Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:32:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1023
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1023 .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_150/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_150_S240_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_150/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_150_S240_L002_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:32:01 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	71,819,383
Mapped reads	65,827,094 / 91.66%
Unmapped reads	5,992,289 / 8.34%
Mapped paired reads	65,827,094 / 91.66%
Mapped reads, first in pair	33,020,383 / 45.98%
Mapped reads, second in pair	32,806,711 / 45.68%
Mapped reads, both in pair	63,851,077 / 88.91%
Mapped reads, singletons	1,976,017 / 2.75%
Read min/max/mean length	30 / 151 / 148.17
Duplicated reads (flagged)	11,809,756 / 16.44%
Clipped reads	15,561,721 / 21.67%

2.2. ACGT Content

Number/percentage of A's	2,806,067,255 / 30.97%
Number/percentage of C's	1,724,200,694 / 19.03%
Number/percentage of T's	2,808,462,684 / 30.99%
Number/percentage of G's	1,722,792,998 / 19.01%
Number/percentage of N's	39,021 / 0%
GC Percentage	38.04%

2.3. Coverage

Mean	29.1545
Standard Deviation	255.825

2.4. Mapping Quality

Mean Mapping Quality	44.05

2.5. Insert size

Mean	257,918.95
Standard Deviation	2,439,175.31
P25/Median/P75	331 / 433 / 569

2.6. Mismatches and indels

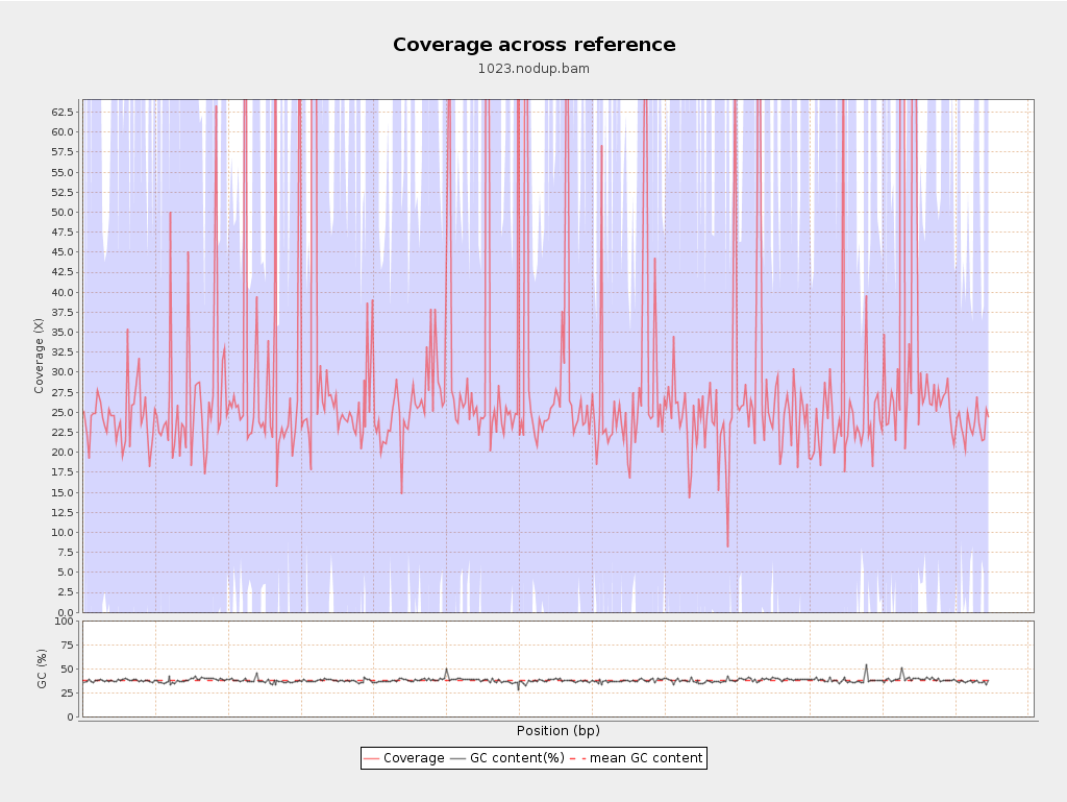
General error rate	2.45%
Mismatches	203,766,903
Insertions	6,585,544
Mapped reads with at least one insertion	8.92%
Deletions	6,420,044
Mapped reads with at least one deletion	8.63%
Homopolymer indels	56.62%

2.7. Chromosome stats

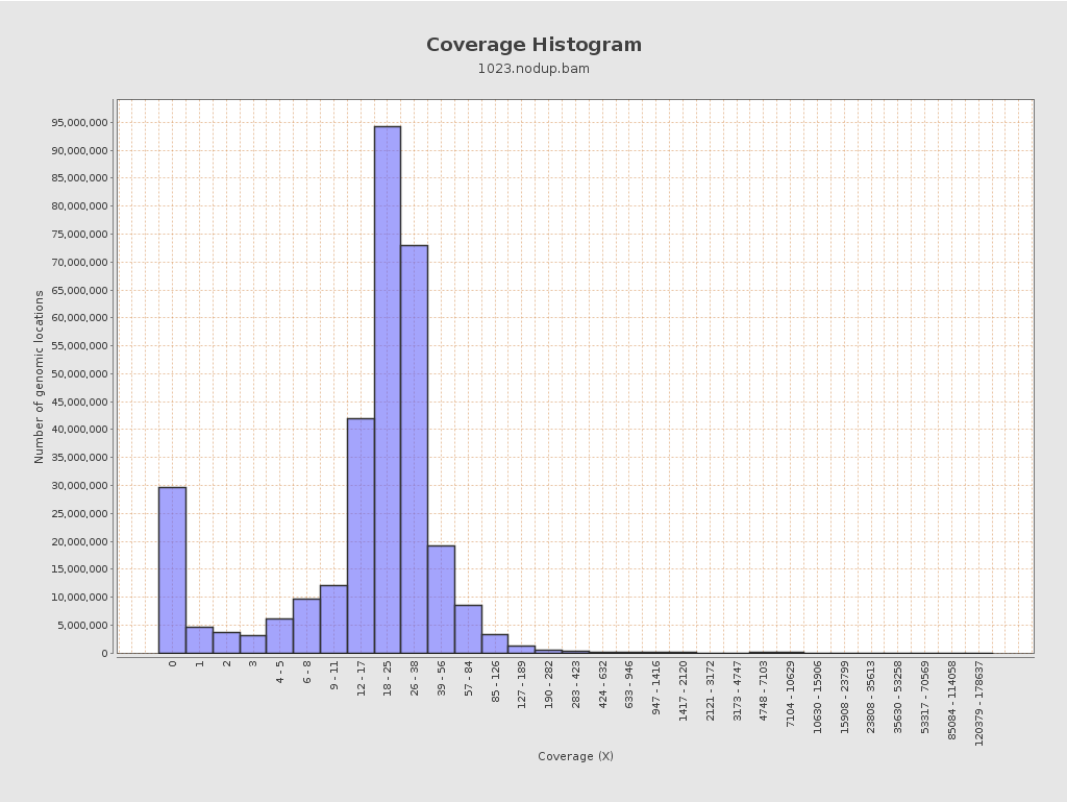
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	717890952	24.1516	94.59

LT669789.1	36598175	1046315297	28.5893	251.5467
LT669790.1	30422129	1053206265	34.6197	340.3672
LT669791.1	52758100	1513987796	28.6968	263.2277
LT669792.1	28376109	843775278	29.7354	287.2567
LT669793.1	33388210	897895031	26.8926	166.2327
LT669794.1	50579949	1359537398	26.879	204.5063
LT669795.1	49795044	1653151487	33.1991	324.7572

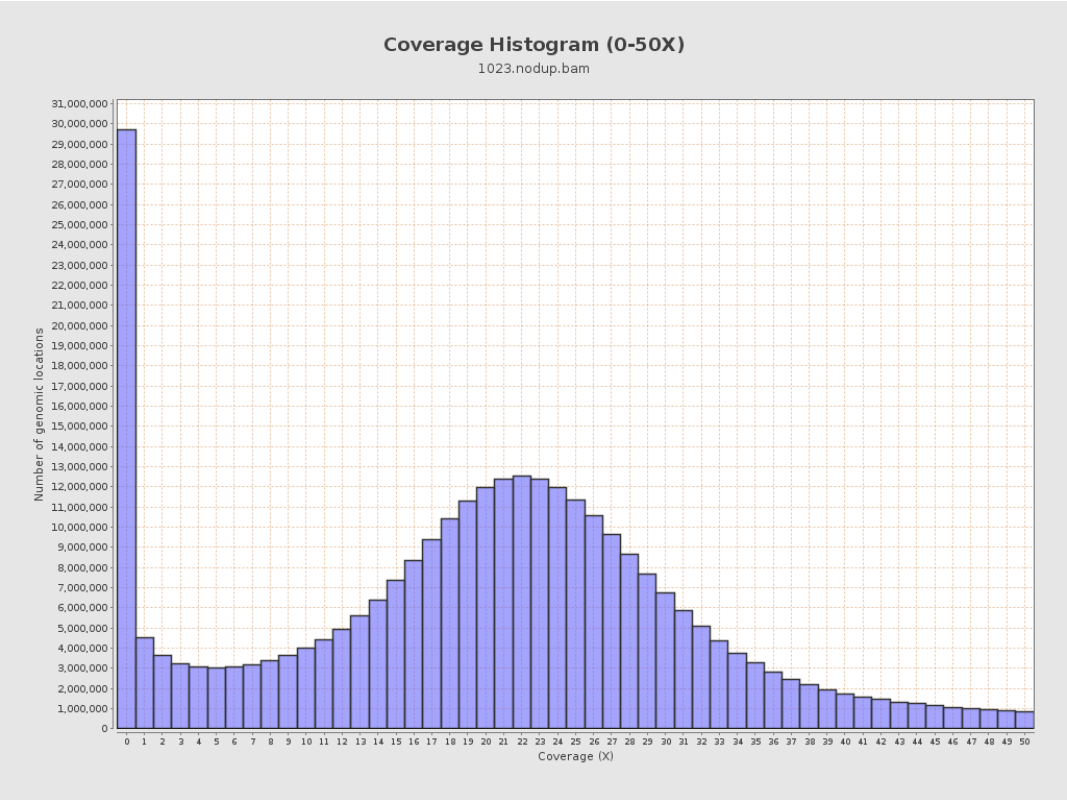
3. Results : Coverage across reference



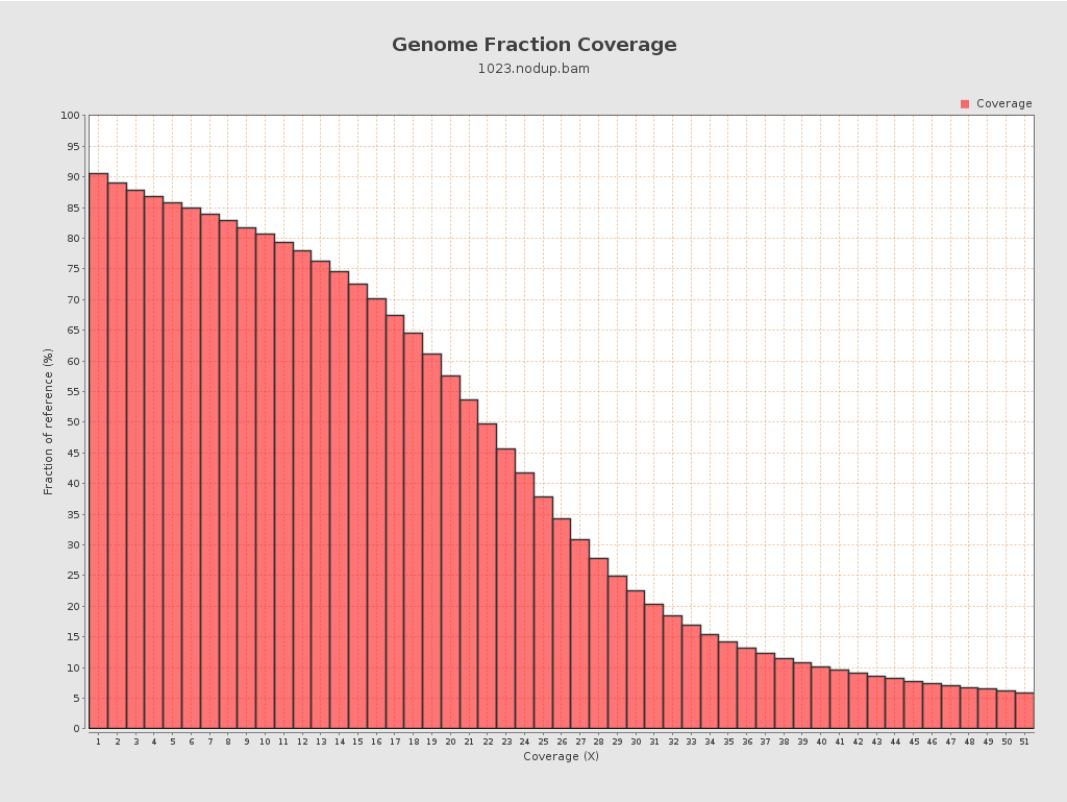
4. Results : Coverage Histogram



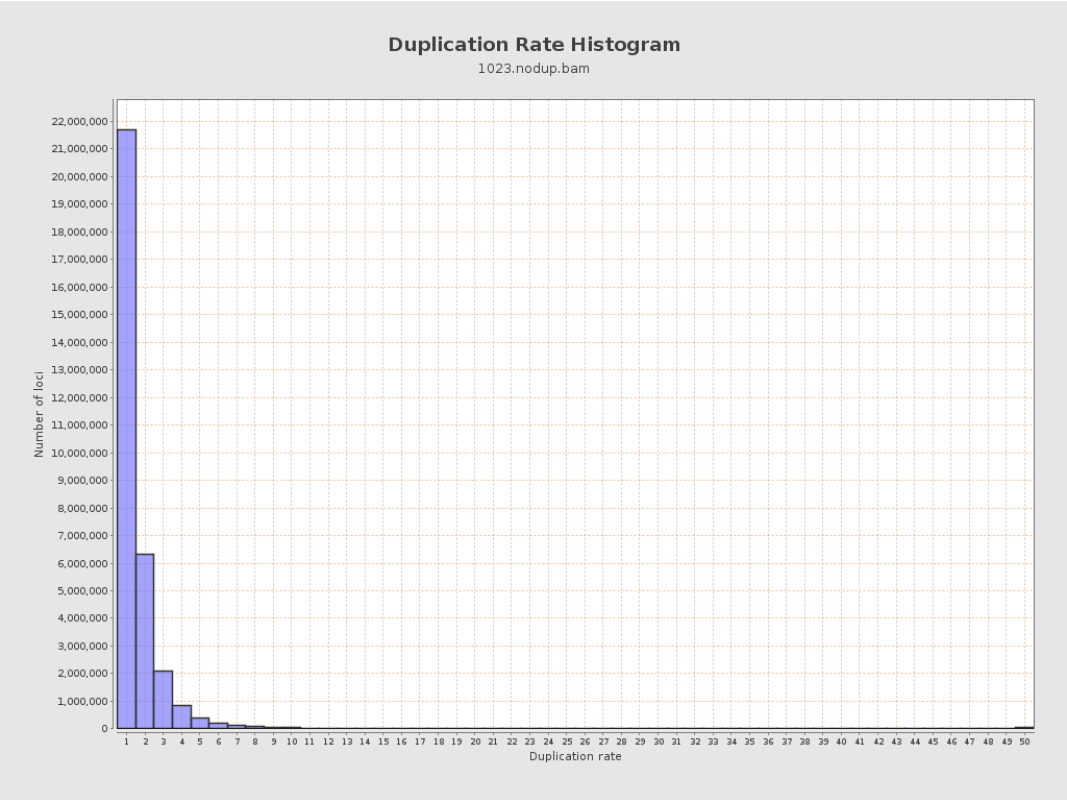
5. Results : Coverage Histogram (0-50X)



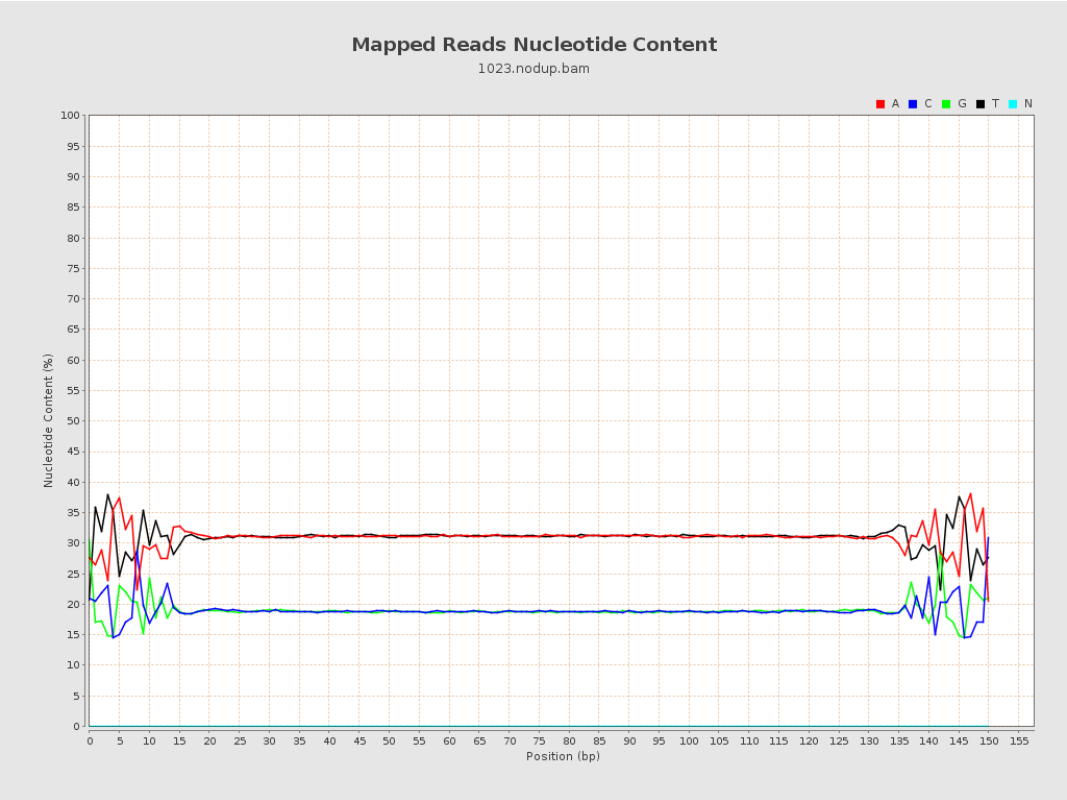
6. Results : Genome Fraction Coverage



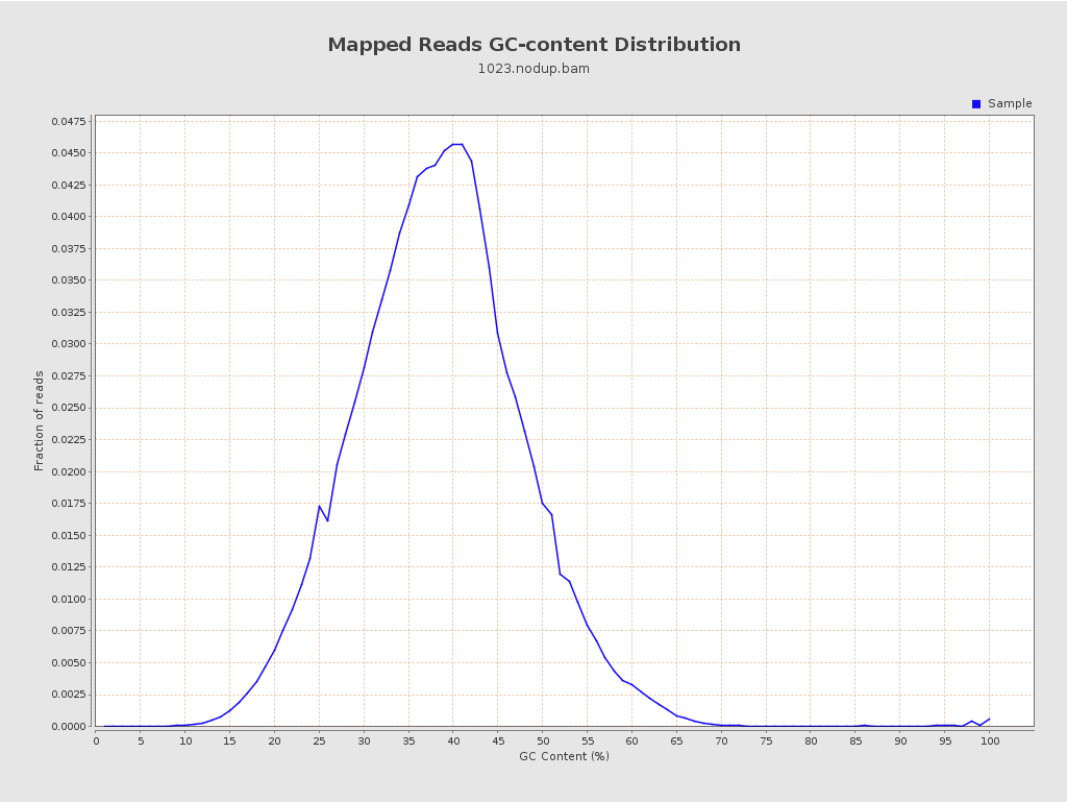
7. Results : Duplication Rate Histogram



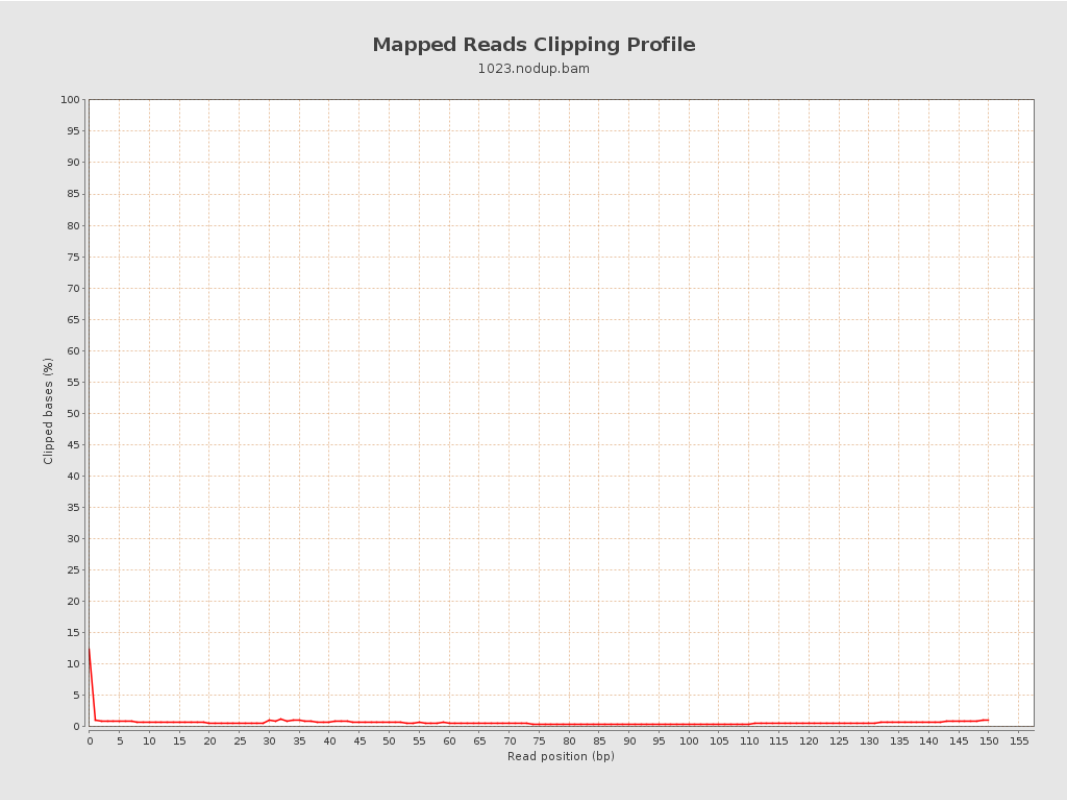
8. Results : Mapped Reads Nucleotide Content



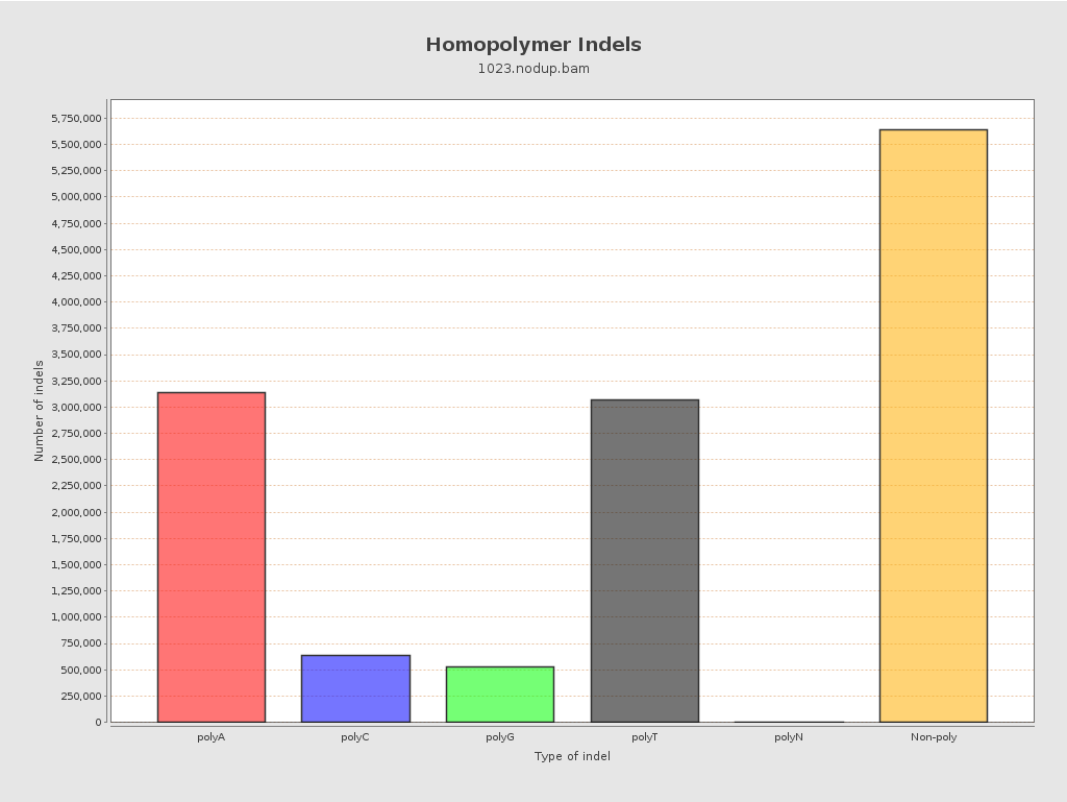
9. Results : Mapped Reads GC-content Distribution



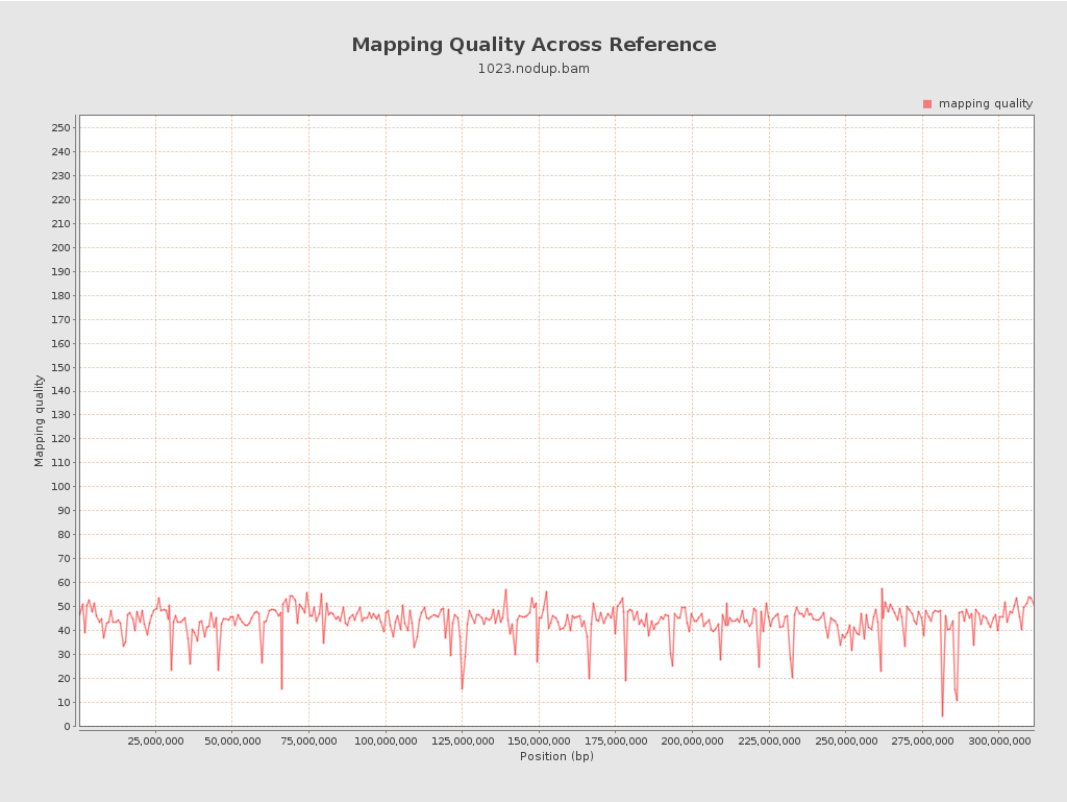
10. Results : Mapped Reads Clipping Profile



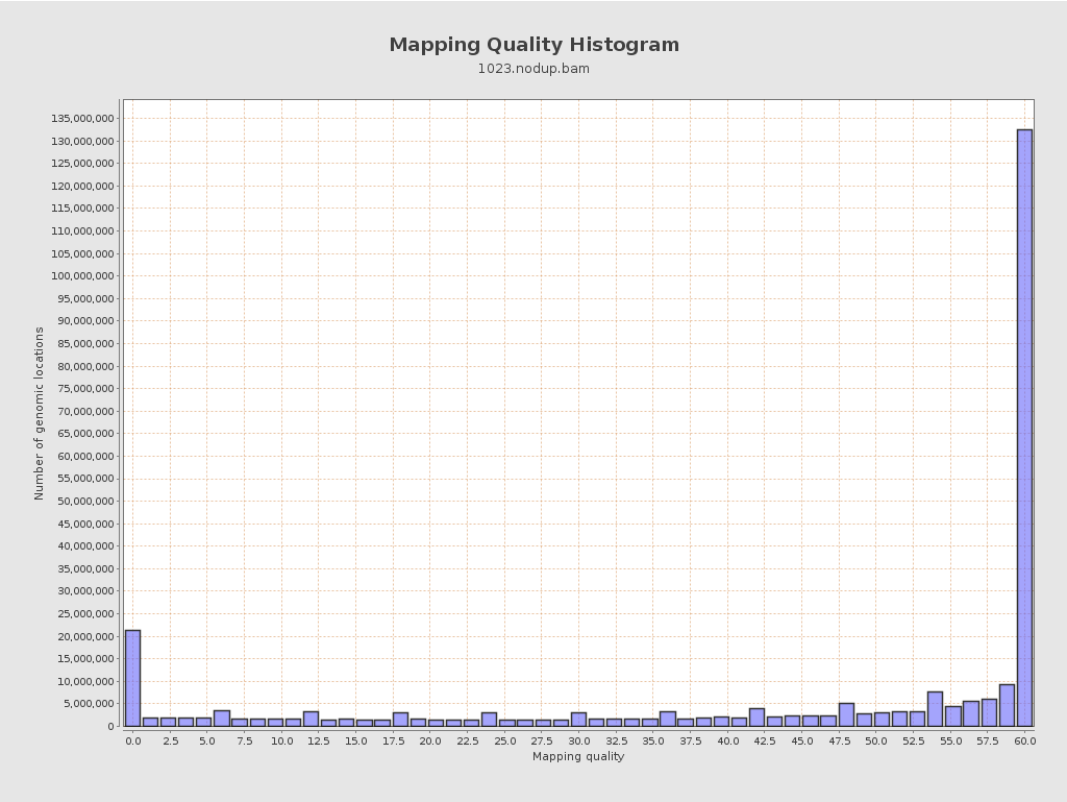
11. Results : Homopolymer Indels



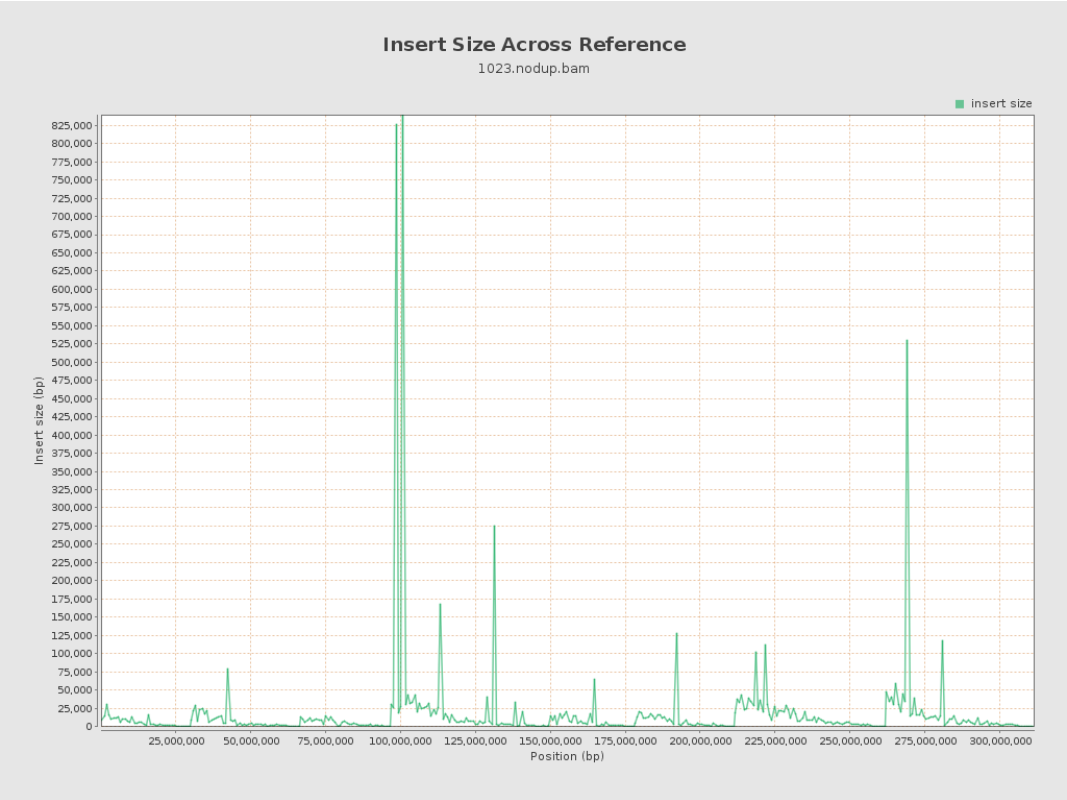
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram