Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.0.1

2015/01/29 23:55:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/harrir/groups/harrisonlab/project_files/rootstock_genetics/m13/analysi
s/m13.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/home/harrir/groups/harrisonlab/project_files/rootstock_genetics/m13/analysis/m13.sorted.bam
Program:	bowtie2 (2.0.5)
Command line:	
Size of a homopolymer:	3
Number of windows:	400
Analysis date:	Thu Jan 29 23:45:39 GMT 2015
Draw chromosome limits:	yes

2. Summary

2.1. Globals

Reference size	578,875,605
Number of reads	399,471,100
Mapped reads	282,460,015 / 70.71%
Unmapped reads	117,011,085 / 29.29%
Paired reads	282,460,015 / 70.71%
Mapped reads, only first in pair	144,088,162 / 36.07%
Mapped reads, only second in pair	138,371,853 / 34.64%
Mapped reads, both in pair	260,515,340 / 65.22%
Mapped reads, singletons	21,944,675 / 5.49%
Read min/max/mean length	101 / 101 / 101
Clipped reads	0 / 0%
Duplication rate	38.26%

2.2. ACGT Content

Number/percentage of A's	8,834,256,266 / 31.03%
Number/percentage of C's	5,392,977,835 / 18.94%
Number/percentage of T's	8,848,170,037 / 31.08%
Number/percentage of G's	5,396,082,532 / 18.95%
Number/percentage of N's	0 / 0%
GC Percentage	37.89%

2.3. Coverage

Mean	49.26
Standard Deviation	298.39

2.4. Mapping Quality

Mean Mapping Quality	21.71

2.5. Insert size

Mean	6,053.4
Standard Deviation	321,577.85
P25/Median/P75	190 / 339 / 364

2.6. Mismatches and indels

General error rate	3.35%
Mismatches	755,024,078
Insertions	24,906,967
Deletions	21,722,454
Homopolymer indels	54.16%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LG10_pht	36966320	1836713307	49.69	225.57
LG11_pht	38535128	1910954090	49.59	218.01
LG12_pht	34924356	1675126976	47.96	406.24
LG13_pht	37956969	2052851076	54.08	264.35

LG14_pht	32305939	1654572058	51.22	644.25
LG15_pht	53078040	2464466580	46.43	217.61
LG16_pht	22123682	1141902538	51.61	357.06
LG17_pht	26512479	1250741606	47.18	136.42
LG1_pht	33466746	1453779911	43.44	185.21
LG2_pht	39136869	1929875534	49.31	322.41
LG3_pht	37898467	1843365438	48.64	306.98
LG4_pht	24311090	1226856481	50.46	201.03
LG5_pht	34832717	1775439109	50.97	247.28
LG6_pht	28552943	1363536322	47.75	278.23
LG7_pht	29555396	1480144971	50.08	250.4
LG8_pht	32612457	1597439108	48.98	245.36
LG9_pht	36106007	1858052271	51.46	249.34

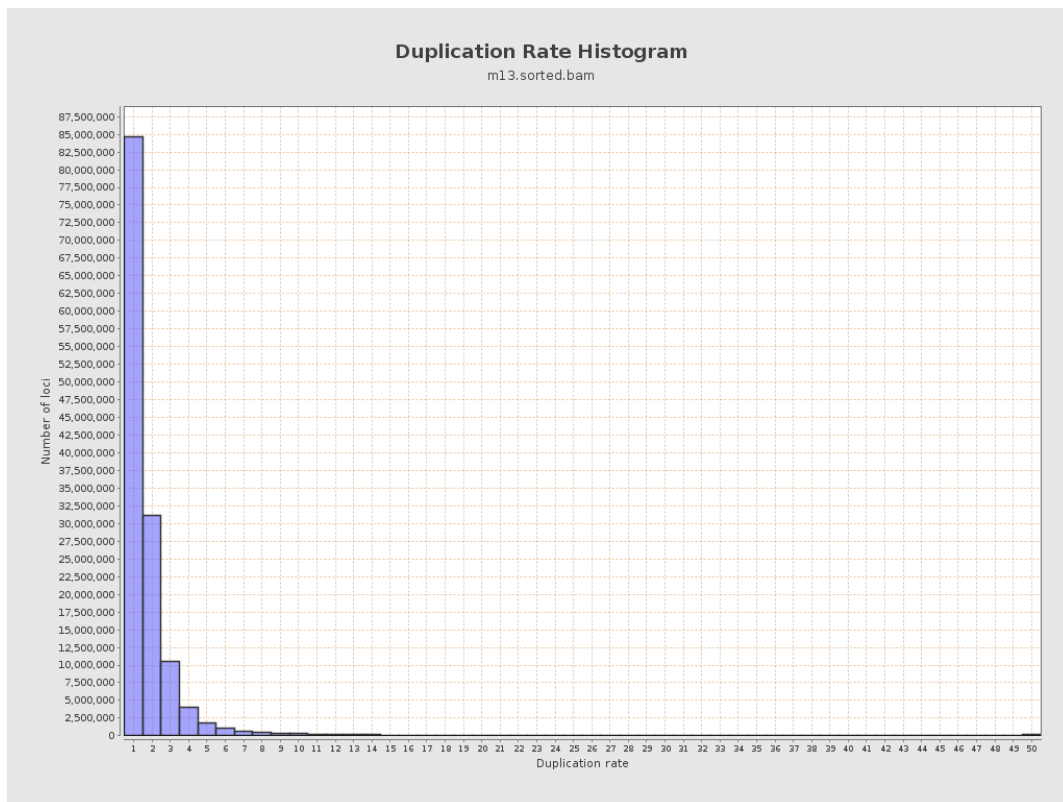# 3. Results : Coverage across reference

4. Results : Coverage Histogram

Coverage Histogram
m13.sorted.bam
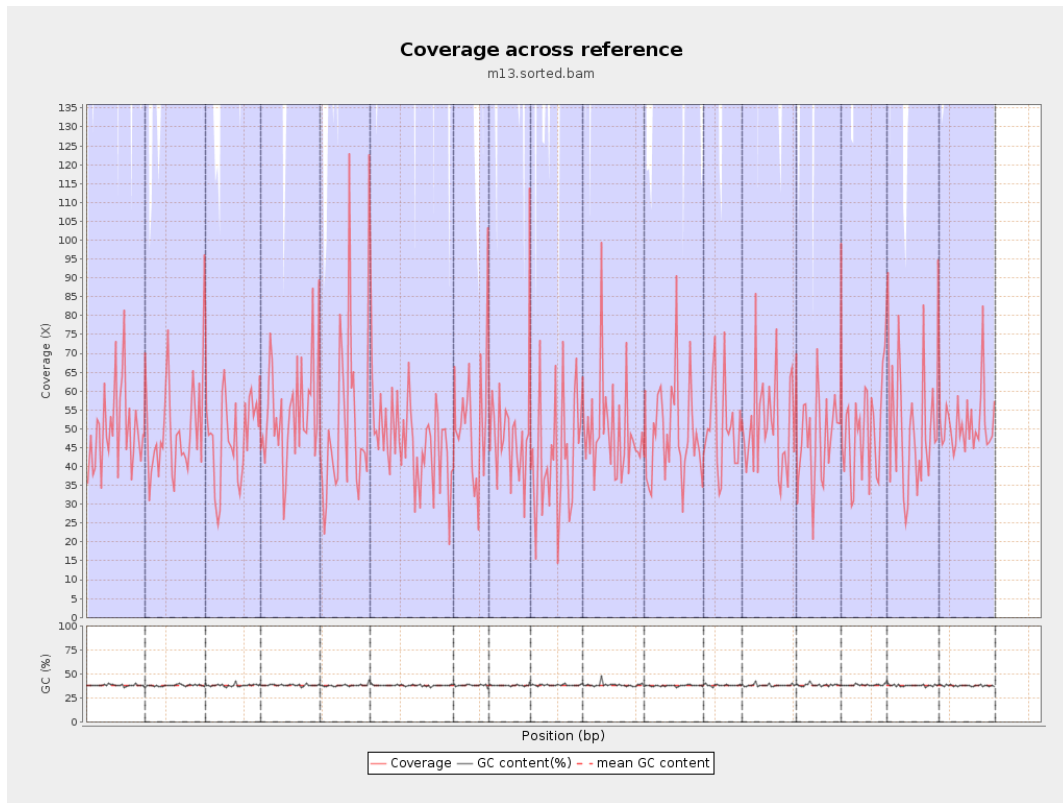
5. Results : Coverage Histogram (0-50X)
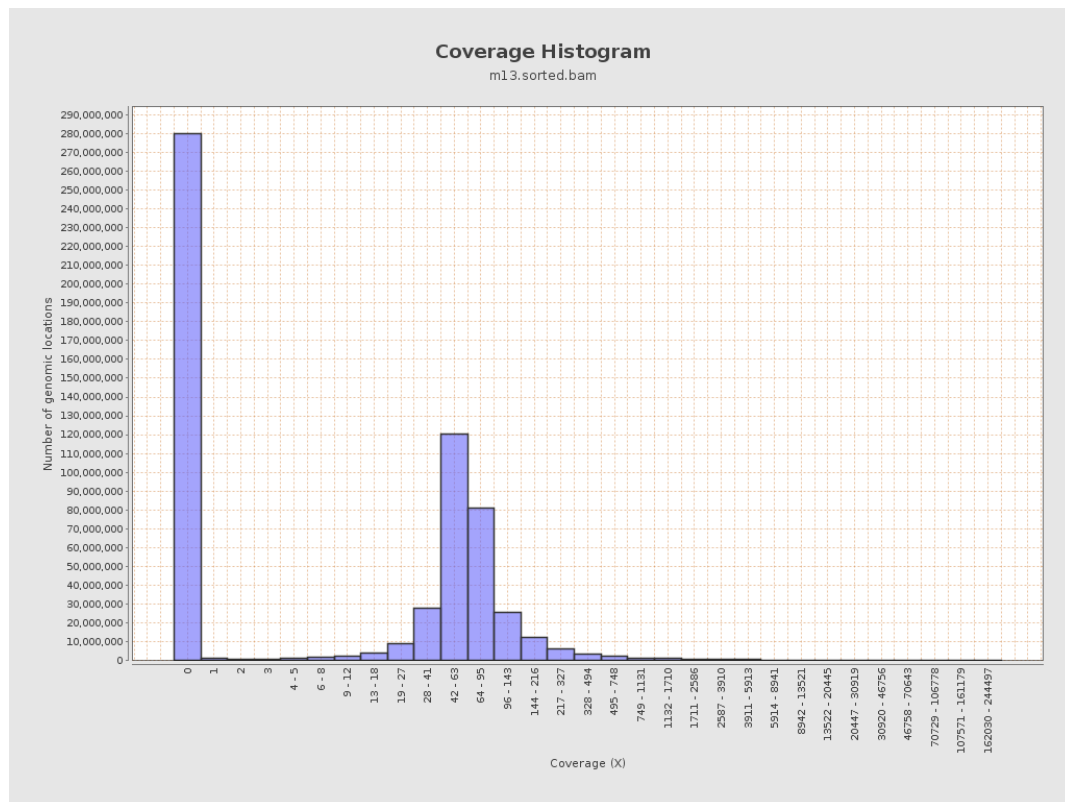
Coverage Histogram (0-50X)
m13.sorted.bam
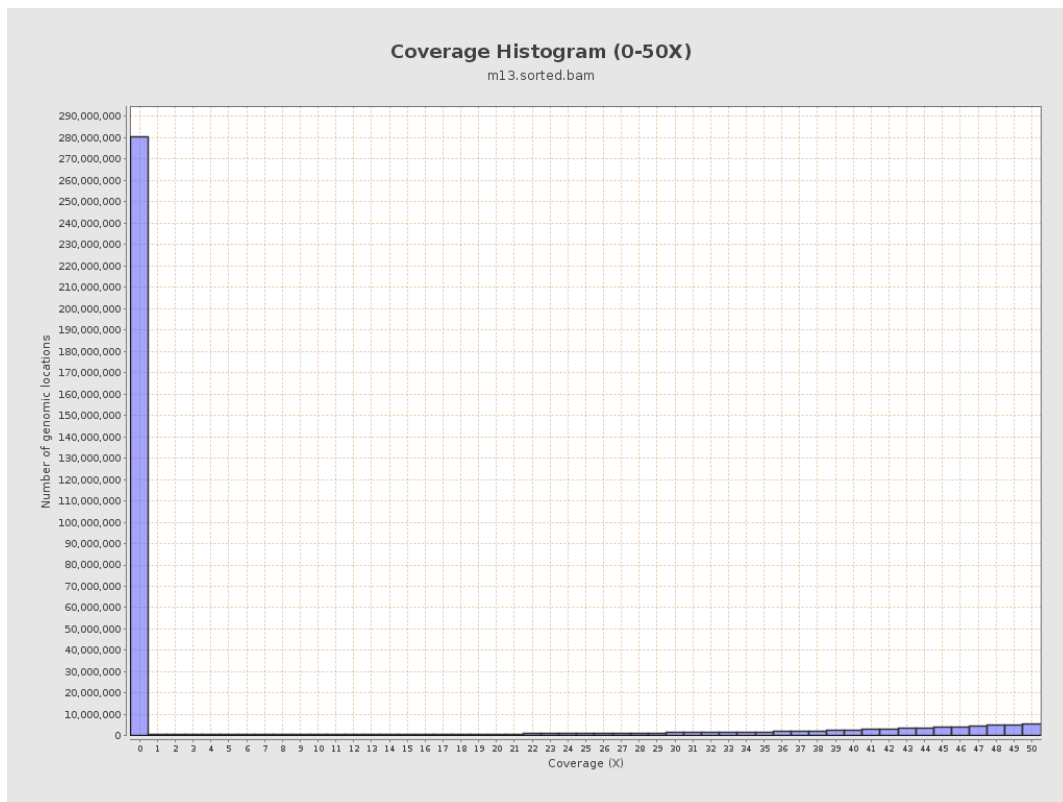
6. Results : Genome Fraction Coverage
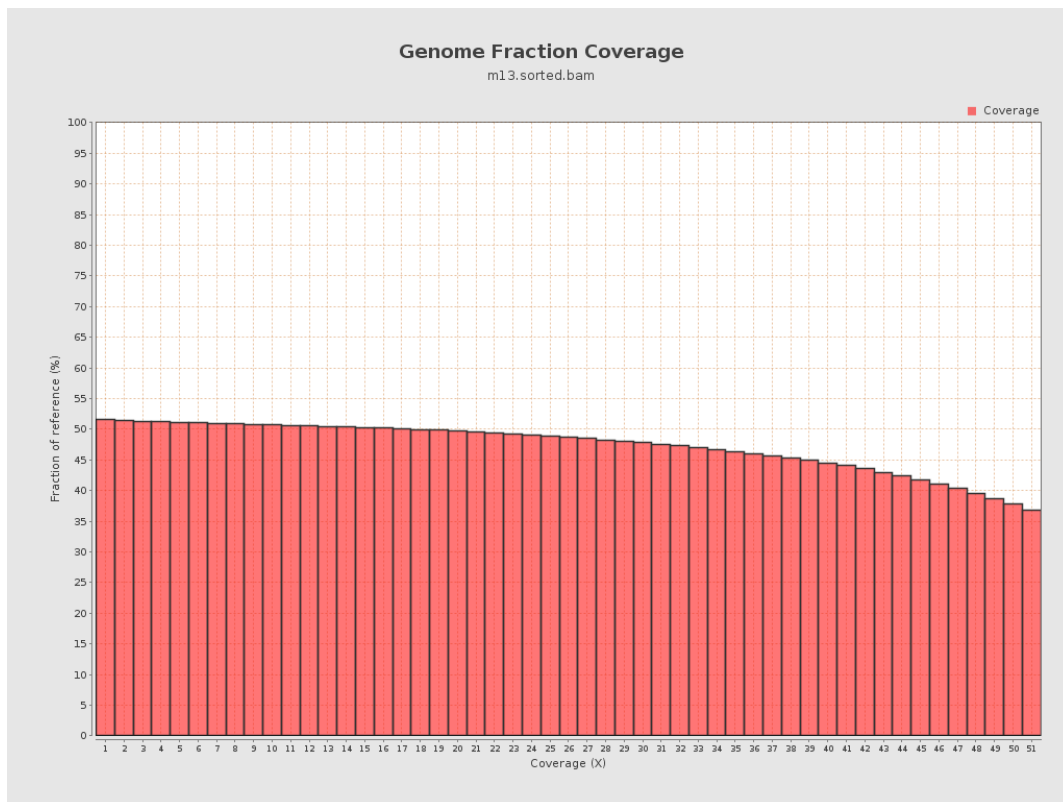
7. Results : Duplication Rate Histogram
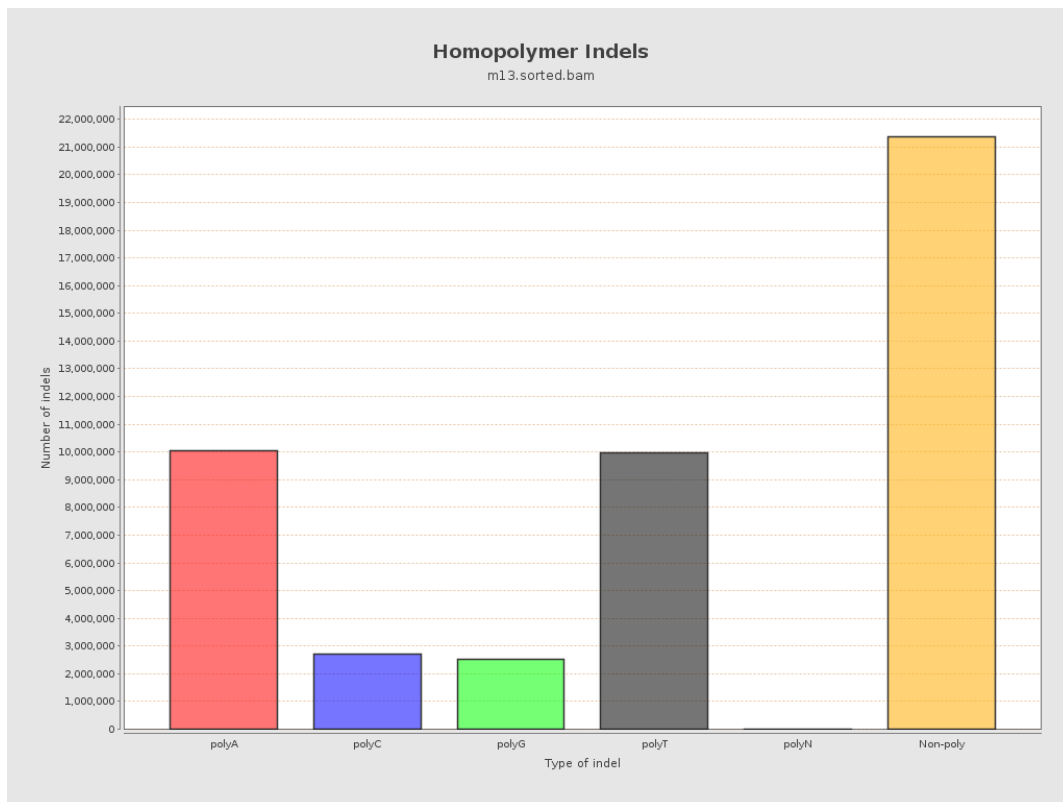

Duplication Rate Histogram
m13.sorted.bam
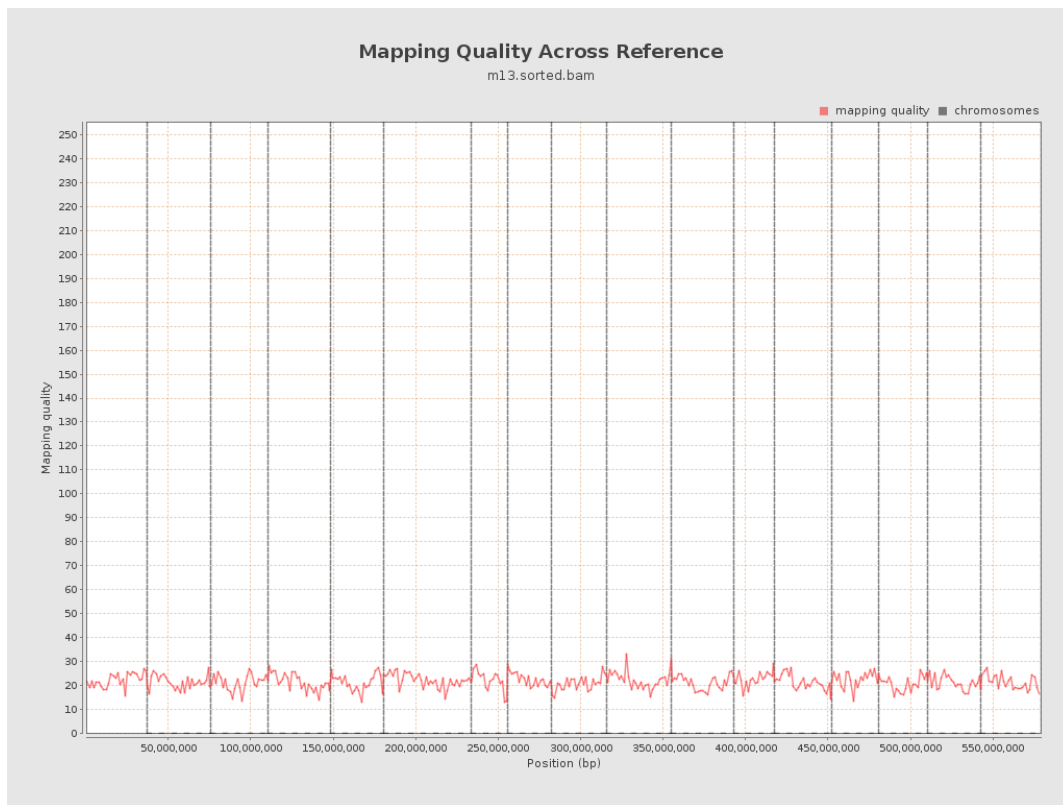
8. Results : Mapped Reads Nucleotide Content
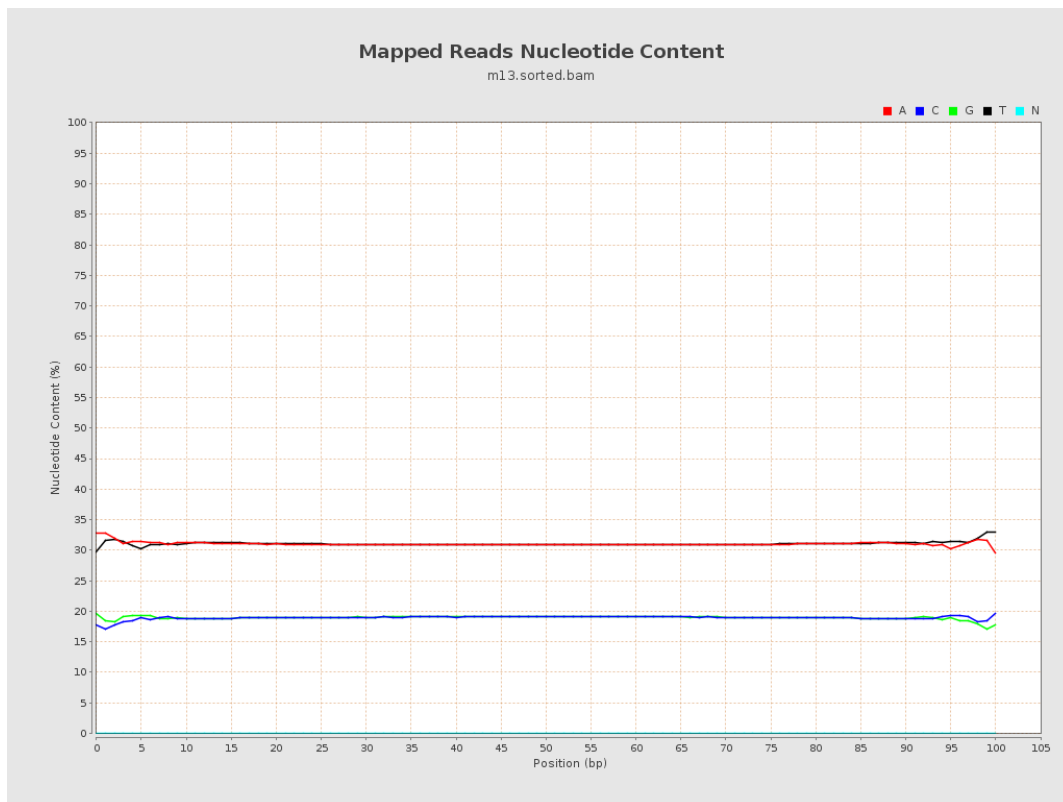
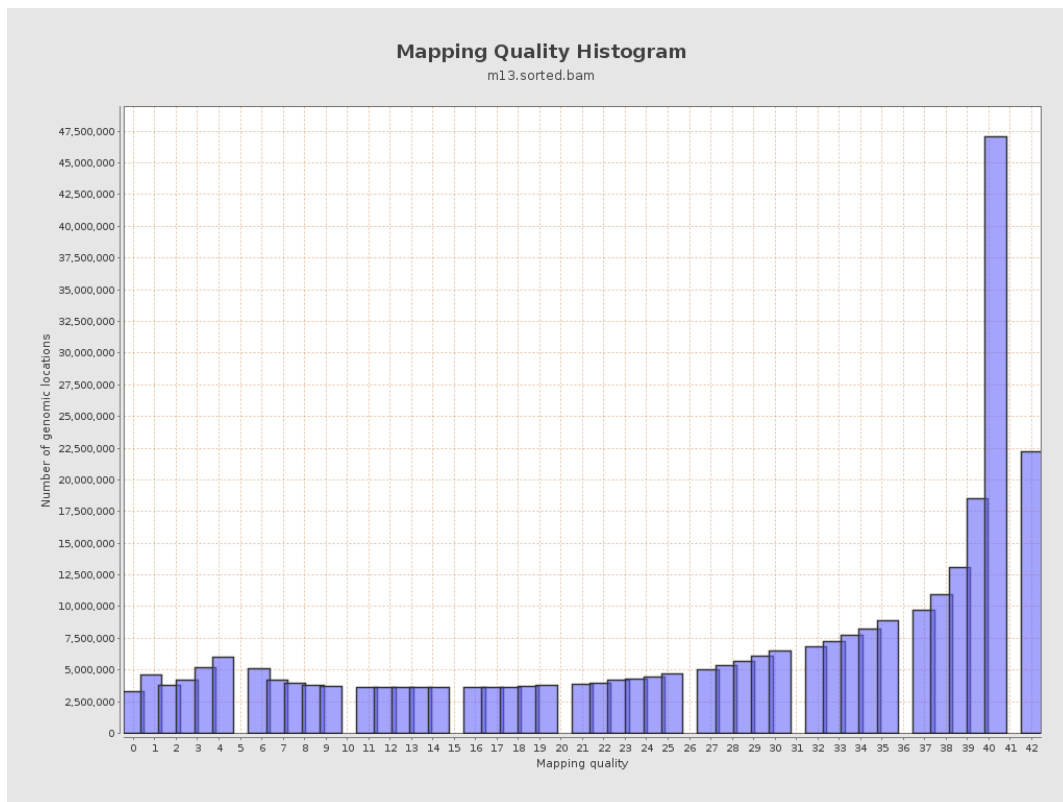# 9. Results : Mapped Reads GC-content Distribution
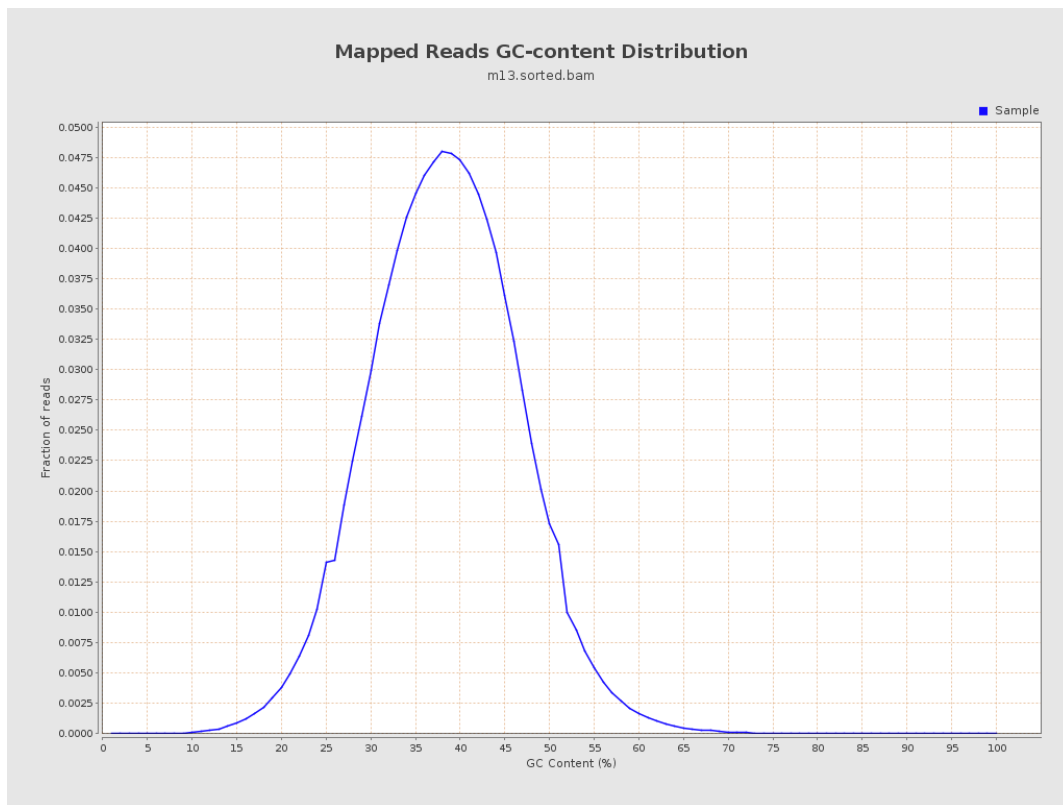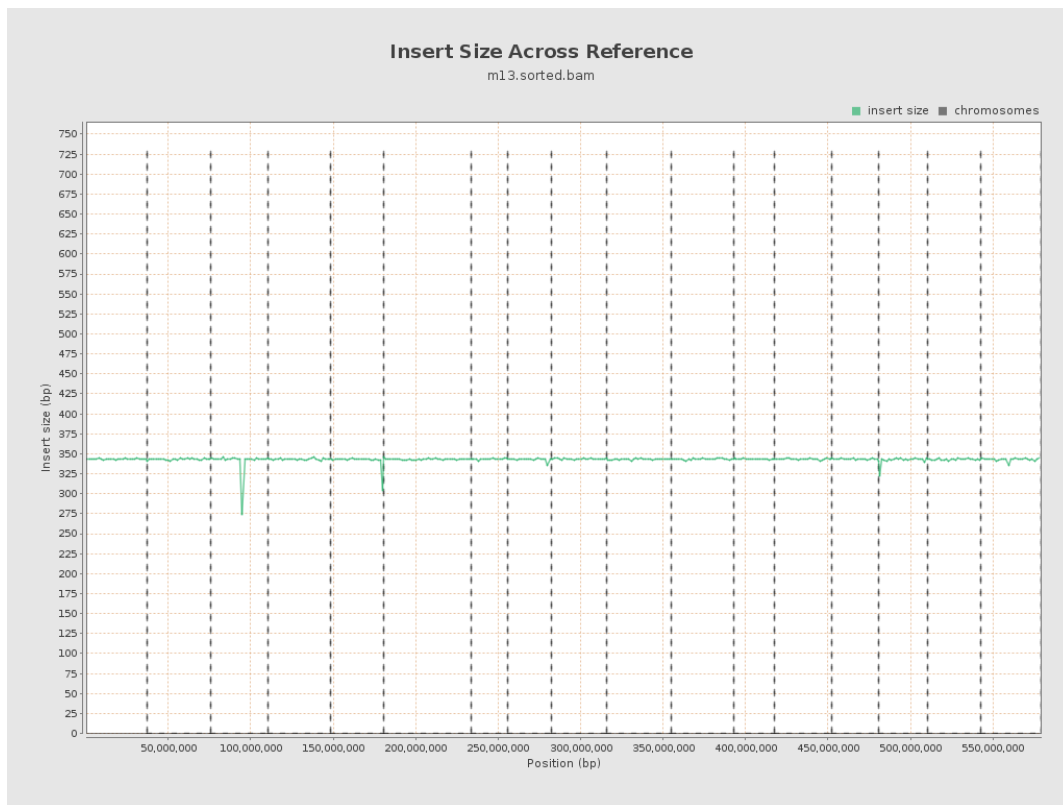
10. Results : Homopolymer Indels

11. Results : Mapping Quality Across Reference

12. Results : Mapping Quality Histogram

13. Results : Insert Size Across Reference

Insert Size Across Reference
m13.sorted.bam

14. Results : Insert Size Histogram