

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:30:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/835
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

| | |
|---------------------------------------|---|
| BAM file: | /proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 835 .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_149/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_149_S239_L002 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_149/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_149_S239_L002 _R2_001.fastq.gz |
| Size of a homopolymer: | 3 |
| Number of windows: | 400 |

| | |
|----------------------------|-------------------------------|
| Analysis date: | Mon May 29 21:30:54 CEST 2023 |
| Draw chromosome limits: | no |
| Skip duplicate alignments: | no |

2. Summary

2.1. Globals

| | |
|------------------------------|---------------------|
| Reference size | 311,642,060 |
| Number of reads | 63,178,421 |
| Mapped reads | 59,502,856 / 94.18% |
| Unmapped reads | 3,675,565 / 5.82% |
| Mapped paired reads | 59,502,856 / 94.18% |
| Mapped reads, first in pair | 29,818,883 / 47.2% |
| Mapped reads, second in pair | 29,683,973 / 46.98% |
| Mapped reads, both in pair | 58,265,872 / 92.22% |
| Mapped reads, singletons | 1,236,984 / 1.96% |
| Read min/max/mean length | 30 / 151 / 148.17 |
| Duplicated reads (flagged) | 9,616,900 / 15.22% |
| Clipped reads | 12,962,749 / 20.52% |

2.2. ACGT Content

| | |
|--------------------------|------------------------|
| Number/percentage of A's | 2,551,708,707 / 30.89% |
| Number/percentage of C's | 1,581,067,609 / 19.14% |
| Number/percentage of T's | 2,553,441,480 / 30.91% |
| Number/percentage of G's | 1,575,604,972 / 19.07% |
| Number/percentage of N's | 35,175 / 0% |
| GC Percentage | 38.21% |

2.3. Coverage

| | |
|--------------------|----------|
| Mean | 26.5757 |
| Standard Deviation | 215.7207 |

2.4. Mapping Quality

| | |
|----------------------|-------|
| Mean Mapping Quality | 44.96 |
|----------------------|-------|

2.5. Insert size

| | |
|--------------------|-----------------|
| Mean | 216,117.37 |
| Standard Deviation | 2,211,308.61 |
| P25/Median/P75 | 323 / 424 / 556 |

2.6. Mismatches and indels

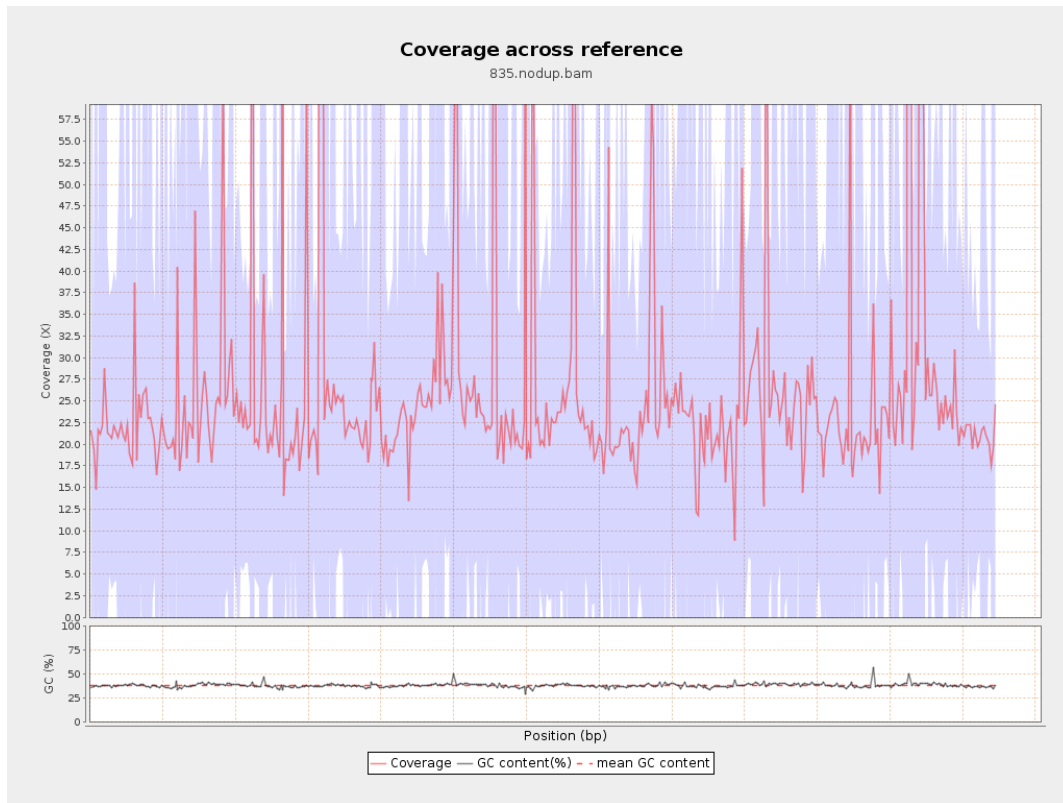
| | |
|--|-------------|
| General error rate | 2.22% |
| Mismatches | 168,497,291 |
| Insertions | 5,463,155 |
| Mapped reads with at least one insertion | 8.26% |
| Deletions | 5,467,843 |
| Mapped reads with at least one deletion | 8.17% |
| Homopolymer indels | 56.94% |

2.7. Chromosome stats

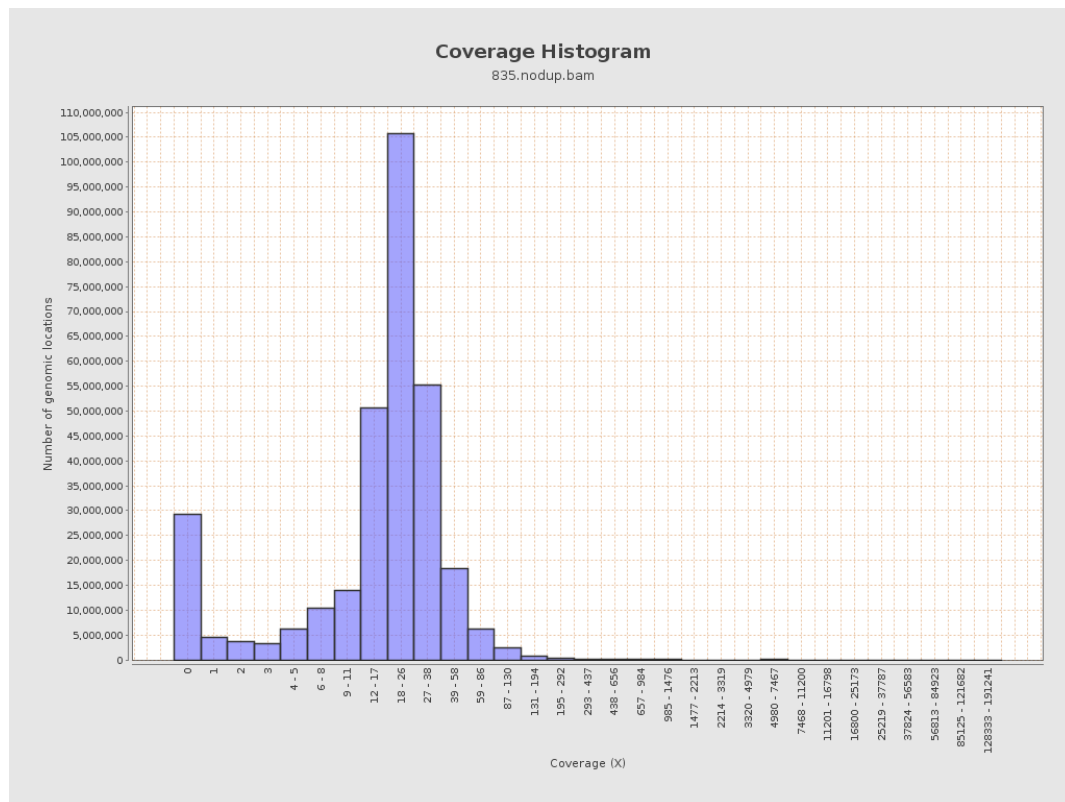
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|------------|----------|--------------|---------------|--------------------|
| LT669788.1 | 29724344 | 645465571 | 21.715 | 65.9748 |
| | | | | |

| | | | | |
|------------|----------|------------|---------|----------|
| LT669789.1 | 36598175 | 976325321 | 26.6769 | 227.3517 |
| LT669790.1 | 30422129 | 878715658 | 28.8841 | 236.2233 |
| LT669791.1 | 52758100 | 1379067405 | 26.1394 | 189.5996 |
| LT669792.1 | 28376109 | 740836075 | 26.1077 | 224.9905 |
| LT669793.1 | 33388210 | 806614995 | 24.1587 | 113.3895 |
| LT669794.1 | 50579949 | 1273802023 | 25.1839 | 193.0733 |
| LT669795.1 | 49795044 | 1581282402 | 31.7558 | 321.0794 |

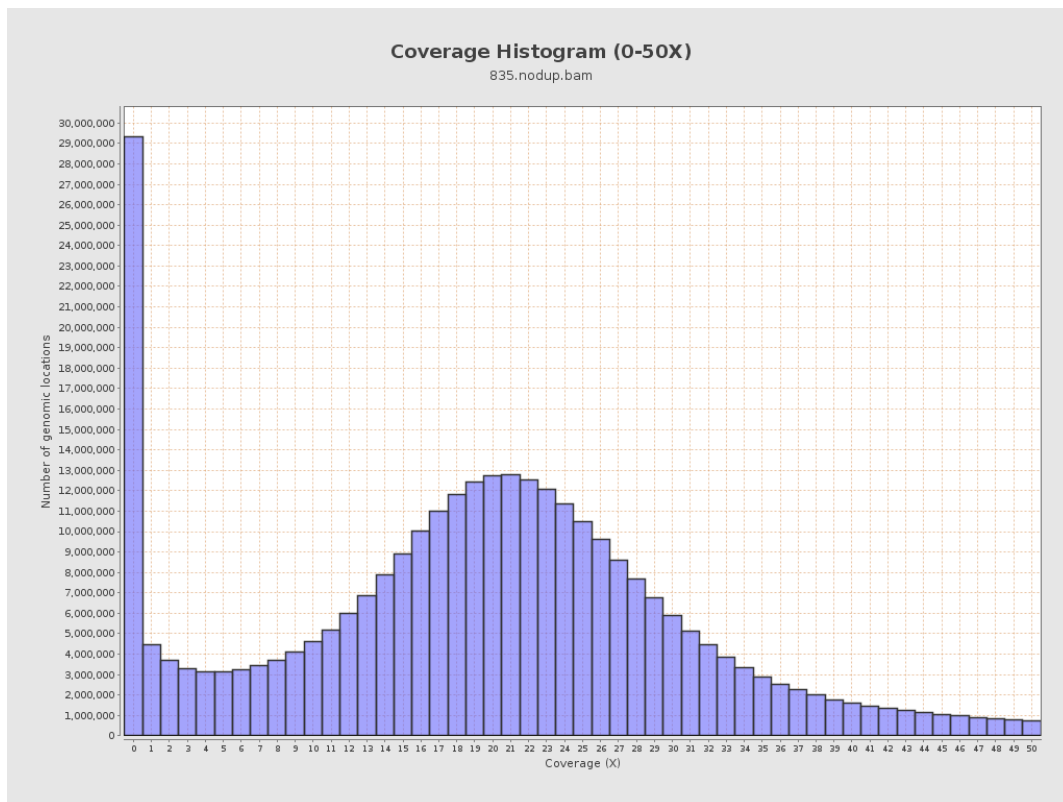
3. Results : Coverage across reference



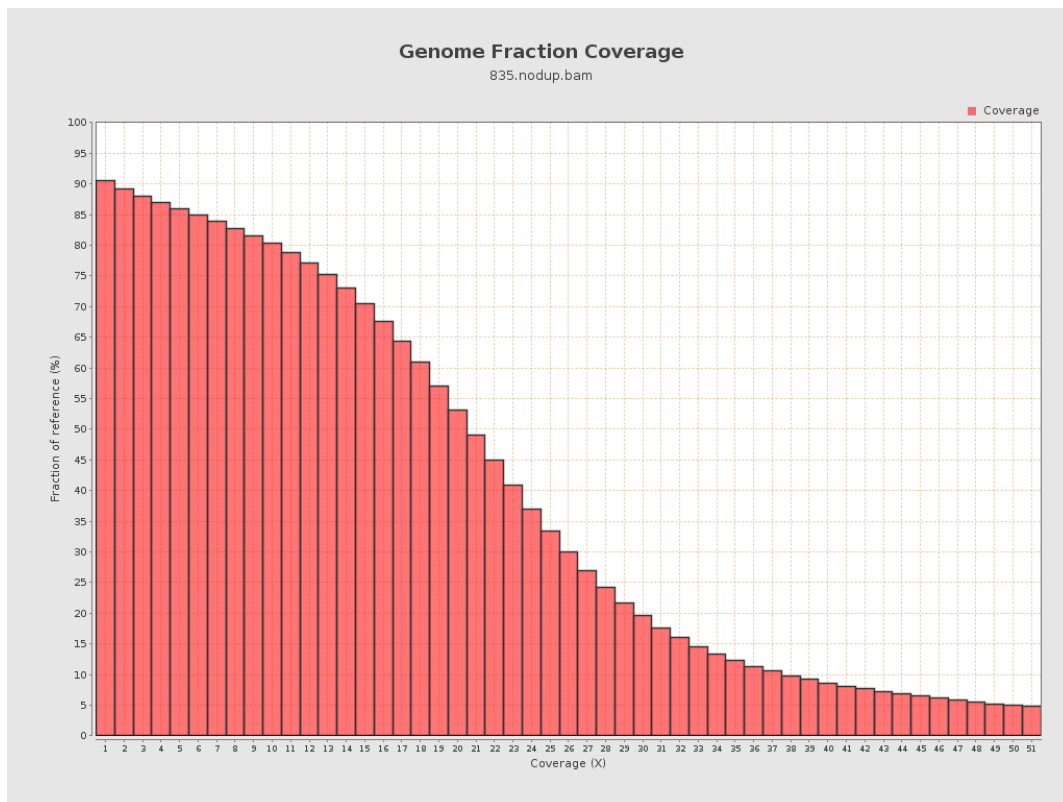
4. Results : Coverage Histogram



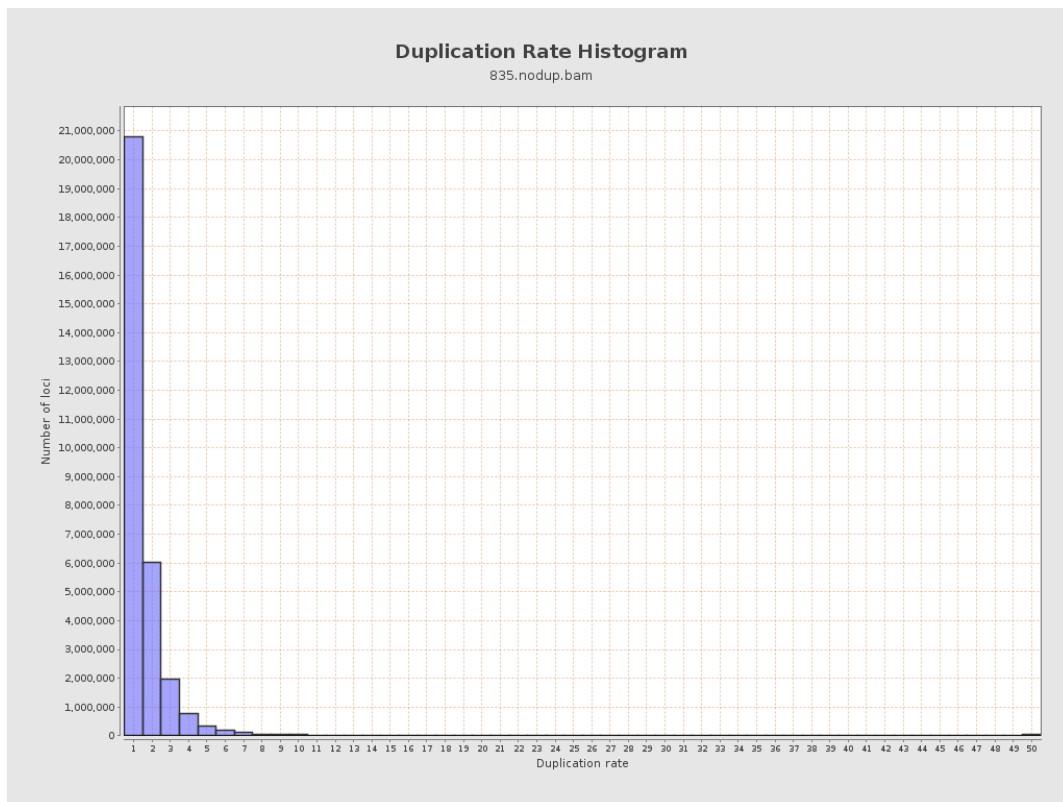
5. Results : Coverage Histogram (0-50X)



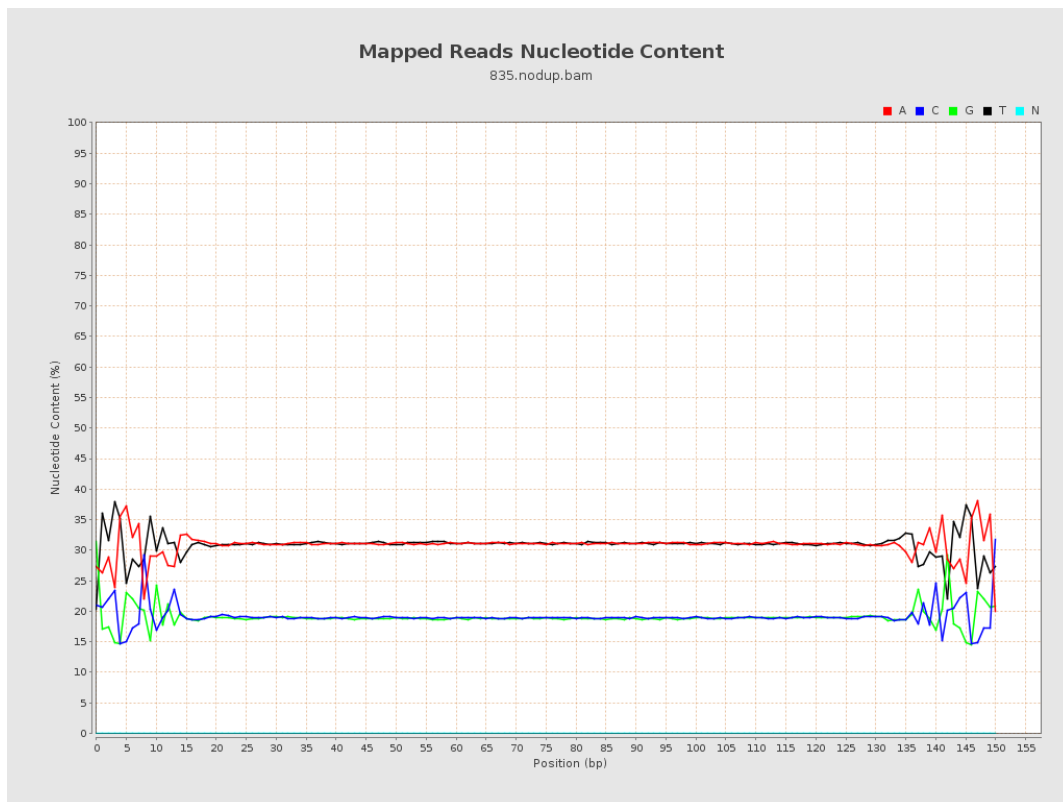
6. Results : Genome Fraction Coverage



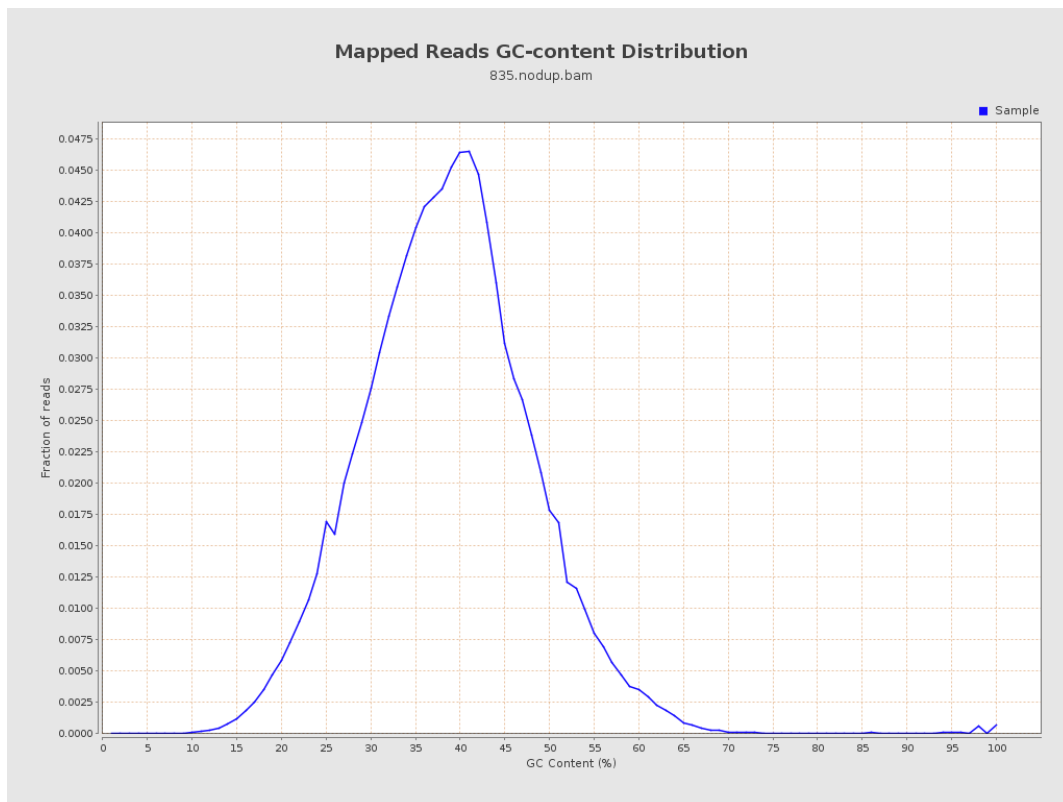
7. Results : Duplication Rate Histogram



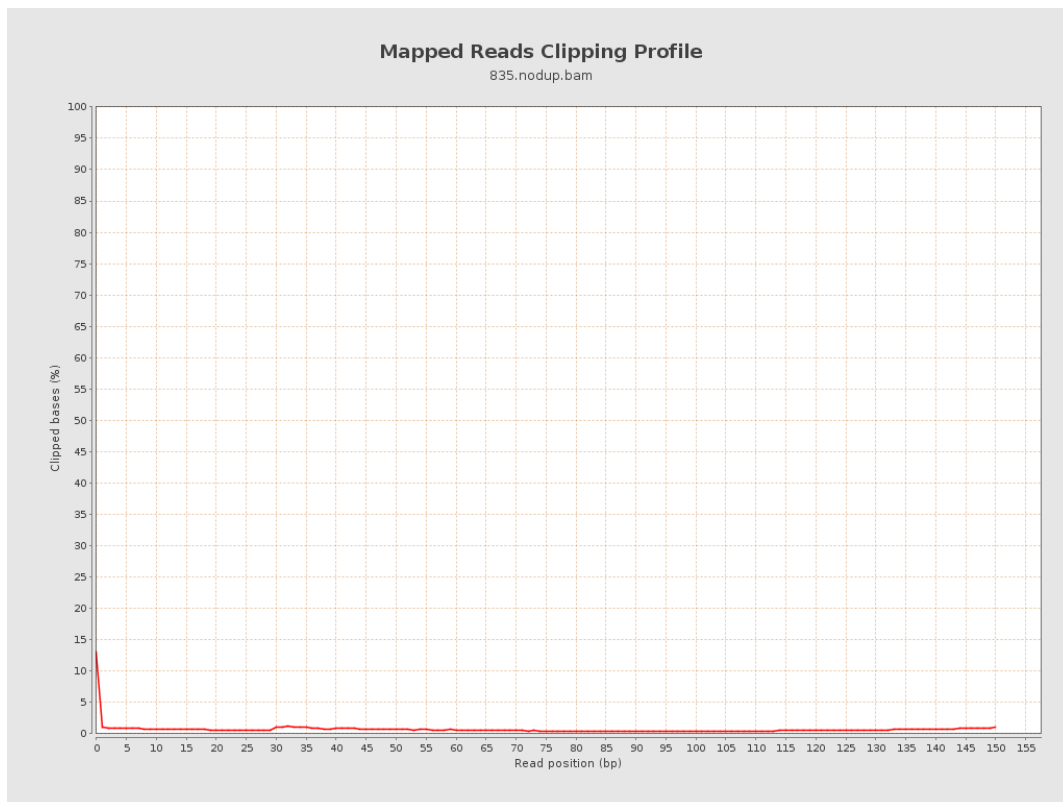
8. Results : Mapped Reads Nucleotide Content



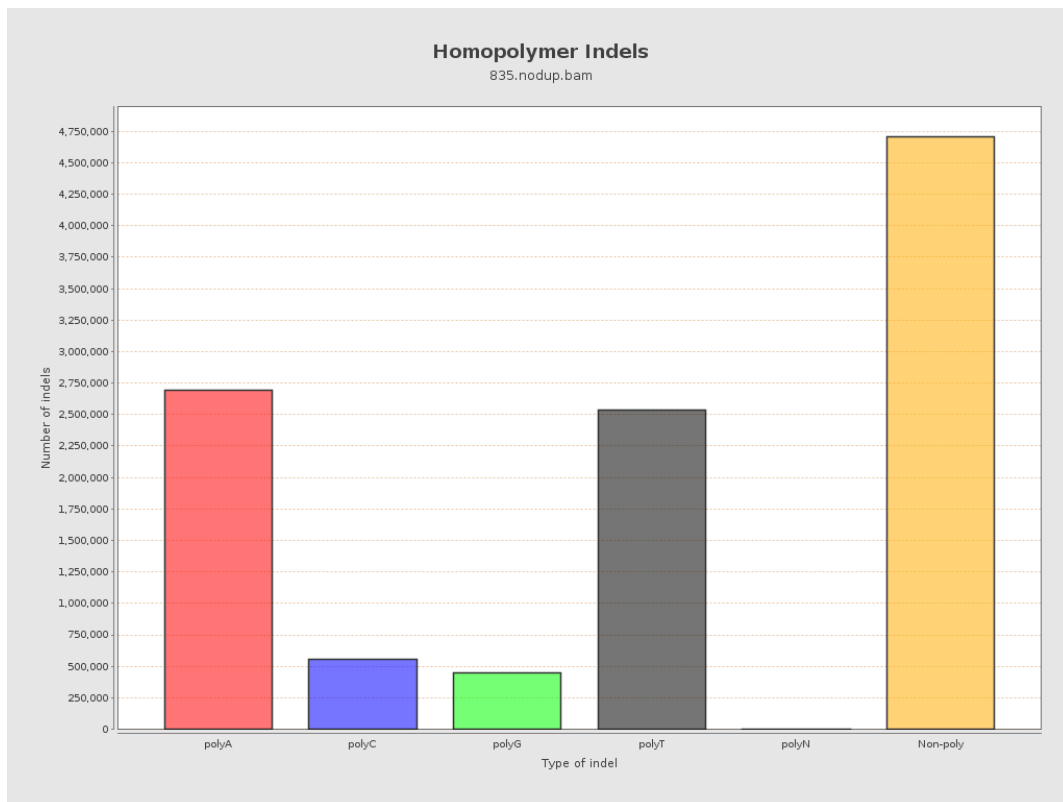
9. Results : Mapped Reads GC-content Distribution



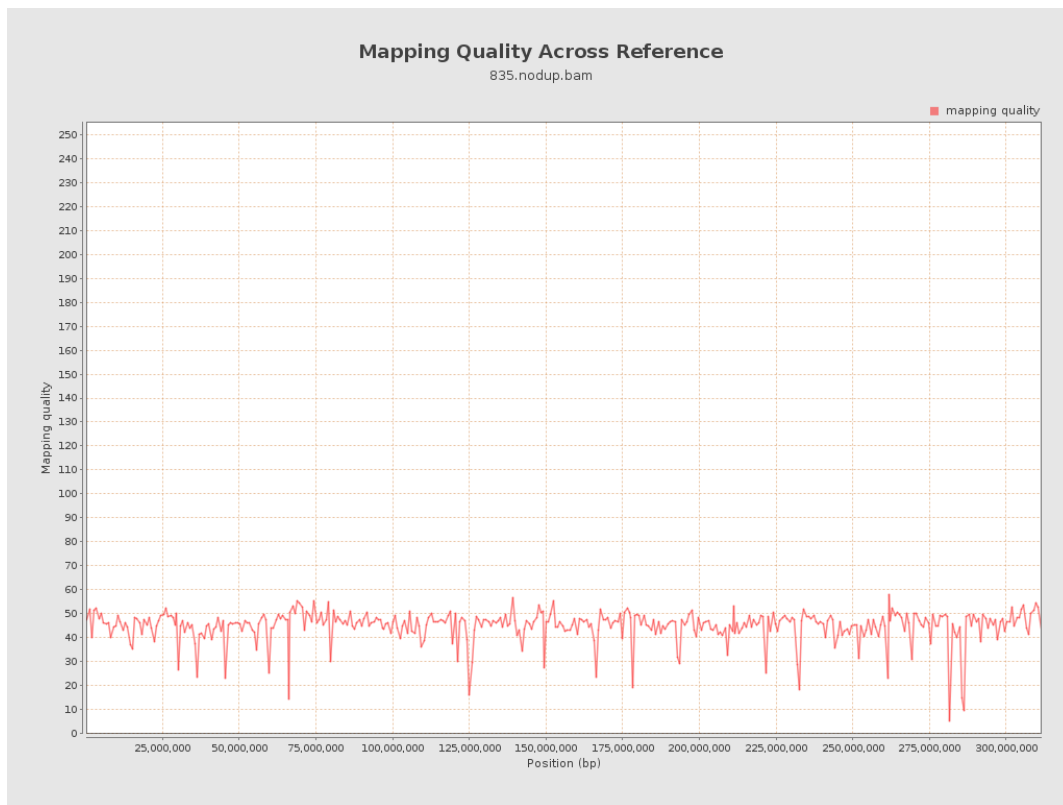
10. Results : Mapped Reads Clipping Profile



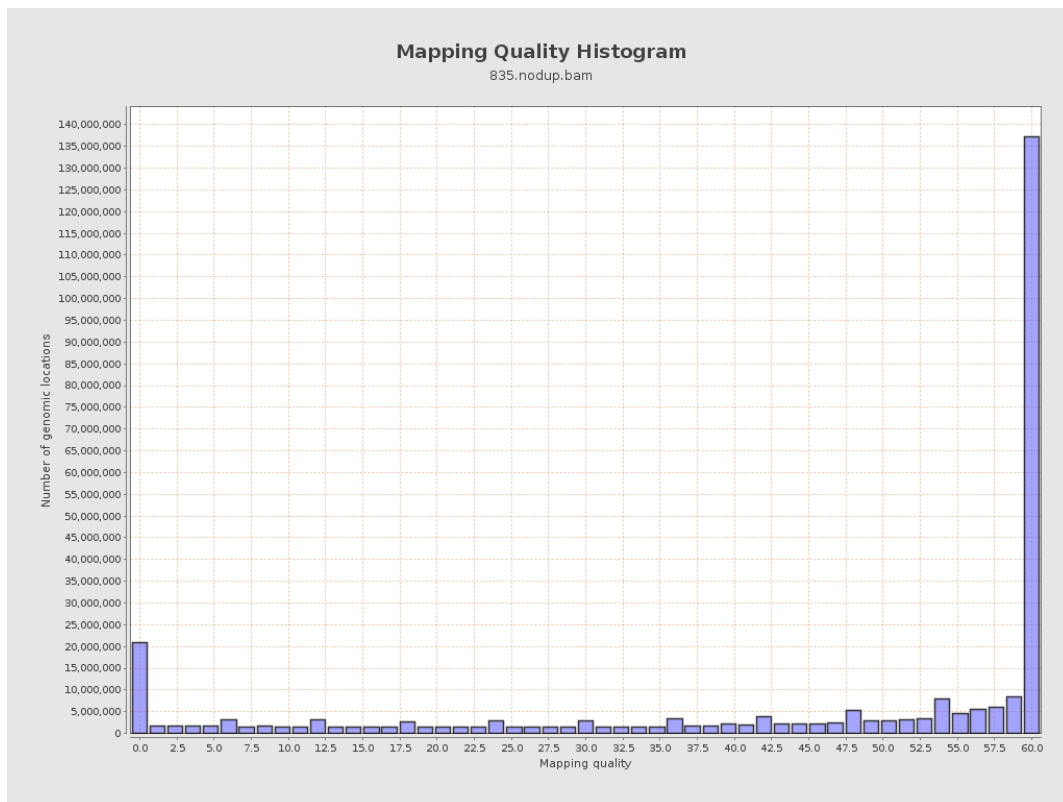
11. Results : Homopolymer Indels



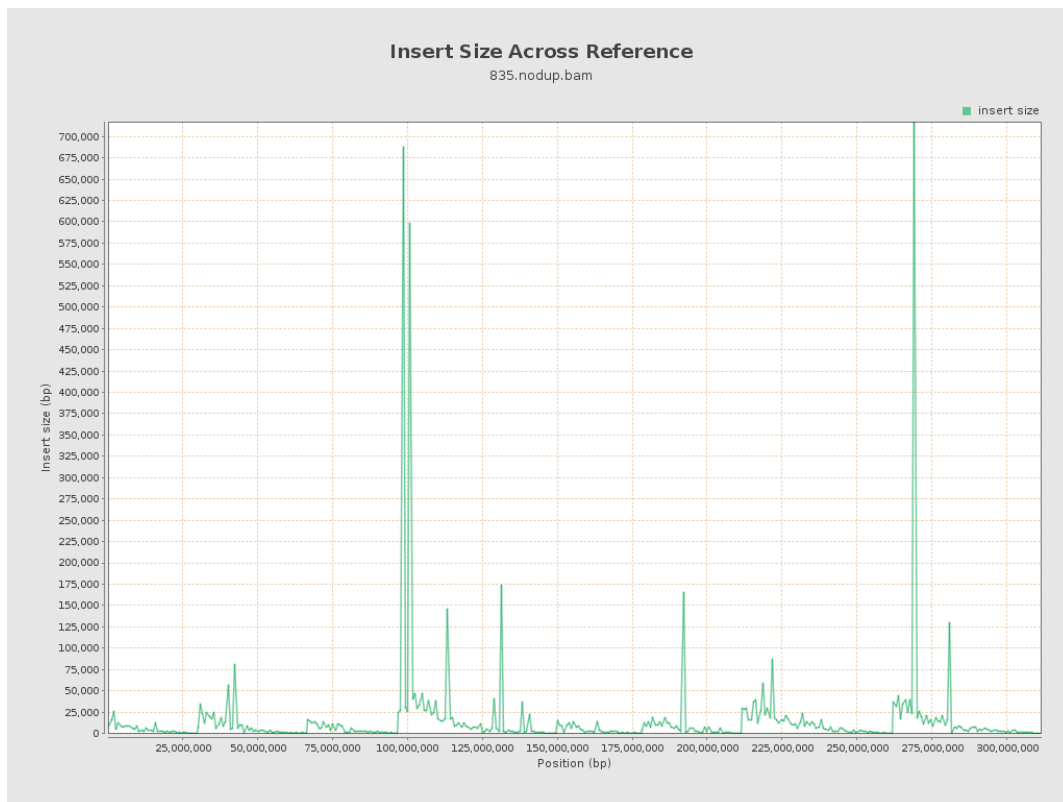
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

