Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:40:48

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/639
.nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/639 .nodup.bam
Program:	bwa (0.7.17-r1188)
Analyze overlapping paired-end reads:	no
Command line:	bwa mem -M -t 8 -R @RG\tID:$unit\tPL:Illumina\tLB:LibA\t SM:$sample /proj/uppstore2018210/Aalpina/data/reference/GCA_900128785.1_MPIPZ. v5_genomic.fa /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_253/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_253_S334_L003 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_253/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_253_S334_L003 _R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:40:47 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	92,803,867
Mapped reads	86,819,937 / 93.55%
Unmapped reads	5,983,930 / 6.45%
Mapped paired reads	86,819,937 / 93.55%
Mapped reads, first in pair	43,477,820 / 46.85%
Mapped reads, second in pair	43,342,117 / 46.7%
Mapped reads, both in pair	84,903,033 / 91.49%
Mapped reads, singletons	1,916,904 / 2.07%
Read min/max/mean length	30 / 151 / 148.01
Duplicated reads (flagged)	14,019,314 / 15.11%
Clipped reads	20,335,743 / 21.91%

2.2. ACGT Content

Number/percentage of A's	3,691,084,789 / 30.83%
Number/percentage of C's	2,294,608,119 / 19.16%
Number/percentage of T's	3,695,569,977 / 30.87%
Number/percentage of G's	2,292,019,527 / 19.14%
Number/percentage of N's	45,666 / 0%
GC Percentage	38.31%

2.3. Coverage

Mean	38.521
Standard Deviation	327.3987

2.4. Mapping Quality

Mean Mapping Quality	44

2.5. Insert size

Mean	232,333.65
Standard Deviation	2,288,916.68
P25/Median/P75	310 / 408 / 534

2.6. Mismatches and indels

General error rate	2.36%
Mismatches	259,904,714
Insertions	8,325,411
Mapped reads with at least one insertion	8.6%
Deletions	8,378,038
Mapped reads with at least one deletion	8.54%
Homopolymer indels	56.13%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	955796002	32.1553	121.4763

LT669789.1	36598175	1431748961	39.1208	353.437
LT669790.1	30422129	1306963218	42.9609	362.1854
LT669791.1	52758100	1986196931	37.6472	321.3608
LT669792.1	28376109	1087774140	38.3342	339.467
LT669793.1	33388210	1188883685	35.6079	213.2598
LT669794.1	50579949	1849949277	36.5748	303.6853
LT669795.1	49795044	2197448436	44.1299	436.7444

3. Results : Coverage across reference

Coverage across reference
639.nodup.bam

4. Results : Coverage Histogram

Coverage Histogram
639.nodup.bam
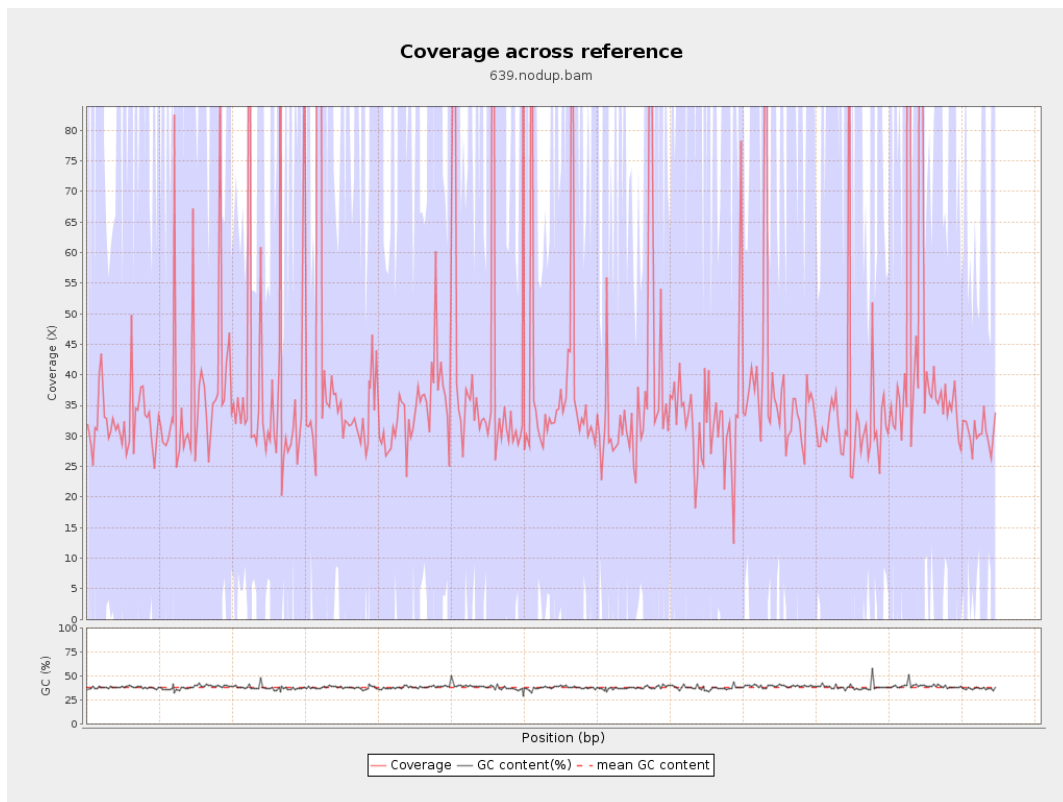
5. Results : Coverage Histogram (0-50X)
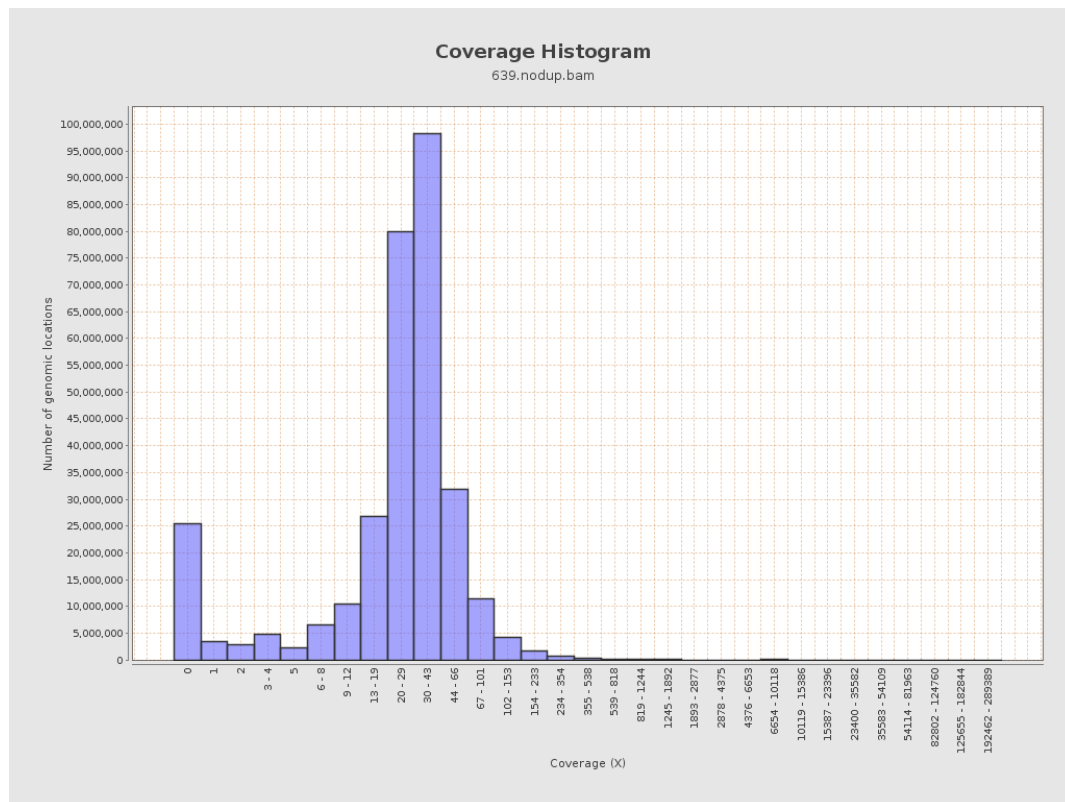
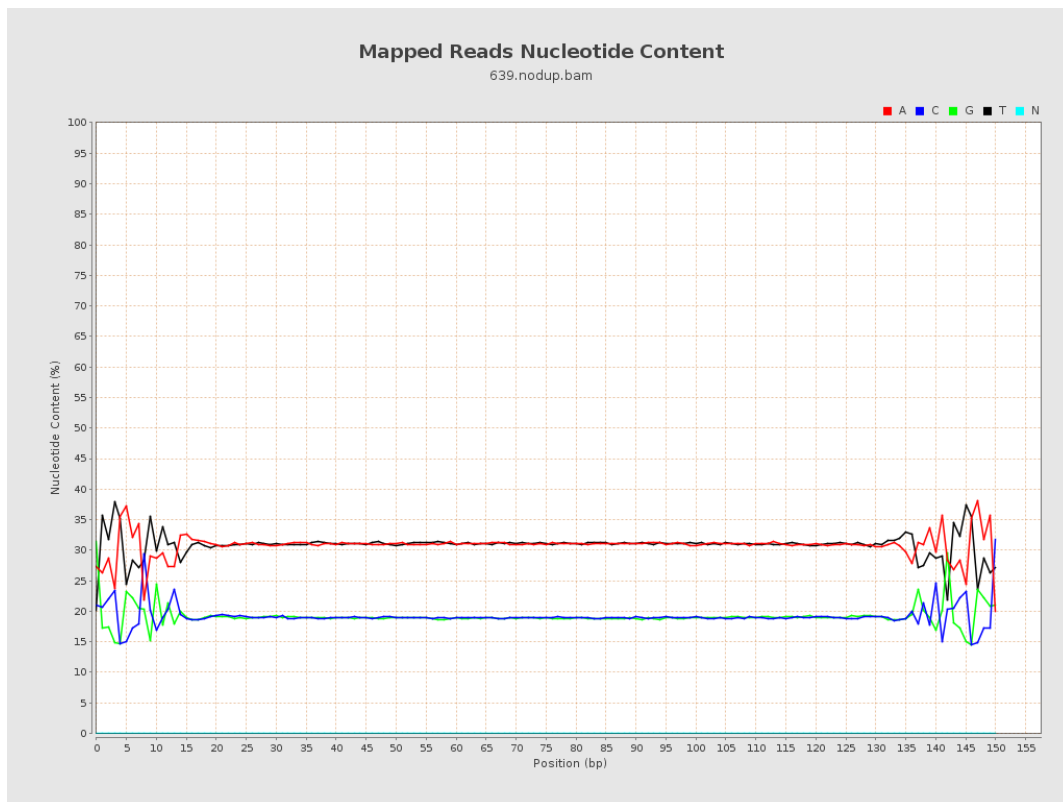Coverage Histogram (0-50X)
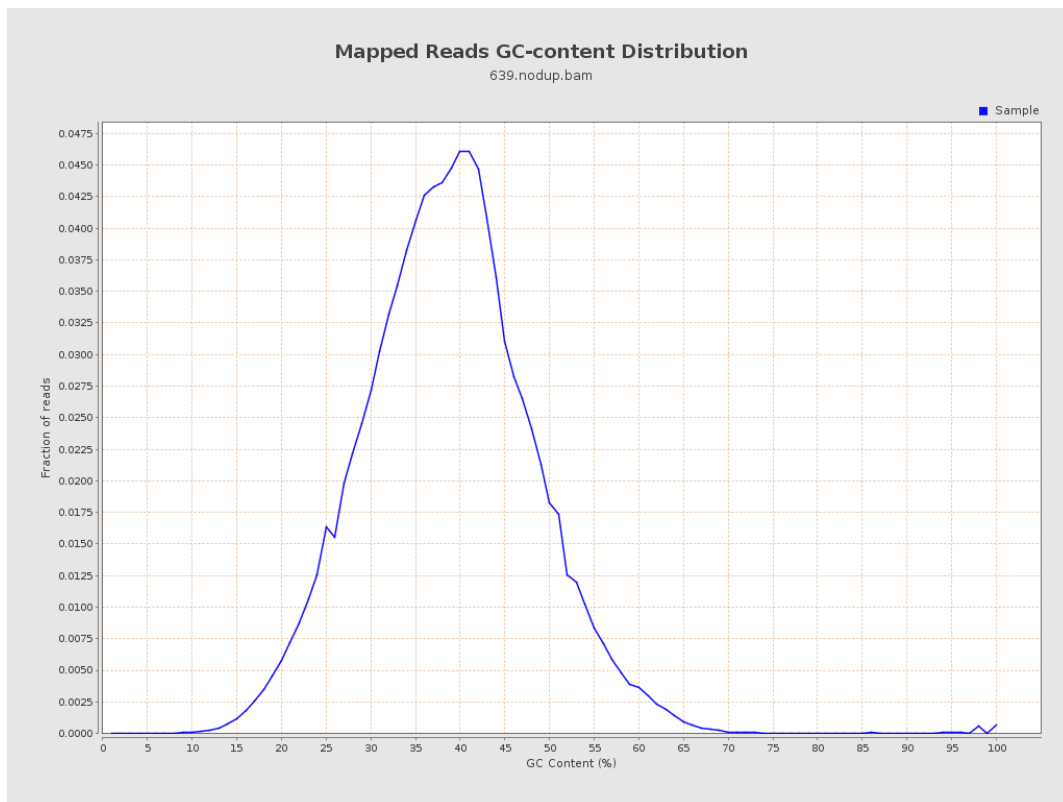639.nodup.bam
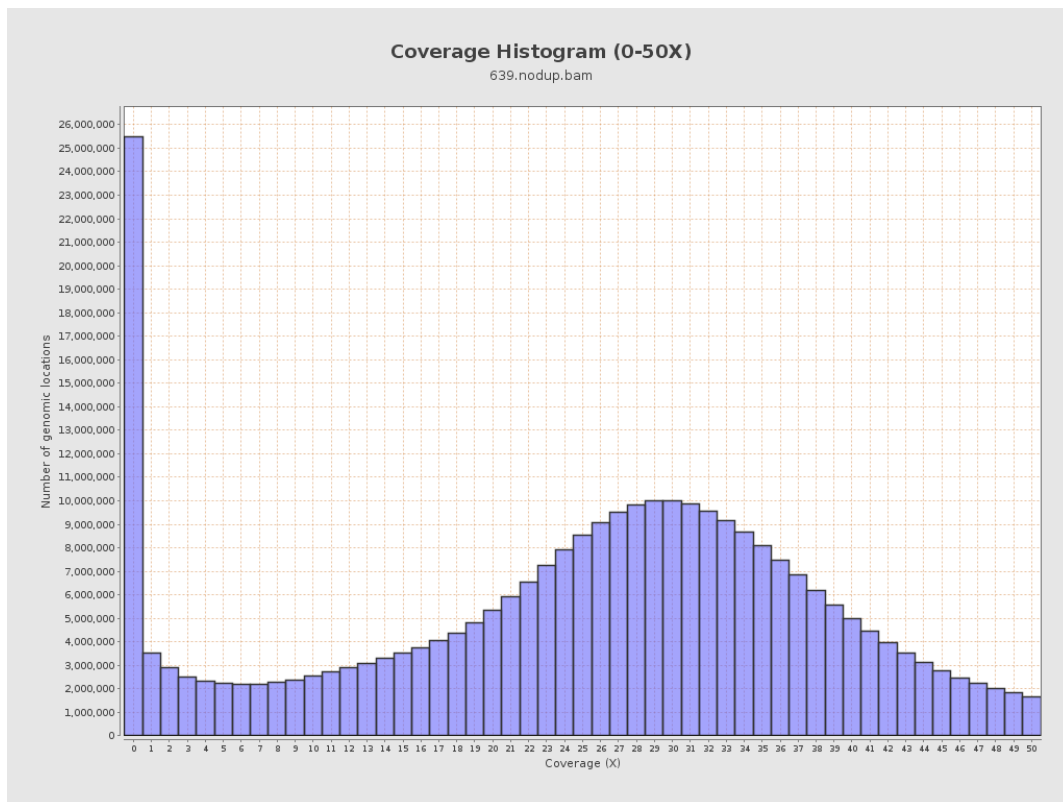
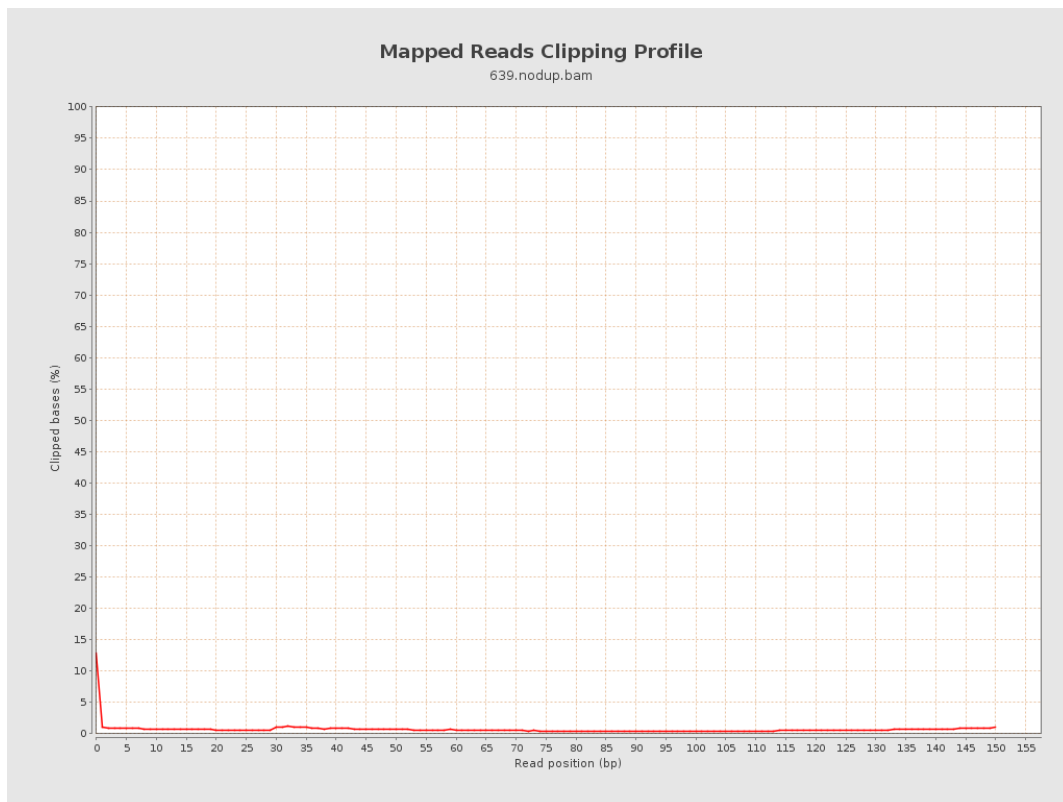# 6. Results : Genome Fraction Coverage
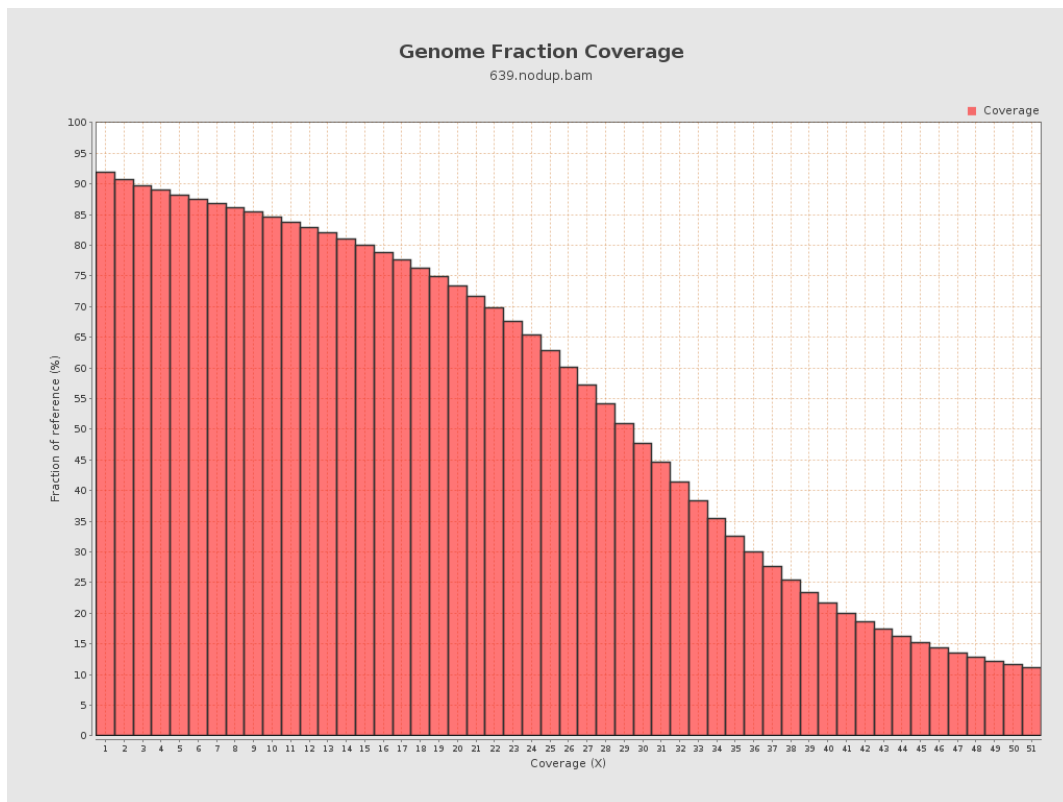
7. Results : Duplication Rate Histogram
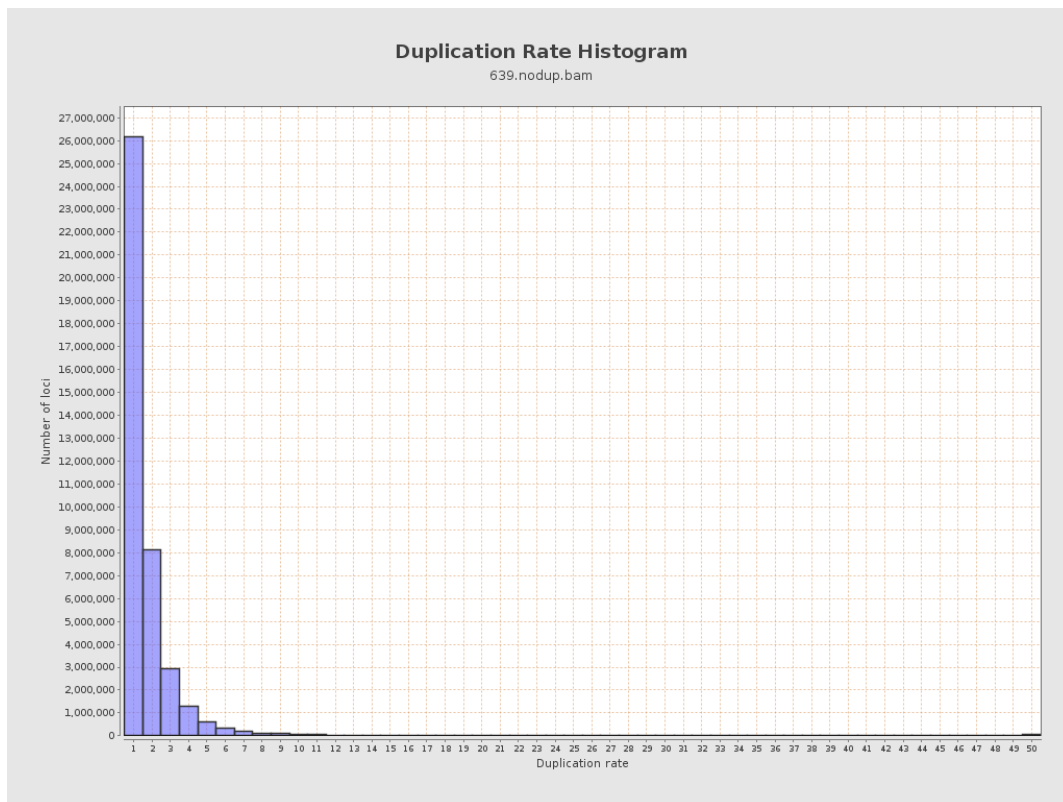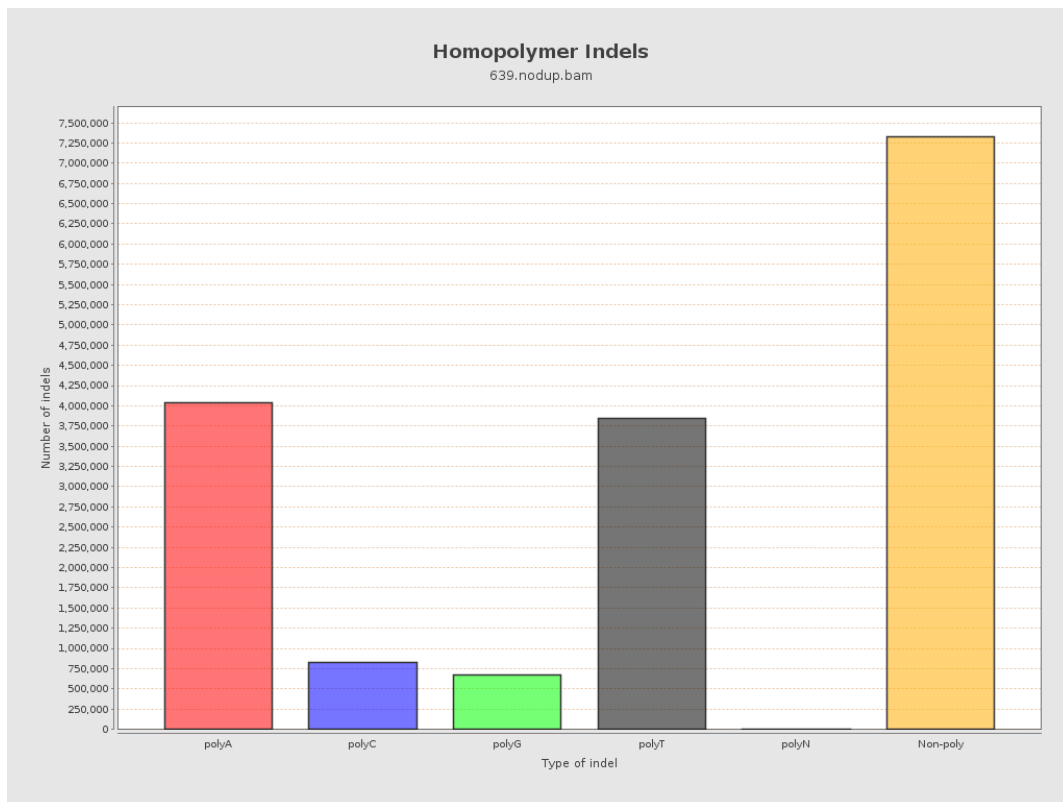
8. Results : Mapped Reads Nucleotide Content
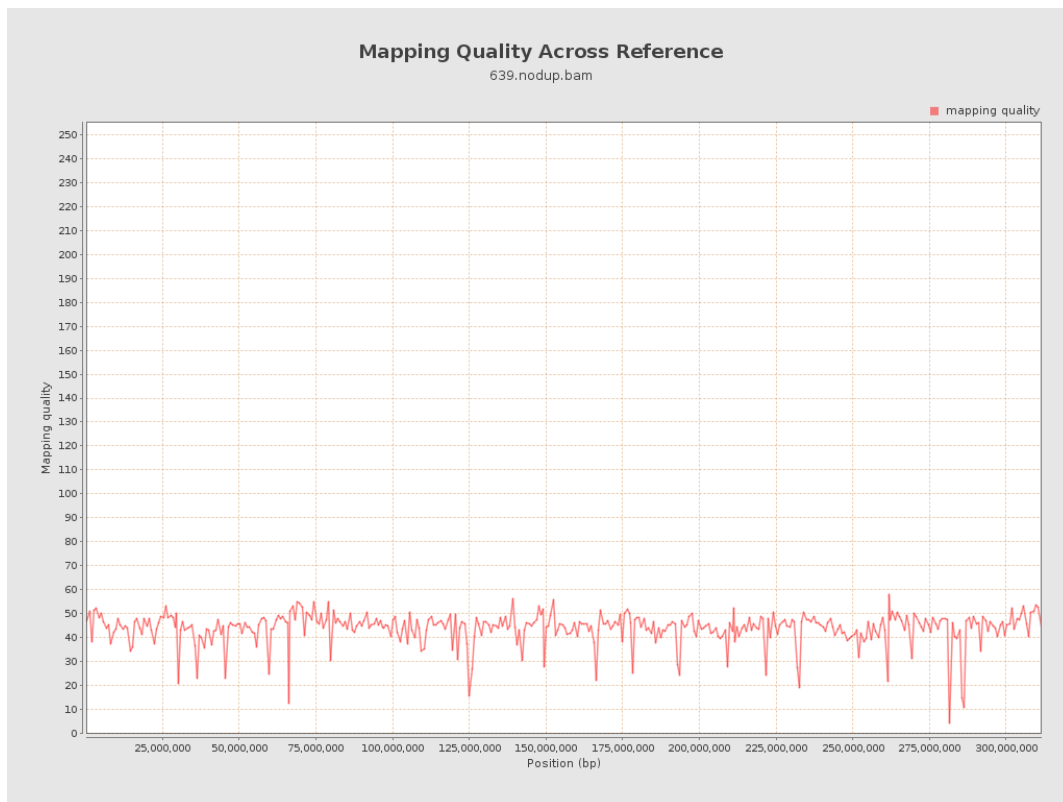
9. Results : Mapped Reads GC-content Distribution

Mapped Reads GC-content Distribution
639.nodup.bam

10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
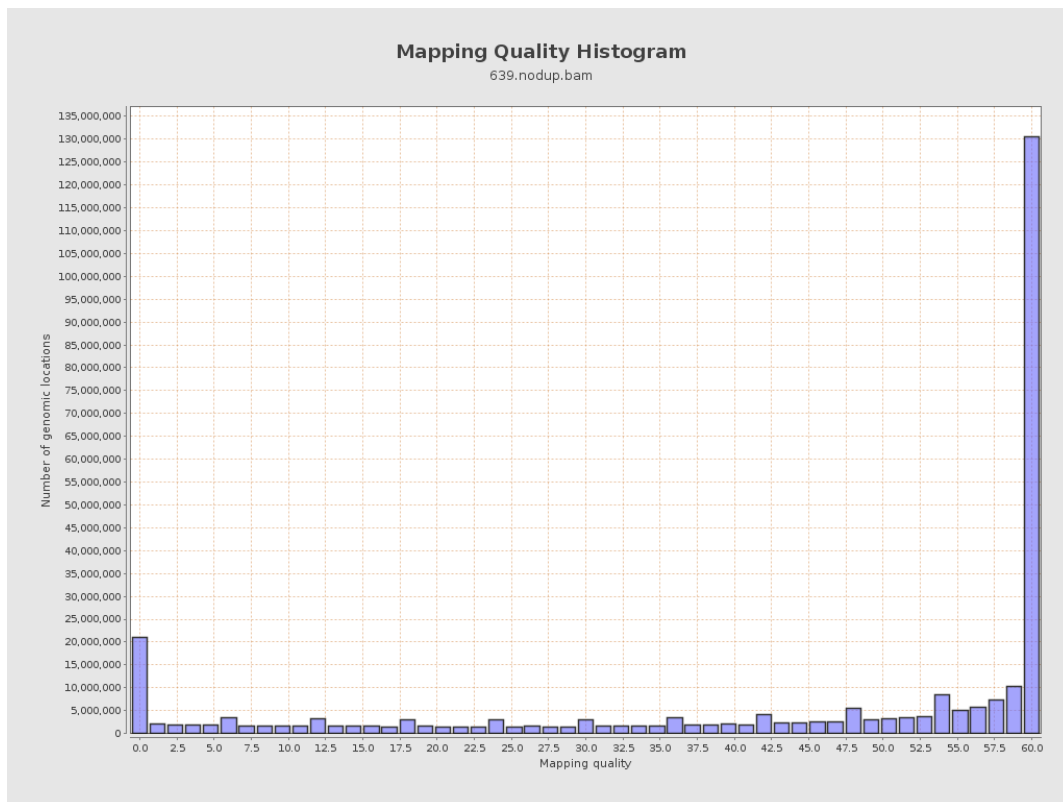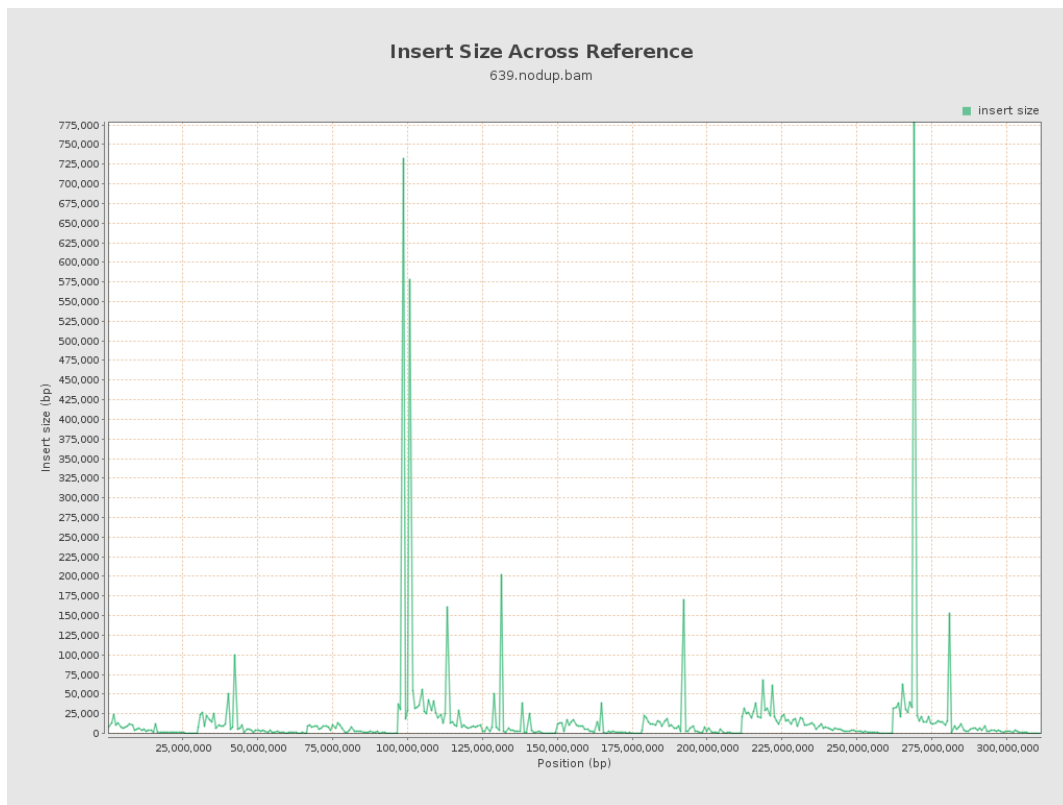639.nodup.bam

11. Results : Homopolymer Indels

12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram

Insert Size Histogram
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