Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:26:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/807.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/807.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_206/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_206_S287_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_206/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_206_S287_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:26:05 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	52,171,114
Mapped reads	49,460,432 / 94.8%
Unmapped reads	2,710,682 / 5.2%
Mapped paired reads	49,460,432 / 94.8%
Mapped reads, first in pair	24,759,668 / 47.46%
Mapped reads, second in pair	24,700,764 / 47.35%
Mapped reads, both in pair	48,548,408 / 93.06%
Mapped reads, singletons	912,024 / 1.75%
Read min/max/mean length	30 / 151 / 147.93
Duplicated reads (flagged)	6,673,422 / 12.79%
Clipped reads	11,514,180 / 22.07%

2.2. ACGT Content

Number/percentage of A's	2,102,356,829 / 30.74%
Number/percentage of C's	1,316,403,703 / 19.25%
Number/percentage of T's	2,106,941,188 / 30.81%
Number/percentage of G's	1,313,323,067 / 19.2%
Number/percentage of N's	25,257 / 0%
GC Percentage	38.45%

2.3. Coverage

Mean	22.0038
Standard Deviation	190.8271

2.4. Mapping Quality

Mean Mapping Quality	43.55

2.5. Insert size

Mean	234,733.21
Standard Deviation	2,287,500.56
P25/Median/P75	321 / 423 / 548

2.6. Mismatches and indels

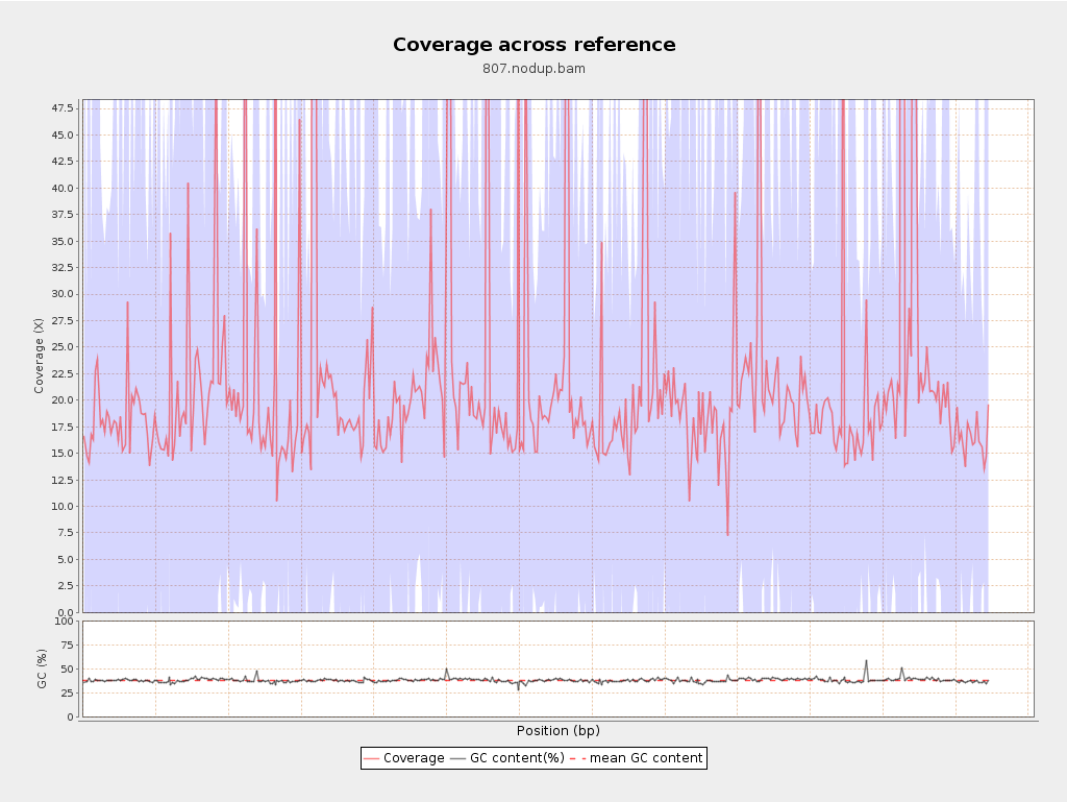
General error rate	2.39%
Mismatches	150,745,537
Insertions	4,704,751
Mapped reads with at least one insertion	8.55%
Deletions	4,826,268
Mapped reads with at least one deletion	8.63%
Homopolymer indels	55.54%

2.7. Chromosome stats

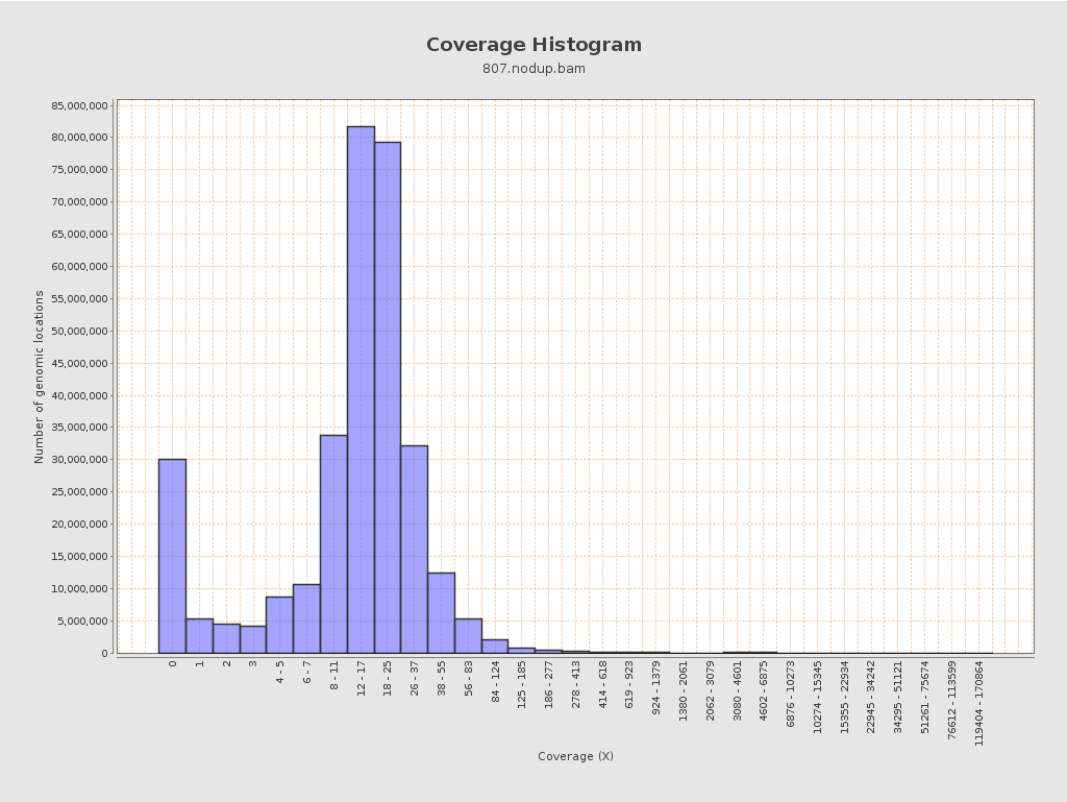
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	528560649	17.7821	65.2664

LT669789.1	36598175	826837787	22.5923	203.7899
LT669790.1	30422129	704872010	23.1697	173.606
LT669791.1	52758100	1146559620	21.7324	179.1712
LT669792.1	28376109	613771420	21.6299	224.6393
LT669793.1	33388210	686523493	20.5619	127.3785
LT669794.1	50579949	1075107607	21.2556	176.1374
LT669795.1	49795044	1275079478	25.6066	266.8978

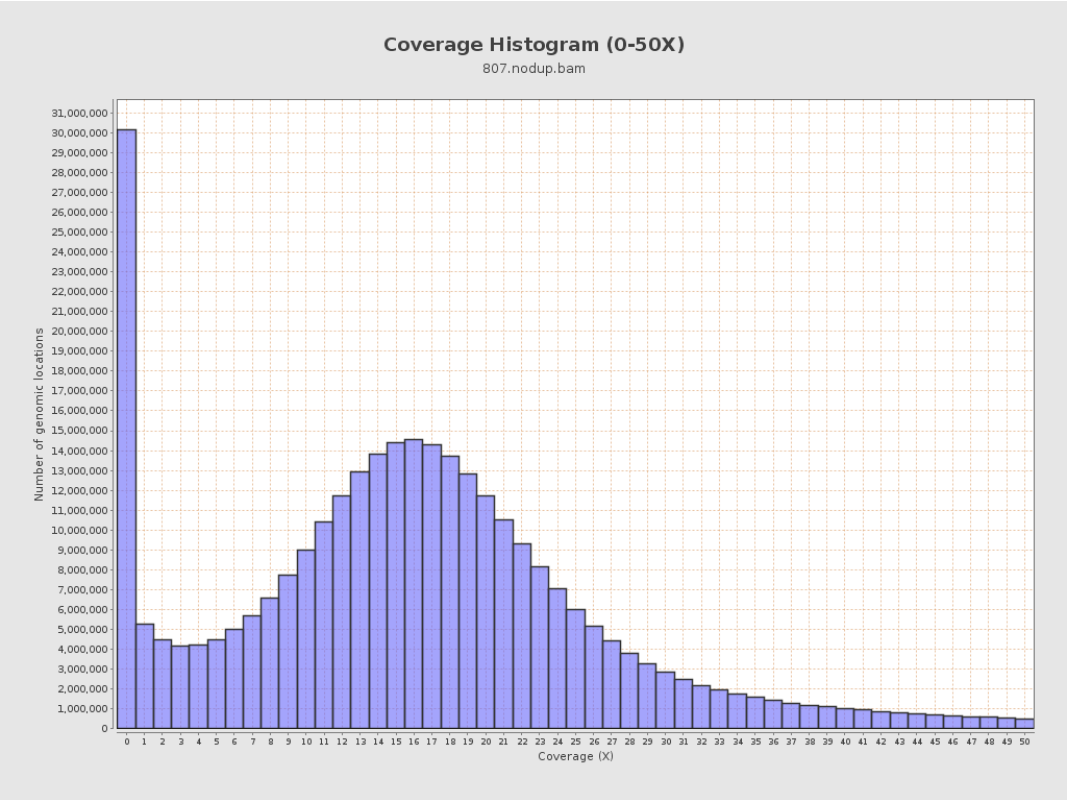
3. Results : Coverage across reference



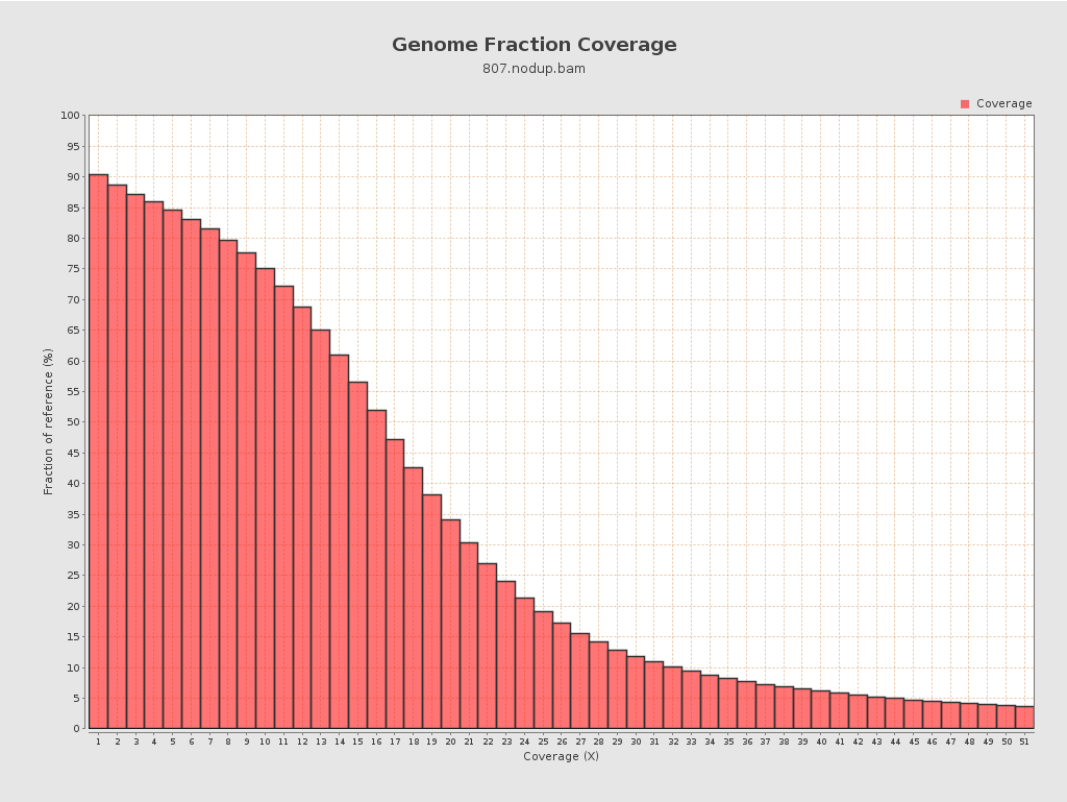
4. Results : Coverage Histogram



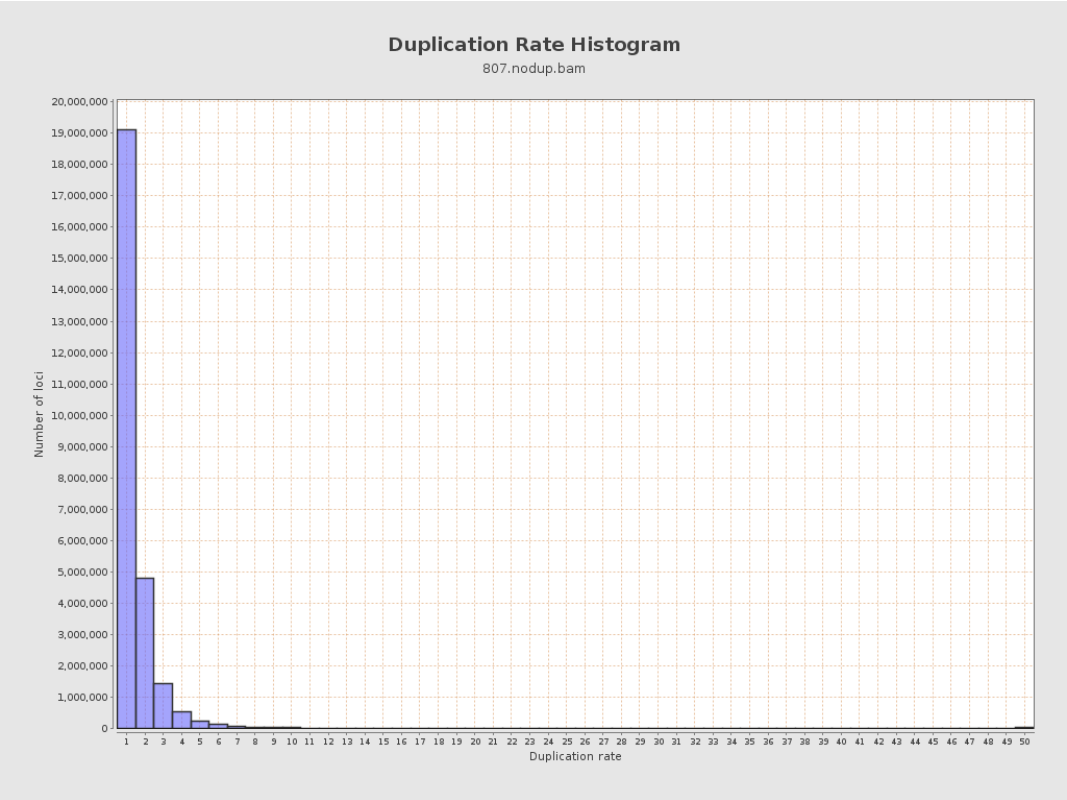
5. Results : Coverage Histogram (0-50X)



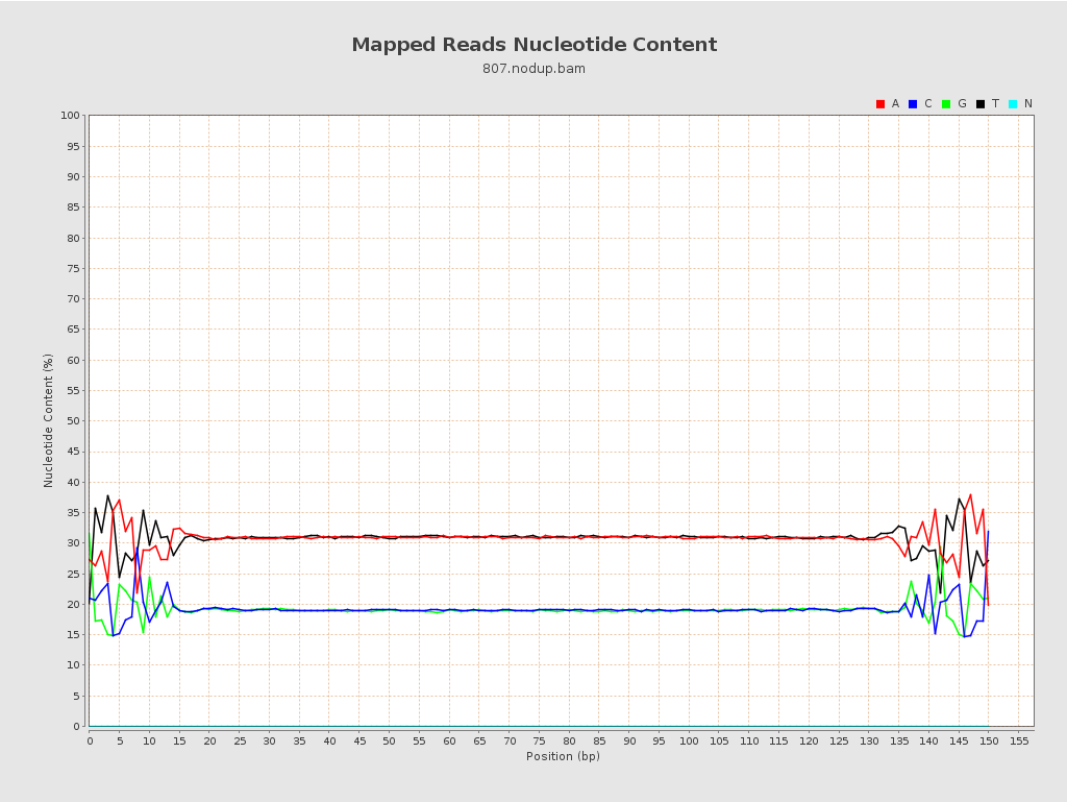
6. Results : Genome Fraction Coverage



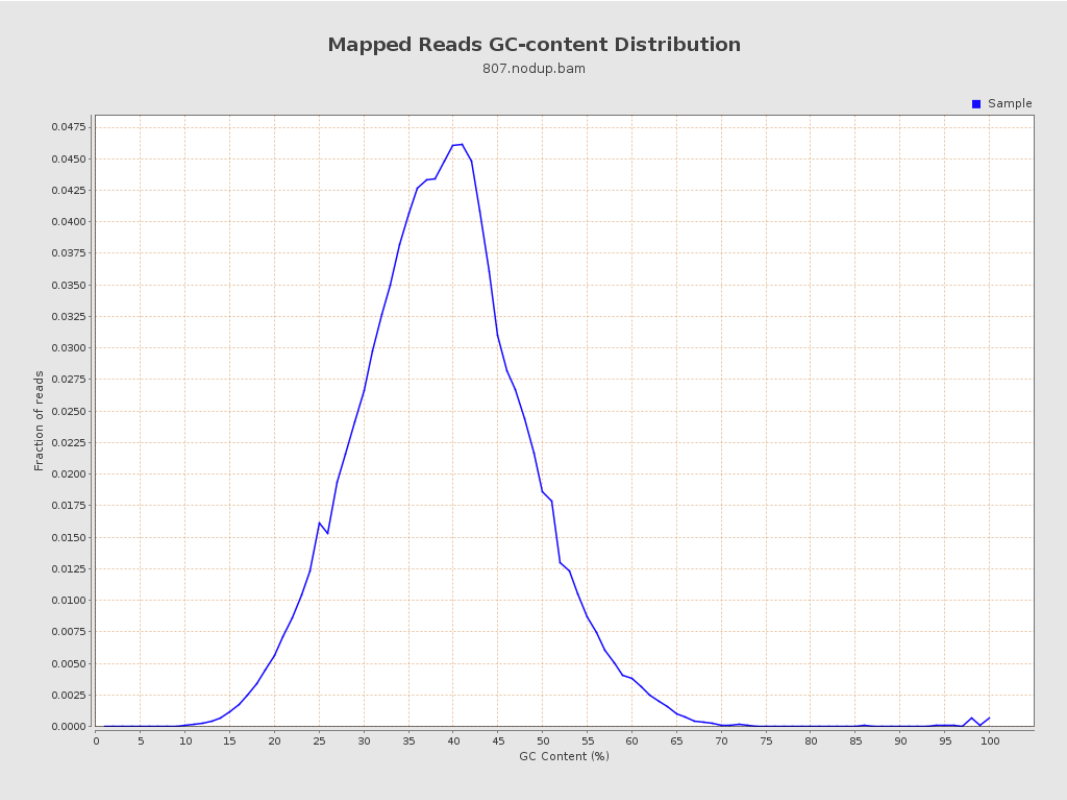
7. Results : Duplication Rate Histogram



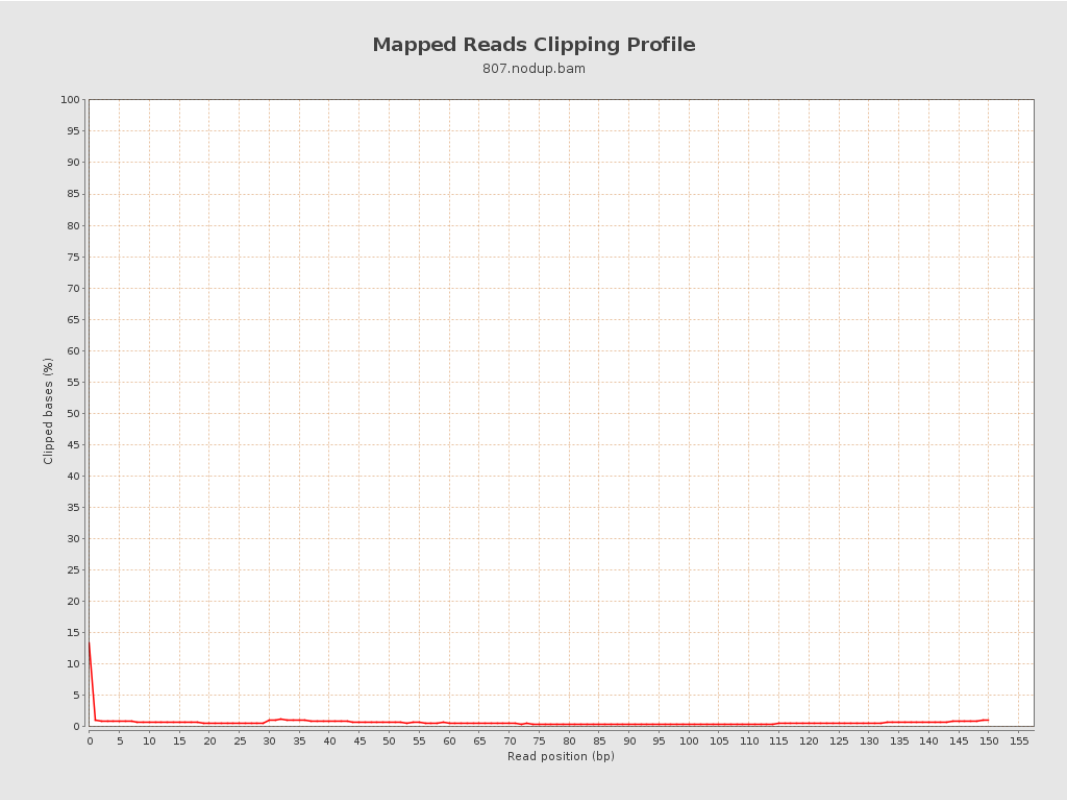
8. Results : Mapped Reads Nucleotide Content



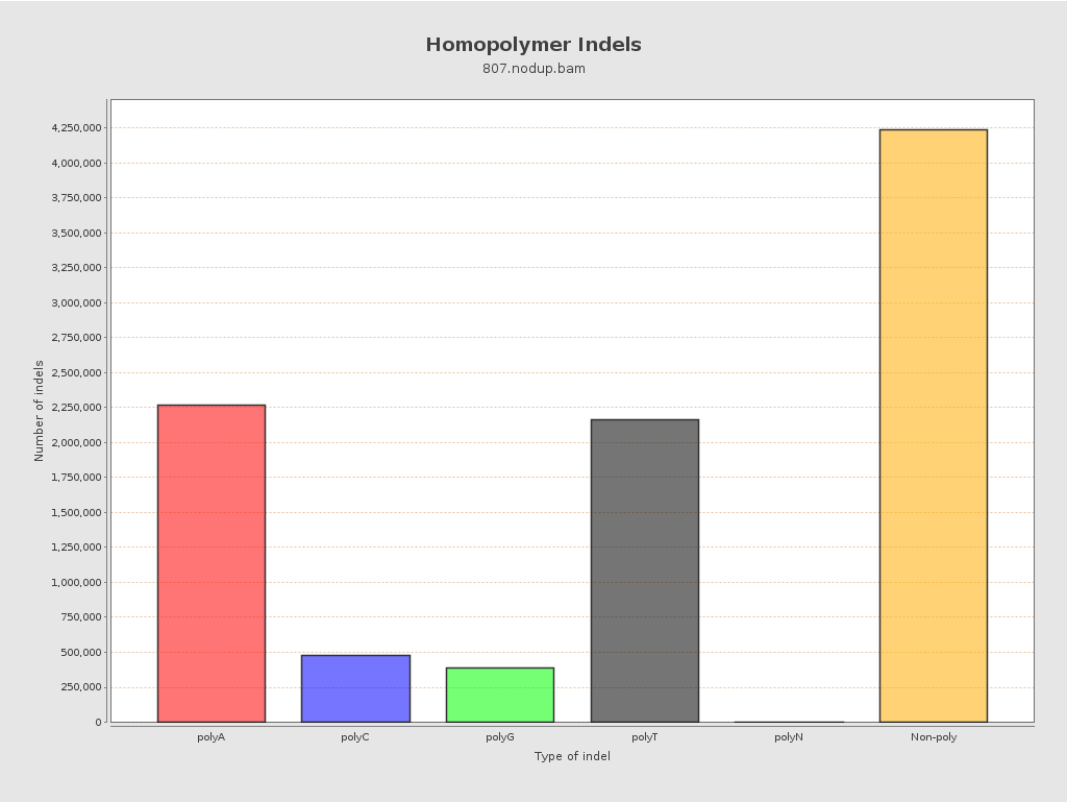
9. Results : Mapped Reads GC-content Distribution



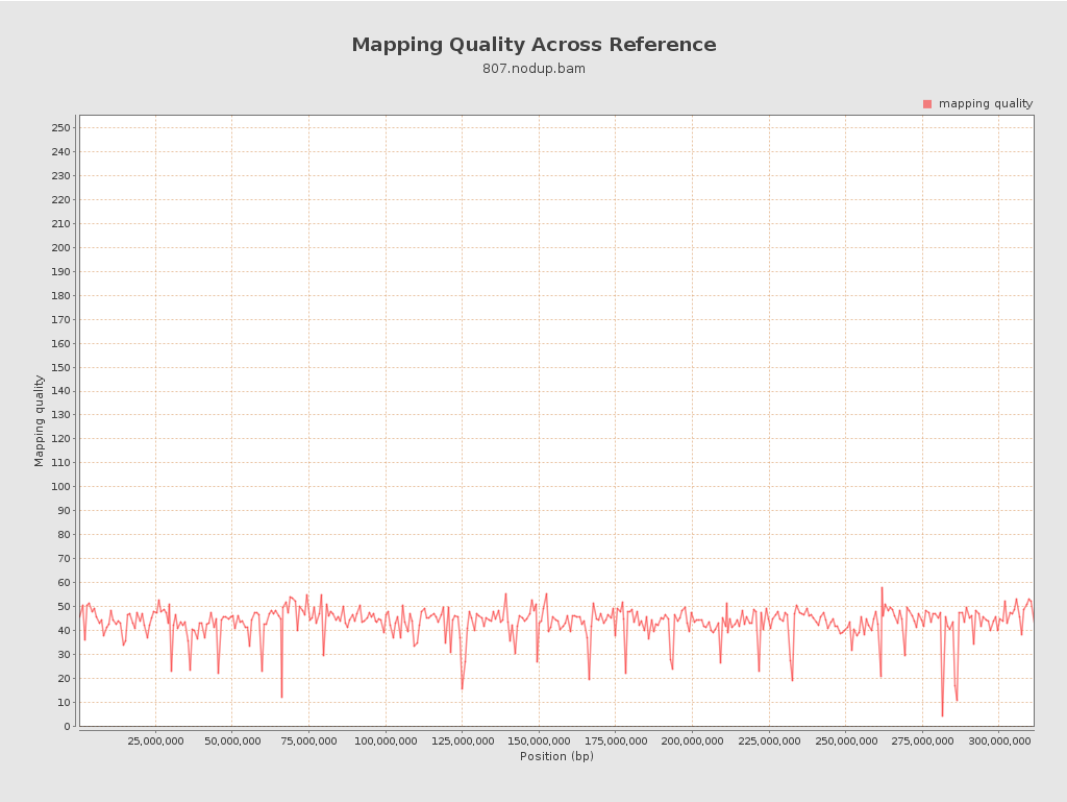
10. Results : Mapped Reads Clipping Profile



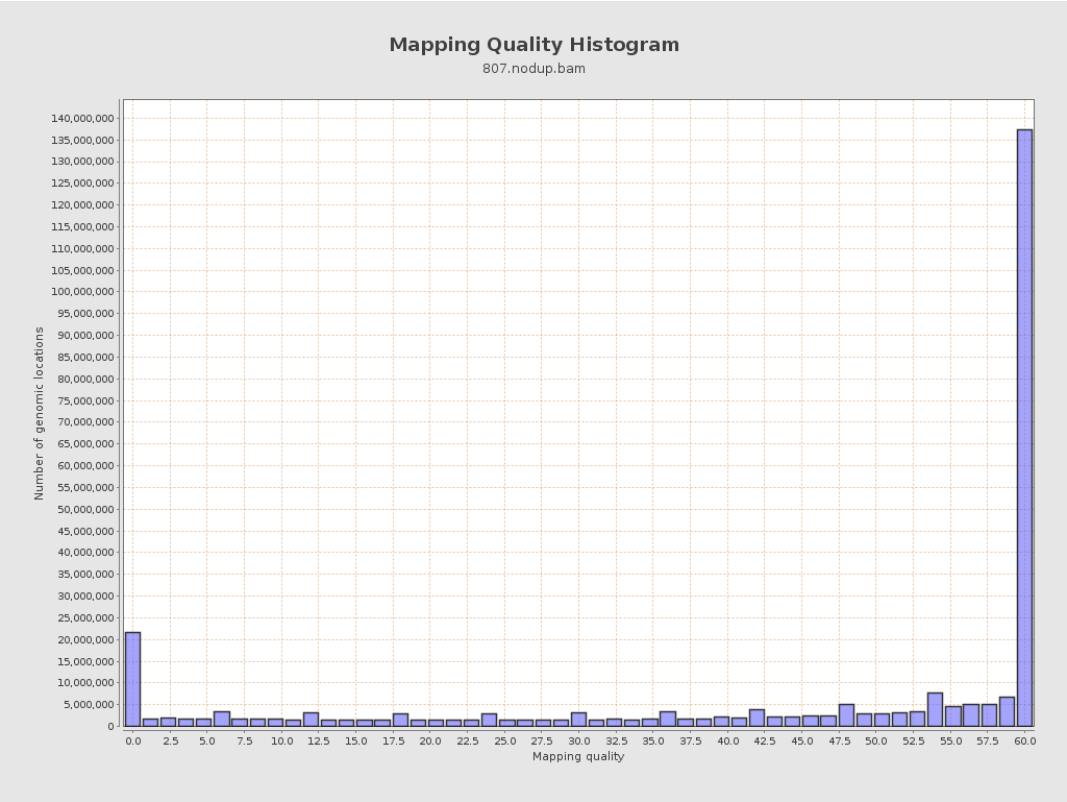
11. Results : Homopolymer Indels



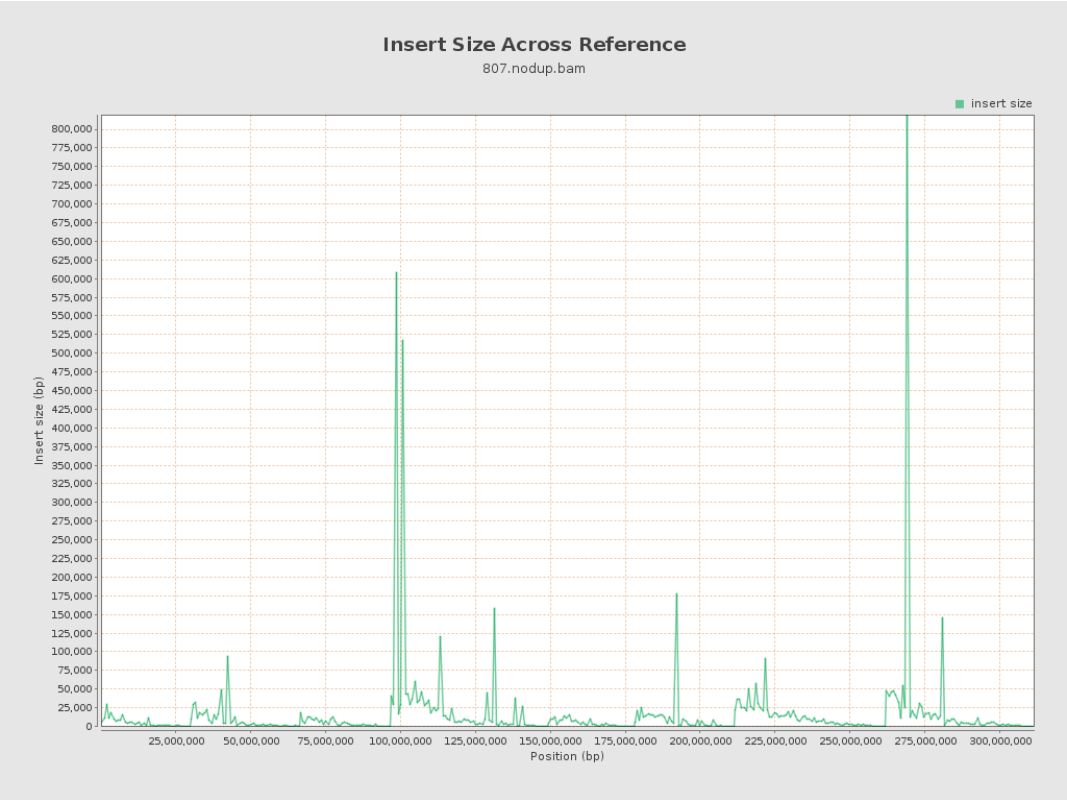
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram