Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:27:30

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/541
.nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/541 .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_268/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_268_S349_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_268/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_268_S349_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:27:29 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	57,455,652
Mapped reads	52,229,120 / 90.9%
Unmapped reads	5,226,532 / 9.1%
Mapped paired reads	52,229,120 / 90.9%
Mapped reads, first in pair	26,179,504 / 45.56%
Mapped reads, second in pair	26,049,616 / 45.34%
Mapped reads, both in pair	50,536,355 / 87.96%
Mapped reads, singletons	1,692,765 / 2.95%
Read min/max/mean length	30 / 151 / 147.91
Duplicated reads (flagged)	8,802,291 / 15.32%
Clipped reads	13,415,082 / 23.35%

2.2. ACGT Content

Number/percentage of A's	2,188,685,329 / 30.85%
Number/percentage of C's	1,356,756,297 / 19.12%
Number/percentage of T's	2,192,187,426 / 30.89%
Number/percentage of G's	1,358,098,601 / 19.14%
Number/percentage of N's	26,865 / 0%
GC Percentage	38.26%

2.3. Coverage

Mean	22.8295
Standard Deviation	238.1713

2.4. Mapping Quality

Mean Mapping Quality	43.67

2.5. Insert size

Mean	268,683.18
Standard Deviation	2,495,623.89
P25/Median/P75	316 / 420 / 551

2.6. Mismatches and indels

General error rate	2.46%
Mismatches	159,832,610
Insertions	5,322,231
Mapped reads with at least one insertion	9.07%
Deletions	5,087,160
Mapped reads with at least one deletion	8.63%
Homopolymer indels	56.88%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	542221147	18.2417	96.1309

| LT669789.1 | 36598175 | 841431415 | 22.9911 | 242.9234 |
LT669790.1	30422129	851447082	27.9878	331.4339
LT669791.1	52758100	1184268057	22.4471	256.7459
LT669792.1	28376109	653632381	23.0346	235.5322
LT669793.1	33388210	692195406	20.7317	186.5708
LT669794.1	50579949	1087465119	21.4999	199.9457
LT669795.1	49795044	1261982009	25.3435	271.2463

3. Results : Coverage across reference

Coverage across reference
541.nodup.bam

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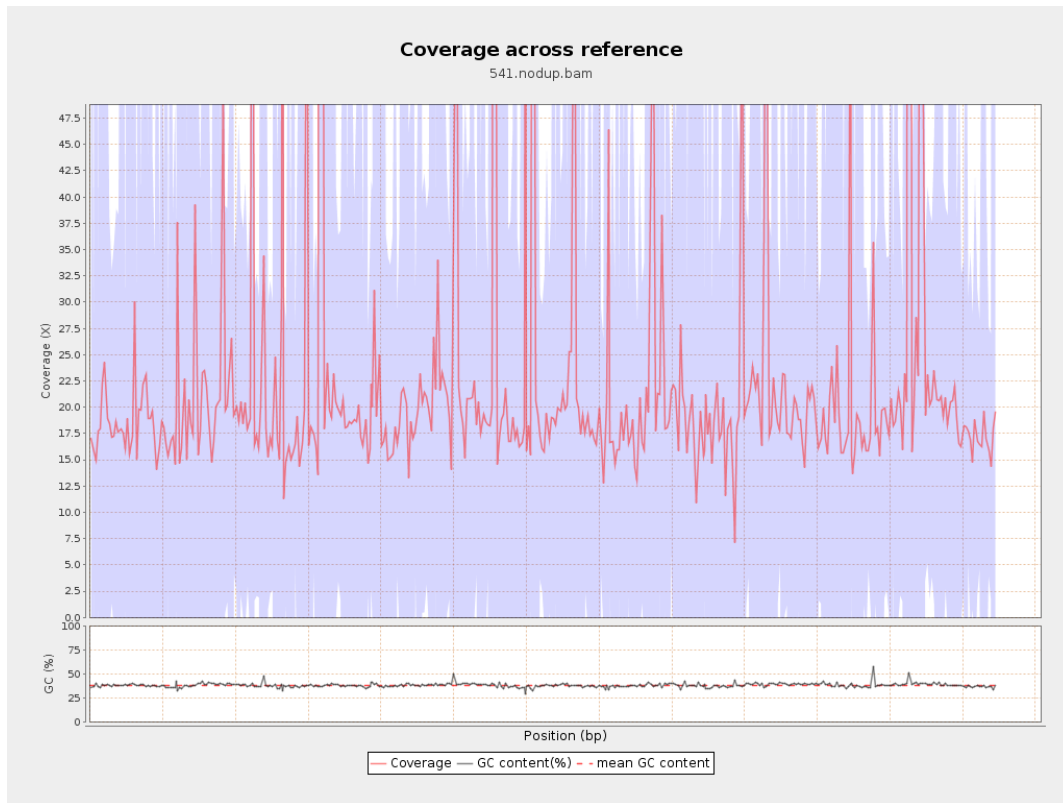
Coverage Histogram
541.nodup.bam
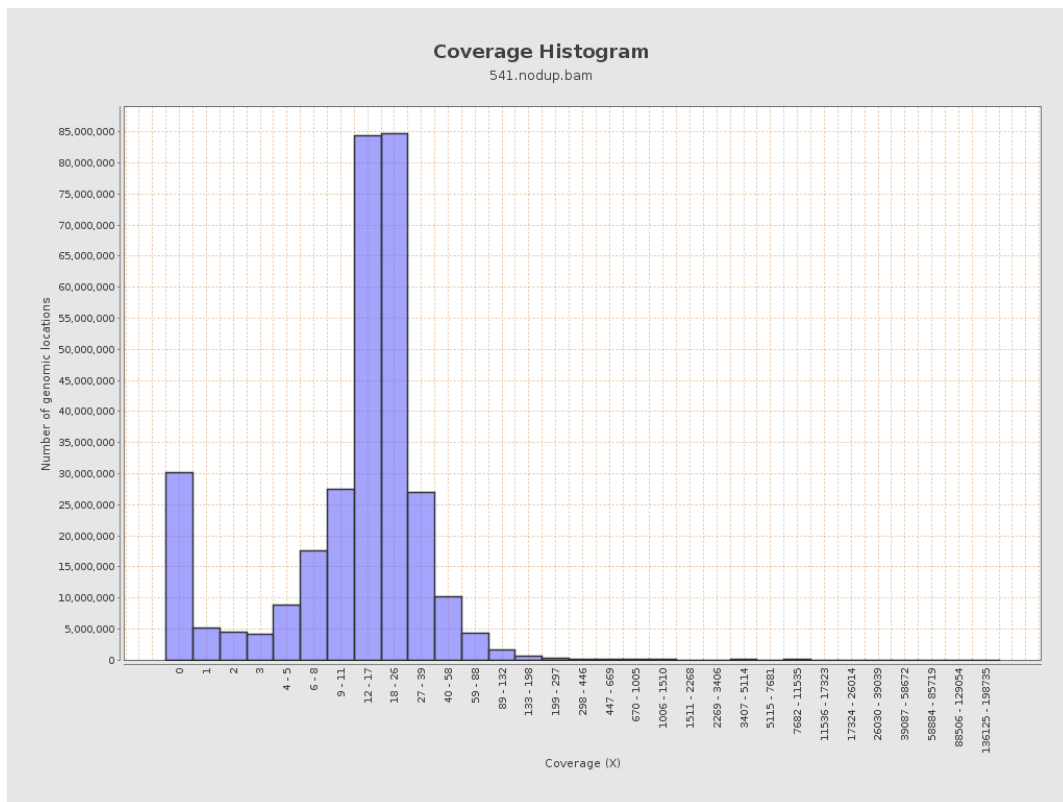
5. Results : Coverage Histogram (0-50X)
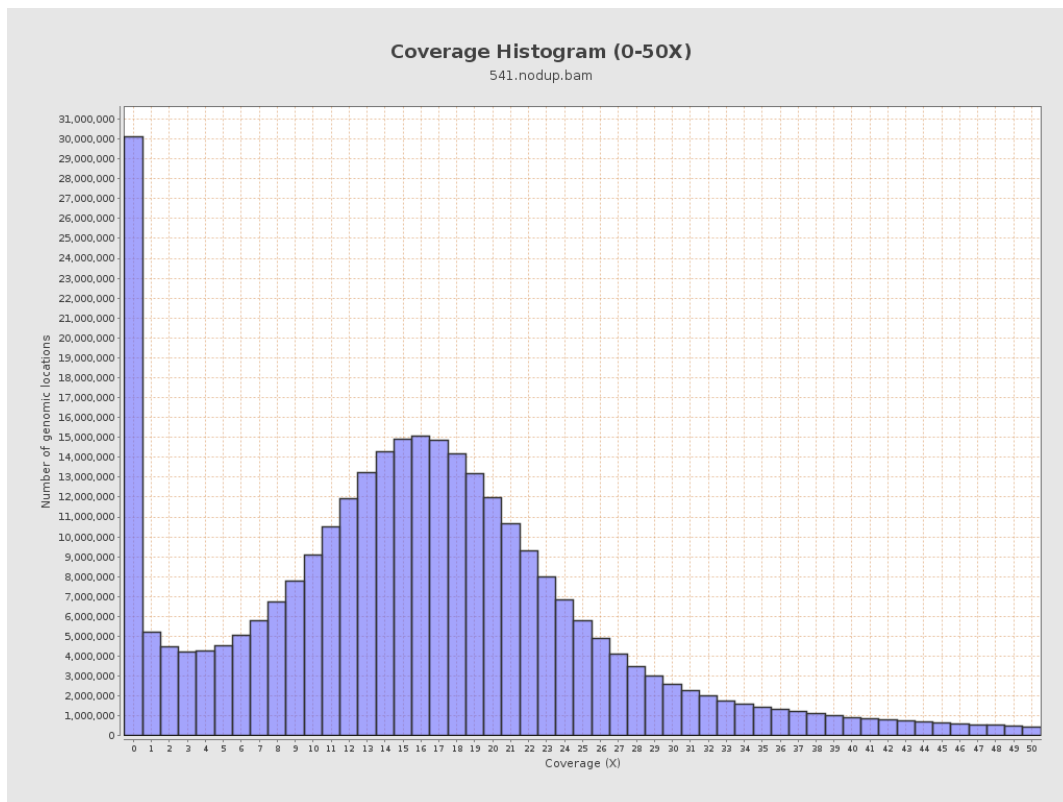
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
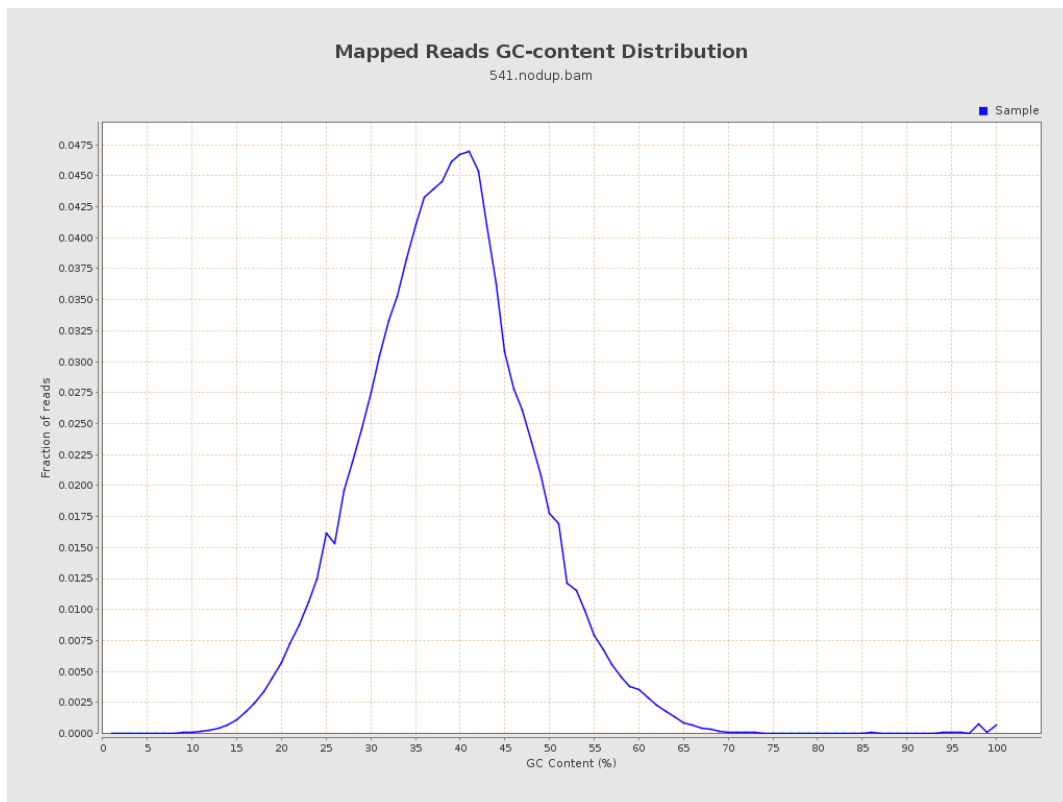541.nodup.bam
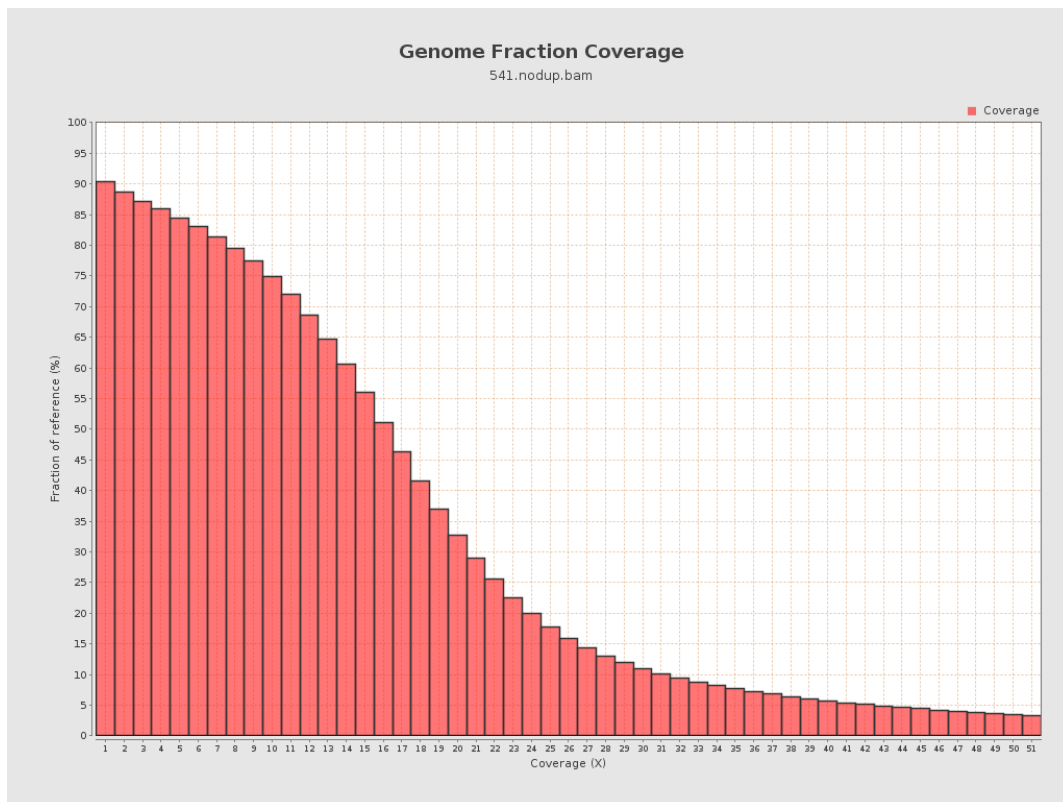
7. Results : Duplication Rate Histogram

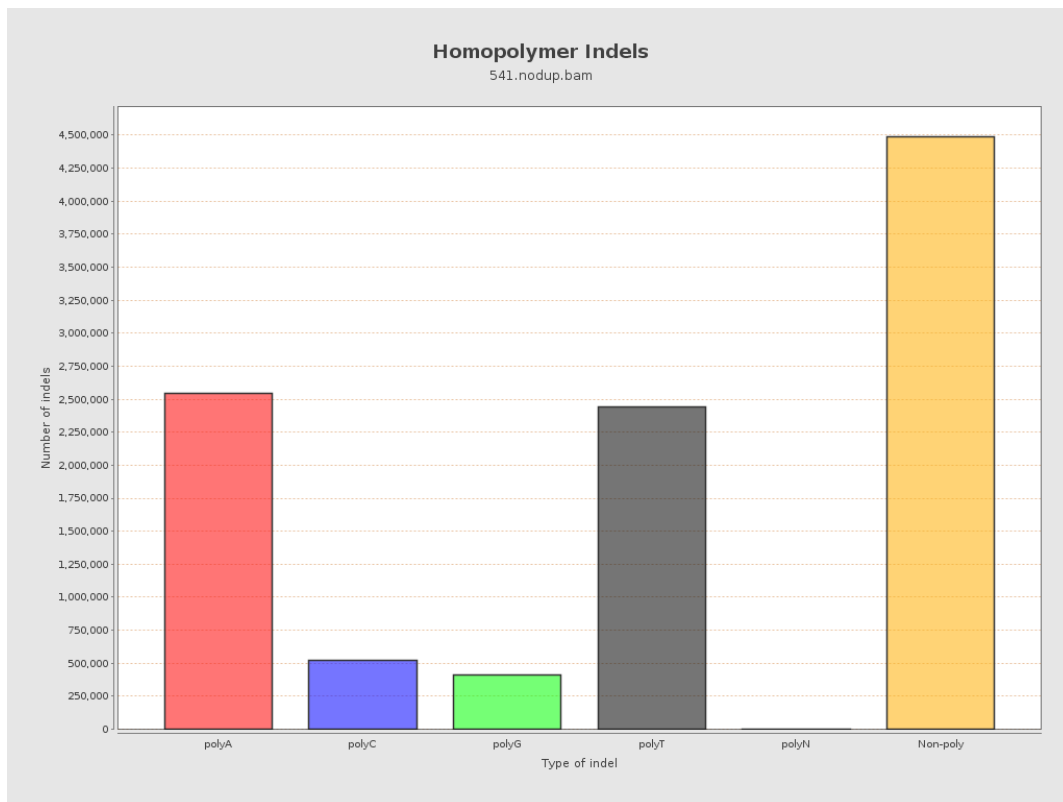Duplication Rate Histogram
541.nodup.bam
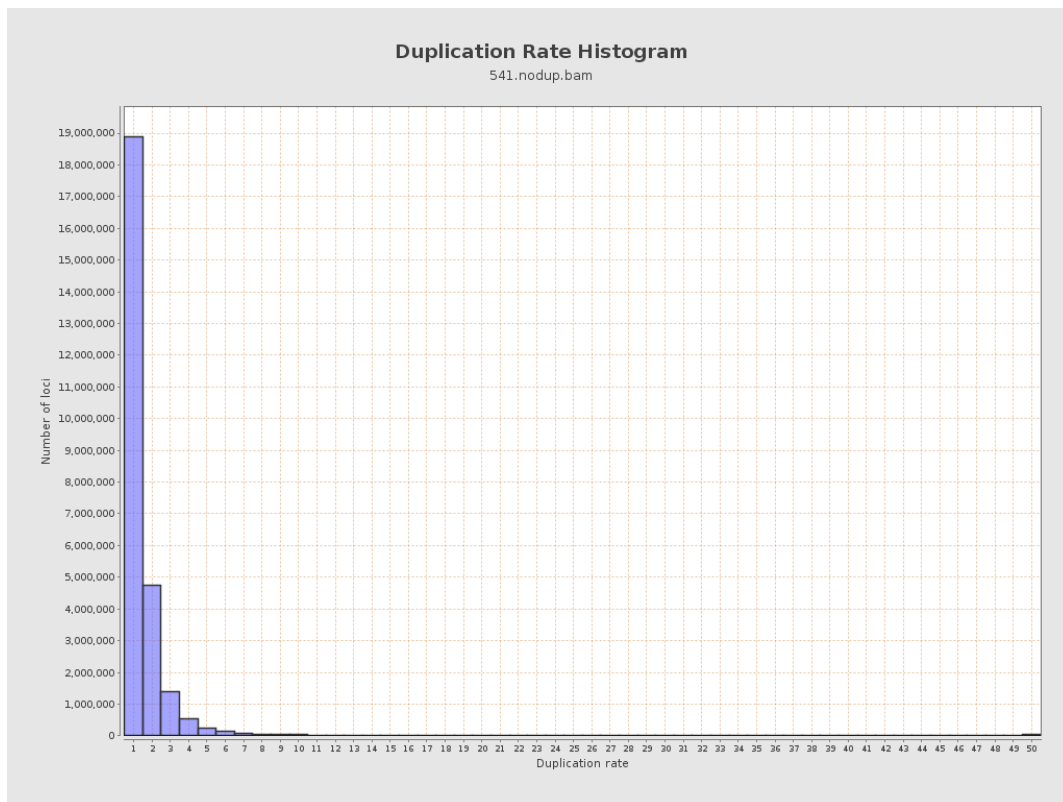
8. Results : Mapped Reads Nucleotide Content
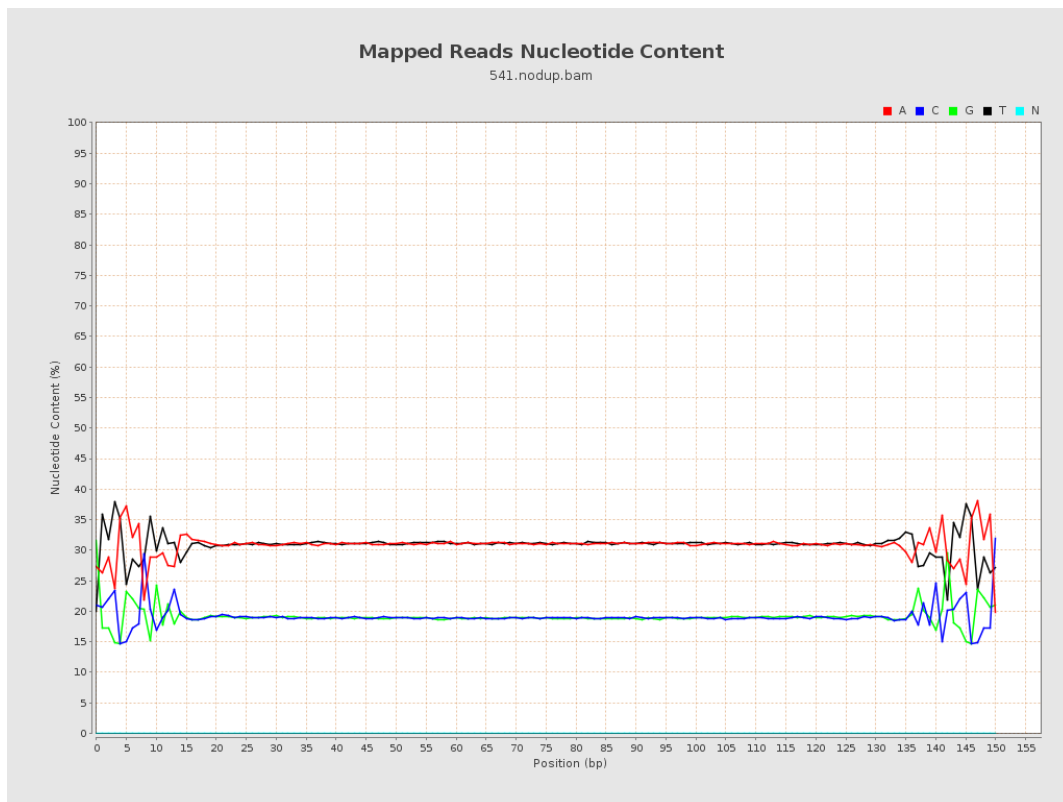
9. Results : Mapped Reads GC-content Distribution

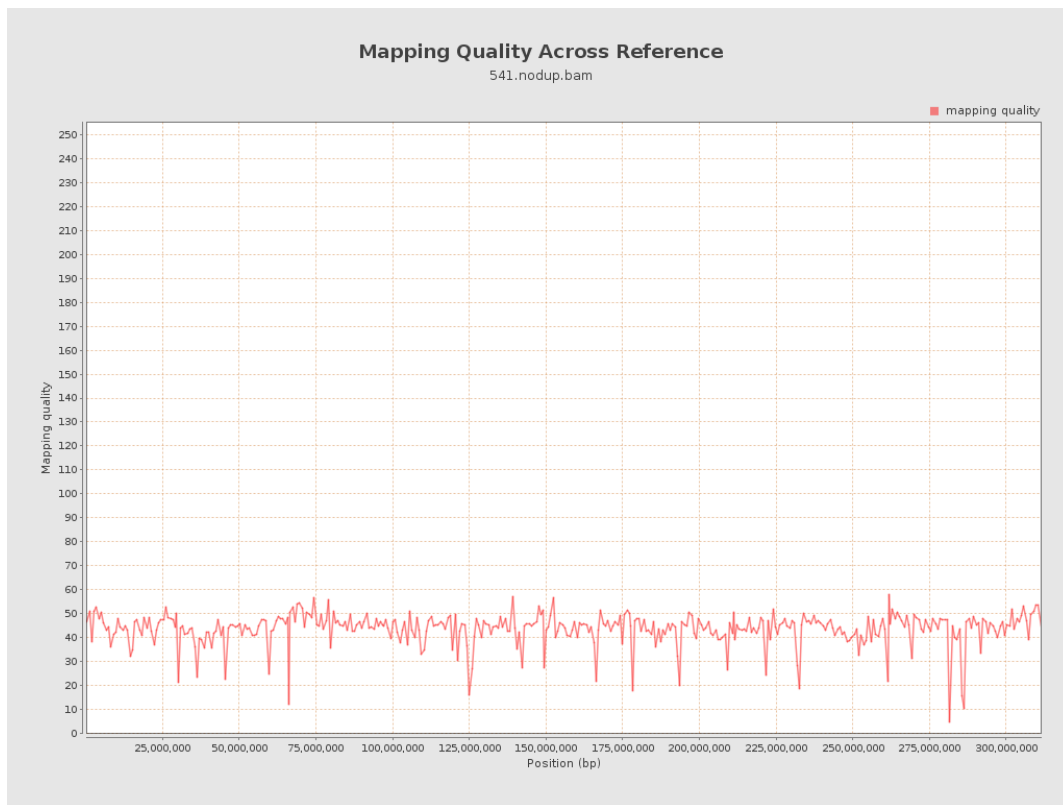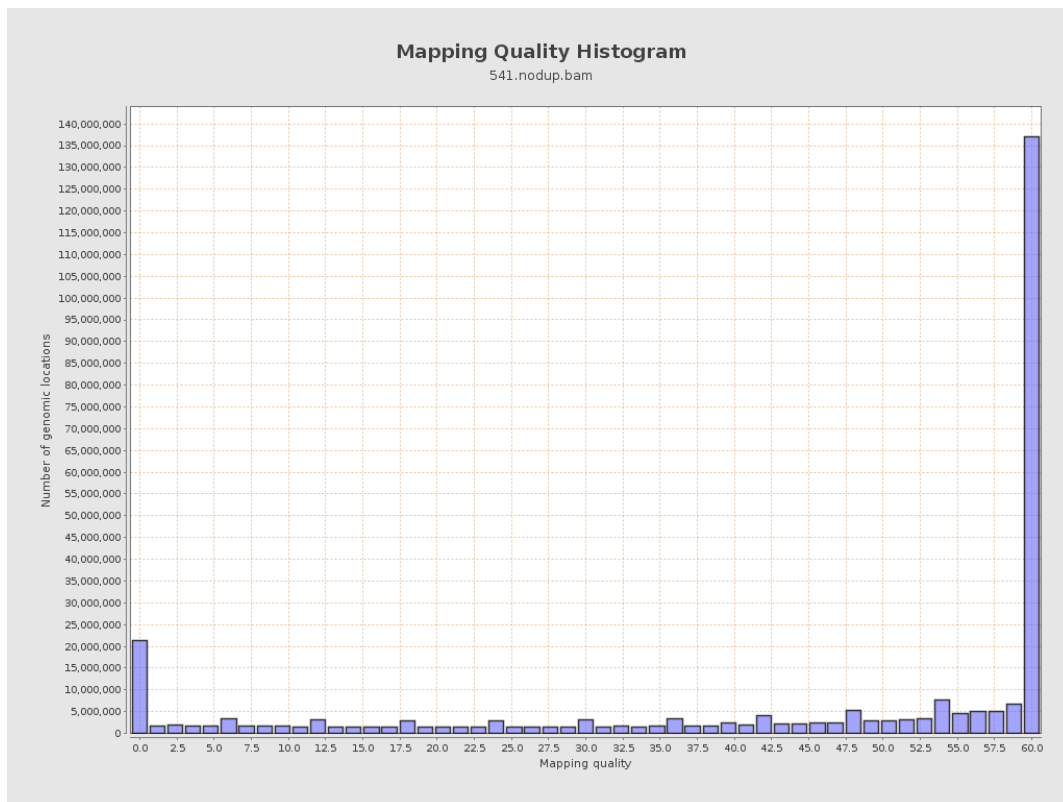# 10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
541.nodup.bam
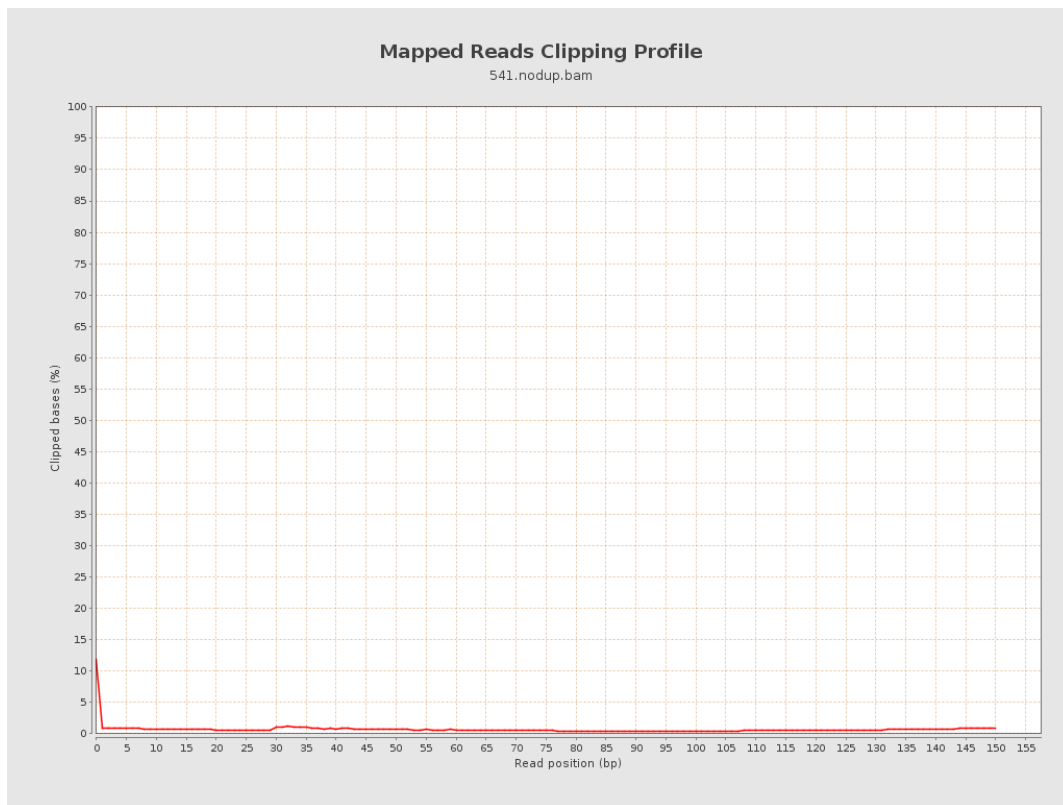
11. Results : Homopolymer Indels

12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
541.nodup.bam

14. Results : Insert Size Across Reference

Insert Size Across Reference
541.nodup.bam
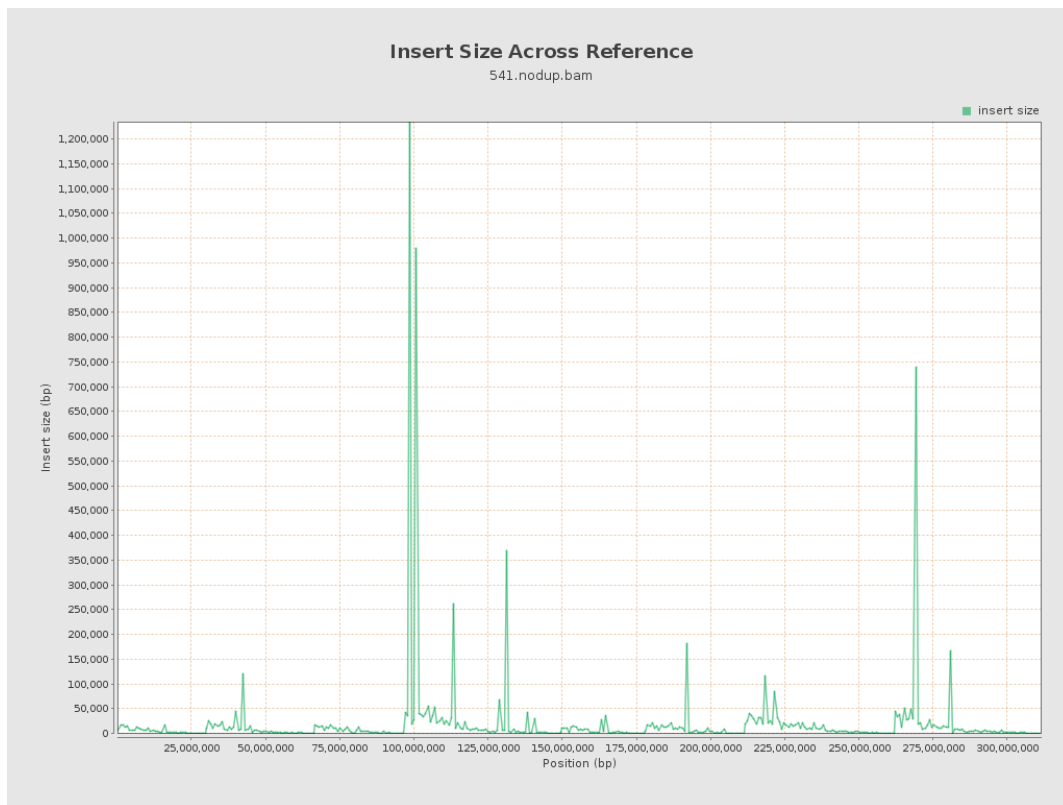
15. Results : Insert Size Histogram