

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2016/10/23 13:18:28*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM124.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-124_CTTGTA_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM-124_CTTGTA_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 13:18:27 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM124.sorted.bam.bam

## 2. Summary

### 2.1. Globals

Reference size	23,958,997
Number of reads	49,017,302
Mapped reads	3,124,724 / 6.37%
Unmapped reads	45,892,578 / 93.63%
Mapped paired reads	3,124,724 / 6.37%
Mapped reads, first in pair	1,563,333 / 3.19%
Mapped reads, second in pair	1,561,391 / 3.19%
Mapped reads, both in pair	2,742,771 / 5.6%
Mapped reads, singletons	381,953 / 0.78%
Read min/max/mean length	30 / 100 / 99.97
Duplicated reads (estimated)	708,330 / 1.45%
Duplication rate	11.6%
Clipped reads	655,690 / 1.34%

### 2.2. ACGT Content

Number/percentage of A's	82,499,340 / 29.42%
Number/percentage of C's	56,809,352 / 20.26%
Number/percentage of T's	84,267,254 / 30.05%
Number/percentage of G's	56,818,143 / 20.26%
Number/percentage of N's	8,767 / 0%
GC Percentage	40.52%

## 2.3. Coverage

Mean	11.7167
Standard Deviation	59.9616

## 2.4. Mapping Quality

Mean Mapping Quality	56.2
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## 2.5. Insert size

Mean	1,004.54
Standard Deviation	31,497.75
P25/Median/P75	224 / 236 / 256

## 2.6. Mismatches and indels

General error rate	1.2%
Mismatches	3,080,118
Insertions	109,366
Mapped reads with at least one insertion	3.24%
Deletions	122,201
Mapped reads with at least one deletion	3.42%
Homopolymer indels	60.63%

## 2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

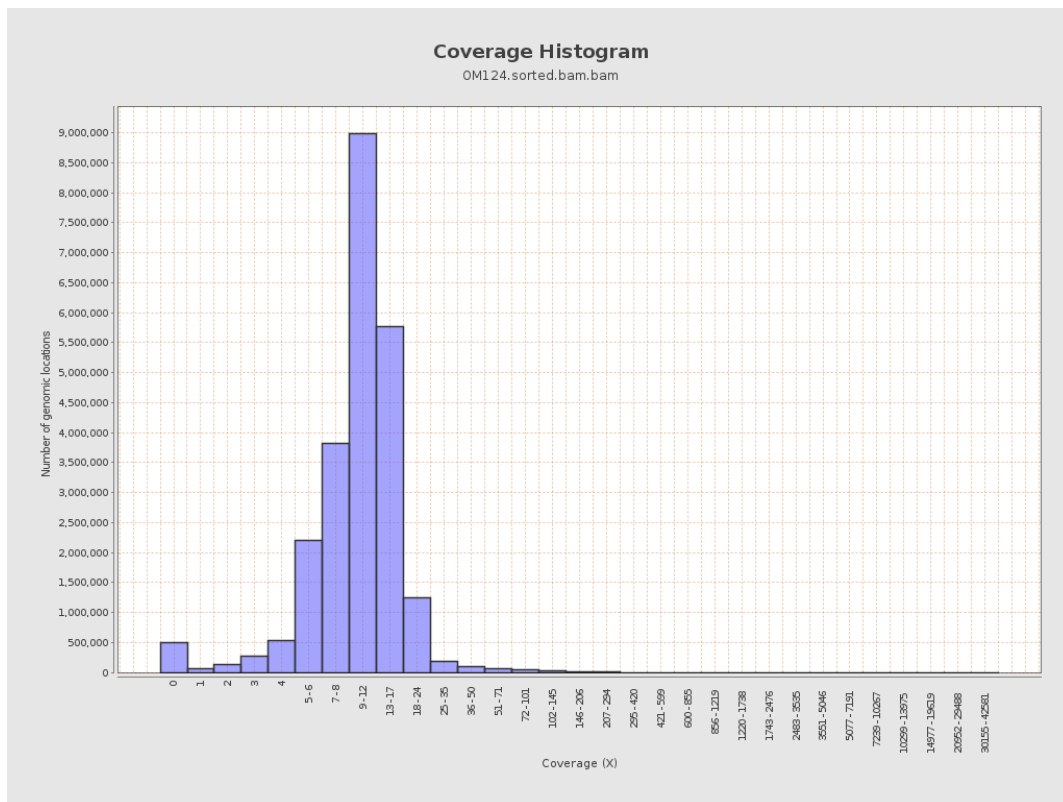
gi 1074120478 emb LT615256.1	977217	10864952	11.1183	14.44
gi 1074120682 emb LT615257.1	860454	9263600	10.7659	24.4172
gi 1074120865 emb LT615258.1	989719	12312662	12.4406	28.2718
gi 1074121086 emb LT615259.1	935450	11215579	11.9895	17.2465
gi 1074121301 emb LT615260.1	1432239	18657784	13.027	33.9667
gi 1074121615 emb LT615261.1	1080962	12523695	11.5857	23.2297
gi 1074121871 emb LT615262.1	1545099	17185303	11.1225	14.6871
gi 1074122235 emb LT615263.1	1585108	19273847	12.1593	85.2632
gi 1074122590 emb LT615264.1	2122358	23721833	11.1771	10.8501
gi 1074123050 emb LT615265.1	1754192	23008679	13.1164	183.3061
gi 1074123421 emb LT615	2150147	25732074	11.9676	23.2232

266.1				
gi 107412389 8 emb LT615 267.1	3031036	34785571	11.4765	53.3698
gi 107412458 8 emb LT615 268.1	2359348	26487641	11.2267	16.555
gi 107412506 5 emb LT615 269.1	3135668	35687667	11.3812	14.0723

### 3. Results : Coverage across reference

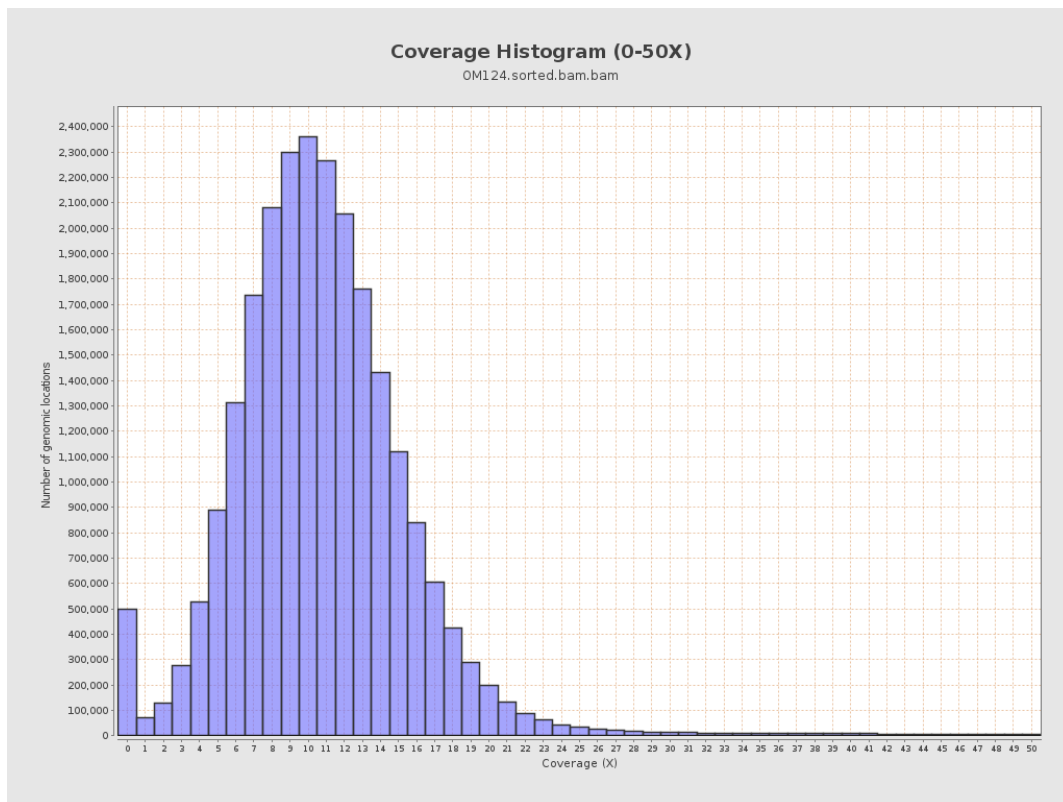


## 4. Results : Coverage Histogram

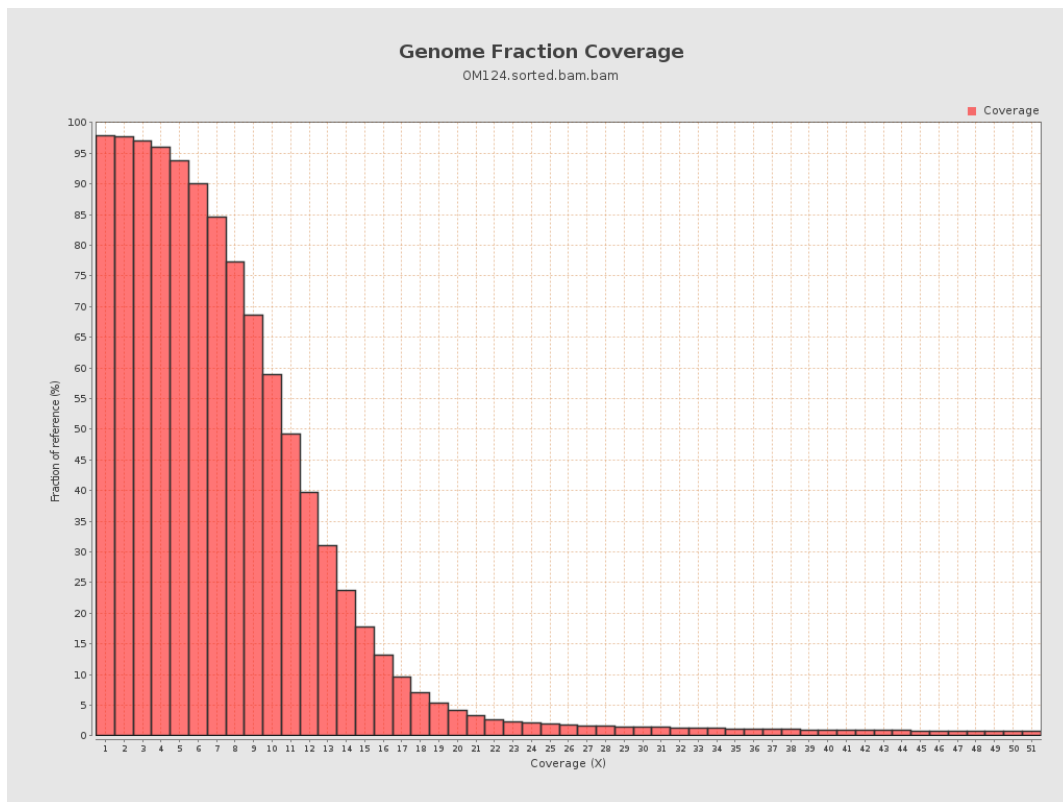




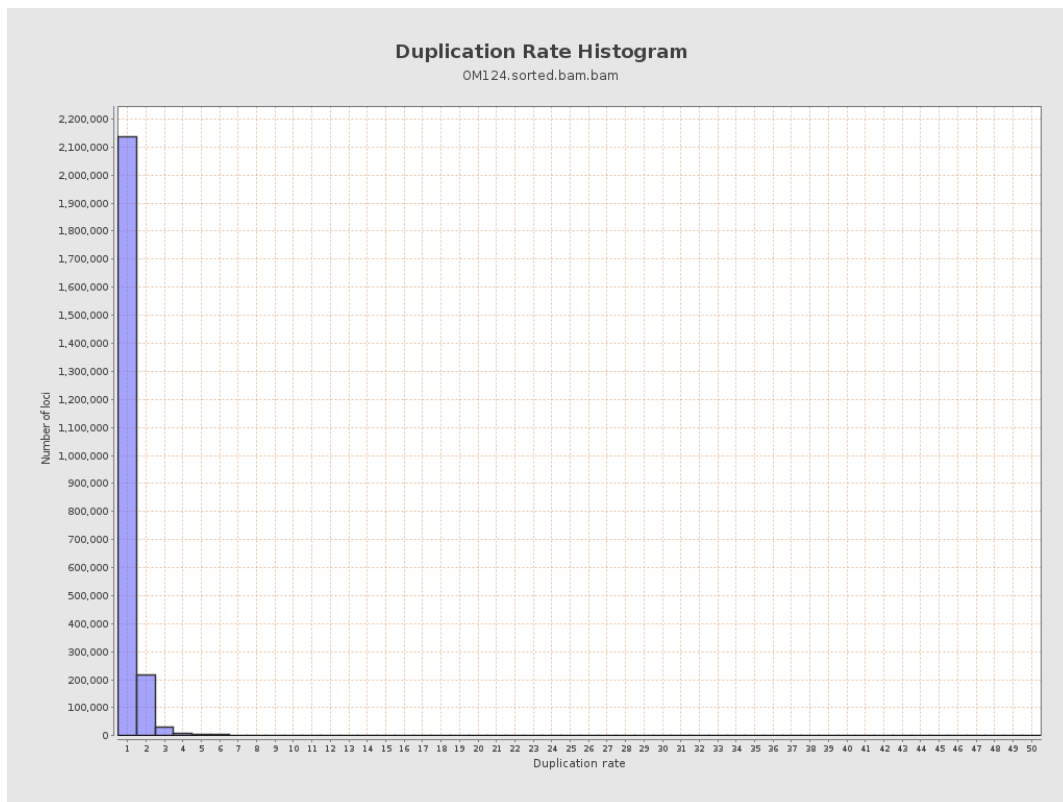
## 5. Results : Coverage Histogram (0-50X)



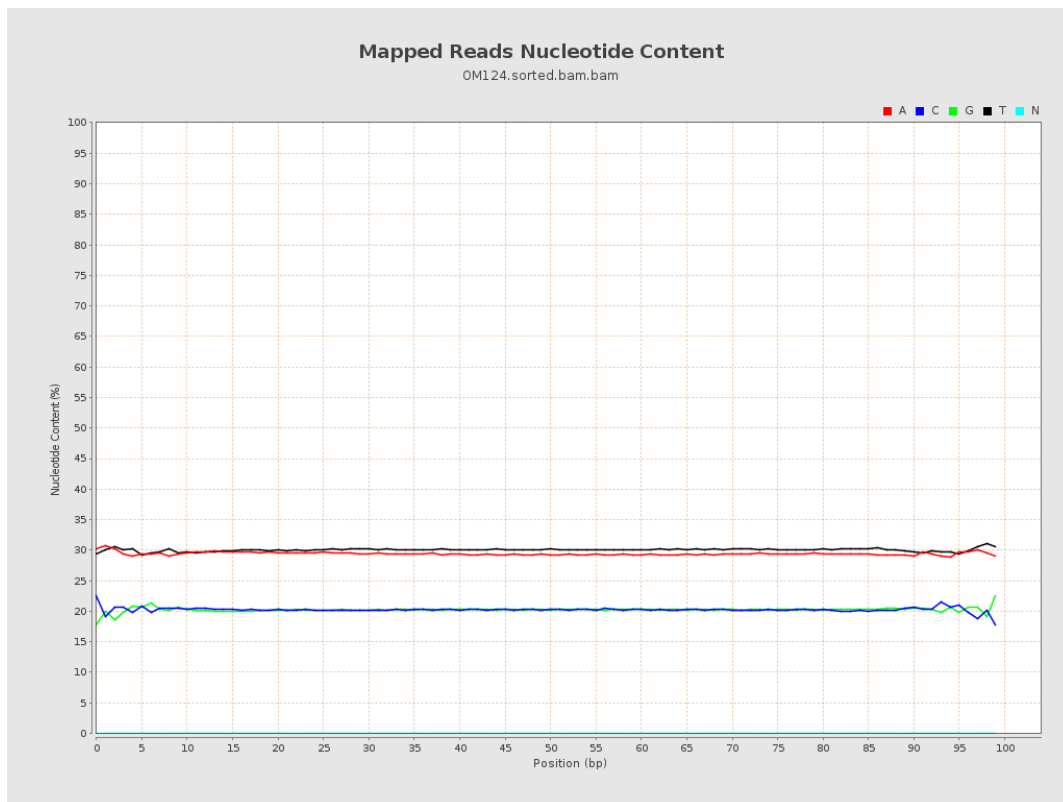
## 6. Results : Genome Fraction Coverage



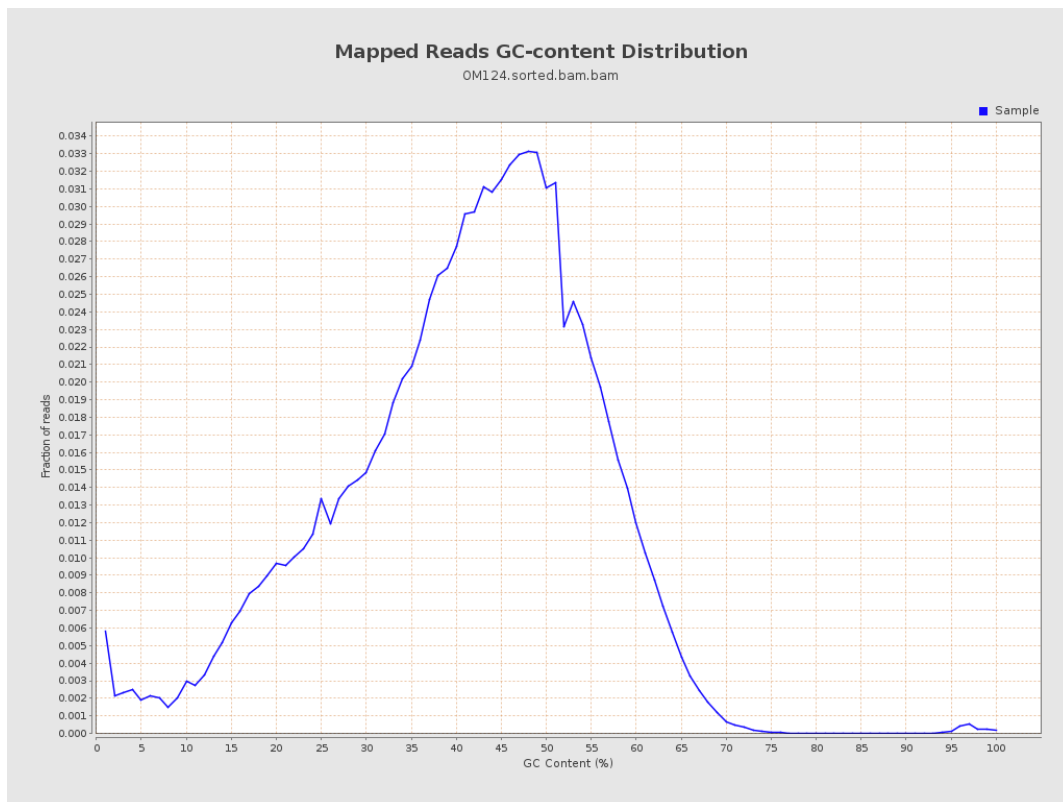
## 7. Results : Duplication Rate Histogram



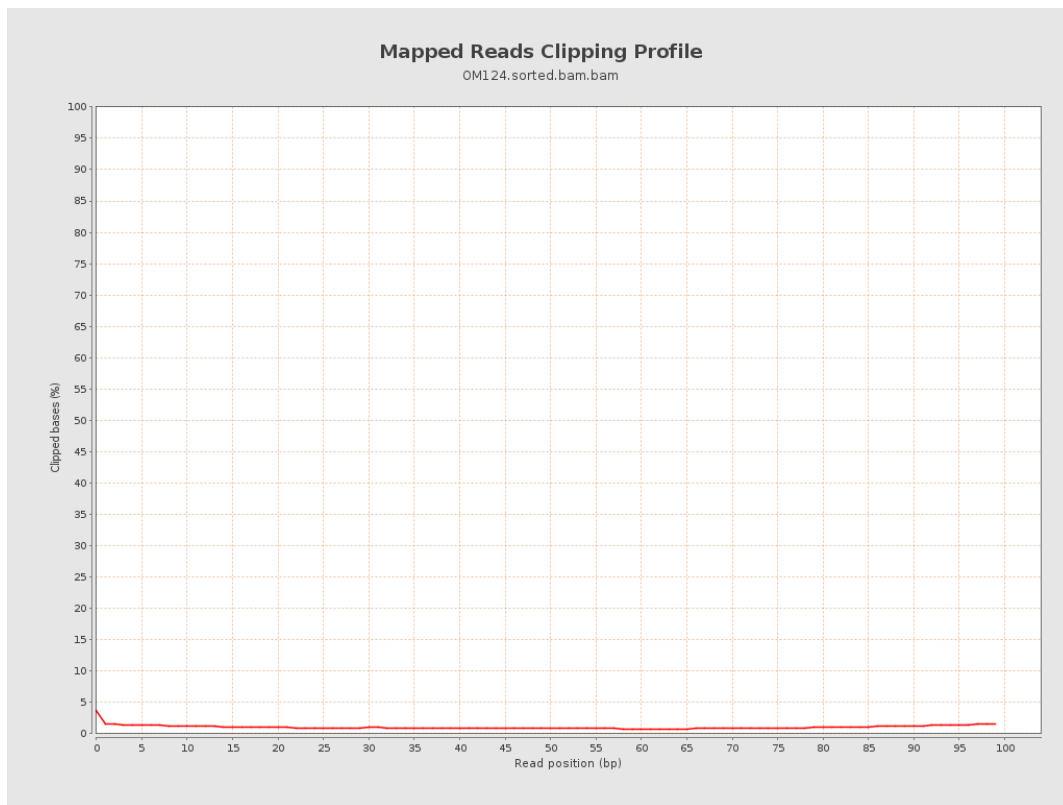
## 8. Results : Mapped Reads Nucleotide Content



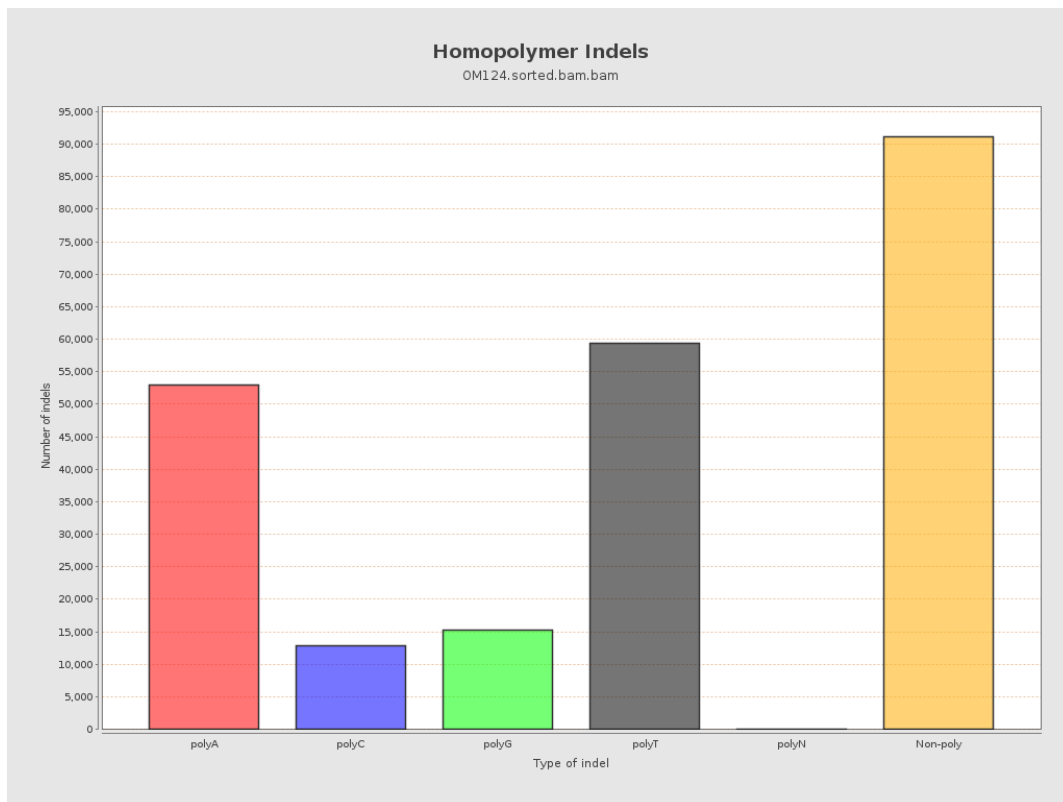
## 9. Results : Mapped Reads GC-content Distribution



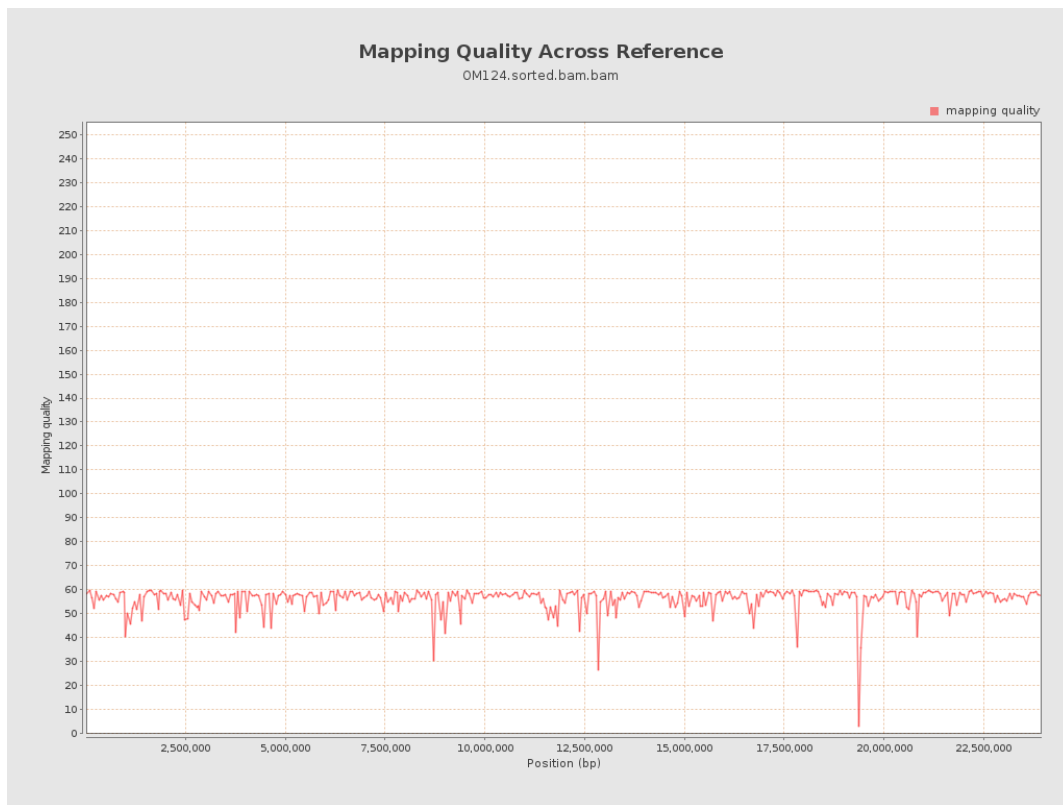
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

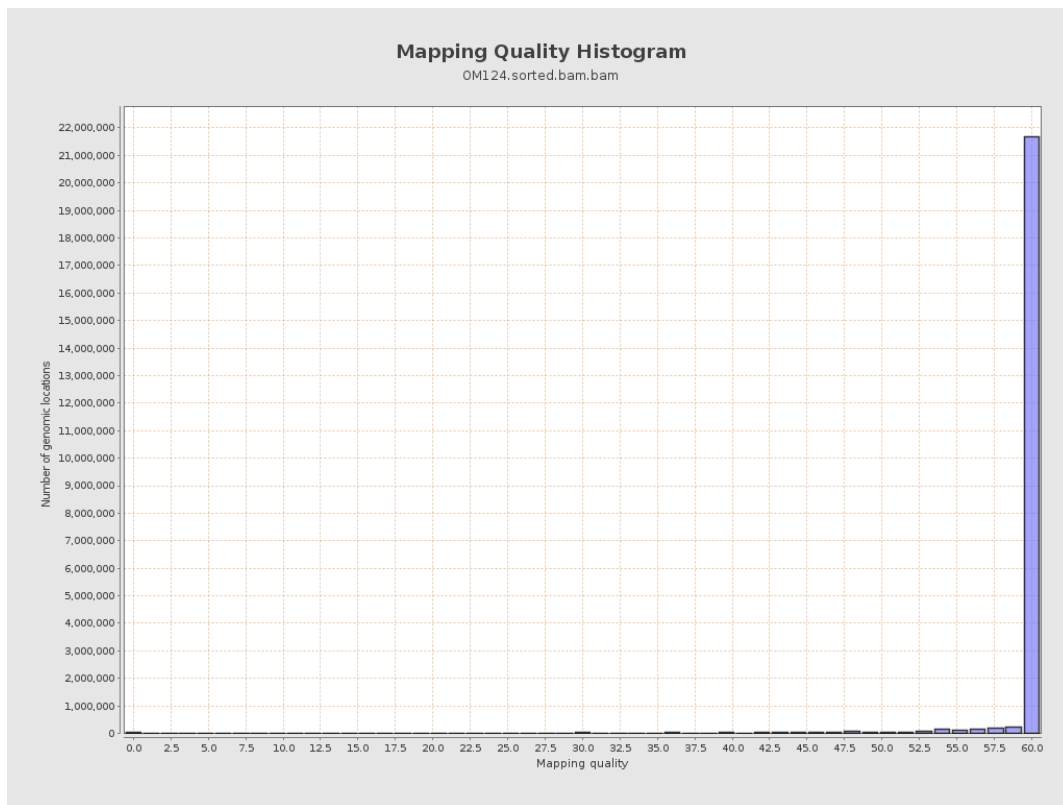


## 12. Results : Mapping Quality Across Reference

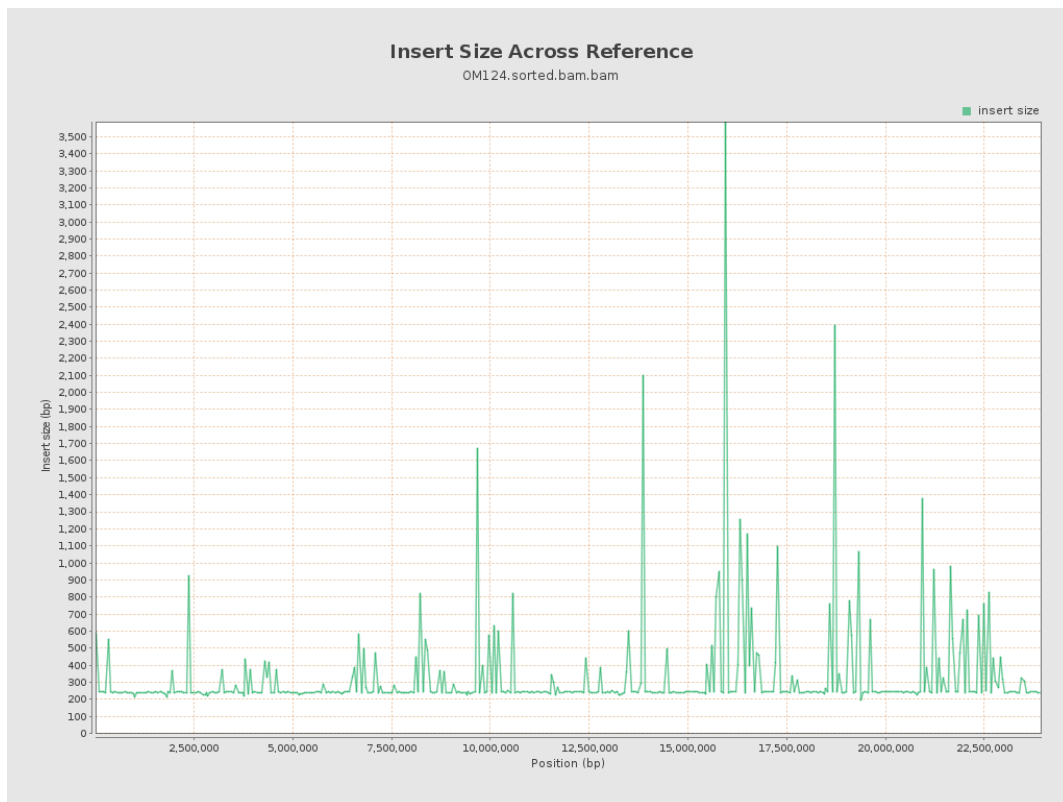




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

