Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:24:51

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/936.nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/936.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_279/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_279_S360_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_279/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_279_S360_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:24:51 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	47,458,728
Mapped reads	45,044,365 / 94.91%
Unmapped reads	2,414,363 / 5.09%
Mapped paired reads	45,044,365 / 94.91%
Mapped reads, first in pair	22,555,982 / 47.53%
Mapped reads, second in pair	22,488,383 / 47.39%
Mapped reads, both in pair	44,231,553 / 93.2%
Mapped reads, singletons	812,812 / 1.71%
Read min/max/mean length	30 / 151 / 148.03
Duplicated reads (flagged)	5,572,257 / 11.74%
Clipped reads	10,100,135 / 21.28%

2.2. ACGT Content

Number/percentage of A's	1,928,207,499 / 30.85%
Number/percentage of C's	1,199,096,722 / 19.18%
Number/percentage of T's	1,927,385,645 / 30.84%
Number/percentage of G's	1,195,782,347 / 19.13%
Number/percentage of N's	22,440 / 0%
GC Percentage	38.32%

2.3. Coverage

Mean	20.1083
Standard Deviation	156.8364

2.4. Mapping Quality

Mean Mapping Quality	43.97

2.5. Insert size

Mean	228,399.68
Standard Deviation	2,258,726.52
P25/Median/P75	327 / 427 / 551

2.6. Mismatches and indels

General error rate	2.31%
Mismatches	132,615,151
Insertions	4,174,990
Mapped reads with at least one insertion	8.35%
Deletions	4,283,800
Mapped reads with at least one deletion	8.45%
Homopolymer indels	56.48%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	481565628	16.2011	44.2966

LT669789.1	36598175	770678079	21.0578	177.4823
LT669790.1	30422129	640785011	21.0631	152.3308
LT669791.1	52758100	1042999978	19.7695	129.4383
LT669792.1	28376109	556204764	19.6012	169.9508
LT669793.1	33388210	621026660	18.6002	89.5987
LT669794.1	50579949	986900651	19.5117	147.6413
LT669795.1	49795044	1166416691	23.4244	231.7026

3. Results : Coverage across reference

Coverage across reference
936.nodup.bam

4. Results : Coverage Histogram

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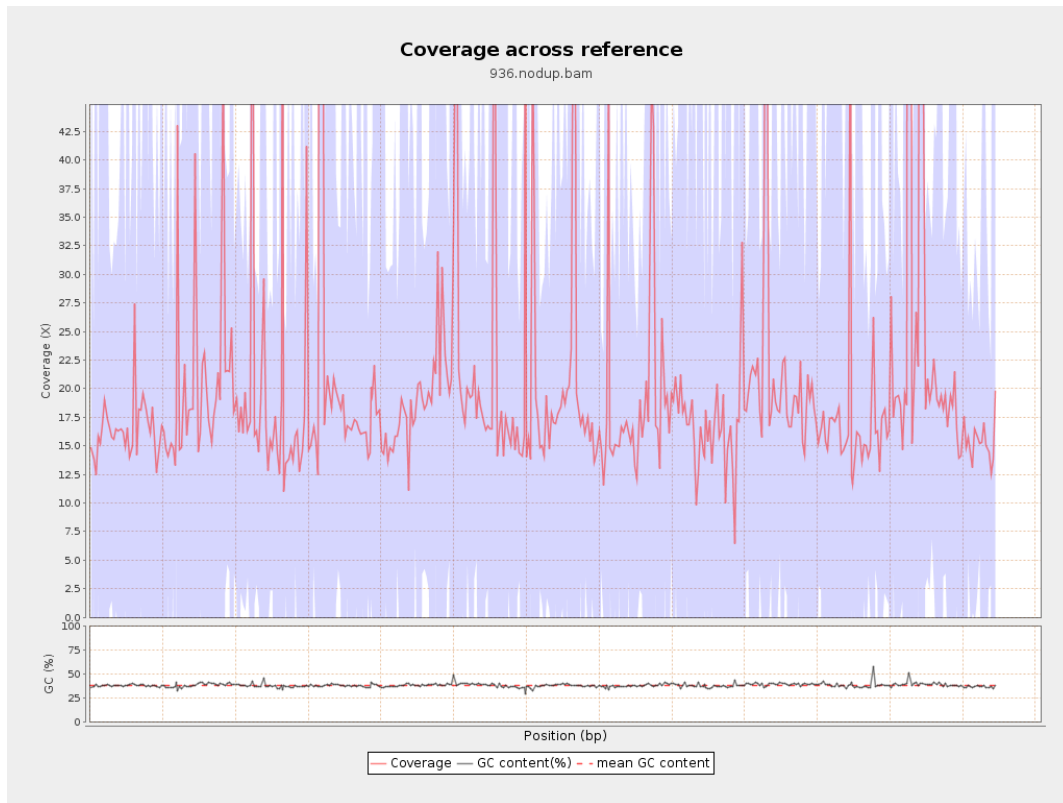
5. Results : Coverage Histogram (0-50X)
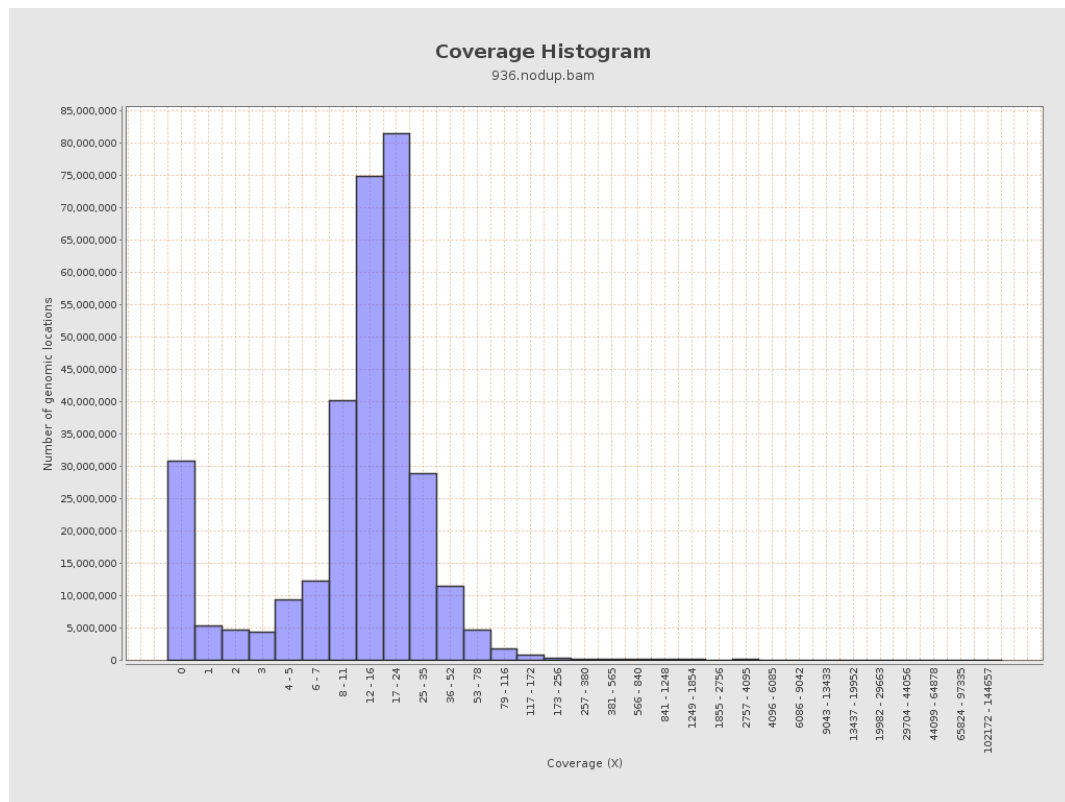
Coverage Histogram (0-50X)
936.nodup.bam
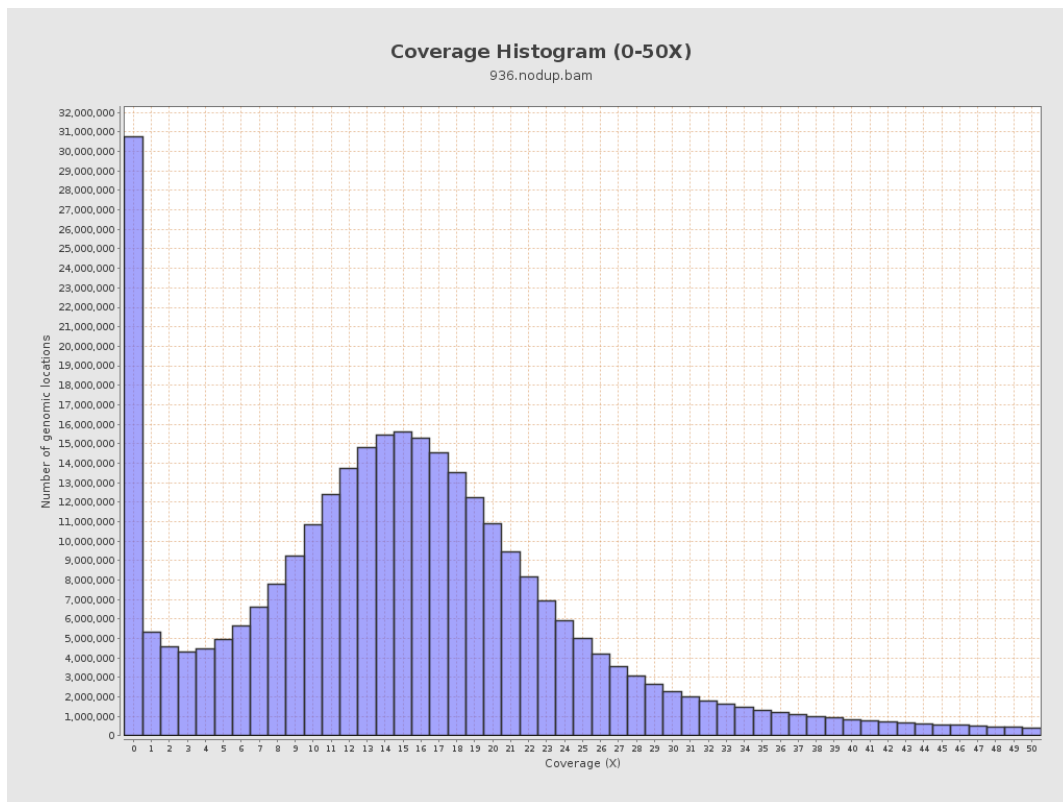
6. Results : Genome Fraction Coverage

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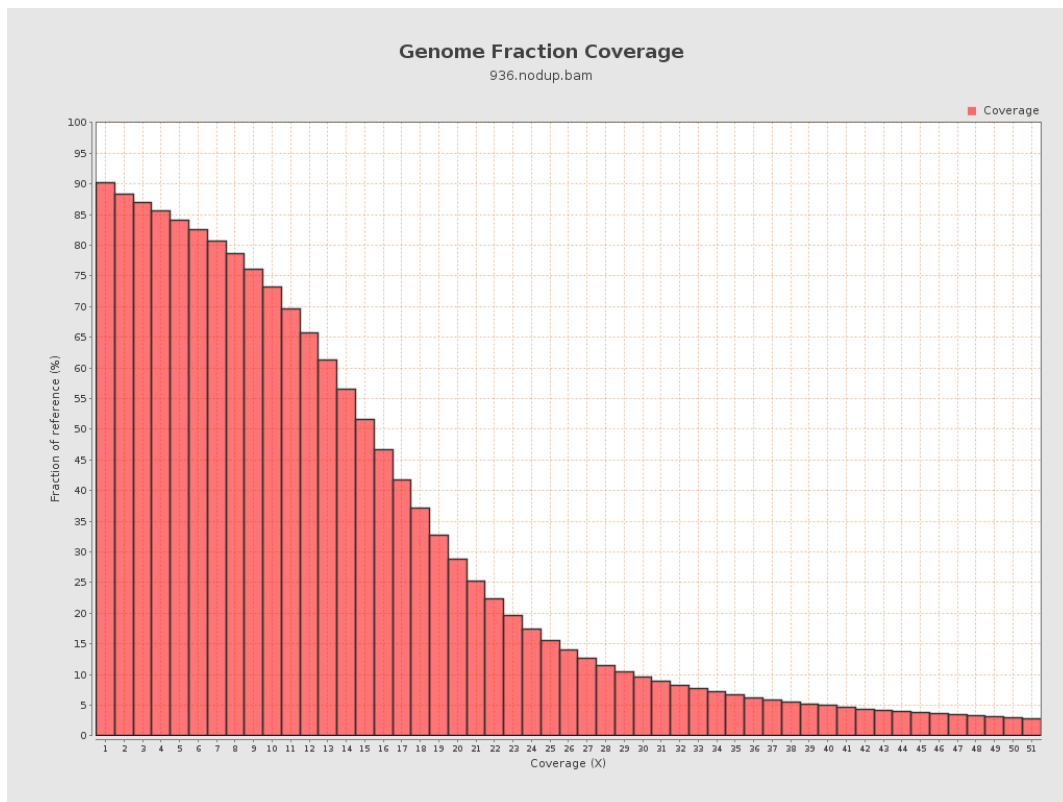
7. Results : Duplication Rate Histogram

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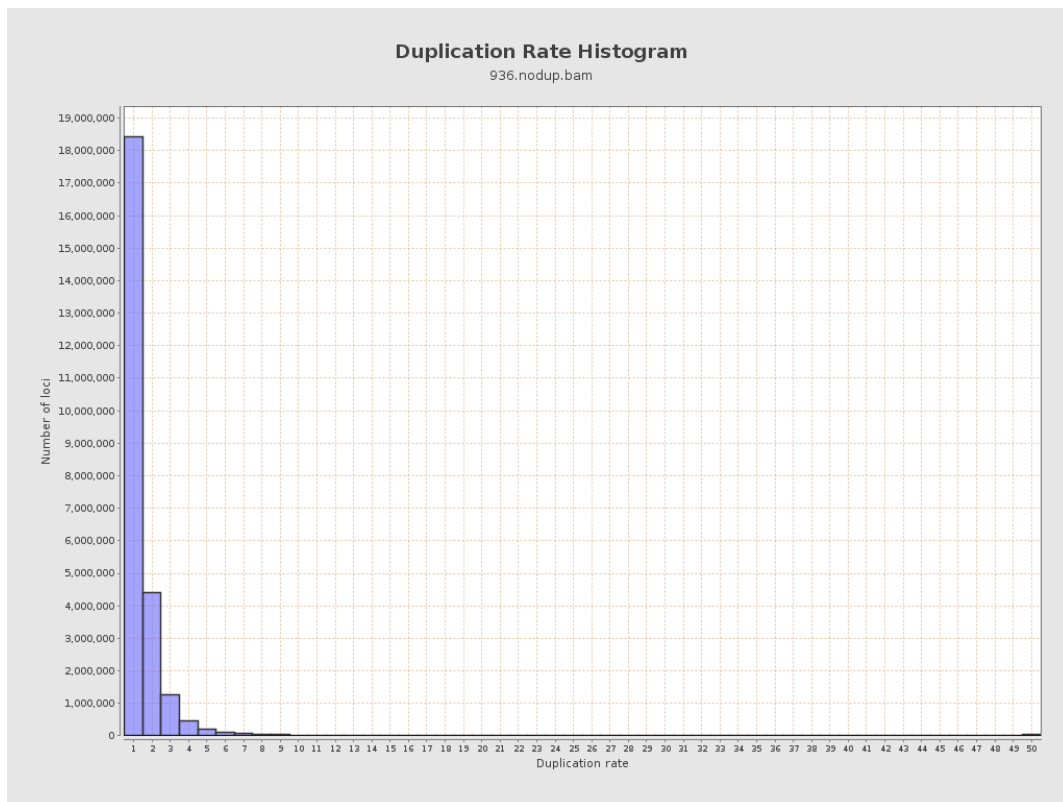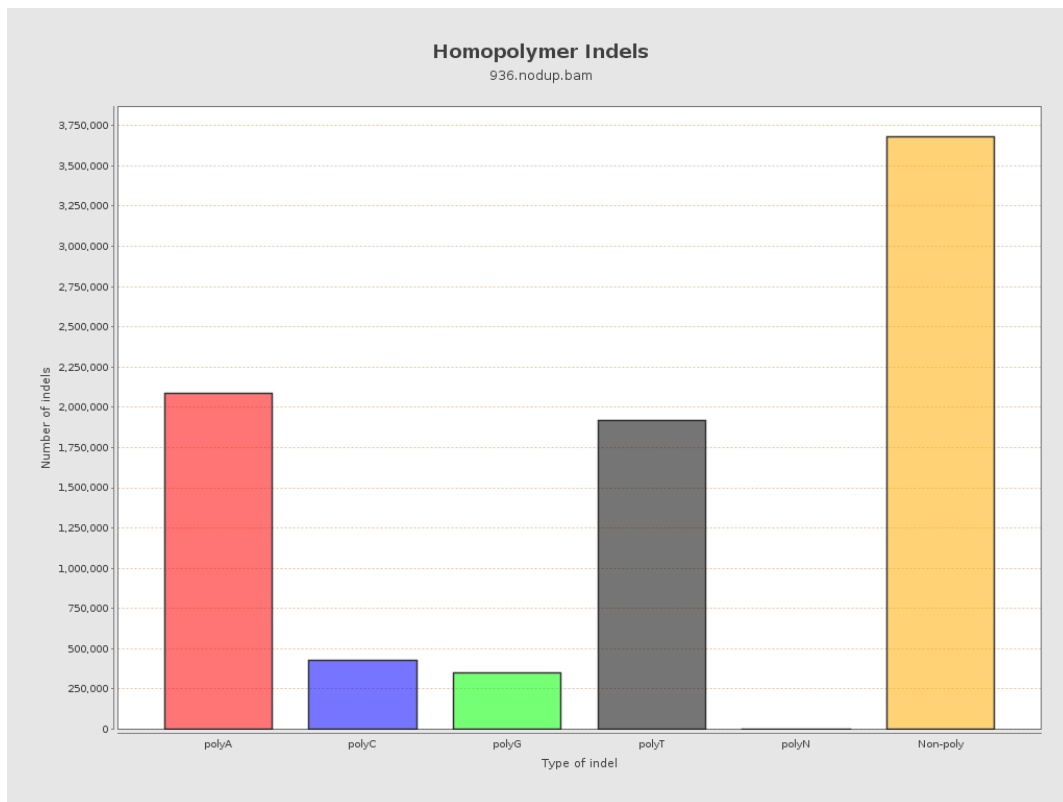
8. Results : Mapped Reads Nucleotide Content
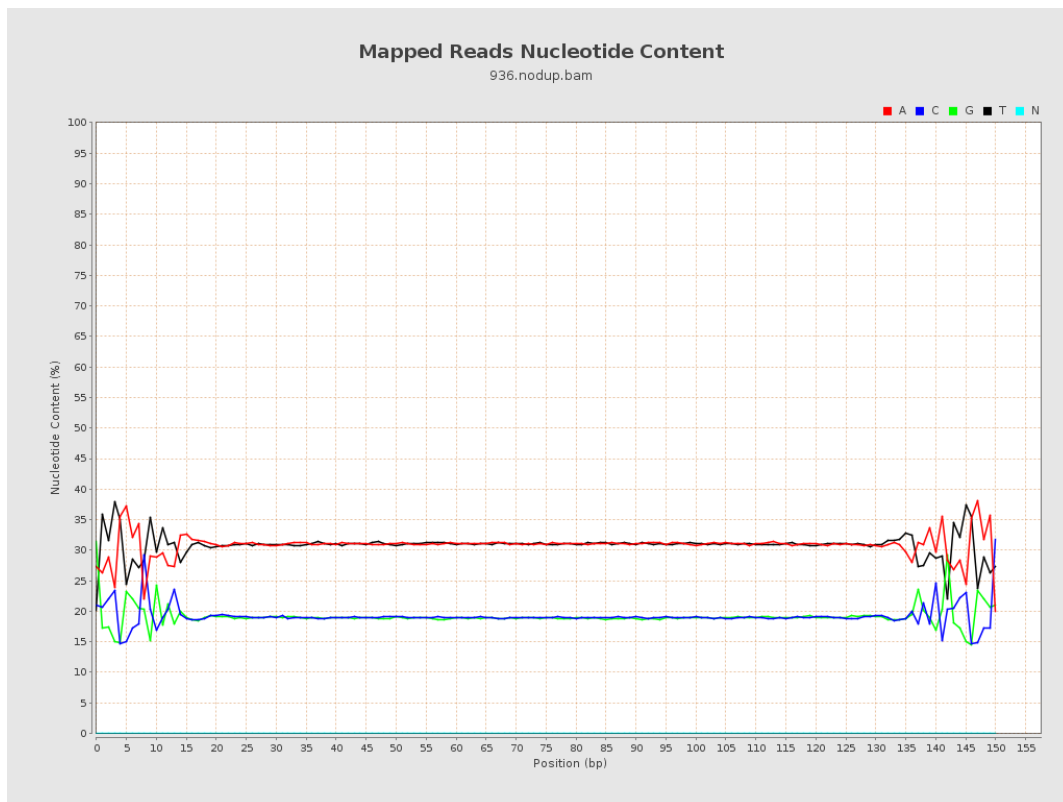
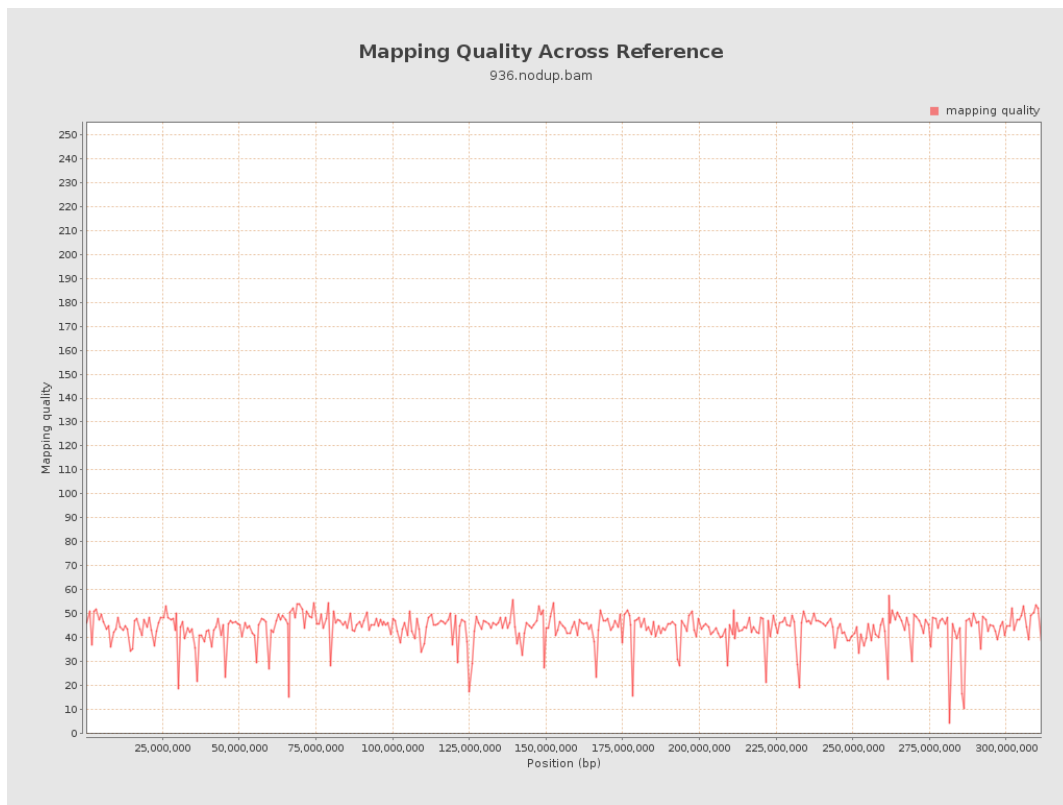# 9. Results : Mapped Reads GC-content Distribution
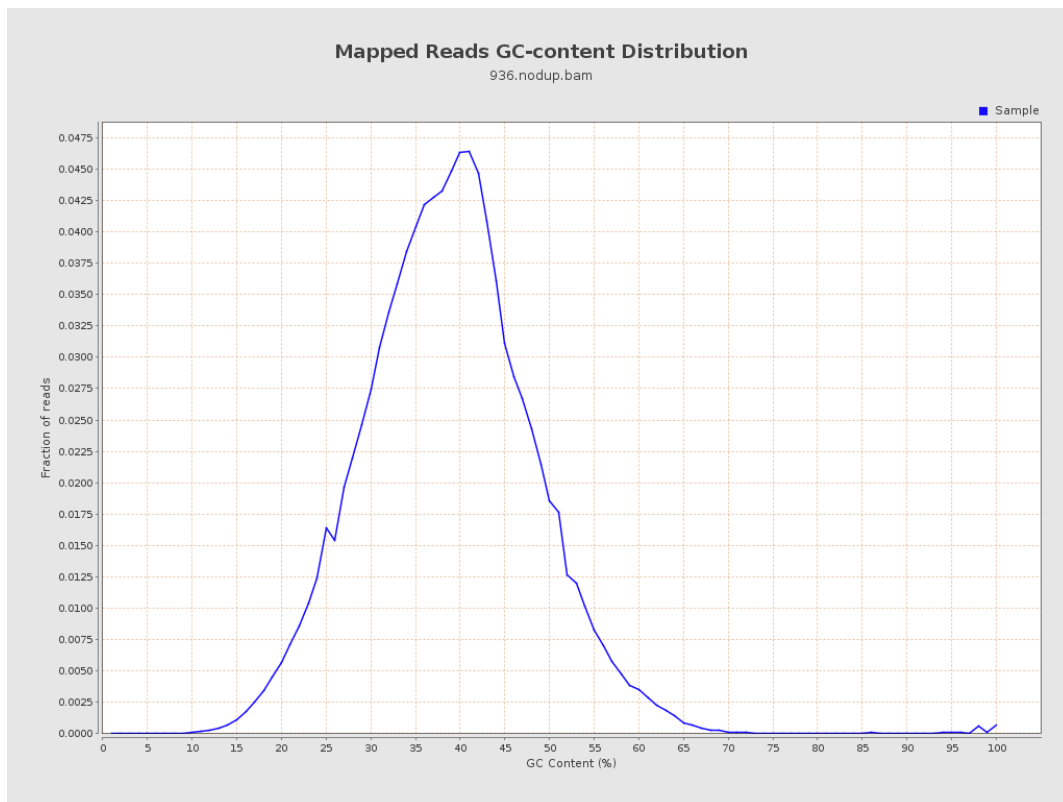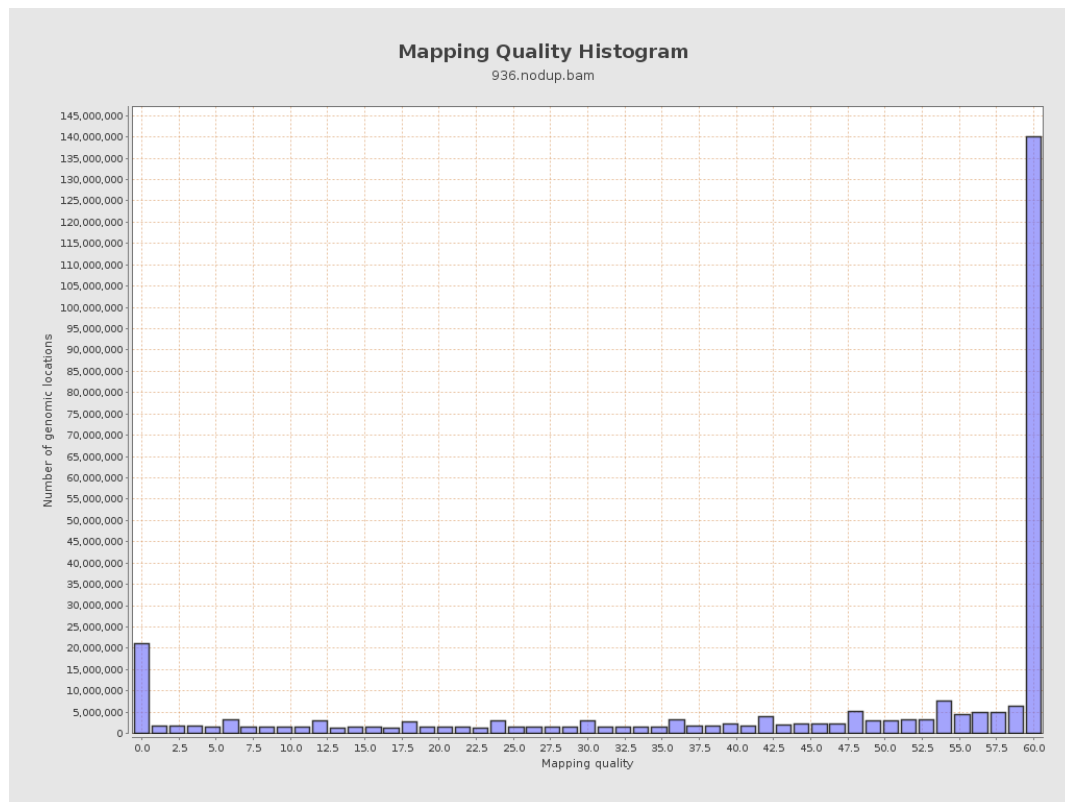
10. Results : Mapped Reads Clipping Profile
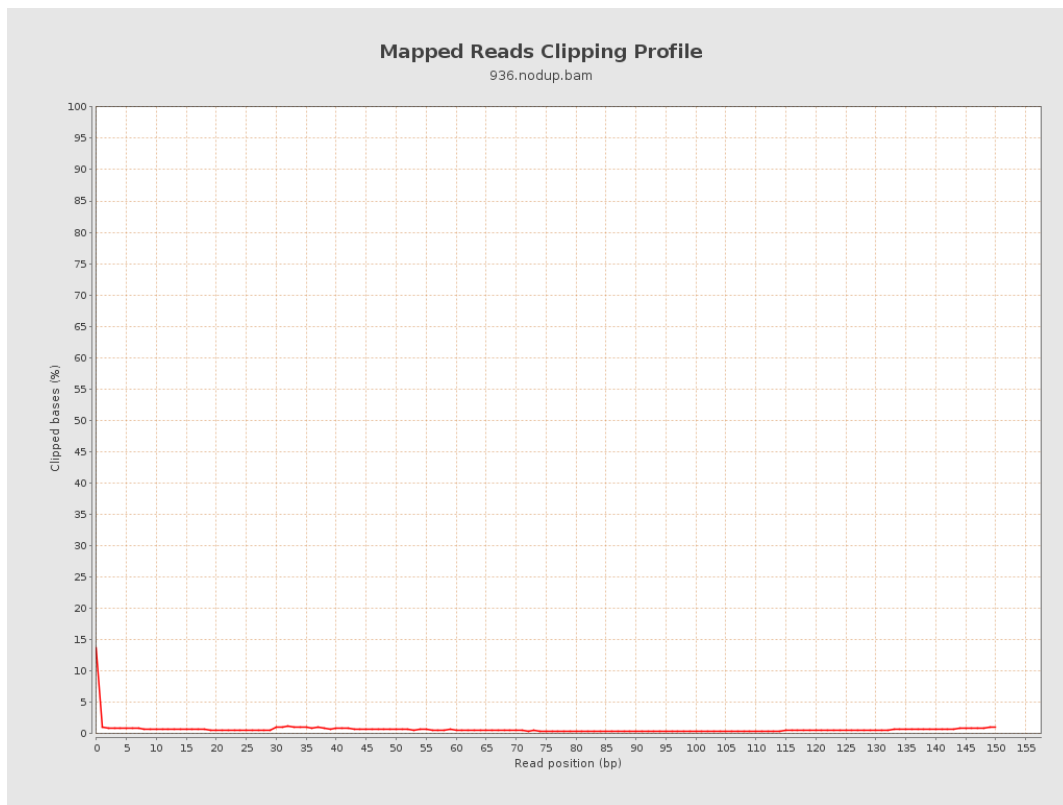
11. Results : Homopolymer Indels

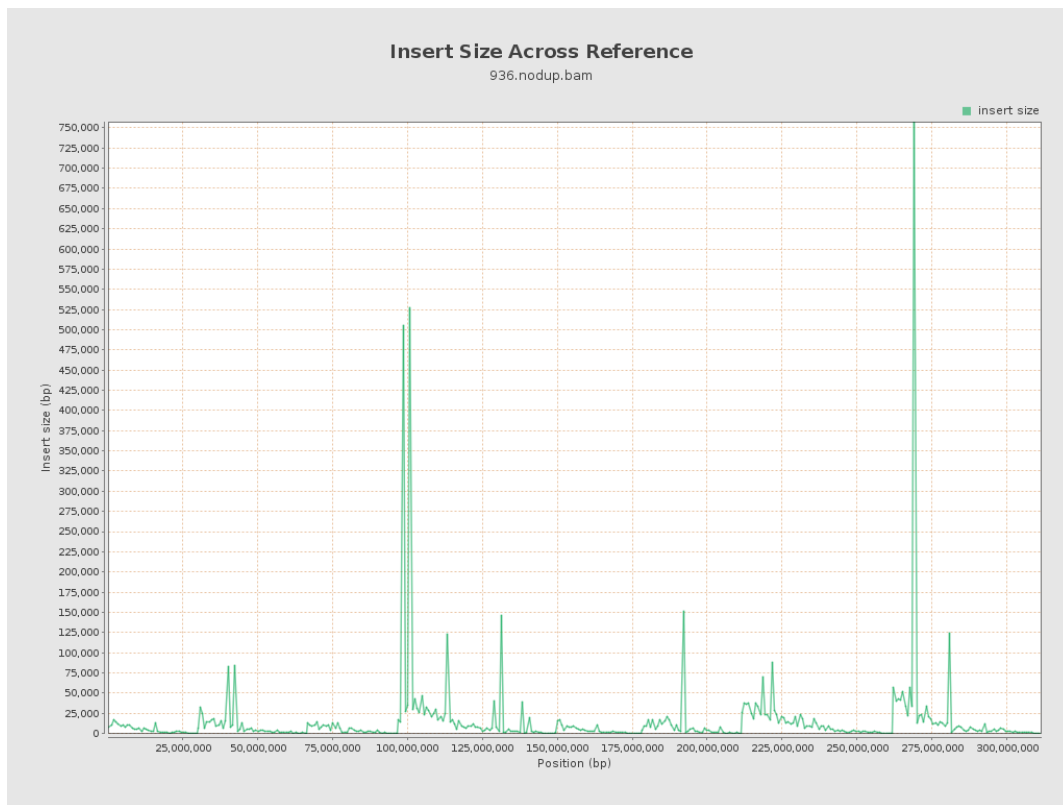# 12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
936.nodup.bam

14. Results : Insert Size Across Reference

Insert Size Across Reference
936.nodup.bam

15. Results : Insert Size Histogram

Insert Size Histogram
936.nodup.bam