Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:36:33

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/979
.nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/979 .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_138/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_138_S228_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_138/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_138_S228_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:36:33 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	80,419,926
Mapped reads	73,166,343 / 90.98%
Unmapped reads	7,253,583 / 9.02%
Mapped paired reads	73,166,343 / 90.98%
Mapped reads, first in pair	36,609,399 / 45.52%
Mapped reads, second in pair	36,556,944 / 45.46%
Mapped reads, both in pair	70,817,562 / 88.06%
Mapped reads, singletons	2,348,781 / 2.92%
Read min/max/mean length	30 / 151 / 148.2
Duplicated reads (flagged)	14,252,607 / 17.72%
Clipped reads	17,050,710 / 21.2%

2.2. ACGT Content

Number/percentage of A's	3,121,952,357 / 31.04%
Number/percentage of C's	1,905,567,191 / 18.95%
Number/percentage of T's	3,125,281,195 / 31.07%
Number/percentage of G's	1,905,319,832 / 18.94%
Number/percentage of N's	40,812 / 0%
GC Percentage	37.89%

2.3. Coverage

Mean	32.359
Standard Deviation	295.7687

2.4. Mapping Quality

Mean Mapping Quality	44.56

2.5. Insert size

Mean	261,958.94
Standard Deviation	2,474,000.11
P25/Median/P75	335 / 437 / 572

2.6. Mismatches and indels

General error rate	2.37%
Mismatches	218,106,596
Insertions	7,326,900
Mapped reads with at least one insertion	8.91%
Deletions	6,997,955
Mapped reads with at least one deletion	8.47%
Homopolymer indels	57.3%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	800507518	26.931	115.5587

LT669789.1	36598175	1160903127	31.7202	303.3409
LT669790.1	30422129	1211998497	39.8394	435.1231
LT669791.1	52758100	1688398099	32.0026	320.9109
LT669792.1	28376109	945793335	33.3306	319.7834
LT669793.1	33388210	982800414	29.4356	187.18
LT669794.1	50579949	1504672987	29.7484	234.8306
LT669795.1	49795044	1789352476	35.9343	330.5209

3. Results : Coverage across reference

4. Results : Coverage Histogram

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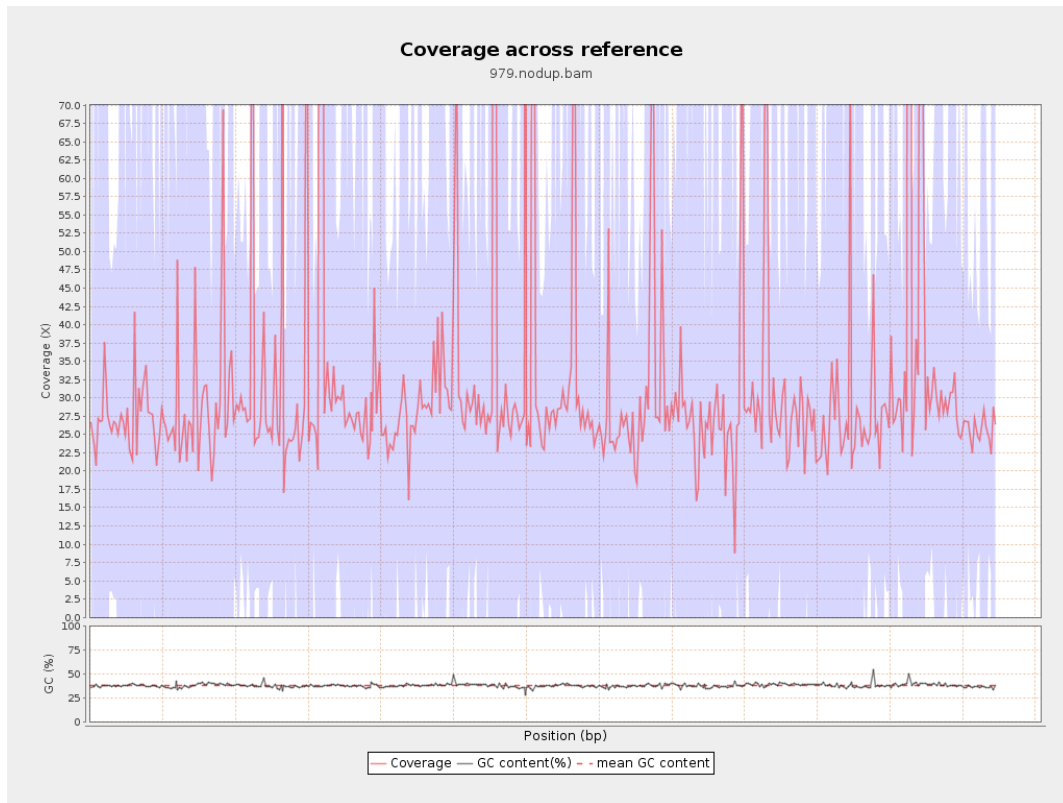
5. Results : Coverage Histogram (0-50X)
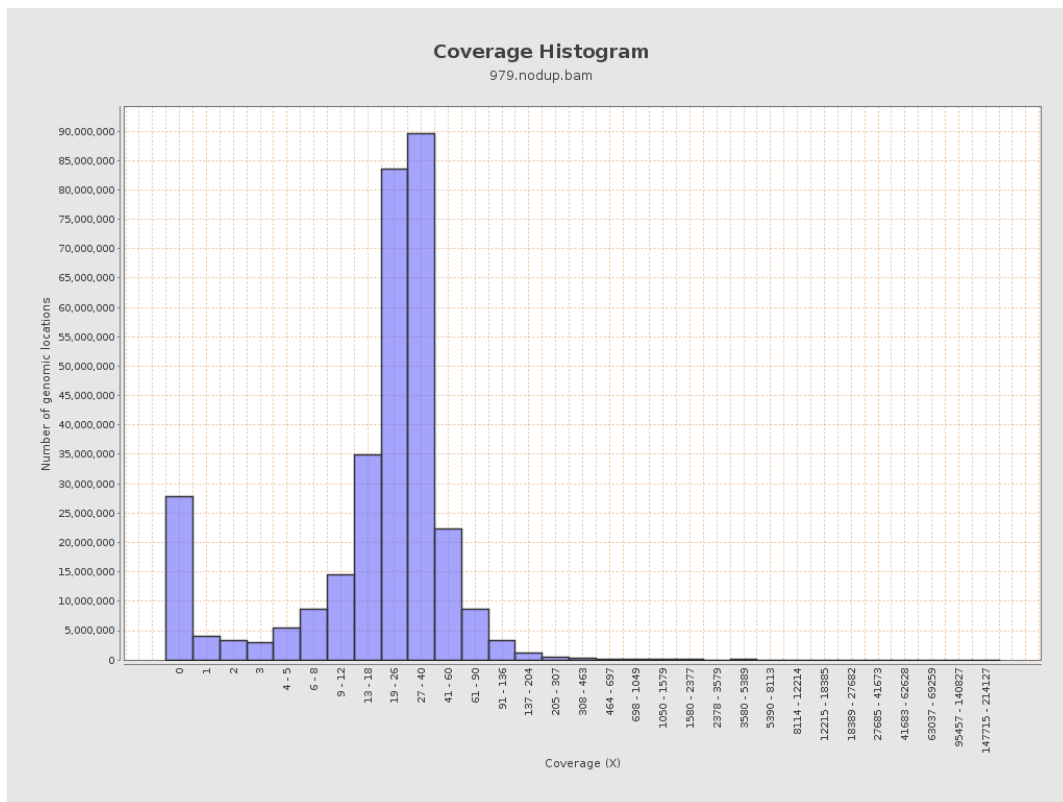
Coverage Histogram (0-50X)
979.nodup.bam
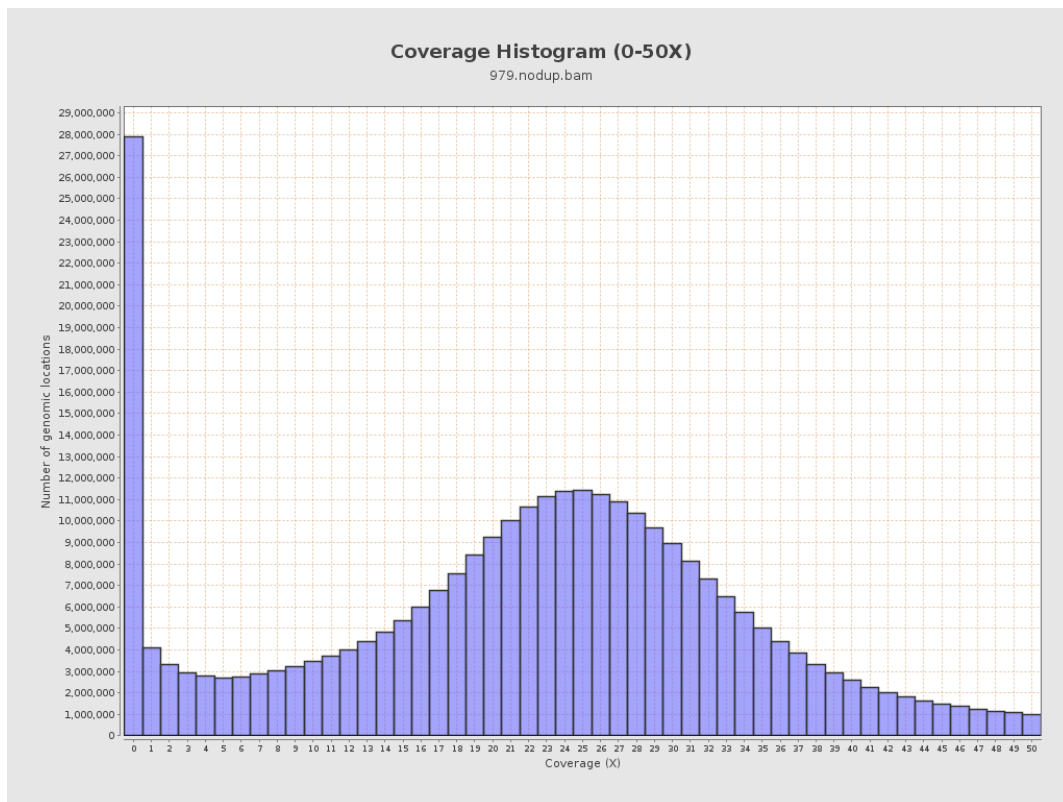
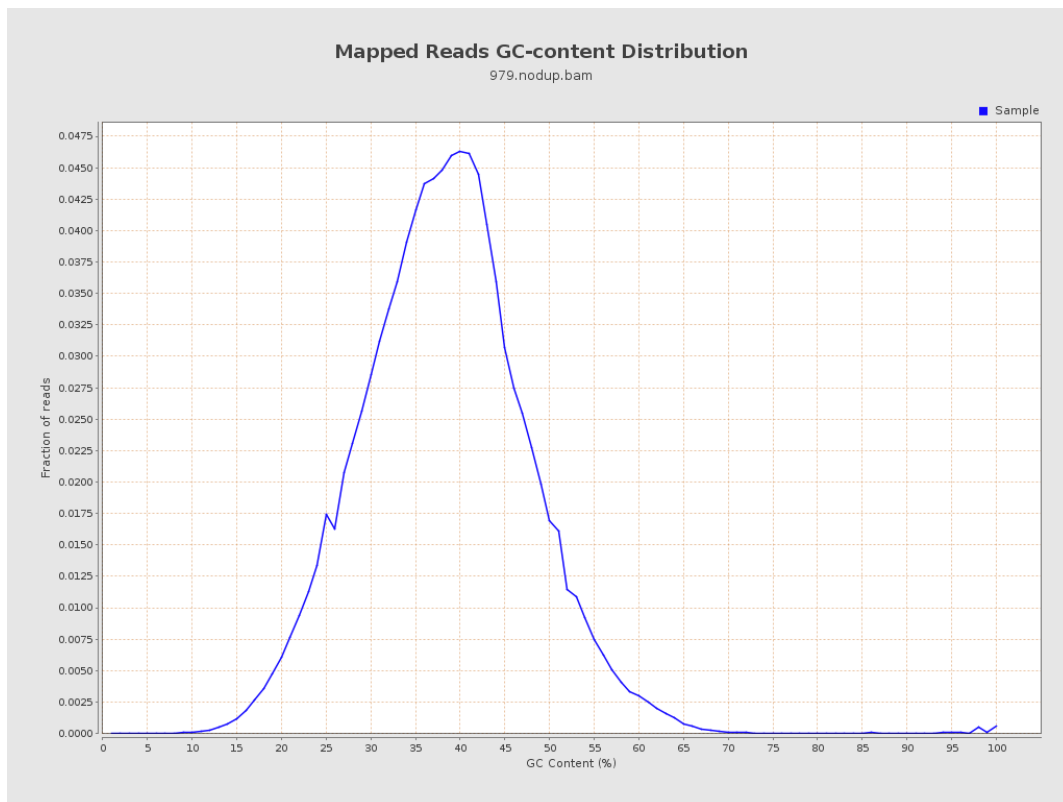# 6. Results : Genome Fraction Coverage
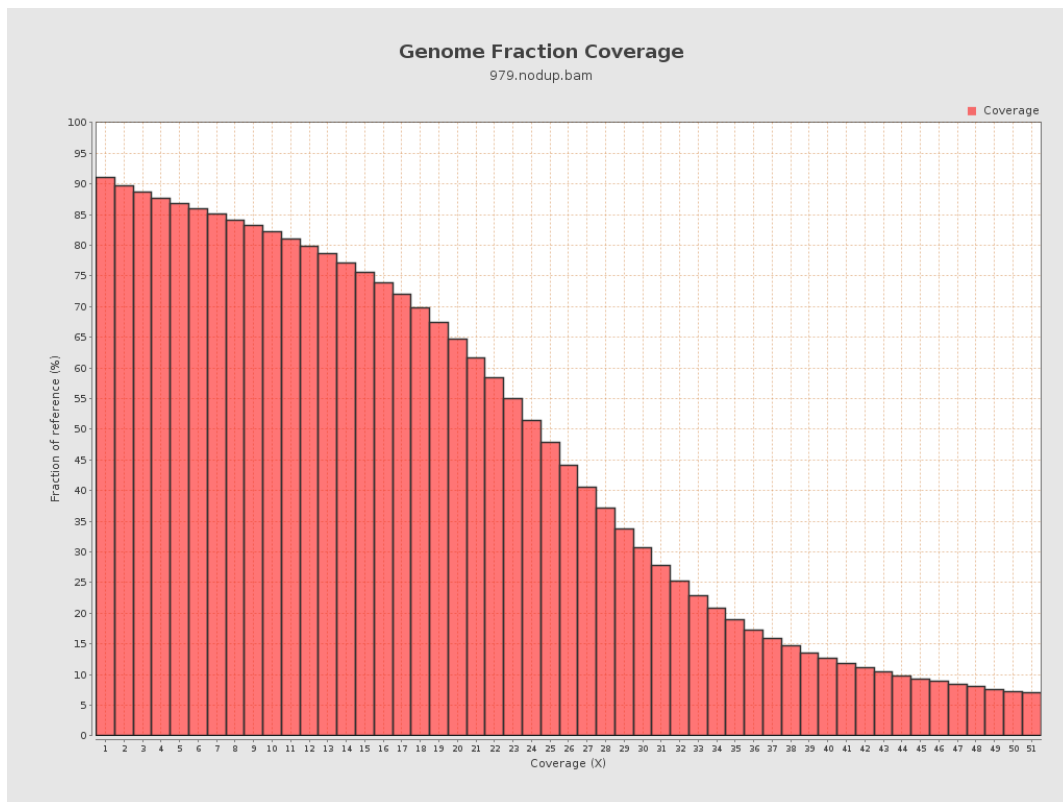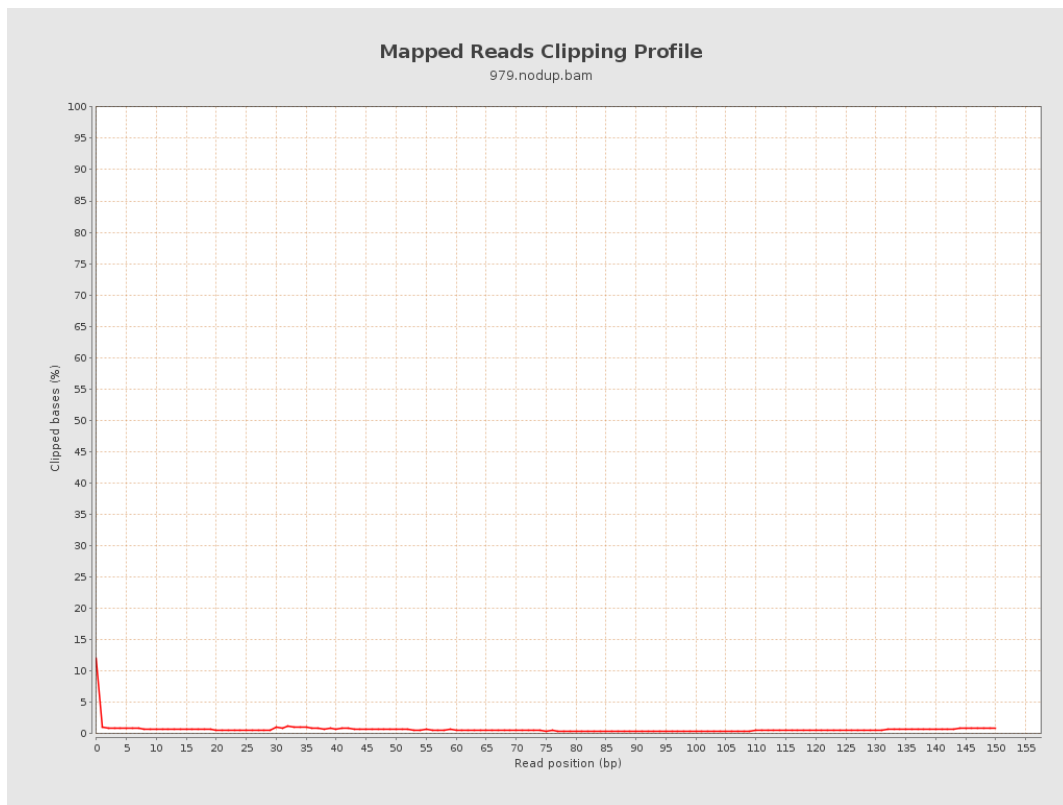
7. Results : Duplication Rate Histogram
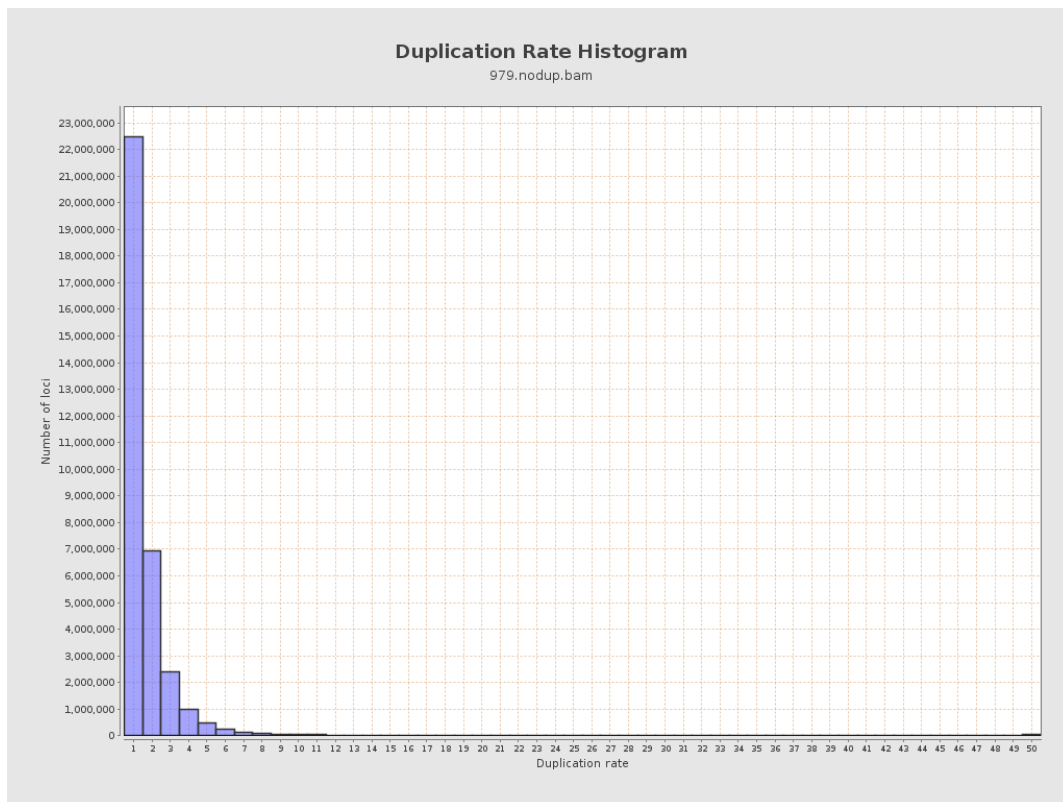
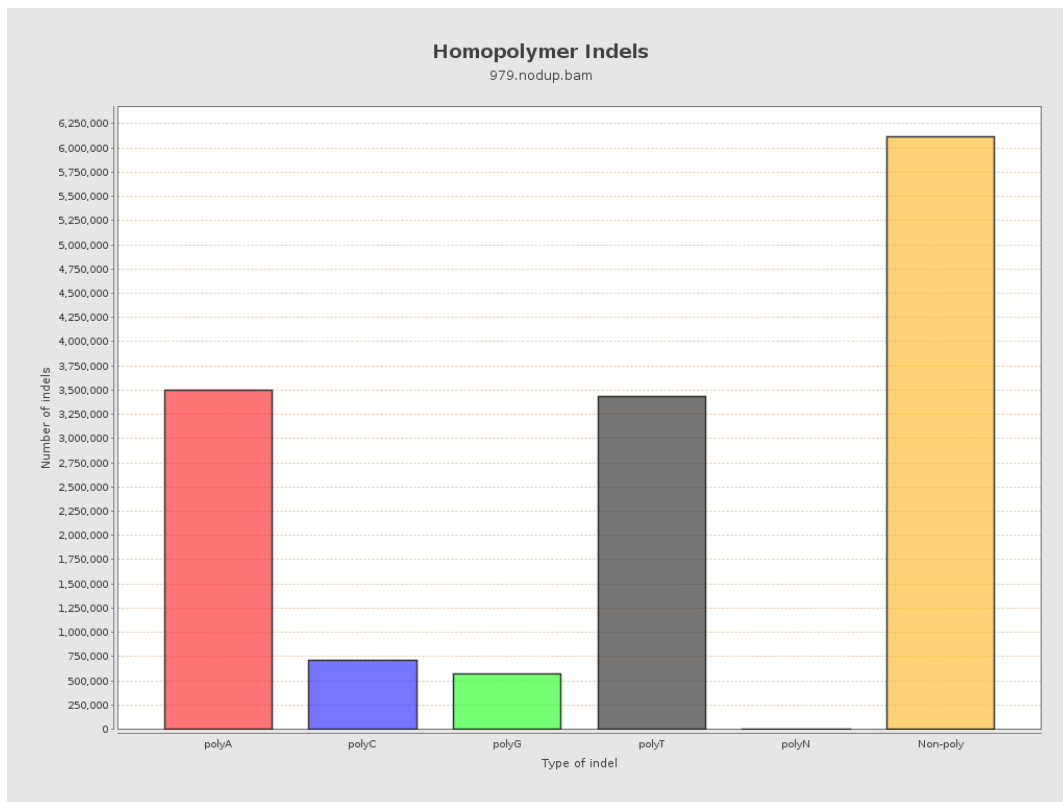# 8. Results : Mapped Reads Nucleotide Content
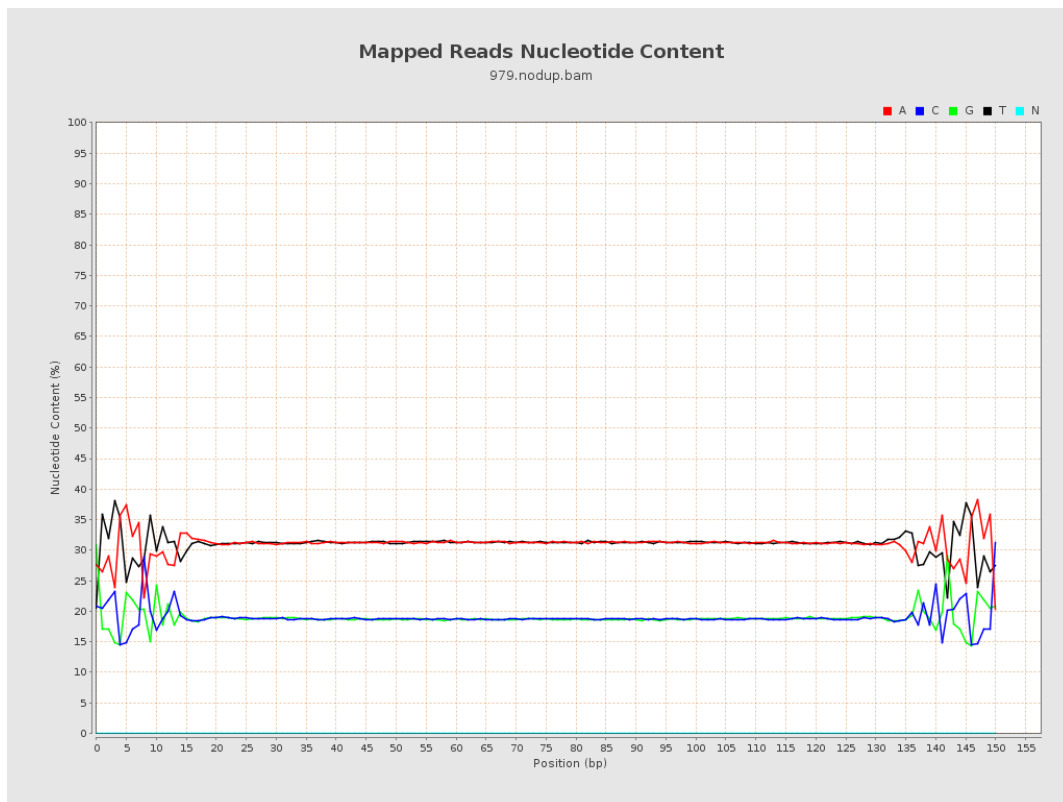
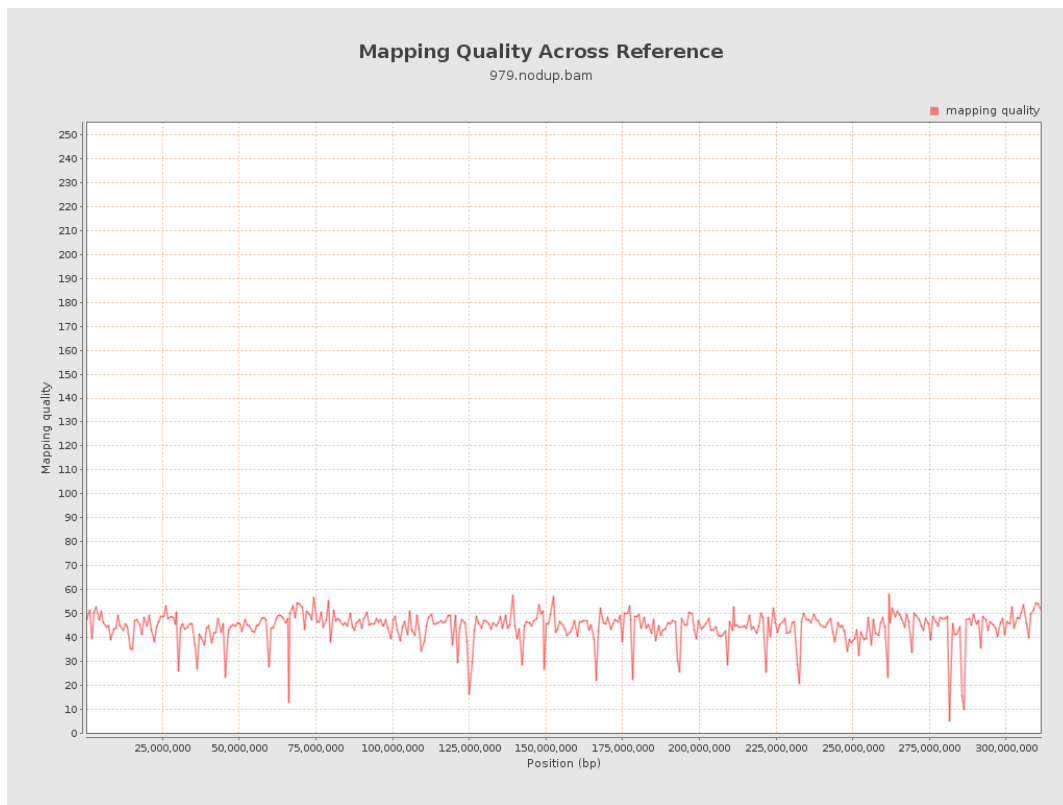# 9. Results : Mapped Reads GC-content Distribution
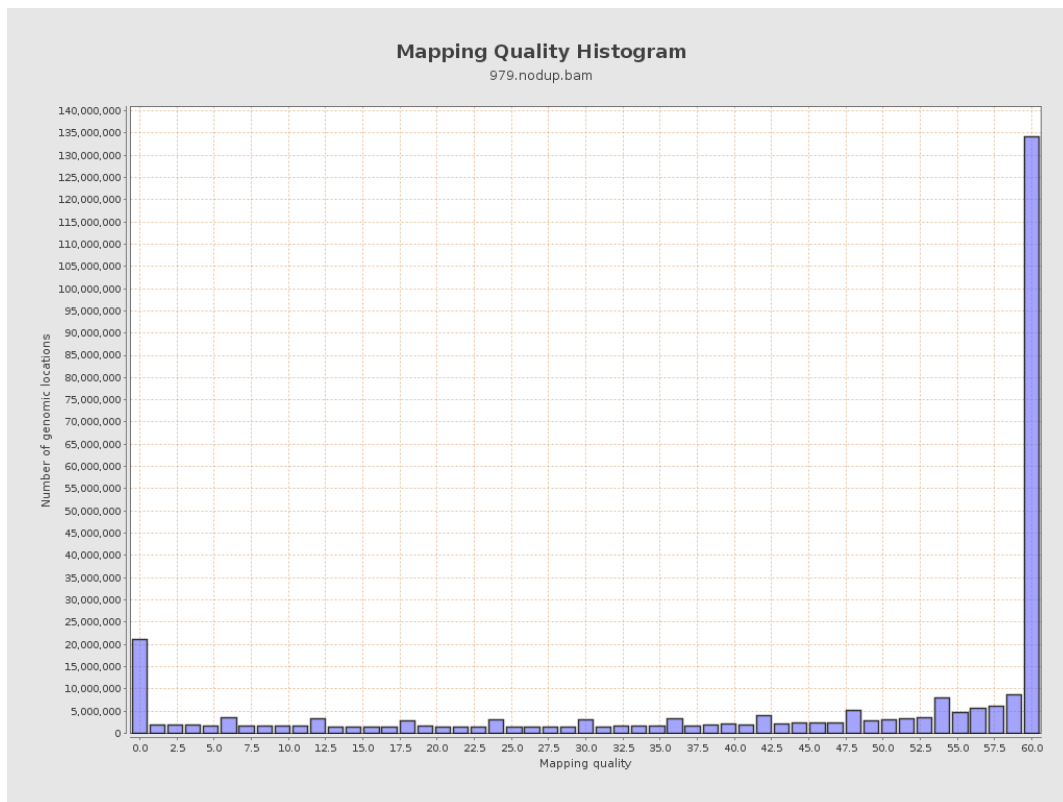
10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels

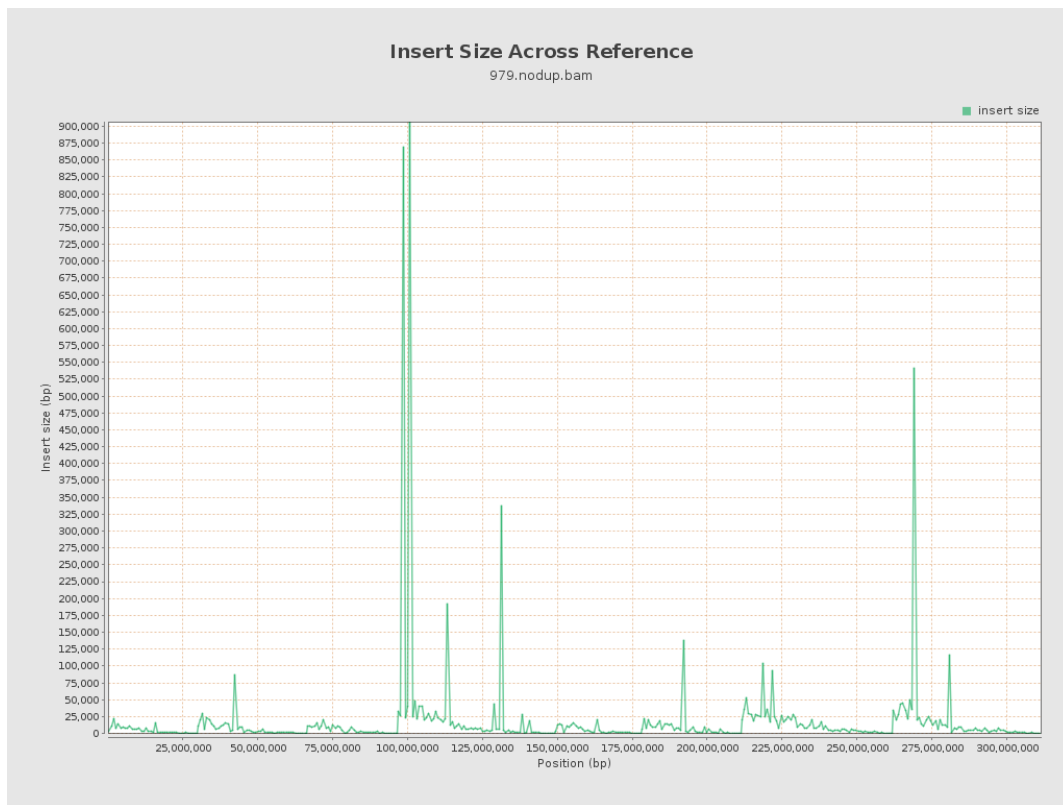# 12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
979.nodup.bam

14. Results : Insert Size Across Reference

Insert Size Across Reference
979.nodup.bam

15. Results : Insert Size Histogram