Qualimap Analysis Results

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

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/808
.nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/808 .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_158/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_158_S248_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_158/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_158_S248_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:30:28 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	63,844,787
Mapped reads	60,387,628 / 94.59%
Unmapped reads	3,457,159 / 5.41%
Mapped paired reads	60,387,628 / 94.59%
Mapped reads, first in pair	30,243,172 / 47.37%
Mapped reads, second in pair	30,144,456 / 47.22%
Mapped reads, both in pair	59,233,866 / 92.78%
Mapped reads, singletons	1,153,762 / 1.81%
Read min/max/mean length	30 / 151 / 148.02
Duplicated reads (flagged)	9,753,637 / 15.28%
Clipped reads	13,754,028 / 21.54%

2.2. ACGT Content

Number/percentage of A's	2,579,856,796 / 30.85%
Number/percentage of C's	1,602,052,720 / 19.16%
Number/percentage of T's	2,583,067,618 / 30.89%
Number/percentage of G's	1,596,822,247 / 19.1%
Number/percentage of N's	35,718 / 0%
GC Percentage	38.26%

2.3. Coverage

Mean	26.9018
Standard Deviation	230.0652

2.4. Mapping Quality

Mean Mapping Quality	43.97

2.5. Insert size

Mean	231,333.4
Standard Deviation	2,267,145.5
P25/Median/P75	329 / 437 / 580

2.6. Mismatches and indels

General error rate	2.32%
Mismatches	178,793,693
Insertions	5,643,479
Mapped reads with at least one insertion	8.41%
Deletions	5,824,364
Mapped reads with at least one deletion	8.56%
Homopolymer indels	56.18%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	624835423	21.021	60.717

LT669789.1	36598175	1009392479	27.5804	230.2048
LT669790.1	30422129	843637259	27.731	207.3122
LT669791.1	52758100	1404973059	26.6305	181.3451
LT669792.1	28376109	737508435	25.9905	241.4218
LT669793.1	33388210	840398150	25.1705	159.6594
LT669794.1	50579949	1311671099	25.9326	201.5995
LT669795.1	49795044	1611313064	32.3589	370.6318

3. Results : Coverage across reference

Coverage across reference
808.nodup.bam

4. Results : Coverage Histogram

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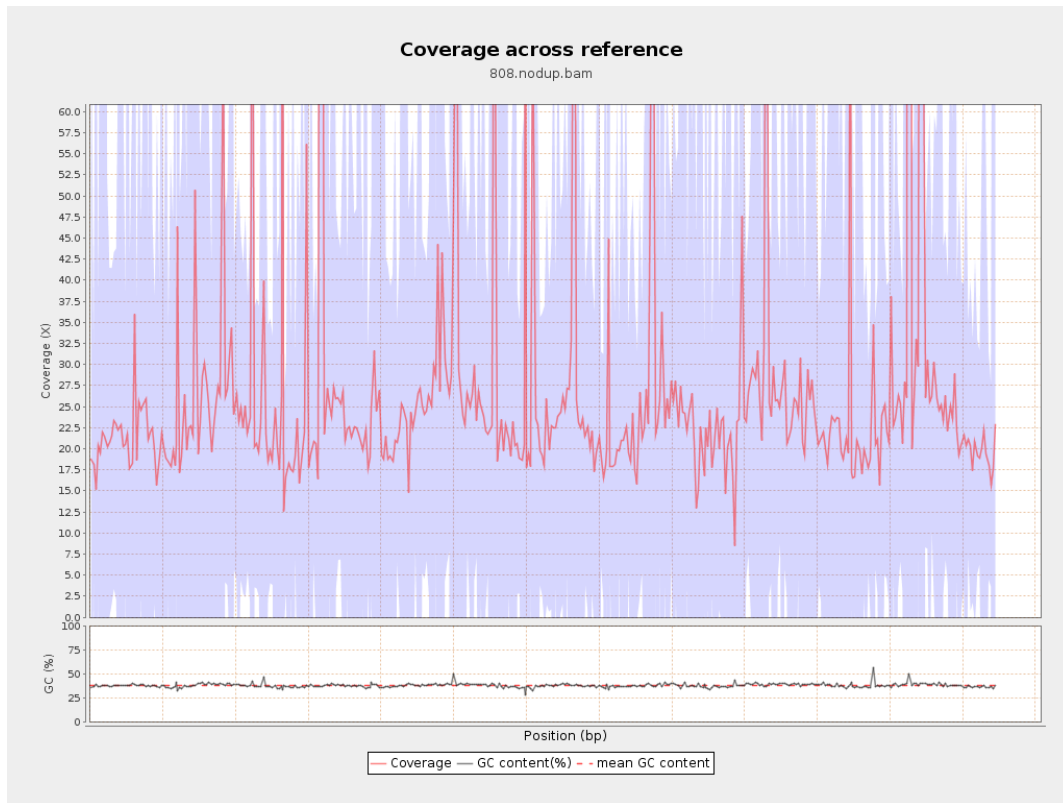
5. Results : Coverage Histogram (0-50X)
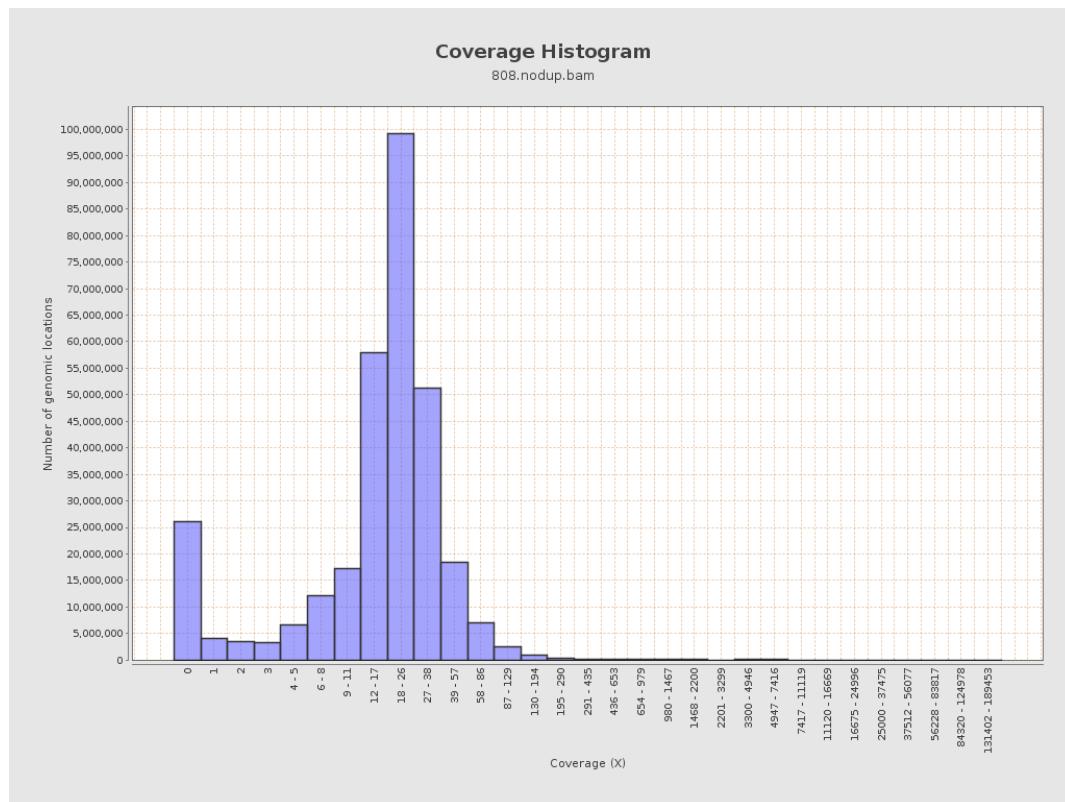
Coverage Histogram (0-50X)
808.nodup.bam
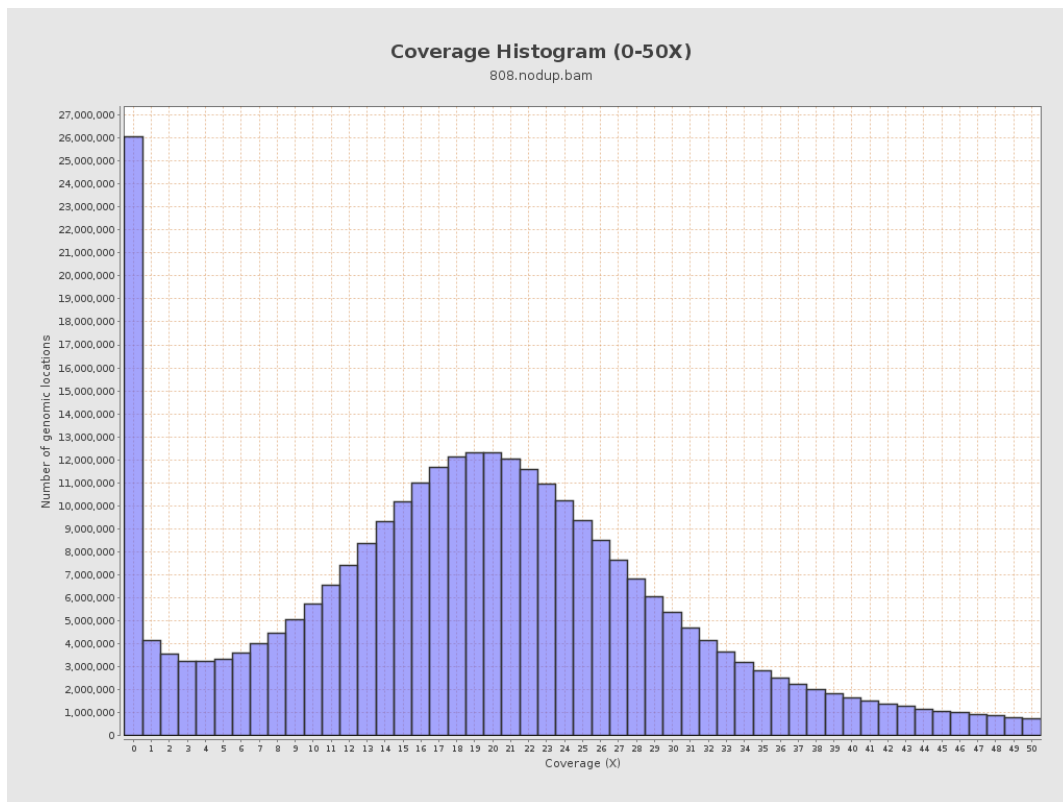
6. Results : Genome Fraction Coverage
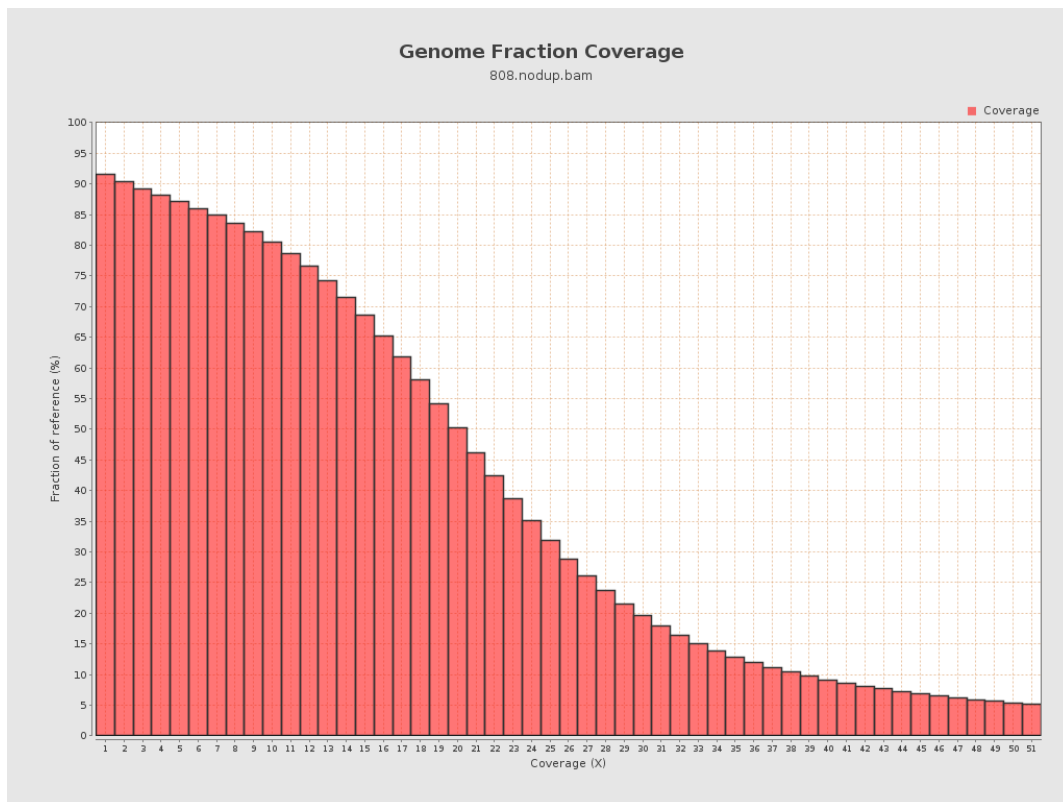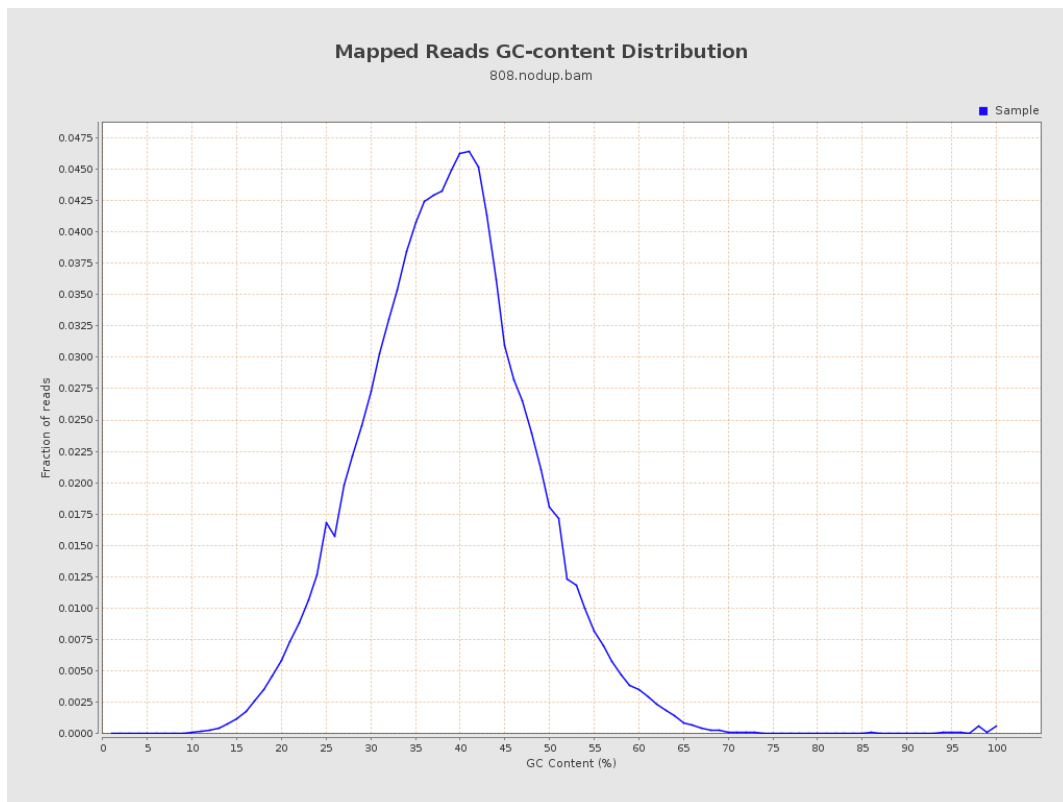
7. Results : Duplication Rate Histogram

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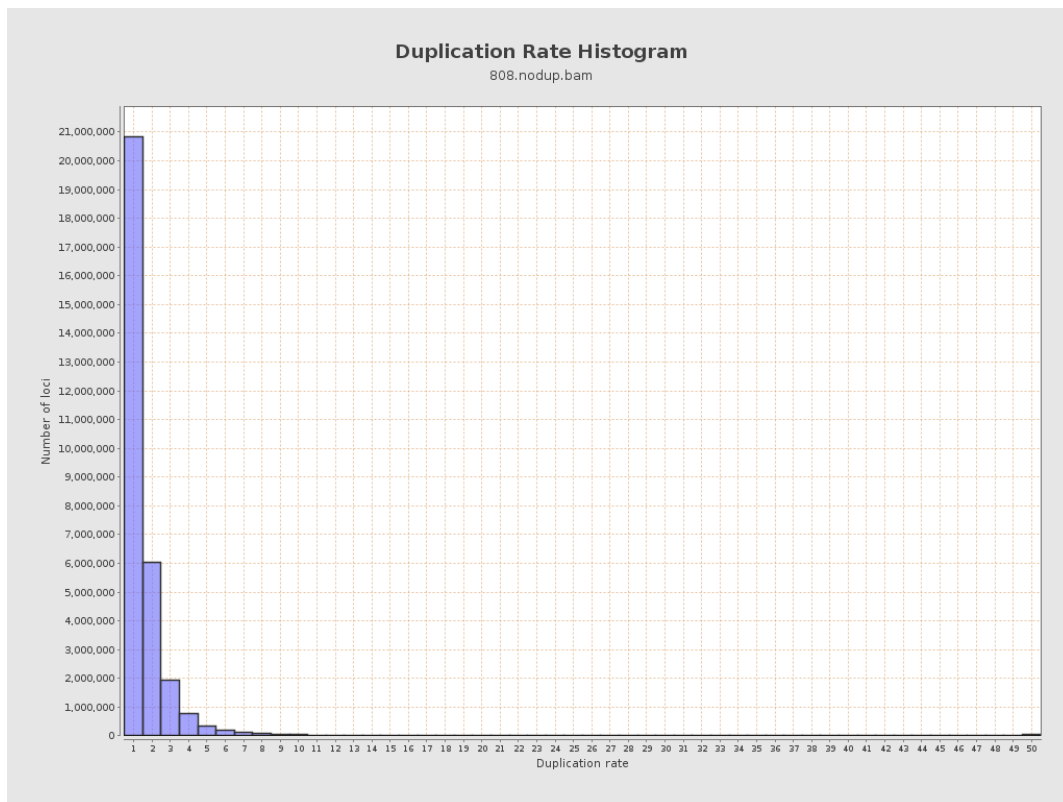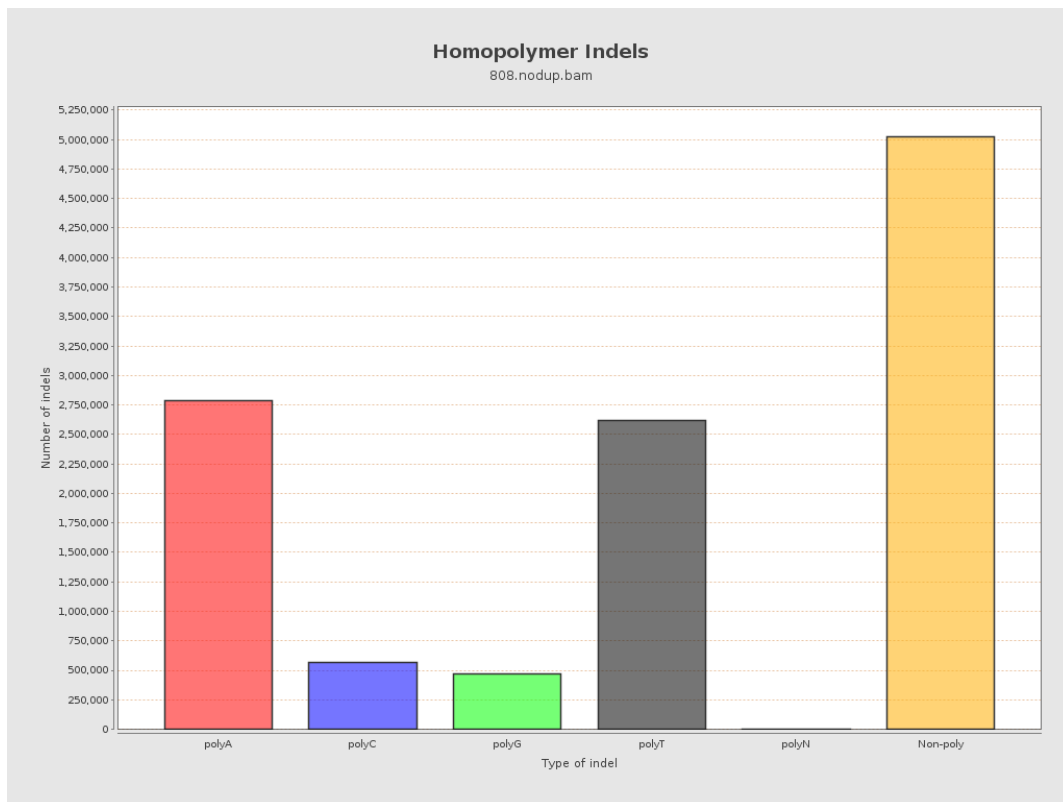
8. Results : Mapped Reads Nucleotide Content
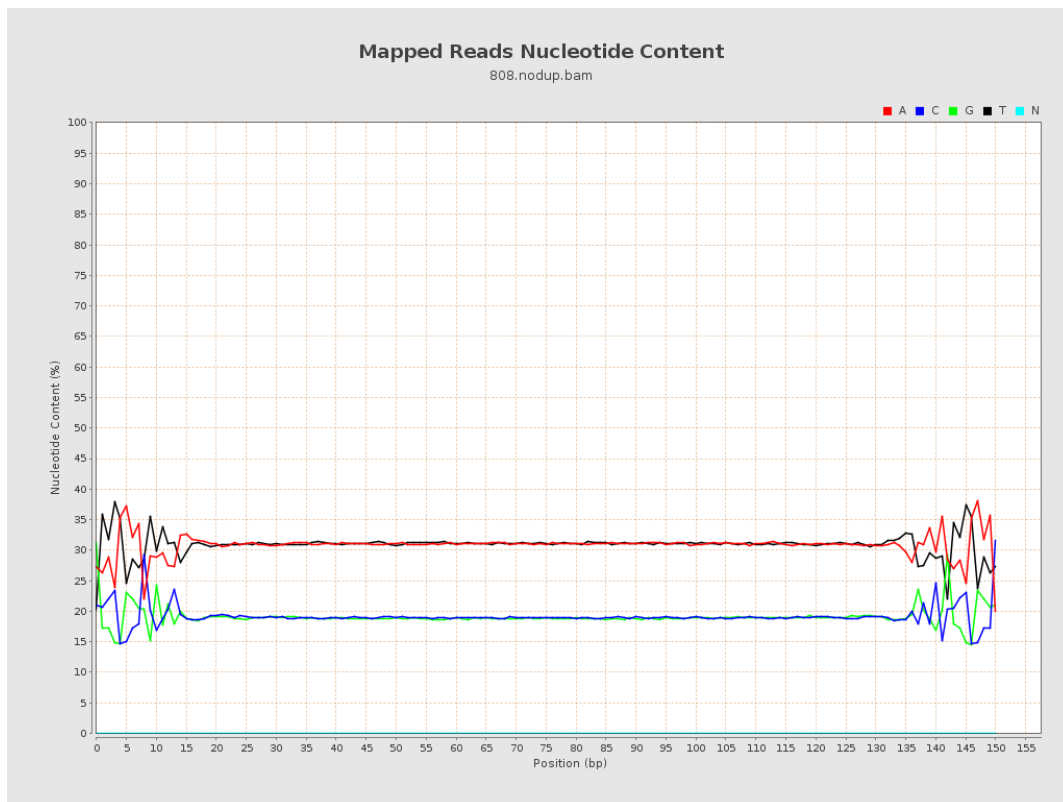
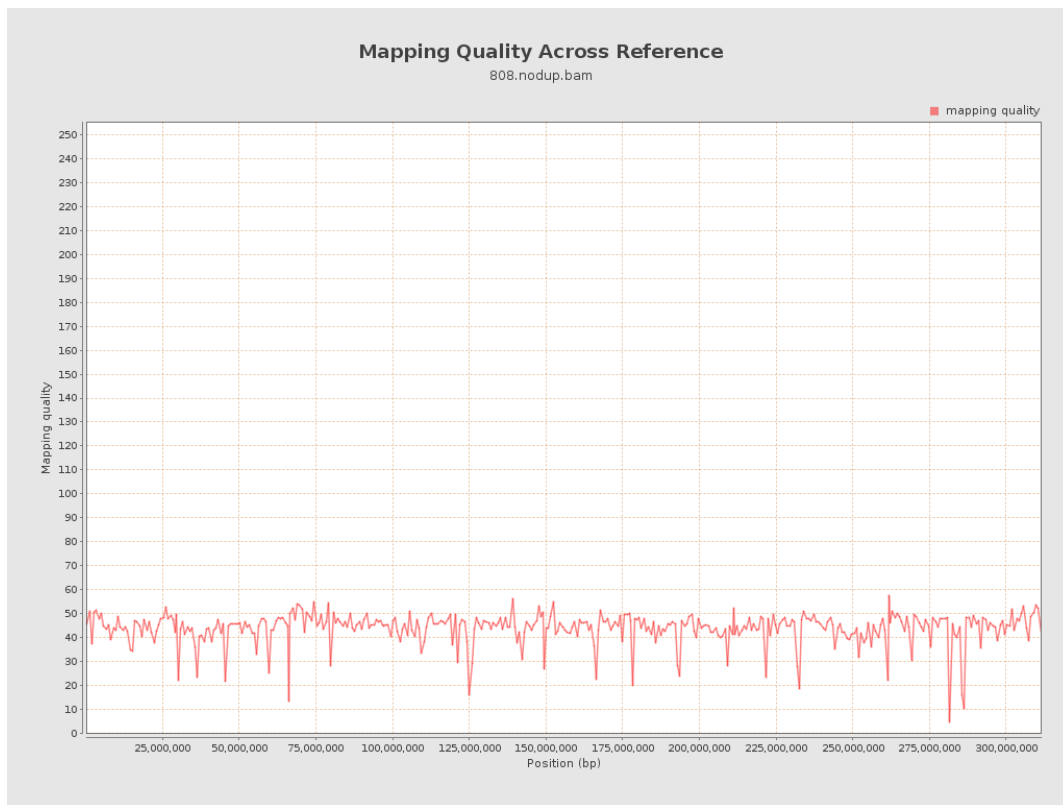# 9. Results : Mapped Reads GC-content Distribution

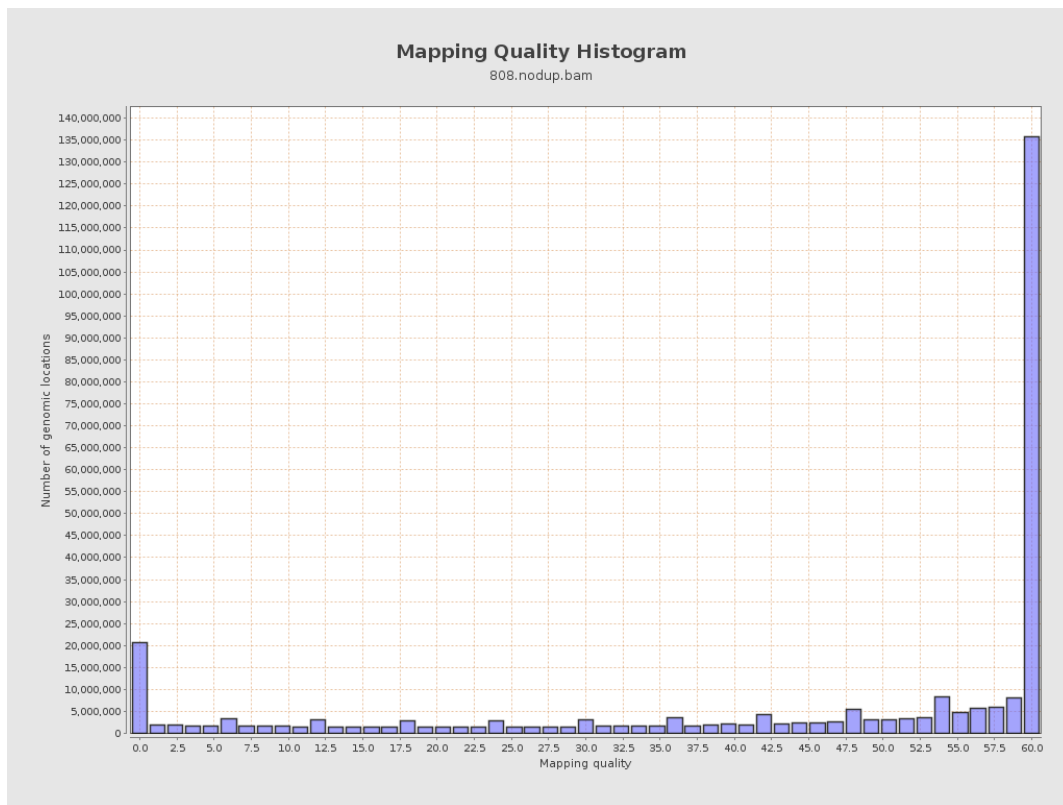# 10. Results : Mapped Reads Clipping Profile
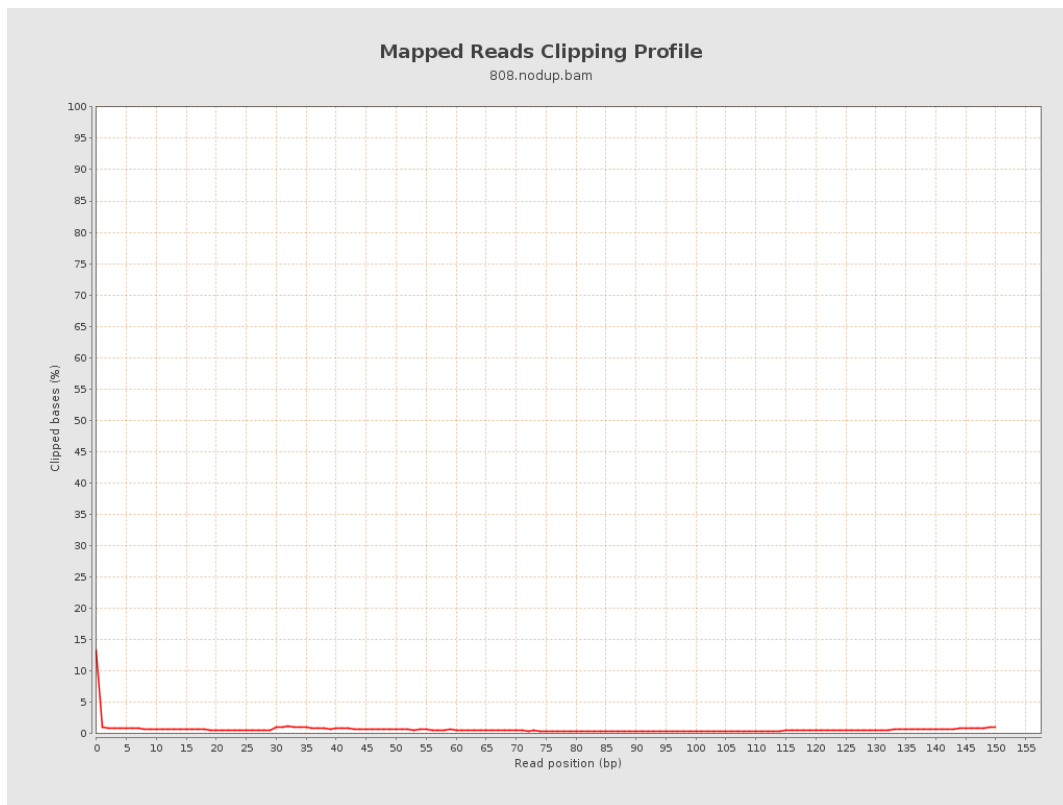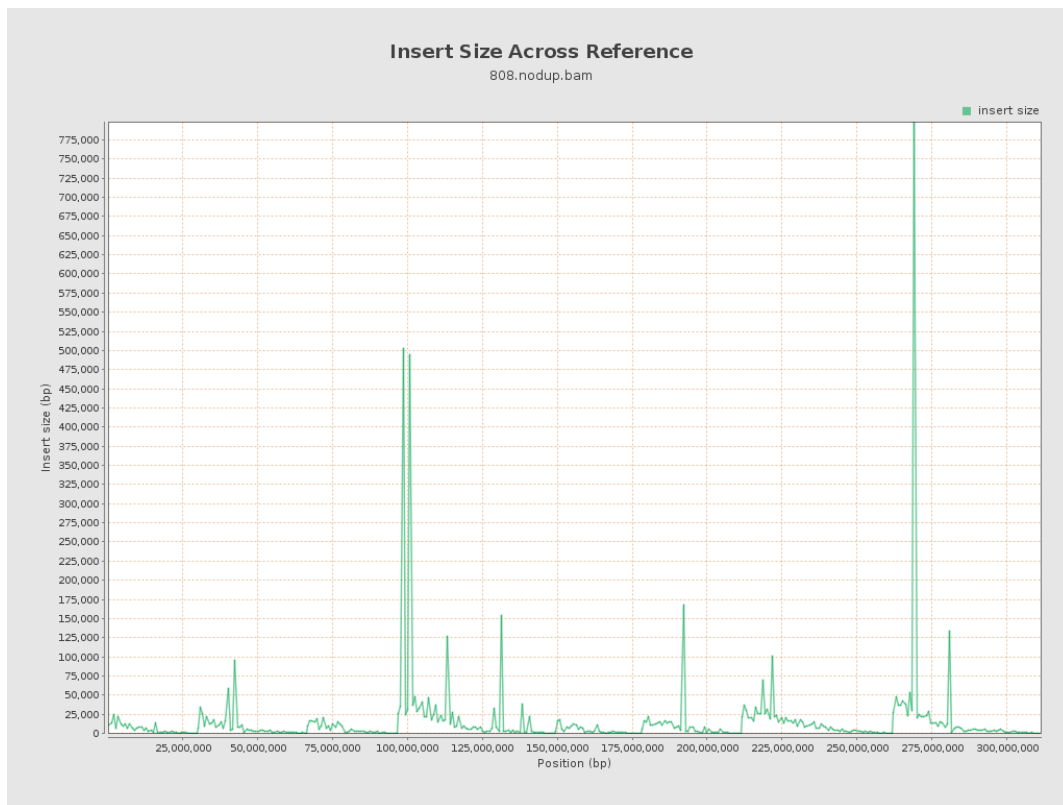
11. Results : Homopolymer Indels

12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

Insert Size Across Reference
808.nodup.bam

15. Results : Insert Size Histogram

Insert Size Histogram
808.nodup.bam