

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/01 02:07:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
output/UF101/UF101_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3
```

1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF101\tSM:UF101\tLB:nan\ tPL:ILLUMINA /data/stonelab/references/M_leprae_ TN/M_leprae_TN.fasta output/UF101/UF101-ancient.sai output/UF101/UF101- ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 01 02:07:05 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF101/UF101_f4_q37_sortc_ markdup.rescaled.bam

2. Summary

2.1. Globals

Reference size	3,268,203
Number of reads	761,891
Mapped reads	761,891 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	30 / 141 / 74.06
Duplicated reads (estimated)	151,988 / 19.95%
Duplication rate	19.24%
Clipped reads	1 / 0%

2.2. ACGT Content

Number/percentage of A's	13,182,418 / 23.36%
Number/percentage of C's	14,263,692 / 25.28%
Number/percentage of T's	13,269,369 / 23.52%
Number/percentage of G's	15,708,094 / 27.84%
Number/percentage of N's	30 / 0%
GC Percentage	53.12%

2.3. Coverage

Mean	17.2655
Standard Deviation	13.2352

2.4. Mapping Quality

Mean Mapping Quality	37
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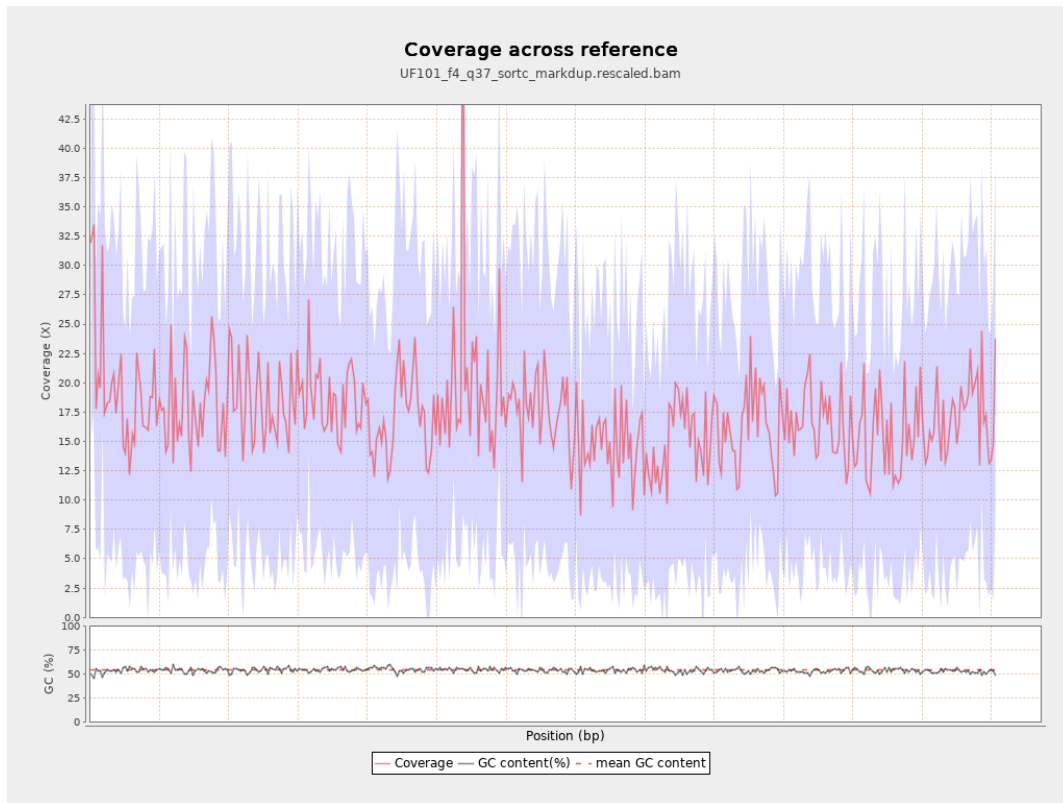
2.5. Mismatches and indels

General error rate	0.84%
Mismatches	474,178
Insertions	1,337
Mapped reads with at least one insertion	0.18%
Deletions	2,943
Mapped reads with at least one deletion	0.39%
Homopolymer indels	50.77%

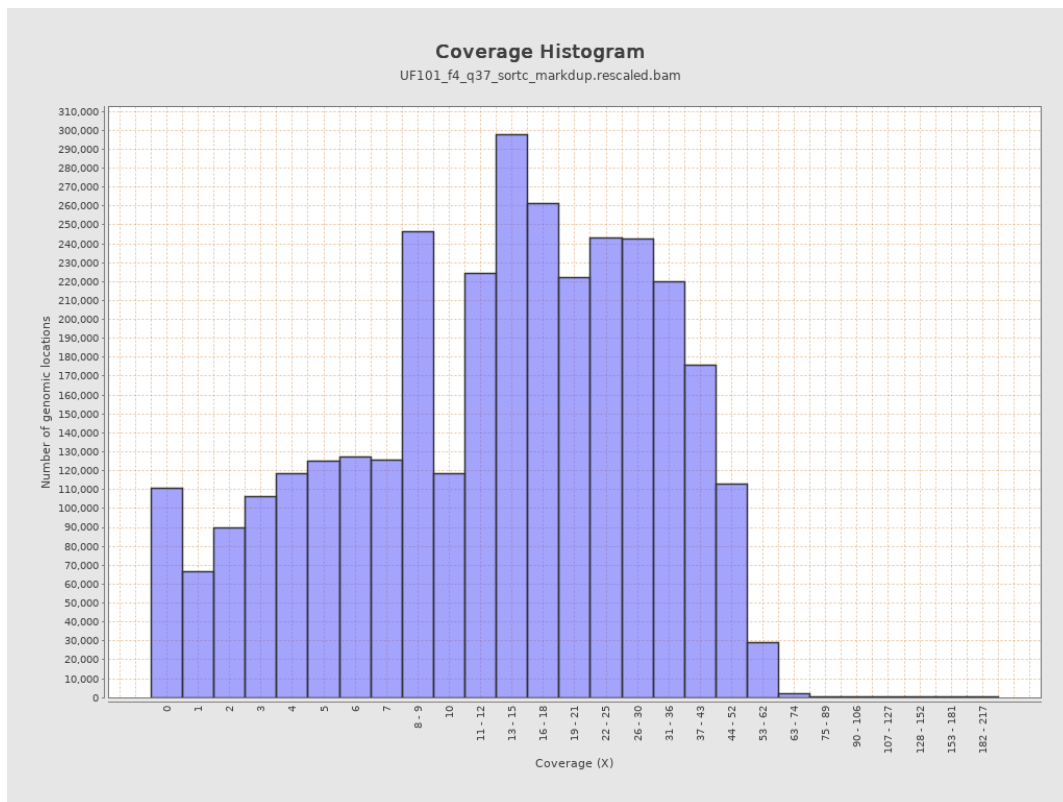
2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
ENA AL450380 AL450380.1	3268203	56427212	17.2655	13.2352

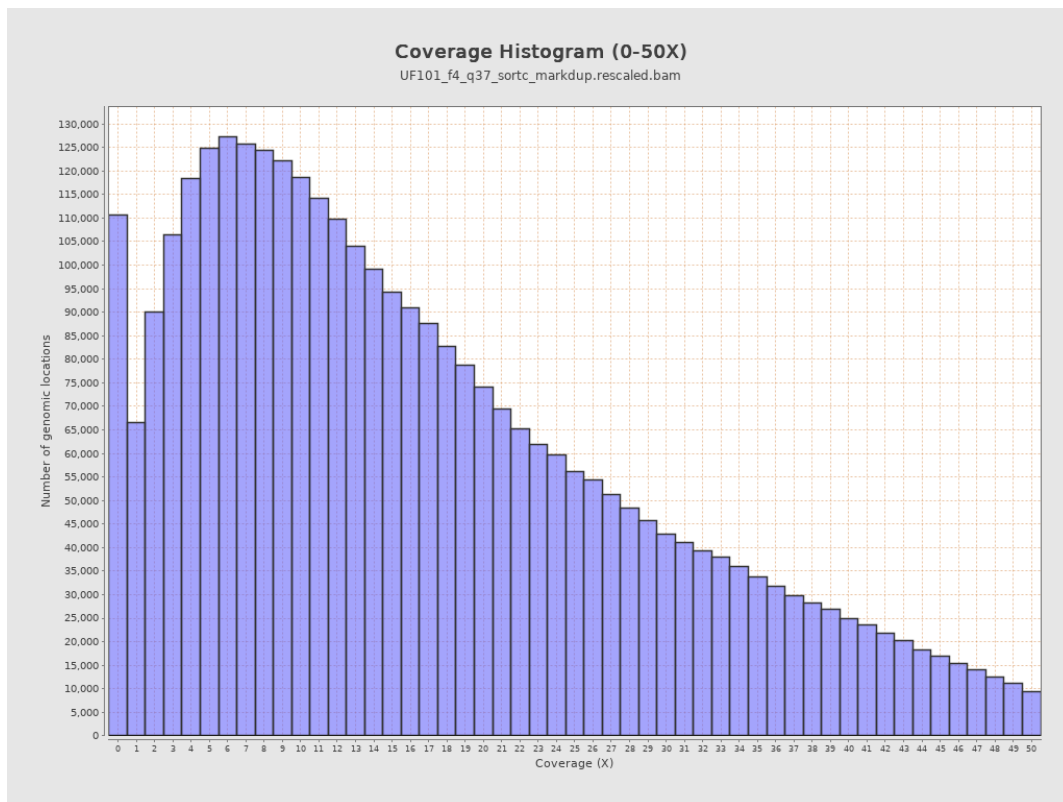
3. Results : Coverage across reference



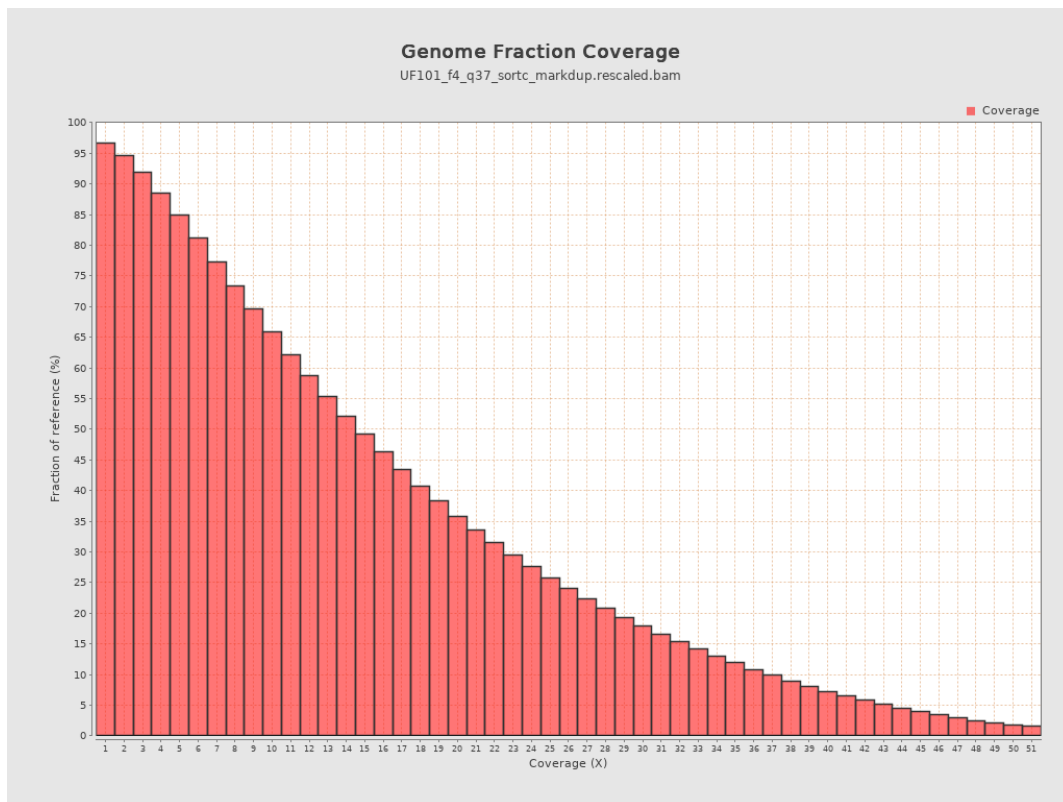
4. Results : Coverage Histogram



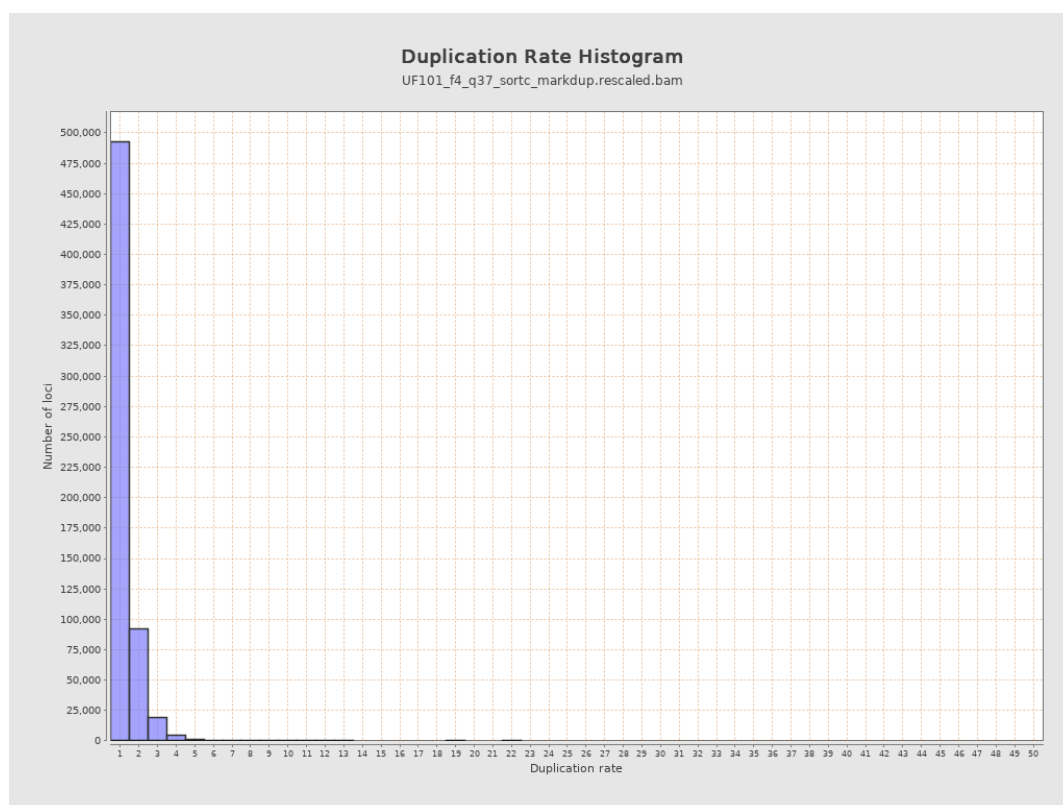
5. Results : Coverage Histogram (0-50X)



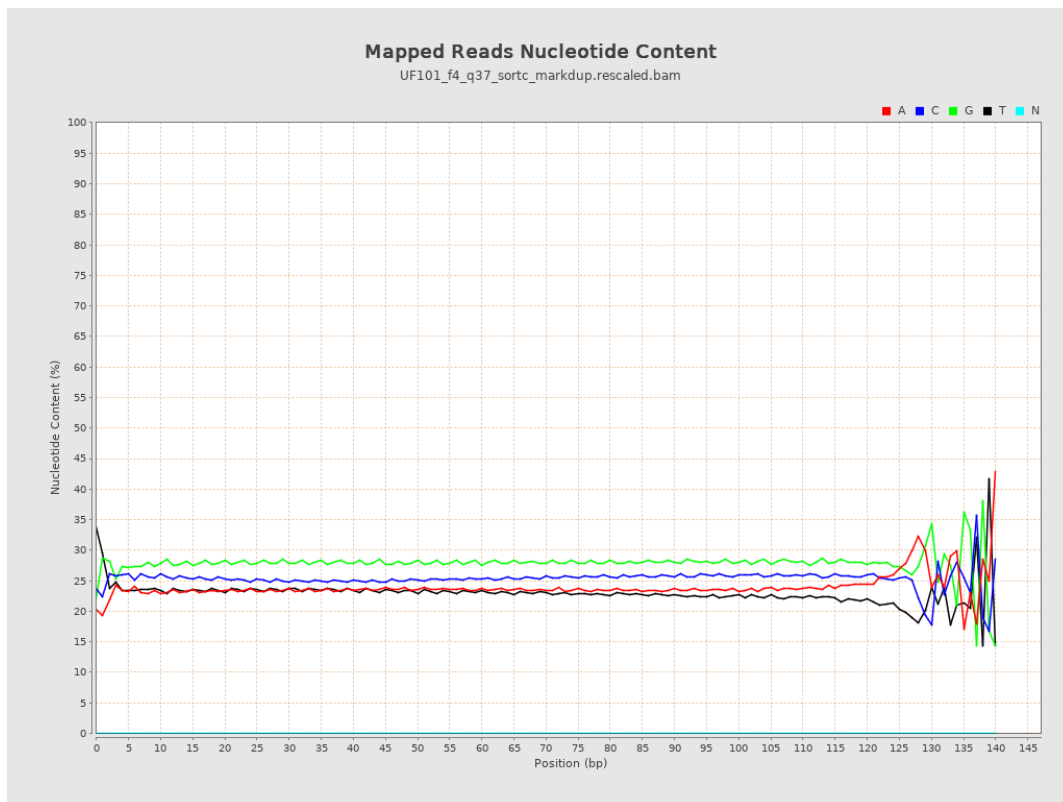
6. Results : Genome Fraction Coverage



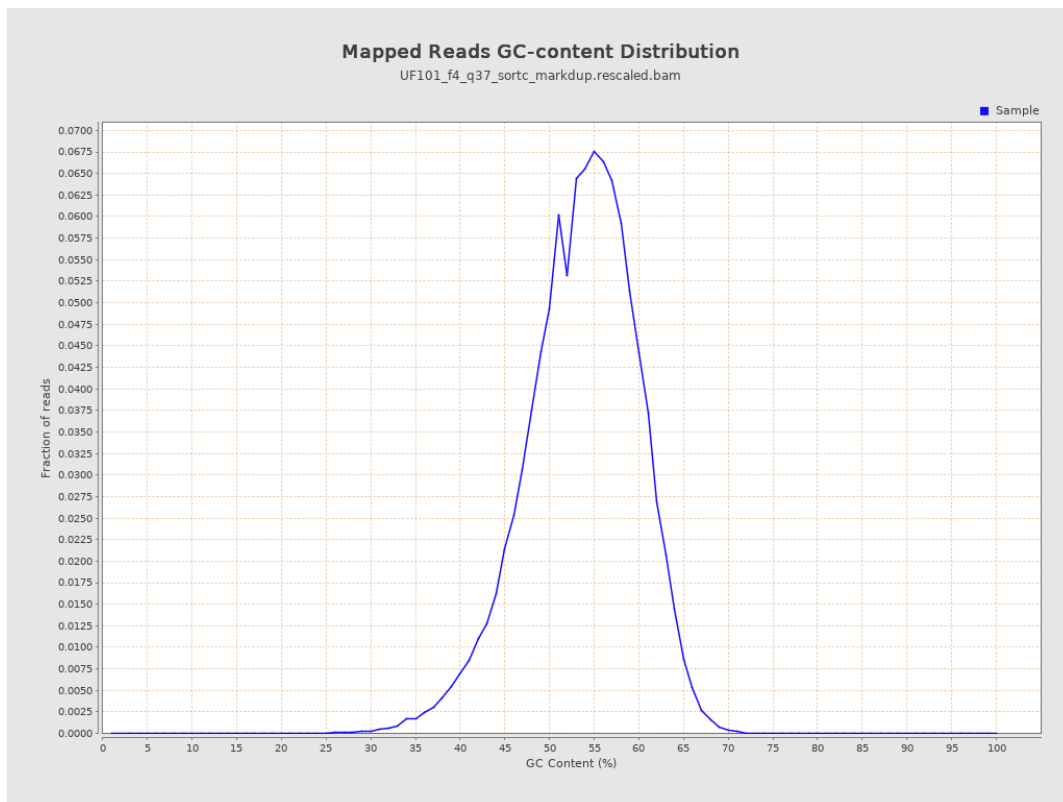
7. Results : Duplication Rate Histogram



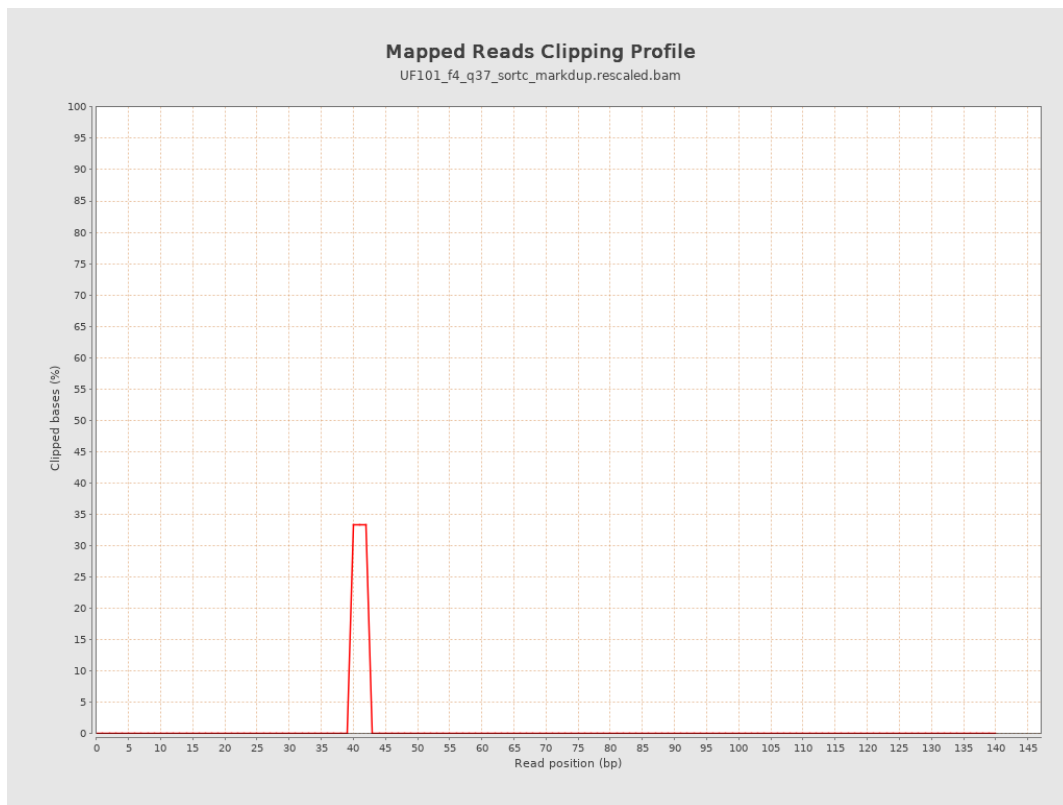
8. Results : Mapped Reads Nucleotide Content



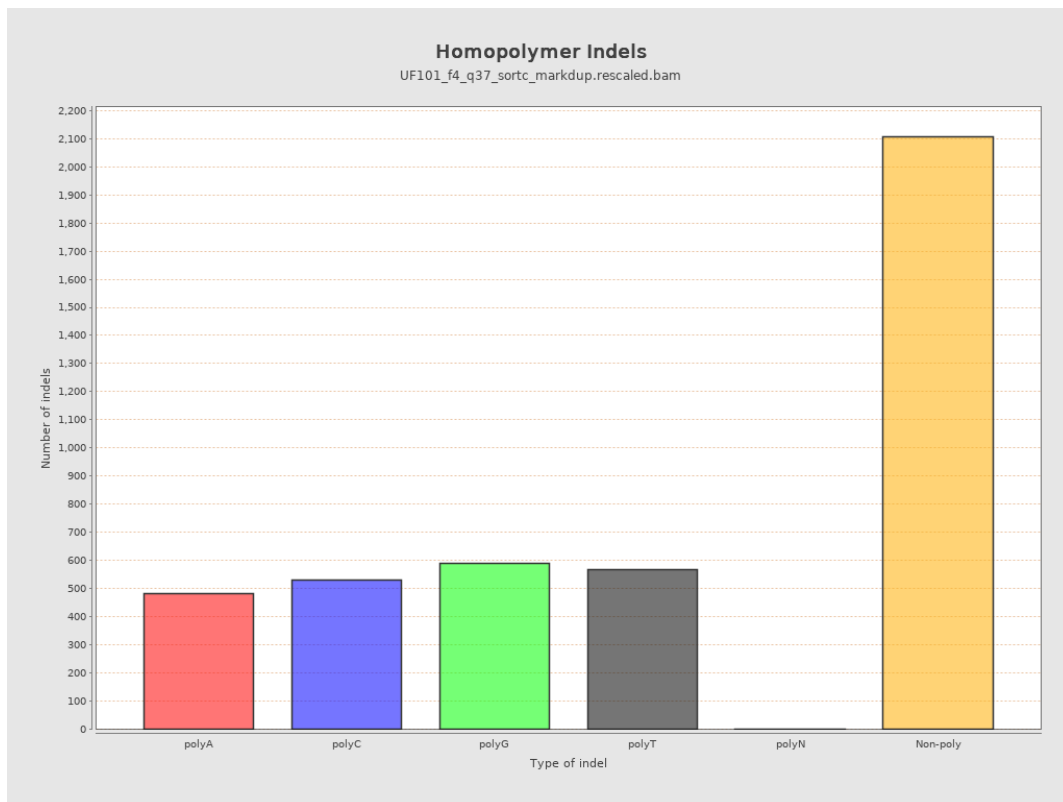
9. Results : Mapped Reads GC-content Distribution



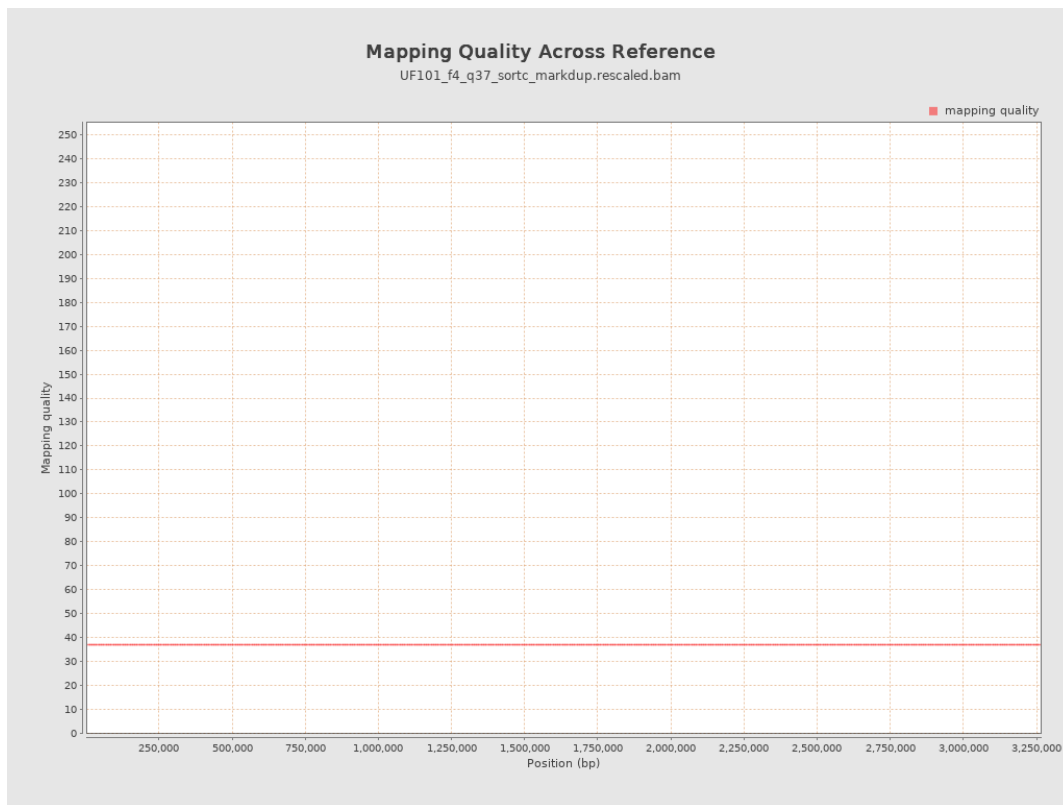
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

