Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:32:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/795.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/795.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_152/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_152_S242_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_152/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_152_S242_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:32:58 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	74,320,311
Mapped reads	67,411,537 / 90.7%
Unmapped reads	6,908,774 / 9.3%
Mapped paired reads	67,411,537 / 90.7%
Mapped reads, first in pair	33,793,587 / 45.47%
Mapped reads, second in pair	33,617,950 / 45.23%
Mapped reads, both in pair	65,211,570 / 87.74%
Mapped reads, singletons	2,199,967 / 2.96%
Read min/max/mean length	30 / 151 / 148.15
Duplicated reads (flagged)	12,540,222 / 16.87%
Clipped reads	15,863,702 / 21.35%

2.2. ACGT Content

Number/percentage of A's	2,871,768,639 / 31.03%
Number/percentage of C's	1,754,061,276 / 18.96%
Number/percentage of T's	2,870,770,344 / 31.02%
Number/percentage of G's	1,756,865,173 / 18.99%
Number/percentage of N's	38,100 / 0%
GC Percentage	37.94%

2.3. Coverage

Mean	29.7688
Standard Deviation	263.9139

2.4. Mapping Quality

Mean Mapping Quality	44.56

2.5. Insert size

Mean	260,863.34
Standard Deviation	2,463,491.49
P25/Median/P75	334 / 437 / 576

2.6. Mismatches and indels

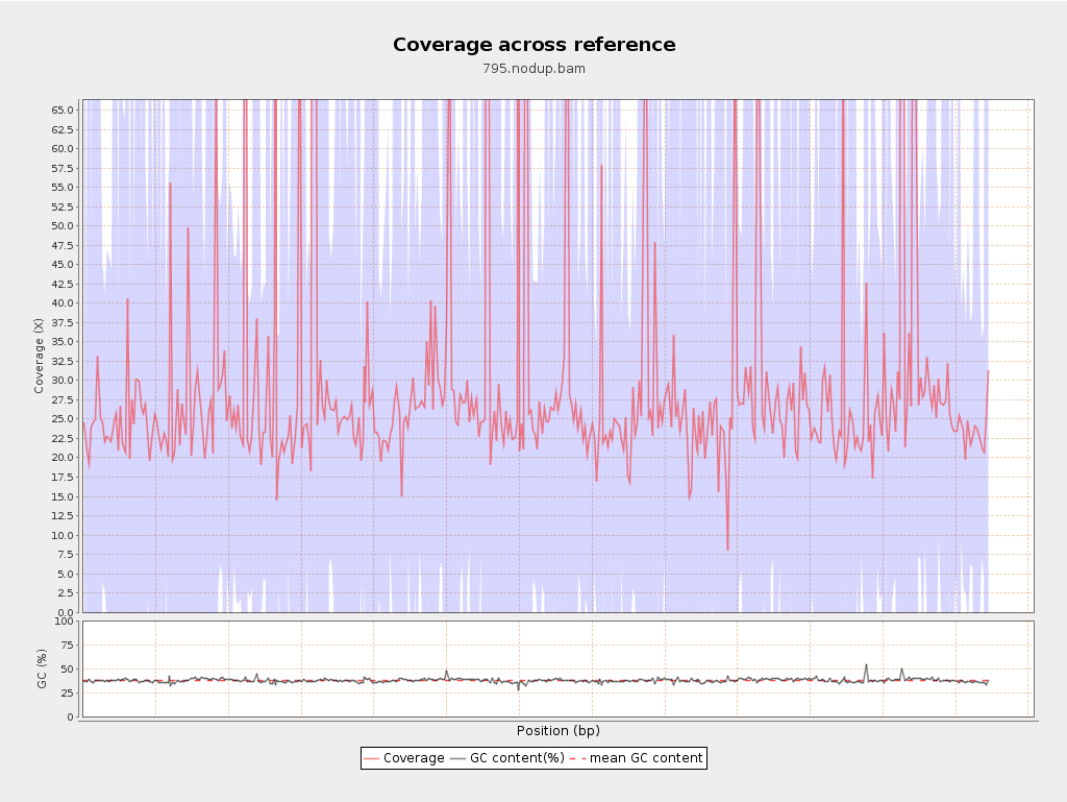
General error rate	2.37%
Mismatches	200,724,830
Insertions	6,698,744
Mapped reads with at least one insertion	8.85%
Deletions	6,410,744
Mapped reads with at least one deletion	8.46%
Homopolymer indels	57.79%

2.7. Chromosome stats

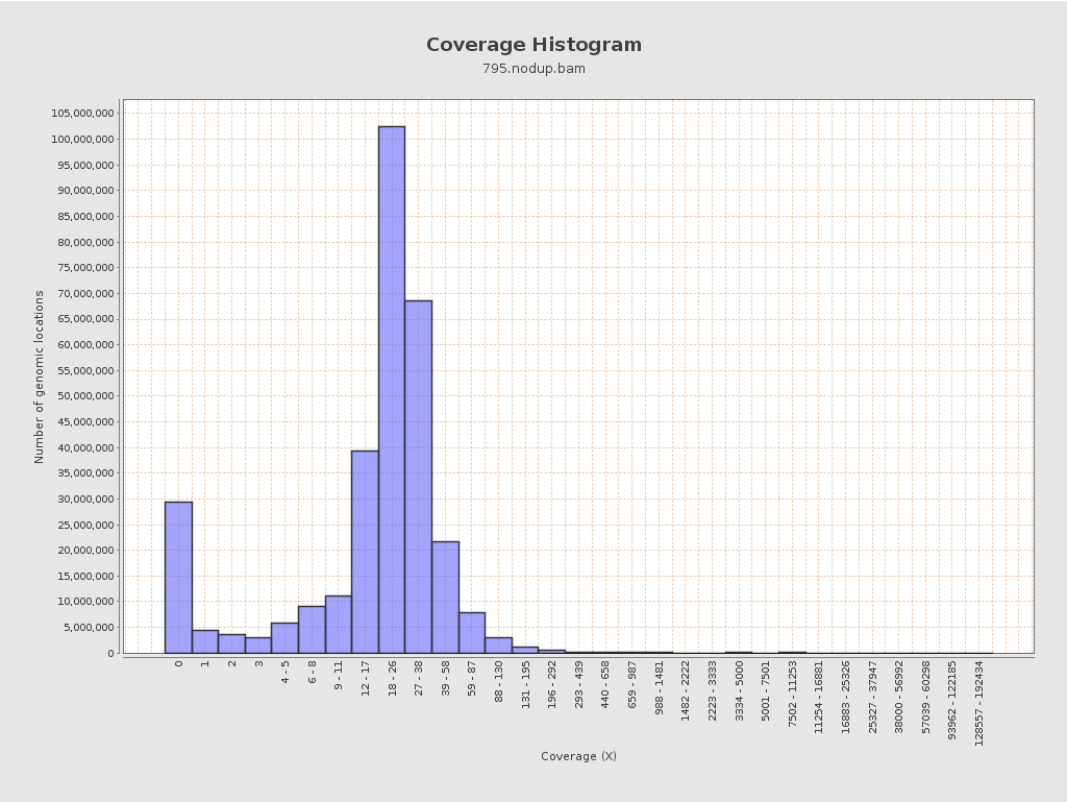
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	727890158	24.488	106.6717

LT669789.1	36598175	1115397665	30.4769	293.0288
LT669790.1	30422129	1081601757	35.5531	382.3754
LT669791.1	52758100	1556236522	29.4976	292.9306
LT669792.1	28376109	861156867	30.348	278.1363
LT669793.1	33388210	918681417	27.5151	178.7169
LT669794.1	50579949	1429601253	28.2642	221.7768
LT669795.1	49795044	1586639488	31.8634	265.0593

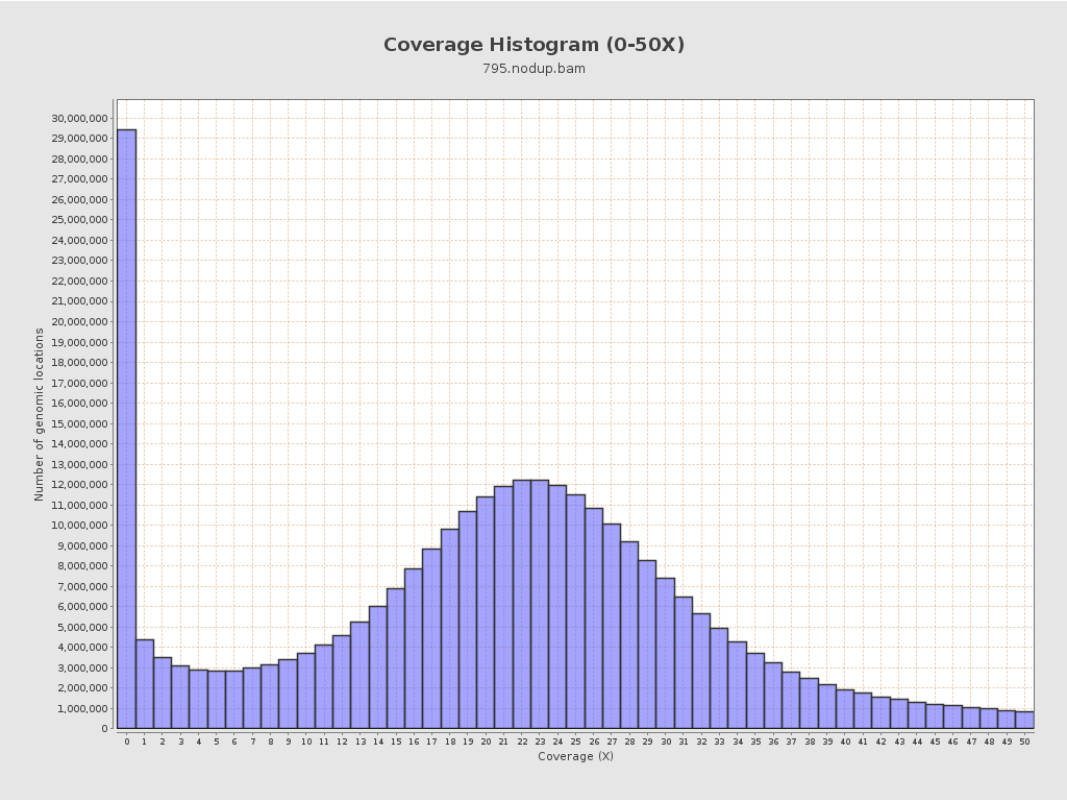
3. Results : Coverage across reference



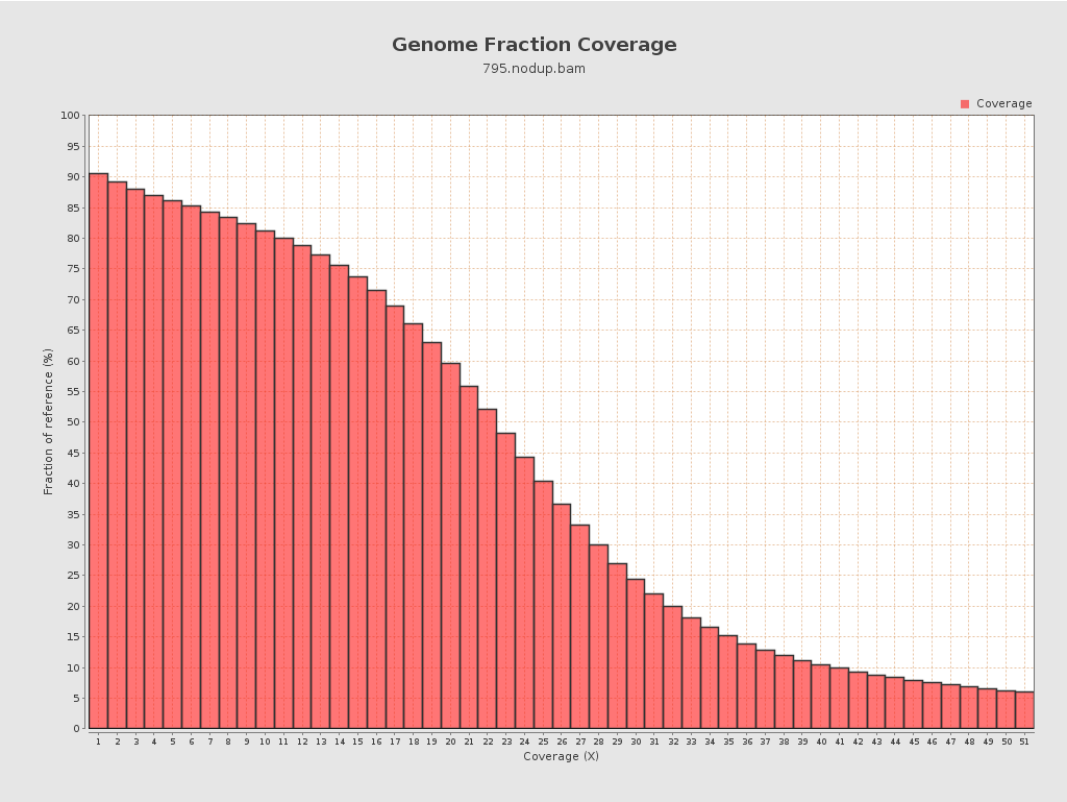
4. Results : Coverage Histogram



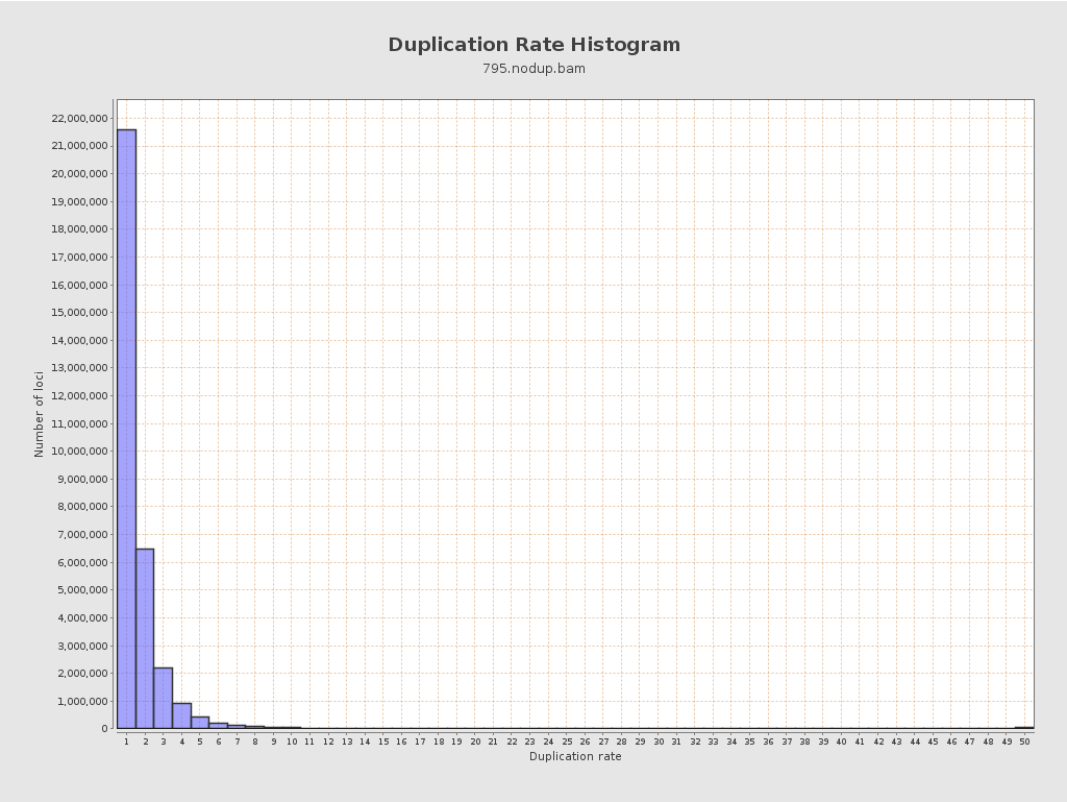
5. Results : Coverage Histogram (0-50X)



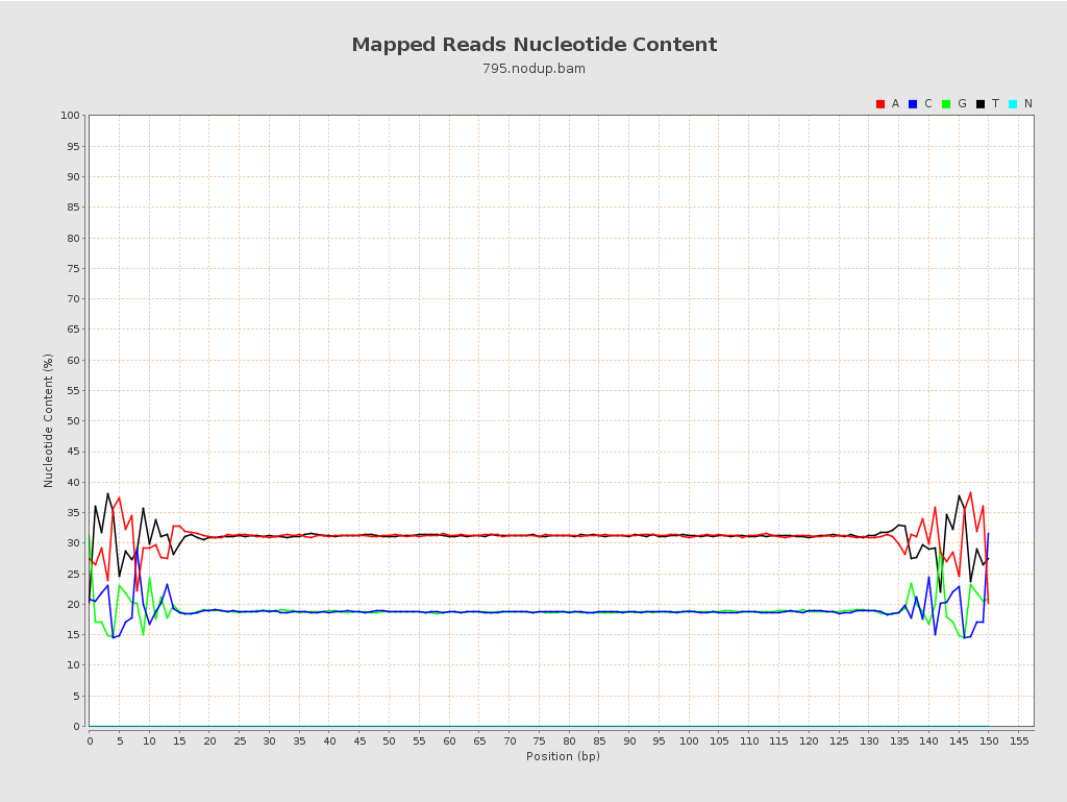
6. Results : Genome Fraction Coverage



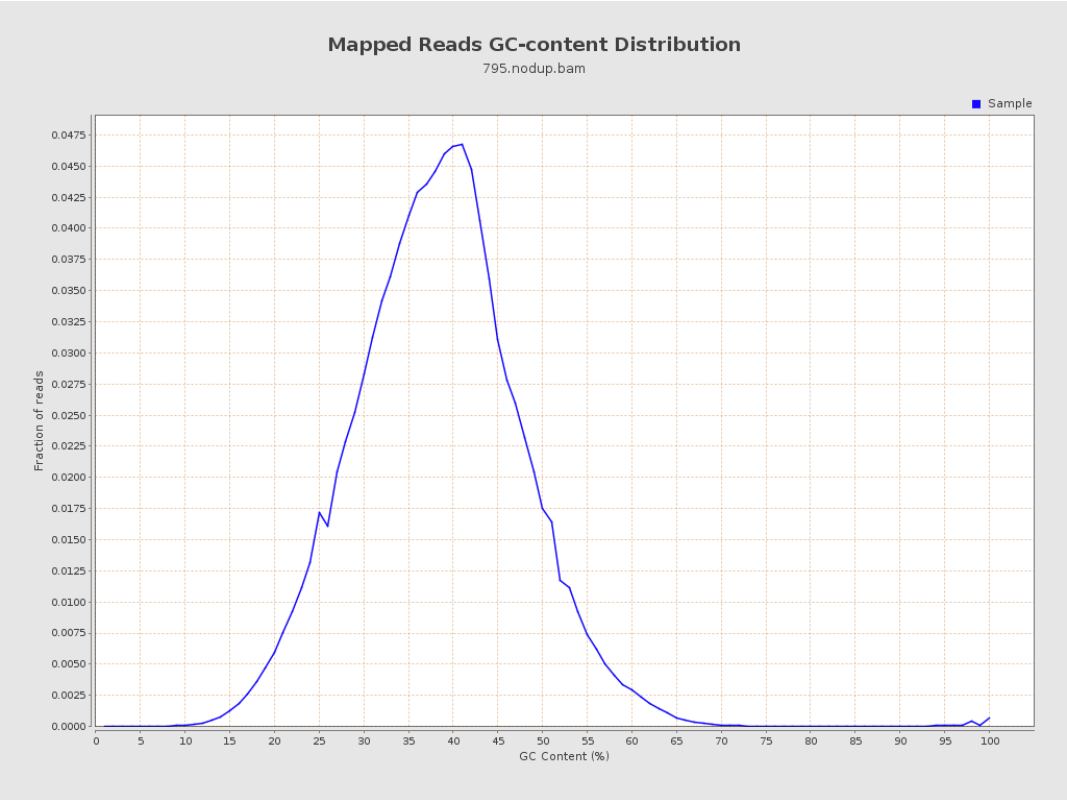
7. Results : Duplication Rate Histogram



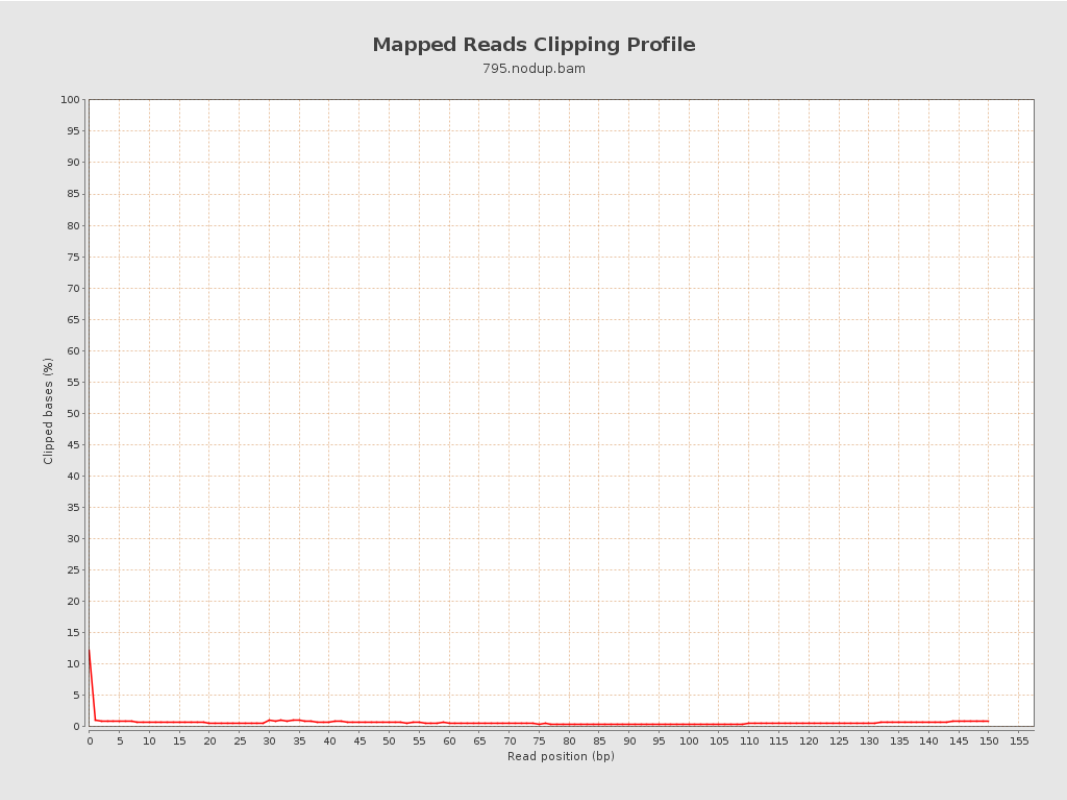
8. Results : Mapped Reads Nucleotide Content



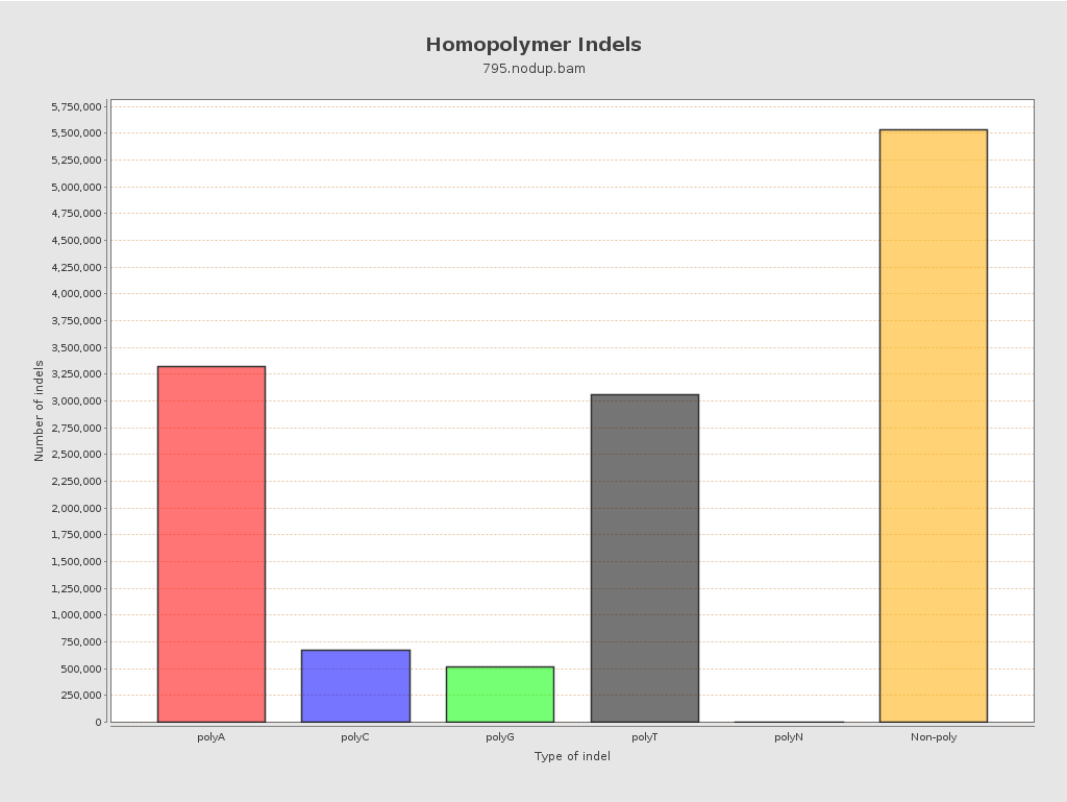
9. Results : Mapped Reads GC-content Distribution



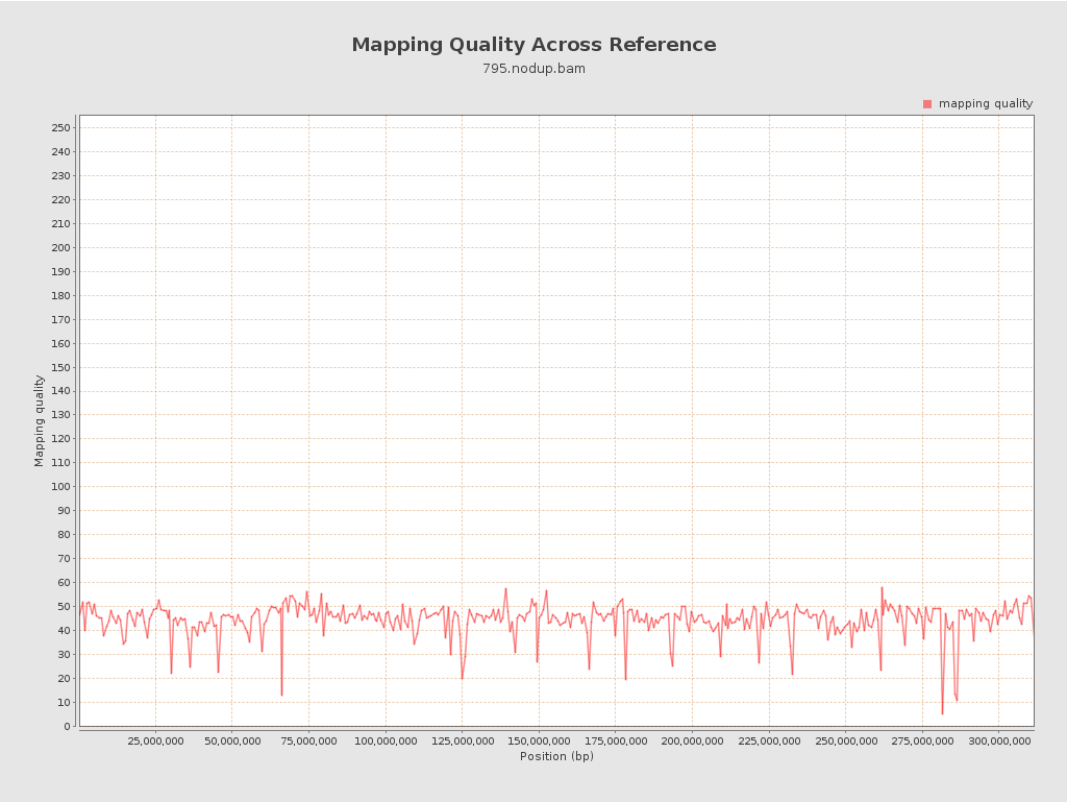
10. Results : Mapped Reads Clipping Profile



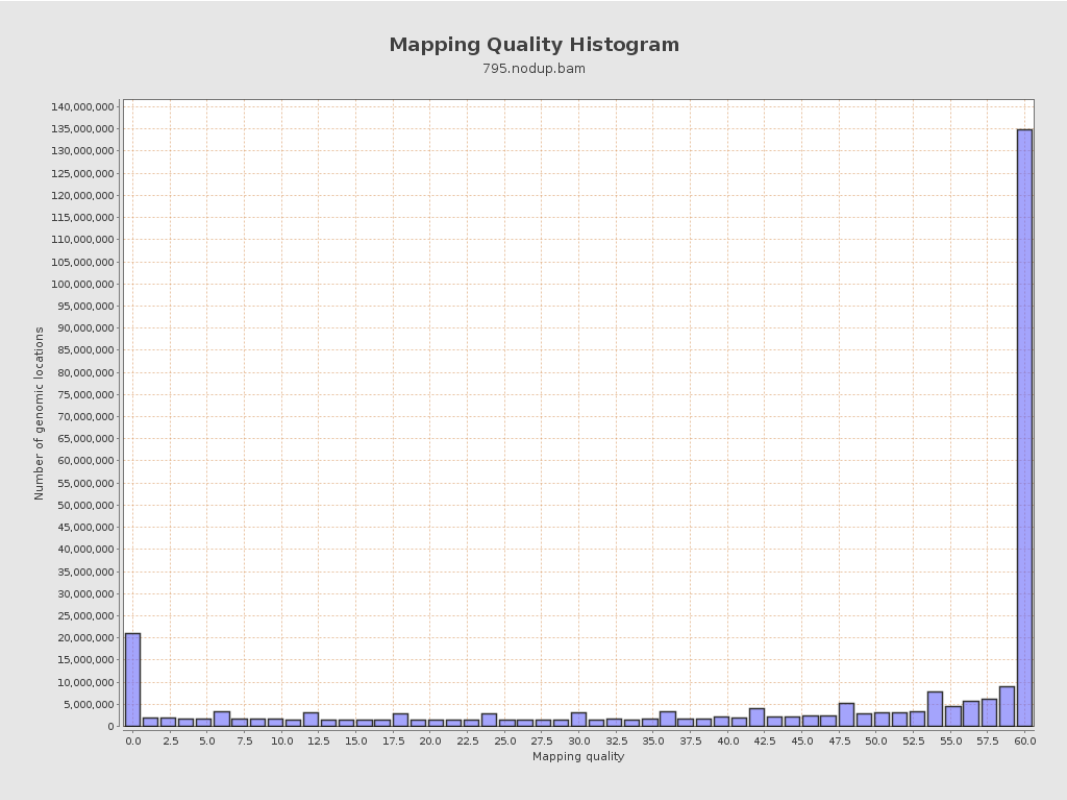
11. Results : Homopolymer Indels



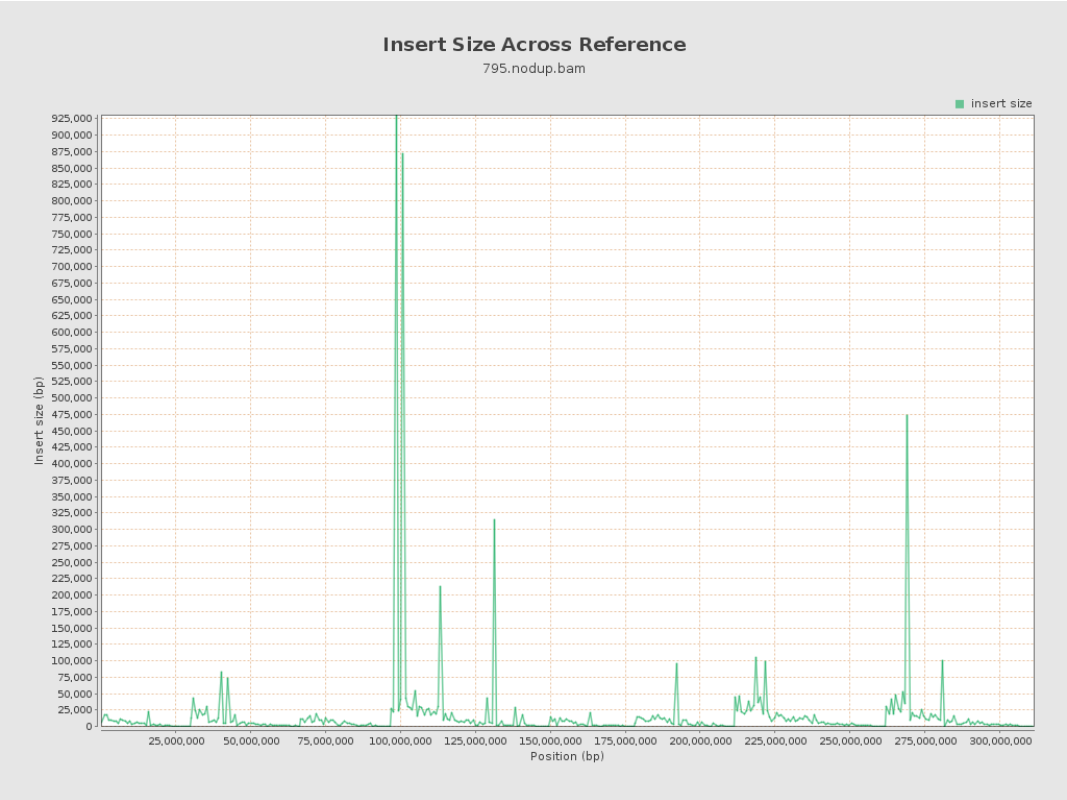
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram