

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2025/02/06 03:22:59*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR16362016.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_SRR16362016 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16362016_1.fastq.gz SRR16362016_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                     |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                      |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                      |
| Analysis date:                        | Thu Feb 06 03:22:58 CST 2025                                                                                                                                                                                            |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                       |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                      |
| Number of windows:                    | 400                                                                                                                                                                                                                     |
| BAM file:                             | SRR16362016.sorted.bam                                                                                                                                                                                                  |

## 2. Summary

### 2.1. Globals

|                              |                      |
|------------------------------|----------------------|
| Reference size               | 3,095,693,983        |
| Number of reads              | 466,978,888          |
| Mapped reads                 | 447,856,148 / 95.91% |
| Unmapped reads               | 19,122,740 / 4.09%   |
| Mapped paired reads          | 447,856,148 / 95.91% |
| Mapped reads, first in pair  | 225,117,761 / 48.21% |
| Mapped reads, second in pair | 222,738,387 / 47.7%  |
| Mapped reads, both in pair   | 444,514,948 / 95.19% |
| Mapped reads, singletons     | 3,341,200 / 0.72%    |
| Secondary alignments         | 0                    |
| Supplementary alignments     | 21,431,751 / 4.59%   |
| Read min/max/mean length     | 30 / 150 / 152.28    |
| Duplicated reads (estimated) | 175,440,742 / 37.57% |
| Duplication rate             | 34.13%               |
| Clipped reads                | 300,688,992 / 64.39% |

### 2.2. ACGT Content

|                          |                         |
|--------------------------|-------------------------|
| Number/percentage of A's | 18,015,916,398 / 29.1%  |
| Number/percentage of C's | 12,916,530,204 / 20.86% |
| Number/percentage of T's | 17,876,367,659 / 28.87% |
| Number/percentage of G's | 13,100,303,254 / 21.16% |
| Number/percentage of N's | 4,725,144 / 0.01%       |
|                          |                         |

|               |        |
|---------------|--------|
| GC Percentage | 42.02% |
|---------------|--------|

## 2.3. Coverage

|                    |          |
|--------------------|----------|
| Mean               | 20.0177  |
| Standard Deviation | 233.8248 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 53.81 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 136,241.57      |
| Standard Deviation | 3,581,443.13    |
| P25/Median/P75     | 180 / 239 / 325 |

## 2.6. Mismatches and indels

|                                          |             |
|------------------------------------------|-------------|
| General error rate                       | 0.89%       |
| Mismatches                               | 526,349,137 |
| Insertions                               | 10,460,351  |
| Mapped reads with at least one insertion | 2.22%       |
| Deletions                                | 31,078,944  |
| Mapped reads with at least one deletion  | 6.65%       |
| Homopolymer indels                       | 44.6%       |

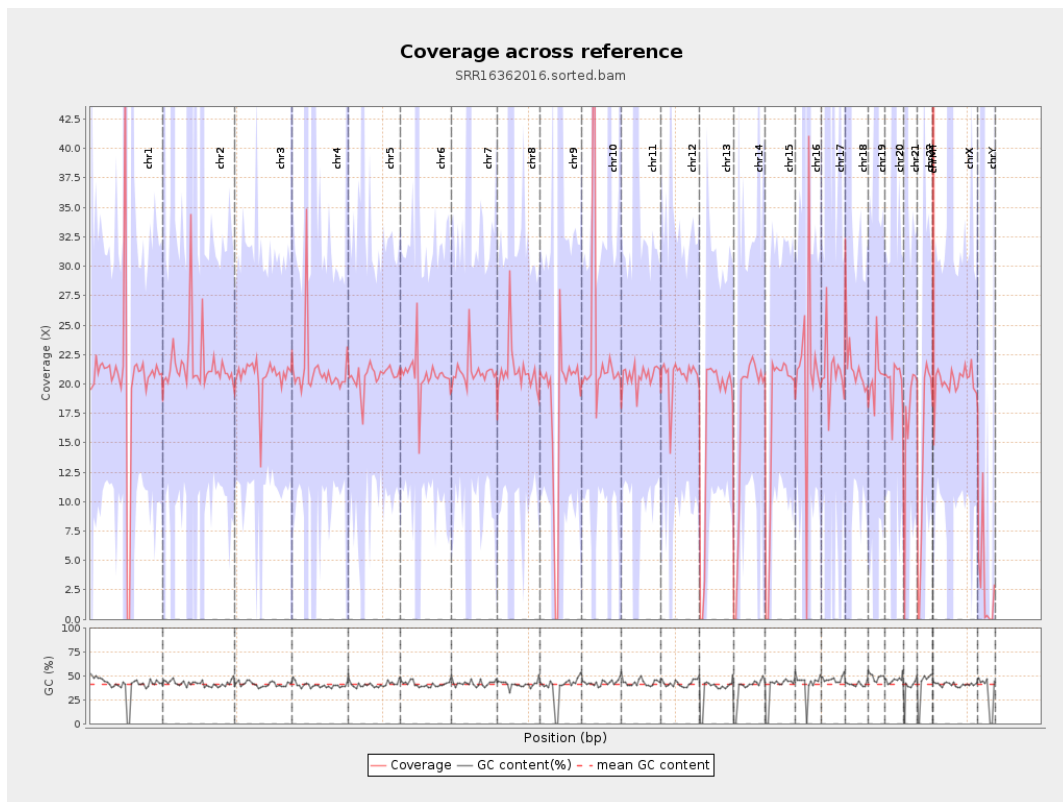
## 2.7. Chromosome stats

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

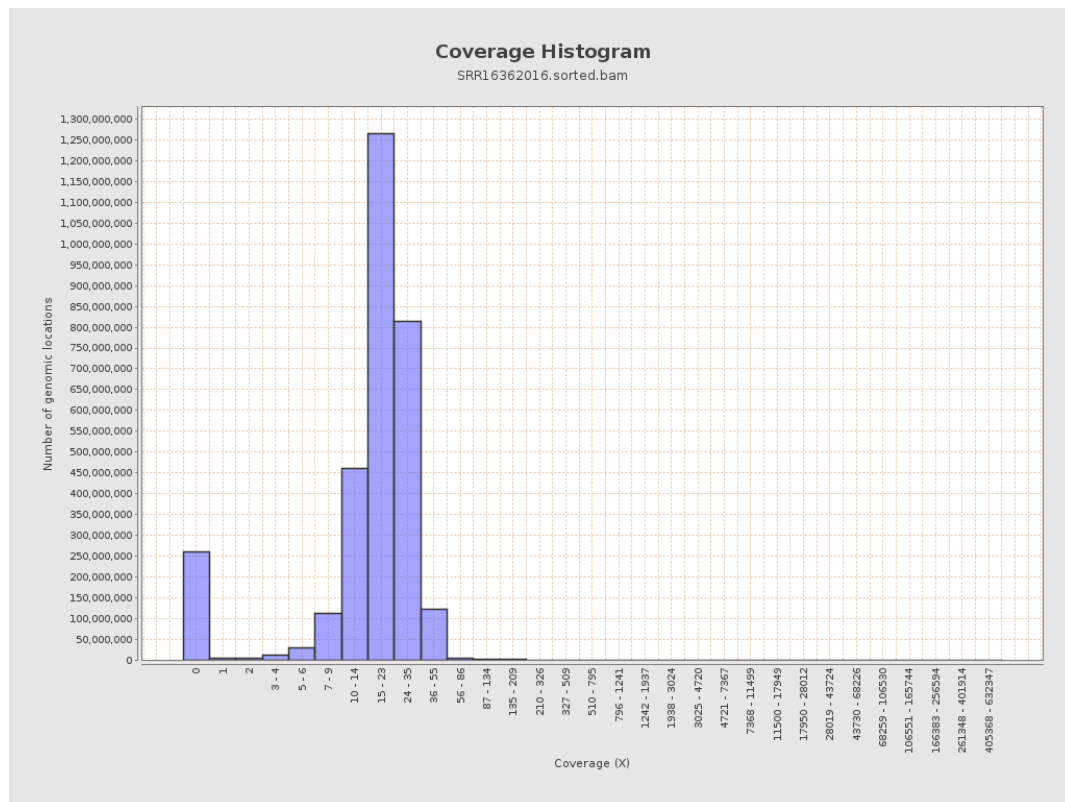
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 5102076664   | 20.4697         | 610.6798         |
| chr2  | 243199373 | 5274522825   | 21.6881         | 140.981          |
| chr3  | 198022430 | 4093339960   | 20.6711         | 17.4388          |
| chr4  | 191154276 | 4044242448   | 21.157          | 132.2831         |
| chr5  | 180915260 | 3731706387   | 20.6268         | 15.7519          |
| chr6  | 171115067 | 3551932548   | 20.7576         | 76.7143          |
| chr7  | 159138663 | 3347292599   | 21.0338         | 140.3092         |
| chr8  | 146364022 | 3095704223   | 21.1507         | 421.8561         |
| chr9  | 141213431 | 2609582937   | 18.4797         | 224.5829         |
| chr10 | 135534747 | 3086104313   | 22.7698         | 317.7323         |
| chr11 | 135006516 | 2789780770   | 20.664          | 81.1858          |
| chr12 | 133851895 | 2772888045   | 20.7161         | 13.6922          |
| chr13 | 115169878 | 1968664744   | 17.0936         | 12.3038          |
| chr14 | 107349540 | 1868268105   | 17.4036         | 17.5242          |
| chr15 | 102531392 | 1765778579   | 17.2218         | 12.9427          |
| chr16 | 90354753  | 1918962491   | 21.2381         | 154.5871         |
| chr17 | 81195210  | 1719075074   | 21.1721         | 104.5694         |
| chr18 | 78077248  | 1676777572   | 21.4759         | 200.5691         |
| chr19 | 59128983  | 1224844023   | 20.7148         | 319.524          |
| chr20 | 63025520  | 1267511694   | 20.1111         | 38.7531          |
| chr21 | 48129895  | 831915221    | 17.2848         | 63.4016          |
| chr22 | 51304566  | 738895872    | 14.4021         | 16.5601          |
| chrMT | 16571     | 186415464    | 11,249.5        | 1,934.182        |
| chrX  | 155270560 | 3132074816   | 20.1717         | 41.0807          |

|      |          |           |        |          |
|------|----------|-----------|--------|----------|
| chrY | 59373566 | 170319905 | 2.8686 | 134.7785 |
|------|----------|-----------|--------|----------|

### 3. Results : Coverage across reference

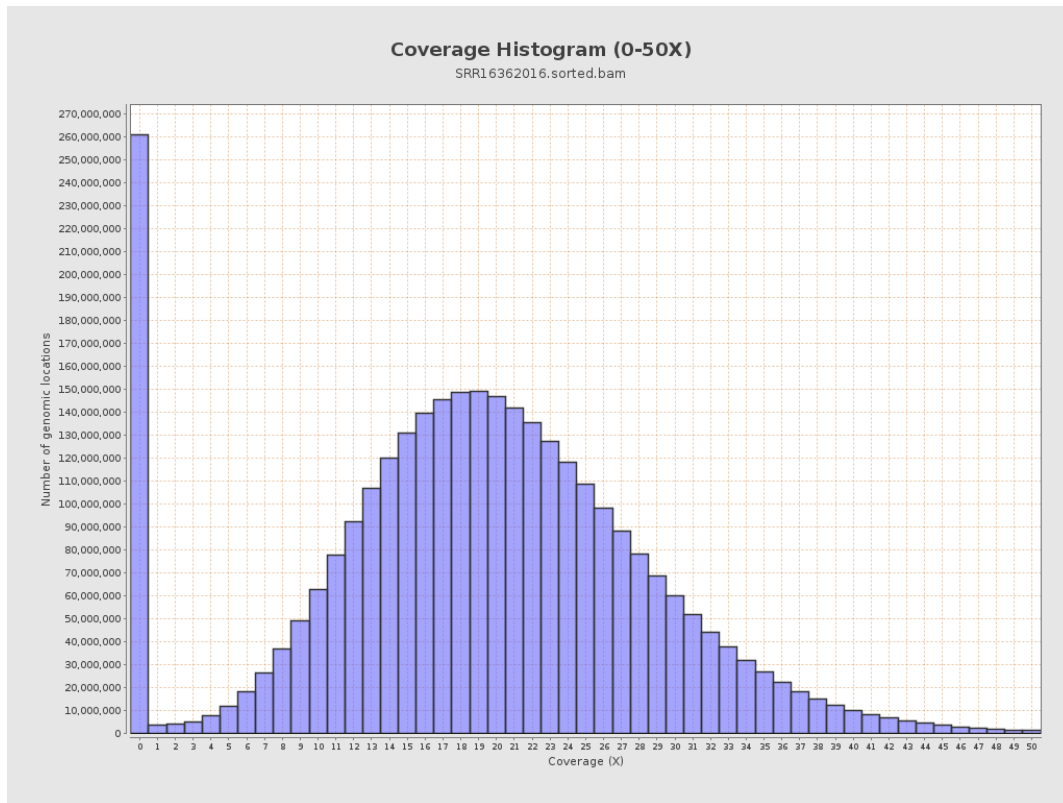


## 4. Results : Coverage Histogram

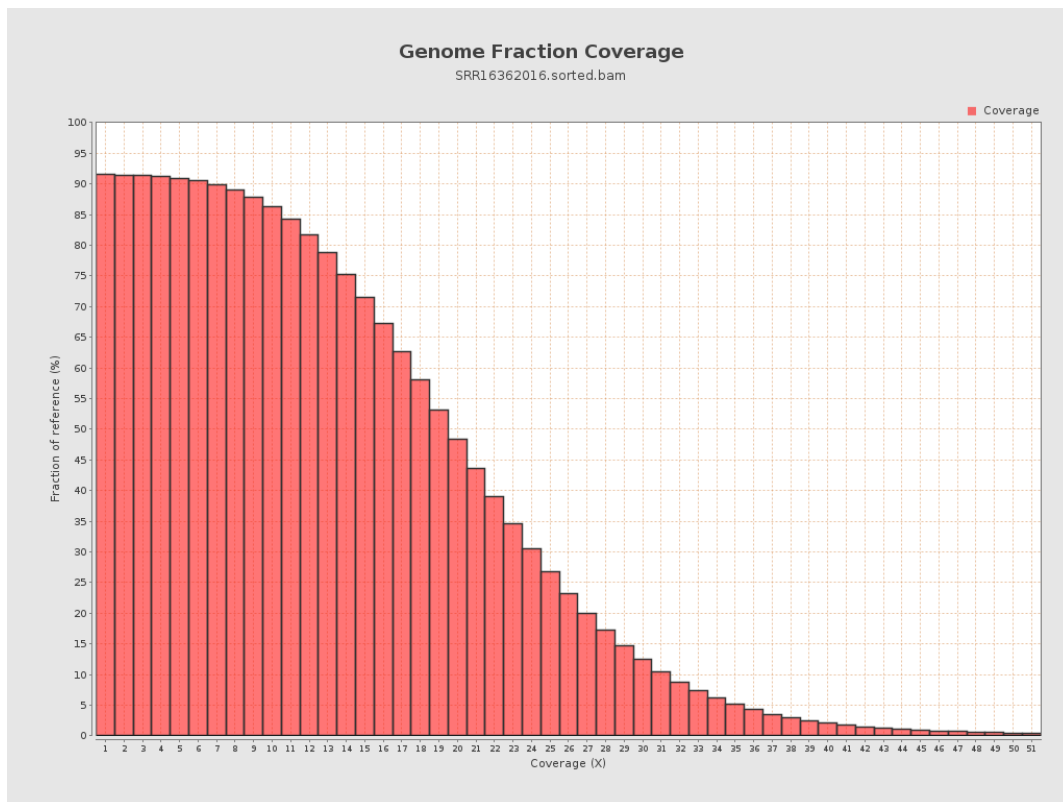




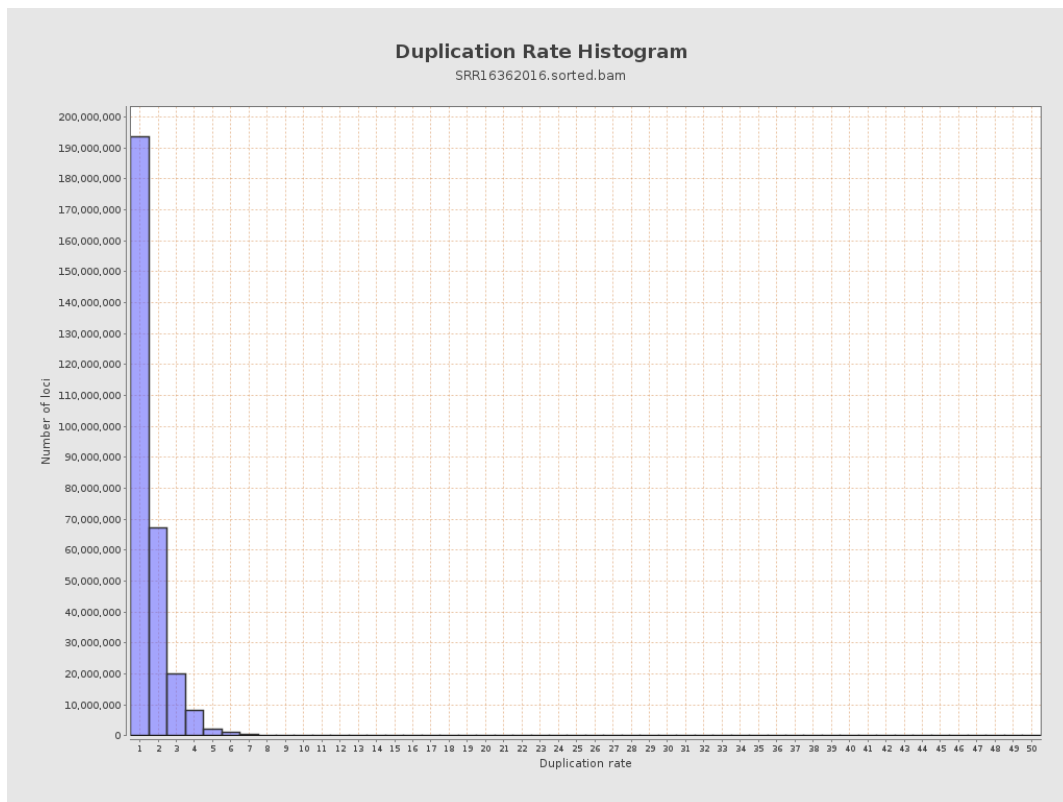
## 5. Results : Coverage Histogram (0-50X)



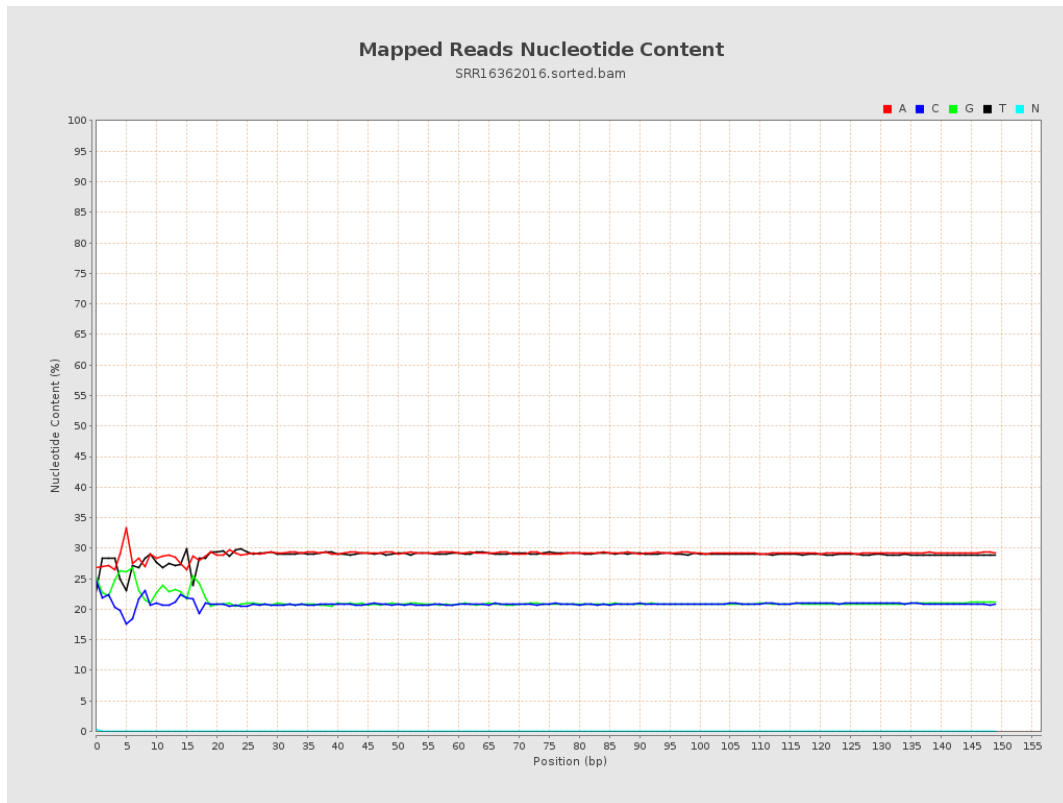
## 6. Results : Genome Fraction Coverage



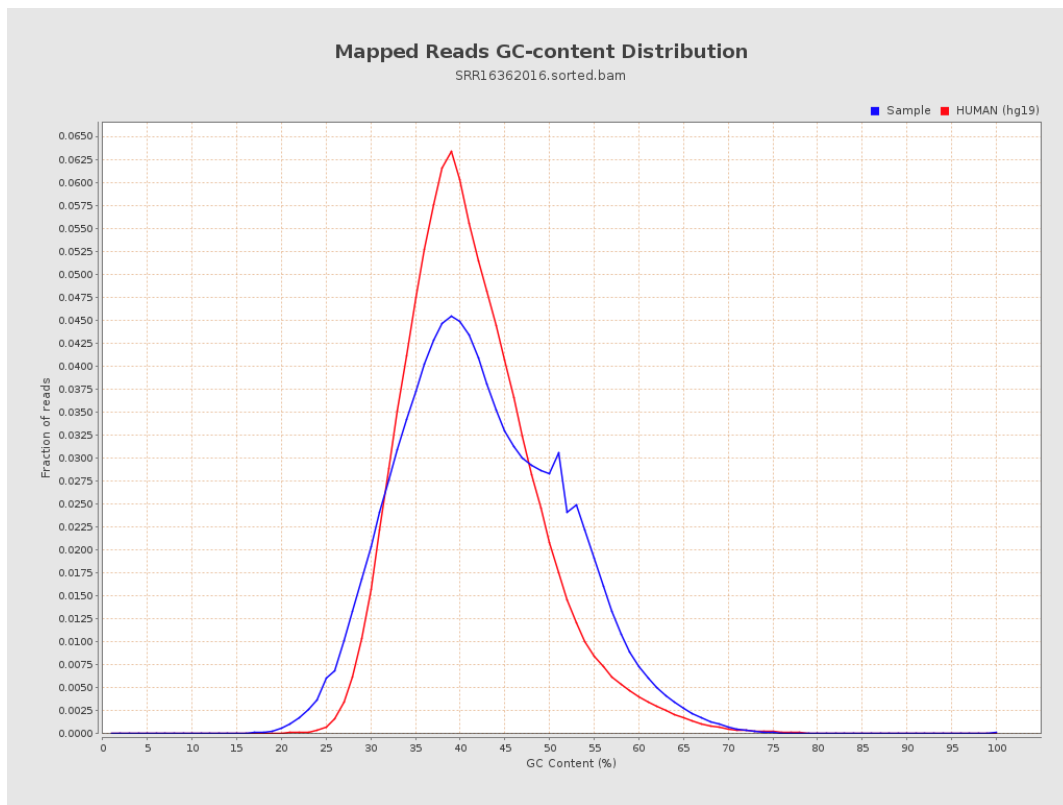
## 7. Results : Duplication Rate Histogram



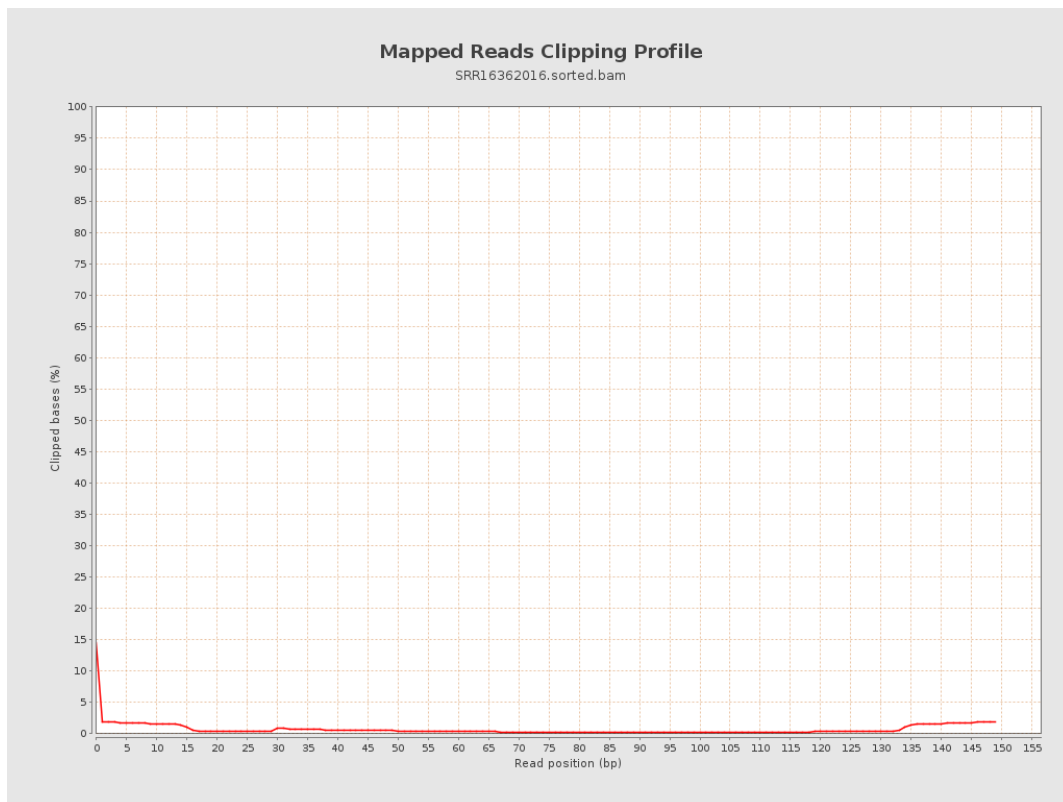
## 8. Results : Mapped Reads Nucleotide Content



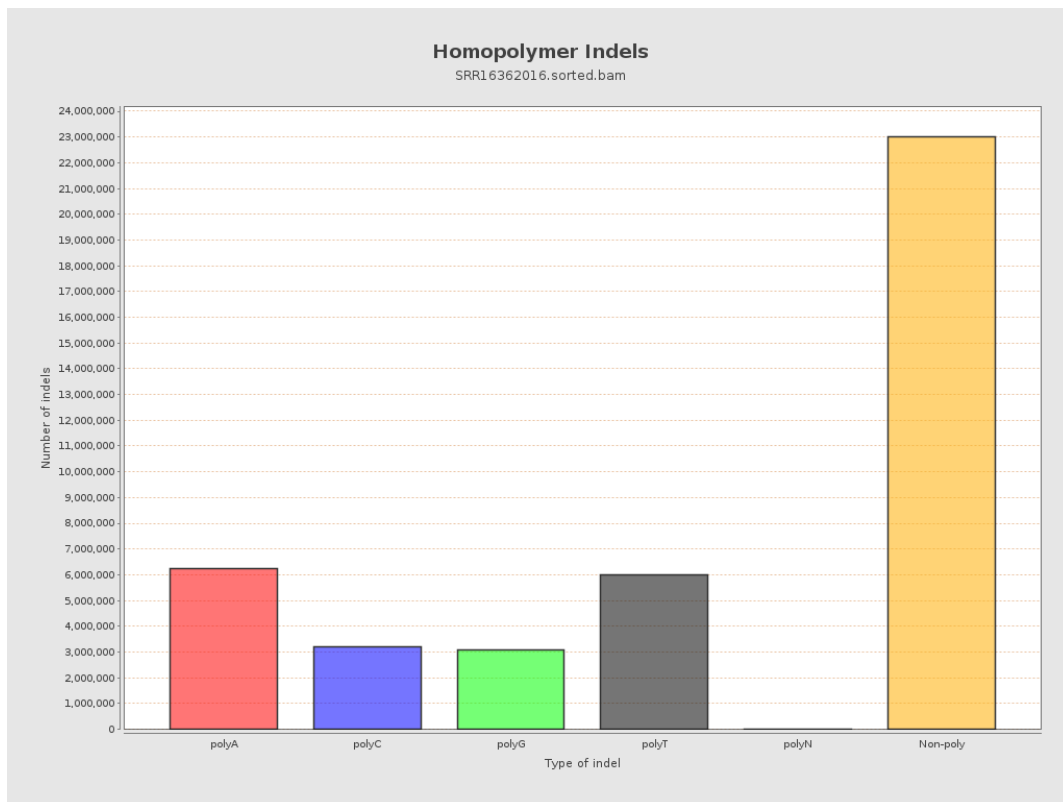
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

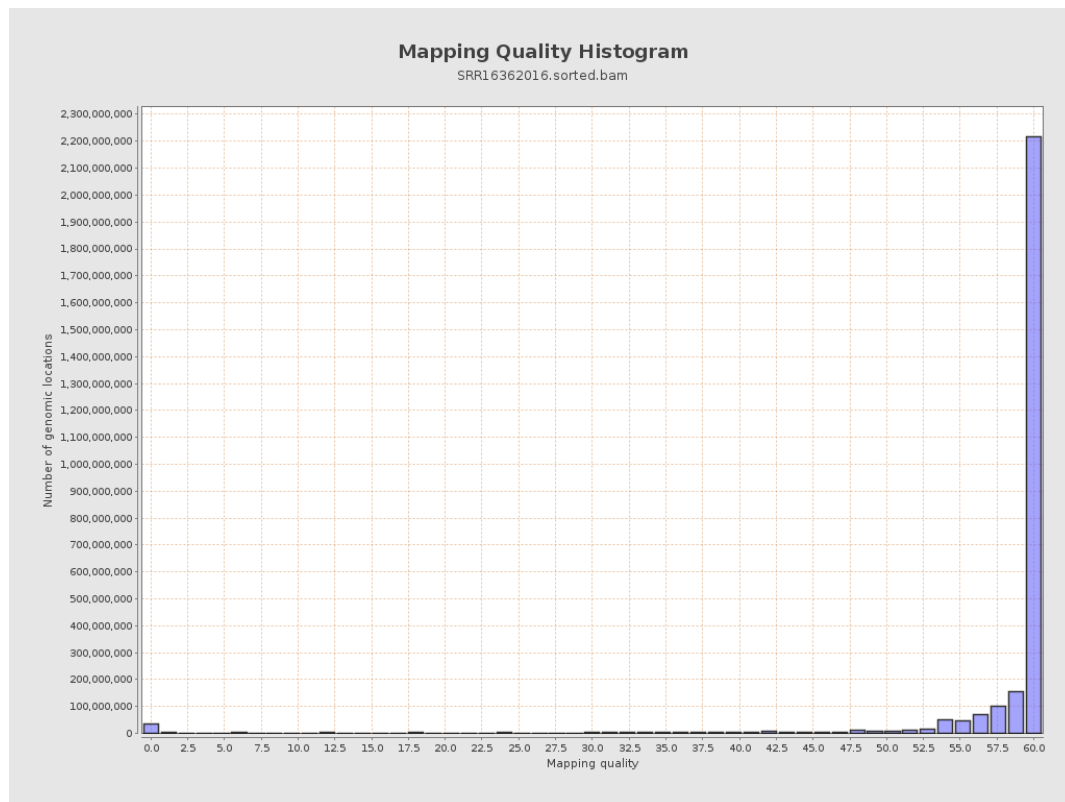


## 12. Results : Mapping Quality Across Reference

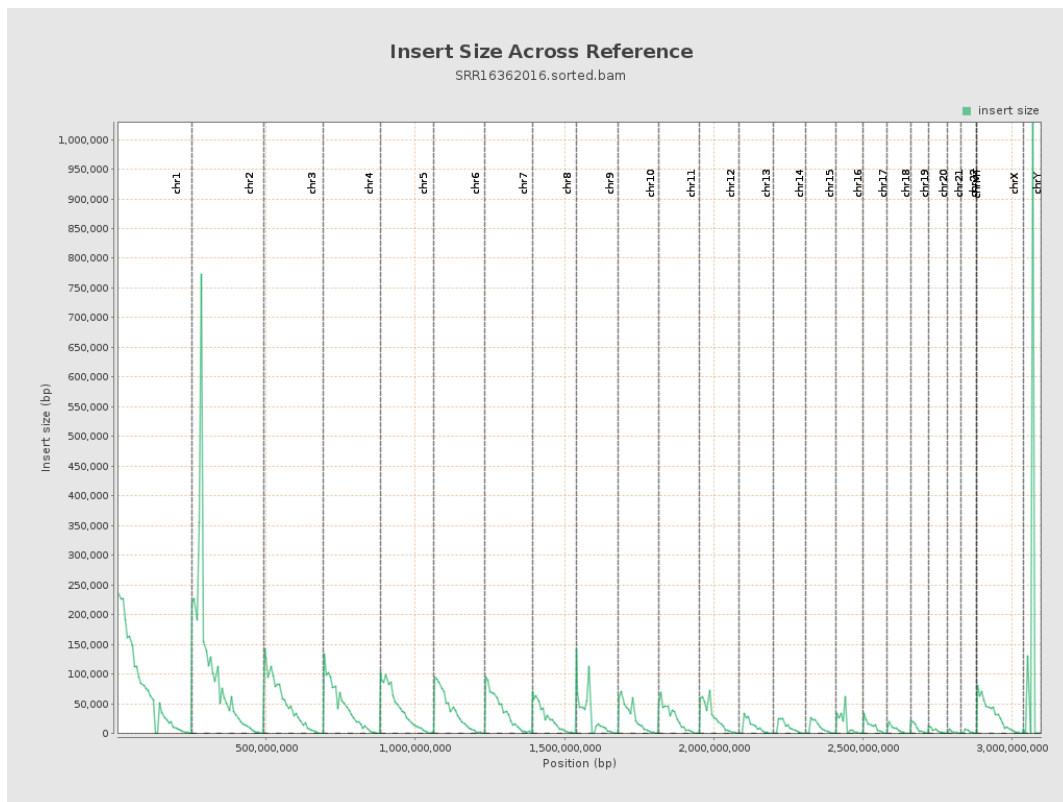




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

