Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:31:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/809.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/809.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_209/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_209_S290_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_209/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_209_S290_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:31:35 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	68,272,791
Mapped reads	64,219,800 / 94.06%
Unmapped reads	4,052,991 / 5.94%
Mapped paired reads	64,219,800 / 94.06%
Mapped reads, first in pair	32,186,349 / 47.14%
Mapped reads, second in pair	32,033,451 / 46.92%
Mapped reads, both in pair	62,836,047 / 92.04%
Mapped reads, singletons	1,383,753 / 2.03%
Read min/max/mean length	30 / 151 / 147.91
Duplicated reads (flagged)	9,927,117 / 14.54%
Clipped reads	15,137,549 / 22.17%

2.2. ACGT Content

Number/percentage of A's	2,721,959,904 / 30.76%
Number/percentage of C's	1,701,916,986 / 19.23%
Number/percentage of T's	2,725,577,142 / 30.8%
Number/percentage of G's	1,699,261,263 / 19.2%
Number/percentage of N's	33,481 / 0%
GC Percentage	38.44%

2.3. Coverage

Mean	28.4678
Standard Deviation	260.8314

2.4. Mapping Quality

Mean Mapping Quality	43.85

2.5. Insert size

Mean	240,768.76
Standard Deviation	2,321,766.66
P25/Median/P75	331 / 436 / 569

2.6. Mismatches and indels

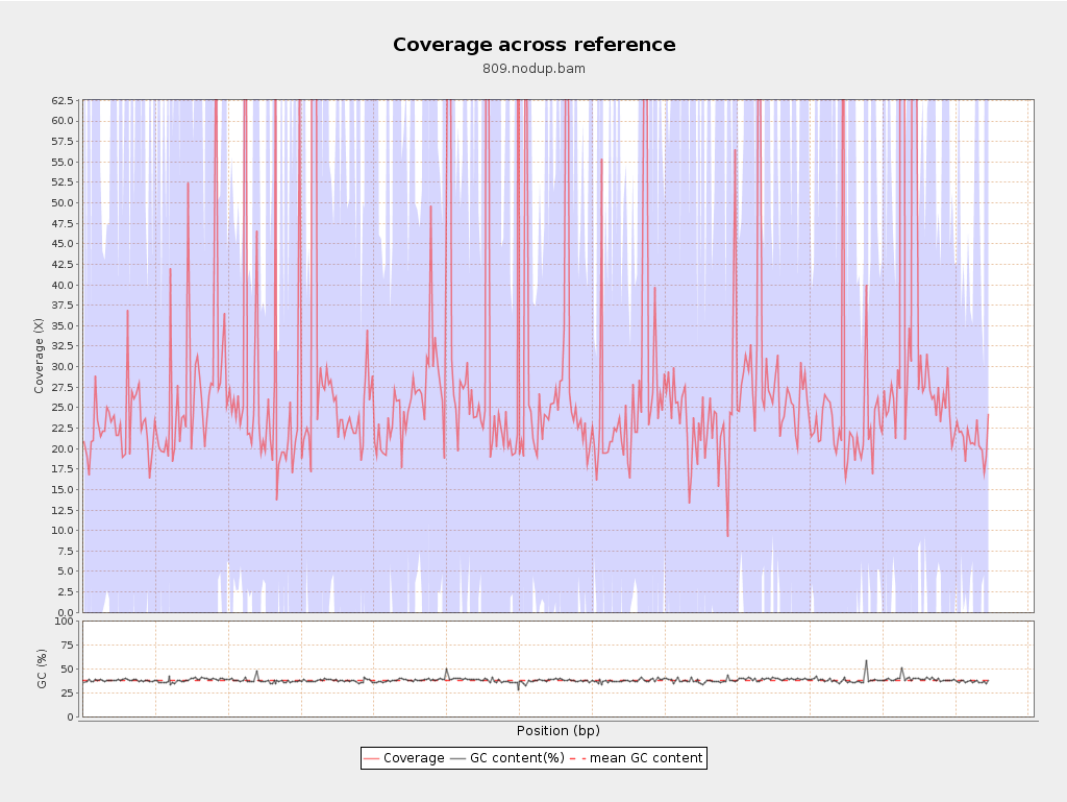
General error rate	2.35%
Mismatches	191,689,139
Insertions	6,077,034
Mapped reads with at least one insertion	8.5%
Deletions	6,156,378
Mapped reads with at least one deletion	8.49%
Homopolymer indels	55.9%

2.7. Chromosome stats

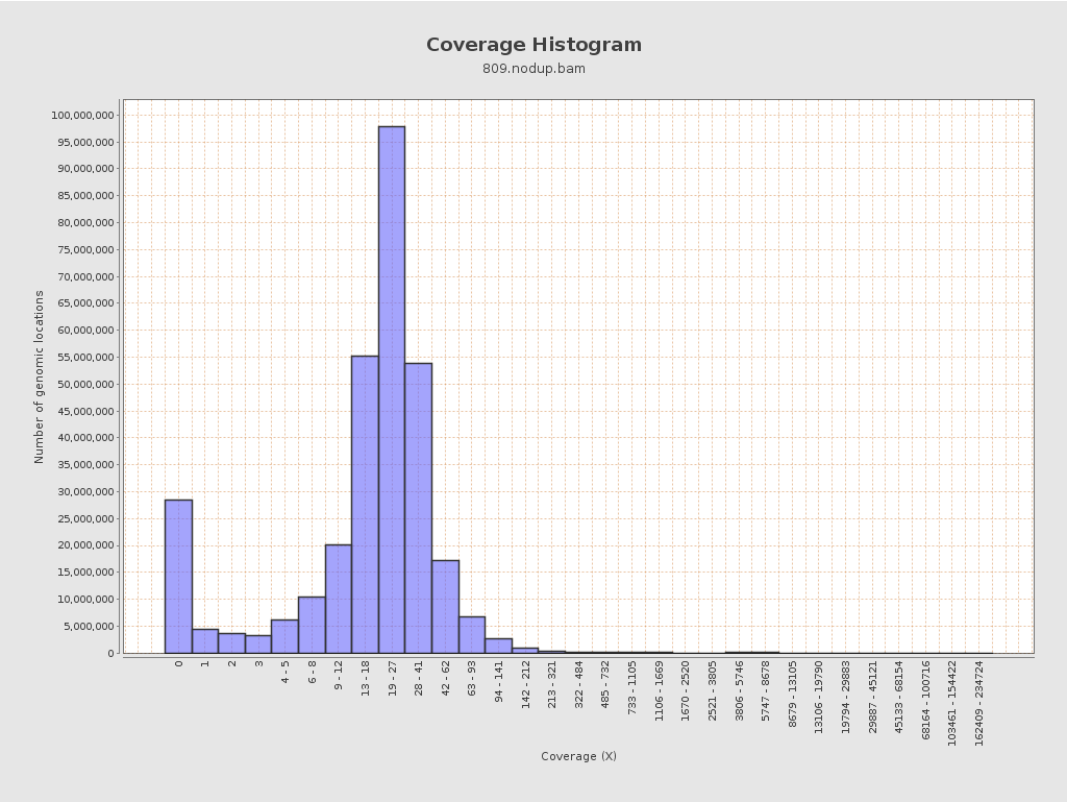
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	667292708	22.4494	88.708

LT669789.1	36598175	1055891671	28.8509	264.6105
LT669790.1	30422129	927575124	30.4901	248.6792
LT669791.1	52758100	1474307643	27.9447	236.8509
LT669792.1	28376109	788813719	27.7985	254.2104
LT669793.1	33388210	888738412	26.6183	174.4835
LT669794.1	50579949	1383985416	27.3623	234.6369
LT669795.1	49795044	1685169834	33.8421	398.9836

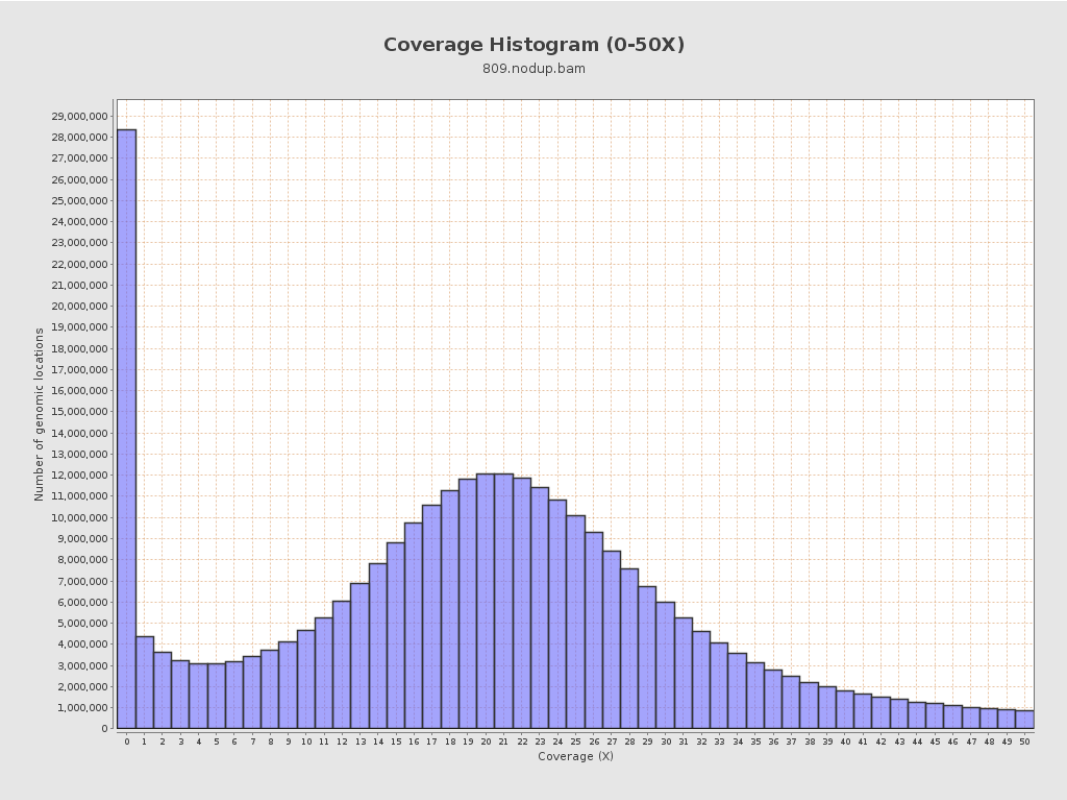
3. Results : Coverage across reference



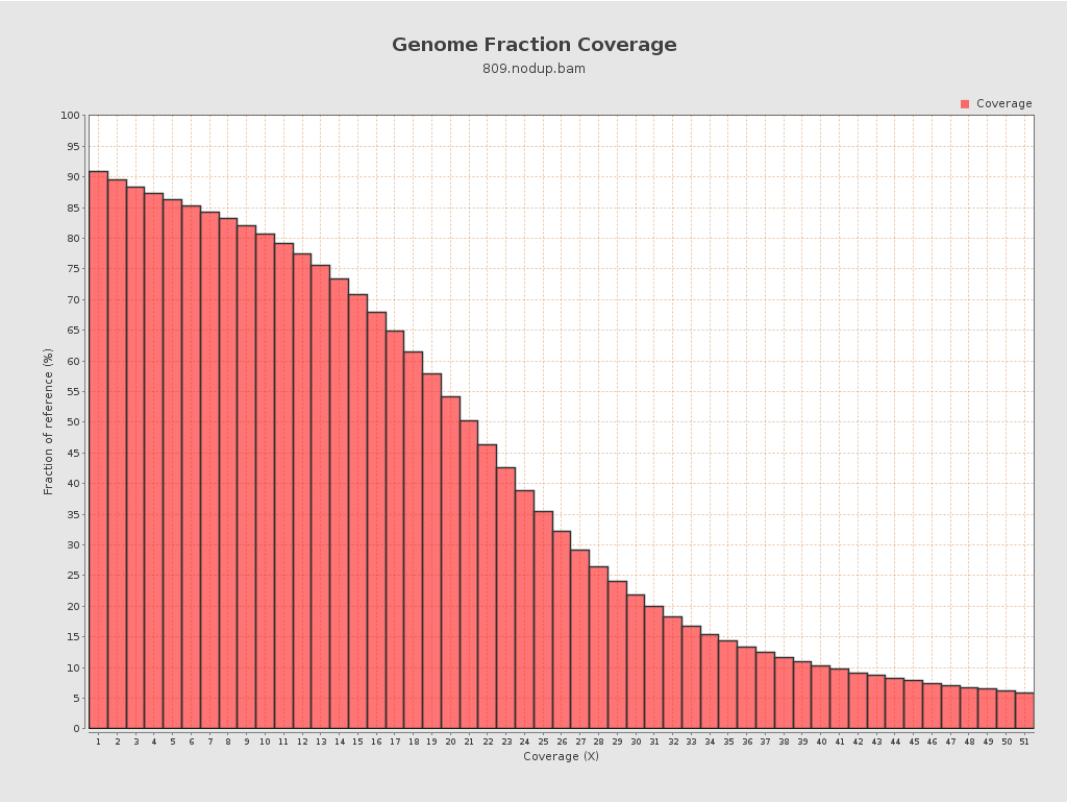
4. Results : Coverage Histogram



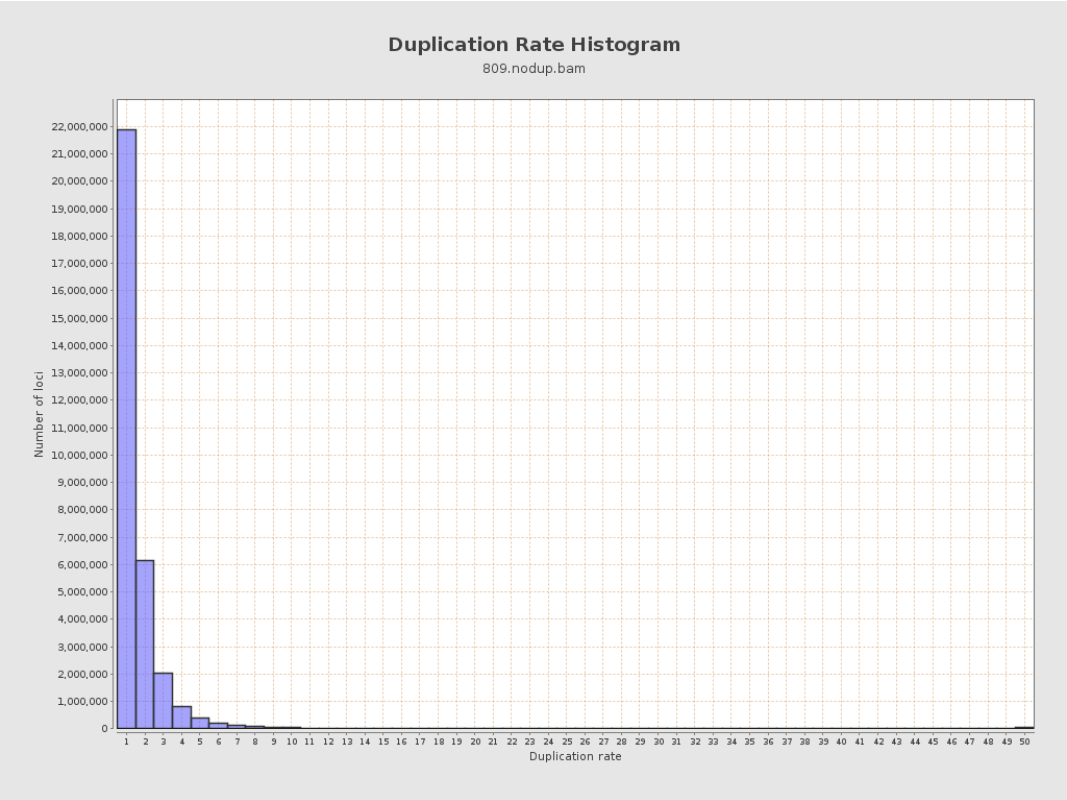
5. Results : Coverage Histogram (0-50X)



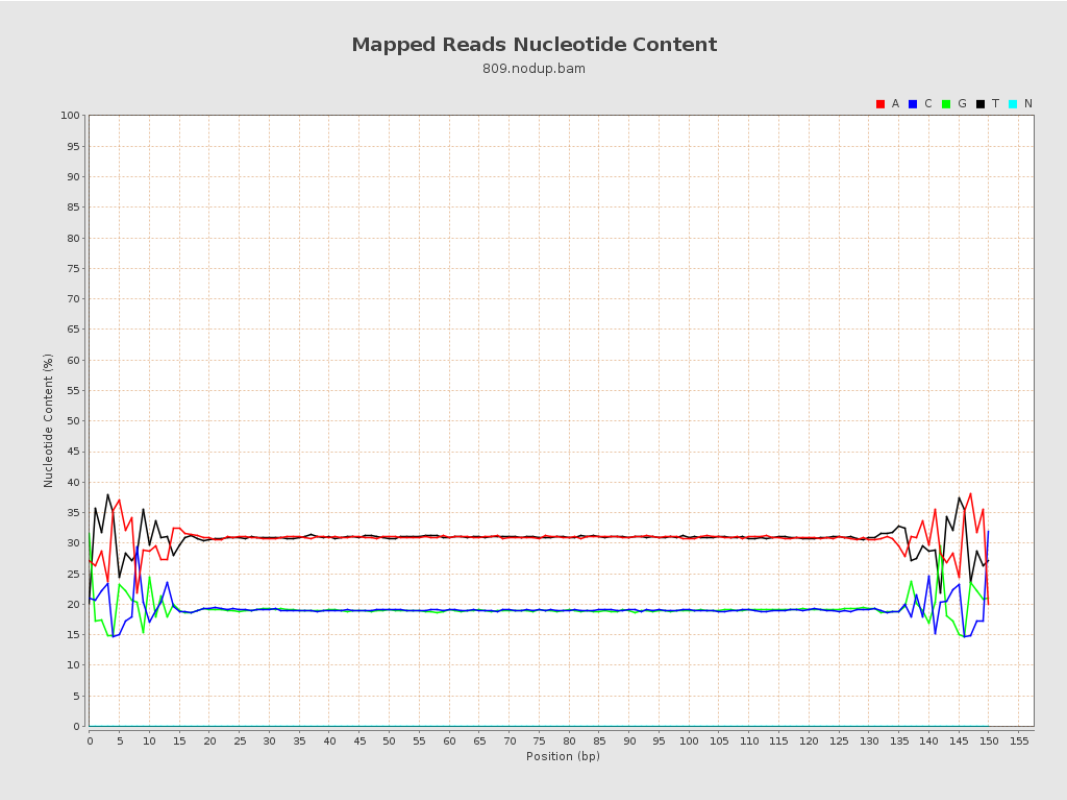
6. Results : Genome Fraction Coverage



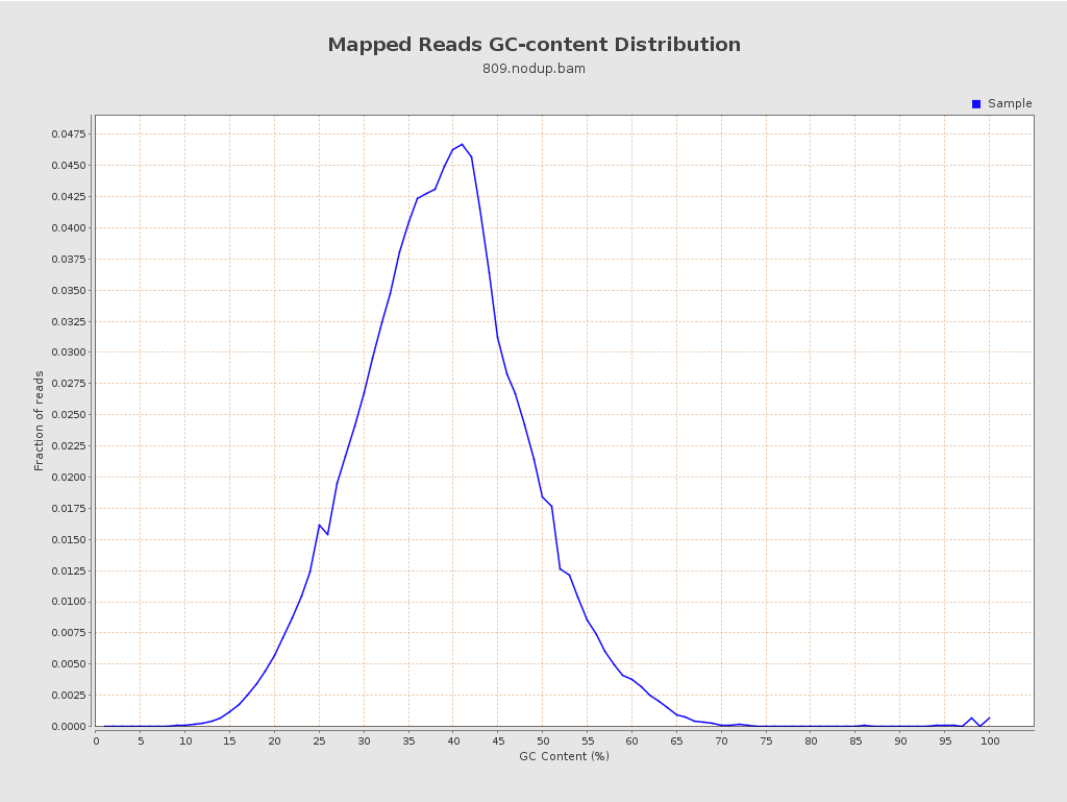
7. Results : Duplication Rate Histogram



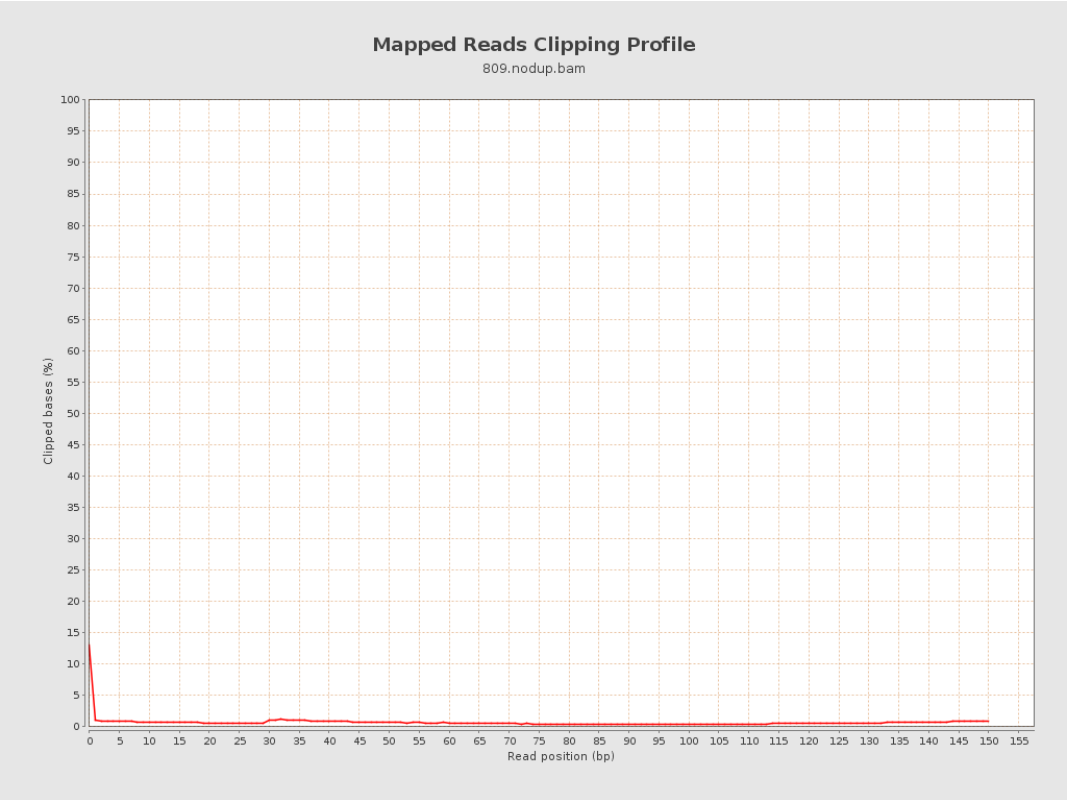
8. Results : Mapped Reads Nucleotide Content



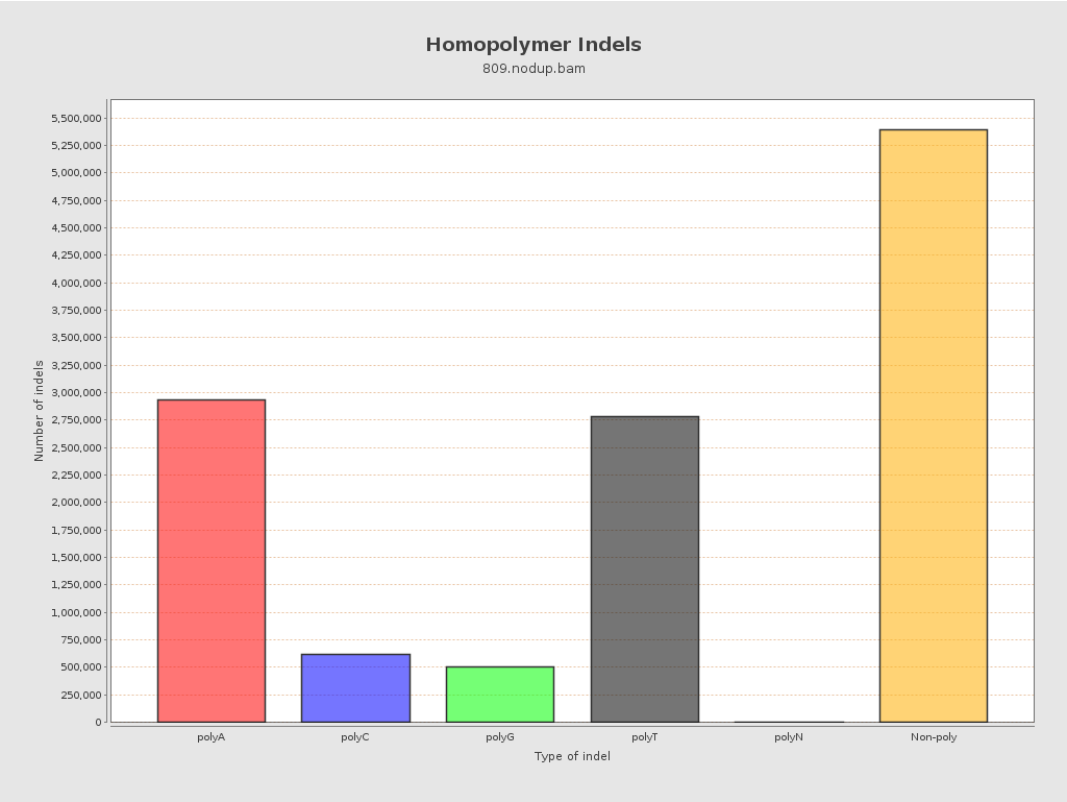
9. Results : Mapped Reads GC-content Distribution



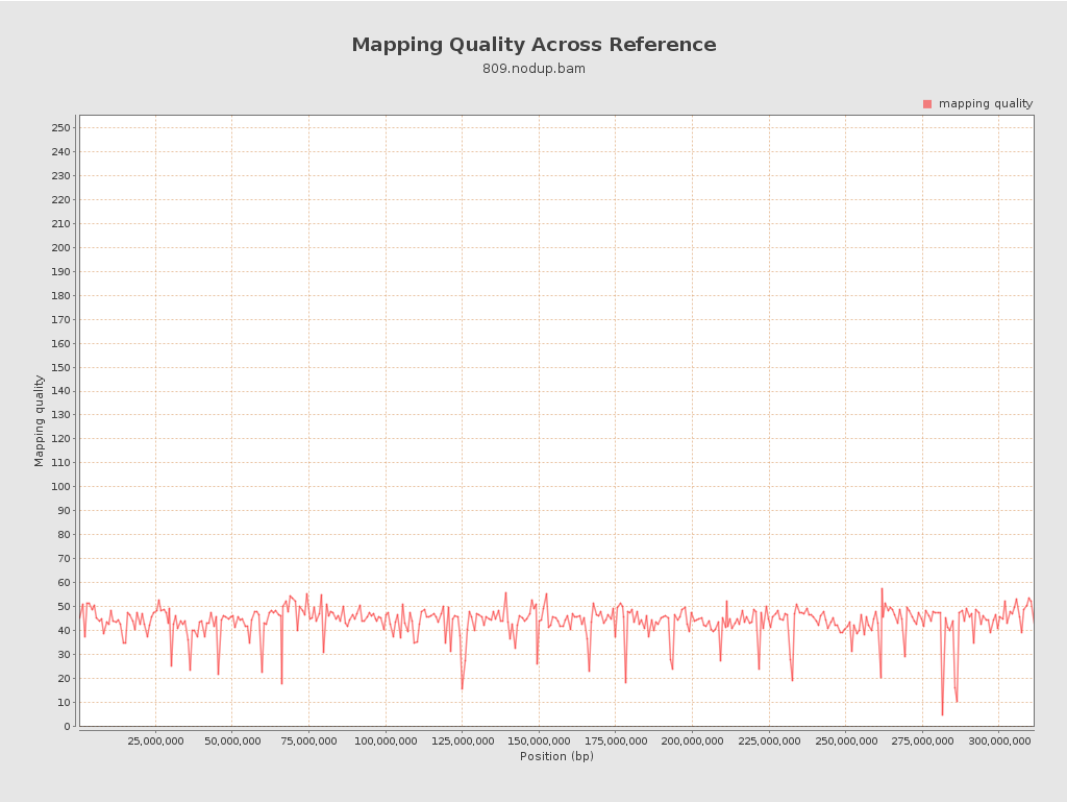
10. Results : Mapped Reads Clipping Profile



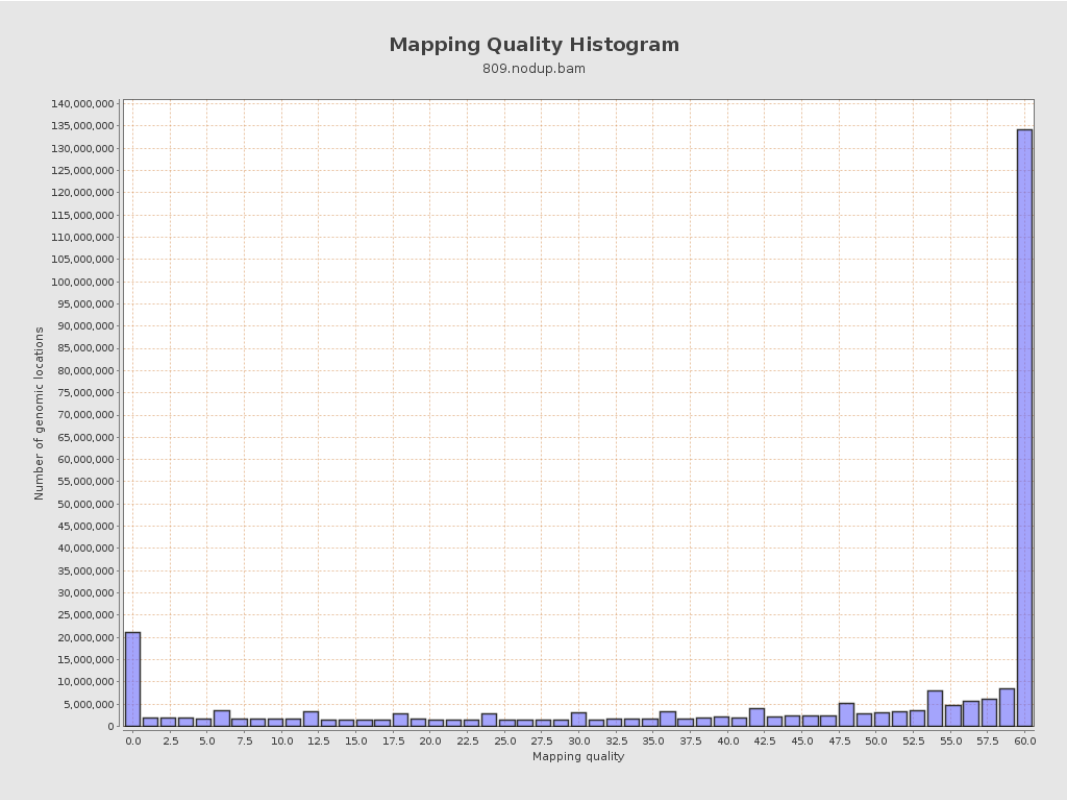
11. Results : Homopolymer Indels



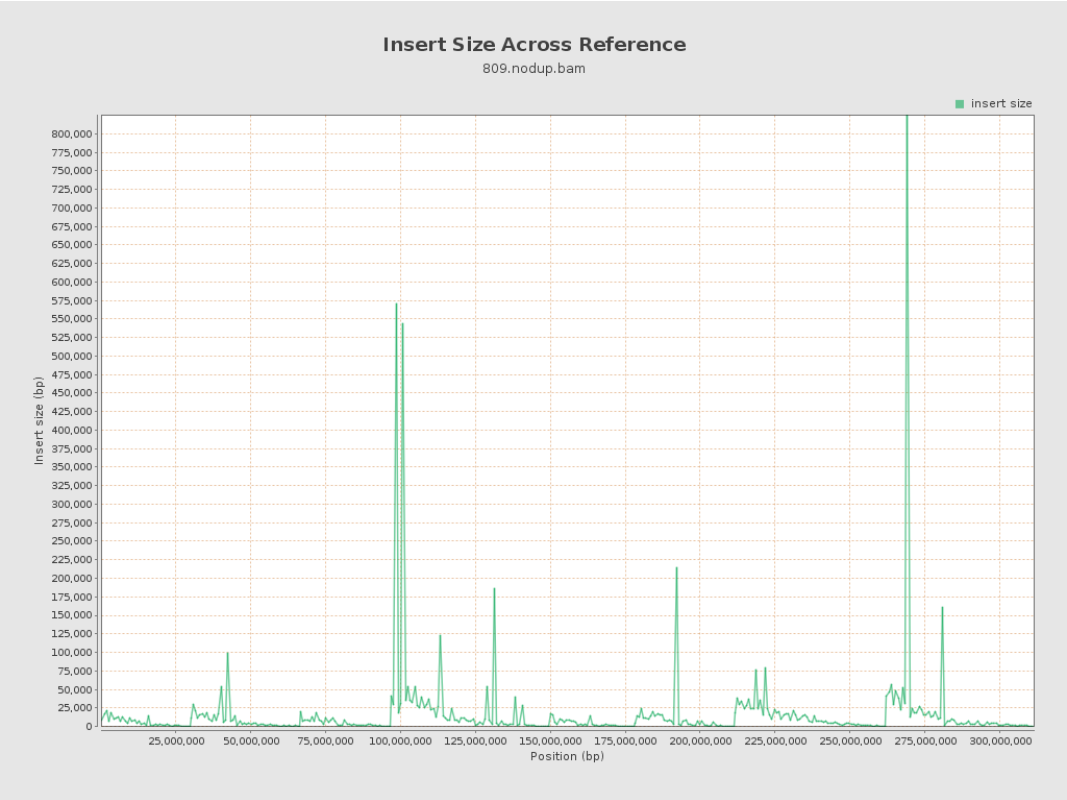
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram