

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/03/02 02:57:24*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
output/UF18/UF18_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3
```

## 1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF18\tSM:UF18\tLB:nan\tP L:ILLUMINA /data/stonelab/references/Human_mit ochondrial/NC_012920.1.fasta output/UF18/UF18-ancient.sai output/UF18/UF18- ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 02 02:57:24 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF18/UF18_f4_q37_sortc_ma rkdup.rescaled.bam

## 2. Summary

### 2.1. Globals

Reference size	16,569
Number of reads	24
Mapped reads	24 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	36 / 122 / 66.29
Duplicated reads (estimated)	1 / 4.17%
Duplication rate	4.35%
Clipped reads	0 / 0%

### 2.2. ACGT Content

Number/percentage of A's	511 / 32.14%
Number/percentage of C's	514 / 32.33%
Number/percentage of T's	375 / 23.58%
Number/percentage of G's	190 / 11.95%
Number/percentage of N's	0 / 0%
GC Percentage	44.28%

### 2.3. Coverage

Mean	0.096
Standard Deviation	0.322

## 2.4. Mapping Quality

Mean Mapping Quality	5.18
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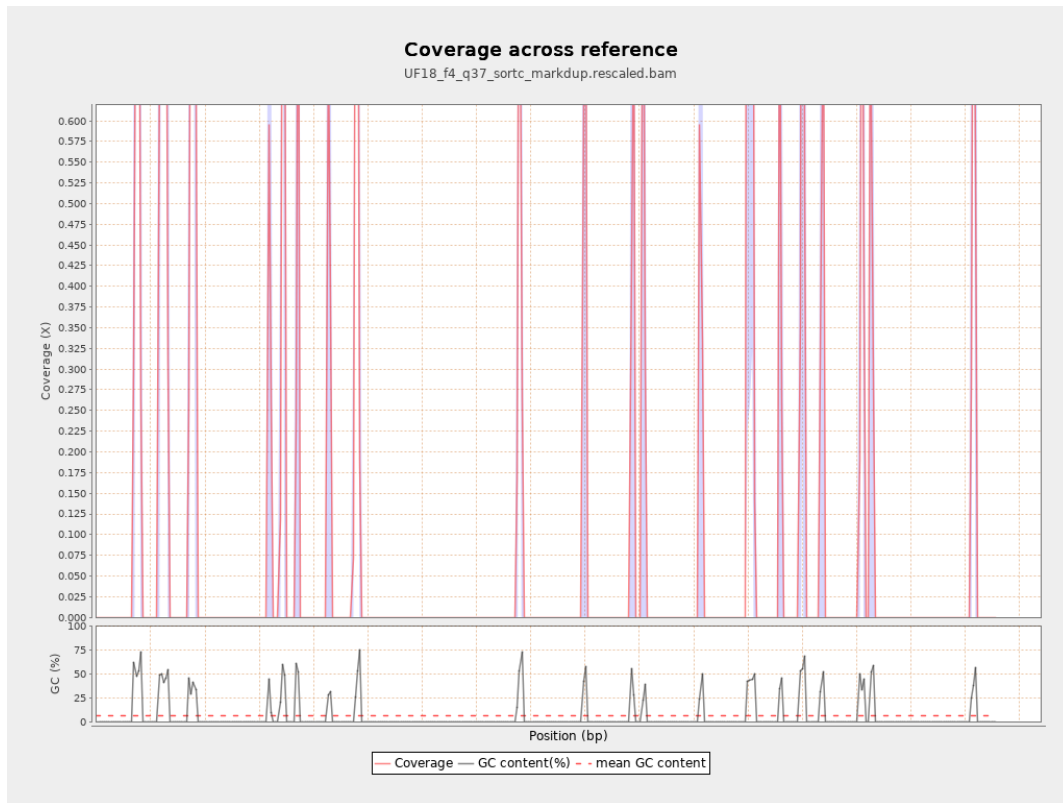
## 2.5. Mismatches and indels

General error rate	1.32%
Mismatches	20
Insertions	1
Mapped reads with at least one insertion	4.17%
Deletions	0
Mapped reads with at least one deletion	0%
Homopolymer indels	0%

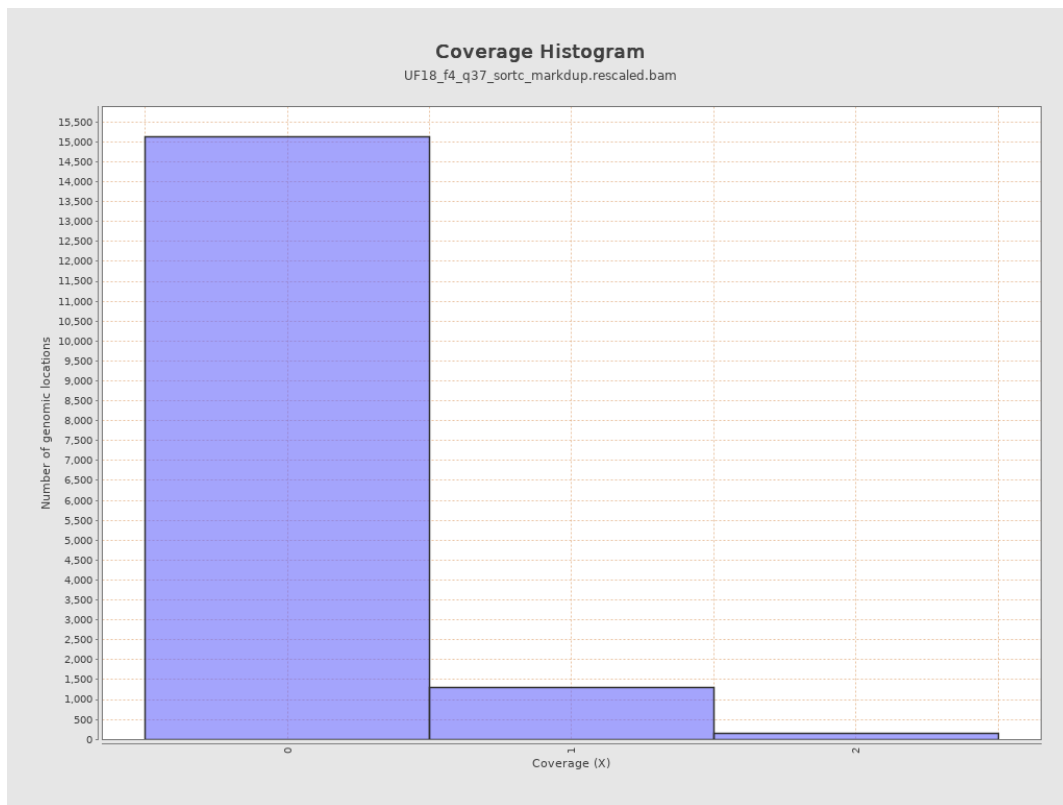
## 2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
NC_012920.1	16569	1590	0.096	0.322

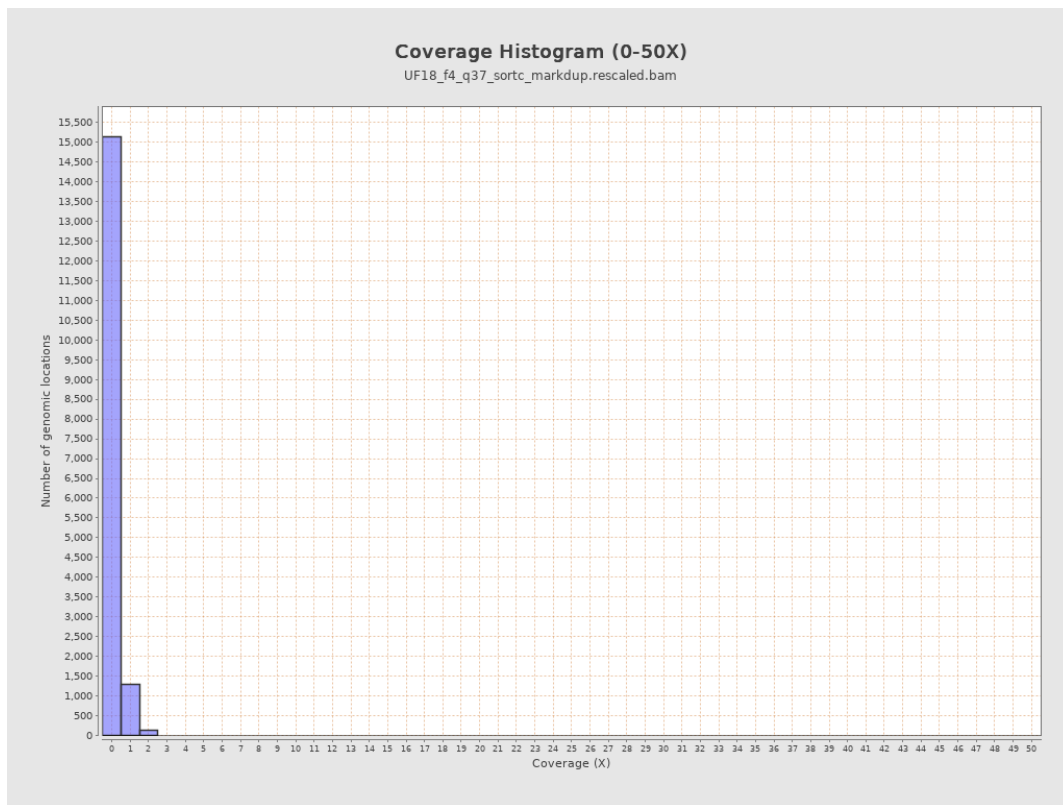
### 3. Results : Coverage across reference



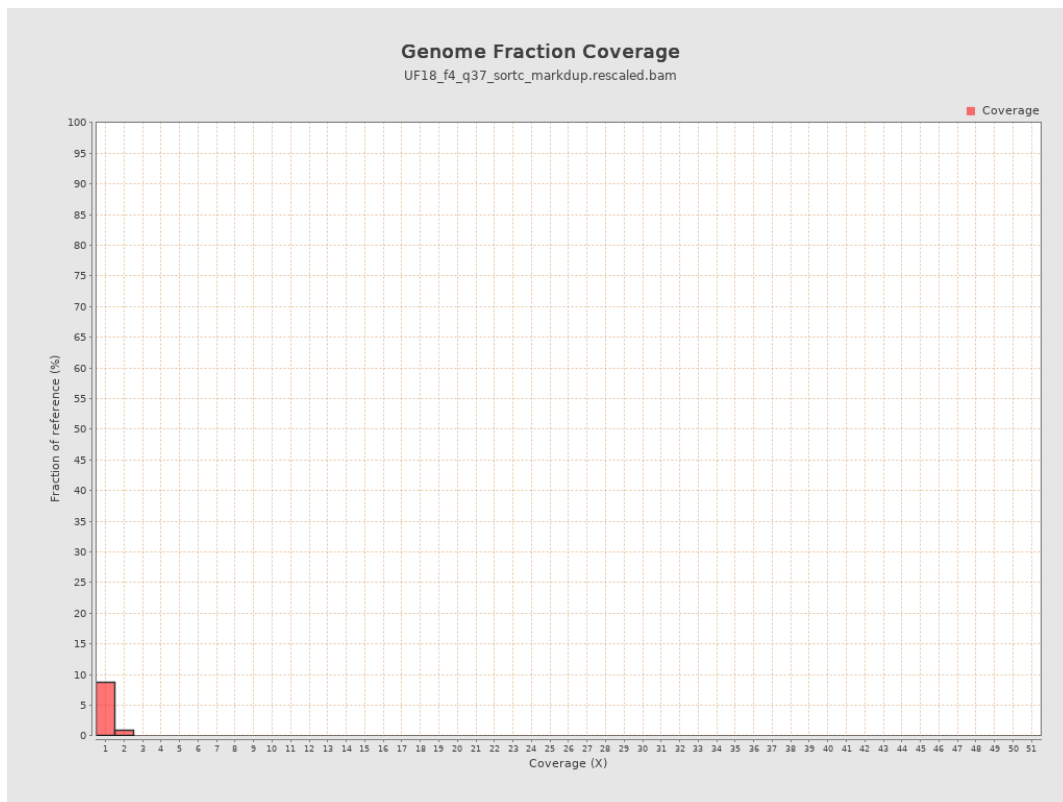
## 4. Results : Coverage Histogram



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

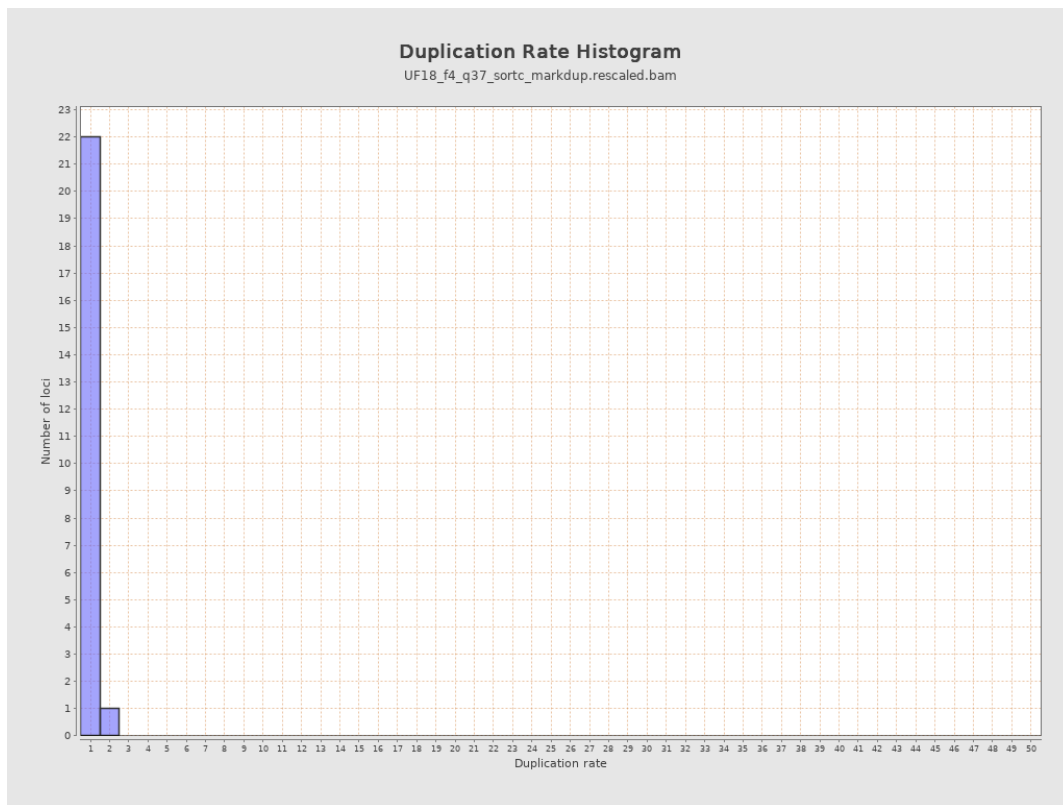


## 6. Results : Genome Fraction Coverage

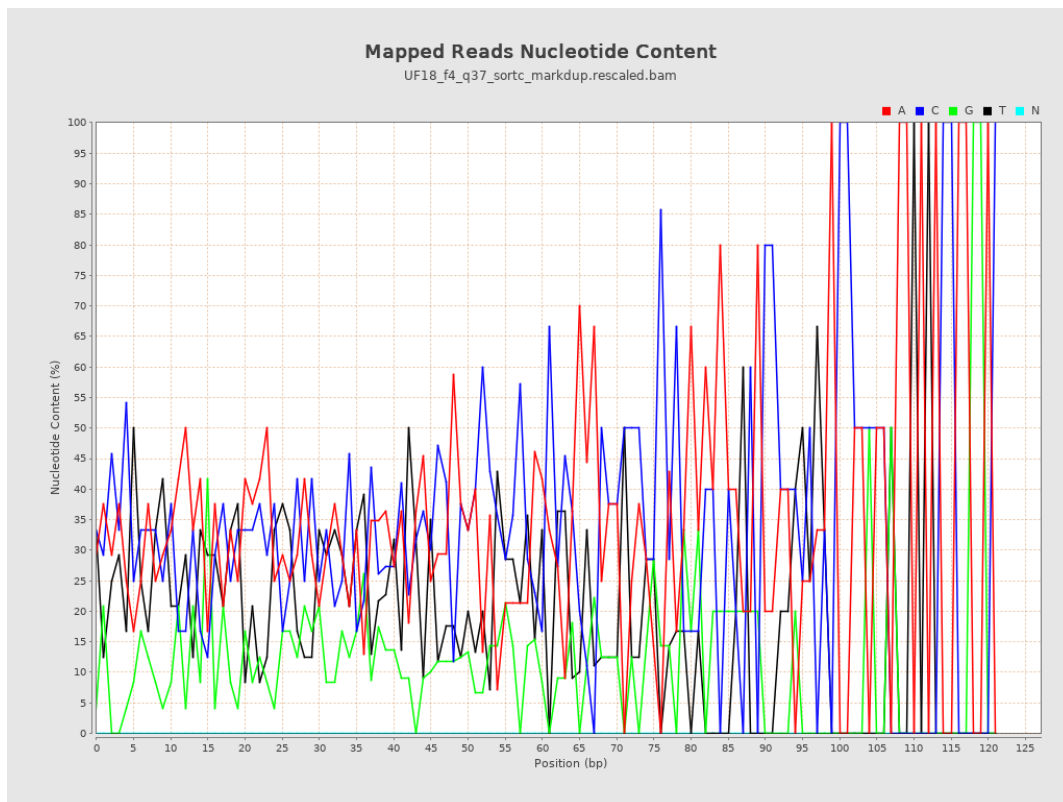




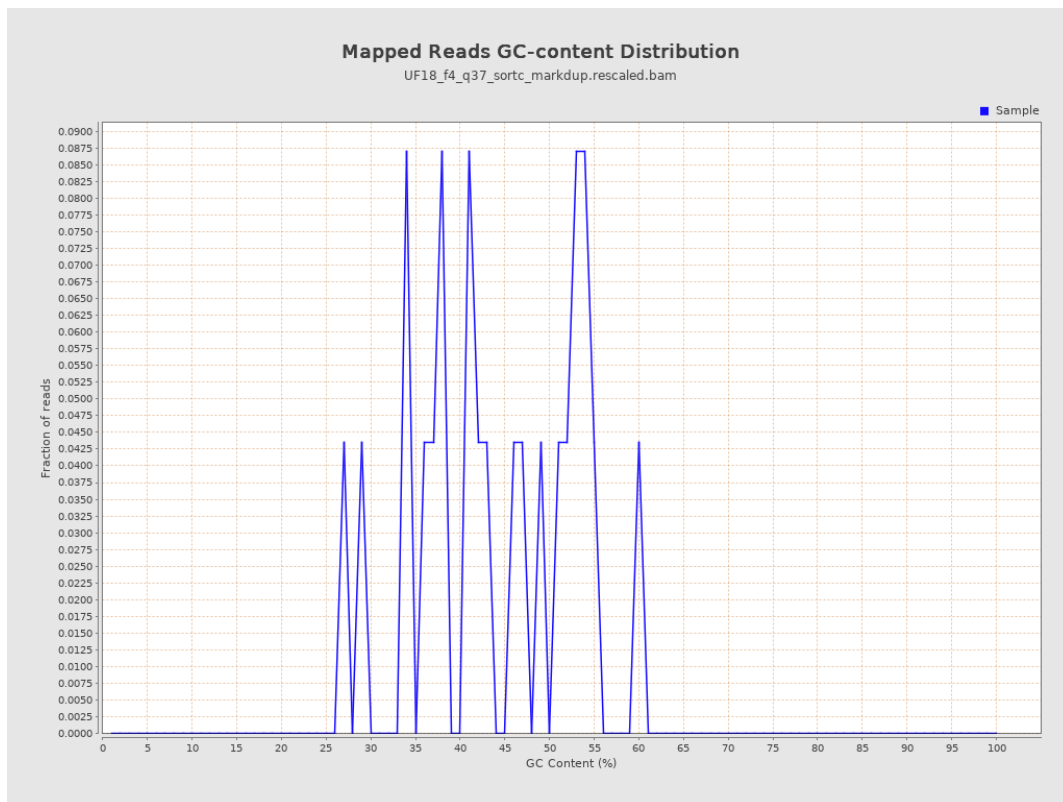
## 7. Results : Duplication Rate Histogram



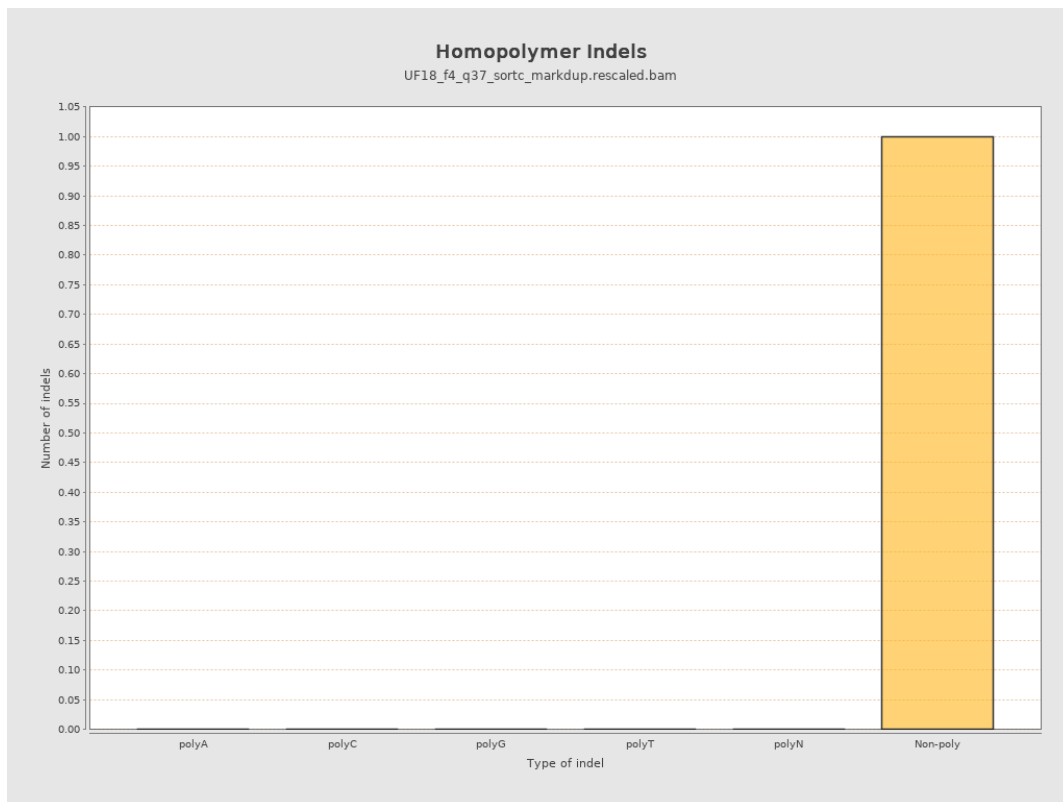
## 8. Results : Mapped Reads Nucleotide Content



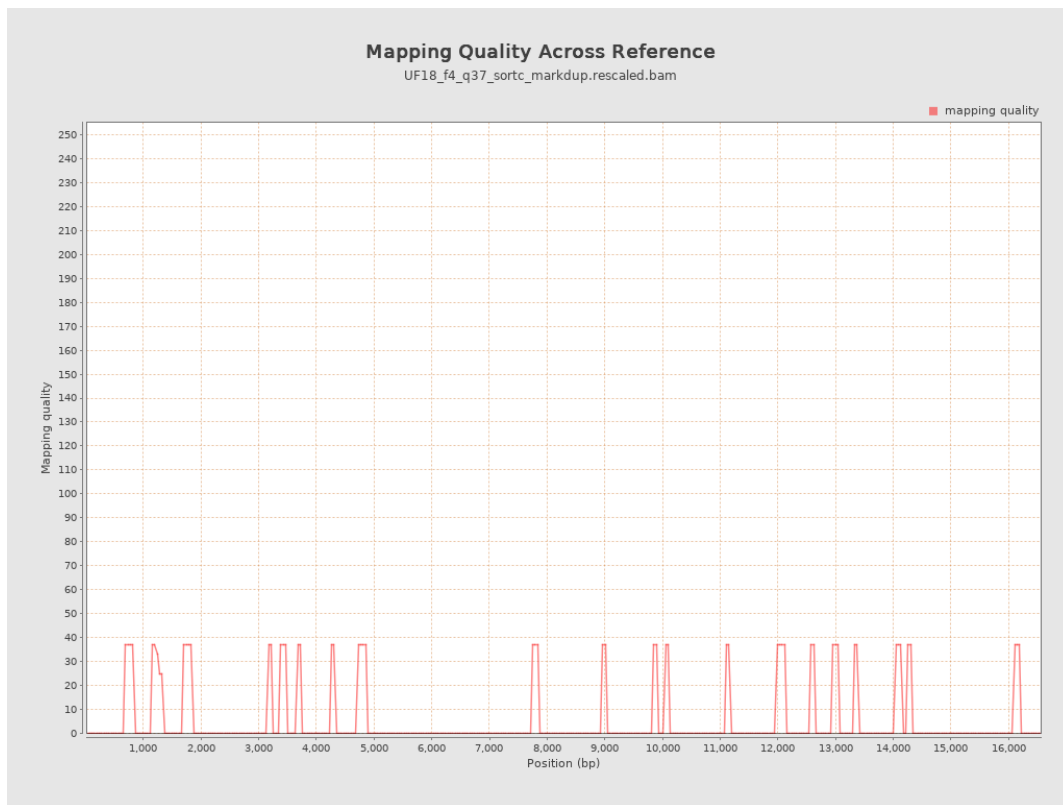
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Homopolymer Indels



## 11. Results : Mapping Quality Across Reference



## 12. Results : Mapping Quality Histogram

