Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:44:31

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1435 .nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1435 .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_464/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_464_S439_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_464/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_464_S439_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:44:31 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	99,709,567
Mapped reads	93,313,659 / 93.59%
Unmapped reads	6,395,908 / 6.41%
Mapped paired reads	93,313,659 / 93.59%
Mapped reads, first in pair	46,753,534 / 46.89%
Mapped reads, second in pair	46,560,125 / 46.7%
Mapped reads, both in pair	91,191,572 / 91.46%
Mapped reads, singletons	2,122,087 / 2.13%
Read min/max/mean length	30 / 151 / 148.02
Duplicated reads (flagged)	16,777,976 / 16.83%
Clipped reads	21,371,486 / 21.43%

2.2. ACGT Content

Number/percentage of A's	3,964,803,905 / 30.77%
Number/percentage of C's	2,476,796,180 / 19.22%
Number/percentage of T's	3,975,402,415 / 30.85%
Number/percentage of G's	2,467,933,691 / 19.15%
Number/percentage of N's	45,088 / 0%
GC Percentage	38.38%

2.3. Coverage

Mean	41.4548
Standard Deviation	353.6363

2.4. Mapping Quality

Mean Mapping Quality	43.81

2.5. Insert size

Mean	245,801.07
Standard Deviation	2,364,540.38
P25/Median/P75	329 / 438 / 583

2.6. Mismatches and indels

General error rate	2.31%
Mismatches	273,164,079
Insertions	8,863,765
Mapped reads with at least one insertion	8.5%
Deletions	8,983,968
Mapped reads with at least one deletion	8.52%
Homopolymer indels	56.53%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	1008033689	33.9127	135.1599

LT669789.1	36598175	1502656904	41.0582	355.2596
LT669790.1	30422129	1368381468	44.9798	379.2369
LT669791.1	52758100	2158060411	40.9048	322.8735
LT669792.1	28376109	1165250870	41.0645	373.2389
LT669793.1	33388210	1271130783	38.0712	233.1615
LT669794.1	50579949	1971728047	38.9824	291.9135
LT669795.1	49795044	2473831194	49.6803	527.4262

3. Results : Coverage across reference

4. Results : Coverage Histogram

Coverage Histogram
1435.nodup.bam
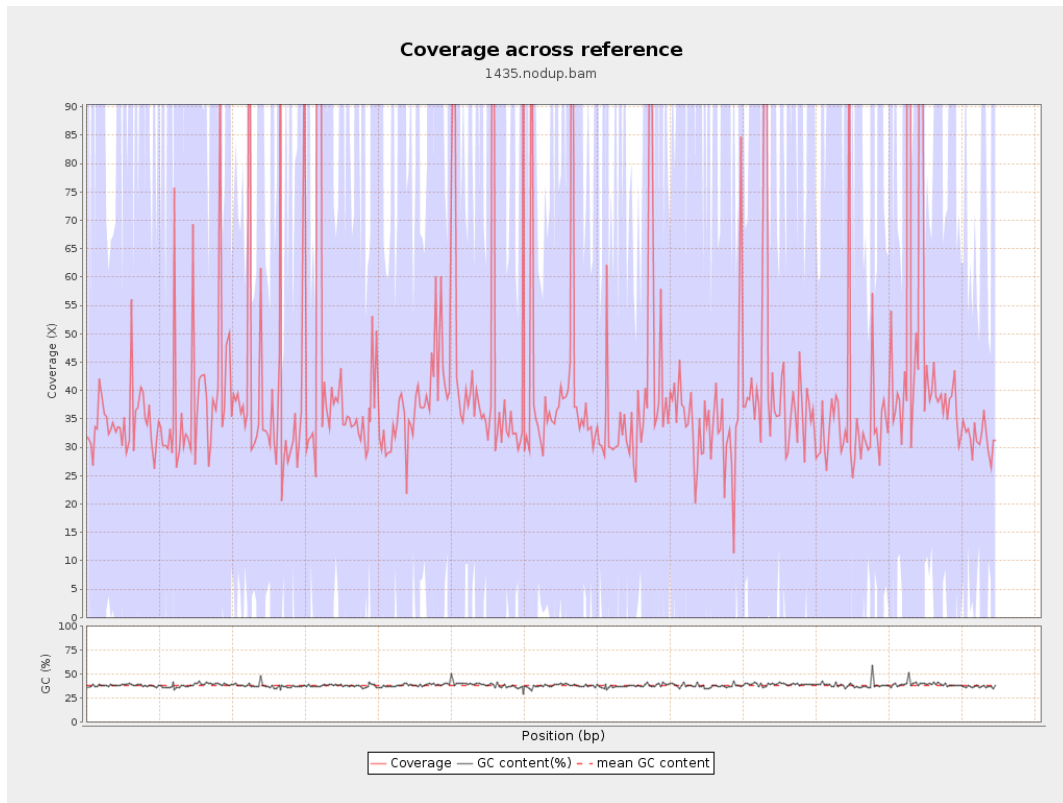
5. Results : Coverage Histogram (0-50X)
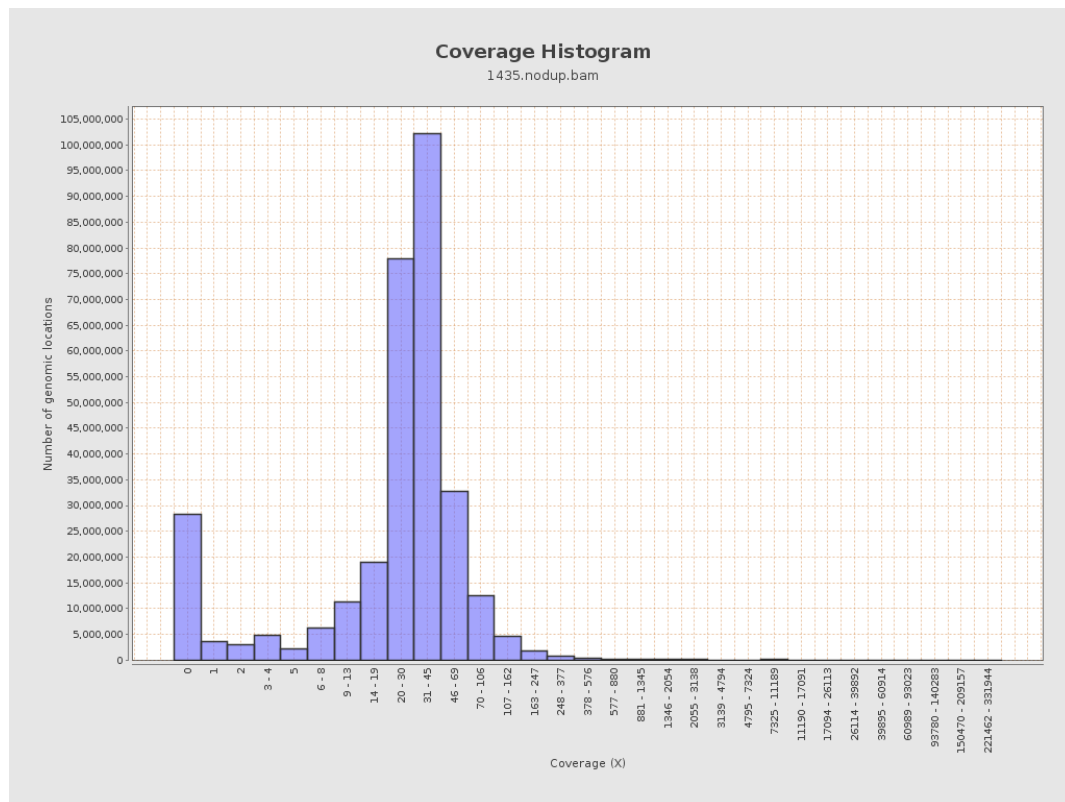
Coverage Histogram (0-50X)
1435.nodup.bam
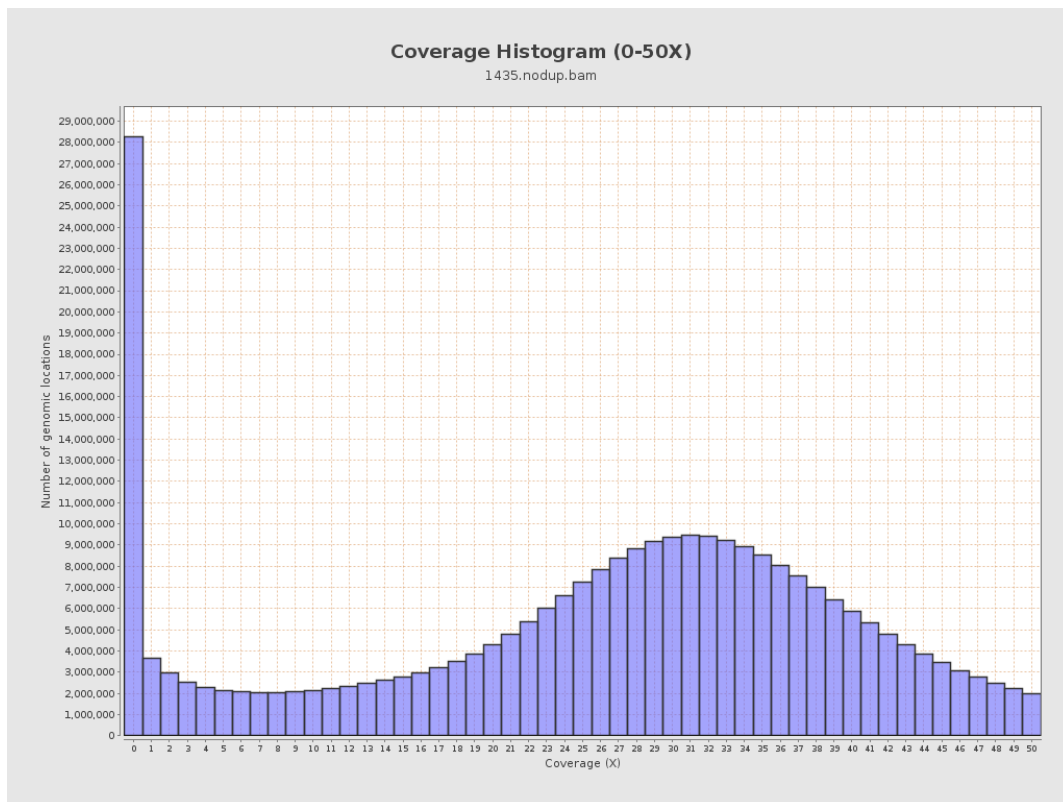
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
1435.nodup.bam
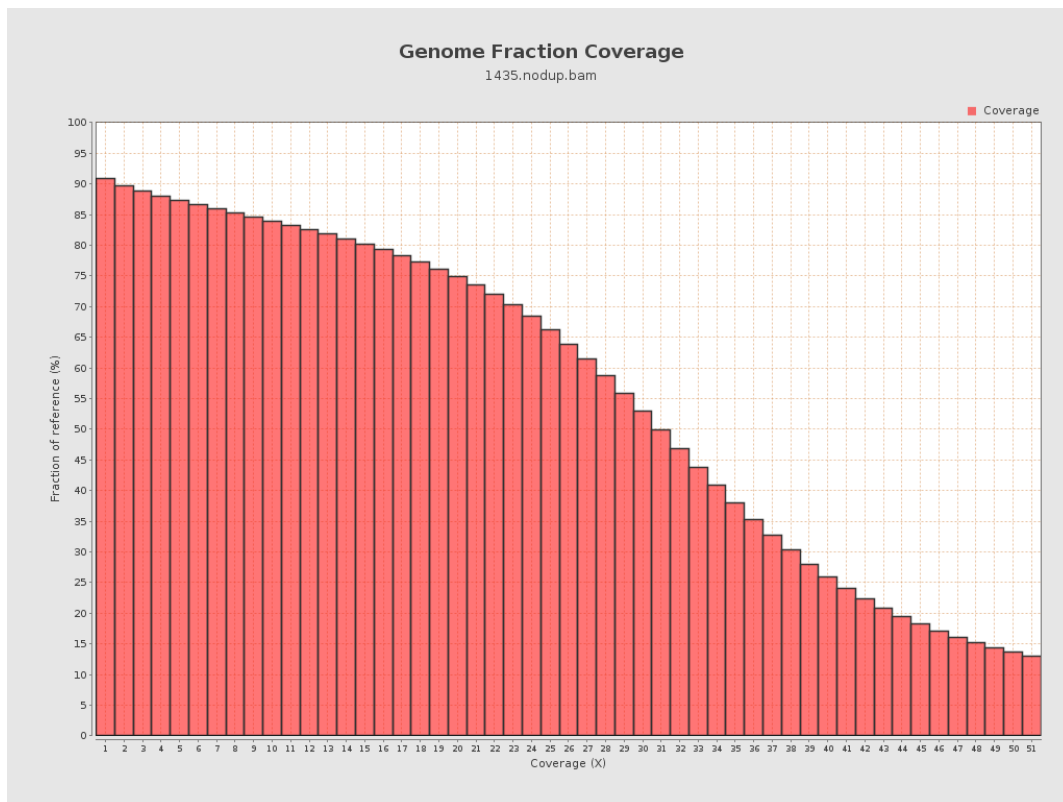
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
1435.nodup.bam
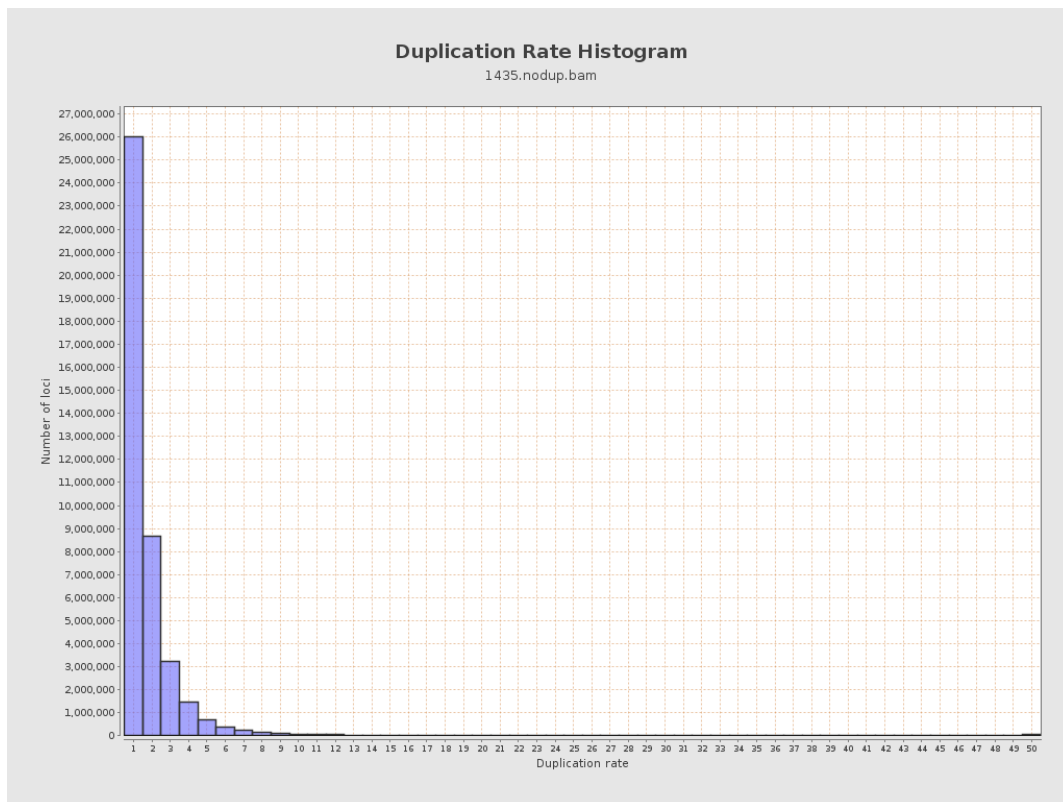
8. Results : Mapped Reads Nucleotide Content
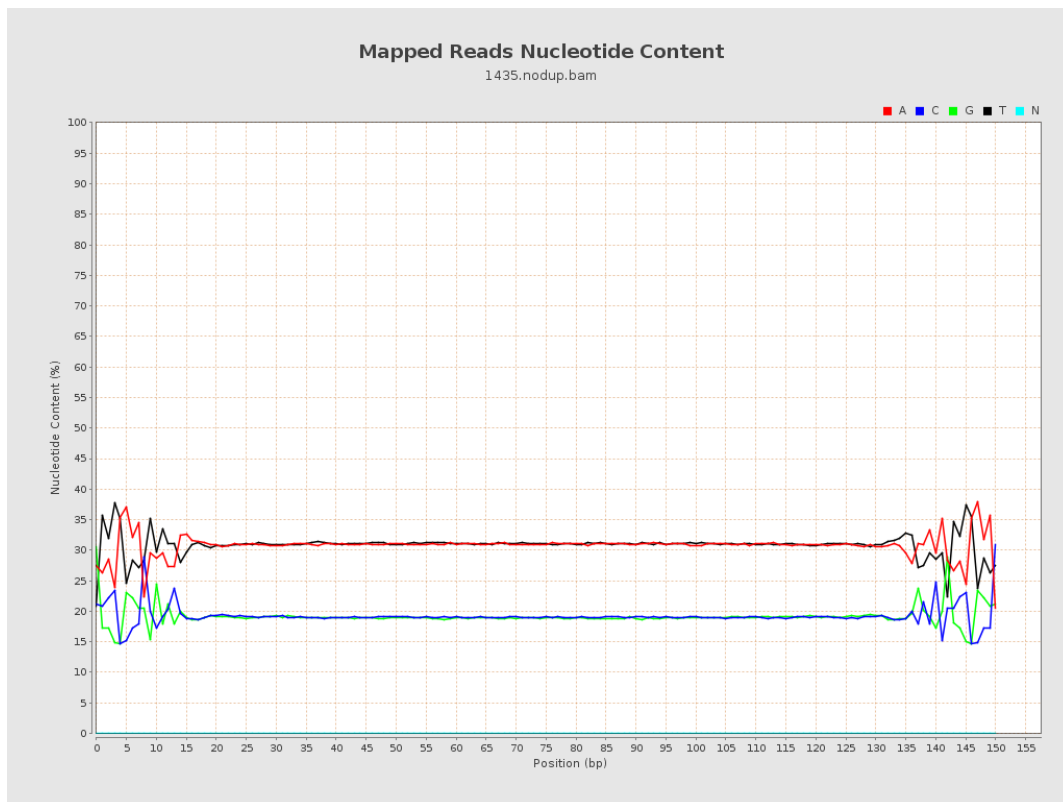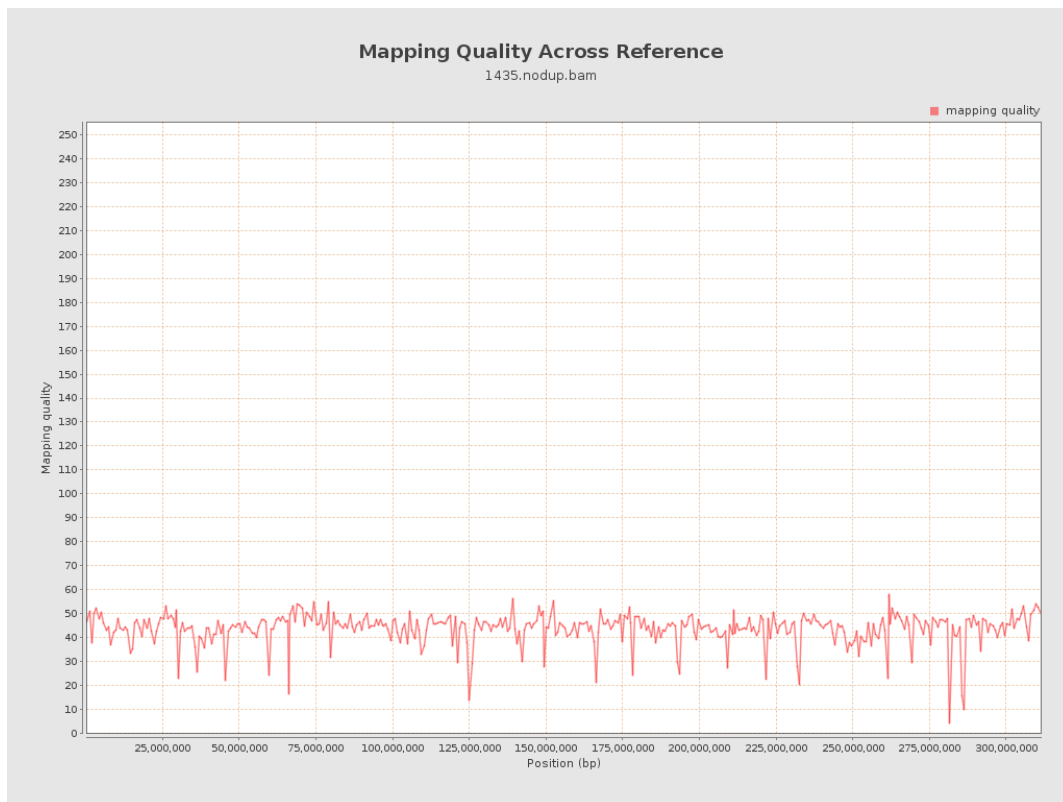
9. Results : Mapped Reads GC-content Distribution
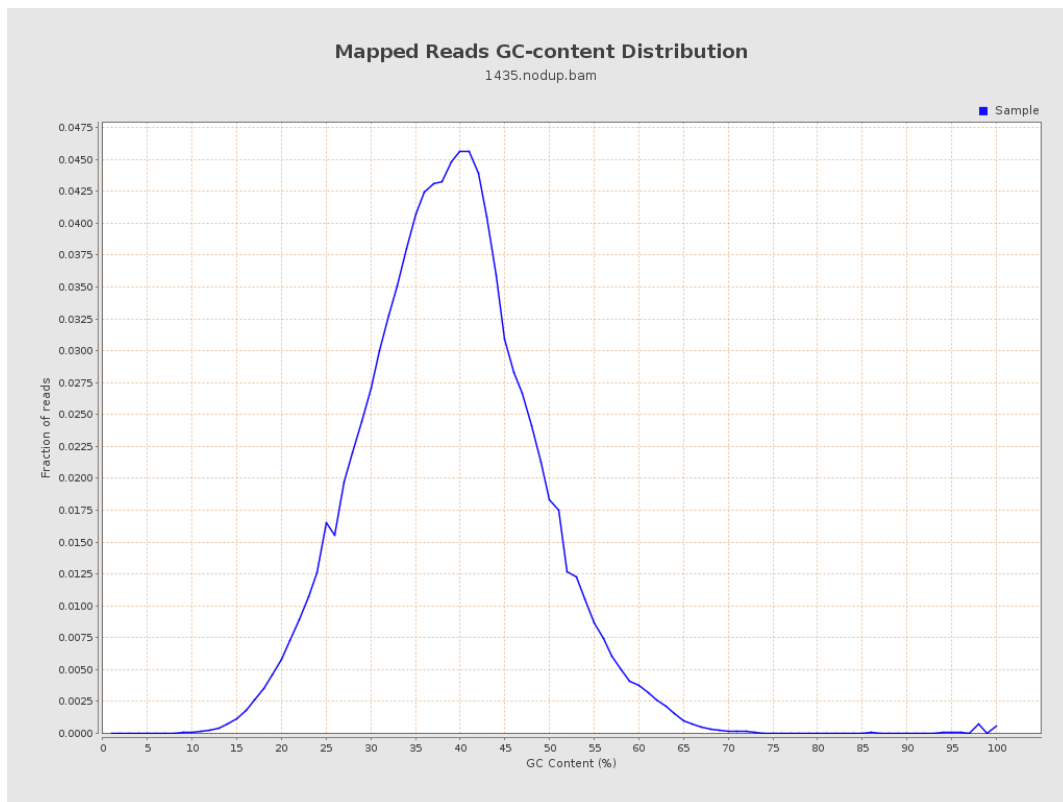
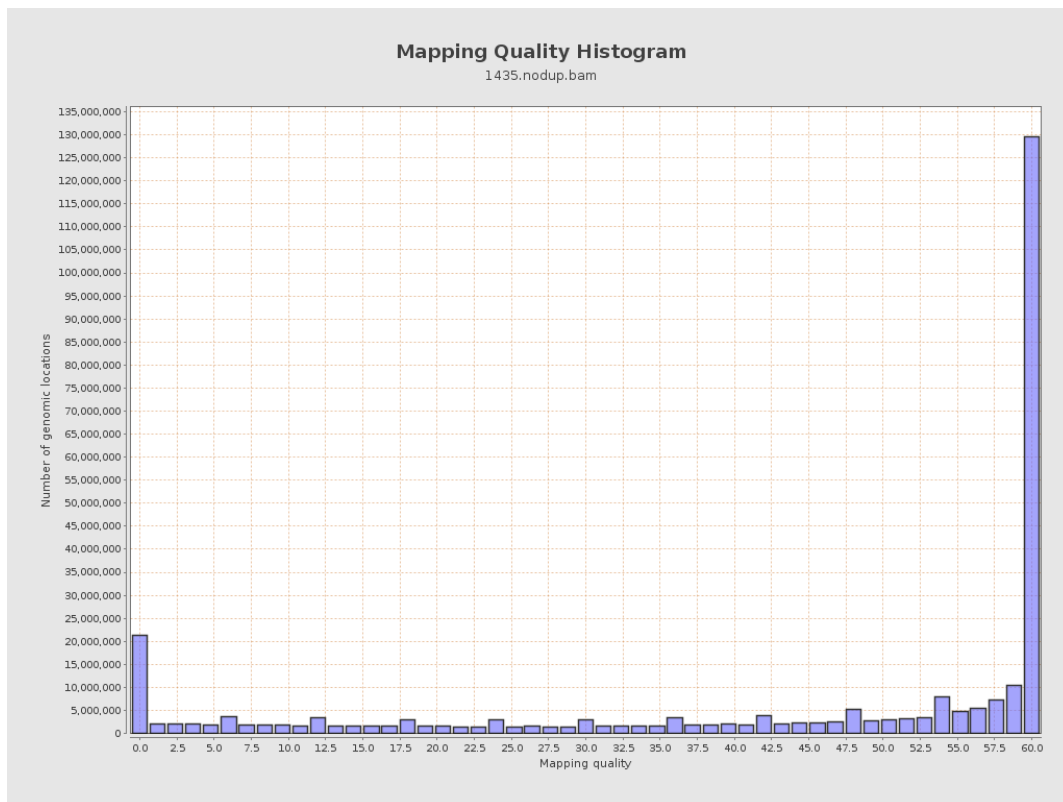# 10. Results : Mapped Reads Clipping Profile
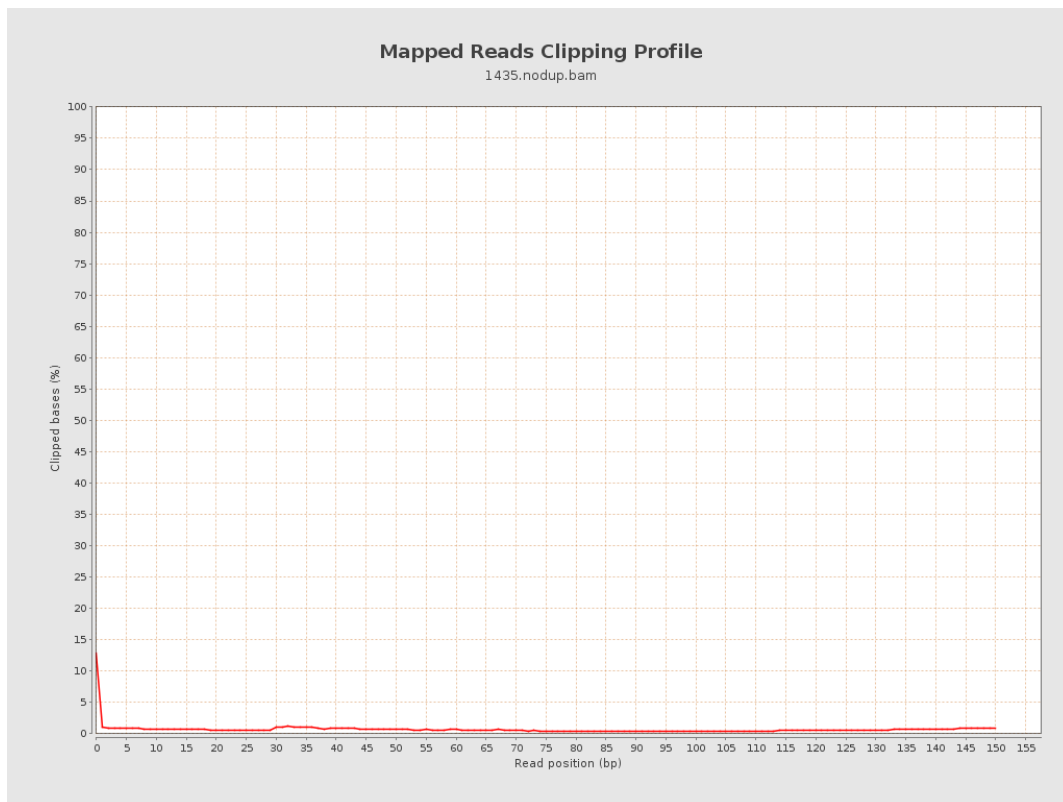
11. Results : Homopolymer Indels
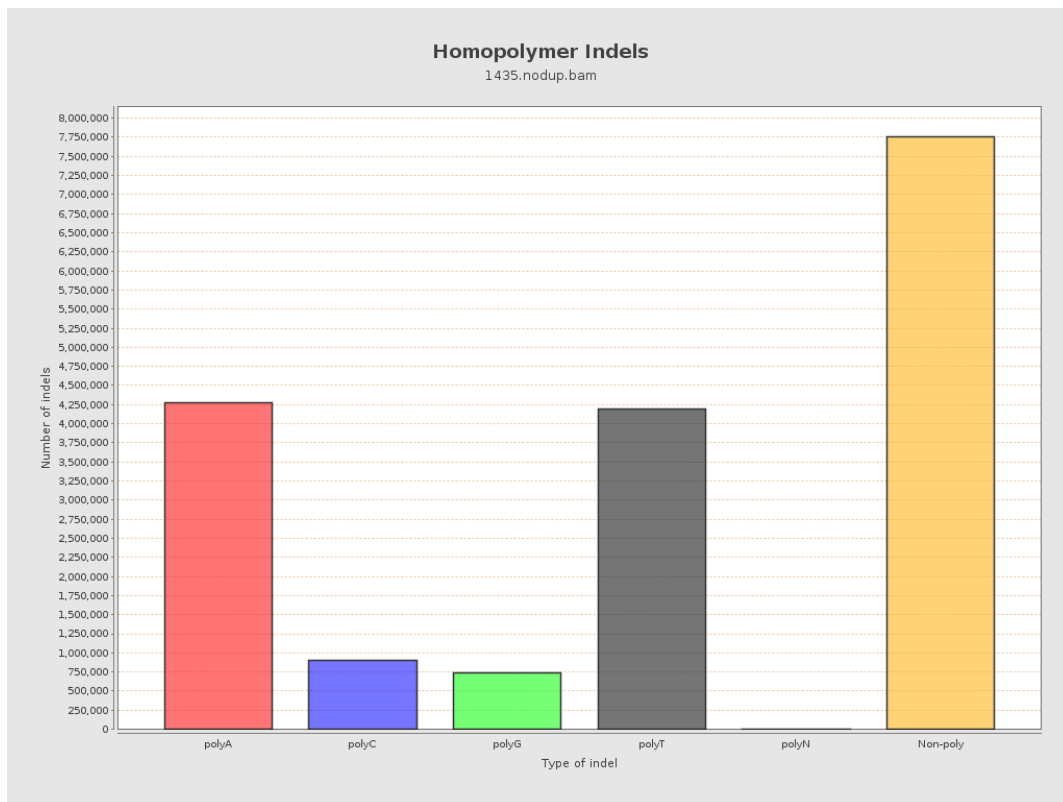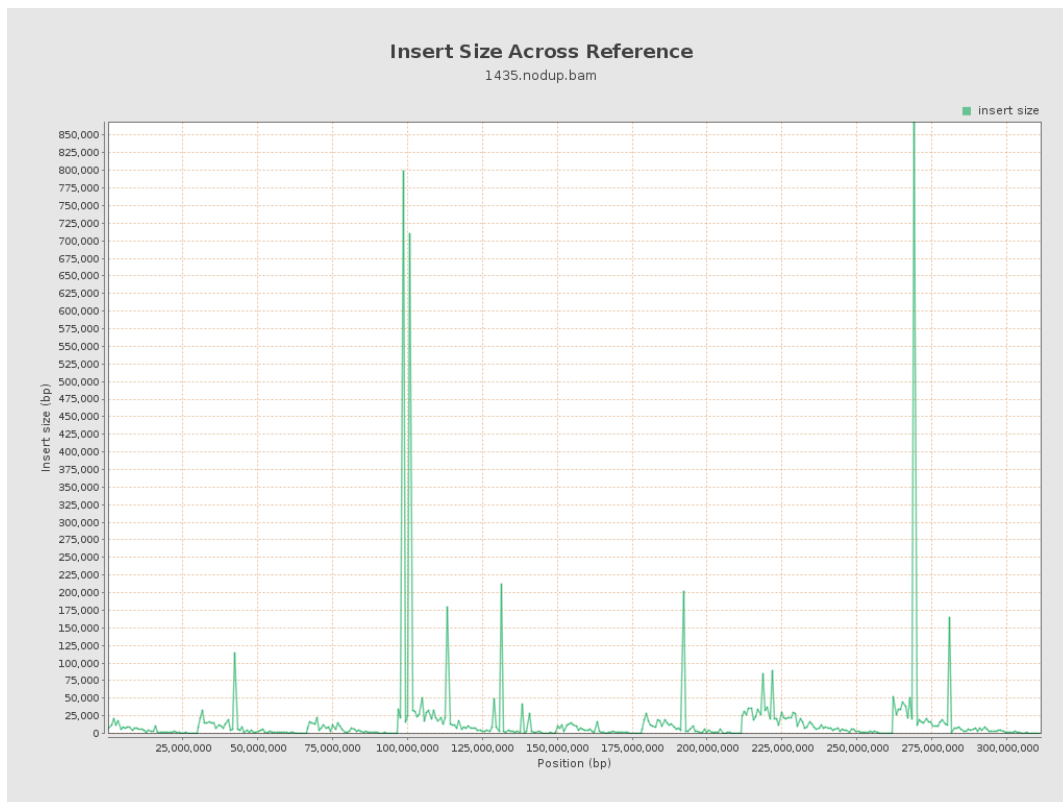
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

Insert Size Across Reference
1435.nodup.bam

15. Results : Insert Size Histogram