

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.0

2016/05/19 11:54:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam  
/export/home/amirh/novoalign_testing/outputBAM/p0sorted.bam -c -nw 400 -  
hm 3
```

1.2. Alignment

BAM file:	/export/home/amirh/novoalign_testing/outputBAM/p0sorted.bam
Program:	novoalign (V3.02.12)
Size of a homopolymer:	3
Number of windows:	400
Analysis date:	Thu May 19 08:46:07 MYT 2016
Draw chromosome limits:	yes

2. Summary

2.1. Globals

Reference size	119,667,750
Number of reads	11,947,007
Mapped reads	498,444 / 4.17%
Unmapped reads	11,448,563 / 95.83%
Paired reads	0 / 0%
Read min/max/mean length	100 / 100 / 100
Clipped reads	0 / 0%
Duplication rate	0.22%

2.2. ACGT Content

Number/percentage of A's	15,967,661 / 32.04%
Number/percentage of C's	8,962,112 / 17.98%
Number/percentage of T's	15,950,906 / 32%
Number/percentage of G's	8,963,721 / 17.98%
Number/percentage of N's	0 / 0%
GC Percentage	35.96%

2.3. Coverage

Mean	0.42
Standard Deviation	0.65

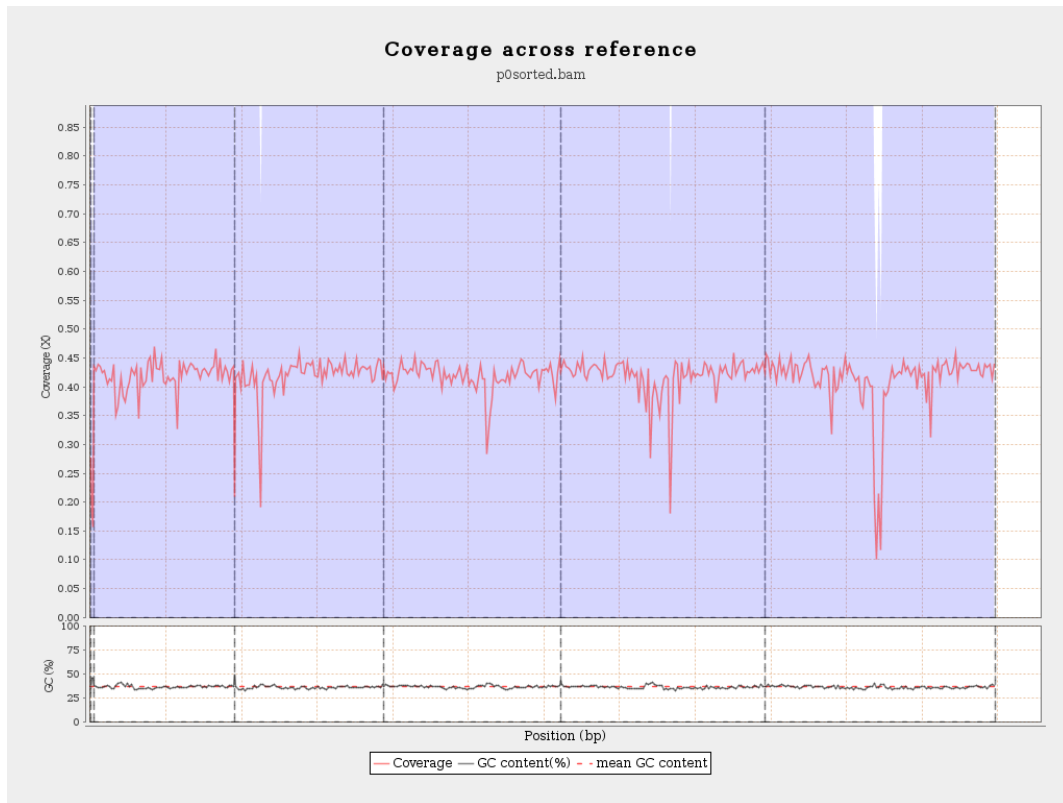
2.4. Mapping Quality

Mean Mapping Quality	68.31
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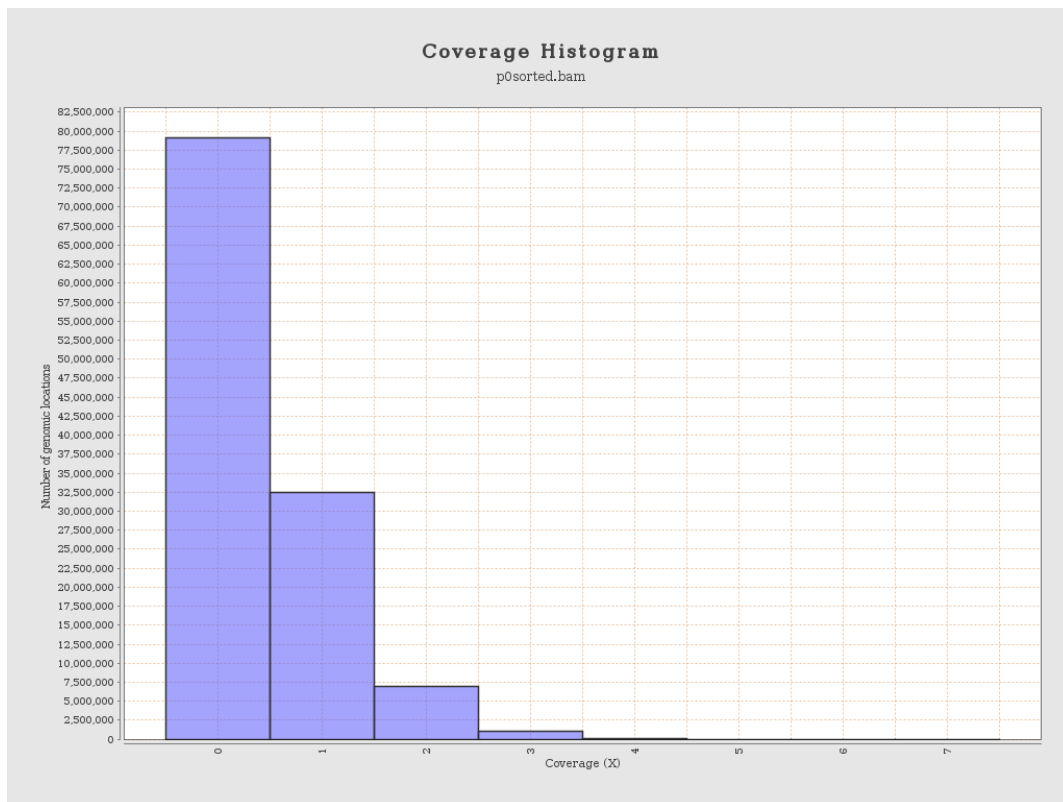
2.5. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
Pt	154478	42600	0.28	0.56
Mt	366924	61400	0.17	0.46
4	18585056	7804100	0.42	0.65
2	19698289	8271900	0.42	0.65
3	23459830	9842500	0.42	0.65
5	26975502	11296200	0.42	0.65
1	30427671	12525700	0.41	0.65

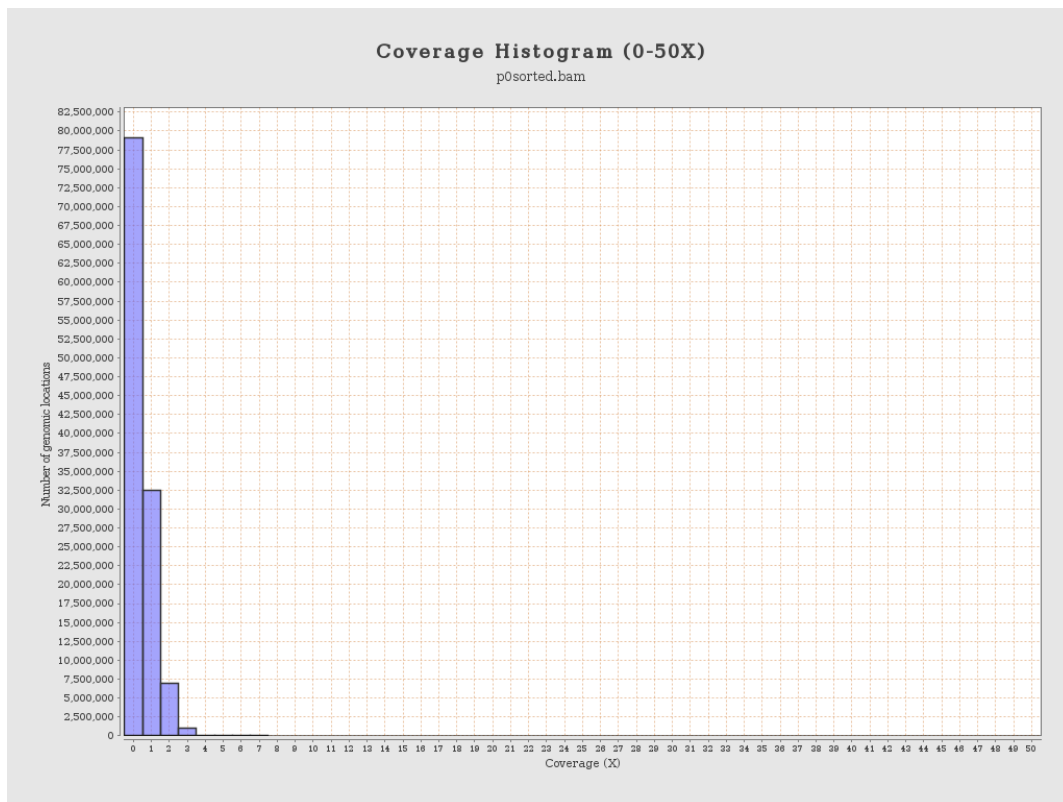
3. Results : Coverage across reference



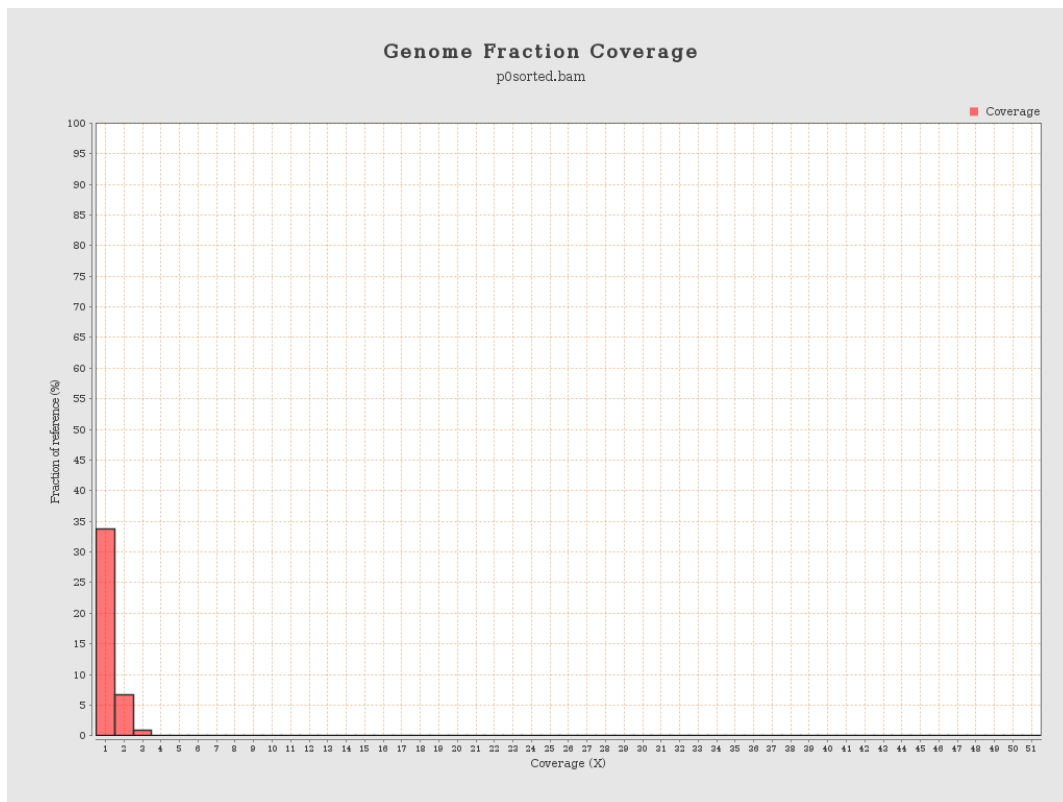
4. Results : Coverage Histogram



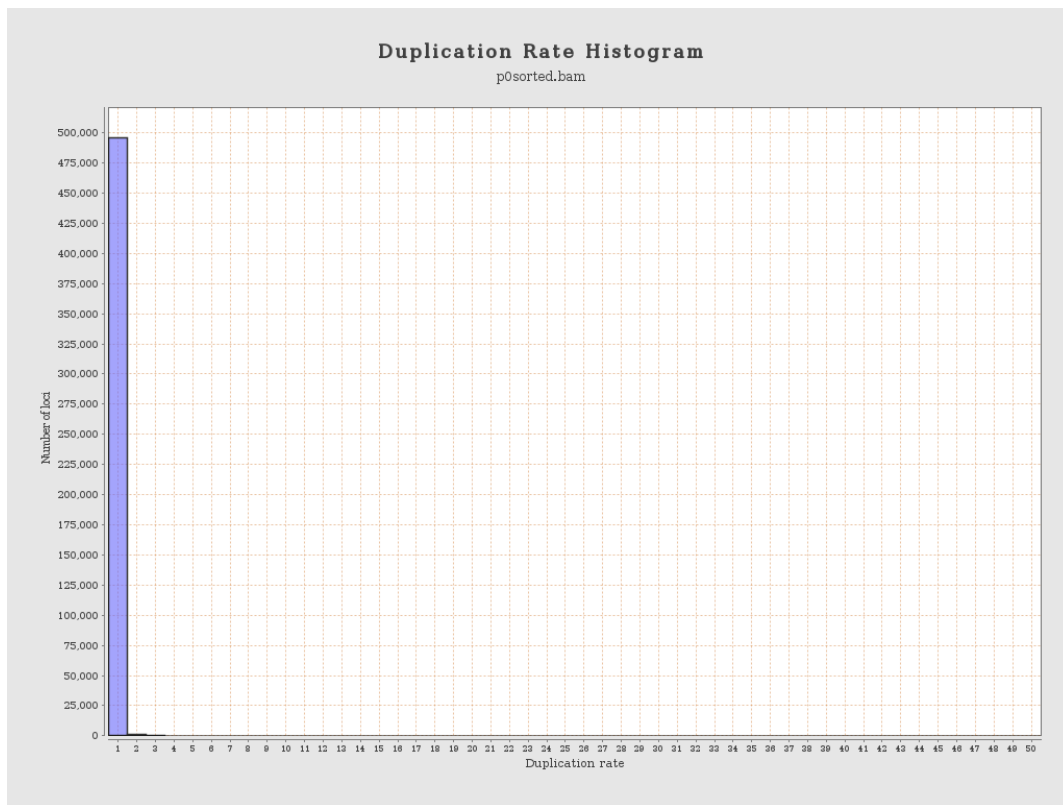
5. Results : Coverage Histogram (0-50X)



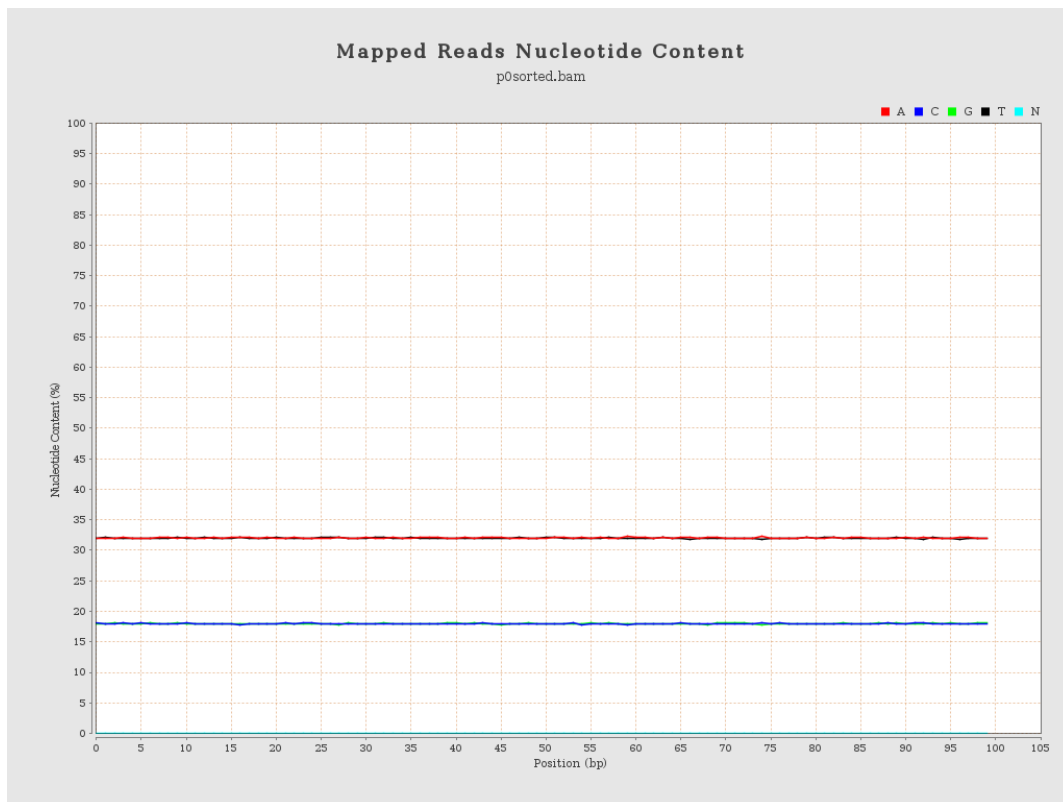
6. Results : Genome Fraction Coverage



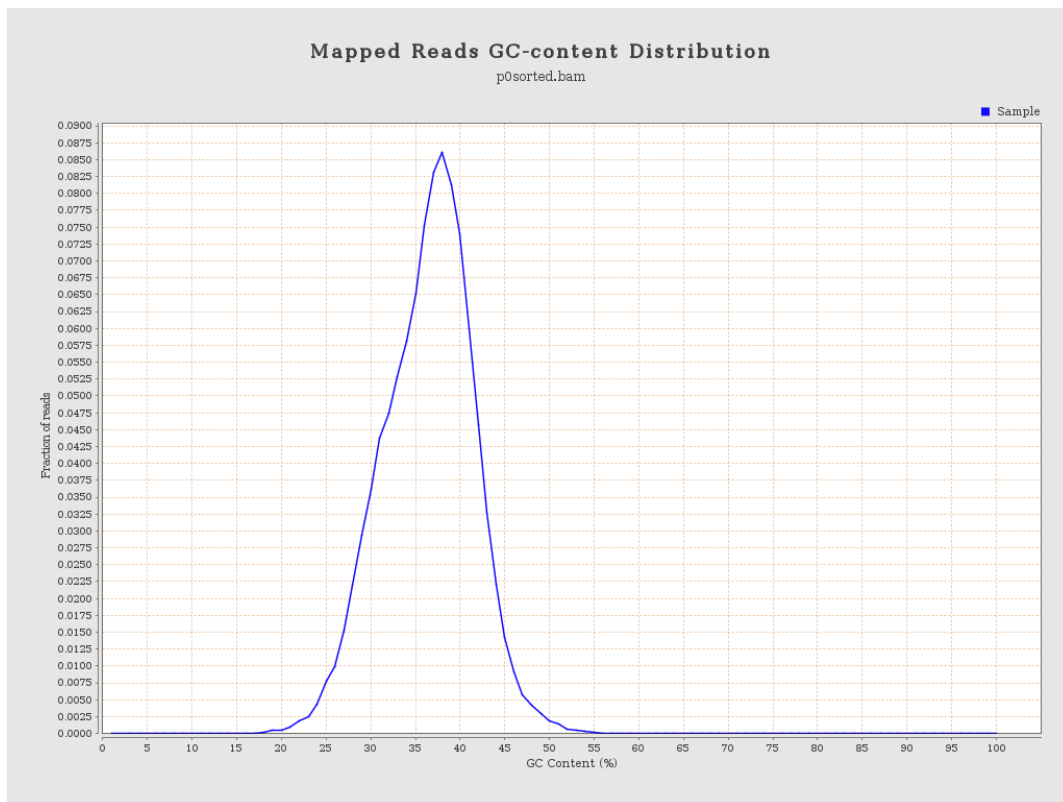
7. Results : Duplication Rate Histogram



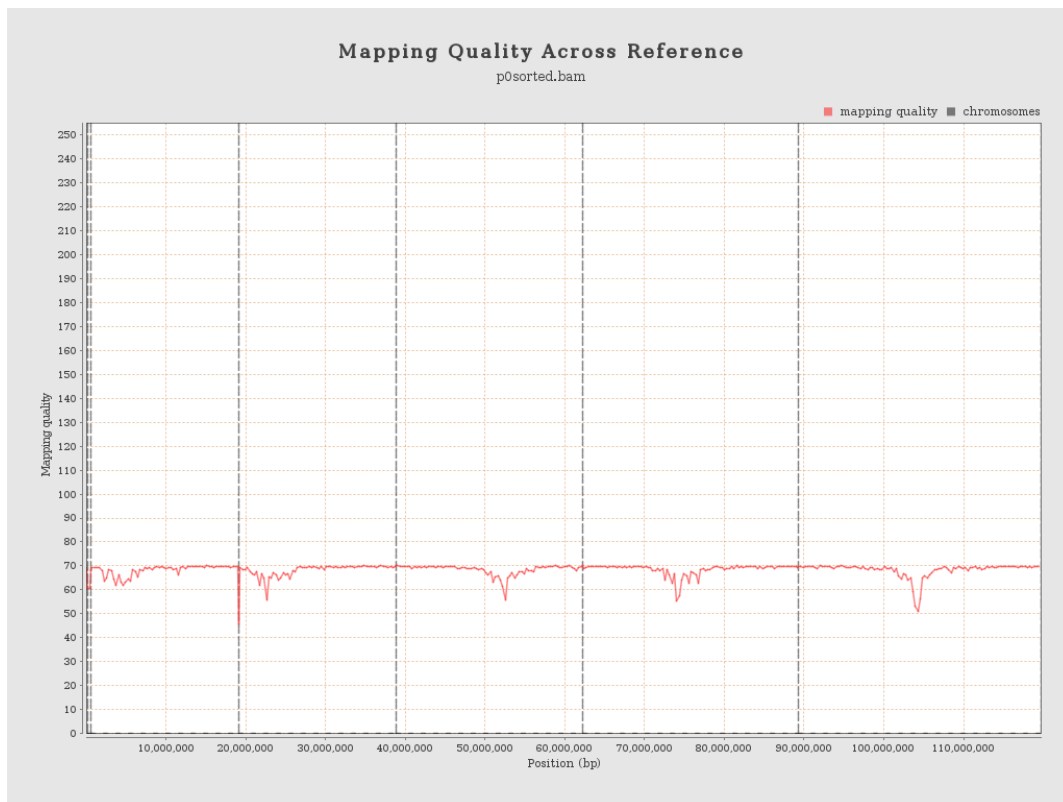
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



10. Results : Mapping Quality Across Reference



11. Results : Mapping Quality Histogram

