Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:30:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/996.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/996.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_120/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_120_S210_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_120/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_120_S210_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:30:12 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	65,494,737
Mapped reads	59,633,439 / 91.05%
Unmapped reads	5,861,298 / 8.95%
Mapped paired reads	59,633,439 / 91.05%
Mapped reads, first in pair	29,842,933 / 45.57%
Mapped reads, second in pair	29,790,506 / 45.49%
Mapped reads, both in pair	57,750,128 / 88.18%
Mapped reads, singletons	1,883,311 / 2.88%
Read min/max/mean length	30 / 151 / 148.09
Duplicated reads (flagged)	10,695,470 / 16.33%
Clipped reads	14,260,760 / 21.77%

2.2. ACGT Content

Number/percentage of A's	2,533,703,576 / 30.98%
Number/percentage of C's	1,555,083,357 / 19.01%
Number/percentage of T's	2,535,422,667 / 31%
Number/percentage of G's	1,554,435,015 / 19.01%
Number/percentage of N's	32,609 / 0%
GC Percentage	38.02%

2.3. Coverage

Mean	26.3128
Standard Deviation	238.7747

2.4. Mapping Quality

Mean Mapping Quality	44.16

2.5. Insert size

Mean	261,905.71
Standard Deviation	2,461,627.74
P25/Median/P75	325 / 425 / 555

2.6. Mismatches and indels

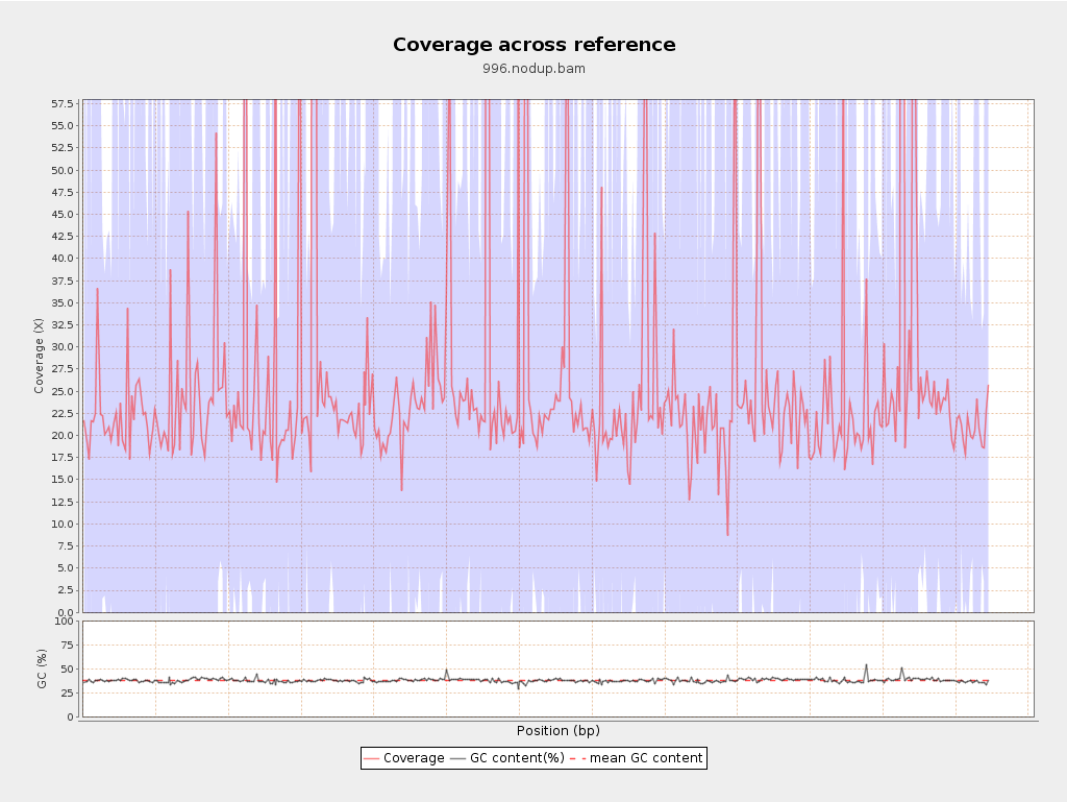
General error rate	2.44%
Mismatches	182,617,643
Insertions	6,054,751
Mapped reads with at least one insertion	9.05%
Deletions	5,785,465
Mapped reads with at least one deletion	8.59%
Homopolymer indels	57.23%

2.7. Chromosome stats

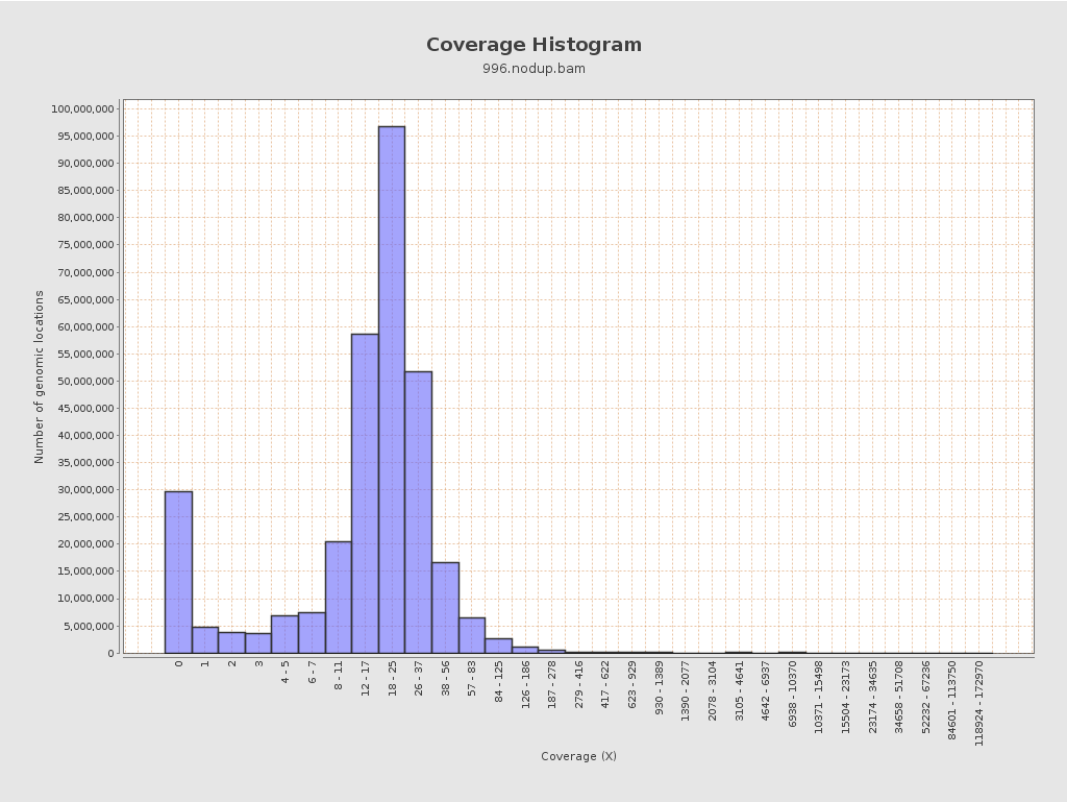
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	650103768	21.8711	96.1115

LT669789.1	36598175	973658032	26.604	257.1486
LT669790.1	30422129	984582894	32.364	354.8999
LT669791.1	52758100	1374087546	26.0451	261.9323
LT669792.1	28376109	756631764	26.6644	254.6863
LT669793.1	33388210	803657410	24.0701	154.1072
LT669794.1	50579949	1237450922	24.4652	195.9069
LT669795.1	49795044	1420017124	28.5172	247.2702

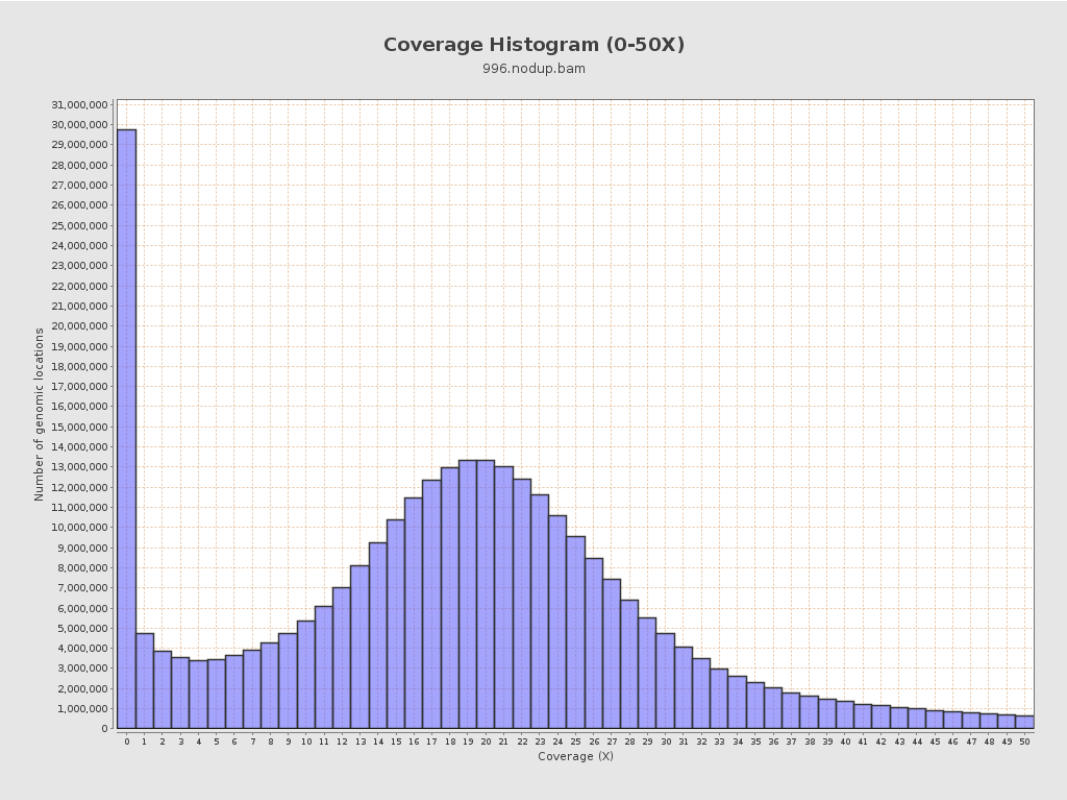
3. Results : Coverage across reference



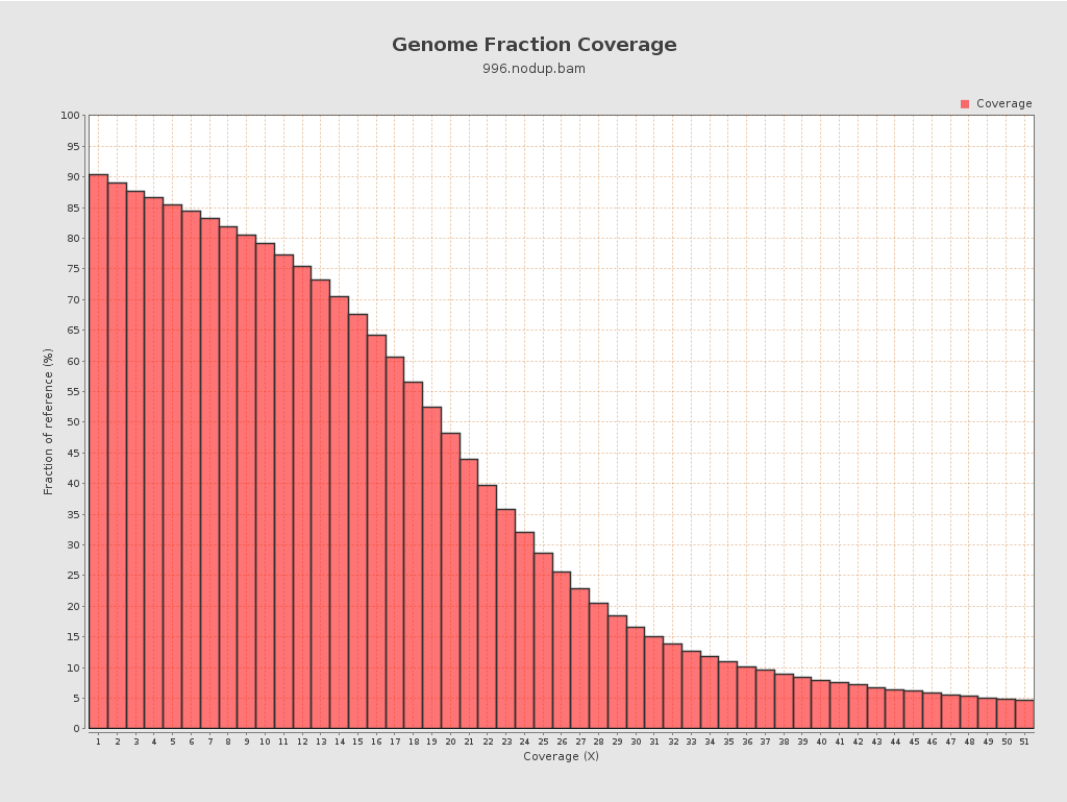
4. Results : Coverage Histogram



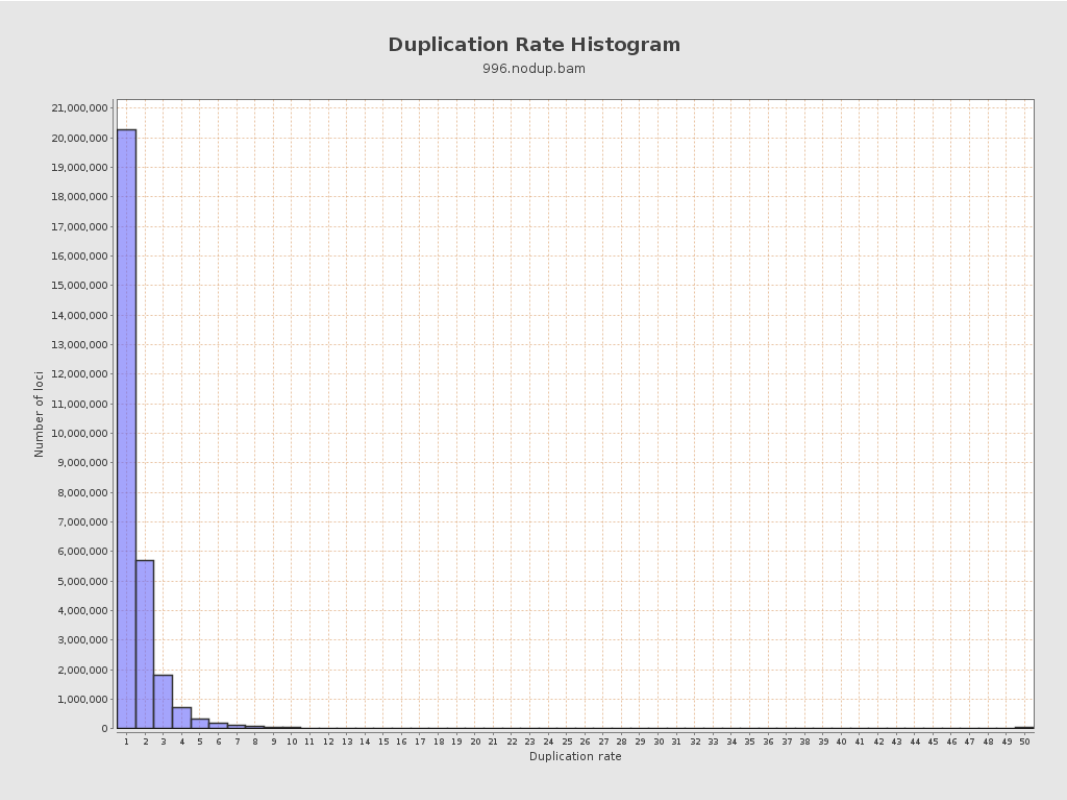
5. Results : Coverage Histogram (0-50X)



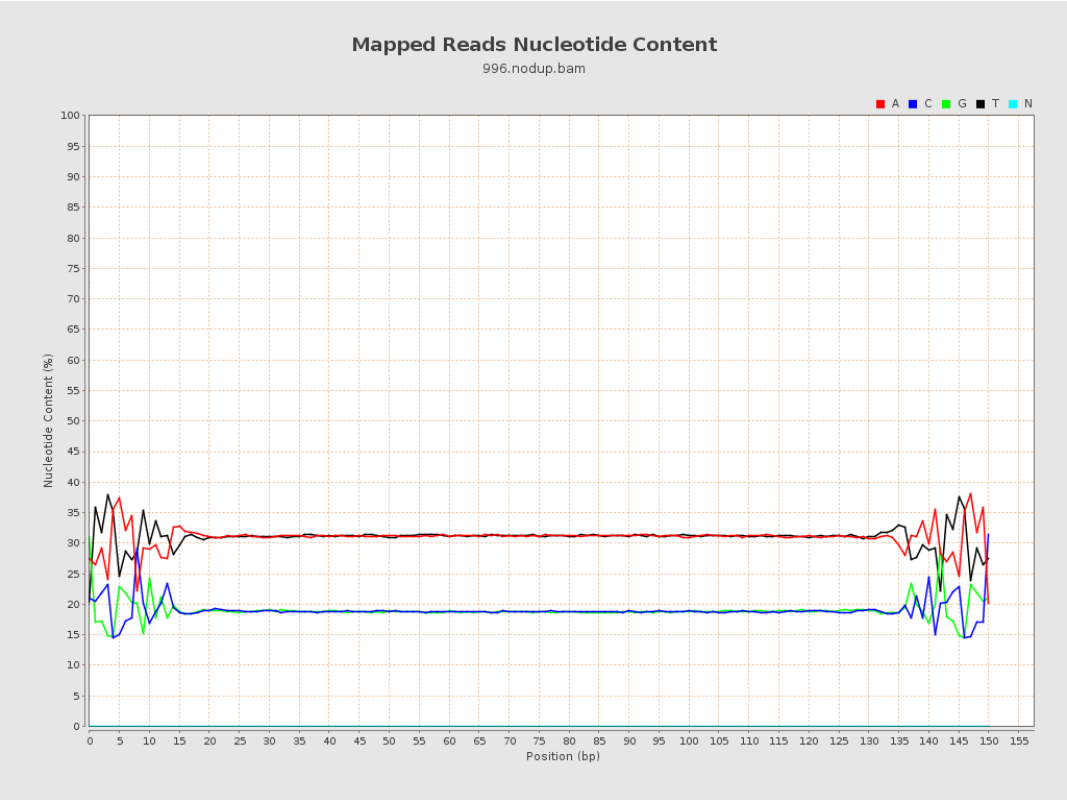
6. Results : Genome Fraction Coverage



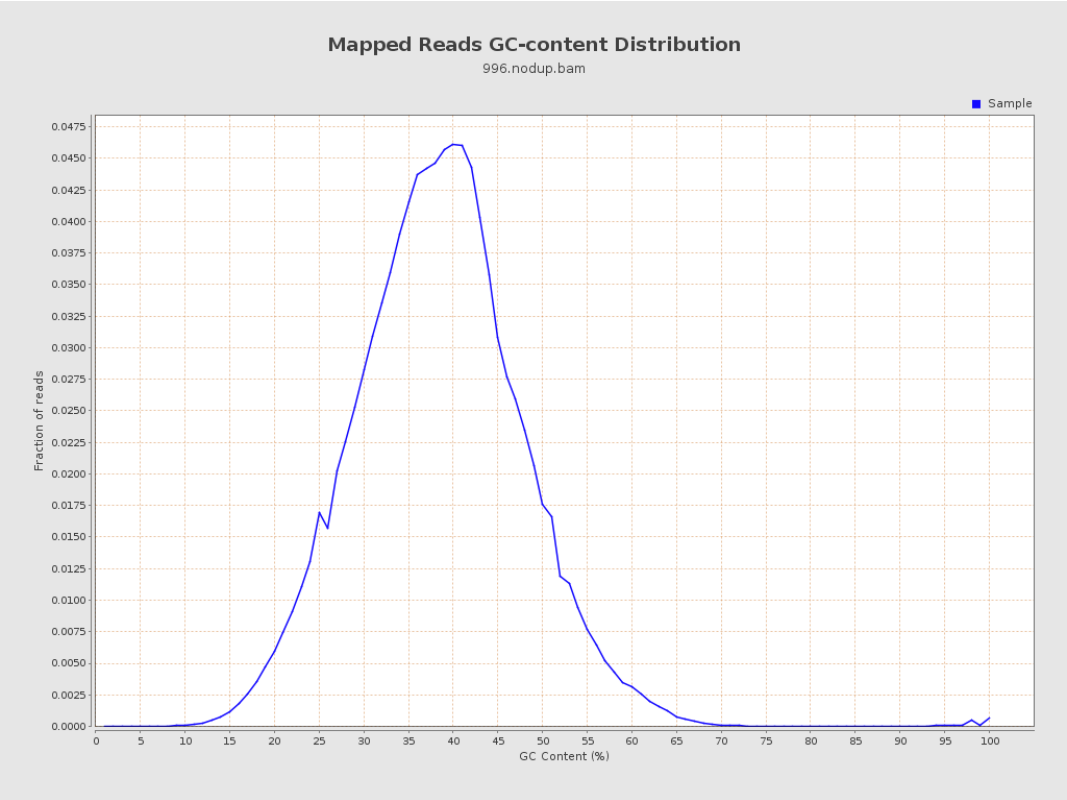
7. Results : Duplication Rate Histogram



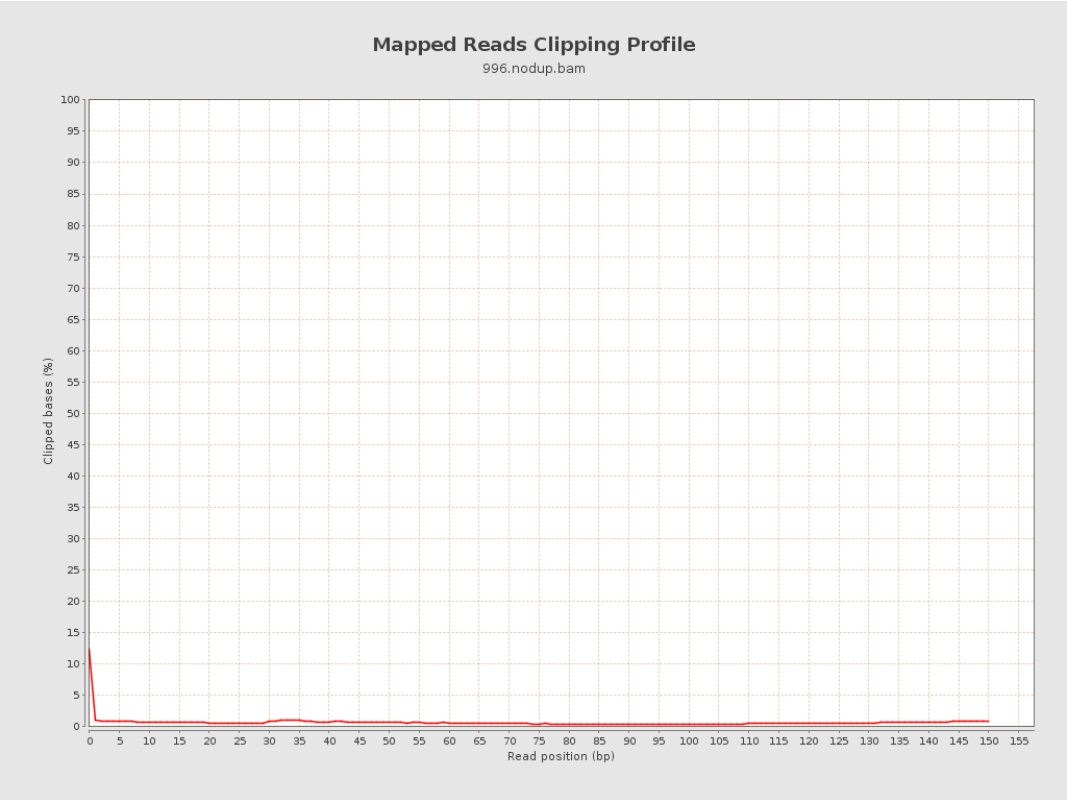
8. Results : Mapped Reads Nucleotide Content



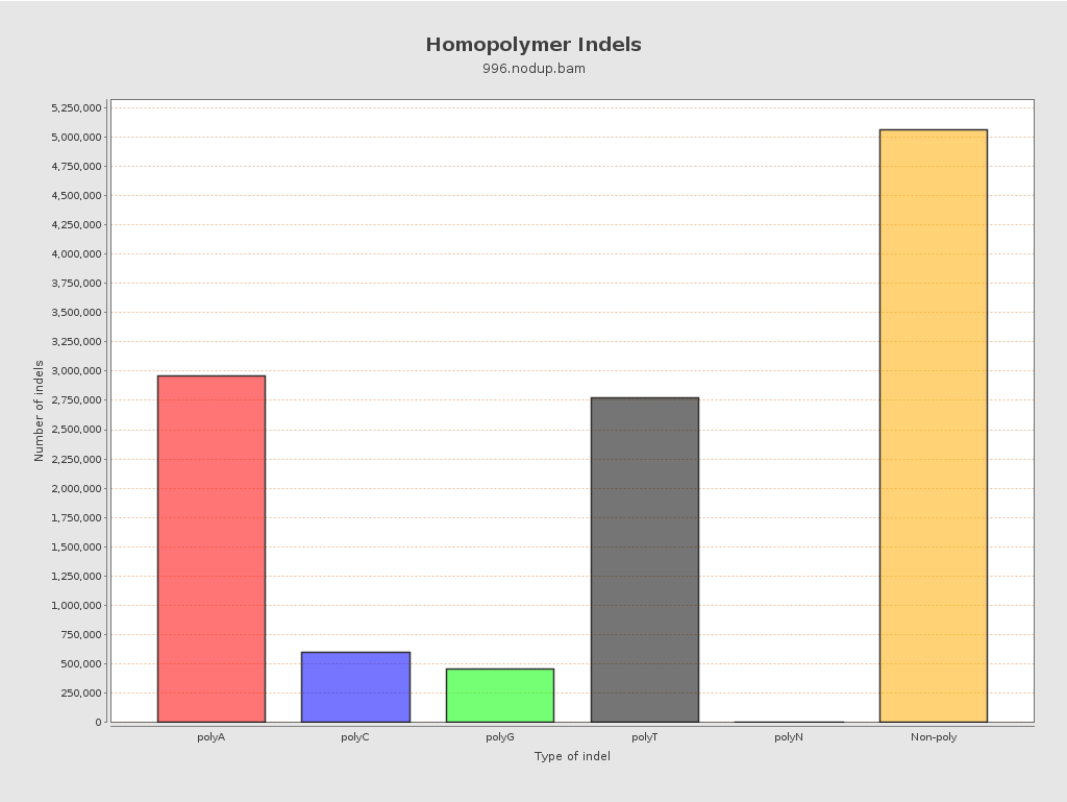
9. Results : Mapped Reads GC-content Distribution



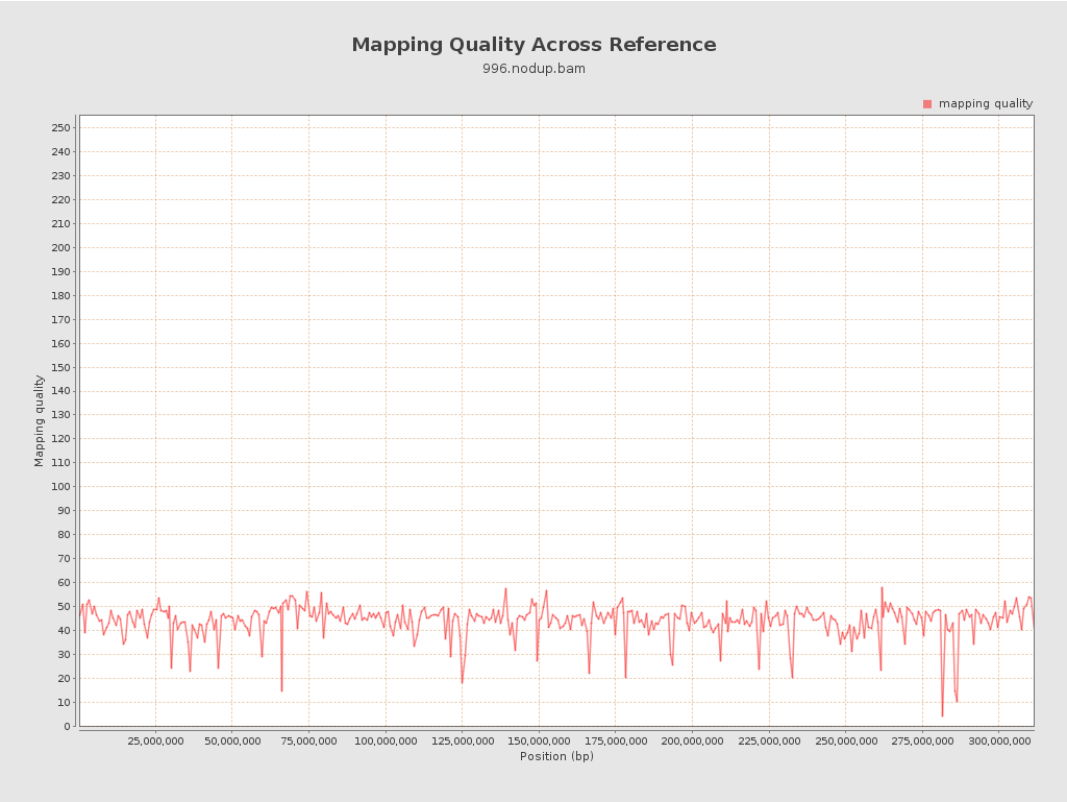
10. Results : Mapped Reads Clipping Profile



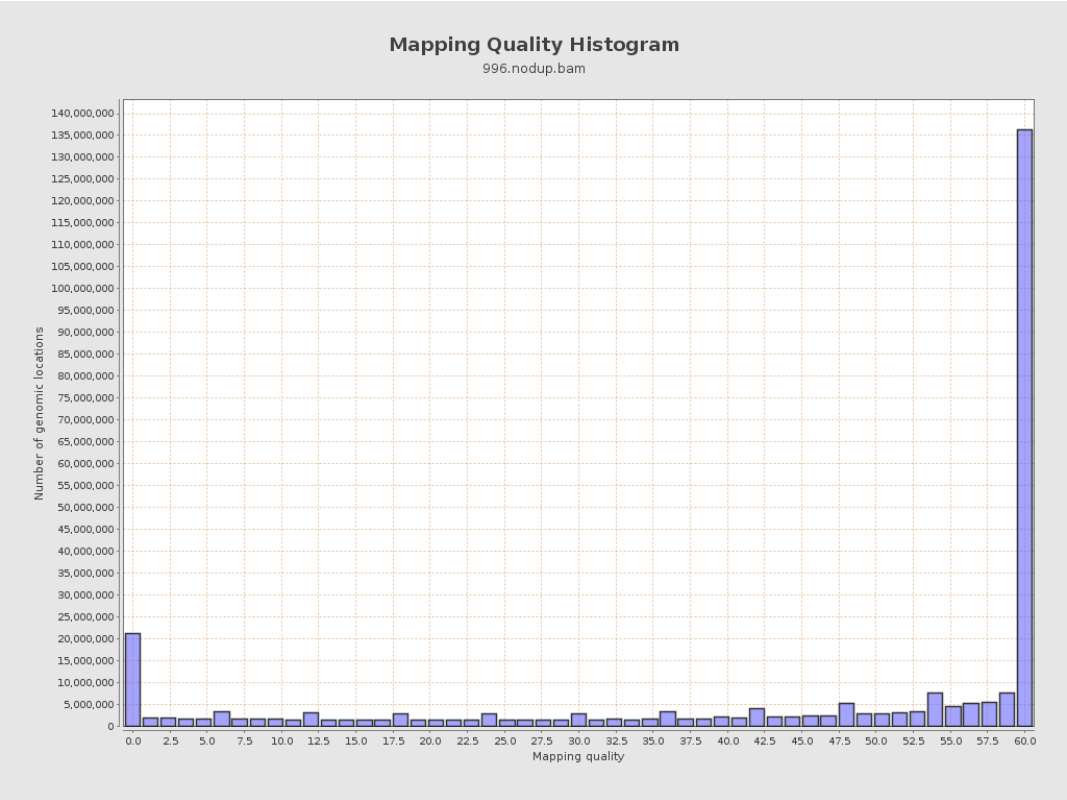
11. Results : Homopolymer Indels



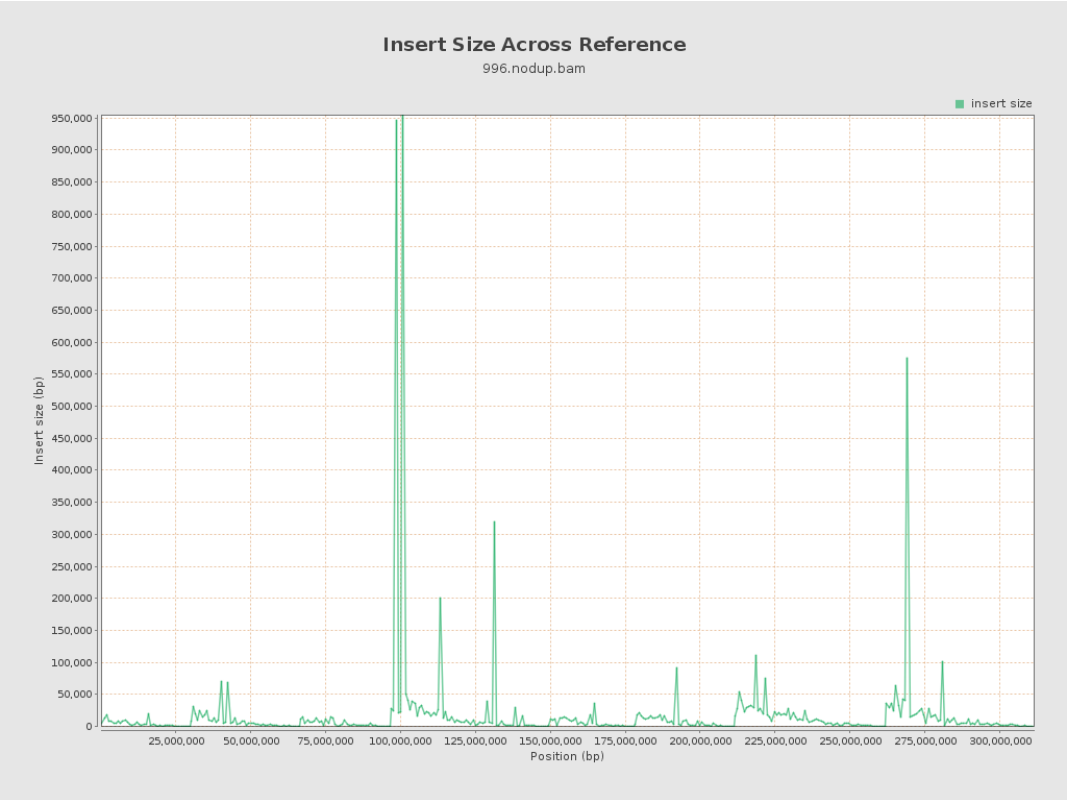
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram