

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:29:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/101
8
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1018 .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_567/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_567_S134_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_567/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_567_S134_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:29:16 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	60,672,780
Mapped reads	57,283,557 / 94.41%
Unmapped reads	3,389,223 / 5.59%
Mapped paired reads	57,283,557 / 94.41%
Mapped reads, first in pair	28,751,275 / 47.39%
Mapped reads, second in pair	28,532,282 / 47.03%
Mapped reads, both in pair	56,111,351 / 92.48%
Mapped reads, singletons	1,172,206 / 1.93%
Read min/max/mean length	30 / 151 / 148.19
Duplicated reads (flagged)	9,020,278 / 14.87%
Clipped reads	13,330,960 / 21.97%

2.2. ACGT Content

Number/percentage of A's	2,446,584,790 / 30.83%
Number/percentage of C's	1,521,952,674 / 19.18%
Number/percentage of T's	2,447,862,409 / 30.85%
Number/percentage of G's	1,518,755,961 / 19.14%
Number/percentage of N's	55,358 / 0%
GC Percentage	38.32%

2.3. Coverage

Mean	25.5259
Standard Deviation	208.1852

2.4. Mapping Quality

Mean Mapping Quality	44.15
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2.5. Insert size

Mean	213,939.4
Standard Deviation	2,186,066.85
P25/Median/P75	316 / 413 / 535

2.6. Mismatches and indels

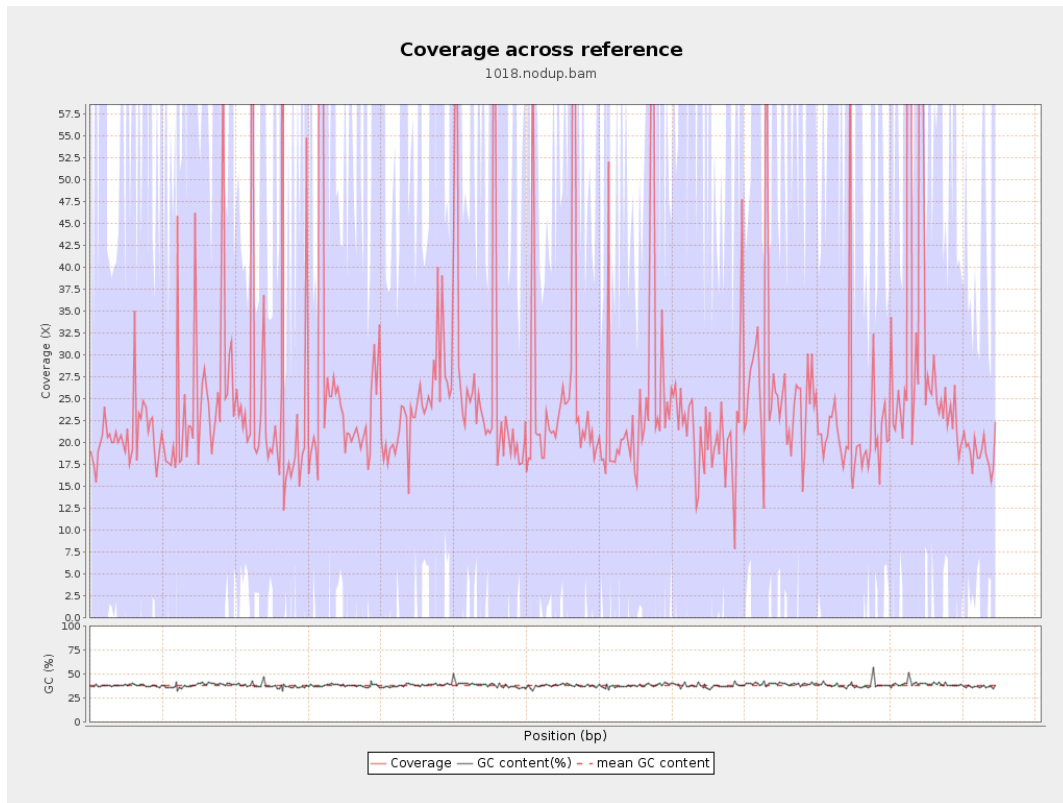
General error rate	2.56%
Mismatches	188,736,806
Insertions	5,214,297
Mapped reads with at least one insertion	8.2%
Deletions	5,317,721
Mapped reads with at least one deletion	8.27%
Homopolymer indels	56.17%

2.7. Chromosome stats

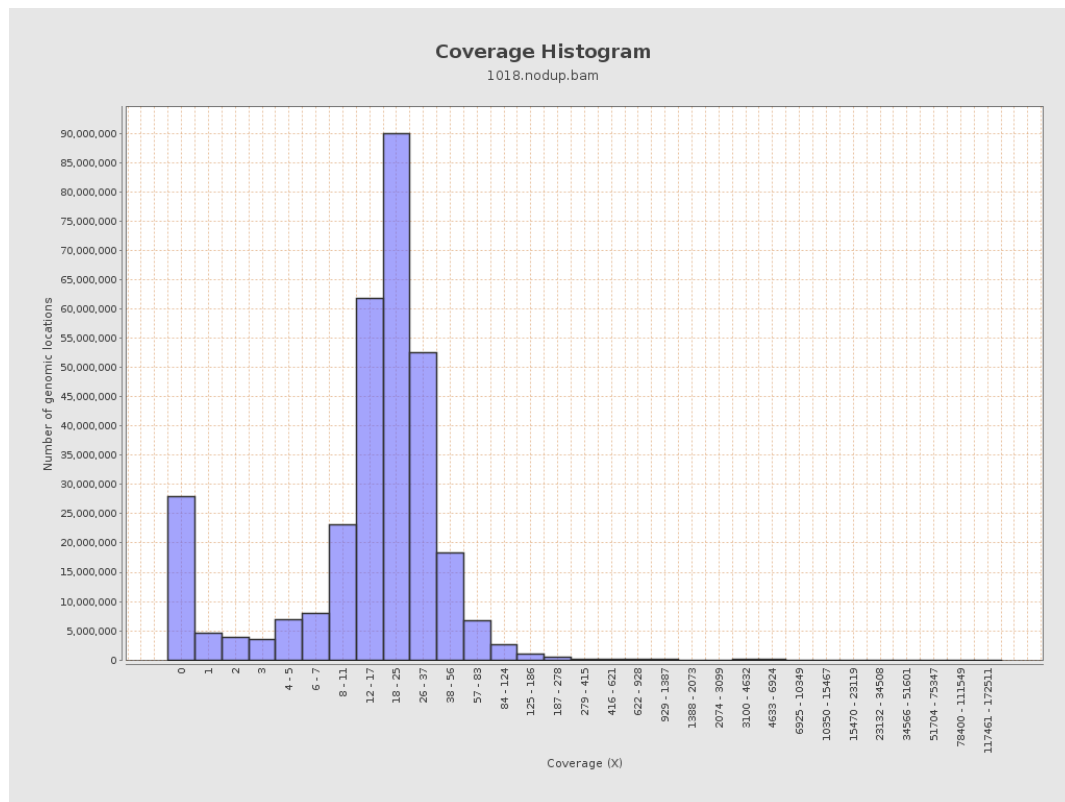
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	605083200	20.3565	61.7602

LT669789.1	36598175	965641452	26.385	220.0866
LT669790.1	30422129	824910146	27.1155	213.8697
LT669791.1	52758100	1350223806	25.5927	184.4262
LT669792.1	28376109	708981773	24.9852	261.562
LT669793.1	33388210	803064854	24.0523	153.4658
LT669794.1	50579949	1241495262	24.5452	187.2804
LT669795.1	49795044	1455532491	29.2305	280.9819

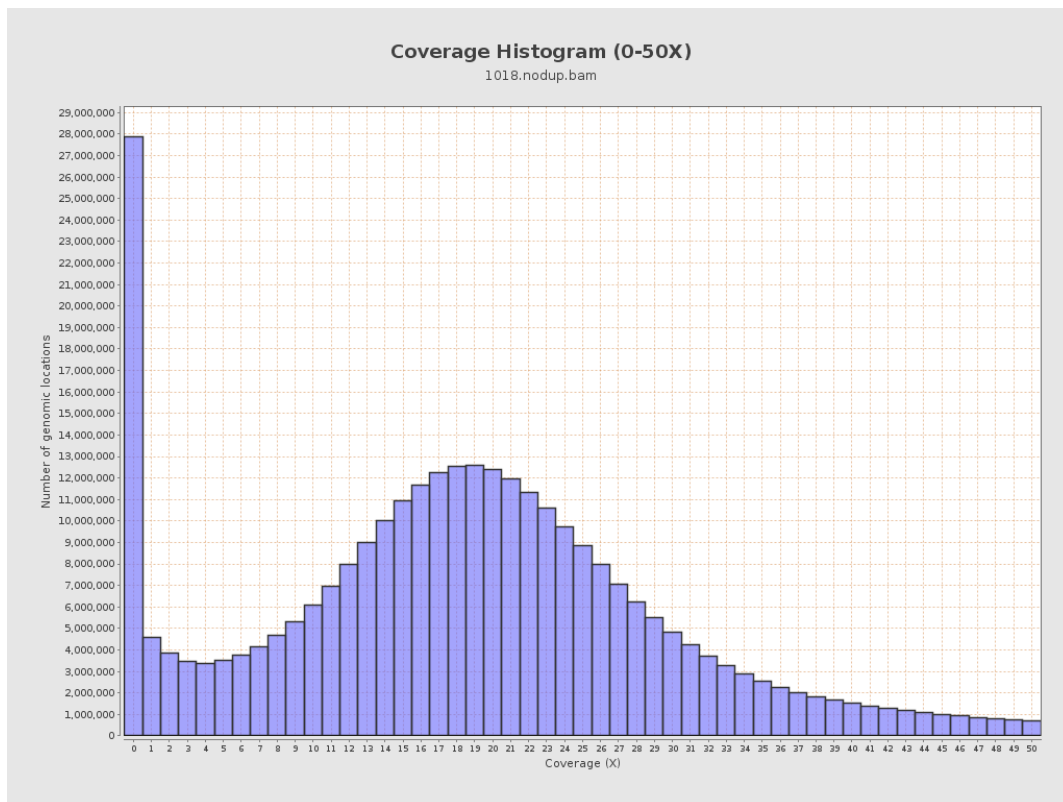
3. Results : Coverage across reference



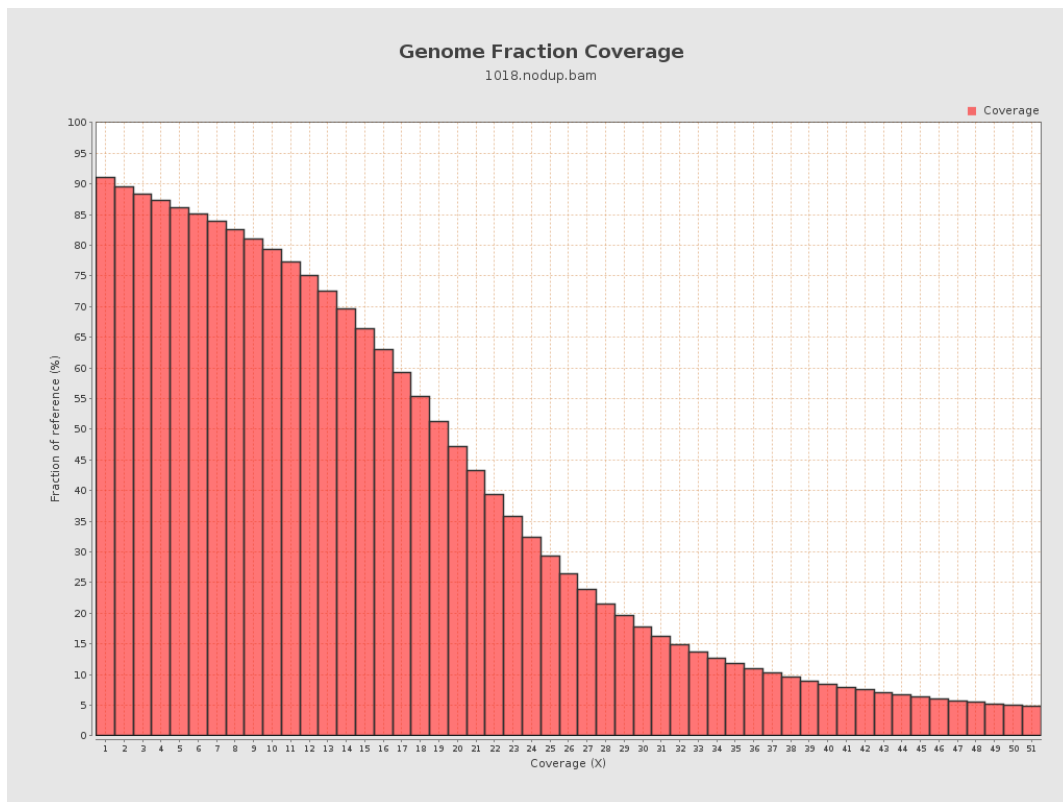
4. Results : Coverage Histogram



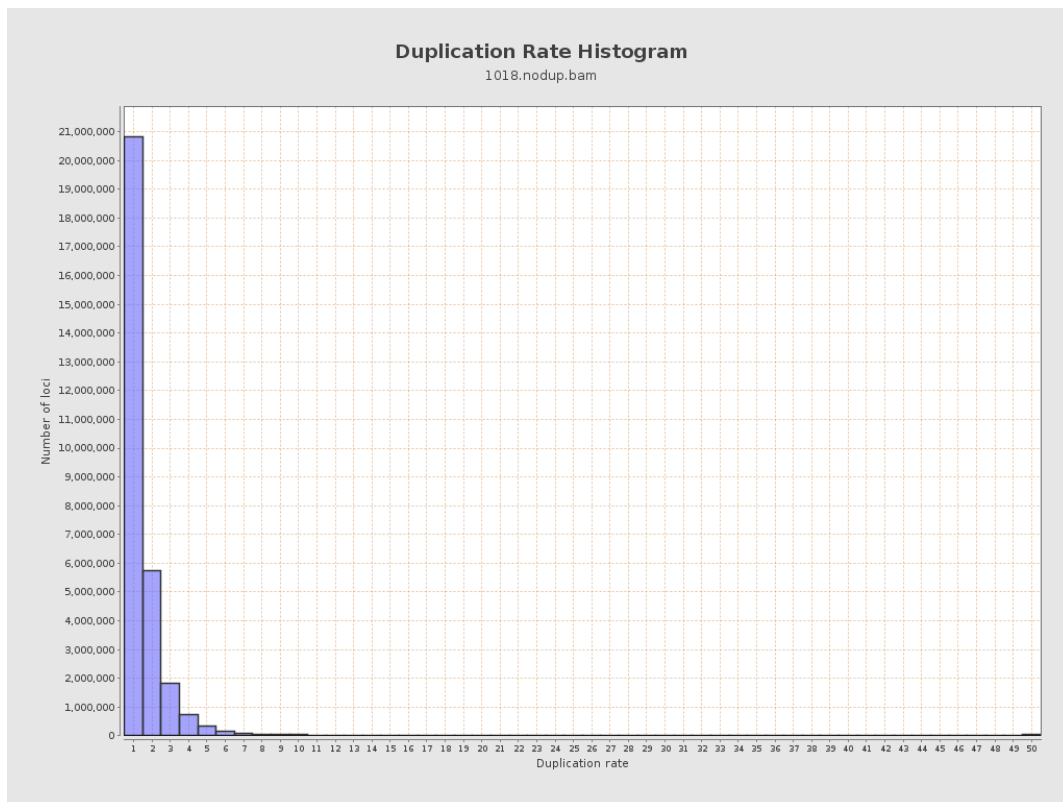
5. Results : Coverage Histogram (0-50X)



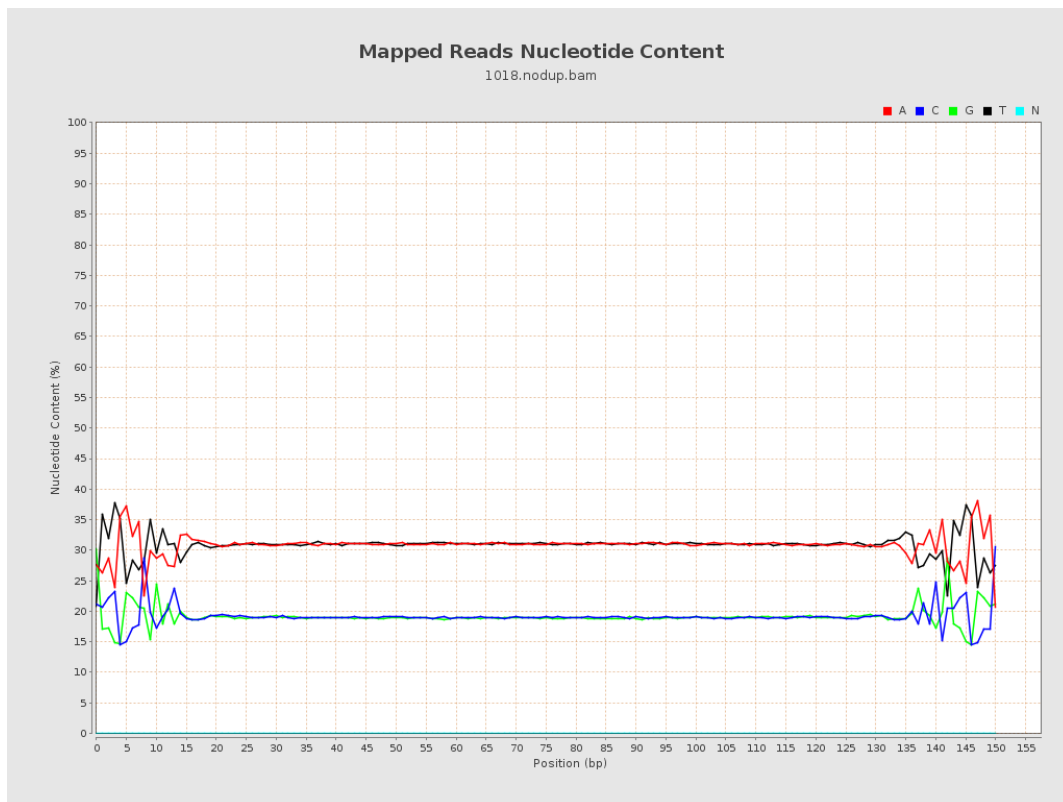
6. Results : Genome Fraction Coverage



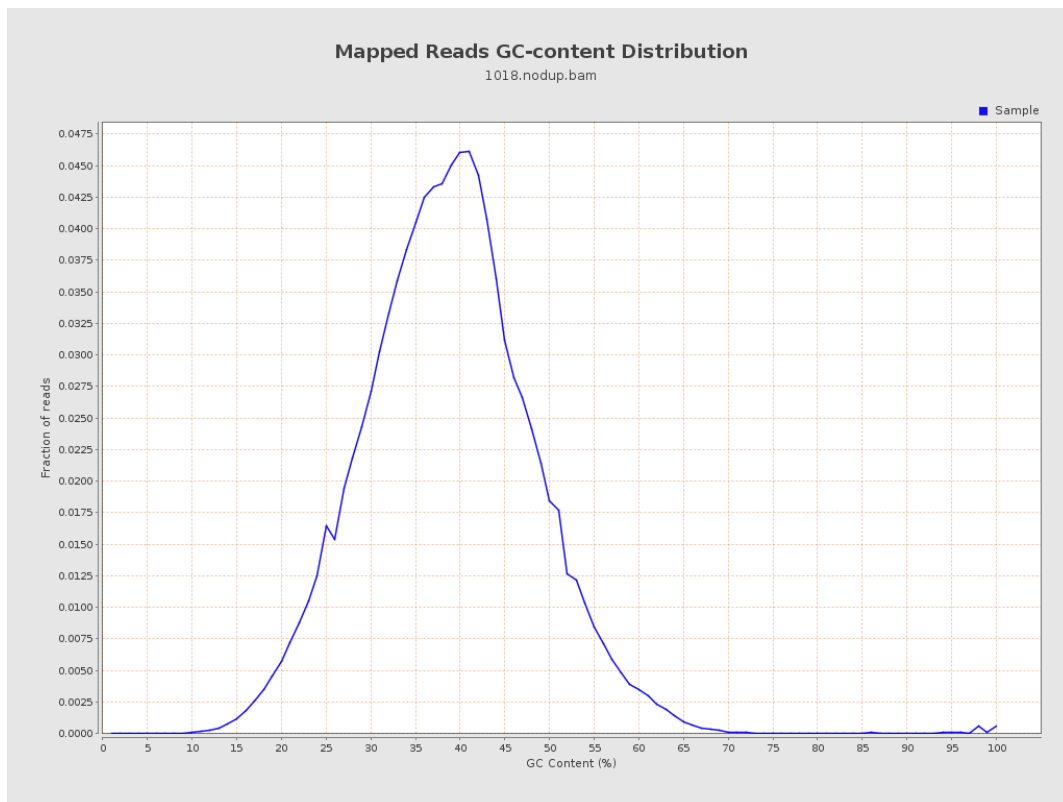
7. Results : Duplication Rate Histogram



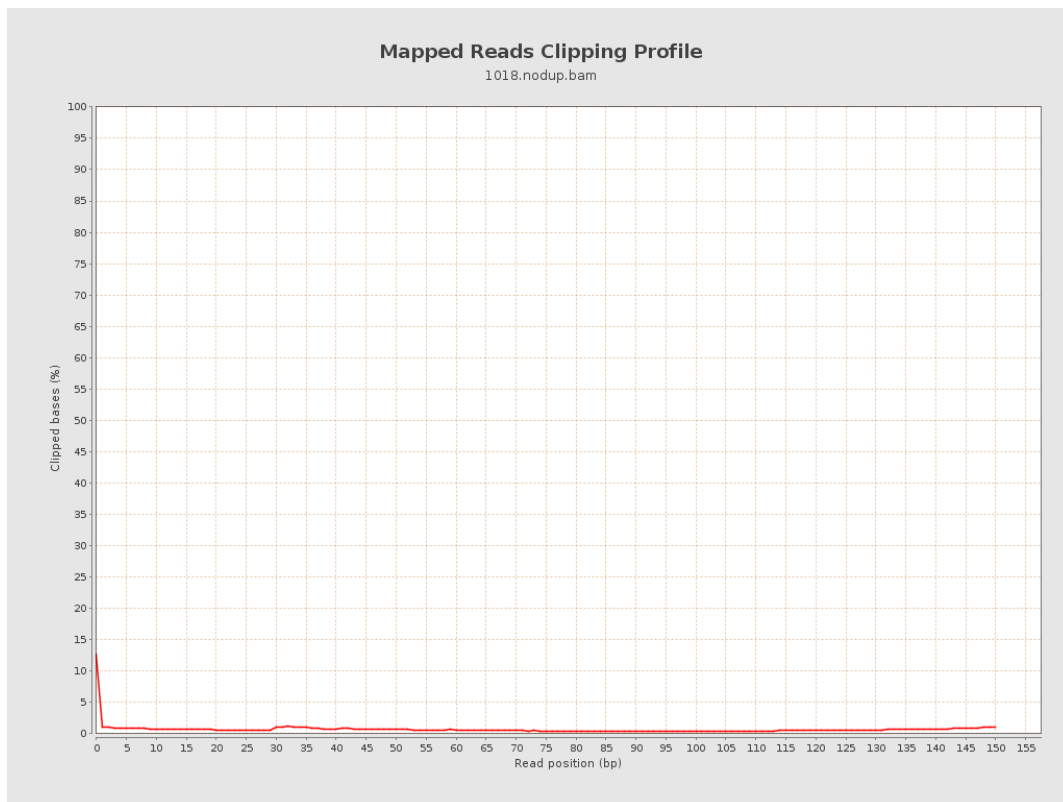
8. Results : Mapped Reads Nucleotide Content



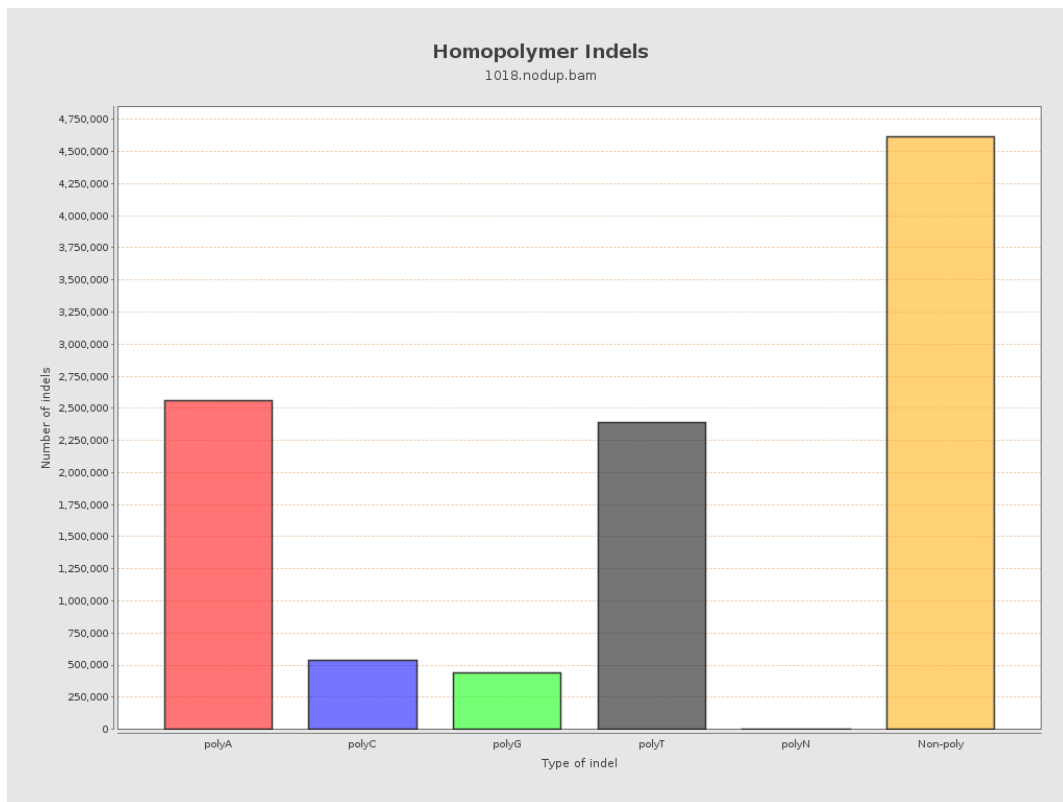
9. Results : Mapped Reads GC-content Distribution



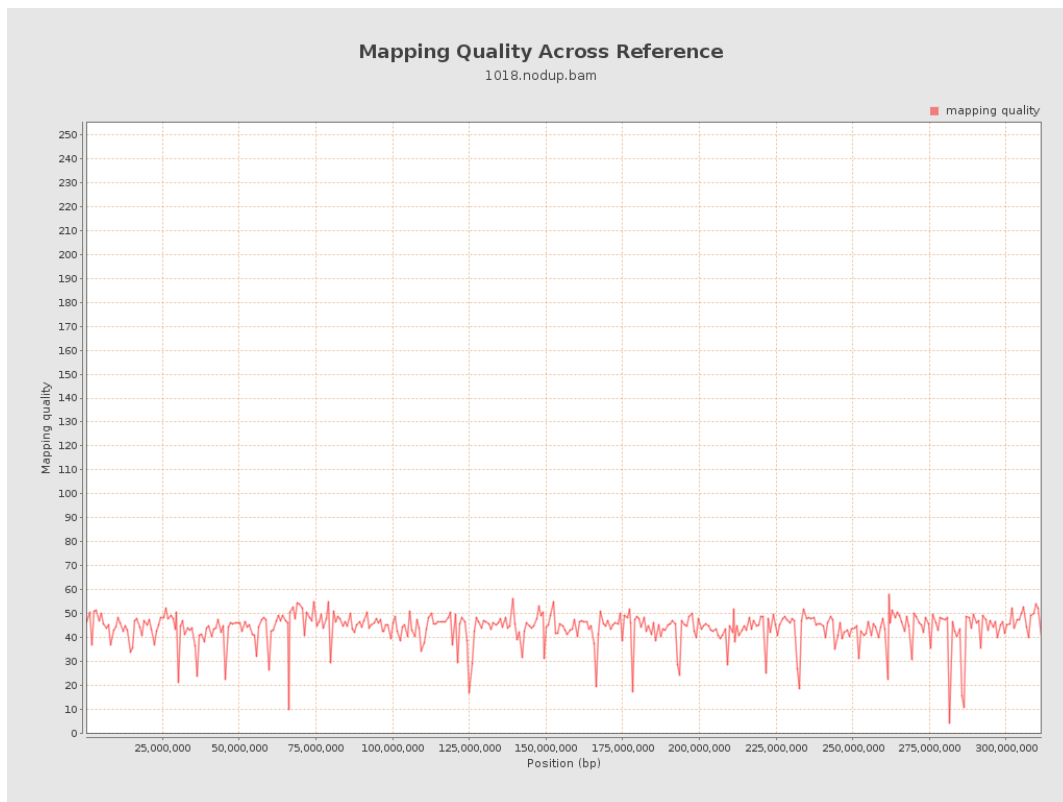
10. Results : Mapped Reads Clipping Profile



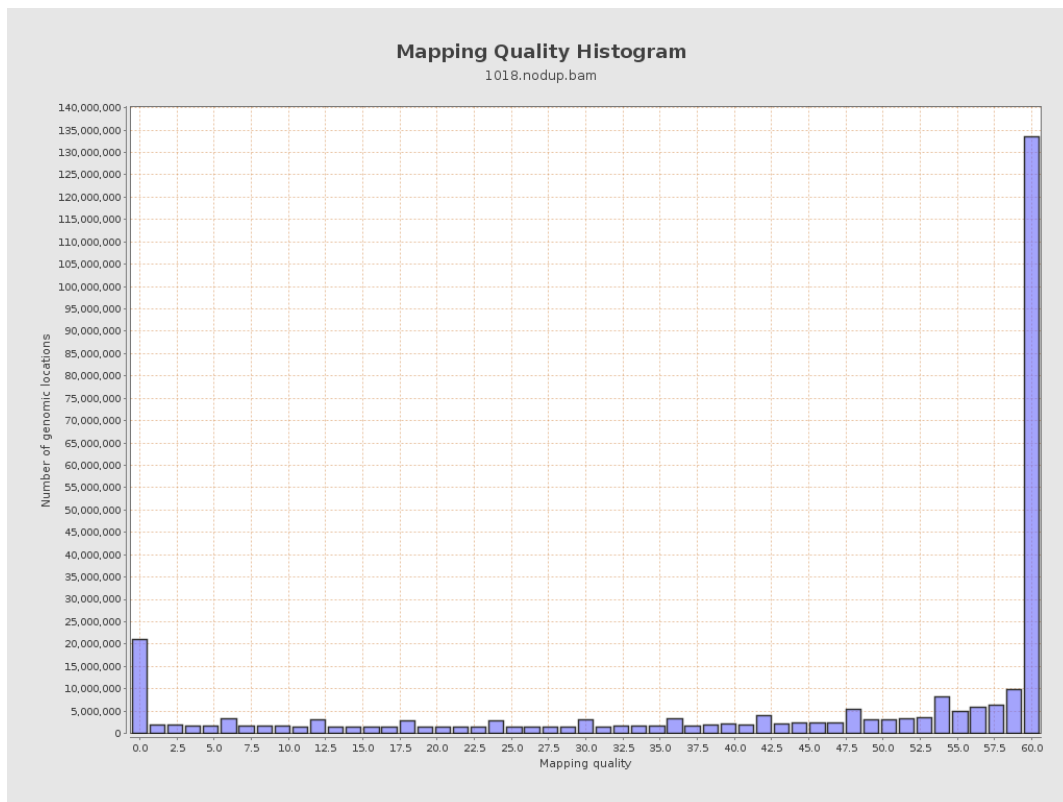
11. Results : Homopolymer Indels



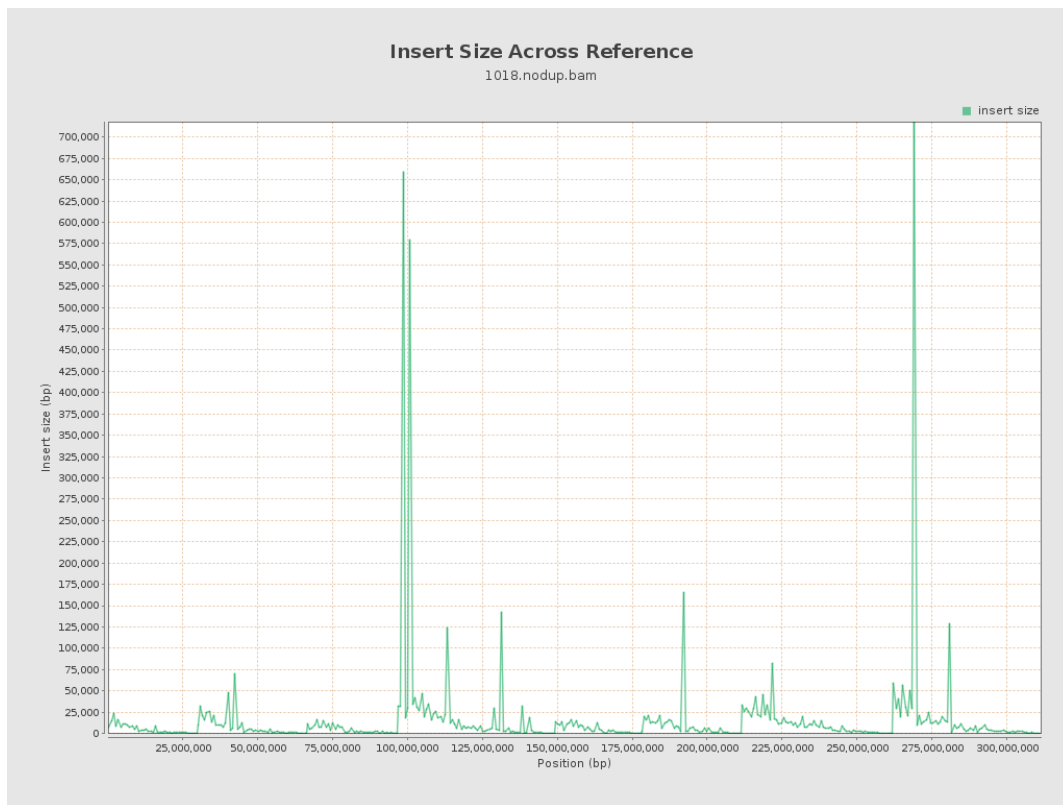
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

