Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:29:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1001
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1001 .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_585/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_585_S152_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_585/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_585_S152_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:29:03 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	56,835,085
Mapped reads	54,215,642 / 95.39%
Unmapped reads	2,619,443 / 4.61%
Mapped paired reads	54,215,642 / 95.39%
Mapped reads, first in pair	27,202,071 / 47.86%
Mapped reads, second in pair	27,013,571 / 47.53%
Mapped reads, both in pair	53,293,936 / 93.77%
Mapped reads, singletons	921,706 / 1.62%
Read min/max/mean length	30 / 151 / 148.05
Duplicated reads (flagged)	7,356,144 / 12.94%
Clipped reads	12,828,750 / 22.57%

2.2. ACGT Content

Number/percentage of A's	2,310,378,197 / 30.81%
Number/percentage of C's	1,440,385,943 / 19.21%
Number/percentage of T's	2,312,546,052 / 30.84%
Number/percentage of G's	1,436,244,151 / 19.15%
Number/percentage of N's	53,172 / 0%
GC Percentage	38.36%

2.3. Coverage

Mean	24.1243
Standard Deviation	192.4818

2.4. Mapping Quality

Mean Mapping Quality	44.05

2.5. Insert size

Mean	214,604.1
Standard Deviation	2,187,368.66
P25/Median/P75	325 / 431 / 560

2.6. Mismatches and indels

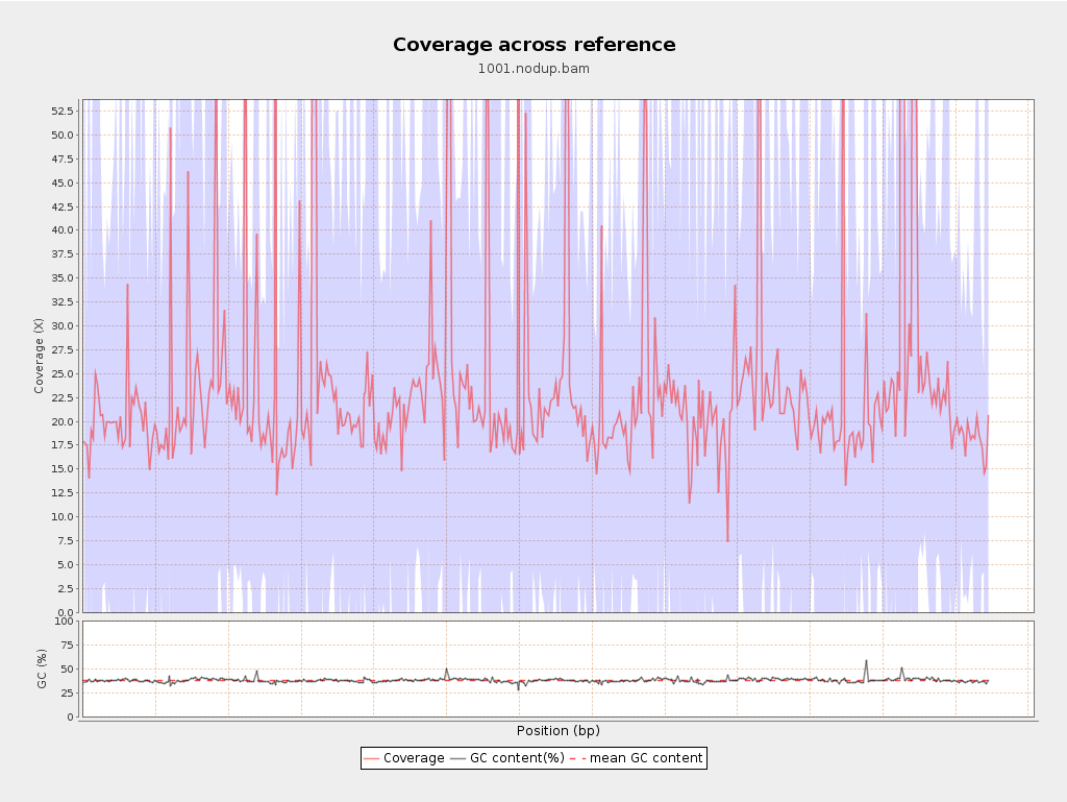
General error rate	2.5%
Mismatches	174,249,363
Insertions	4,813,142
Mapped reads with at least one insertion	8.02%
Deletions	4,992,970
Mapped reads with at least one deletion	8.18%
Homopolymer indels	55.43%

2.7. Chromosome stats

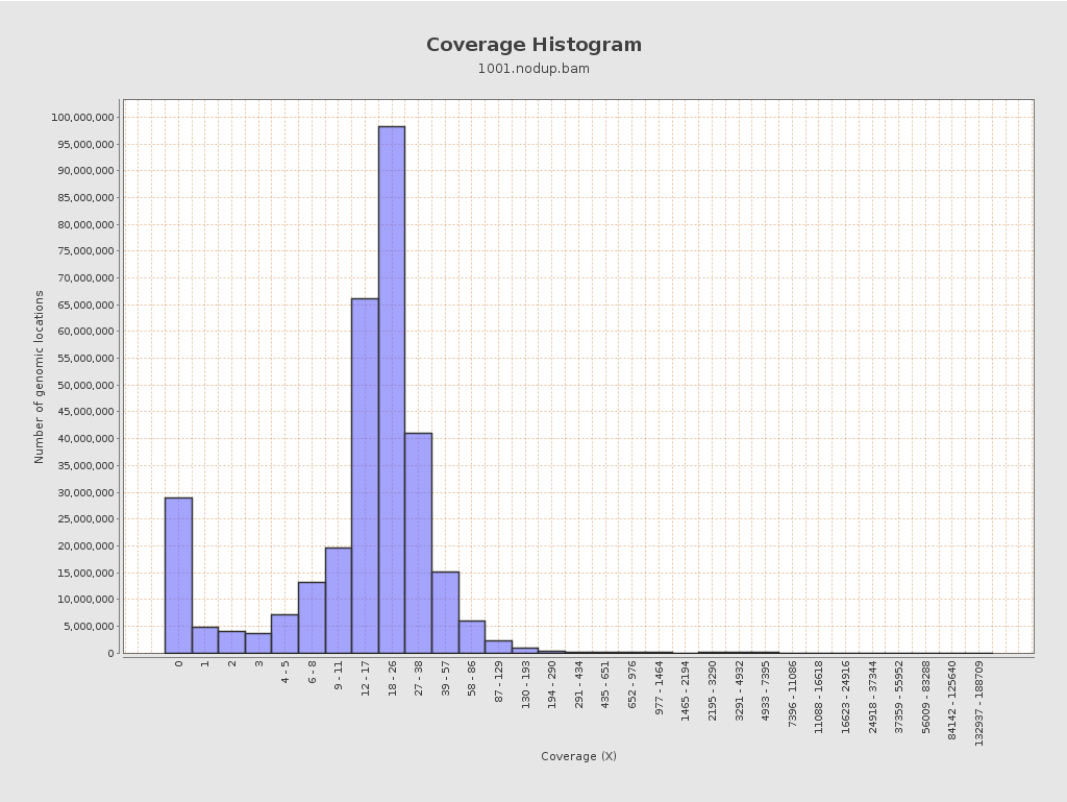
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	586320269	19.7253	67.6294

LT669789.1	36598175	910402148	24.8756	214.9193
LT669790.1	30422129	746888750	24.5508	146.36
LT669791.1	52758100	1246668706	23.6299	174.6668
LT669792.1	28376109	671401885	23.6608	196.8179
LT669793.1	33388210	743657142	22.273	99.8524
LT669794.1	50579949	1177018111	23.2704	185.138
LT669795.1	49795044	1435795110	28.8341	293.5442

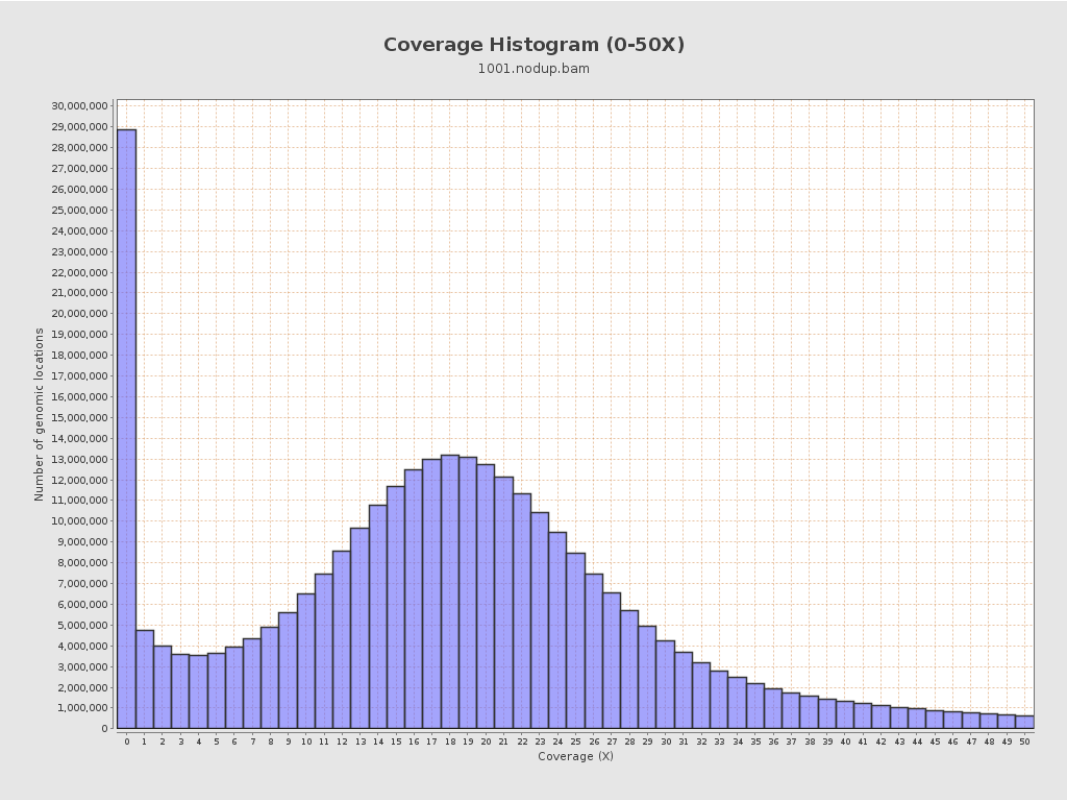
3. Results : Coverage across reference



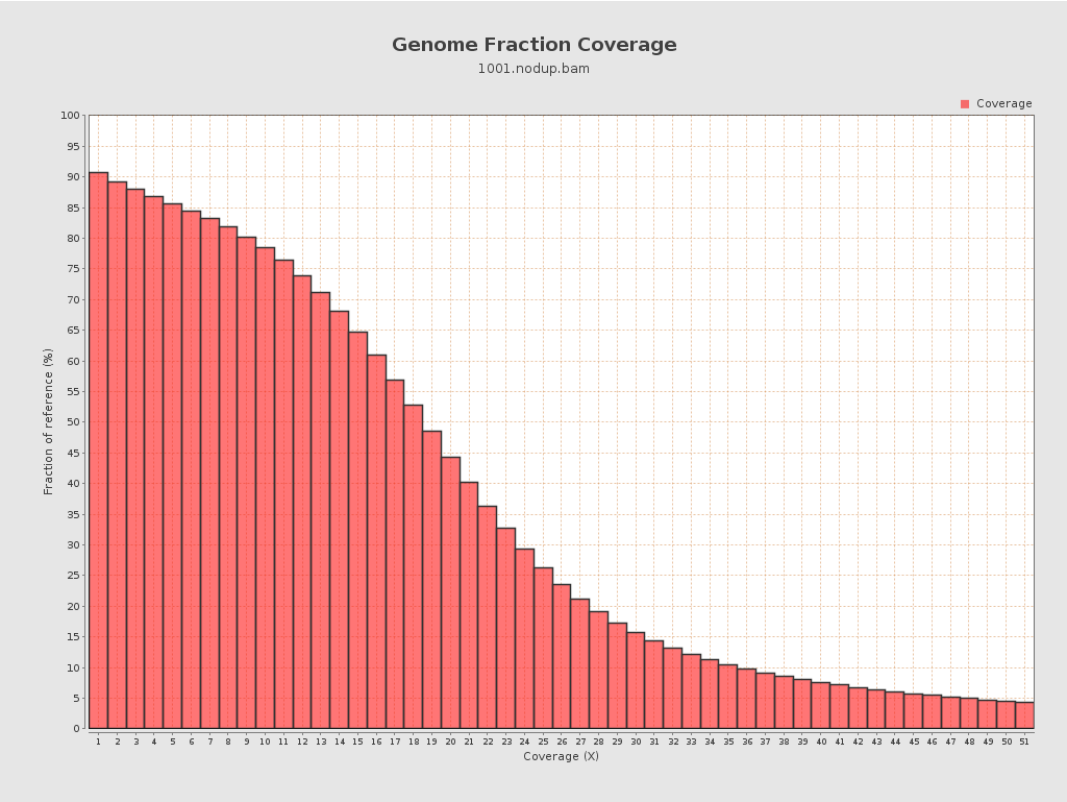
4. Results : Coverage Histogram



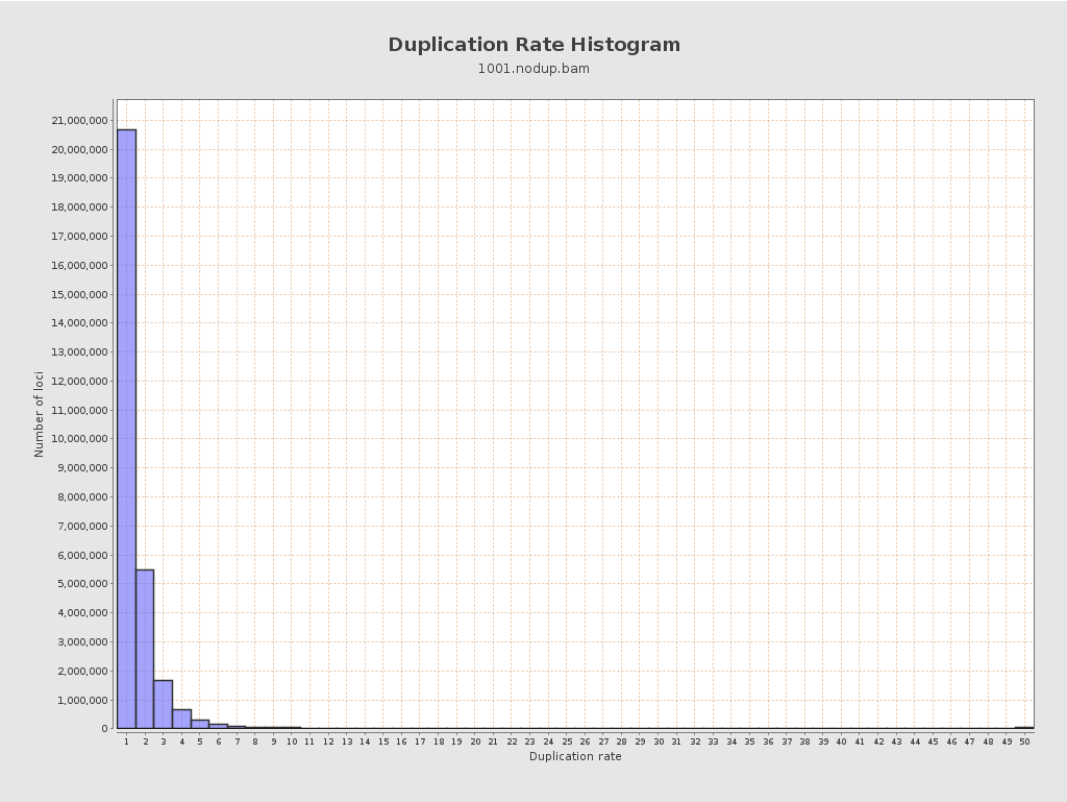
5. Results : Coverage Histogram (0-50X)



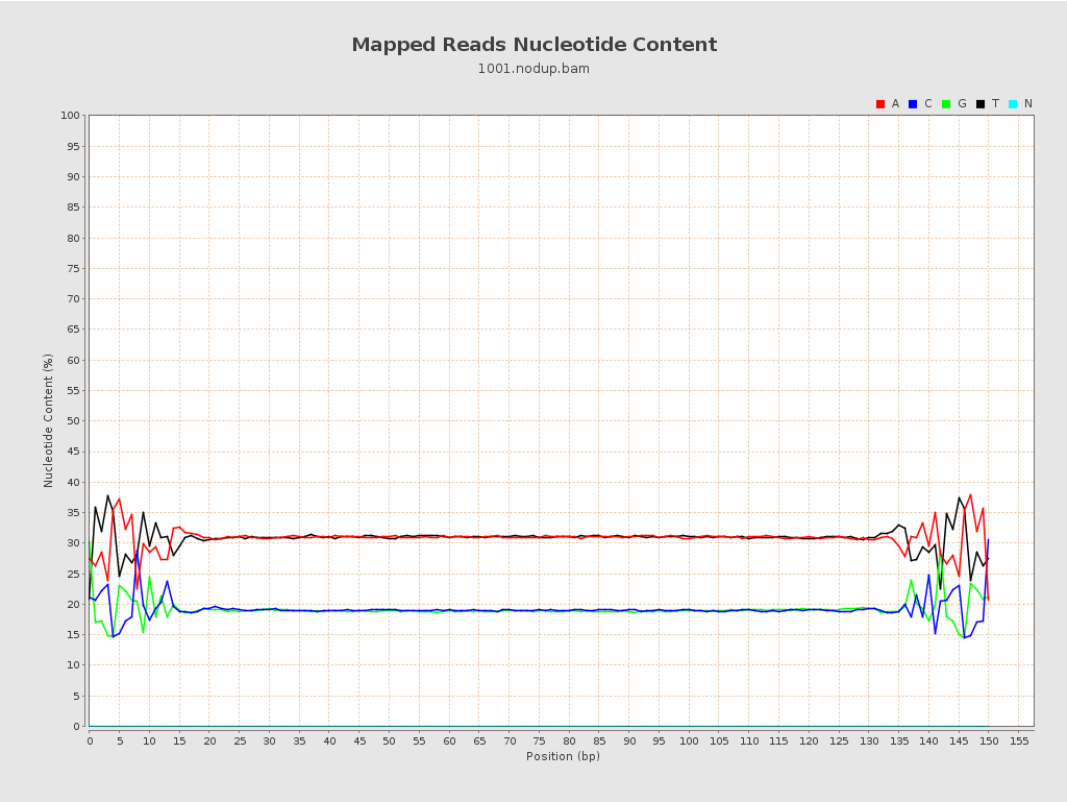
6. Results : Genome Fraction Coverage



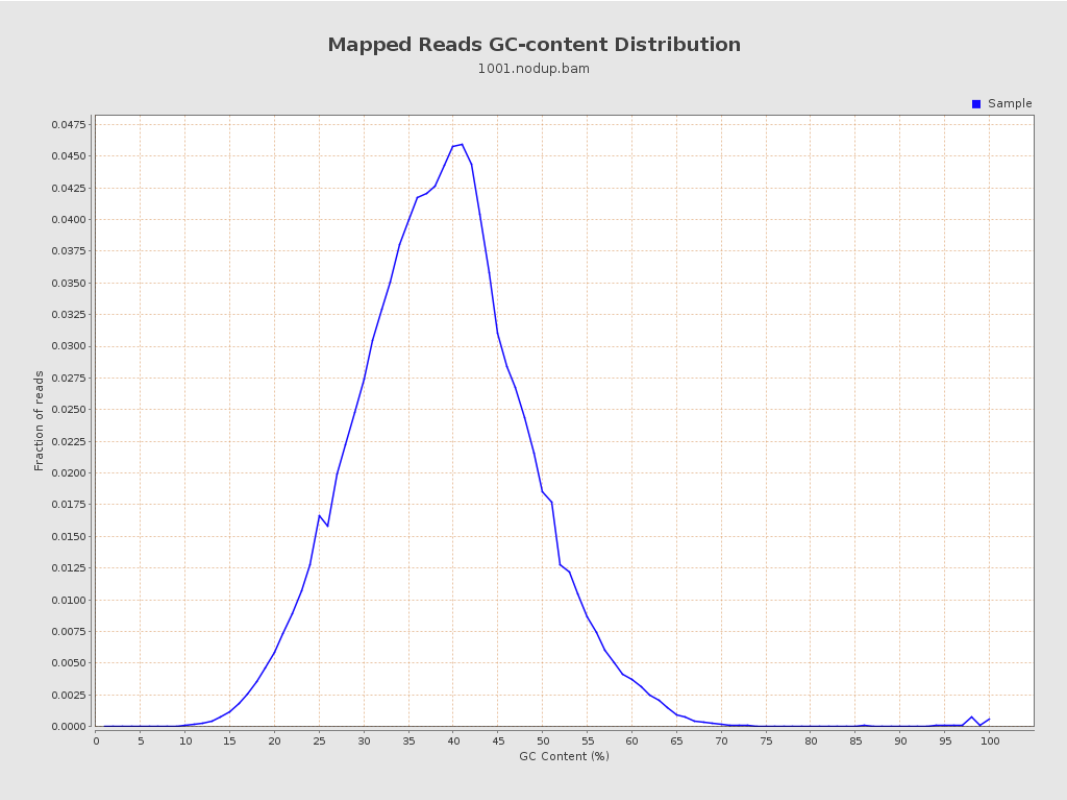
7. Results : Duplication Rate Histogram



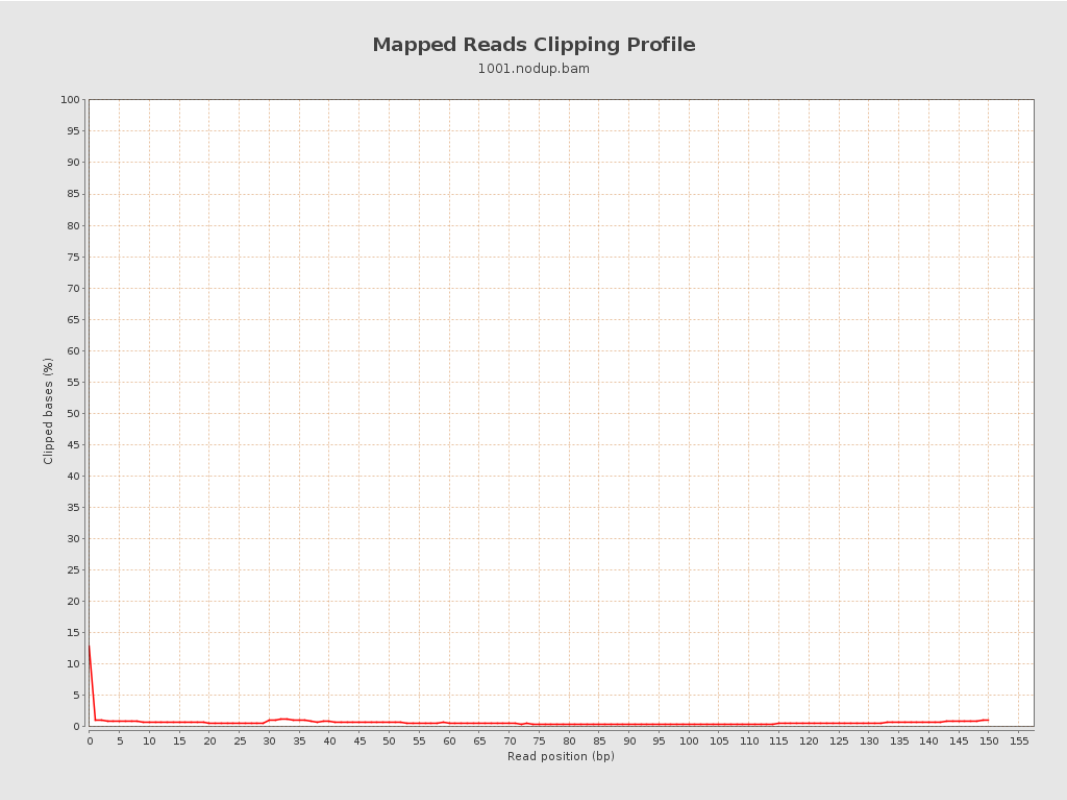
8. Results : Mapped Reads Nucleotide Content



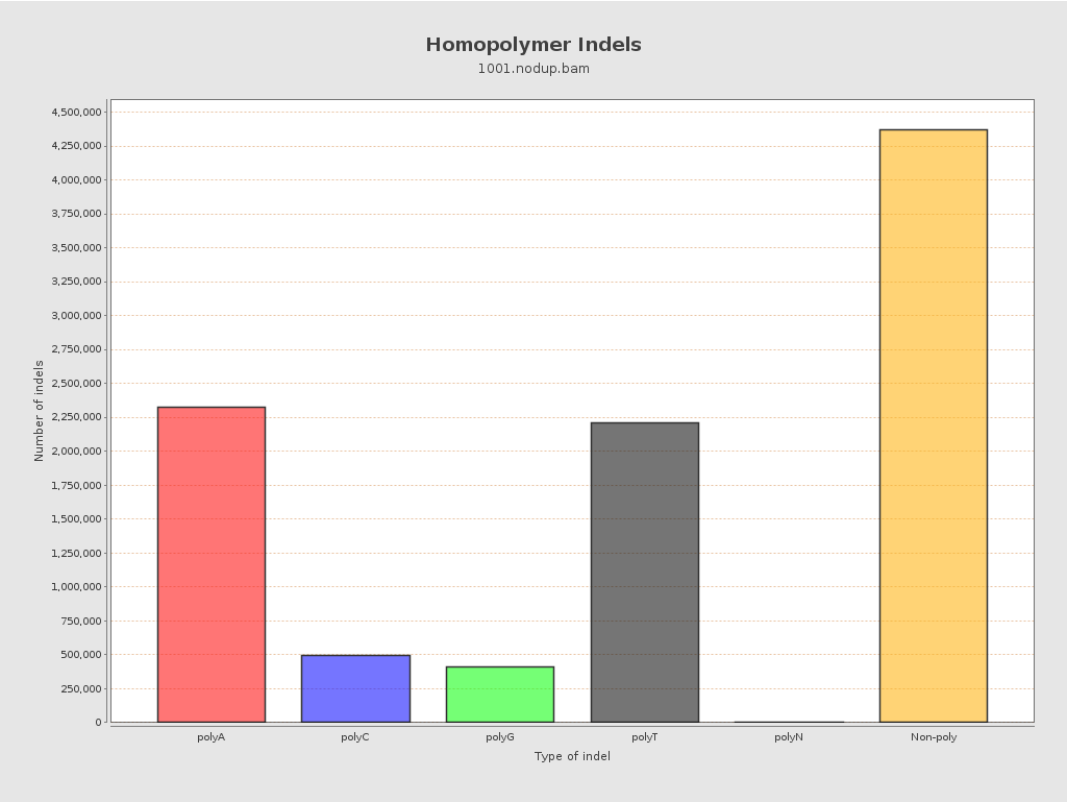
9. Results : Mapped Reads GC-content Distribution



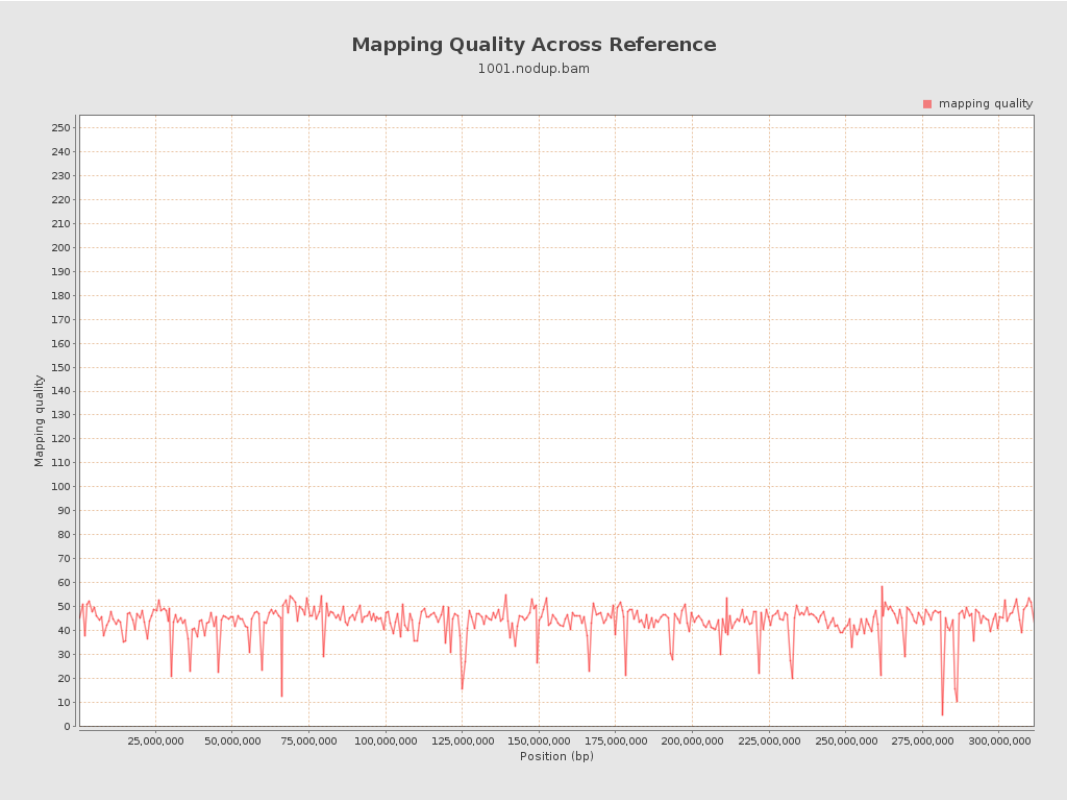
10. Results : Mapped Reads Clipping Profile



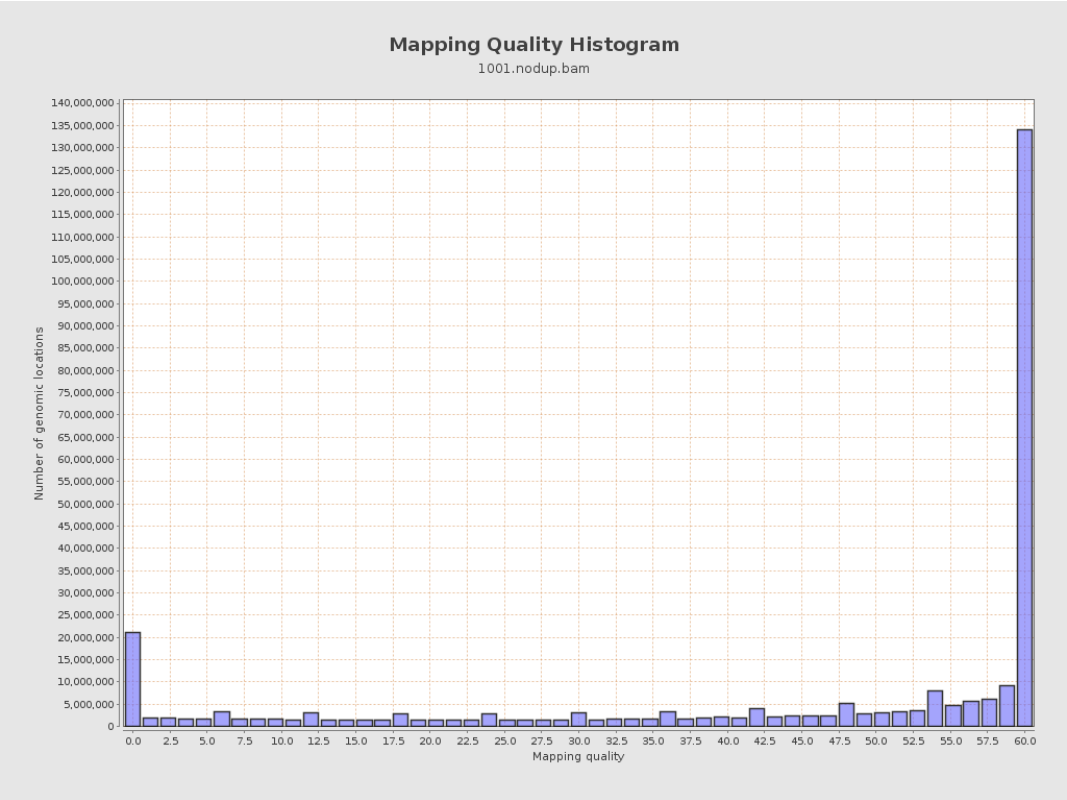
11. Results : Homopolymer Indels



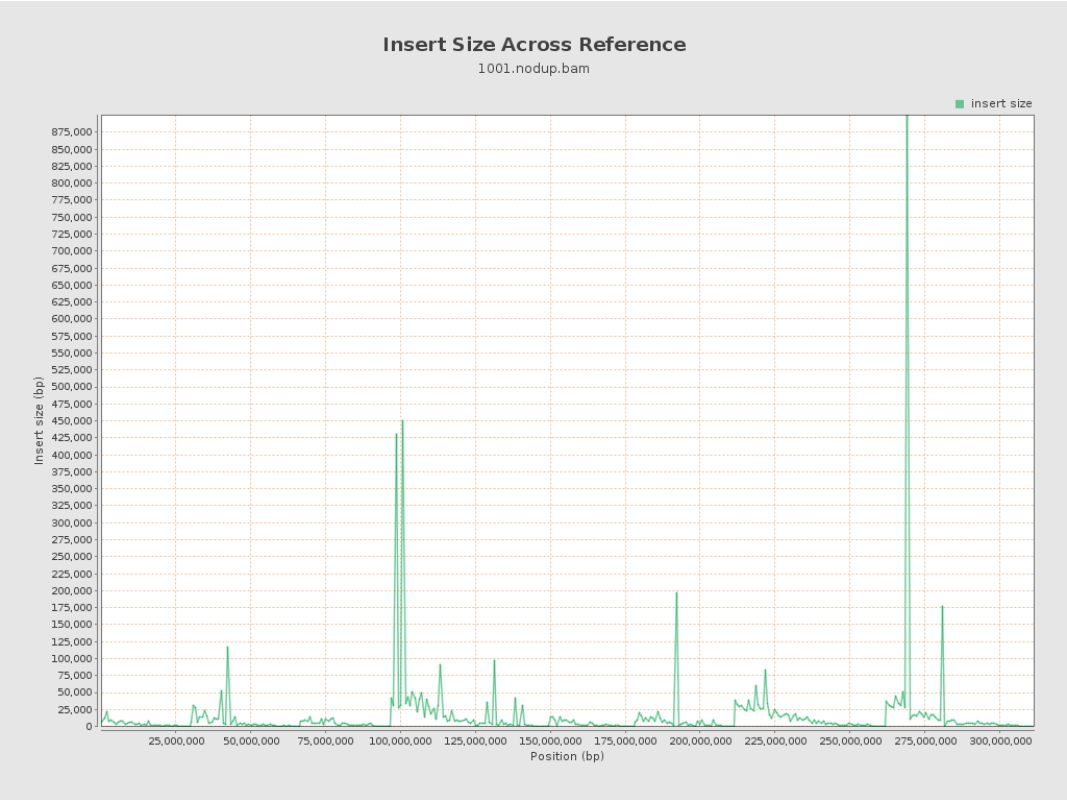
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram