# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:36:11*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/968.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| BAM file: | /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/968.nodup.bam |
| Program: | bwa (0.7.17-r1188) |
| Analyze overlapping paired-end reads: | no |
| Command line: | bwa mem -M -t 8 -R @RG\tID:$unit\tPL:Illumina\tLB:LibA\tSM:$sample /proj/uppstore2018210/Aalpina/data/reference/GCA_900128785.1_MPIPZ.v5_genomic.fa /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_108/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_108_S198_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_108/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_108_S198_L002_R2_001.fastq.gz |
| Size of a homopolymer: | 3 |
| Number of windows: | 400 |

| | |
|---|---|
| Analysis date: | Mon May 29 21:36:11 CEST 2023 |
| Draw chromosome limits: | no |
| Skip duplicate alignments: | no |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 311,642,060 |
| Number of reads | 82,012,290 |
| Mapped reads | 74,506,172 / 90.85% |
| Unmapped reads | 7,506,118 / 9.15% |
| Mapped paired reads | 74,506,172 / 90.85% |
| Mapped reads, first in pair | 37,323,409 / 45.51% |
| Mapped reads,  second in pair | 37,182,763 / 45.34% |
| Mapped reads, both in pair | 72,076,776 / 87.89% |
| Mapped reads, singletons | 2,429,396 / 2.96% |
| Read min/max/mean length | 30 / 151 / 148.14 |
| Duplicated reads (flagged) | 14,727,121 / 17.96% |
| Clipped reads | 17,387,001 / 21.2% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 3,171,637,521 / 31.02% |
| Number/percentage of C's | 1,938,707,936 / 18.96% |
| Number/percentage of T's | 3,176,938,182 / 31.08% |
| Number/percentage of G's | 1,935,622,018 / 18.93% |
| Number/percentage of N's | 42,690 / 0% |
| GC Percentage | 37.9% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 32.8882 |
| Standard Deviation | 305.0447 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.77 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 258,462.59 |
| Standard Deviation | 2,468,982.59 |
| P25/Median/P75 | 319 / 419 / 553 |

## 2.6. Mismatches and indels

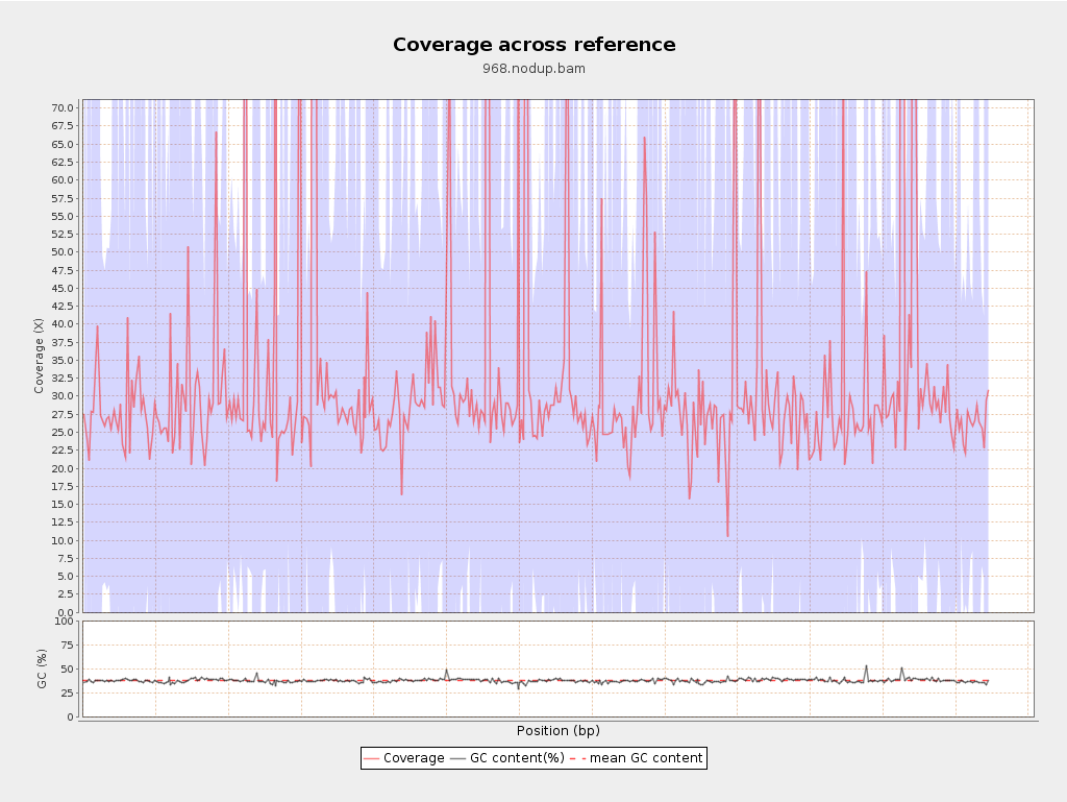
| | |
|---|---|
| General error rate | 2.31% |
| Mismatches | 215,089,914 |
| Insertions | 7,511,484 |
| Mapped reads with at least one insertion | 8.96% |
| Deletions | 7,091,985 |
| Mapped reads with at least one deletion | 8.42% |
| Homopolymer indels | 57.69% |

## 2.7. Chromosome stats

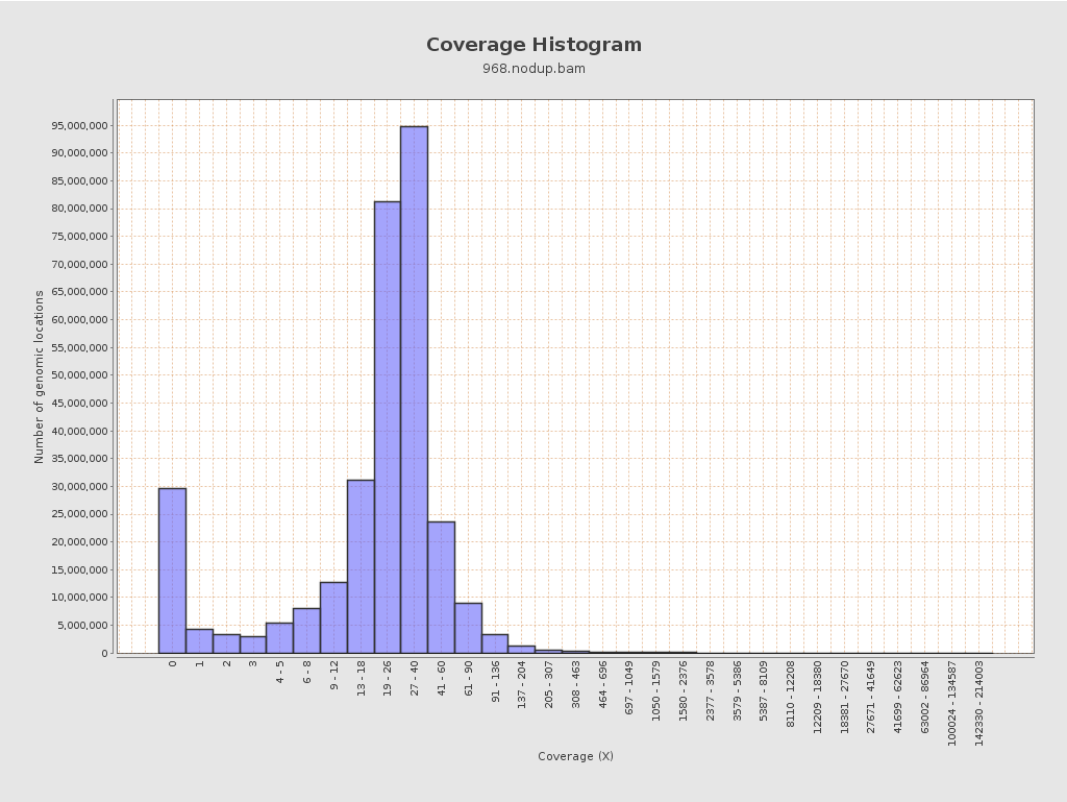
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| LT669788.1 | 29724344 | 818139659 | 27.5242 | 137.6756 |

| | | | | |
|---|---|---|---|---|
| LT669789.1 | 36598175 | 1211775241 | 33.1103 | 334.5033 |
| LT669790.1 | 30422129 | 1244632671 | 40.9121 | 458.5081 |
| LT669791.1 | 52758100 | 1714976062 | 32.5064 | 344.1801 |
| LT669792.1 | 28376109 | 944131327 | 33.2721 | 294.3738 |
| LT669793.1 | 33388210 | 978991479 | 29.3215 | 161.8341 |
| LT669794.1 | 50579949 | 1515625995 | 29.965 | 233.0729 |
| LT669795.1 | 49795044 | 1821058704 | 36.5711 | 335.6448 |

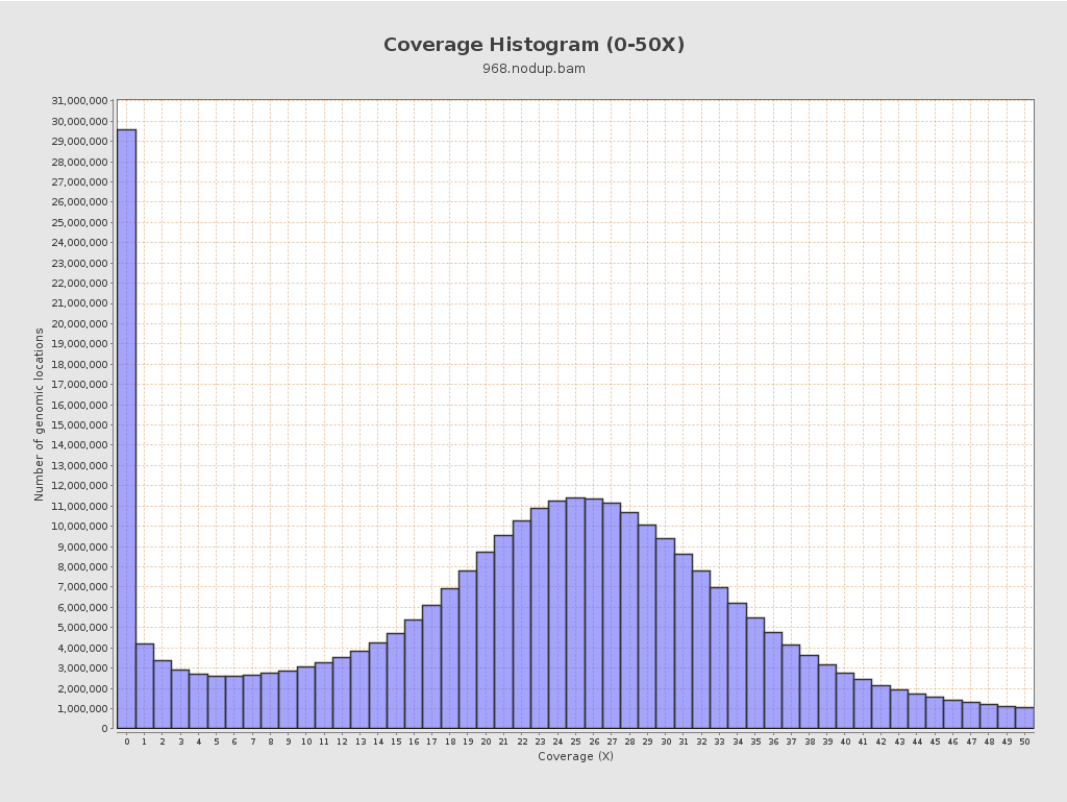
# 3. Results : Coverage across reference



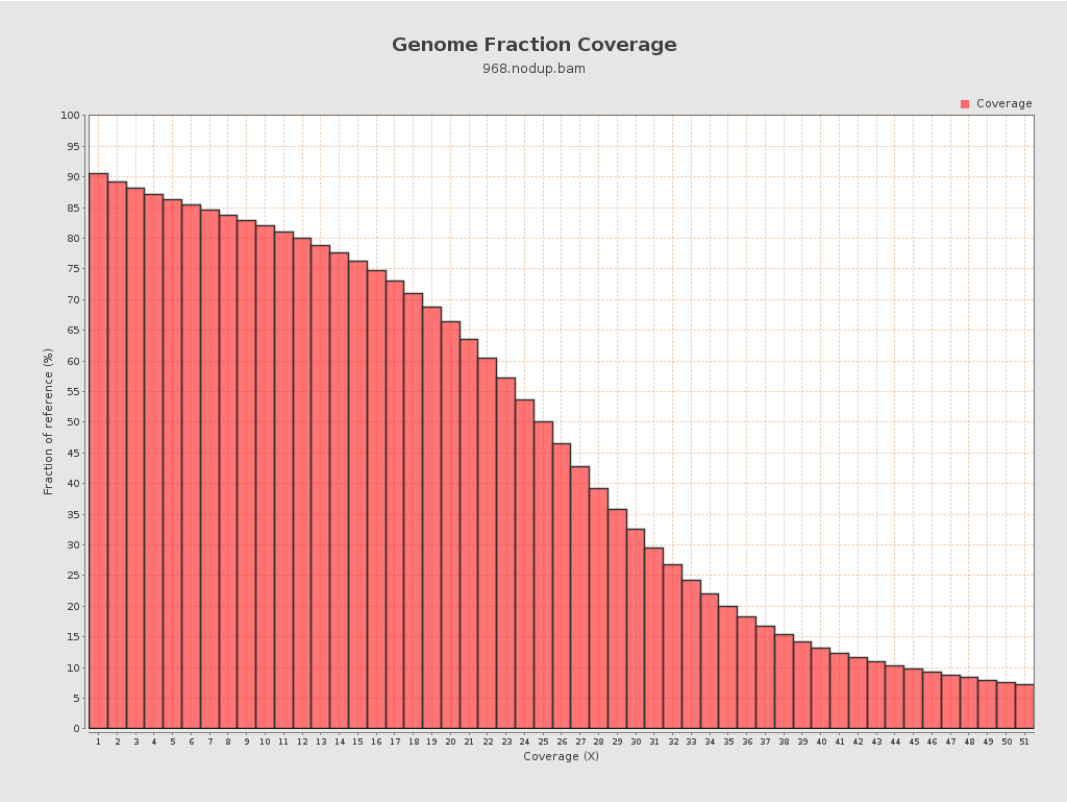
# 4. Results : Coverage Histogram



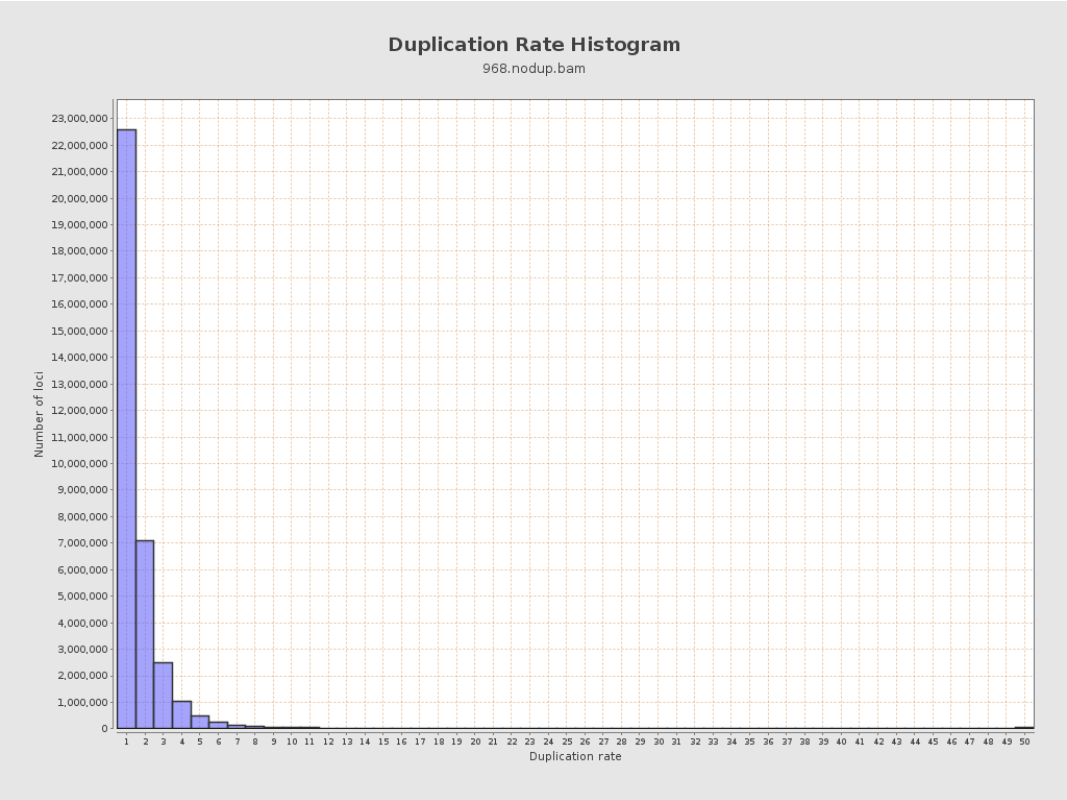
# 5. Results : Coverage Histogram (0-50X)



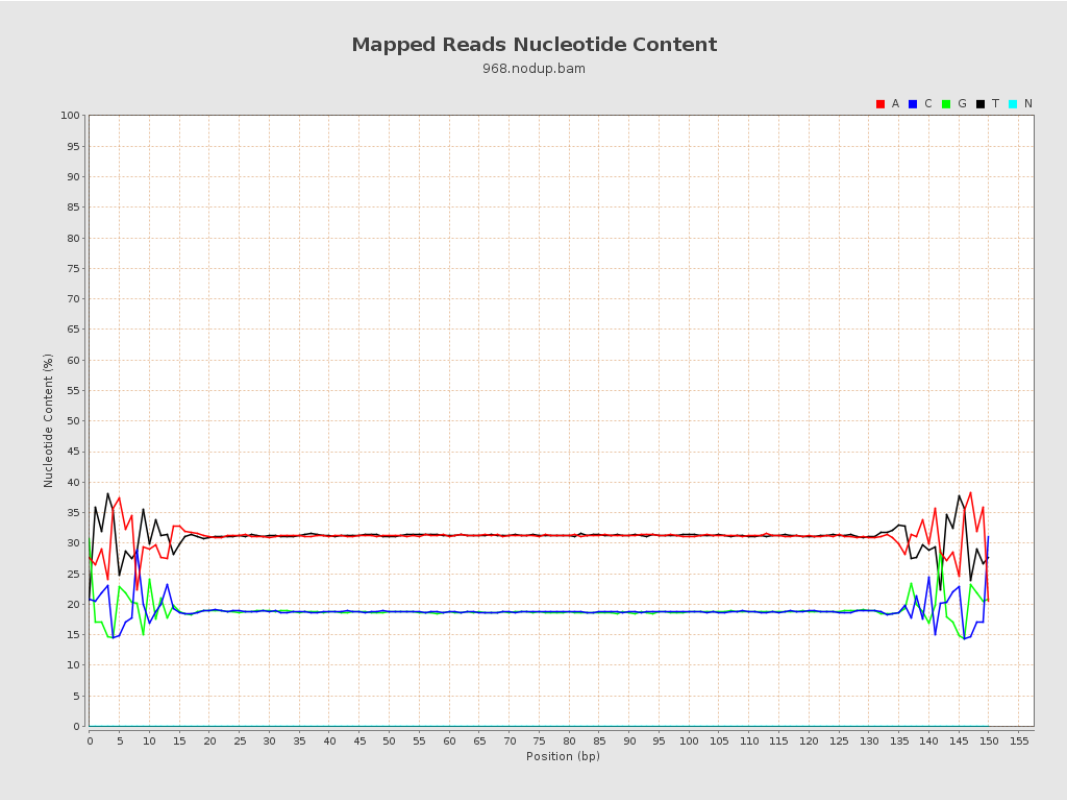
# 6. Results : Genome Fraction Coverage



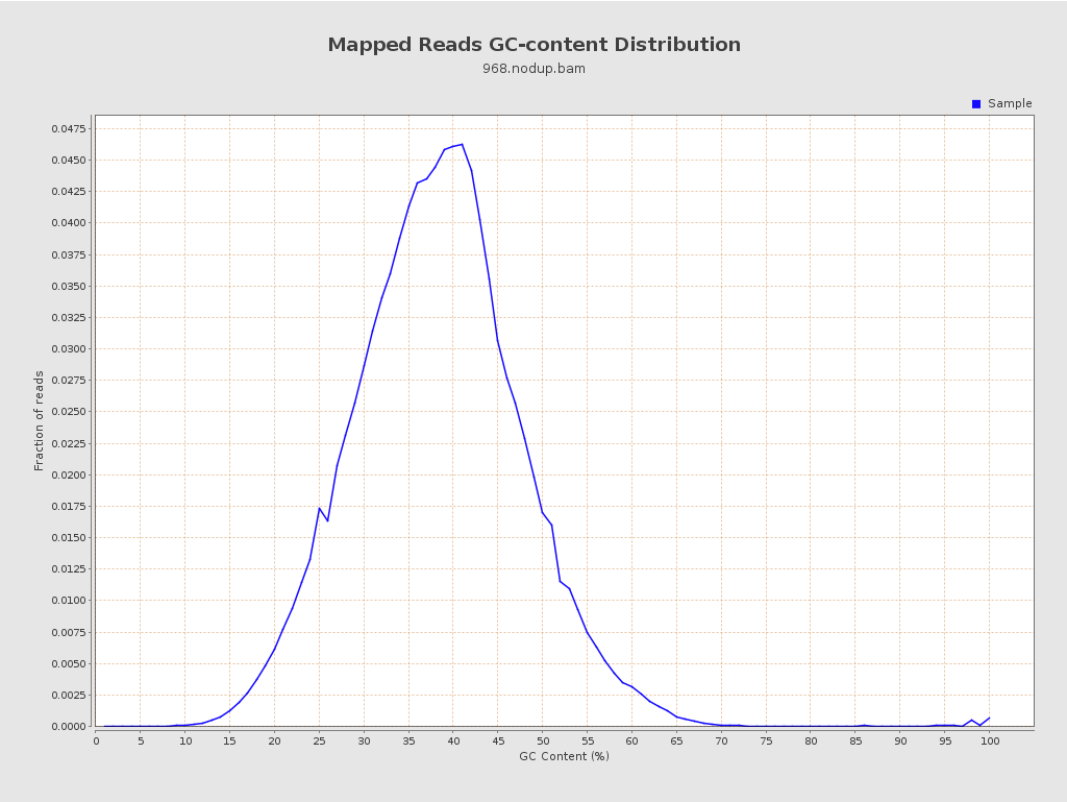
# 7. Results : Duplication Rate Histogram



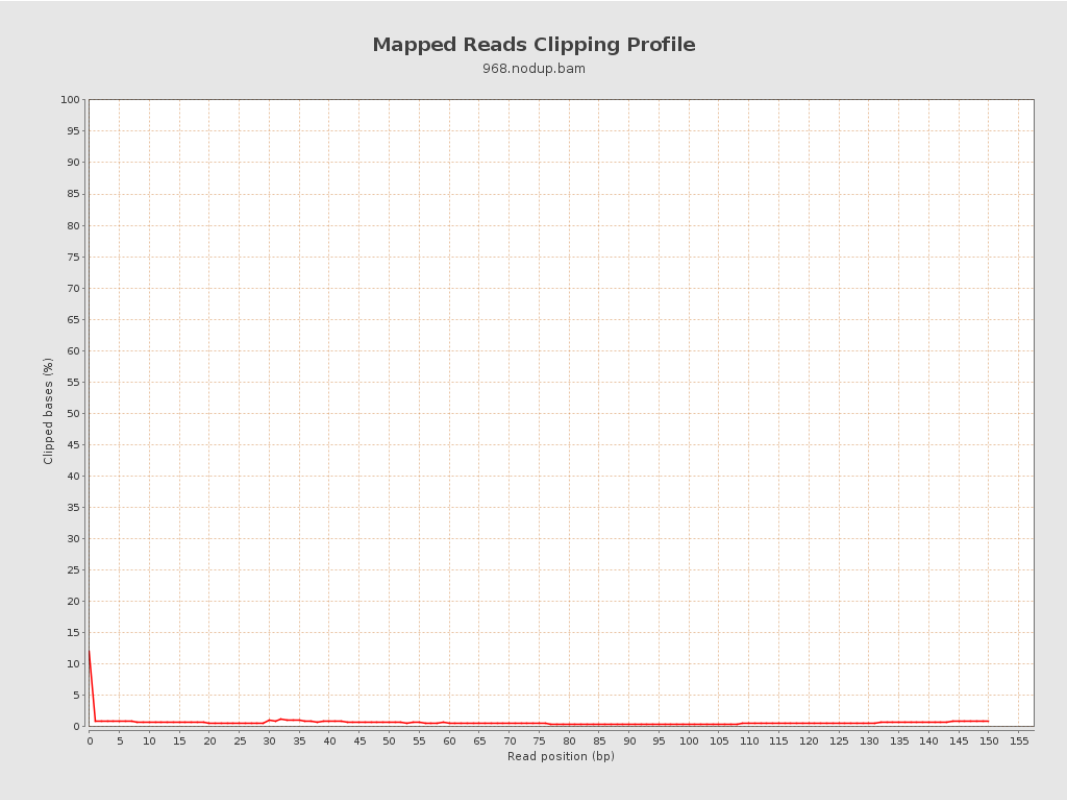
# 8. Results : Mapped Reads Nucleotide Content



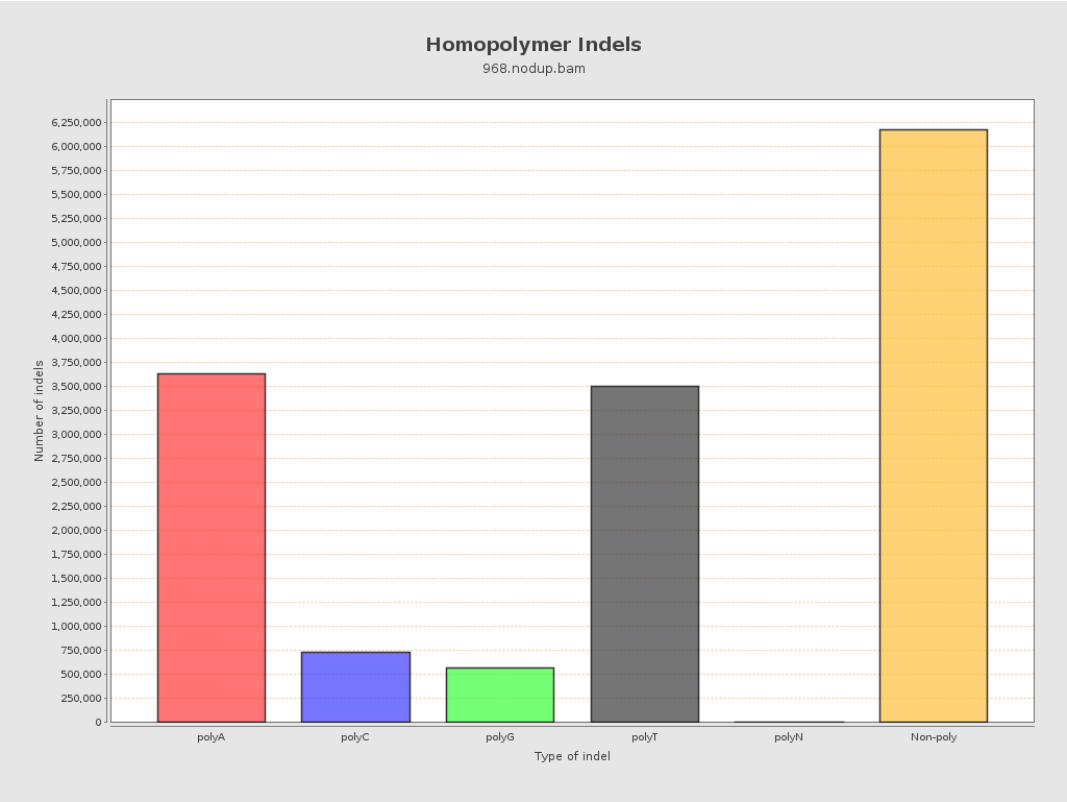
# 9. Results : Mapped Reads GC-content Distribution



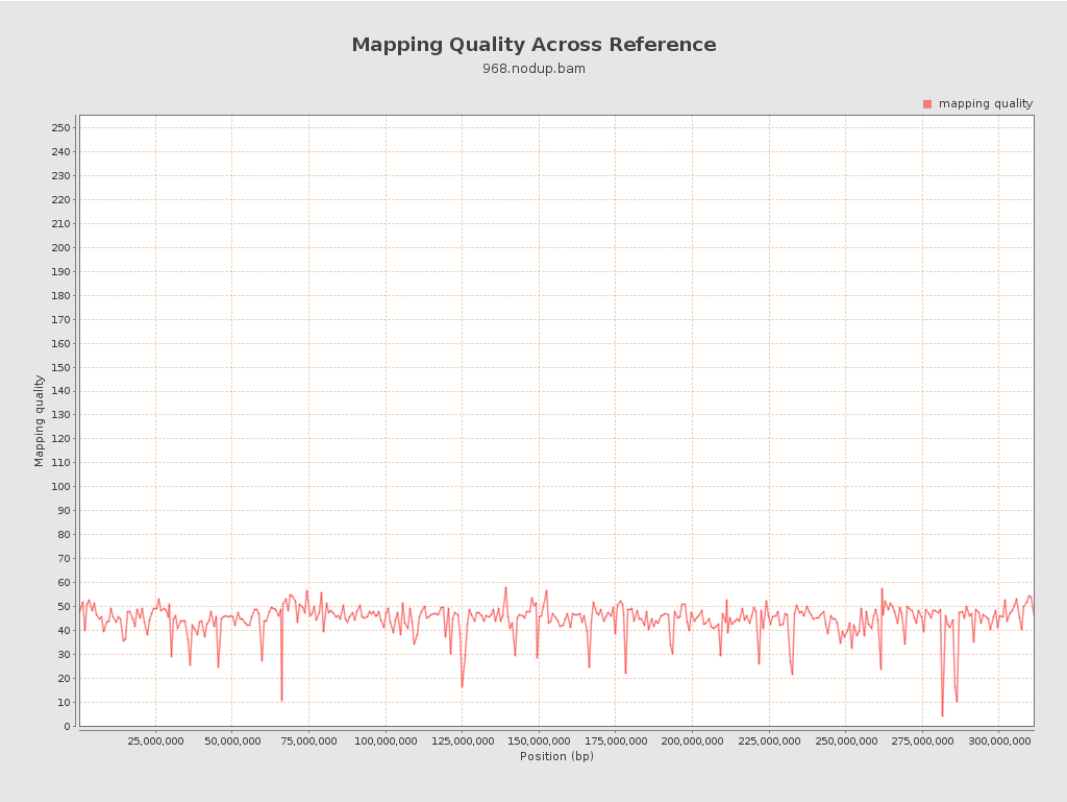
# 10. Results : Mapped Reads Clipping Profile



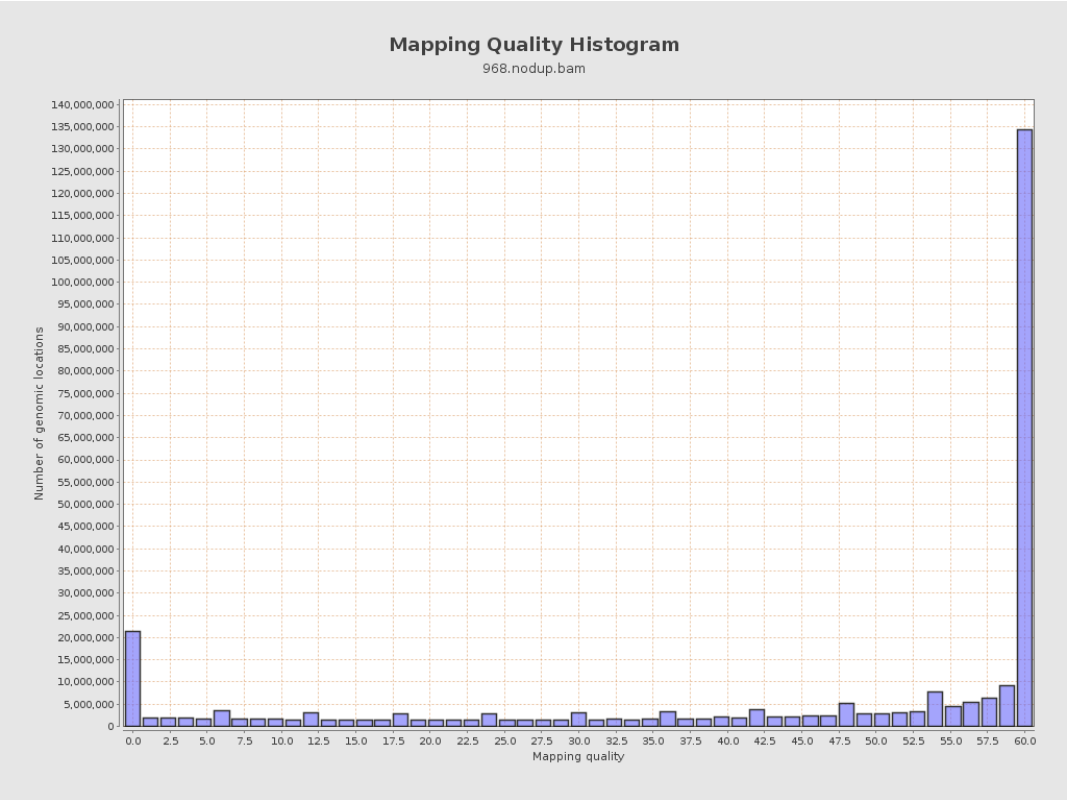
# 11. Results : Homopolymer Indels



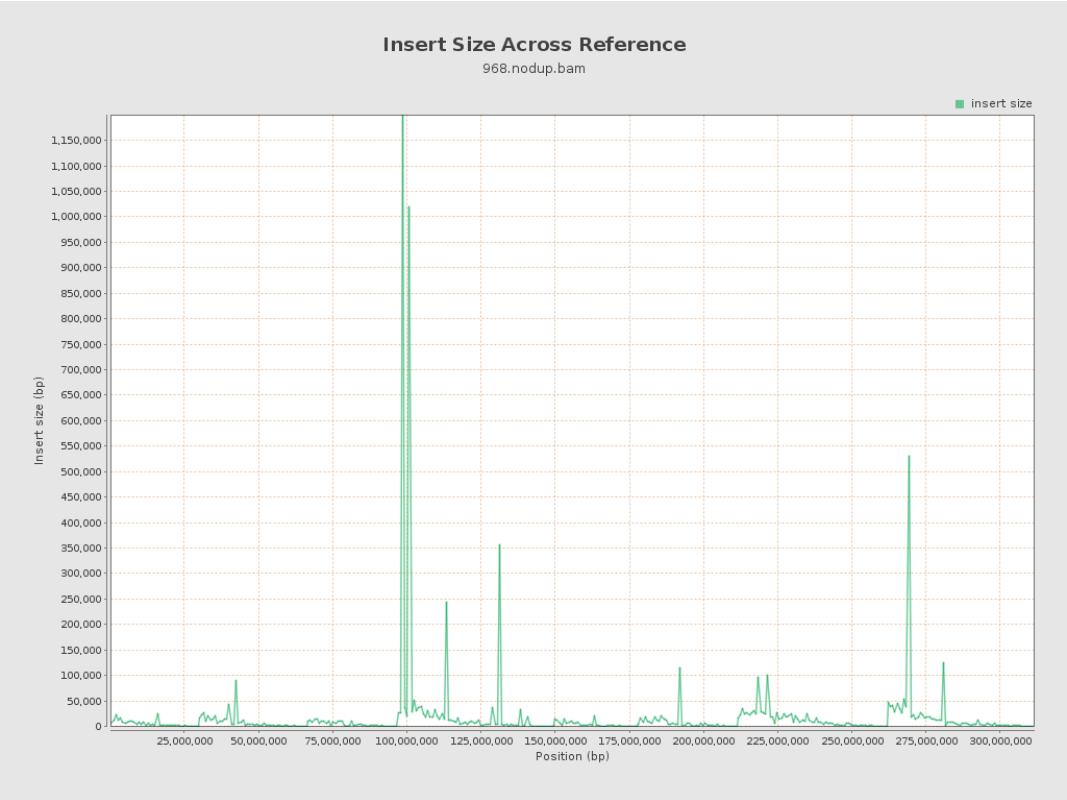
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram