Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/876.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/876.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_220/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_220_S301_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_220/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_220_S301_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:35:46 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	85,314,678
Mapped reads	77,662,844 / 91.03%
Unmapped reads	7,651,834 / 8.97%
Mapped paired reads	77,662,844 / 91.03%
Mapped reads, first in pair	38,911,354 / 45.61%
Mapped reads, second in pair	38,751,490 / 45.42%
Mapped reads, both in pair	75,313,588 / 88.28%
Mapped reads, singletons	2,349,256 / 2.75%
Read min/max/mean length	30 / 151 / 148.01
Duplicated reads (flagged)	13,821,754 / 16.2%
Clipped reads	18,955,806 / 22.22%

2.2. ACGT Content

Number/percentage of A's	3,284,949,580 / 30.96%
Number/percentage of C's	2,017,672,044 / 19.02%
Number/percentage of T's	3,288,313,884 / 30.99%
Number/percentage of G's	2,019,282,155 / 19.03%
Number/percentage of N's	39,329 / 0%
GC Percentage	38.05%

2.3. Coverage

Mean	34.1335
Standard Deviation	331.8102

2.4. Mapping Quality

Mean Mapping Quality	44.59

2.5. Insert size

Mean	252,420.89
Standard Deviation	2,425,248.82
P25/Median/P75	315 / 417 / 546

2.6. Mismatches and indels

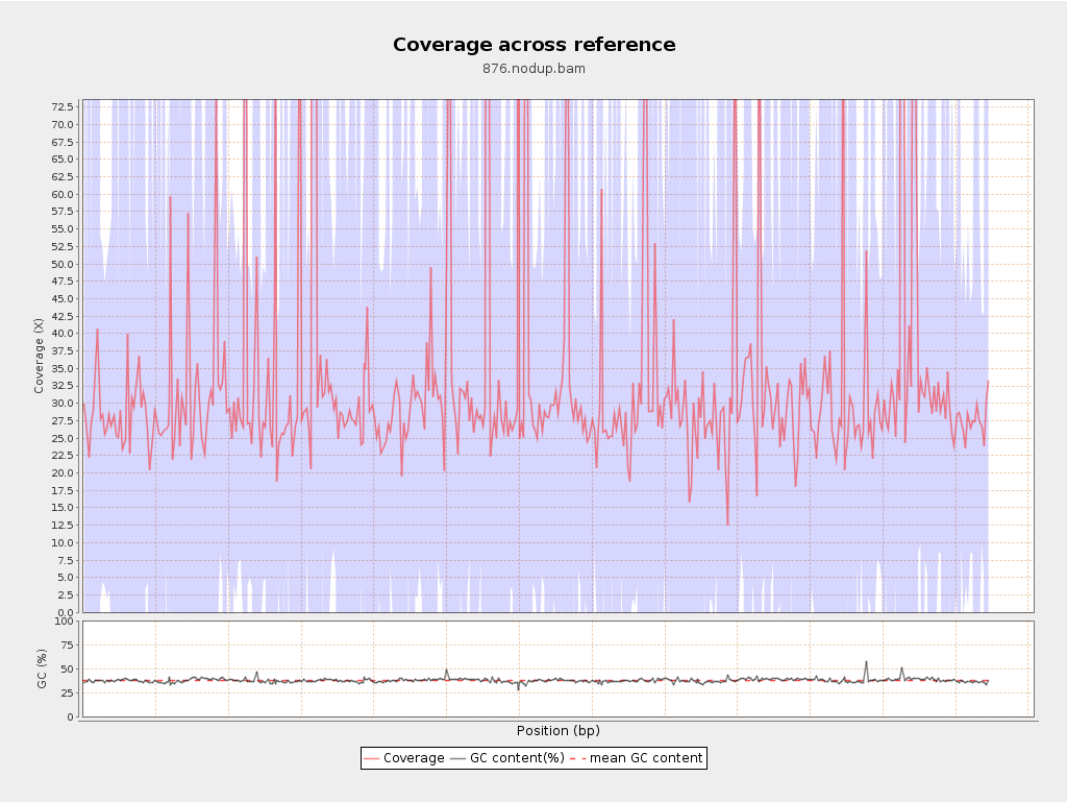
General error rate	2.34%
Mismatches	226,866,083
Insertions	7,755,572
Mapped reads with at least one insertion	8.9%
Deletions	7,360,738
Mapped reads with at least one deletion	8.4%
Homopolymer indels	57.33%

2.7. Chromosome stats

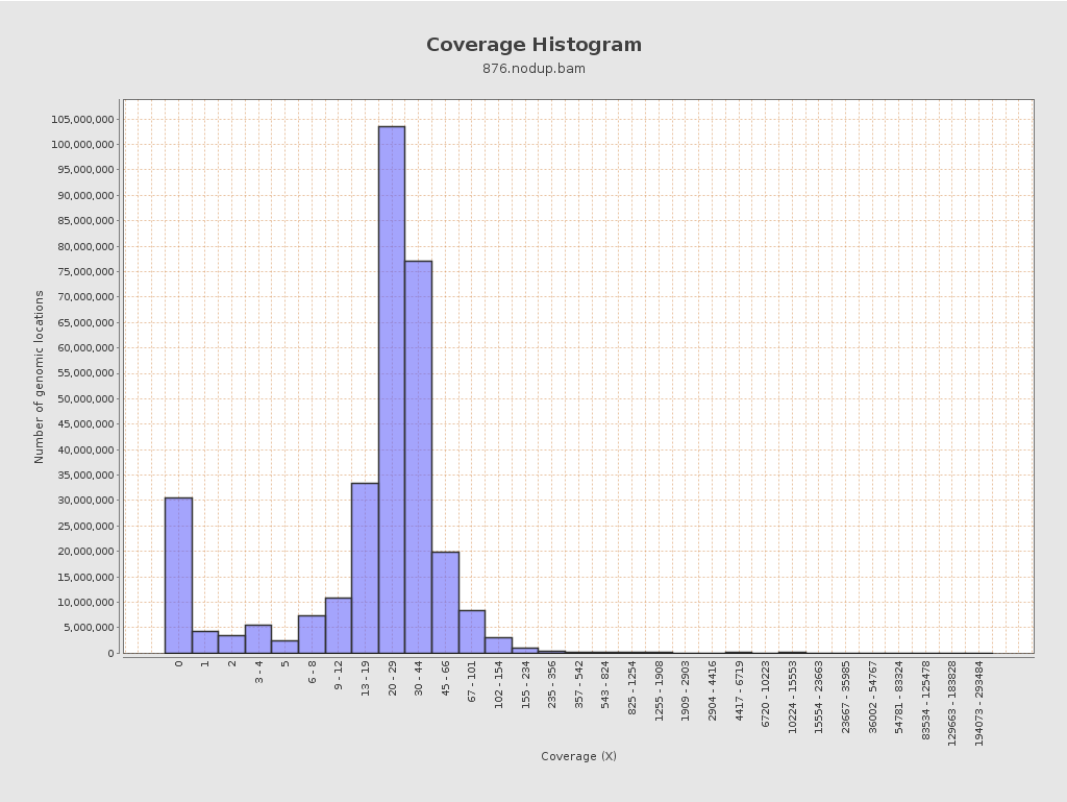
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	837526279	28.1764	137.5866

LT669789.1	36598175	1254148993	34.2681	351.0752
LT669790.1	30422129	1292118328	42.473	468.599
LT669791.1	52758100	1756900052	33.301	361.6182
LT669792.1	28376109	980363880	34.5489	313.6565
LT669793.1	33388210	1043119300	31.2421	209.2492
LT669794.1	50579949	1609170127	31.8144	279.0009
LT669795.1	49795044	1864100495	37.4355	387.1424

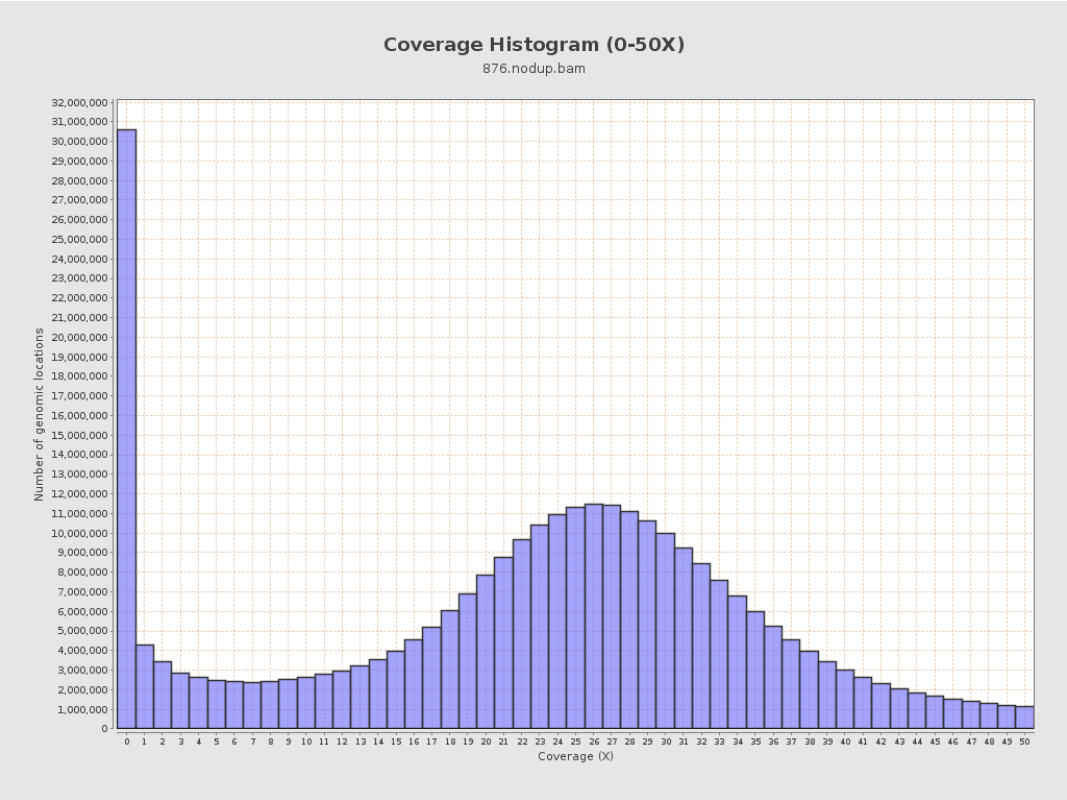
3. Results : Coverage across reference



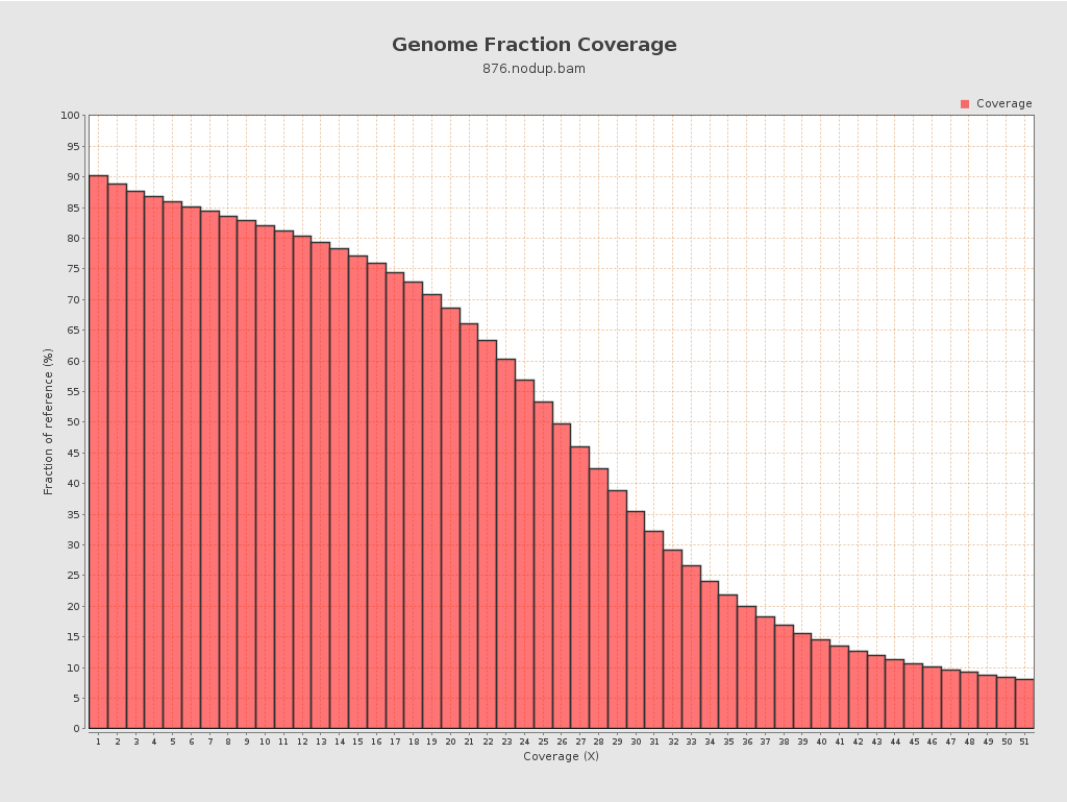
4. Results : Coverage Histogram



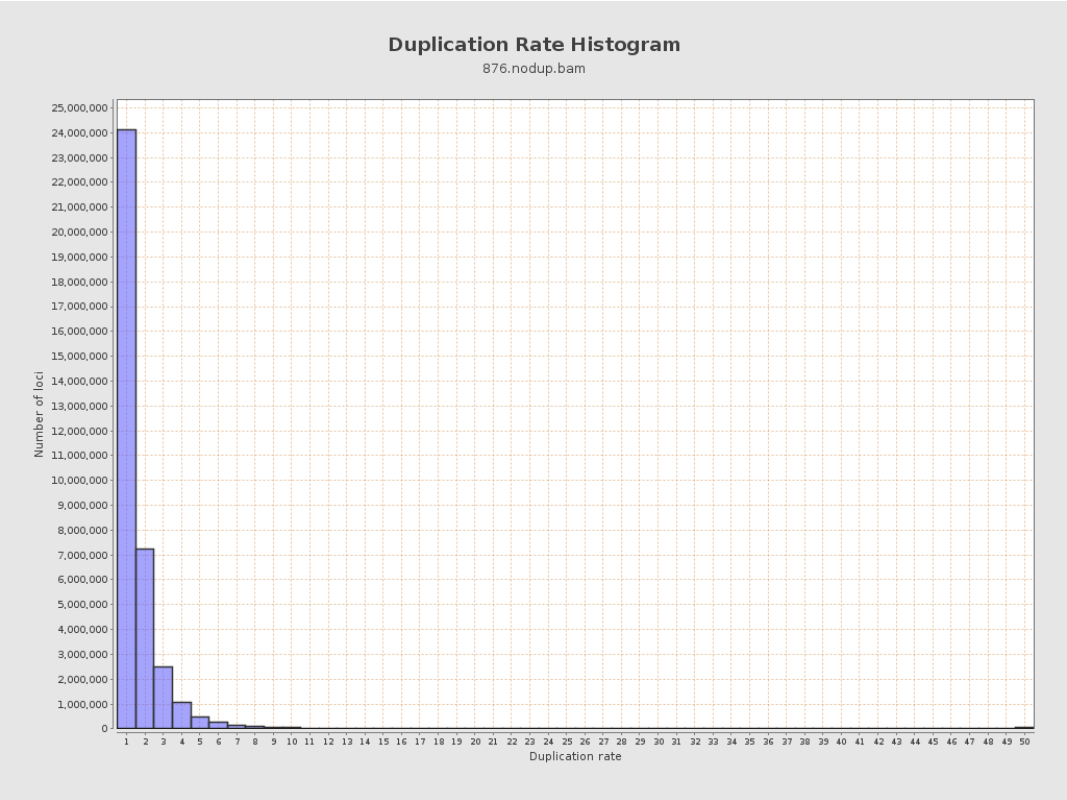
5. Results : Coverage Histogram (0-50X)



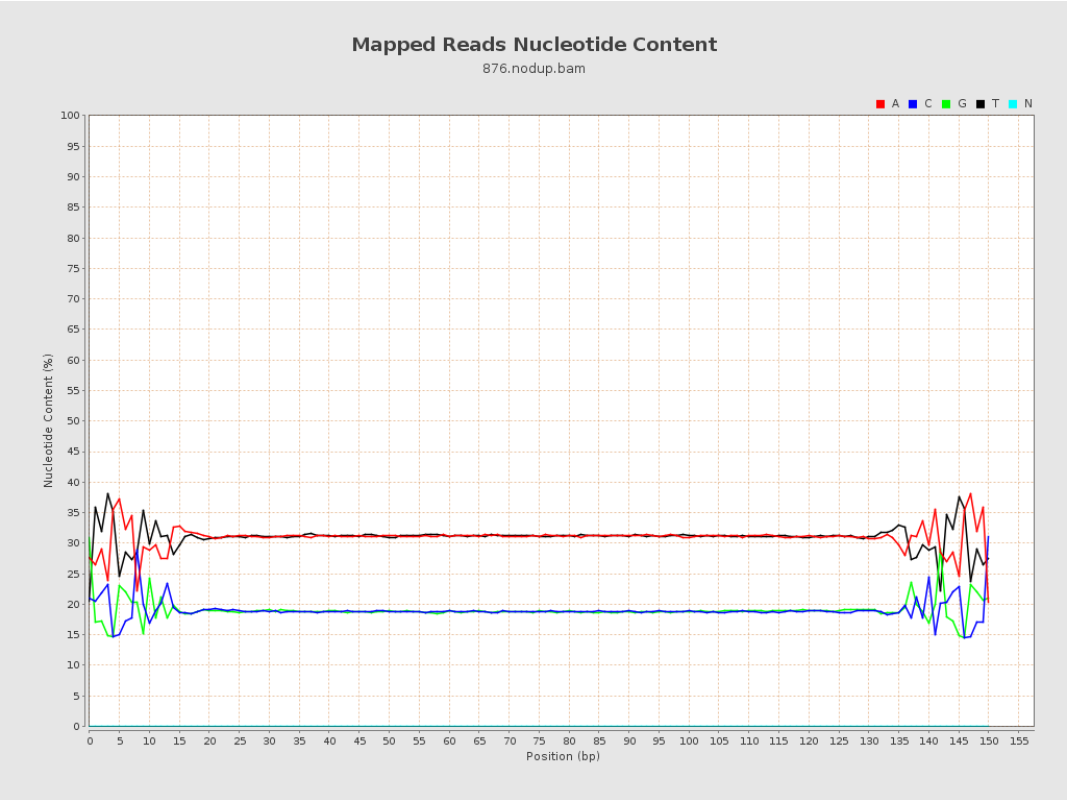
6. Results : Genome Fraction Coverage



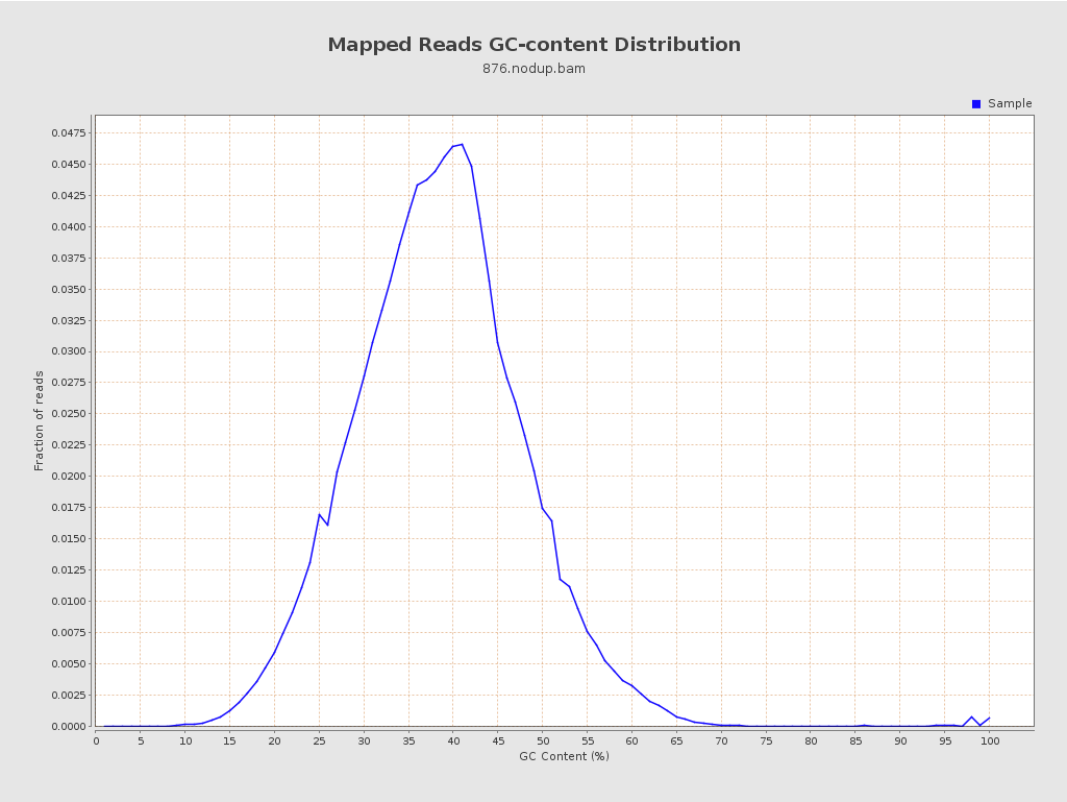
7. Results : Duplication Rate Histogram



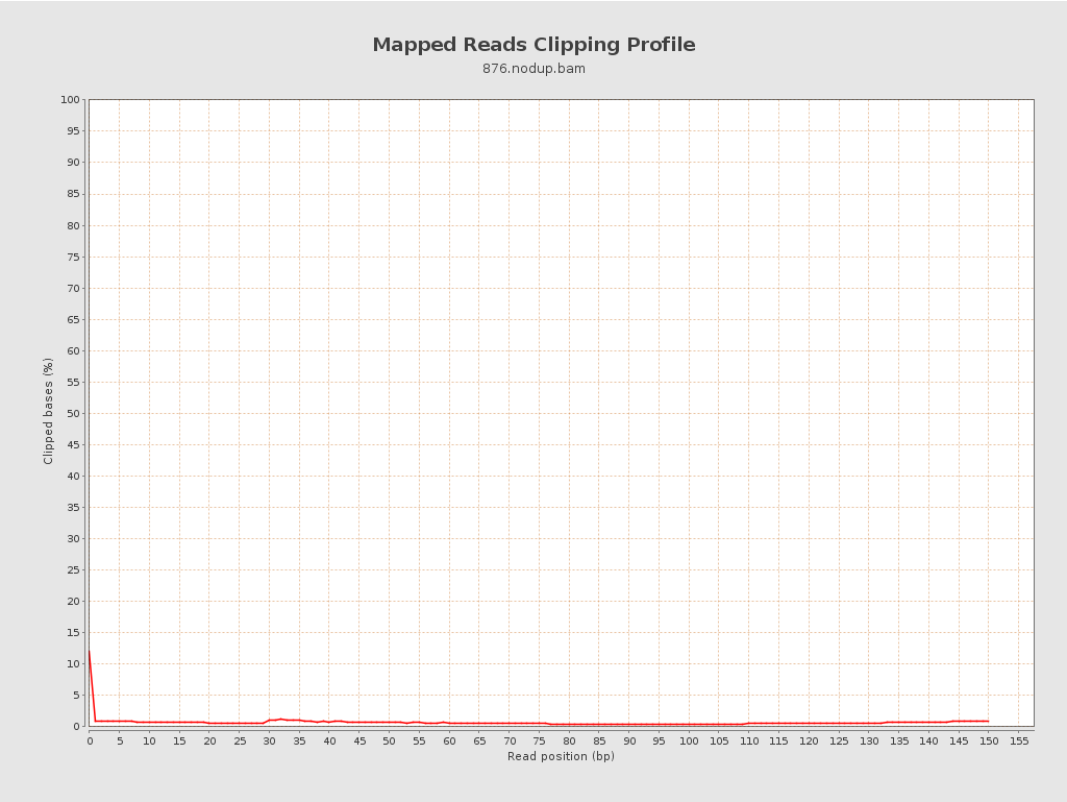
8. Results : Mapped Reads Nucleotide Content



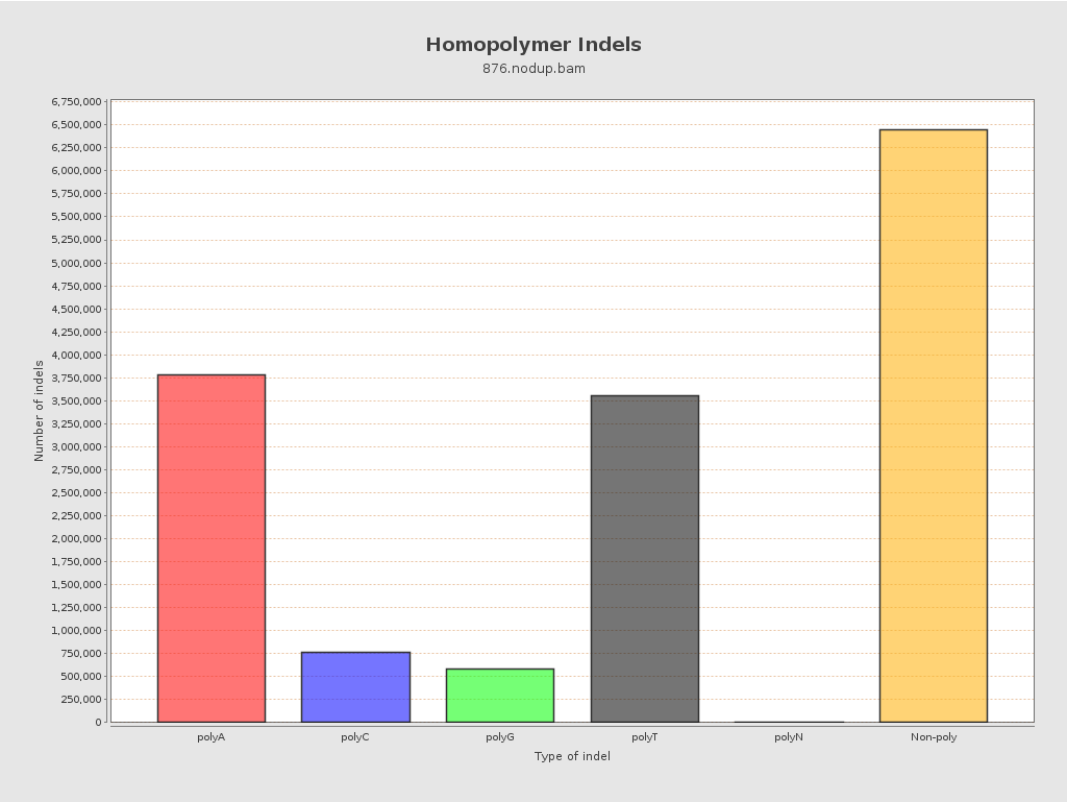
9. Results : Mapped Reads GC-content Distribution



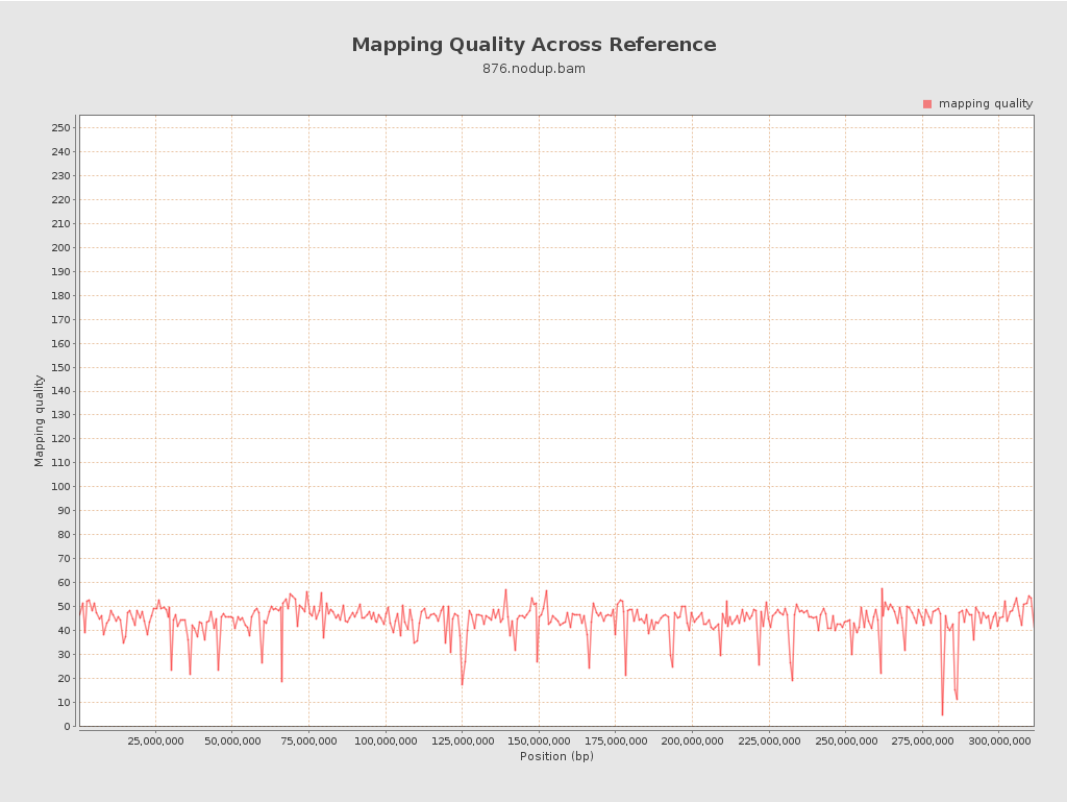
10. Results : Mapped Reads Clipping Profile



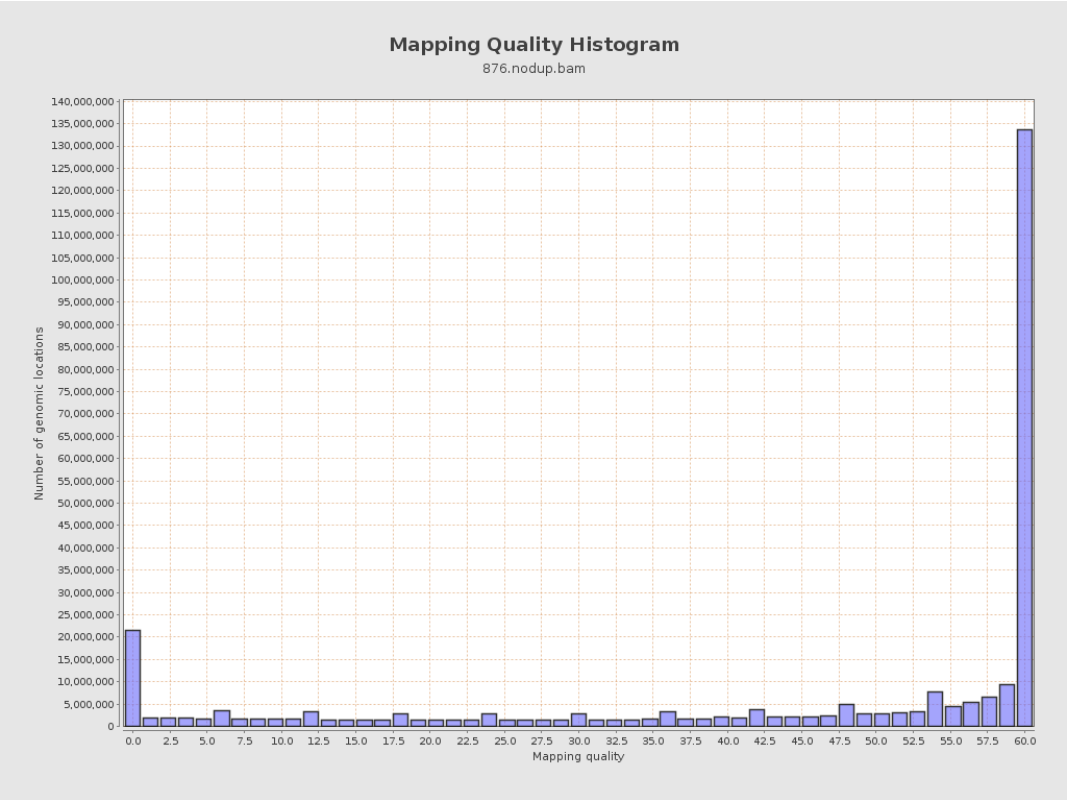
11. Results : Homopolymer Indels



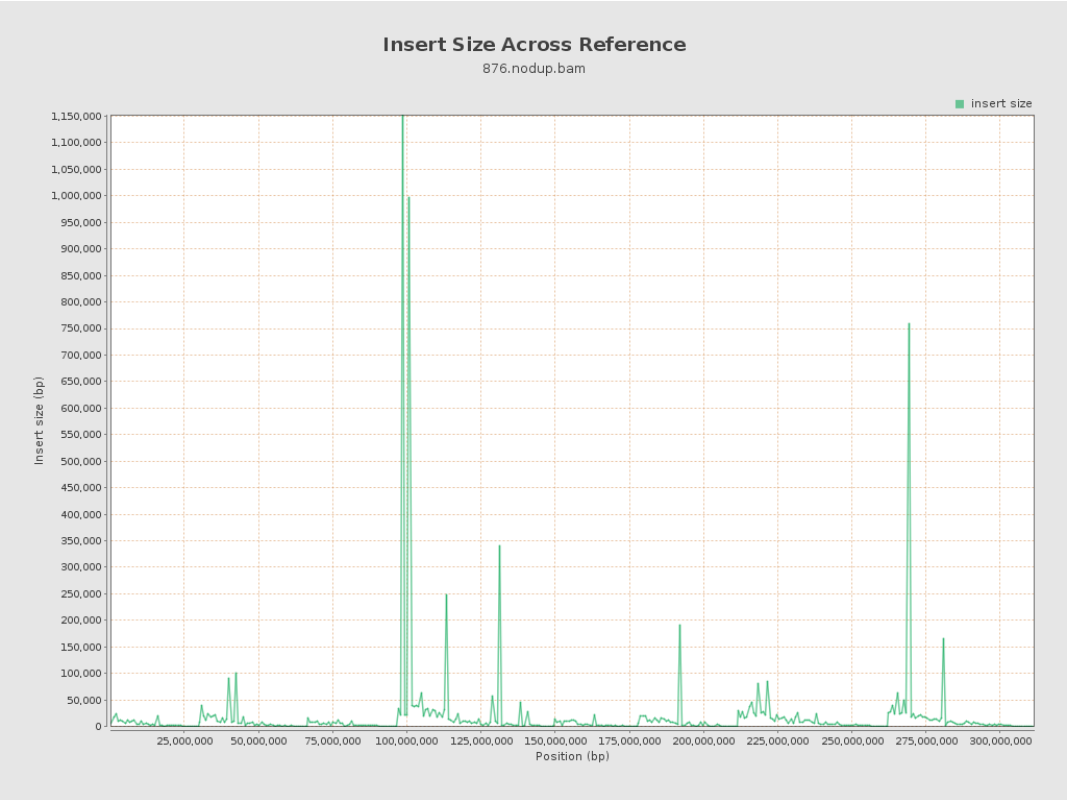
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram