Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:27:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1434
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1434 .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_278/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_278_S359_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_278/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_278_S359_L003_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:27:43 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	56,886,805
Mapped reads	52,771,663 / 92.77%
Unmapped reads	4,115,142 / 7.23%
Mapped paired reads	52,771,663 / 92.77%
Mapped reads, first in pair	26,447,755 / 46.49%
Mapped reads, second in pair	26,323,908 / 46.27%
Mapped reads, both in pair	51,554,405 / 90.63%
Mapped reads, singletons	1,217,258 / 2.14%
Read min/max/mean length	30 / 151 / 147.85
Duplicated reads (flagged)	7,433,262 / 13.07%
Clipped reads	12,729,489 / 22.38%

2.2. ACGT Content

Number/percentage of A's	2,226,361,422 / 30.71%
Number/percentage of C's	1,397,272,299 / 19.27%
Number/percentage of T's	2,230,322,085 / 30.76%
Number/percentage of G's	1,395,780,653 / 19.25%
Number/percentage of N's	27,370 / 0%
GC Percentage	38.53%

2.3. Coverage

Mean	23.327
Standard Deviation	198.2961

2.4. Mapping Quality

Mean Mapping Quality	43.2

2.5. Insert size

Mean	253,812.87
Standard Deviation	2,388,277.59
P25/Median/P75	323 / 426 / 558

2.6. Mismatches and indels

General error rate	2.4%
Mismatches	159,974,318
Insertions	5,140,115
Mapped reads with at least one insertion	8.73%
Deletions	5,218,871
Mapped reads with at least one deletion	8.74%
Homopolymer indels	56.09%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	577752321	19.437	72.2512

LT669789.1	36598175	887050848	24.2376	222.7683
LT669790.1	30422129	775657688	25.4965	206.4341
LT669791.1	52758100	1210861898	22.9512	193.4263
LT669792.1	28376109	660193136	23.2658	213.439
LT669793.1	33388210	726137008	21.7483	126.3191
LT669794.1	50579949	1115520813	22.0546	169.9982
LT669795.1	49795044	1316487899	26.4381	273.4722

3. Results : Coverage across reference

Coverage across reference
1434.nodup.bam

4. Results : Coverage Histogram

Coverage Histogram
1434.nodup.bam
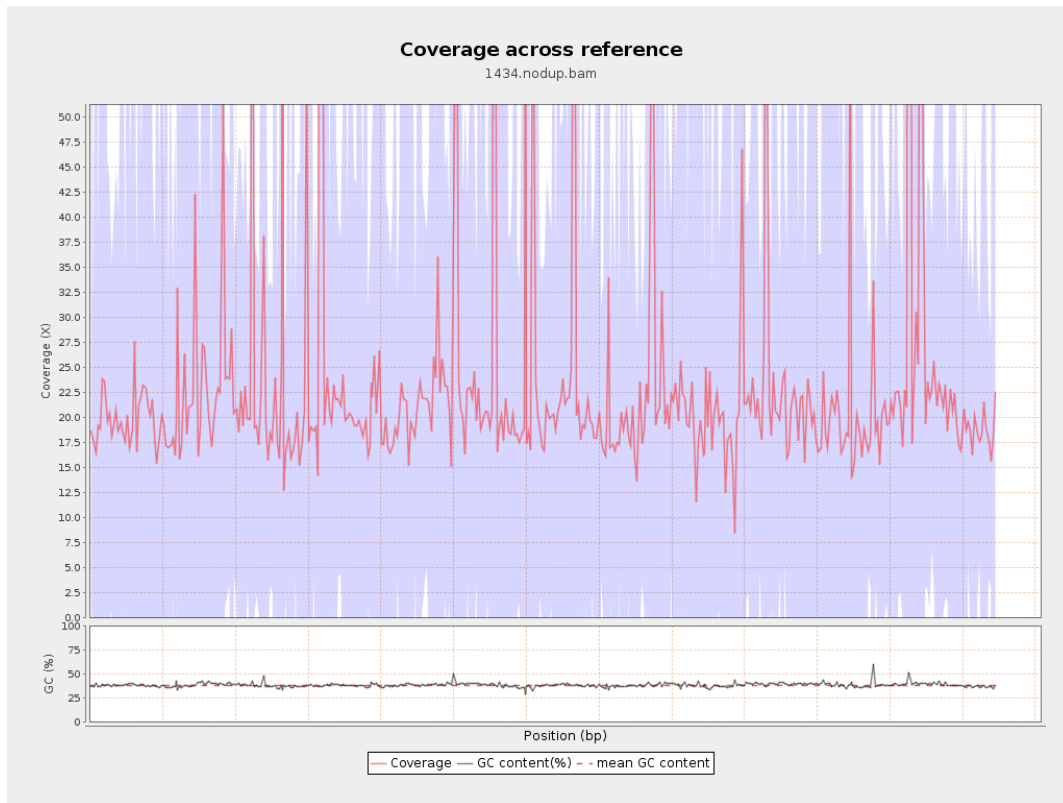
5. Results : Coverage Histogram (0-50X)
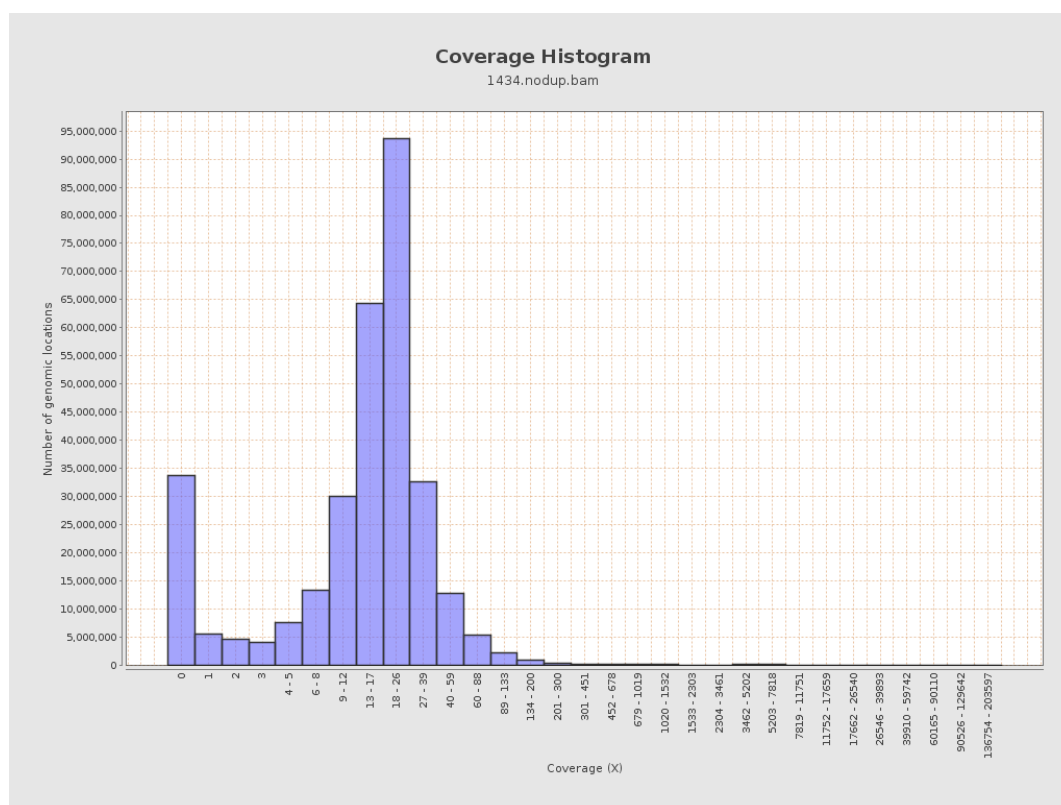
Coverage Histogram (0-50X)
1434.nodup.bam
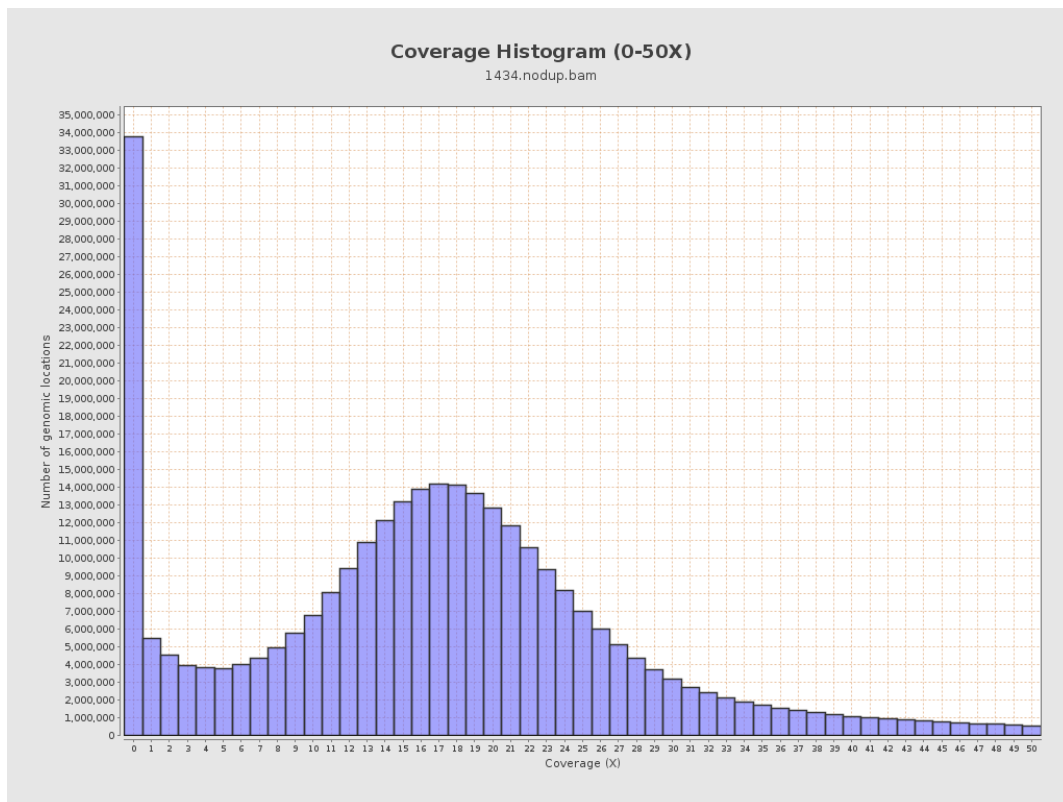
6. Results : Genome Fraction Coverage
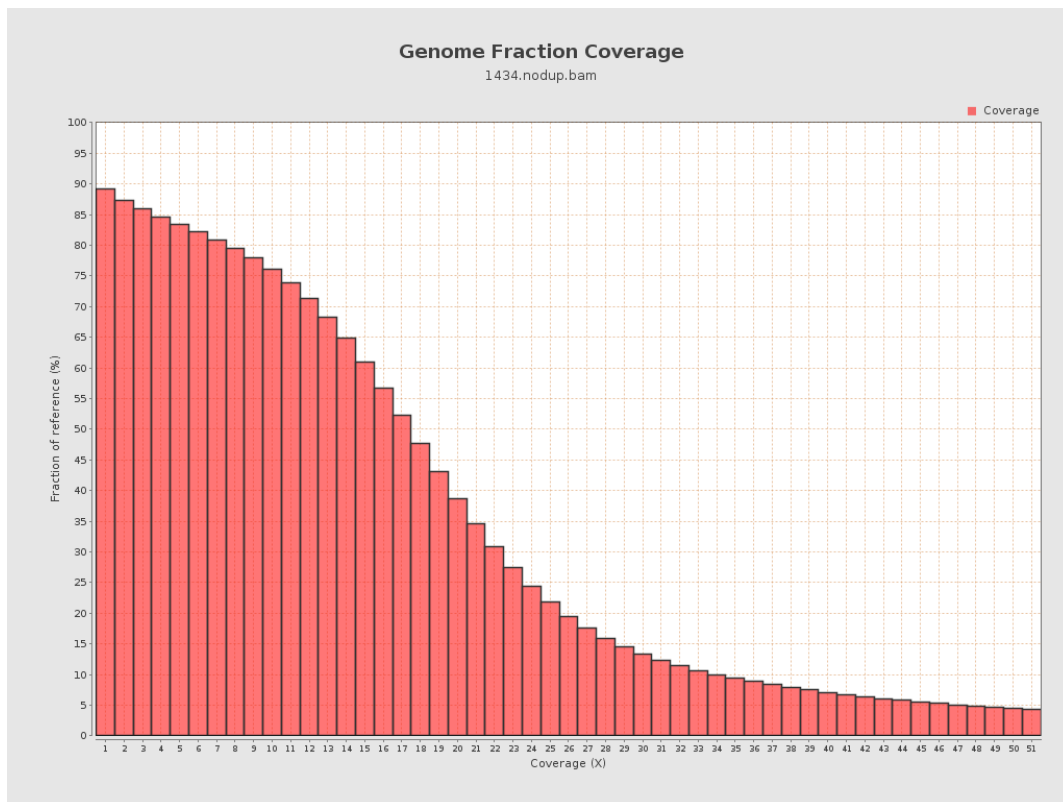
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
1434.nodup.bam
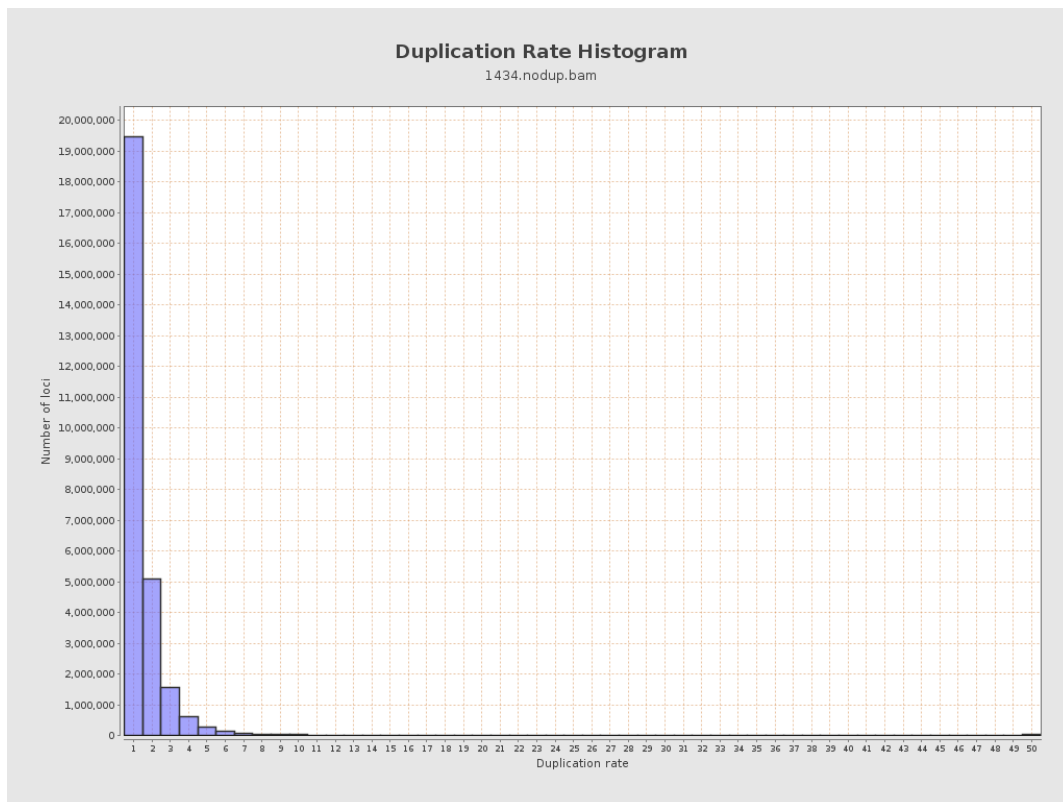
8. Results : Mapped Reads Nucleotide Content
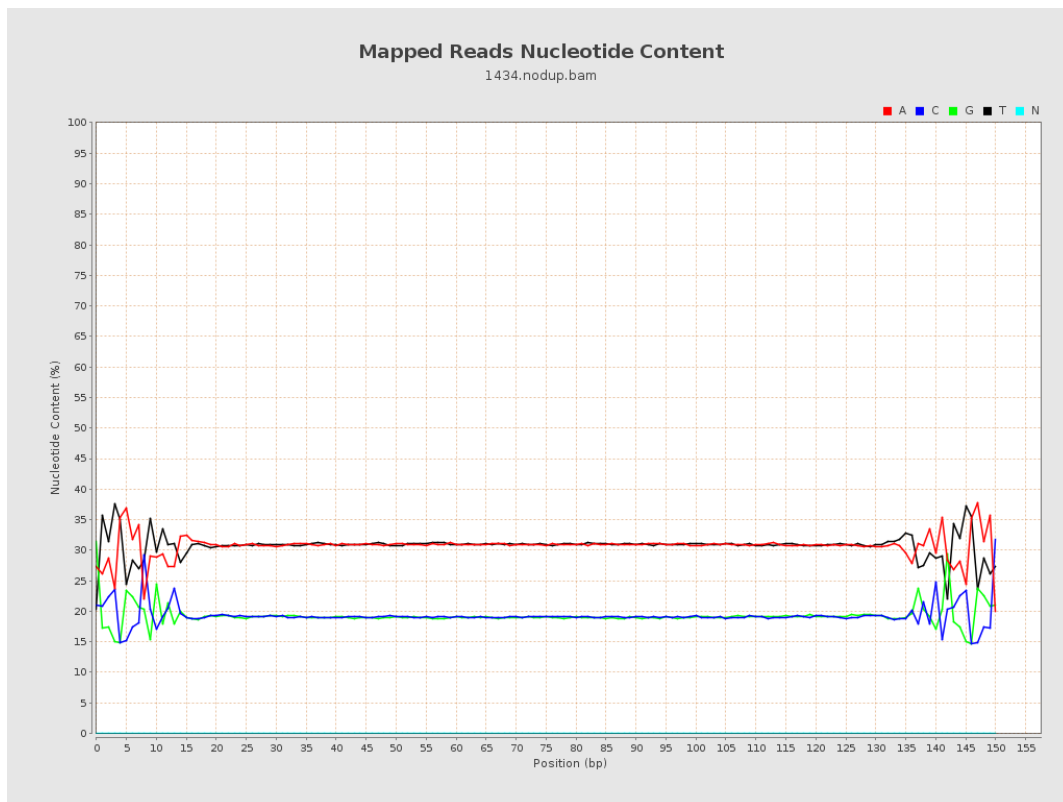
9. Results : Mapped Reads GC-content Distribution
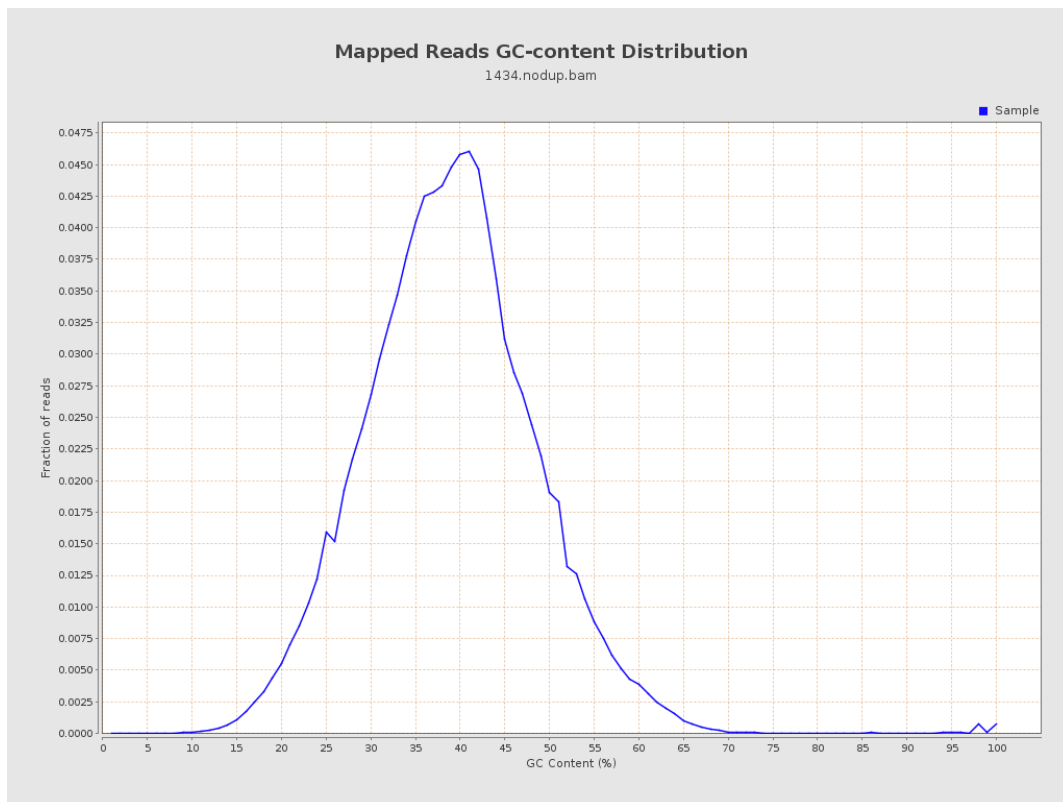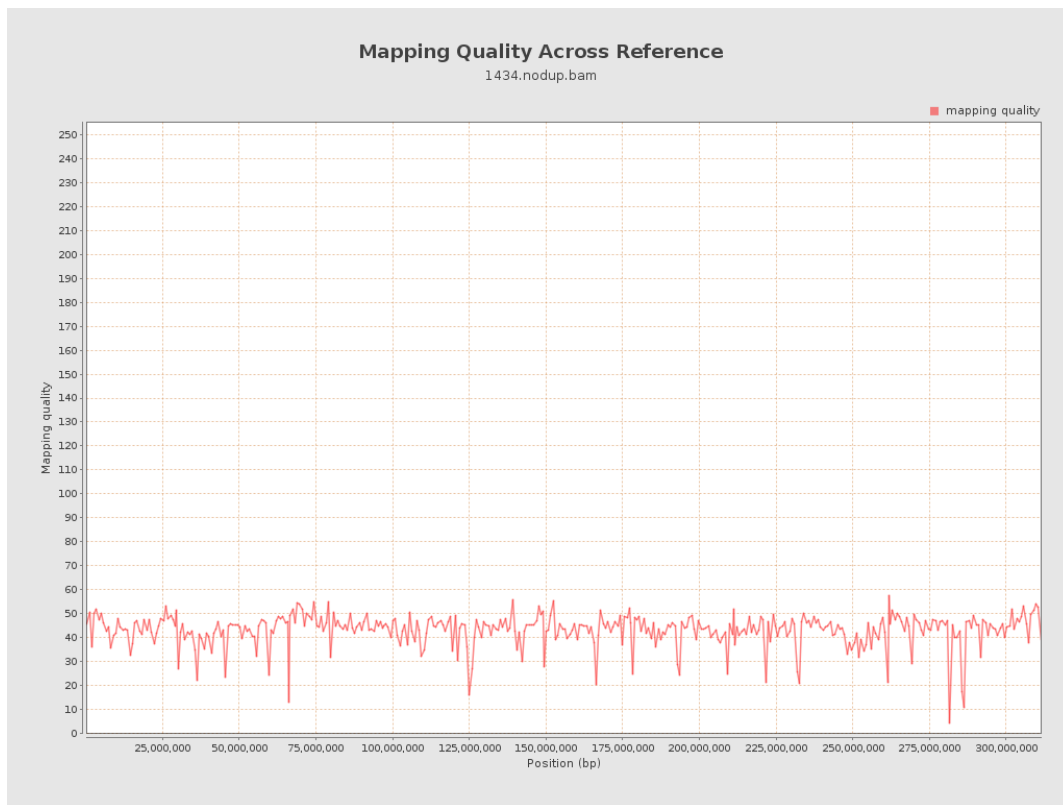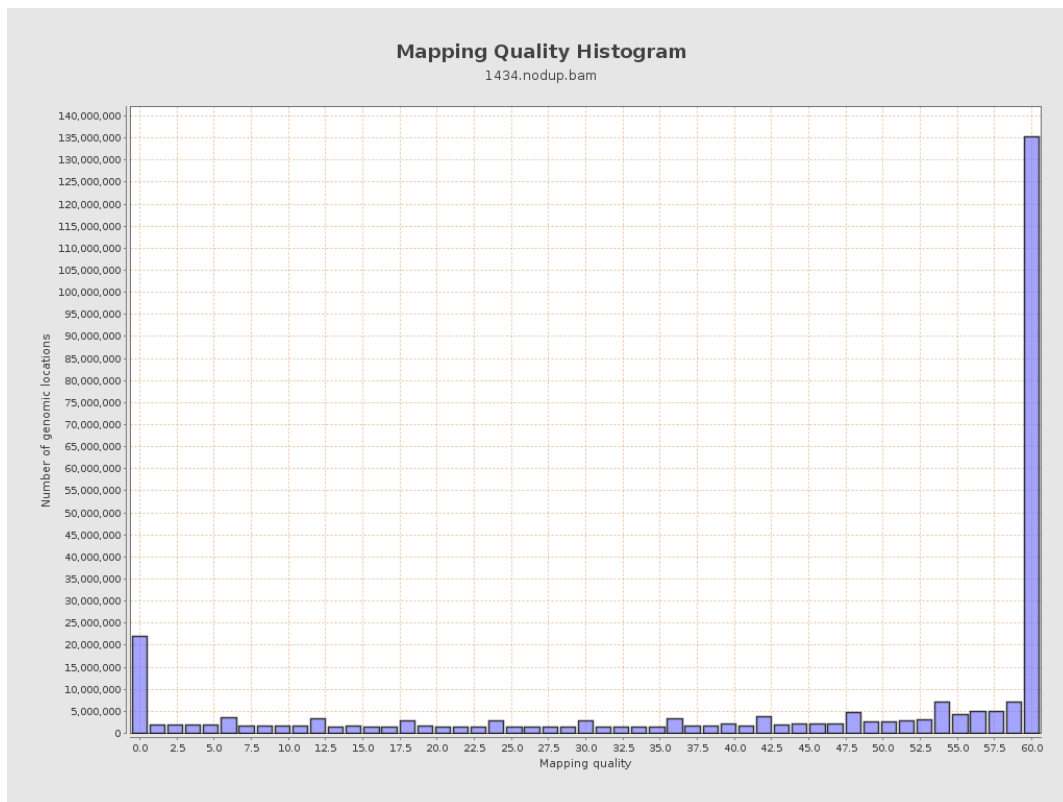
10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
1434.nodup.bam
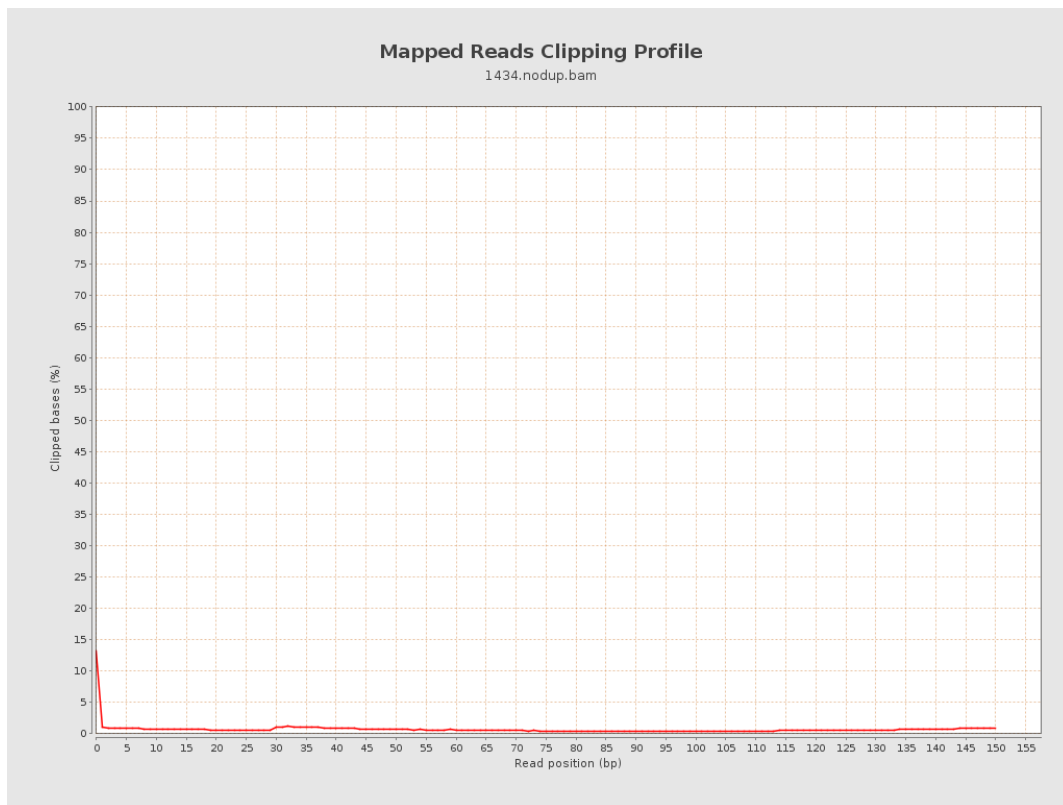
11. Results : Homopolymer Indels
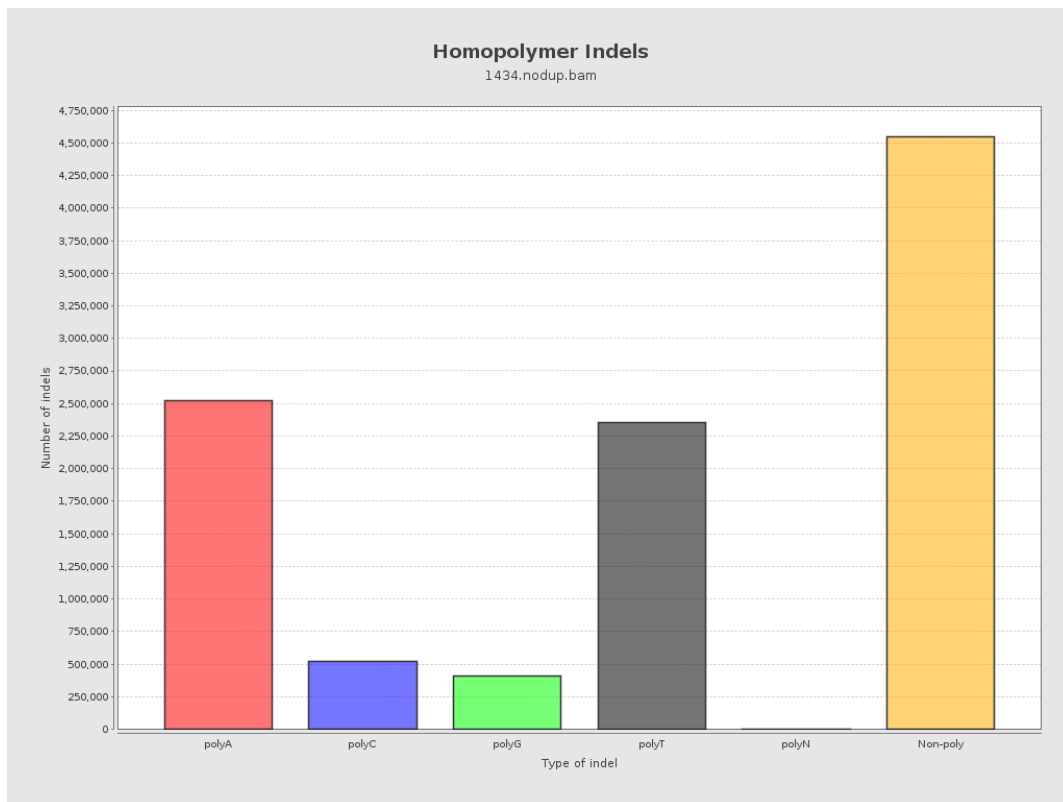
12. Results : Mapping Quality Across Reference
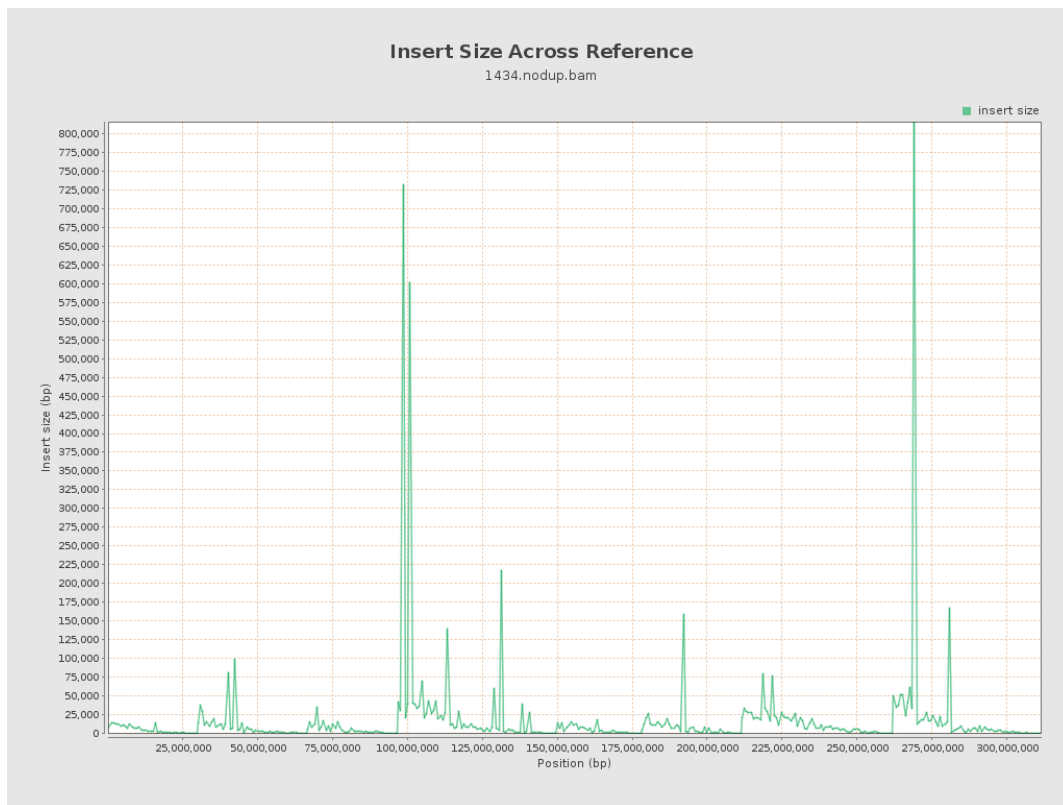
13. Results : Mapping Quality Histogram

Mapping Quality Histogram
1434.nodup.bam

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram

Insert Size Histogram
1434.nodup.bam