

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2016/10/23 14:09:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM303.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/OM303-BiooBarcode35_CATTTT_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM303-BiooBarcode35_CATTTT_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 14:09:18 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM303.sorted.bam.

	bam
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2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	12,186,688
Mapped reads	2,241,937 / 18.4%
Unmapped reads	9,944,751 / 81.6%
Mapped paired reads	2,241,937 / 18.4%
Mapped reads, first in pair	1,125,915 / 9.24%
Mapped reads, second in pair	1,116,022 / 9.16%
Mapped reads, both in pair	2,141,027 / 17.57%
Mapped reads, singletons	100,910 / 0.83%
Read min/max/mean length	30 / 100 / 99.96
Duplicated reads (estimated)	658,815 / 5.41%
Duplication rate	27.54%
Clipped reads	285,978 / 2.35%

2.2. ACGT Content

Number/percentage of A's	62,921,492 / 29.49%
Number/percentage of C's	43,630,723 / 20.45%
Number/percentage of T's	63,270,951 / 29.66%
Number/percentage of G's	43,517,194 / 20.4%
Number/percentage of N's	11,339 / 0.01%
GC Percentage	40.85%

2.3. Coverage

Mean	8.9138
Standard Deviation	13.7307

2.4. Mapping Quality

Mean Mapping Quality	58.1
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2.5. Insert size

Mean	794.78
Standard Deviation	23,682.77
P25/Median/P75	287 / 305 / 319

2.6. Mismatches and indels

General error rate	1.29%
Mismatches	2,586,788
Insertions	67,771
Mapped reads with at least one insertion	2.85%
Deletions	77,208
Mapped reads with at least one deletion	3.2%
Homopolymer indels	62.87%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

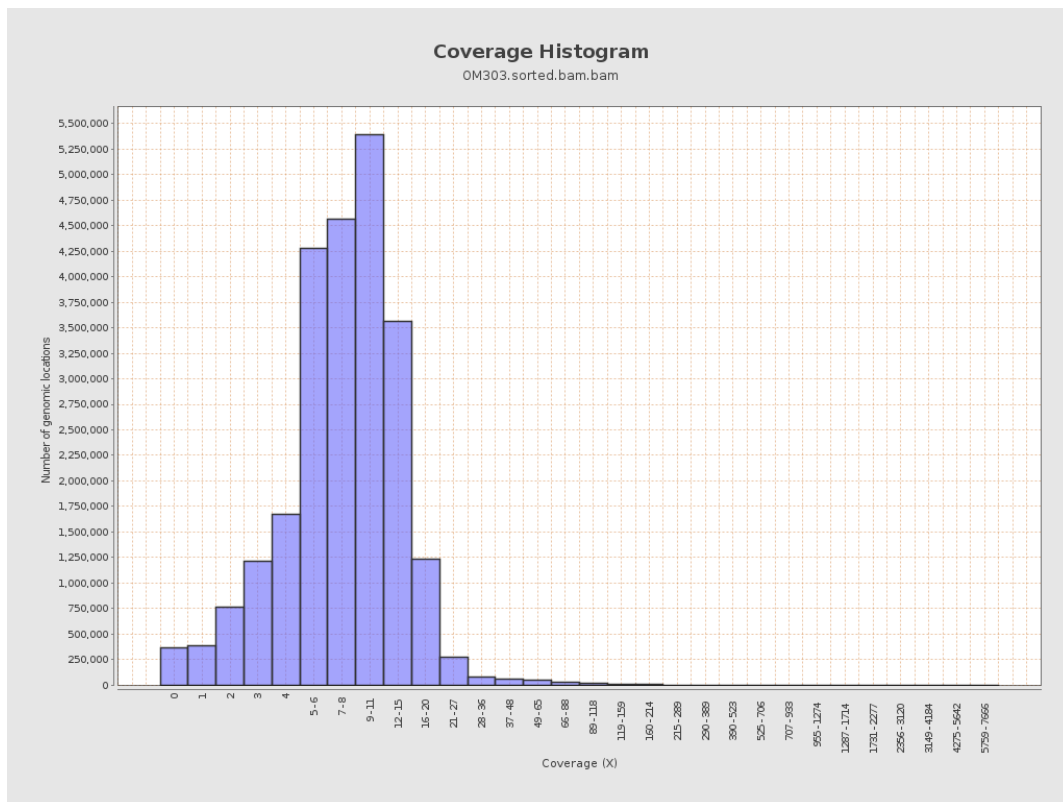
gi 1074120478 emb LT615256.1	977217	7951662	8.137	5.555
gi 1074120682 emb LT615257.1	860454	7570126	8.7978	7.6286
gi 1074120865 emb LT615258.1	989719	9929973	10.0331	13.3991
gi 1074121086 emb LT615259.1	935450	9118357	9.7476	14.1315
gi 1074121301 emb LT615260.1	1432239	13261705	9.2594	11.009
gi 1074121615 emb LT615261.1	1080962	9705964	8.979	8.4987
gi 1074121871 emb LT615262.1	1545099	13212635	8.5513	5.1582
gi 1074122235 emb LT615263.1	1585108	14092668	8.8907	14.6689
gi 1074122590 emb LT615264.1	2122358	18092153	8.5246	5.403
gi 1074123050 emb LT615265.1	1754192	16047123	9.1479	33.2558
gi 1074123421 emb LT615	2150147	20324019	9.4524	20.6235

266.1				
gi 107412389 8 emb LT615 267.1	3031036	26414787	8.7148	9.373
gi 107412458 8 emb LT615 268.1	2359348	20075954	8.5091	8.6973
gi 107412506 5 emb LT615 269.1	3135668	27768265	8.8556	4.8178

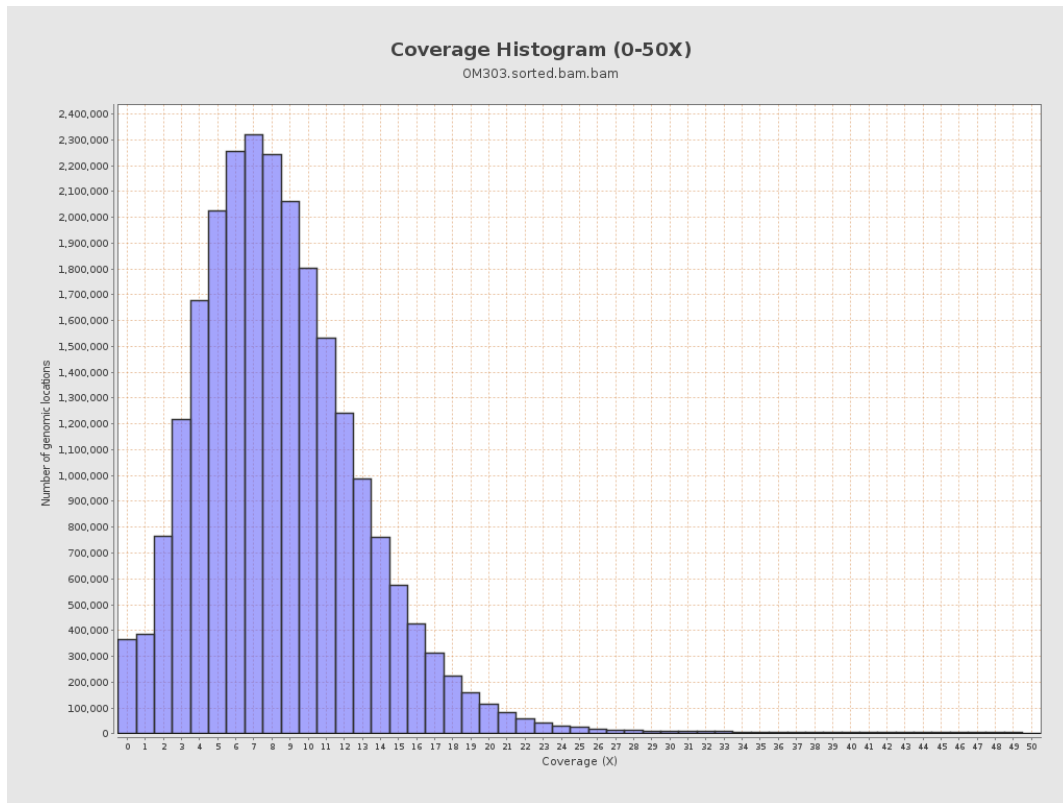
3. Results : Coverage across reference



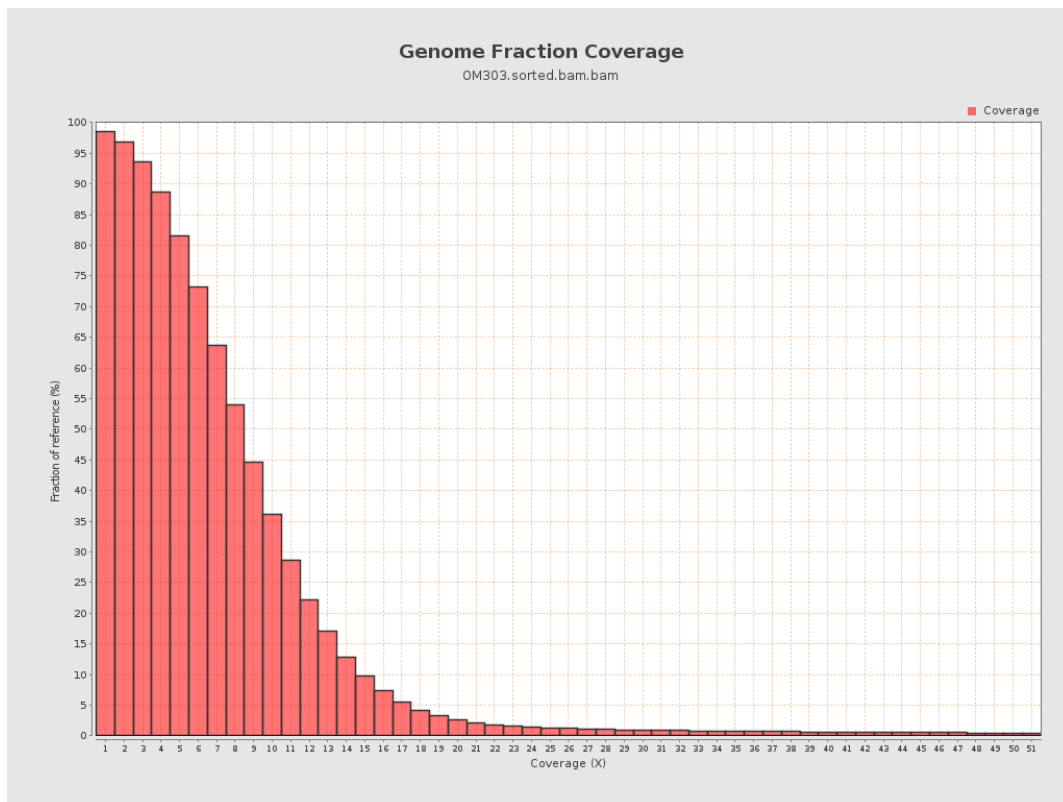
4. Results : Coverage Histogram



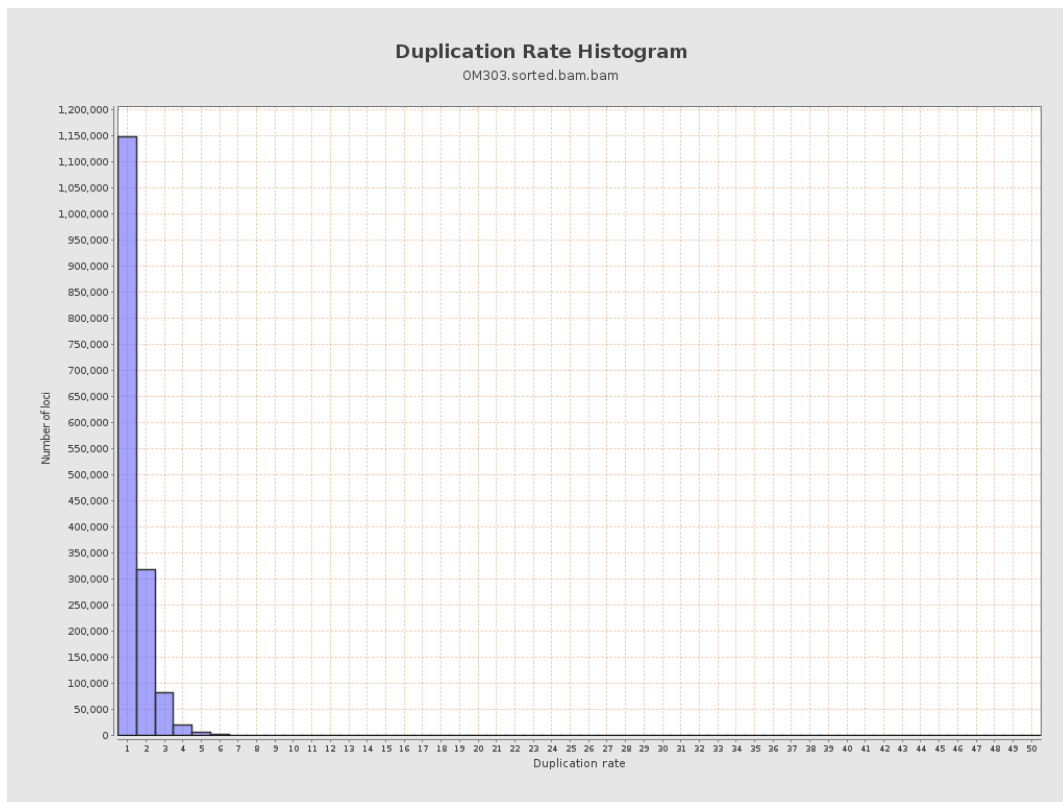
5. Results : Coverage Histogram (0-50X)



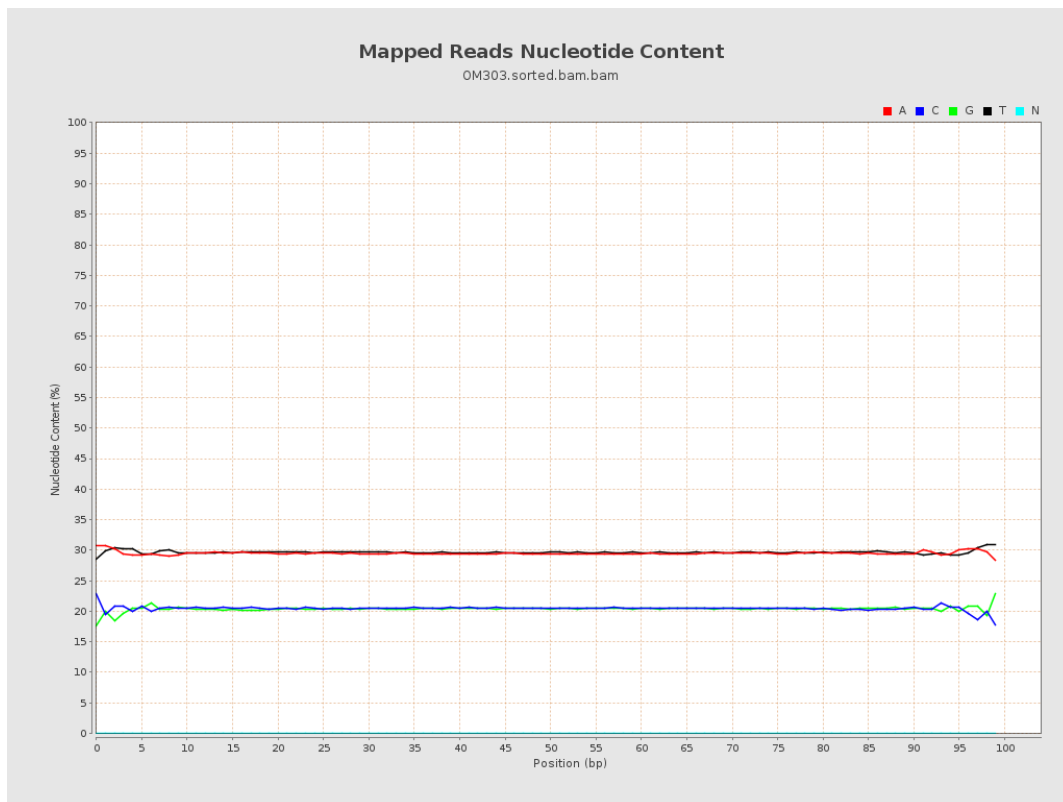
6. Results : Genome Fraction Coverage



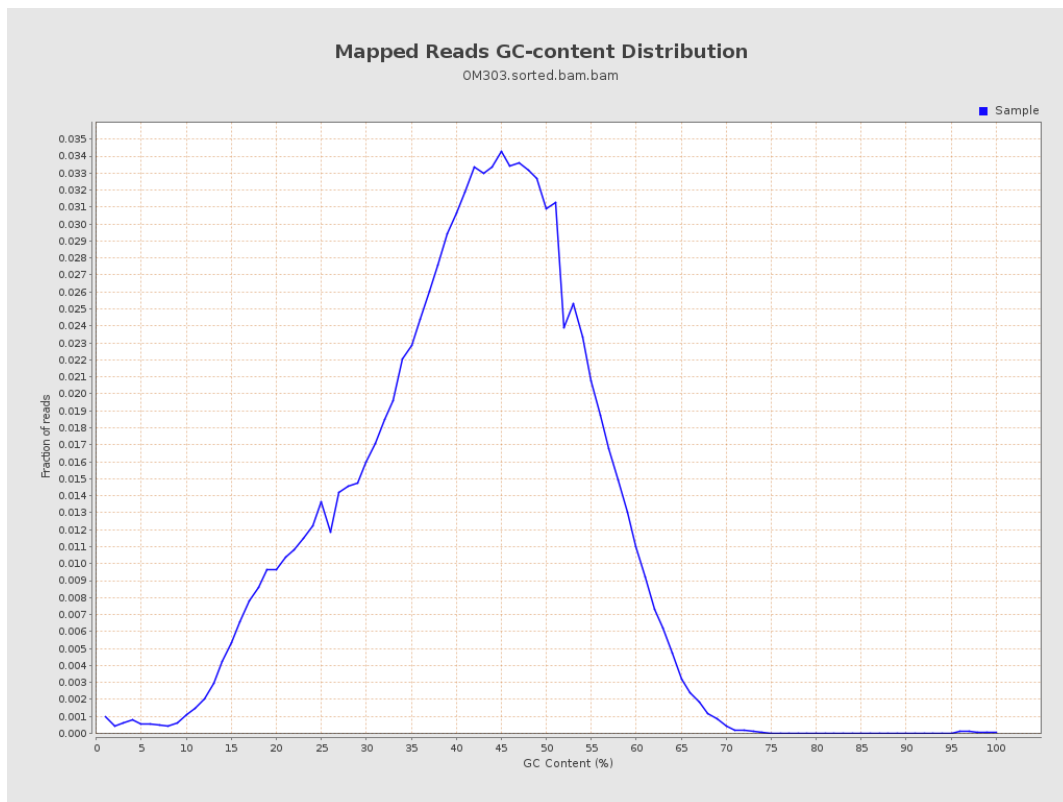
7. Results : Duplication Rate Histogram



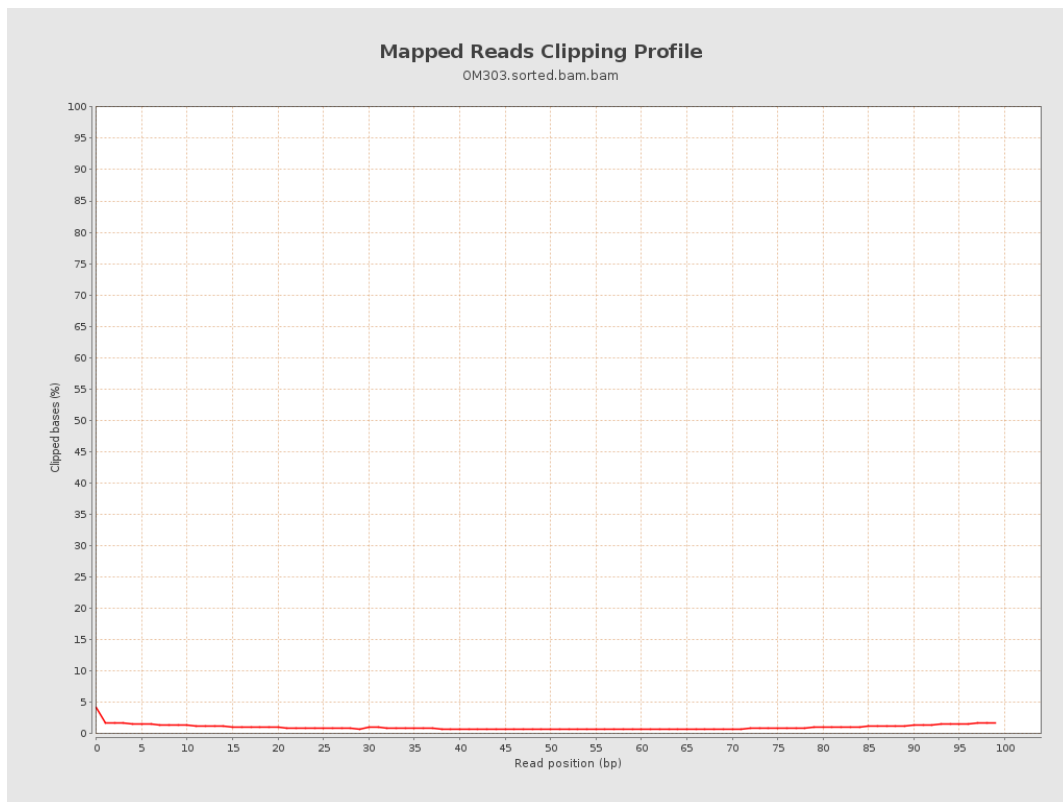
8. Results : Mapped Reads Nucleotide Content



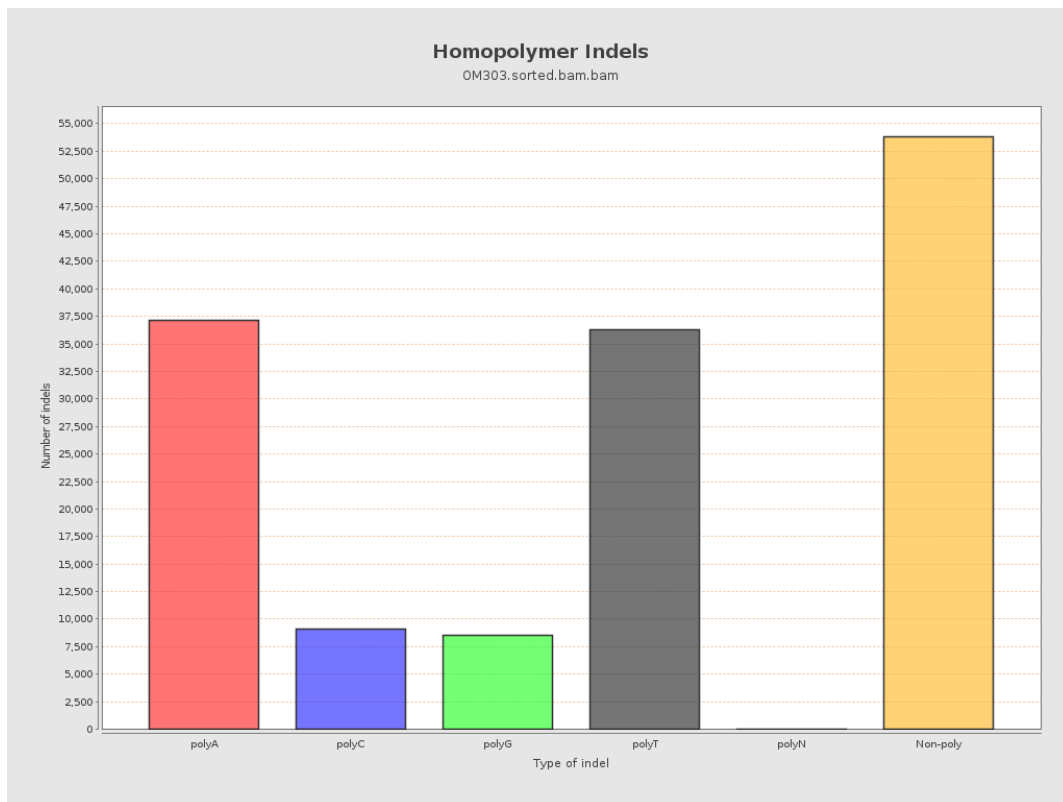
9. Results : Mapped Reads GC-content Distribution



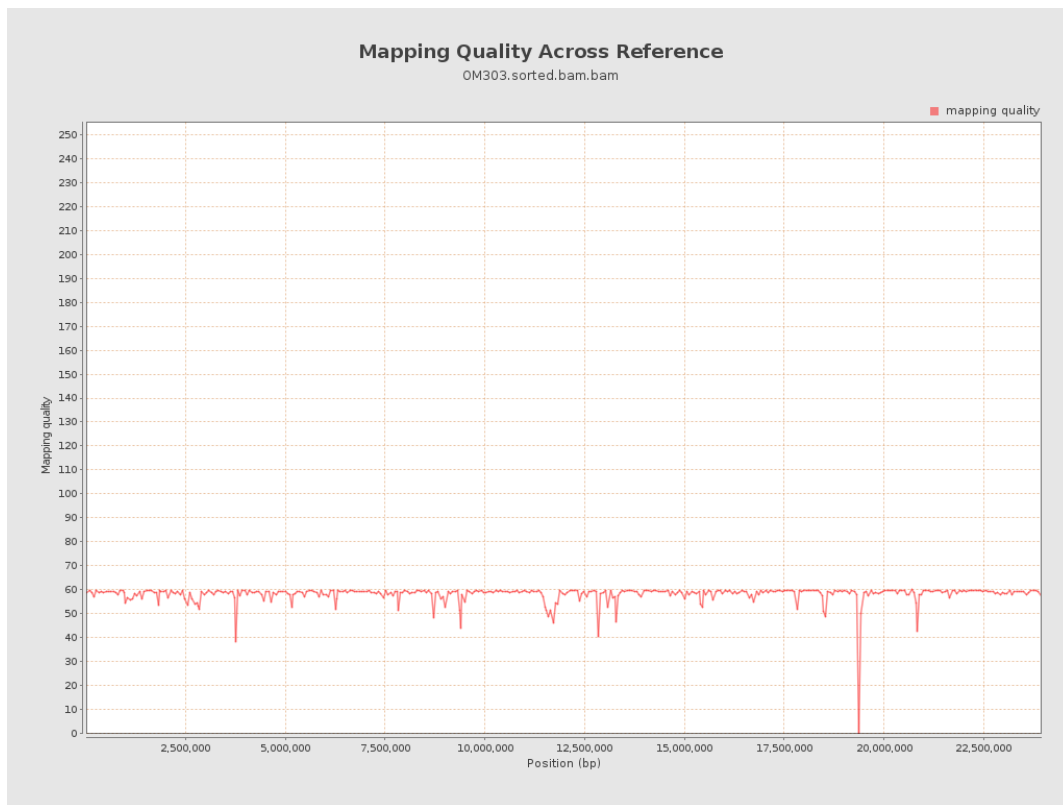
10. Results : Mapped Reads Clipping Profile



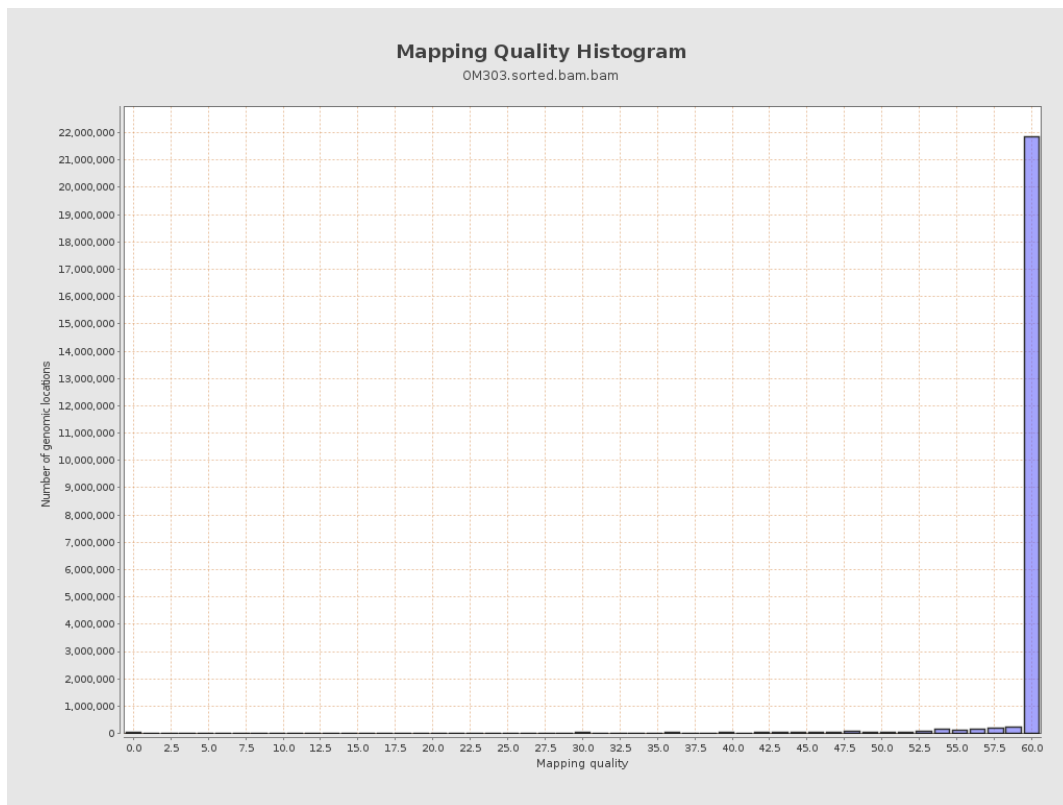
11. Results : Homopolymer Indels



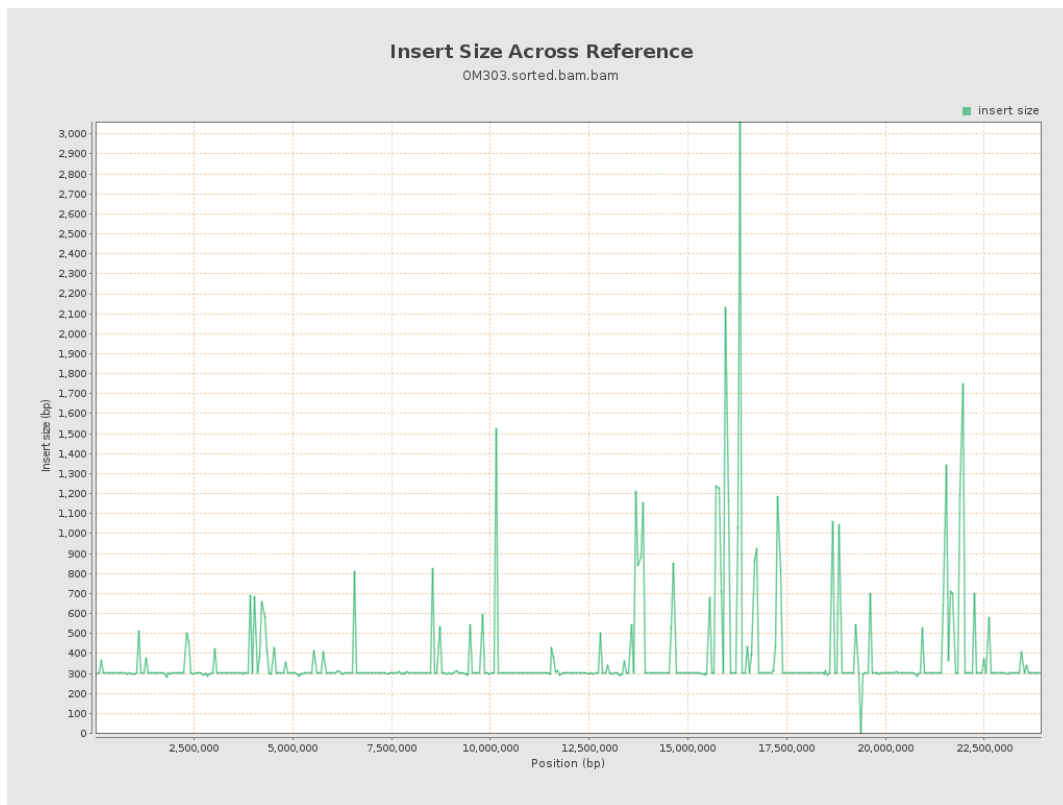
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

