Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:35:22

1. Input data & parameters

1.1. QualiMap command line

> qualimap bamqc -bam
> /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/111
> 0
> .nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1110 .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_560/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_560_S127_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_560/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_560_S127_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:35:21 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	78,967,861
Mapped reads	72,217,562 / 91.45%
Unmapped reads	6,750,299 / 8.55%
Mapped paired reads	72,217,562 / 91.45%
Mapped reads, first in pair	36,967,744 / 46.81%
Mapped reads, second in pair	35,249,818 / 44.64%
Mapped reads, both in pair	69,626,722 / 88.17%
Mapped reads, singletons	2,590,840 / 3.28%
Read min/max/mean length	30 / 151 / 148.51
Duplicated reads (flagged)	11,275,121 / 14.28%
Clipped reads	21,092,886 / 26.71%

2.2. ACGT Content

Number/percentage of A's	3,039,012,035 / 30.94%
Number/percentage of C's	1,869,204,606 / 19.03%
Number/percentage of T's	3,042,358,637 / 30.97%
Number/percentage of G's	1,872,236,961 / 19.06%
Number/percentage of N's	41,499 / 0%
GC Percentage	38.09%

2.3. Coverage

Mean	31.5961
Standard Deviation	237.9397

2.4. Mapping Quality

Mean Mapping Quality	43.98

2.5. Insert size

Mean	202,438.66
Standard Deviation	2,143,536.16
P25/Median/P75	306 / 401 / 513

2.6. Mismatches and indels

General error rate	3.55%
Mismatches	331,245,754
Insertions	6,490,546
Mapped reads with at least one insertion	8.09%
Deletions	6,528,003
Mapped reads with at least one deletion	8.07%
Homopolymer indels	54.78%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	808276173	27.1924	92.007

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LT669789.1	36598175	1174937343	32.1037	249.7165
LT669790.1	30422129	1054648674	34.6672	258.7224
LT669791.1	52758100	1622015550	30.7444	235.6457
LT669792.1	28376109	904937804	31.8908	255.6831
LT669793.1	33388210	994177862	29.7763	168.9604
LT669794.1	50579949	1524778506	30.1459	219.6431
LT669795.1	49795044	1762886467	35.4028	313.4919

3. Results : Coverage across reference

Coverage across reference
1110.nodup.bam
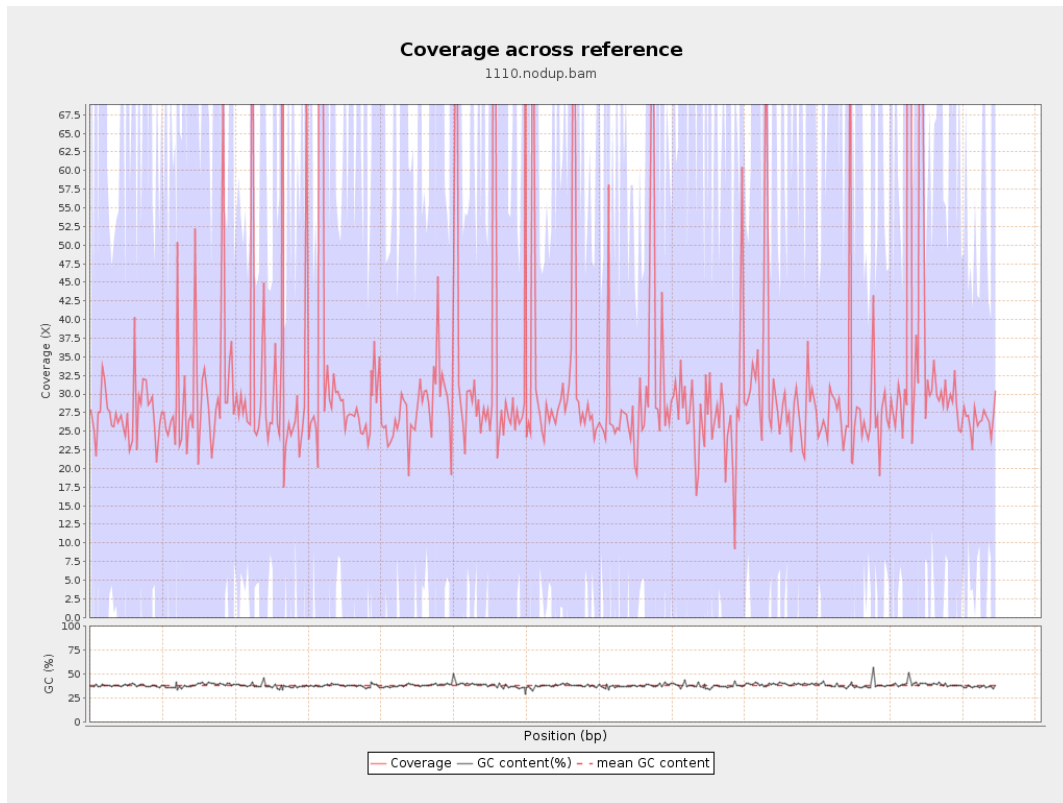
4. Results : Coverage Histogram

5. Results : Coverage Histogram (0-50X)
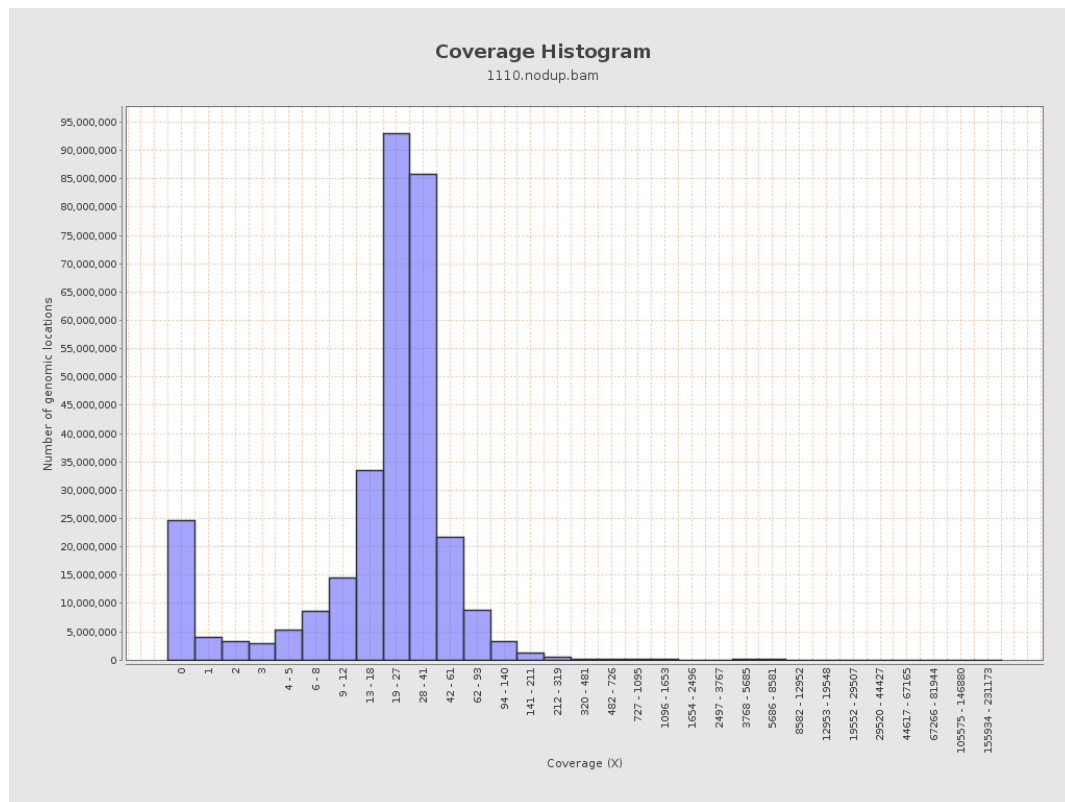
Coverage Histogram (0-50X)
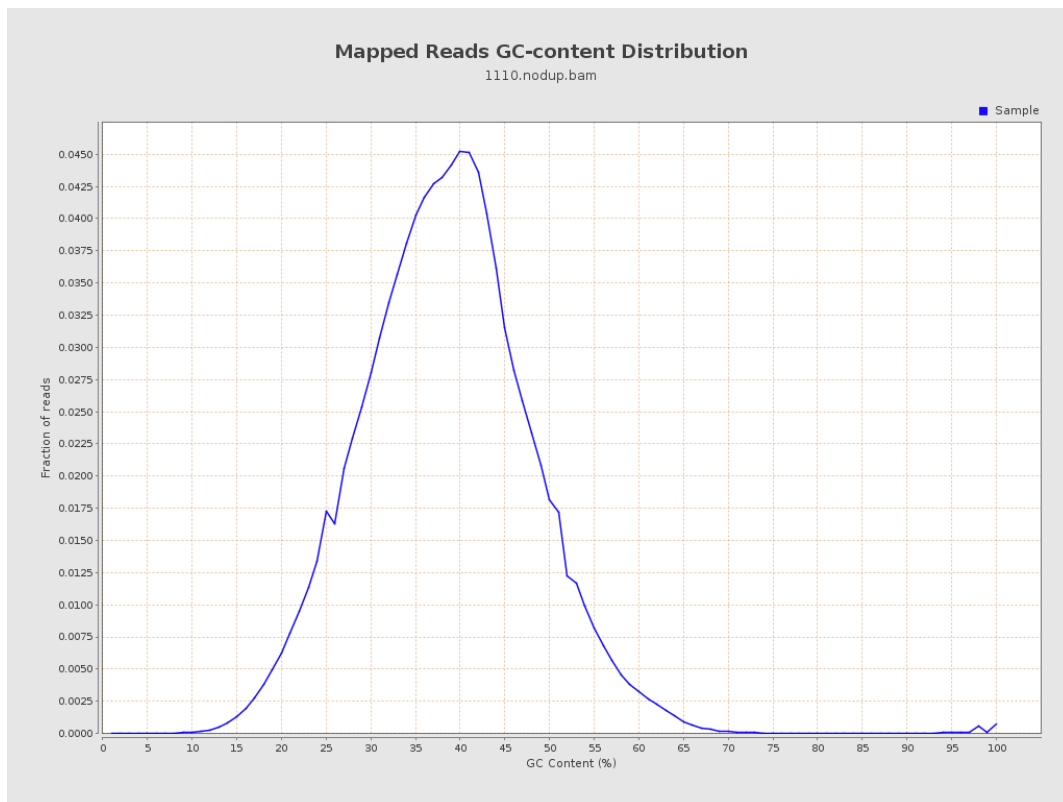1110.nodup.bam
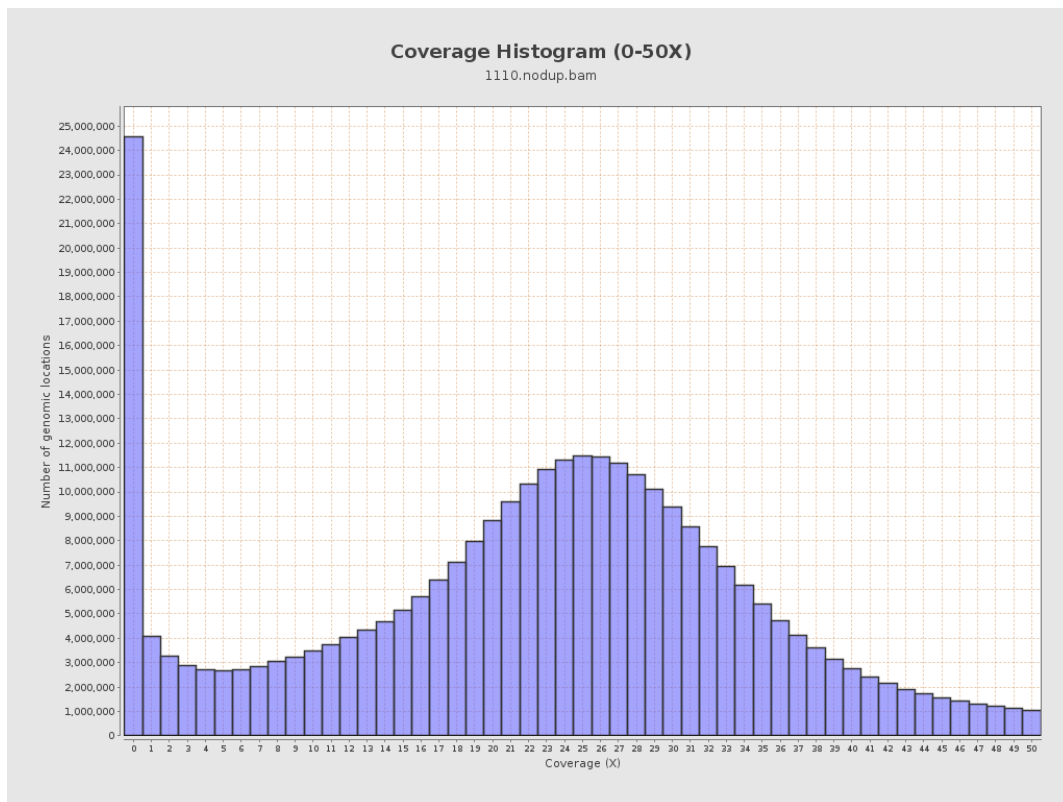
6. Results : Genome Fraction Coverage
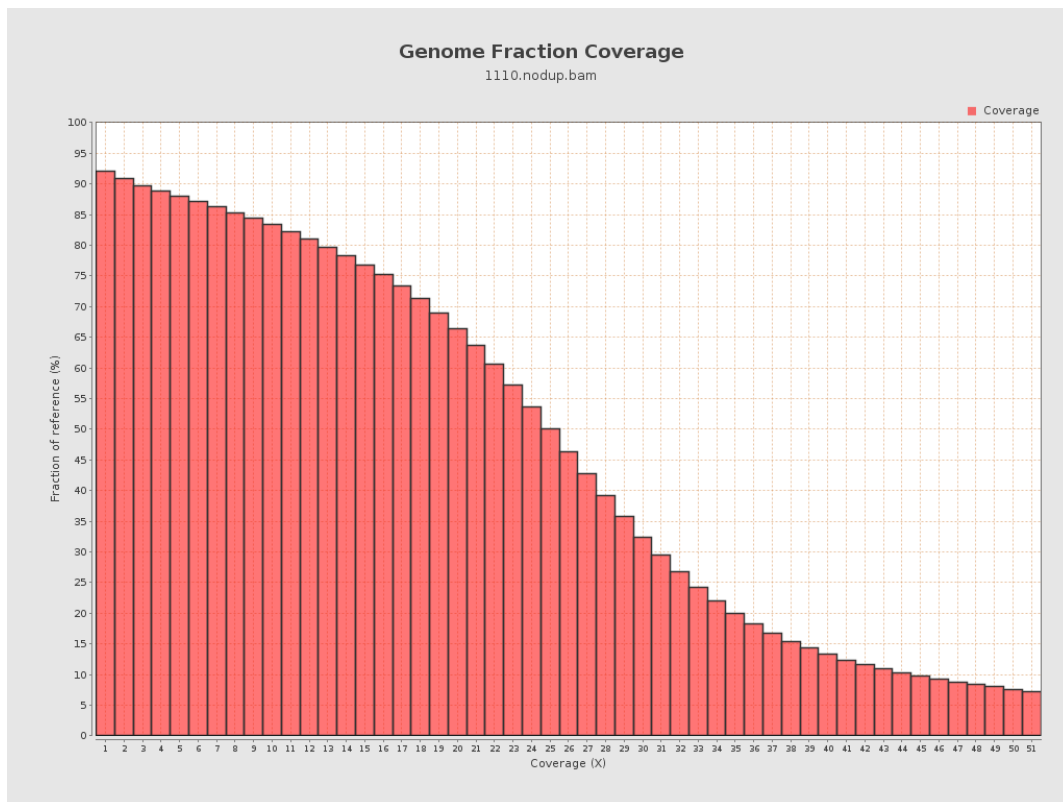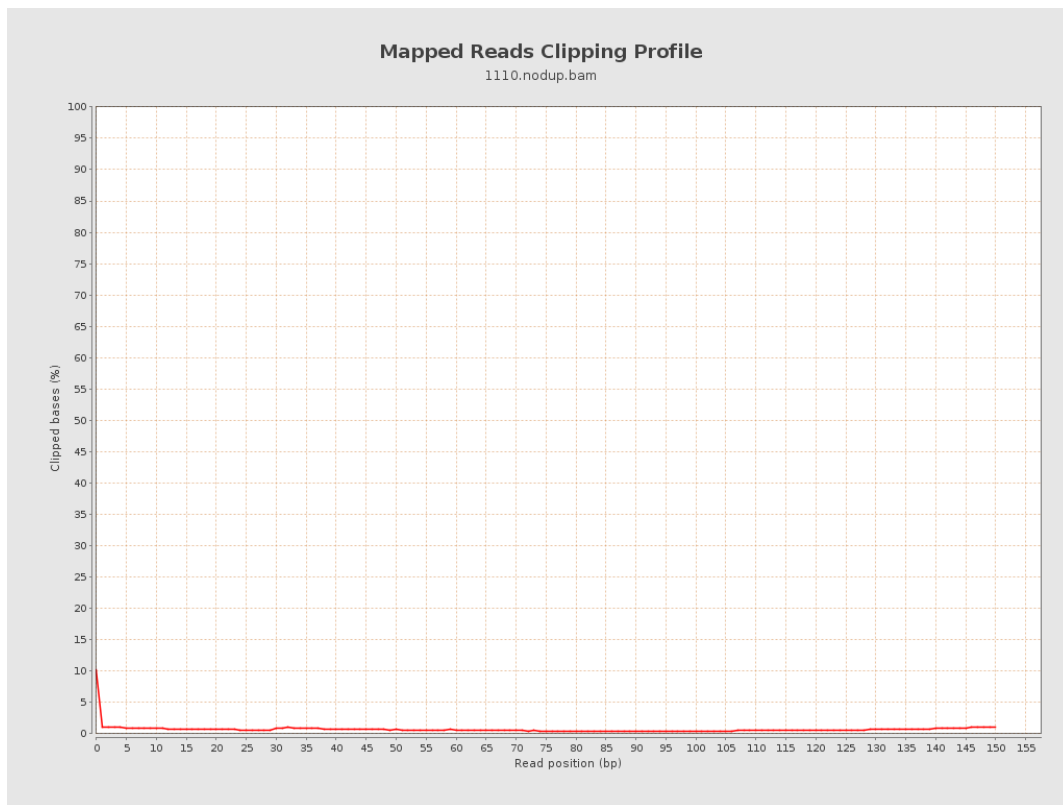
7. Results : Duplication Rate Histogram
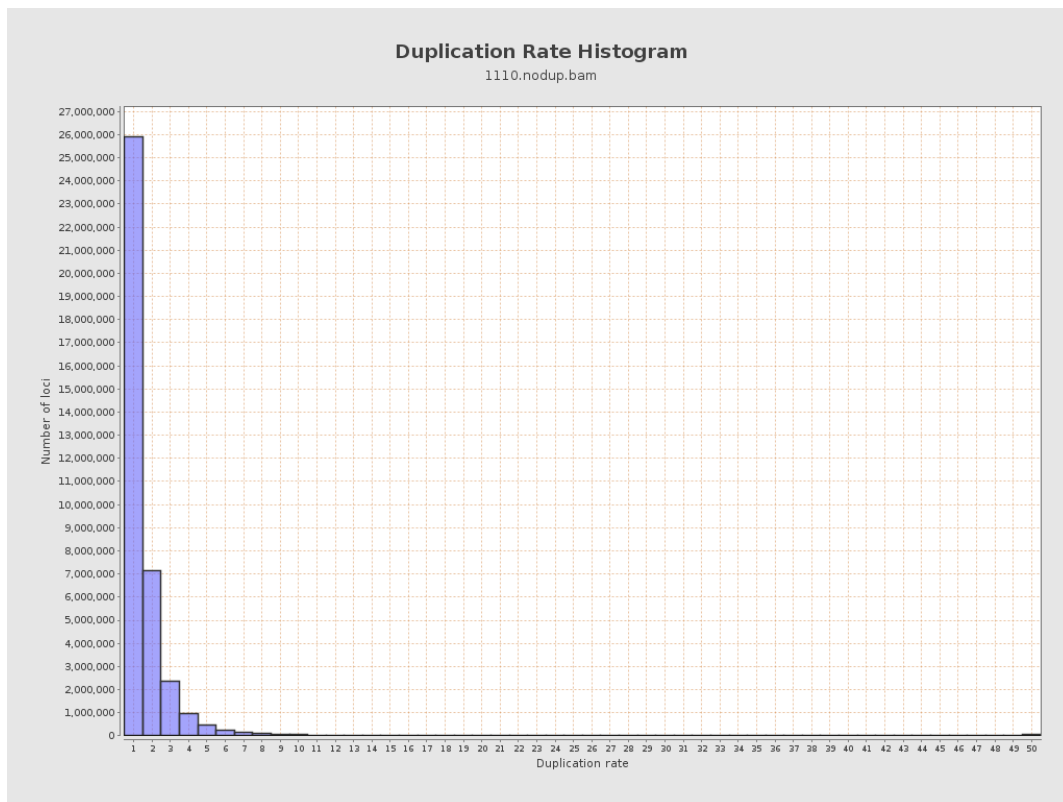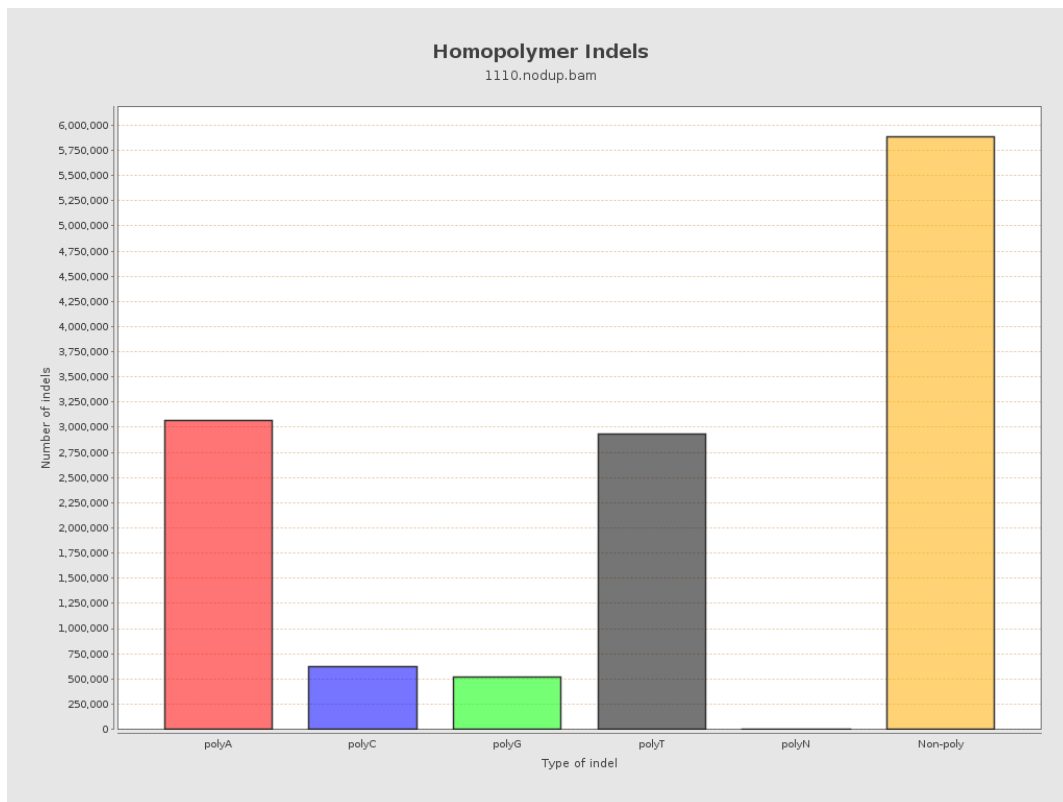
8. Results : Mapped Reads Nucleotide Content
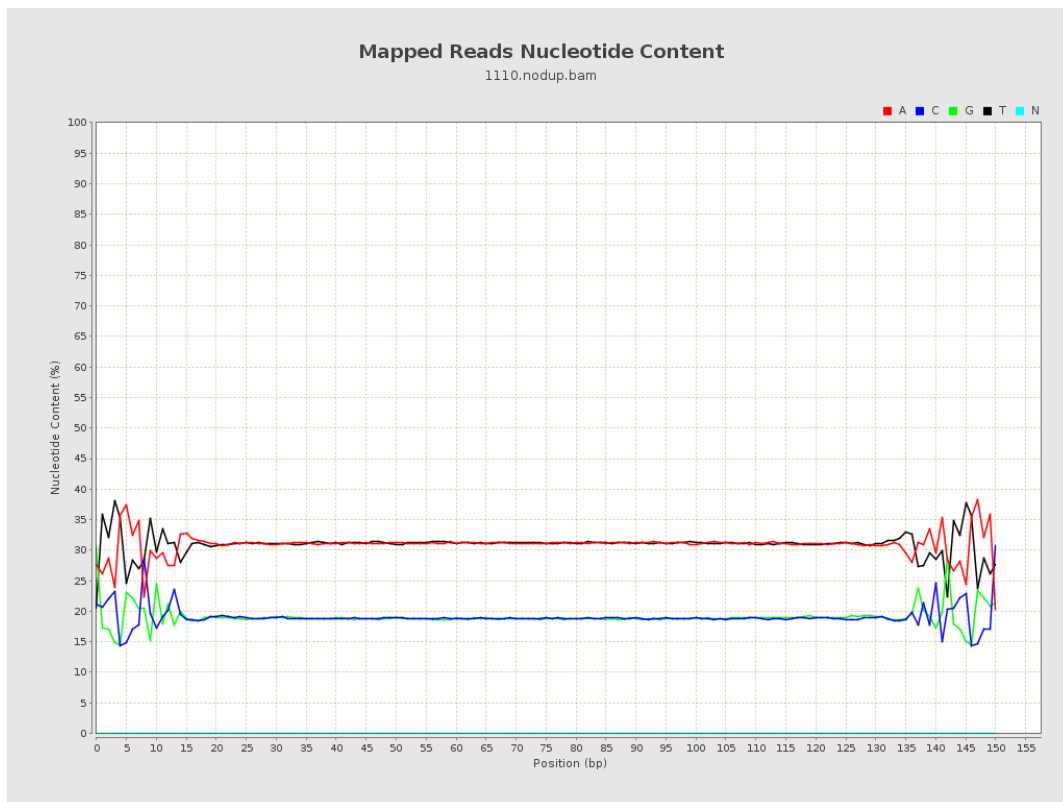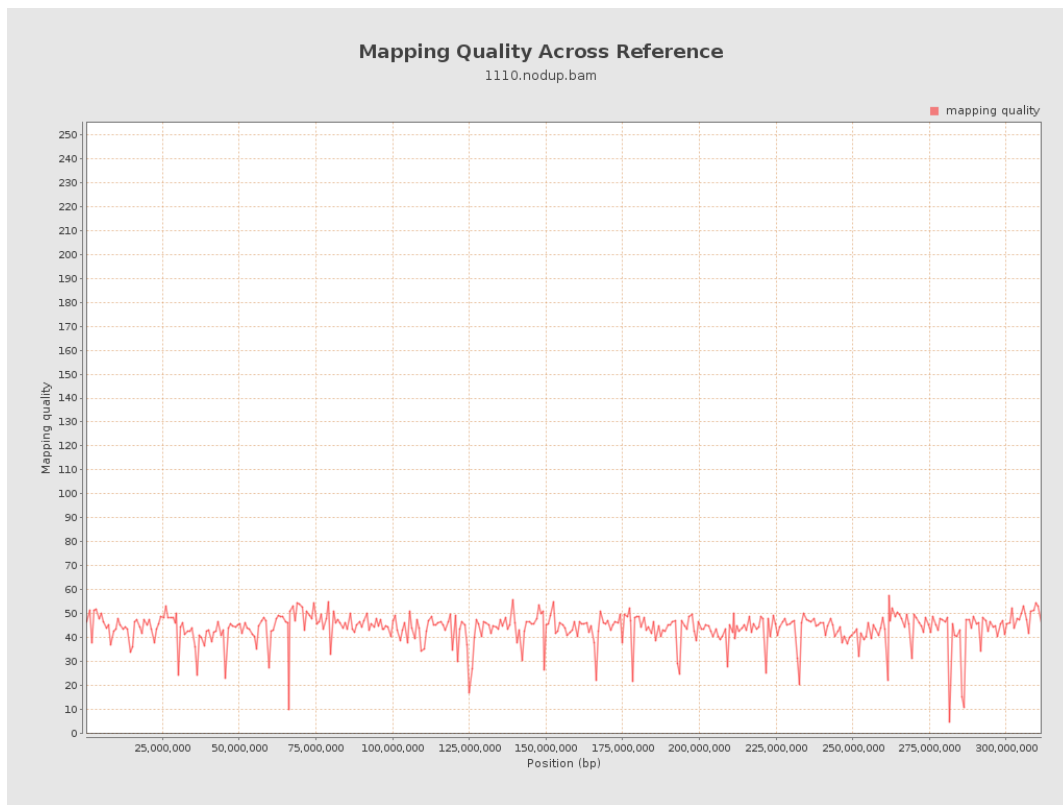
9. Results : Mapped Reads GC-content Distribution

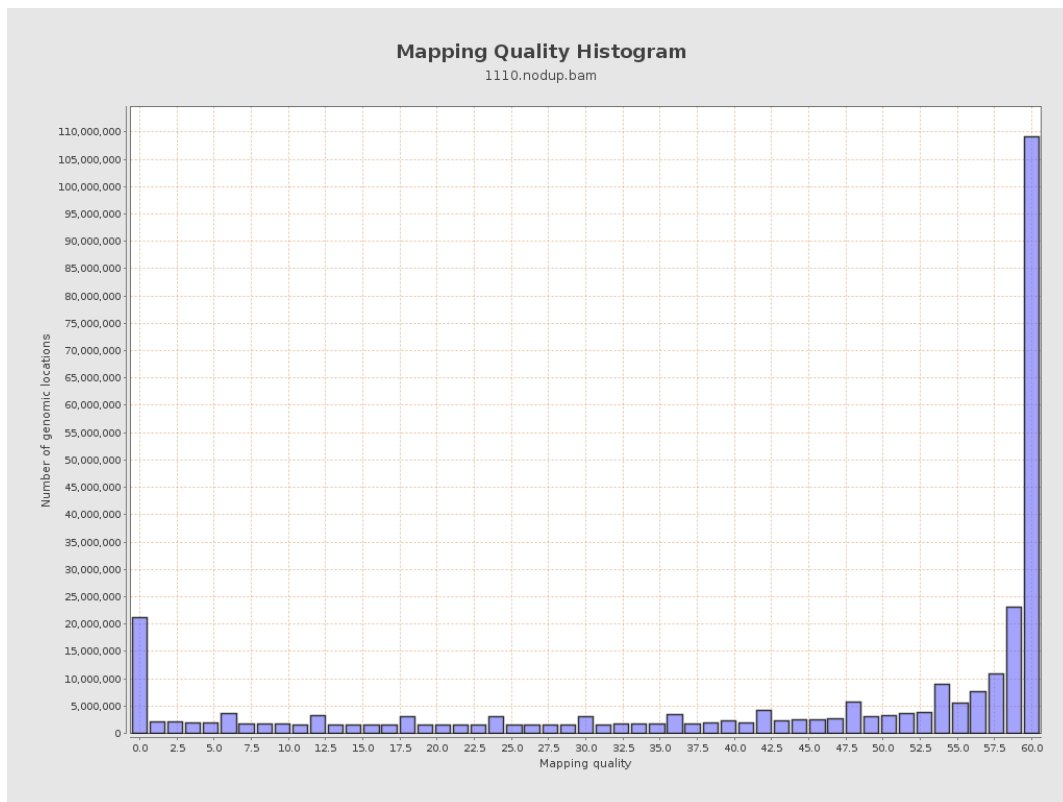# 10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels
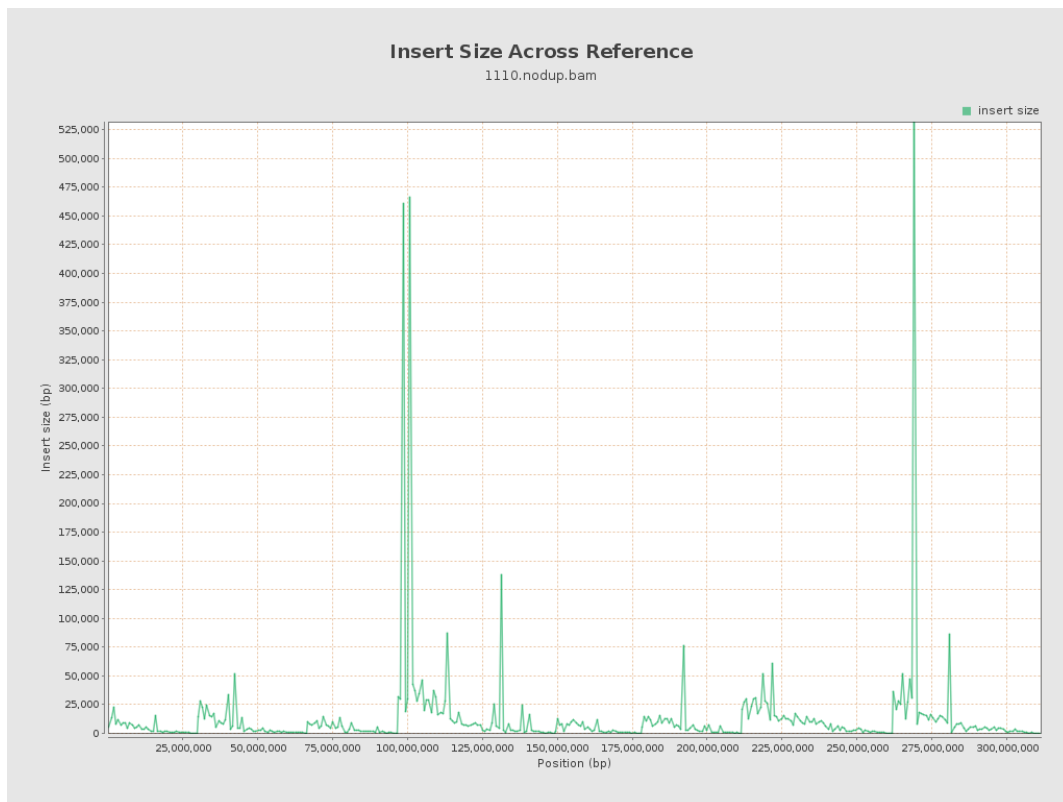
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram

Insert Size Histogram
1110.nodup.bam