Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:37:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/804.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/804.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_475/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_475_S450_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_475/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_475_S450_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:37:44 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	79,923,274
Mapped reads	75,913,972 / 94.98%
Unmapped reads	4,009,302 / 5.02%
Mapped paired reads	75,913,972 / 94.98%
Mapped reads, first in pair	38,018,289 / 47.57%
Mapped reads, second in pair	37,895,683 / 47.42%
Mapped reads, both in pair	74,491,775 / 93.2%
Mapped reads, singletons	1,422,197 / 1.78%
Read min/max/mean length	30 / 151 / 148.17
Duplicated reads (flagged)	12,768,450 / 15.98%
Clipped reads	16,379,435 / 20.49%

2.2. ACGT Content

Number/percentage of A's	3,254,718,951 / 30.77%
Number/percentage of C's	2,036,378,124 / 19.25%
Number/percentage of T's	3,261,515,264 / 30.83%
Number/percentage of G's	2,026,576,098 / 19.16%
Number/percentage of N's	36,975 / 0%
GC Percentage	38.41%

2.3. Coverage

Mean	34.0336
Standard Deviation	285.0767

2.4. Mapping Quality

Mean Mapping Quality	43.94

2.5. Insert size

Mean	231,318.64
Standard Deviation	2,267,672.52
P25/Median/P75	350 / 460 / 609

2.6. Mismatches and indels

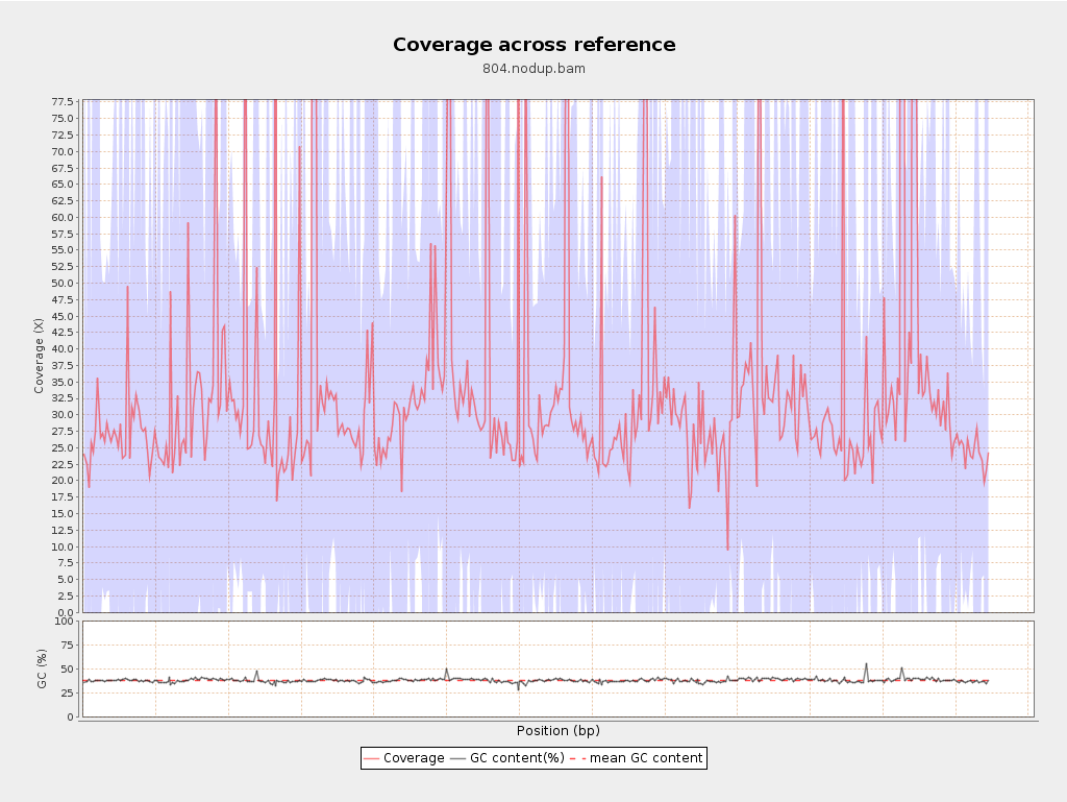
General error rate	2.31%
Mismatches	225,306,249
Insertions	7,001,125
Mapped reads with at least one insertion	8.3%
Deletions	7,193,423
Mapped reads with at least one deletion	8.41%
Homopolymer indels	56.04%

2.7. Chromosome stats

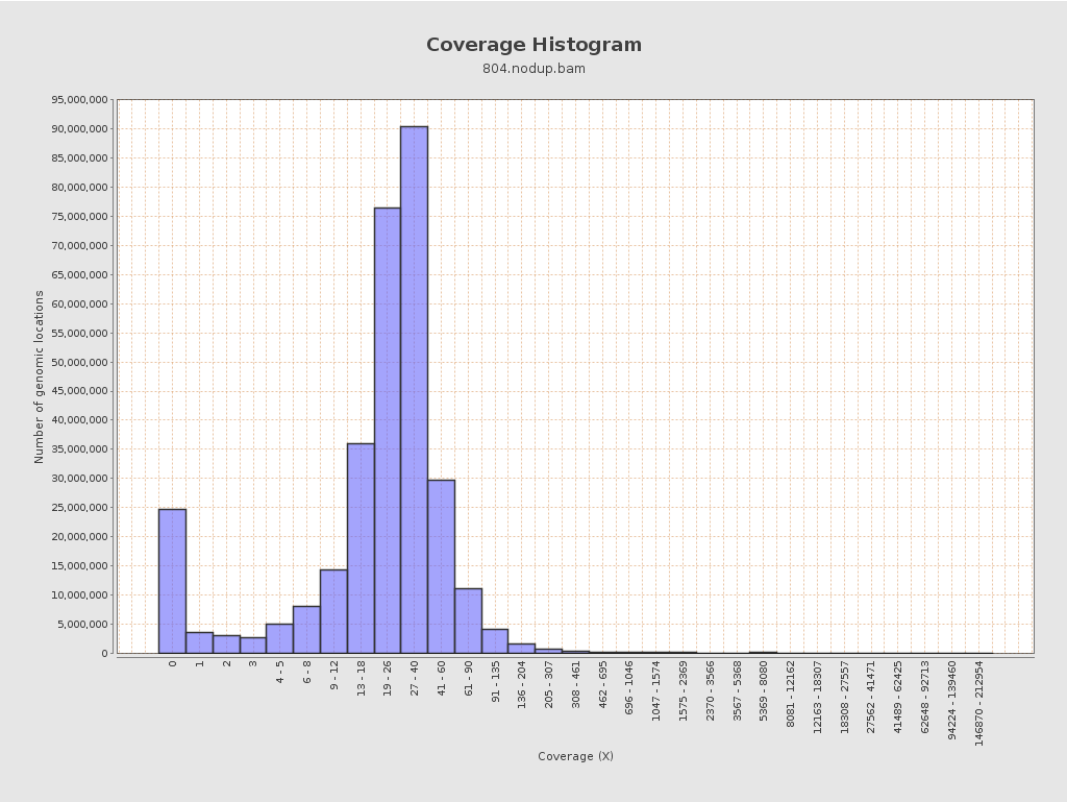
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	794439356	26.7269	77.186

LT669789.1	36598175	1255098531	34.294	302.2887
LT669790.1	30422129	1063663203	34.9635	262.4032
LT669791.1	52758100	1793801988	34.0005	237.1166
LT669792.1	28376109	941293534	33.172	331.7525
LT669793.1	33388210	1063932384	31.8655	204.7595
LT669794.1	50579949	1645561438	32.5339	253.0276
LT669795.1	49795044	2048524229	41.1391	424.6344

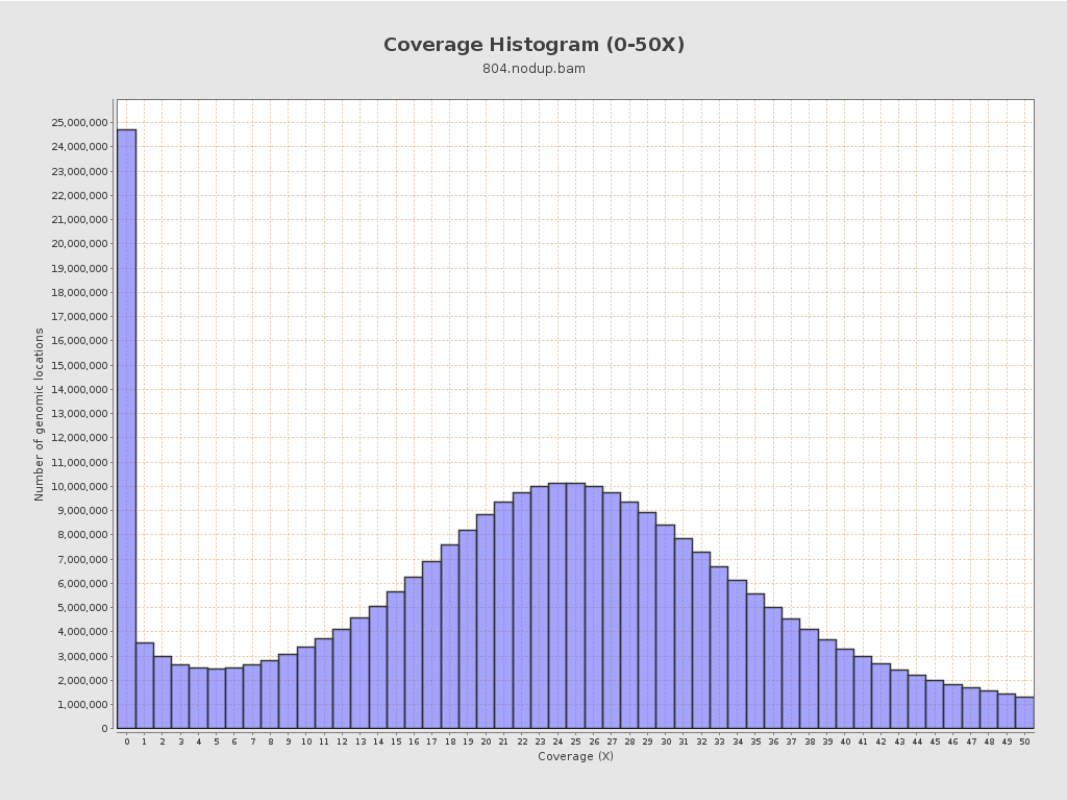
3. Results : Coverage across reference



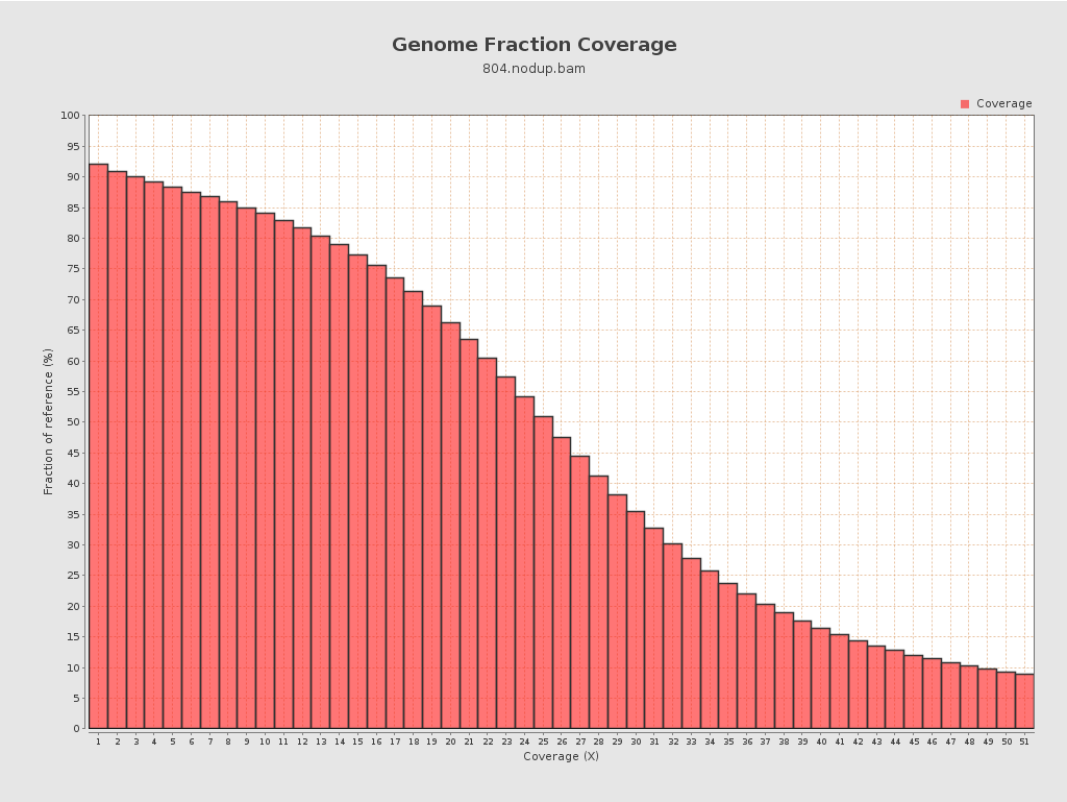
4. Results : Coverage Histogram



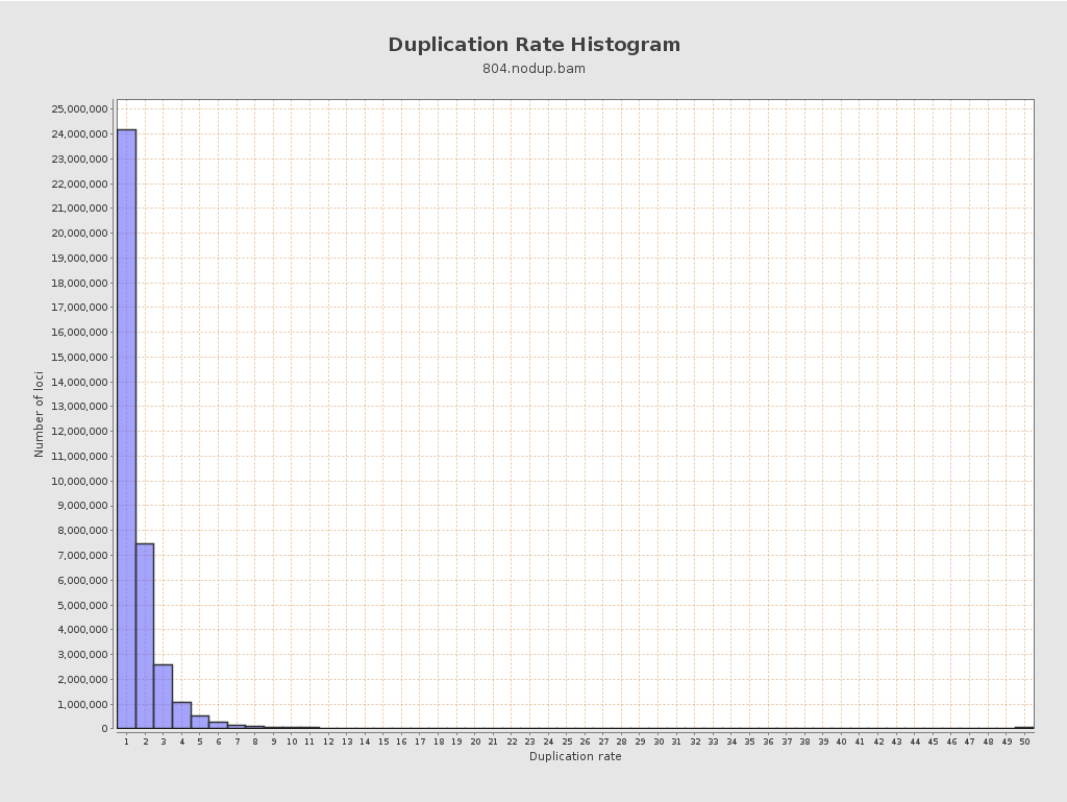
5. Results : Coverage Histogram (0-50X)



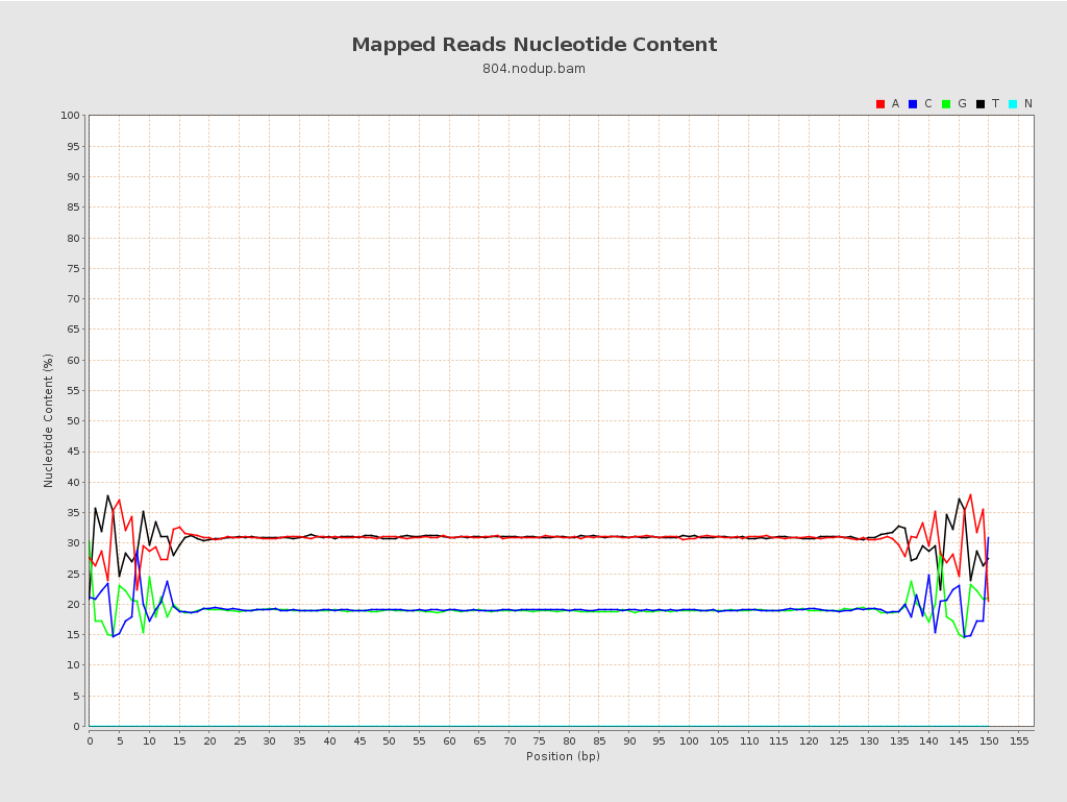
6. Results : Genome Fraction Coverage



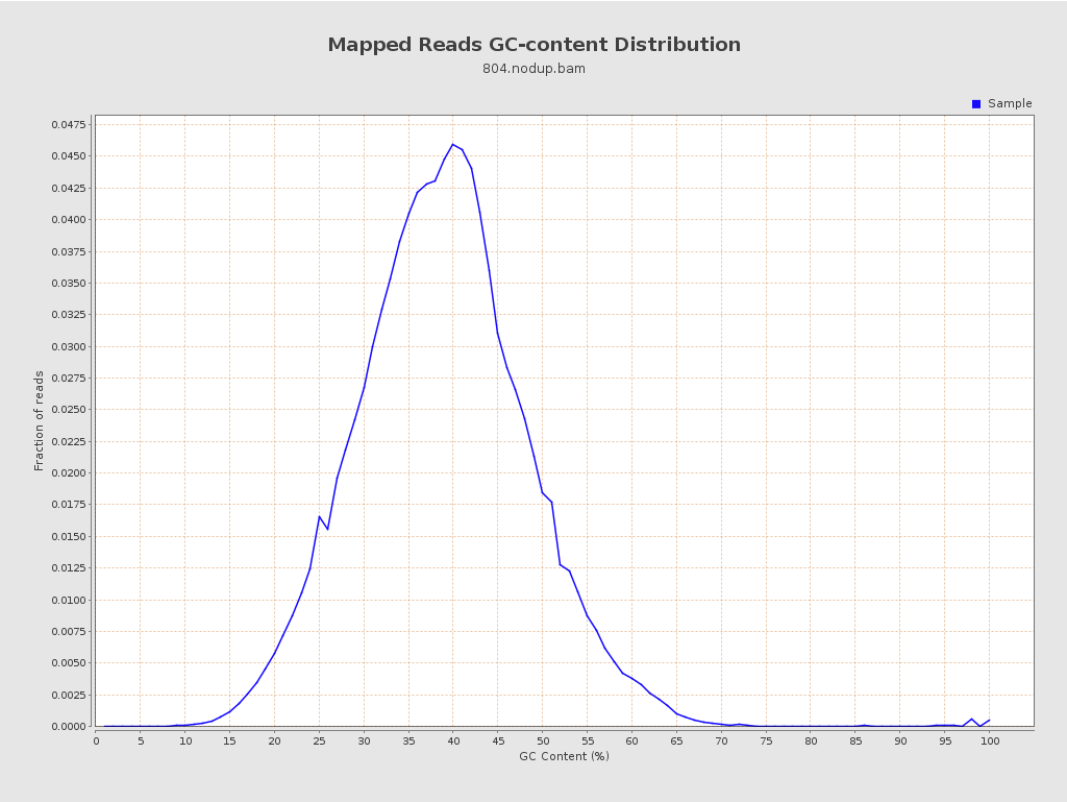
7. Results : Duplication Rate Histogram



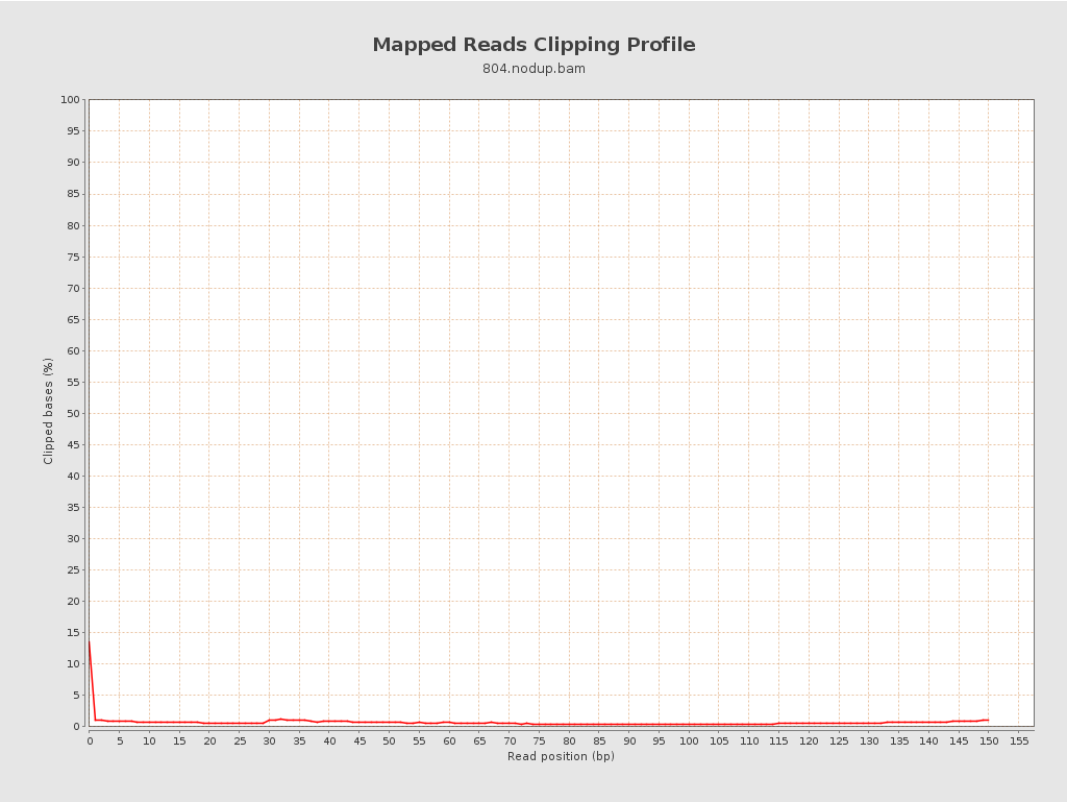
8. Results : Mapped Reads Nucleotide Content



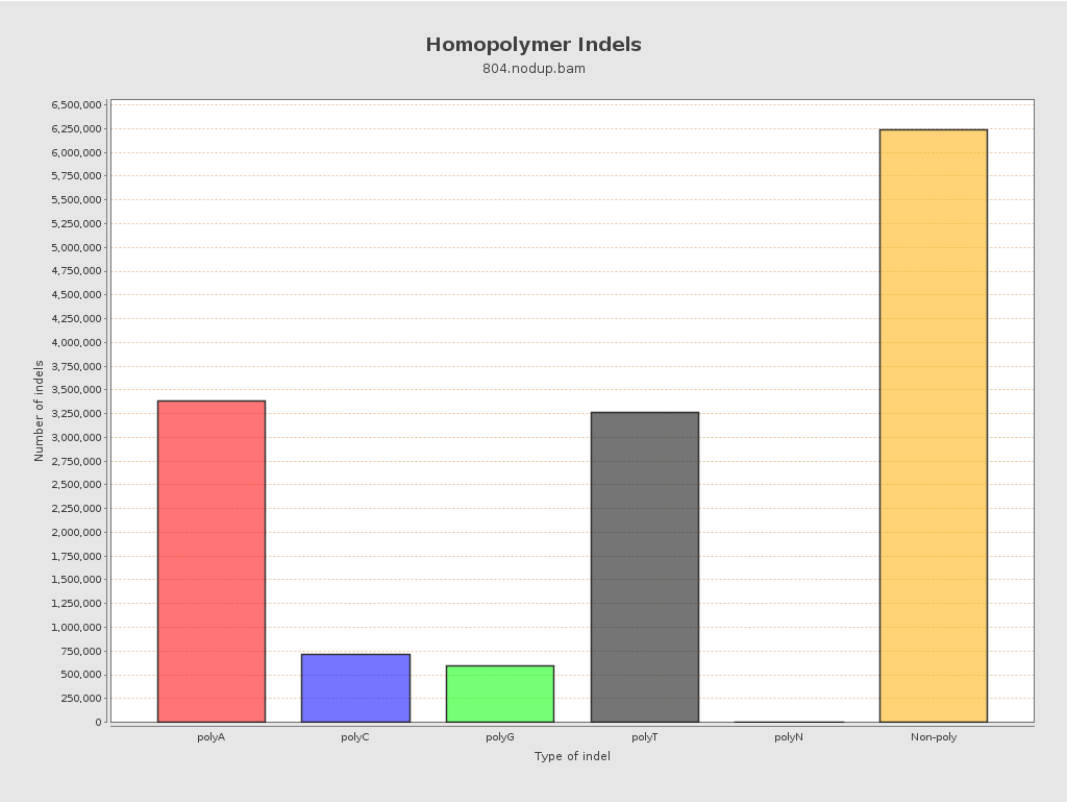
9. Results : Mapped Reads GC-content Distribution



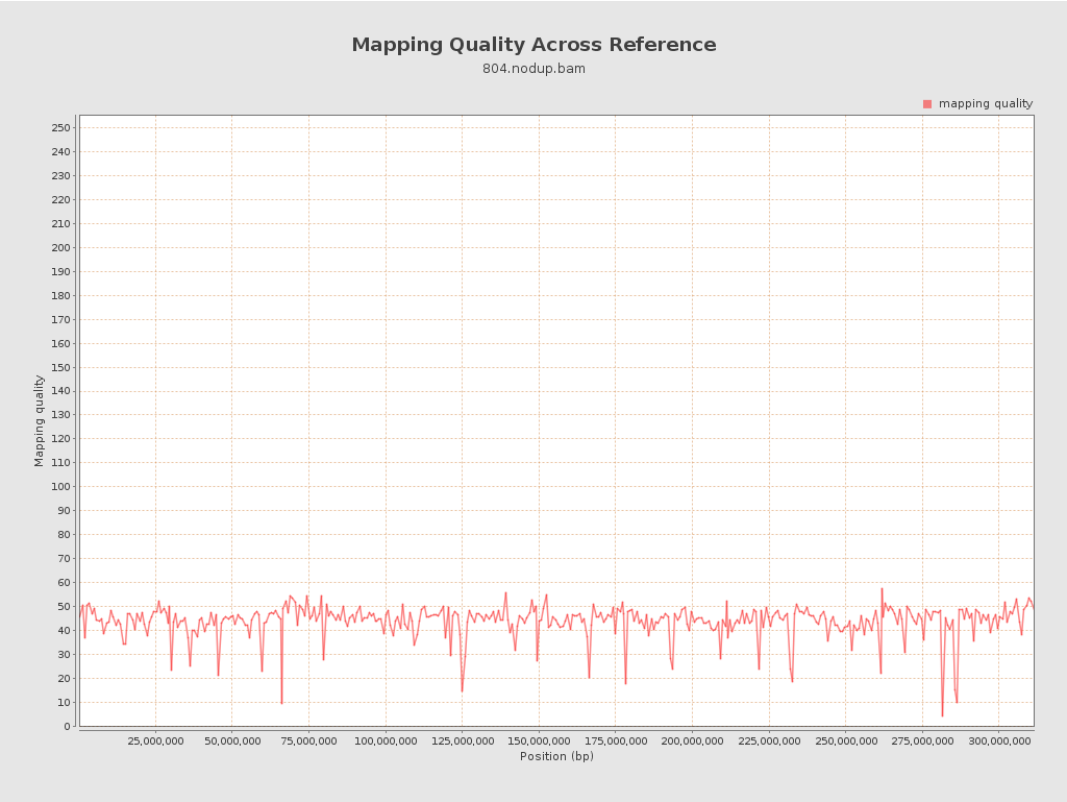
10. Results : Mapped Reads Clipping Profile



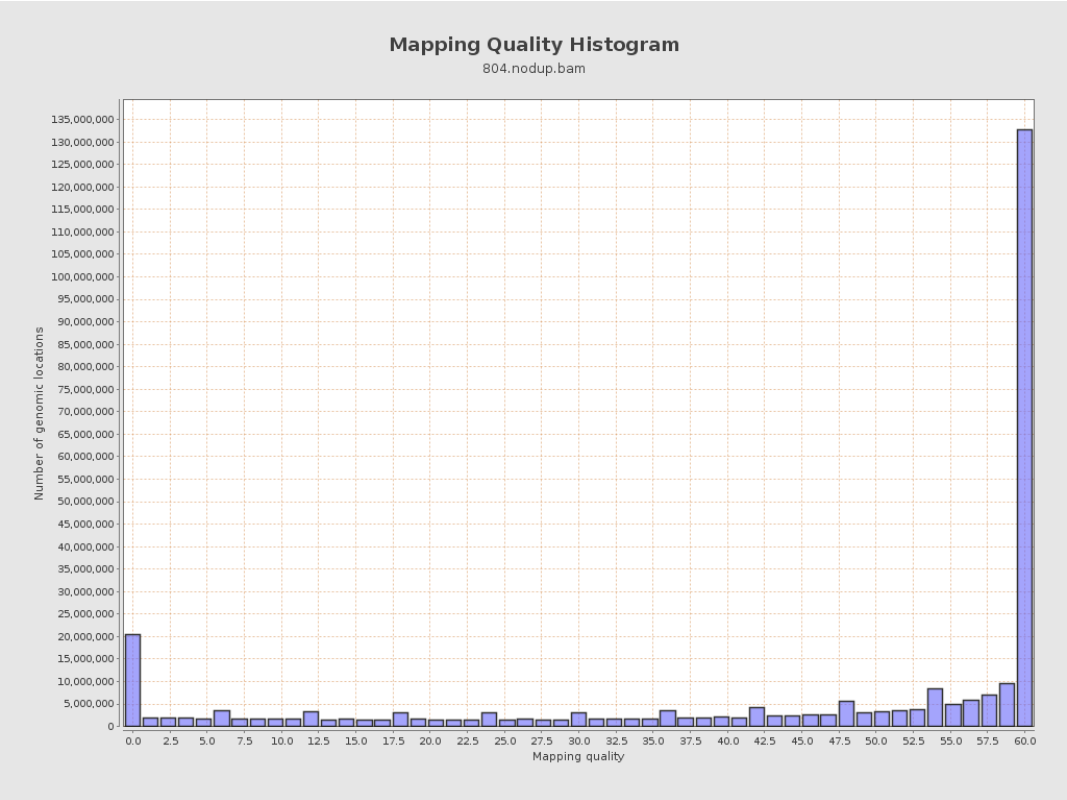
11. Results : Homopolymer Indels



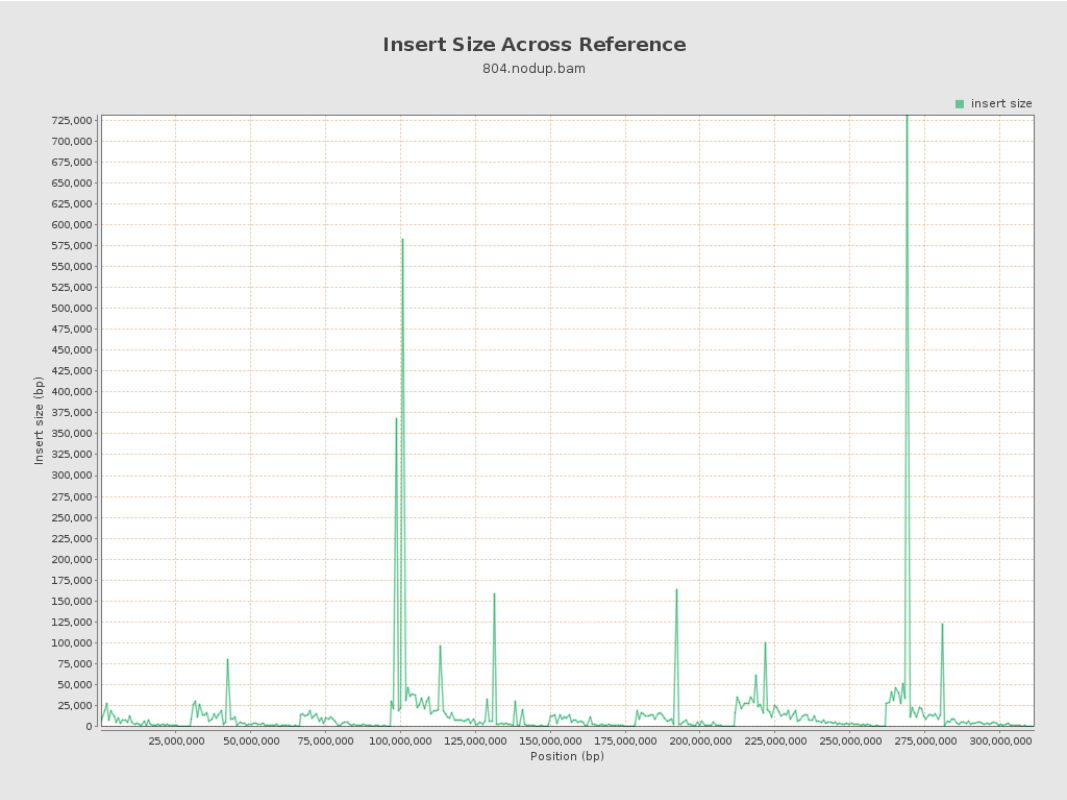
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram