Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 12:17:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM074.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/OM074-BiooBarcode10_GATCAG_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM074-BiooBarcode10_GATCAG_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 12:17:50 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM074.sorted.bam.

	bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	37,871,978
Mapped reads	2,268,581 / 5.99%
Unmapped reads	35,603,397 / 94.01%
Mapped paired reads	2,268,581 / 5.99%
Mapped reads, first in pair	1,136,652 / 3%
Mapped reads, second in pair	1,131,929 / 2.99%
Mapped reads, both in pair	1,549,657 / 4.09%
Mapped reads, singletons	718,924 / 1.9%
Read min/max/mean length	30 / 100 / 99.93
Duplicated reads (estimated)	1,010,882 / 2.67%
Duplication rate	14.04%
Clipped reads	1,061,411 / 2.8%

2.2. ACGT Content

Number/percentage of A's	54,765,467 / 32.7%
Number/percentage of C's	28,819,064 / 17.21%
Number/percentage of T's	55,373,019 / 33.06%
Number/percentage of G's	28,541,317 / 17.04%
Number/percentage of N's	7,419 / 0%
GC Percentage	34.25%

2.3. Coverage

Mean	7.001
Standard Deviation	75.7505

2.4. Mapping Quality

Mean Mapping Quality	49.21

2.5. Insert size

Mean	7,815.73
Standard Deviation	95,771.46
P25/Median/P75	272 / 284 / 293

2.6. Mismatches and indels

General error rate	1.55%
Mismatches	2,309,166
Insertions	105,586
Mapped reads with at least one insertion	4.23%
Deletions	97,739
Mapped reads with at least one deletion	3.79%
Homopolymer indels	49.99%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|1074120478|emb|LT615256.1|	977217	5947198	6.0859	18.7231
gi|1074120682|emb|LT615257.1|	860454	5906925	6.8649	36.7822
gi|1074120865|emb|LT615258.1|	989719	7059071	7.1324	34.075
gi|1074121086|emb|LT615259.1|	935450	6207312	6.6356	34.5708
gi|1074121301|emb|LT615260.1|	1432239	11038779	7.7074	79.9771
gi|1074121615|emb|LT615261.1|	1080962	7139022	6.6043	38.0844
gi|1074121871|emb|LT615262.1|	1545099	11534904	7.4655	101.4677
gi|1074122235|emb|LT615263.1|	1585108	11565820	7.2966	77.9791
gi|1074122590|emb|LT615264.1|	2122358	14389215	6.7798	108.5797
gi|1074123050|emb|LT615265.1|	1754192	14185923	8.0869	140.177
gi|1074123421|emb|LT615	2150147	16263406	7.5639	91.0213

266.1|				
gi|1074123898|emb|LT615267.1|	3031036	20631895	6.8069	59.7893
gi|1074124588|emb|LT615268.1|	2359348	14738487	6.2468	31.3983
gi|1074125065|emb|LT615269.1|	3135668	21128115	6.738	47.1074

3. Results : Coverage across reference

Coverage across reference
OM074.sorted.bam.bam

4. Results : Coverage Histogram

Coverage Histogram
OM074.sorted.bam.bam
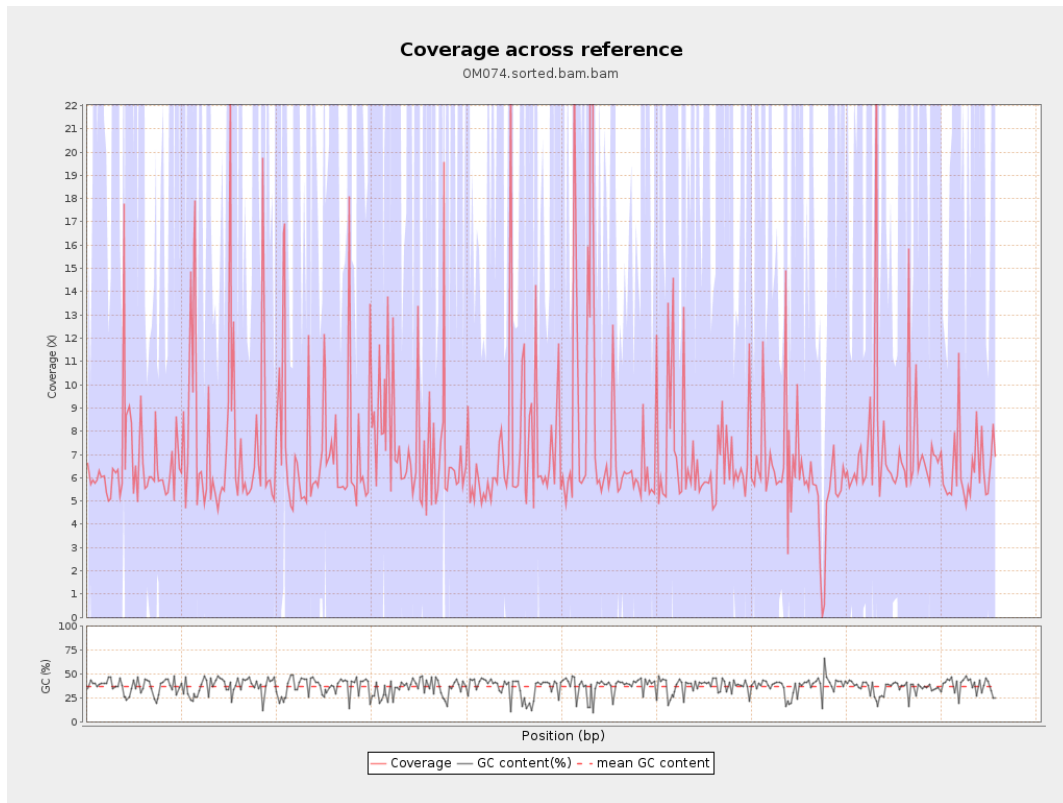
5. Results : Coverage Histogram (0-50X)
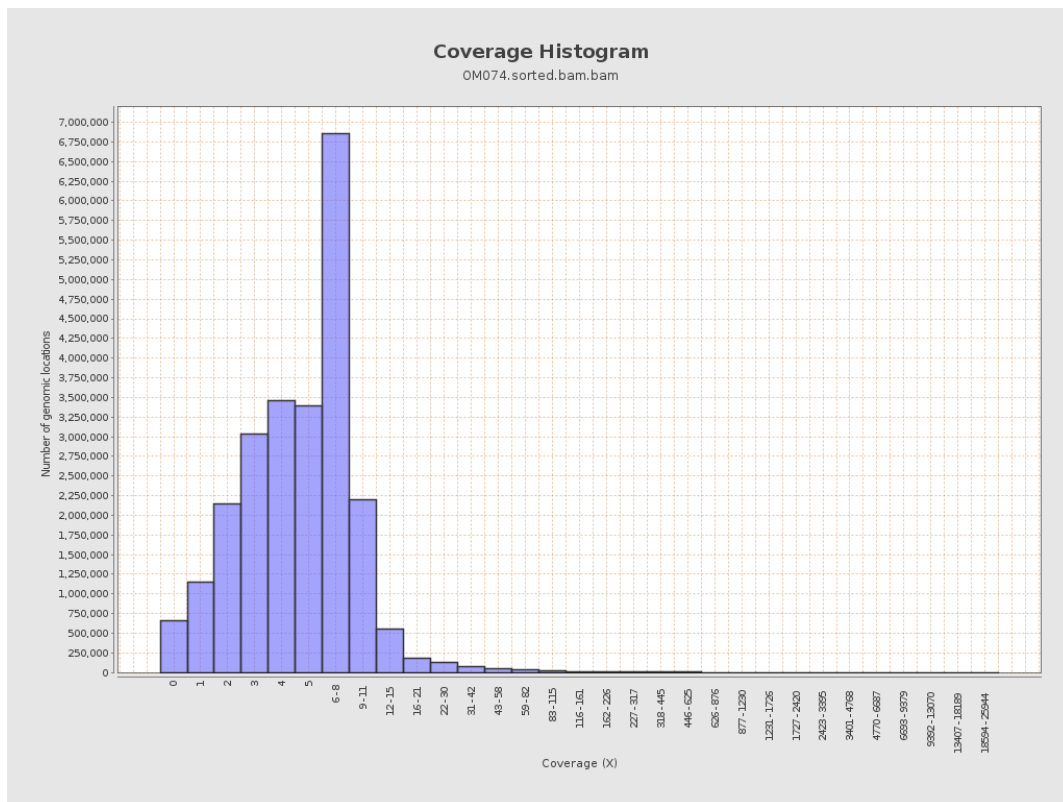
Coverage Histogram (0-50X)
OM074.sorted.bam.bam
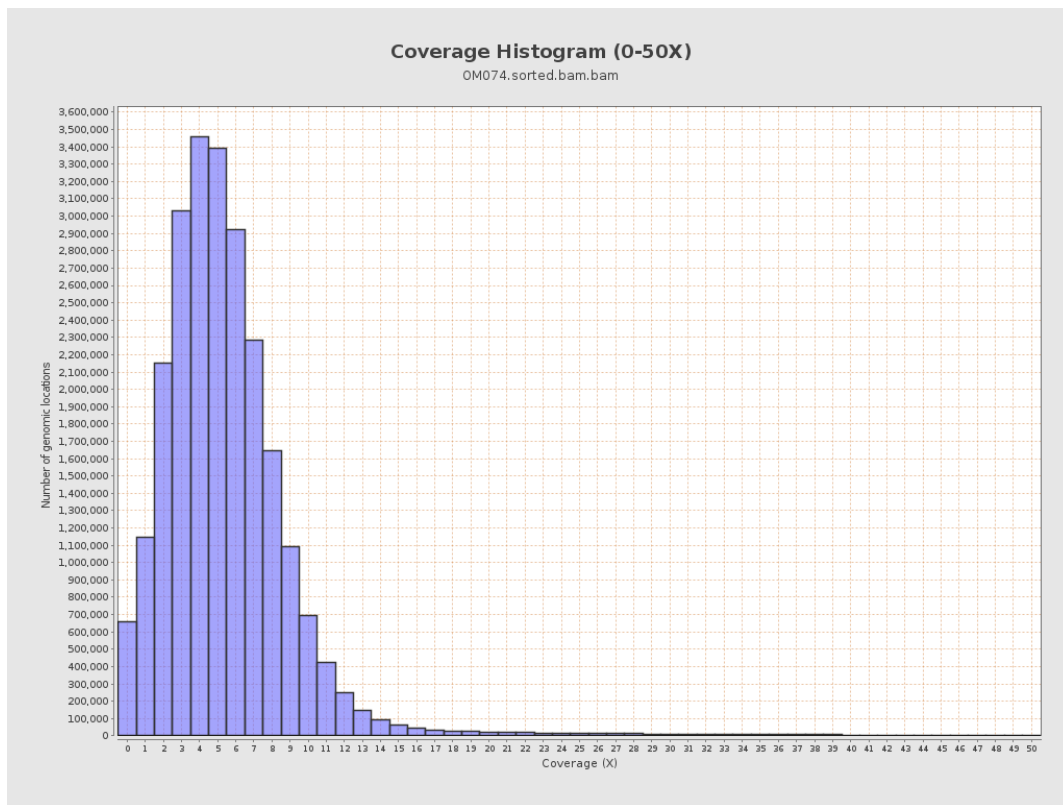
6. Results : Genome Fraction Coverage

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PRINCIPE FELIPE
CENTRO DE INVESTIGACION
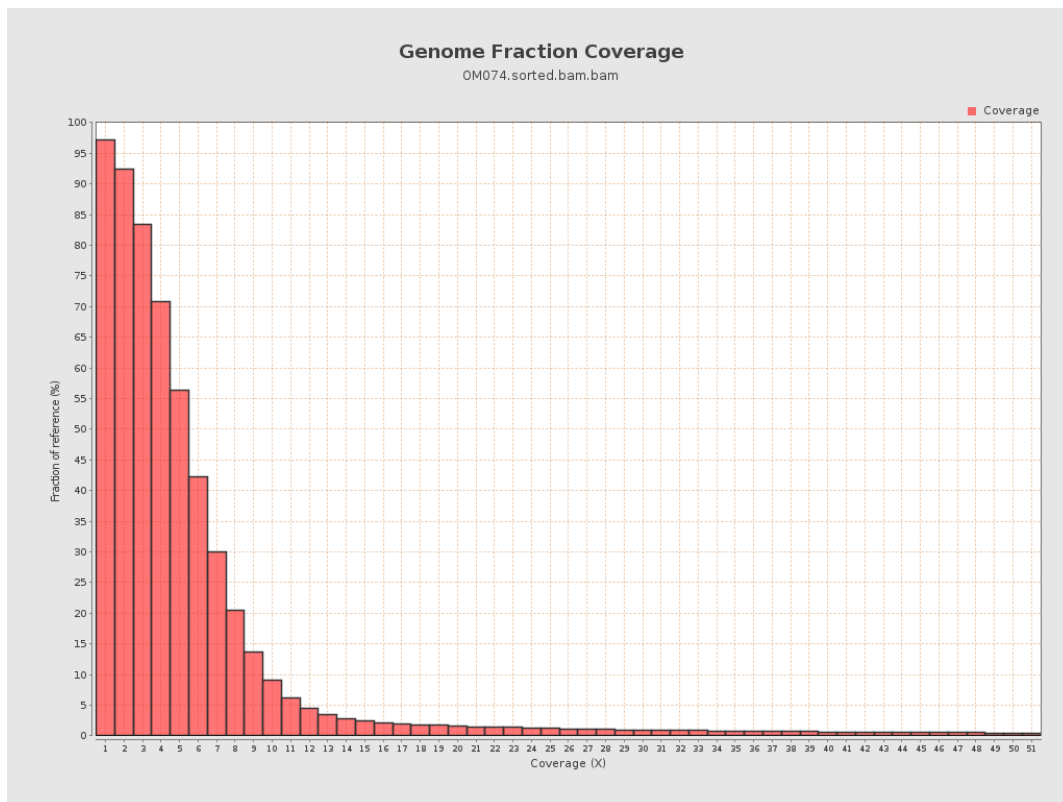
7. Results : Duplication Rate Histogram

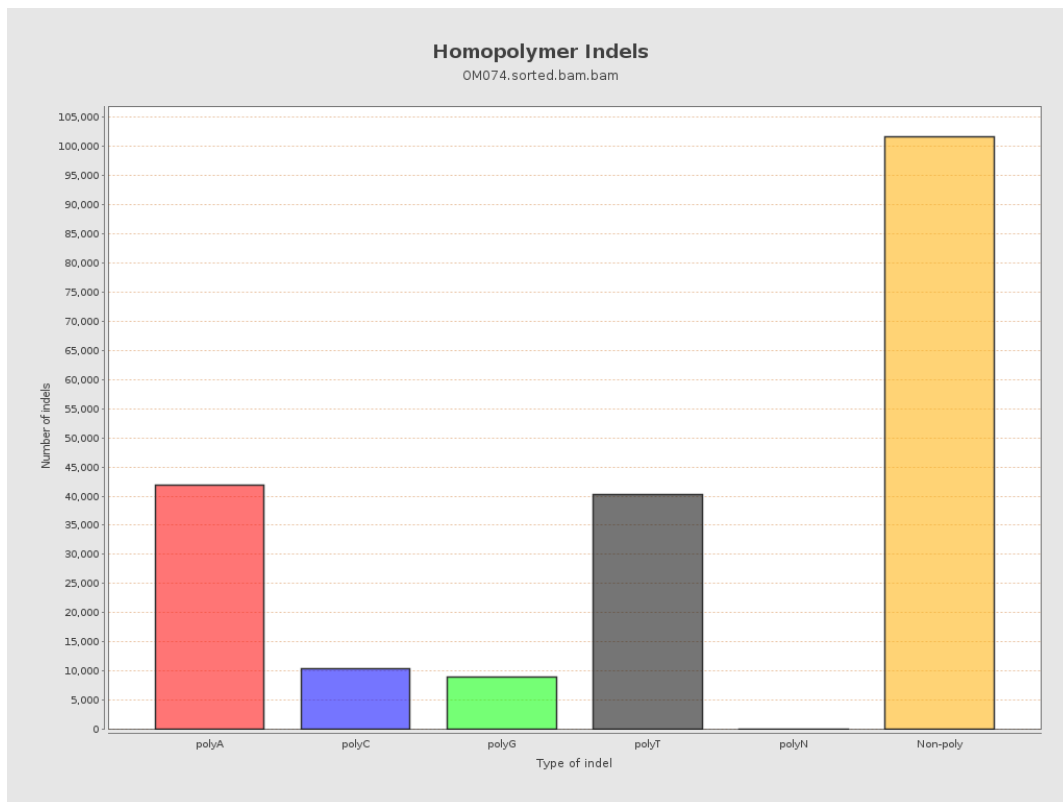Duplication Rate Histogram
OM074.sorted.bam.bam
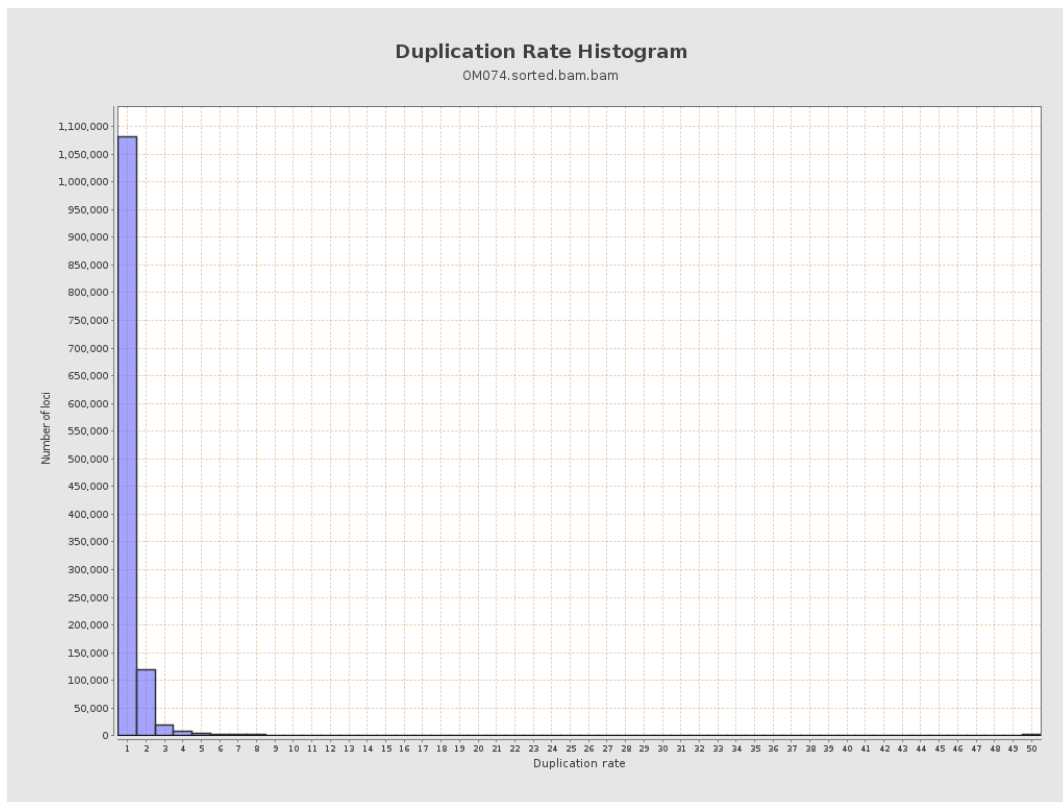
8. Results : Mapped Reads Nucleotide Content
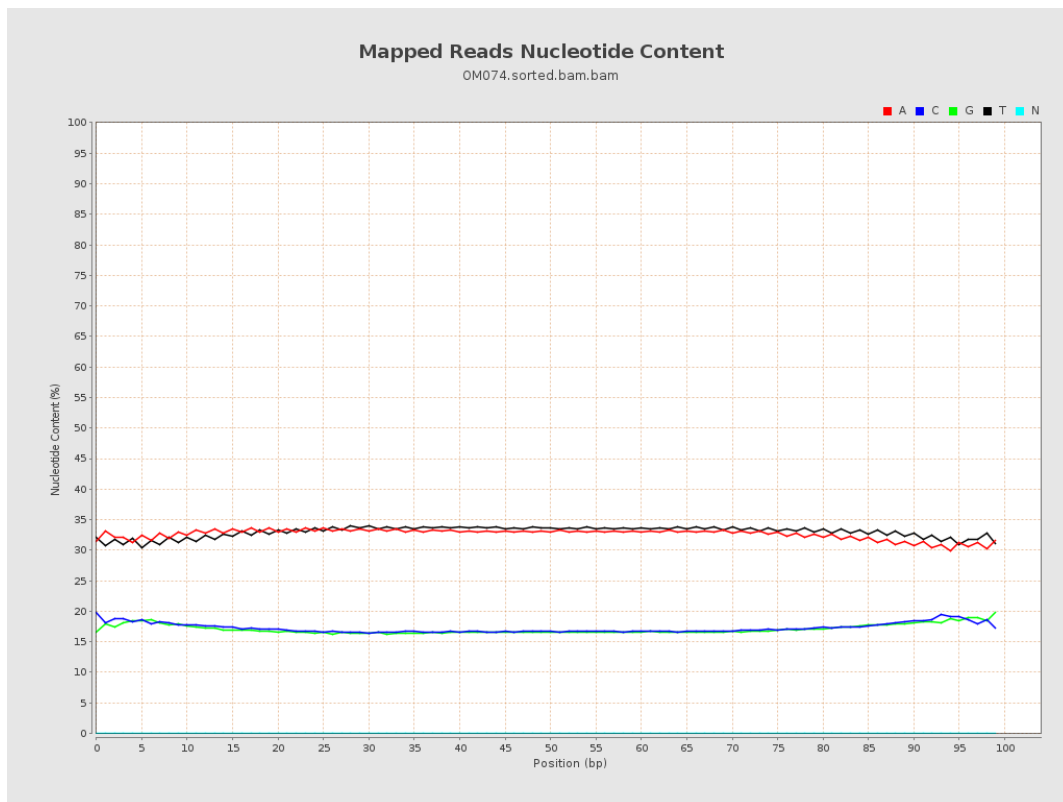
9. Results : Mapped Reads GC-content Distribution
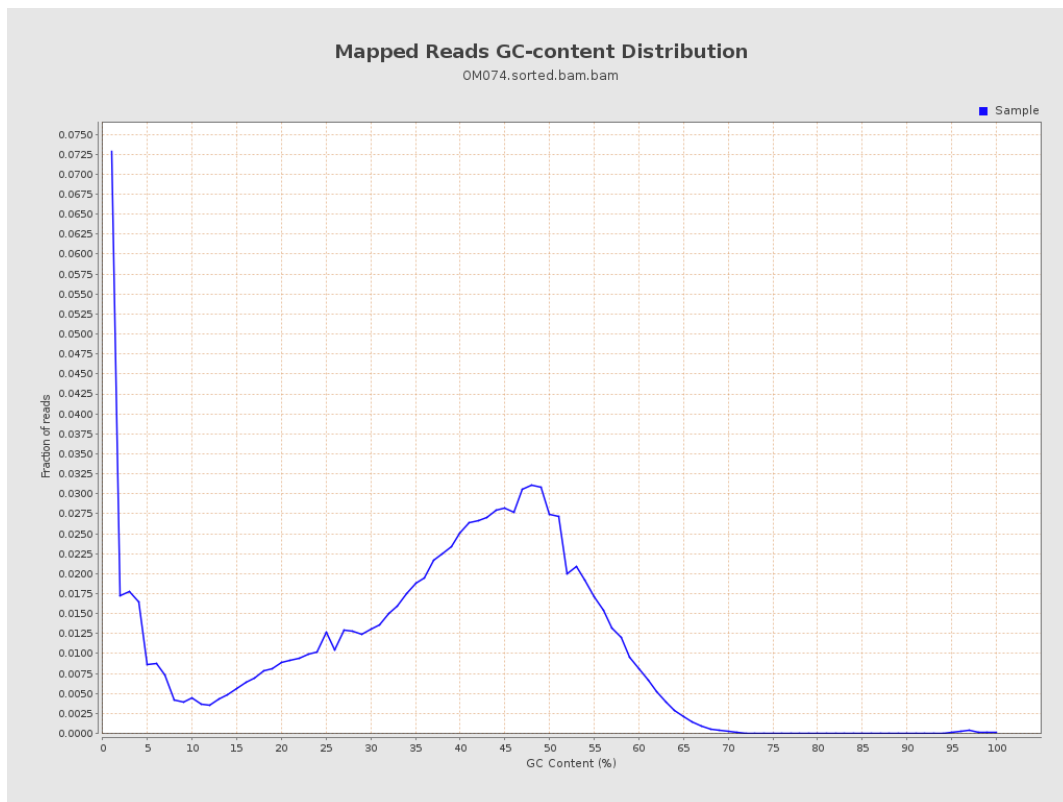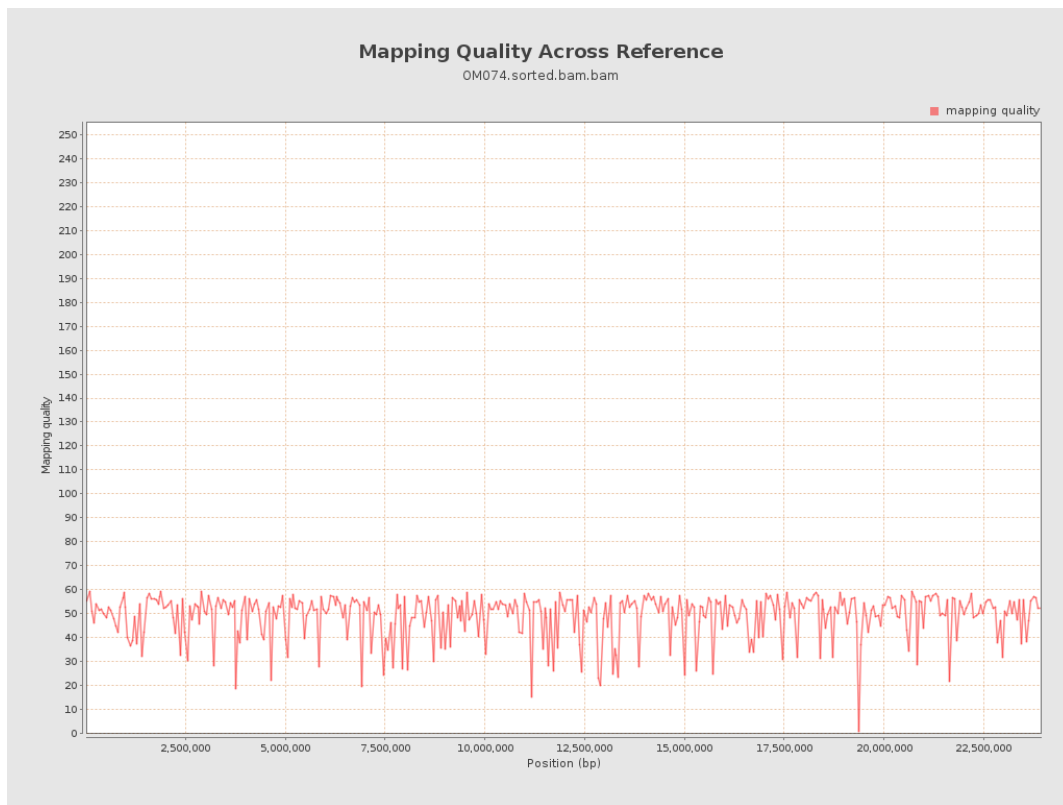
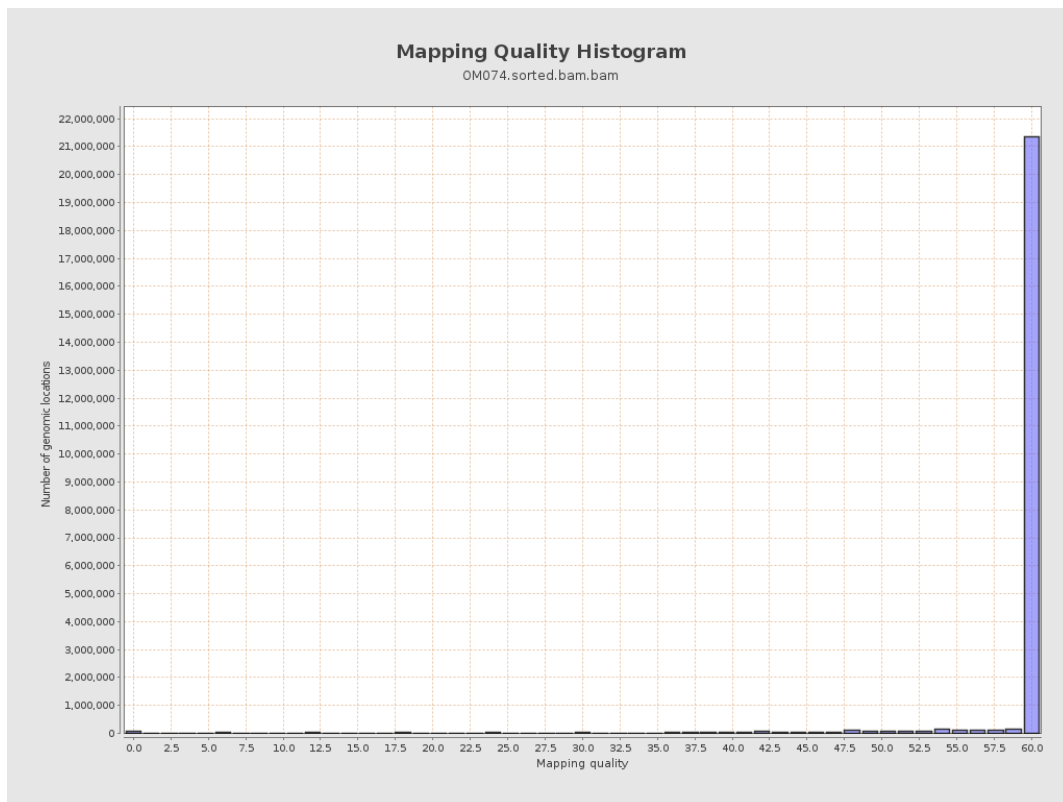# 10. Results : Mapped Reads Clipping Profile
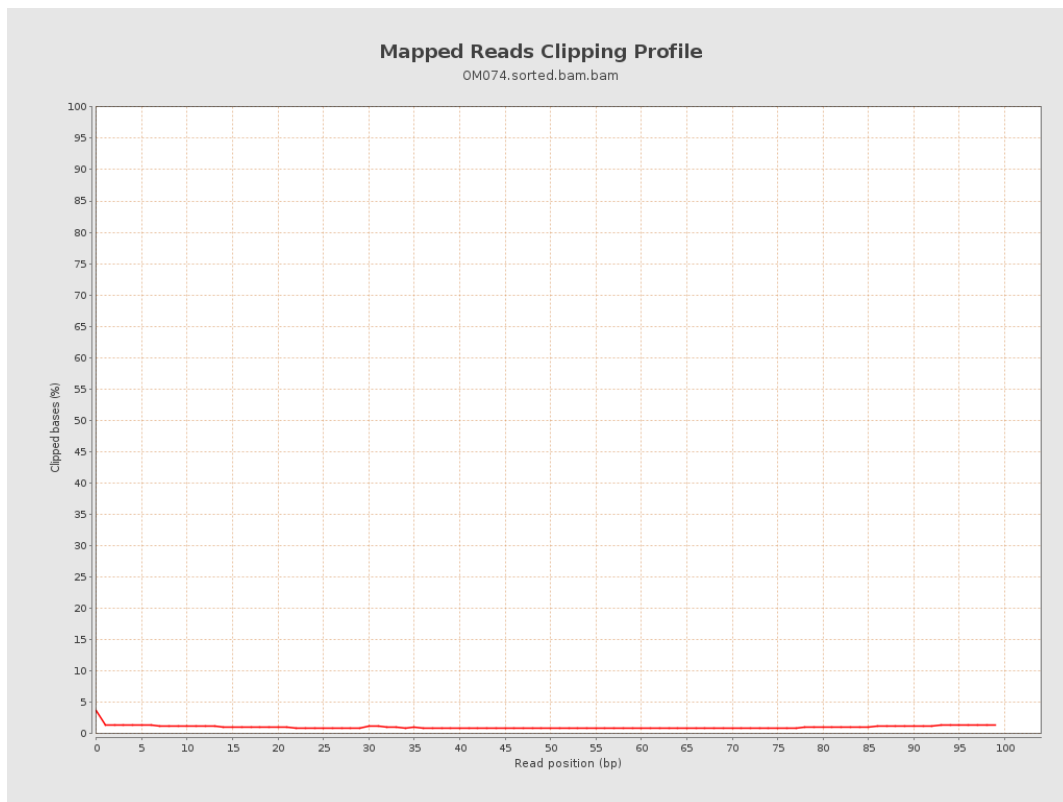
11. Results : Homopolymer Indels

Homopolymer Indels
OM074.sorted.bam.bam
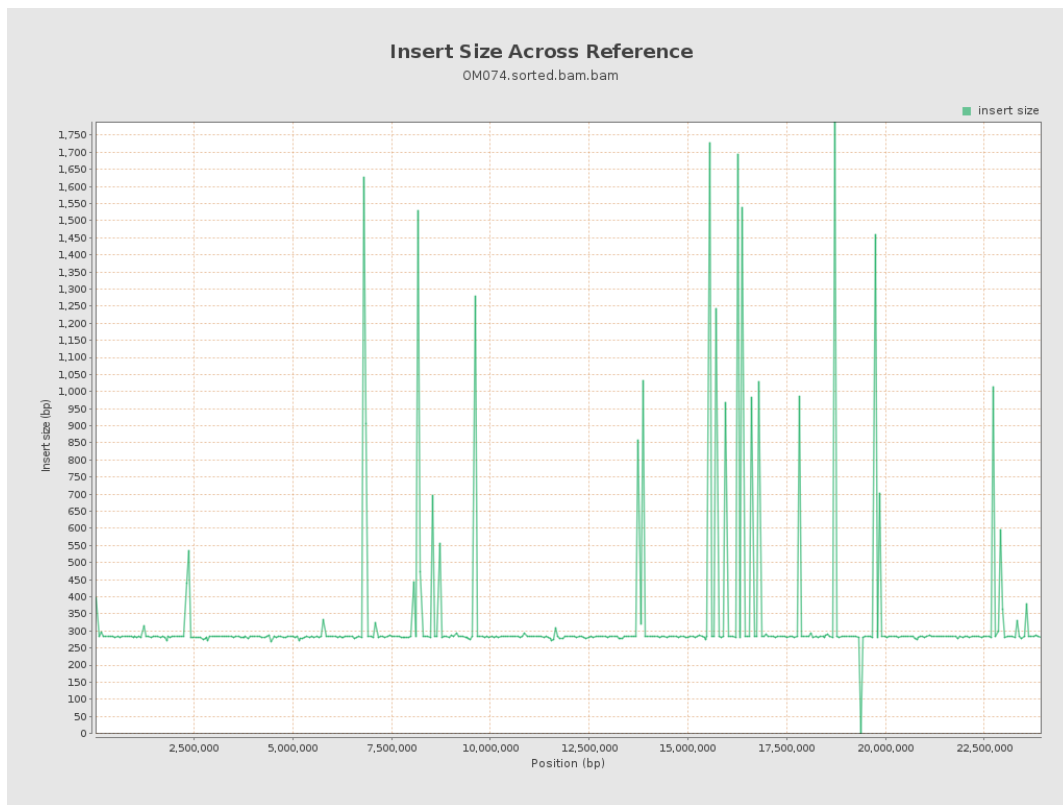
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

Insert Size Across Reference
OM074.sorted.bam.bam

15. Results : Insert Size Histogram