Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:35:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/115
1
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1151 .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_539/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_539_S106_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_539/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_539_S106_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:35:31 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	80,048,024
Mapped reads	74,697,776 / 93.32%
Unmapped reads	5,350,248 / 6.68%
Mapped paired reads	74,697,776 / 93.32%
Mapped reads, first in pair	37,468,463 / 46.81%
Mapped reads, second in pair	37,229,313 / 46.51%
Mapped reads, both in pair	72,922,494 / 91.1%
Mapped reads, singletons	1,775,282 / 2.22%
Read min/max/mean length	30 / 151 / 148.1
Duplicated reads (flagged)	12,984,807 / 16.22%
Clipped reads	18,350,175 / 22.92%

2.2. ACGT Content

Number/percentage of A's	3,160,476,659 / 30.78%
Number/percentage of C's	1,972,750,237 / 19.21%
Number/percentage of T's	3,162,493,984 / 30.8%
Number/percentage of G's	1,972,690,235 / 19.21%
Number/percentage of N's	72,987 / 0%
GC Percentage	38.42%

2.3. Coverage

Mean	33.0356
Standard Deviation	292.562

2.4. Mapping Quality

Mean Mapping Quality	43.28

2.5. Insert size

Mean	238,967.61
Standard Deviation	2,314,242
P25/Median/P75	311 / 409 / 528

2.6. Mismatches and indels

General error rate	2.63%
Mismatches	250,260,299
Insertions	7,121,295
Mapped reads with at least one insertion	8.52%
Deletions	7,198,197
Mapped reads with at least one deletion	8.54%
Homopolymer indels	56.35%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	773904446	26.036	85.2789

LT669789.1	36598175	1237953702	33.8256	284.2784
LT669790.1	30422129	1122989211	36.9136	345.9087
LT669791.1	52758100	1780778549	33.7537	330.6289
LT669792.1	28376109	920826288	32.4508	313.9617
LT669793.1	33388210	1021517330	30.5952	228.9573
LT669794.1	50579949	1622208401	32.0722	290.4001
LT669795.1	49795044	1815102441	36.4515	325.5488

3. Results : Coverage across reference

Coverage across reference
1151.nodup.bam

4. Results : Coverage Histogram

Coverage Histogram
1151.nodup.bam
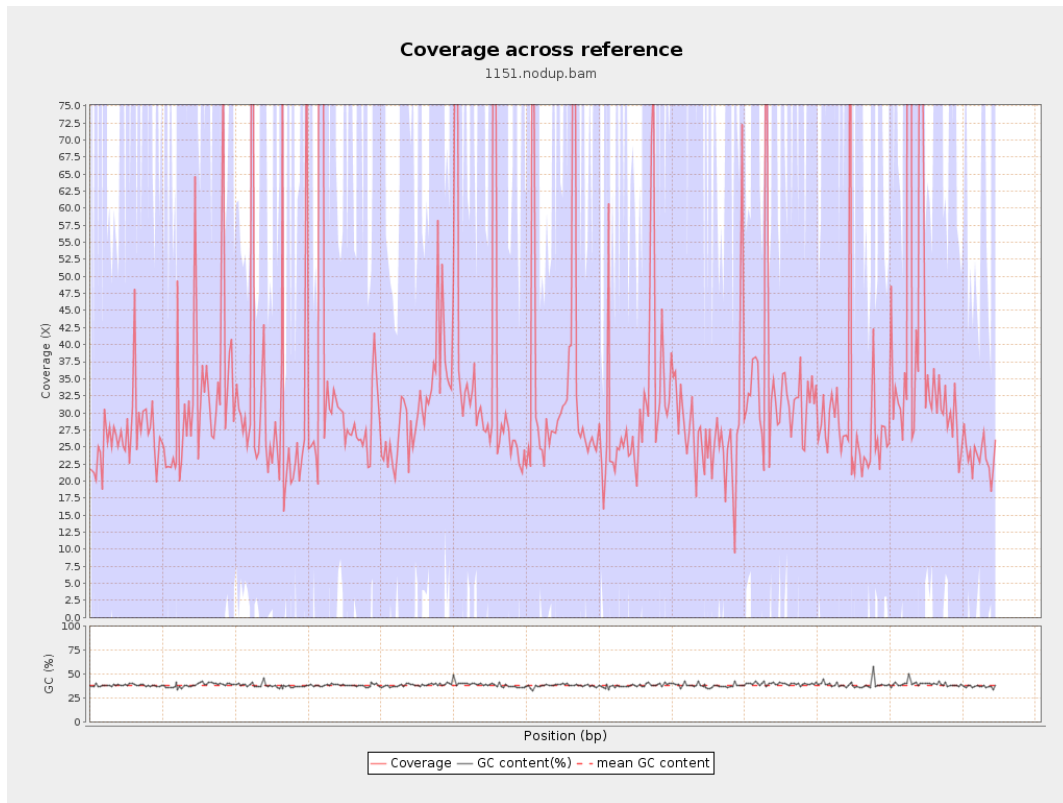
5. Results : Coverage Histogram (0-50X)
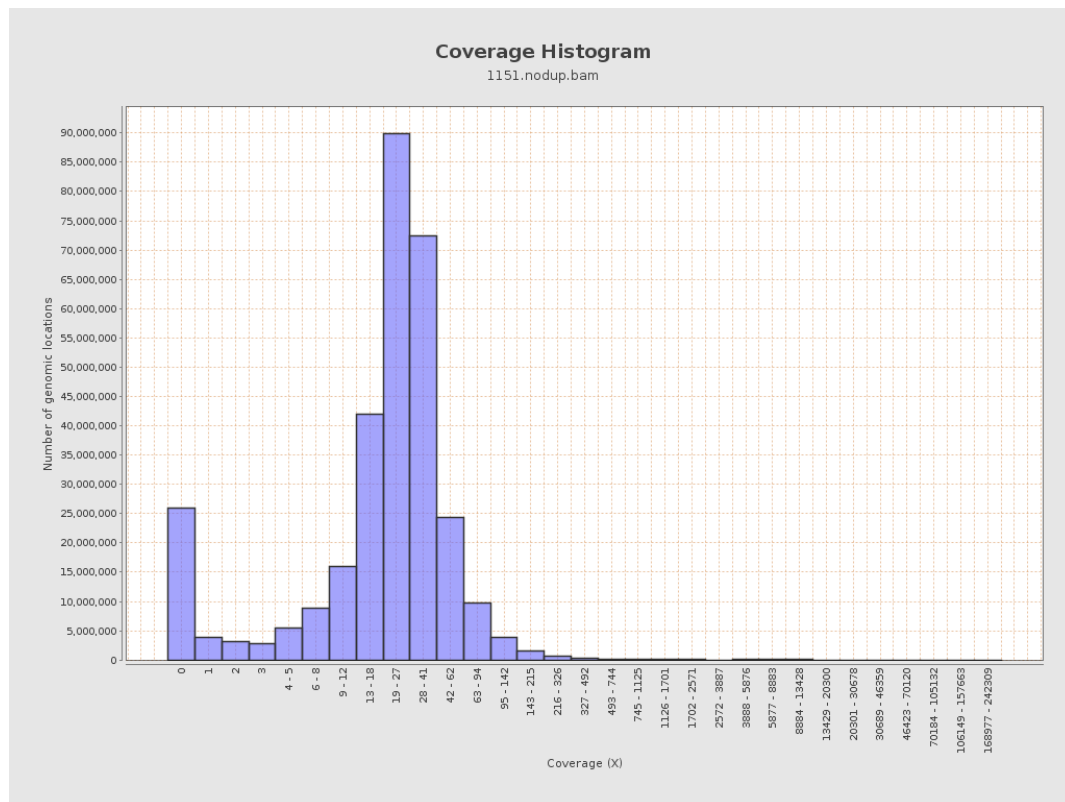
Coverage Histogram (0-50X)
1151.nodup.bam
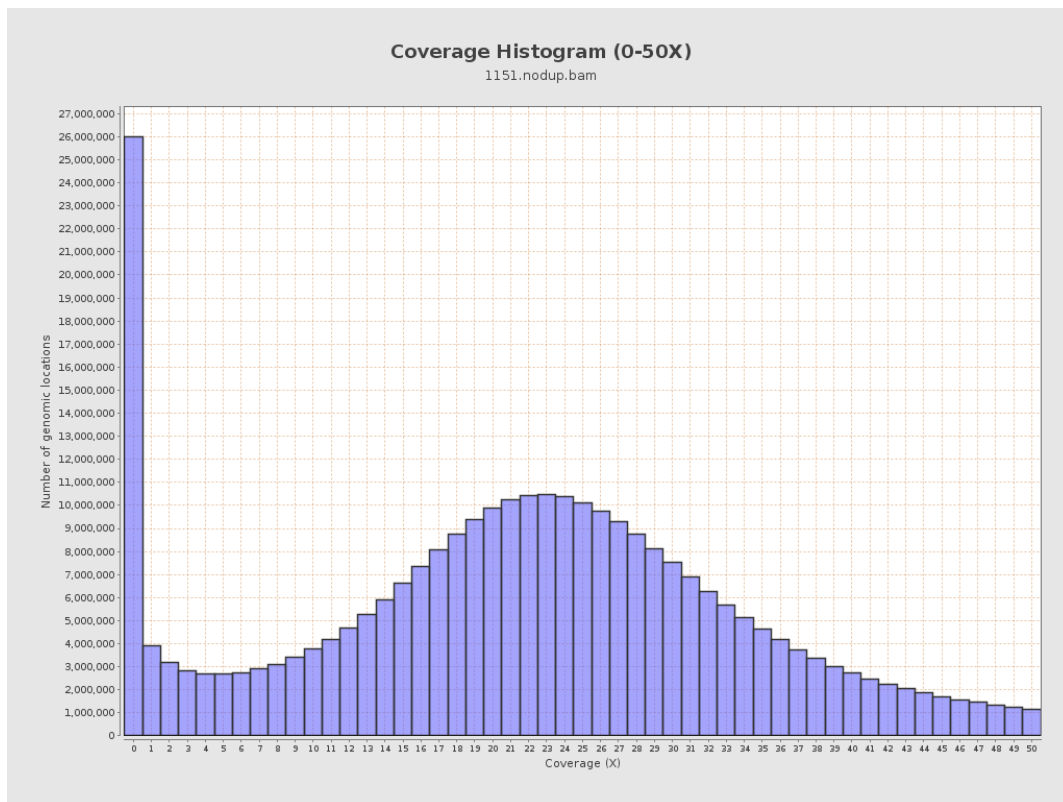
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
1151.nodup.bam
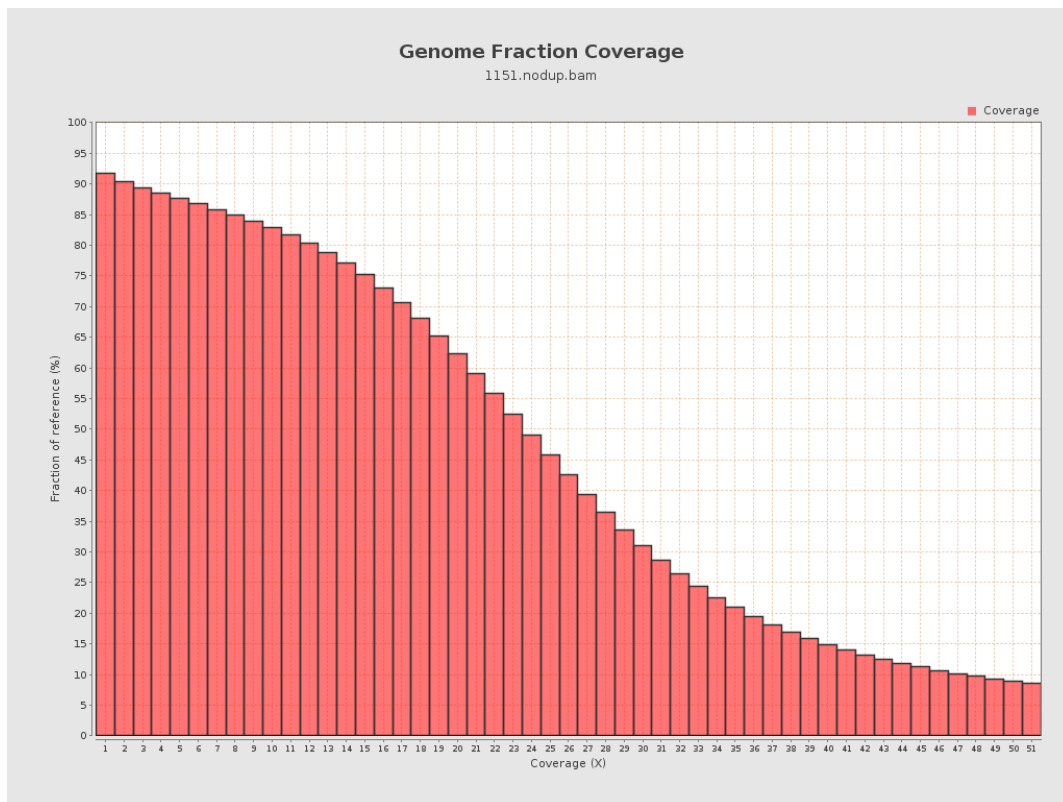
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
1151.nodup.bam
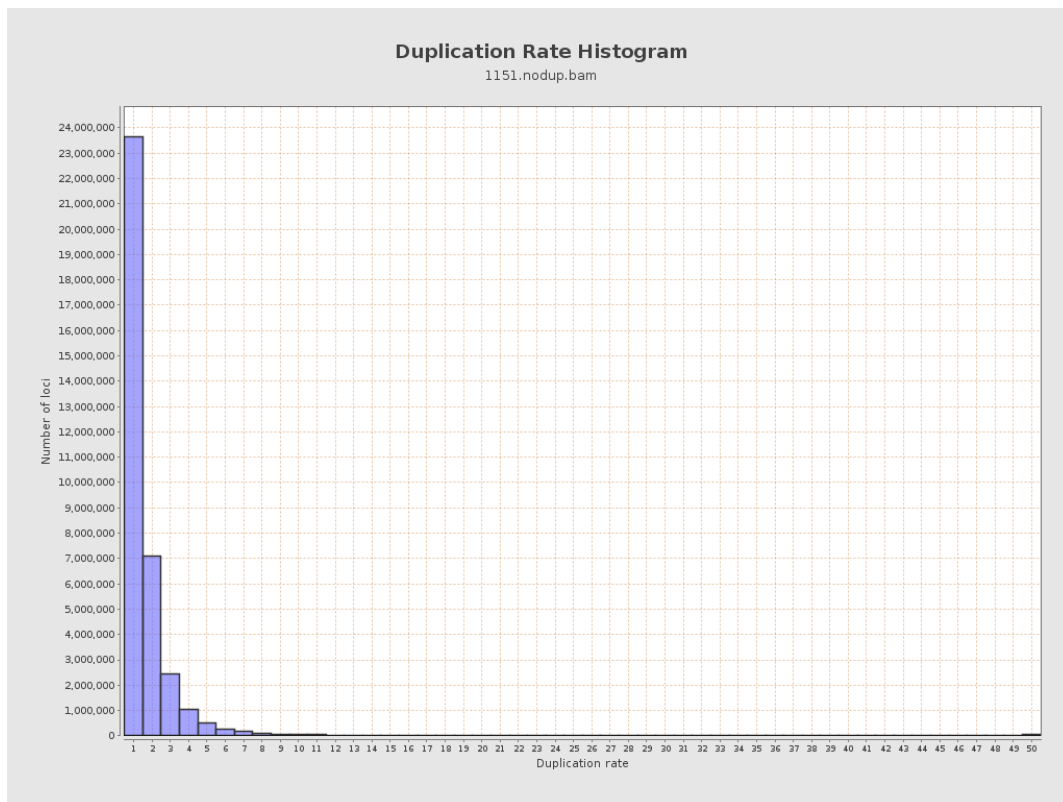
8. Results : Mapped Reads Nucleotide Content
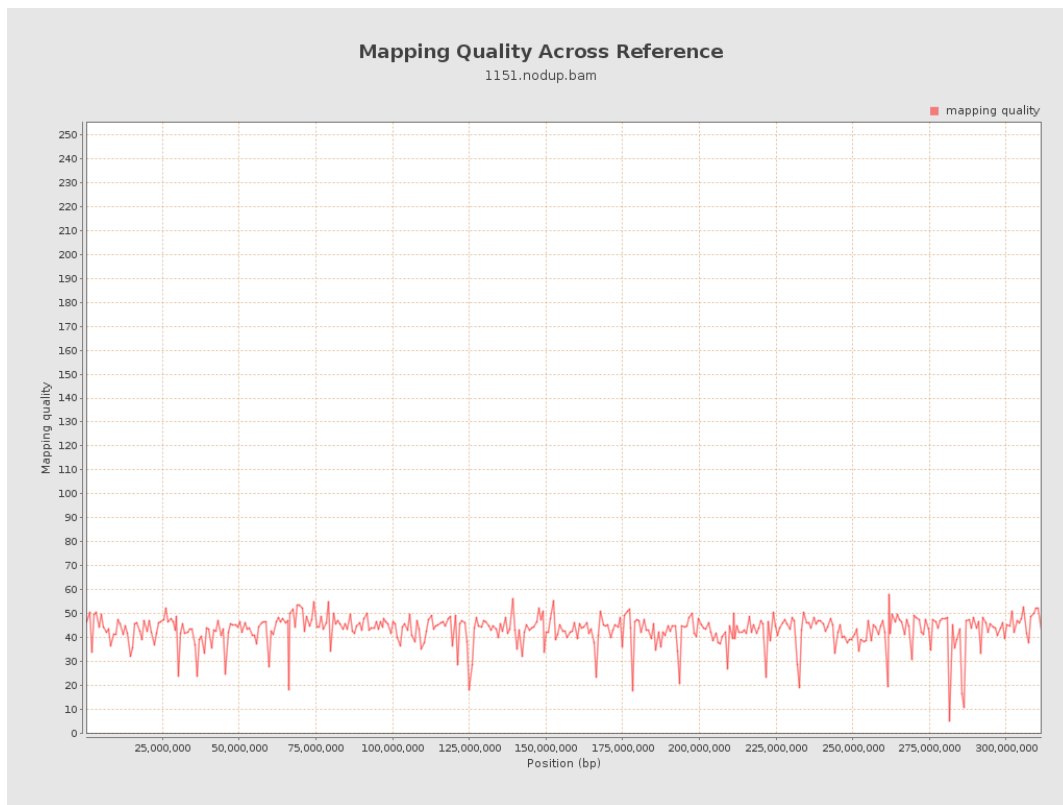
9. Results : Mapped Reads GC-content Distribution
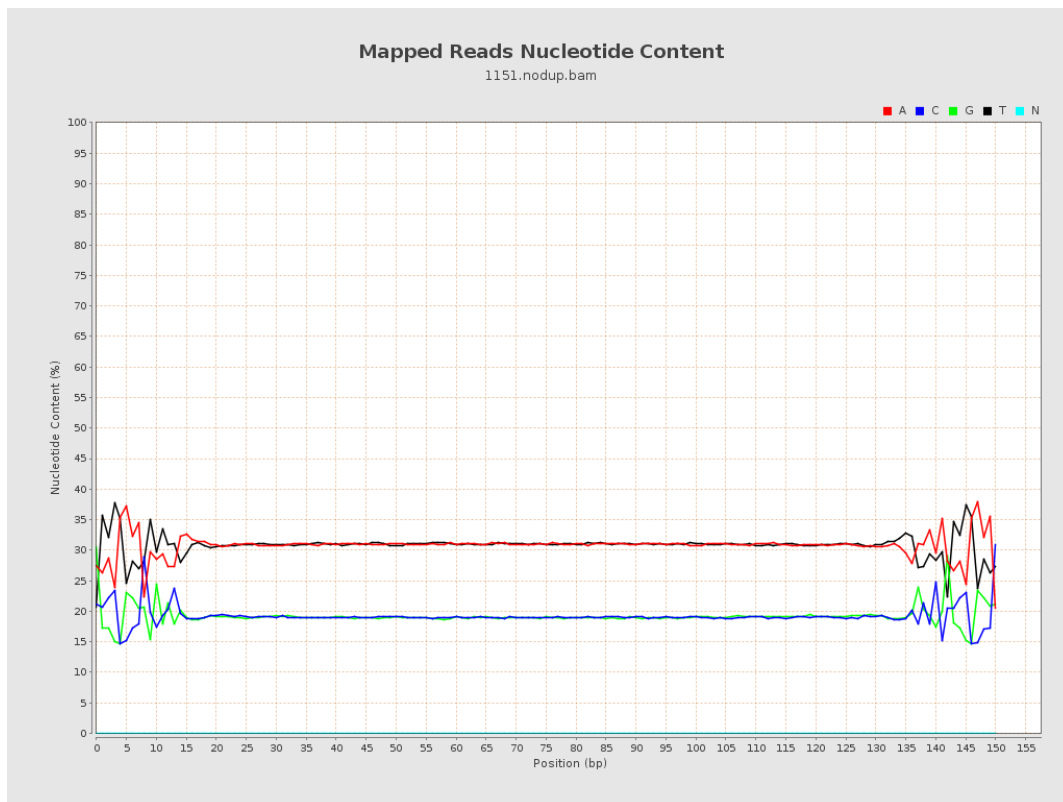
Mapped Reads GC-content Distribution
1151.nodup.bam
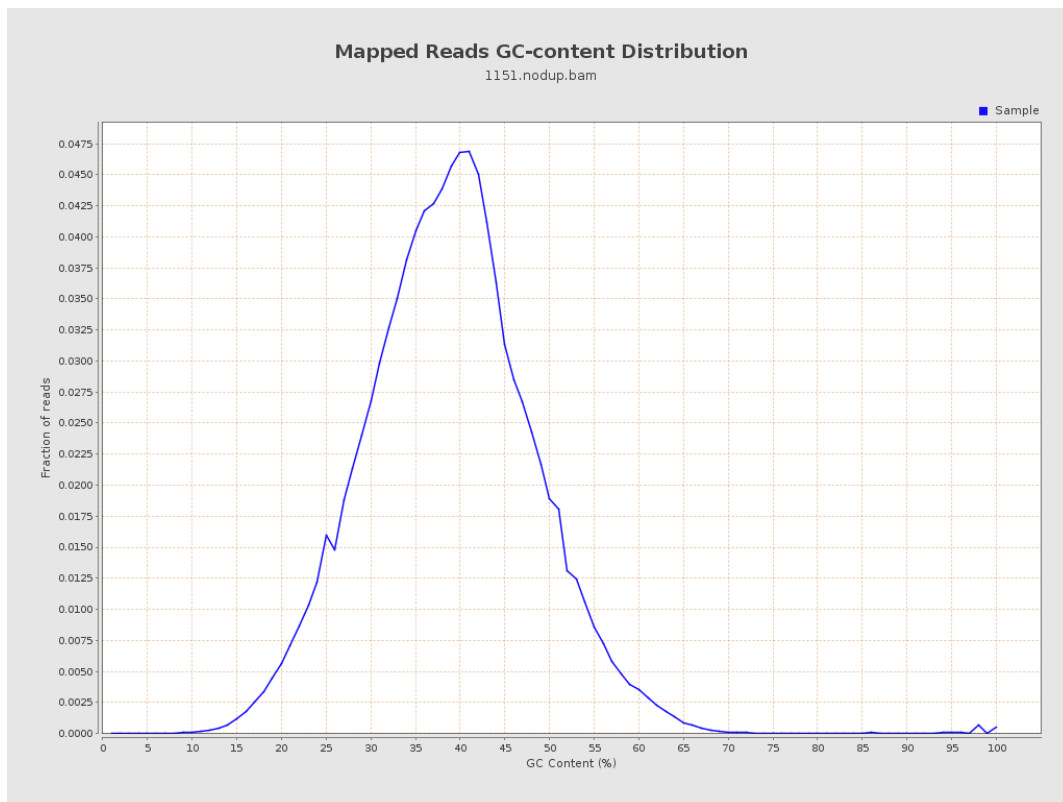
10. Results : Mapped Reads Clipping Profile
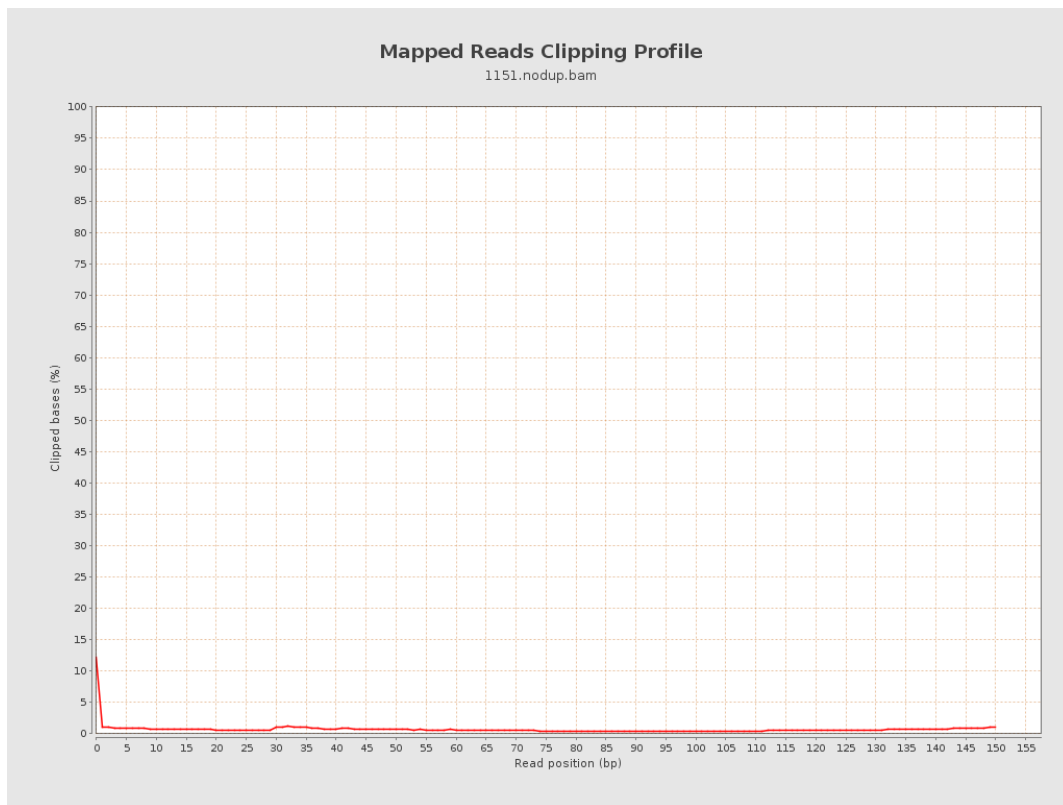
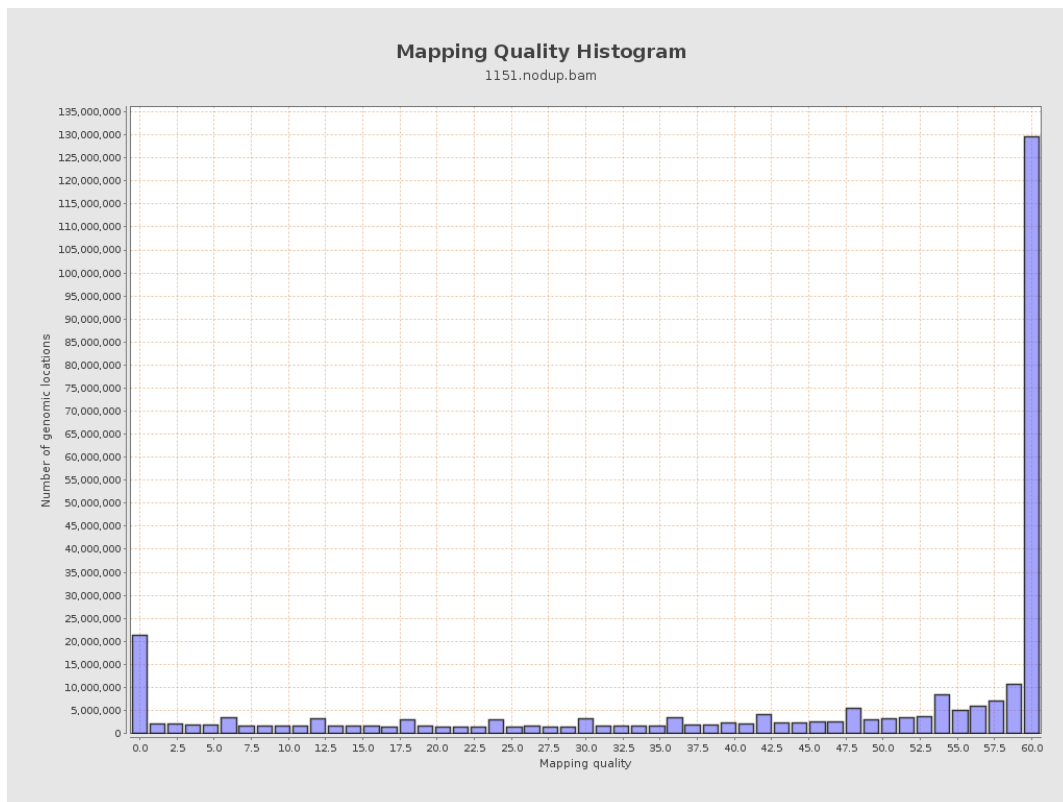# 11. Results : Homopolymer Indels

Homopolymer Indels
1151.nodup.bam
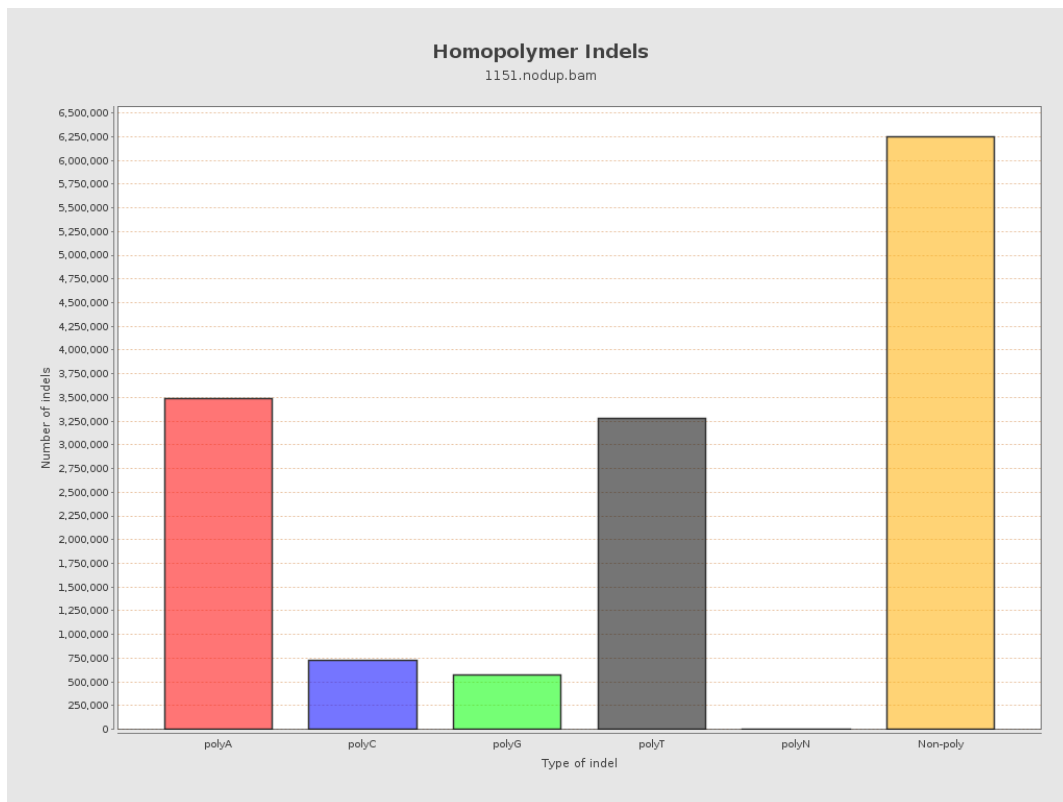
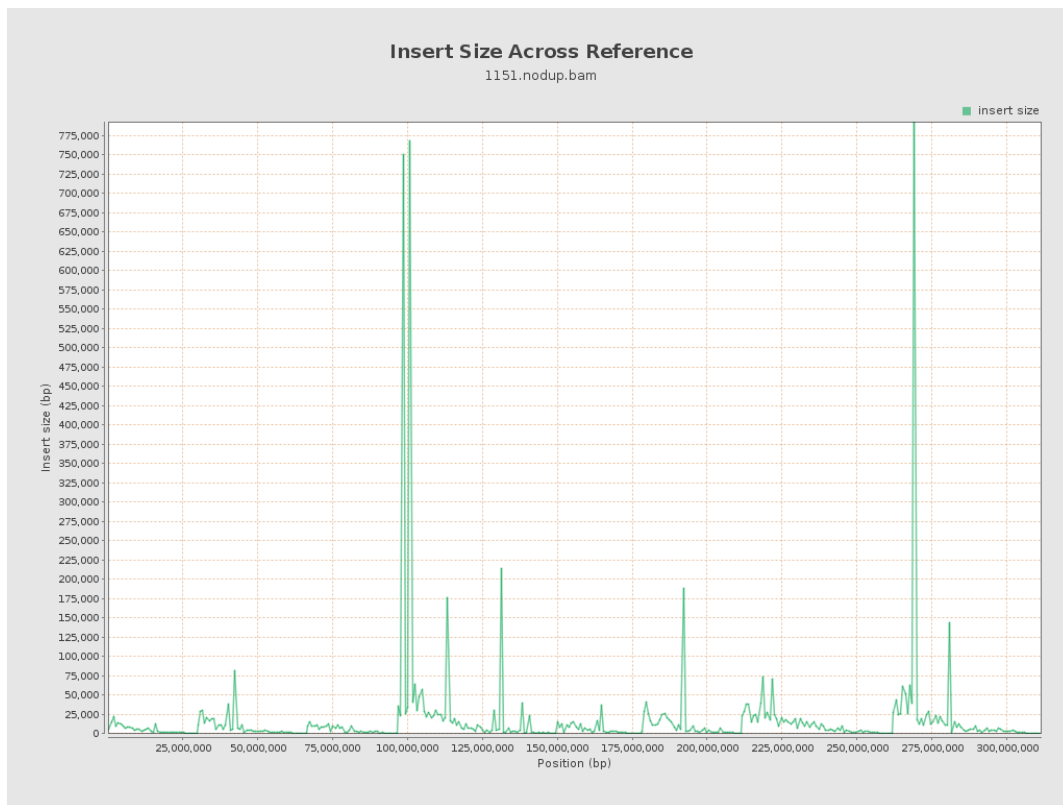# 12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram