

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2025/01/19 12:36:19*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR618620.sorted.bam -c -nw 400 -hm 3
```

## 1.2. Alignment

|                                       |                                                                                                                                                                                                                   |
|---------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Command line:                         | /home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR618620 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618620_1.fastq.gz SRR618620_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                               |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                |
| Analysis date:                        | Sun Jan 19 12:36:16 CST 2025                                                                                                                                                                                      |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                 |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                |
| Number of windows:                    | 400                                                                                                                                                                                                               |
| BAM file:                             | SRR618620.sorted.bam                                                                                                                                                                                              |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 44,456,872          |
| Mapped reads                 | 40,661,702 / 91.46% |
| Unmapped reads               | 3,795,170 / 8.54%   |
| Mapped paired reads          | 40,661,702 / 91.46% |
| Mapped reads, first in pair  | 21,203,548 / 47.69% |
| Mapped reads, second in pair | 19,458,154 / 43.77% |
| Mapped reads, both in pair   | 38,080,734 / 85.66% |
| Mapped reads, singletons     | 2,580,968 / 5.81%   |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 197,596 / 0.44%     |
| Read min/max/mean length     | 30 / 100 / 100.18   |
| Duplicated reads (estimated) | 18,944,226 / 42.61% |
| Duplication rate             | 34.65%              |
| Clipped reads                | 10,602,255 / 23.85% |

### 2.2. ACGT Content

|                          |                        |
|--------------------------|------------------------|
| Number/percentage of A's | 1,057,943,807 / 28%    |
| Number/percentage of C's | 793,356,534 / 21%      |
| Number/percentage of T's | 1,082,945,364 / 28.66% |
| Number/percentage of G's | 841,962,593 / 22.28%   |
| Number/percentage of N's | 2,072,059 / 0.05%      |
|                          |                        |

|               |        |
|---------------|--------|
| GC Percentage | 43.28% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 1.2214 |
| Standard Deviation | 5.8749 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 52.84 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 163,631.4       |
| Standard Deviation | 4,038,615.35    |
| P25/Median/P75     | 199 / 232 / 276 |

## 2.6. Mismatches and indels

|                                          |            |
|------------------------------------------|------------|
| General error rate                       | 1.49%      |
| Mismatches                               | 55,193,166 |
| Insertions                               | 728,075    |
| Mapped reads with at least one insertion | 1.76%      |
| Deletions                                | 1,983,273  |
| Mapped reads with at least one deletion  | 4.75%      |
| Homopolymer indels                       | 52.48%     |

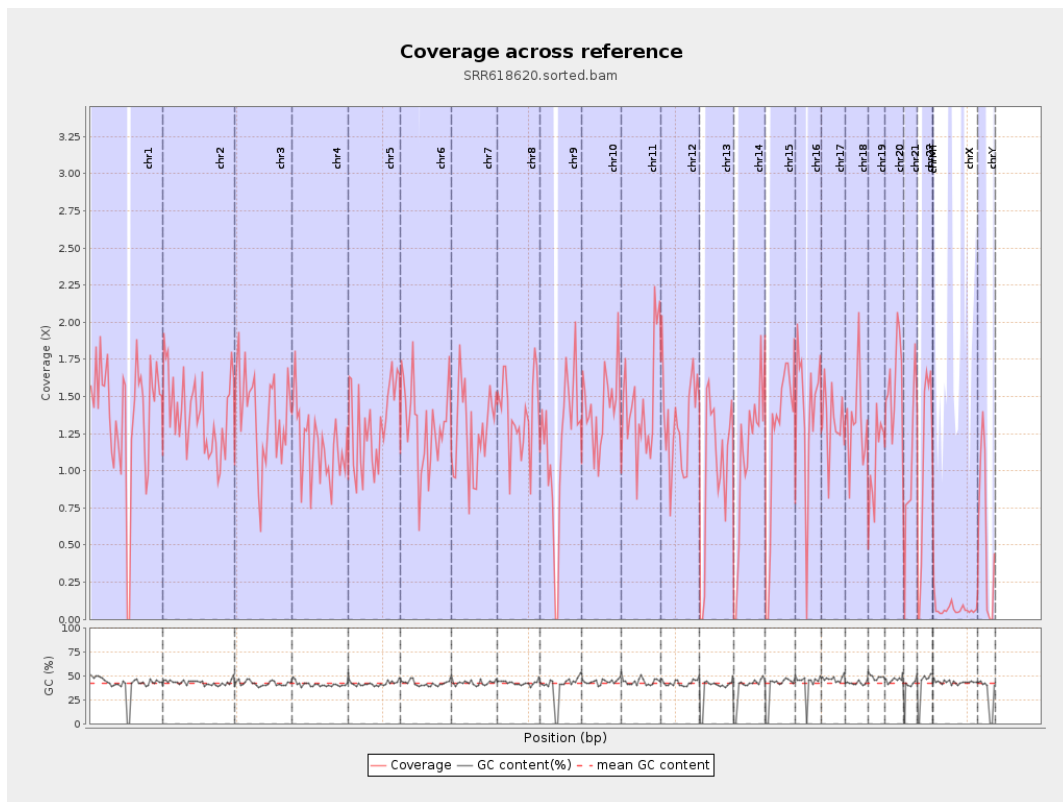
## 2.7. Chromosome stats

| Name | Length | Mapped | Mean | Standard |
|------|--------|--------|------|----------|
|------|--------|--------|------|----------|

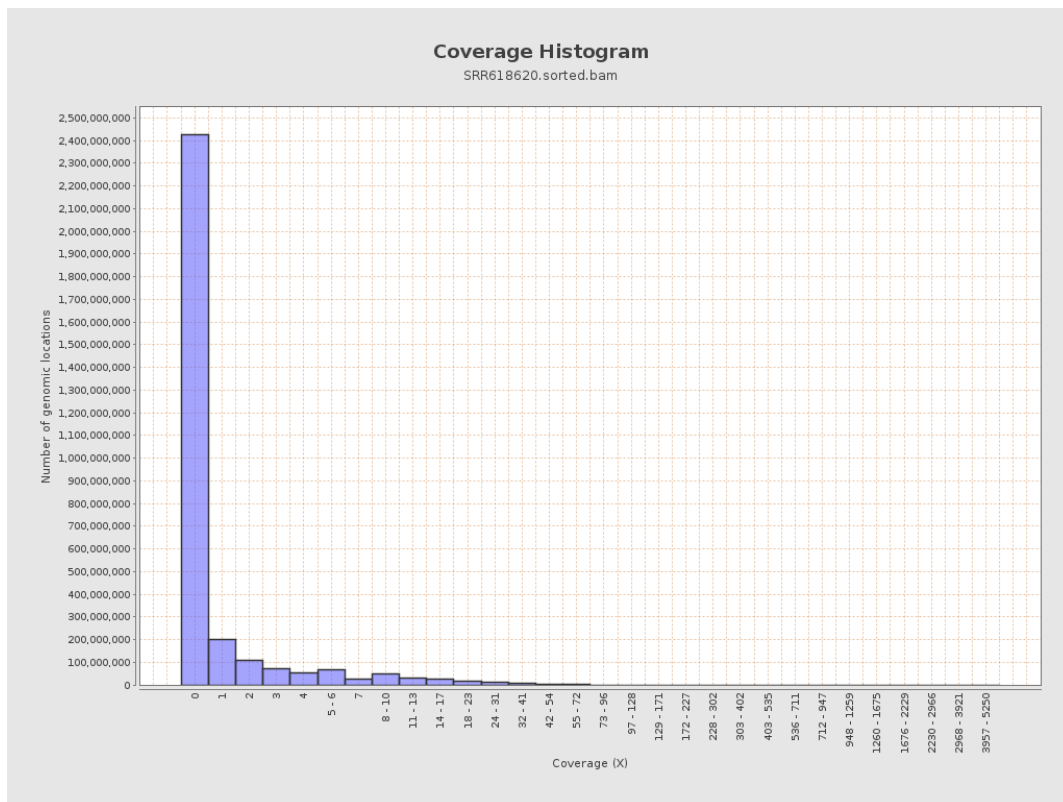
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 342196484    | 1.3729          | 6.9078           |
| chr2  | 243199373 | 336988500    | 1.3856          | 6.1984           |
| chr3  | 198022430 | 269782282    | 1.3624          | 5.4577           |
| chr4  | 191154276 | 222872035    | 1.1659          | 5.4594           |
| chr5  | 180915260 | 237654393    | 1.3136          | 5.6409           |
| chr6  | 171115067 | 223491045    | 1.3061          | 5.2998           |
| chr7  | 159138663 | 200872119    | 1.2622          | 5.7023           |
| chr8  | 146364022 | 201598243    | 1.3774          | 6.3686           |
| chr9  | 141213431 | 165474169    | 1.1718          | 6.1997           |
| chr10 | 135534747 | 193117421    | 1.4249          | 7.0633           |
| chr11 | 135006516 | 195198394    | 1.4458          | 6.2478           |
| chr12 | 133851895 | 179061851    | 1.3378          | 7.7437           |
| chr13 | 115169878 | 117454753    | 1.0198          | 4.5417           |
| chr14 | 107349540 | 117081276    | 1.0907          | 5.03             |
| chr15 | 102531392 | 124317006    | 1.2125          | 5.0938           |
| chr16 | 90354753  | 125849358    | 1.3928          | 7.3051           |
| chr17 | 81195210  | 108360538    | 1.3346          | 5.665            |
| chr18 | 78077248  | 103168731    | 1.3214          | 5.8795           |
| chr19 | 59128983  | 63402857     | 1.0723          | 5.1996           |
| chr20 | 63025520  | 101199336    | 1.6057          | 5.6011           |
| chr21 | 48129895  | 50415587     | 1.0475          | 5.6513           |
| chr22 | 51304566  | 54686232     | 1.0659          | 5.718            |
| chrMT | 16571     | 12799        | 0.7724          | 3.7282           |
| chrX  | 155270560 | 10911071     | 0.0703          | 2.5102           |

|      |          |          |        |        |
|------|----------|----------|--------|--------|
| chrY | 59373566 | 35782779 | 0.6027 | 3.9223 |
|------|----------|----------|--------|--------|

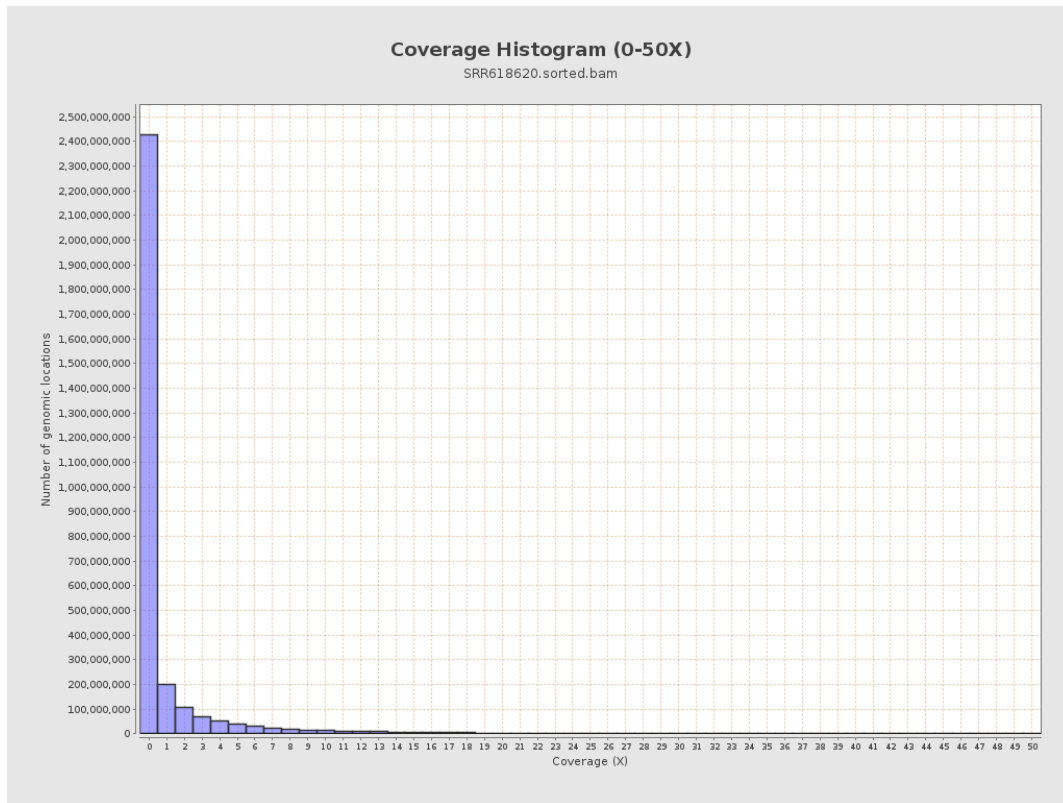
### 3. Results : Coverage across reference



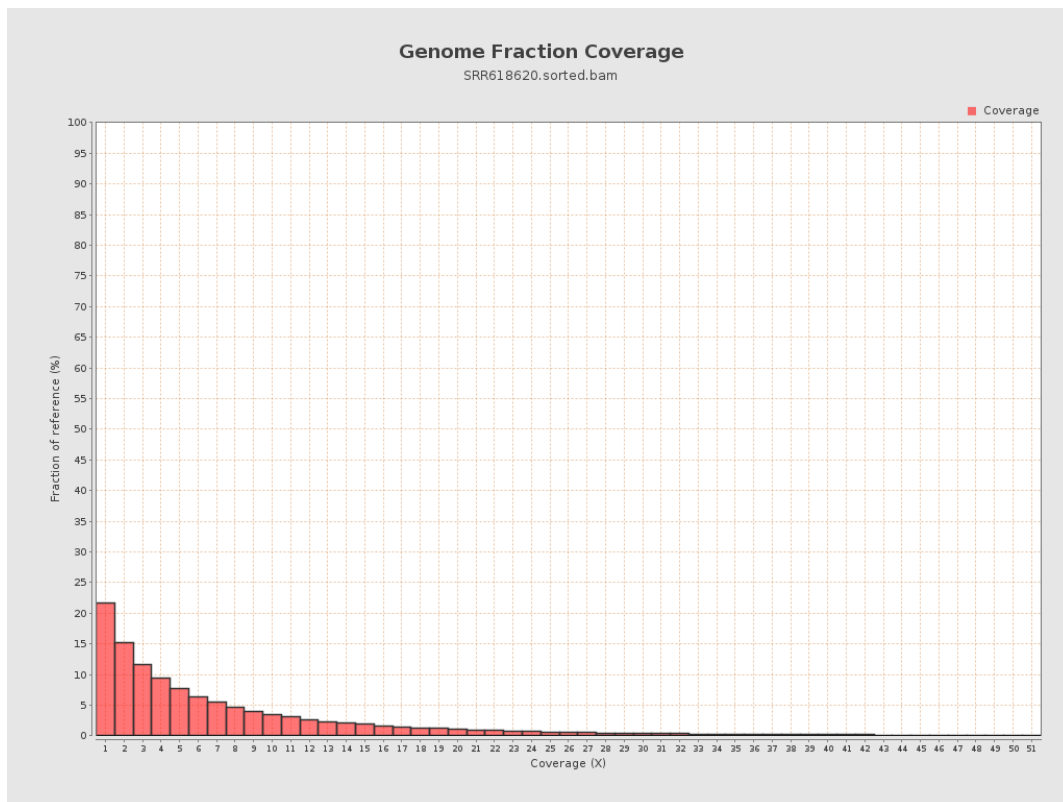
## 4. Results : Coverage Histogram



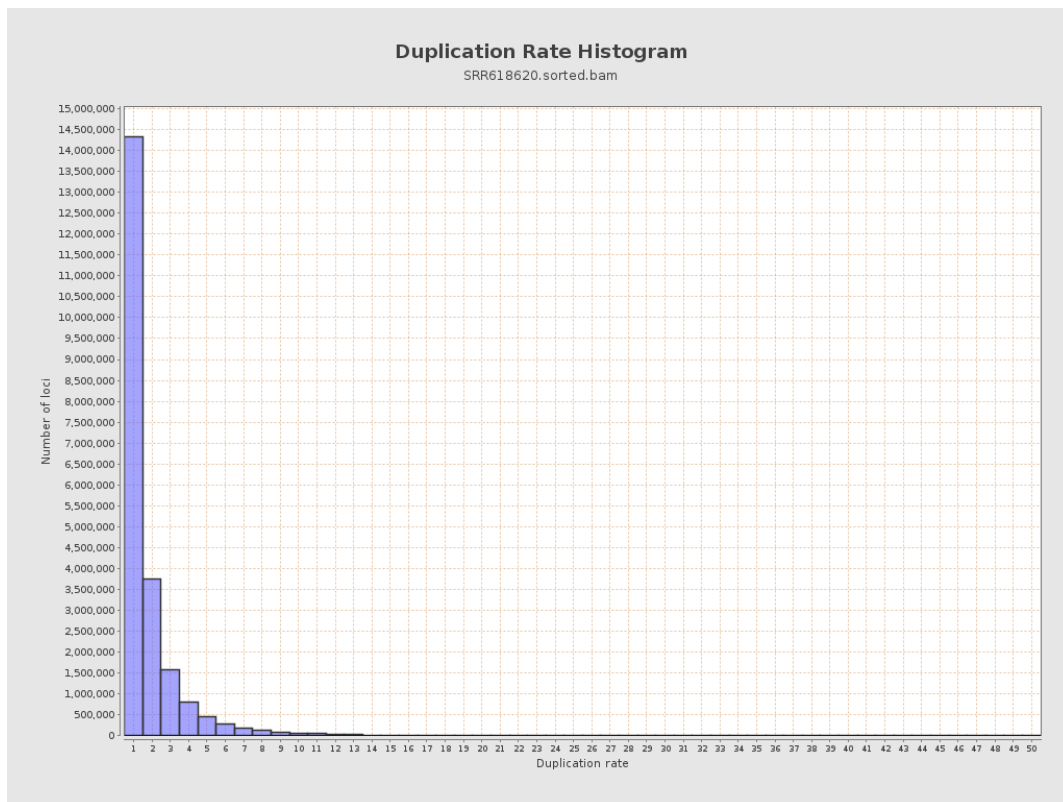
## 5. Results : Coverage Histogram (0-50X)



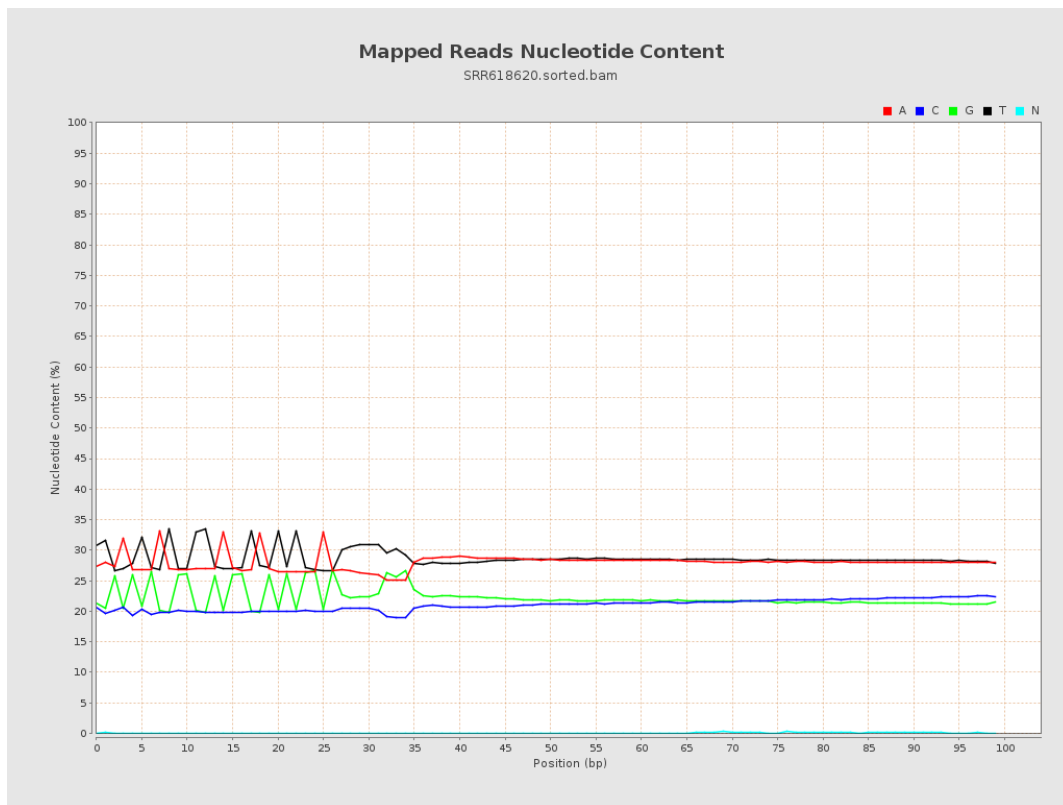
## 6. Results : Genome Fraction Coverage



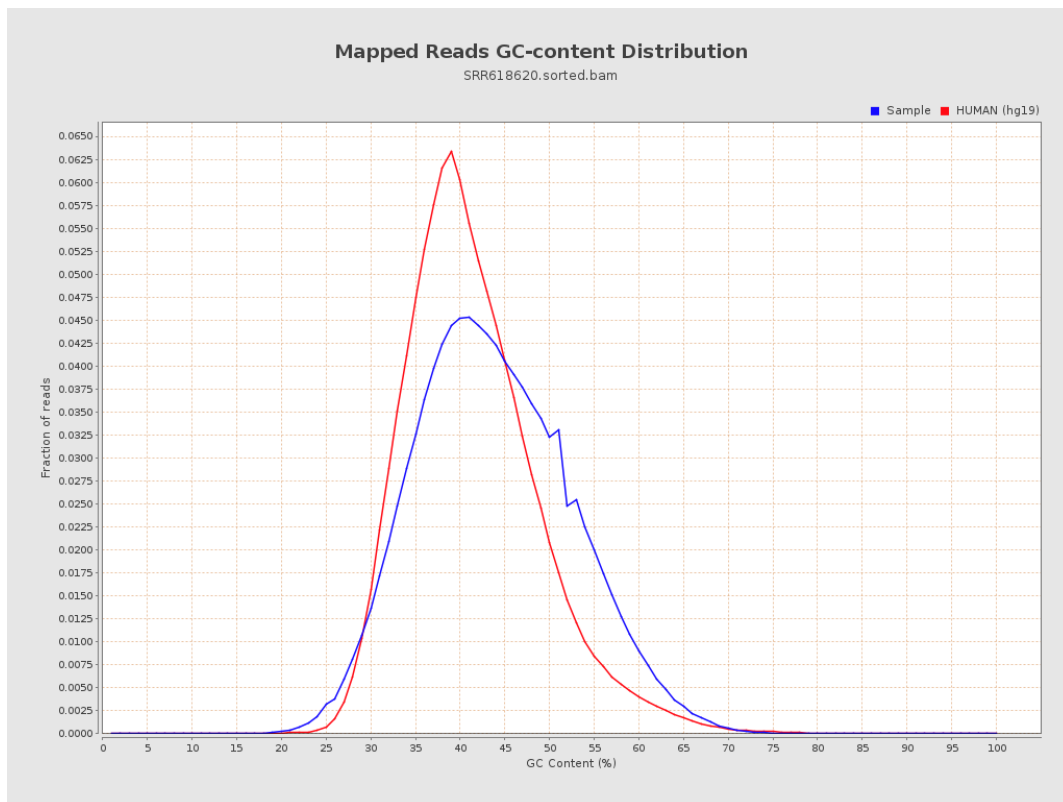
## 7. Results : Duplication Rate Histogram



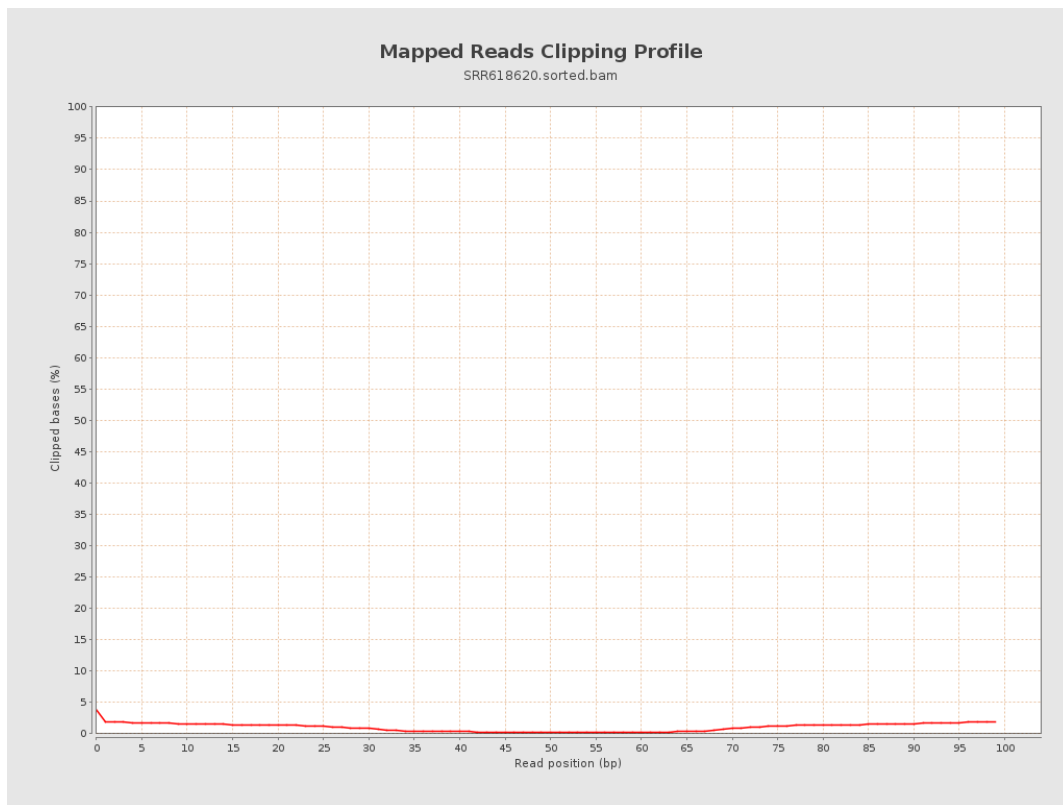
## 8. Results : Mapped Reads Nucleotide Content



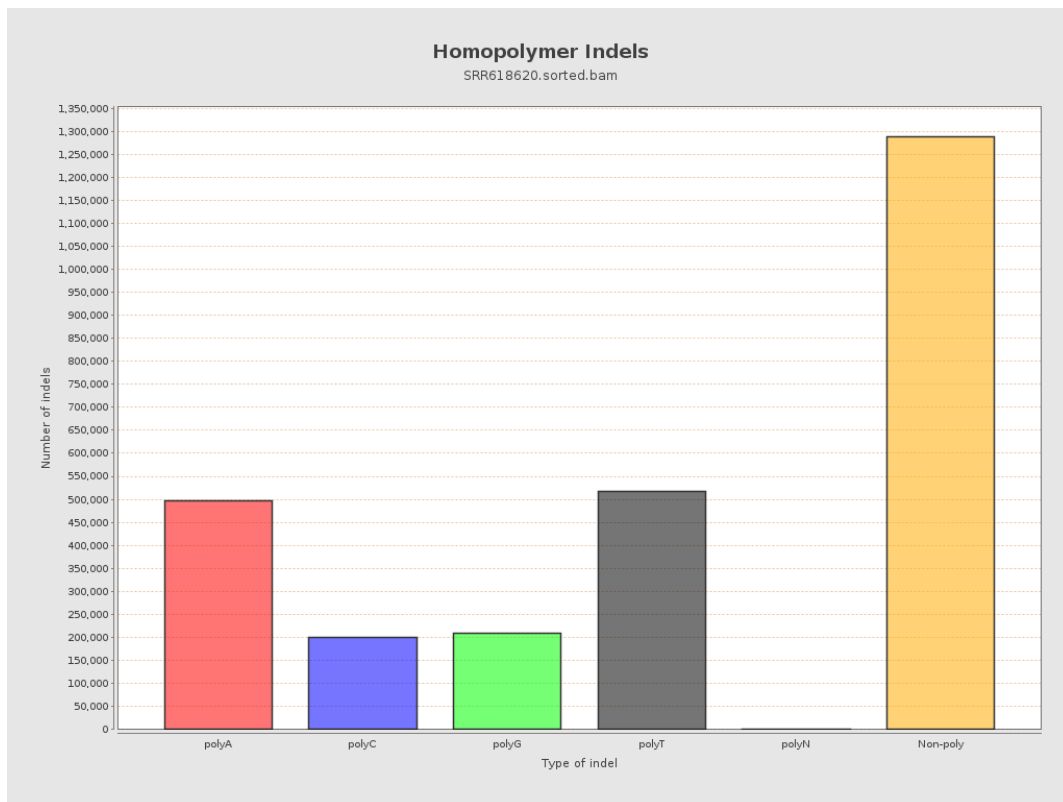
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



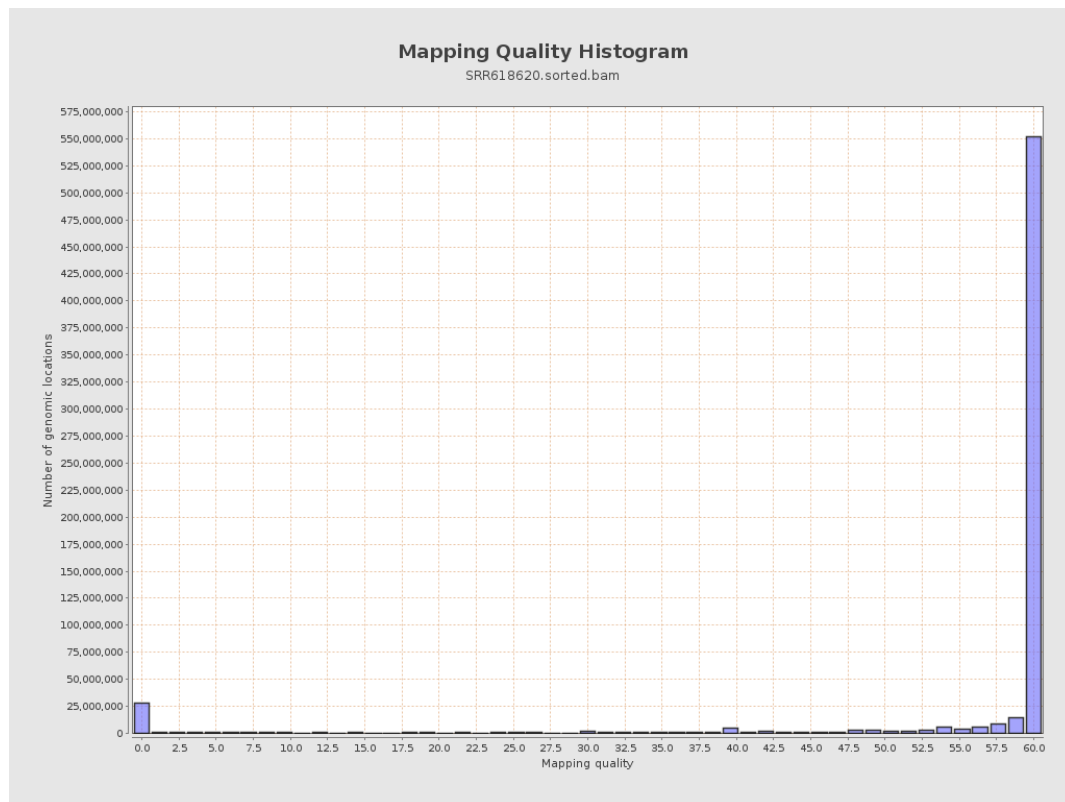
## 11. Results : Homopolymer Indels



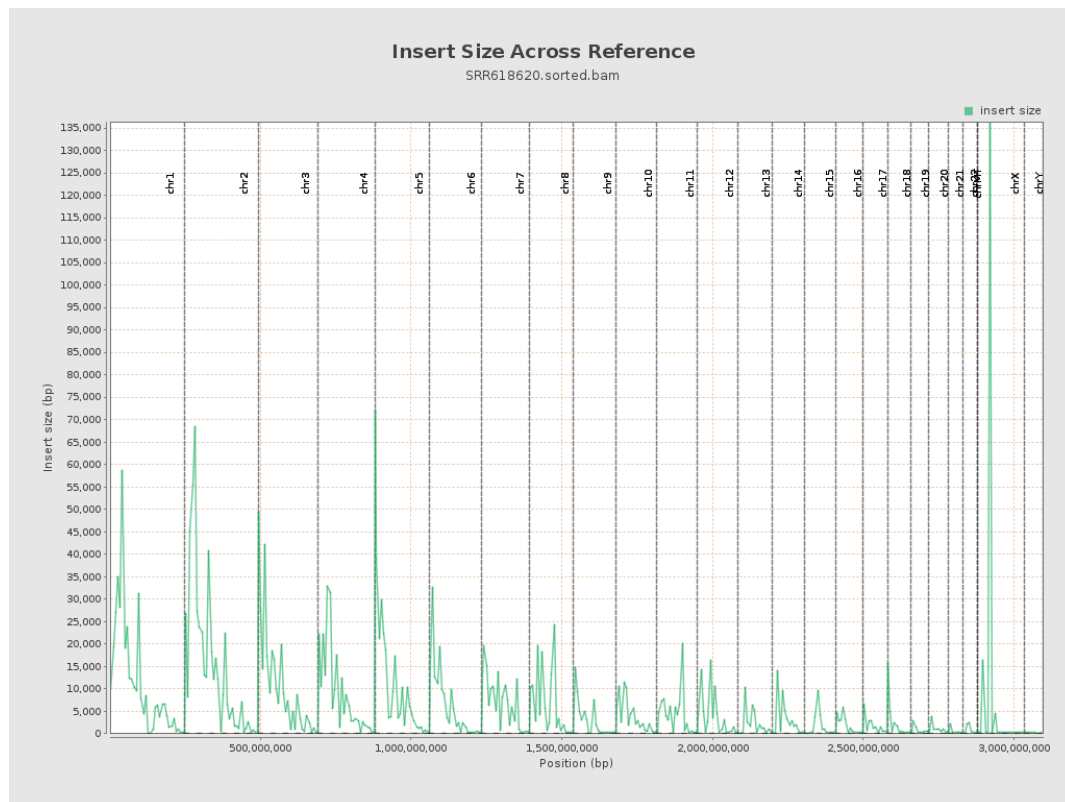
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

