Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:39:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/800.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/800.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_262/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_262_S343_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_262/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_262_S343_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:39:31 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	89,776,724
Mapped reads	84,345,338 / 93.95%
Unmapped reads	5,431,386 / 6.05%
Mapped paired reads	84,345,338 / 93.95%
Mapped reads, first in pair	42,230,325 / 47.04%
Mapped reads, second in pair	42,115,013 / 46.91%
Mapped reads, both in pair	82,586,075 / 91.99%
Mapped reads, singletons	1,759,263 / 1.96%
Read min/max/mean length	30 / 151 / 147.87
Duplicated reads (flagged)	13,696,094 / 15.26%
Clipped reads	20,851,270 / 23.23%

2.2. ACGT Content

Number/percentage of A's	3,557,261,371 / 30.8%
Number/percentage of C's	2,216,228,533 / 19.19%
Number/percentage of T's	3,562,710,549 / 30.84%
Number/percentage of G's	2,215,034,827 / 19.18%
Number/percentage of N's	40,761 / 0%
GC Percentage	38.36%

2.3. Coverage

Mean	37.1618
Standard Deviation	346.5681

2.4. Mapping Quality

Mean Mapping Quality	44.07

2.5. Insert size

Mean	229,927.77
Standard Deviation	2,287,892.34
P25/Median/P75	300 / 402 / 525

2.6. Mismatches and indels

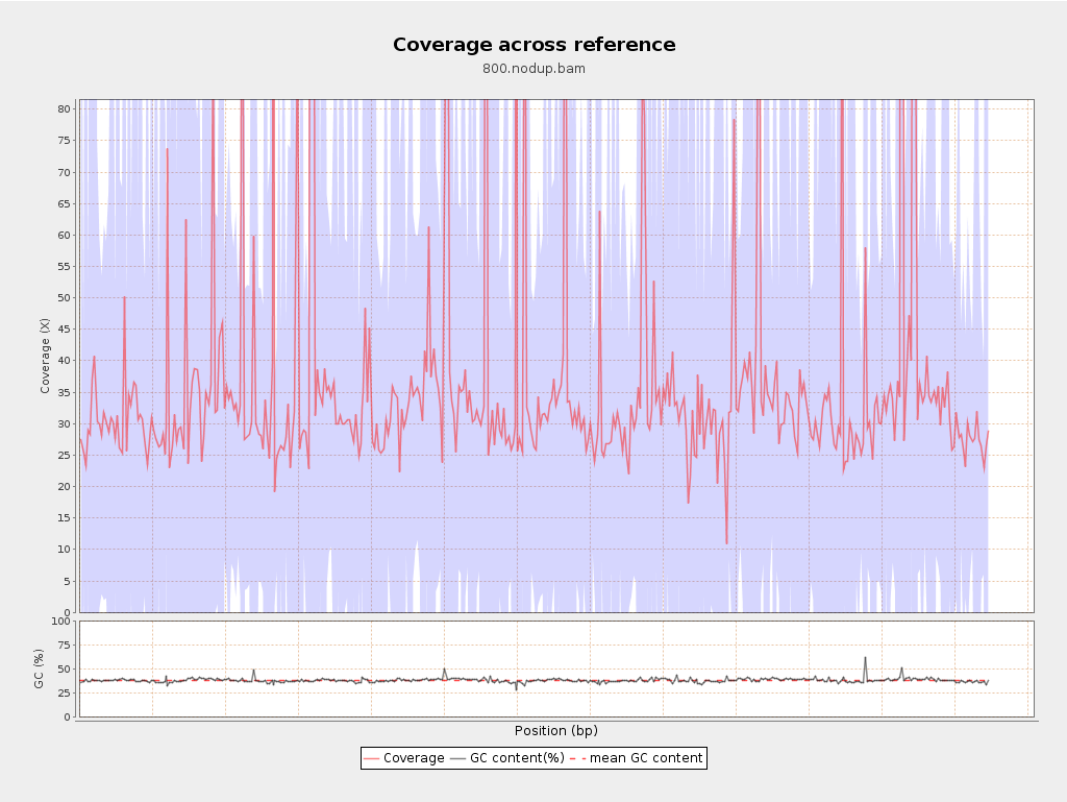
General error rate	2.39%
Mismatches	253,905,034
Insertions	8,019,309
Mapped reads with at least one insertion	8.52%
Deletions	7,994,317
Mapped reads with at least one deletion	8.4%
Homopolymer indels	56.06%

2.7. Chromosome stats

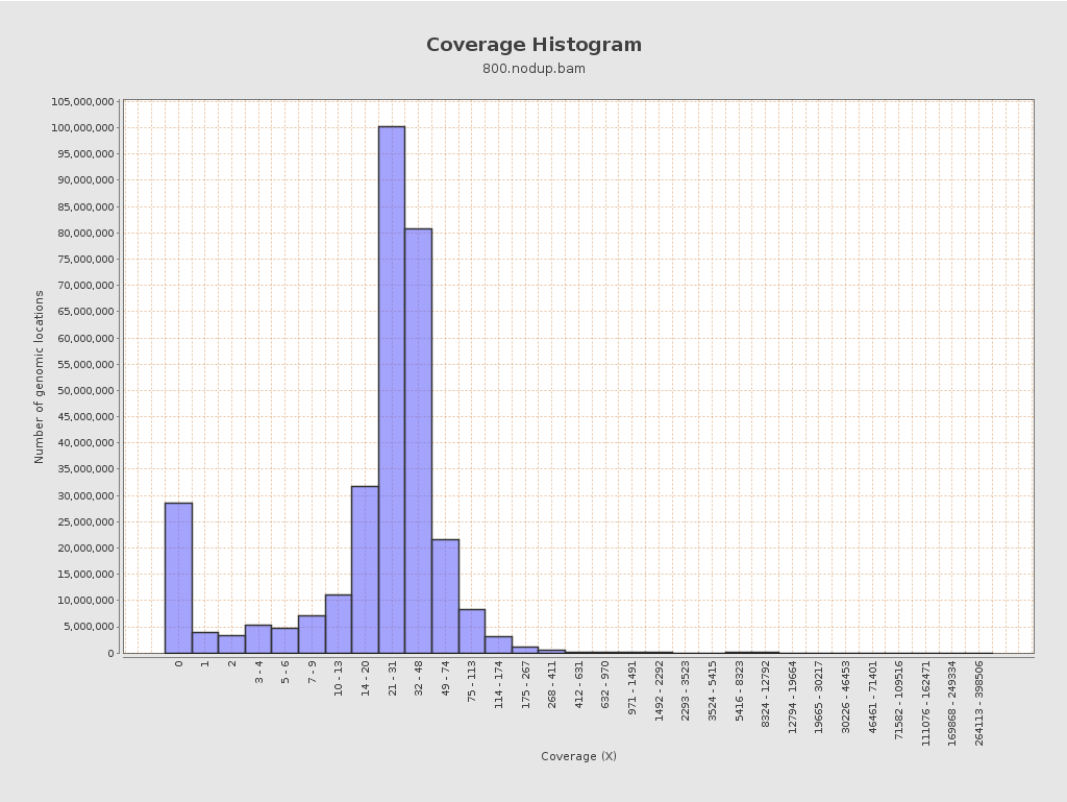
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	894783275	30.1027	121.6409

LT669789.1	36598175	1365886360	37.3212	355.7035
LT669790.1	30422129	1249518676	41.0727	360.5901
LT669791.1	52758100	1936068358	36.6971	331.1658
LT669792.1	28376109	1056113953	37.2184	358.7158
LT669793.1	33388210	1124226355	33.6714	179.6343
LT669794.1	50579949	1798319043	35.554	301.8237
LT669795.1	49795044	2156264084	43.3028	516.39

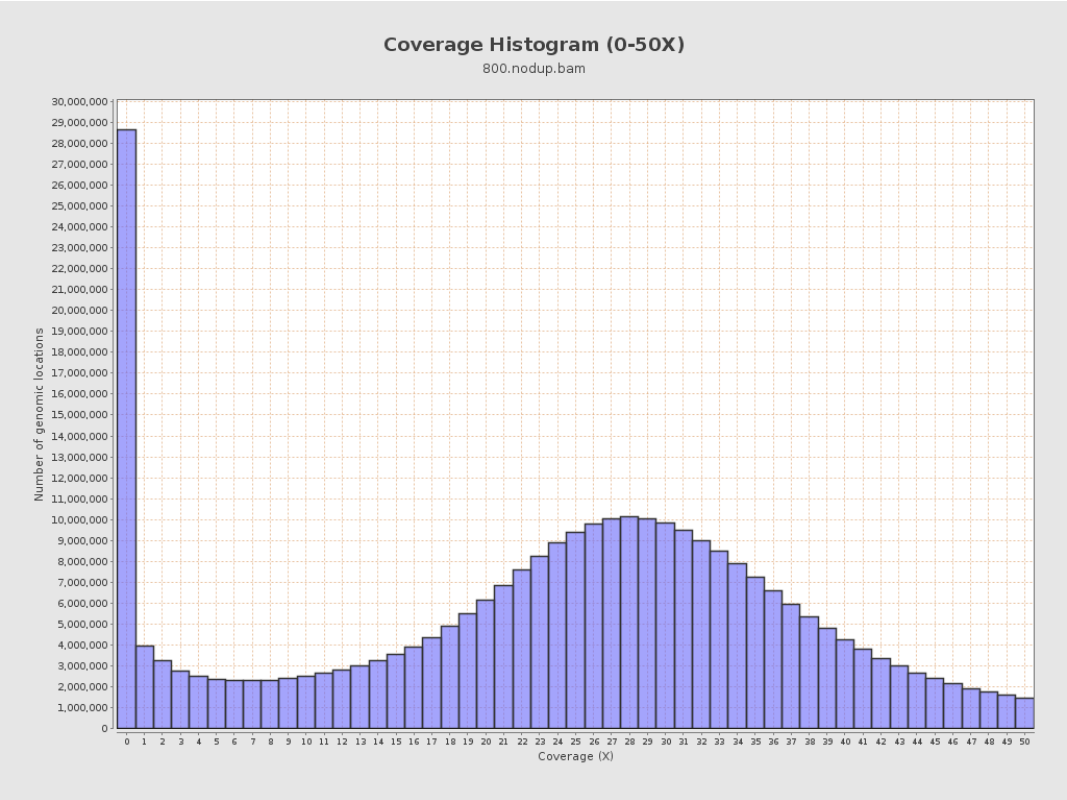
3. Results : Coverage across reference



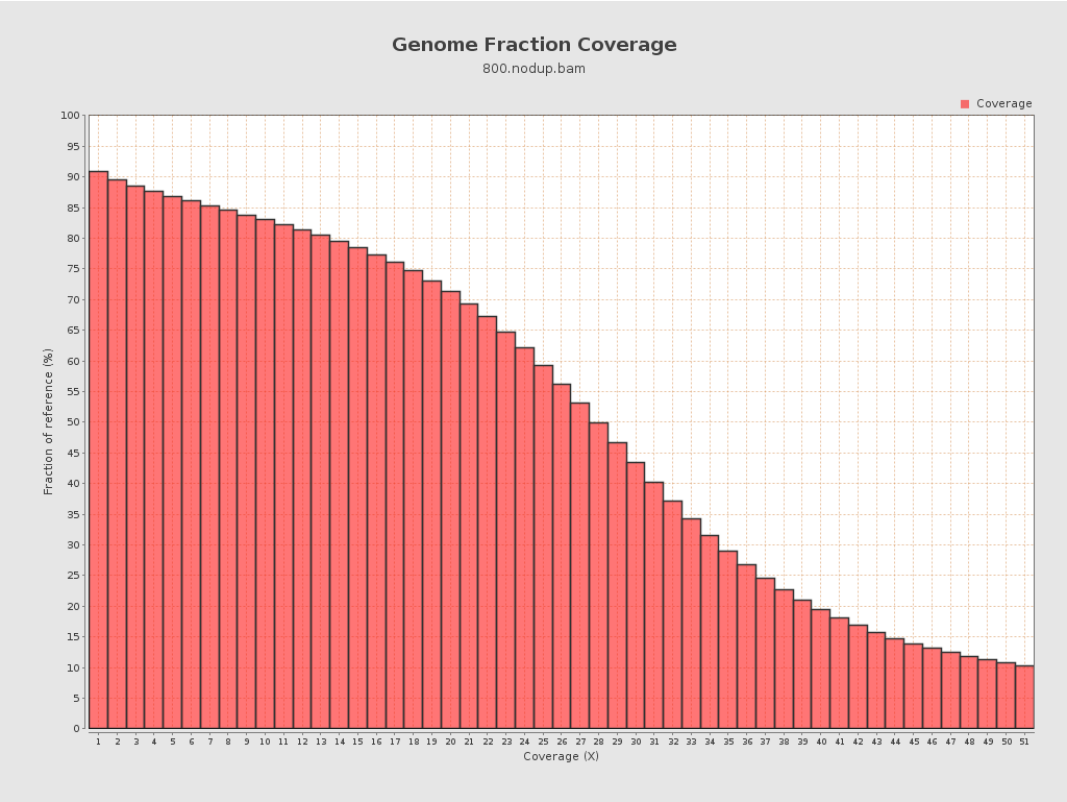
4. Results : Coverage Histogram



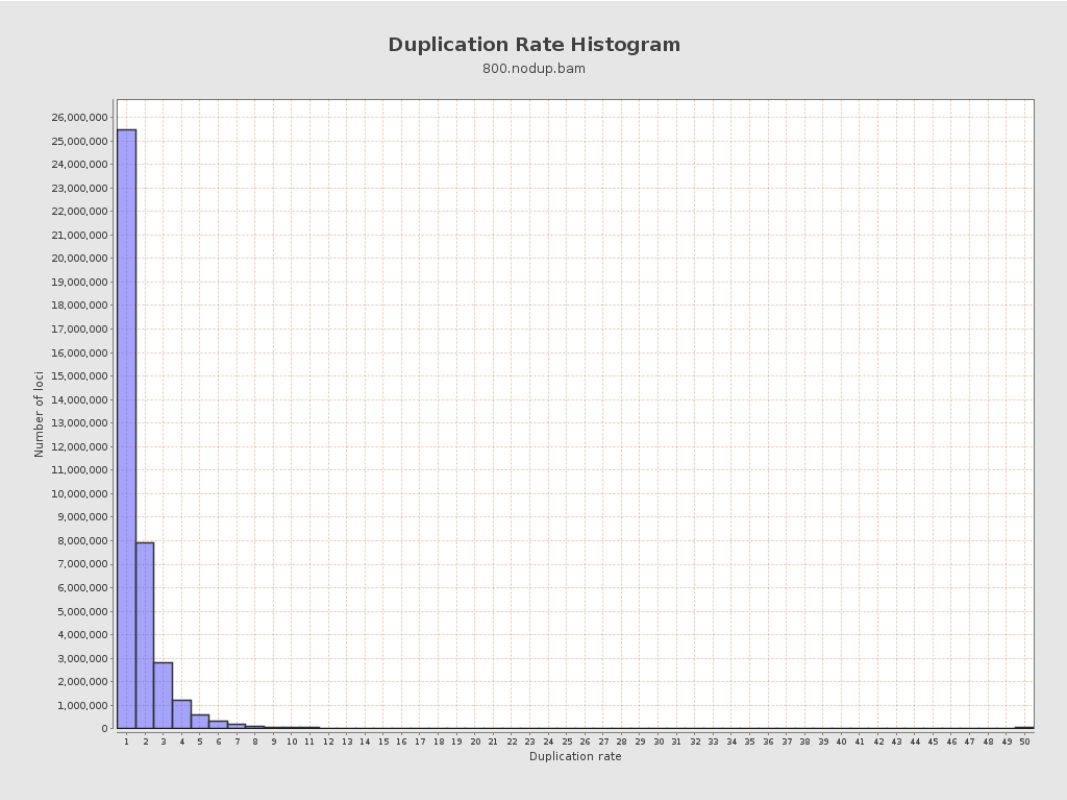
5. Results : Coverage Histogram (0-50X)



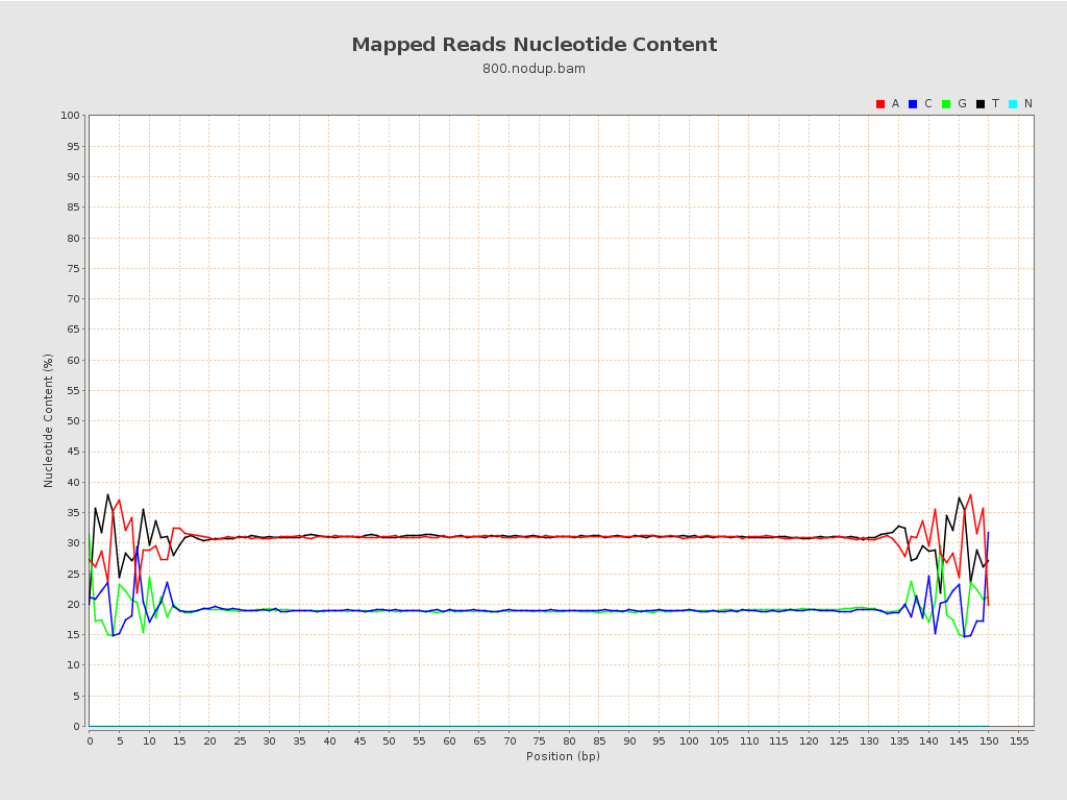
6. Results : Genome Fraction Coverage



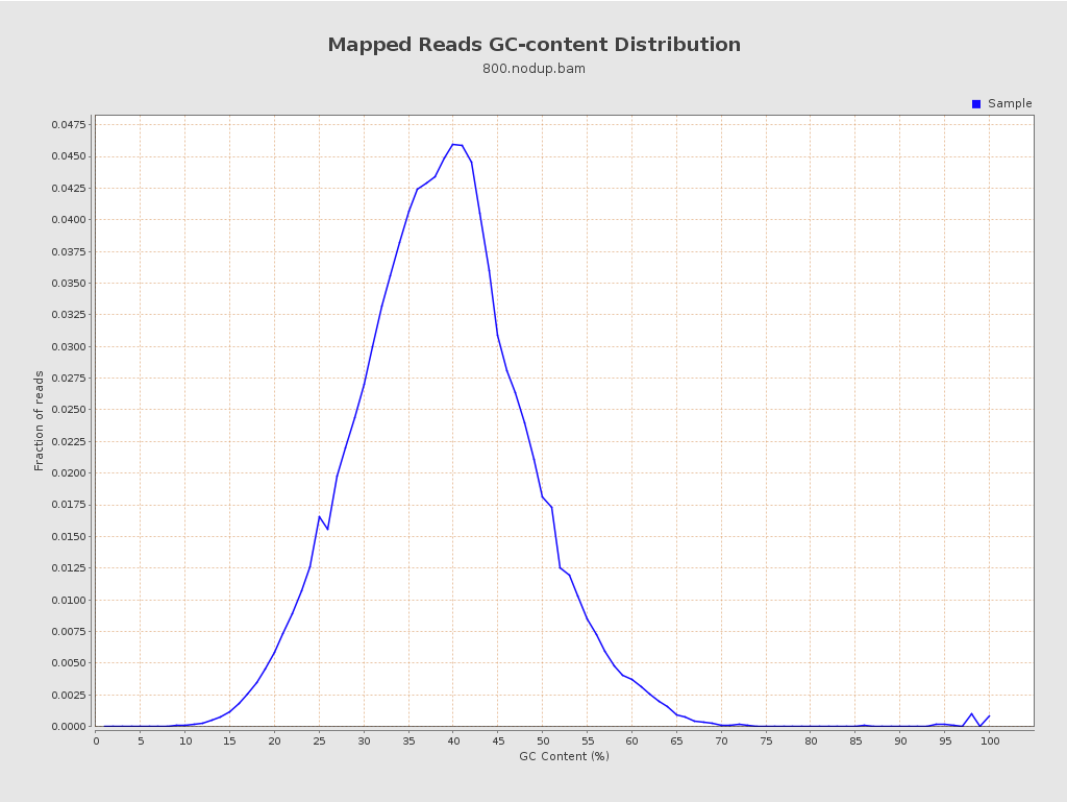
7. Results : Duplication Rate Histogram



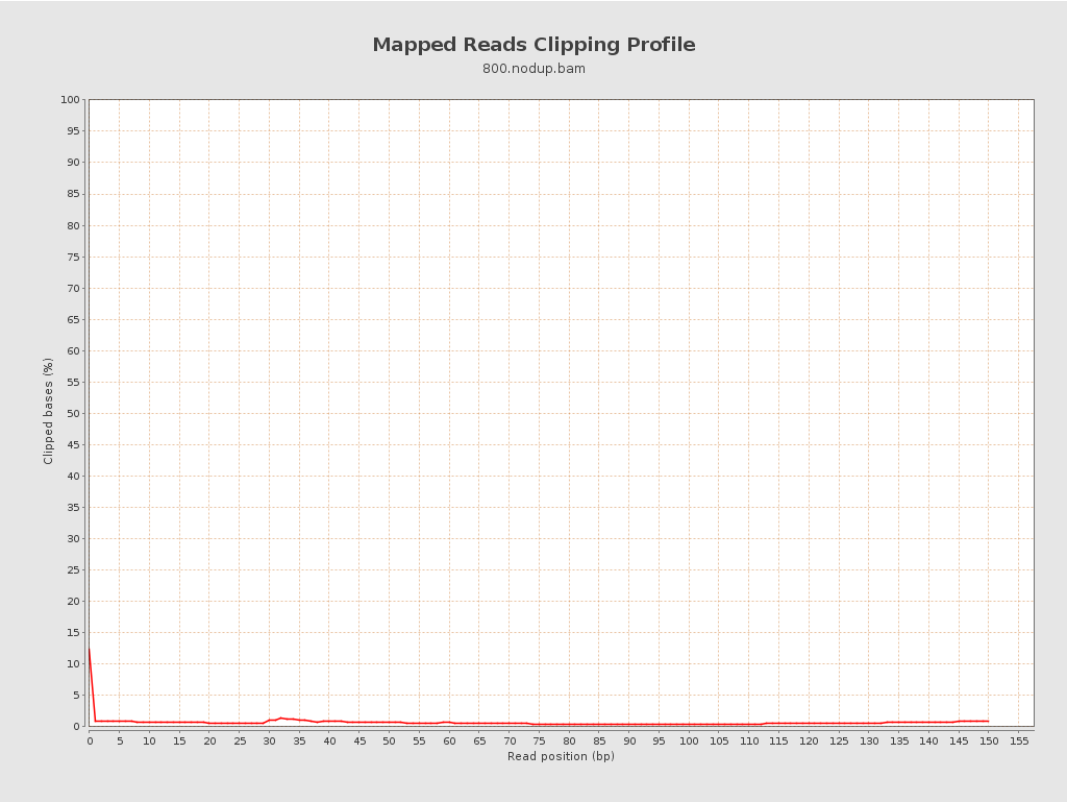
8. Results : Mapped Reads Nucleotide Content



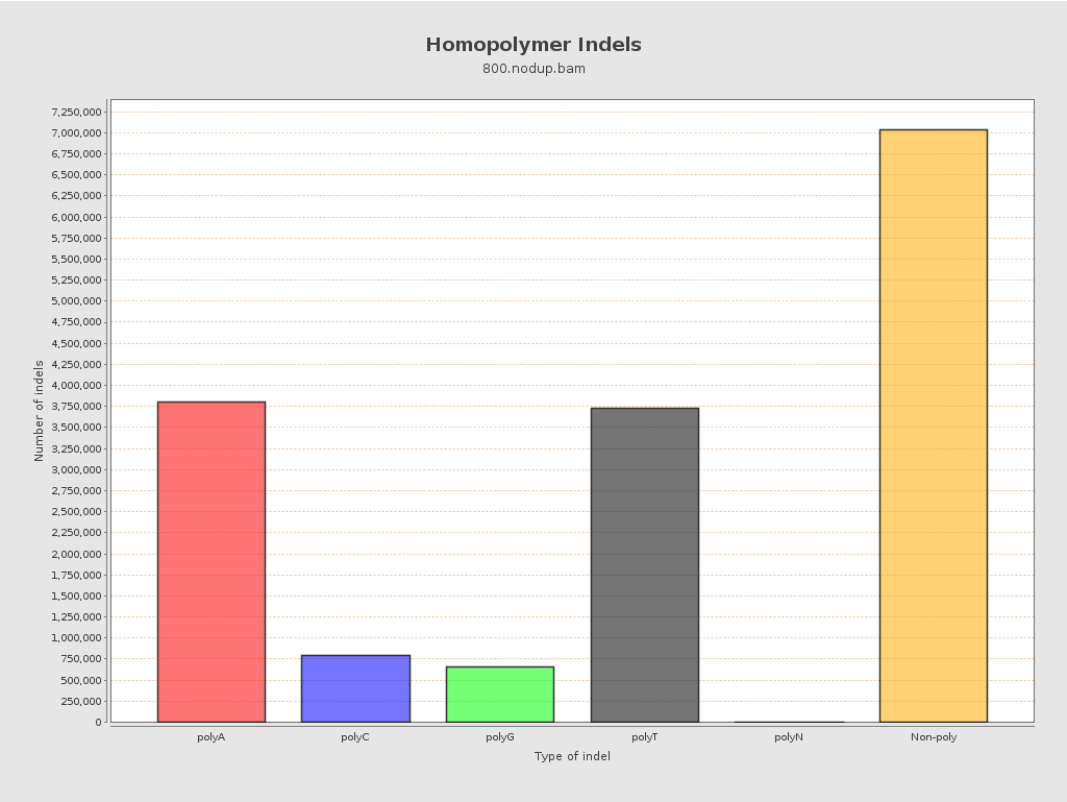
9. Results : Mapped Reads GC-content Distribution



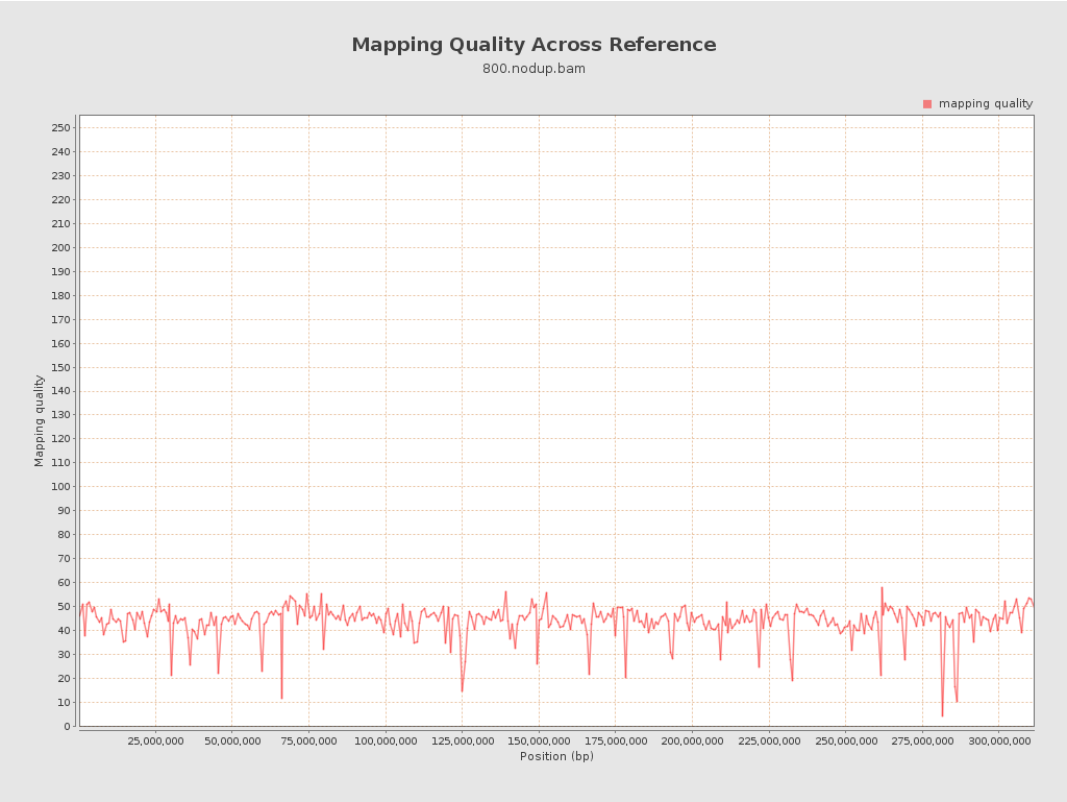
10. Results : Mapped Reads Clipping Profile



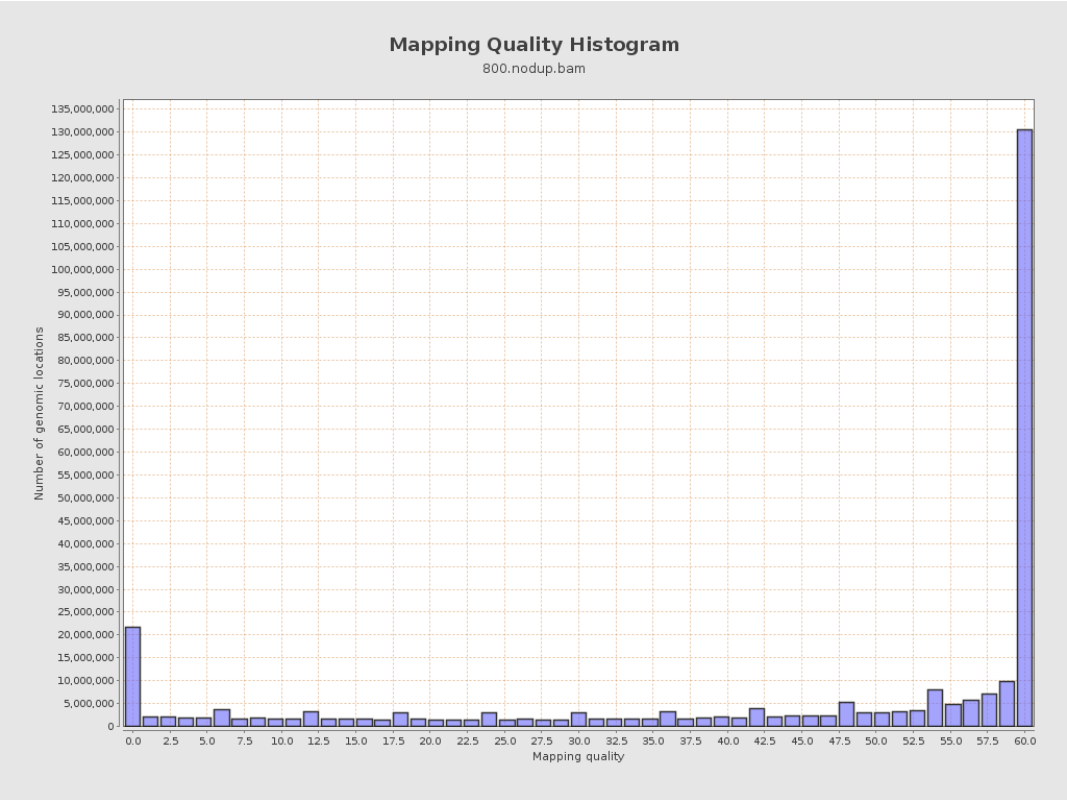
11. Results : Homopolymer Indels



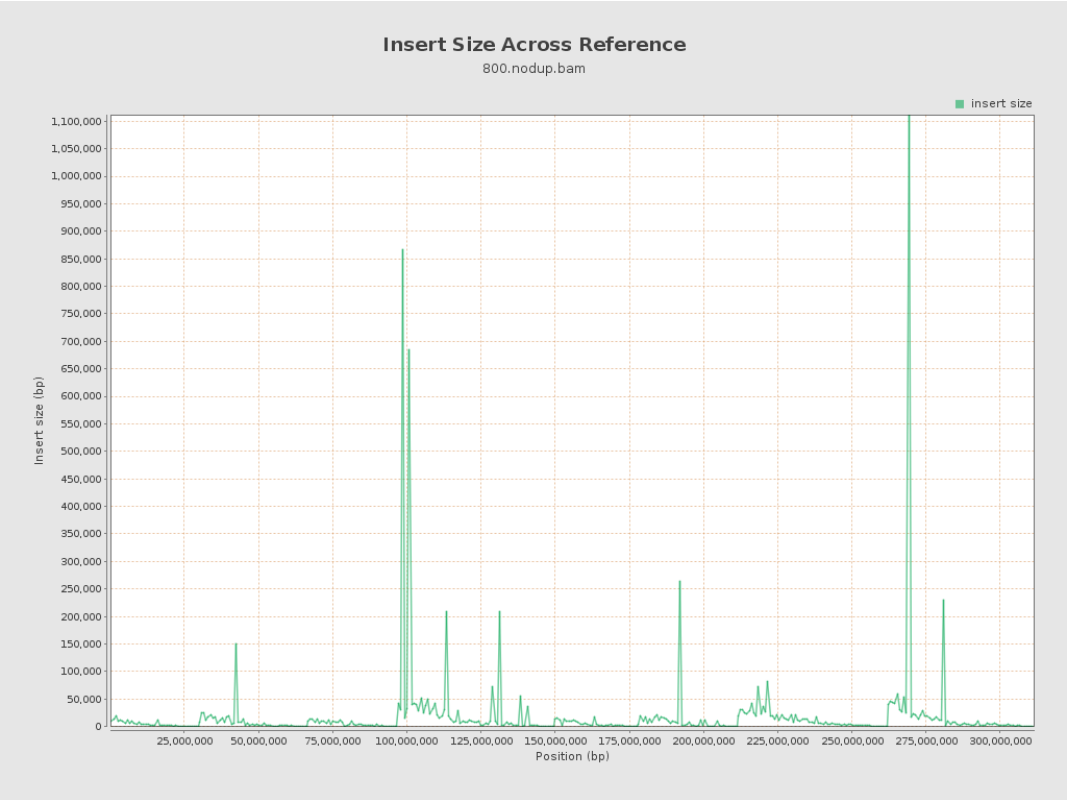
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram