Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:26:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/401.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/401.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_282/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_282_S363_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_282/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_282_S363_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:26:01 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	51,306,084
Mapped reads	47,741,928 / 93.05%
Unmapped reads	3,564,156 / 6.95%
Mapped paired reads	47,741,928 / 93.05%
Mapped reads, first in pair	23,928,832 / 46.64%
Mapped reads, second in pair	23,813,096 / 46.41%
Mapped reads, both in pair	46,654,586 / 90.93%
Mapped reads, singletons	1,087,342 / 2.12%
Read min/max/mean length	30 / 151 / 148.09
Duplicated reads (flagged)	6,567,803 / 12.8%
Clipped reads	11,370,178 / 22.16%

2.2. ACGT Content

Number/percentage of A's	2,025,885,575 / 30.9%
Number/percentage of C's	1,252,103,324 / 19.1%
Number/percentage of T's	2,028,873,022 / 30.94%
Number/percentage of G's	1,249,660,166 / 19.06%
Number/percentage of N's	24,170 / 0%
GC Percentage	38.16%

2.3. Coverage

Mean	21.0906
Standard Deviation	180.5652

2.4. Mapping Quality

Mean Mapping Quality	44.77

2.5. Insert size

Mean	219,219.26
Standard Deviation	2,233,624.98
P25/Median/P75	307 / 413 / 537

2.6. Mismatches and indels

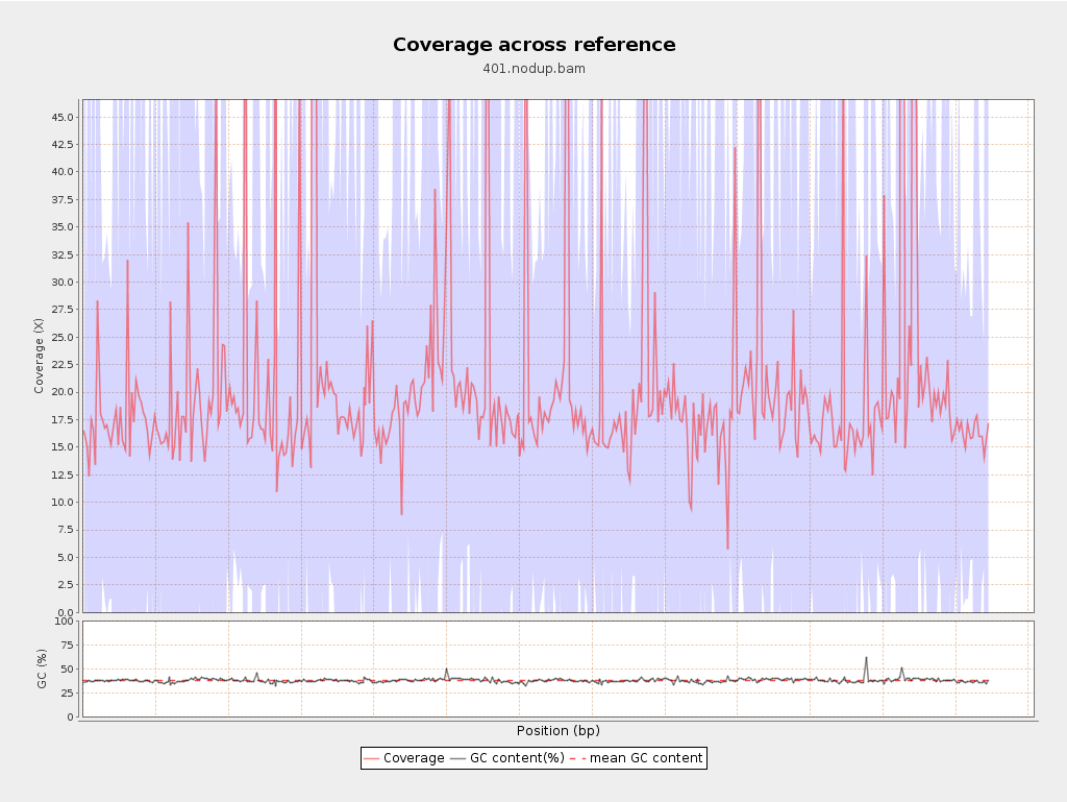
General error rate	2.26%
Mismatches	136,337,099
Insertions	4,338,932
Mapped reads with at least one insertion	8.16%
Deletions	4,321,587
Mapped reads with at least one deletion	8.05%
Homopolymer indels	56.94%

2.7. Chromosome stats

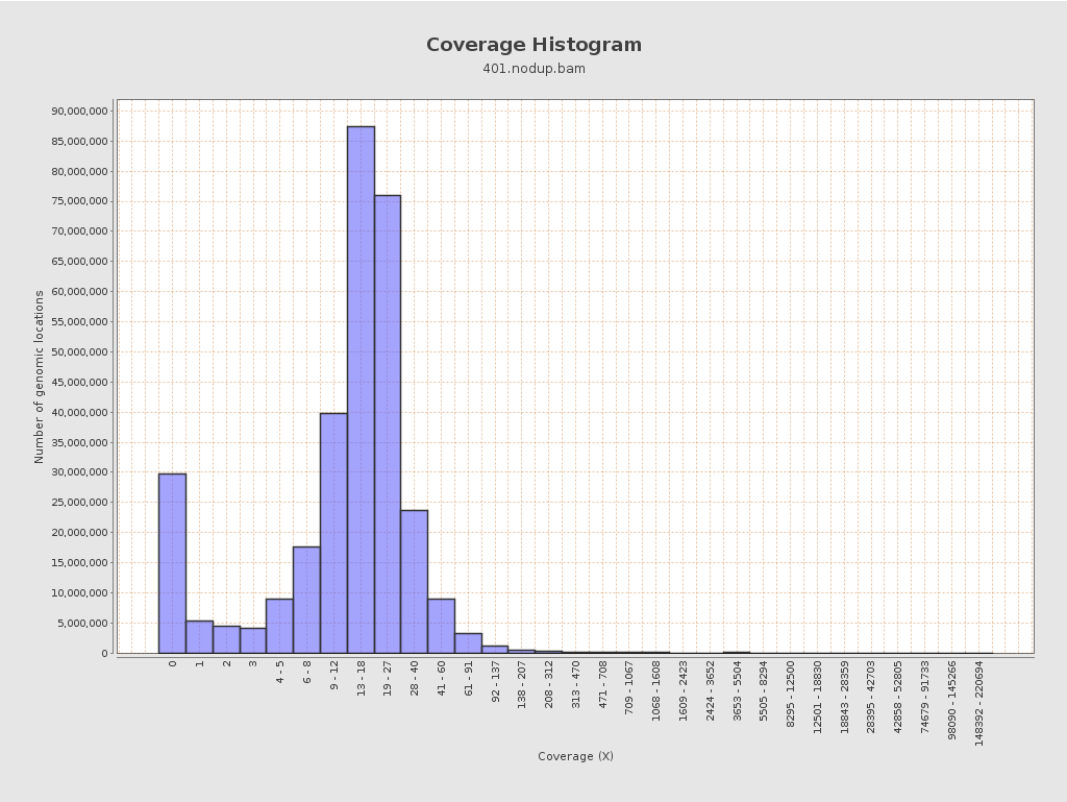
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	515600292	17.3461	53.3511

LT669789.1	36598175	760378631	20.7764	169.7616
LT669790.1	30422129	713470900	23.4524	196.8841
LT669791.1	52758100	1107547849	20.9929	155.9843
LT669792.1	28376109	588238863	20.7301	199.1347
LT669793.1	33388210	655470854	19.6318	133.7877
LT669794.1	50579949	996997444	19.7113	142.2937
LT669795.1	49795044	1235020825	24.8021	276.6124

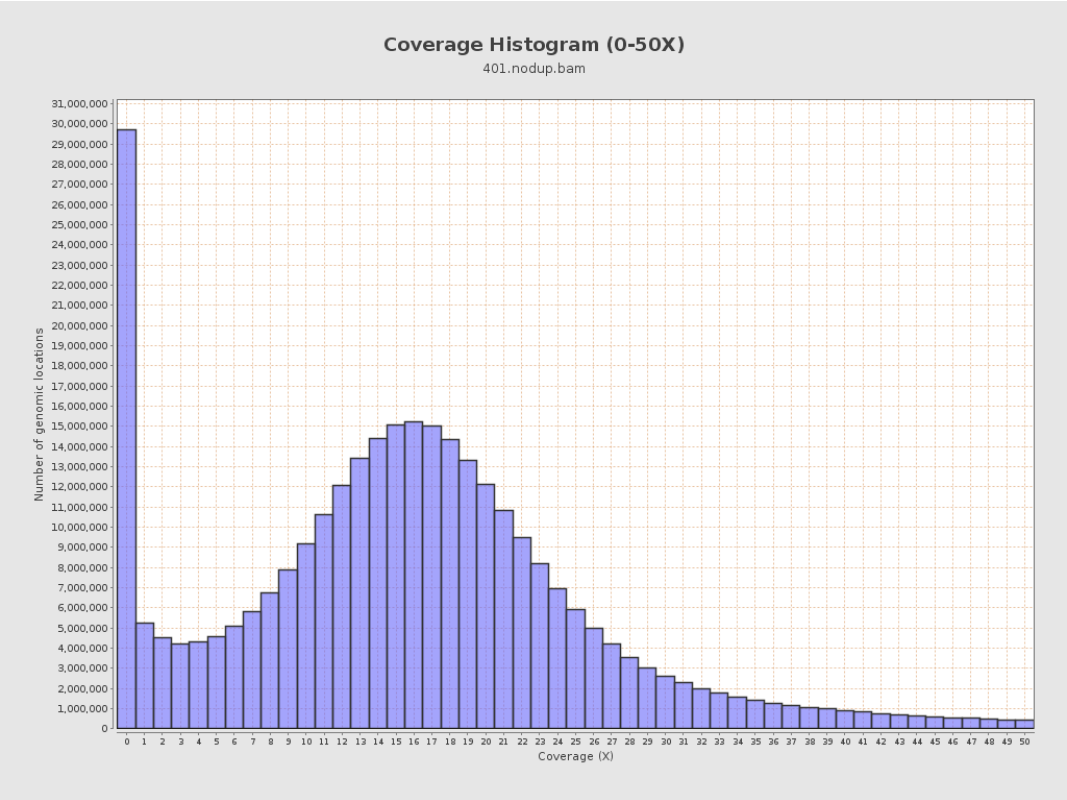
3. Results : Coverage across reference



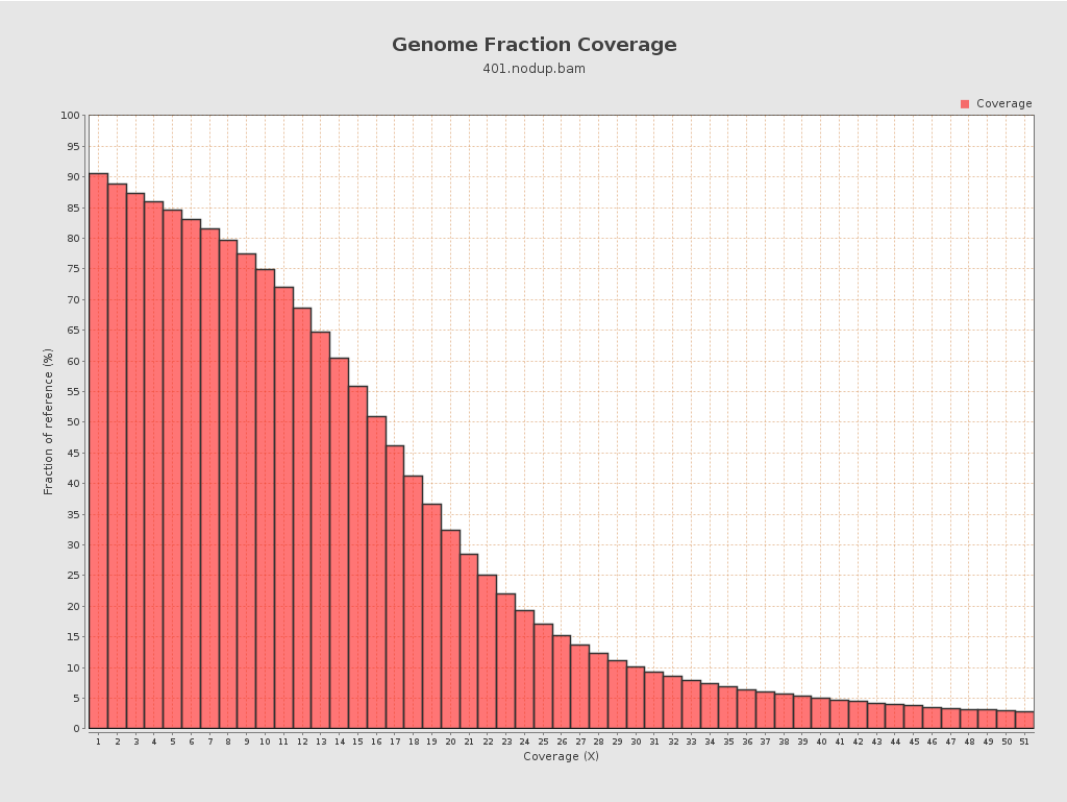
4. Results : Coverage Histogram



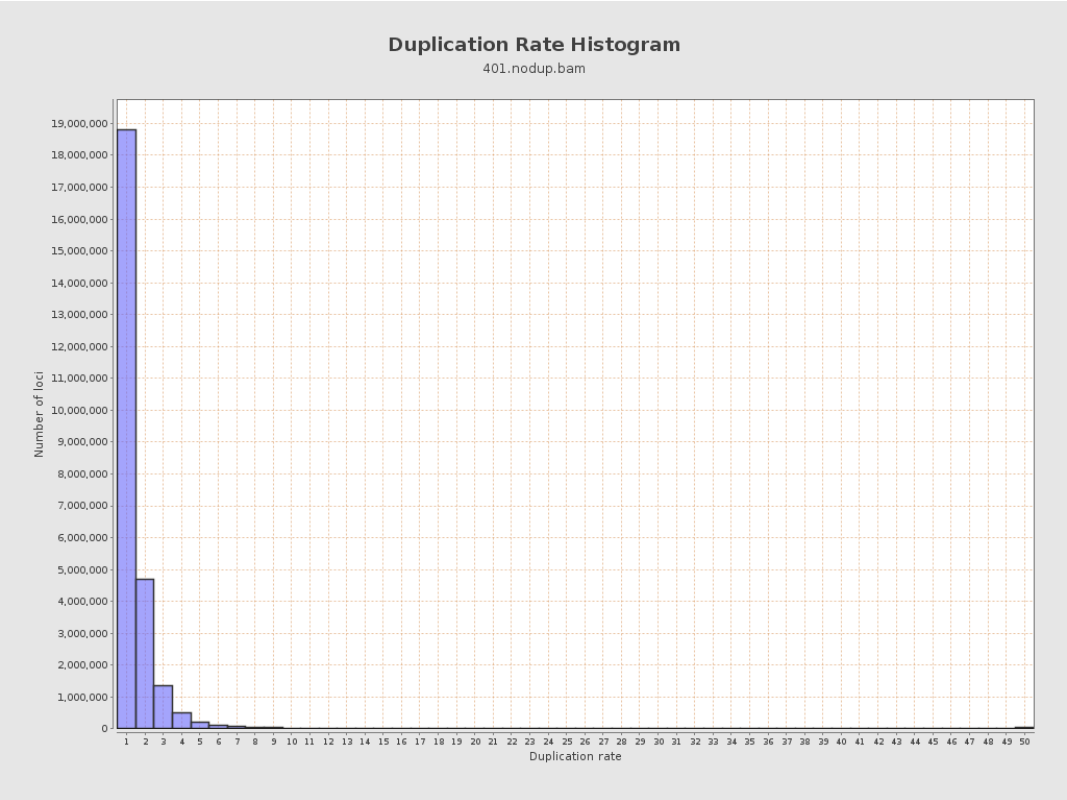
5. Results : Coverage Histogram (0-50X)



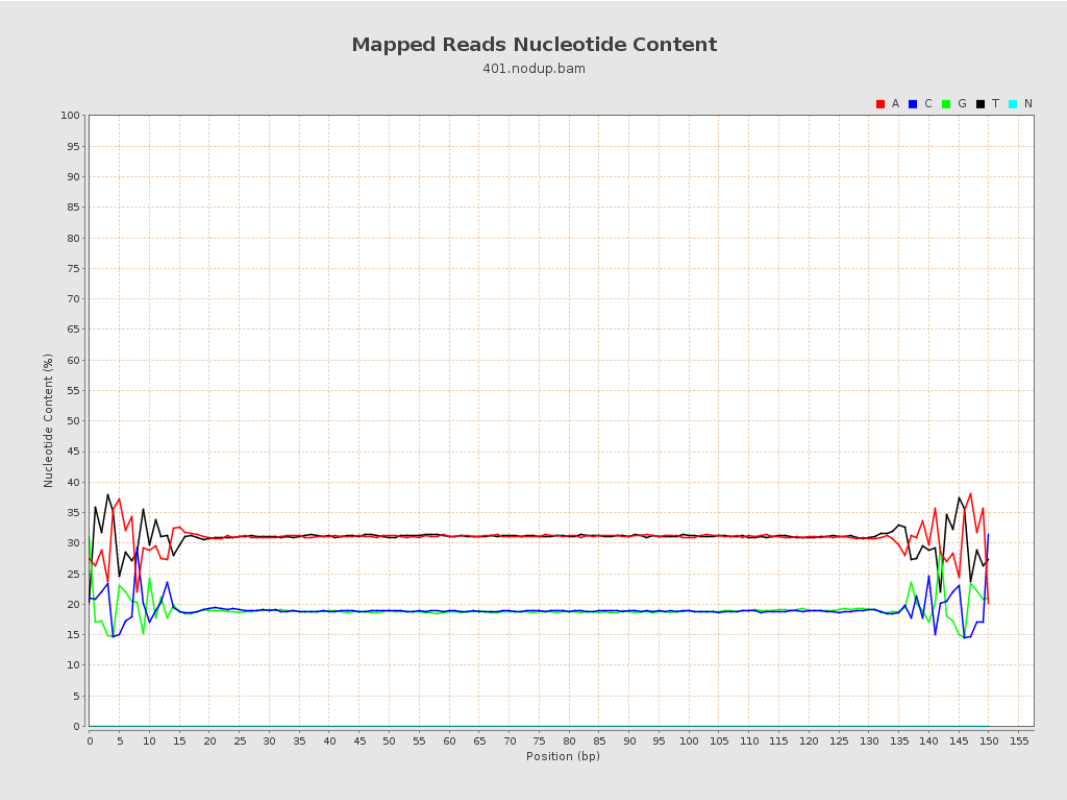
6. Results : Genome Fraction Coverage



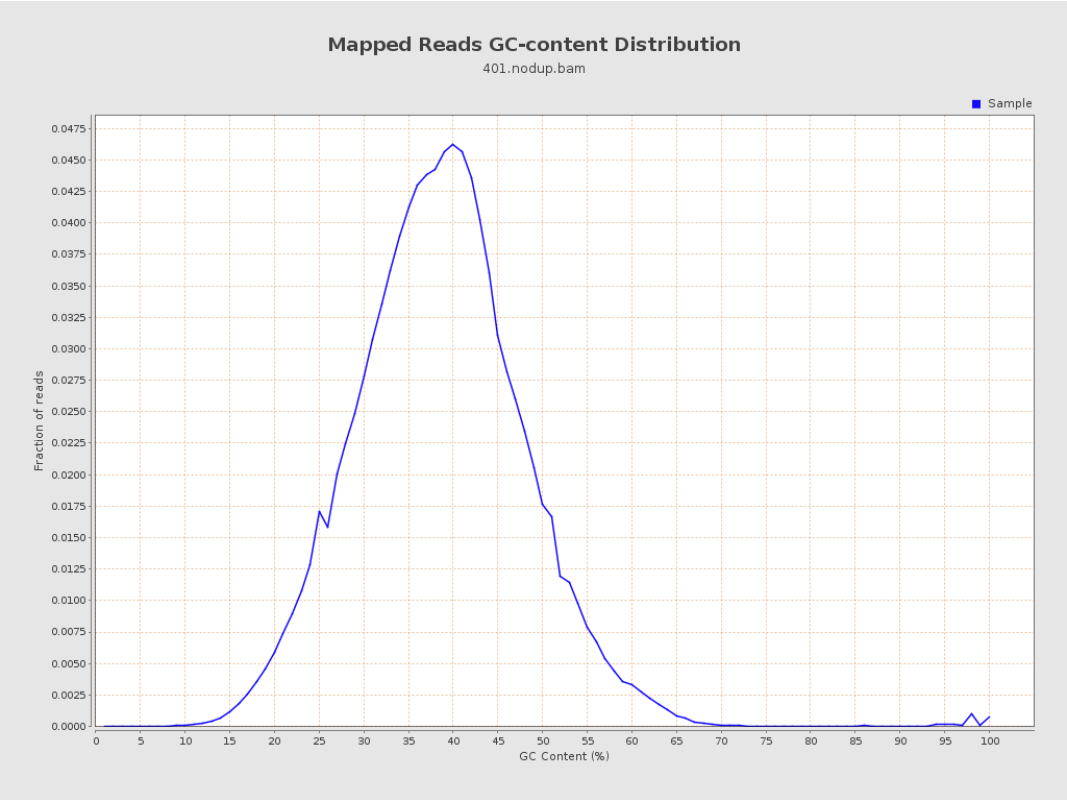
7. Results : Duplication Rate Histogram



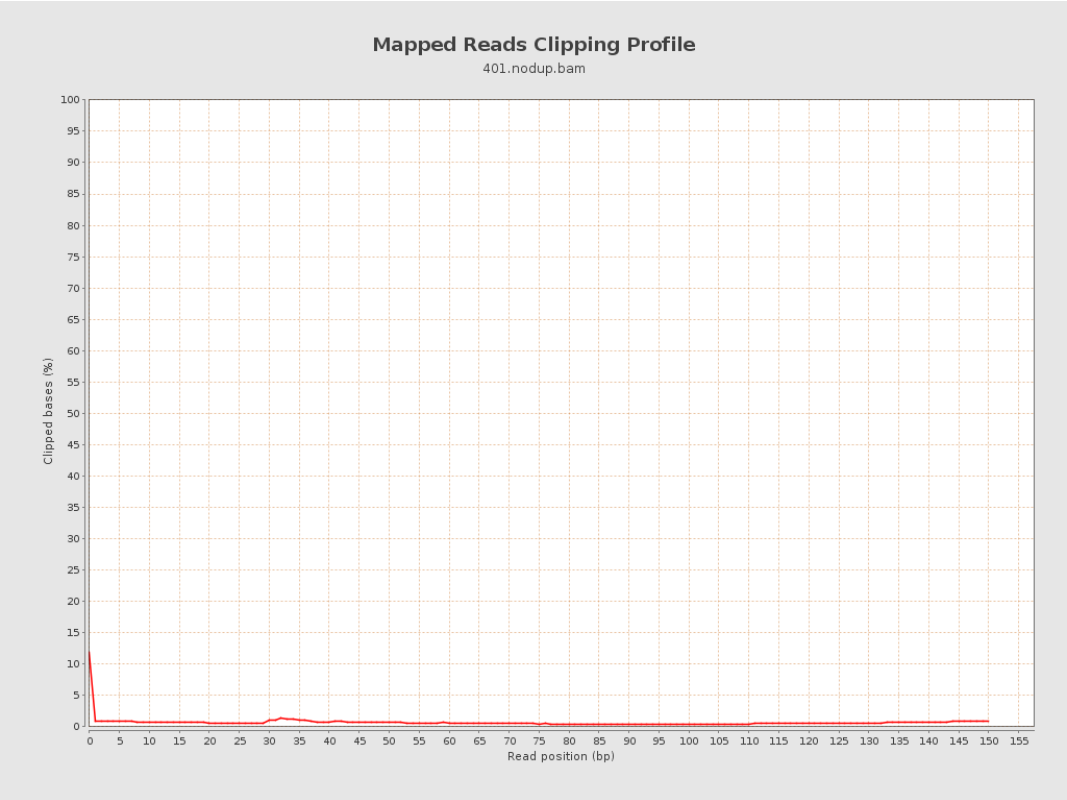
8. Results : Mapped Reads Nucleotide Content



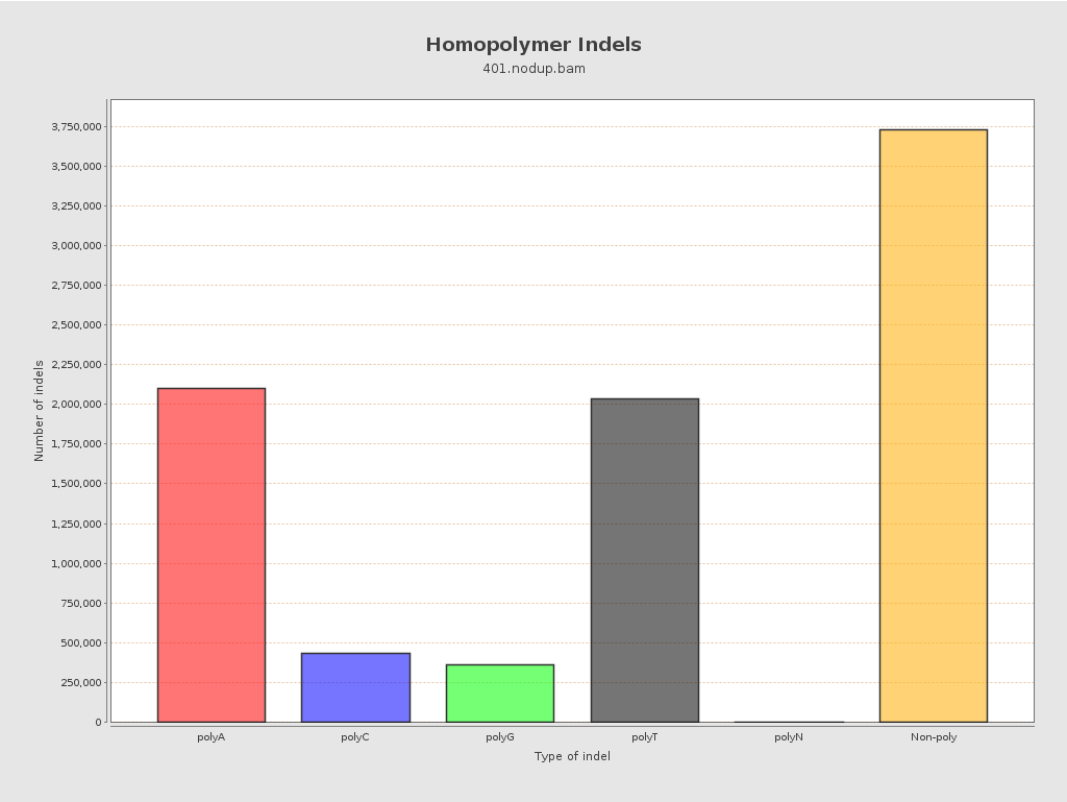
9. Results : Mapped Reads GC-content Distribution



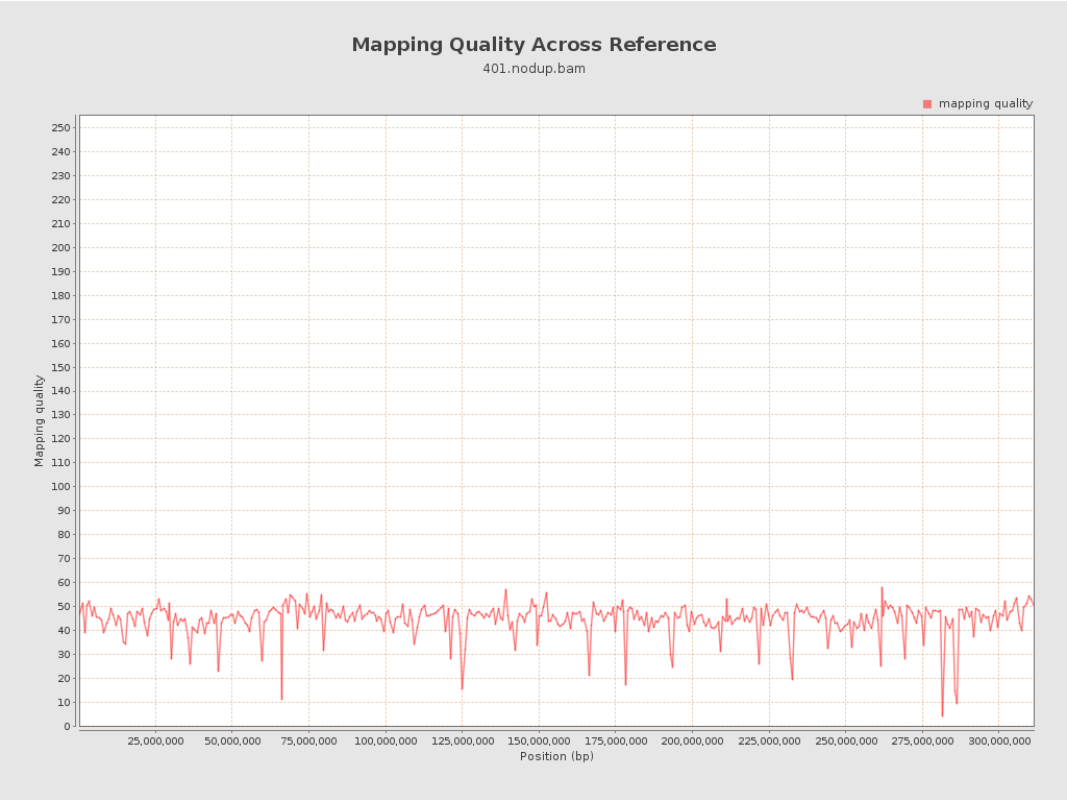
10. Results : Mapped Reads Clipping Profile



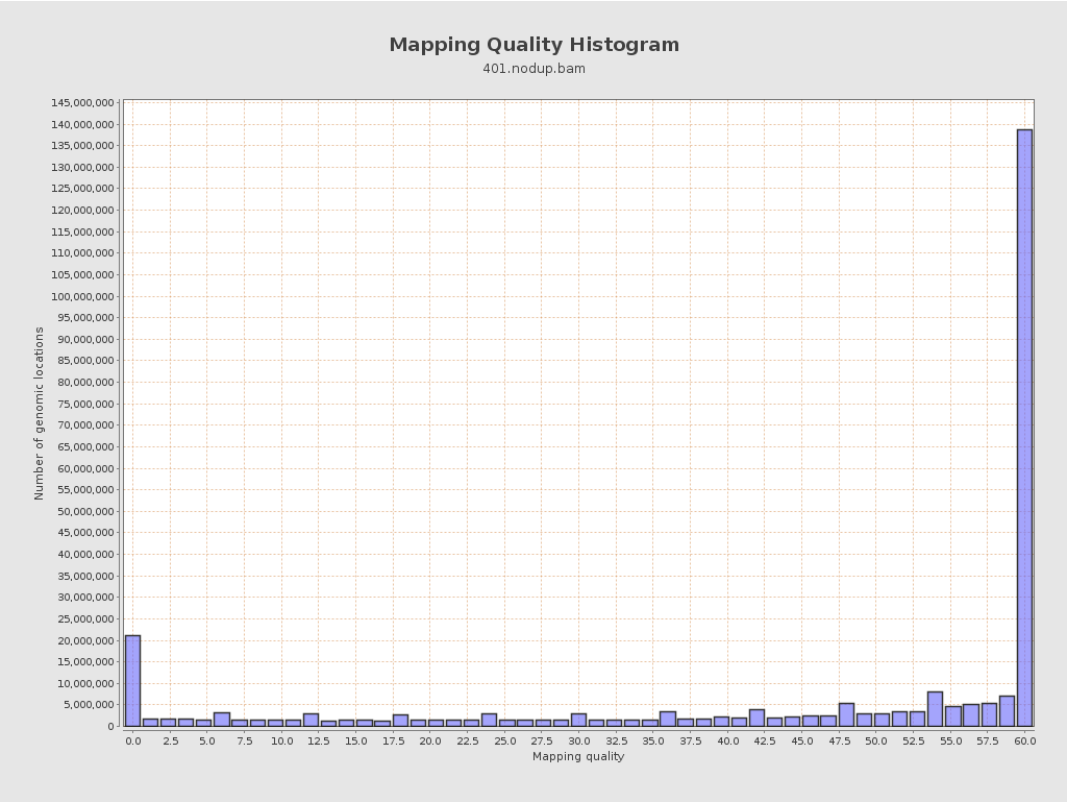
11. Results : Homopolymer Indels



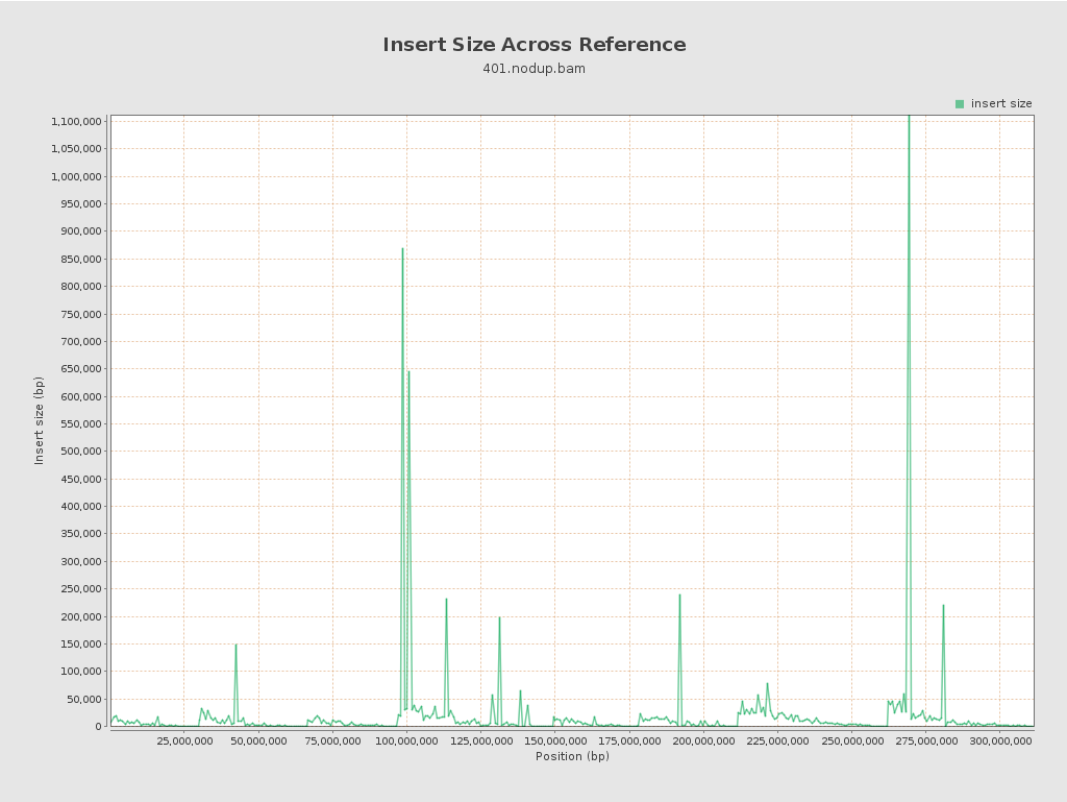
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram