

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2016/10/23 14:09:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM304.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/OM304-BiooBarcode36_CCAACA_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM304-BiooBarcode36_CCAACA_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 14:09:42 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM304.sorted.bam.

	bam
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2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	2,235,094
Mapped reads	886,695 / 39.67%
Unmapped reads	1,348,399 / 60.33%
Mapped paired reads	886,695 / 39.67%
Mapped reads, first in pair	439,753 / 19.67%
Mapped reads, second in pair	446,942 / 20%
Mapped reads, both in pair	858,591 / 38.41%
Mapped reads, singletons	28,104 / 1.26%
Read min/max/mean length	30 / 100 / 99.93
Duplicated reads (estimated)	57,541 / 2.57%
Duplication rate	4.95%
Clipped reads	105,762 / 4.73%

2.2. ACGT Content

Number/percentage of A's	25,787,575 / 30.21%
Number/percentage of C's	16,880,093 / 19.78%
Number/percentage of T's	25,863,410 / 30.3%
Number/percentage of G's	16,818,567 / 19.71%
Number/percentage of N's	6,892 / 0.01%
GC Percentage	39.48%

2.3. Coverage

Mean	3.5662
Standard Deviation	3.995

2.4. Mapping Quality

Mean Mapping Quality	58.48
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2.5. Insert size

Mean	1,031.05
Standard Deviation	30,946.81
P25/Median/P75	335 / 345 / 353

2.6. Mismatches and indels

General error rate	1.63%
Mismatches	1,329,924
Insertions	28,397
Mapped reads with at least one insertion	3.04%
Deletions	32,937
Mapped reads with at least one deletion	3.48%
Homopolymer indels	62.42%

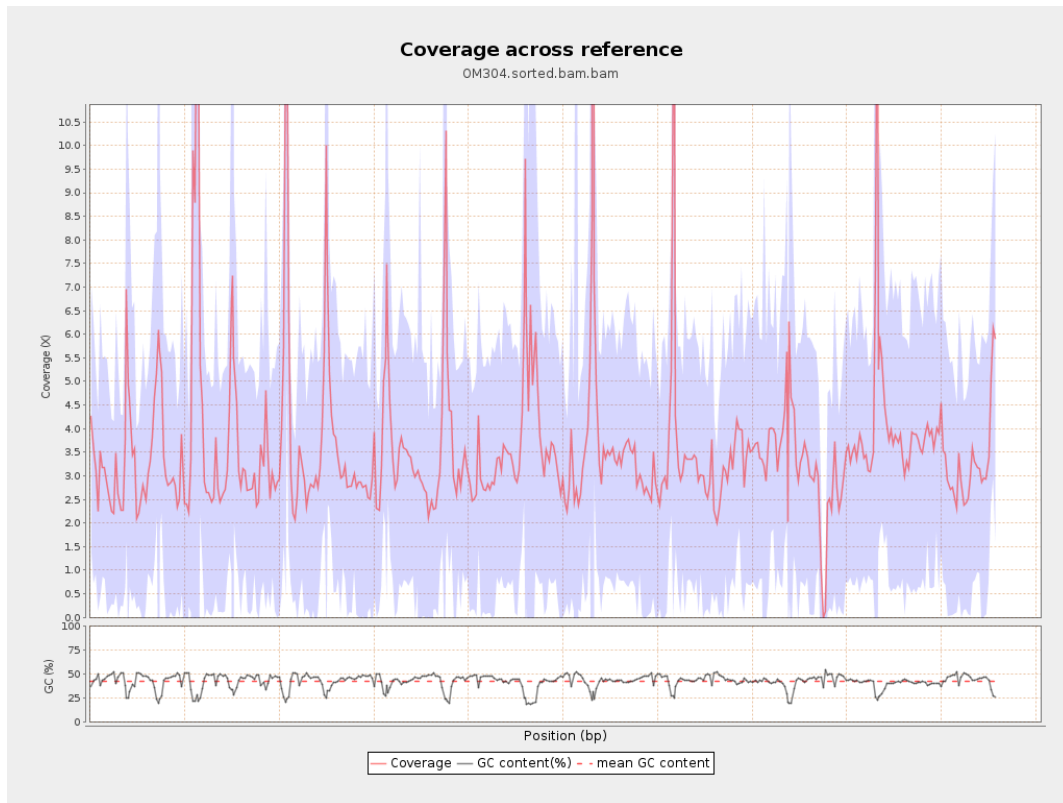
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

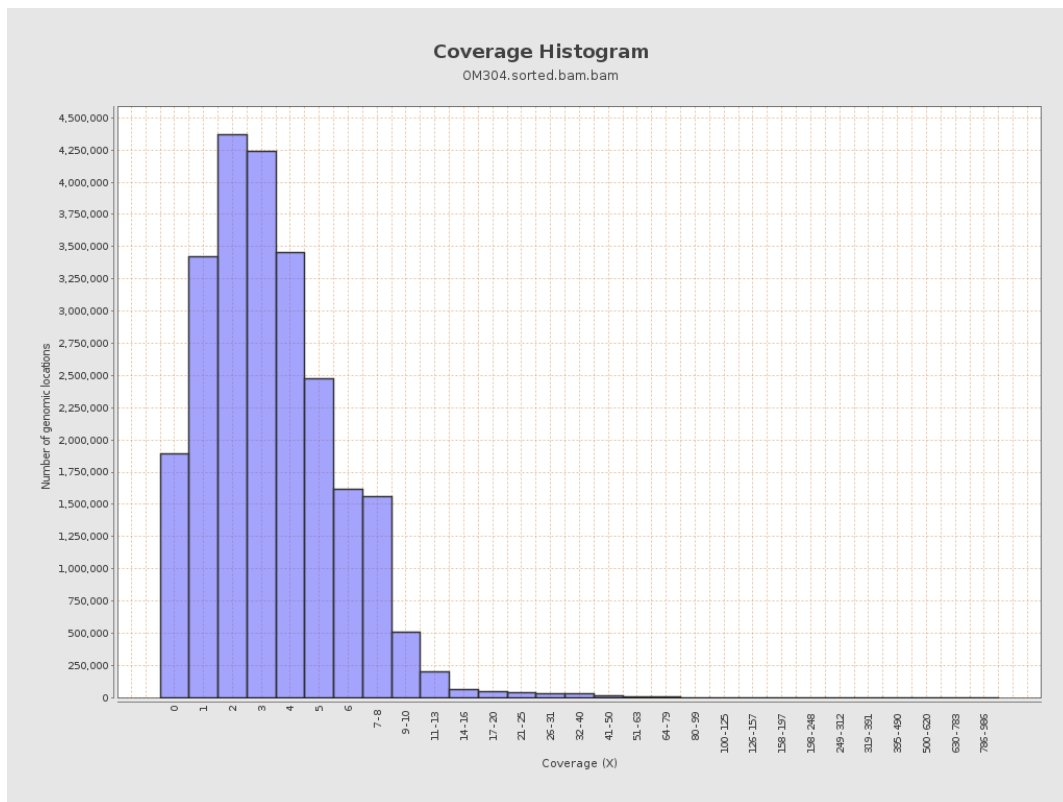
gi 1074120478 emb LT615256.1	977217	2952383	3.0212	2.2416
gi 1074120682 emb LT615257.1	860454	3071307	3.5694	3.4328
gi 1074120865 emb LT615258.1	989719	3927617	3.9684	5.8533
gi 1074121086 emb LT615259.1	935450	3663496	3.9163	5.697
gi 1074121301 emb LT615260.1	1432239	5235630	3.6556	4.0224
gi 1074121615 emb LT615261.1	1080962	3998147	3.6987	3.7634
gi 1074121871 emb LT615262.1	1545099	5072338	3.2829	2.3647
gi 1074122235 emb LT615263.1	1585108	5563735	3.51	3.4925
gi 1074122590 emb LT615264.1	2122358	7271986	3.4264	2.645
gi 1074123050 emb LT615265.1	1754192	6616907	3.7721	4.8694
gi 1074123421 emb LT615	2150147	8177020	3.803	6.95

266.1				
gi 107412389 8 emb LT615 267.1	3031036	10431047	3.4414	2.6753
gi 107412458 8 emb LT615 268.1	2359348	7997810	3.3898	3.917
gi 107412506 5 emb LT615 269.1	3135668	11462585	3.6555	2.3503

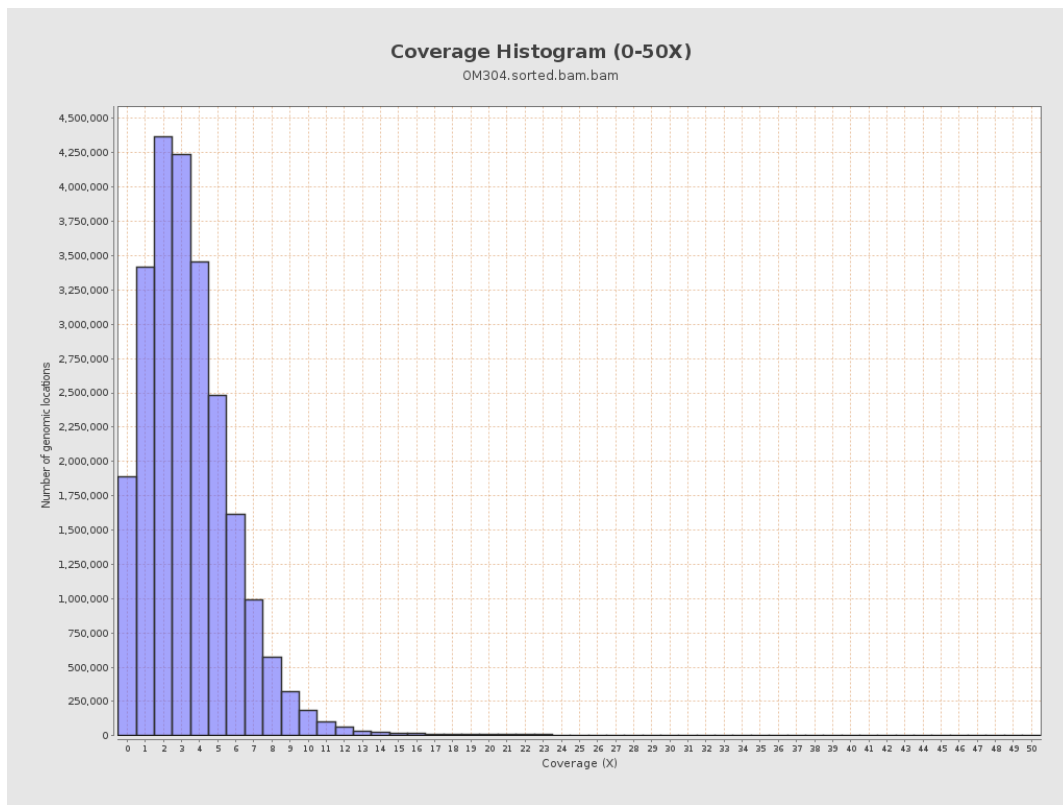
3. Results : Coverage across reference



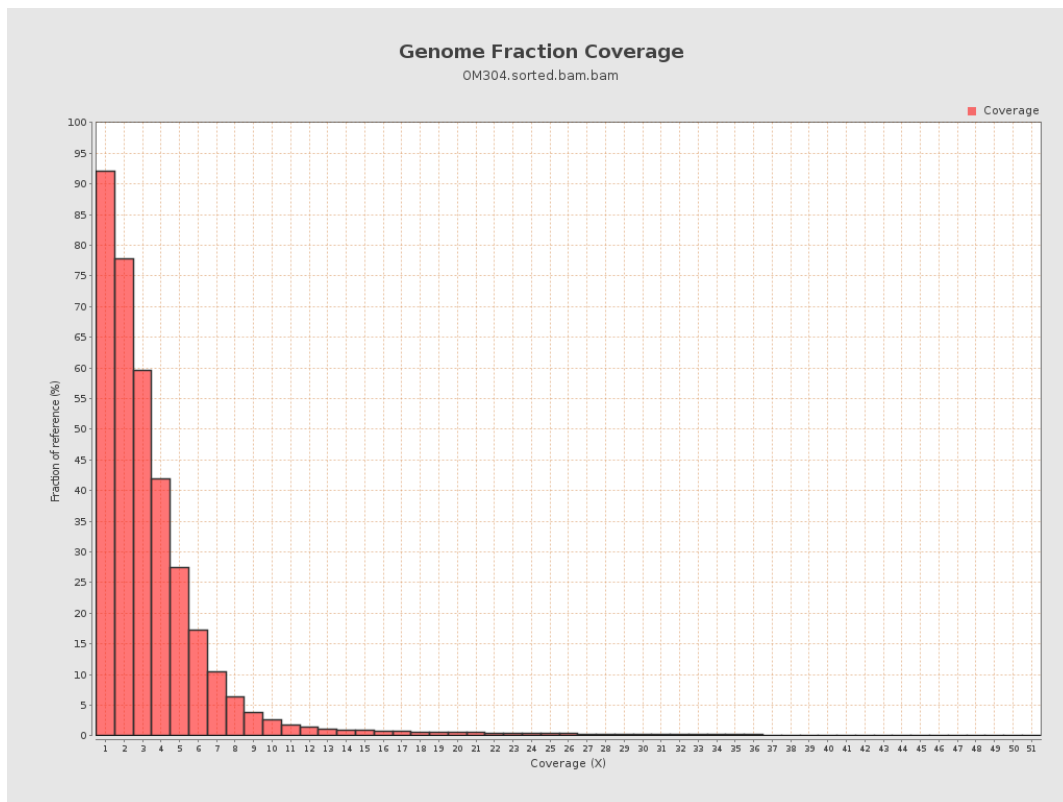
4. Results : Coverage Histogram



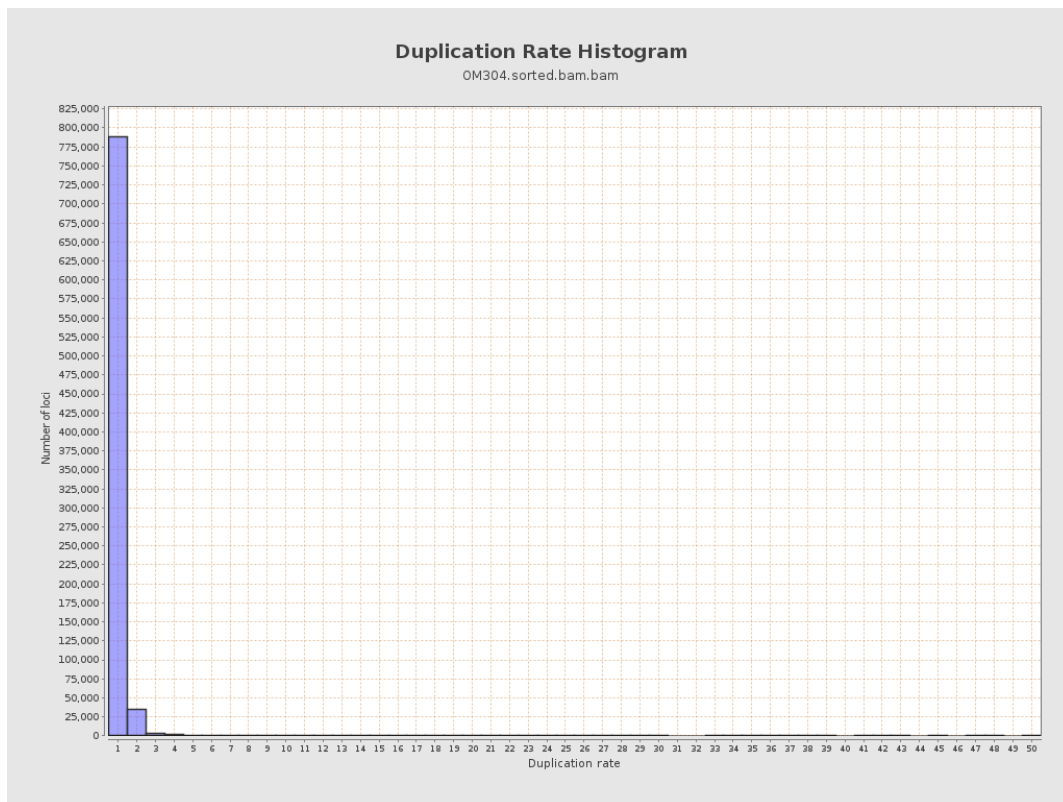
5. Results : Coverage Histogram (0-50X)



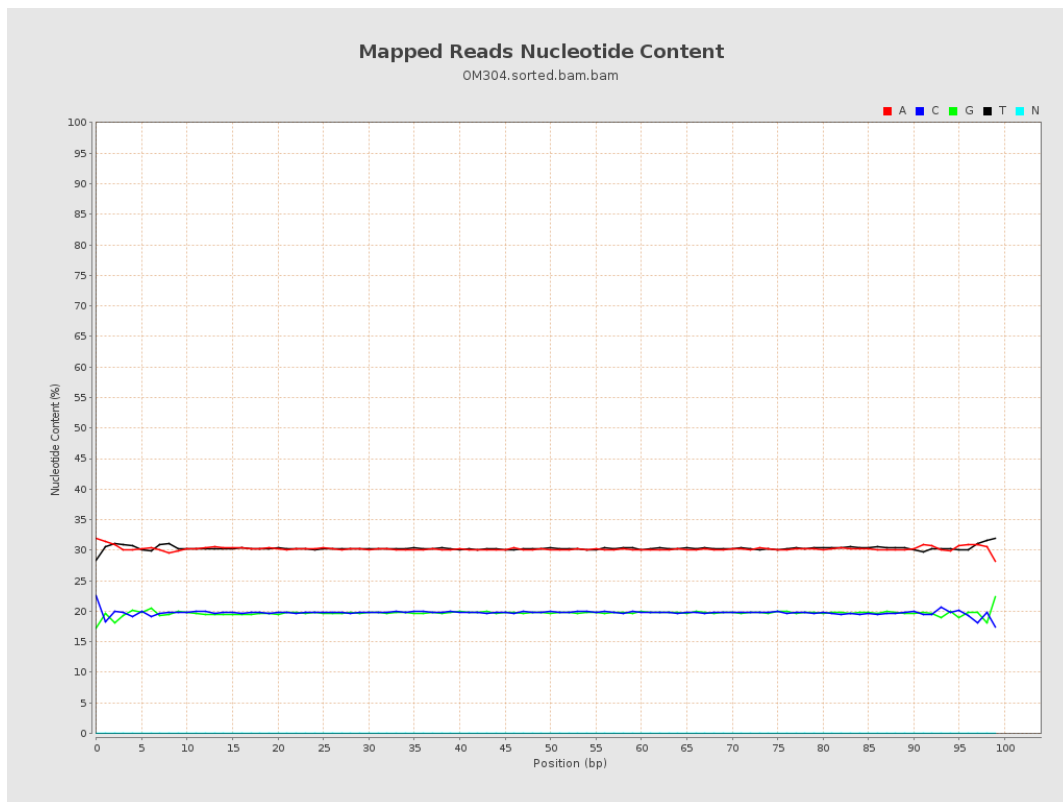
6. Results : Genome Fraction Coverage



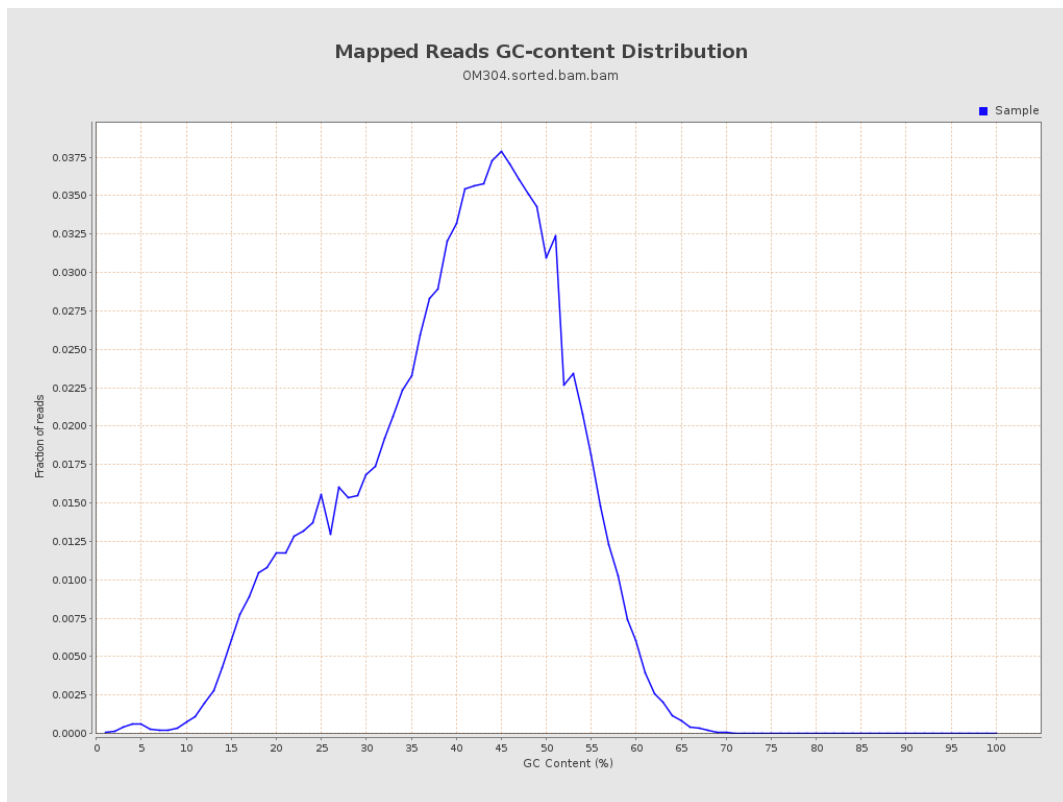
7. Results : Duplication Rate Histogram



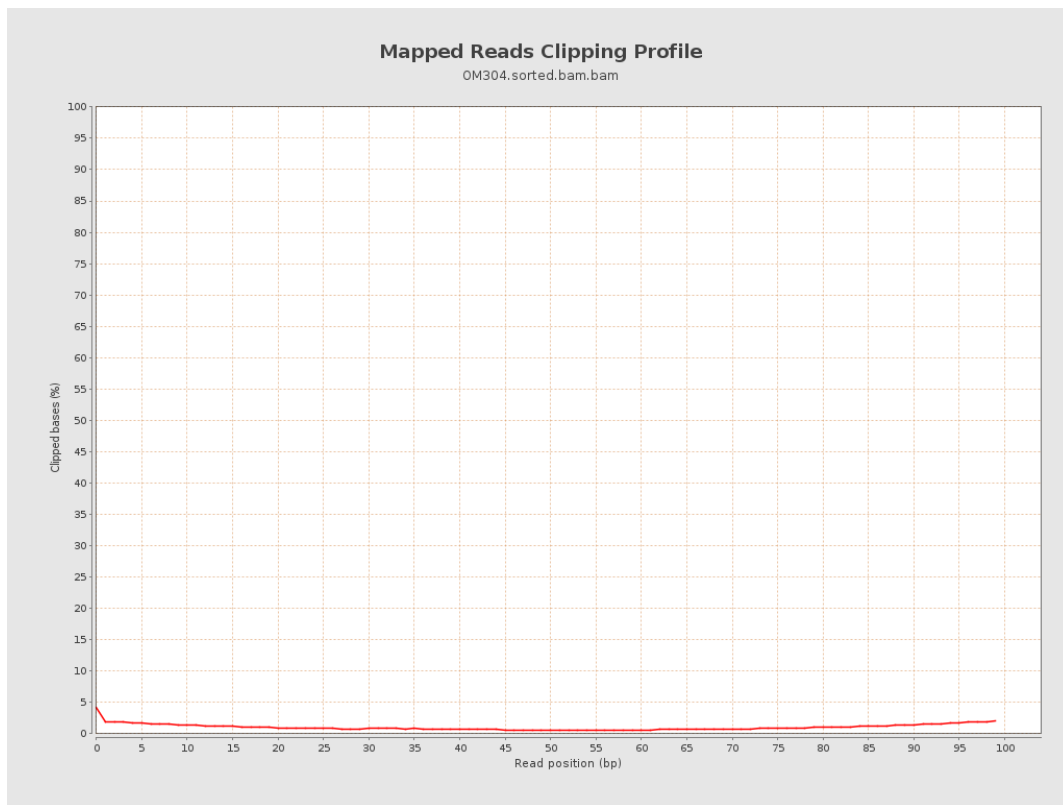
8. Results : Mapped Reads Nucleotide Content



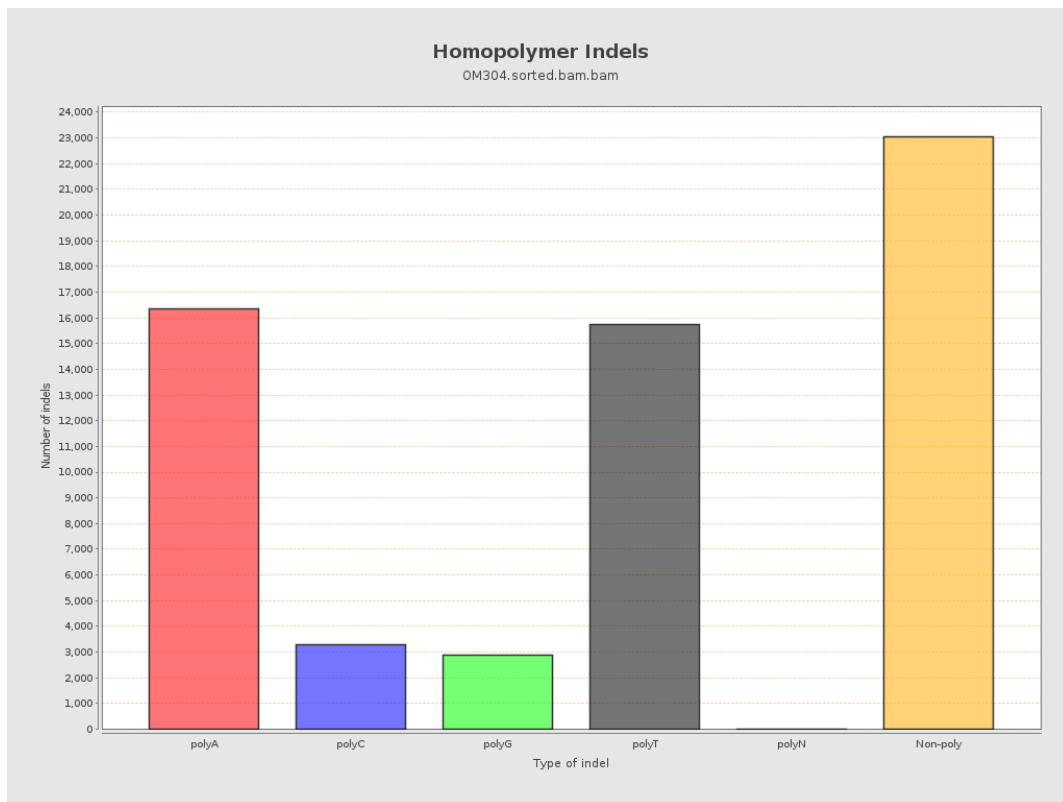
9. Results : Mapped Reads GC-content Distribution



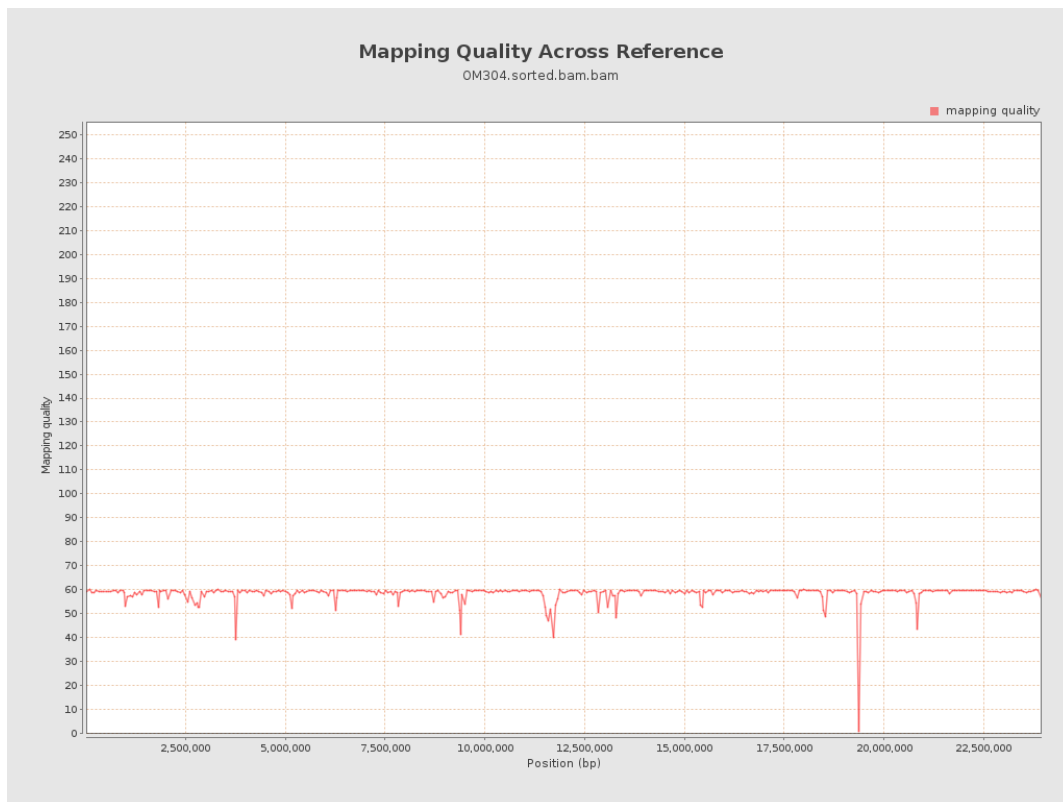
10. Results : Mapped Reads Clipping Profile



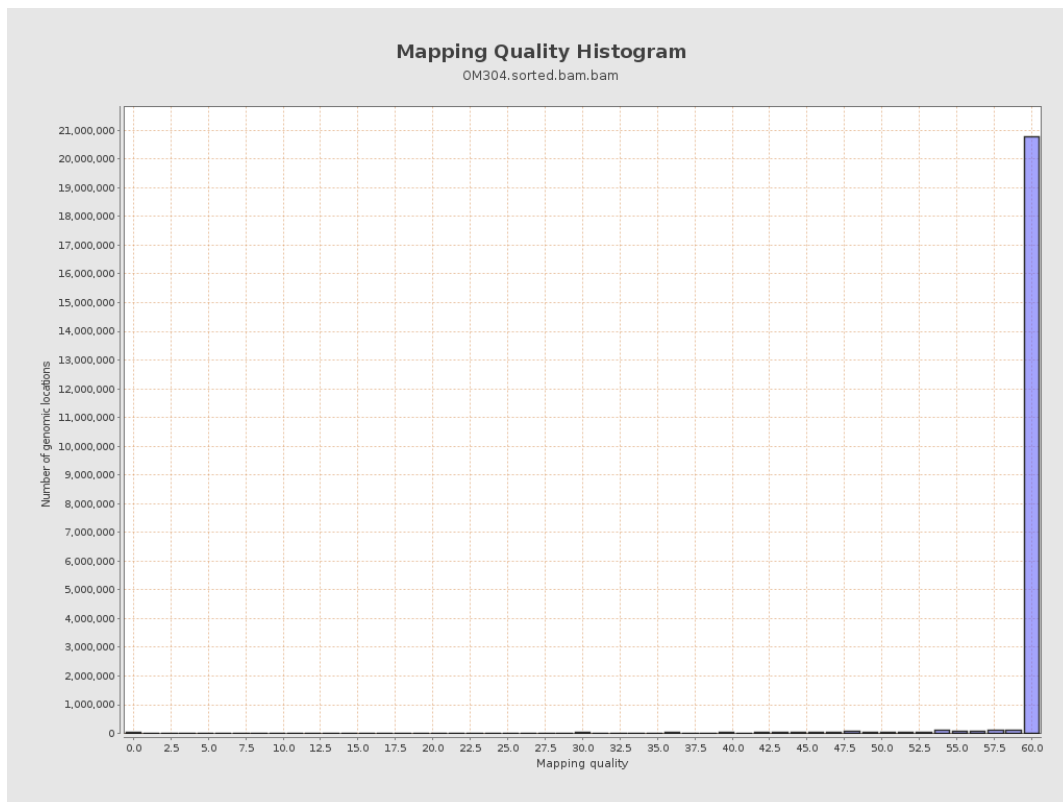
11. Results : Homopolymer Indels



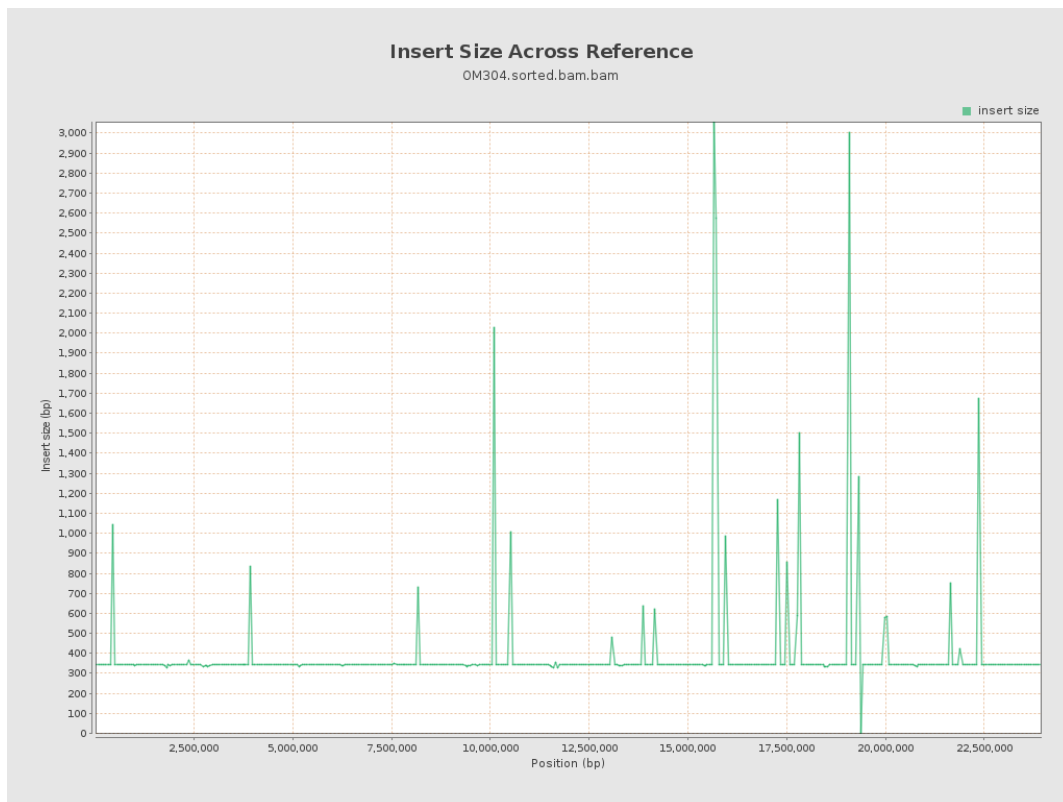
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

