

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:33:51*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/507
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/507.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/awdata/P26207/P26207_156/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_156_S246_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_156/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_156_S246_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:33:51 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	73,513,655
Mapped reads	68,146,642 / 92.7%
Unmapped reads	5,367,013 / 7.3%
Mapped paired reads	68,146,642 / 92.7%
Mapped reads, first in pair	34,148,047 / 46.45%
Mapped reads, second in pair	33,998,595 / 46.25%
Mapped reads, both in pair	66,423,685 / 90.36%
Mapped reads, singletons	1,722,957 / 2.34%
Read min/max/mean length	30 / 151 / 148.2
Duplicated reads (flagged)	11,736,679 / 15.97%
Clipped reads	15,073,400 / 20.5%

### 2.2. ACGT Content

Number/percentage of A's	2,906,605,331 / 30.77%
Number/percentage of C's	1,814,488,596 / 19.21%
Number/percentage of T's	2,913,290,595 / 30.84%
Number/percentage of G's	1,811,535,842 / 19.18%
Number/percentage of N's	40,170 / 0%
GC Percentage	38.39%

### 2.3. Coverage

Mean	30.3876
Standard Deviation	252.0125

## 2.4. Mapping Quality

Mean Mapping Quality	44.15
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## 2.5. Insert size

Mean	241,495.29
Standard Deviation	2,348,825.78
P25/Median/P75	331 / 433 / 574

## 2.6. Mismatches and indels

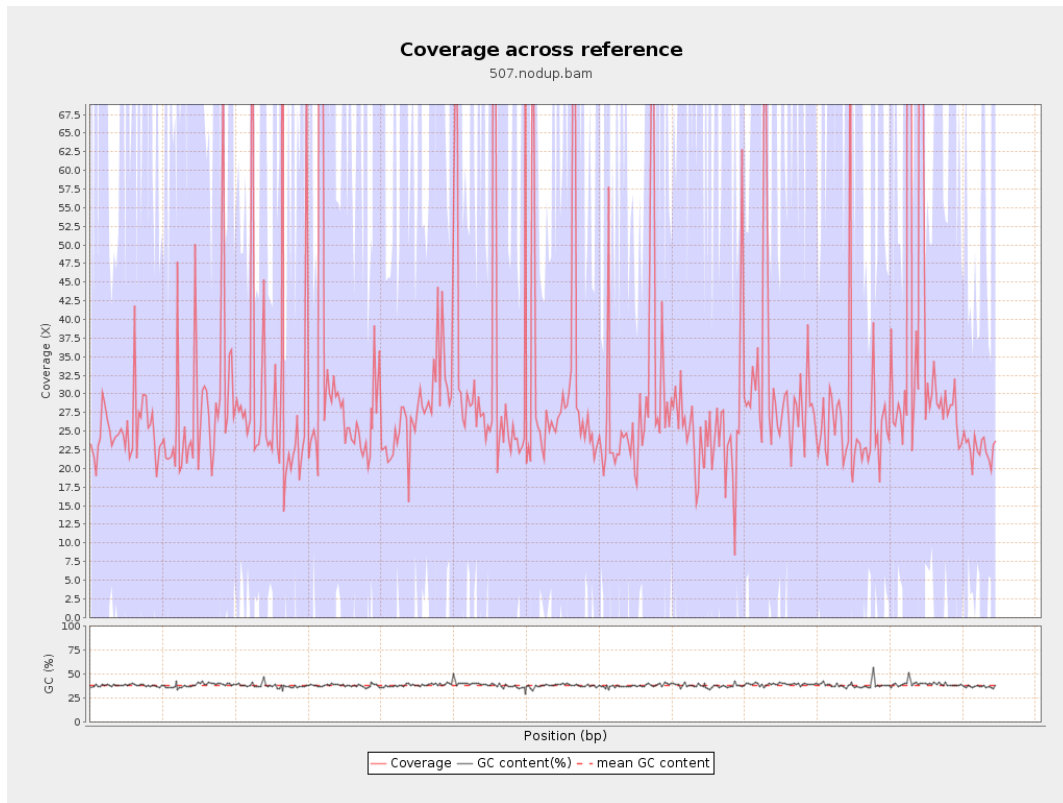
General error rate	2.3%
Mismatches	199,710,647
Insertions	6,424,903
Mapped reads with at least one insertion	8.44%
Deletions	6,355,198
Mapped reads with at least one deletion	8.27%
Homopolymer indels	56.37%

## 2.7. Chromosome stats

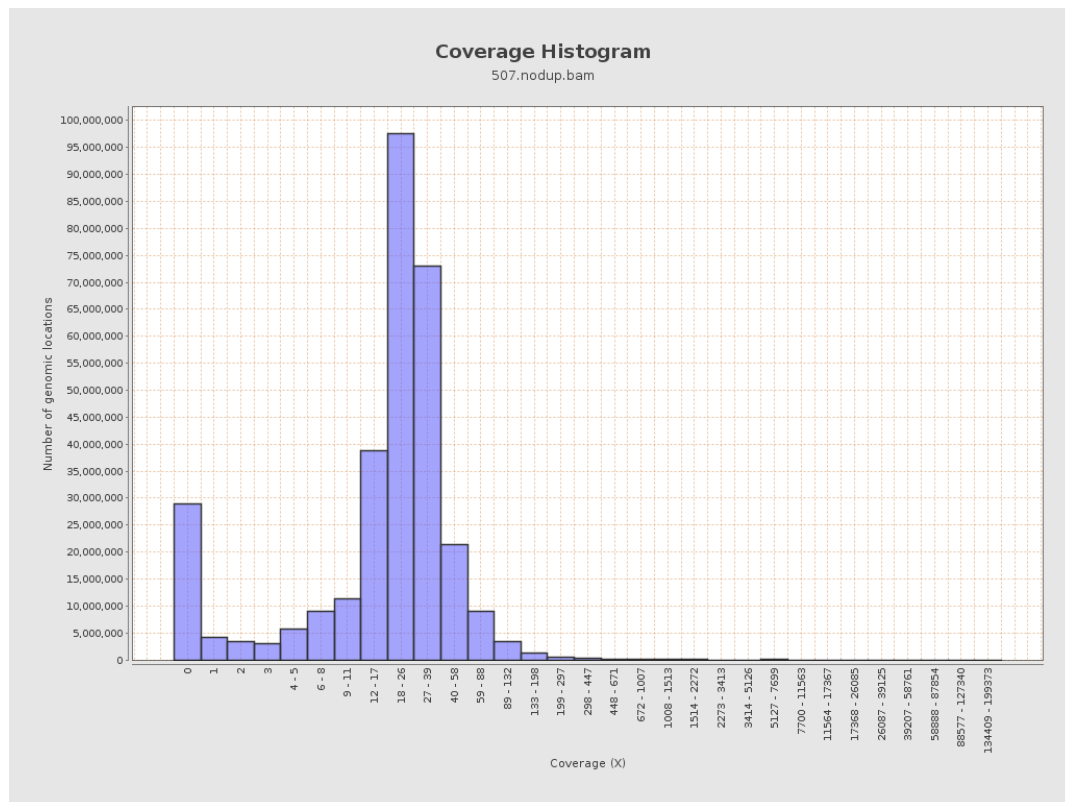
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	732572582	24.6455	100.027

LT669789.1	36598175	1109261083	30.3092	270.3425
LT669790.1	30422129	1004495364	33.0186	276.0587
LT669791.1	52758100	1589526198	30.1286	239.2787
LT669792.1	28376109	850462505	29.9711	281.1505
LT669793.1	33388210	933323911	27.9537	173.2669
LT669794.1	50579949	1475314141	29.168	199.9828
LT669795.1	49795044	1775095062	35.648	353.1501

### 3. Results : Coverage across reference

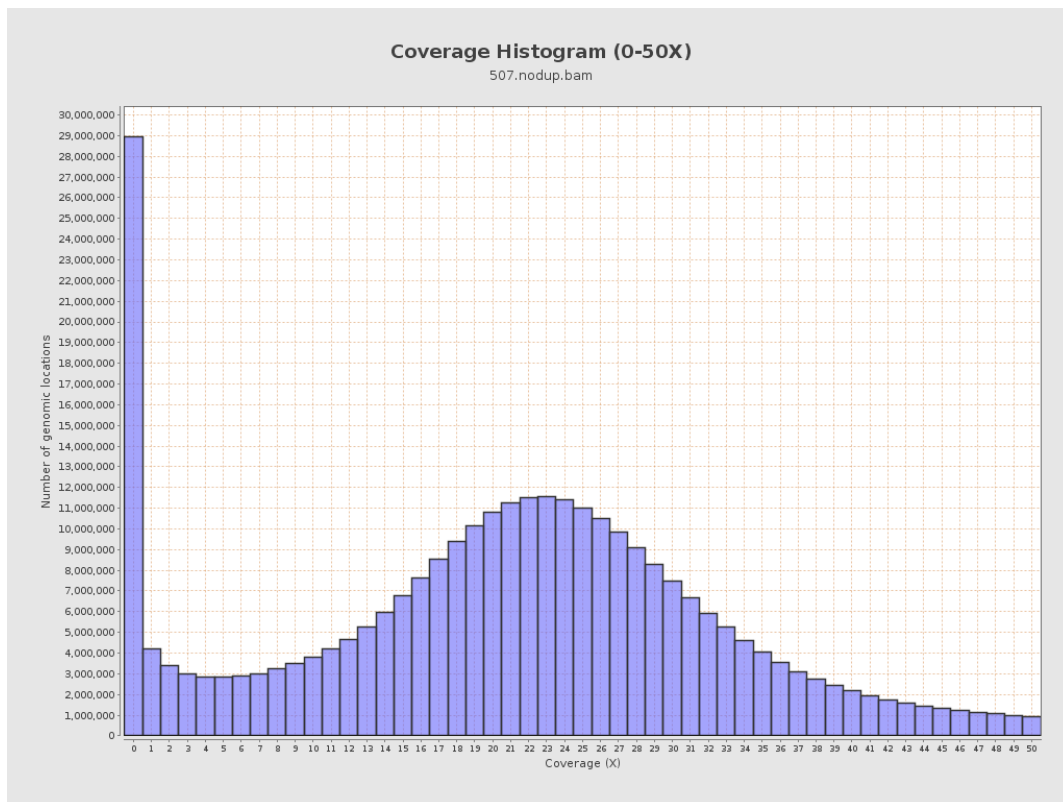


## 4. Results : Coverage Histogram

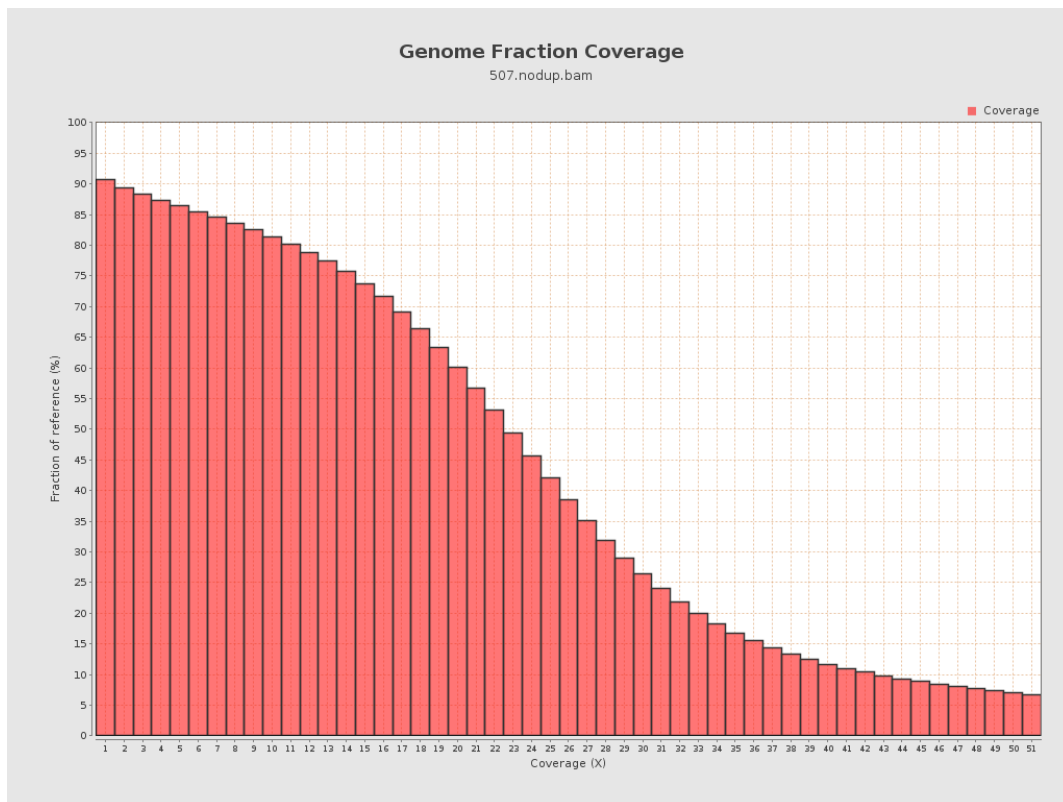




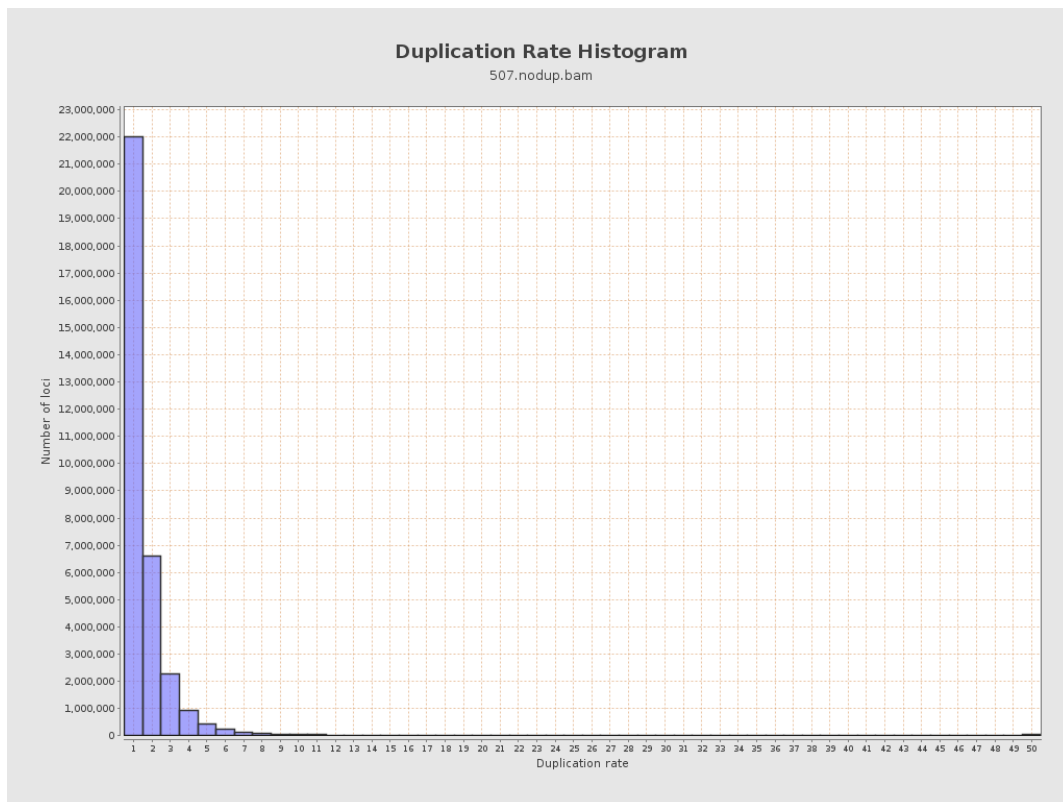
## 5. Results : Coverage Histogram (0-50X)



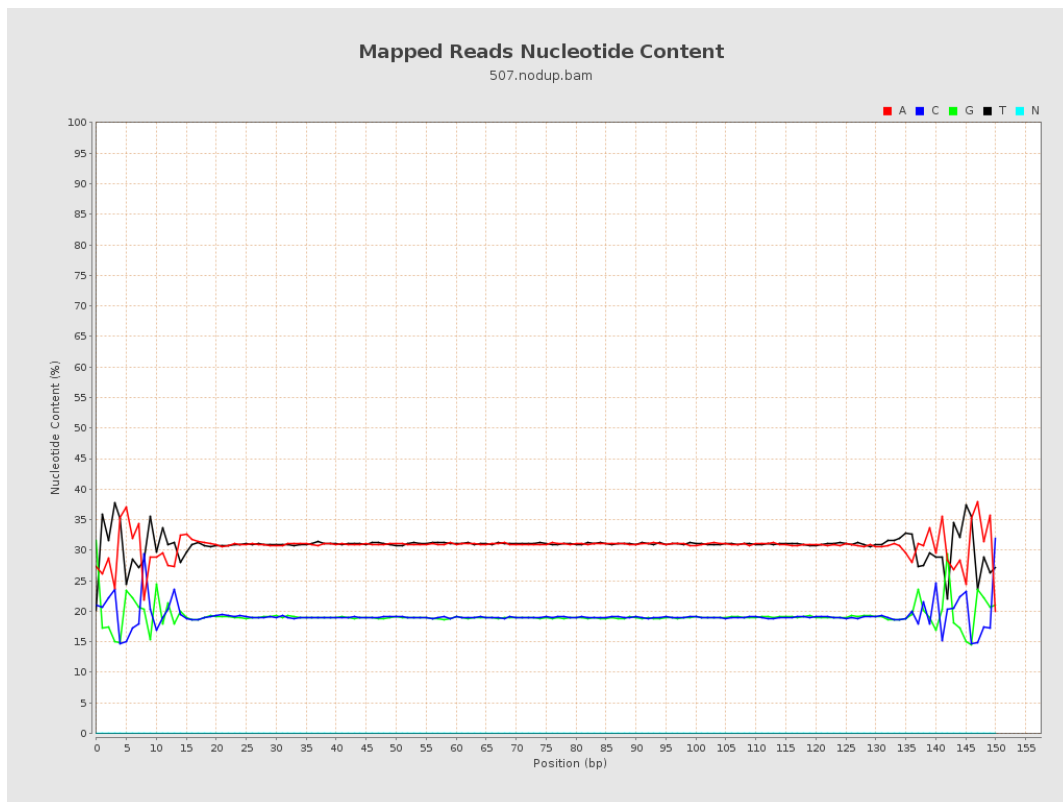
## 6. Results : Genome Fraction Coverage



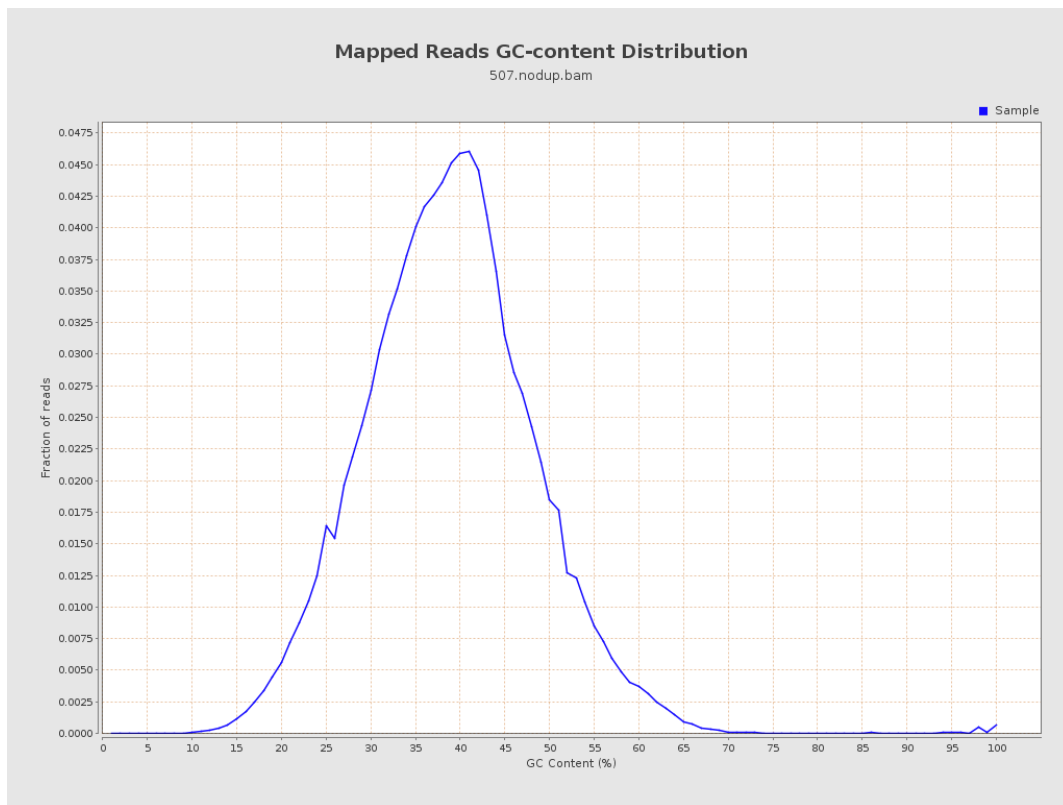
## 7. Results : Duplication Rate Histogram



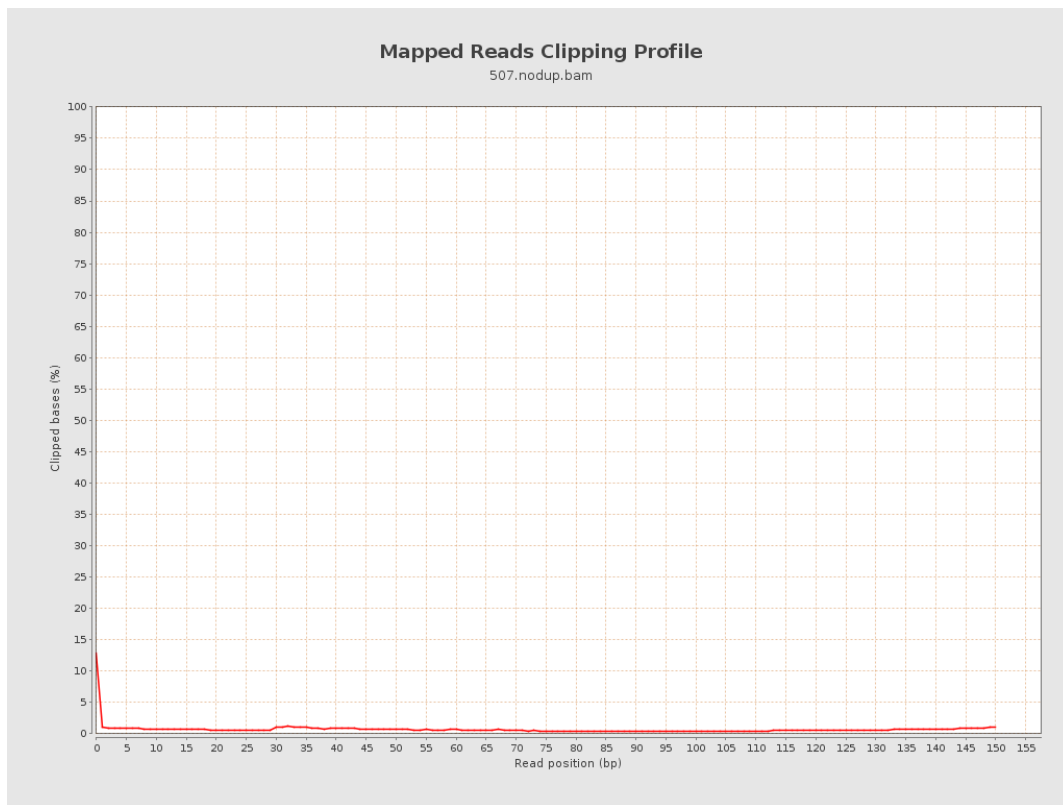
## 8. Results : Mapped Reads Nucleotide Content



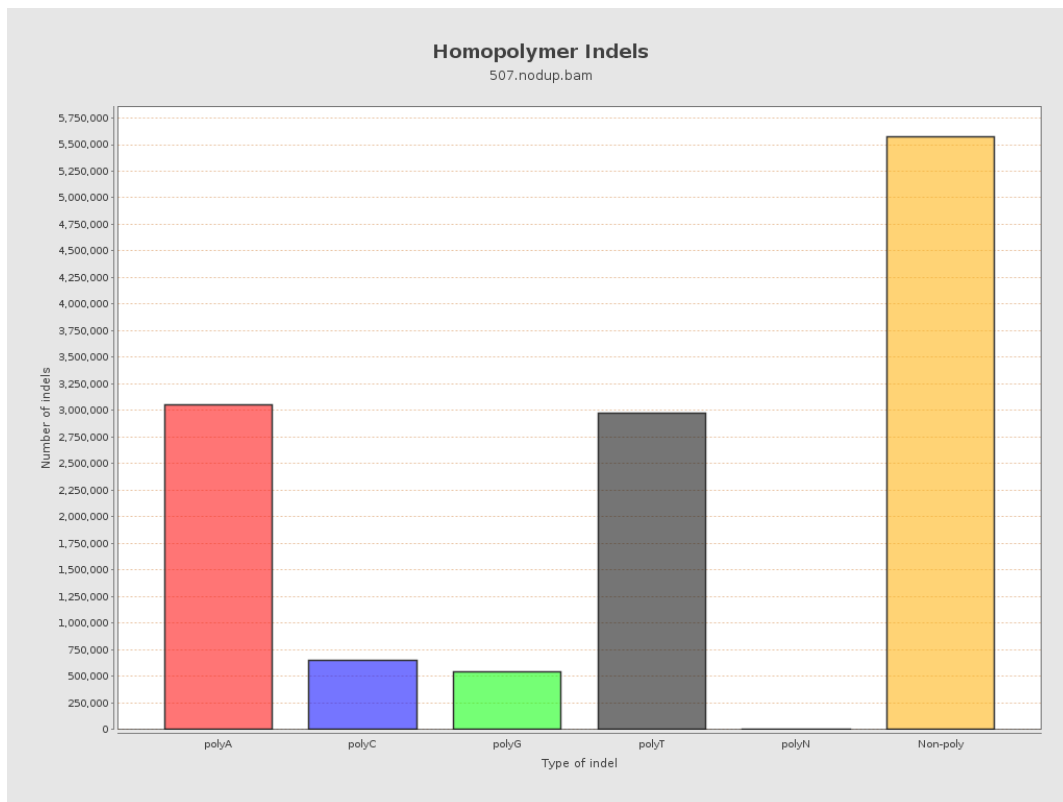
## 9. Results : Mapped Reads GC-content Distribution



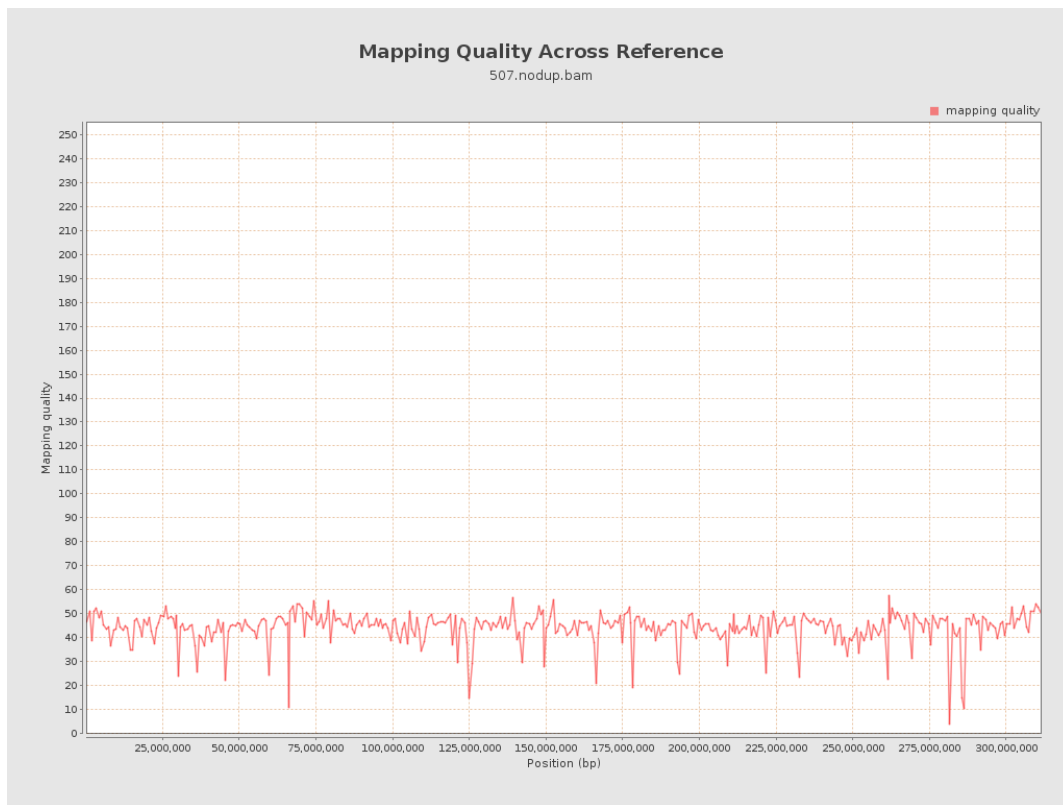
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

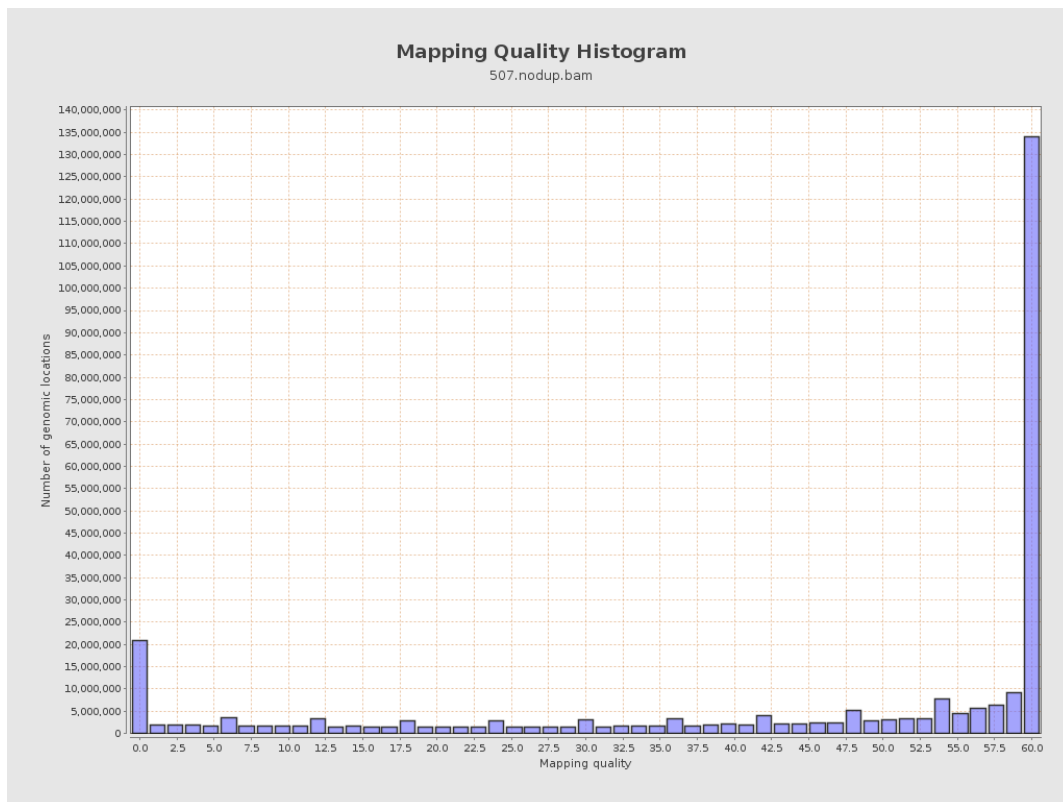


## 12. Results : Mapping Quality Across Reference

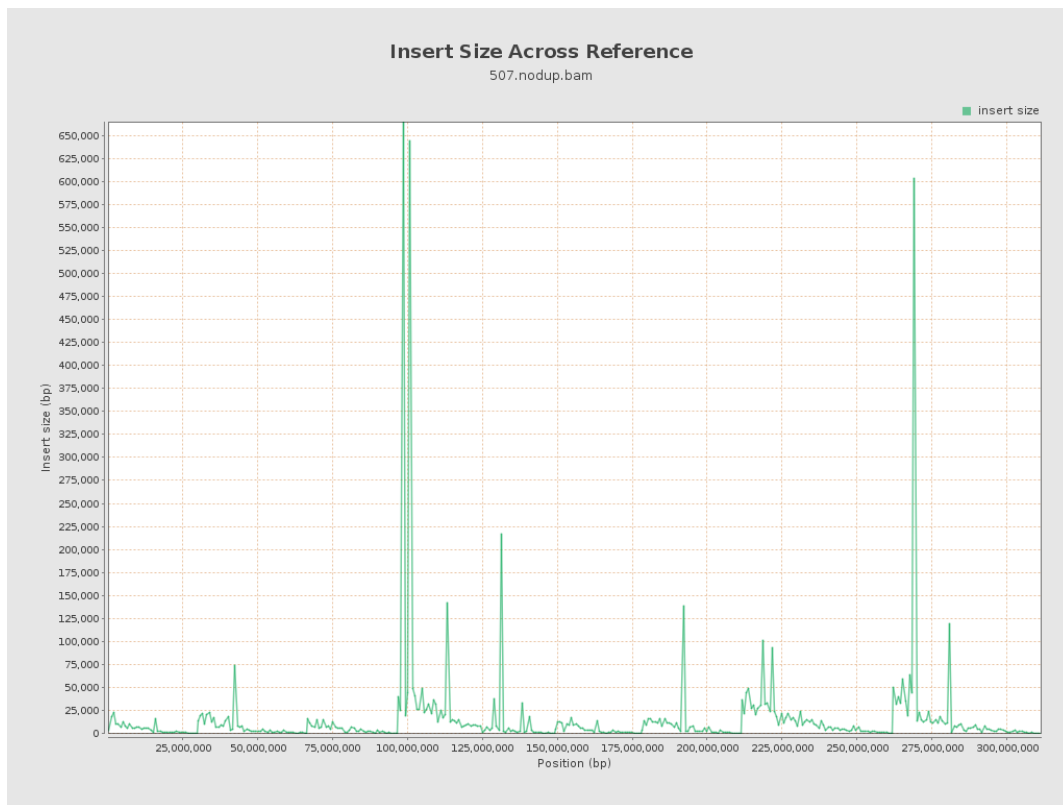




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

