Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:32:46

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/596
.nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/596 .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_488/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_488_S463_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_488/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_488_S463_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:32:46 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	72,885,411
Mapped reads	66,501,996 / 91.24%
Unmapped reads	6,383,415 / 8.76%
Mapped paired reads	66,501,996 / 91.24%
Mapped reads, first in pair	33,299,449 / 45.69%
Mapped reads, second in pair	33,202,547 / 45.55%
Mapped reads, both in pair	64,428,785 / 88.4%
Mapped reads, singletons	2,073,211 / 2.84%
Read min/max/mean length	30 / 151 / 148.21
Duplicated reads (flagged)	12,027,472 / 16.5%
Clipped reads	15,066,650 / 20.67%

2.2. ACGT Content

Number/percentage of A's	2,828,646,702 / 30.87%
Number/percentage of C's	1,752,371,306 / 19.12%
Number/percentage of T's	2,833,341,166 / 30.92%
Number/percentage of G's	1,749,320,192 / 19.09%
Number/percentage of N's	30,417 / 0%
GC Percentage	38.21%

2.3. Coverage

Mean	29.4796
Standard Deviation	279.2221

2.4. Mapping Quality

Mean Mapping Quality	44.27

2.5. Insert size

| Mean	255,038.07
Standard Deviation	2,431,669.4
P25/Median/P75	331 / 431 / 564

2.6. Mismatches and indels

| General error rate	2.3%
Mismatches	192,707,050
Insertions	6,598,749
Mapped reads with at least one insertion	8.84%
Deletions	6,289,082
Mapped reads with at least one deletion	8.4%
Homopolymer indels	57.37%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	691448746	23.262	107.049

| LT669789.1 | 36598175 | 1085818259 | 29.6686 | 306.578 |
LT669790.1	30422129	1058118711	34.7812	391.7069
LT669791.1	52758100	1547489569	29.3318	298.8683
LT669792.1	28376109	822617355	28.9898	292.8588
LT669793.1	33388210	898854321	26.9213	185.2418
LT669794.1	50579949	1415795228	27.9912	223.563
LT669795.1	49795044	1666931554	33.4759	317.6964

3. Results : Coverage across reference

Coverage across reference
596.nodup.bam

4. Results : Coverage Histogram

Coverage Histogram
596.nodup.bam
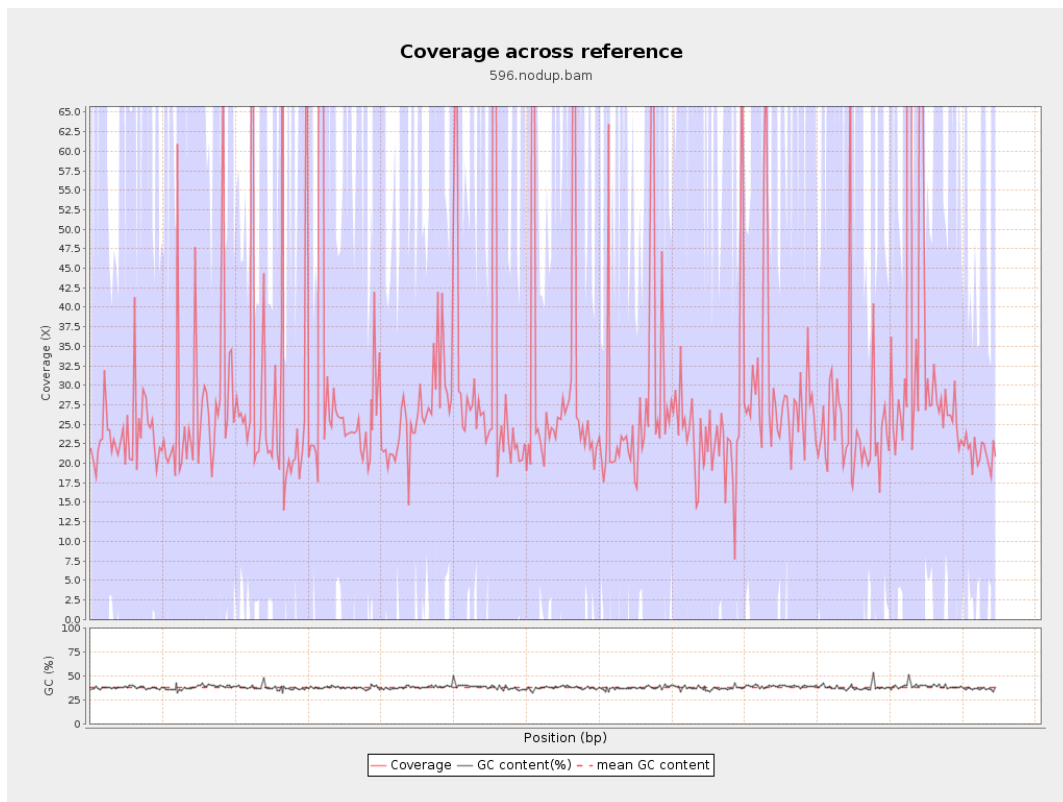
5. Results : Coverage Histogram (0-50X)
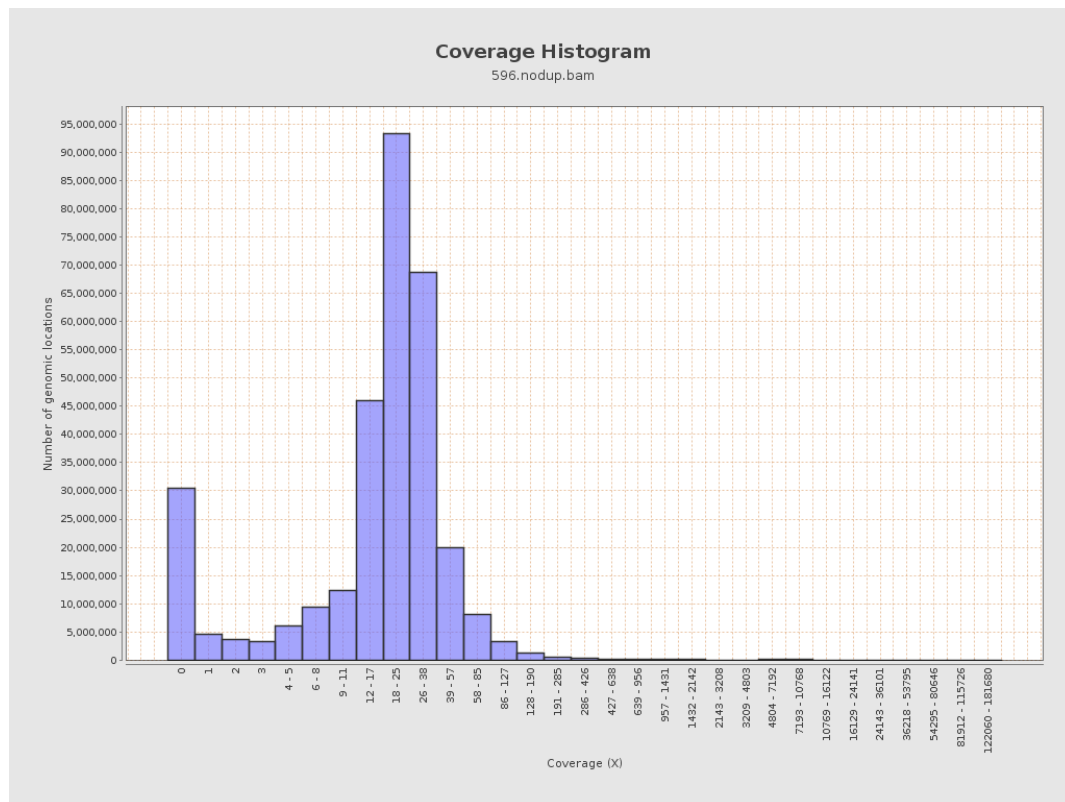
Coverage Histogram (0-50X)
596.nodup.bam
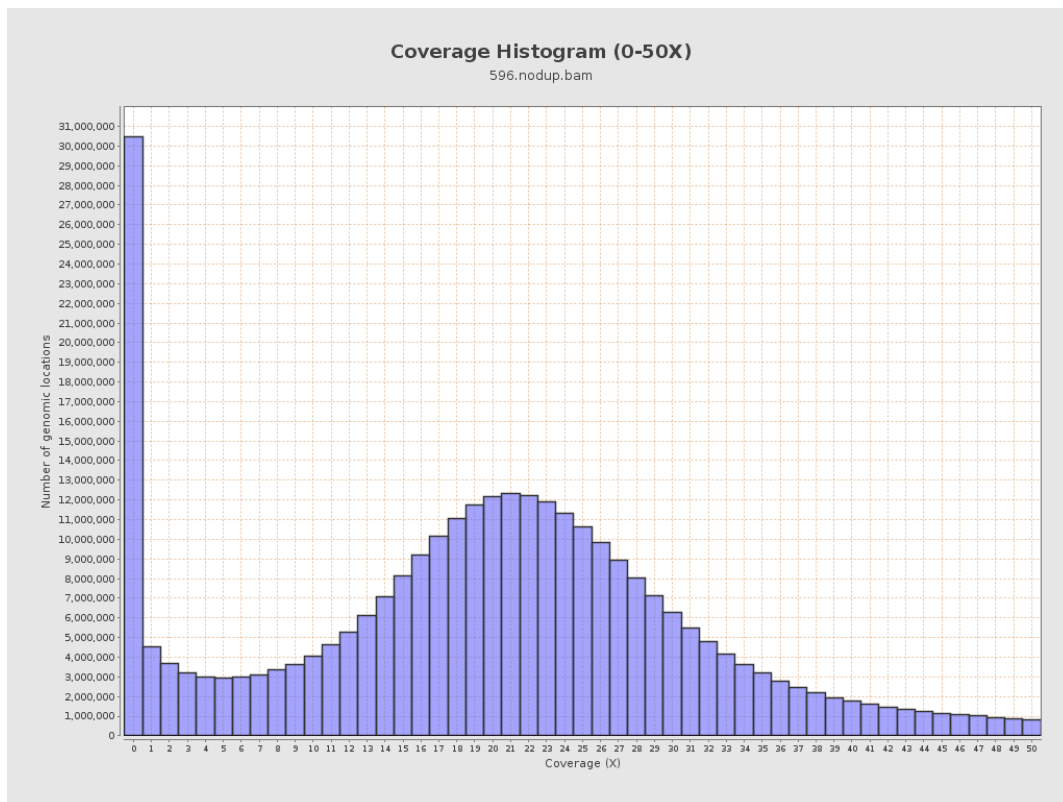
6. Results : Genome Fraction Coverage
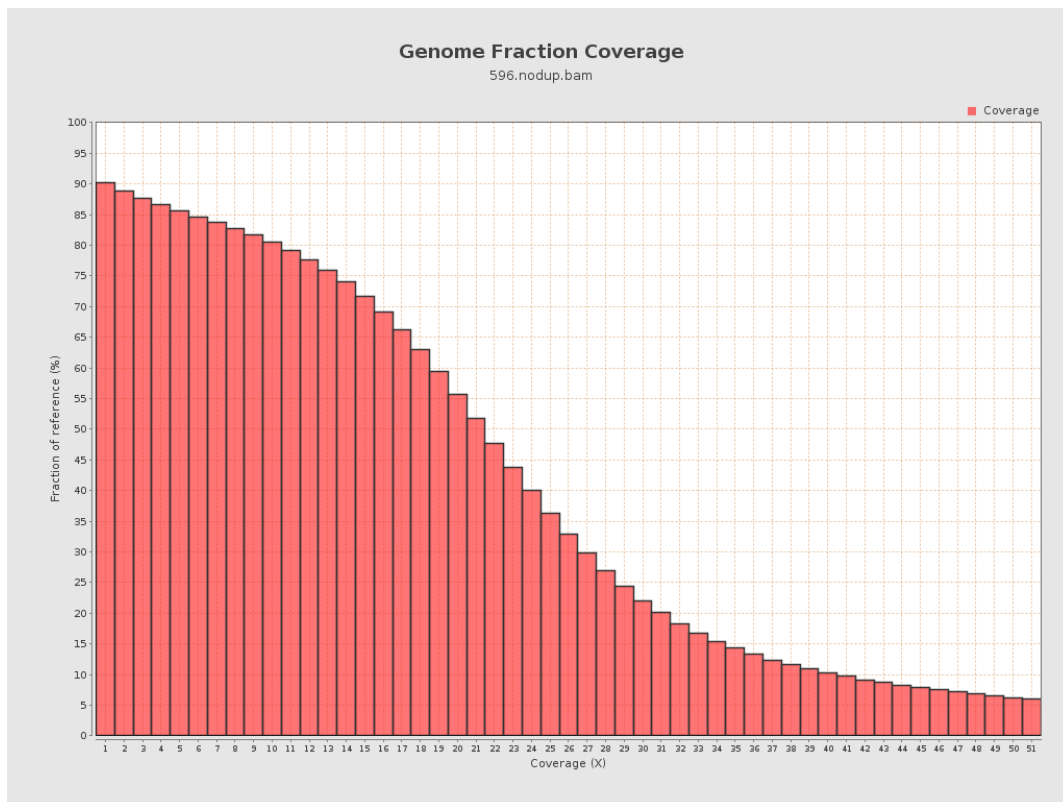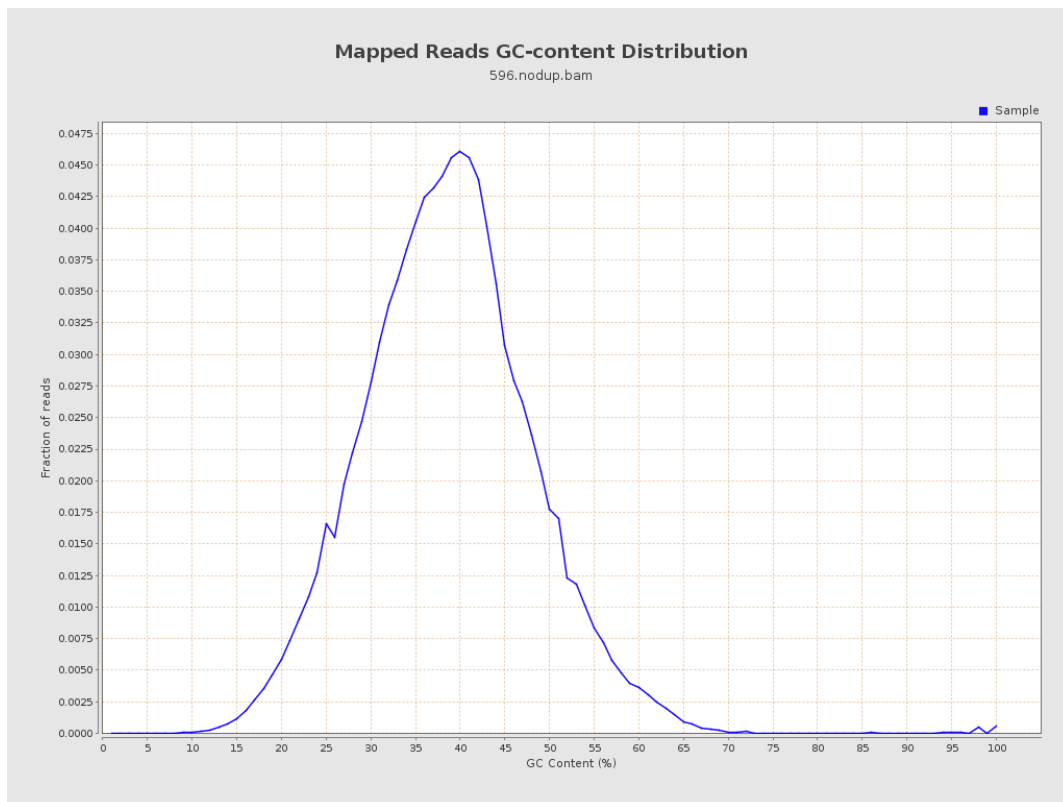
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
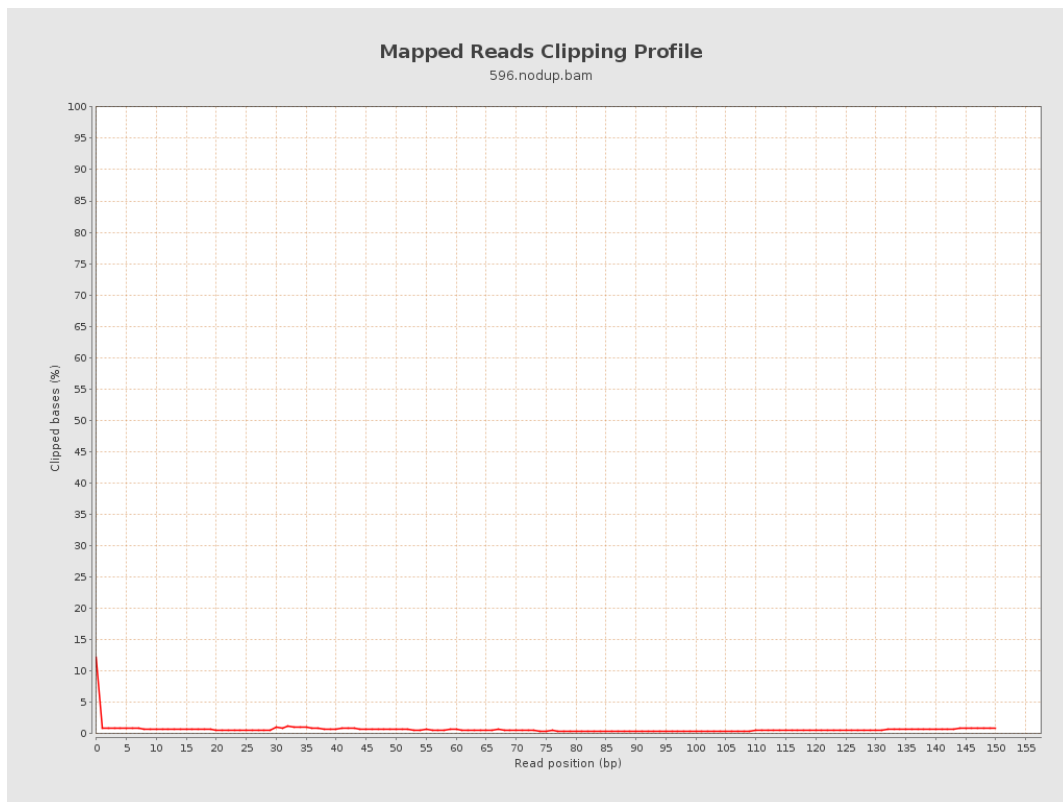596.nodup.bam
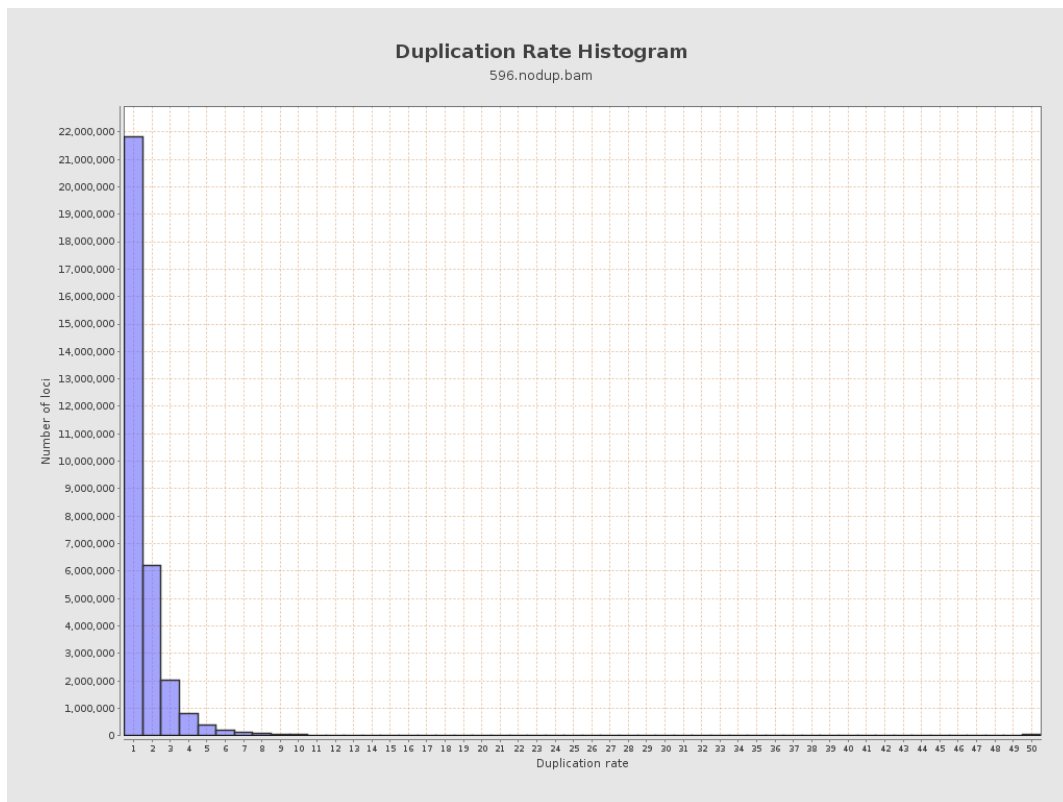
8. Results : Mapped Reads Nucleotide Content
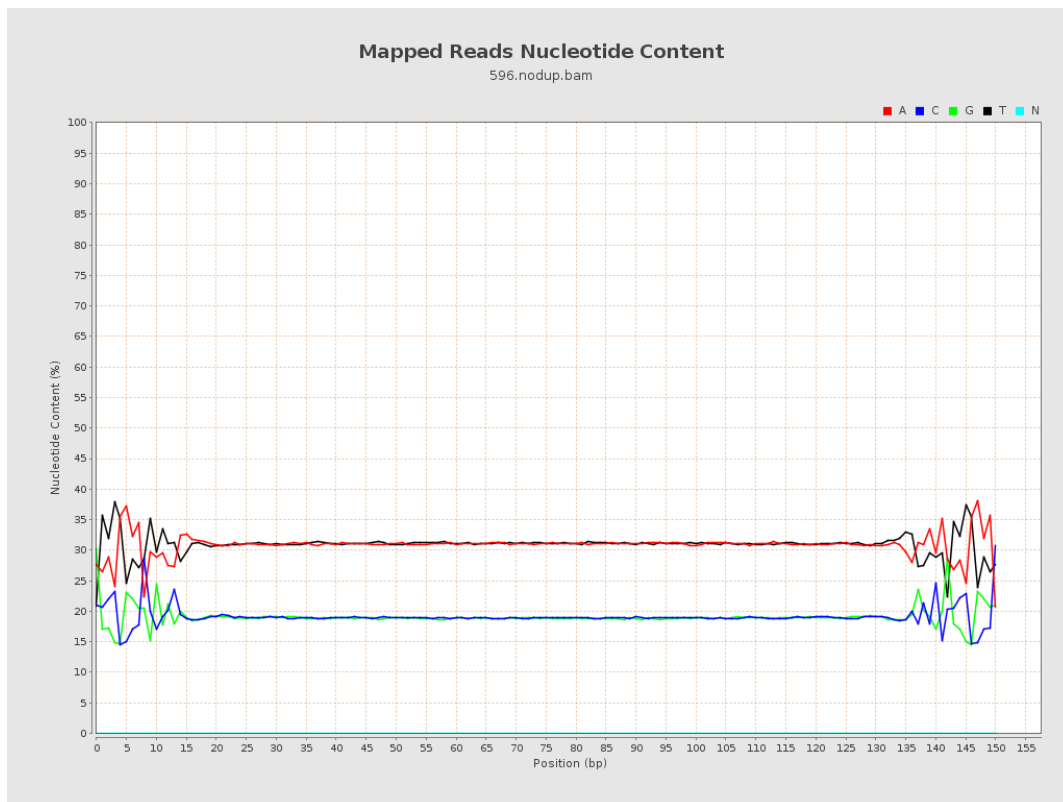
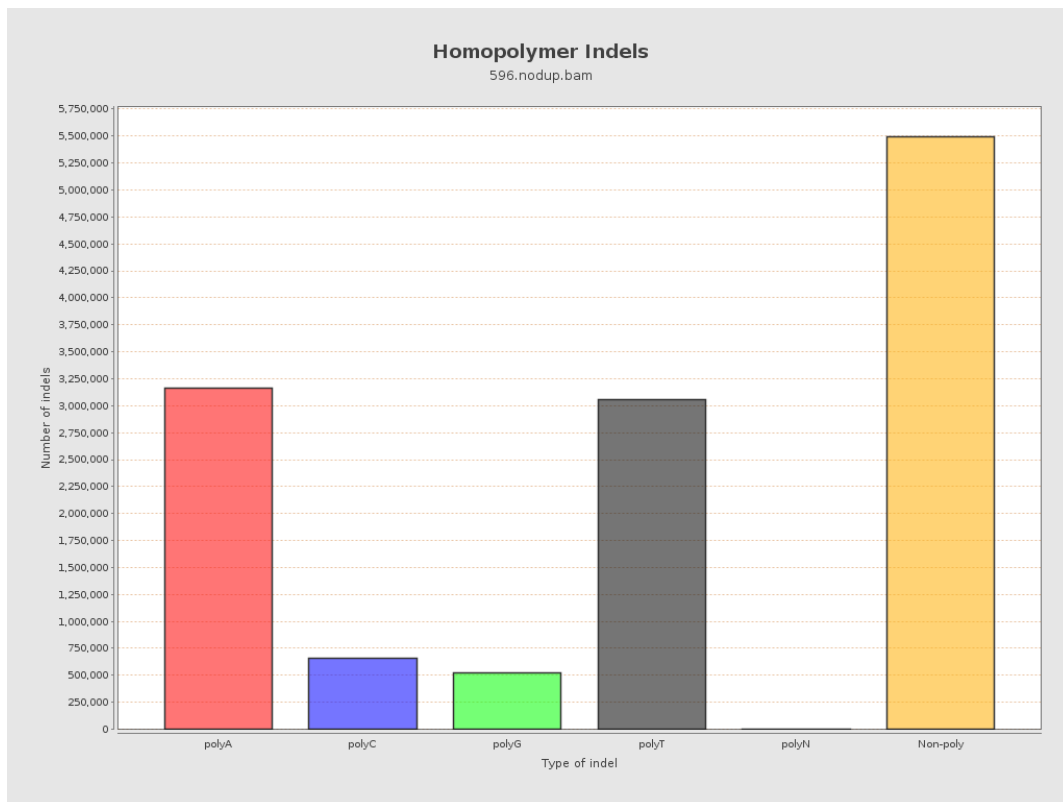# 9. Results : Mapped Reads GC-content Distribution

10. Results : Mapped Reads Clipping Profile

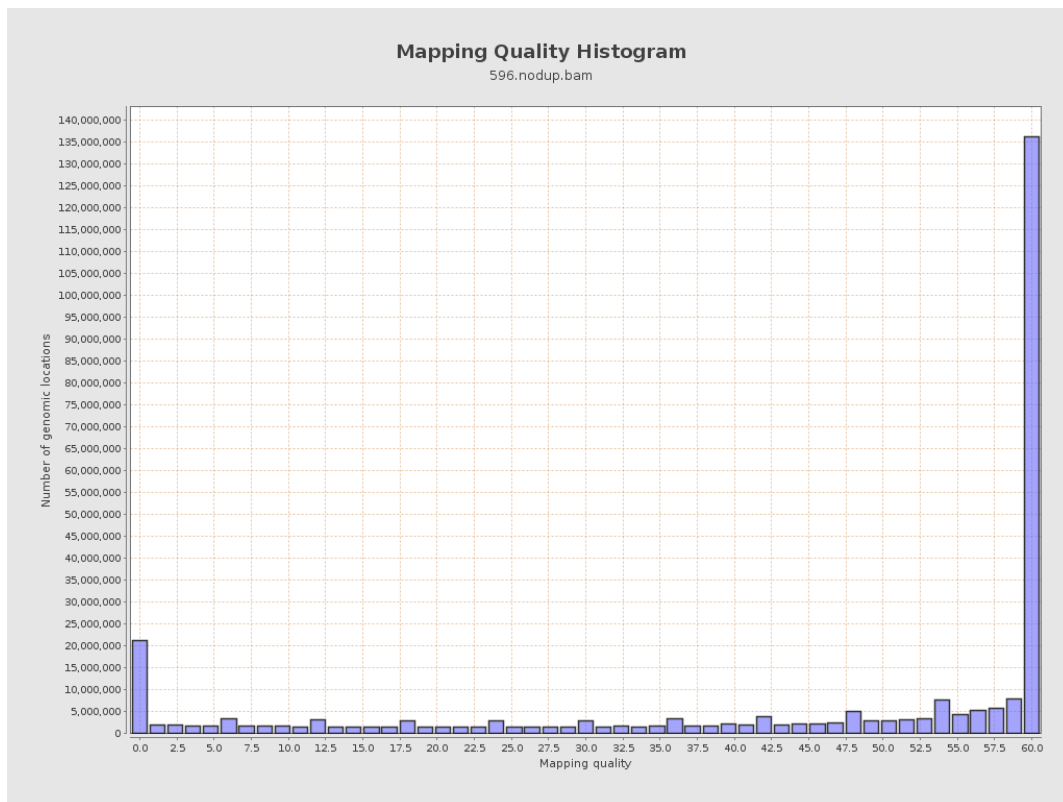
Mapped Reads Clipping Profile
596.nodup.bam

11. Results : Homopolymer Indels

Homopolymer Indels
596.nodup.bam

12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram
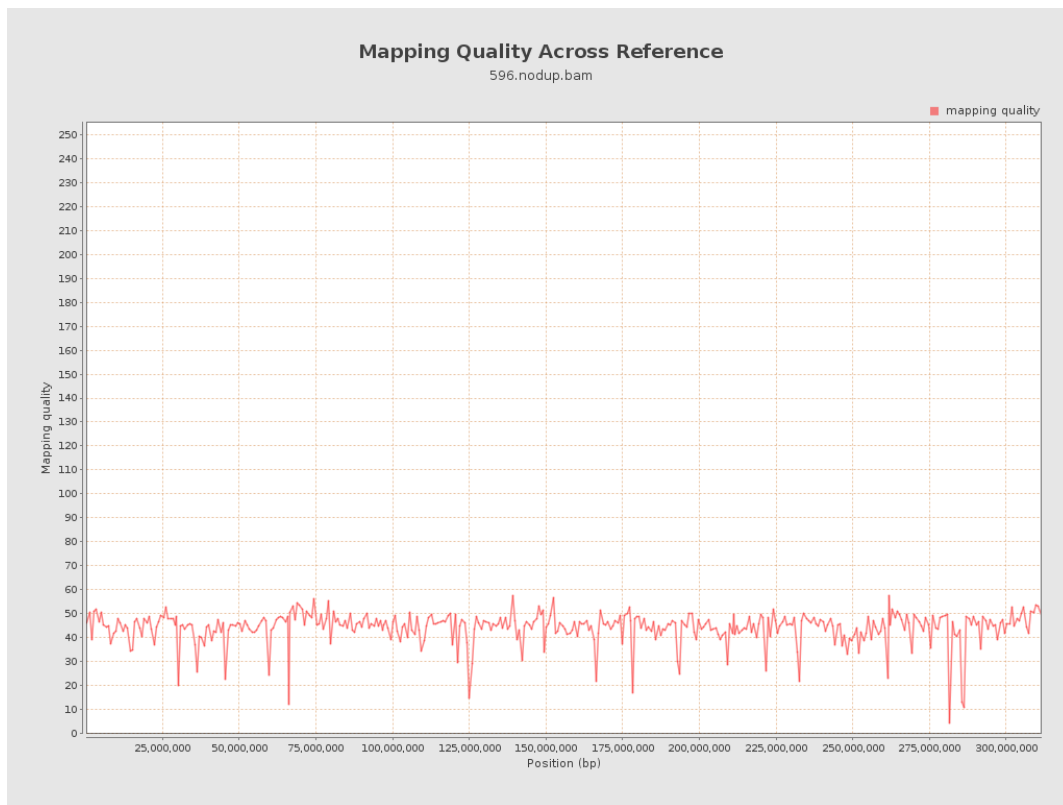
Mapping Quality Histogram
596.nodup.bam

14. Results : Insert Size Across Reference
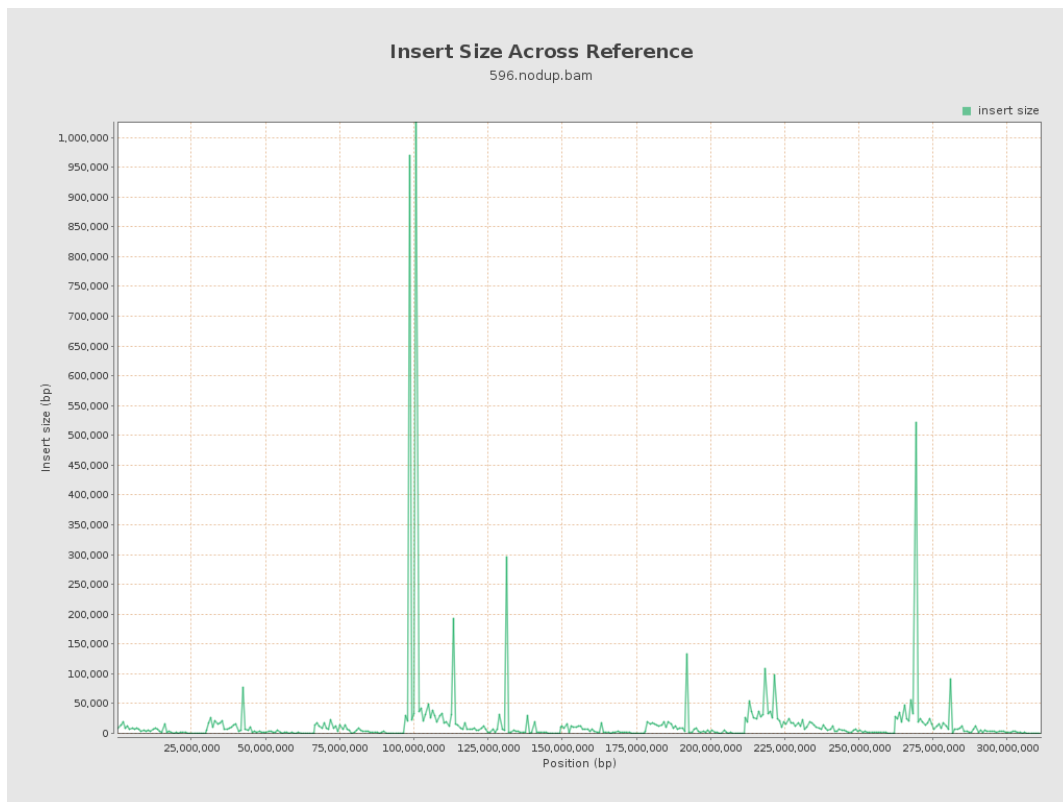
15. Results : Insert Size Histogram