

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:31:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/652
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/652 .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_203/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_203_S284_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_203/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_203_S284_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:31:49 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	68,514,081
Mapped reads	63,833,316 / 93.17%
Unmapped reads	4,680,765 / 6.83%
Mapped paired reads	63,833,316 / 93.17%
Mapped reads, first in pair	31,980,611 / 46.68%
Mapped reads, second in pair	31,852,705 / 46.49%
Mapped reads, both in pair	62,475,344 / 91.19%
Mapped reads, singletons	1,357,972 / 1.98%
Read min/max/mean length	30 / 151 / 148.03
Duplicated reads (flagged)	9,298,160 / 13.57%
Clipped reads	14,643,016 / 21.37%

2.2. ACGT Content

Number/percentage of A's	2,720,559,556 / 30.85%
Number/percentage of C's	1,690,330,366 / 19.17%
Number/percentage of T's	2,722,520,286 / 30.87%
Number/percentage of G's	1,686,163,994 / 19.12%
Number/percentage of N's	32,077 / 0%
GC Percentage	38.28%

2.3. Coverage

Mean	28.3727
Standard Deviation	238.7925

2.4. Mapping Quality

Mean Mapping Quality	44.19
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2.5. Insert size

Mean	229,679.77
Standard Deviation	2,276,941.84
P25/Median/P75	316 / 414 / 539

2.6. Mismatches and indels

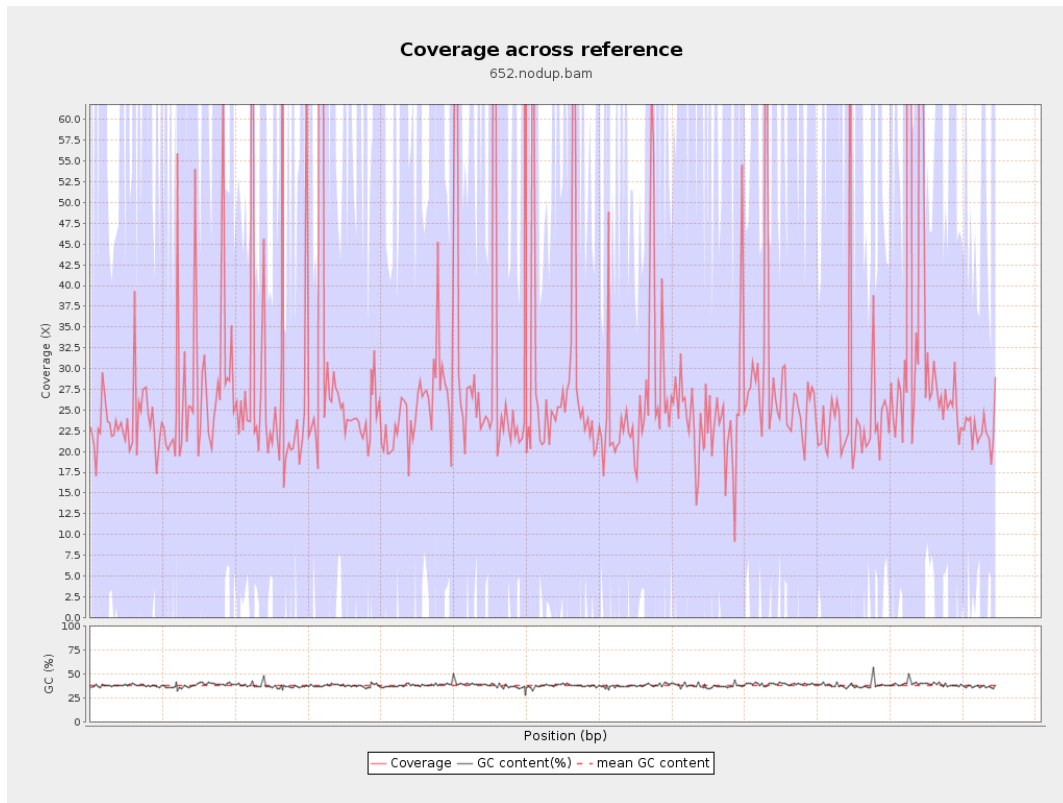
General error rate	2.31%
Mismatches	186,554,960
Insertions	6,084,040
Mapped reads with at least one insertion	8.56%
Deletions	6,080,135
Mapped reads with at least one deletion	8.44%
Homopolymer indels	56.64%

2.7. Chromosome stats

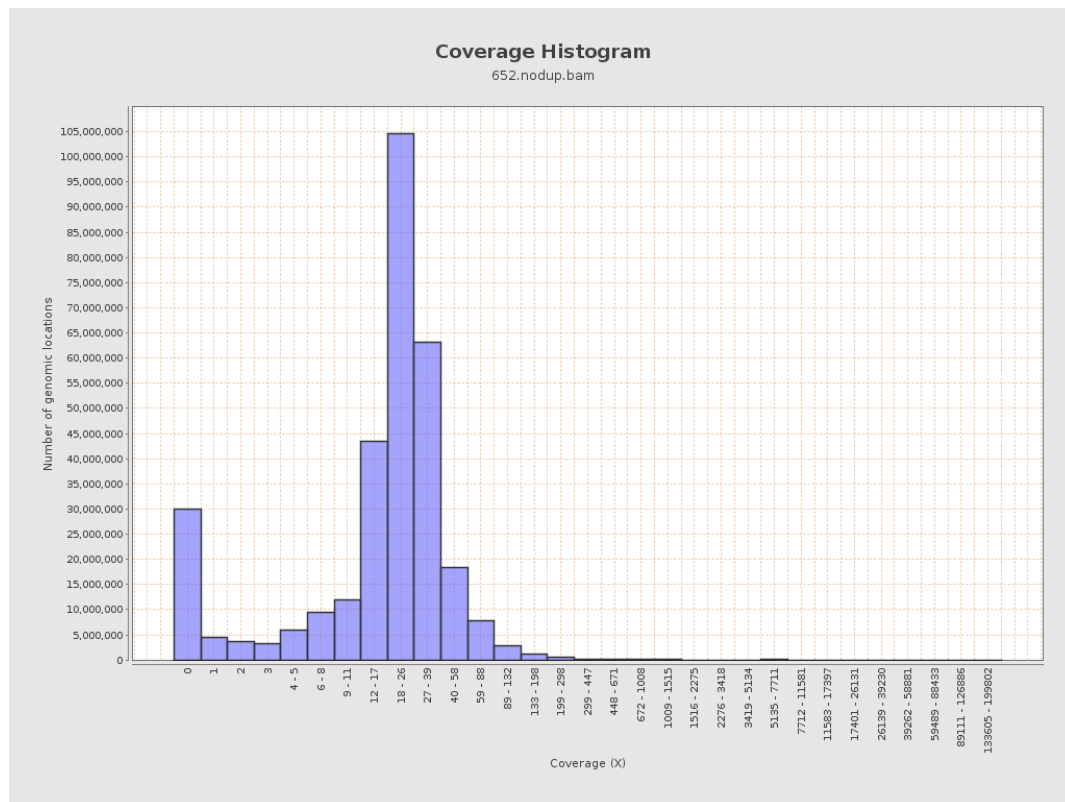
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	688734186	23.1707	88.6218

LT669789.1	36598175	1076265031	29.4076	278.1612
LT669790.1	30422129	952738751	31.3173	261.3152
LT669791.1	52758100	1457094743	27.6184	234.1061
LT669792.1	28376109	797553355	28.1065	235.1825
LT669793.1	33388210	863285402	25.856	117.8598
LT669794.1	50579949	1358690311	26.8622	219.1883
LT669795.1	49795044	1647771889	33.0911	325.336

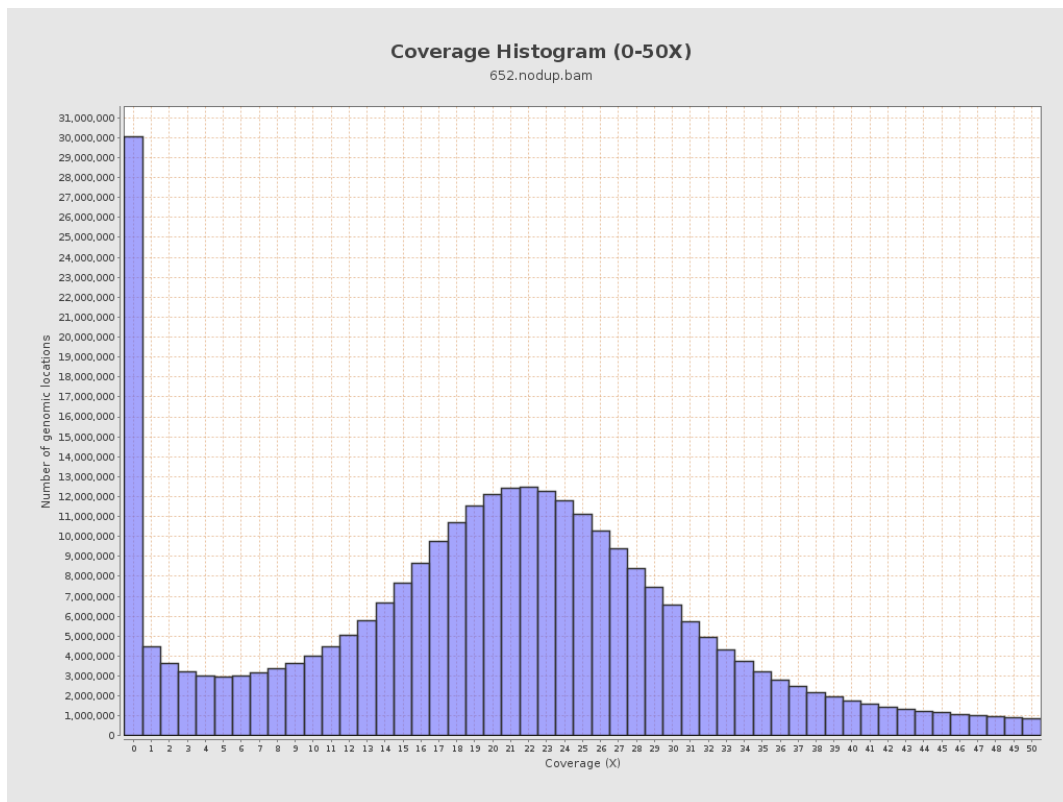
3. Results : Coverage across reference



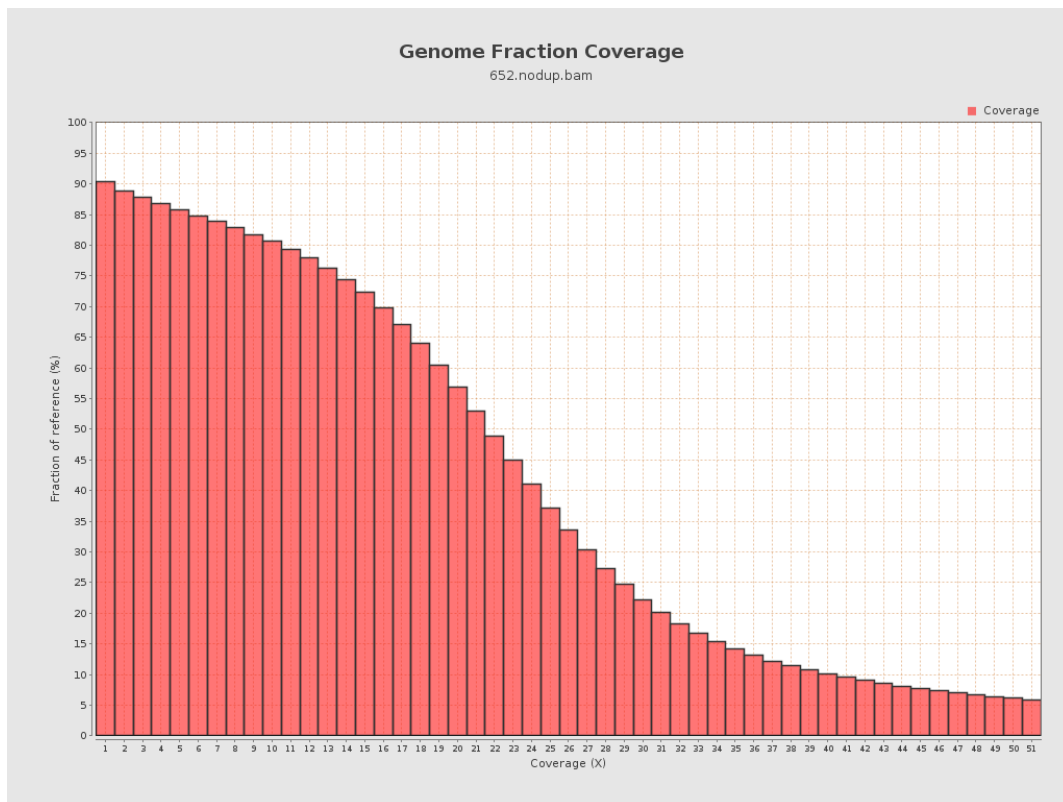
4. Results : Coverage Histogram



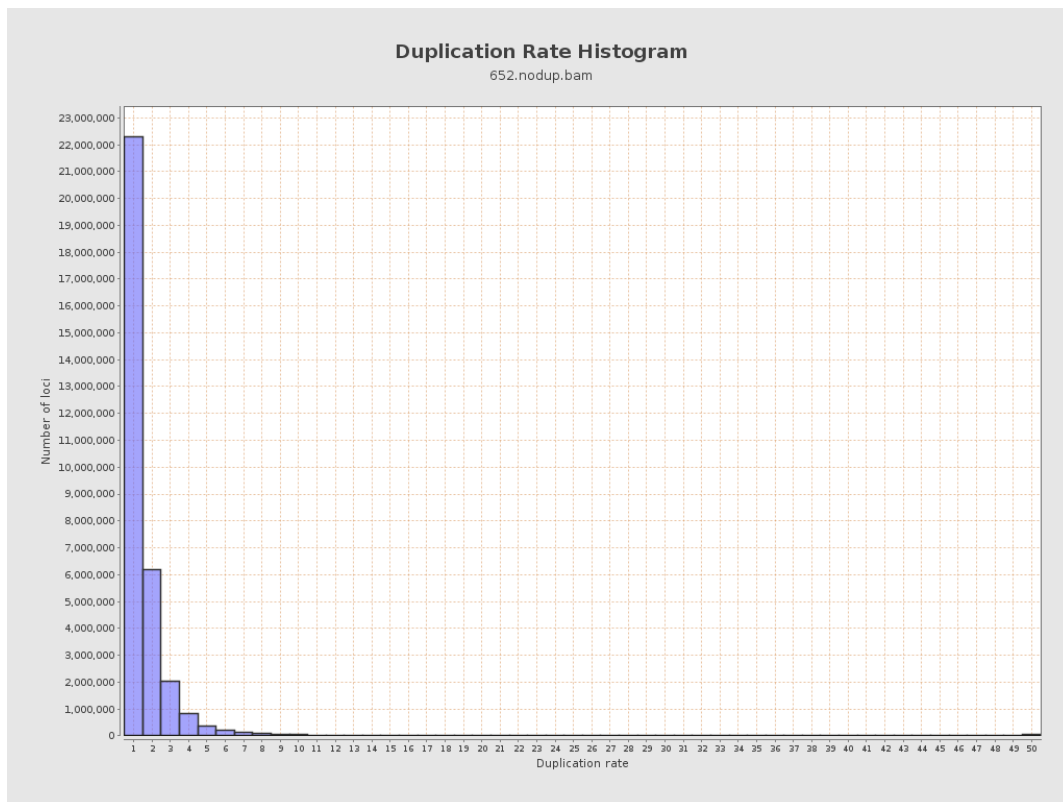
5. Results : Coverage Histogram (0-50X)



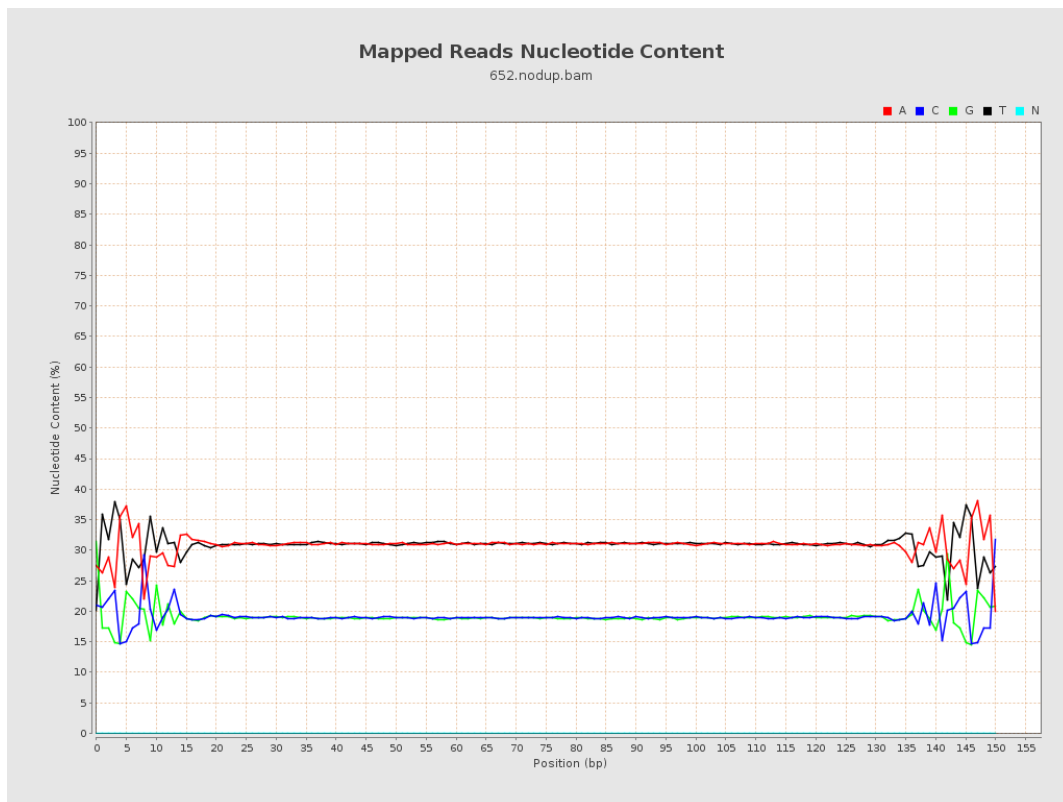
6. Results : Genome Fraction Coverage



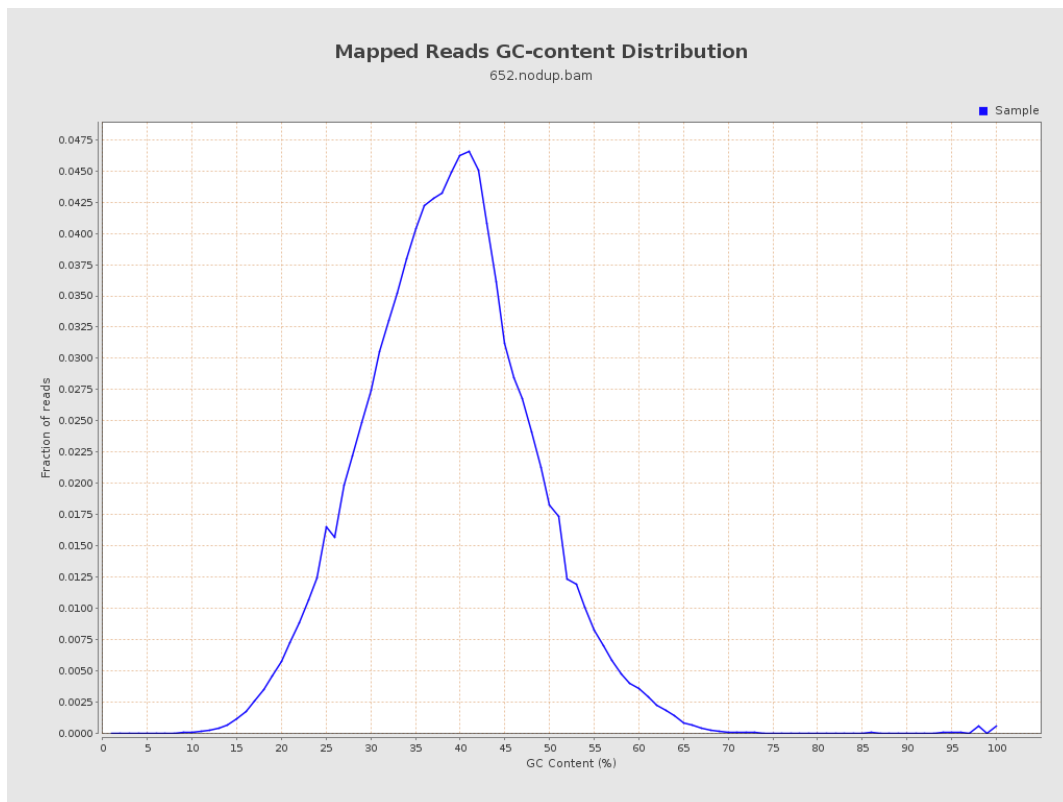
7. Results : Duplication Rate Histogram



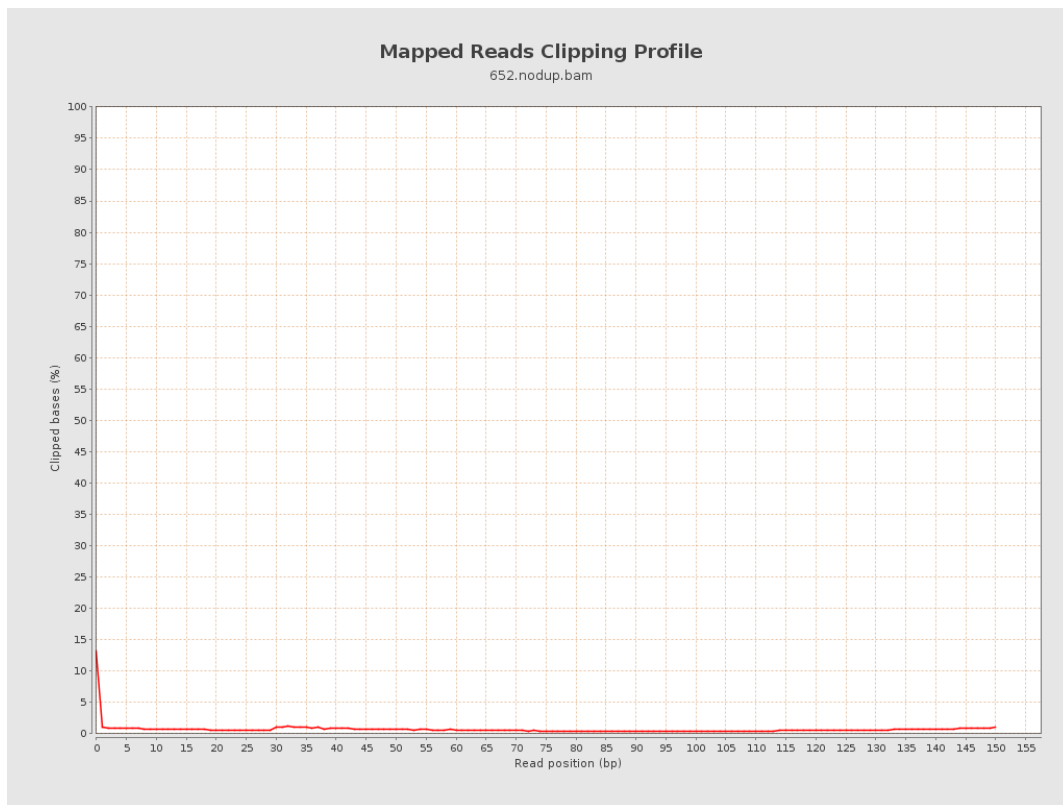
8. Results : Mapped Reads Nucleotide Content



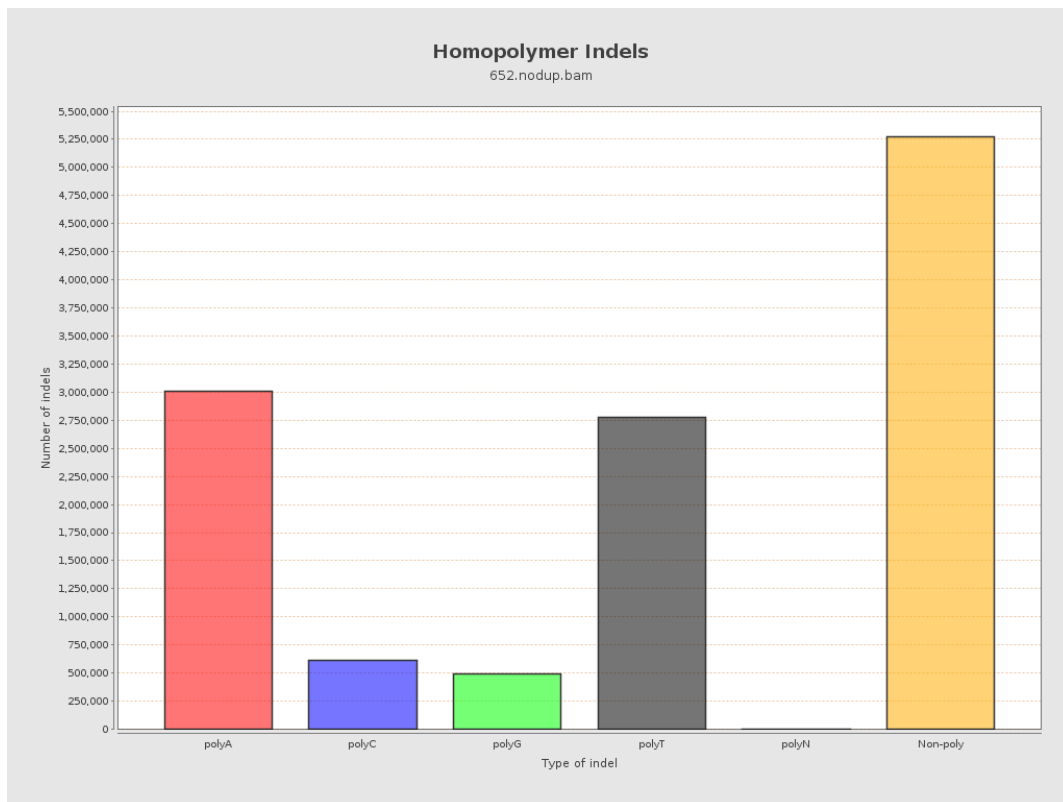
9. Results : Mapped Reads GC-content Distribution



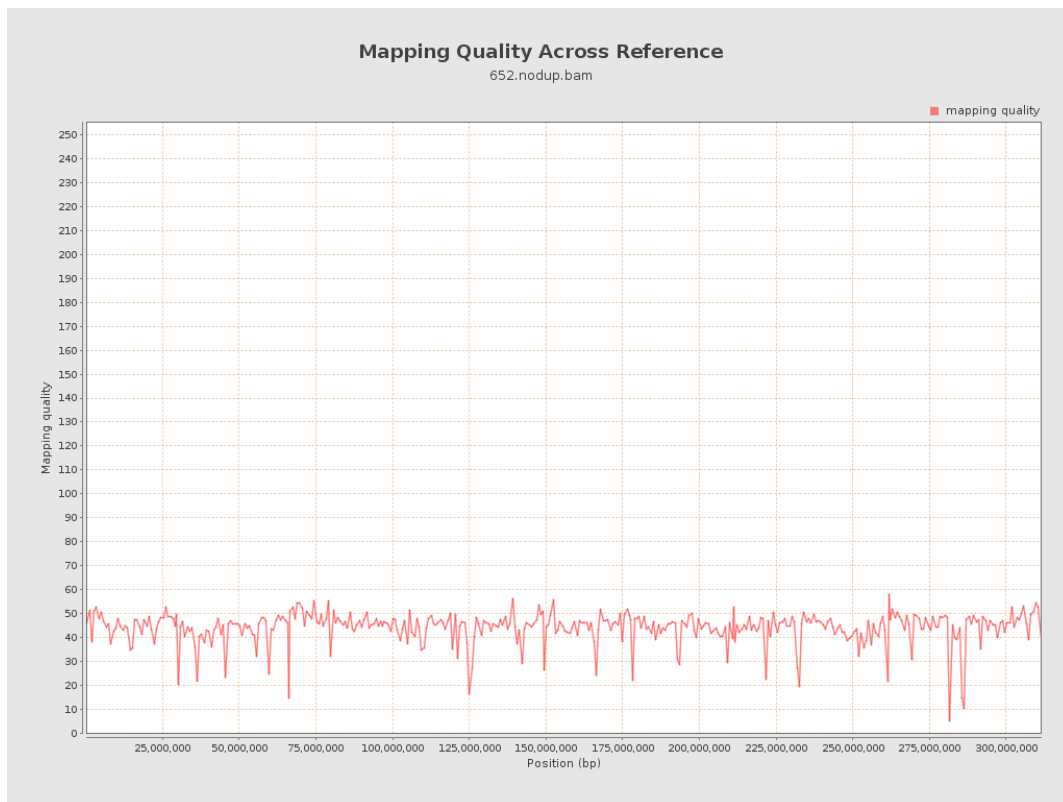
10. Results : Mapped Reads Clipping Profile



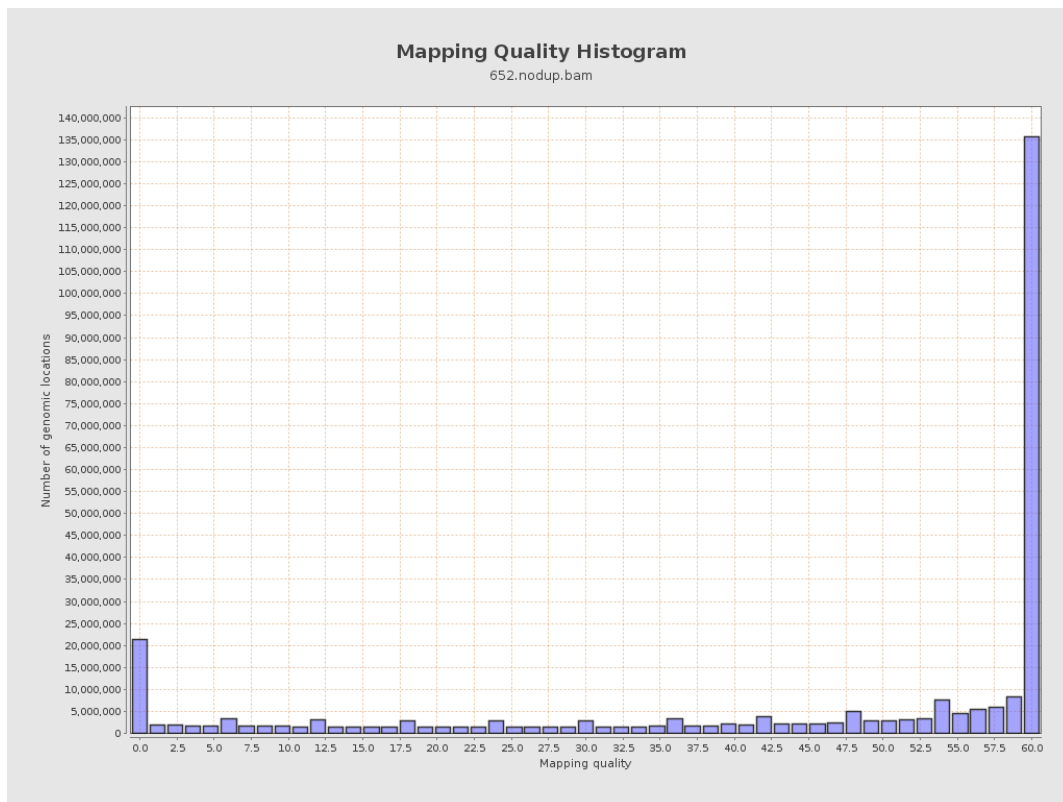
11. Results : Homopolymer Indels



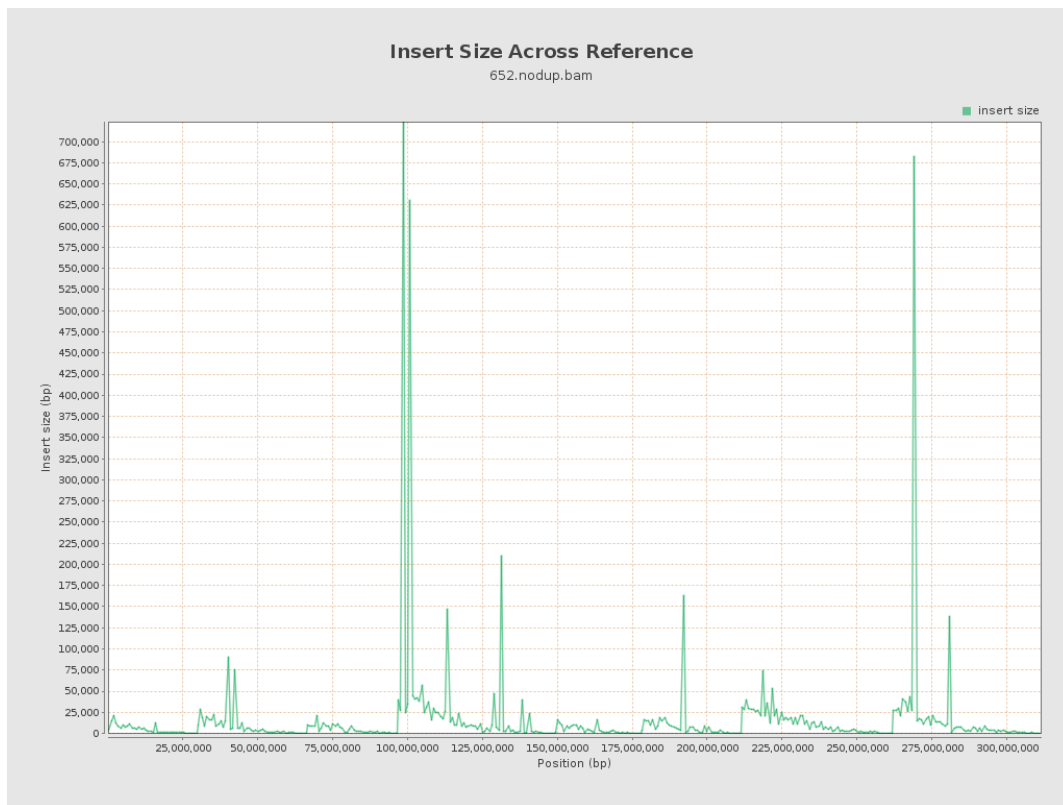
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

