Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:36:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/609.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/609.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_263/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_263_S344_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_263/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_263_S344_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:36:06 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	84,770,230
Mapped reads	76,225,144 / 89.92%
Unmapped reads	8,545,086 / 10.08%
Mapped paired reads	76,225,144 / 89.92%
Mapped reads, first in pair	38,191,729 / 45.05%
Mapped reads, second in pair	38,033,415 / 44.87%
Mapped reads, both in pair	73,560,618 / 86.78%
Mapped reads, singletons	2,664,526 / 3.14%
Read min/max/mean length	30 / 151 / 147.9
Duplicated reads (flagged)	14,966,812 / 17.66%
Clipped reads	20,047,610 / 23.65%

2.2. ACGT Content

Number/percentage of A's	3,173,043,880 / 30.84%
Number/percentage of C's	1,970,181,161 / 19.15%
Number/percentage of T's	3,176,587,690 / 30.87%
Number/percentage of G's	1,968,859,375 / 19.14%
Number/percentage of N's	38,868 / 0%
GC Percentage	38.29%

2.3. Coverage

Mean	33.0989
Standard Deviation	383.4483

2.4. Mapping Quality

Mean Mapping Quality	44

2.5. Insert size

Mean	261,567.3
Standard Deviation	2,473,624.04
P25/Median/P75	297 / 399 / 525

2.6. Mismatches and indels

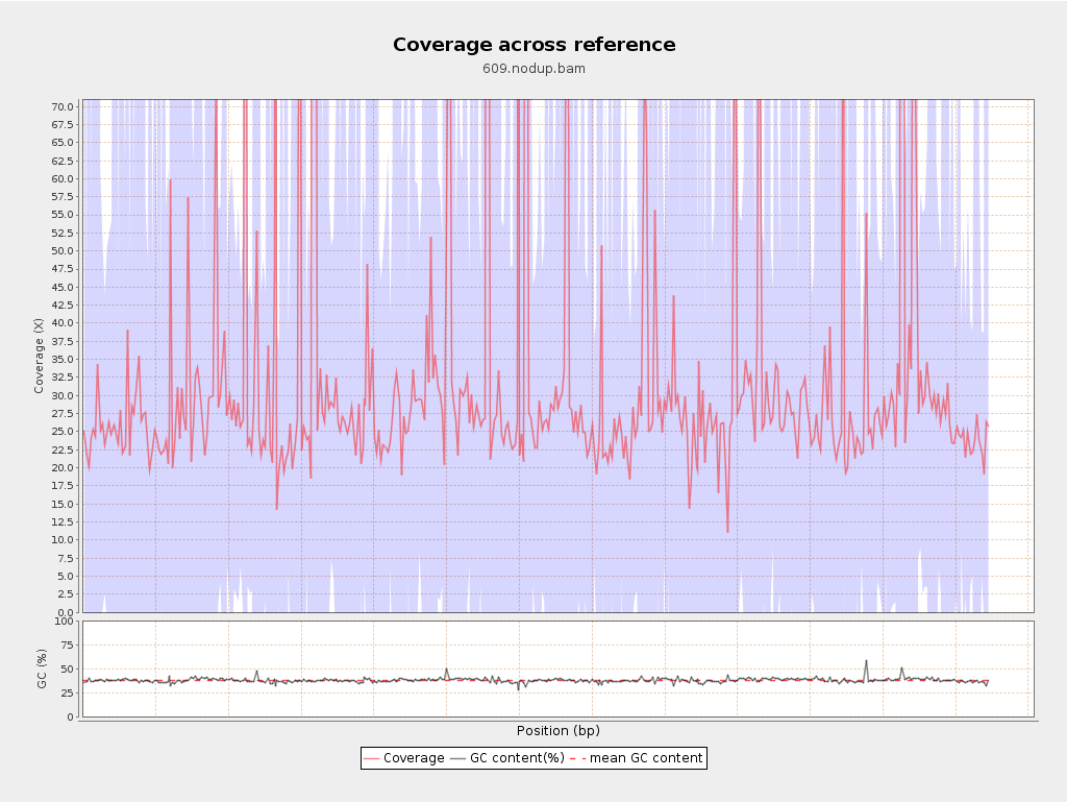
General error rate	2.41%
Mismatches	226,466,107
Insertions	7,887,004
Mapped reads with at least one insertion	9.2%
Deletions	7,227,417
Mapped reads with at least one deletion	8.4%
Homopolymer indels	57.56%

2.7. Chromosome stats

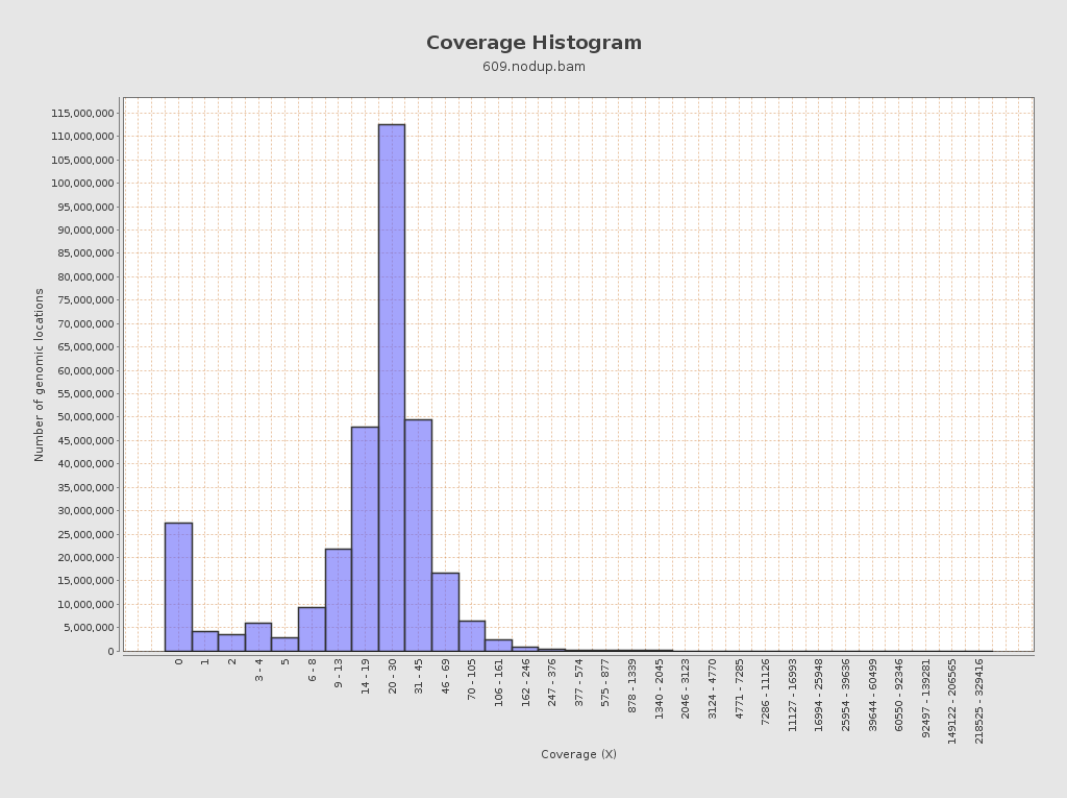
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	753695498	25.3562	147.9187

LT669789.1	36598175	1239154577	33.8584	405.6963
LT669790.1	30422129	1282799376	42.1667	567.2355
LT669791.1	52758100	1748207769	33.1363	429.3842
LT669792.1	28376109	958861953	33.7912	392.2489
LT669793.1	33388210	962434271	28.8256	200.306
LT669794.1	50579949	1565131843	30.9437	308.6948
LT669795.1	49795044	1804728838	36.2431	427.5125

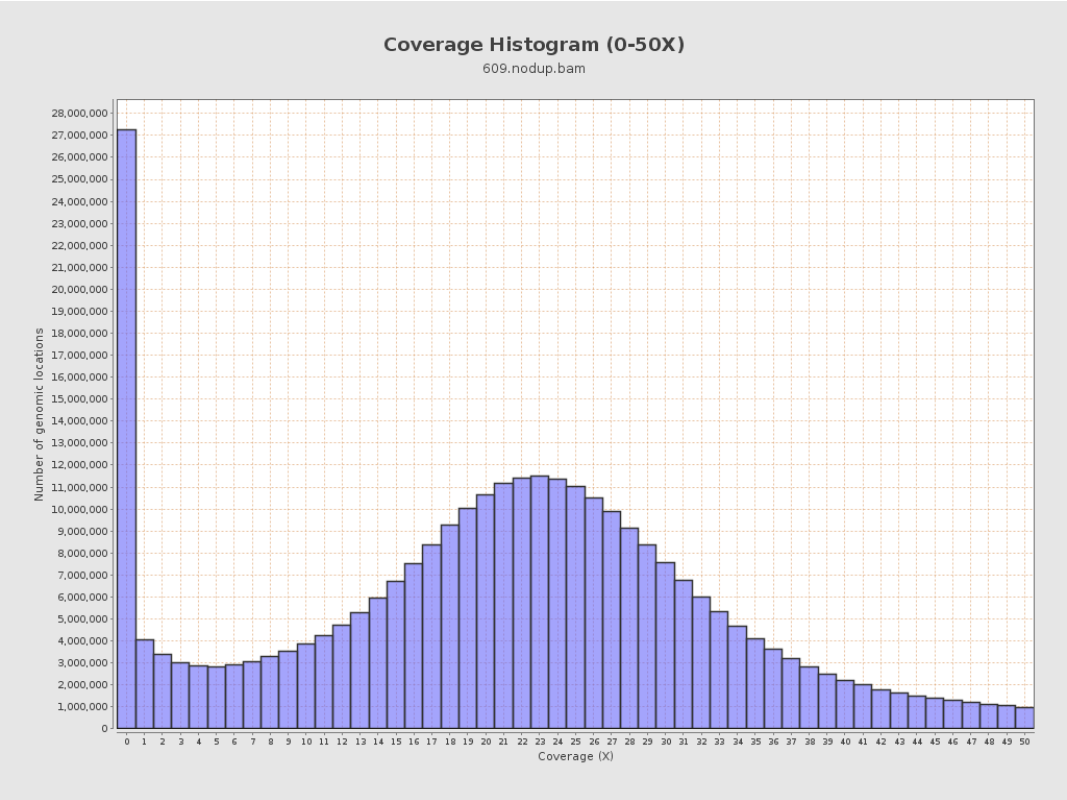
3. Results : Coverage across reference



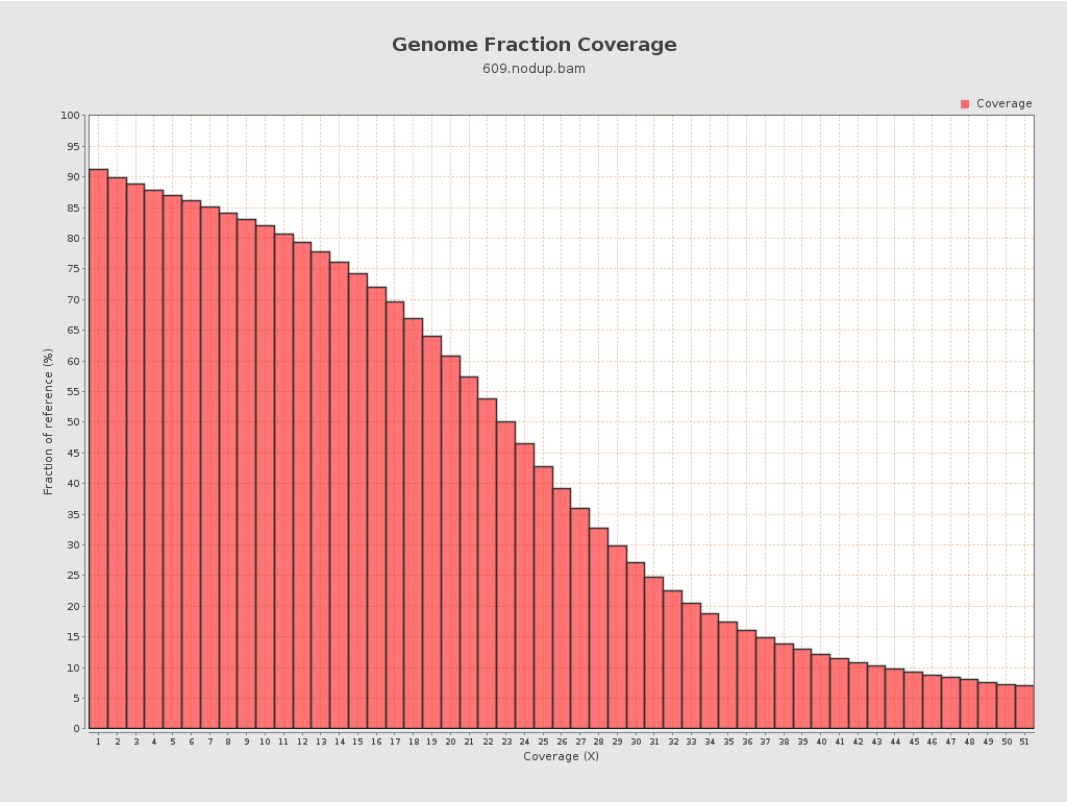
4. Results : Coverage Histogram



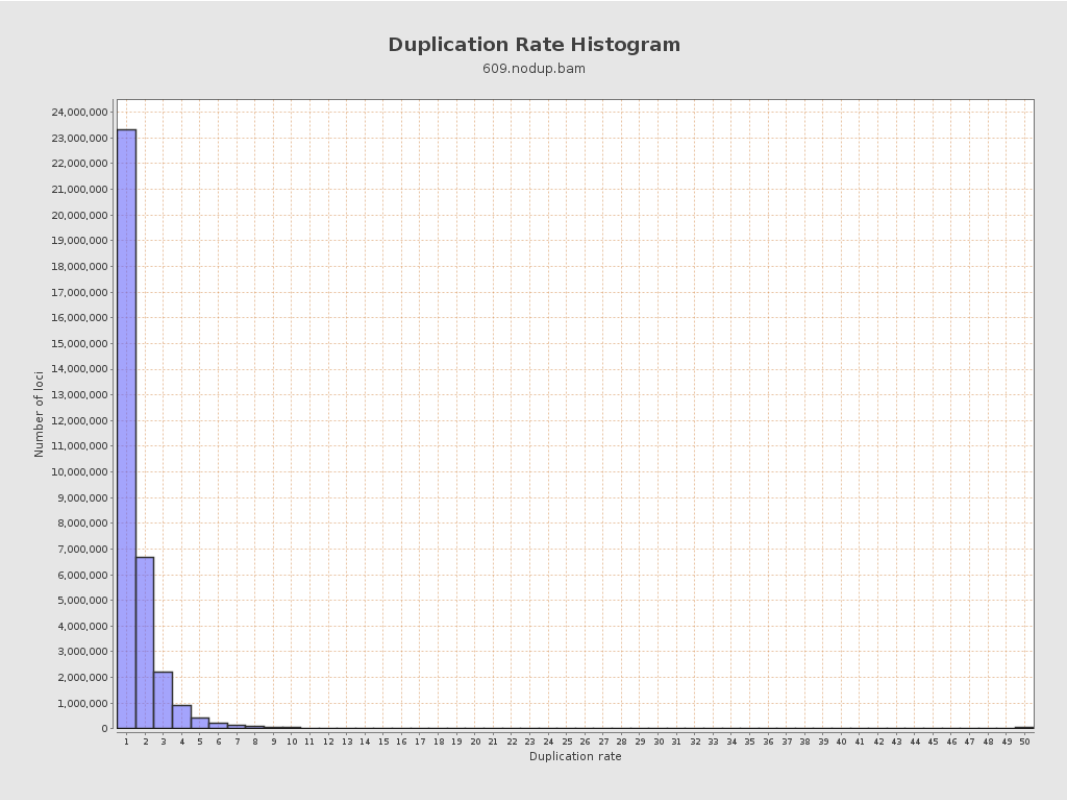
5. Results : Coverage Histogram (0-50X)



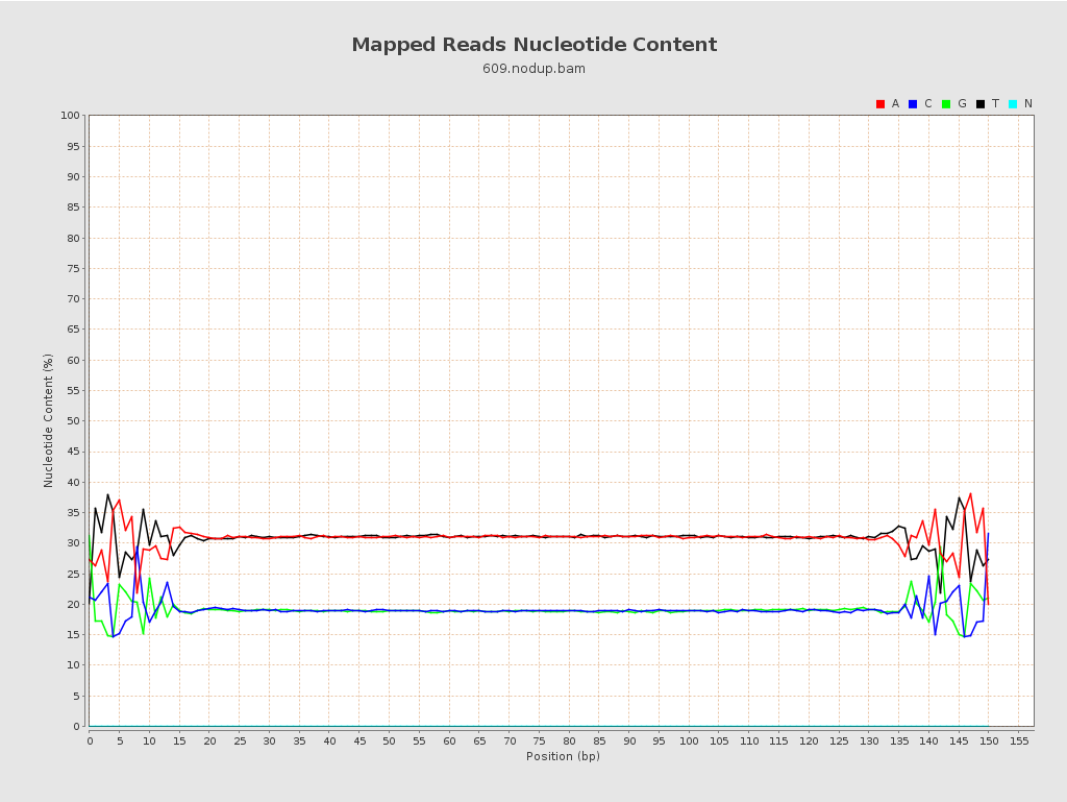
6. Results : Genome Fraction Coverage



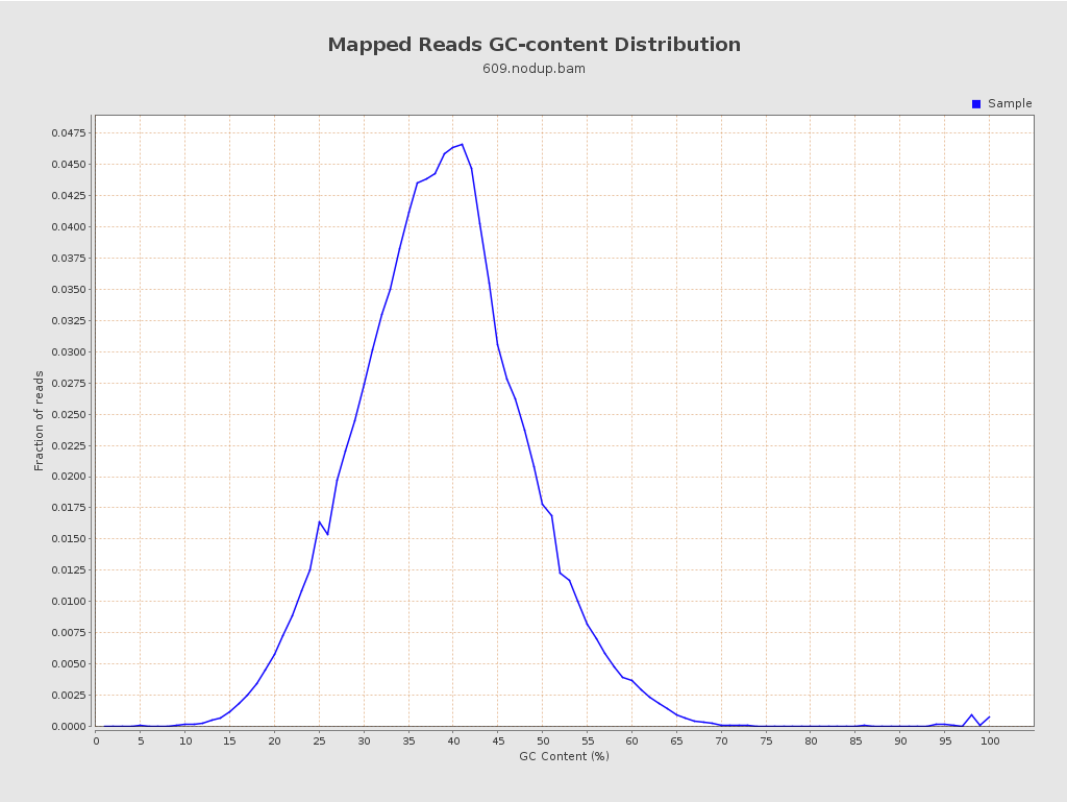
7. Results : Duplication Rate Histogram



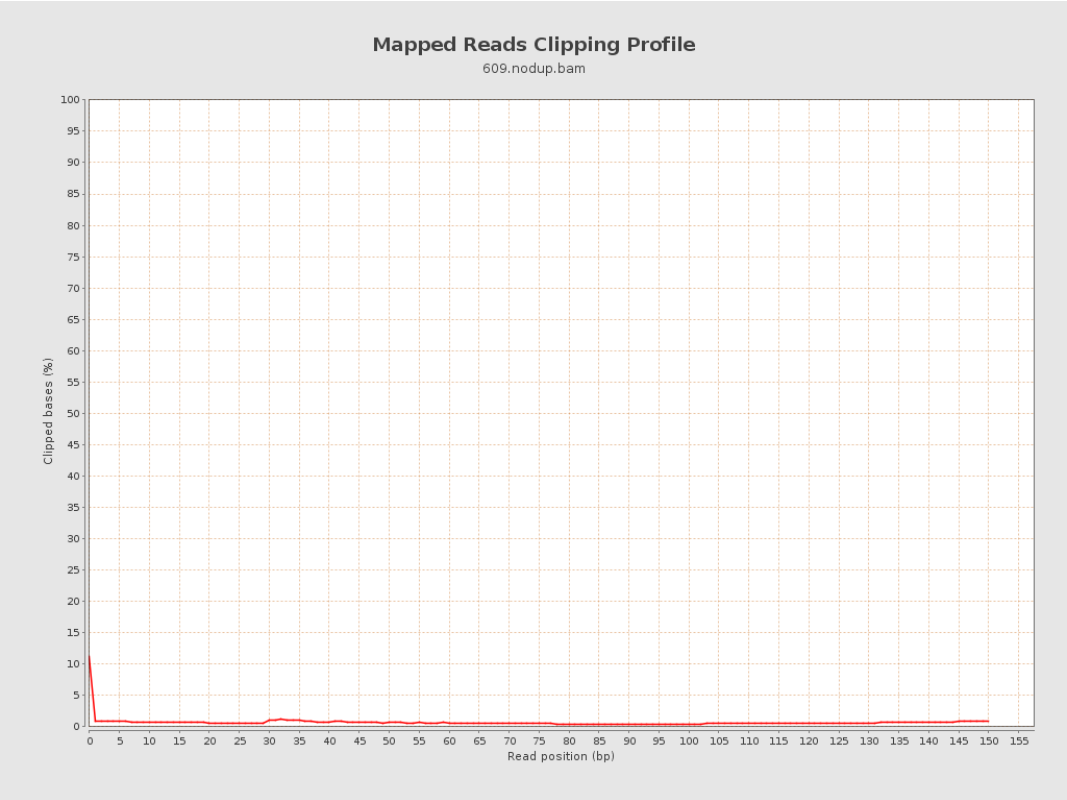
8. Results : Mapped Reads Nucleotide Content



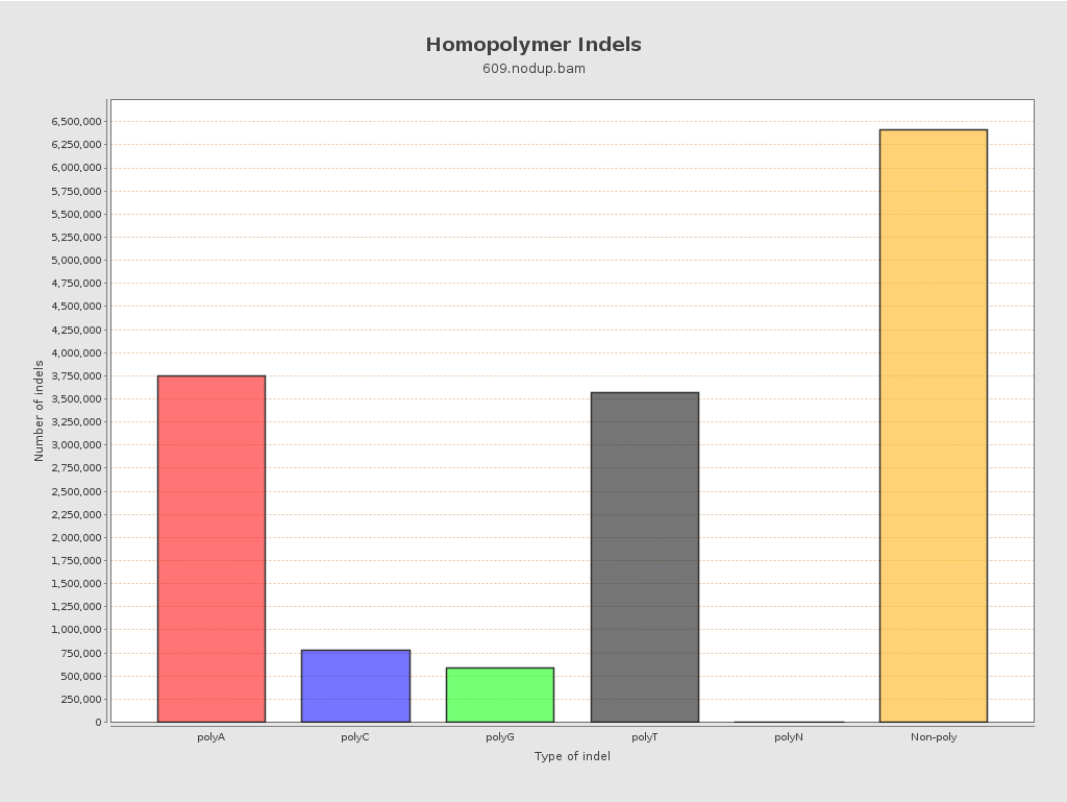
9. Results : Mapped Reads GC-content Distribution



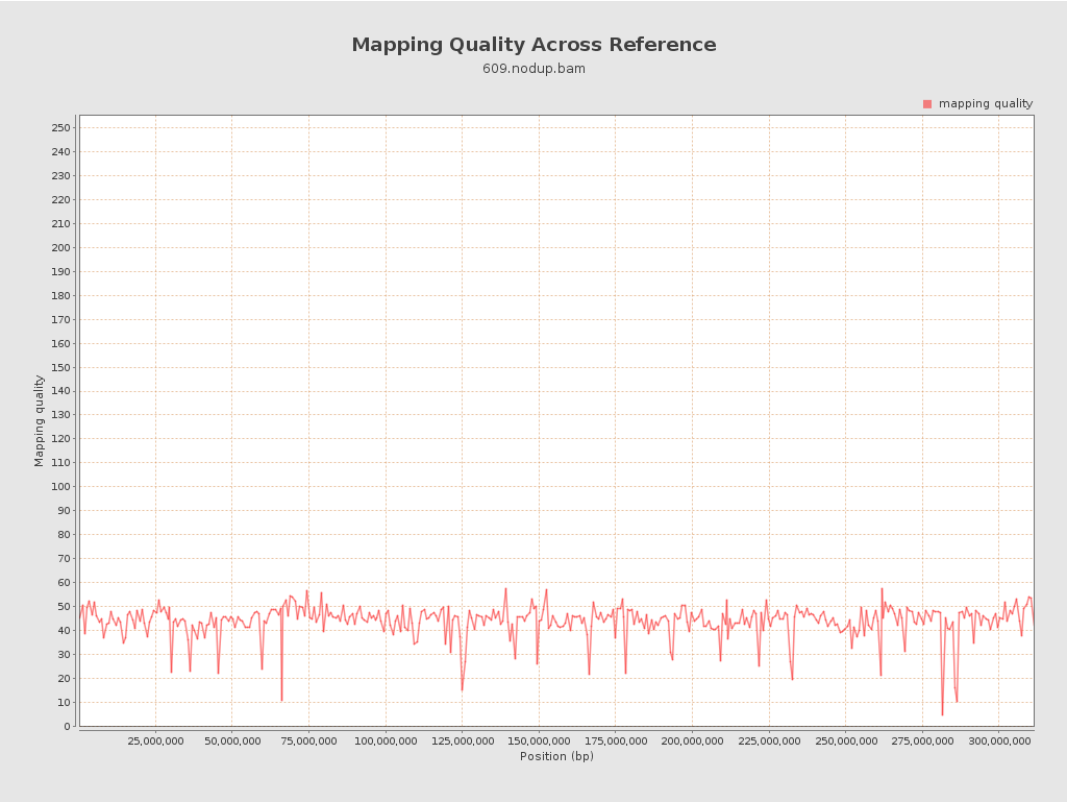
10. Results : Mapped Reads Clipping Profile



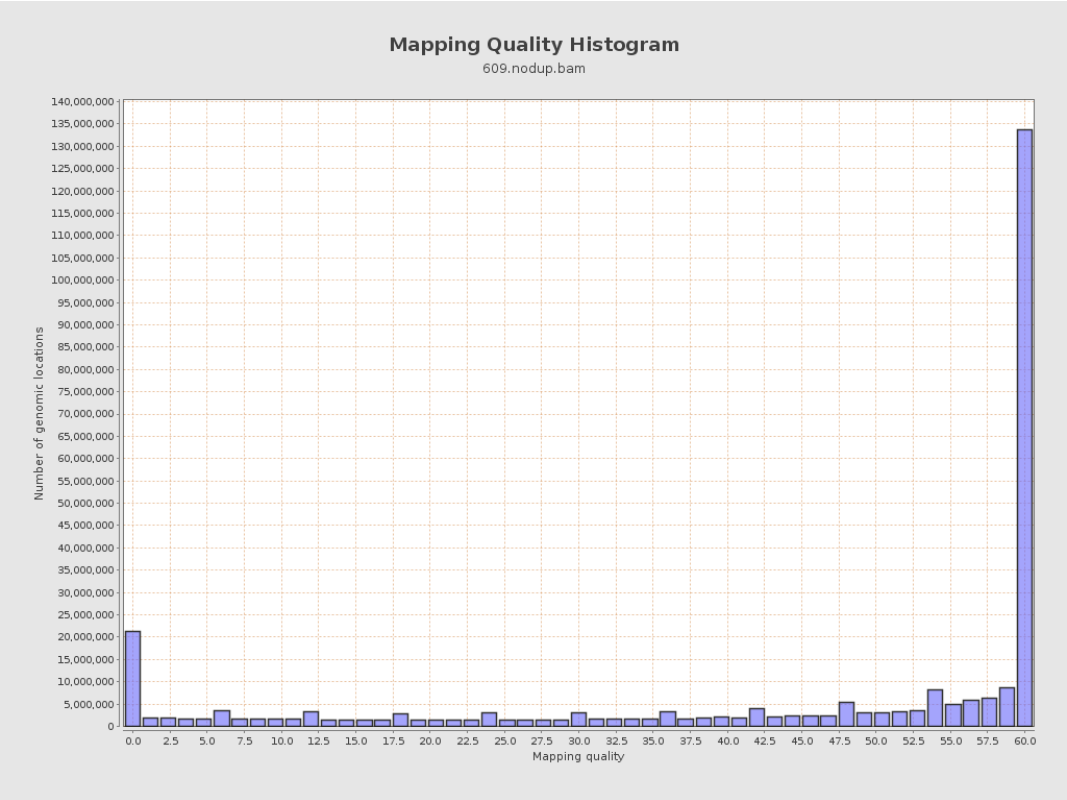
11. Results : Homopolymer Indels



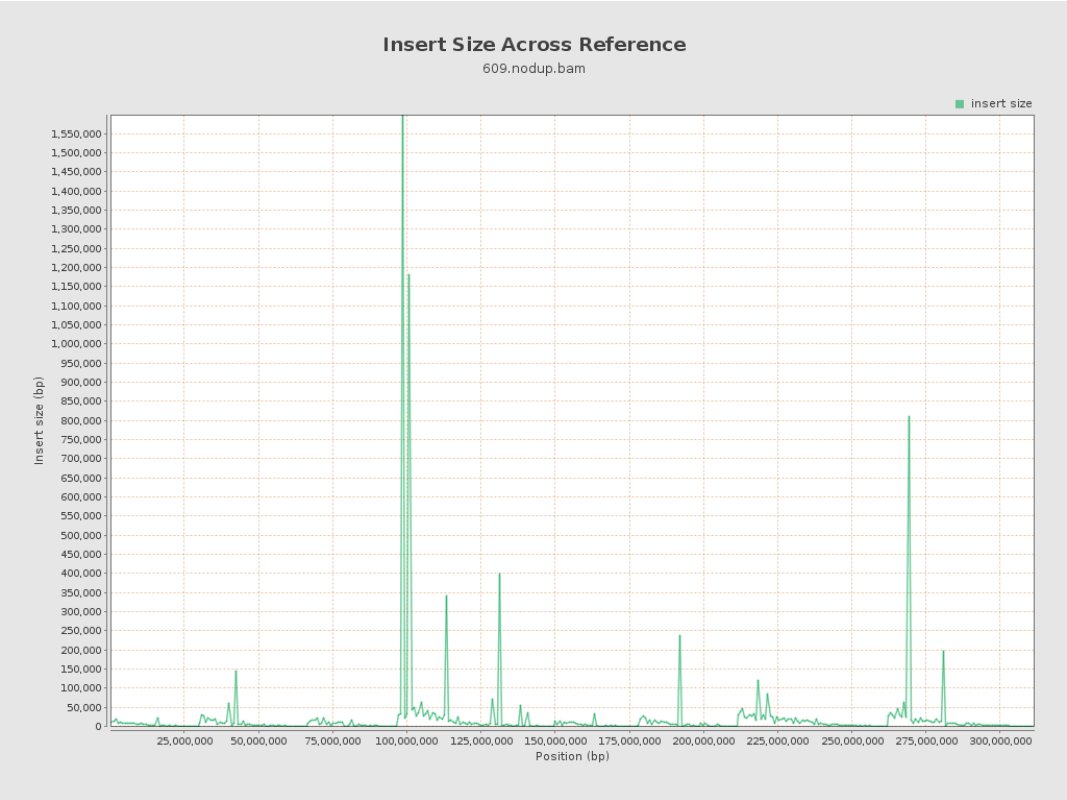
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram