

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2016/10/23 14:07:54*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM302.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/OM302-BiooBarcode34_CATGGC_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM302-BiooBarcode34_CATGGC_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 14:07:54 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM302.sorted.bam.

	bam
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## 2. Summary

### 2.1. Globals

Reference size	23,958,997
Number of reads	5,829,367
Mapped reads	1,387,667 / 23.8%
Unmapped reads	4,441,700 / 76.2%
Mapped paired reads	1,387,667 / 23.8%
Mapped reads, first in pair	698,202 / 11.98%
Mapped reads, second in pair	689,465 / 11.83%
Mapped reads, both in pair	1,332,827 / 22.86%
Mapped reads, singletons	54,840 / 0.94%
Read min/max/mean length	30 / 100 / 99.96
Duplicated reads (estimated)	139,088 / 2.39%
Duplication rate	6.95%
Clipped reads	184,538 / 3.17%

### 2.2. ACGT Content

Number/percentage of A's	39,954,735 / 30.19%
Number/percentage of C's	26,156,025 / 19.77%
Number/percentage of T's	40,143,627 / 30.34%
Number/percentage of G's	26,074,651 / 19.7%
Number/percentage of N's	10,486 / 0.01%
GC Percentage	39.47%

## 2.3. Coverage

Mean	5.5291
Standard Deviation	6.7152

## 2.4. Mapping Quality

Mean Mapping Quality	58.25
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## 2.5. Insert size

Mean	972.84
Standard Deviation	26,317.52
P25/Median/P75	331 / 352 / 362

## 2.6. Mismatches and indels

General error rate	1.63%
Mismatches	2,057,522
Insertions	45,113
Mapped reads with at least one insertion	3.07%
Deletions	50,311
Mapped reads with at least one deletion	3.4%
Homopolymer indels	60.86%

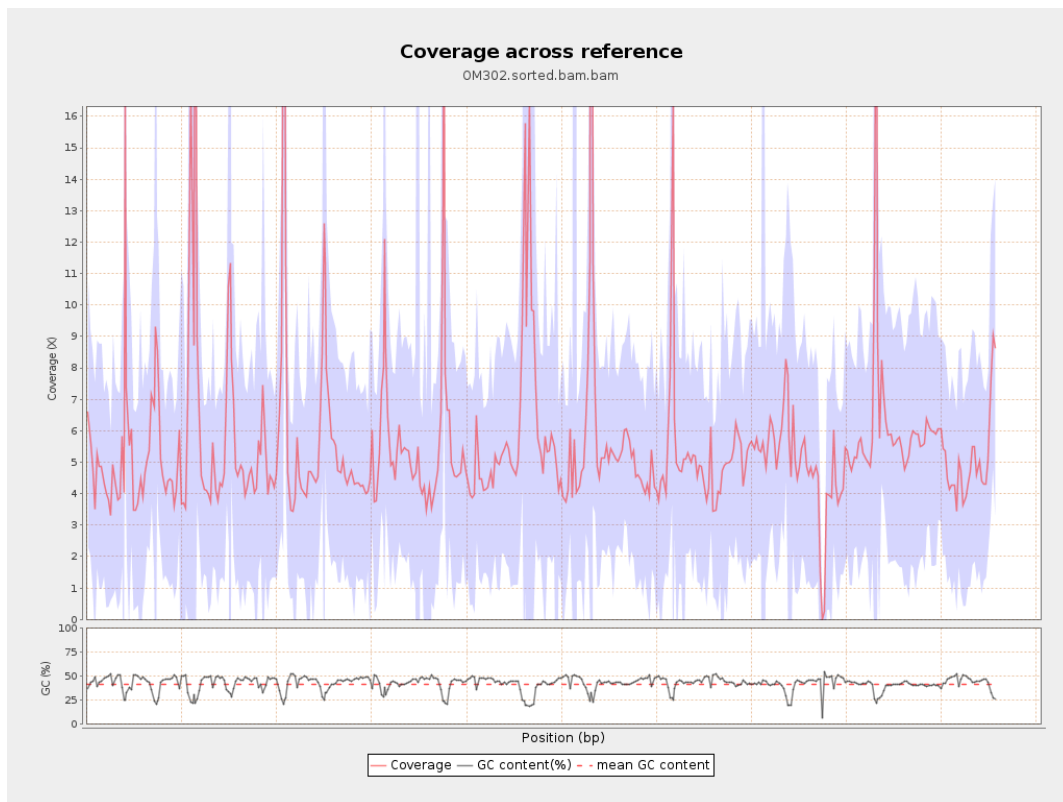
## 2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi 1074120478 emb LT615256.1	977217	4484444	4.589	3.0525
gi 1074120682 emb LT615257.1	860454	5068763	5.8908	5.5747
gi 1074120865 emb LT615258.1	989719	5942527	6.0043	7.6251
gi 1074121086 emb LT615259.1	935450	6047343	6.4646	9.351
gi 1074121301 emb LT615260.1	1432239	8333553	5.8185	6.3799
gi 1074121615 emb LT615261.1	1080962	6220121	5.7542	6.0503
gi 1074121871 emb LT615262.1	1545099	7876778	5.0979	3.1846
gi 1074122235 emb LT615263.1	1585108	8644730	5.4537	7.7461
gi 1074122590 emb LT615264.1	2122358	11144660	5.2511	3.695
gi 1074123050 emb LT615265.1	1754192	11155509	6.3593	13.7088
gi 1074123421 emb LT615	2150147	12138420	5.6454	8.5028

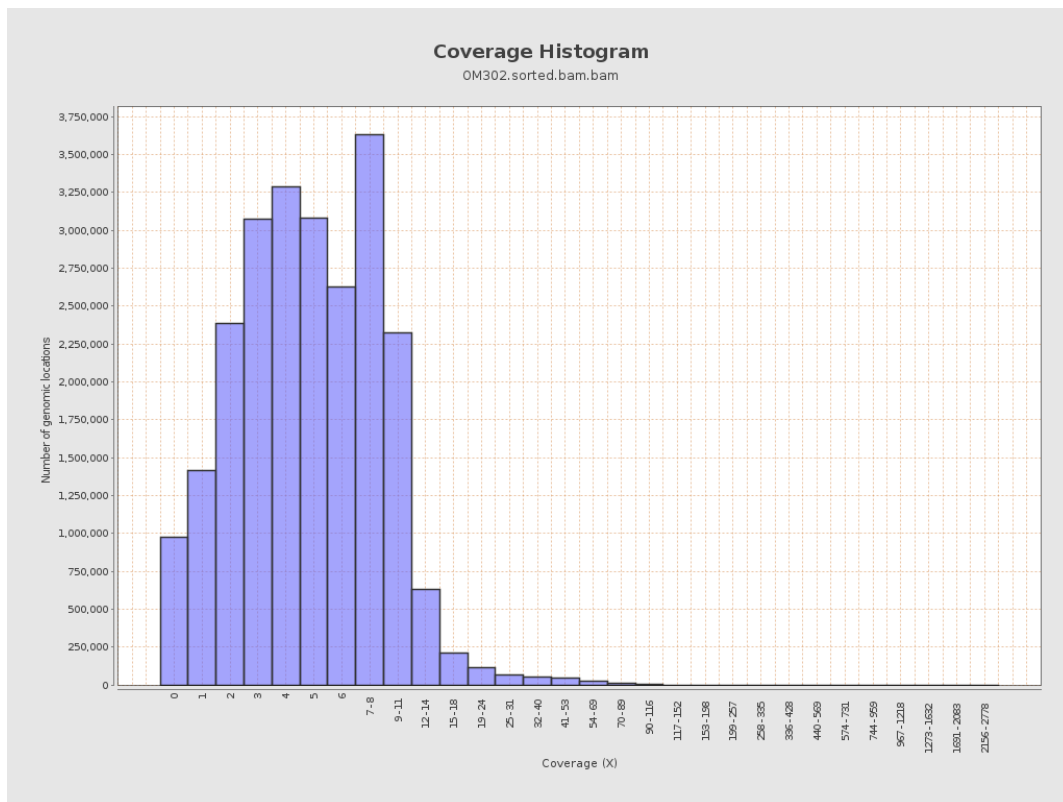
266.1				
gi 107412389 8 emb LT615 267.1	3031036	16093556	5.3096	4.7157
gi 107412458 8 emb LT615 268.1	2359348	11954980	5.0671	5.7224
gi 107412506 5 emb LT615 269.1	3135668	17366070	5.5382	3.2581

### 3. Results : Coverage across reference

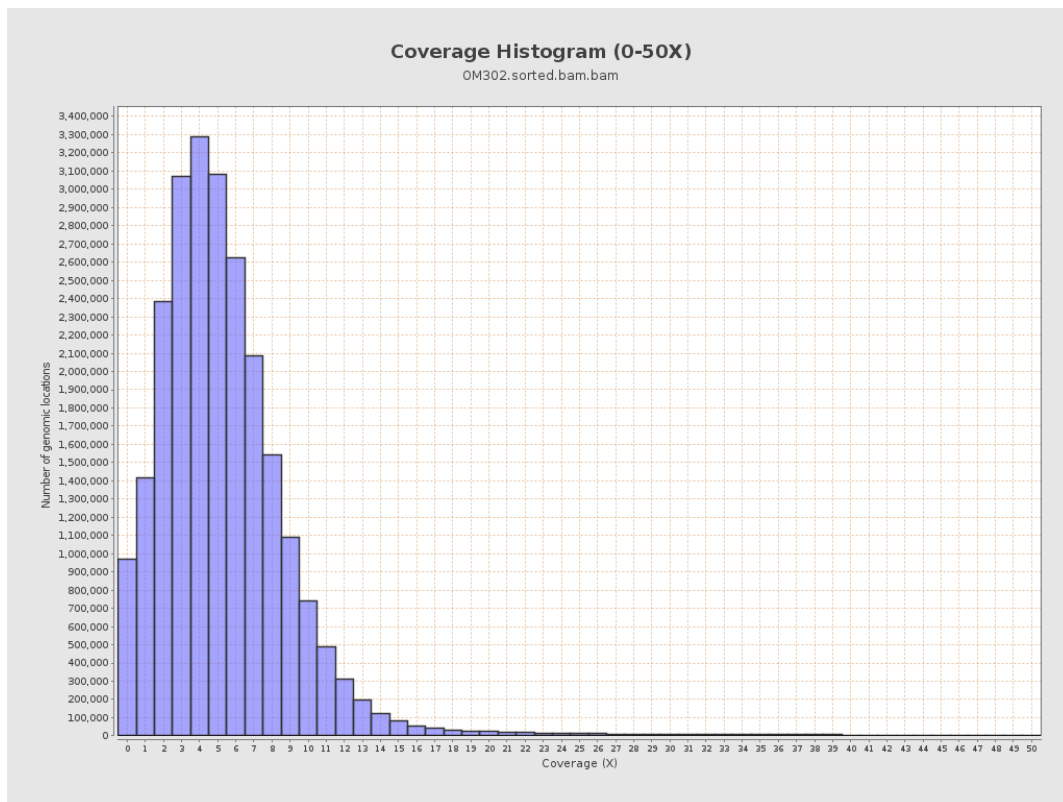




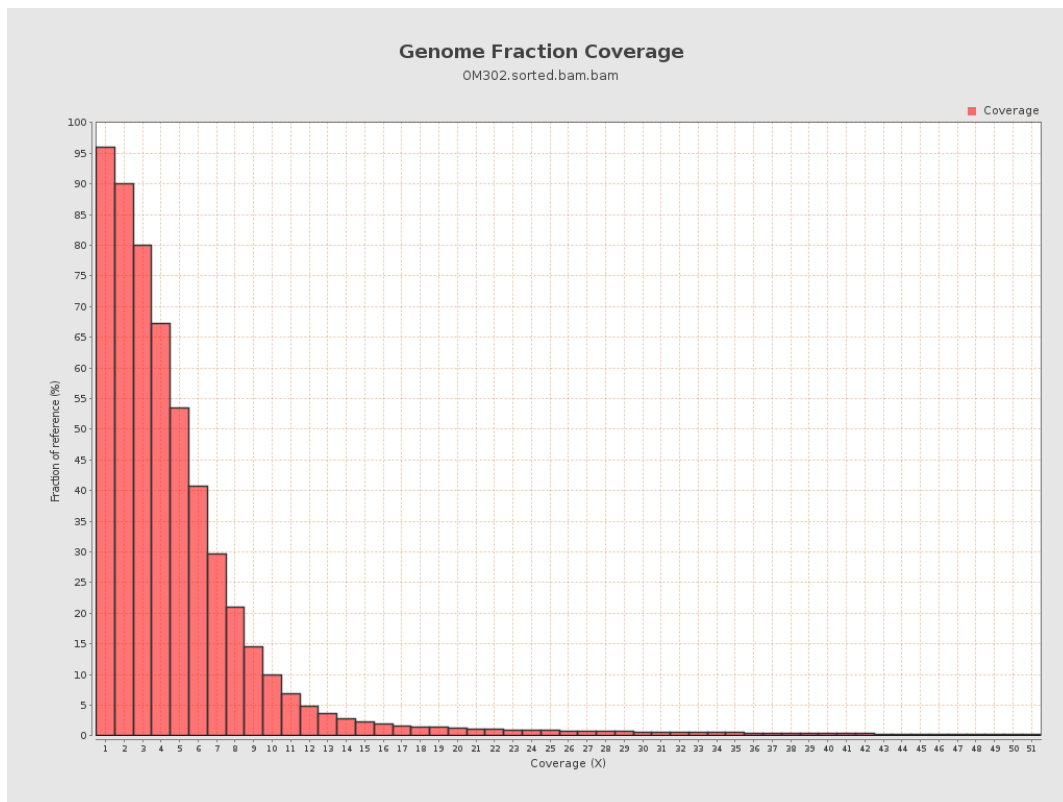
## 4. Results : Coverage Histogram



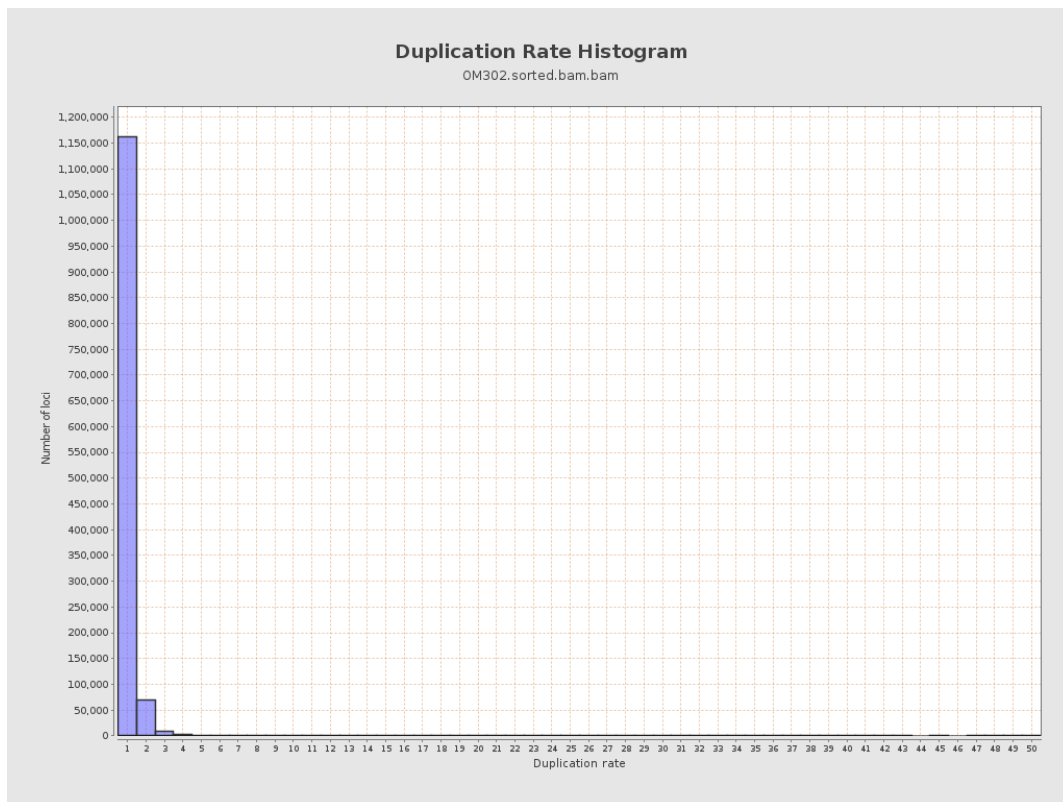
## 5. Results : Coverage Histogram (0-50X)



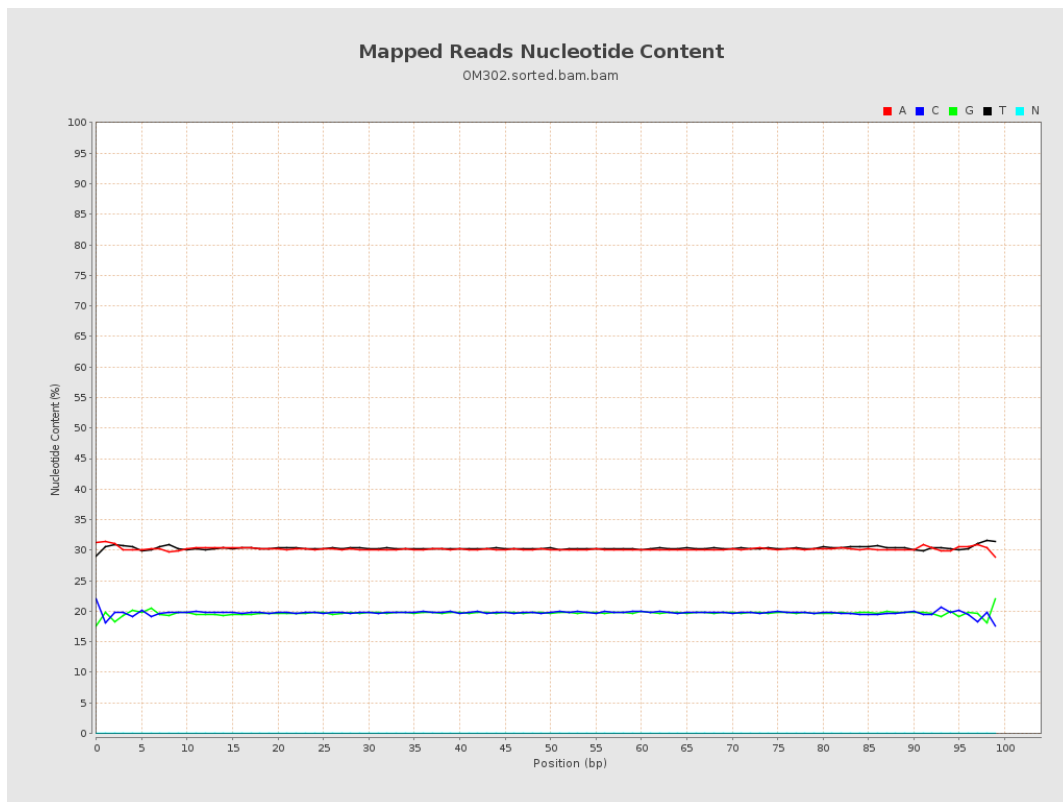
## 6. Results : Genome Fraction Coverage



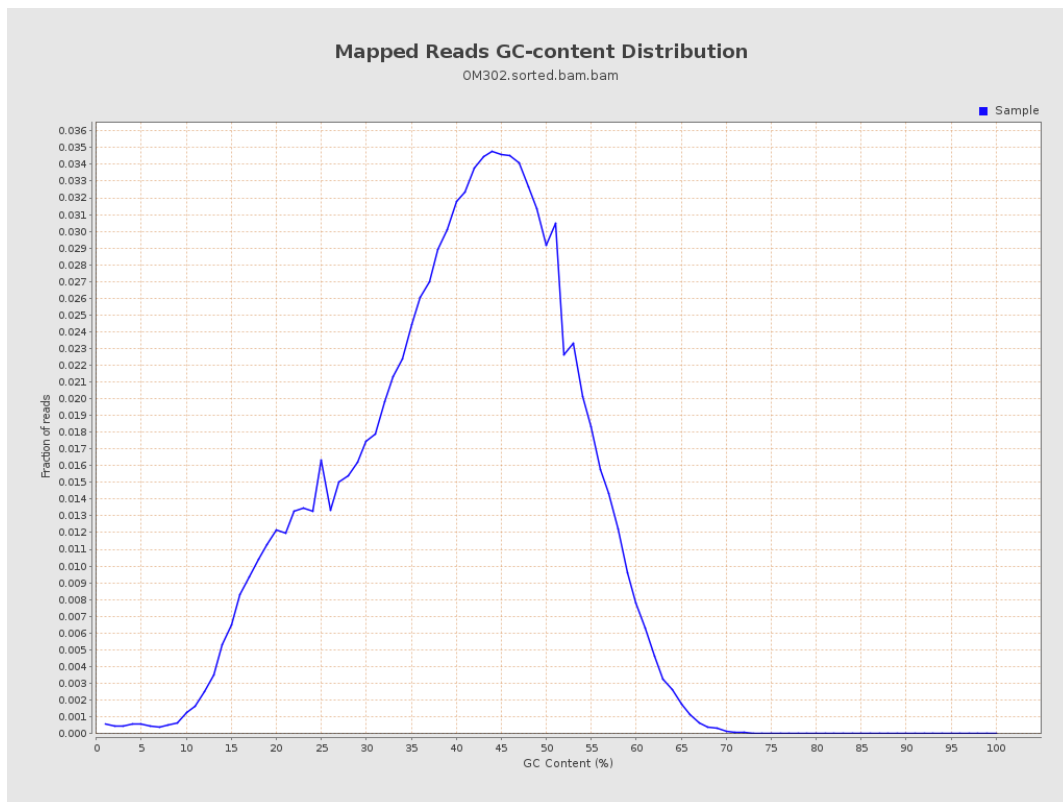
## 7. Results : Duplication Rate Histogram



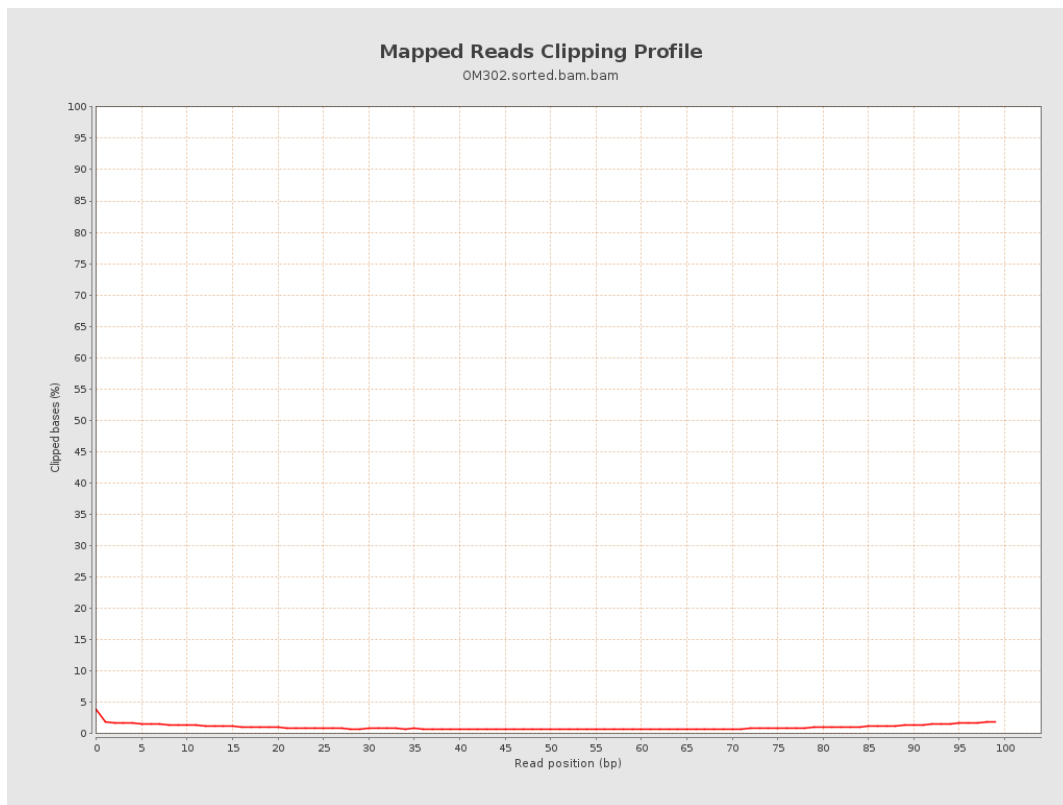
## 8. Results : Mapped Reads Nucleotide Content



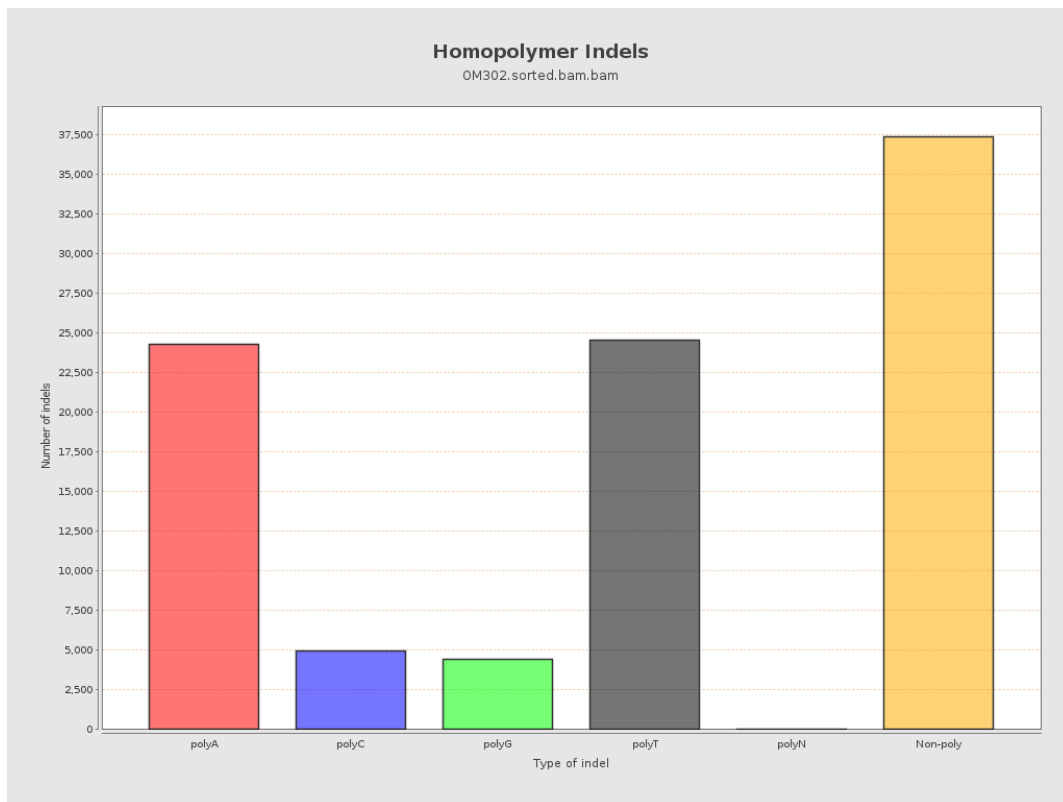
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile

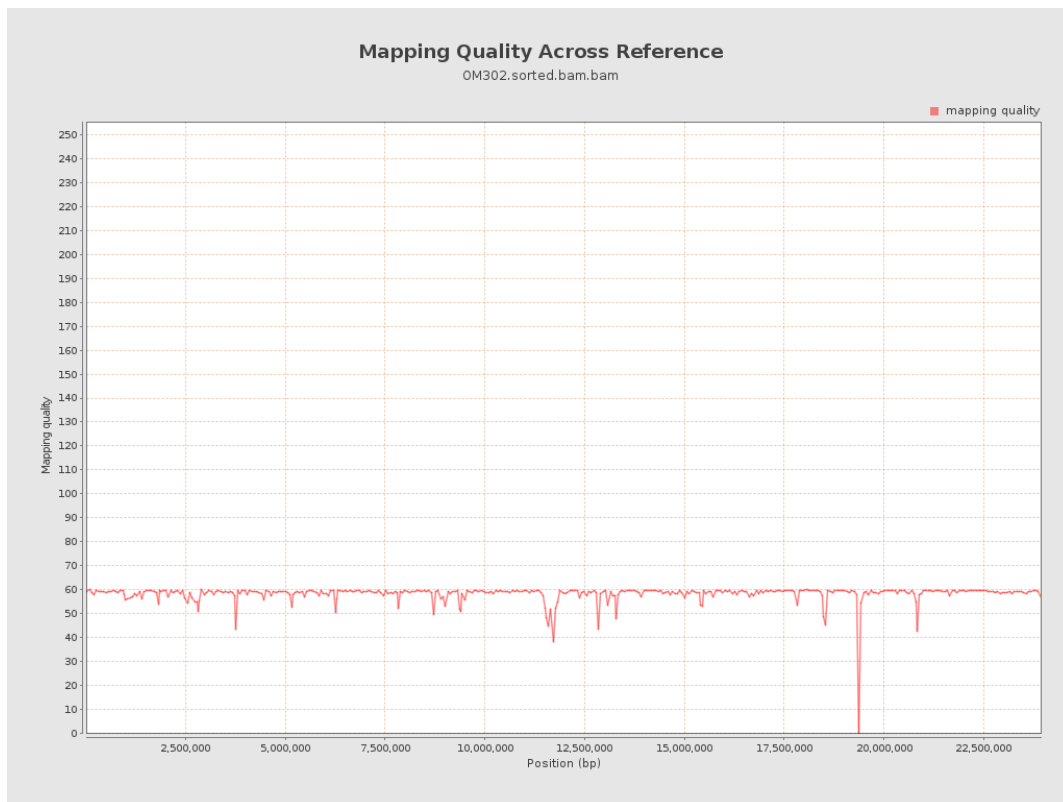


## 11. Results : Homopolymer Indels

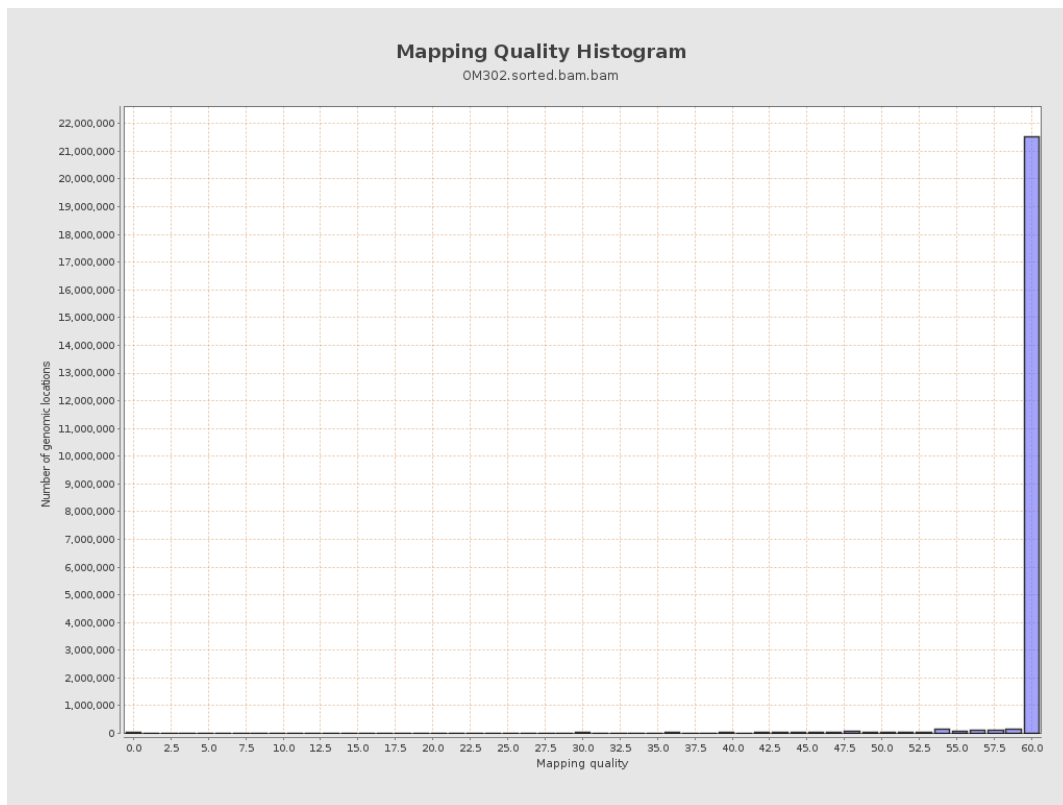




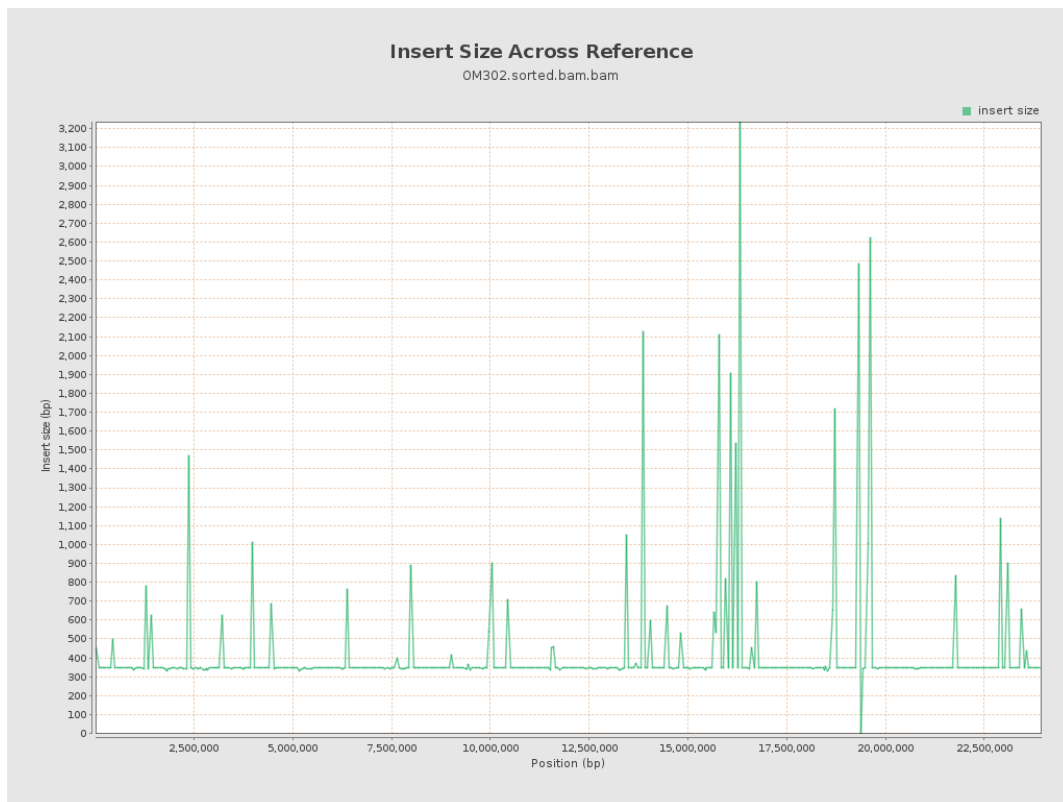
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

