

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:28:12*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/514
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/514.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_286/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_286_S367_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_286/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_286_S367_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:28:11 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	58,594,779
Mapped reads	52,731,881 / 89.99%
Unmapped reads	5,862,898 / 10.01%
Mapped paired reads	52,731,881 / 89.99%
Mapped reads, first in pair	26,425,954 / 45.1%
Mapped reads, second in pair	26,305,927 / 44.89%
Mapped reads, both in pair	50,924,616 / 86.91%
Mapped reads, singletons	1,807,265 / 3.08%
Read min/max/mean length	30 / 151 / 148.17
Duplicated reads (flagged)	9,134,070 / 15.59%
Clipped reads	12,840,367 / 21.91%

### 2.2. ACGT Content

Number/percentage of A's	2,229,601,055 / 30.98%
Number/percentage of C's	1,368,598,113 / 19.02%
Number/percentage of T's	2,231,884,292 / 31.01%
Number/percentage of G's	1,367,244,031 / 19%
Number/percentage of N's	25,930 / 0%
GC Percentage	38.01%

### 2.3. Coverage

Mean	23.1536
Standard Deviation	241.6641

## 2.4. Mapping Quality

Mean Mapping Quality	44.92
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## 2.5. Insert size

Mean	248,985.86
Standard Deviation	2,421,083.44
P25/Median/P75	310 / 405 / 523

## 2.6. Mismatches and indels

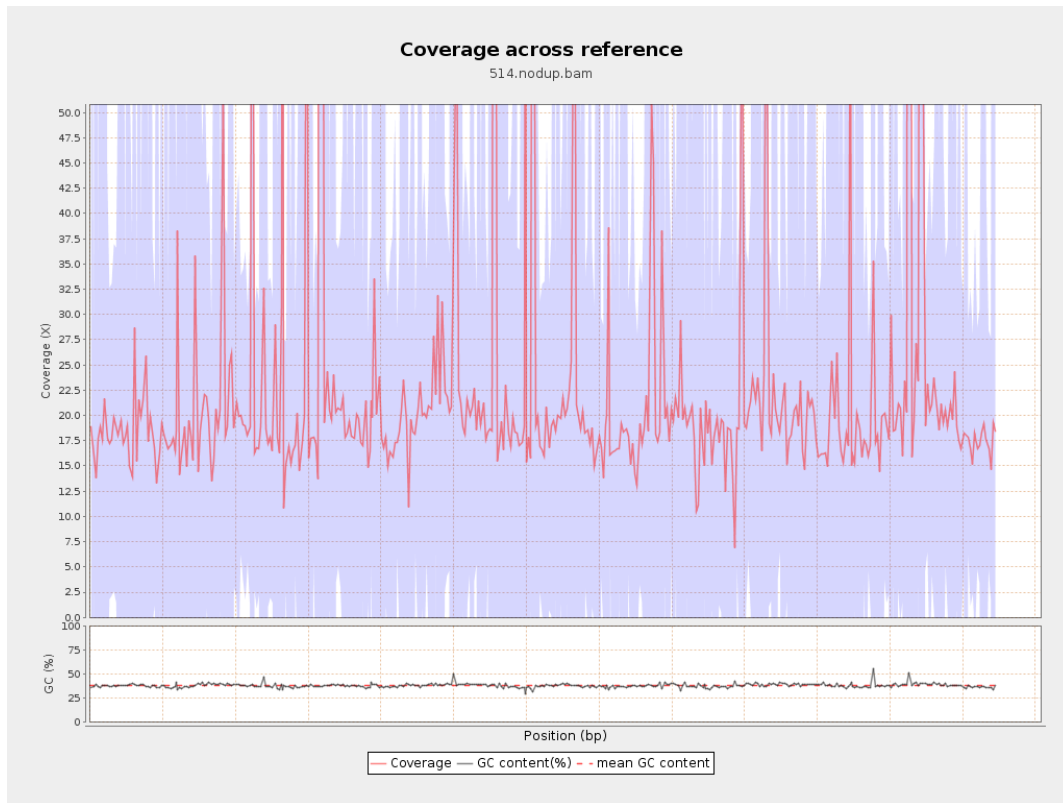
General error rate	2.36%
Mismatches	155,189,362
Insertions	5,331,293
Mapped reads with at least one insertion	8.99%
Deletions	4,973,926
Mapped reads with at least one deletion	8.36%
Homopolymer indels	57.61%

## 2.7. Chromosome stats

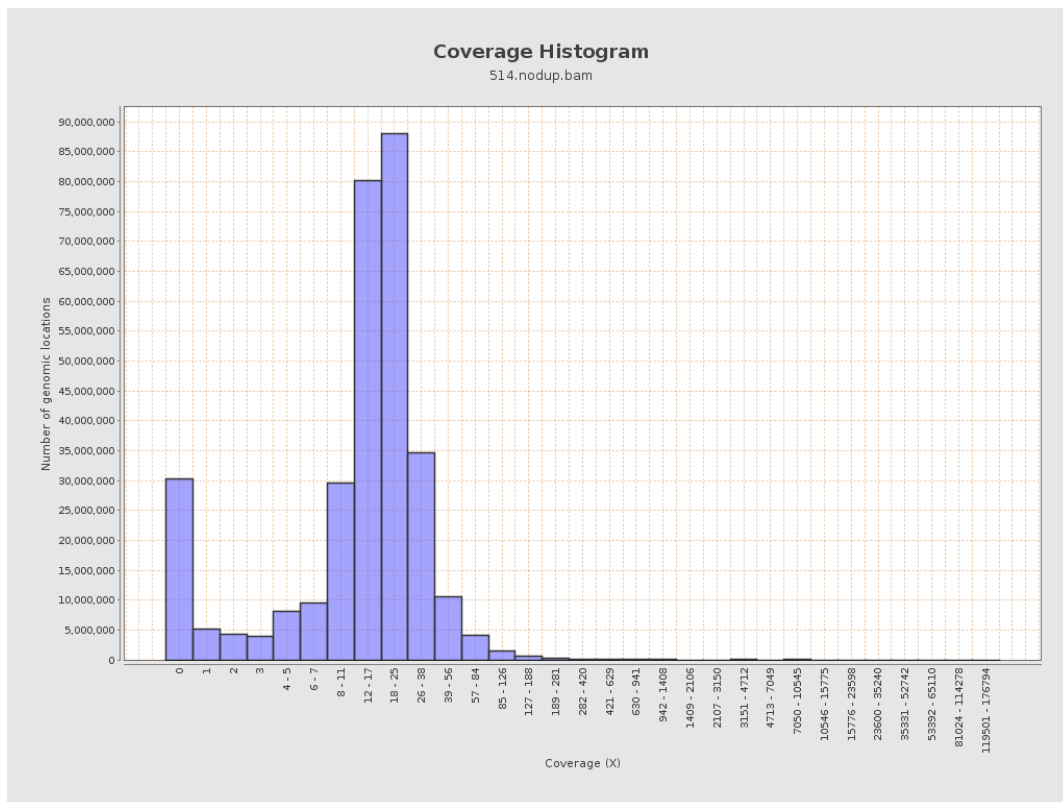
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	543006956	18.2681	93.7027

LT669789.1	36598175	832875443	22.7573	248.0194
LT669790.1	30422129	882491268	29.0082	352.1956
LT669791.1	52758100	1213860220	23.008	259.5538
LT669792.1	28376109	659977203	23.2582	237.6341
LT669793.1	33388210	680773085	20.3896	126.3113
LT669794.1	50579949	1080901769	21.3702	188.4371
LT669795.1	49795044	1321748222	26.5438	298.149

### 3. Results : Coverage across reference

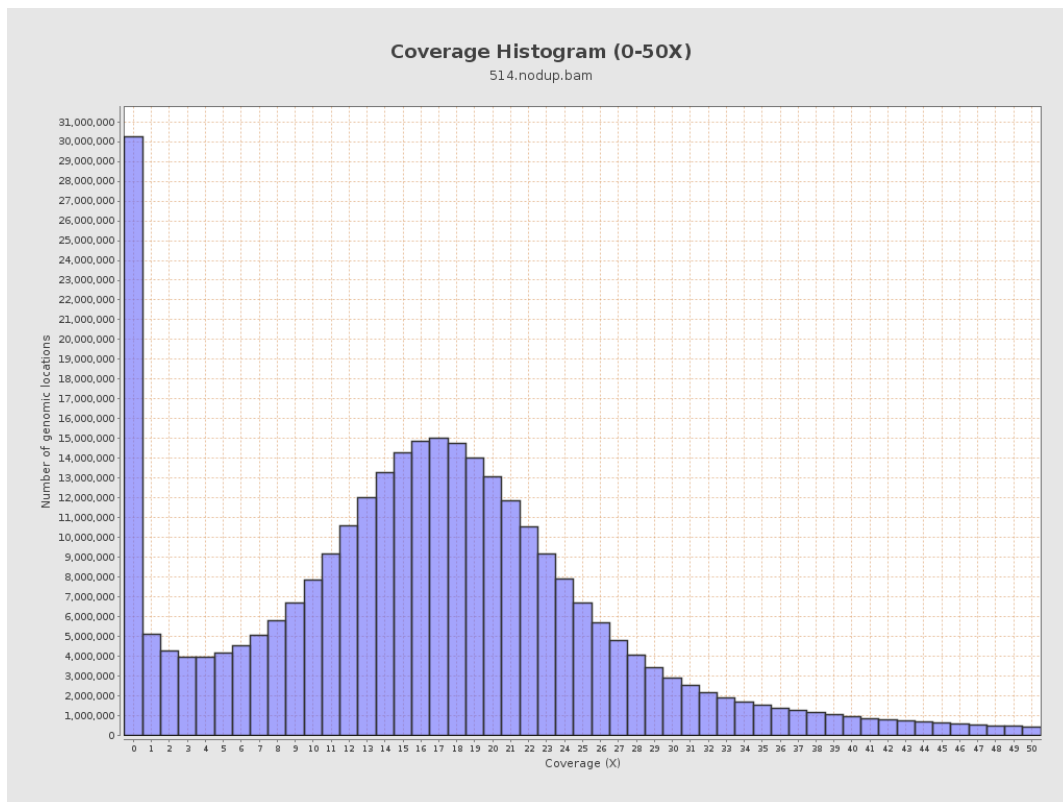


## 4. Results : Coverage Histogram

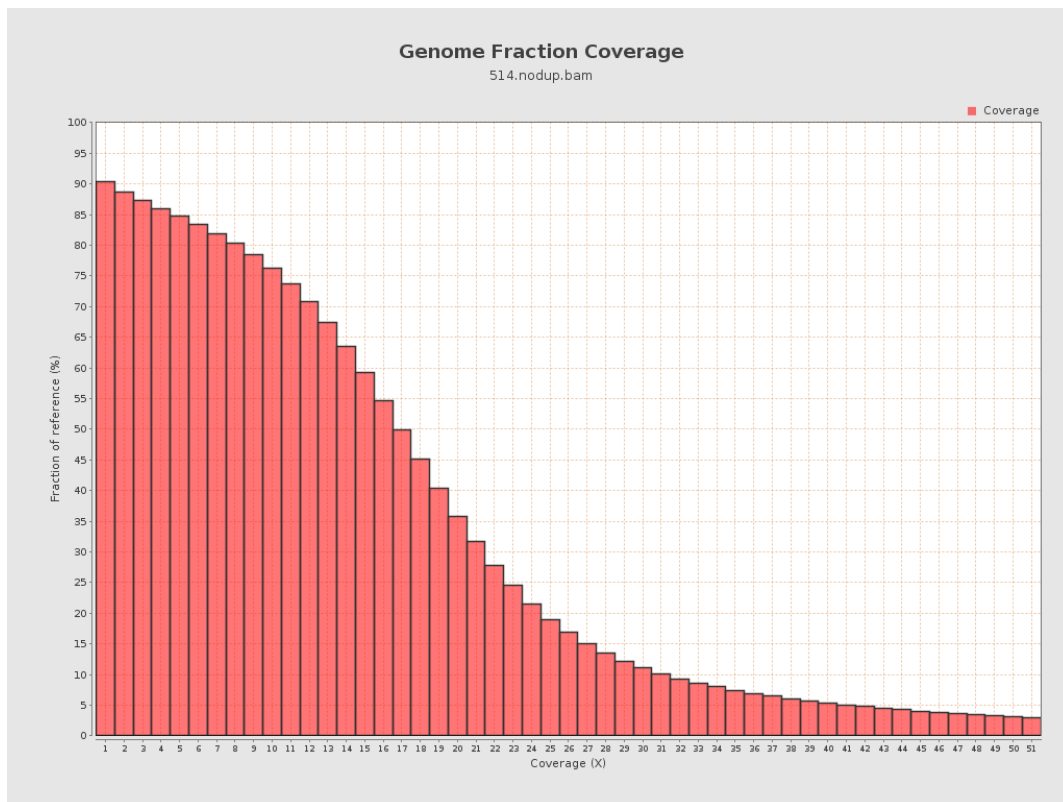




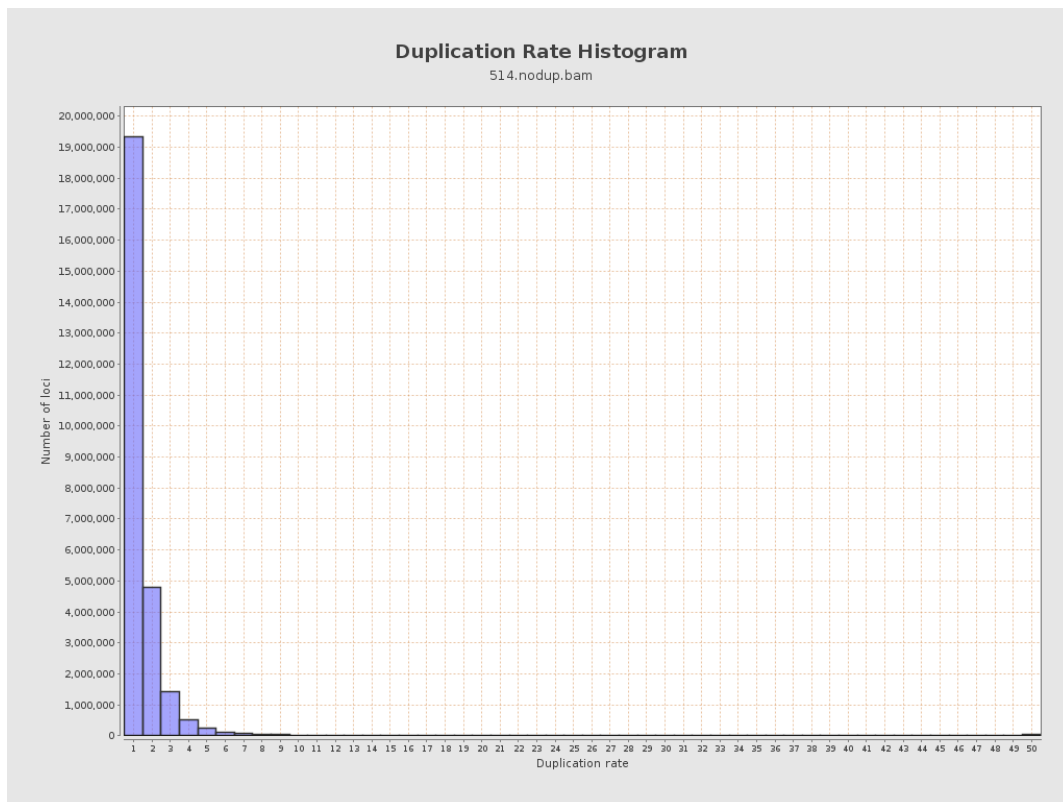
## 5. Results : Coverage Histogram (0-50X)



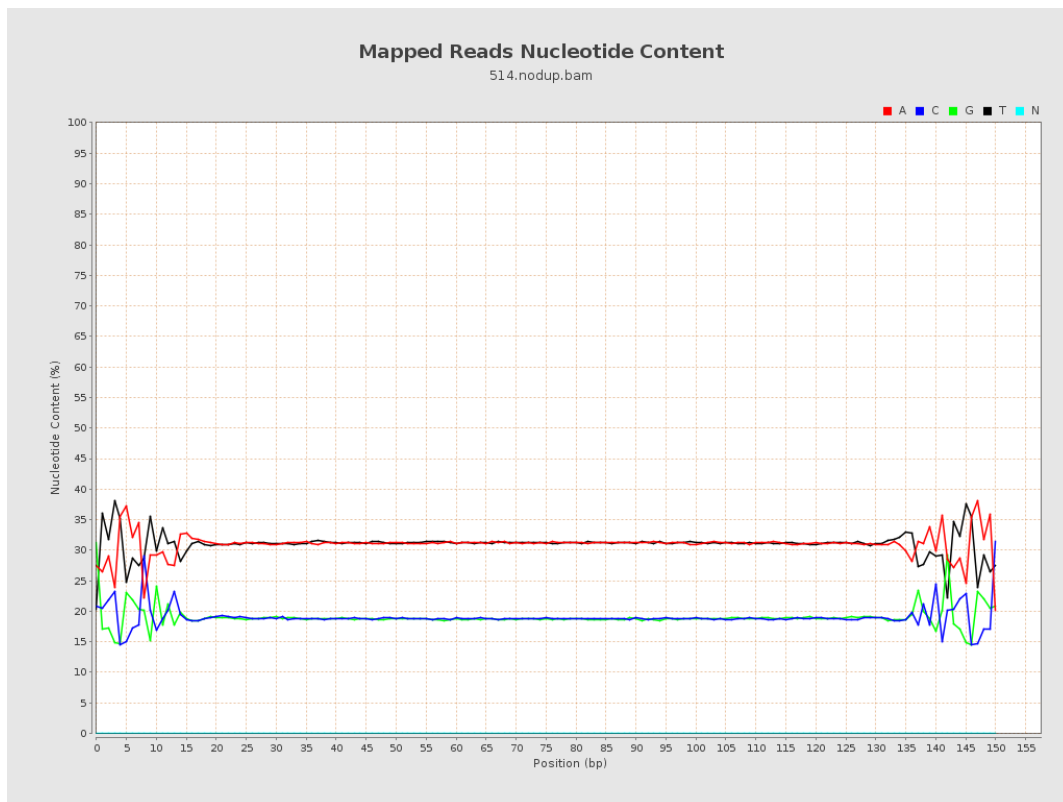
## 6. Results : Genome Fraction Coverage



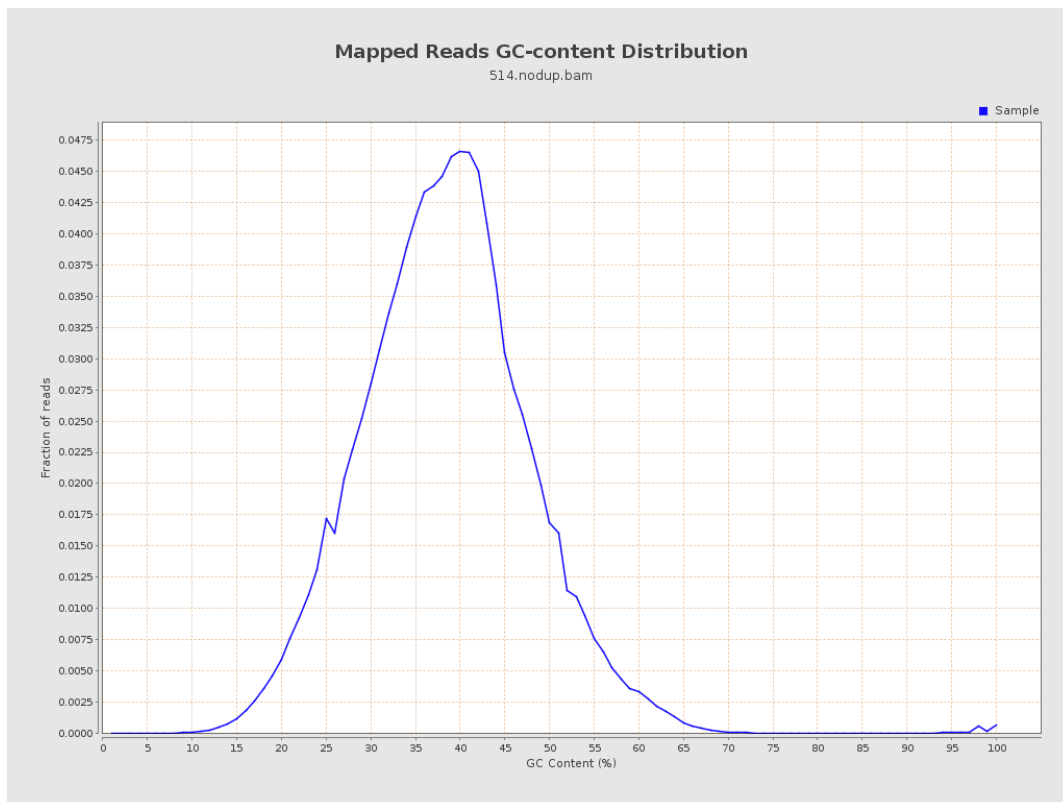
## 7. Results : Duplication Rate Histogram



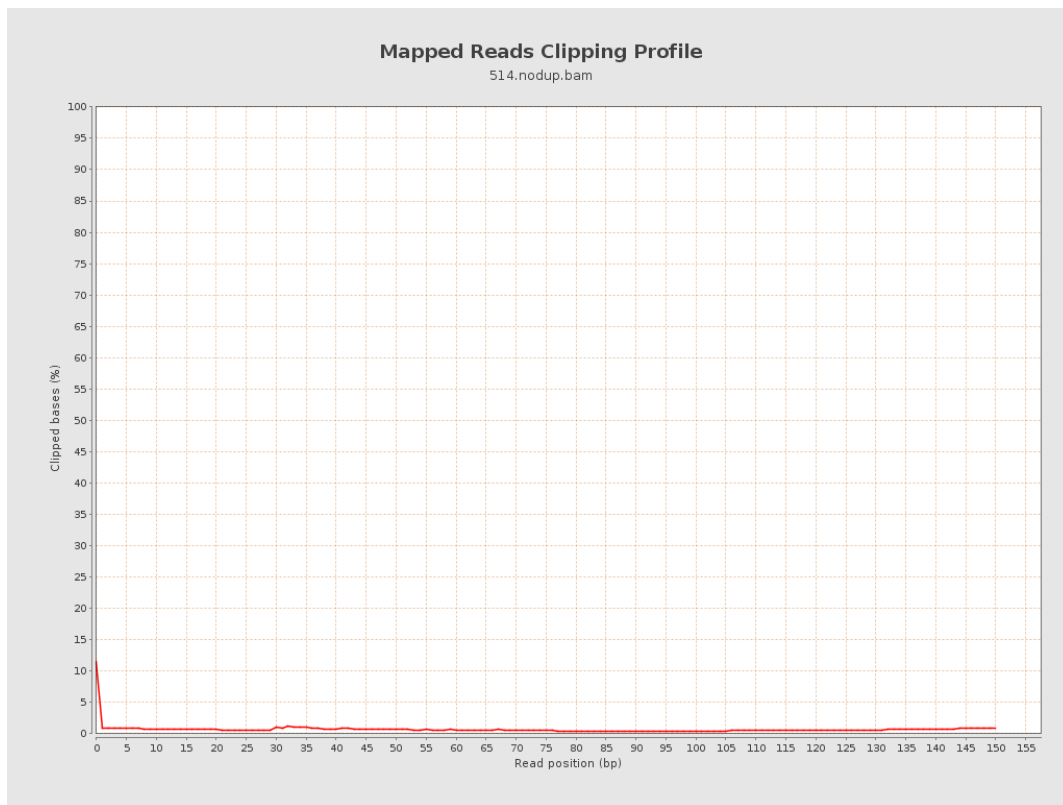
## 8. Results : Mapped Reads Nucleotide Content



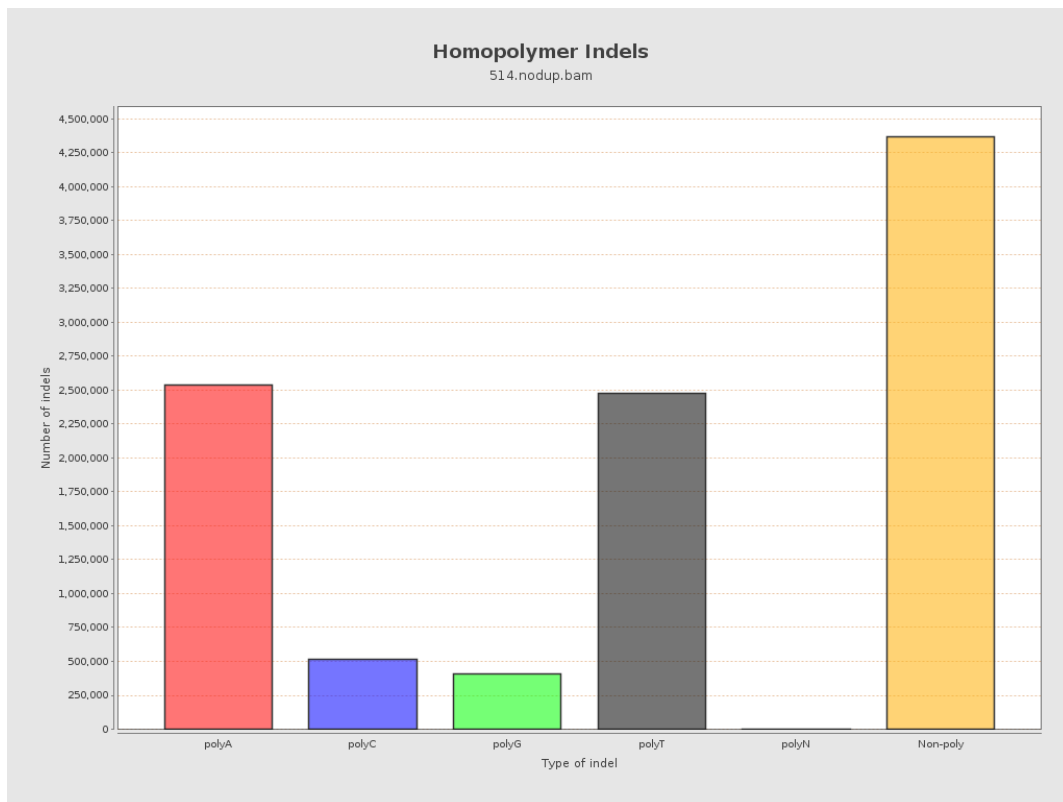
## 9. Results : Mapped Reads GC-content Distribution



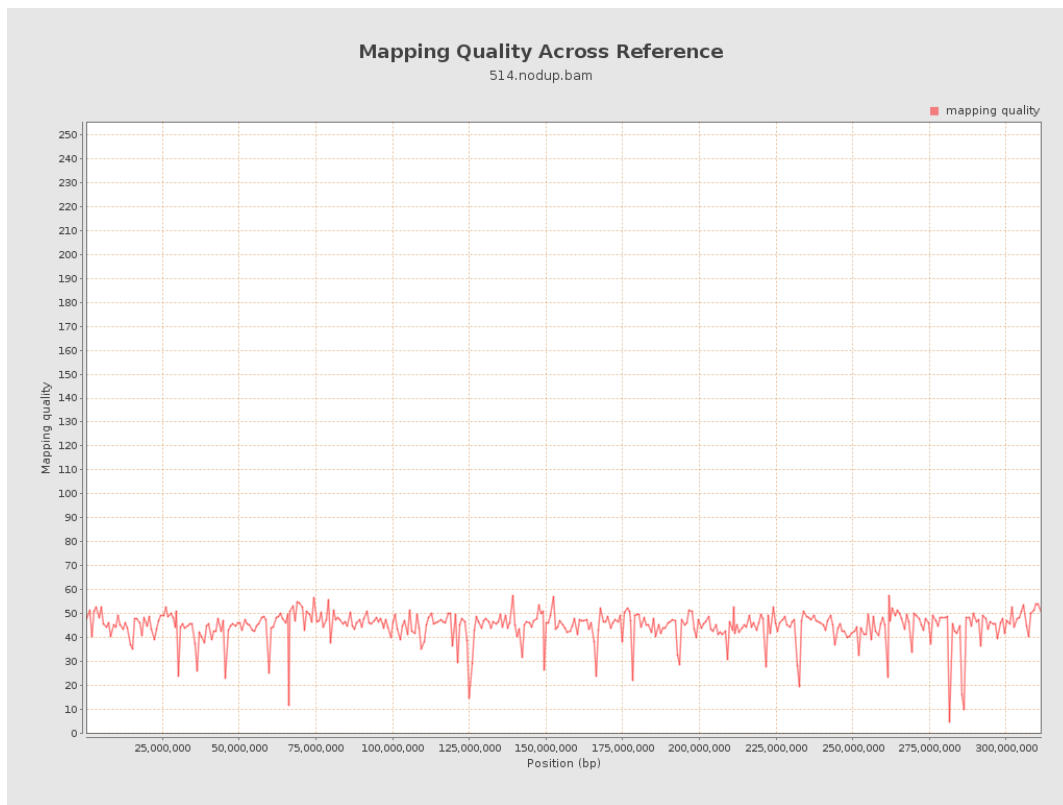
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

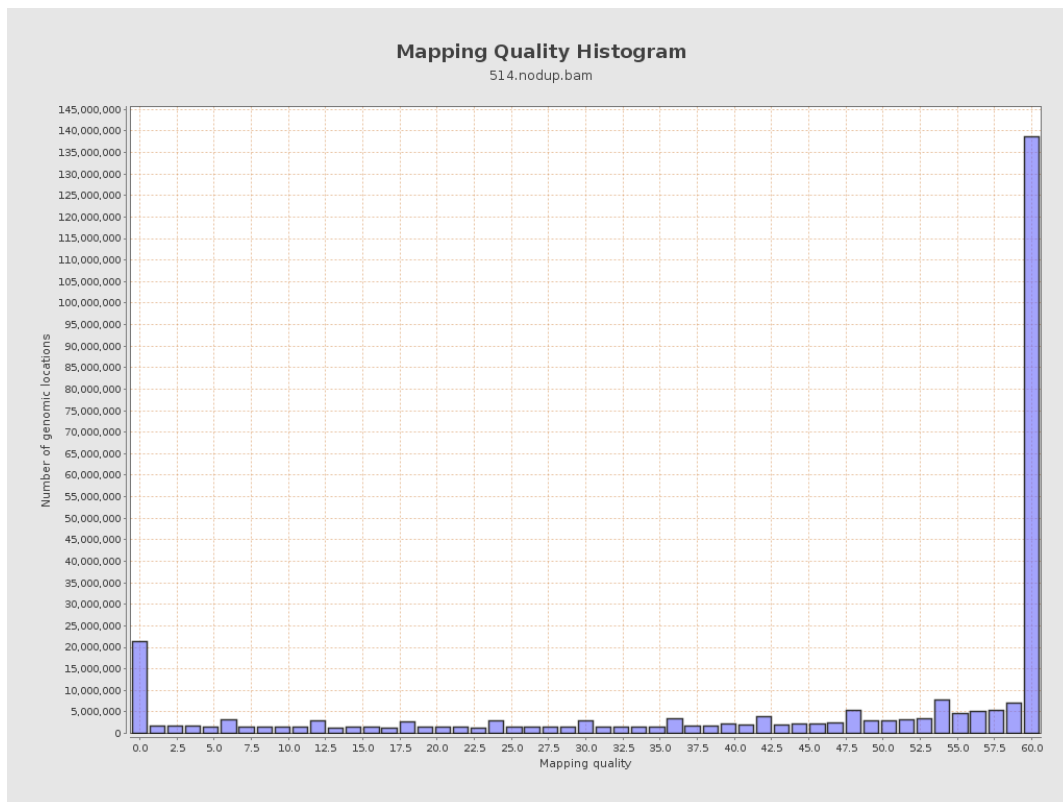


## 12. Results : Mapping Quality Across Reference

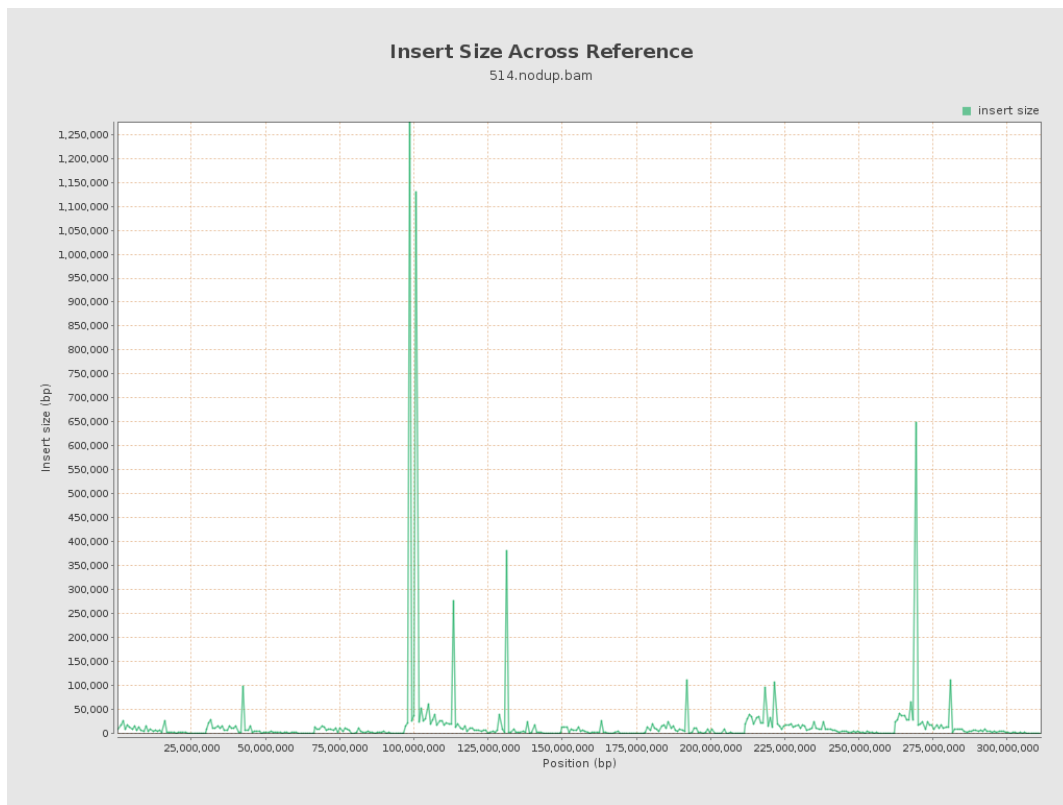




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

