Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:41:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1386
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1386 .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_432/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_432_S407_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_432/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_432_S407_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:41:31 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	93,798,063
Mapped reads	89,006,200 / 94.89%
Unmapped reads	4,791,863 / 5.11%
Mapped paired reads	89,006,200 / 94.89%
Mapped reads, first in pair	44,640,247 / 47.59%
Mapped reads, second in pair	44,365,953 / 47.3%
Mapped reads, both in pair	87,264,731 / 93.03%
Mapped reads, singletons	1,741,469 / 1.86%
Read min/max/mean length	30 / 151 / 148.14
Duplicated reads (flagged)	15,237,727 / 16.25%
Clipped reads	19,494,327 / 20.78%

2.2. ACGT Content

Number/percentage of A's	3,806,385,550 / 30.68%
Number/percentage of C's	2,400,057,560 / 19.34%
Number/percentage of T's	3,813,017,905 / 30.73%
Number/percentage of G's	2,387,415,626 / 19.24%
Number/percentage of N's	41,889 / 0%
GC Percentage	38.59%

2.3. Coverage

Mean	39.9156
Standard Deviation	330.8093

2.4. Mapping Quality

Mean Mapping Quality	43.38

2.5. Insert size

Mean	241,082.03
Standard Deviation	2,304,886.17
P25/Median/P75	367 / 479 / 632

2.6. Mismatches and indels

General error rate	2.41%
Mismatches	277,346,586
Insertions	8,249,009
Mapped reads with at least one insertion	8.36%
Deletions	8,575,586
Mapped reads with at least one deletion	8.56%
Homopolymer indels	55.64%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	926770890	31.1789	86.5961

LT669789.1	36598175	1504353625	41.1046	347.1731
LT669790.1	30422129	1215190586	39.9443	288.8549
LT669791.1	52758100	2107382742	39.9443	270.5071
LT669792.1	28376109	1106900544	39.0082	433.1308
LT669793.1	33388210	1253668946	37.5483	240.3211
LT669794.1	50579949	1962792652	38.8057	302.8472
LT669795.1	49795044	2362321038	47.4409	473.7389

3. Results : Coverage across reference
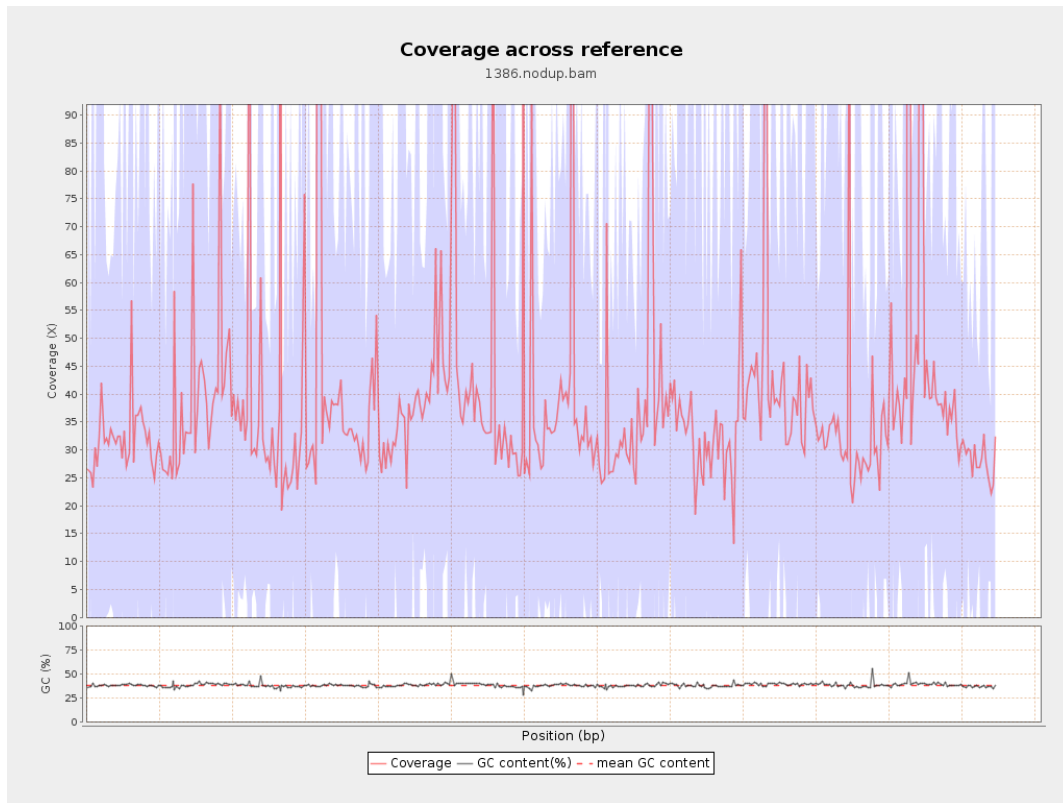
4. Results : Coverage Histogram

5. Results : Coverage Histogram (0-50X)
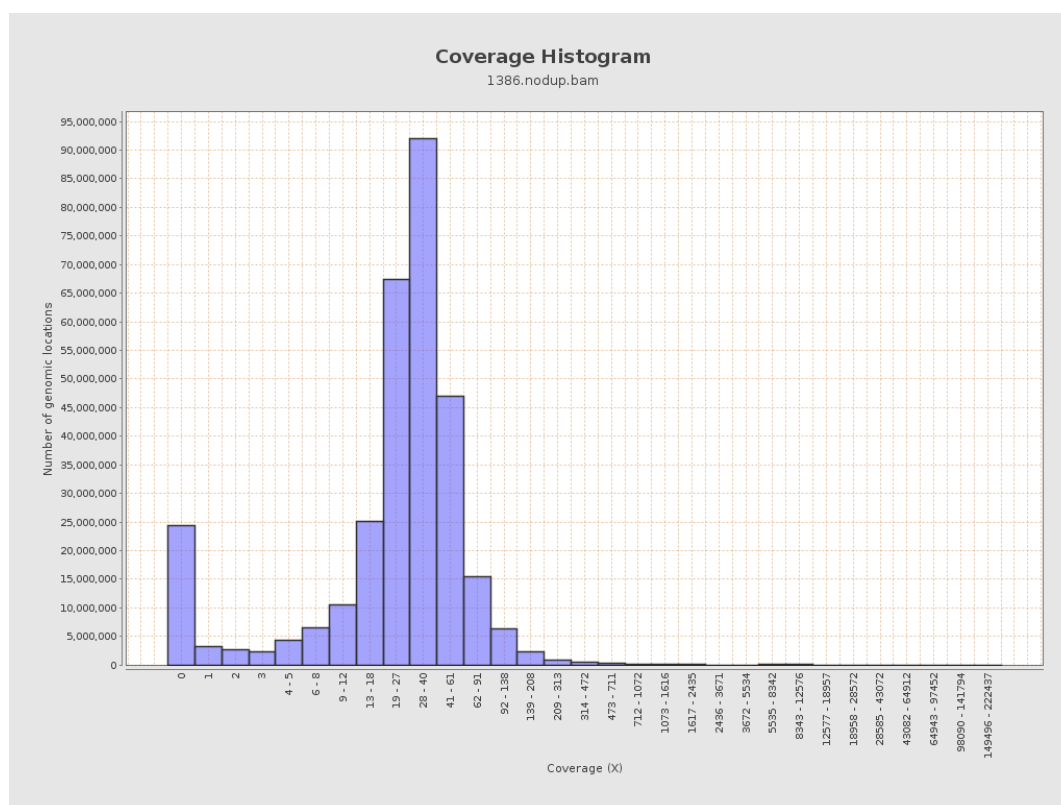
Coverage Histogram (0-50X)
1386.nodup.bam
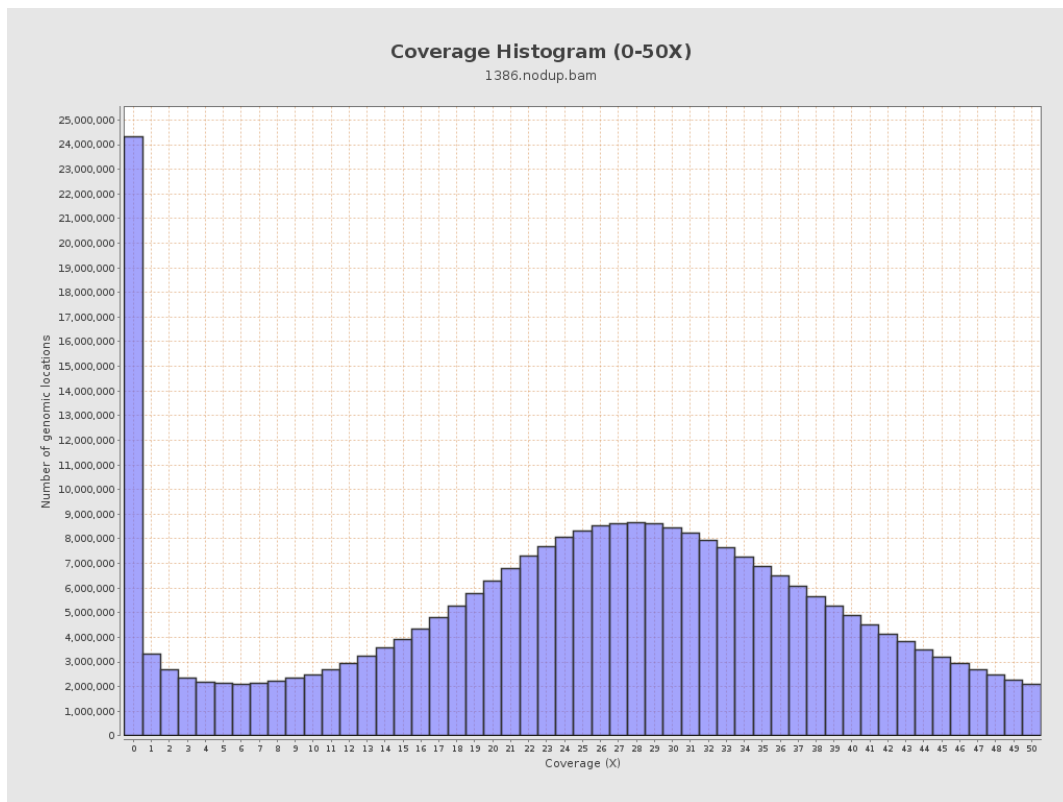
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
1386.nodup.bam
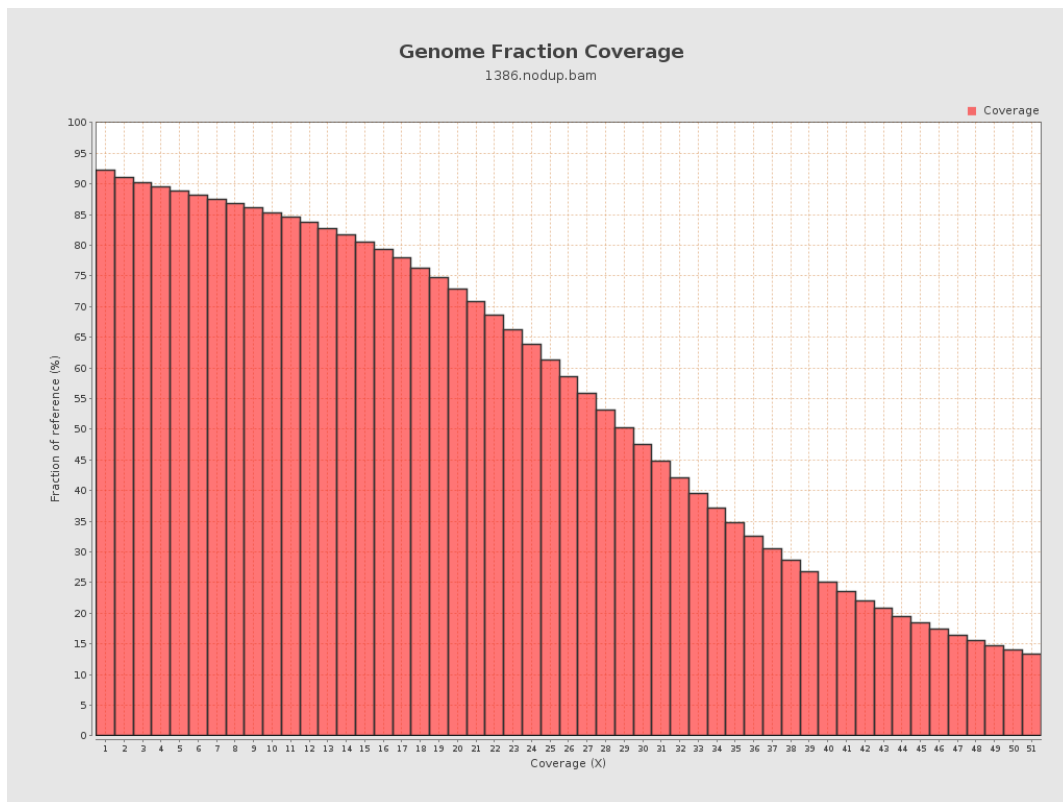
7. Results : Duplication Rate Histogram
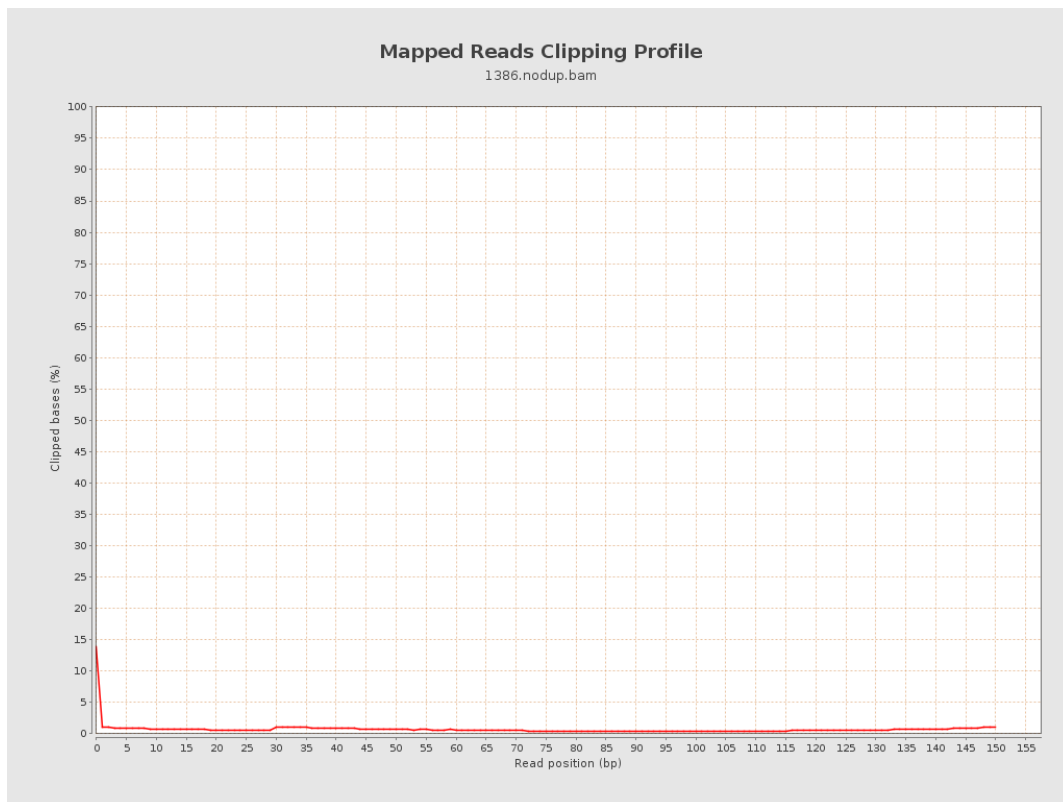

Duplication Rate Histogram
1386.nodup.bam
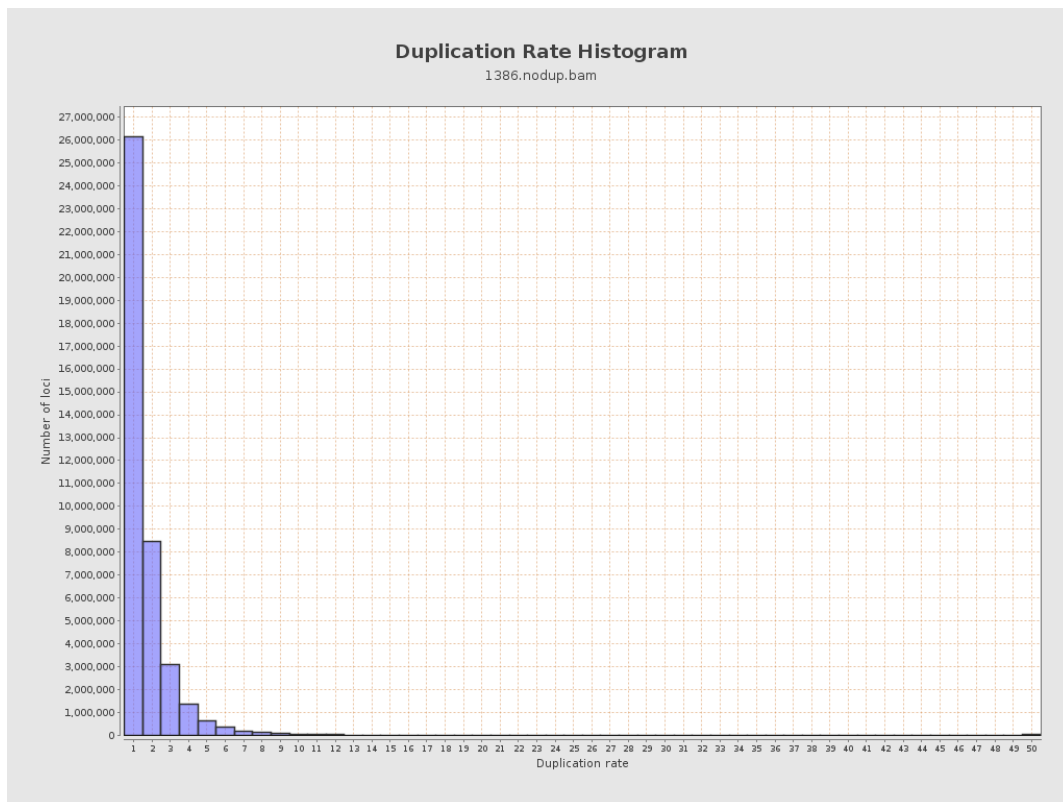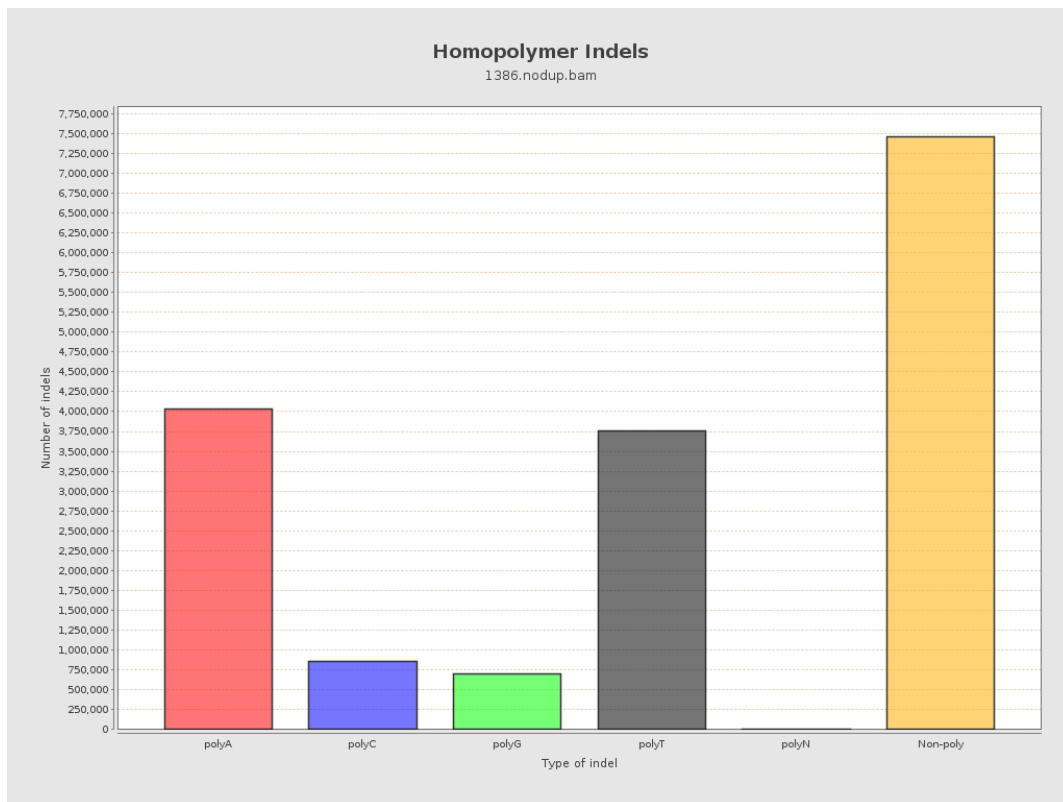
8. Results : Mapped Reads Nucleotide Content
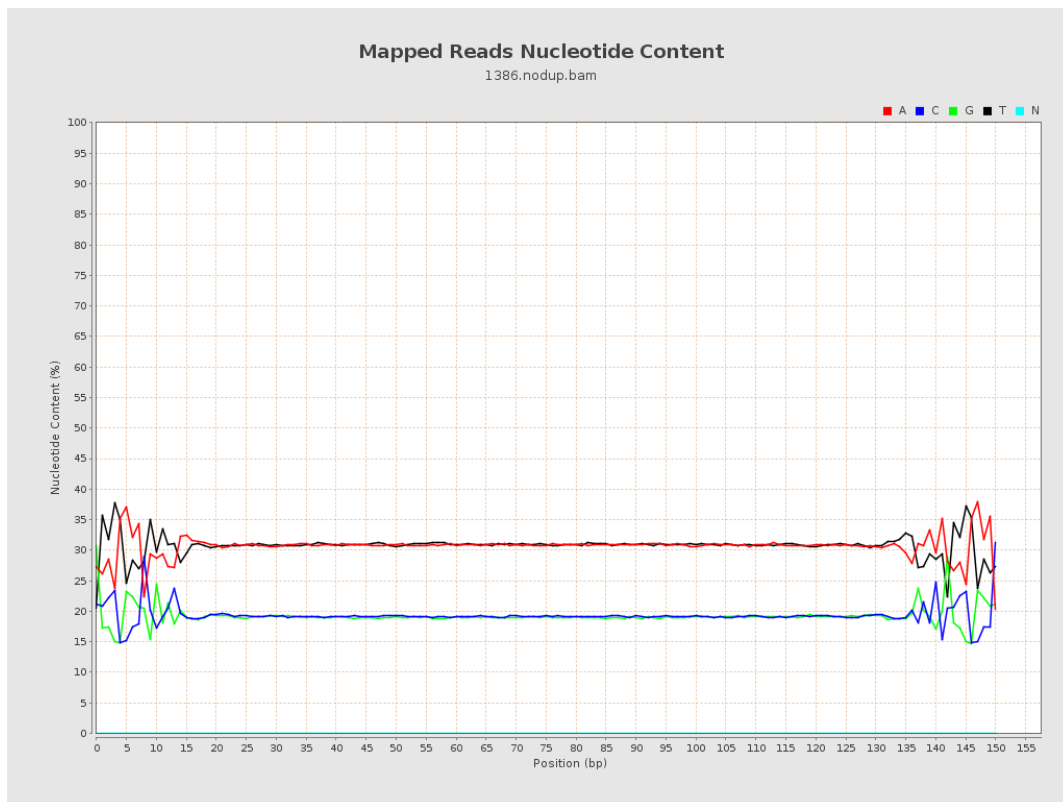
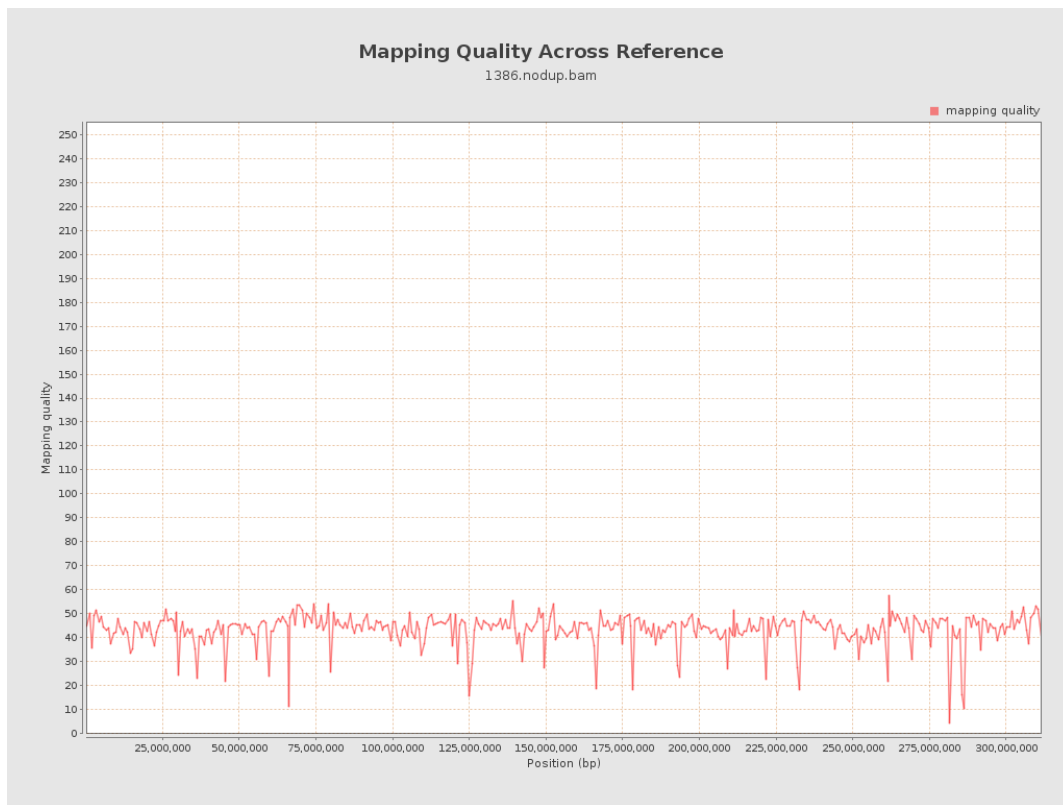# 9. Results : Mapped Reads GC-content Distribution
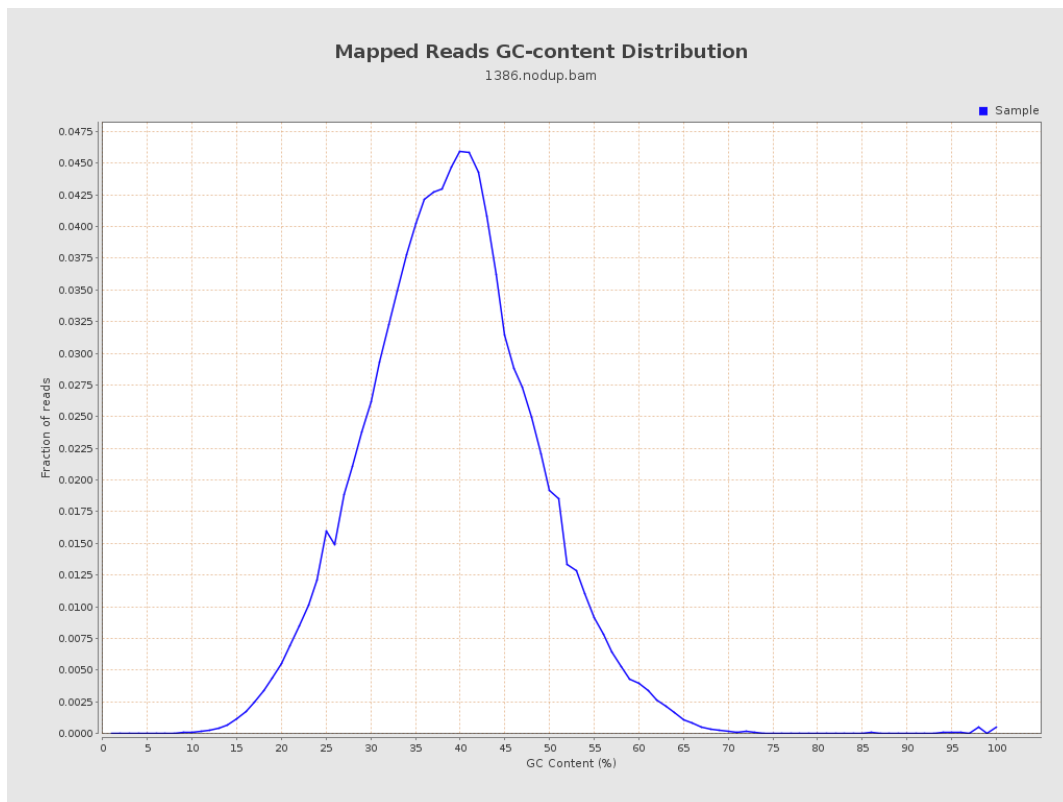
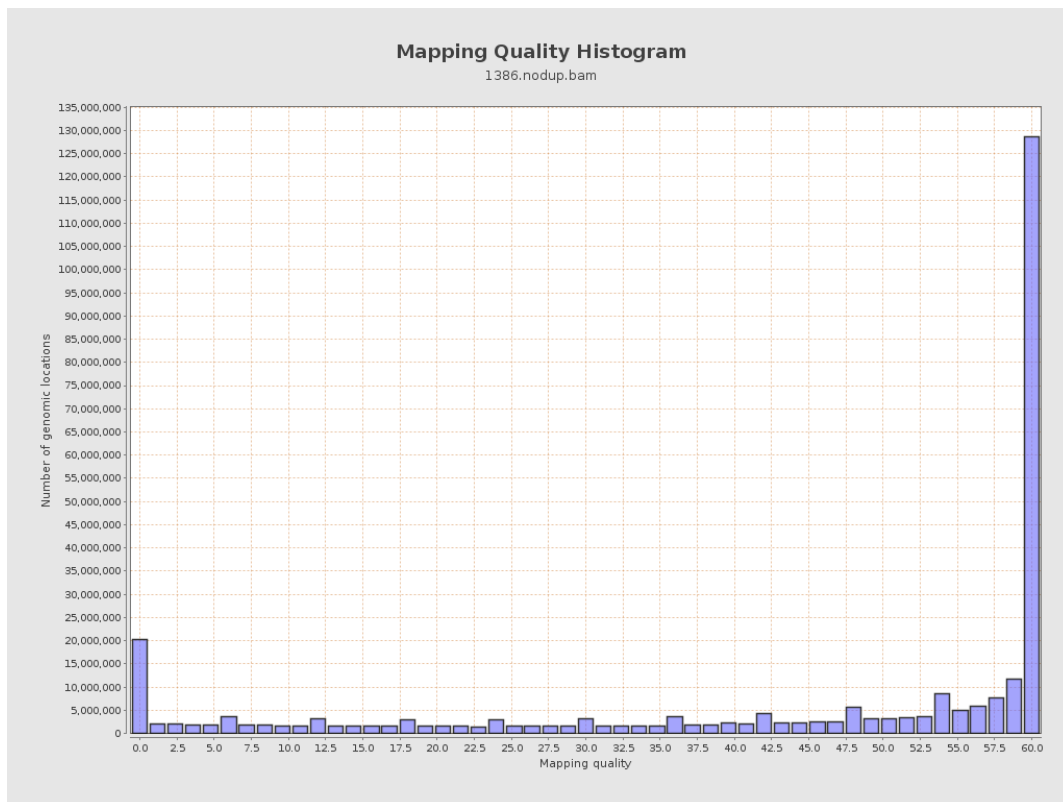# 10. Results : Mapped Reads Clipping Profile
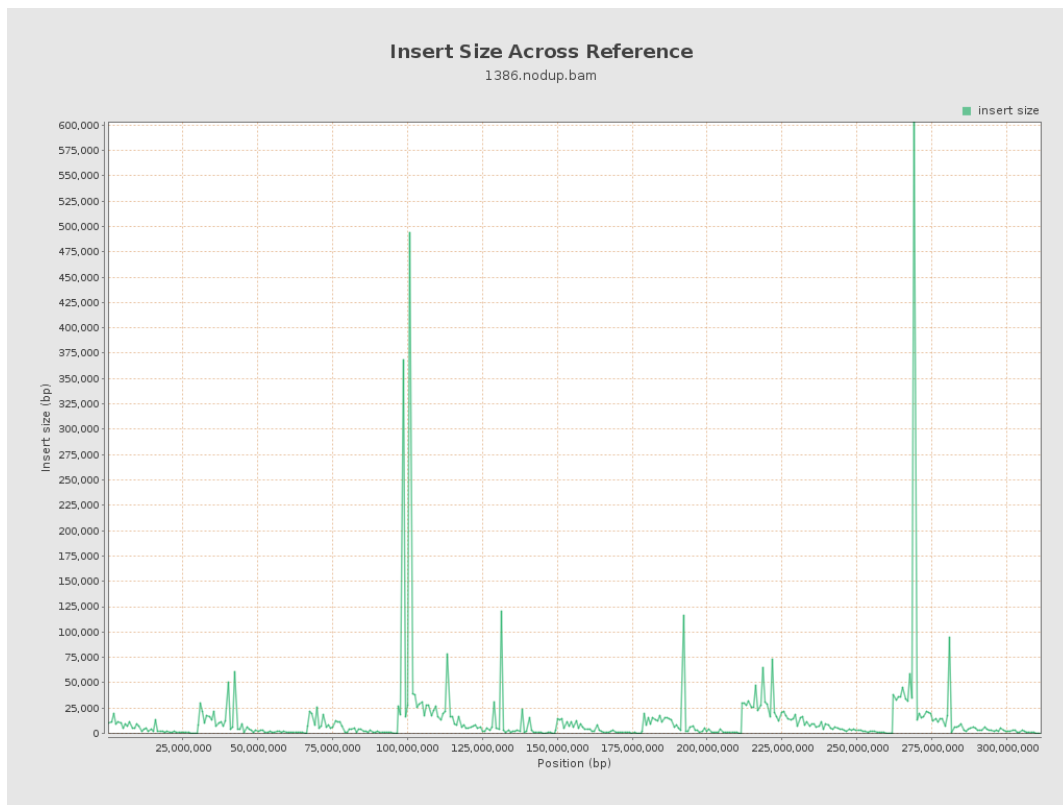
11. Results : Homopolymer Indels

12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

Insert Size Across Reference
1386.nodup.bam

15. Results : Insert Size Histogram

Insert Size Histogram
1386.nodup.bam