

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2016/10/23 13:57:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM273.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/OM273-BiooBarcode26_ATGAGC_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM273-BiooBarcode26_ATGAGC_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 13:57:54 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM273.sorted.bam.

	bam
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2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	4,237,400
Mapped reads	2,039,732 / 48.14%
Unmapped reads	2,197,668 / 51.86%
Mapped paired reads	2,039,732 / 48.14%
Mapped reads, first in pair	1,016,775 / 24%
Mapped reads, second in pair	1,022,957 / 24.14%
Mapped reads, both in pair	1,991,830 / 47.01%
Mapped reads, singletons	47,902 / 1.13%
Read min/max/mean length	30 / 100 / 99.92
Duplicated reads (estimated)	238,009 / 5.62%
Duplication rate	8.04%
Clipped reads	258,100 / 6.09%

2.2. ACGT Content

Number/percentage of A's	59,114,480 / 30.2%
Number/percentage of C's	38,717,087 / 19.78%
Number/percentage of T's	59,257,637 / 30.27%
Number/percentage of G's	38,655,180 / 19.75%
Number/percentage of N's	16,248 / 0.01%
GC Percentage	39.53%

2.3. Coverage

Mean	8.1792
Standard Deviation	9.403

2.4. Mapping Quality

Mean Mapping Quality	58.69
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2.5. Insert size

Mean	820.91
Standard Deviation	23,783.59
P25/Median/P75	302 / 326 / 340

2.6. Mismatches and indels

General error rate	1.69%
Mismatches	3,155,416
Insertions	68,389
Mapped reads with at least one insertion	3.18%
Deletions	77,963
Mapped reads with at least one deletion	3.6%
Homopolymer indels	61.41%

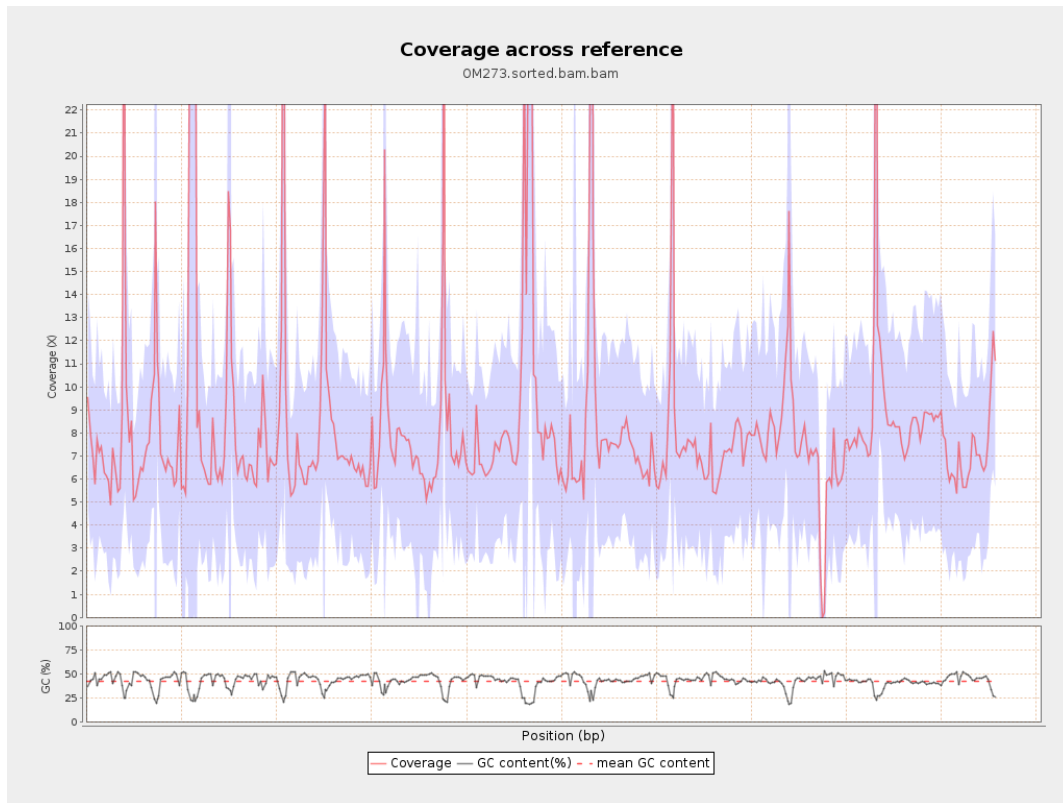
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

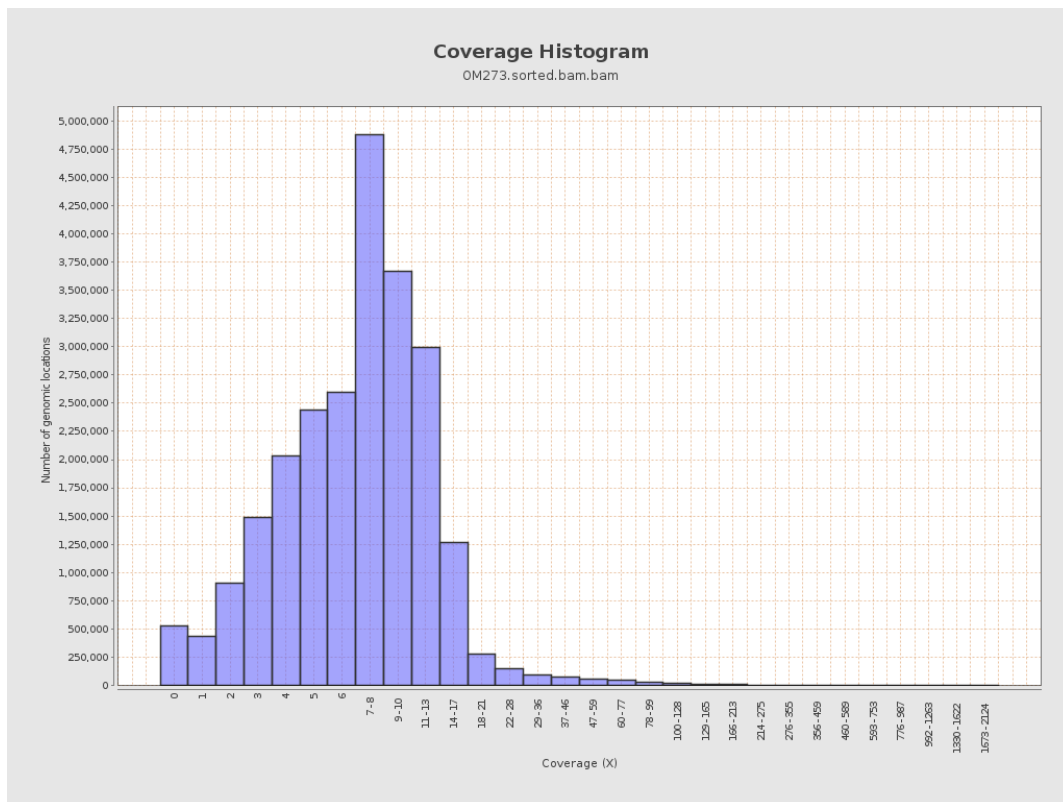
gi 1074120478 emb LT615256.1	977217	7160608	7.3276	6.3051
gi 1074120682 emb LT615257.1	860454	7190549	8.3567	8.0449
gi 1074120865 emb LT615258.1	989719	10100717	10.2056	15.8769
gi 1074121086 emb LT615259.1	935450	8430348	9.0121	16.4675
gi 1074121301 emb LT615260.1	1432239	12321096	8.6027	10.1308
gi 1074121615 emb LT615261.1	1080962	8516515	7.8786	7.4002
gi 1074121871 emb LT615262.1	1545099	11519468	7.4555	4.2475
gi 1074122235 emb LT615263.1	1585108	12384542	7.8131	6.3324
gi 1074122590 emb LT615264.1	2122358	16303651	7.6819	5.524
gi 1074123050 emb LT615265.1	1754192	17069468	9.7307	12.2508
gi 1074123421 emb LT615	2150147	18196150	8.4627	15.484

266.1				
gi 107412389 8 emb LT615 267.1	3031036	23272998	7.6782	4.5115
gi 107412458 8 emb LT615 268.1	2359348	18328376	7.7684	10.4605
gi 107412506 5 emb LT615 269.1	3135668	25171558	8.0275	3.861

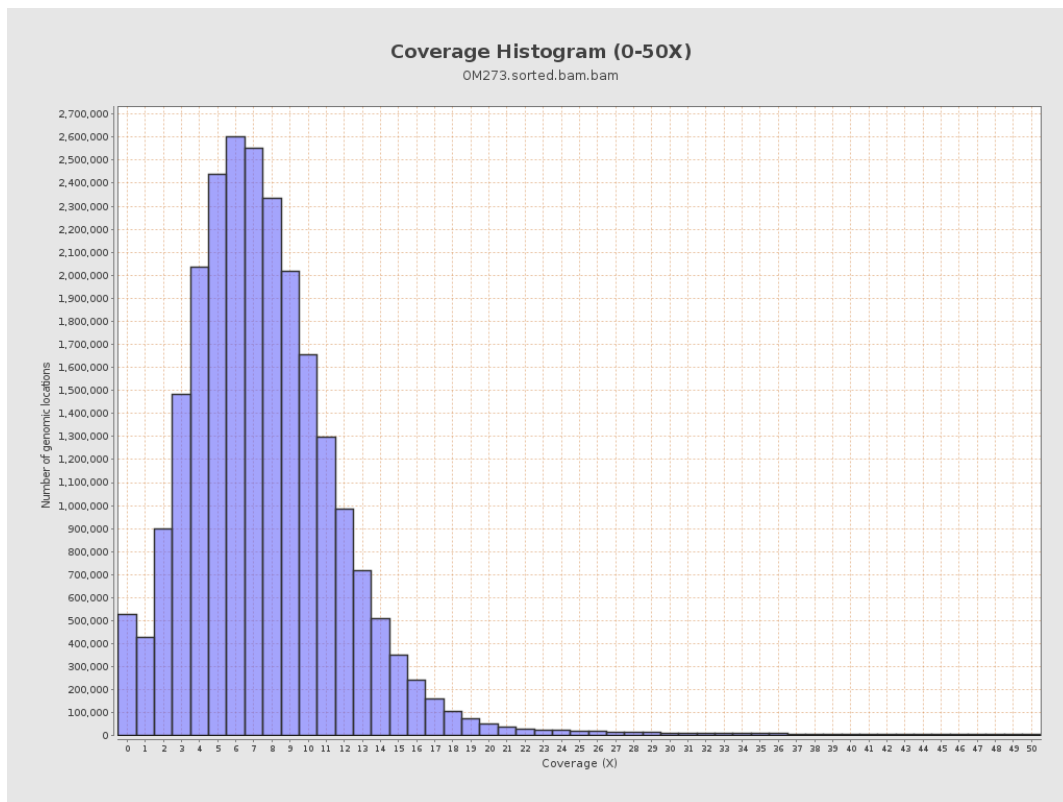
3. Results : Coverage across reference



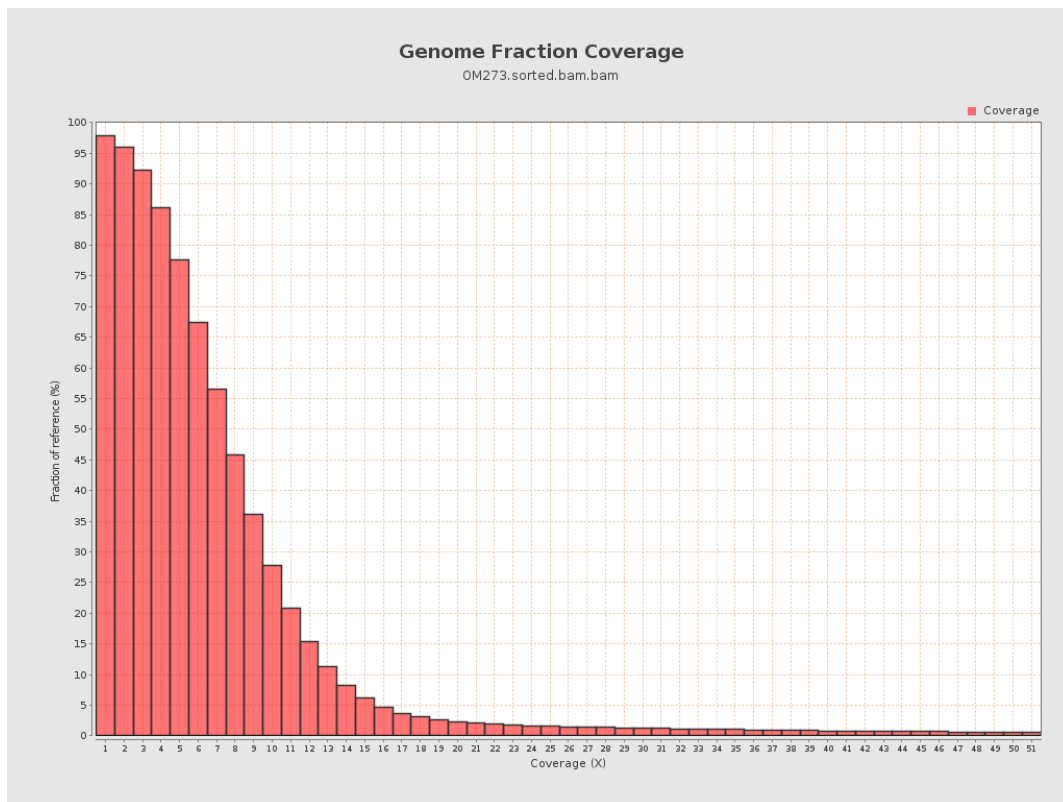
4. Results : Coverage Histogram



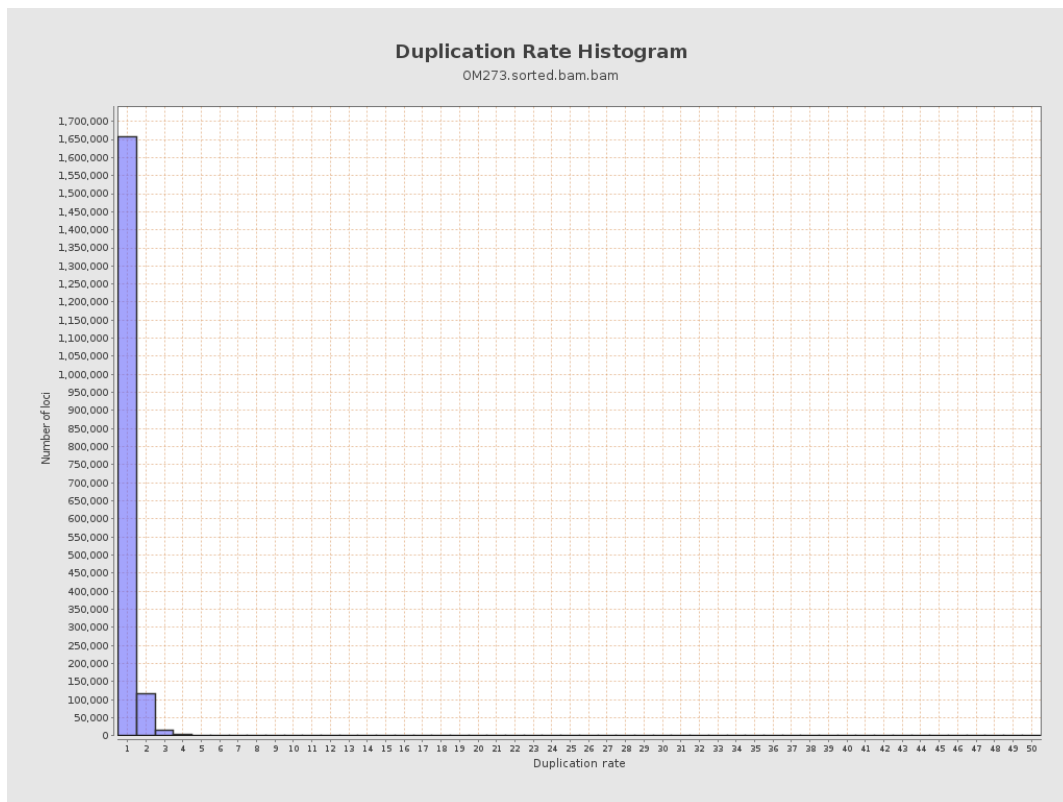
5. Results : Coverage Histogram (0-50X)



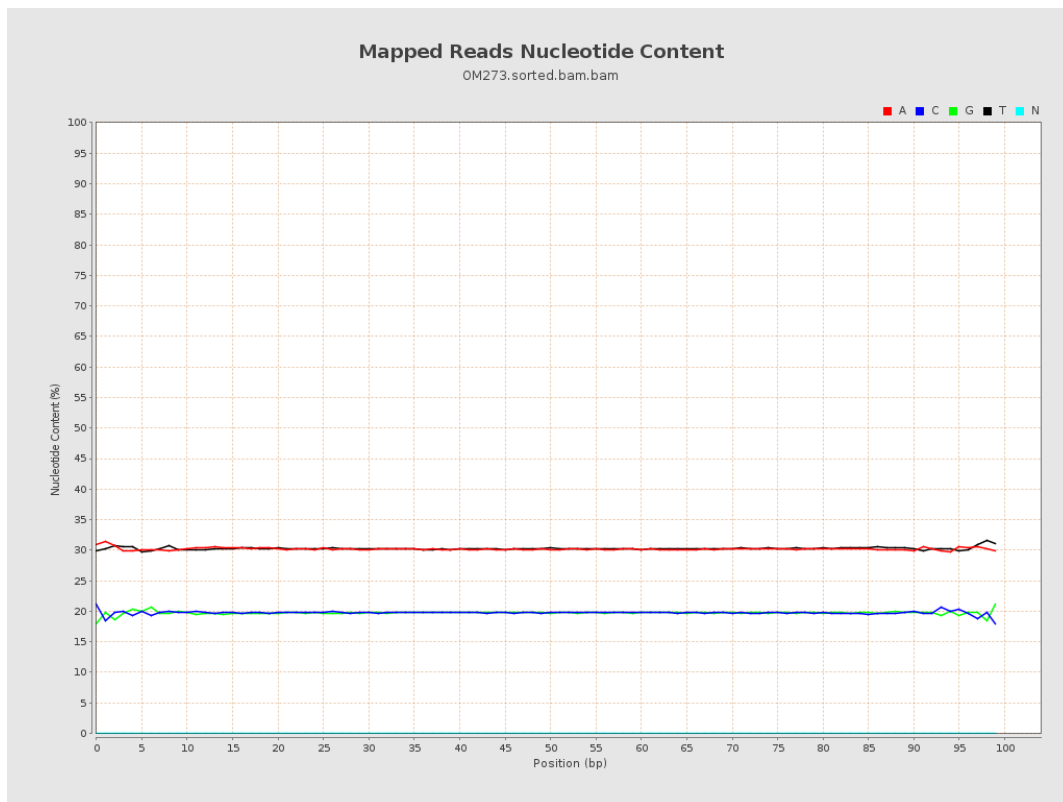
6. Results : Genome Fraction Coverage



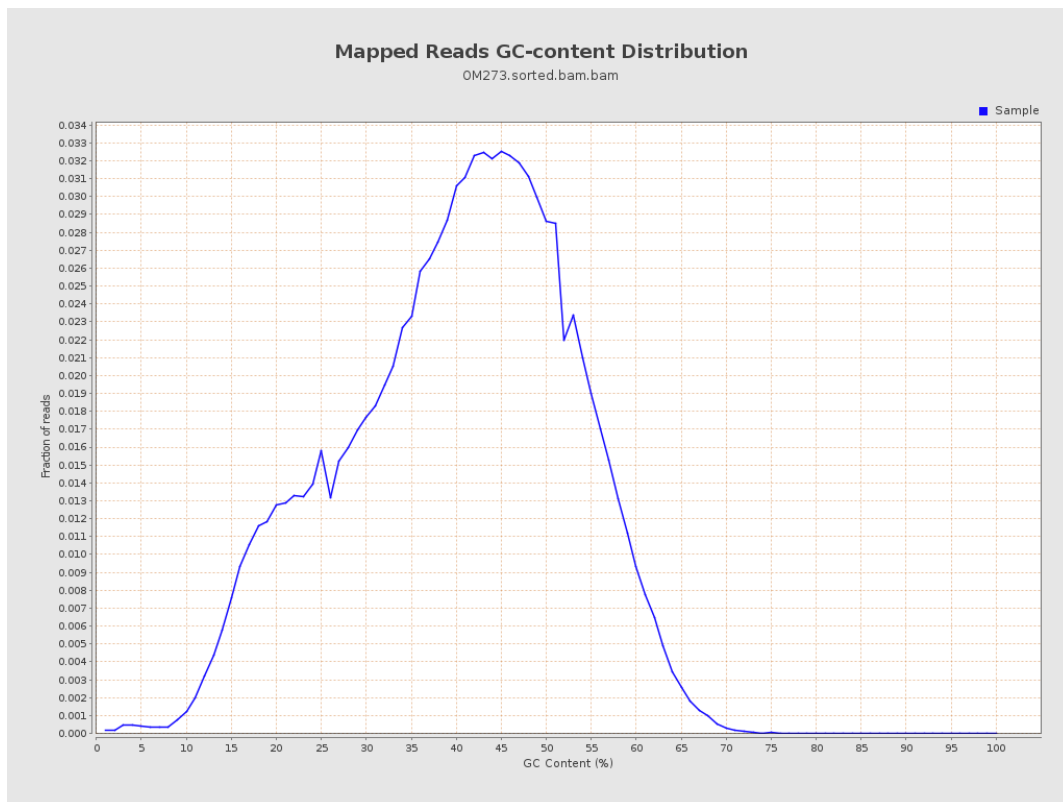
7. Results : Duplication Rate Histogram



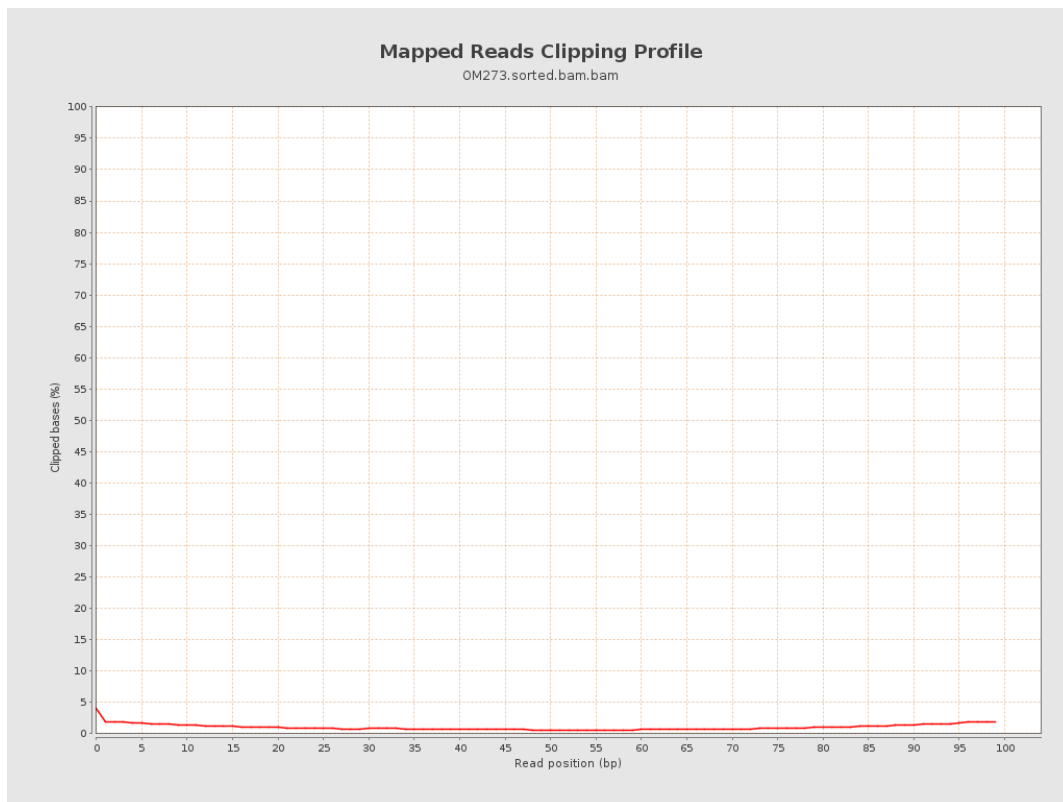
8. Results : Mapped Reads Nucleotide Content



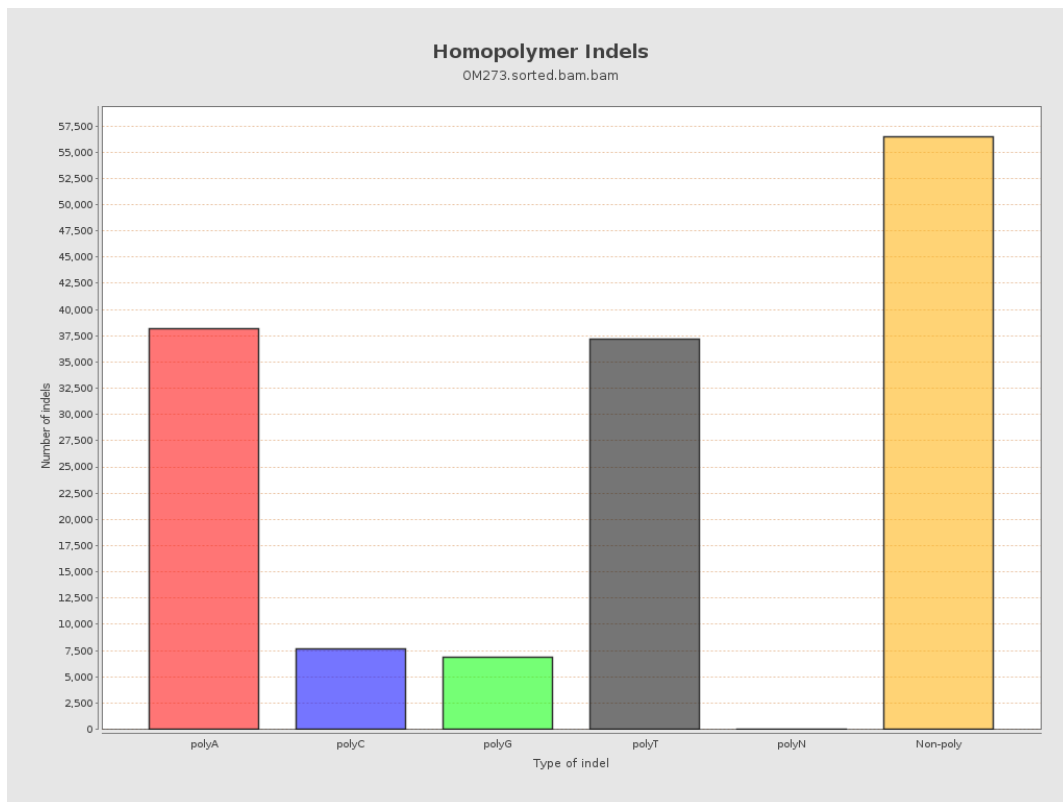
9. Results : Mapped Reads GC-content Distribution



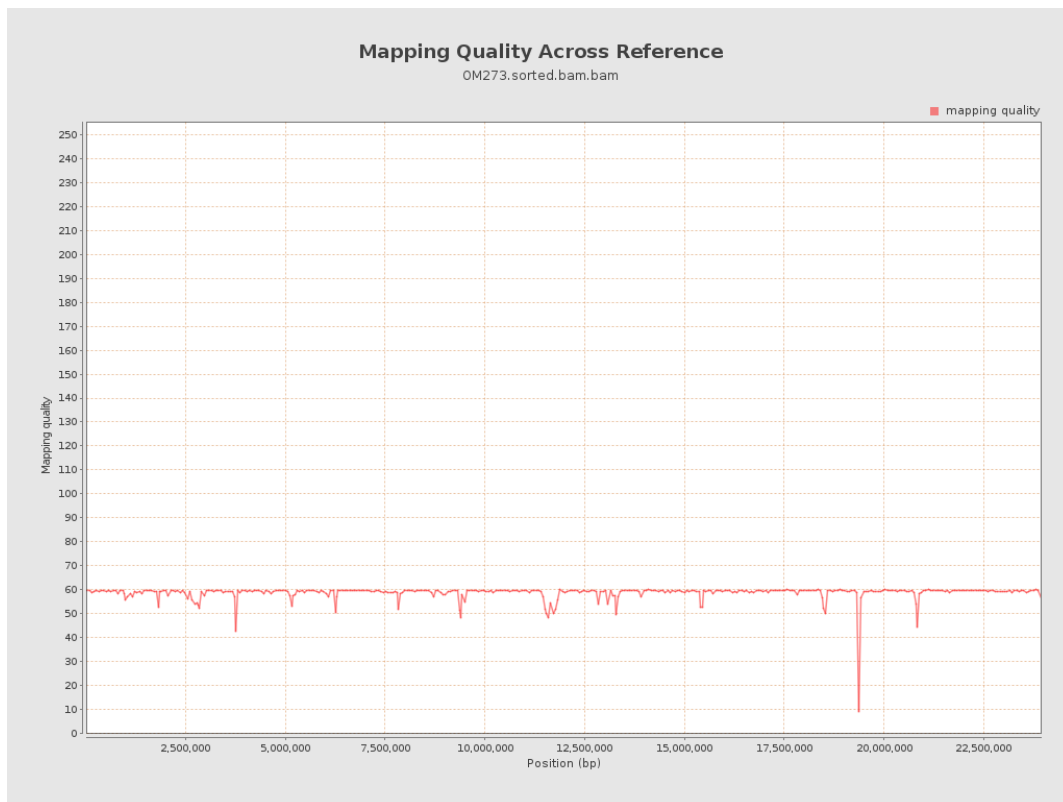
10. Results : Mapped Reads Clipping Profile



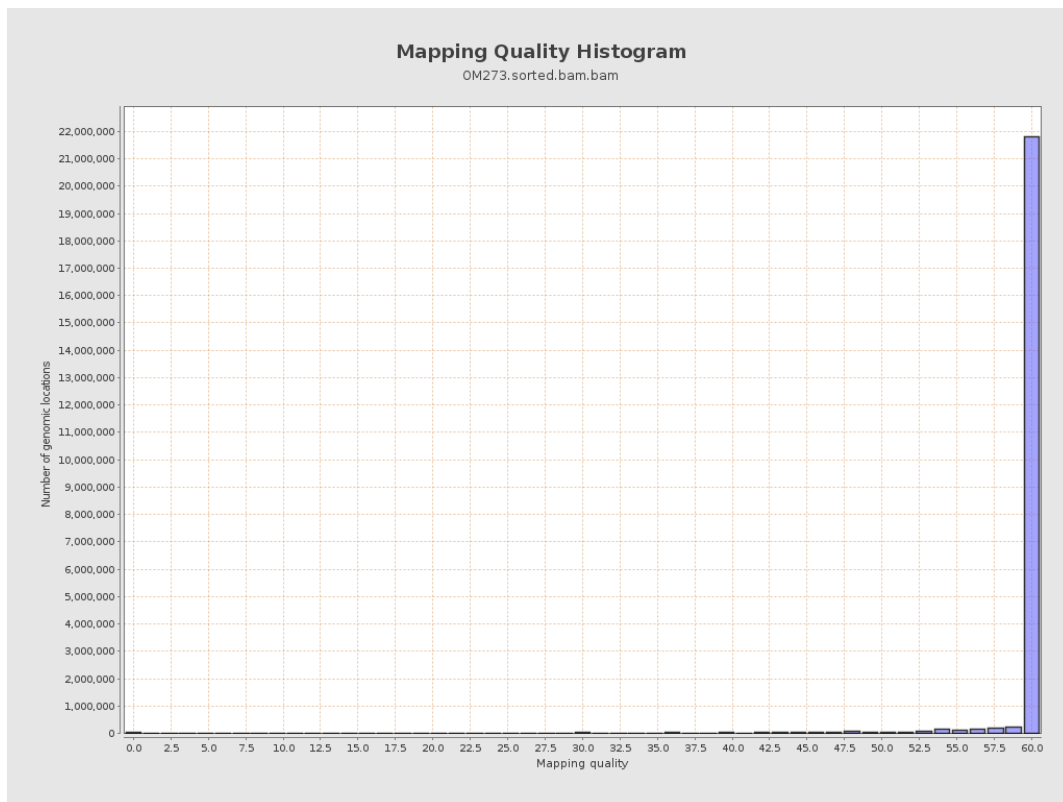
11. Results : Homopolymer Indels



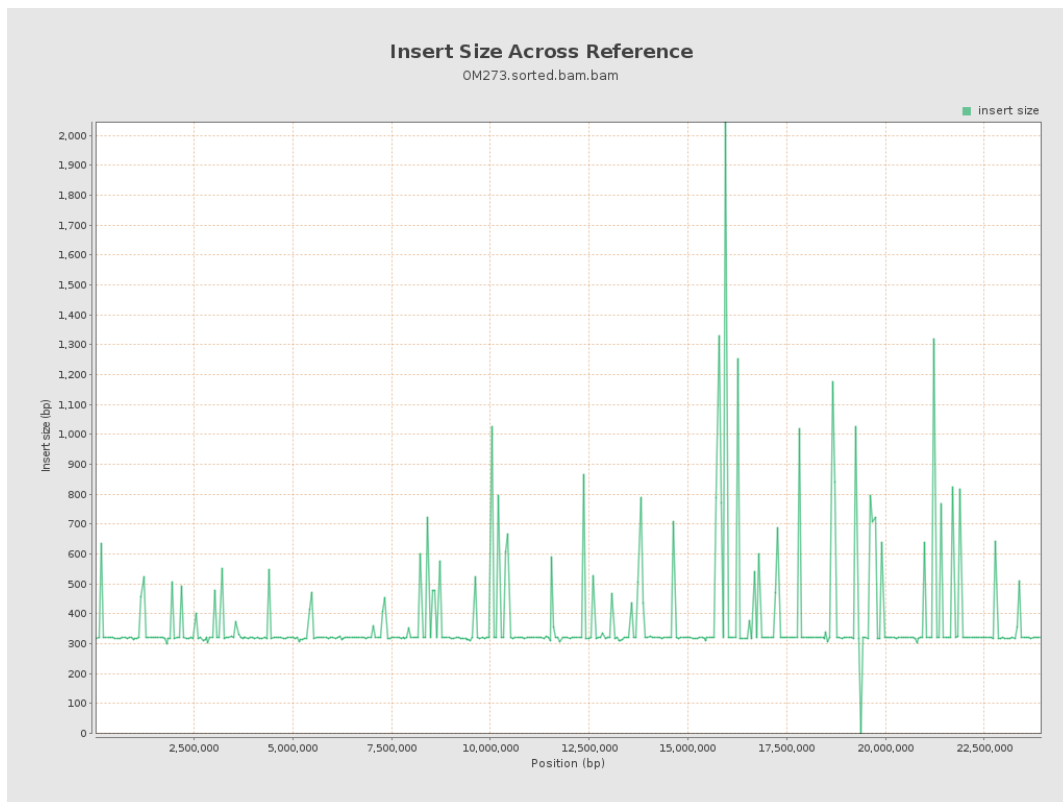
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

