

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:37:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/831
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/831.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_550/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_550_S117_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_550/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_550_S117_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:37:32 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	82,752,063
Mapped reads	77,157,575 / 93.24%
Unmapped reads	5,594,488 / 6.76%
Mapped paired reads	77,157,575 / 93.24%
Mapped reads, first in pair	38,758,329 / 46.84%
Mapped reads, second in pair	38,399,246 / 46.4%
Mapped reads, both in pair	75,416,905 / 91.14%
Mapped reads, singletons	1,740,670 / 2.1%
Read min/max/mean length	30 / 151 / 148.11
Duplicated reads (flagged)	12,313,827 / 14.88%
Clipped reads	19,034,038 / 23%

2.2. ACGT Content

Number/percentage of A's	3,279,529,468 / 30.94%
Number/percentage of C's	2,019,539,960 / 19.05%
Number/percentage of T's	3,286,446,417 / 31%
Number/percentage of G's	2,015,013,886 / 19.01%
Number/percentage of N's	75,345 / 0%
GC Percentage	38.06%

2.3. Coverage

Mean	34.1026
Standard Deviation	262.9725

2.4. Mapping Quality

Mean Mapping Quality	44.26
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2.5. Insert size

Mean	226,559.71
Standard Deviation	2,268,494.82
P25/Median/P75	323 / 431 / 562

2.6. Mismatches and indels

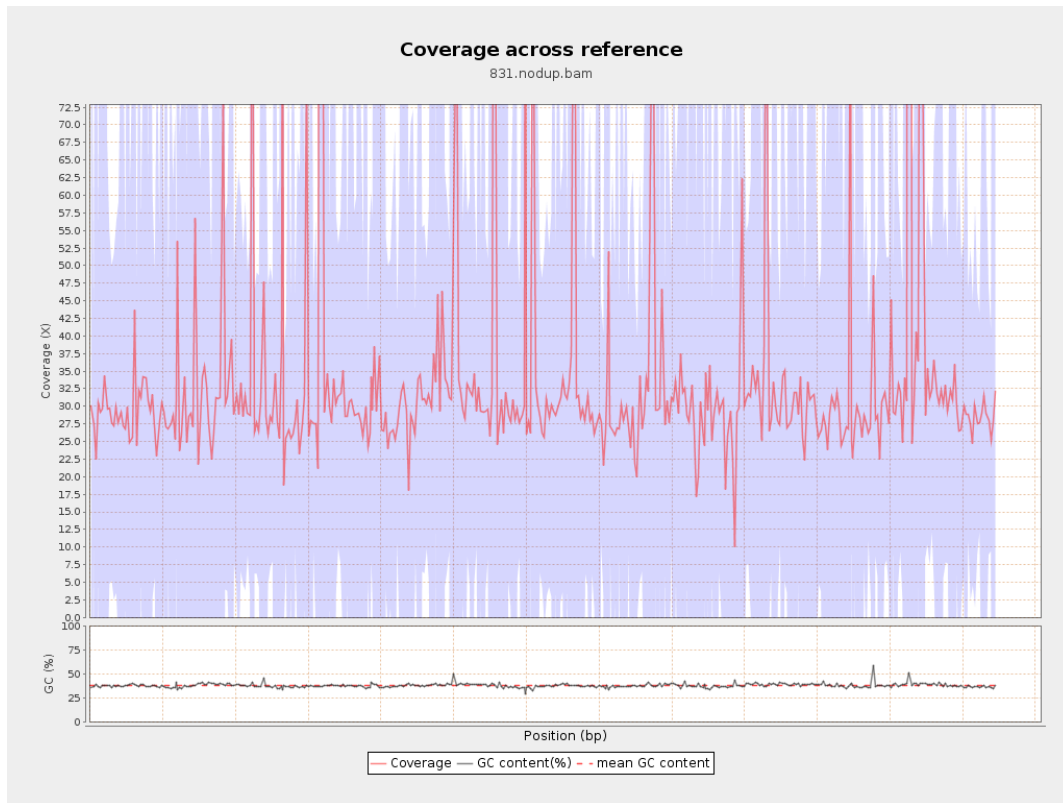
General error rate	2.55%
Mismatches	250,324,525
Insertions	7,115,764
Mapped reads with at least one insertion	8.28%
Deletions	7,212,696
Mapped reads with at least one deletion	8.31%
Homopolymer indels	56.4%

2.7. Chromosome stats

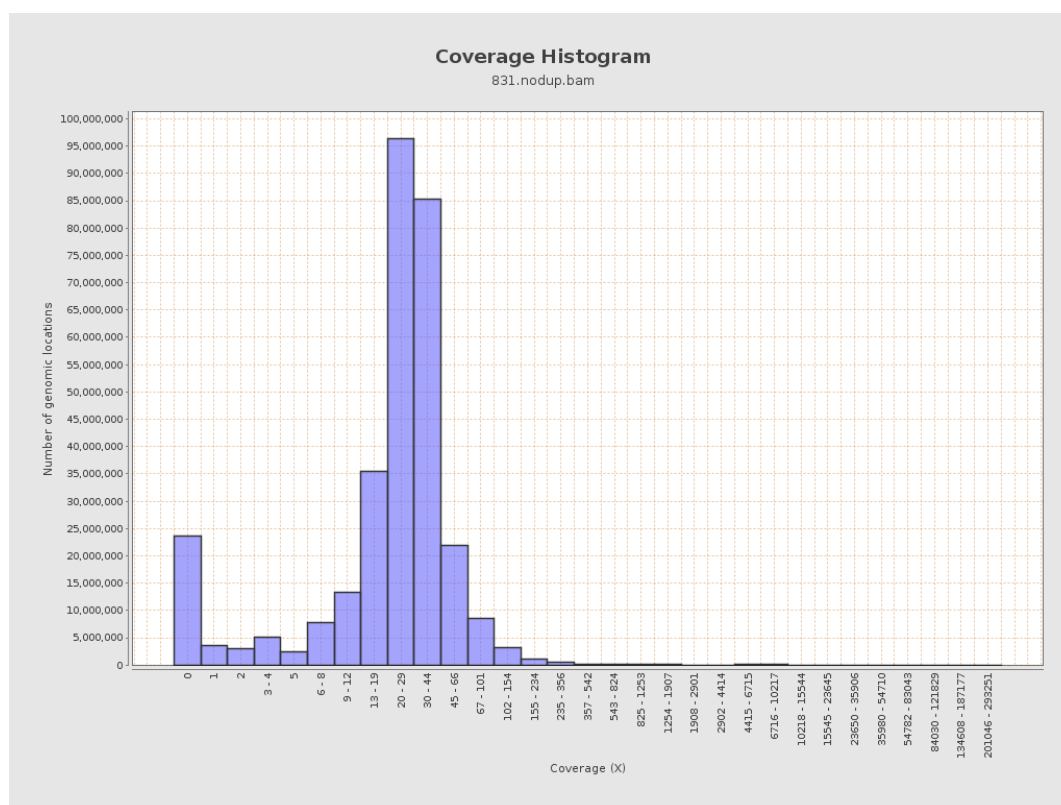
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	863622329	29.0544	81.7794

LT669789.1	36598175	1241541204	33.9236	254.9666
LT669790.1	30422129	1127064778	37.0475	279.182
LT669791.1	52758100	1758553565	33.3324	232.5296
LT669792.1	28376109	971463008	34.2352	281.8555
LT669793.1	33388210	1060005577	31.7479	186.516
LT669794.1	50579949	1610363020	31.838	213.3674
LT669795.1	49795044	1995178862	40.0678	401.5221

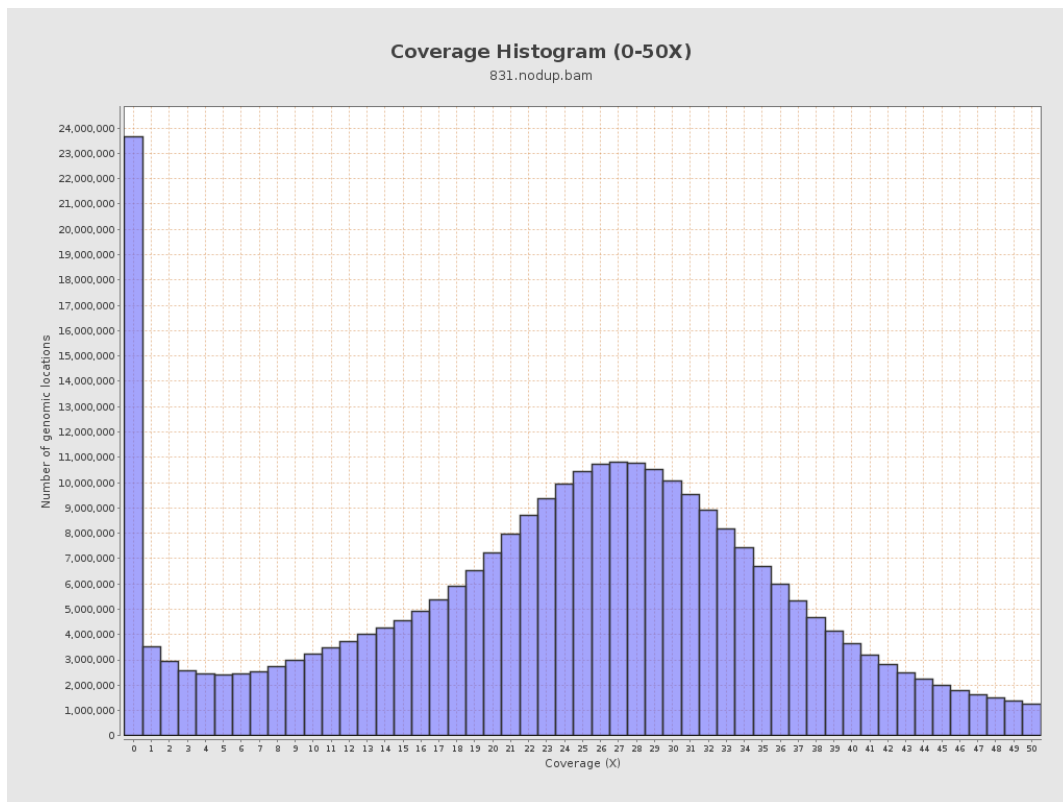
3. Results : Coverage across reference



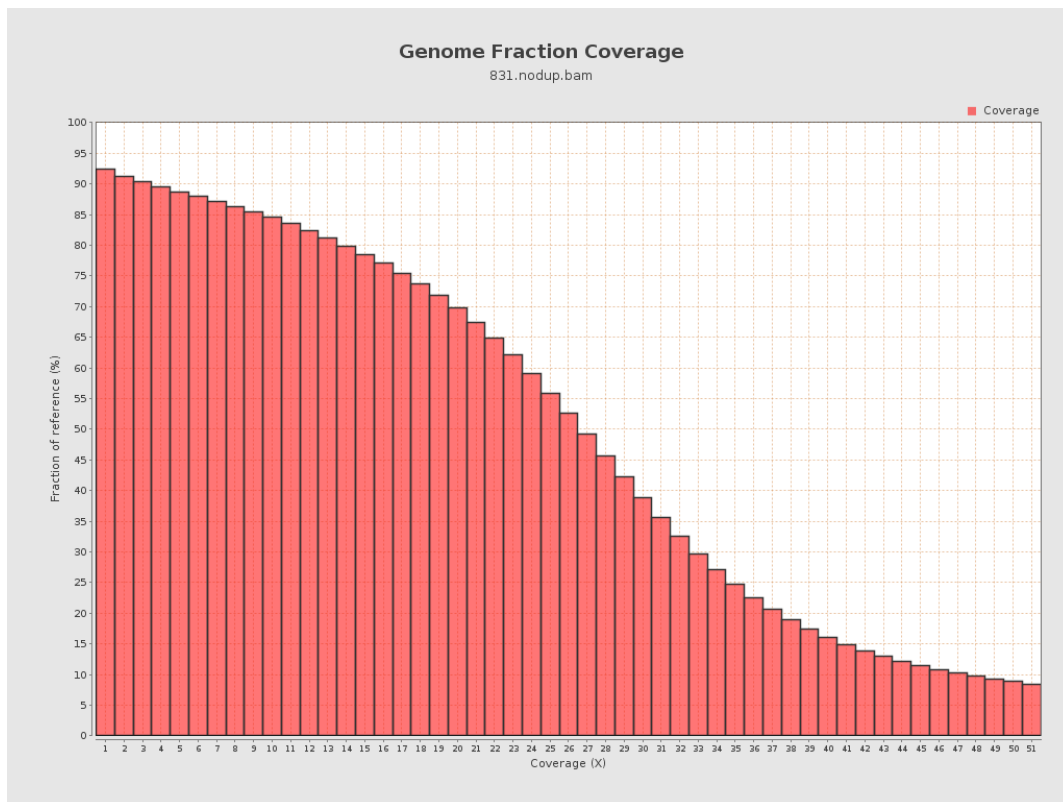
4. Results : Coverage Histogram



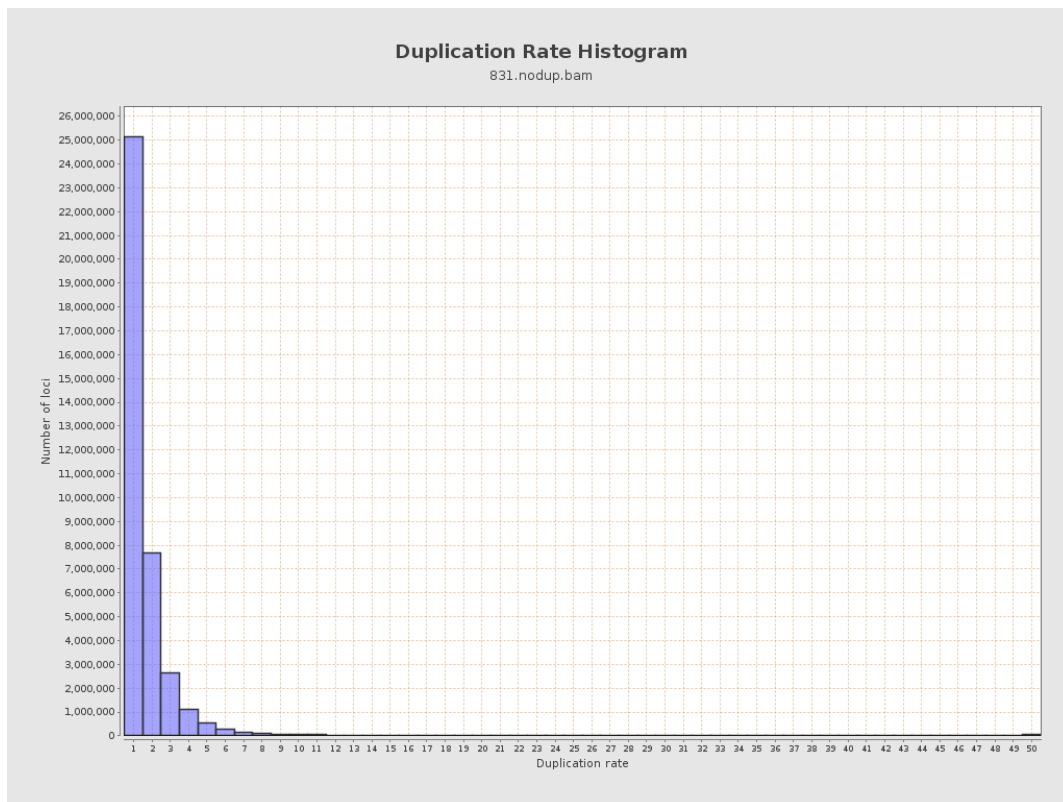
5. Results : Coverage Histogram (0-50X)



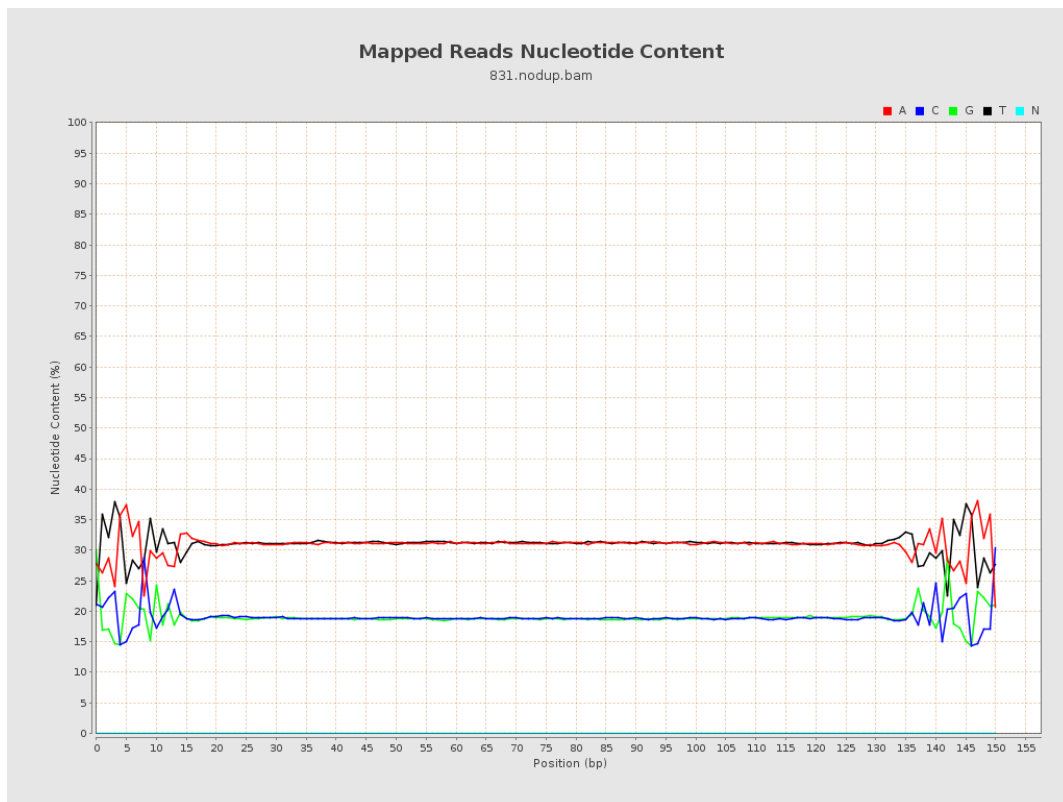
6. Results : Genome Fraction Coverage



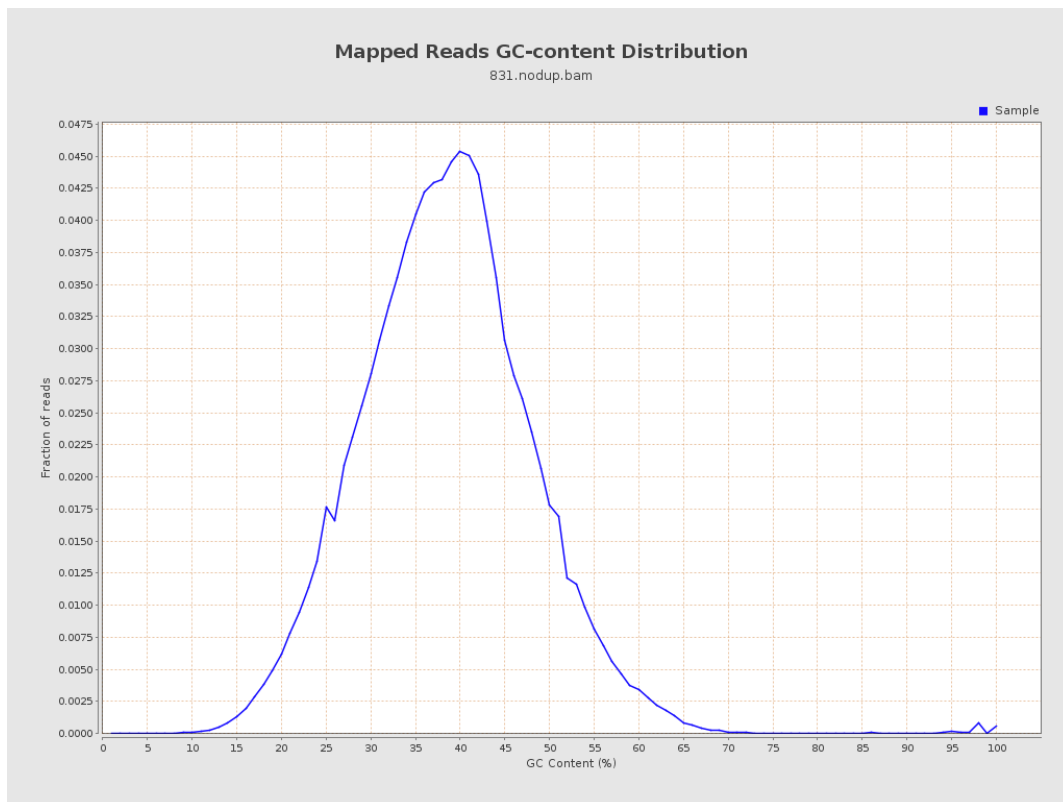
7. Results : Duplication Rate Histogram



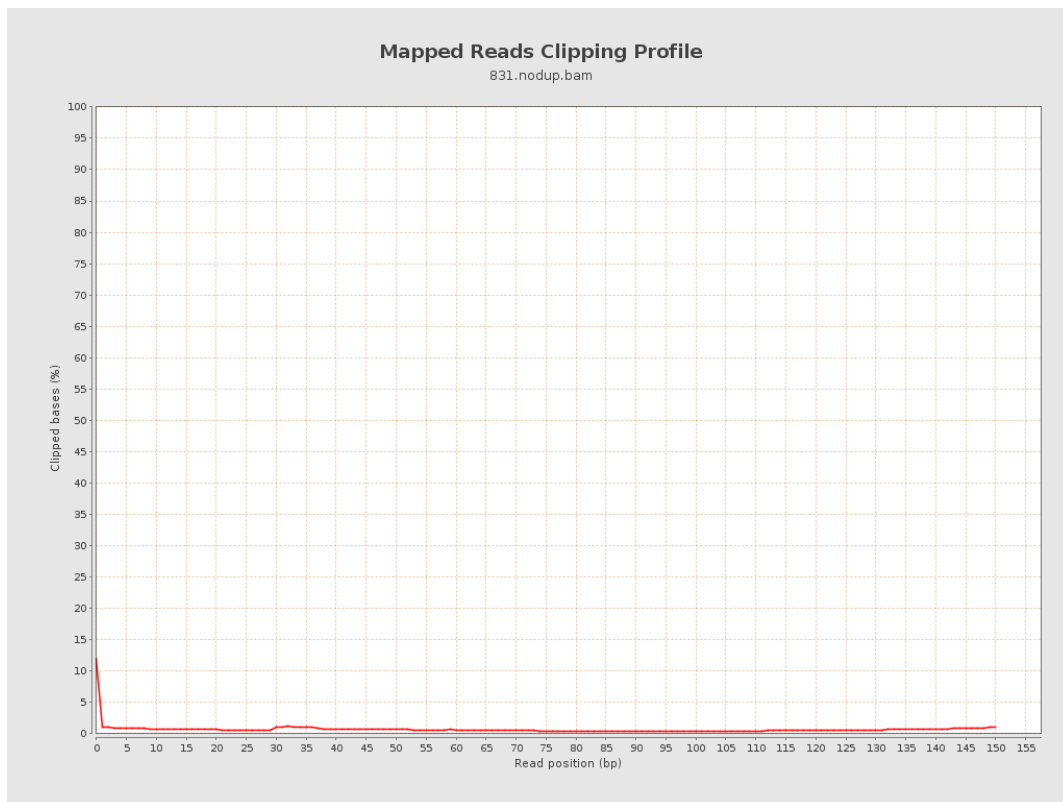
8. Results : Mapped Reads Nucleotide Content



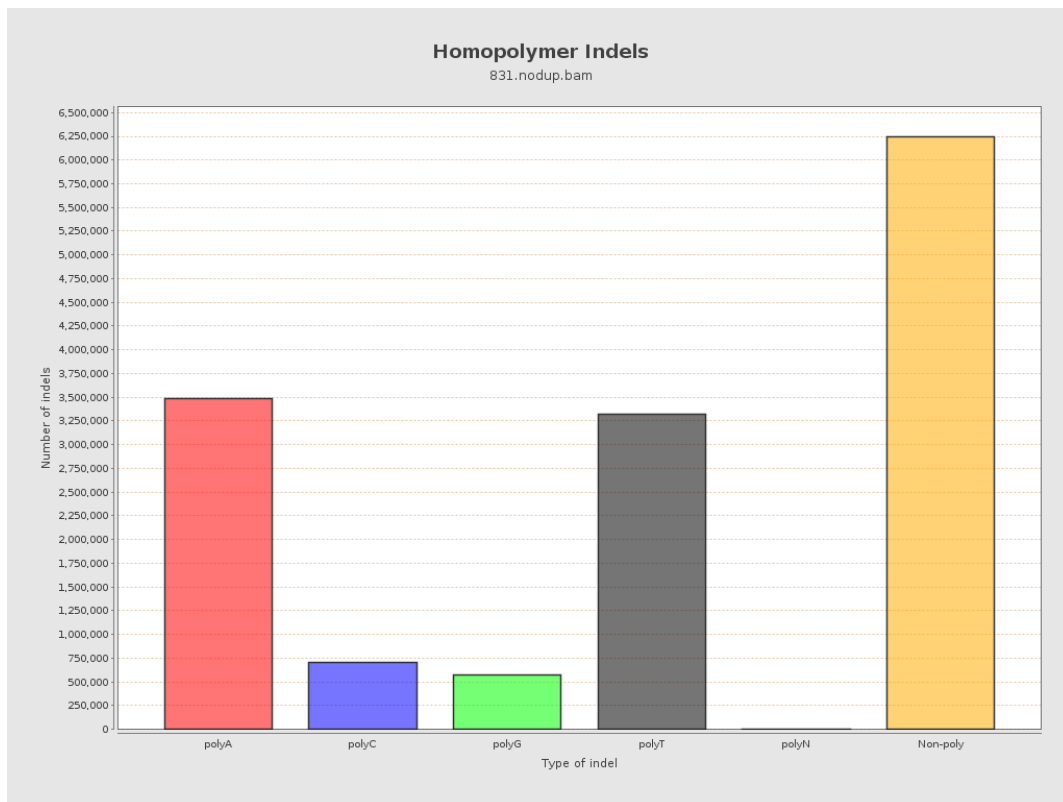
9. Results : Mapped Reads GC-content Distribution



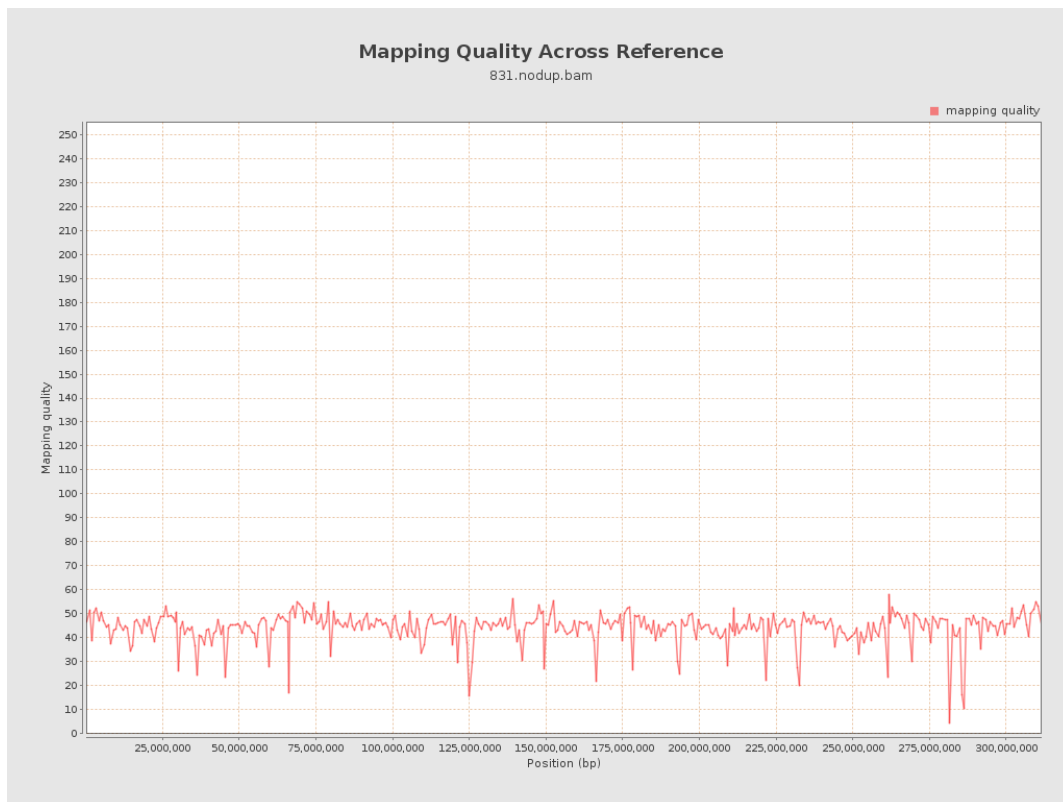
10. Results : Mapped Reads Clipping Profile



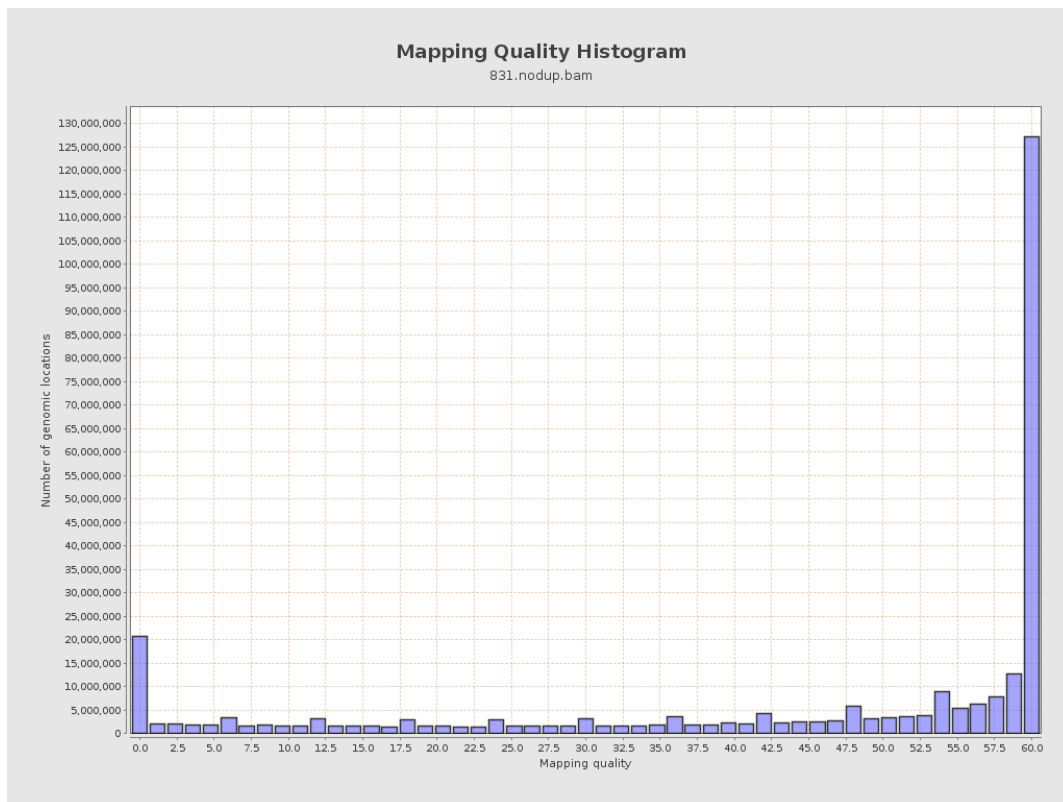
11. Results : Homopolymer Indels



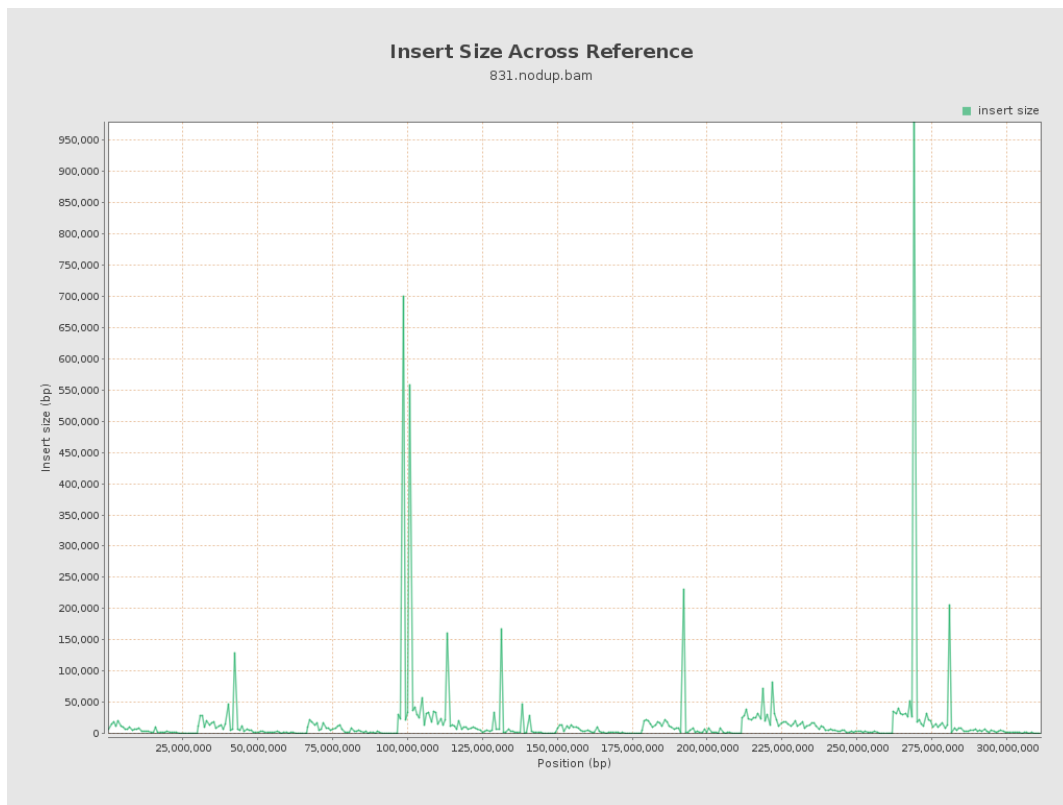
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

