

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2016/10/23 14:14:49*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM312.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/OM312-BiooBarcode25_ACTGAT_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM312-BiooBarcode25_ACTGAT_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 14:14:48 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM312.sorted.bam.

	bam
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## 2. Summary

### 2.1. Globals

Reference size	23,958,997
Number of reads	38,764,803
Mapped reads	5,241,454 / 13.52%
Unmapped reads	33,523,349 / 86.48%
Mapped paired reads	5,241,454 / 13.52%
Mapped reads, first in pair	2,632,469 / 6.79%
Mapped reads, second in pair	2,608,985 / 6.73%
Mapped reads, both in pair	4,935,066 / 12.73%
Mapped reads, singletons	306,388 / 0.79%
Read min/max/mean length	30 / 100 / 99.97
Duplicated reads (estimated)	1,160,321 / 2.99%
Duplication rate	16%
Clipped reads	796,839 / 2.06%

### 2.2. ACGT Content

Number/percentage of A's	148,714,116 / 30.16%
Number/percentage of C's	97,446,726 / 19.76%
Number/percentage of T's	149,654,005 / 30.35%
Number/percentage of G's	97,331,749 / 19.74%
Number/percentage of N's	40,663 / 0.01%
GC Percentage	39.5%

## 2.3. Coverage

Mean	20.6059
Standard Deviation	37.3116

## 2.4. Mapping Quality

Mean Mapping Quality	57.71
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## 2.5. Insert size

Mean	892.97
Standard Deviation	26,611.55
P25/Median/P75	323 / 342 / 352

## 2.6. Mismatches and indels

General error rate	1.62%
Mismatches	7,602,623
Insertions	173,474
Mapped reads with at least one insertion	3.11%
Deletions	196,648
Mapped reads with at least one deletion	3.47%
Homopolymer indels	61.36%

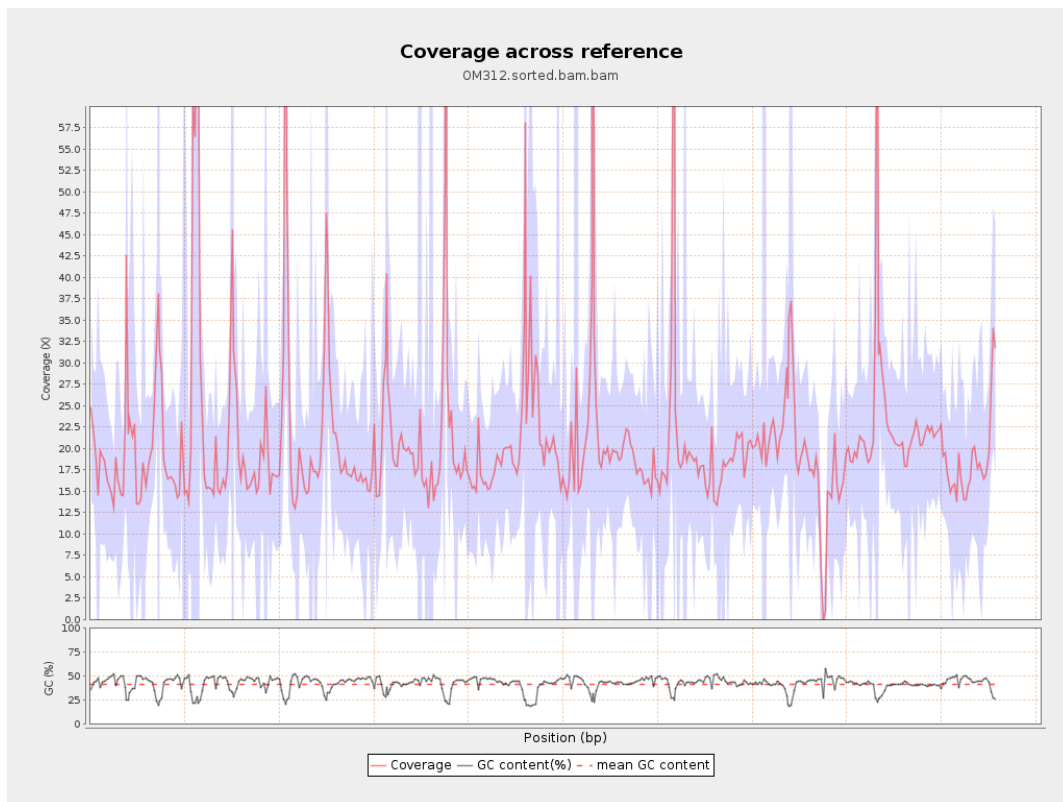
## 2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi 1074120478 emb LT615256.1	977217	17772060	18.1864	12.1477
gi 1074120682 emb LT615257.1	860454	17839238	20.7324	22.4777
gi 1074120865 emb LT615258.1	989719	23283094	23.525	35.7101
gi 1074121086 emb LT615259.1	935450	20875501	22.316	32.9218
gi 1074121301 emb LT615260.1	1432239	31594216	22.0593	26.2996
gi 1074121615 emb LT615261.1	1080962	21892660	20.2529	21.0194
gi 1074121871 emb LT615262.1	1545099	29682531	19.2108	11.9352
gi 1074122235 emb LT615263.1	1585108	32749359	20.6606	48.9317
gi 1074122590 emb LT615264.1	2122358	41462405	19.536	13.2203
gi 1074123050 emb LT615265.1	1754192	38262775	21.8122	97.6261
gi 1074123421 emb LT615	2150147	46726506	21.7318	42.138

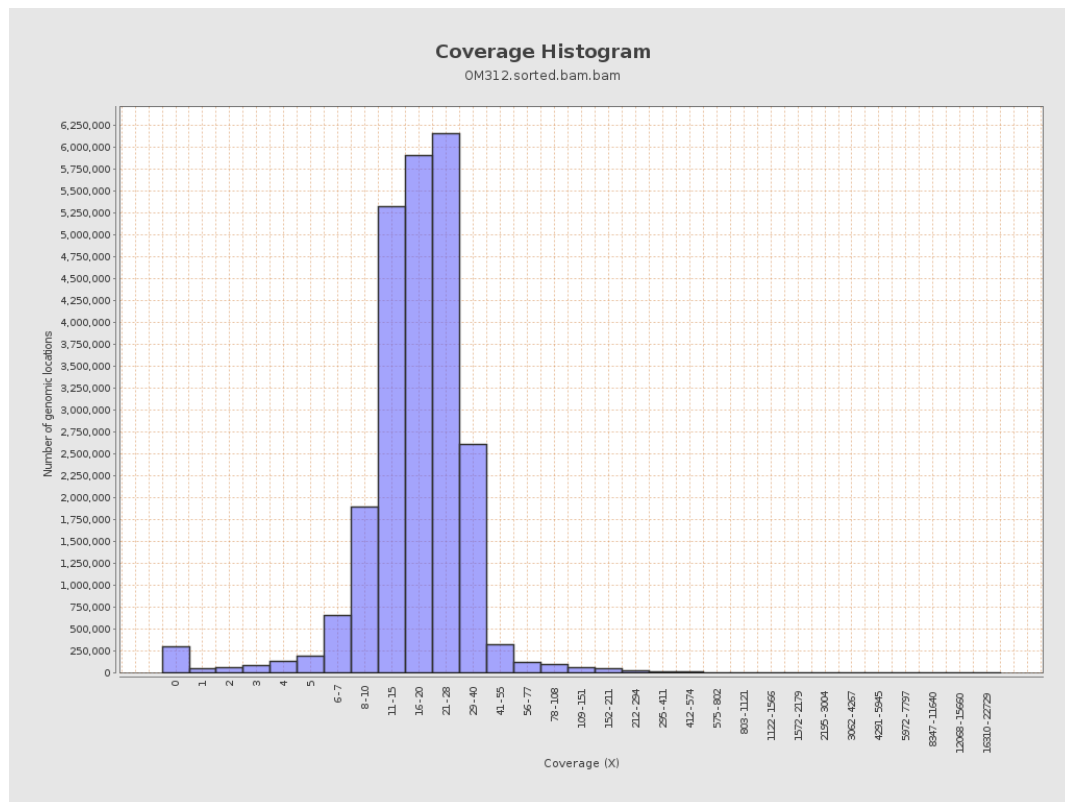
266.1				
gi 107412389 8 emb LT615 267.1	3031036	60445843	19.9423	29.0677
gi 107412458 8 emb LT615 268.1	2359348	46349933	19.6452	21.6848
gi 107412506 5 emb LT615 269.1	3135668	64761191	20.6531	11.3495

### 3. Results : Coverage across reference

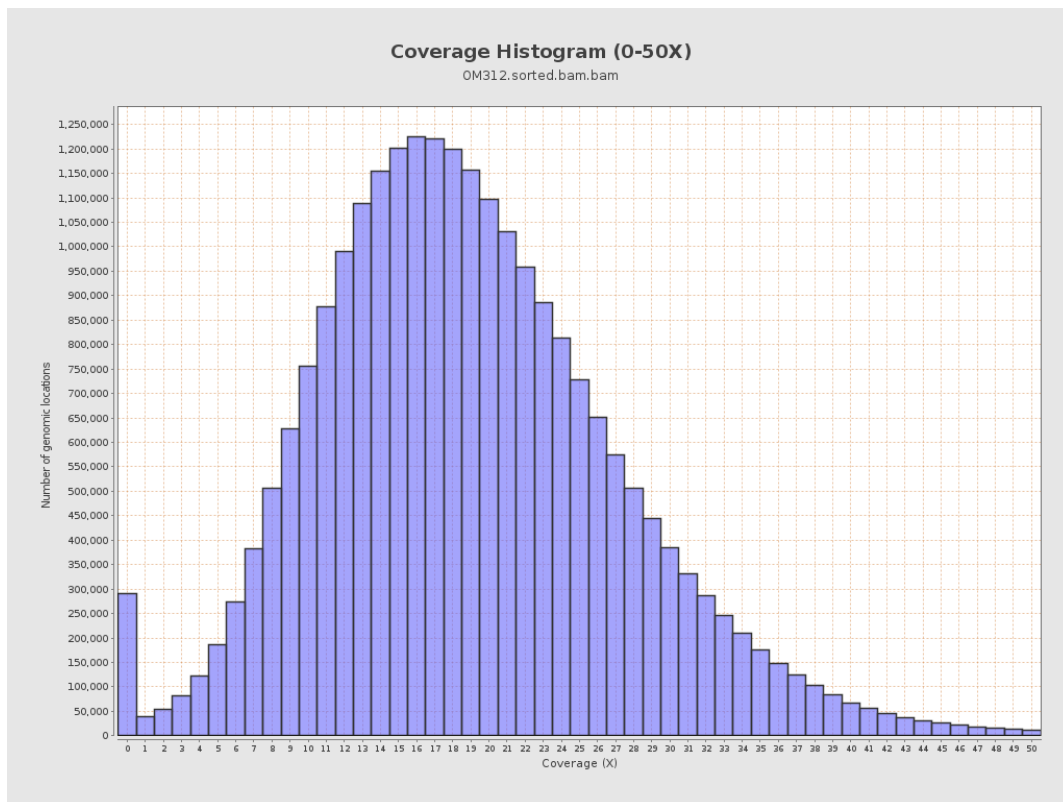




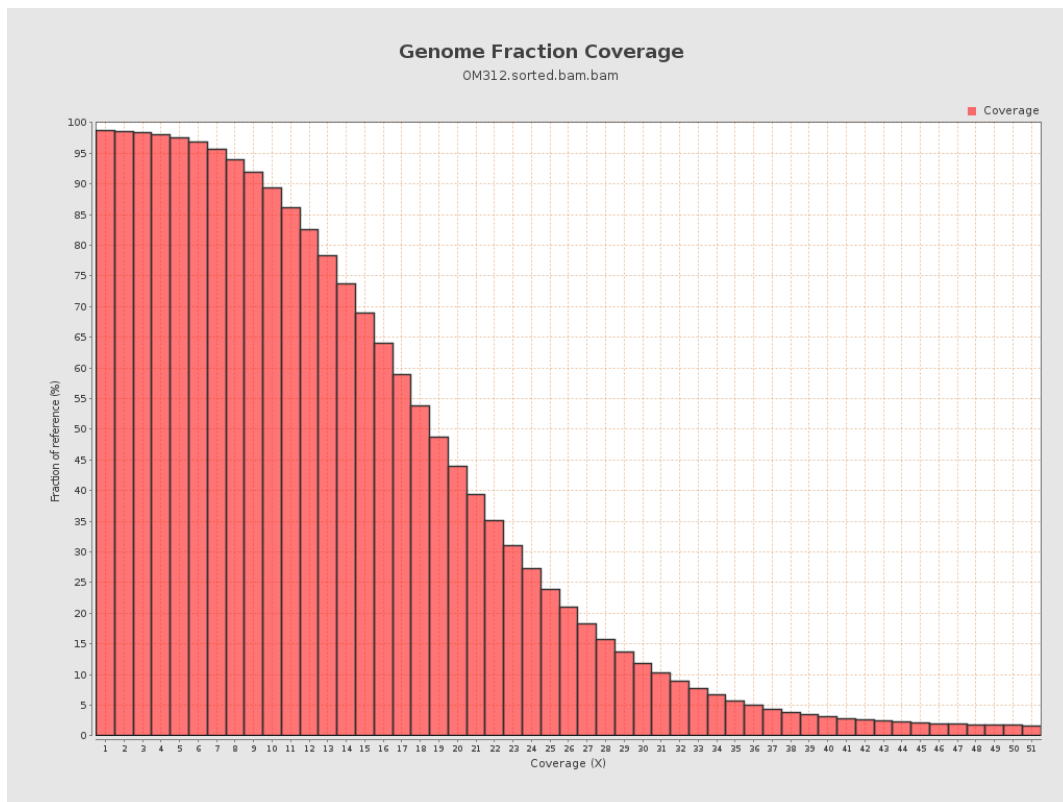
## 4. Results : Coverage Histogram



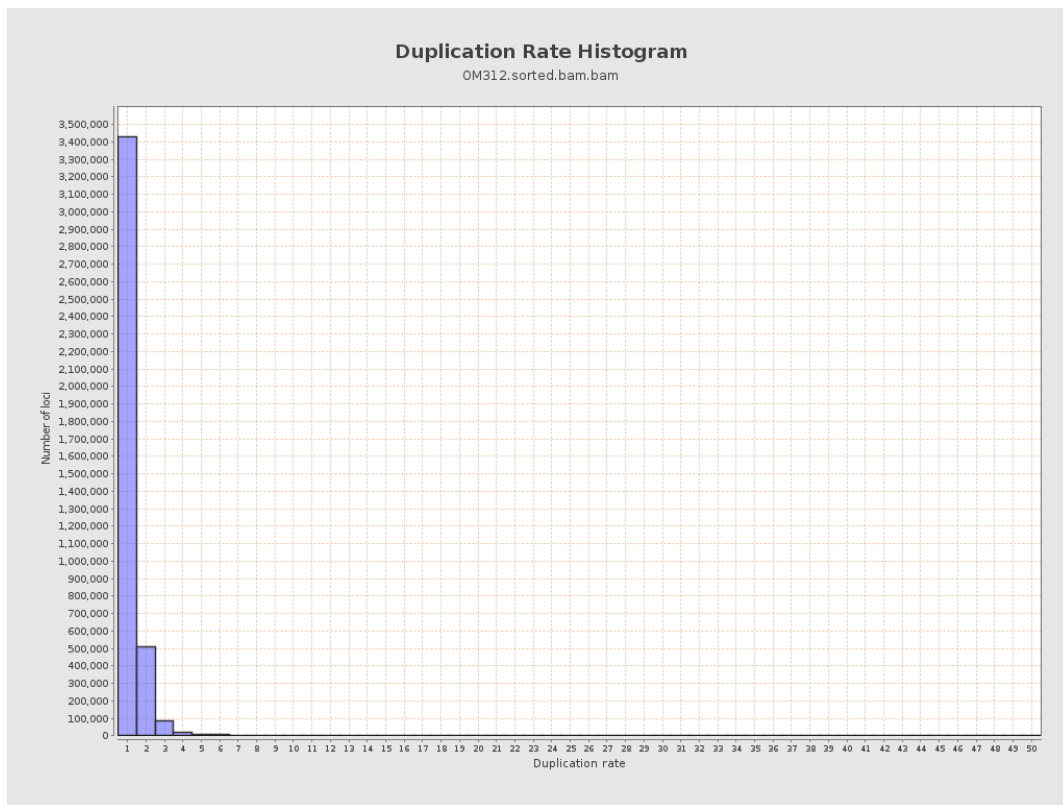
## 5. Results : Coverage Histogram (0-50X)



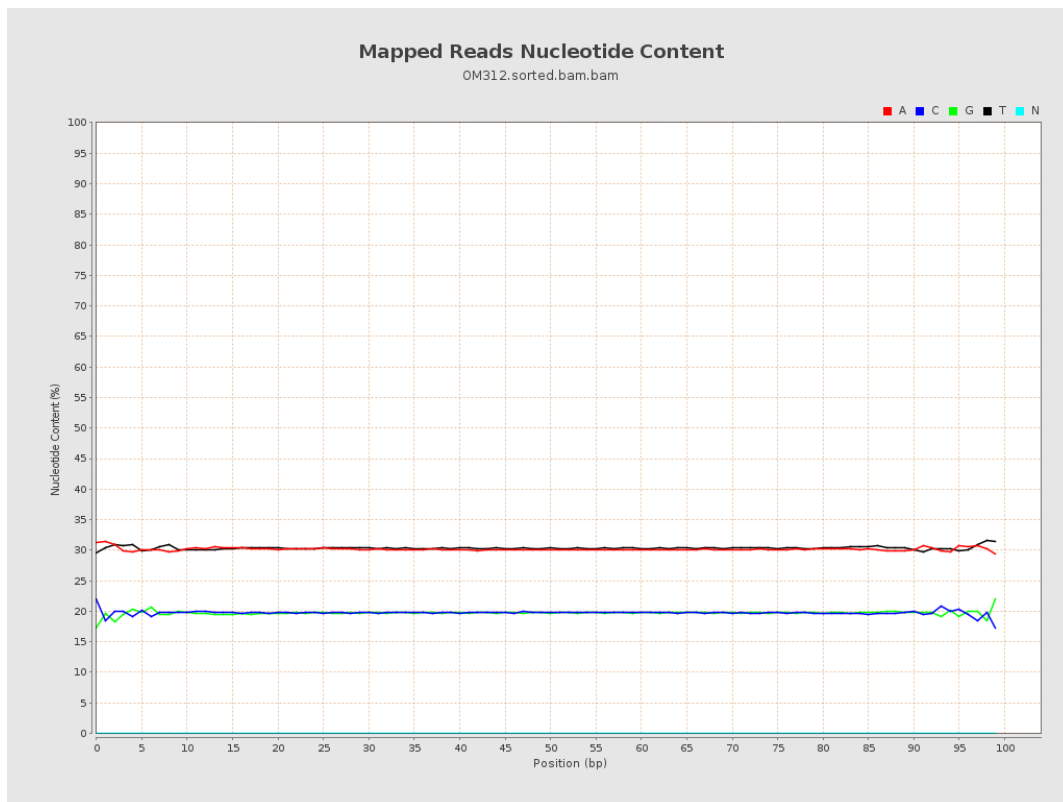
## 6. Results : Genome Fraction Coverage



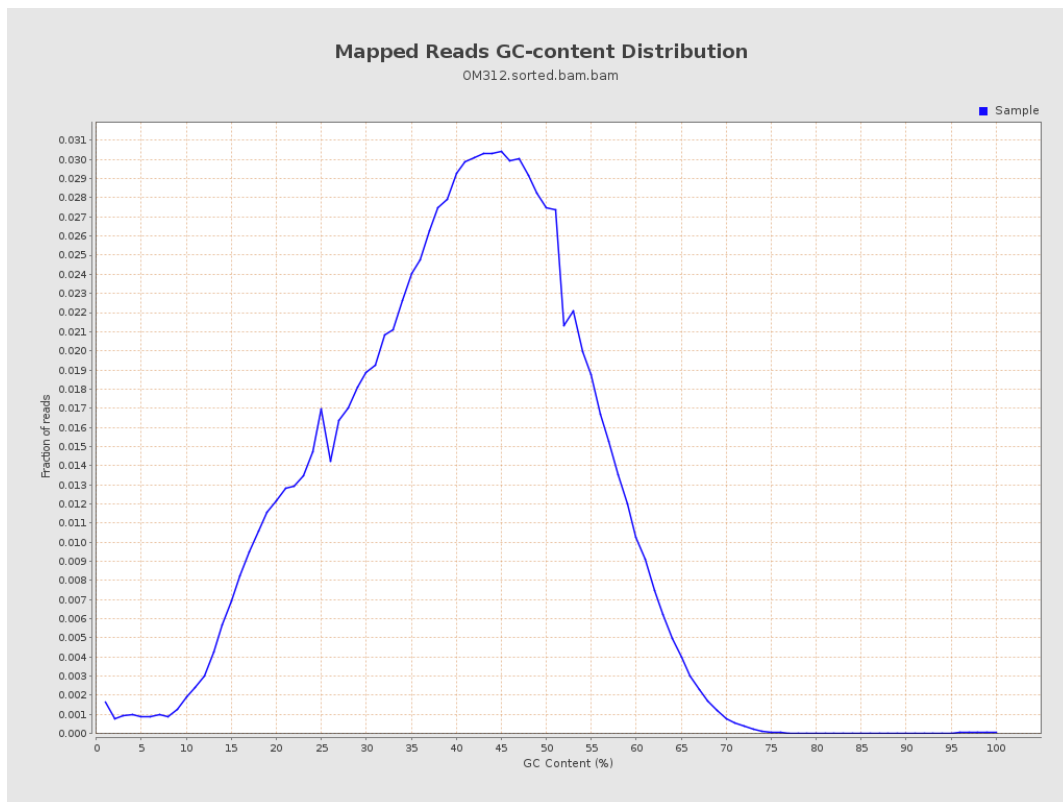
## 7. Results : Duplication Rate Histogram



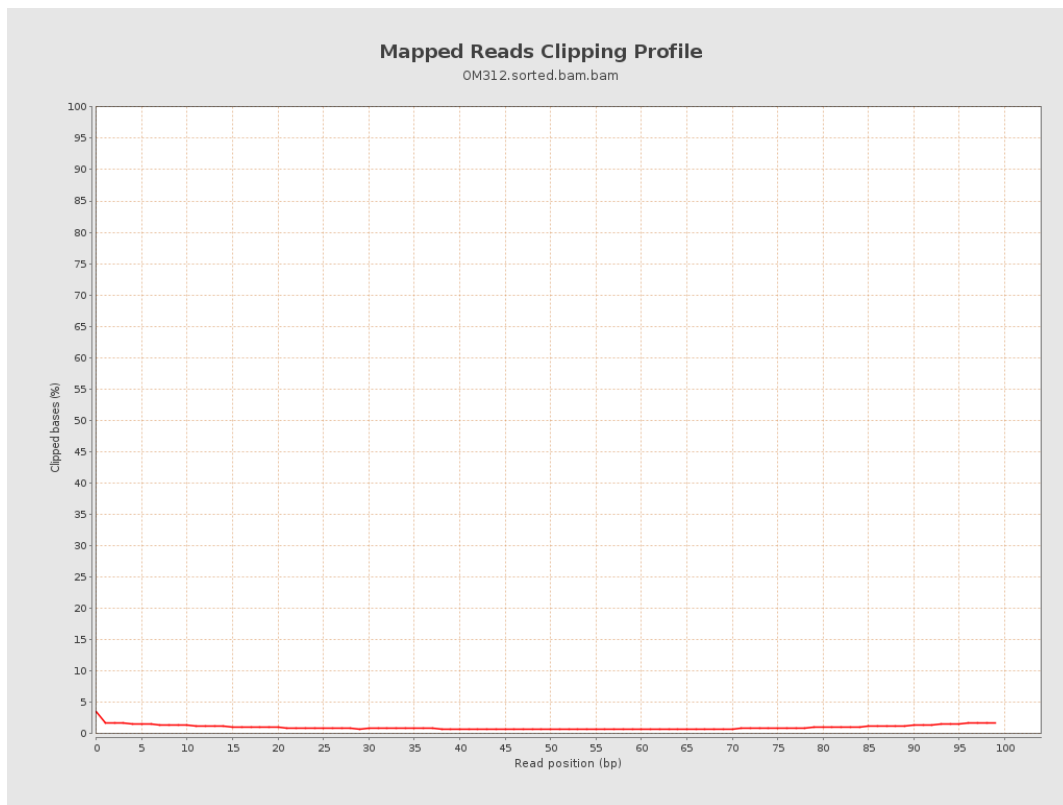
## 8. Results : Mapped Reads Nucleotide Content



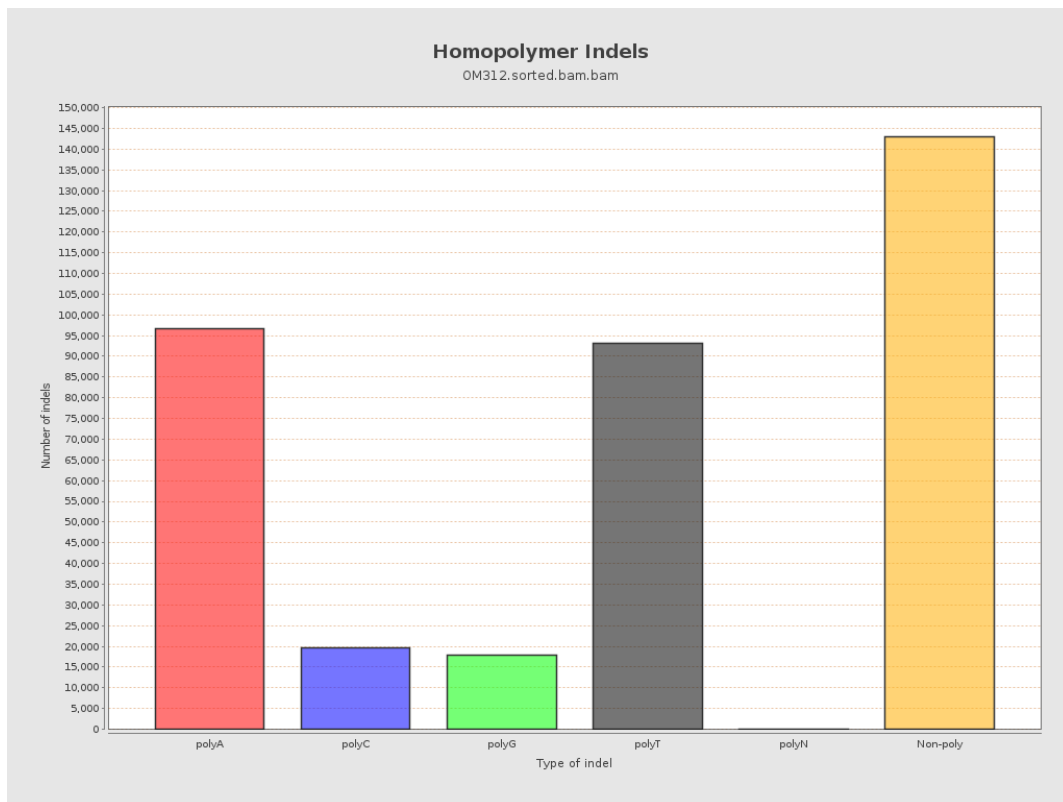
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile

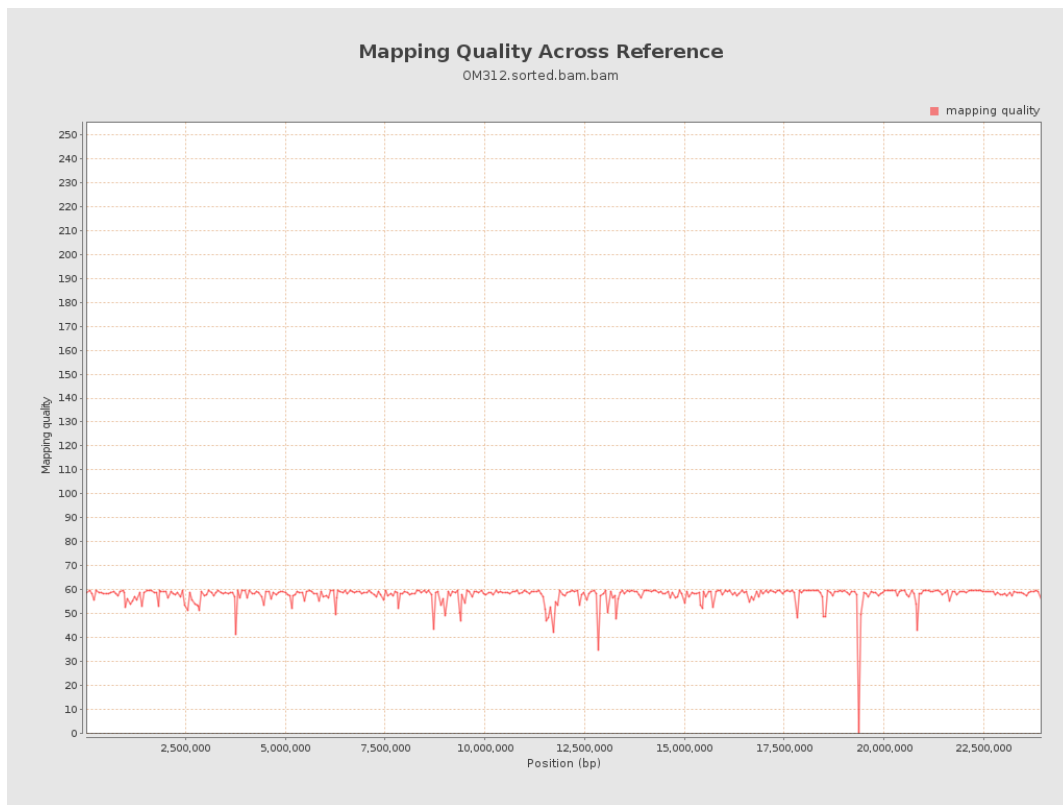


## 11. Results : Homopolymer Indels

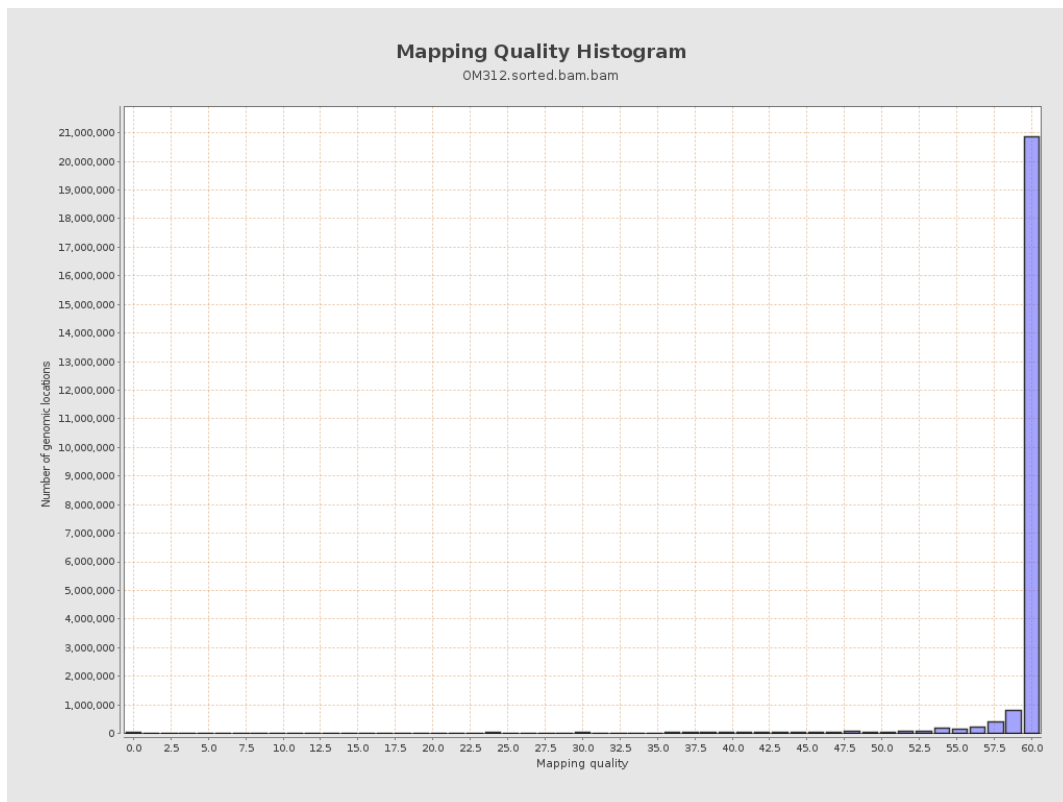




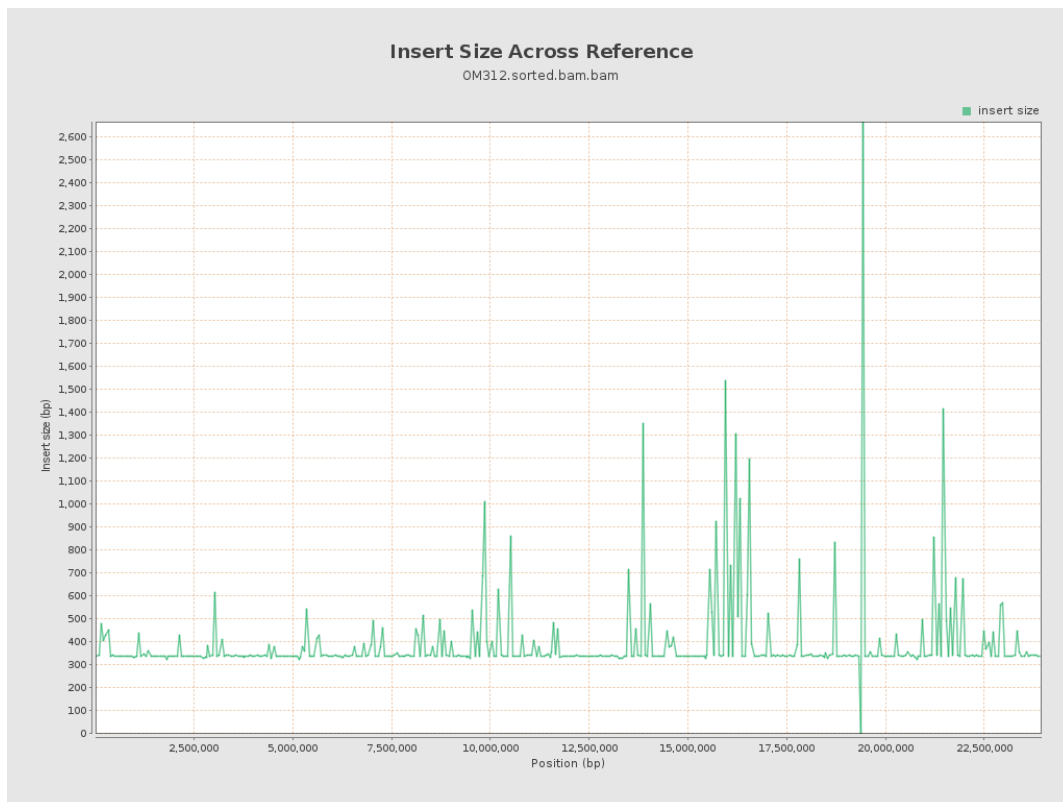
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

