Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2022/03/01 02:29:25

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam output/UF803/UF803_f4_q37_sortc_markdup.rescaled.bam -nw 400 -hm 3

1.2. Alignment

Command line:	bwa samse -r @RG\tID:UF803\tSM:UF803\tLB:nan\tPL:ILLUMINA /data/stonelab/references/M_leprae_TN/M_leprae_TN.fasta output/UF803/UF803-ancient.sai output/UF803/UF803-ancient.trimmed.fq
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 01 02:29:25 MST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	output/UF803/UF803_f4_q37_sortc_markdup.rescaled.bam

2. Summary

2.1. Globals

Reference size	3,268,203
Number of reads	238,128
Mapped reads	238,128 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	30 / 139 / 72.63
Duplicated reads (estimated)	21,406 / 8.99%
Duplication rate	8.47%
Clipped reads	2 / 0%

2.2. ACGT Content

Number/percentage of A's	3,992,092 / 23.08%
Number/percentage of C's	4,305,404 / 24.89%
Number/percentage of T's	4,061,976 / 23.49%
Number/percentage of G's	4,935,768 / 28.54%
Number/percentage of N's	10 / 0%
GC Percentage	53.43%

2.3. Coverage

Mean	5.2924
Standard Deviation	6.2973

2.4. Mapping Quality

Mean Mapping Quality	37

2.5. Mismatches and indels

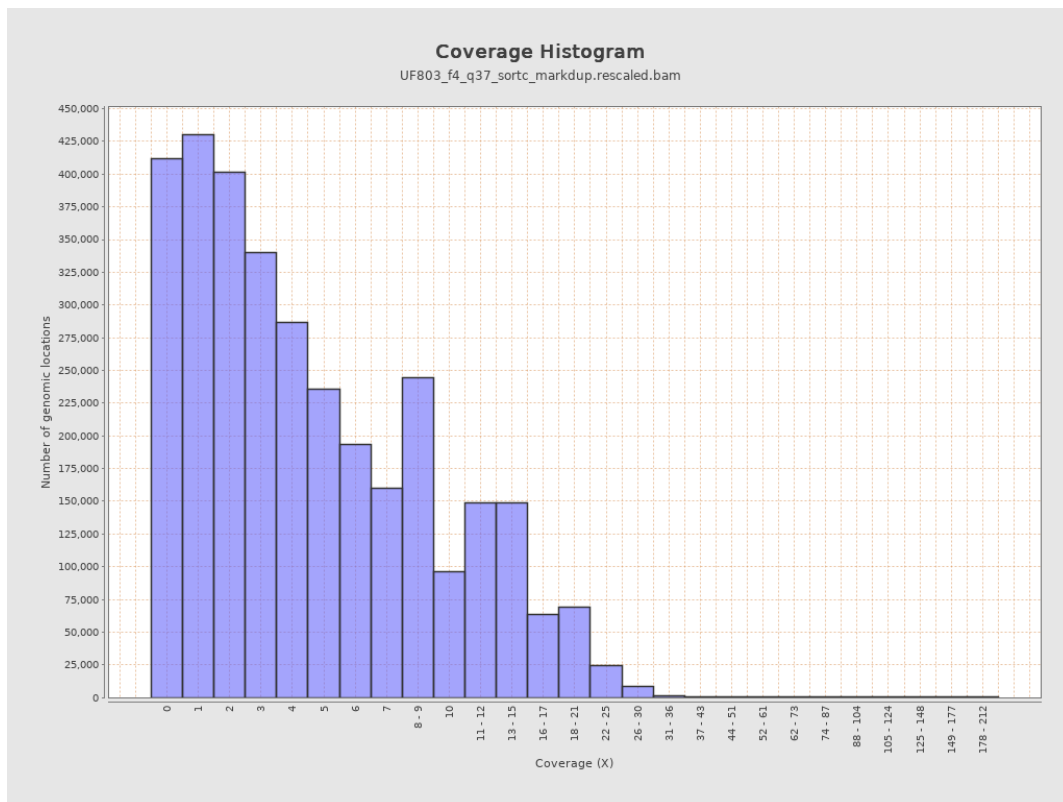|	
General error rate	0.31%
Mismatches	51,888
Insertions	871
Mapped reads with at least one insertion	0.37%
Deletions	1,302
Mapped reads with at least one deletion	0.55%
Homopolymer indels	39.16%

2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
ENA|AL450380|AL450380.1	3268203	17296764	5.2924	6.2973

3. Results : Coverage across reference

Coverage across reference
UF803_f4_q37_sortc_markdup.rescaled.bam

4. Results : Coverage Histogram
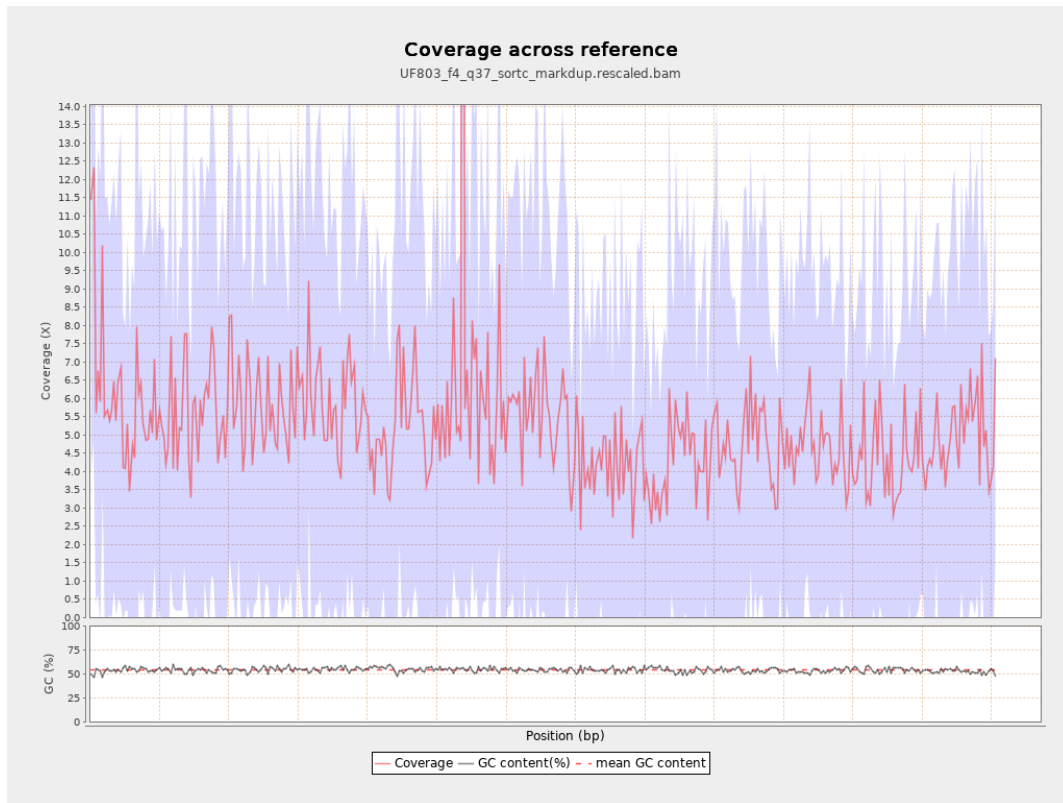
Coverage Histogram
UF803_f4_q37_sortc_markdup.rescaled.bam
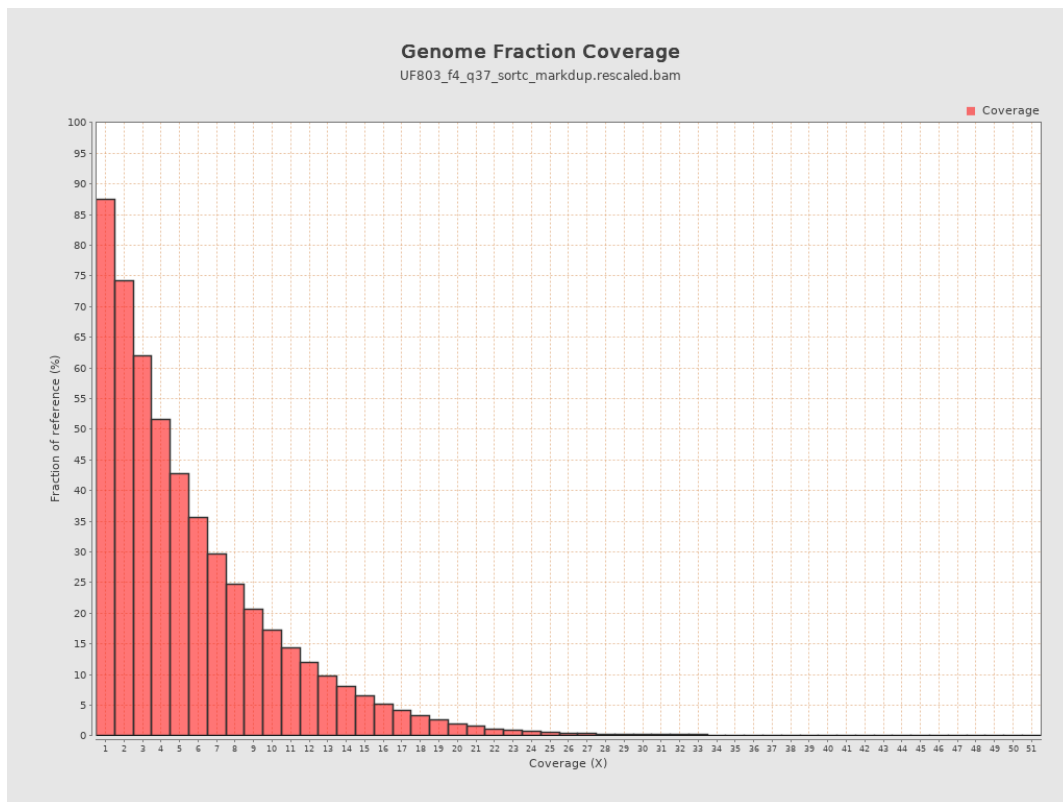
5. Results : Coverage Histogram (0-50X)
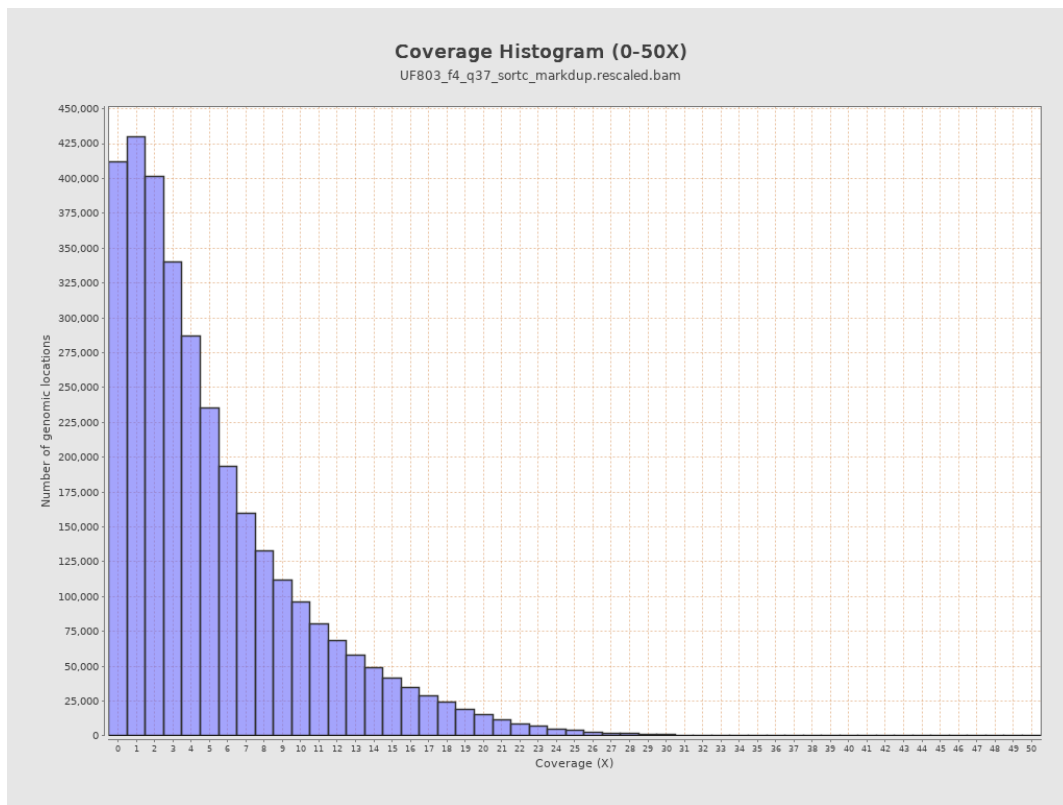
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
UF803_f4_q37_sortc_markdup.rescaled.bam

7. Results : Duplication Rate Histogram
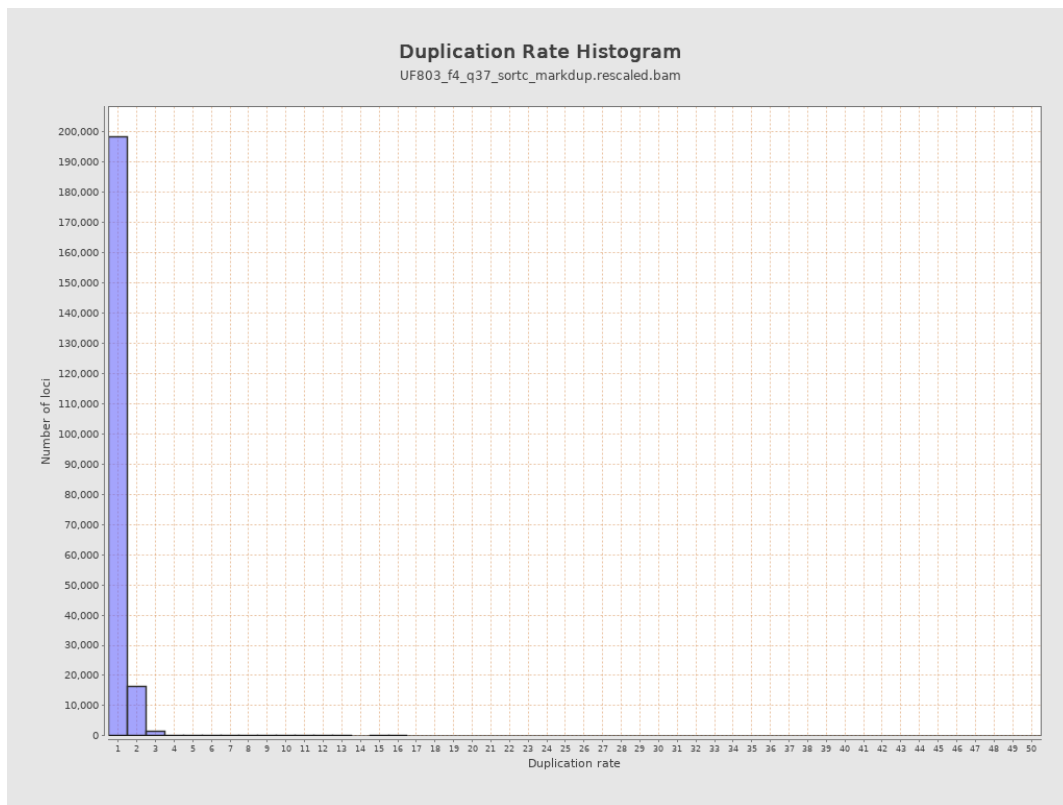
Duplication Rate Histogram

UF803_f4_q37_sortc_markdup.rescaled.bam

8. Results : Mapped Reads Nucleotide Content

Mapped Reads Nucleotide Content
UF803_f4_q37_sortc_markdup.rescaled.bam

9. Results : Mapped Reads GC-content Distribution

Mapped Reads GC-content Distribution
UF803_f4_q37_sortc_markdup.rescaled.bam
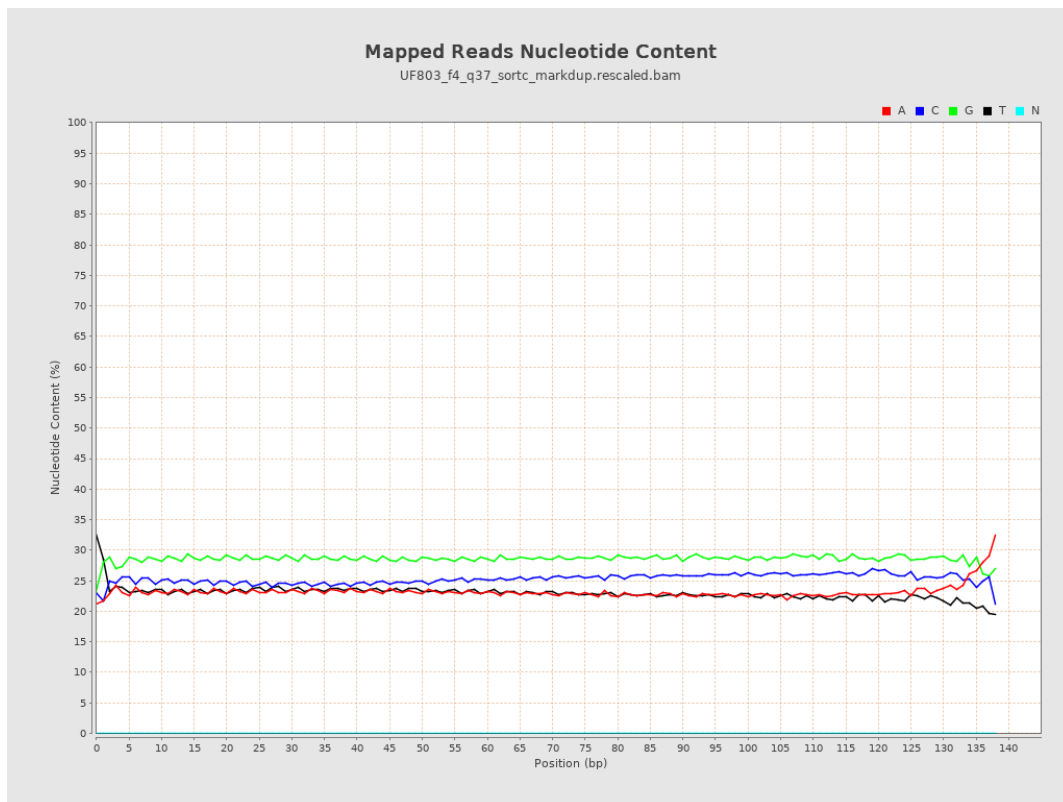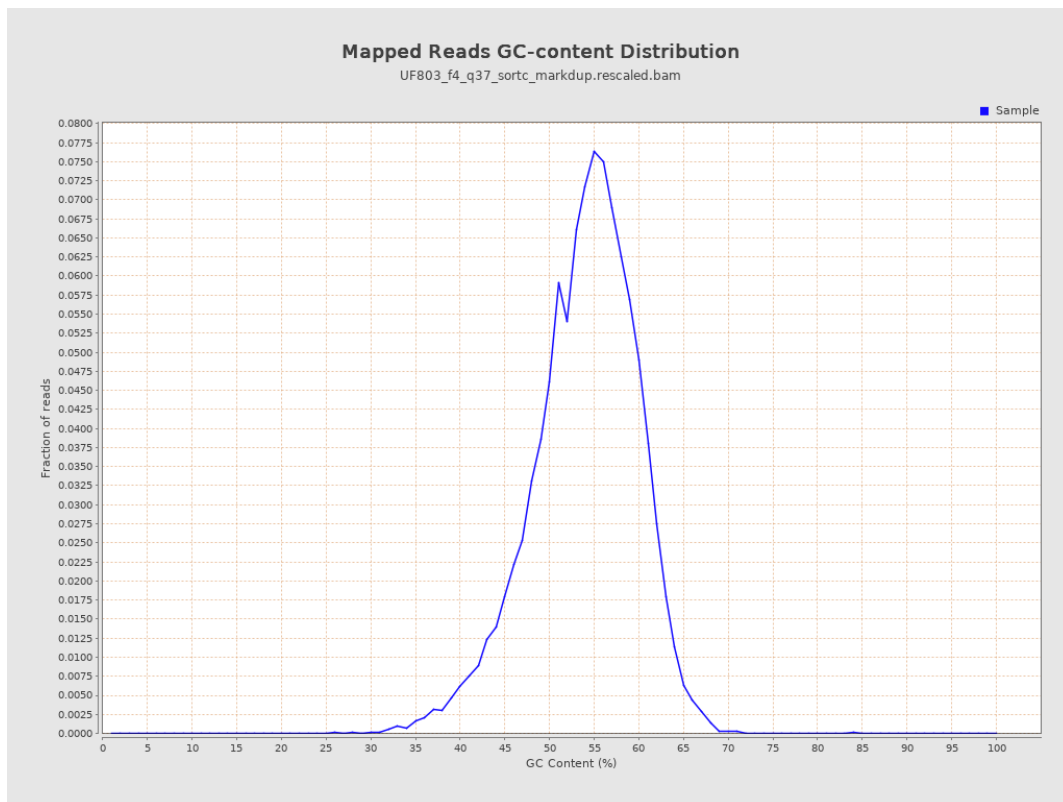
10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
UF803_f4_q37_sortc_markdup.rescaled.bam
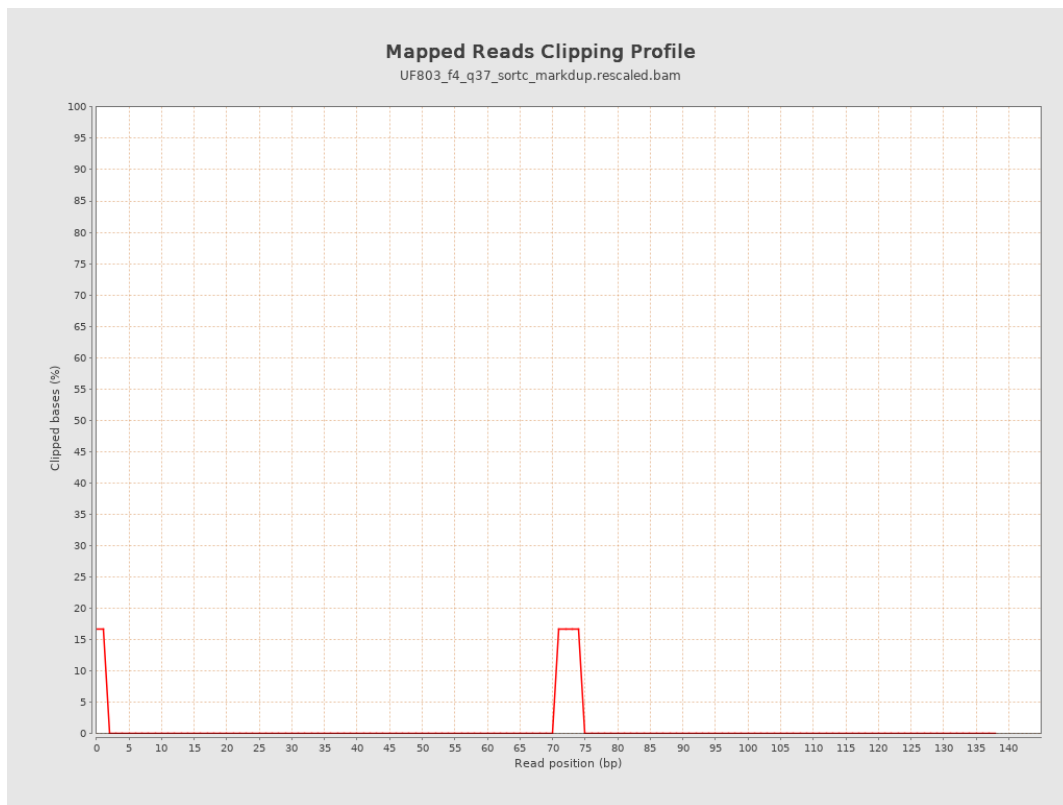
11. Results : Homopolymer Indels

Homopolymer Indels
UF803_f4_q37_sortc_markdup.rescaled.bam

12. Results : Mapping Quality Across Reference

Mapping Quality Across Reference
UF803_f4_q37_sortc_markdup.rescaled.bam

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
UF803_f4_q37_sortc_markdup.rescaled.bam