

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/03/01 01:51:54*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
output/UF701/UF701_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3
```

## 1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF701\tSM:UF701\tLB:nan\ tPL:ILLUMINA /data/stonelab/references/M_leprae_ TN/M_leprae_TN.fasta output/UF701/UF701-ancient.sai output/UF701/UF701- ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 01 01:51:53 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF701/UF701_f4_q37_sortc_ markdup.rescaled.bam

## 2. Summary

### 2.1. Globals

Reference size	3,268,203
Number of reads	807
Mapped reads	807 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	30 / 127 / 48.95
Duplicated reads (estimated)	167 / 20.69%
Duplication rate	19.06%
Clipped reads	0 / 0%

### 2.2. ACGT Content

Number/percentage of A's	9,669 / 24.49%
Number/percentage of C's	9,769 / 24.74%
Number/percentage of T's	7,511 / 19.02%
Number/percentage of G's	12,539 / 31.75%
Number/percentage of N's	0 / 0%
GC Percentage	56.49%

### 2.3. Coverage

Mean	0.0121
Standard Deviation	0.5727

## 2.4. Mapping Quality

Mean Mapping Quality	6.29
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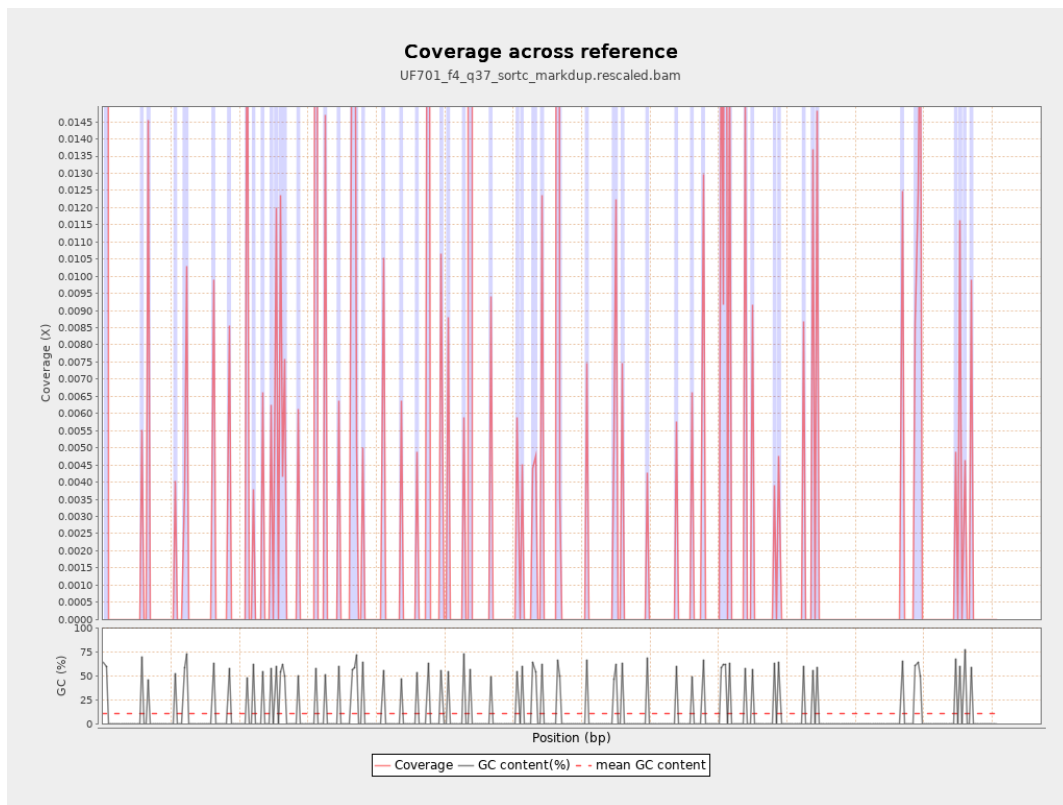
## 2.5. Mismatches and indels

General error rate	4.1%
Mismatches	1,605
Insertions	15
Mapped reads with at least one insertion	1.86%
Deletions	12
Mapped reads with at least one deletion	1.49%
Homopolymer indels	14.81%

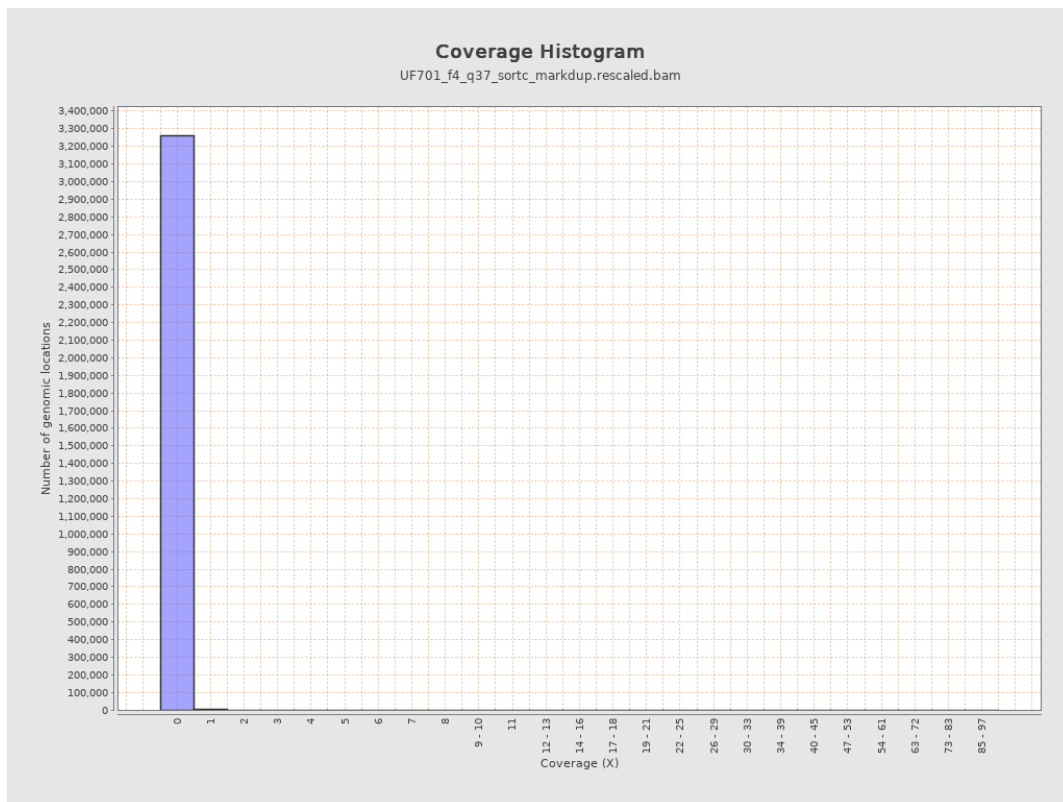
## 2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
ENA AL450380 AL450380.1	3268203	39500	0.0121	0.5727

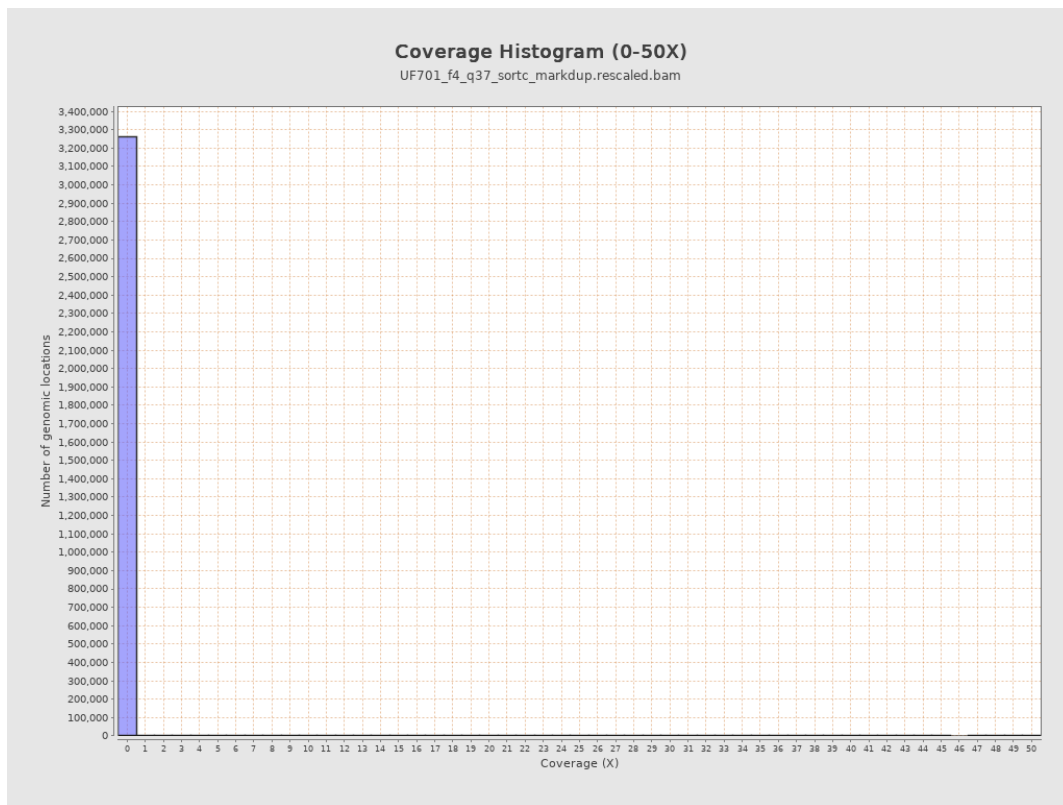
### 3. Results : Coverage across reference



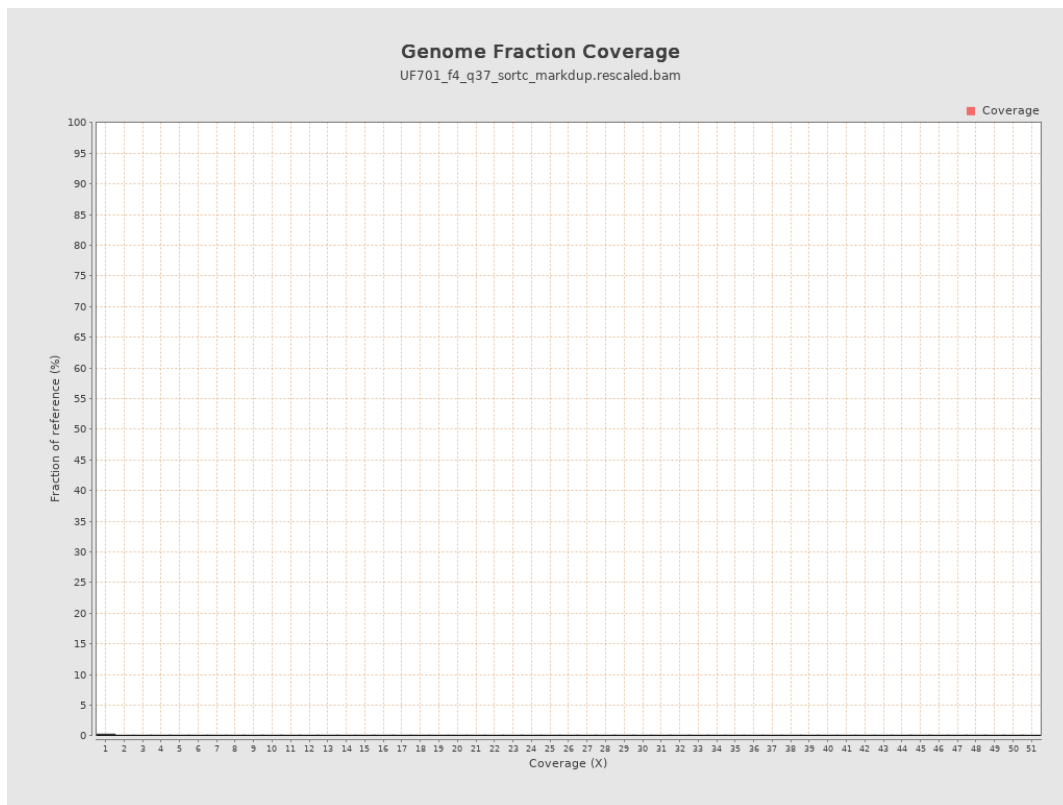
## 4. Results : Coverage Histogram



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

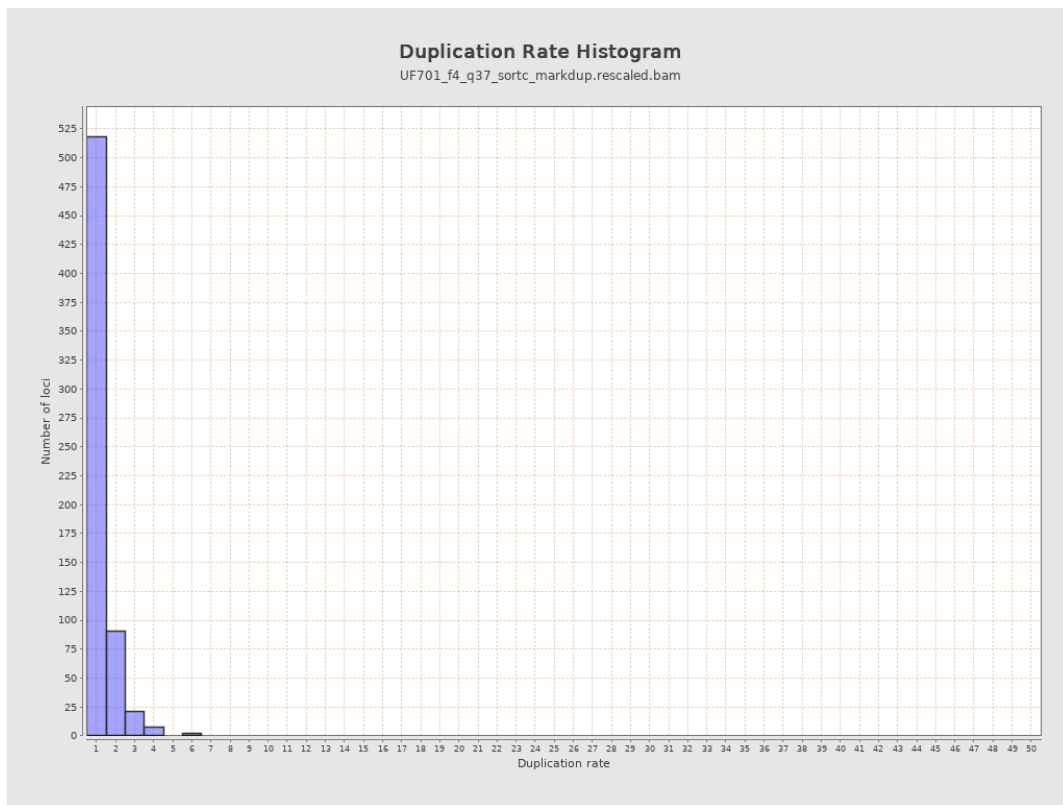


## 6. Results : Genome Fraction Coverage

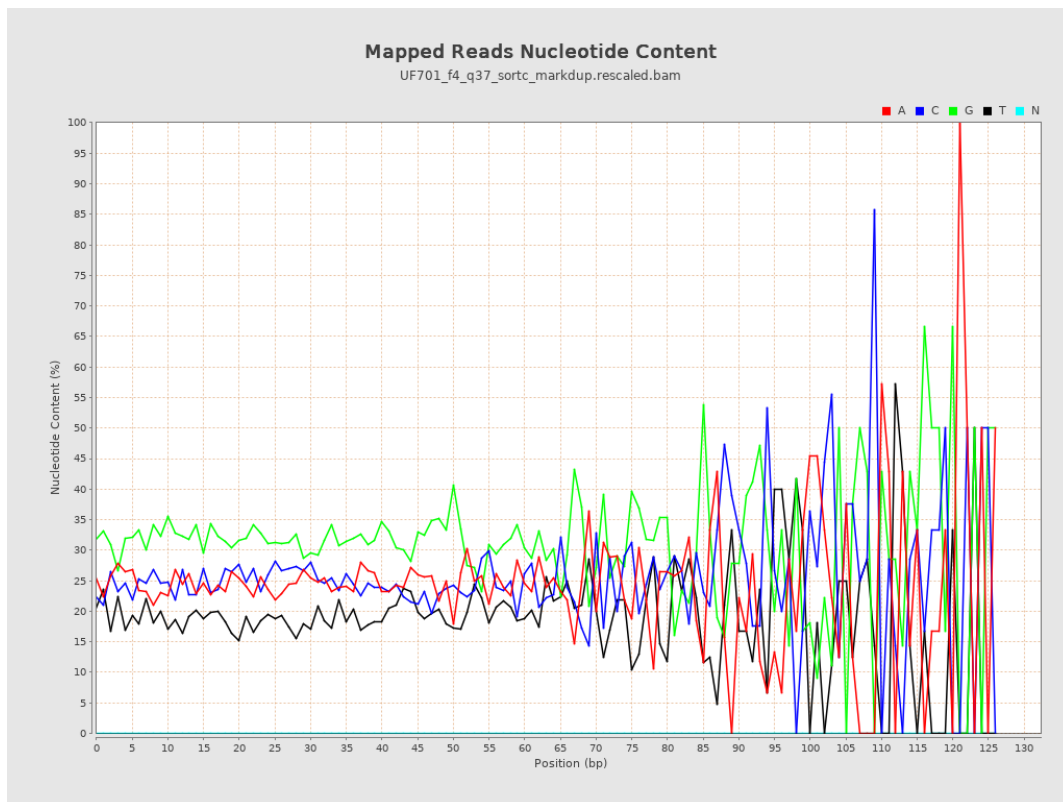




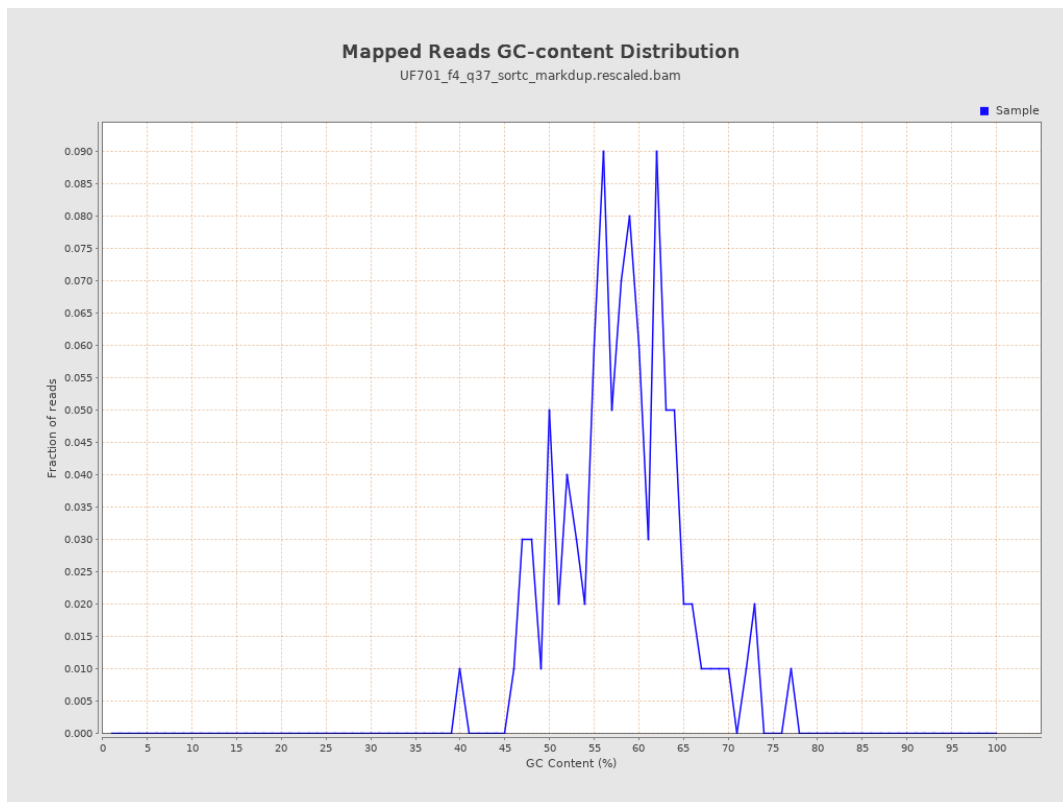
## 7. Results : Duplication Rate Histogram



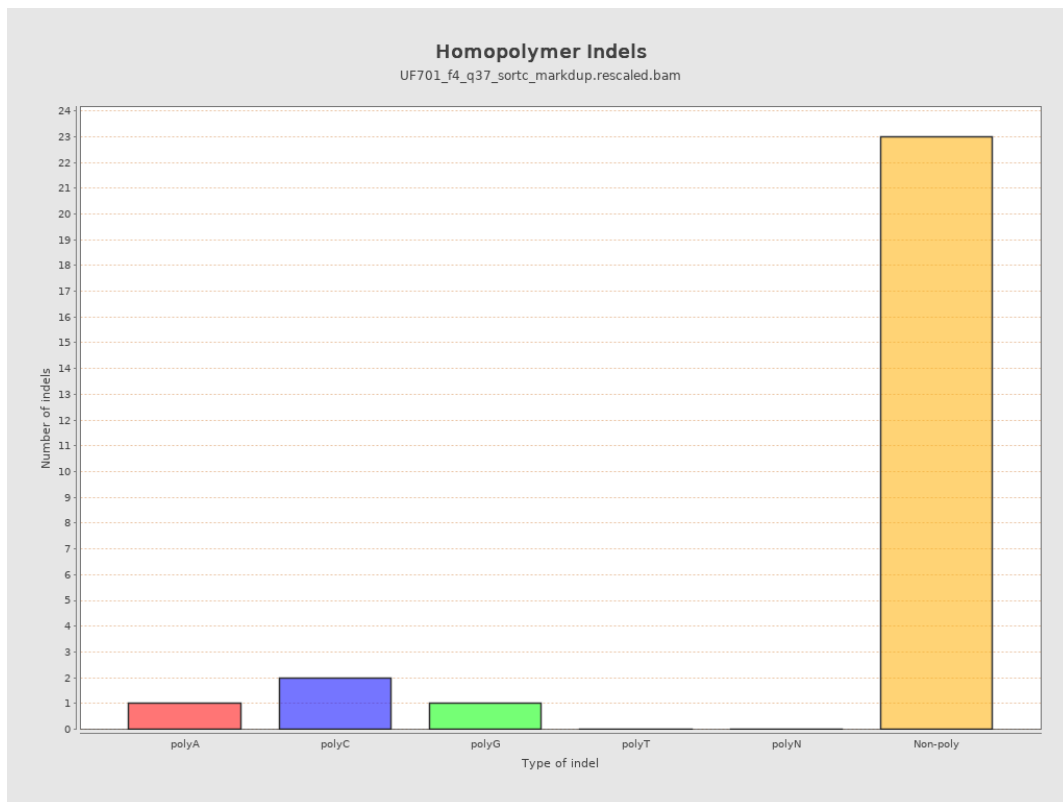
## 8. Results : Mapped Reads Nucleotide Content



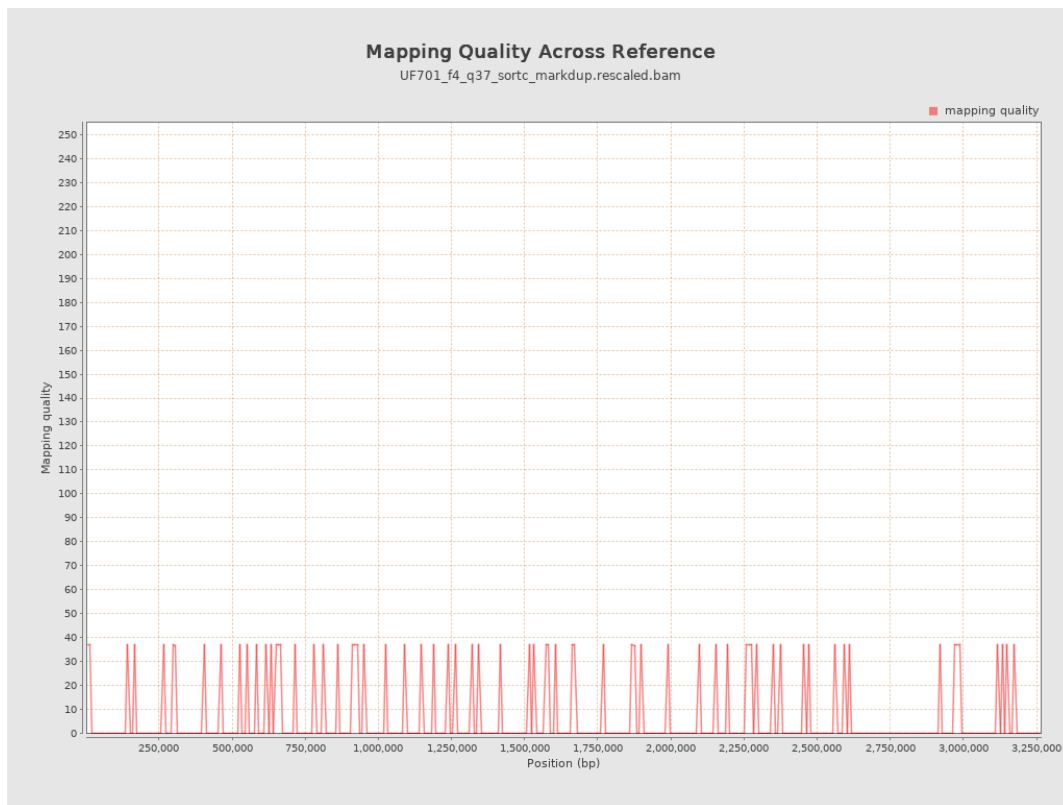
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Homopolymer Indels



# 11. Results : Mapping Quality Across Reference



## 12. Results : Mapping Quality Histogram

