

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:29:22*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/110
0
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1100 .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_409/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_409_S384_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_409/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_409_S384_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

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

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	58,451,066
Mapped reads	54,931,587 / 93.98%
Unmapped reads	3,519,479 / 6.02%
Mapped paired reads	54,931,587 / 93.98%
Mapped reads, first in pair	27,544,931 / 47.12%
Mapped reads, second in pair	27,386,656 / 46.85%
Mapped reads, both in pair	53,721,652 / 91.91%
Mapped reads, singletons	1,209,935 / 2.07%
Read min/max/mean length	30 / 151 / 148.05
Duplicated reads (flagged)	8,261,201 / 14.13%
Clipped reads	12,318,533 / 21.07%

### 2.2. ACGT Content

Number/percentage of A's	2,347,064,427 / 30.78%
Number/percentage of C's	1,464,504,909 / 19.21%
Number/percentage of T's	2,350,604,487 / 30.83%
Number/percentage of G's	1,463,015,728 / 19.19%
Number/percentage of N's	25,904 / 0%
GC Percentage	38.39%

### 2.3. Coverage

Mean	24.5334
Standard Deviation	205.5481

## 2.4. Mapping Quality

Mean Mapping Quality	43.59
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## 2.5. Insert size

Mean	255,087.02
Standard Deviation	2,397,652.43
P25/Median/P75	372 / 482 / 623

## 2.6. Mismatches and indels

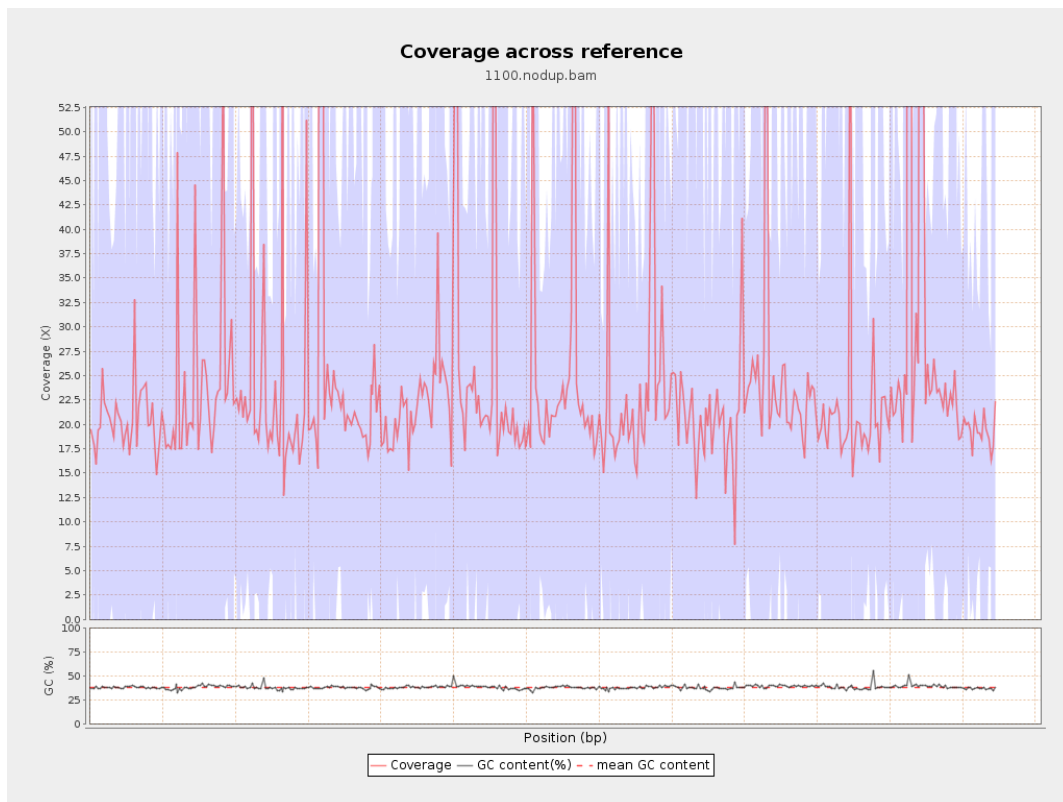
General error rate	2.41%
Mismatches	169,252,922
Insertions	5,175,264
Mapped reads with at least one insertion	8.47%
Deletions	5,379,704
Mapped reads with at least one deletion	8.68%
Homopolymer indels	55.84%

## 2.7. Chromosome stats

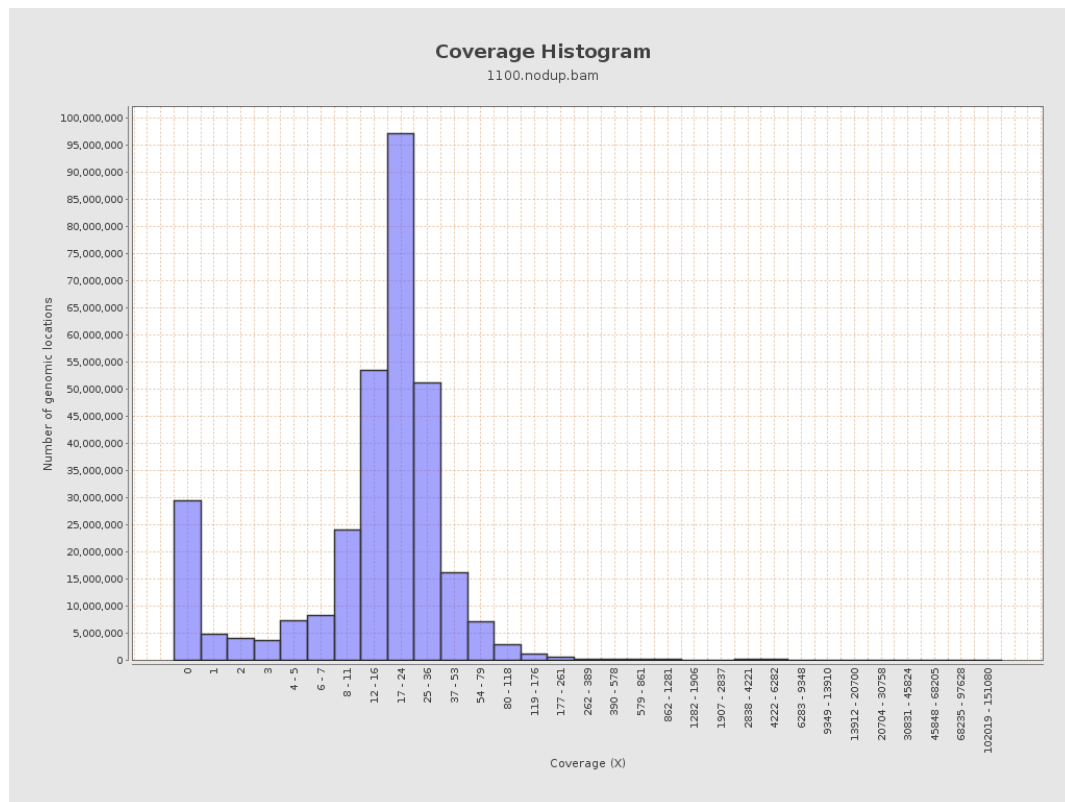
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	599930252	20.1831	73.3741

LT669789.1	36598175	915598289	25.0176	211.4173
LT669790.1	30422129	790740334	25.9923	188.1777
LT669791.1	52758100	1256551494	23.8172	184.4579
LT669792.1	28376109	675444119	23.8033	194.4948
LT669793.1	33388210	772779126	23.1453	193.1967
LT669794.1	50579949	1181783856	23.3647	189.8059
LT669795.1	49795044	1452809447	29.1758	295.732

### 3. Results : Coverage across reference

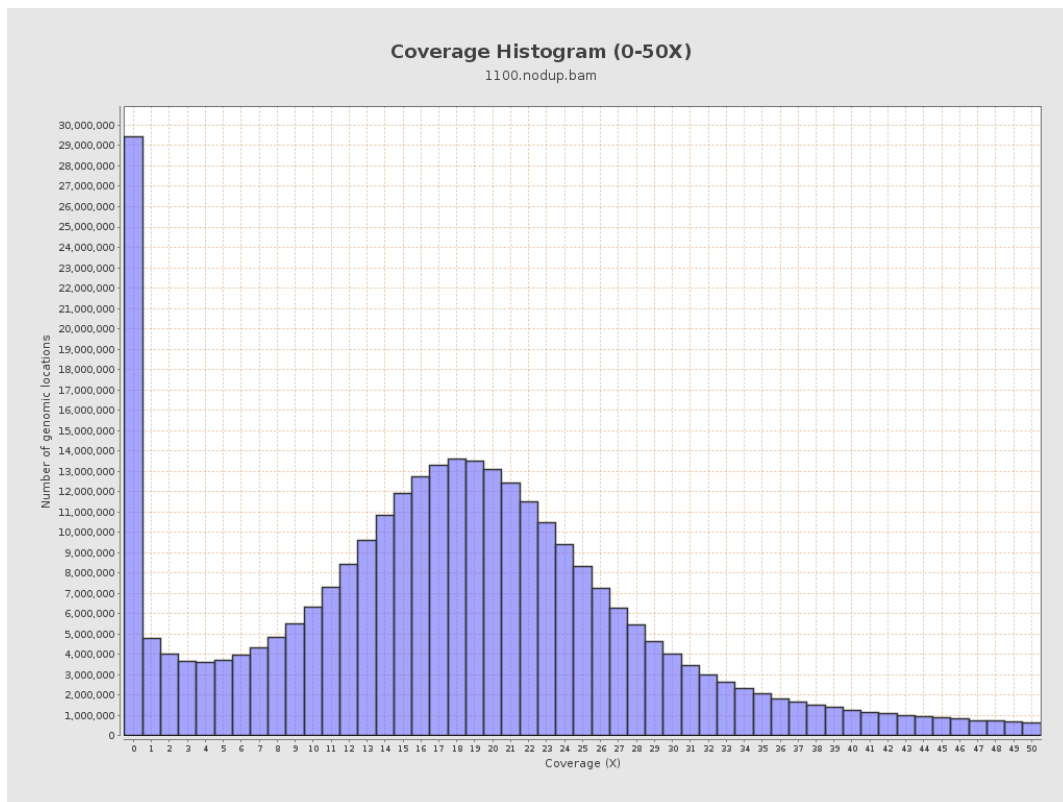


## 4. Results : Coverage Histogram

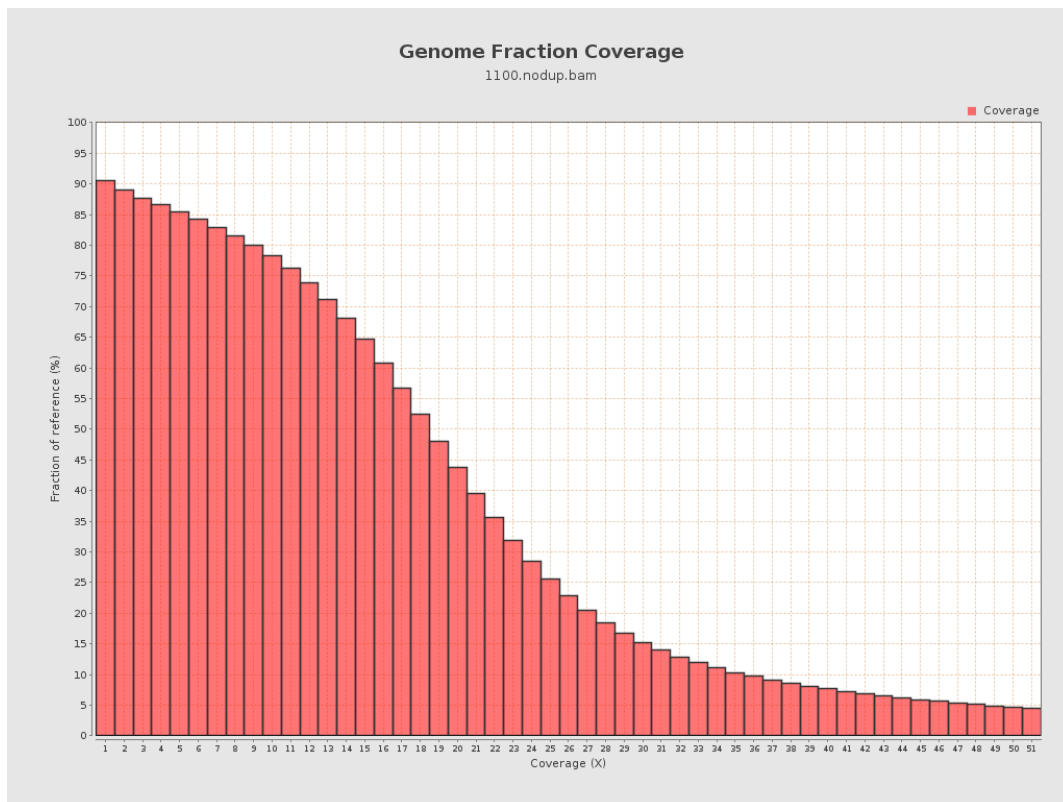




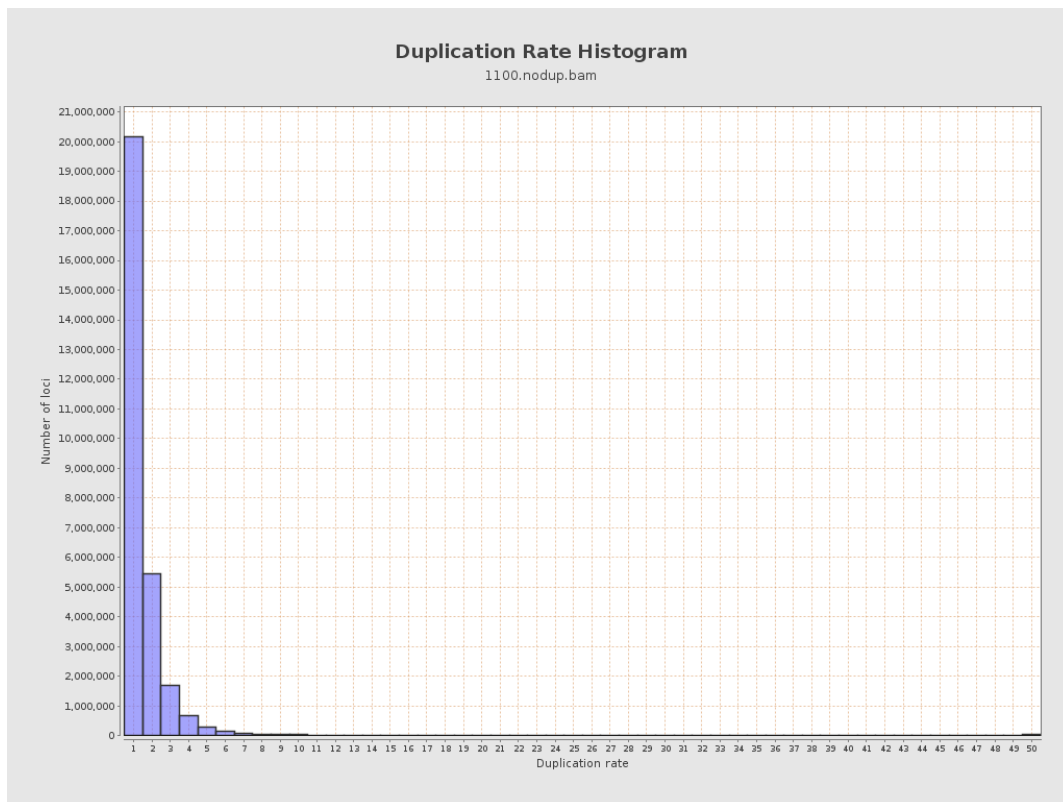
## 5. Results : Coverage Histogram (0-50X)



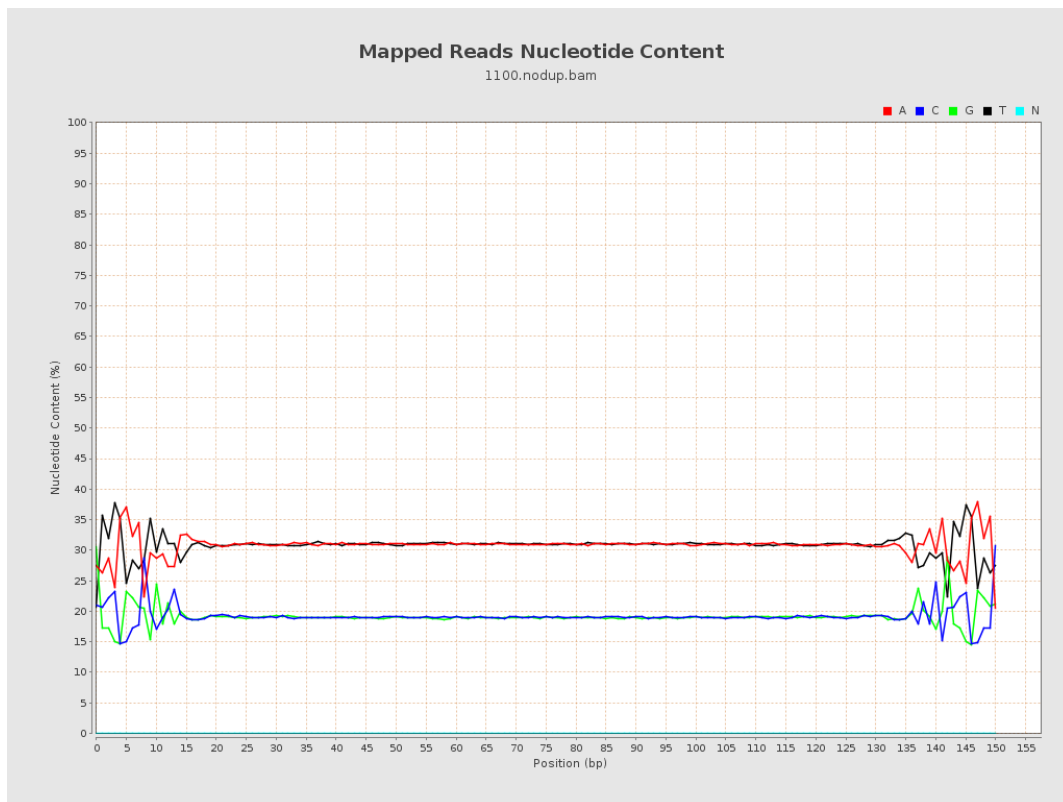
## 6. Results : Genome Fraction Coverage



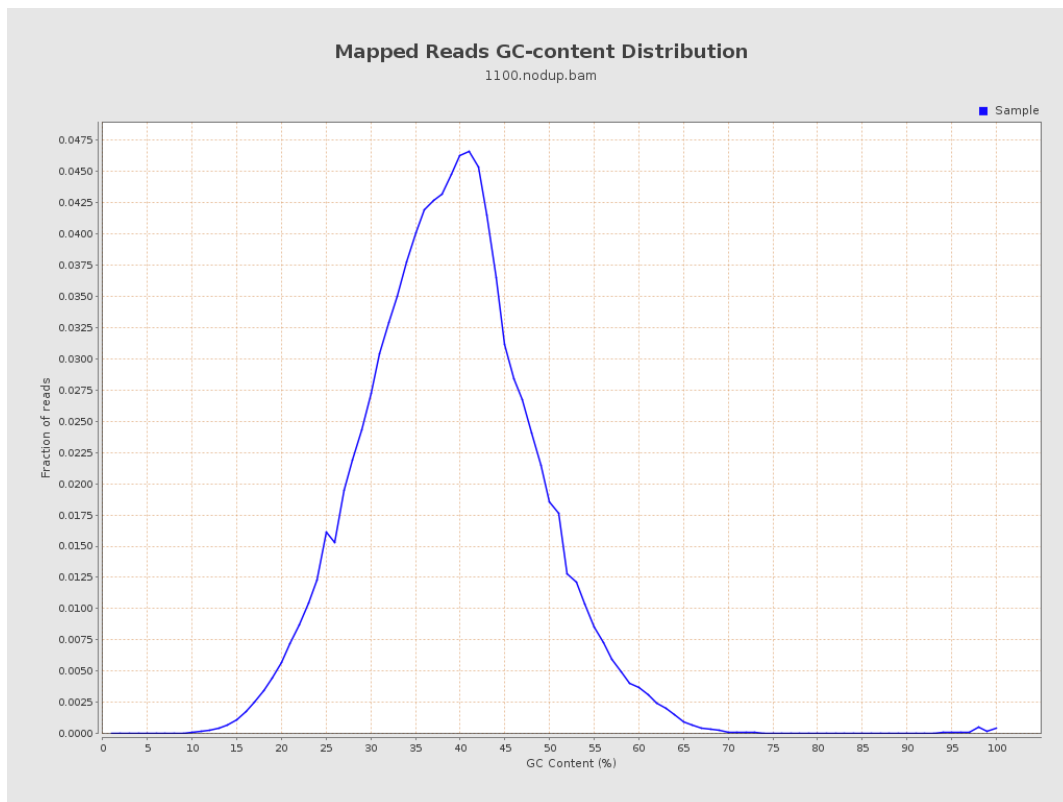
## 7. Results : Duplication Rate Histogram



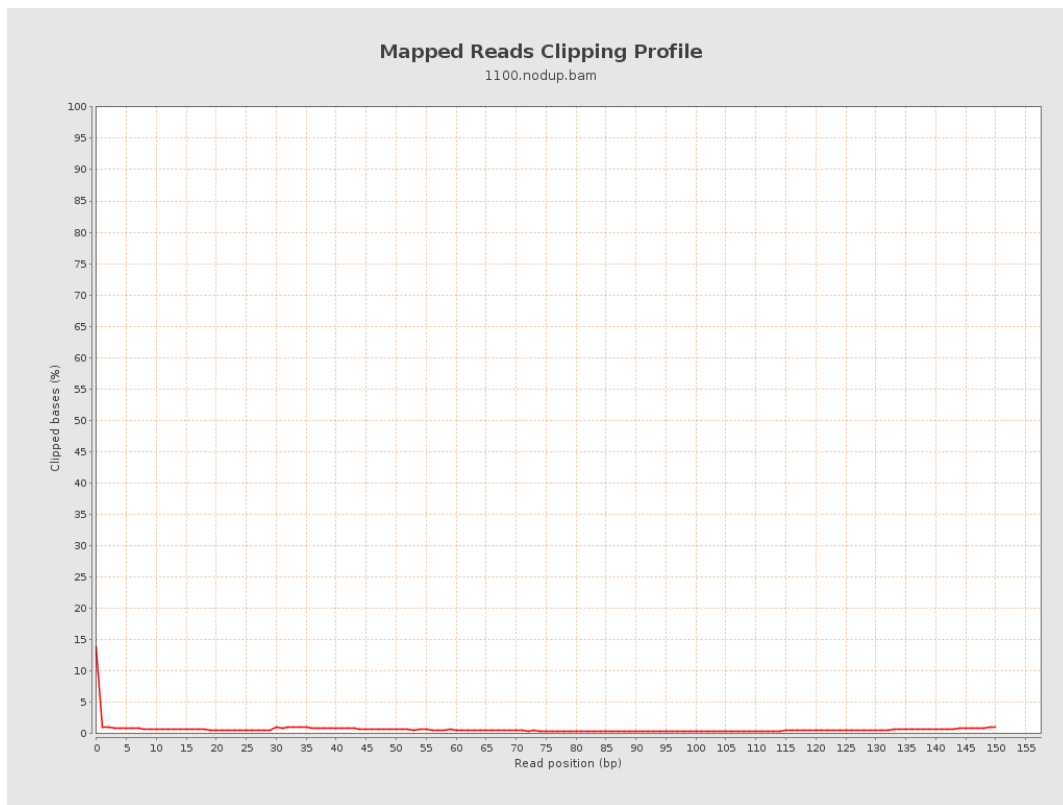
## 8. Results : Mapped Reads Nucleotide Content



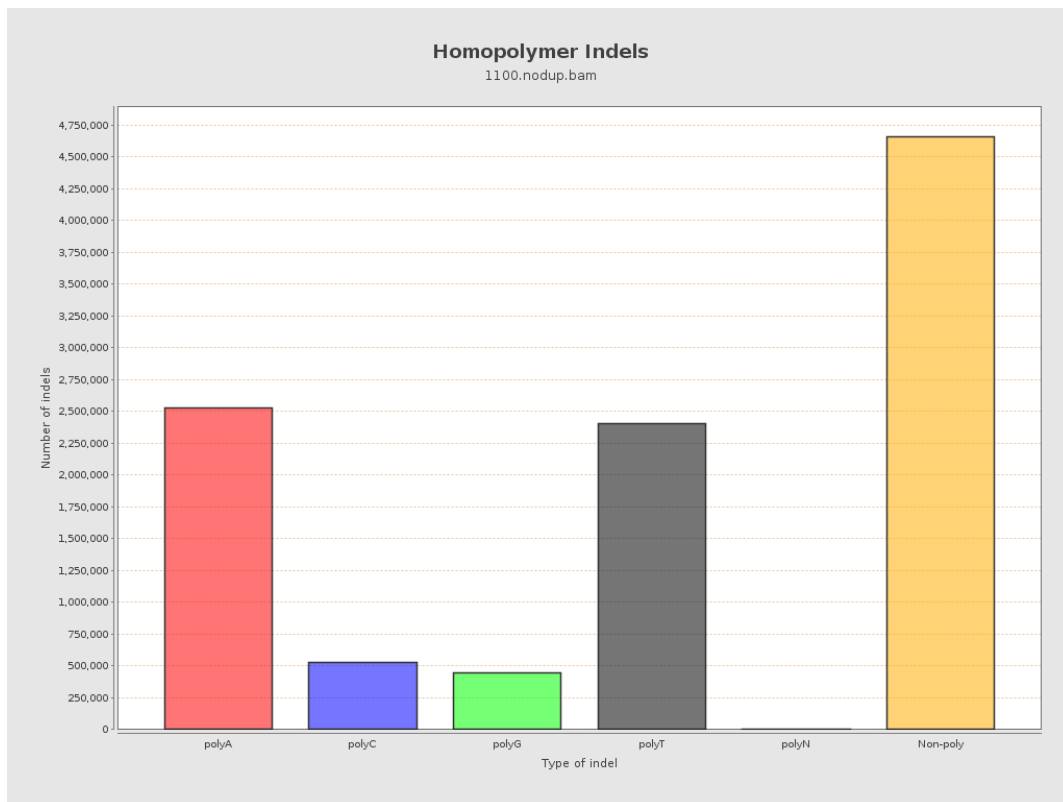
## 9. Results : Mapped Reads GC-content Distribution



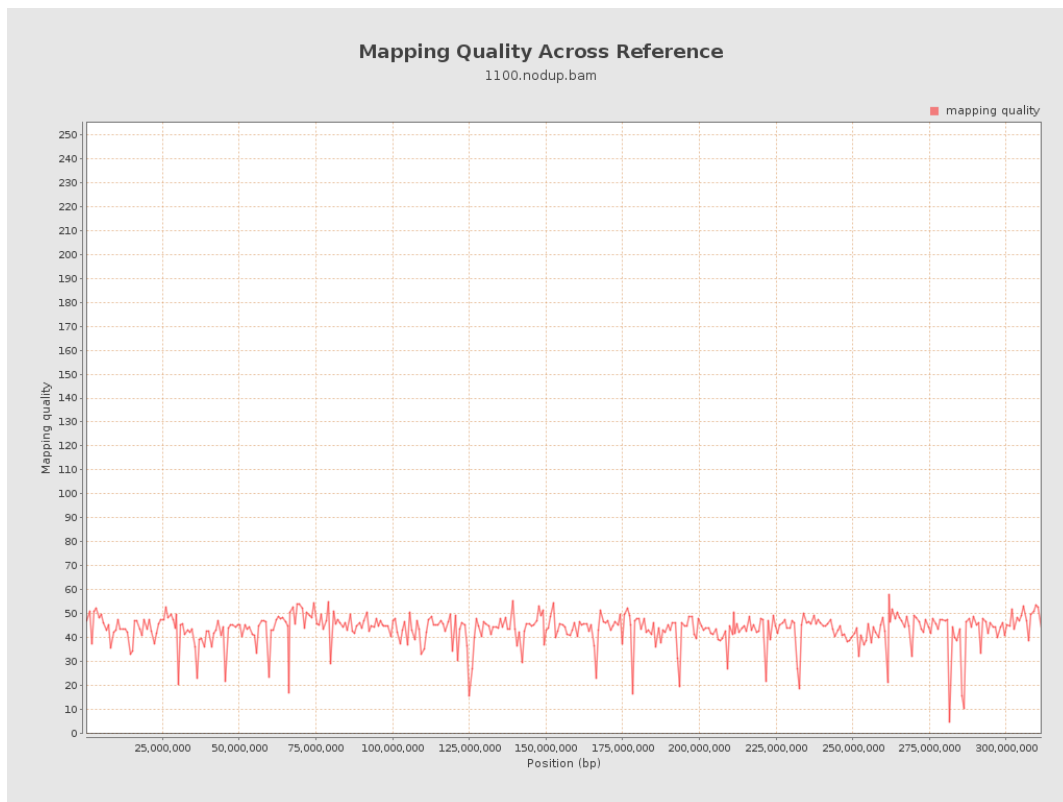
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

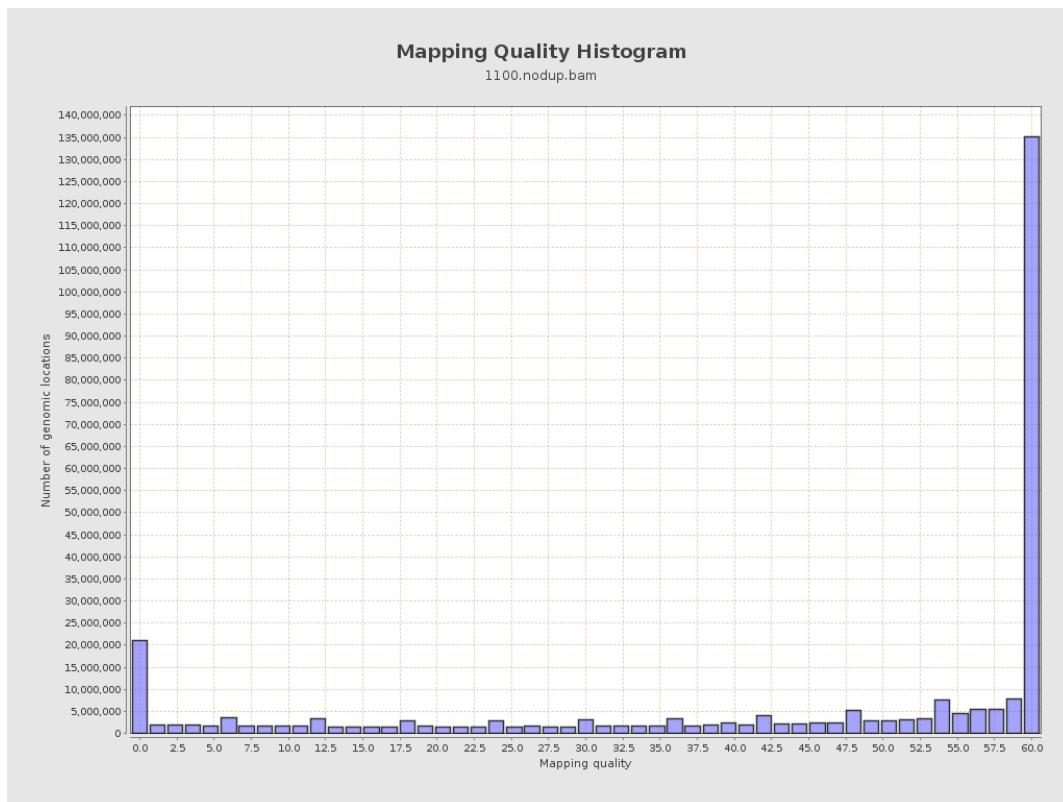


## 12. Results : Mapping Quality Across Reference

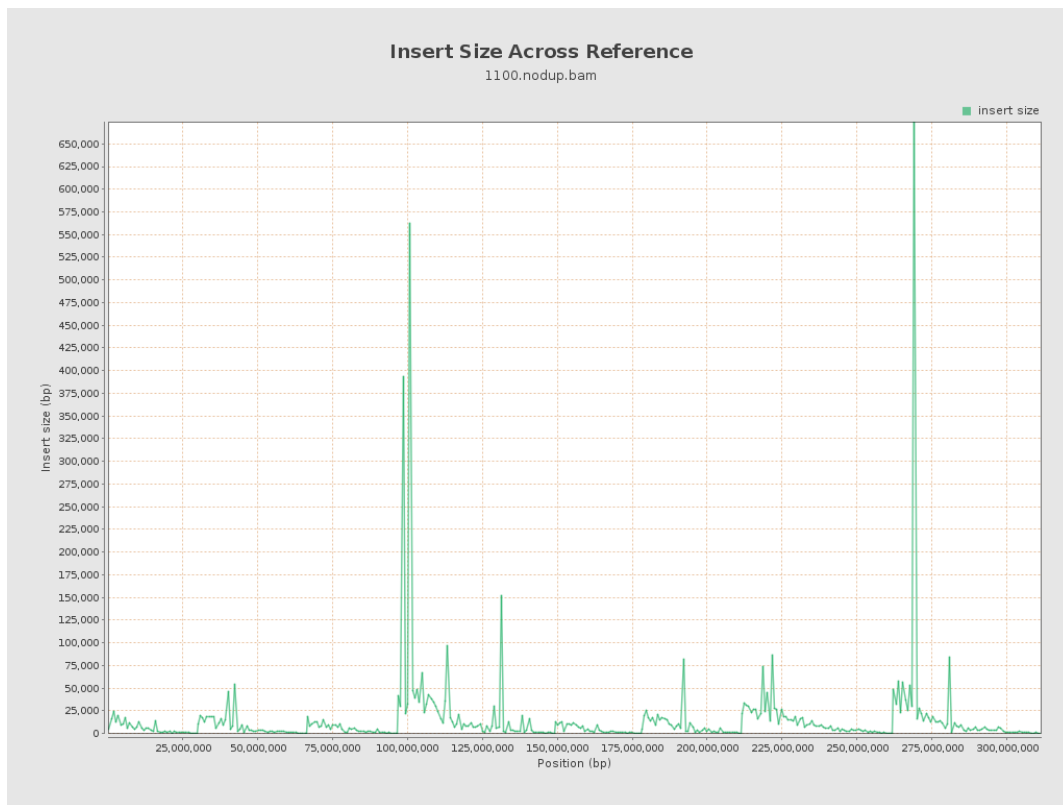




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

