

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:38:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/971
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/971.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/awdata/P26207/P26207_433/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_433_S408_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_433/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_433_S408_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:38:52 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	85,932,888
Mapped reads	79,660,476 / 92.7%
Unmapped reads	6,272,412 / 7.3%
Mapped paired reads	79,660,476 / 92.7%
Mapped reads, first in pair	39,856,395 / 46.38%
Mapped reads, second in pair	39,804,081 / 46.32%
Mapped reads, both in pair	77,701,303 / 90.42%
Mapped reads, singletons	1,959,173 / 2.28%
Read min/max/mean length	30 / 151 / 148.15
Duplicated reads (flagged)	14,640,042 / 17.04%
Clipped reads	17,687,285 / 20.58%

2.2. ACGT Content

Number/percentage of A's	3,393,725,028 / 30.77%
Number/percentage of C's	2,122,889,312 / 19.24%
Number/percentage of T's	3,398,862,401 / 30.81%
Number/percentage of G's	2,115,522,682 / 19.18%
Number/percentage of N's	37,150 / 0%
GC Percentage	38.42%

2.3. Coverage

Mean	35.491
Standard Deviation	302.8249

2.4. Mapping Quality

Mean Mapping Quality	43.85
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2.5. Insert size

Mean	236,578.15
Standard Deviation	2,320,882.52
P25/Median/P75	311 / 405 / 527

2.6. Mismatches and indels

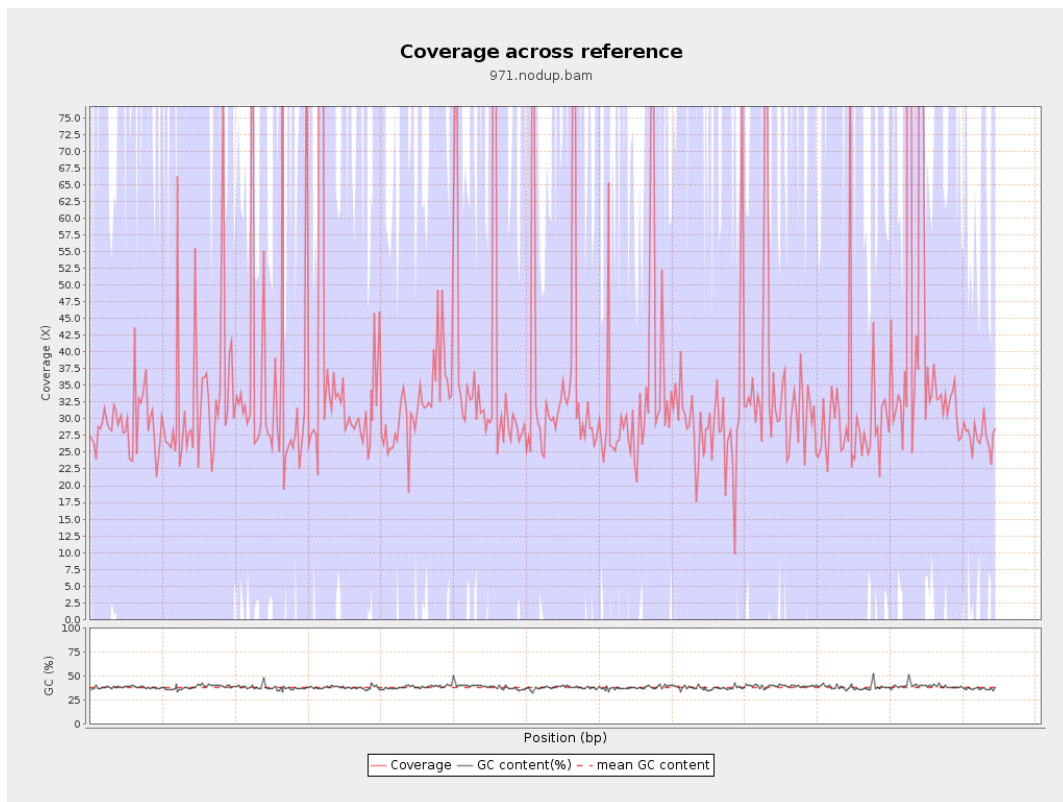
General error rate	2.32%
Mismatches	234,590,909
Insertions	7,739,701
Mapped reads with at least one insertion	8.68%
Deletions	7,731,446
Mapped reads with at least one deletion	8.58%
Homopolymer indels	56.52%

2.7. Chromosome stats

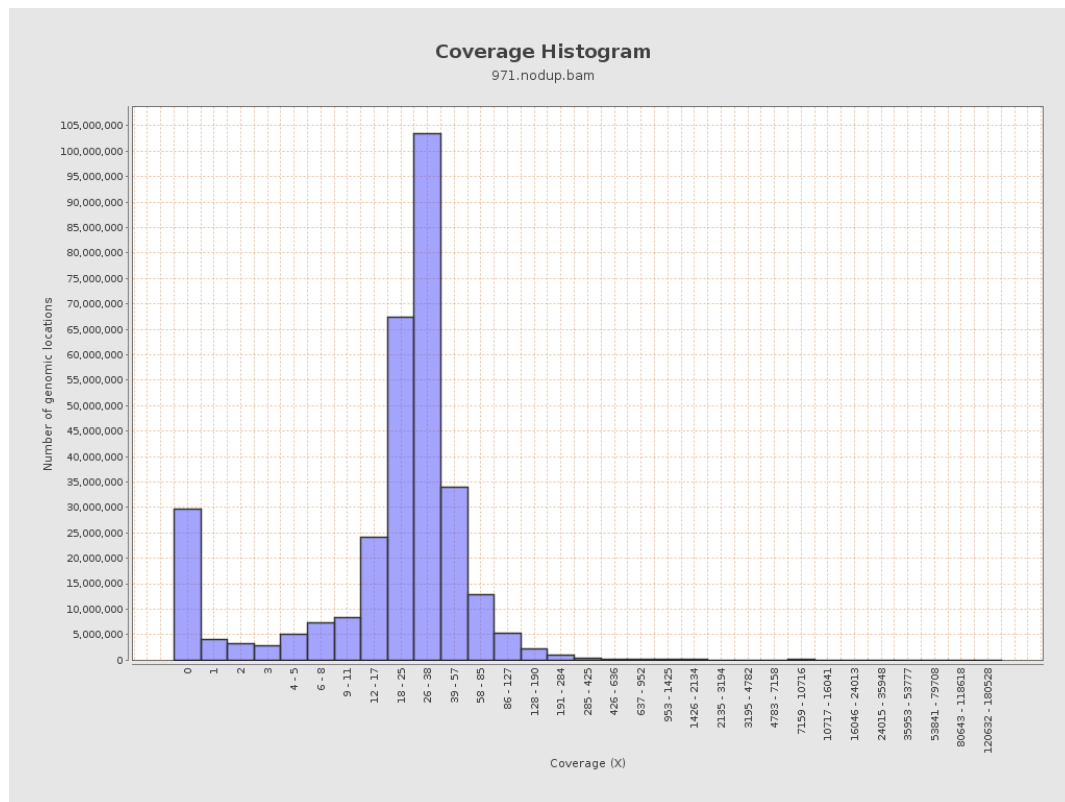
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	858543249	28.8835	104.5662

LT669789.1	36598175	1296198306	35.417	323.6792
LT669790.1	30422129	1223637586	40.222	362.1879
LT669791.1	52758100	1856546168	35.1898	292.7039
LT669792.1	28376109	996387780	35.1136	344.9589
LT669793.1	33388210	1091968229	32.7052	195.6556
LT669794.1	50579949	1676147353	33.1386	242.3283
LT669795.1	49795044	2061067126	41.391	407.7528

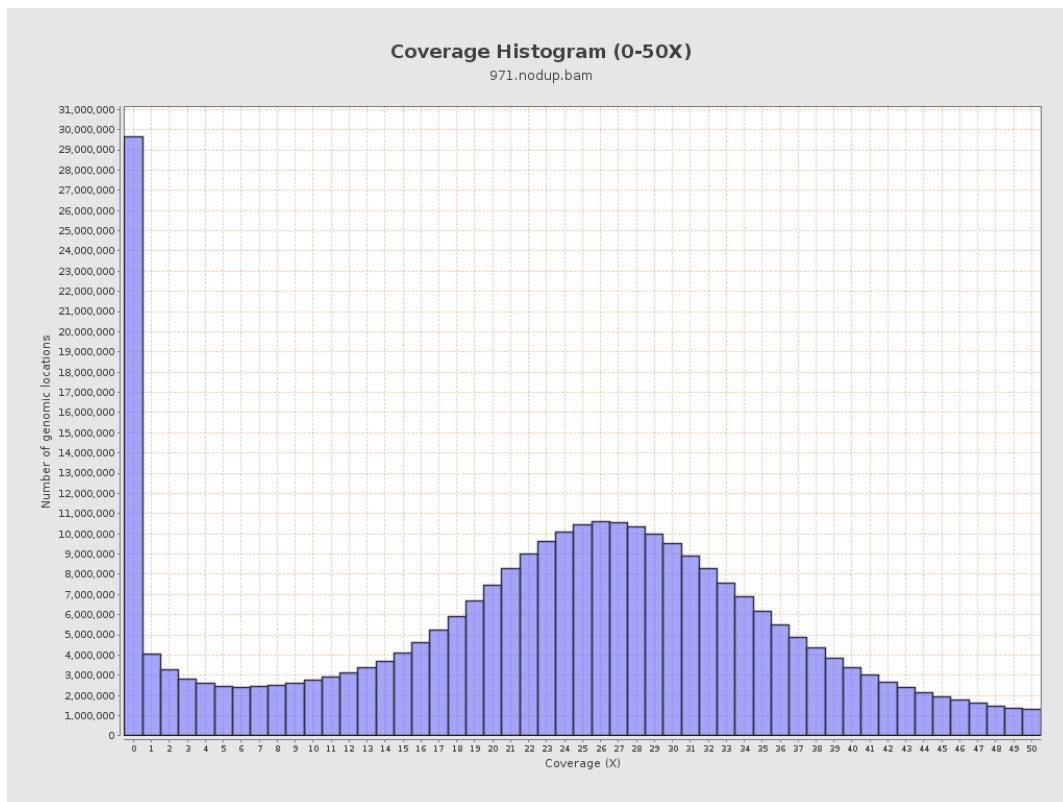
3. Results : Coverage across reference



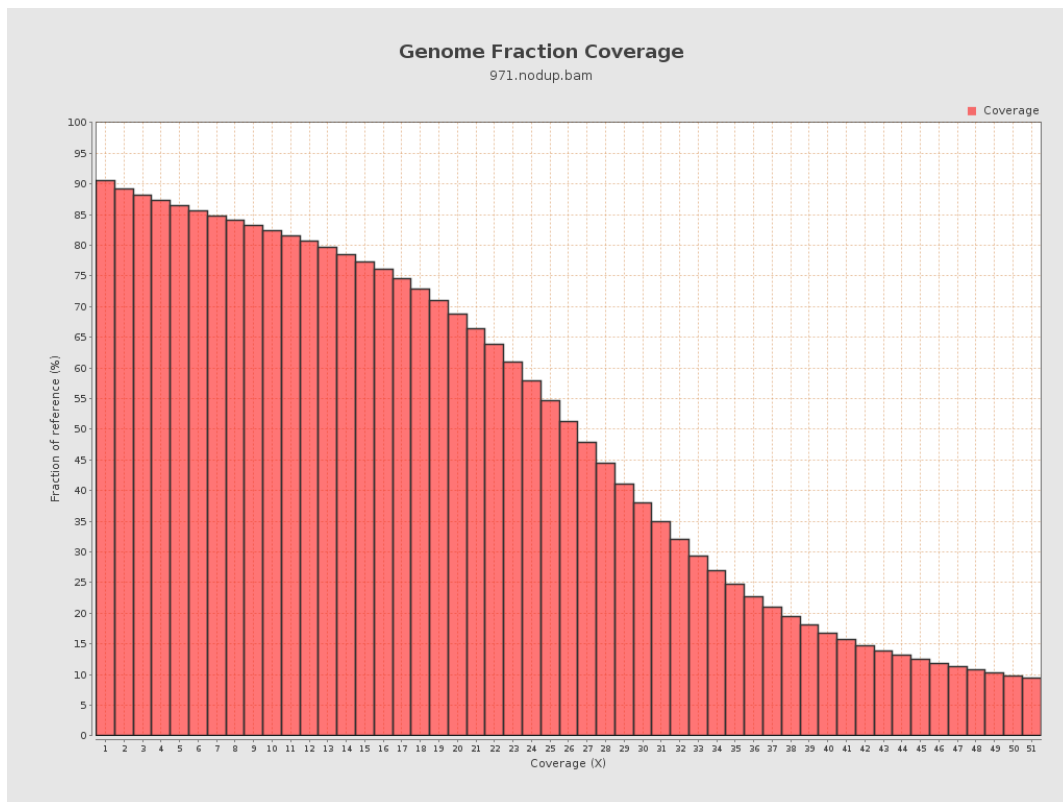
4. Results : Coverage Histogram



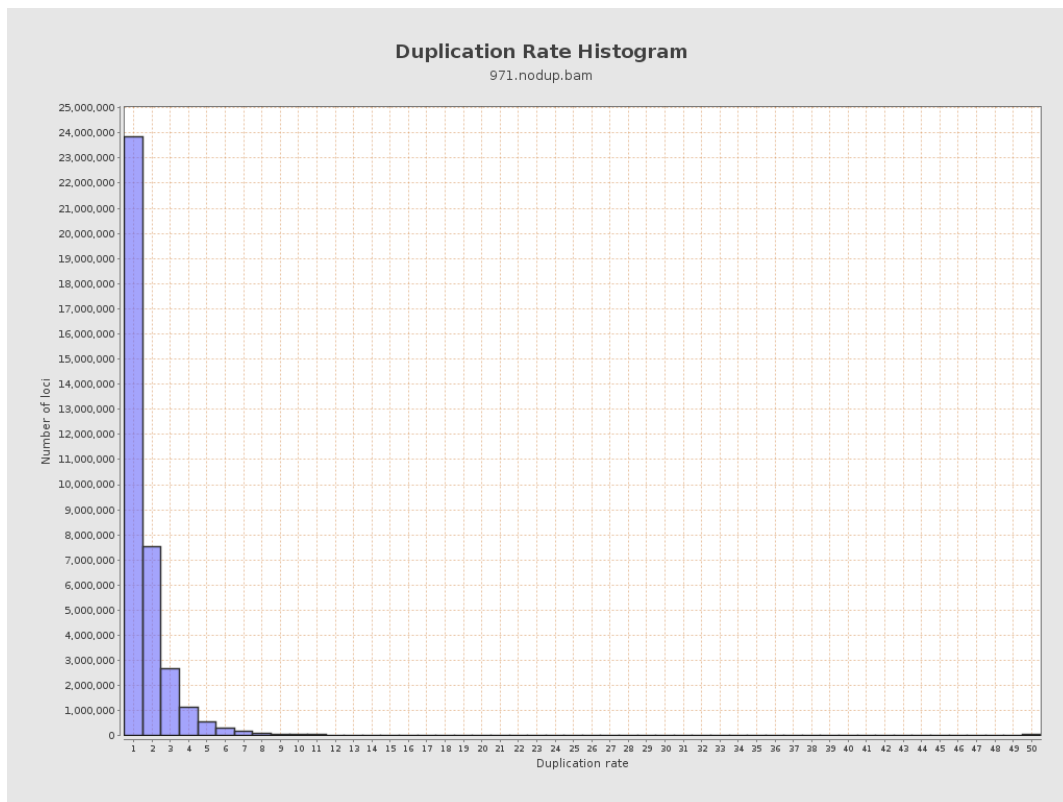
5. Results : Coverage Histogram (0-50X)



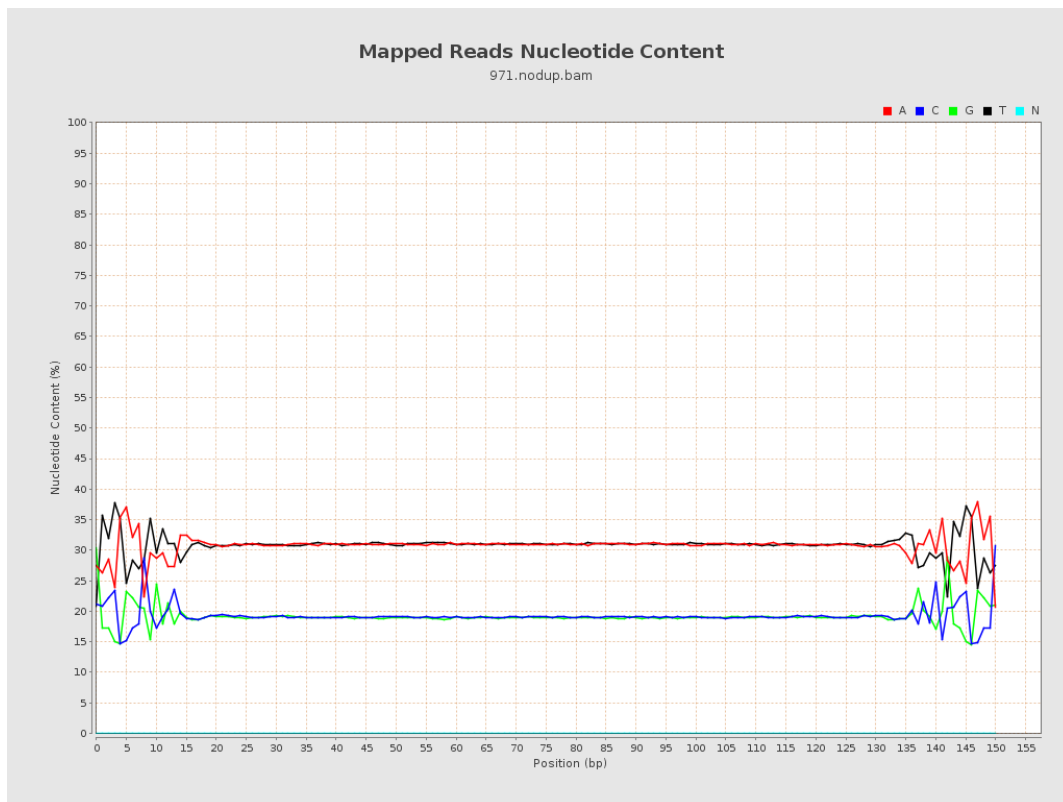
6. Results : Genome Fraction Coverage



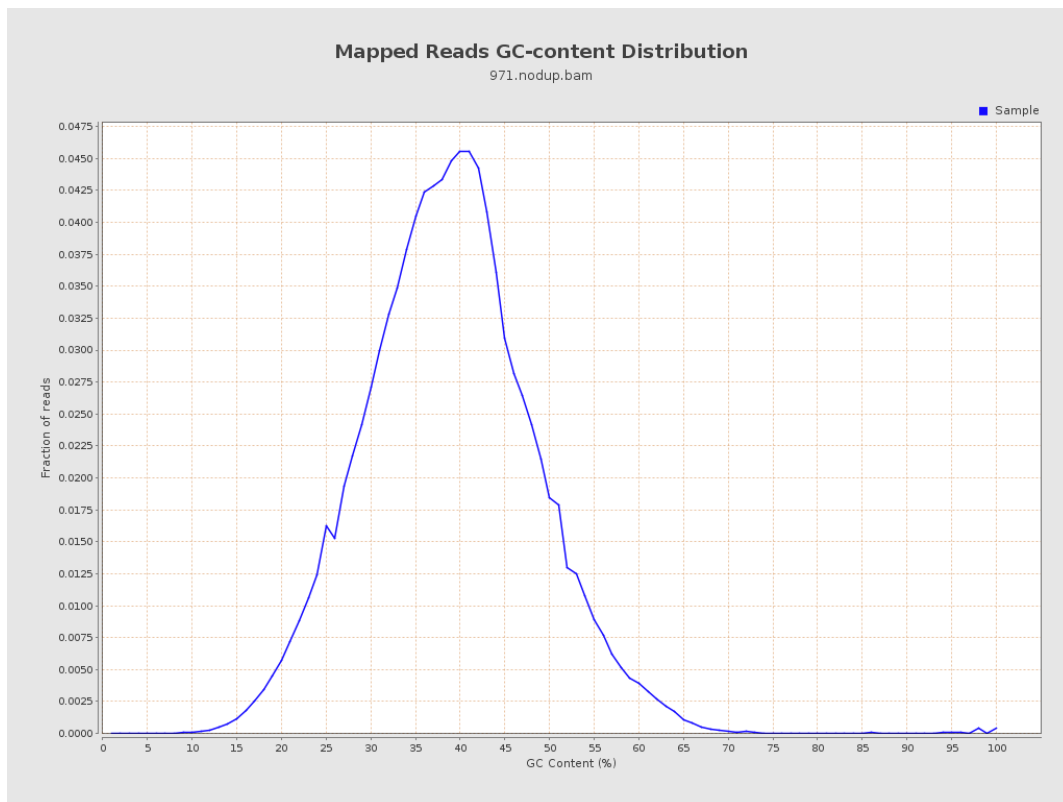
7. Results : Duplication Rate Histogram



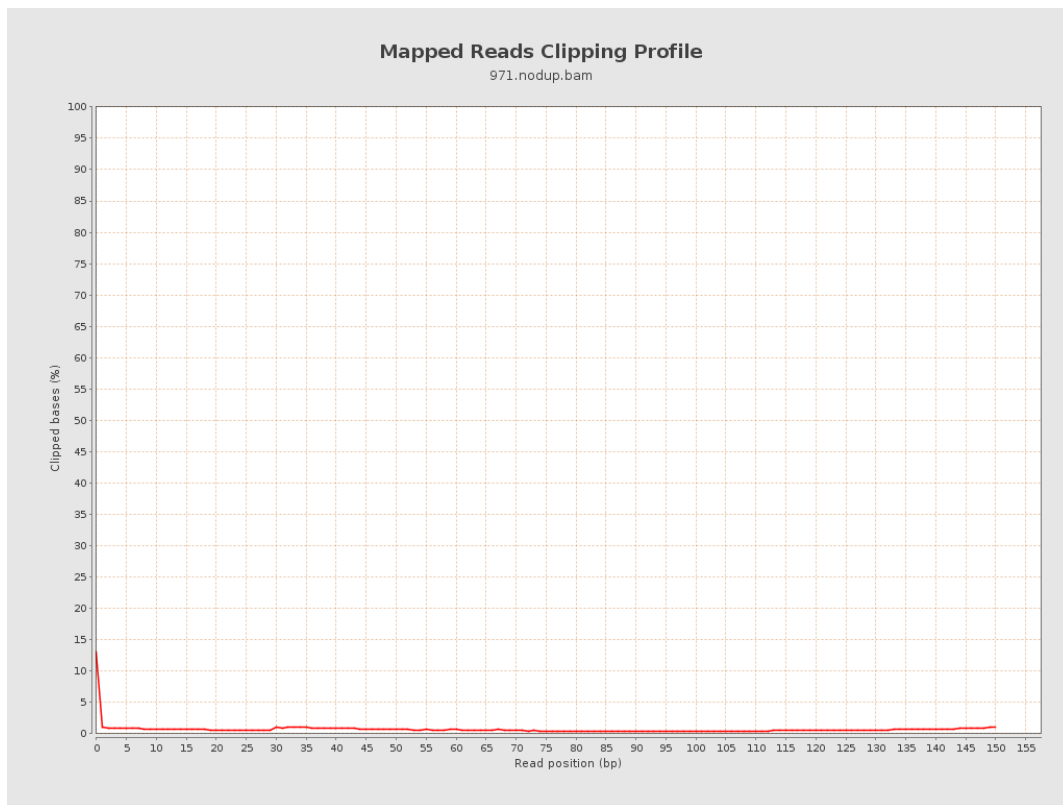
8. Results : Mapped Reads Nucleotide Content



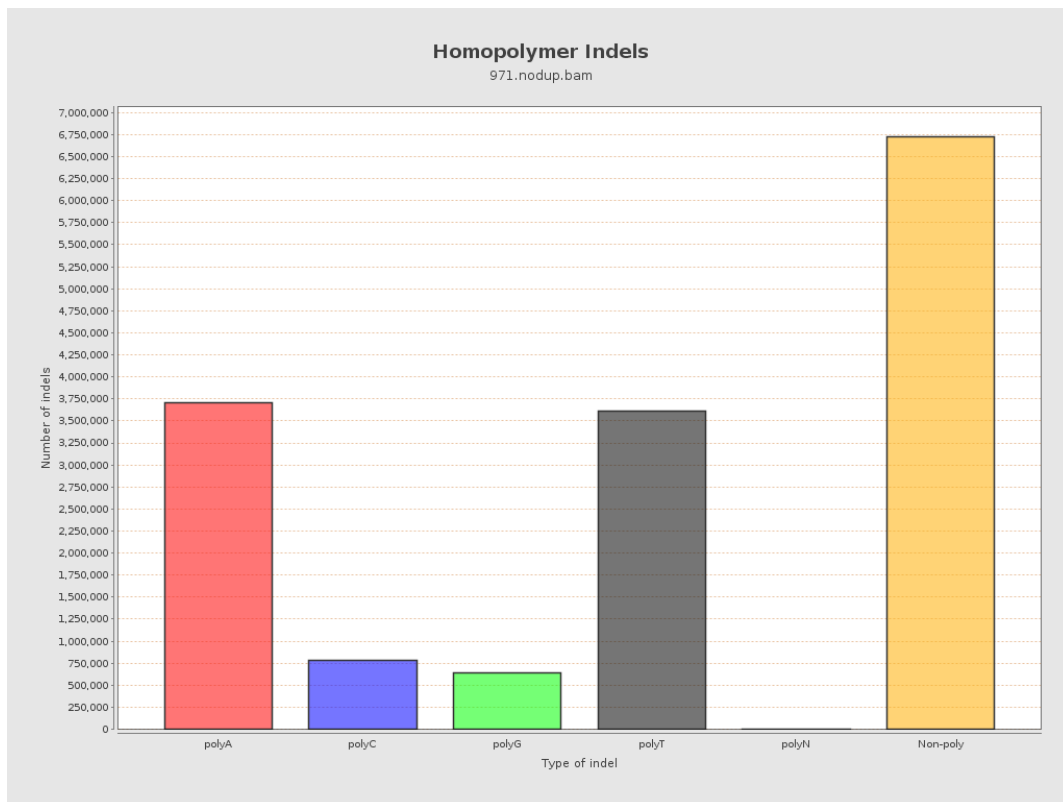
9. Results : Mapped Reads GC-content Distribution



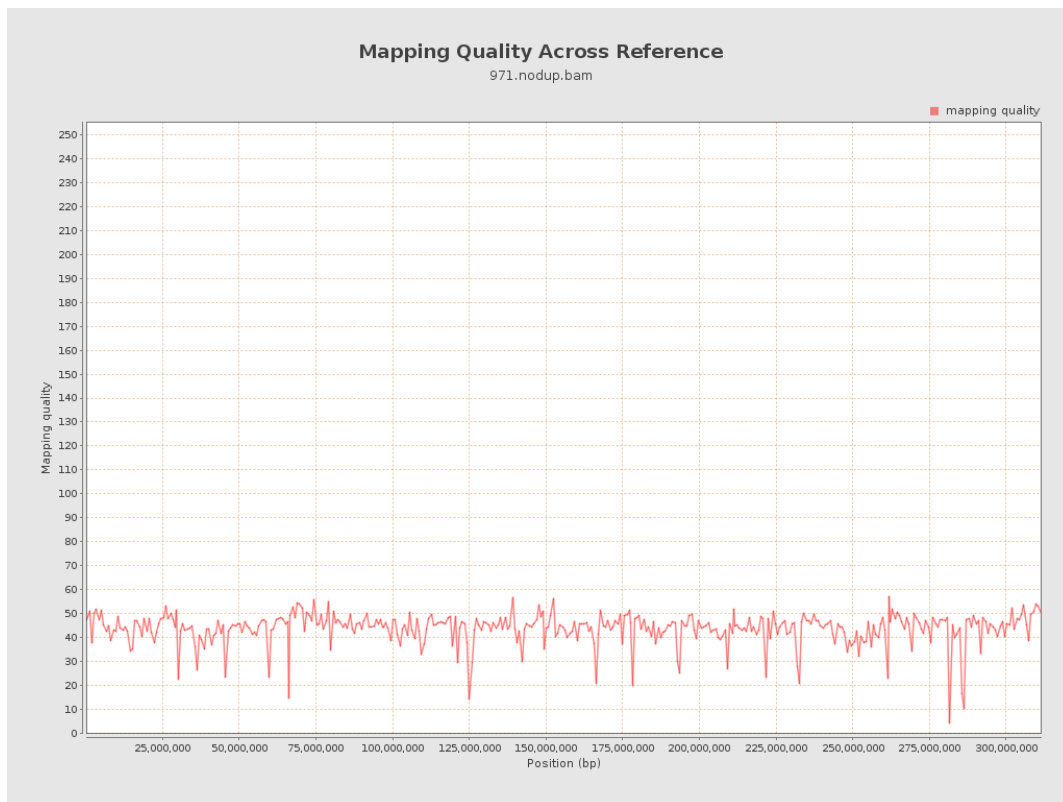
10. Results : Mapped Reads Clipping Profile



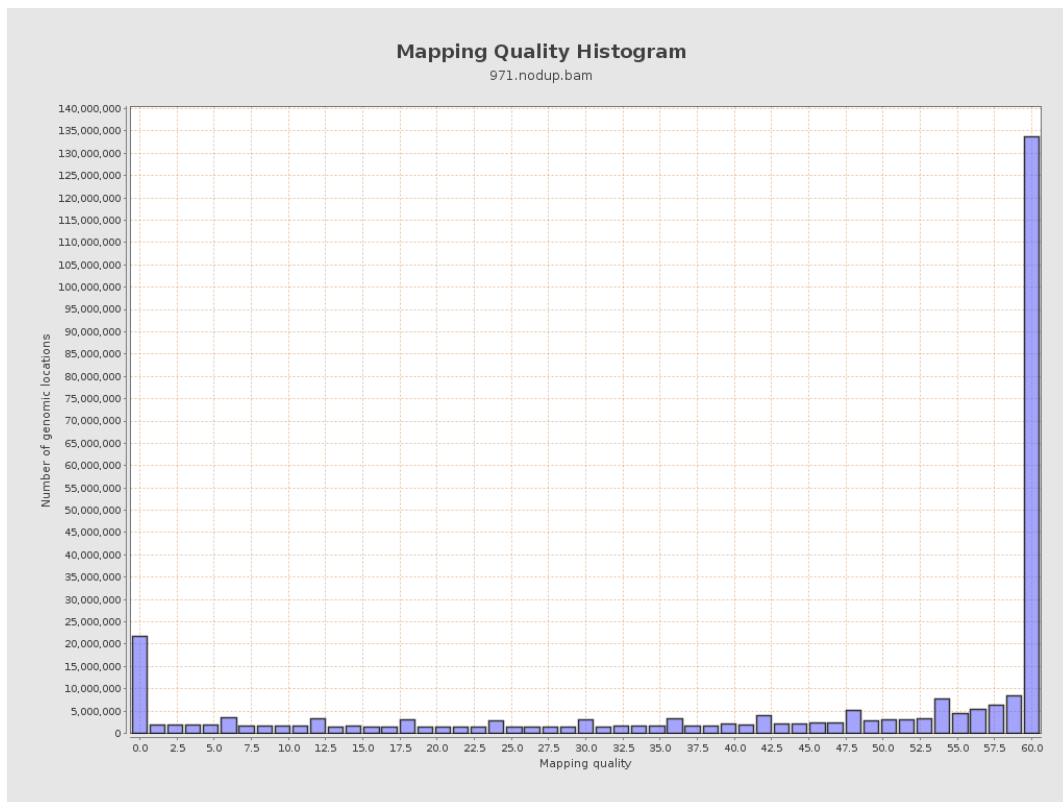
11. Results : Homopolymer Indels



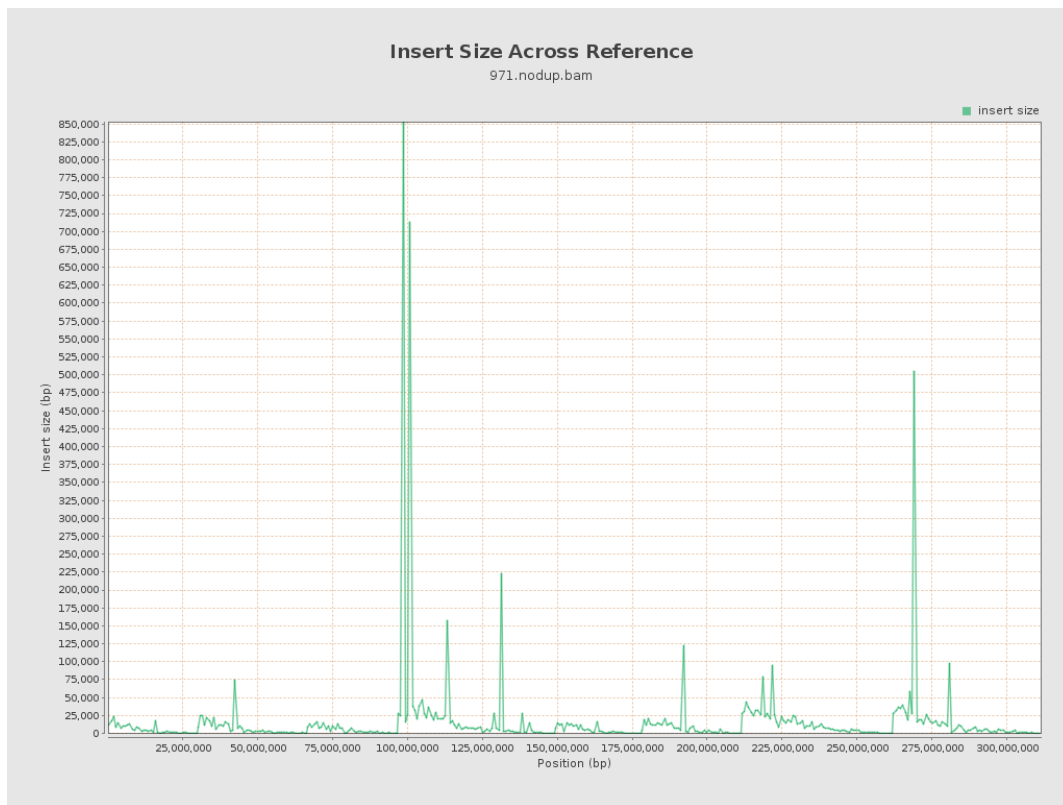
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

