

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/03/01 02:00:23*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
output/UF11/UF11_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3
```

## 1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF11\tSM:UF11\tLB:nan\tP L:ILLUMINA /data/stonelab/references/M_leprae_ TN/M_leprae_TN.fasta output/UF11/UF11-ancient.sai output/UF11/UF11- ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 01 02:00:22 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF11/UF11_f4_q37_sortc_ma rkdup.rescaled.bam

## 2. Summary

### 2.1. Globals

Reference size	3,268,203
Number of reads	329,469
Mapped reads	329,469 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	30 / 141 / 62.18
Duplicated reads (estimated)	49,758 / 15.1%
Duplication rate	14.32%
Clipped reads	1 / 0%

### 2.2. ACGT Content

Number/percentage of A's	4,921,774 / 24.03%
Number/percentage of C's	4,861,928 / 23.73%
Number/percentage of T's	4,976,365 / 24.29%
Number/percentage of G's	5,724,171 / 27.94%
Number/percentage of N's	14 / 0%
GC Percentage	51.68%

### 2.3. Coverage

Mean	6.2682
Standard Deviation	7.9391

## 2.4. Mapping Quality

Mean Mapping Quality	37
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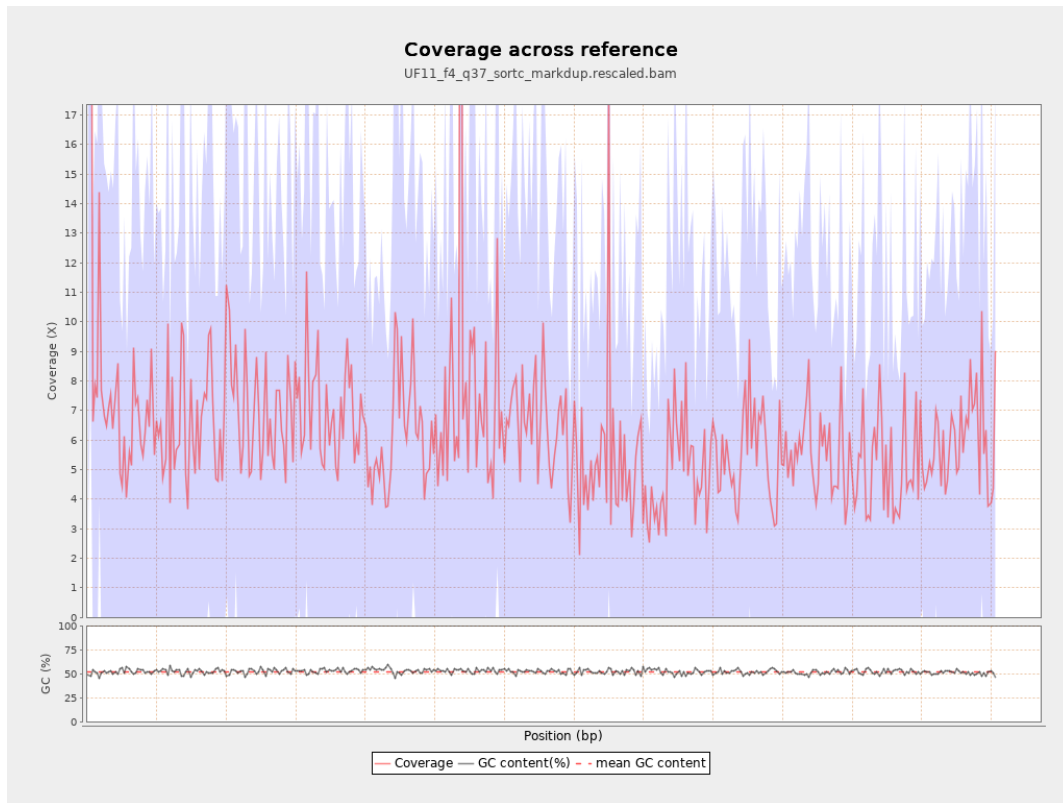
## 2.5. Mismatches and indels

General error rate	0.26%
Mismatches	52,741
Insertions	467
Mapped reads with at least one insertion	0.14%
Deletions	1,342
Mapped reads with at least one deletion	0.41%
Homopolymer indels	42.18%

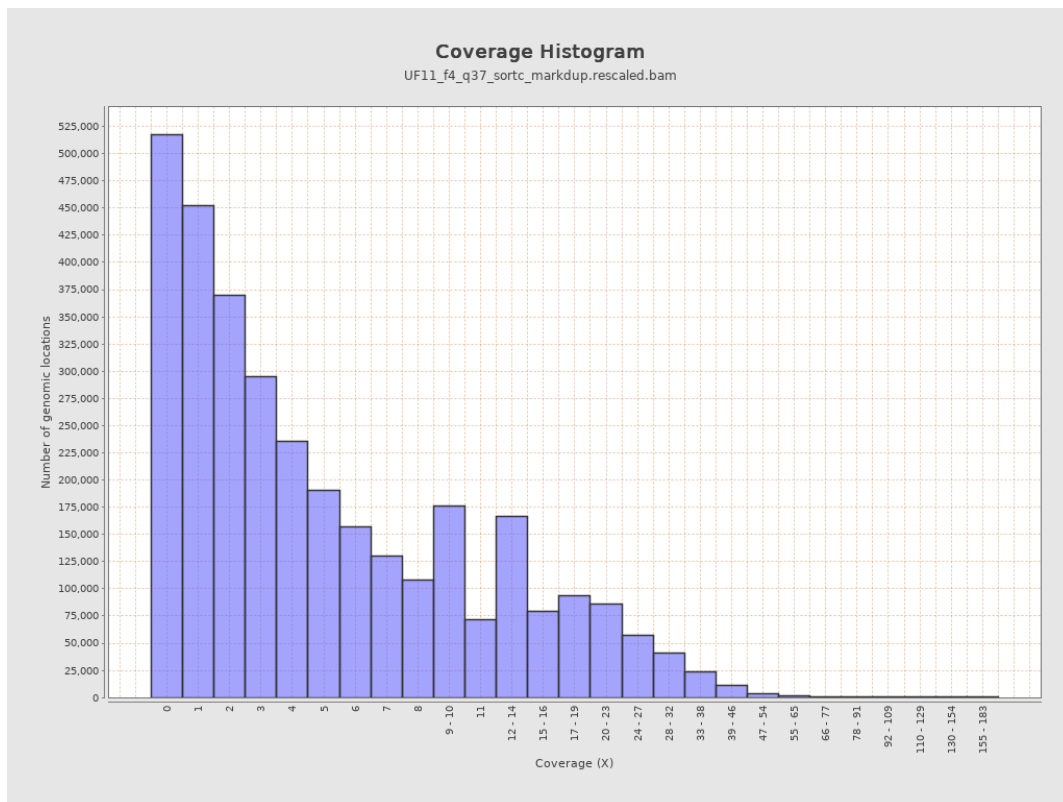
## 2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
ENA AL450380 AL450380.1	3268203	20485773	6.2682	7.9391

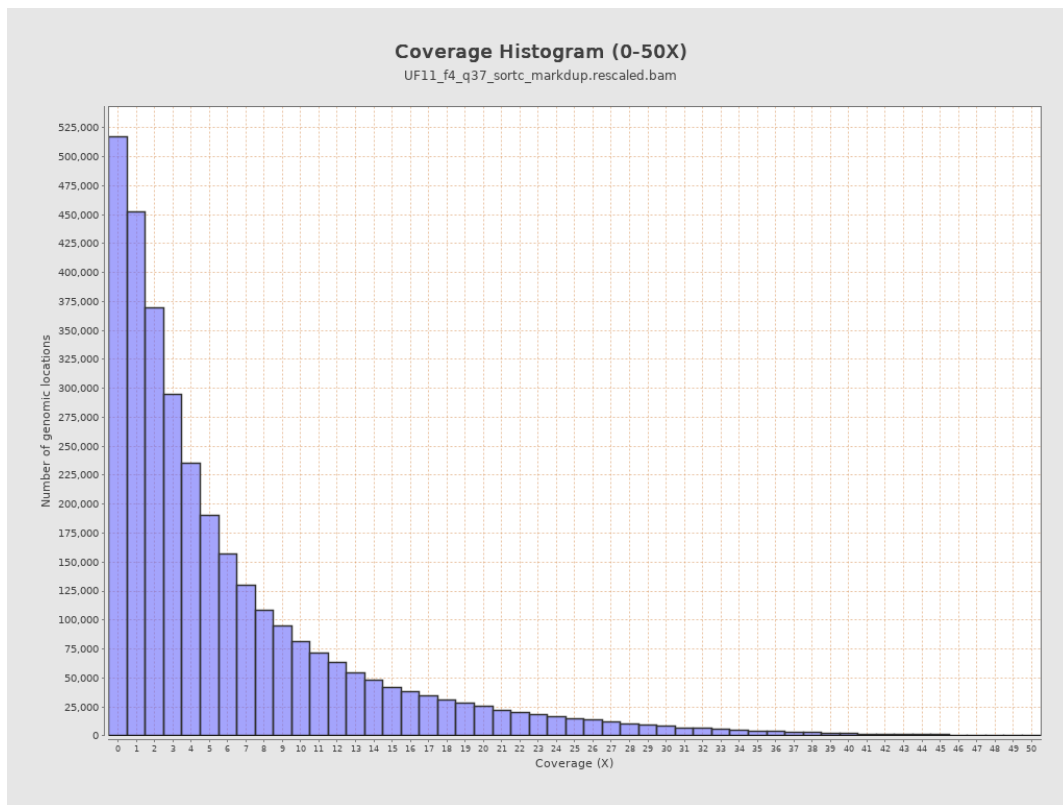
### 3. Results : Coverage across reference



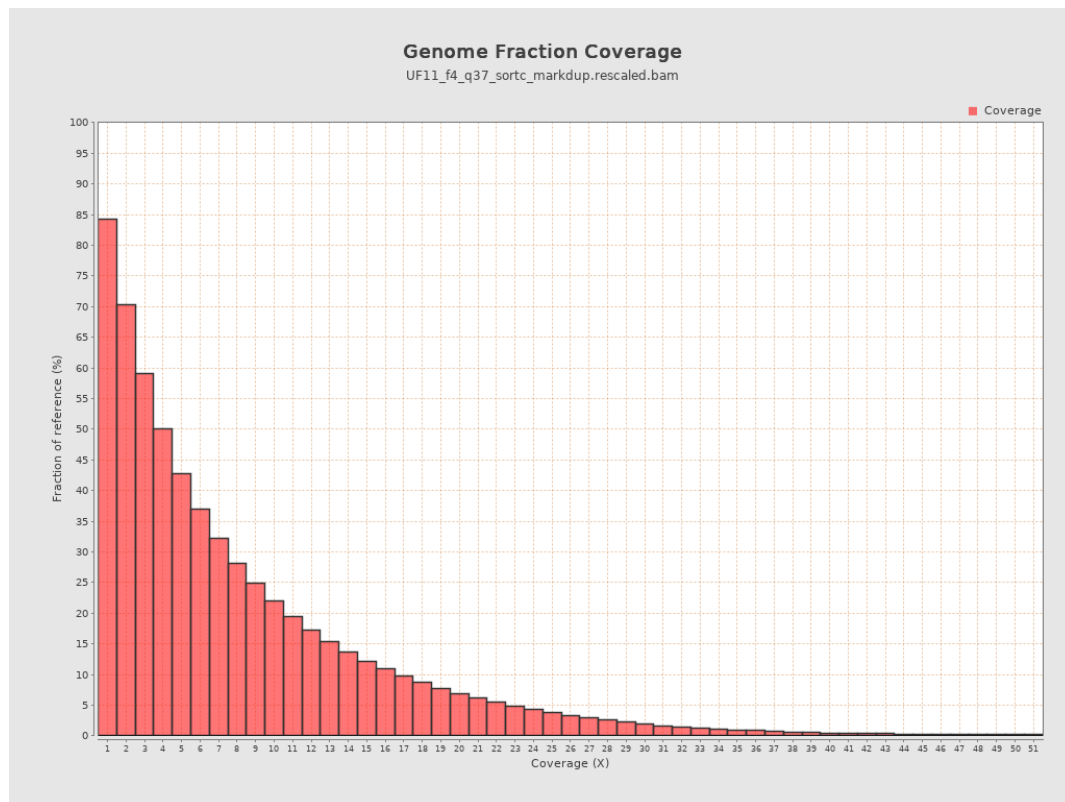
## 4. Results : Coverage Histogram



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

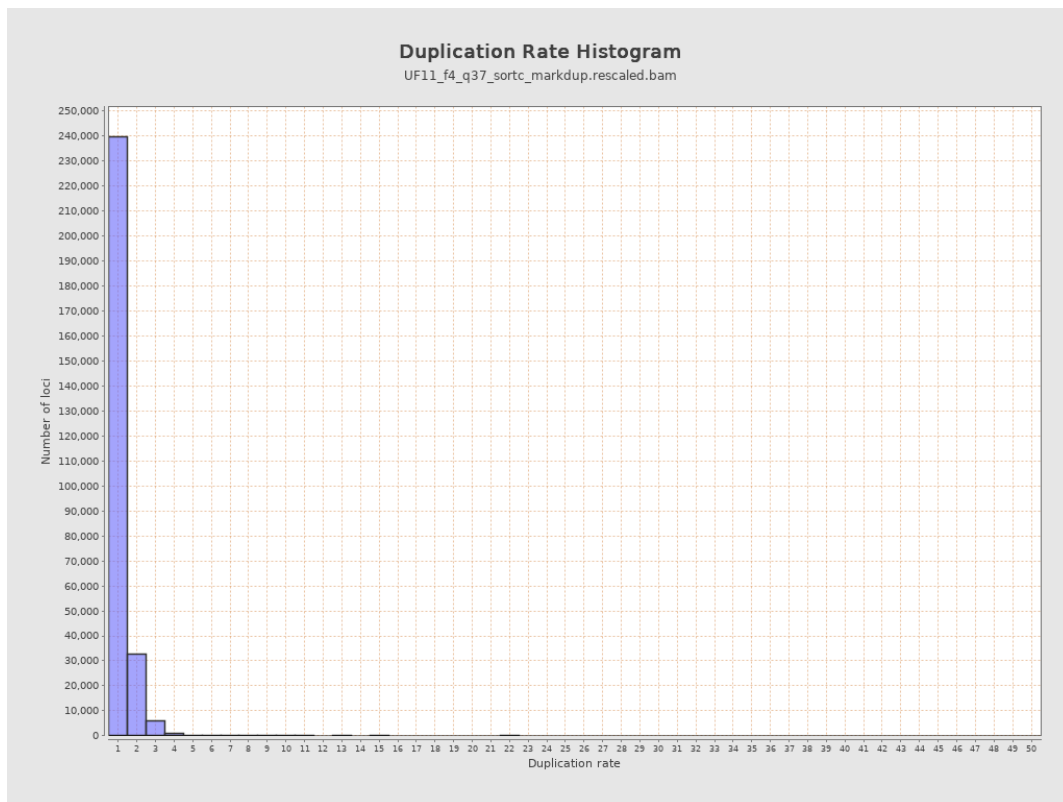


## 6. Results : Genome Fraction Coverage

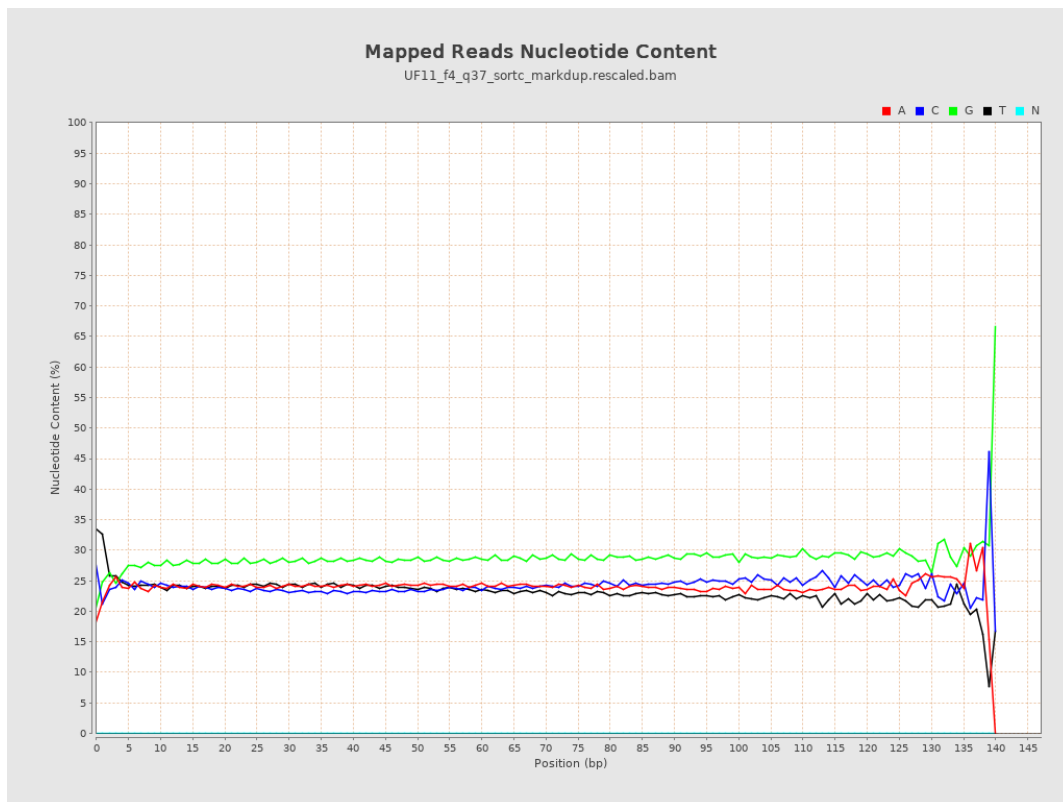




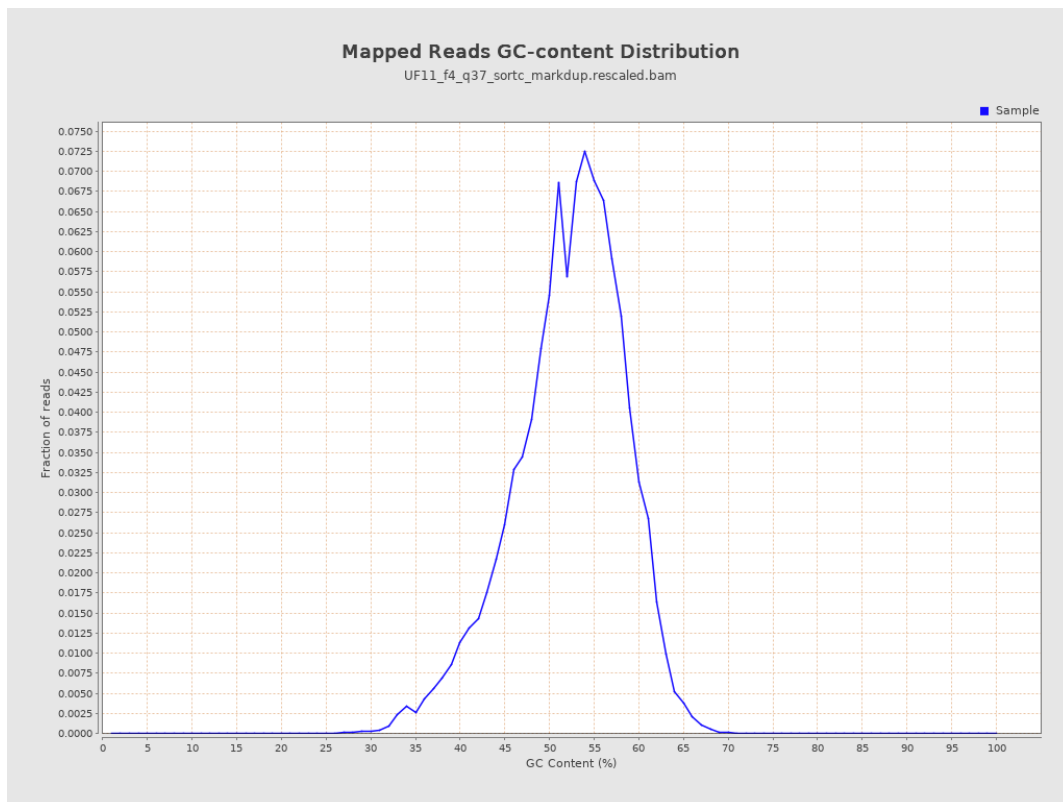
## 7. Results : Duplication Rate Histogram



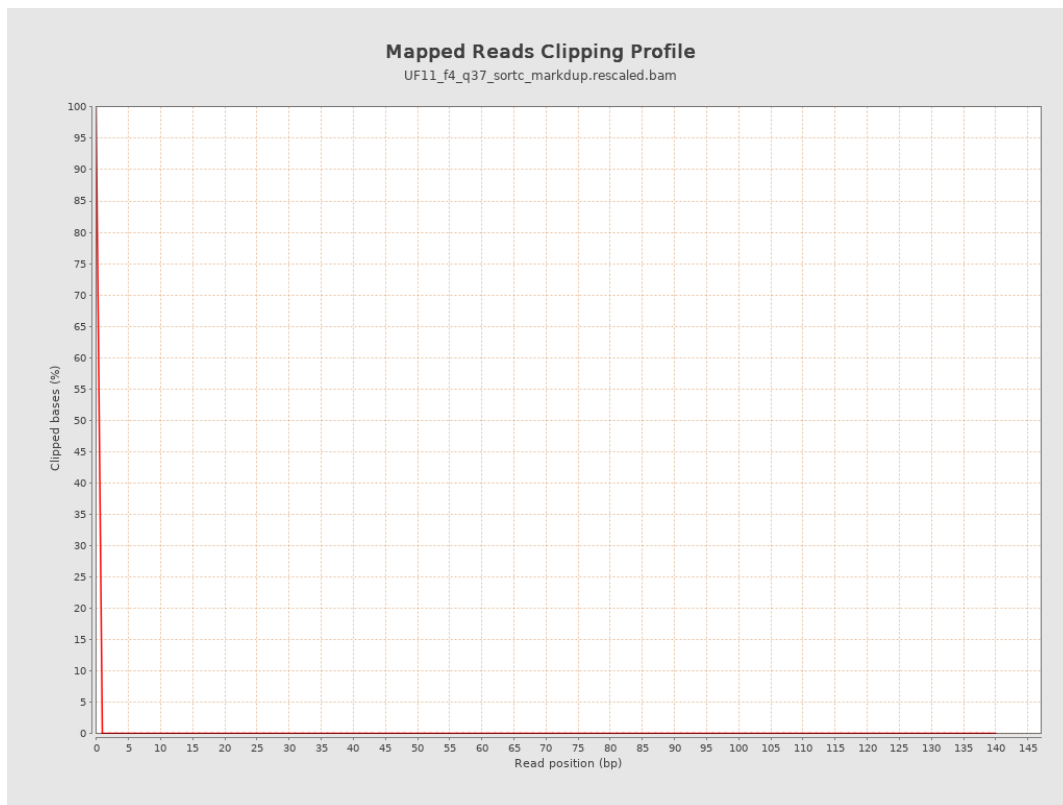
## 8. Results : Mapped Reads Nucleotide Content



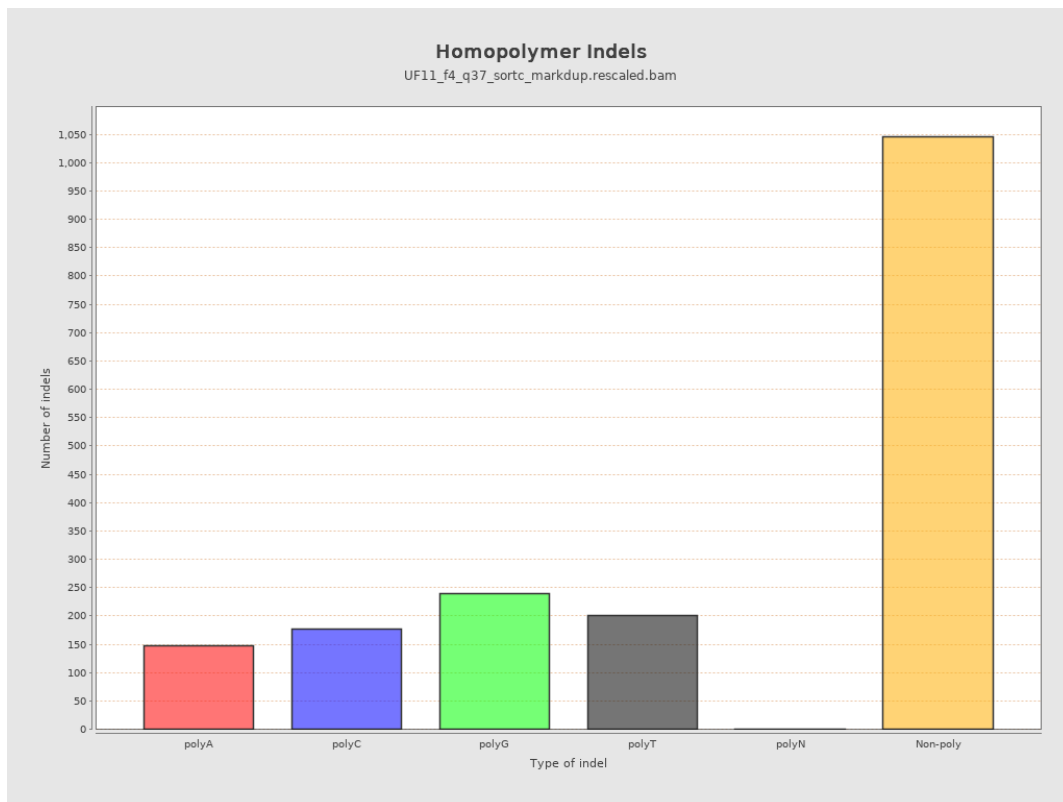
## 9. Results : Mapped Reads GC-content Distribution



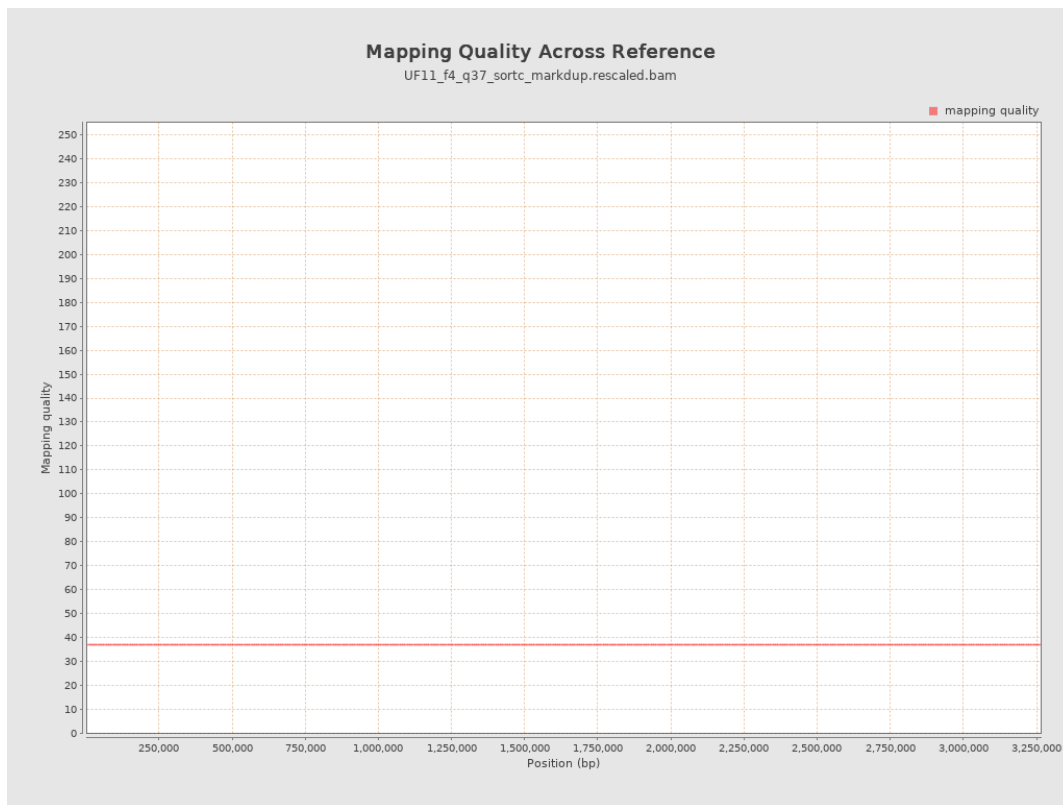
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

