Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 13:38:57

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam /home/vdp5/data/cambodia_samples/sequences_bam/OM146.sorted.bam.bam -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-146_TTAGGC_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM-146_TTAGGC_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 13:38:57 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM146.sorted.bam.bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	41,639,451
Mapped reads	5,074,862 / 12.19%
Unmapped reads	36,564,589 / 87.81%
Mapped paired reads	5,074,862 / 12.19%
Mapped reads, first in pair	2,536,658 / 6.09%
Mapped reads, second in pair	2,538,204 / 6.1%
Mapped reads, both in pair	4,759,672 / 11.43%
Mapped reads, singletons	315,190 / 0.76%
Read min/max/mean length	30 / 100 / 99.96
Duplicated reads (estimated)	1,168,599 / 2.81%
Duplication rate	16.36%
Clipped reads	754,213 / 1.81%

2.2. ACGT Content

Number/percentage of A's	139,992,003 / 29.46%
Number/percentage of C's	97,004,046 / 20.42%
Number/percentage of T's	141,398,198 / 29.76%
Number/percentage of G's	96,762,081 / 20.36%
Number/percentage of N's	14,883 / 0%
GC Percentage	40.78%

2.3. Coverage

Mean	19.8537
Standard Deviation	47.5692

2.4. Mapping Quality

Mean Mapping Quality	57.43

2.5. Insert size

Mean	760.6
Standard Deviation	24,302.17
P25/Median/P75	198 / 211 / 224

2.6. Mismatches and indels

General error rate	1.17%
Mismatches	5,116,565
Insertions	168,066
Mapped reads with at least one insertion	3.09%
Deletions	184,918
Mapped reads with at least one deletion	3.3%
Homopolymer indels	63.73%

2.7. Chromosome stats

| Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|1074120478|emb|LT615256.1|	977217	17835321	18.2511	13.0386
gi|1074120682|emb|LT615257.1|	860454	16284181	18.9251	22.7944
gi|1074120865|emb|LT615258.1|	989719	23267719	23.5094	33.9349
gi|1074121086|emb|LT615259.1|	935450	19936750	21.3125	28.5523
gi|1074121301|emb|LT615260.1|	1432239	29306311	20.4619	33.7049
gi|1074121615|emb|LT615261.1|	1080962	22025610	20.3759	23.1558
gi|1074121871|emb|LT615262.1|	1545099	29234419	18.9207	13.2477
gi|1074122235|emb|LT615263.1|	1585108	31911128	20.1318	67.7802
gi|1074122590|emb|LT615264.1|	2122358	40097413	18.8929	10.8634
gi|1074123050|emb|LT615265.1|	1754192	36438044	20.772	134.652
gi|1074123421|emb|LT615	2150147	43929527	20.4309	38.7482

266.1|				
gi|1074123898|emb|LT615267.1|	3031036	59063713	19.4863	39.845
gi|1074124588|emb|LT615268.1|	2359348	44820717	18.9971	23.7923
gi|1074125065|emb|LT615269.1|	3135668	61524266	19.6208	12.3795

3. Results : Coverage across reference

Coverage across reference
OM146.sorted.bam.bam

4. Results : Coverage Histogram

Coverage Histogram
OM146.sorted.bam.bam

5. Results : Coverage Histogram (0-50X)
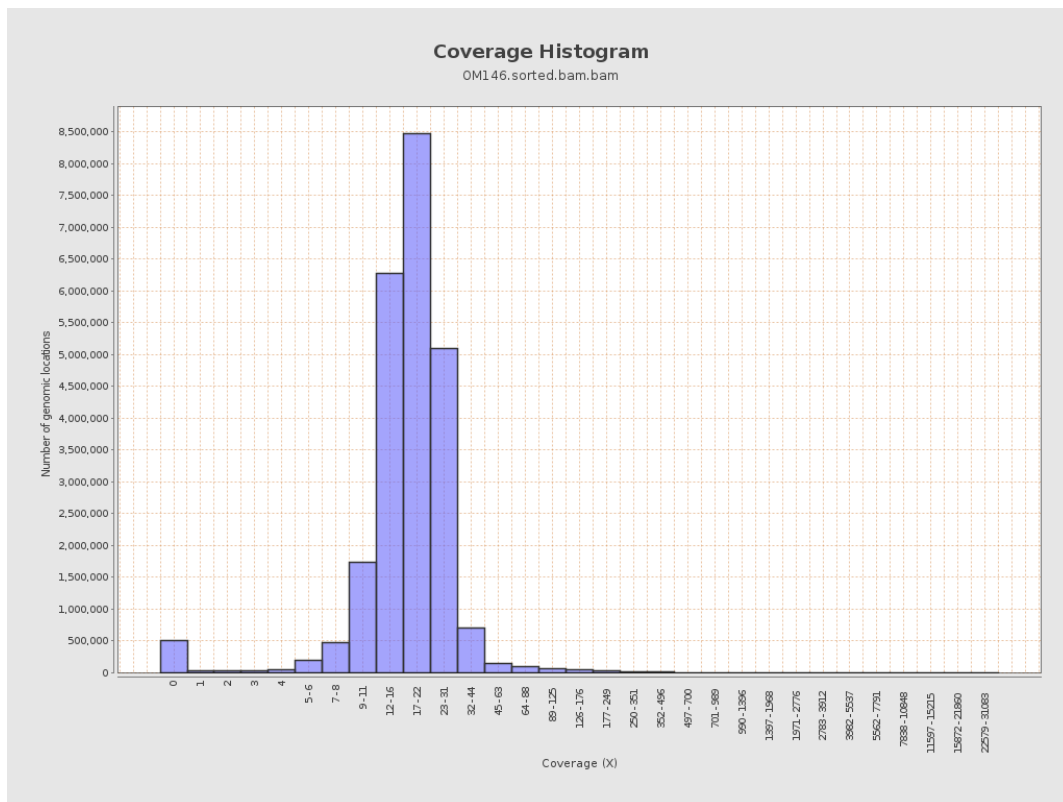
Coverage Histogram (0-50X)
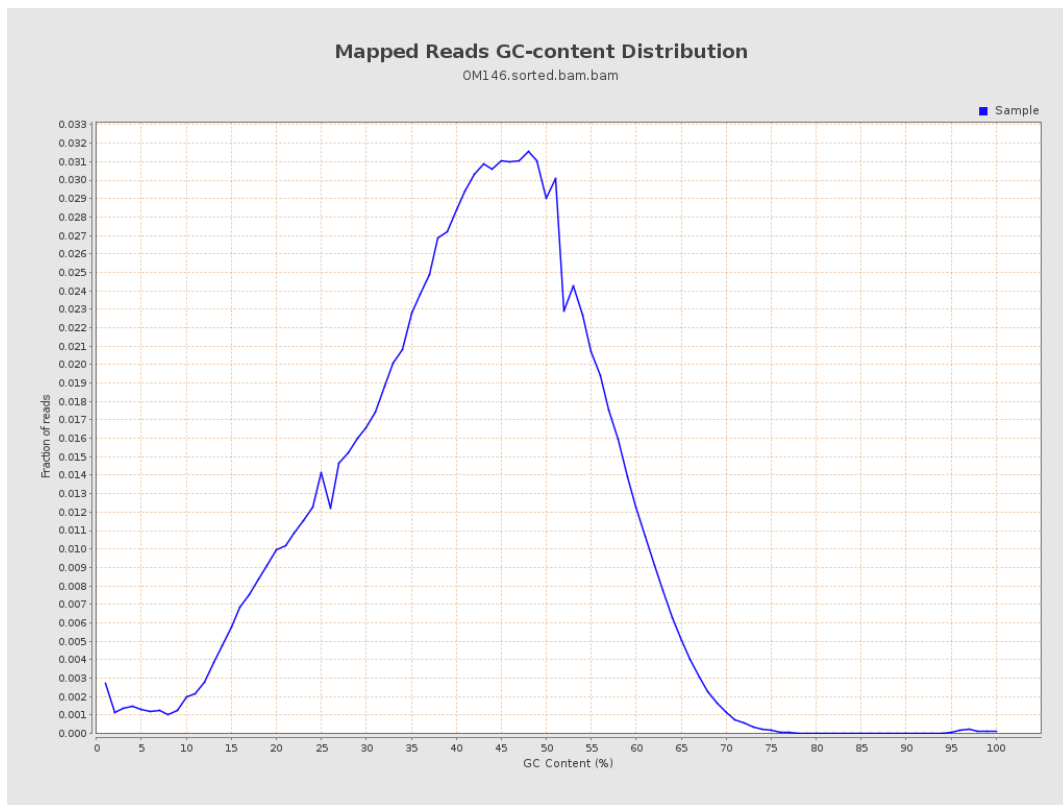OM146.sorted.bam.bam
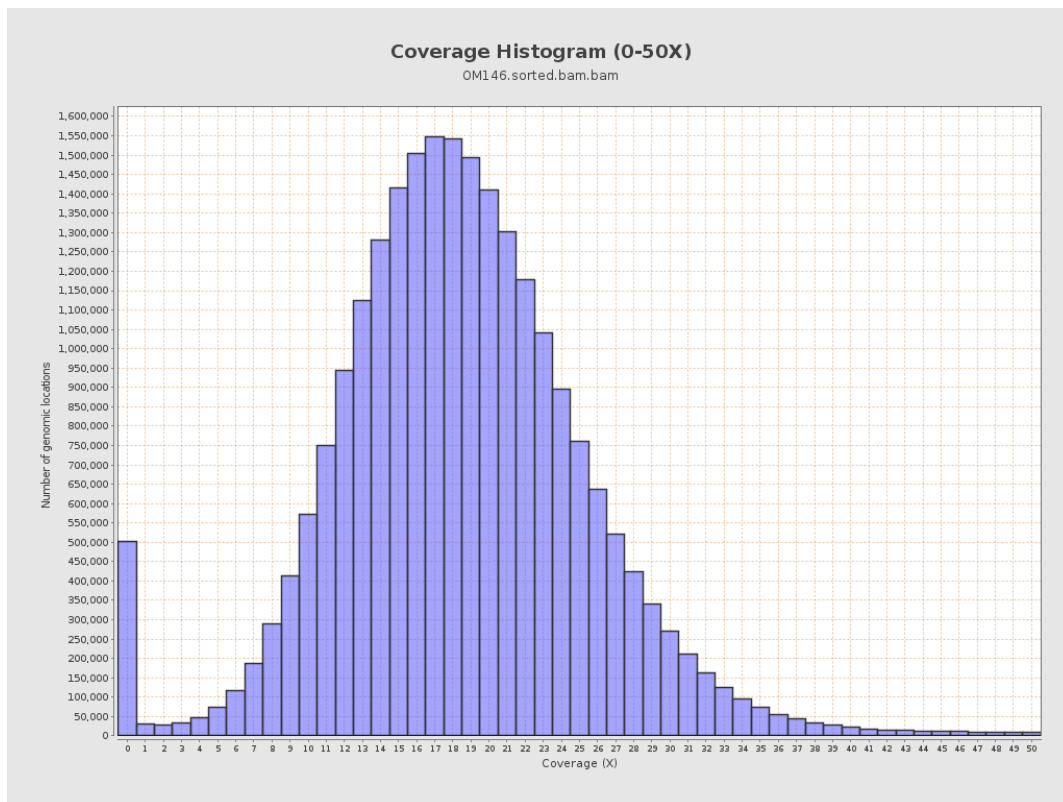
6. Results : Genome Fraction Coverage
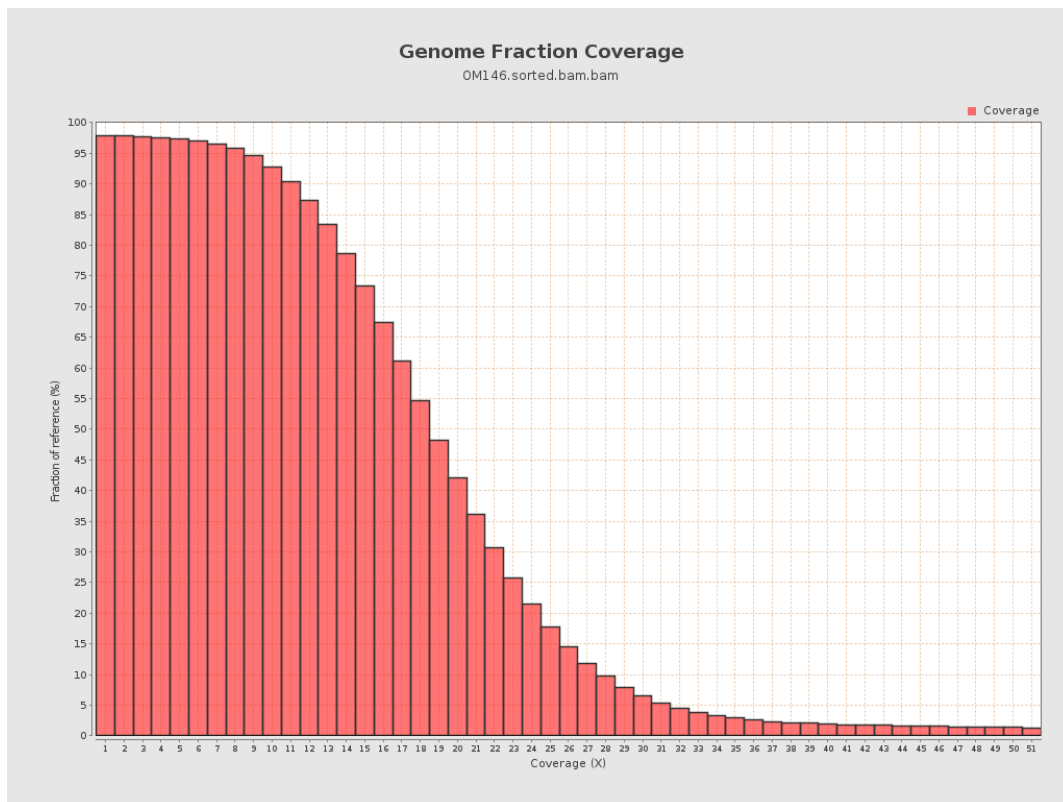
7. Results : Duplication Rate Histogram
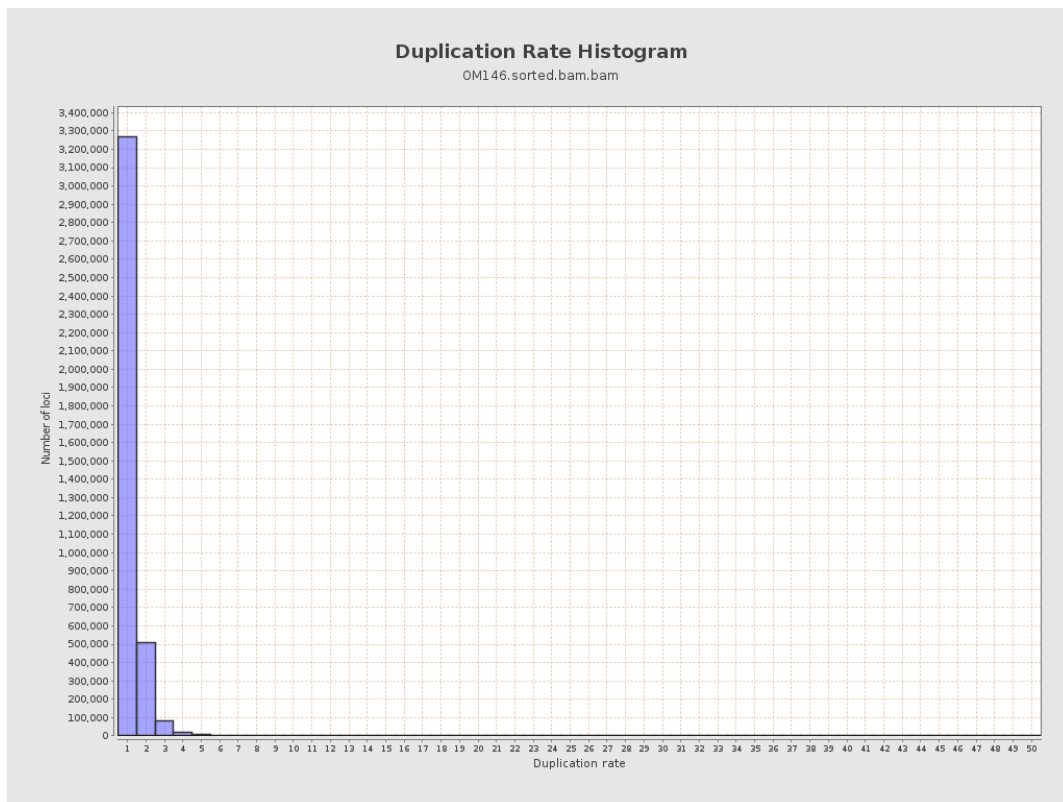
8. Results : Mapped Reads Nucleotide Content
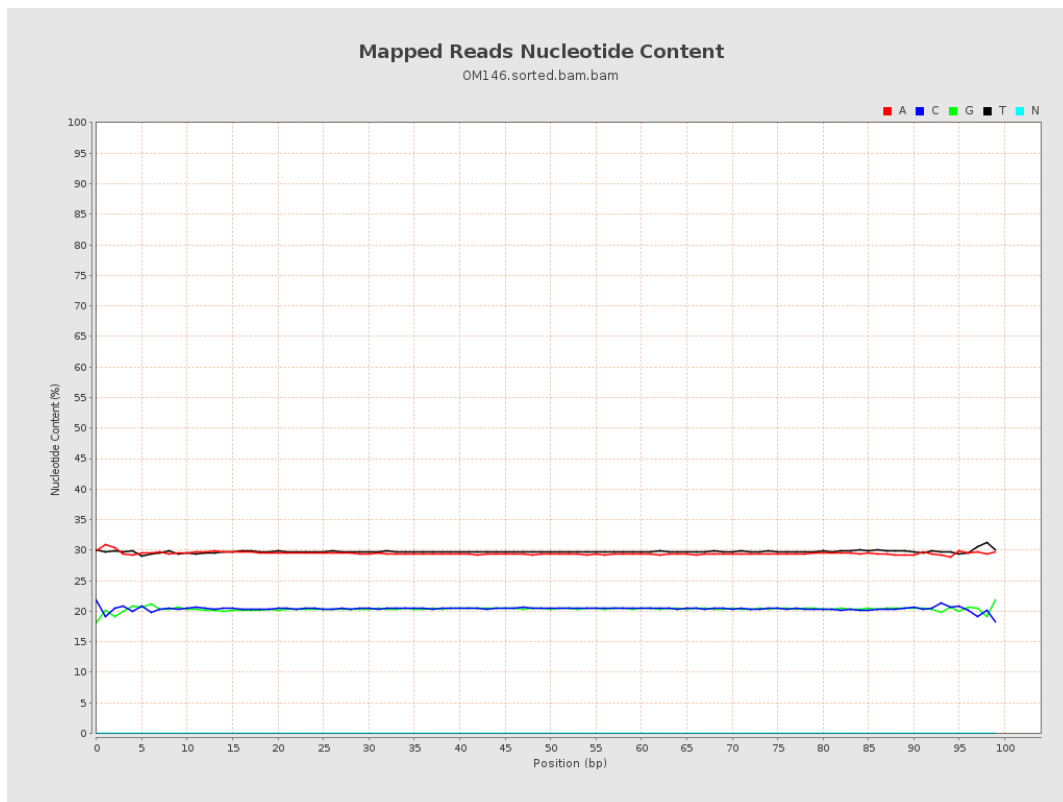
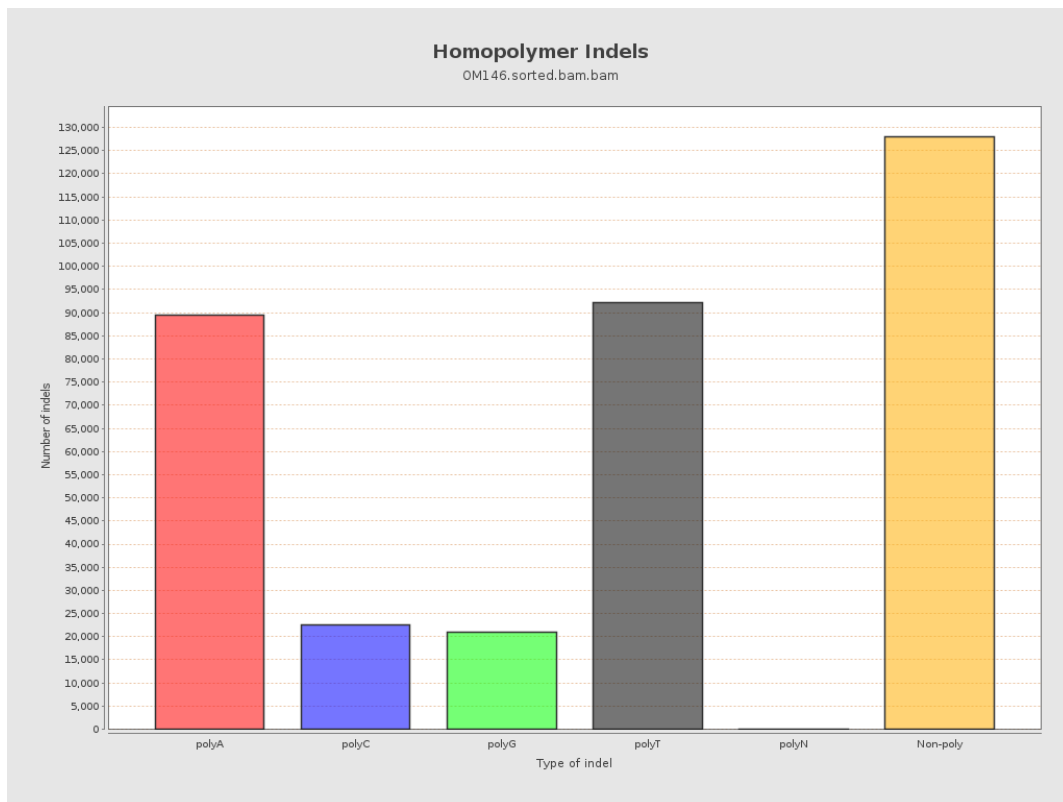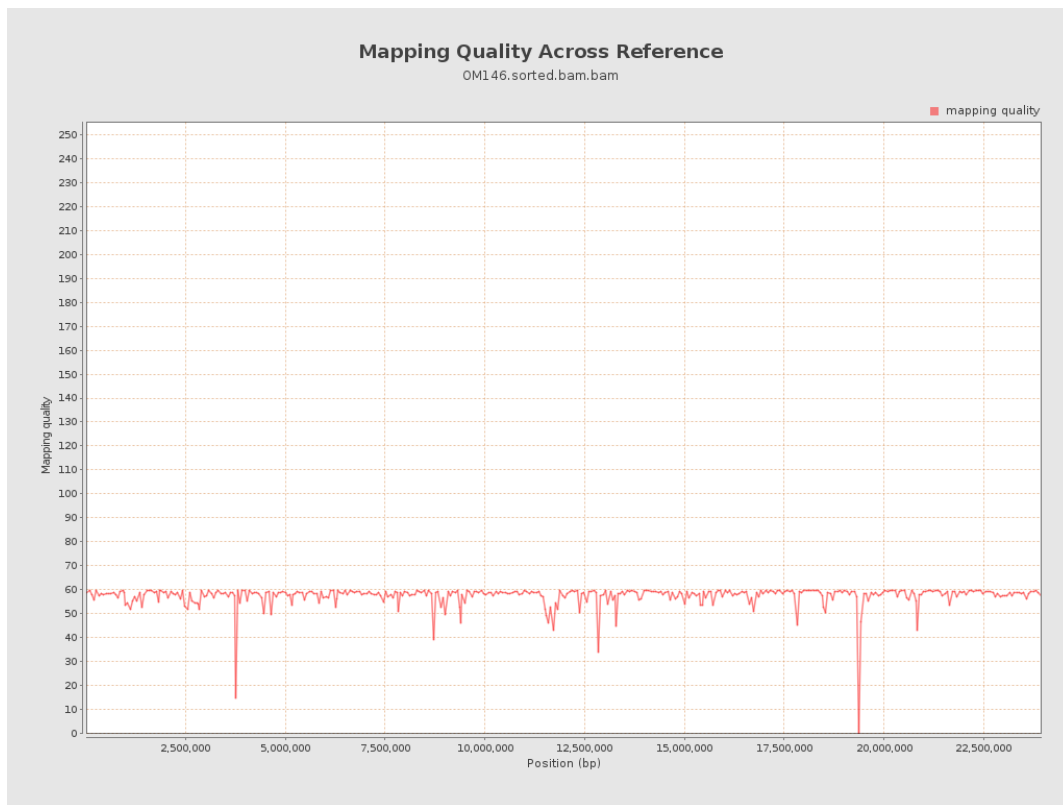# 9. Results : Mapped Reads GC-content Distribution
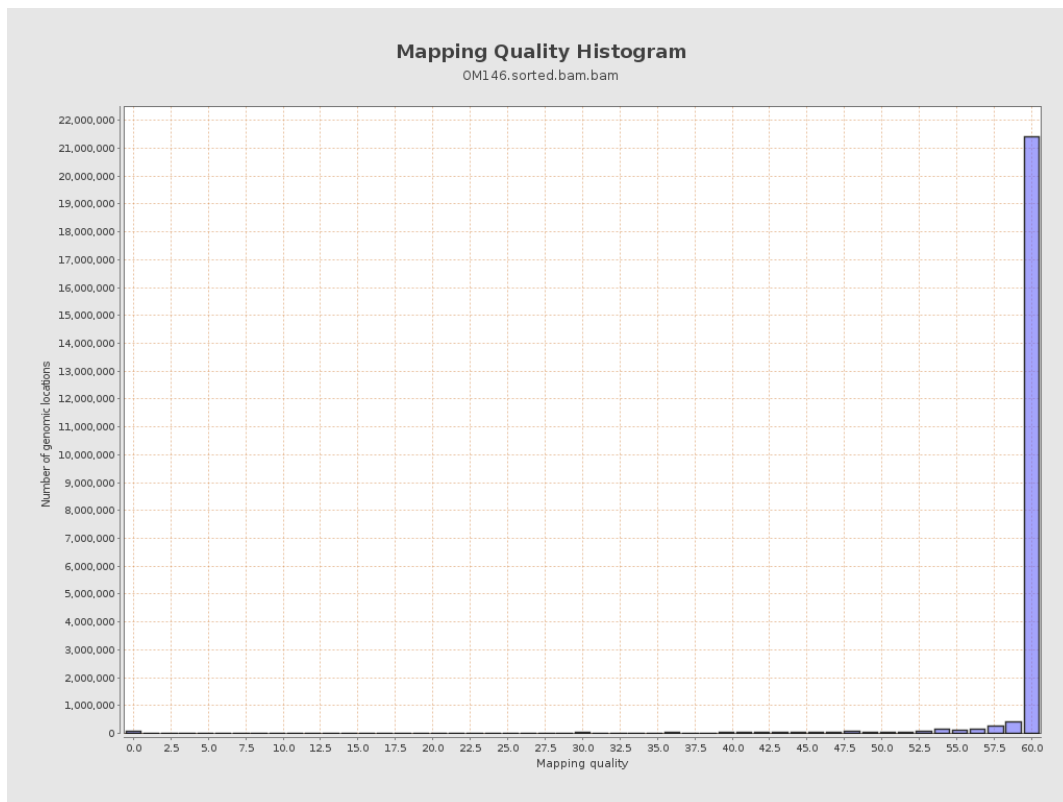
10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
OM146.sorted.bam.bam

11. Results : Homopolymer Indels

Homopolymer Indels
OM146.sorted.bam.bam

12. Results : Mapping Quality Across Reference

Mapping Quality Across Reference
OM146.sorted.bam.bam

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

Insert Size Across Reference
OM146.sorted.bam.bam
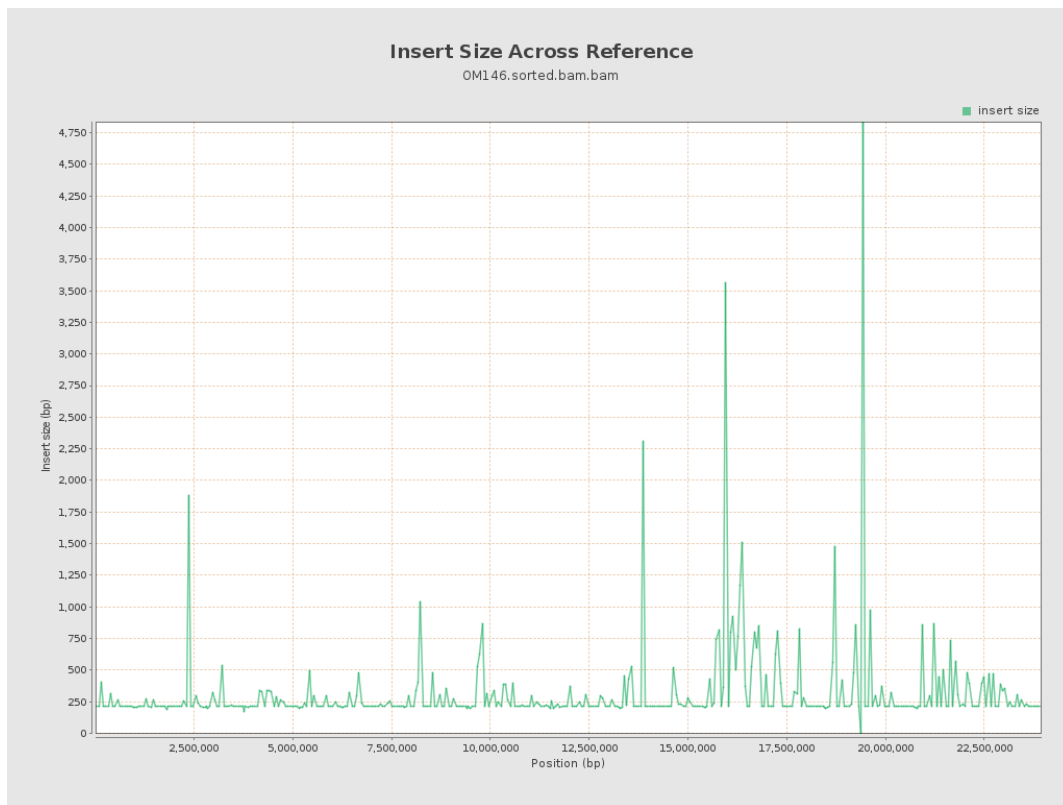
15. Results : Insert Size Histogram

Insert Size Histogram
OM146.sorted.bam.bam