Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:35:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/115
2
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1152 .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_559/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_559_S126_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_559/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_559_S126_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:35:12 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	75,660,865
Mapped reads	70,647,952 / 93.37%
Unmapped reads	5,012,913 / 6.63%
Mapped paired reads	70,647,952 / 93.37%
Mapped reads, first in pair	35,436,745 / 46.84%
Mapped reads, second in pair	35,211,207 / 46.54%
Mapped reads, both in pair	68,966,199 / 91.15%
Mapped reads, singletons	1,681,753 / 2.22%
Read min/max/mean length	30 / 151 / 148.09
Duplicated reads (flagged)	11,921,143 / 15.76%
Clipped reads	17,217,663 / 22.76%

2.2. ACGT Content

Number/percentage of A's	3,004,040,110 / 30.93%
Number/percentage of C's	1,852,427,219 / 19.08%
Number/percentage of T's	3,005,949,736 / 30.95%
Number/percentage of G's	1,848,466,539 / 19.03%
Number/percentage of N's	70,195 / 0%
GC Percentage	38.11%

2.3. Coverage

Mean	31.24
Standard Deviation	275.5036

2.4. Mapping Quality

Mean Mapping Quality	44.05

2.5. Insert size

Mean	226,749.2
Standard Deviation	2,257,557.31
P25/Median/P75	305 / 403 / 523

2.6. Mismatches and indels

General error rate	2.54%
Mismatches	228,132,572
Insertions	6,786,643
Mapped reads with at least one insertion	8.61%
Deletions	6,695,107
Mapped reads with at least one deletion	8.42%
Homopolymer indels	56.53%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	737704583	24.8182	88.6629

LT669789.1	36598175	1165492098	31.8456	279.9112
LT669790.1	30422129	1068044417	35.1075	326.3098
LT669791.1	52758100	1636658309	31.0219	262.3512
LT669792.1	28376109	876725865	30.8966	321.6888
LT669793.1	33388210	948446092	28.4066	148.257
LT669794.1	50579949	1501621827	29.6881	225.7441
LT669795.1	49795044	1801014978	36.1686	386.3167

3. Results : Coverage across reference

Coverage across reference
1152.nodup.bam

4. Results : Coverage Histogram

Coverage Histogram
1152.nodup.bam
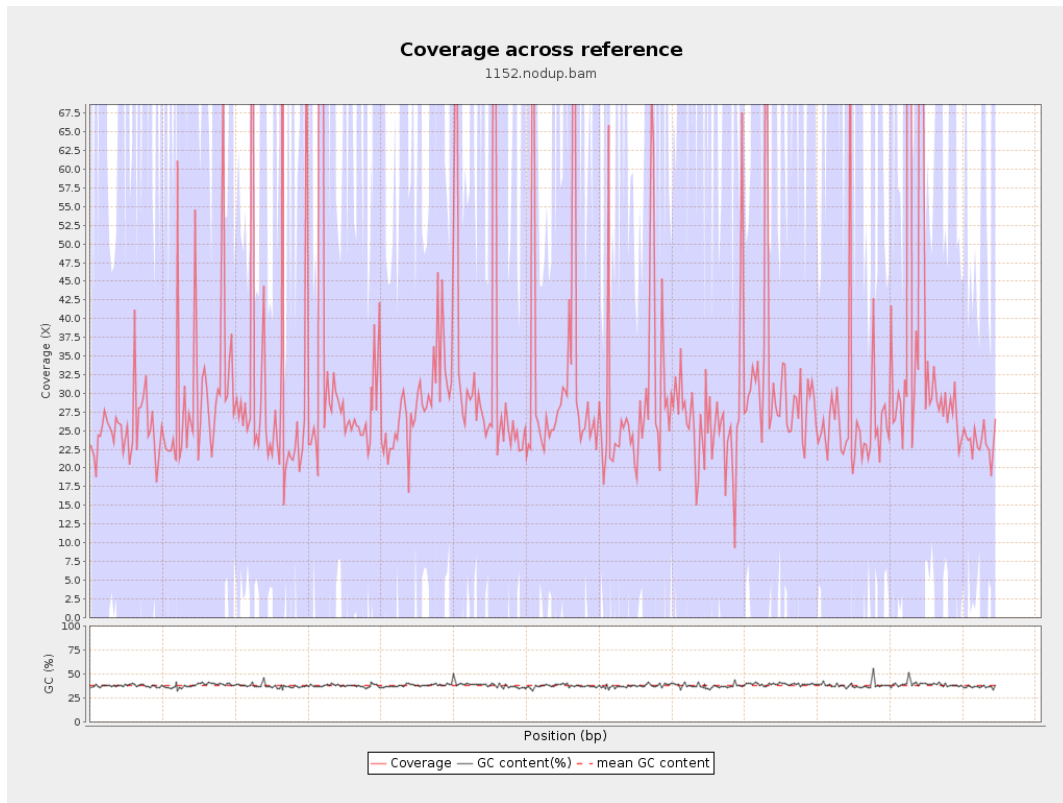
5. Results : Coverage Histogram (0-50X)
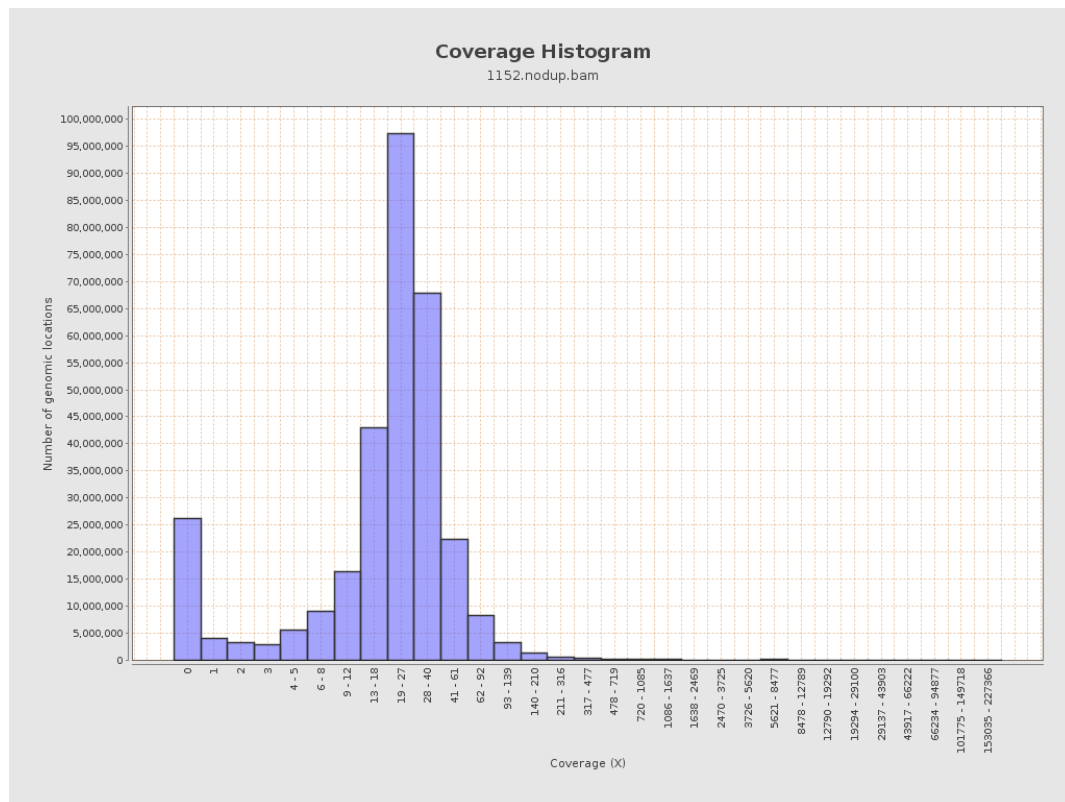
Coverage Histogram (0-50X)
1152.nodup.bam
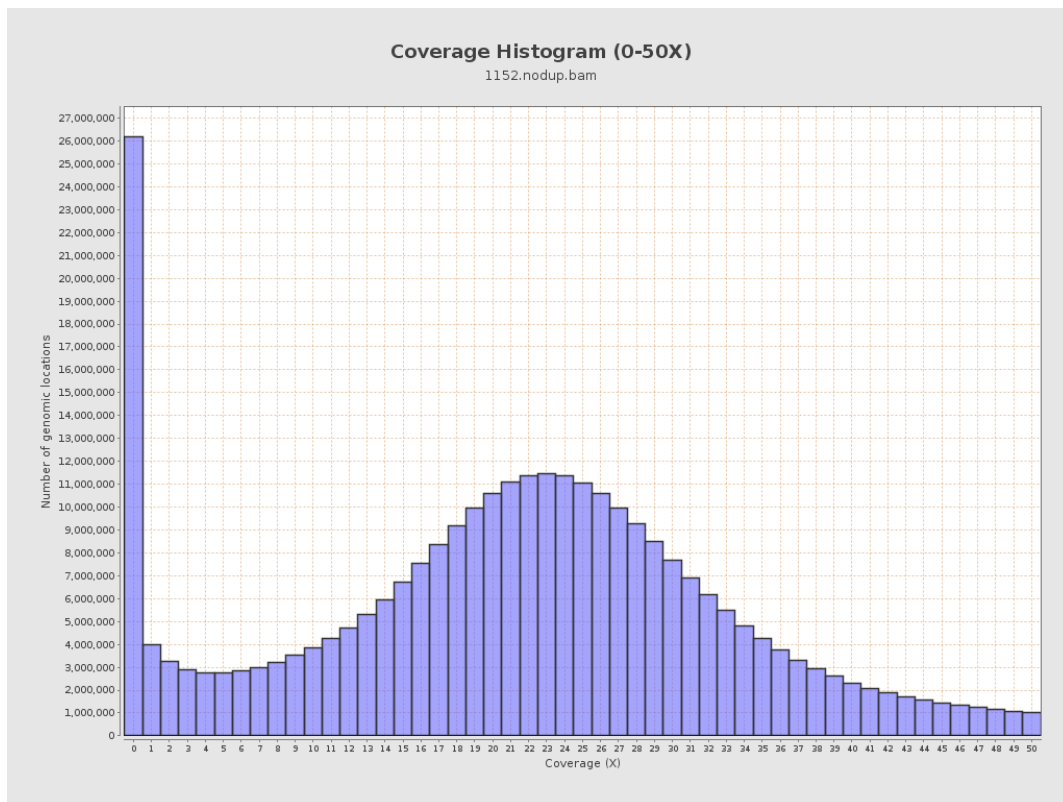
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
1152.nodup.bam
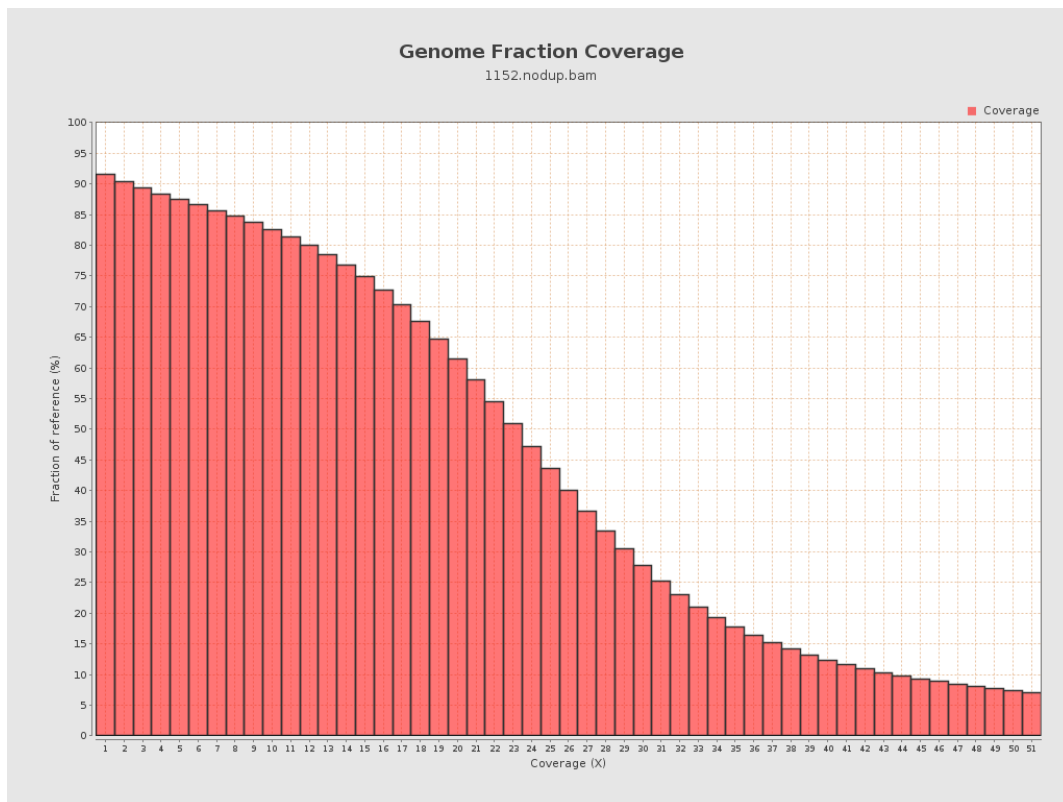
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
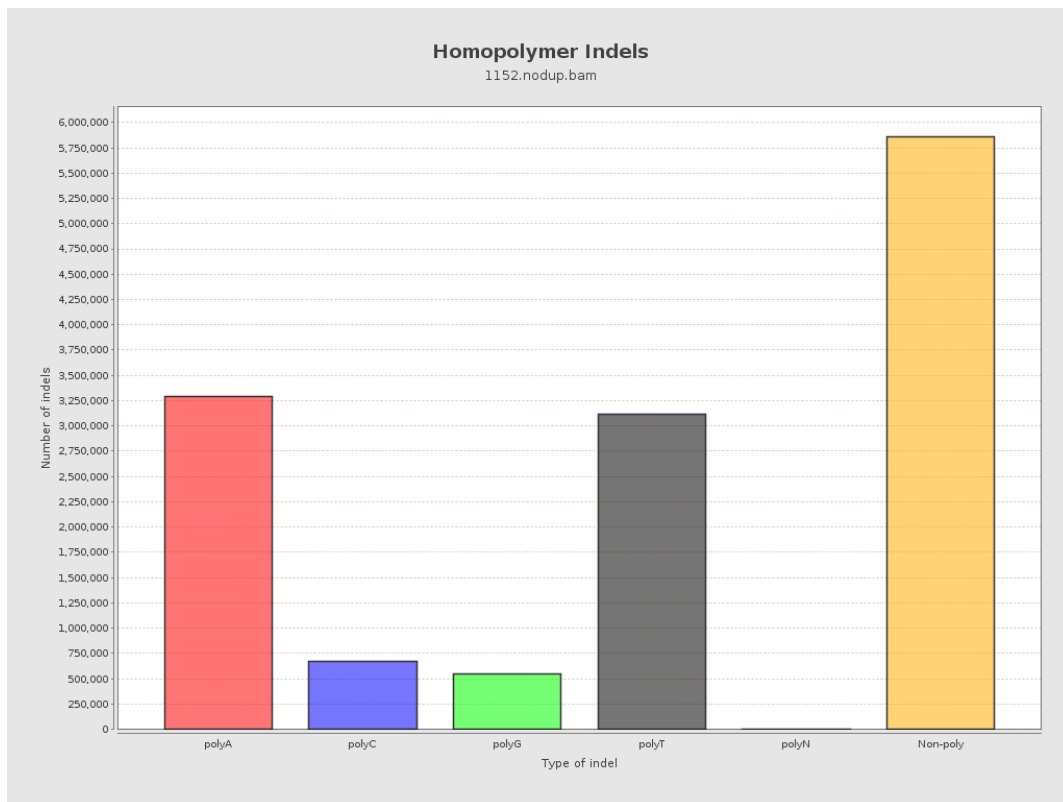1152.nodup.bam
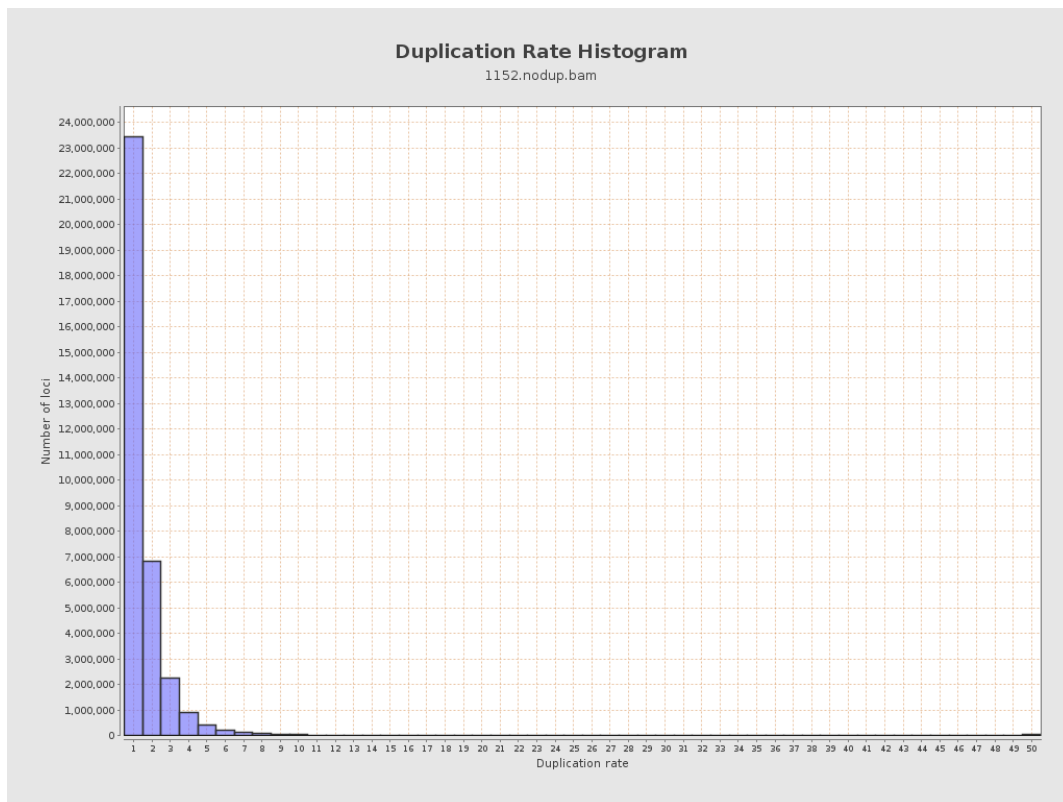
8. Results : Mapped Reads Nucleotide Content
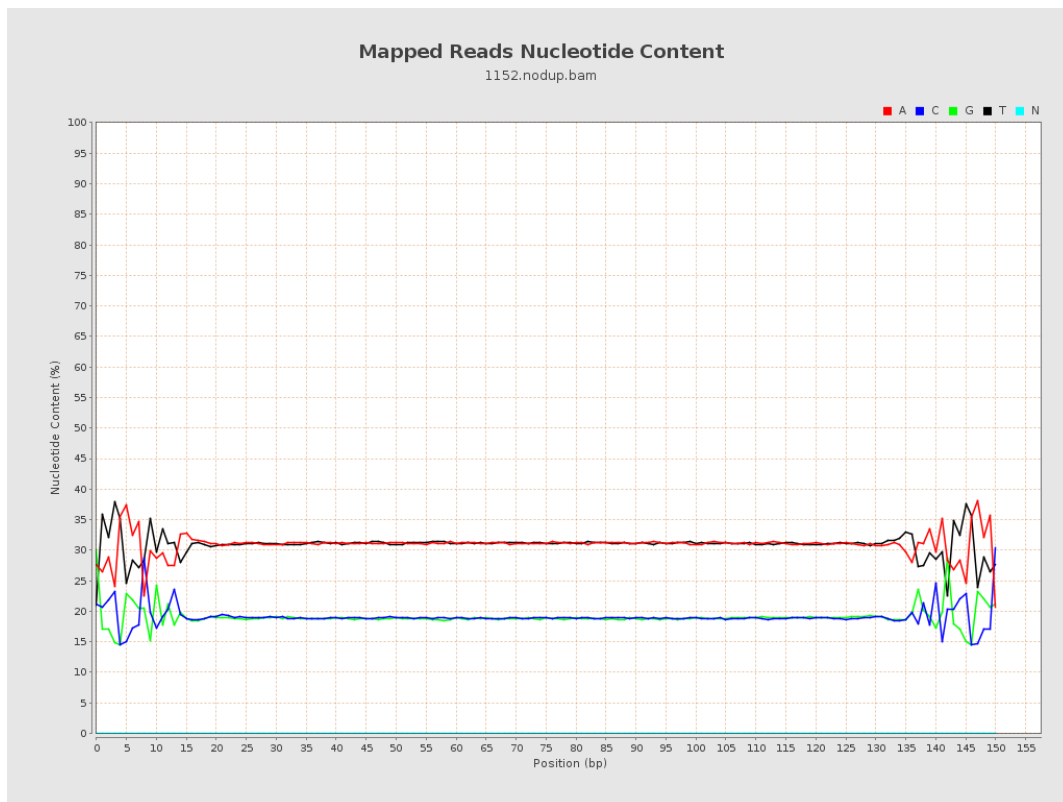
9. Results : Mapped Reads GC-content Distribution
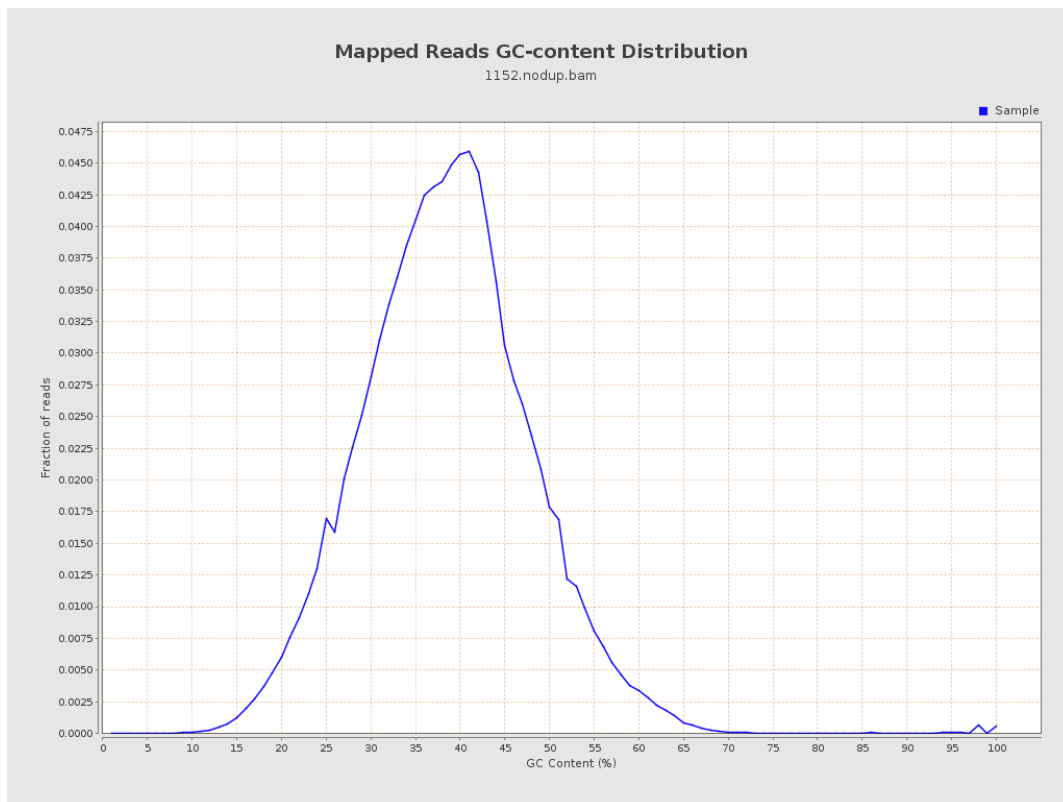
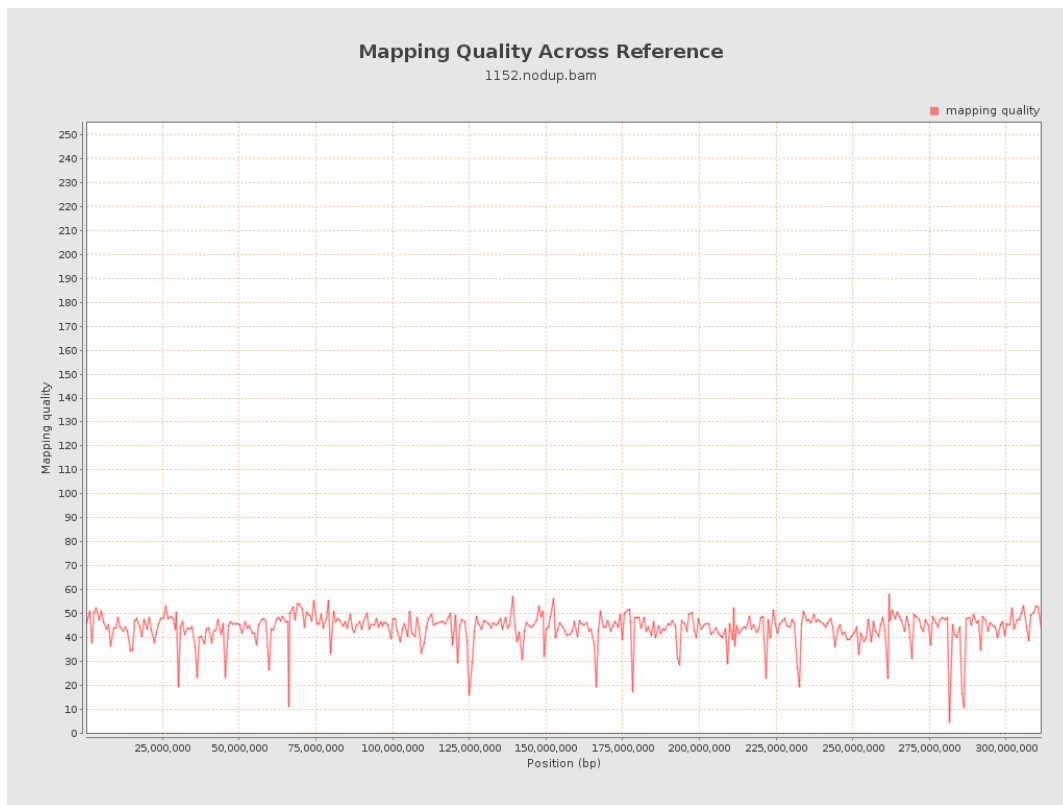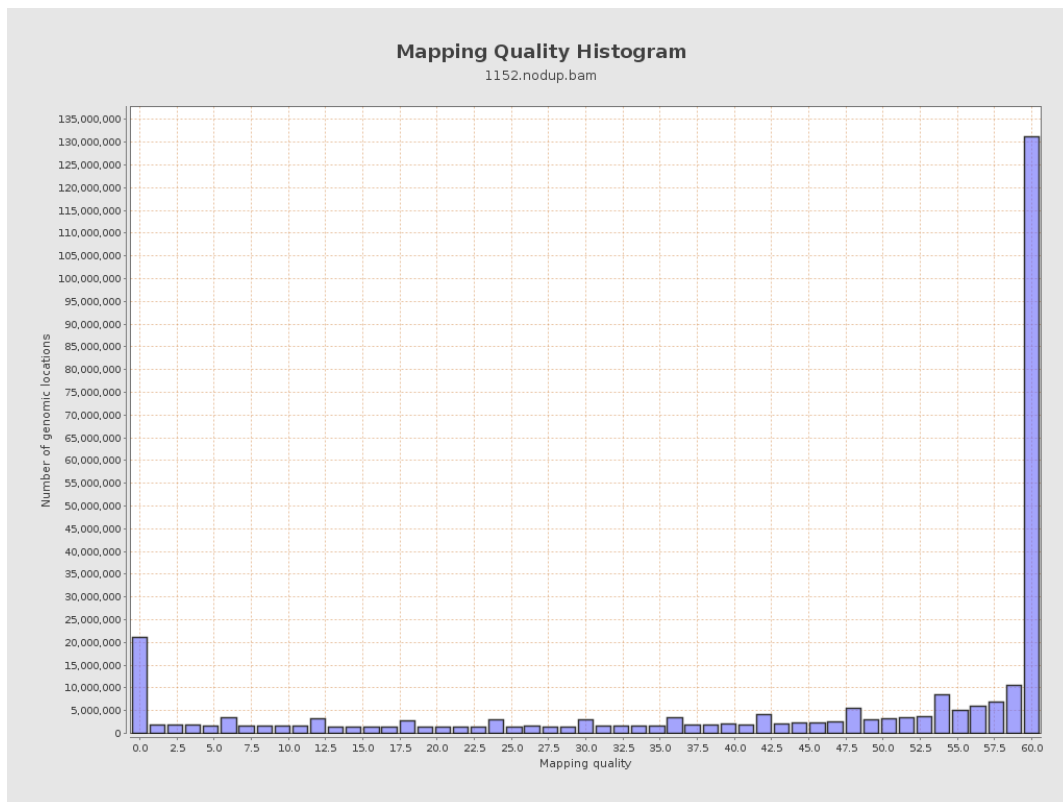# 10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
1152.nodup.bam
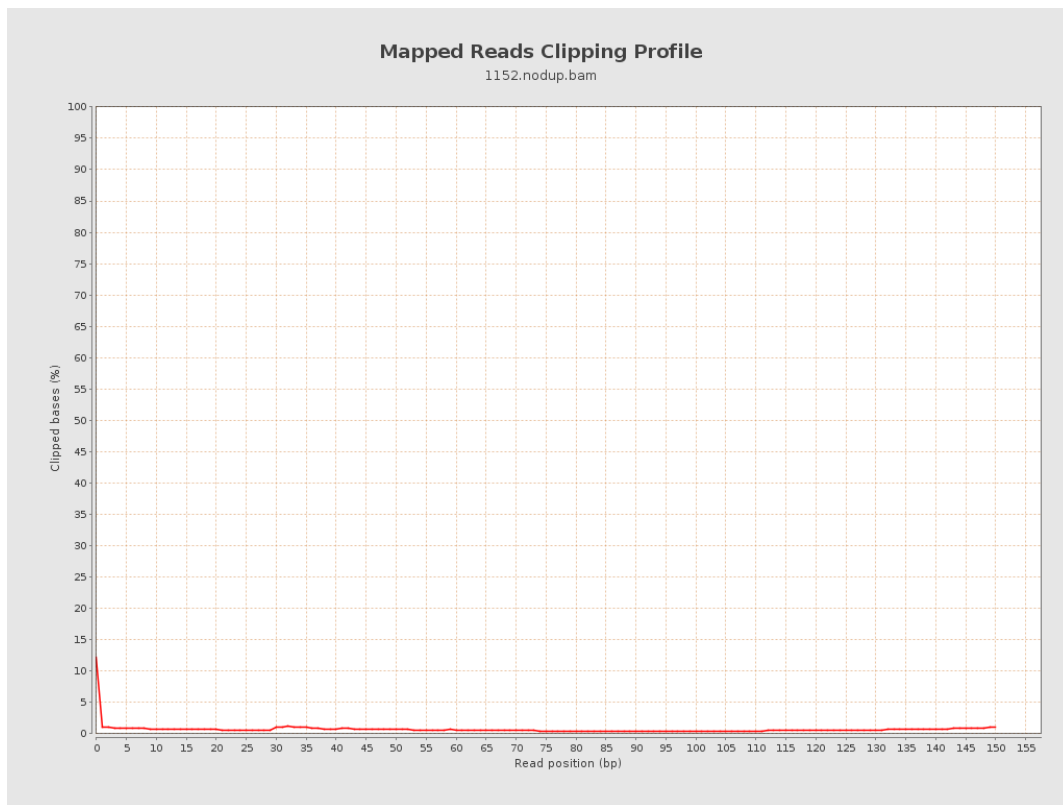
11. Results : Homopolymer Indels

12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
1152.nodup.bam

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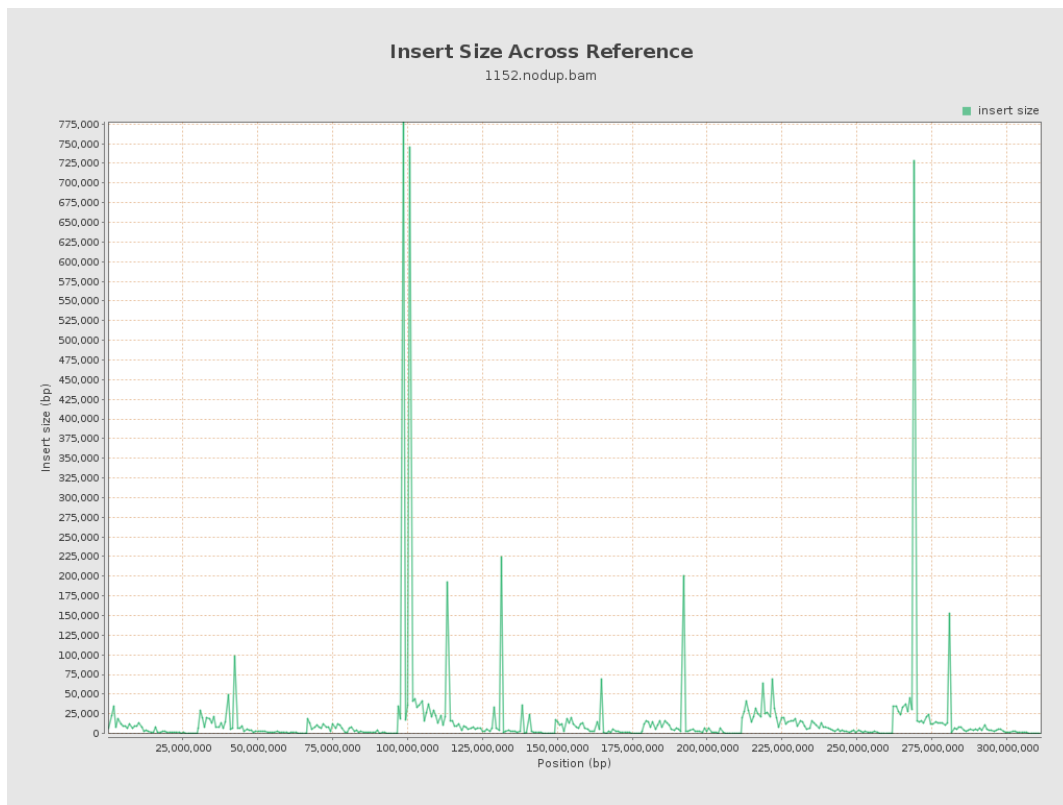
15. Results : Insert Size Histogram

Insert Size Histogram
1152.nodup.bam