Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:38:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/803.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/803.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_424/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_424_S399_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_424/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_424_S399_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:38:15 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	83,517,454
Mapped reads	77,636,208 / 92.96%
Unmapped reads	5,881,246 / 7.04%
Mapped paired reads	77,636,208 / 92.96%
Mapped reads, first in pair	38,895,576 / 46.57%
Mapped reads, second in pair	38,740,632 / 46.39%
Mapped reads, both in pair	75,582,258 / 90.5%
Mapped reads, singletons	2,053,950 / 2.46%
Read min/max/mean length	30 / 151 / 148.24
Duplicated reads (flagged)	13,783,961 / 16.5%
Clipped reads	16,797,153 / 20.11%

2.2. ACGT Content

Number/percentage of A's	3,333,913,124 / 30.93%
Number/percentage of C's	2,056,929,828 / 19.08%
Number/percentage of T's	3,339,150,359 / 30.98%
Number/percentage of G's	2,050,109,949 / 19.02%
Number/percentage of N's	37,511 / 0%
GC Percentage	38.1%

2.3. Coverage

Mean	34.6781
Standard Deviation	287.5047

2.4. Mapping Quality

Mean Mapping Quality	44.74

2.5. Insert size

Mean	247,955.07
Standard Deviation	2,397,695.76
P25/Median/P75	358 / 466 / 607

2.6. Mismatches and indels

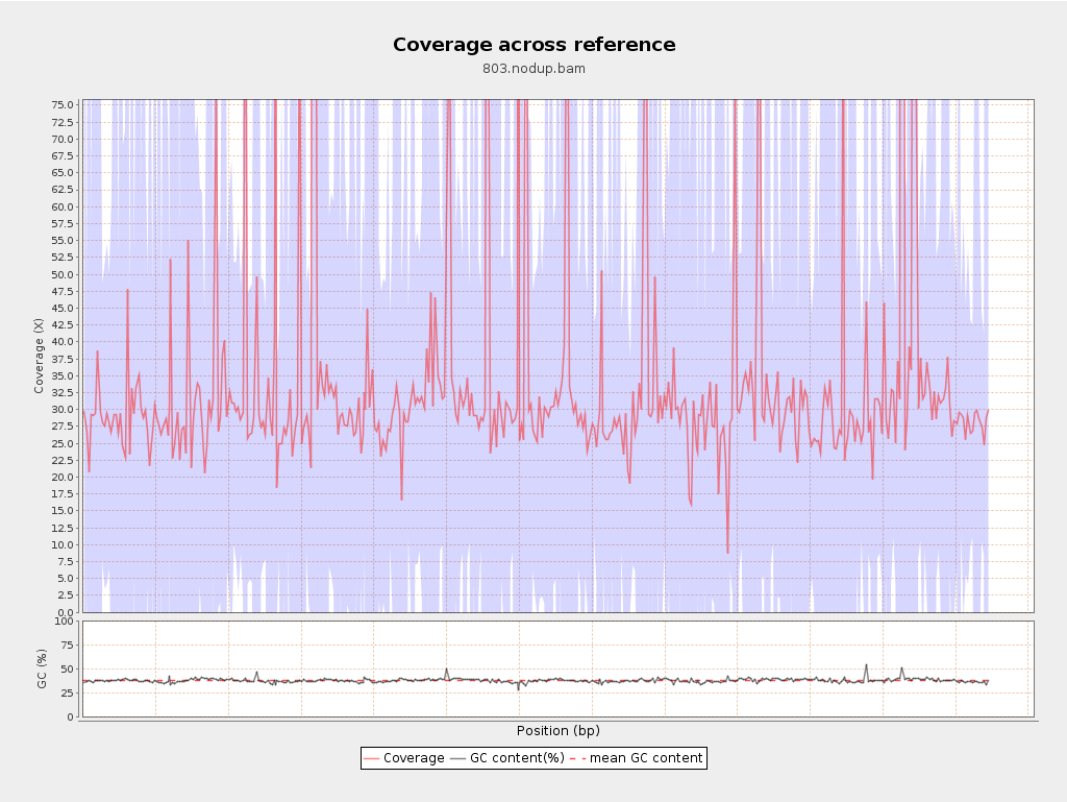
General error rate	2.27%
Mismatches	224,211,384
Insertions	7,363,740
Mapped reads with at least one insertion	8.49%
Deletions	7,235,937
Mapped reads with at least one deletion	8.26%
Homopolymer indels	56.92%

2.7. Chromosome stats

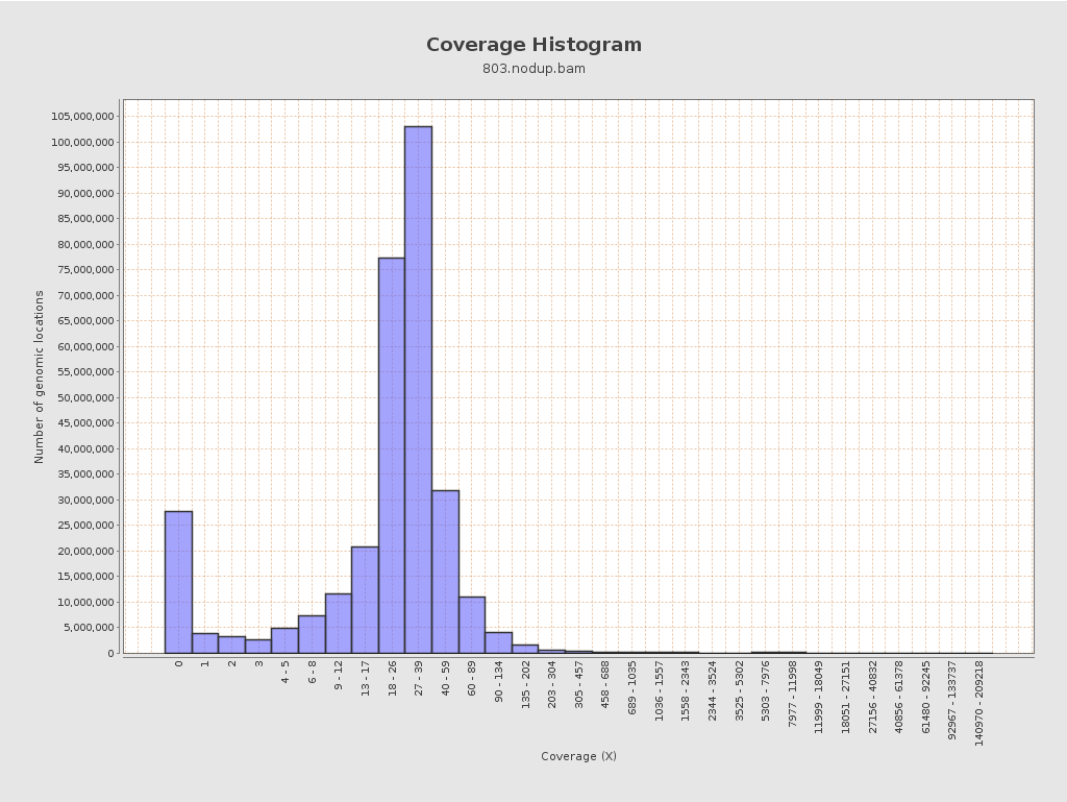
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	858855405	28.894	104.4802

LT669789.1	36598175	1232834503	33.6857	295.5671
LT669790.1	30422129	1218284502	40.046	365.4974
LT669791.1	52758100	1789387216	33.9168	281.9847
LT669792.1	28376109	986601803	34.7687	291.2952
LT669793.1	33388210	1050849624	31.4737	189.6178
LT669794.1	50579949	1634151858	32.3083	242.4654
LT669795.1	49795044	2036203354	40.8917	385.313

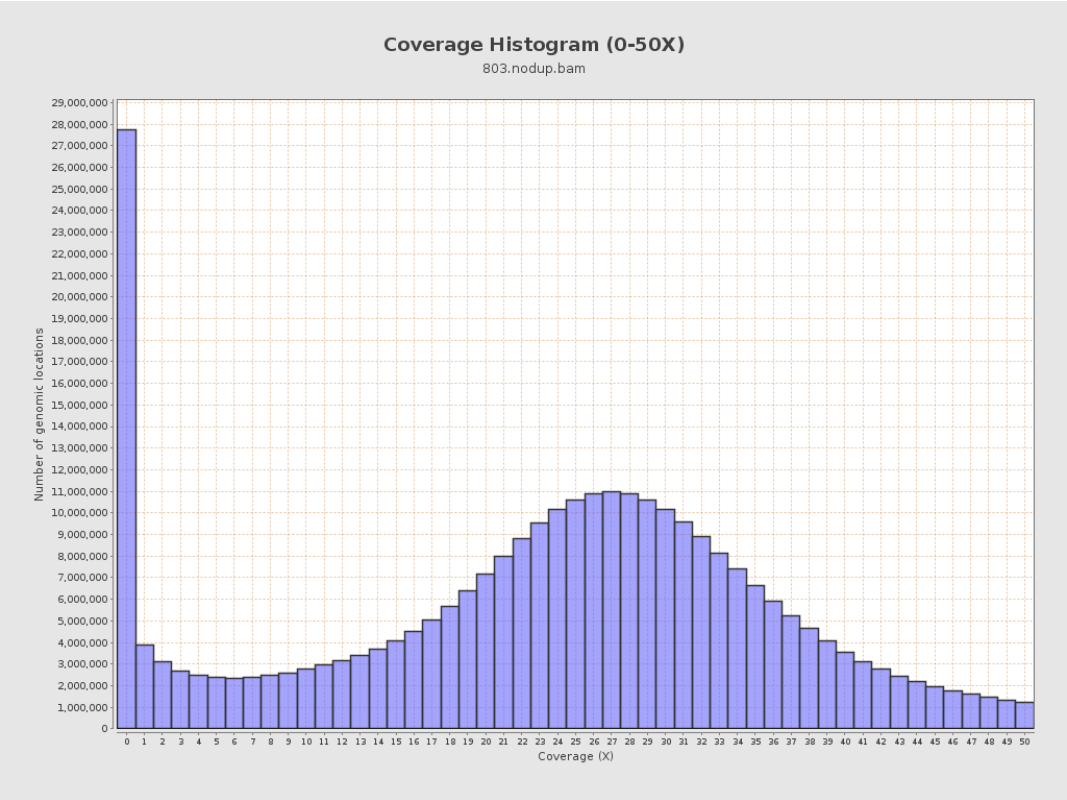
3. Results : Coverage across reference



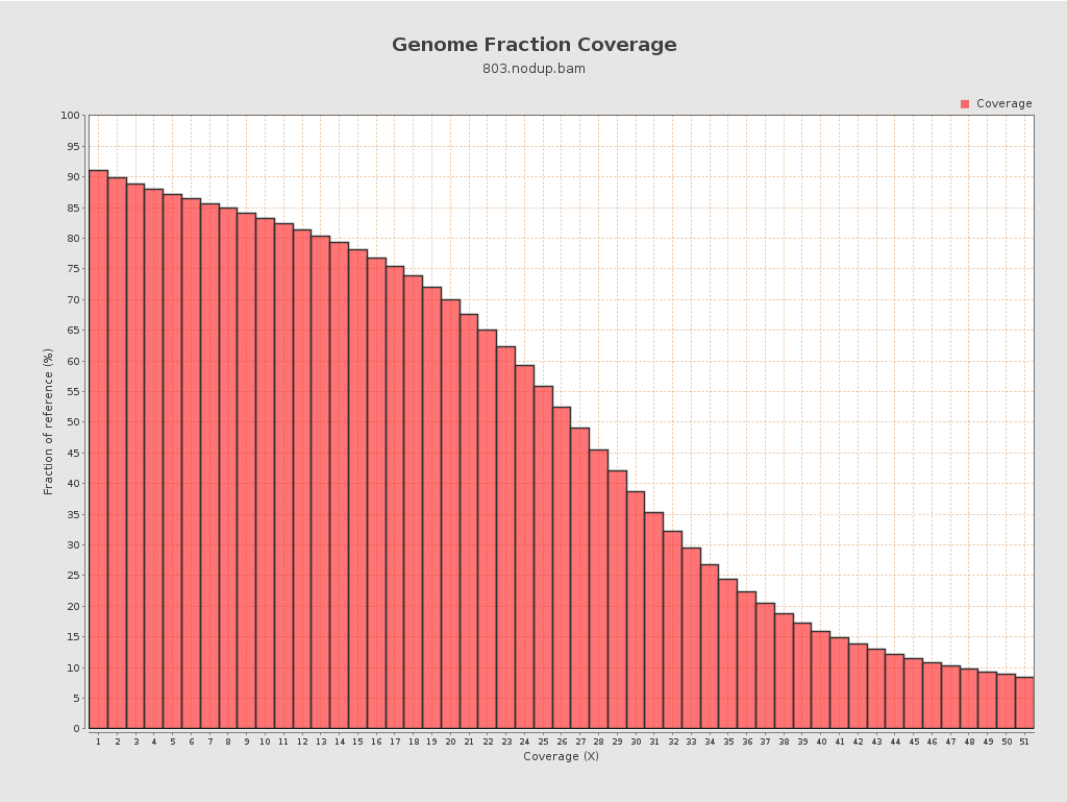
4. Results : Coverage Histogram



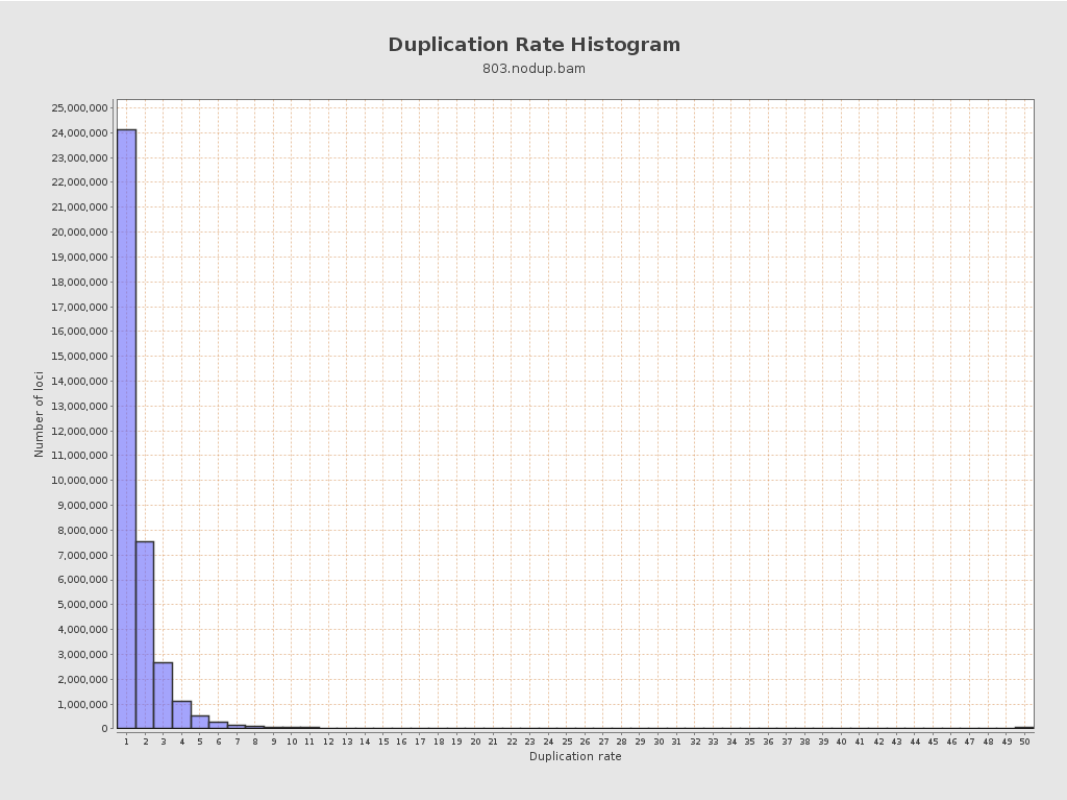
5. Results : Coverage Histogram (0-50X)



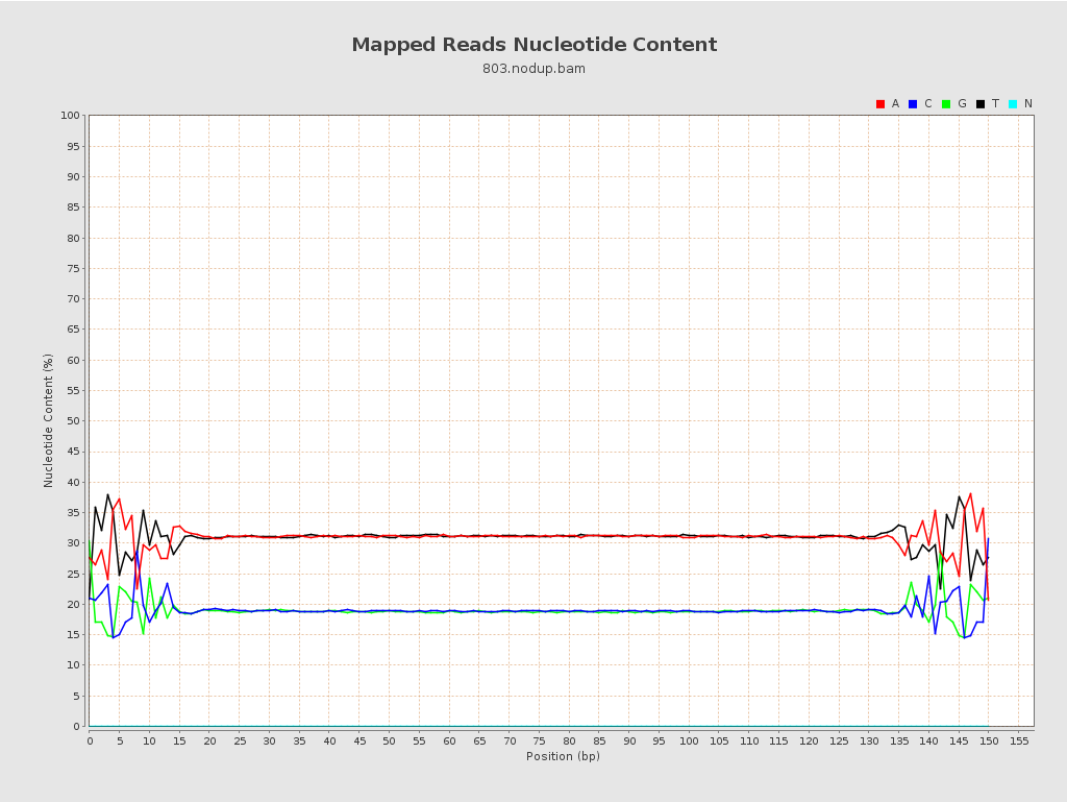
6. Results : Genome Fraction Coverage



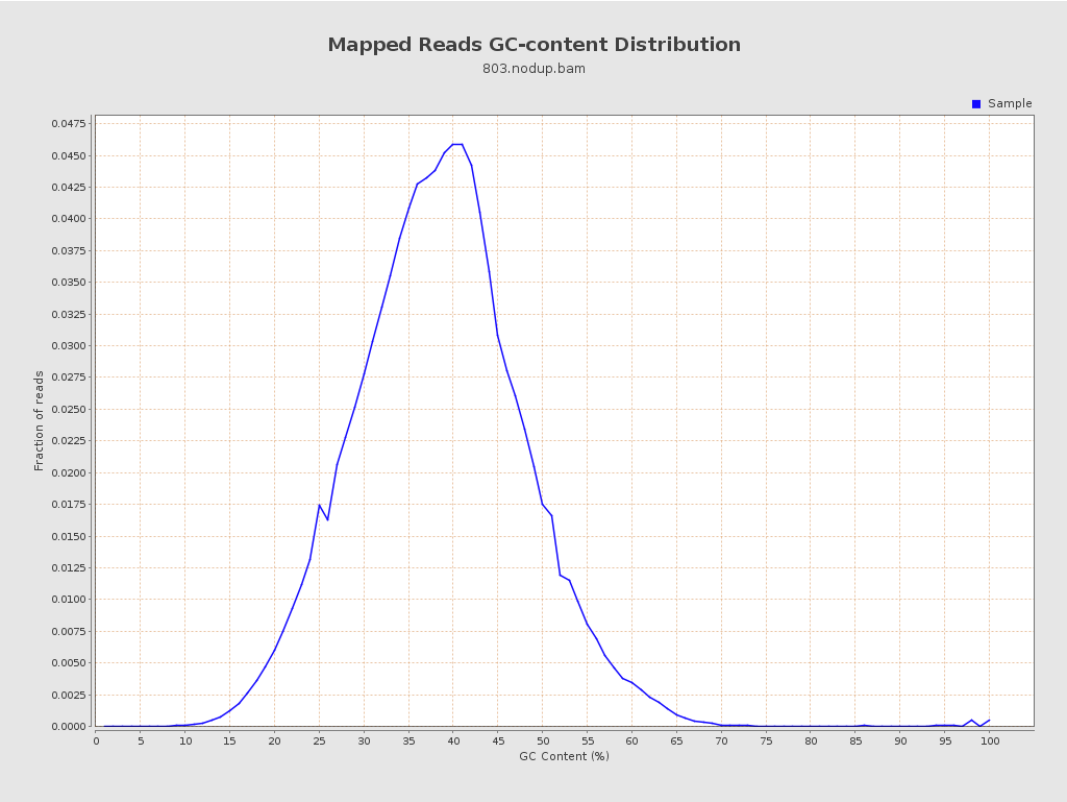
7. Results : Duplication Rate Histogram



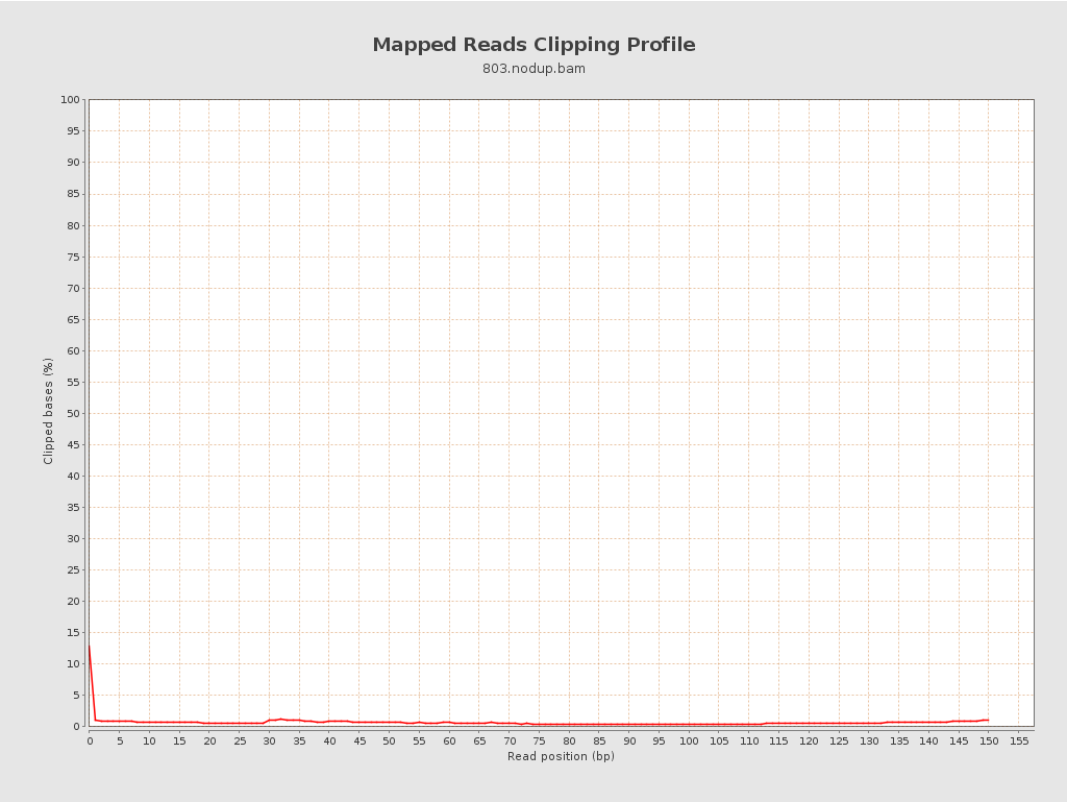
8. Results : Mapped Reads Nucleotide Content



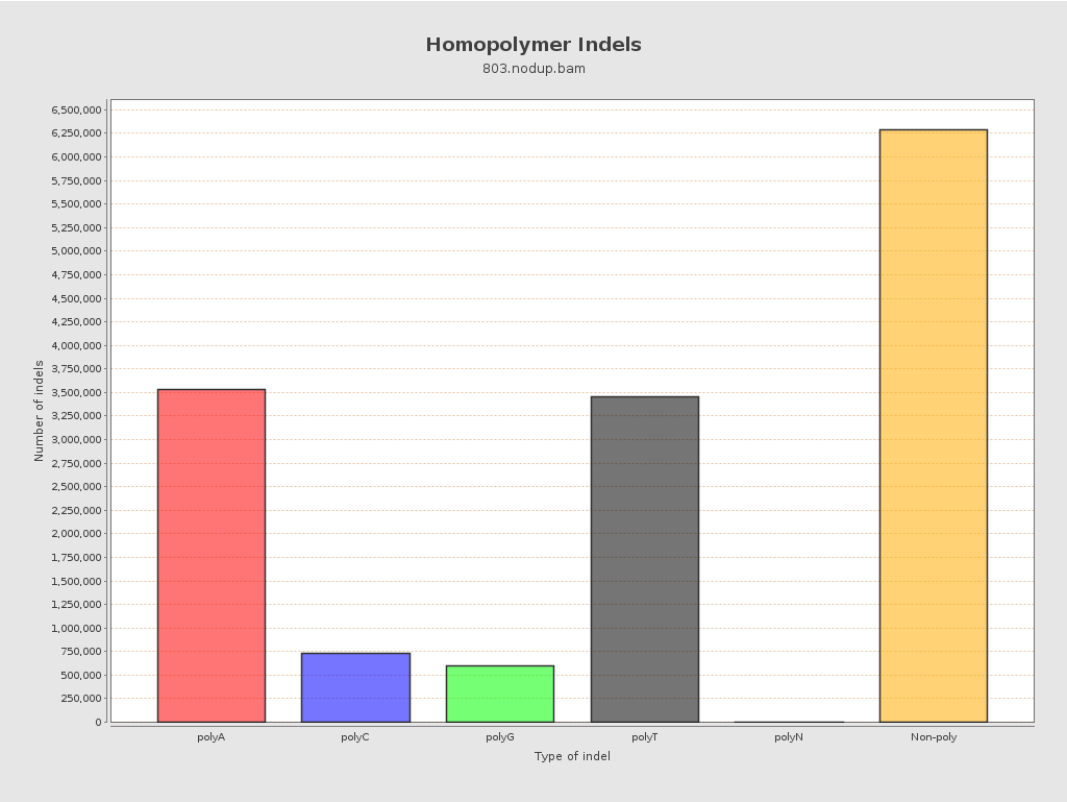
9. Results : Mapped Reads GC-content Distribution



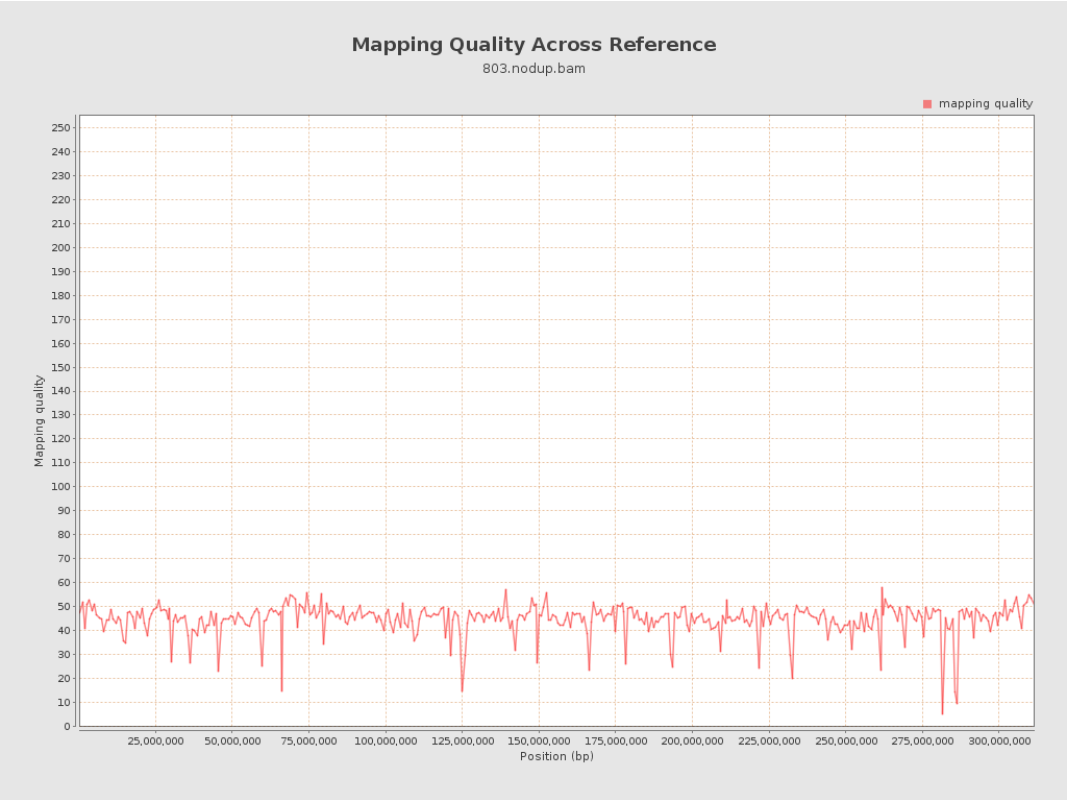
10. Results : Mapped Reads Clipping Profile



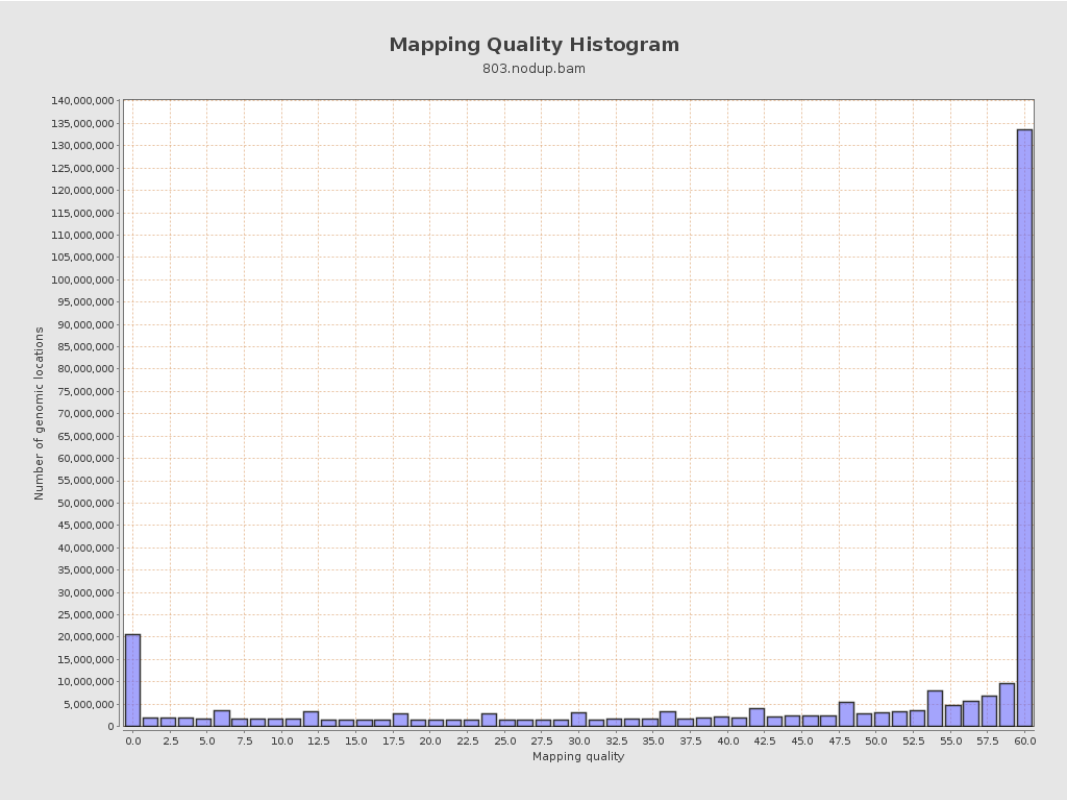
11. Results : Homopolymer Indels



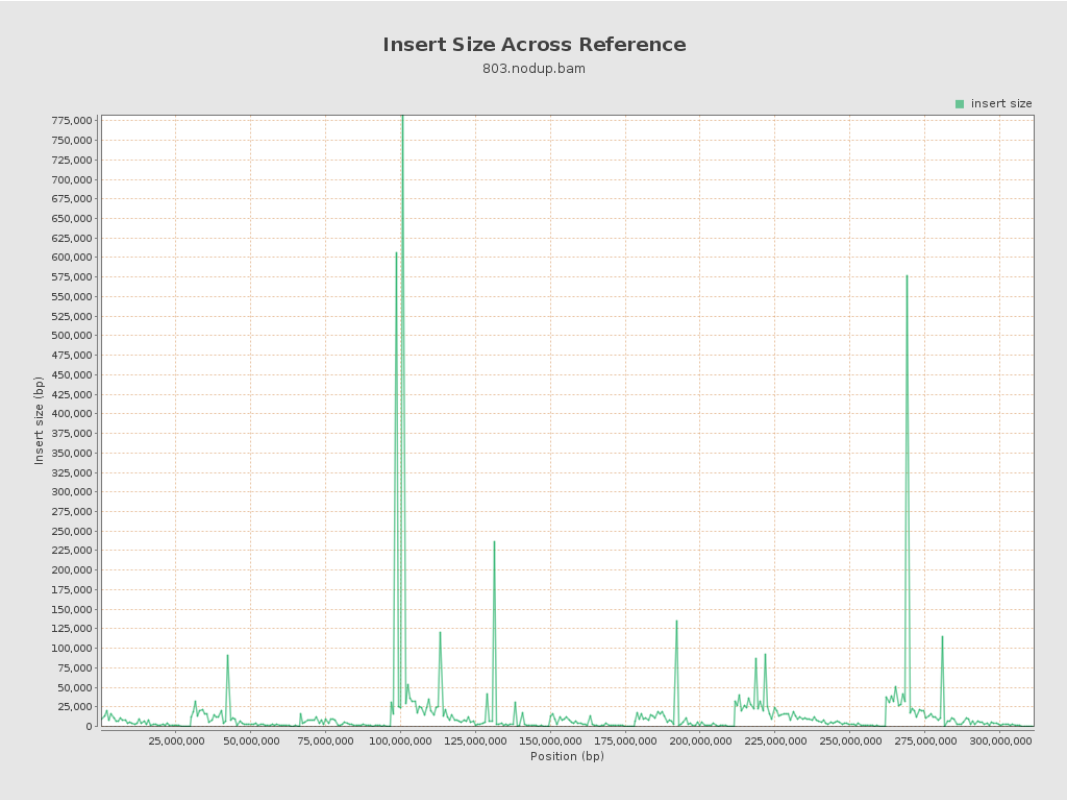
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram