

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:33:20*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/909
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/909 .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_215/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_215_S296_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_215/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_215_S296_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:33:20 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

## 2. Summary

### 2.1. Globals

Reference size	311,642,060
Number of reads	72,232,542
Mapped reads	67,831,177 / 93.91%
Unmapped reads	4,401,365 / 6.09%
Mapped paired reads	67,831,177 / 93.91%
Mapped reads, first in pair	33,962,800 / 47.02%
Mapped reads, second in pair	33,868,377 / 46.89%
Mapped reads, both in pair	66,484,254 / 92.04%
Mapped reads, singletons	1,346,923 / 1.86%
Read min/max/mean length	30 / 151 / 148
Duplicated reads (flagged)	9,858,032 / 13.65%
Clipped reads	15,607,059 / 21.61%

### 2.2. ACGT Content

Number/percentage of A's	2,889,432,971 / 30.84%
Number/percentage of C's	1,794,653,393 / 19.15%
Number/percentage of T's	2,889,786,646 / 30.84%
Number/percentage of G's	1,795,393,360 / 19.16%
Number/percentage of N's	34,803 / 0%
GC Percentage	38.32%

### 2.3. Coverage

Mean	30.1432
Standard Deviation	243.8461

## 2.4. Mapping Quality

Mean Mapping Quality	43.78
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## 2.5. Insert size

Mean	231,922.28
Standard Deviation	2,281,546.94
P25/Median/P75	306 / 404 / 531

## 2.6. Mismatches and indels

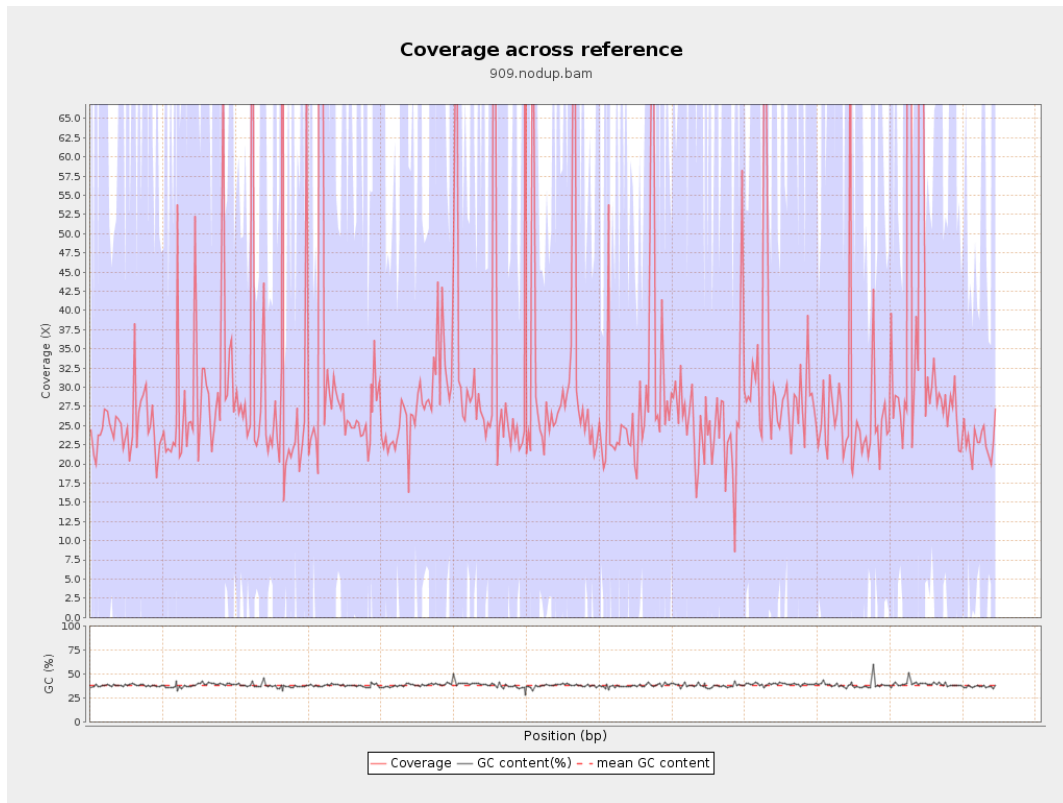
General error rate	2.3%
Mismatches	198,166,259
Insertions	6,354,926
Mapped reads with at least one insertion	8.41%
Deletions	6,482,082
Mapped reads with at least one deletion	8.5%
Homopolymer indels	56.82%

## 2.7. Chromosome stats

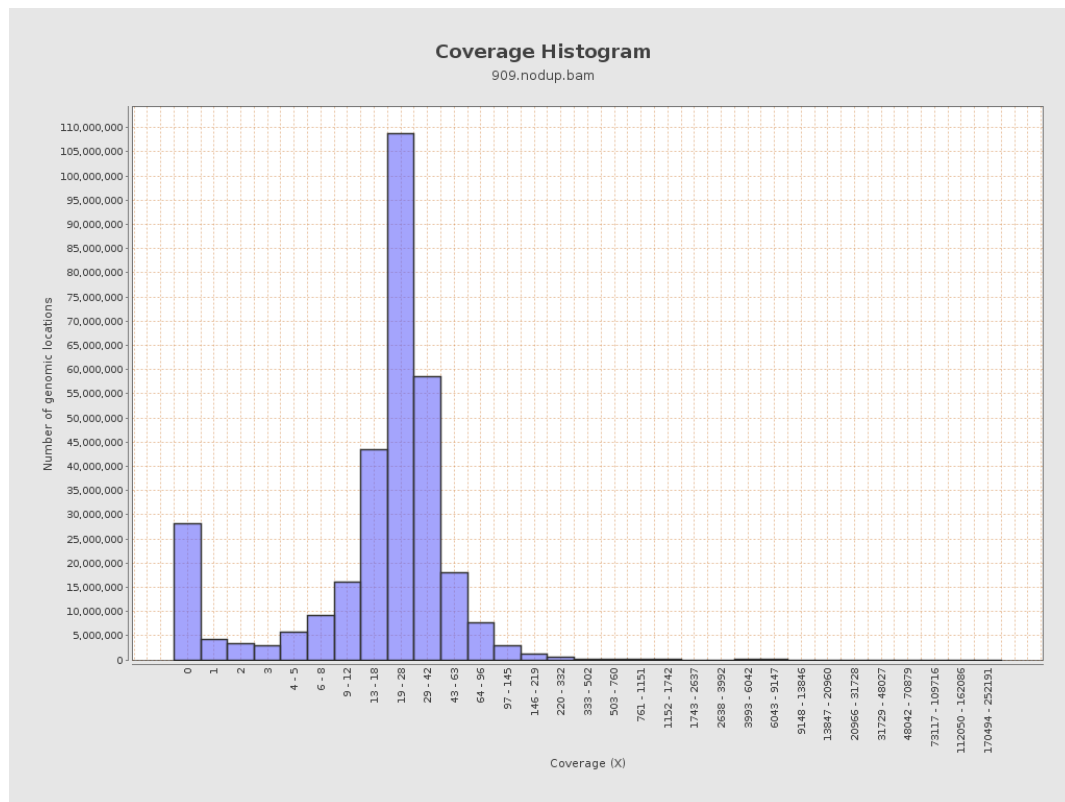
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	726882296	24.4541	73.0702

LT669789.1	36598175	1133651576	30.9756	259.4521
LT669790.1	30422129	979576494	32.1995	245.4917
LT669791.1	52758100	1560161810	29.572	207.2895
LT669792.1	28376109	848725421	29.9099	249.4487
LT669793.1	33388210	938427263	28.1065	168.3886
LT669794.1	50579949	1478195093	29.2249	195.7149
LT669795.1	49795044	1728268747	34.7076	379.0798

### 3. Results : Coverage across reference

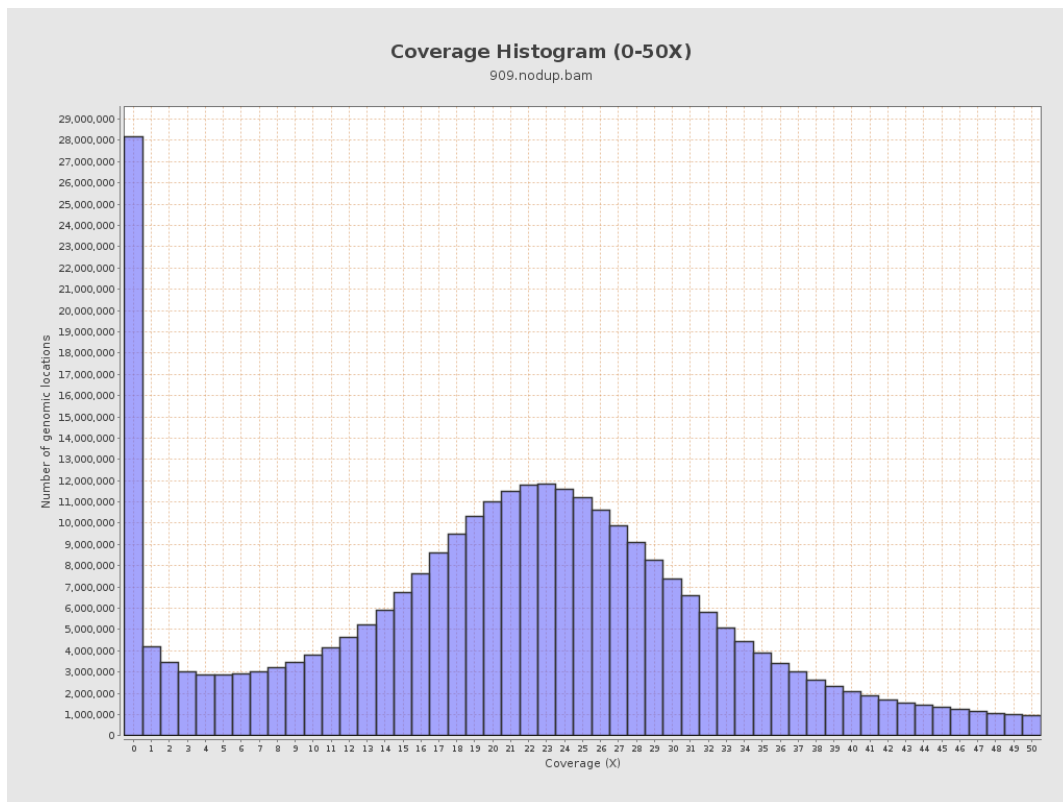


## 4. Results : Coverage Histogram

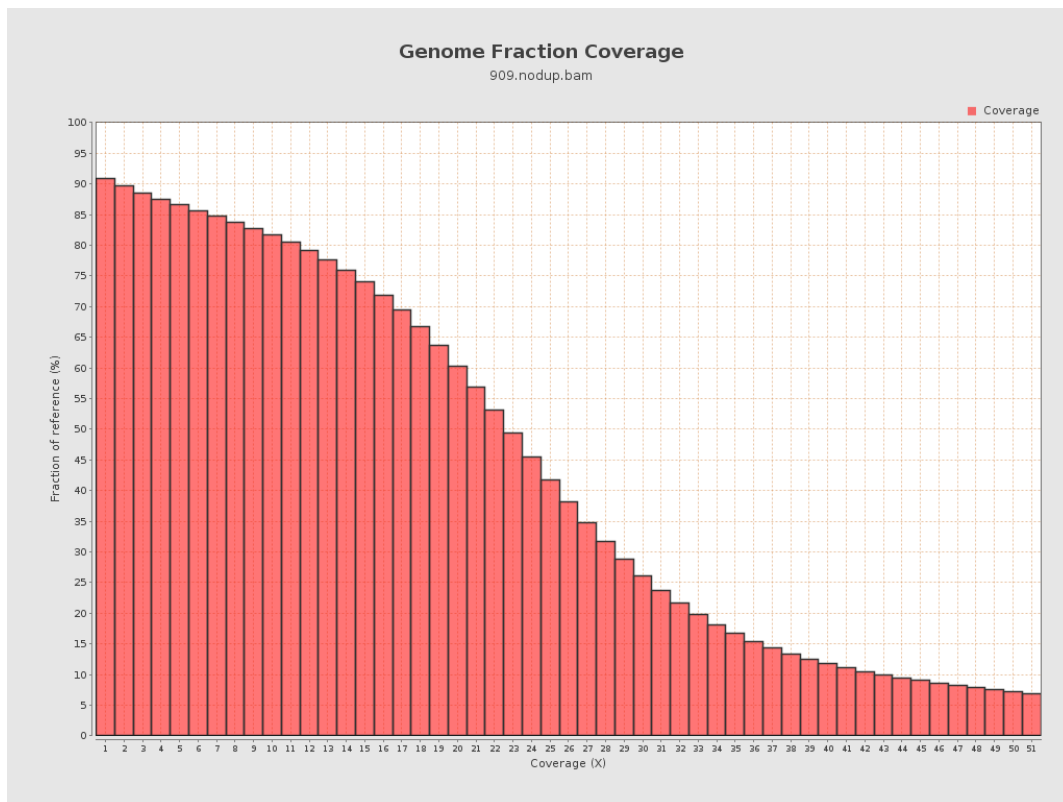




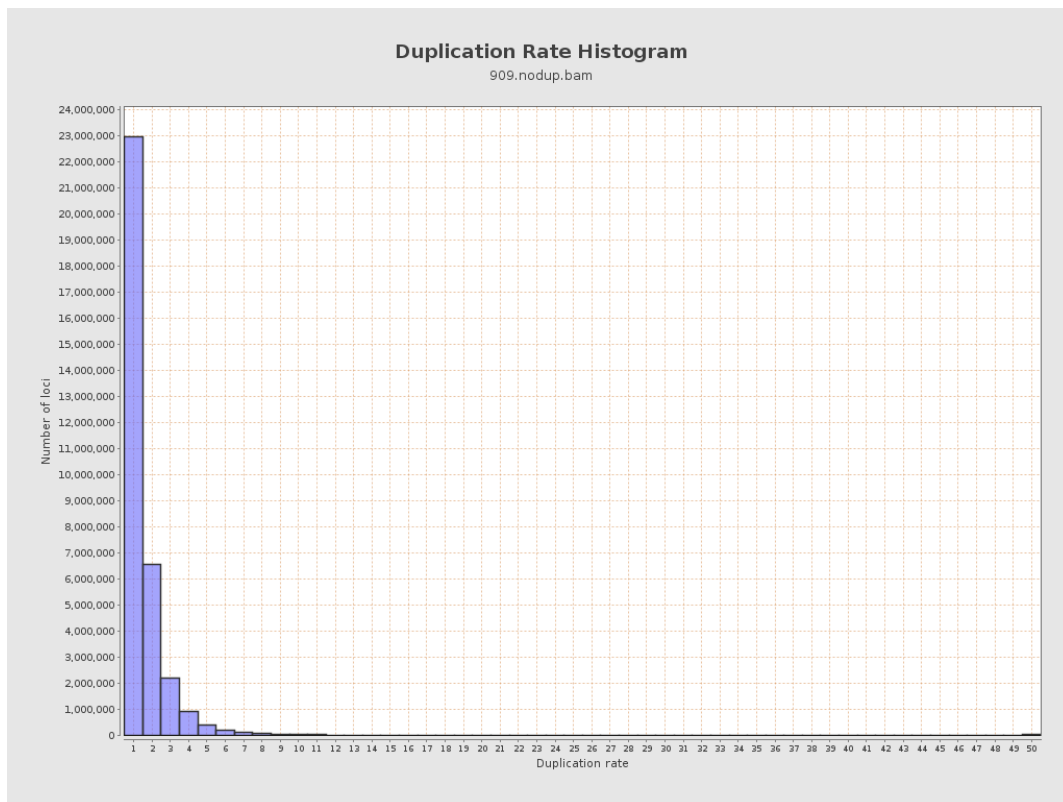
## 5. Results : Coverage Histogram (0-50X)



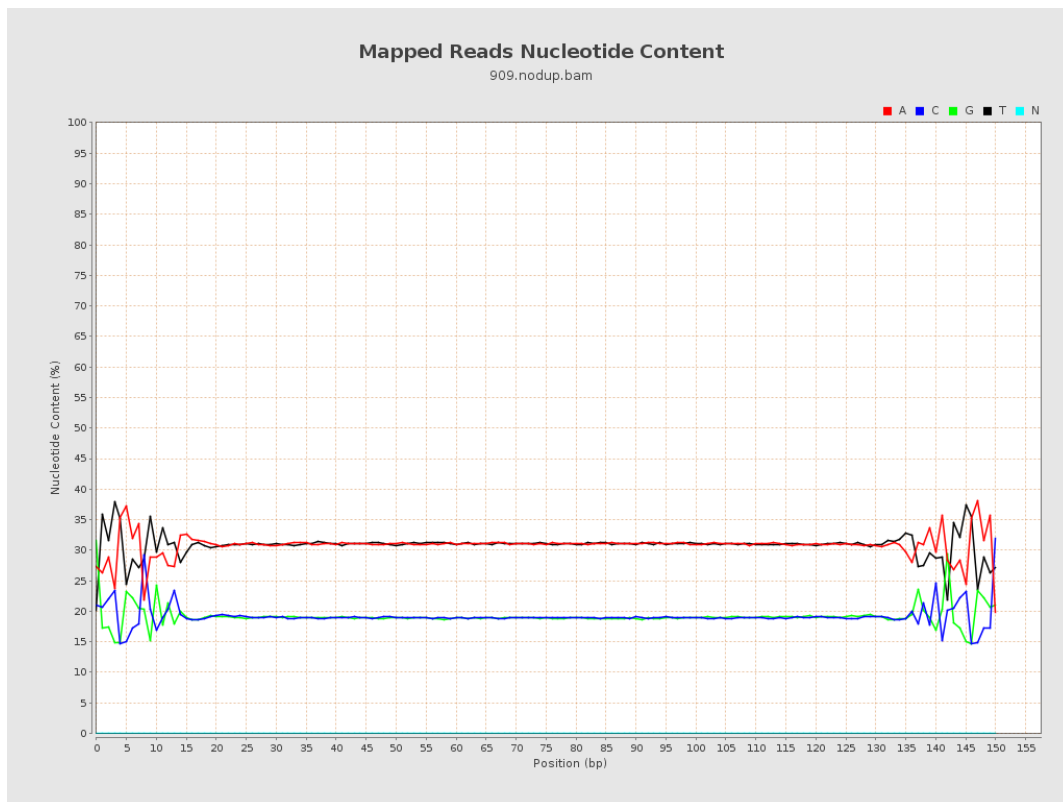
## 6. Results : Genome Fraction Coverage



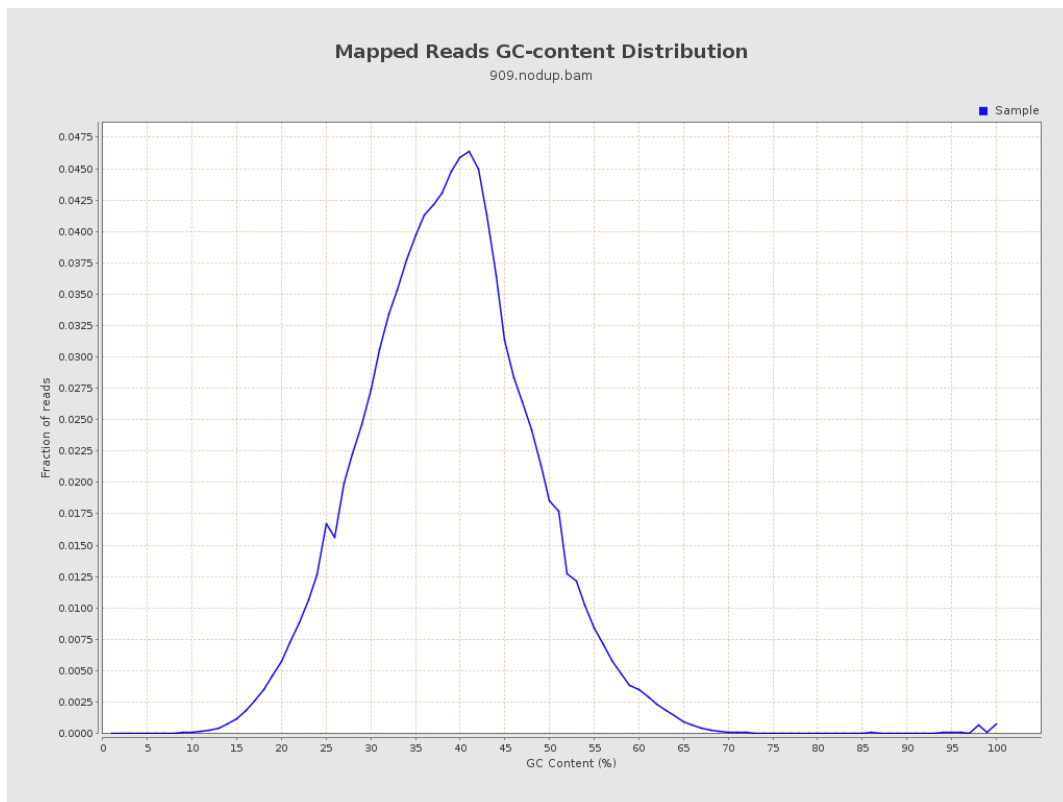
## 7. Results : Duplication Rate Histogram



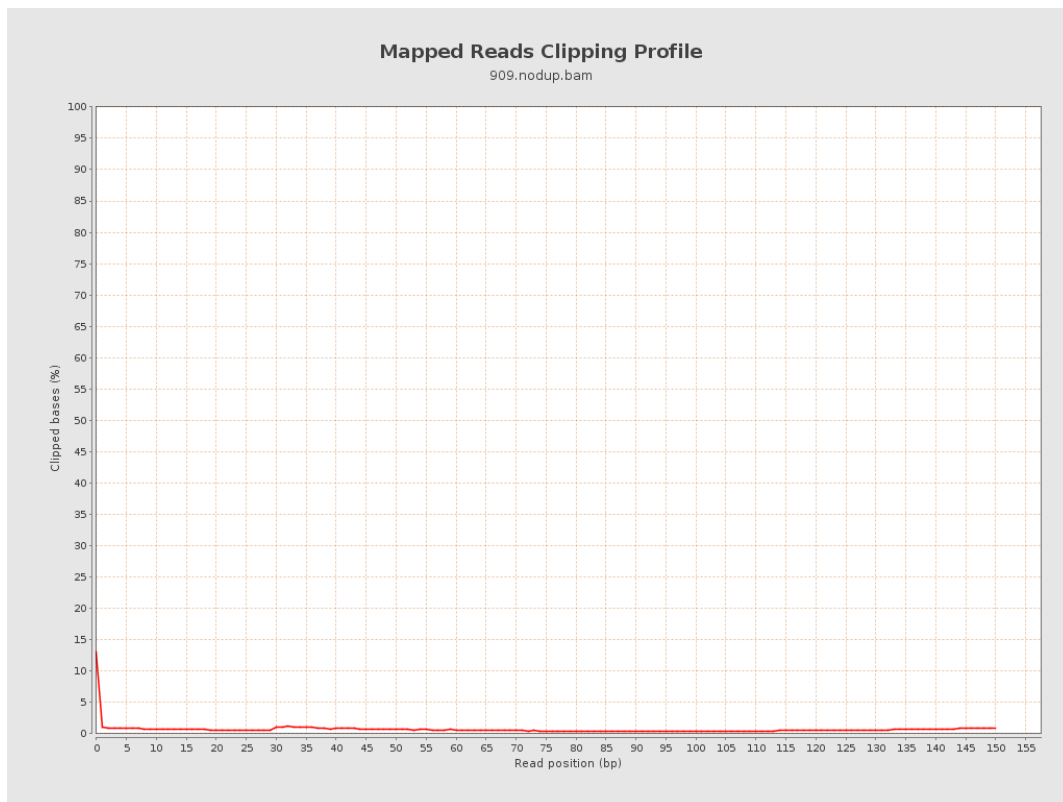
## 8. Results : Mapped Reads Nucleotide Content



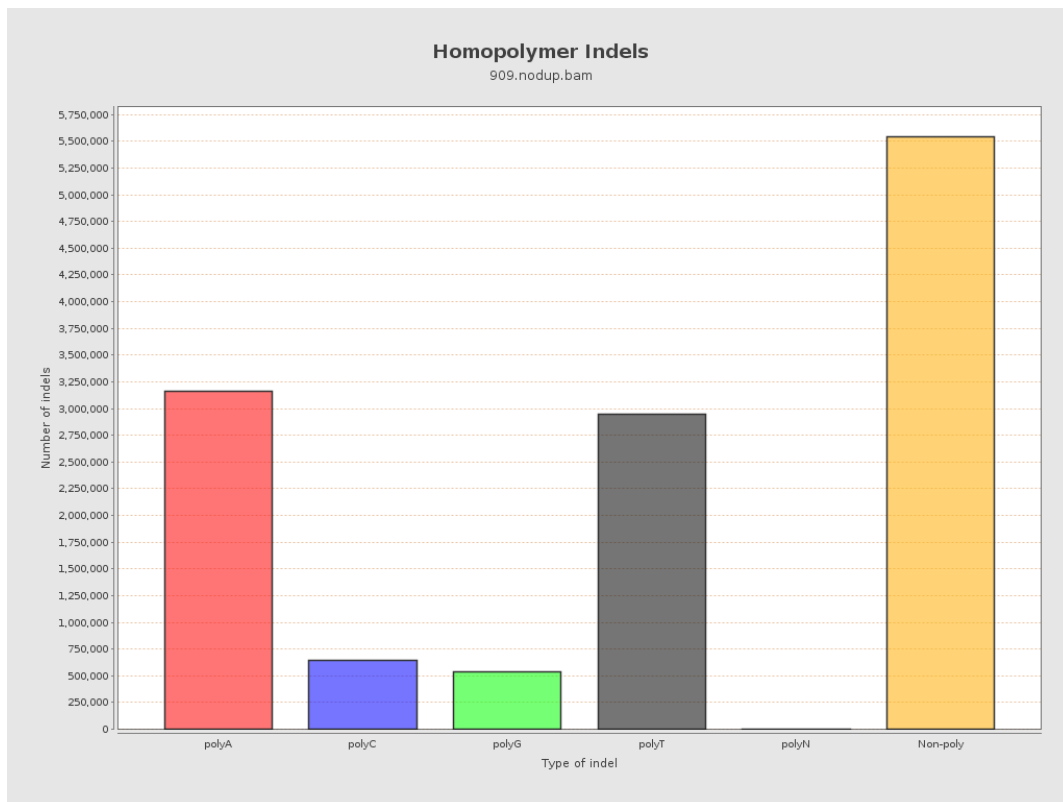
## 9. Results : Mapped Reads GC-content Distribution



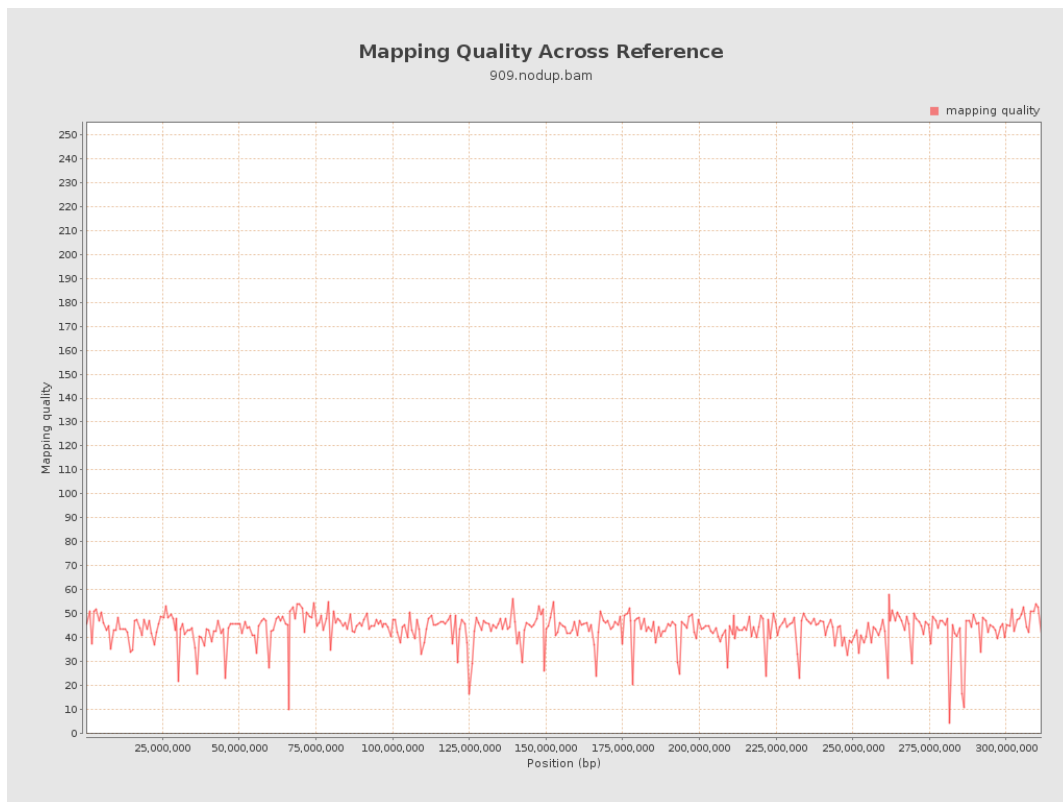
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

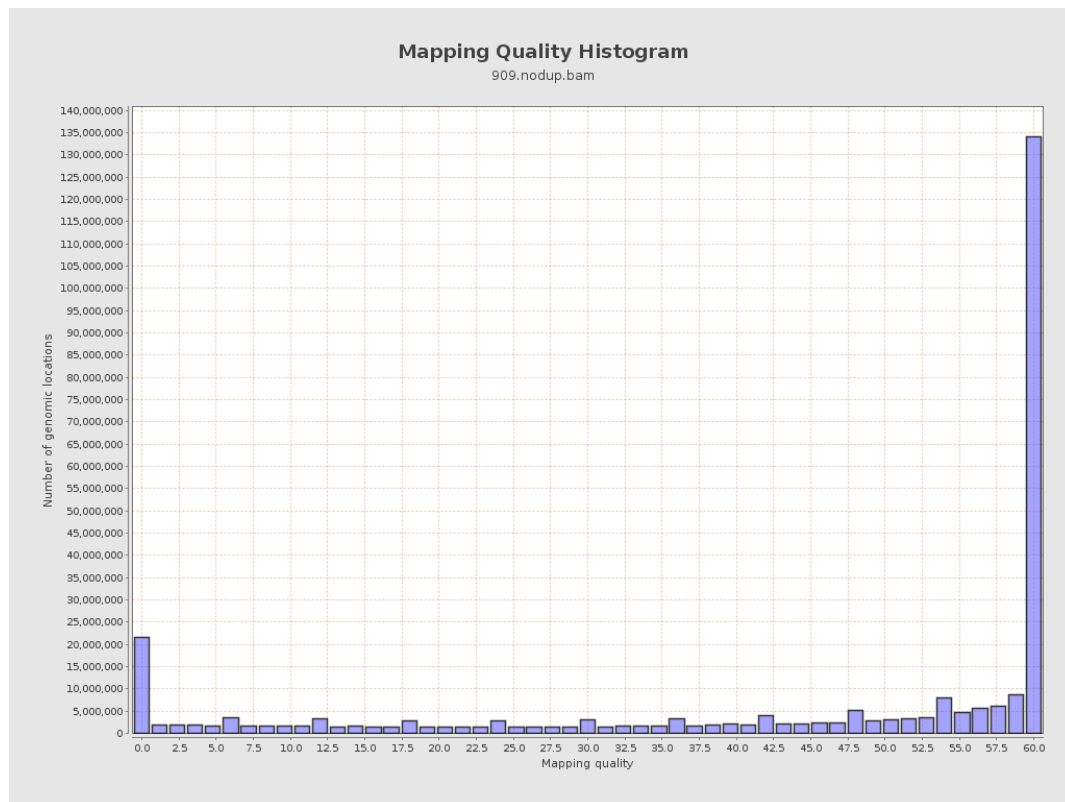


## 12. Results : Mapping Quality Across Reference

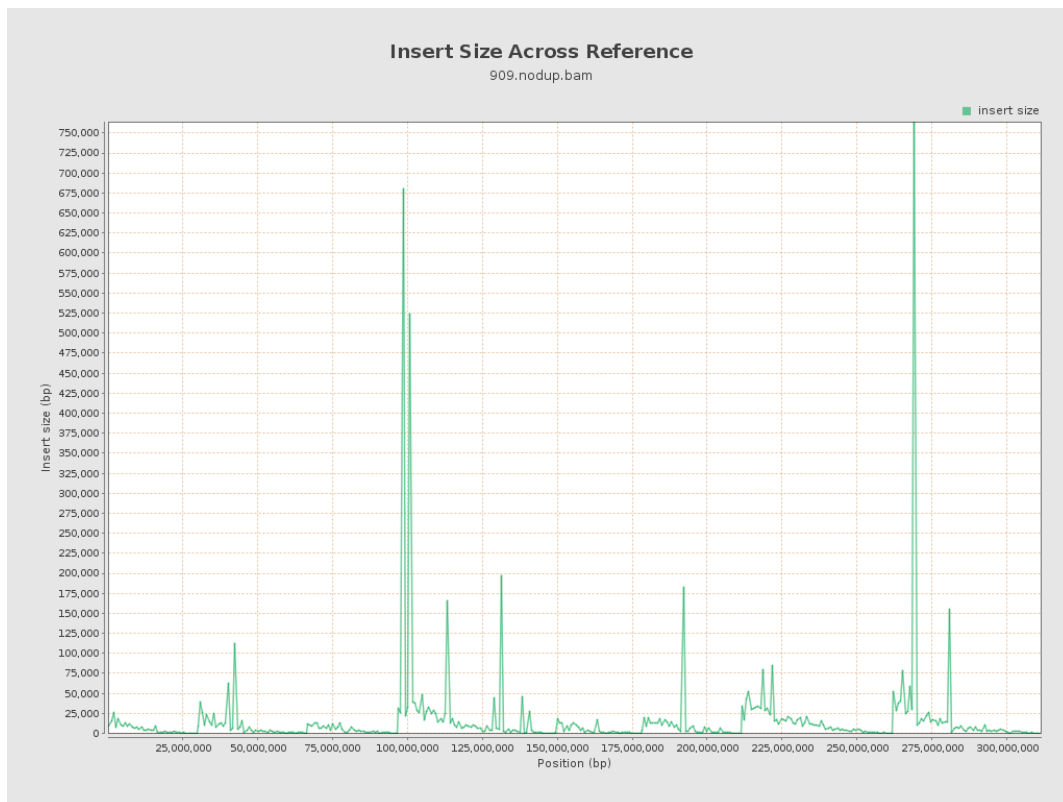




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

