

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2016/10/23 13:46:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM220.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/OM220-BiooBarcode20_GTGGCC_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM220-BiooBarcode20_GTGGCC_R1.fastq.gz |
| Draw chromosome limits: | no |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.15-r1140) |
| Analysis date: | Sun Oct 23 13:46:19 EDT 2016 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | /home/vdp5/data/cambodia_samples/sequences_bam/OM220.sorted.bam. |

| | |
|--|-----|
| | bam |
|--|-----|

2. Summary

2.1. Globals

| | |
|------------------------------|--------------------|
| Reference size | 23,958,997 |
| Number of reads | 8,001,365 |
| Mapped reads | 2,460,718 / 30.75% |
| Unmapped reads | 5,540,647 / 69.25% |
| Mapped paired reads | 2,460,718 / 30.75% |
| Mapped reads, first in pair | 1,226,934 / 15.33% |
| Mapped reads, second in pair | 1,233,784 / 15.42% |
| Mapped reads, both in pair | 2,385,524 / 29.81% |
| Mapped reads, singletons | 75,194 / 0.94% |
| Read min/max/mean length | 30 / 100 / 99.95 |
| Duplicated reads (estimated) | 308,829 / 3.86% |
| Duplication rate | 9.28% |
| Clipped reads | 292,671 / 3.66% |

2.2. ACGT Content

| | |
|--------------------------|---------------------|
| Number/percentage of A's | 70,980,930 / 30.02% |
| Number/percentage of C's | 47,095,417 / 19.92% |
| Number/percentage of T's | 71,297,169 / 30.16% |
| Number/percentage of G's | 47,035,608 / 19.9% |
| Number/percentage of N's | 19,122 / 0.01% |
| GC Percentage | 39.82% |

2.3. Coverage

| | |
|--------------------|---------|
| Mean | 9.8778 |
| Standard Deviation | 10.3543 |

2.4. Mapping Quality

| | |
|----------------------|-------|
| Mean Mapping Quality | 58.46 |
|----------------------|-------|

2.5. Insert size

| | |
|--------------------|-----------------|
| Mean | 848.82 |
| Standard Deviation | 27,791.66 |
| P25/Median/P75 | 319 / 331 / 339 |

2.6. Mismatches and indels

| | |
|--|-----------|
| General error rate | 1.54% |
| Mismatches | 3,461,463 |
| Insertions | 76,705 |
| Mapped reads with at least one insertion | 2.95% |
| Deletions | 87,029 |
| Mapped reads with at least one deletion | 3.32% |
| Homopolymer indels | 62.69% |

2.7. Chromosome stats

| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|------|--------|--------------|---------------|--------------------|
| | | | | |

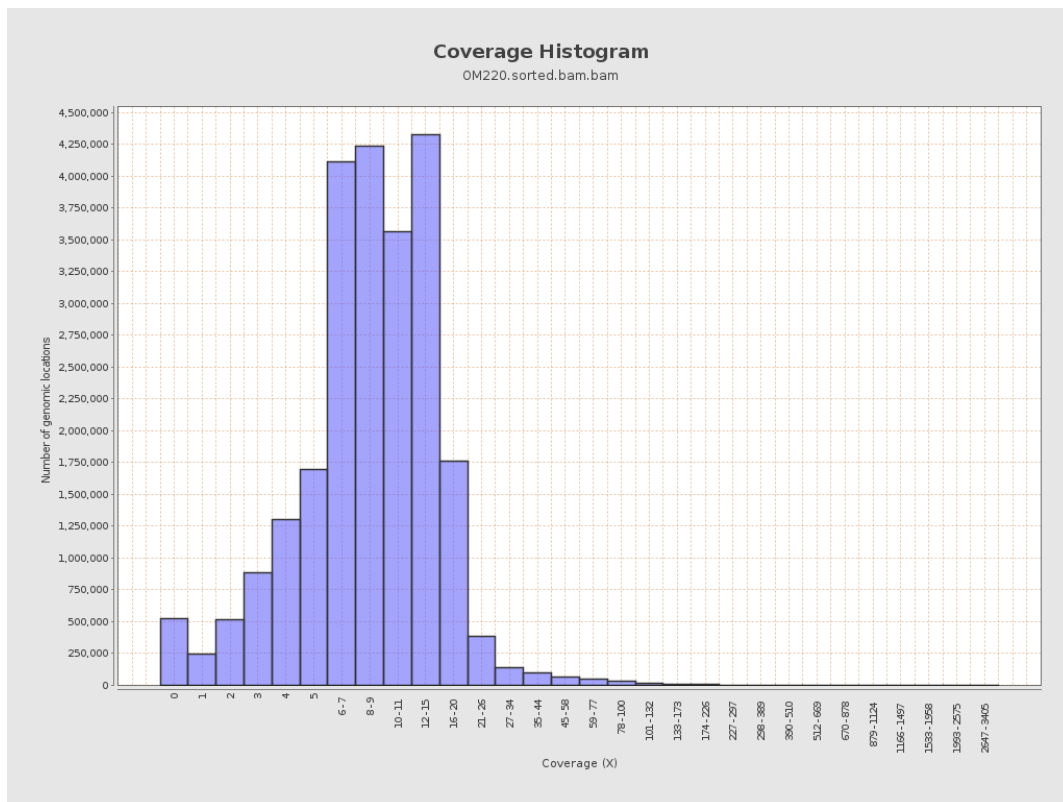
| | | | | |
|------------------------------|---------|----------|---------|---------|
| gi 1074120478 emb LT615256.1 | 977217 | 8321453 | 8.5155 | 5.2318 |
| gi 1074120682 emb LT615257.1 | 860454 | 8735783 | 10.1525 | 8.1966 |
| gi 1074120865 emb LT615258.1 | 989719 | 11333032 | 11.4508 | 15.9967 |
| gi 1074121086 emb LT615259.1 | 935450 | 9743964 | 10.4163 | 14.9467 |
| gi 1074121301 emb LT615260.1 | 1432239 | 14588499 | 10.1858 | 9.8214 |
| gi 1074121615 emb LT615261.1 | 1080962 | 11068775 | 10.2397 | 10.1995 |
| gi 1074121871 emb LT615262.1 | 1545099 | 14283127 | 9.2442 | 5.0799 |
| gi 1074122235 emb LT615263.1 | 1585108 | 15433933 | 9.7368 | 10.3479 |
| gi 1074122590 emb LT615264.1 | 2122358 | 20396562 | 9.6103 | 6.5262 |
| gi 1074123050 emb LT615265.1 | 1754192 | 18335616 | 10.4525 | 17.5397 |
| gi 1074123421 emb LT615 | 2150147 | 22317330 | 10.3794 | 14.9904 |

| | | | | |
|--------------------------------------|---------|----------|---------|---------|
| 266.1 | | | | |
| gi 107412389 8 emb LT615 267.1 | 3031036 | 28555808 | 9.4211 | 6.1684 |
| gi 107412458 8 emb LT615 268.1 | 2359348 | 22109974 | 9.3712 | 10.2795 |
| gi 107412506 5 emb LT615 269.1 | 3135668 | 31439507 | 10.0264 | 4.9148 |

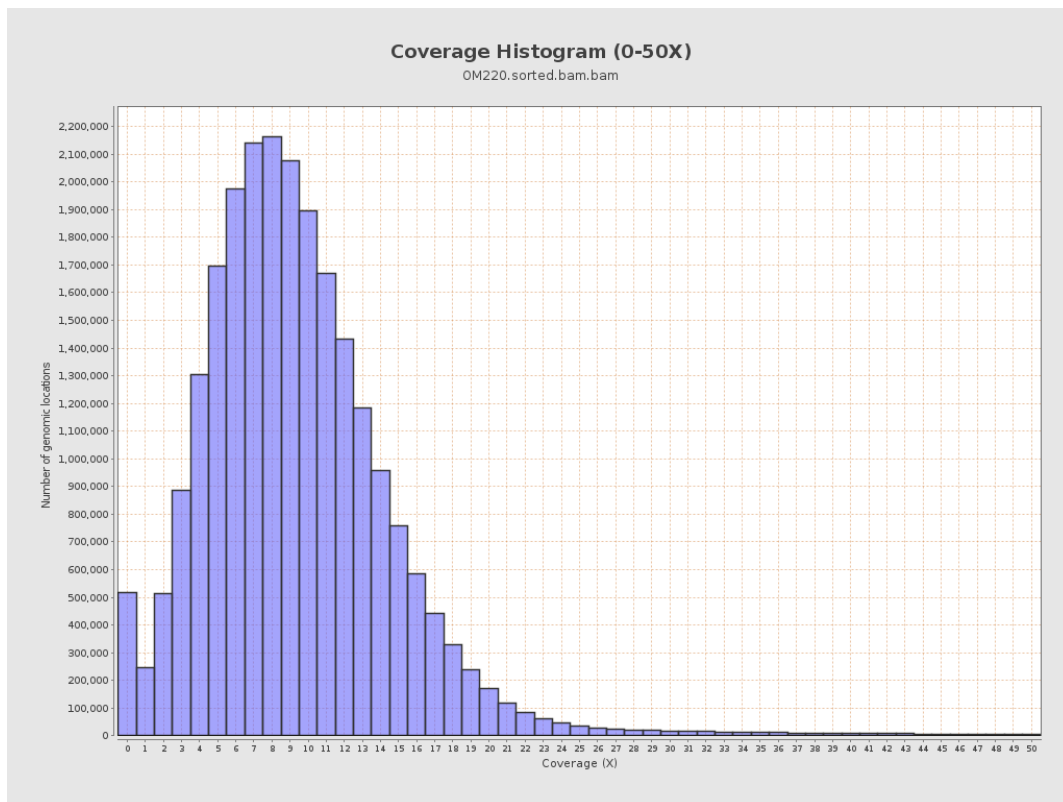
3. Results : Coverage across reference



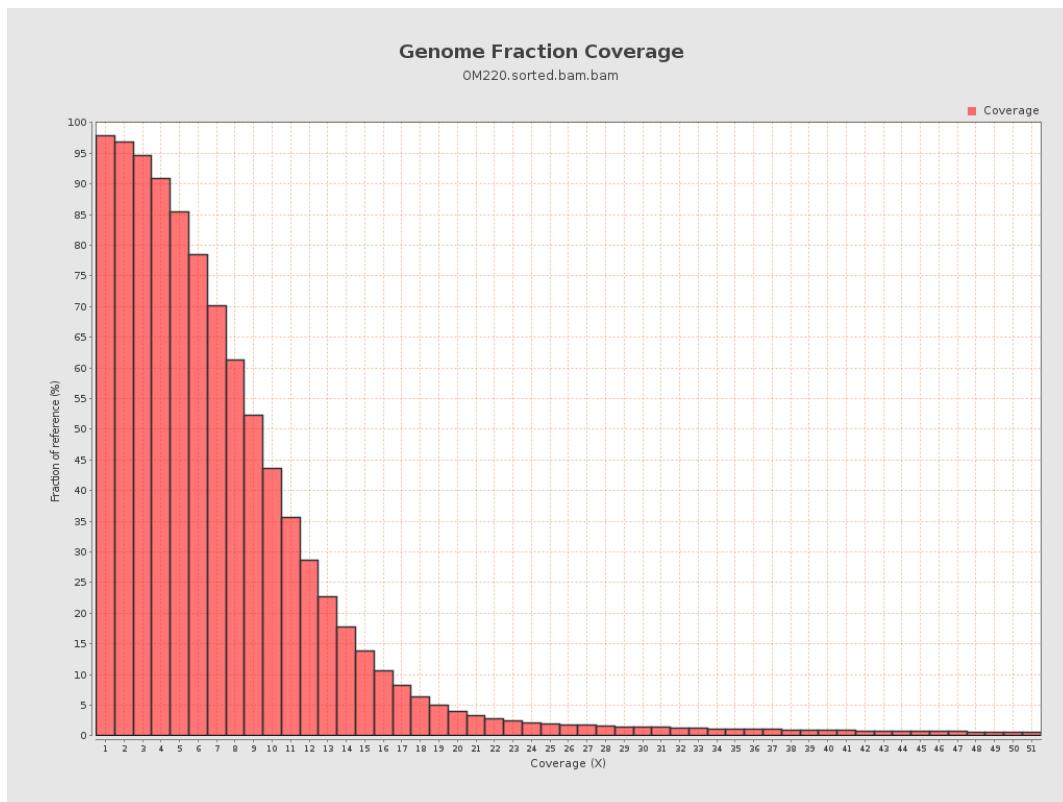
4. Results : Coverage Histogram



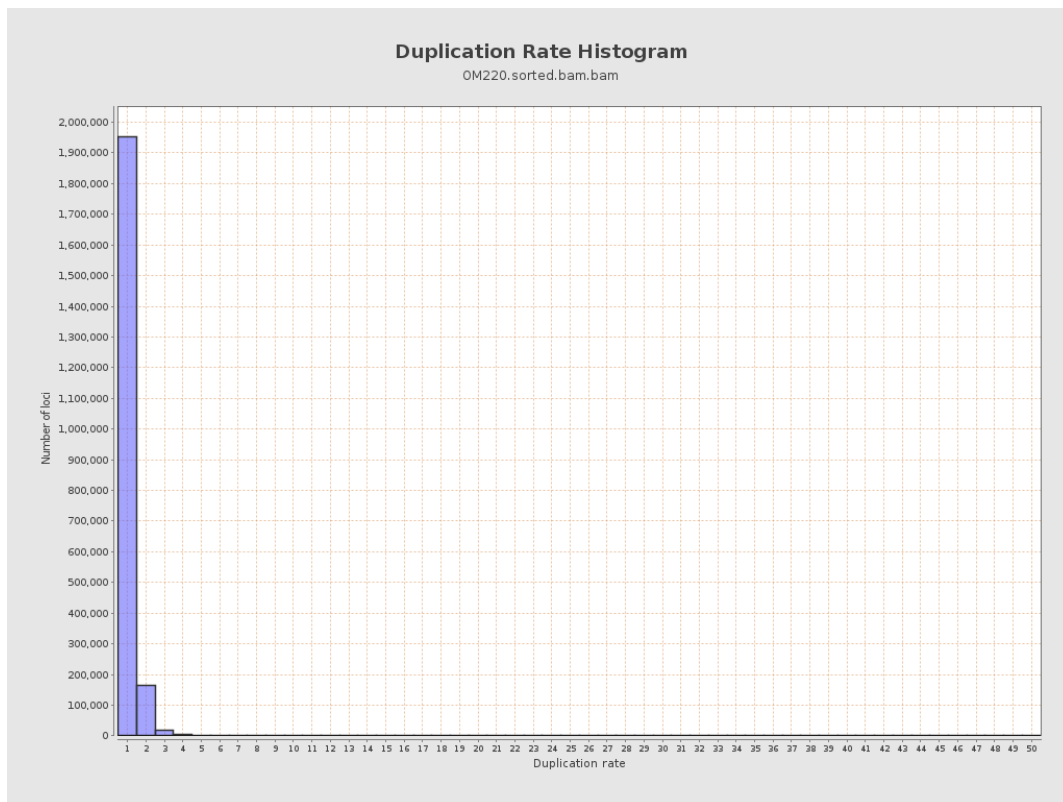
5. Results : Coverage Histogram (0-50X)



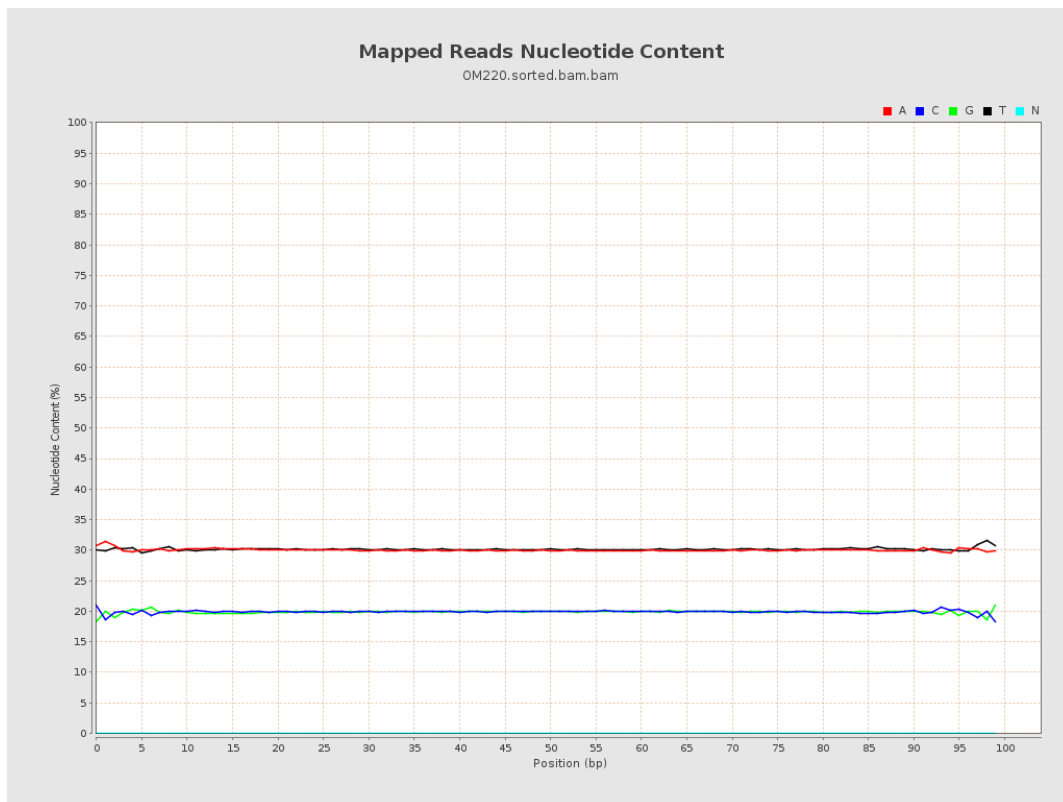
6. Results : Genome Fraction Coverage



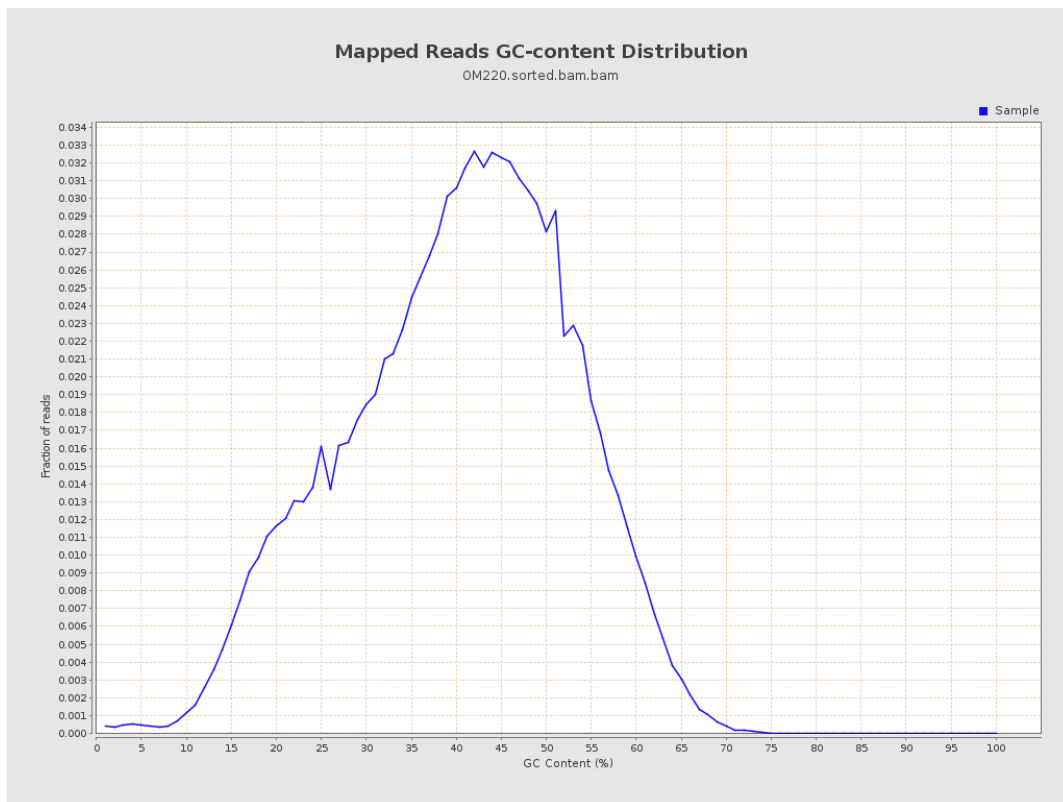
7. Results : Duplication Rate Histogram



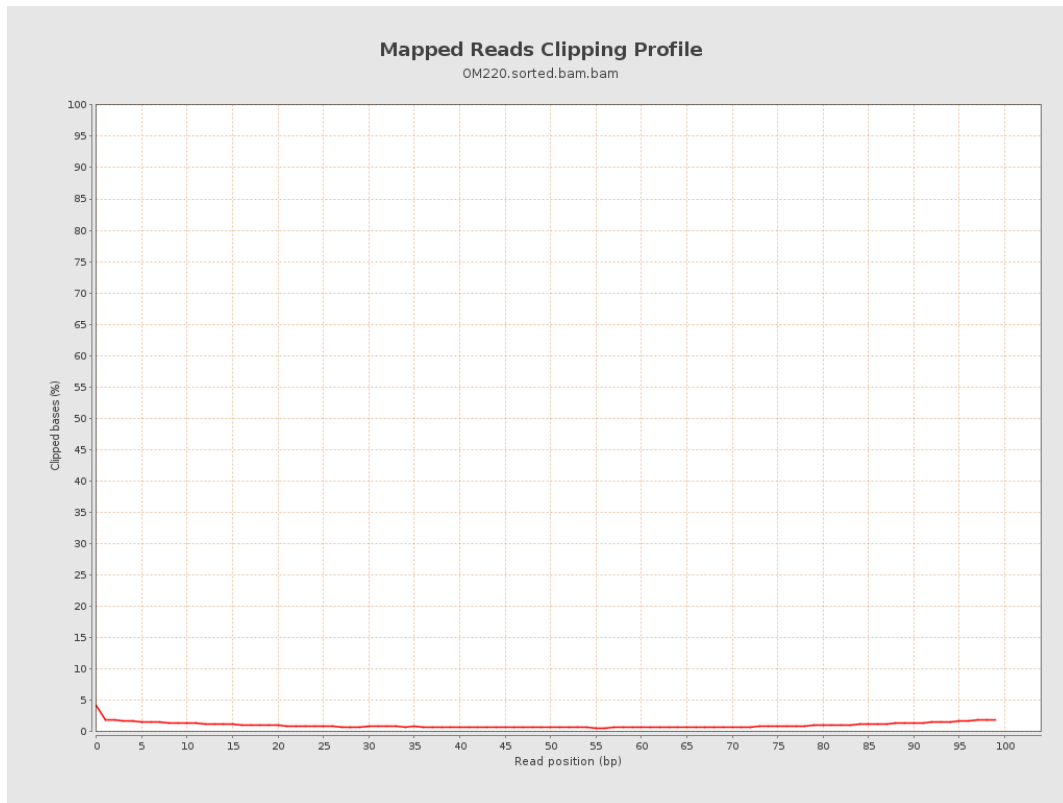
8. Results : Mapped Reads Nucleotide Content



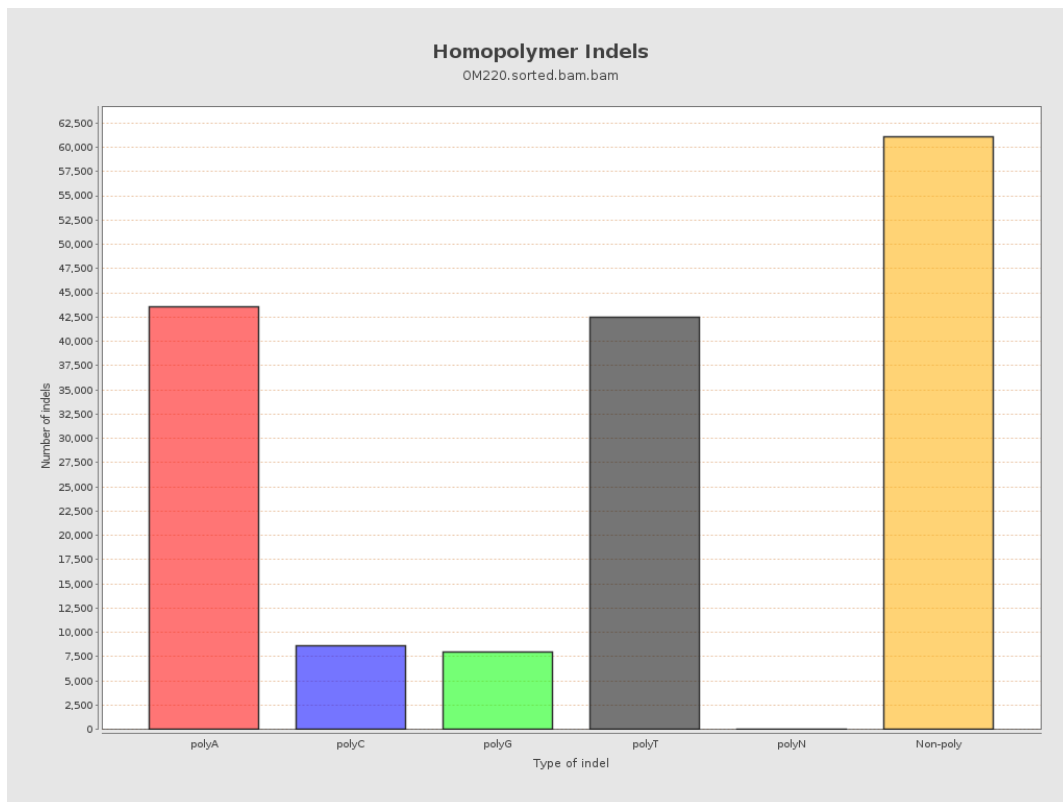
9. Results : Mapped Reads GC-content Distribution



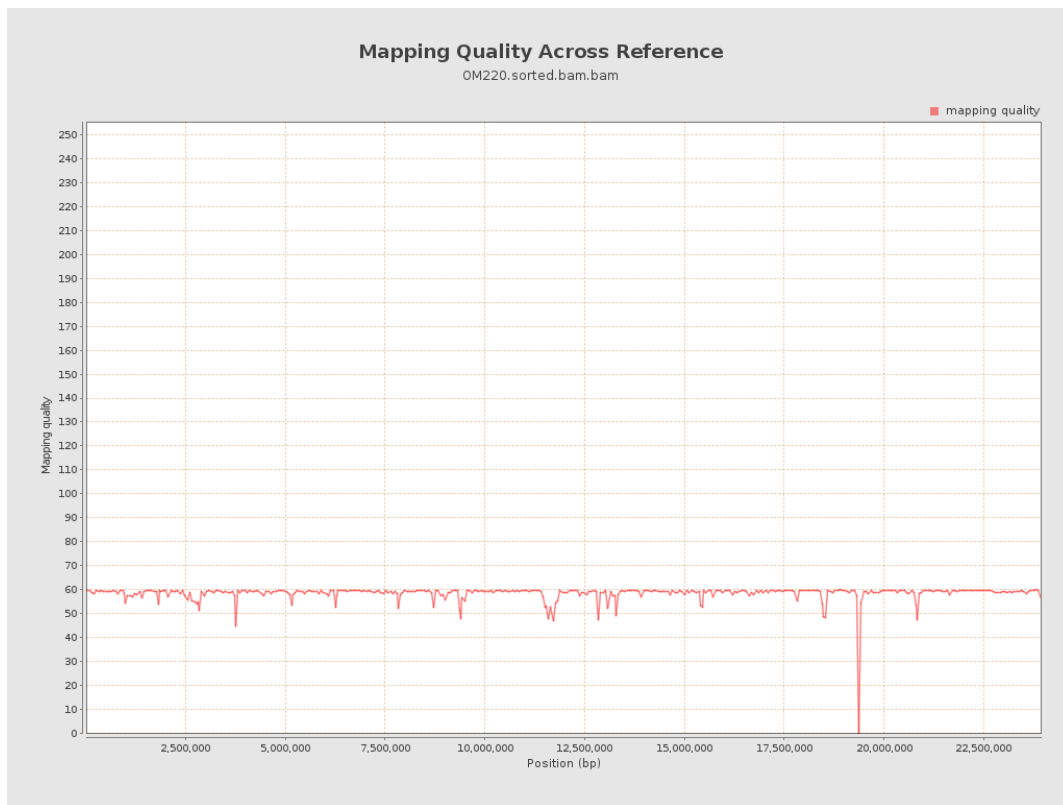
10. Results : Mapped Reads Clipping Profile



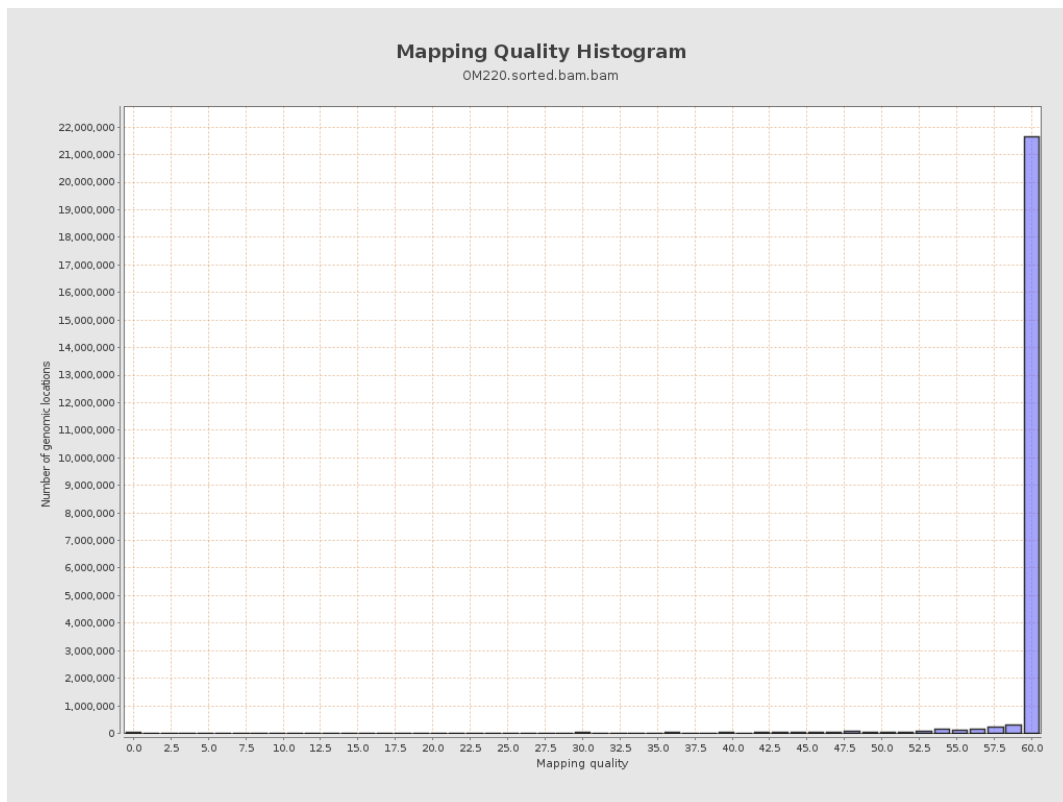
11. Results : Homopolymer Indels



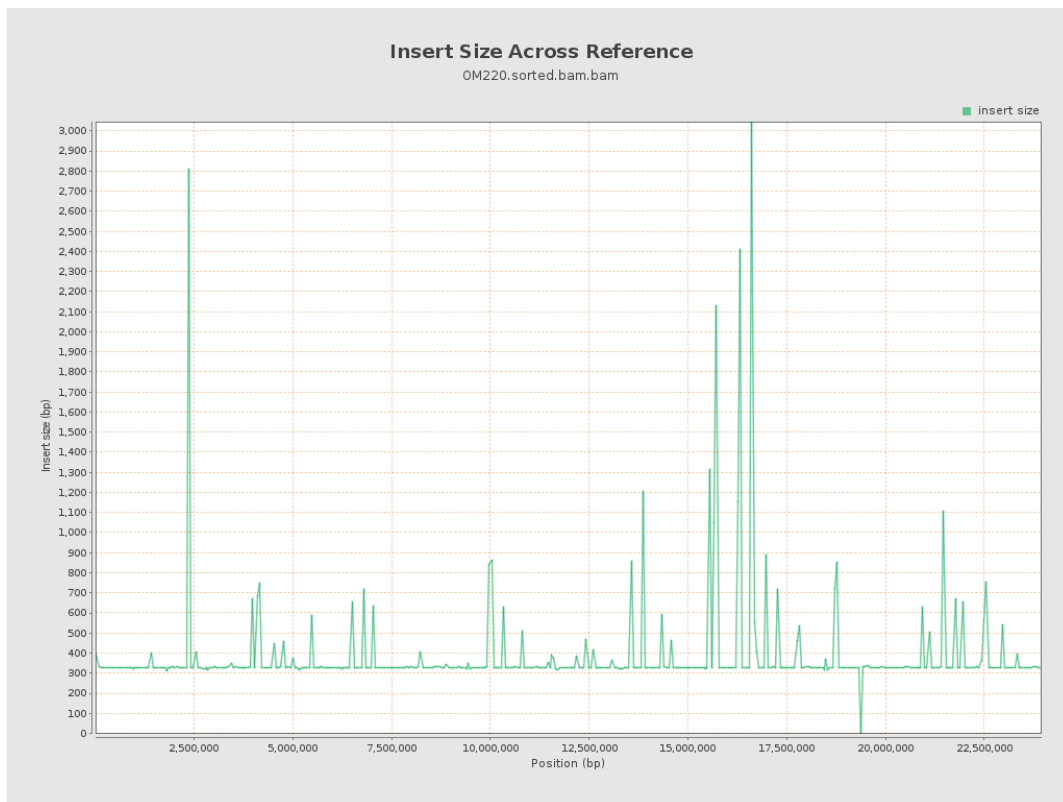
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

