

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2016/10/23 14:25:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM325.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/OM325-BiooBarcode35_CATTTT_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM325-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 14:25:48 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM325.sorted.bam.

	bam
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2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	27,168,106
Mapped reads	3,538,026 / 13.02%
Unmapped reads	23,630,080 / 86.98%
Mapped paired reads	3,538,026 / 13.02%
Mapped reads, first in pair	1,780,337 / 6.55%
Mapped reads, second in pair	1,757,689 / 6.47%
Mapped reads, both in pair	3,312,826 / 12.19%
Mapped reads, singletons	225,200 / 0.83%
Read min/max/mean length	30 / 100 / 99.97
Duplicated reads (estimated)	725,468 / 2.67%
Duplication rate	14.6%
Clipped reads	542,354 / 2%

2.2. ACGT Content

Number/percentage of A's	100,504,678 / 30.21%
Number/percentage of C's	65,530,841 / 19.7%
Number/percentage of T's	101,243,231 / 30.44%
Number/percentage of G's	65,374,123 / 19.65%
Number/percentage of N's	27,060 / 0.01%
GC Percentage	39.35%

2.3. Coverage

Mean	13.8999
Standard Deviation	27.1862

2.4. Mapping Quality

Mean Mapping Quality	57.57
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2.5. Insert size

Mean	1,002.59
Standard Deviation	31,250.27
P25/Median/P75	333 / 348 / 357

2.6. Mismatches and indels

General error rate	1.63%
Mismatches	5,149,736
Insertions	116,034
Mapped reads with at least one insertion	3.08%
Deletions	133,381
Mapped reads with at least one deletion	3.48%
Homopolymer indels	61.8%

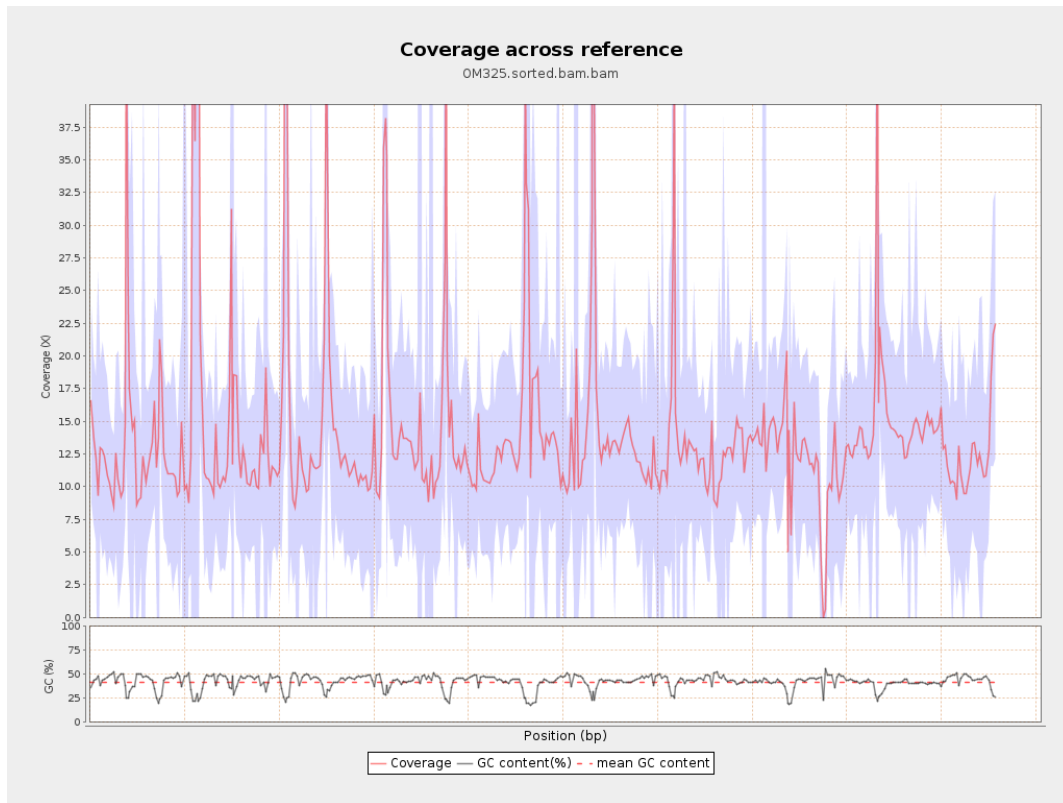
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

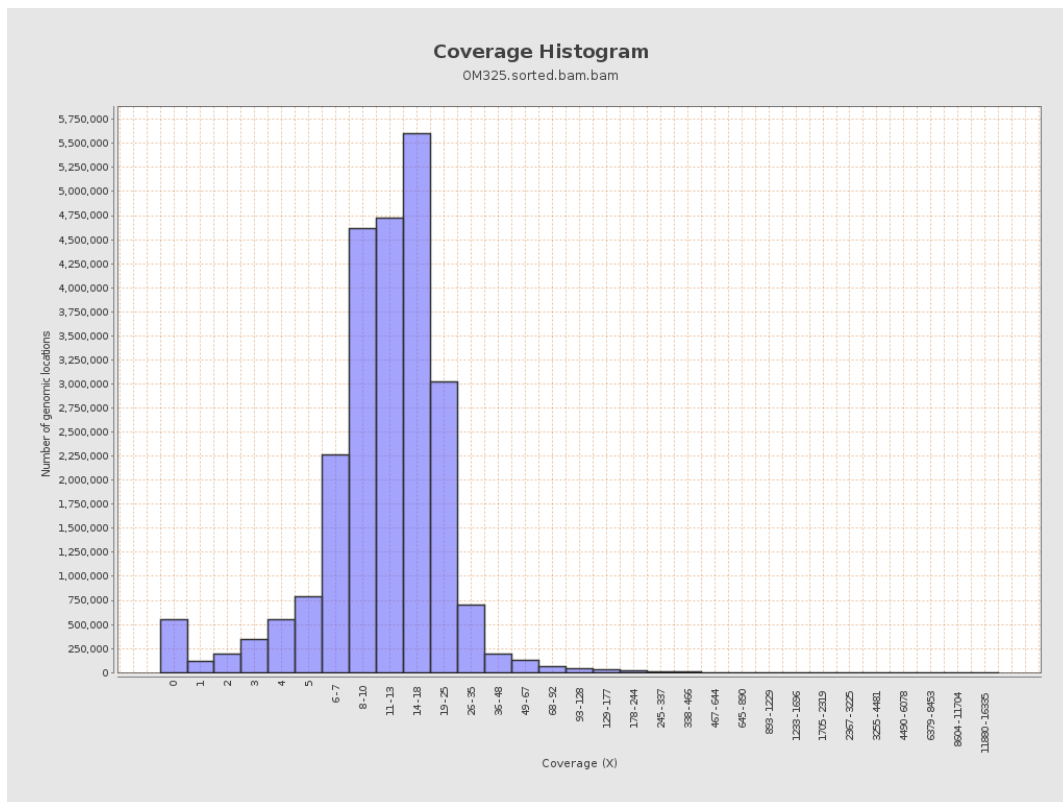
gi 1074120478 emb LT615256.1	977217	12006795	12.2867	10.1688
gi 1074120682 emb LT615257.1	860454	11188978	13.0036	14.6832
gi 1074120865 emb LT615258.1	989719	15940100	16.1057	28.4497
gi 1074121086 emb LT615259.1	935450	15306841	16.3631	24.4316
gi 1074121301 emb LT615260.1	1432239	21071704	14.7124	19.3799
gi 1074121615 emb LT615261.1	1080962	15365088	14.2143	18.1391
gi 1074121871 emb LT615262.1	1545099	21436059	13.8736	10.4907
gi 1074122235 emb LT615263.1	1585108	21945363	13.8447	35.8548
gi 1074122590 emb LT615264.1	2122358	27875925	13.1344	10.0617
gi 1074123050 emb LT615265.1	1754192	26065872	14.8592	70.5704
gi 1074123421 emb LT615	2150147	32097776	14.9282	30.8219

266.1				
gi 107412389 8 emb LT615 267.1	3031036	40361063	13.3159	21.1227
gi 107412458 8 emb LT615 268.1	2359348	28820475	12.2154	12.4583
gi 107412506 5 emb LT615 269.1	3135668	43545072	13.887	8.3915

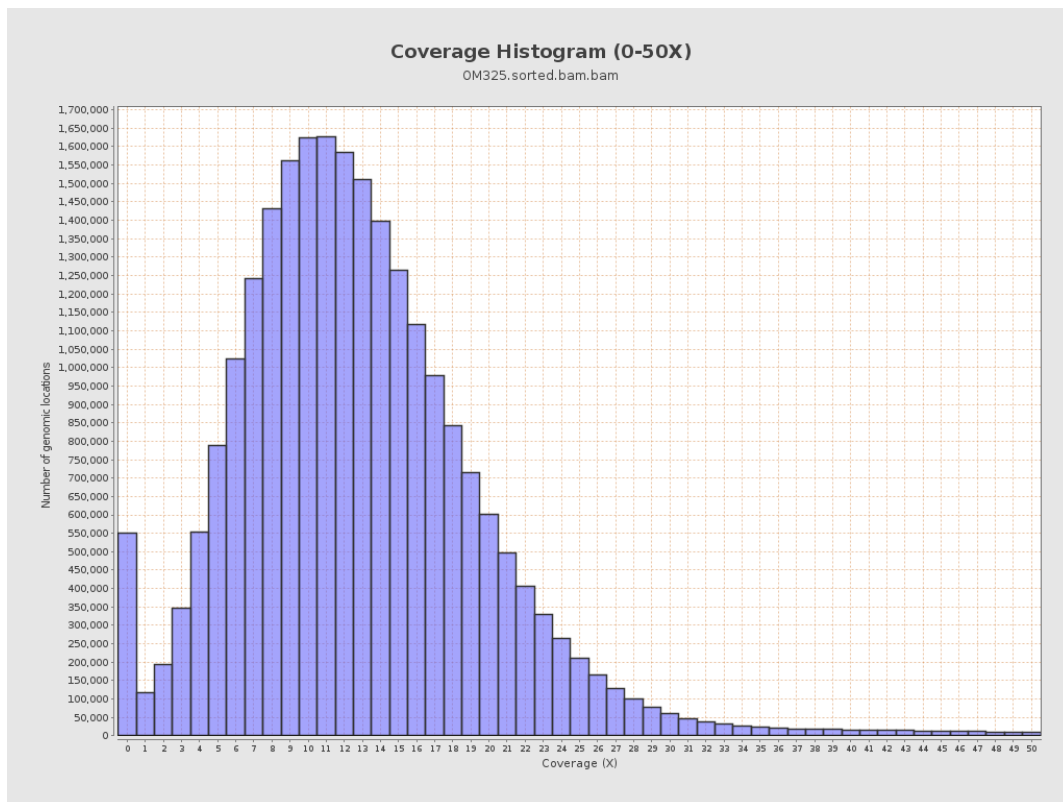
3. Results : Coverage across reference



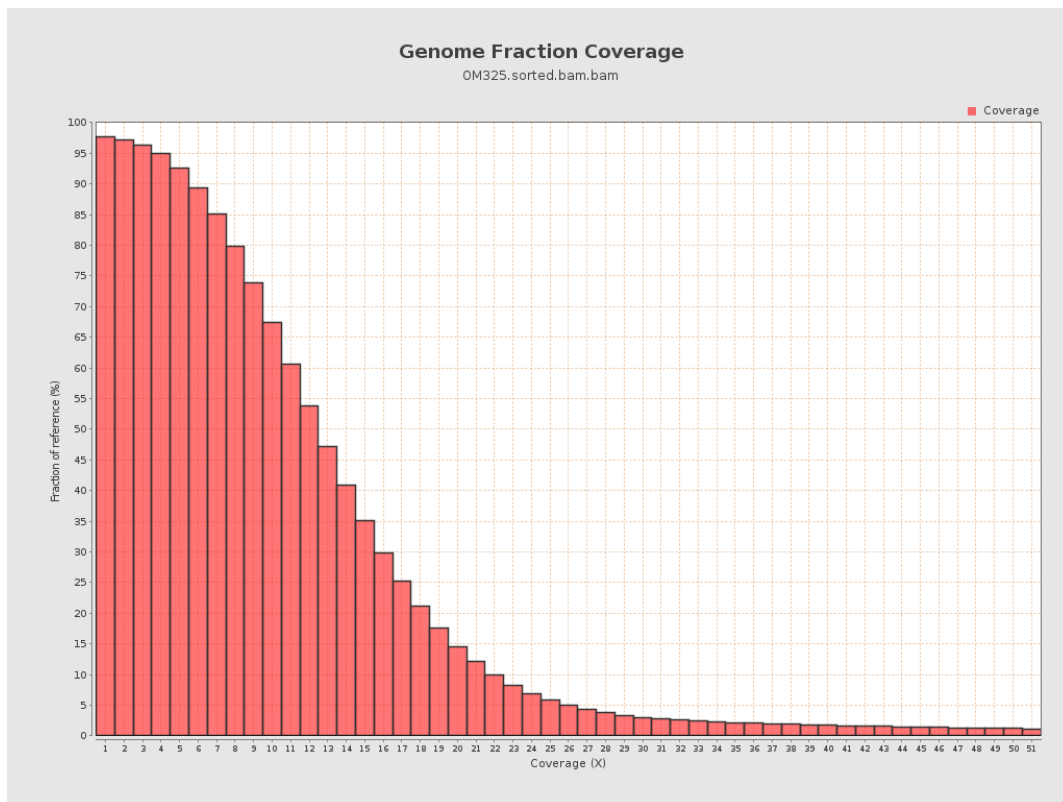
4. Results : Coverage Histogram



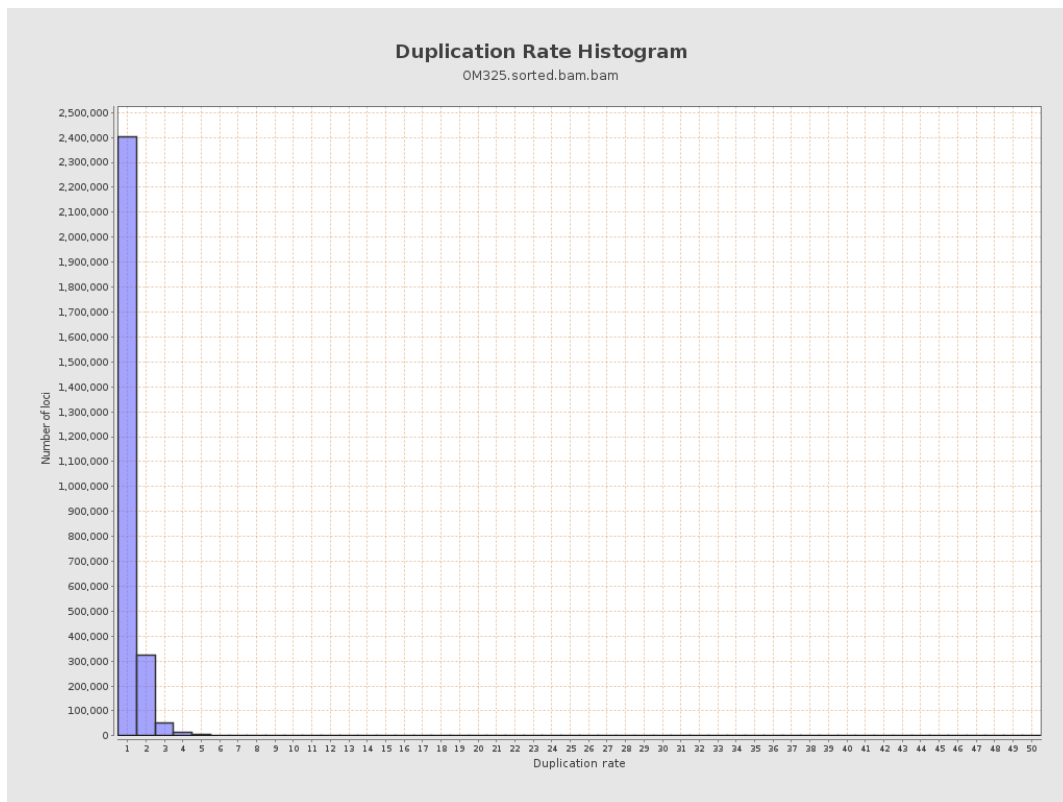
5. Results : Coverage Histogram (0-50X)



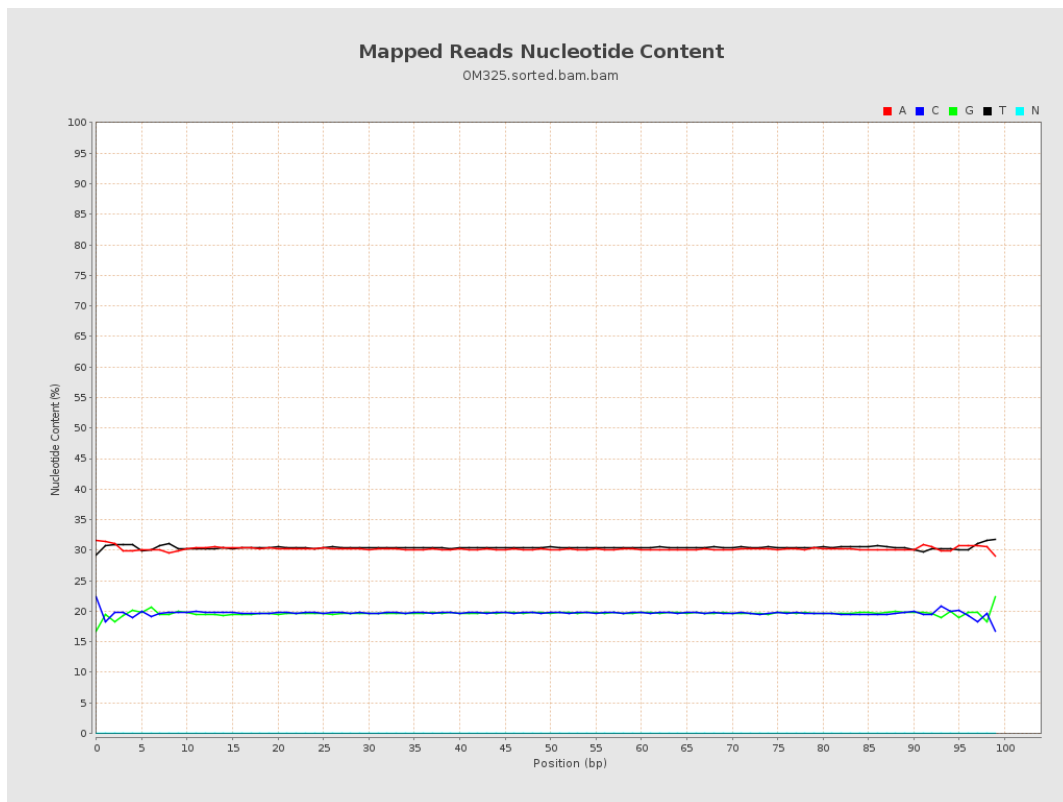
6. Results : Genome Fraction Coverage



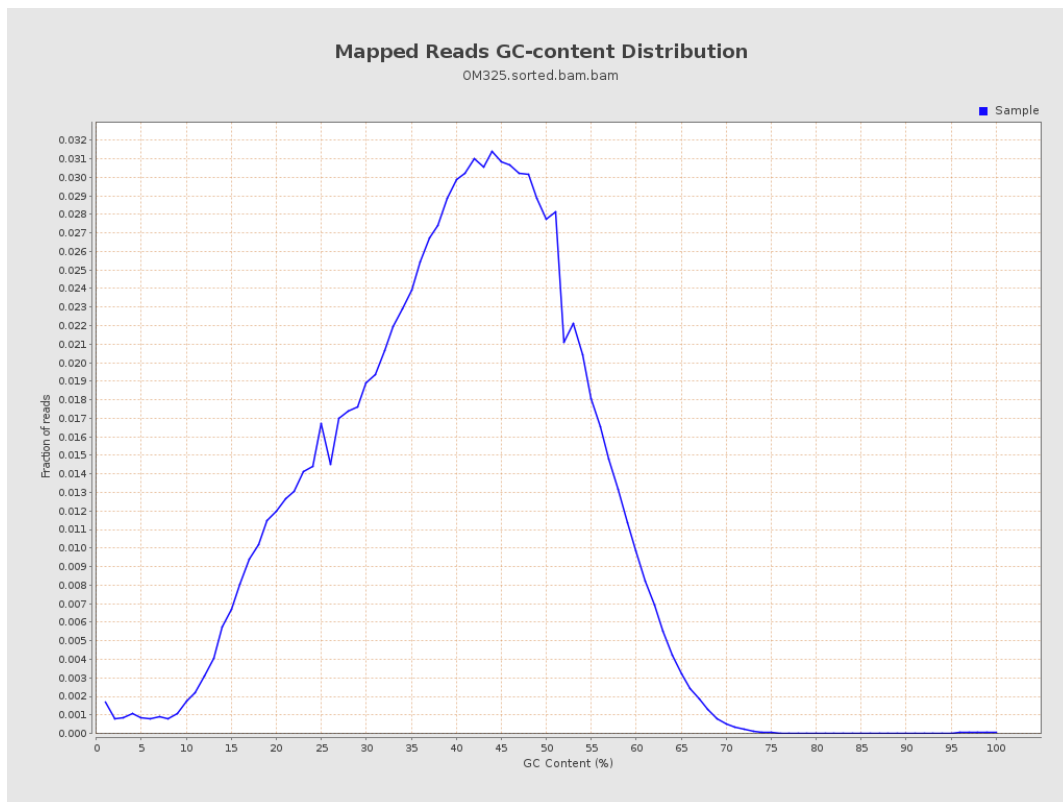
7. Results : Duplication Rate Histogram



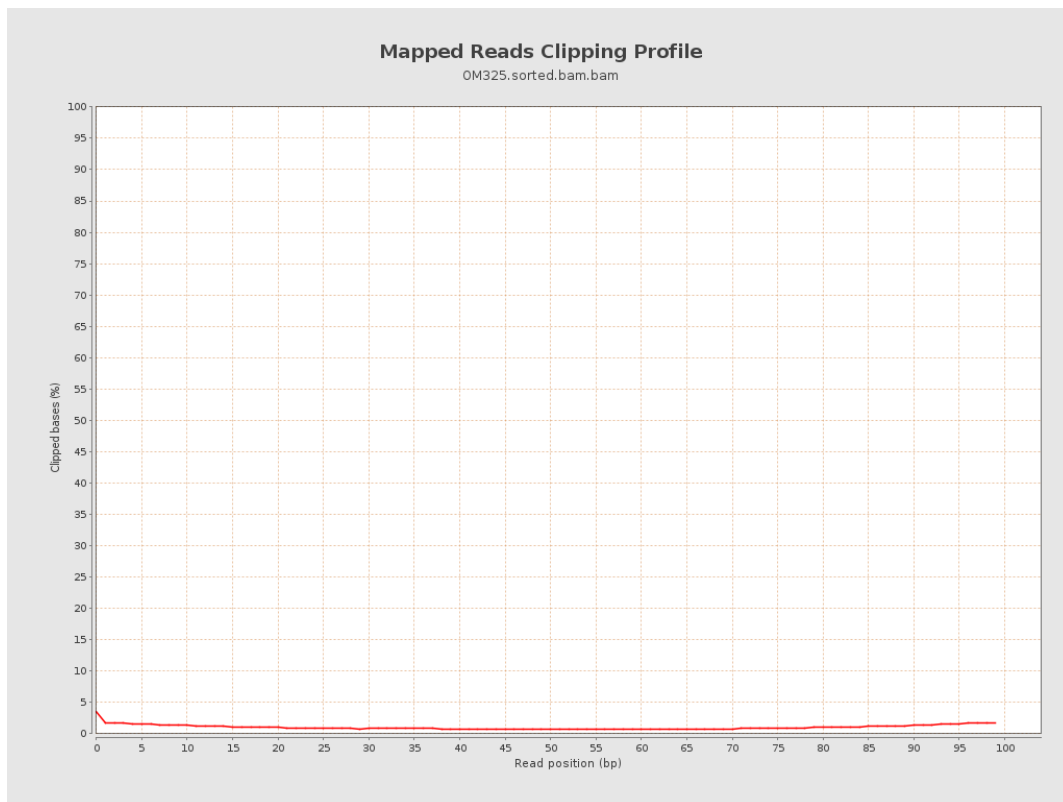
8. Results : Mapped Reads Nucleotide Content



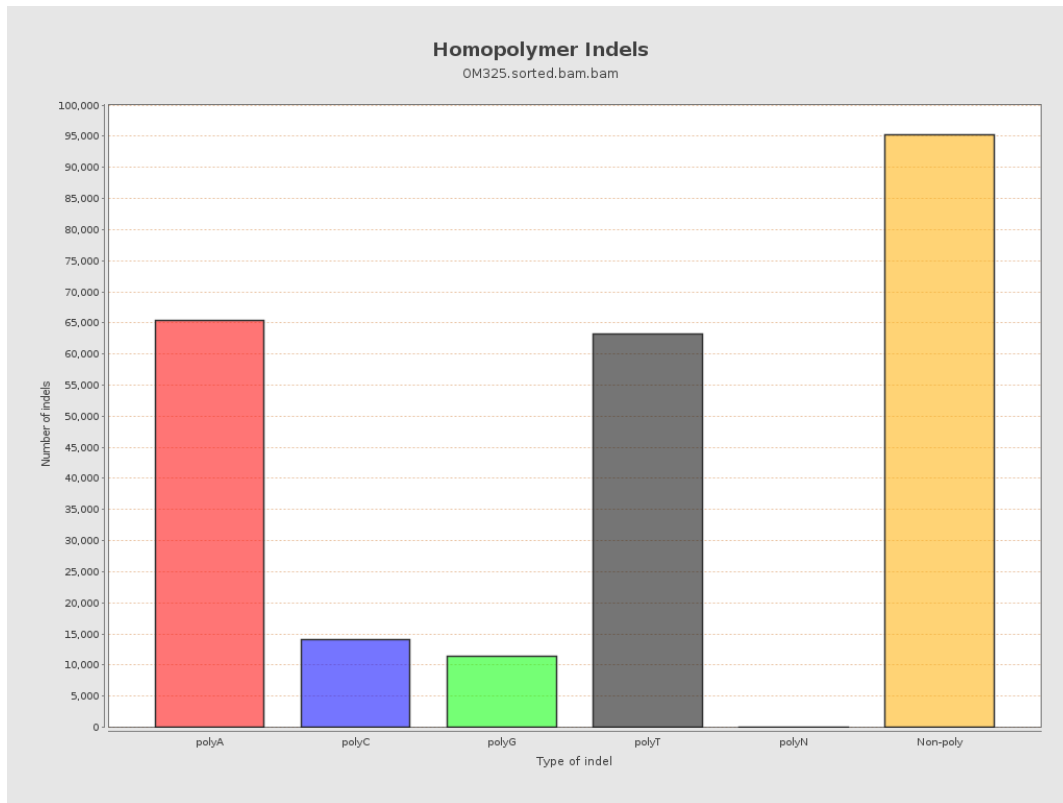
9. Results : Mapped Reads GC-content Distribution



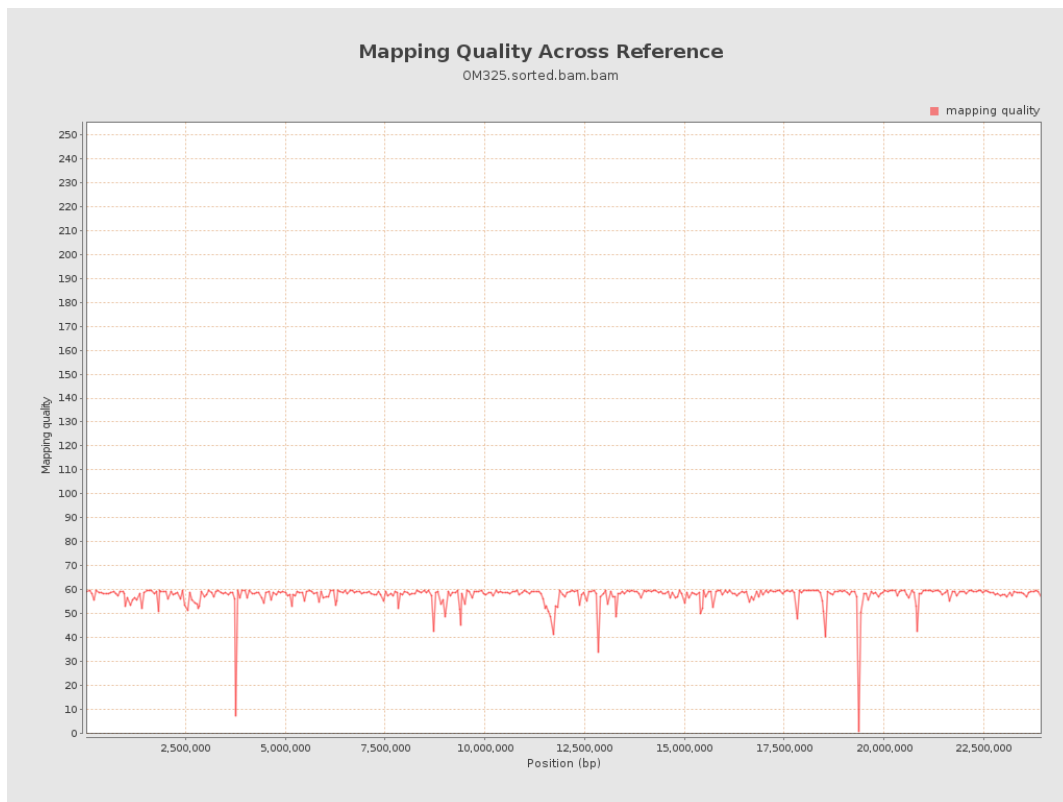
10. Results : Mapped Reads Clipping Profile



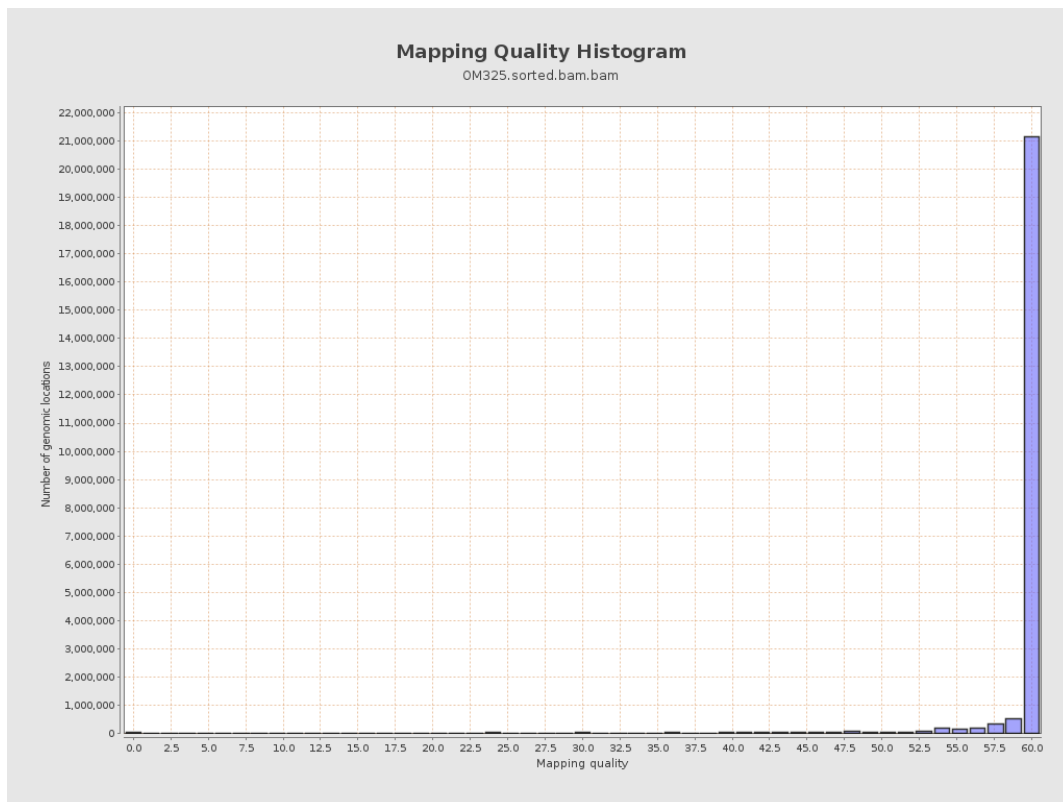
11. Results : Homopolymer Indels



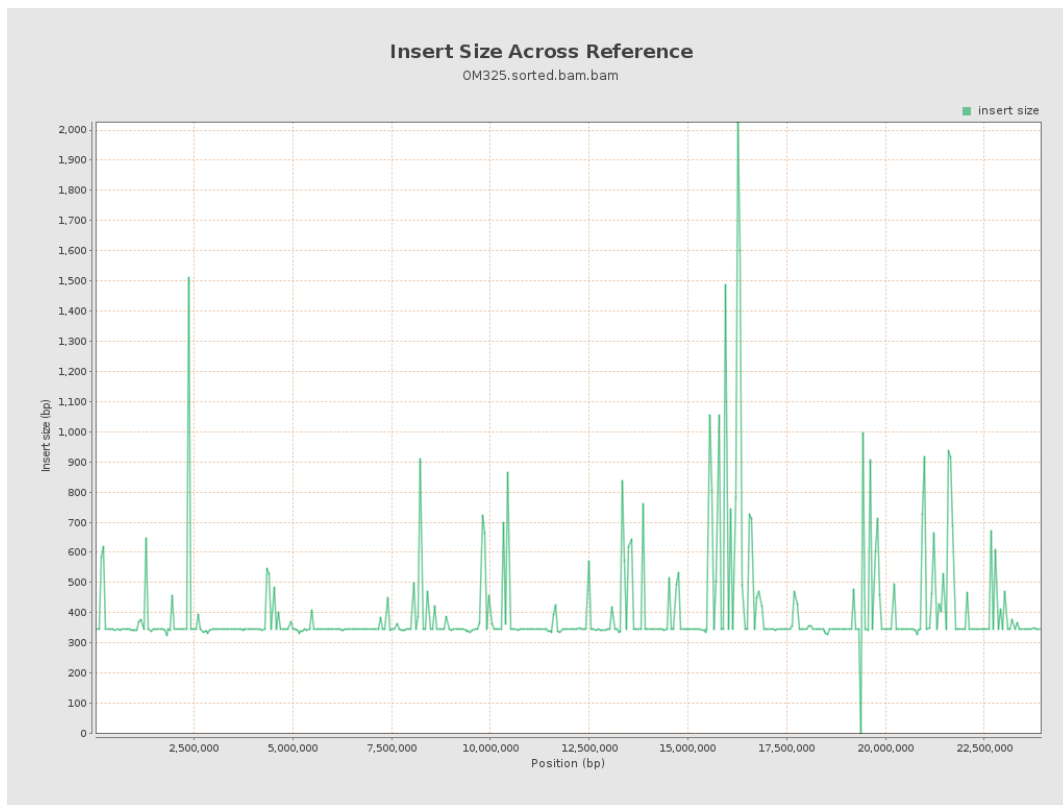
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

