Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 13:01:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM108.sorted.bam.ba
m -nw 400 -hm 3
```

1.2. Alignment

Command line:	bwa mem -M /home/vdp5/data/salvador_vivax_asia_2016/first-SAMEA2376790/pvivax_sal1_SAMEA2376790.fasta /home/vdp5/data/cambodia_samples/sequences_gz/OM-108_GCCAAT_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM-108_GCCAAT_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 13:01:50 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM108.sorted.bam.bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	78,828,230
Mapped reads	1,876,860 / 2.38%
Unmapped reads	76,951,370 / 97.62%
Mapped paired reads	1,876,860 / 2.38%
Mapped reads, first in pair	941,918 / 1.19%
Mapped reads, second in pair	934,942 / 1.19%
Mapped reads, both in pair	1,291,826 / 1.64%
Mapped reads, singletons	585,034 / 0.74%
Read min/max/mean length	30 / 100 / 99.98
Duplicated reads (estimated)	715,516 / 0.91%
Duplication rate	12.67%
Clipped reads	746,296 / 0.95%

2.2. ACGT Content

Number/percentage of A's	44,270,467 / 30.28%
Number/percentage of C's	27,631,874 / 18.9%
Number/percentage of T's	46,467,550 / 31.78%
Number/percentage of G's	27,841,556 / 19.04%
Number/percentage of N's	4,209 / 0%
GC Percentage	37.94%

2.3. Coverage

Mean	6.1119
Standard Deviation	96.4121

2.4. Mapping Quality

Mean Mapping Quality	51.71

2.5. Insert size

Mean	1,860.47
Standard Deviation	43,072.33
P25/Median/P75	219 / 230 / 242

2.6. Mismatches and indels

General error rate	1.37%
Mismatches	1,797,965
Insertions	80,611
Mapped reads with at least one insertion	3.86%
Deletions	92,564
Mapped reads with at least one deletion	3.77%
Homopolymer indels	56.26%

2.7. Chromosome stats

| Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|1074120478|emb|LT615256.1|	977217	5401417	5.5273	21.2711
gi|1074120682|emb|LT615257.1|	860454	5634994	6.5489	41.7758
gi|1074120865|emb|LT615258.1|	989719	6541698	6.6097	41.2706
gi|1074121086|emb|LT615259.1|	935450	5729923	6.1253	16.4185
gi|1074121301|emb|LT615260.1|	1432239	9464704	6.6083	46.8998
gi|1074121615|emb|LT615261.1|	1080962	6422153	5.9411	36.7577
gi|1074121871|emb|LT615262.1|	1545099	8178713	5.2933	22.9646
gi|1074122235|emb|LT615263.1|	1585108	11075903	6.9875	129.0799
gi|1074122590|emb|LT615264.1|	2122358	11803997	5.5617	15.4189
gi|1074123050|emb|LT615265.1|	1754192	14045890	8.007	307.7926
gi|1074123421|emb|LT615	2150147	13160201	6.1206	28.5527

|				
266.1|				
gi|1074123898|emb|LT615267.1|	3031036	18236943	6.0167	72.8454
gi|1074124588|emb|LT615268.1|	2359348	12988684	5.5052	21.3587
gi|1074125065|emb|LT615269.1|	3135668	17750798	5.6609	20.9245

3. Results : Coverage across reference
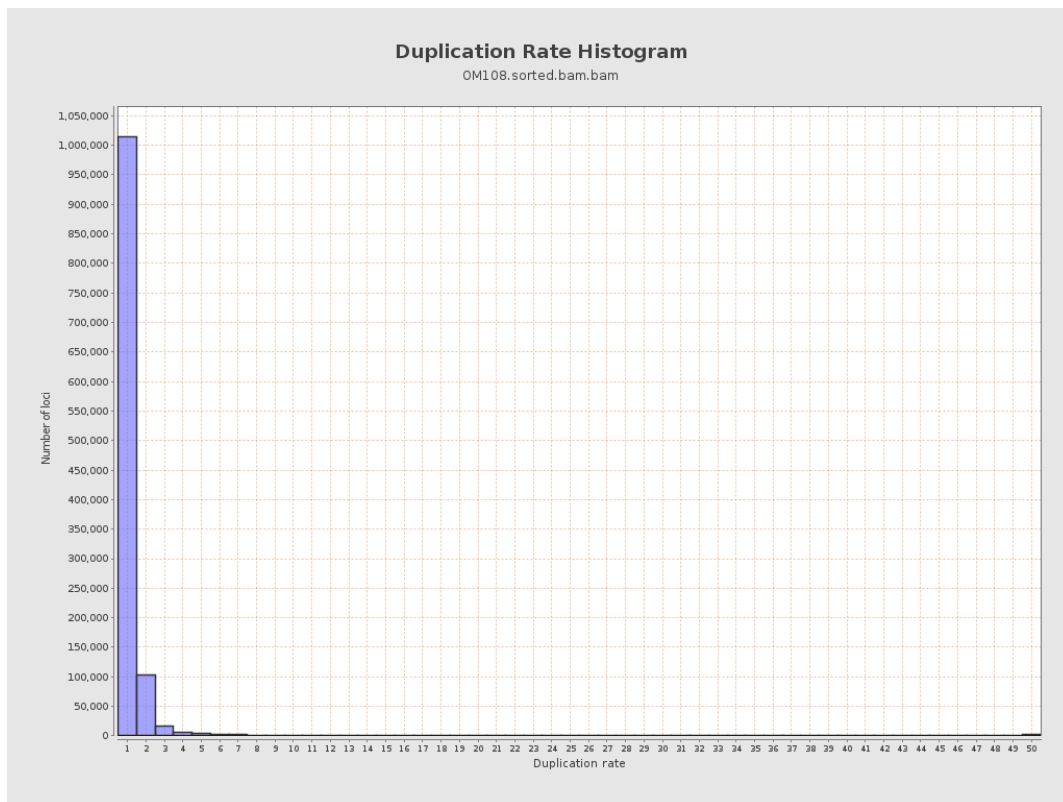
4. Results : Coverage Histogram

Coverage Histogram
OM108.sorted.bam.bam
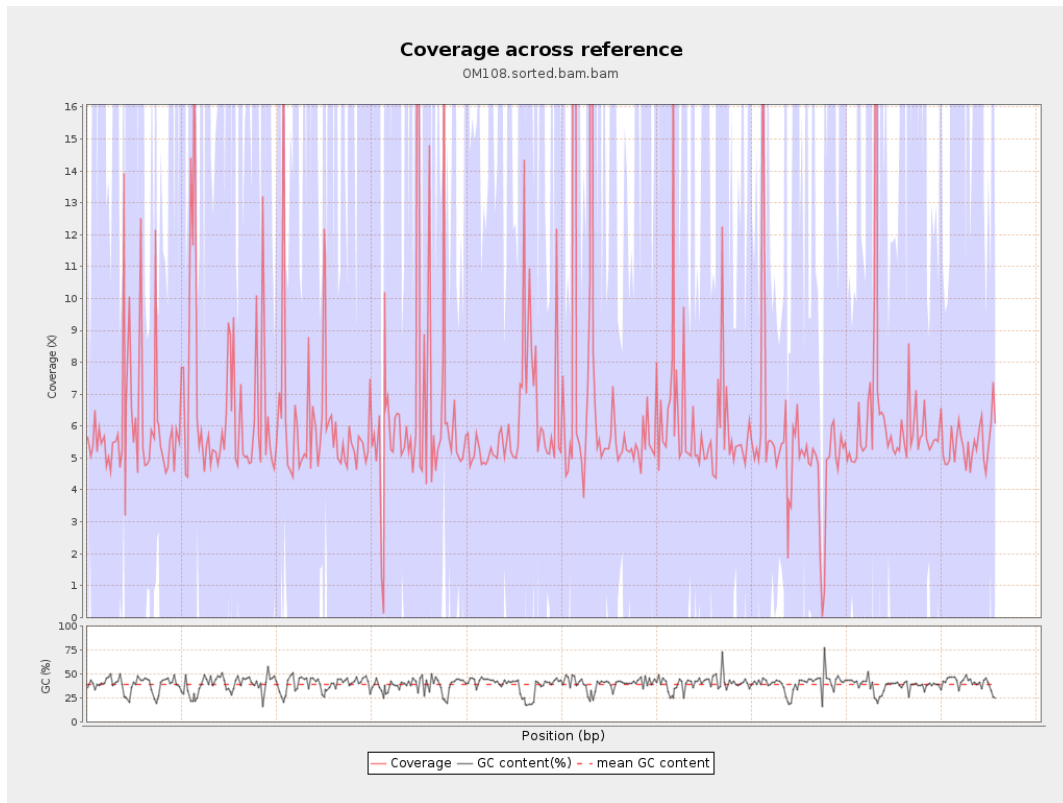
5. Results : Coverage Histogram (0-50X)
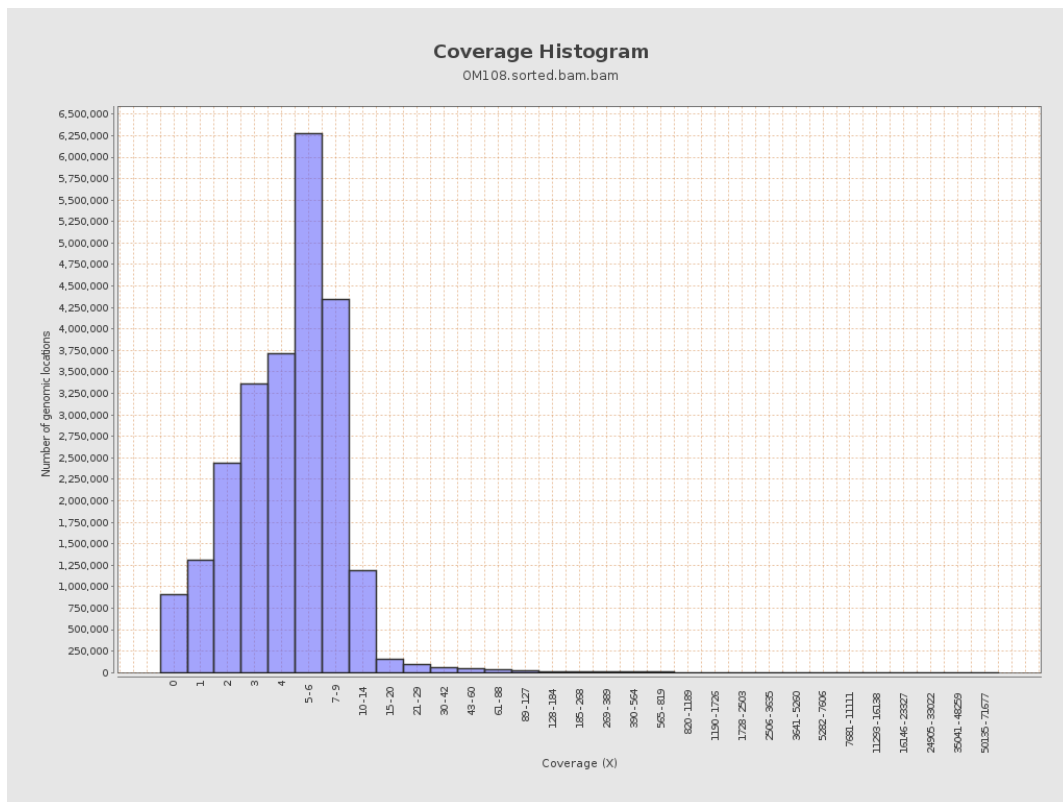
Coverage Histogram (0-50X)
OM108.sorted.bam.bam
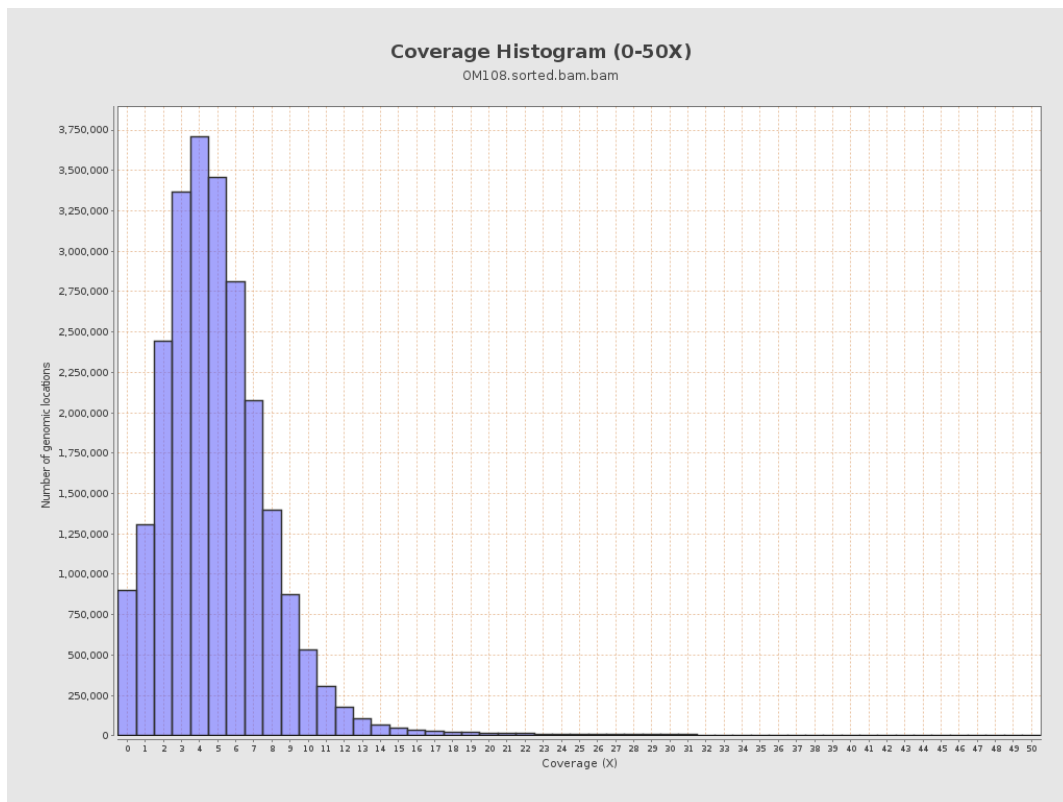
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
OM108.sorted.bam.bam
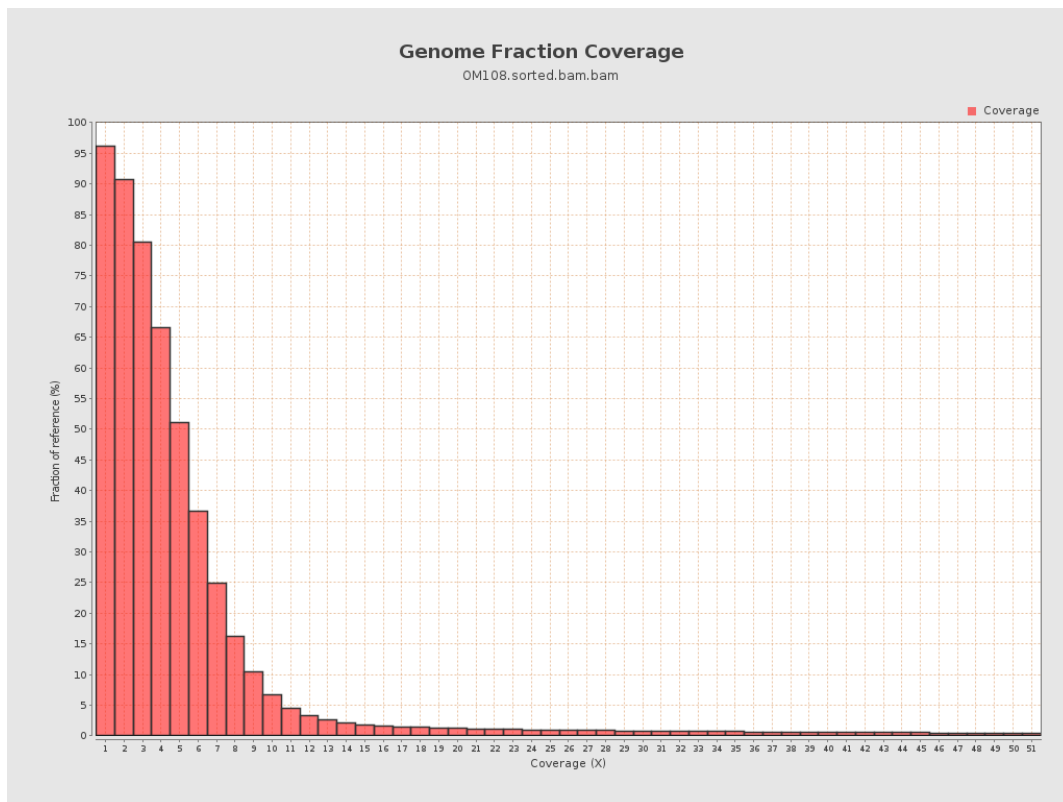
7. Results : Duplication Rate Histogram
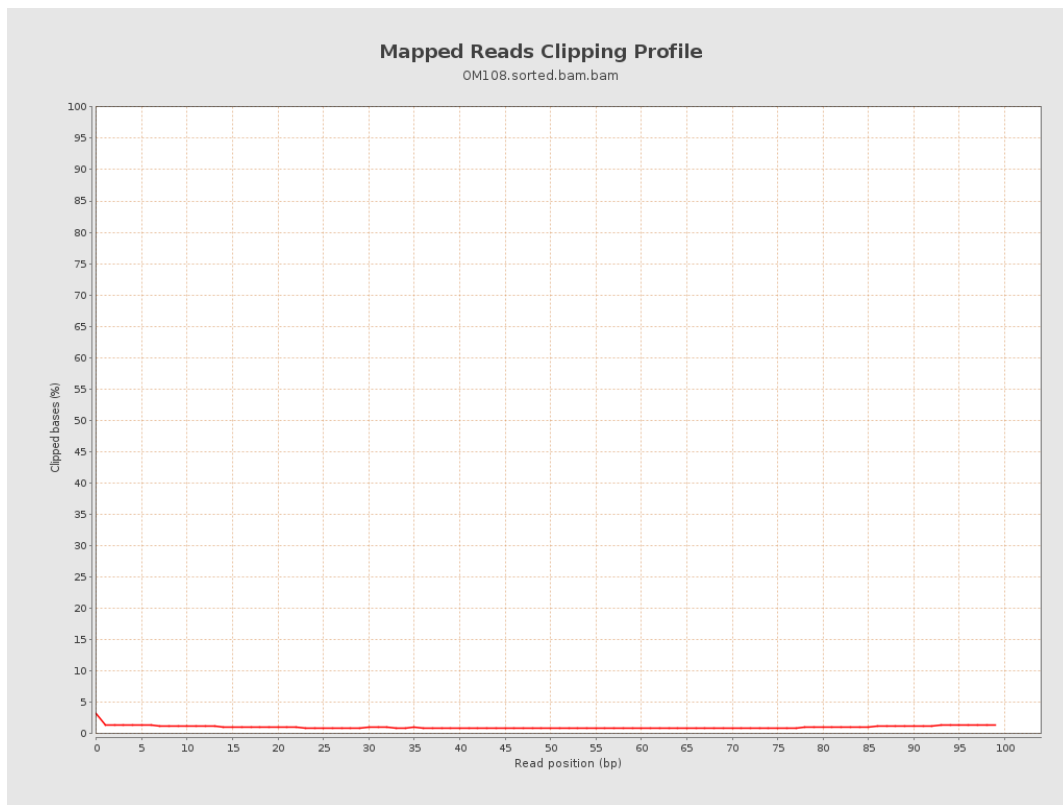

Duplication Rate Histogram
OM108.sorted.bam.bam

8. Results : Mapped Reads Nucleotide Content
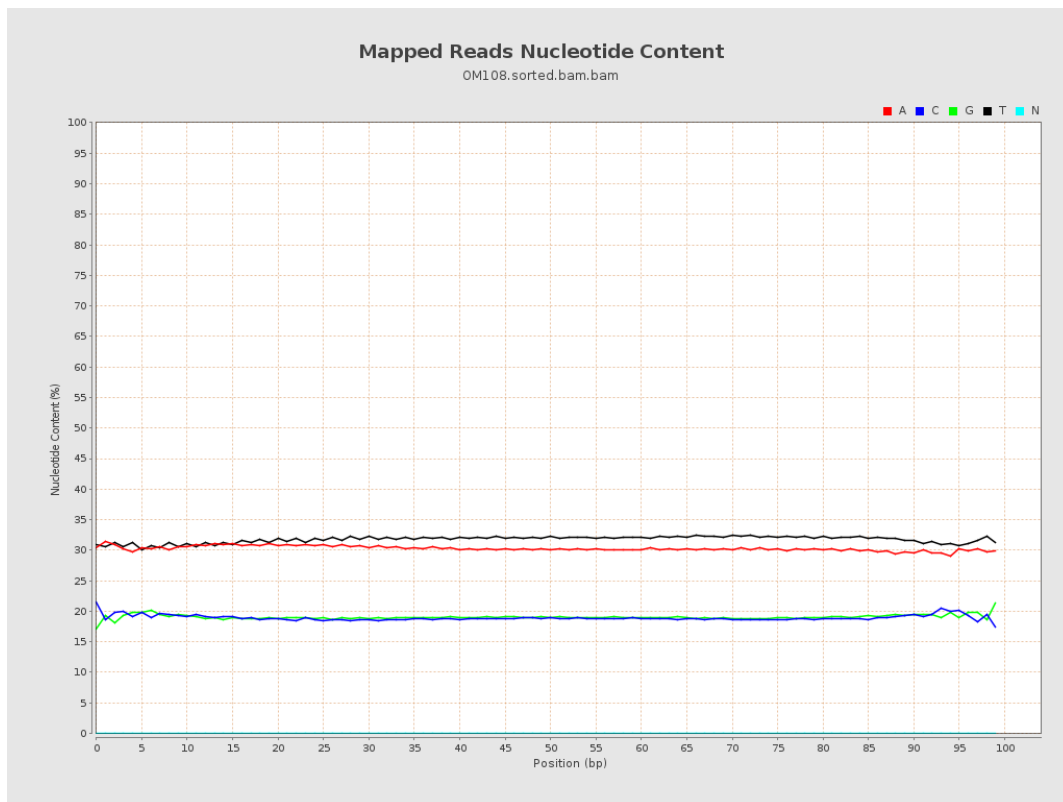
9. Results : Mapped Reads GC-content Distribution
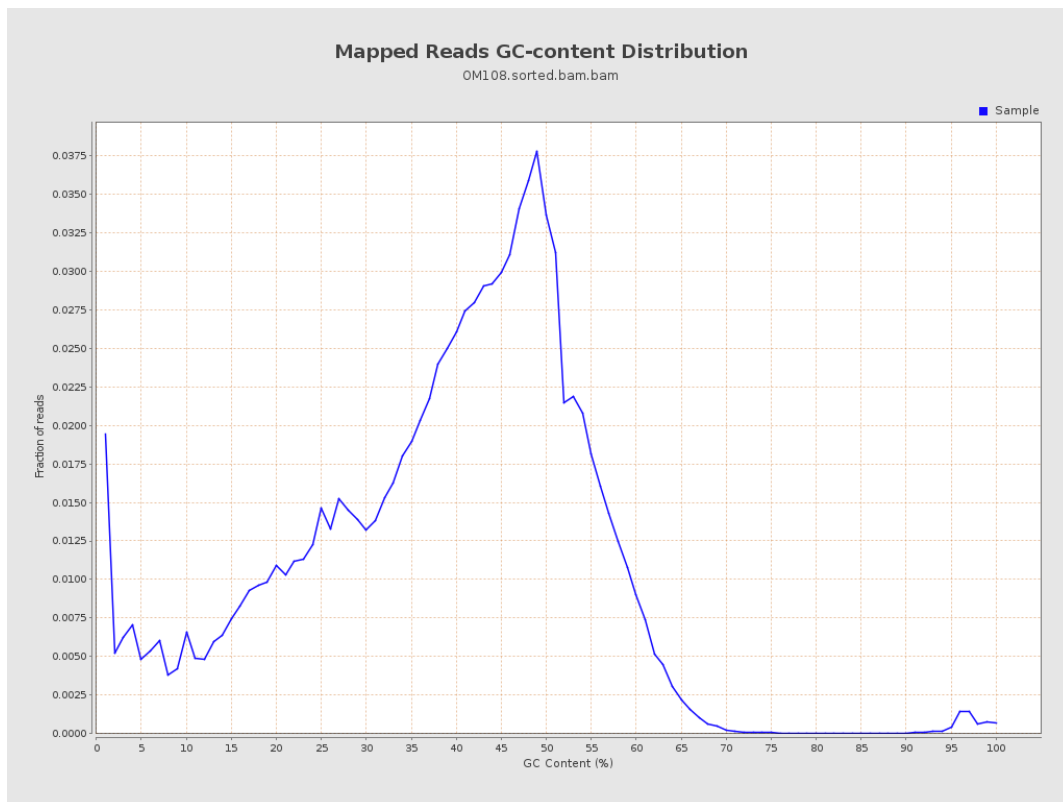
10. Results : Mapped Reads Clipping Profile
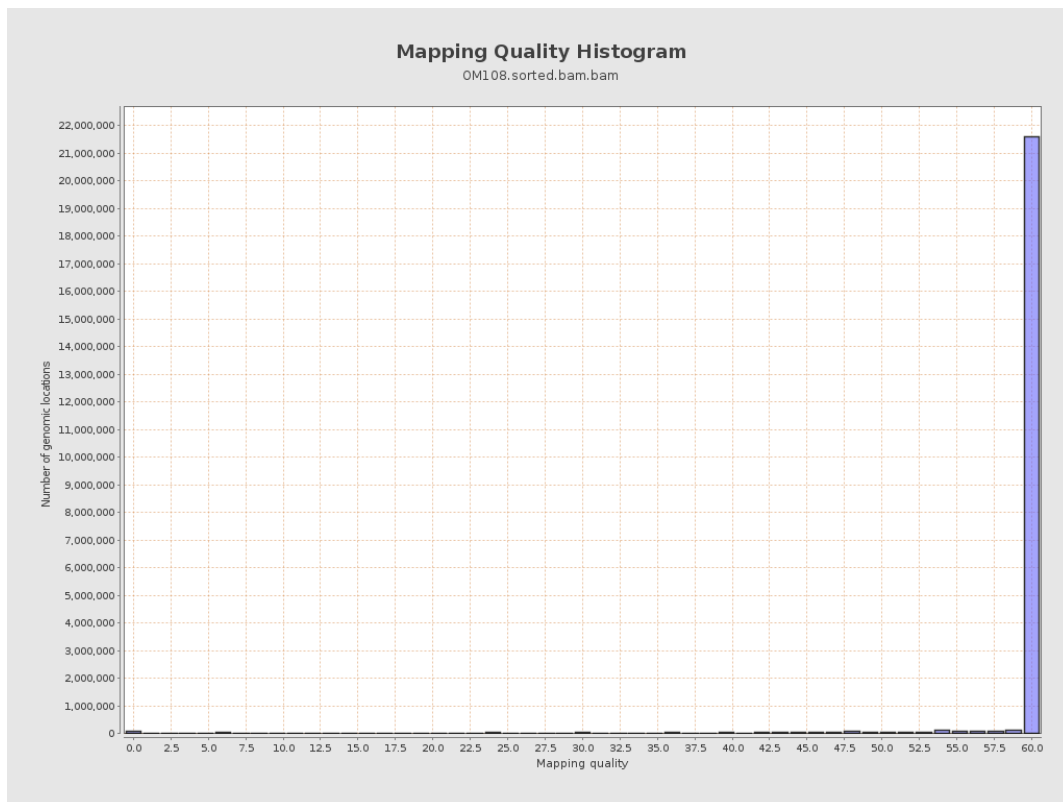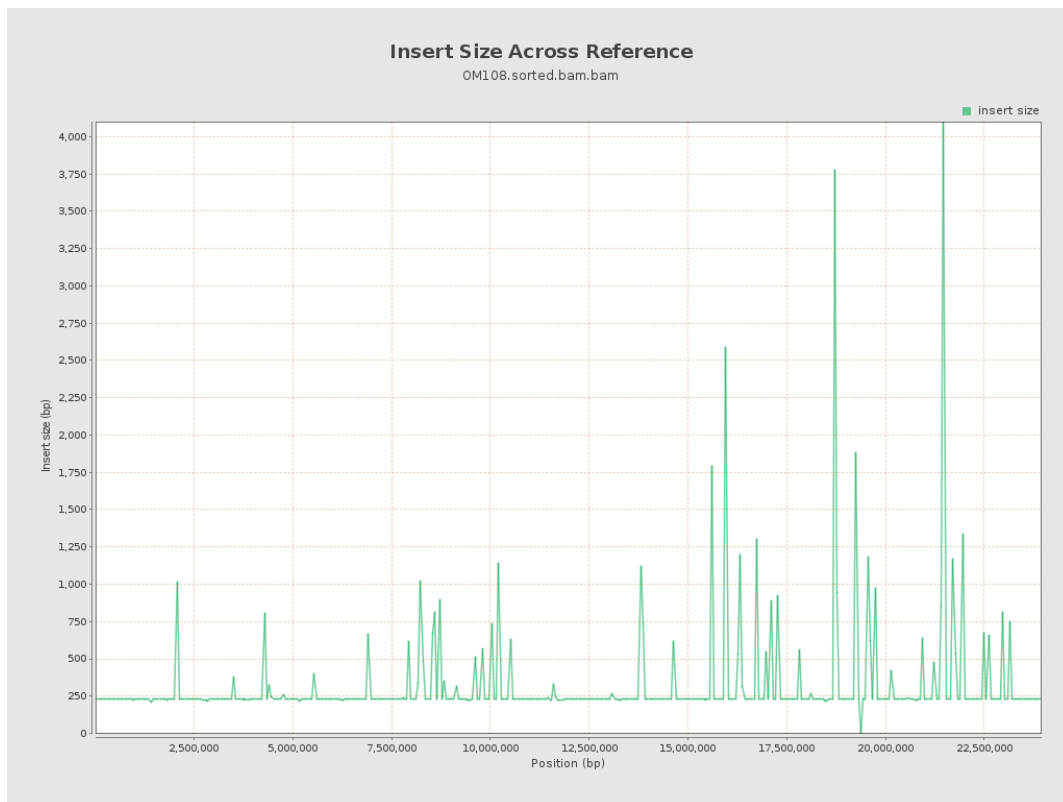

Mapped Reads Clipping Profile
OM108.sorted.bam.bam

11. Results : Homopolymer Indels

Homopolymer Indels
OM108.sorted.bam.bam
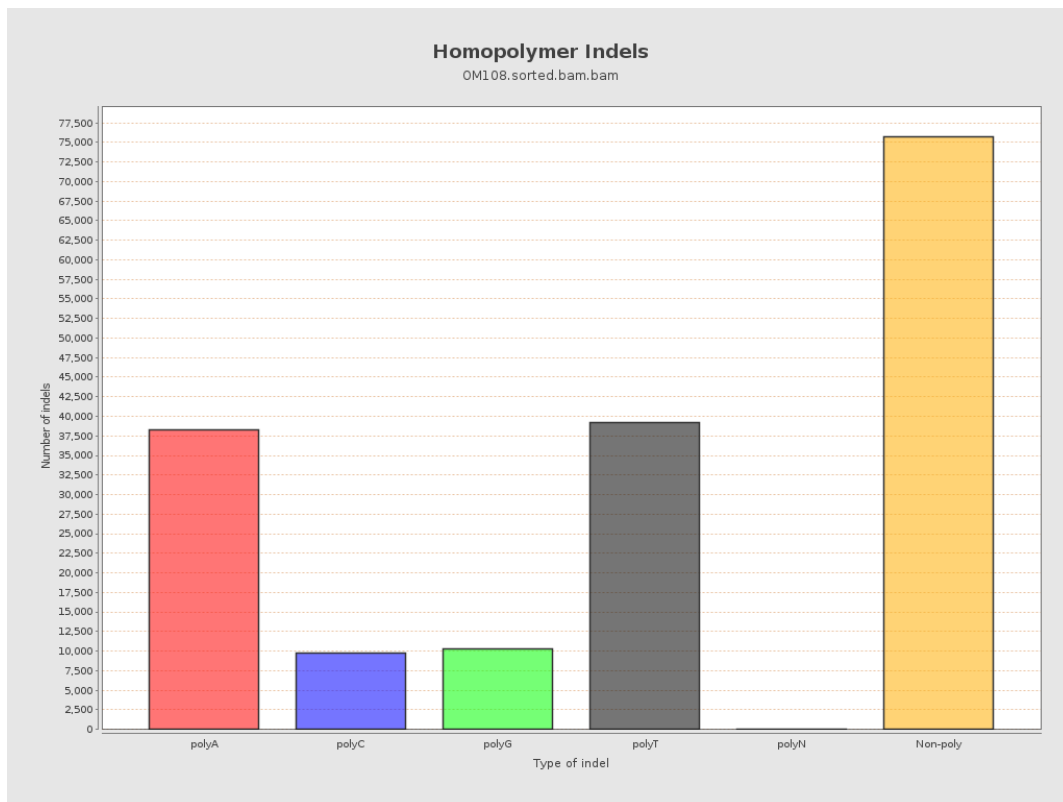
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
OM108.sorted.bam.bam

14. Results : Insert Size Across Reference

Insert Size Across Reference
OM108.sorted.bam.bam

15. Results : Insert Size Histogram

Insert Size Histogram
OM108.sorted.bam.bam