

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:35:23*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/112
0
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1120 .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/r eference/GCA_900128785.1_MPIPZ. v5_genomic.fa /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_555/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_555_S122_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_555/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_555_S122_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:35:22 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	79,834,055
Mapped reads	73,857,012 / 92.51%
Unmapped reads	5,977,043 / 7.49%
Mapped paired reads	73,857,012 / 92.51%
Mapped reads, first in pair	37,047,232 / 46.41%
Mapped reads, second in pair	36,809,780 / 46.11%
Mapped reads, both in pair	71,946,018 / 90.12%
Mapped reads, singletons	1,910,994 / 2.39%
Read min/max/mean length	30 / 151 / 147.9
Duplicated reads (flagged)	12,420,844 / 15.56%
Clipped reads	19,307,084 / 24.18%

### 2.2. ACGT Content

Number/percentage of A's	3,113,442,100 / 31.01%
Number/percentage of C's	1,905,053,867 / 18.98%
Number/percentage of T's	3,114,410,172 / 31.02%
Number/percentage of G's	1,905,756,866 / 18.98%
Number/percentage of N's	74,003 / 0%
GC Percentage	37.96%

### 2.3. Coverage

Mean	32.2983
Standard Deviation	291.186

## 2.4. Mapping Quality

Mean Mapping Quality	43.79
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## 2.5. Insert size

Mean	235,271.15
Standard Deviation	2,318,306.14
P25/Median/P75	285 / 383 / 500

## 2.6. Mismatches and indels

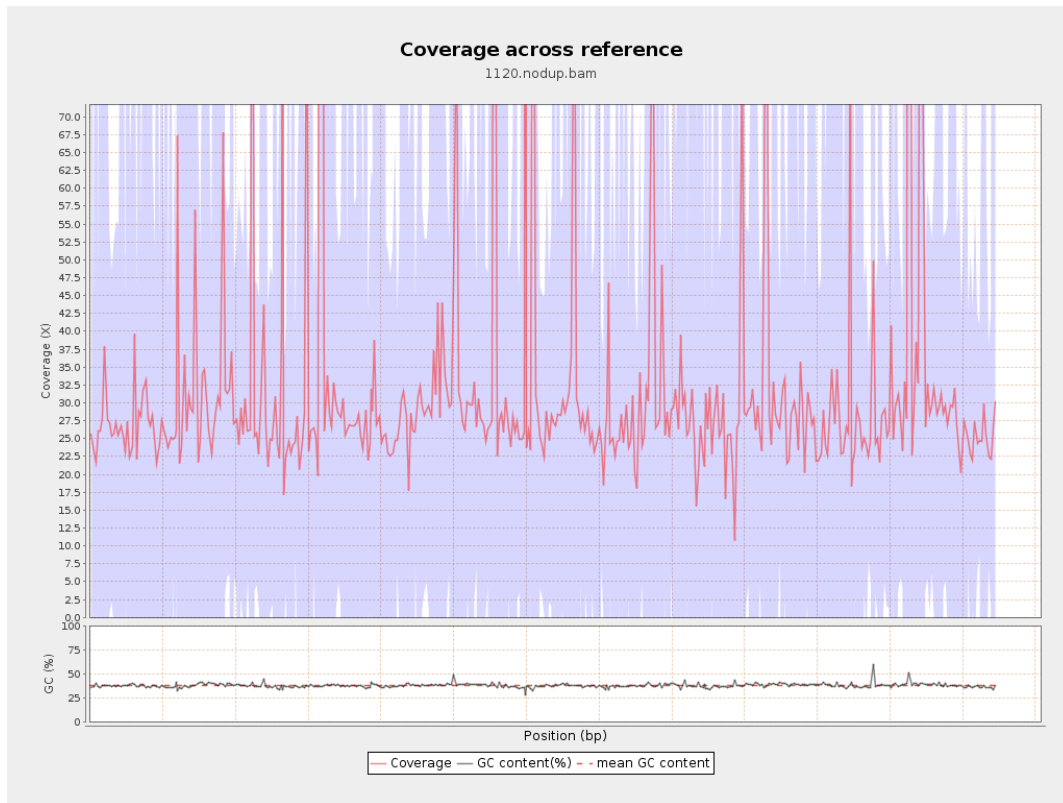
General error rate	2.58%
Mismatches	238,778,318
Insertions	7,311,720
Mapped reads with at least one insertion	8.84%
Deletions	7,152,597
Mapped reads with at least one deletion	8.59%
Homopolymer indels	57.01%

## 2.7. Chromosome stats

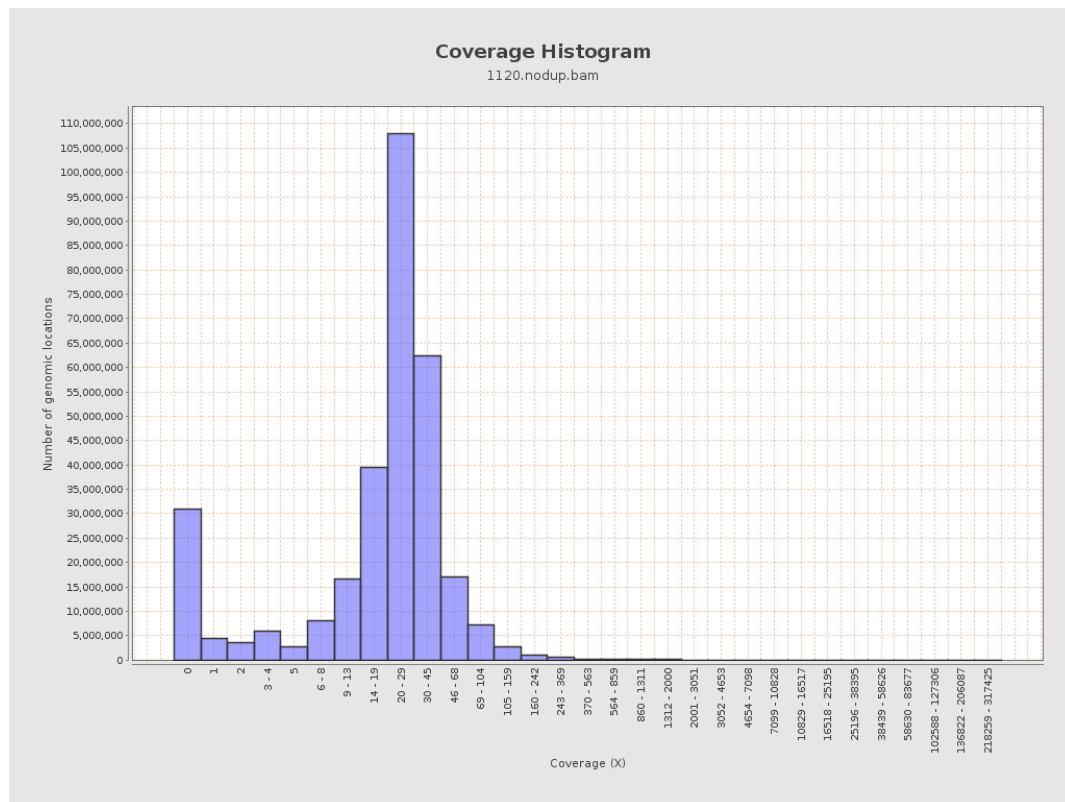
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	790986097	26.6107	103.8532

LT669789.1	36598175	1210073158	33.0638	296.178
LT669790.1	30422129	1167360671	38.3721	395.3382
LT669791.1	52758100	1672343171	31.6983	283.5564
LT669792.1	28376109	925061290	32.6	283.5638
LT669793.1	33388210	996053757	29.8325	196.4879
LT669794.1	50579949	1542016311	30.4867	243.8904
LT669795.1	49795044	1761610059	35.3772	383.2484

### 3. Results : Coverage across reference

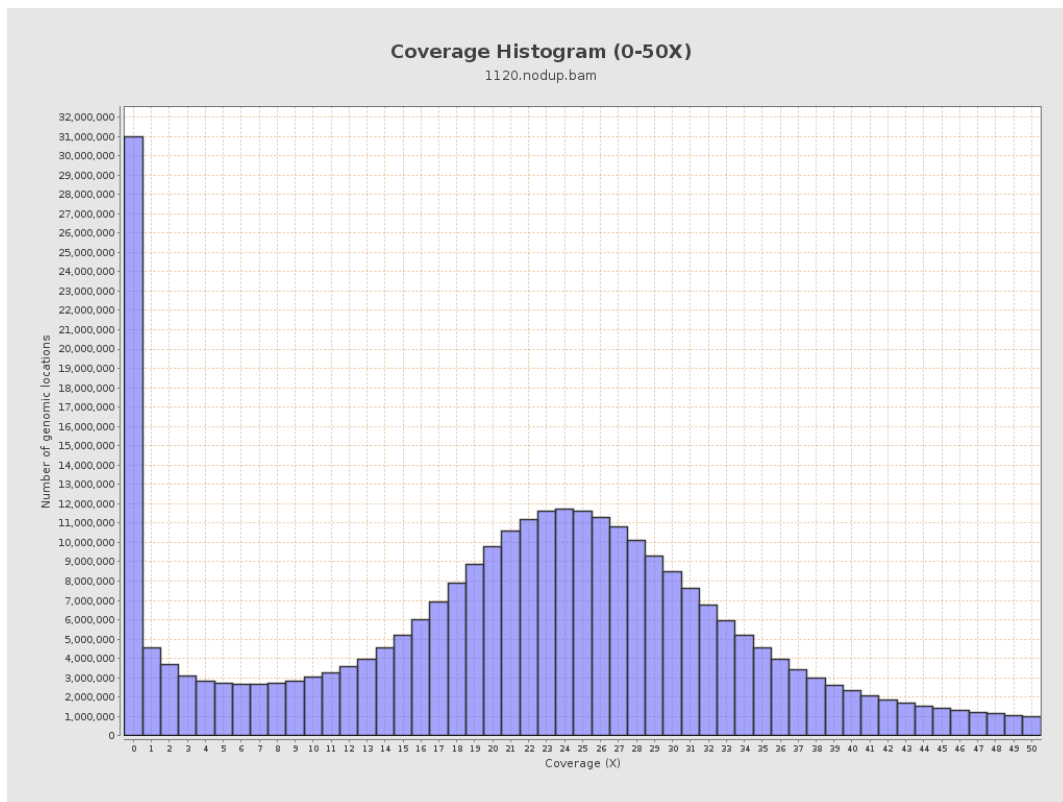


## 4. Results : Coverage Histogram

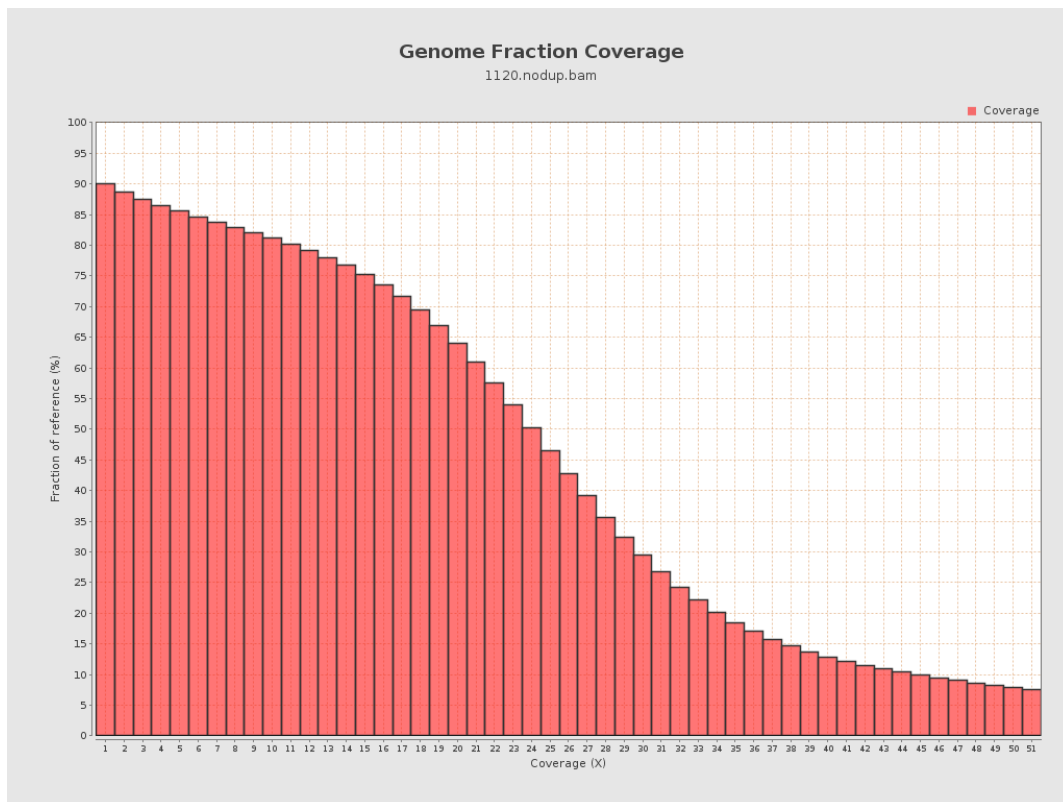




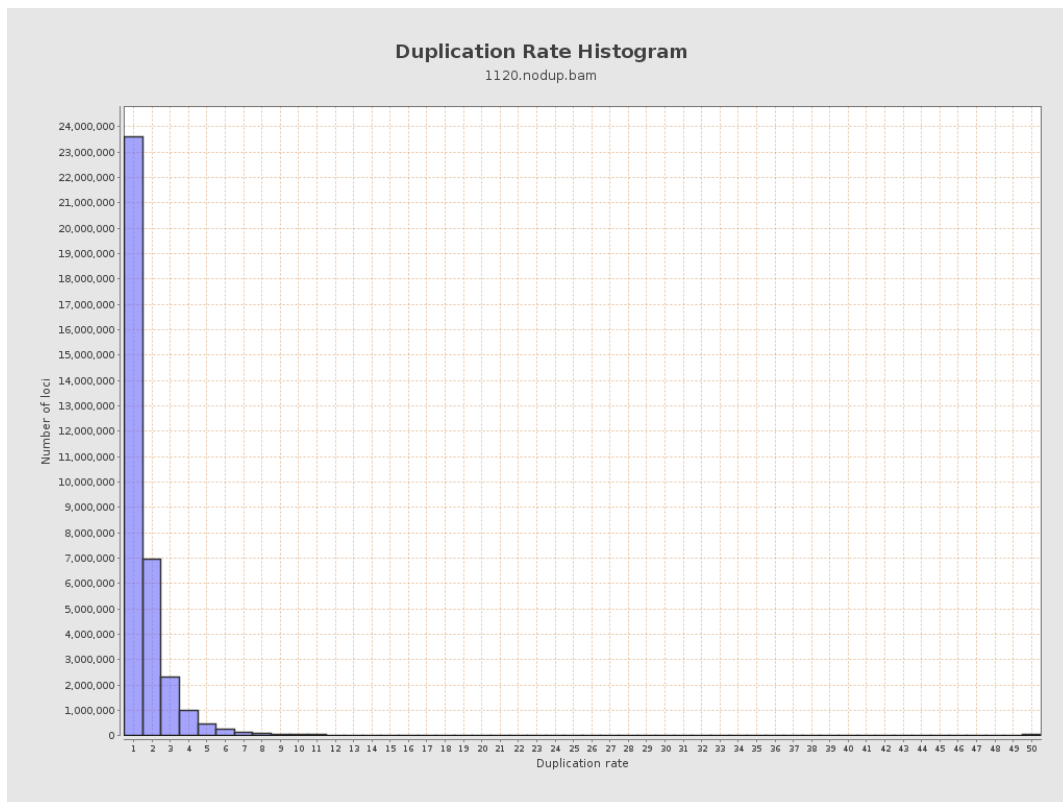
## 5. Results : Coverage Histogram (0-50X)



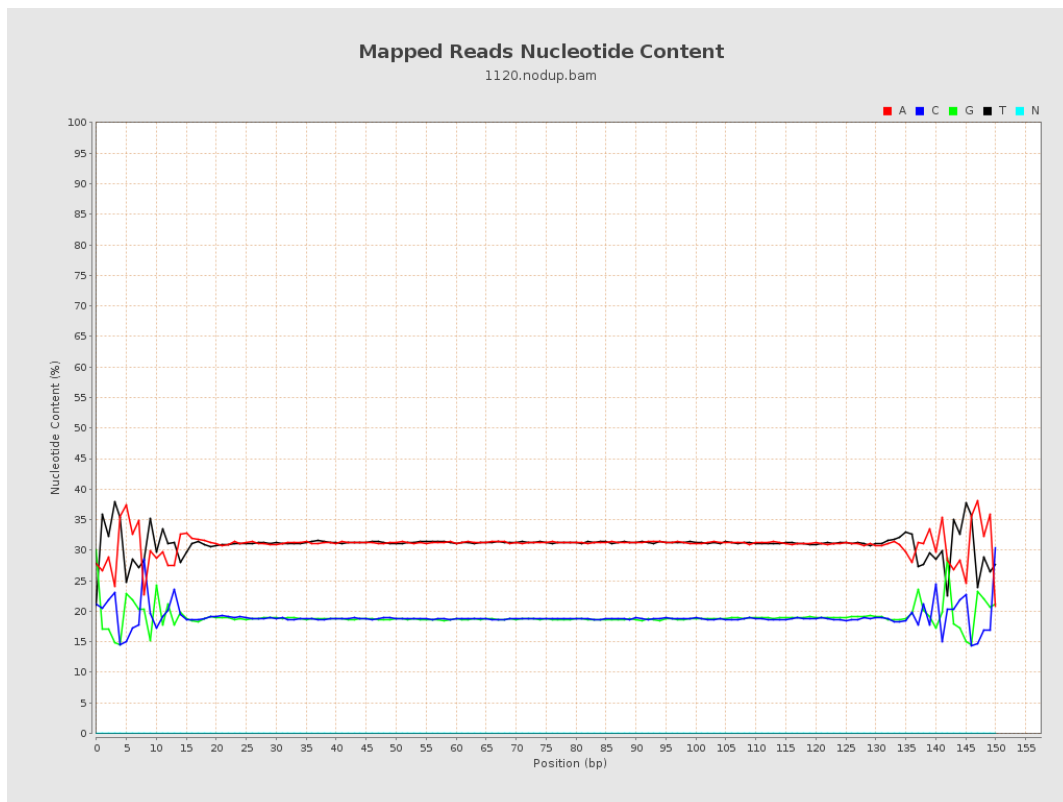
## 6. Results : Genome Fraction Coverage



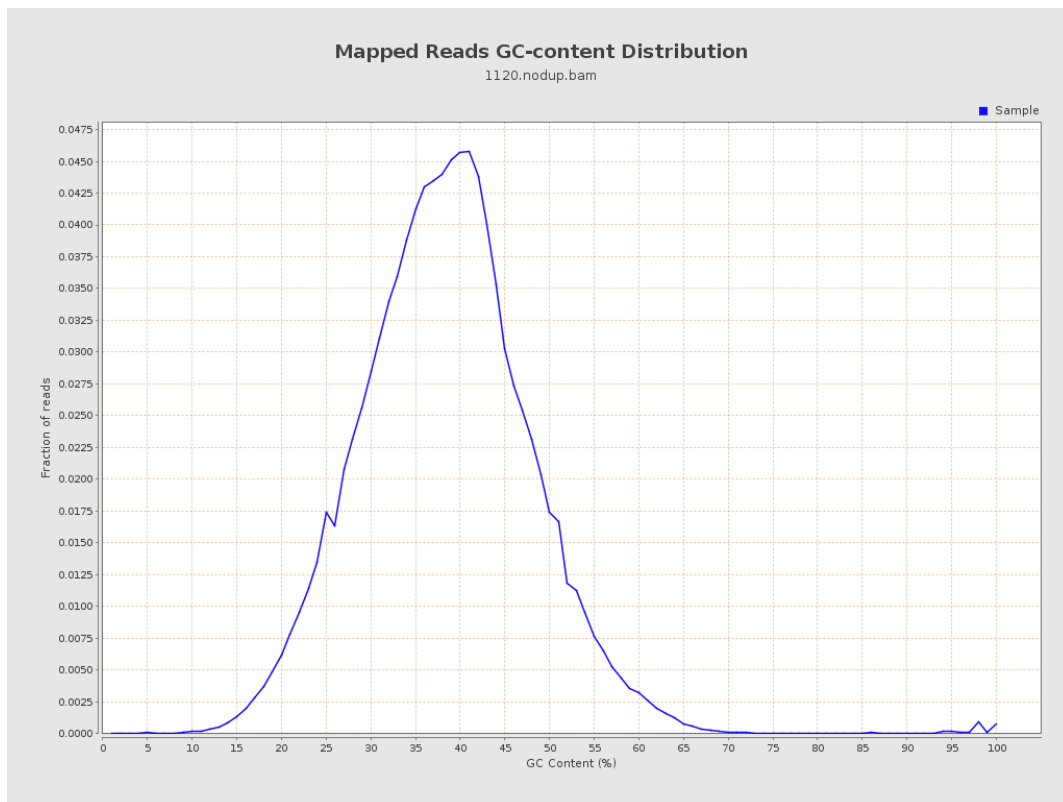
## 7. Results : Duplication Rate Histogram



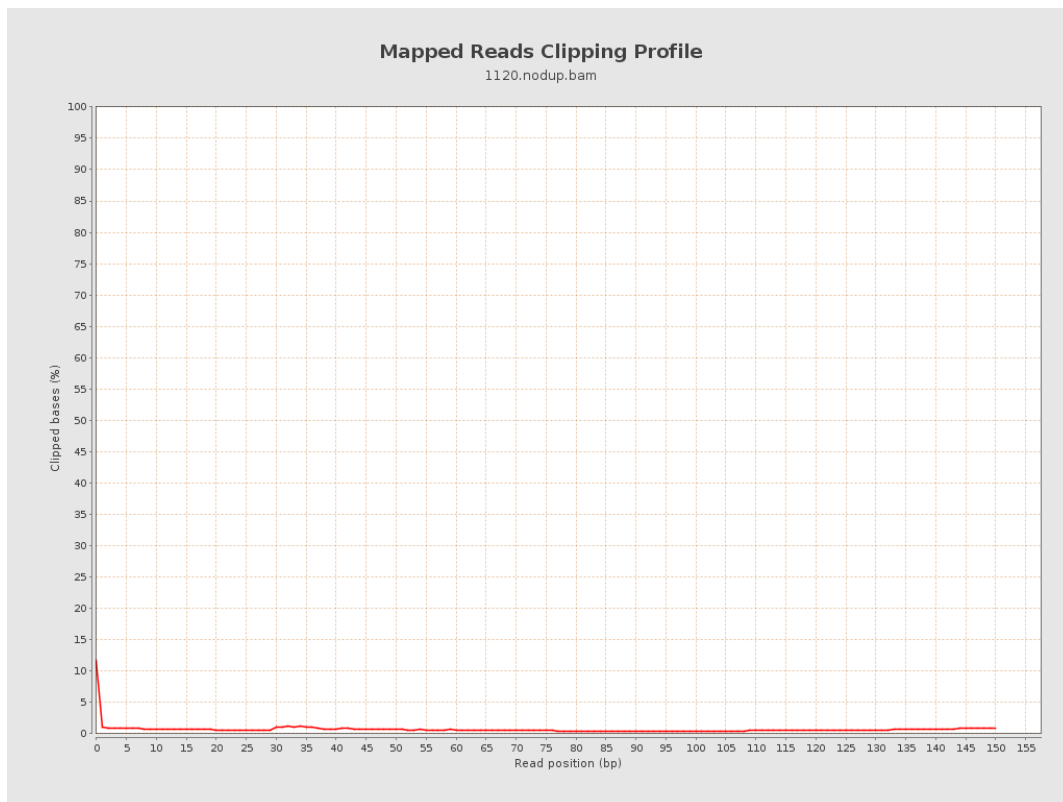
## 8. Results : Mapped Reads Nucleotide Content



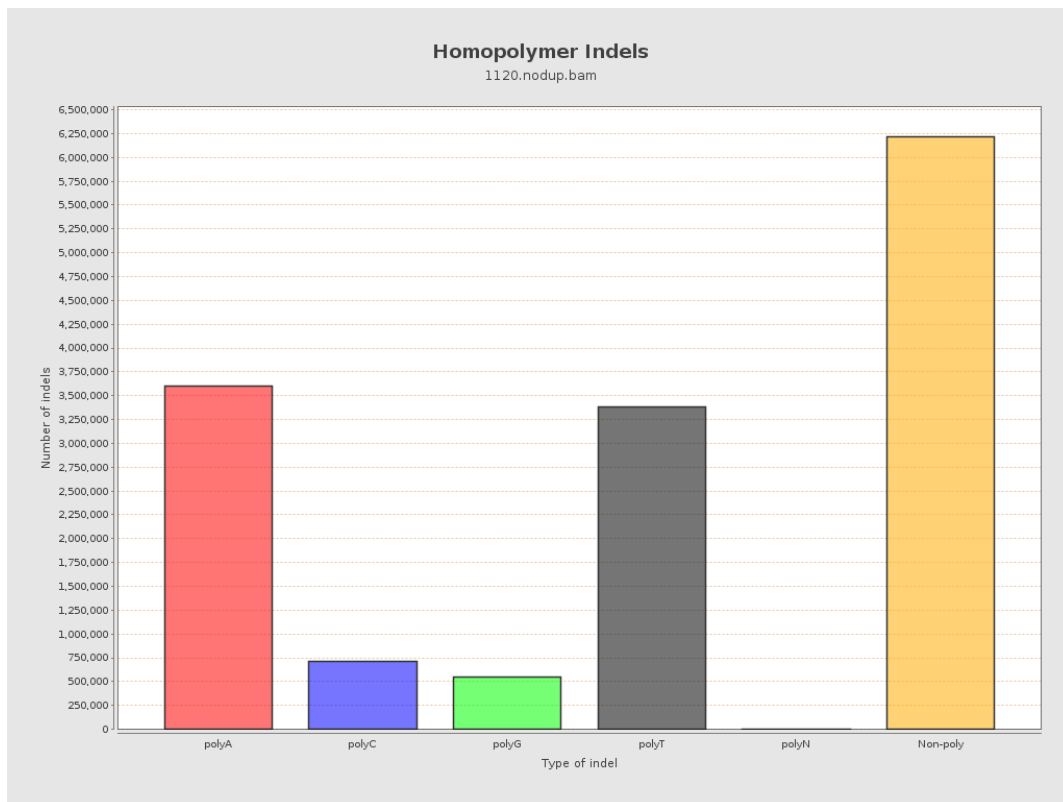
## 9. Results : Mapped Reads GC-content Distribution



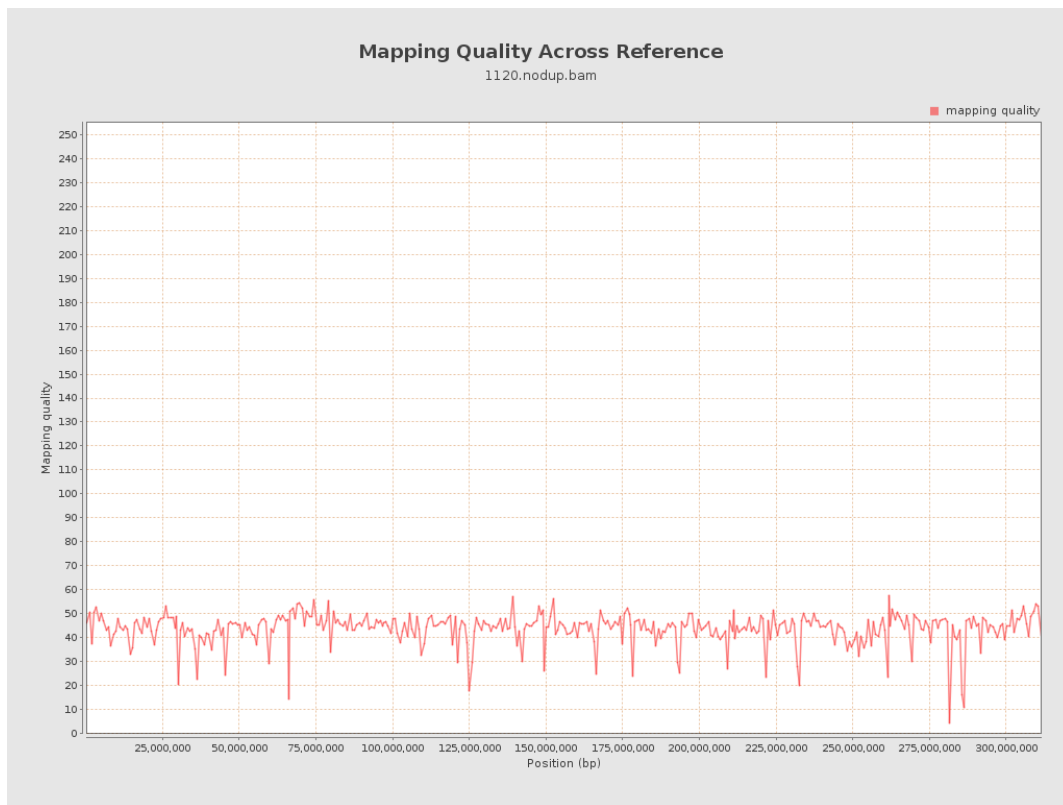
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

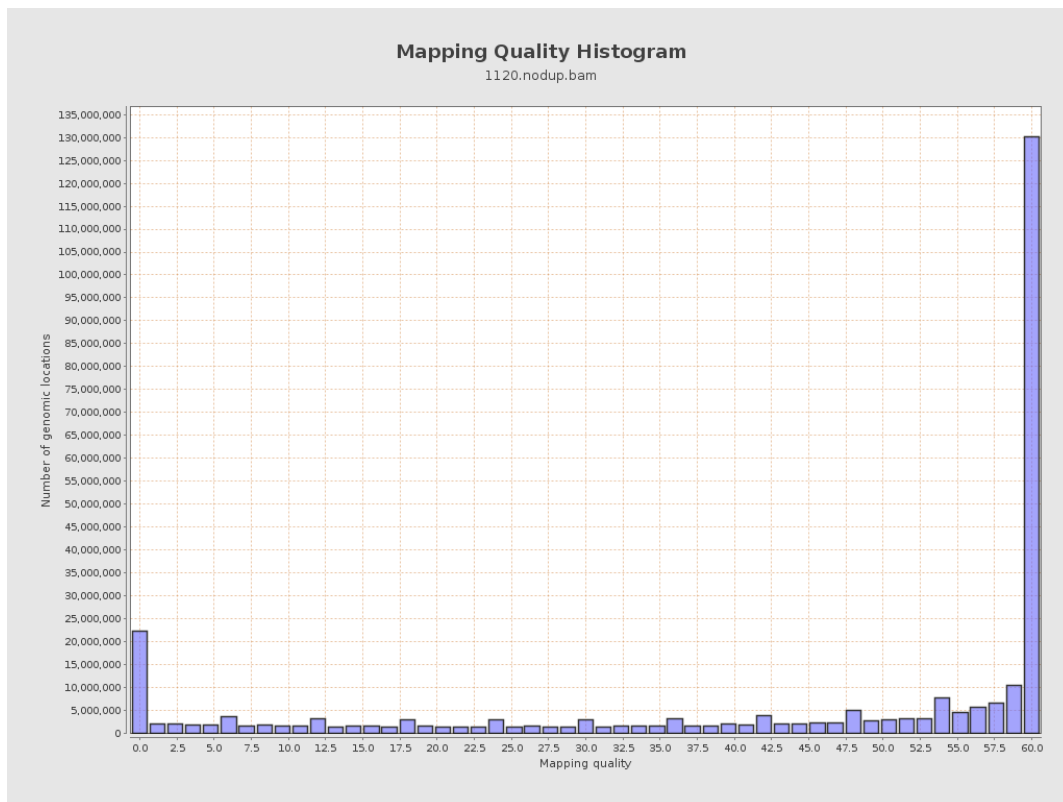


## 12. Results : Mapping Quality Across Reference

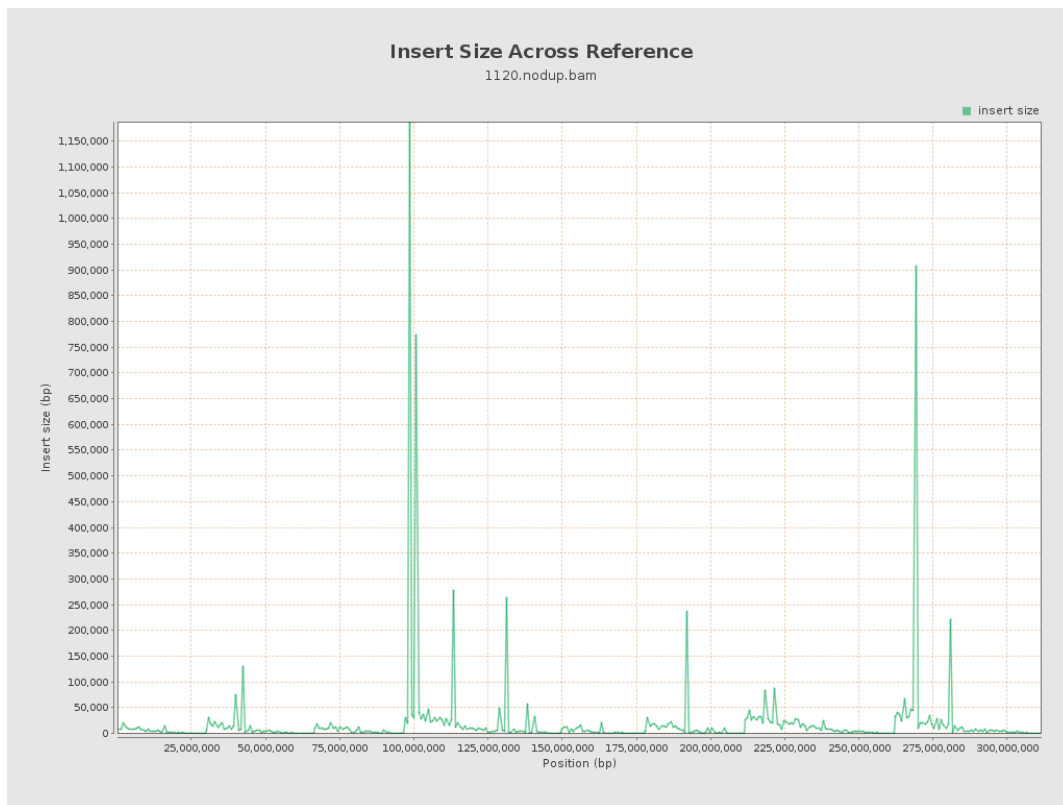




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

