Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:30:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/603.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/603.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_481/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_481_S456_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_481/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_481_S456_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:30:48 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	65,089,020
Mapped reads	59,964,435 / 92.13%
Unmapped reads	5,124,585 / 7.87%
Mapped paired reads	59,964,435 / 92.13%
Mapped reads, first in pair	30,056,844 / 46.18%
Mapped reads, second in pair	29,907,591 / 45.95%
Mapped reads, both in pair	58,486,417 / 89.86%
Mapped reads, singletons	1,478,018 / 2.27%
Read min/max/mean length	30 / 151 / 148.24
Duplicated reads (flagged)	9,213,040 / 14.15%
Clipped reads	13,363,196 / 20.53%

2.2. ACGT Content

Number/percentage of A's	2,570,174,199 / 30.88%
Number/percentage of C's	1,592,169,496 / 19.13%
Number/percentage of T's	2,571,206,231 / 30.9%
Number/percentage of G's	1,588,515,029 / 19.09%
Number/percentage of N's	29,285 / 0%
GC Percentage	38.22%

2.3. Coverage

Mean	26.7742
Standard Deviation	208.1601

2.4. Mapping Quality

Mean Mapping Quality	43.96

2.5. Insert size

Mean	251,448.85
Standard Deviation	2,394,293.41
P25/Median/P75	355 / 463 / 610

2.6. Mismatches and indels

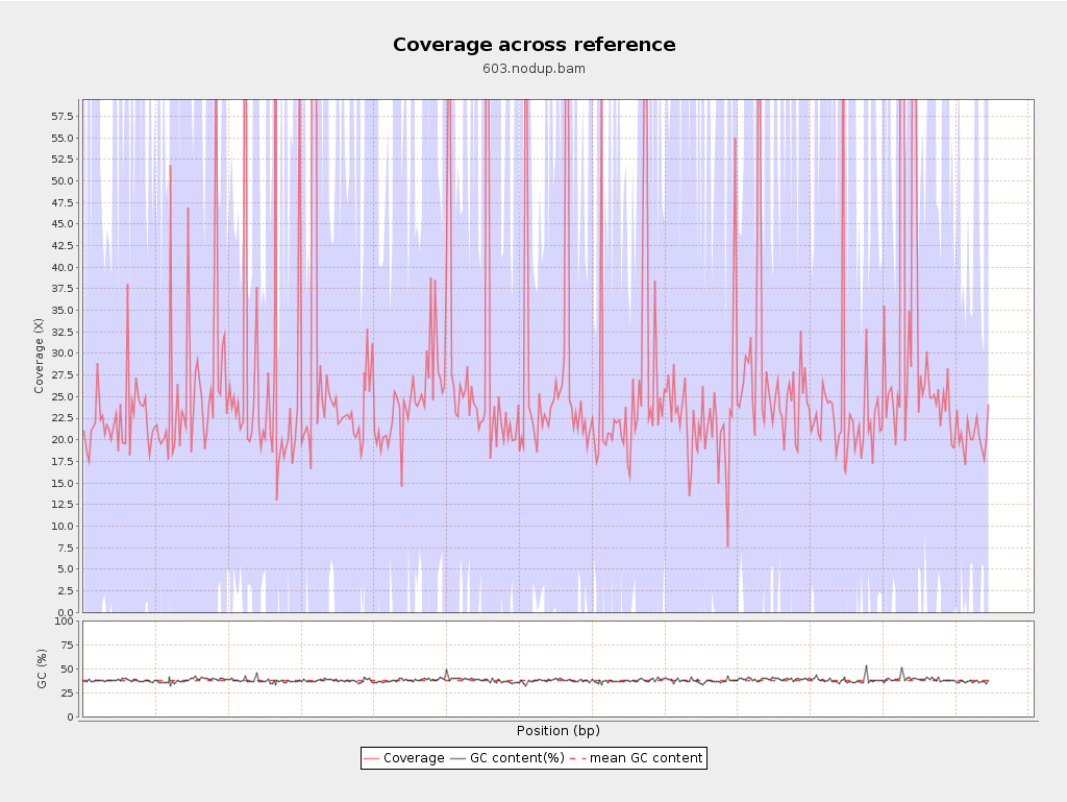
General error rate	2.39%
Mismatches	183,233,453
Insertions	5,744,651
Mapped reads with at least one insertion	8.59%
Deletions	5,827,516
Mapped reads with at least one deletion	8.64%
Homopolymer indels	56.85%

2.7. Chromosome stats

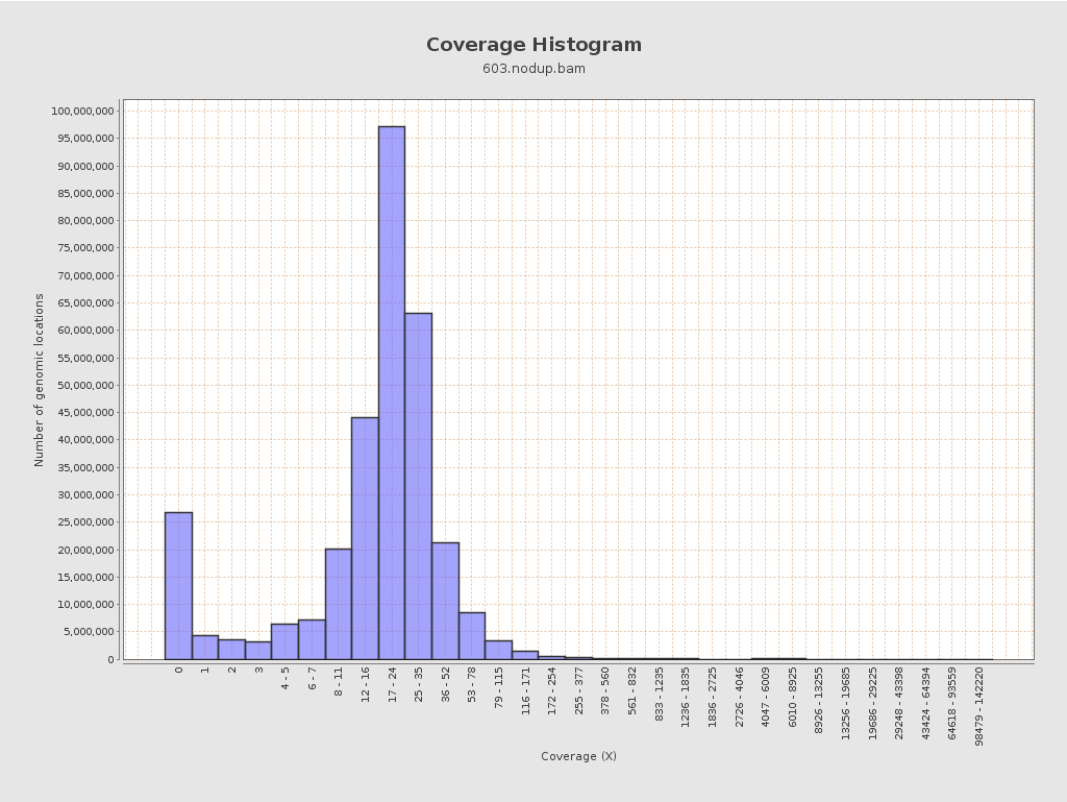
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	654024845	22.003	69.6818

LT669789.1	36598175	1006693735	27.5067	224.2262
LT669790.1	30422129	893080351	29.3563	252.2904
LT669791.1	52758100	1396601167	26.4718	200.3034
LT669792.1	28376109	750588869	26.4514	244.2079
LT669793.1	33388210	846393067	25.3501	159.8893
LT669794.1	50579949	1303827667	25.7776	198.7326
LT669795.1	49795044	1492761952	29.9781	242.2049

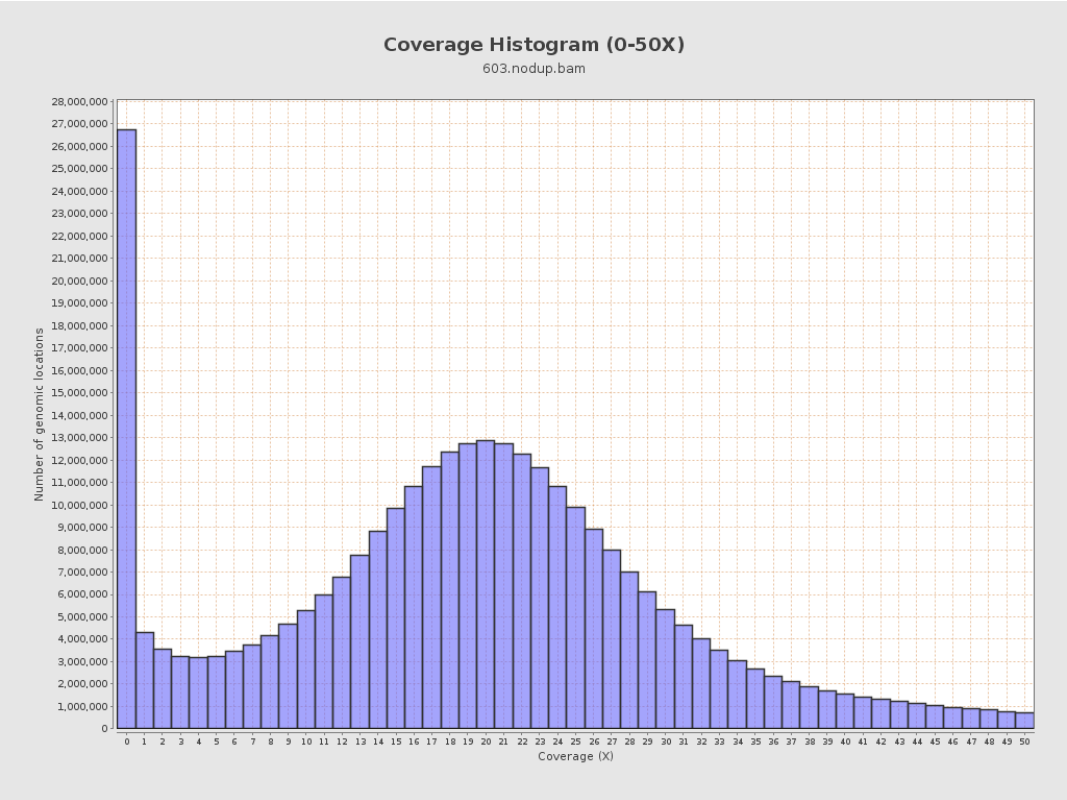
3. Results : Coverage across reference



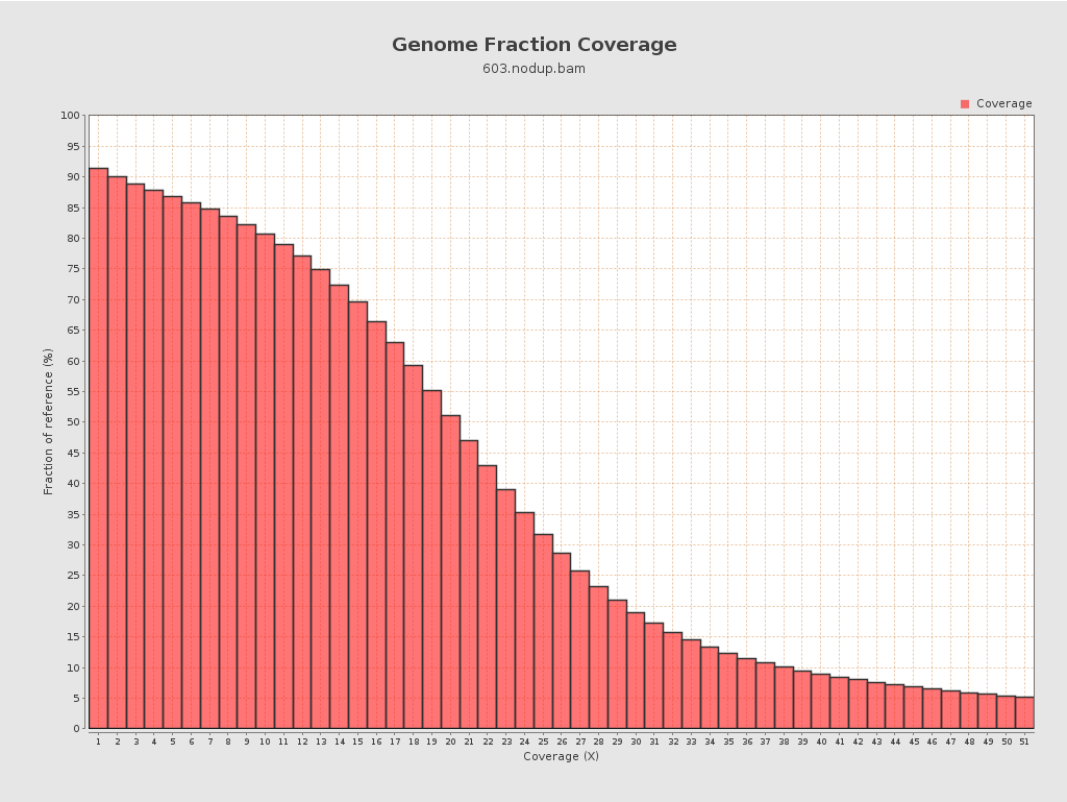
4. Results : Coverage Histogram



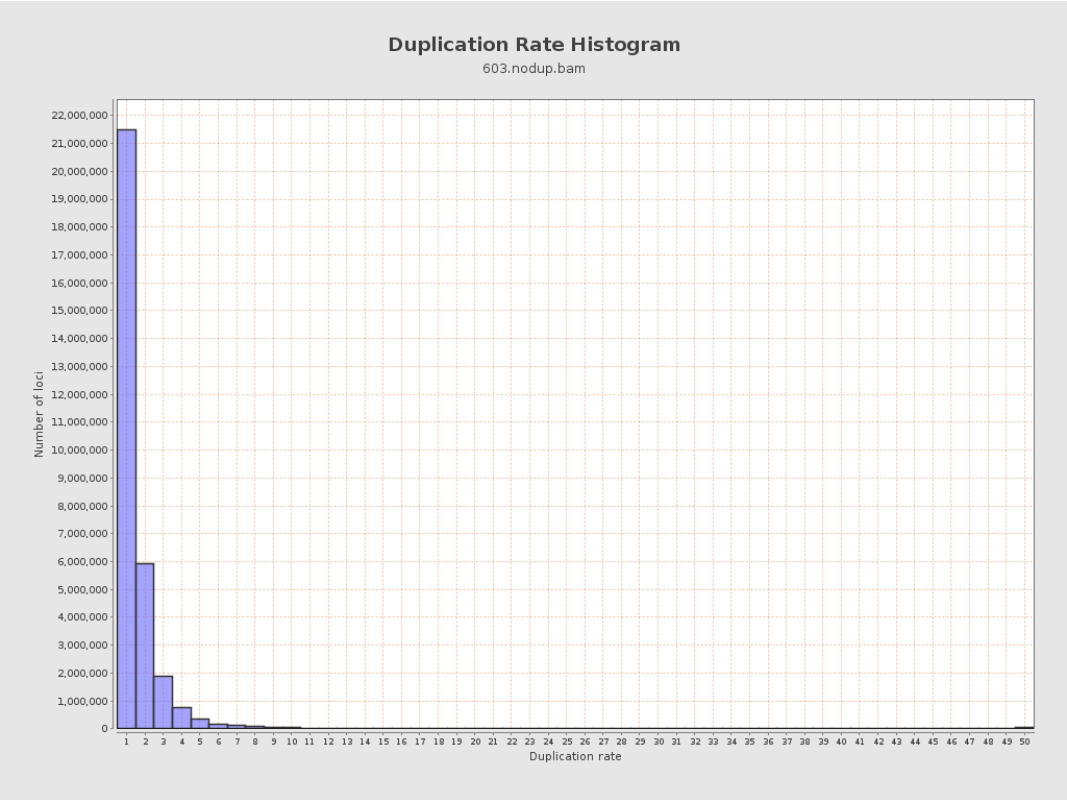
5. Results : Coverage Histogram (0-50X)



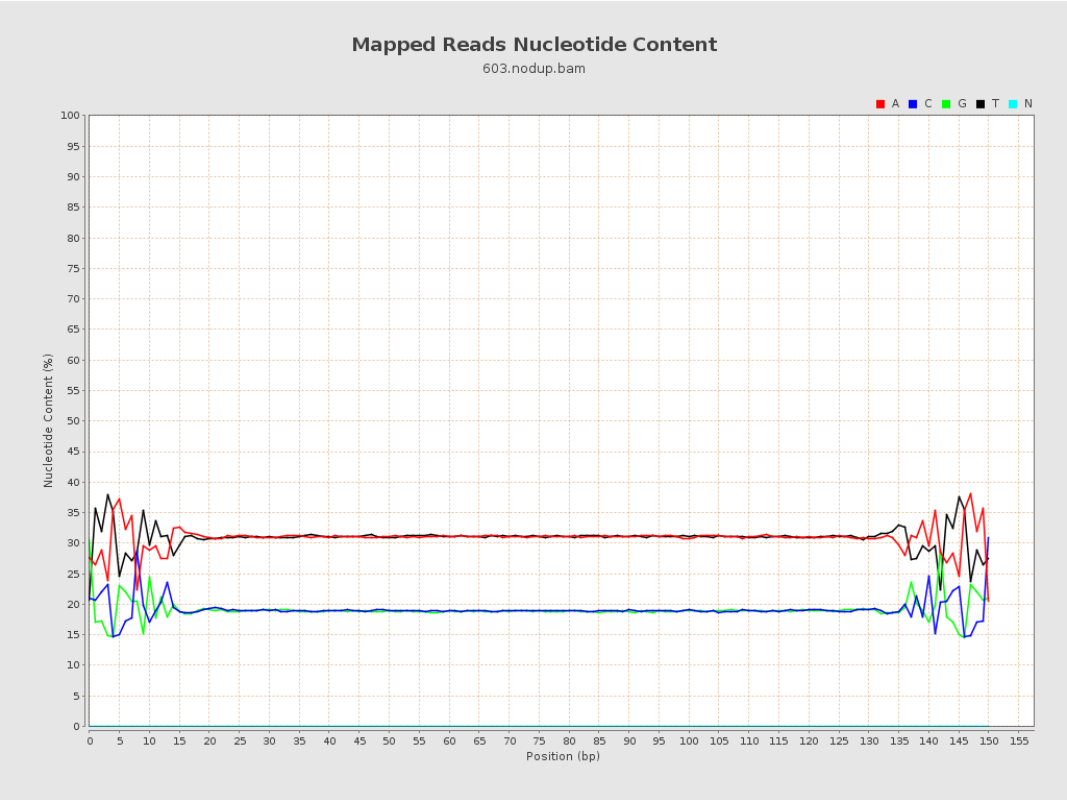
6. Results : Genome Fraction Coverage



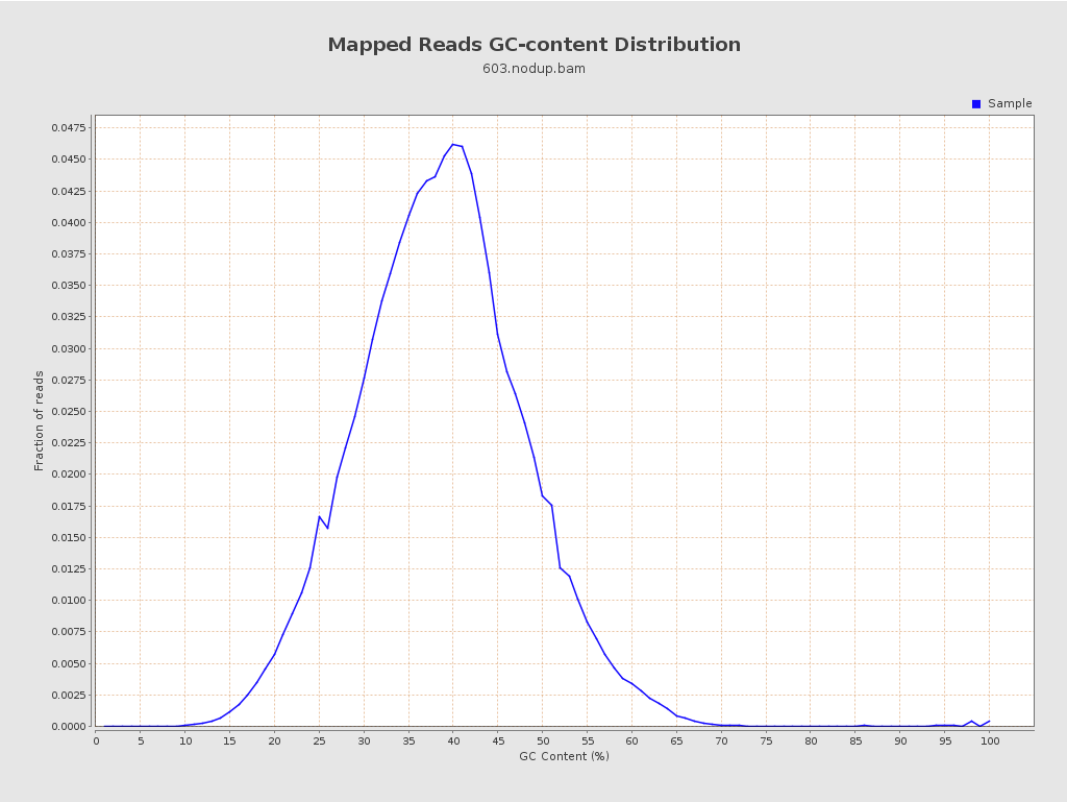
7. Results : Duplication Rate Histogram



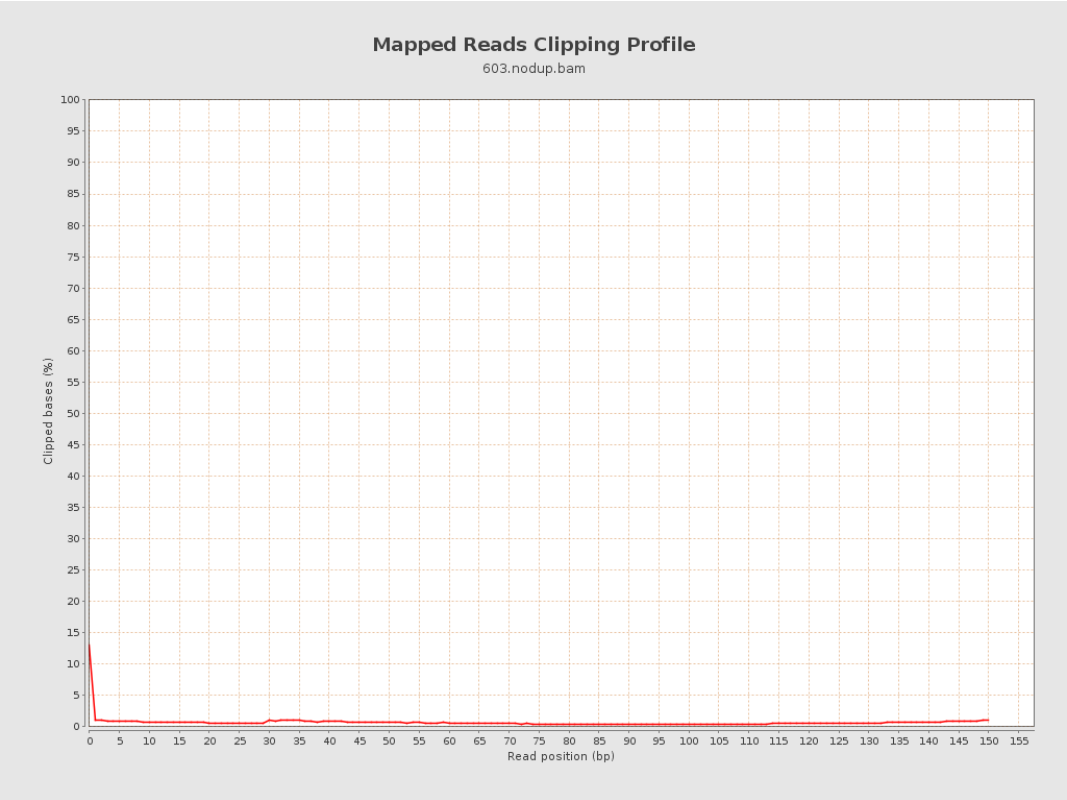
8. Results : Mapped Reads Nucleotide Content



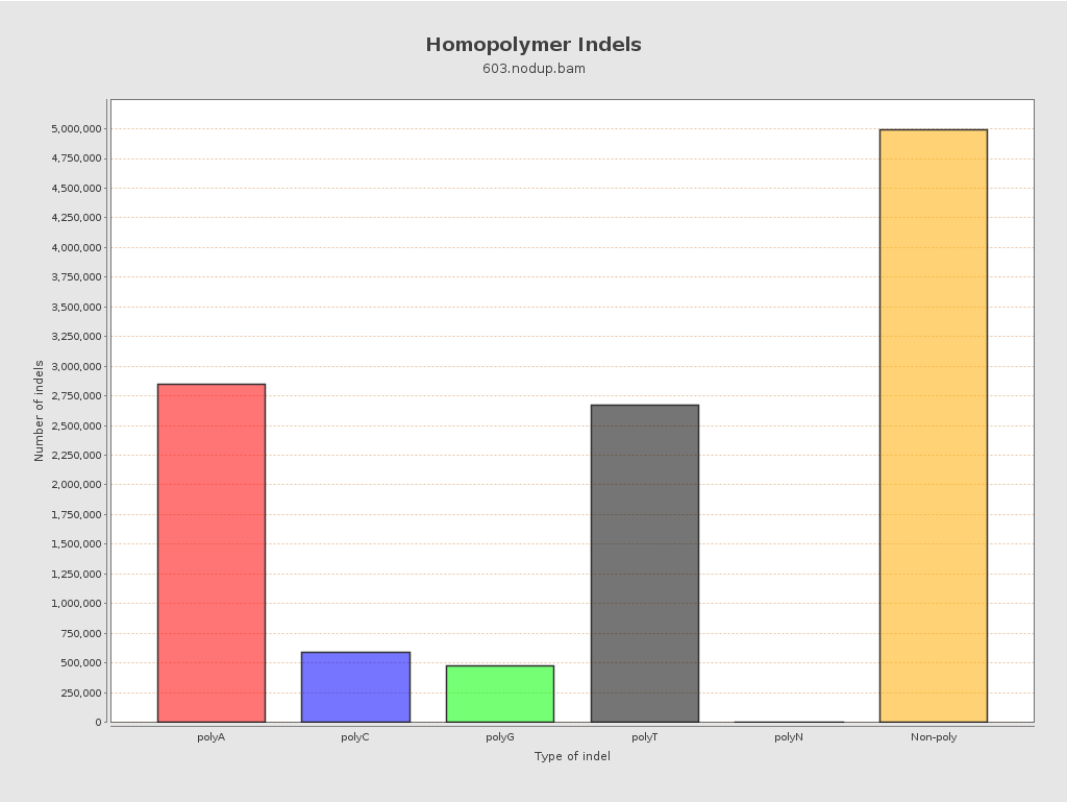
9. Results : Mapped Reads GC-content Distribution



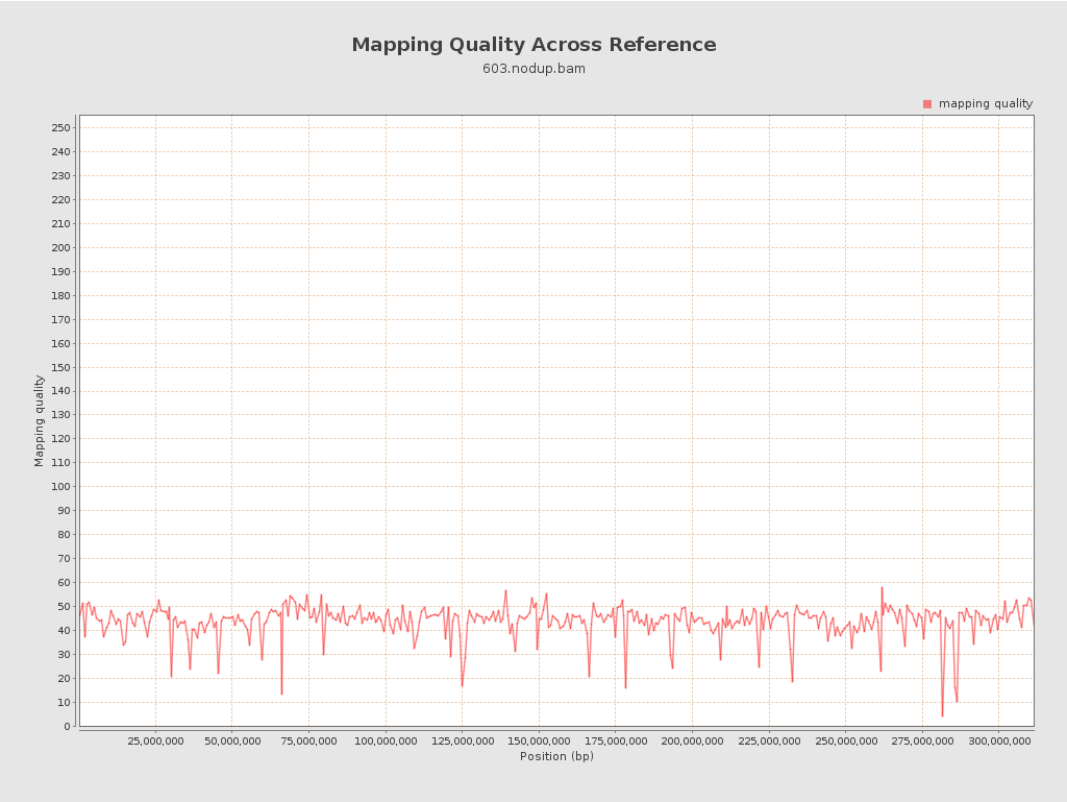
10. Results : Mapped Reads Clipping Profile



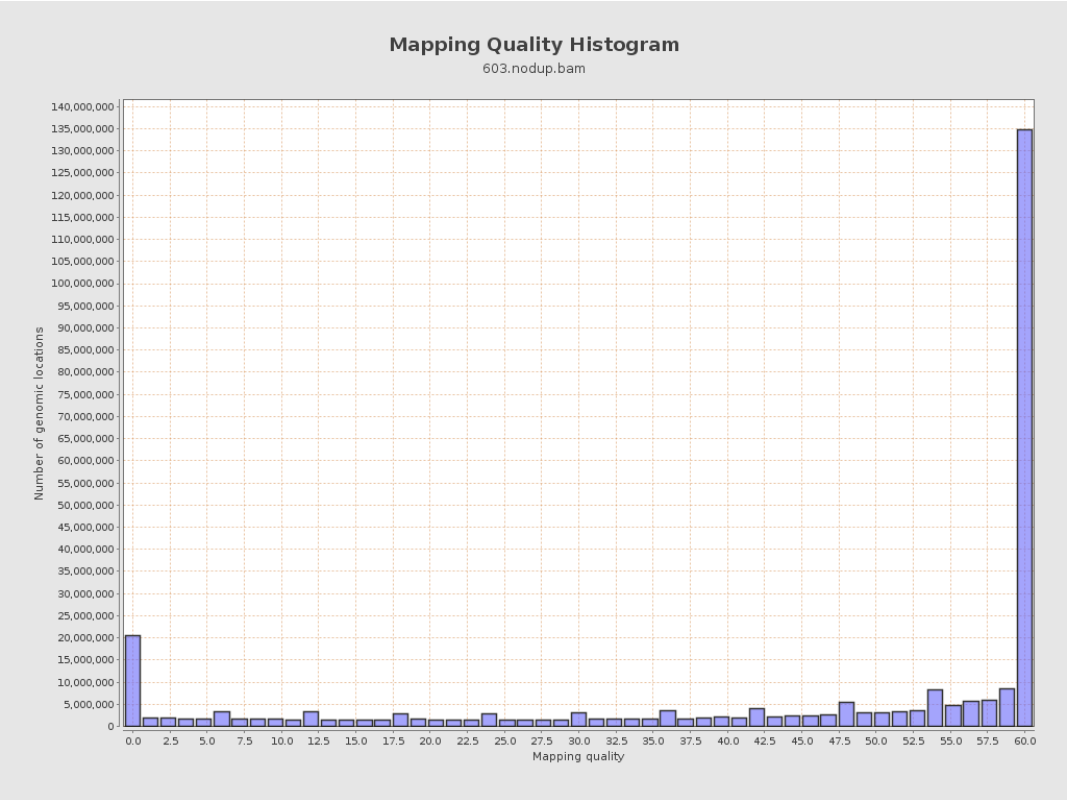
11. Results : Homopolymer Indels



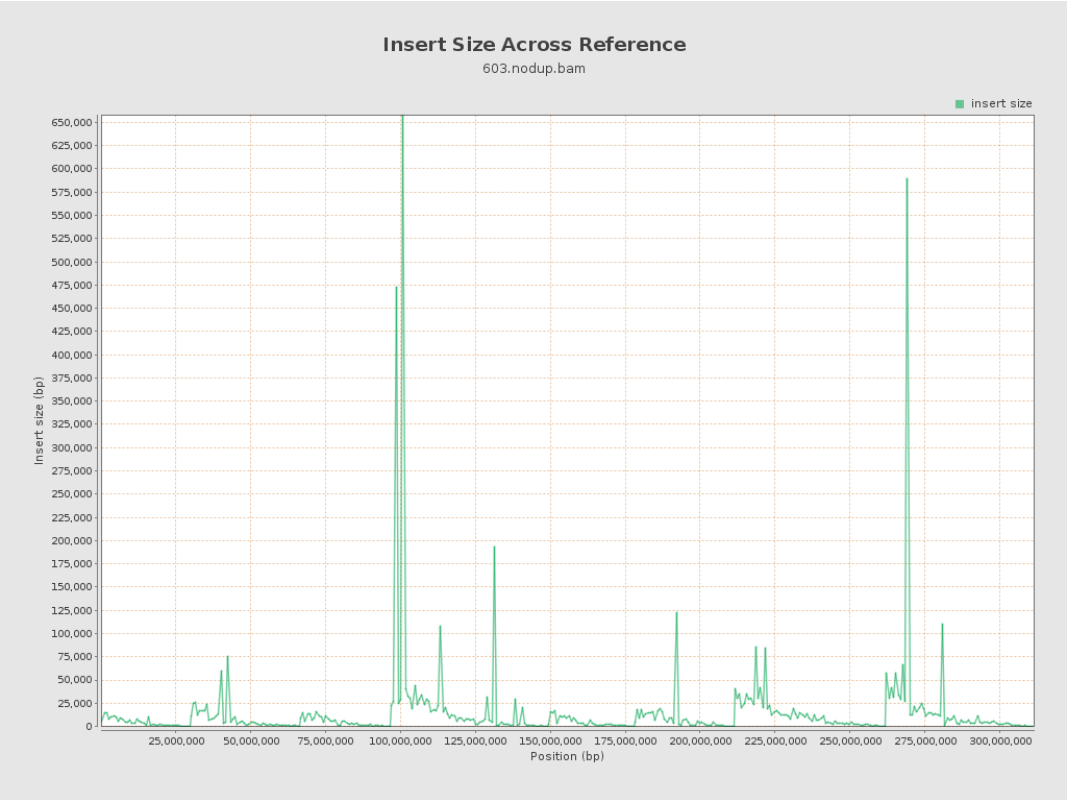
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram