Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:29:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/608.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/608.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_465/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_465_S440_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_465/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_465_S440_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

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

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	59,296,182
Mapped reads	56,351,680 / 95.03%
Unmapped reads	2,944,502 / 4.97%
Mapped paired reads	56,351,680 / 95.03%
Mapped reads, first in pair	28,226,295 / 47.6%
Mapped reads, second in pair	28,125,385 / 47.43%
Mapped reads, both in pair	55,284,160 / 93.23%
Mapped reads, singletons	1,067,520 / 1.8%
Read min/max/mean length	30 / 151 / 148.18
Duplicated reads (flagged)	8,340,288 / 14.07%
Clipped reads	11,989,673 / 20.22%

2.2. ACGT Content

Number/percentage of A's	2,427,694,199 / 30.85%
Number/percentage of C's	1,509,654,392 / 19.18%
Number/percentage of T's	2,428,173,014 / 30.85%
Number/percentage of G's	1,504,387,620 / 19.12%
Number/percentage of N's	27,525 / 0%
GC Percentage	38.3%

2.3. Coverage

Mean	25.3187
Standard Deviation	209.8158

2.4. Mapping Quality

Mean Mapping Quality	43.86

2.5. Insert size

Mean	237,097.42
Standard Deviation	2,295,540.89
P25/Median/P75	362 / 472 / 622

2.6. Mismatches and indels

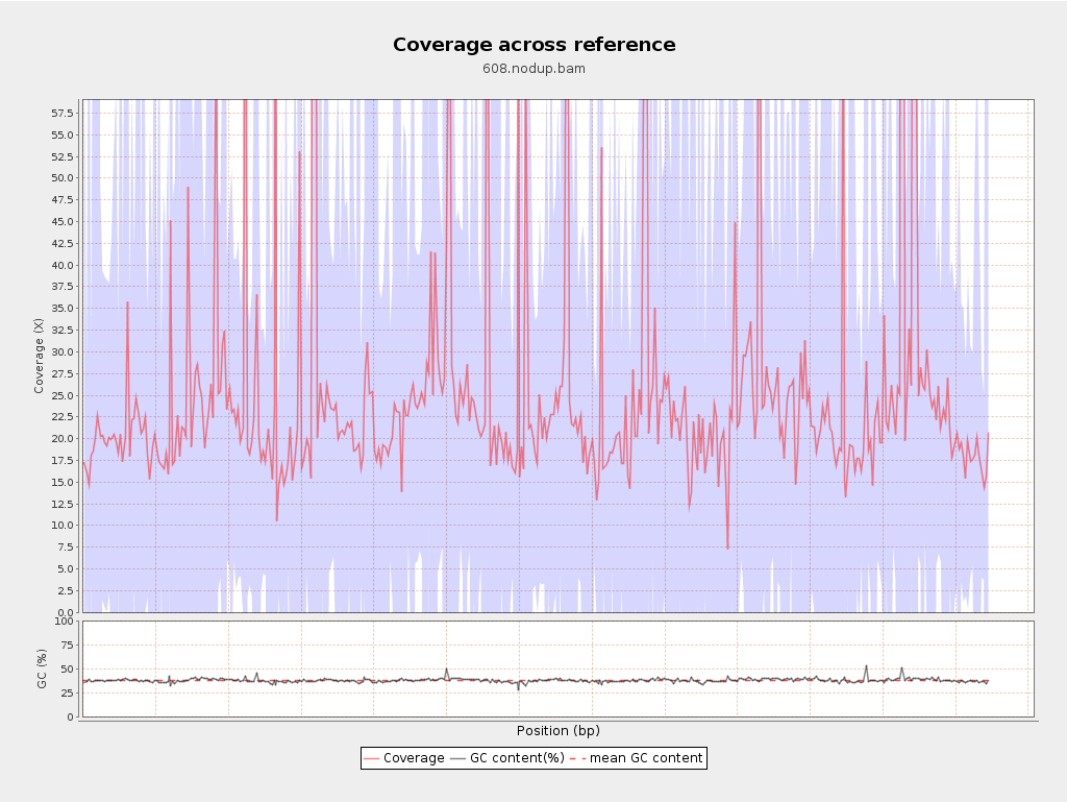
General error rate	2.34%
Mismatches	169,665,809
Insertions	5,190,586
Mapped reads with at least one insertion	8.3%
Deletions	5,446,929
Mapped reads with at least one deletion	8.61%
Homopolymer indels	56.53%

2.7. Chromosome stats

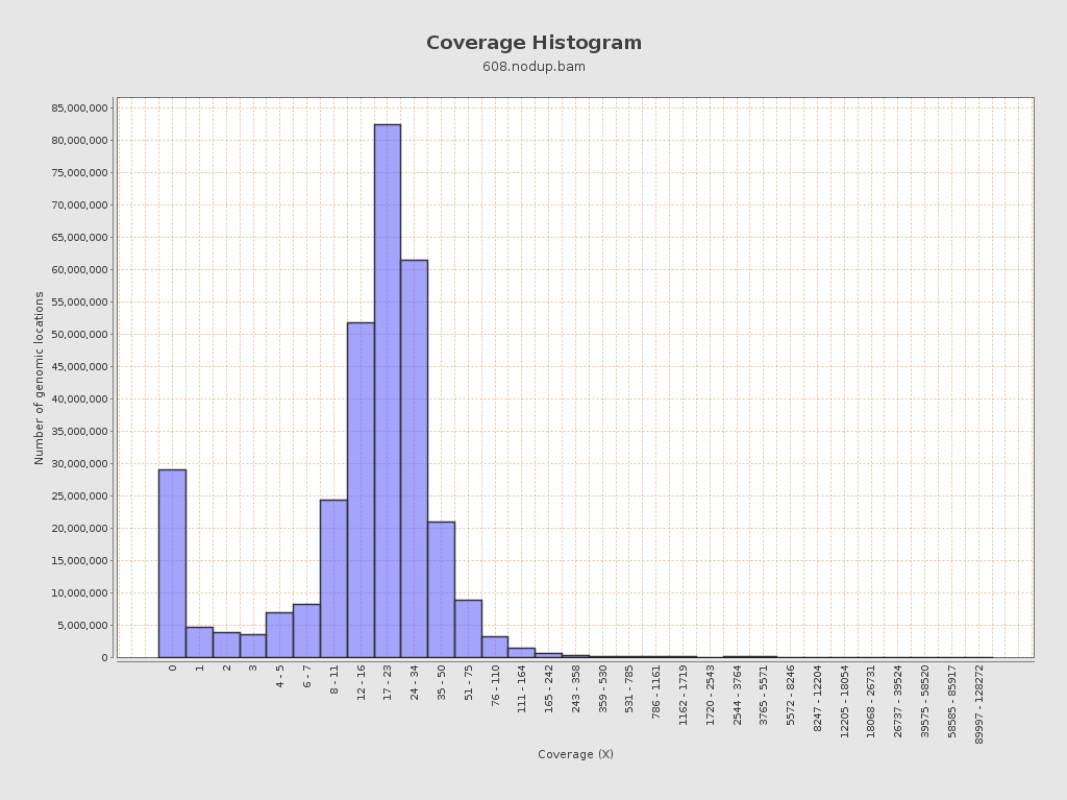
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	587282310	19.7576	56.7793

LT669789.1	36598175	957692858	26.1678	213.2733
LT669790.1	30422129	794327164	26.1102	217.414
LT669791.1	52758100	1331731541	25.2422	173.2714
LT669792.1	28376109	691018835	24.3521	220.8235
LT669793.1	33388210	822345892	24.6298	225.7596
LT669794.1	50579949	1256871887	24.8492	215.5583
LT669795.1	49795044	1449090759	29.1011	265.0991

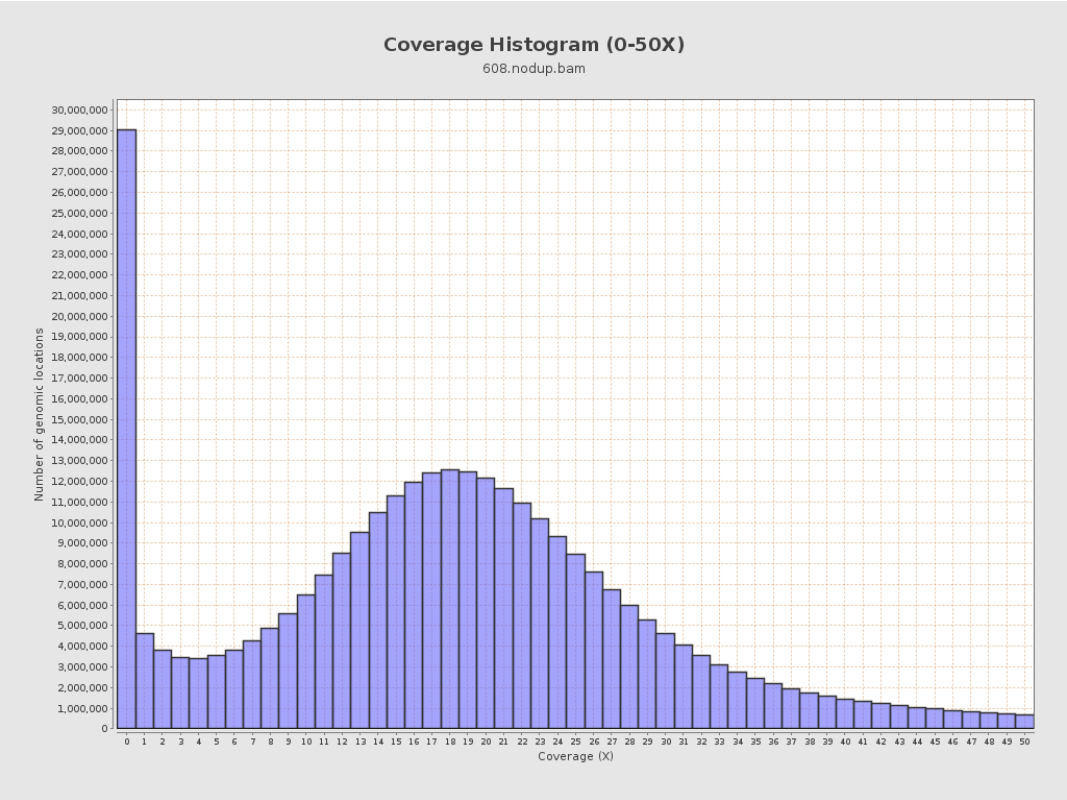
3. Results : Coverage across reference



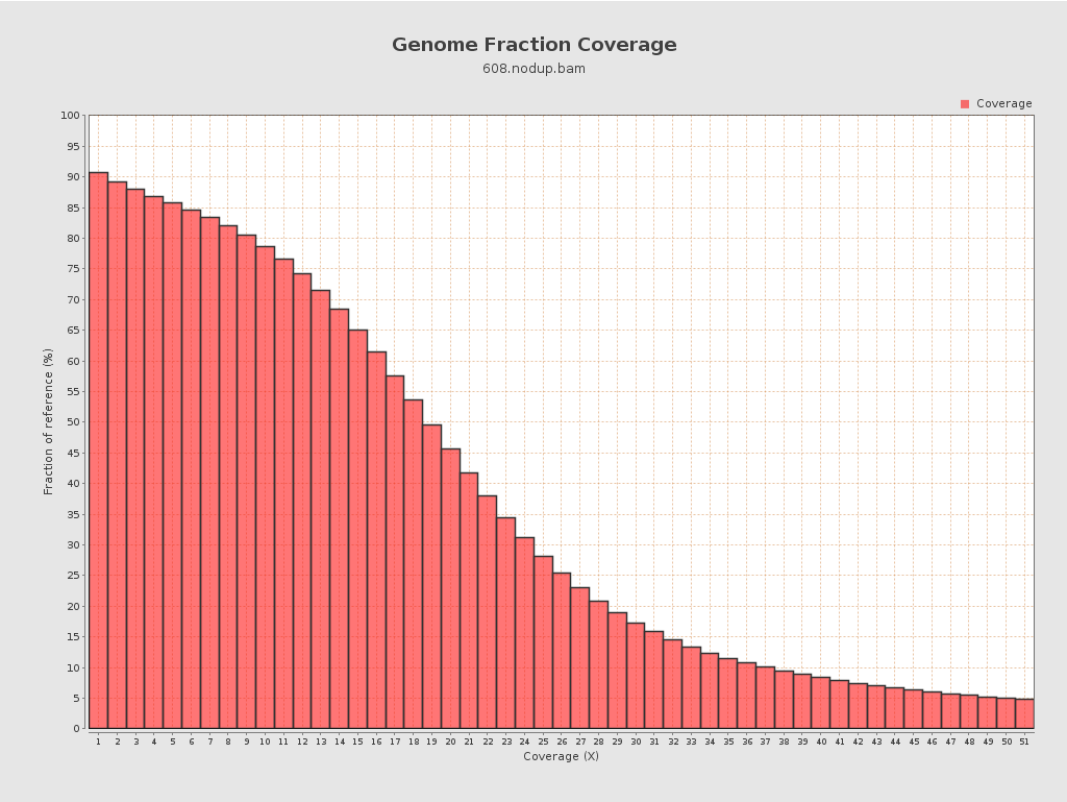
4. Results : Coverage Histogram



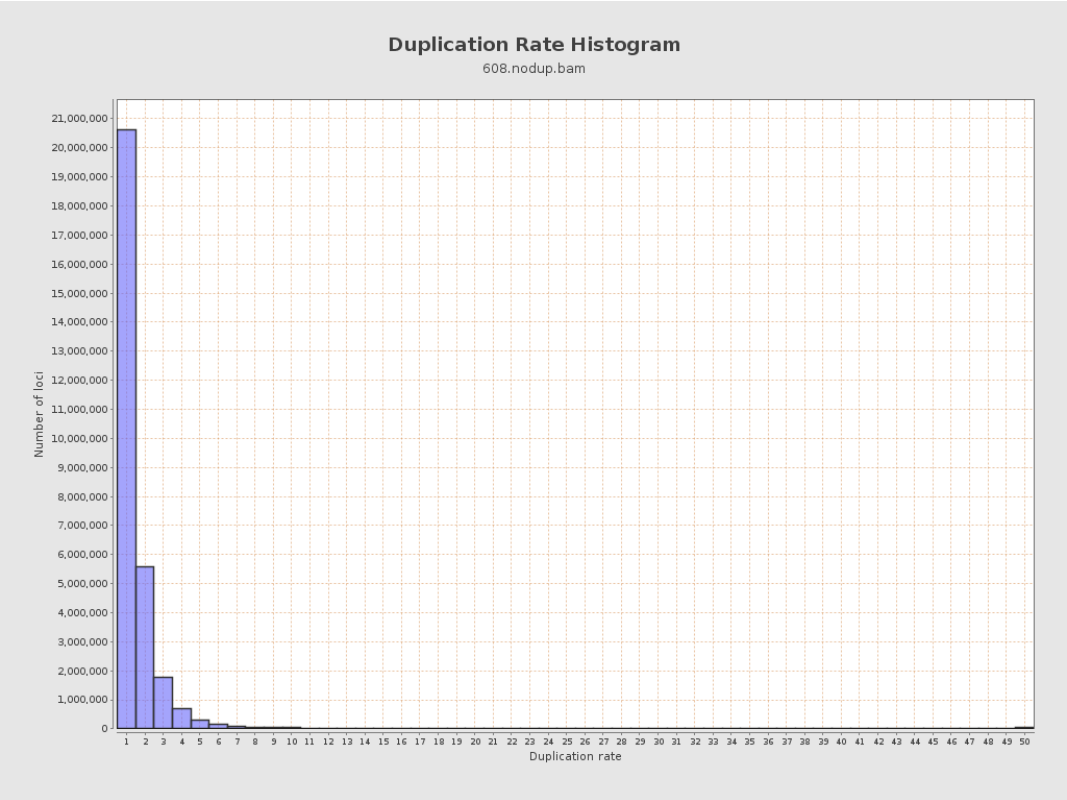
5. Results : Coverage Histogram (0-50X)



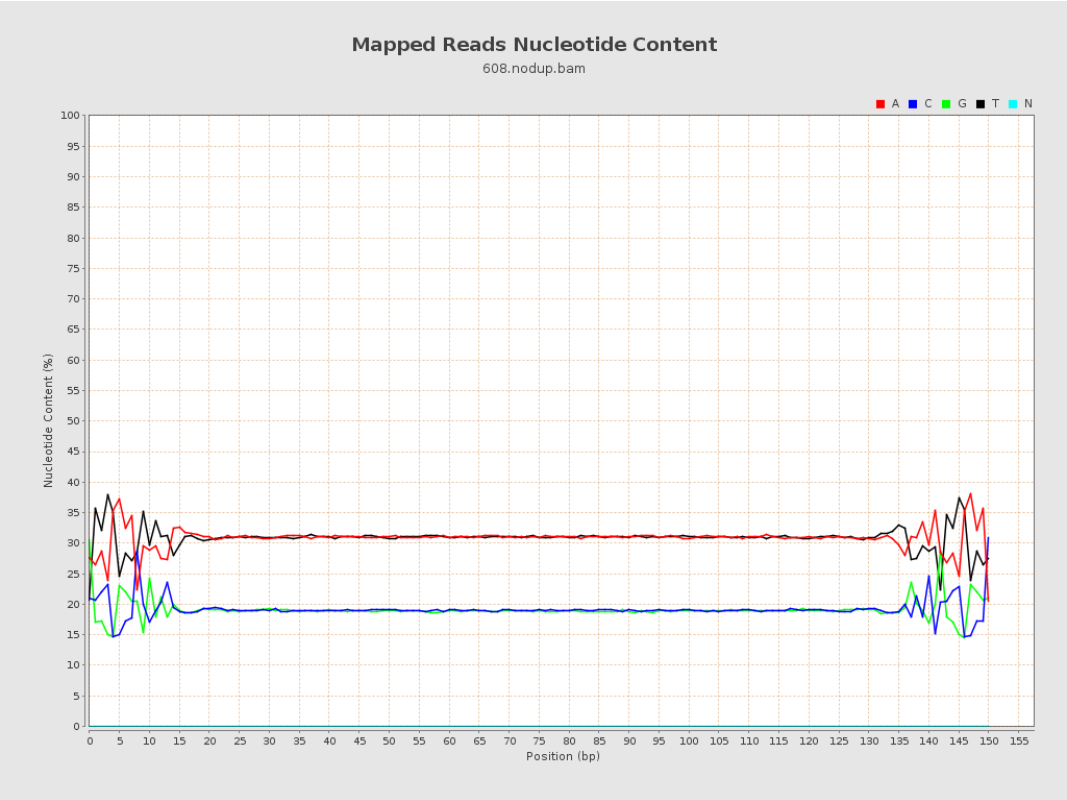
6. Results : Genome Fraction Coverage



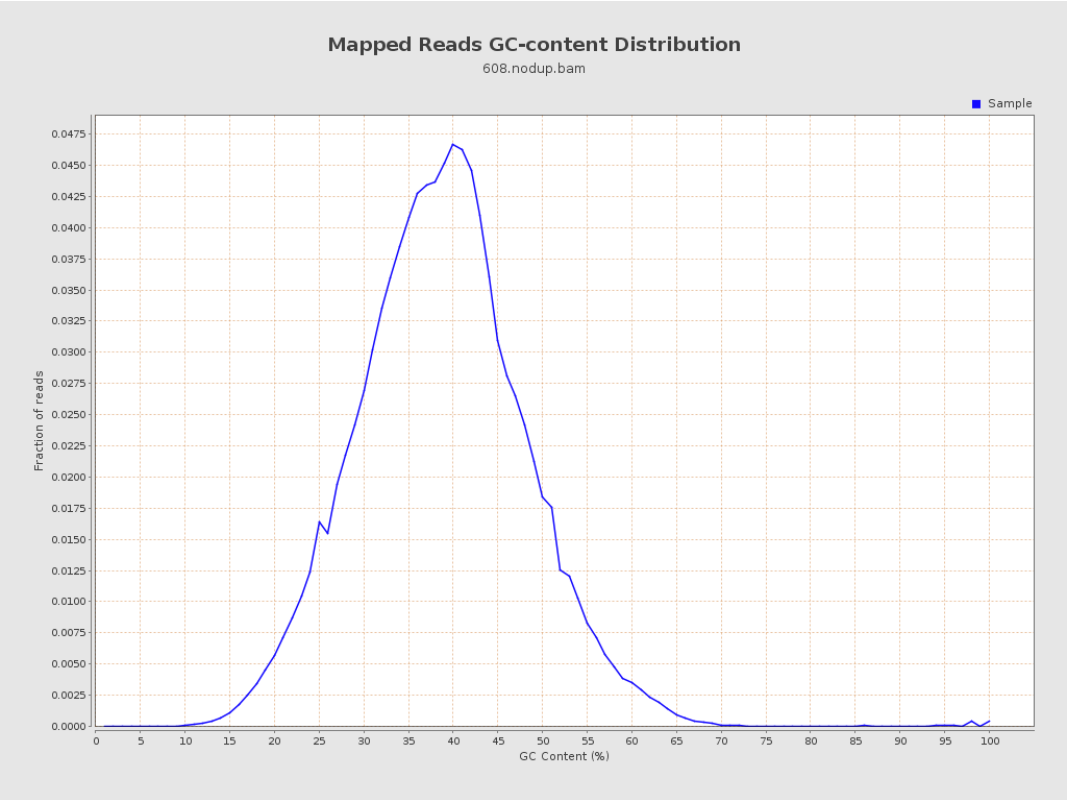
7. Results : Duplication Rate Histogram



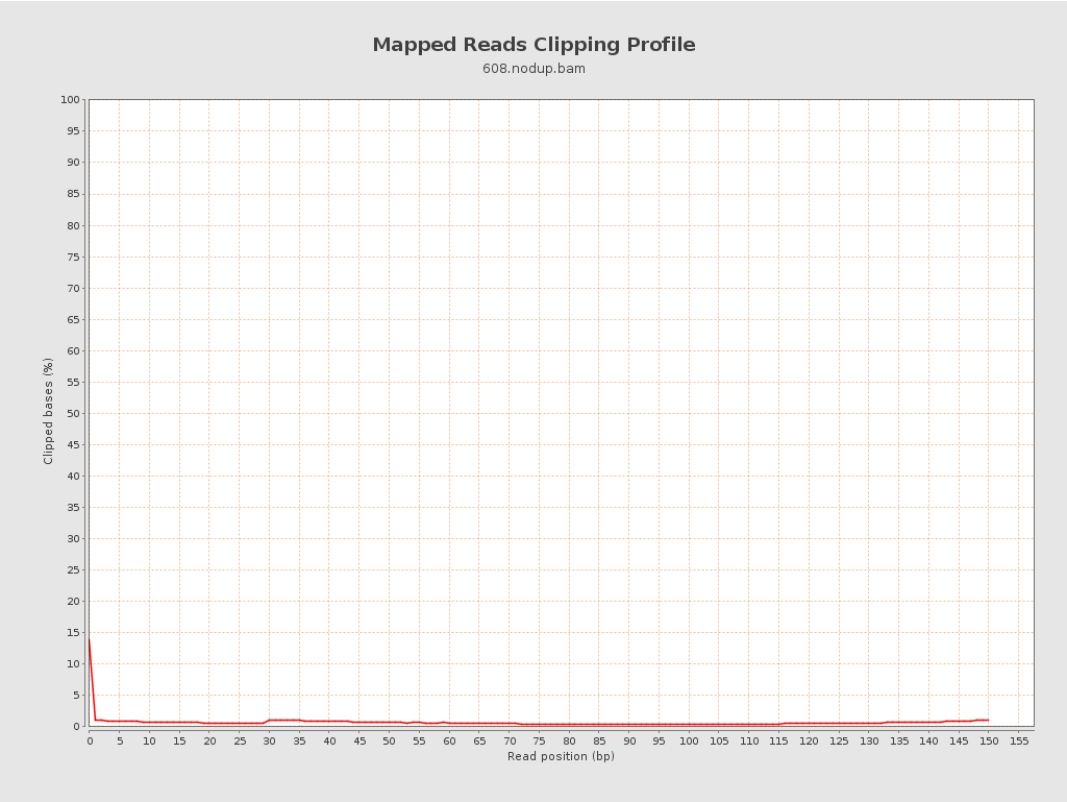
8. Results : Mapped Reads Nucleotide Content



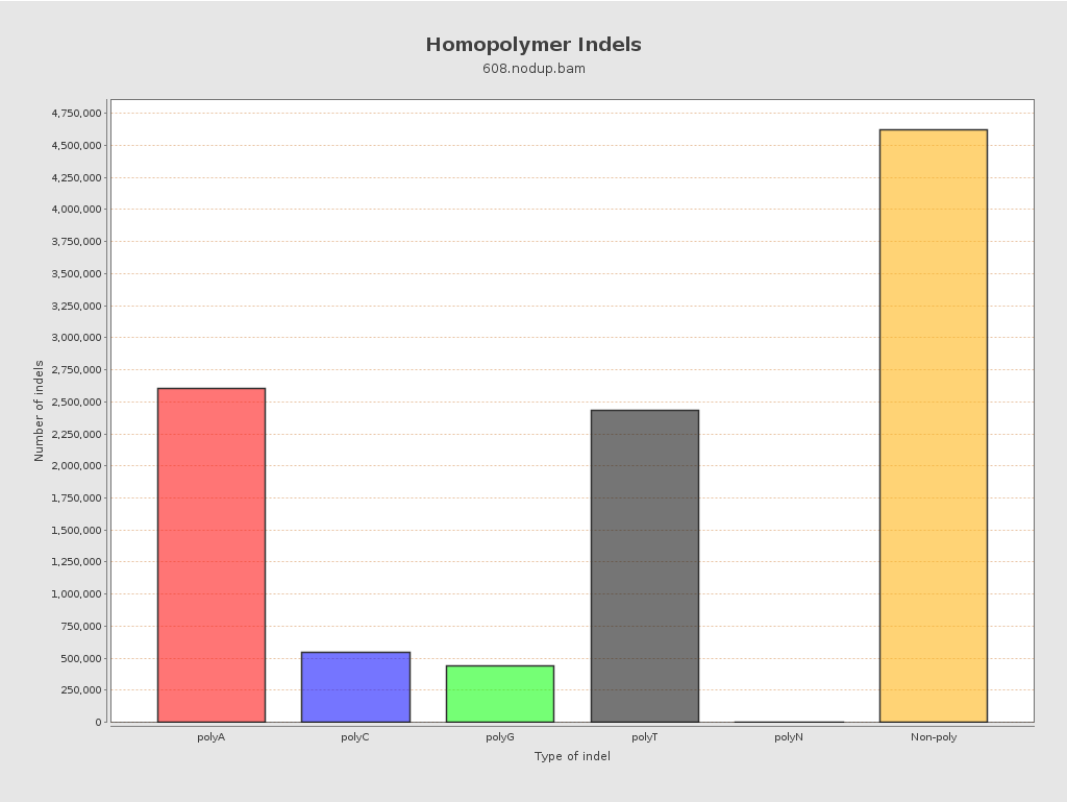
9. Results : Mapped Reads GC-content Distribution



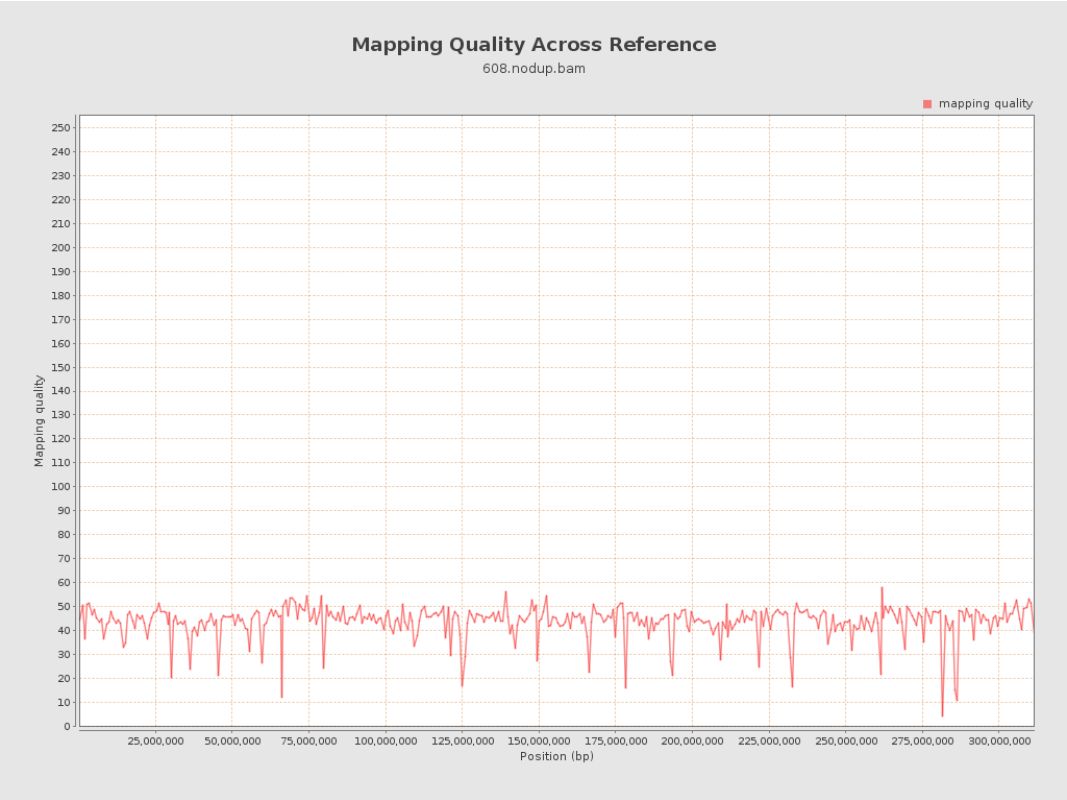
10. Results : Mapped Reads Clipping Profile



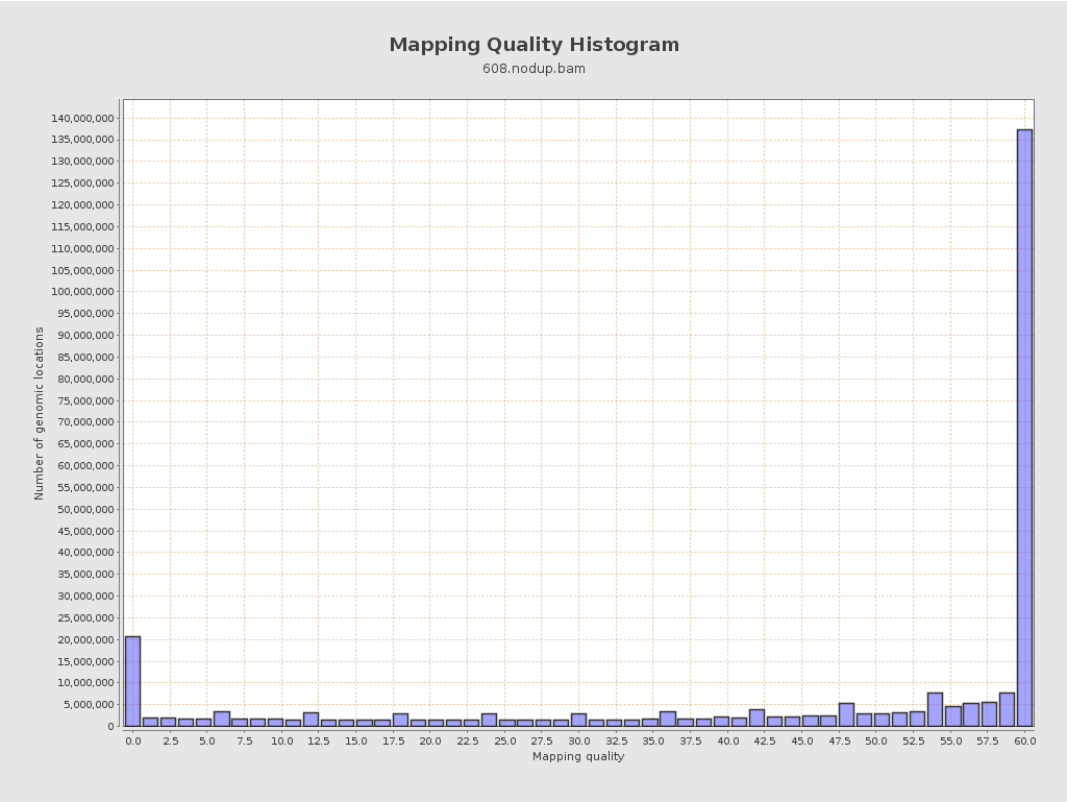
11. Results : Homopolymer Indels



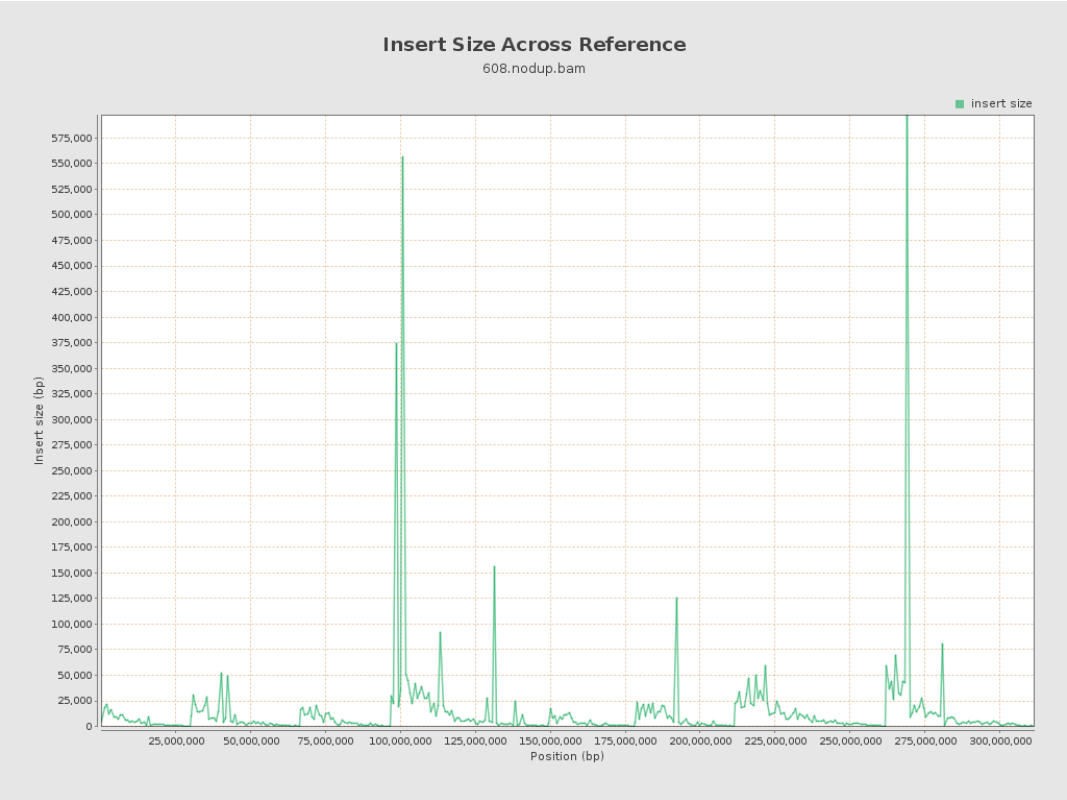
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram