Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:30:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/612.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/612.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_187/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_187_S277_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_187/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_187_S277_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:30:45 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	61,981,585
Mapped reads	58,518,045 / 94.41%
Unmapped reads	3,463,540 / 5.59%
Mapped paired reads	58,518,045 / 94.41%
Mapped reads, first in pair	29,313,729 / 47.29%
Mapped reads, second in pair	29,204,316 / 47.12%
Mapped reads, both in pair	57,384,540 / 92.58%
Mapped reads, singletons	1,133,505 / 1.83%
Read min/max/mean length	30 / 151 / 148.08
Duplicated reads (flagged)	9,311,363 / 15.02%
Clipped reads	12,848,010 / 20.73%

2.2. ACGT Content

Number/percentage of A's	2,513,359,372 / 30.86%
Number/percentage of C's	1,560,188,319 / 19.16%
Number/percentage of T's	2,514,878,755 / 30.88%
Number/percentage of G's	1,555,019,034 / 19.1%
Number/percentage of N's	35,277 / 0%
GC Percentage	38.25%

2.3. Coverage

Mean	26.2018
Standard Deviation	206.1702

2.4. Mapping Quality

Mean Mapping Quality	43.64

2.5. Insert size

Mean	234,366.72
Standard Deviation	2,279,065.68
P25/Median/P75	336 / 437 / 570

2.6. Mismatches and indels

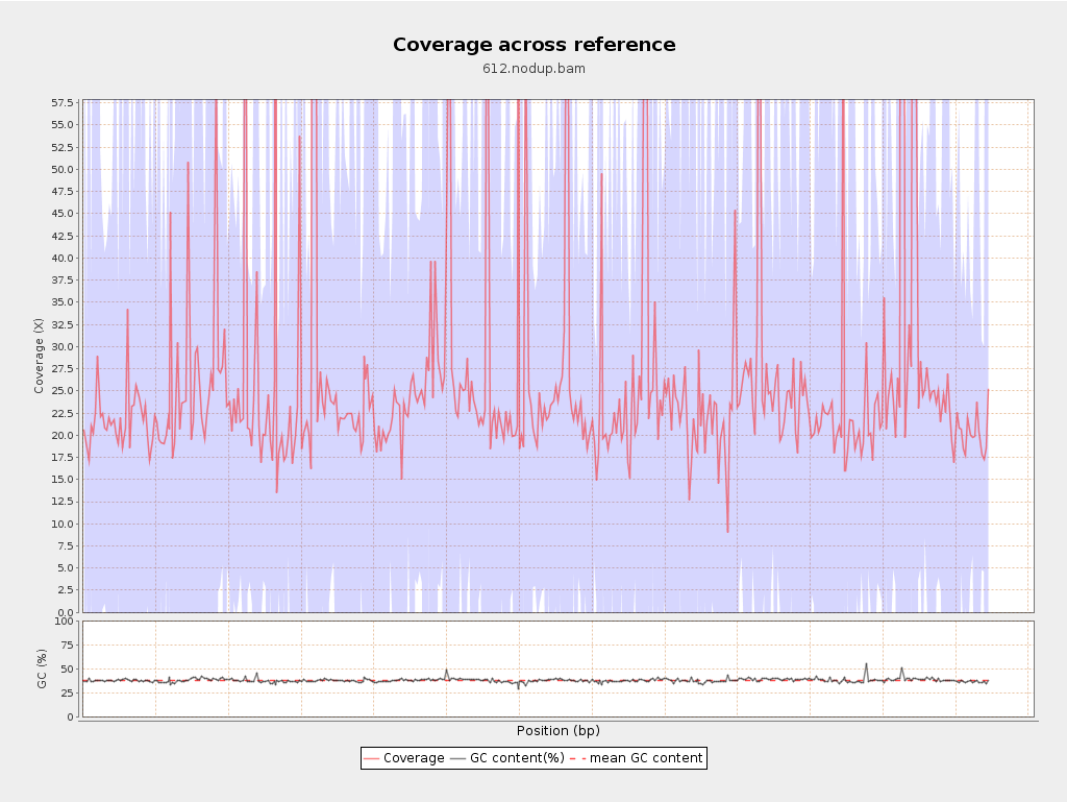
General error rate	2.35%
Mismatches	175,928,849
Insertions	5,569,297
Mapped reads with at least one insertion	8.56%
Deletions	5,798,841
Mapped reads with at least one deletion	8.8%
Homopolymer indels	56.35%

2.7. Chromosome stats

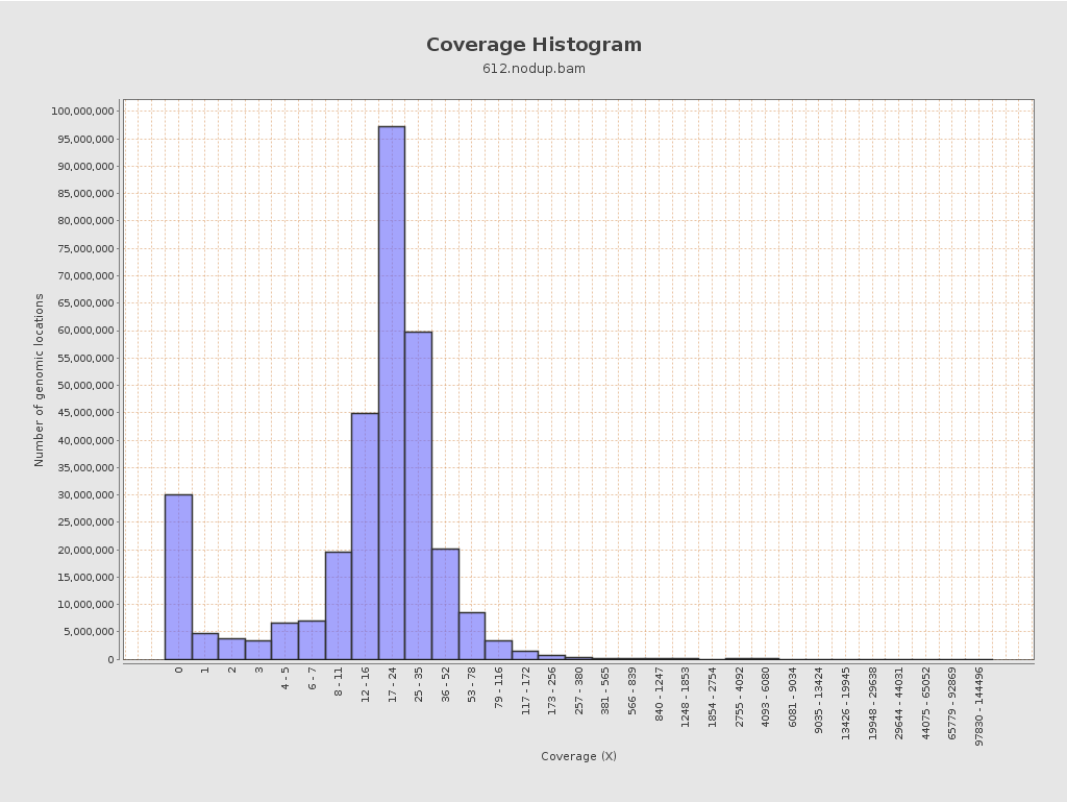
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	639234677	21.5054	56.3164

LT669789.1	36598175	993109743	27.1355	224.0343
LT669790.1	30422129	839483758	27.5945	211.7678
LT669791.1	52758100	1355017779	25.6836	164.8935
LT669792.1	28376109	725810150	25.5782	212.995
LT669793.1	33388210	848599556	25.4161	213.2063
LT669794.1	50579949	1272939945	25.1669	199.3466
LT669795.1	49795044	1491377565	29.9503	272.5939

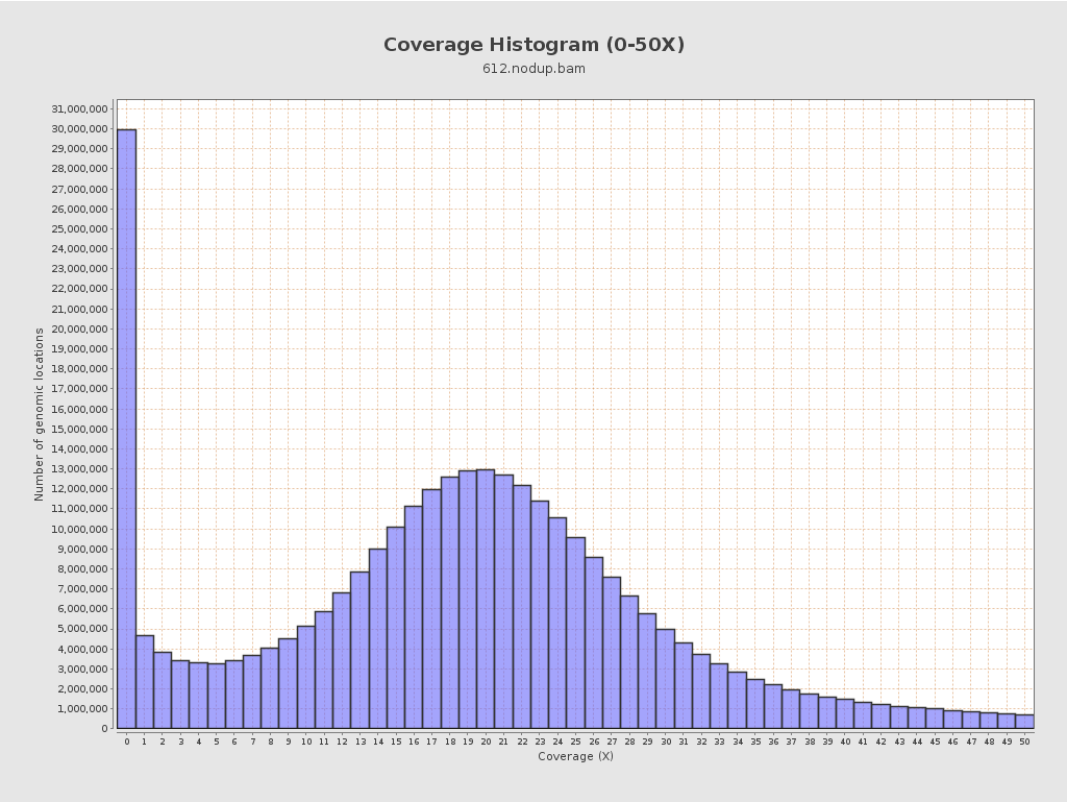
3. Results : Coverage across reference



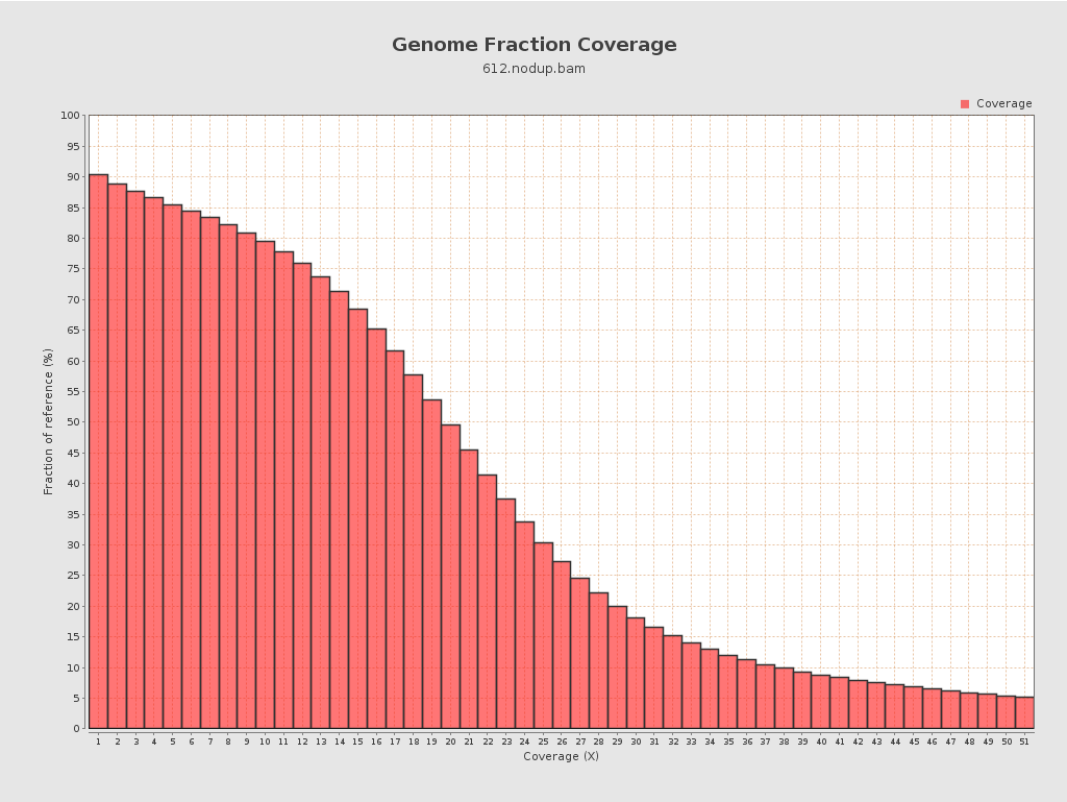
4. Results : Coverage Histogram



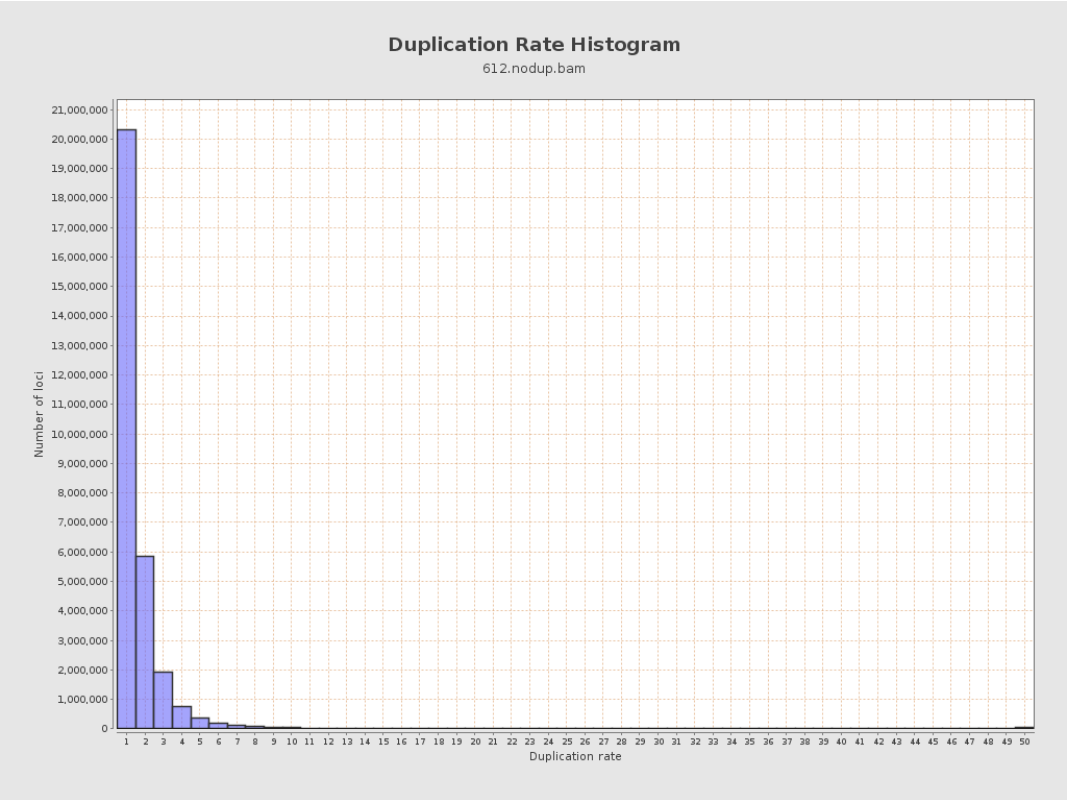
5. Results : Coverage Histogram (0-50X)



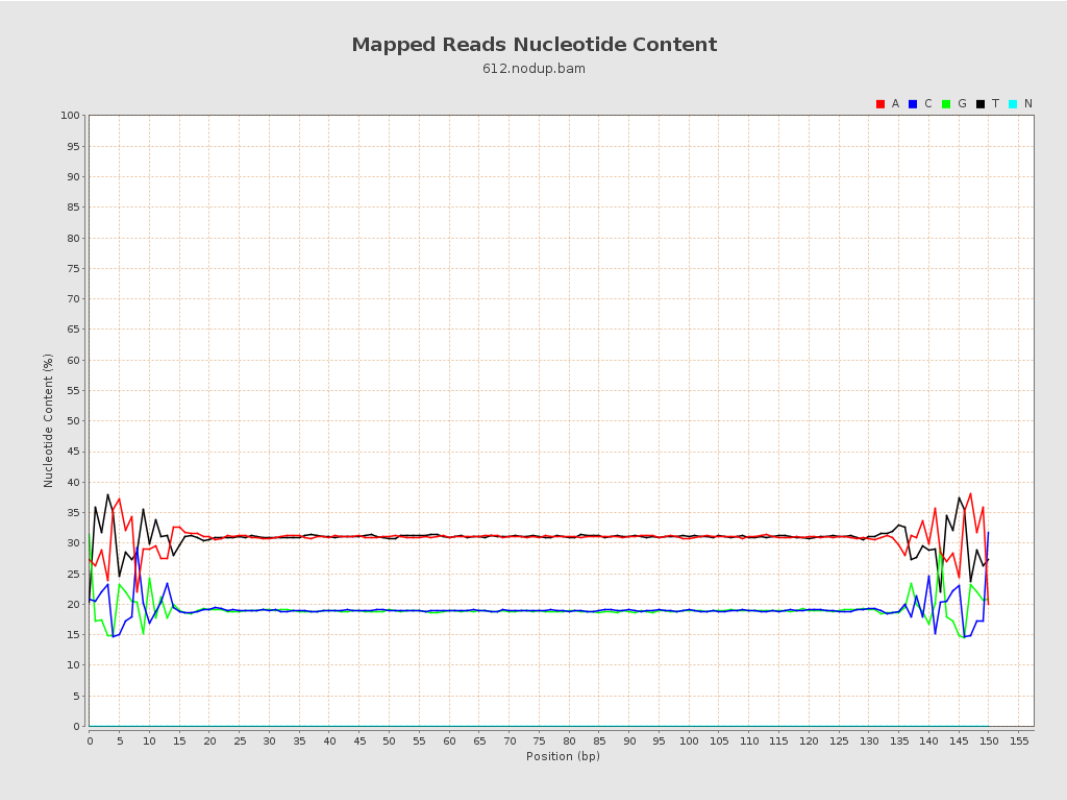
6. Results : Genome Fraction Coverage



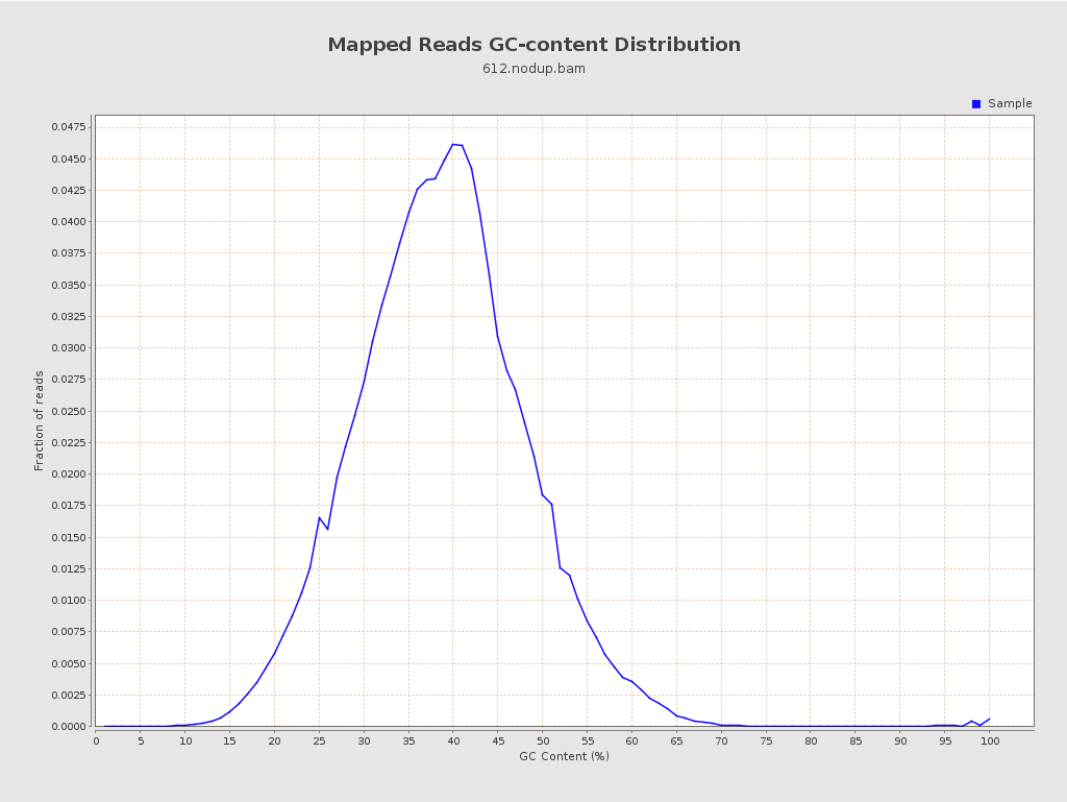
7. Results : Duplication Rate Histogram



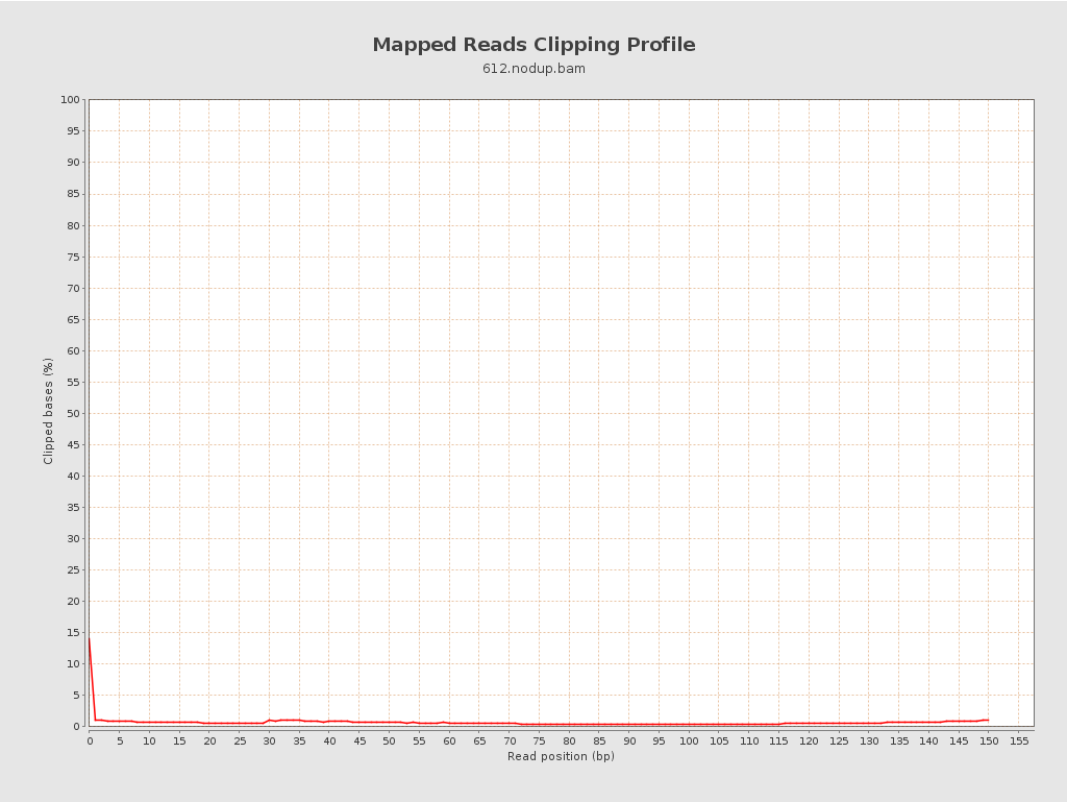
8. Results : Mapped Reads Nucleotide Content



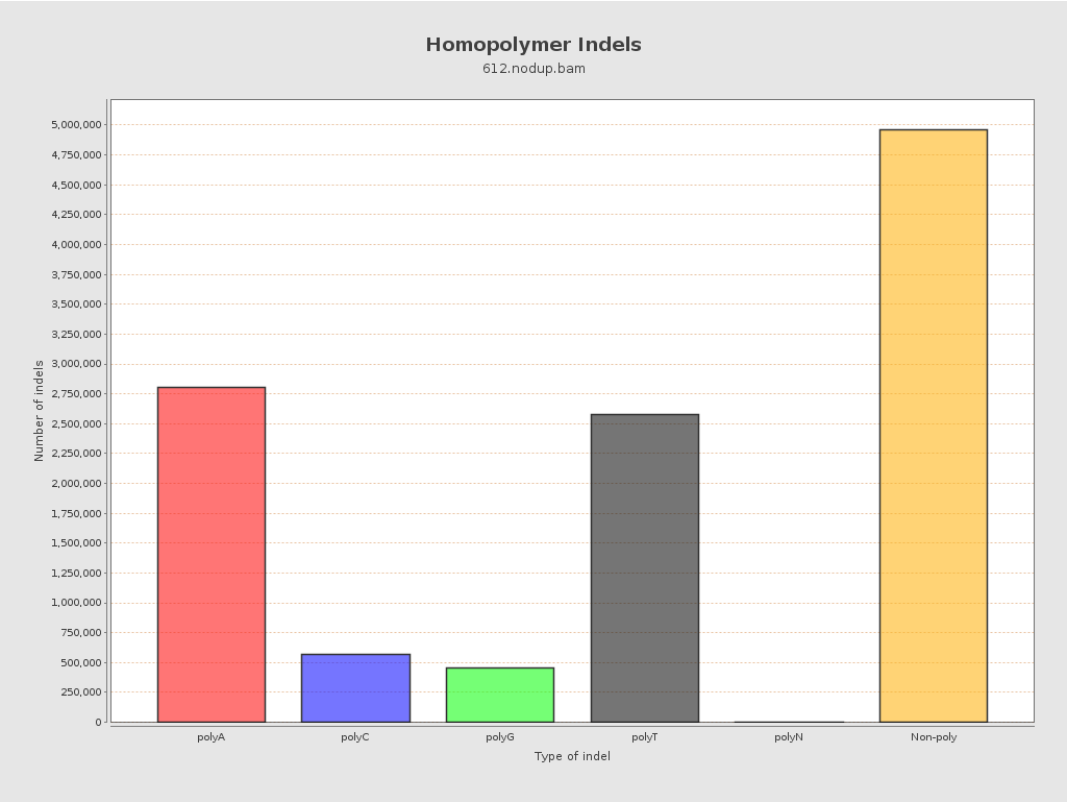
9. Results : Mapped Reads GC-content Distribution



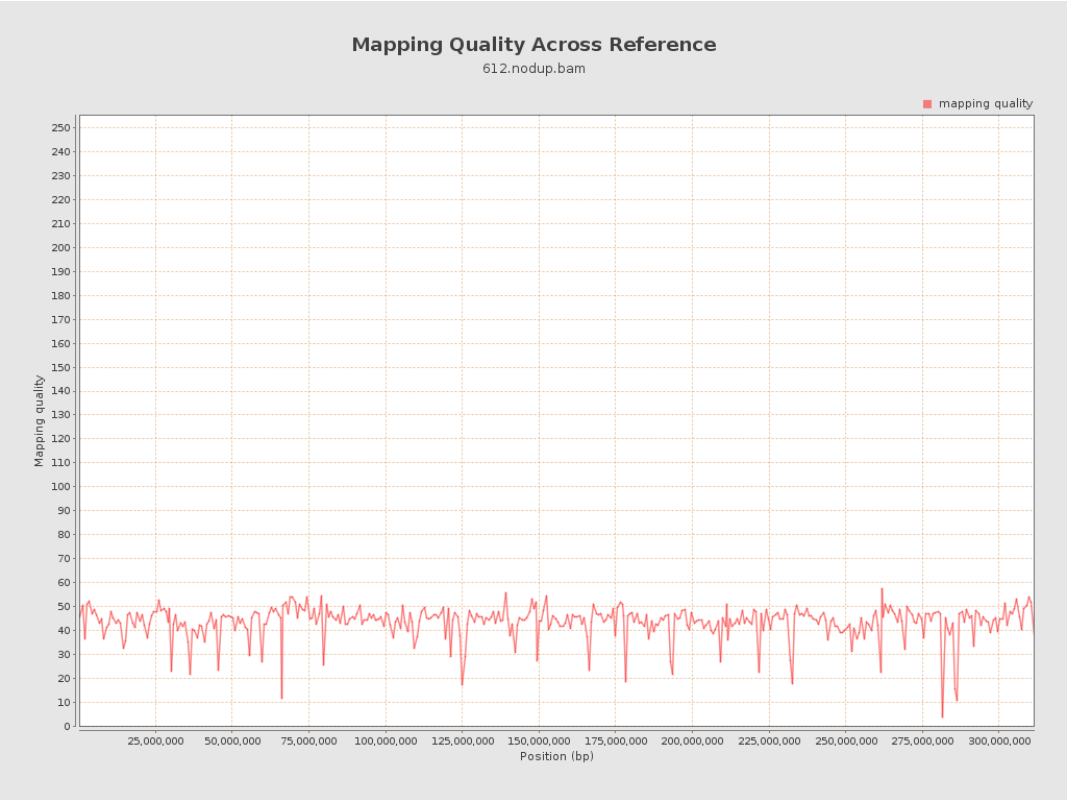
10. Results : Mapped Reads Clipping Profile



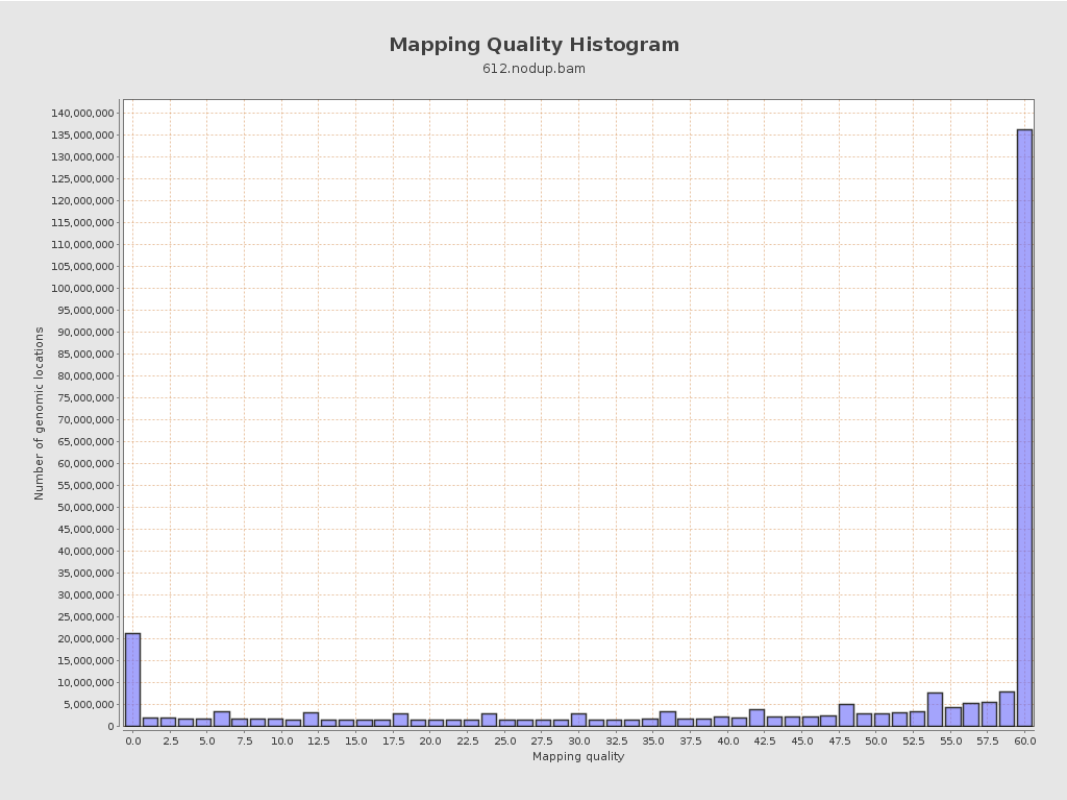
11. Results : Homopolymer Indels



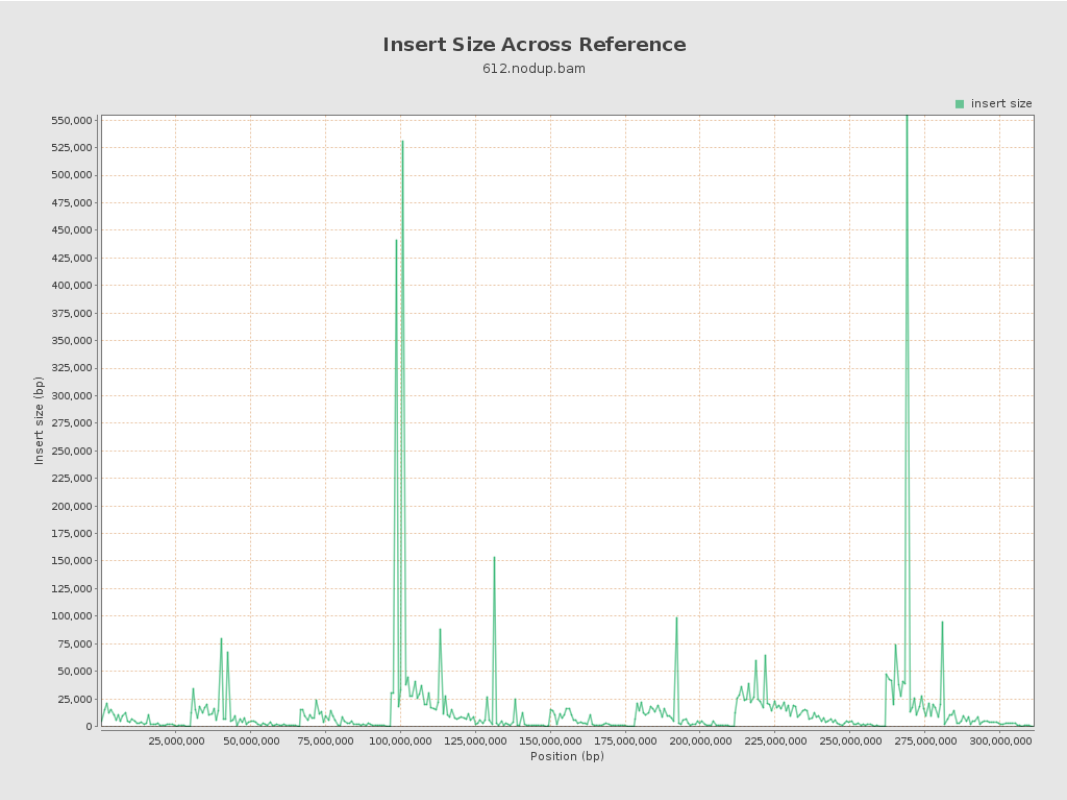
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram