Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:32:08

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/611 .nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/611 .nodup.bam
Program:	bwa (0.7.17-r1188)
Analyze overlapping paired-end reads:	no
Command line:	bwa mem -M -t 8 -R @RG\tID:$unit\tPL:Illumina\tLB:LibA\tSM:$sample /proj/uppstore2018210/Aalpina/data/reference/GCA_900128785.1_MPIPZ.v5_genomic.fa /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_208/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_208_S289_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_208/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_208_S289_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:32:07 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	70,683,741
Mapped reads	65,275,368 / 92.35%
Unmapped reads	5,408,373 / 7.65%
Mapped paired reads	65,275,368 / 92.35%
Mapped reads, first in pair	32,677,152 / 46.23%
Mapped reads, second in pair	32,598,216 / 46.12%
Mapped reads, both in pair	63,581,588 / 89.95%
Mapped reads, singletons	1,693,780 / 2.4%
Read min/max/mean length	30 / 151 / 148.16
Duplicated reads (flagged)	10,338,621 / 14.63%
Clipped reads	15,169,680 / 21.46%

2.2. ACGT Content

Number/percentage of A's	2,767,528,386 / 30.78%
Number/percentage of C's	1,729,498,743 / 19.23%
Number/percentage of T's	2,773,434,331 / 30.85%
Number/percentage of G's	1,721,044,829 / 19.14%
Number/percentage of N's	33,258 / 0%
GC Percentage	38.38%

2.3. Coverage

Mean	28.9253
Standard Deviation	256.3191

2.4. Mapping Quality

Mean Mapping Quality	44.35

2.5. Insert size

| Mean	234,099.1
Standard Deviation	2,320,155.48
P25/Median/P75	305 / 400 / 522

2.6. Mismatches and indels

General error rate	2.34%
Mismatches	192,937,090
Insertions	6,341,279
Mapped reads with at least one insertion	8.69%
Deletions	6,122,533
Mapped reads with at least one deletion	8.32%
Homopolymer indels	57%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	689362832	23.1919	95.0648

|				
LT669789.1	36598175	1057597983	28.8976	275.4027
LT669790.1	30422129	1021855213	33.5892	341.606
LT669791.1	52758100	1522211601	28.8527	264.3576
LT669792.1	28376109	817406794	28.8062	281.0262
LT669793.1	33388210	860302315	25.7666	131.7052
LT669794.1	50579949	1373121854	27.1476	210.5486
LT669795.1	49795044	1672492883	33.5875	320.8935

3. Results : Coverage across reference

Coverage across reference

611.nodup.bam
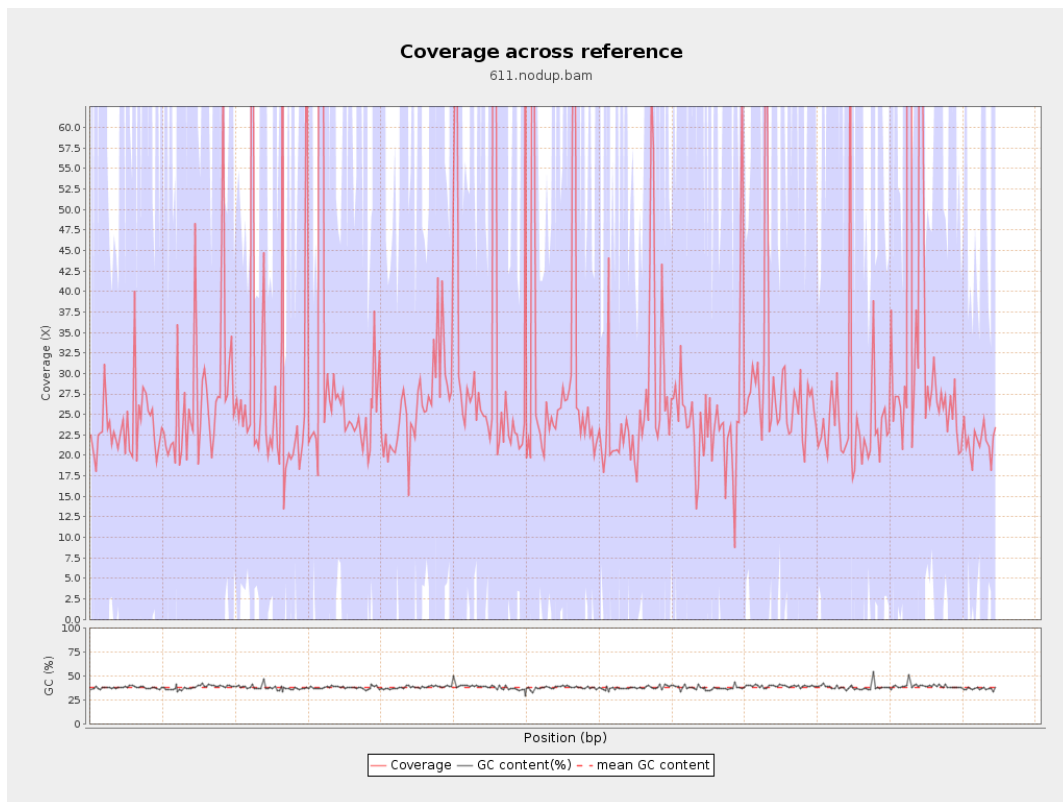
4. Results : Coverage Histogram
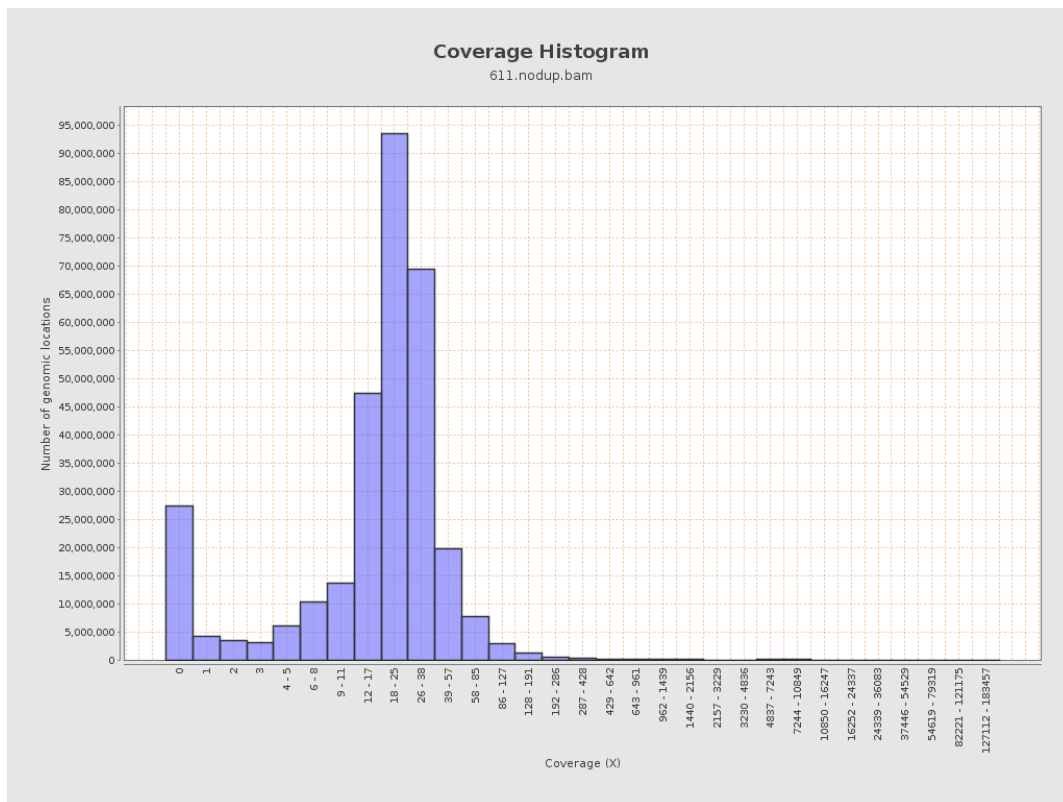
5. Results : Coverage Histogram (0-50X)
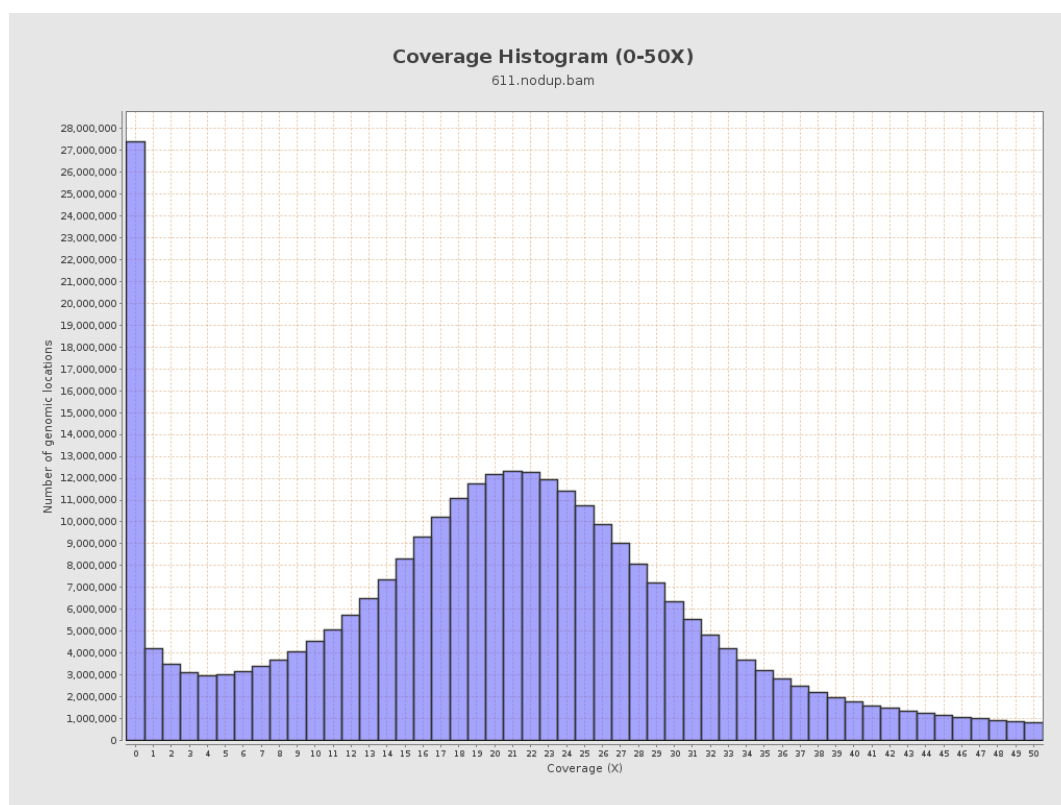
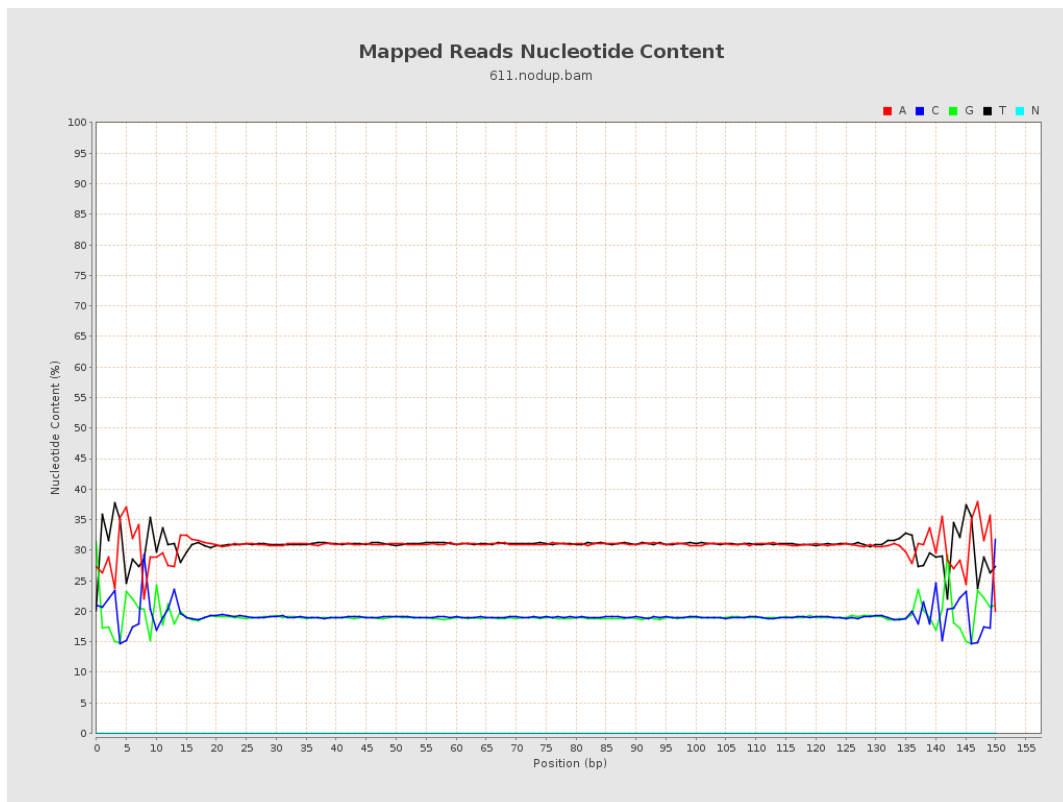# 6. Results : Genome Fraction Coverage

Genome Fraction Coverage
611.nodup.bam
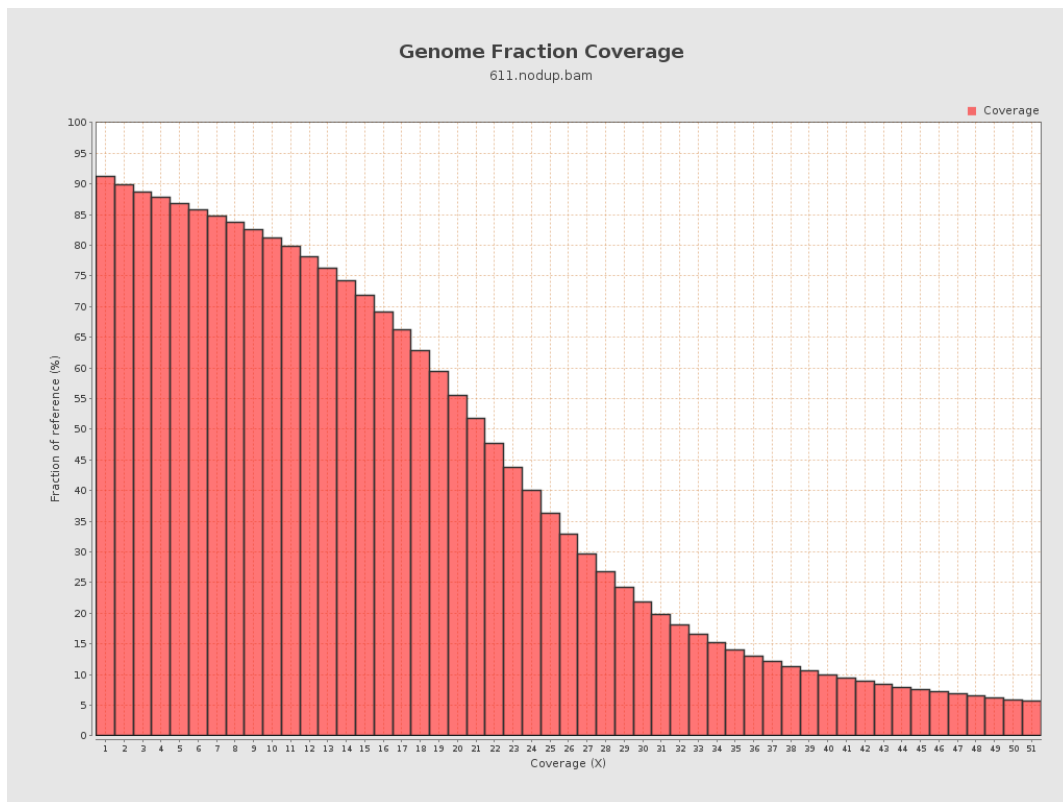
7. Results : Duplication Rate Histogram
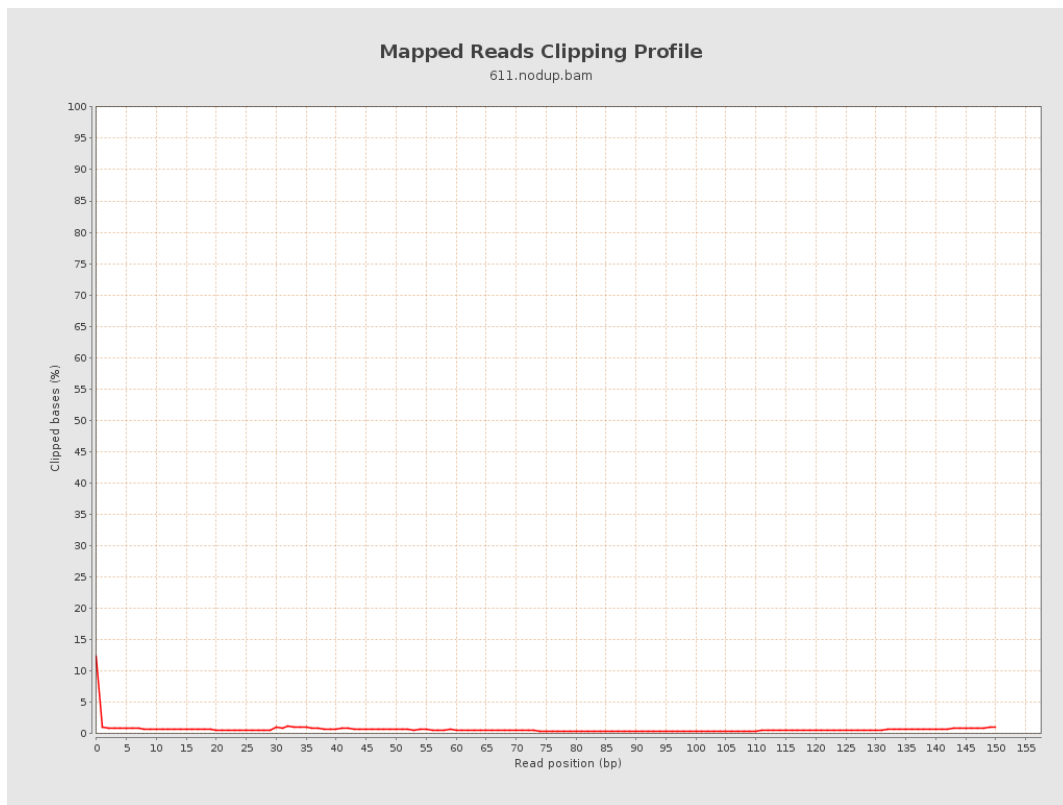
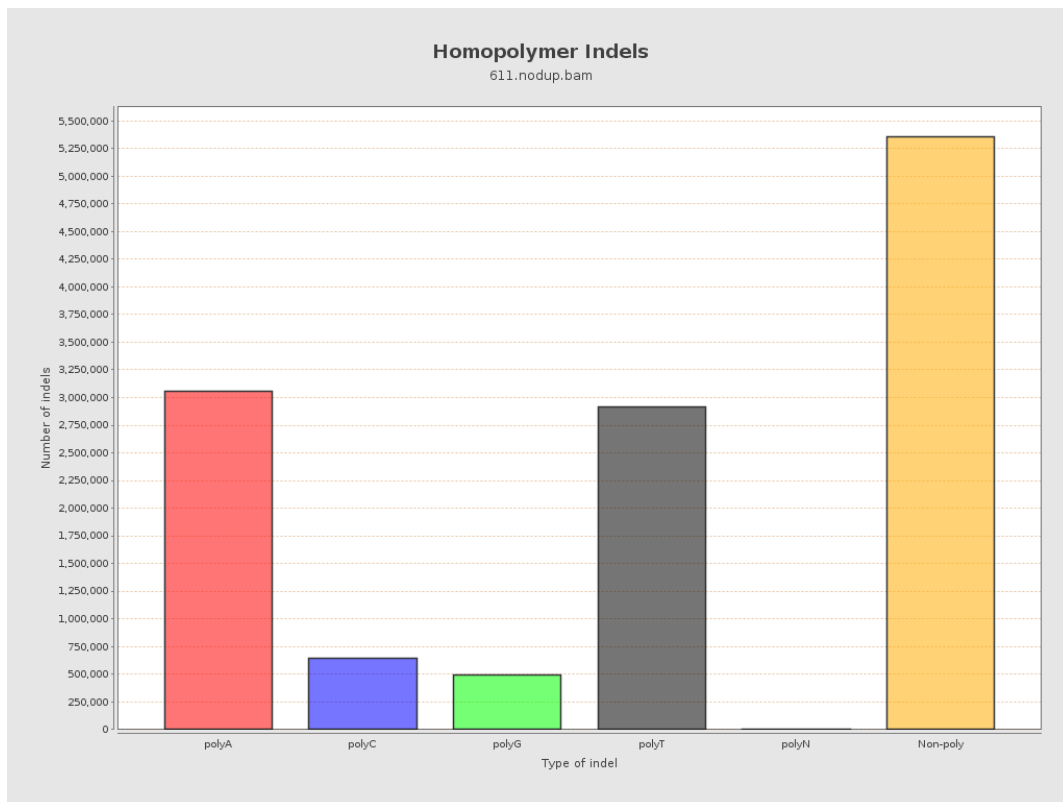# 8. Results : Mapped Reads Nucleotide Content
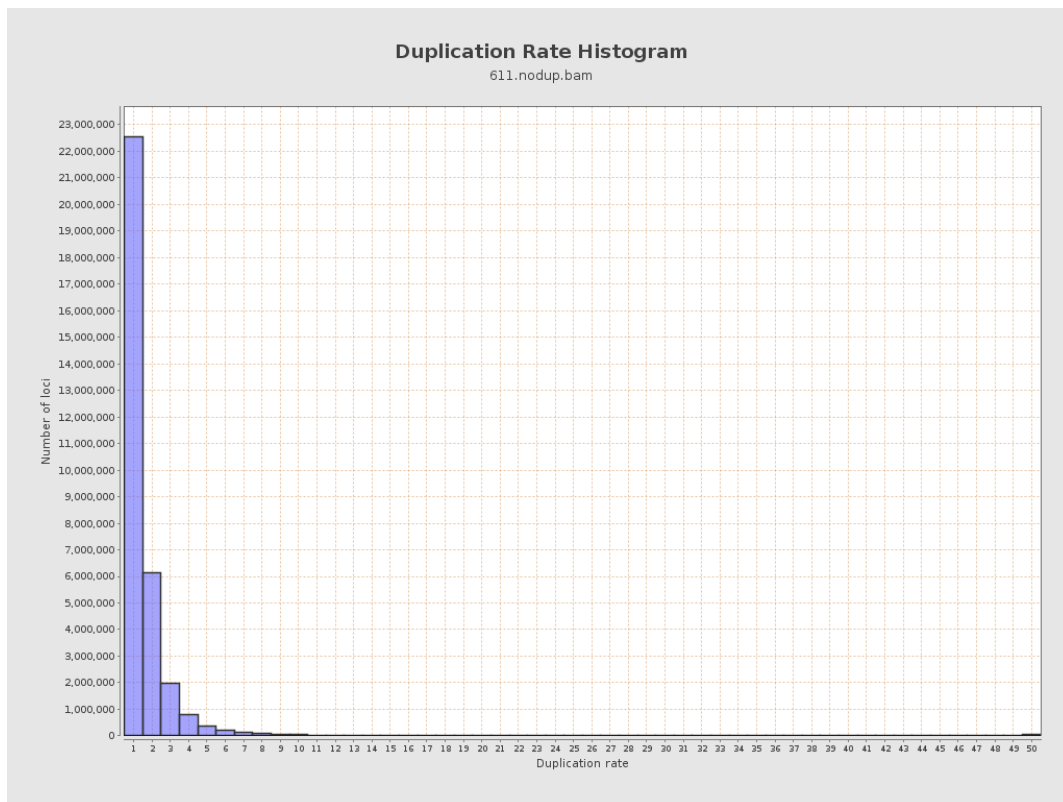
Mapped Reads Nucleotide Content
611.nodup.bam

9. Results : Mapped Reads GC-content Distribution
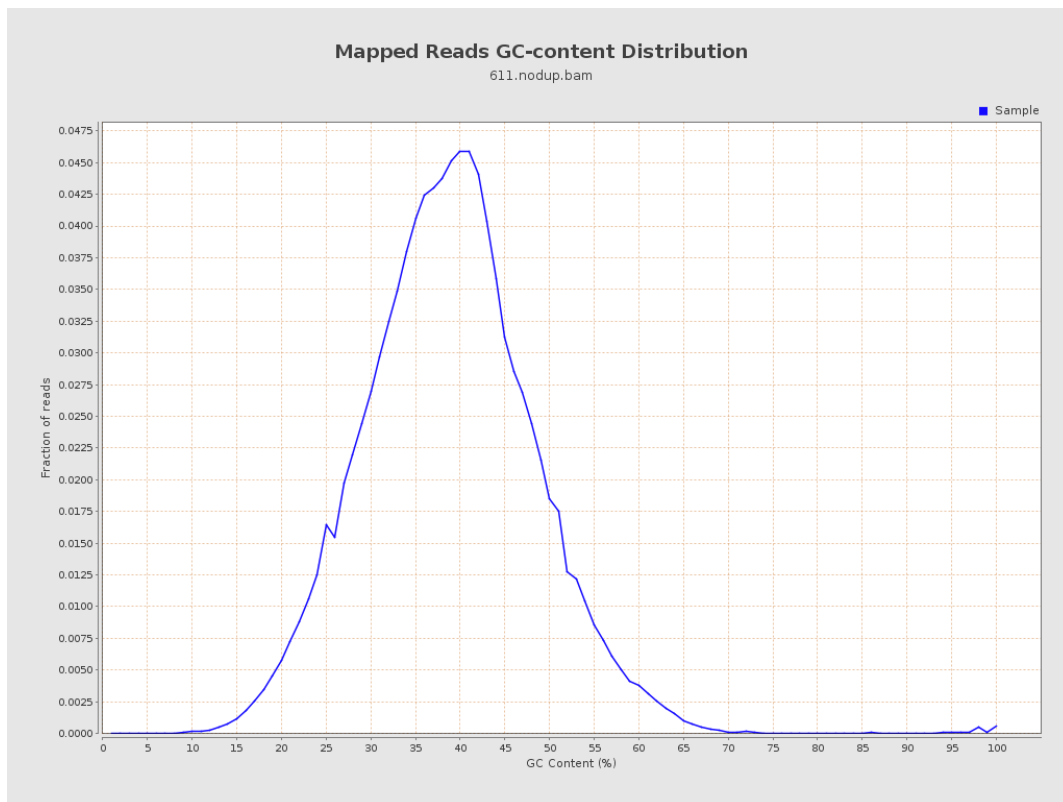
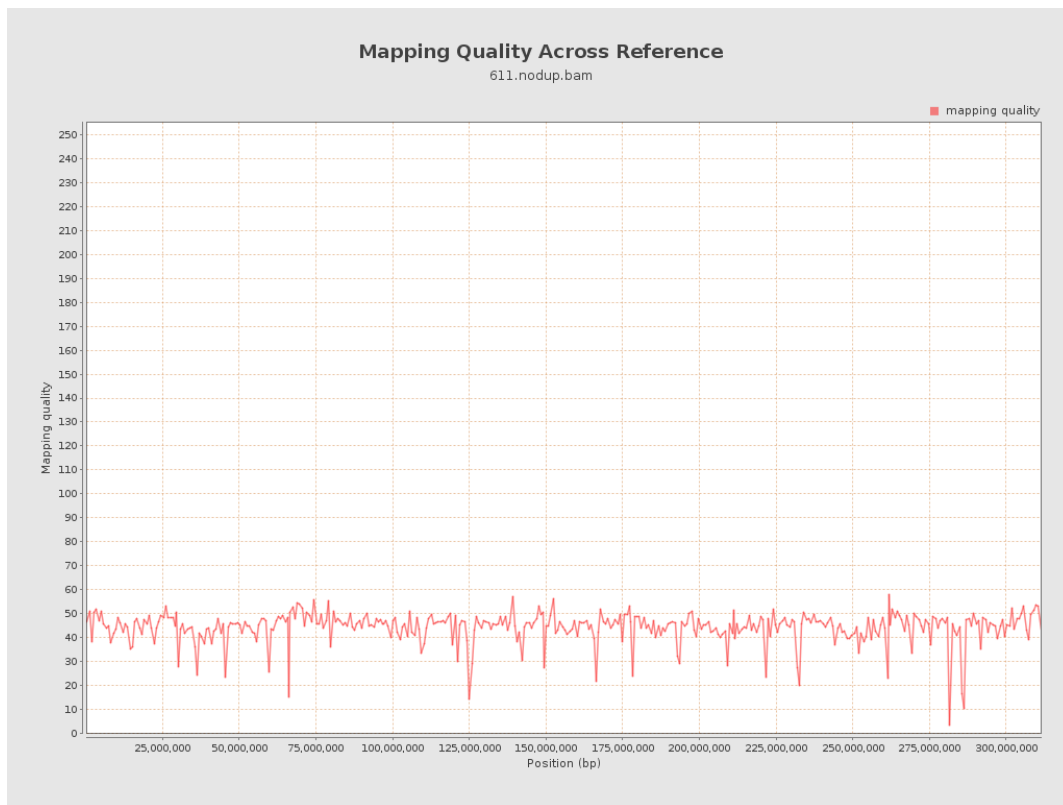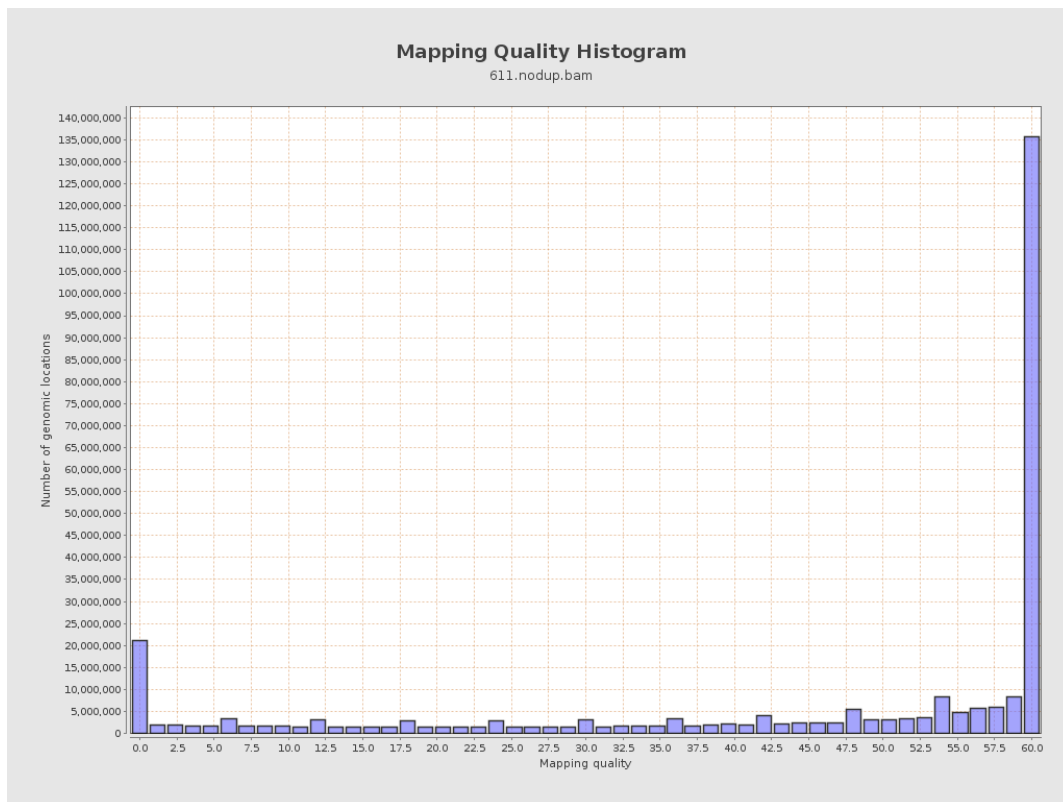# 10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
611.nodup.bam

11. Results : Homopolymer Indels

12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
611.nodup.bam

14. Results : Insert Size Across Reference
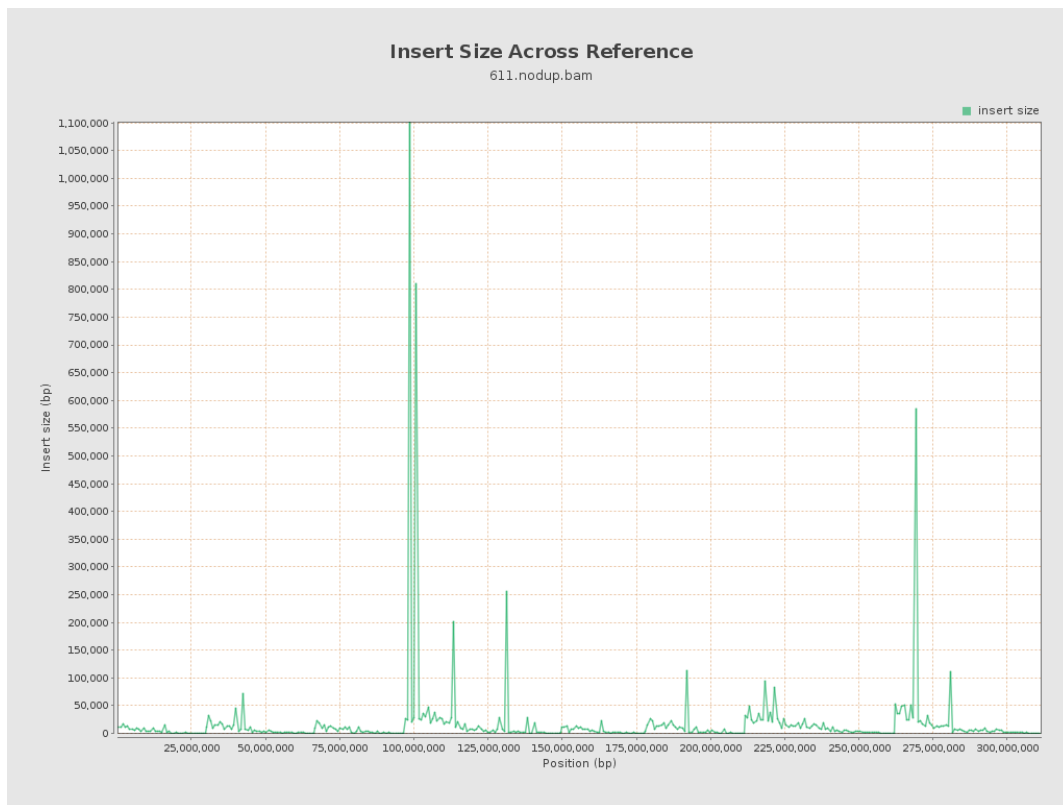
15. Results : Insert Size Histogram