Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:30:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/591.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/591.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_480/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_480_S455_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_480/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_480_S455_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:30:11 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	65,197,228
Mapped reads	59,863,833 / 91.82%
Unmapped reads	5,333,395 / 8.18%
Mapped paired reads	59,863,833 / 91.82%
Mapped reads, first in pair	29,964,695 / 45.96%
Mapped reads, second in pair	29,899,138 / 45.86%
Mapped reads, both in pair	58,118,047 / 89.14%
Mapped reads, singletons	1,745,786 / 2.68%
Read min/max/mean length	30 / 151 / 148.18
Duplicated reads (flagged)	9,923,483 / 15.22%
Clipped reads	13,484,158 / 20.68%

2.2. ACGT Content

Number/percentage of A's	2,544,605,124 / 30.79%
Number/percentage of C's	1,586,166,552 / 19.19%
Number/percentage of T's	2,551,573,061 / 30.88%
Number/percentage of G's	1,581,828,006 / 19.14%
Number/percentage of N's	28,592 / 0%
GC Percentage	38.33%

2.3. Coverage

Mean	26.5845
Standard Deviation	242.7372

2.4. Mapping Quality

Mean Mapping Quality	44.59

2.5. Insert size

Mean	251,415.46
Standard Deviation	2,417,929.91
P25/Median/P75	341 / 446 / 586

2.6. Mismatches and indels

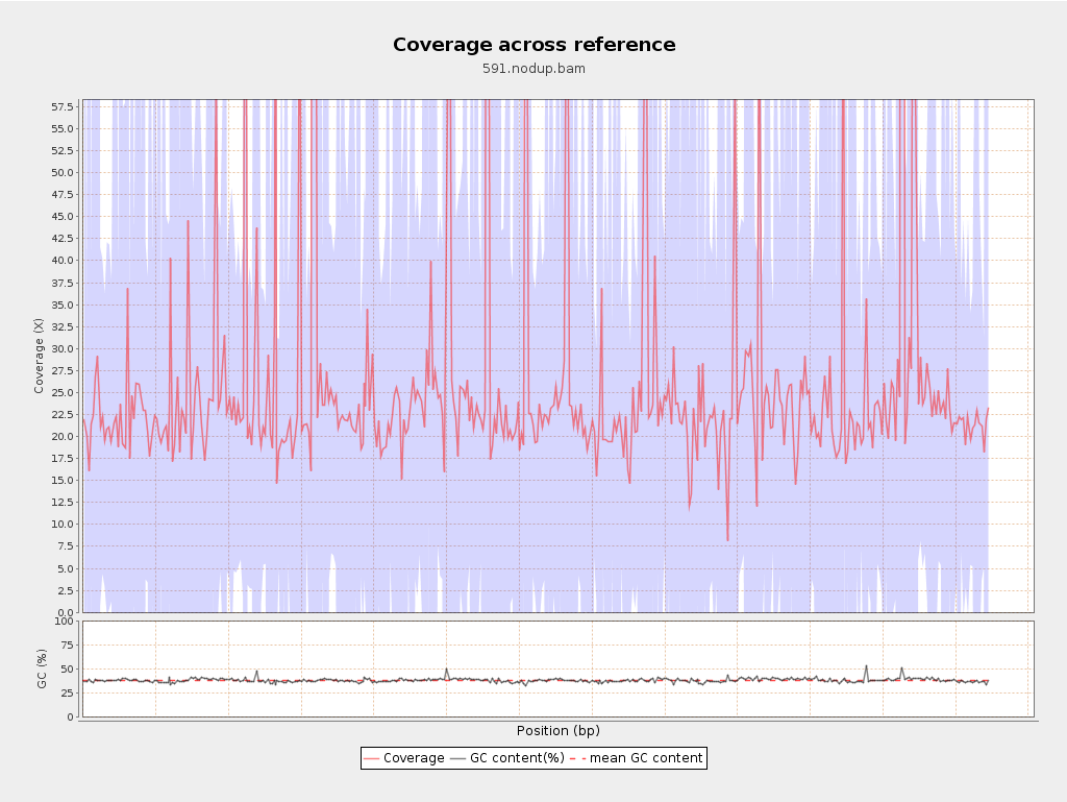
General error rate	2.31%
Mismatches	174,687,821
Insertions	5,823,952
Mapped reads with at least one insertion	8.69%
Deletions	5,575,580
Mapped reads with at least one deletion	8.26%
Homopolymer indels	56.83%

2.7. Chromosome stats

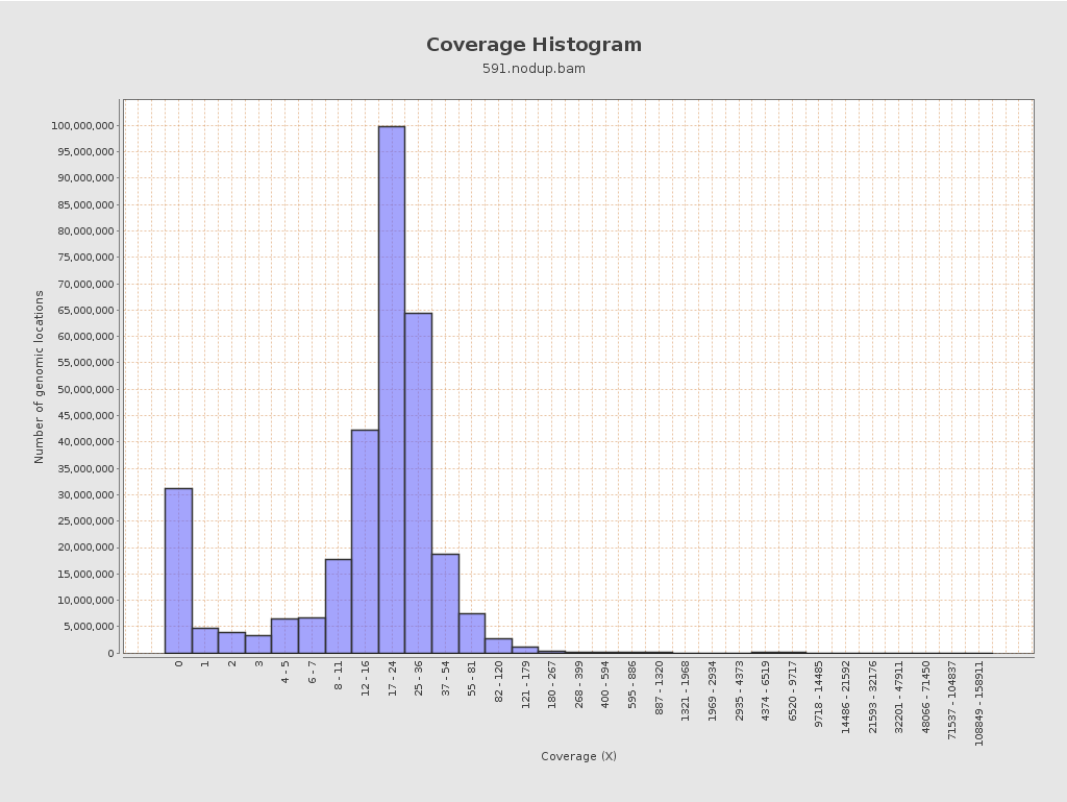
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	651928886	21.9325	102.0905

LT669789.1	36598175	980651118	26.7951	271.5437
LT669790.1	30422129	949228642	31.2019	315.9873
LT669791.1	52758100	1381894368	26.193	266.8065
LT669792.1	28376109	744835560	26.2487	248.1296
LT669793.1	33388210	804601316	24.0984	152.142
LT669794.1	50579949	1255005654	24.8123	210.4416
LT669795.1	49795044	1516707644	30.459	276.1921

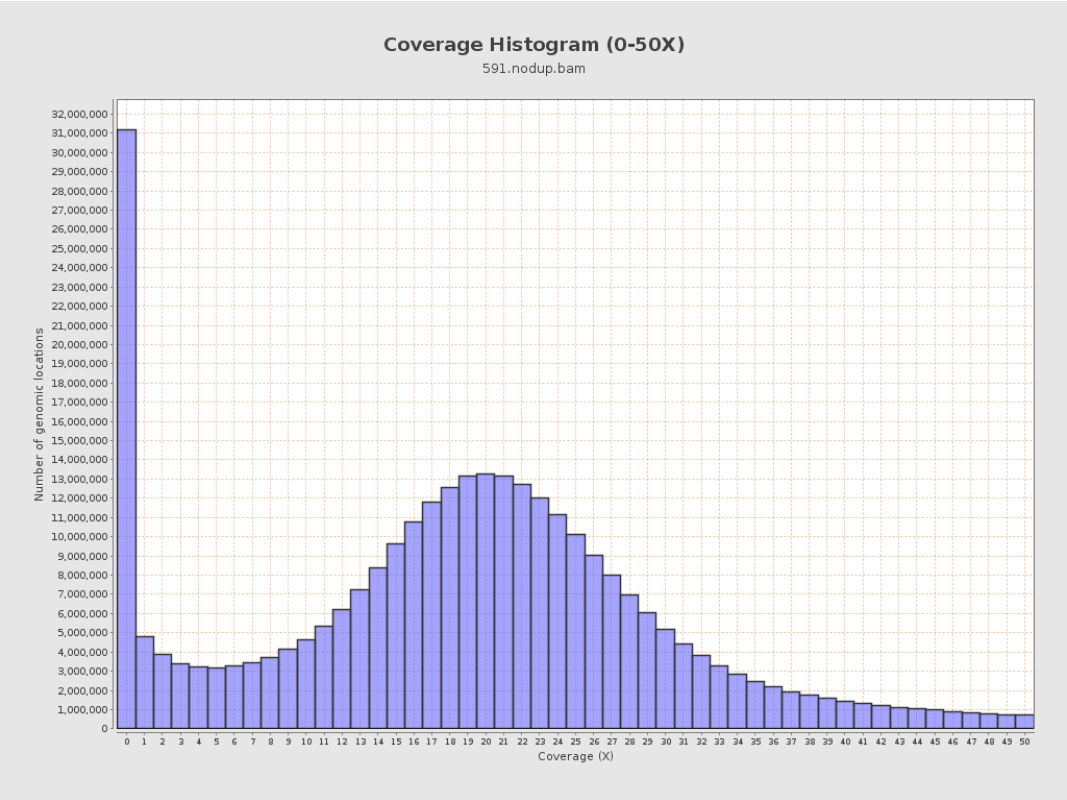
3. Results : Coverage across reference



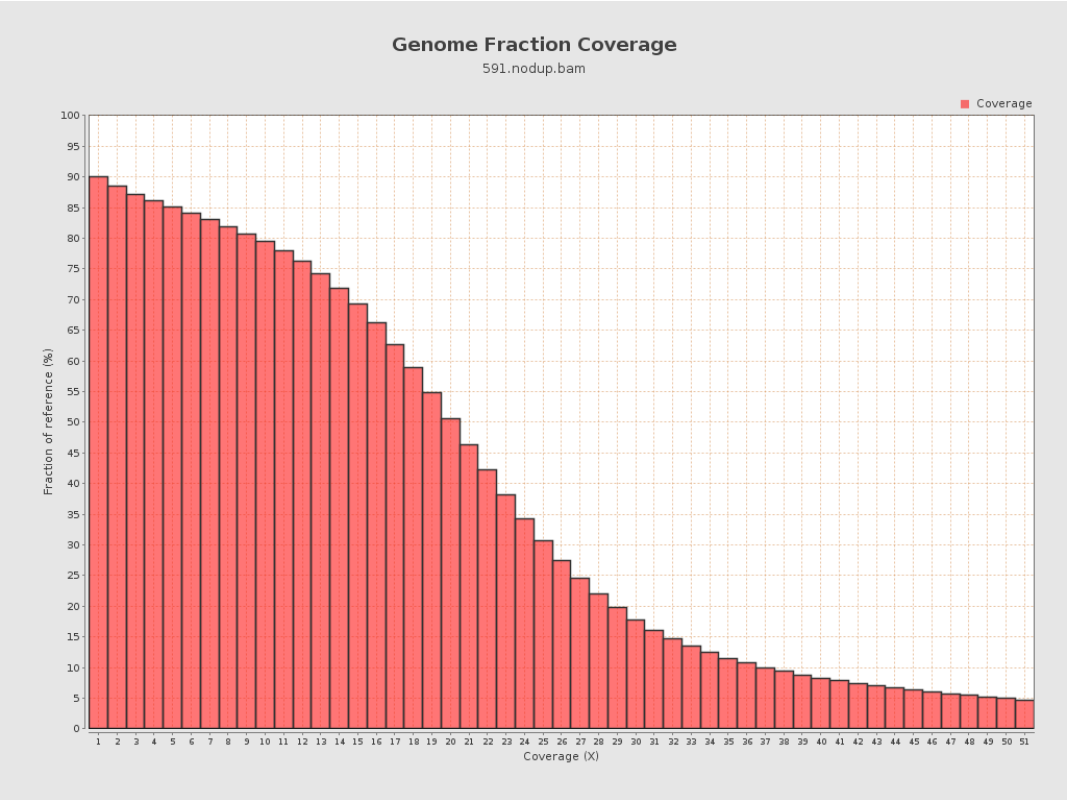
4. Results : Coverage Histogram



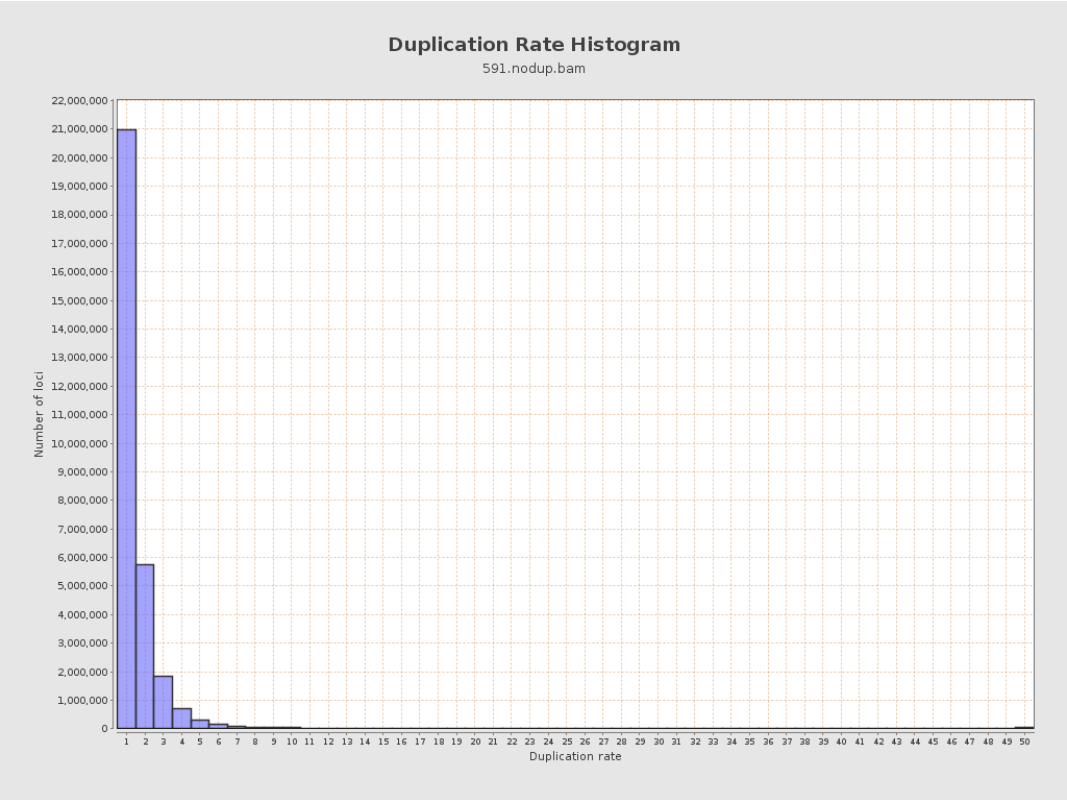
5. Results : Coverage Histogram (0-50X)



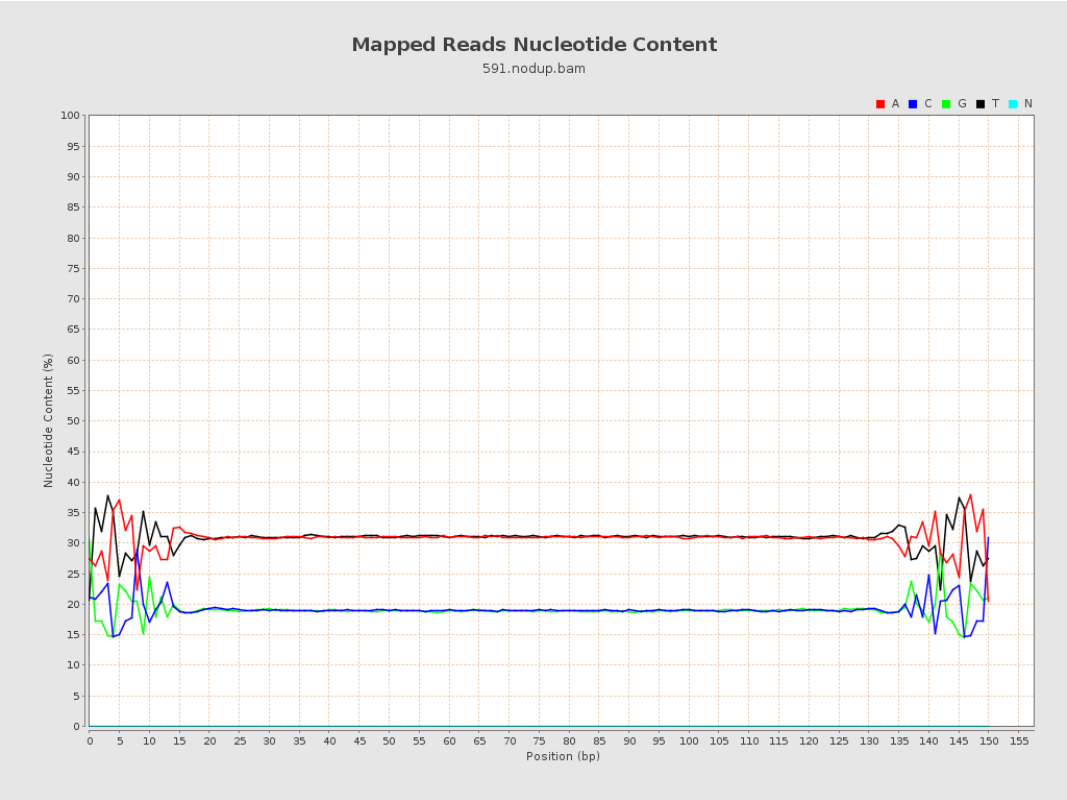
6. Results : Genome Fraction Coverage



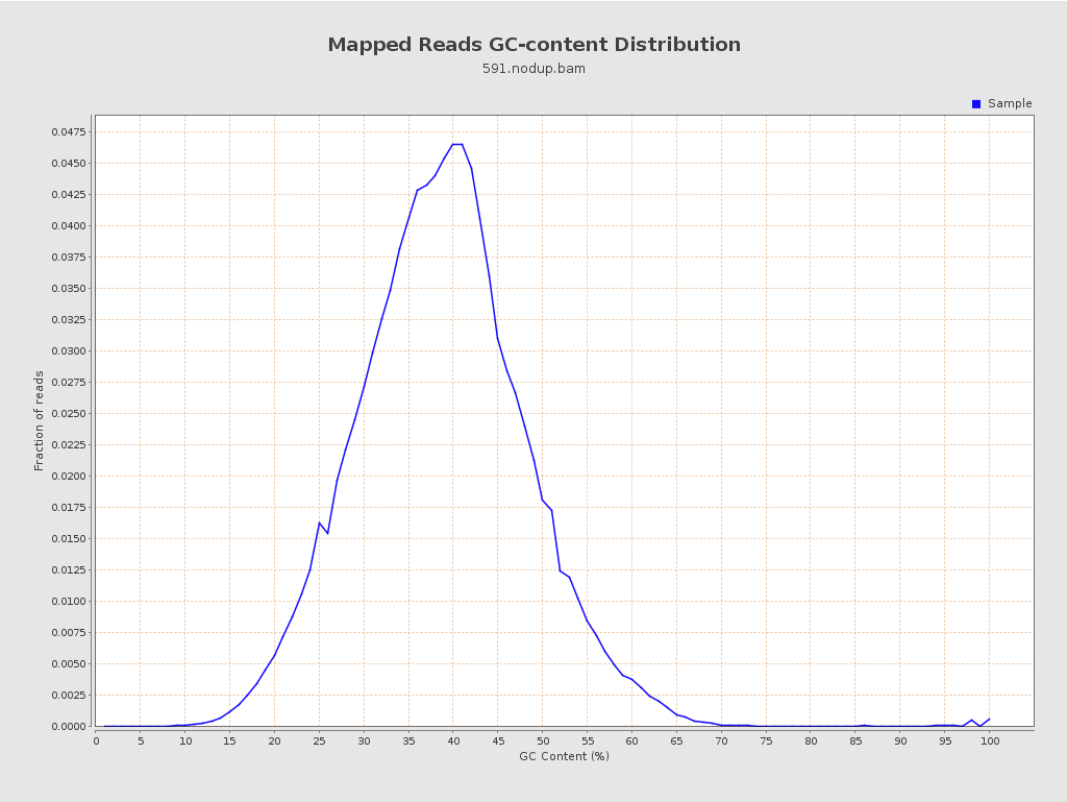
7. Results : Duplication Rate Histogram



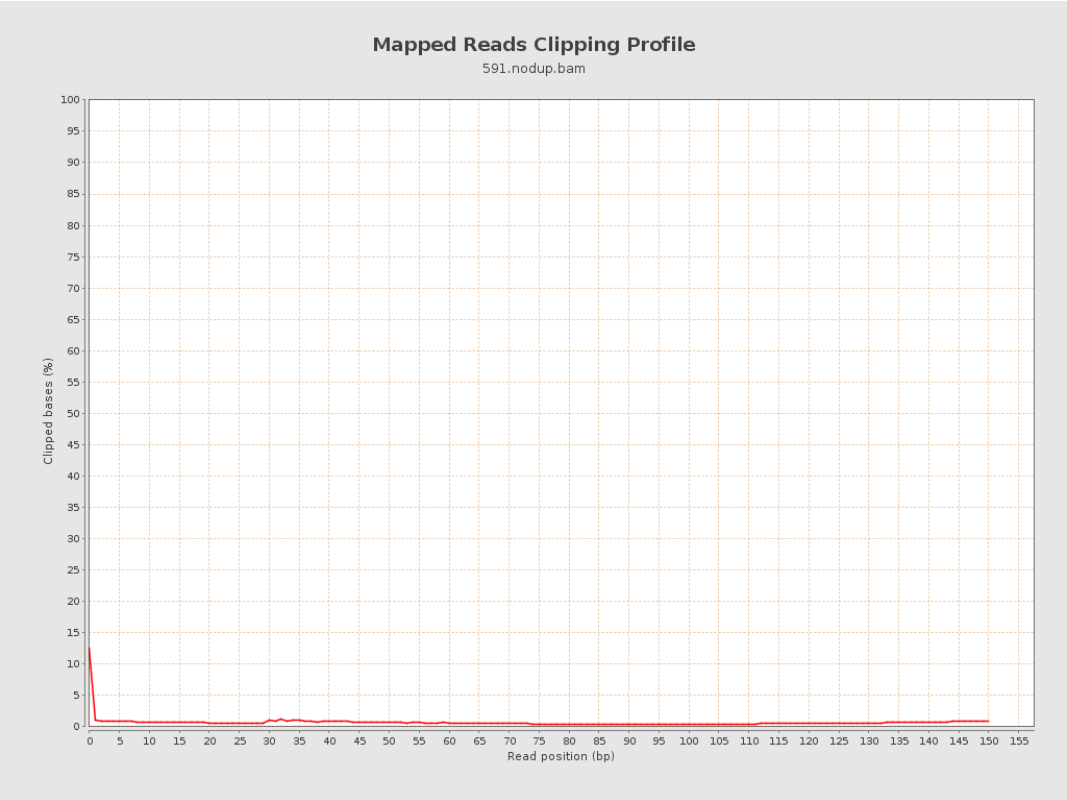
8. Results : Mapped Reads Nucleotide Content



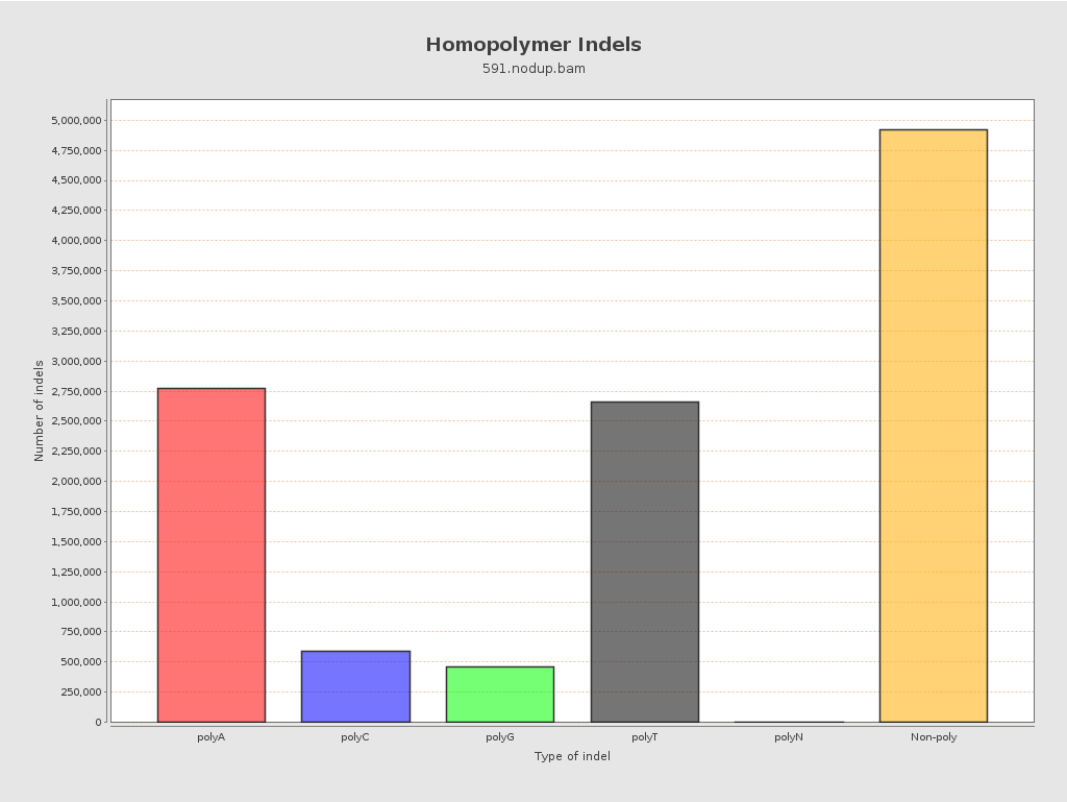
9. Results : Mapped Reads GC-content Distribution



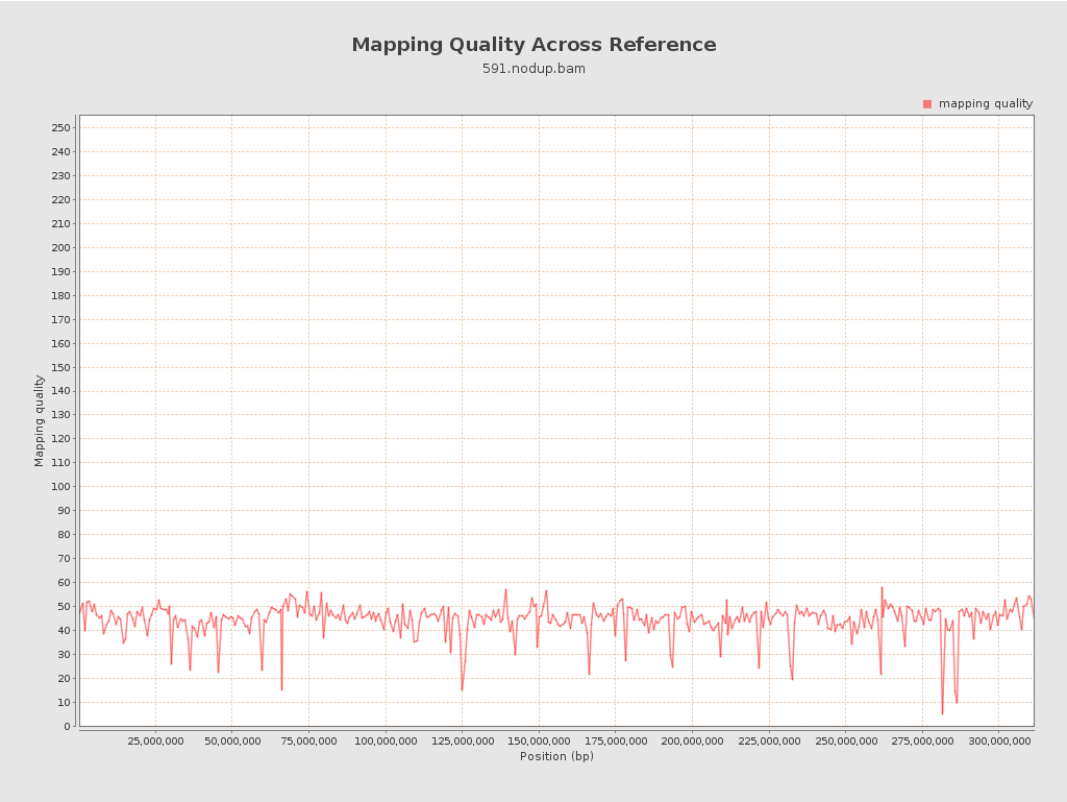
10. Results : Mapped Reads Clipping Profile



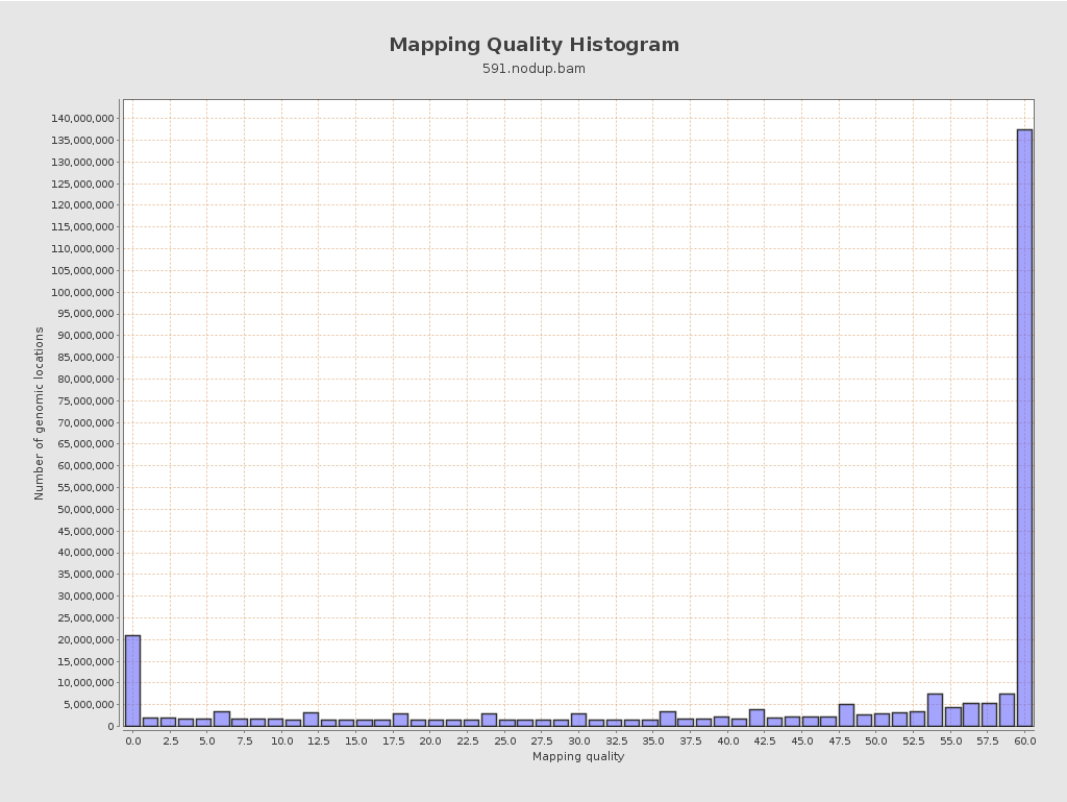
11. Results : Homopolymer Indels



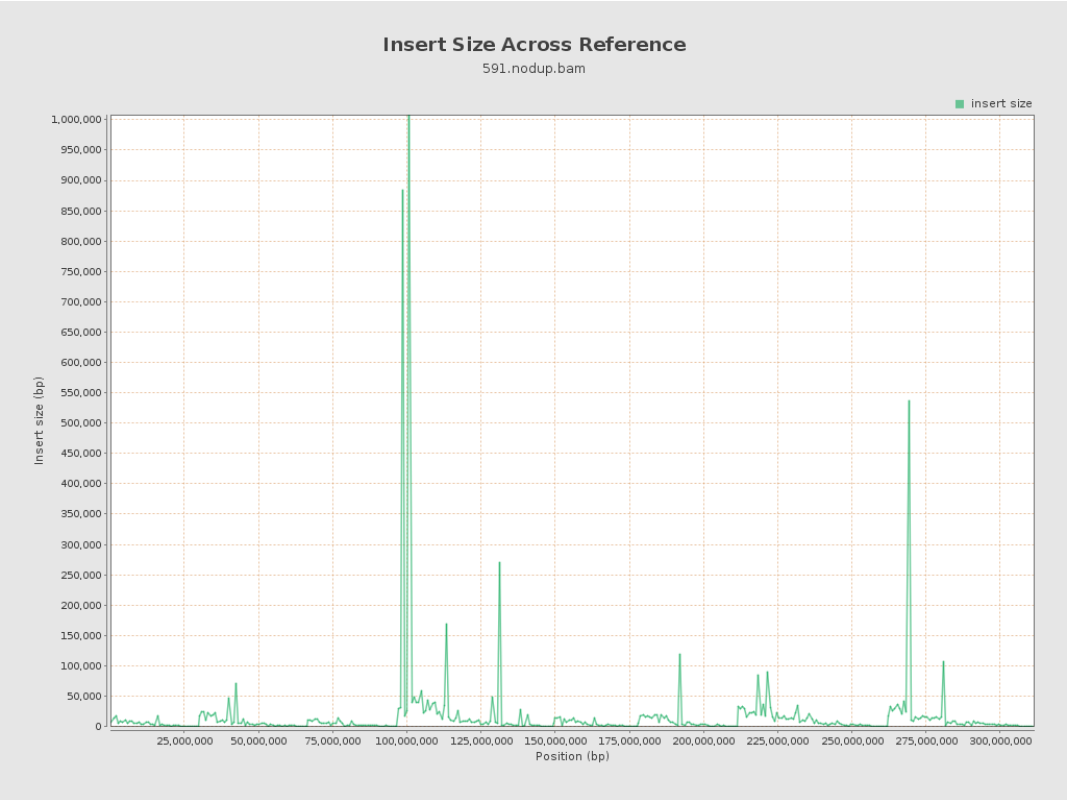
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram