Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:37:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/796.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/796.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_431/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_431_S406_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_431/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_431_S406_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:37:57 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	85,039,631
Mapped reads	80,389,530 / 94.53%
Unmapped reads	4,650,101 / 5.47%
Mapped paired reads	80,389,530 / 94.53%
Mapped reads, first in pair	40,265,369 / 47.35%
Mapped reads, second in pair	40,124,161 / 47.18%
Mapped reads, both in pair	78,774,593 / 92.63%
Mapped reads, singletons	1,614,937 / 1.9%
Read min/max/mean length	30 / 151 / 148.18
Duplicated reads (flagged)	13,451,566 / 15.82%
Clipped reads	17,283,005 / 20.32%

2.2. ACGT Content

Number/percentage of A's	3,456,489,349 / 30.88%
Number/percentage of C's	2,143,302,957 / 19.15%
Number/percentage of T's	3,460,556,355 / 30.92%
Number/percentage of G's	2,133,266,311 / 19.06%
Number/percentage of N's	38,947 / 0%
GC Percentage	38.21%

2.3. Coverage

Mean	36.0111
Standard Deviation	289.1749

2.4. Mapping Quality

Mean Mapping Quality	44.12

2.5. Insert size

Mean	231,637.89
Standard Deviation	2,272,572.13
P25/Median/P75	347 / 454 / 593

2.6. Mismatches and indels

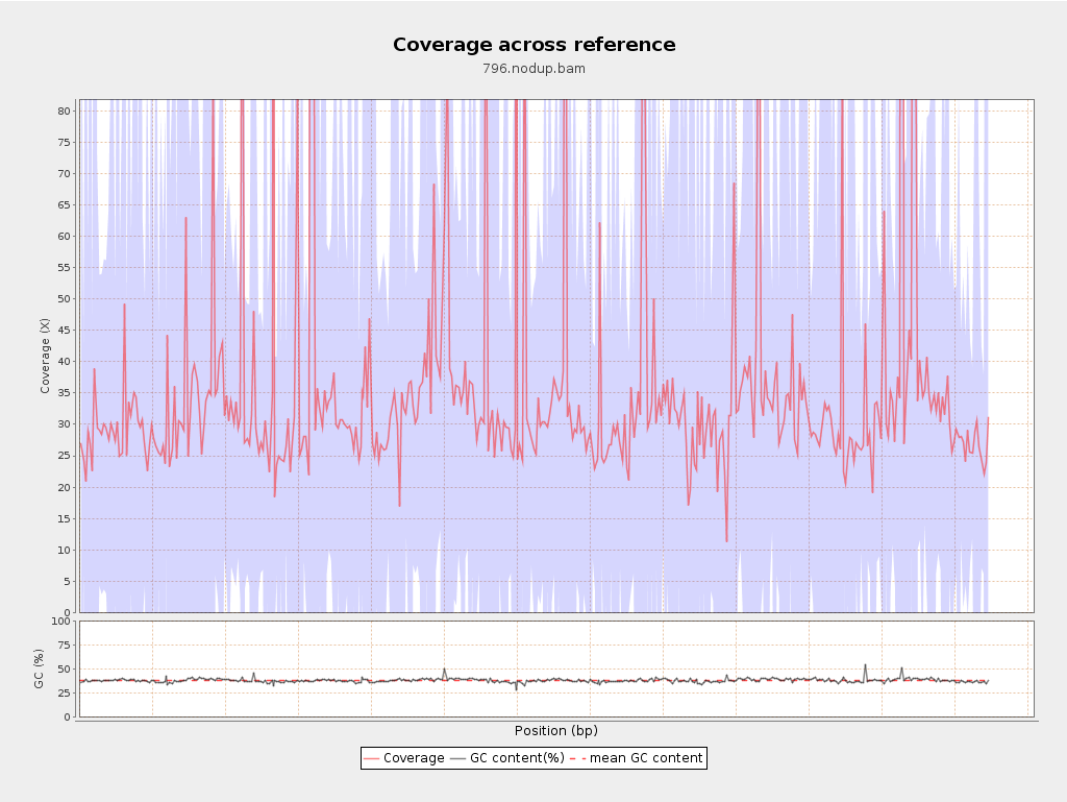
General error rate	2.28%
Mismatches	234,449,162
Insertions	7,523,222
Mapped reads with at least one insertion	8.41%
Deletions	7,635,295
Mapped reads with at least one deletion	8.45%
Homopolymer indels	56.82%

2.7. Chromosome stats

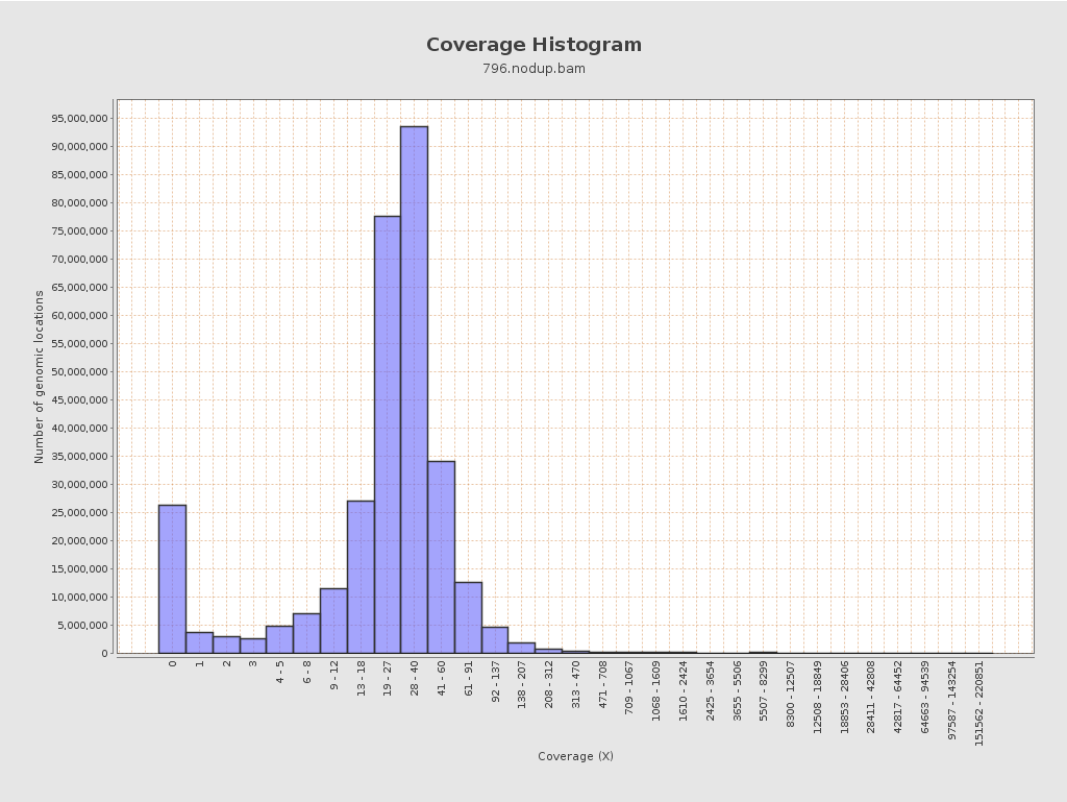
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	854318820	28.7414	74.0708

LT669789.1	36598175	1321643882	36.1123	282.9445
LT669790.1	30422129	1159855925	38.1254	303.1738
LT669791.1	52758100	1898987702	35.9942	242.7637
LT669792.1	28376109	1025151521	36.1273	376.5423
LT669793.1	33388210	1113911526	33.3624	206.6023
LT669794.1	50579949	1744890131	34.4977	241.8715
LT669795.1	49795044	2103828168	42.2498	416.7926

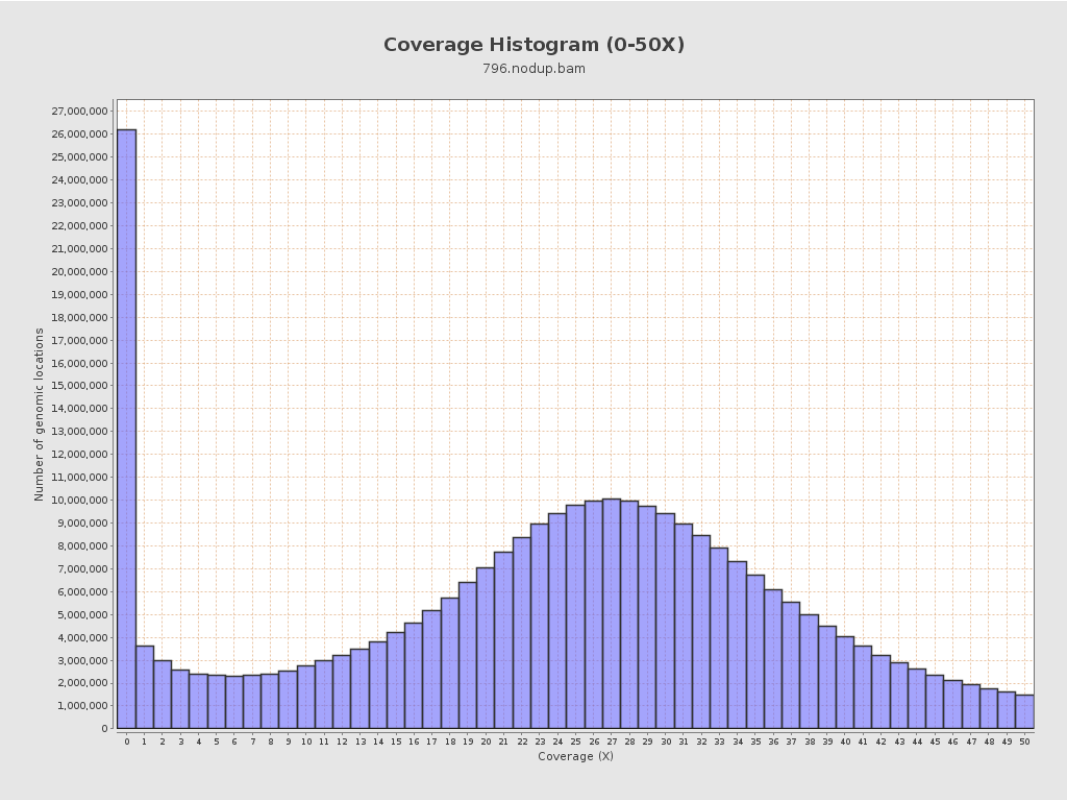
3. Results : Coverage across reference



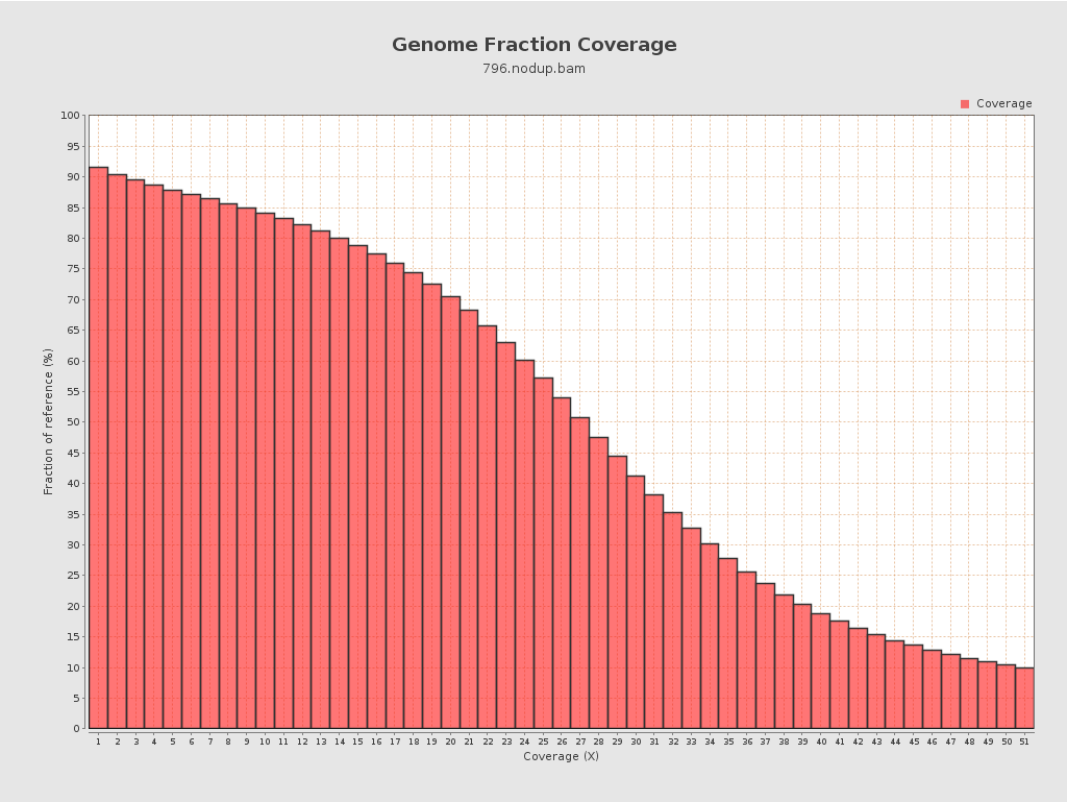
4. Results : Coverage Histogram



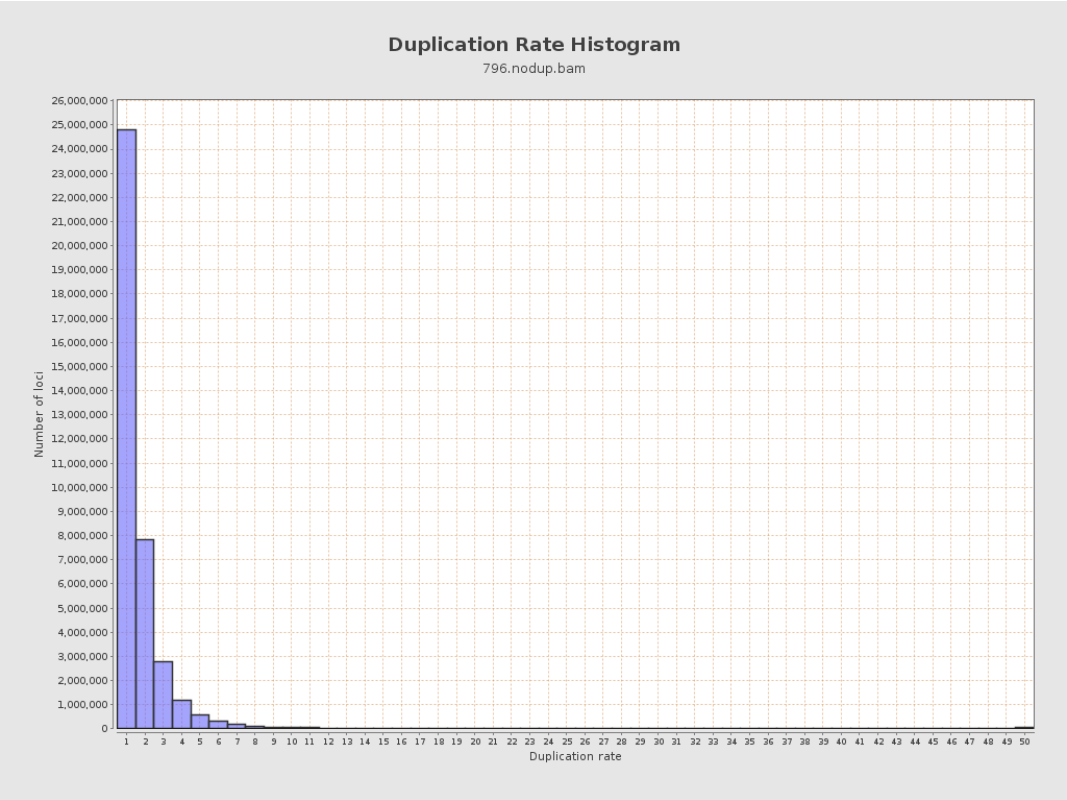
5. Results : Coverage Histogram (0-50X)



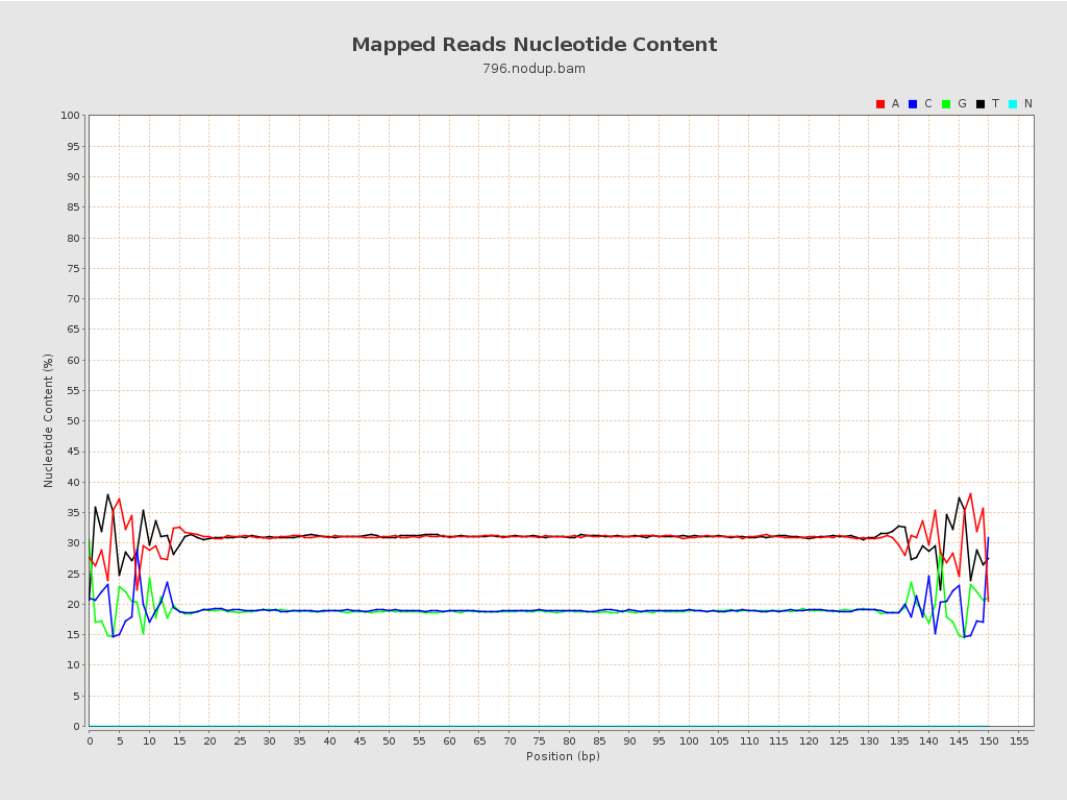
6. Results : Genome Fraction Coverage



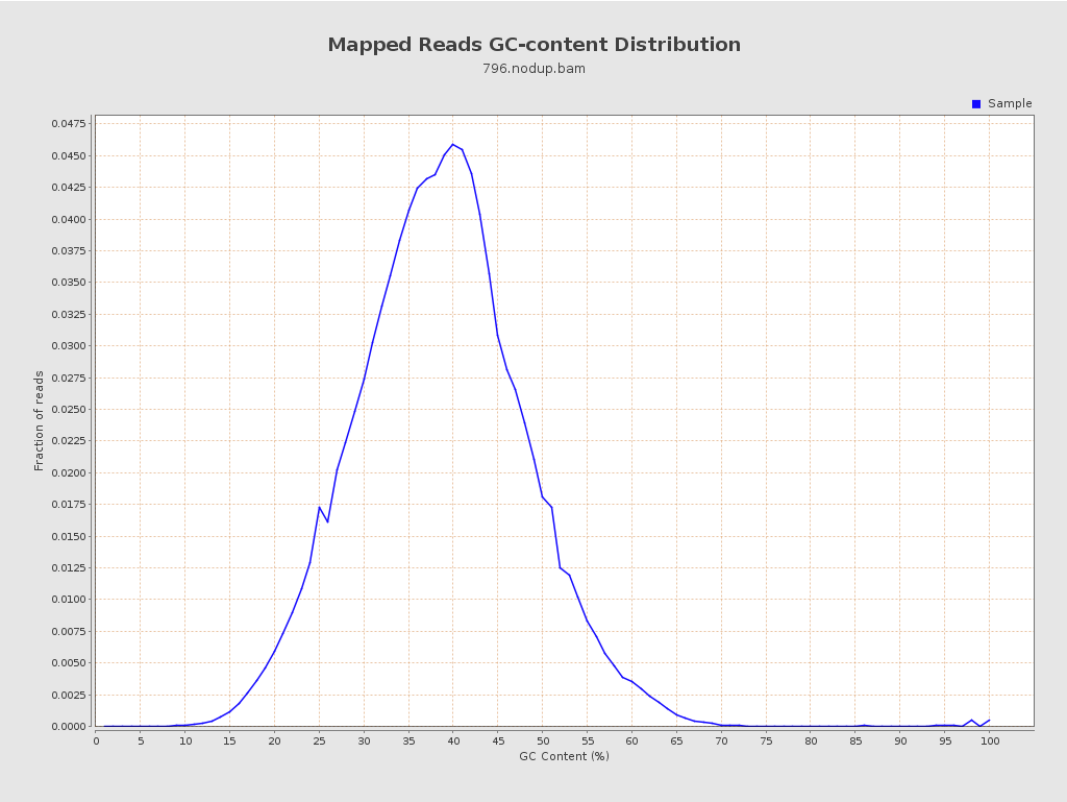
7. Results : Duplication Rate Histogram



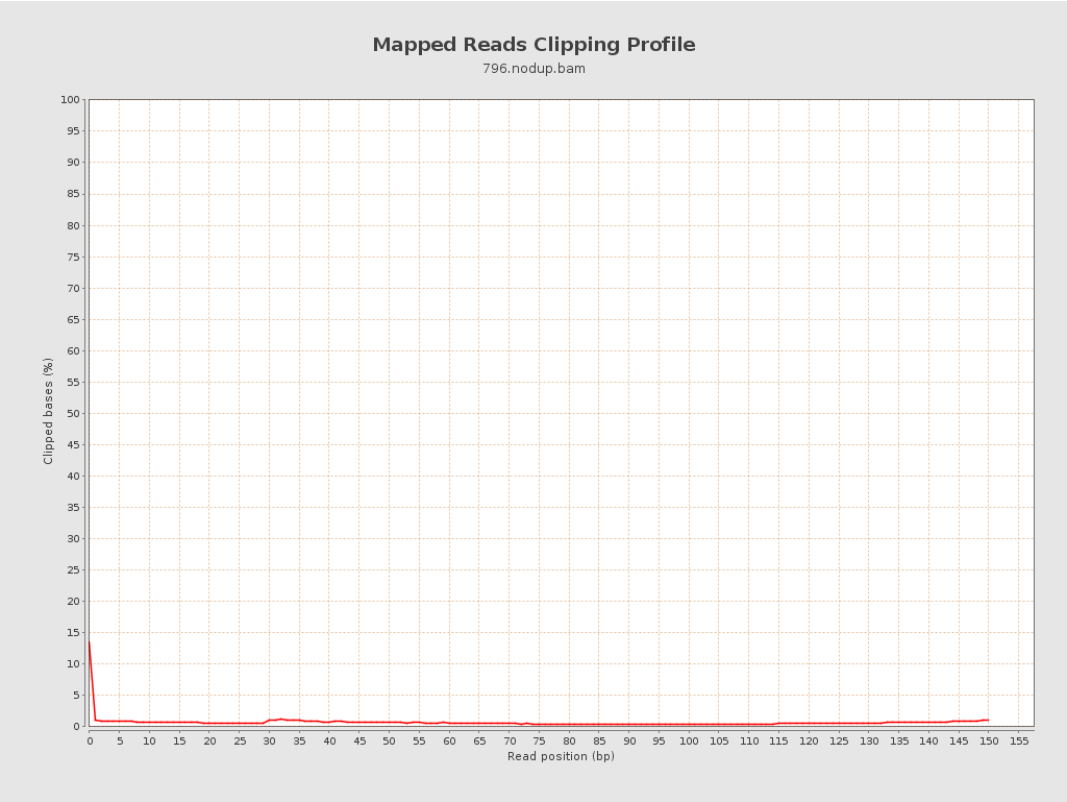
8. Results : Mapped Reads Nucleotide Content



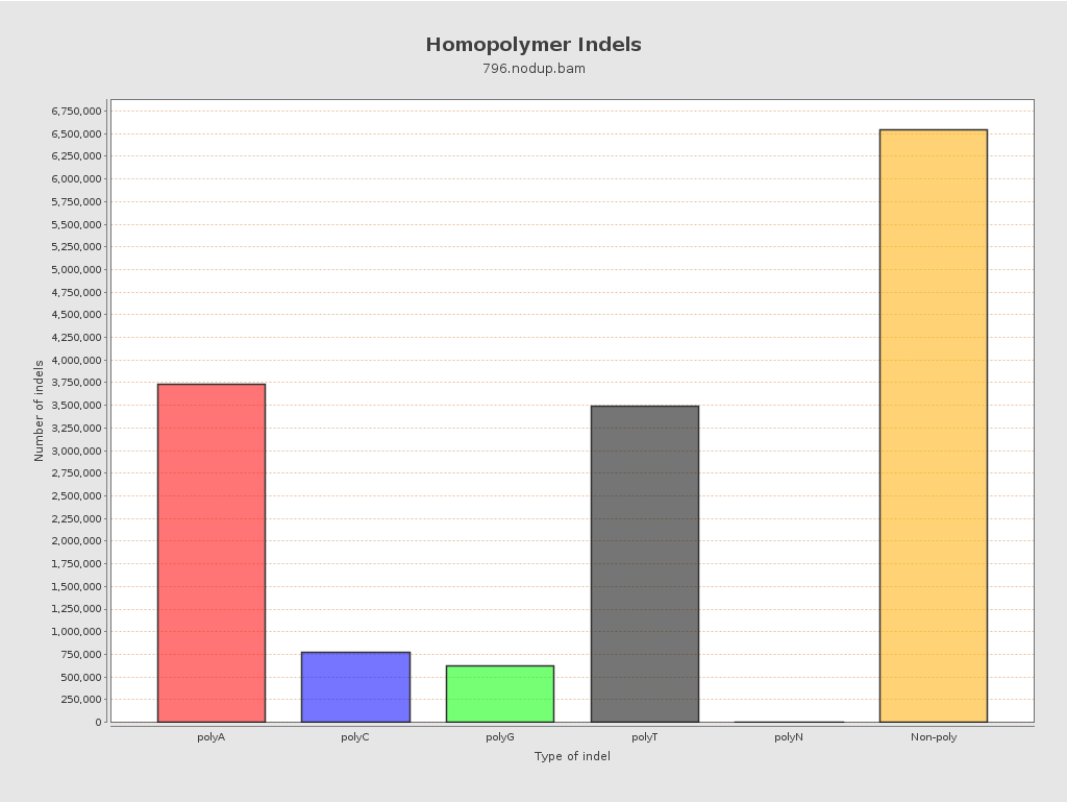
9. Results : Mapped Reads GC-content Distribution



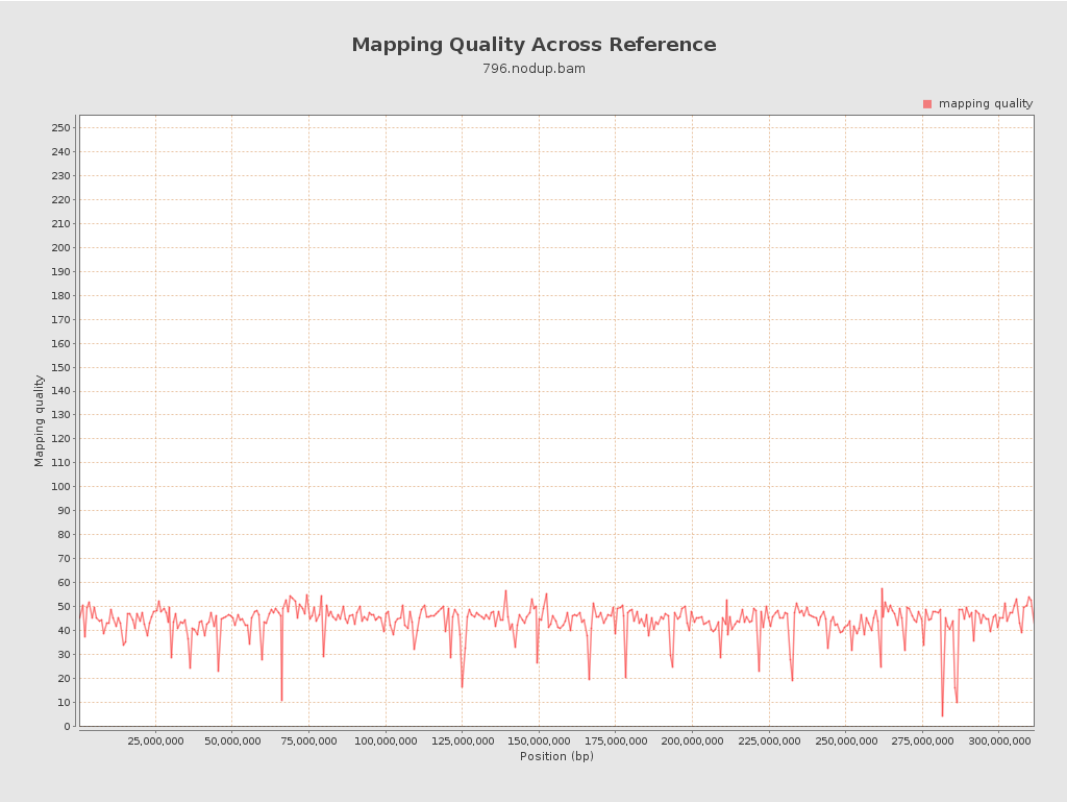
10. Results : Mapped Reads Clipping Profile



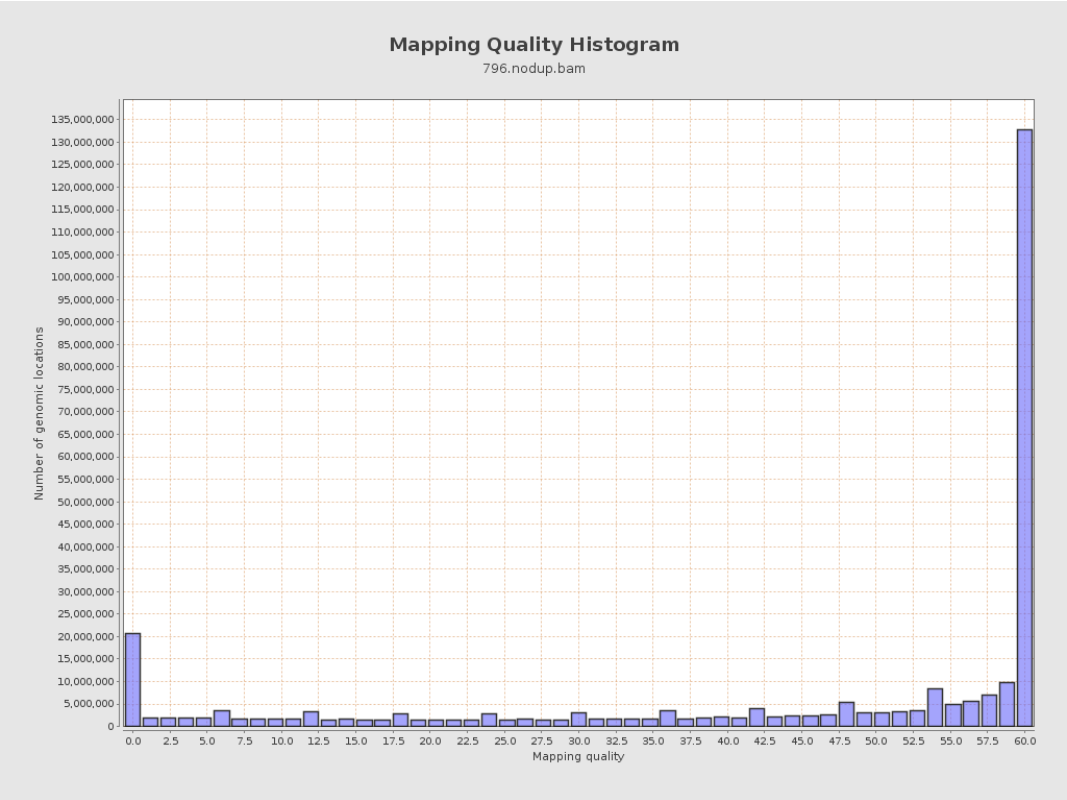
11. Results : Homopolymer Indels



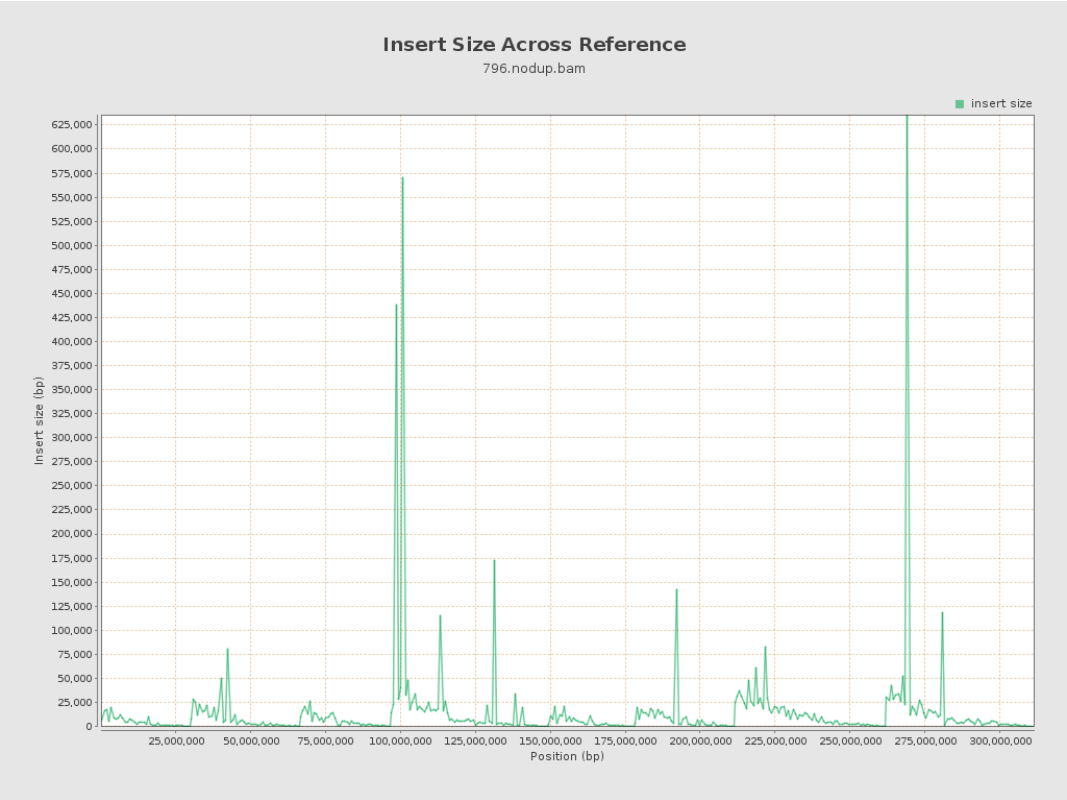
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram