

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2016/10/23 11:56:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM012.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/OM012-BiooBarcode1_CGATGT_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM012-BiooBarcode1_CGATGT_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 11:56:28 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM012.sorted.bam.bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	3,908,464
Mapped reads	887,242 / 22.7%
Unmapped reads	3,021,222 / 77.3%
Mapped paired reads	887,242 / 22.7%
Mapped reads, first in pair	445,045 / 11.39%
Mapped reads, second in pair	442,197 / 11.31%
Mapped reads, both in pair	852,331 / 21.81%
Mapped reads, singletons	34,911 / 0.89%
Read min/max/mean length	30 / 100 / 99.96
Duplicated reads (estimated)	71,546 / 1.83%
Duplication rate	5.67%
Clipped reads	114,763 / 2.94%

2.2. ACGT Content

Number/percentage of A's	25,422,112 / 30.05%
Number/percentage of C's	16,840,918 / 19.9%
Number/percentage of T's	25,562,037 / 30.21%
Number/percentage of G's	16,781,417 / 19.83%
Number/percentage of N's	7,137 / 0.01%
GC Percentage	39.74%

2.3. Coverage

Mean	3.5352
Standard Deviation	4.7246

2.4. Mapping Quality

Mean Mapping Quality	58.14
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2.5. Insert size

Mean	858.2
Standard Deviation	27,229.01
P25/Median/P75	286 / 297 / 308

2.6. Mismatches and indels

General error rate	1.52%
Mismatches	1,215,316
Insertions	28,974
Mapped reads with at least one insertion	3.09%
Deletions	33,037
Mapped reads with at least one deletion	3.48%
Homopolymer indels	63.1%

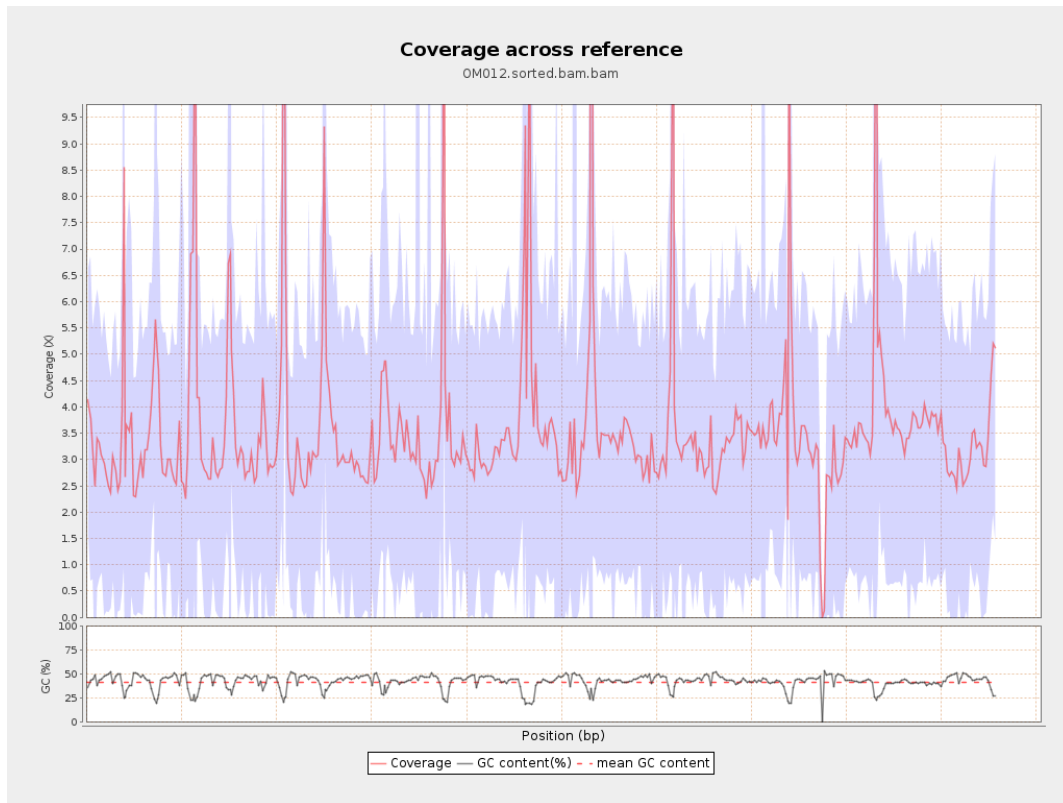
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

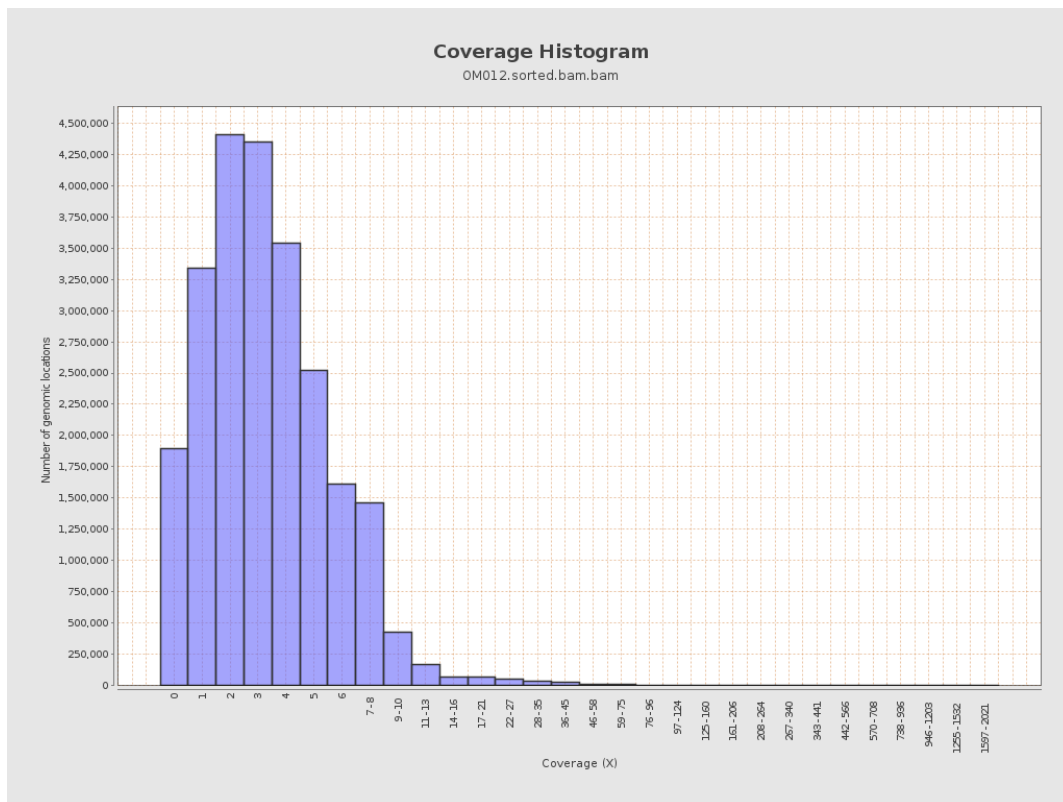
gi 1074120478 emb LT615256.1	977217	3069919	3.1415	2.5278
gi 1074120682 emb LT615257.1	860454	2921790	3.3956	3.3363
gi 1074120865 emb LT615258.1	989719	3532099	3.5688	4.3192
gi 1074121086 emb LT615259.1	935450	3595075	3.8432	5.6513
gi 1074121301 emb LT615260.1	1432239	5243600	3.6611	4.2548
gi 1074121615 emb LT615261.1	1080962	3954566	3.6584	4.0761
gi 1074121871 emb LT615262.1	1545099	5063255	3.277	2.3406
gi 1074122235 emb LT615263.1	1585108	5566126	3.5115	5.8989
gi 1074122590 emb LT615264.1	2122358	7067088	3.3298	2.4336
gi 1074123050 emb LT615265.1	1754192	6776749	3.8632	9.4144
gi 1074123421 emb LT615	2150147	7842896	3.6476	6.6679

266.1				
gi 107412389 8 emb LT615 267.1	3031036	10509842	3.4674	3.6278
gi 107412458 8 emb LT615 268.1	2359348	8381414	3.5524	4.1673
gi 107412506 5 emb LT615 269.1	3135668	11174580	3.5637	2.3896

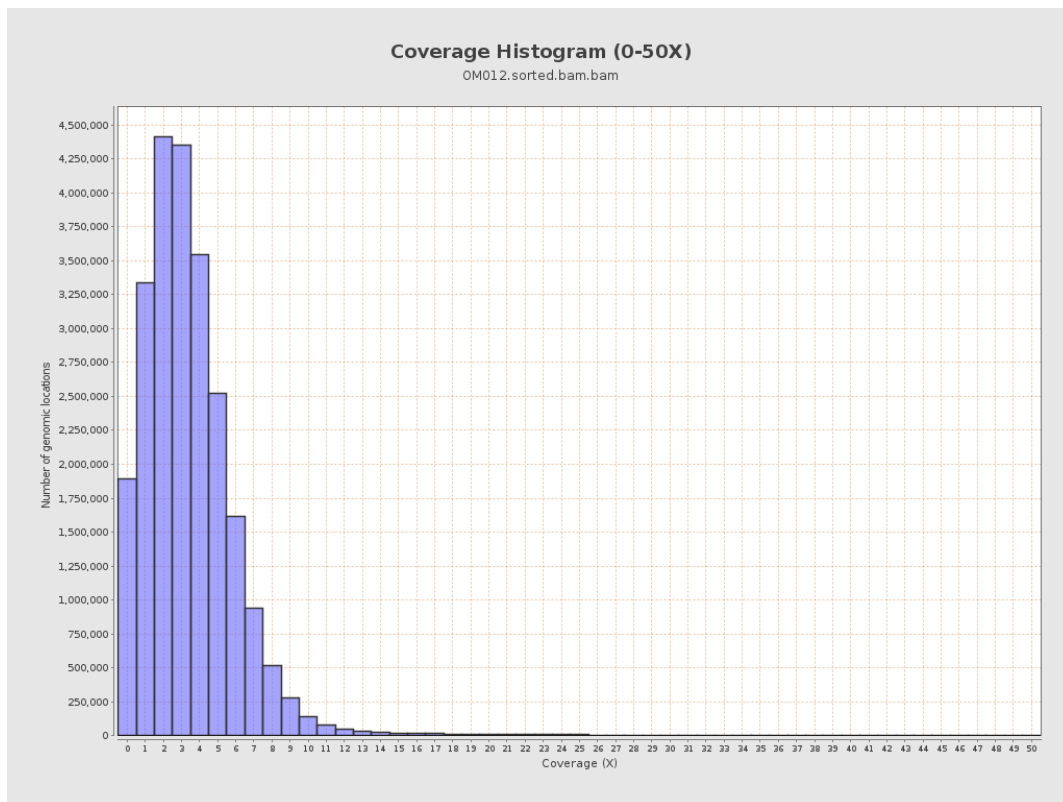
3. Results : Coverage across reference



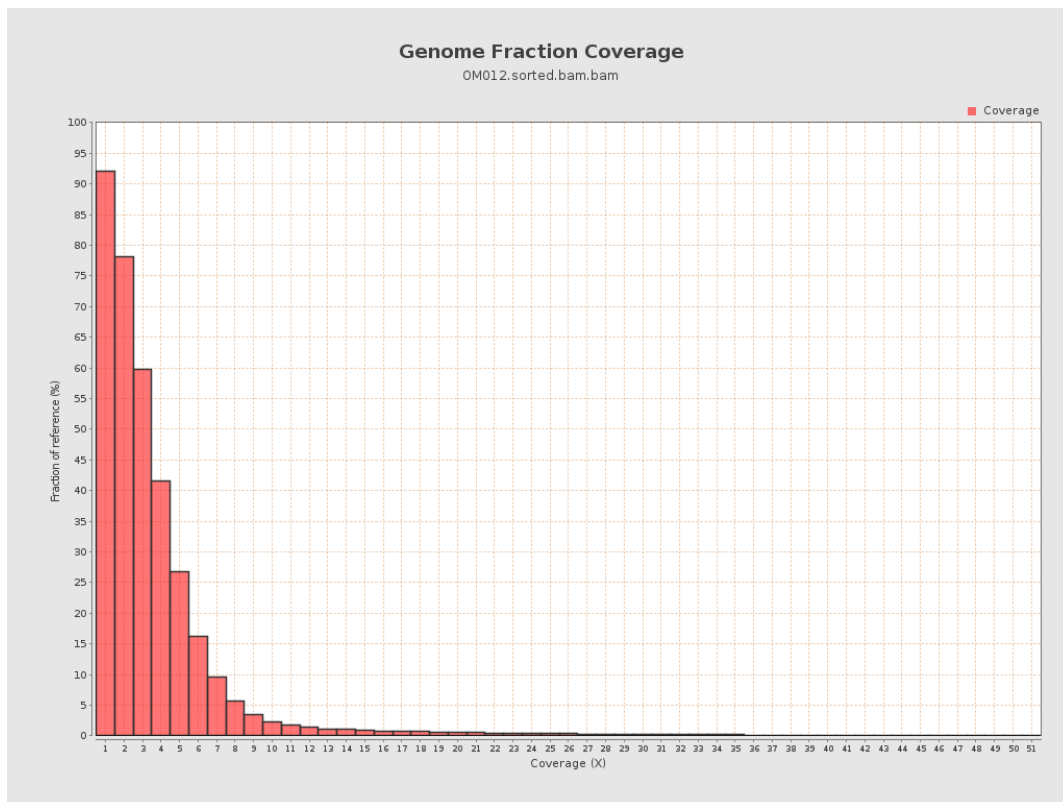
4. Results : Coverage Histogram



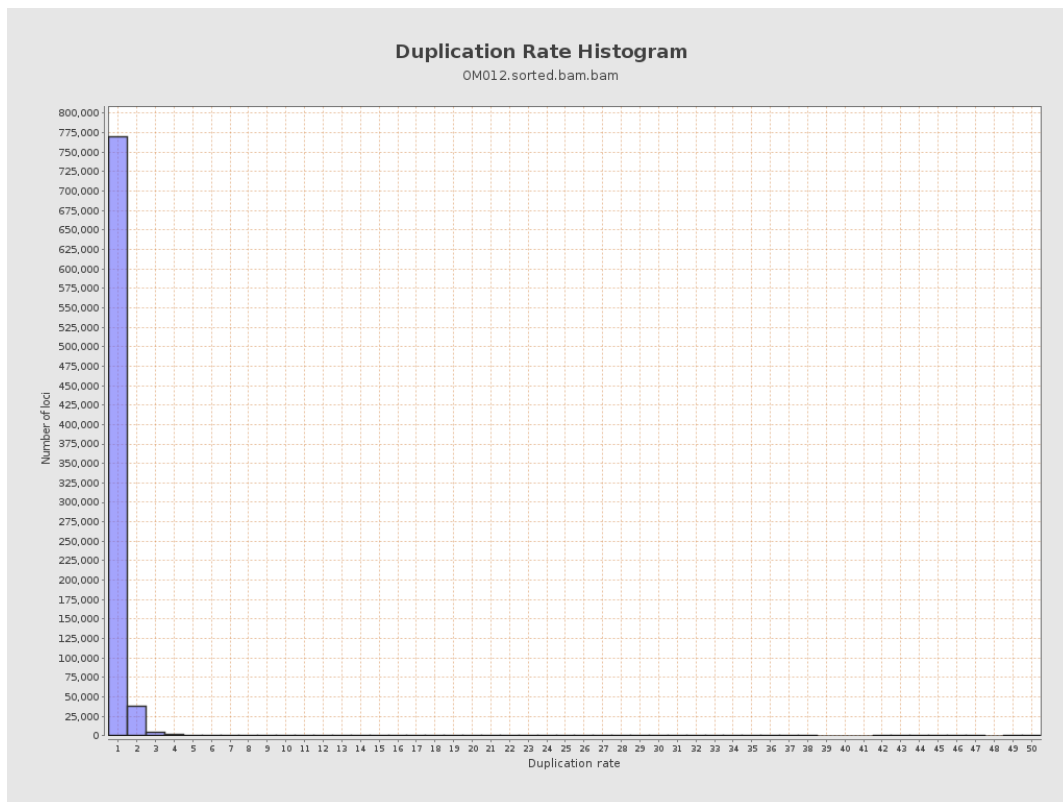
5. Results : Coverage Histogram (0-50X)



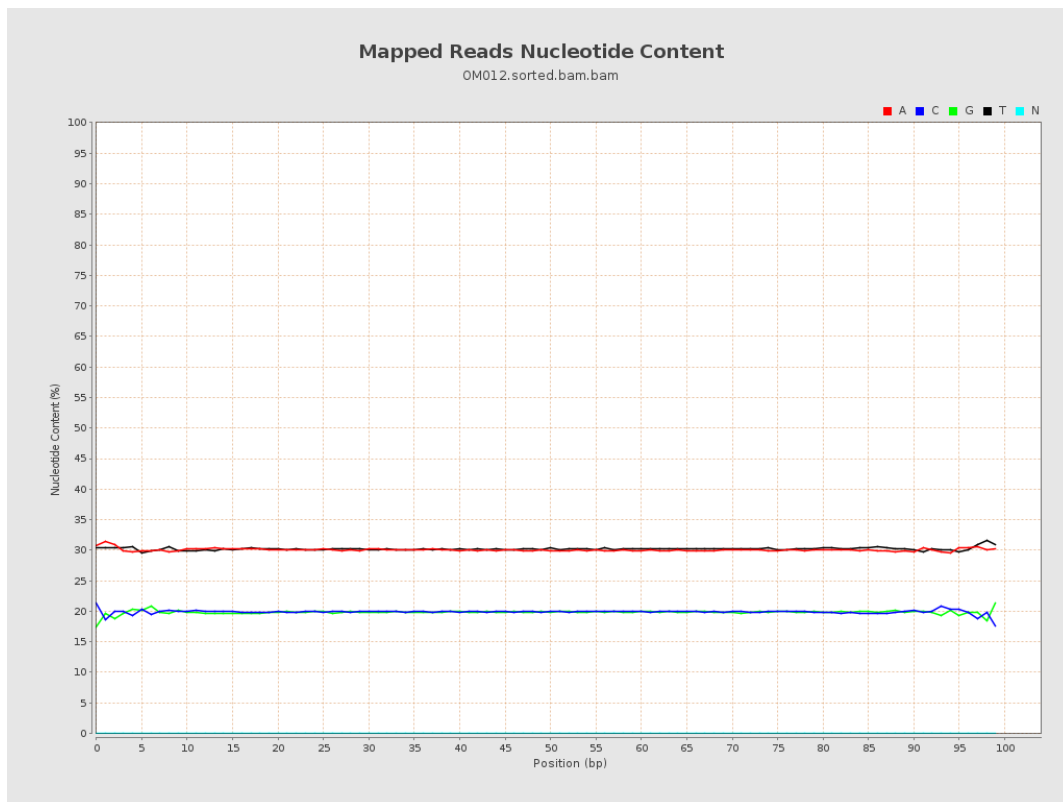
6. Results : Genome Fraction Coverage



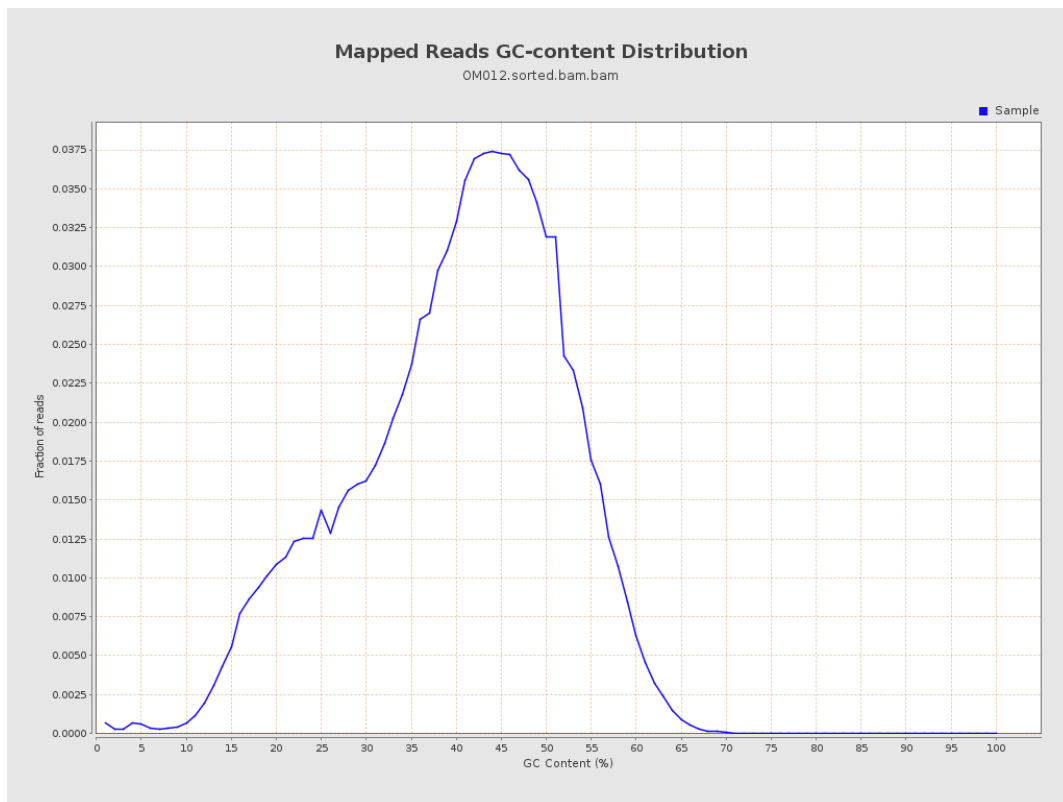
7. Results : Duplication Rate Histogram



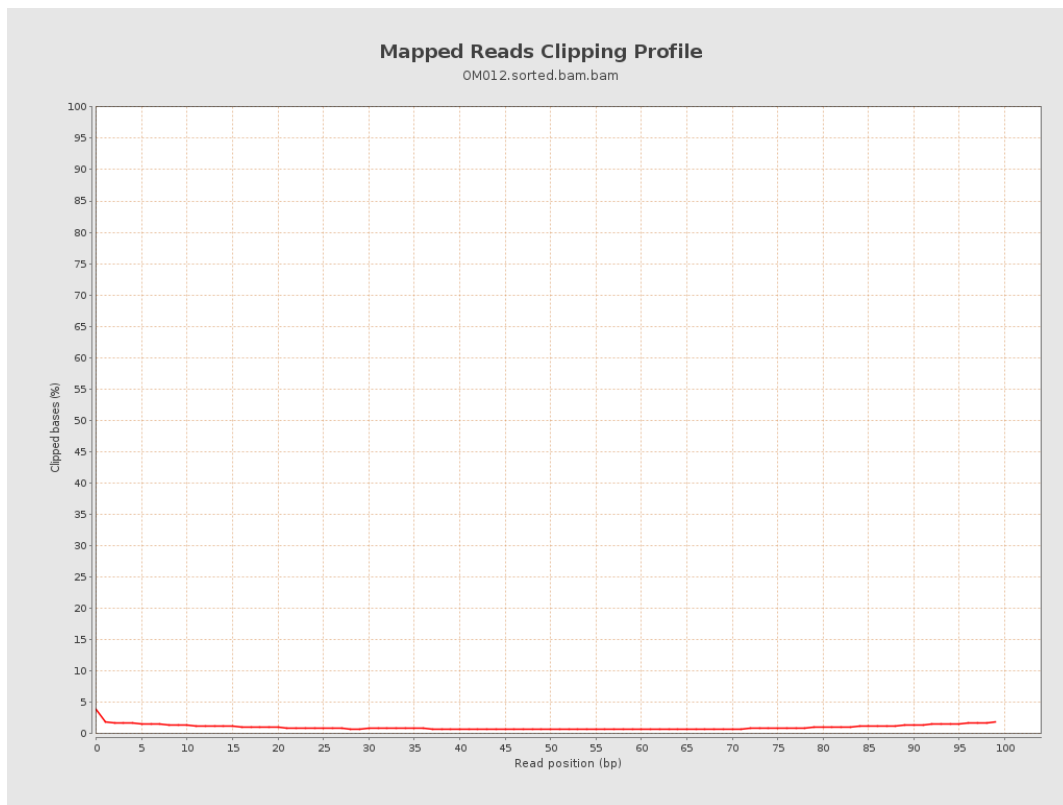
8. Results : Mapped Reads Nucleotide Content



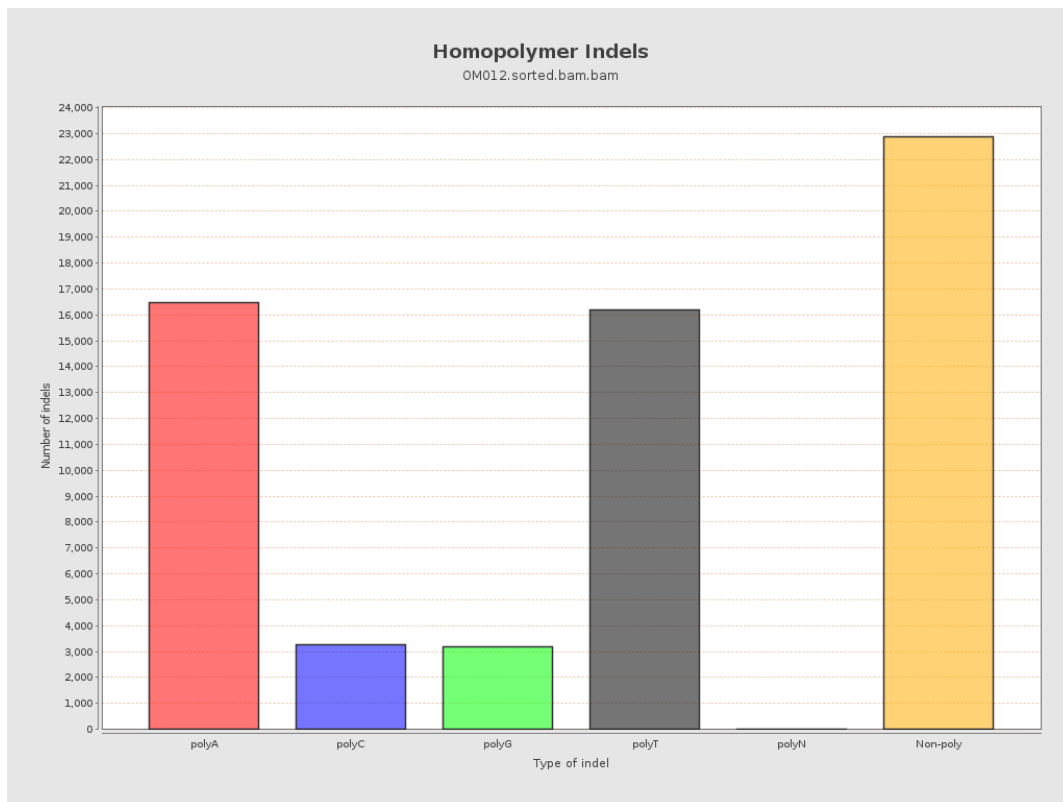
9. Results : Mapped Reads GC-content Distribution



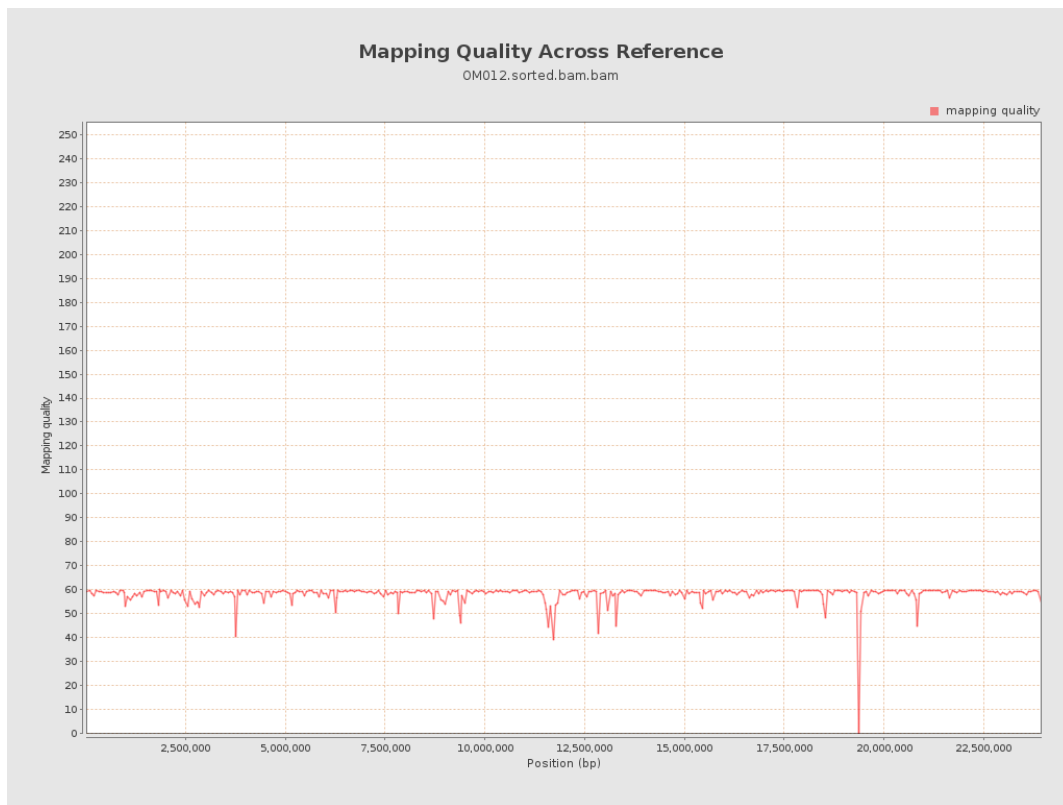
10. Results : Mapped Reads Clipping Profile



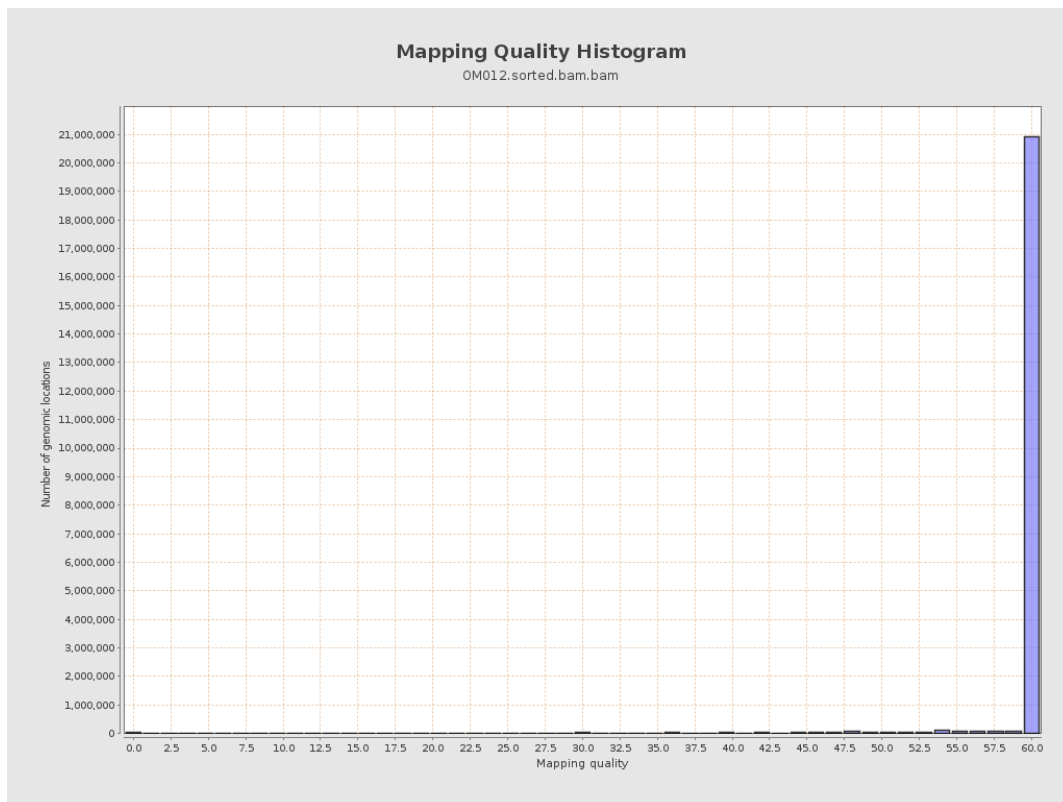
11. Results : Homopolymer Indels



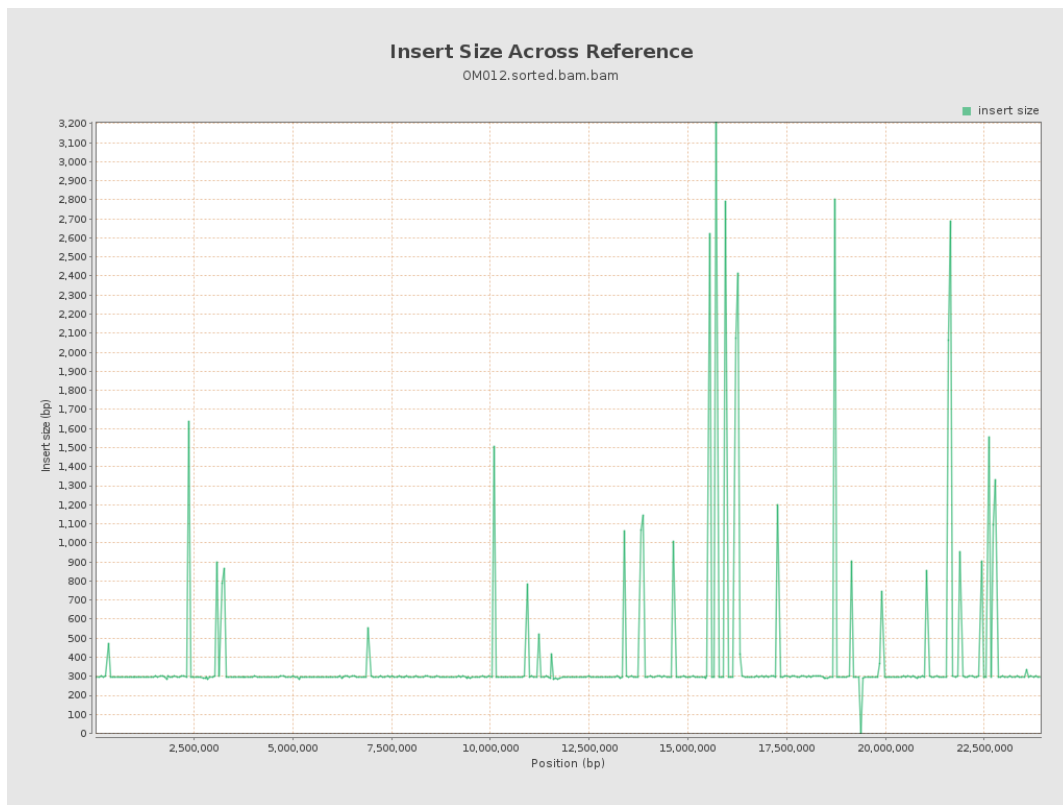
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

