

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.0

2016/05/20 09:31:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam  
/export/home/amirh/art_bin_GreatSmokyMountains/testing/try_sorted.bam -c  
-nw 400 -hm 3
```

1.2. Alignment

BAM file:	/export/home/amirh/art_bin_GreatSmokyMountains/testing/try_sorted.bam
Program:	01
Size of a homopolymer:	3
Number of windows:	400
Analysis date:	Fri May 20 09:30:29 MYT 2016
Draw chromosome limits:	yes

2. Summary

2.1. Globals

Reference size	119,667,750
Number of reads	11,946,761
Mapped reads	11,946,761 / 100%
Unmapped reads	0 / 0%
Paired reads	0 / 0%
Read min/max/mean length	100 / 100 / 100
Clipped reads	0 / 0%
Duplication rate	4.92%

2.2. ACGT Content

Number/percentage of A's	378,556,826 / 31.69%
Number/percentage of C's	214,670,378 / 17.97%
Number/percentage of T's	378,059,956 / 31.65%
Number/percentage of G's	214,452,030 / 17.95%
Number/percentage of N's	0 / 0%
GC Percentage	35.92%

2.3. Coverage

Mean	9.98
Standard Deviation	3.18

2.4. Mapping Quality

Mean Mapping Quality	99
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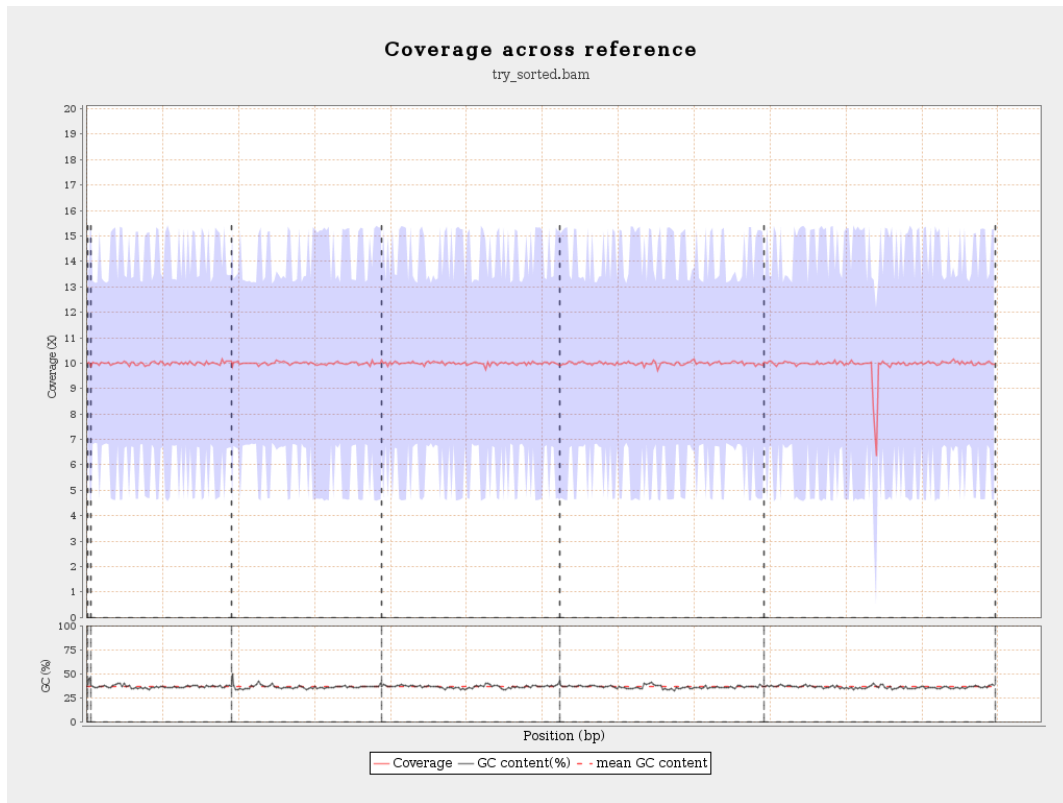
2.5. Mismatches and indels

Insertions	522
Deletions	698
Homopolymer indels	22.05%

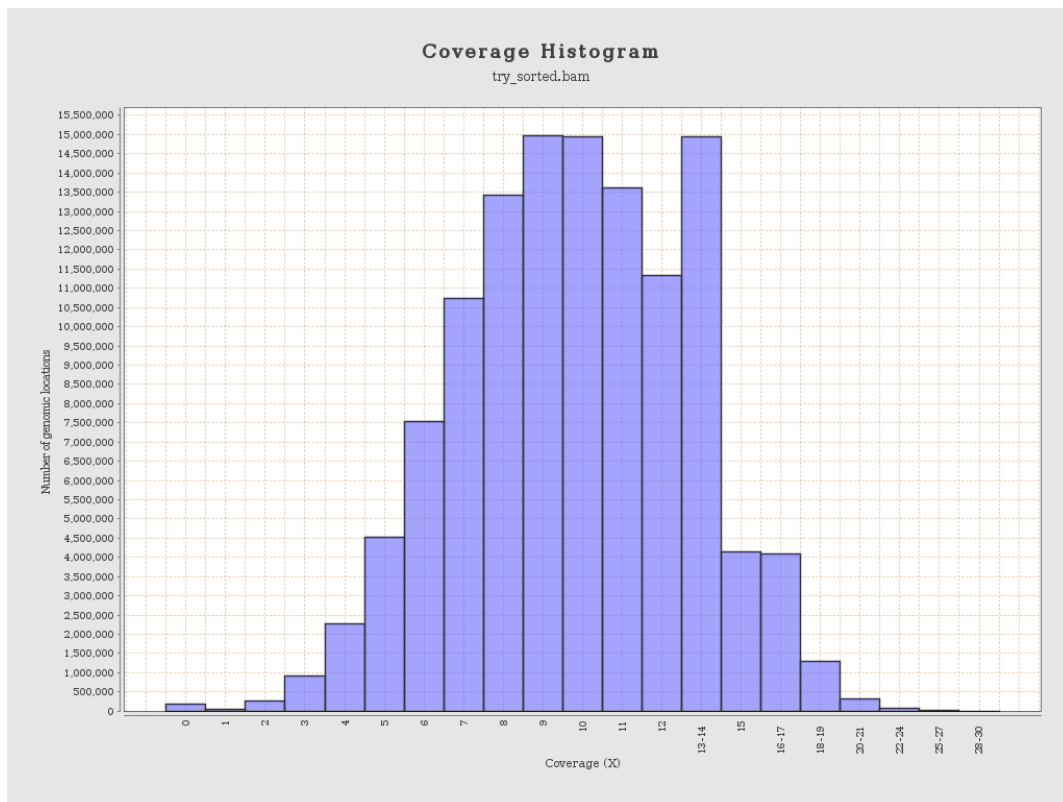
2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
Pt	154478	1544000	9.99	3.13
Mt	366924	3668999	10	3.17
4	18585056	185813634	10	3.16
2	19698289	196947450	10	3.17
3	23459830	234477445	9.99	3.16
5	26975502	269628319	10	3.17
1	30427671	302596429	9.94	3.24

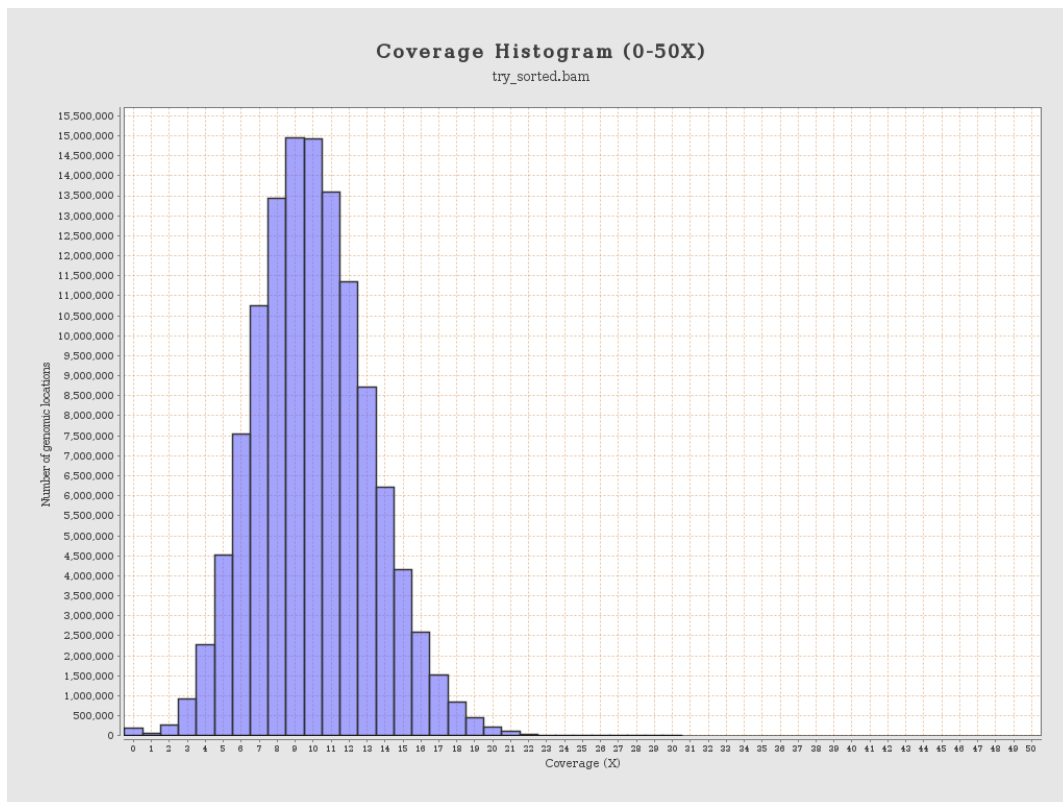
3. Results : Coverage across reference



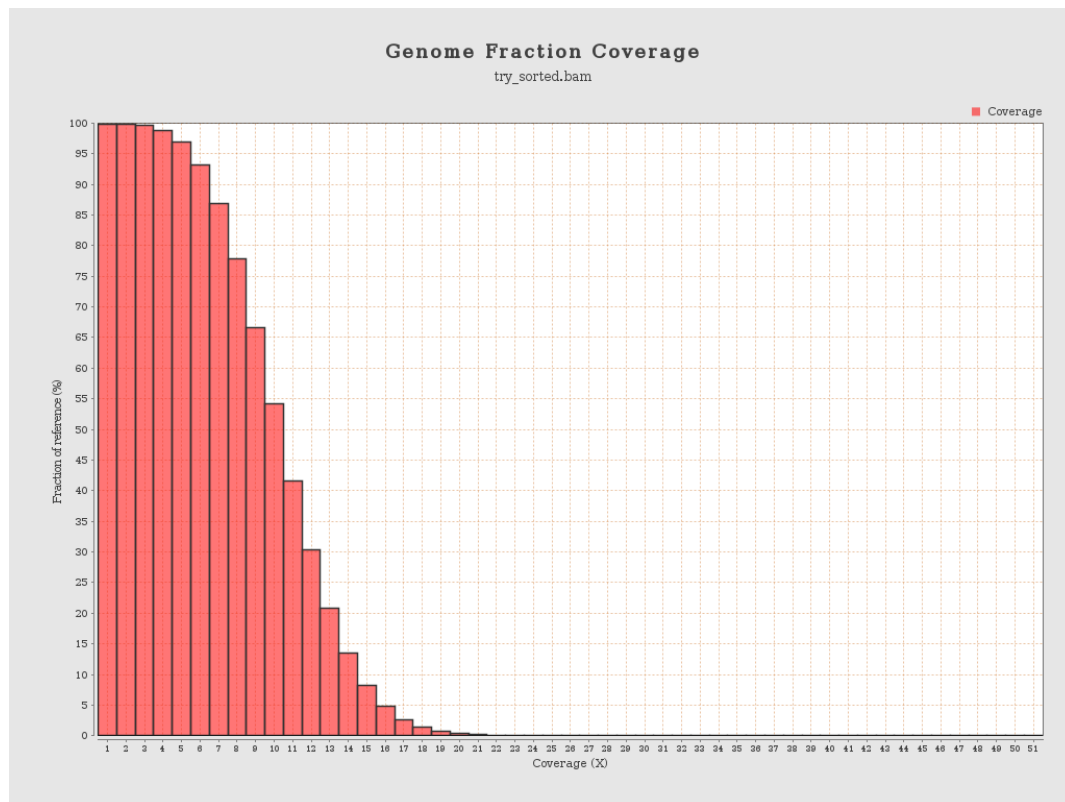
4. Results : Coverage Histogram



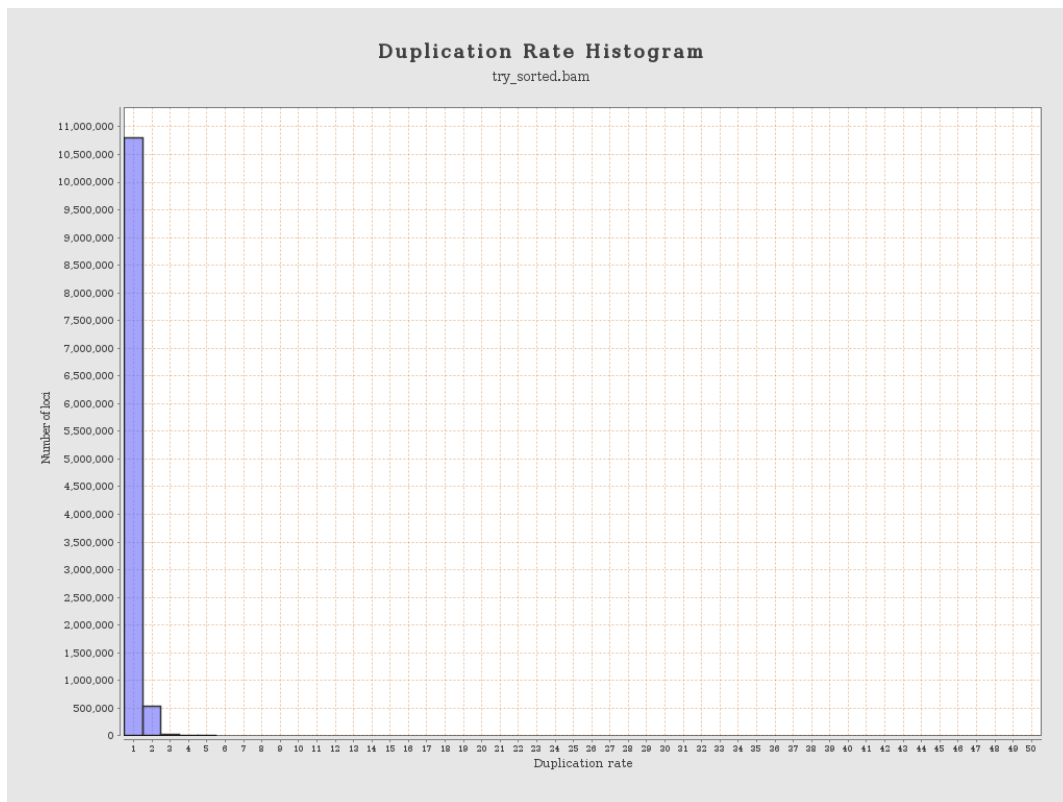
5. Results : Coverage Histogram (0-50X)



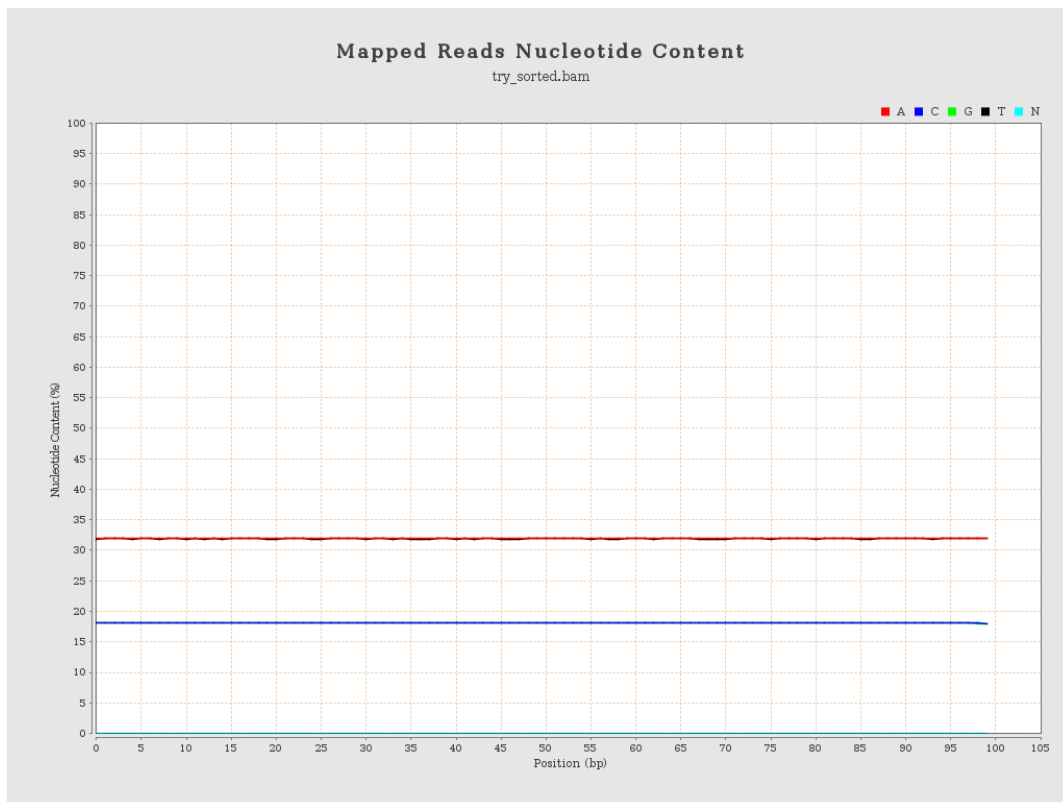
6. Results : Genome Fraction Coverage



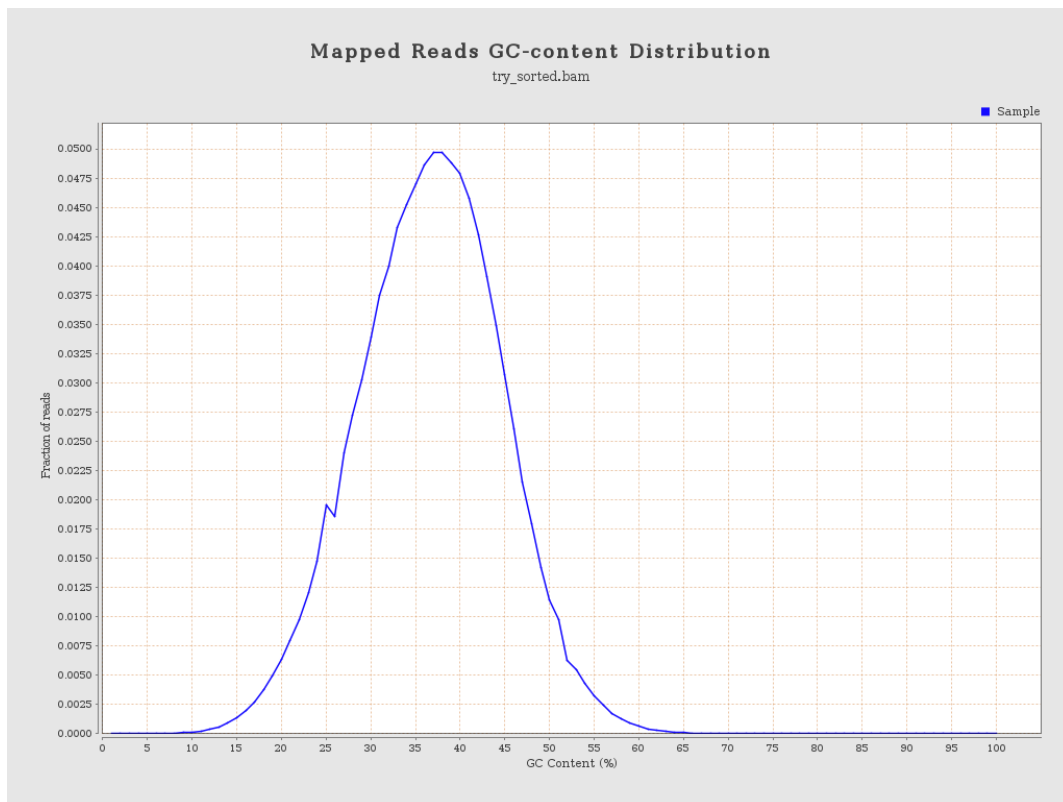
7. Results : Duplication Rate Histogram



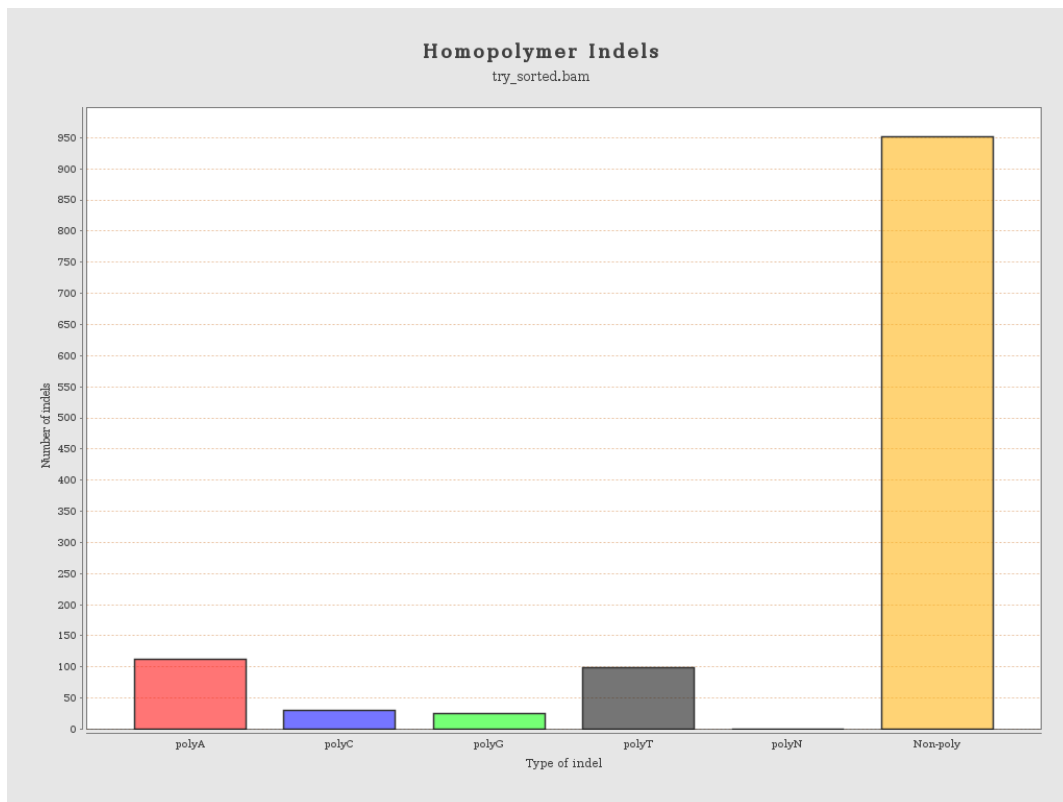
8. Results : Mapped Reads Nucleotide Content



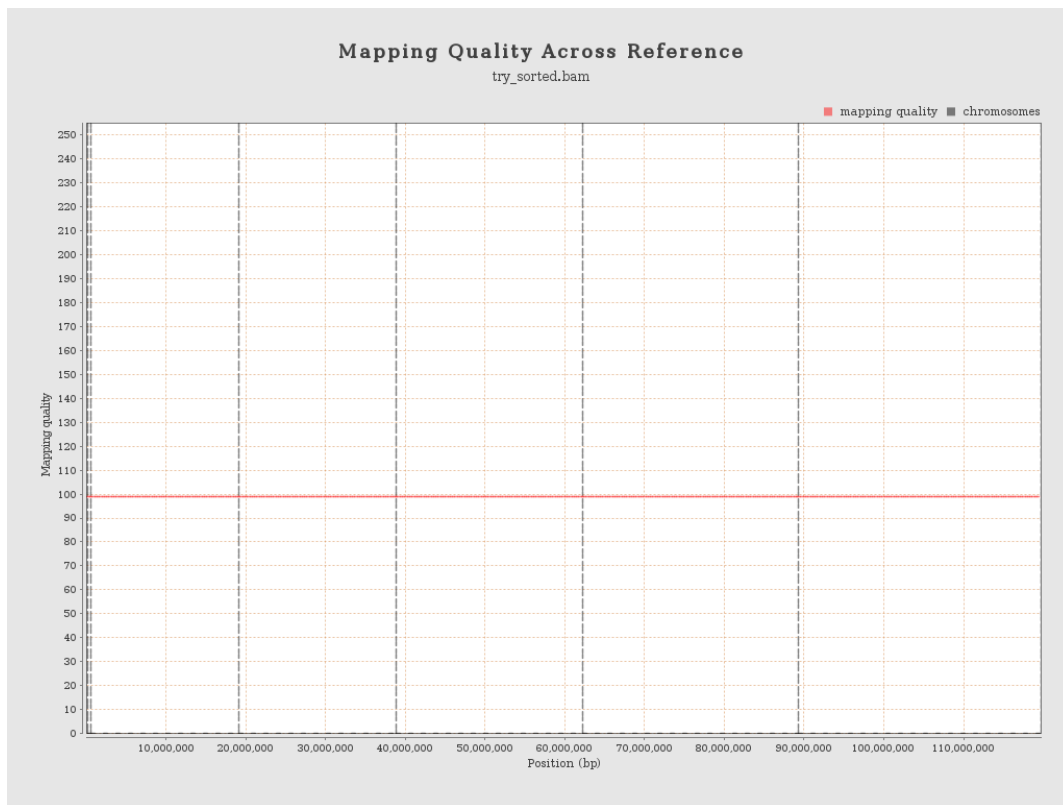
9. Results : Mapped Reads GC-content Distribution



10. Results : Homopolymer Indels



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

