

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2016/10/23 13:59:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM284.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/OM284-BiooBarcode30_CACCGG_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM284-BiooBarcode30_CACCGG_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 13:59:58 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM284.sorted.bam.

	bam
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2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	6,525,218
Mapped reads	1,574,511 / 24.13%
Unmapped reads	4,950,707 / 75.87%
Mapped paired reads	1,574,511 / 24.13%
Mapped reads, first in pair	783,608 / 12.01%
Mapped reads, second in pair	790,903 / 12.12%
Mapped reads, both in pair	1,513,340 / 23.19%
Mapped reads, singletons	61,171 / 0.94%
Read min/max/mean length	30 / 100 / 99.96
Duplicated reads (estimated)	162,346 / 2.49%
Duplication rate	7.22%
Clipped reads	206,929 / 3.17%

2.2. ACGT Content

Number/percentage of A's	45,573,820 / 30.31%
Number/percentage of C's	29,546,888 / 19.65%
Number/percentage of T's	45,768,293 / 30.44%
Number/percentage of G's	29,482,932 / 19.61%
Number/percentage of N's	12,188 / 0.01%
GC Percentage	39.26%

2.3. Coverage

Mean	6.2833
Standard Deviation	7.987

2.4. Mapping Quality

Mean Mapping Quality	58.22
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2.5. Insert size

Mean	945.1
Standard Deviation	29,201.48
P25/Median/P75	313 / 325 / 335

2.6. Mismatches and indels

General error rate	1.65%
Mismatches	2,362,861
Insertions	52,718
Mapped reads with at least one insertion	3.17%
Deletions	60,048
Mapped reads with at least one deletion	3.57%
Homopolymer indels	62.33%

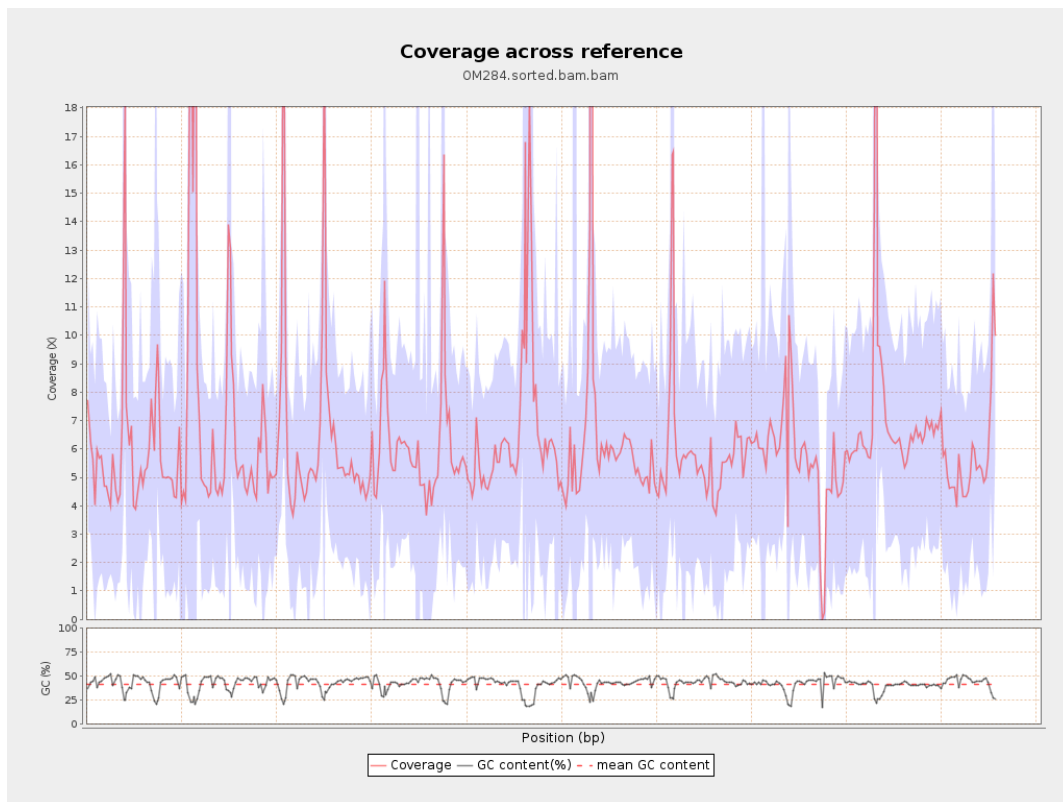
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

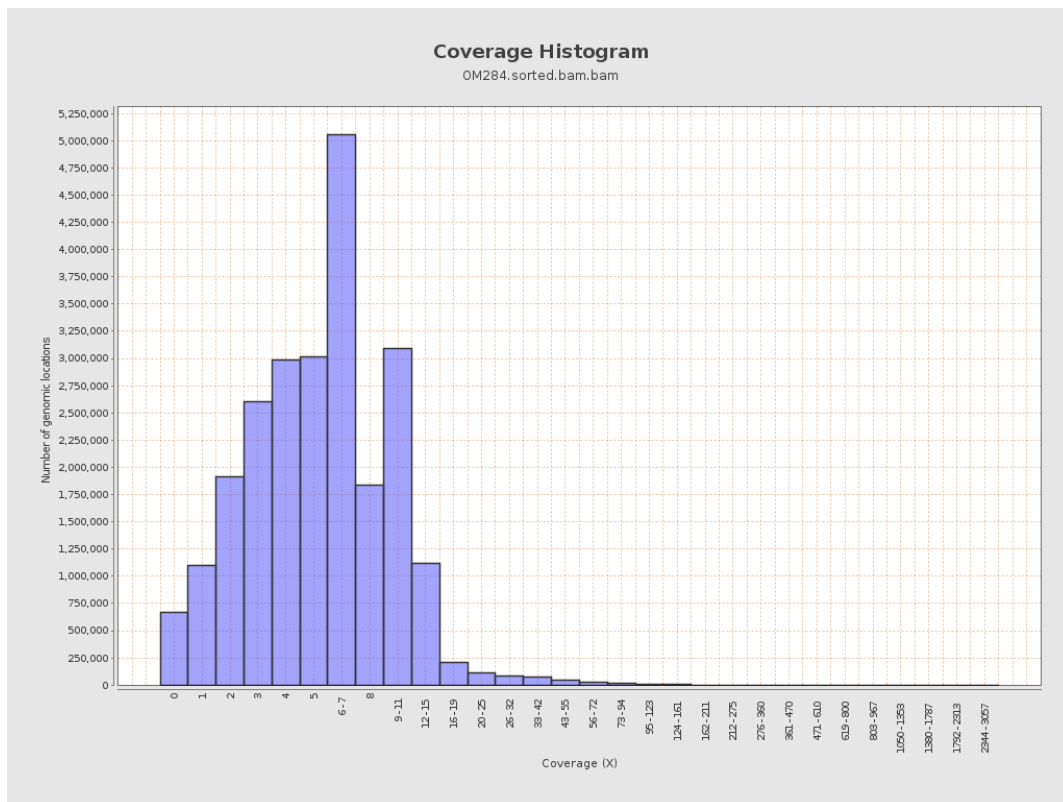
gi 1074120478 emb LT615256.1	977217	5348900	5.4736	3.8016
gi 1074120682 emb LT615257.1	860454	5451566	6.3357	6.4537
gi 1074120865 emb LT615258.1	989719	7411320	7.4883	10.817
gi 1074121086 emb LT615259.1	935450	6868624	7.3426	11.8195
gi 1074121301 emb LT615260.1	1432239	9374866	6.5456	7.0378
gi 1074121615 emb LT615261.1	1080962	6811079	6.3009	6.8375
gi 1074121871 emb LT615262.1	1545099	8899638	5.7599	3.5671
gi 1074122235 emb LT615263.1	1585108	9628794	6.0745	8.3345
gi 1074122590 emb LT615264.1	2122358	12387954	5.8369	3.8567
gi 1074123050 emb LT615265.1	1754192	12372764	7.0533	14.7649
gi 1074123421 emb LT615	2150147	13654787	6.3506	11.8136

266.1				
gi 107412389 8 emb LT615 267.1	3031036	17969181	5.9284	4.9472
gi 107412458 8 emb LT615 268.1	2359348	14640641	6.2054	7.7425
gi 107412506 5 emb LT615 269.1	3135668	19720308	6.289	3.8082

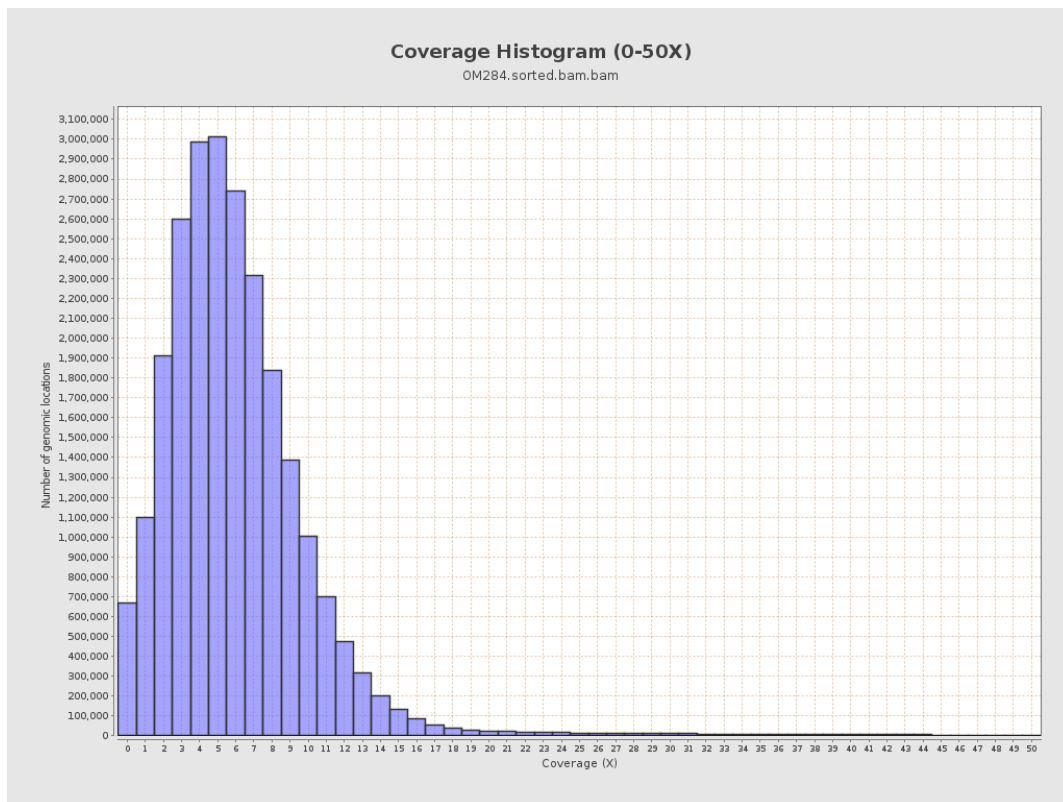
3. Results : Coverage across reference



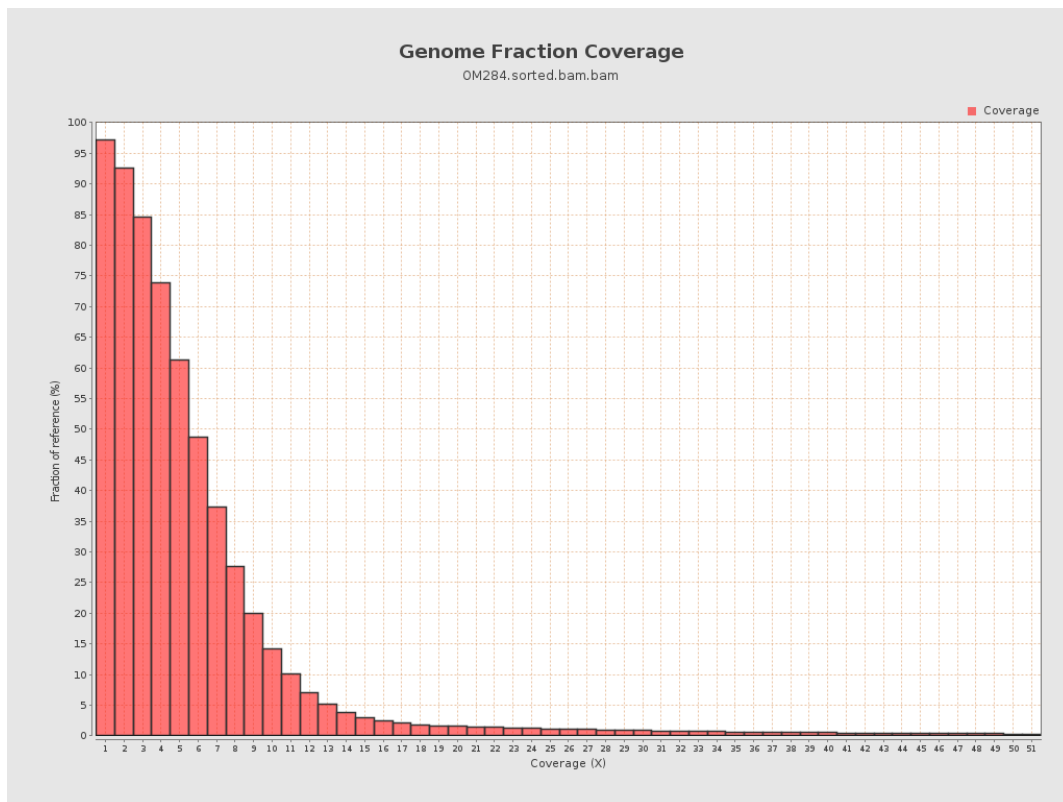
4. Results : Coverage Histogram



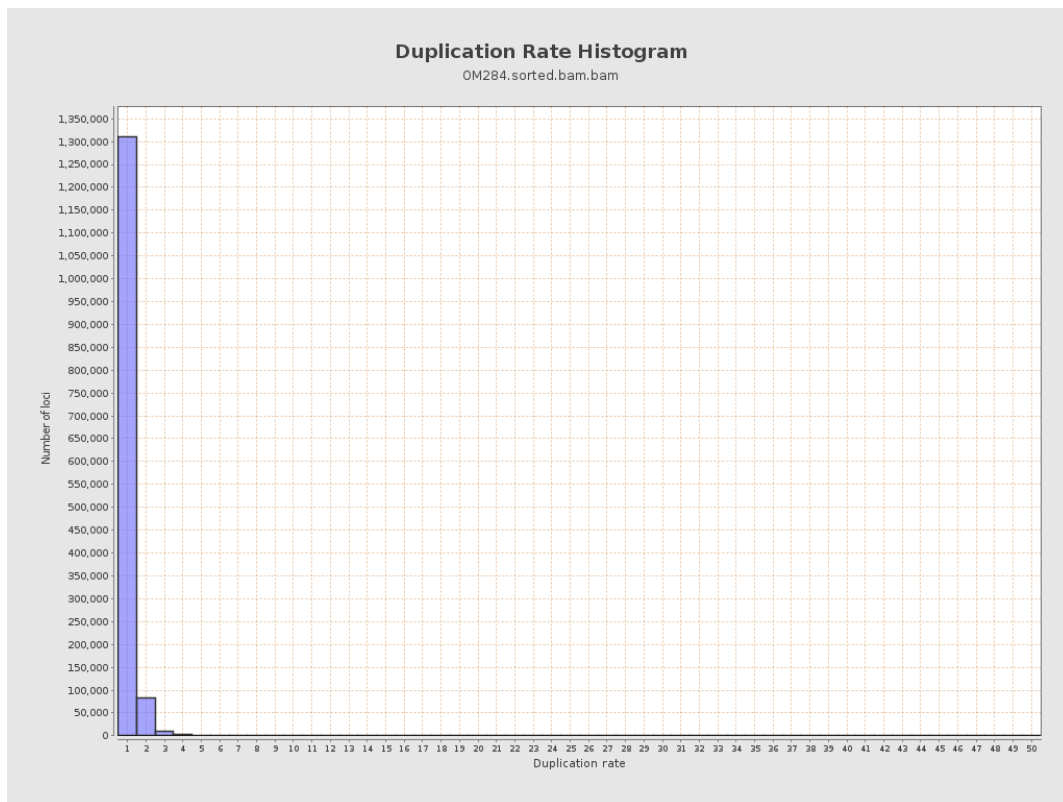
5. Results : Coverage Histogram (0-50X)



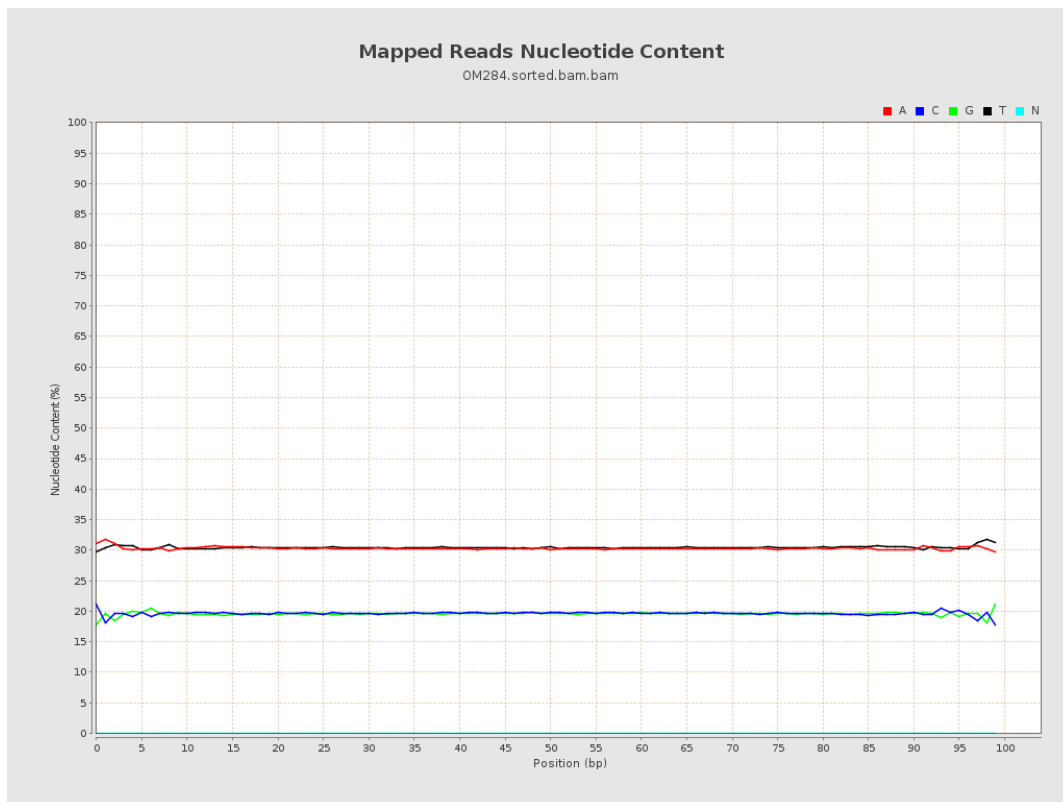
6. Results : Genome Fraction Coverage



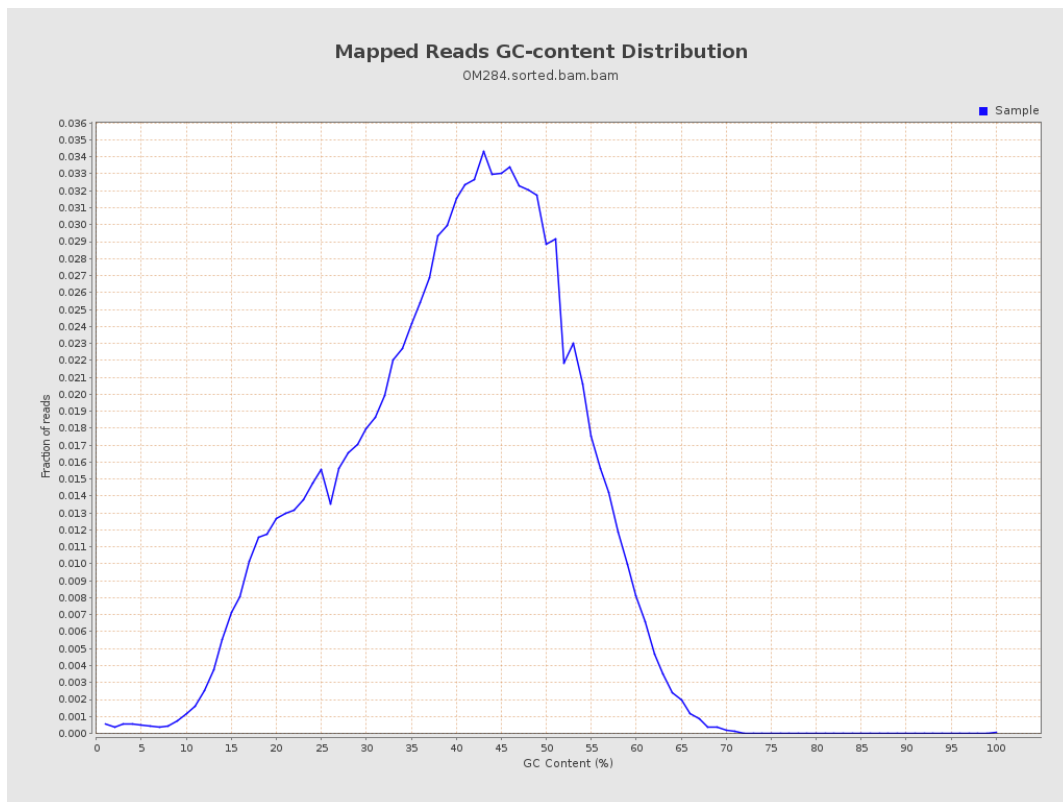
7. Results : Duplication Rate Histogram



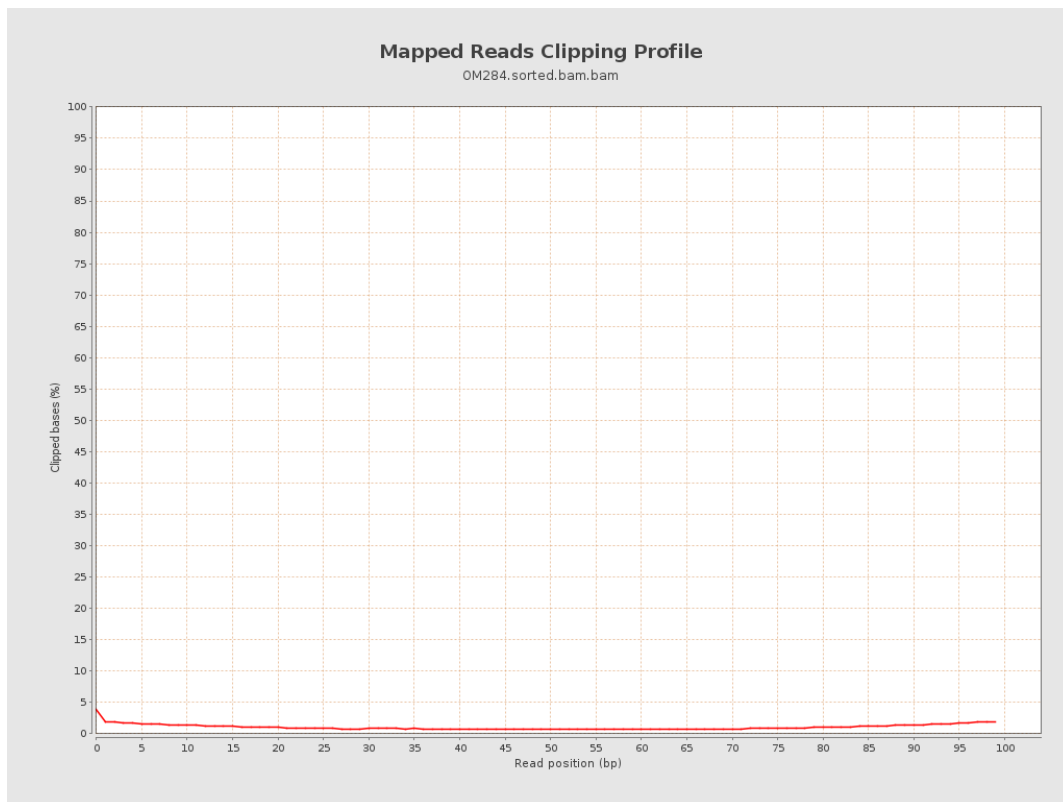
8. Results : Mapped Reads Nucleotide Content



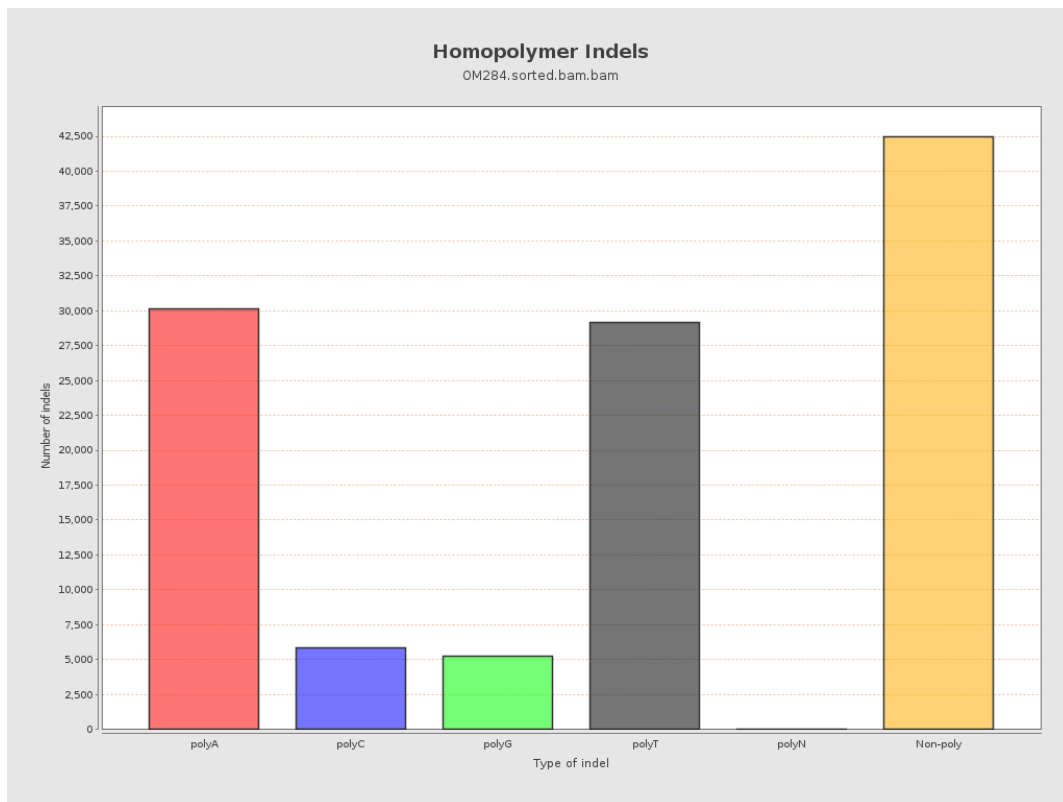
9. Results : Mapped Reads GC-content Distribution



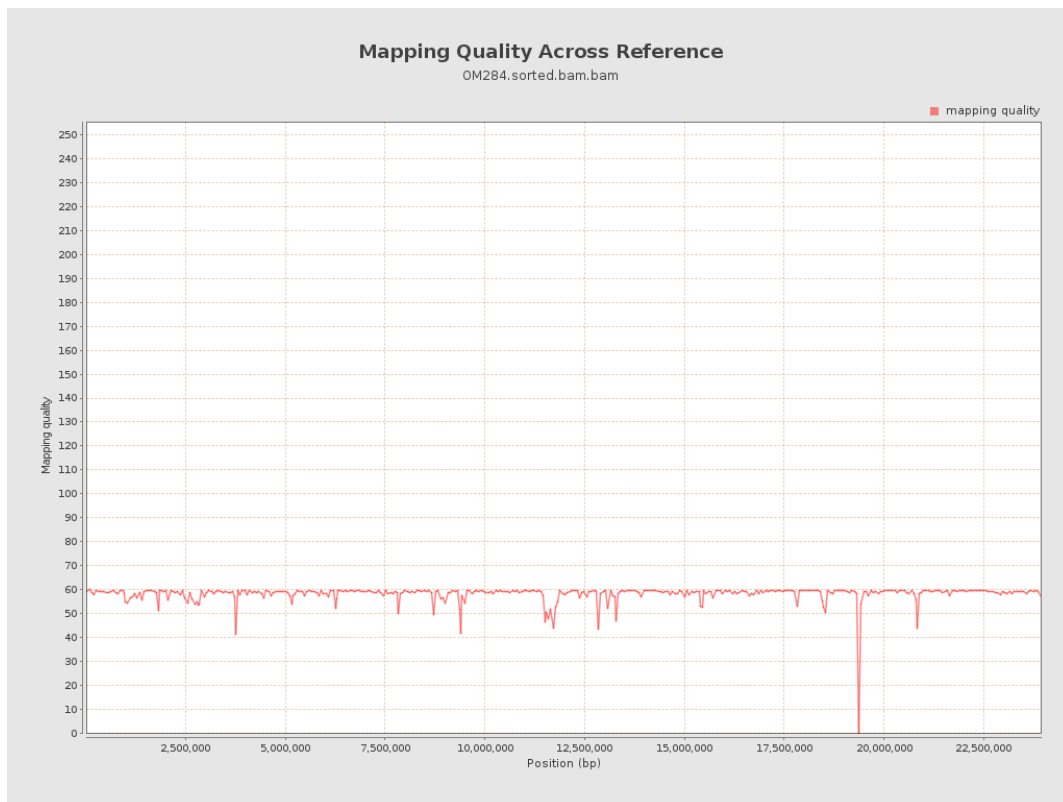
10. Results : Mapped Reads Clipping Profile



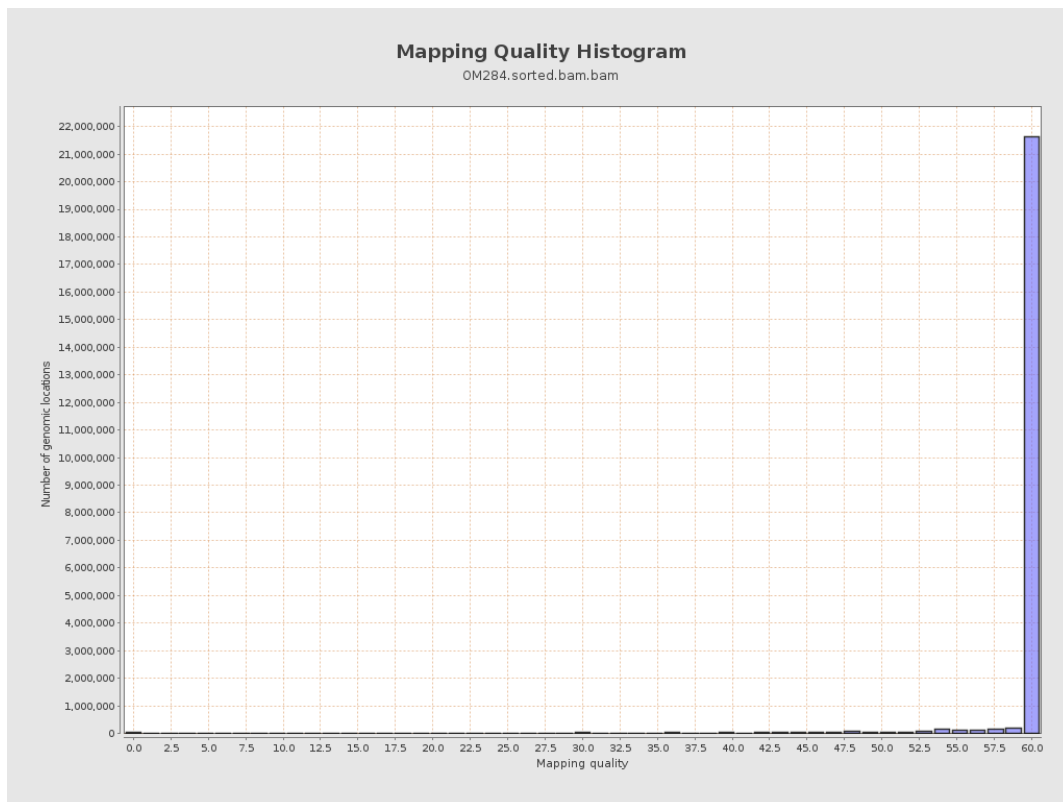
11. Results : Homopolymer Indels



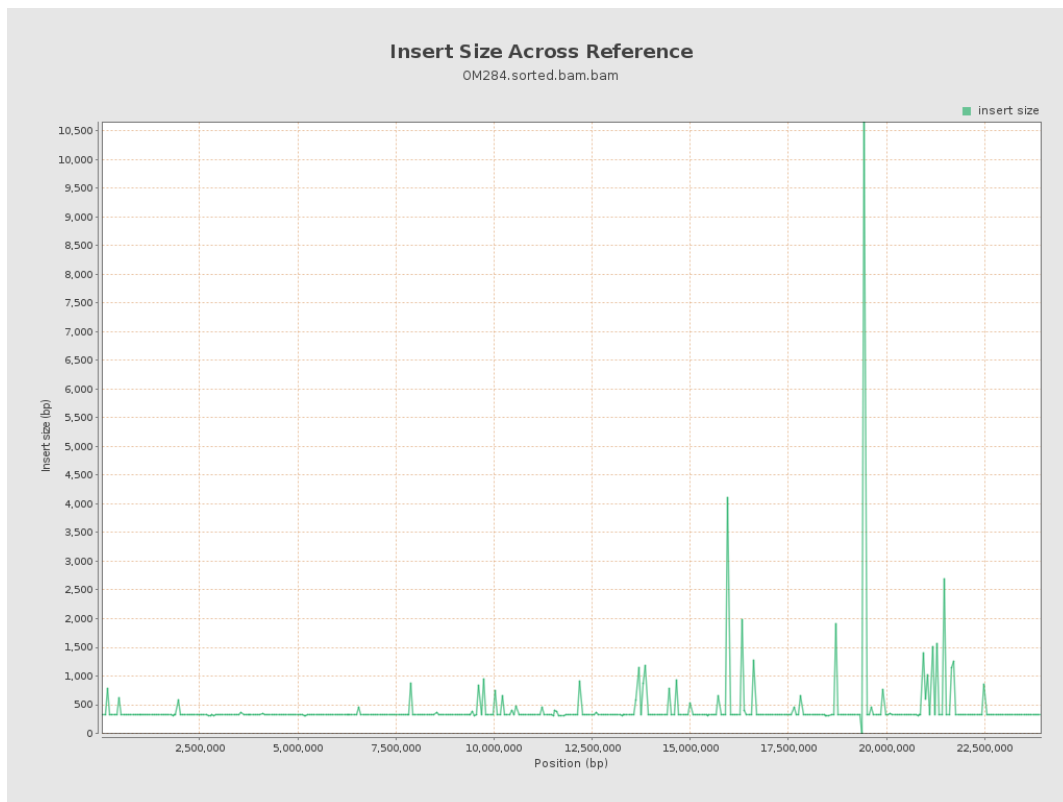
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

