

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2016/10/23 14:10:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM310.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/OM310-BiooBarcode38_CTAGCT_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM310-BiooBarcode38_CTAGCT_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 14:10:22 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM310.sorted.bam.

	bam
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2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	1,863,529
Mapped reads	1,198,678 / 64.32%
Unmapped reads	664,851 / 35.68%
Mapped paired reads	1,198,678 / 64.32%
Mapped reads, first in pair	597,081 / 32.04%
Mapped reads, second in pair	601,597 / 32.28%
Mapped reads, both in pair	1,171,986 / 62.89%
Mapped reads, singletons	26,692 / 1.43%
Read min/max/mean length	30 / 100 / 99.9
Duplicated reads (estimated)	91,250 / 4.9%
Duplication rate	5.67%
Clipped reads	138,995 / 7.46%

2.2. ACGT Content

Number/percentage of A's	34,790,597 / 30.06%
Number/percentage of C's	23,080,624 / 19.94%
Number/percentage of T's	34,888,402 / 30.14%
Number/percentage of G's	22,983,818 / 19.86%
Number/percentage of N's	9,129 / 0.01%
GC Percentage	39.8%

2.3. Coverage

Mean	4.8363
Standard Deviation	5.6216

2.4. Mapping Quality

Mean Mapping Quality	58.67
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2.5. Insert size

Mean	885.46
Standard Deviation	27,665.34
P25/Median/P75	340 / 351 / 360

2.6. Mismatches and indels

General error rate	1.66%
Mismatches	1,828,378
Insertions	40,114
Mapped reads with at least one insertion	3.17%
Deletions	44,651
Mapped reads with at least one deletion	3.52%
Homopolymer indels	62.6%

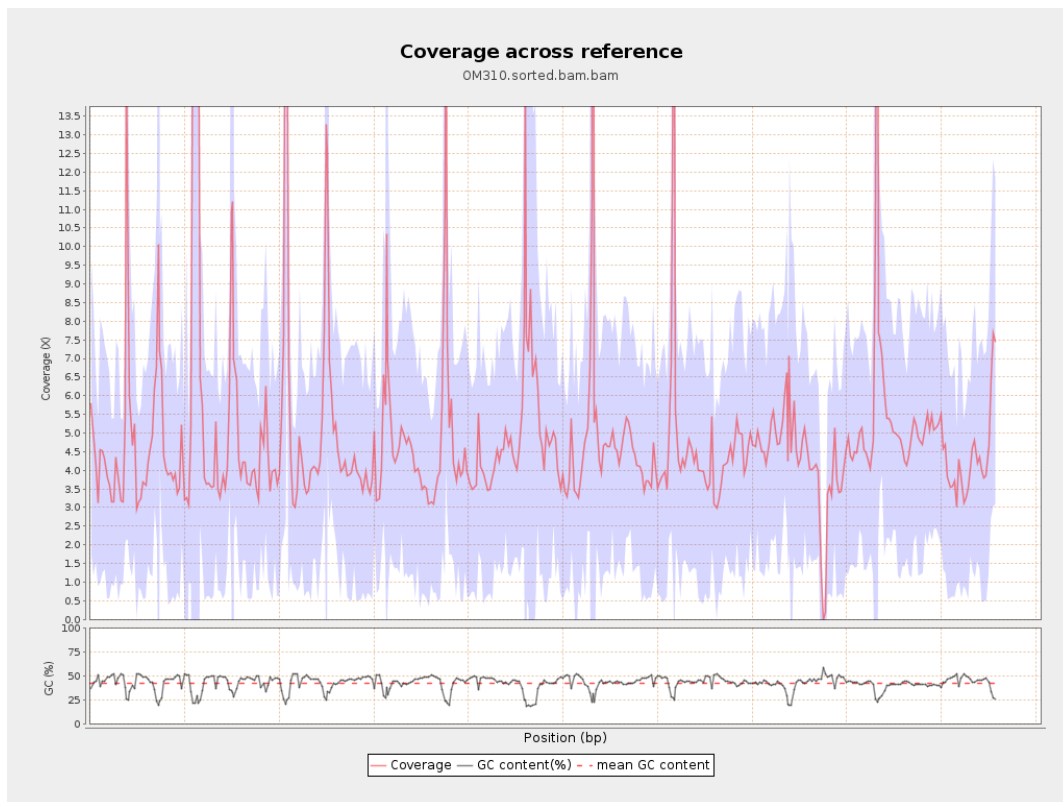
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

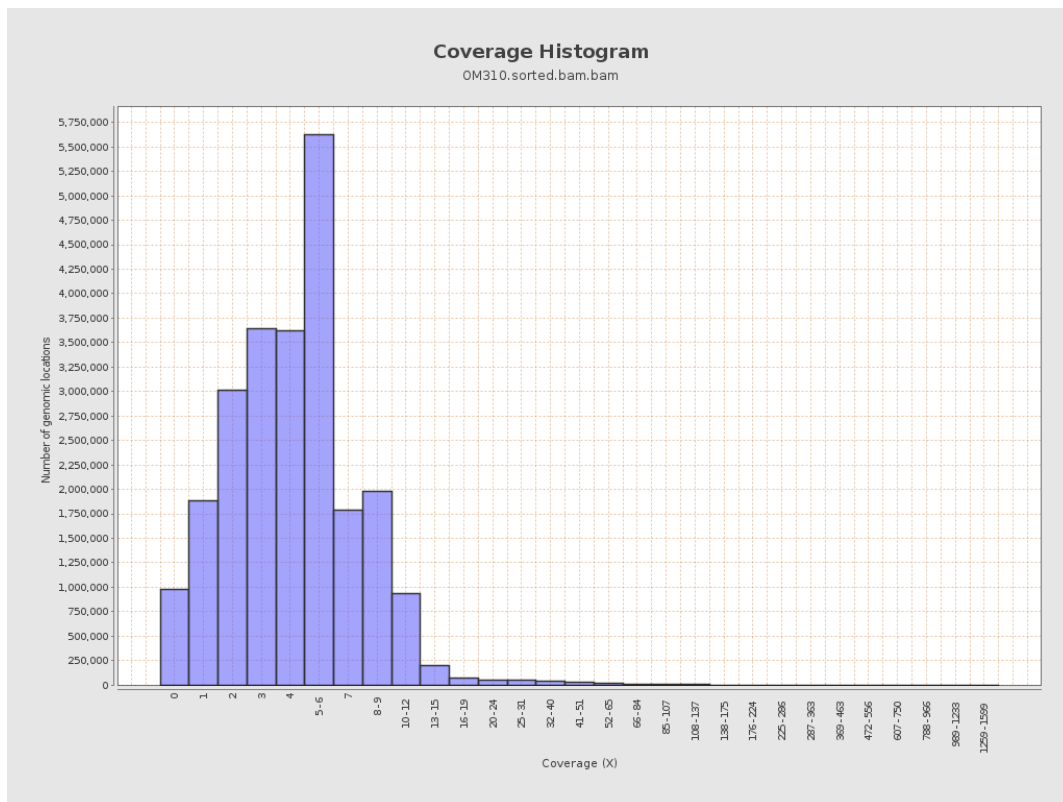
gi 1074120478 emb LT615256.1	977217	4176813	4.2742	3.4236
gi 1074120682 emb LT615257.1	860454	4312908	5.0124	4.4073
gi 1074120865 emb LT615258.1	989719	5712343	5.7717	9.1599
gi 1074121086 emb LT615259.1	935450	5112572	5.4654	8.3411
gi 1074121301 emb LT615260.1	1432239	7302274	5.0985	5.9123
gi 1074121615 emb LT615261.1	1080962	5338462	4.9386	5.1575
gi 1074121871 emb LT615262.1	1545099	6833877	4.4229	2.7486
gi 1074122235 emb LT615263.1	1585108	7448520	4.6991	3.9126
gi 1074122590 emb LT615264.1	2122358	9796658	4.6159	3.61
gi 1074123050 emb LT615265.1	1754192	8879996	5.0622	4.9347
gi 1074123421 emb LT615	2150147	10951084	5.0932	10.9645

266.1				
gi 107412389 8 emb LT615 267.1	3031036	13953723	4.6036	3.0993
gi 107412458 8 emb LT615 268.1	2359348	10849974	4.5987	5.8886
gi 107412506 5 emb LT615 269.1	3135668	15202532	4.8483	2.7506

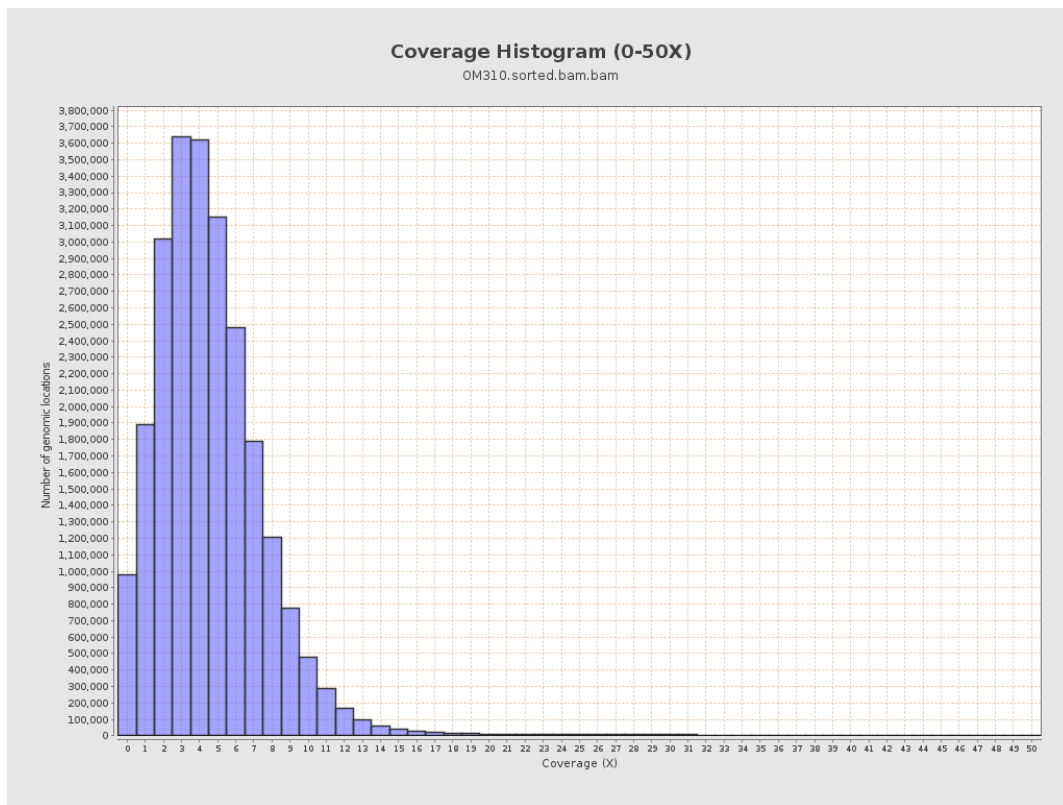
3. Results : Coverage across reference



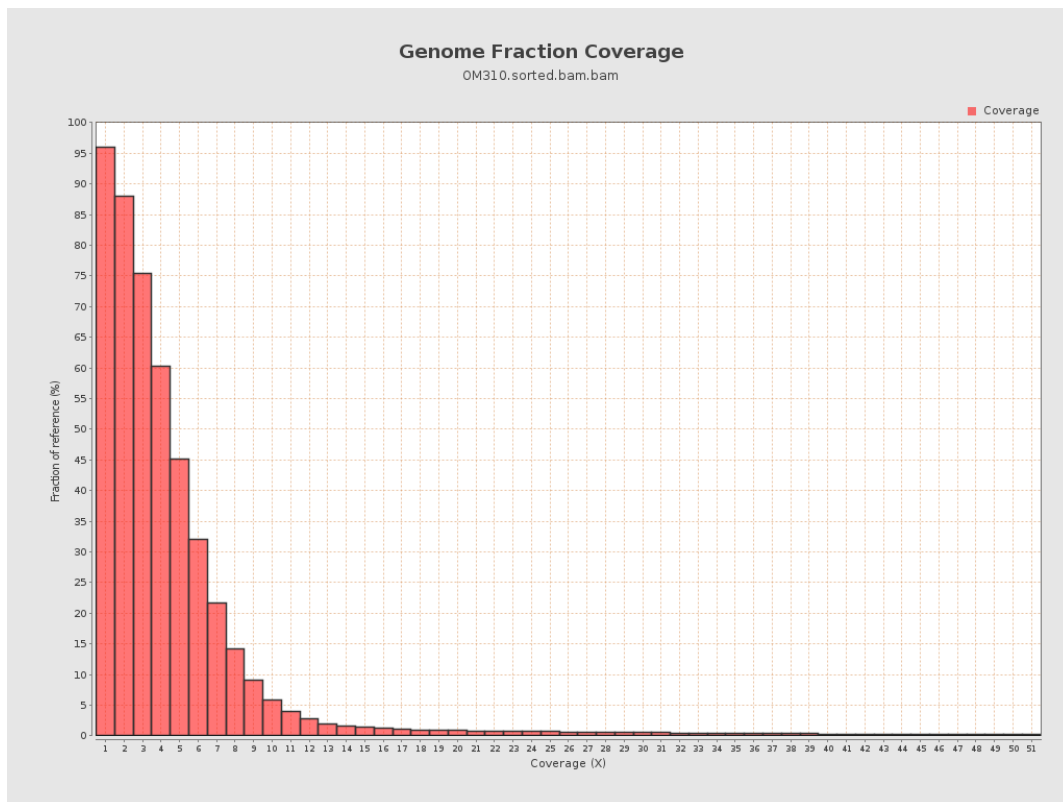
4. Results : Coverage Histogram



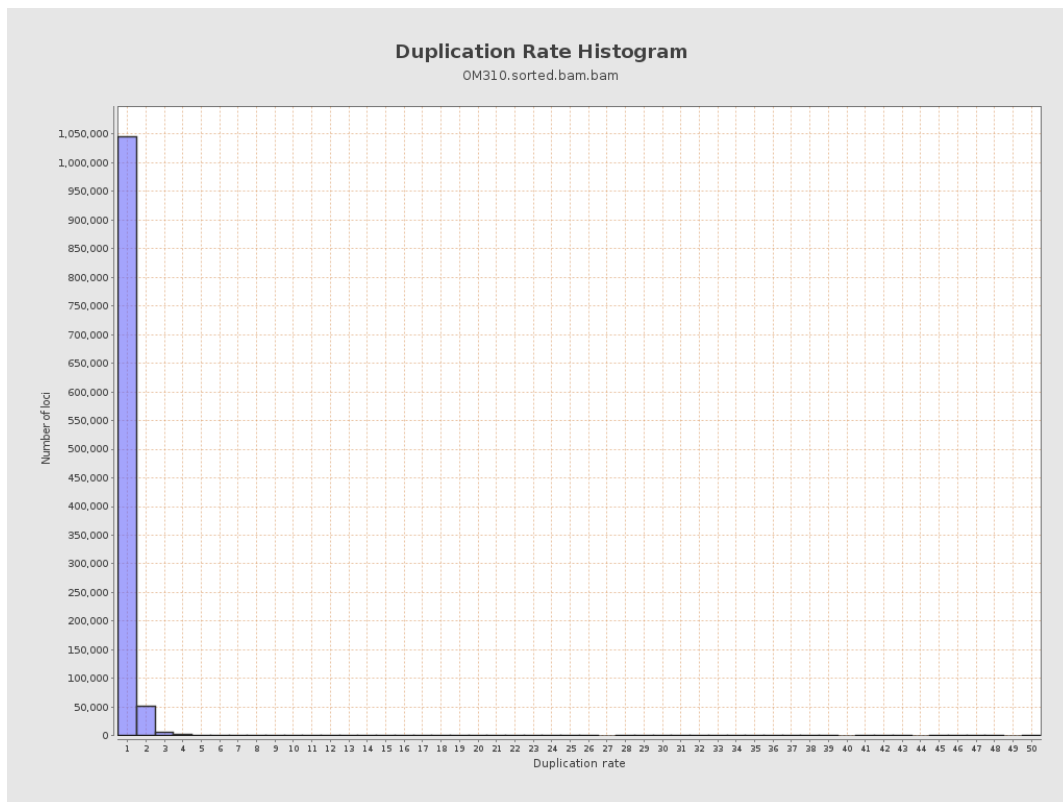
5. Results : Coverage Histogram (0-50X)



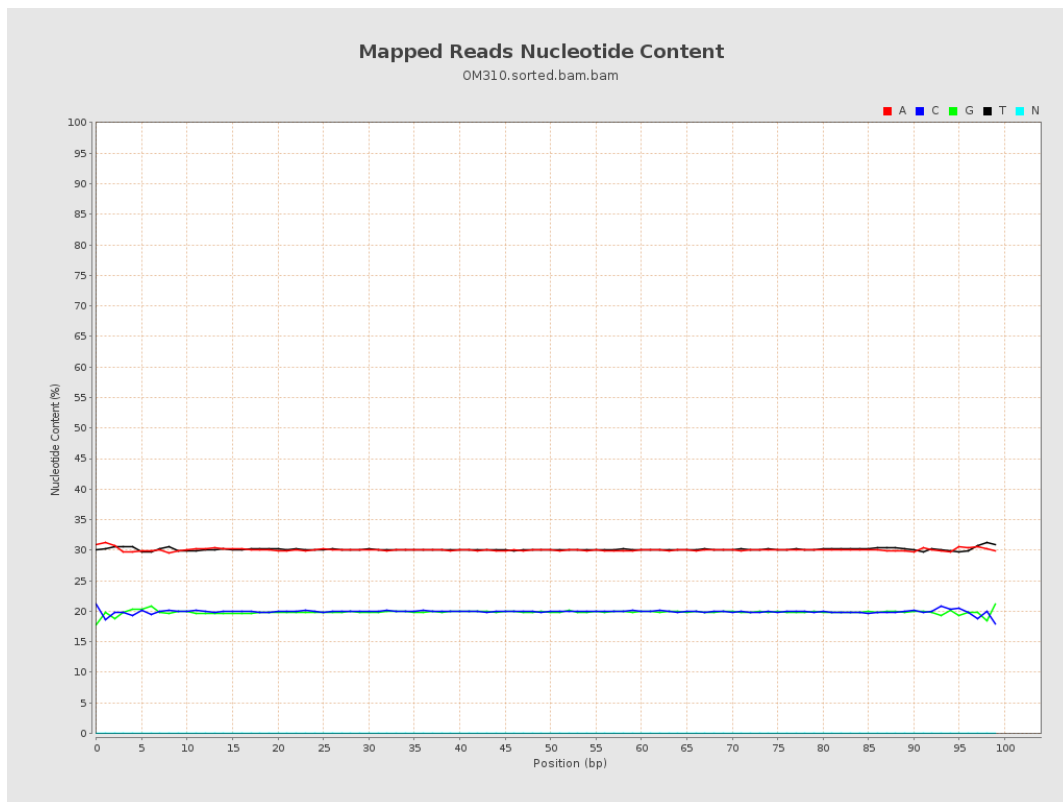
6. Results : Genome Fraction Coverage



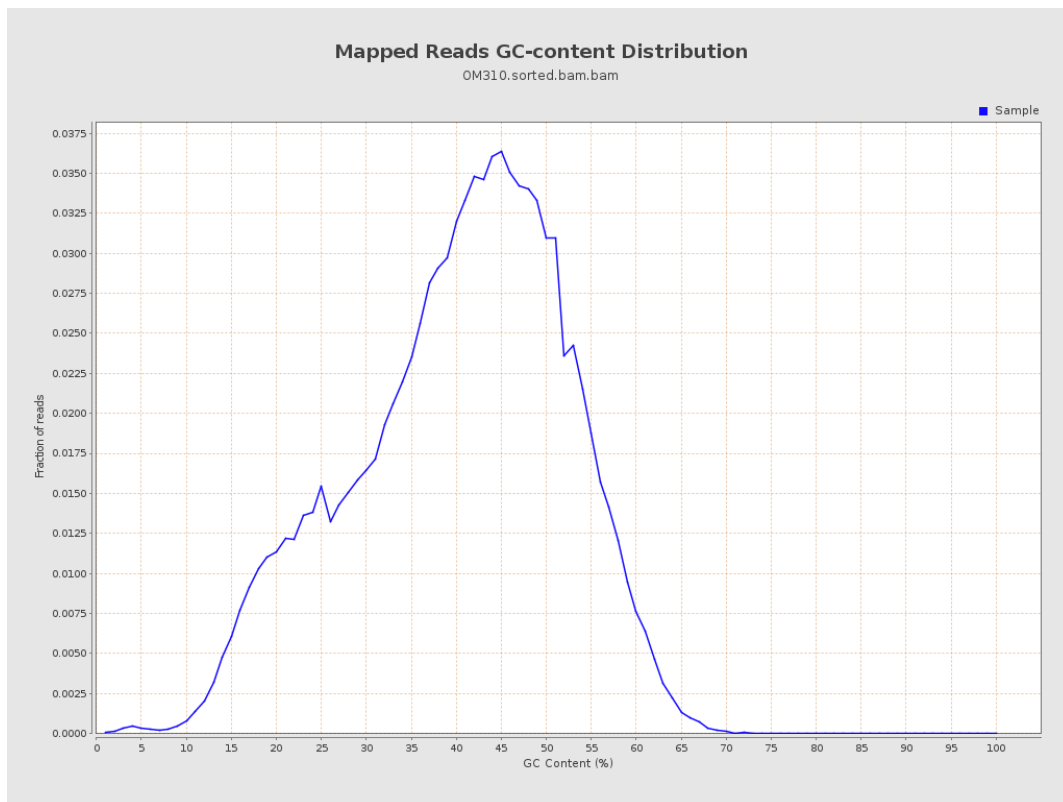
7. Results : Duplication Rate Histogram



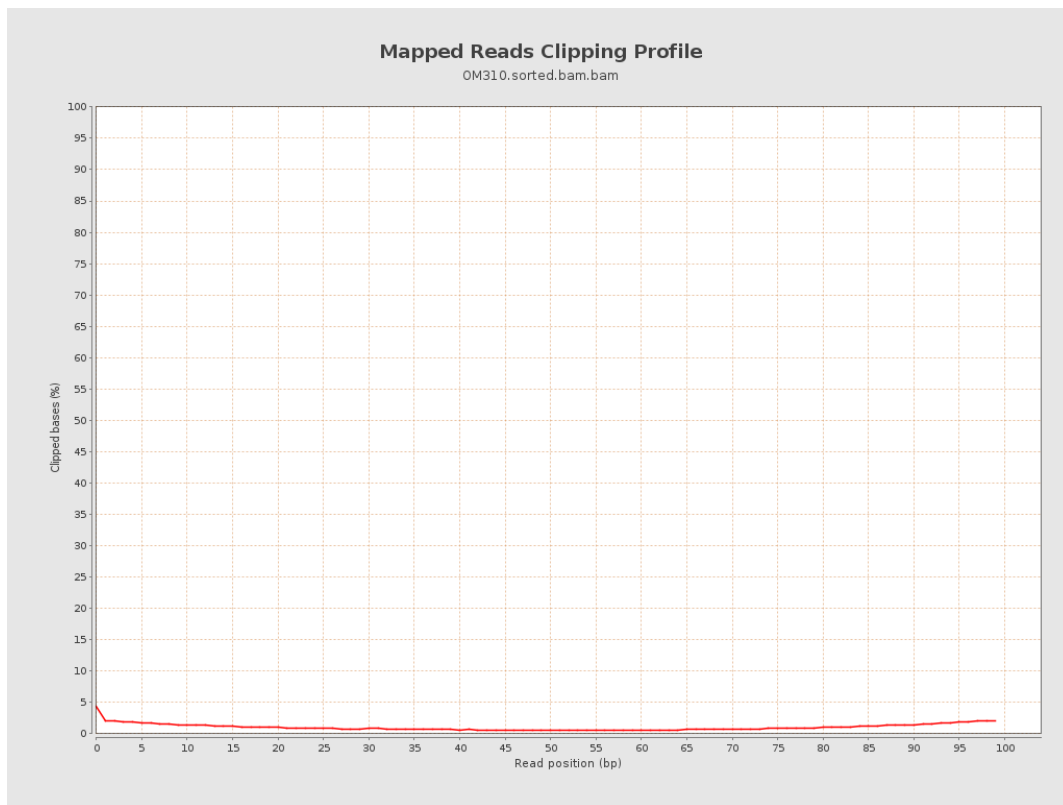
8. Results : Mapped Reads Nucleotide Content



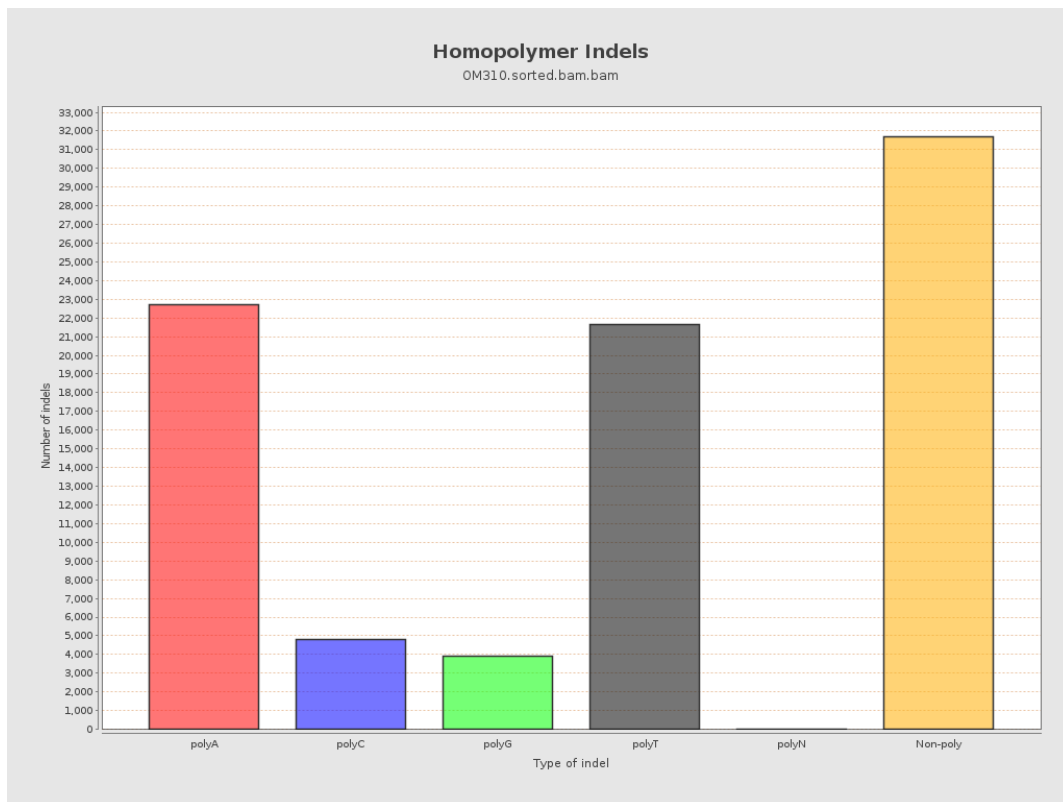
9. Results : Mapped Reads GC-content Distribution



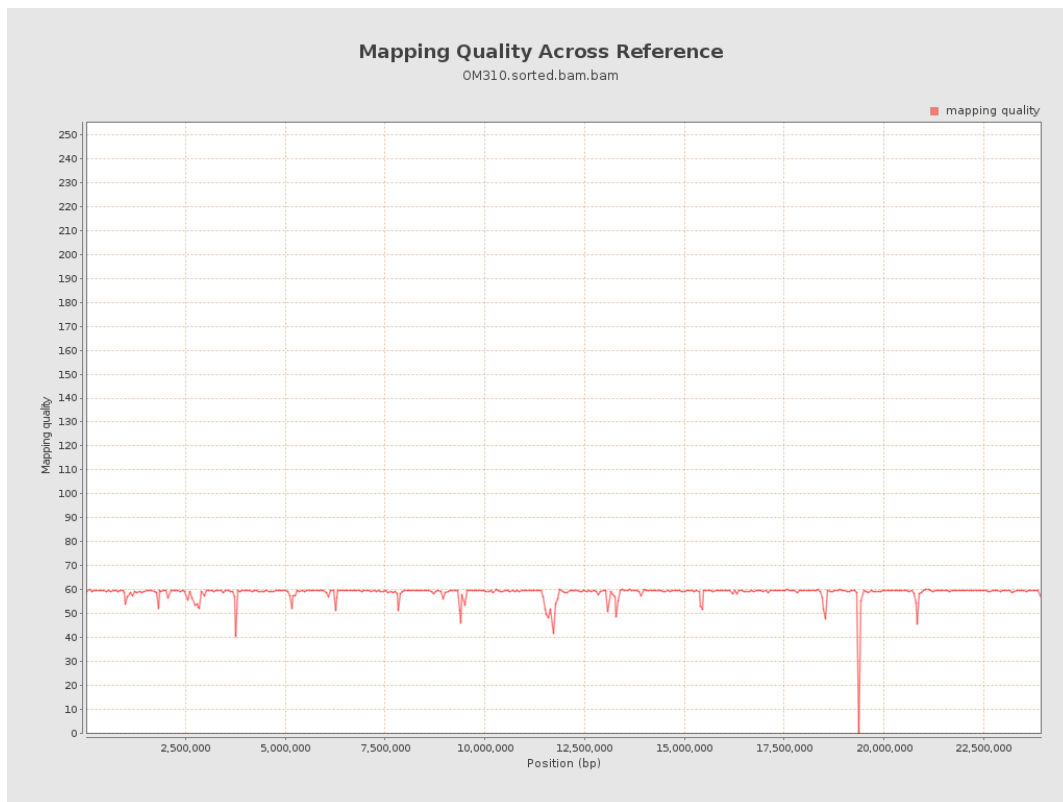
10. Results : Mapped Reads Clipping Profile



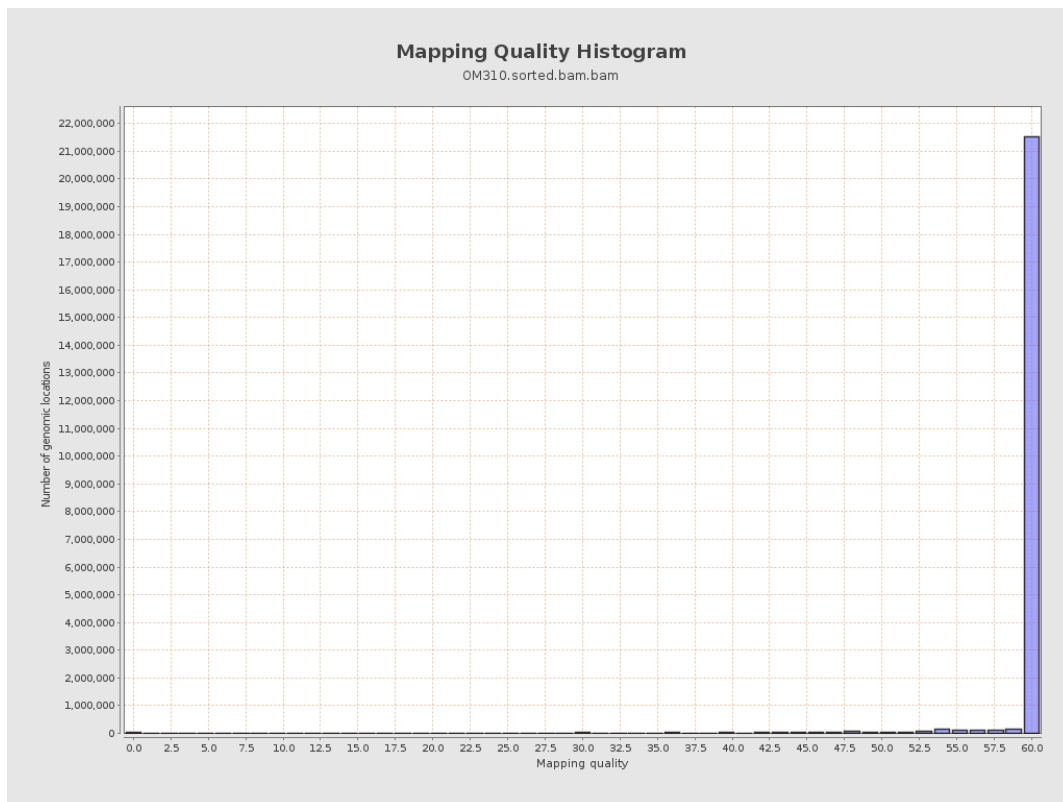
11. Results : Homopolymer Indels



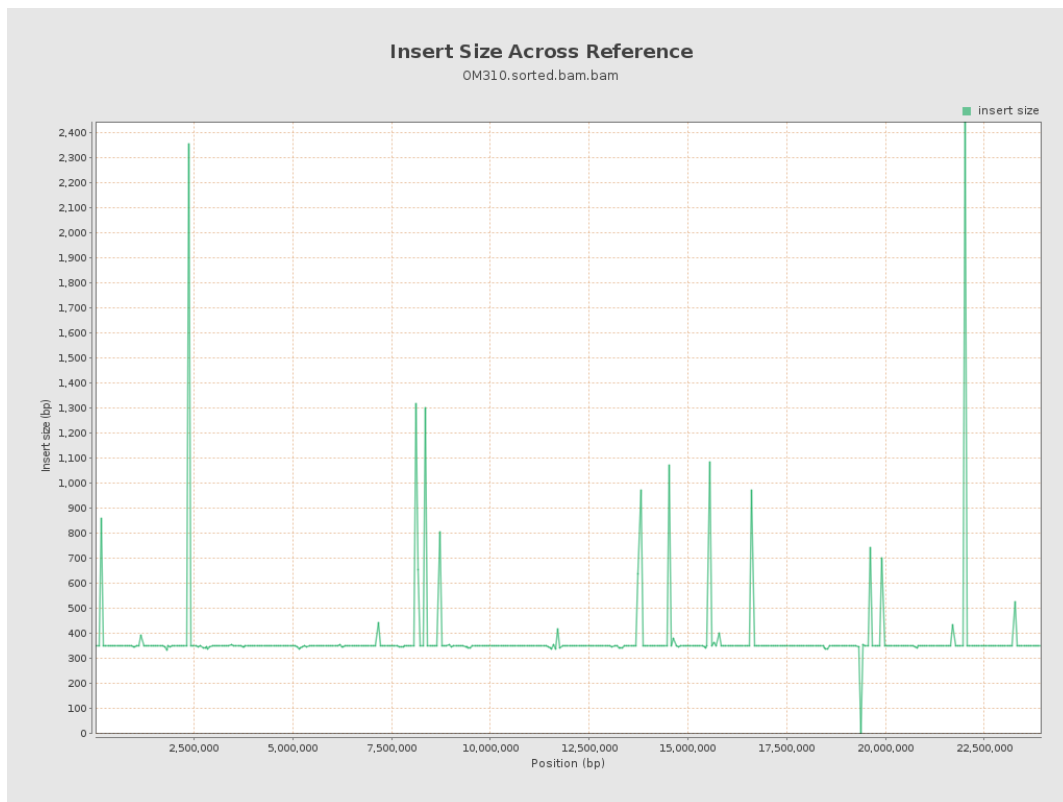
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

