

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2016/10/23 13:48:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM269.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/OM269-BiooBarcode24_GGTAGC_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM269-BiooBarcode24_GGTAGC_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 13:48:31 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM269.sorted.bam.

	bam
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2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	4,057,644
Mapped reads	2,236,789 / 55.13%
Unmapped reads	1,820,855 / 44.87%
Mapped paired reads	2,236,789 / 55.13%
Mapped reads, first in pair	1,114,749 / 27.47%
Mapped reads, second in pair	1,122,040 / 27.65%
Mapped reads, both in pair	2,185,850 / 53.87%
Mapped reads, singletons	50,939 / 1.26%
Read min/max/mean length	30 / 100 / 99.92
Duplicated reads (estimated)	277,555 / 6.84%
Duplication rate	8.79%
Clipped reads	279,200 / 6.88%

2.2. ACGT Content

Number/percentage of A's	64,854,439 / 30.16%
Number/percentage of C's	42,602,074 / 19.81%
Number/percentage of T's	65,077,322 / 30.27%
Number/percentage of G's	42,480,925 / 19.76%
Number/percentage of N's	16,886 / 0.01%
GC Percentage	39.57%

2.3. Coverage

Mean	8.984
Standard Deviation	10.4801

2.4. Mapping Quality

Mean Mapping Quality	58.61
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2.5. Insert size

Mean	853.4
Standard Deviation	24,061.37
P25/Median/P75	337 / 359 / 371

2.6. Mismatches and indels

General error rate	1.72%
Mismatches	3,532,860
Insertions	72,815
Mapped reads with at least one insertion	3.08%
Deletions	84,091
Mapped reads with at least one deletion	3.55%
Homopolymer indels	61.59%

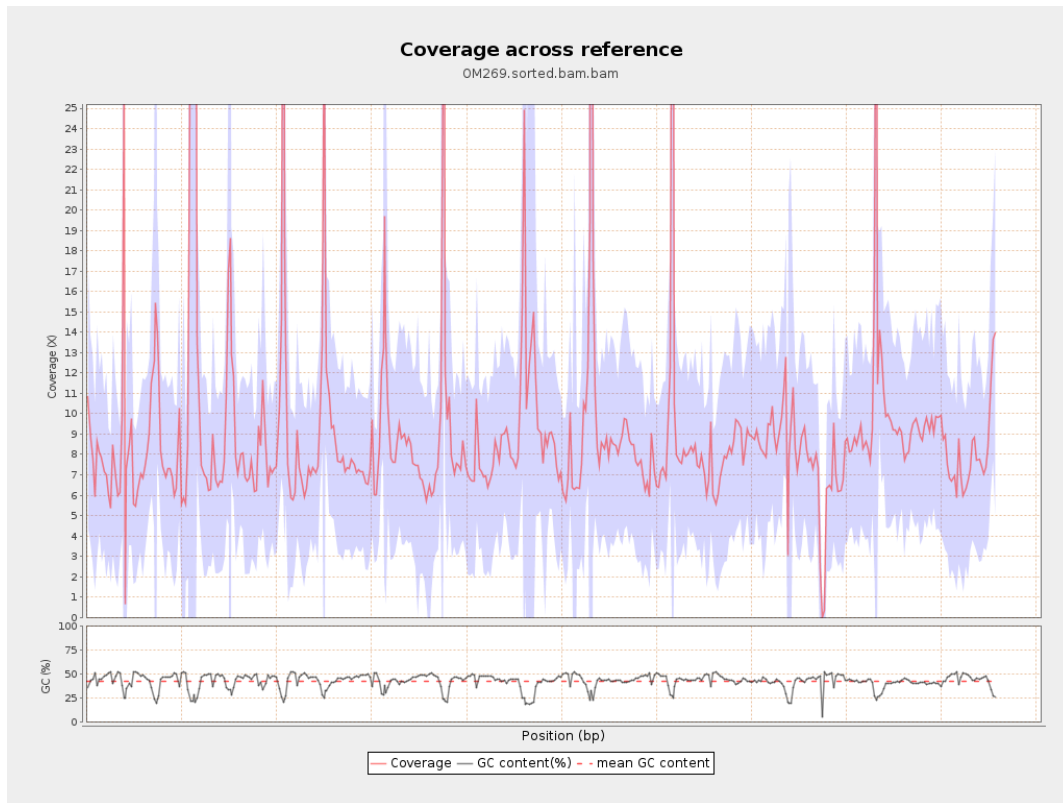
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

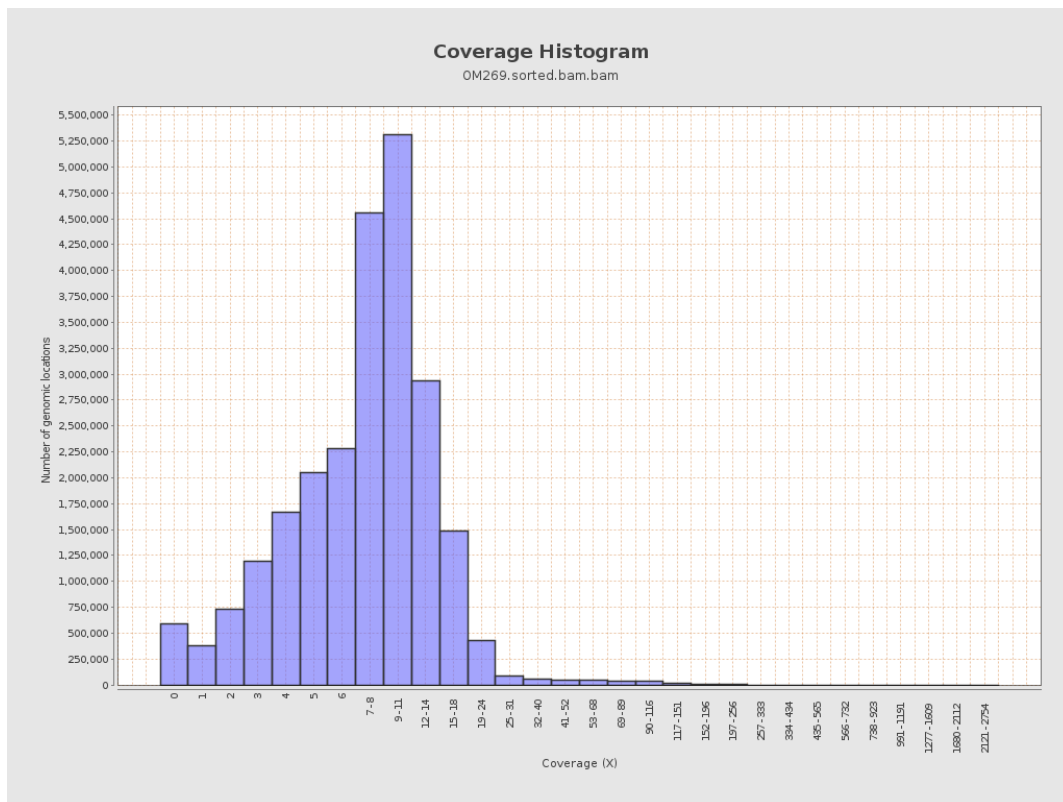
gi 1074120478 emb LT615256.1	977217	7755460	7.9363	6.2772
gi 1074120682 emb LT615257.1	860454	6967975	8.098	7.9255
gi 1074120865 emb LT615258.1	989719	10848599	10.9613	19.3812
gi 1074121086 emb LT615259.1	935450	10336238	11.0495	18.7701
gi 1074121301 emb LT615260.1	1432239	13879760	9.691	11.6894
gi 1074121615 emb LT615261.1	1080962	9706048	8.9791	10.3484
gi 1074121871 emb LT615262.1	1545099	12777471	8.2697	4.2514
gi 1074122235 emb LT615263.1	1585108	14242227	8.985	9.039
gi 1074122590 emb LT615264.1	2122358	18060077	8.5094	5.6752
gi 1074123050 emb LT615265.1	1754192	16374181	9.3343	9.9456
gi 1074123421 emb LT615	2150147	20778465	9.6637	19.0472

266.1				
gi 107412389 8 emb LT615 267.1	3031036	25889569	8.5415	5.4392
gi 107412458 8 emb LT615 268.1	2359348	19508984	8.2688	8.8669
gi 107412506 5 emb LT615 269.1	3135668	28123422	8.9689	4.2672

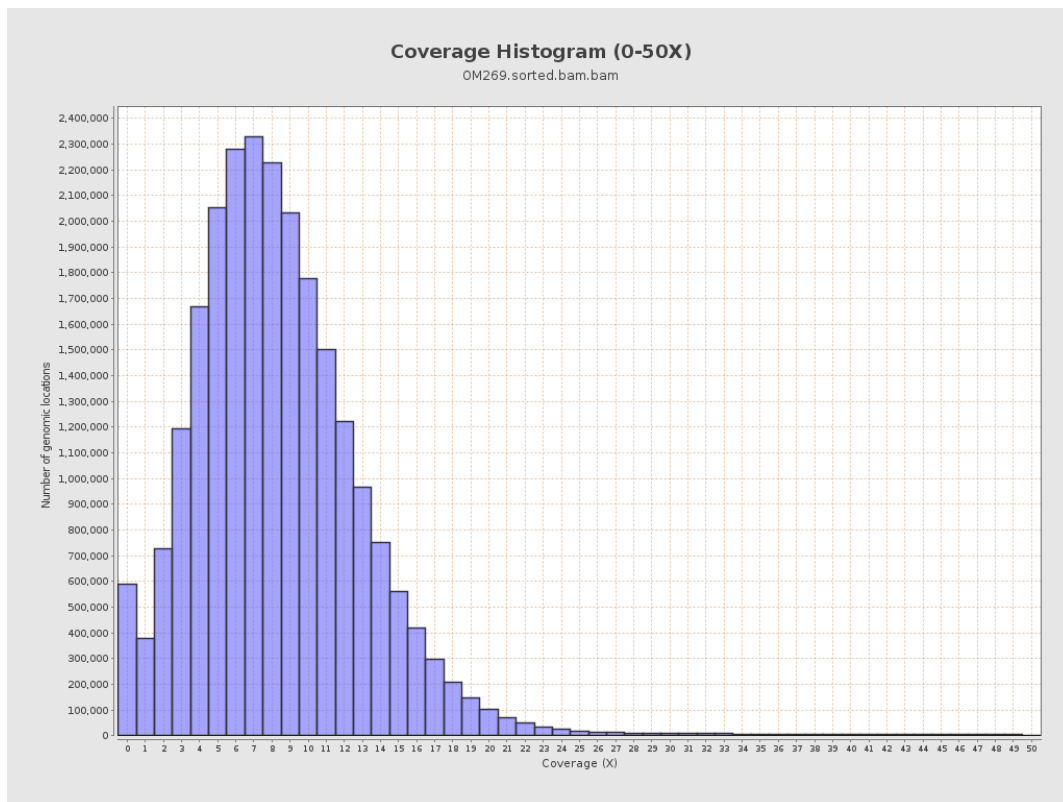
3. Results : Coverage across reference



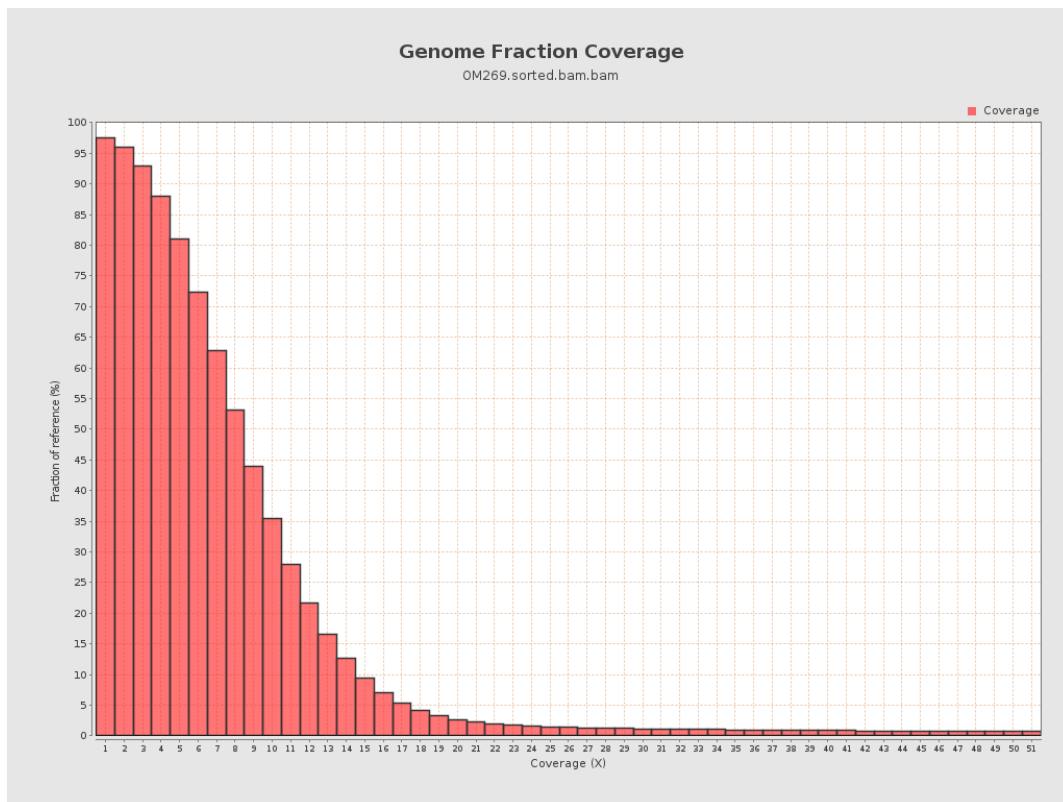
4. Results : Coverage Histogram



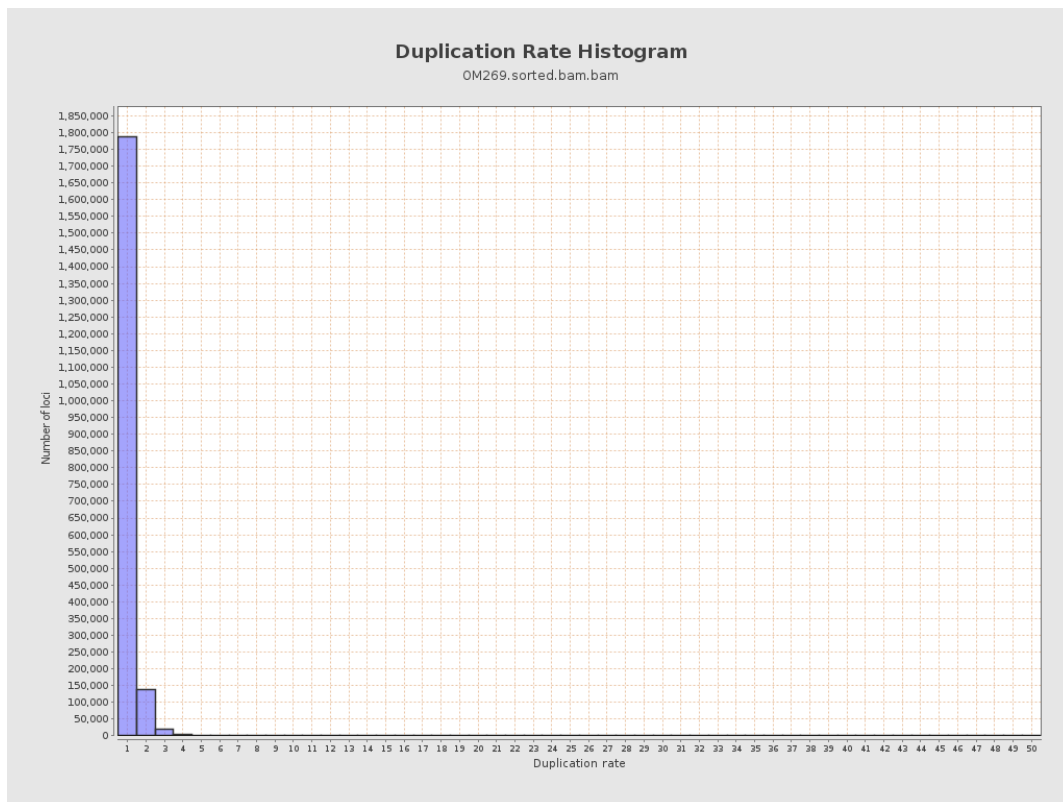
5. Results : Coverage Histogram (0-50X)



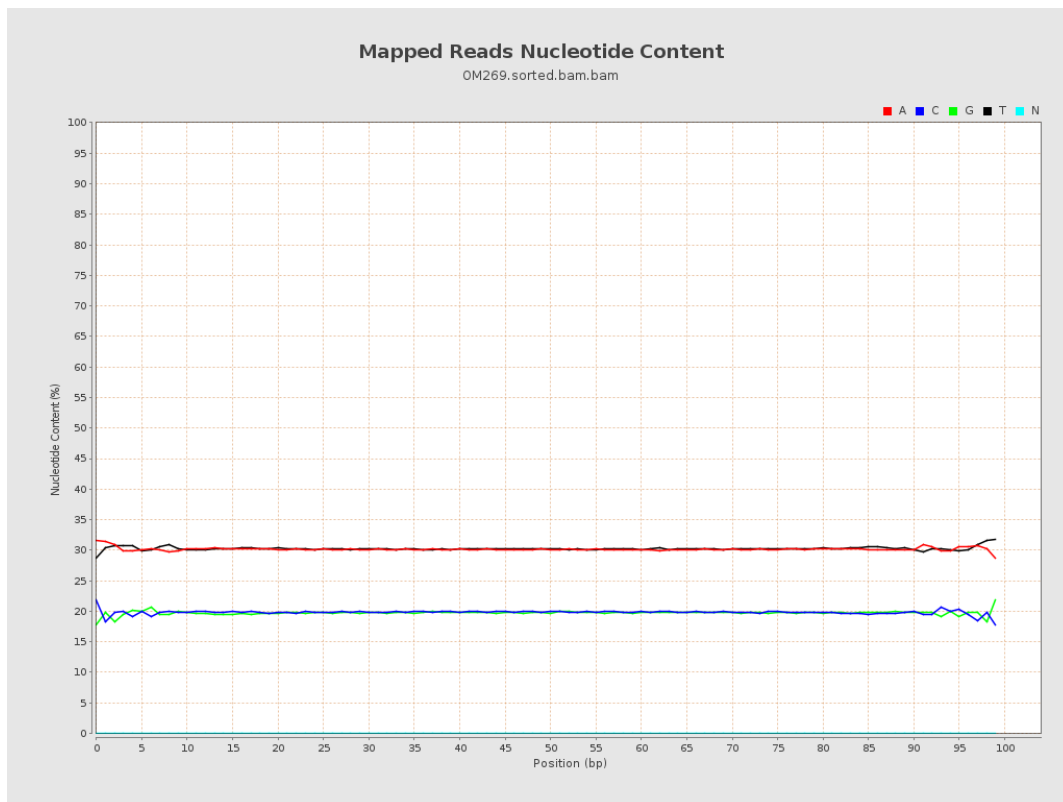
6. Results : Genome Fraction Coverage



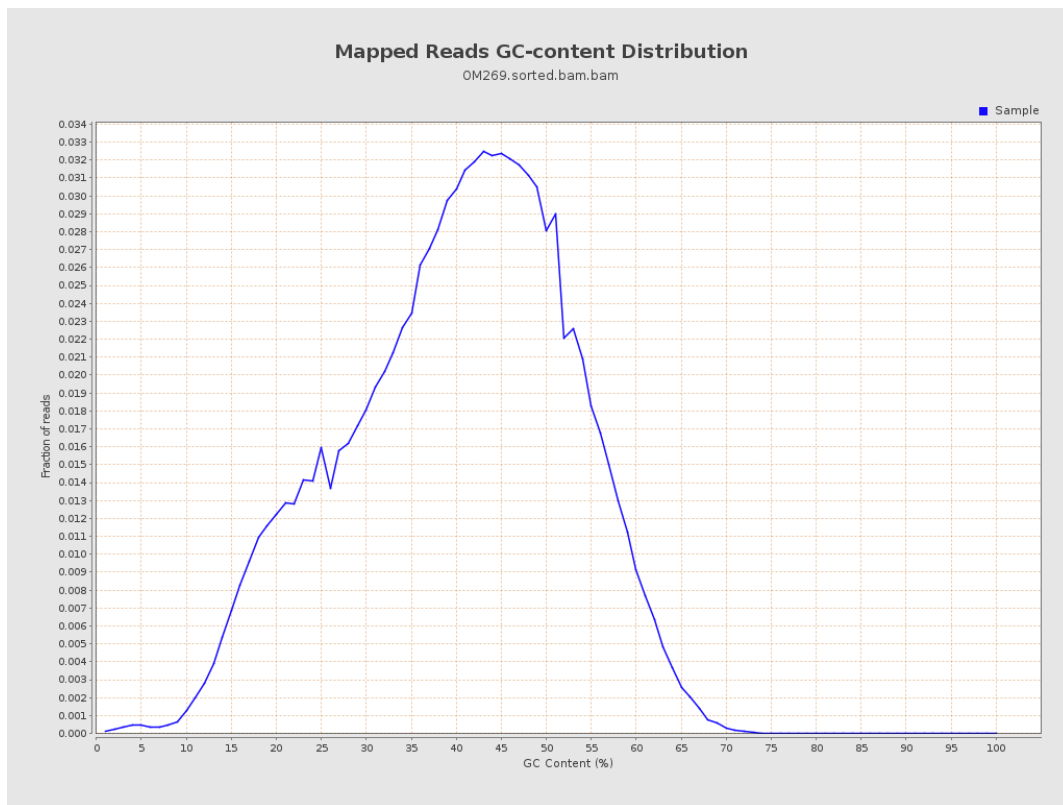
7. Results : Duplication Rate Histogram



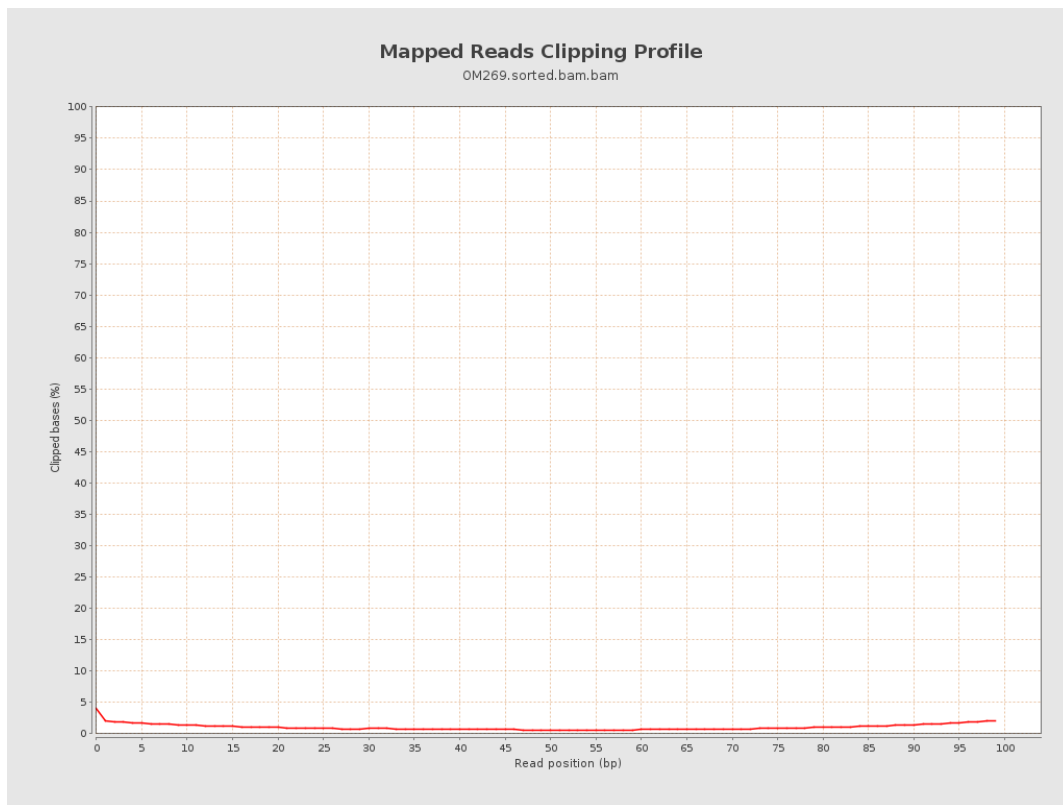
8. Results : Mapped Reads Nucleotide Content



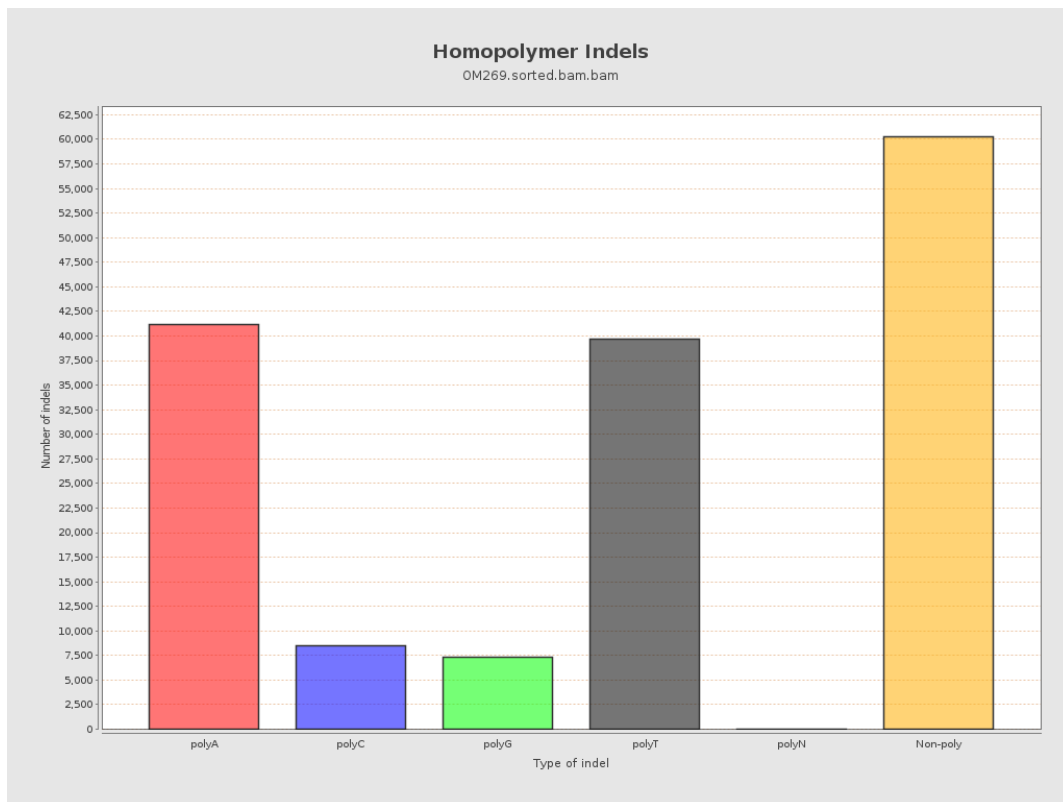
9. Results : Mapped Reads GC-content Distribution



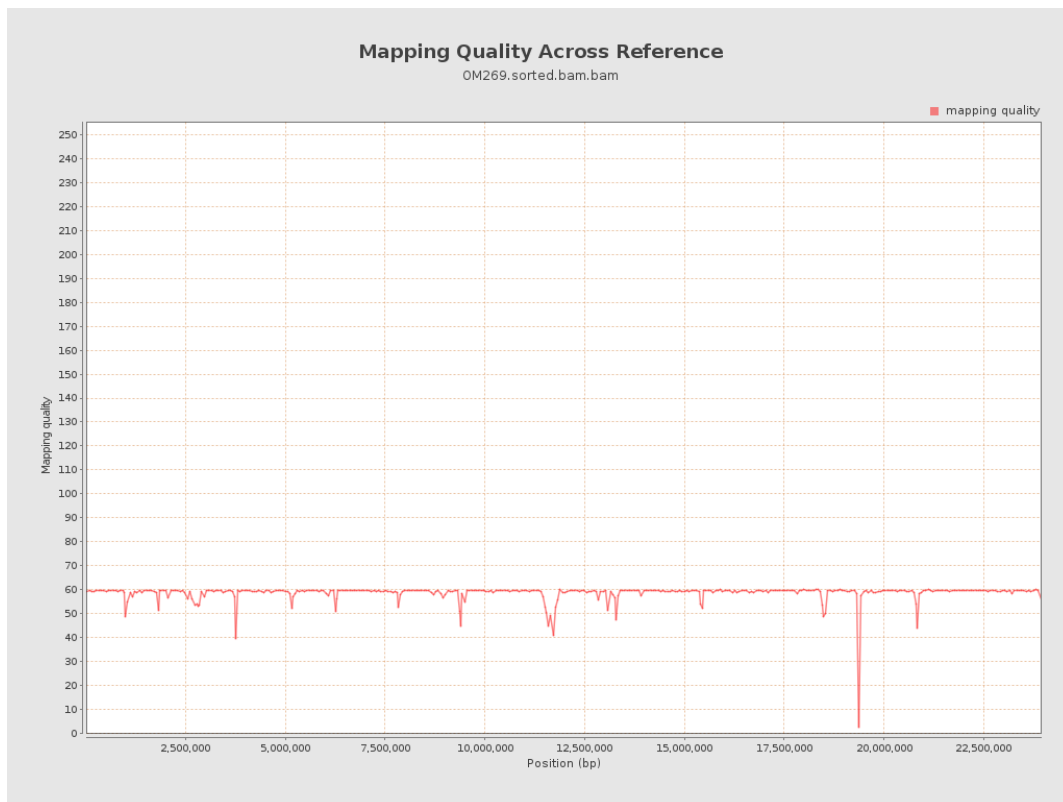
10. Results : Mapped Reads Clipping Profile



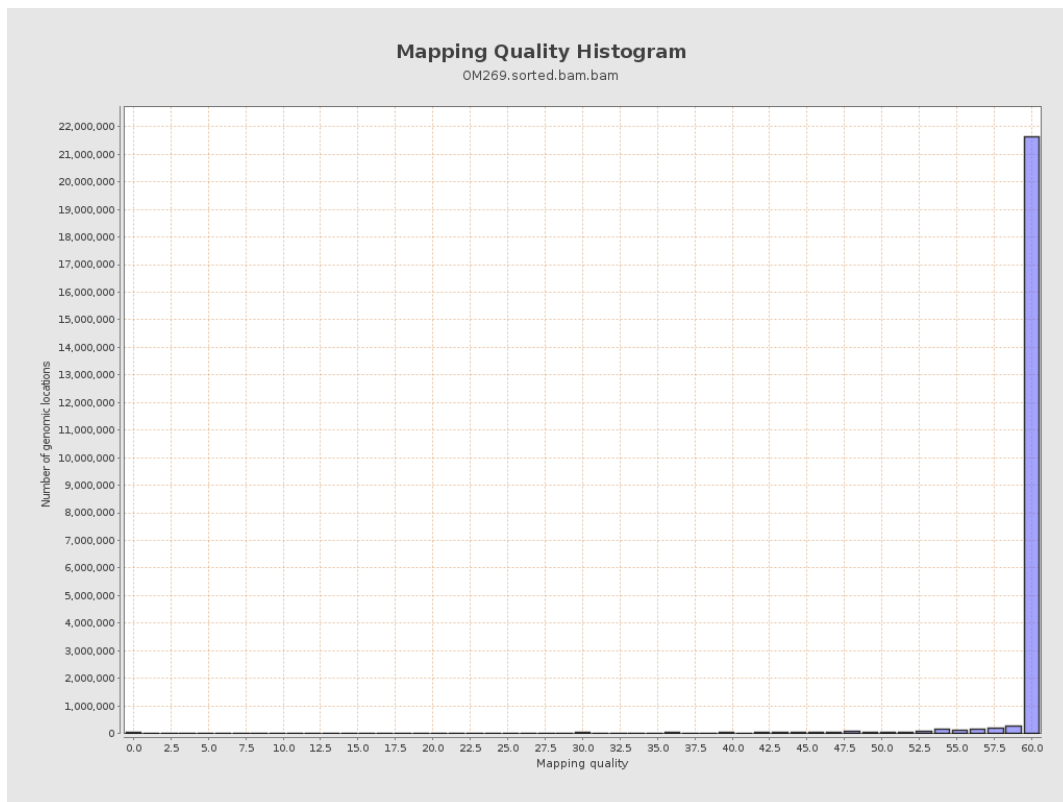
11. Results : Homopolymer Indels



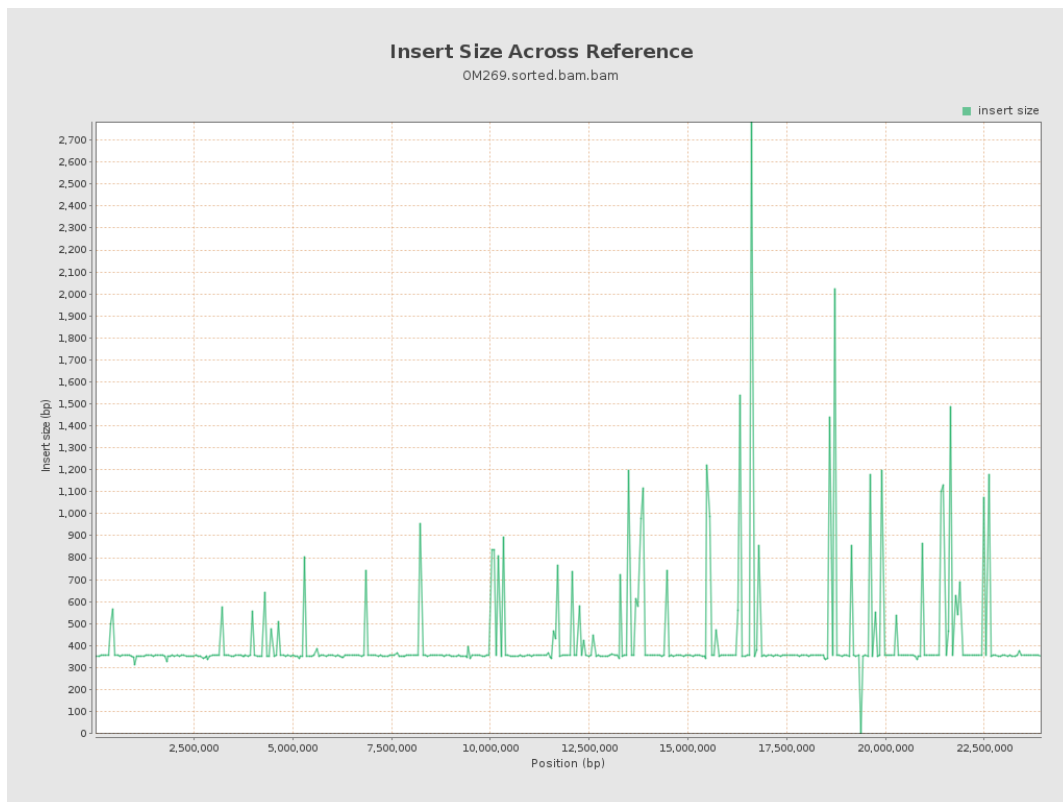
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

