Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:32:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/142
7
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1427 .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_412/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_412_S387_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_412/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_412_S387_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:32:42 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	70,342,829
Mapped reads	66,536,200 / 94.59%
Unmapped reads	3,806,629 / 5.41%
Mapped paired reads	66,536,200 / 94.59%
Mapped reads, first in pair	33,317,317 / 47.36%
Mapped reads, second in pair	33,218,883 / 47.22%
Mapped reads, both in pair	65,311,028 / 92.85%
Mapped reads, singletons	1,225,172 / 1.74%
Read min/max/mean length	30 / 151 / 148.31
Duplicated reads (flagged)	10,300,149 / 14.64%
Clipped reads	13,489,478 / 19.18%

2.2. ACGT Content

Number/percentage of A's	2,872,257,433 / 30.84%
Number/percentage of C's	1,788,978,938 / 19.21%
Number/percentage of T's	2,872,870,880 / 30.84%
Number/percentage of G's	1,779,986,274 / 19.11%
Number/percentage of N's	32,232 / 0%
GC Percentage	38.32%

2.3. Coverage

Mean	29.9625
Standard Deviation	228.7992

2.4. Mapping Quality

Mean Mapping Quality	44.6

2.5. Insert size

Mean	215,674.52
Standard Deviation	2,191,579.05
P25/Median/P75	342 / 443 / 576

2.6. Mismatches and indels

General error rate	2.18%
Mismatches	186,165,951
Insertions	5,948,312
Mapped reads with at least one insertion	8.05%
Deletions	6,147,445
Mapped reads with at least one deletion	8.22%
Homopolymer indels	56.63%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	728023909	24.4925	55.5539

LT669789.1	36598175	1084096662	29.6216	221.9847
LT669790.1	30422129	951275607	31.2692	210.438
LT669791.1	52758100	1570297796	29.7641	173.8443
LT669792.1	28376109	831959181	29.319	268.0002
LT669793.1	33388210	914280933	27.3833	115.5038
LT669794.1	50579949	1438118071	28.4326	188.0783
LT669795.1	49795044	1819515044	36.5401	380.2838

3. Results : Coverage across reference

Coverage across reference
1427.nodup.bam

4. Results : Coverage Histogram

Coverage Histogram
1427.nodup.bam
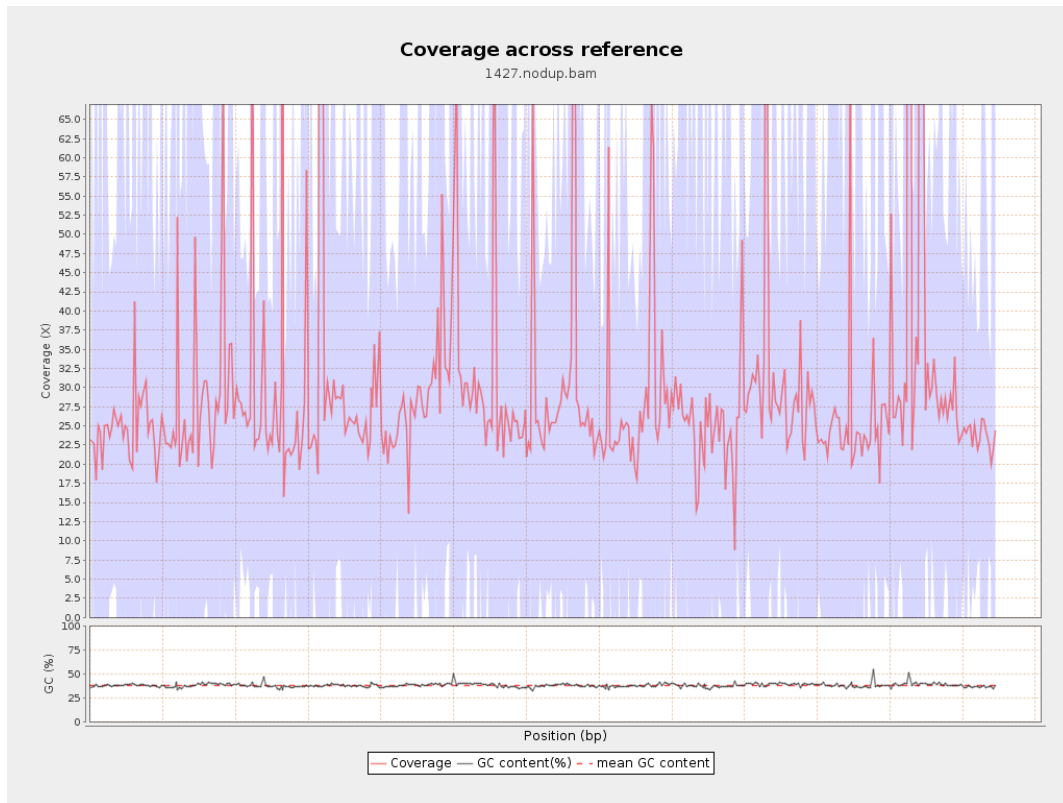
5. Results : Coverage Histogram (0-50X)
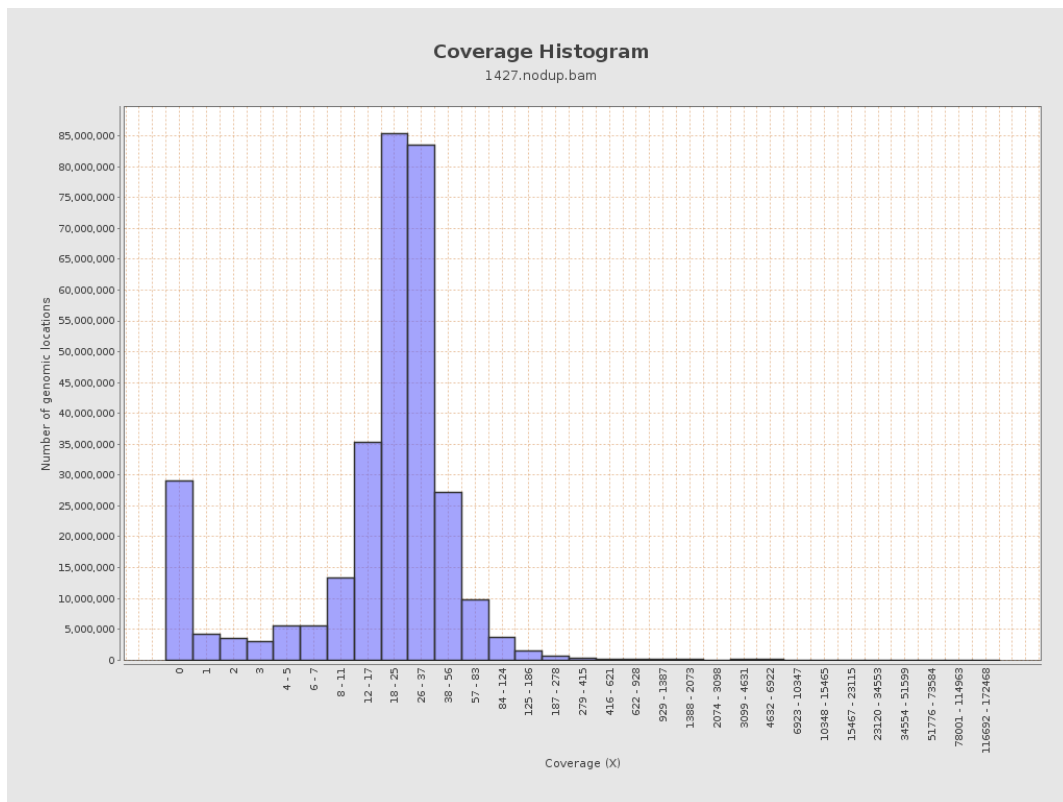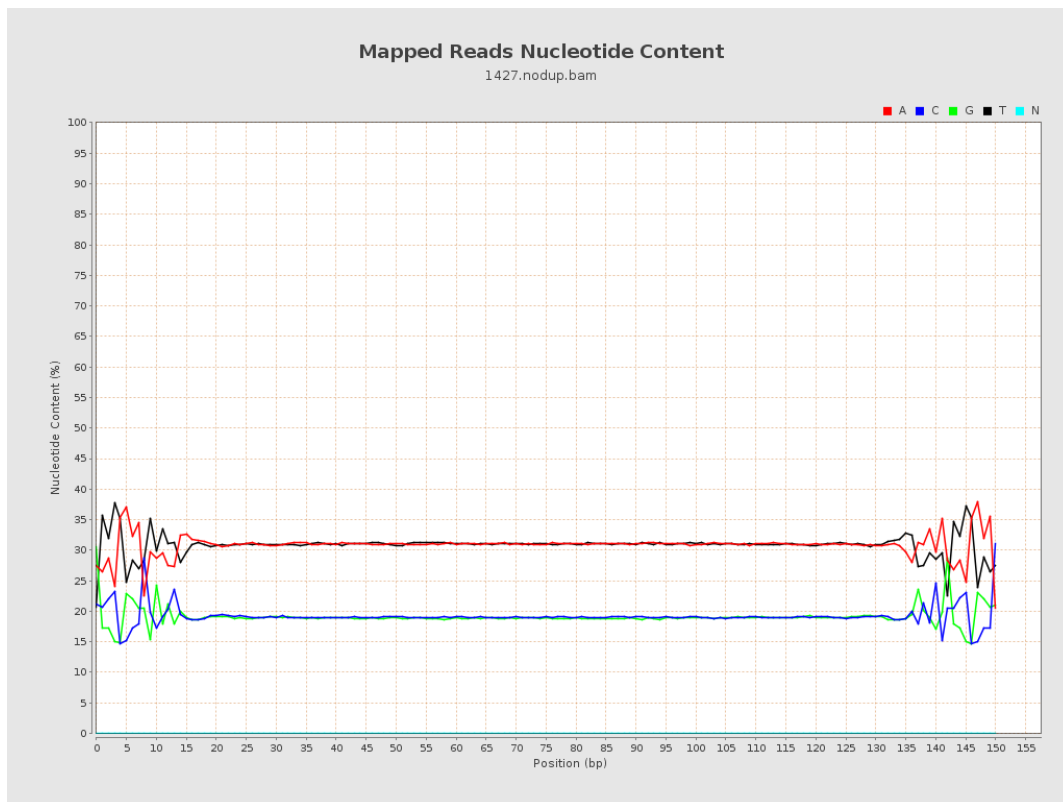
Coverage Histogram (0-50X)
1427.nodup.bam
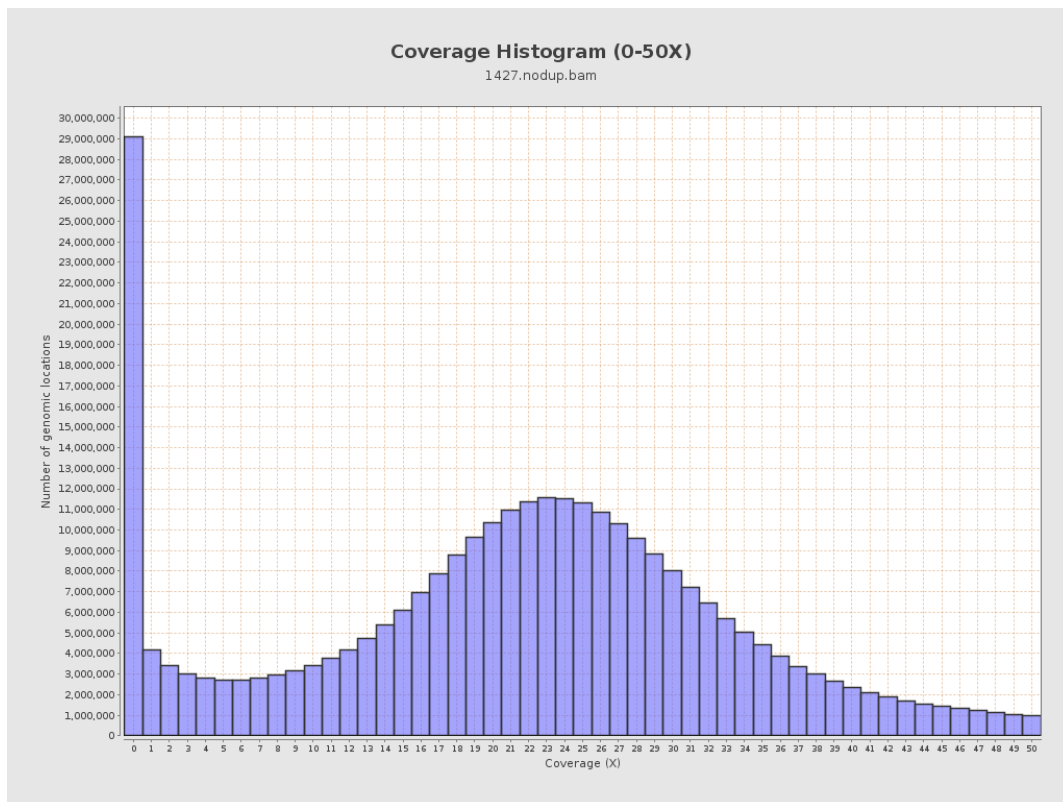
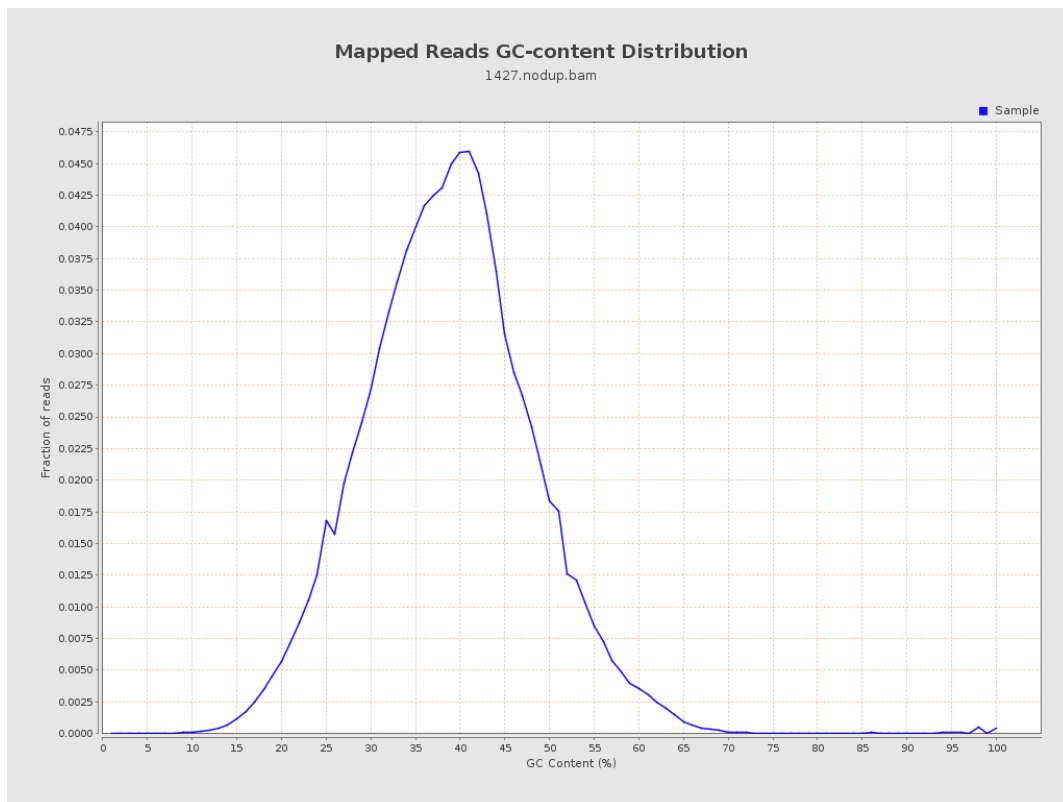# 6. Results : Genome Fraction Coverage
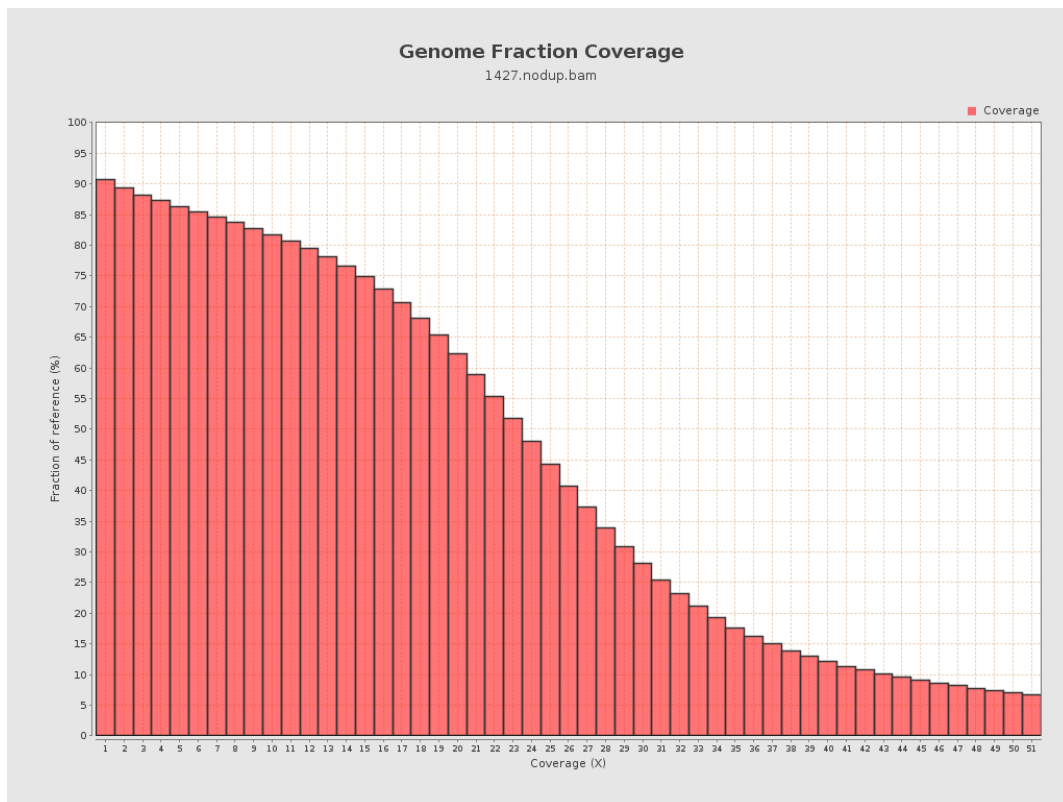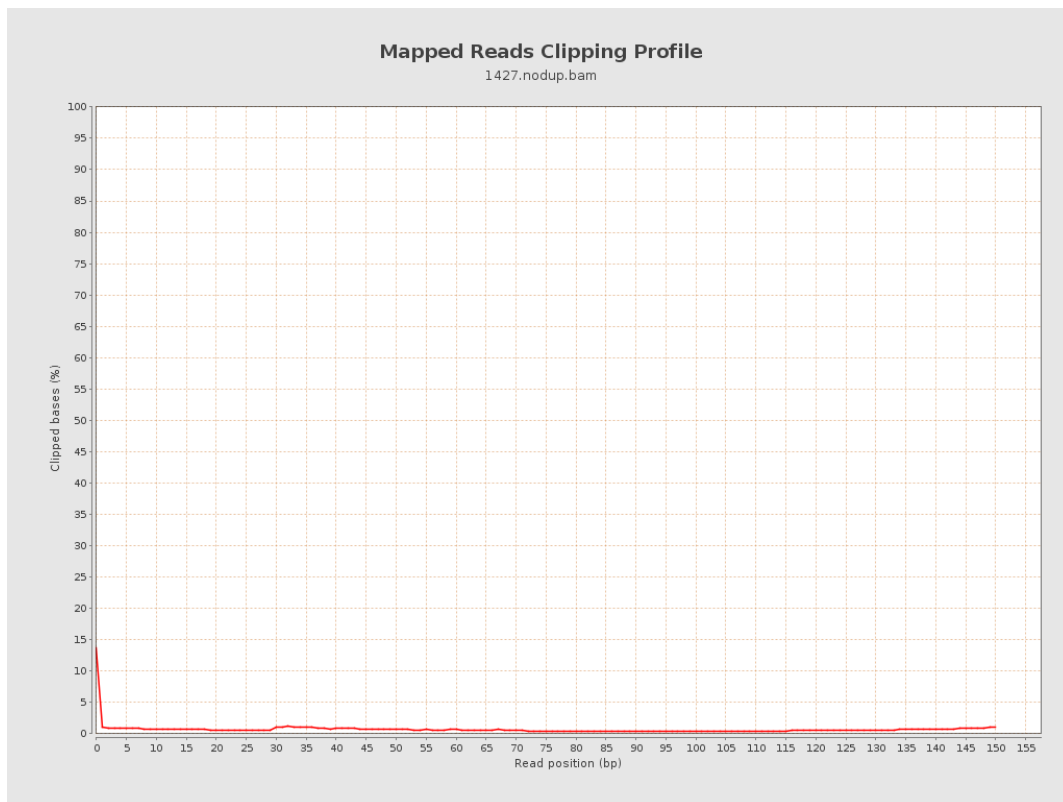
7. Results : Duplication Rate Histogram
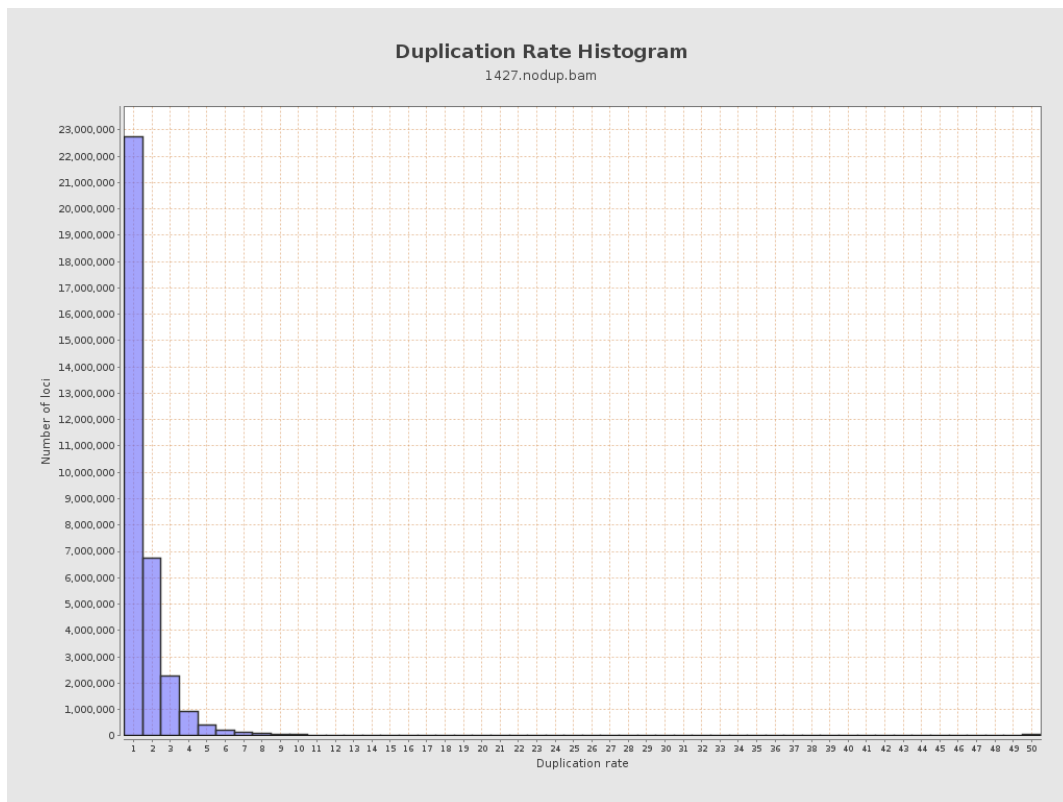
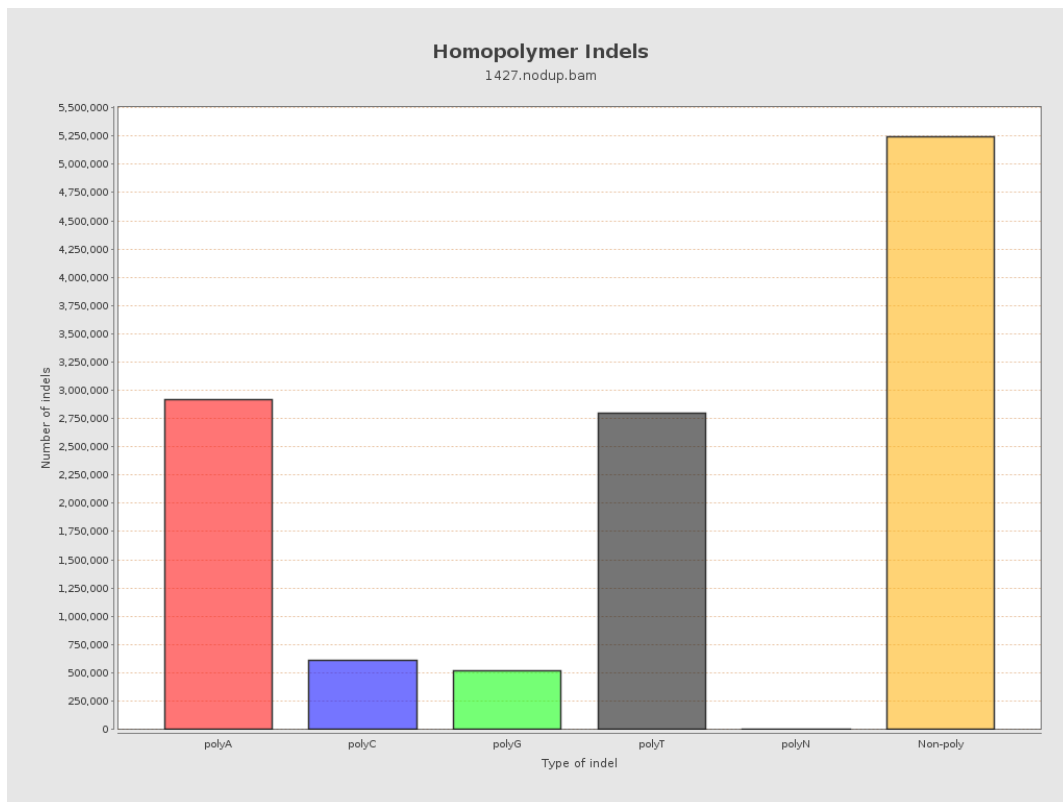# 8. Results : Mapped Reads Nucleotide Content

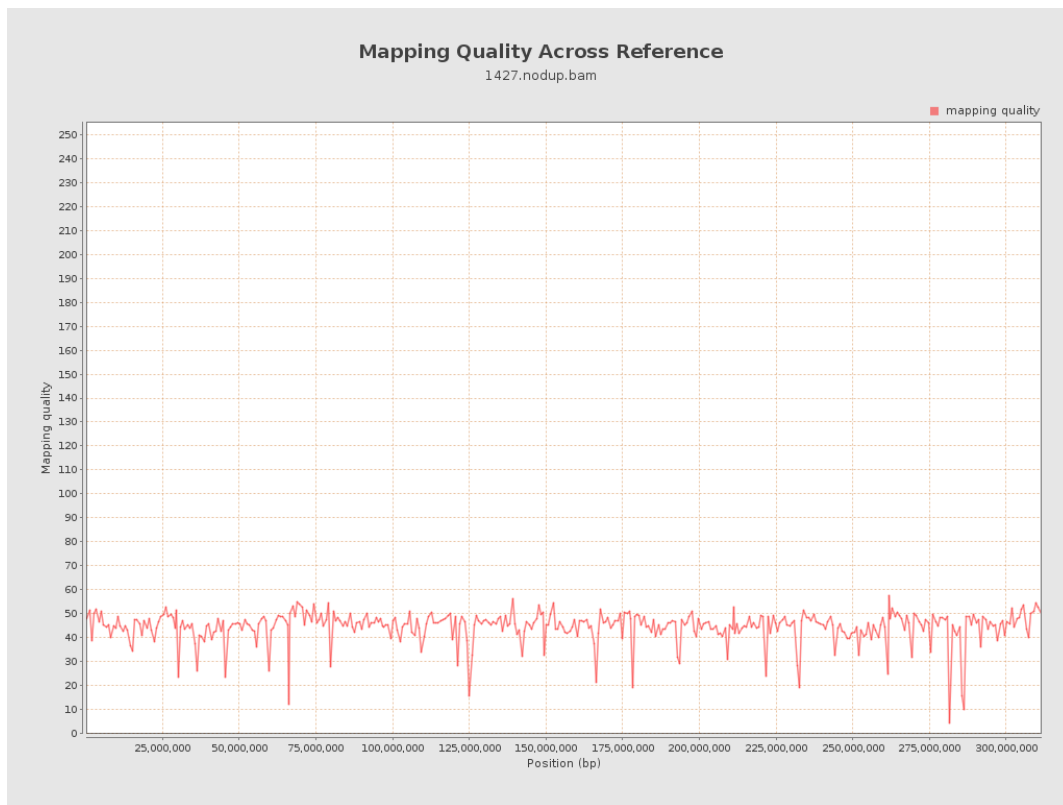# 9. Results : Mapped Reads GC-content Distribution
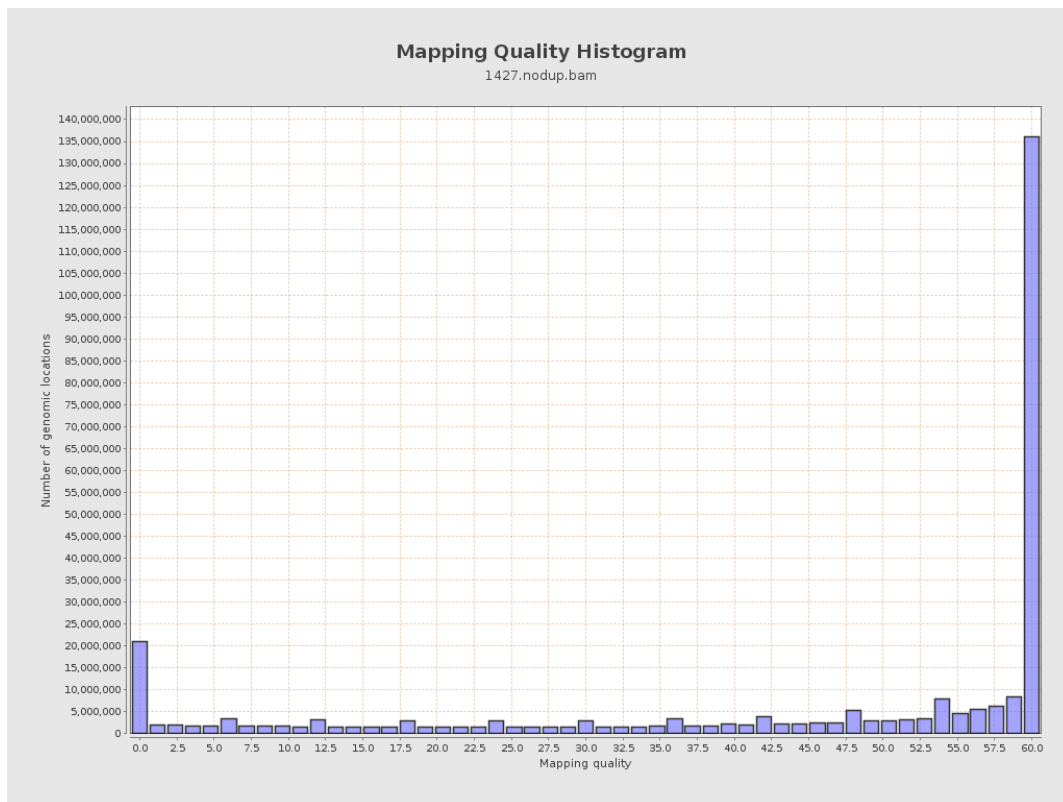
10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels

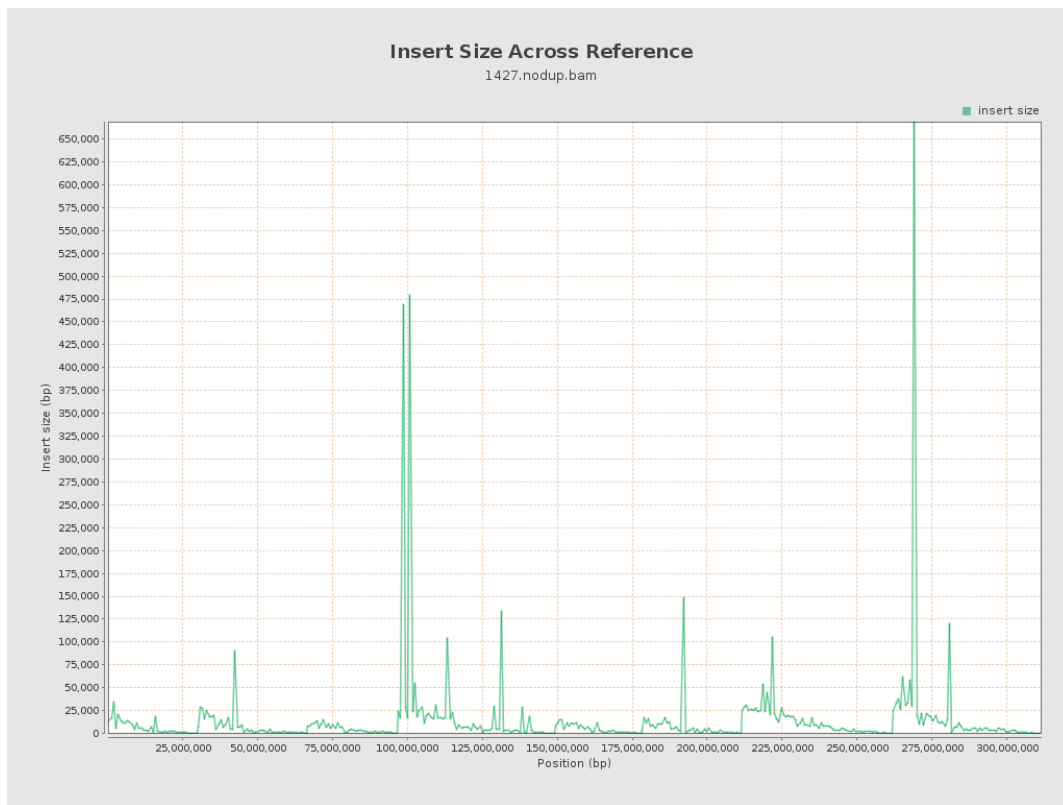# 12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
1427.nodup.bam

14. Results : Insert Size Across Reference

Insert Size Across Reference
1427.nodup.bam

15. Results : Insert Size Histogram

Insert Size Histogram
1427.nodup.bam