Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/875.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/875.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_234/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_234_S315_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_234/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_234_S315_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:35:52 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	80,468,678
Mapped reads	72,588,673 / 90.21%
Unmapped reads	7,880,005 / 9.79%
Mapped paired reads	72,588,673 / 90.21%
Mapped reads, first in pair	36,393,602 / 45.23%
Mapped reads, second in pair	36,195,071 / 44.98%
Mapped reads, both in pair	70,157,472 / 87.19%
Mapped reads, singletons	2,431,201 / 3.02%
Read min/max/mean length	30 / 151 / 148.08
Duplicated reads (flagged)	13,002,184 / 16.16%
Clipped reads	18,127,392 / 22.53%

2.2. ACGT Content

Number/percentage of A's	3,059,788,174 / 30.96%
Number/percentage of C's	1,879,661,764 / 19.02%
Number/percentage of T's	3,060,804,160 / 30.97%
Number/percentage of G's	1,881,323,670 / 19.04%
Number/percentage of N's	36,884 / 0%
GC Percentage	38.06%

2.3. Coverage

Mean	31.7905
Standard Deviation	323.1429

2.4. Mapping Quality

Mean Mapping Quality	44.37

2.5. Insert size

Mean	258,581.33
Standard Deviation	2,460,444.77
P25/Median/P75	306 / 404 / 524

2.6. Mismatches and indels

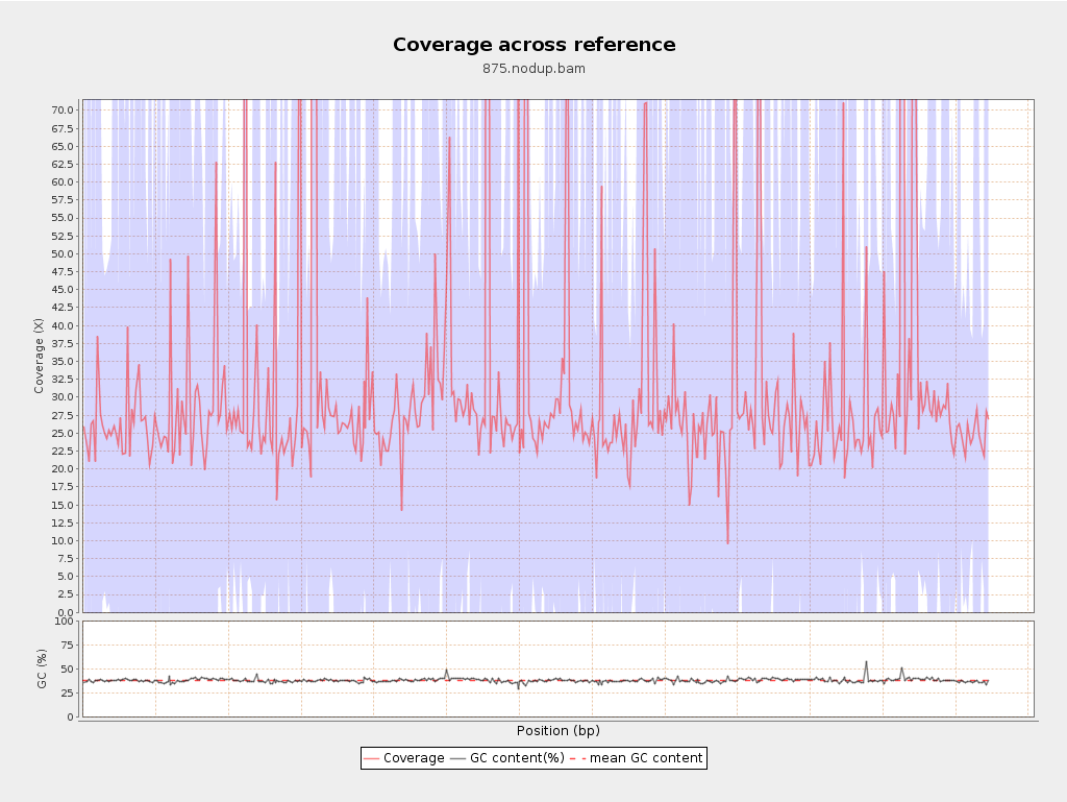
General error rate	2.39%
Mismatches	215,495,269
Insertions	7,313,023
Mapped reads with at least one insertion	8.96%
Deletions	6,880,000
Mapped reads with at least one deletion	8.41%
Homopolymer indels	57.87%

2.7. Chromosome stats

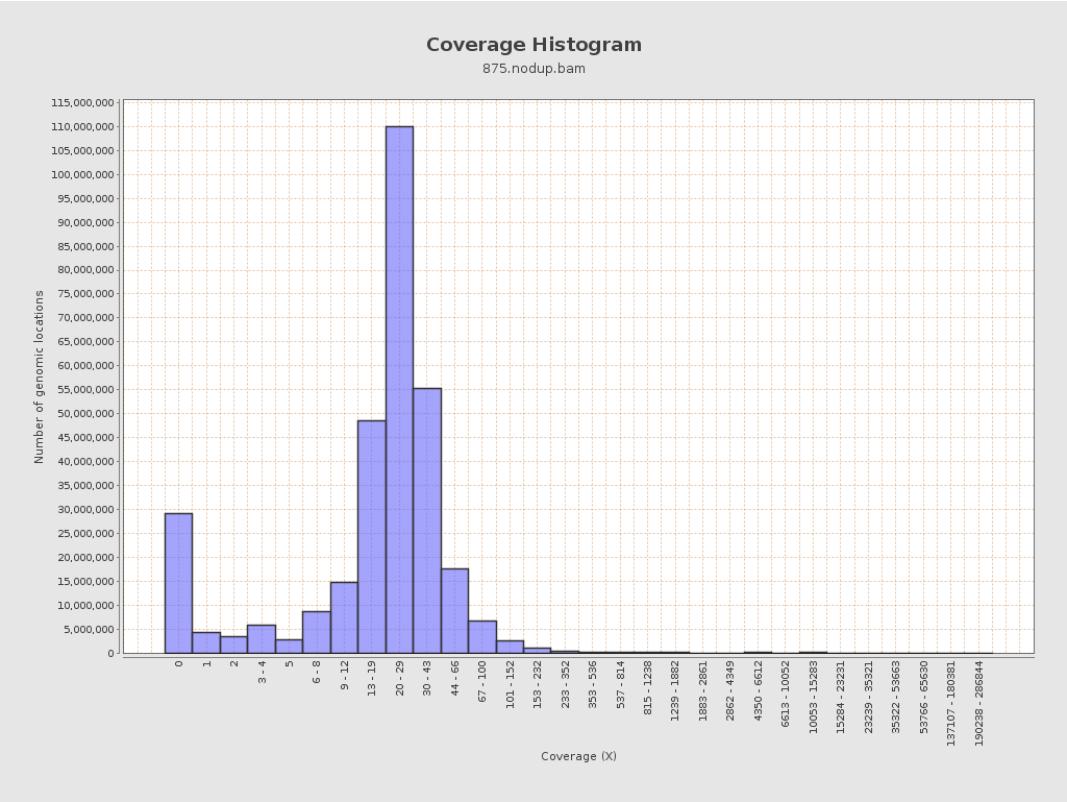
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	770192202	25.9112	130.9218

LT669789.1	36598175	1142283217	31.2115	317.7304
LT669790.1	30422129	1223338851	40.2121	489.2041
LT669791.1	52758100	1680402335	31.8511	359.3833
LT669792.1	28376109	910194100	32.0761	310.4541
LT669793.1	33388210	961808742	28.8068	198.652
LT669794.1	50579949	1476180364	29.1851	248.5895
LT669795.1	49795044	1742842994	35.0003	376.5568

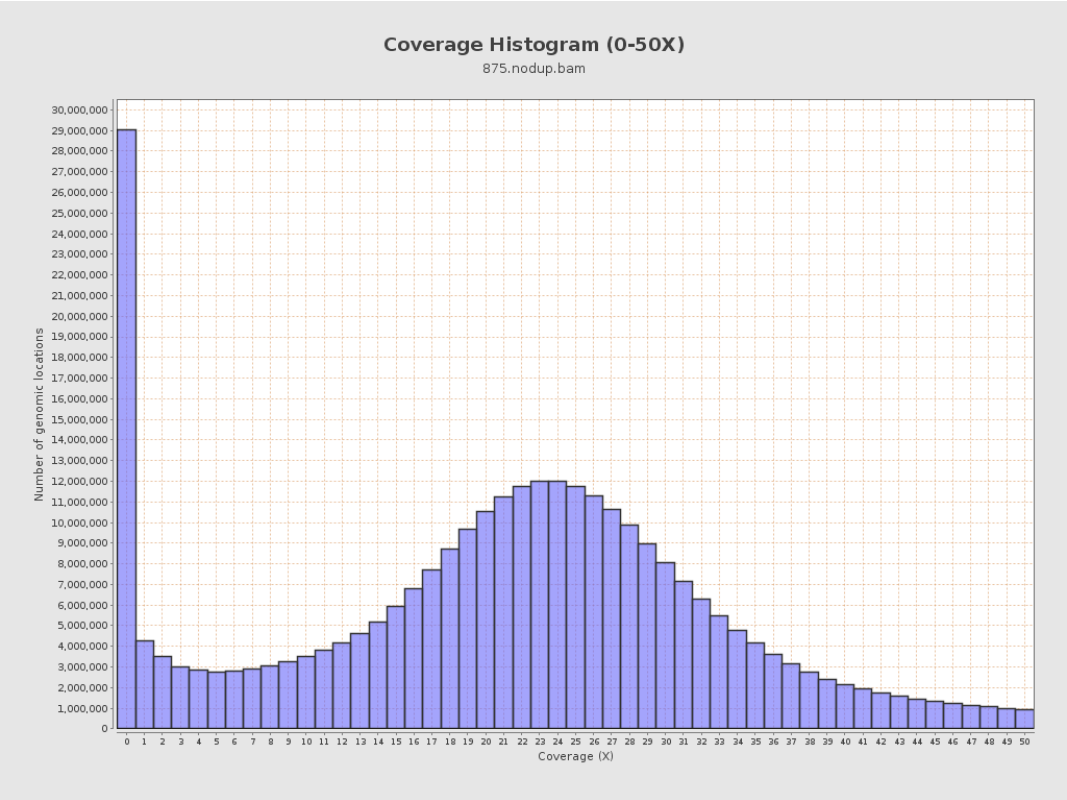
3. Results : Coverage across reference



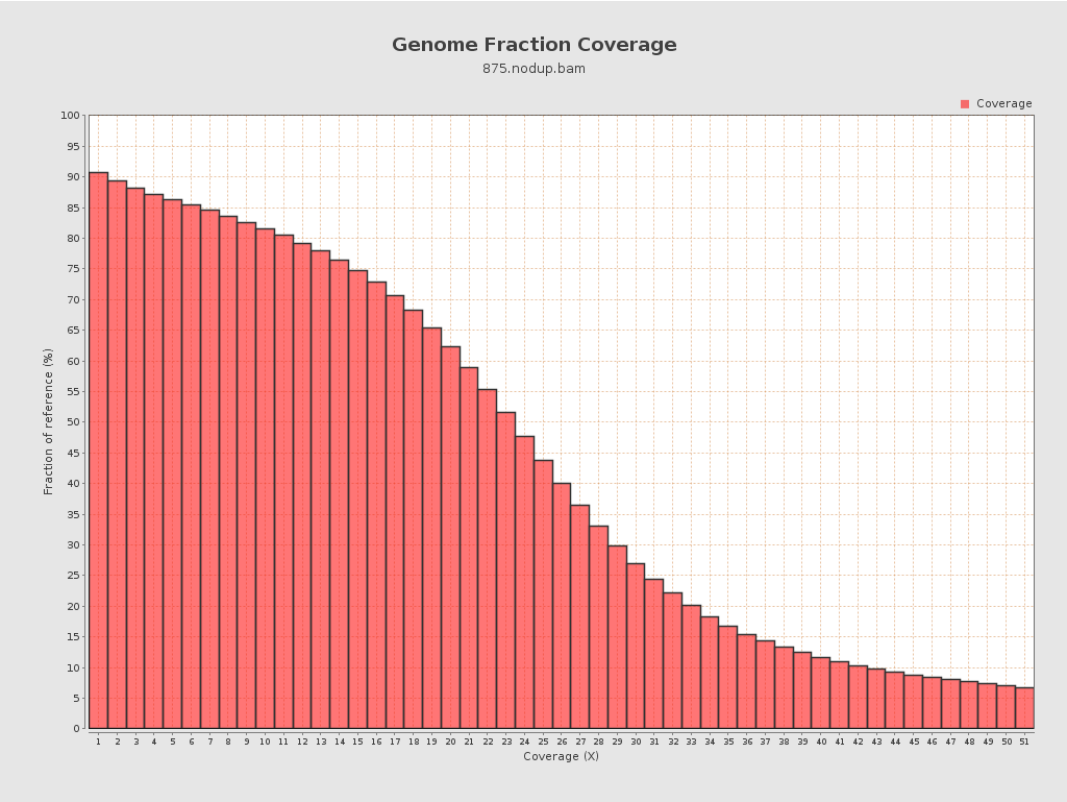
4. Results : Coverage Histogram



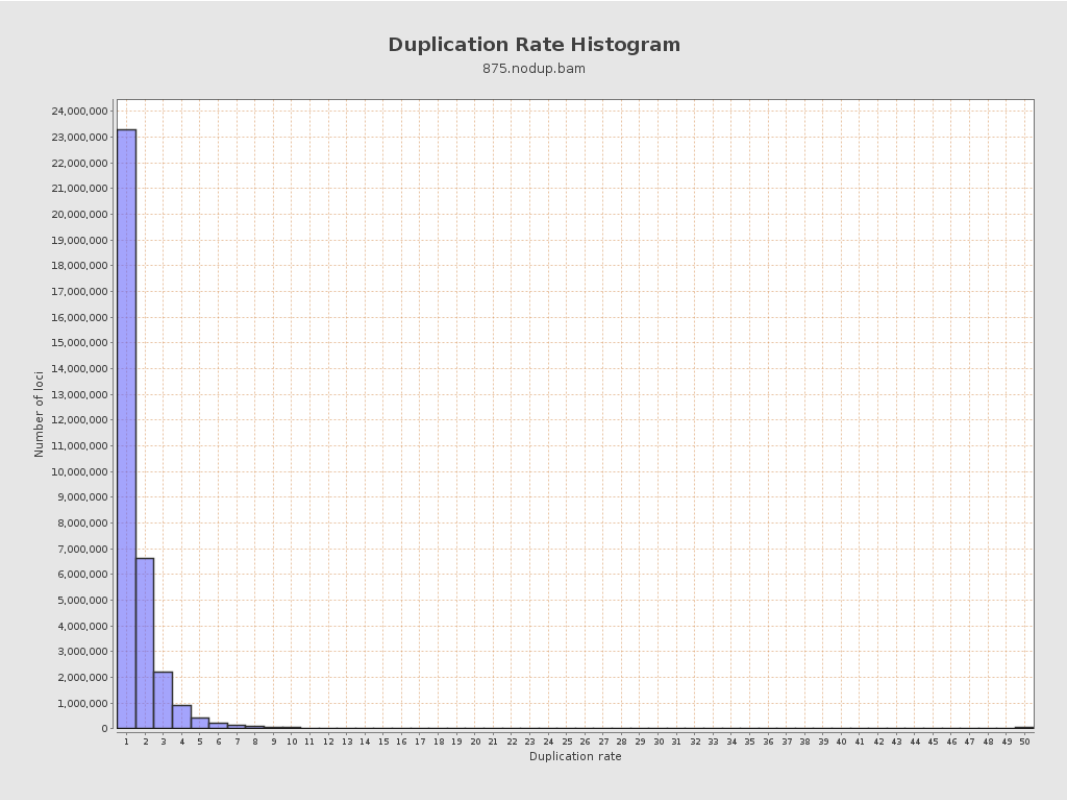
5. Results : Coverage Histogram (0-50X)



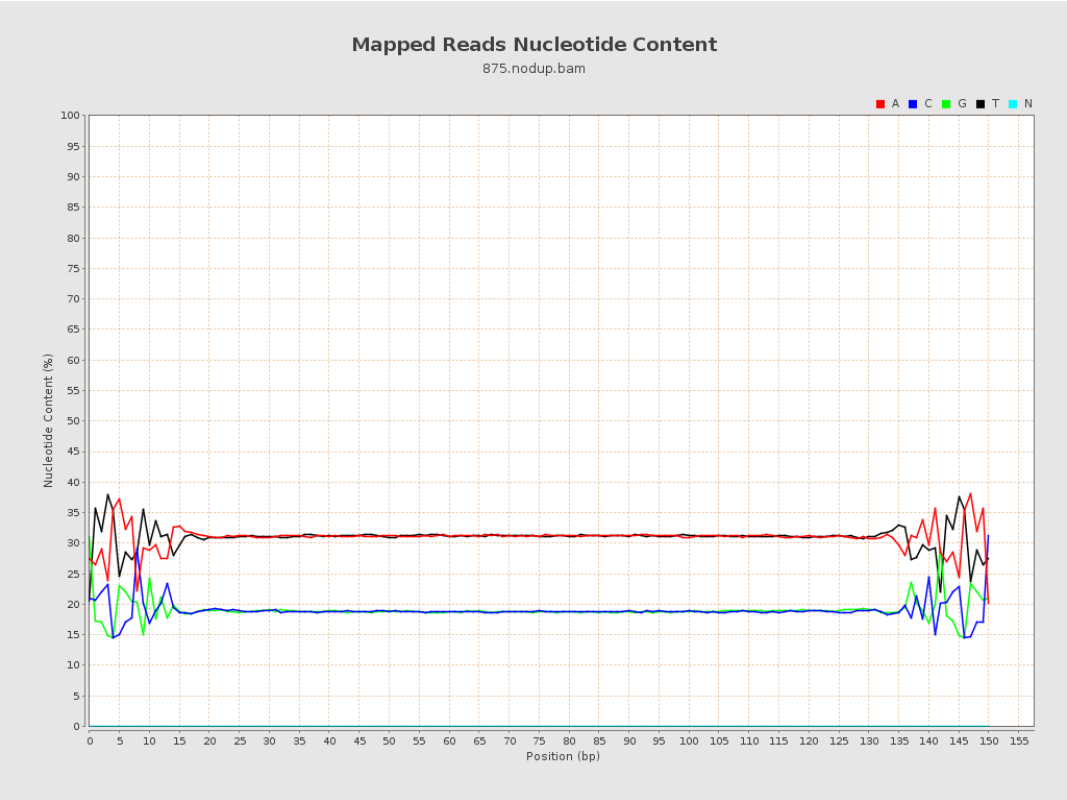
6. Results : Genome Fraction Coverage



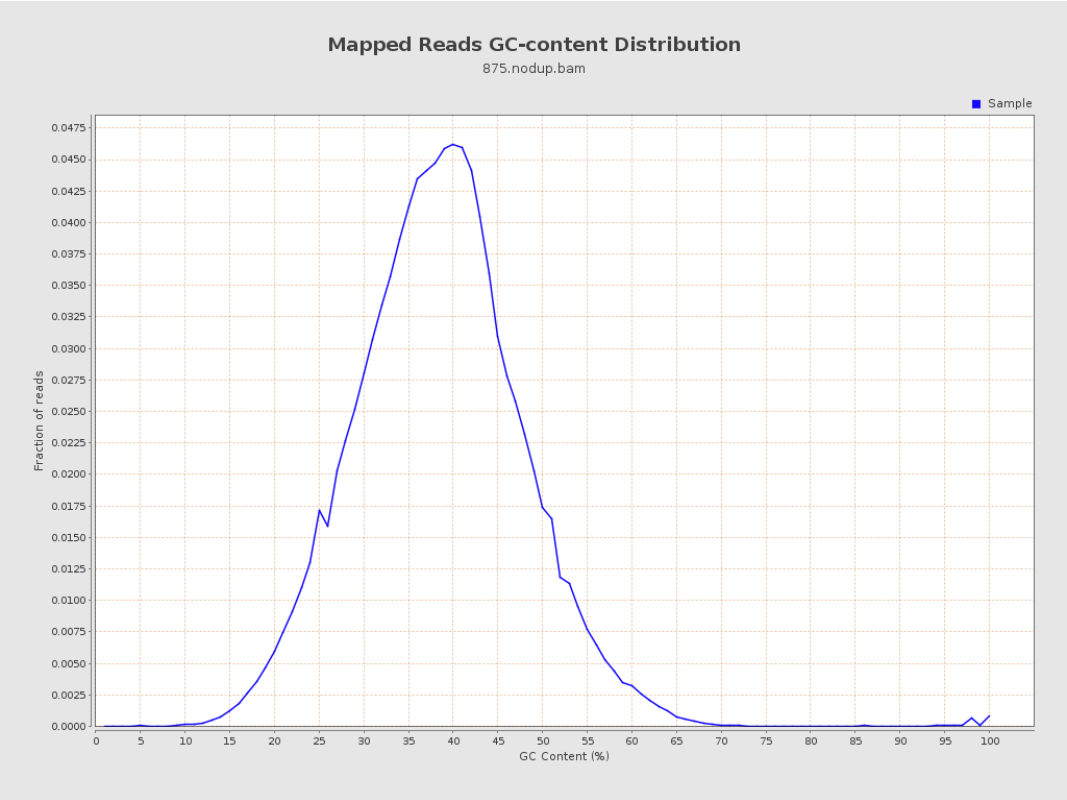
7. Results : Duplication Rate Histogram



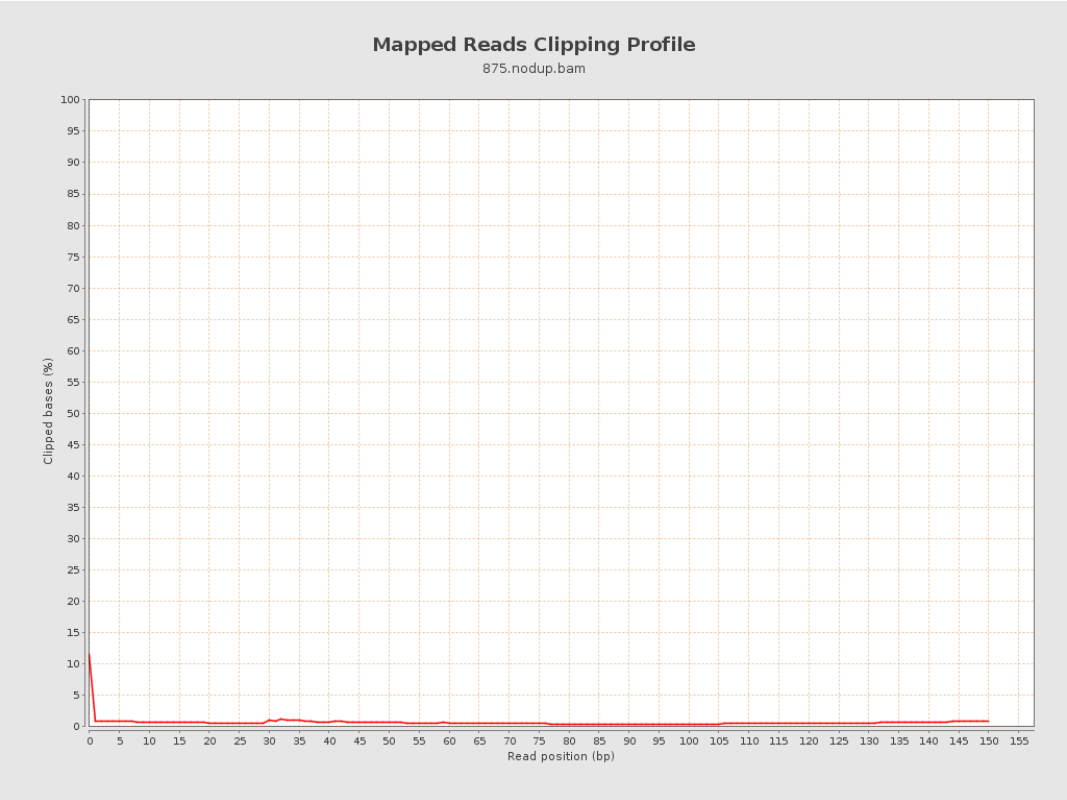
8. Results : Mapped Reads Nucleotide Content



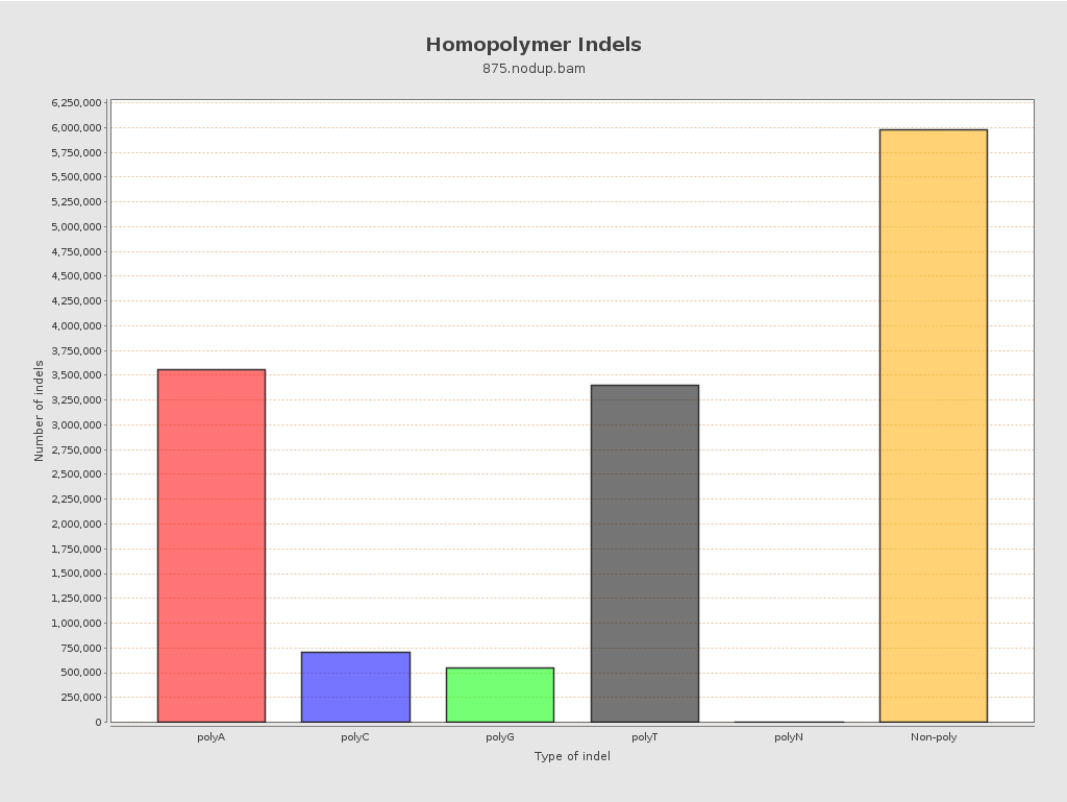
9. Results : Mapped Reads GC-content Distribution



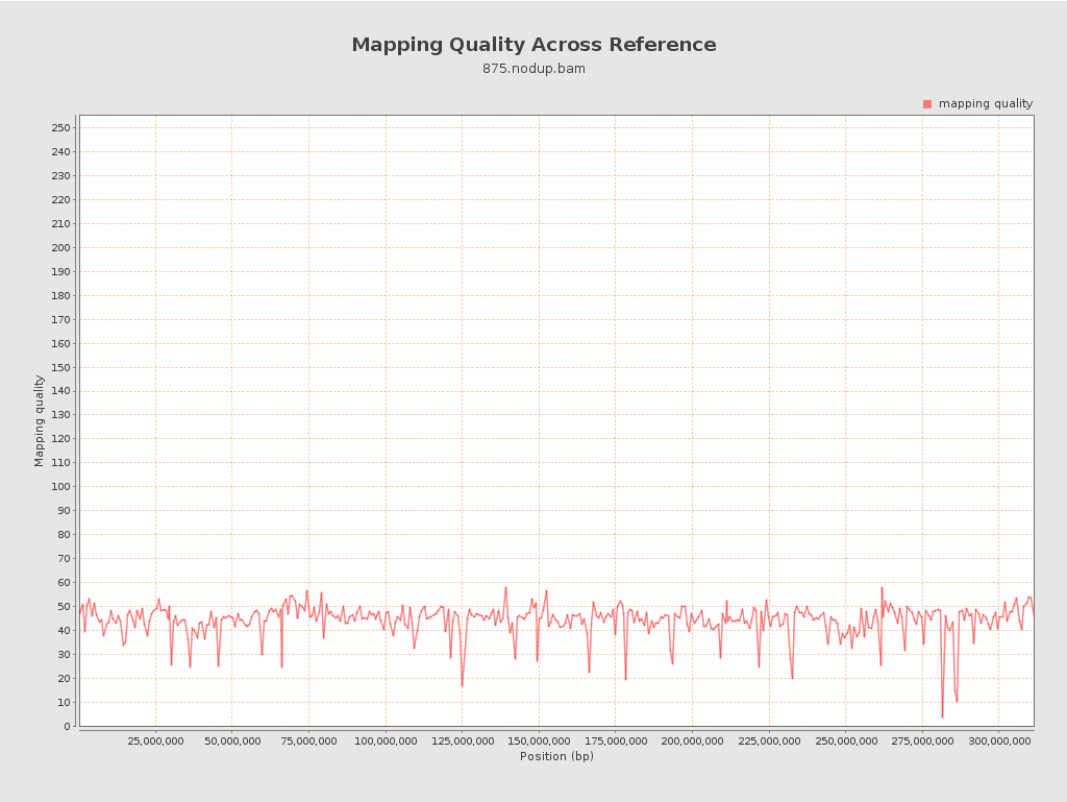
10. Results : Mapped Reads Clipping Profile



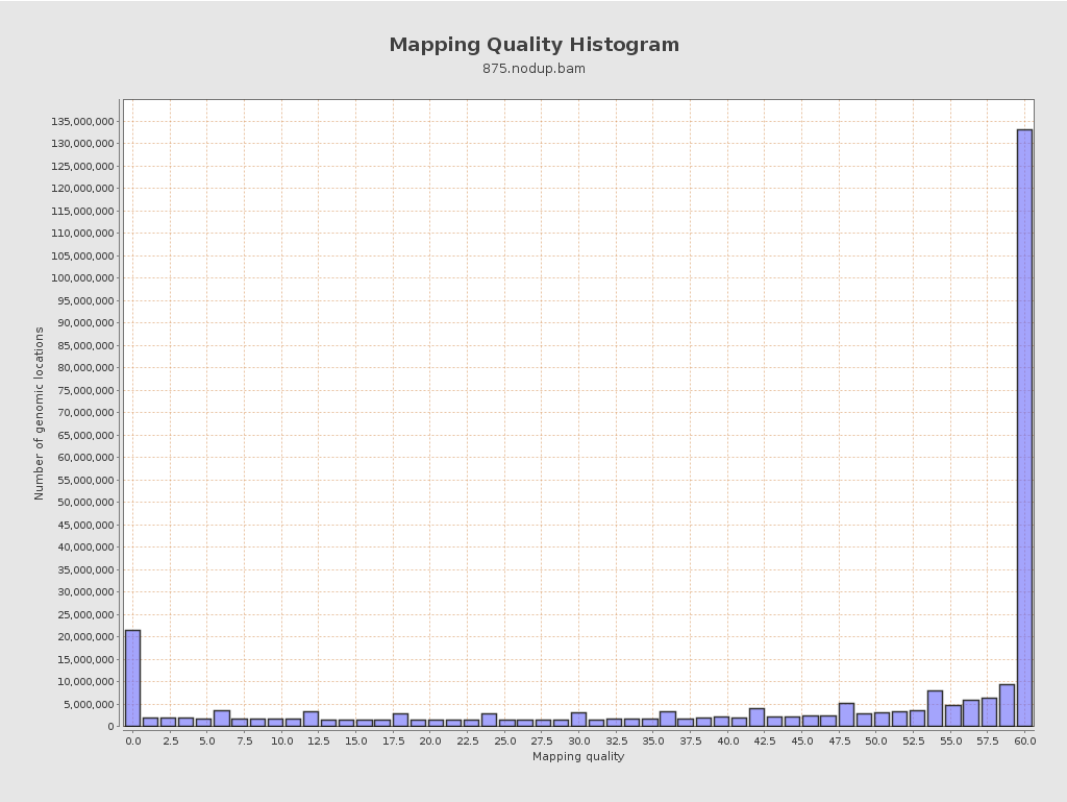
11. Results : Homopolymer Indels



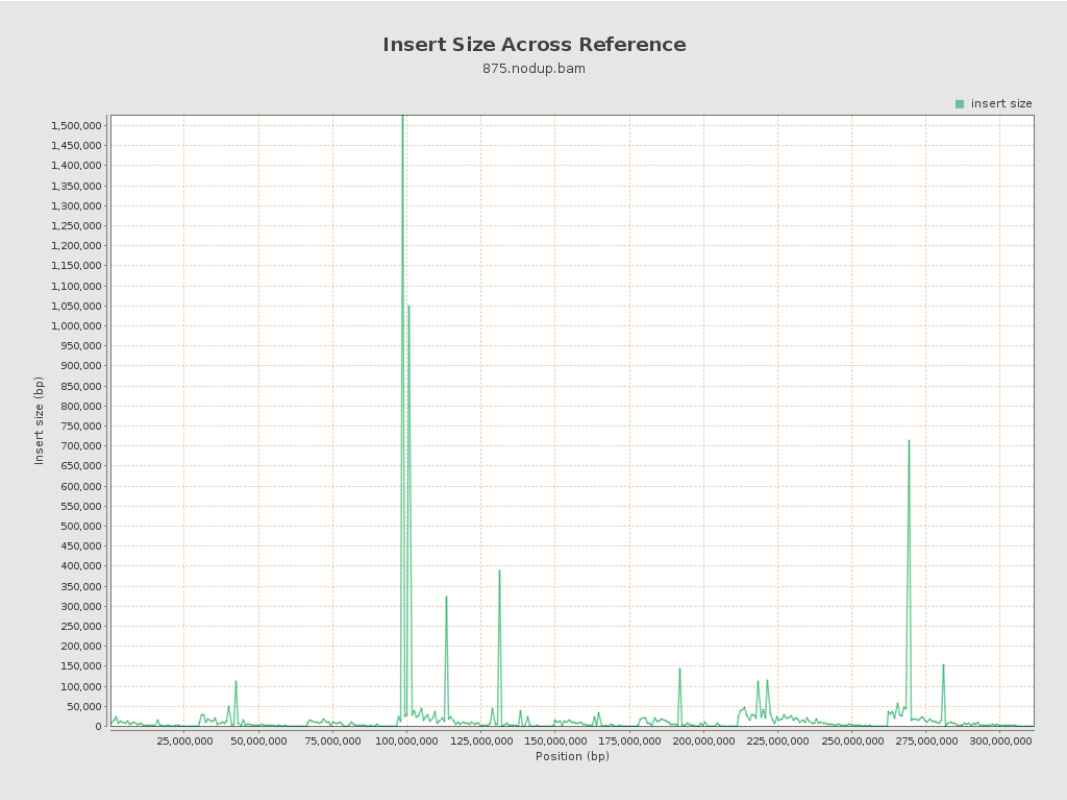
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram