

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2016/10/23 12:13:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM046.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/OM046-BiooBarcode9_ACTTGA_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM046-BiooBarcode9_ACTTGA_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 12:13:15 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM046.sorted.bam.bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	17,783,164
Mapped reads	6,401,395 / 36%
Unmapped reads	11,381,769 / 64%
Mapped paired reads	6,401,395 / 36%
Mapped reads, first in pair	3,191,991 / 17.95%
Mapped reads, second in pair	3,209,404 / 18.05%
Mapped reads, both in pair	6,238,951 / 35.08%
Mapped reads, singletons	162,444 / 0.91%
Read min/max/mean length	30 / 100 / 99.94
Duplicated reads (estimated)	1,369,729 / 7.7%
Duplication rate	17.4%
Clipped reads	722,196 / 4.06%

2.2. ACGT Content

Number/percentage of A's	183,380,971 / 29.74%
Number/percentage of C's	124,732,738 / 20.23%
Number/percentage of T's	184,044,718 / 29.85%
Number/percentage of G's	124,409,162 / 20.18%
Number/percentage of N's	54,328 / 0.01%
GC Percentage	40.41%

2.3. Coverage

Mean	25.7619
Standard Deviation	25.9907

2.4. Mapping Quality

Mean Mapping Quality	58.53
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2.5. Insert size

Mean	739.73
Standard Deviation	25,336.25
P25/Median/P75	267 / 280 / 290

2.6. Mismatches and indels

General error rate	1.46%
Mismatches	8,539,625
Insertions	196,817
Mapped reads with at least one insertion	2.9%
Deletions	226,556
Mapped reads with at least one deletion	3.33%
Homopolymer indels	63.26%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

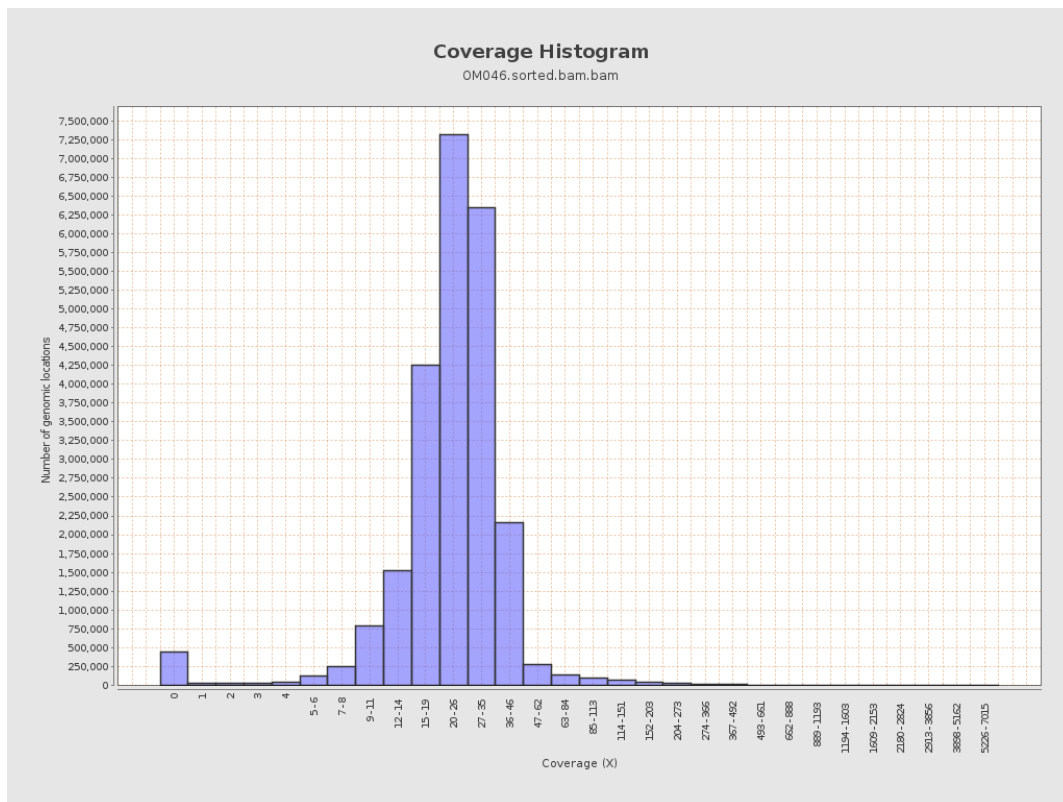
gi 1074120478 emb LT615256.1	977217	22206601	22.7243	9.8954
gi 1074120682 emb LT615257.1	860454	23426464	27.2257	21.3185
gi 1074120865 emb LT615258.1	989719	29587507	29.8949	38.3116
gi 1074121086 emb LT615259.1	935450	26506244	28.3353	42.2833
gi 1074121301 emb LT615260.1	1432239	37834811	26.4165	25.5039
gi 1074121615 emb LT615261.1	1080962	29581898	27.3663	24.786
gi 1074121871 emb LT615262.1	1545099	37208246	24.0815	9.2266
gi 1074122235 emb LT615263.1	1585108	39855957	25.144	20.9451
gi 1074122590 emb LT615264.1	2122358	52396318	24.6878	14.4104
gi 1074123050 emb LT615265.1	1754192	44616979	25.4345	34.411
gi 1074123421 emb LT615	2150147	58486242	27.201	46.5074

266.1				
gi 107412389 8 emb LT615 267.1	3031036	75835526	25.0197	14.2267
gi 107412458 8 emb LT615 268.1	2359348	58777546	24.9126	29.5148
gi 107412506 5 emb LT615 269.1	3135668	80909294	25.8029	9.1159

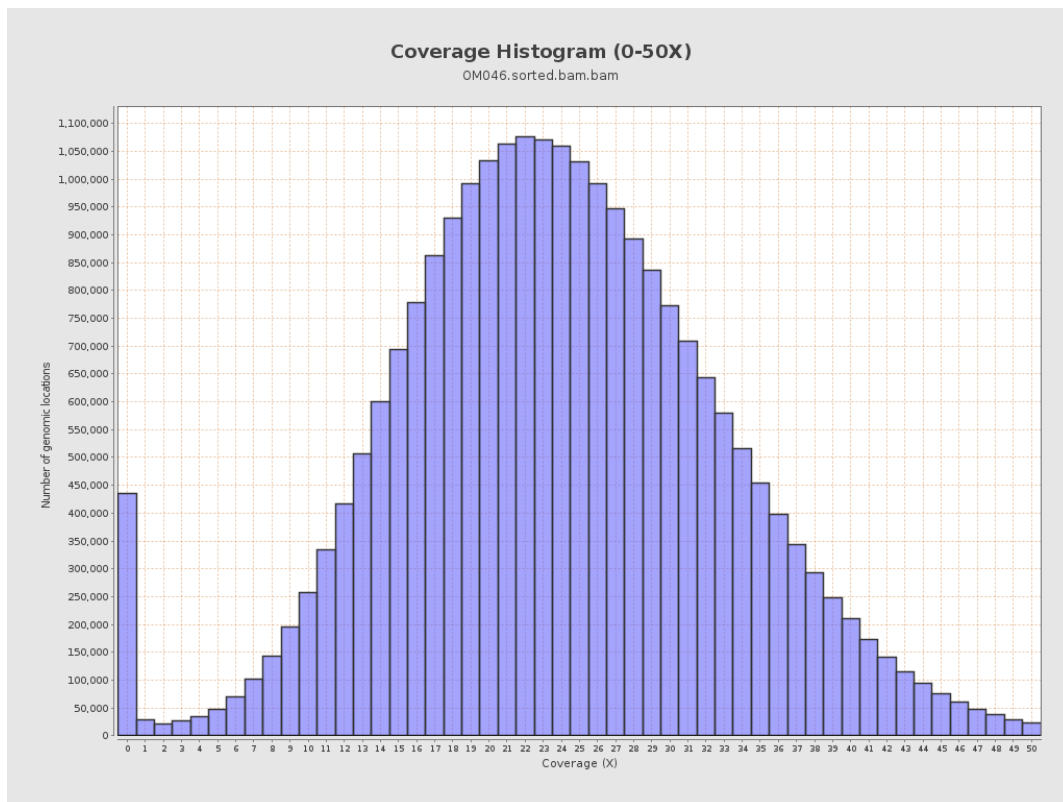
3. Results : Coverage across reference



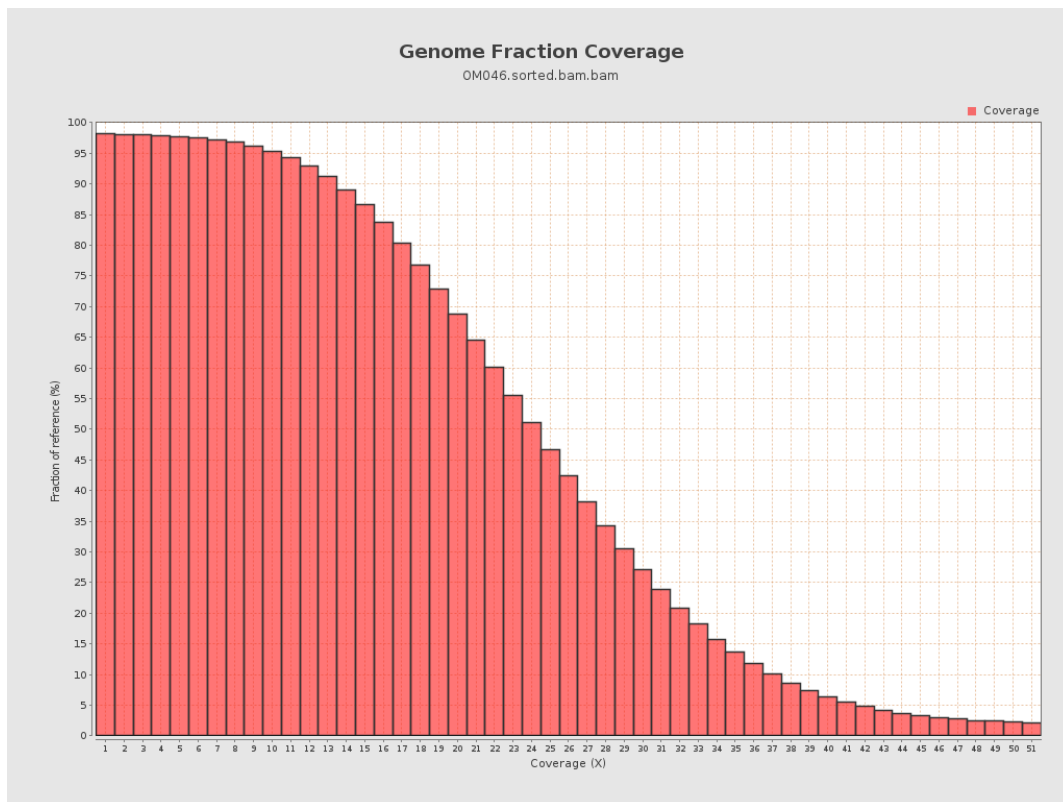
4. Results : Coverage Histogram



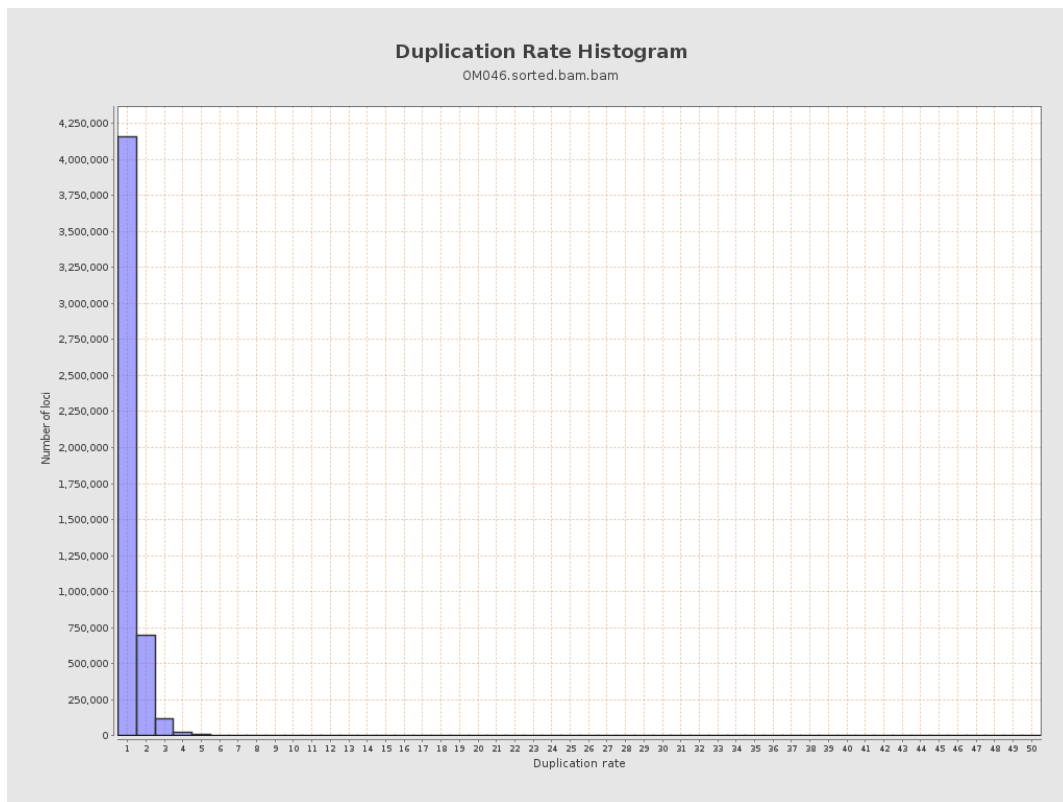
5. Results : Coverage Histogram (0-50X)



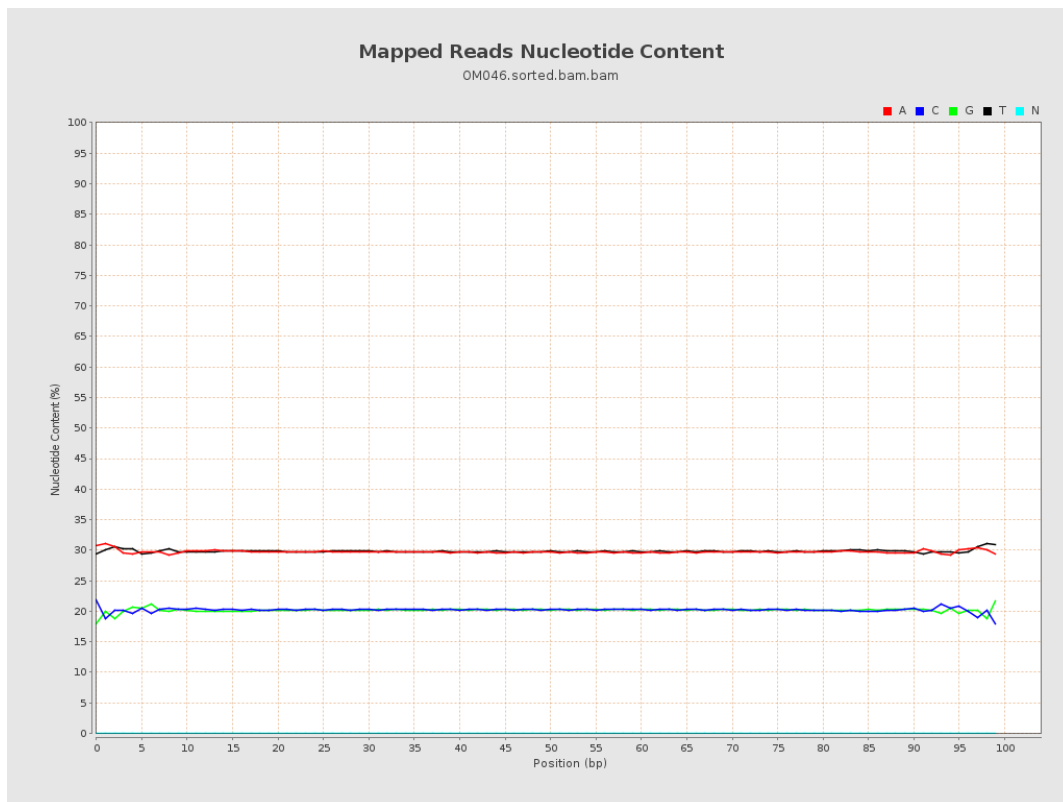
6. Results : Genome Fraction Coverage



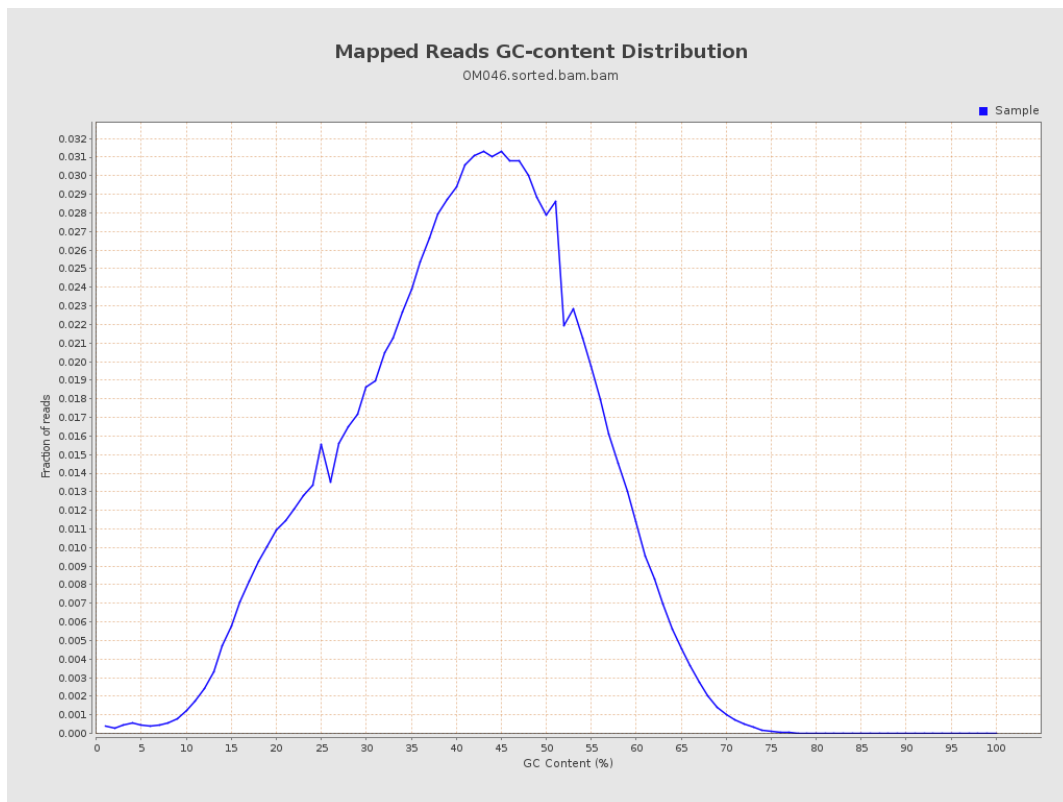
7. Results : Duplication Rate Histogram



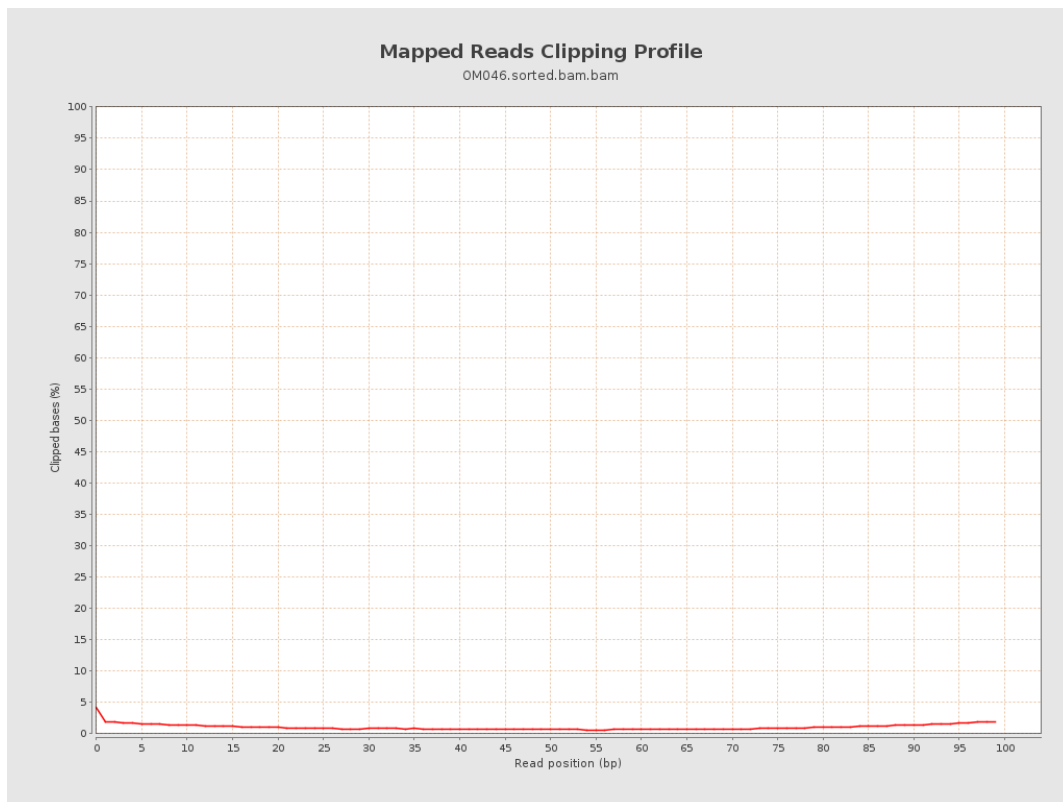
8. Results : Mapped Reads Nucleotide Content



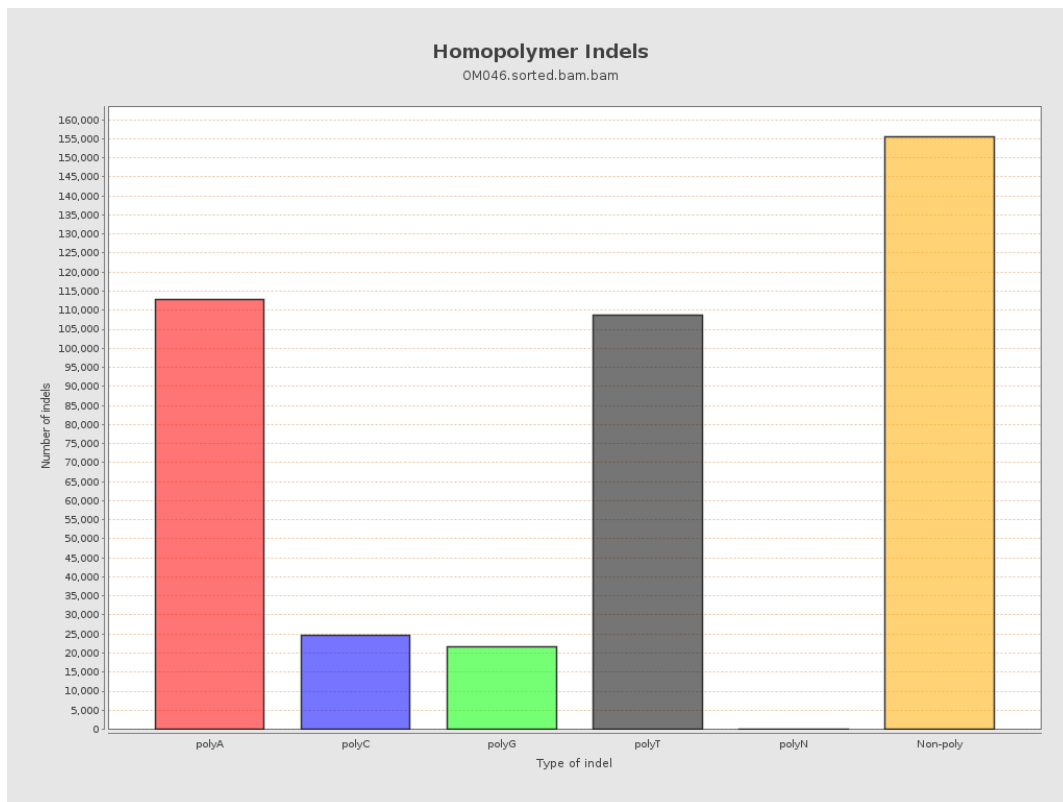
9. Results : Mapped Reads GC-content Distribution



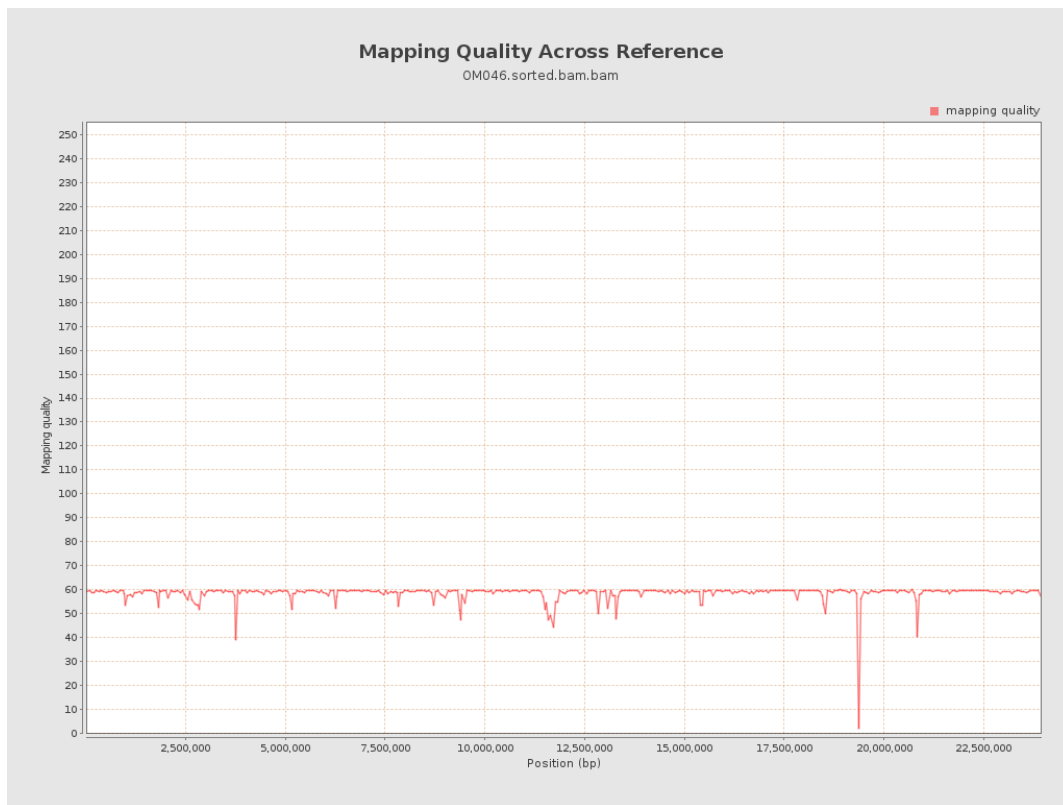
10. Results : Mapped Reads Clipping Profile



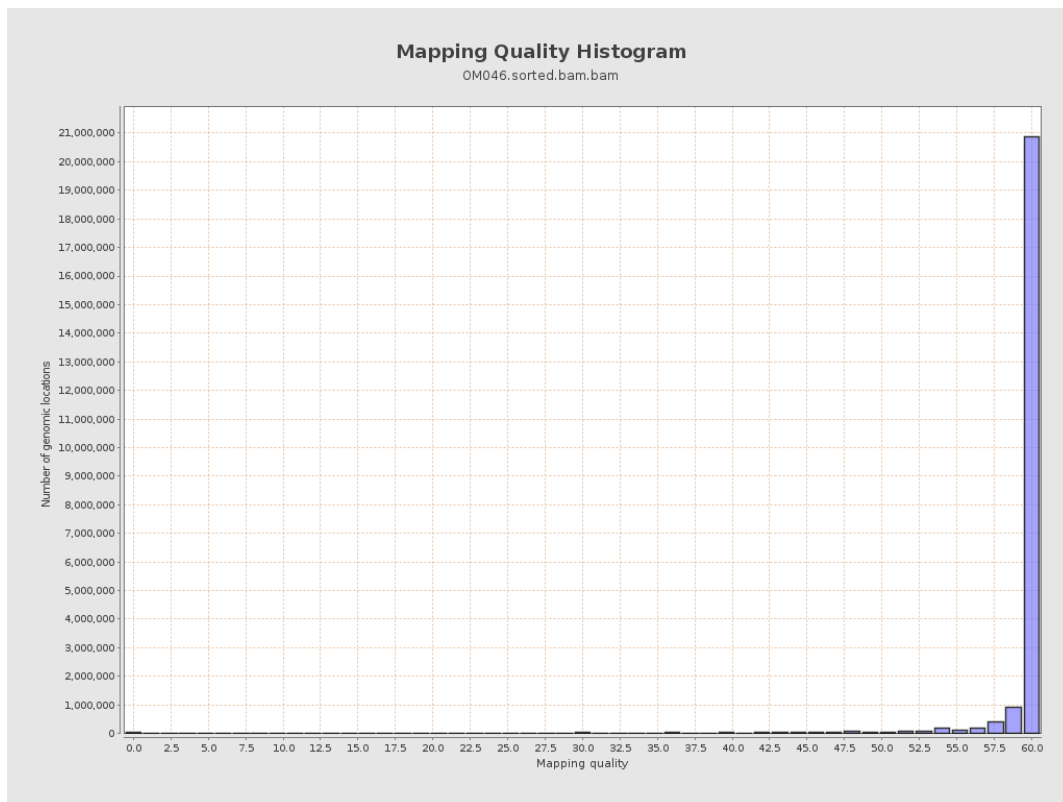
11. Results : Homopolymer Indels



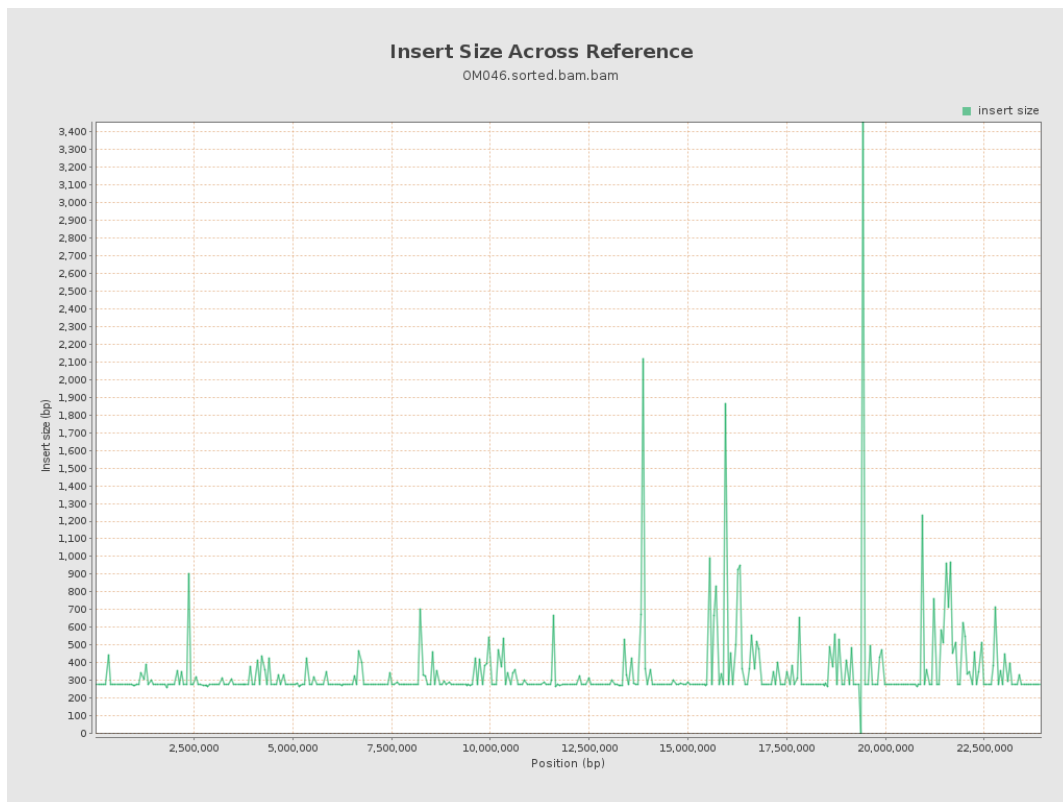
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

