

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:32:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/148
2
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

| | |
|---------------------------------------|---|
| BAM file: | /proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1482 .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_416/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_416_S391_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_416/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_416_S391_L004 _R2_001.fastq.gz |
| Size of a homopolymer: | 3 |
| | |

| | |
|----------------------------|-------------------------------|
| Number of windows: | 400 |
| Analysis date: | Mon May 29 21:32:51 CEST 2023 |
| Draw chromosome limits: | no |
| Skip duplicate alignments: | no |

2. Summary

2.1. Globals

| | |
|------------------------------|---------------------|
| Reference size | 311,642,060 |
| Number of reads | 67,300,609 |
| Mapped reads | 63,182,307 / 93.88% |
| Unmapped reads | 4,118,302 / 6.12% |
| Mapped paired reads | 63,182,307 / 93.88% |
| Mapped reads, first in pair | 31,616,674 / 46.98% |
| Mapped reads, second in pair | 31,565,633 / 46.9% |
| Mapped reads, both in pair | 61,845,899 / 91.9% |
| Mapped reads, singletons | 1,336,408 / 1.99% |
| Read min/max/mean length | 30 / 151 / 148.26 |
| Duplicated reads (flagged) | 9,743,722 / 14.48% |
| Clipped reads | 13,363,722 / 19.86% |

2.2. ACGT Content

| | |
|--------------------------|------------------------|
| Number/percentage of A's | 2,732,492,688 / 31% |
| Number/percentage of C's | 1,675,920,644 / 19.01% |
| Number/percentage of T's | 2,731,101,958 / 30.99% |
| Number/percentage of G's | 1,674,462,531 / 19% |
| Number/percentage of N's | 29,312 / 0% |
| GC Percentage | 38.01% |

2.3. Coverage

| | |
|--------------------|----------|
| Mean | 28.3551 |
| Standard Deviation | 195.0521 |

2.4. Mapping Quality

| | |
|----------------------|-------|
| Mean Mapping Quality | 44.43 |
|----------------------|-------|

2.5. Insert size

| | |
|--------------------|-----------------|
| Mean | 238,958.38 |
| Standard Deviation | 2,329,486.07 |
| P25/Median/P75 | 351 / 456 / 595 |

2.6. Mismatches and indels

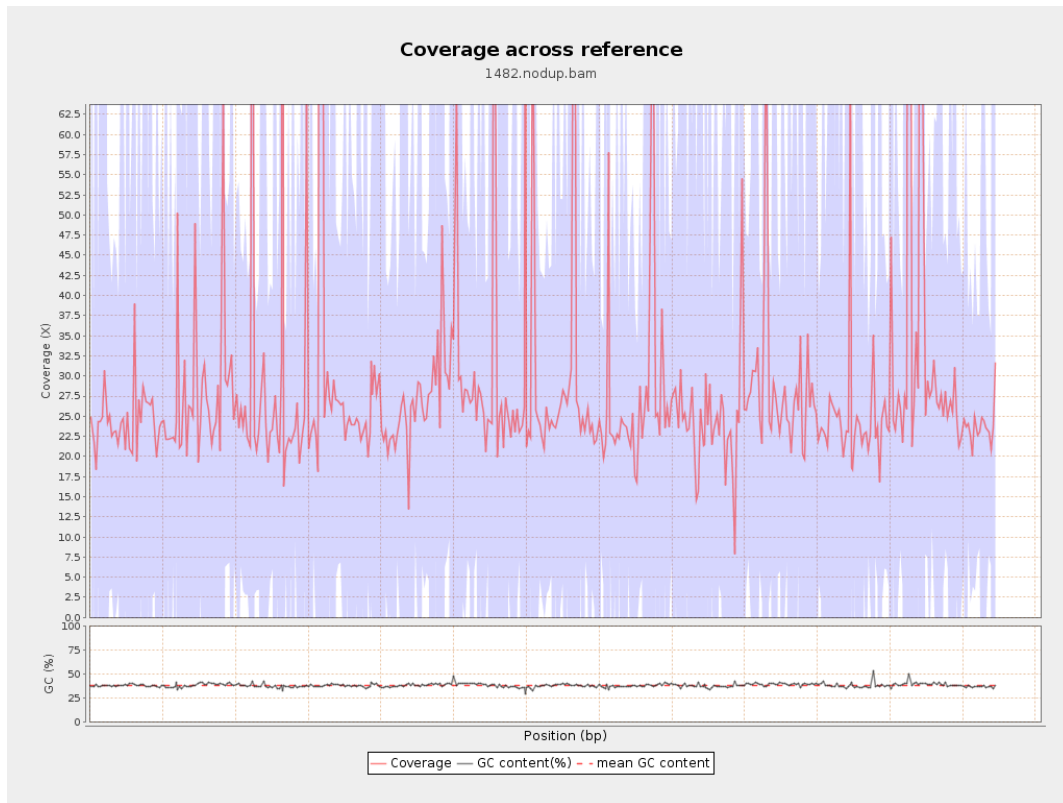
| | |
|--|-------------|
| General error rate | 2.29% |
| Mismatches | 185,630,102 |
| Insertions | 5,891,321 |
| Mapped reads with at least one insertion | 8.37% |
| Deletions | 6,015,987 |
| Mapped reads with at least one deletion | 8.47% |
| Homopolymer indels | 57.35% |

2.7. Chromosome stats

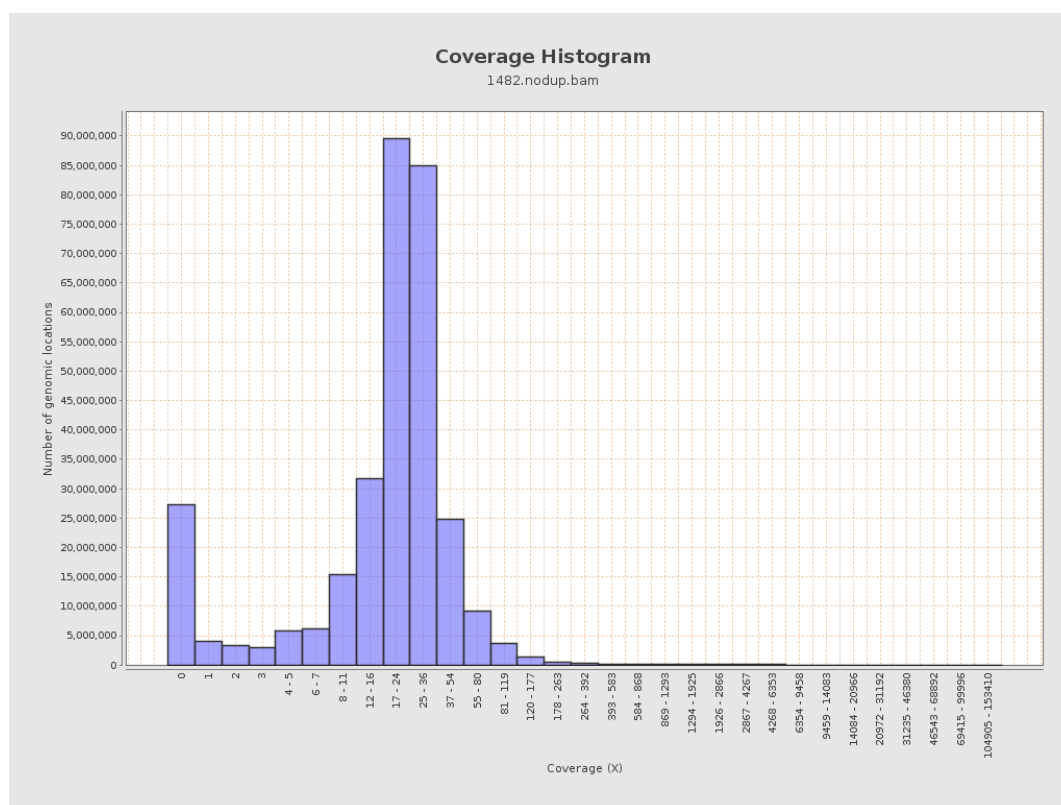
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|------------|----------|--------------|---------------|--------------------|
| LT669788.1 | 29724344 | 717551313 | 24.1402 | 68.1765 |

| | | | | |
|------------|----------|------------|---------|----------|
| LT669789.1 | 36598175 | 1073875111 | 29.3423 | 221.3924 |
| LT669790.1 | 30422129 | 948865783 | 31.19 | 235.0536 |
| LT669791.1 | 52758100 | 1485597901 | 28.1587 | 177.655 |
| LT669792.1 | 28376109 | 806841888 | 28.4338 | 239.9528 |
| LT669793.1 | 33388210 | 891379875 | 26.6974 | 150.9784 |
| LT669794.1 | 50579949 | 1374065376 | 27.1662 | 172.7546 |
| LT669795.1 | 49795044 | 1538460014 | 30.8958 | 231.6842 |

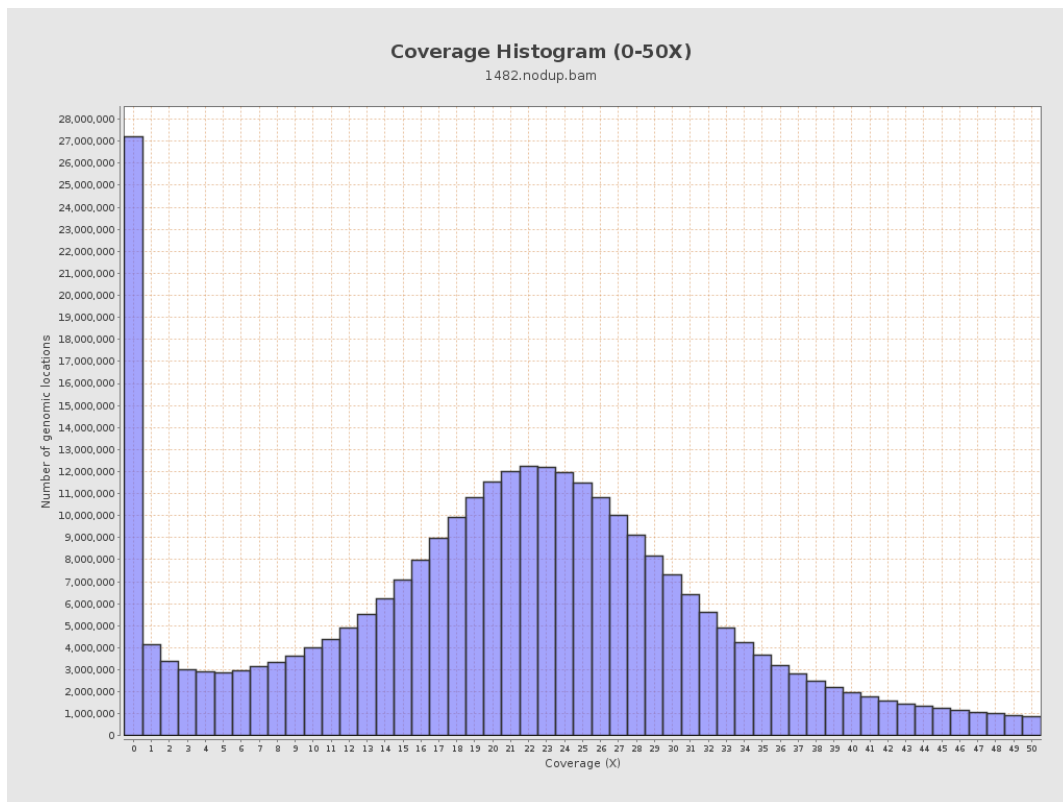
3. Results : Coverage across reference



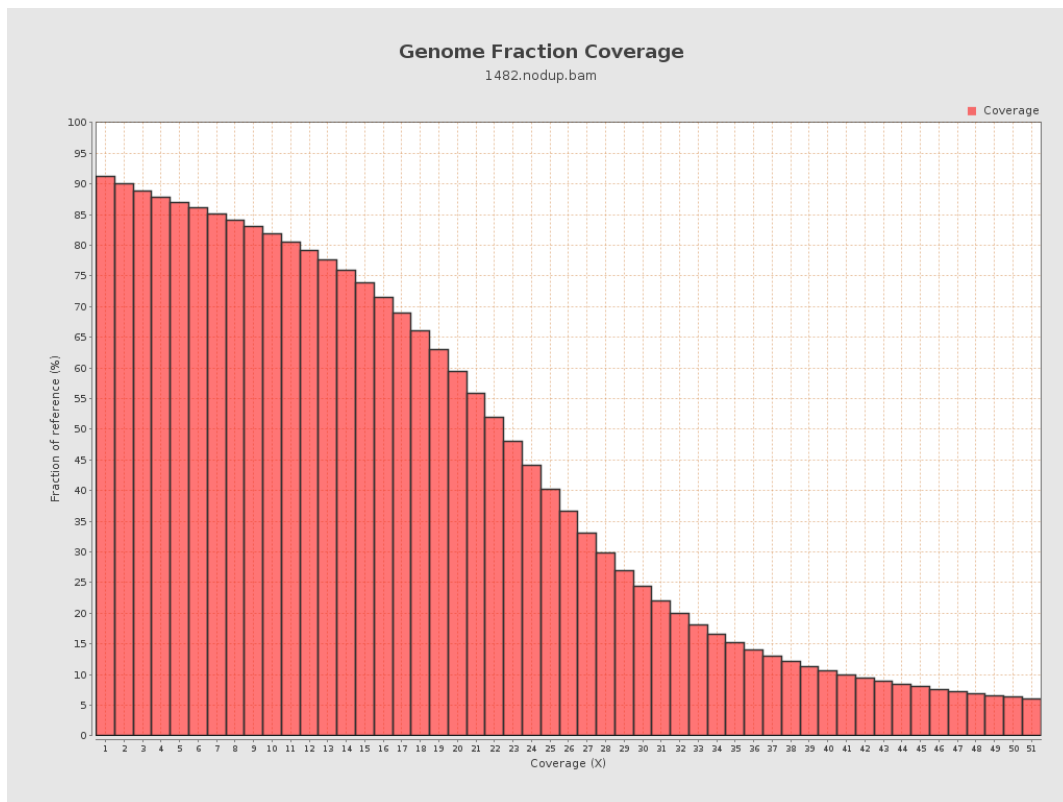
4. Results : Coverage Histogram



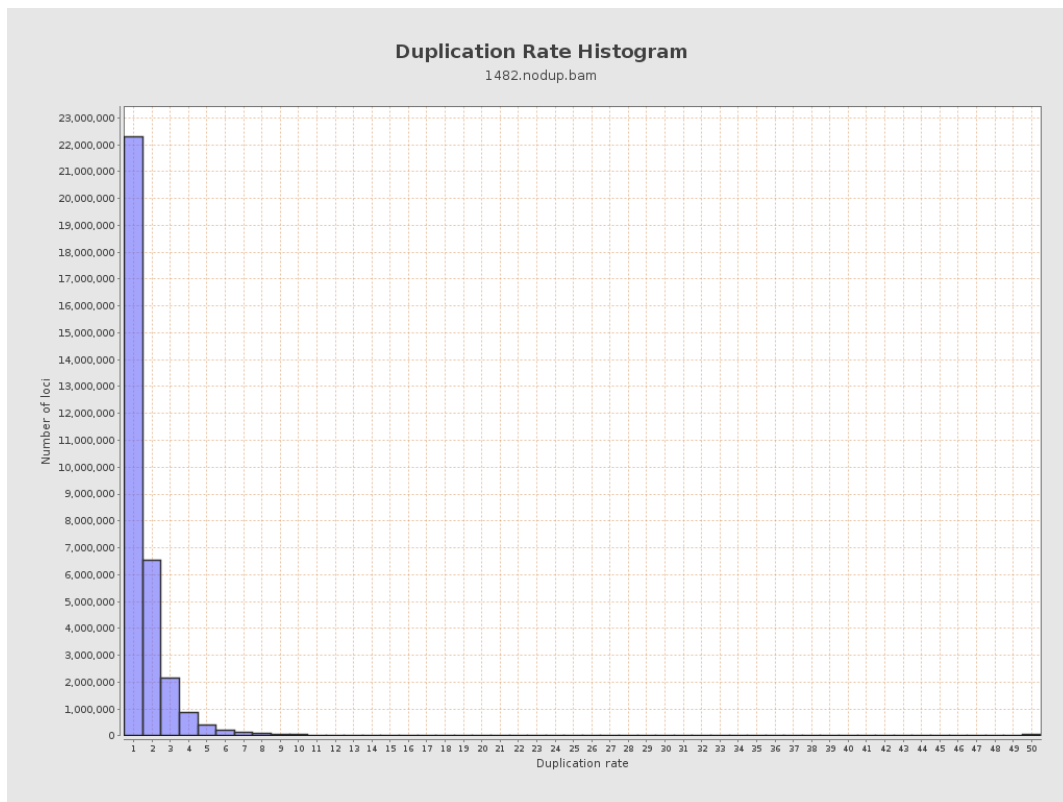
5. Results : Coverage Histogram (0-50X)



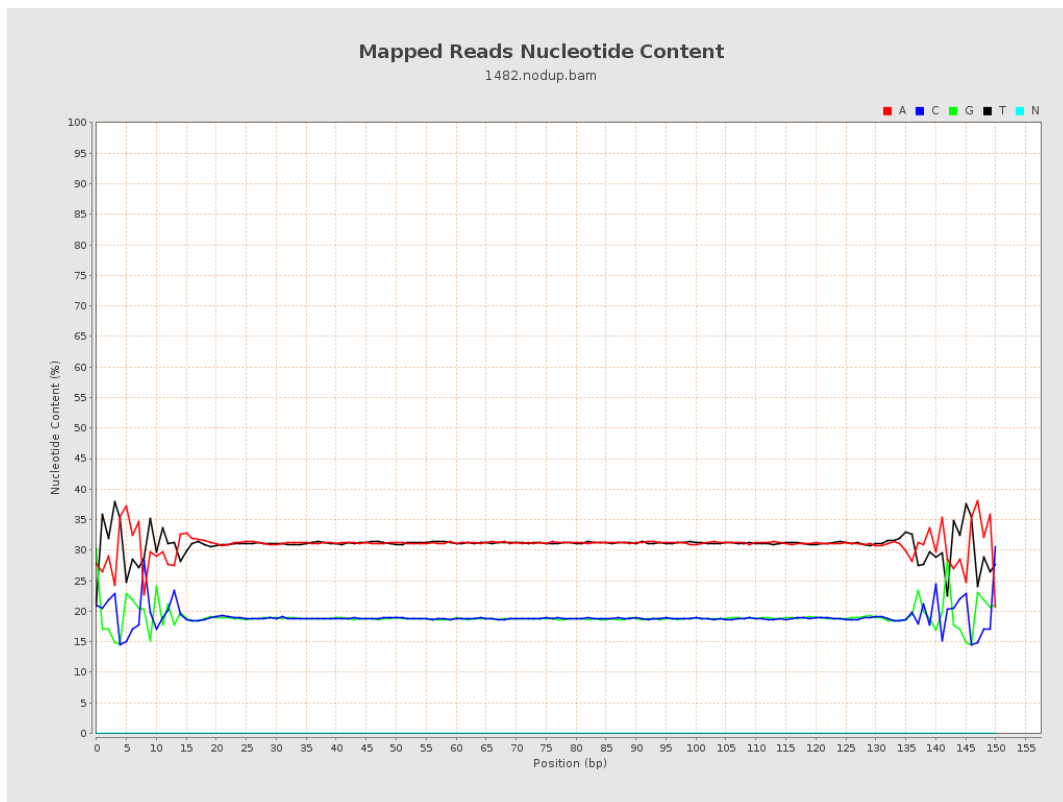
6. Results : Genome Fraction Coverage



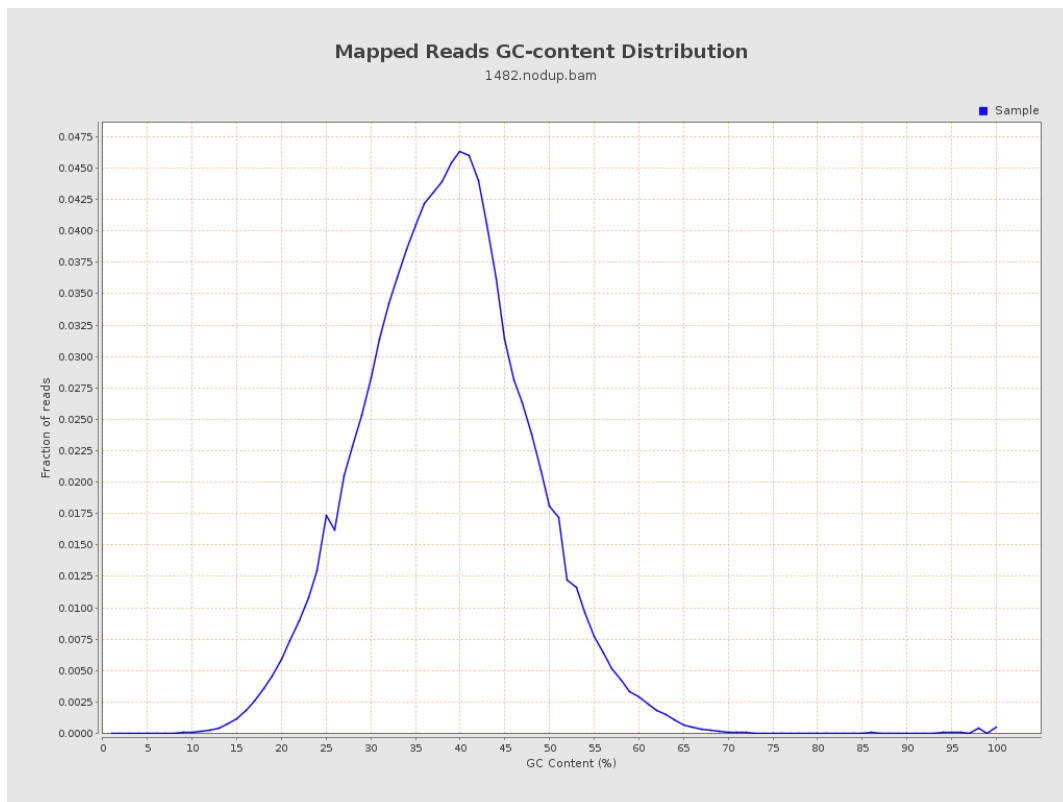
7. Results : Duplication Rate Histogram



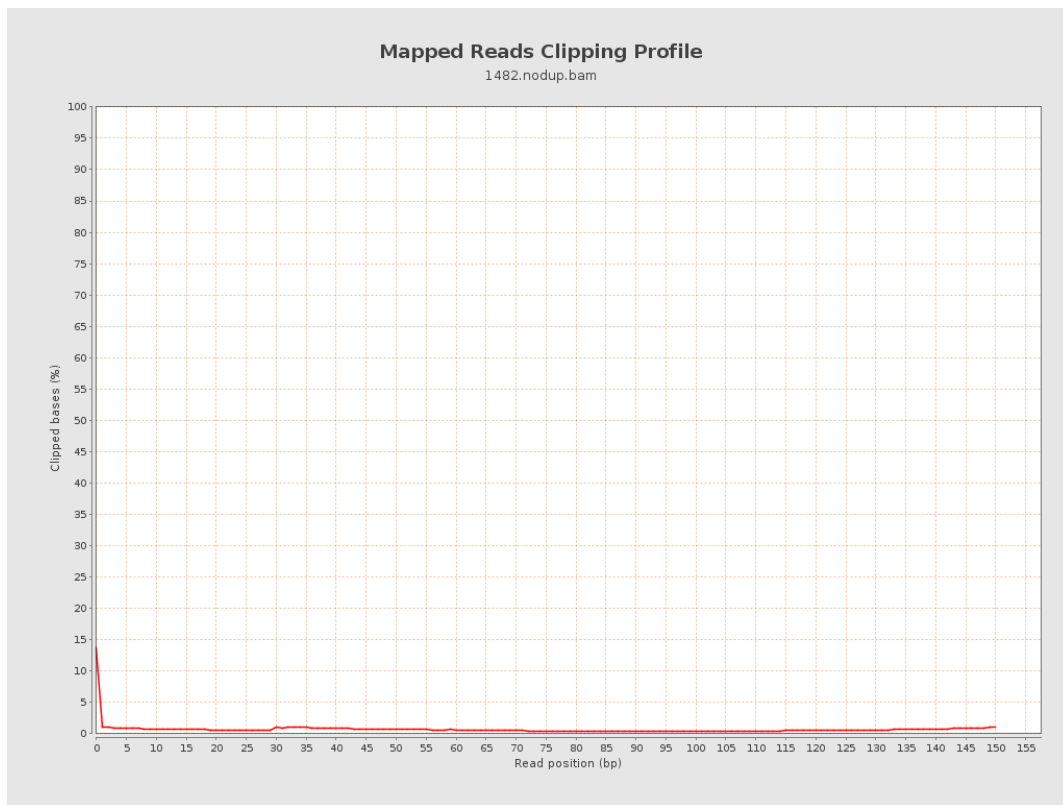
8. Results : Mapped Reads Nucleotide Content



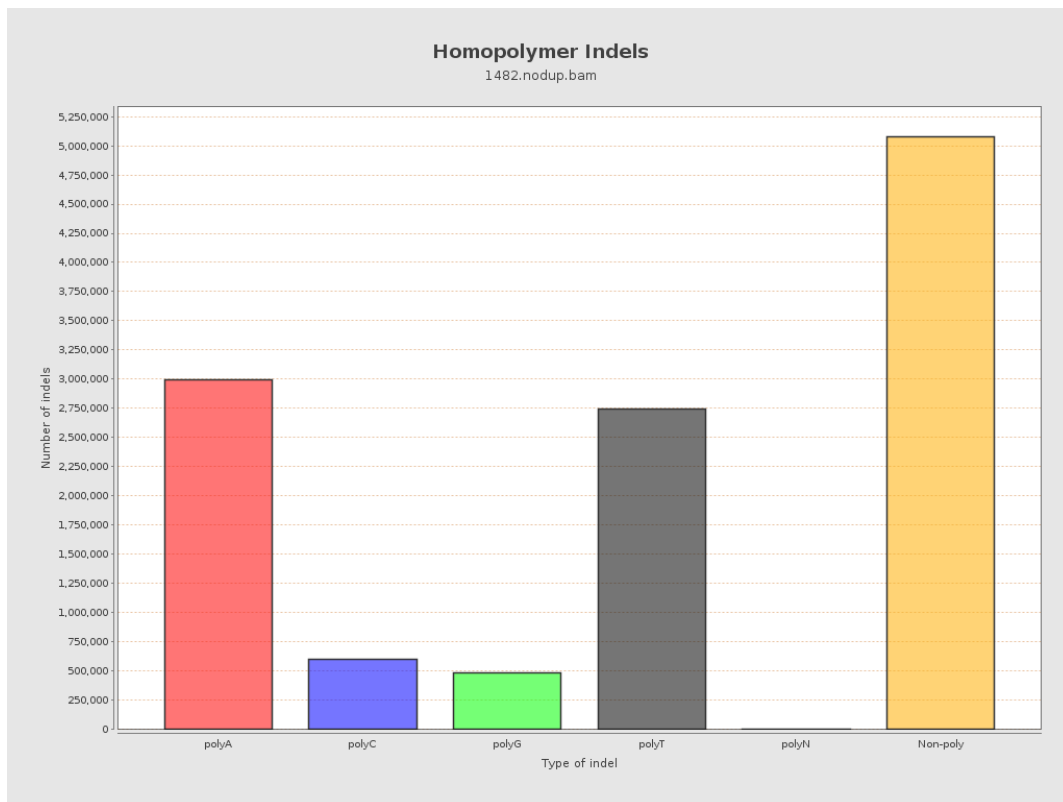
9. Results : Mapped Reads GC-content Distribution



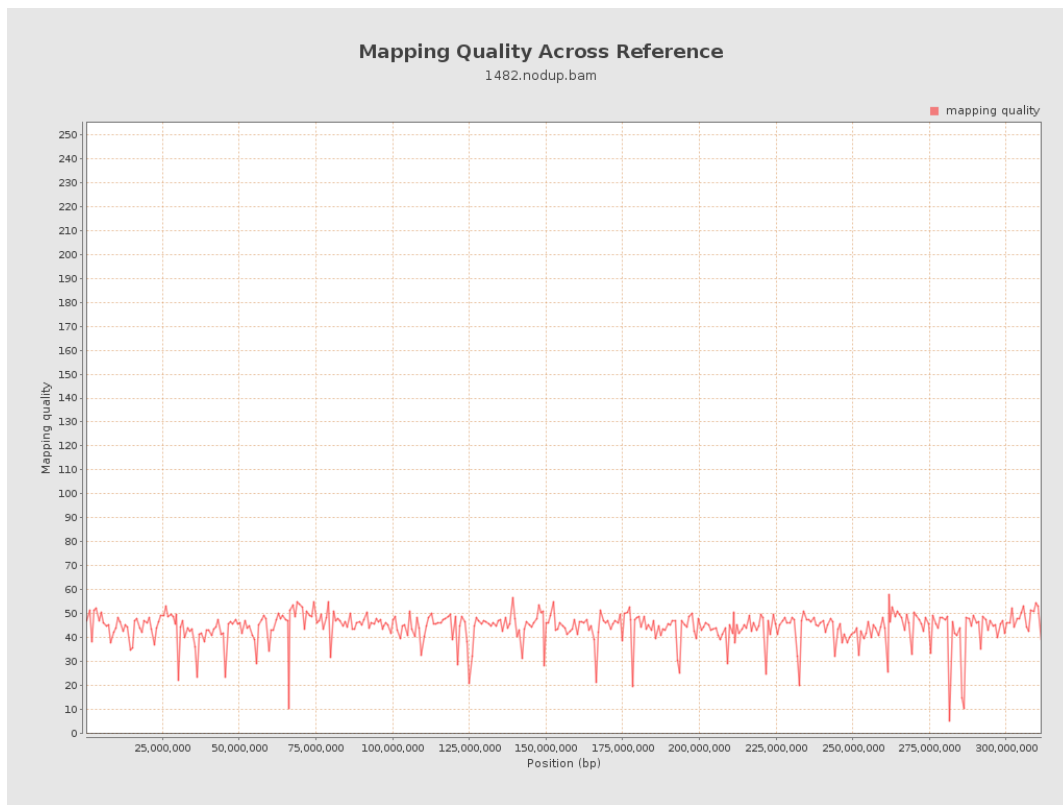
10. Results : Mapped Reads Clipping Profile



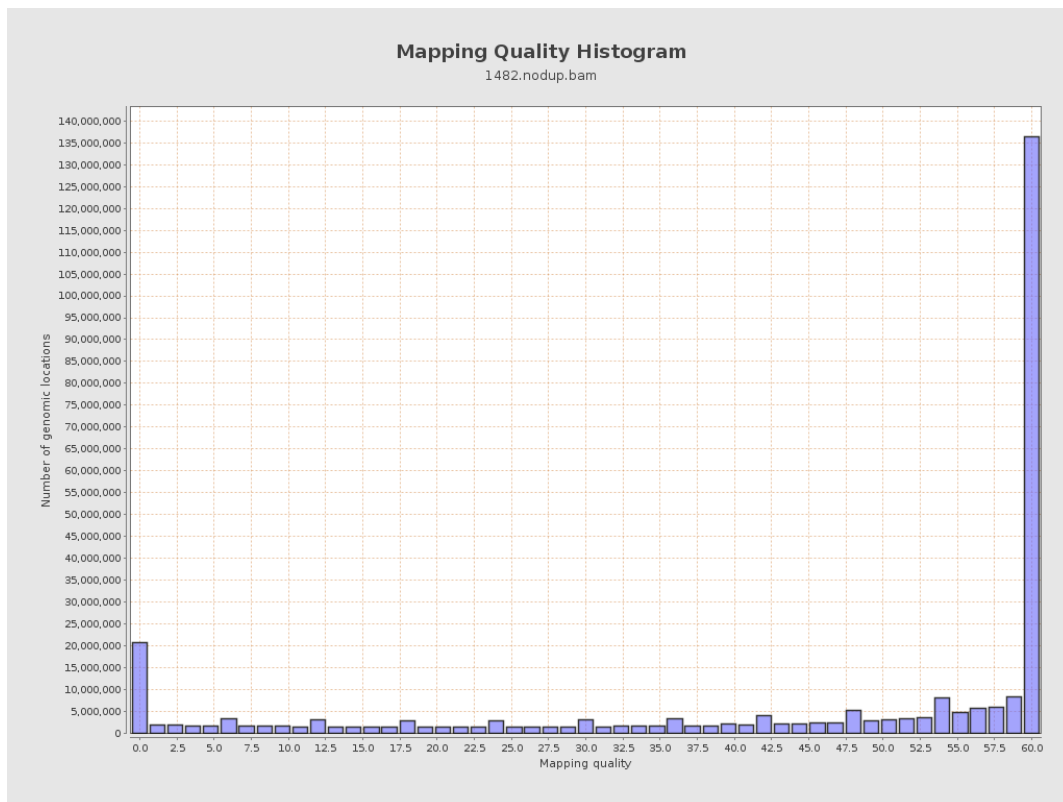
11. Results : Homopolymer Indels



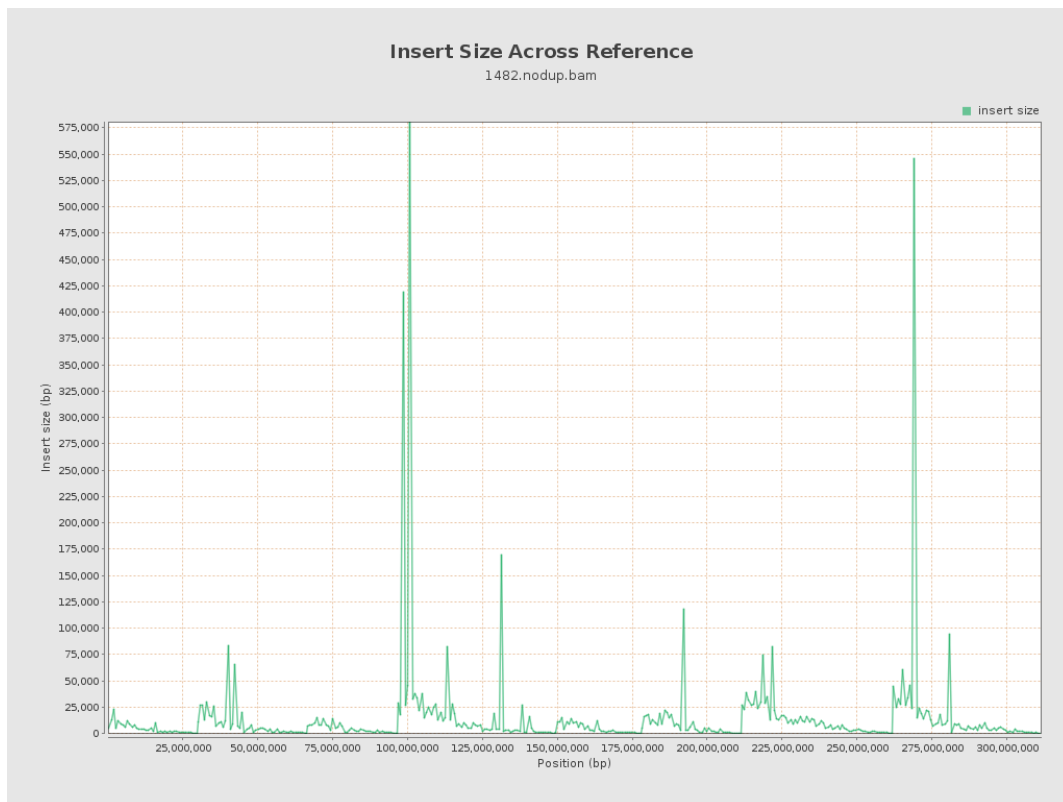
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

