Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:22:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1176
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1176 .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_581/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_581_S148_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_581/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_581_S148_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:22:31 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	40,770,523
Mapped reads	37,963,764 / 93.12%
Unmapped reads	2,806,759 / 6.88%
Mapped paired reads	37,963,764 / 93.12%
Mapped reads, first in pair	19,032,799 / 46.68%
Mapped reads, second in pair	18,930,965 / 46.43%
Mapped reads, both in pair	37,023,353 / 90.81%
Mapped reads, singletons	940,411 / 2.31%
Read min/max/mean length	30 / 151 / 148.18
Duplicated reads (flagged)	5,630,282 / 13.81%
Clipped reads	9,180,804 / 22.52%

2.2. ACGT Content

Number/percentage of A's	1,615,483,694 / 30.92%
Number/percentage of C's	998,392,365 / 19.11%
Number/percentage of T's	1,615,934,297 / 30.93%
Number/percentage of G's	994,714,899 / 19.04%
Number/percentage of N's	34,176 / 0%
GC Percentage	38.15%

2.3. Coverage

Mean	16.806
Standard Deviation	146.2679

2.4. Mapping Quality

Mean Mapping Quality	44.37

2.5. Insert size

Mean	230,447.62
Standard Deviation	2,292,135.92
P25/Median/P75	331 / 435 / 554

2.6. Mismatches and indels

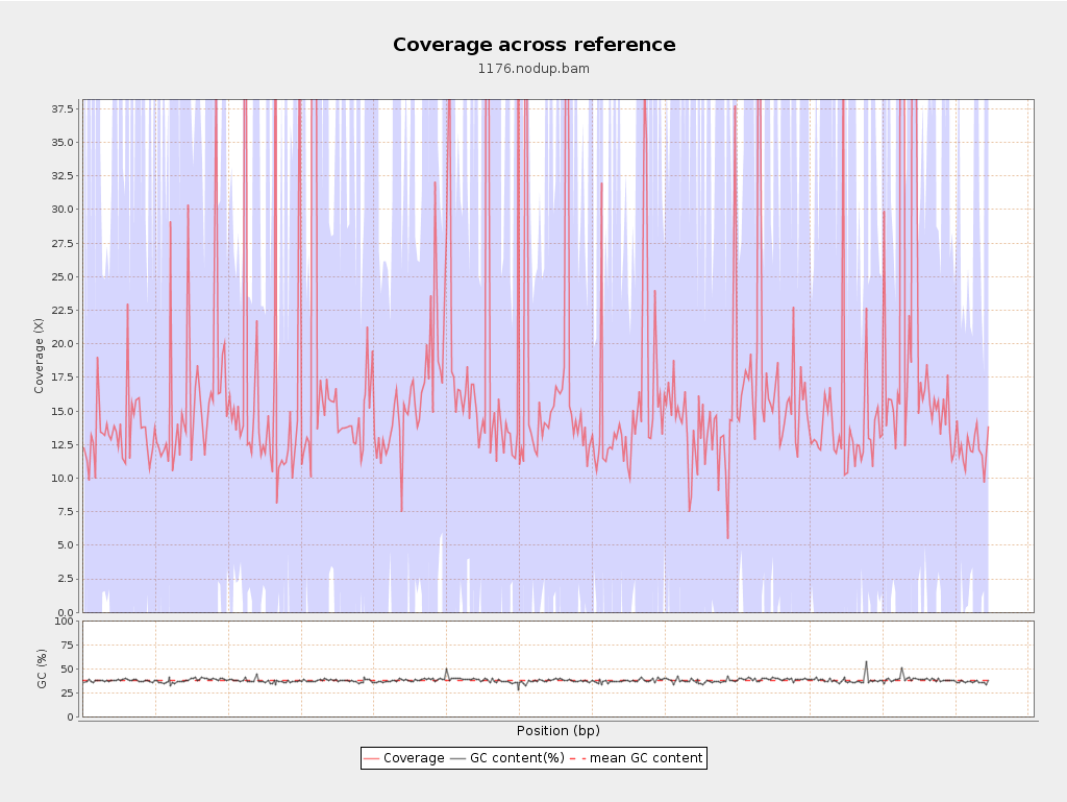
General error rate	2.56%
Mismatches	123,876,390
Insertions	3,548,410
Mapped reads with at least one insertion	8.39%
Deletions	3,489,591
Mapped reads with at least one deletion	8.19%
Homopolymer indels	56.86%

2.7. Chromosome stats

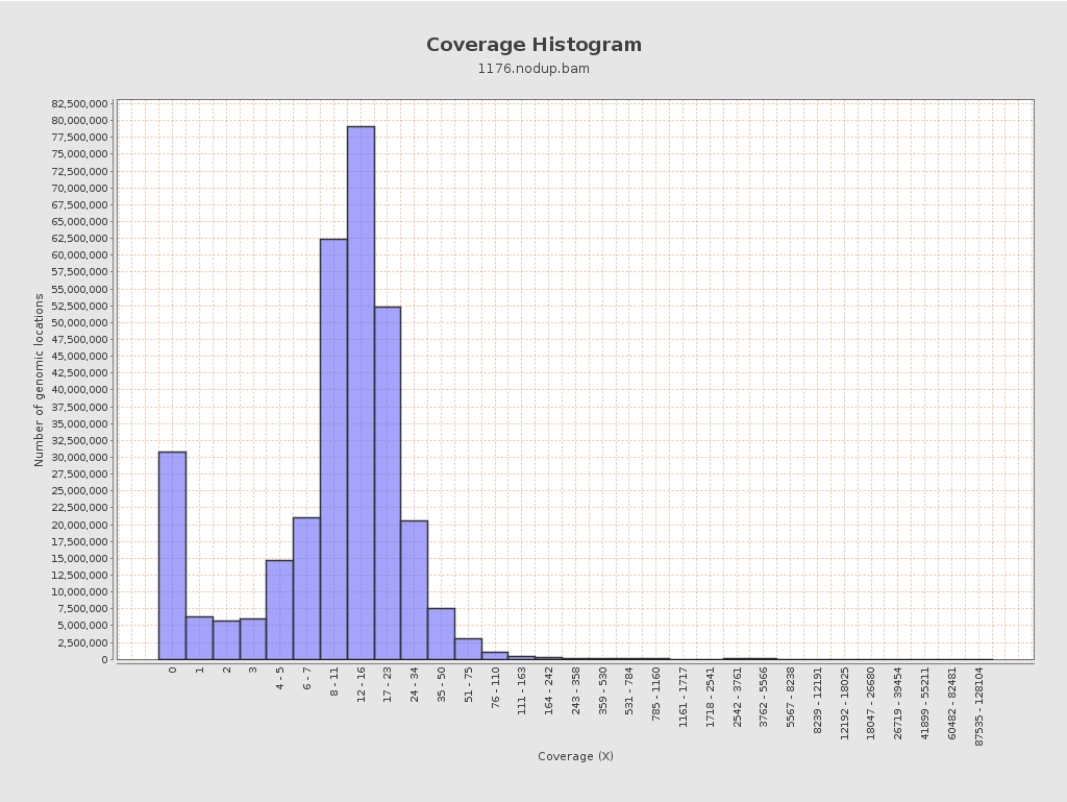
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	393771199	13.2474	45.9123

LT669789.1	36598175	618091027	16.8886	145.11
LT669790.1	30422129	573846432	18.8628	177.6181
LT669791.1	52758100	892050083	16.9083	137.878
LT669792.1	28376109	470922019	16.5957	166.378
LT669793.1	33388210	506187566	15.1607	79.9822
LT669794.1	50579949	811405029	16.042	121.7085
LT669795.1	49795044	971198347	19.5039	206.4352

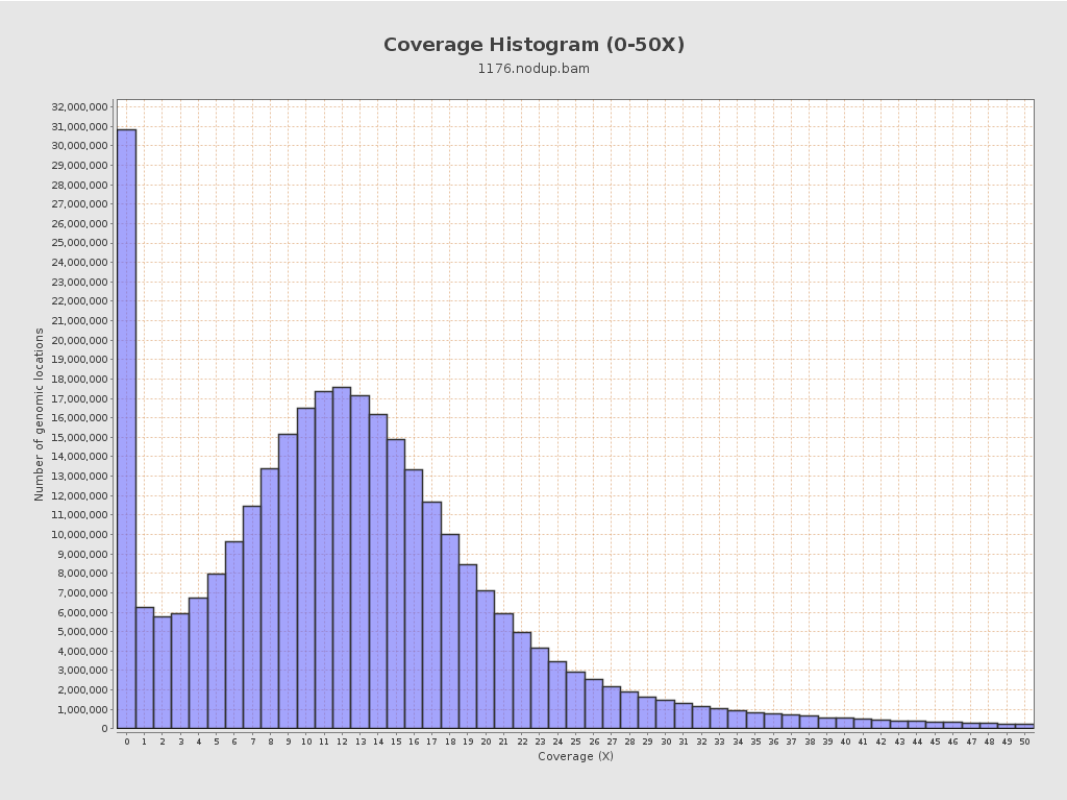
3. Results : Coverage across reference



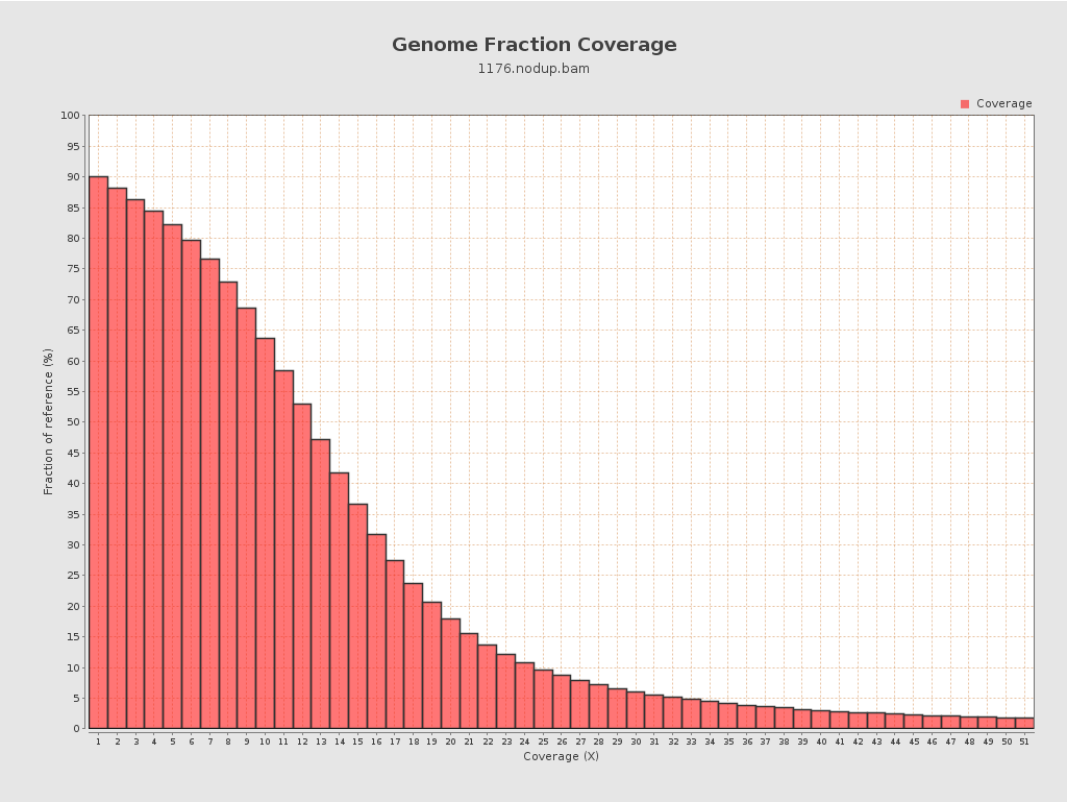
4. Results : Coverage Histogram



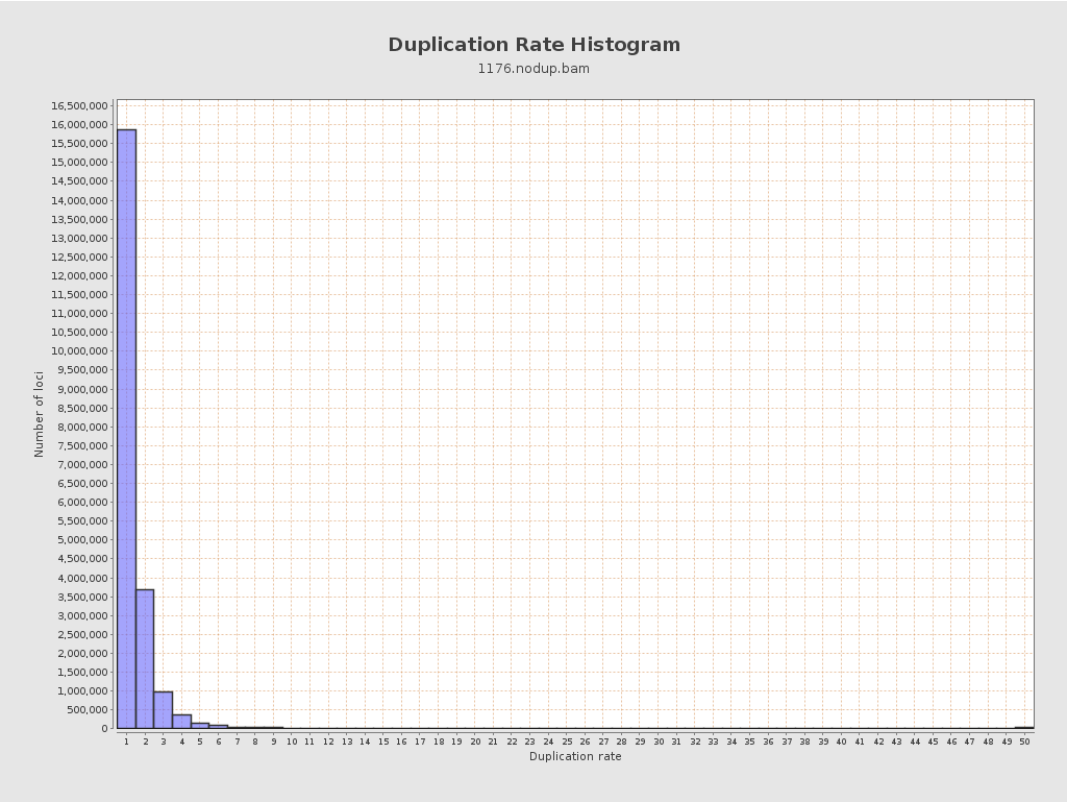
5. Results : Coverage Histogram (0-50X)



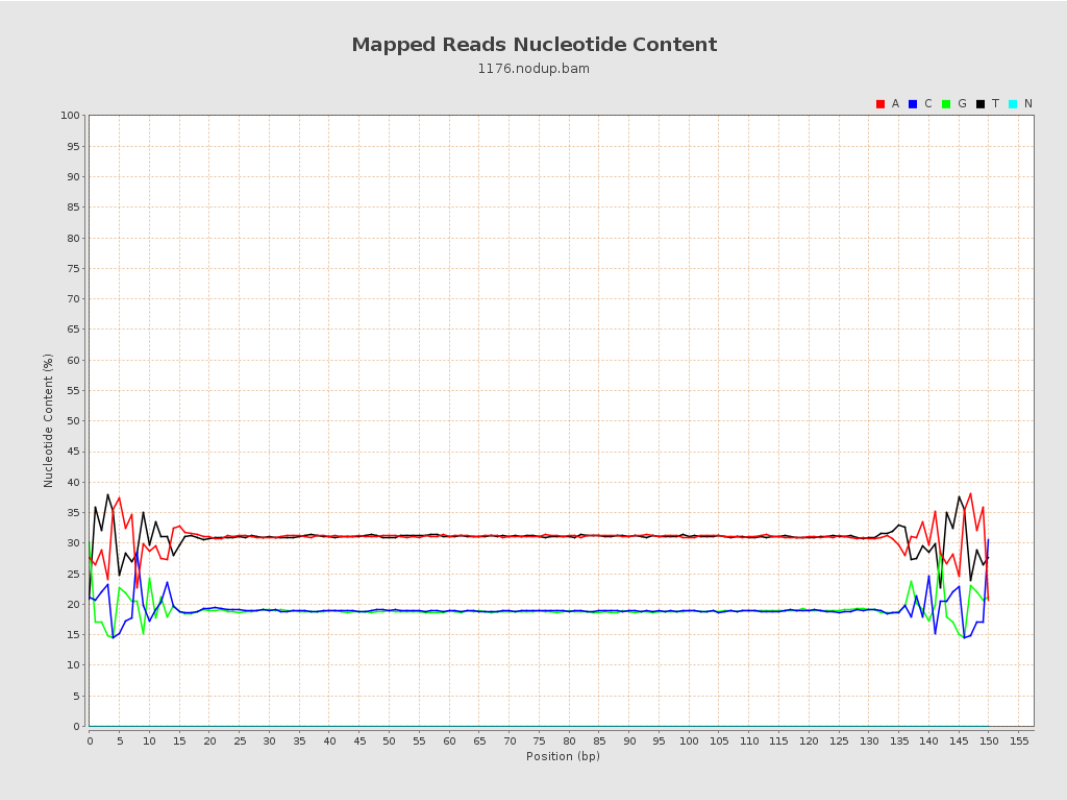
6. Results : Genome Fraction Coverage



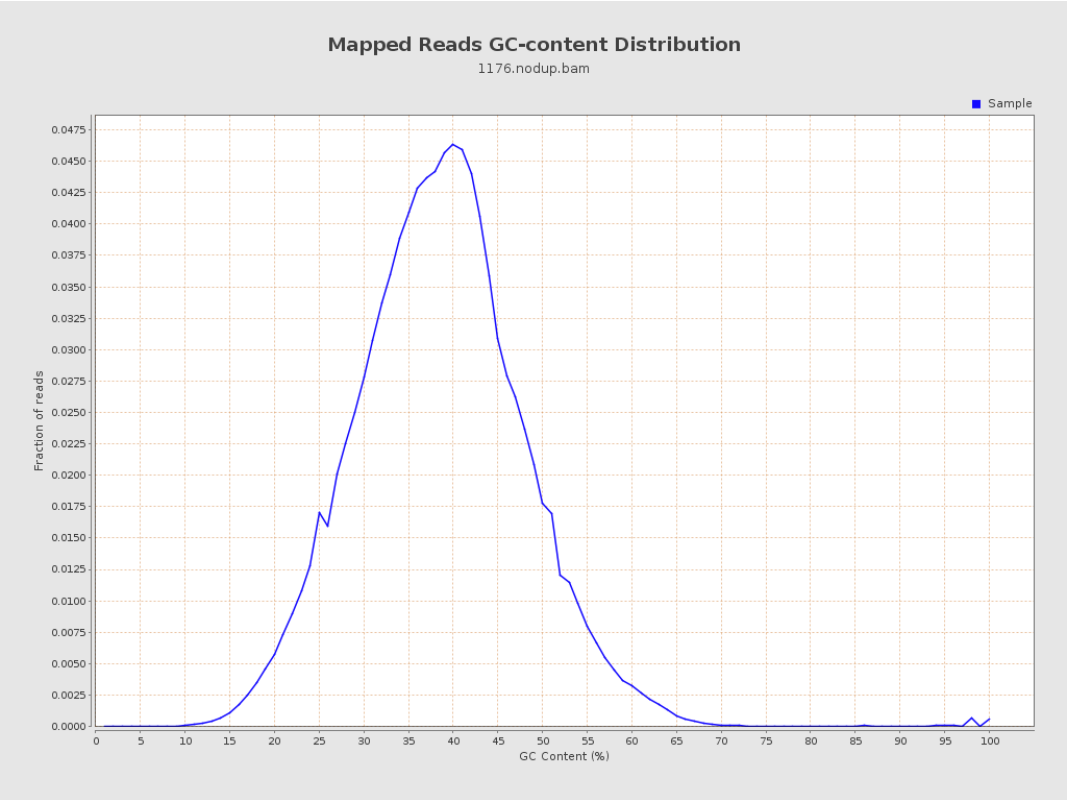
7. Results : Duplication Rate Histogram



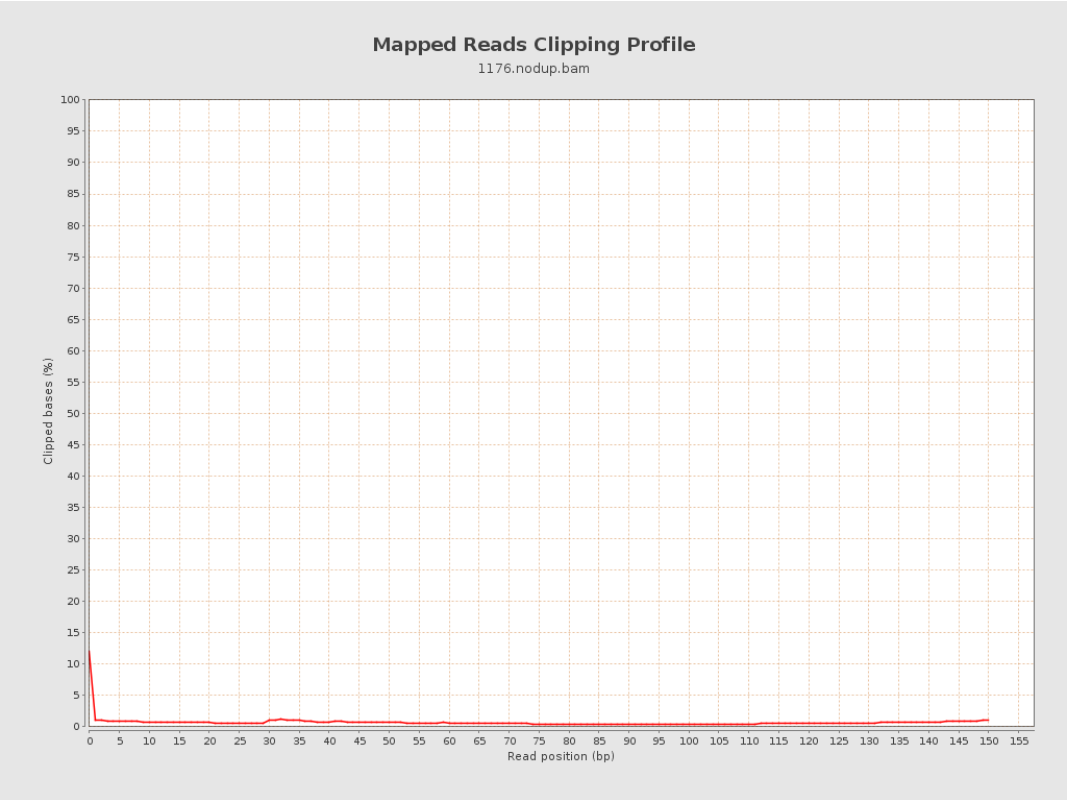
8. Results : Mapped Reads Nucleotide Content



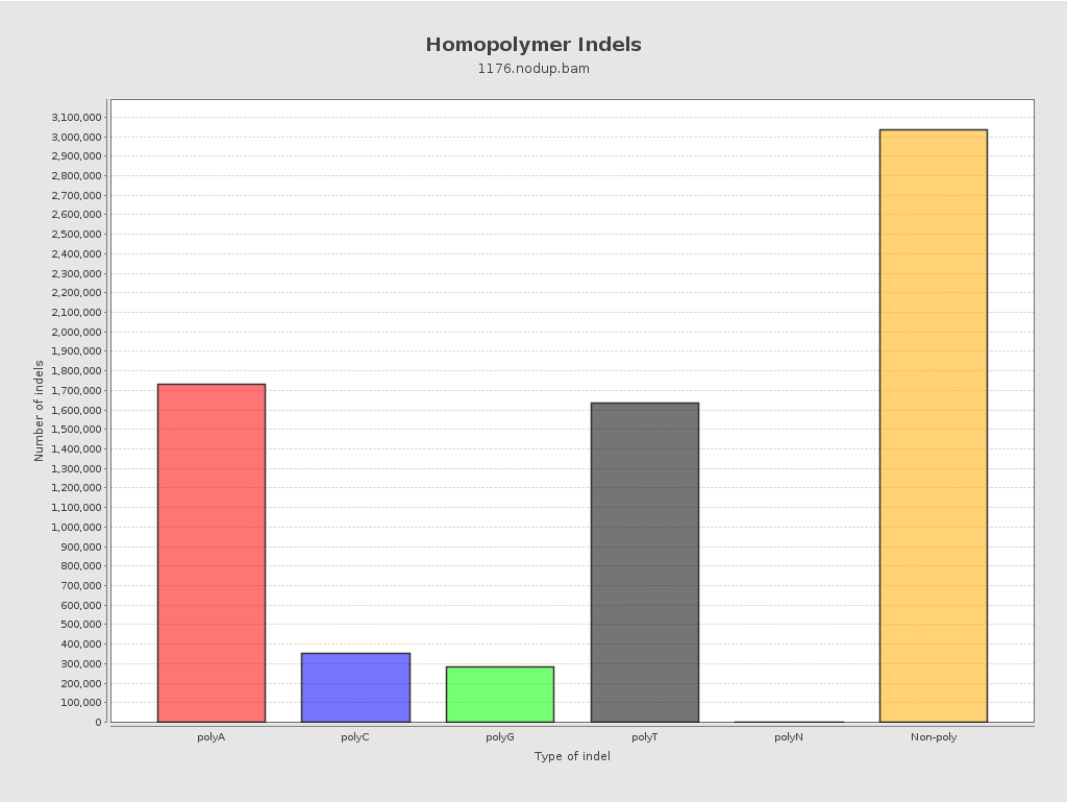
9. Results : Mapped Reads GC-content Distribution



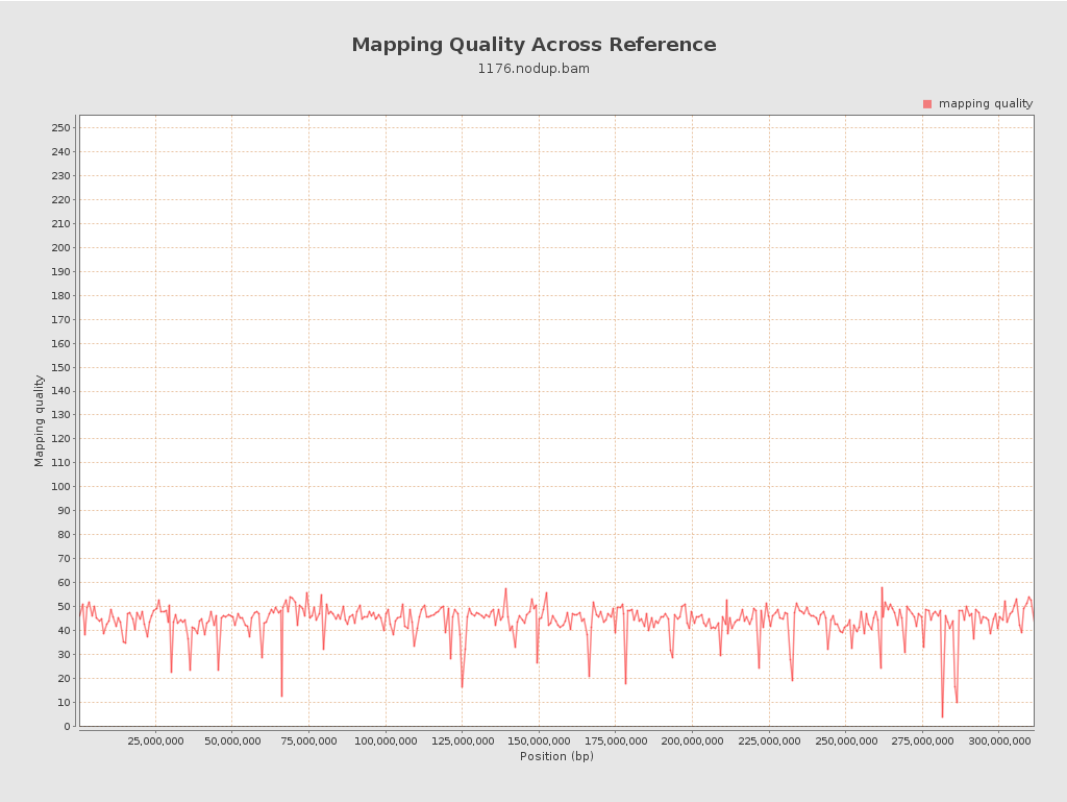
10. Results : Mapped Reads Clipping Profile



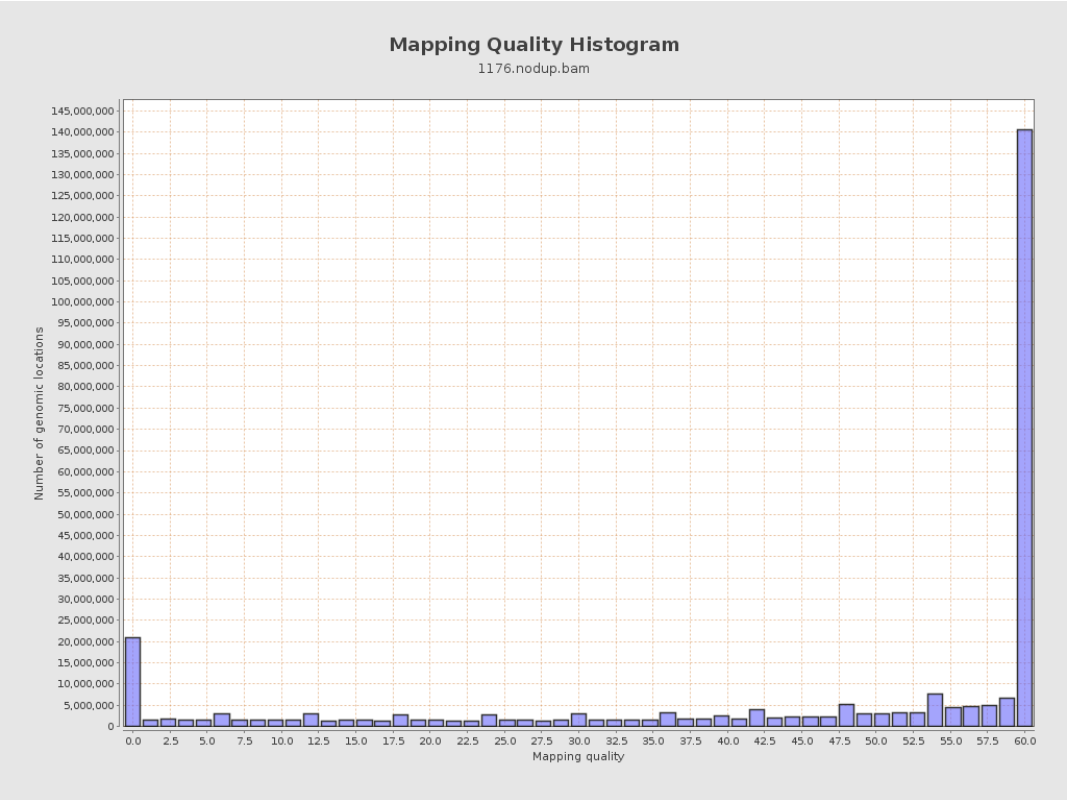
11. Results : Homopolymer Indels



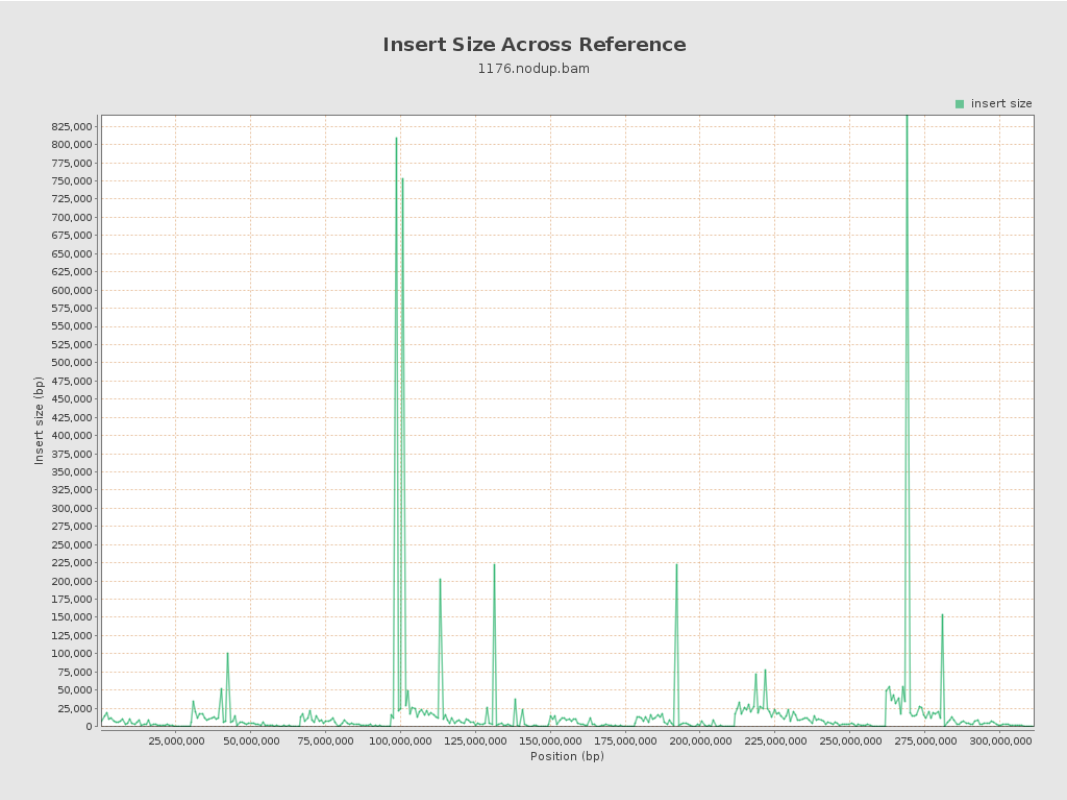
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram