Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:39:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/123
3
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1233 .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_246/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_246_S327_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_246/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_246_S327_L003_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:39:26 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	88,282,959
Mapped reads	81,481,331 / 92.3%
Unmapped reads	6,801,628 / 7.7%
Mapped paired reads	81,481,331 / 92.3%
Mapped reads, first in pair	40,818,286 / 46.24%
Mapped reads, second in pair	40,663,045 / 46.06%
Mapped reads, both in pair	79,375,593 / 89.91%
Mapped reads, singletons	2,105,738 / 2.39%
Read min/max/mean length	30 / 151 / 147.91
Duplicated reads (flagged)	12,887,431 / 14.6%
Clipped reads	19,963,579 / 22.61%

2.2. ACGT Content

Number/percentage of A's	3,446,521,549 / 30.91%
Number/percentage of C's	2,126,824,944 / 19.07%
Number/percentage of T's	3,448,437,938 / 30.93%
Number/percentage of G's	2,128,305,852 / 19.09%
Number/percentage of N's	41,666 / 0%
GC Percentage	38.16%

2.3. Coverage

Mean	35.8753
Standard Deviation	301.0461

2.4. Mapping Quality

Mean Mapping Quality	43.73

2.5. Insert size

Mean	249,670.78
Standard Deviation	2,386,034.84
P25/Median/P75	307 / 407 / 534

2.6. Mismatches and indels

General error rate	2.37%
Mismatches	242,004,717
Insertions	8,000,530
Mapped reads with at least one insertion	8.77%
Deletions	7,910,274
Mapped reads with at least one deletion	8.59%
Homopolymer indels	56.65%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	893375018	30.0553	106.3318

|				
LT669789.1	36598175	1328212502	36.2918	305.898
LT669790.1	30422129	1274021631	41.8781	373.5738
LT669791.1	52758100	1854039424	35.1423	287.671
LT669792.1	28376109	1036610052	36.5311	313.9505
LT669793.1	33388210	1132695909	33.925	264.3807
LT669794.1	50579949	1687889125	33.3707	234.8211
LT669795.1	49795044	1973404589	39.6305	399.5298

3. Results : Coverage across reference

Coverage across reference
1233.nodup.bam

4. Results : Coverage Histogram

Coverage Histogram
1233.nodup.bam
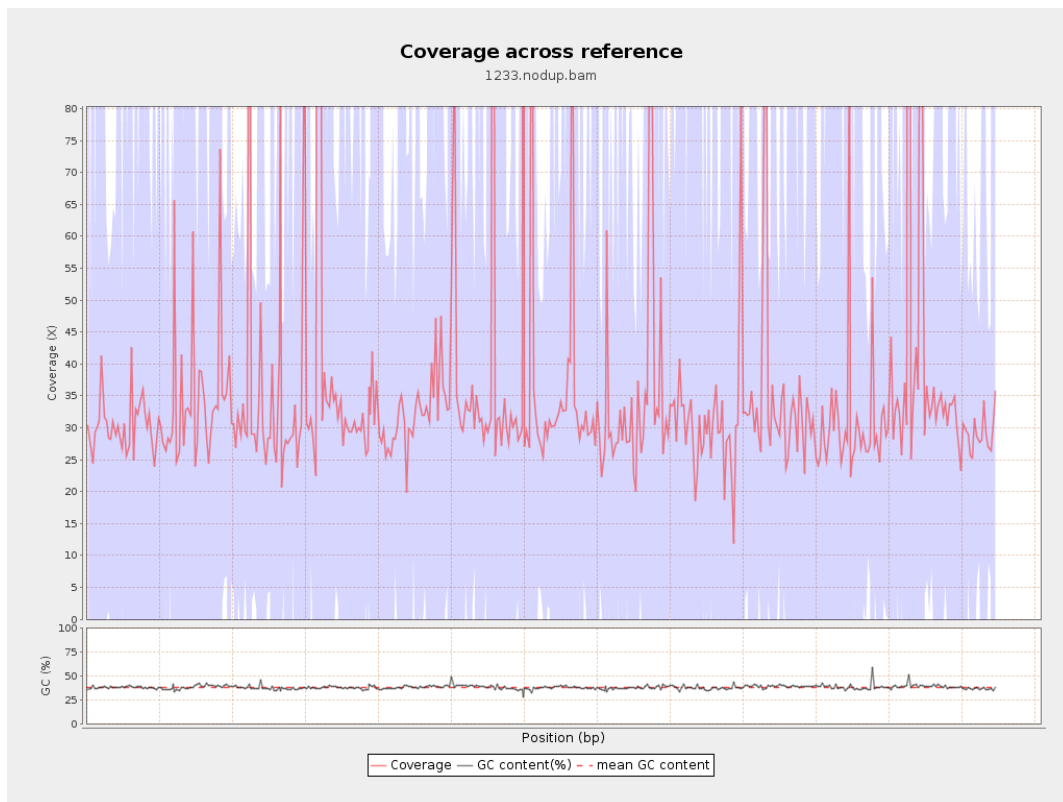
5. Results : Coverage Histogram (0-50X)
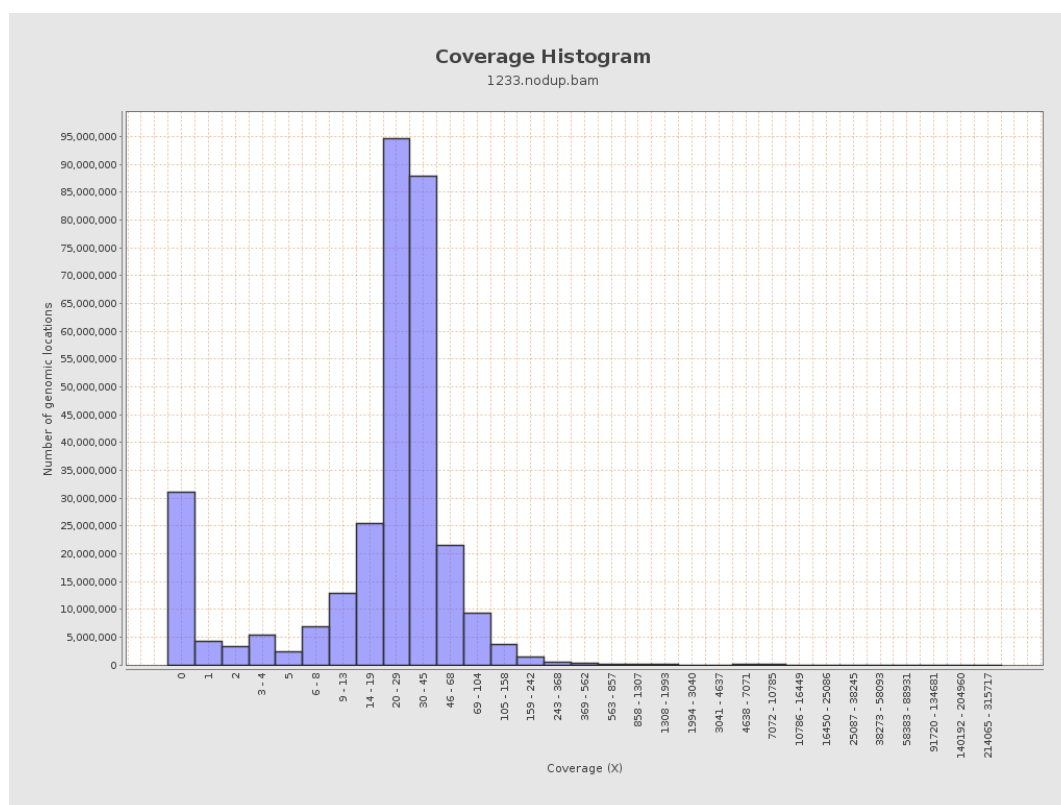
Coverage Histogram (0-50X)
1233.nodup.bam
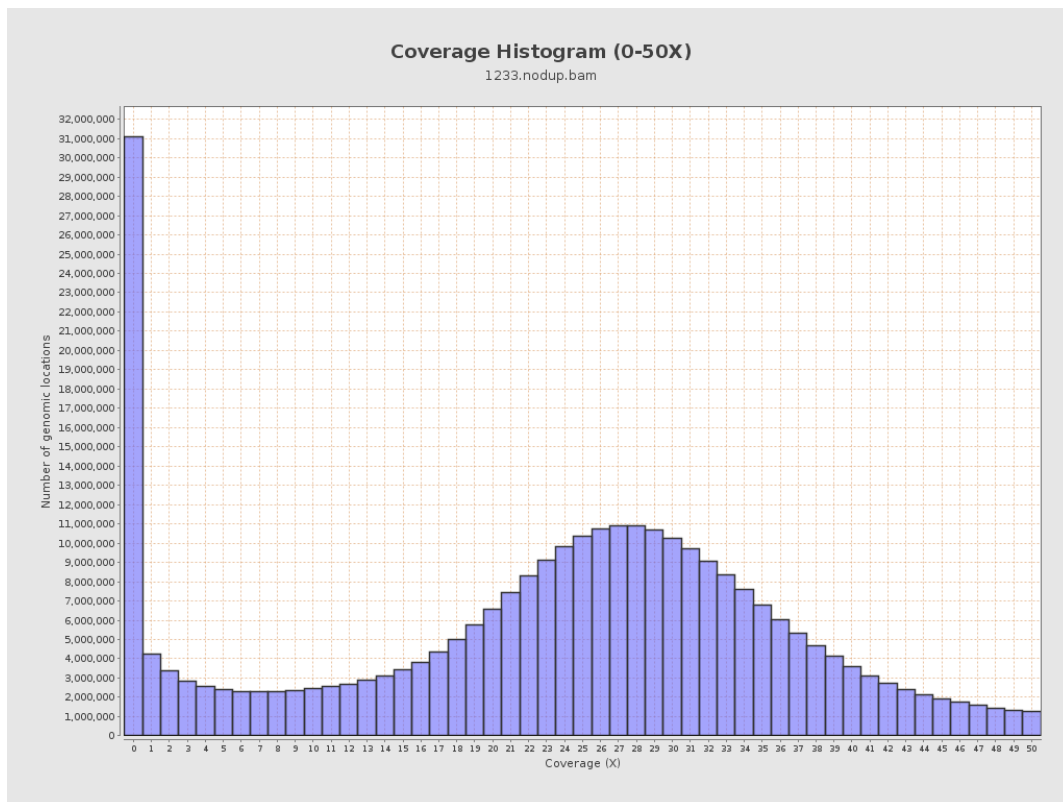
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
1233.nodup.bam
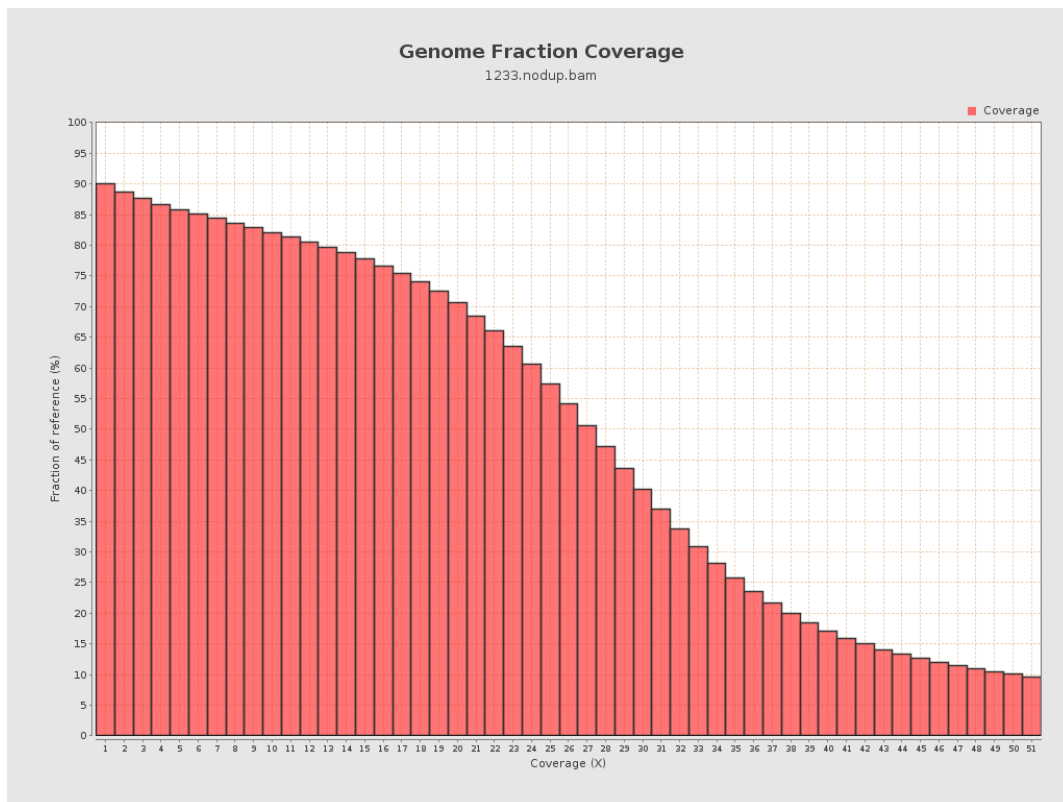
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
1233.nodup.bam
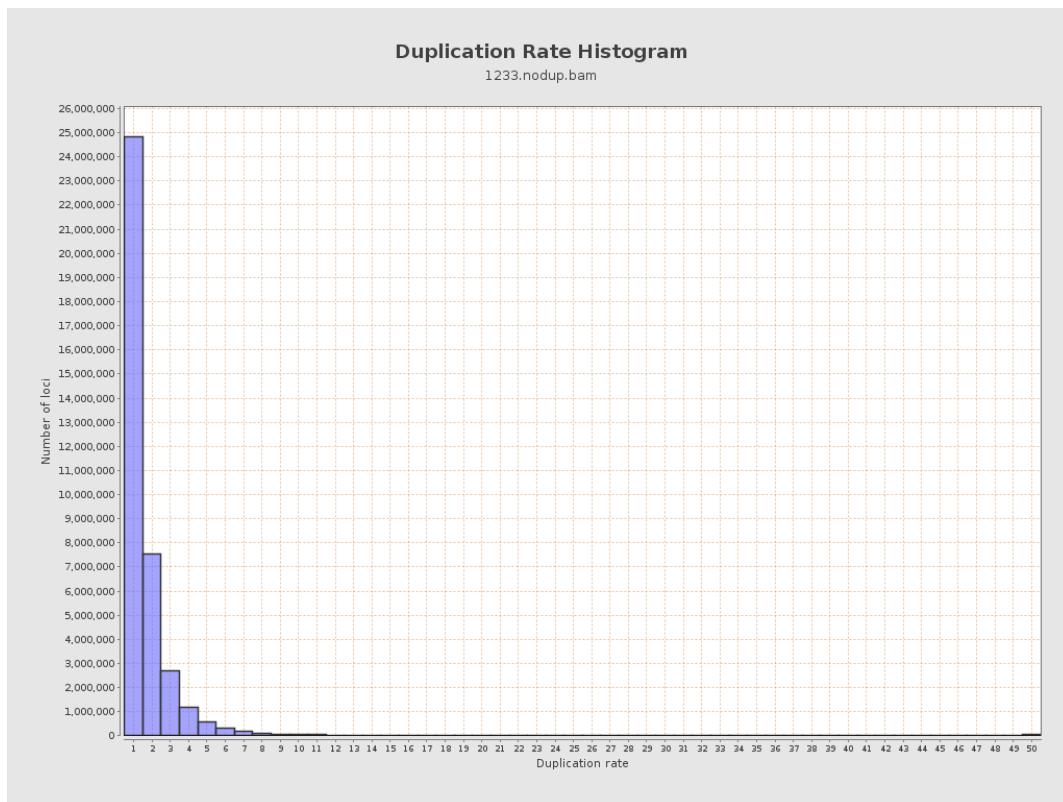
8. Results : Mapped Reads Nucleotide Content
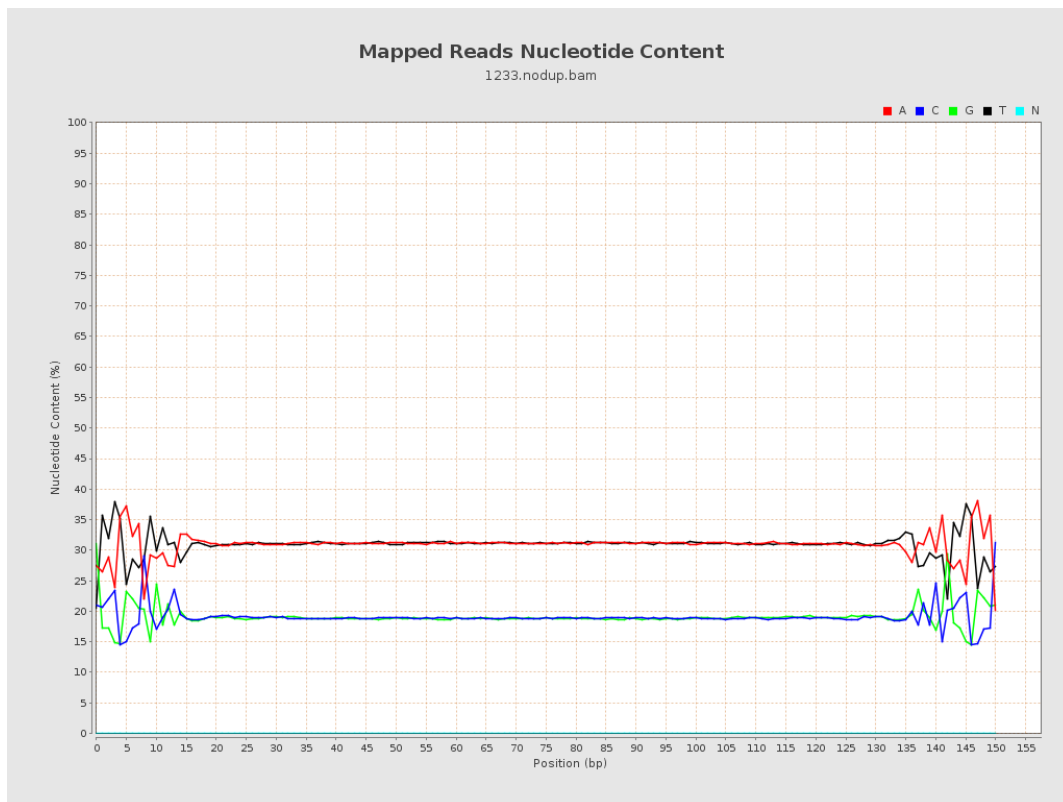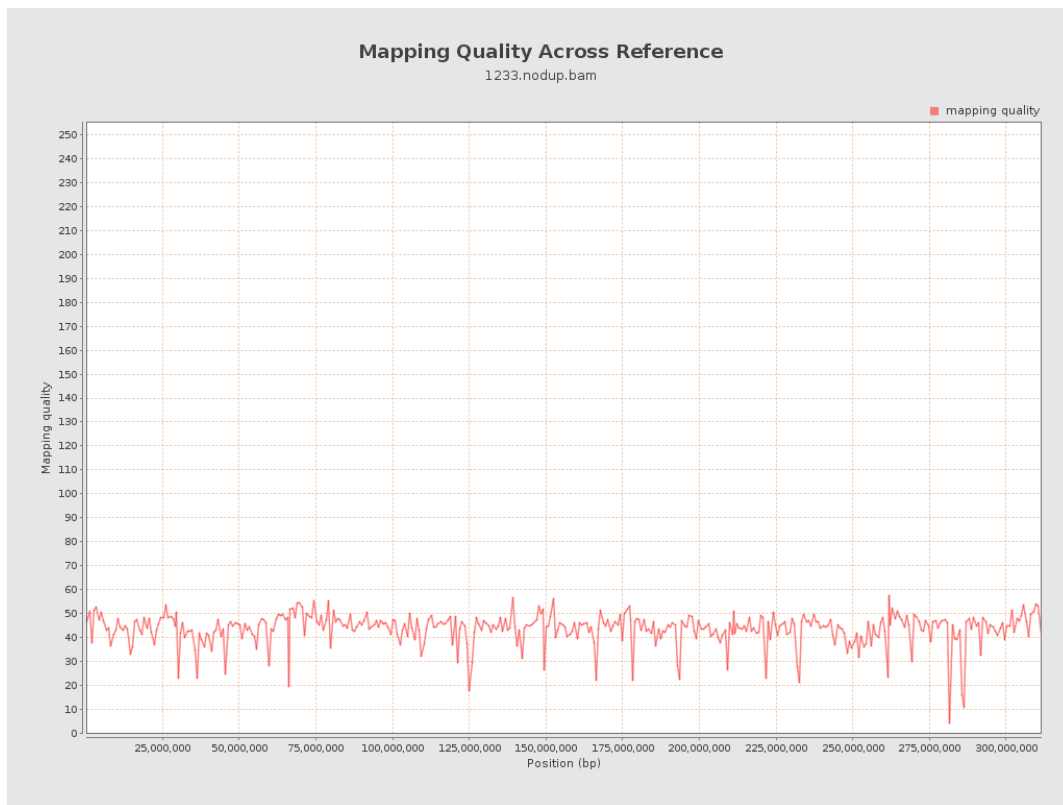
9. Results : Mapped Reads GC-content Distribution
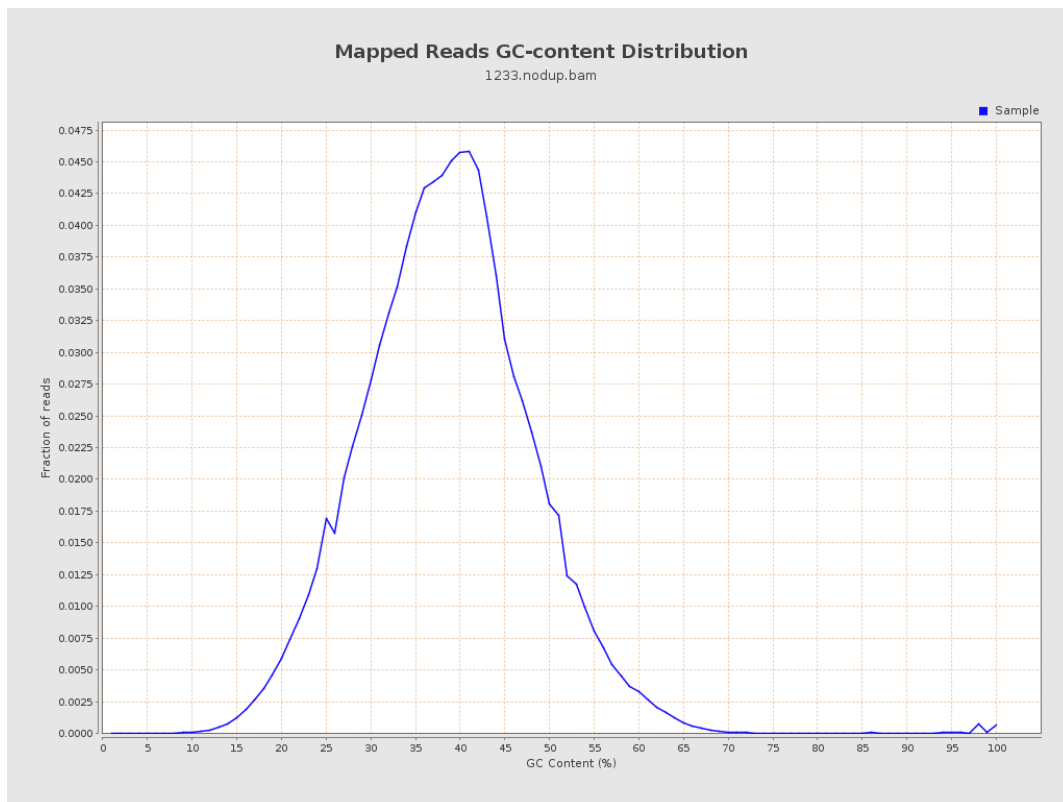
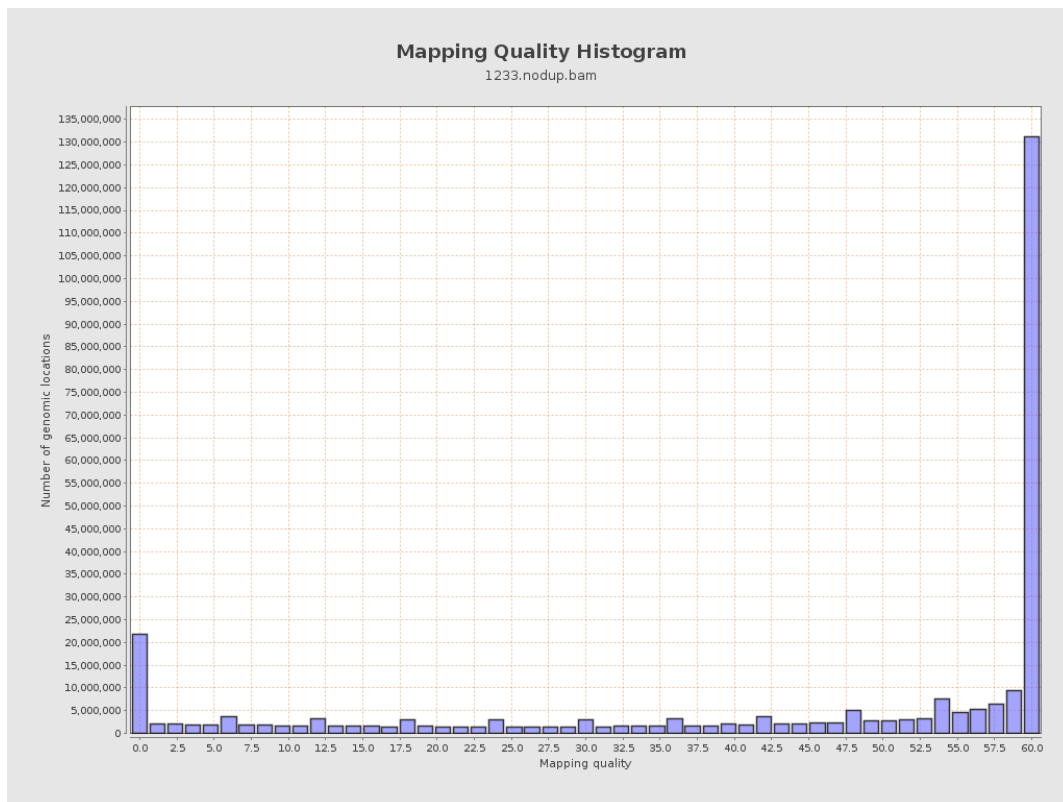# 10. Results : Mapped Reads Clipping Profile
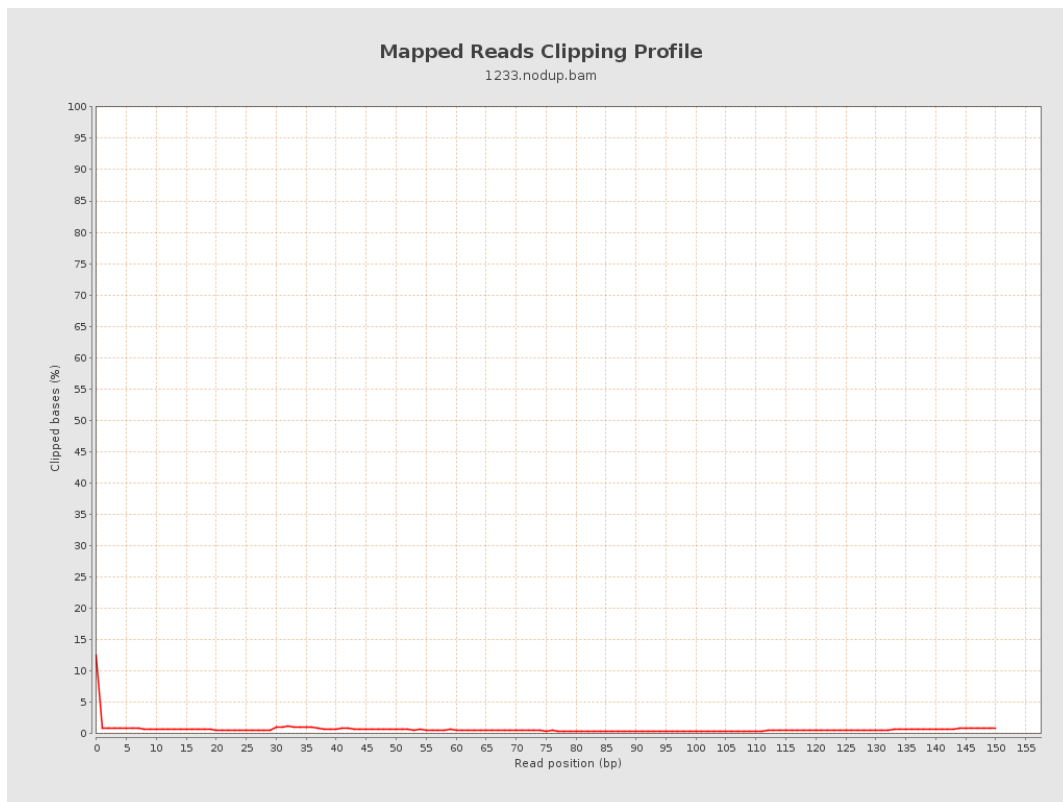
11. Results : Homopolymer Indels
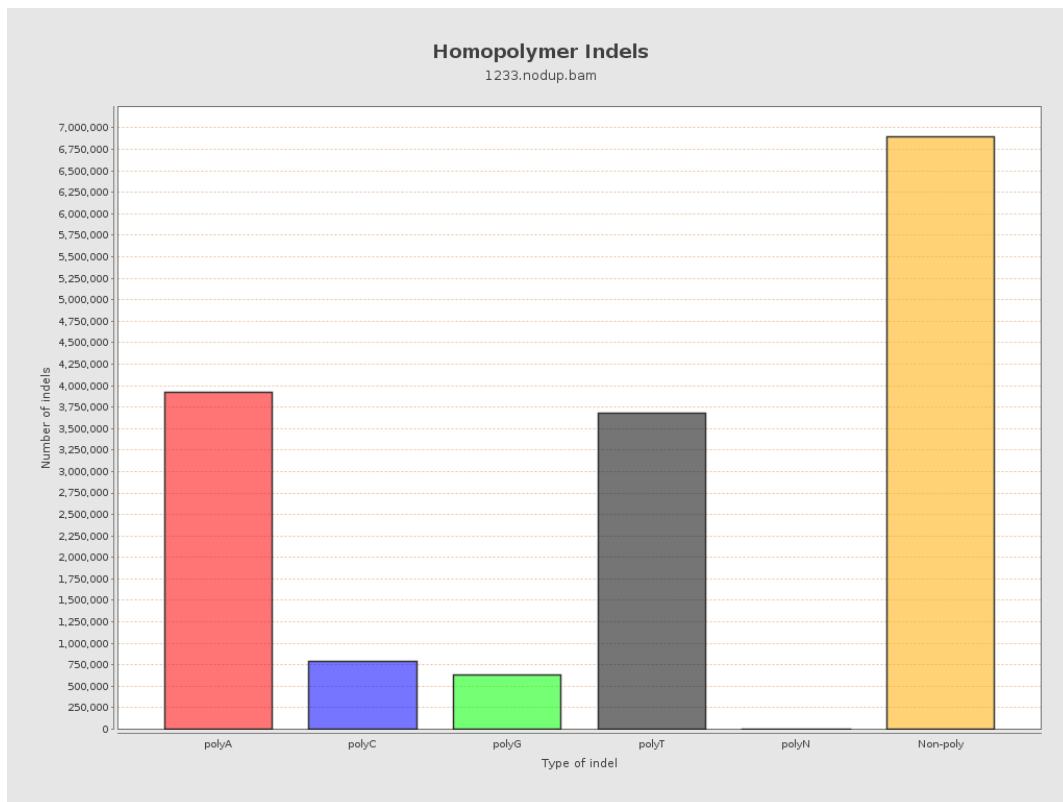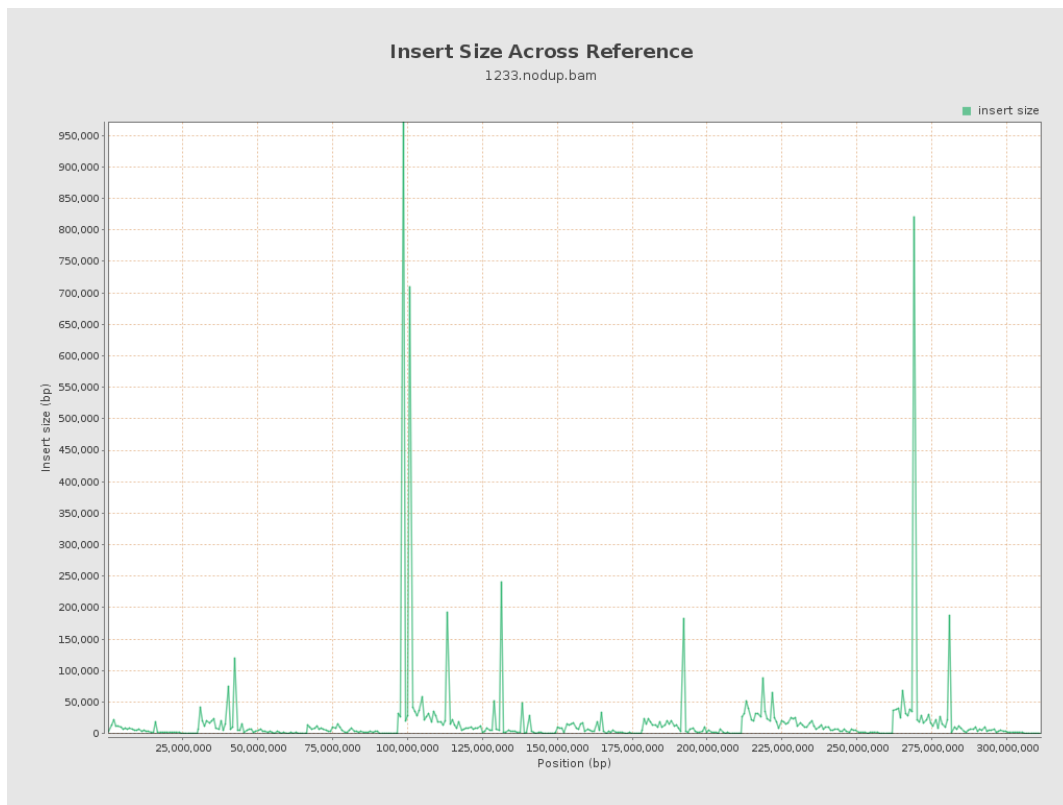
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

Insert Size Across Reference
1233.nodup.bam

15. Results : Insert Size Histogram