

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/03/01 01:50:03*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
output/UF702/UF702_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3
```

## 1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF702\tSM:UF702\tLB:nan\ tPL:ILLUMINA /data/stonelab/references/M_leprae_ TN/M_leprae_TN.fasta output/UF702/UF702-ancient.sai output/UF702/UF702- ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 01 01:50:02 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF702/UF702_f4_q37_sortc_ markdup.rescaled.bam

## 2. Summary

### 2.1. Globals

Reference size	3,268,203
Number of reads	849
Mapped reads	849 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	30 / 126 / 47.53
Duplicated reads (estimated)	189 / 22.26%
Duplication rate	22.27%
Clipped reads	0 / 0%

### 2.2. ACGT Content

Number/percentage of A's	9,774 / 24.23%
Number/percentage of C's	9,619 / 23.85%
Number/percentage of T's	7,951 / 19.71%
Number/percentage of G's	12,990 / 32.21%
Number/percentage of N's	0 / 0%
GC Percentage	56.05%

### 2.3. Coverage

Mean	0.0123
Standard Deviation	0.5821

## 2.4. Mapping Quality

Mean Mapping Quality	4.9
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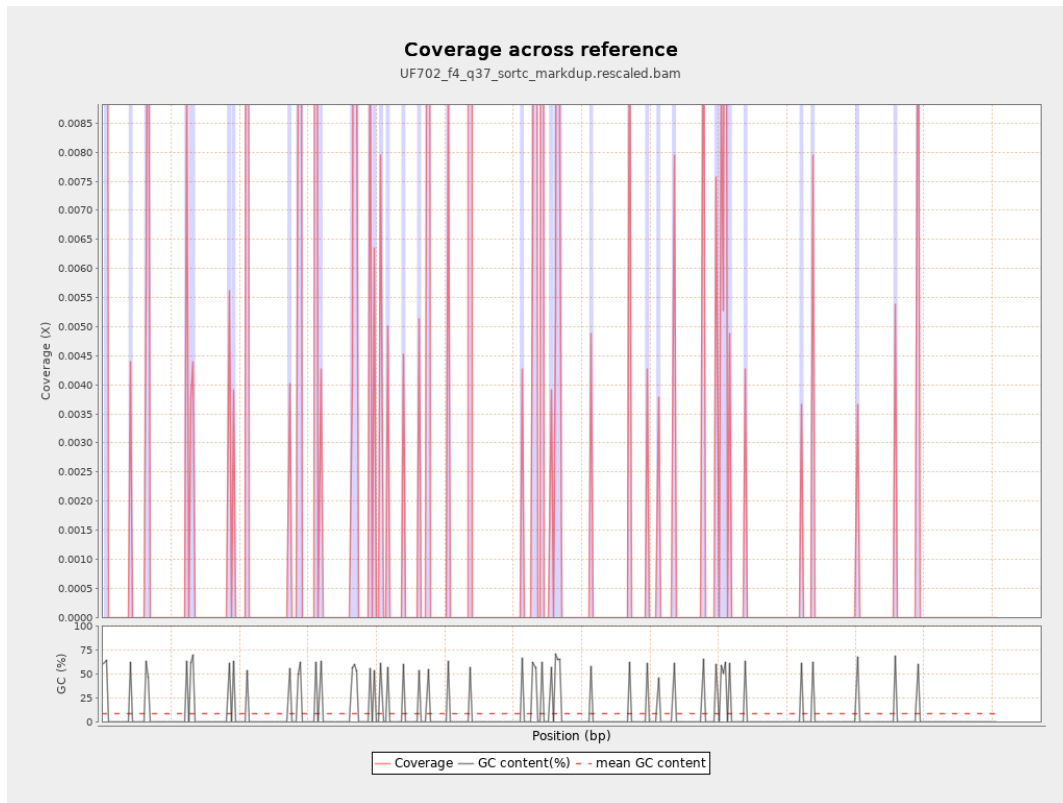
## 2.5. Mismatches and indels

General error rate	4.39%
Mismatches	1,755
Insertions	16
Mapped reads with at least one insertion	1.88%
Deletions	20
Mapped reads with at least one deletion	2.36%
Homopolymer indels	16.67%

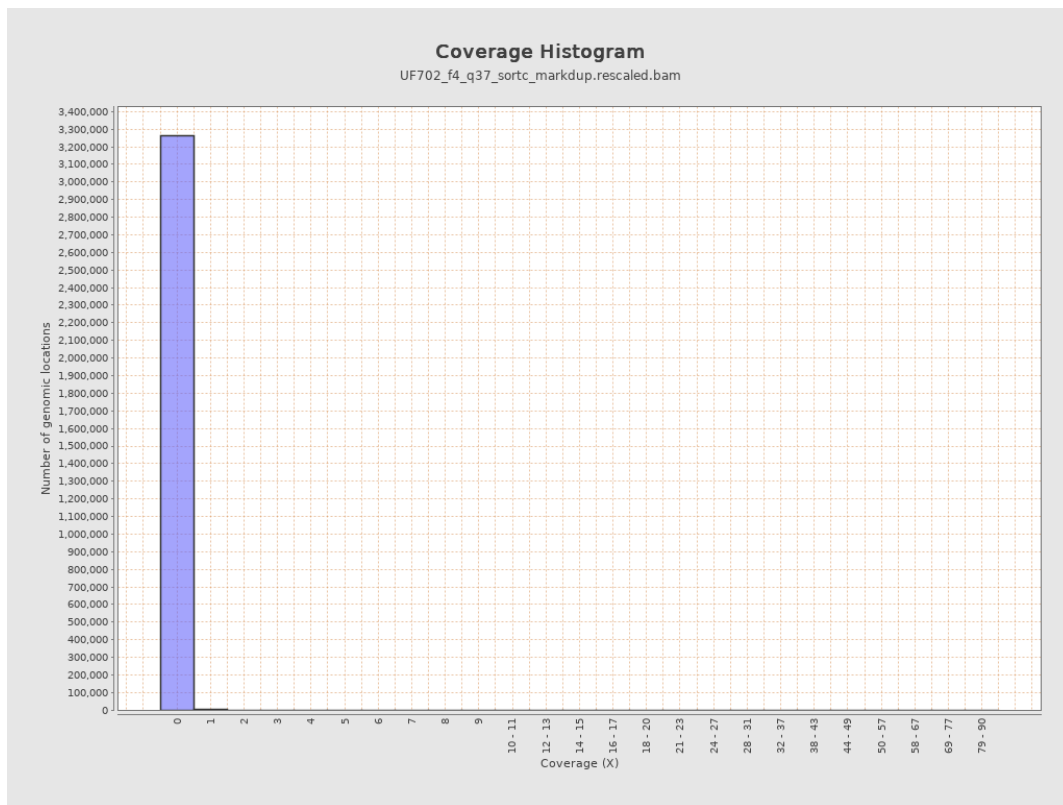
## 2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
ENA AL450380 AL450380.1	3268203	40354	0.0123	0.5821

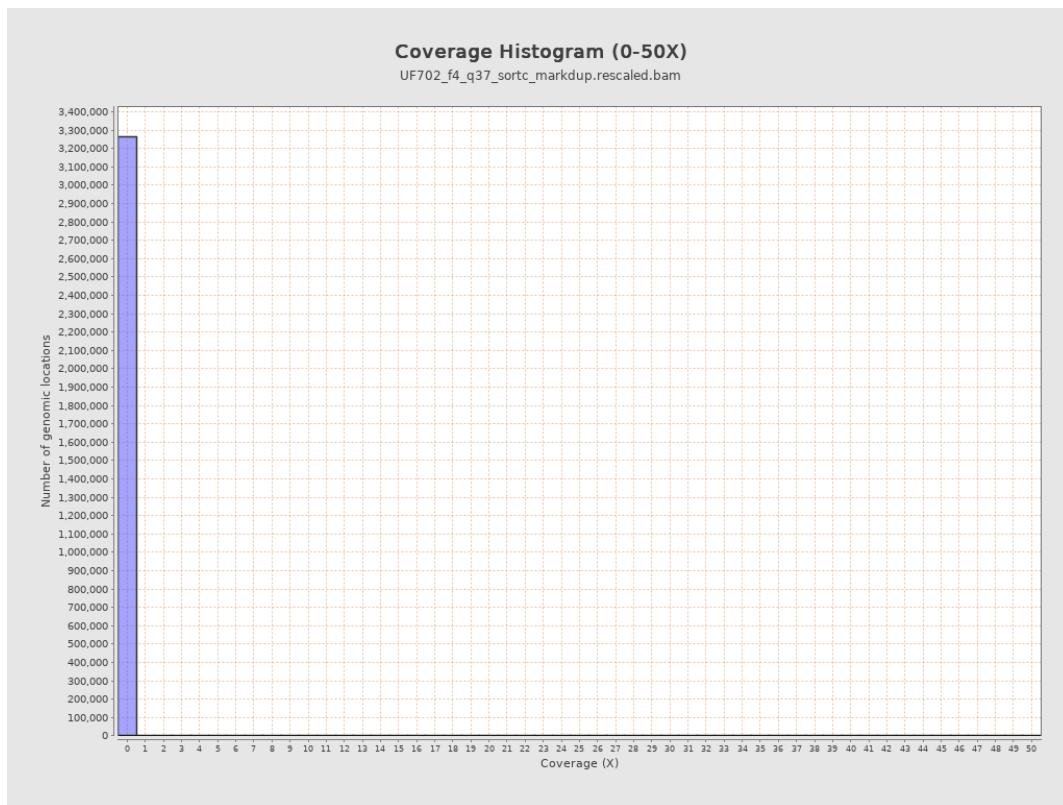
### 3. Results : Coverage across reference



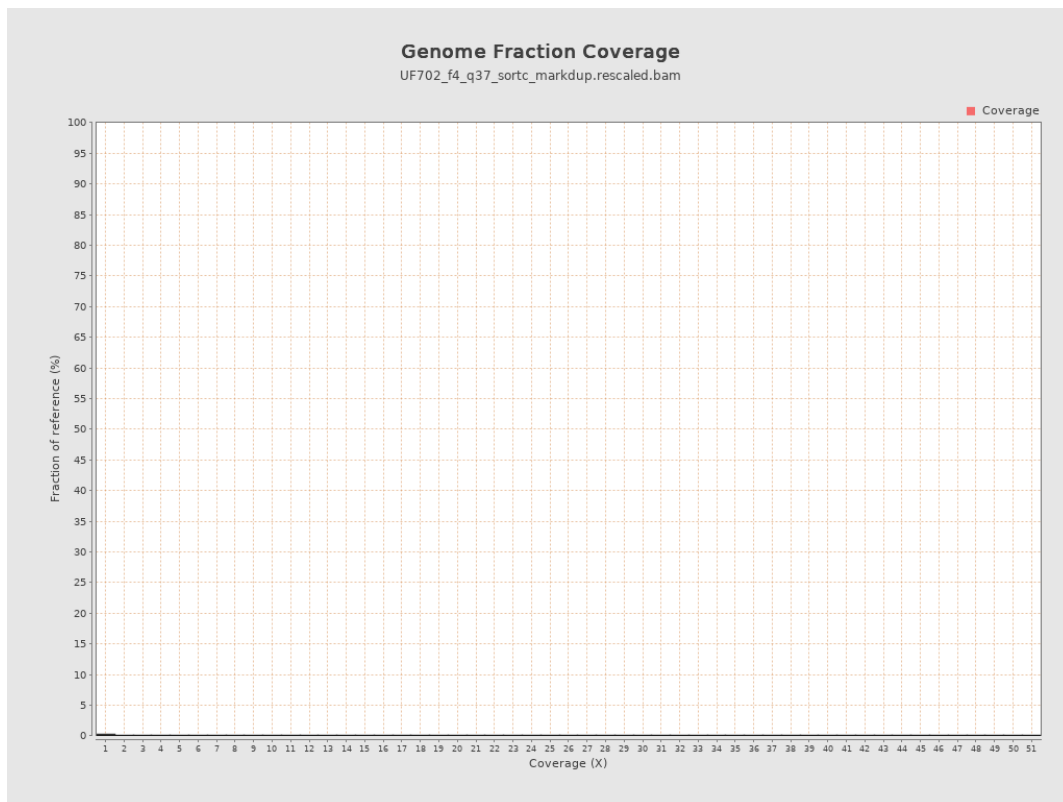
## 4. Results : Coverage Histogram



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

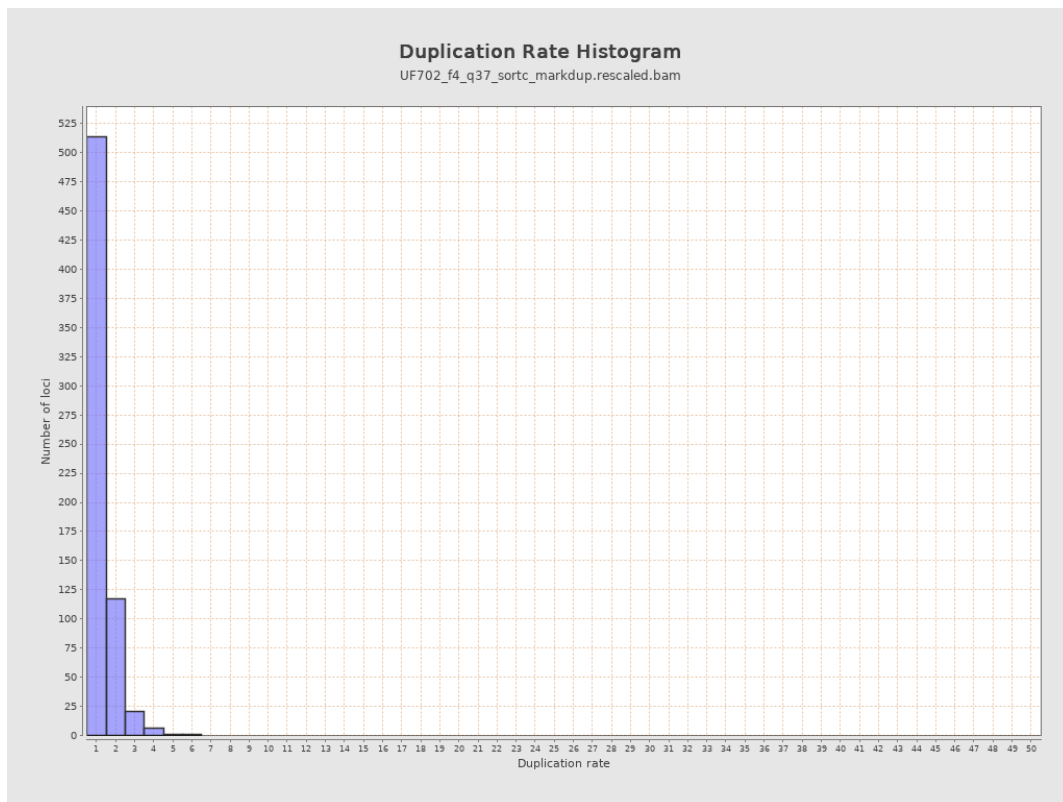


## 6. Results : Genome Fraction Coverage

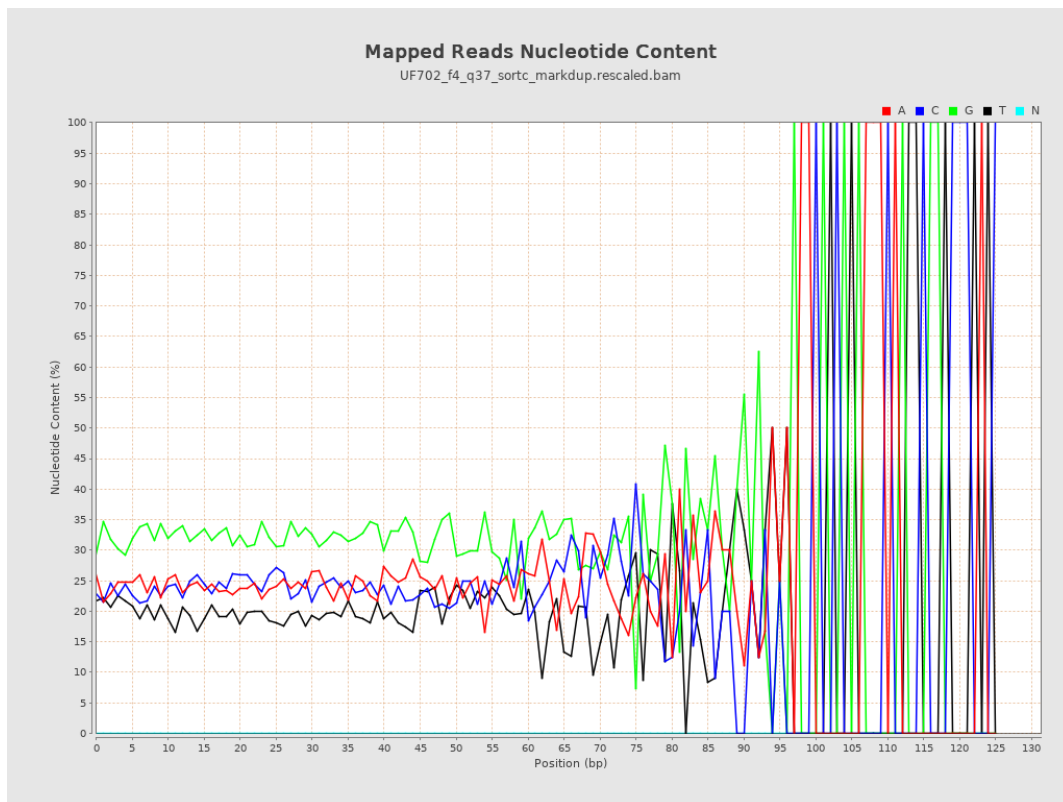




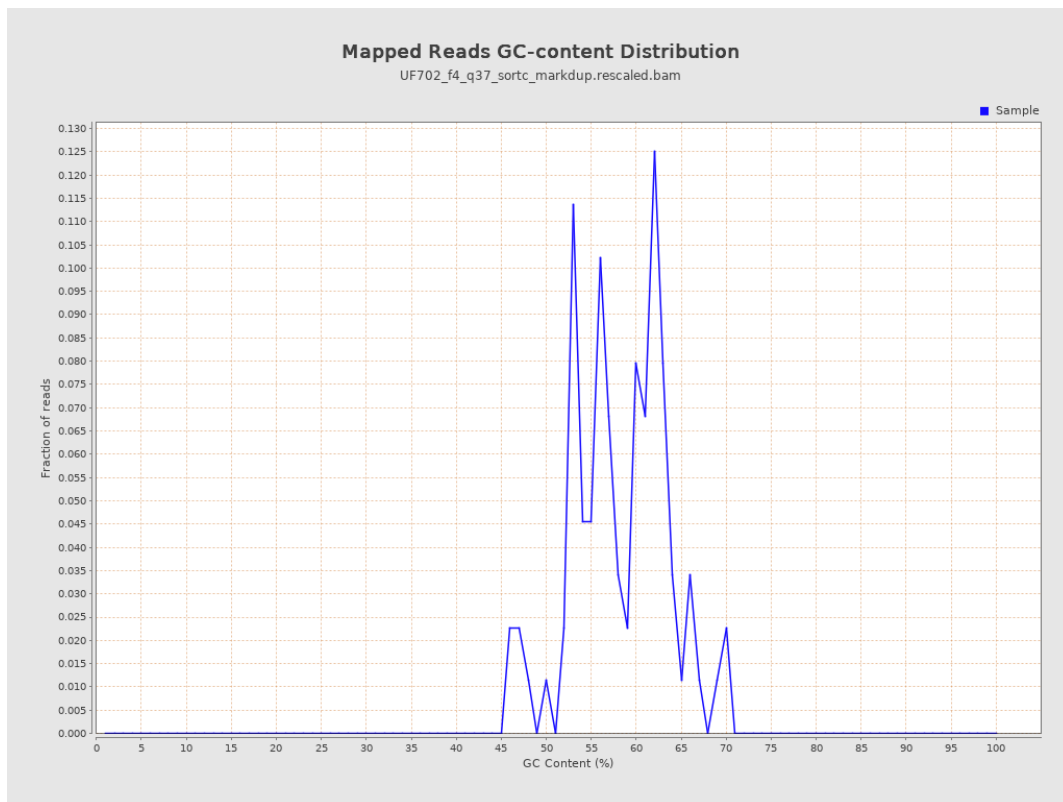
## 7. Results : Duplication Rate Histogram



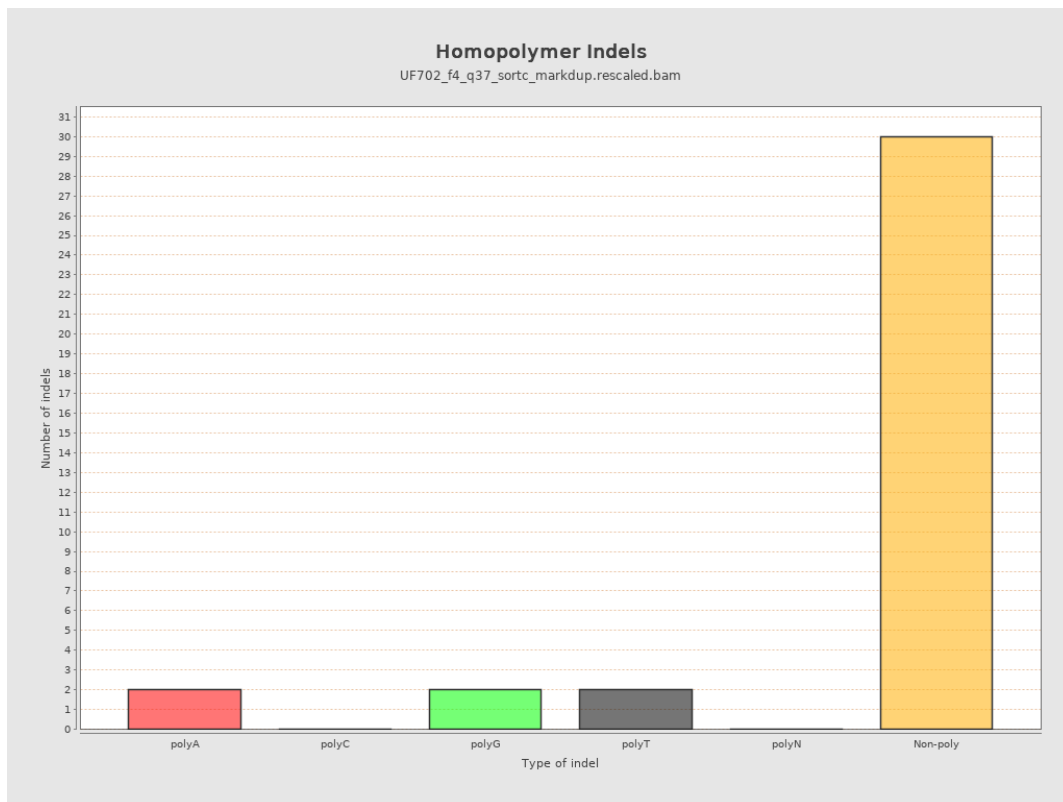
## 8. Results : Mapped Reads Nucleotide Content



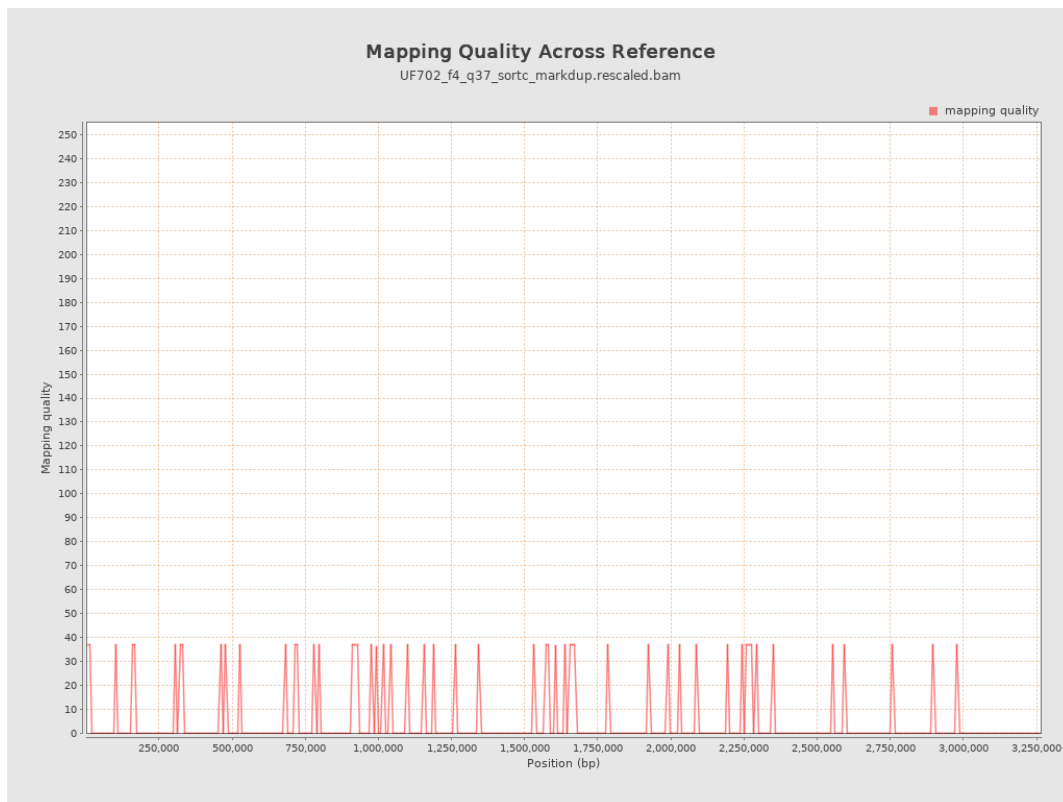
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Homopolymer Indels



## 11. Results : Mapping Quality Across Reference



## 12. Results : Mapping Quality Histogram

