

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:39:15*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/528
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/528.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_242/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_242_S323_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_242/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_242_S323_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:39:15 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	93,878,414
Mapped reads	85,442,830 / 91.01%
Unmapped reads	8,435,584 / 8.99%
Mapped paired reads	85,442,830 / 91.01%
Mapped reads, first in pair	42,812,198 / 45.6%
Mapped reads, second in pair	42,630,632 / 45.41%
Mapped reads, both in pair	82,712,941 / 88.11%
Mapped reads, singletons	2,729,889 / 2.91%
Read min/max/mean length	30 / 151 / 148.18
Duplicated reads (flagged)	15,866,169 / 16.9%
Clipped reads	20,312,491 / 21.64%

### 2.2. ACGT Content

Number/percentage of A's	3,637,424,141 / 31.08%
Number/percentage of C's	2,214,018,386 / 18.92%
Number/percentage of T's	3,638,595,818 / 31.09%
Number/percentage of G's	2,212,370,778 / 18.91%
Number/percentage of N's	42,484 / 0%
GC Percentage	37.82%

### 2.3. Coverage

Mean	37.645
Standard Deviation	367.1073

## 2.4. Mapping Quality

Mean Mapping Quality	45
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## 2.5. Insert size

Mean	245,450.23
Standard Deviation	2,397,978.27
P25/Median/P75	311 / 409 / 531

## 2.6. Mismatches and indels

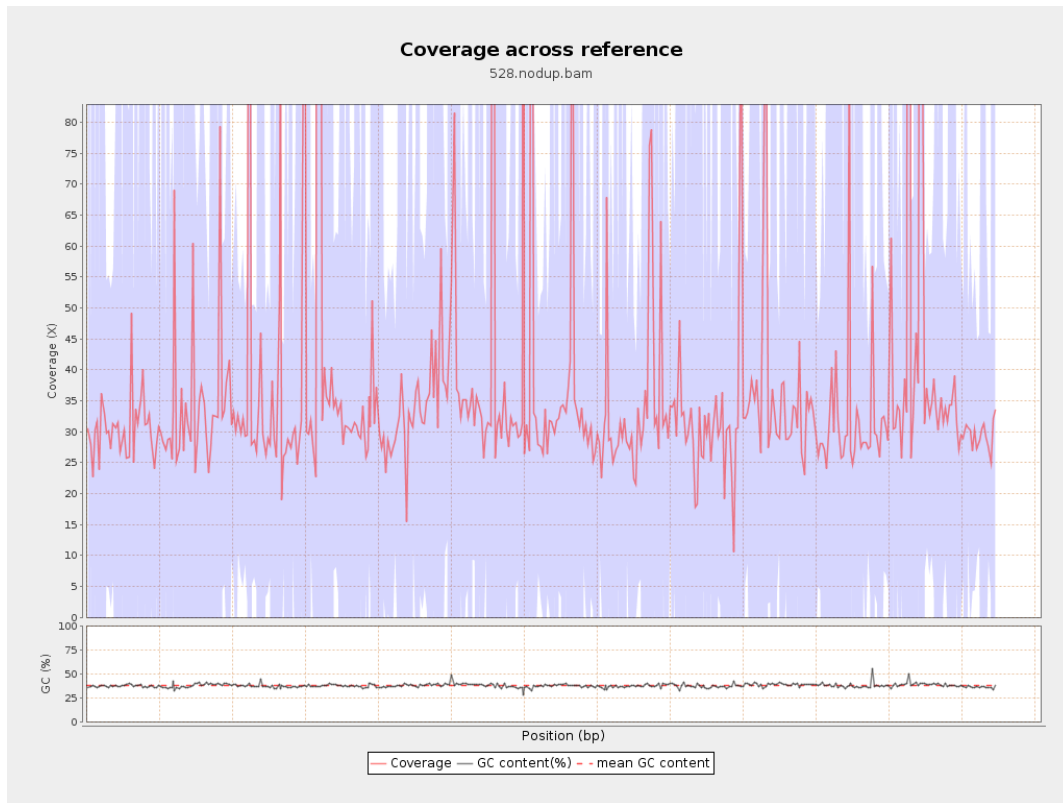
General error rate	2.31%
Mismatches	246,515,109
Insertions	8,505,691
Mapped reads with at least one insertion	8.86%
Deletions	7,926,376
Mapped reads with at least one deletion	8.24%
Homopolymer indels	58.16%

## 2.7. Chromosome stats

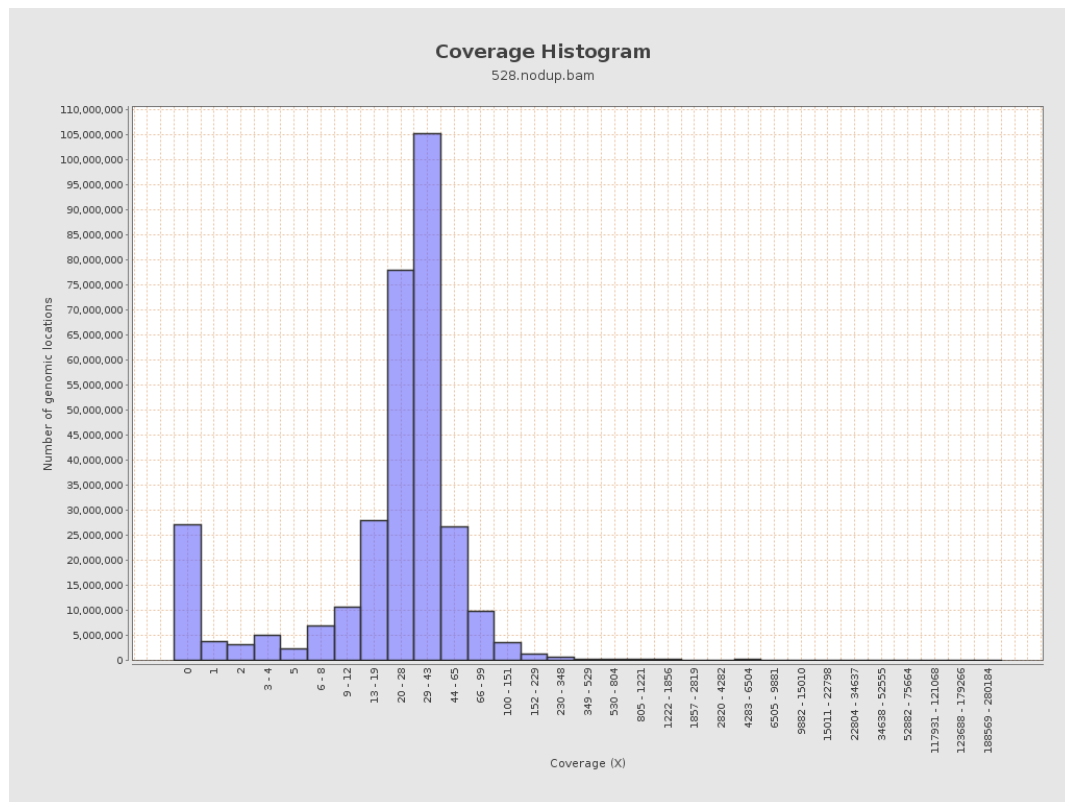
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	894726729	30.1008	145.0905

LT669789.1	36598175	1355896924	37.0482	368.1351
LT669790.1	30422129	1442346703	47.4111	556.7541
LT669791.1	52758100	1970390327	37.3476	393.2621
LT669792.1	28376109	1091275382	38.4575	380.5026
LT669793.1	33388210	1118358924	33.4956	239.4751
LT669794.1	50579949	1762746856	34.8507	281.5665
LT669795.1	49795044	2096014244	42.0928	420.0183

### 3. Results : Coverage across reference

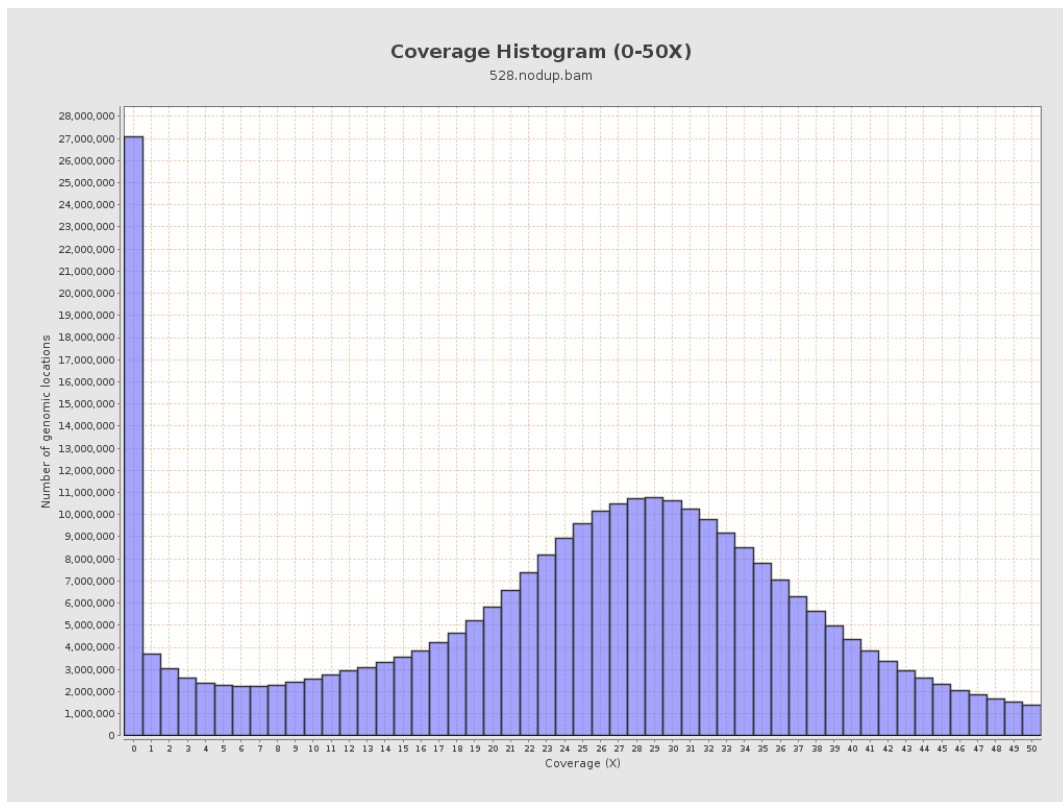


## 4. Results : Coverage Histogram

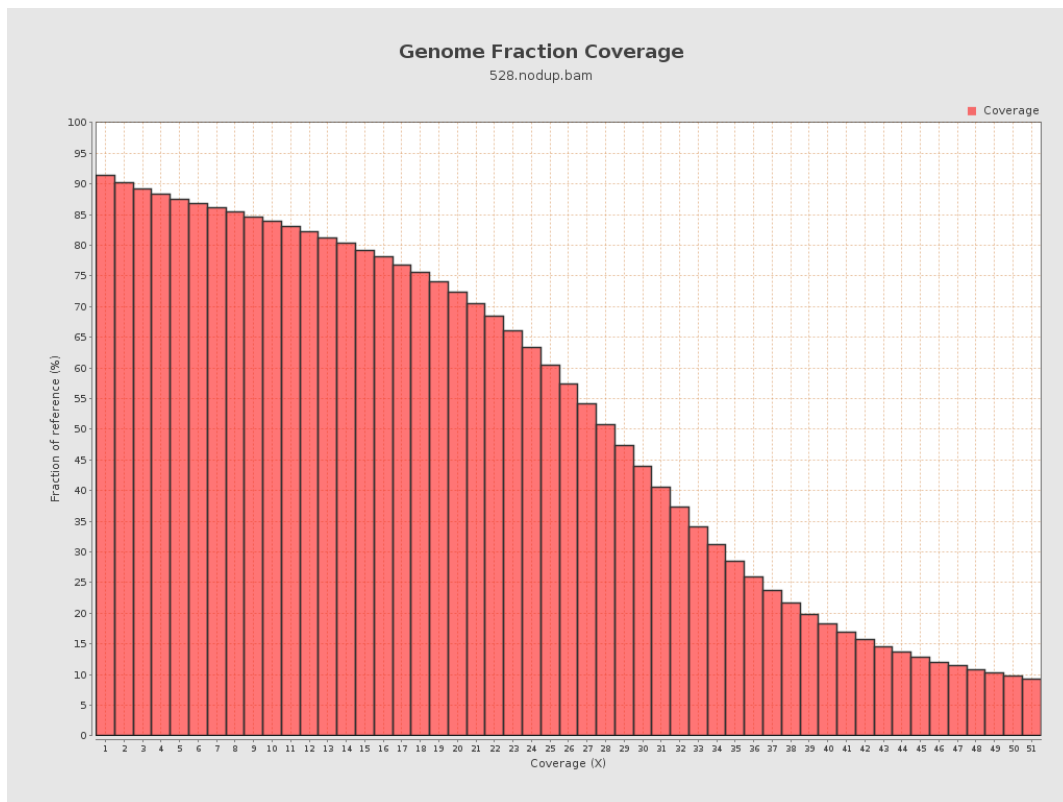




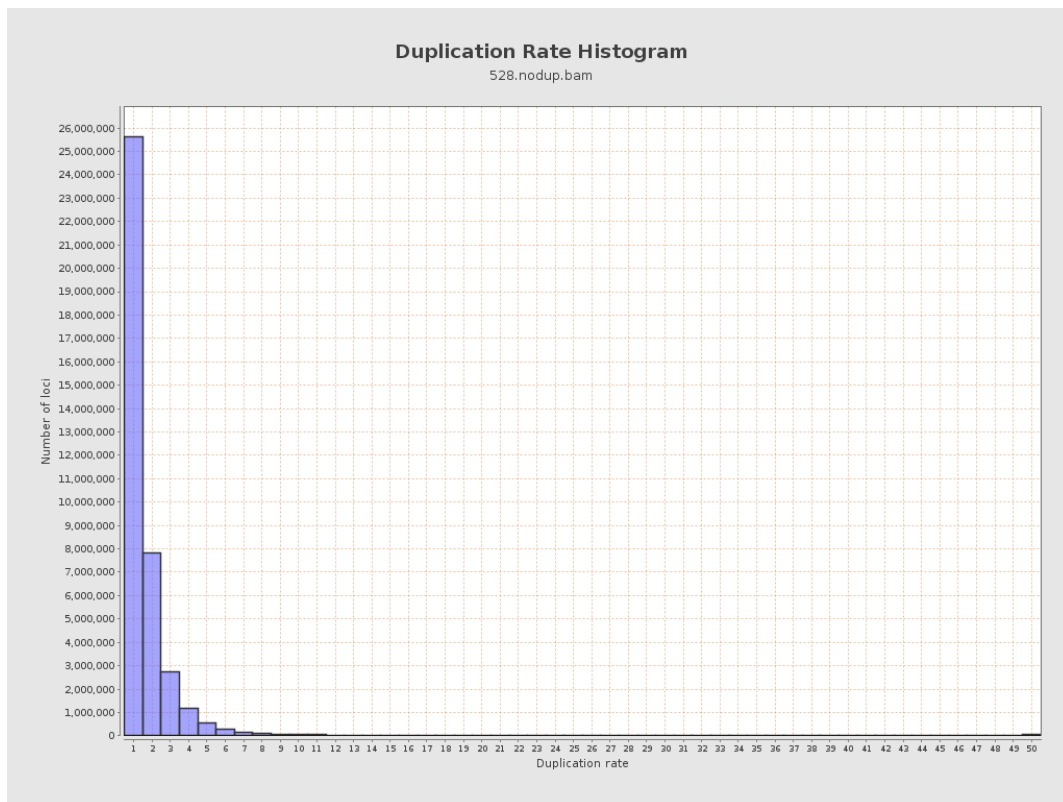
## 5. Results : Coverage Histogram (0-50X)



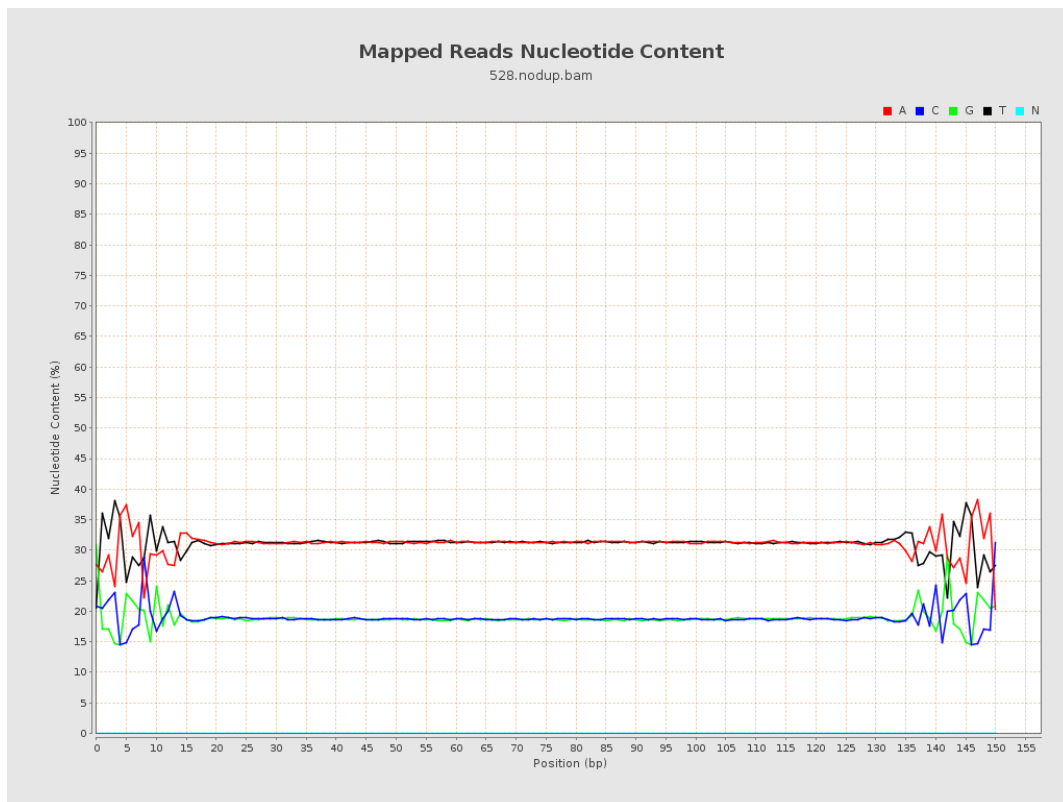
## 6. Results : Genome Fraction Coverage



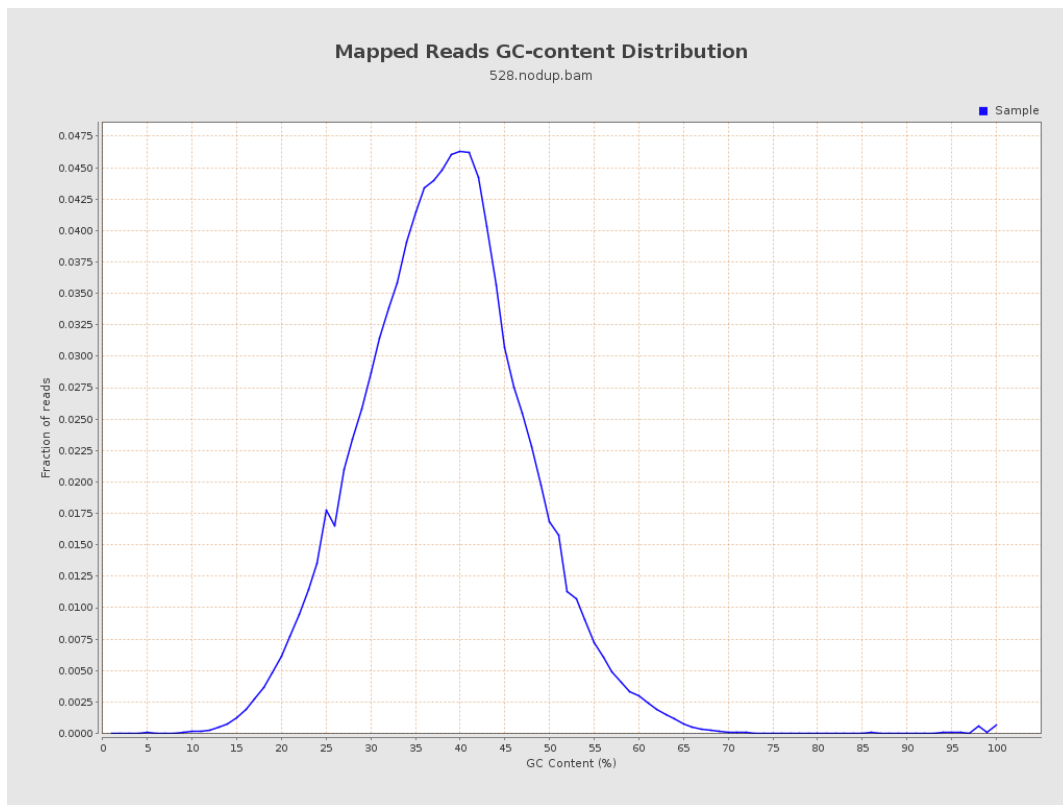
## 7. Results : Duplication Rate Histogram



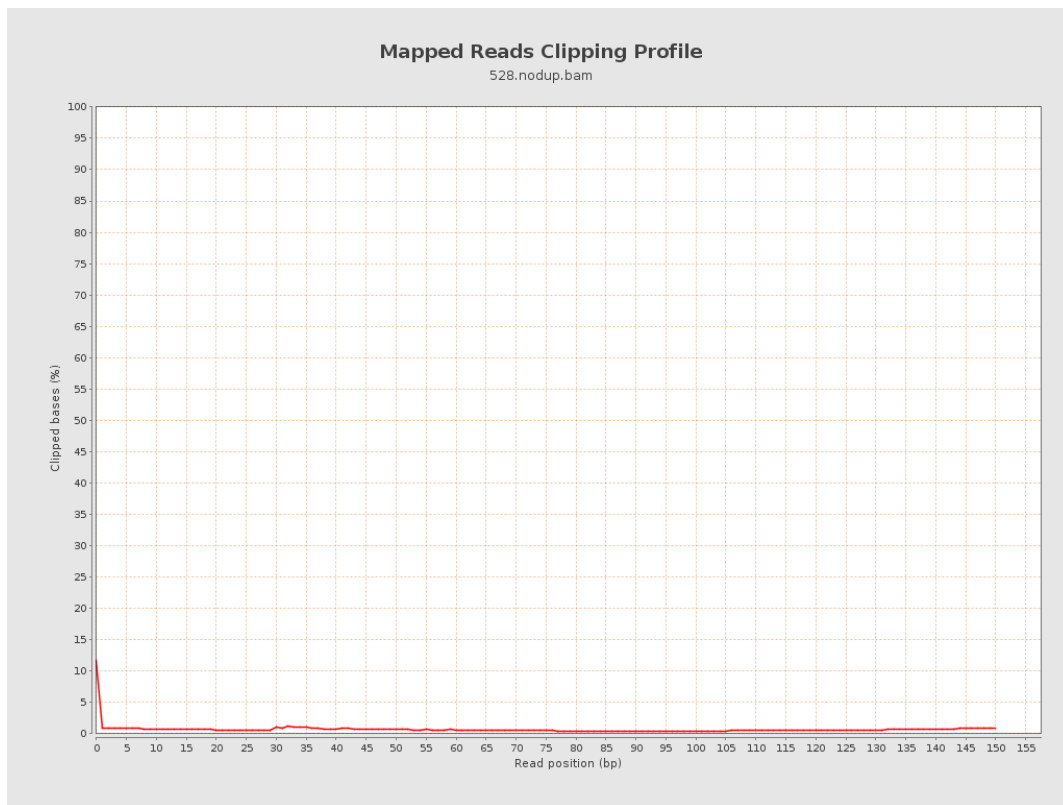
## 8. Results : Mapped Reads Nucleotide Content



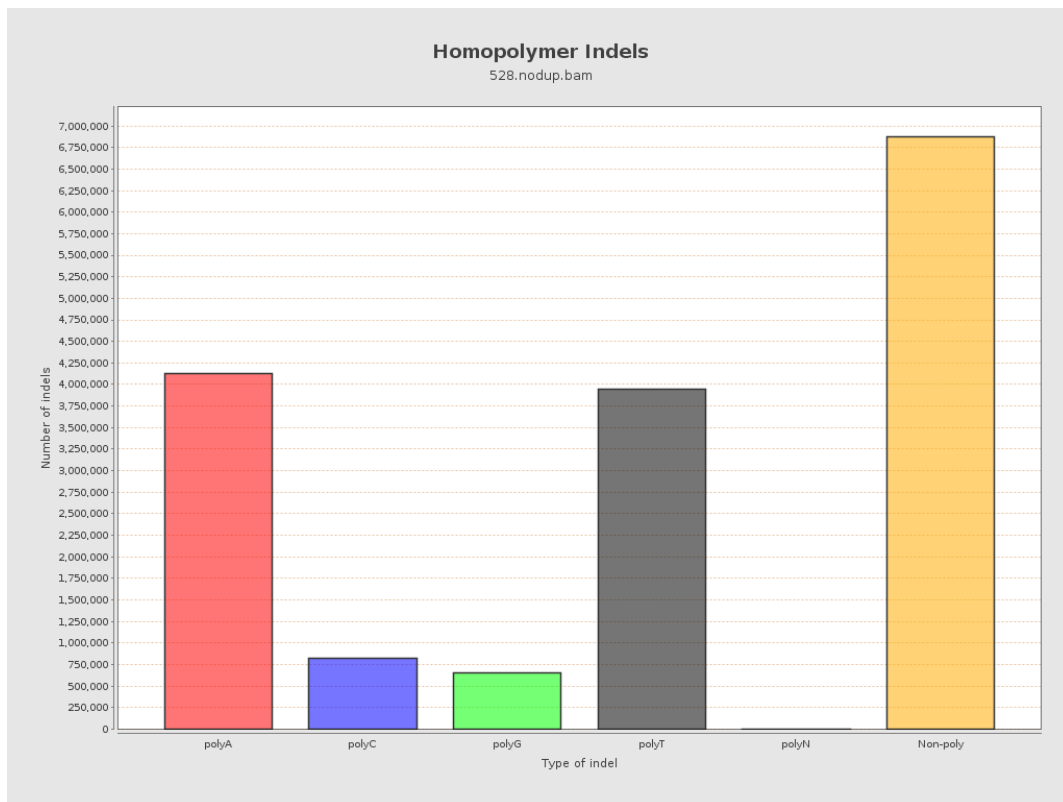
## 9. Results : Mapped Reads GC-content Distribution



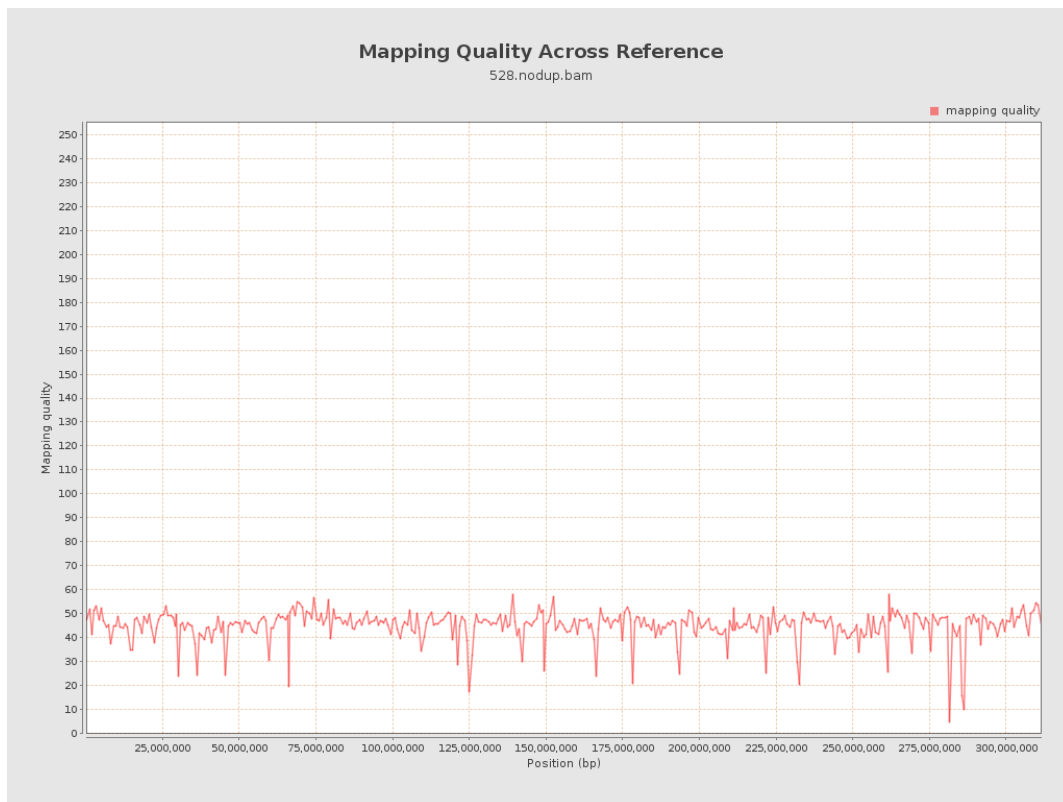
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

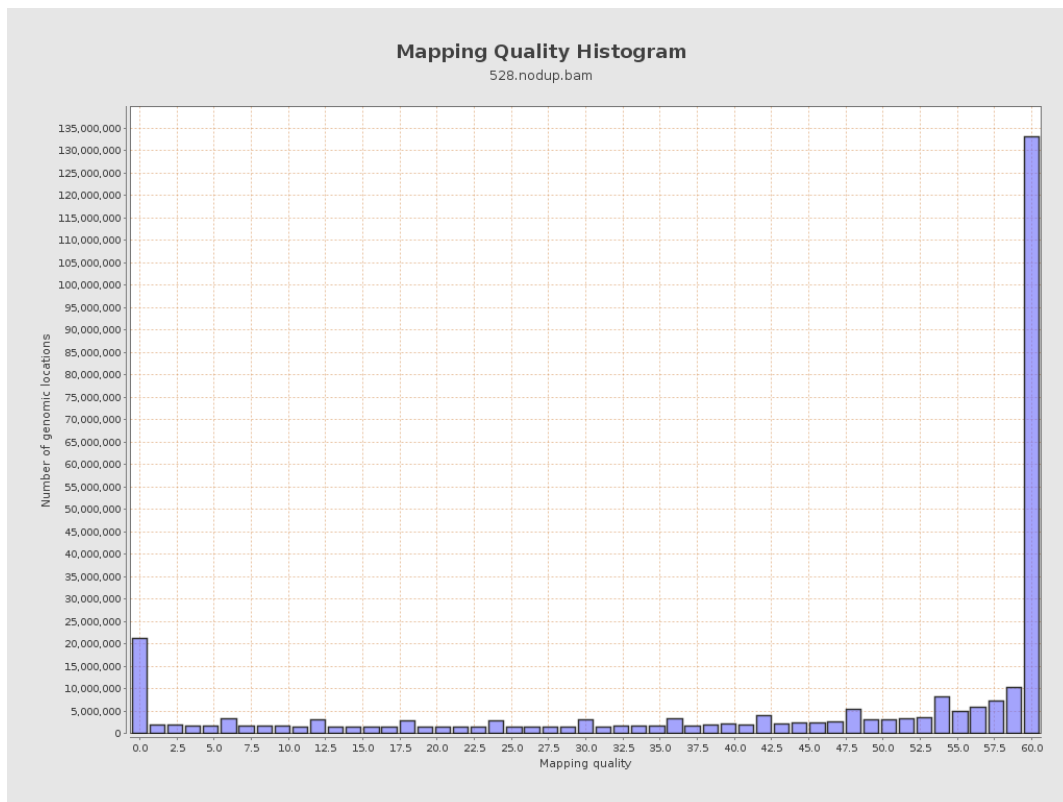


## 12. Results : Mapping Quality Across Reference

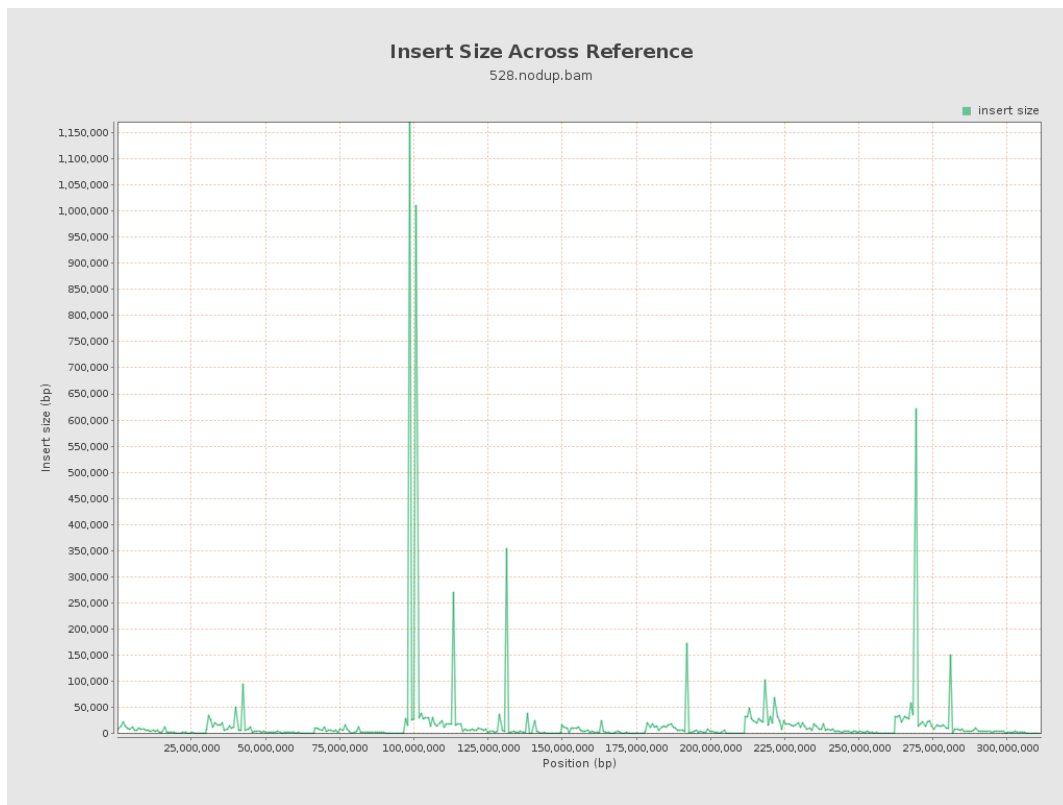




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

