

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2016/10/23 14:01:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM299.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/OM299-BiooBarcode33_CAGGCG_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM299-BiooBarcode33_CAGGCG_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 14:01:24 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM299.sorted.bam.

	bam
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2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	2,096,324
Mapped reads	1,338,286 / 63.84%
Unmapped reads	758,038 / 36.16%
Mapped paired reads	1,338,286 / 63.84%
Mapped reads, first in pair	671,840 / 32.05%
Mapped reads, second in pair	666,446 / 31.79%
Mapped reads, both in pair	1,306,844 / 62.34%
Mapped reads, singletons	31,442 / 1.5%
Read min/max/mean length	30 / 100 / 99.91
Duplicated reads (estimated)	127,490 / 6.08%
Duplication rate	6.69%
Clipped reads	168,651 / 8.05%

2.2. ACGT Content

Number/percentage of A's	39,061,165 / 30.35%
Number/percentage of C's	25,273,616 / 19.64%
Number/percentage of T's	39,138,016 / 30.41%
Number/percentage of G's	25,242,104 / 19.61%
Number/percentage of N's	10,422 / 0.01%
GC Percentage	39.25%

2.3. Coverage

Mean	5.3782
Standard Deviation	6.3028

2.4. Mapping Quality

Mean Mapping Quality	58.68
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2.5. Insert size

Mean	906.54
Standard Deviation	25,462.99
P25/Median/P75	340 / 356 / 365

2.6. Mismatches and indels

General error rate	1.77%
Mismatches	2,176,344
Insertions	45,337
Mapped reads with at least one insertion	3.21%
Deletions	52,332
Mapped reads with at least one deletion	3.68%
Homopolymer indels	62.16%

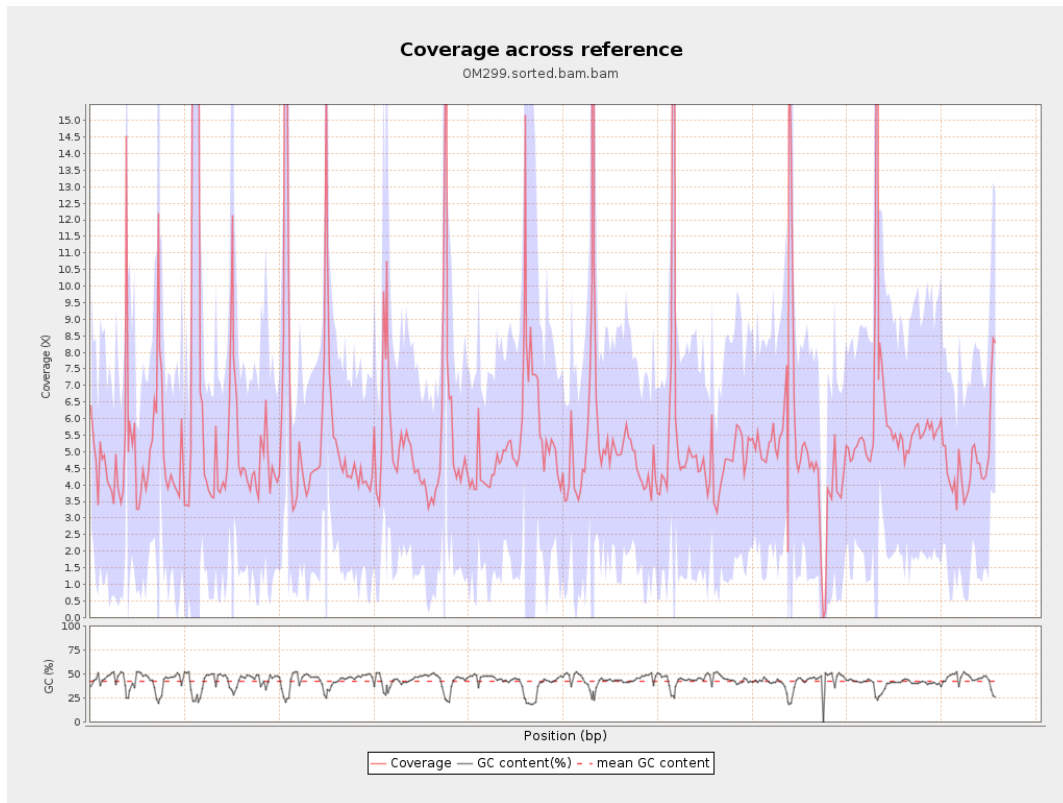
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

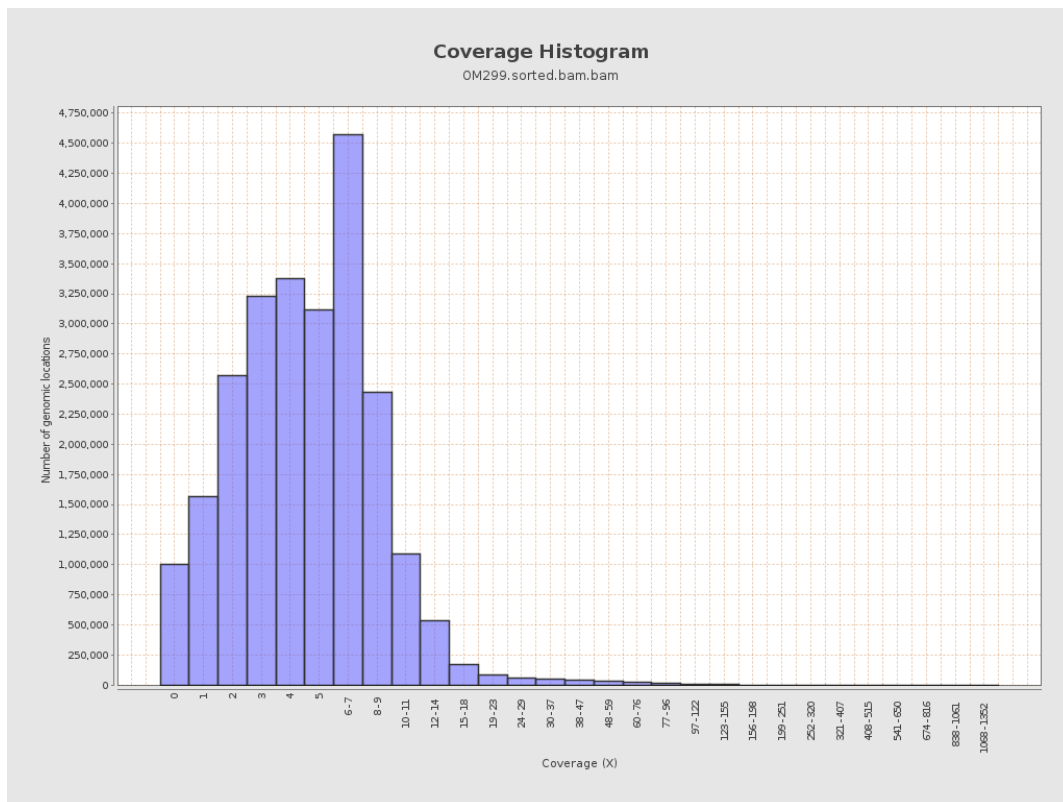
gi 1074120478 emb LT615256.1	977217	4573684	4.6803	3.2456
gi 1074120682 emb LT615257.1	860454	4481604	5.2084	5.0173
gi 1074120865 emb LT615258.1	989719	6542335	6.6103	11.735
gi 1074121086 emb LT615259.1	935450	5524325	5.9055	10.4719
gi 1074121301 emb LT615260.1	1432239	8302398	5.7968	7.5724
gi 1074121615 emb LT615261.1	1080962	5967022	5.5201	6.1838
gi 1074121871 emb LT615262.1	1545099	7693292	4.9792	3.1579
gi 1074122235 emb LT615263.1	1585108	8376322	5.2844	5.2764
gi 1074122590 emb LT615264.1	2122358	10724181	5.053	3.7546
gi 1074123050 emb LT615265.1	1754192	9448876	5.3865	4.8779
gi 1074123421 emb LT615	2150147	12252439	5.6984	10.1295

266.1				
gi 107412389 8 emb LT615 267.1	3031036	15366848	5.0698	3.8481
gi 107412458 8 emb LT615 268.1	2359348	12889062	5.463	7.4012
gi 107412506 5 emb LT615 269.1	3135668	16714218	5.3304	2.9901

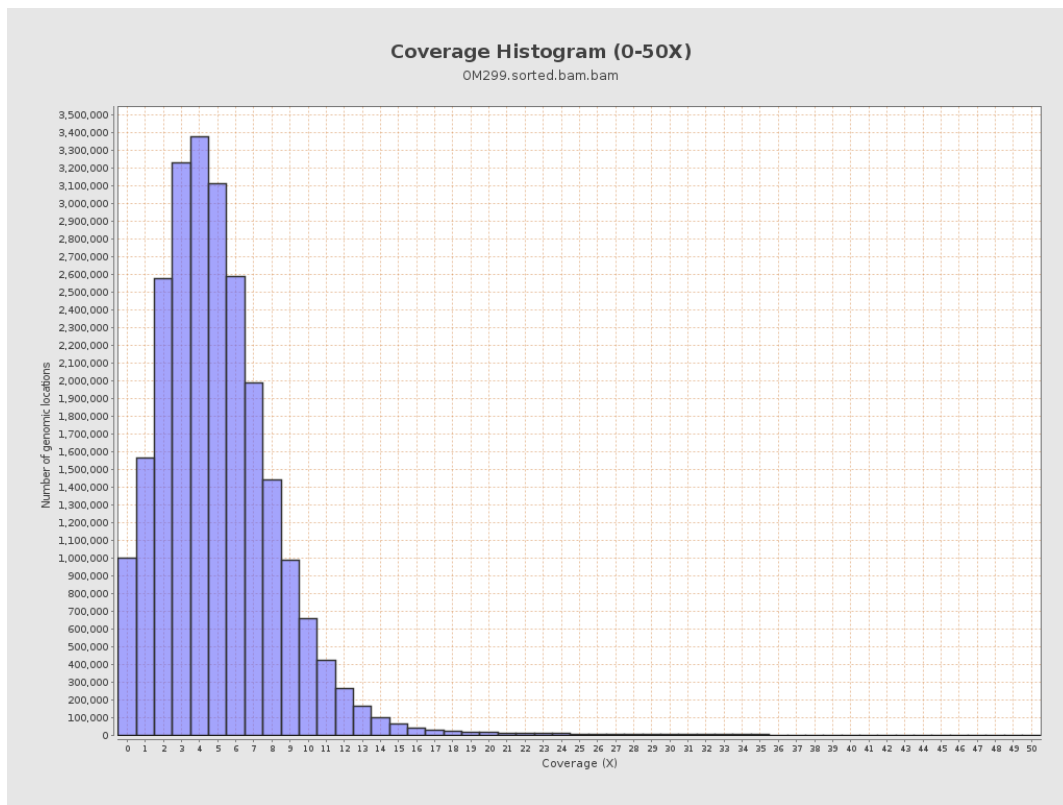
3. Results : Coverage across reference



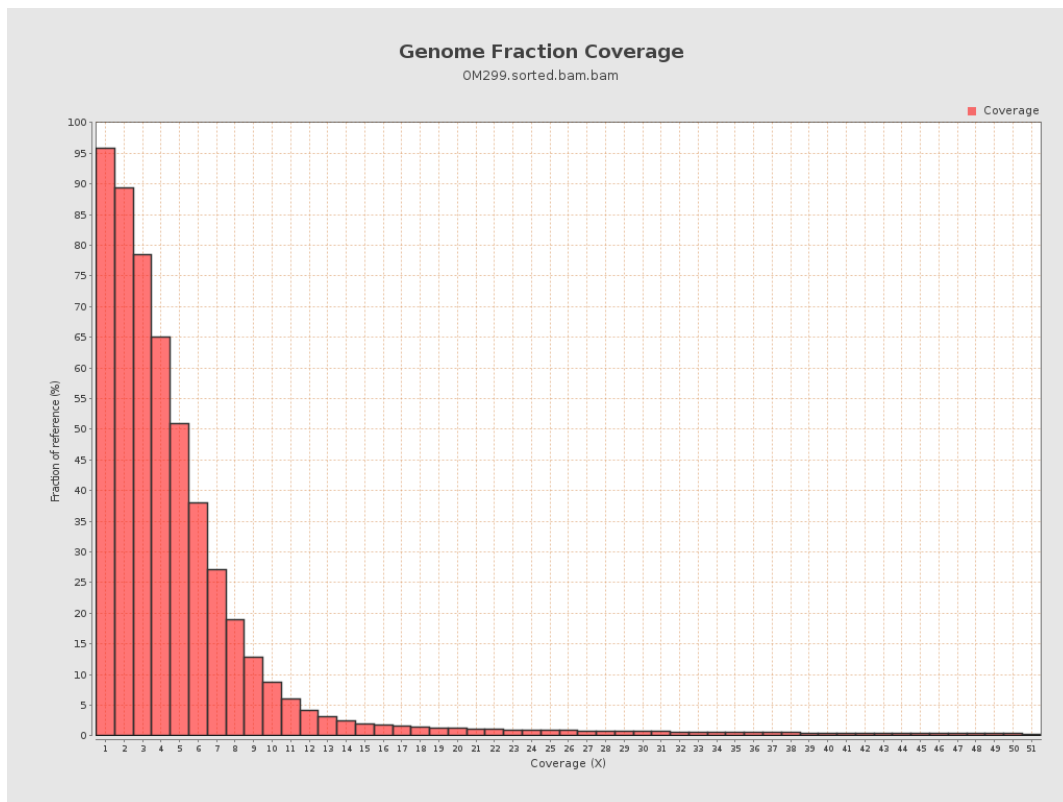
4. Results : Coverage Histogram



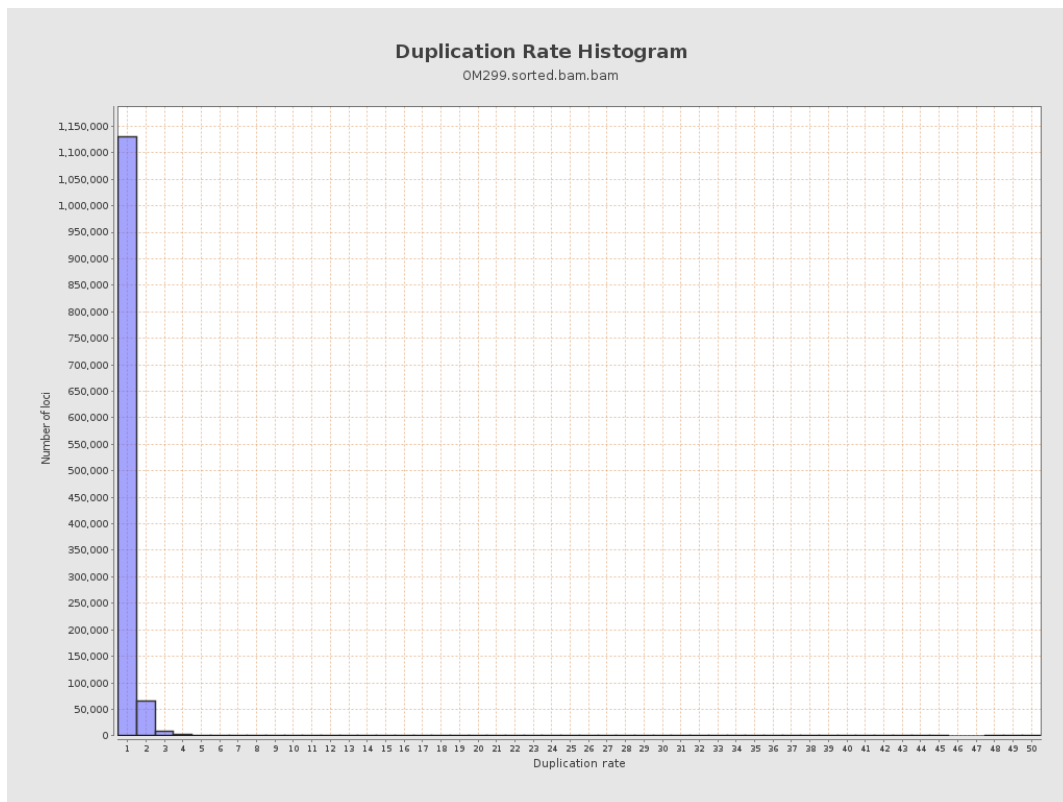
5. Results : Coverage Histogram (0-50X)



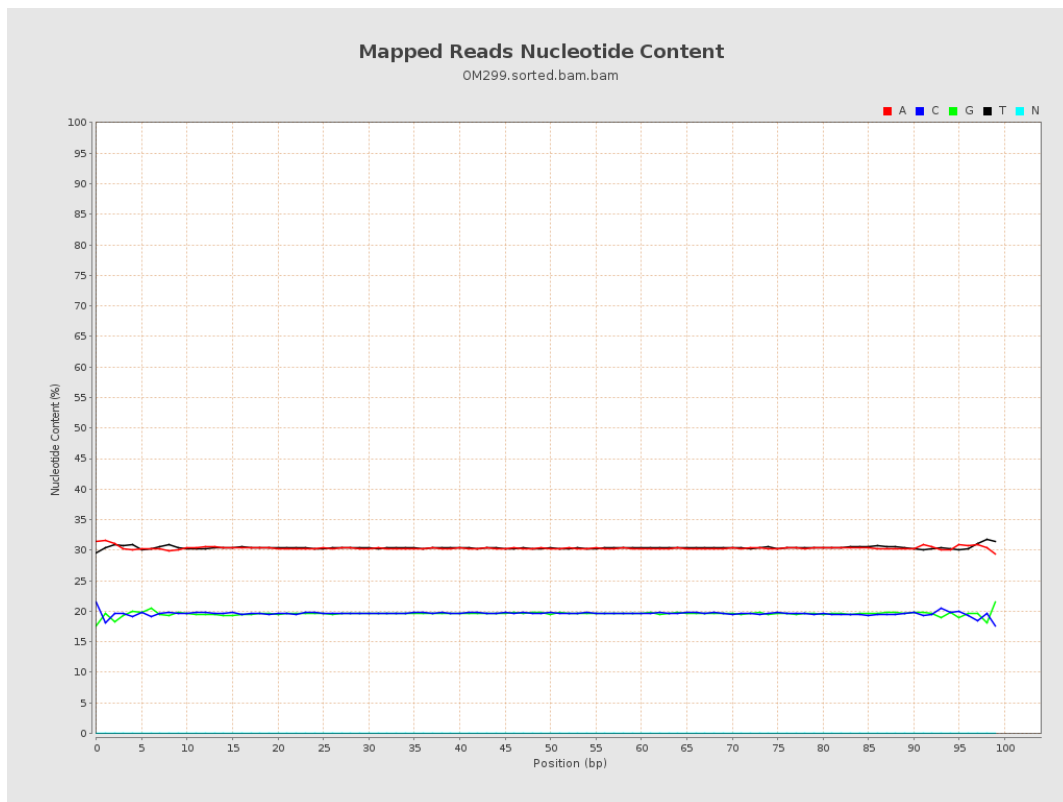
6. Results : Genome Fraction Coverage



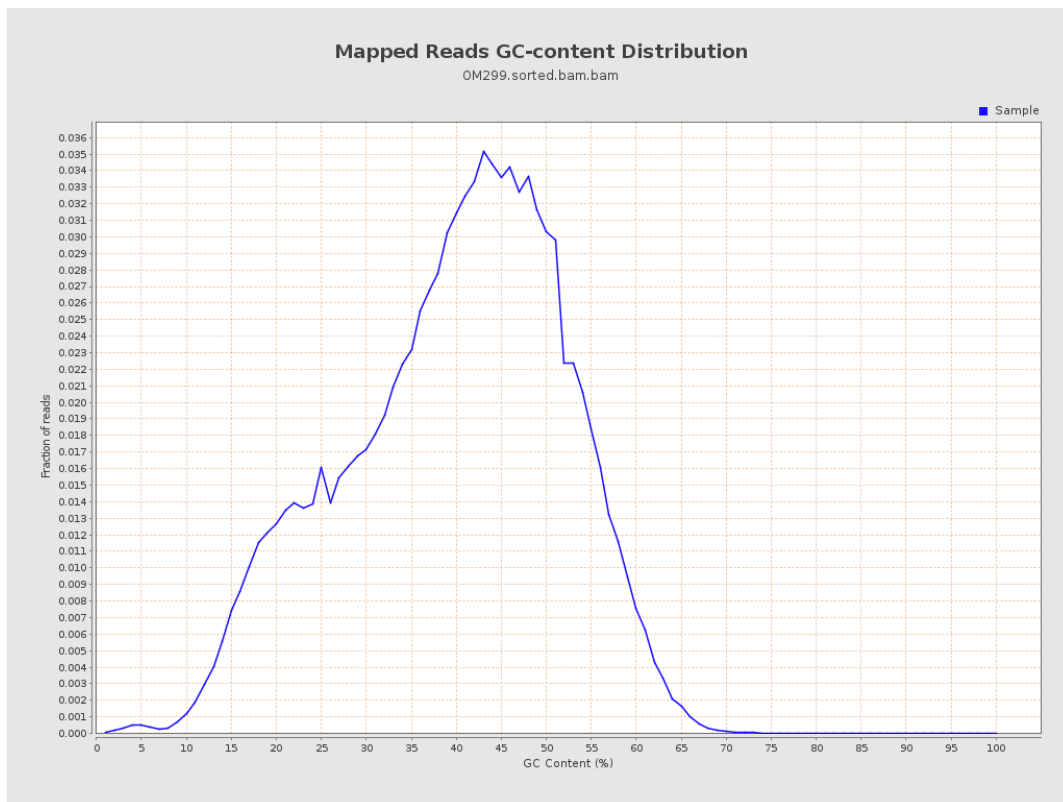
7. Results : Duplication Rate Histogram



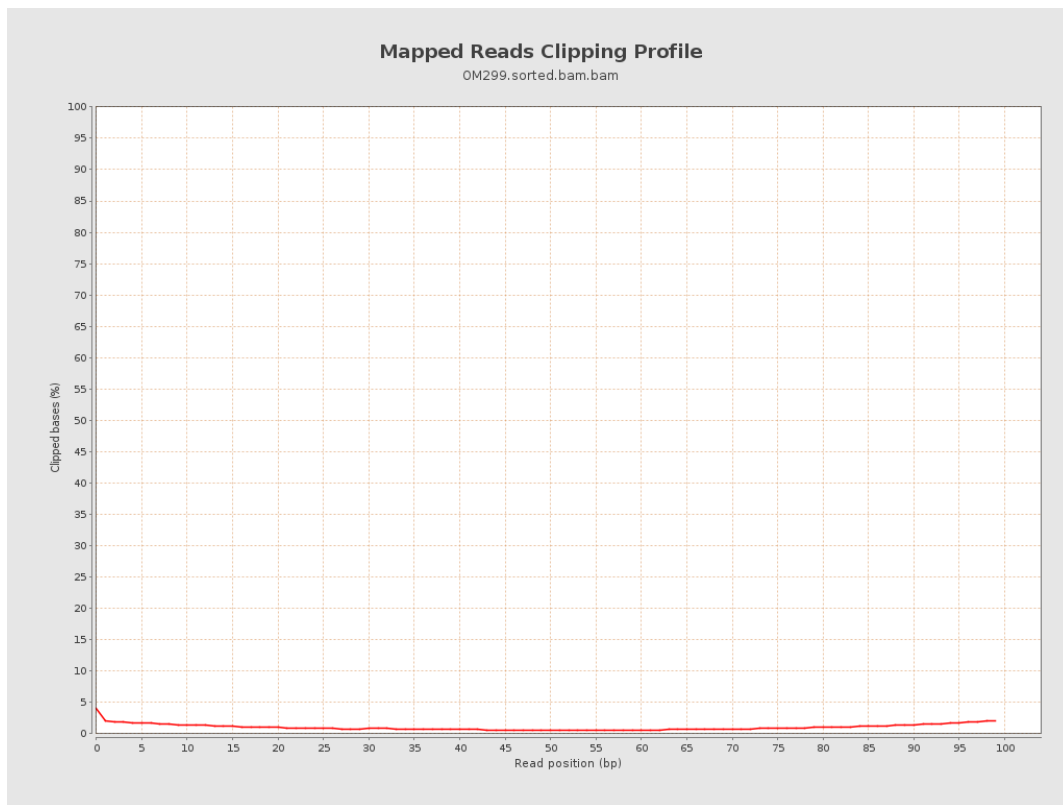
8. Results : Mapped Reads Nucleotide Content



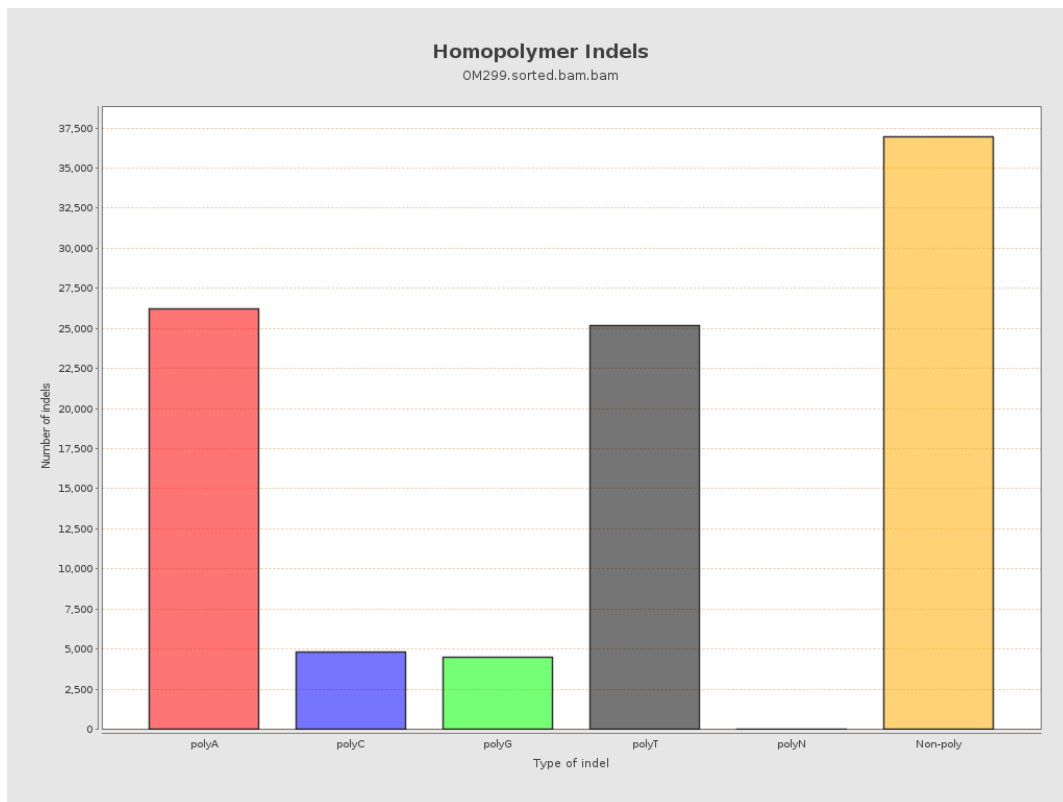
9. Results : Mapped Reads GC-content Distribution



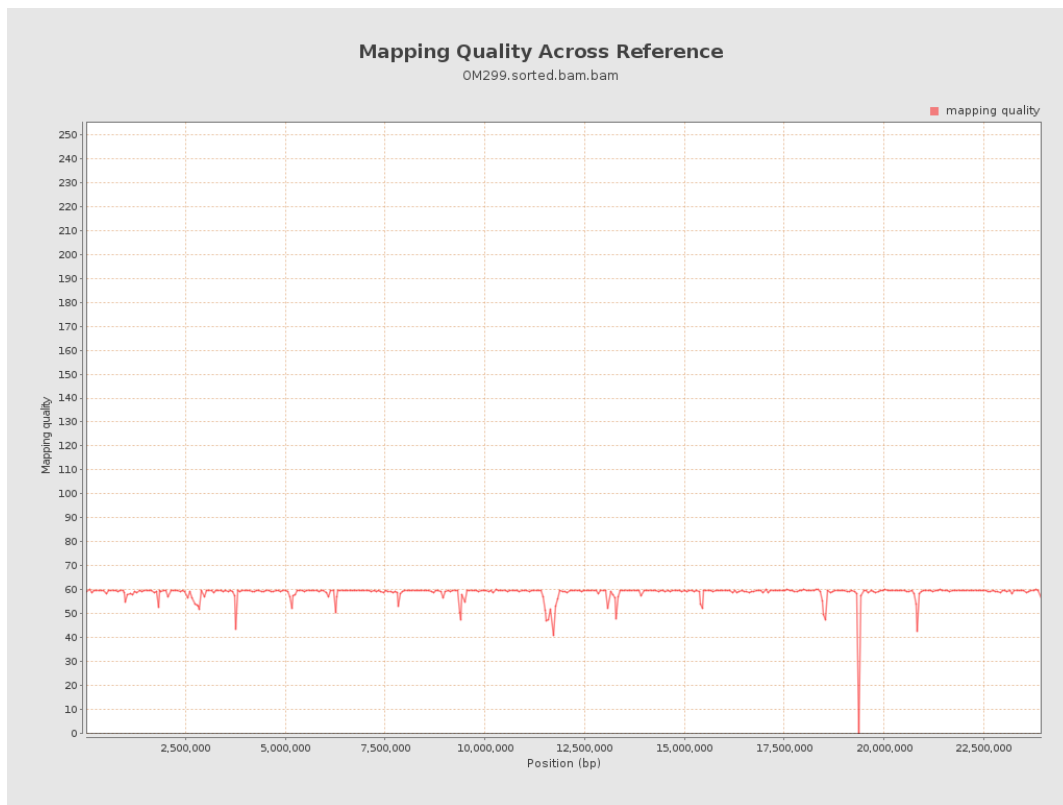
10. Results : Mapped Reads Clipping Profile



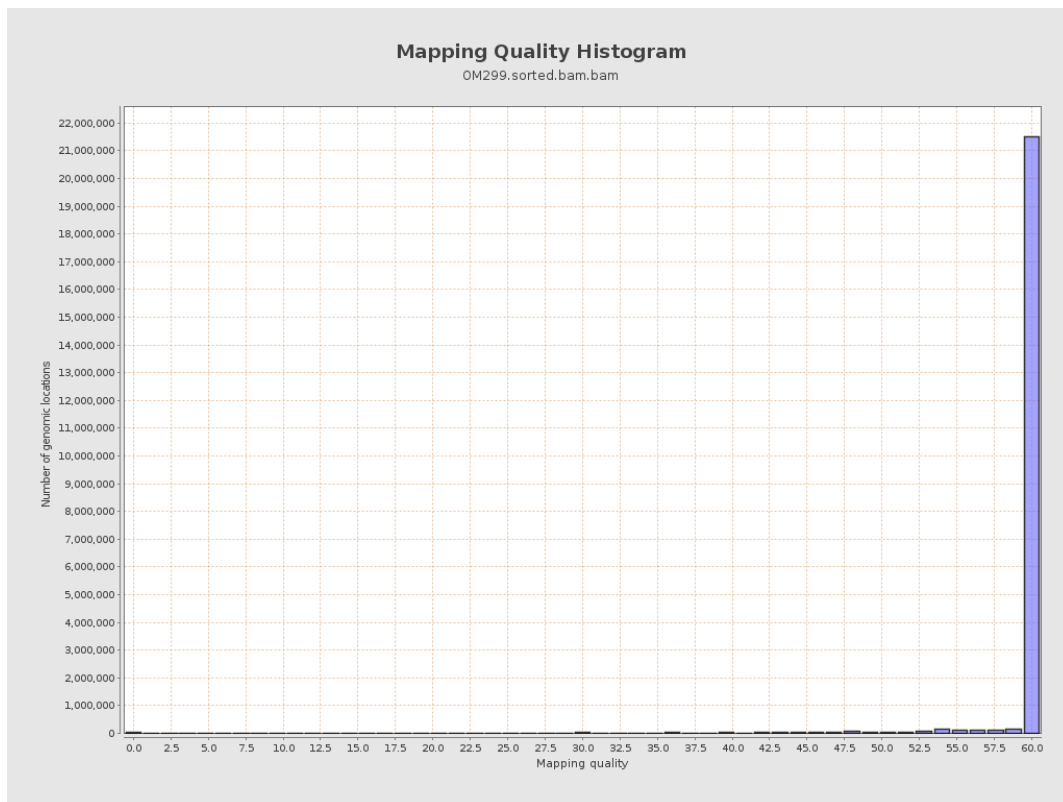
11. Results : Homopolymer Indels



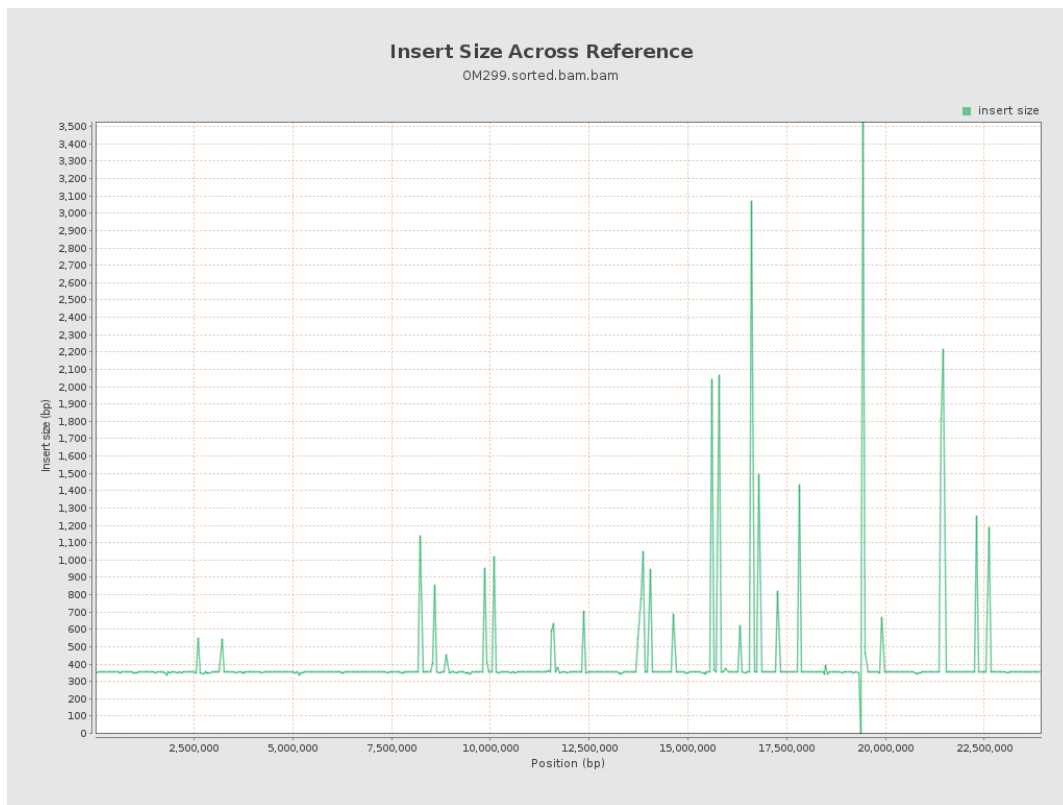
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

