Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:31:46

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/661
.nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/661 .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_174/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_174_S264_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_174/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_174_S264_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:31:45 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	67,784,088
Mapped reads	62,891,598 / 92.78%
Unmapped reads	4,892,490 / 7.22%
Mapped paired reads	62,891,598 / 92.78%
Mapped reads, first in pair	31,525,837 / 46.51%
Mapped reads, second in pair	31,365,761 / 46.27%
Mapped reads, both in pair	61,412,495 / 90.6%
Mapped reads, singletons	1,479,103 / 2.18%
Read min/max/mean length	30 / 151 / 148.16
Duplicated reads (flagged)	10,854,460 / 16.01%
Clipped reads	14,206,439 / 20.96%

2.2. ACGT Content

Number/percentage of A's	2,687,344,809 / 30.82%
Number/percentage of C's	1,672,328,893 / 19.18%
Number/percentage of T's	2,692,439,439 / 30.88%
Number/percentage of G's	1,667,046,382 / 19.12%
Number/percentage of N's	36,608 / 0%
GC Percentage	38.3%

2.3. Coverage

Mean	28.0518
Standard Deviation	228.7091

2.4. Mapping Quality

Mean Mapping Quality	43.67

2.5. Insert size

Mean	255,269.35
Standard Deviation	2,406,186.67
P25/Median/P75	359 / 470 / 619

2.6. Mismatches and indels

General error rate	2.38%
Mismatches	191,173,783
Insertions	6,022,779
Mapped reads with at least one insertion	8.6%
Deletions	6,076,683
Mapped reads with at least one deletion	8.55%
Homopolymer indels	56.21%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	678186616	22.8159	70.7954

| LT669789.1	36598175	1051321056	28.7261	246.2749
LT669790.1	30422129	913731415	30.0351	242.1017
LT669791.1	52758100	1469029777	27.8446	210.8723
LT669792.1	28376109	783327149	27.6052	288.454
LT669793.1	33388210	878404896	26.3088	168.0781
LT669794.1	50579949	1349967499	26.6898	202.3615
LT669795.1	49795044	1618143799	32.4961	298.1283

3. Results : Coverage across reference

Coverage across reference
661.nodup.bam
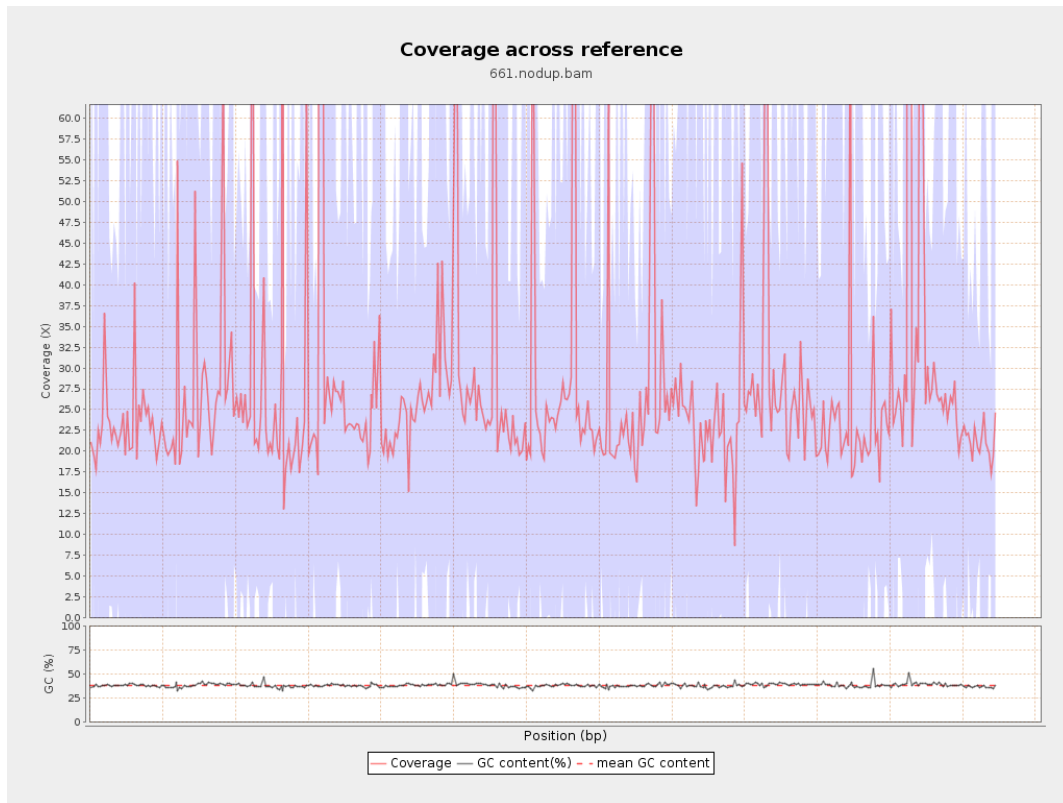
4. Results : Coverage Histogram

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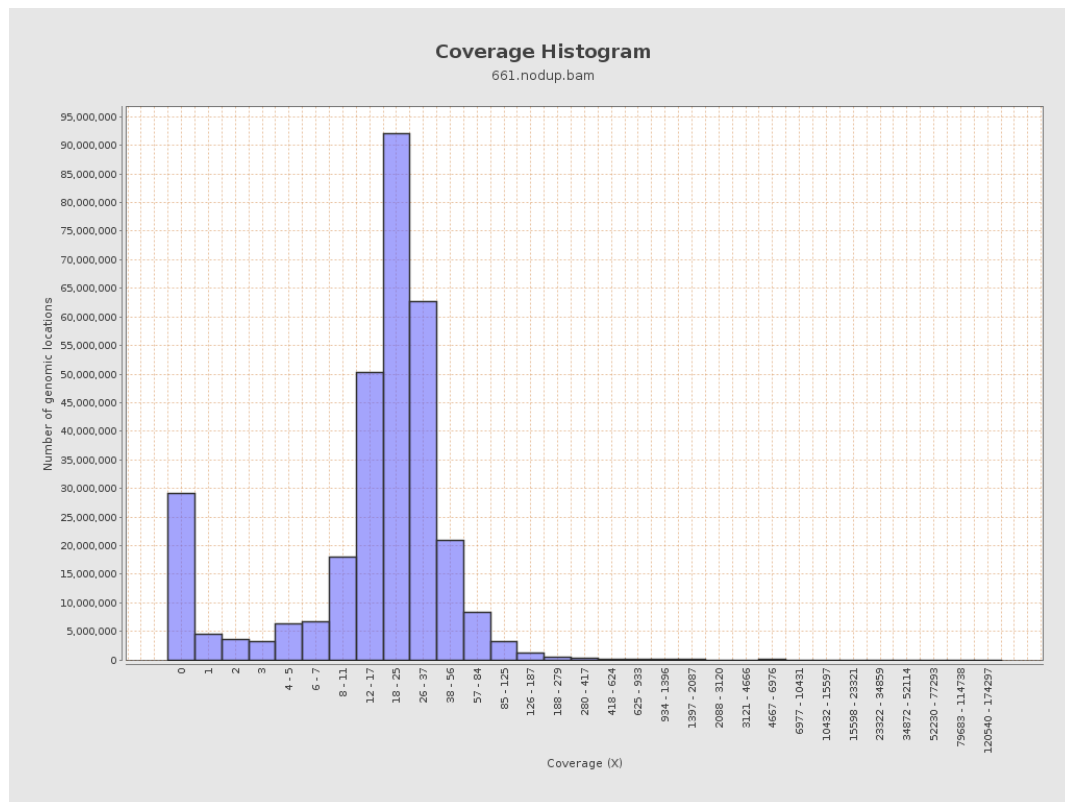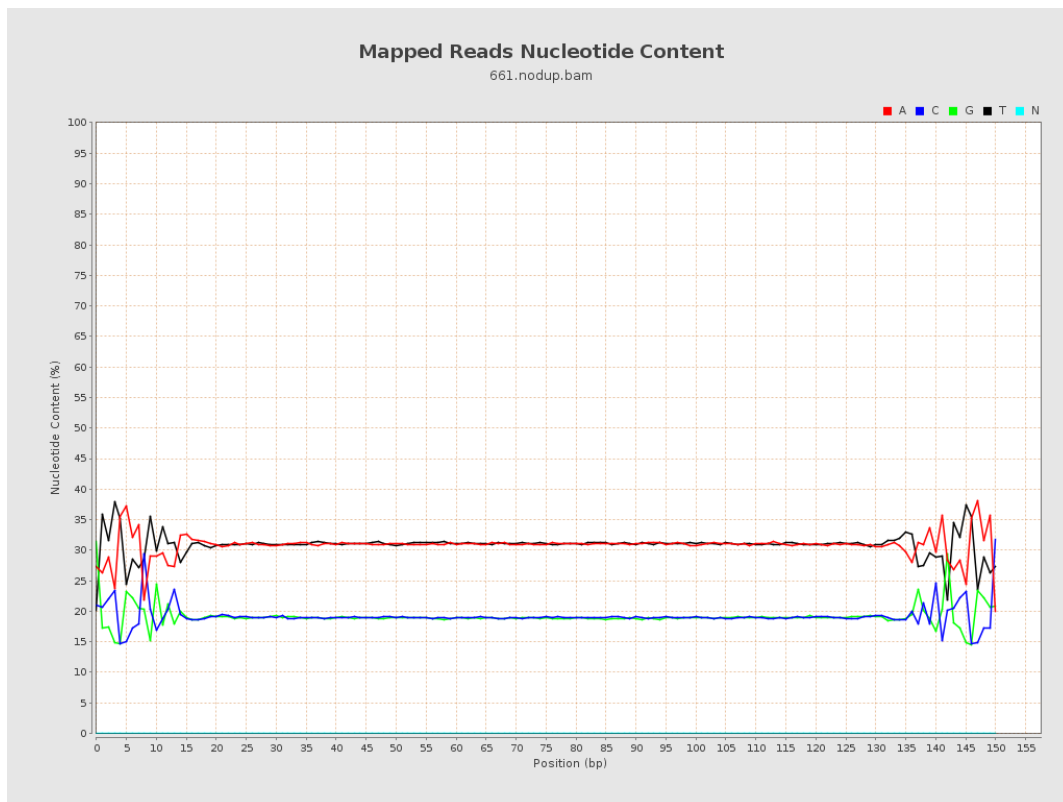

Coverage Histogram (0-50X)
661.nodup.bam
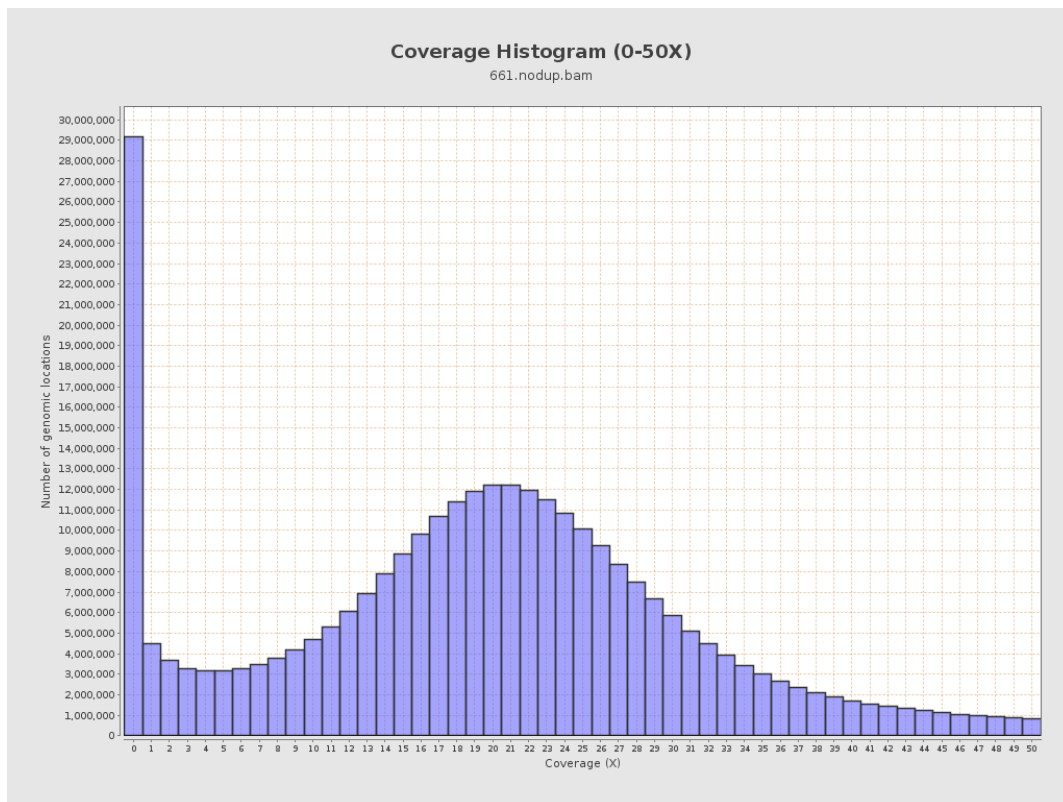
6. Results : Genome Fraction Coverage
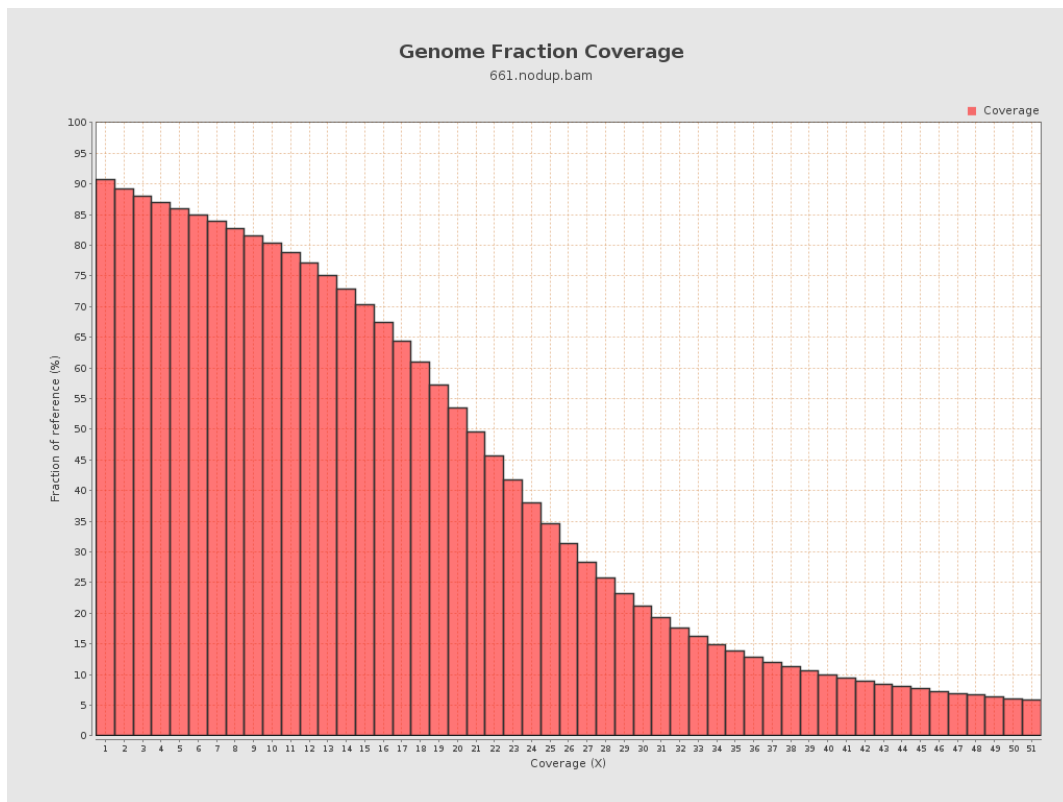
7. Results : Duplication Rate Histogram
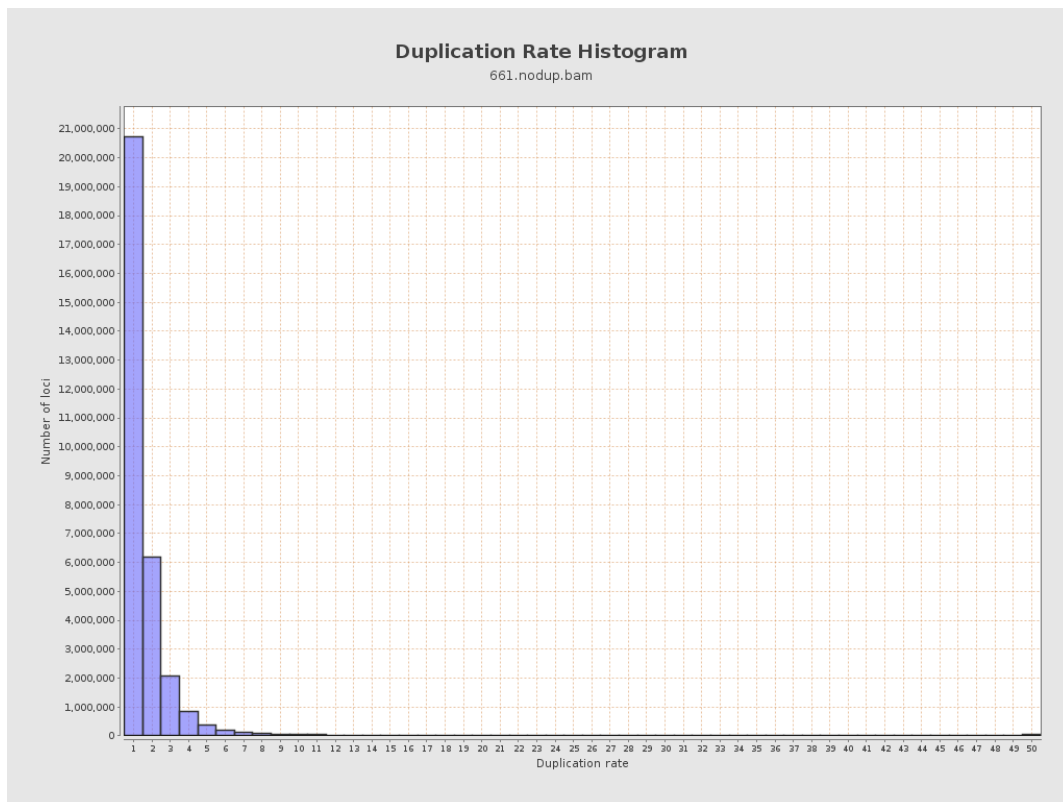
8. Results : Mapped Reads Nucleotide Content

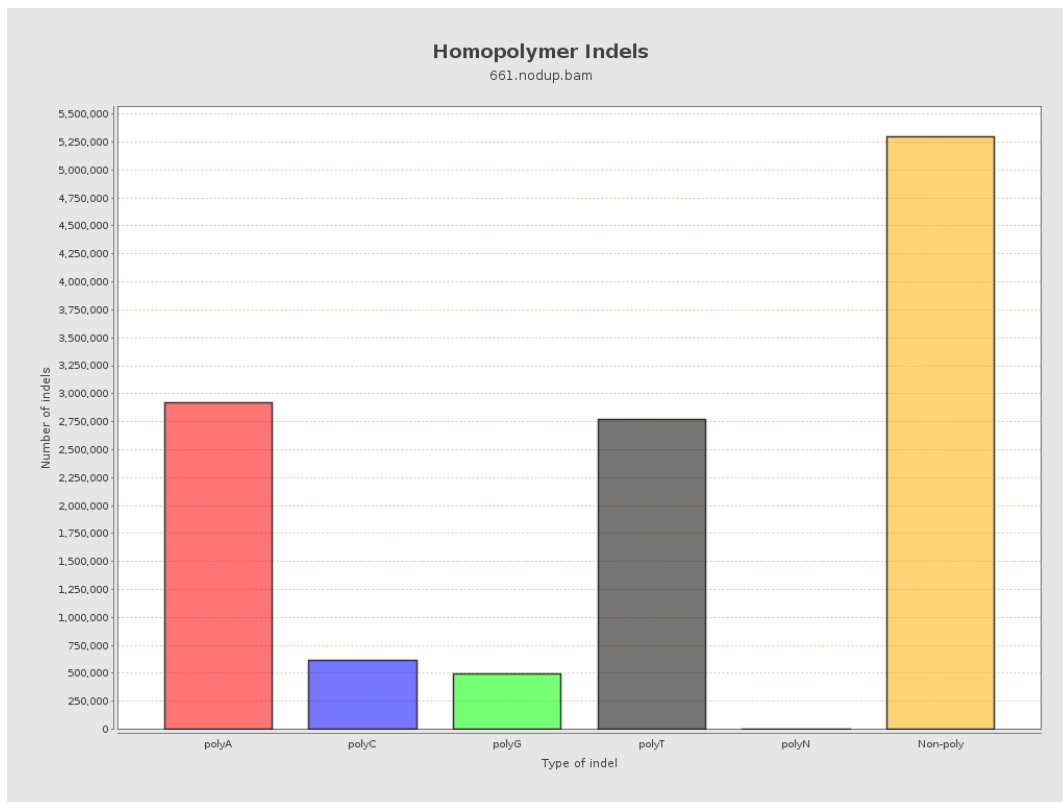Mapped Reads Nucleotide Content
661.nodup.bam

9. Results : Mapped Reads GC-content Distribution
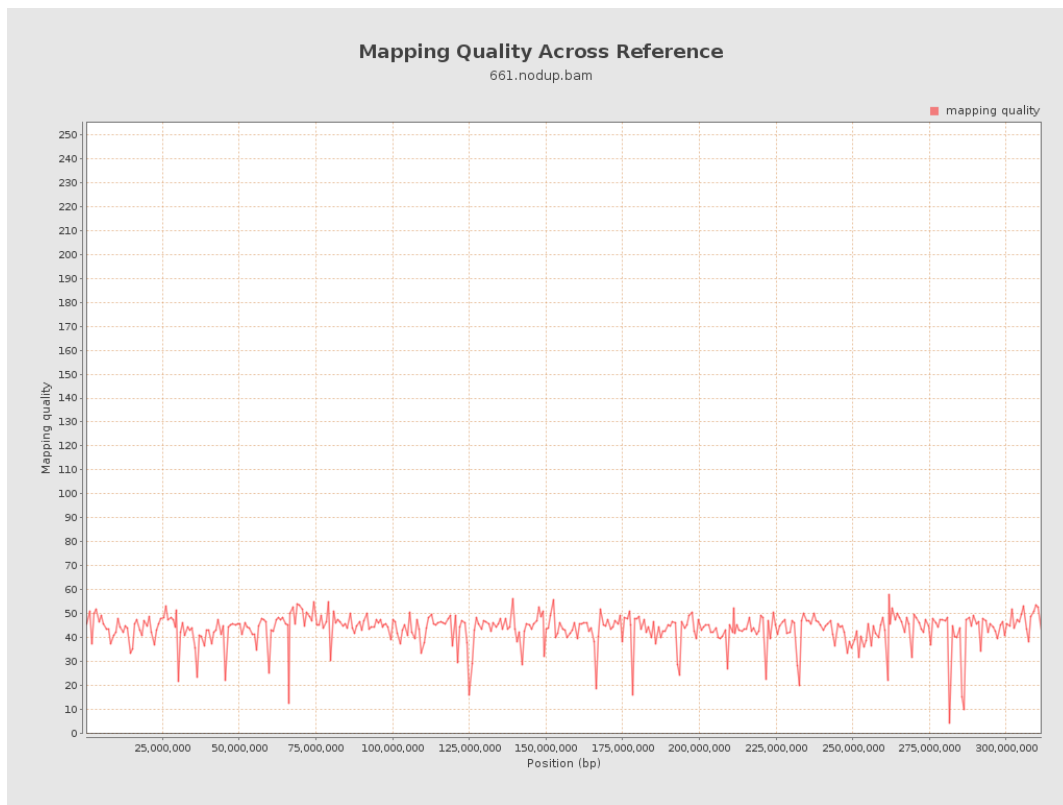

Mapped Reads GC-content Distribution
661.nodup.bam
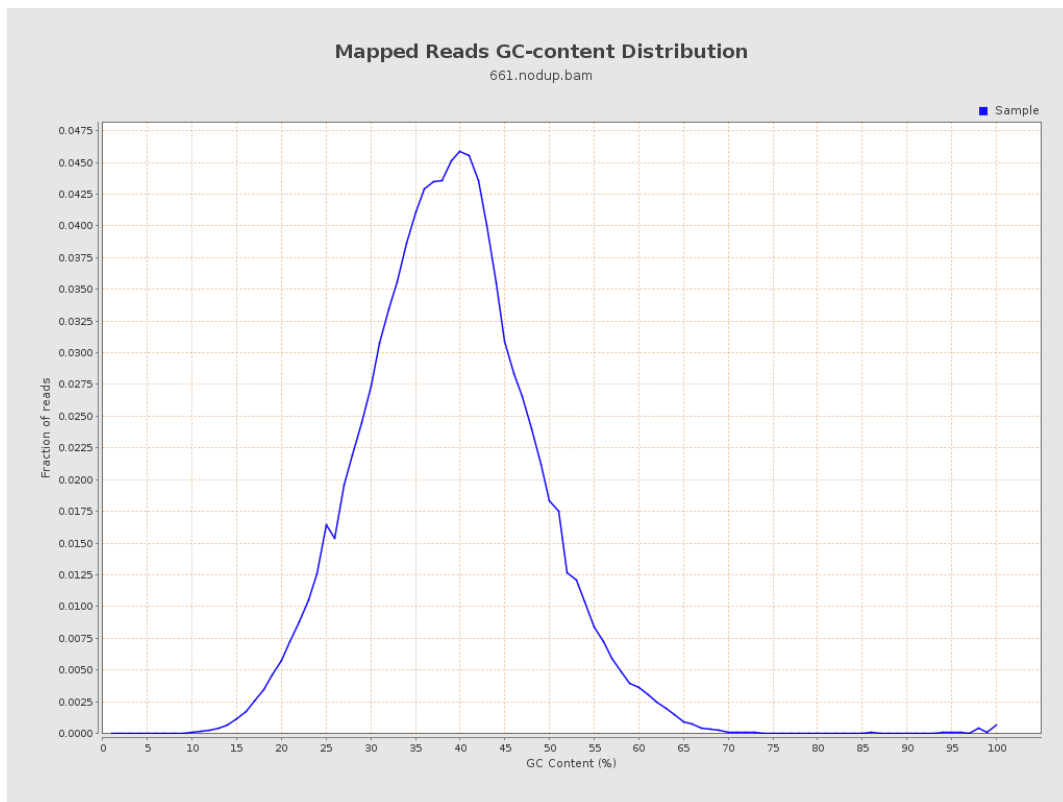
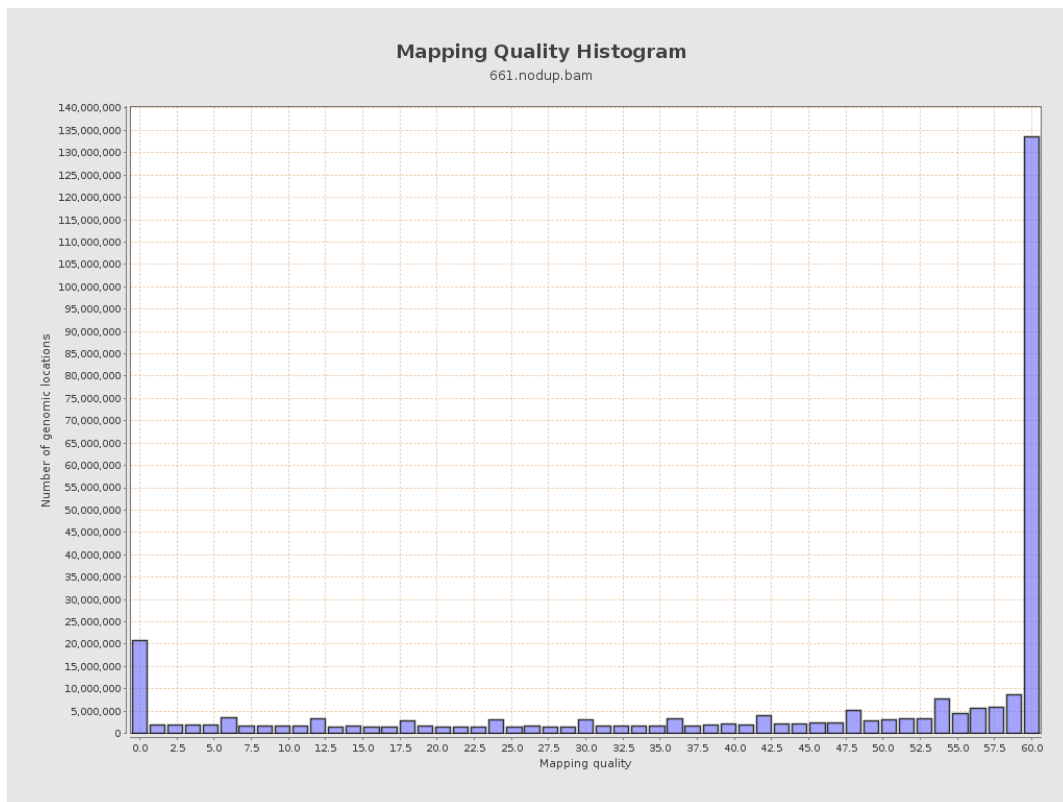# 10. Results : Mapped Reads Clipping Profile
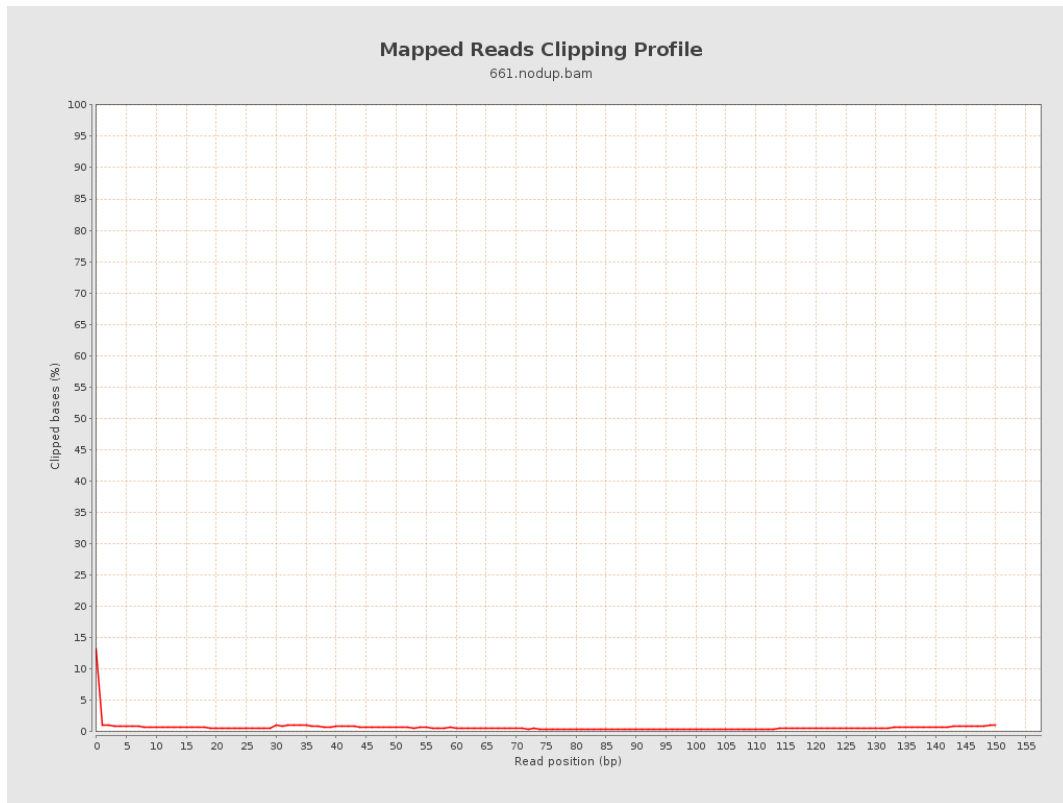
11. Results : Homopolymer Indels

12. Results : Mapping Quality Across Reference

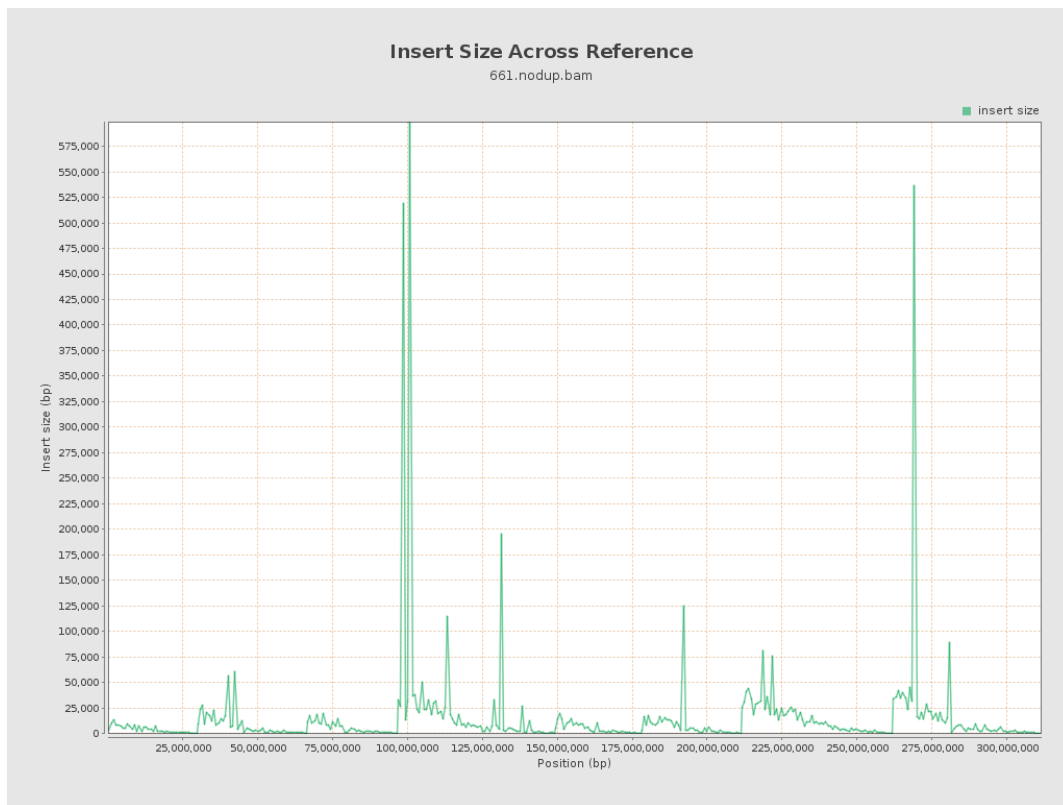# 13. Results : Mapping Quality Histogram

Mapping Quality Histogram
661.nodup.bam

14. Results : Insert Size Across Reference

Insert Size Across Reference
661.nodup.bam

15. Results : Insert Size Histogram

Insert Size Histogram
661.nodup.bam