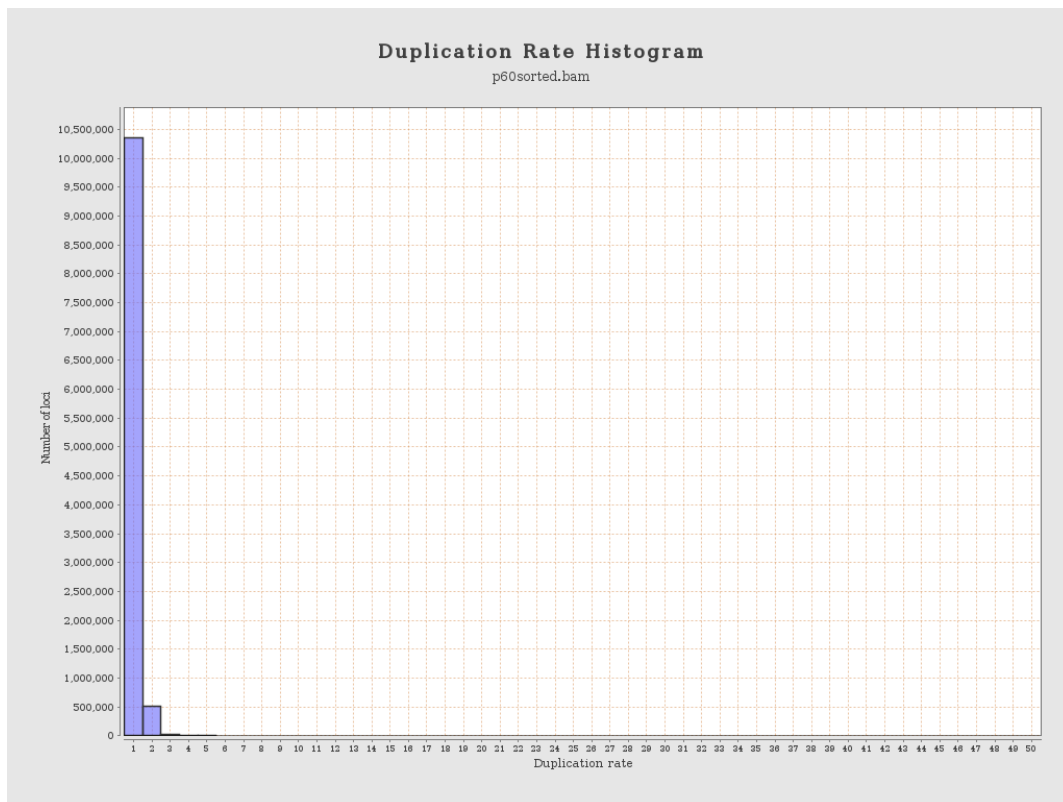
5. Results : Coverage Histogram (0-50X)



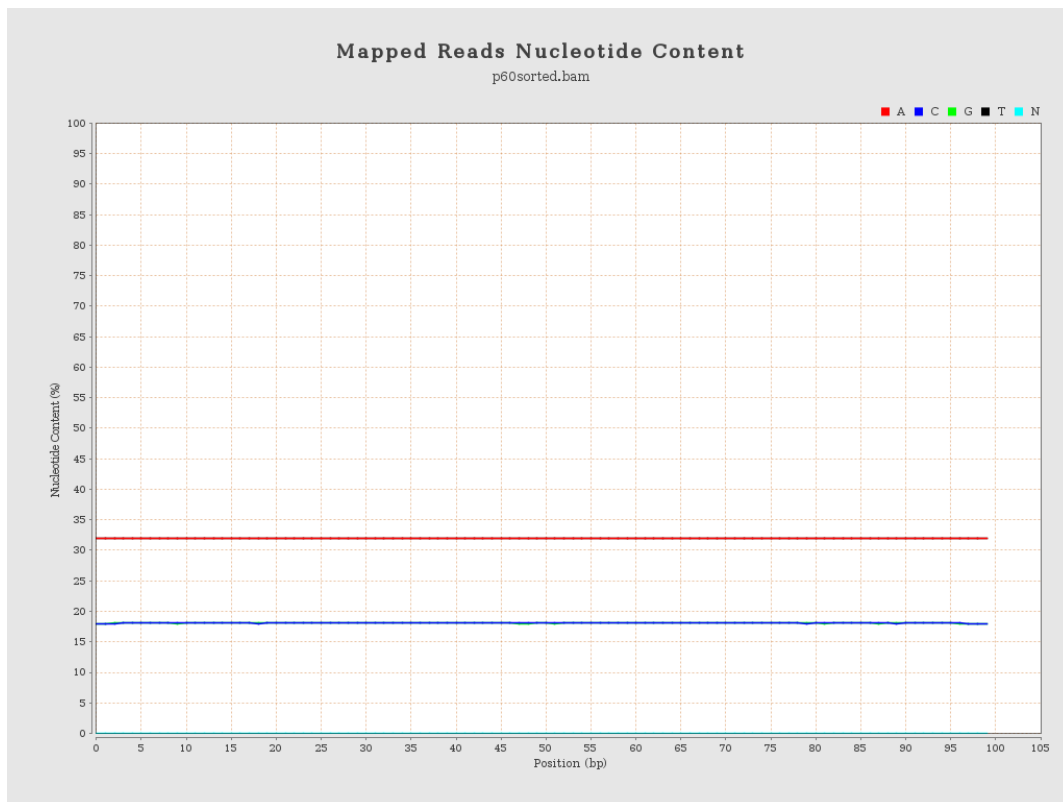
6. Results : Genome Fraction Coverage



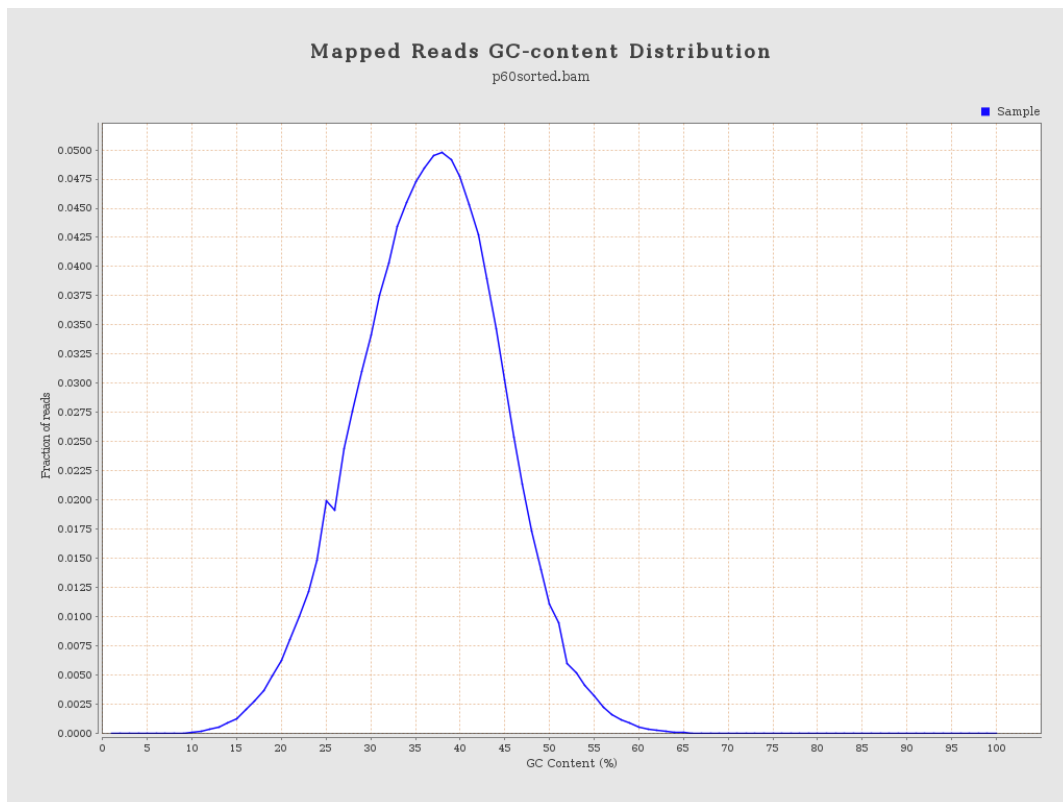
7. Results : Duplication Rate Histogram



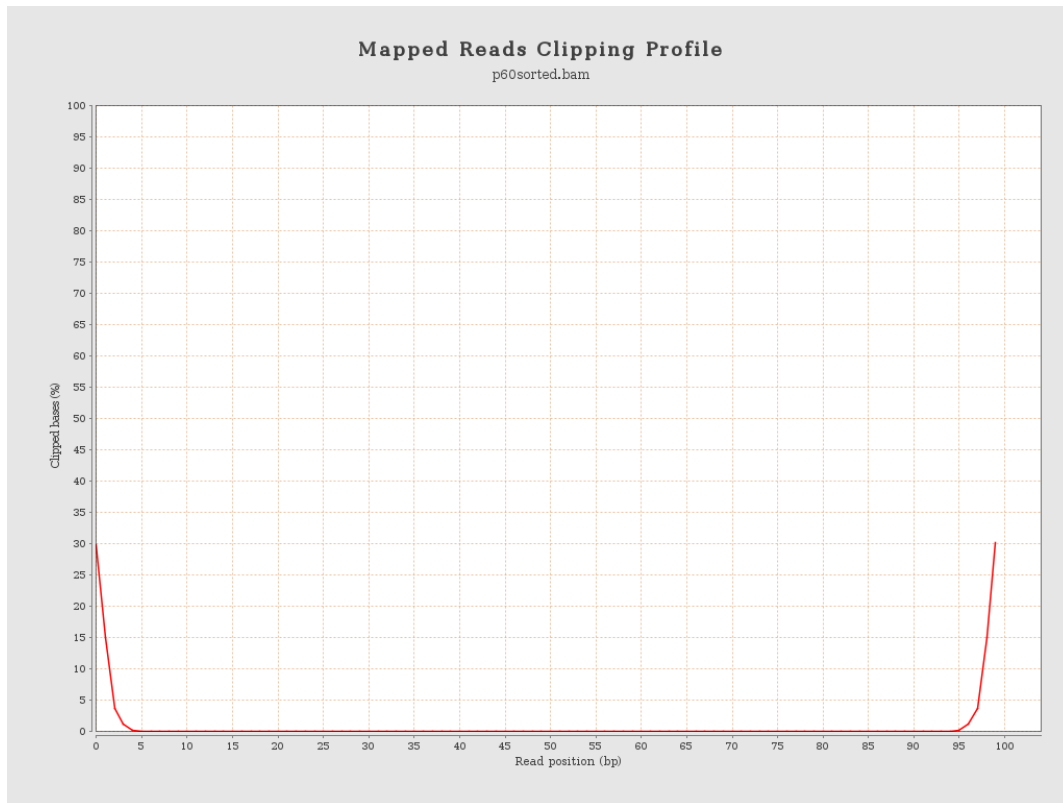
8. Results : Mapped Reads Nucleotide Content



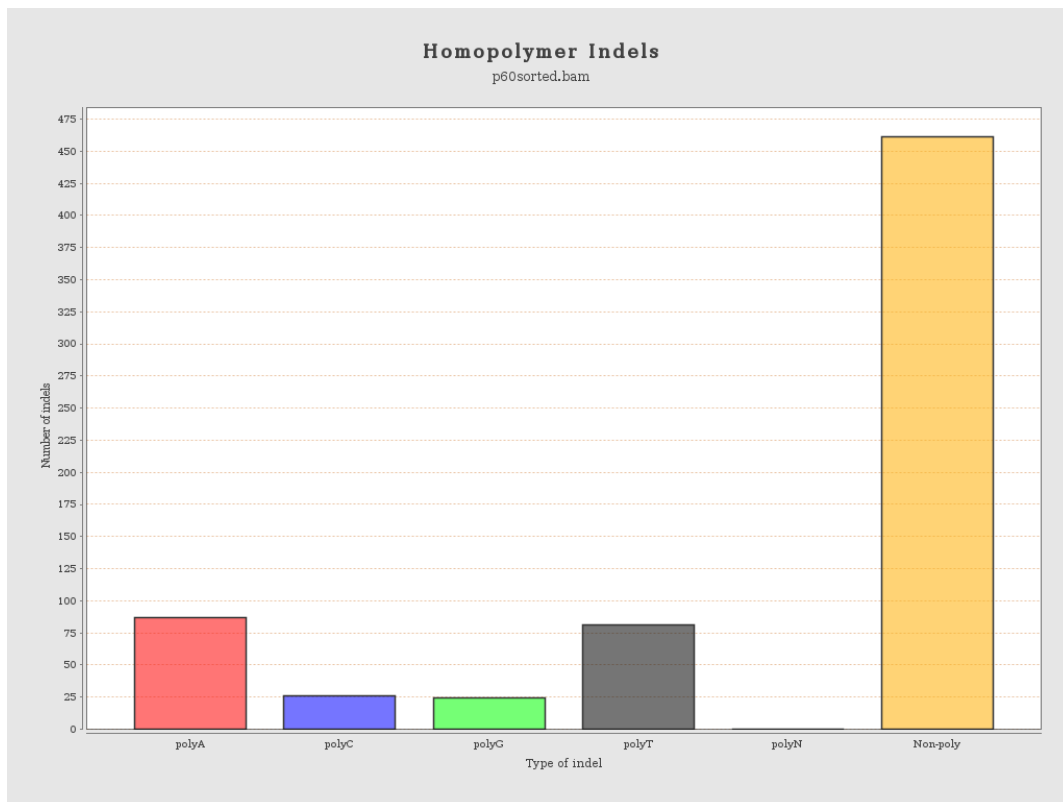
9. Results : Mapped Reads GC-content Distribution



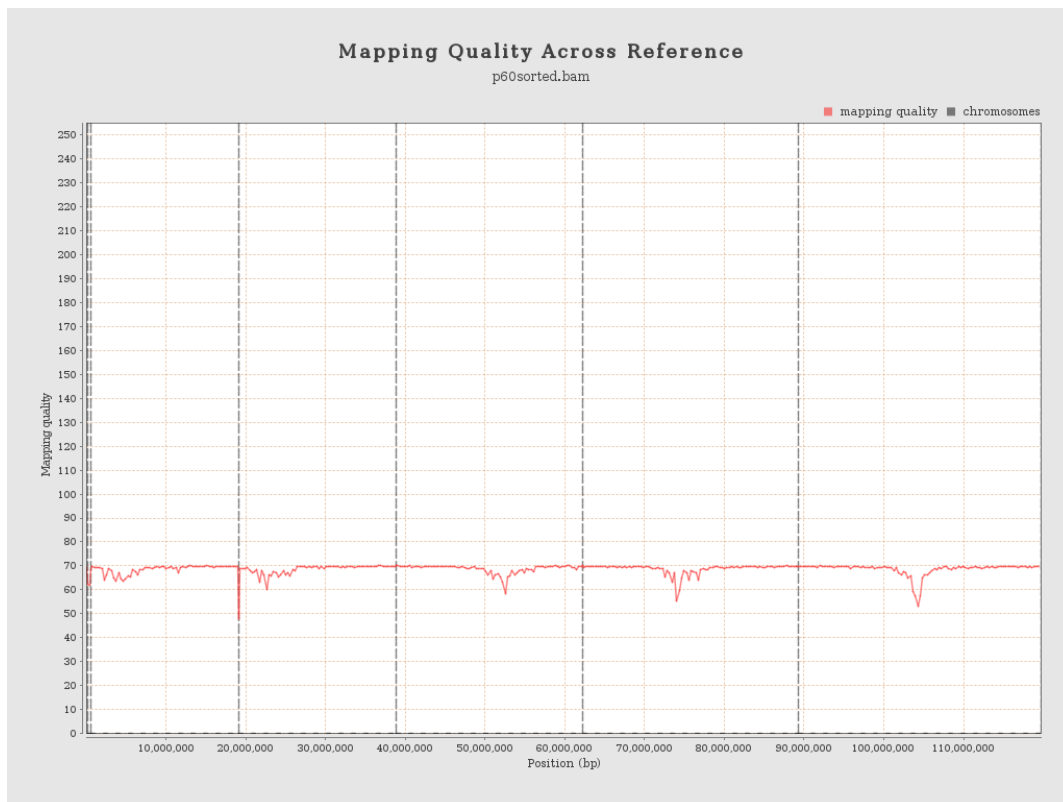
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

