

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2016/10/23 13:58:38*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM282.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/OM282-BiooBarcode28_CAAAAG_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM282-BiooBarcode28_CAAAAG_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 13:58:37 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM282.sorted.bam.

	bam
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## 2. Summary

### 2.1. Globals

Reference size	23,958,997
Number of reads	1,274,577
Mapped reads	808,312 / 63.42%
Unmapped reads	466,265 / 36.58%
Mapped paired reads	808,312 / 63.42%
Mapped reads, first in pair	402,742 / 31.6%
Mapped reads, second in pair	405,570 / 31.82%
Mapped reads, both in pair	793,316 / 62.24%
Mapped reads, singletons	14,996 / 1.18%
Read min/max/mean length	30 / 100 / 99.9
Duplicated reads (estimated)	43,018 / 3.38%
Duplication rate	4.2%
Clipped reads	83,003 / 6.51%

### 2.2. ACGT Content

Number/percentage of A's	23,285,609 / 29.72%
Number/percentage of C's	15,879,649 / 20.27%
Number/percentage of T's	23,360,044 / 29.81%
Number/percentage of G's	15,834,211 / 20.21%
Number/percentage of N's	6,487 / 0.01%
GC Percentage	40.47%

## 2.3. Coverage

Mean	3.274
Standard Deviation	3.2886

## 2.4. Mapping Quality

Mean Mapping Quality	58.68
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## 2.5. Insert size

Mean	733.66
Standard Deviation	21,300.13
P25/Median/P75	303 / 314 / 322

## 2.6. Mismatches and indels

General error rate	1.47%
Mismatches	1,092,964
Insertions	24,251
Mapped reads with at least one insertion	2.86%
Deletions	27,435
Mapped reads with at least one deletion	3.22%
Homopolymer indels	64.96%

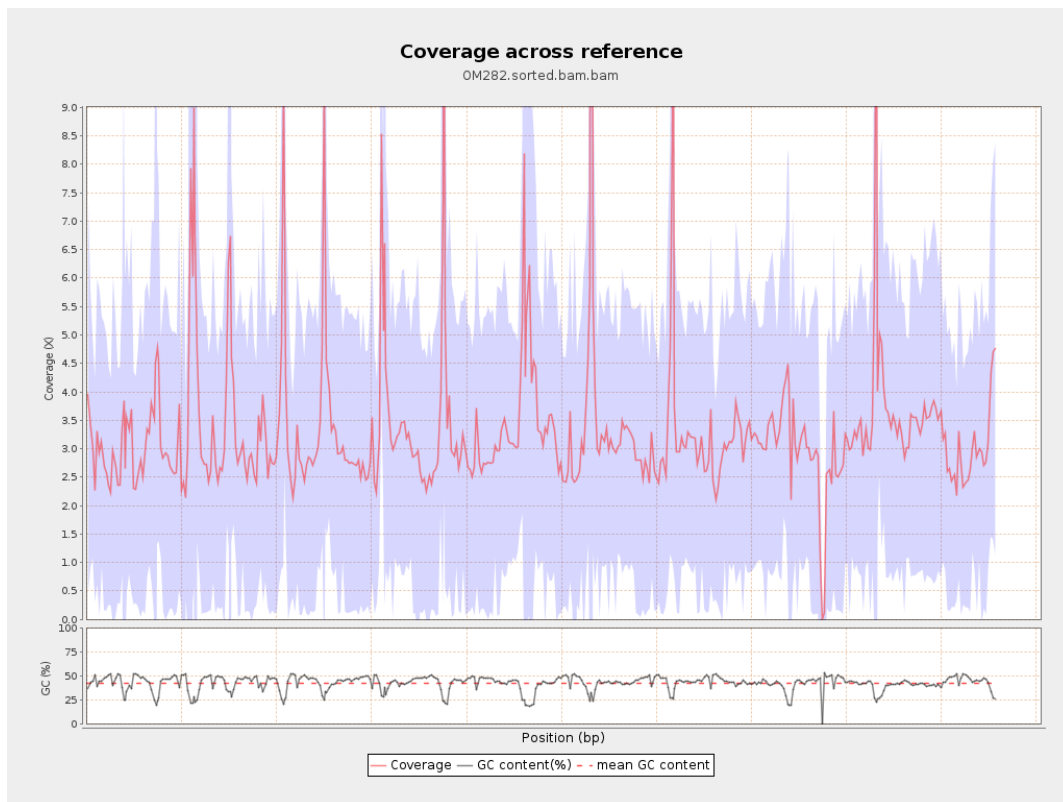
## 2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi 1074120478 emb LT615256.1	977217	2801843	2.8672	2.0923
gi 1074120682 emb LT615257.1	860454	2681327	3.1162	2.6738
gi 1074120865 emb LT615258.1	989719	3448182	3.484	4.1825
gi 1074121086 emb LT615259.1	935450	3187340	3.4073	4.4965
gi 1074121301 emb LT615260.1	1432239	4827849	3.3708	3.3856
gi 1074121615 emb LT615261.1	1080962	3607380	3.3372	3.2278
gi 1074121871 emb LT615262.1	1545099	5037787	3.2605	2.3941
gi 1074122235 emb LT615263.1	1585108	5179101	3.2673	2.7199
gi 1074122590 emb LT615264.1	2122358	6824830	3.2157	2.456
gi 1074123050 emb LT615265.1	1754192	6095778	3.475	3.1354
gi 1074123421 emb LT615	2150147	7322157	3.4054	6.0989

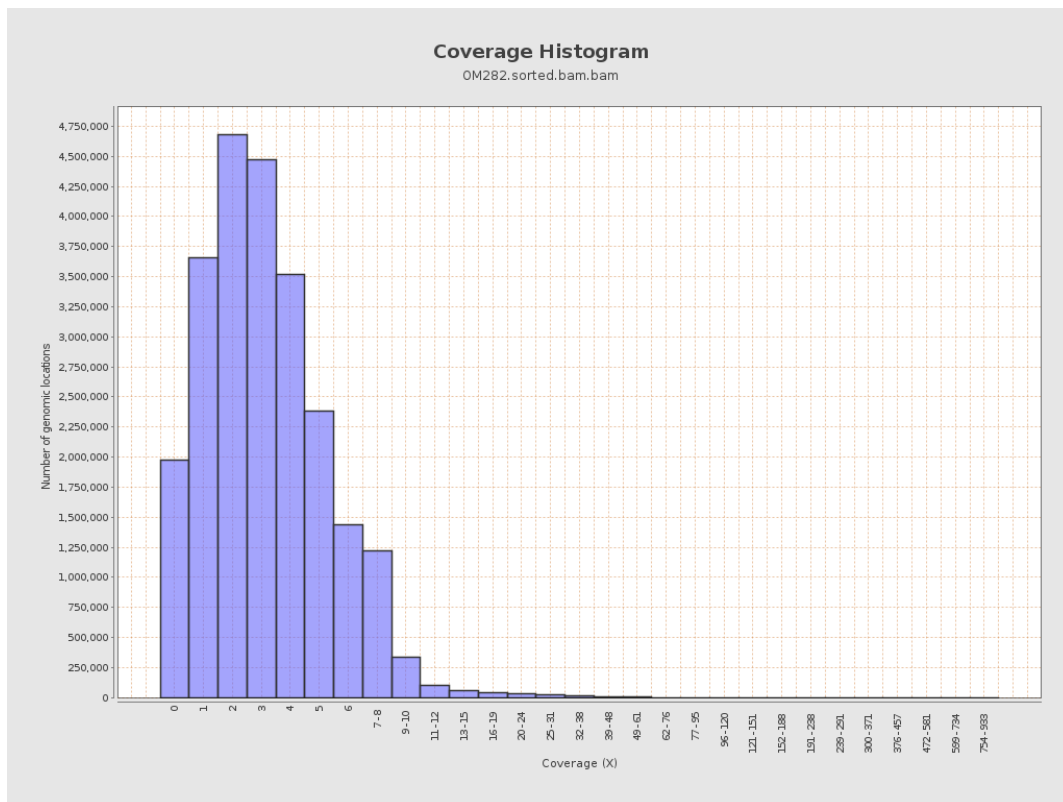
266.1				
gi 107412389 8 emb LT615 267.1	3031036	9757055	3.219	2.2652
gi 107412458 8 emb LT615 268.1	2359348	7226089	3.0627	3.2071
gi 107412506 5 emb LT615 269.1	3135668	10443963	3.3307	2.102

### 3. Results : Coverage across reference

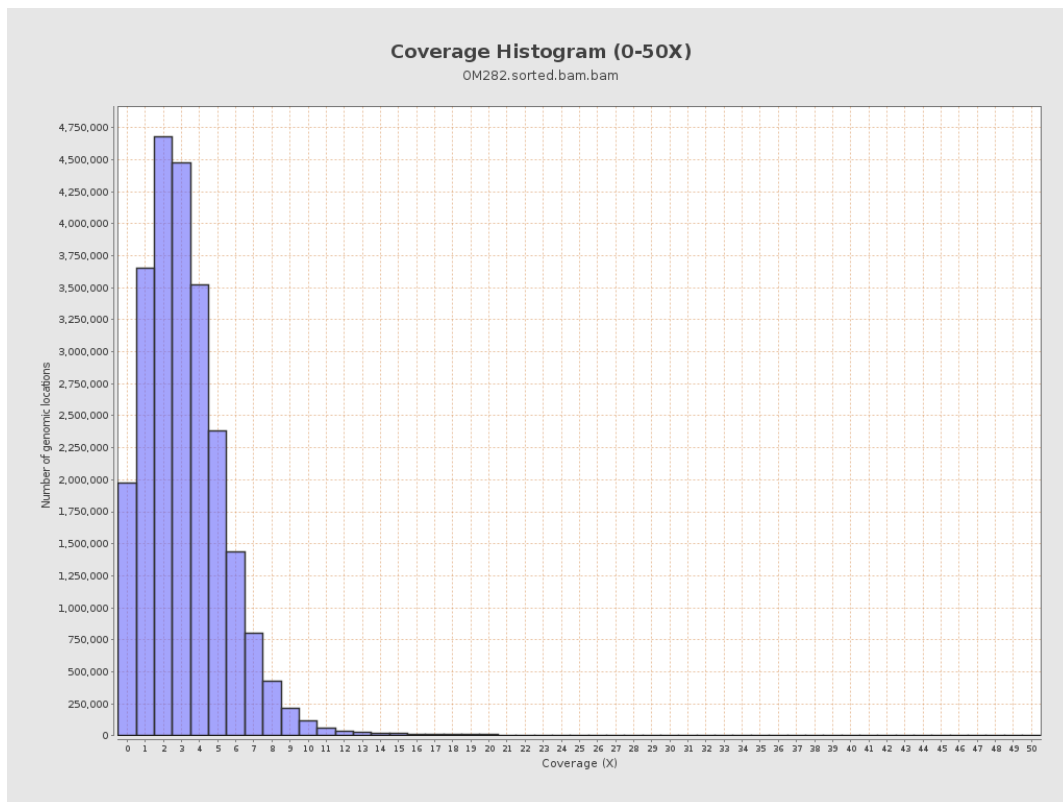




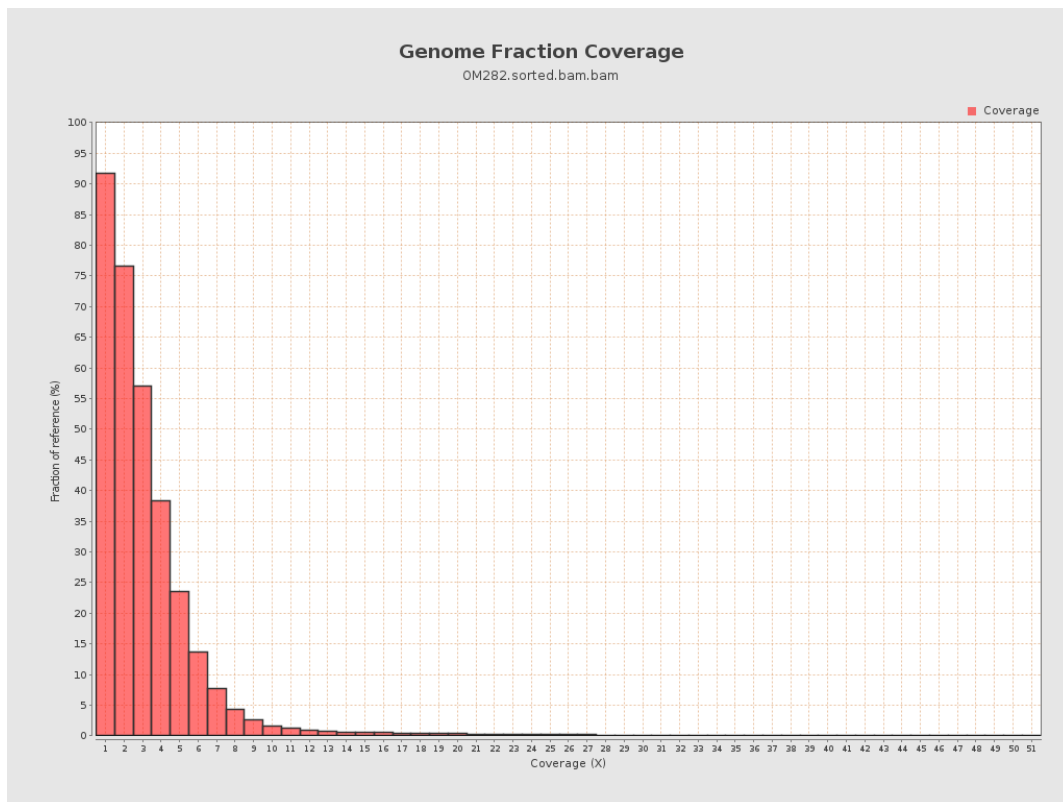
## 4. Results : Coverage Histogram



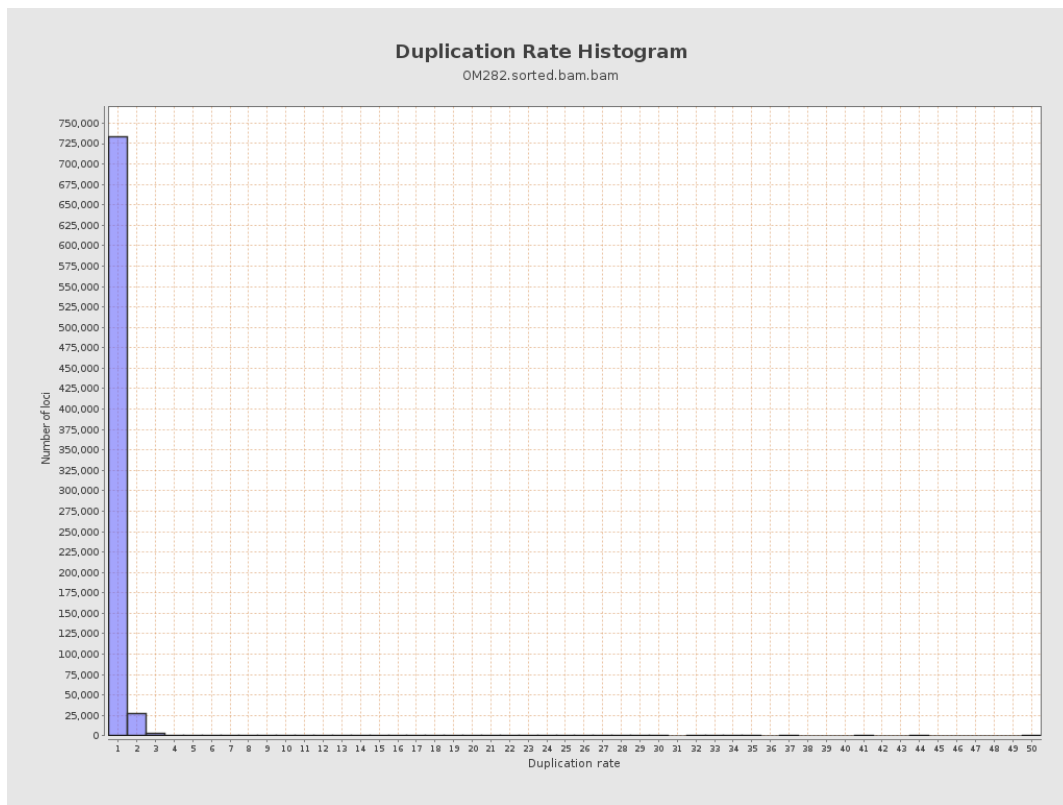
## 5. Results : Coverage Histogram (0-50X)



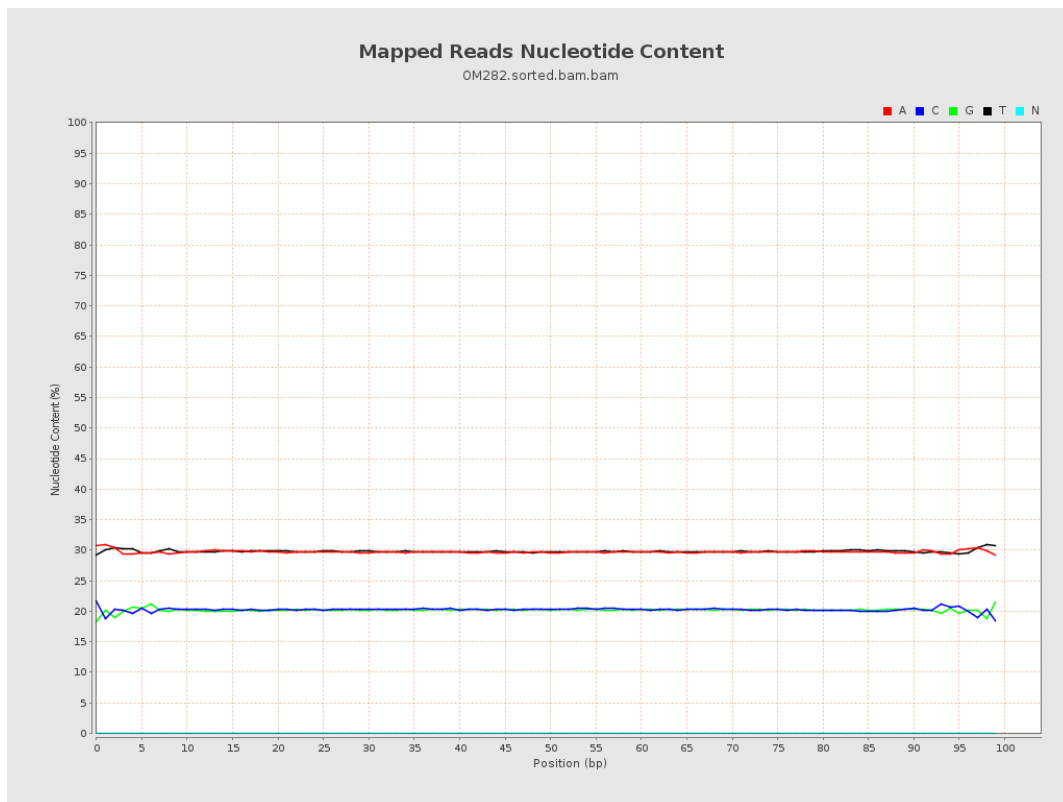
## 6. Results : Genome Fraction Coverage



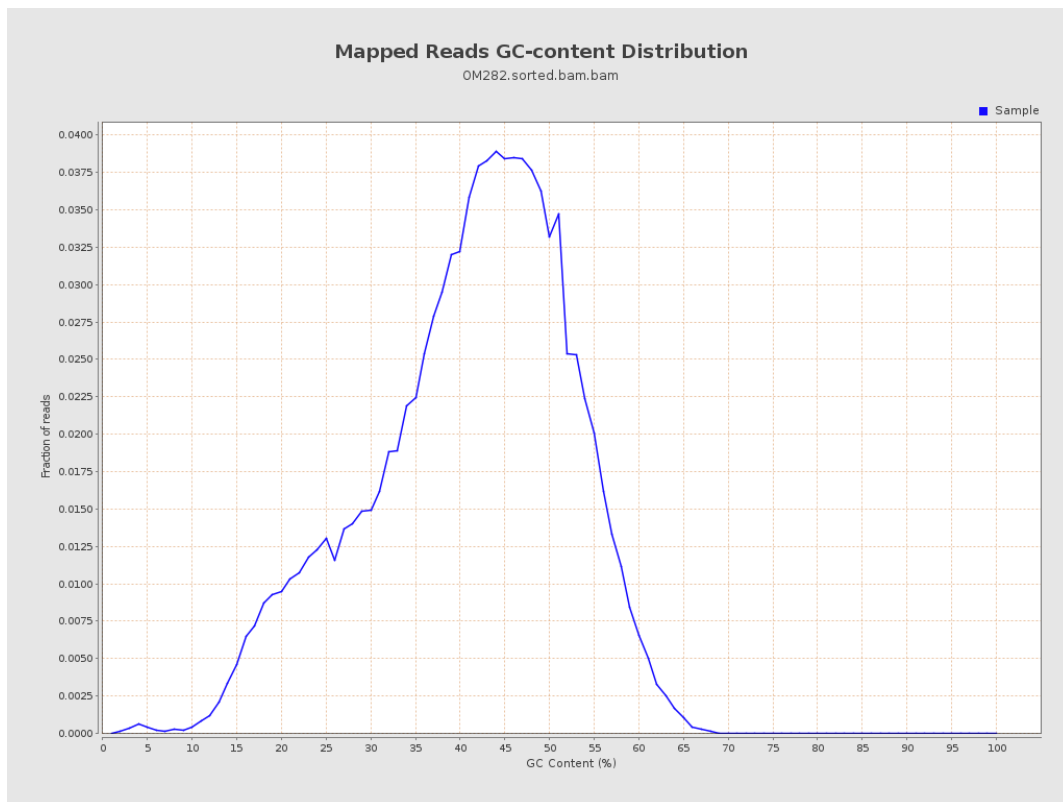
## 7. Results : Duplication Rate Histogram



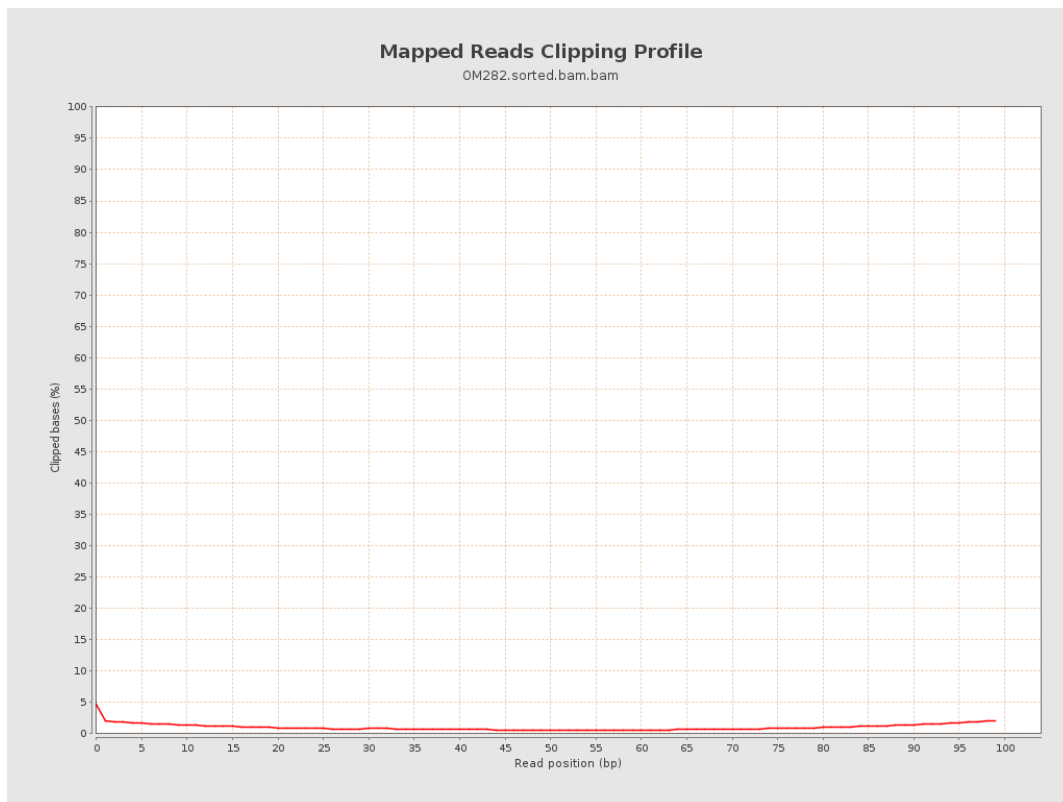
## 8. Results : Mapped Reads Nucleotide Content



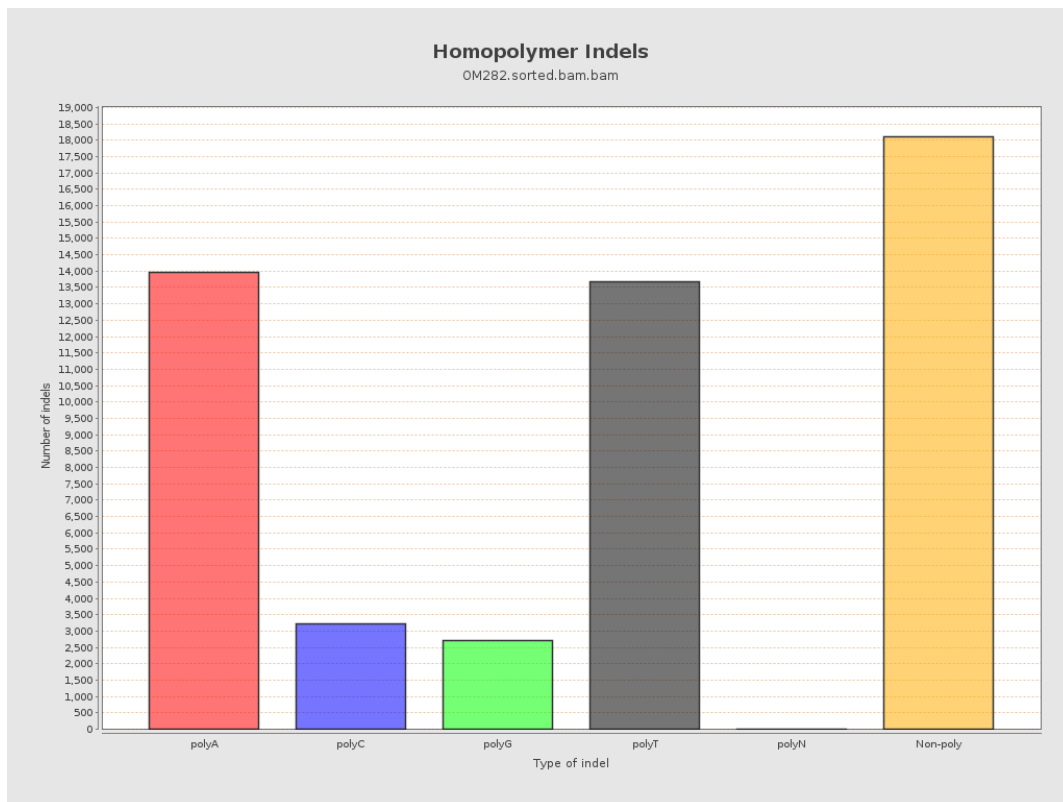
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile

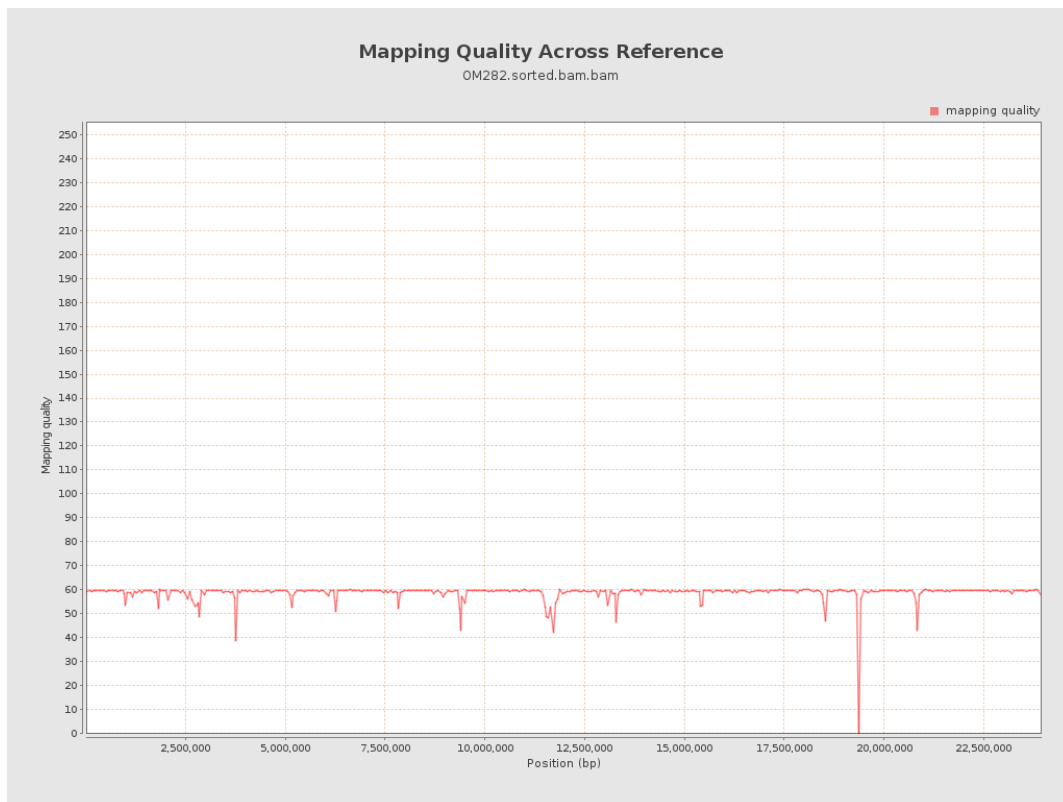


## 11. Results : Homopolymer Indels

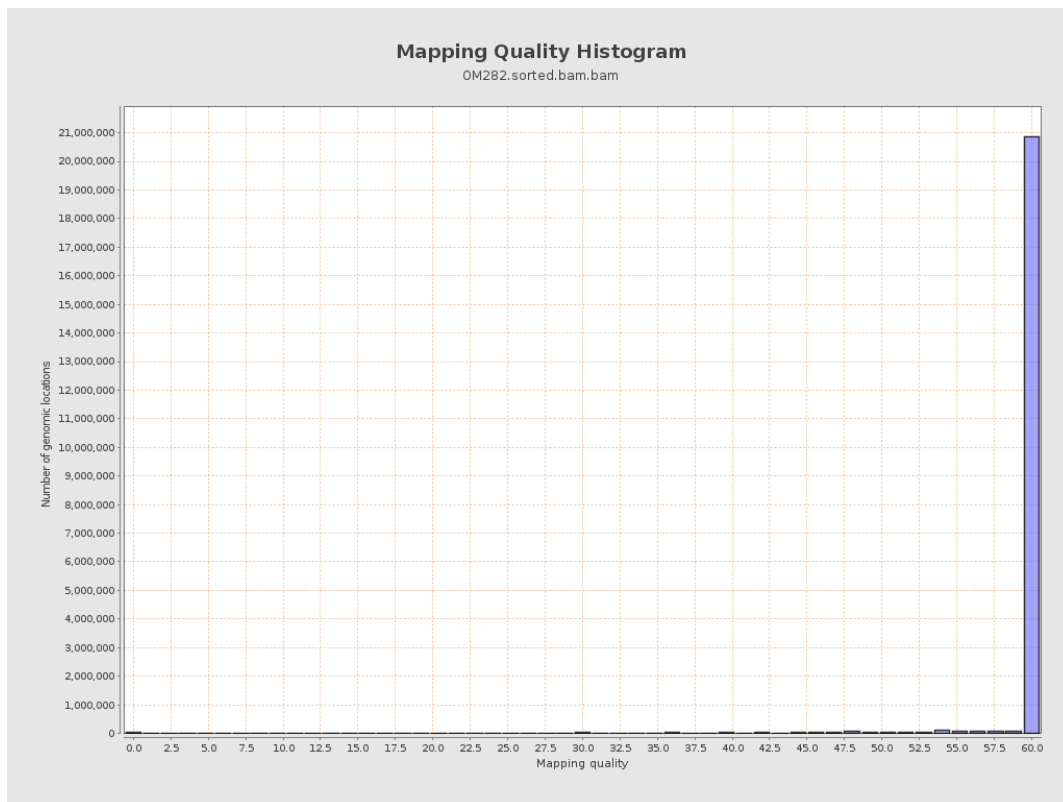




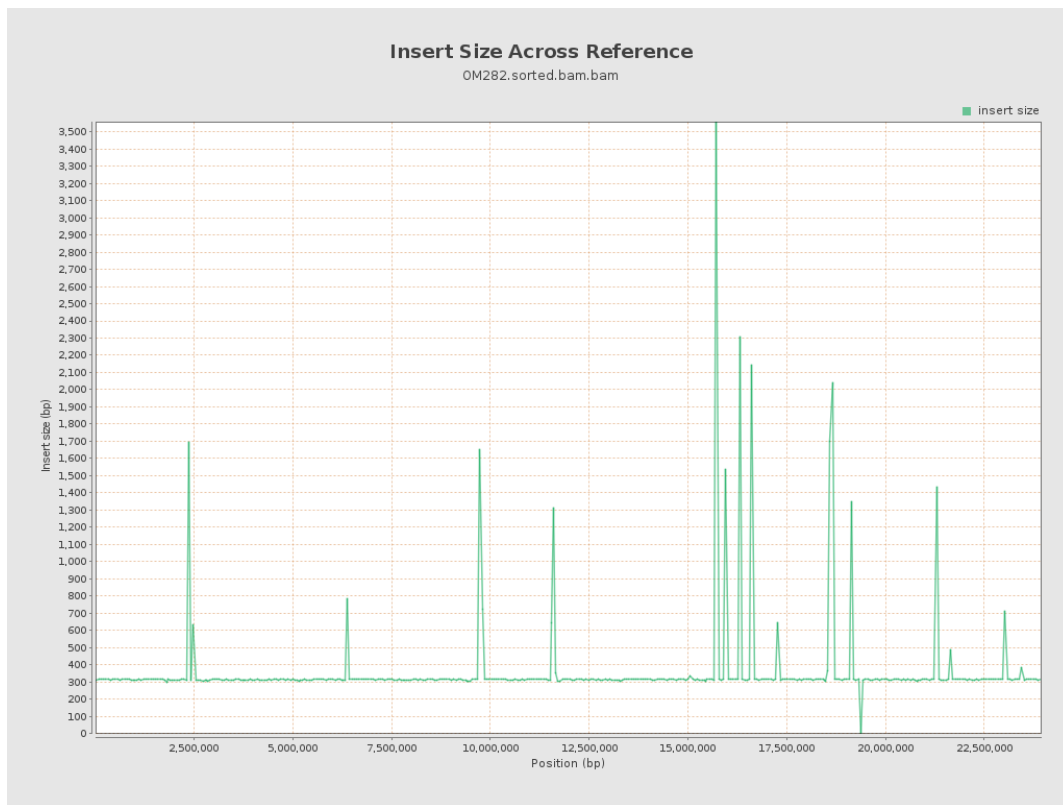
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

