Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:30:46

1. Input data & parameters

1.1. QualiMap command line

> qualimap bamqc -bam
> /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1437
> .nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1437 .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_562/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_562_S129_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_562/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_562_S129_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:30:45 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	60,480,316
Mapped reads	57,548,201 / 95.15%
Unmapped reads	2,932,115 / 4.85%
Mapped paired reads	57,548,201 / 95.15%
Mapped reads, first in pair	28,846,816 / 47.7%
Mapped reads, second in pair	28,701,385 / 47.46%
Mapped reads, both in pair	56,588,023 / 93.56%
Mapped reads, singletons	960,178 / 1.59%
Read min/max/mean length	30 / 151 / 148.09
Duplicated reads (flagged)	7,822,395 / 12.93%
Clipped reads	13,302,839 / 22%

2.2. ACGT Content

Number/percentage of A's	2,467,842,252 / 30.95%
Number/percentage of C's	1,519,811,218 / 19.06%
Number/percentage of T's	2,468,934,635 / 30.97%
Number/percentage of G's	1,516,454,349 / 19.02%
Number/percentage of N's	59,902 / 0%
GC Percentage	38.08%

2.3. Coverage

Mean	25.6498
Standard Deviation	201.8073

2.4. Mapping Quality

Mean Mapping Quality	44.23

2.5. Insert size

Mean	206,801.62
Standard Deviation	2,136,541.76
P25/Median/P75	306 / 403 / 522

2.6. Mismatches and indels

General error rate	2.44%
Mismatches	180,269,609
Insertions	5,245,617
Mapped reads with at least one insertion	8.22%
Deletions	5,428,362
Mapped reads with at least one deletion	8.41%
Homopolymer indels	56.22%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	619904581	20.8551	44.3469

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LT669789.1	36598175	977636551	26.7127	216.5278
LT669790.1	30422129	807939028	26.5576	178.7853
LT669791.1	52758100	1326467386	25.1424	155.5692
LT669792.1	28376109	724101821	25.518	228.6529
LT669793.1	33388210	805202576	24.1164	142.7832
LT669794.1	50579949	1247290298	24.6598	177.3352
LT669795.1	49795044	1485008116	29.8224	314.0693

3. Results : Coverage across reference

Coverage across reference
1437.nodup.bam

4. Results : Coverage Histogram
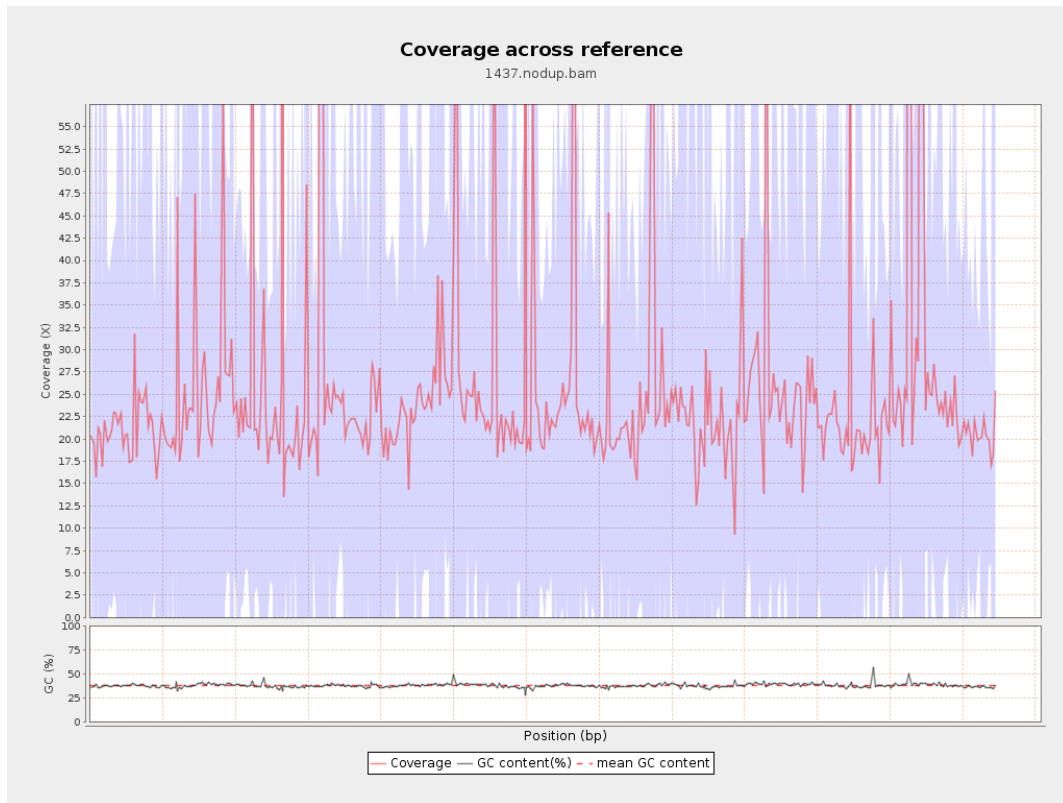
Coverage Histogram
1437.nodup.bam
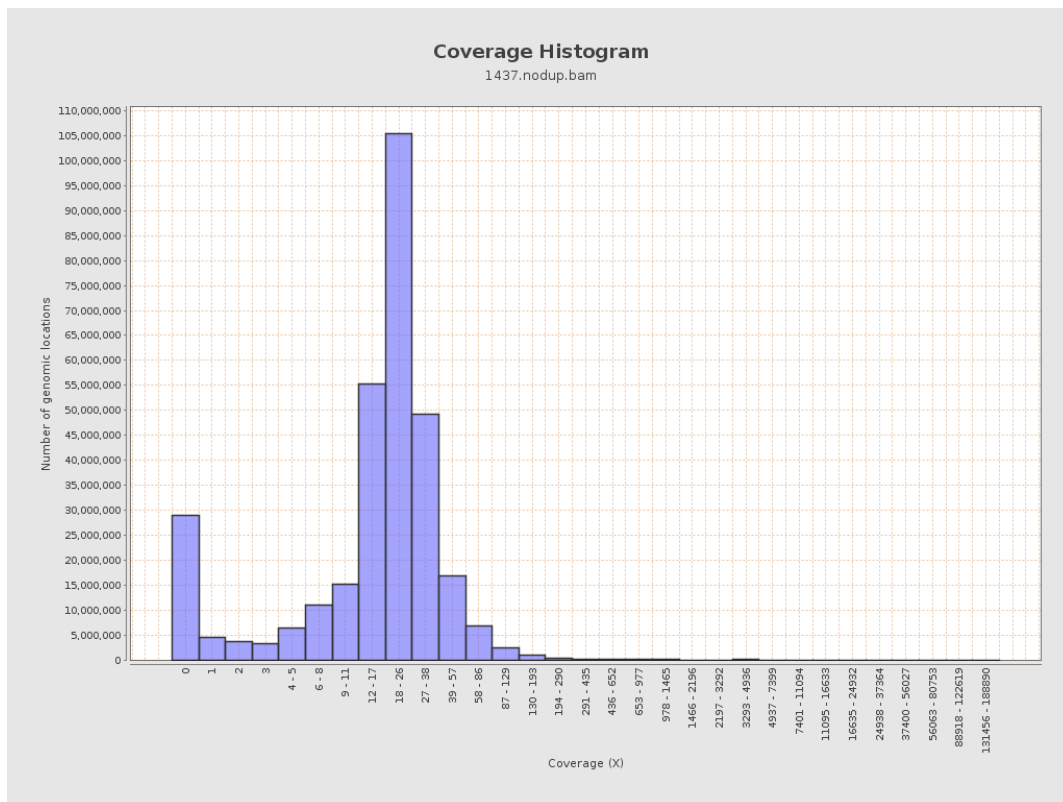
5. Results : Coverage Histogram (0-50X)
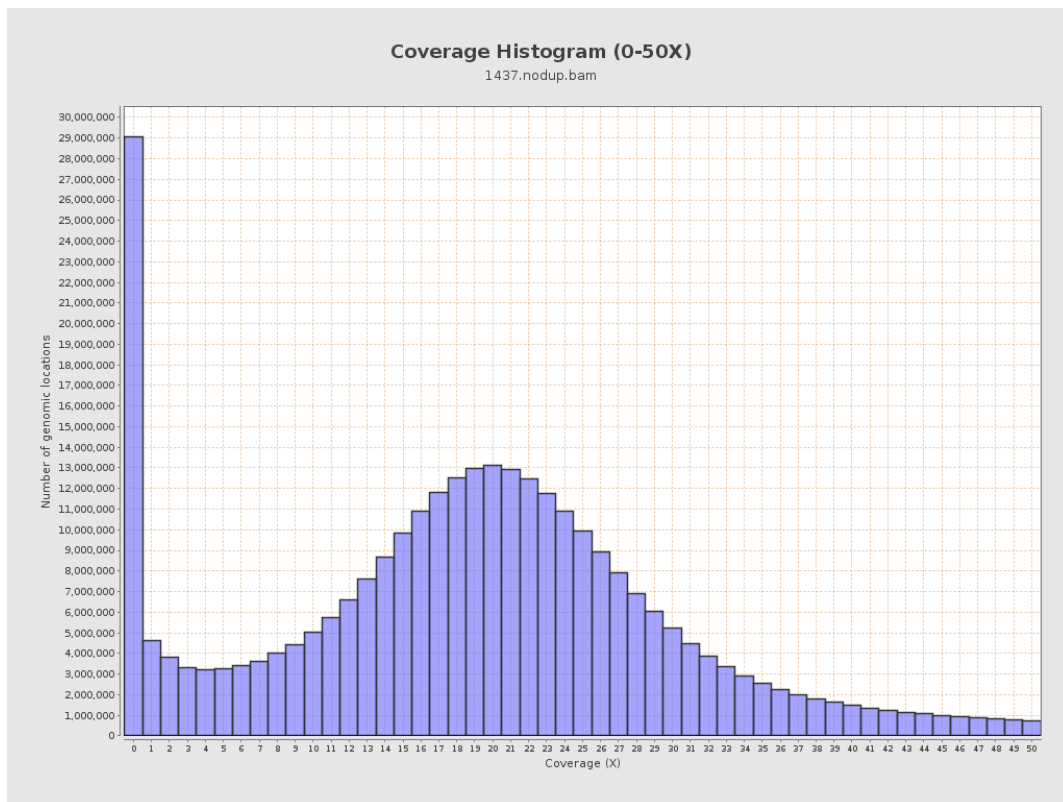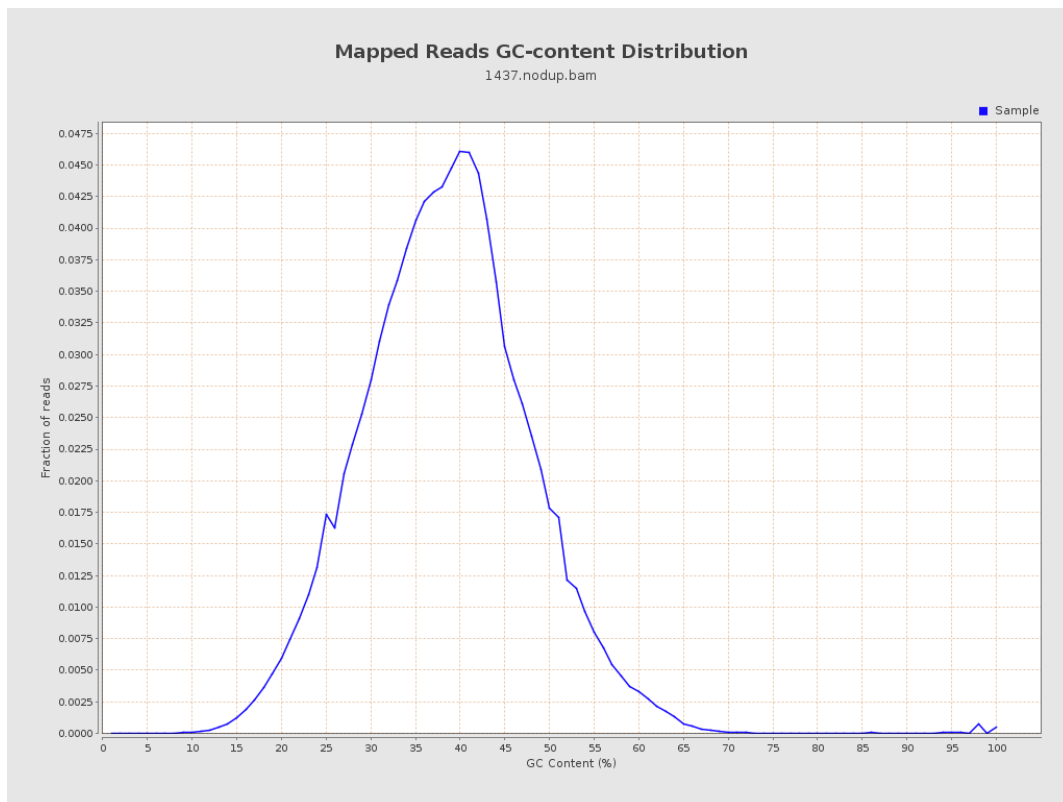
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
1437.nodup.bam
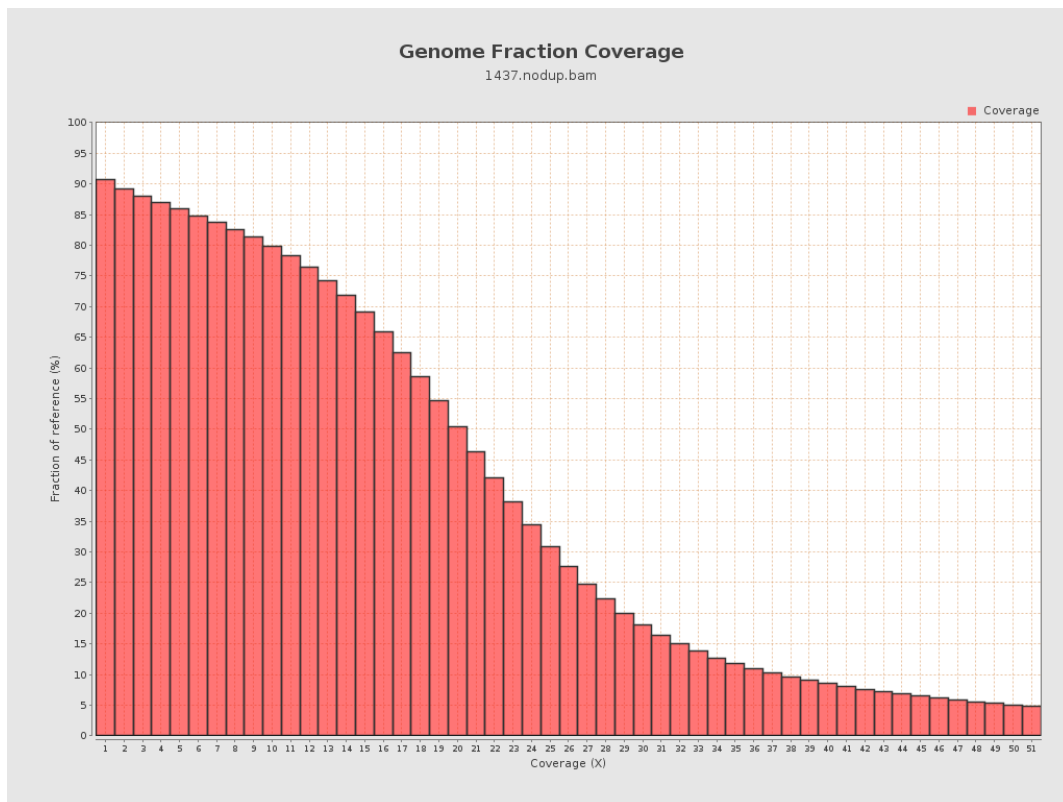
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
1437.nodup.bam
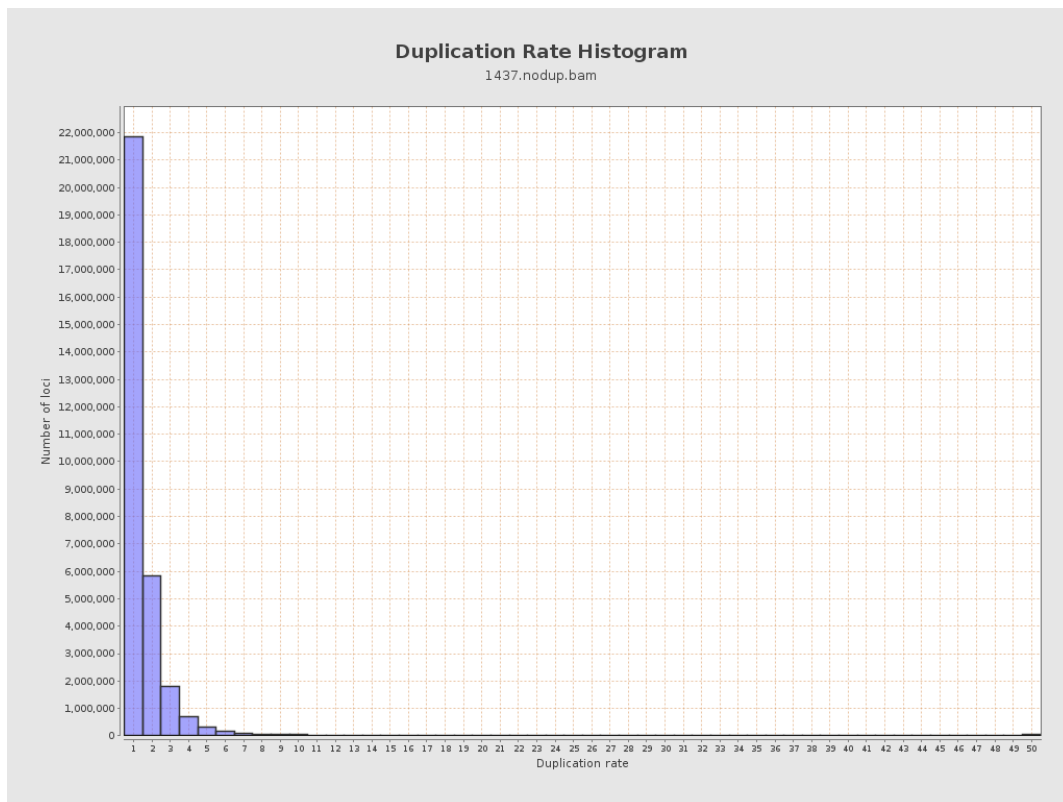
8. Results : Mapped Reads Nucleotide Content

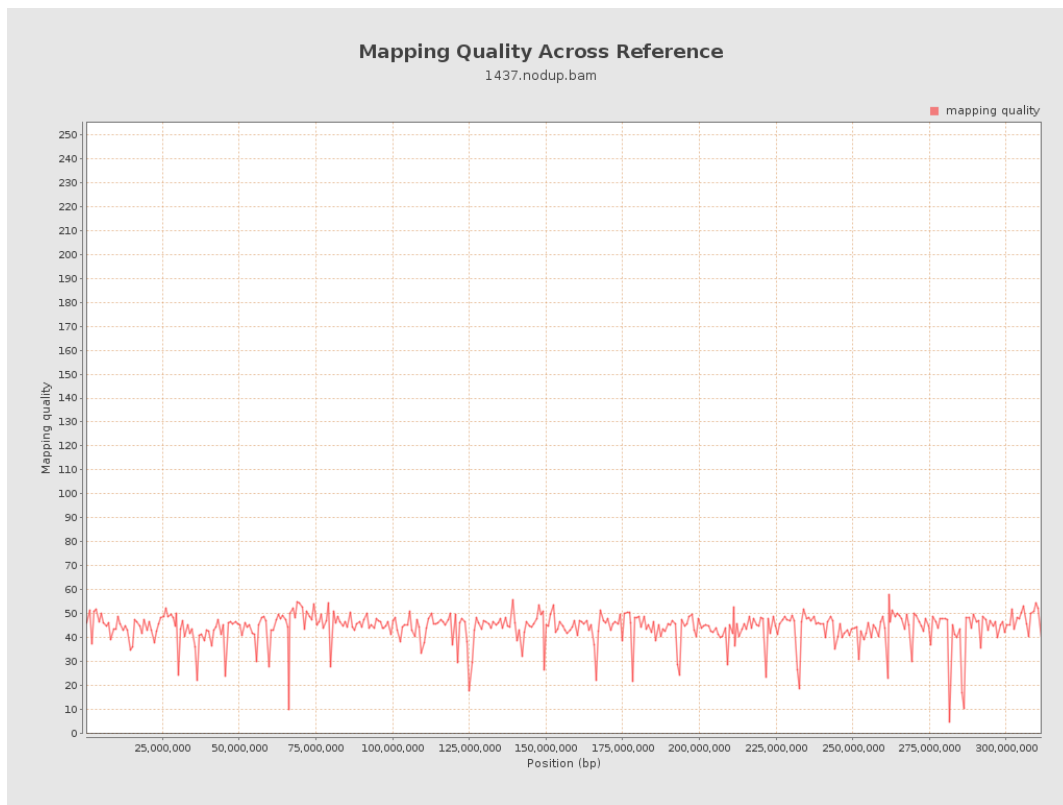# 9. Results : Mapped Reads GC-content Distribution
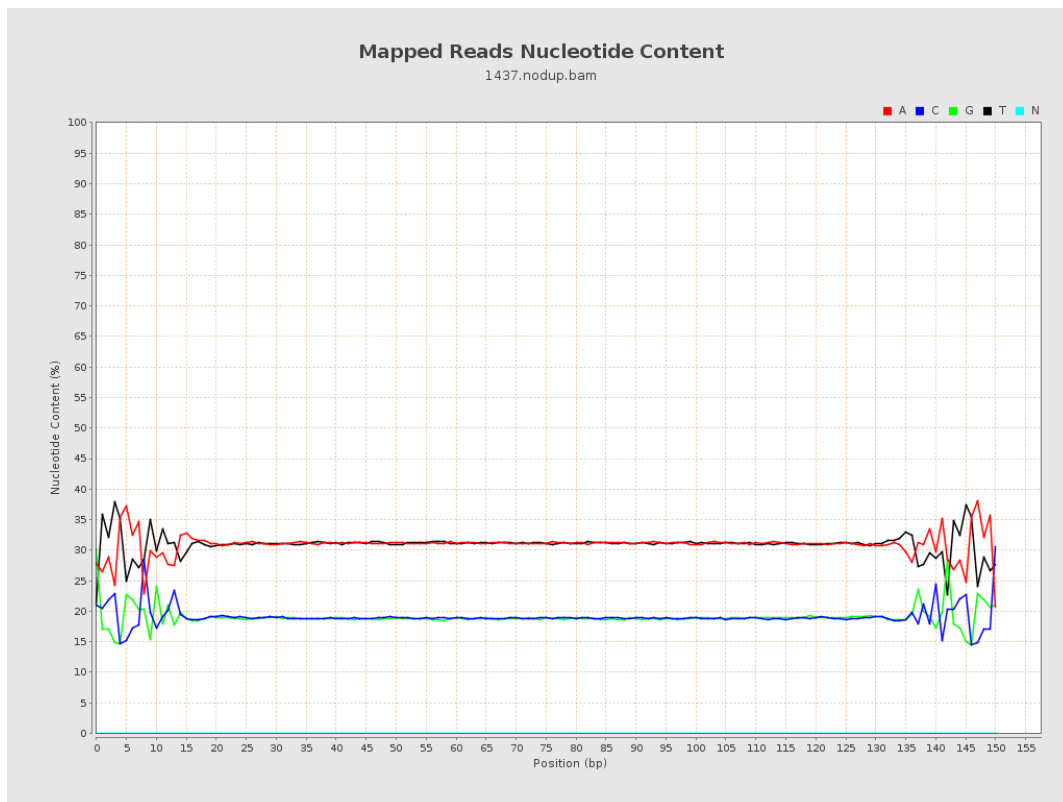
Mapped Reads GC-content Distribution
1437.nodup.bam

10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
1437.nodup.bam
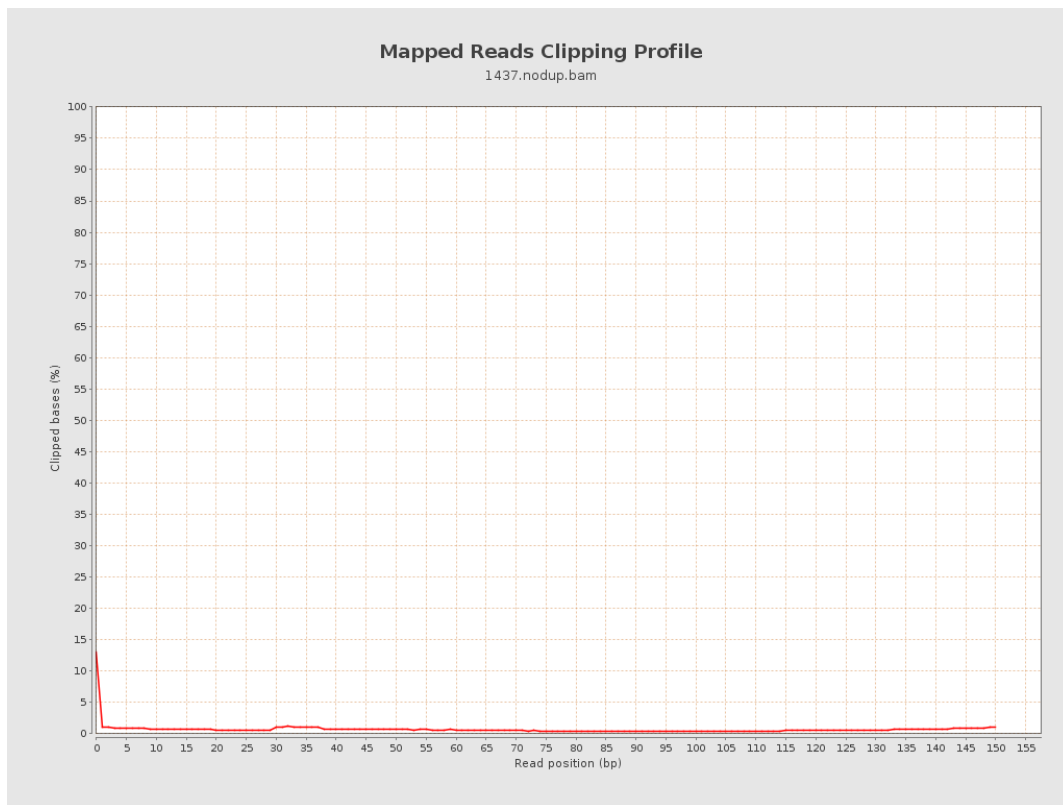
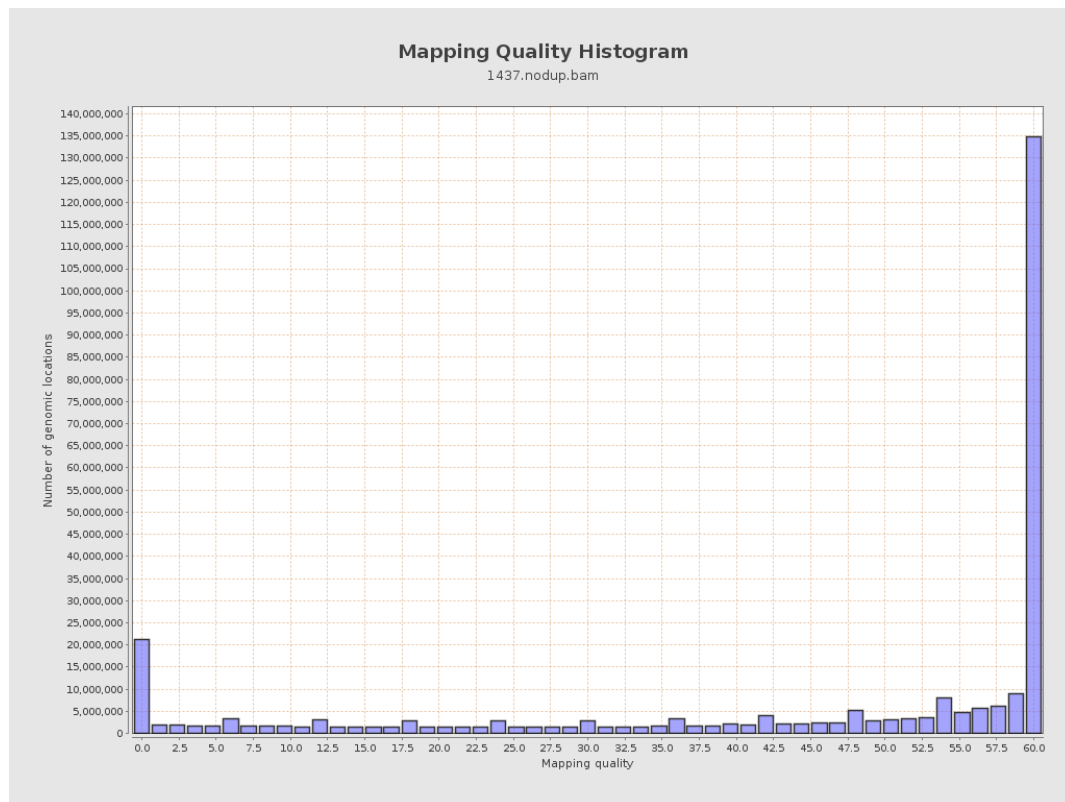# 11. Results : Homopolymer Indels

Homopolymer Indels
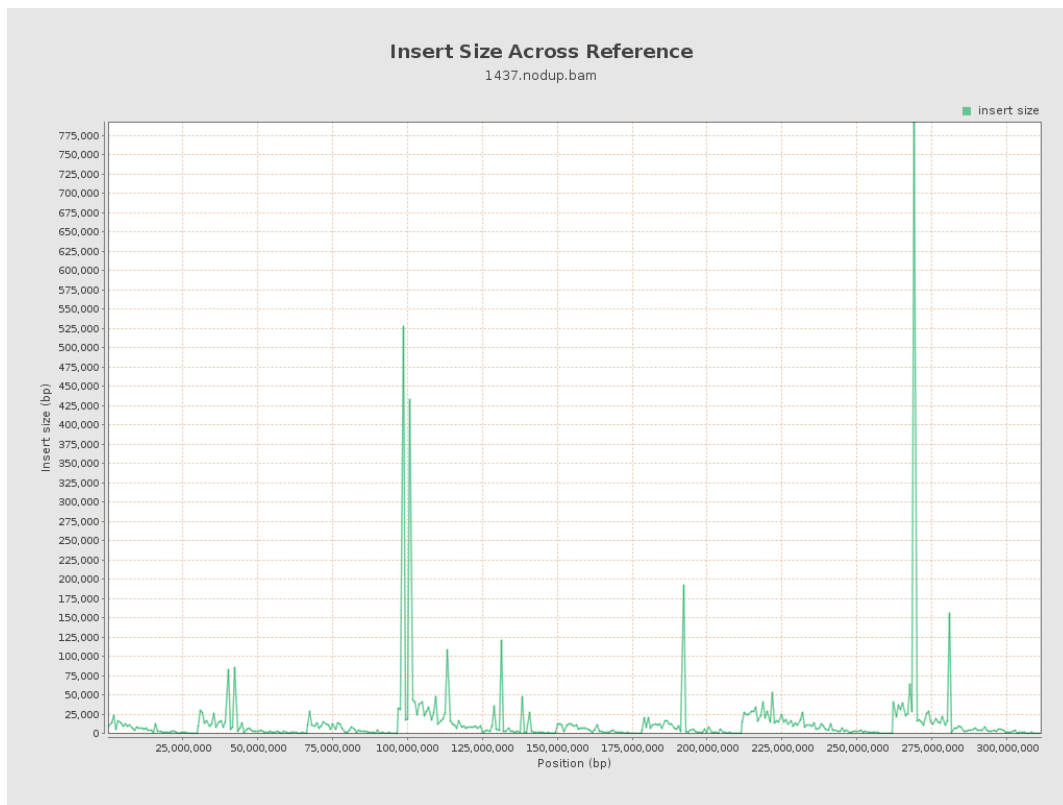1437.nodup.bam
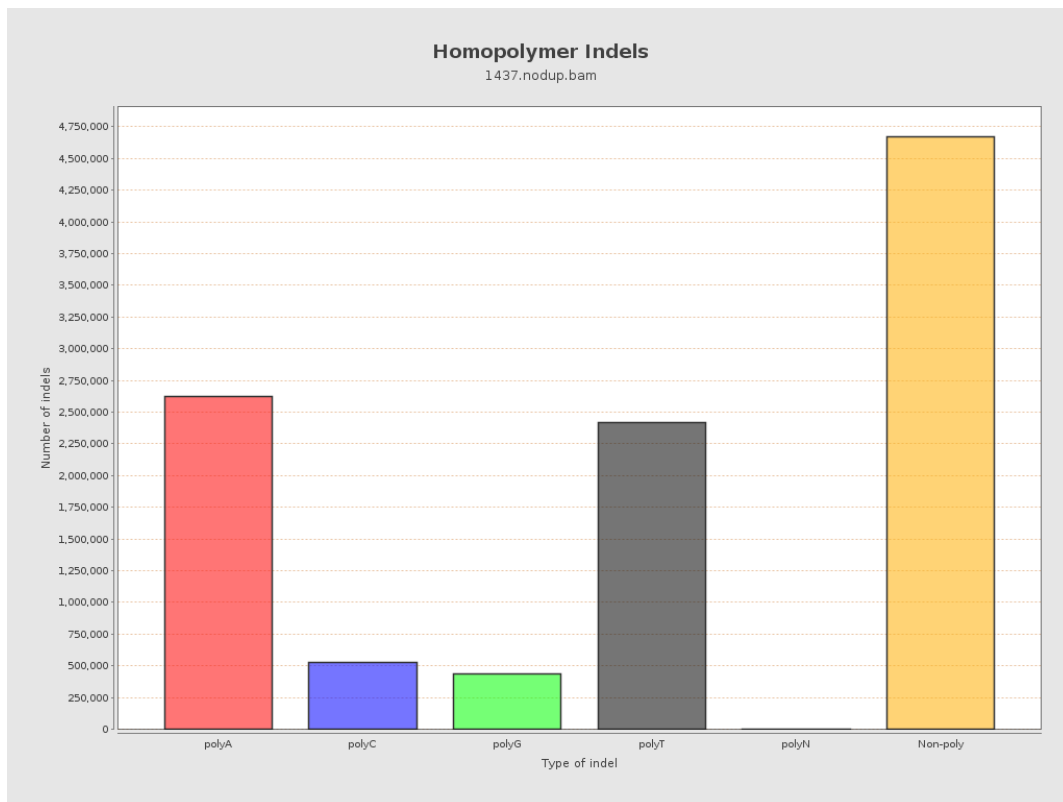
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram

Insert Size Histogram
1437.nodup.bam