Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:30:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/441.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/441.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_122/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_122_S212_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_122/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_122_S212_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:30:02 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	68,381,183
Mapped reads	57,083,760 / 83.48%
Unmapped reads	11,297,423 / 16.52%
Mapped paired reads	57,083,760 / 83.48%
Mapped reads, first in pair	28,599,802 / 41.82%
Mapped reads, second in pair	28,483,958 / 41.65%
Mapped reads, both in pair	55,292,188 / 80.86%
Mapped reads, singletons	1,791,572 / 2.62%
Read min/max/mean length	30 / 151 / 148.31
Duplicated reads (flagged)	10,500,765 / 15.36%
Clipped reads	13,592,790 / 19.88%

2.2. ACGT Content

Number/percentage of A's	2,417,040,402 / 30.95%
Number/percentage of C's	1,487,260,120 / 19.04%
Number/percentage of T's	2,416,481,154 / 30.94%
Number/percentage of G's	1,489,100,897 / 19.07%
Number/percentage of N's	33,067 / 0%
GC Percentage	38.11%

2.3. Coverage

Mean	25.1237
Standard Deviation	224.9191

2.4. Mapping Quality

Mean Mapping Quality	44.51

2.5. Insert size

Mean	254,756.76
Standard Deviation	2,434,655.68
P25/Median/P75	320 / 422 / 557

2.6. Mismatches and indels

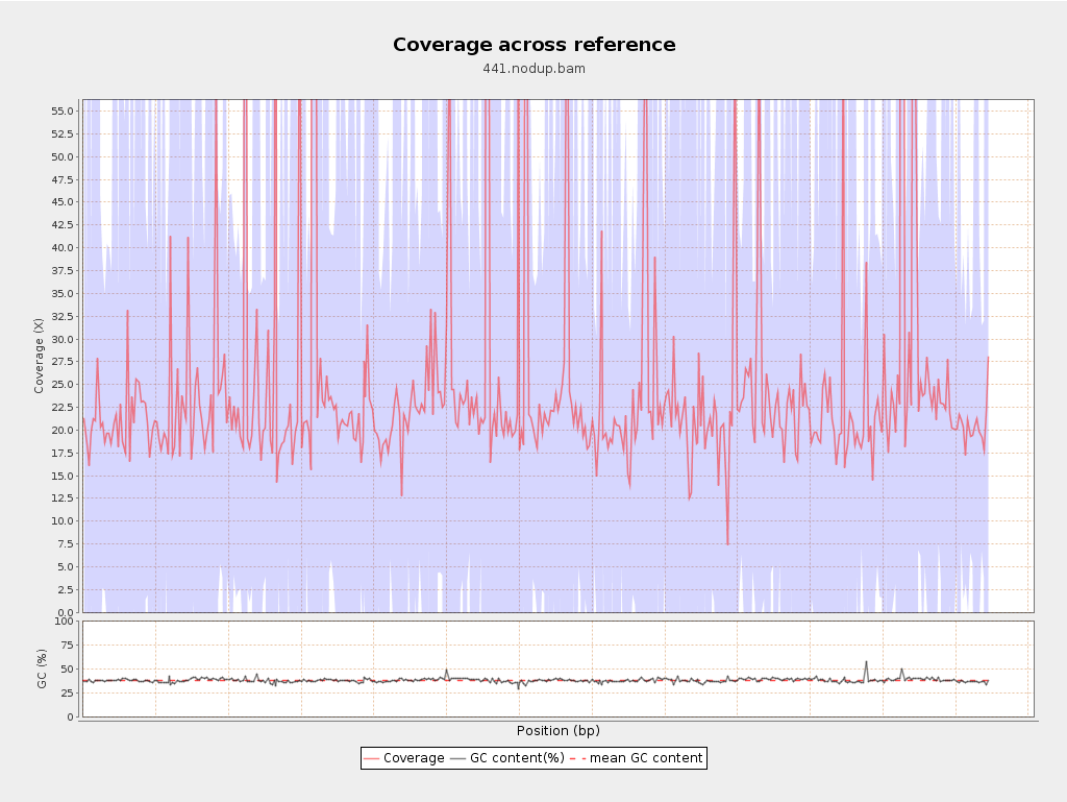
General error rate	2.3%
Mismatches	163,716,731
Insertions	5,554,027
Mapped reads with at least one insertion	8.68%
Deletions	5,361,804
Mapped reads with at least one deletion	8.34%
Homopolymer indels	57.84%

2.7. Chromosome stats

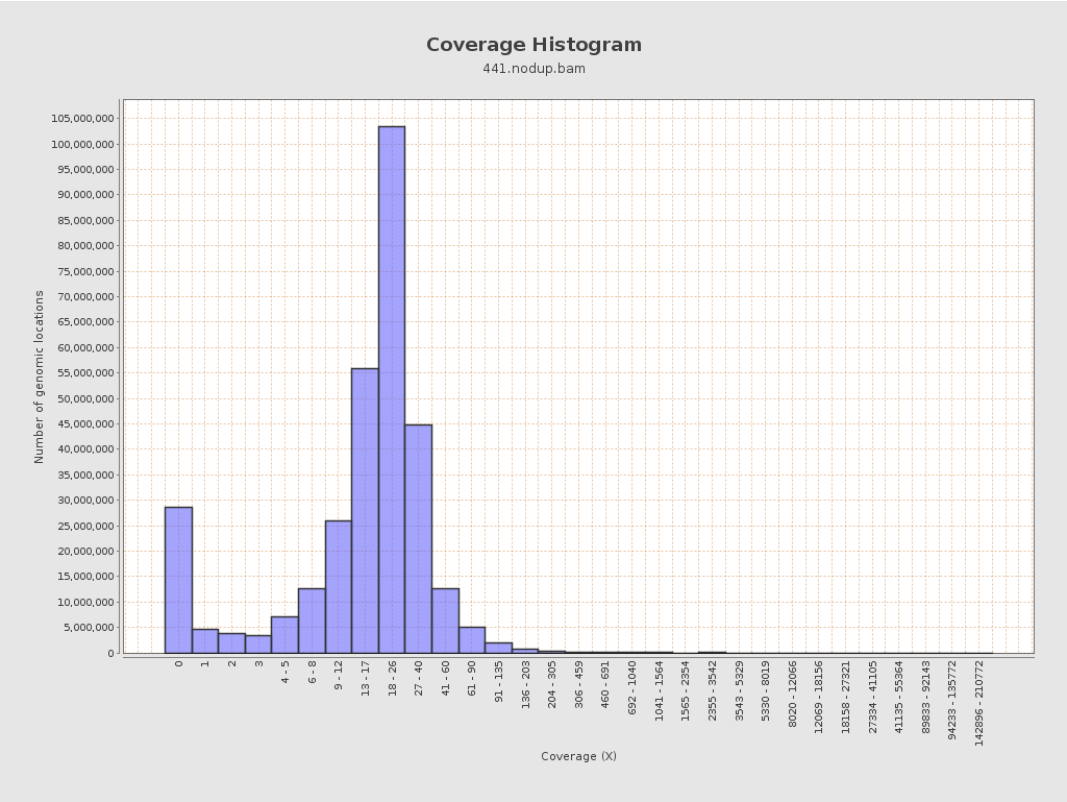
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	618365367	20.8033	88.8641

LT669789.1	36598175	954022736	26.0675	255.2414
LT669790.1	30422129	918708941	30.1987	314.877
LT669791.1	52758100	1308566558	24.8031	242.208
LT669792.1	28376109	715919220	25.2296	223.3205
LT669793.1	33388210	769114563	23.0355	148.161
LT669794.1	50579949	1197320705	23.6718	182.7172
LT669795.1	49795044	1347582220	27.0626	253.3689

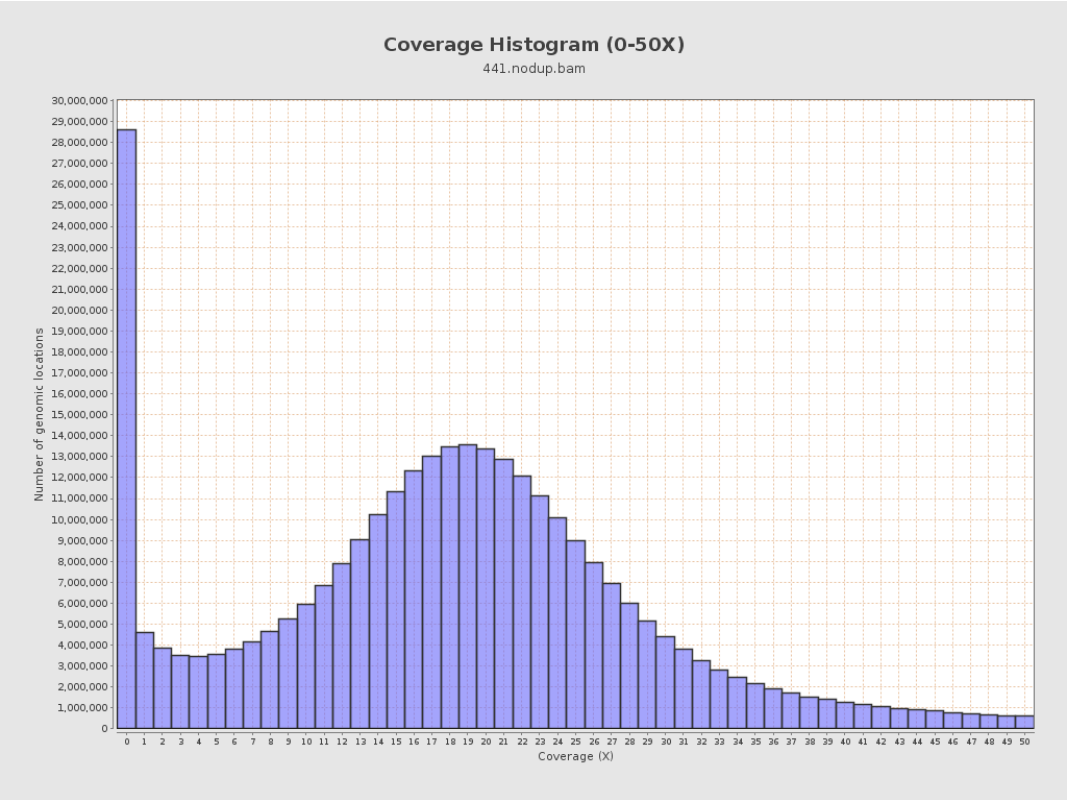
3. Results : Coverage across reference



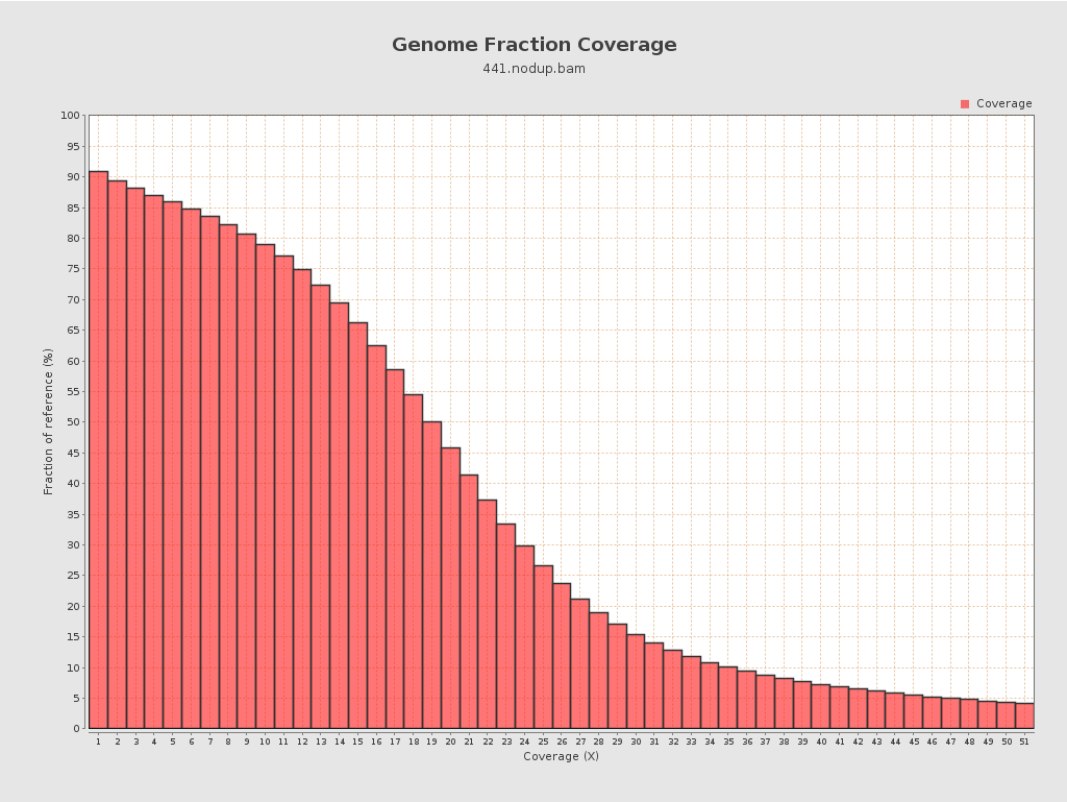
4. Results : Coverage Histogram



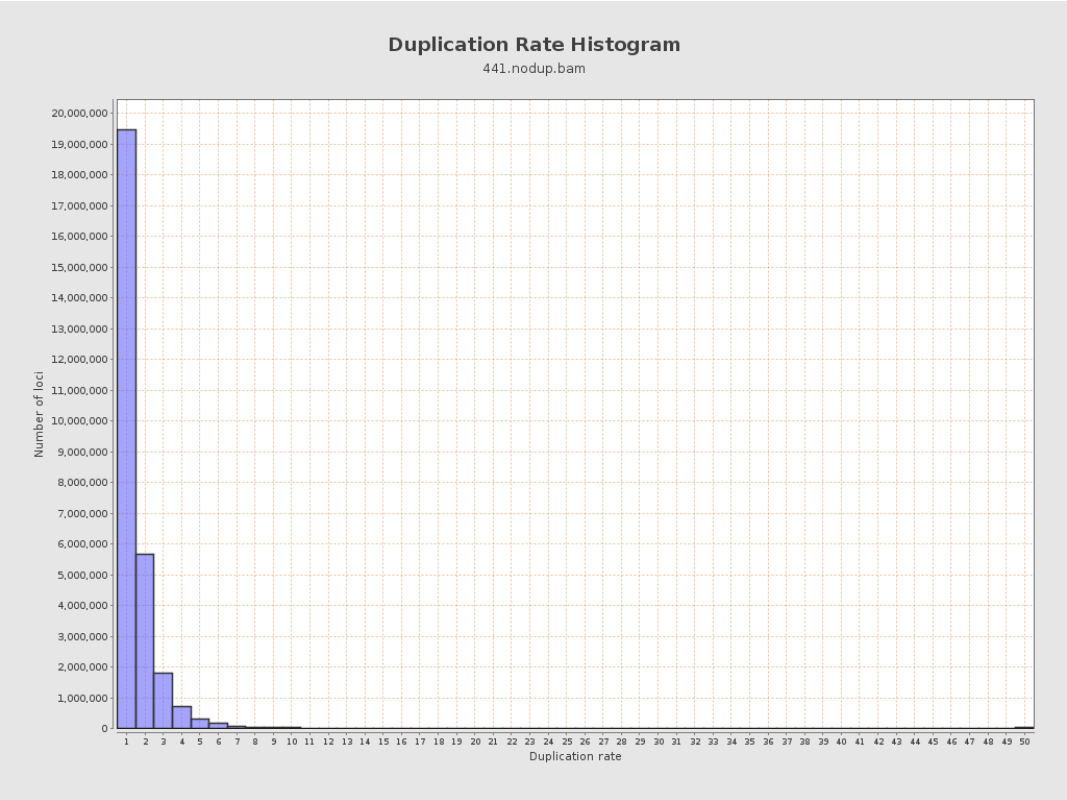
5. Results : Coverage Histogram (0-50X)



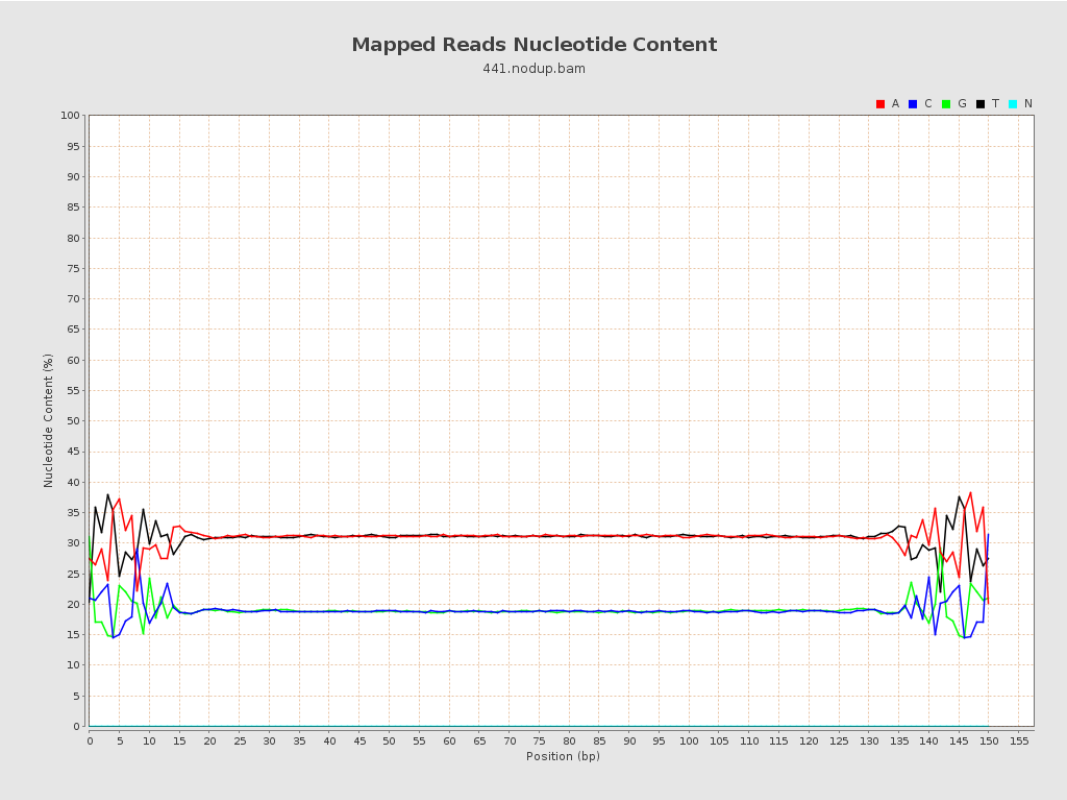
6. Results : Genome Fraction Coverage



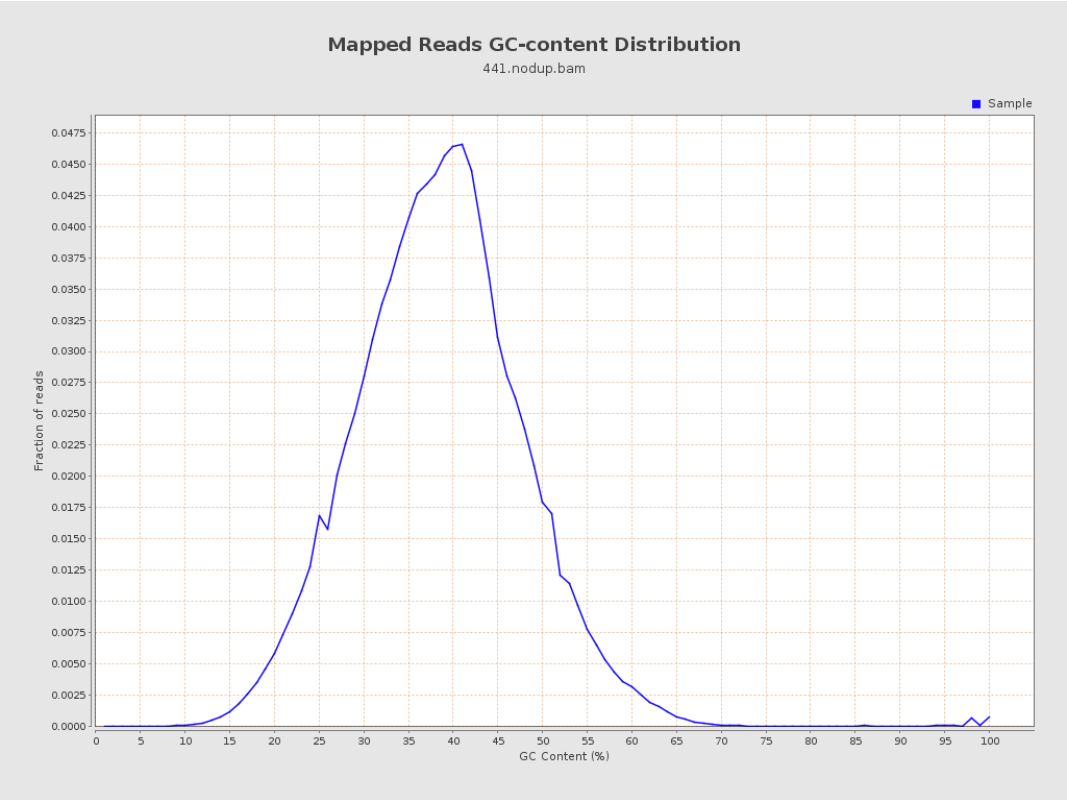
7. Results : Duplication Rate Histogram



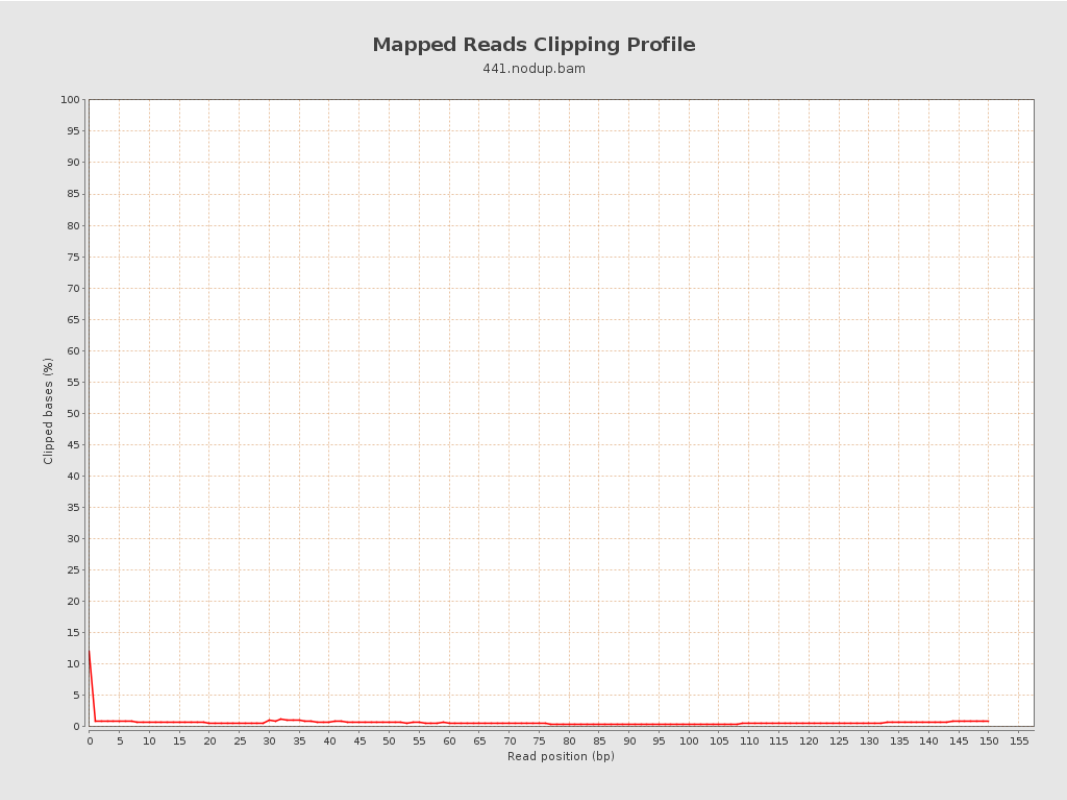
8. Results : Mapped Reads Nucleotide Content



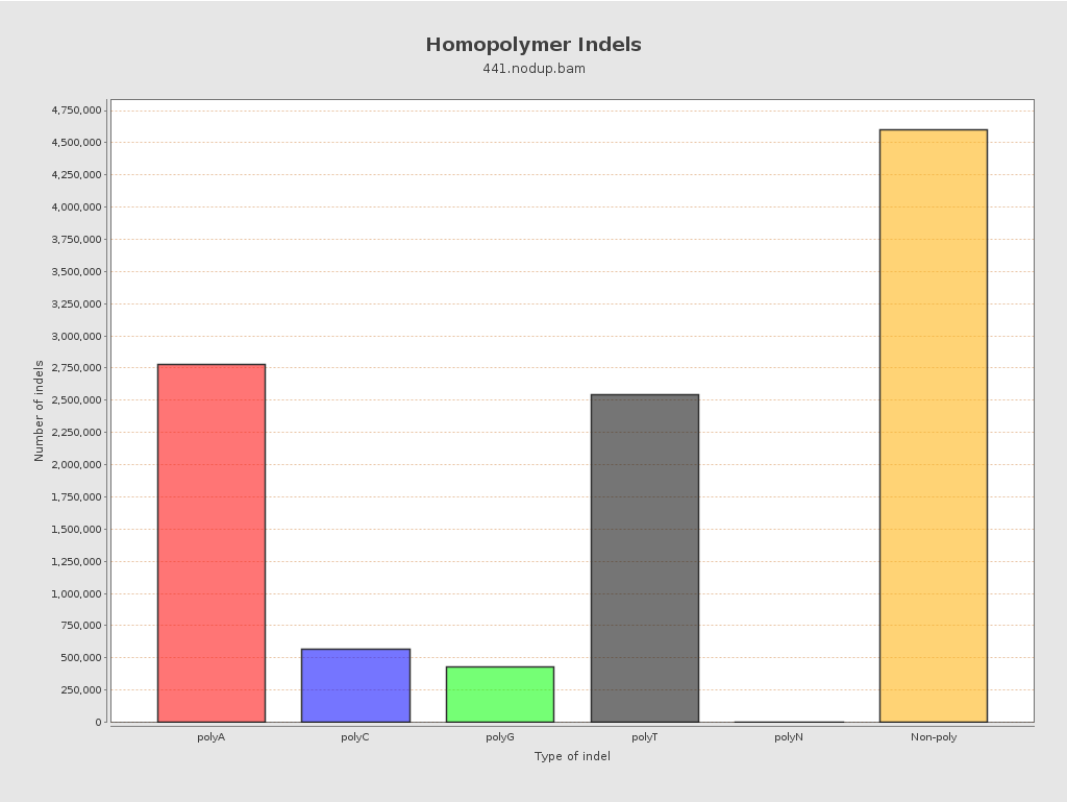
9. Results : Mapped Reads GC-content Distribution



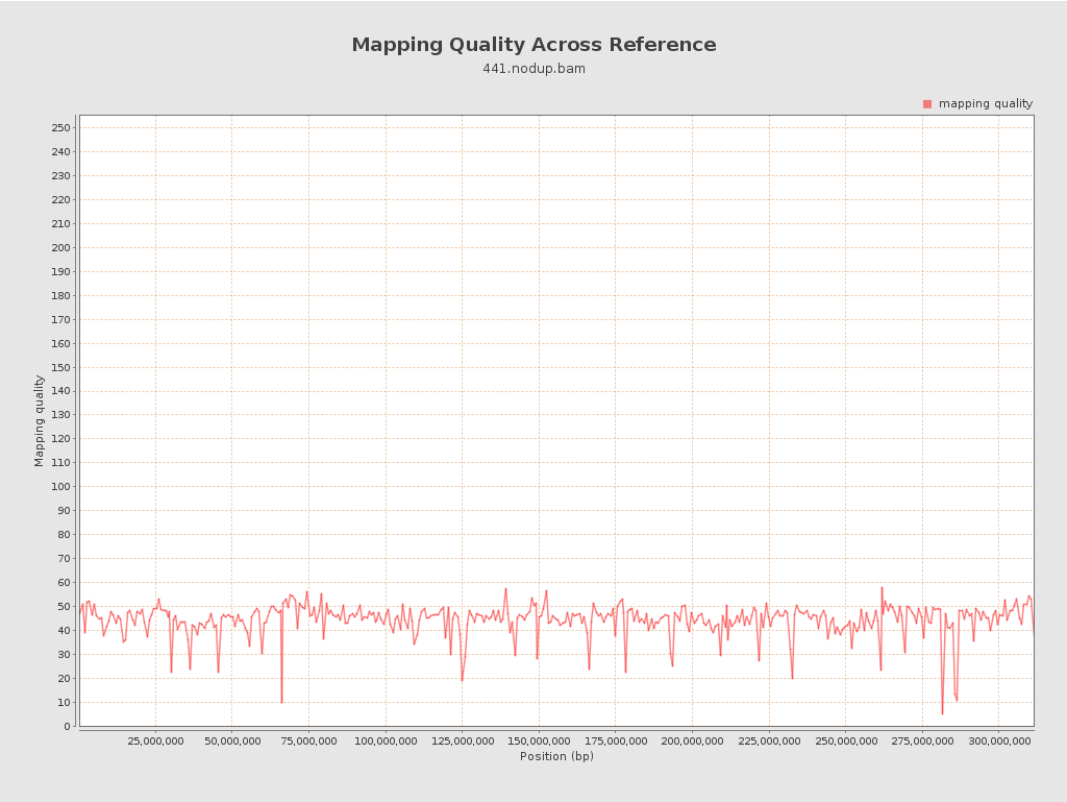
10. Results : Mapped Reads Clipping Profile



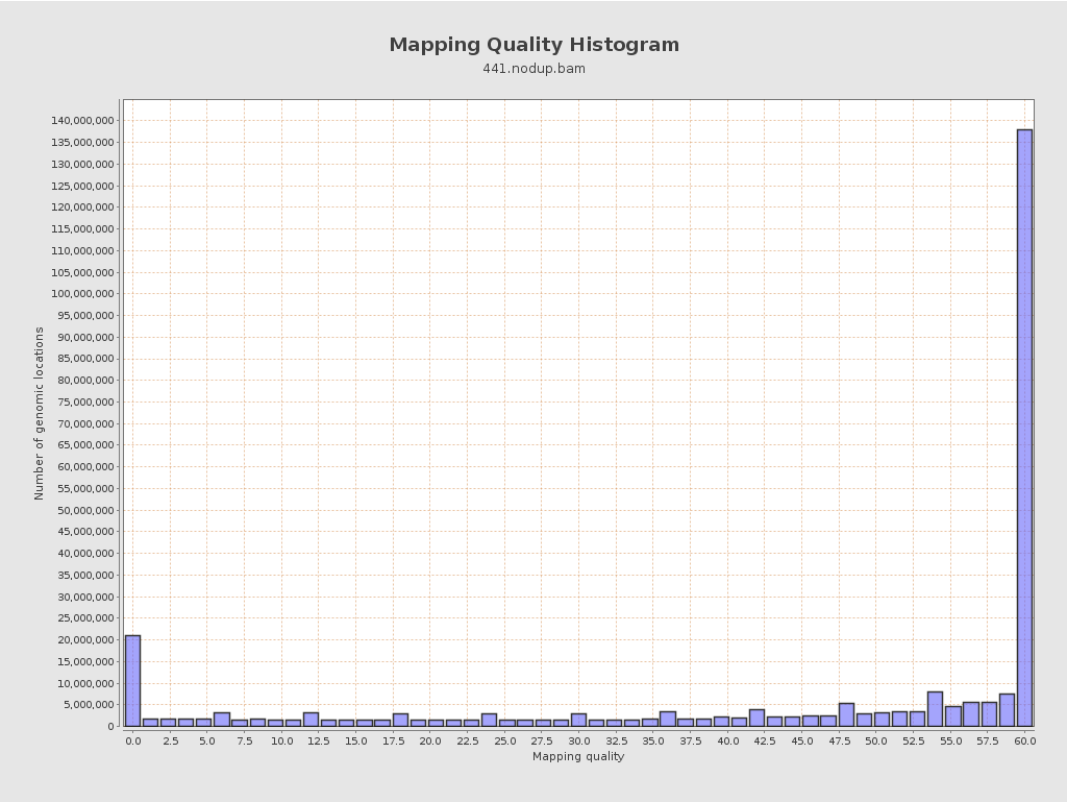
11. Results : Homopolymer Indels



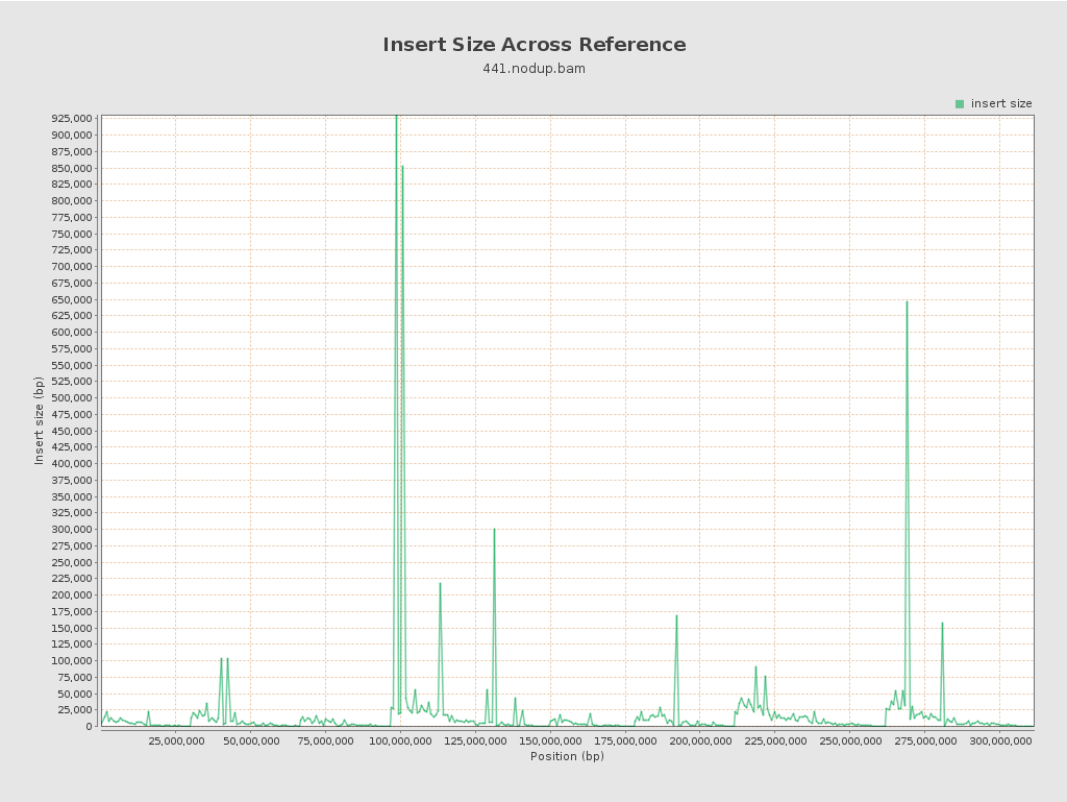
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram