

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2016/10/23 14:00:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM292.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/OM292-BiooBarcode31_CACGAT_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM292-BiooBarcode31_CACGAT_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 14:00:37 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM292.sorted.bam.

	bam
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2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	4,187,474
Mapped reads	1,167,887 / 27.89%
Unmapped reads	3,019,587 / 72.11%
Mapped paired reads	1,167,887 / 27.89%
Mapped reads, first in pair	588,135 / 14.05%
Mapped reads, second in pair	579,752 / 13.84%
Mapped reads, both in pair	1,124,387 / 26.85%
Mapped reads, singletons	43,500 / 1.04%
Read min/max/mean length	30 / 100 / 99.95
Duplicated reads (estimated)	102,105 / 2.44%
Duplication rate	6.17%
Clipped reads	147,588 / 3.52%

2.2. ACGT Content

Number/percentage of A's	33,658,881 / 30.11%
Number/percentage of C's	22,188,994 / 19.85%
Number/percentage of T's	33,819,449 / 30.25%
Number/percentage of G's	22,127,260 / 19.79%
Number/percentage of N's	8,973 / 0.01%
GC Percentage	39.64%

2.3. Coverage

Mean	4.6713
Standard Deviation	5.5849

2.4. Mapping Quality

Mean Mapping Quality	58.35
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2.5. Insert size

Mean	960.22
Standard Deviation	30,772.75
P25/Median/P75	323 / 339 / 349

2.6. Mismatches and indels

General error rate	1.61%
Mismatches	1,710,948
Insertions	38,358
Mapped reads with at least one insertion	3.1%
Deletions	43,351
Mapped reads with at least one deletion	3.48%
Homopolymer indels	62.84%

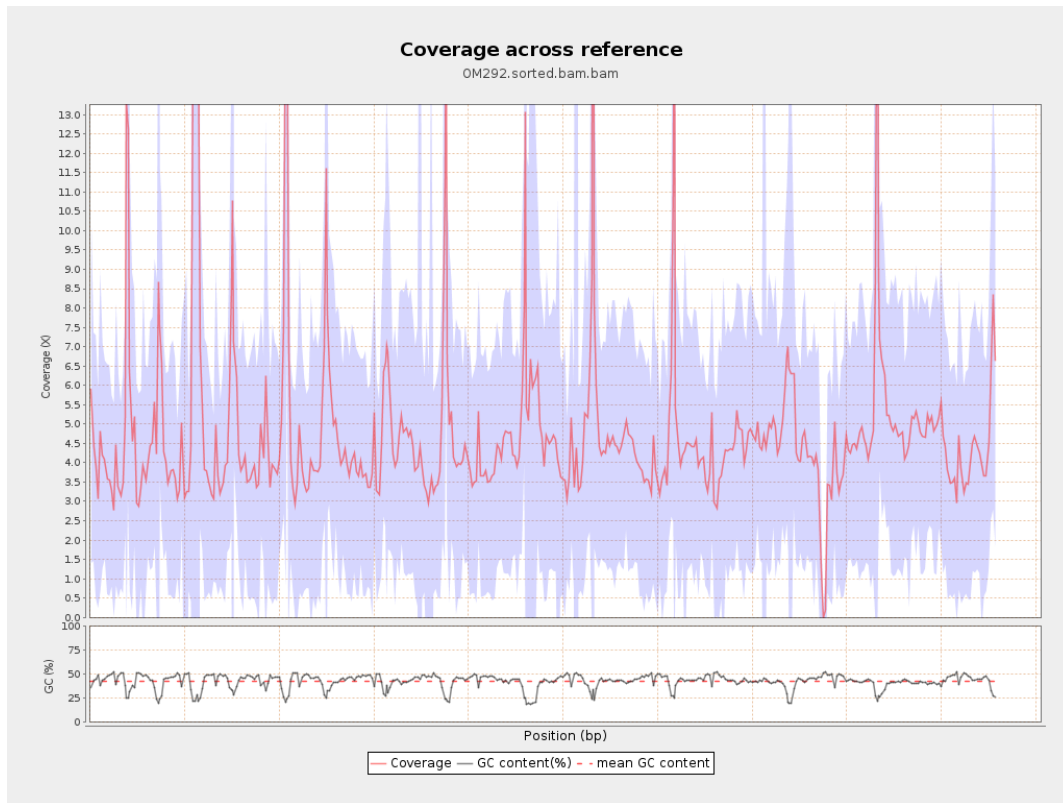
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

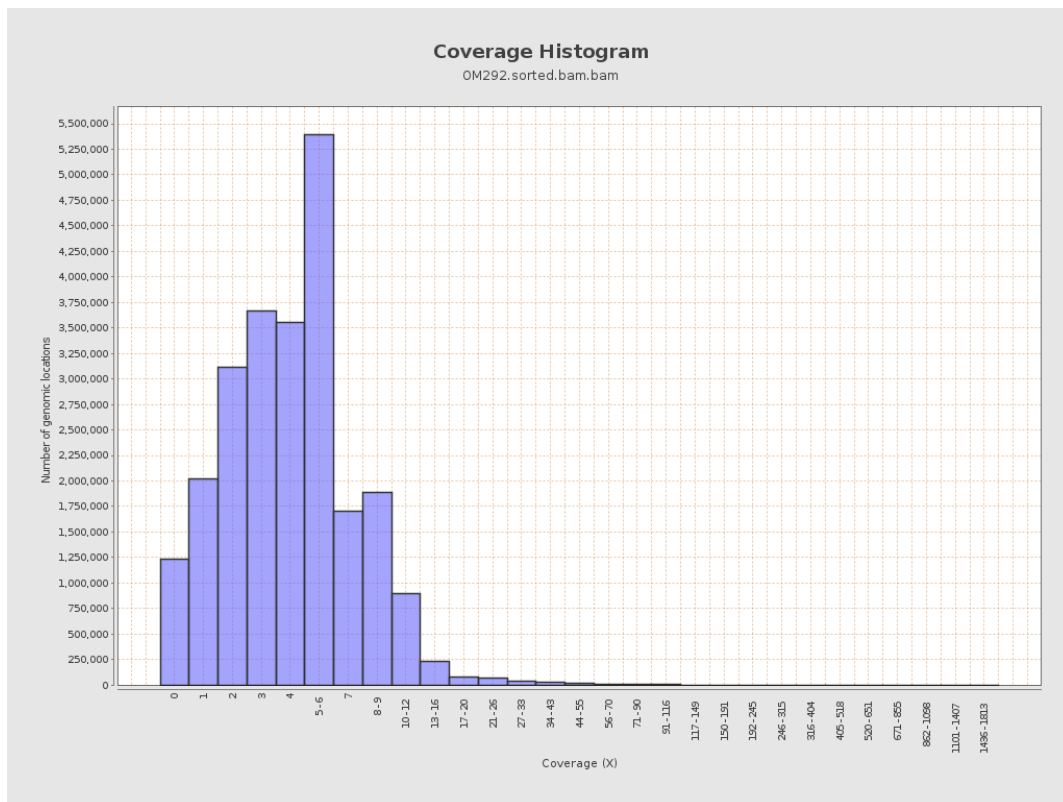
gi 1074120478 emb LT615256.1	977217	4034440	4.1285	3.4506
gi 1074120682 emb LT615257.1	860454	4200985	4.8823	4.9766
gi 1074120865 emb LT615258.1	989719	5395620	5.4517	8.6287
gi 1074121086 emb LT615259.1	935450	4719078	5.0447	8.006
gi 1074121301 emb LT615260.1	1432239	7014814	4.8978	5.3717
gi 1074121615 emb LT615261.1	1080962	5107317	4.7248	4.9317
gi 1074121871 emb LT615262.1	1545099	6731554	4.3567	2.7307
gi 1074122235 emb LT615263.1	1585108	7303864	4.6078	5.5916
gi 1074122590 emb LT615264.1	2122358	9516924	4.4841	3.3171
gi 1074123050 emb LT615265.1	1754192	8315342	4.7403	8.7817
gi 1074123421 emb LT615	2150147	10238366	4.7617	8.6473

266.1				
gi 107412389 8 emb LT615 267.1	3031036	13837096	4.5651	4.0094
gi 107412458 8 emb LT615 268.1	2359348	10482859	4.4431	4.8358
gi 107412506 5 emb LT615 269.1	3135668	15020352	4.7902	2.9413

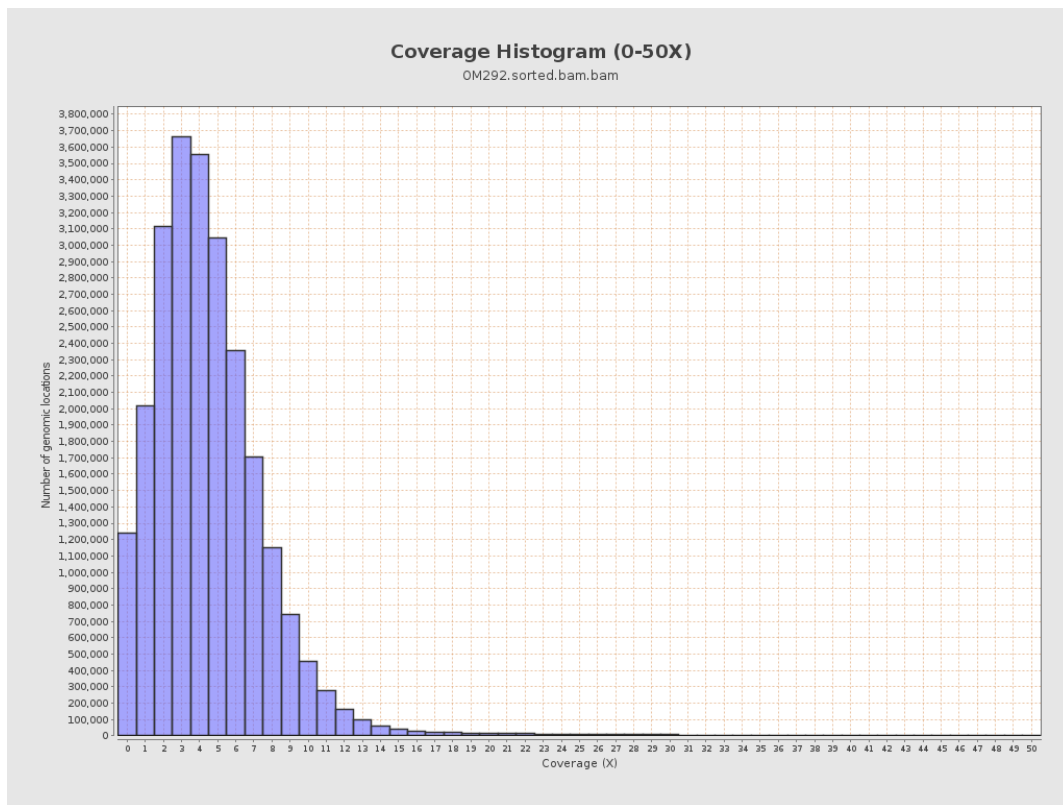
3. Results : Coverage across reference



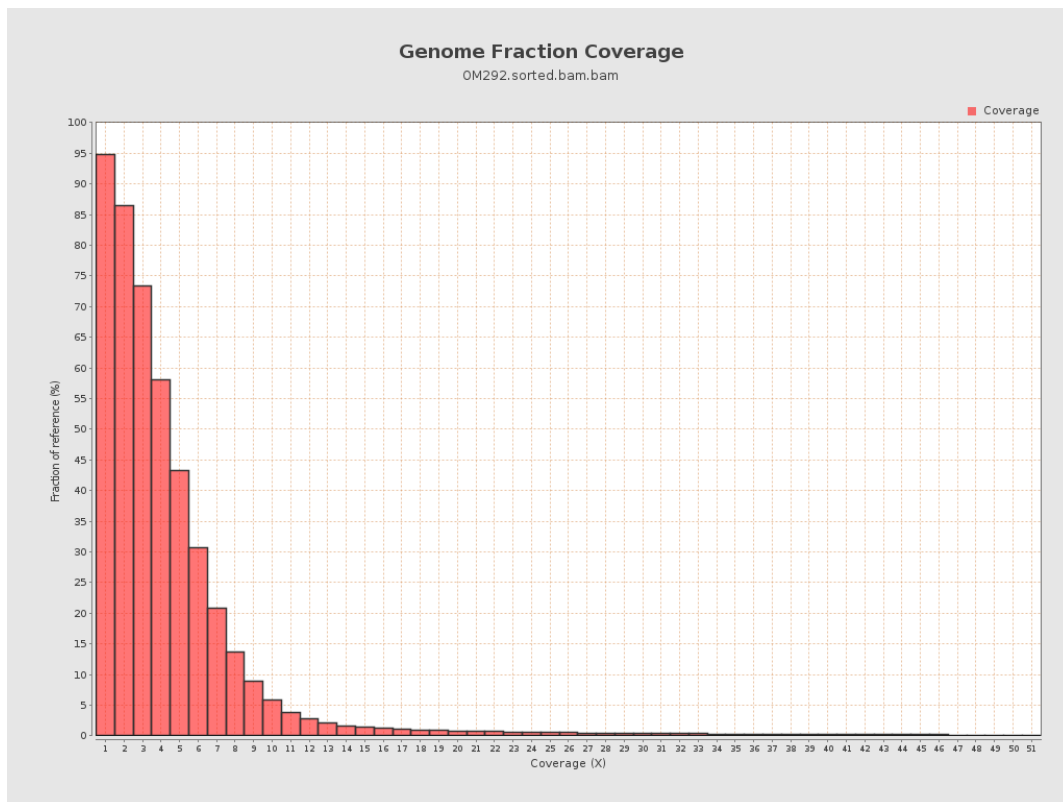
4. Results : Coverage Histogram



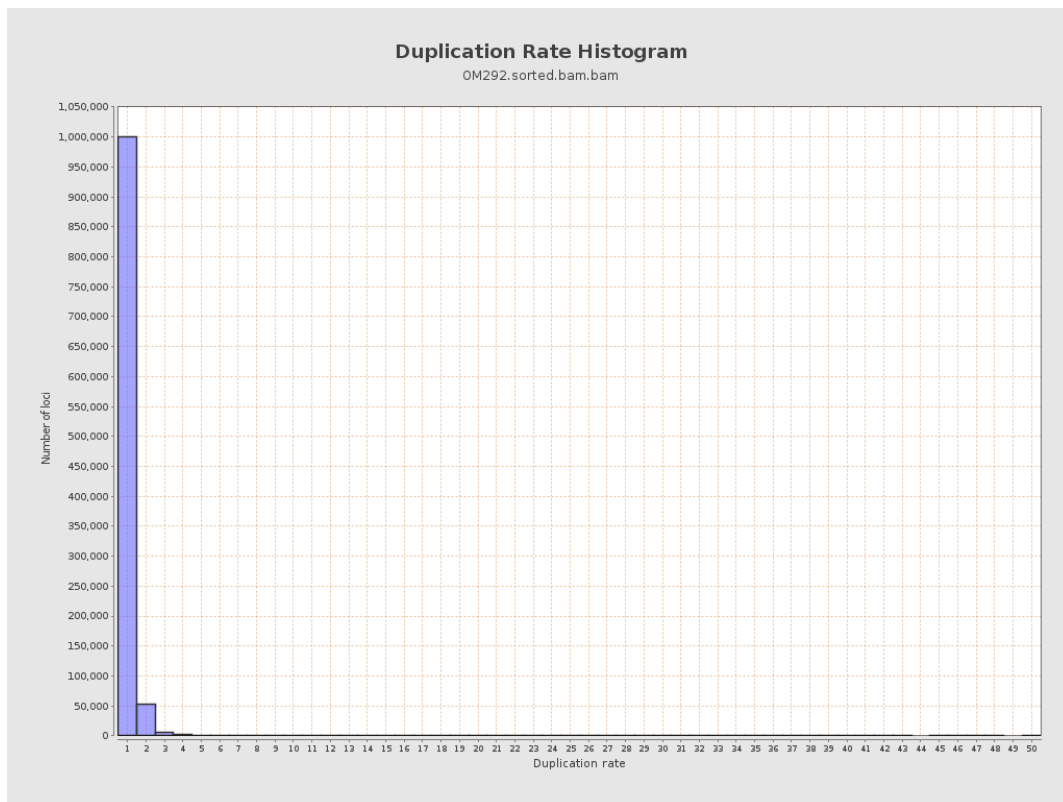
5. Results : Coverage Histogram (0-50X)



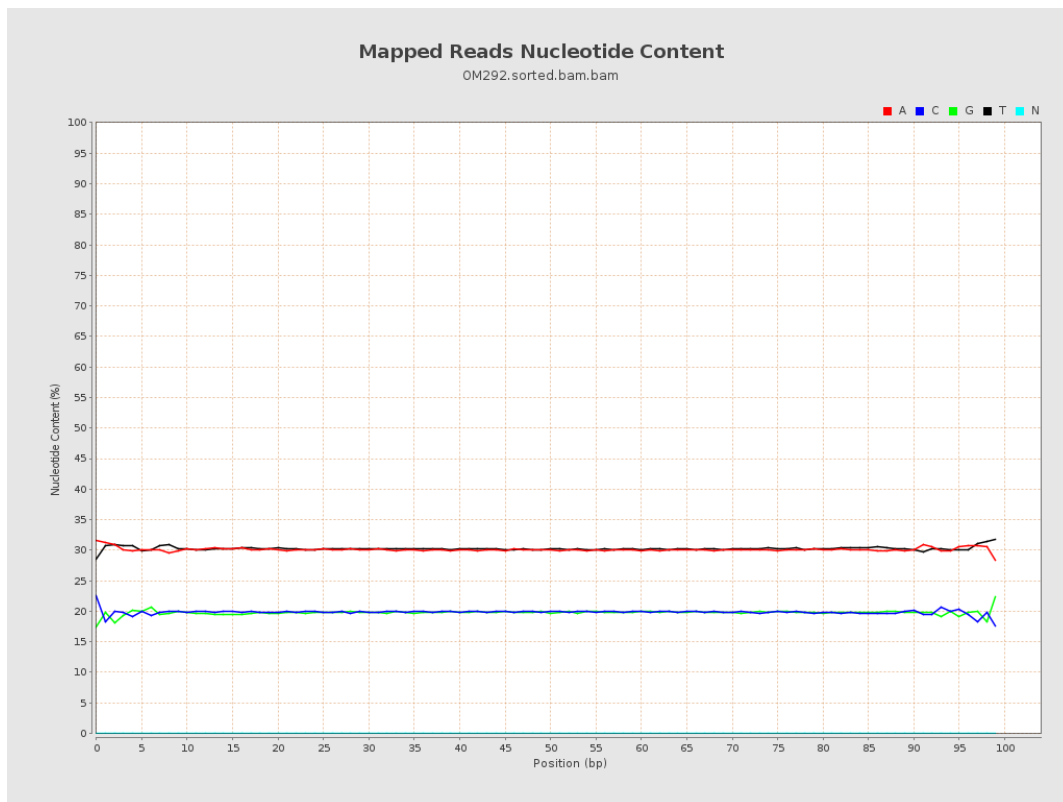
6. Results : Genome Fraction Coverage



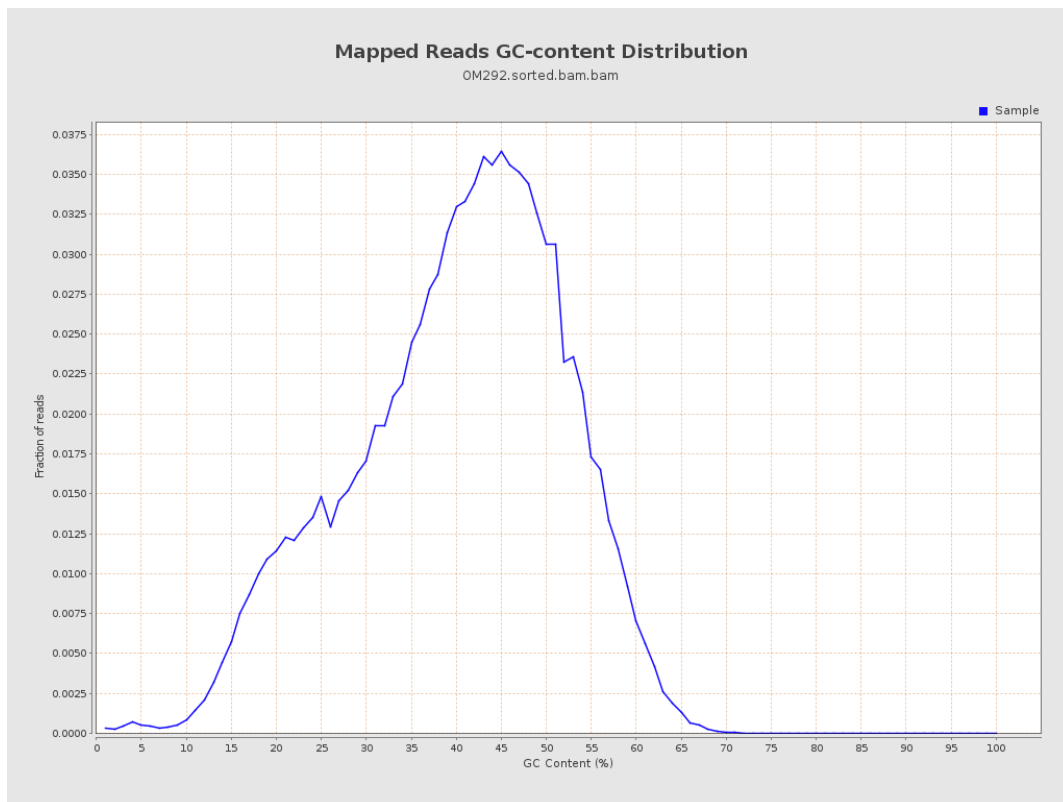
7. Results : Duplication Rate Histogram



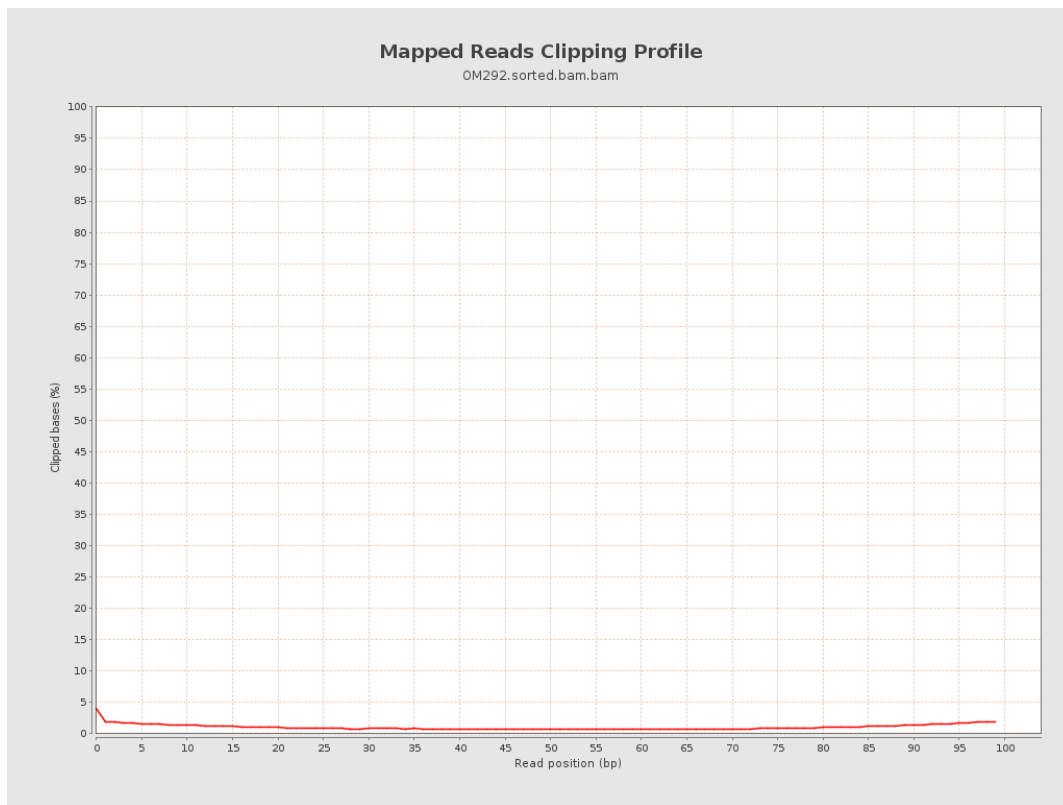
8. Results : Mapped Reads Nucleotide Content



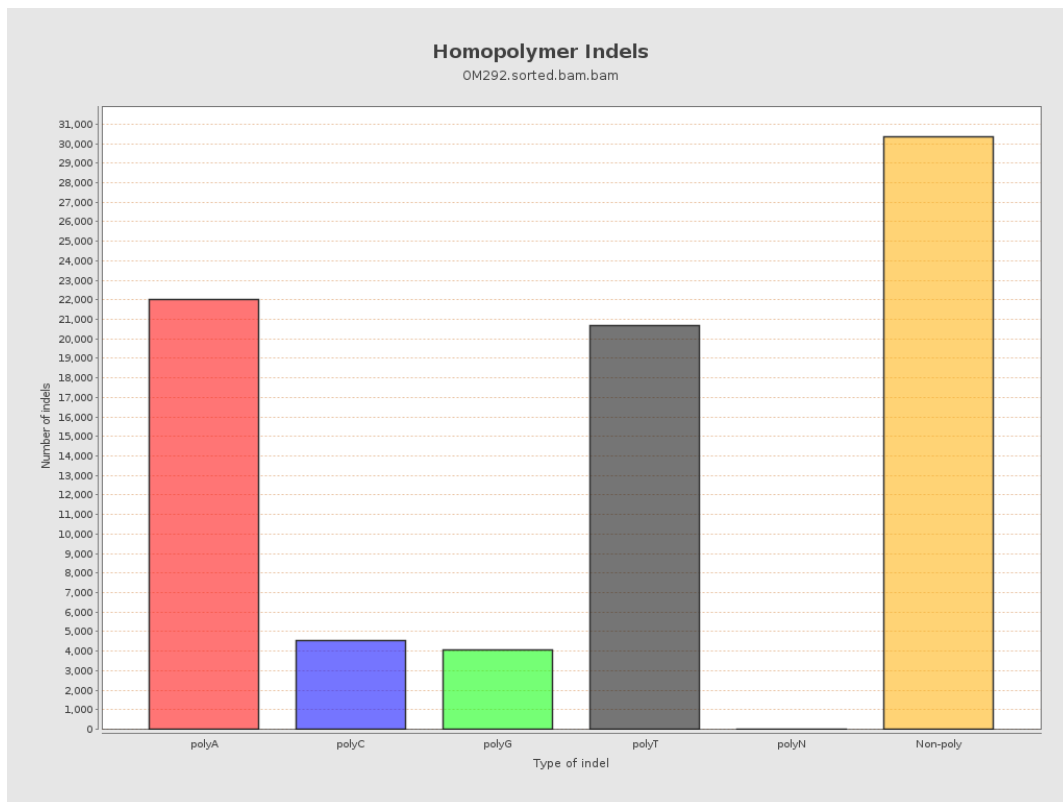
9. Results : Mapped Reads GC-content Distribution



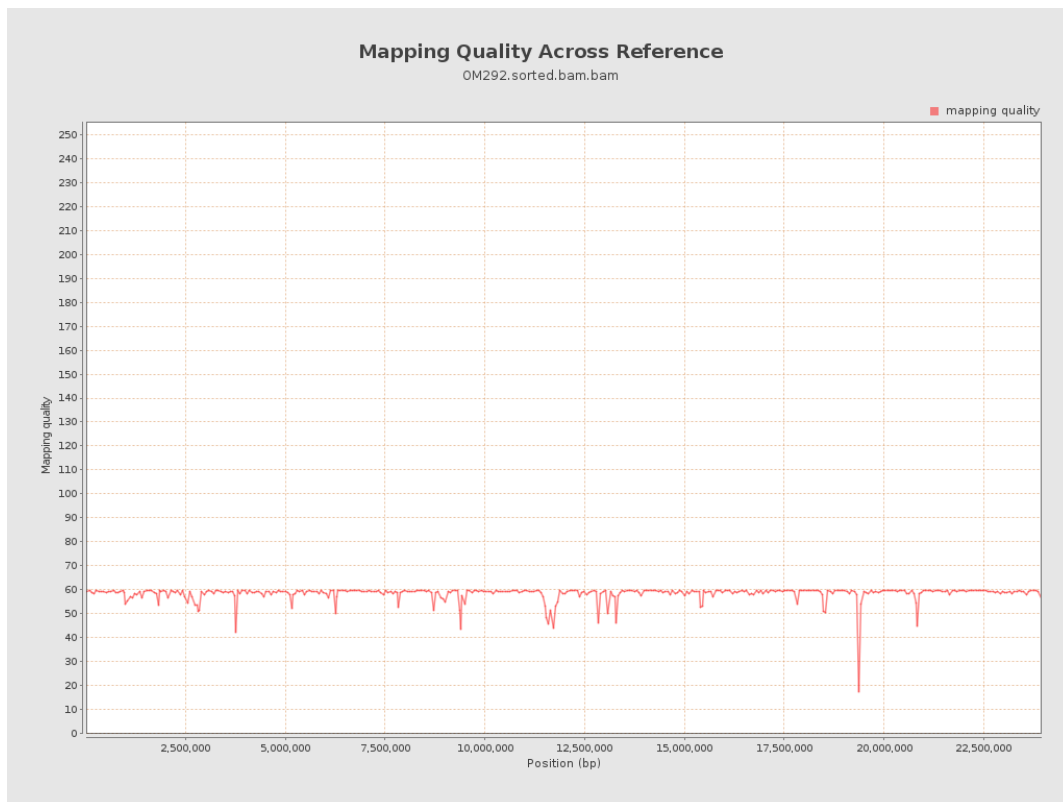
10. Results : Mapped Reads Clipping Profile



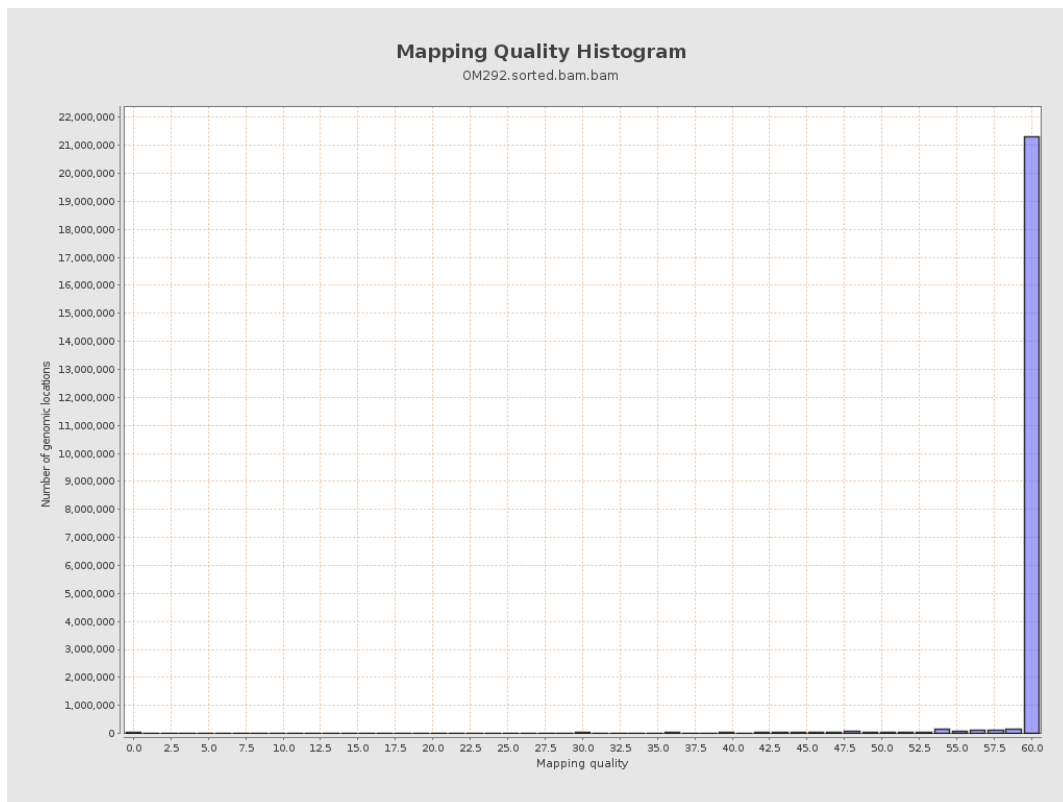
11. Results : Homopolymer Indels



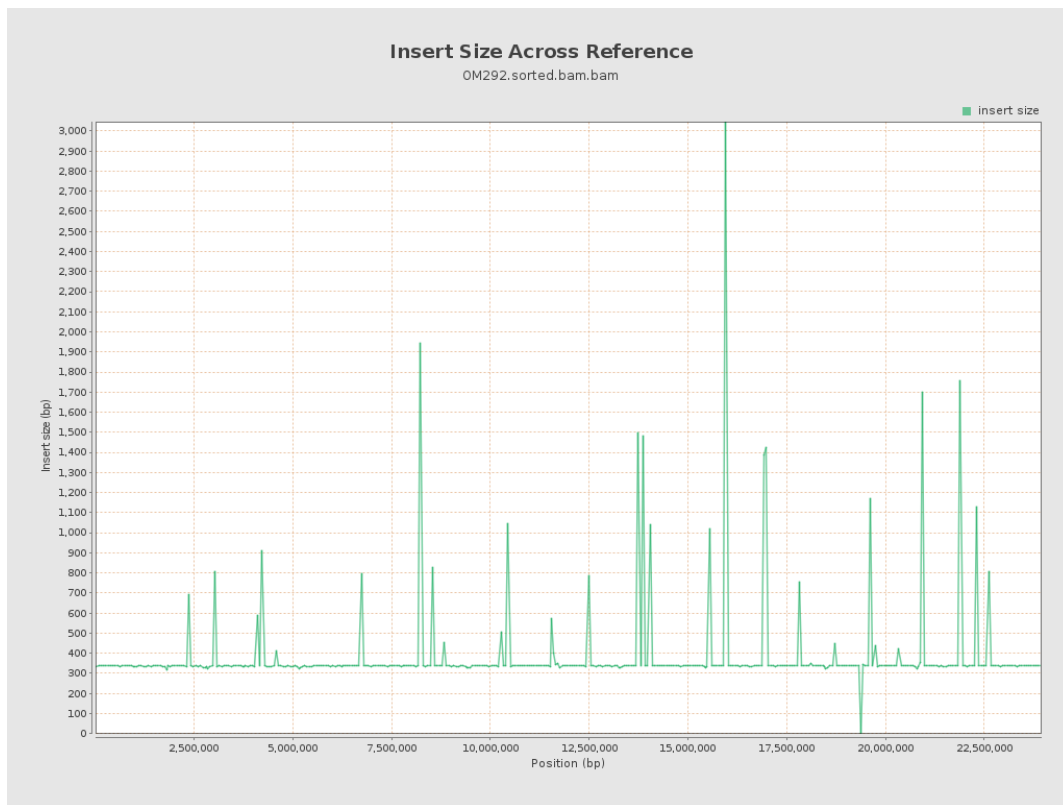
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

