

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/02 02:56:19

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/Human_mit ochondrial/NC_012920.1.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:	Wed Mar 02 02:56:19 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	16,569
Number of reads	271
Mapped reads	271 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	31 / 127 / 56.61
Duplicated reads (estimated)	10 / 3.69%
Duplication rate	3.83%
Clipped reads	1 / 0.37%

2.2. ACGT Content

Number/percentage of A's	4,992 / 32.54%
Number/percentage of C's	4,571 / 29.8%
Number/percentage of T's	3,878 / 25.28%
Number/percentage of G's	1,900 / 12.39%
Number/percentage of N's	0 / 0%
GC Percentage	42.18%

2.3. Coverage

Mean	0.9259
Standard Deviation	1.9305

2.4. Mapping Quality

Mean Mapping Quality	26.87
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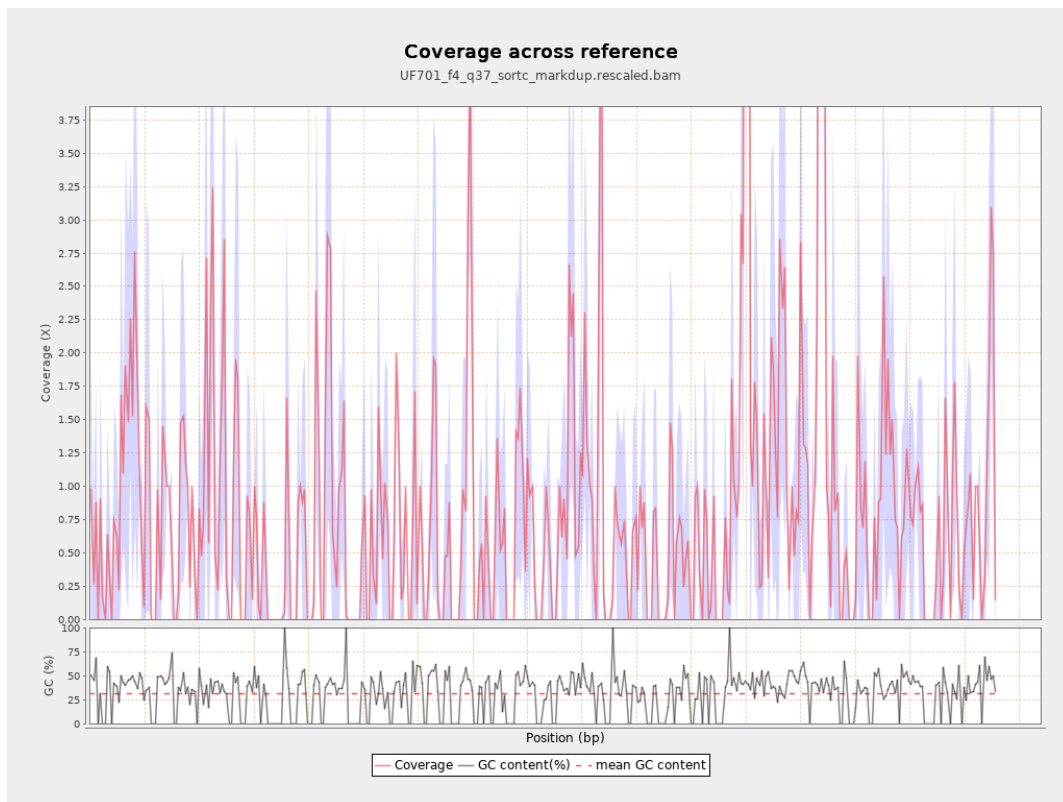
2.5. Mismatches and indels

General error rate	2.3%
Mismatches	353

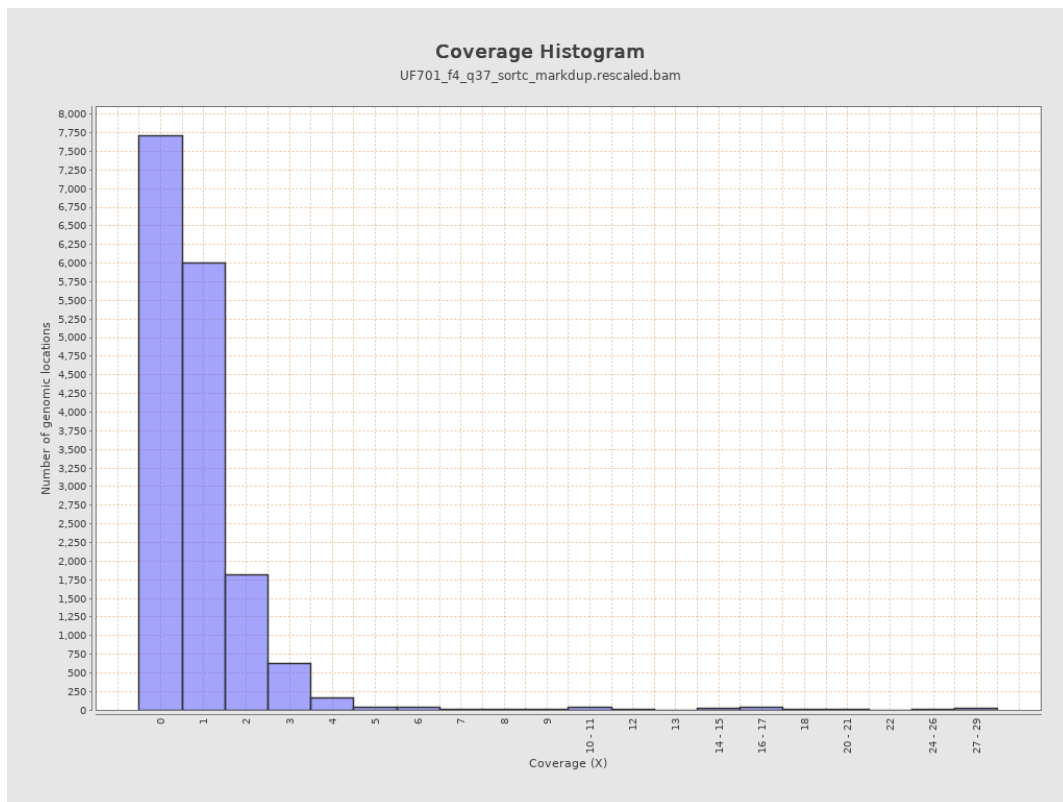
2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
NC_012920.1	16569	15341	0.9259	1.9305

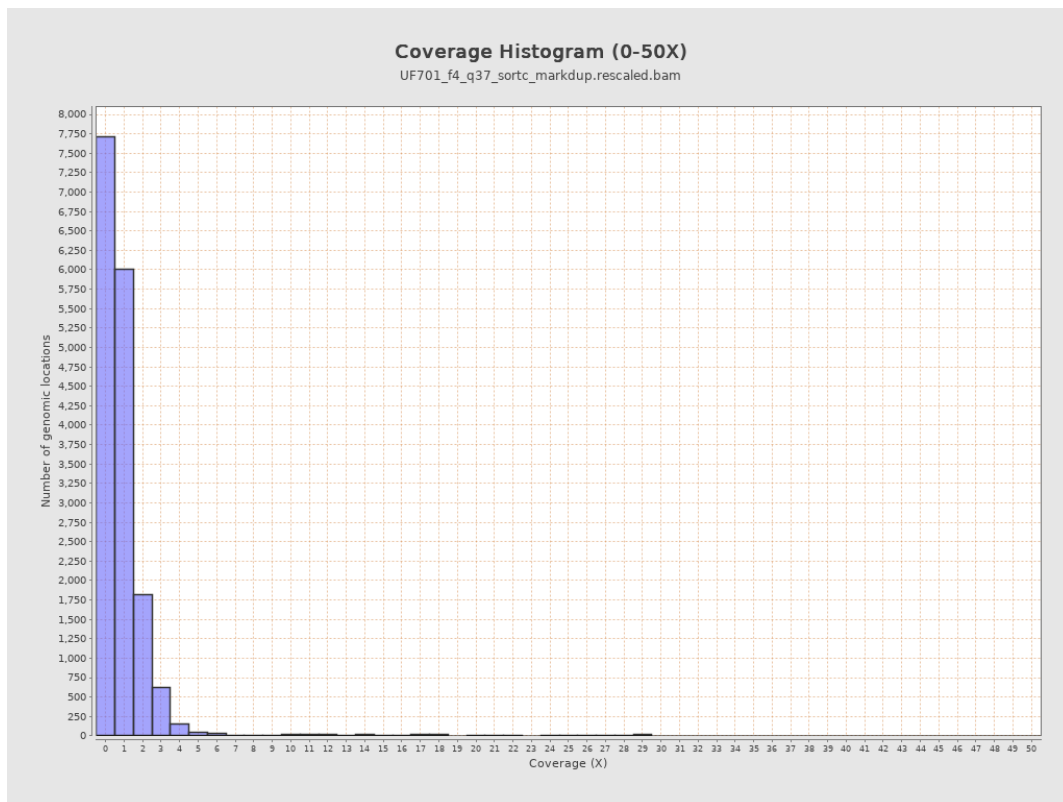
3. Results : Coverage across reference



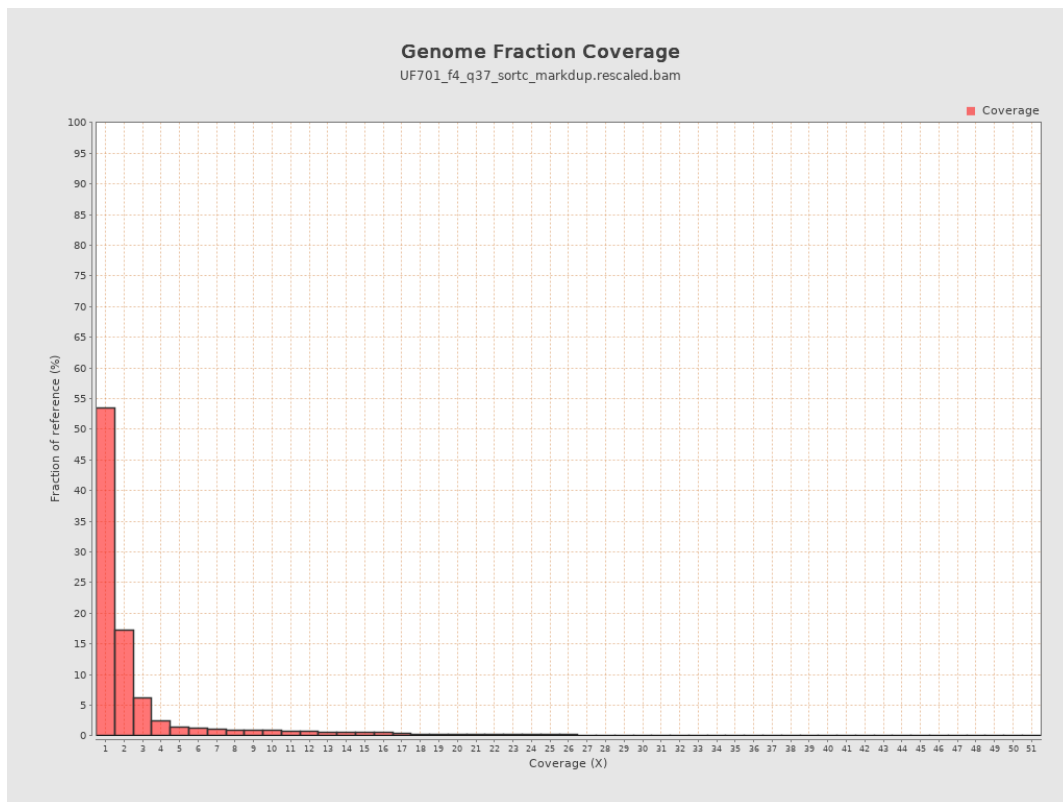
4. Results : Coverage Histogram



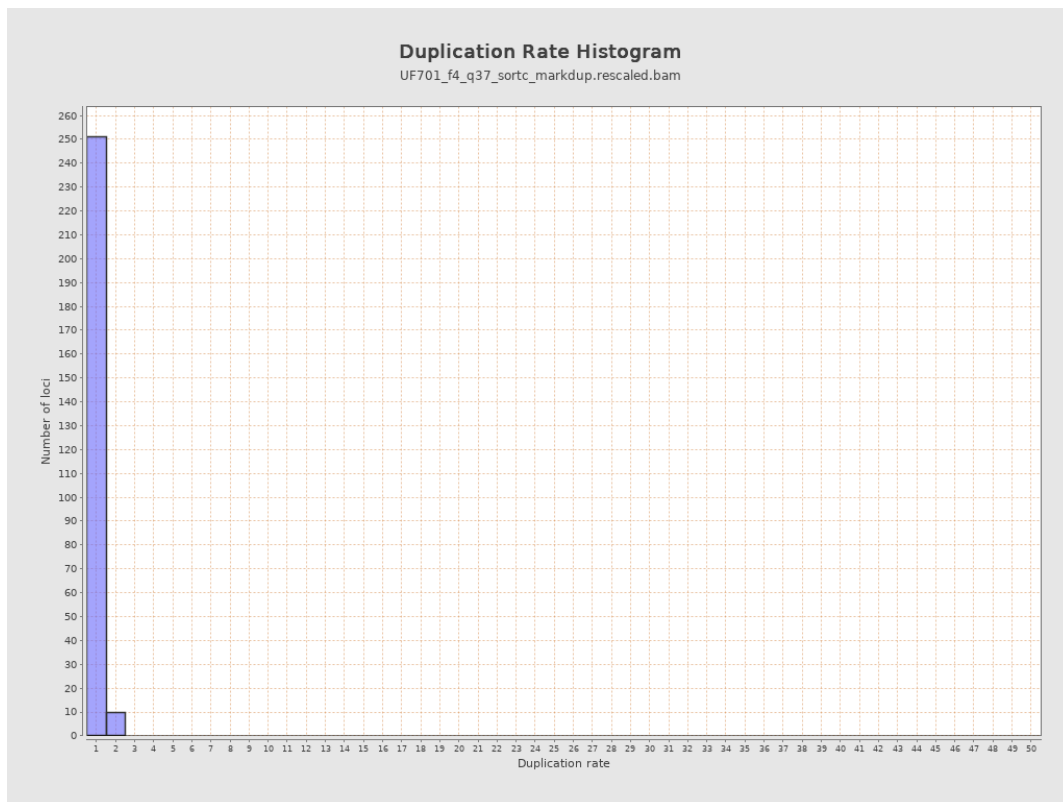
5. Results : Coverage Histogram (0-50X)



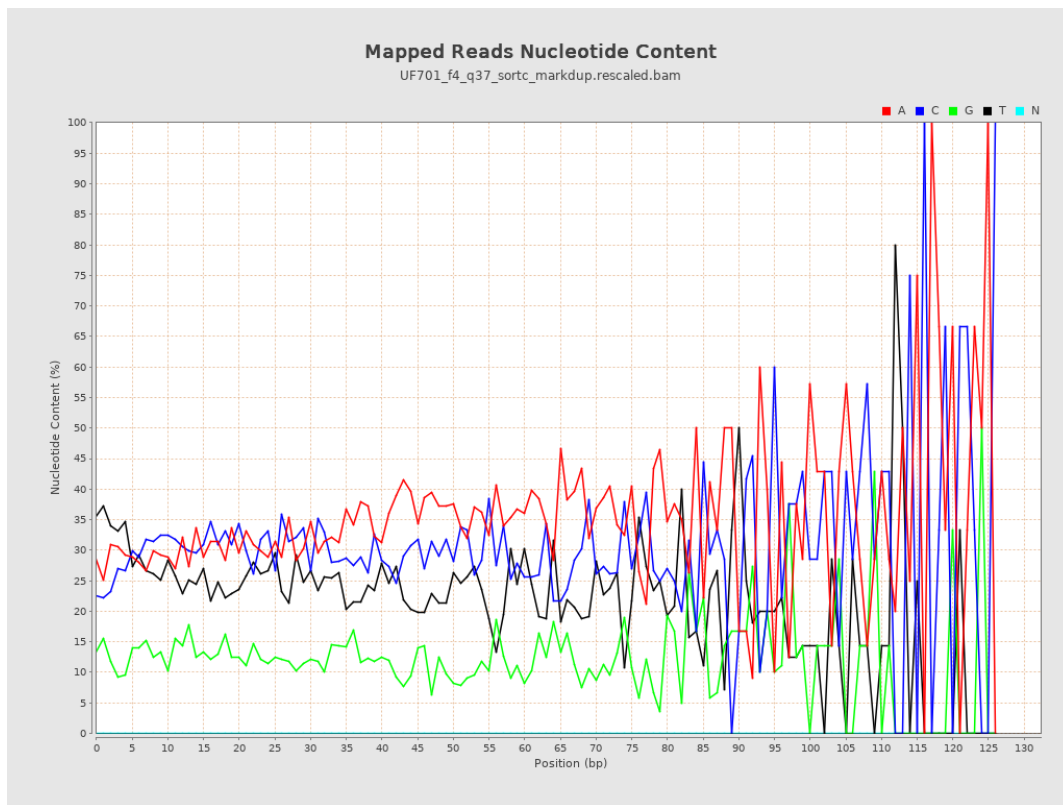
6. Results : Genome Fraction Coverage



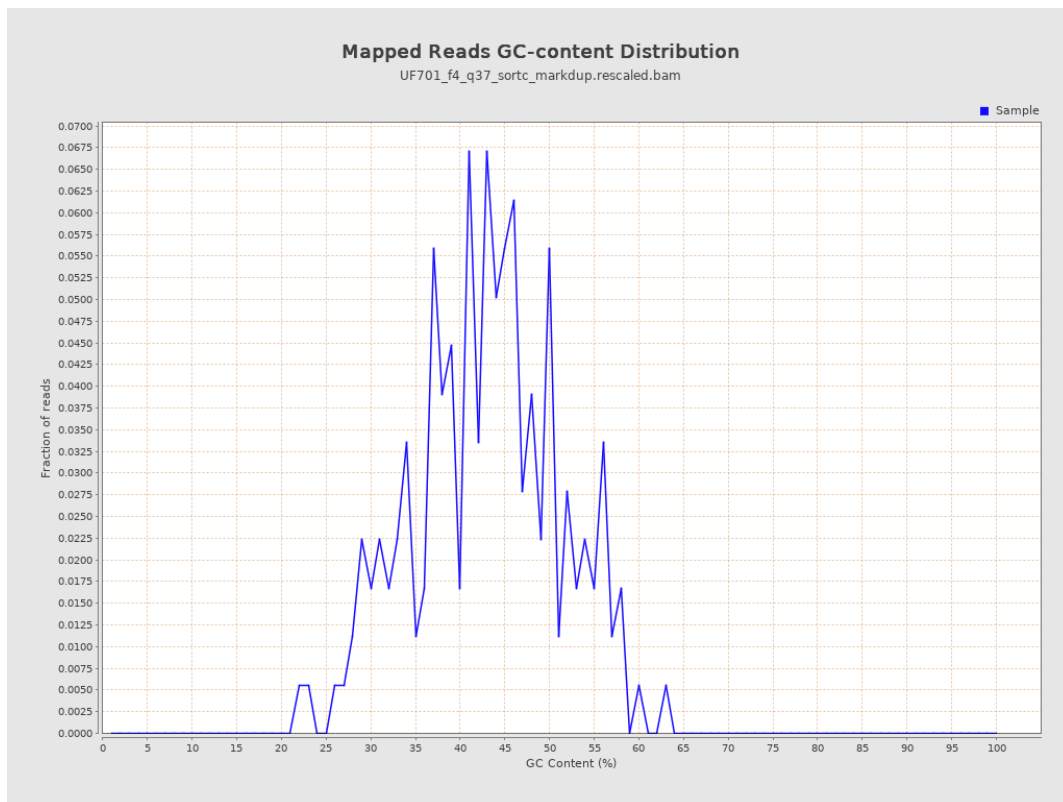
7. Results : Duplication Rate Histogram



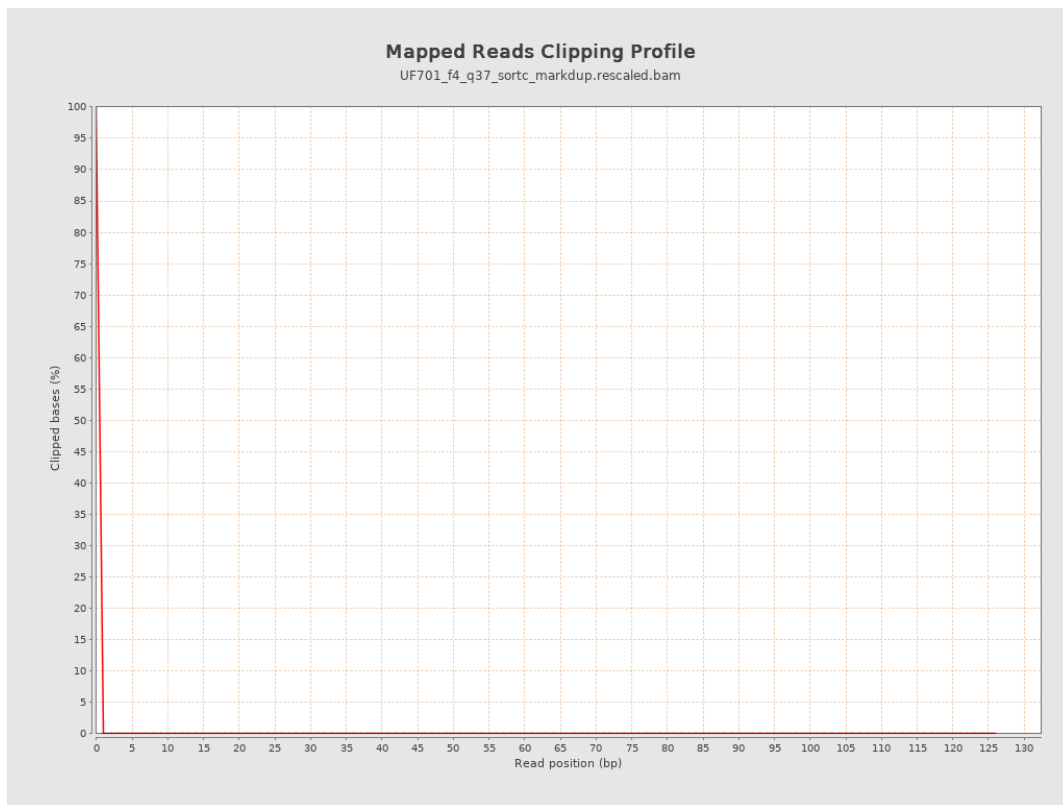
8. Results : Mapped Reads Nucleotide Content



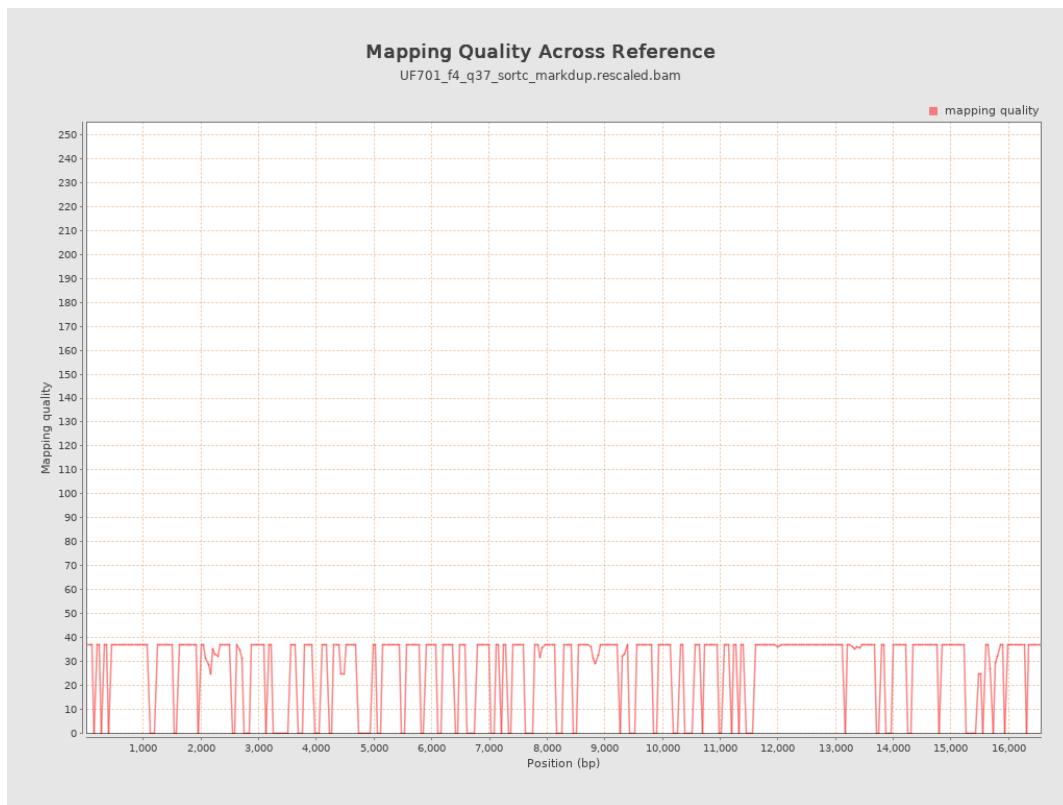
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

