

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/15 05:45:37*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038432.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_SRR5038432 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038432_1.fastq.gz SRR5038432_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                  |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                   |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                   |
| Analysis date:                        | Fri Apr 15 05:45:36 CST 2022                                                                                                                                                                                         |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                    |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                   |
| Number of windows:                    | 400                                                                                                                                                                                                                  |
| BAM file:                             | SRR5038432.sorted.bam                                                                                                                                                                                                |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 14,577,296          |
| Mapped reads                 | 13,857,489 / 95.06% |
| Unmapped reads               | 719,807 / 4.94%     |
| Mapped paired reads          | 13,857,489 / 95.06% |
| Mapped reads, first in pair  | 7,021,391 / 48.17%  |
| Mapped reads, second in pair | 6,836,098 / 46.9%   |
| Mapped reads, both in pair   | 13,635,988 / 93.54% |
| Mapped reads, singletons     | 221,501 / 1.52%     |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 216,768 / 1.49%     |
| Read min/max/mean length     | 30 / 150 / 150.74   |
| Duplicated reads (estimated) | 2,102,187 / 14.42%  |
| Duplication rate             | 10.56%              |
| Clipped reads                | 6,273,451 / 43.04%  |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 536,296,893 / 28.56% |
| Number/percentage of C's | 373,343,974 / 19.88% |
| Number/percentage of T's | 546,962,055 / 29.13% |
| Number/percentage of G's | 421,062,040 / 22.42% |
| Number/percentage of N's | 148,487 / 0.01%      |
|                          |                      |

|               |       |
|---------------|-------|
| GC Percentage | 42.3% |
|---------------|-------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.607  |
| Standard Deviation | 8.0422 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 53.46 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 98,196.36       |
| Standard Deviation | 3,034,004.89    |
| P25/Median/P75     | 216 / 268 / 334 |

## 2.6. Mismatches and indels

|                                          |            |
|------------------------------------------|------------|
| General error rate                       | 1.29%      |
| Mismatches                               | 23,455,492 |
| Insertions                               | 309,223    |
| Mapped reads with at least one insertion | 2.12%      |
| Deletions                                | 640,417    |
| Mapped reads with at least one deletion  | 4.46%      |
| Homopolymer indels                       | 47.64%     |

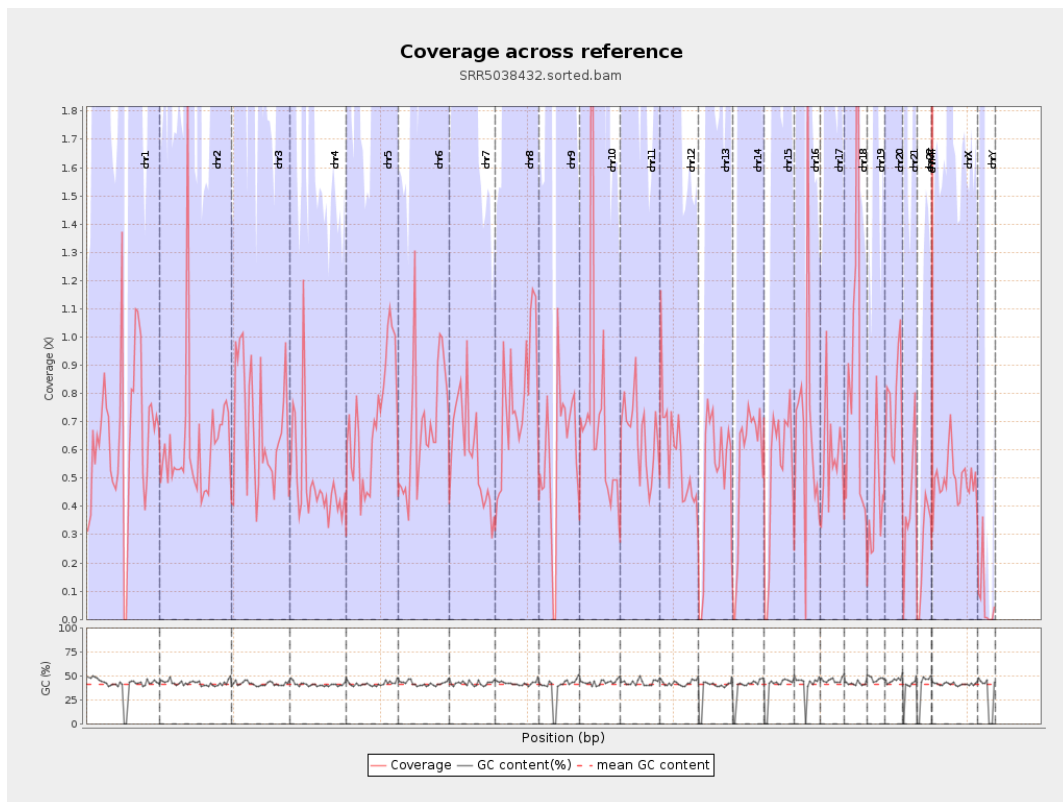
## 2.7. Chromosome stats

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

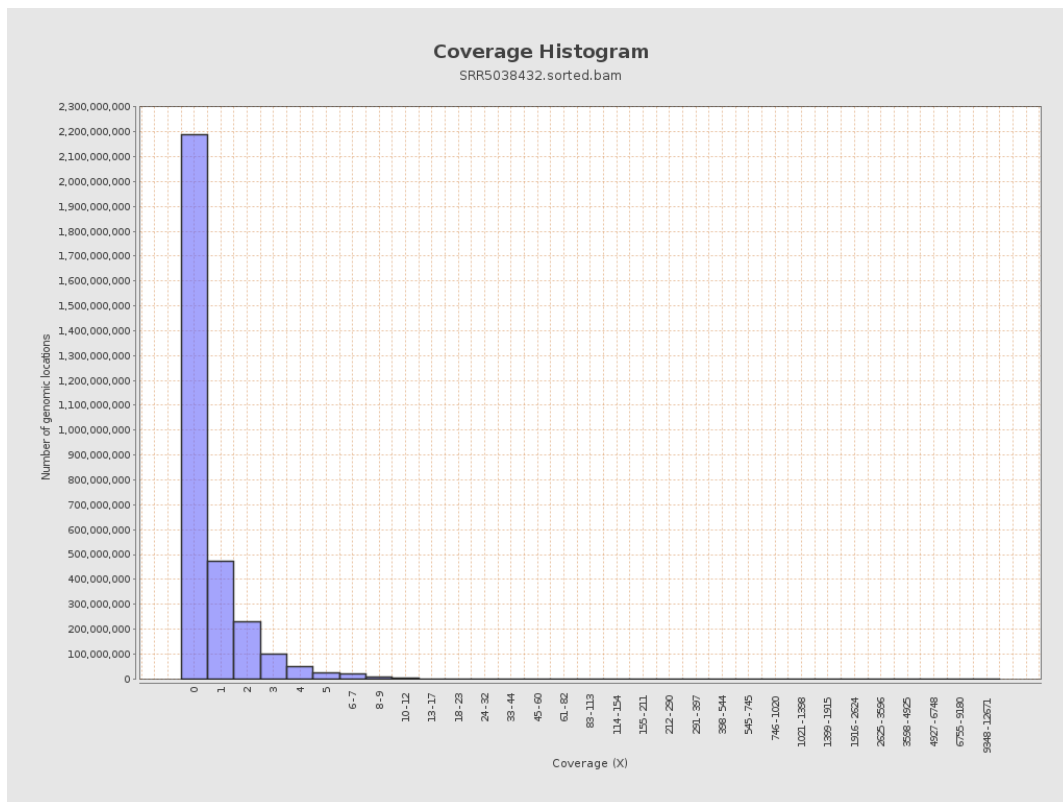
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 161180342    | 0.6467          | 12.596           |
| chr2  | 243199373 | 151362771    | 0.6224          | 8.2114           |
| chr3  | 198022430 | 135129068    | 0.6824          | 1.3727           |
| chr4  | 191154276 | 93237974     | 0.4878          | 6.1287           |
| chr5  | 180915260 | 126625112    | 0.6999          | 1.3346           |
| chr6  | 171115067 | 118950711    | 0.6952          | 6.8099           |
| chr7  | 159138663 | 93167463     | 0.5854          | 7.9661           |
| chr8  | 146364022 | 114278892    | 0.7808          | 3.0424           |
| chr9  | 141213431 | 81061180     | 0.574           | 13.4501          |
| chr10 | 135534747 | 103202530    | 0.7614          | 20.6159          |
| chr11 | 135006516 | 87221137     | 0.6461          | 6.996            |
| chr12 | 133851895 | 78790943     | 0.5886          | 1.3267           |
| chr13 | 115169878 | 59385676     | 0.5156          | 1.1125           |
| chr14 | 107349540 | 59195603     | 0.5514          | 1.2391           |
| chr15 | 102531392 | 52621546     | 0.5132          | 1.1326           |
| chr16 | 90354753  | 60345424     | 0.6679          | 9.2196           |
| chr17 | 81195210  | 46223986     | 0.5693          | 9.3504           |
| chr18 | 78077248  | 68972723     | 0.8834          | 8.9682           |
| chr19 | 59128983  | 24236149     | 0.4099          | 5.4414           |
| chr20 | 63025520  | 48617776     | 0.7714          | 2.3322           |
| chr21 | 48129895  | 20278037     | 0.4213          | 2.8729           |
| chr22 | 51304566  | 13240995     | 0.2581          | 0.7983           |
| chrMT | 16571     | 943578       | 56.9415         | 28.8363          |
| chrX  | 155270560 | 76517911     | 0.4928          | 2.2067           |

|      |          |         |        |        |
|------|----------|---------|--------|--------|
| chrY | 59373566 | 4271265 | 0.0719 | 5.9712 |
|------|----------|---------|--------|--------|

### 3. Results : Coverage across reference

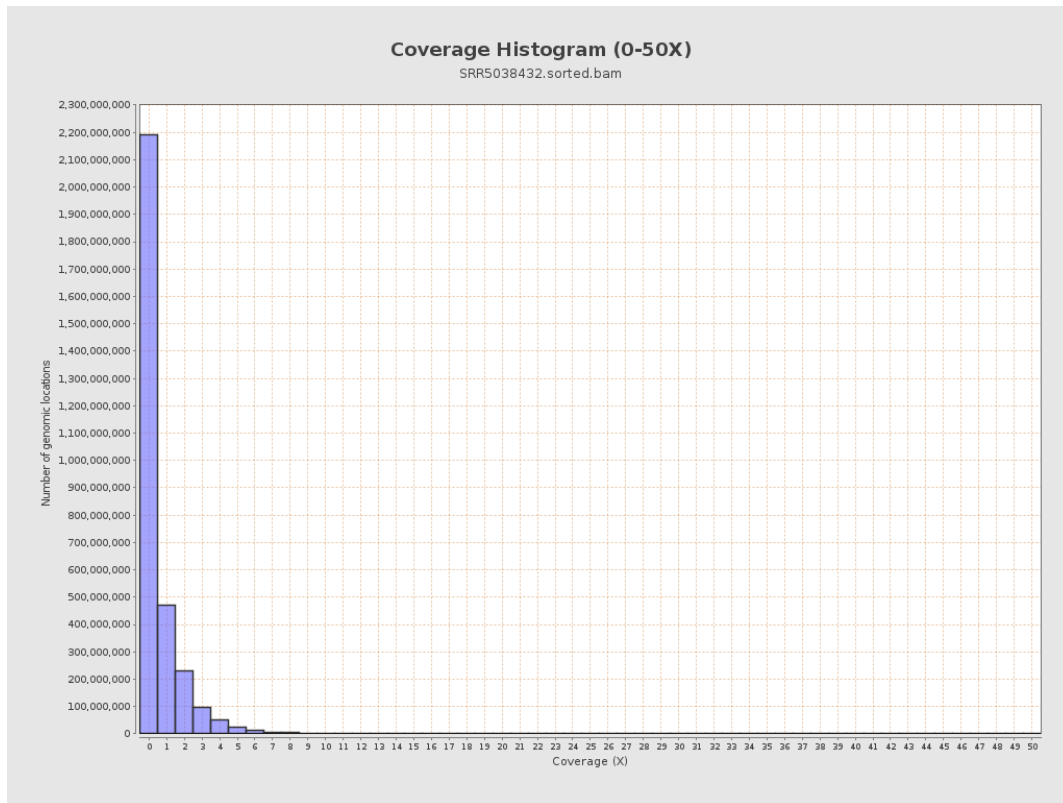


## 4. Results : Coverage Histogram

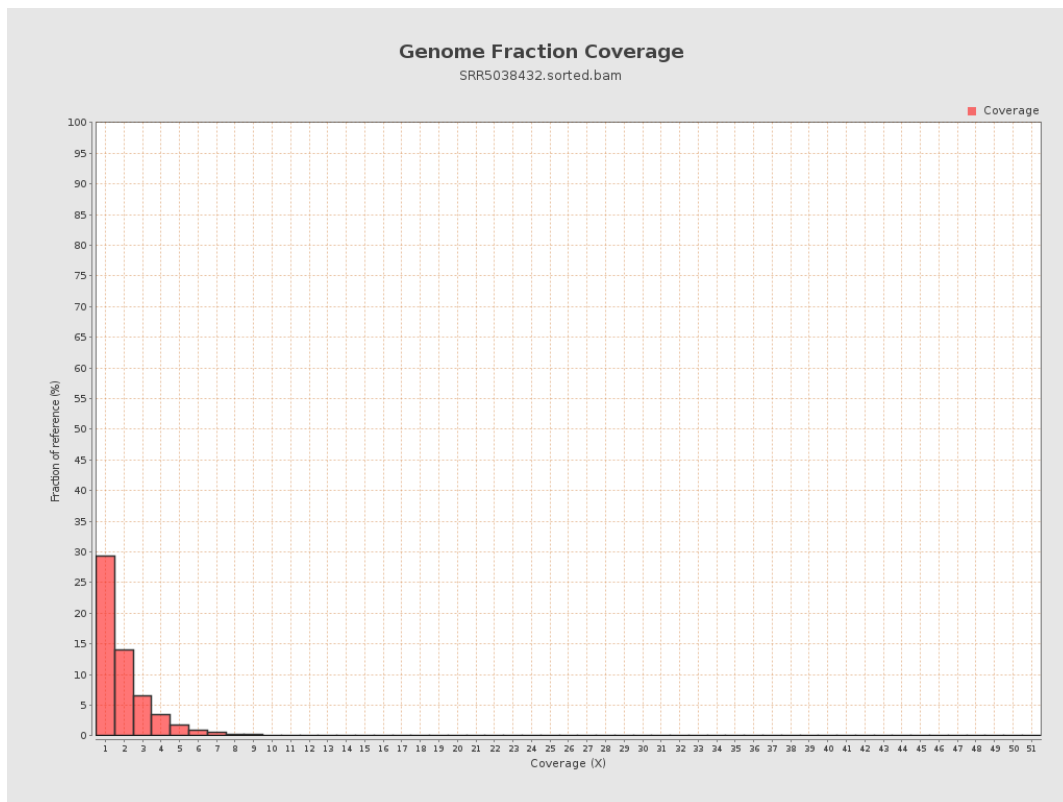




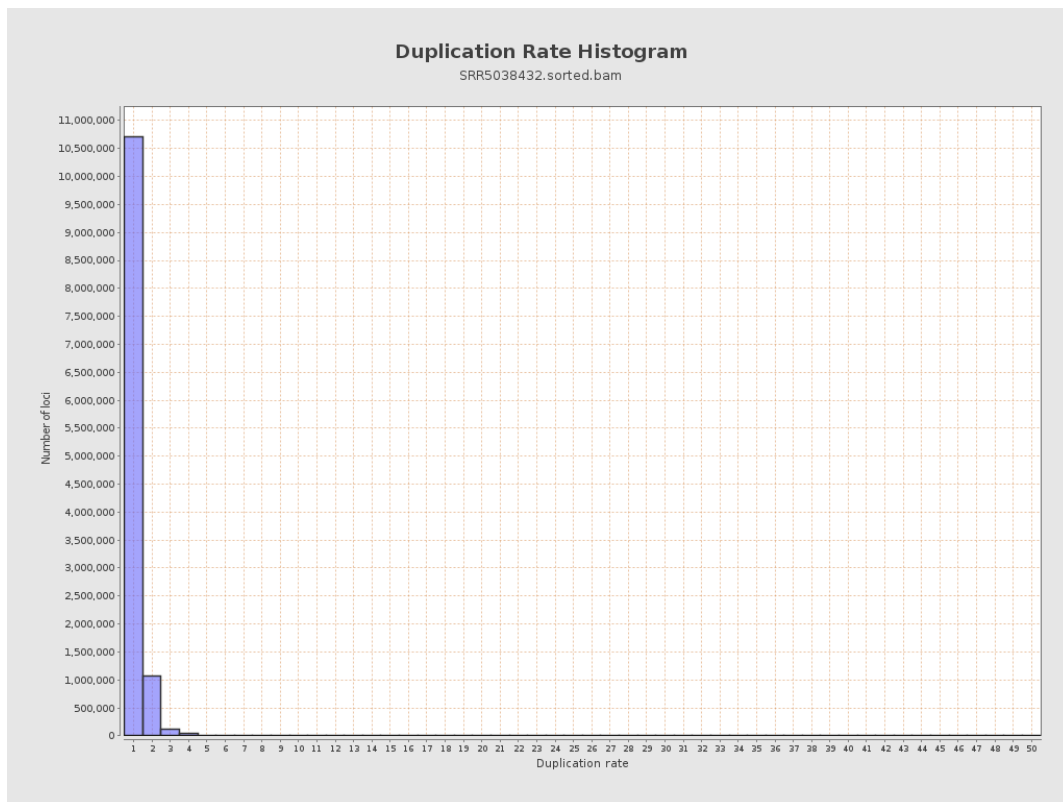
## 5. Results : Coverage Histogram (0-50X)



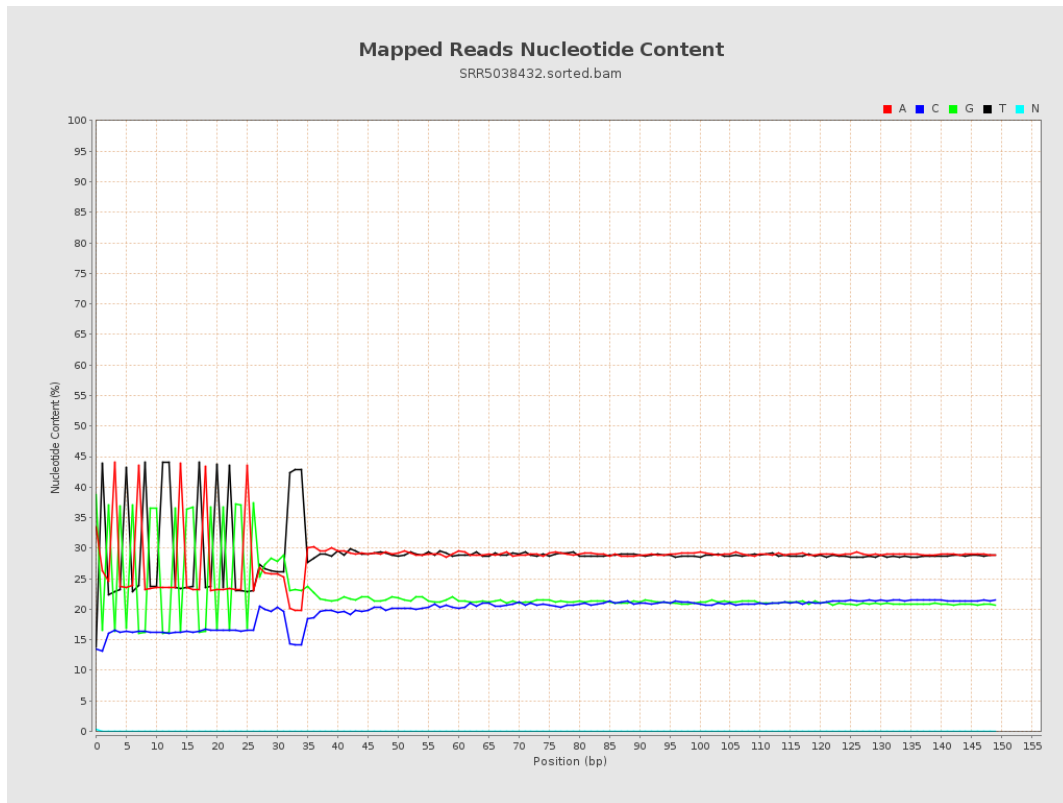
## 6. Results : Genome Fraction Coverage



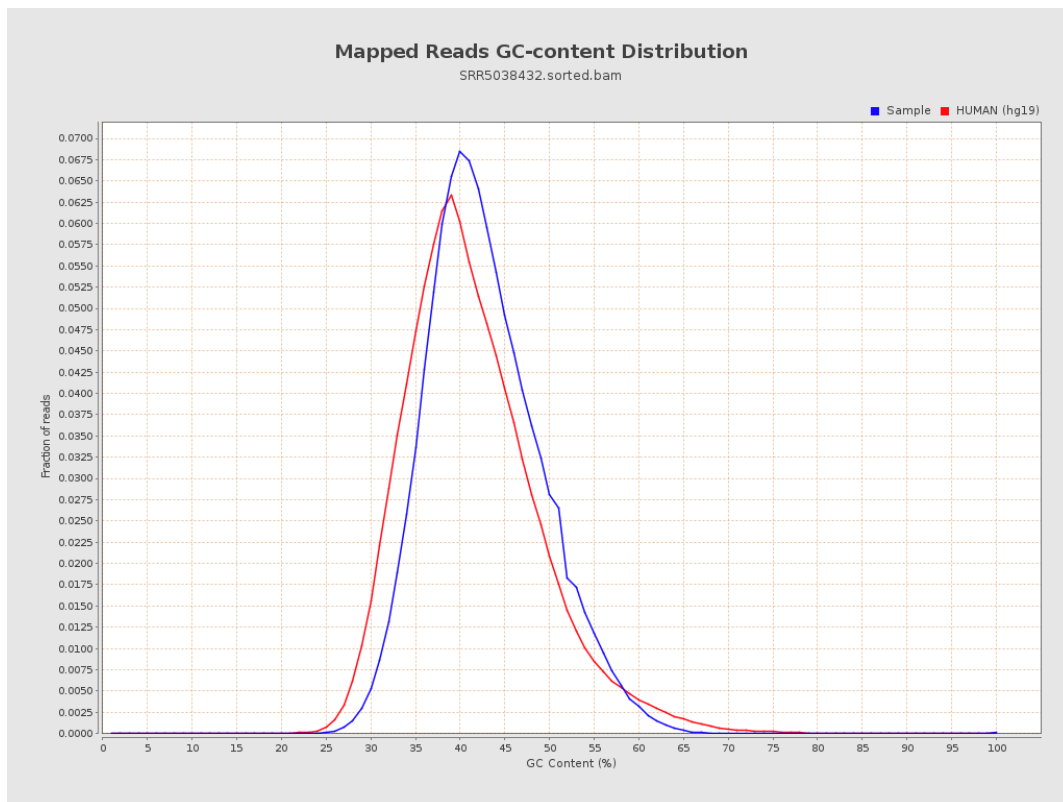
## 7. Results : Duplication Rate Histogram



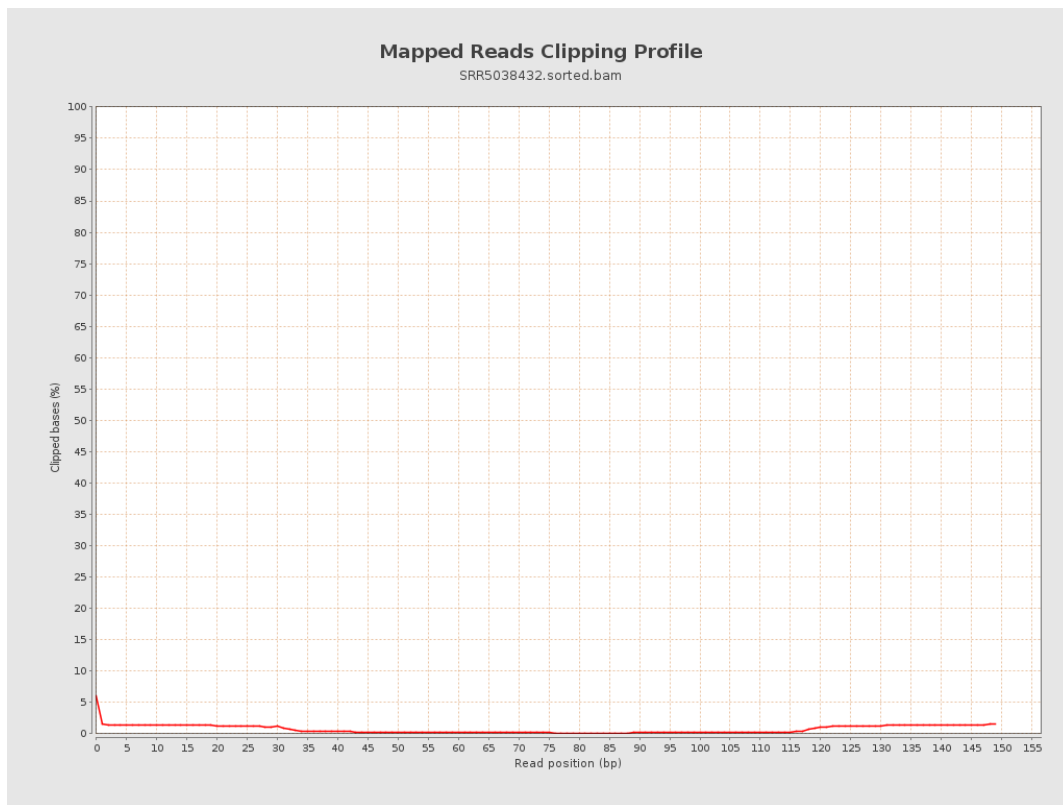
## 8. Results : Mapped Reads Nucleotide Content



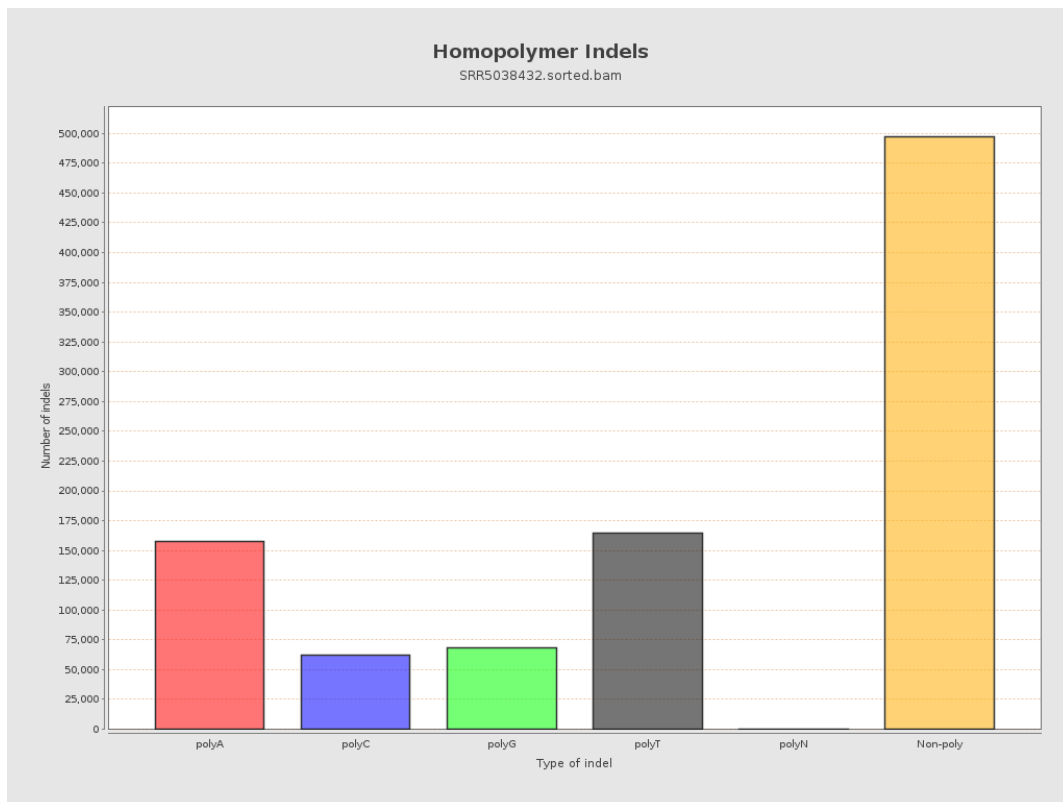
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

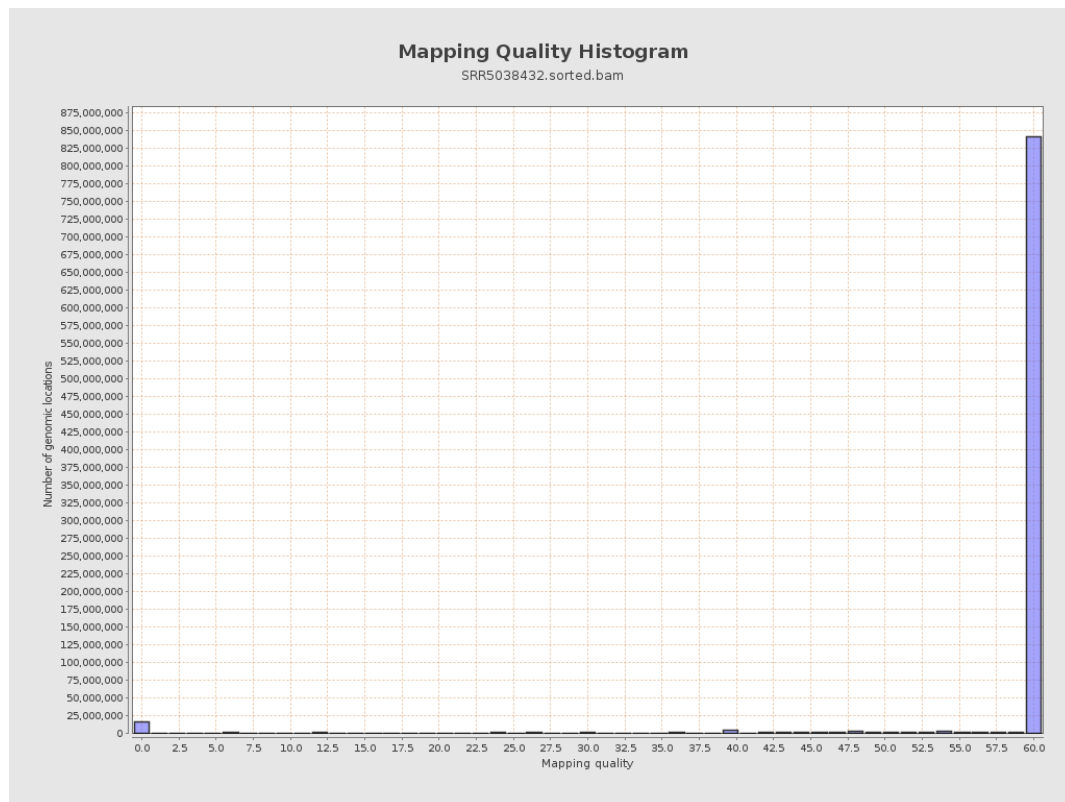


## 12. Results : Mapping Quality Across Reference

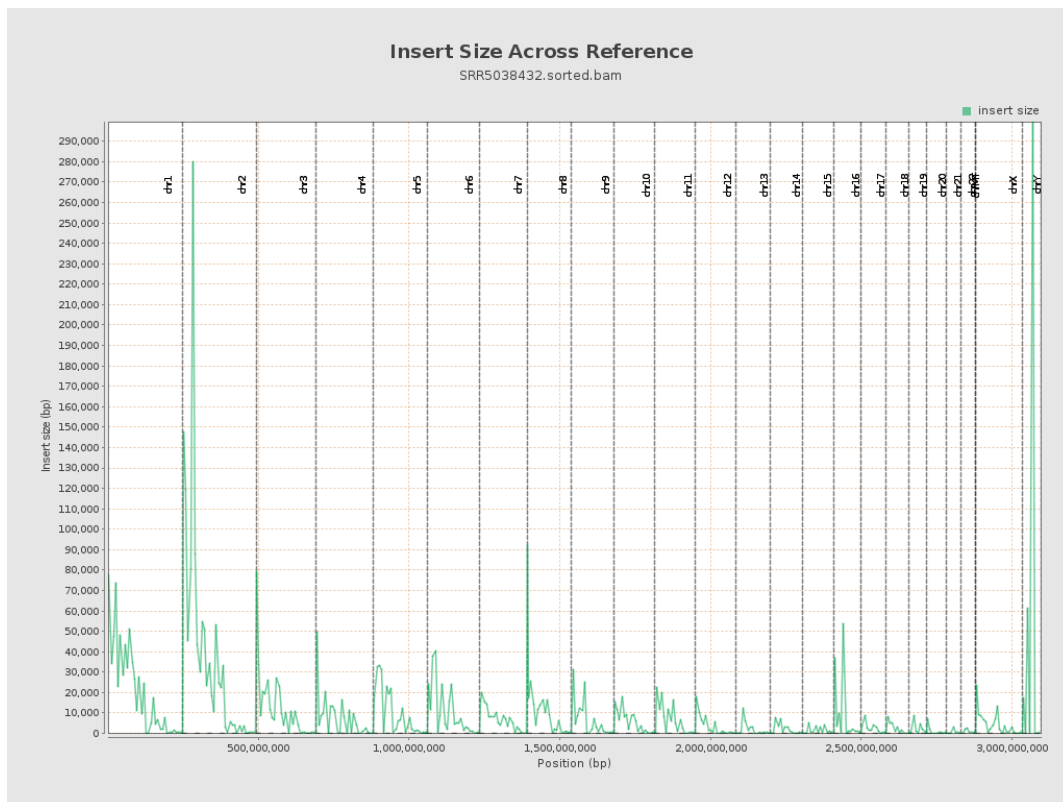




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

