Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:41:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/711.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/711.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_264/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_264_S345_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_264/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_264_S345_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:41:23 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	101,575,760
Mapped reads	92,242,356 / 90.81%
Unmapped reads	9,333,404 / 9.19%
Mapped paired reads	92,242,356 / 90.81%
Mapped reads, first in pair	46,222,312 / 45.51%
Mapped reads, second in pair	46,020,044 / 45.31%
Mapped reads, both in pair	89,343,702 / 87.96%
Mapped reads, singletons	2,898,654 / 2.85%
Read min/max/mean length	30 / 151 / 147.99
Duplicated reads (flagged)	17,494,560 / 17.22%
Clipped reads	23,281,089 / 22.92%

2.2. ACGT Content

Number/percentage of A's	3,871,225,119 / 30.88%
Number/percentage of C's	2,393,814,504 / 19.09%
Number/percentage of T's	3,881,640,390 / 30.96%
Number/percentage of G's	2,390,224,199 / 19.07%
Number/percentage of N's	47,137 / 0%
GC Percentage	38.16%

2.3. Coverage

Mean	40.332
Standard Deviation	413.9148

2.4. Mapping Quality

Mean Mapping Quality	44.36

2.5. Insert size

Mean	245,930.48
Standard Deviation	2,385,275.35
P25/Median/P75	296 / 394 / 518

2.6. Mismatches and indels

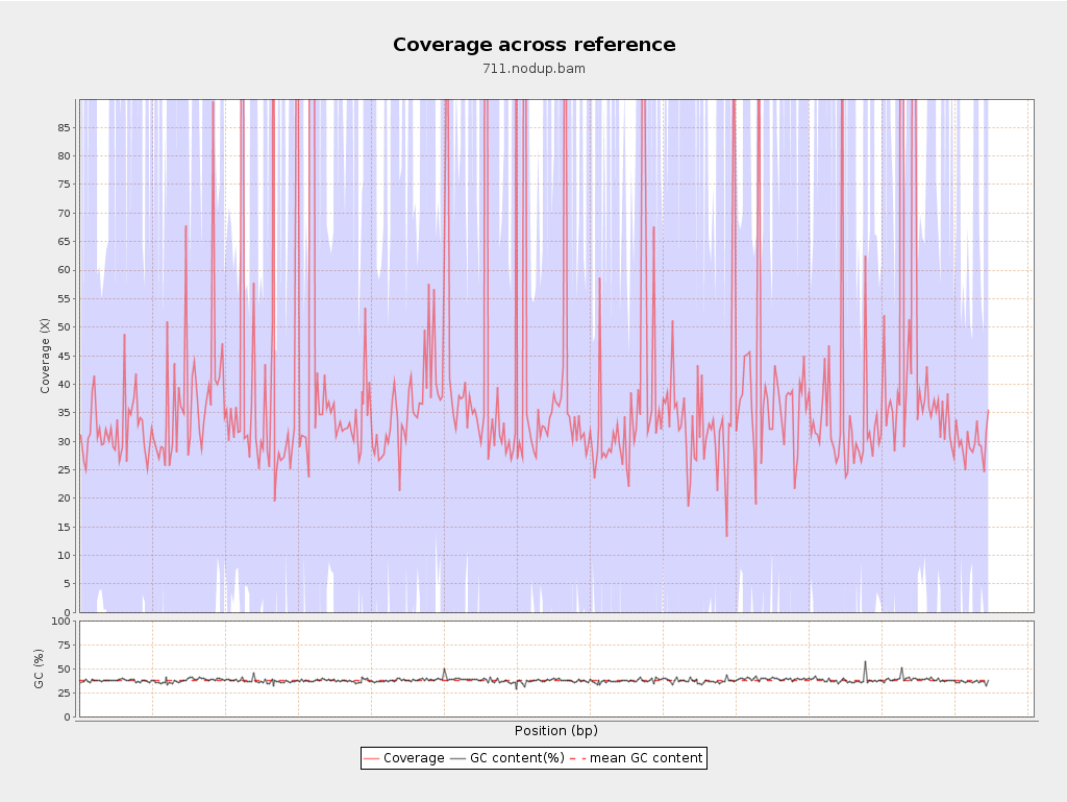
General error rate	2.37%
Mismatches	270,939,054
Insertions	9,322,796
Mapped reads with at least one insertion	8.99%
Deletions	8,702,718
Mapped reads with at least one deletion	8.38%
Homopolymer indels	57.54%

2.7. Chromosome stats

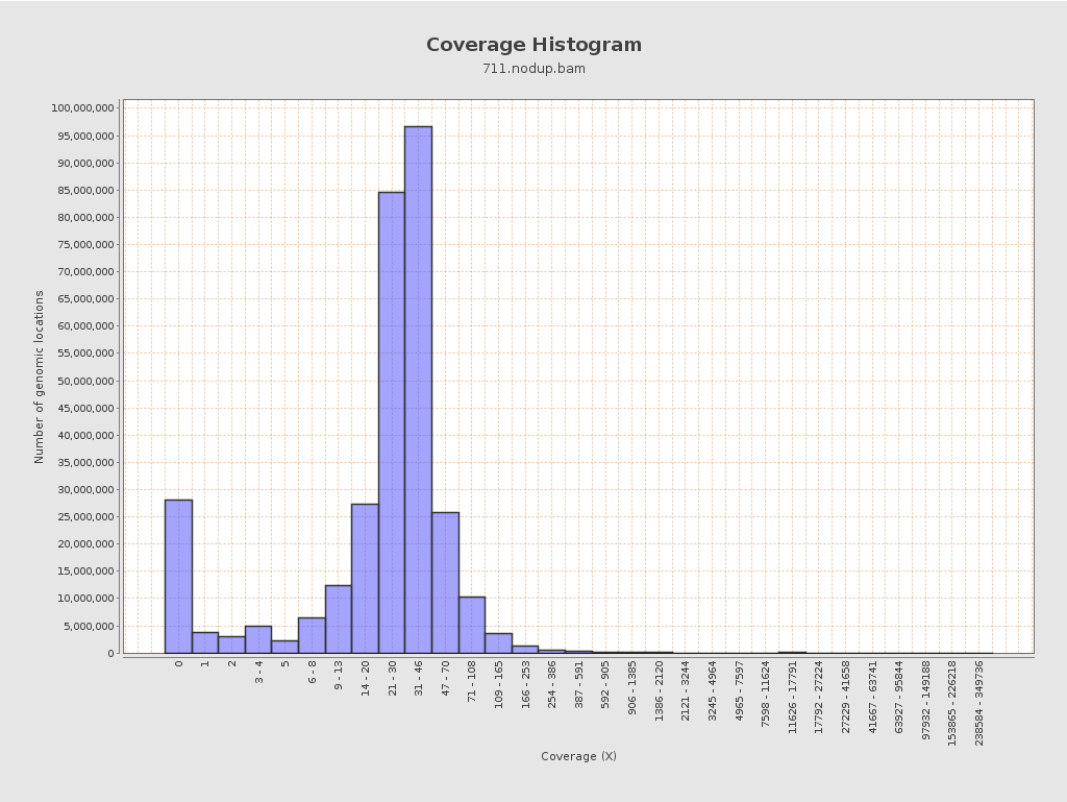
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	937613310	31.5436	172.1373

LT669789.1	36598175	1503934122	41.0931	425.7552
LT669790.1	30422129	1512607741	49.7206	601.3922
LT669791.1	52758100	2111306341	40.0186	427.6898
LT669792.1	28376109	1149806793	40.5202	438.4871
LT669793.1	33388210	1216211221	36.4264	263.8928
LT669794.1	50579949	1906669295	37.6961	319.8298
LT669795.1	49795044	2231006170	44.8038	496.2424

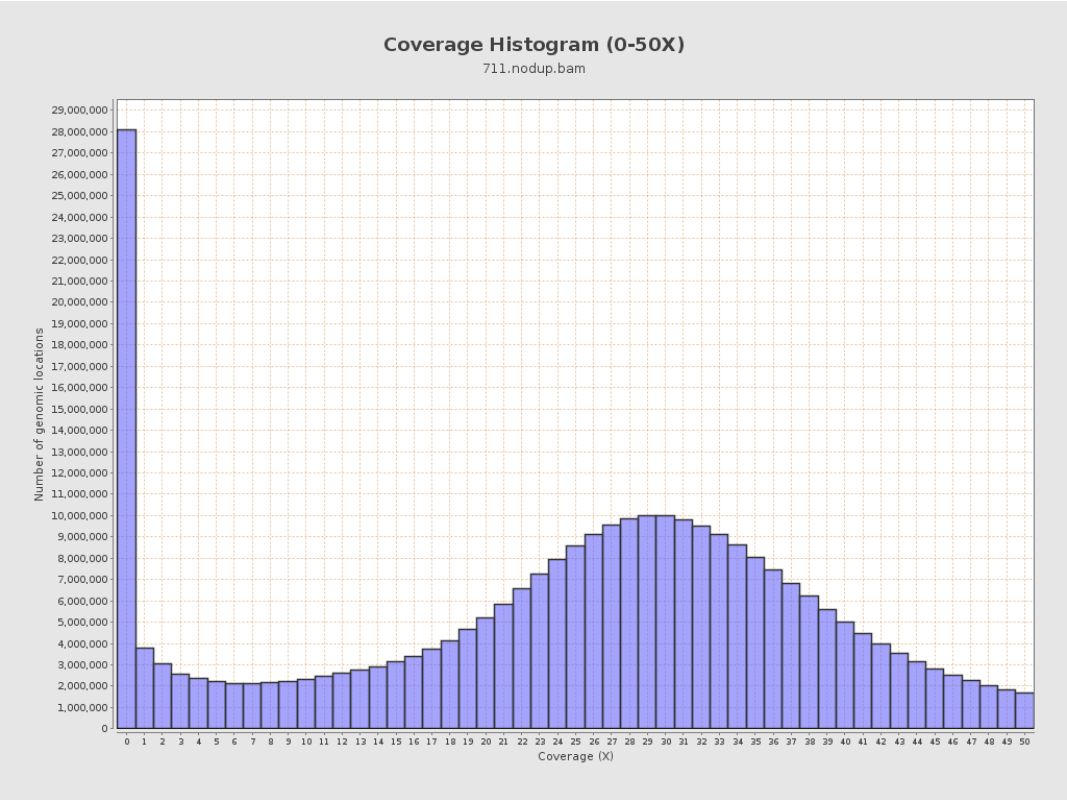
3. Results : Coverage across reference



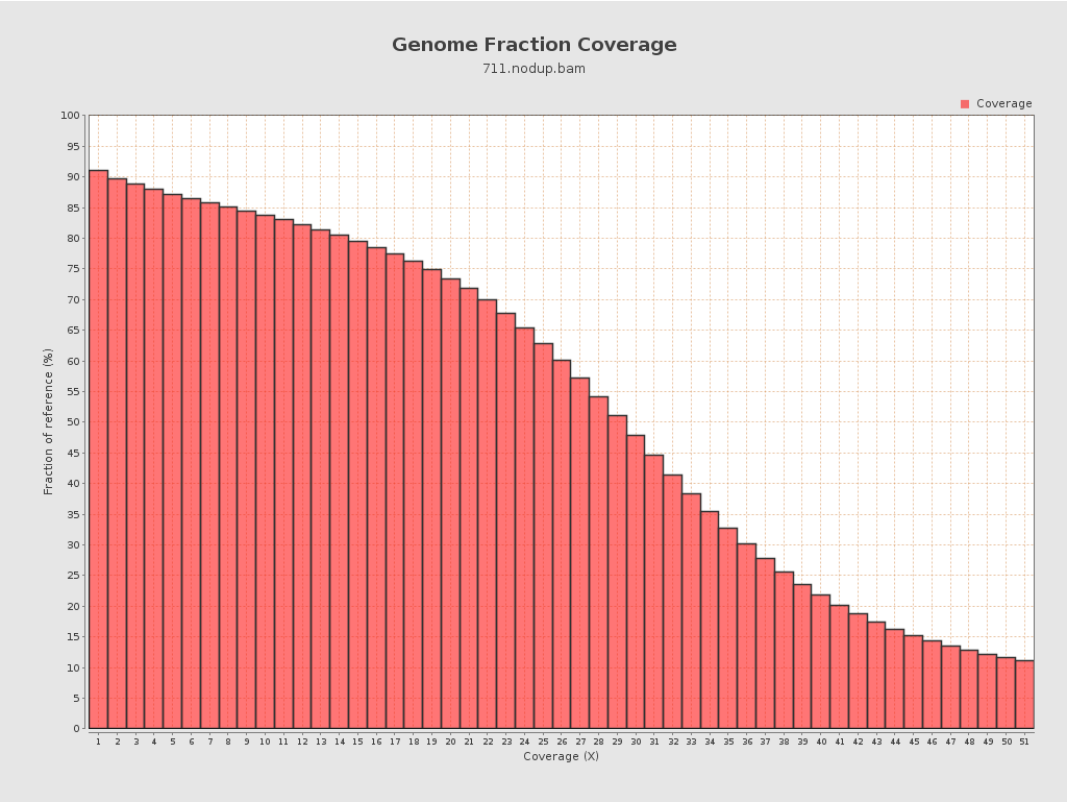
4. Results : Coverage Histogram



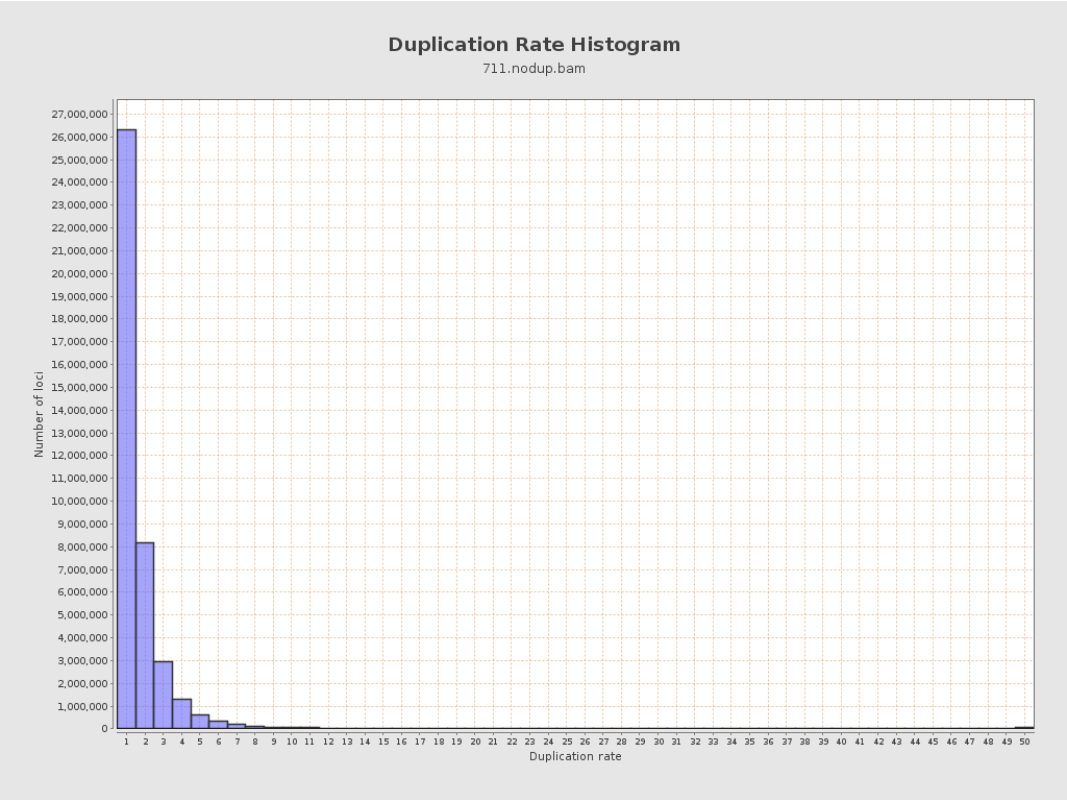
5. Results : Coverage Histogram (0-50X)



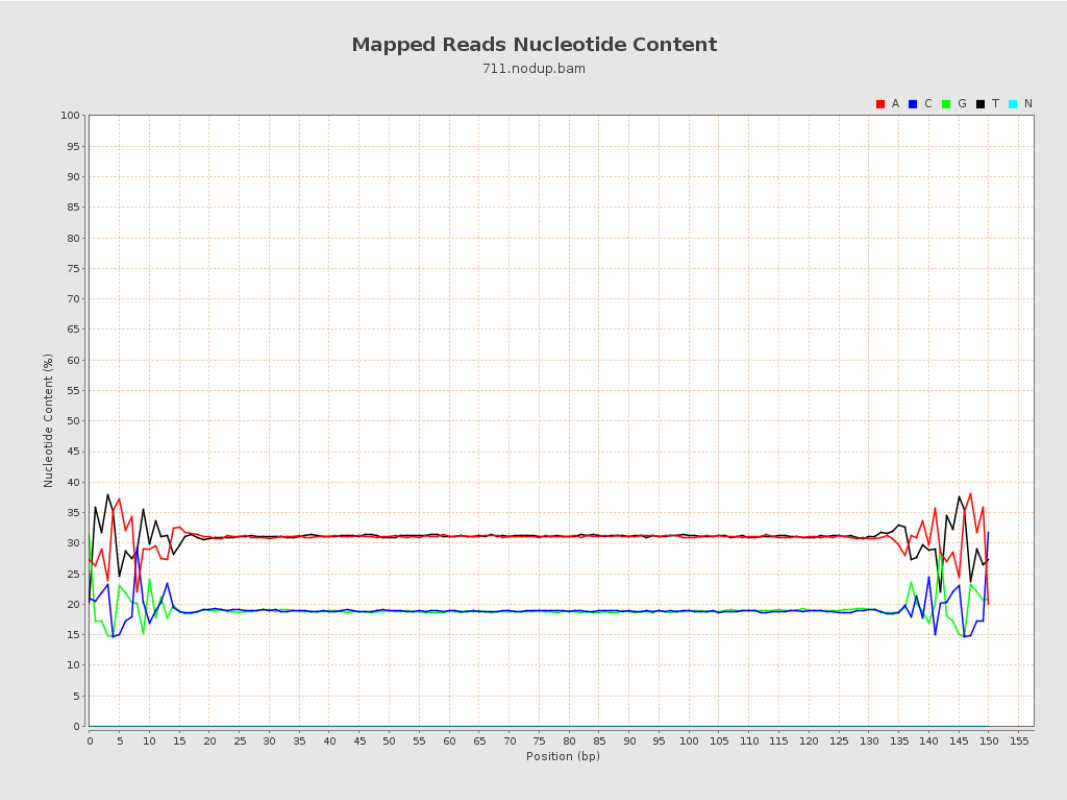
6. Results : Genome Fraction Coverage



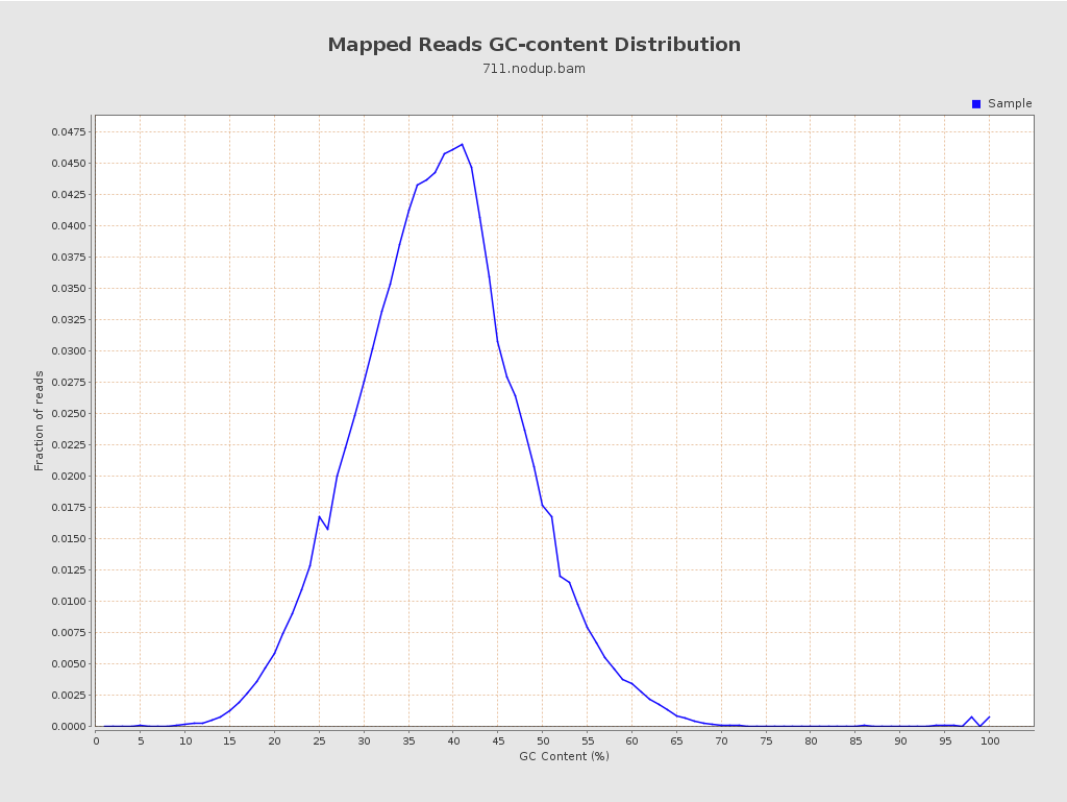
7. Results : Duplication Rate Histogram



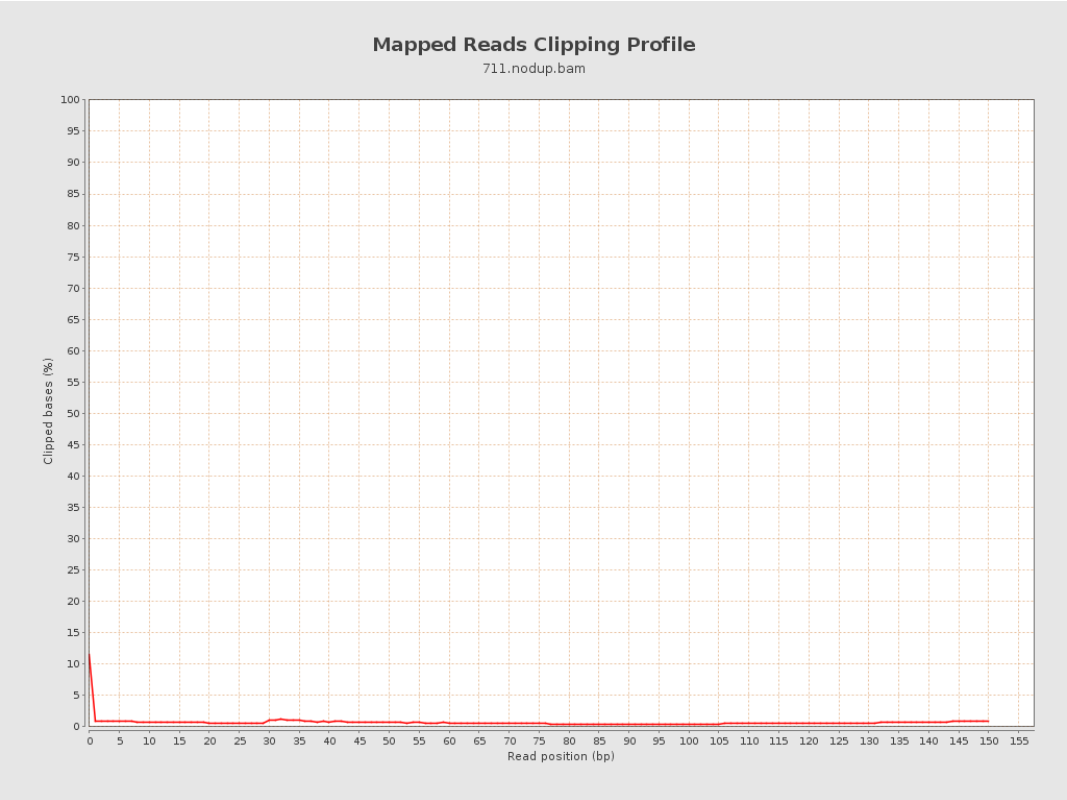
8. Results : Mapped Reads Nucleotide Content



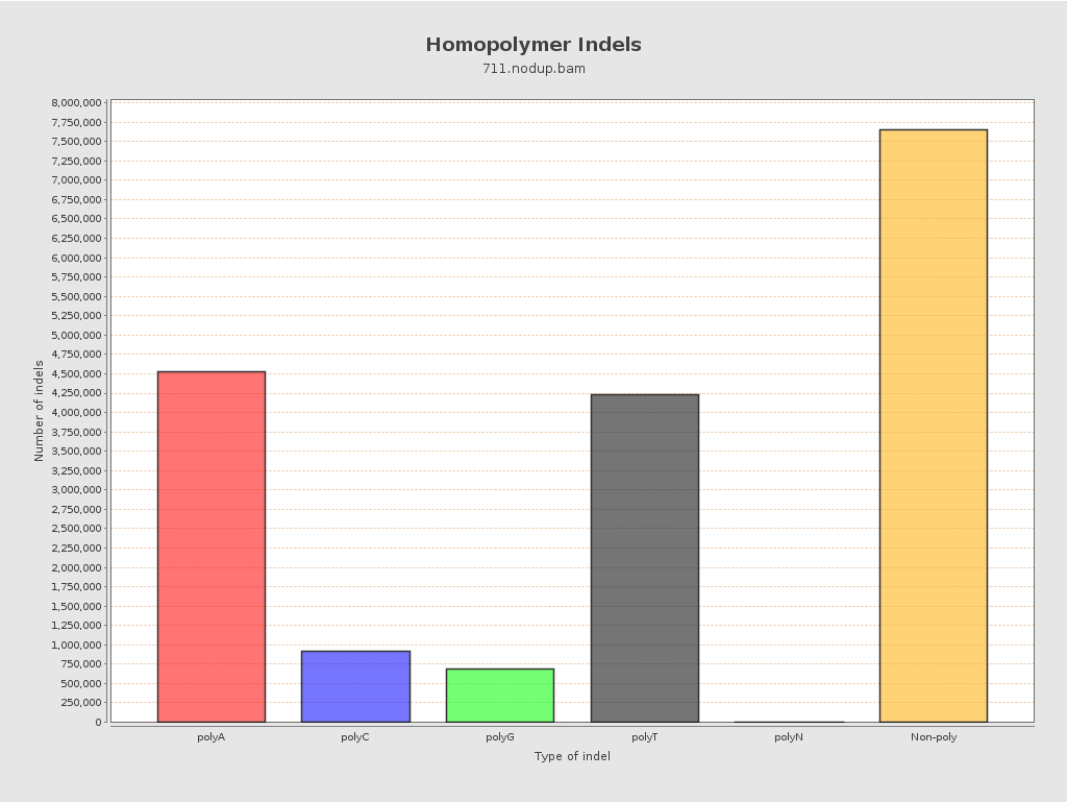
9. Results : Mapped Reads GC-content Distribution



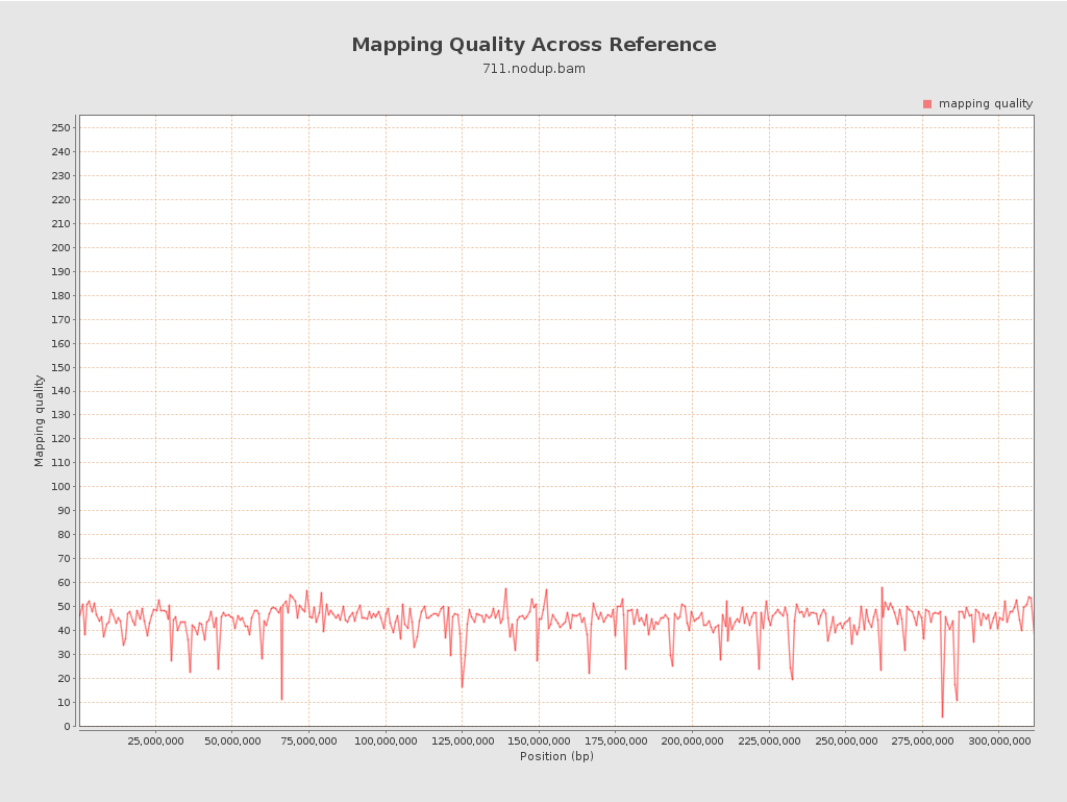
10. Results : Mapped Reads Clipping Profile



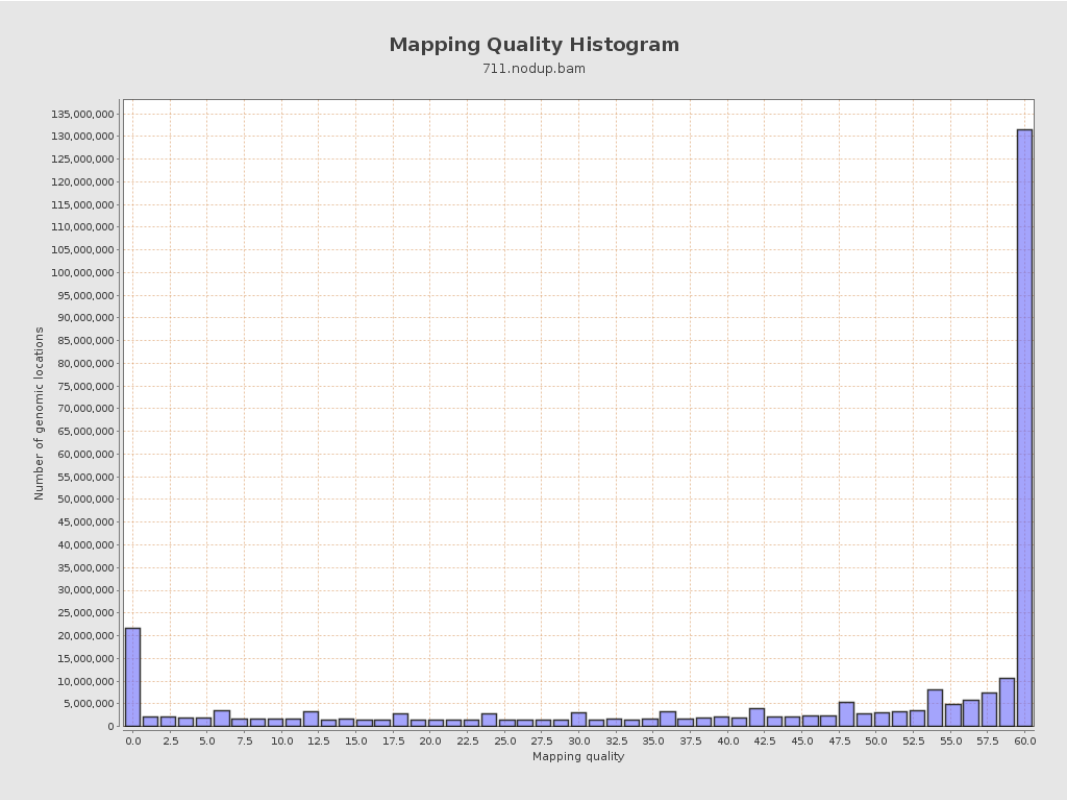
11. Results : Homopolymer Indels



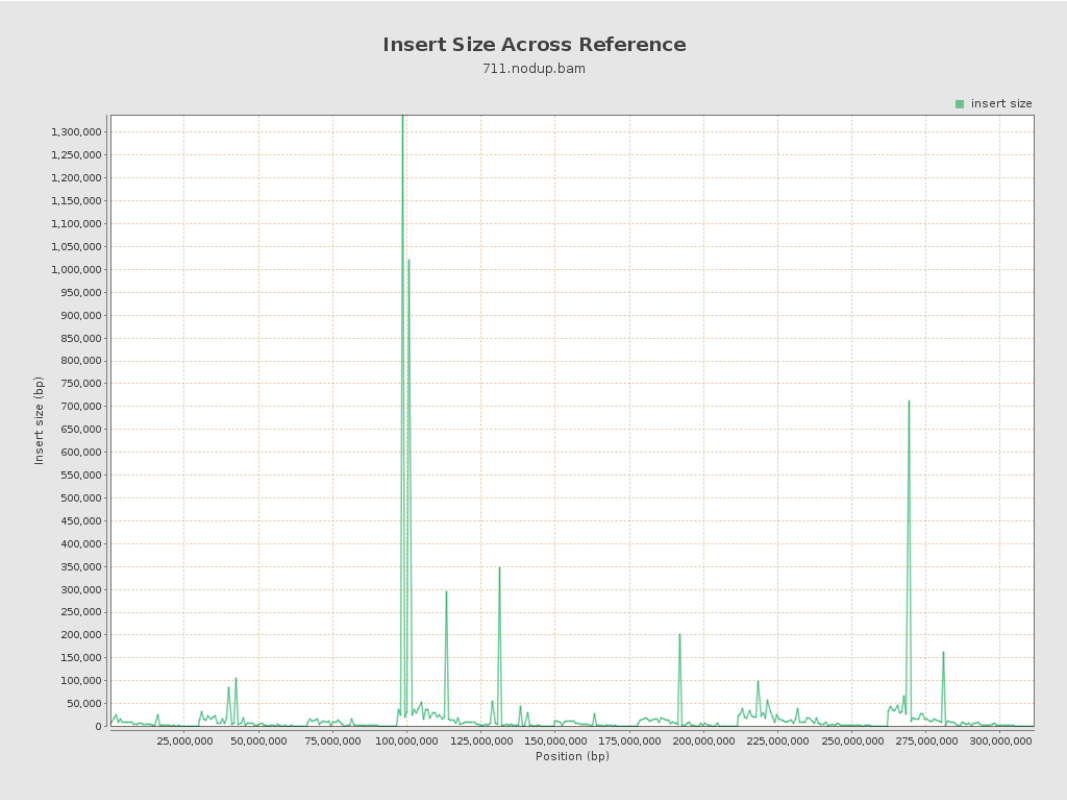
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram