Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:27:38

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/871 .nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/871 .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_280/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_280_S361_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_280/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_280_S361_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:27:37 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	59,531,453
Mapped reads	52,536,535 / 88.25%
Unmapped reads	6,994,918 / 11.75%
Mapped paired reads	52,536,535 / 88.25%
Mapped reads, first in pair	26,292,688 / 44.17%
Mapped reads, second in pair	26,243,847 / 44.08%
Mapped reads, both in pair	50,307,832 / 84.51%
Mapped reads, singletons	2,228,703 / 3.74%
Read min/max/mean length	30 / 151 / 147.92
Duplicated reads (flagged)	10,392,516 / 17.46%
Clipped reads	14,153,802 / 23.78%

2.2. ACGT Content

Number/percentage of A's	2,185,951,893 / 30.9%
Number/percentage of C's	1,348,277,686 / 19.06%
Number/percentage of T's	2,188,652,763 / 30.94%
Number/percentage of G's	1,350,738,903 / 19.1%
Number/percentage of N's	23,970 / 0%
GC Percentage	38.16%

2.3. Coverage

Mean	22.761
Standard Deviation	293.6711

2.4. Mapping Quality

Mean Mapping Quality	43.45

2.5. Insert size

Mean	296,506.3
Standard Deviation	2,644,577.23
P25/Median/P75	307 / 403 / 524

2.6. Mismatches and indels

General error rate	2.61%
Mismatches	168,410,817
Insertions	5,850,571
Mapped reads with at least one insertion	9.84%
Deletions	5,282,584
Mapped reads with at least one deletion	8.88%
Homopolymer indels	57.39%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	532488169	17.9142	133.242

LT669789.1	36598175	823524201	22.5018	298.0745
LT669790.1	30422129	962341480	31.6329	477.9495
LT669791.1	52758100	1196017530	22.6698	351.6737
LT669792.1	28376109	656182248	23.1245	281.2429
LT669793.1	33388210	685644414	20.5355	195.3756
LT669794.1	50579949	1053098745	20.8205	226.0759
LT669795.1	49795044	1183983159	23.7771	265.7066

3. Results : Coverage across reference

Coverage across reference
871.nodup.bam

4. Results : Coverage Histogram

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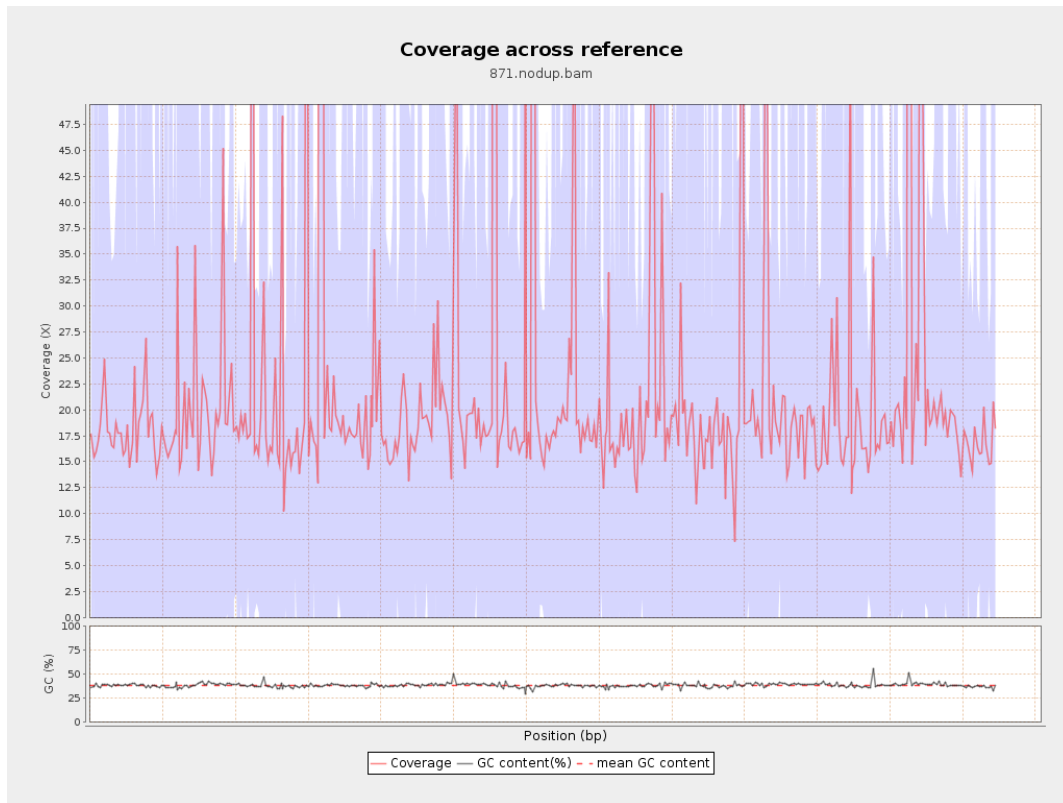
5. Results : Coverage Histogram (0-50X)
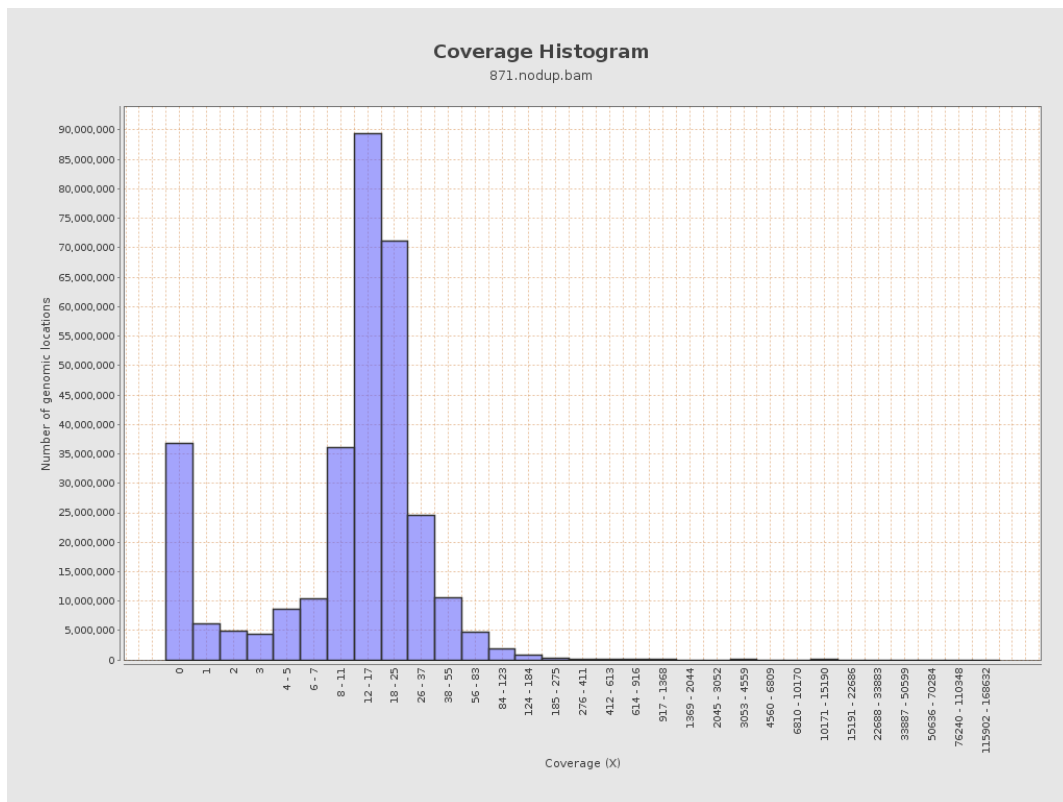
Coverage Histogram (0-50X)
871.nodup.bam
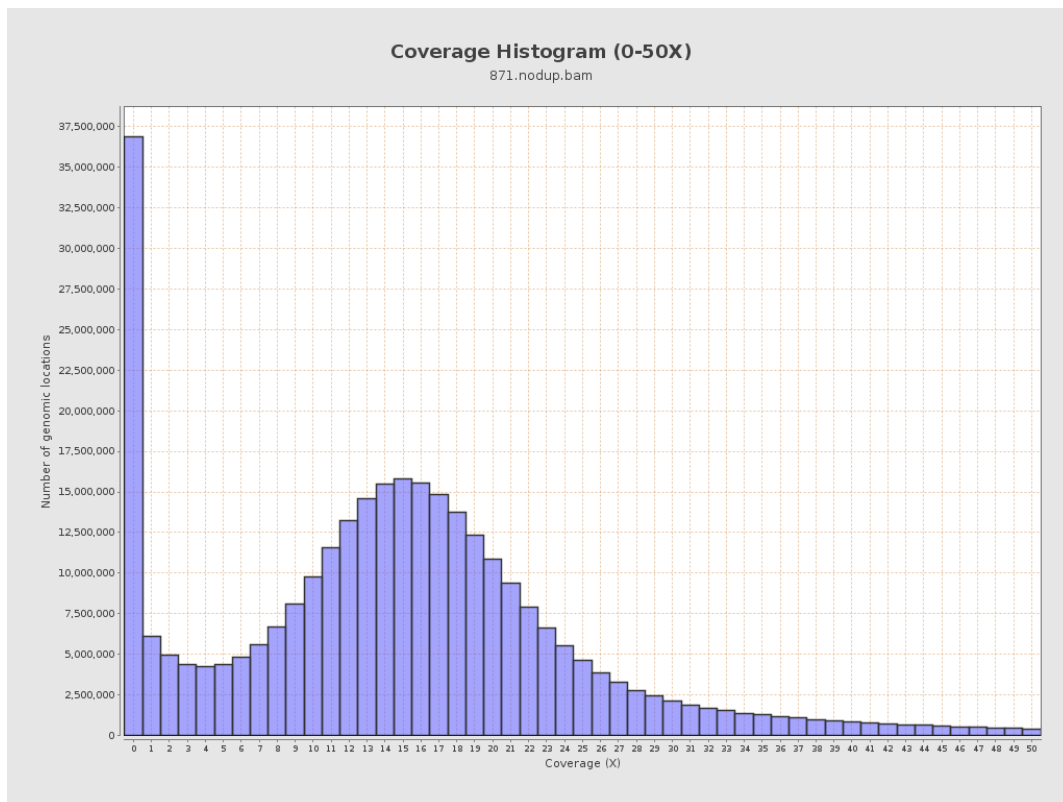
6. Results : Genome Fraction Coverage

BioinformaticsandGenomics
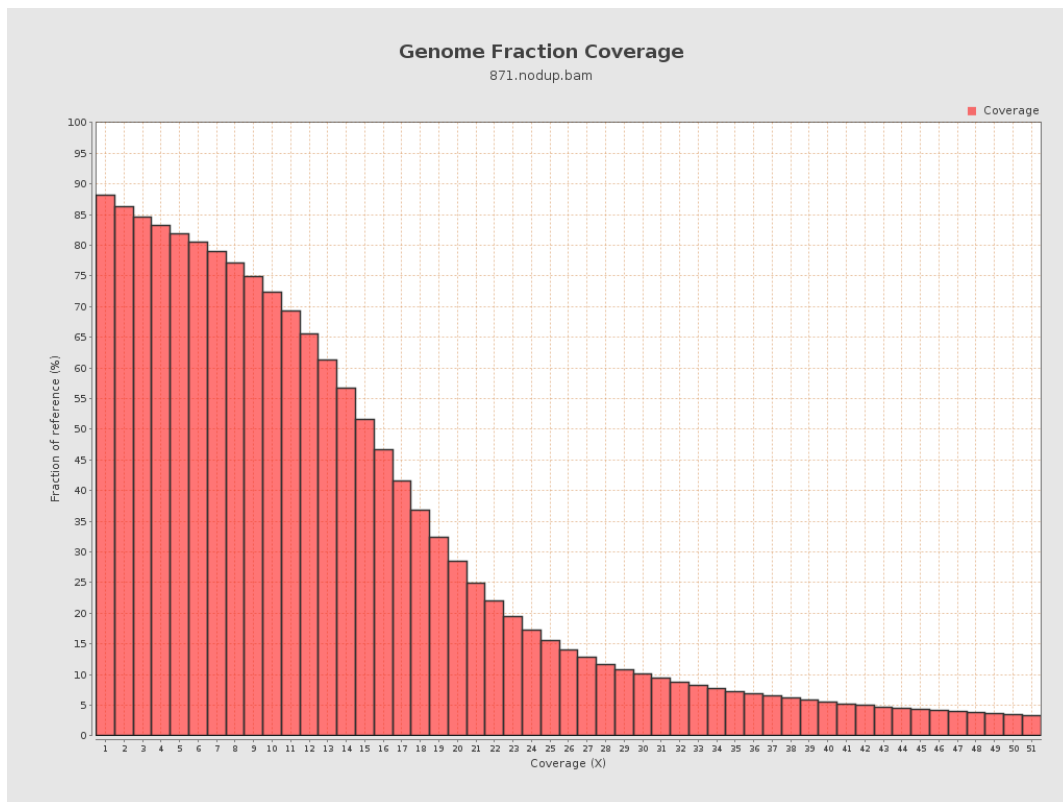
7. Results : Duplication Rate Histogram

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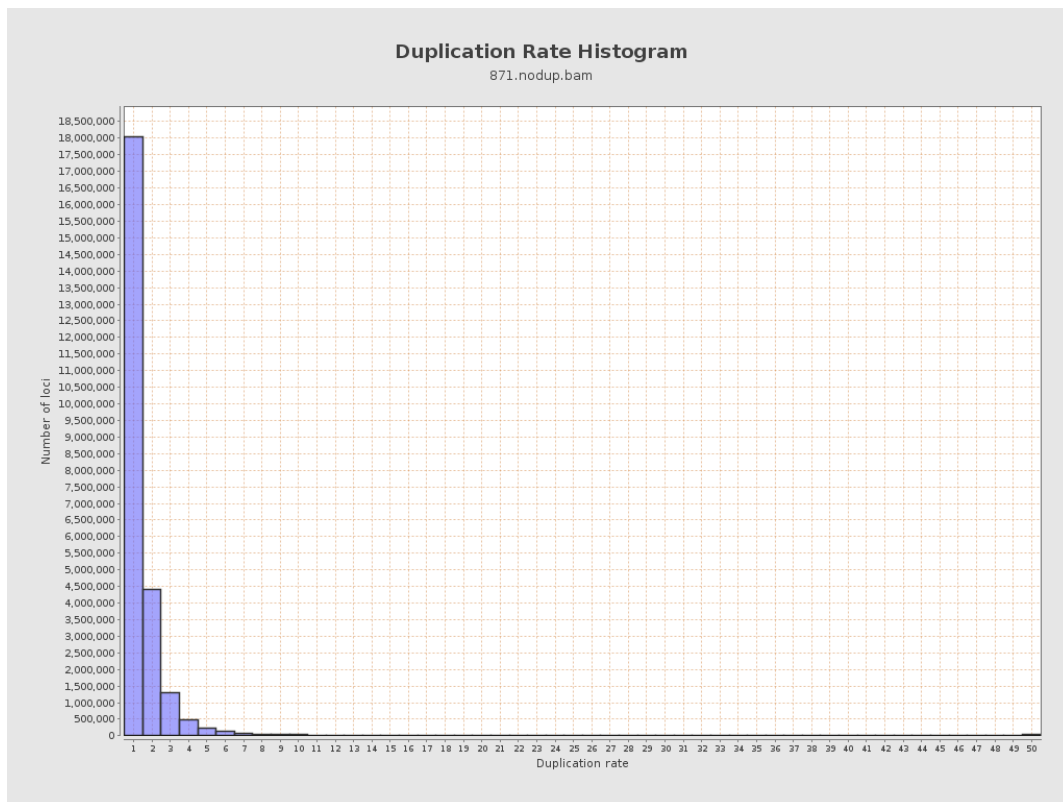
8. Results : Mapped Reads Nucleotide Content
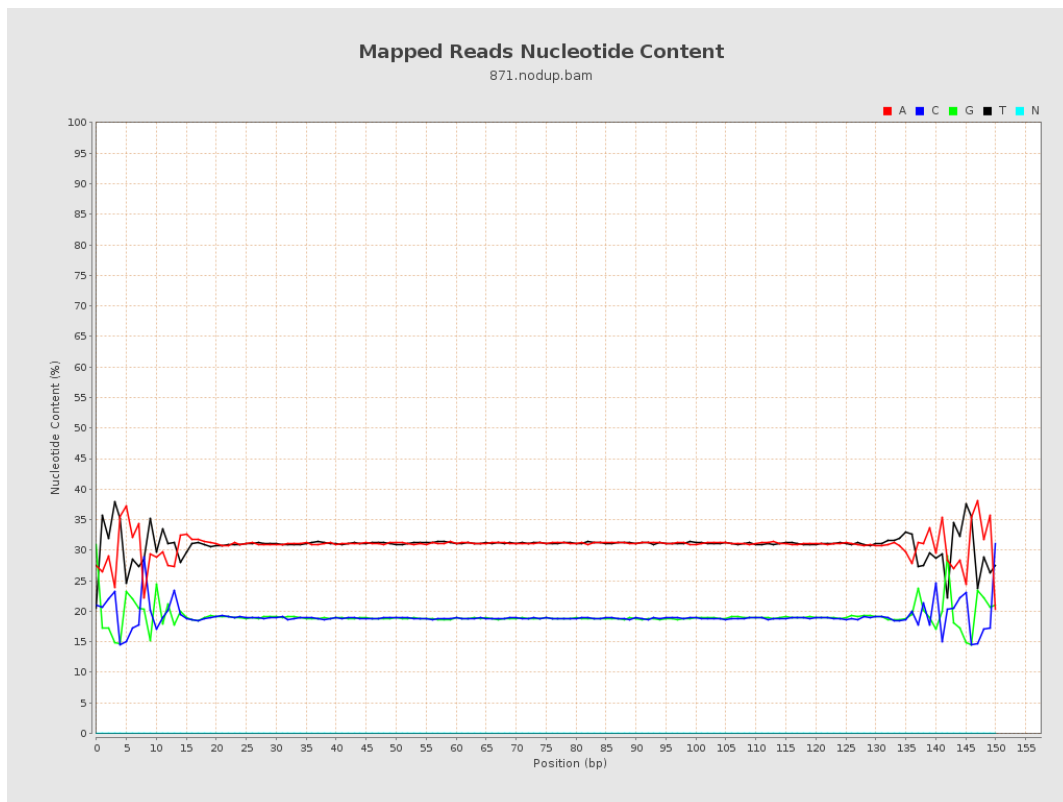
9. Results : Mapped Reads GC-content Distribution
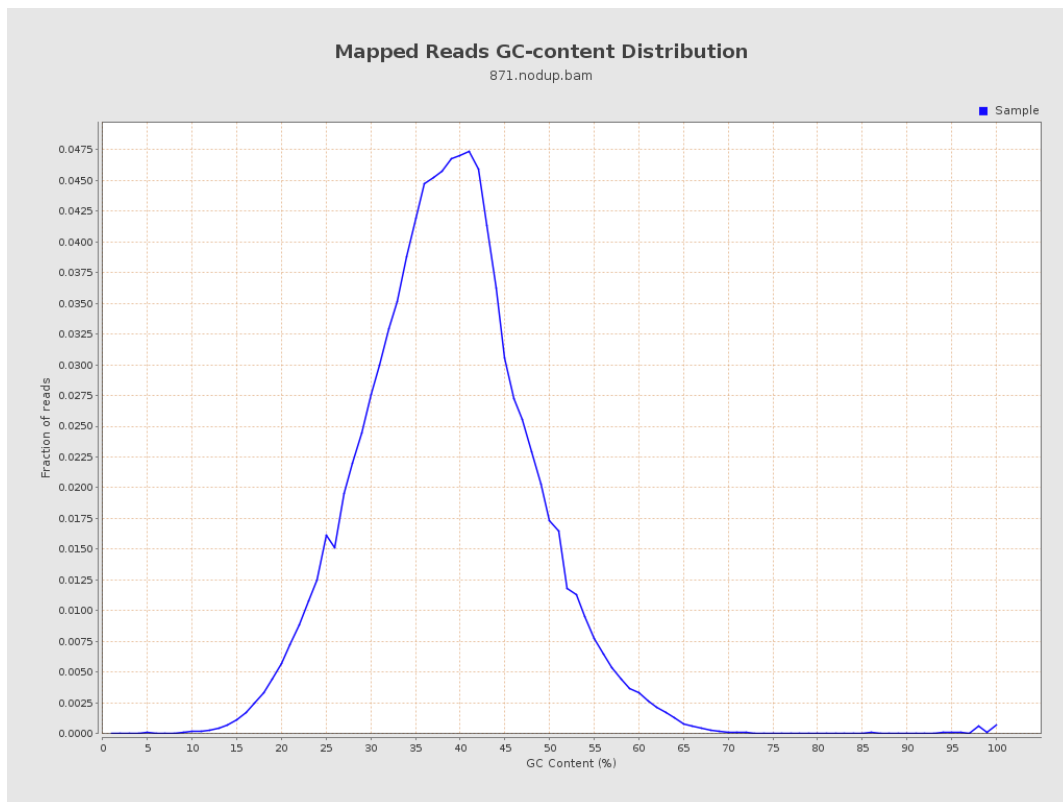
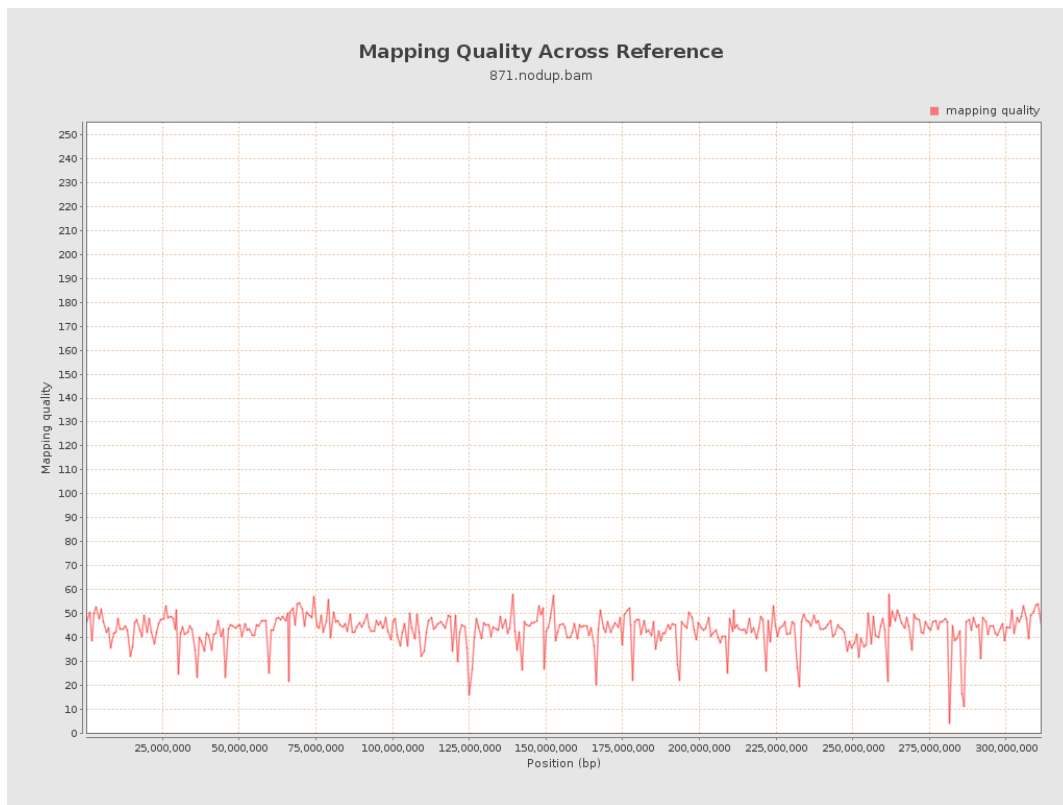# 10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
871.nodup.bam
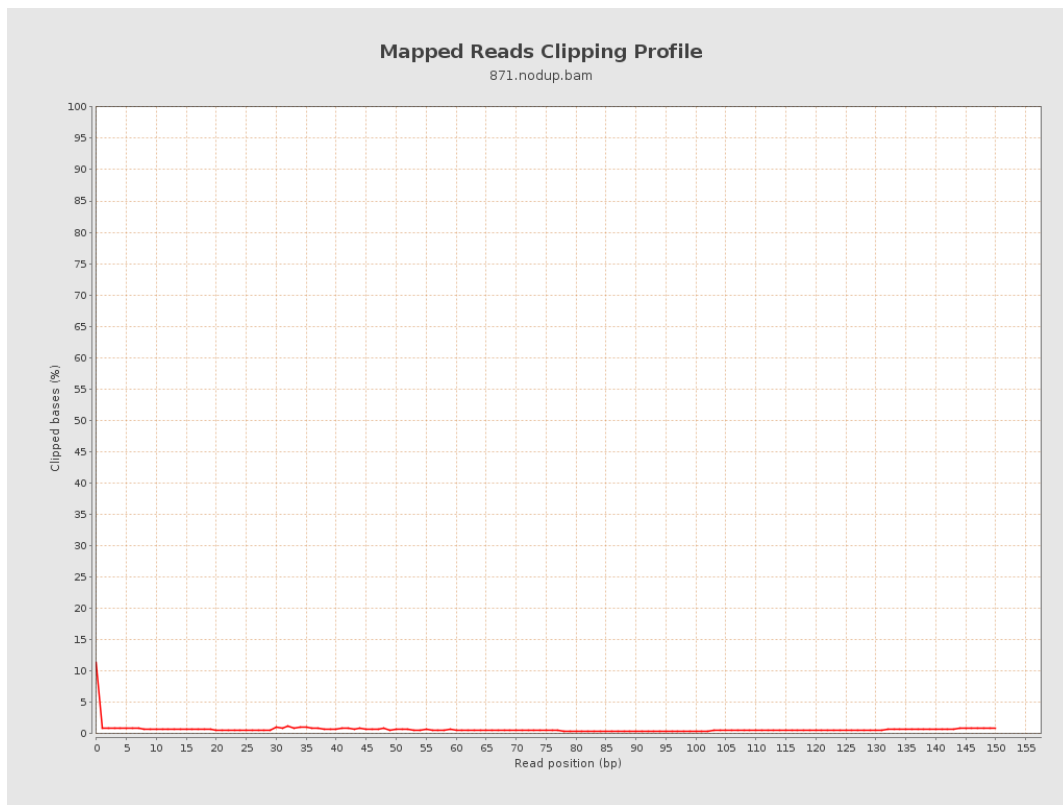
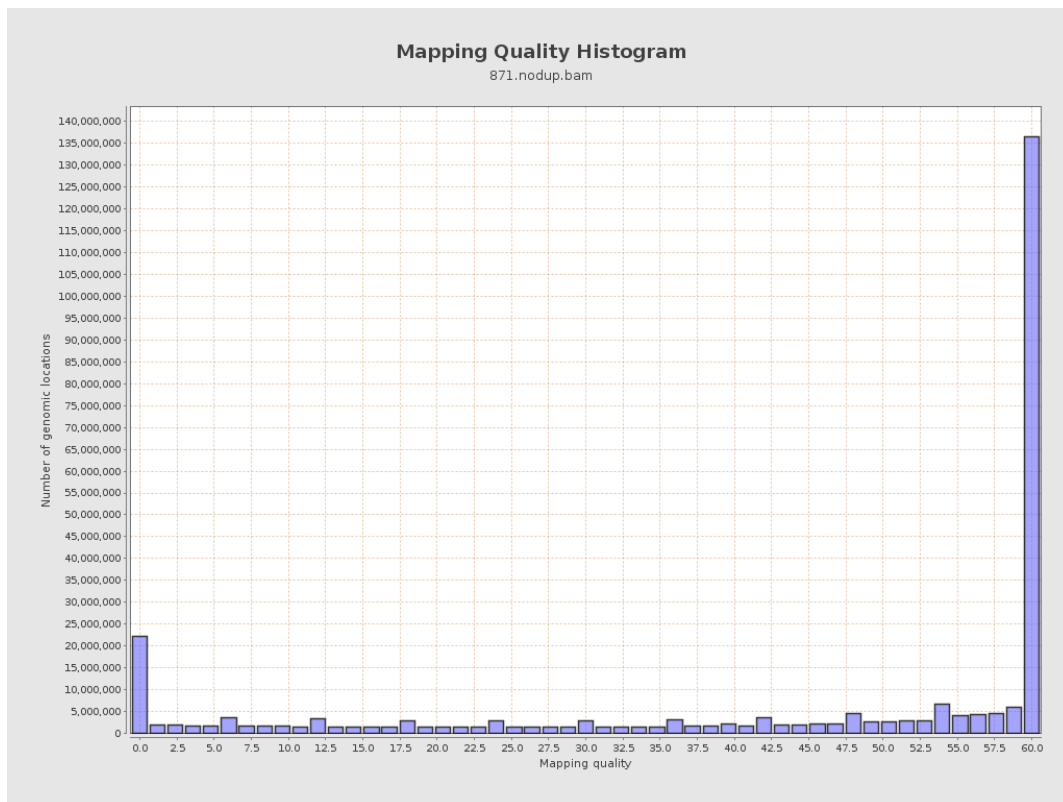# 11. Results : Homopolymer Indels

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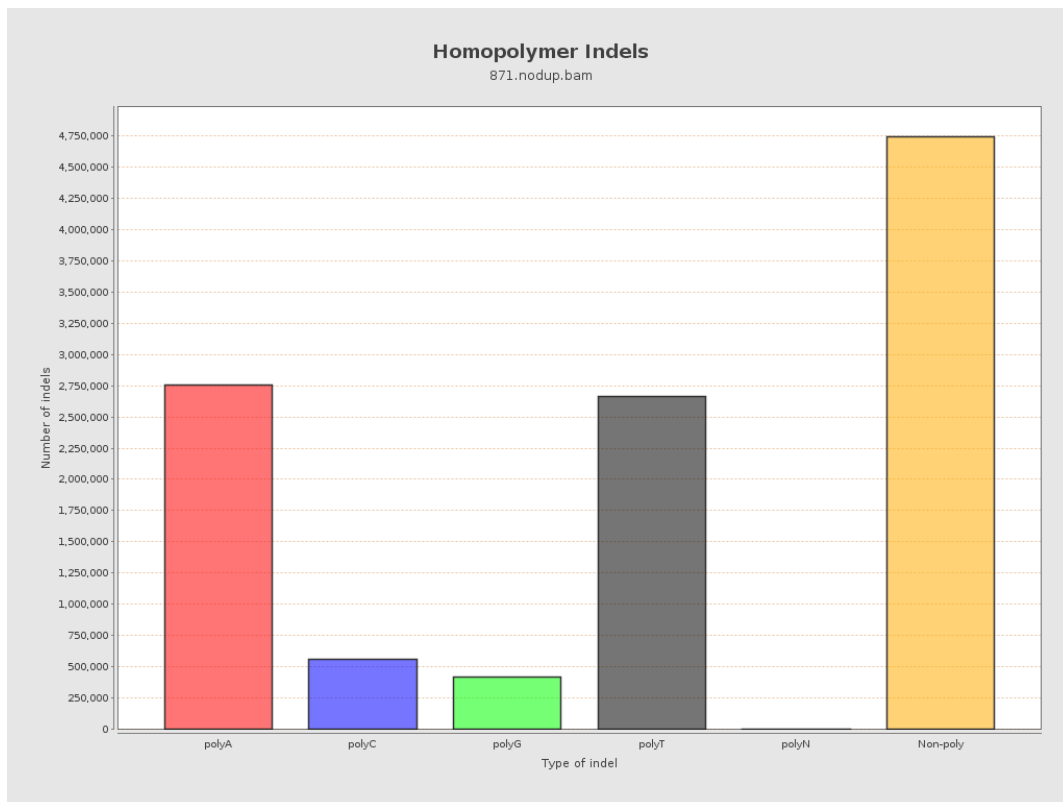
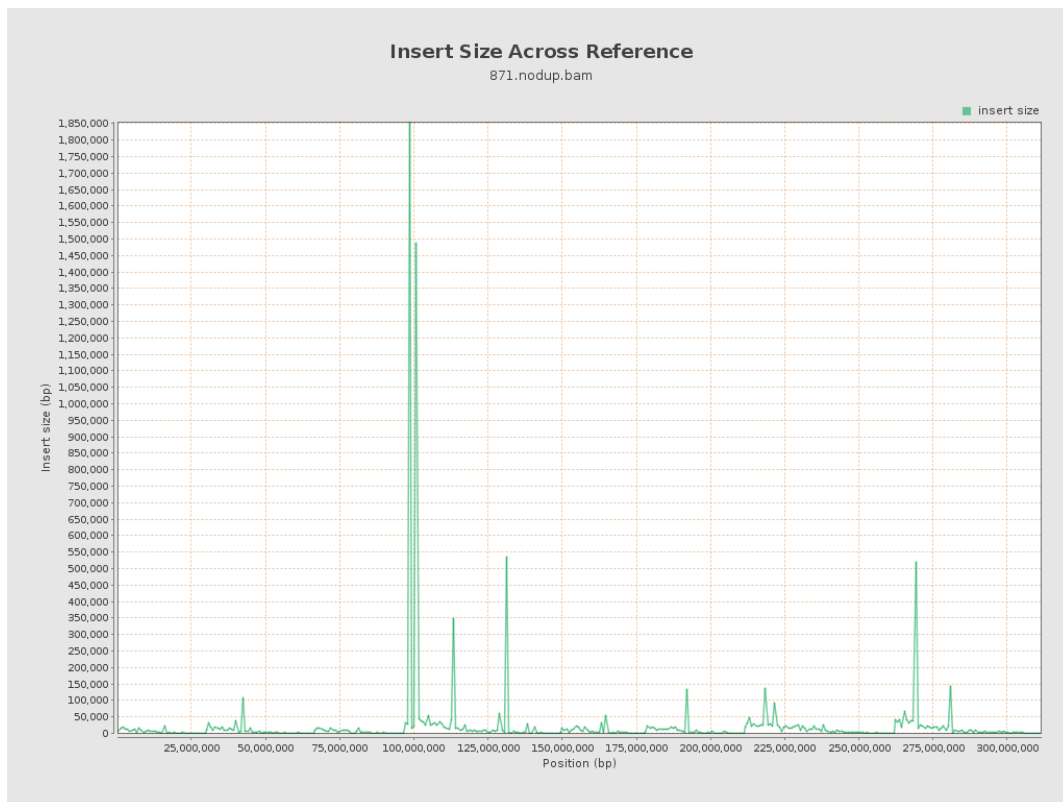# 12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram