Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:31:28

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/493
.nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/493 .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_410/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_410_S385_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_410/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_410_S385_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:31:27 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	65,848,940
Mapped reads	62,536,758 / 94.97%
Unmapped reads	3,312,182 / 5.03%
Mapped paired reads	62,536,758 / 94.97%
Mapped reads, first in pair	31,296,512 / 47.53%
Mapped reads, second in pair	31,240,246 / 47.44%
Mapped reads, both in pair	61,416,893 / 93.27%
Mapped reads, singletons	1,119,865 / 1.7%
Read min/max/mean length	30 / 151 / 148.3
Duplicated reads (flagged)	9,262,339 / 14.07%
Clipped reads	12,981,711 / 19.71%

2.2. ACGT Content

Number/percentage of A's	2,692,956,195 / 30.79%
Number/percentage of C's	1,683,109,944 / 19.24%
Number/percentage of T's	2,696,850,742 / 30.83%
Number/percentage of G's	1,673,760,112 / 19.14%
Number/percentage of N's	28,628 / 0%
GC Percentage	38.38%

2.3. Coverage

Mean	28.1349
Standard Deviation	217.472

2.4. Mapping Quality

Mean Mapping Quality	44.73

2.5. Insert size

Mean	218,520.17
Standard Deviation	2,220,764.76
P25/Median/P75	349 / 455 / 596

2.6. Mismatches and indels

General error rate	2.25%
Mismatches	181,083,157
Insertions	5,567,270
Mapped reads with at least one insertion	8.03%
Deletions	5,673,052
Mapped reads with at least one deletion	8.08%
Homopolymer indels	56.24%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	683871928	23.0071	53.378

LT669789.1	36598175	1009818535	27.592	221.0267
LT669790.1	30422129	893524675	29.3709	192.0487
LT669791.1	52758100	1466960438	27.8054	183.2602
LT669792.1	28376109	784018457	27.6295	254.9632
LT669793.1	33388210	854238995	25.585	106.5839
LT669794.1	50579949	1349033766	26.6713	187.1055
LT669795.1	49795044	1726550150	34.6731	346.3801

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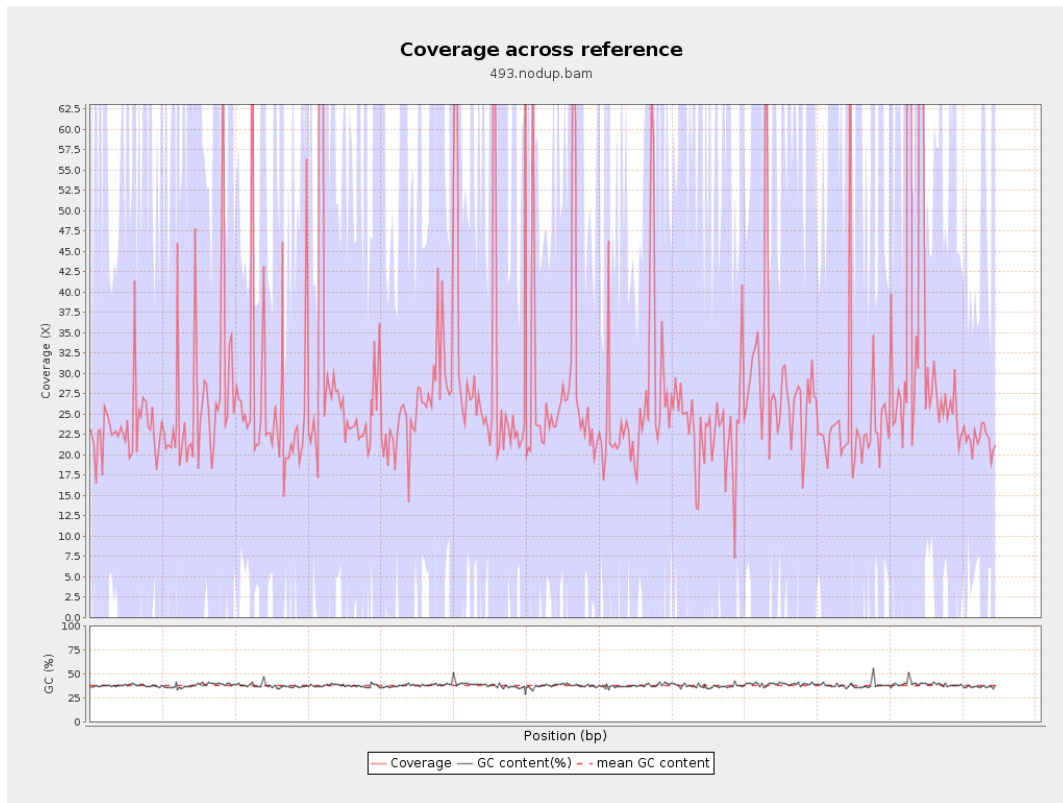
4. Results : Coverage Histogram
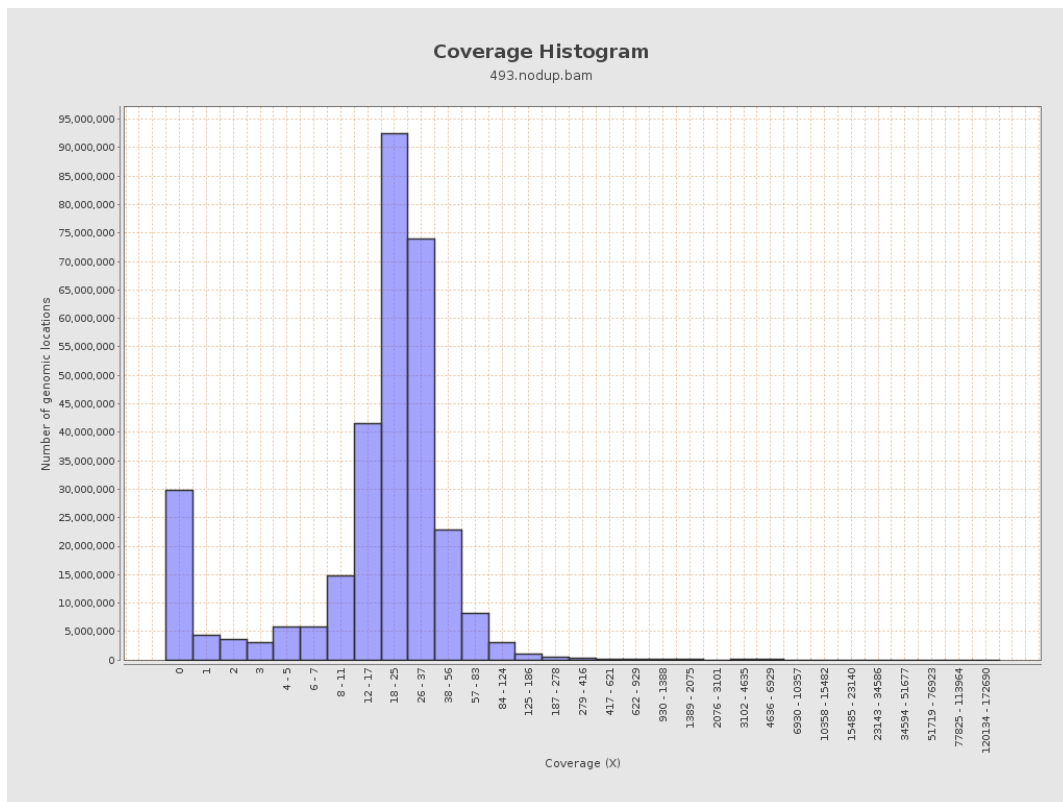
5. Results : Coverage Histogram (0-50X)
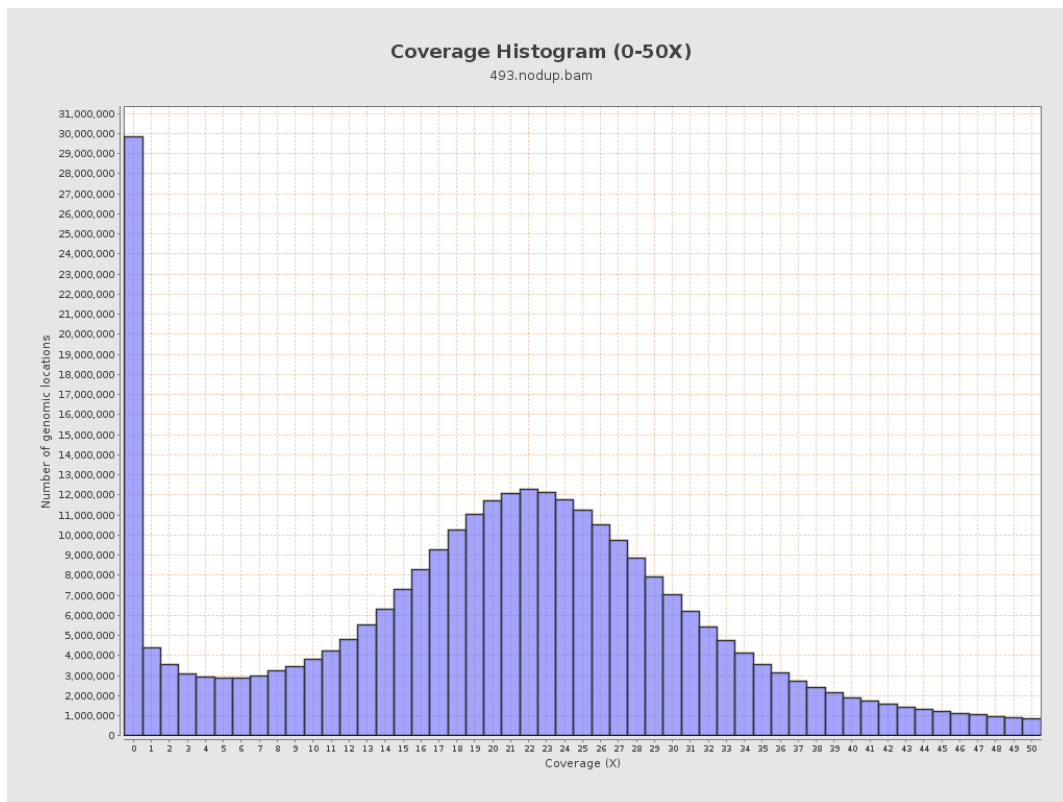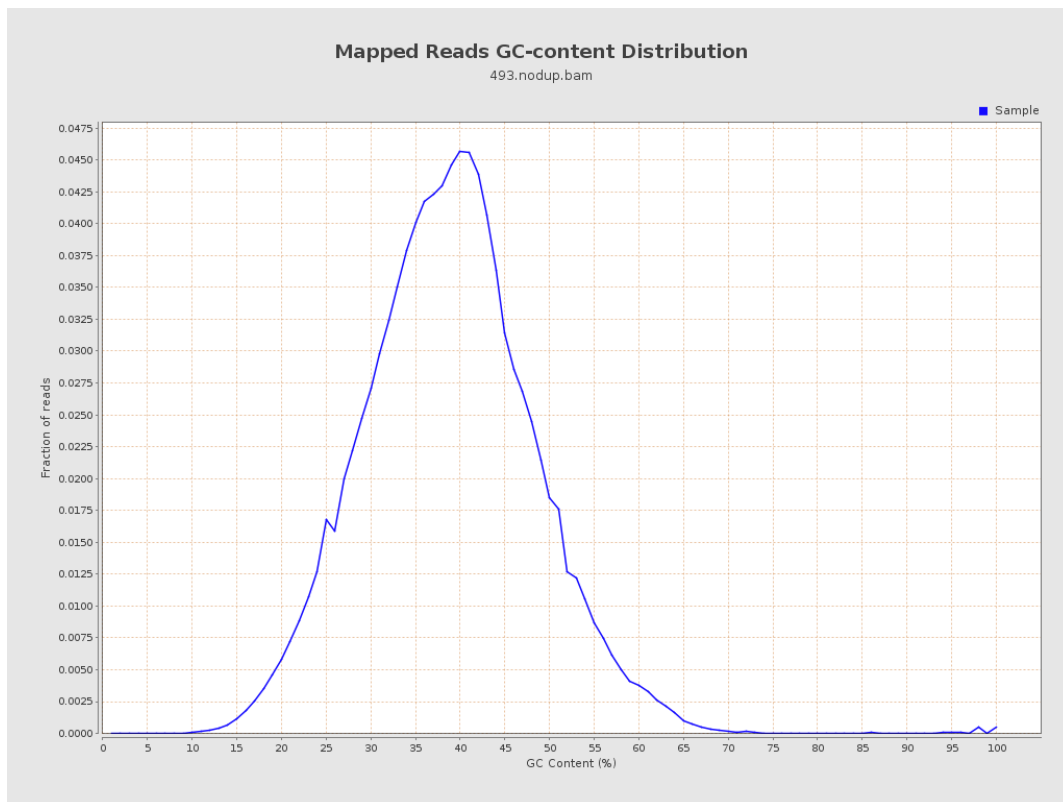
6. Results : Genome Fraction Coverage
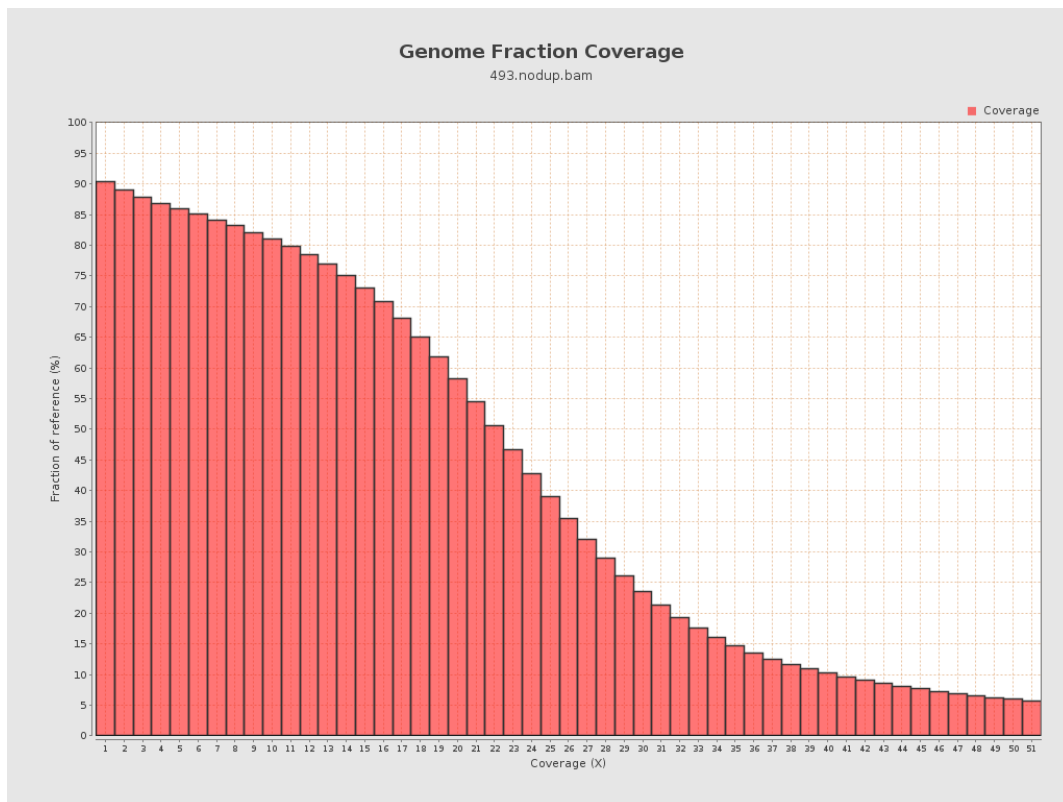
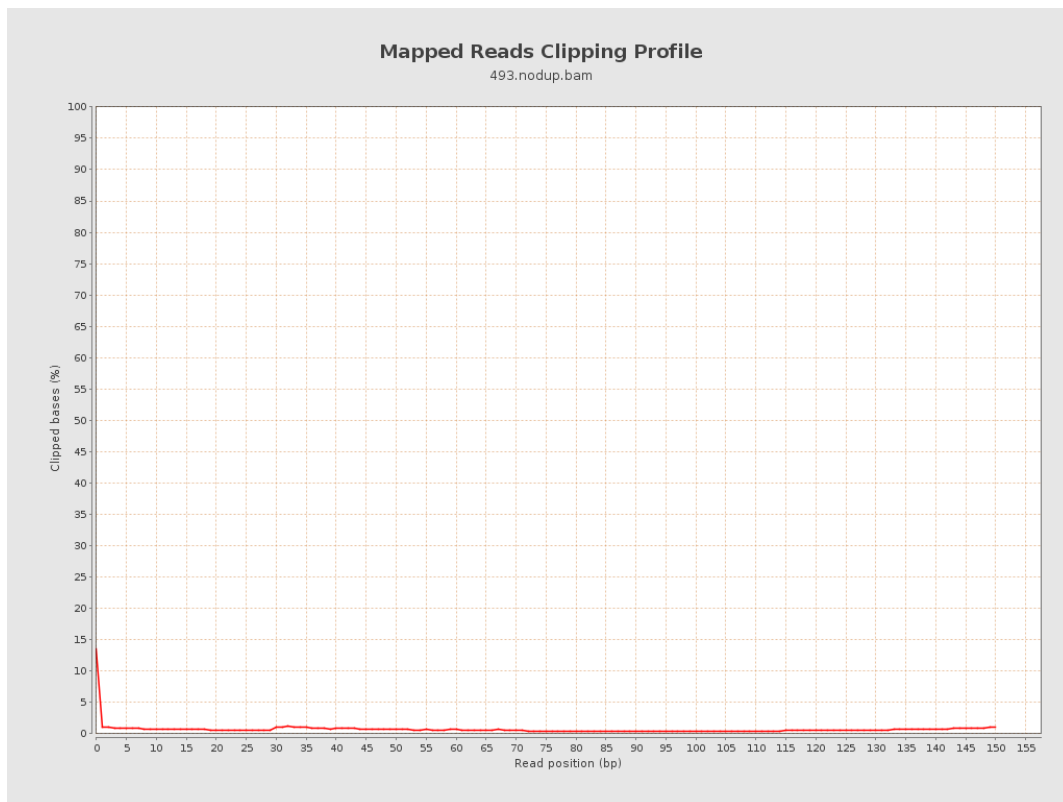# 7. Results : Duplication Rate Histogram
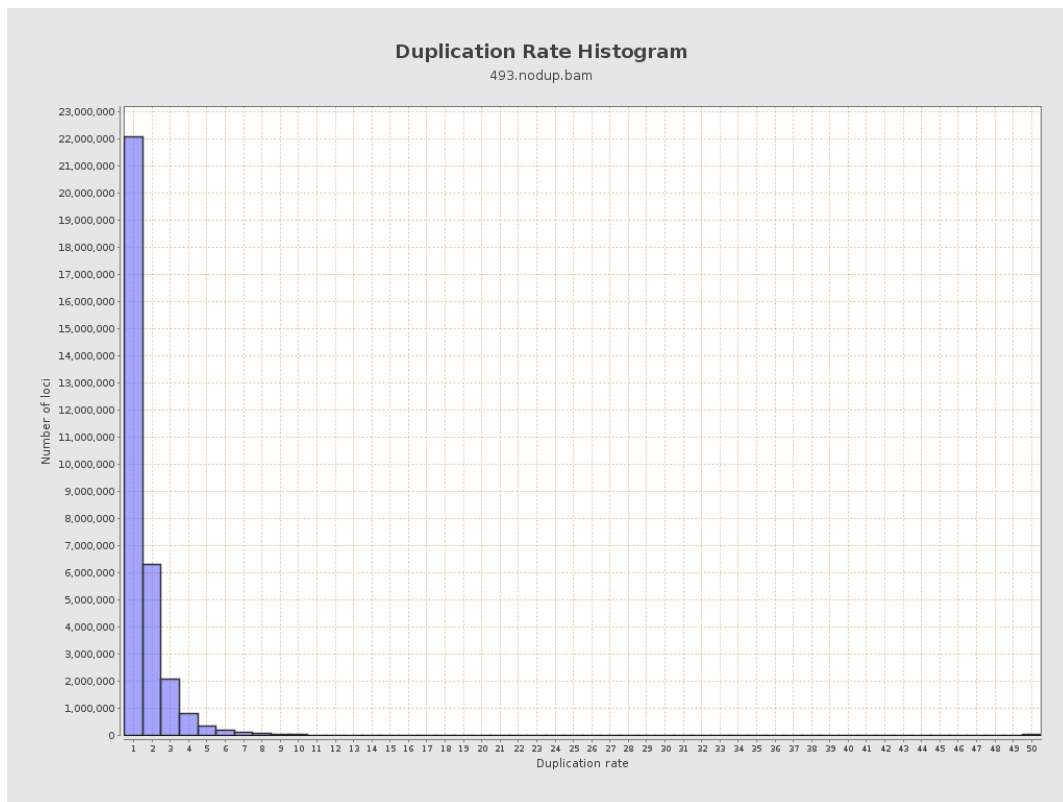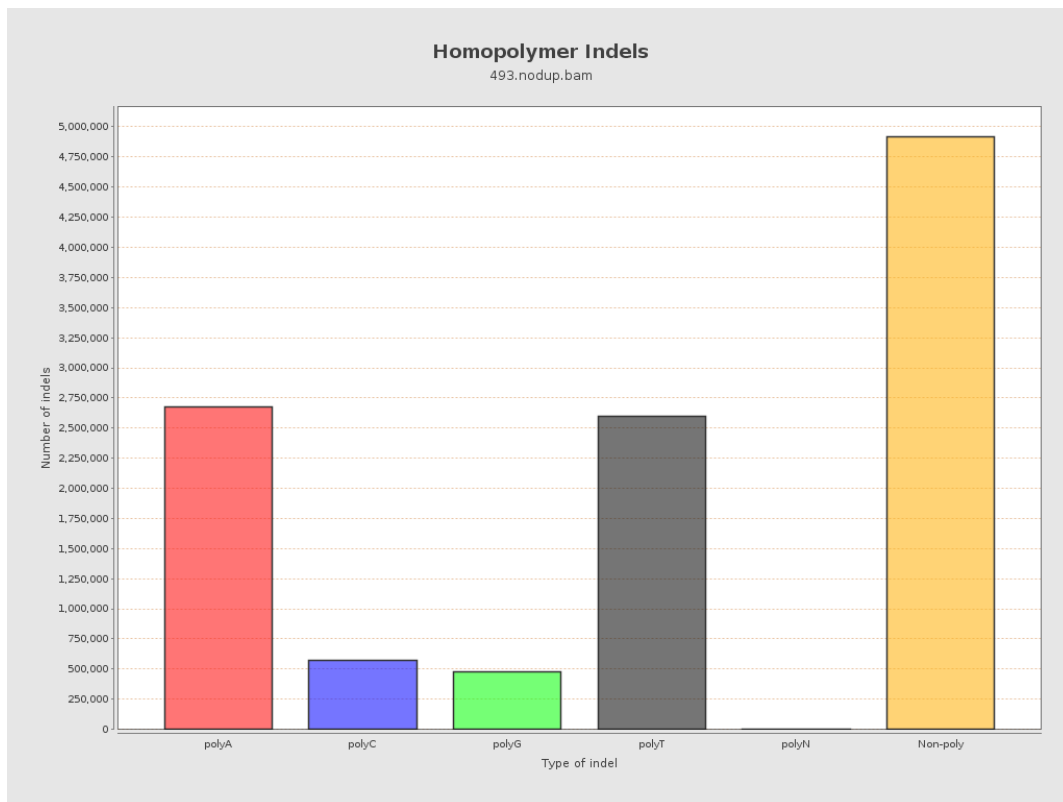
8. Results : Mapped Reads Nucleotide Content
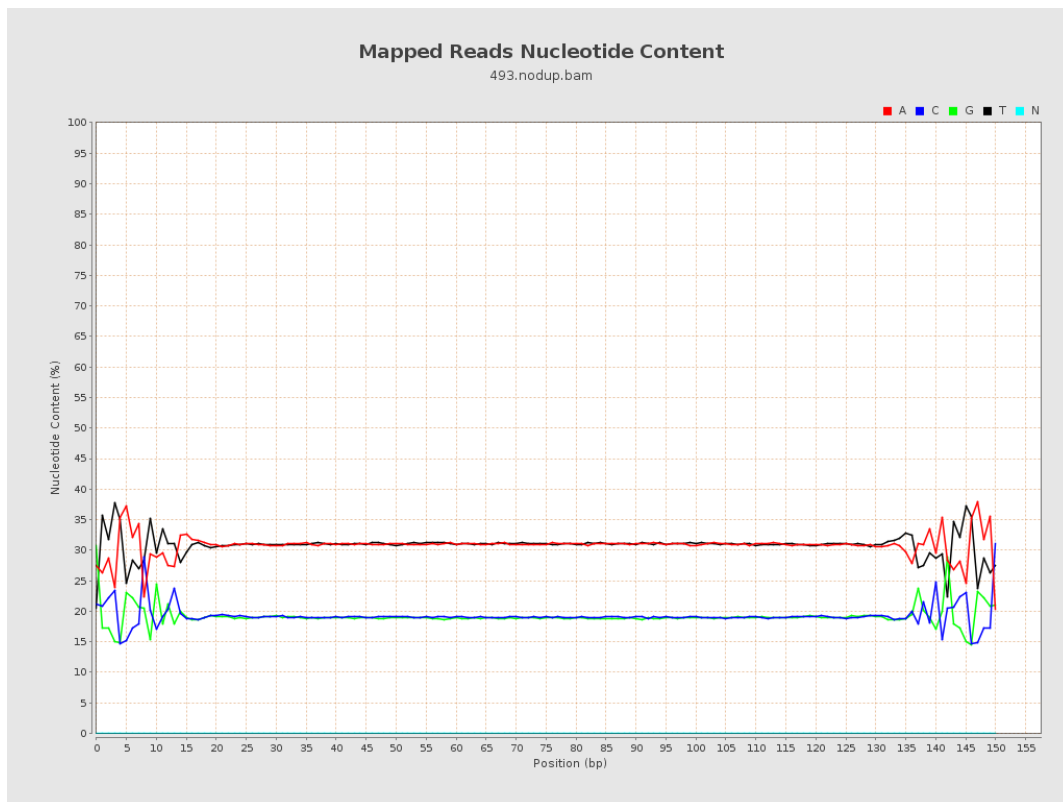
9. Results : Mapped Reads GC-content Distribution
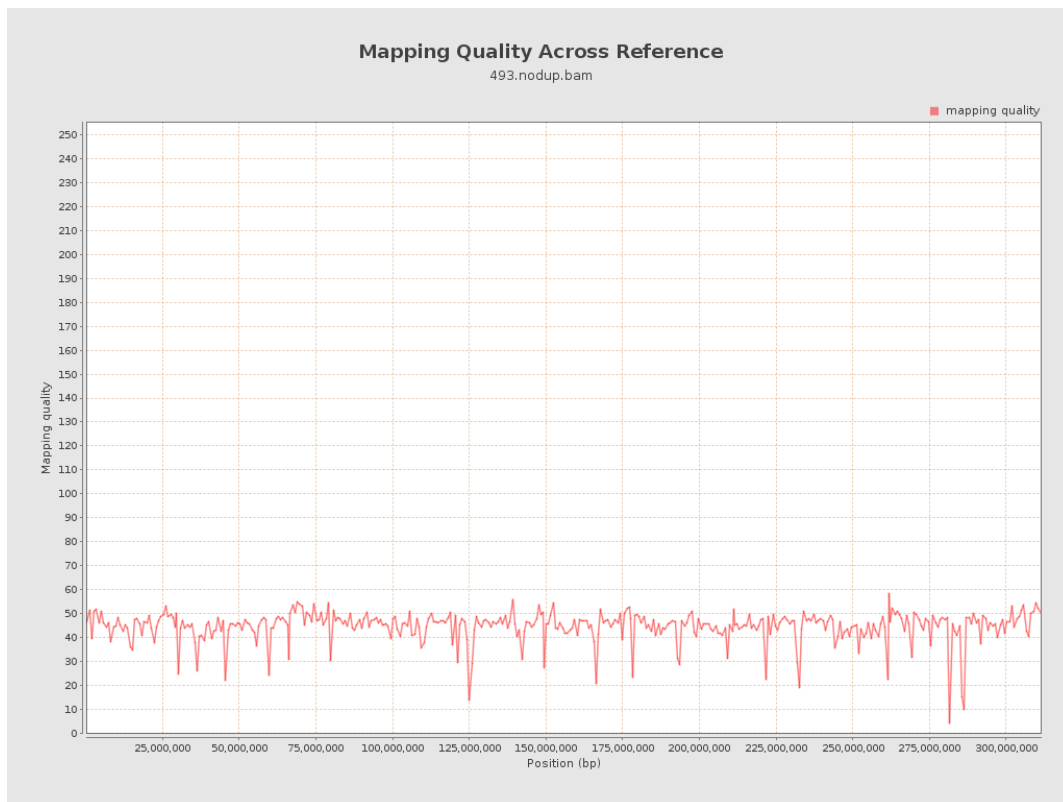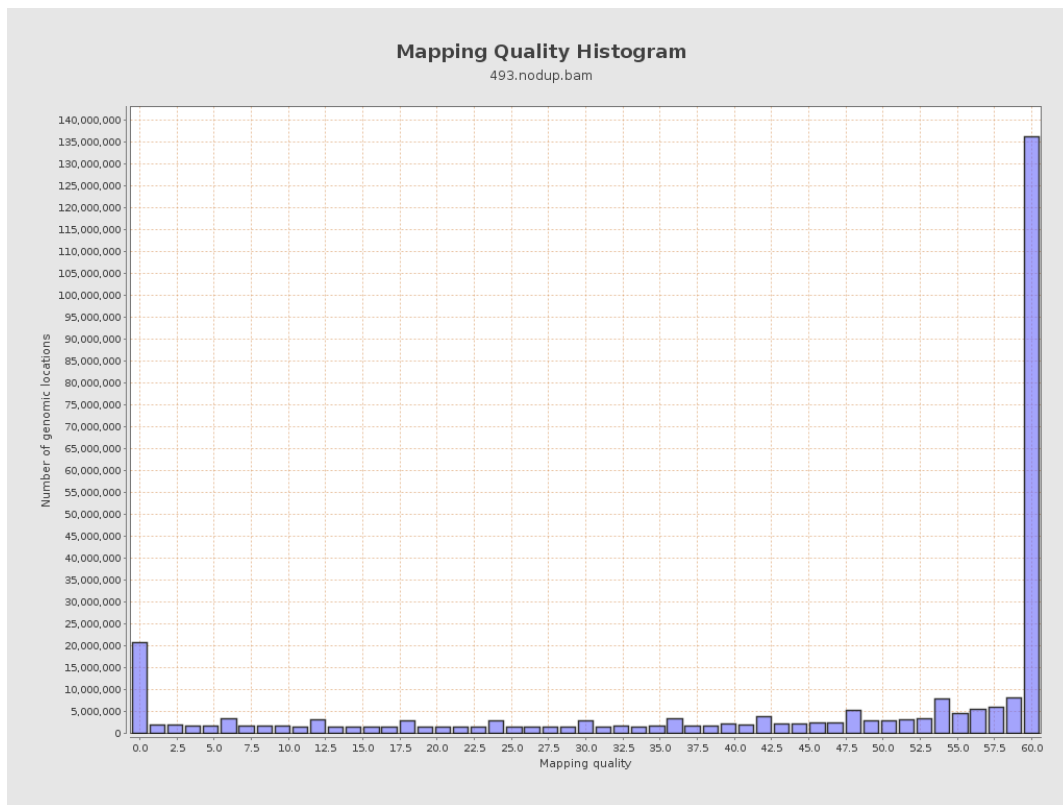
10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels

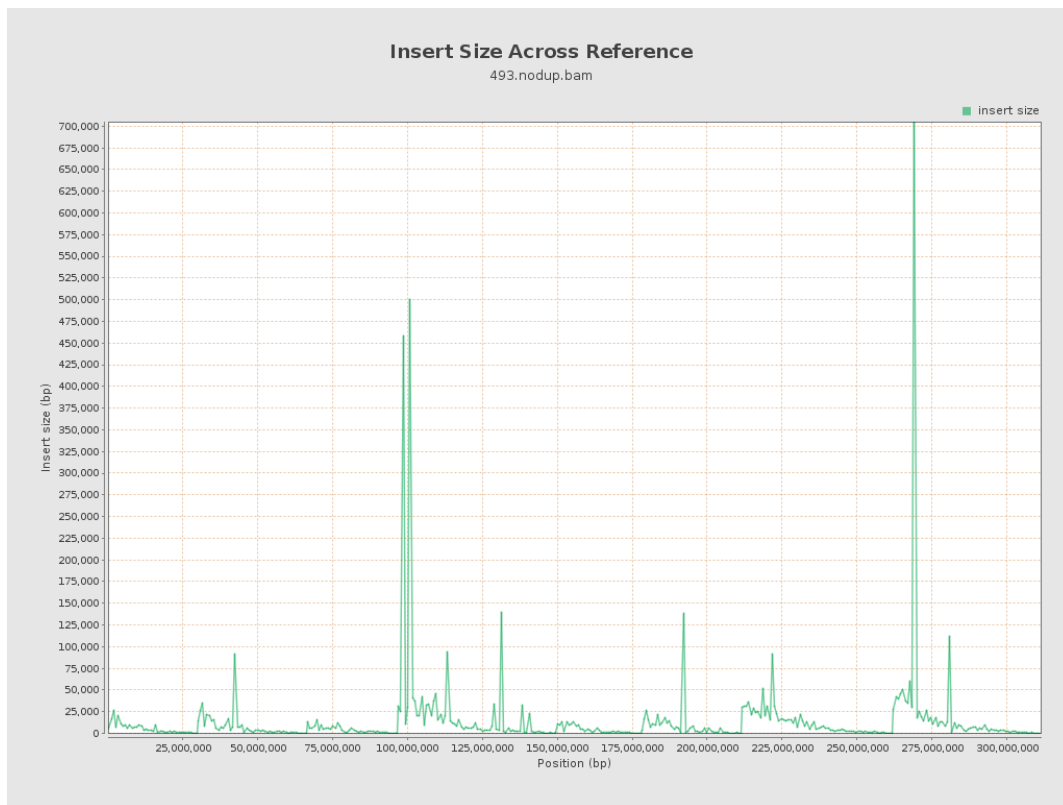# 12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
493.nodup.bam

14. Results : Insert Size Across Reference

Insert Size Across Reference
493.nodup.bam

15. Results : Insert Size Histogram

Insert Size Histogram
493.nodup.bam