Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/02 02:57:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam output/UF703/UF703_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3
```

1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF703\tSM:UF703\tLB:nan\tPL:ILLUMINA /data/stonelab/references/Human_mitochondrial/NC_012920.1.fasta output/UF703/UF703-ancient.sai output/UF703/UF703-ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 02 02:57:26 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF703/UF703_f4_q37_sortc_markdup.rescaled.bam

2. Summary

2.1. Globals

Reference size	16,569
Number of reads	322
Mapped reads	322 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	31 / 135 / 61.49
Duplicated reads (estimated)	10 / 3.11%
Duplication rate	2.88%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	6,494 / 32.8%
Number/percentage of C's	6,034 / 30.47%
Number/percentage of T's	5,066 / 25.58%
Number/percentage of G's	2,207 / 11.15%
Number/percentage of N's	0 / 0%
GC Percentage	41.62%

2.3. Coverage

Mean	1.1951
Standard Deviation	2.0615

2.4. Mapping Quality

Mean Mapping Quality	28.44

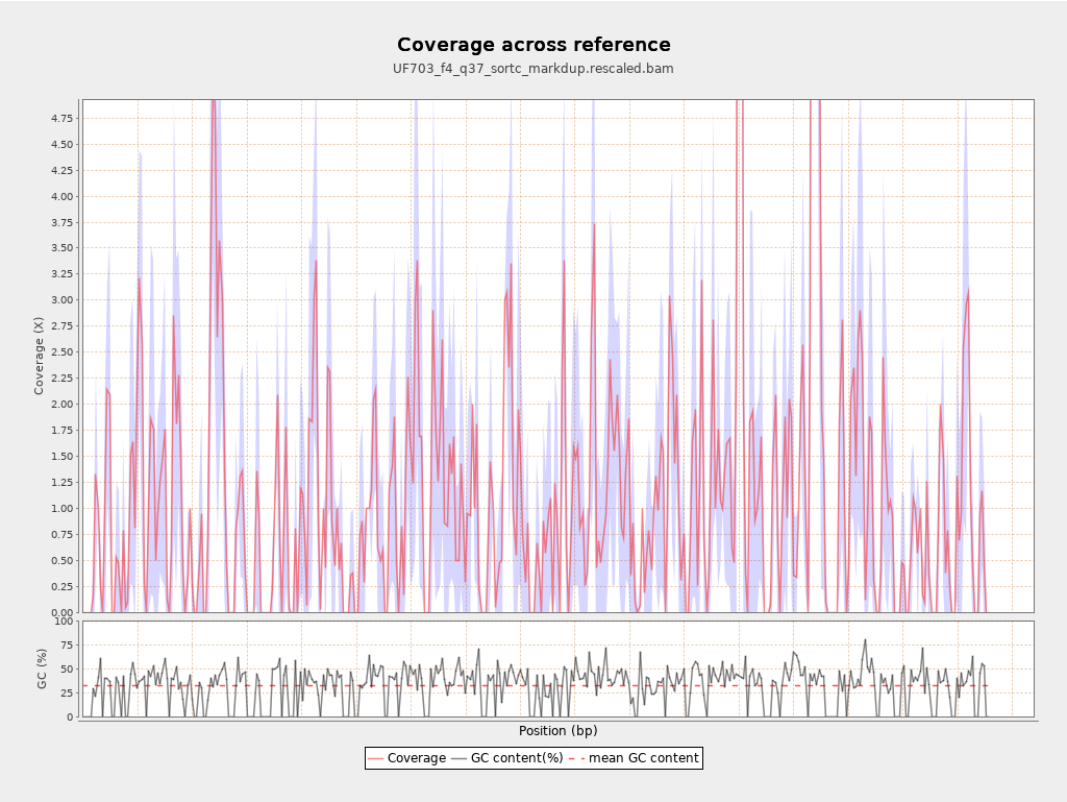
2.5. Mismatches and indels

General error rate	2.27%
Mismatches	450

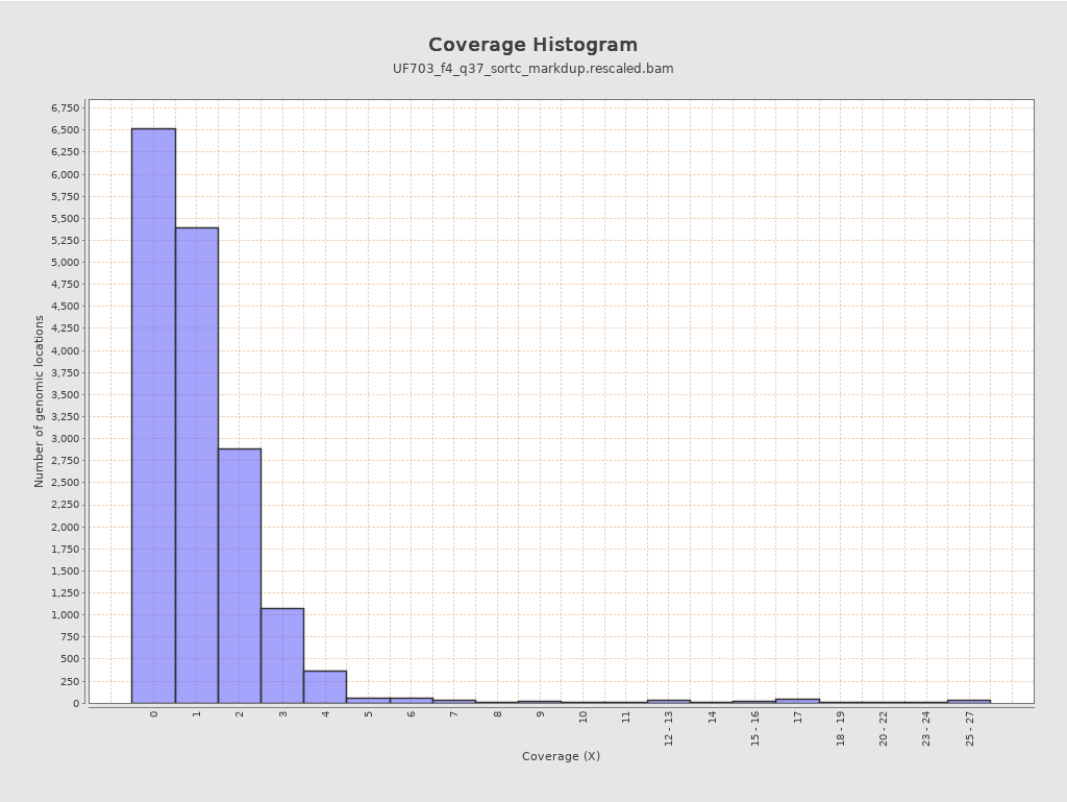
2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
NC_012920.1	16569	19801	1.1951	2.0615

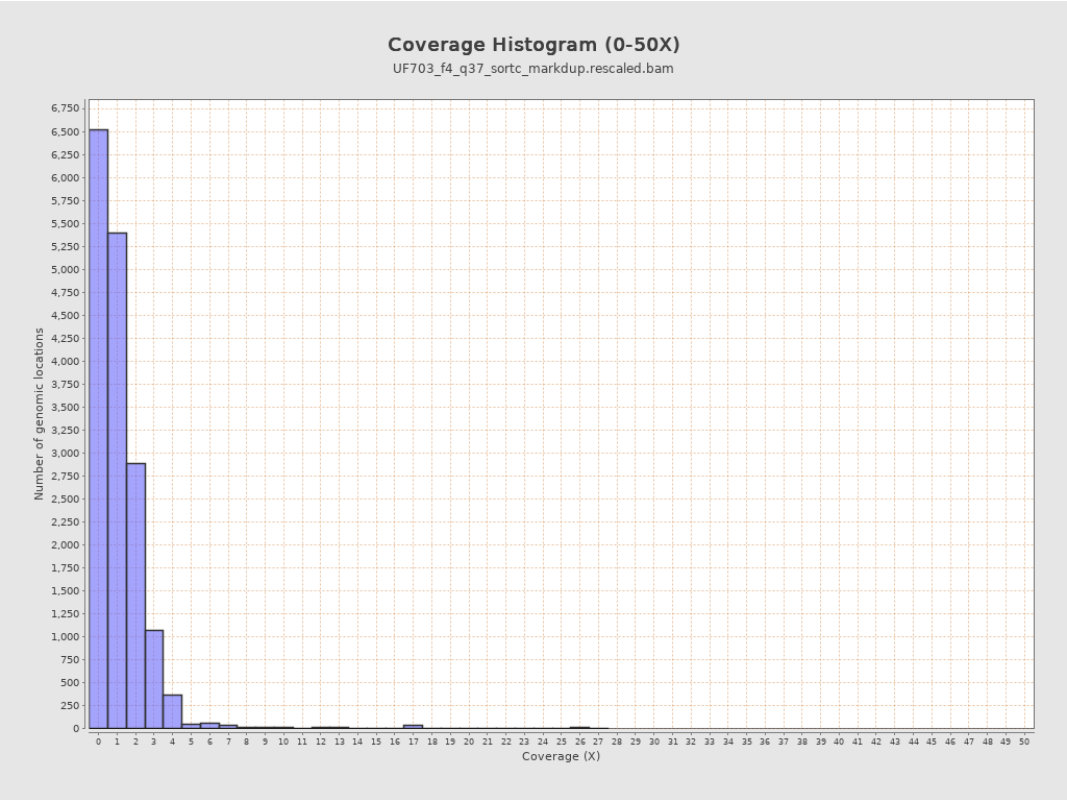
3. Results : Coverage across reference



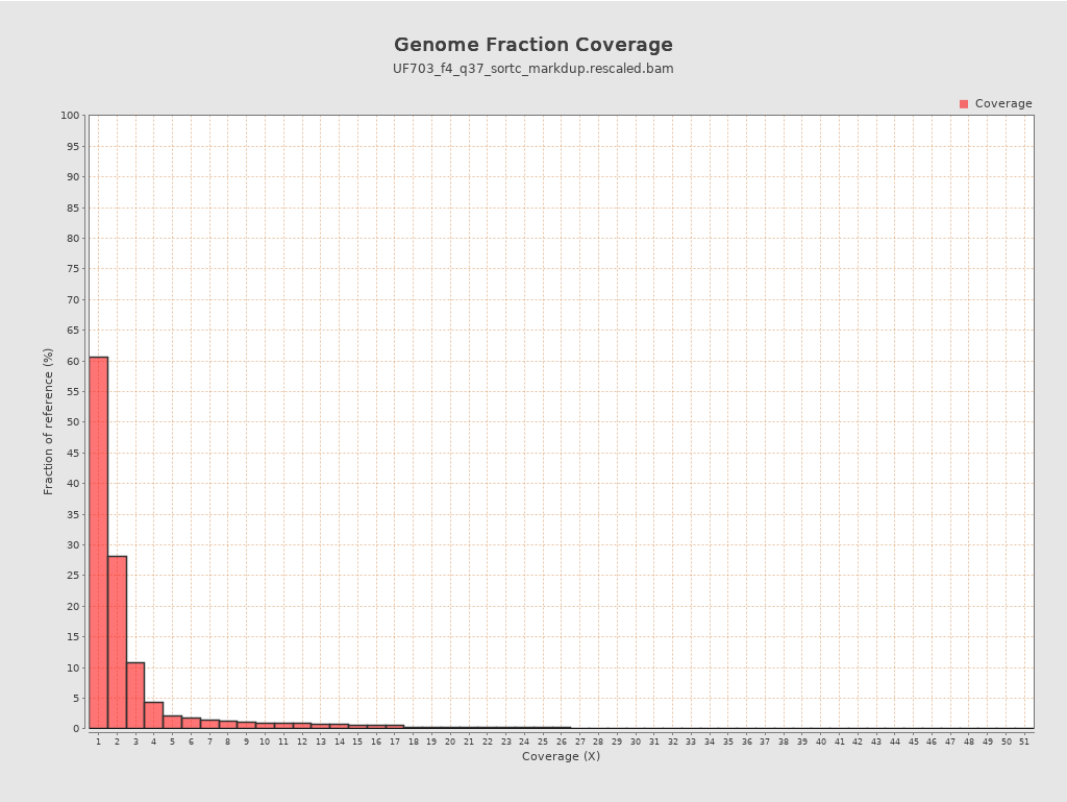
4. Results : Coverage Histogram



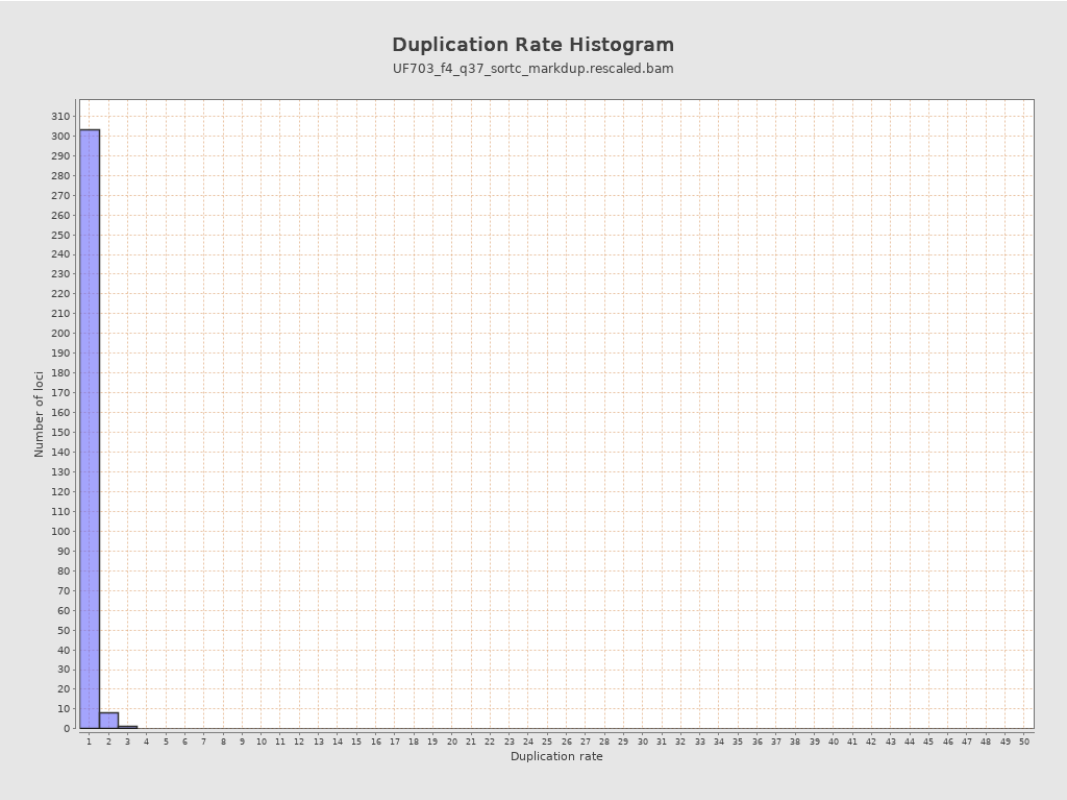
5. Results : Coverage Histogram (0-50X)



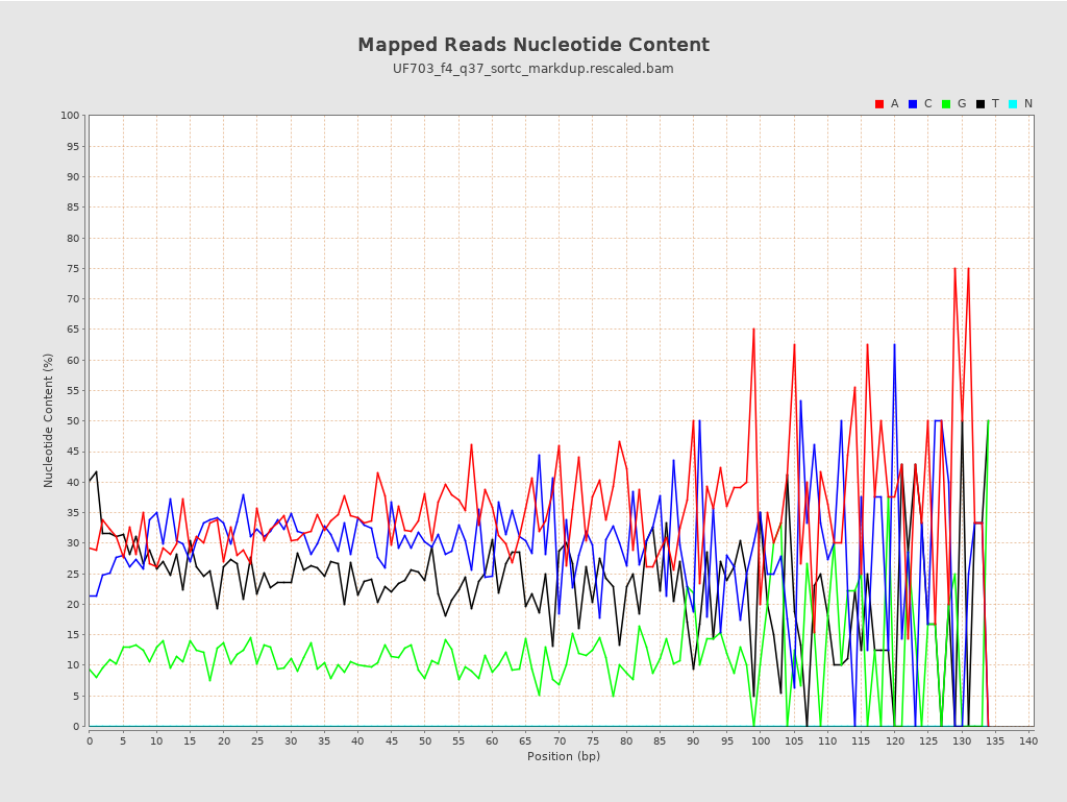
6. Results : Genome Fraction Coverage



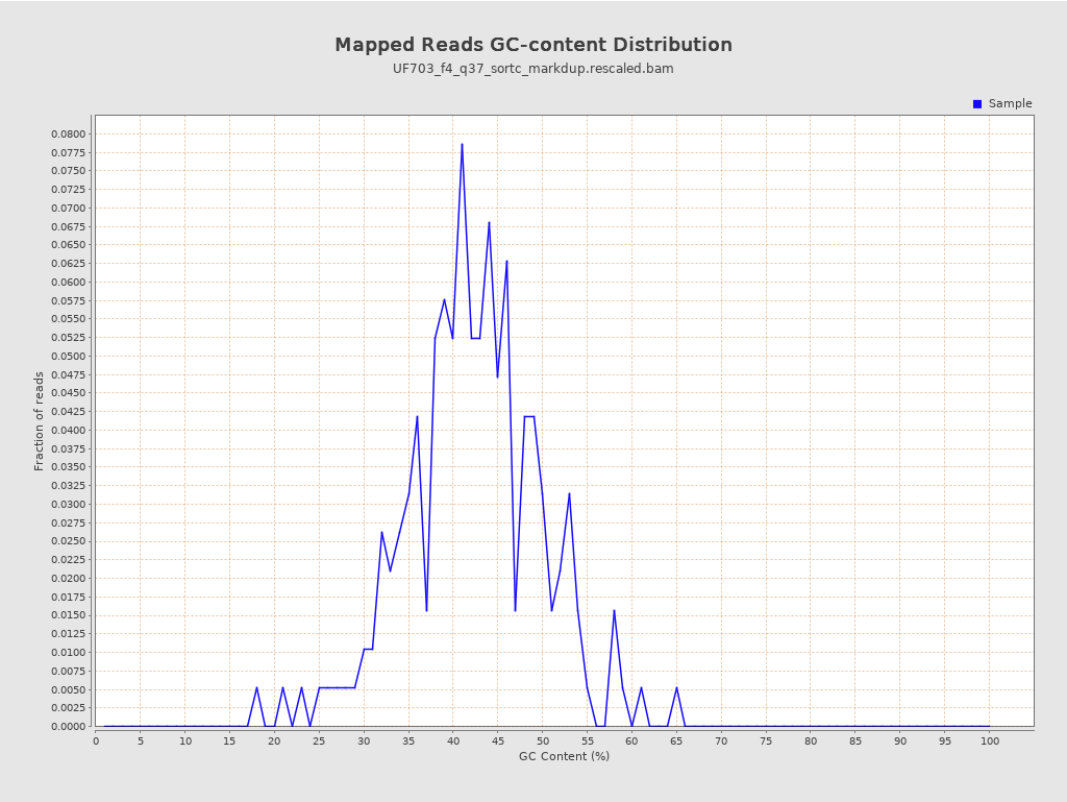
7. Results : Duplication Rate Histogram



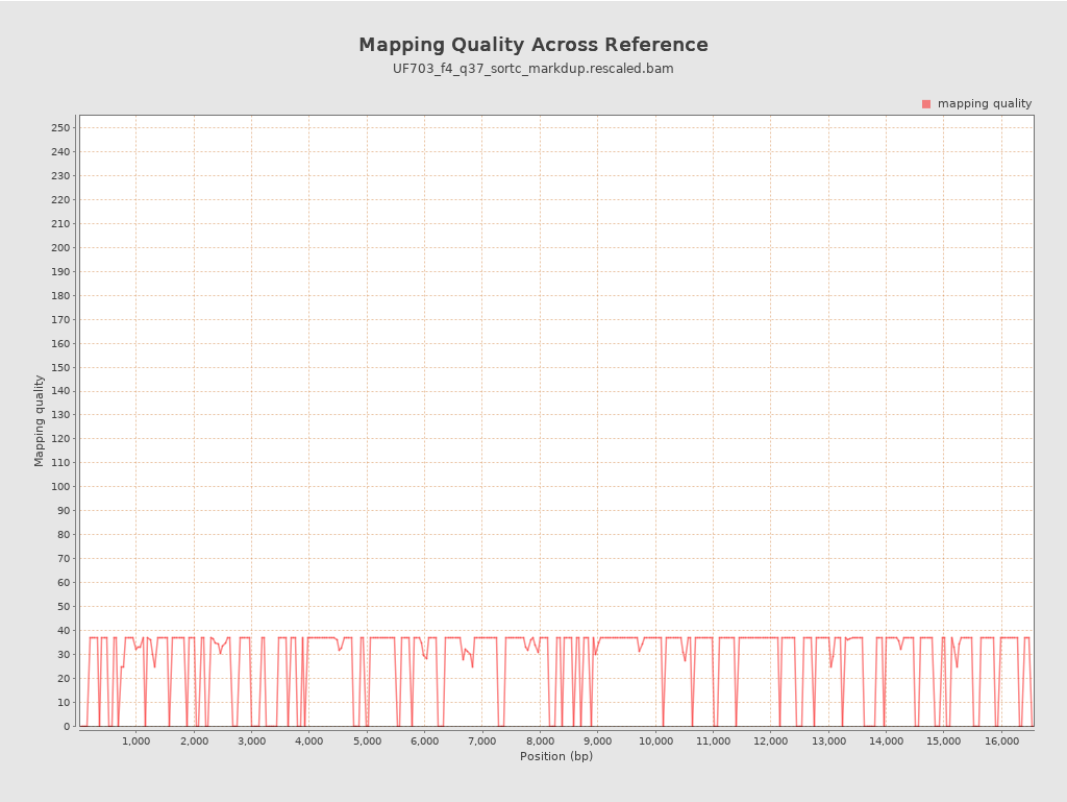
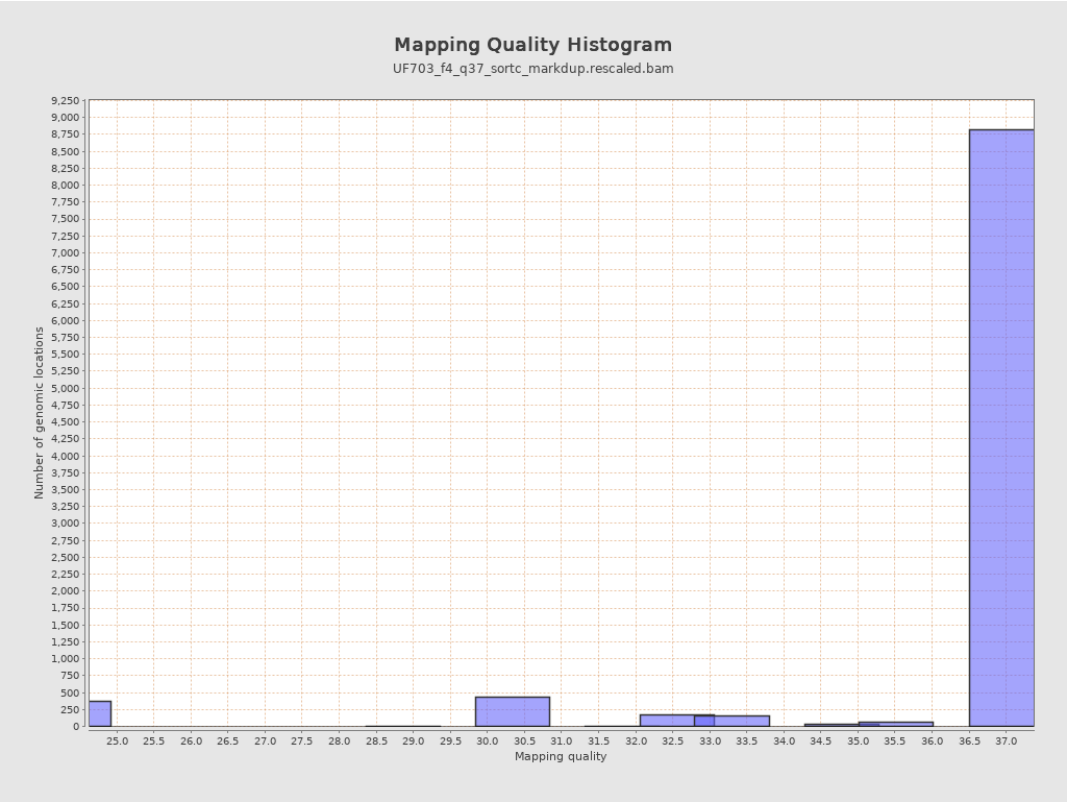
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



10. Results : Mapping Quality Across Reference



11. Results : Mapping Quality Histogram