Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:32:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1440
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1440 .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_553/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_553_S120_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_553/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_553_S120_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:32:09 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	66,260,284
Mapped reads	63,225,572 / 95.42%
Unmapped reads	3,034,712 / 4.58%
Mapped paired reads	63,225,572 / 95.42%
Mapped reads, first in pair	31,686,198 / 47.82%
Mapped reads, second in pair	31,539,374 / 47.6%
Mapped reads, both in pair	62,199,093 / 93.87%
Mapped reads, singletons	1,026,479 / 1.55%
Read min/max/mean length	30 / 151 / 148.11
Duplicated reads (flagged)	8,955,247 / 13.52%
Clipped reads	14,643,392 / 22.1%

2.2. ACGT Content

Number/percentage of A's	2,711,203,716 / 30.93%
Number/percentage of C's	1,672,271,033 / 19.08%
Number/percentage of T's	2,714,328,428 / 30.97%
Number/percentage of G's	1,667,938,200 / 19.03%
Number/percentage of N's	60,769 / 0%
GC Percentage	38.11%

2.3. Coverage

Mean	28.1999
Standard Deviation	203.6759

2.4. Mapping Quality

Mean Mapping Quality	44.06

2.5. Insert size

Mean	206,562.36
Standard Deviation	2,146,713.83
P25/Median/P75	306 / 402 / 517

2.6. Mismatches and indels

General error rate	2.47%
Mismatches	200,774,870
Insertions	5,711,117
Mapped reads with at least one insertion	8.15%
Deletions	5,936,073
Mapped reads with at least one deletion	8.35%
Homopolymer indels	55.92%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	714640015	24.0422	56.6704

|				
LT669789.1	36598175	1053203536	28.7775	217.2253
LT669790.1	30422129	888963955	29.221	183.3557
LT669791.1	52758100	1462837056	27.7273	167.1188
LT669792.1	28376109	789462446	27.8214	241.6882
LT669793.1	33388210	893799923	26.7699	161.3982
LT669794.1	50579949	1363987271	26.967	188.3481
LT669795.1	49795044	1621366635	32.5608	293.3888

3. Results : Coverage across reference

Coverage across reference
1440.nodup.bam

4. Results : Coverage Histogram
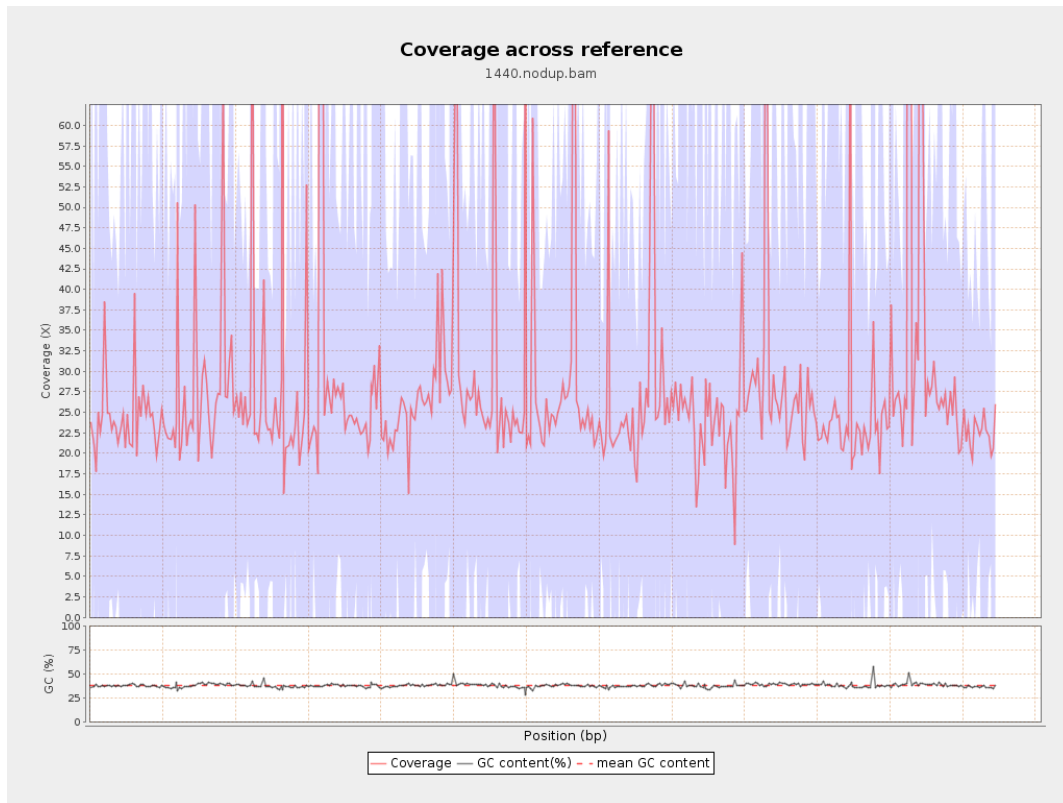
Coverage Histogram
1440.nodup.bam
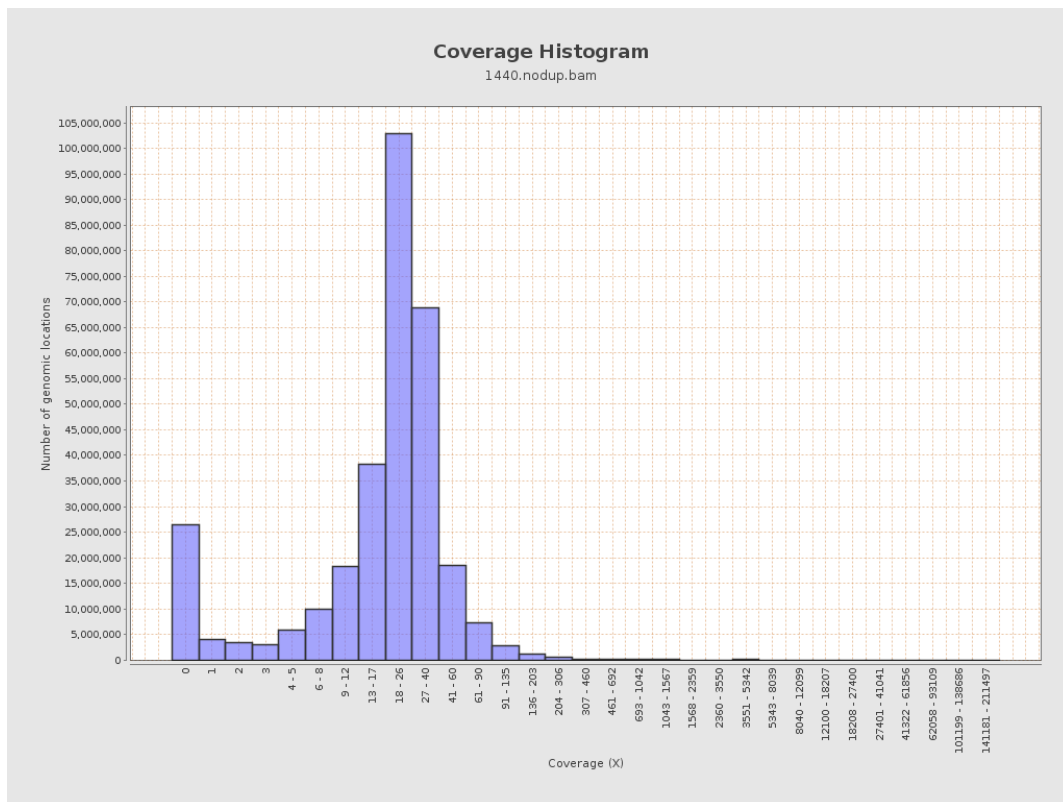
5. Results : Coverage Histogram (0-50X)
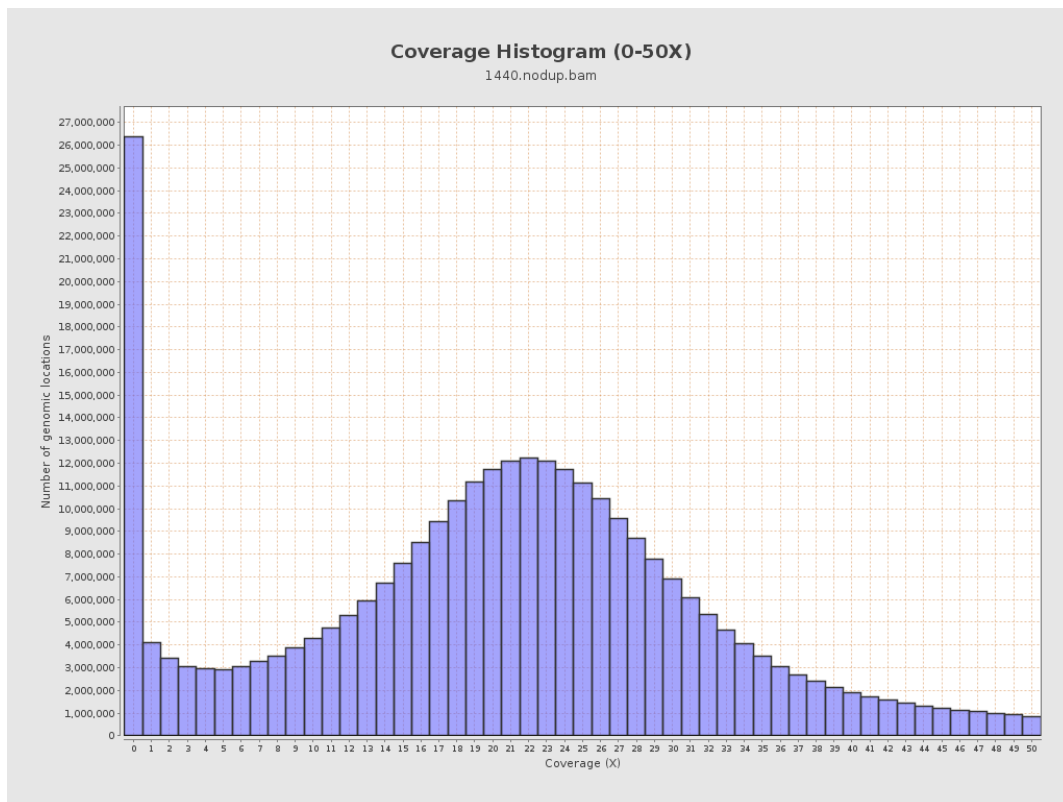
6. Results : Genome Fraction Coverage
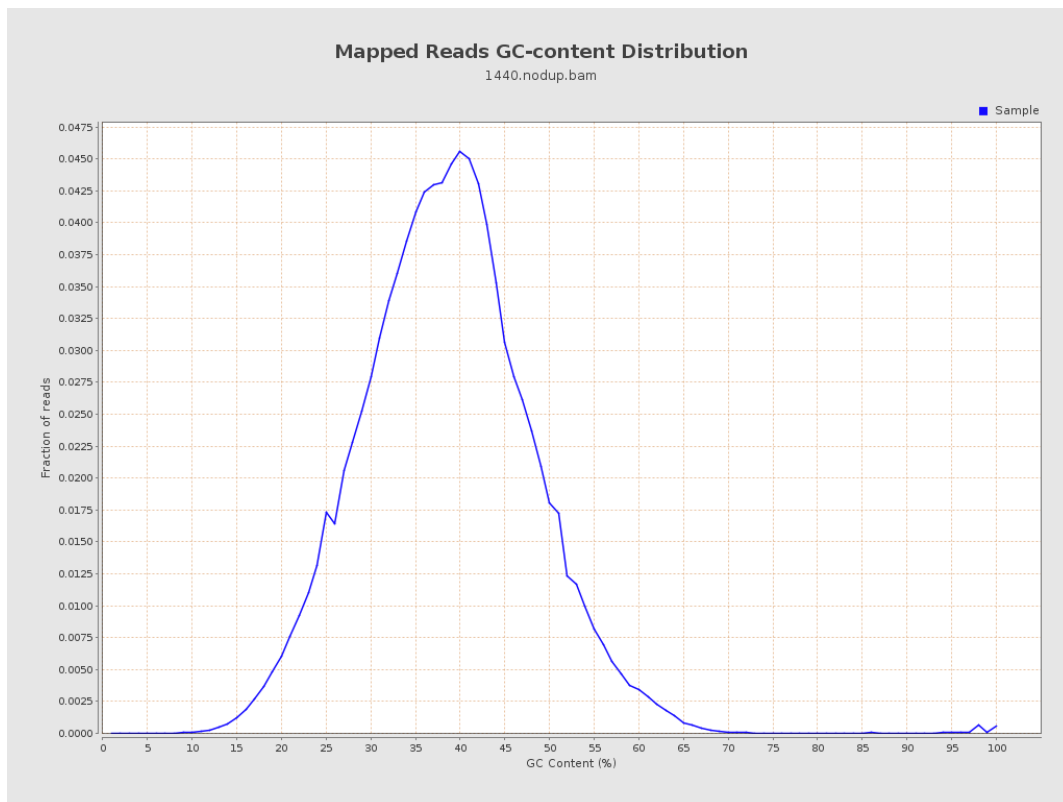

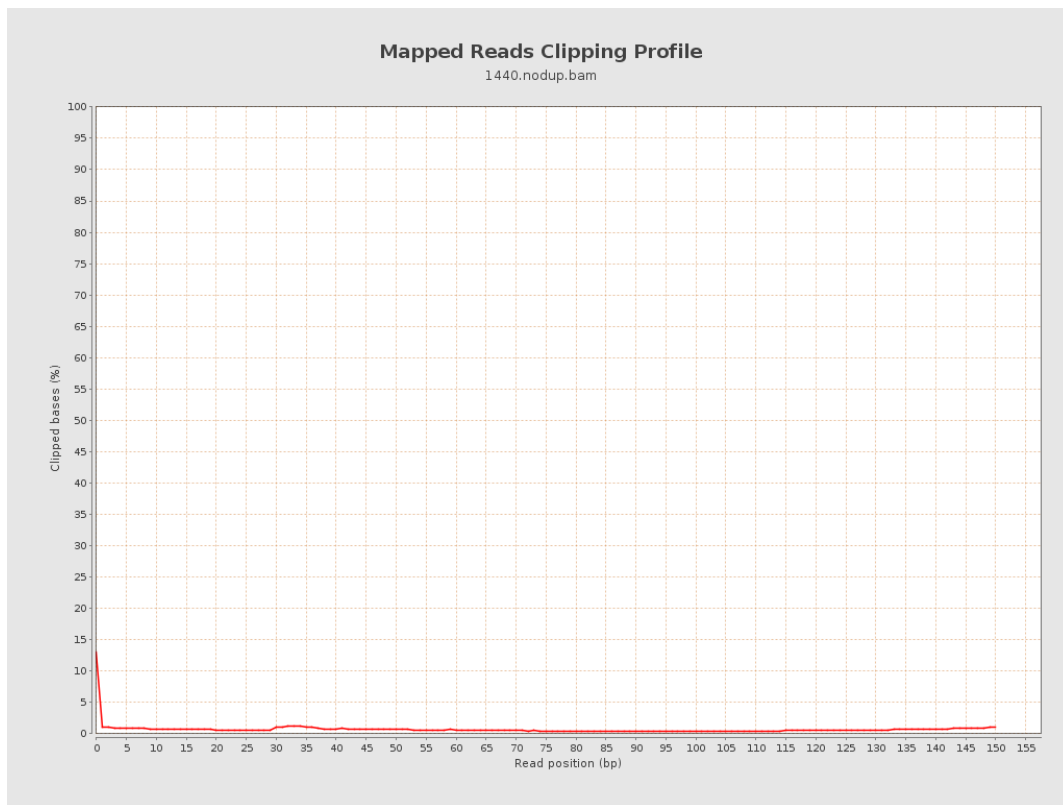Genome Fraction Coverage
1440.nodup.bam
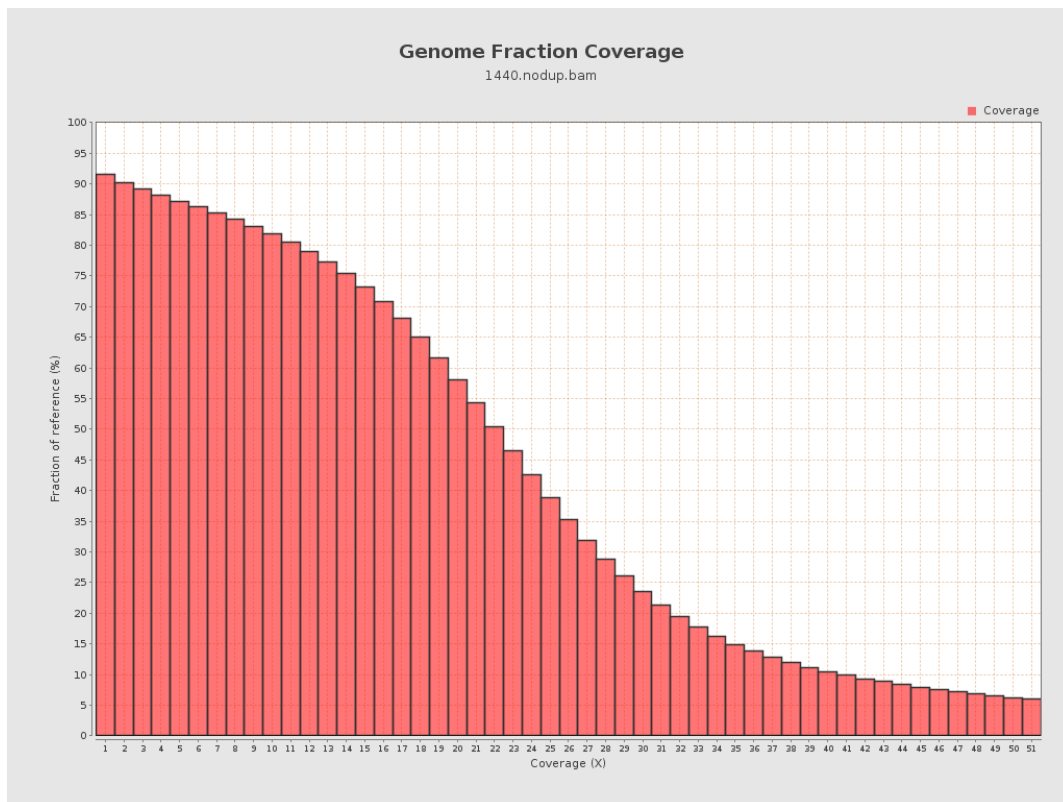
7. Results : Duplication Rate Histogram
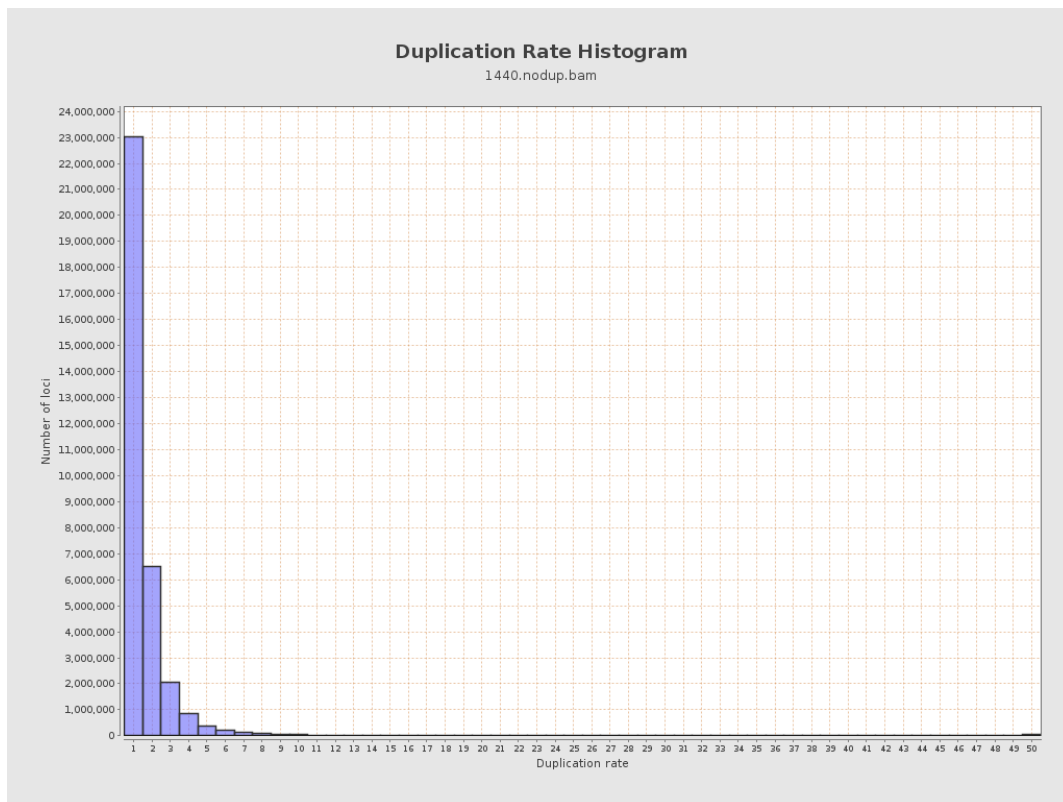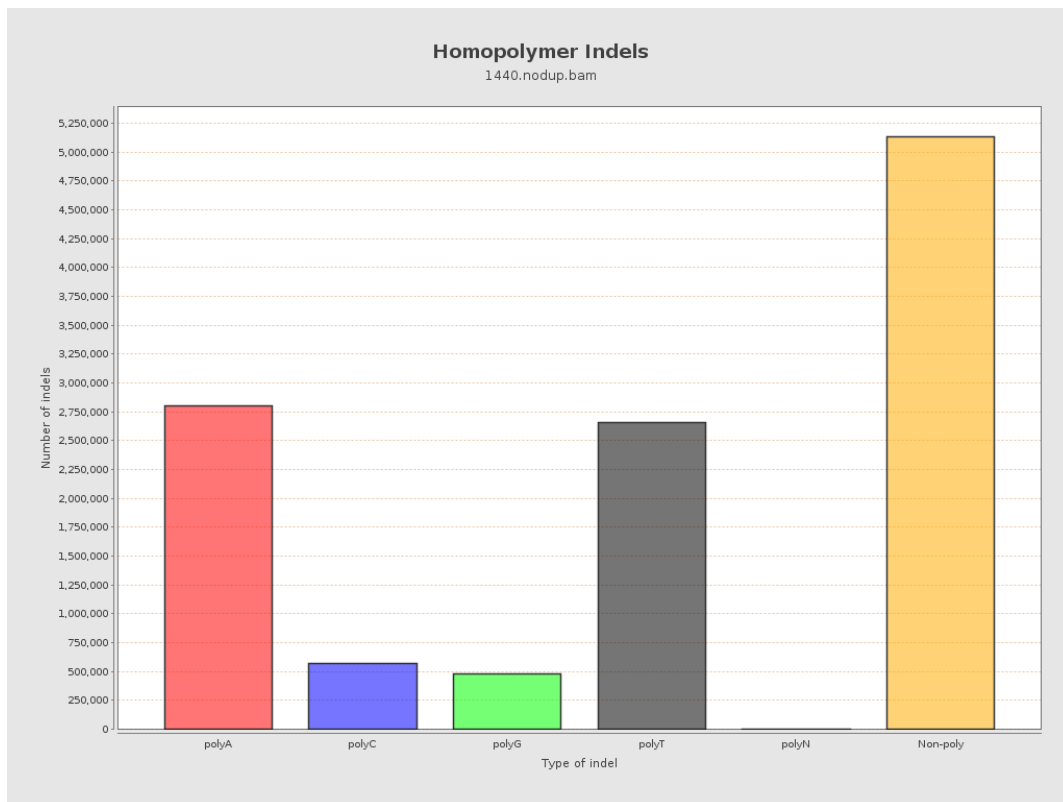
8. Results : Mapped Reads Nucleotide Content
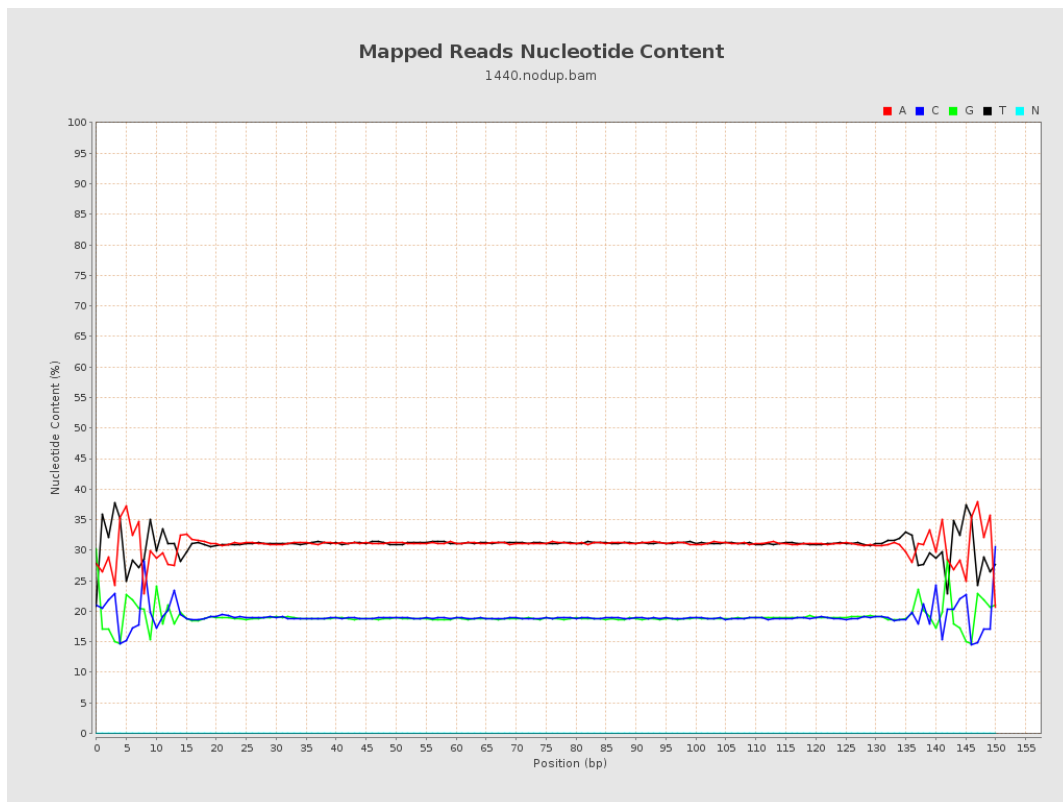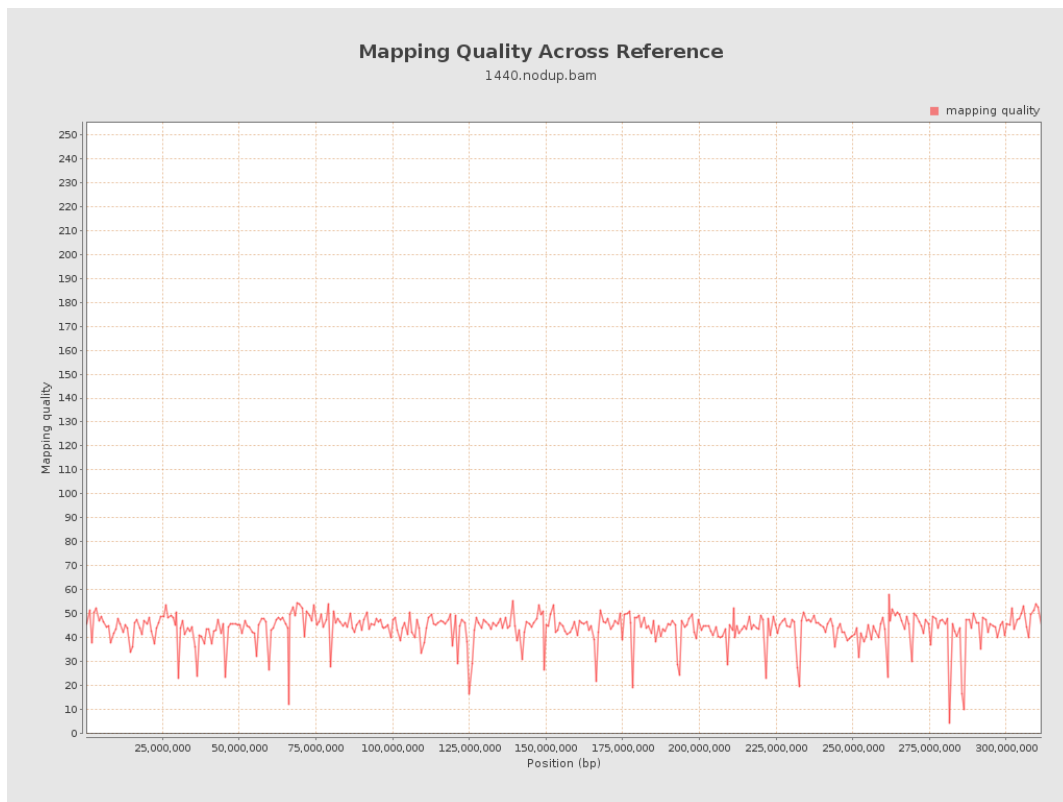
9. Results : Mapped Reads GC-content Distribution

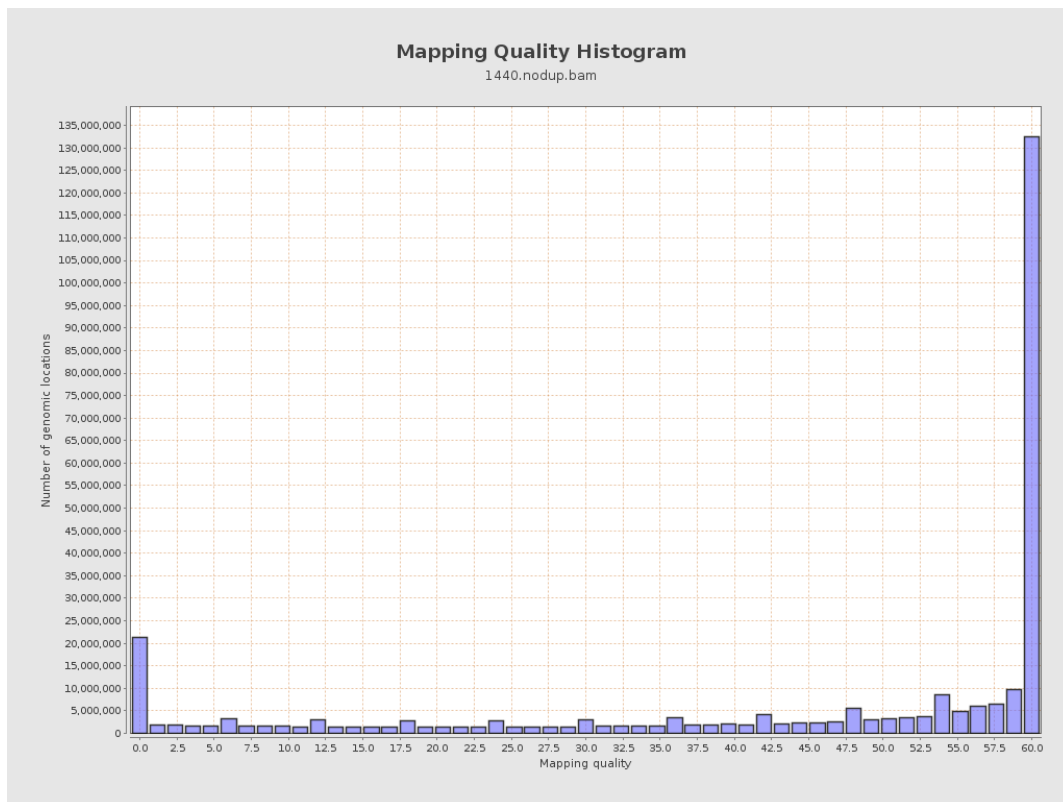# 10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels
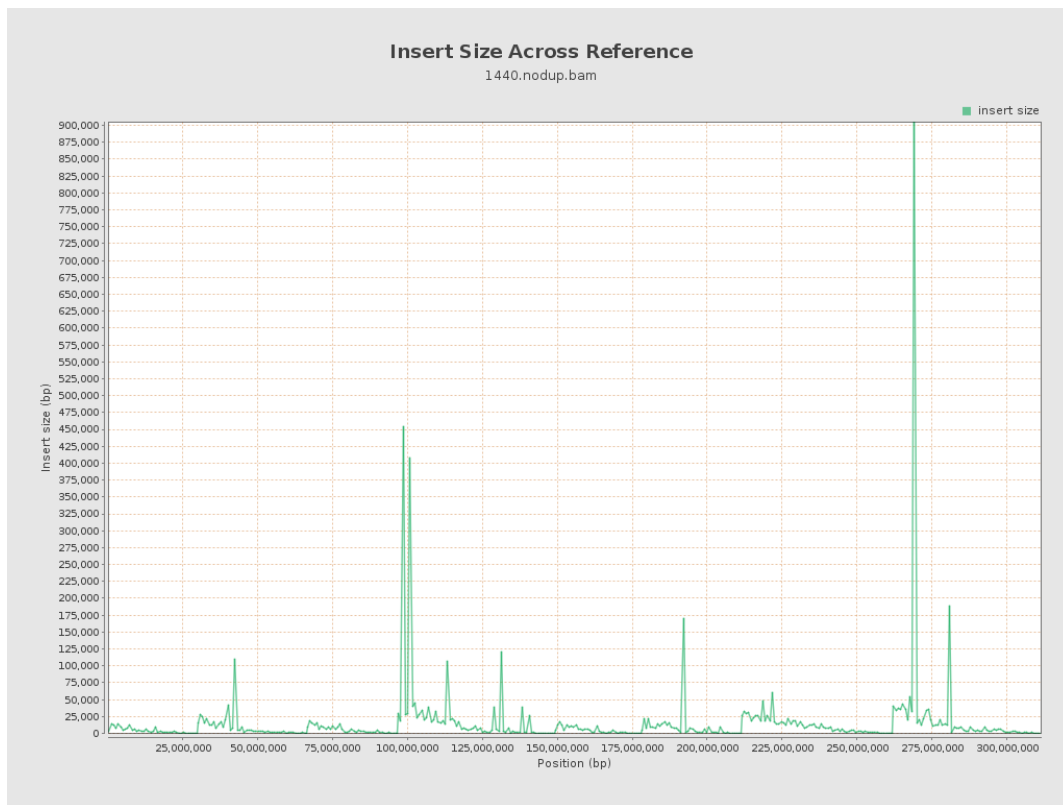
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
1440.nodup.bam

14. Results : Insert Size Across Reference

Insert Size Across Reference
1440.nodup.bam

15. Results : Insert Size Histogram