

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:30:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/110
4
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1104 .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\t SM:\$sample /proj/uppstore2018210/Aalpina/data/r eference/GCA_900128785.1_MPIPZ. v5_genomic.fa /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_491/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_491_S466_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_491/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_491_S466_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:30:39 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	67,011,410
Mapped reads	59,235,784 / 88.4%
Unmapped reads	7,775,626 / 11.6%
Mapped paired reads	59,235,784 / 88.4%
Mapped reads, first in pair	29,624,069 / 44.21%
Mapped reads, second in pair	29,611,715 / 44.19%
Mapped reads, both in pair	57,814,605 / 86.28%
Mapped reads, singletons	1,421,179 / 2.12%
Read min/max/mean length	30 / 151 / 148.46
Duplicated reads (flagged)	9,177,933 / 13.7%
Clipped reads	12,473,300 / 18.61%

2.2. ACGT Content

Number/percentage of A's	2,551,138,584 / 30.9%
Number/percentage of C's	1,576,944,559 / 19.1%
Number/percentage of T's	2,553,874,442 / 30.93%
Number/percentage of G's	1,574,116,027 / 19.07%
Number/percentage of N's	26,591 / 0%
GC Percentage	38.17%

2.3. Coverage

Mean	26.5593
Standard Deviation	201.006

2.4. Mapping Quality

Mean Mapping Quality	44.62
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2.5. Insert size

Mean	237,660.57
Standard Deviation	2,322,191.21
P25/Median/P75	353 / 458 / 600

2.6. Mismatches and indels

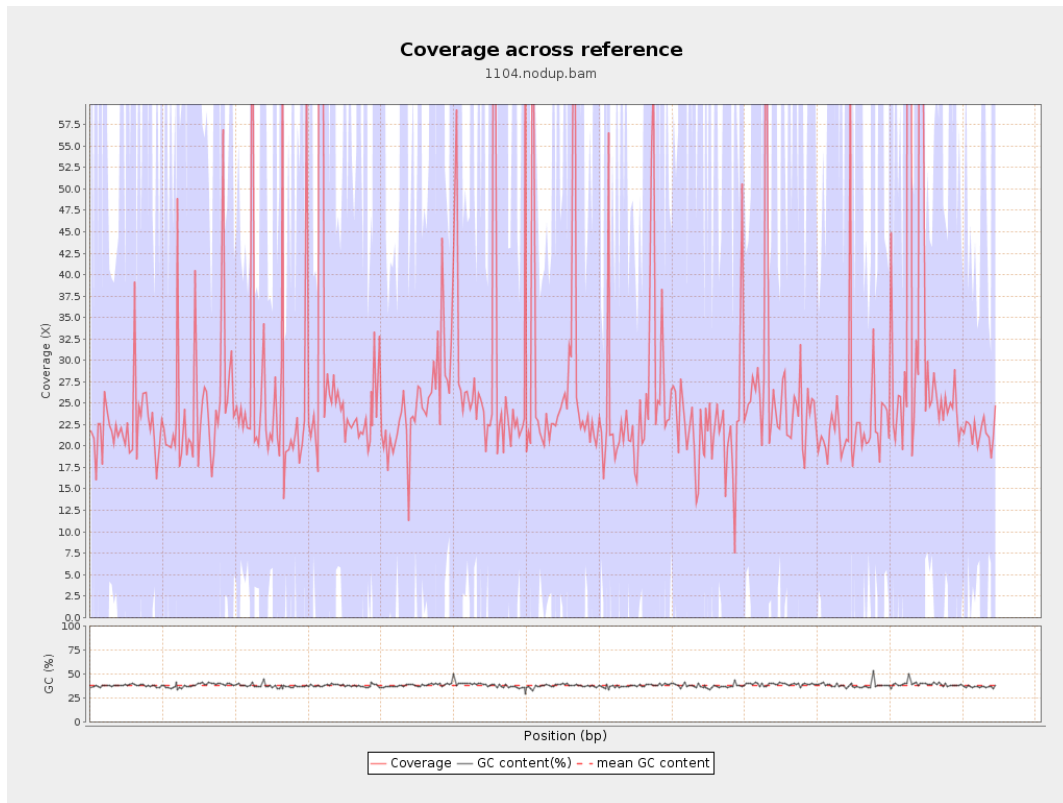
General error rate	2.28%
Mismatches	173,138,627
Insertions	5,513,076
Mapped reads with at least one insertion	8.34%
Deletions	5,515,630
Mapped reads with at least one deletion	8.28%
Homopolymer indels	56.76%

2.7. Chromosome stats

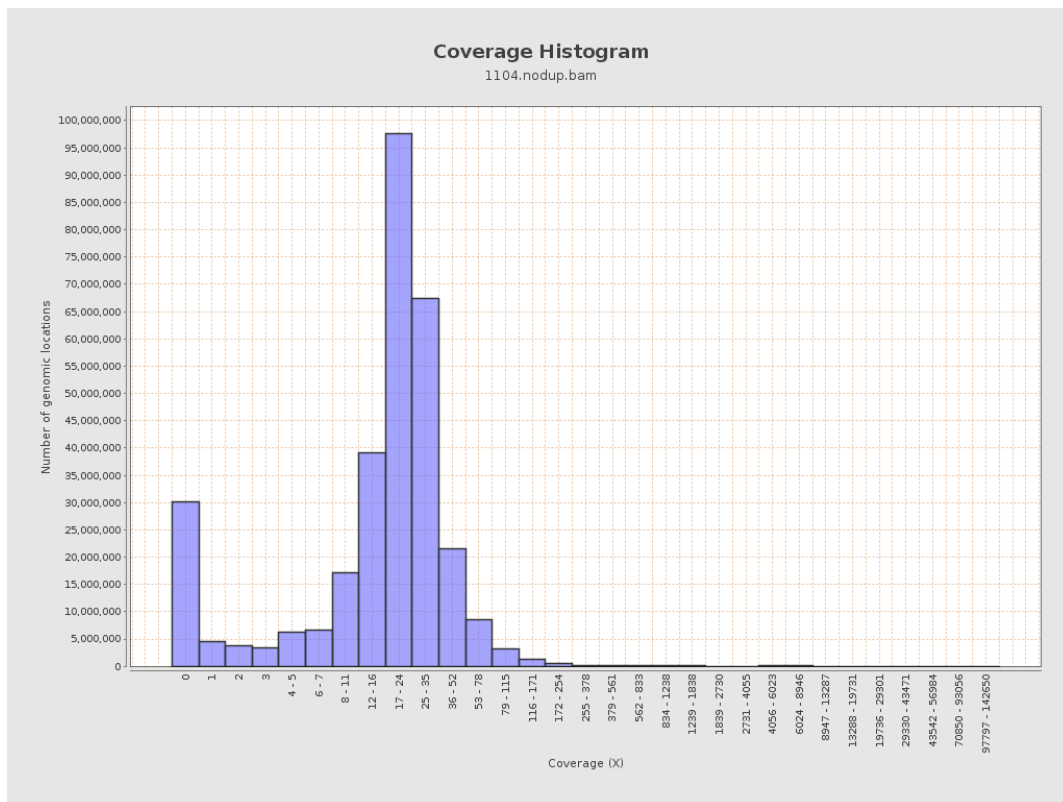
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	653764930	21.9943	65.5355

LT669789.1	36598175	953655347	26.0575	194.845
LT669790.1	30422129	901722828	29.6404	231.9071
LT669791.1	52758100	1390247318	26.3514	184.3046
LT669792.1	28376109	749830676	26.4247	220.8534
LT669793.1	33388210	819070455	24.5317	197.0351
LT669794.1	50579949	1249385718	24.7012	156.3196
LT669795.1	49795044	1559317741	31.3147	273.5981

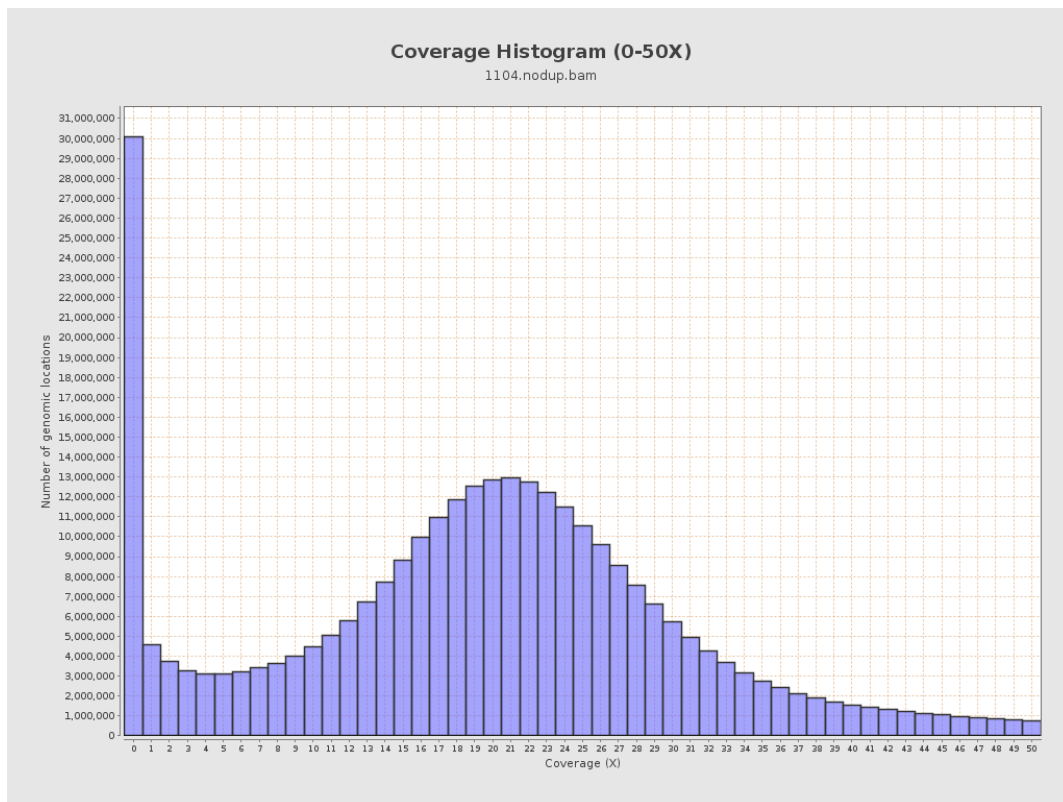
3. Results : Coverage across reference



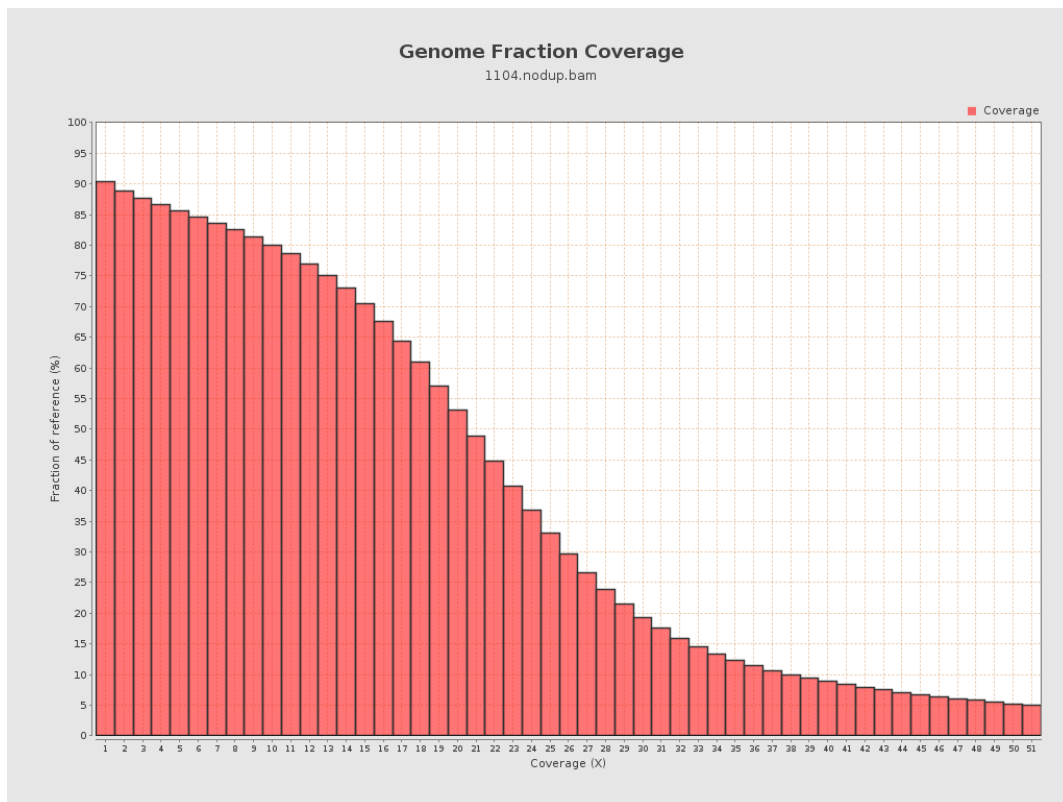
4. Results : Coverage Histogram



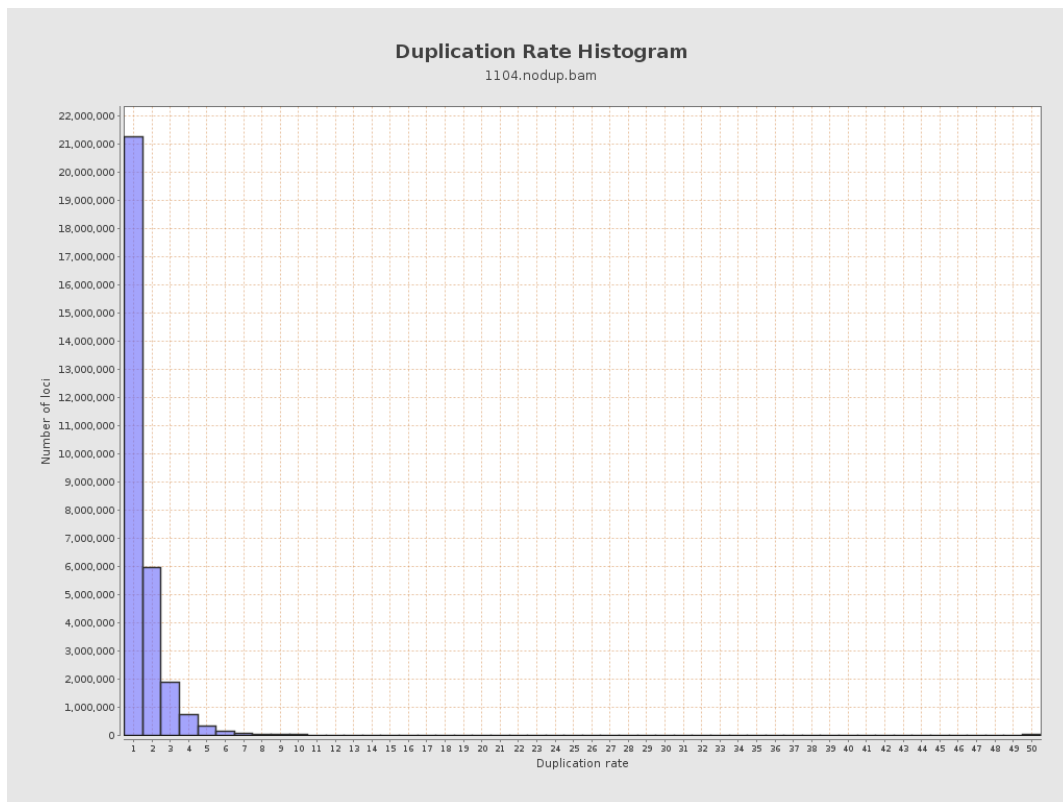
5. Results : Coverage Histogram (0-50X)



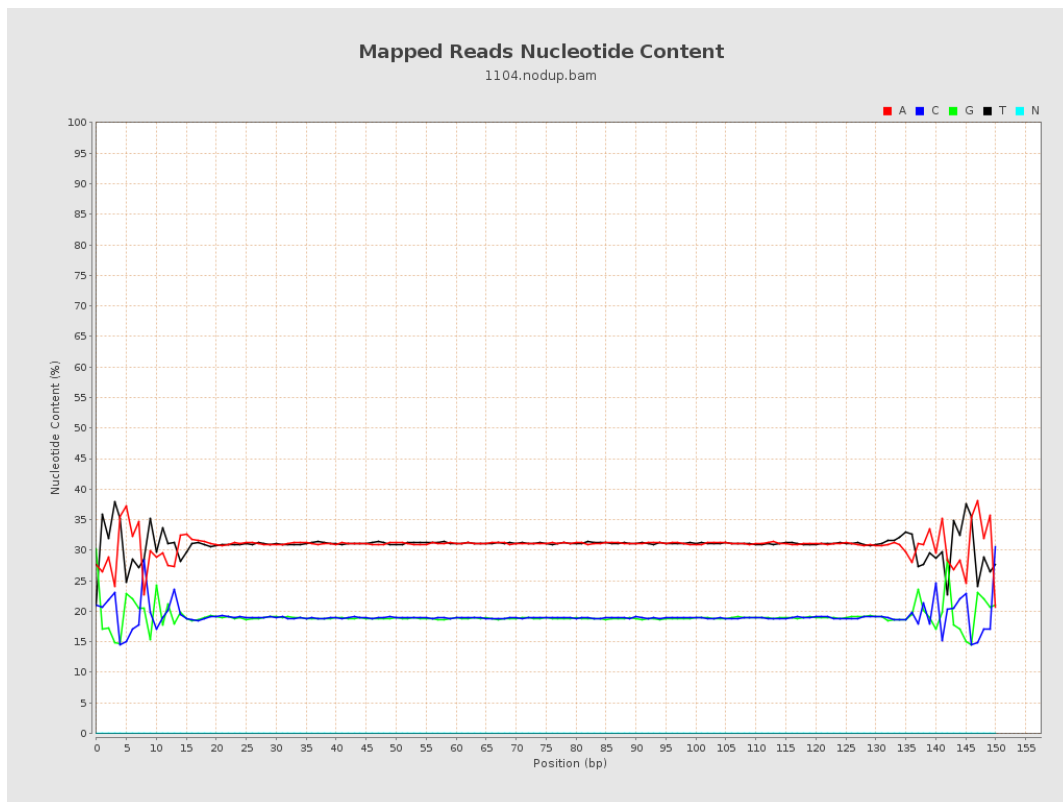
6. Results : Genome Fraction Coverage



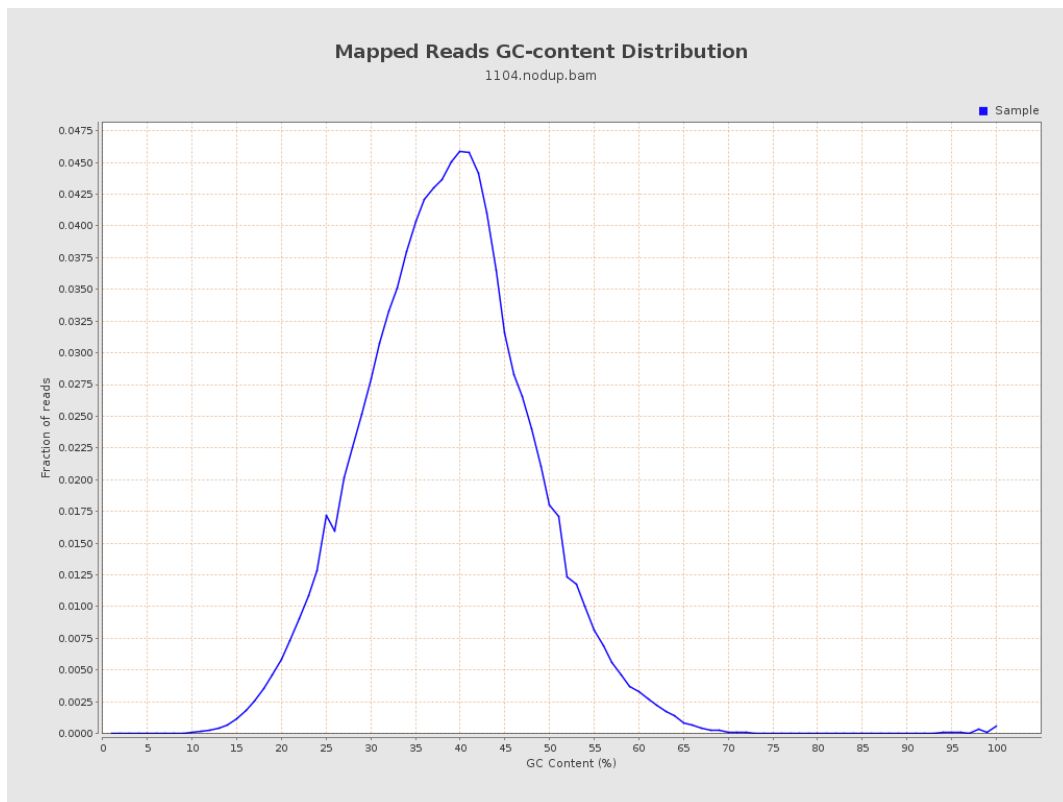
7. Results : Duplication Rate Histogram



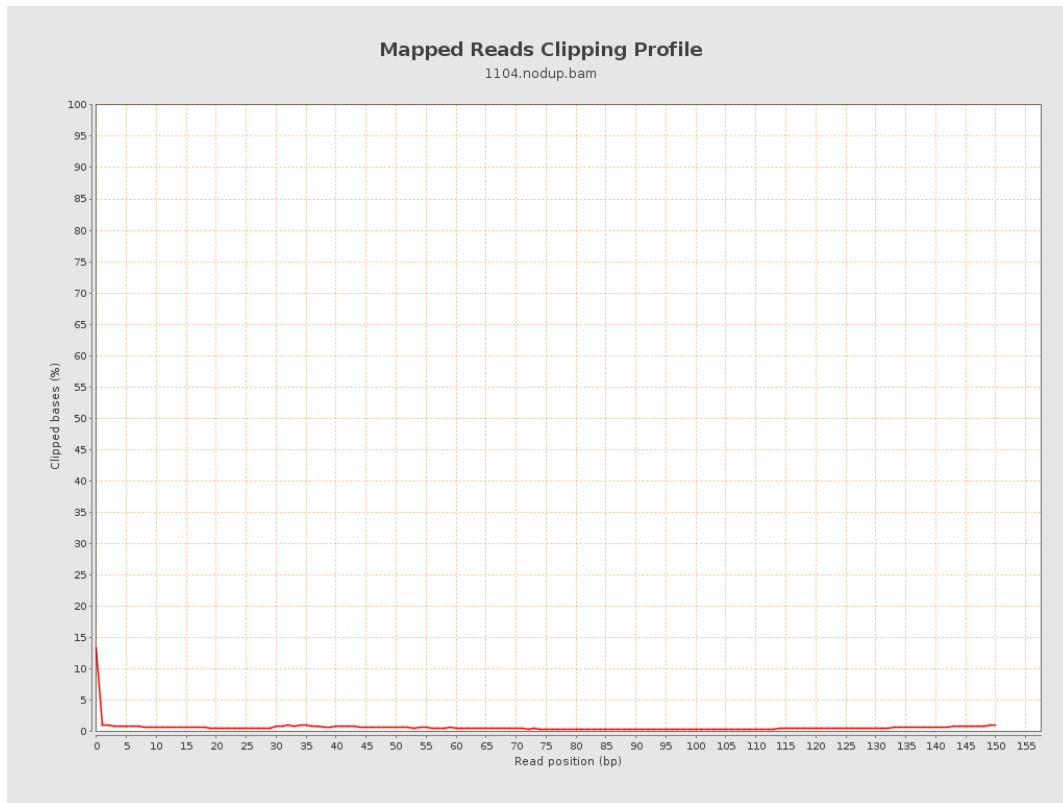
8. Results : Mapped Reads Nucleotide Content



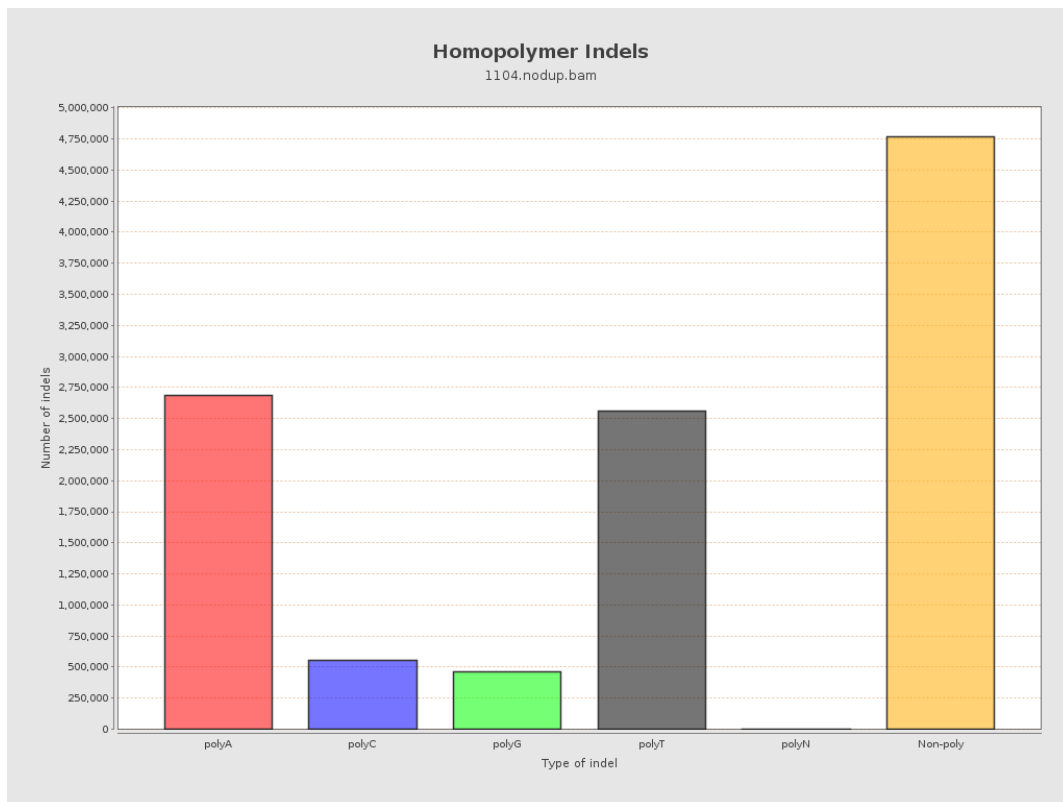
9. Results : Mapped Reads GC-content Distribution



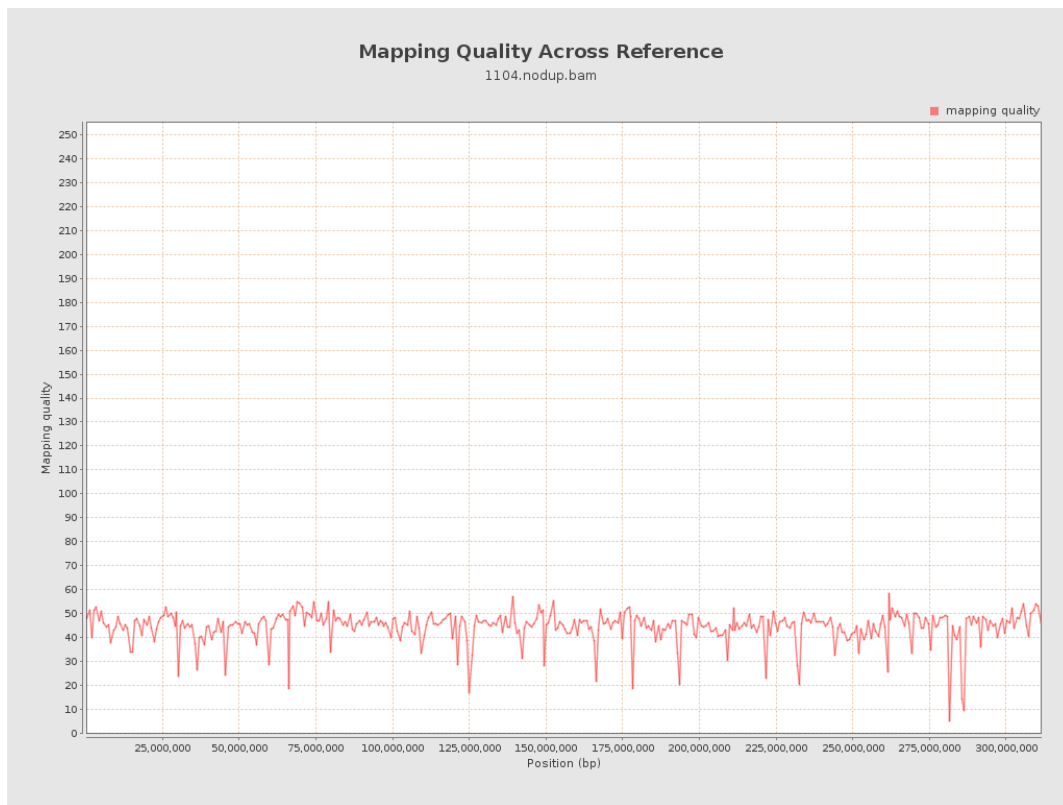
10. Results : Mapped Reads Clipping Profile



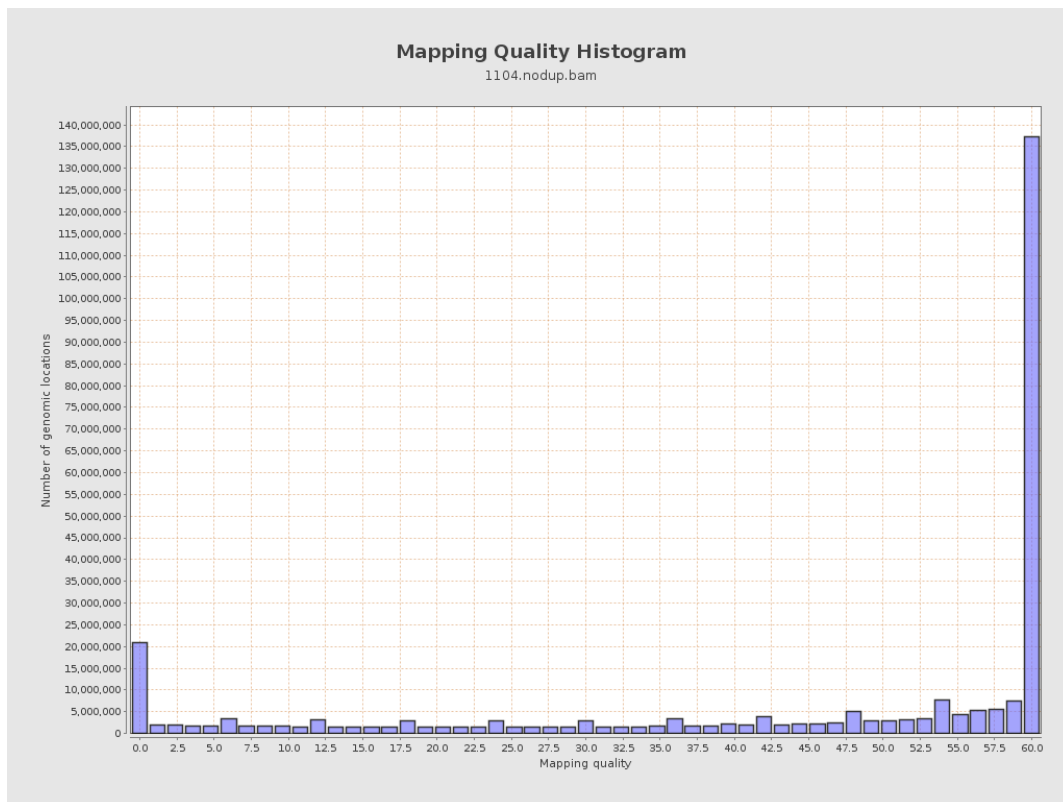
11. Results : Homopolymer Indels



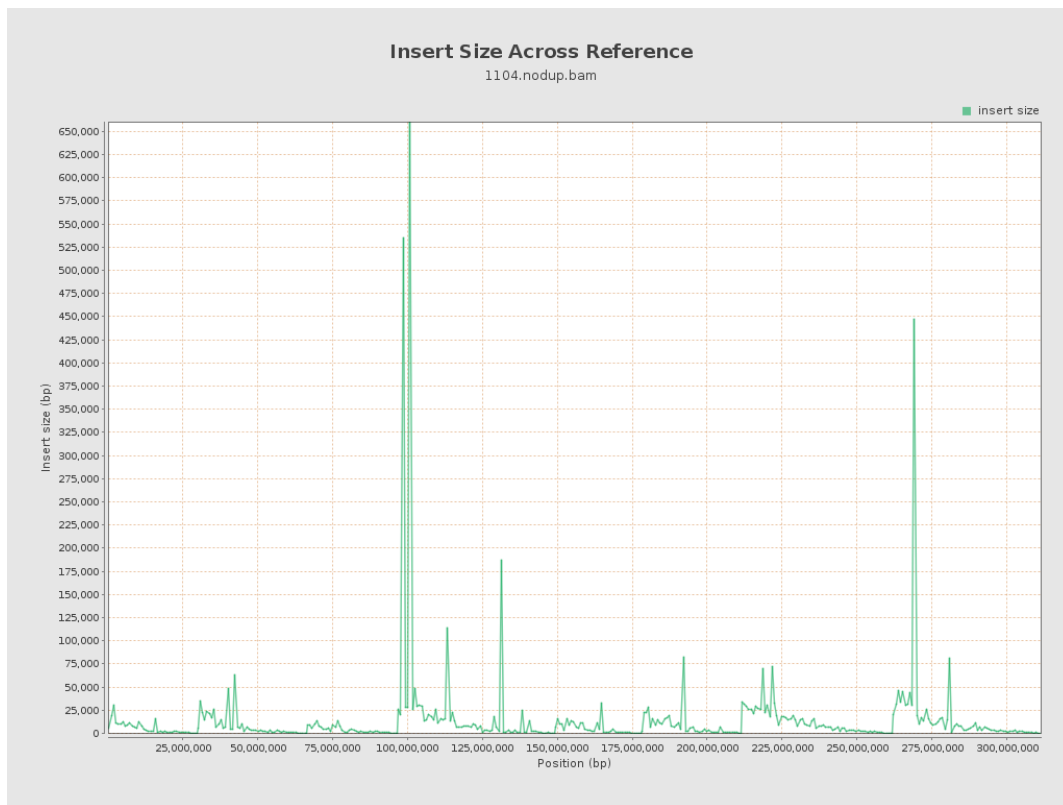
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

