Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:34:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/874.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/874.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_129/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_129_S219_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_129/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_129_S219_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:34:57 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	78,156,289
Mapped reads	70,981,147 / 90.82%
Unmapped reads	7,175,142 / 9.18%
Mapped paired reads	70,981,147 / 90.82%
Mapped reads, first in pair	35,521,090 / 45.45%
Mapped reads, second in pair	35,460,057 / 45.37%
Mapped reads, both in pair	68,864,895 / 88.11%
Mapped reads, singletons	2,116,252 / 2.71%
Read min/max/mean length	30 / 151 / 148.24
Duplicated reads (flagged)	13,965,639 / 17.87%
Clipped reads	16,220,225 / 20.75%

2.2. ACGT Content

Number/percentage of A's	3,030,984,898 / 31.05%
Number/percentage of C's	1,850,725,042 / 18.96%
Number/percentage of T's	3,031,955,447 / 31.06%
Number/percentage of G's	1,848,341,890 / 18.93%
Number/percentage of N's	41,026 / 0%
GC Percentage	37.89%

2.3. Coverage

Mean	31.4035
Standard Deviation	300.0294

2.4. Mapping Quality

Mean Mapping Quality	44.89

2.5. Insert size

Mean	238,337.77
Standard Deviation	2,360,882.6
P25/Median/P75	297 / 388 / 505

2.6. Mismatches and indels

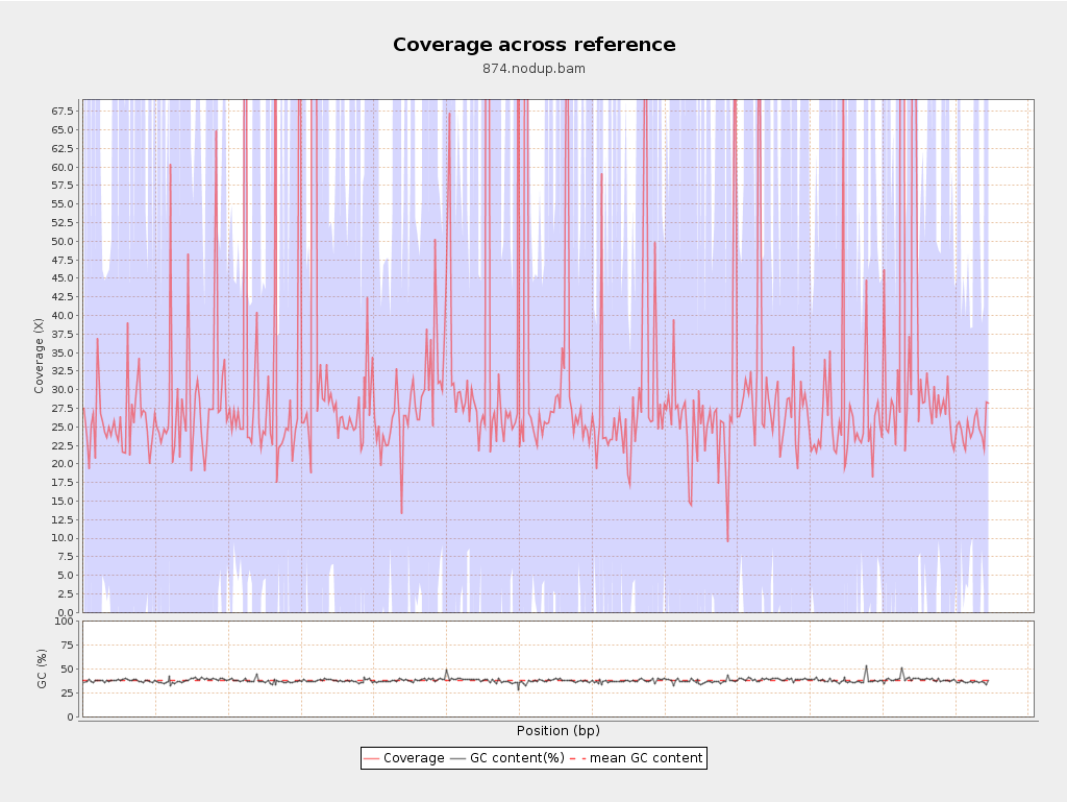
General error rate	2.27%
Mismatches	201,905,089
Insertions	7,105,133
Mapped reads with at least one insertion	8.91%
Deletions	6,641,103
Mapped reads with at least one deletion	8.31%
Homopolymer indels	58.04%

2.7. Chromosome stats

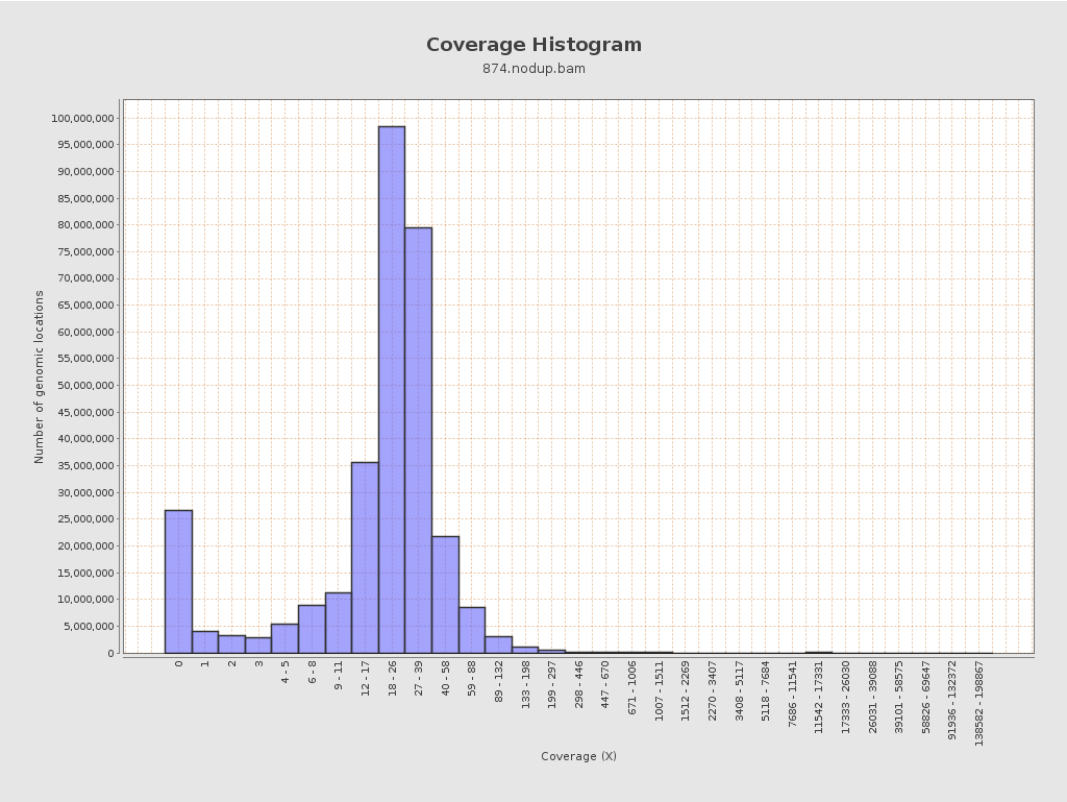
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	759226109	25.5422	120.2582

LT669789.1	36598175	1137243119	31.0738	312.0213
LT669790.1	30422129	1205073634	39.6117	456.3264
LT669791.1	52758100	1651235798	31.2982	329.6887
LT669792.1	28376109	901767574	31.7791	308.9982
LT669793.1	33388210	946649757	28.3528	191.7033
LT669794.1	50579949	1456984437	28.8056	227.7375
LT669795.1	49795044	1728463661	34.7116	330.1294

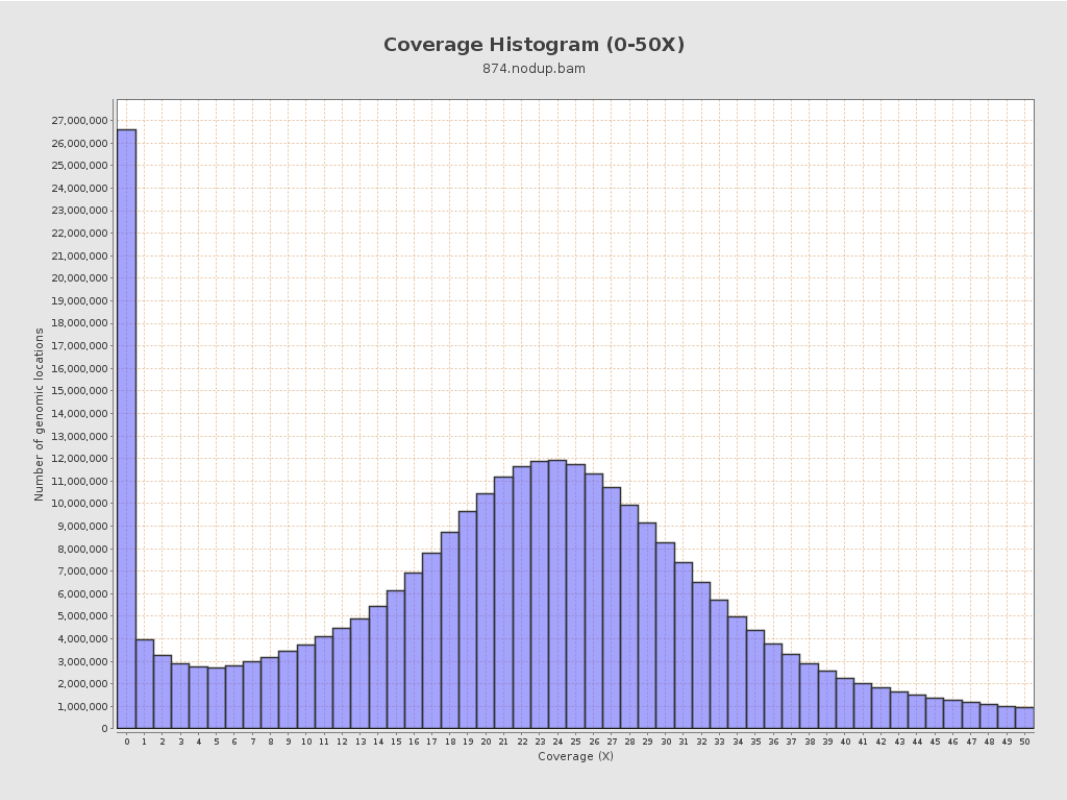
3. Results : Coverage across reference



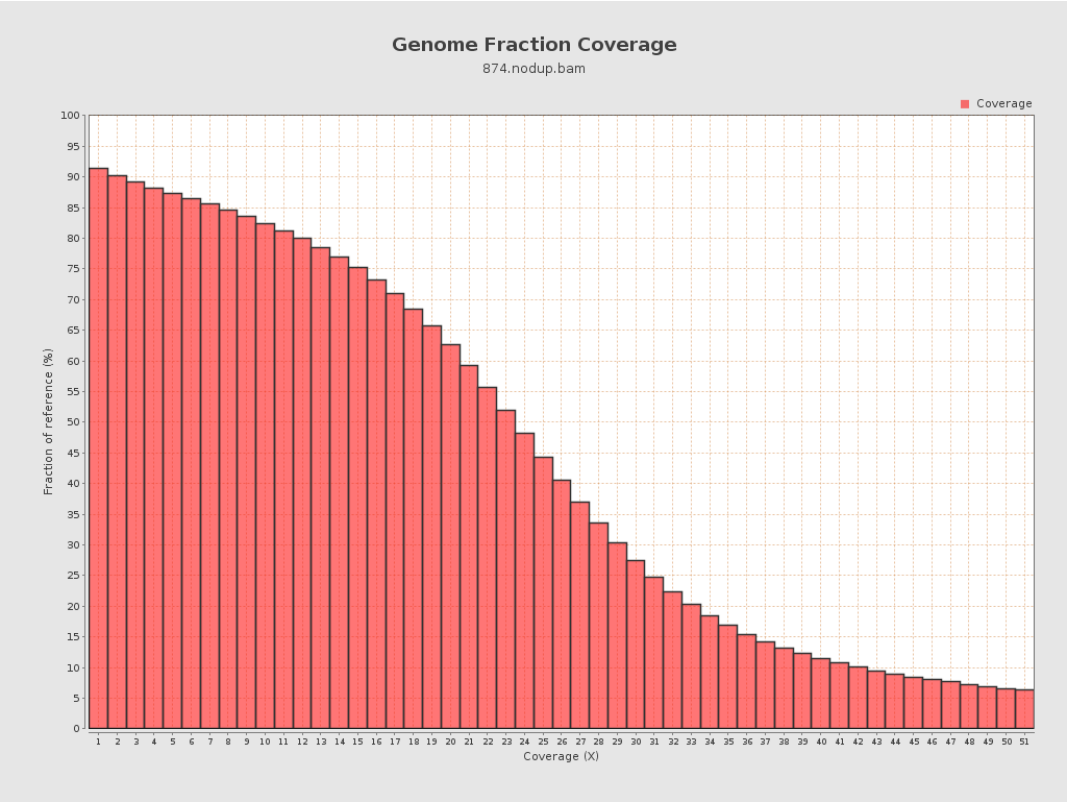
4. Results : Coverage Histogram



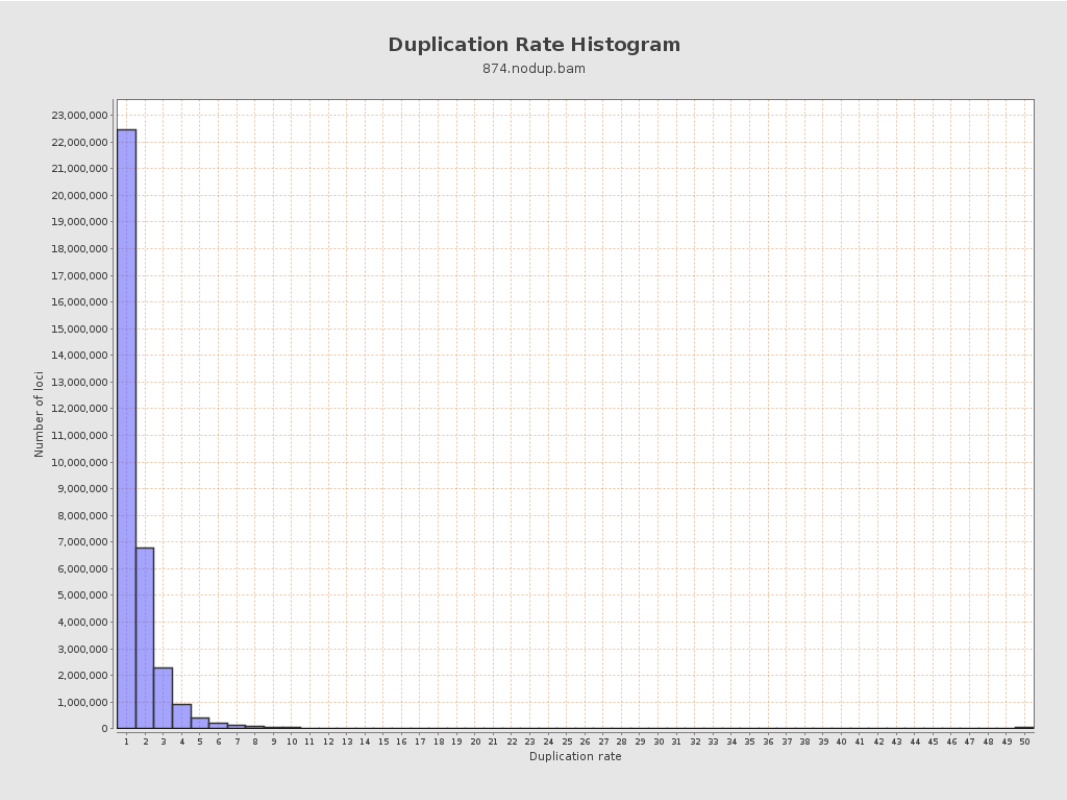
5. Results : Coverage Histogram (0-50X)



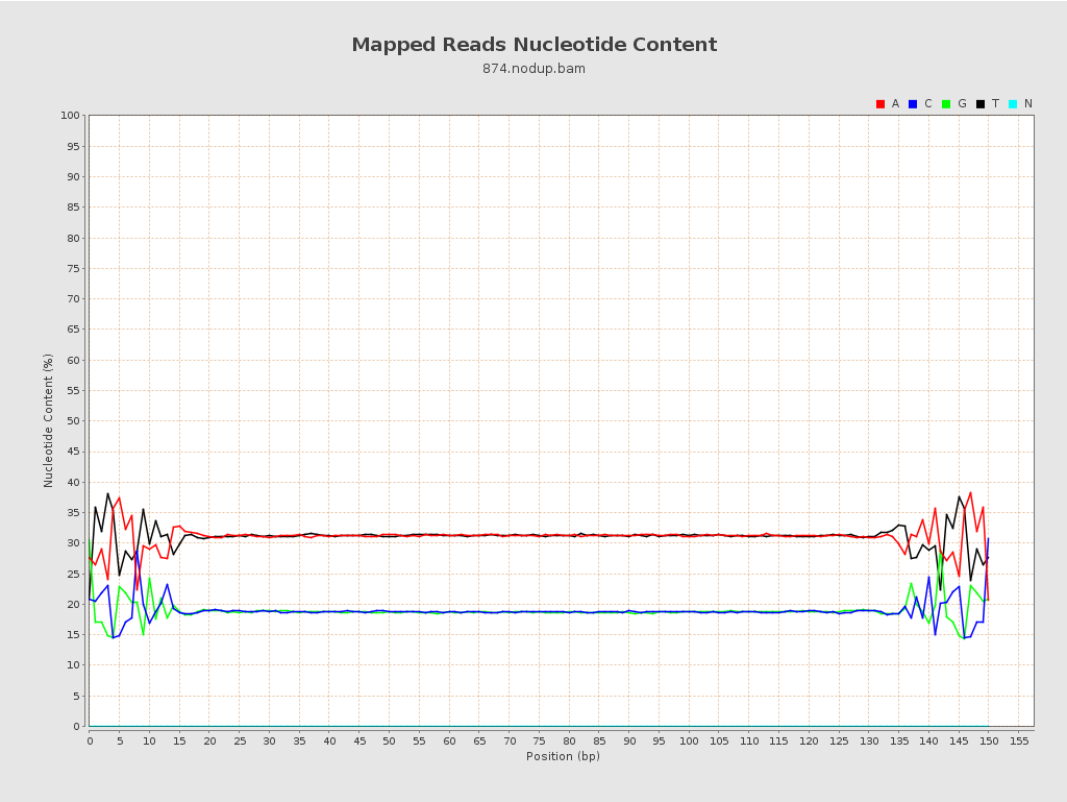
6. Results : Genome Fraction Coverage



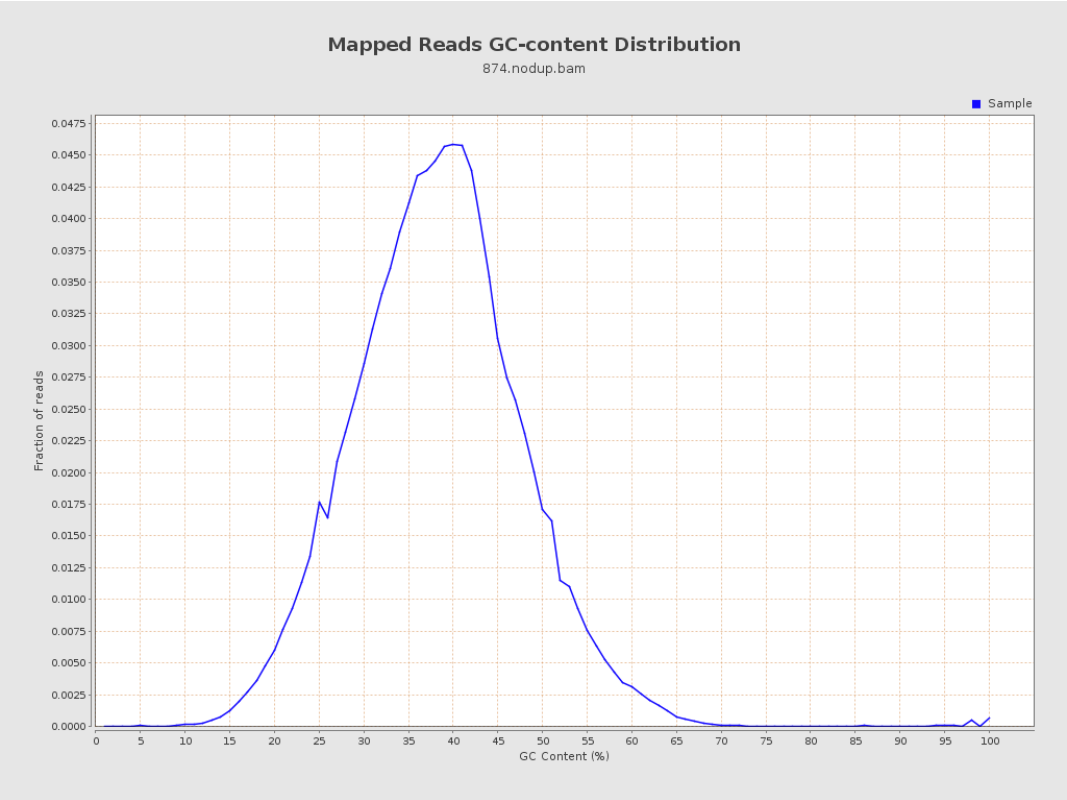
7. Results : Duplication Rate Histogram



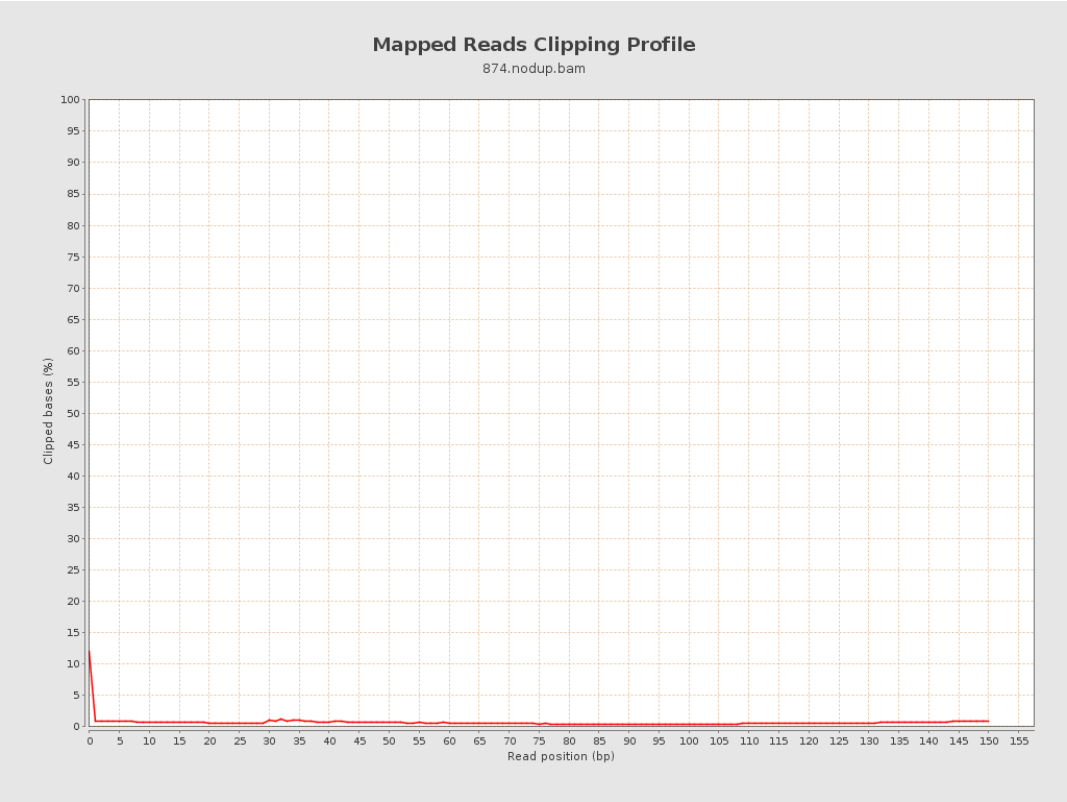
8. Results : Mapped Reads Nucleotide Content



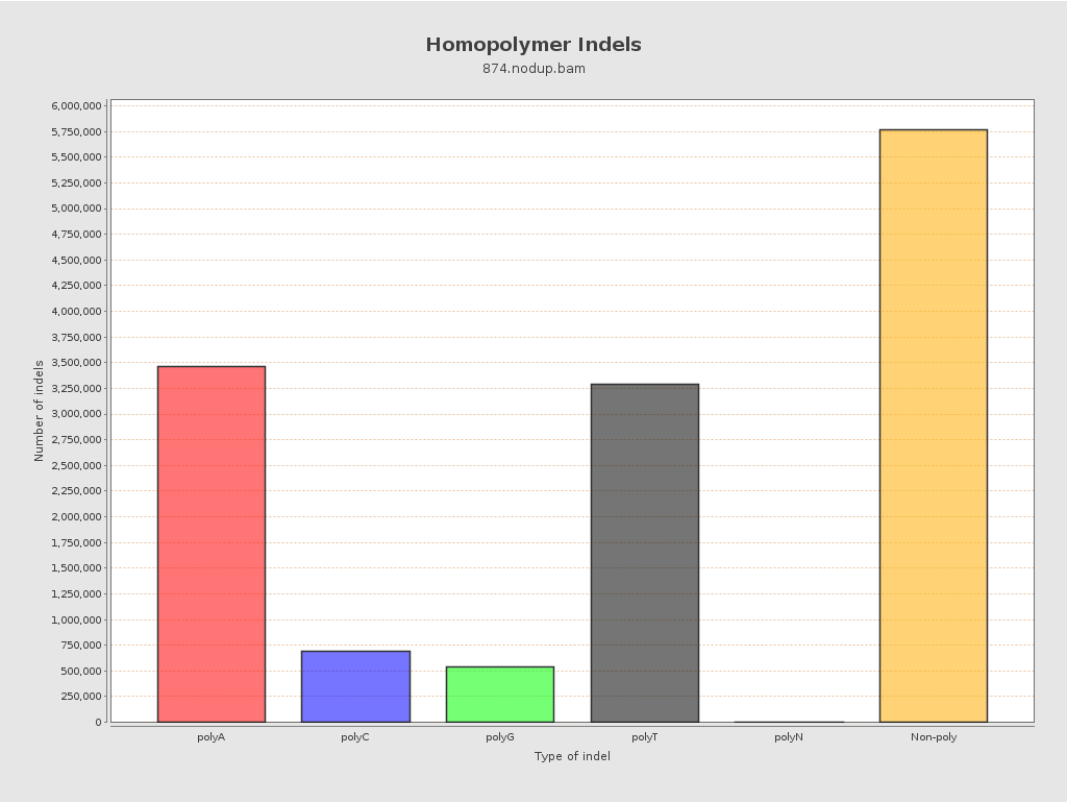
9. Results : Mapped Reads GC-content Distribution



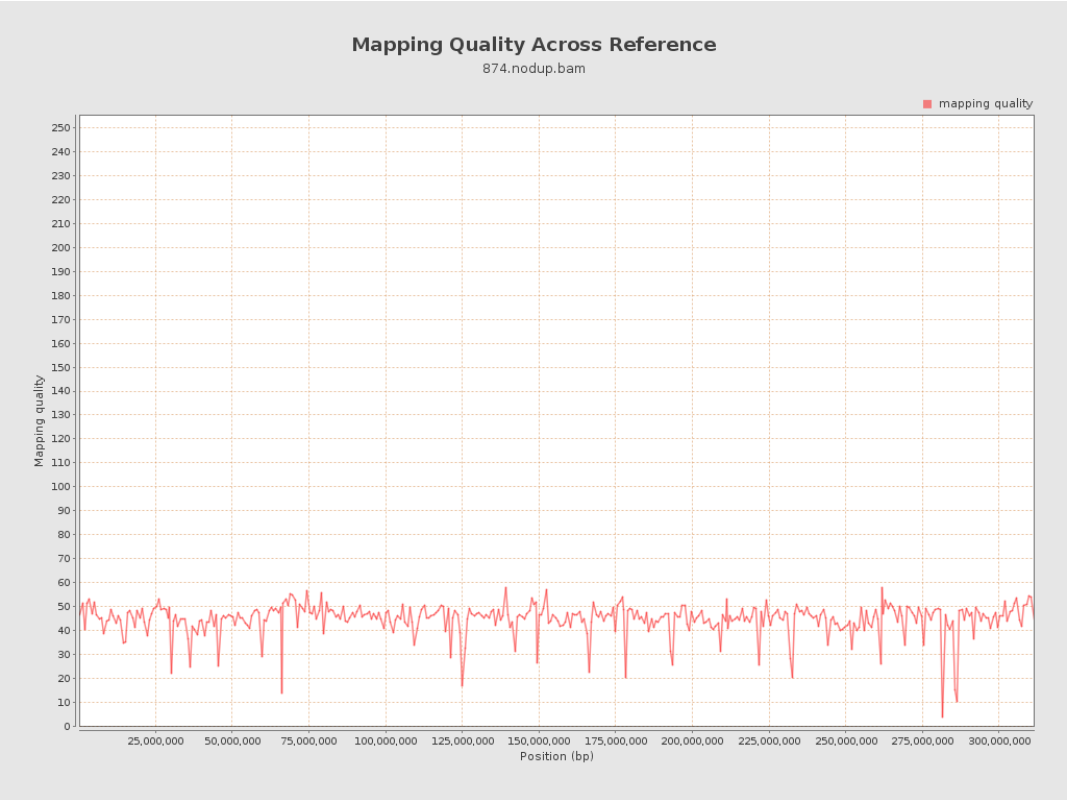
10. Results : Mapped Reads Clipping Profile



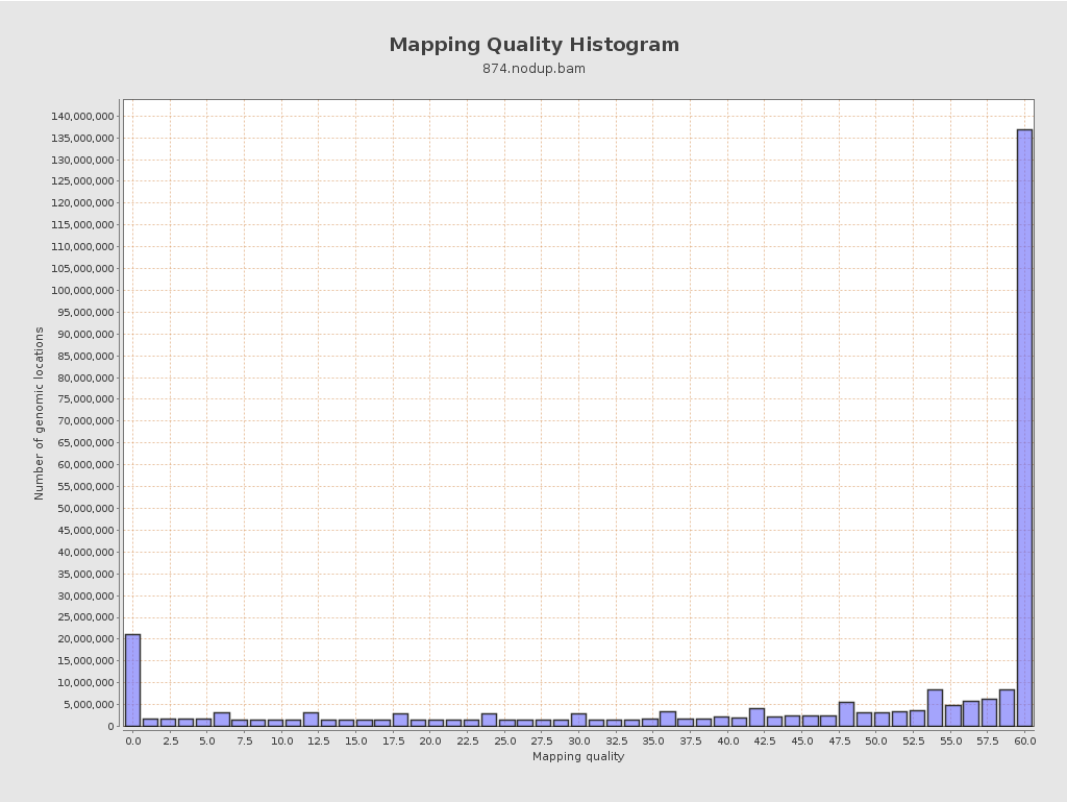
11. Results : Homopolymer Indels



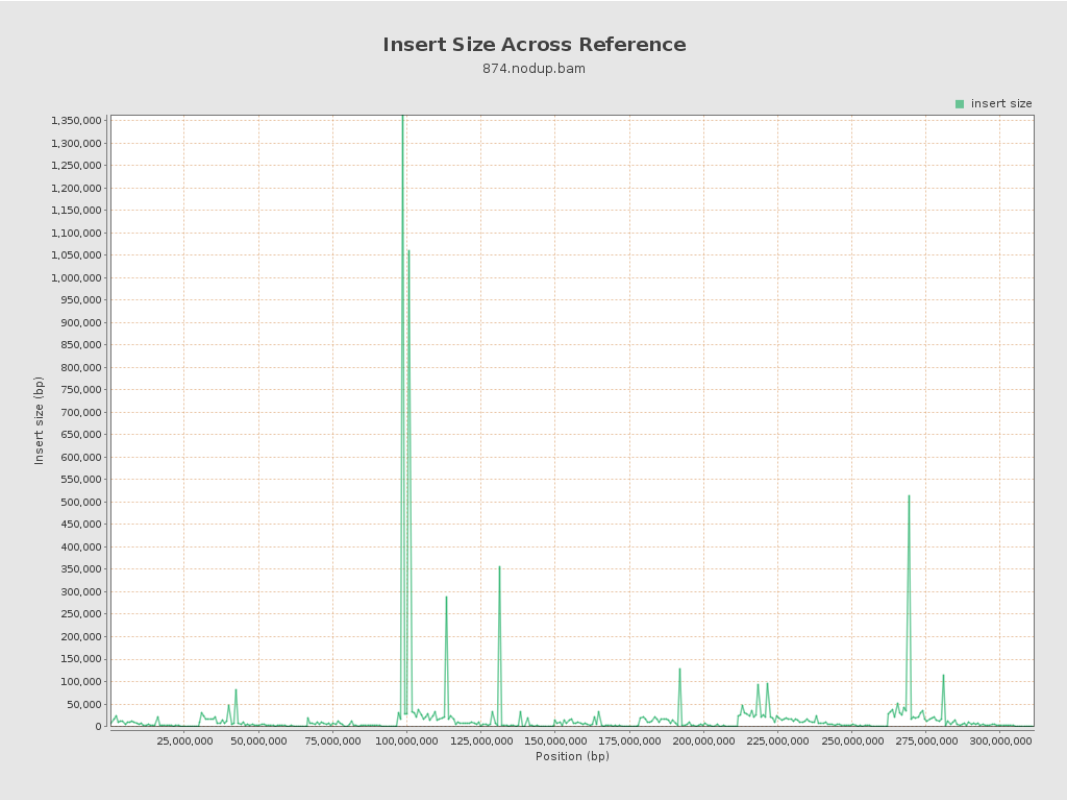
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram