

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:33:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/146
7
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

| | |
|---------------------------------------|---|
| BAM file: | /proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1467 .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_109/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_109_S199_L002 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_109/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_109_S199_L002 _R2_001.fastq.gz |
| Size of a homopolymer: | 3 |
| | |

| | |
|----------------------------|-------------------------------|
| Number of windows: | 400 |
| Analysis date: | Mon May 29 21:33:40 CEST 2023 |
| Draw chromosome limits: | no |
| Skip duplicate alignments: | no |

2. Summary

2.1. Globals

| | |
|------------------------------|---------------------|
| Reference size | 311,642,060 |
| Number of reads | 75,555,748 |
| Mapped reads | 68,847,751 / 91.12% |
| Unmapped reads | 6,707,997 / 8.88% |
| Mapped paired reads | 68,847,751 / 91.12% |
| Mapped reads, first in pair | 34,482,653 / 45.64% |
| Mapped reads, second in pair | 34,365,098 / 45.48% |
| Mapped reads, both in pair | 66,826,331 / 88.45% |
| Mapped reads, singletons | 2,021,420 / 2.68% |
| Read min/max/mean length | 30 / 151 / 148.09 |
| Duplicated reads (flagged) | 12,913,762 / 17.09% |
| Clipped reads | 16,093,506 / 21.3% |

2.2. ACGT Content

| | |
|--------------------------|------------------------|
| Number/percentage of A's | 2,932,011,393 / 30.97% |
| Number/percentage of C's | 1,801,513,394 / 19.03% |
| Number/percentage of T's | 2,933,654,686 / 30.99% |
| Number/percentage of G's | 1,799,897,832 / 19.01% |
| Number/percentage of N's | 39,441 / 0% |
| GC Percentage | 38.04% |

2.3. Coverage

| | |
|--------------------|----------|
| Mean | 30.4598 |
| Standard Deviation | 257.3336 |

2.4. Mapping Quality

| | |
|----------------------|-------|
| Mean Mapping Quality | 44.07 |
|----------------------|-------|

2.5. Insert size

| | |
|--------------------|-----------------|
| Mean | 254,205.88 |
| Standard Deviation | 2,417,531.12 |
| P25/Median/P75 | 317 / 412 / 531 |

2.6. Mismatches and indels

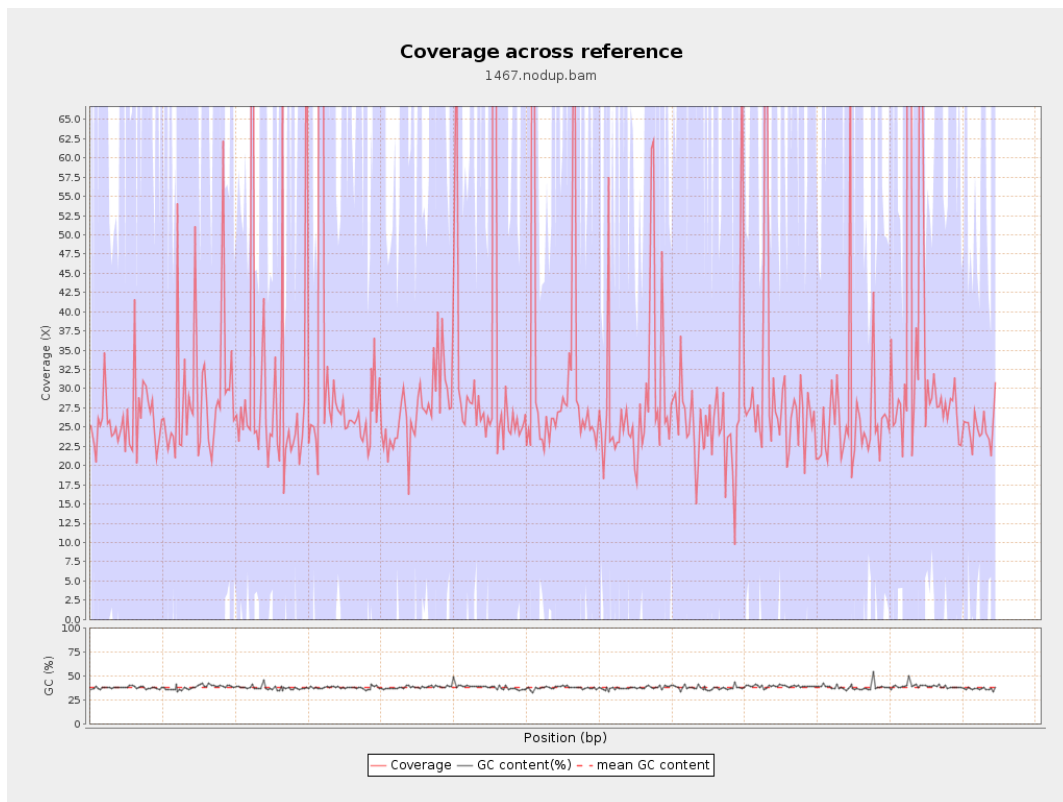
| | |
|--|-------------|
| General error rate | 2.38% |
| Mismatches | 205,698,622 |
| Insertions | 6,926,700 |
| Mapped reads with at least one insertion | 8.98% |
| Deletions | 6,772,329 |
| Mapped reads with at least one deletion | 8.71% |
| Homopolymer indels | 57.28% |

2.7. Chromosome stats

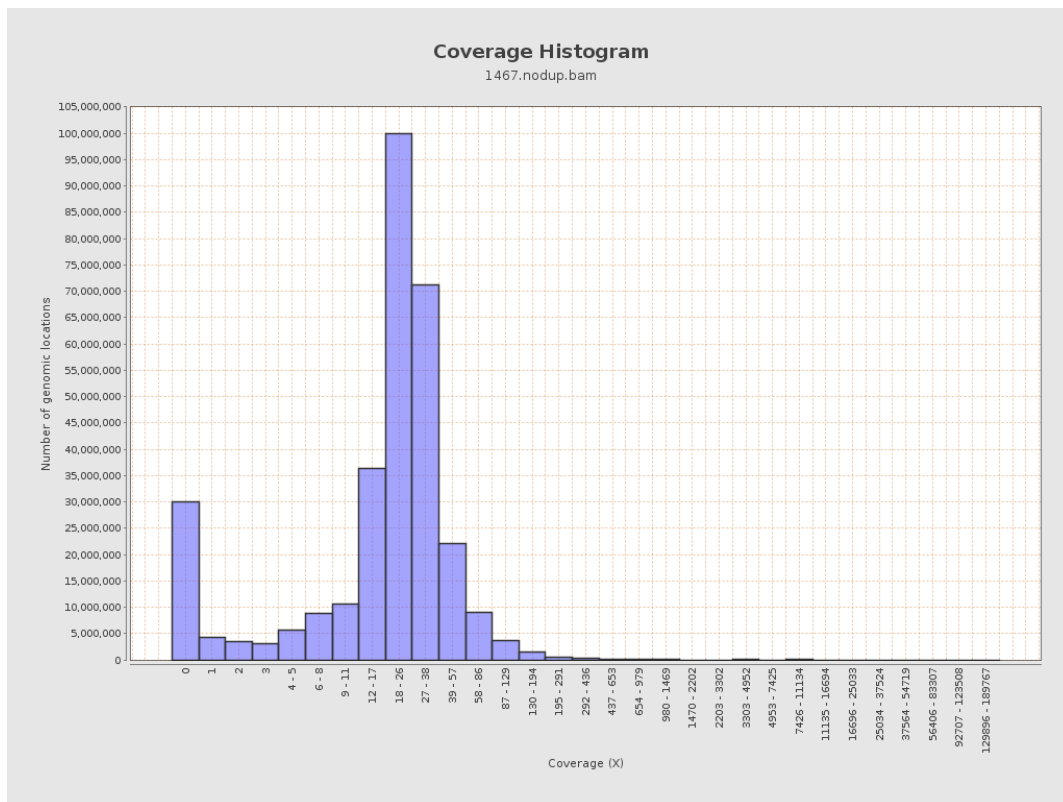
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|------------|----------|--------------|---------------|--------------------|
| LT669788.1 | 29724344 | 760157466 | 25.5736 | 100.9821 |

| | | | | |
|------------|----------|------------|---------|----------|
| LT669789.1 | 36598175 | 1134534772 | 30.9998 | 279.8638 |
| LT669790.1 | 30422129 | 1106038466 | 36.3564 | 370.129 |
| LT669791.1 | 52758100 | 1586011229 | 30.0619 | 274.4363 |
| LT669792.1 | 28376109 | 867083139 | 30.5568 | 268.5849 |
| LT669793.1 | 33388210 | 927881161 | 27.7907 | 167.4511 |
| LT669794.1 | 50579949 | 1436949396 | 28.4095 | 219.9632 |
| LT669795.1 | 49795044 | 1673901559 | 33.6158 | 279.6136 |

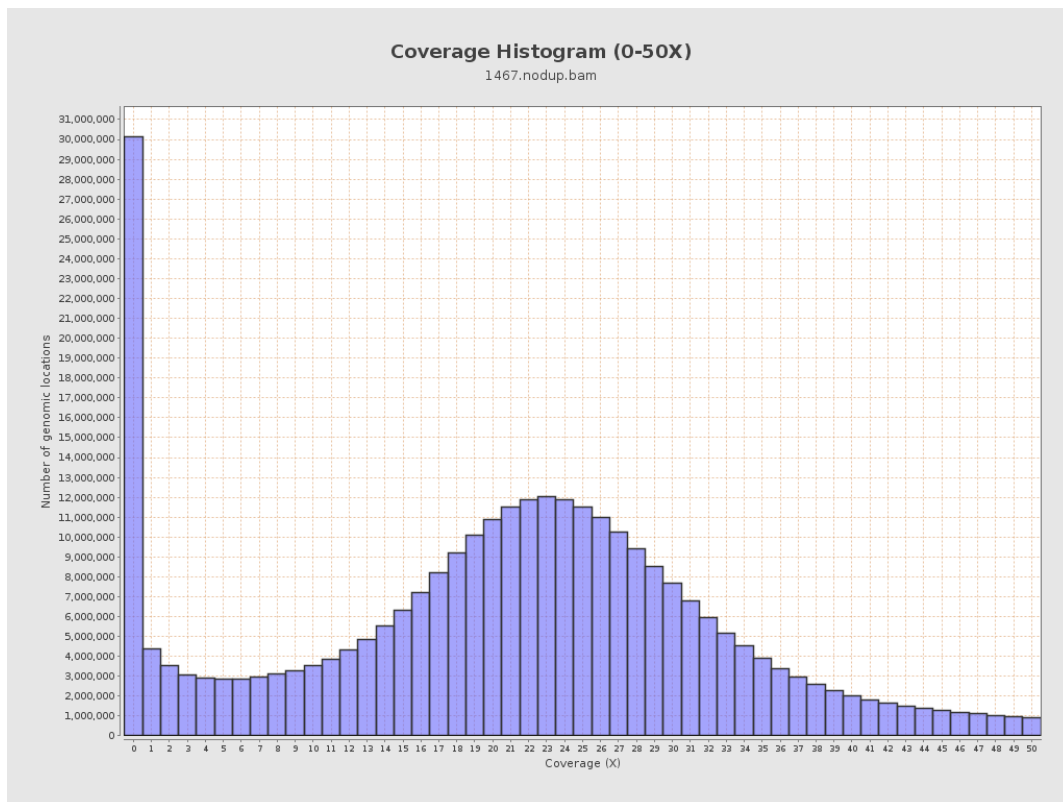
3. Results : Coverage across reference



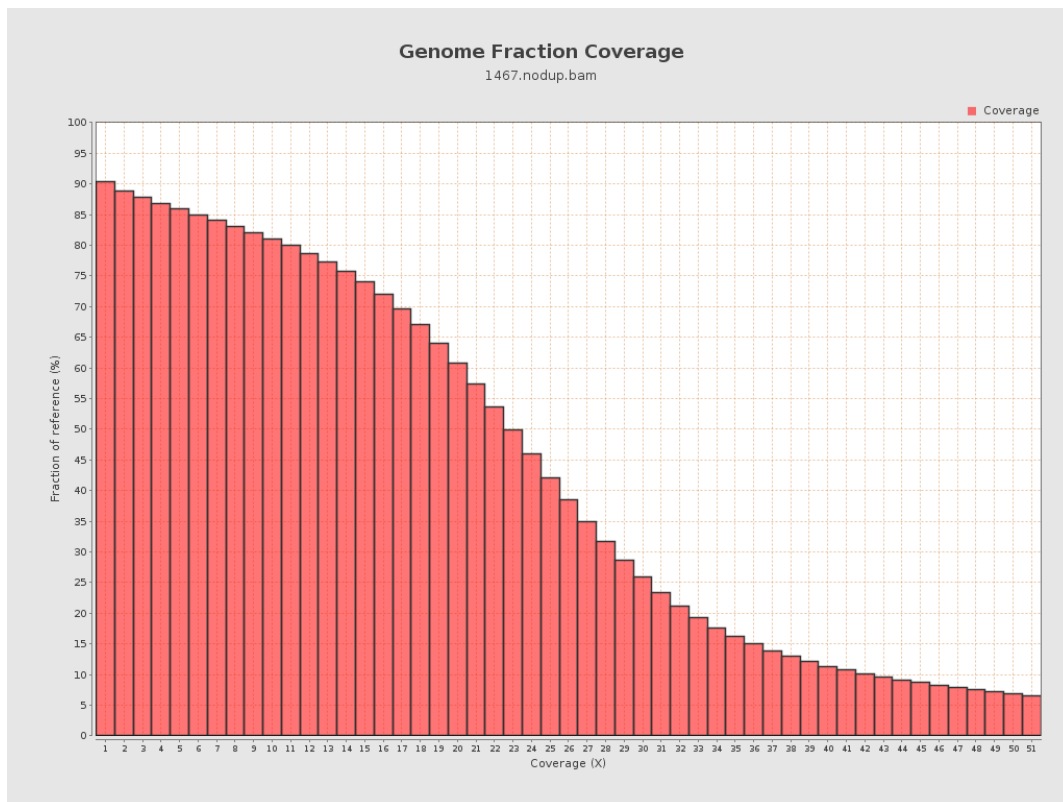
4. Results : Coverage Histogram



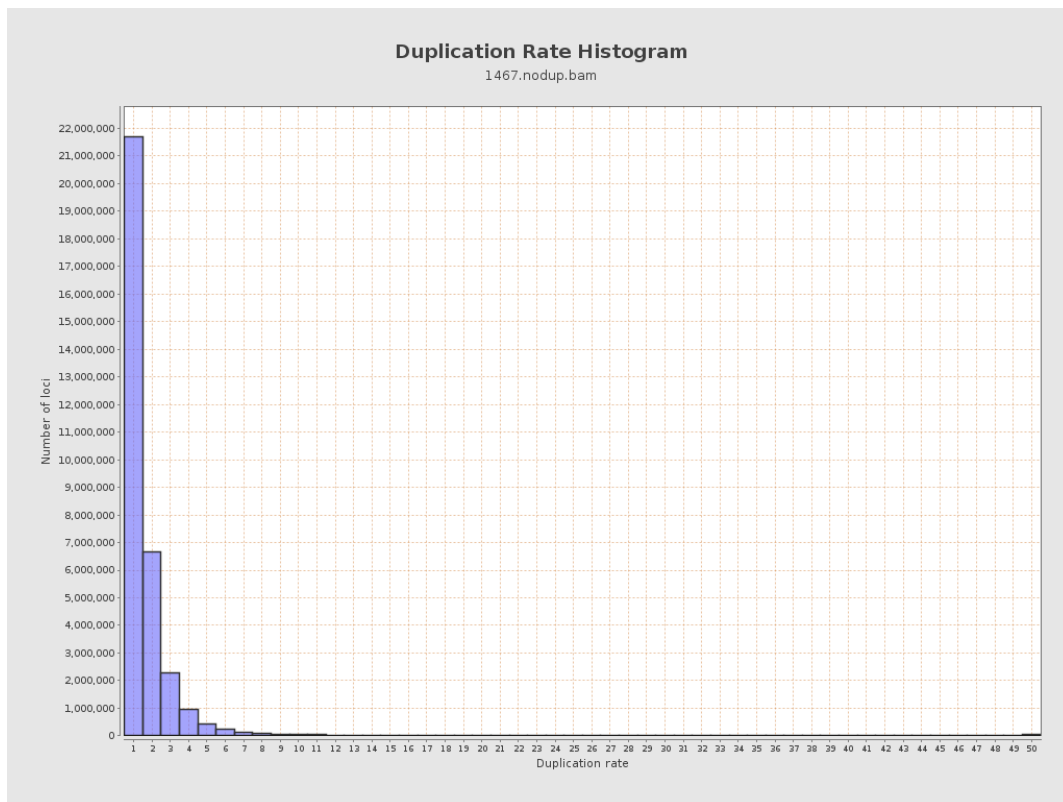
5. Results : Coverage Histogram (0-50X)



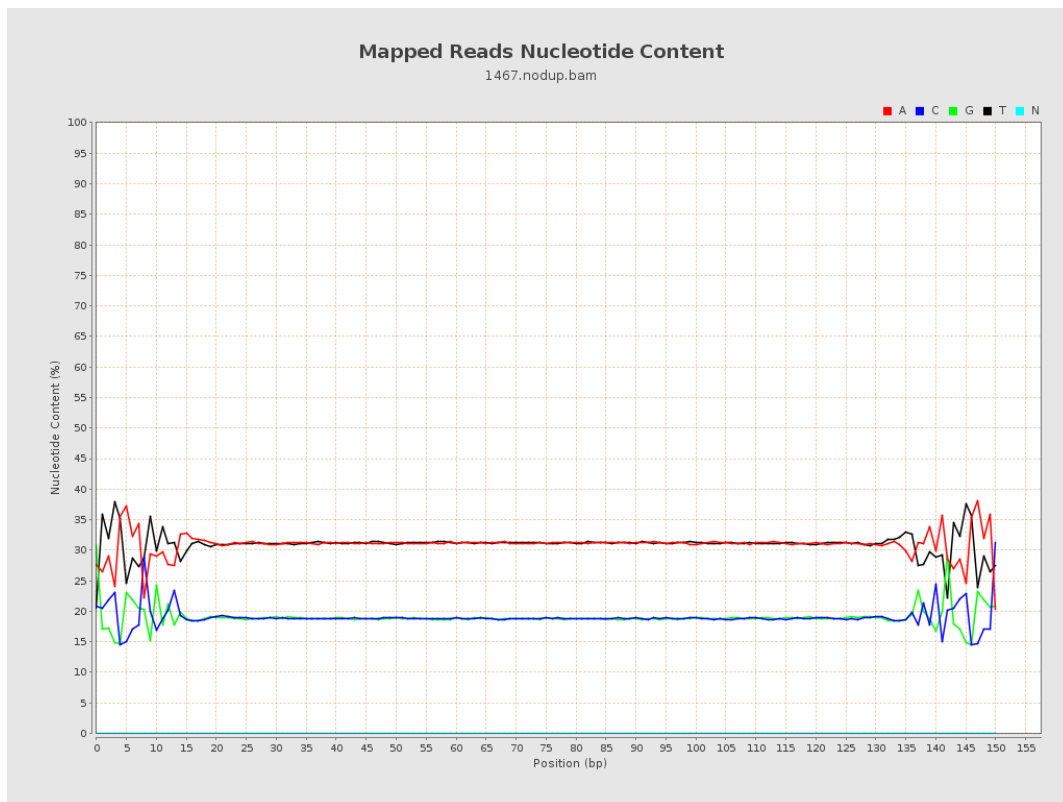
6. Results : Genome Fraction Coverage



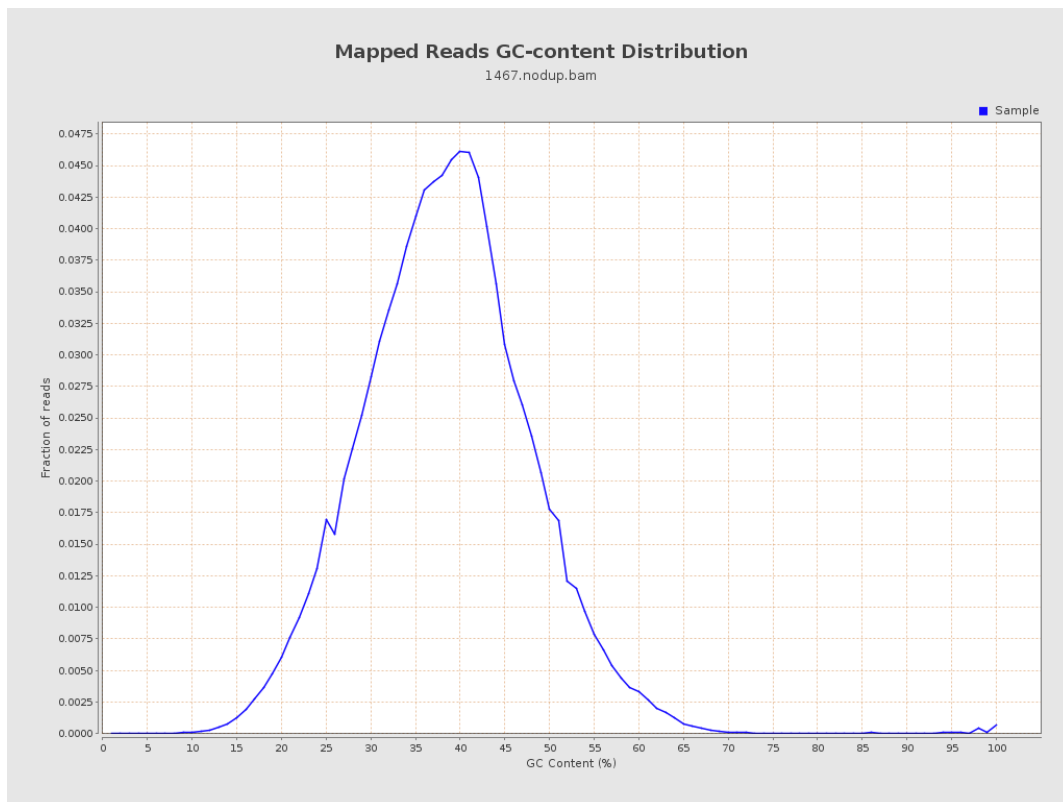
7. Results : Duplication Rate Histogram



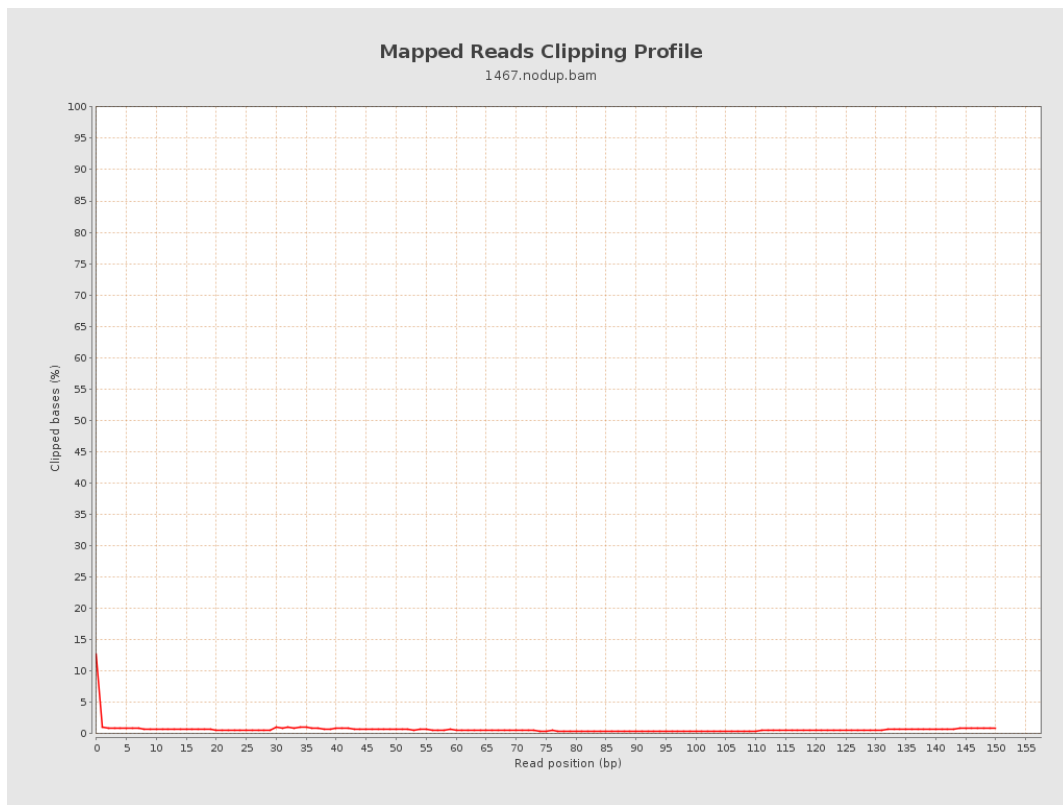
8. Results : Mapped Reads Nucleotide Content



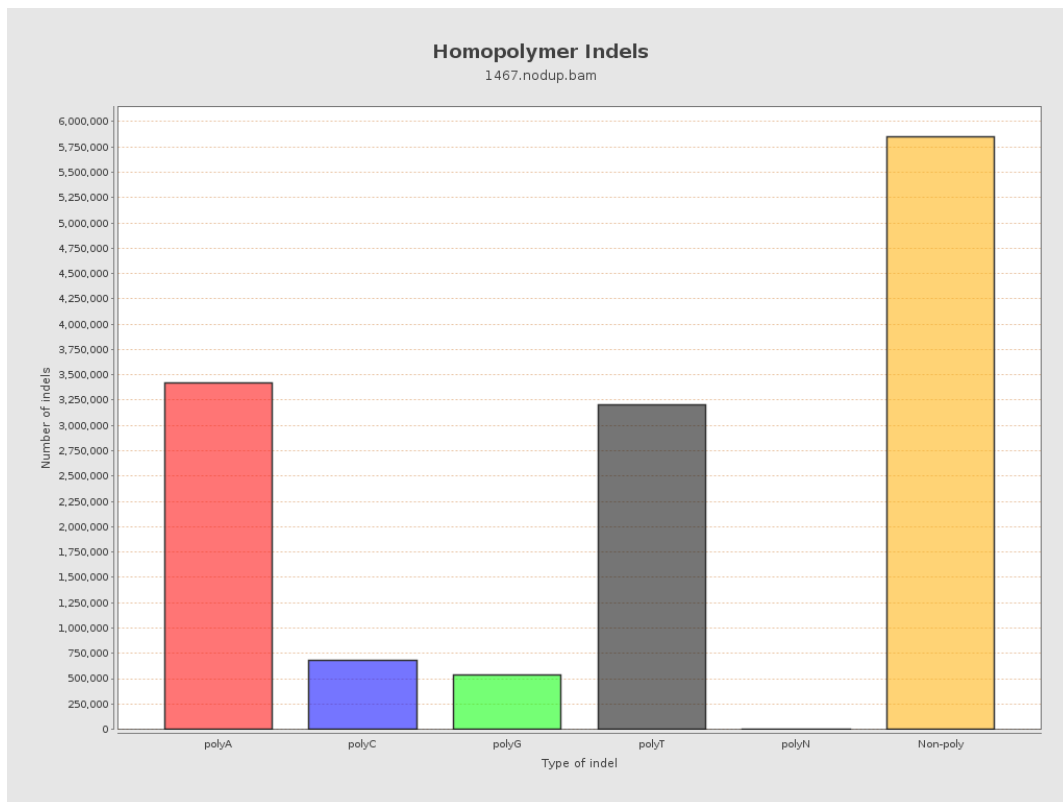
9. Results : Mapped Reads GC-content Distribution



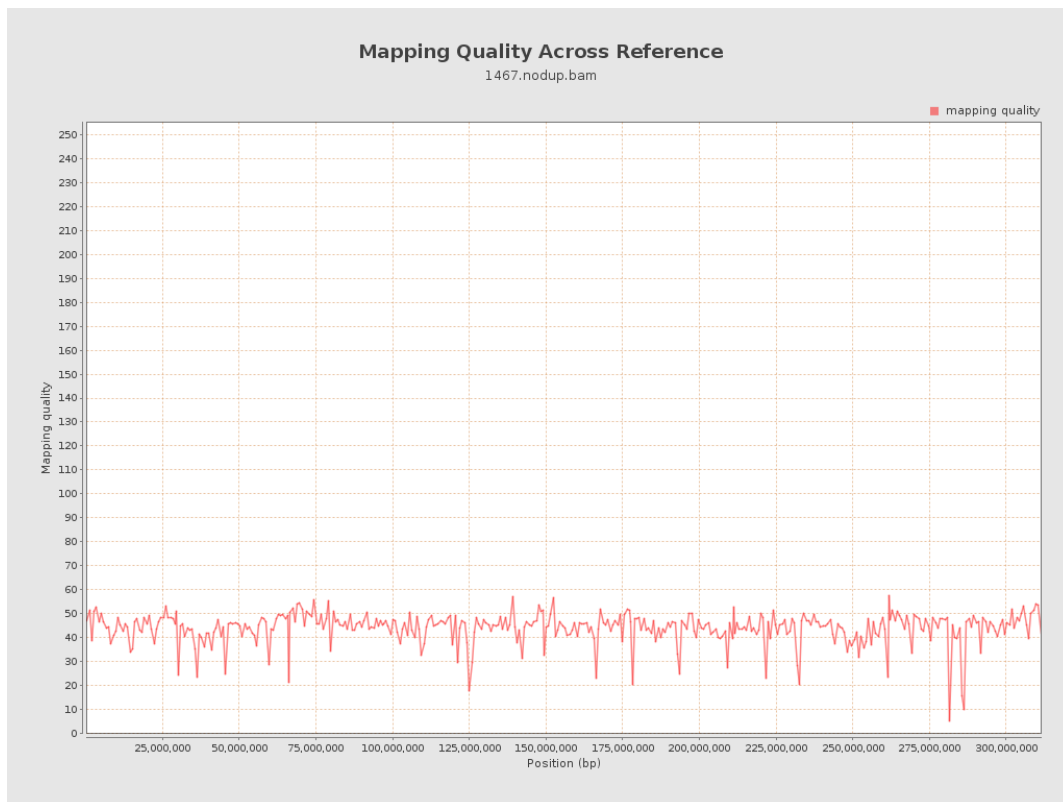
10. Results : Mapped Reads Clipping Profile



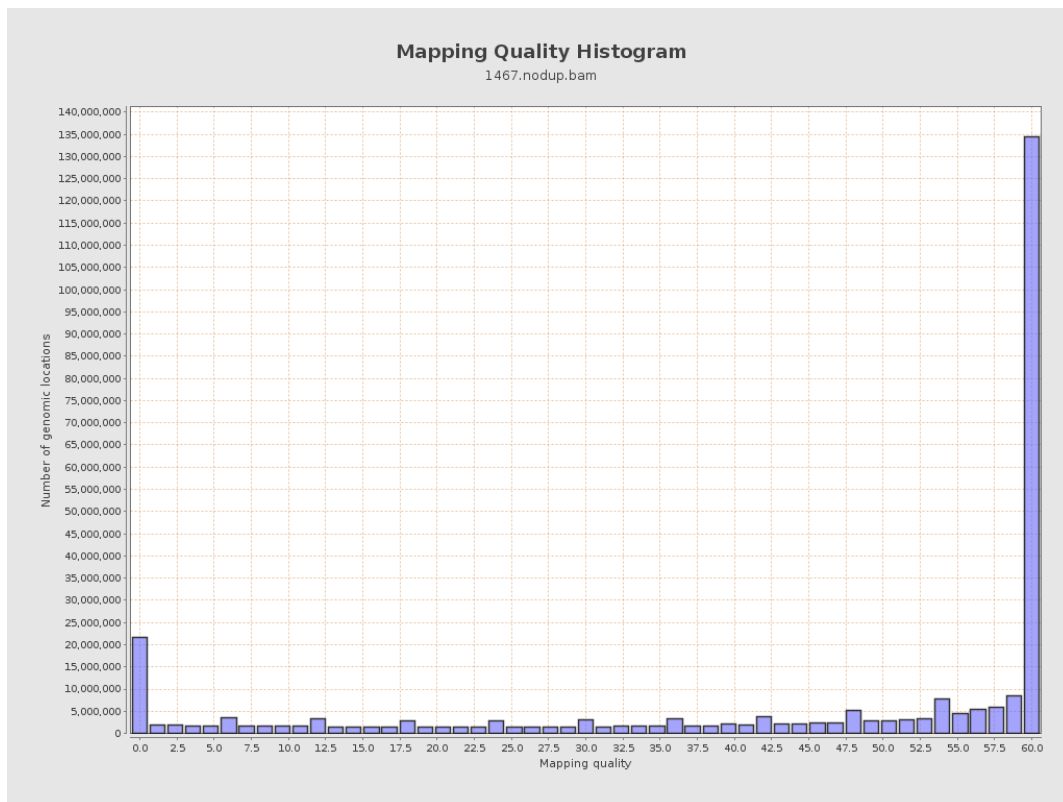
11. Results : Homopolymer Indels



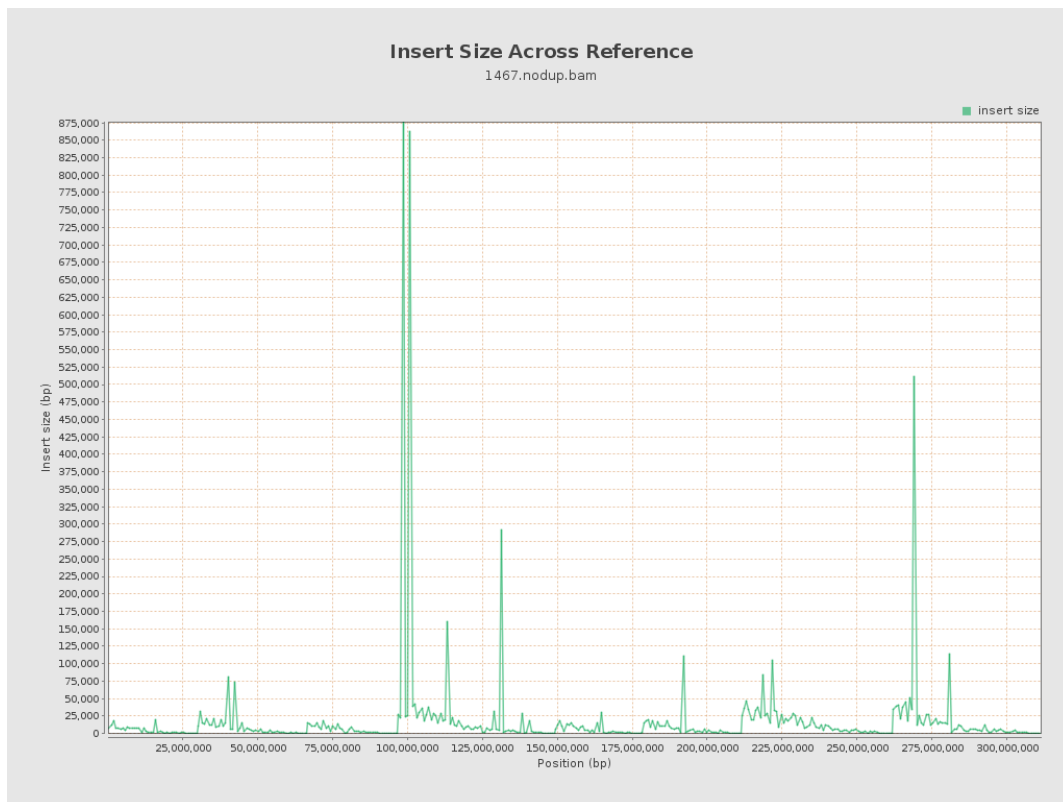
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

