

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2016/10/23 14:01:01*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM296.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/OM296-BiooBarcode32_CACTCA_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM296-BiooBarcode32_CACTCA_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 14:01:00 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM296.sorted.bam.

	bam
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## 2. Summary

### 2.1. Globals

Reference size	23,958,997
Number of reads	1,991,410
Mapped reads	879,662 / 44.17%
Unmapped reads	1,111,748 / 55.83%
Mapped paired reads	879,662 / 44.17%
Mapped reads, first in pair	437,451 / 21.97%
Mapped reads, second in pair	442,211 / 22.21%
Mapped reads, both in pair	854,773 / 42.92%
Mapped reads, singletons	24,889 / 1.25%
Read min/max/mean length	30 / 100 / 99.93
Duplicated reads (estimated)	65,551 / 3.29%
Duplication rate	5.37%
Clipped reads	108,534 / 5.45%

### 2.2. ACGT Content

Number/percentage of A's	25,527,687 / 30.19%
Number/percentage of C's	16,720,698 / 19.77%
Number/percentage of T's	25,620,665 / 30.29%
Number/percentage of G's	16,701,557 / 19.75%
Number/percentage of N's	6,342 / 0.01%
GC Percentage	39.52%

## 2.3. Coverage

Mean	3.5337
Standard Deviation	4.2617

## 2.4. Mapping Quality

Mean Mapping Quality	58.52
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## 2.5. Insert size

Mean	816.01
Standard Deviation	22,456.11
P25/Median/P75	334 / 347 / 356

## 2.6. Mismatches and indels

General error rate	1.68%
Mismatches	1,357,726
Insertions	29,195
Mapped reads with at least one insertion	3.14%
Deletions	33,031
Mapped reads with at least one deletion	3.54%
Homopolymer indels	62.14%

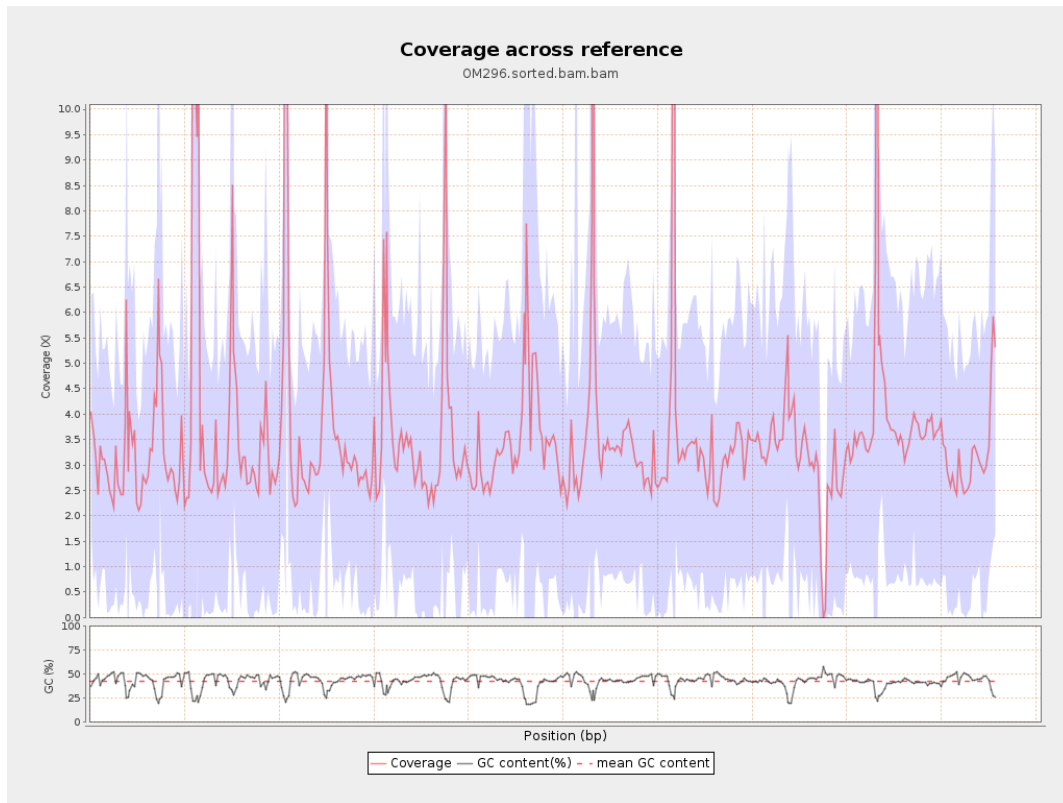
## 2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi 1074120478 emb LT615256.1	977217	2943177	3.0118	2.1614
gi 1074120682 emb LT615257.1	860454	2850367	3.3126	3.2726
gi 1074120865 emb LT615258.1	989719	4159407	4.2026	7.0317
gi 1074121086 emb LT615259.1	935450	3446573	3.6844	6.2679
gi 1074121301 emb LT615260.1	1432239	5643855	3.9406	5.6525
gi 1074121615 emb LT615261.1	1080962	3996032	3.6967	4.5767
gi 1074121871 emb LT615262.1	1545099	5258030	3.403	2.4448
gi 1074122235 emb LT615263.1	1585108	5513494	3.4783	3.5955
gi 1074122590 emb LT615264.1	2122358	6913335	3.2574	2.5218
gi 1074123050 emb LT615265.1	1754192	6353088	3.6217	4.4037
gi 1074123421 emb LT615	2150147	8112803	3.7731	6.8806

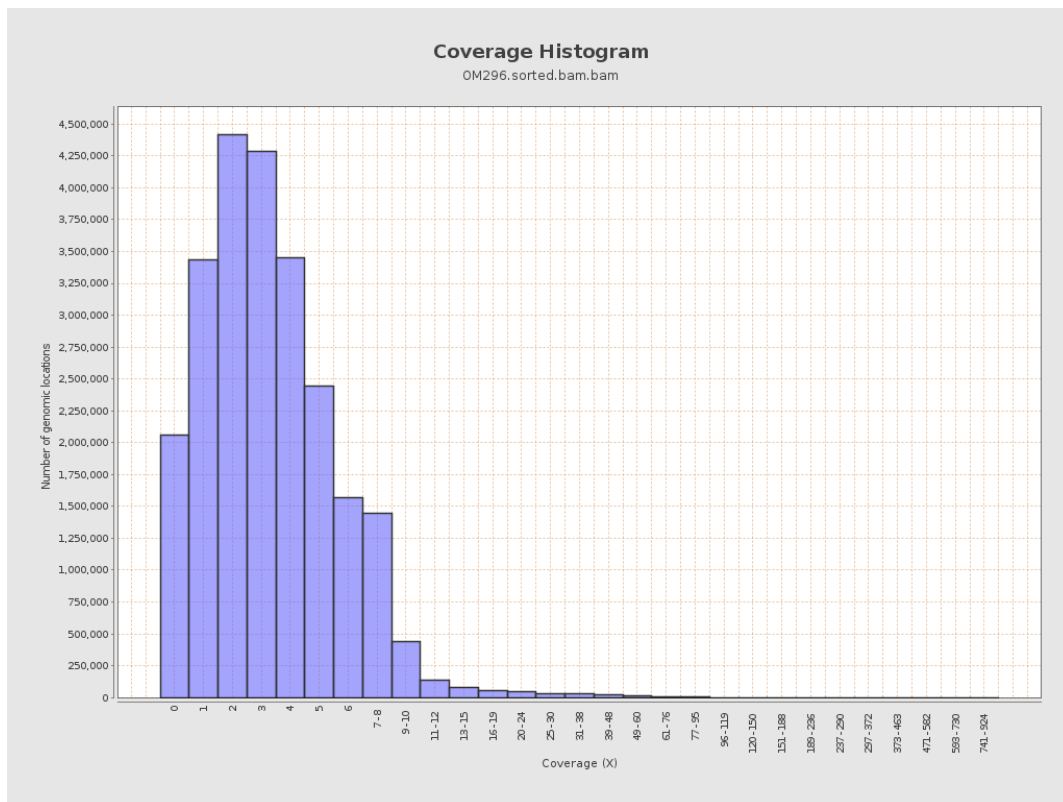
266.1				
gi 107412389 8 emb LT615 267.1	3031036	10361603	3.4185	2.8626
gi 107412458 8 emb LT615 268.1	2359348	7973250	3.3794	4.3962
gi 107412506 5 emb LT615 269.1	3135668	11138527	3.5522	2.2829

### 3. Results : Coverage across reference

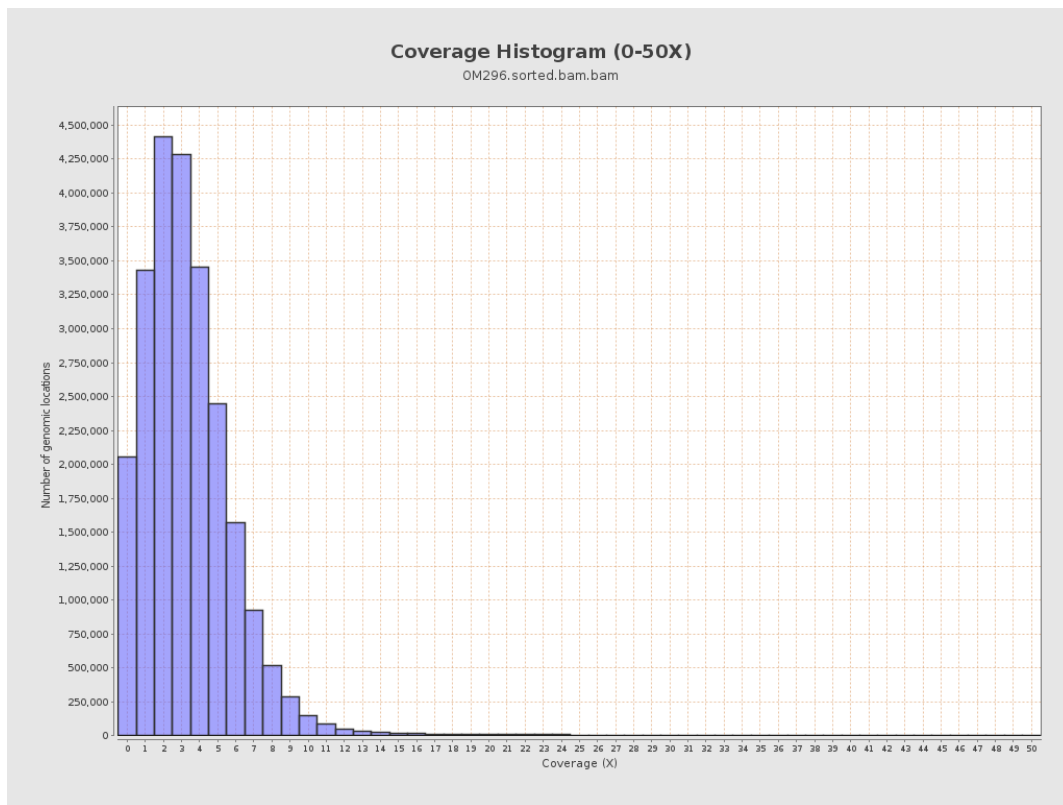




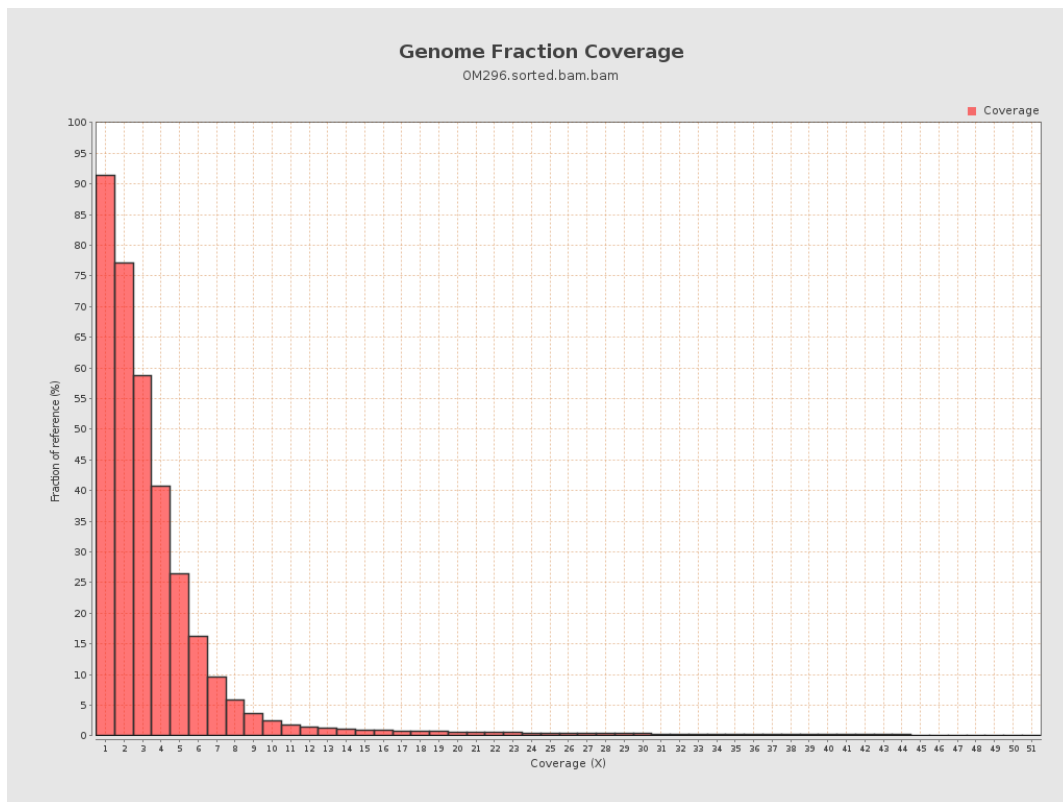
## 4. Results : Coverage Histogram



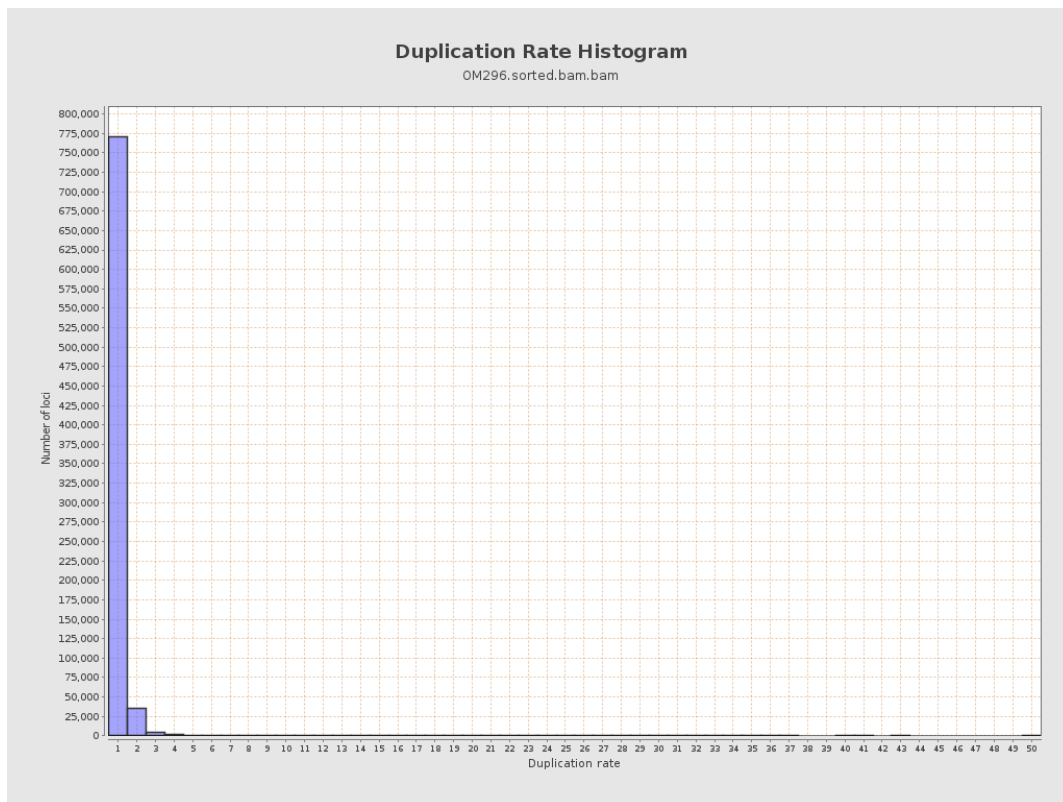
## 5. Results : Coverage Histogram (0-50X)



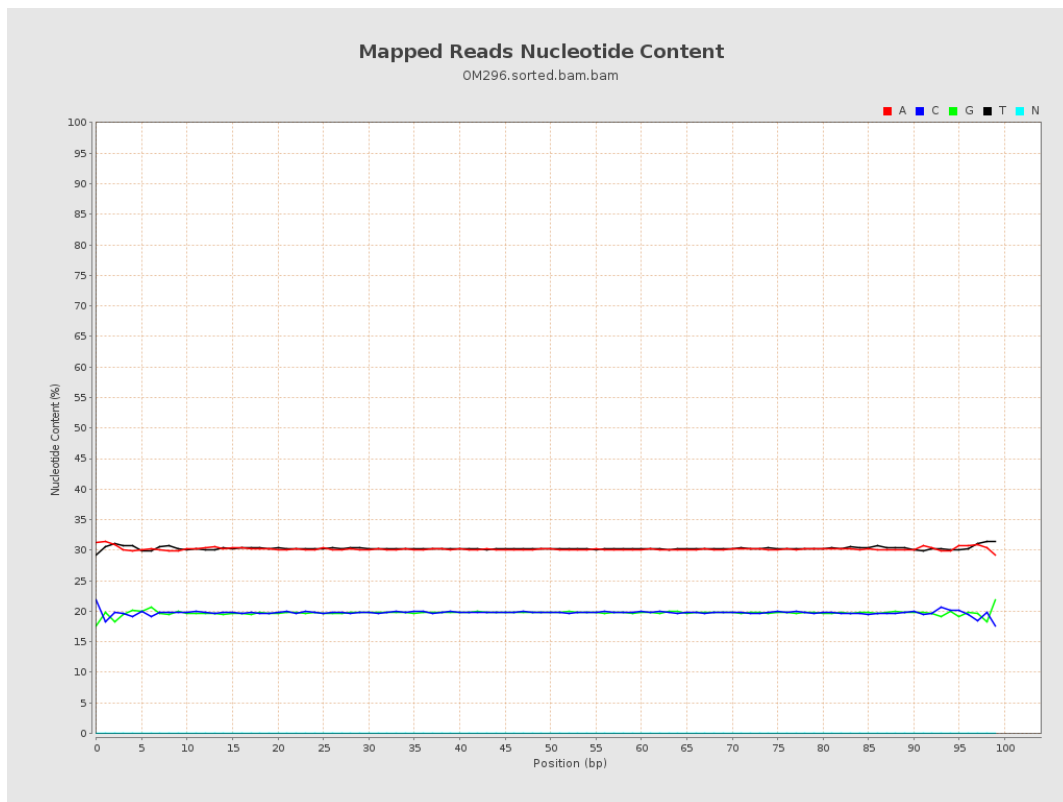
## 6. Results : Genome Fraction Coverage



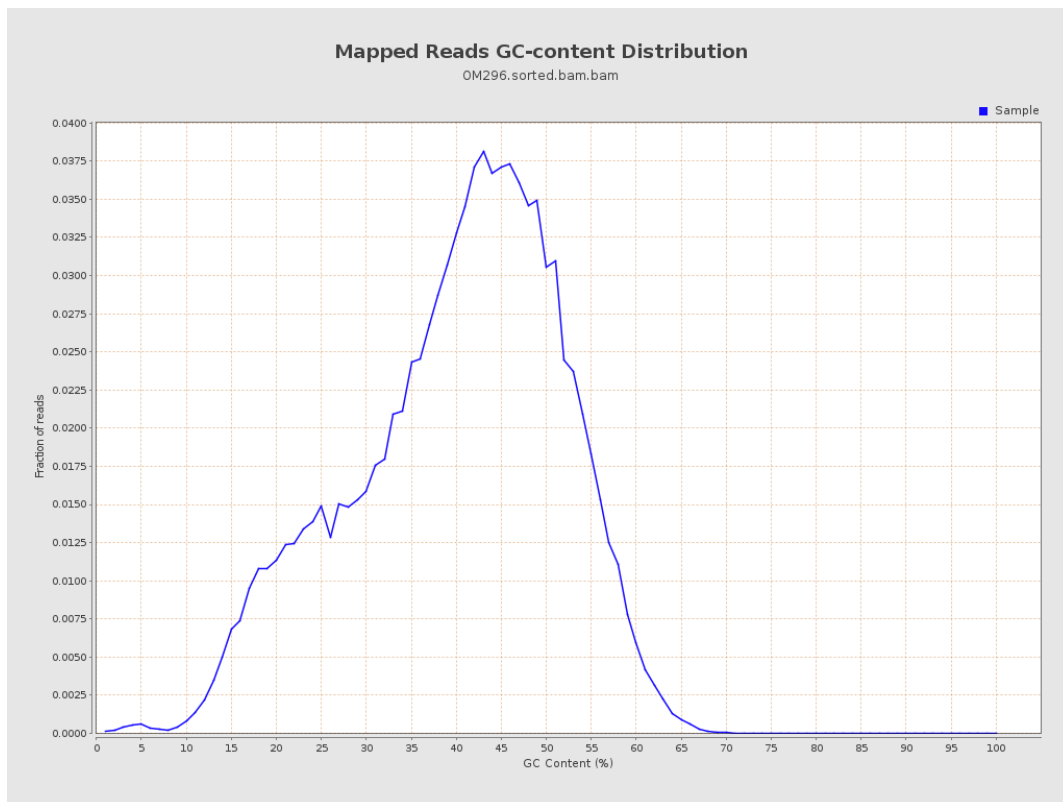
## 7. Results : Duplication Rate Histogram



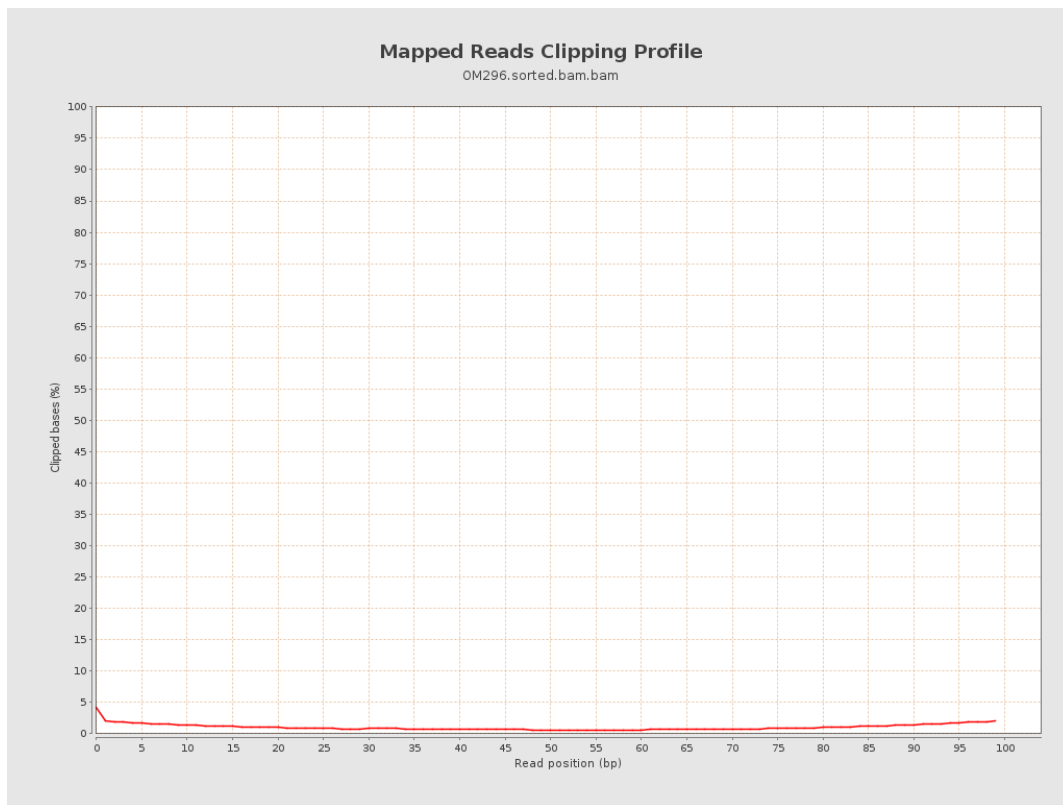
## 8. Results : Mapped Reads Nucleotide Content



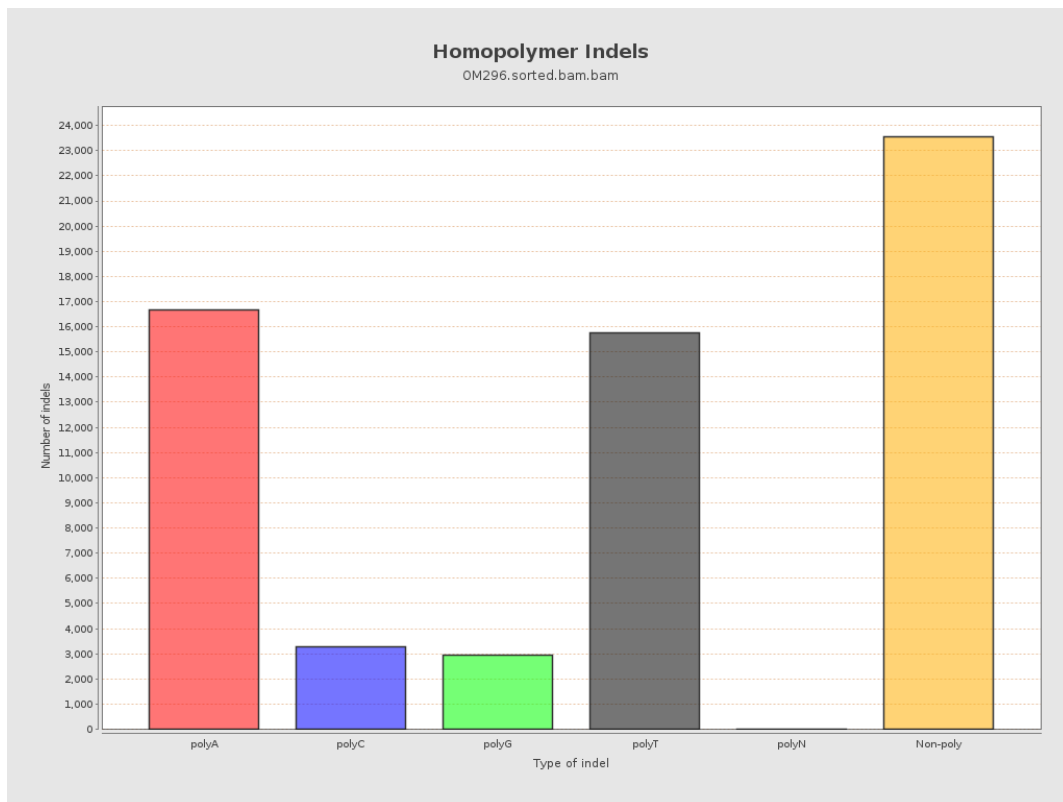
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile

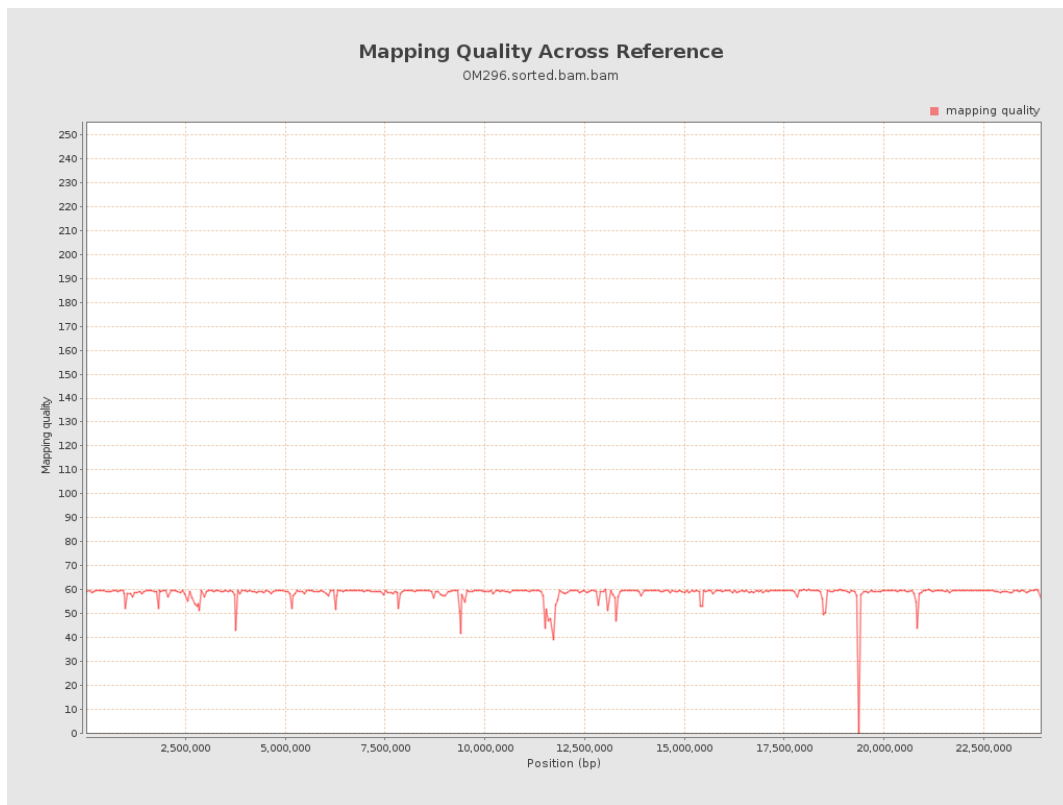


## 11. Results : Homopolymer Indels

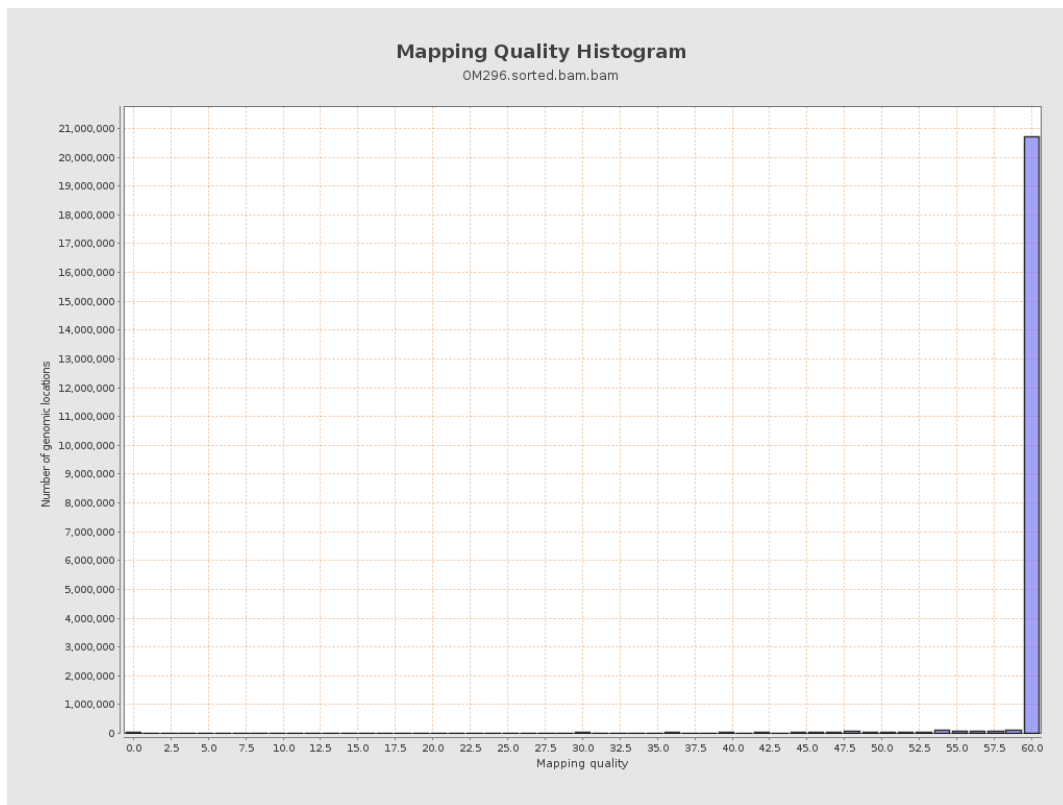




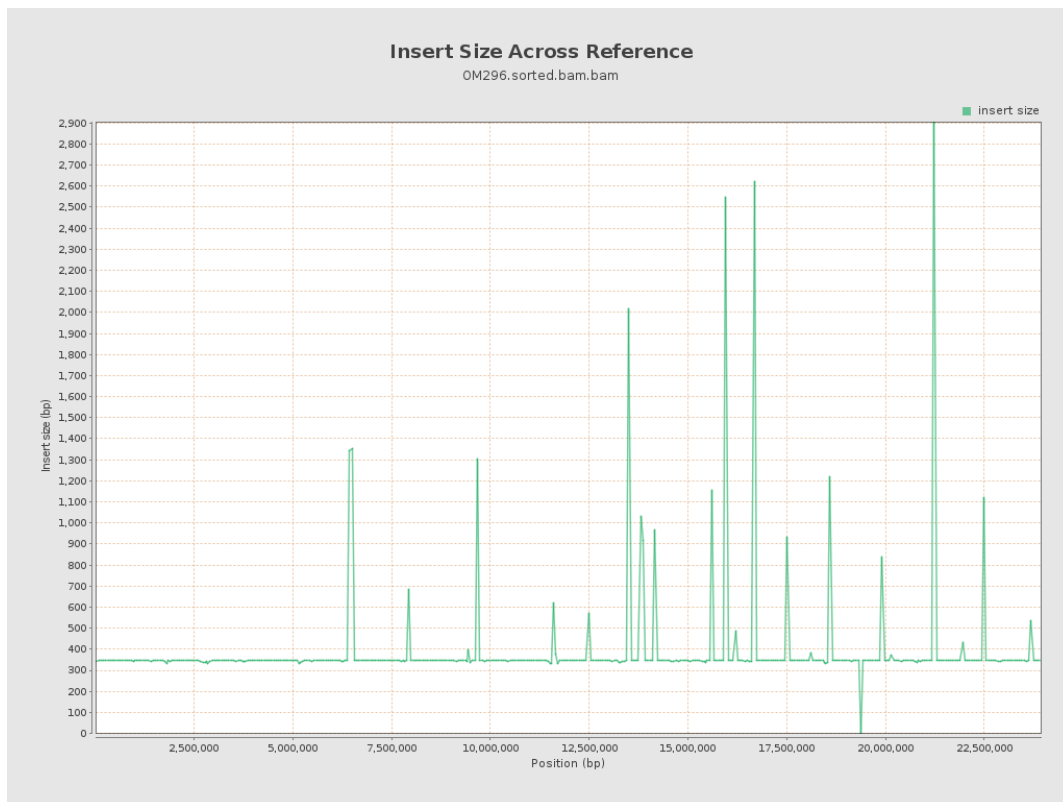
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

