Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:33:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1101
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1101 .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_549/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_549_S116_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_549/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_549_S116_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:32:59 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	68,366,025
Mapped reads	64,174,058 / 93.87%
Unmapped reads	4,191,967 / 6.13%
Mapped paired reads	64,174,058 / 93.87%
Mapped reads, first in pair	32,229,837 / 47.14%
Mapped reads, second in pair	31,944,221 / 46.73%
Mapped reads, both in pair	62,827,077 / 91.9%
Mapped reads, singletons	1,346,981 / 1.97%
Read min/max/mean length	30 / 151 / 148.18
Duplicated reads (flagged)	9,556,640 / 13.98%
Clipped reads	15,173,671 / 22.19%

2.2. ACGT Content

Number/percentage of A's	2,739,381,951 / 30.88%
Number/percentage of C's	1,697,748,379 / 19.14%
Number/percentage of T's	2,740,204,934 / 30.88%
Number/percentage of G's	1,694,960,768 / 19.1%
Number/percentage of N's	60,655 / 0%
GC Percentage	38.24%

2.3. Coverage

Mean	28.5408
Standard Deviation	223.474

2.4. Mapping Quality

Mean Mapping Quality	44.34

2.5. Insert size

Mean	209,611.37
Standard Deviation	2,161,598.04
P25/Median/P75	312 / 408 / 527

2.6. Mismatches and indels

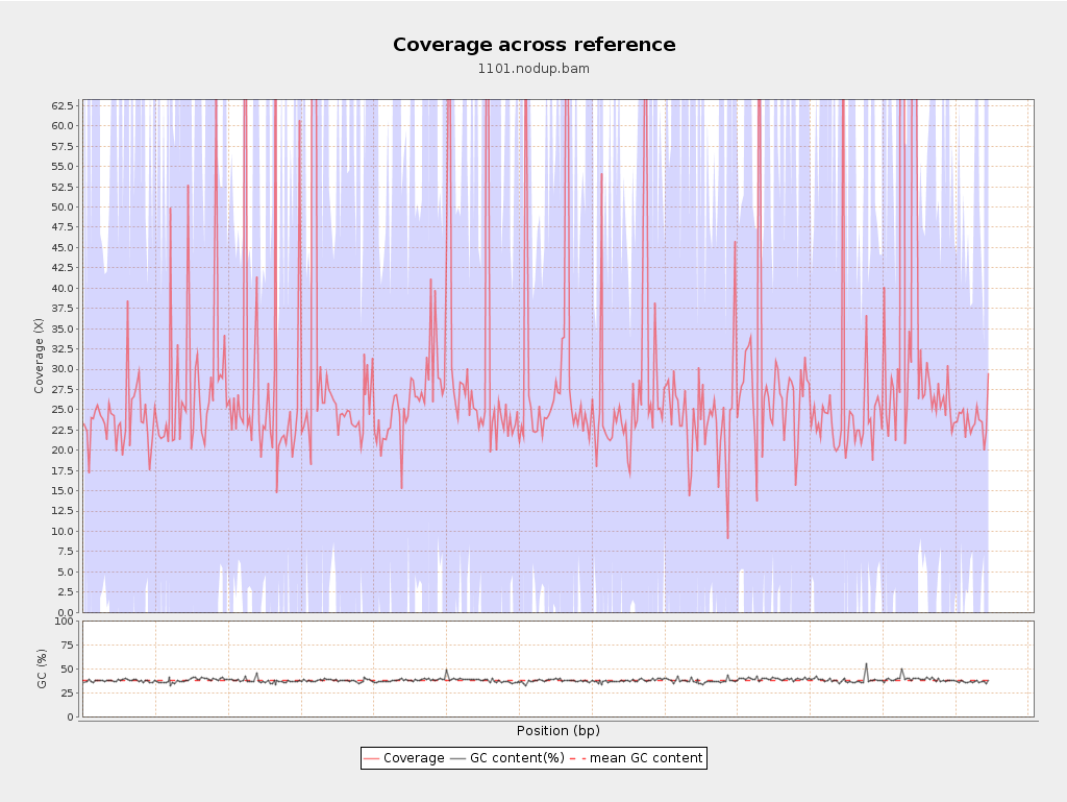
General error rate	2.59%
Mismatches	213,613,770
Insertions	5,839,158
Mapped reads with at least one insertion	8.2%
Deletions	5,930,747
Mapped reads with at least one deletion	8.24%
Homopolymer indels	56.05%

2.7. Chromosome stats

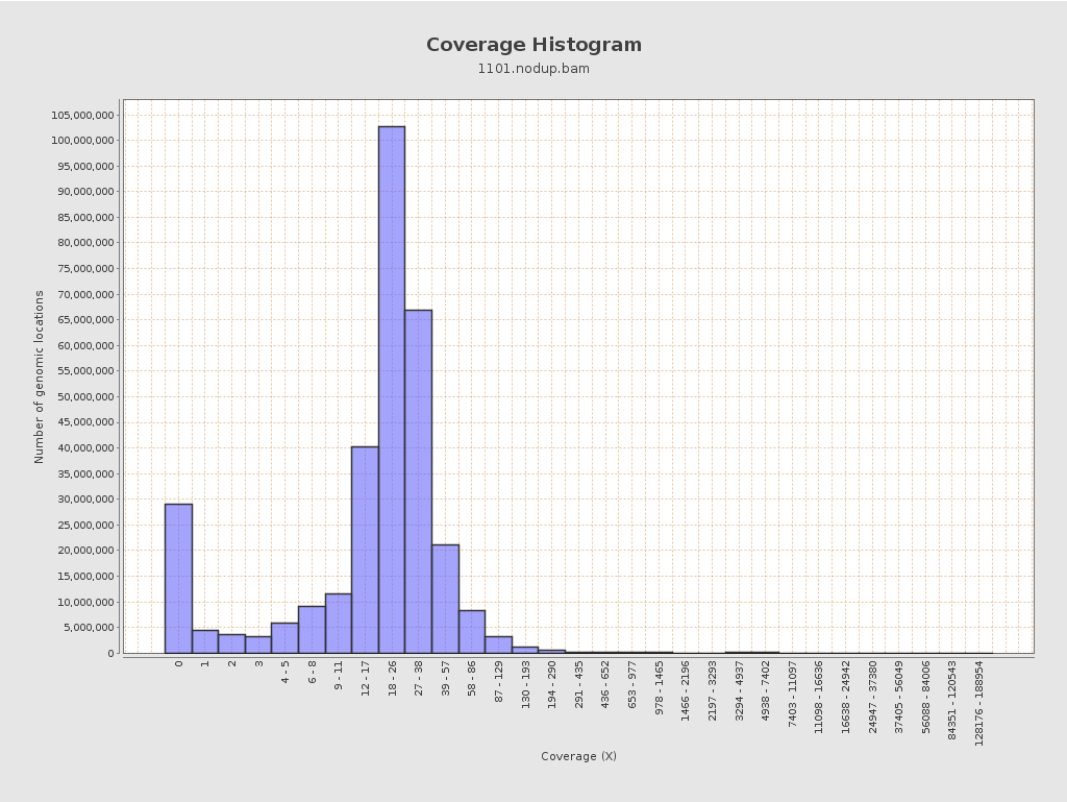
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	702276645	23.6263	66.2913

LT669789.1	36598175	1070301907	29.2447	233.3987
LT669790.1	30422129	932738435	30.6599	223.6338
LT669791.1	52758100	1471321465	27.8881	188.3298
LT669792.1	28376109	797617079	28.1088	244.9822
LT669793.1	33388210	883588227	26.4641	157.2992
LT669794.1	50579949	1361725019	26.9222	190.2176
LT669795.1	49795044	1674951835	33.6369	337.8831

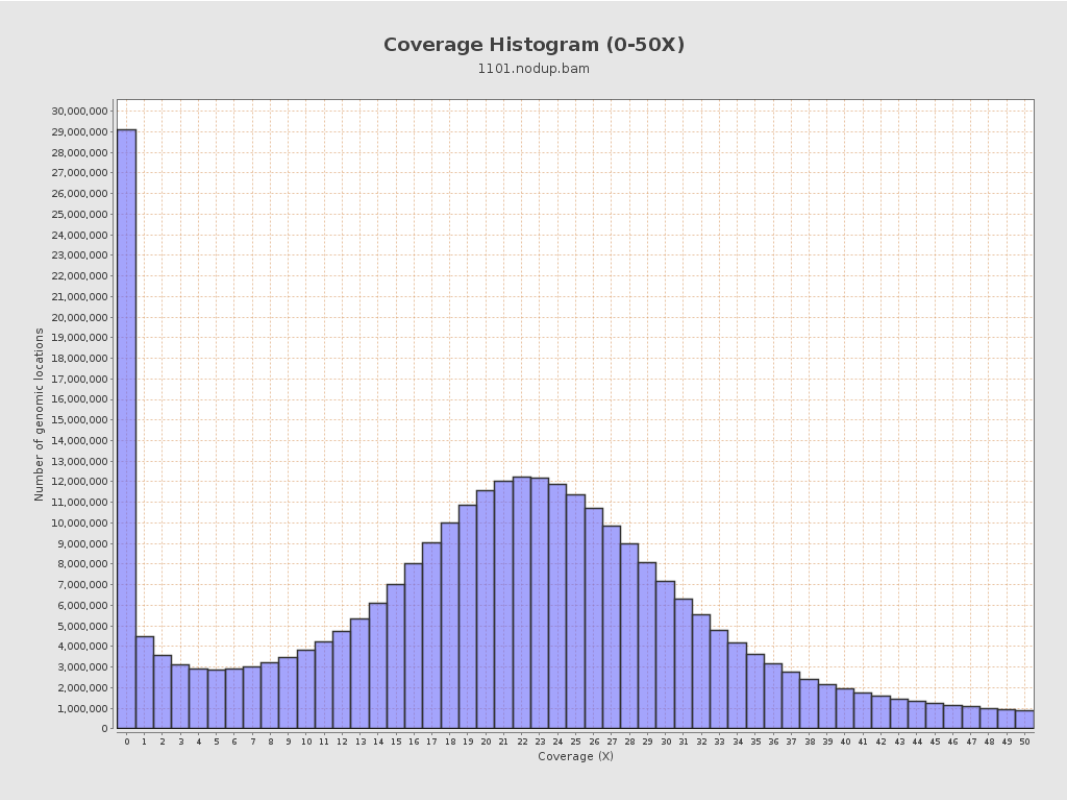
3. Results : Coverage across reference



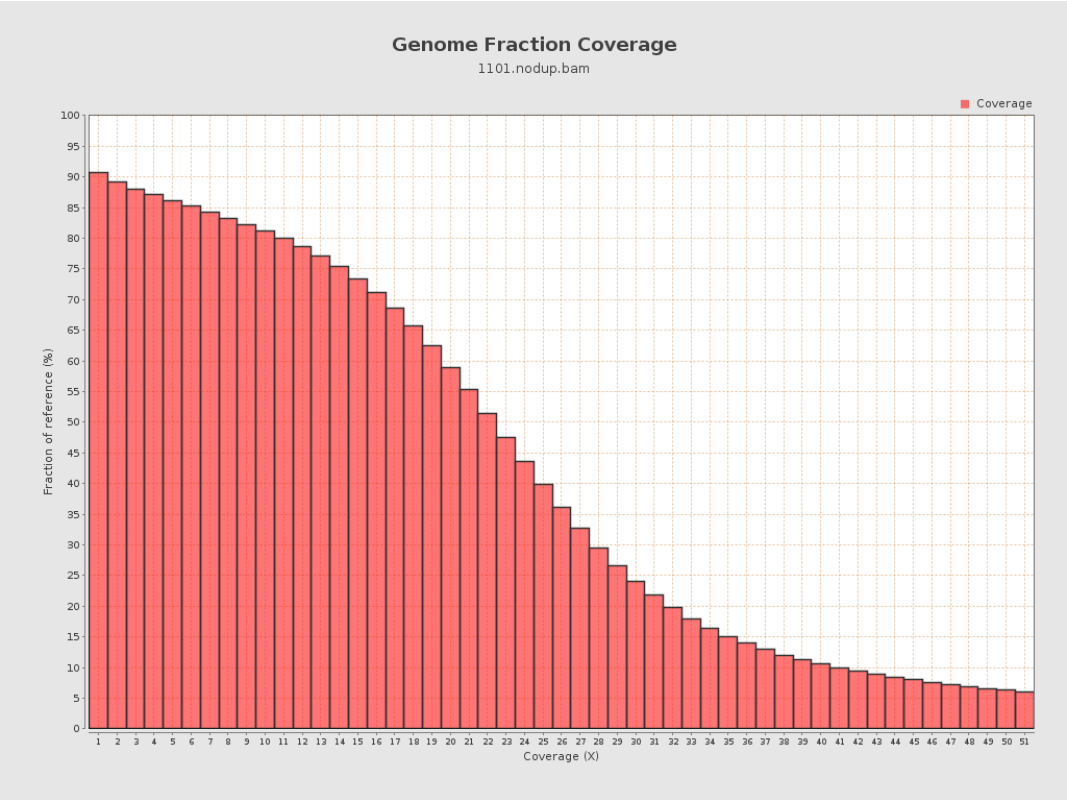
4. Results : Coverage Histogram



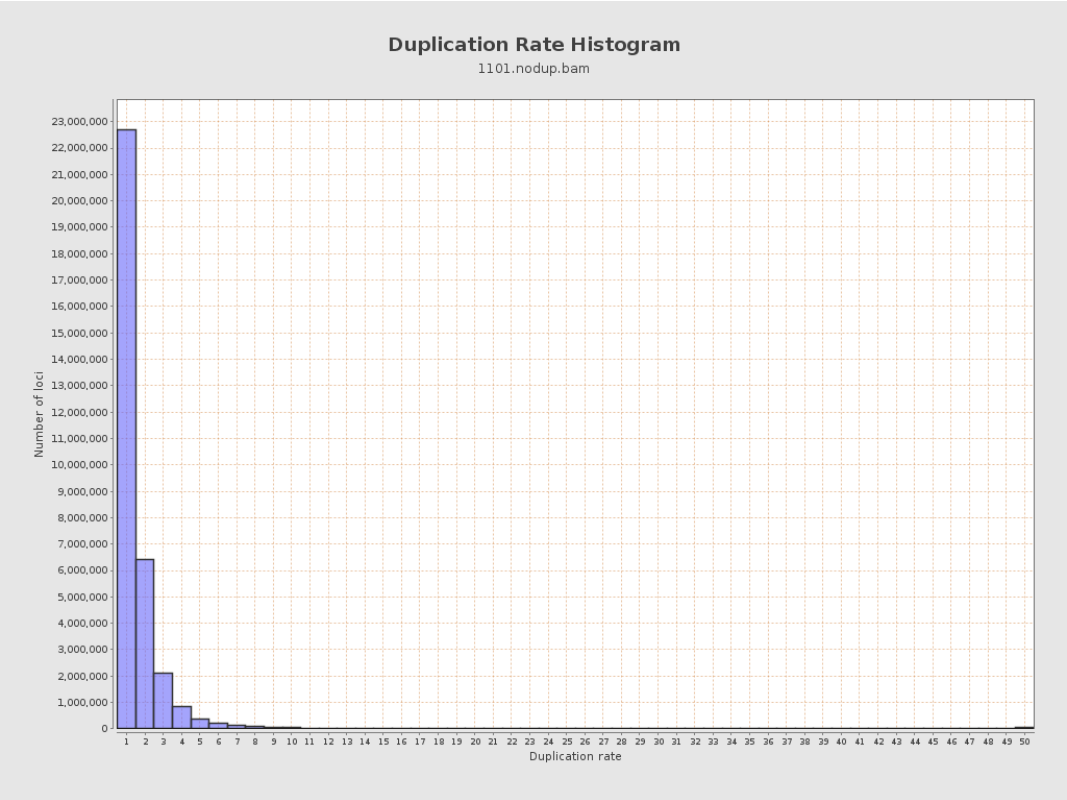
5. Results : Coverage Histogram (0-50X)



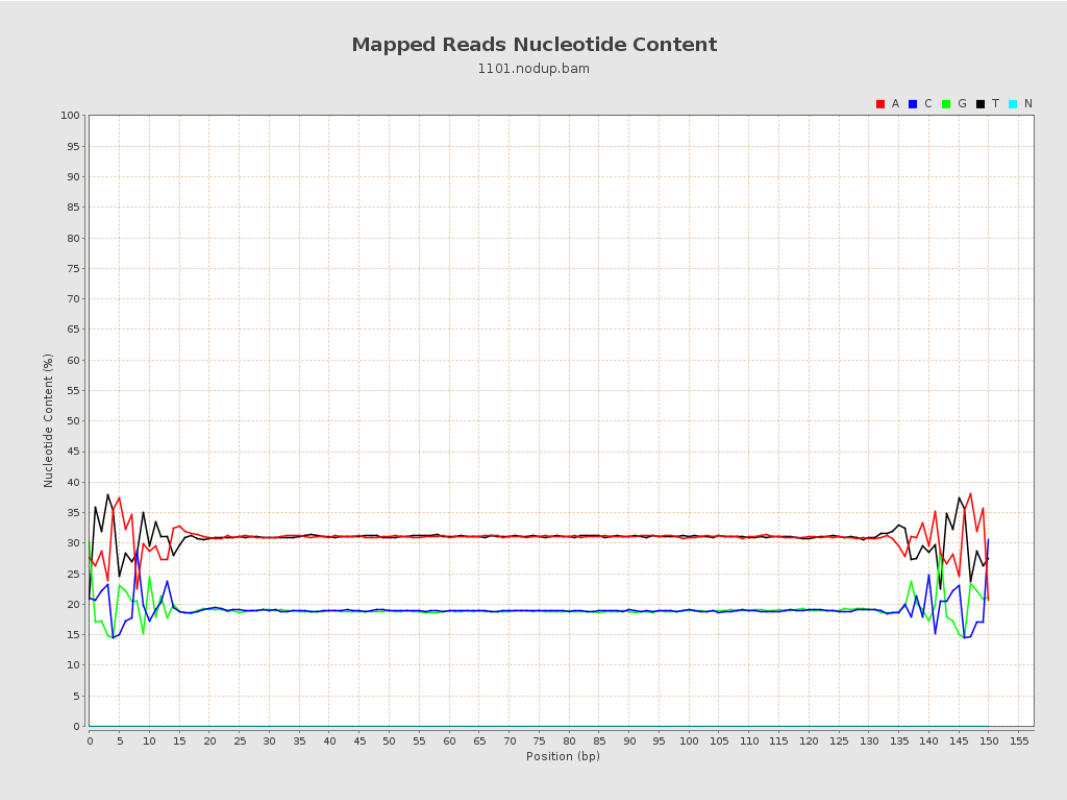
6. Results : Genome Fraction Coverage



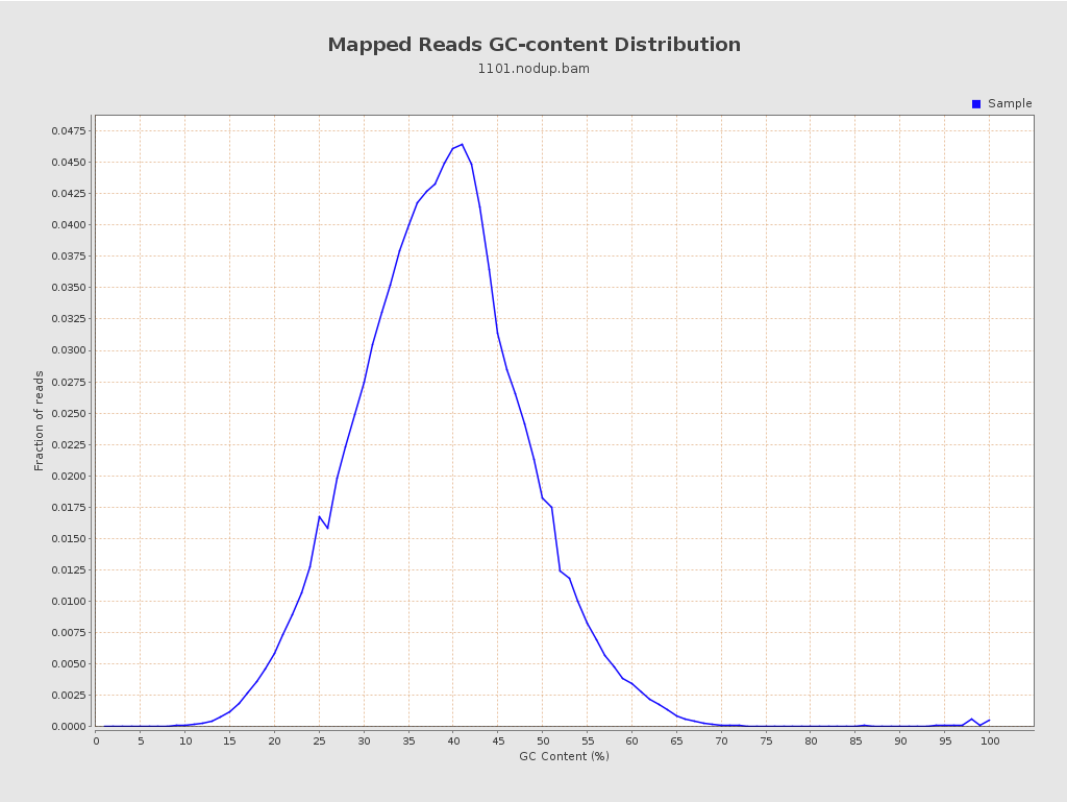
7. Results : Duplication Rate Histogram



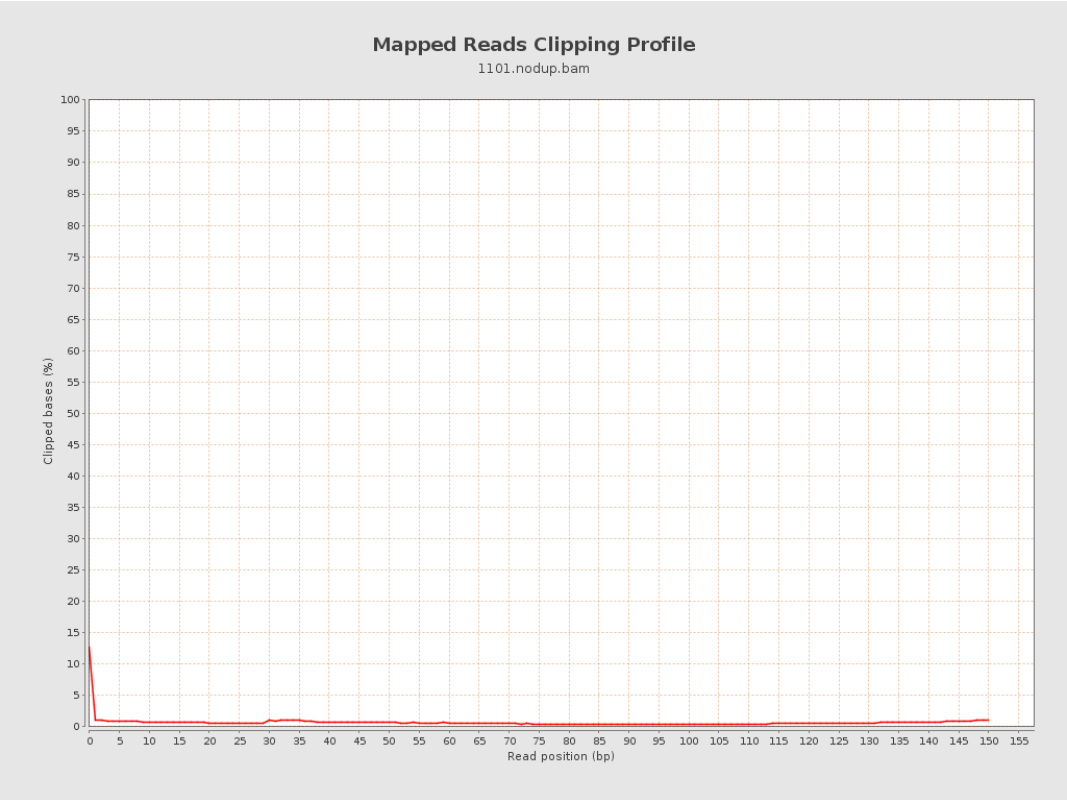
8. Results : Mapped Reads Nucleotide Content



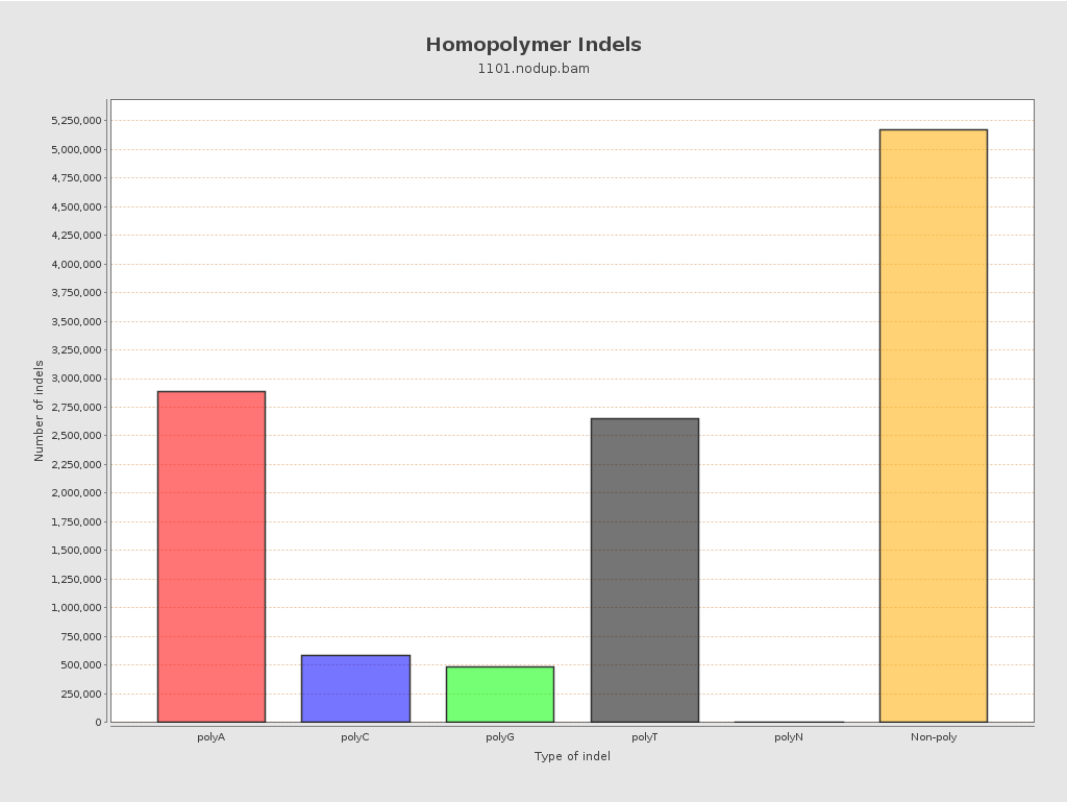
9. Results : Mapped Reads GC-content Distribution



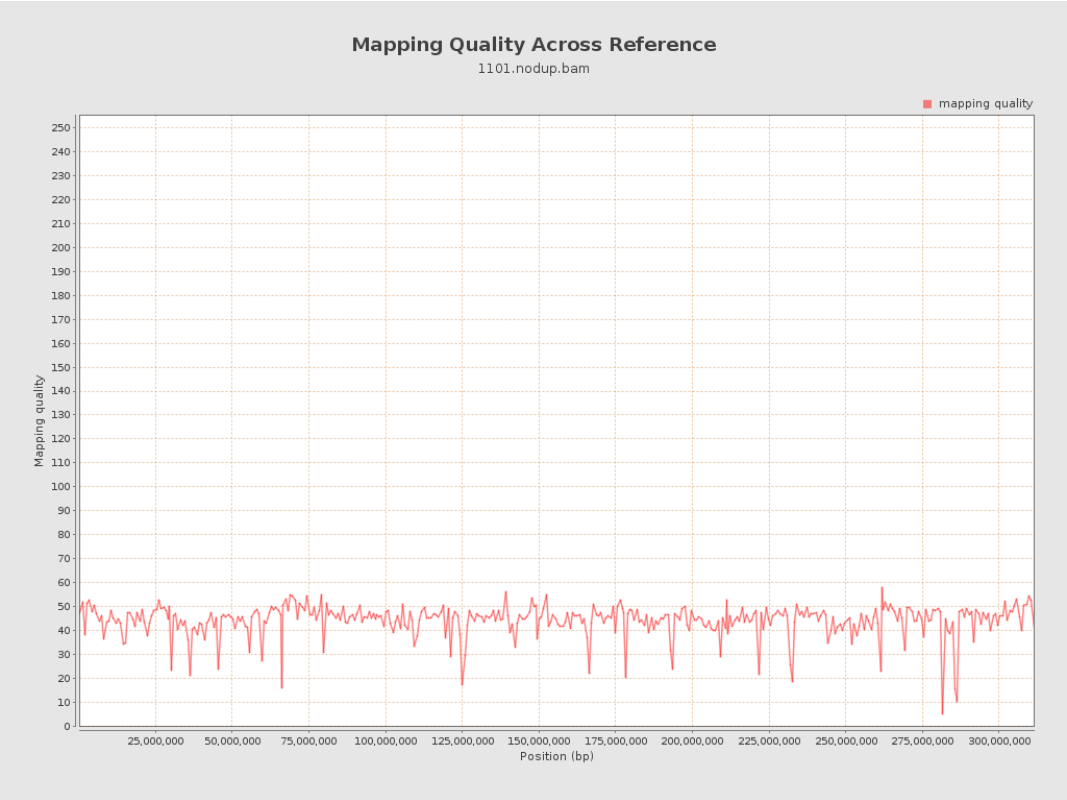
10. Results : Mapped Reads Clipping Profile



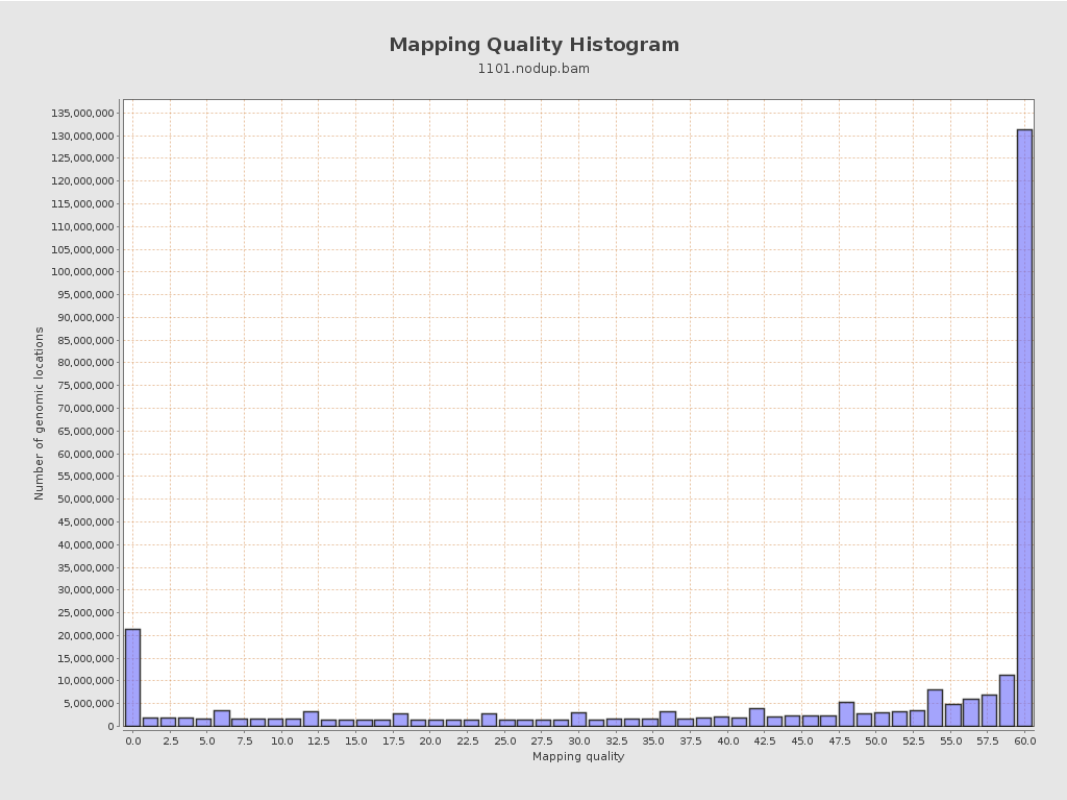
11. Results : Homopolymer Indels



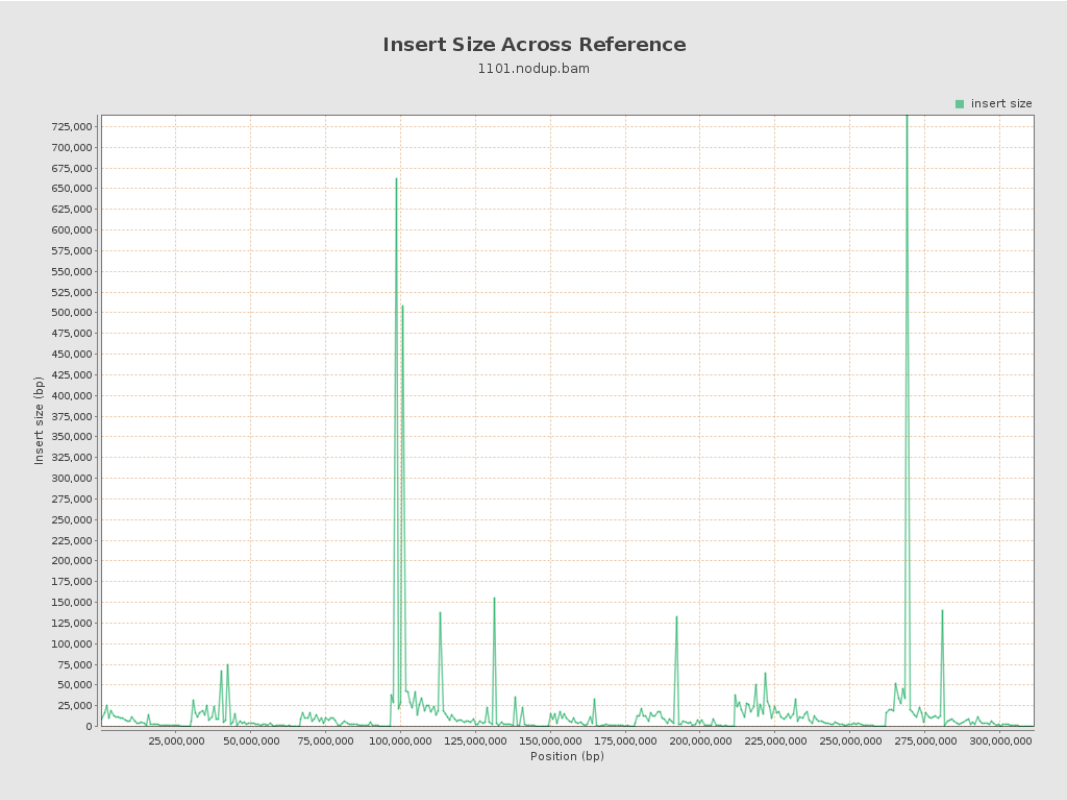
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram