

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:27:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/147
9
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

| | |
|---------------------------------------|---|
| BAM file: | /proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1479 .nodup.bam |
| Program: | bwa (0.7.17-r1188) |
| Analyze overlapping paired-end reads: | no |
| Command line: | bwa mem -M -t 8 -R @RG\tID:\$unit\tPL:Illumina\tLB:LibA\t SM:\$sample /proj/uppstore2018210/Aalpina/data/r eference/GCA_900128785.1_MPIPZ. v5_genomic.fa /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_538/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_538_S105_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_538/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_538_S105_L004 _R2_001.fastq.gz |
| Size of a homopolymer: | 3 |
| | |

| | |
|----------------------------|-------------------------------|
| Number of windows: | 400 |
| Analysis date: | Mon May 29 21:27:12 CEST 2023 |
| Draw chromosome limits: | no |
| Skip duplicate alignments: | no |

2. Summary

2.1. Globals

| | |
|------------------------------|---------------------|
| Reference size | 311,642,060 |
| Number of reads | 54,959,118 |
| Mapped reads | 50,737,668 / 92.32% |
| Unmapped reads | 4,221,450 / 7.68% |
| Mapped paired reads | 50,737,668 / 92.32% |
| Mapped reads, first in pair | 25,478,874 / 46.36% |
| Mapped reads, second in pair | 25,258,794 / 45.96% |
| Mapped reads, both in pair | 49,298,726 / 89.7% |
| Mapped reads, singletons | 1,438,942 / 2.62% |
| Read min/max/mean length | 30 / 151 / 147.97 |
| Duplicated reads (flagged) | 7,591,122 / 13.81% |
| Clipped reads | 12,985,543 / 23.63% |

2.2. ACGT Content

| | |
|--------------------------|------------------------|
| Number/percentage of A's | 2,146,854,799 / 30.99% |
| Number/percentage of C's | 1,315,334,359 / 18.99% |
| Number/percentage of T's | 2,146,606,454 / 30.99% |
| Number/percentage of G's | 1,318,137,457 / 19.03% |
| Number/percentage of N's | 47,870 / 0% |
| GC Percentage | 38.02% |

2.3. Coverage

| | |
|--------------------|----------|
| Mean | 22.2859 |
| Standard Deviation | 198.0774 |

2.4. Mapping Quality

| | |
|----------------------|-------|
| Mean Mapping Quality | 43.71 |
|----------------------|-------|

2.5. Insert size

| | |
|--------------------|-----------------|
| Mean | 253,154.22 |
| Standard Deviation | 2,414,990.8 |
| P25/Median/P75 | 315 / 415 / 535 |

2.6. Mismatches and indels

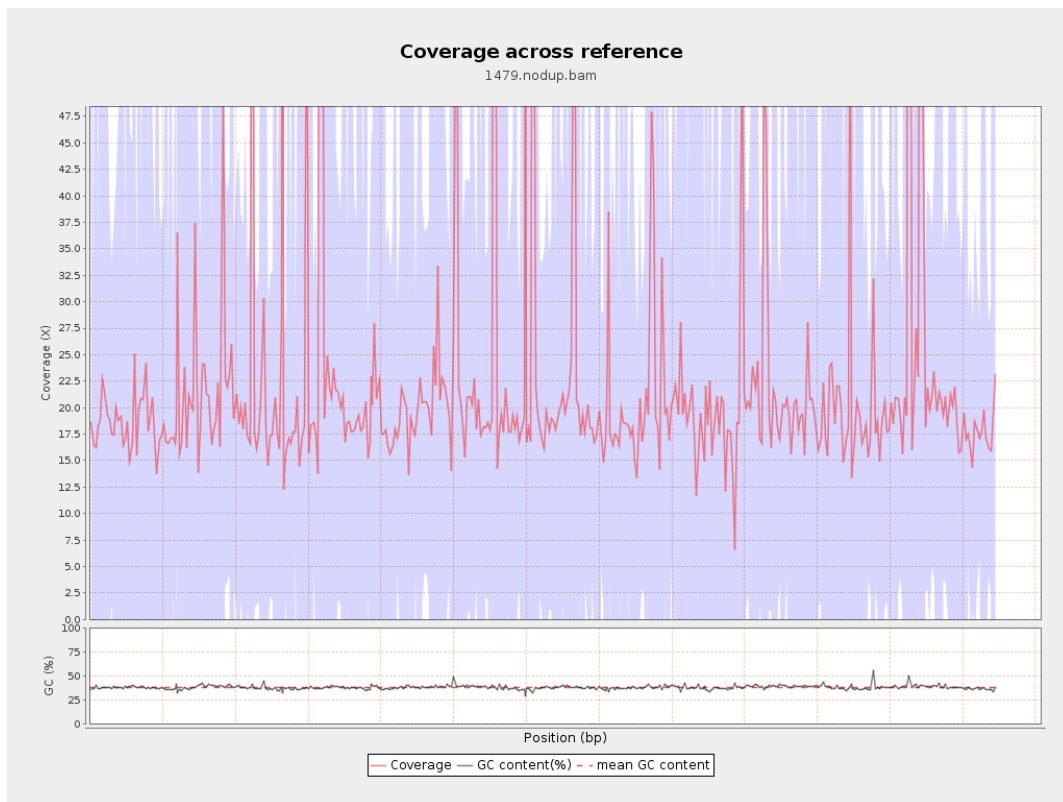
| | |
|--|-------------|
| General error rate | 2.65% |
| Mismatches | 169,926,442 |
| Insertions | 5,044,234 |
| Mapped reads with at least one insertion | 8.87% |
| Deletions | 4,907,092 |
| Mapped reads with at least one deletion | 8.58% |
| Homopolymer indels | 56.83% |

2.7. Chromosome stats

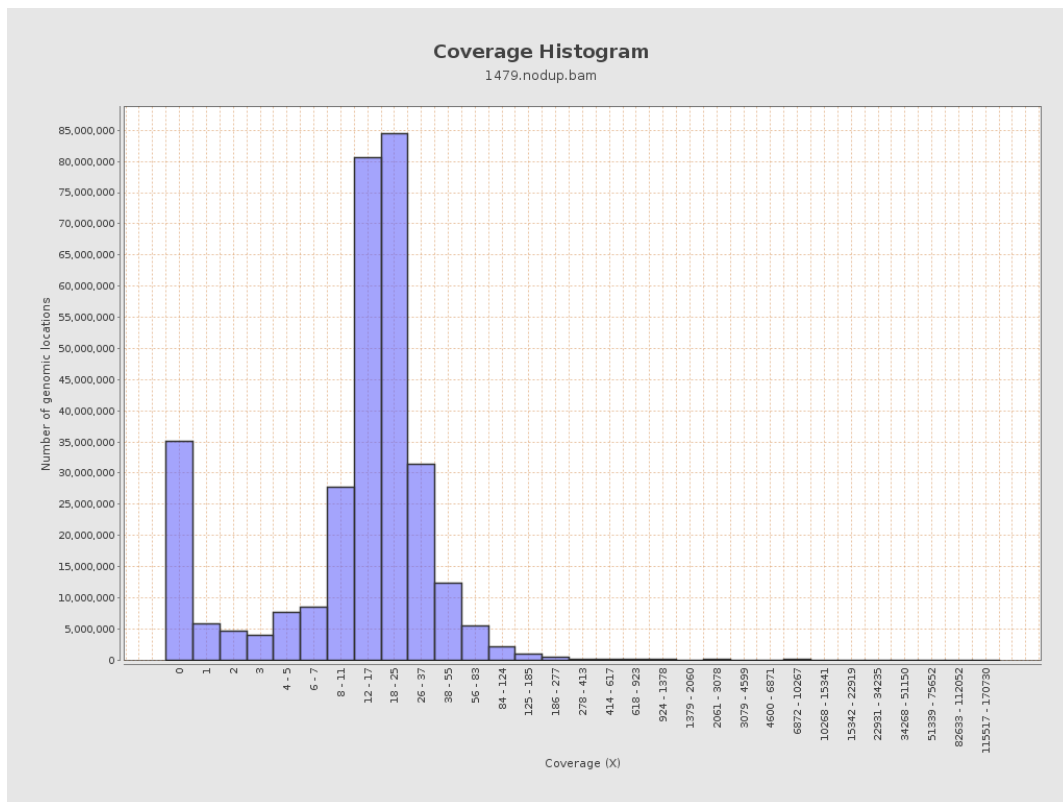
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|------------|----------|--------------|---------------|--------------------|
| LT669788.1 | 29724344 | 547728033 | 18.4269 | 81.5777 |
| | | | | |

| | | | | |
|------------|----------|------------|---------|----------|
| LT669789.1 | 36598175 | 843509753 | 23.0479 | 210.1281 |
| LT669790.1 | 30422129 | 802556746 | 26.3807 | 263.7921 |
| LT669791.1 | 52758100 | 1158626484 | 21.9611 | 217.0047 |
| LT669792.1 | 28376109 | 644603454 | 22.7164 | 209.3898 |
| LT669793.1 | 33388210 | 681267430 | 20.4044 | 108.3817 |
| LT669794.1 | 50579949 | 1084495802 | 21.4412 | 165.1775 |
| LT669795.1 | 49795044 | 1182422143 | 23.7458 | 236.8942 |

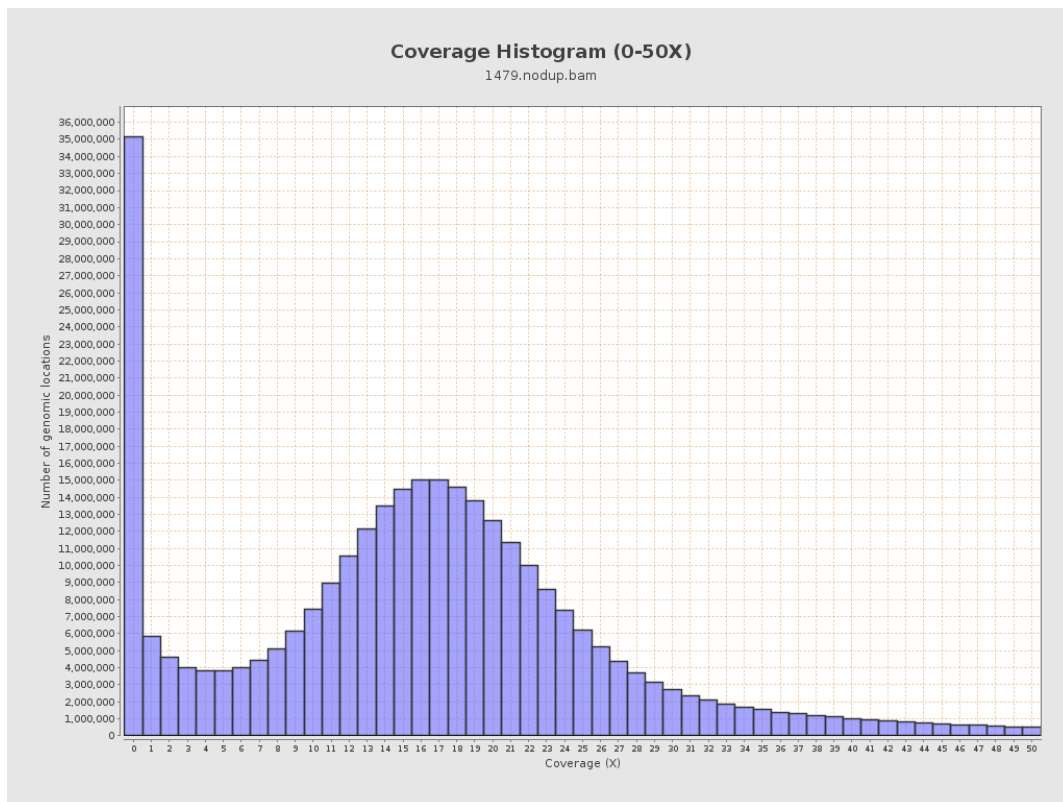
3. Results : Coverage across reference



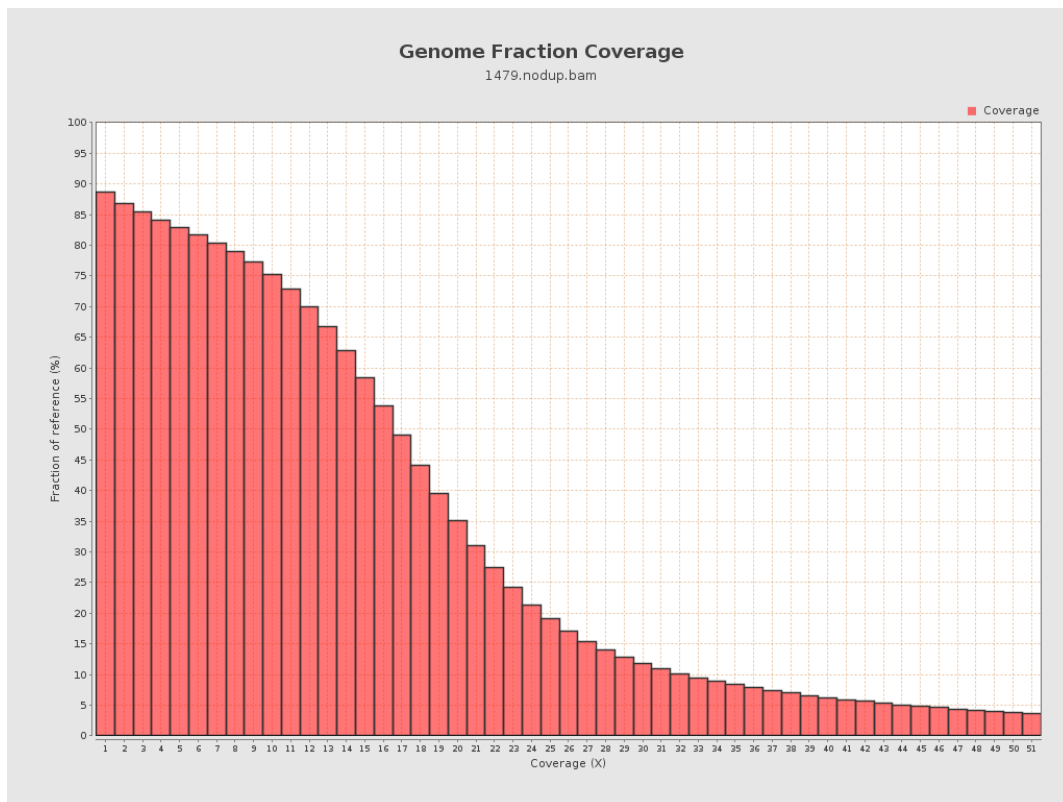
4. Results : Coverage Histogram



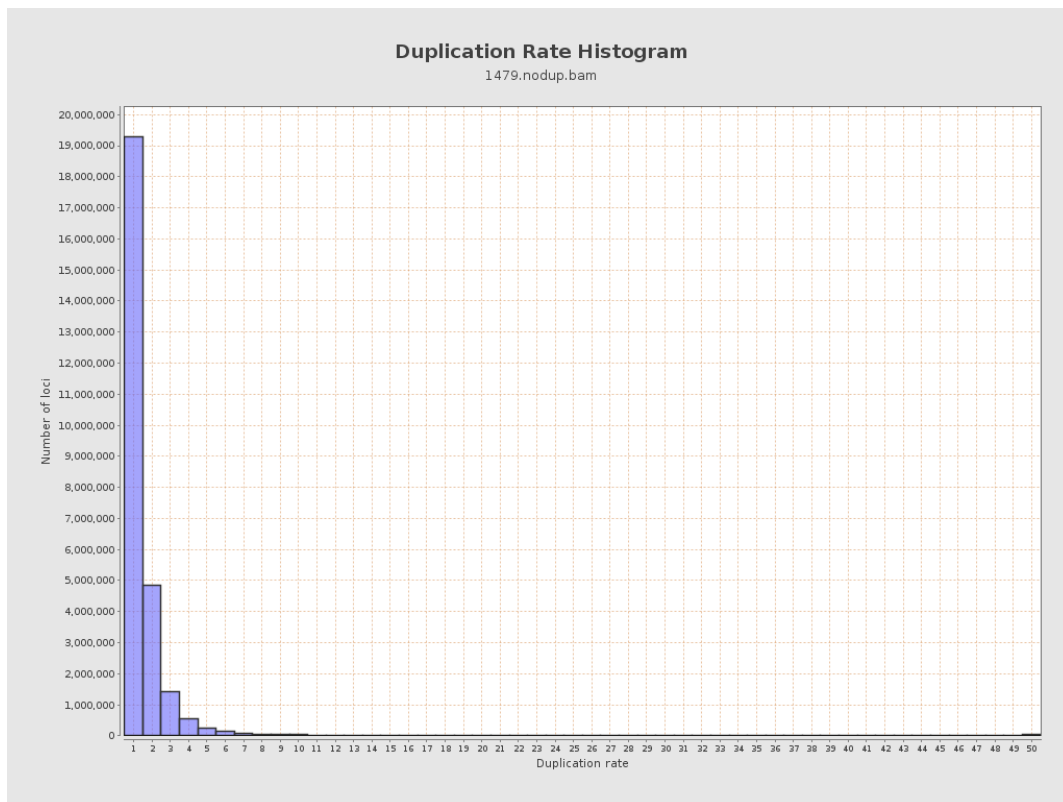
5. Results : Coverage Histogram (0-50X)



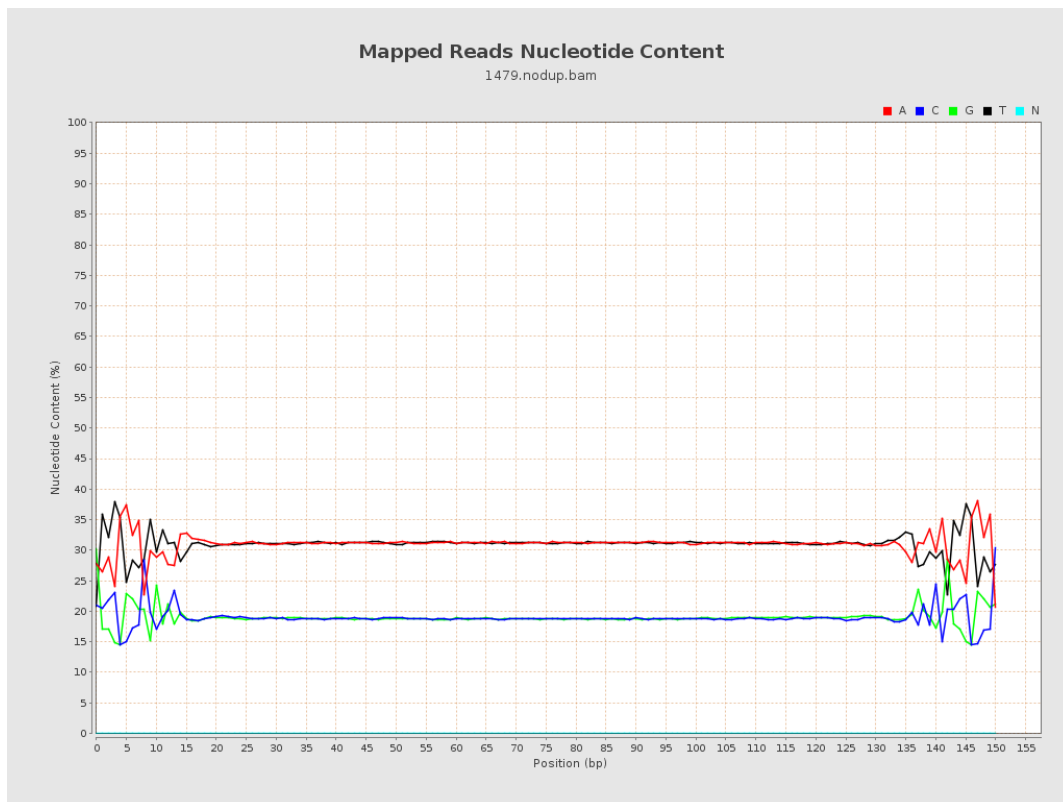
6. Results : Genome Fraction Coverage



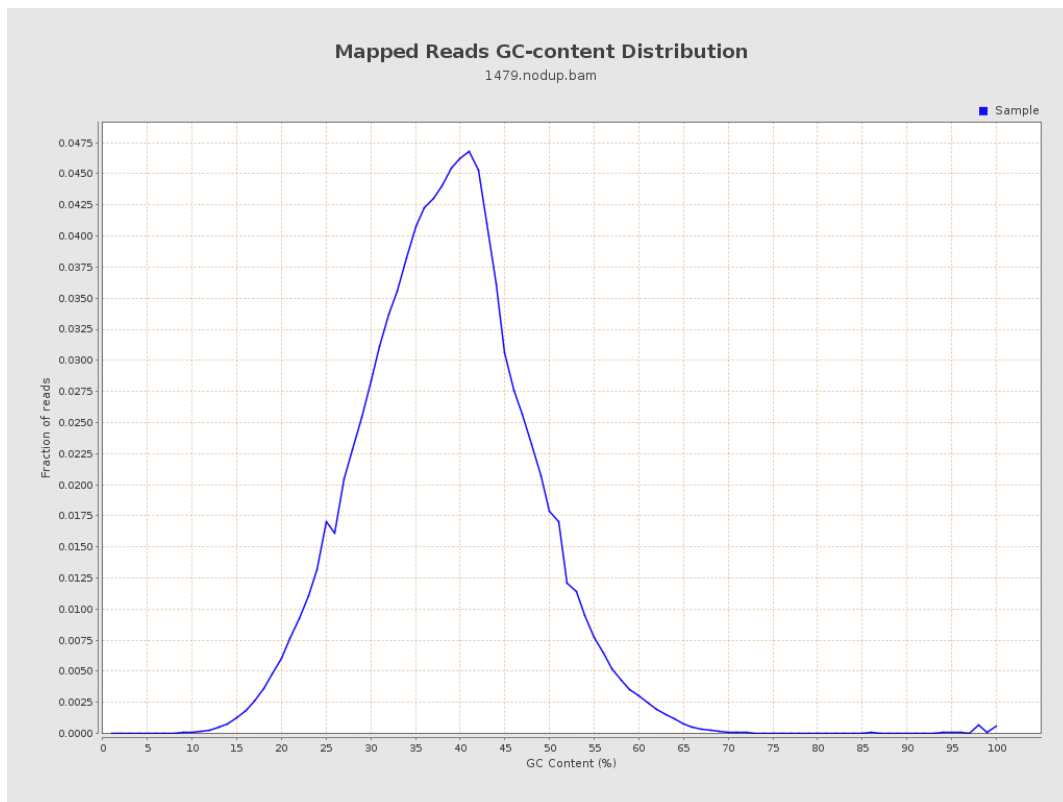
7. Results : Duplication Rate Histogram



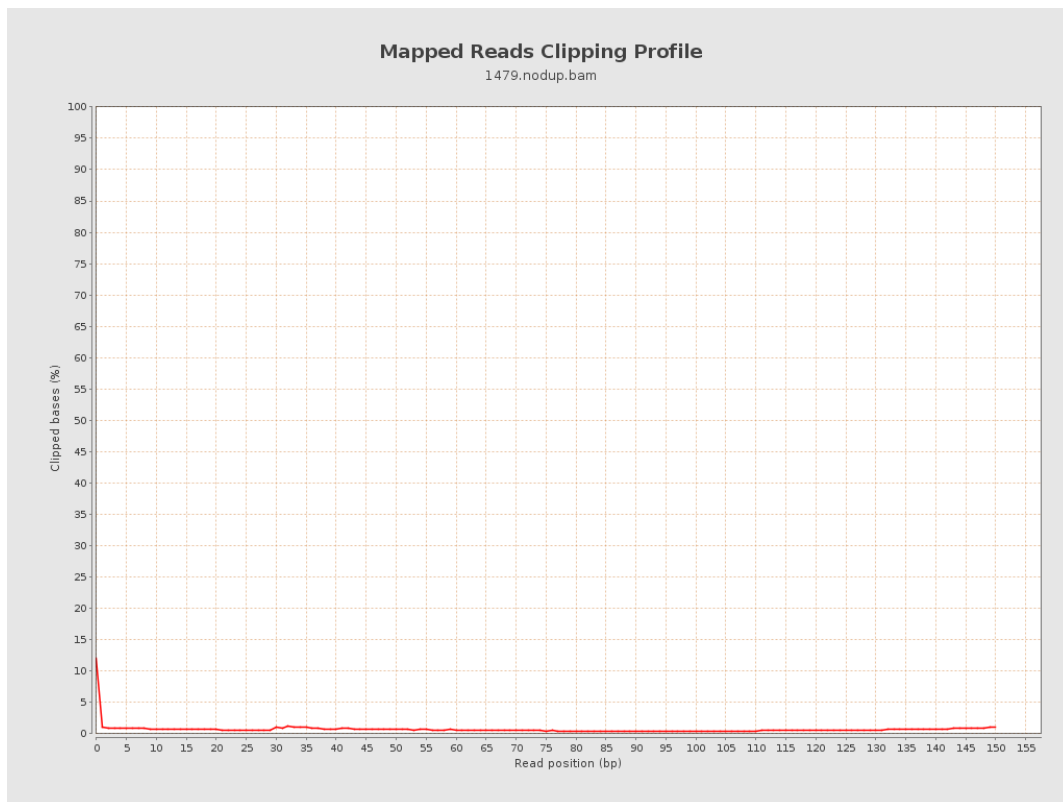
8. Results : Mapped Reads Nucleotide Content



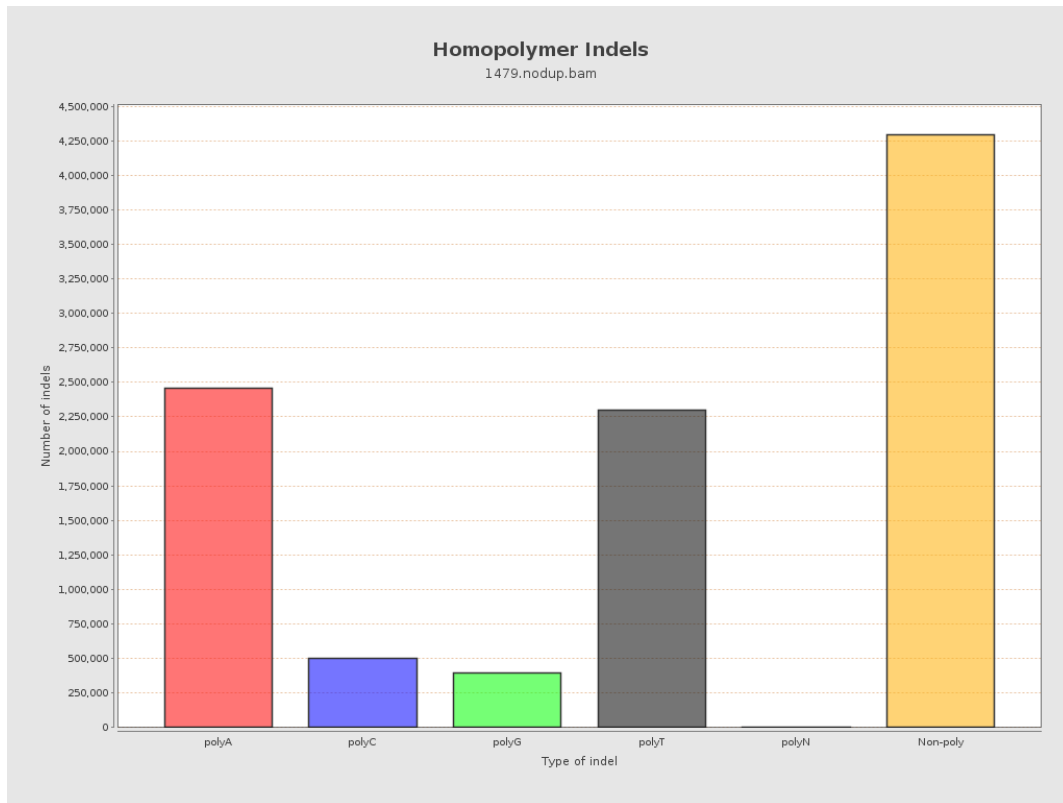
9. Results : Mapped Reads GC-content Distribution



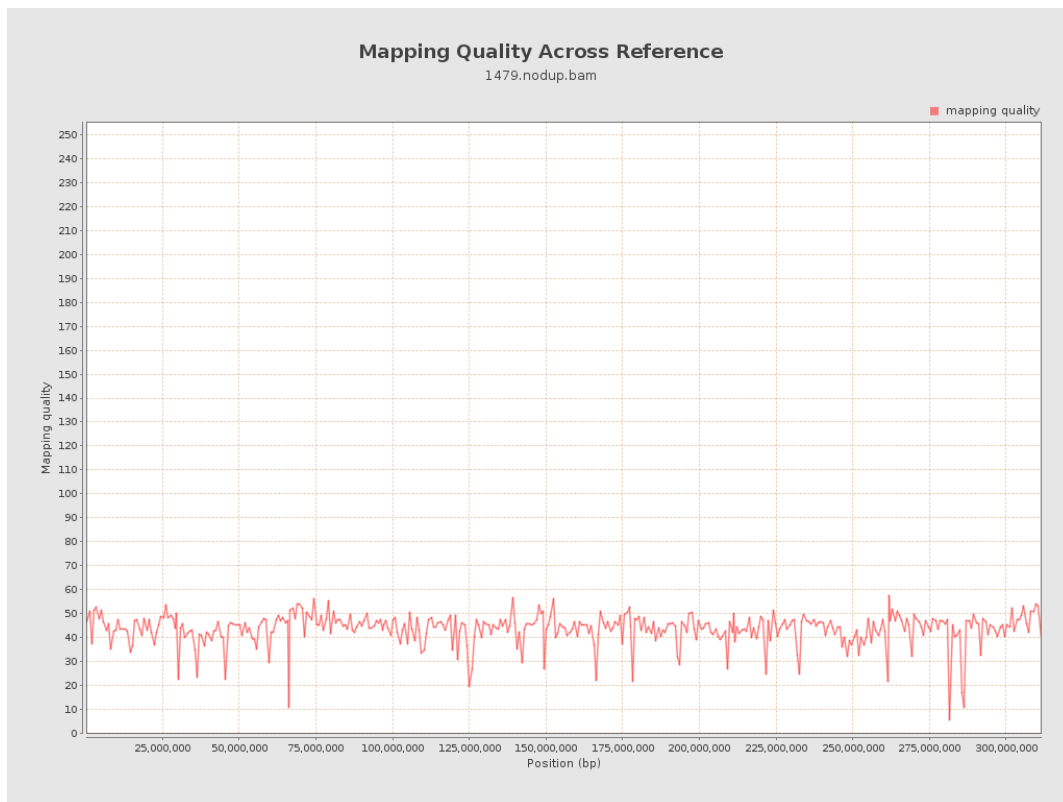
10. Results : Mapped Reads Clipping Profile



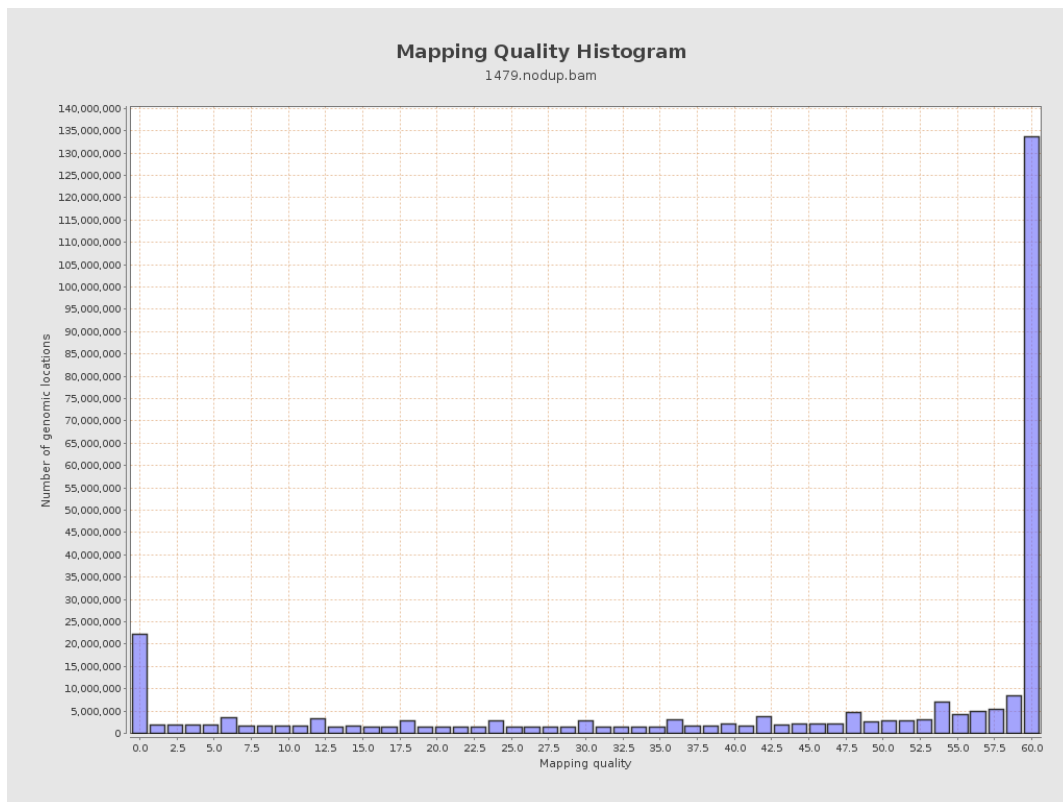
11. Results : Homopolymer Indels



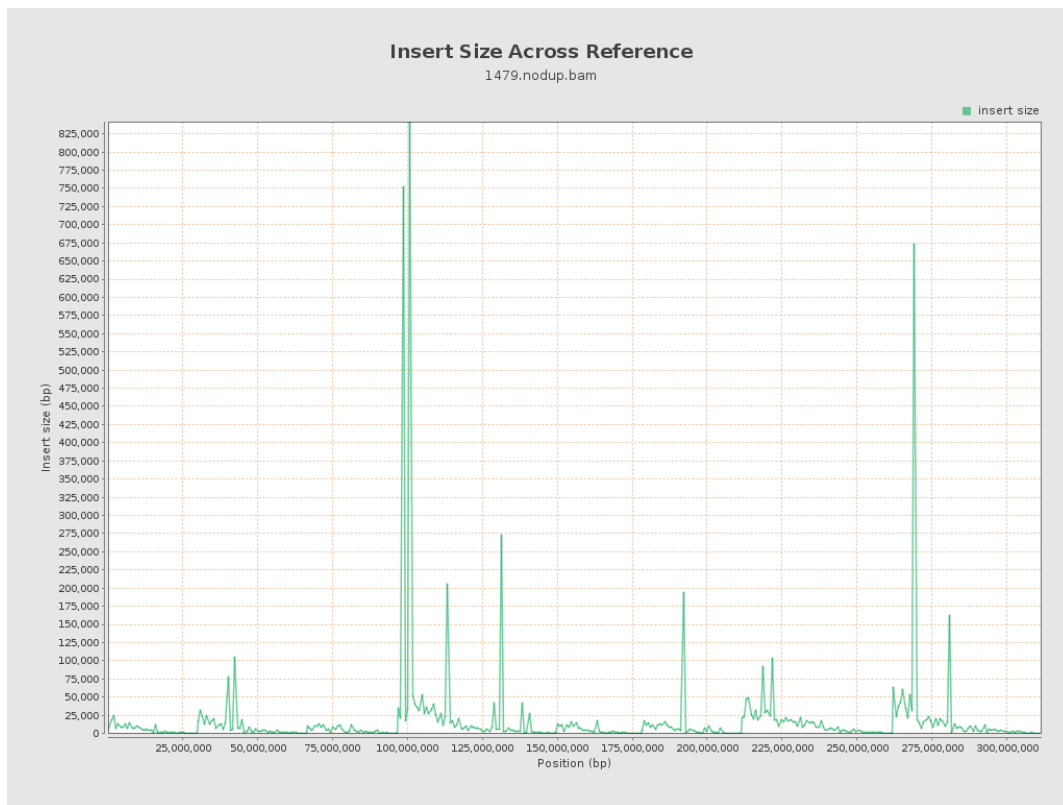
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

