Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:36:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/810.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/810.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_244/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_244_S325_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_244/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_244_S325_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:36:18 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	75,826,549
Mapped reads	71,546,990 / 94.36%
Unmapped reads	4,279,559 / 5.64%
Mapped paired reads	71,546,990 / 94.36%
Mapped reads, first in pair	35,848,330 / 47.28%
Mapped reads, second in pair	35,698,660 / 47.08%
Mapped reads, both in pair	70,148,831 / 92.51%
Mapped reads, singletons	1,398,159 / 1.84%
Read min/max/mean length	30 / 151 / 148.11
Duplicated reads (flagged)	10,236,965 / 13.5%
Clipped reads	16,136,201 / 21.28%

2.2. ACGT Content

Number/percentage of A's	3,055,028,192 / 30.79%
Number/percentage of C's	1,905,925,163 / 19.21%
Number/percentage of T's	3,059,789,462 / 30.84%
Number/percentage of G's	1,899,917,443 / 19.15%
Number/percentage of N's	38,563 / 0%
GC Percentage	38.36%

2.3. Coverage

Mean	31.9147
Standard Deviation	266.6172

2.4. Mapping Quality

Mean Mapping Quality	44.02

2.5. Insert size

Mean	223,095.64
Standard Deviation	2,229,265.13
P25/Median/P75	320 / 421 / 553

2.6. Mismatches and indels

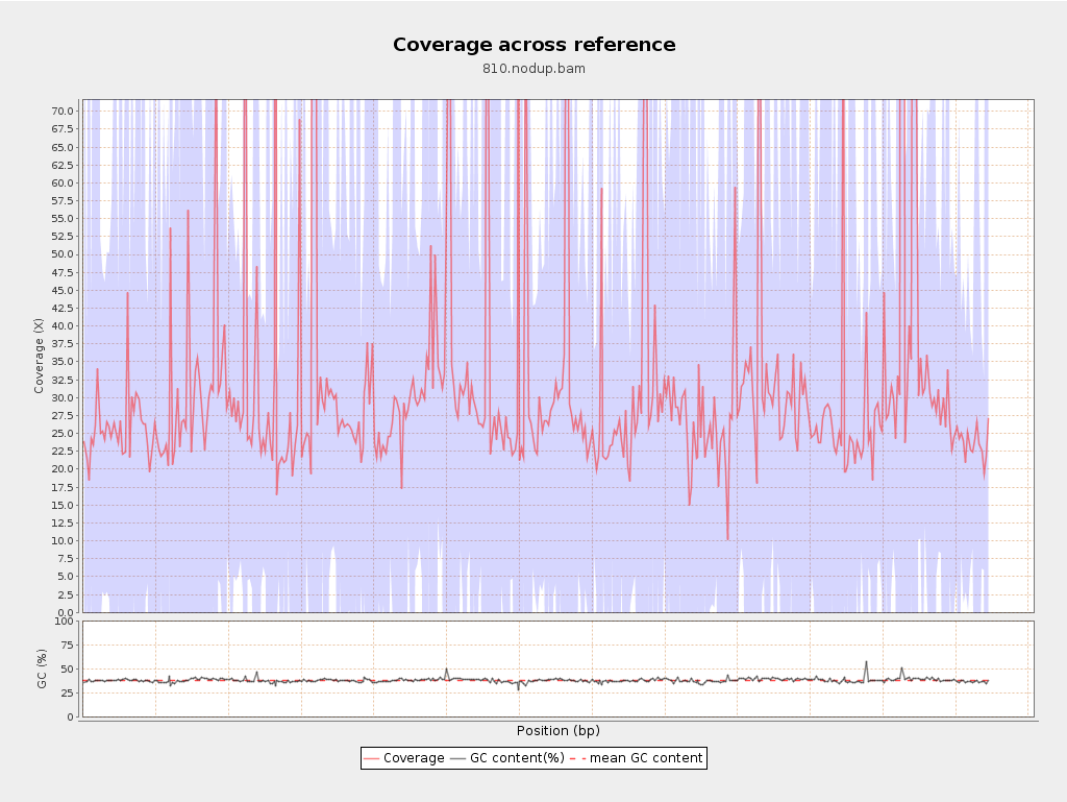
General error rate	2.32%
Mismatches	212,308,754
Insertions	6,622,817
Mapped reads with at least one insertion	8.33%
Deletions	6,743,732
Mapped reads with at least one deletion	8.37%
Homopolymer indels	56.24%

2.7. Chromosome stats

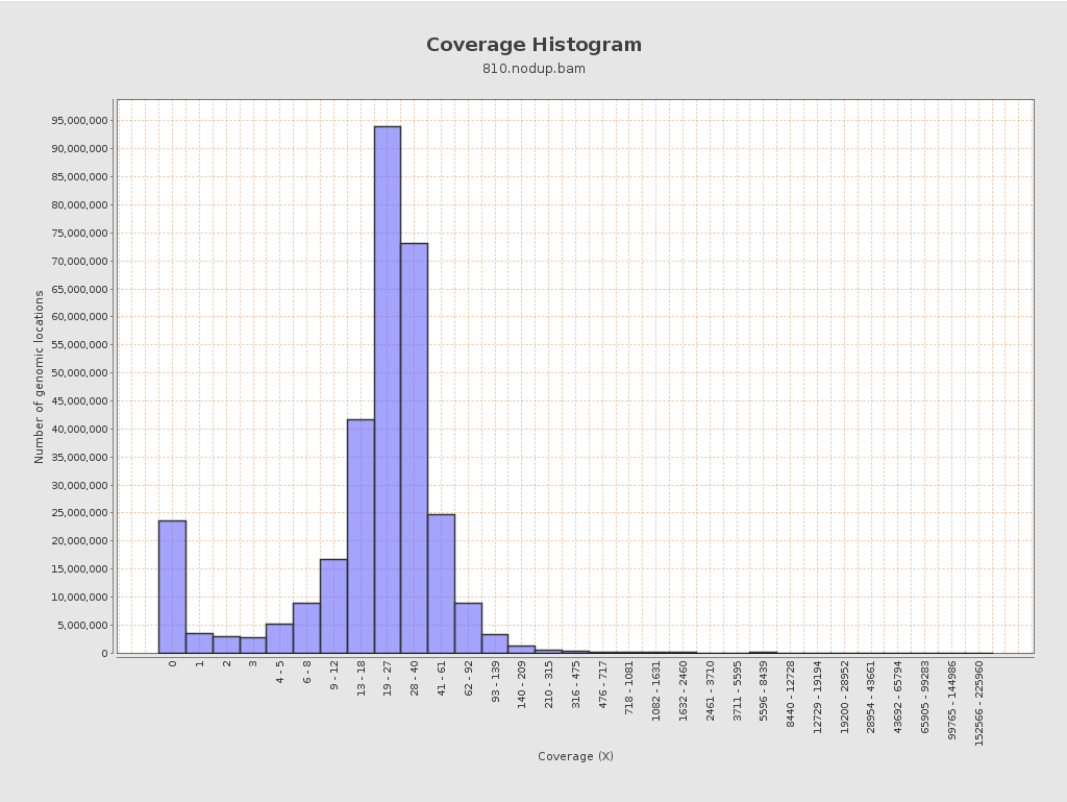
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	753566802	25.3518	75.6749

LT669789.1	36598175	1204139288	32.9016	292.4944
LT669790.1	30422129	1021404707	33.5744	263.1339
LT669791.1	52758100	1673043222	31.7116	225.3322
LT669792.1	28376109	884197119	31.1599	307.5311
LT669793.1	33388210	996872487	29.857	189.7263
LT669794.1	50579949	1538043995	30.4082	234.3277
LT669795.1	49795044	1874697783	37.6483	385.508

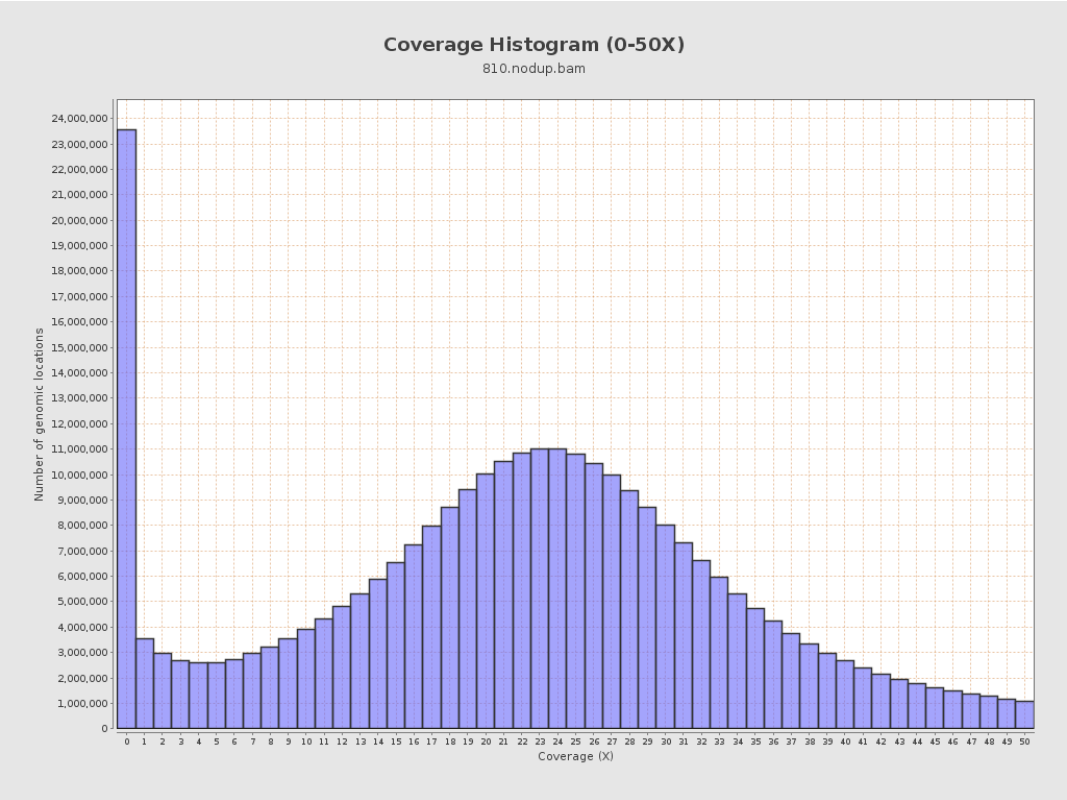
3. Results : Coverage across reference



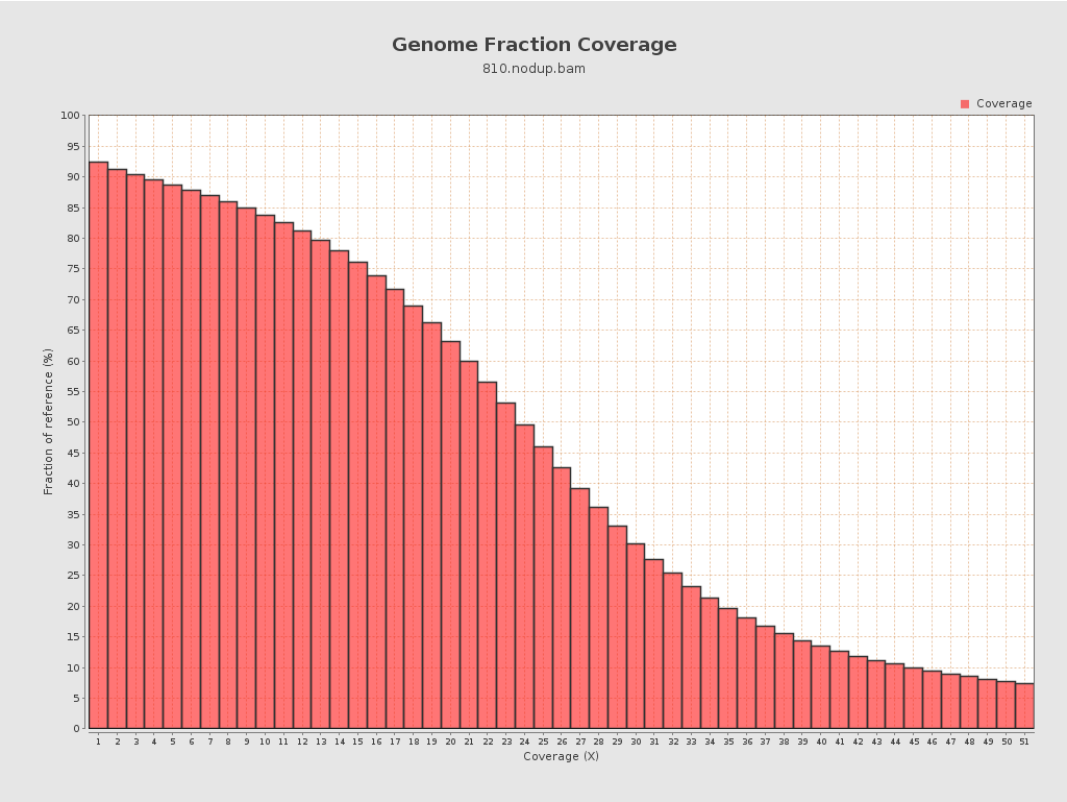
4. Results : Coverage Histogram



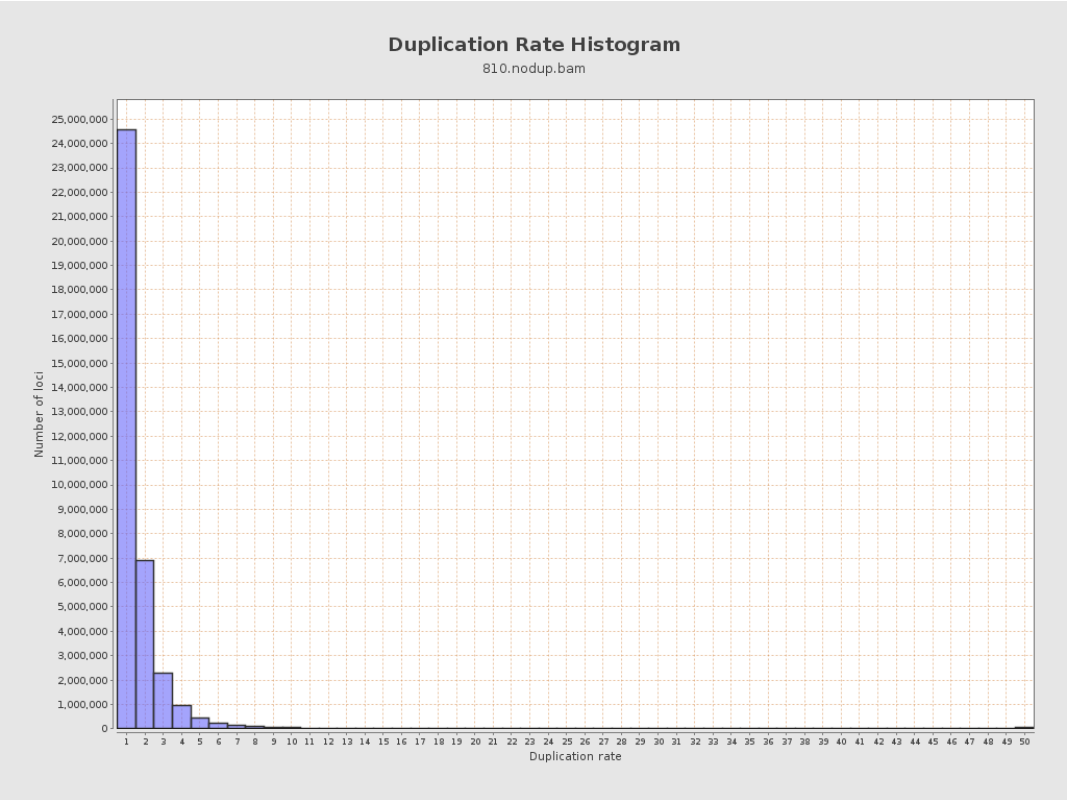
5. Results : Coverage Histogram (0-50X)



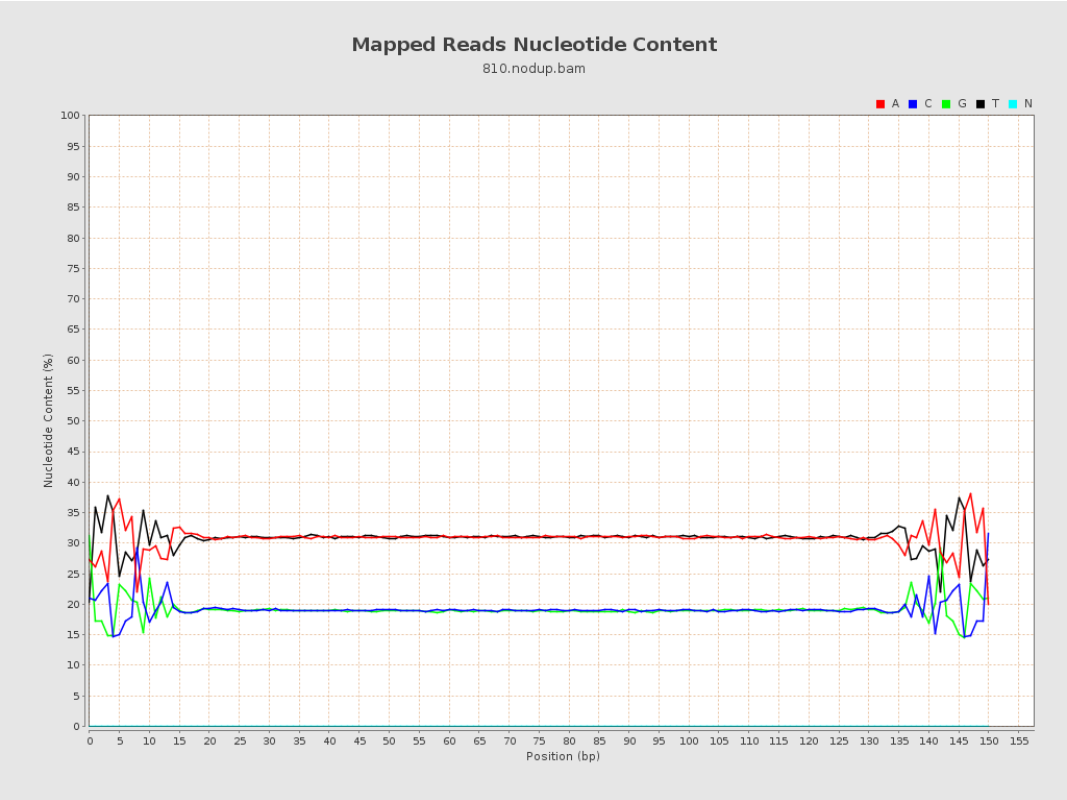
6. Results : Genome Fraction Coverage



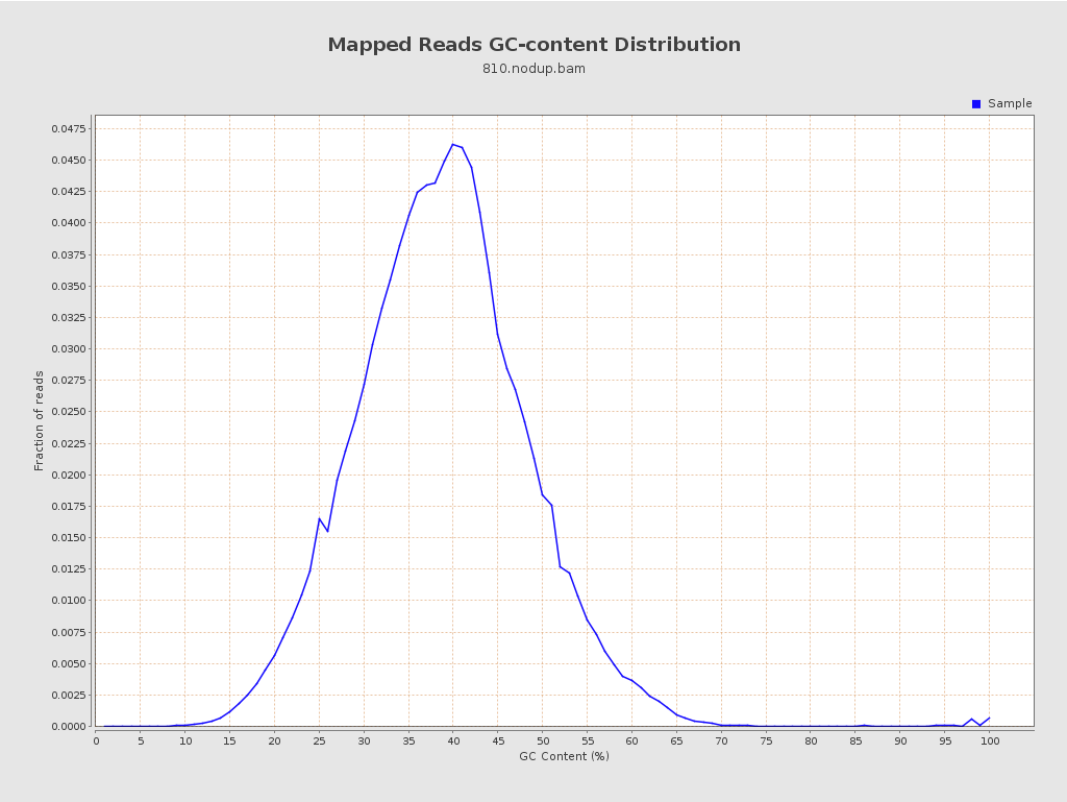
7. Results : Duplication Rate Histogram



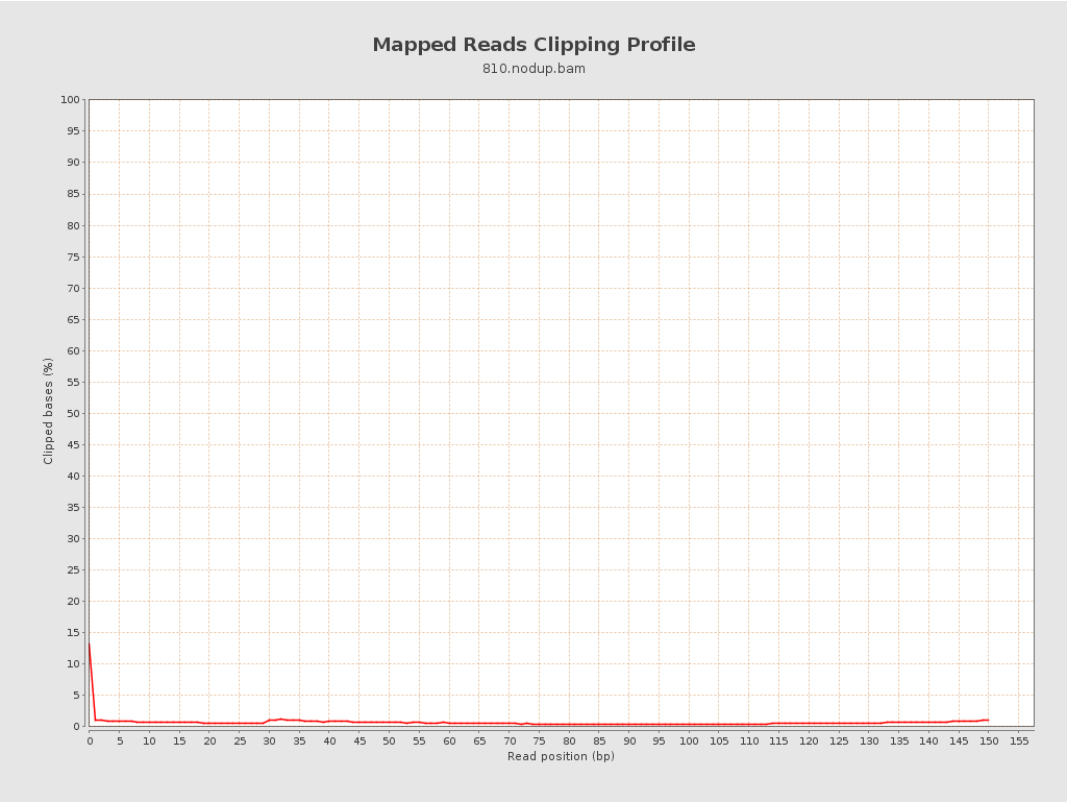
8. Results : Mapped Reads Nucleotide Content



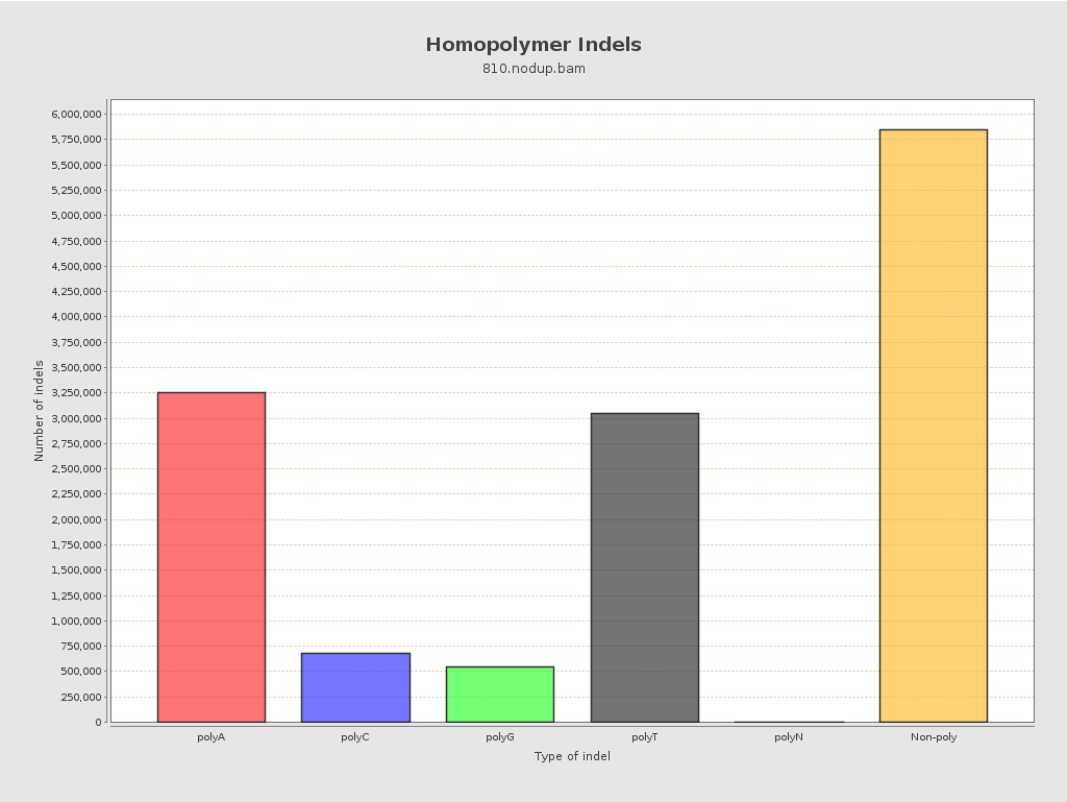
9. Results : Mapped Reads GC-content Distribution



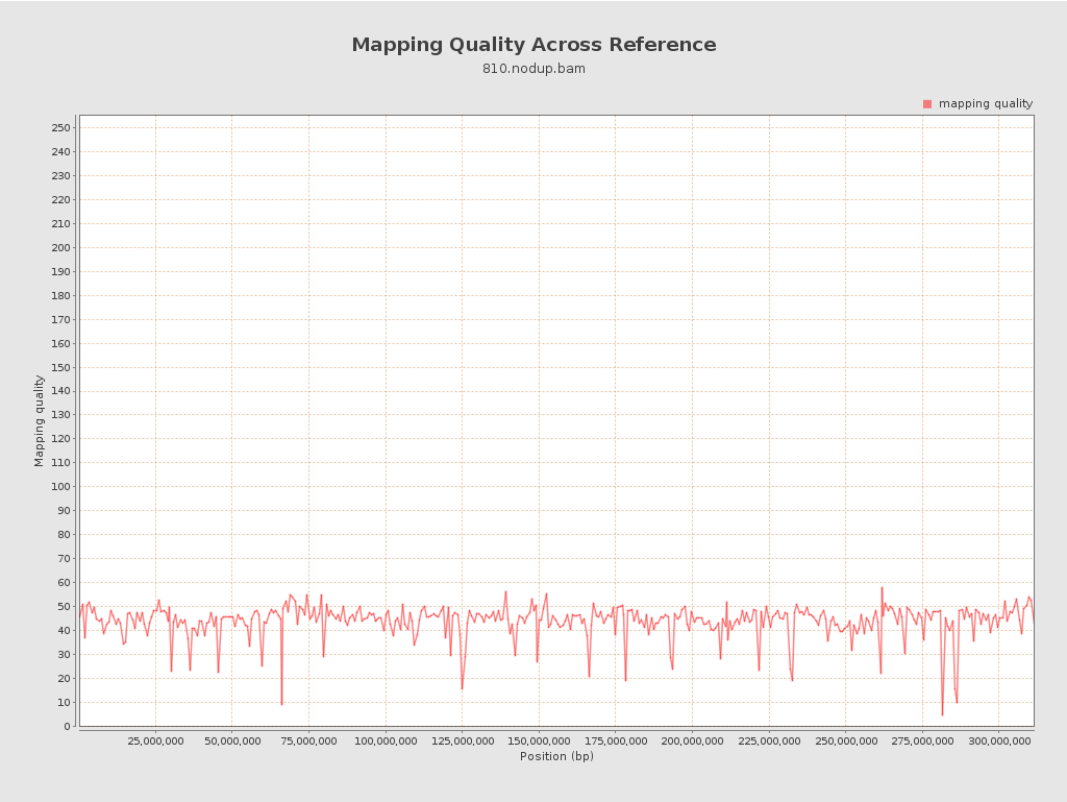
10. Results : Mapped Reads Clipping Profile



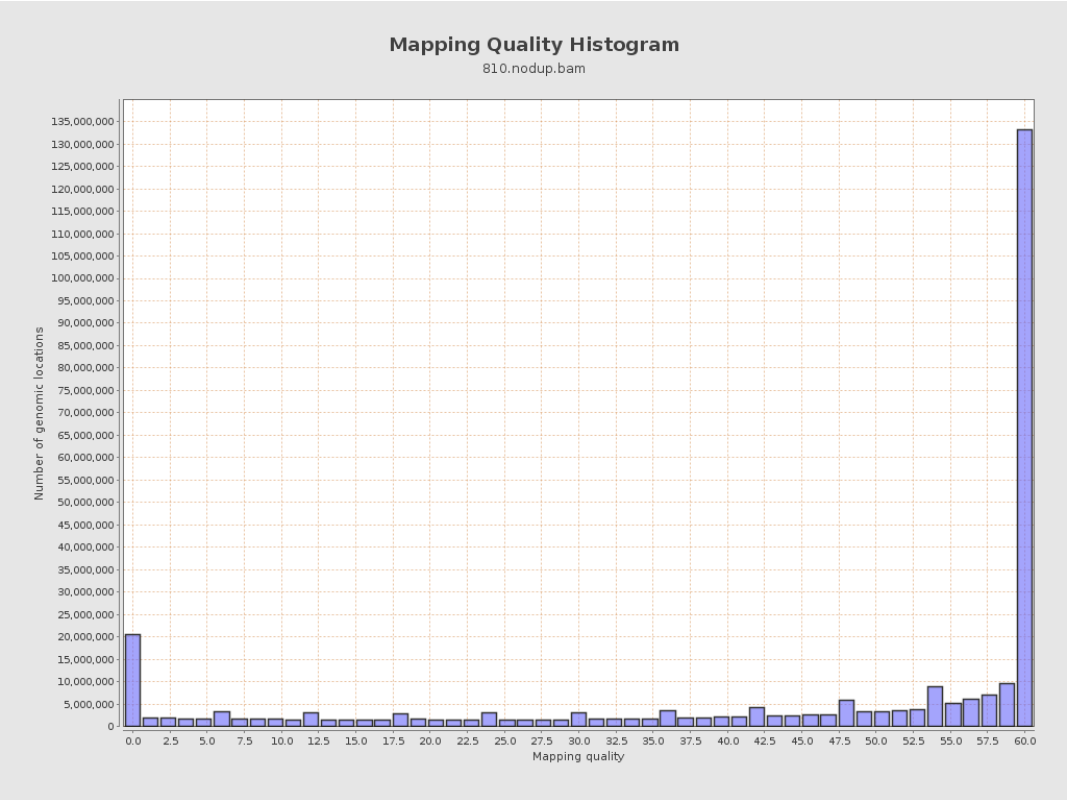
11. Results : Homopolymer Indels



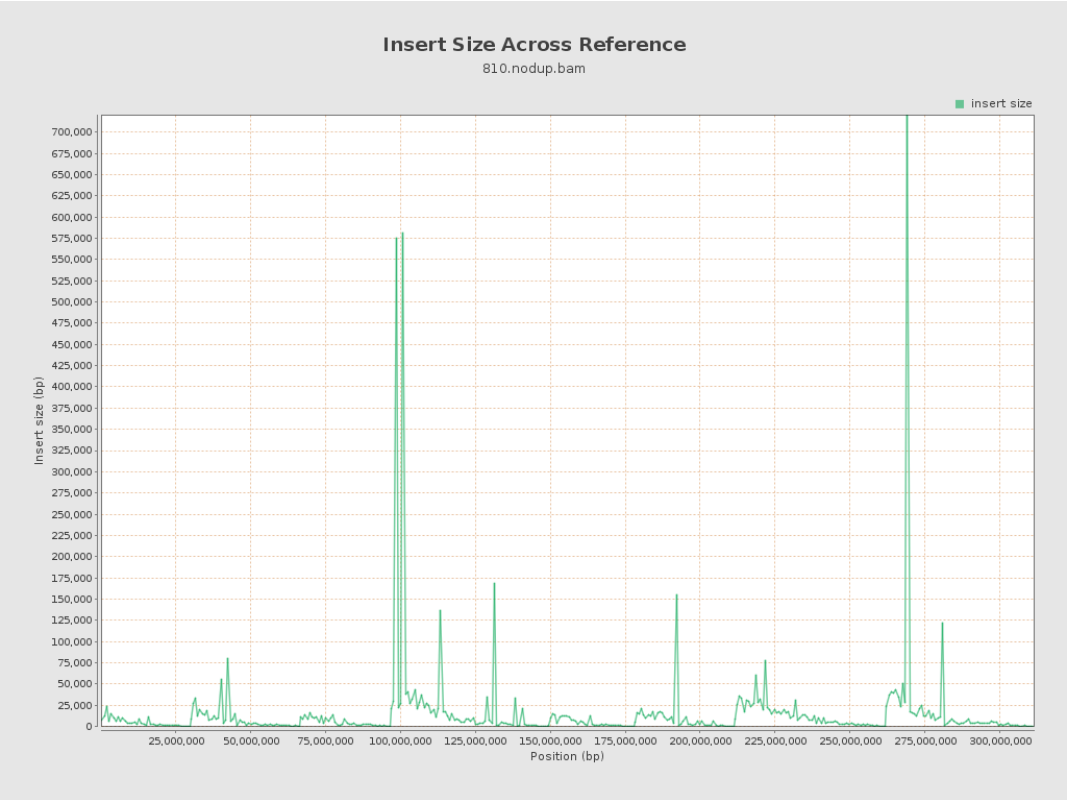
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram