

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/01 01:48:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
output/UF104/UF104_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3
```

1.2. Alignment

| | |
|---------------------------------------|---|
| Command line: | bwa samse -r @RG\tID:UF104\tSM:UF104\tLB:nan\ \tPL:ILLUMINA /data/stonelab/references/M_leprae_ TN/M_leprae_TN.fasta output/UF104/UF104-ancient.sai output/UF104/UF104- ancient.trimmed.fq |
| Draw chromosome limits: | no |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Mar 01 01:48:56 MST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | output/UF104/UF104_f4_q37_sortc_ markdup.rescaled.bam |

2. Summary

2.1. Globals

| | |
|------------------------------|-----------------|
| Reference size | 3,268,203 |
| Number of reads | 213 |
| Mapped reads | 213 / 100% |
| Unmapped reads | 0 / 0% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Read min/max/mean length | 30 / 97 / 46.38 |
| Duplicated reads (estimated) | 33 / 15.49% |
| Duplication rate | 11.67% |
| Clipped reads | 0 / 0% |

2.2. ACGT Content

| | |
|--------------------------|----------------|
| Number/percentage of A's | 2,402 / 24.32% |
| Number/percentage of C's | 2,480 / 25.11% |
| Number/percentage of T's | 1,811 / 18.34% |
| Number/percentage of G's | 3,183 / 32.23% |
| Number/percentage of N's | 0 / 0% |
| GC Percentage | 57.34% |

2.3. Coverage

| | |
|--------------------|--------|
| Mean | 0.003 |
| Standard Deviation | 0.2212 |

2.4. Mapping Quality

| | |
|----------------------|------|
| Mean Mapping Quality | 1.85 |
|----------------------|------|

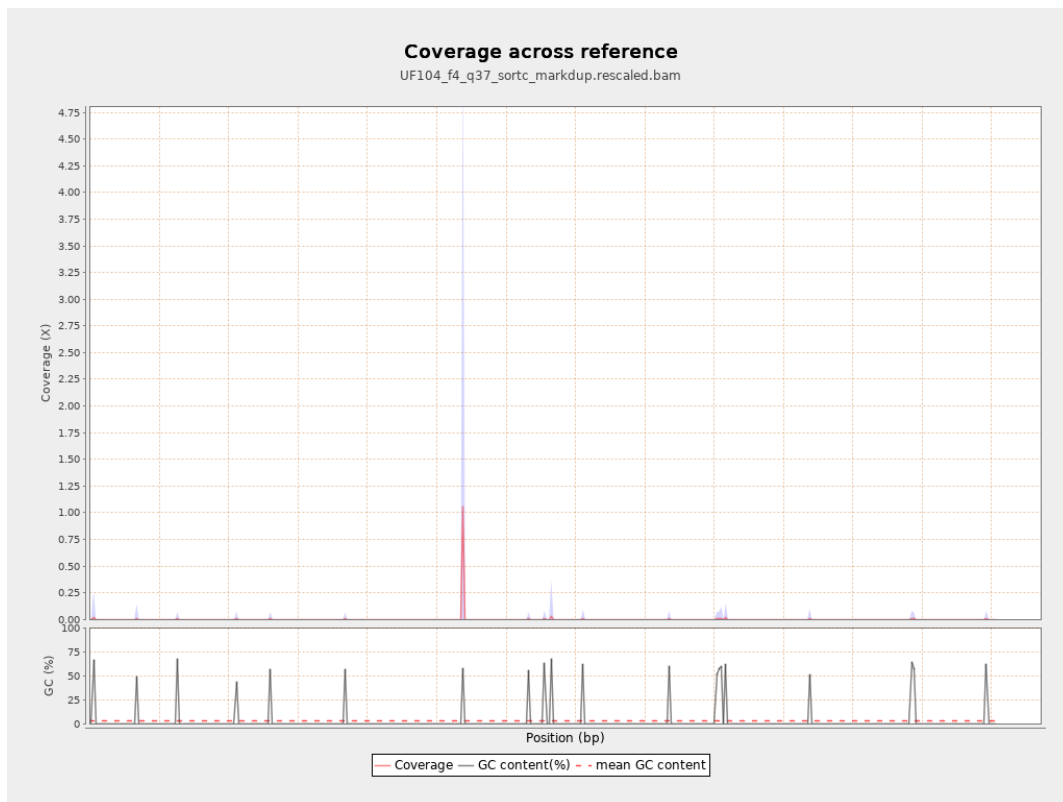
2.5. Mismatches and indels

| | |
|--|-------|
| General error rate | 4.63% |
| Mismatches | 455 |
| Insertions | 2 |
| Mapped reads with at least one insertion | 0.94% |
| Deletions | 3 |
| Mapped reads with at least one deletion | 1.41% |
| Homopolymer indels | 20% |

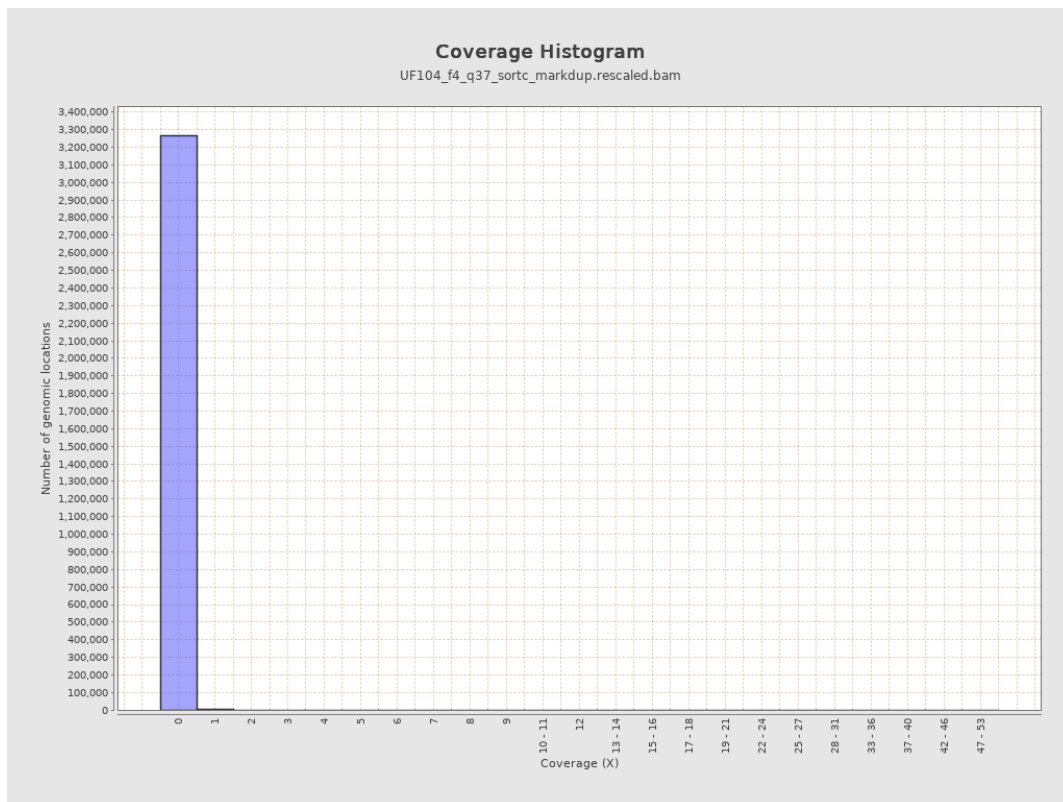
2.6. Chromosome stats

| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|-------------------------|---------|--------------|---------------|--------------------|
| ENA AL450380 AL450380.1 | 3268203 | 9879 | 0.003 | 0.2212 |

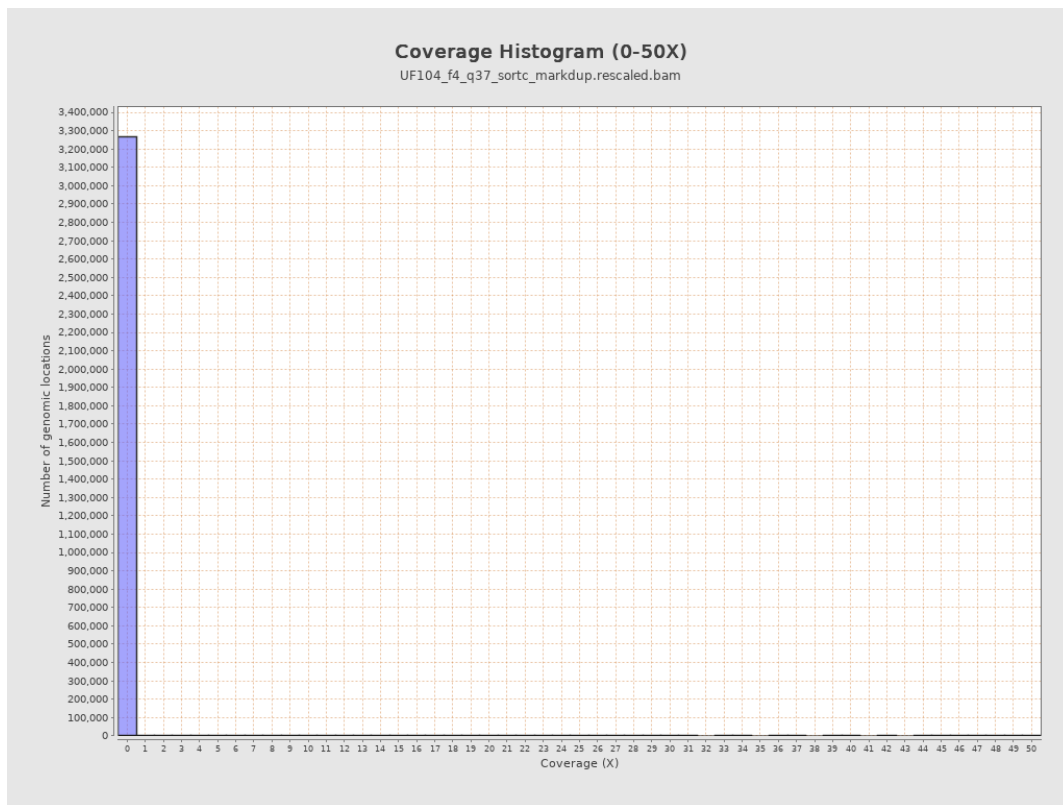
3. Results : Coverage across reference



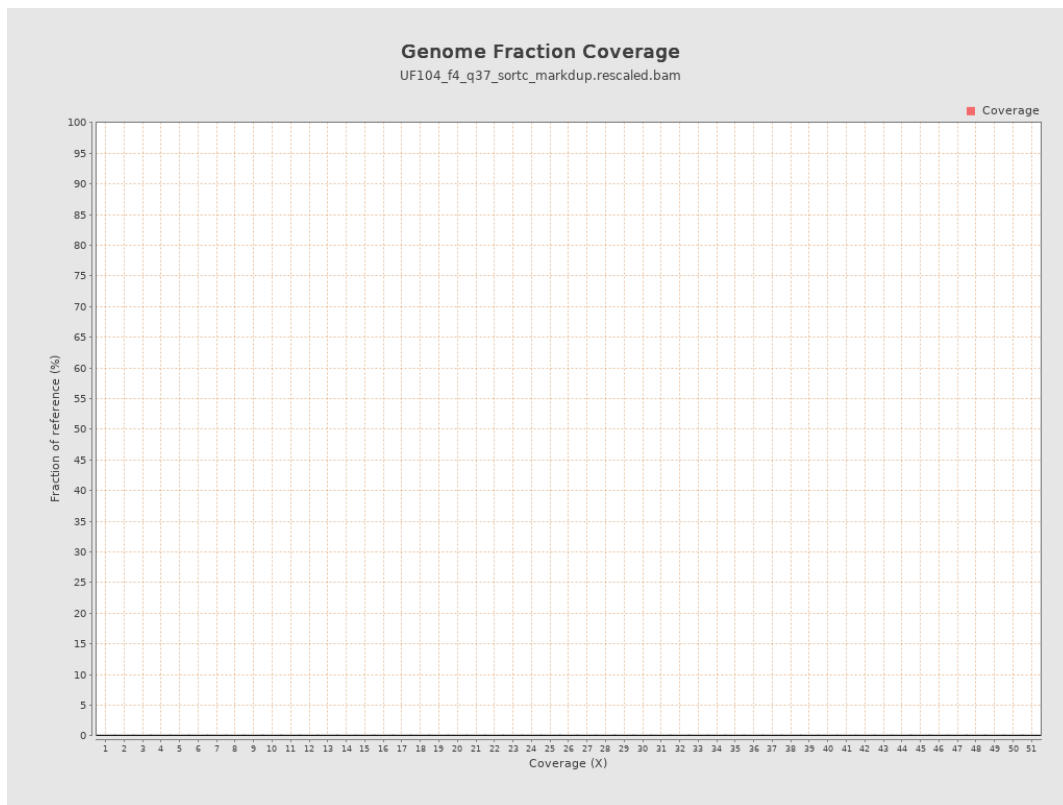
4. Results : Coverage Histogram



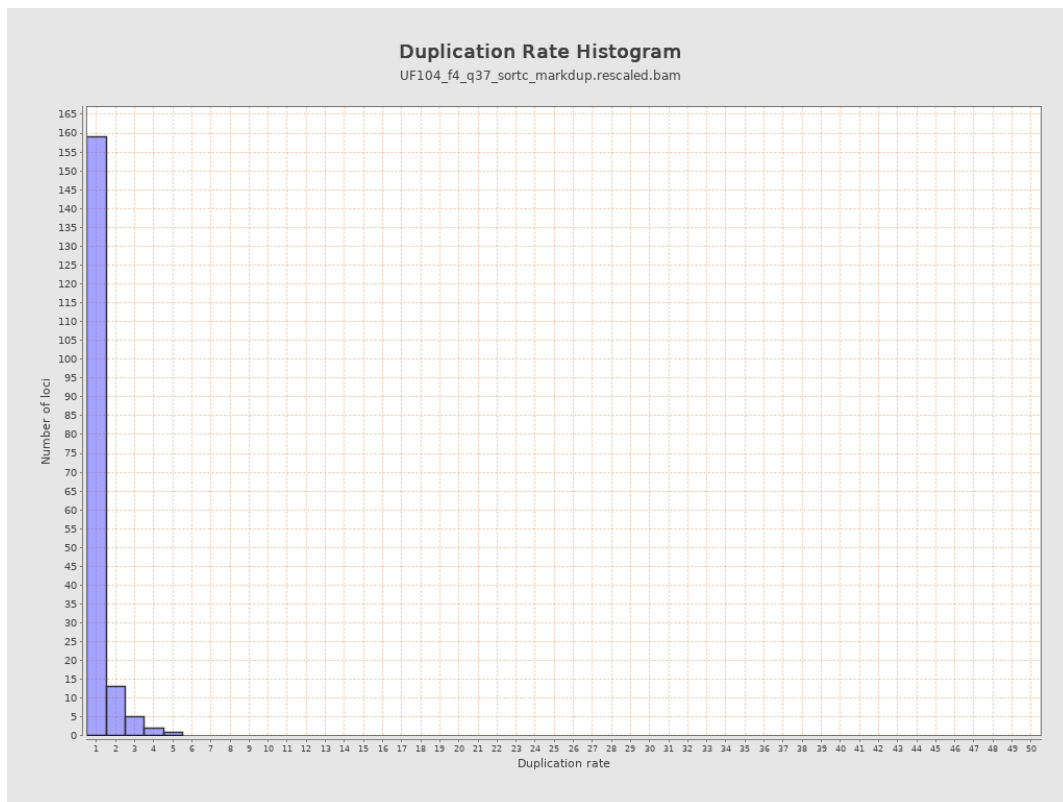
5. Results : Coverage Histogram (0-50X)



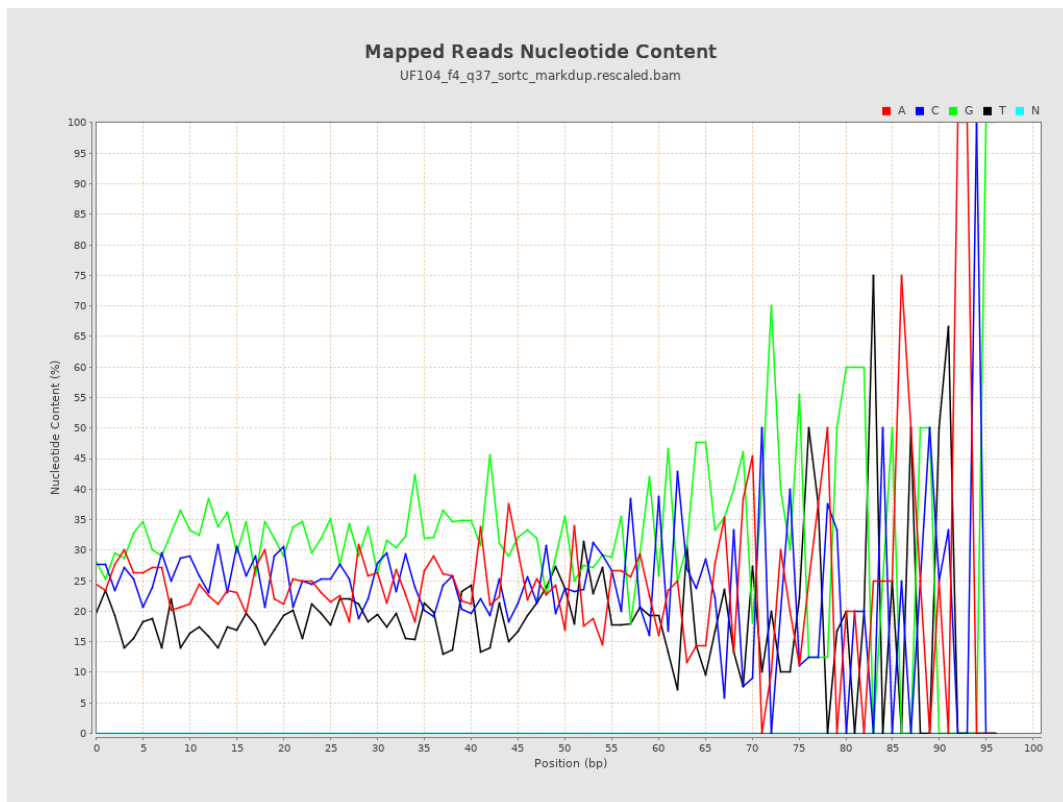
6. Results : Genome Fraction Coverage



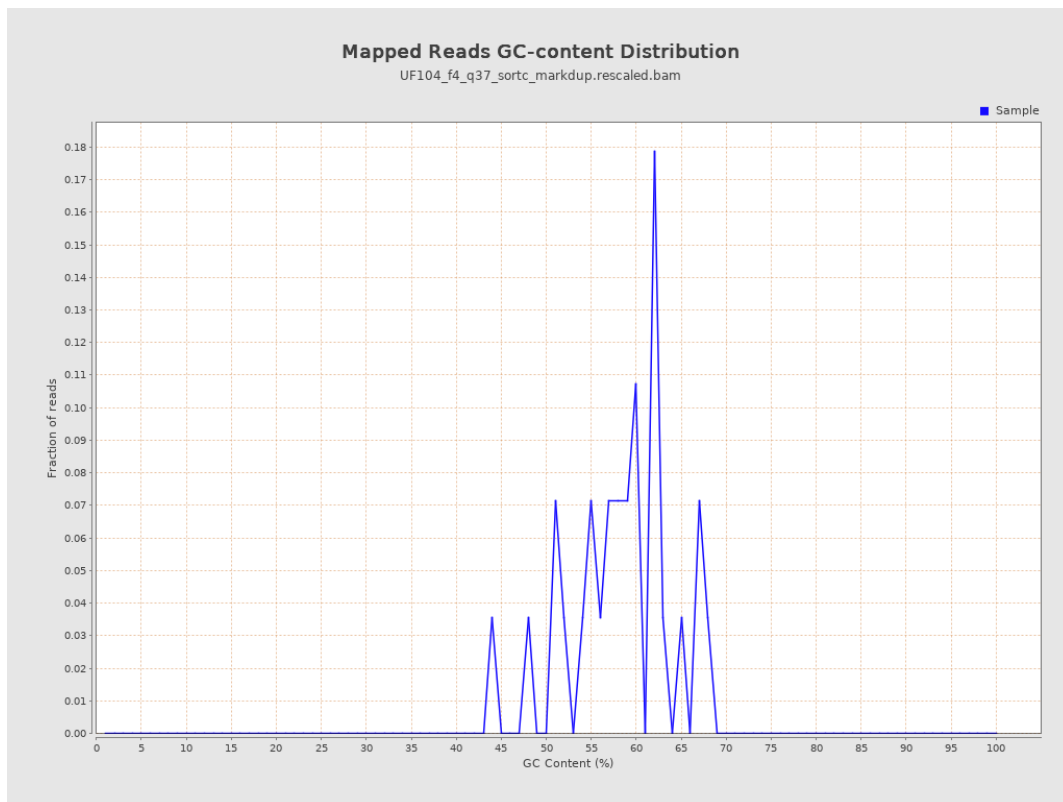
7. Results : Duplication Rate Histogram



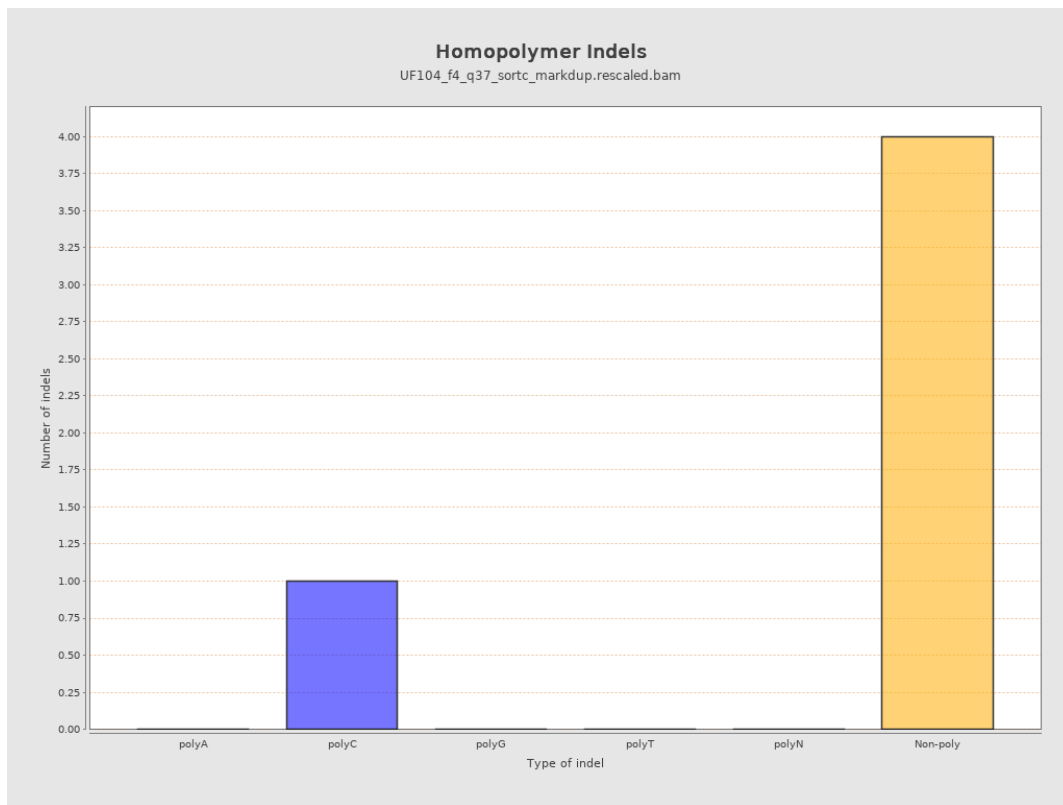
8. Results : Mapped Reads Nucleotide Content



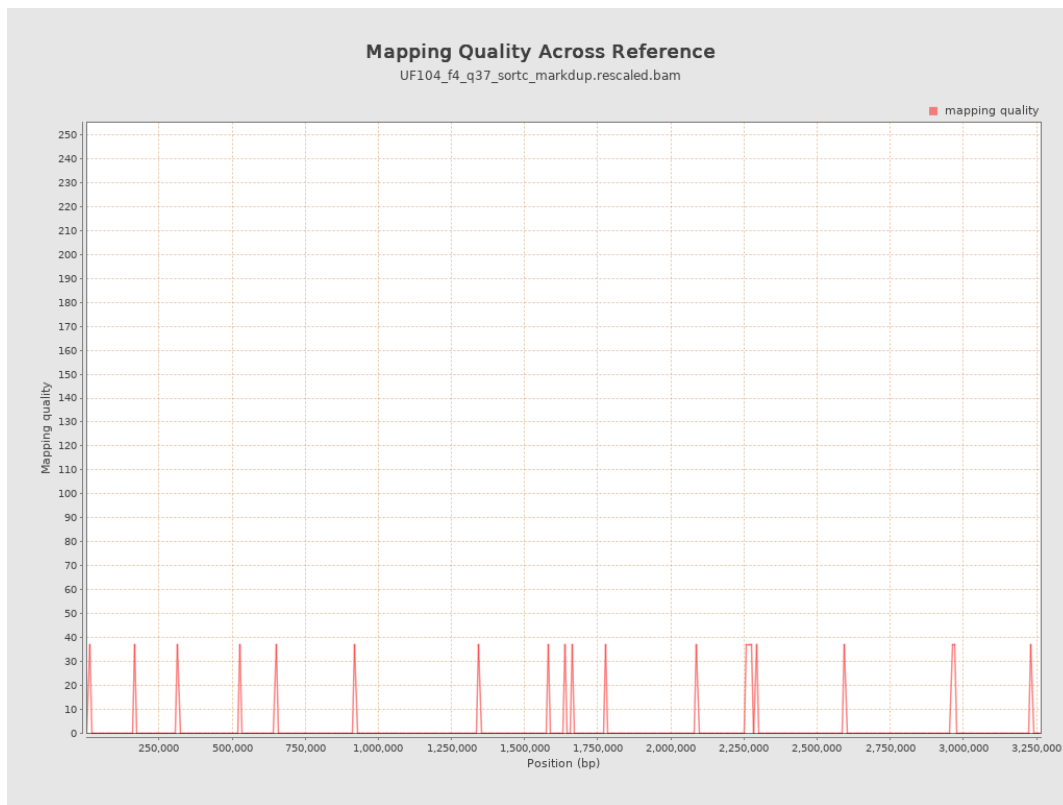
9. Results : Mapped Reads GC-content Distribution



10. Results : Homopolymer Indels



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

