Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:32:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/601.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/601.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_182/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_182_S272_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_182/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_182_S272_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:32:15 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	71,216,608
Mapped reads	66,553,536 / 93.45%
Unmapped reads	4,663,072 / 6.55%
Mapped paired reads	66,553,536 / 93.45%
Mapped reads, first in pair	33,354,182 / 46.83%
Mapped reads, second in pair	33,199,354 / 46.62%
Mapped reads, both in pair	64,954,448 / 91.21%
Mapped reads, singletons	1,599,088 / 2.25%
Read min/max/mean length	30 / 151 / 148.19
Duplicated reads (flagged)	11,517,347 / 16.17%
Clipped reads	14,697,932 / 20.64%

2.2. ACGT Content

Number/percentage of A's	2,847,161,098 / 30.81%
Number/percentage of C's	1,772,948,796 / 19.19%
Number/percentage of T's	2,853,829,507 / 30.89%
Number/percentage of G's	1,765,951,764 / 19.11%
Number/percentage of N's	39,064 / 0%
GC Percentage	38.3%

2.3. Coverage

Mean	29.7265
Standard Deviation	245.5983

2.4. Mapping Quality

Mean Mapping Quality	44.16

2.5. Insert size

Mean	242,092.84
Standard Deviation	2,350,683.78
P25/Median/P75	342 / 447 / 587

2.6. Mismatches and indels

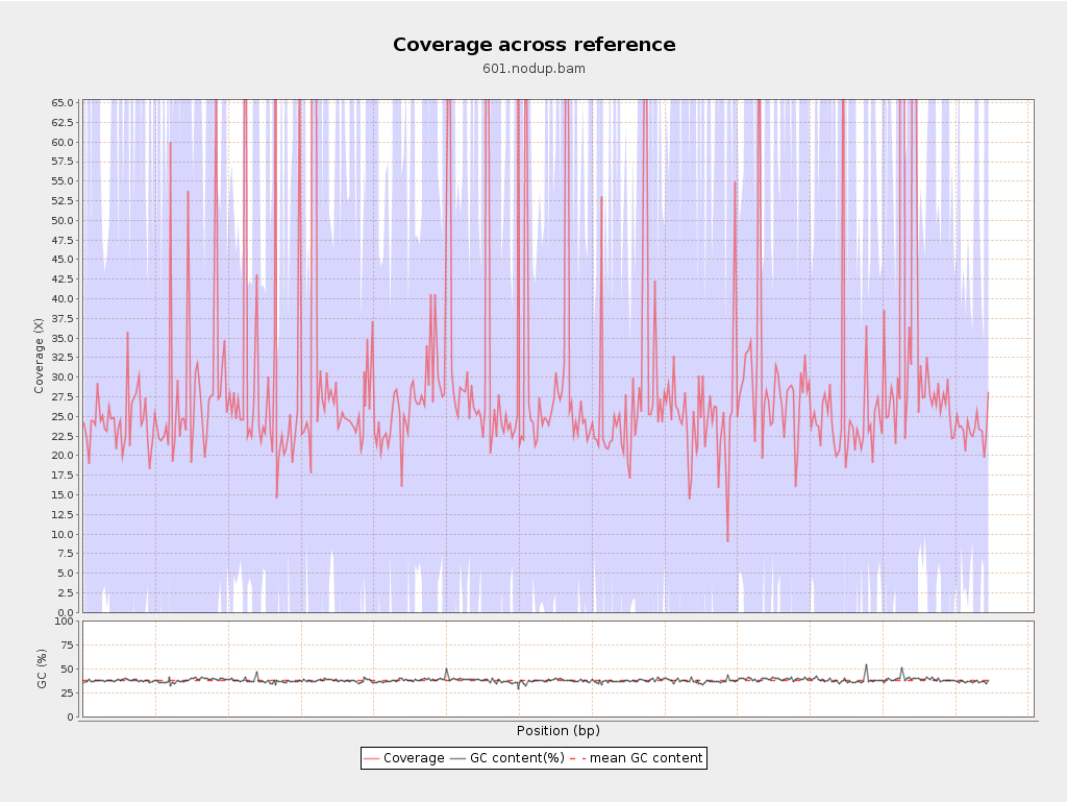
General error rate	2.32%
Mismatches	197,031,767
Insertions	6,379,782
Mapped reads with at least one insertion	8.59%
Deletions	6,365,749
Mapped reads with at least one deletion	8.5%
Homopolymer indels	56.8%

2.7. Chromosome stats

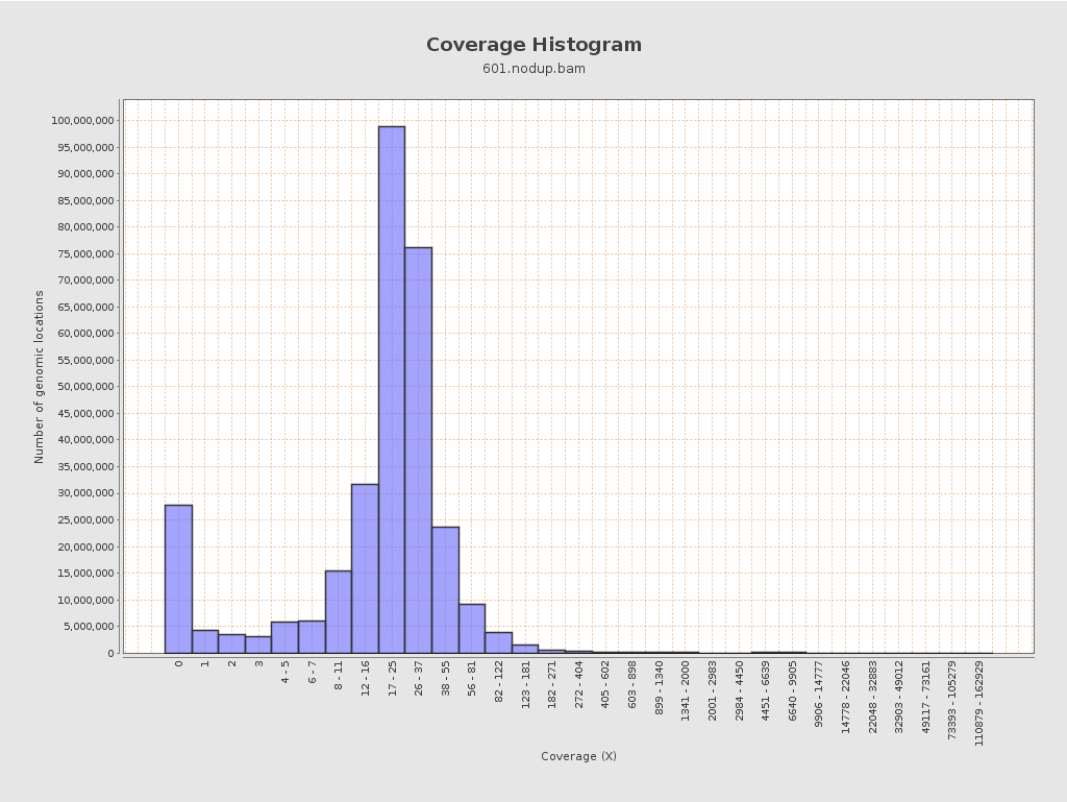
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	718648311	24.1771	78.0741

LT669789.1	36598175	1103638697	30.1556	254.7405
LT669790.1	30422129	987473192	32.459	270.8001
LT669791.1	52758100	1537721050	29.1466	223.075
LT669792.1	28376109	834180438	29.3973	287.0795
LT669793.1	33388210	910366117	27.2661	162.2256
LT669794.1	50579949	1418458904	28.0439	196.576
LT669795.1	49795044	1753555303	35.2155	353.1597

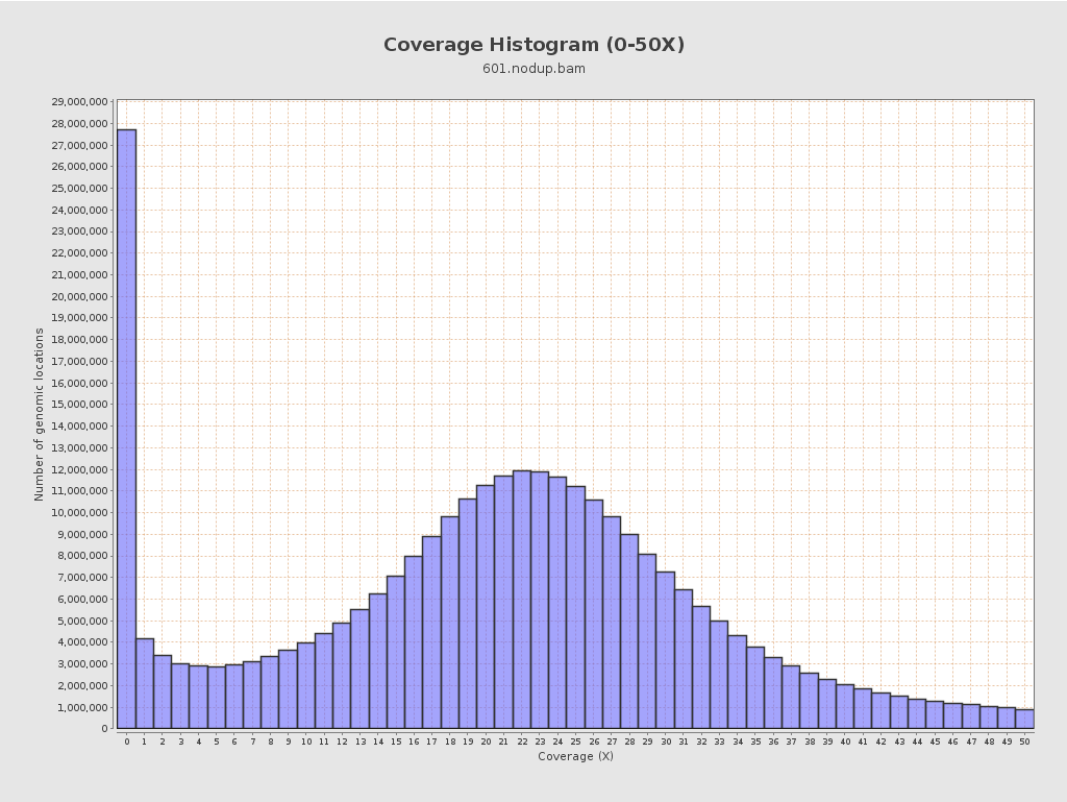
3. Results : Coverage across reference



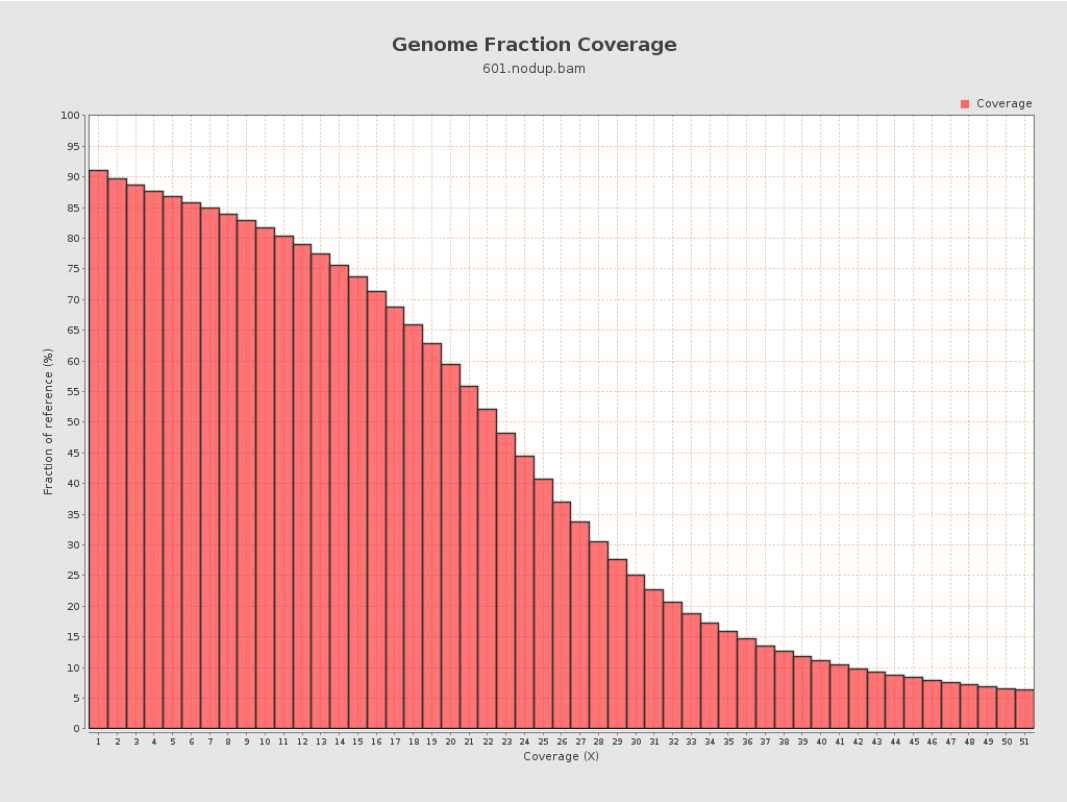
4. Results : Coverage Histogram



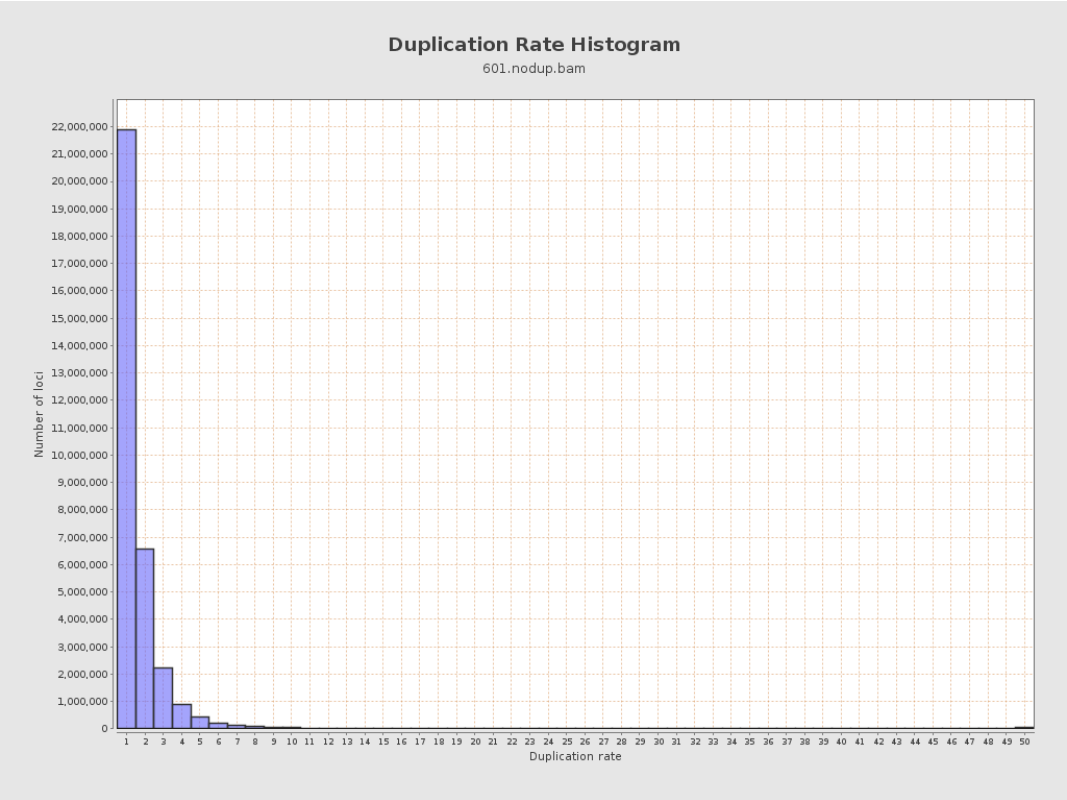
5. Results : Coverage Histogram (0-50X)



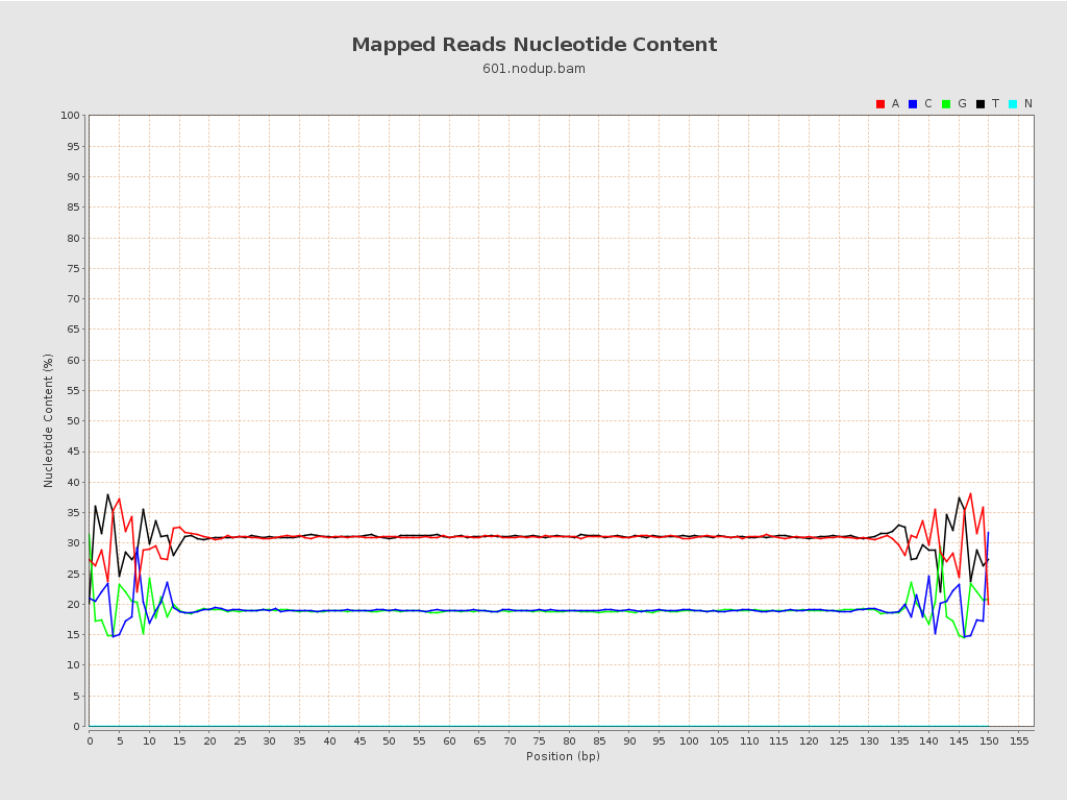
6. Results : Genome Fraction Coverage



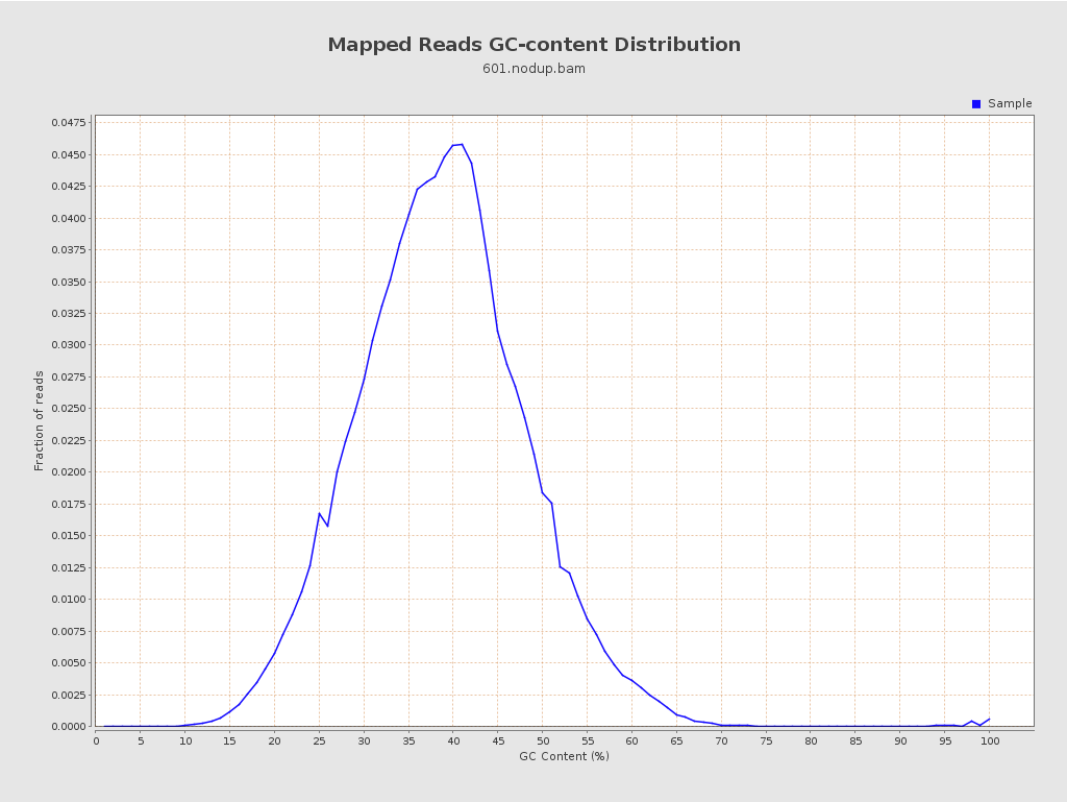
7. Results : Duplication Rate Histogram



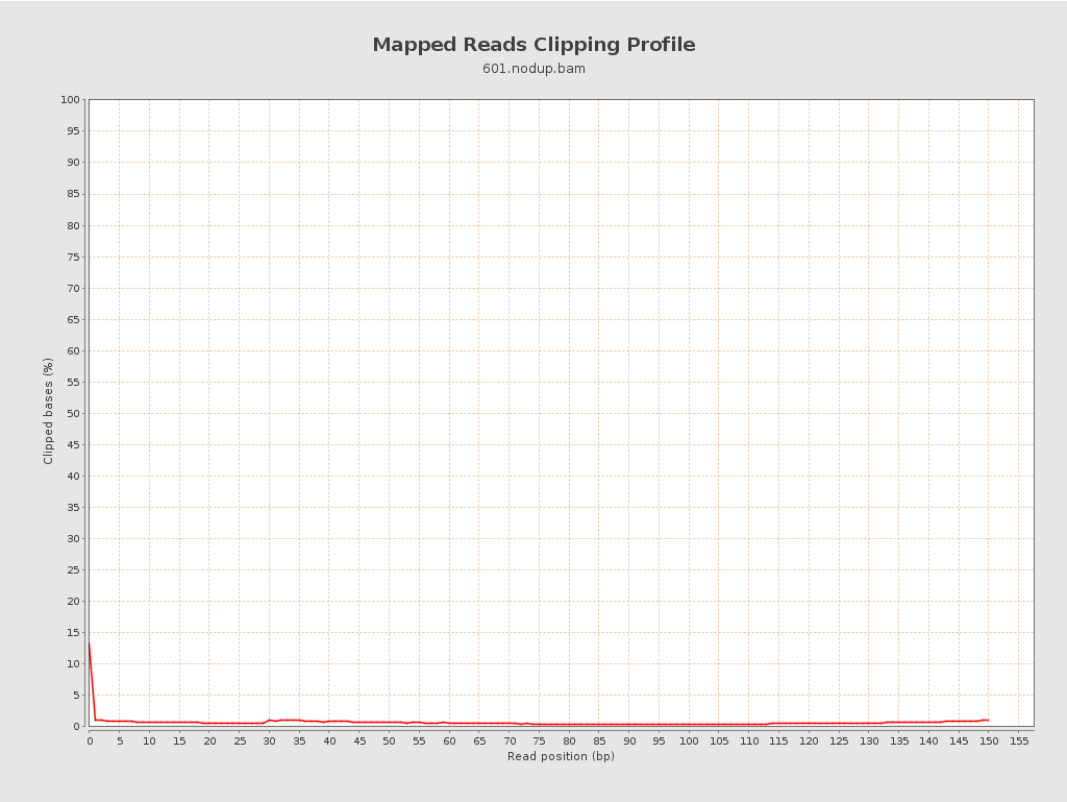
8. Results : Mapped Reads Nucleotide Content



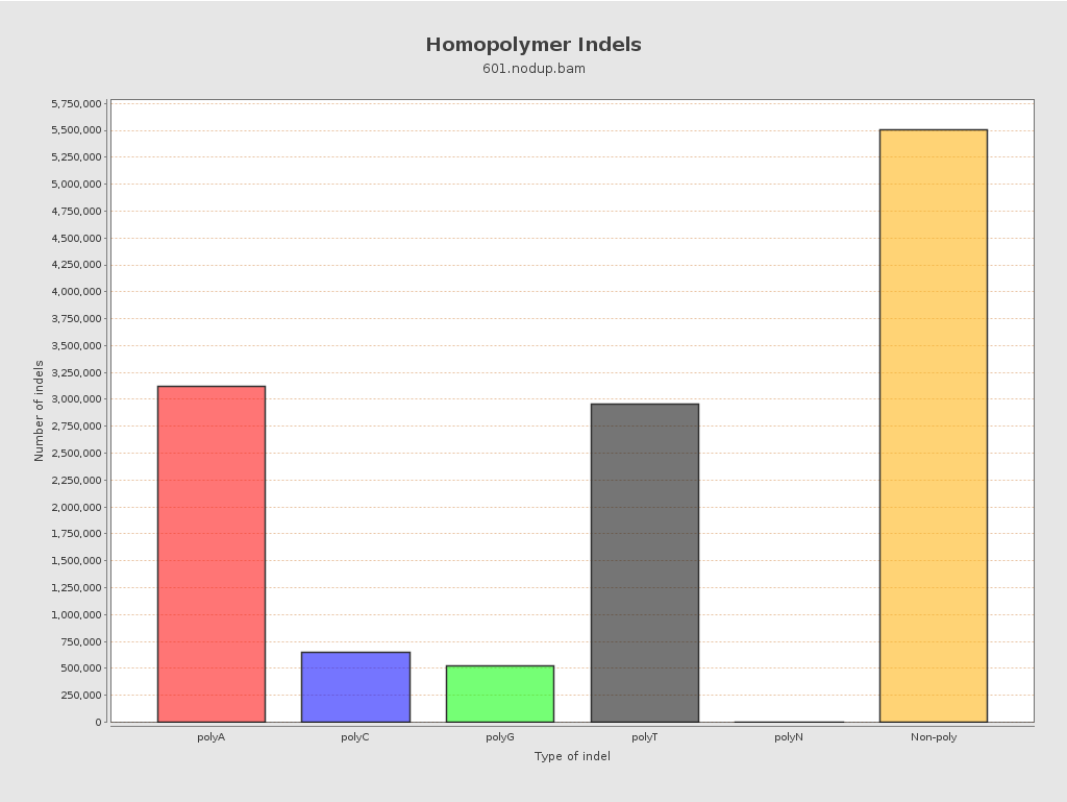
9. Results : Mapped Reads GC-content Distribution



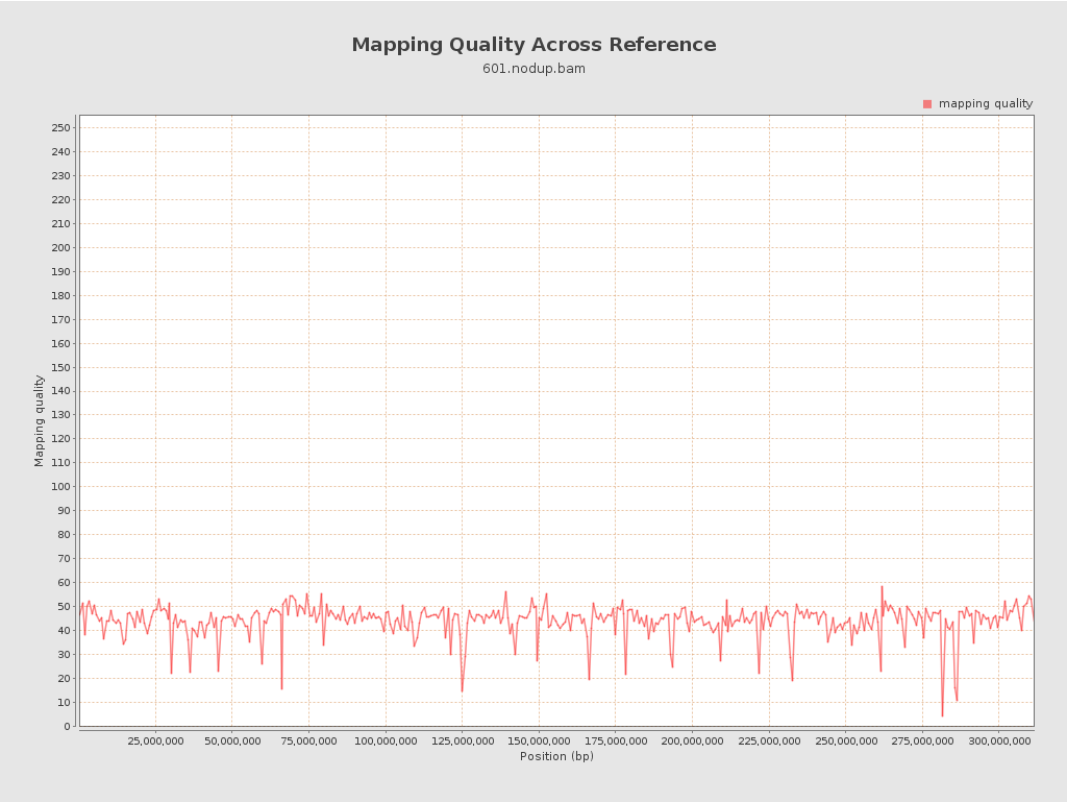
10. Results : Mapped Reads Clipping Profile



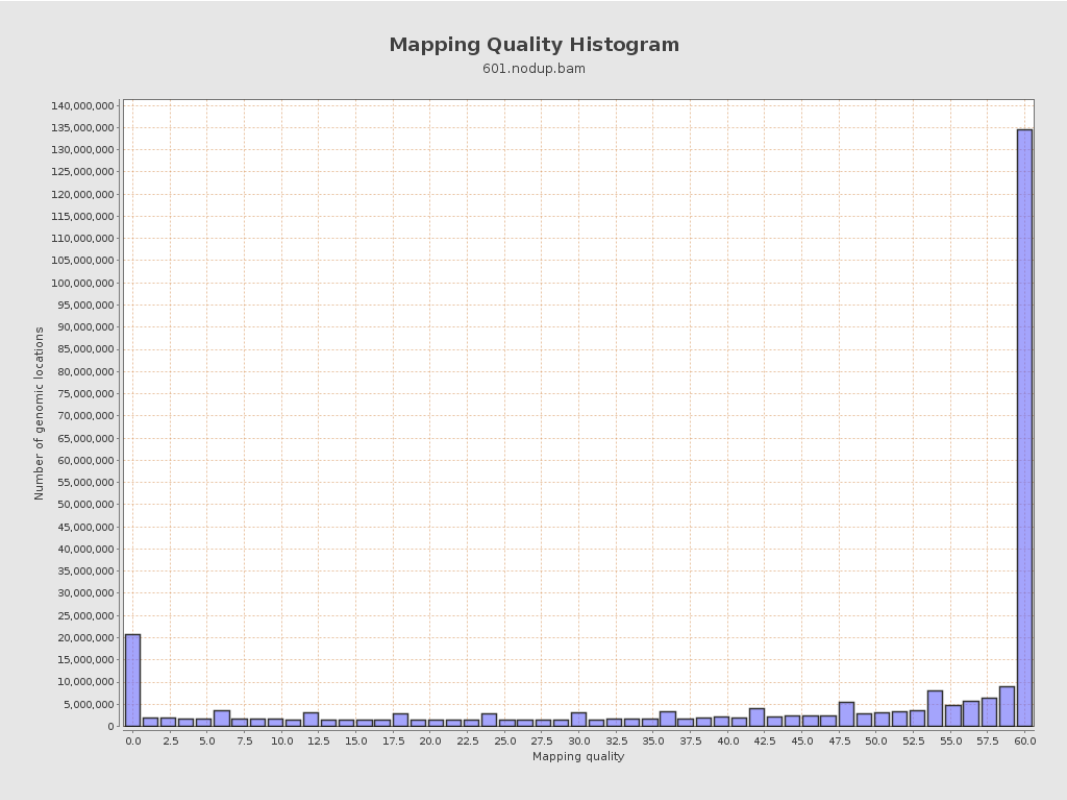
11. Results : Homopolymer Indels



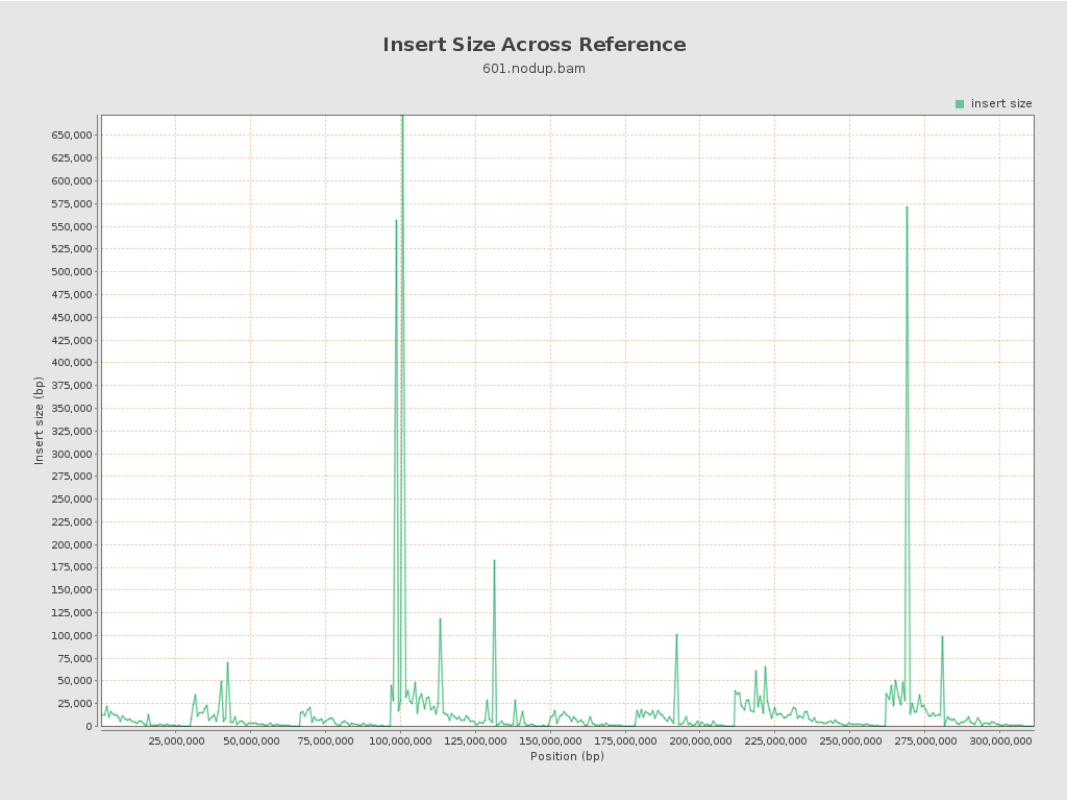
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram