Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.0.1

2015/01/30 14:18:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/harrir/groups/harrisonlab/project_files/rootstock_genetics/m116/analys
is/m116.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/home/harrir/groups/harrisonlab/project_files/rootstock_genetics/m116/analysis/m116.sorted.bam
Program:	bowtie2 (2.0.5)
Command line:	
Size of a homopolymer:	3
Number of windows:	400
Analysis date:	Fri Jan 30 08:58:42 GMT 2015
Draw chromosome limits:	yes

2. Summary

2.1. Globals

Reference size	578,875,605
Number of reads	350,574,924
Mapped reads	253,241,902 / 72.24%
Unmapped reads	97,333,022 / 27.76%
Paired reads	253,241,902 / 72.24%
Mapped reads, only first in pair	129,499,393 / 36.94%
Mapped reads, only second in pair	123,742,509 / 35.3%
Mapped reads, both in pair	229,426,598 / 65.44%
Mapped reads, singletons	23,815,304 / 6.79%
Read min/max/mean length	90 / 90 / 90
Clipped reads	0 / 0%
Duplication rate	36.11%

2.2. ACGT Content

Number/percentage of A's	6,998,476,152 / 30.76%
Number/percentage of C's	4,374,499,203 / 19.23%
Number/percentage of T's	7,005,586,191 / 30.79%
Number/percentage of G's	4,373,372,100 / 19.22%
Number/percentage of N's	0 / 0%
GC Percentage	38.45%

2.3. Coverage

Mean	39.36
Standard Deviation	287.94

2.4. Mapping Quality

Mean Mapping Quality	21.74

2.5. Insert size

Mean	8,959.93
Standard Deviation	385,126.25
P25/Median/P75	0 / 455 / 471

2.6. Mismatches and indels

General error rate	2.85%
Mismatches	496,027,388
Insertions	19,109,020
Deletions	16,126,979
Homopolymer indels	53.2%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LG10_pht	36966320	1457084826	39.42	214.27
LG11_pht	38535128	1540489186	39.98	261.84
LG12_pht	34924356	1335668664	38.24	419.31
LG13_pht	37956969	1658403371	43.69	252.97

LG14_pht	32305939	1330096883	41.17	545.8
LG15_pht	53078040	2013225599	37.93	270.61
LG16_pht	22123682	896081299	40.5	276.79
LG17_pht	26512479	984971093	37.15	130.47
LG1_pht	33466746	1149899399	34.36	194.38
LG2_pht	39136869	1495990184	38.22	236.02
LG3_pht	37898467	1487489665	39.25	300.7
LG4_pht	24311090	975922036	40.14	208.43
LG5_pht	34832717	1495672108	42.94	378.81
LG6_pht	28552943	1058035567	37.06	206.05
LG7_pht	29555396	1169325023	39.56	219.4
LG8_pht	32612457	1257304515	38.55	230.18
LG9_pht	36106007	1476184412	40.88	243.34

3. Results : Coverage across reference

Coverage across reference
m116.sorted.bam

4. Results : Coverage Histogram

Coverage Histogram
m116.sorted.bam
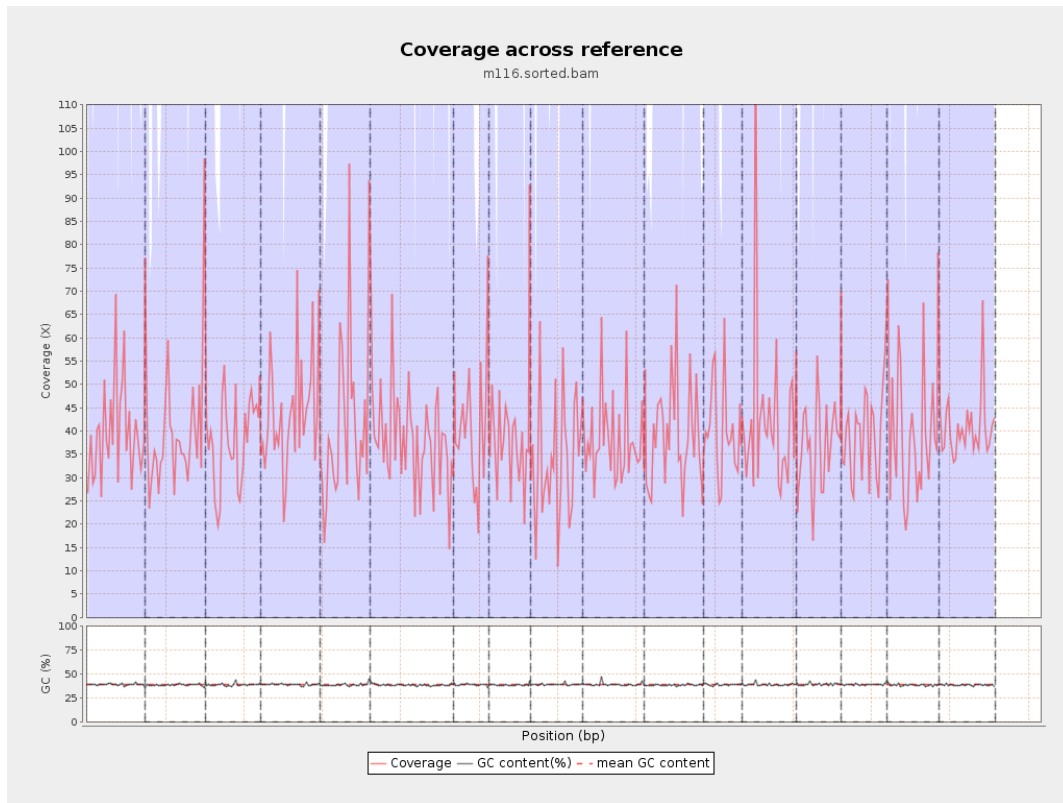
5. Results : Coverage Histogram (0-50X)
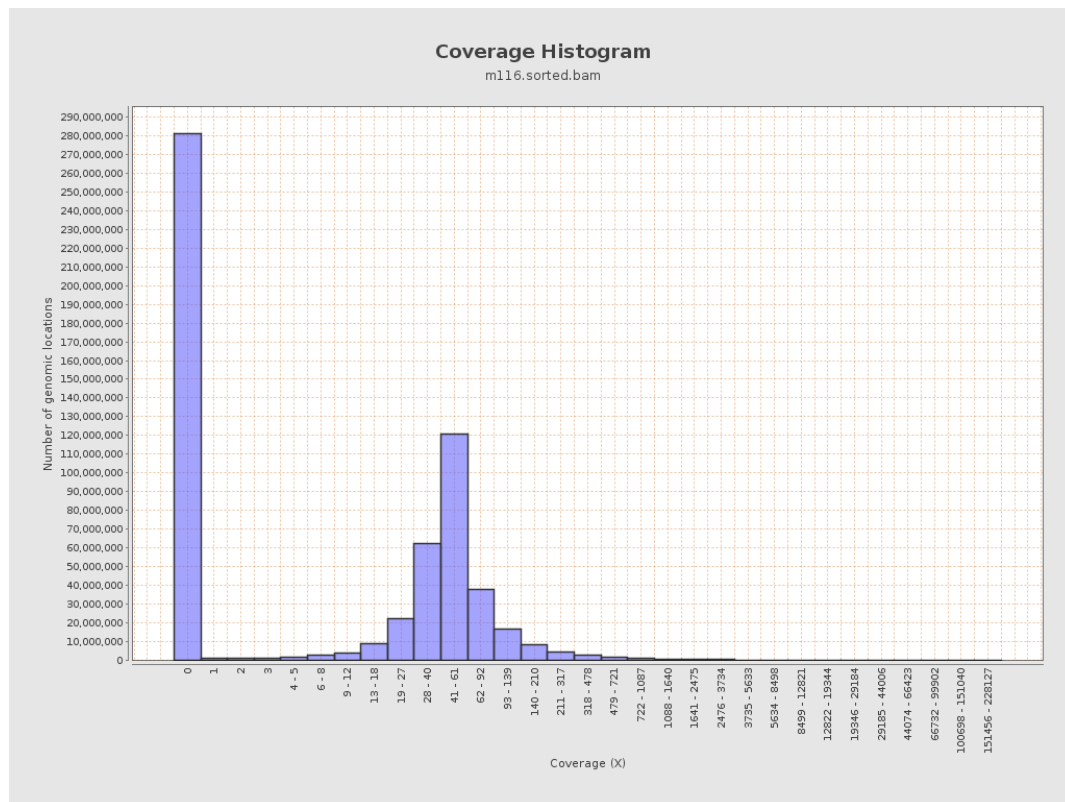
Coverage Histogram (0-50X)
m116.sorted.bam
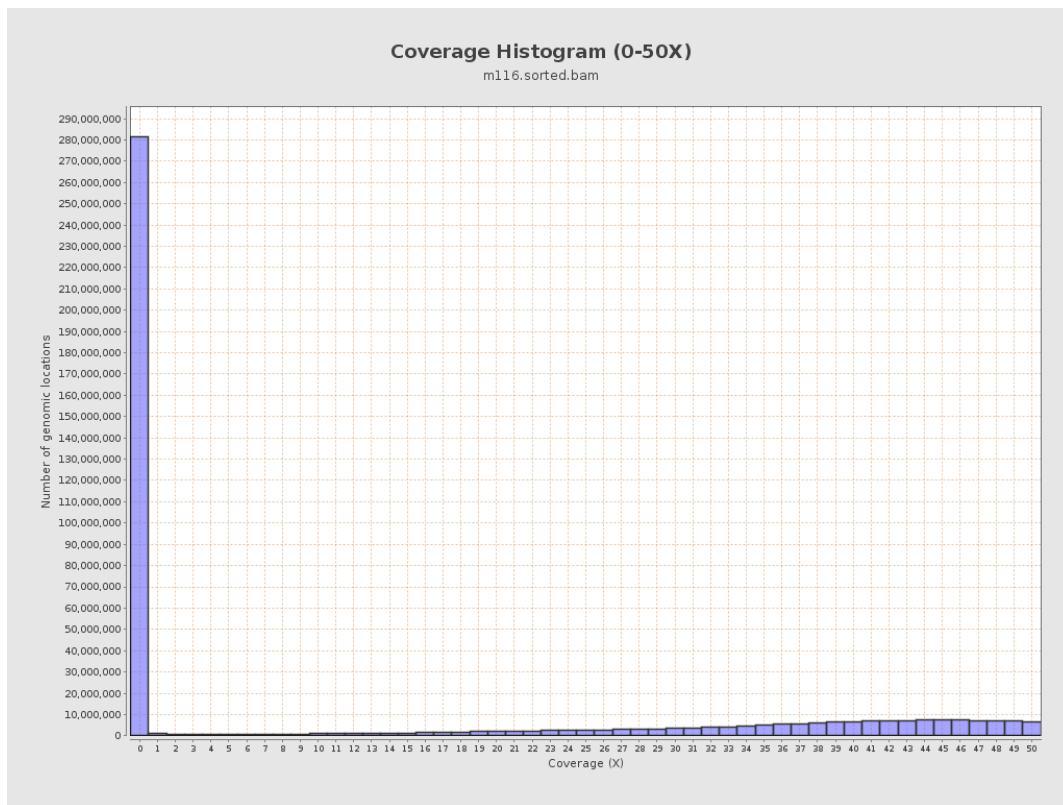
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
m116.sorted.bam
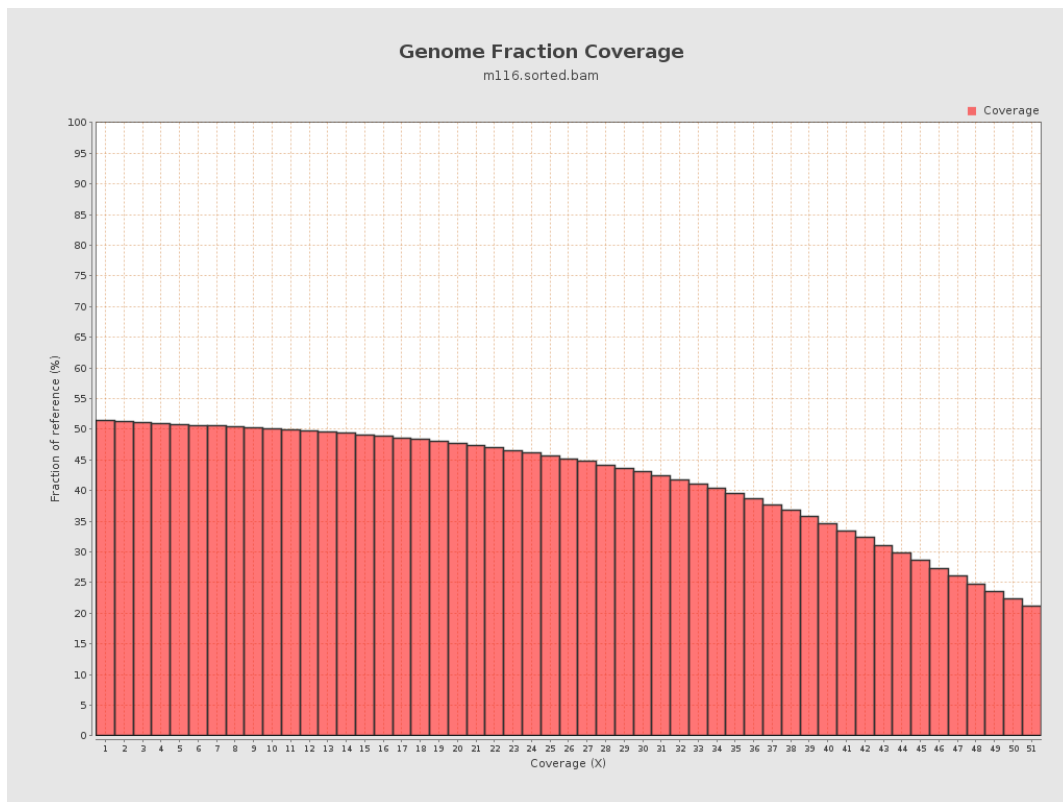
7. Results : Duplication Rate Histogram
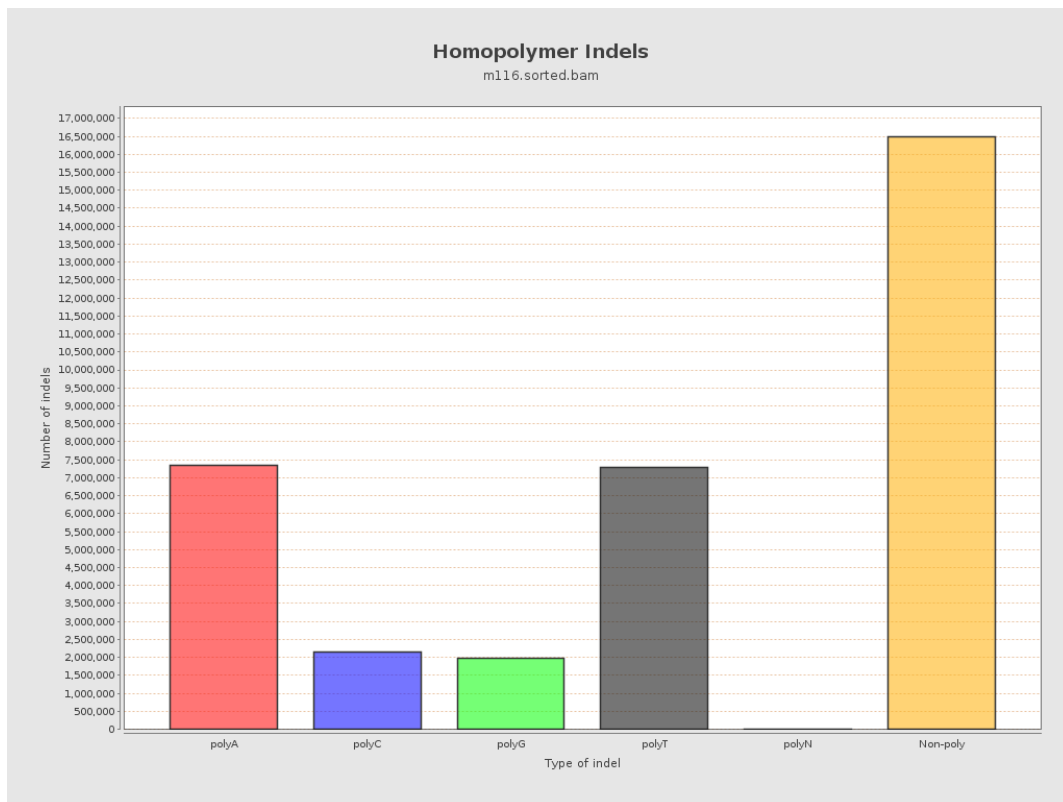
Duplication Rate Histogram
m116.sorted.bam
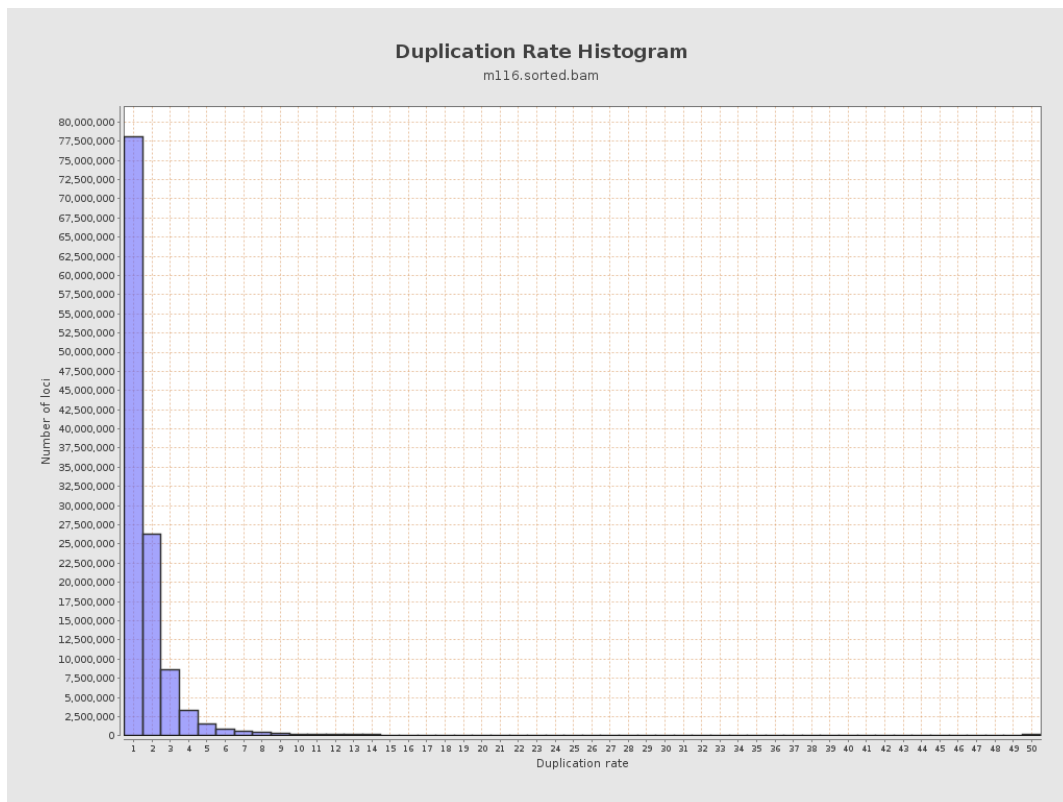
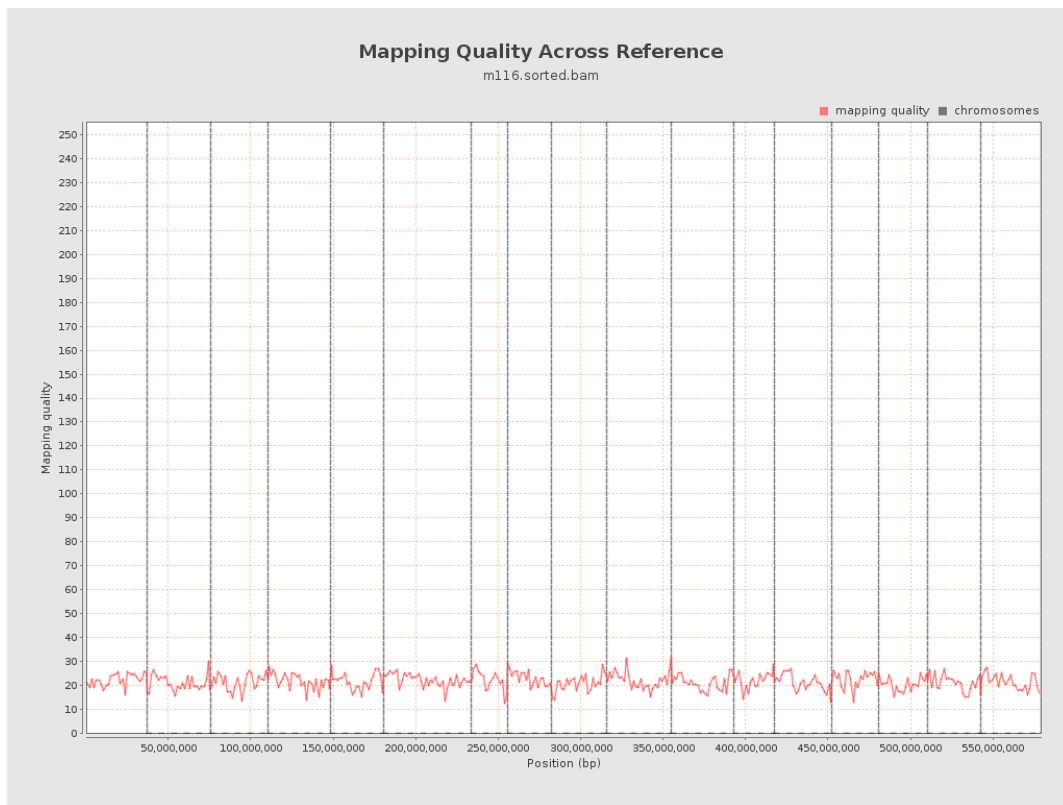# 8. Results : Mapped Reads Nucleotide Content
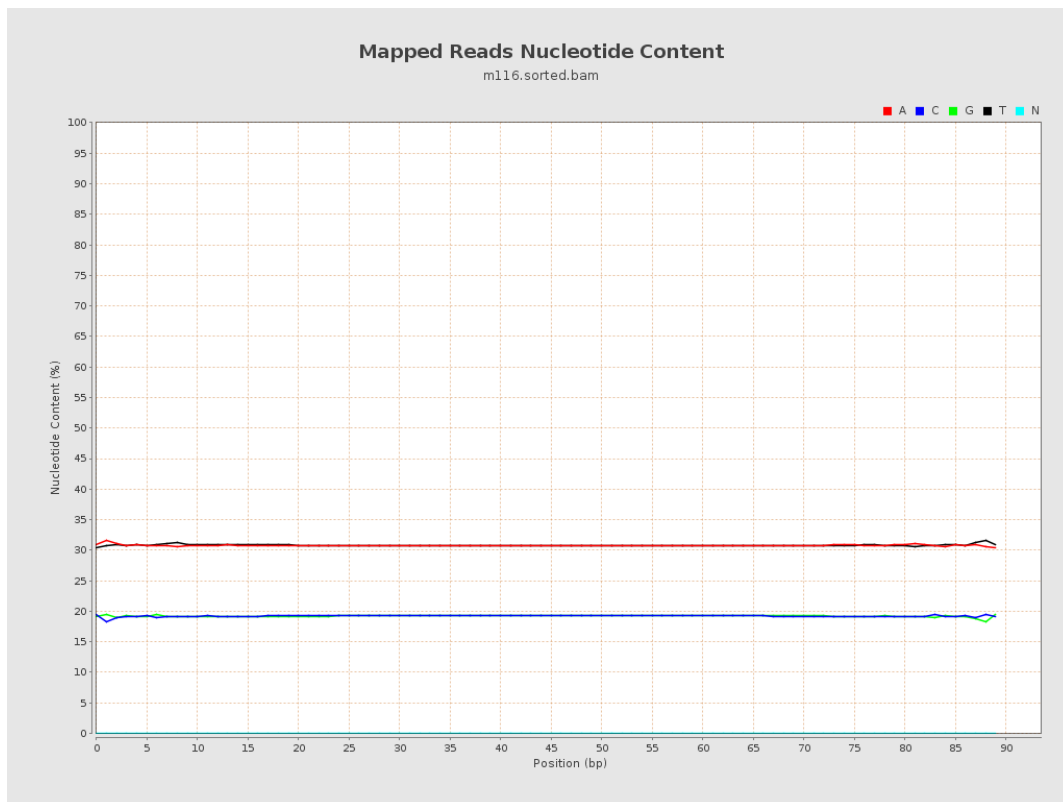
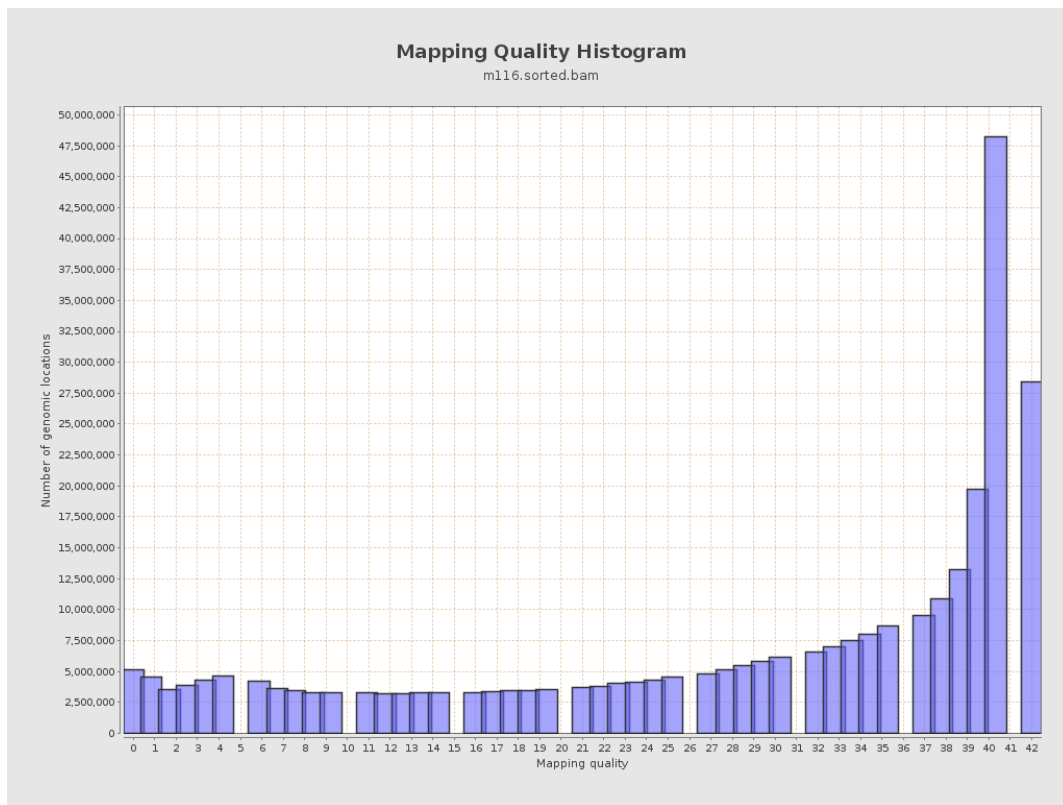# 9. Results : Mapped Reads GC-content Distribution
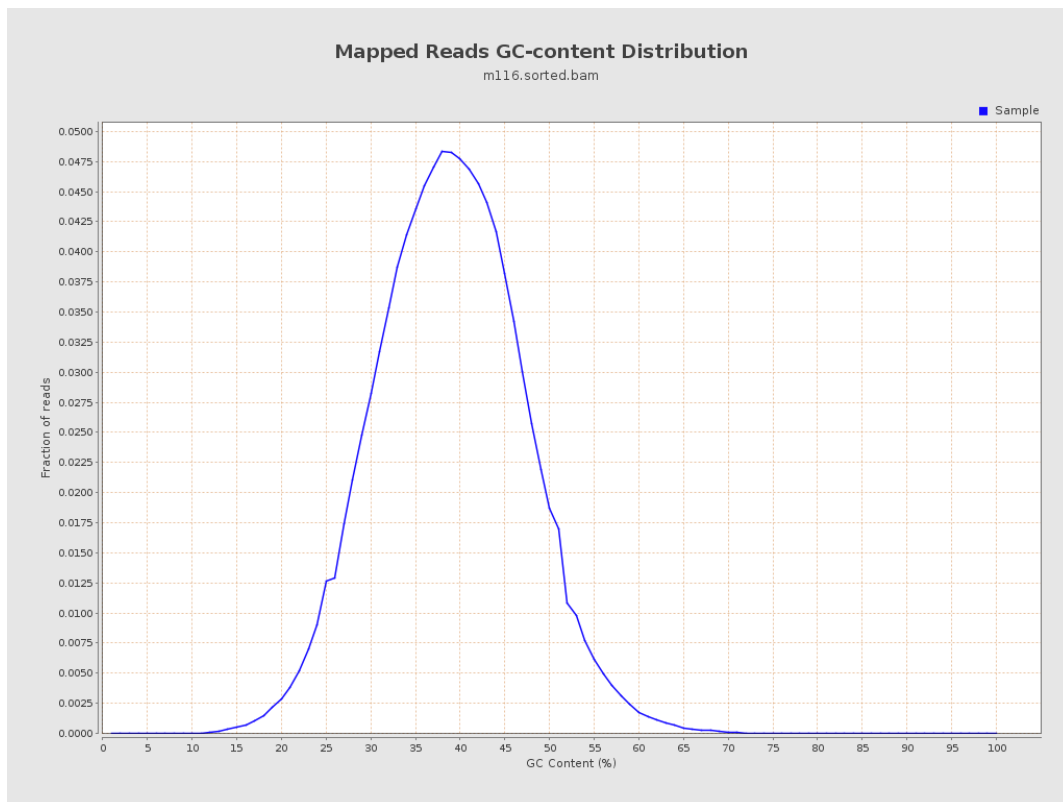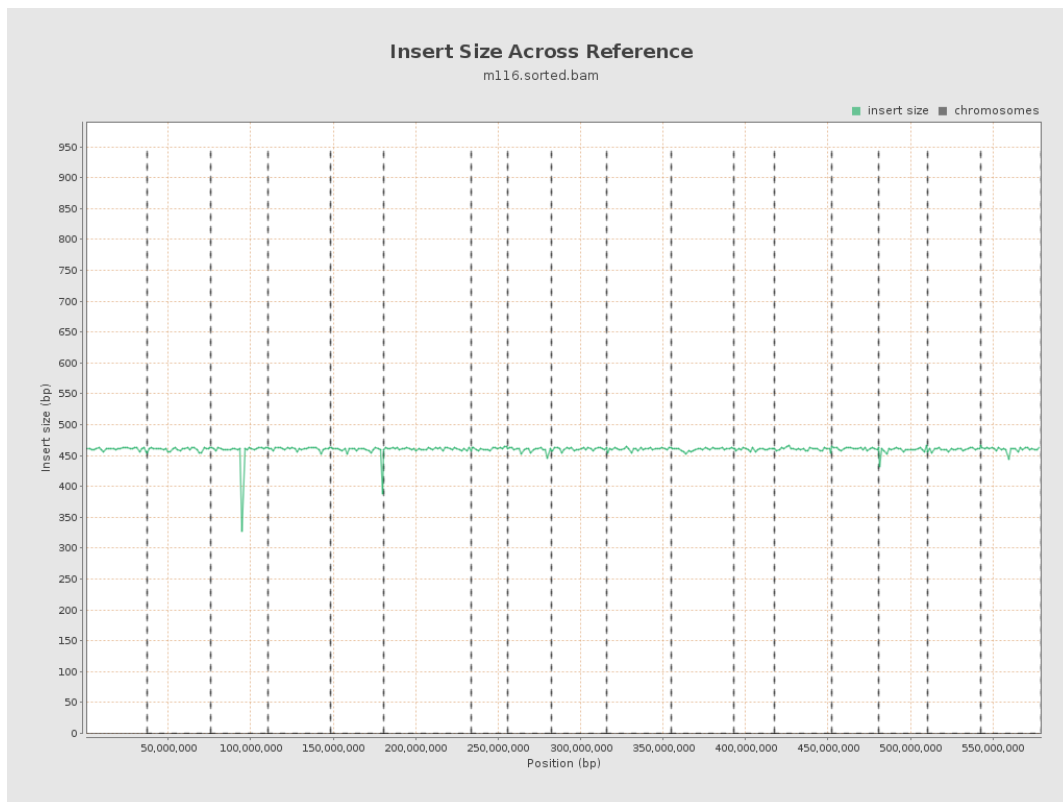
10. Results : Homopolymer Indels

11. Results : Mapping Quality Across Reference

12. Results : Mapping Quality Histogram

13. Results : Insert Size Across Reference

14. Results : Insert Size Histogram

Insert Size Histogram
m116.sorted.bam