Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:26:27

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/Fr2
.nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/Fr2 .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_104/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_104_S194_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_104/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_104_S194_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:26:27 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	52,673,842
Mapped reads	48,386,496 / 91.86%
Unmapped reads	4,287,346 / 8.14%
Mapped paired reads	48,386,496 / 91.86%
Mapped reads, first in pair	24,228,996 / 46%
Mapped reads, second in pair	24,157,500 / 45.86%
Mapped reads, both in pair	47,720,969 / 90.6%
Mapped reads, singletons	665,527 / 1.26%
Read min/max/mean length	30 / 151 / 148.55
Duplicated reads (flagged)	6,819,266 / 12.95%
Clipped reads	9,425,023 / 17.89%

2.2. ACGT Content

Number/percentage of A's	2,099,244,078 / 30.89%
Number/percentage of C's	1,300,054,288 / 19.13%
Number/percentage of T's	2,102,098,136 / 30.93%
Number/percentage of G's	1,293,975,406 / 19.04%
Number/percentage of N's	28,600 / 0%
GC Percentage	38.17%

2.3. Coverage

Mean	21.8547
Standard Deviation	150.4733

2.4. Mapping Quality

Mean Mapping Quality	45.52

2.5. Insert size

| Mean	183,017.58
Standard Deviation	2,021,074.58
P25/Median/P75	323 / 421 / 548

2.6. Mismatches and indels

| General error rate	2.02%
Mismatches	126,060,458
Insertions	3,972,469
Mapped reads with at least one insertion	7.44%
Deletions	4,149,966
Mapped reads with at least one deletion	7.67%
Homopolymer indels	57.17%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	558989546	18.8058	31.7425

|				
LT669789.1	36598175	797412533	21.7883	159.1668
LT669790.1	30422129	673540626	22.1398	112.0379
LT669791.1	52758100	1128562031	21.3913	101.8124
LT669792.1	28376109	613656573	21.6258	165.3274
LT669793.1	33388210	660861225	19.7933	77.0959
LT669794.1	50579949	1032169228	20.4067	124.8361
LT669795.1	49795044	1345660861	27.024	261.543

3. Results : Coverage across reference

Coverage across reference
Fr2.nodup.bam

4. Results : Coverage Histogram

Coverage Histogram
Fr2.nodup.bam
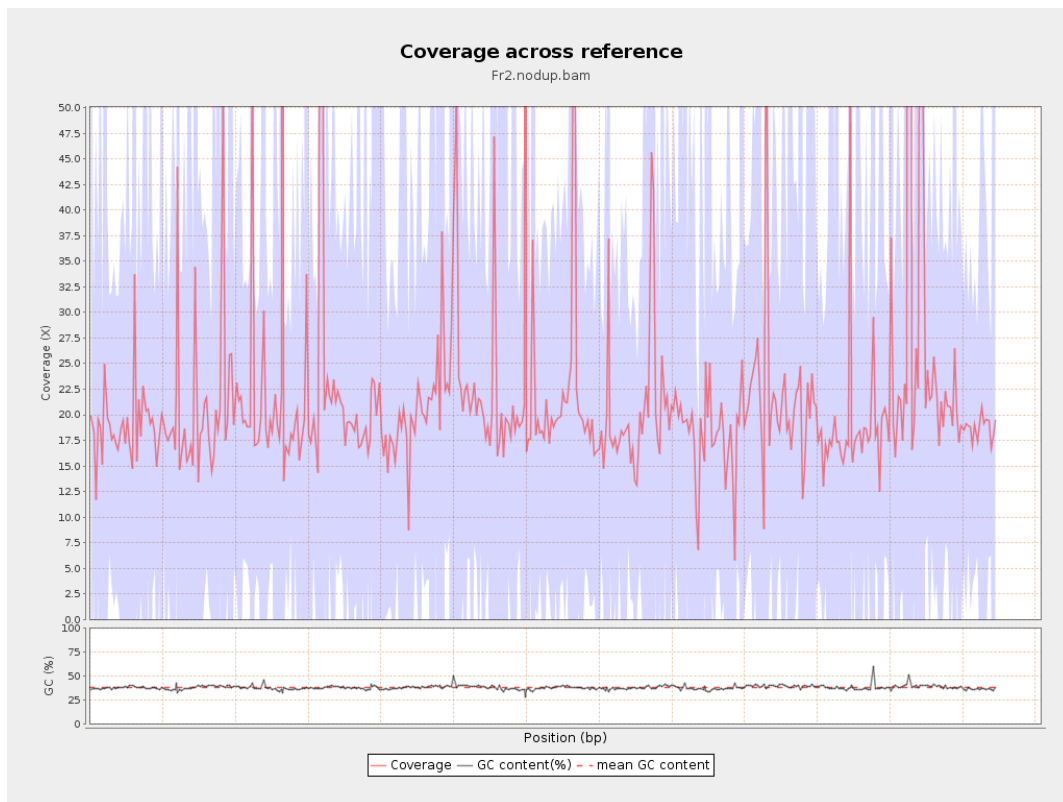
5. Results : Coverage Histogram (0-50X)
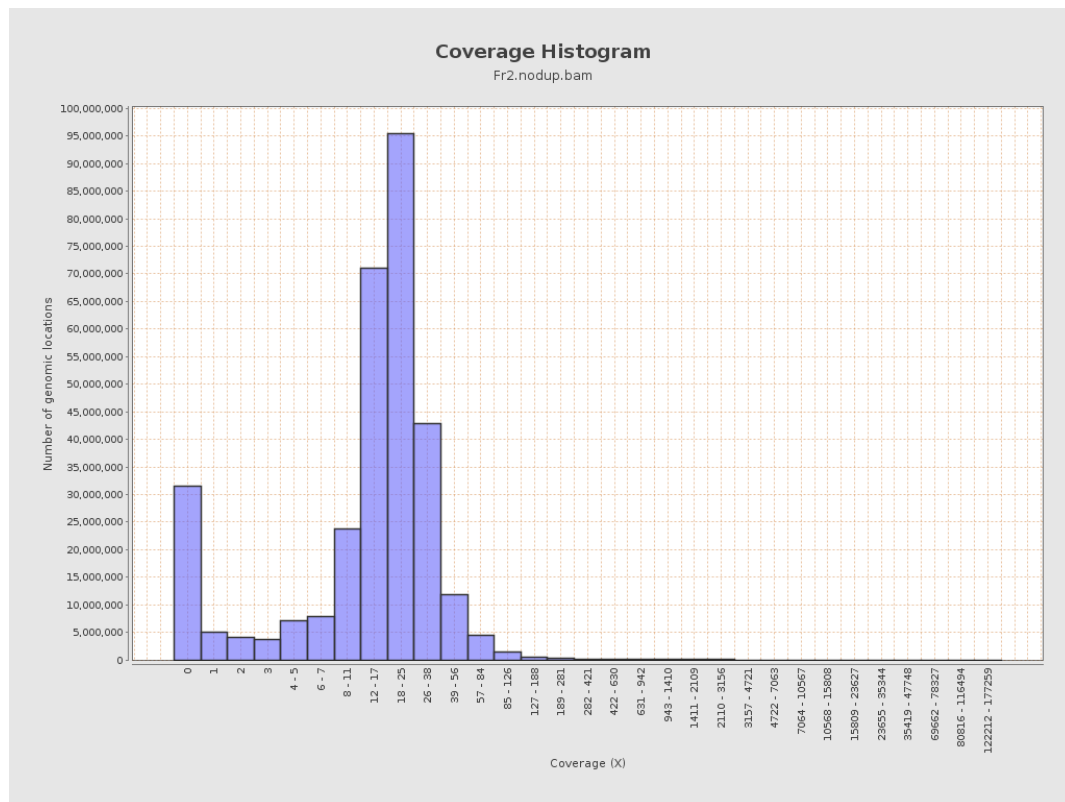
Coverage Histogram (0-50X)
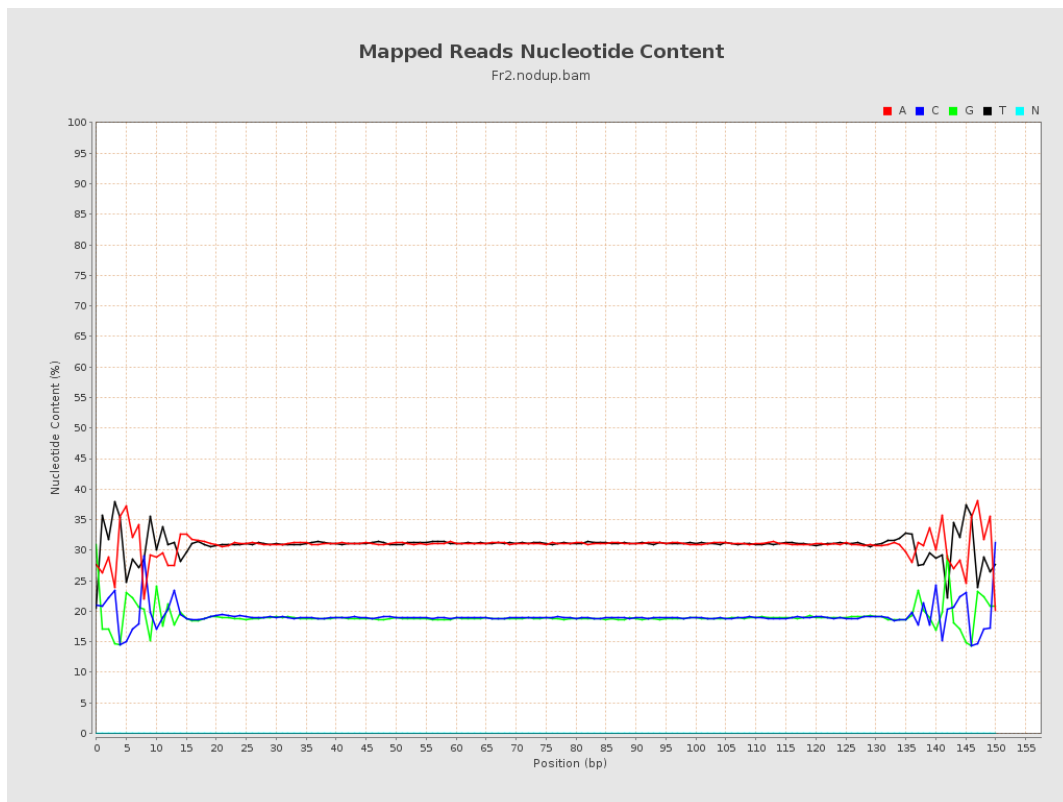Fr2.nodup.bam
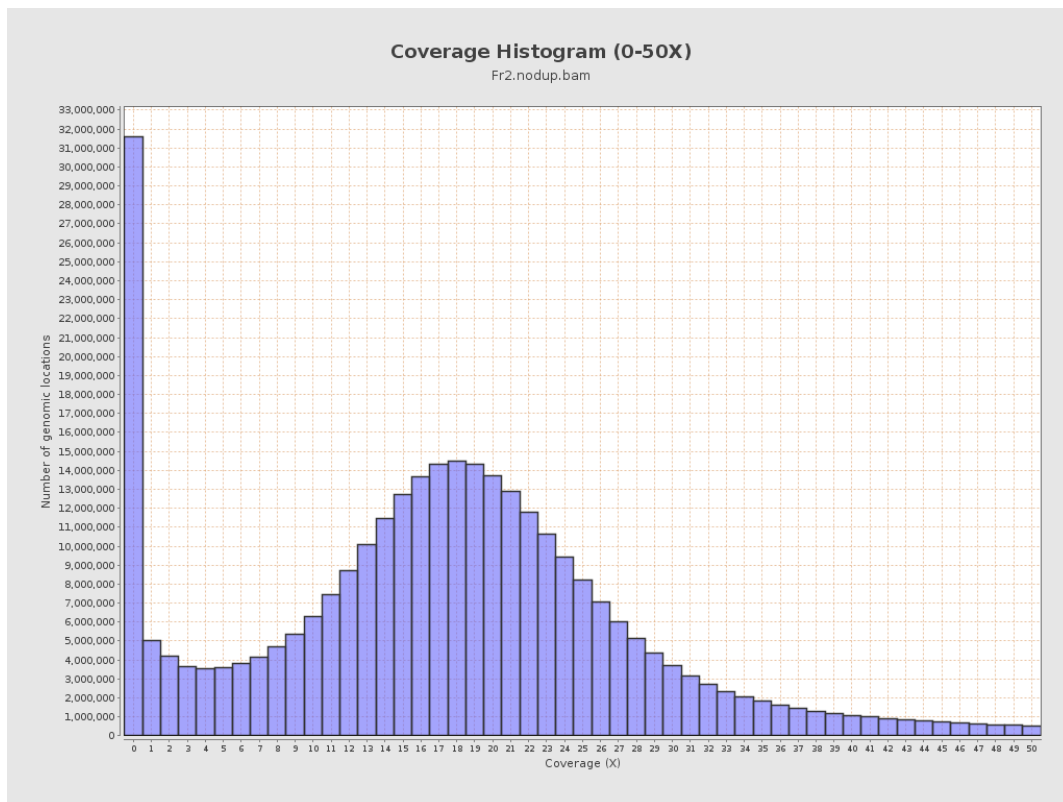
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
Fr2.nodup.bam
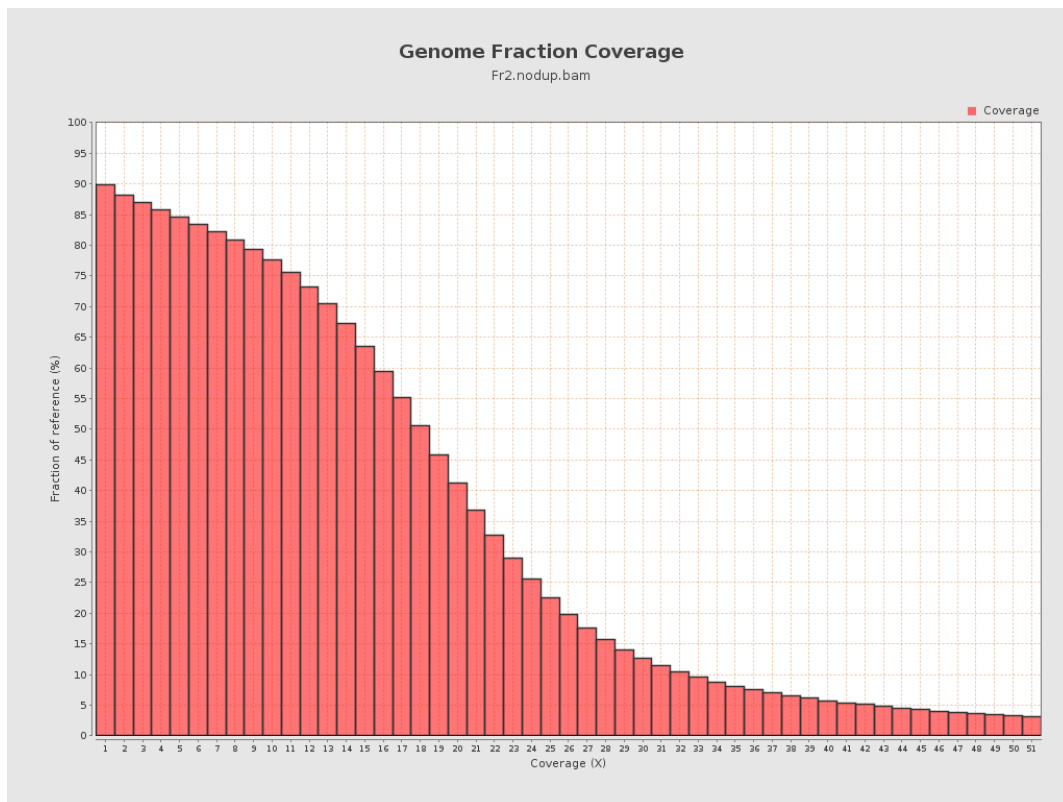
7. Results : Duplication Rate Histogram
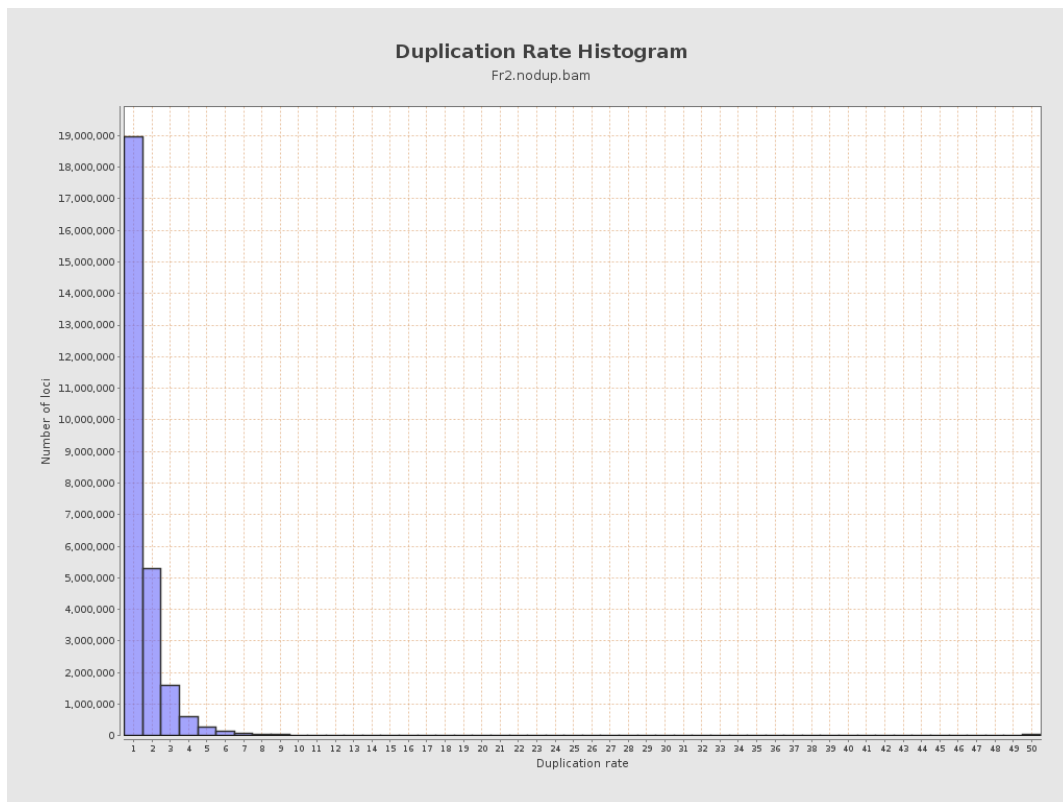
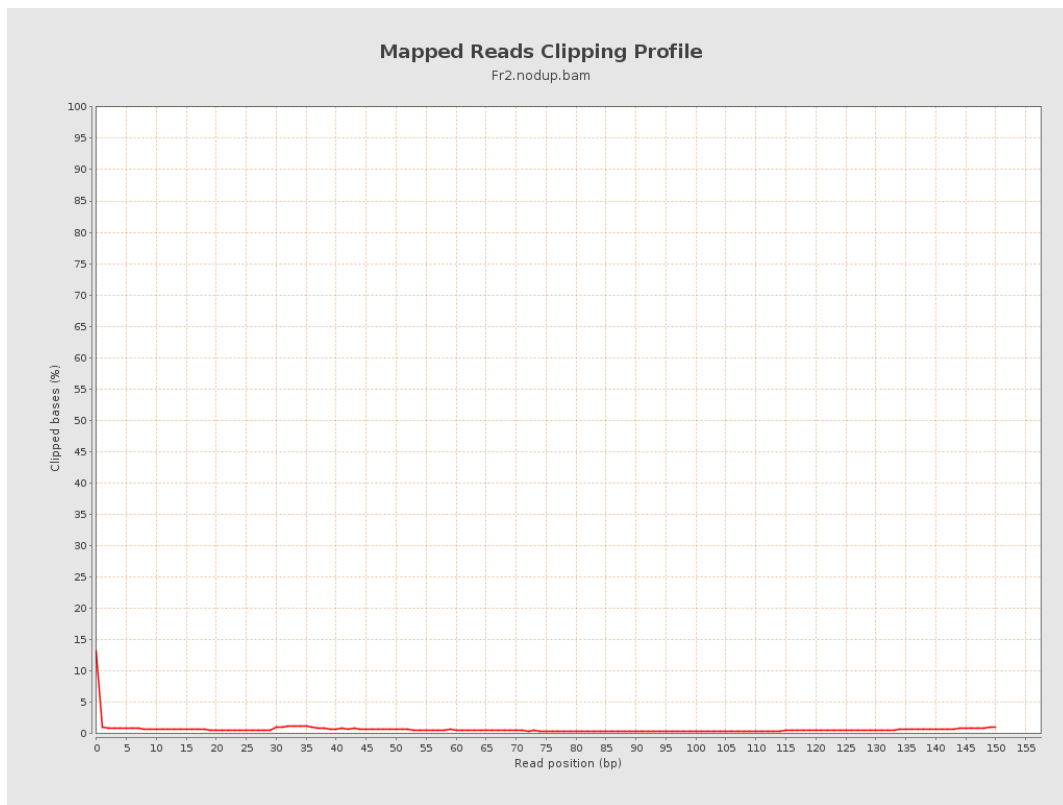# 8. Results : Mapped Reads Nucleotide Content

Mapped Reads Nucleotide Content
Fr2.nodup.bam

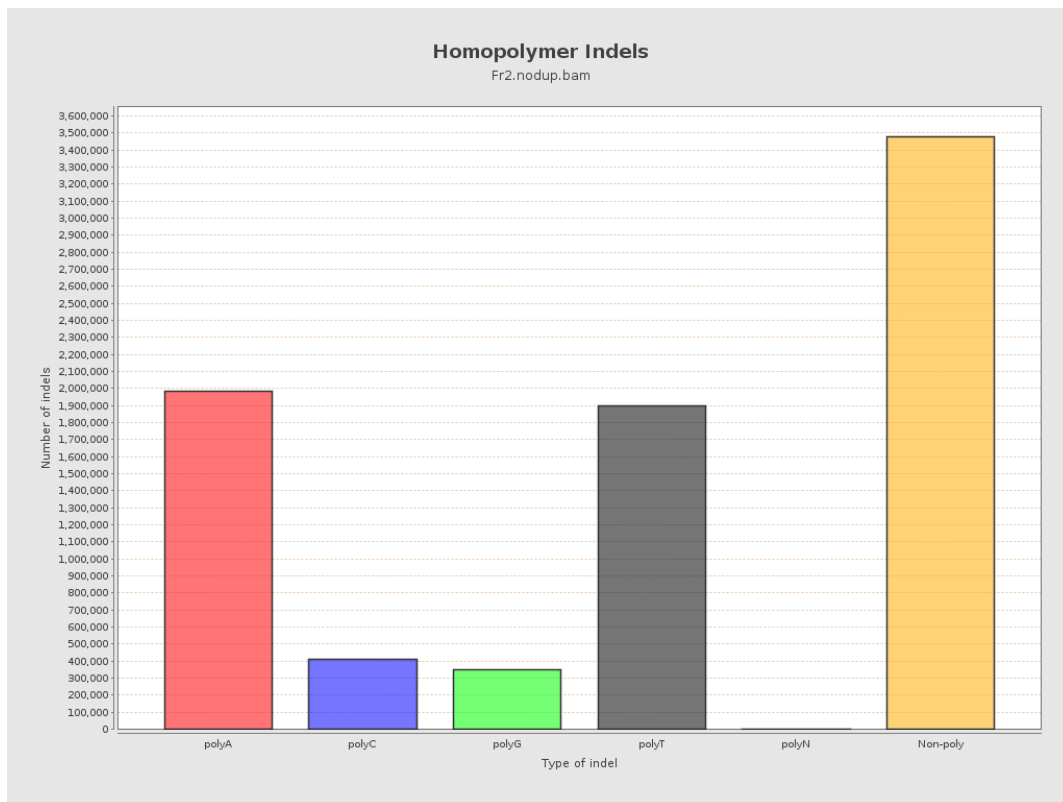# 9. Results : Mapped Reads GC-content Distribution
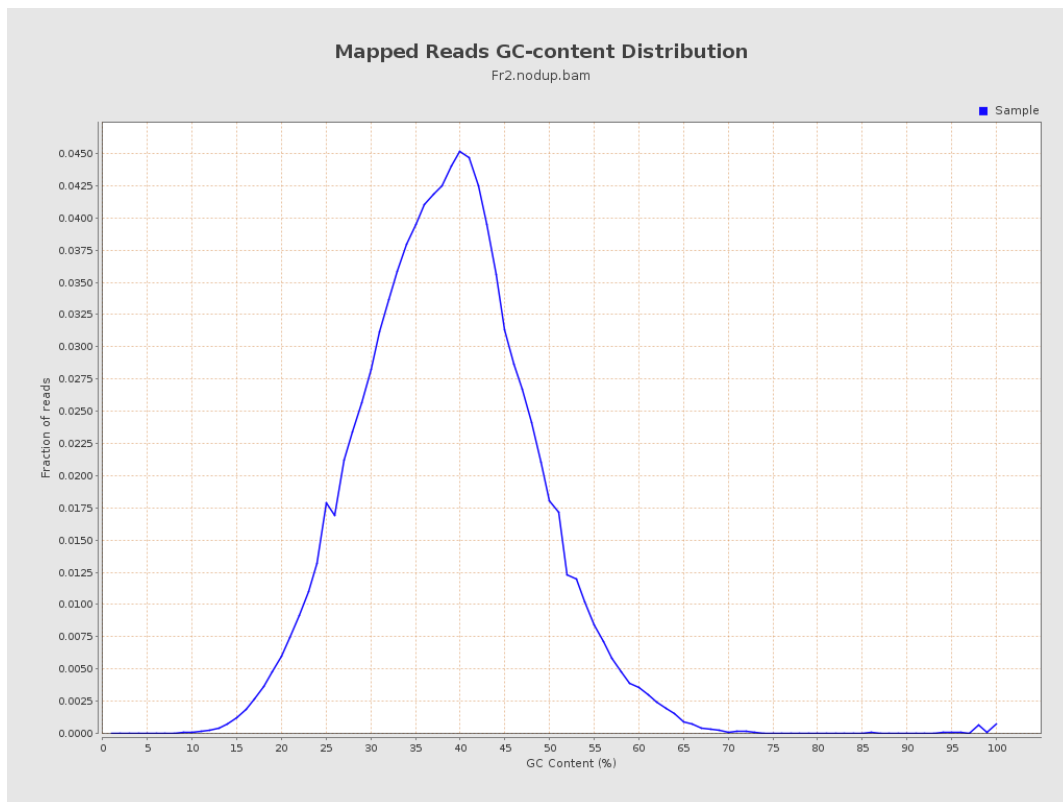
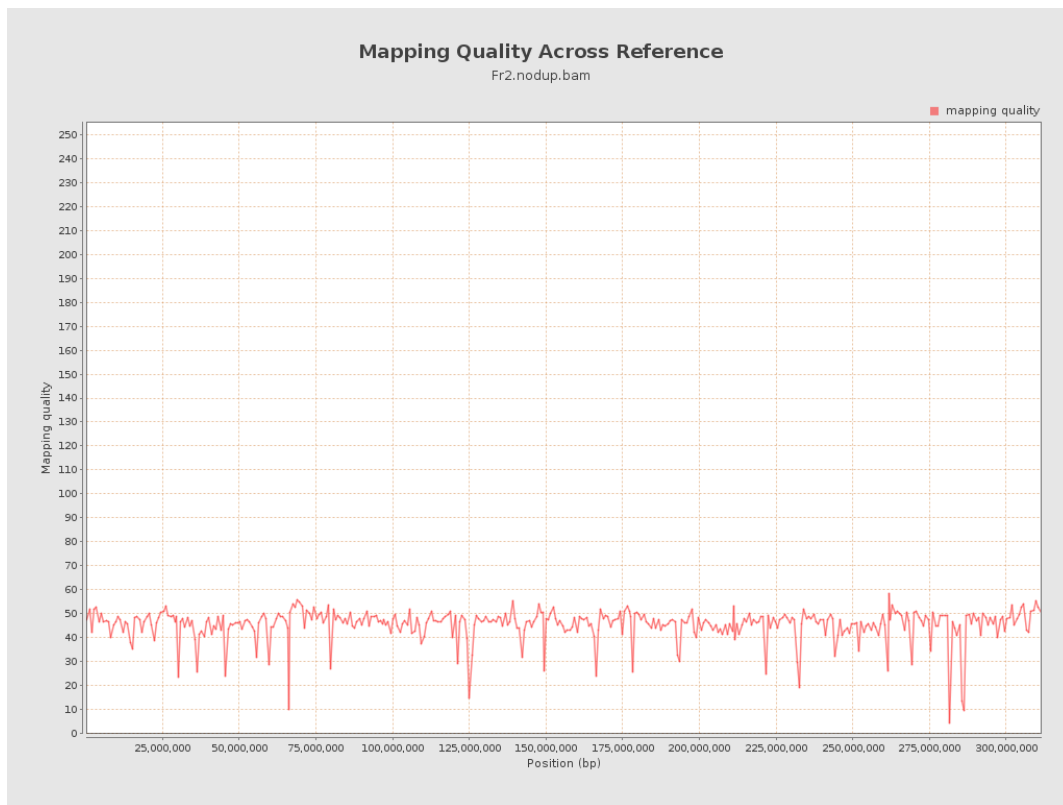# 10. Results : Mapped Reads Clipping Profile

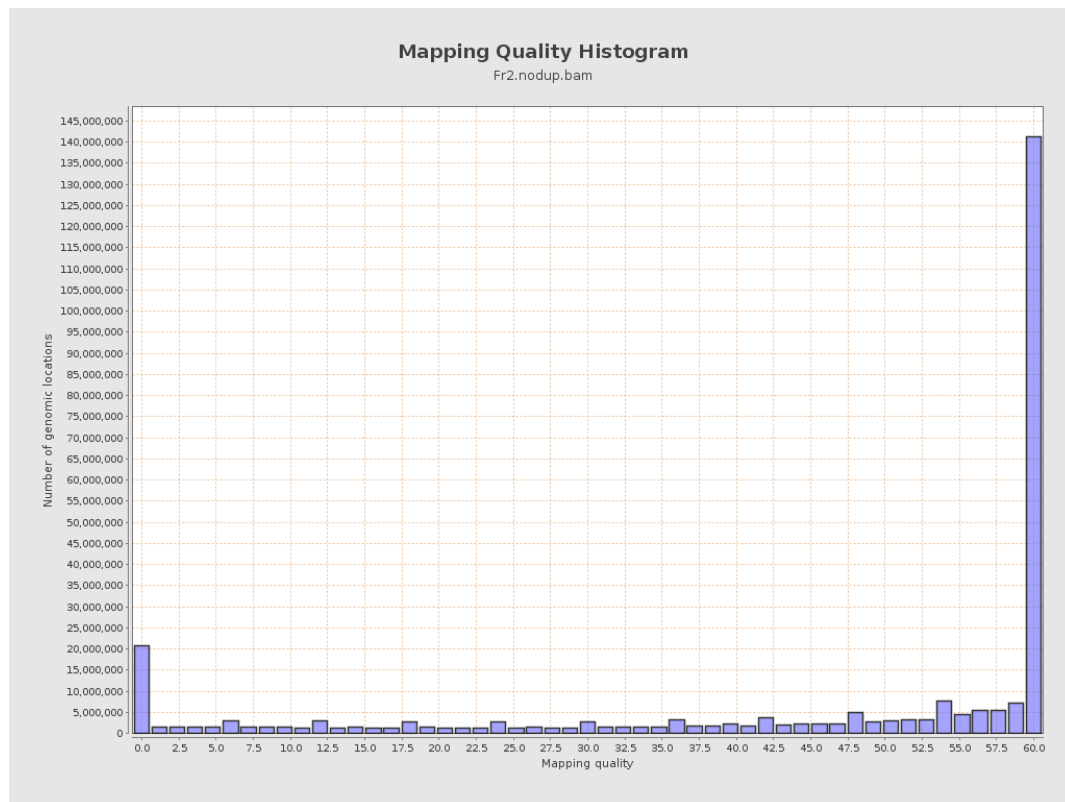Mapped Reads Clipping Profile
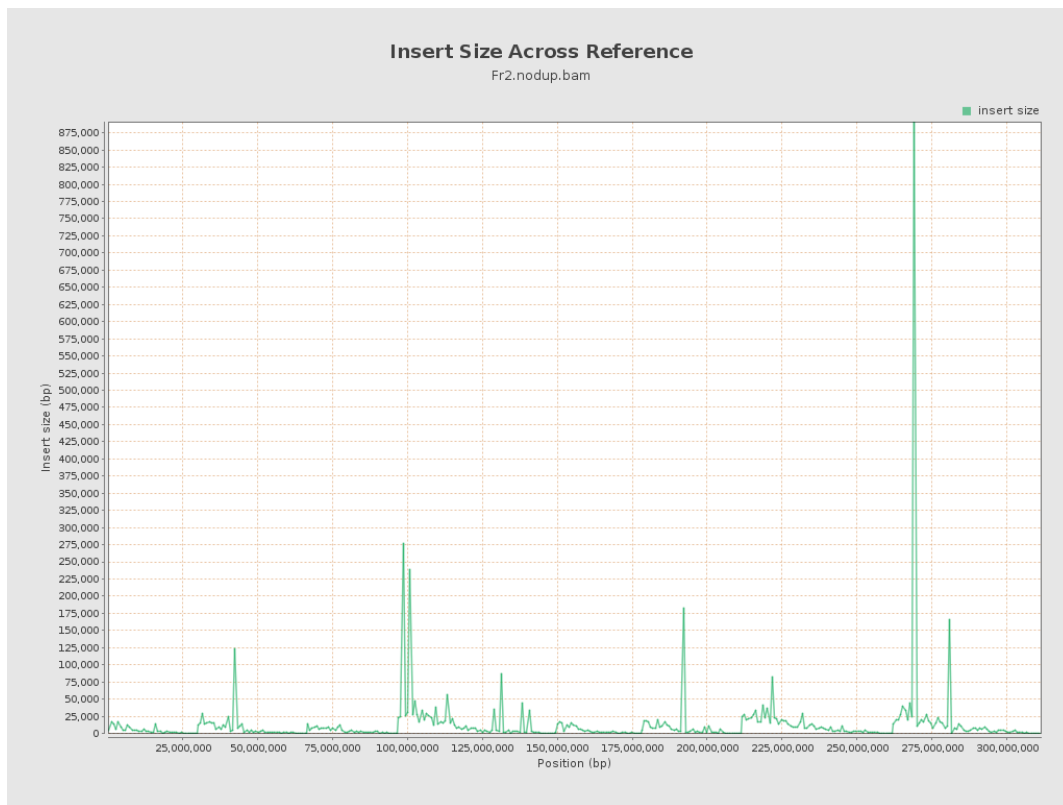Fr2.nodup.bam

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
Fr2.nodup.bam

15. Results : Insert Size Histogram

Insert Size Histogram
Fr2.nodup.bam