Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:38:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/799.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/799.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_259/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_259_S340_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_259/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_259_S340_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:38:15 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	83,764,850
Mapped reads	78,039,847 / 93.17%
Unmapped reads	5,725,003 / 6.83%
Mapped paired reads	78,039,847 / 93.17%
Mapped reads, first in pair	39,091,460 / 46.67%
Mapped reads, second in pair	38,948,387 / 46.5%
Mapped reads, both in pair	76,252,518 / 91.03%
Mapped reads, singletons	1,787,329 / 2.13%
Read min/max/mean length	30 / 151 / 148.07
Duplicated reads (flagged)	13,154,330 / 15.7%
Clipped reads	18,384,876 / 21.95%

2.2. ACGT Content

Number/percentage of A's	3,315,362,274 / 30.84%
Number/percentage of C's	2,059,263,295 / 19.15%
Number/percentage of T's	3,320,864,208 / 30.89%
Number/percentage of G's	2,055,484,928 / 19.12%
Number/percentage of N's	39,617 / 0%
GC Percentage	38.27%

2.3. Coverage

Mean	34.5868
Standard Deviation	310.2569

2.4. Mapping Quality

Mean Mapping Quality	44.17

2.5. Insert size

Mean	229,381.83
Standard Deviation	2,280,509.51
P25/Median/P75	307 / 406 / 532

2.6. Mismatches and indels

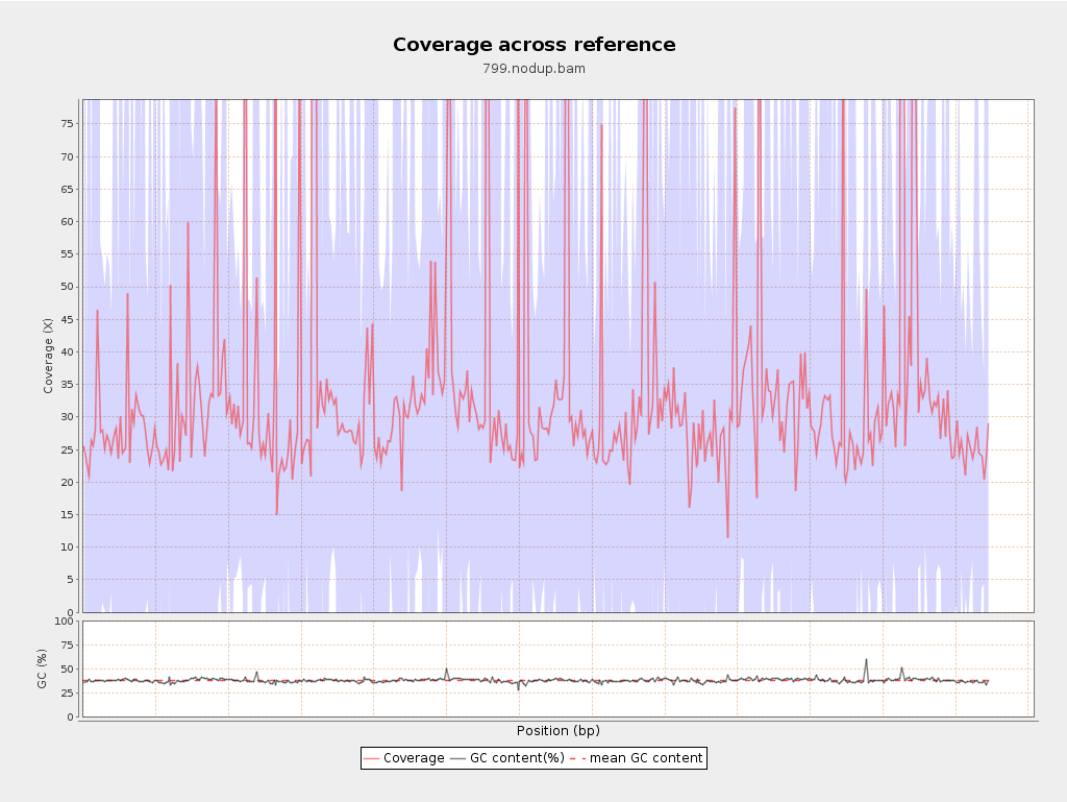
General error rate	2.37%
Mismatches	234,586,663
Insertions	7,485,863
Mapped reads with at least one insertion	8.6%
Deletions	7,396,409
Mapped reads with at least one deletion	8.42%
Homopolymer indels	56.57%

2.7. Chromosome stats

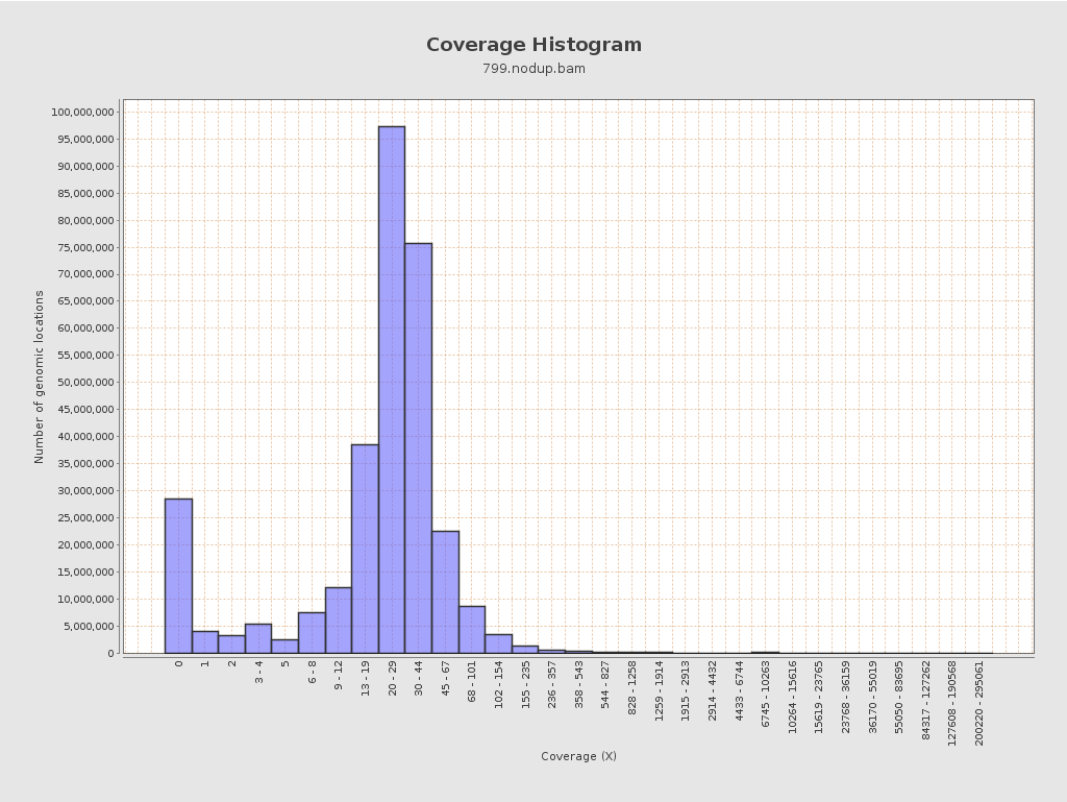
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	816208710	27.4593	97.8072

LT669789.1	36598175	1282105811	35.032	316.2727
LT669790.1	30422129	1163951272	38.26	360.9843
LT669791.1	52758100	1832015969	34.7248	290.9169
LT669792.1	28376109	978124568	34.47	377.204
LT669793.1	33388210	1077372141	32.268	218.5565
LT669794.1	50579949	1667982604	32.9772	269.3517
LT669795.1	49795044	1960931653	39.3801	408.7271

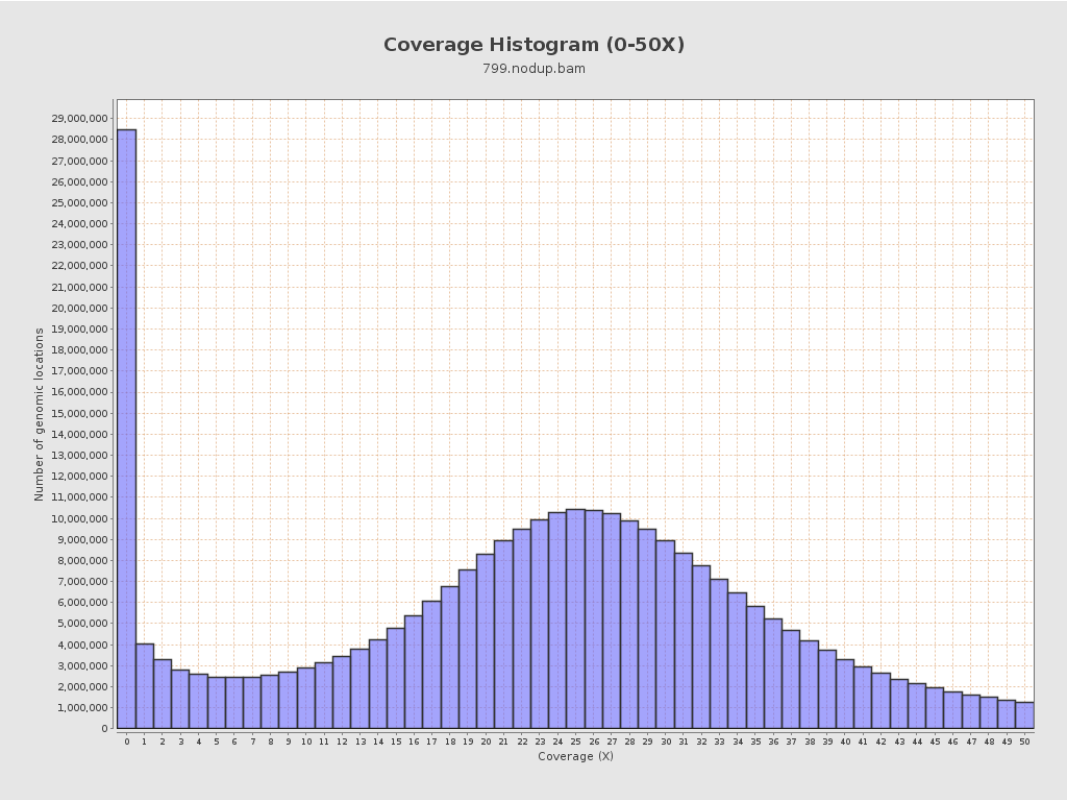
3. Results : Coverage across reference



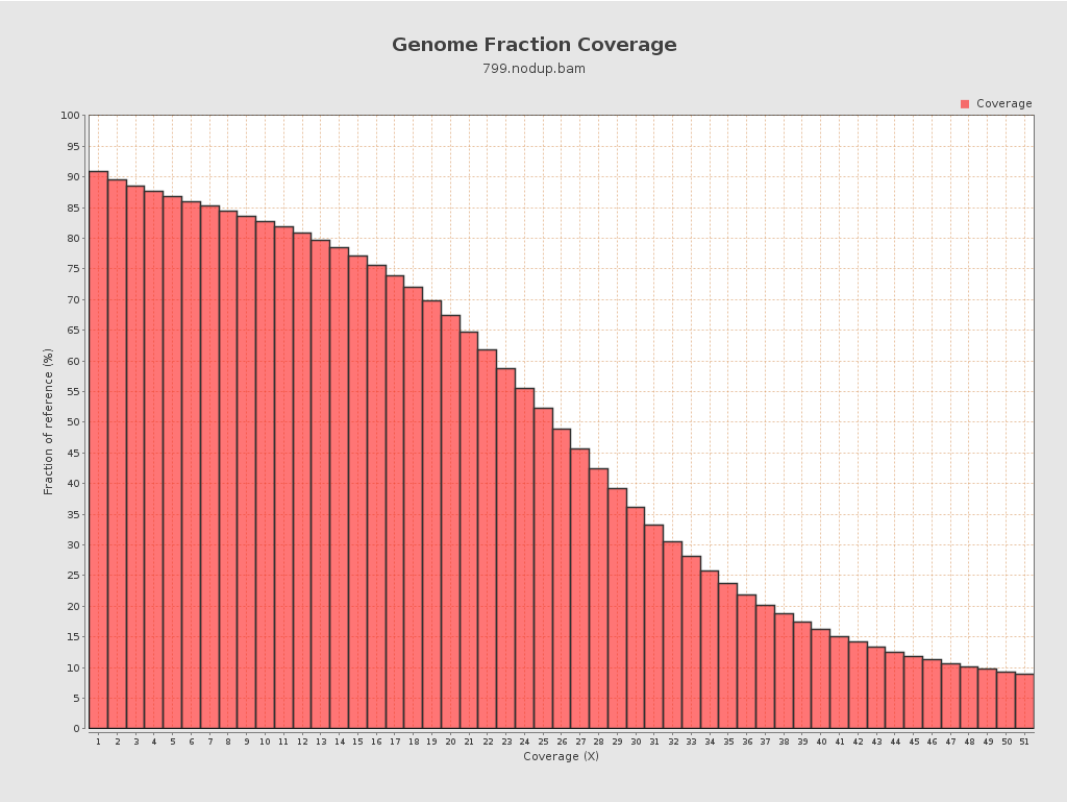
4. Results : Coverage Histogram



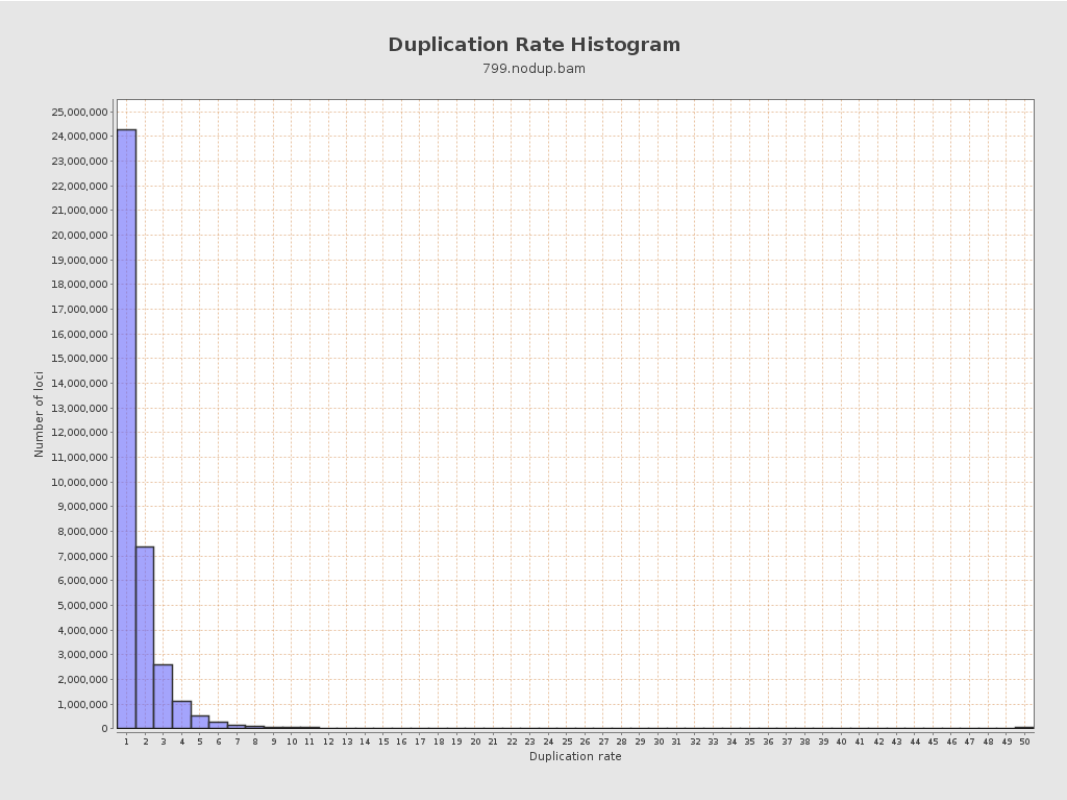
5. Results : Coverage Histogram (0-50X)



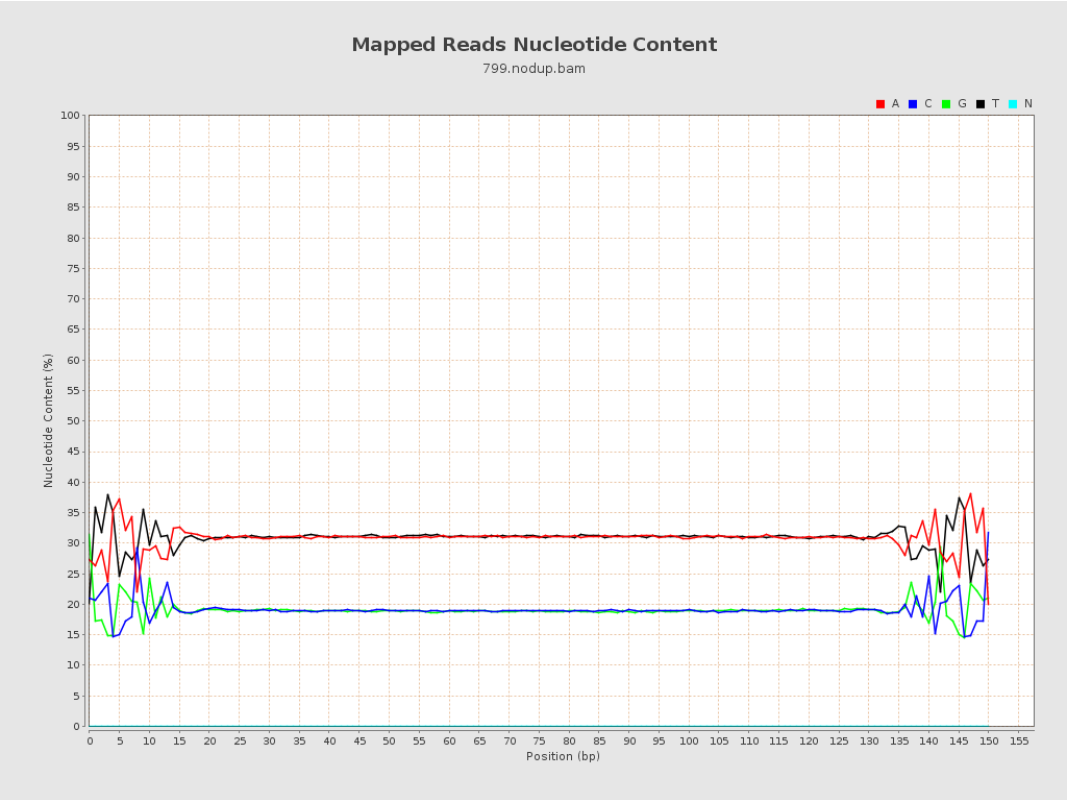
6. Results : Genome Fraction Coverage



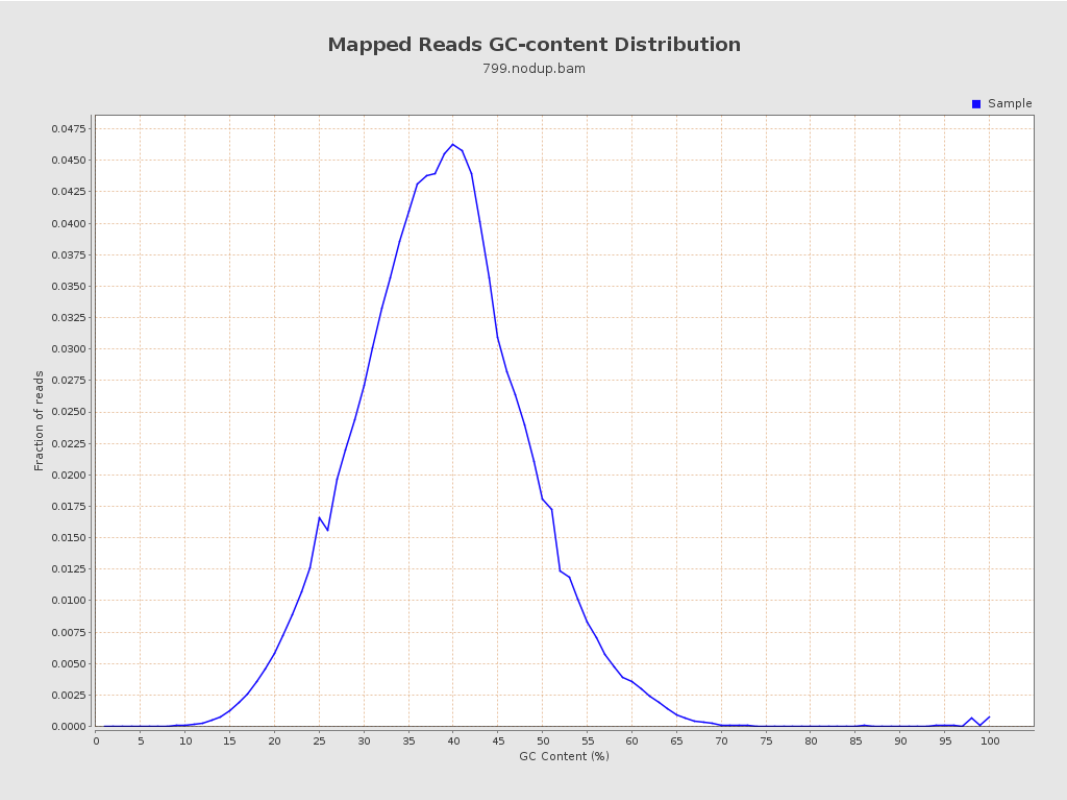
7. Results : Duplication Rate Histogram



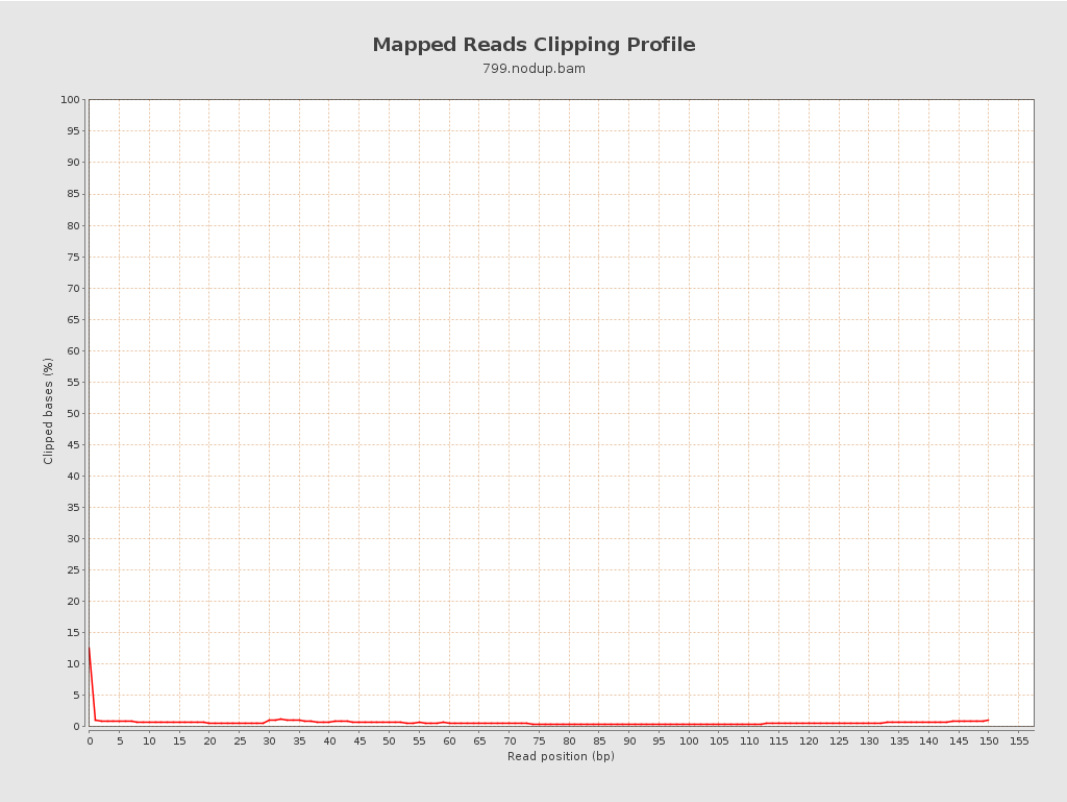
8. Results : Mapped Reads Nucleotide Content



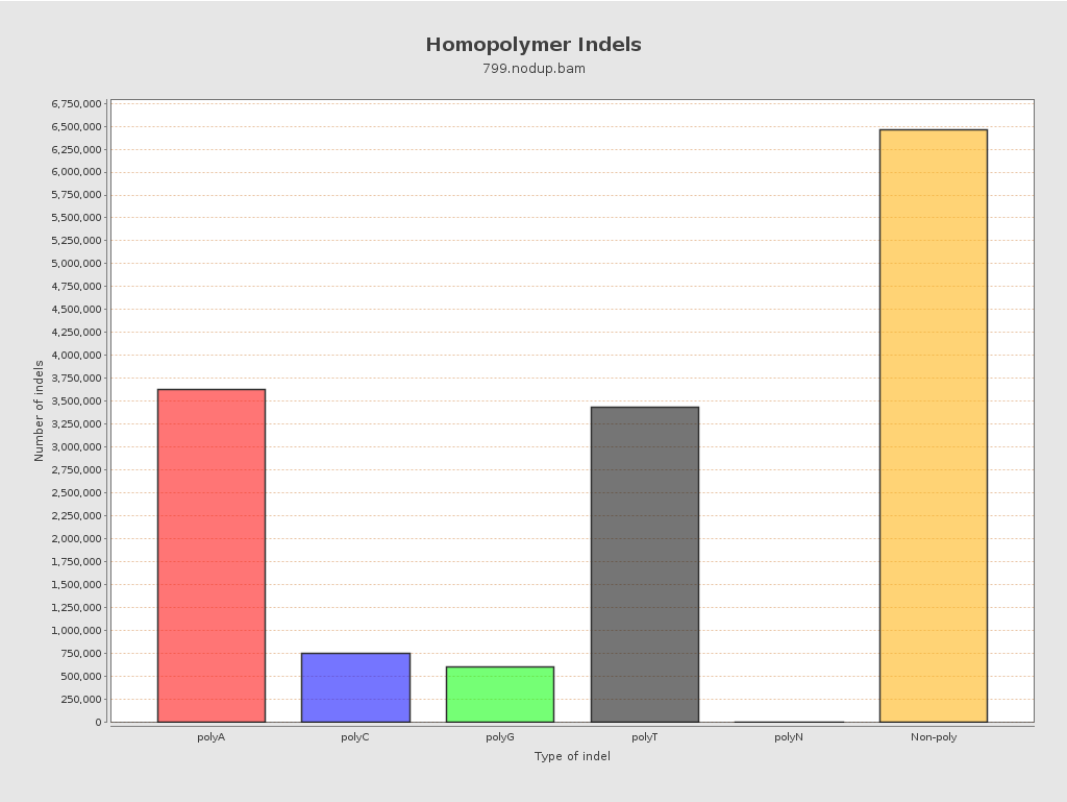
9. Results : Mapped Reads GC-content Distribution



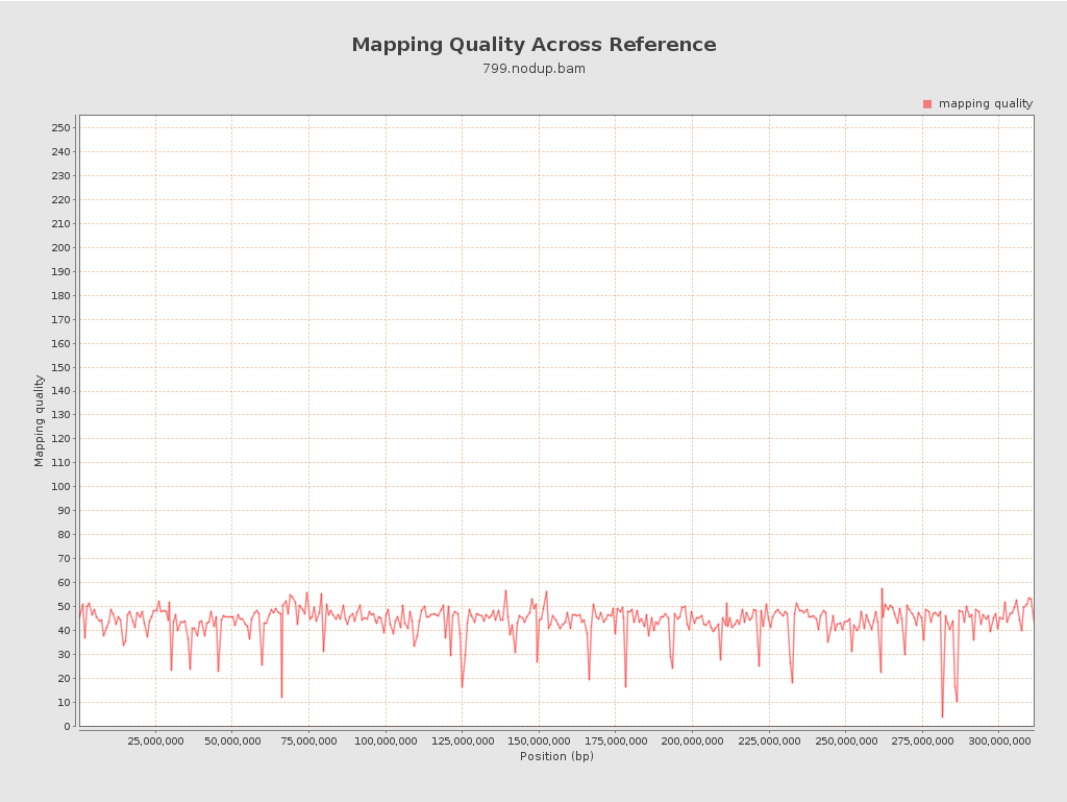
10. Results : Mapped Reads Clipping Profile



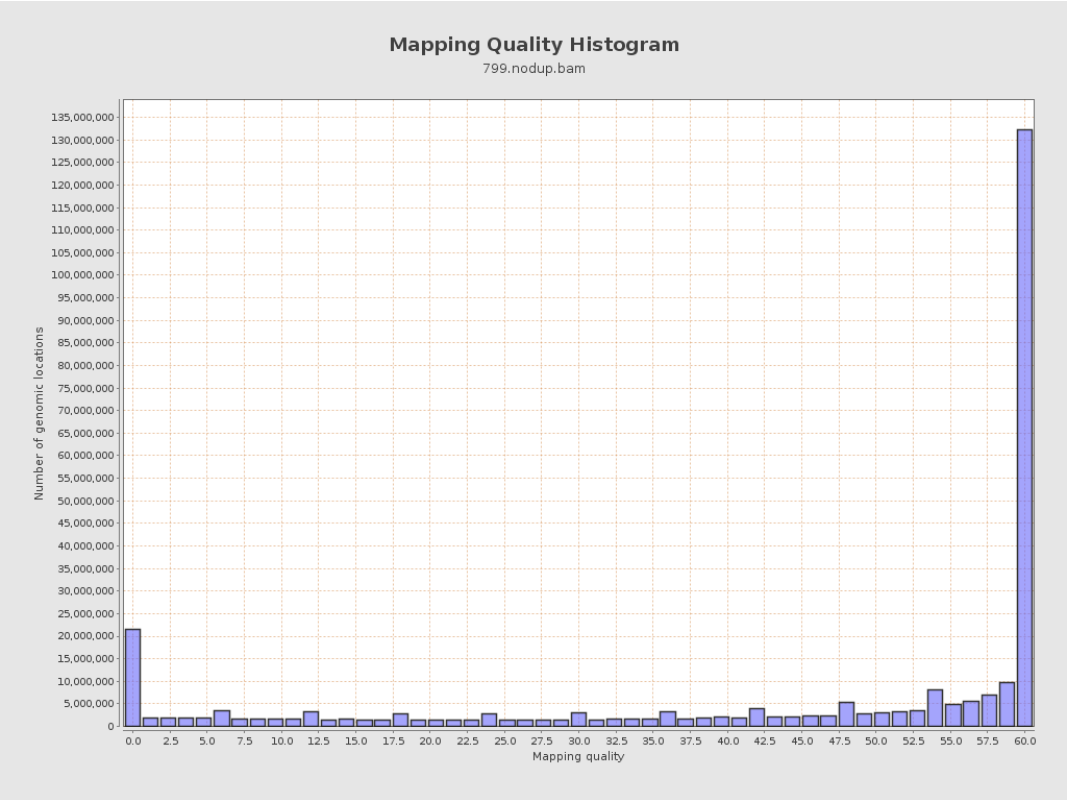
11. Results : Homopolymer Indels



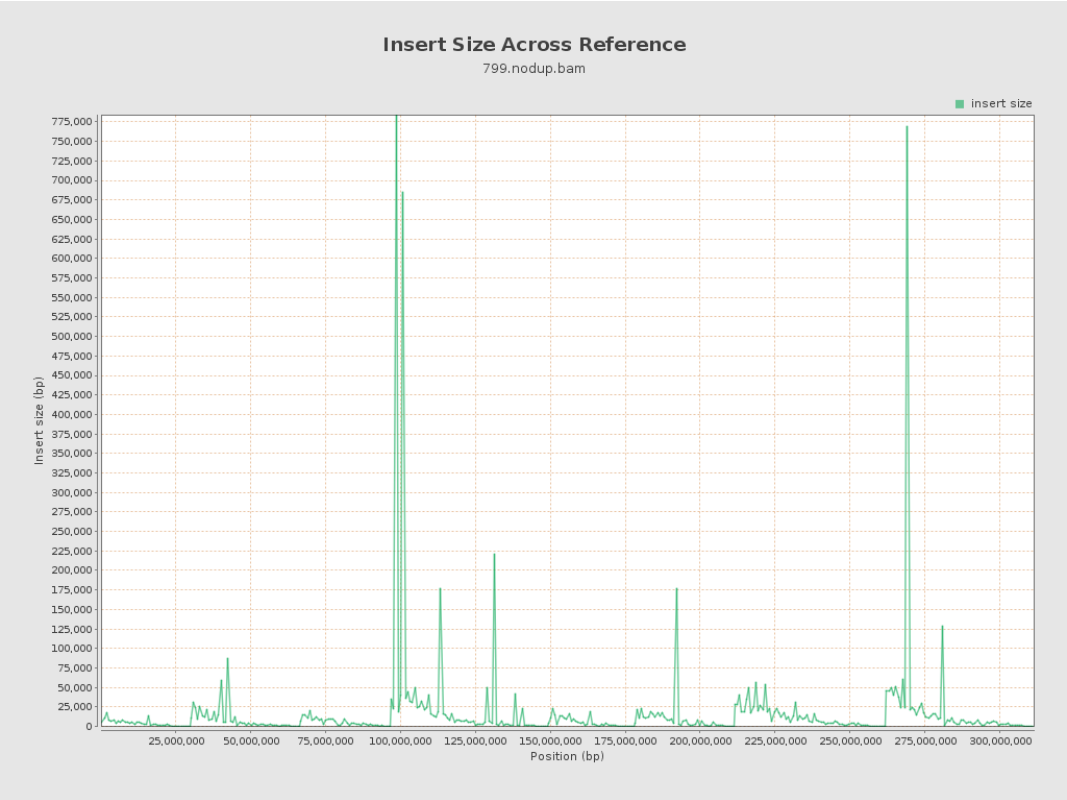
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram