Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:27:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/801.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/801.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_401/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_401_S376_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_401/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_401_S376_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:27:02 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	55,422,937
Mapped reads	51,527,798 / 92.97%
Unmapped reads	3,895,139 / 7.03%
Mapped paired reads	51,527,798 / 92.97%
Mapped reads, first in pair	25,829,343 / 46.6%
Mapped reads, second in pair	25,698,455 / 46.37%
Mapped reads, both in pair	50,225,480 / 90.62%
Mapped reads, singletons	1,302,318 / 2.35%
Read min/max/mean length	30 / 151 / 148.25
Duplicated reads (flagged)	8,157,066 / 14.72%
Clipped reads	11,313,674 / 20.41%

2.2. ACGT Content

Number/percentage of A's	2,207,074,436 / 30.83%
Number/percentage of C's	1,372,639,425 / 19.17%
Number/percentage of T's	2,213,330,799 / 30.91%
Number/percentage of G's	1,366,529,776 / 19.09%
Number/percentage of N's	24,885 / 0%
GC Percentage	38.26%

2.3. Coverage

Mean	23.0332
Standard Deviation	199.0497

2.4. Mapping Quality

Mean Mapping Quality	44.14

2.5. Insert size

Mean	258,653.02
Standard Deviation	2,428,404.89
P25/Median/P75	390 / 509 / 664

2.6. Mismatches and indels

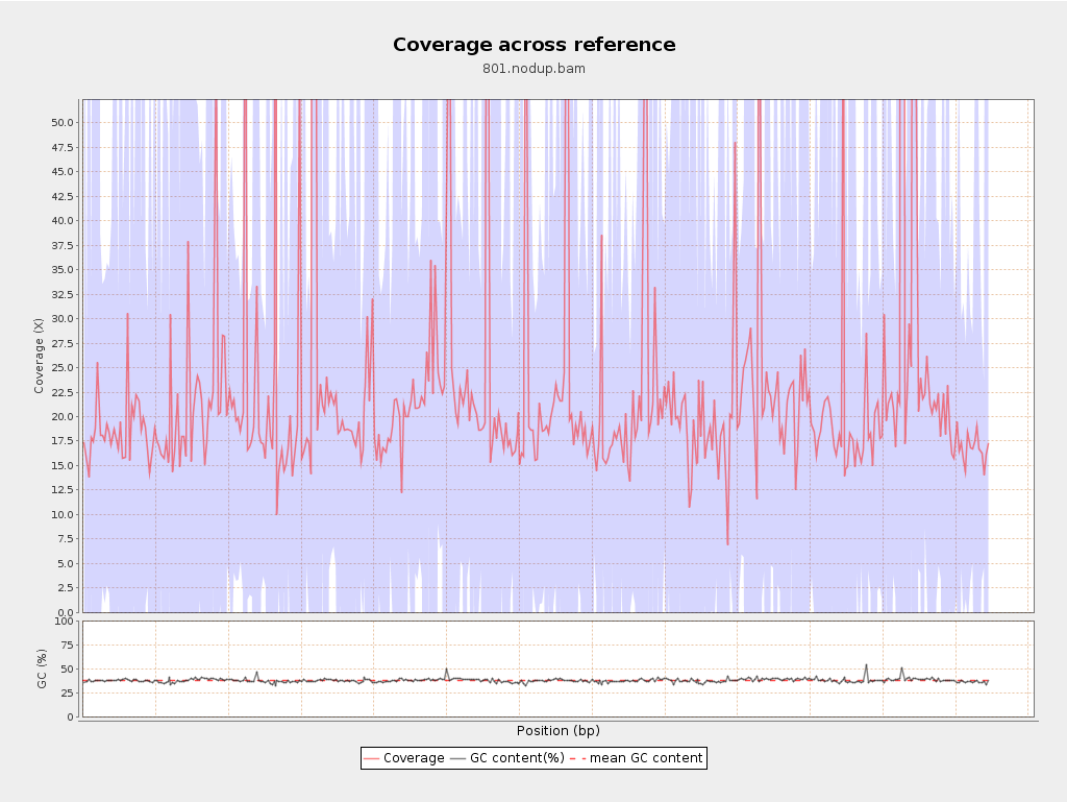
General error rate	2.35%
Mismatches	154,877,462
Insertions	4,909,743
Mapped reads with at least one insertion	8.54%
Deletions	4,911,781
Mapped reads with at least one deletion	8.47%
Homopolymer indels	56.43%

2.7. Chromosome stats

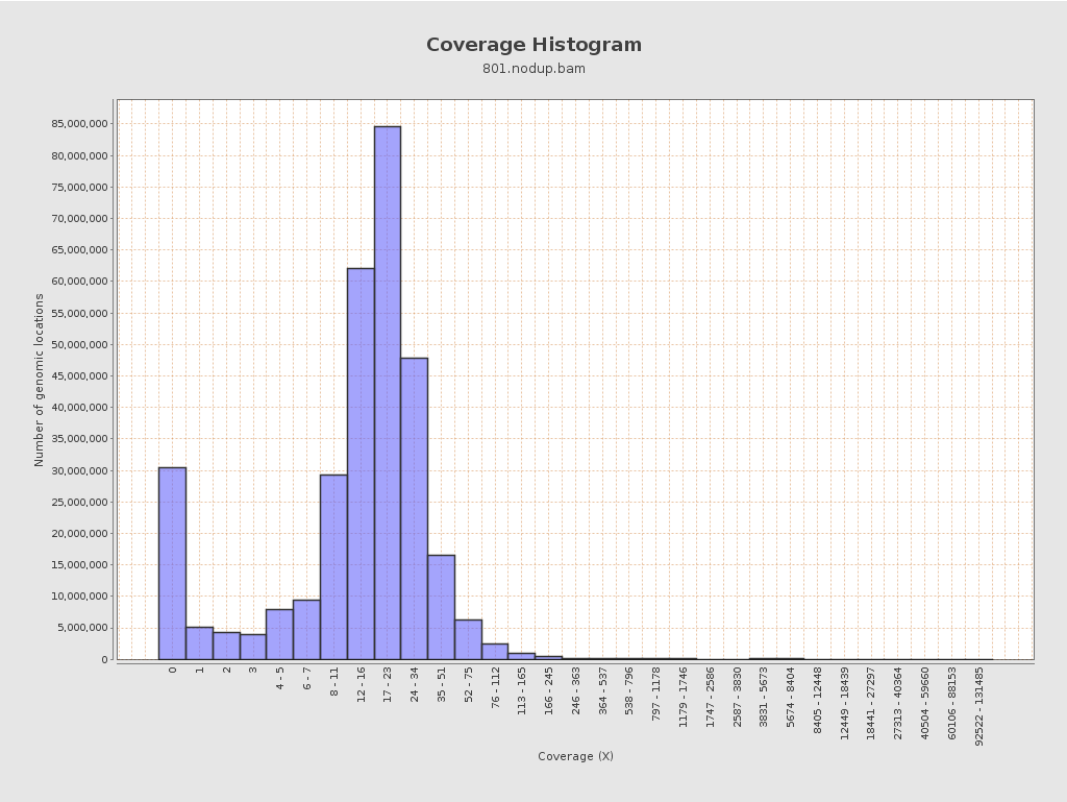
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	542310397	18.2447	60.8823

LT669789.1	36598175	845127996	23.0921	207.2466
LT669790.1	30422129	765361879	25.1581	223.2529
LT669791.1	52758100	1215221798	23.0338	181.5929
LT669792.1	28376109	640401308	22.5683	239.907
LT669793.1	33388210	710180724	21.2704	134.2226
LT669794.1	50579949	1113135512	22.0074	175.0702
LT669795.1	49795044	1346361036	27.0381	269.7228

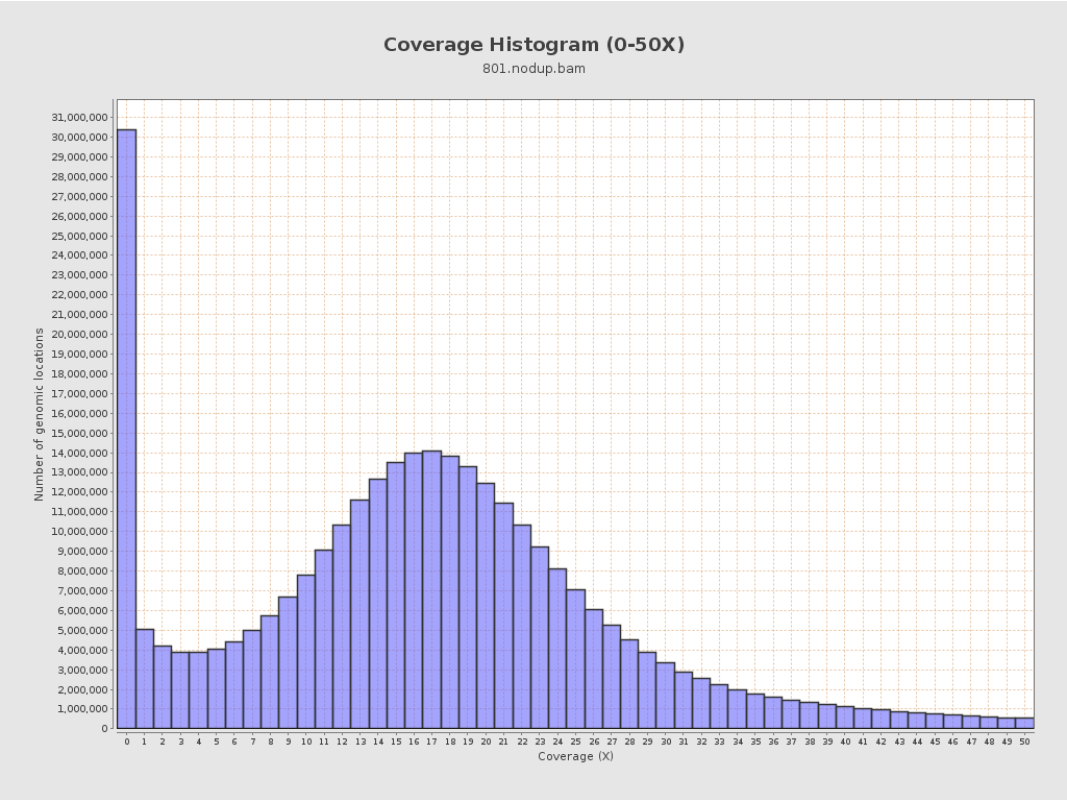
3. Results : Coverage across reference



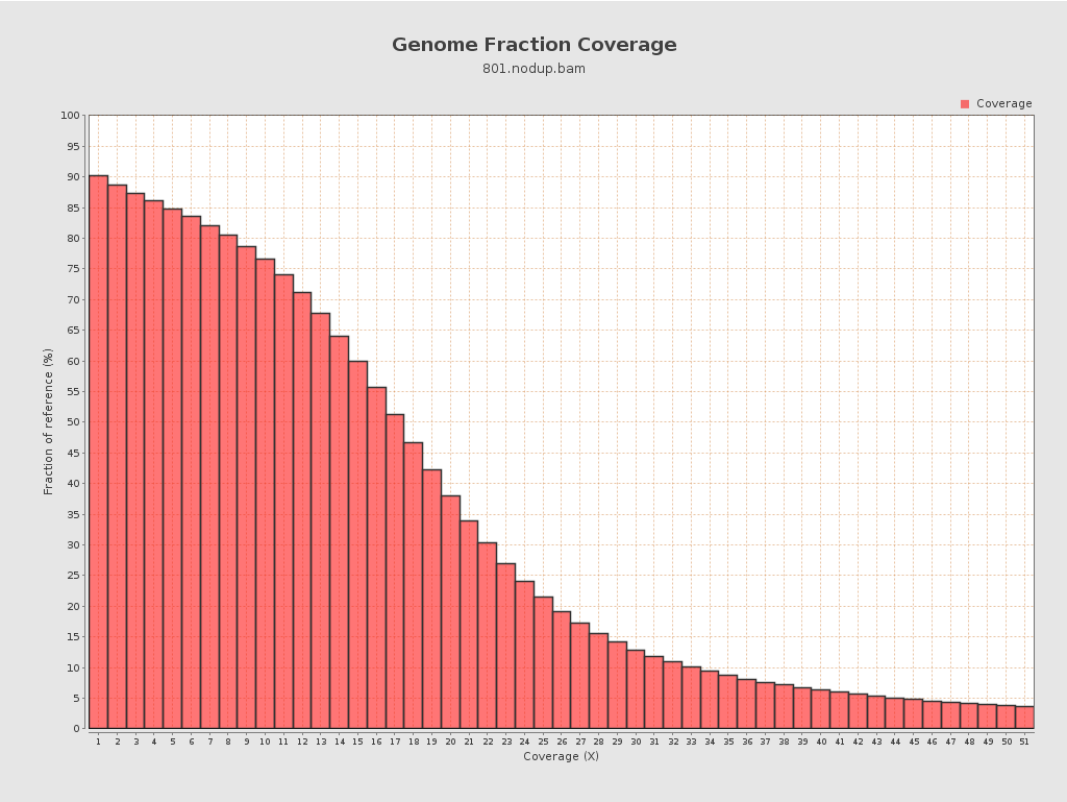
4. Results : Coverage Histogram



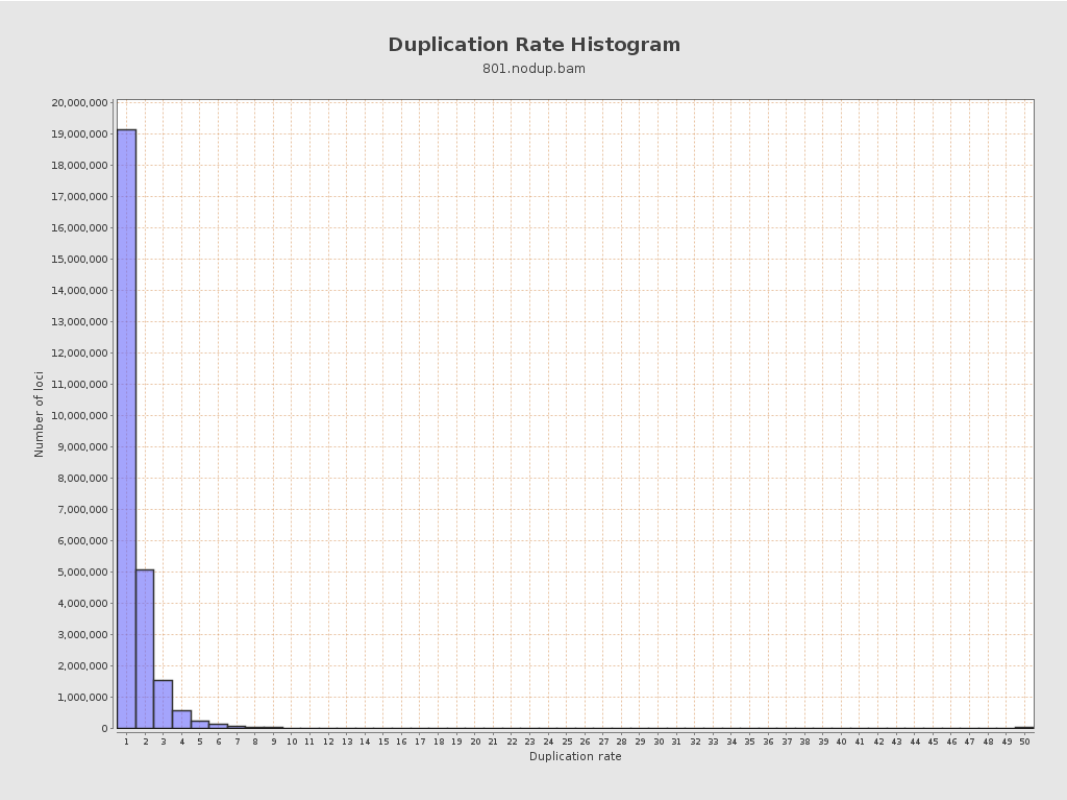
5. Results : Coverage Histogram (0-50X)



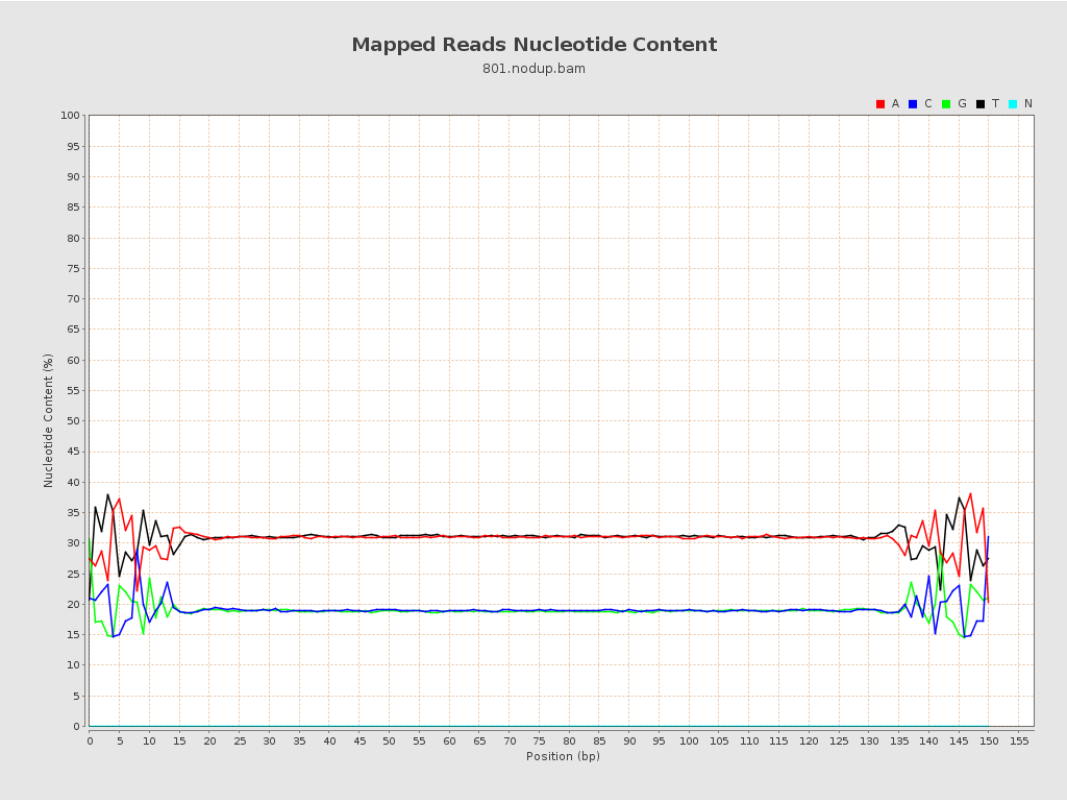
6. Results : Genome Fraction Coverage



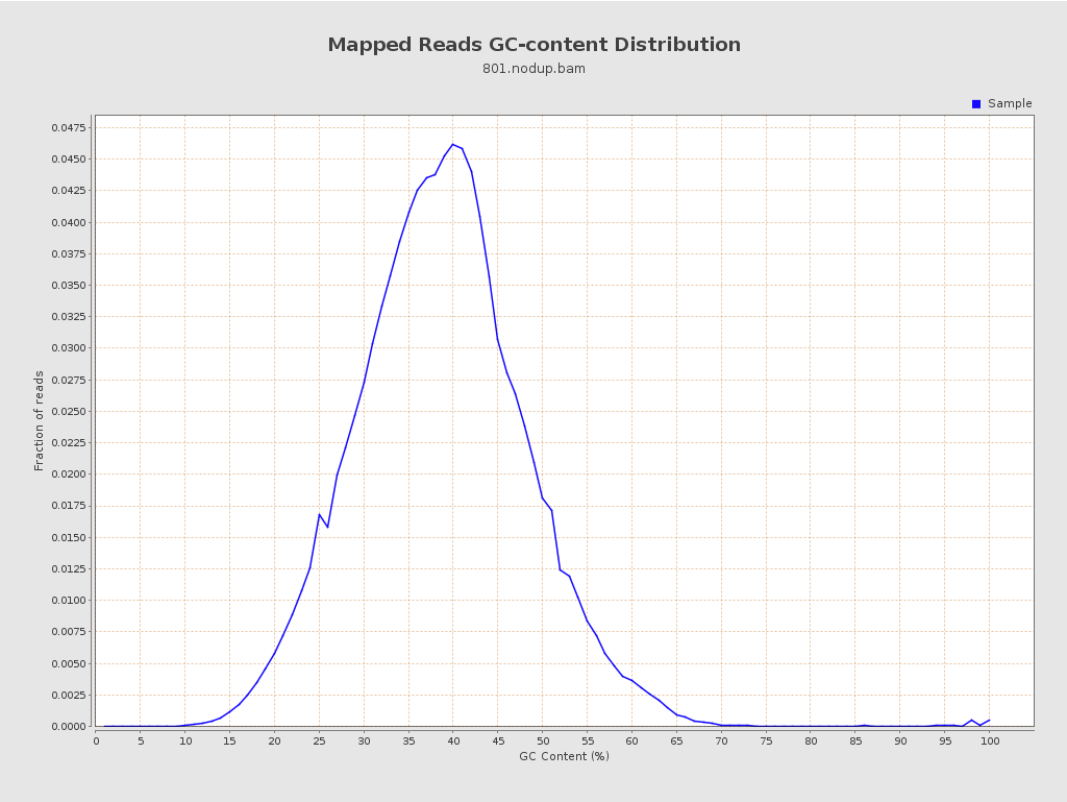
7. Results : Duplication Rate Histogram



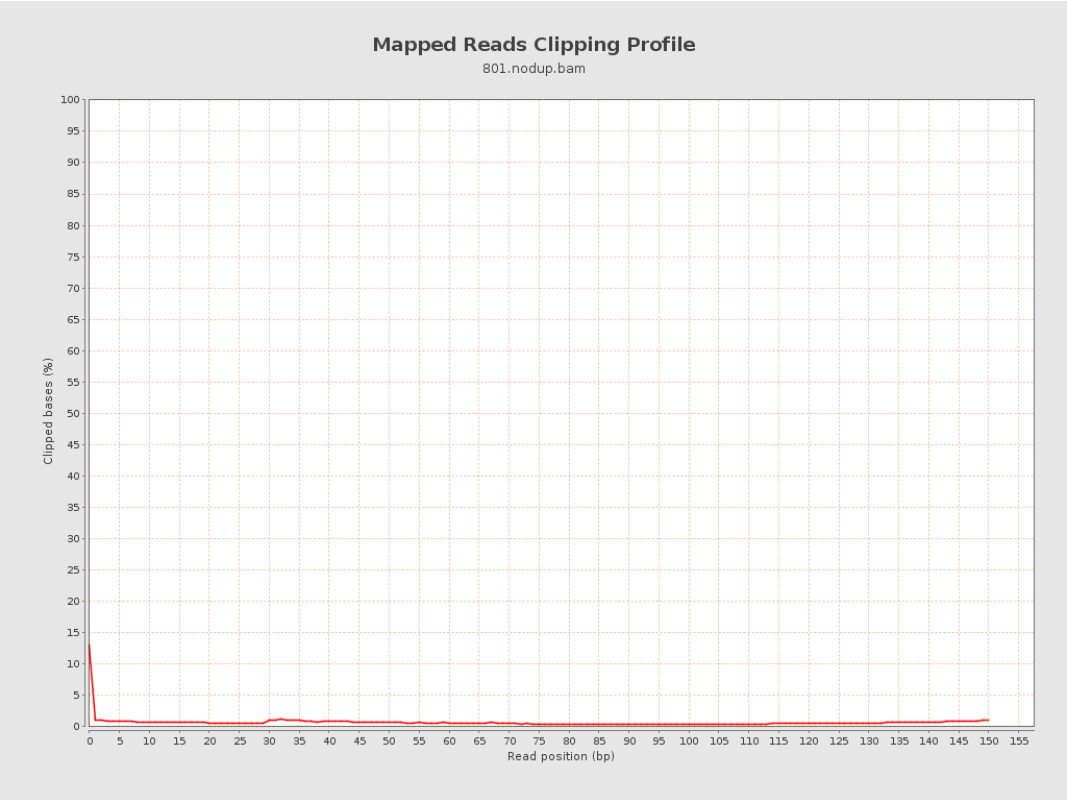
8. Results : Mapped Reads Nucleotide Content



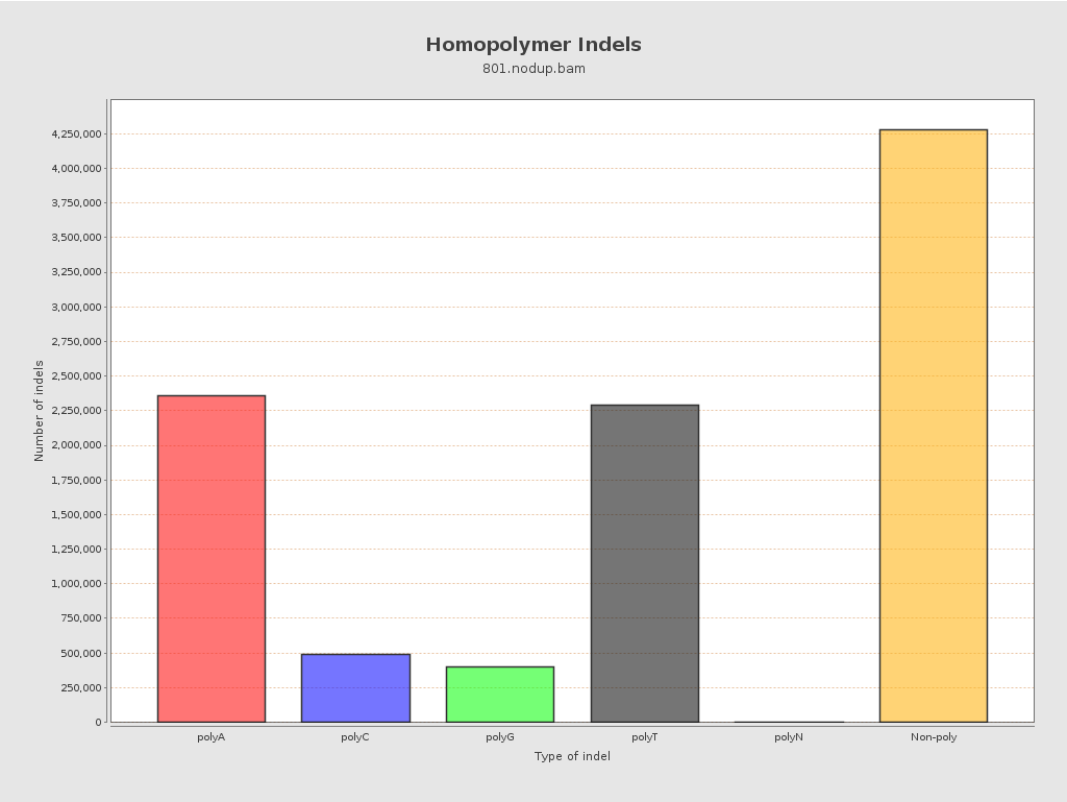
9. Results : Mapped Reads GC-content Distribution



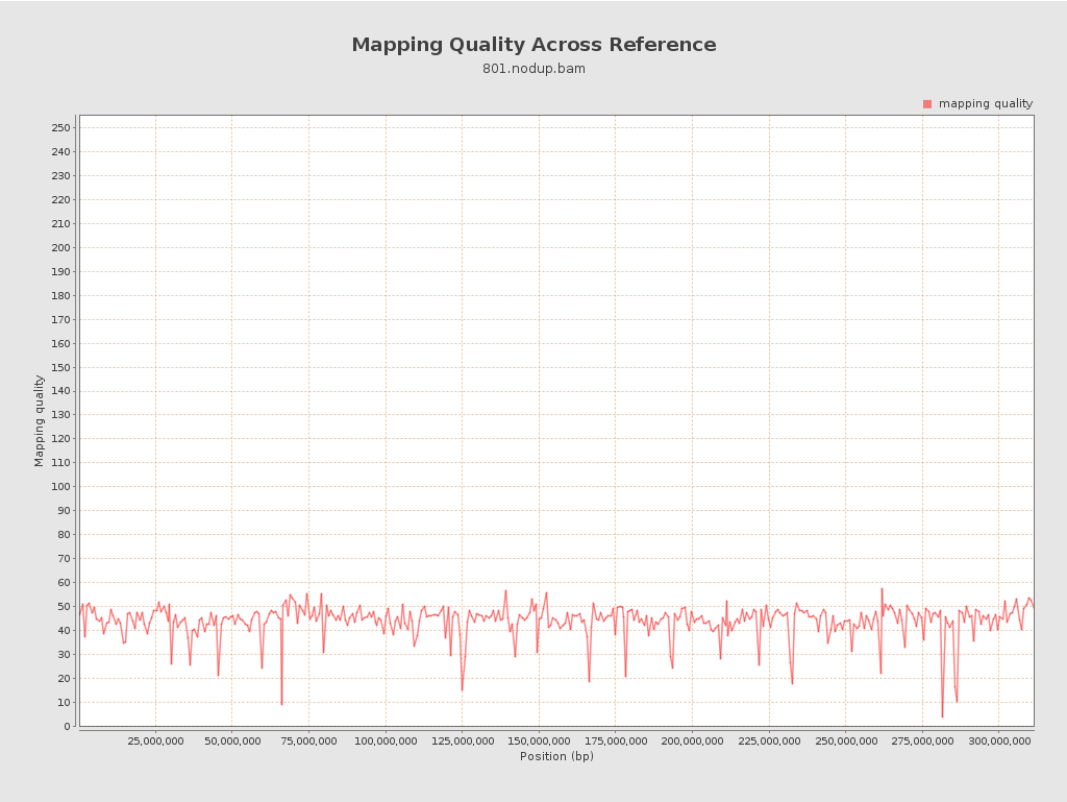
10. Results : Mapped Reads Clipping Profile



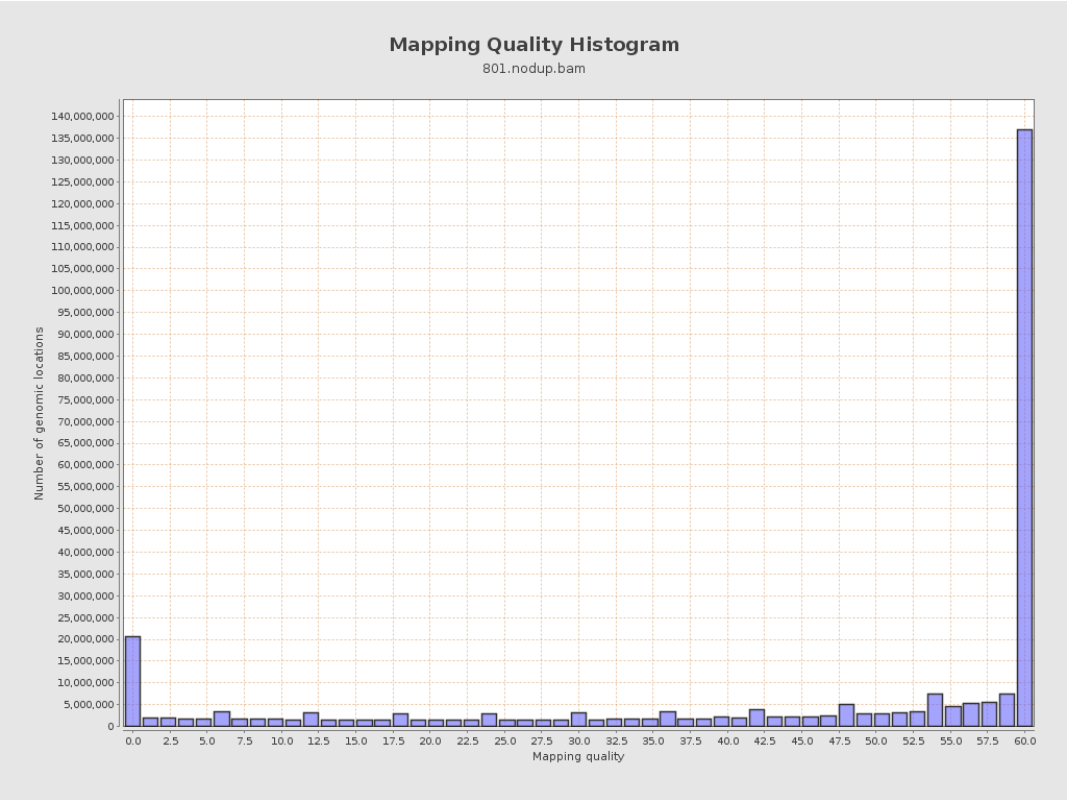
11. Results : Homopolymer Indels



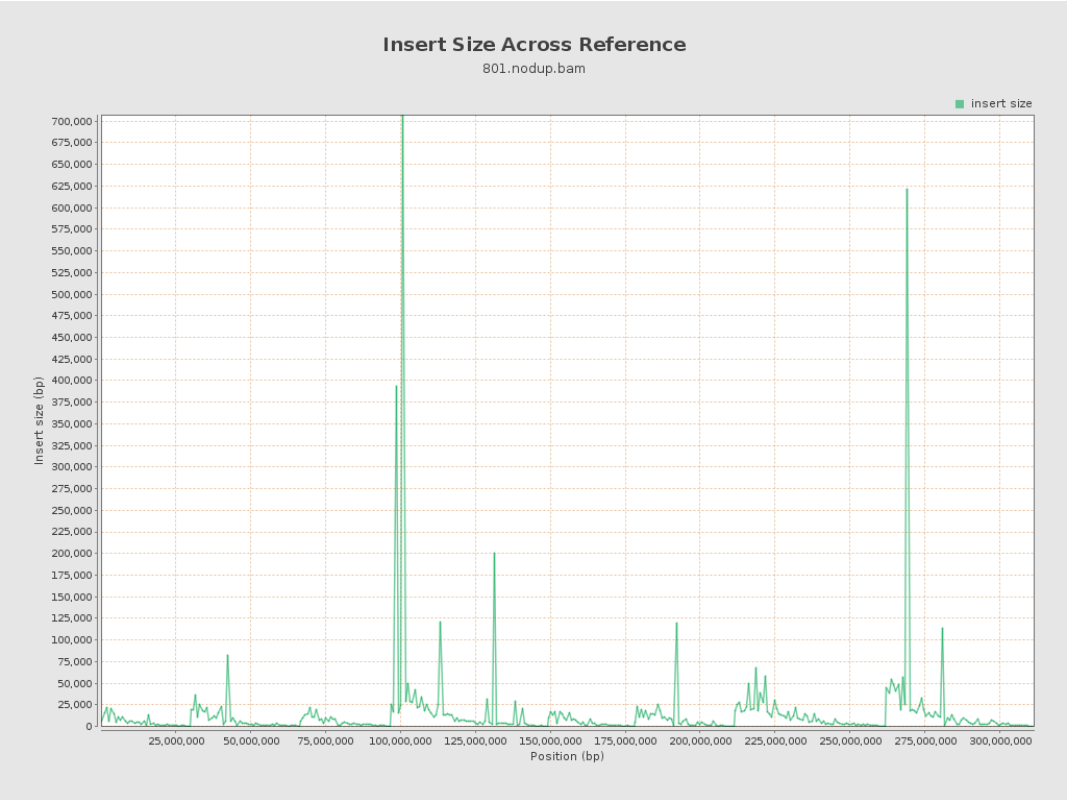
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram