Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:26:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/960.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/960.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_493/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_493_S468_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_493/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_493_S468_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:26:15 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	50,204,819
Mapped reads	47,591,923 / 94.8%
Unmapped reads	2,612,896 / 5.2%
Mapped paired reads	47,591,923 / 94.8%
Mapped reads, first in pair	23,858,214 / 47.52%
Mapped reads, second in pair	23,733,709 / 47.27%
Mapped reads, both in pair	46,651,636 / 92.92%
Mapped reads, singletons	940,287 / 1.87%
Read min/max/mean length	30 / 151 / 148.26
Duplicated reads (flagged)	7,905,805 / 15.75%
Clipped reads	10,192,534 / 20.3%

2.2. ACGT Content

Number/percentage of A's	2,041,147,636 / 30.76%
Number/percentage of C's	1,280,188,914 / 19.29%
Number/percentage of T's	2,043,426,260 / 30.79%
Number/percentage of G's	1,271,576,823 / 19.16%
Number/percentage of N's	23,060 / 0%
GC Percentage	38.45%

2.3. Coverage

Mean	21.3471
Standard Deviation	194.813

2.4. Mapping Quality

Mean Mapping Quality	44.3

2.5. Insert size

Mean	232,219.42
Standard Deviation	2,272,164.29
P25/Median/P75	387 / 506 / 661

2.6. Mismatches and indels

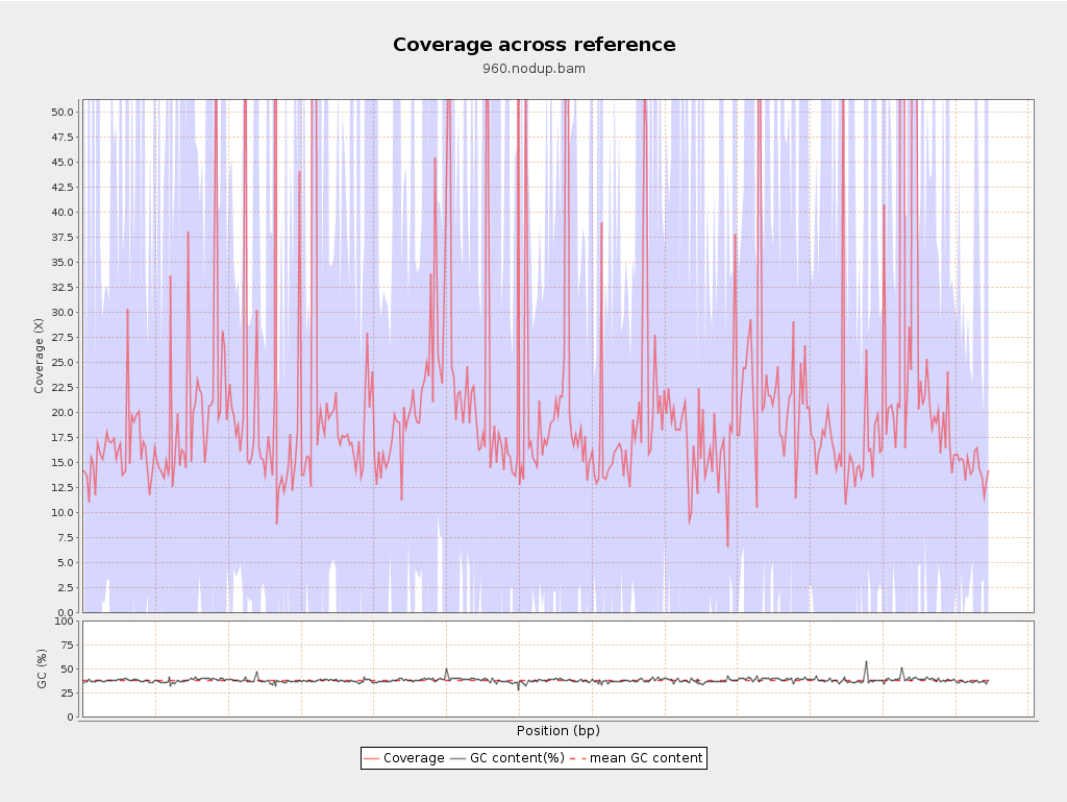
General error rate	2.28%
Mismatches	139,610,957
Insertions	4,271,863
Mapped reads with at least one insertion	8.1%
Deletions	4,371,985
Mapped reads with at least one deletion	8.21%
Homopolymer indels	56.57%

2.7. Chromosome stats

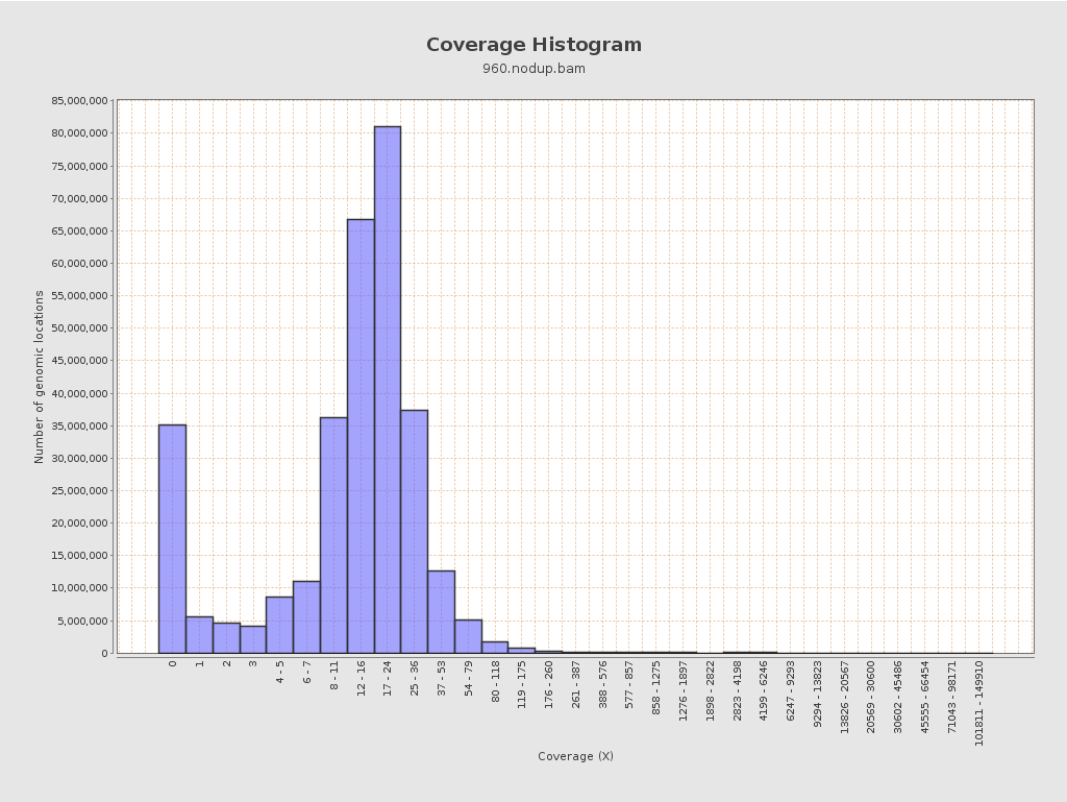
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	474961714	15.9789	42.5993

LT669789.1	36598175	798527078	21.8188	203.5546
LT669790.1	30422129	654381141	21.51	175.3056
LT669791.1	52758100	1136351213	21.5389	141.8706
LT669792.1	28376109	577203499	20.3412	205.0687
LT669793.1	33388210	639225325	19.1452	90.5294
LT669794.1	50579949	1045015080	20.6607	170.4988
LT669795.1	49795044	1326999072	26.6492	326.877

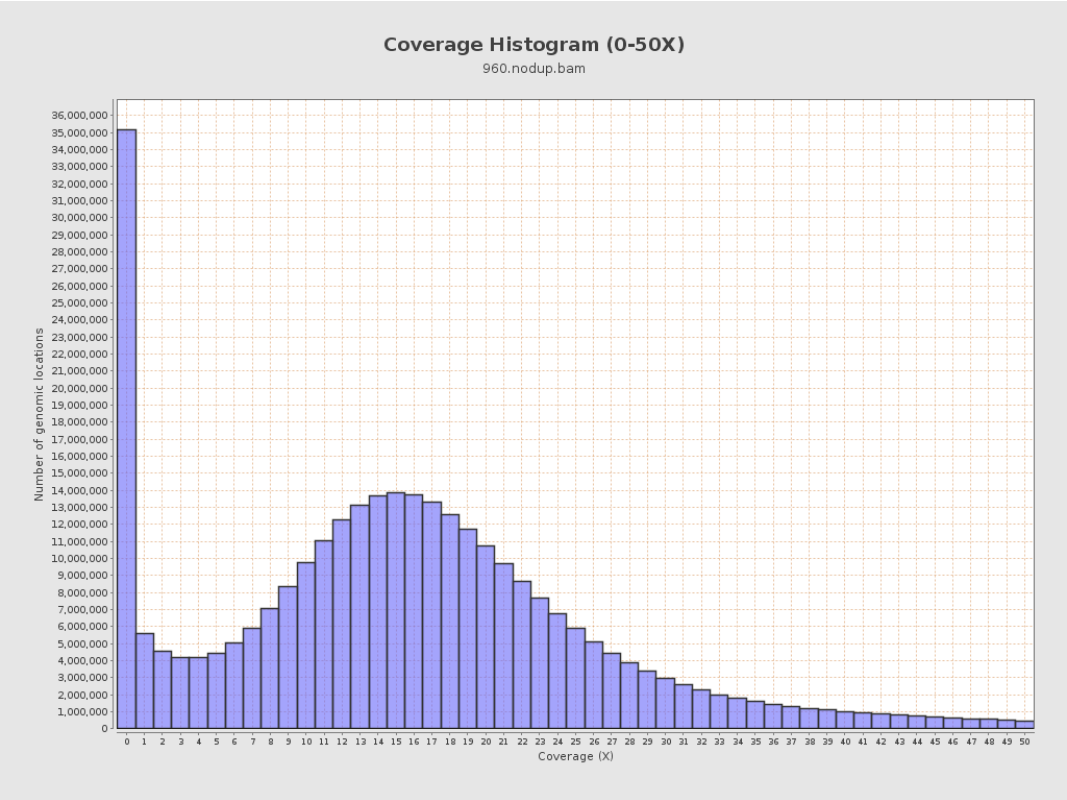
3. Results : Coverage across reference



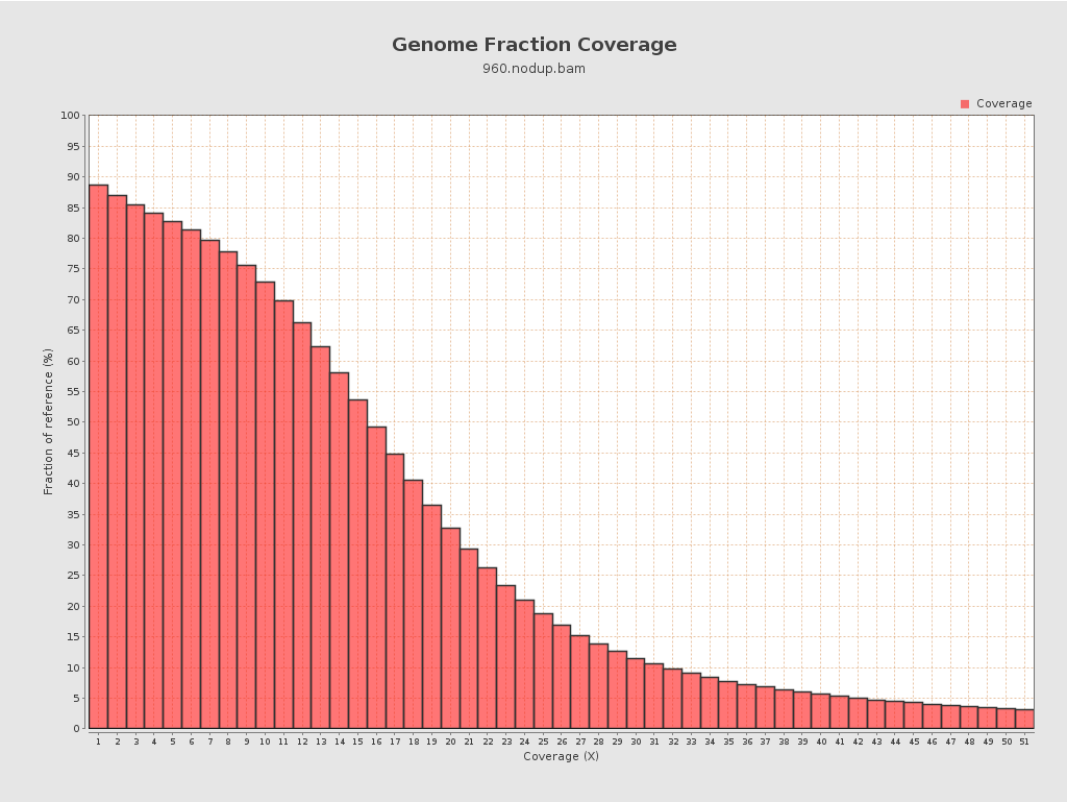
4. Results : Coverage Histogram



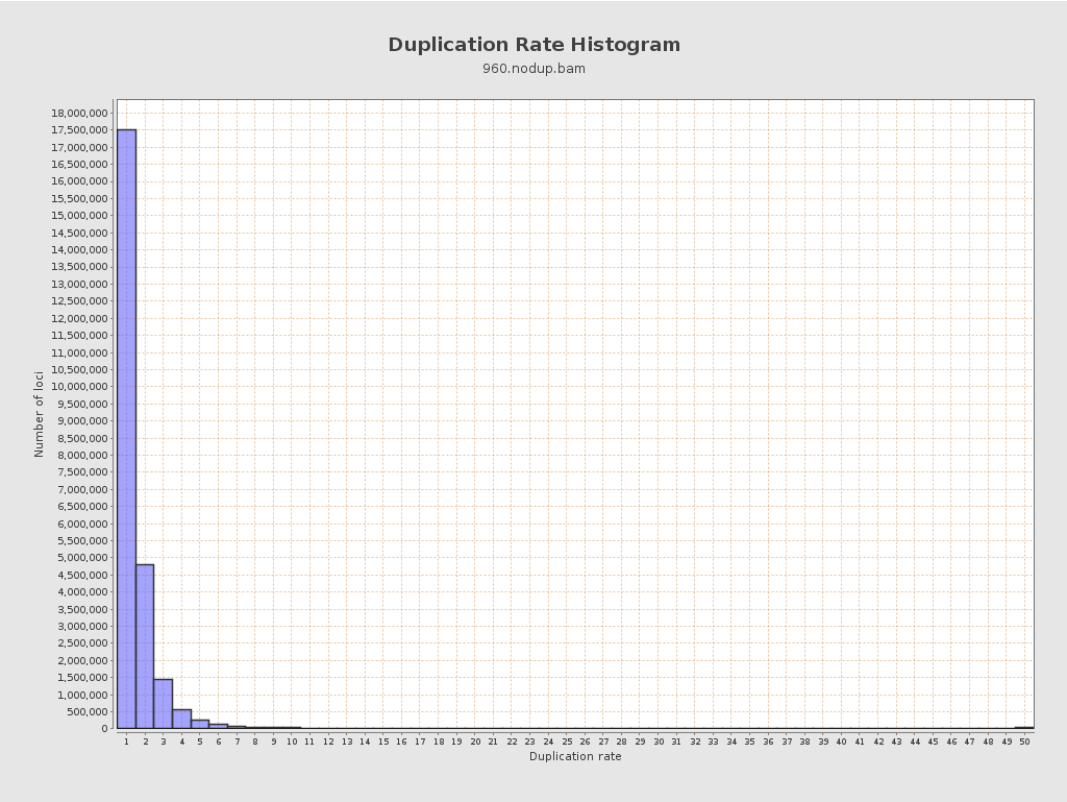
5. Results : Coverage Histogram (0-50X)



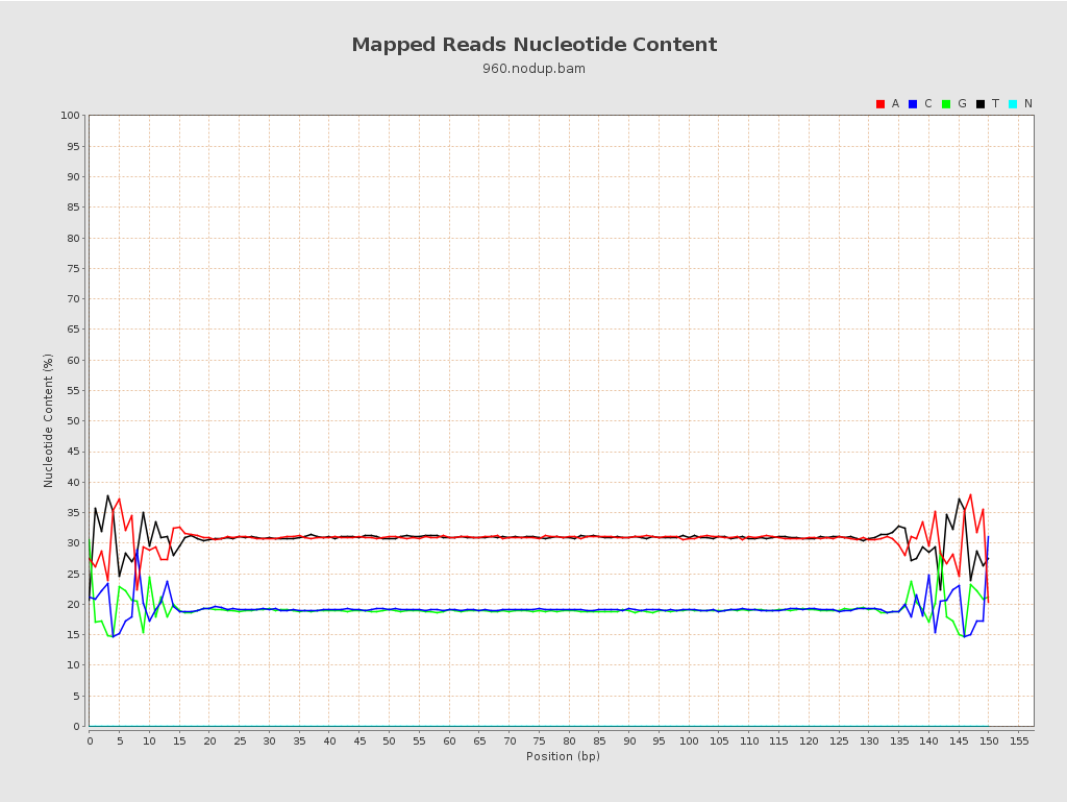
6. Results : Genome Fraction Coverage



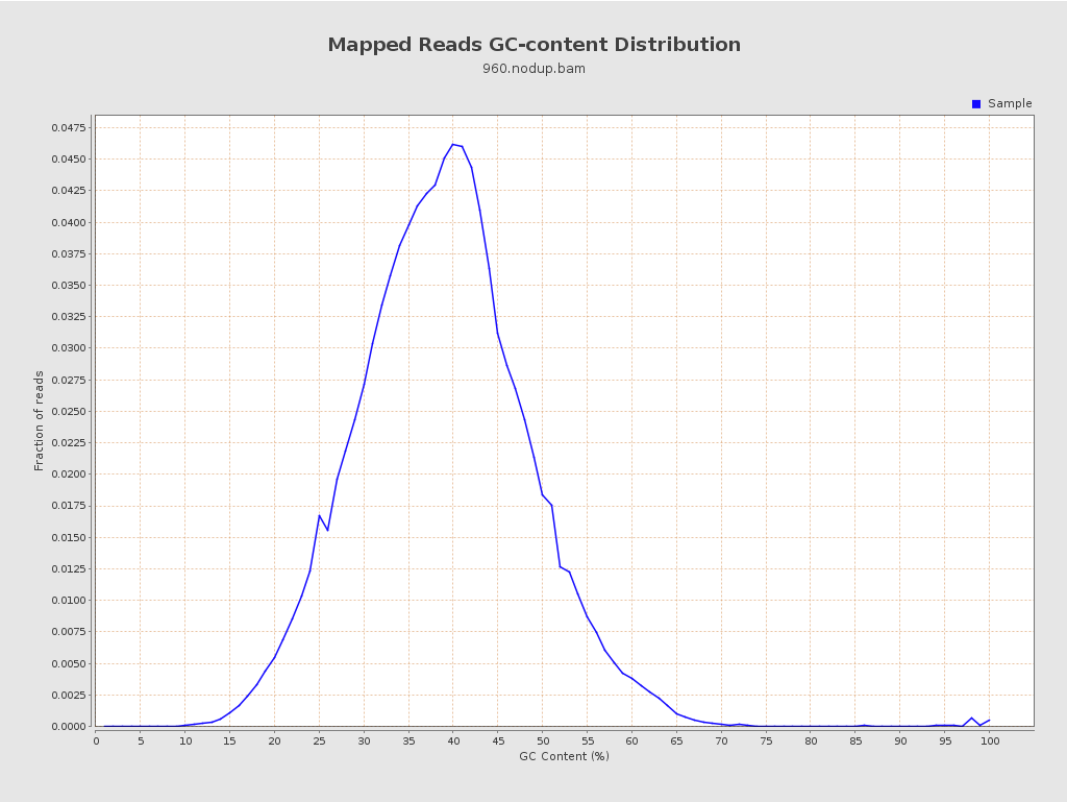
7. Results : Duplication Rate Histogram



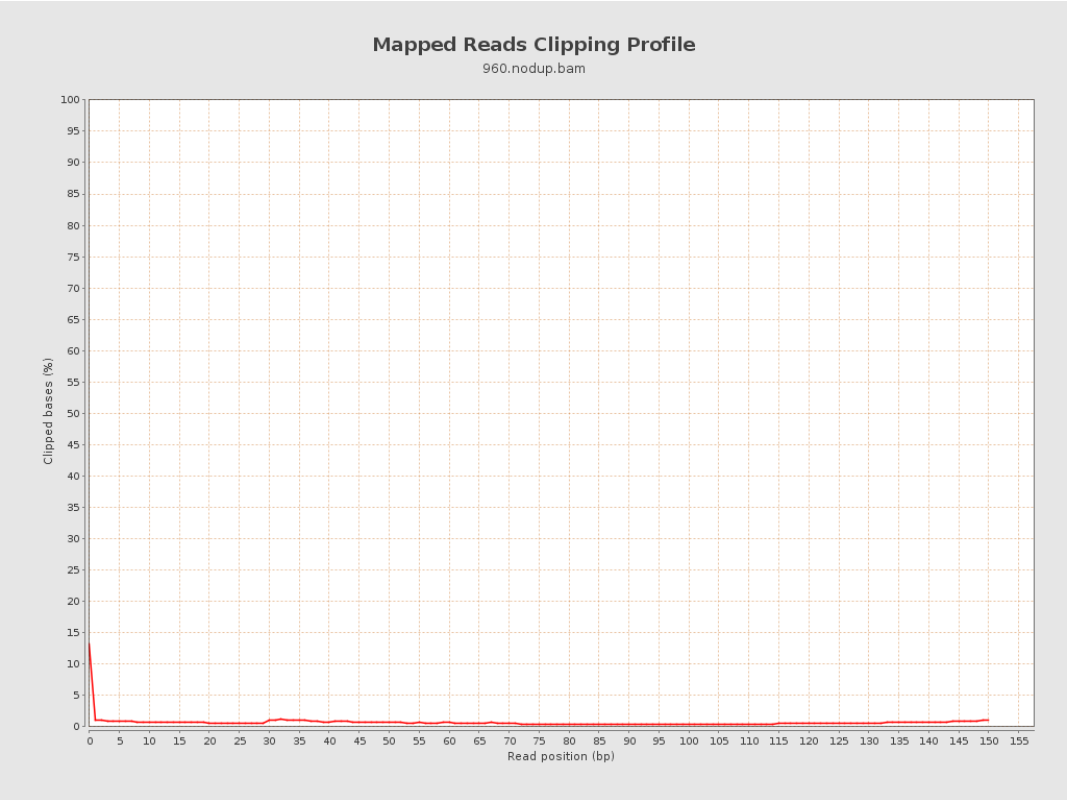
8. Results : Mapped Reads Nucleotide Content



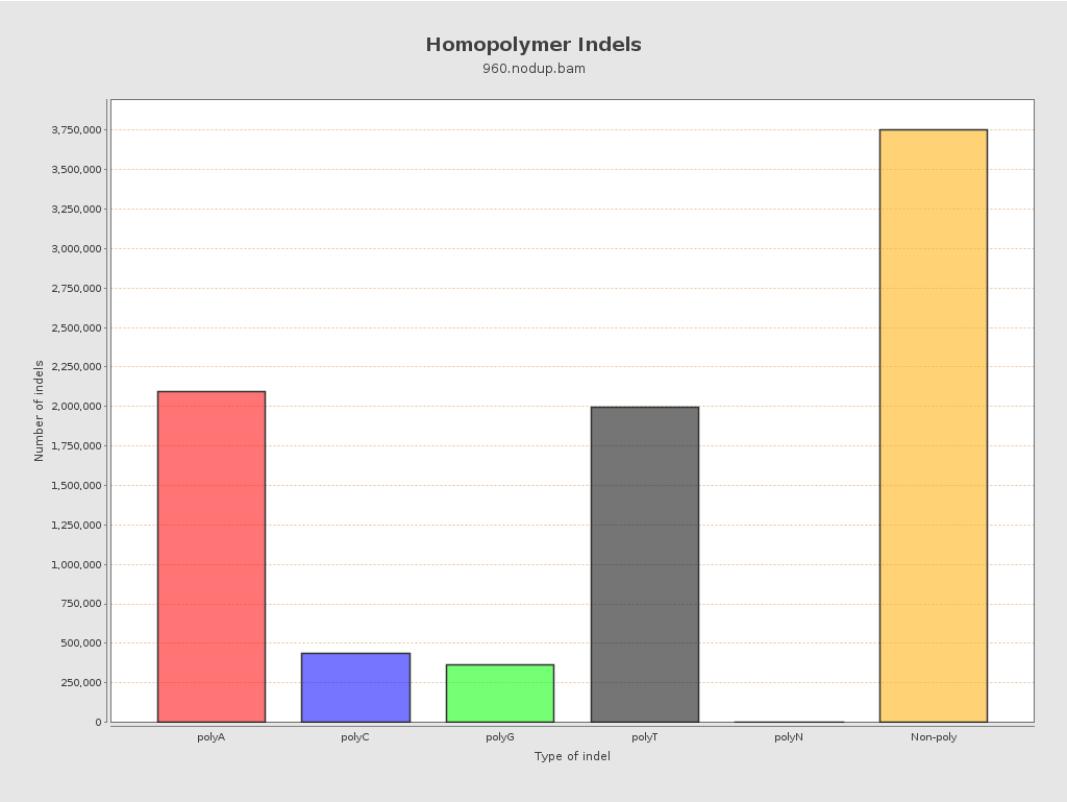
9. Results : Mapped Reads GC-content Distribution



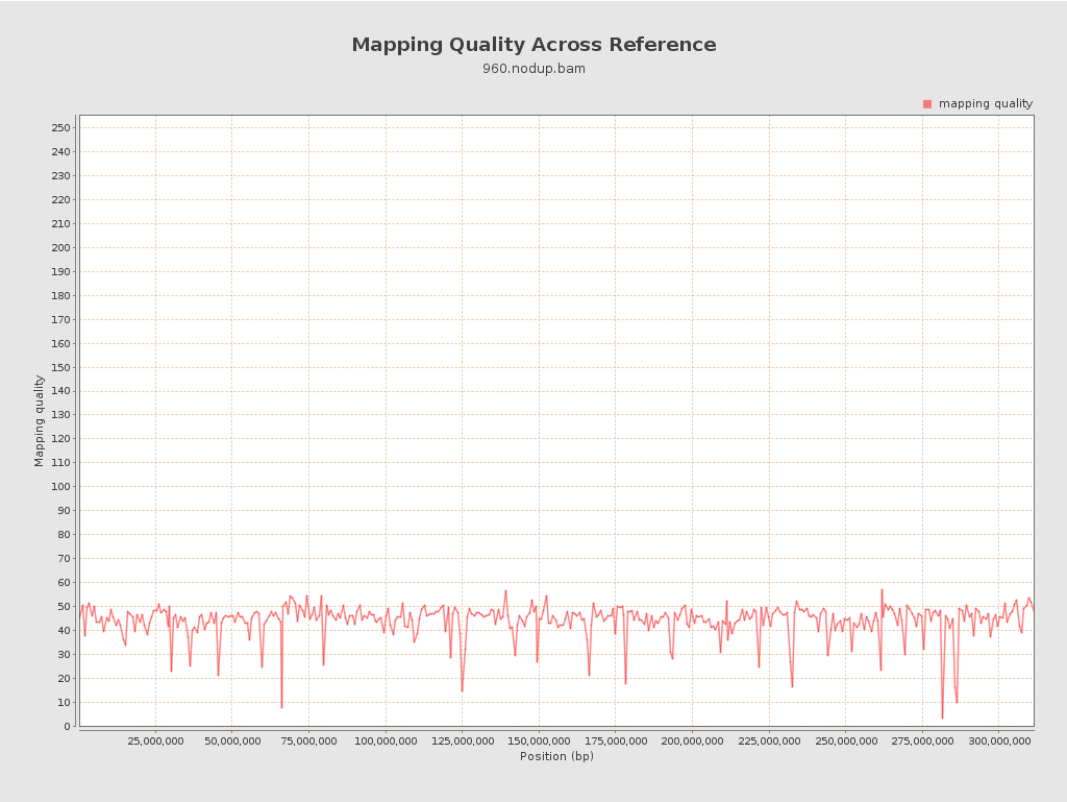
10. Results : Mapped Reads Clipping Profile



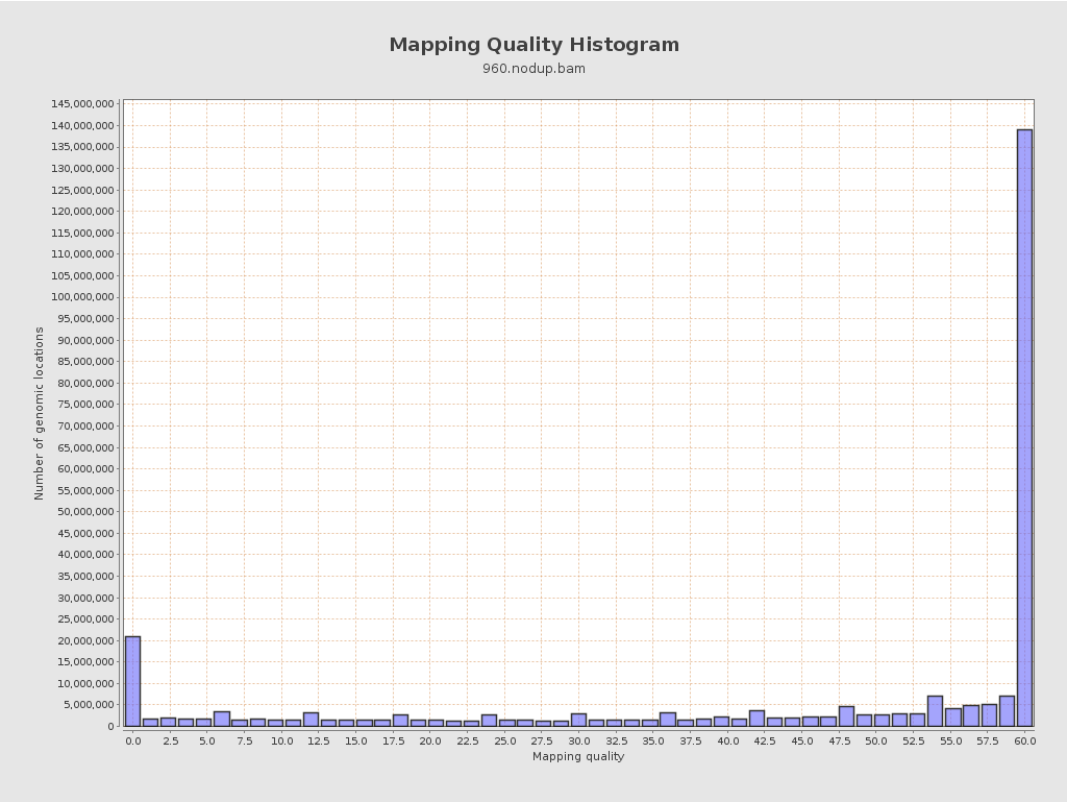
11. Results : Homopolymer Indels



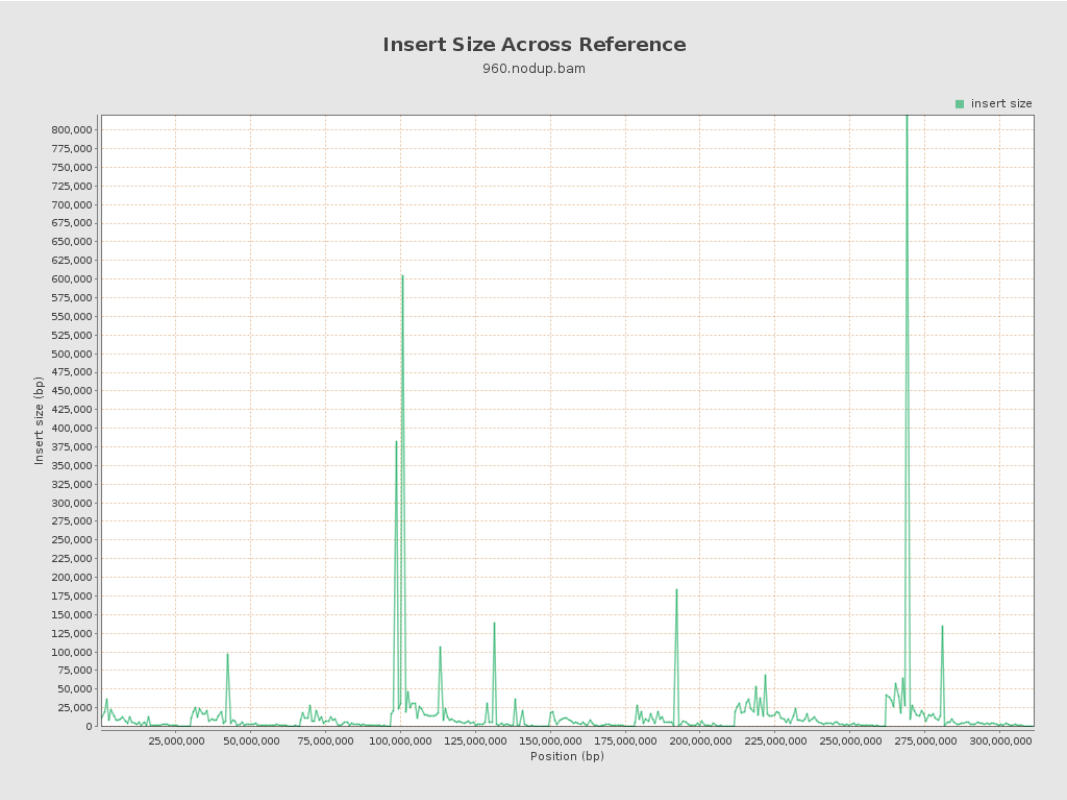
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram