Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 14:10:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM305.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/OM305-BiooBarcode37_CGGAAT_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM305-BiooBarcode37_CGGAAT_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 14:10:01 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM305.sorted.bam.

	bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	1,479,395
Mapped reads	948,534 / 64.12%
Unmapped reads	530,861 / 35.88%
Mapped paired reads	948,534 / 64.12%
Mapped reads, first in pair	470,445 / 31.8%
Mapped reads, second in pair	478,089 / 32.32%
Mapped reads, both in pair	924,301 / 62.48%
Mapped reads, singletons	24,233 / 1.64%
Read min/max/mean length	30 / 100 / 99.9
Duplicated reads (estimated)	63,024 / 4.26%
Duplication rate	4.88%
Clipped reads	111,753 / 7.55%

2.2. ACGT Content

Number/percentage of A's	27,537,065 / 30.1%
Number/percentage of C's	18,183,760 / 19.87%
Number/percentage of T's	27,654,315 / 30.22%
Number/percentage of G's	18,122,877 / 19.81%
Number/percentage of N's	7,629 / 0.01%
GC Percentage	39.68%

2.3. Coverage

Mean	3.8231
Standard Deviation	3.9783

2.4. Mapping Quality

Mean Mapping Quality	58.63

2.5. Insert size

Mean	1,037.31
Standard Deviation	28,826.05
P25/Median/P75	345 / 356 / 365

2.6. Mismatches and indels

General error rate	1.67%
Mismatches	1,457,695
Insertions	30,876
Mapped reads with at least one insertion	3.07%
Deletions	34,625
Mapped reads with at least one deletion	3.46%
Homopolymer indels	63.01%

2.7. Chromosome stats

| Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|107412047 8|emb|LT615 256.1|	977217	3283902	3.3605	2.534
gi|107412068 2|emb|LT615 257.1|	860454	3303479	3.8392	3.2012
gi|107412086 5|emb|LT615 258.1|	989719	4090613	4.1331	5.5824
gi|107412108 6|emb|LT615 259.1|	935450	3948028	4.2205	5.7307
gi|107412130 1|emb|LT615 260.1|	1432239	5867308	4.0966	4.975
gi|107412161 5|emb|LT615 261.1|	1080962	4074224	3.7691	3.7313
gi|107412187 1|emb|LT615 262.1|	1545099	5713030	3.6975	2.6526
gi|107412223 5|emb|LT615 263.1|	1585108	5953167	3.7557	3.1509
gi|107412259 0|emb|LT615 264.1|	2122358	7625867	3.5931	2.5859
gi|107412305 0|emb|LT615 265.1|	1754192	6941170	3.9569	3.9471
gi|107412342 1|emb|LT615	2150147	8364131	3.89	6.6663

266.1|				
gi|1074123898|emb|LT615267.1|	3031036	11106281	3.6642	2.3876
gi|1074124588|emb|LT615268.1|	2359348	9194920	3.8972	4.7064
gi|1074125065|emb|LT615269.1|	3135668	12131739	3.8689	2.3952

3. Results : Coverage across reference

Coverage across reference
OM305.sorted.bam.bam

4. Results : Coverage Histogram

Coverage Histogram
OM305.sorted.bam.bam
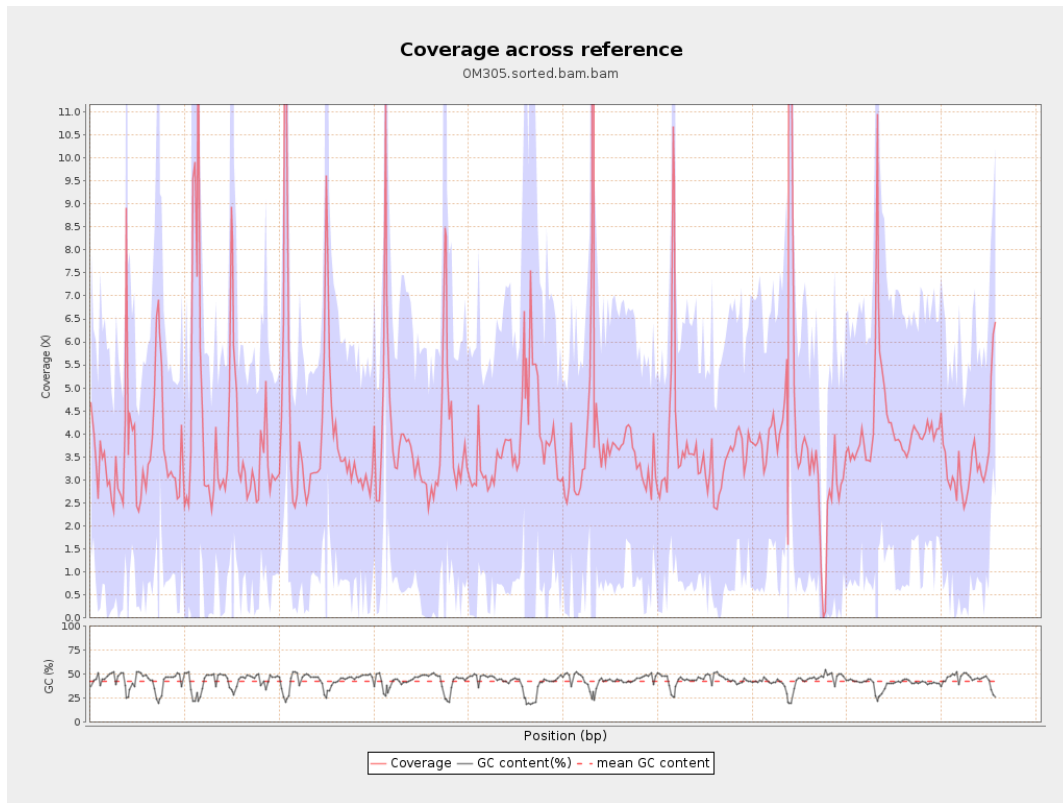
5. Results : Coverage Histogram (0-50X)
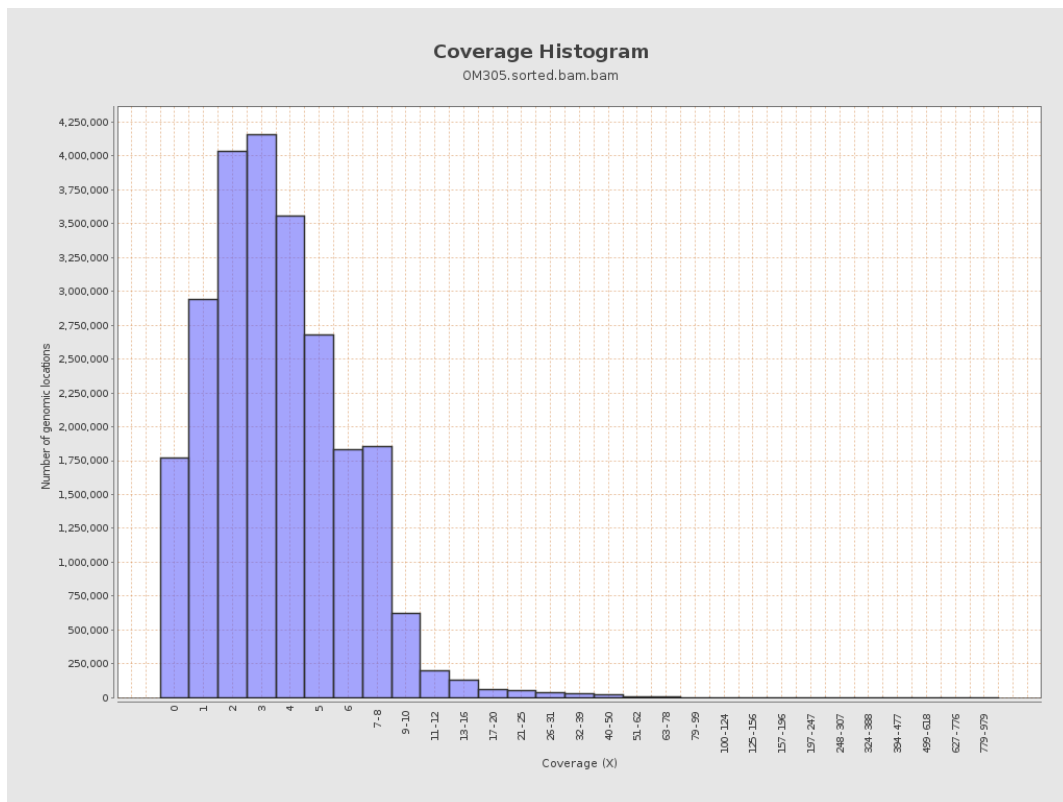
Coverage Histogram (0-50X)
OM305.sorted.bam.bam
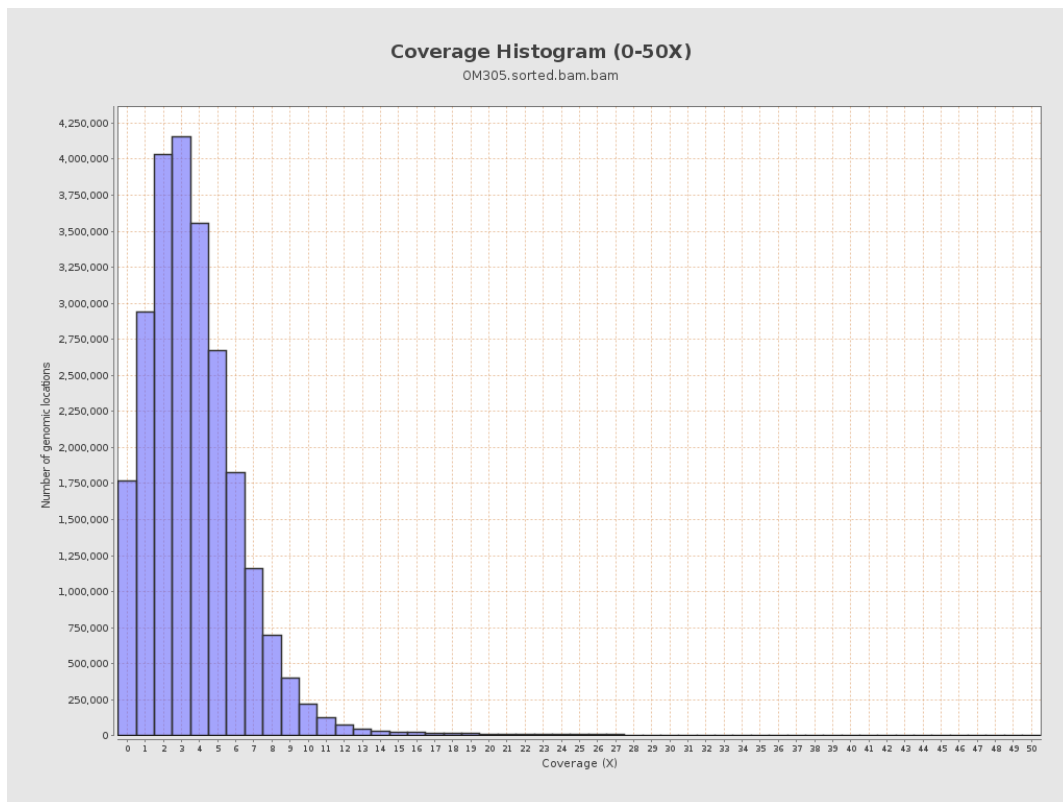
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
OM305.sorted.bam.bam
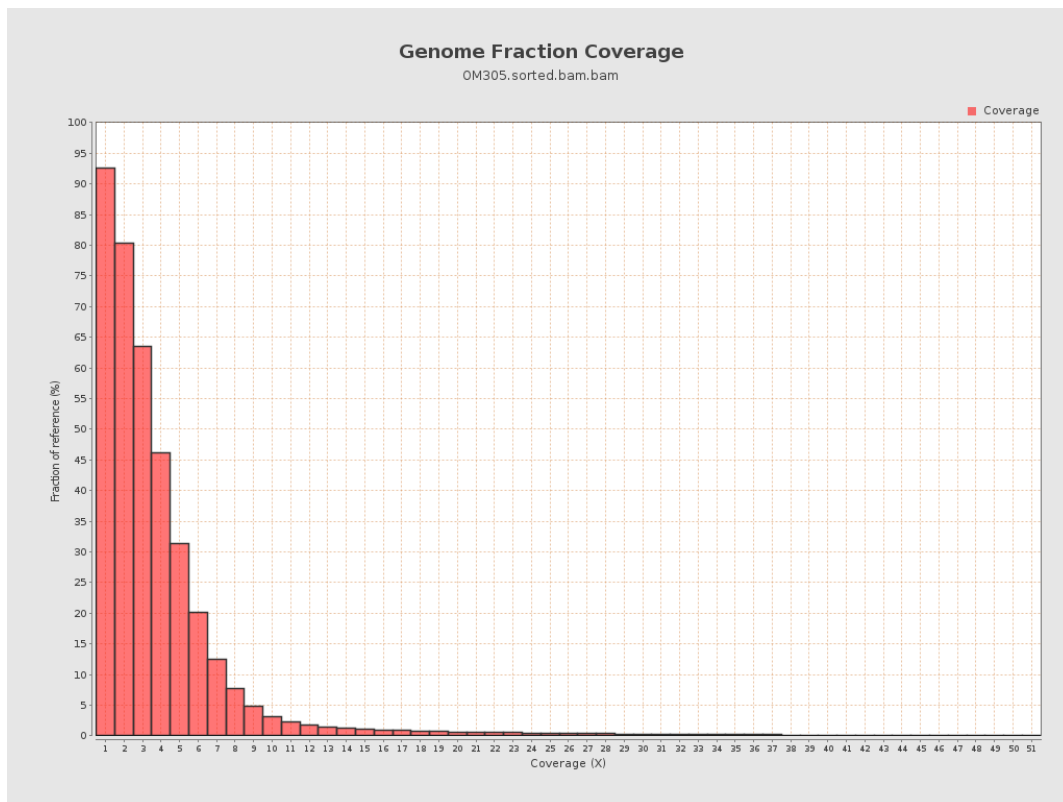
7. Results : Duplication Rate Histogram

8. Results : Mapped Reads Nucleotide Content
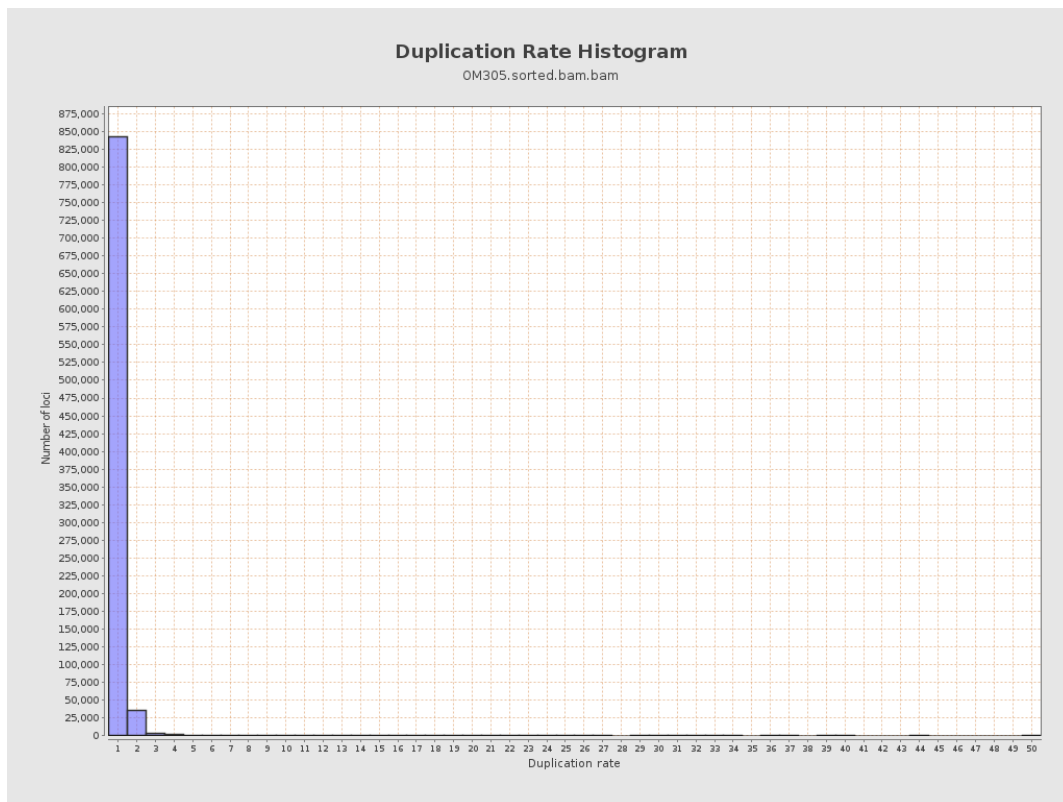
Mapped Reads Nucleotide Content
OM305.sorted.bam.bam
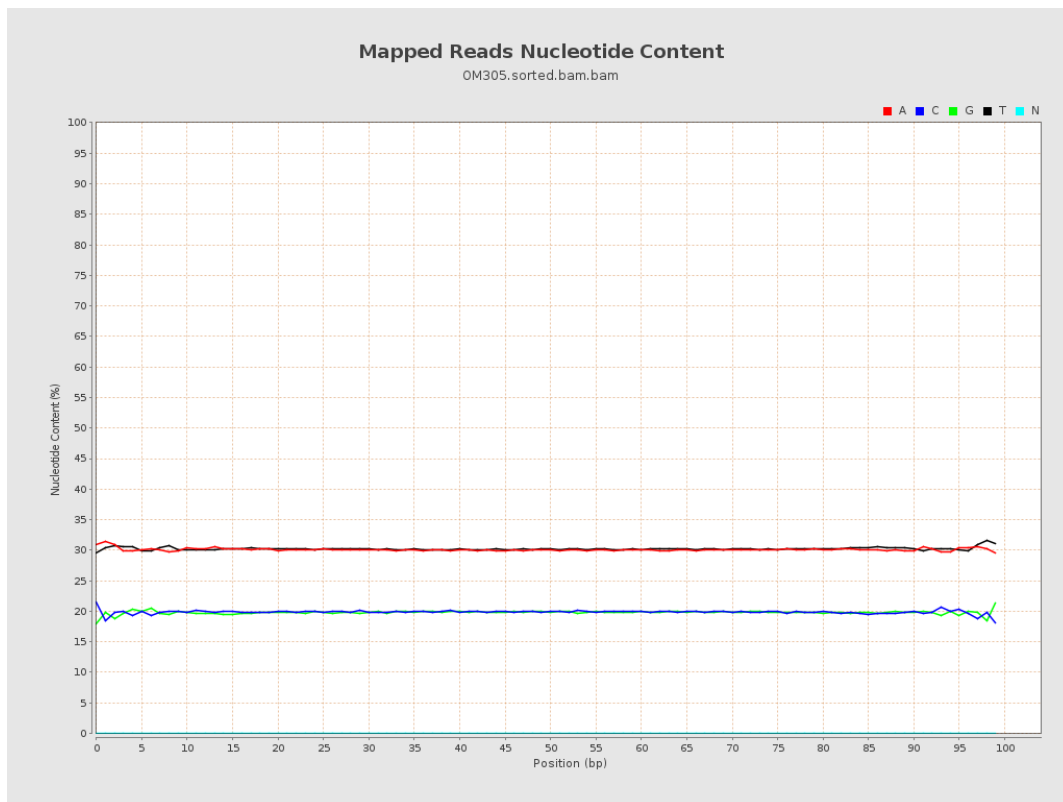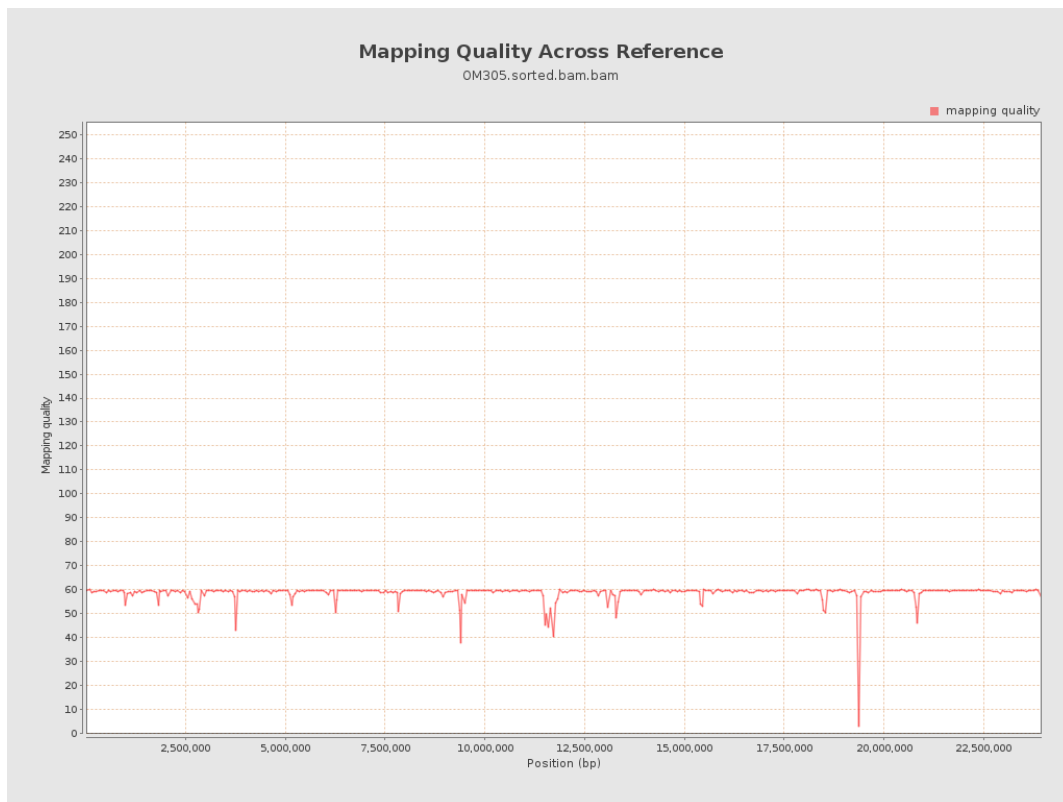
9. Results : Mapped Reads GC-content Distribution
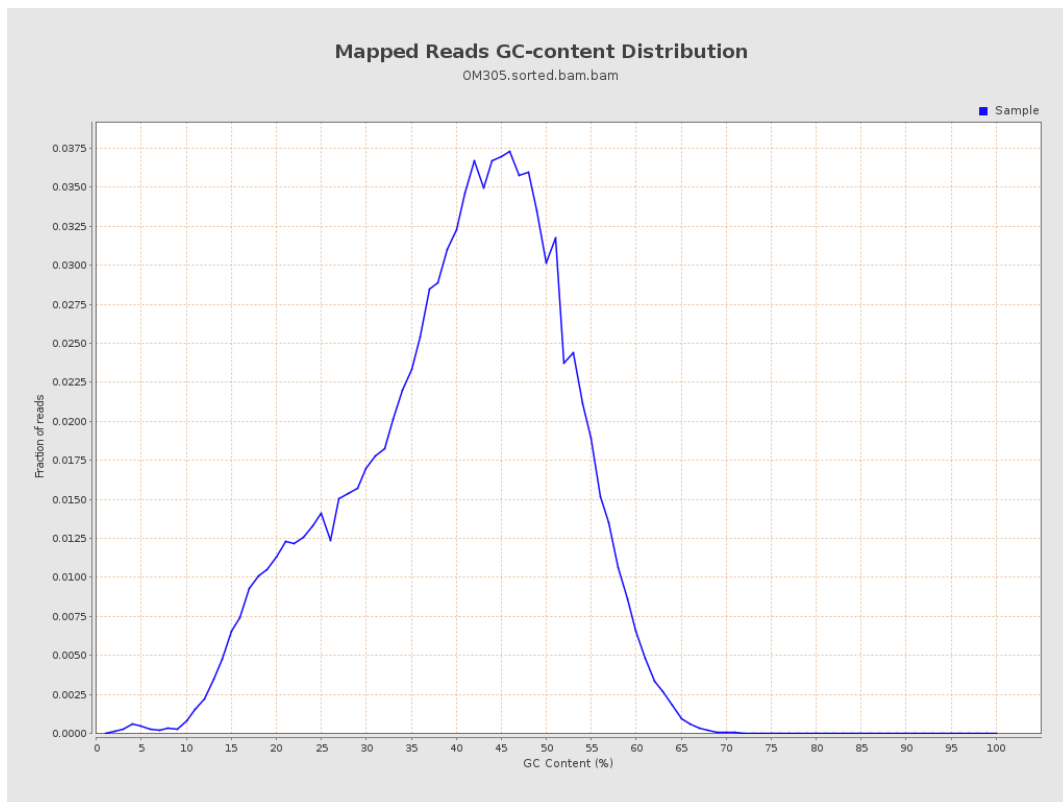
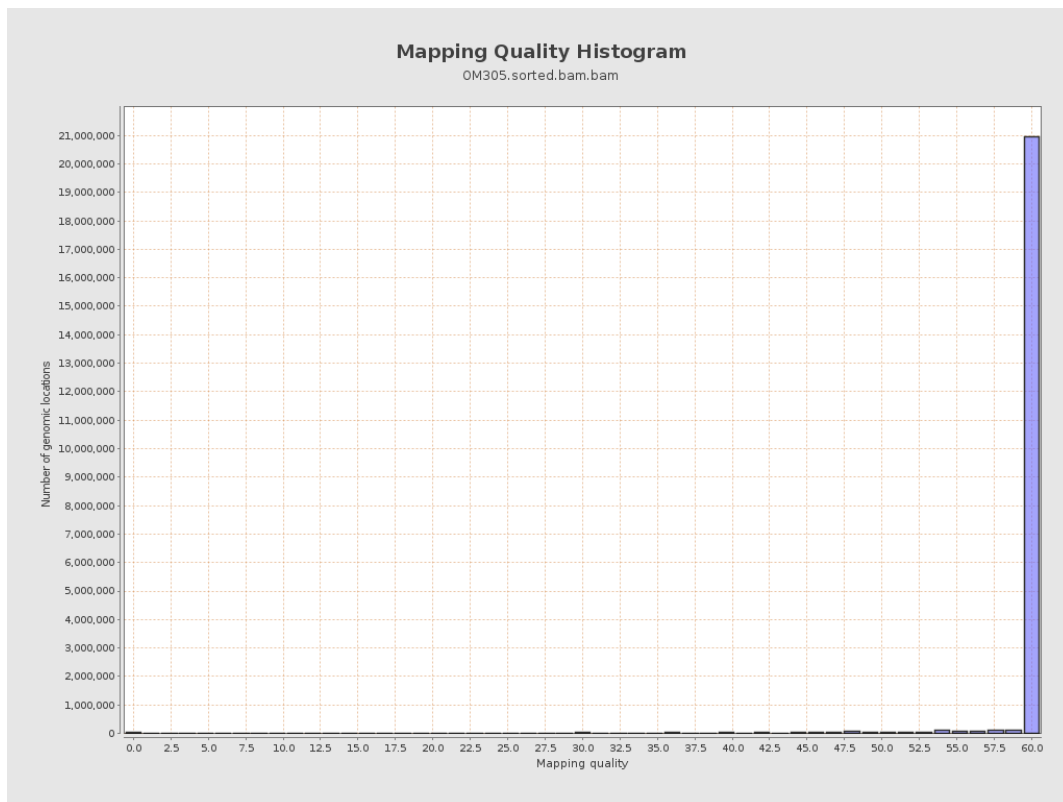# 10. Results : Mapped Reads Clipping Profile
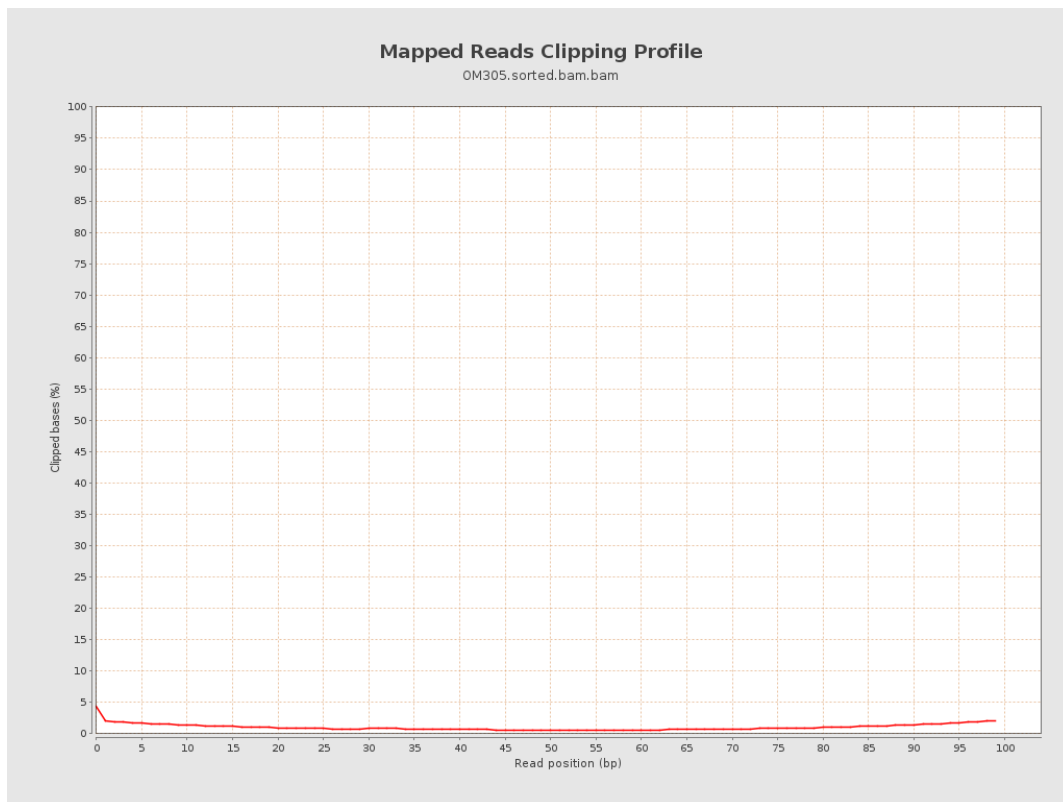
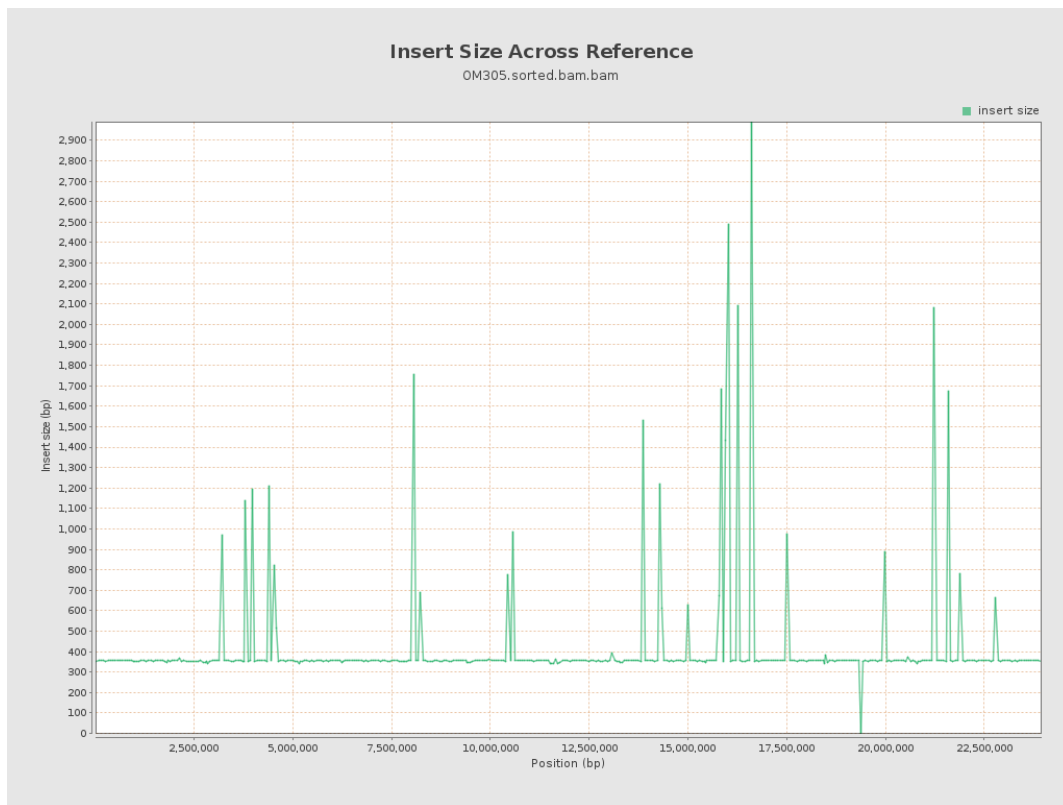# 11. Results : Homopolymer Indels
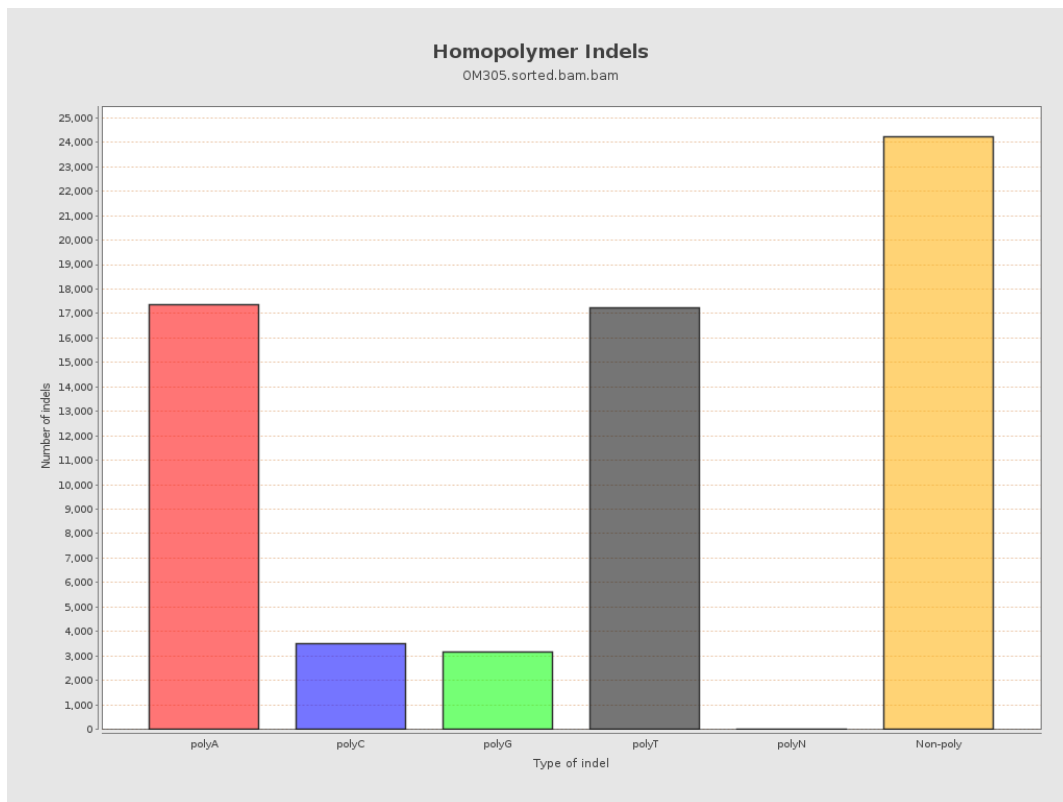
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram

Insert Size Histogram
OM305.sorted.bam.bam