

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:28:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/104
5
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

| | |
|---------------------------------------|---|
| BAM file: | /proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1045 .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_119/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_119_S209_L002 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_119/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_119_S209_L002 _R2_001.fastq.gz |
| Size of a homopolymer: | 3 |
| | |

| | |
|----------------------------|-------------------------------|
| Number of windows: | 400 |
| Analysis date: | Mon May 29 21:28:51 CEST 2023 |
| Draw chromosome limits: | no |
| Skip duplicate alignments: | no |

2. Summary

2.1. Globals

| | |
|------------------------------|---------------------|
| Reference size | 311,642,060 |
| Number of reads | 61,046,750 |
| Mapped reads | 55,381,765 / 90.72% |
| Unmapped reads | 5,664,985 / 9.28% |
| Mapped paired reads | 55,381,765 / 90.72% |
| Mapped reads, first in pair | 27,710,569 / 45.39% |
| Mapped reads, second in pair | 27,671,196 / 45.33% |
| Mapped reads, both in pair | 53,627,792 / 87.85% |
| Mapped reads, singletons | 1,753,973 / 2.87% |
| Read min/max/mean length | 30 / 151 / 148.09 |
| Duplicated reads (flagged) | 9,709,340 / 15.9% |
| Clipped reads | 13,136,963 / 21.52% |

2.2. ACGT Content

| | |
|--------------------------|------------------------|
| Number/percentage of A's | 2,346,040,040 / 30.89% |
| Number/percentage of C's | 1,450,619,841 / 19.1% |
| Number/percentage of T's | 2,349,297,910 / 30.93% |
| Number/percentage of G's | 1,449,741,008 / 19.09% |
| Number/percentage of N's | 32,389 / 0% |
| GC Percentage | 38.18% |

2.3. Coverage

| | |
|--------------------|----------|
| Mean | 24.4386 |
| Standard Deviation | 224.9114 |

2.4. Mapping Quality

| | |
|----------------------|-------|
| Mean Mapping Quality | 43.99 |
|----------------------|-------|

2.5. Insert size

| | |
|--------------------|-----------------|
| Mean | 262,267.65 |
| Standard Deviation | 2,464,856.73 |
| P25/Median/P75 | 318 / 416 / 546 |

2.6. Mismatches and indels

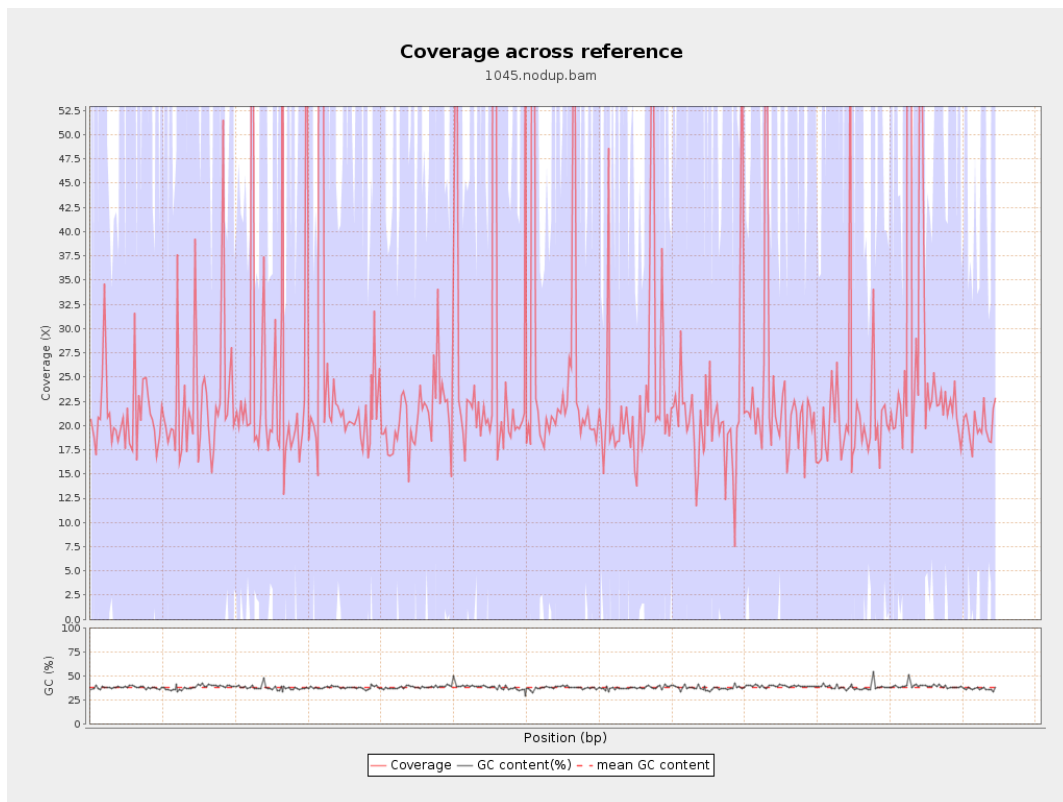
| | |
|--|-------------|
| General error rate | 2.39% |
| Mismatches | 165,976,083 |
| Insertions | 5,659,845 |
| Mapped reads with at least one insertion | 9.1% |
| Deletions | 5,425,484 |
| Mapped reads with at least one deletion | 8.66% |
| Homopolymer indels | 56.81% |

2.7. Chromosome stats

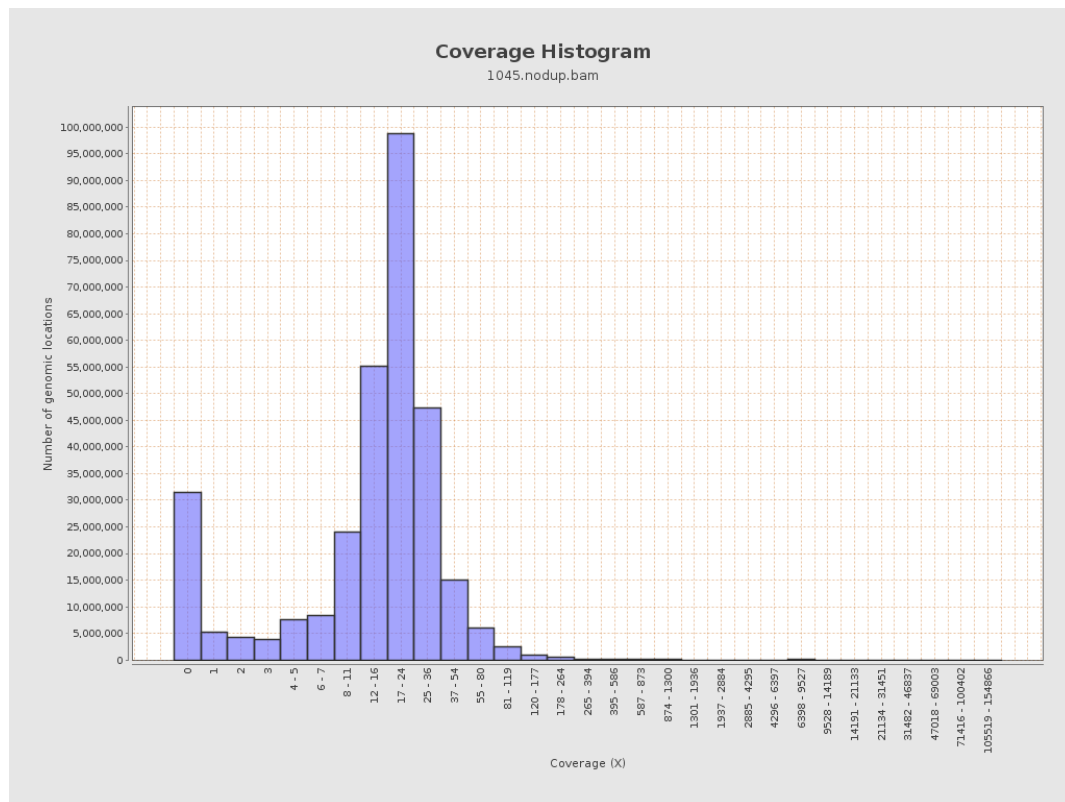
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|------------|----------|--------------|---------------|--------------------|
| LT669788.1 | 29724344 | 618361937 | 20.8032 | 97.0417 |
| | | | | |

| | | | | |
|------------|----------|------------|---------|----------|
| LT669789.1 | 36598175 | 895863575 | 24.4784 | 242.6949 |
| LT669790.1 | 30422129 | 907853285 | 29.8419 | 323.4813 |
| LT669791.1 | 52758100 | 1259383899 | 23.8709 | 252.2867 |
| LT669792.1 | 28376109 | 701947519 | 24.7373 | 225.0888 |
| LT669793.1 | 33388210 | 752581999 | 22.5404 | 143.709 |
| LT669794.1 | 50579949 | 1138237554 | 22.5037 | 194.3186 |
| LT669795.1 | 49795044 | 1341874307 | 26.9479 | 234.9393 |

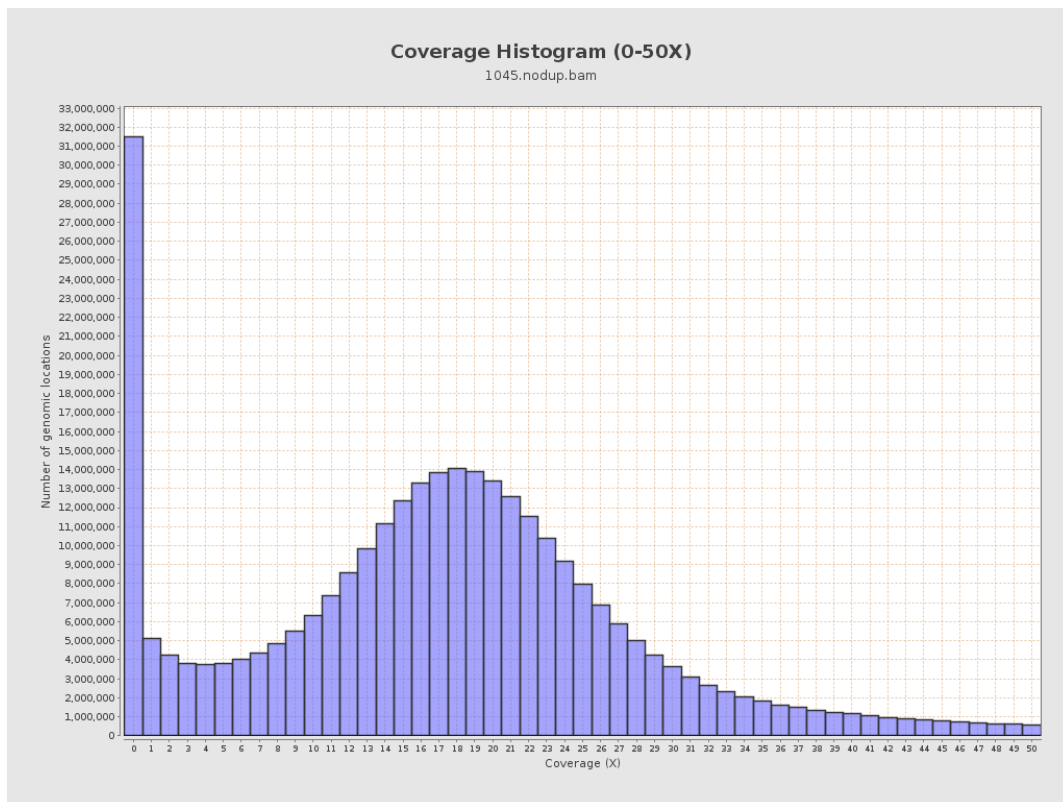
3. Results : Coverage across reference



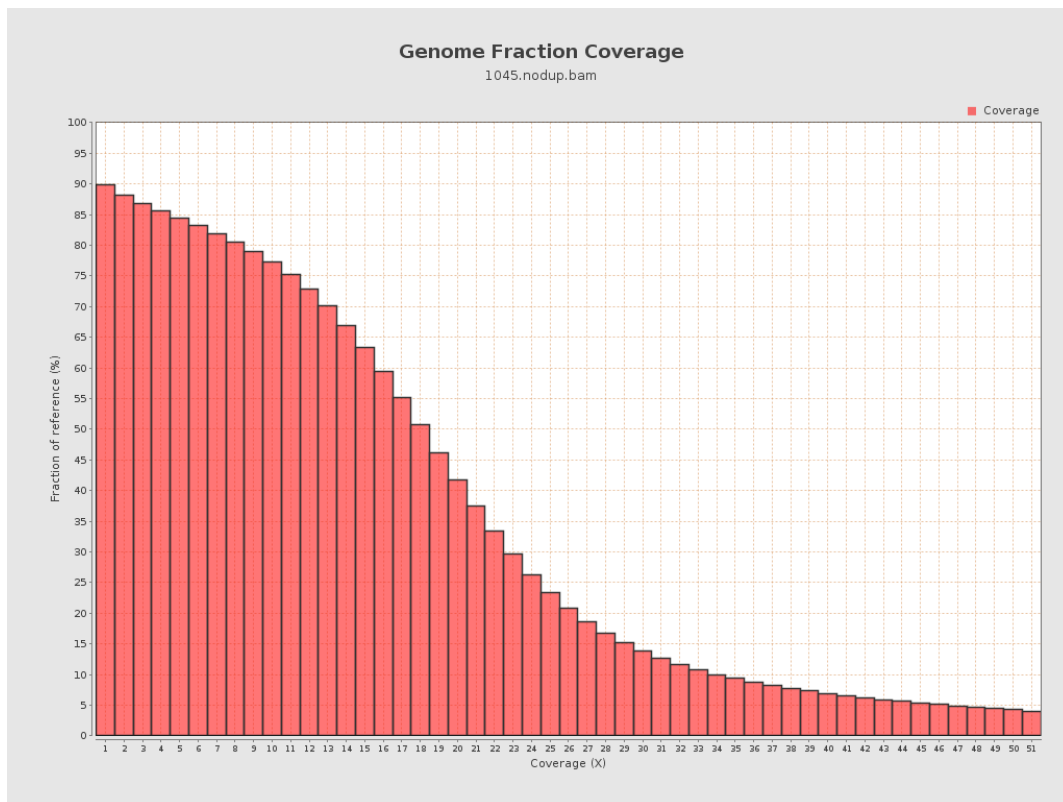
4. Results : Coverage Histogram



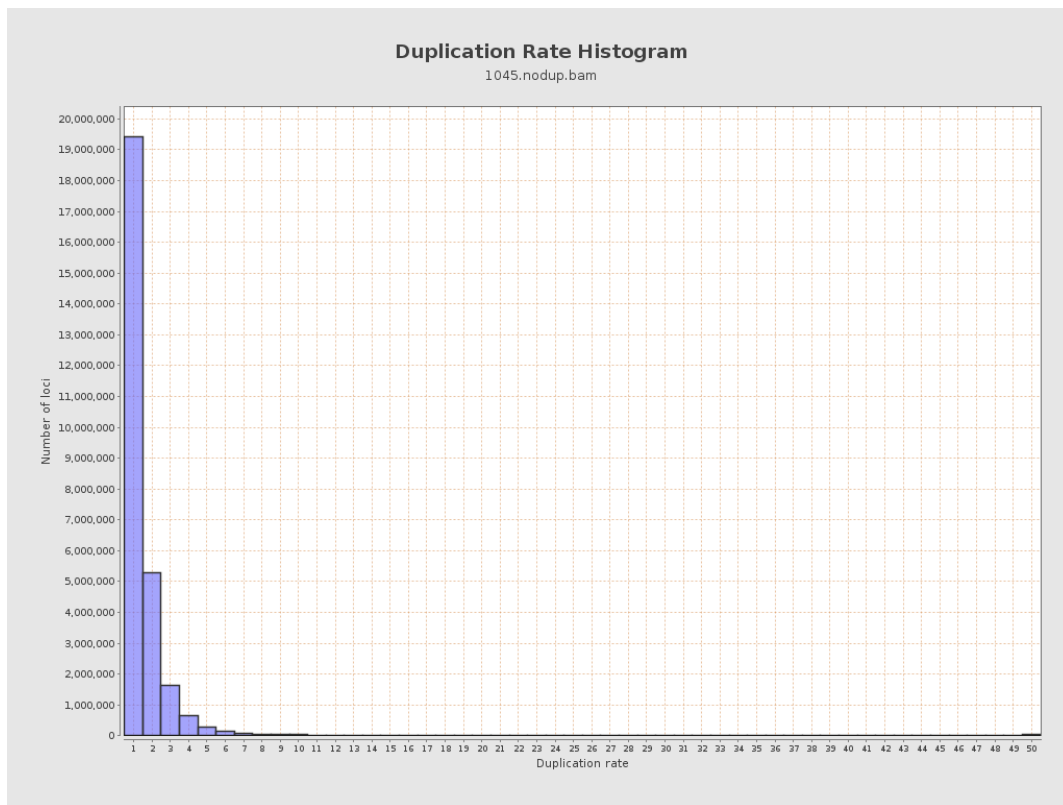
5. Results : Coverage Histogram (0-50X)



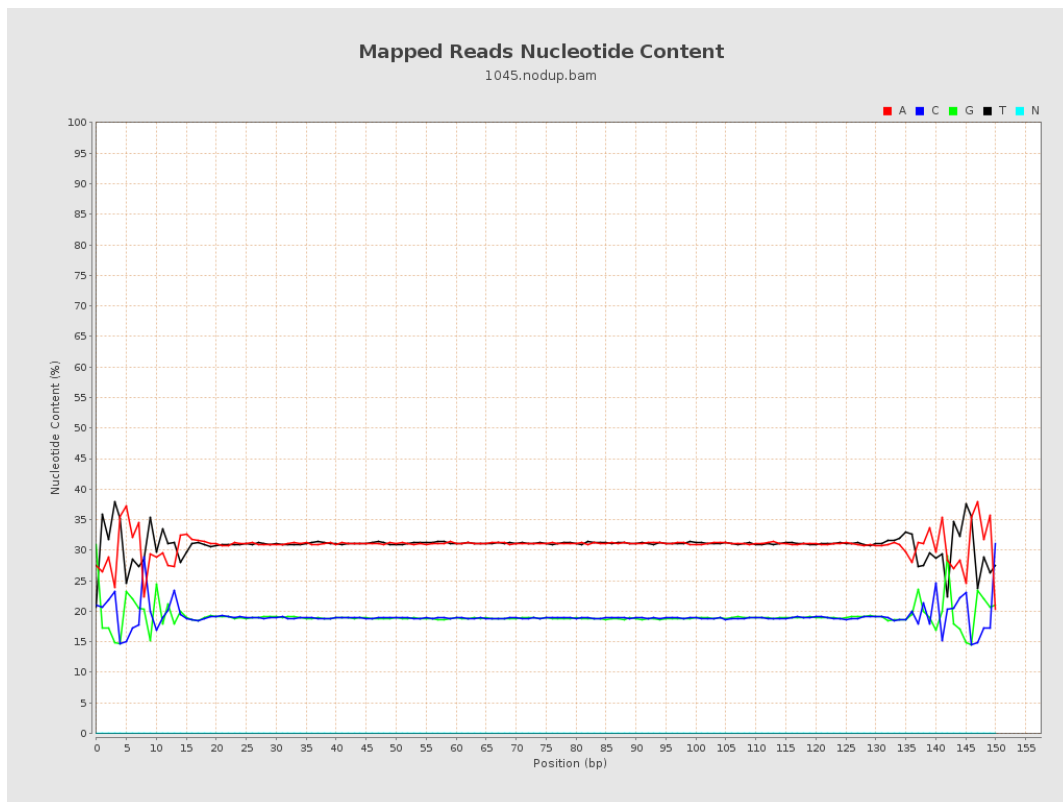
6. Results : Genome Fraction Coverage



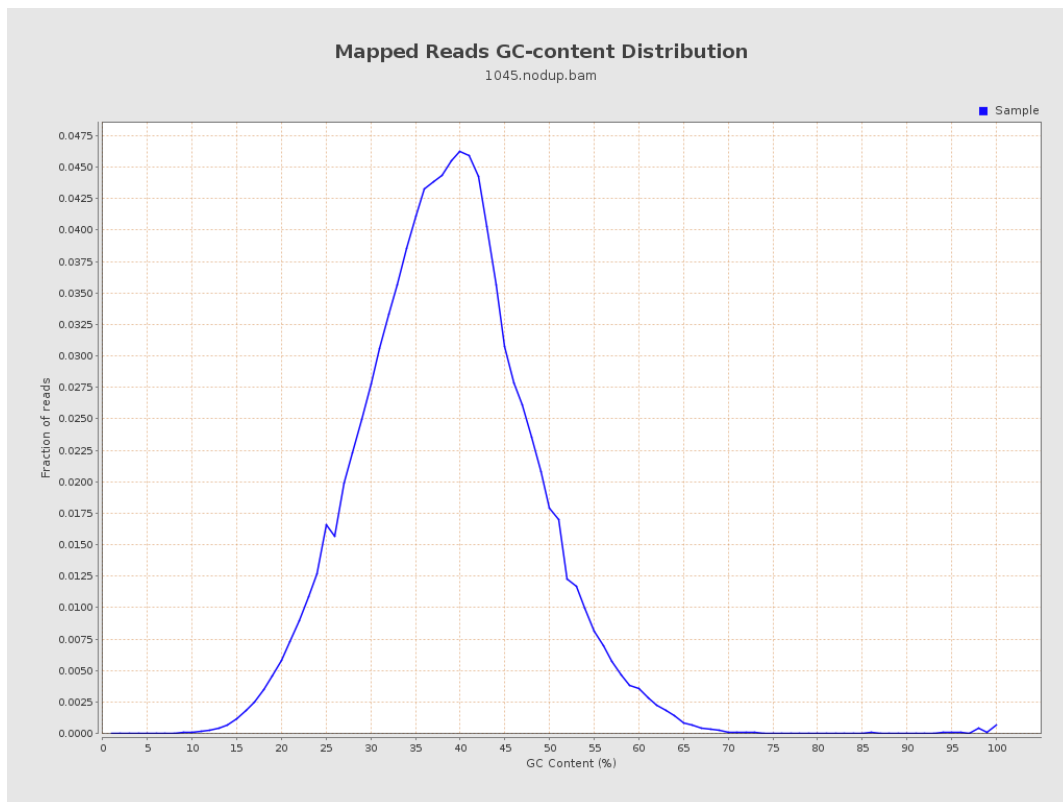
7. Results : Duplication Rate Histogram



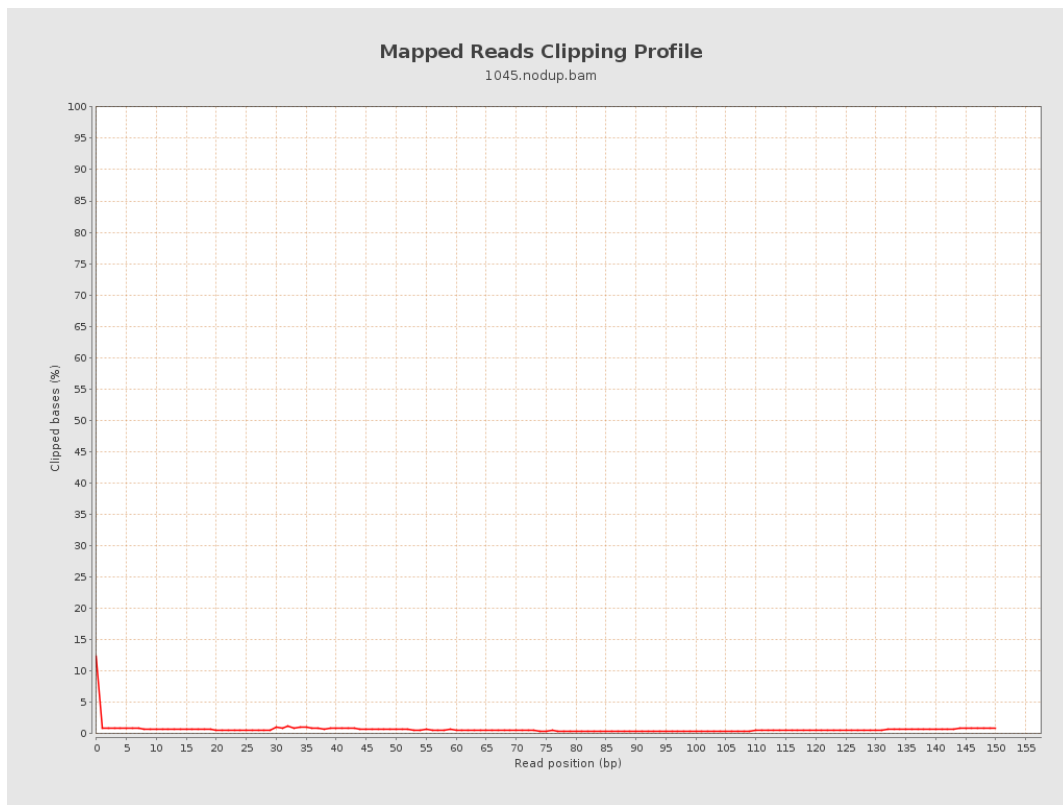
8. Results : Mapped Reads Nucleotide Content



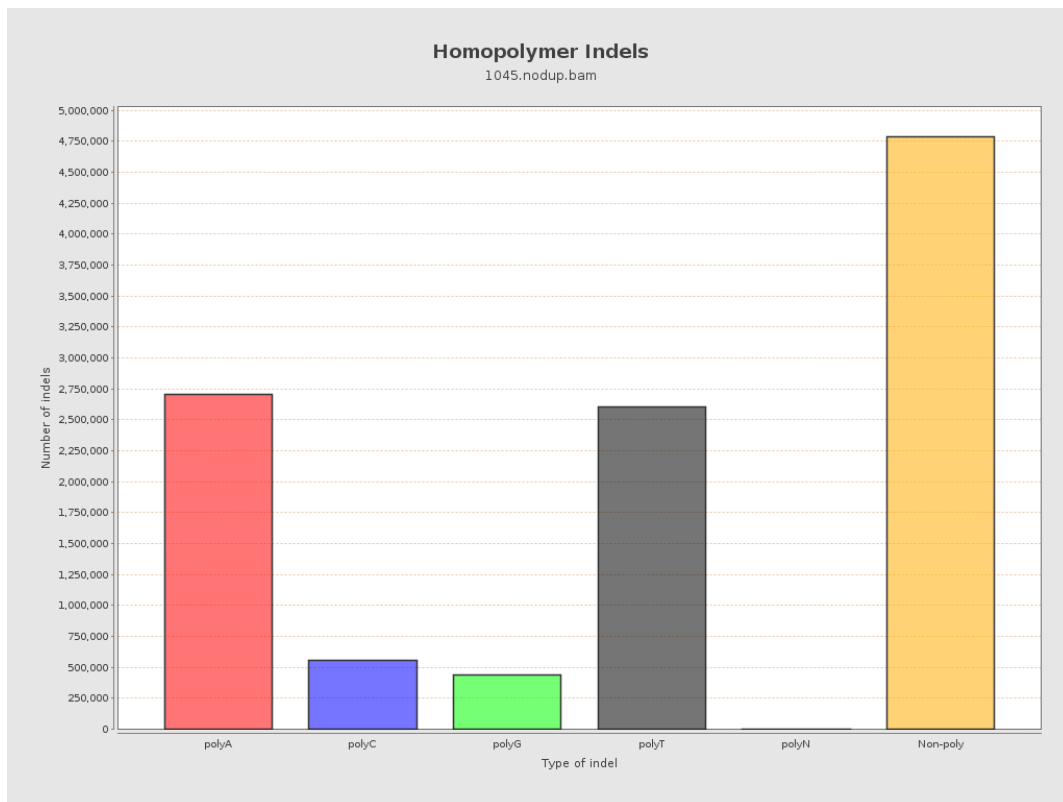
9. Results : Mapped Reads GC-content Distribution



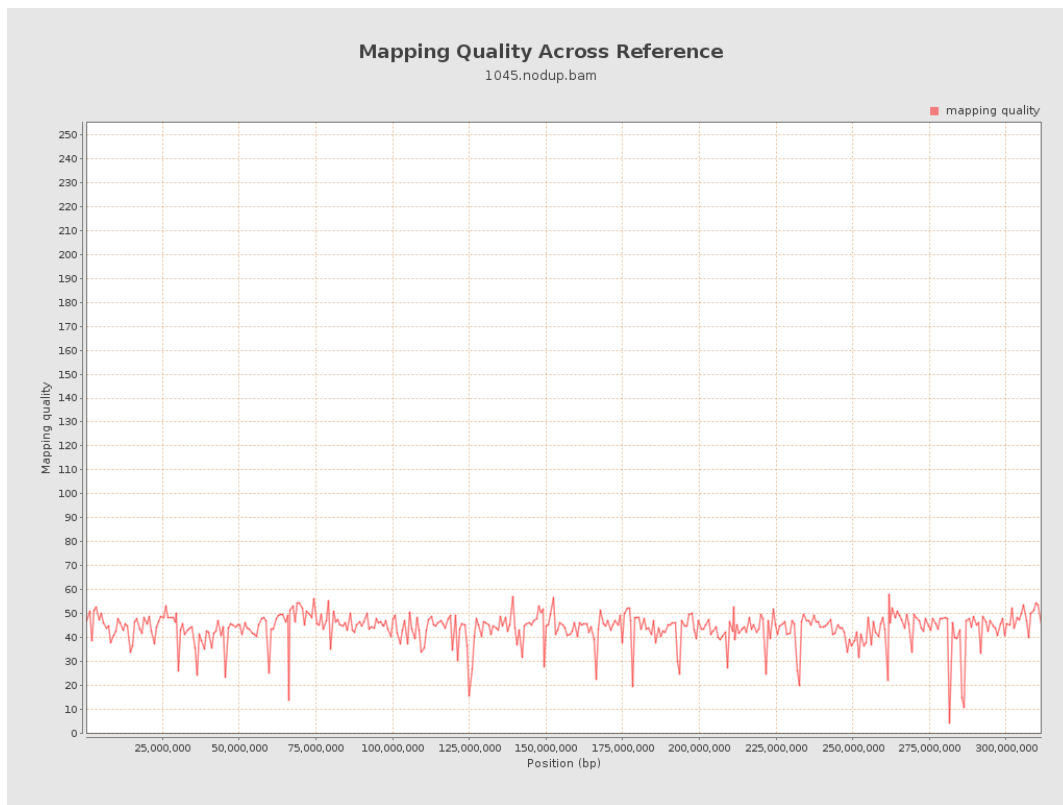
10. Results : Mapped Reads Clipping Profile



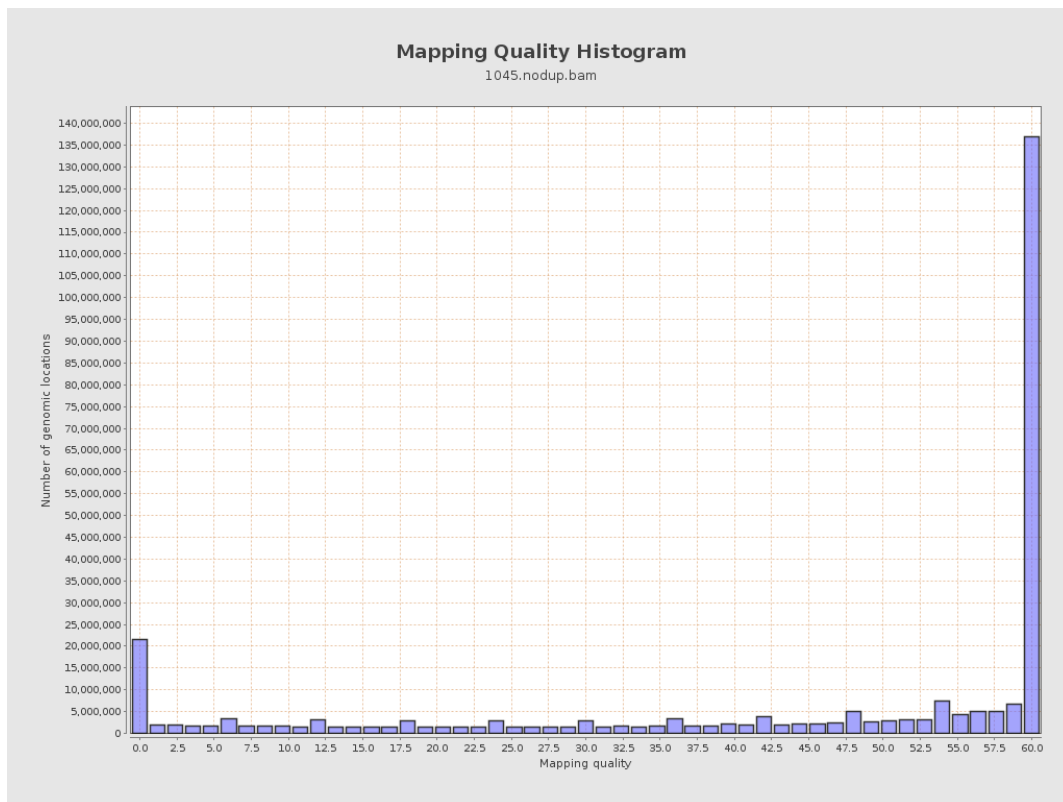
11. Results : Homopolymer Indels



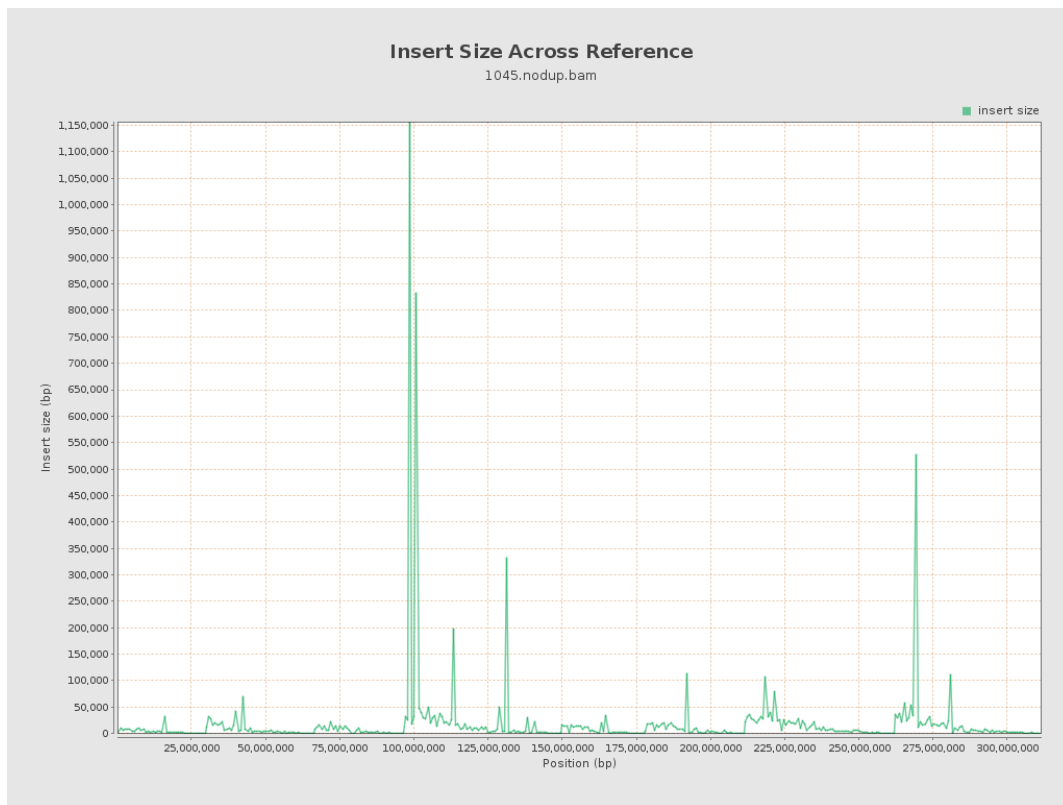
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

