Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:33:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1105
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1105 .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_547/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_547_S114_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_547/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_547_S114_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:33:43 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	80,308,034
Mapped reads	72,562,445 / 90.36%
Unmapped reads	7,745,589 / 9.64%
Mapped paired reads	72,562,445 / 90.36%
Mapped reads, first in pair	36,403,149 / 45.33%
Mapped reads, second in pair	36,159,296 / 45.03%
Mapped reads, both in pair	70,982,916 / 88.39%
Mapped reads, singletons	1,579,529 / 1.97%
Read min/max/mean length	30 / 151 / 148.28
Duplicated reads (flagged)	11,445,754 / 14.25%
Clipped reads	17,132,975 / 21.33%

2.2. ACGT Content

Number/percentage of A's	3,101,832,577 / 30.98%
Number/percentage of C's	1,903,650,404 / 19.01%
Number/percentage of T's	3,105,066,307 / 31.02%
Number/percentage of G's	1,900,890,332 / 18.99%
Number/percentage of N's	70,458 / 0%
GC Percentage	38%

2.3. Coverage

Mean	32.2062
Standard Deviation	241.1921

2.4. Mapping Quality

Mean Mapping Quality	44.5

2.5. Insert size

Mean	210,493.39
Standard Deviation	2,180,056.23
P25/Median/P75	296 / 388 / 504

2.6. Mismatches and indels

General error rate	2.49%
Mismatches	231,237,306
Insertions	6,709,896
Mapped reads with at least one insertion	8.3%
Deletions	6,768,665
Mapped reads with at least one deletion	8.29%
Homopolymer indels	56.4%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	815173508	27.4244	80.7243

LT669789.1	36598175	1171289391	32.004	247.4849
LT669790.1	30422129	1083961280	35.6307	270.7612
LT669791.1	52758100	1657837320	31.4234	221.6496
LT669792.1	28376109	912306788	32.1505	254.7013
LT669793.1	33388210	993101344	29.7441	171.6571
LT669794.1	50579949	1521338224	30.0779	201.0896
LT669795.1	49795044	1881798199	37.7909	347.0885

3. Results : Coverage across reference

Coverage across reference
1105.nodup.bam

4. Results : Coverage Histogram

Coverage Histogram
1105.nodup.bam
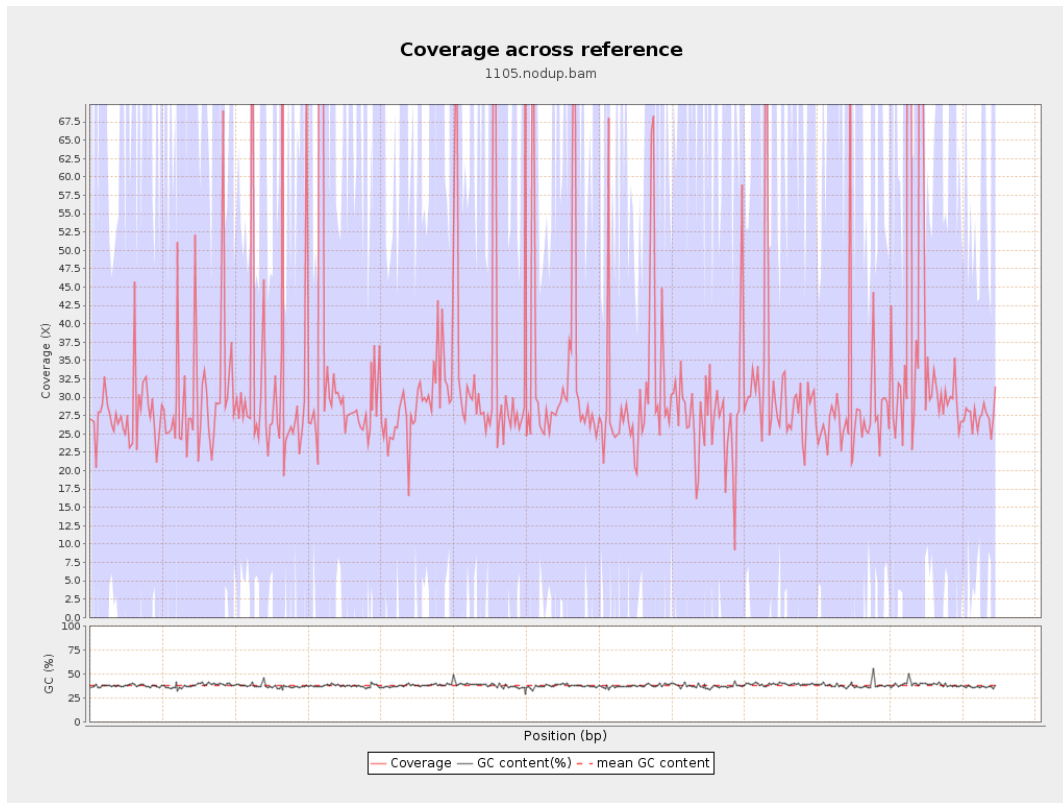
5. Results : Coverage Histogram (0-50X)
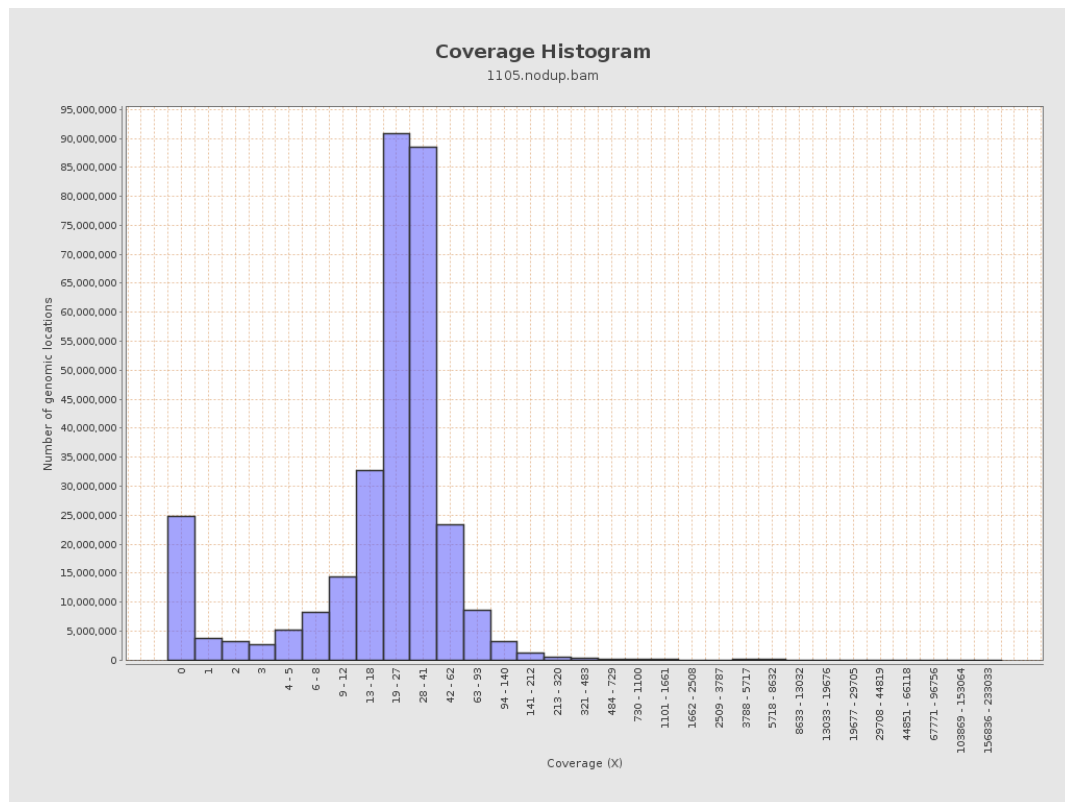
Coverage Histogram (0-50X)
1105.nodup.bam
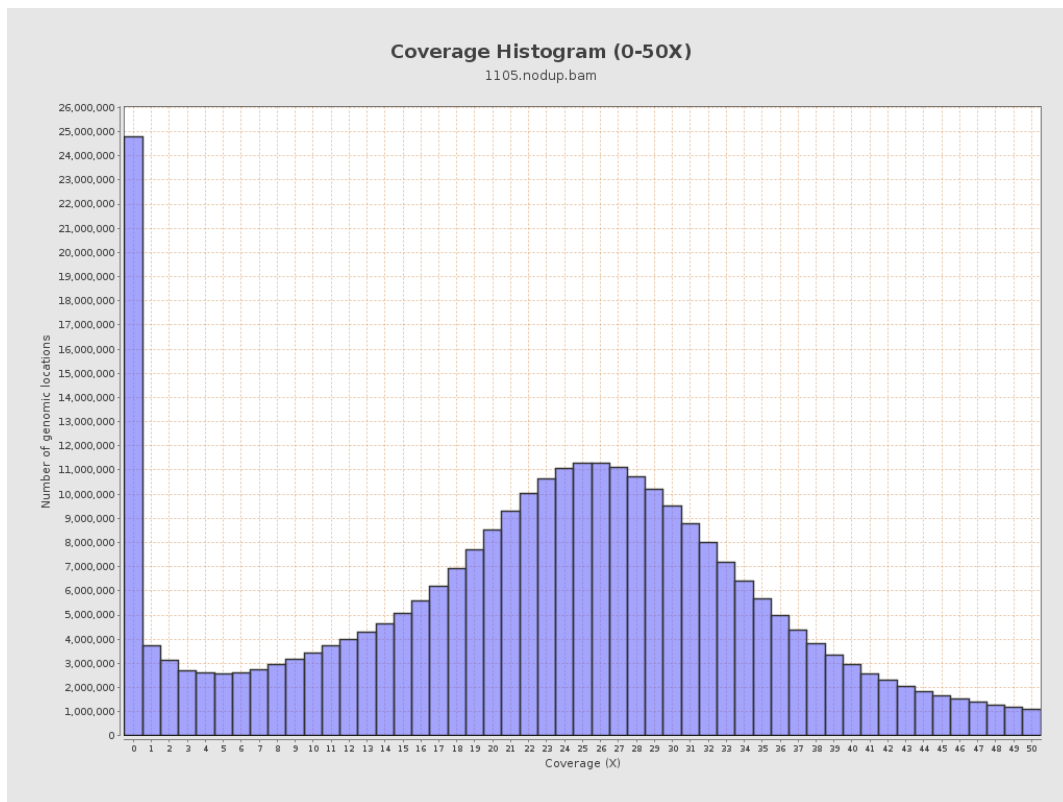
6. Results : Genome Fraction Coverage
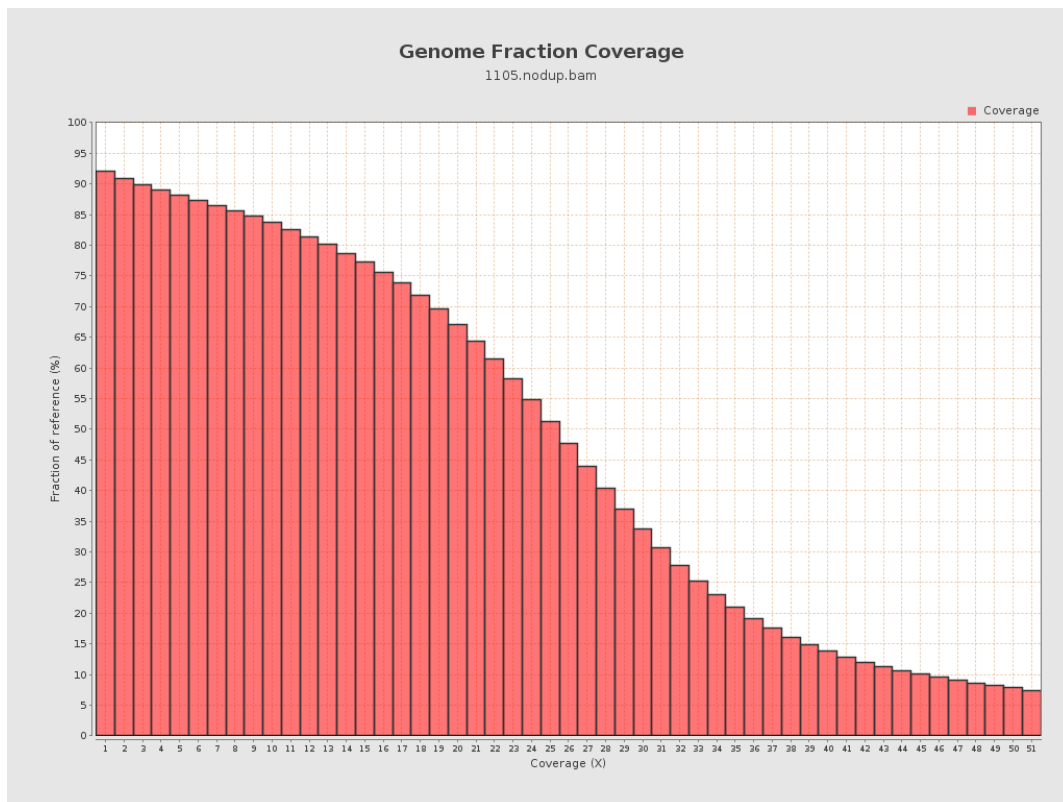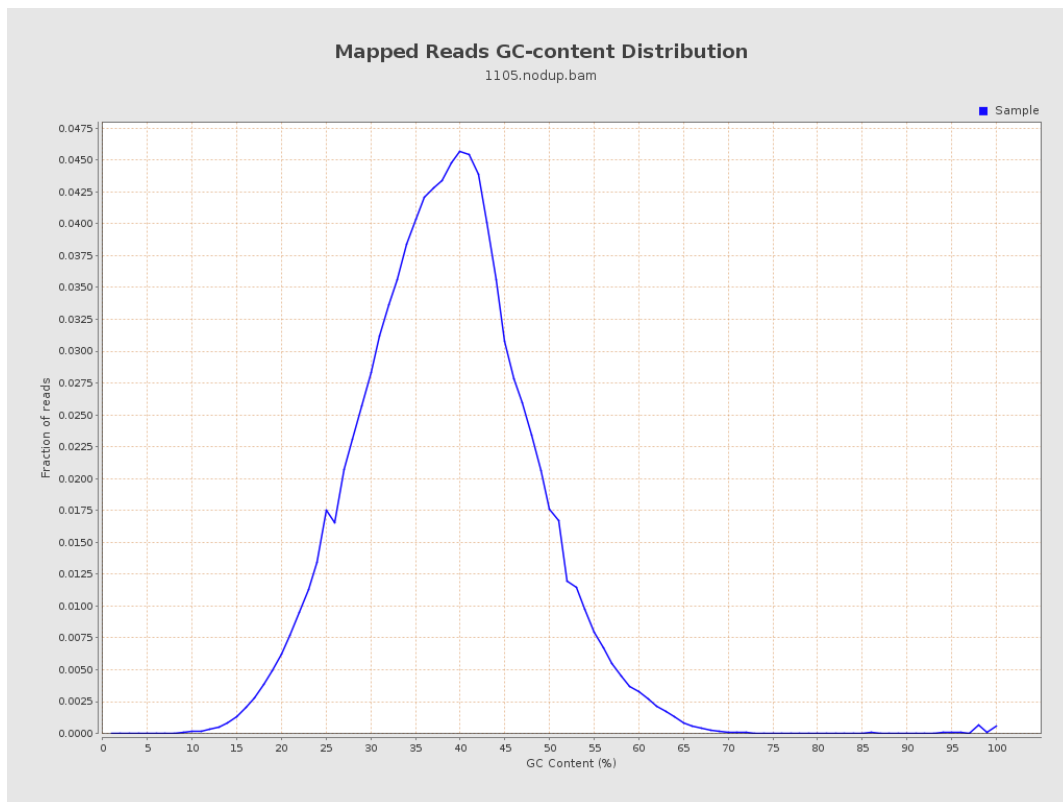
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
1105.nodup.bam
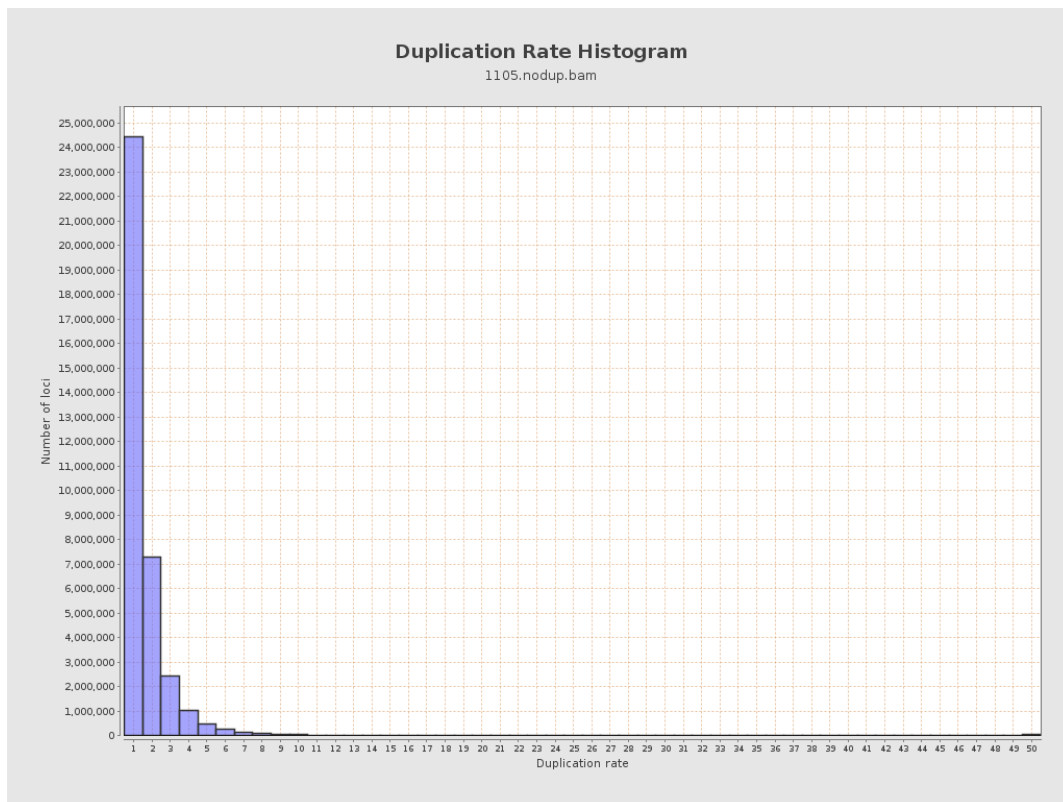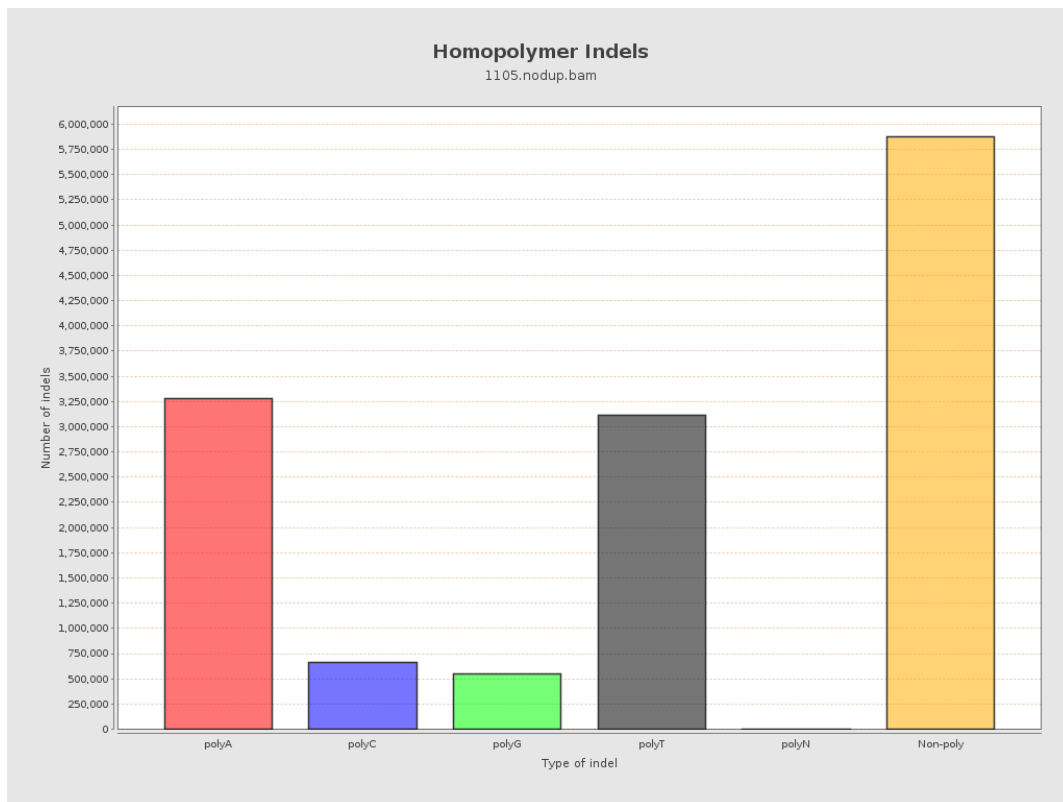
8. Results : Mapped Reads Nucleotide Content
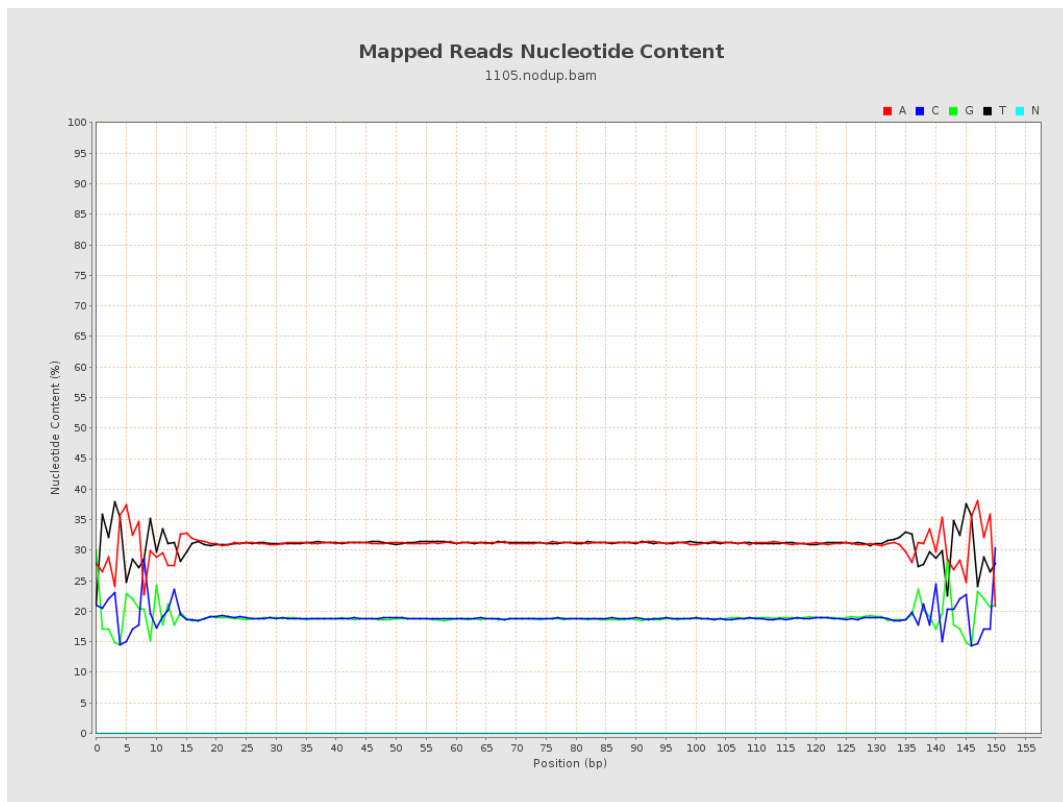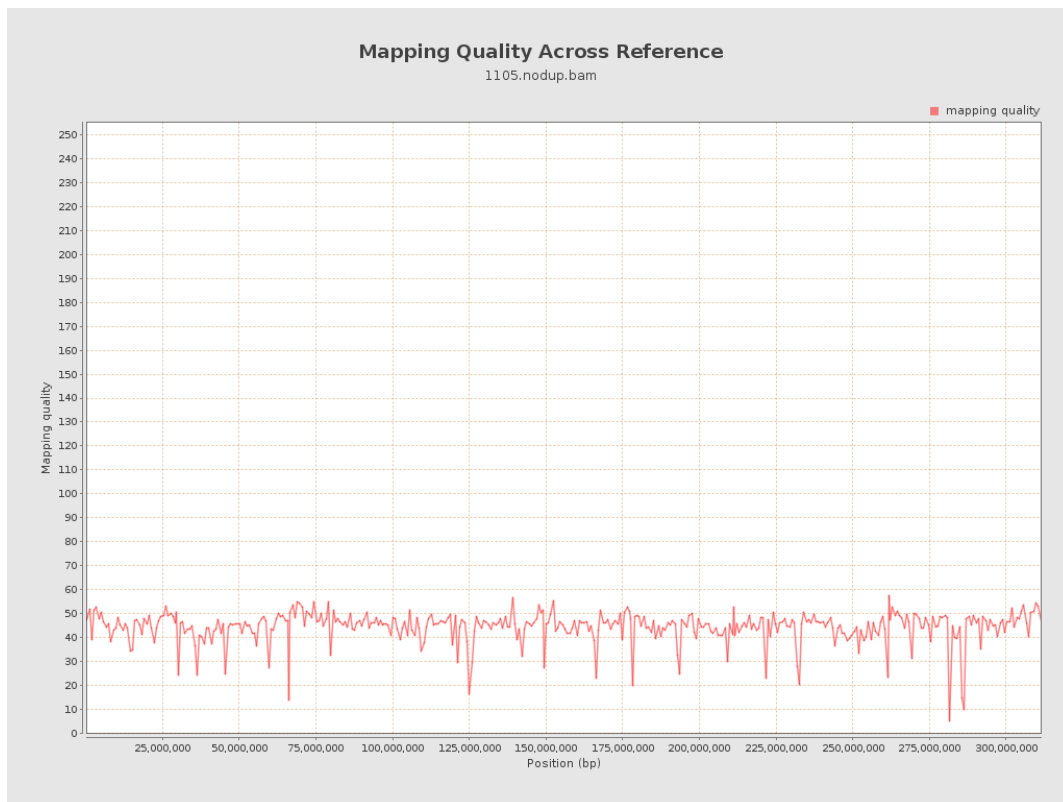
9. Results : Mapped Reads GC-content Distribution
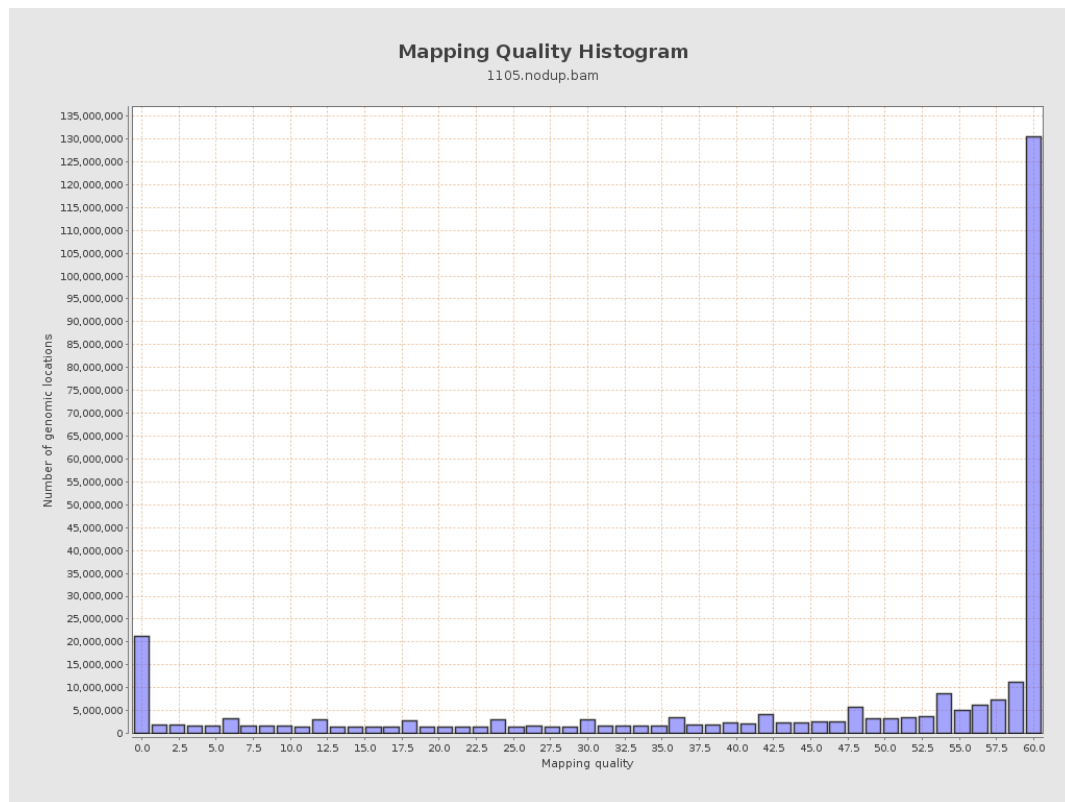
10. Results : Mapped Reads Clipping Profile
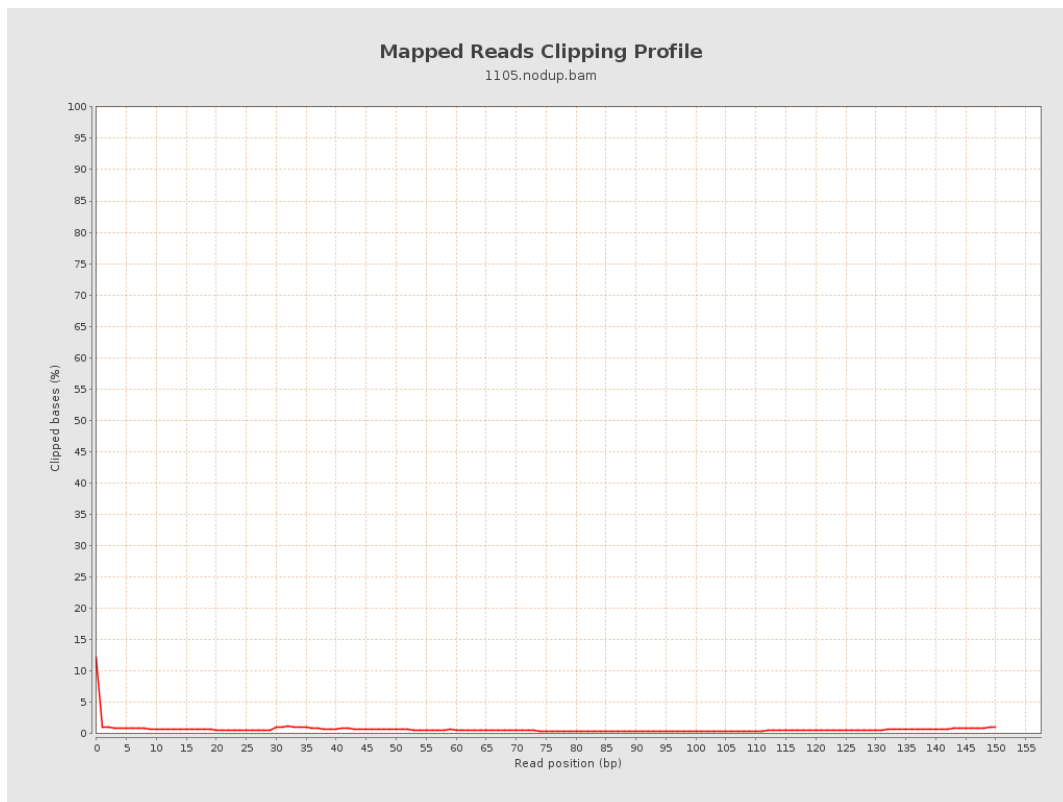
11. Results : Homopolymer Indels

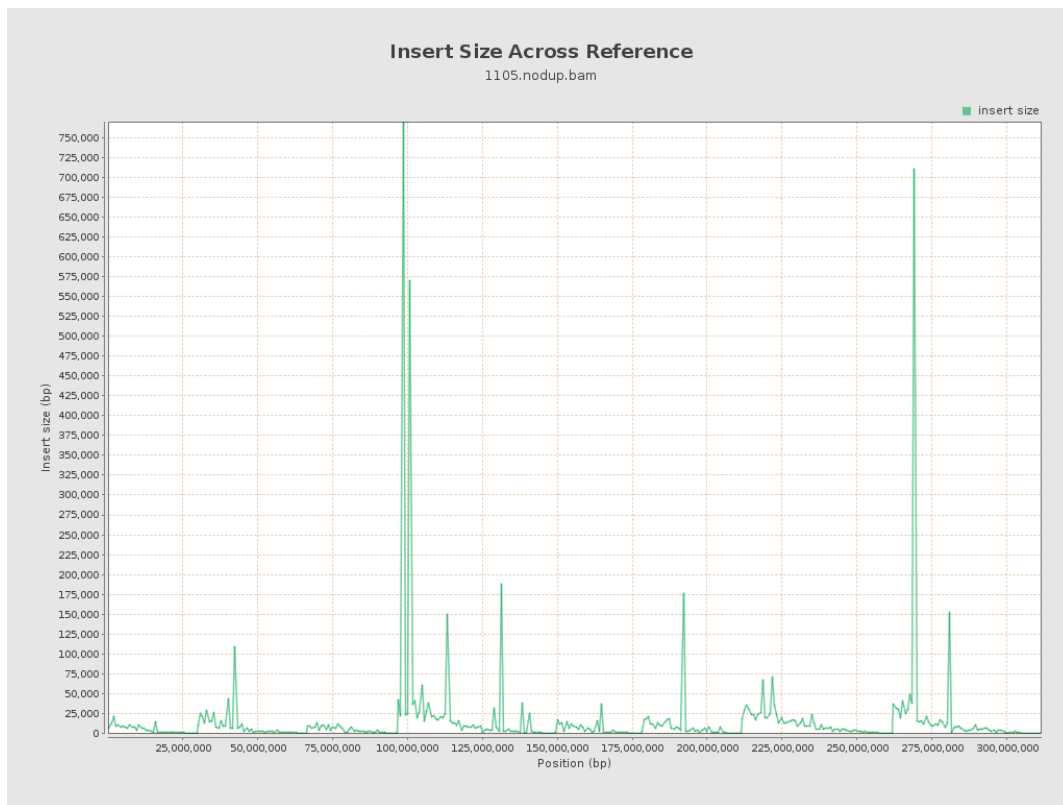# 12. Results : Mapping Quality Across Reference

Mapping Quality Across Reference
1105.nodup.bam

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
1105.nodup.bam

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram

Insert Size Histogram
1105.nodup.bam