Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:28:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/834.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/834.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_267/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_267_S348_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_267/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_267_S348_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:28:05 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	58,162,093
Mapped reads	53,868,205 / 92.62%
Unmapped reads	4,293,888 / 7.38%
Mapped paired reads	53,868,205 / 92.62%
Mapped reads, first in pair	26,988,901 / 46.4%
Mapped reads, second in pair	26,879,304 / 46.21%
Mapped reads, both in pair	52,419,800 / 90.13%
Mapped reads, singletons	1,448,405 / 2.49%
Read min/max/mean length	30 / 151 / 148.27
Duplicated reads (flagged)	8,339,961 / 14.34%
Clipped reads	12,113,676 / 20.83%

2.2. ACGT Content

Number/percentage of A's	2,299,374,613 / 30.87%
Number/percentage of C's	1,425,288,905 / 19.14%
Number/percentage of T's	2,303,666,364 / 30.93%
Number/percentage of G's	1,419,728,025 / 19.06%
Number/percentage of N's	27,751 / 0%
GC Percentage	38.2%

2.3. Coverage

Mean	23.9585
Standard Deviation	218.4765

2.4. Mapping Quality

Mean Mapping Quality	44.64

2.5. Insert size

Mean	237,505.32
Standard Deviation	2,333,860.31
P25/Median/P75	335 / 437 / 564

2.6. Mismatches and indels

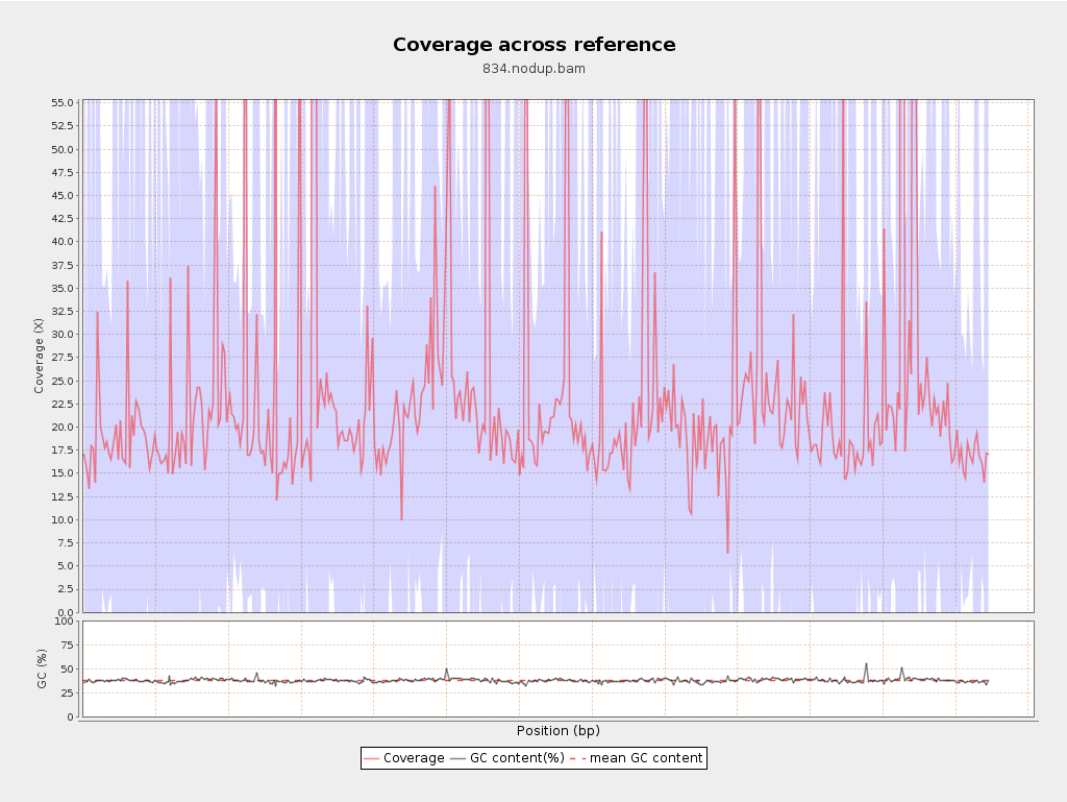
General error rate	2.3%
Mismatches	156,868,789
Insertions	5,096,073
Mapped reads with at least one insertion	8.46%
Deletions	4,931,143
Mapped reads with at least one deletion	8.15%
Homopolymer indels	57.25%

2.7. Chromosome stats

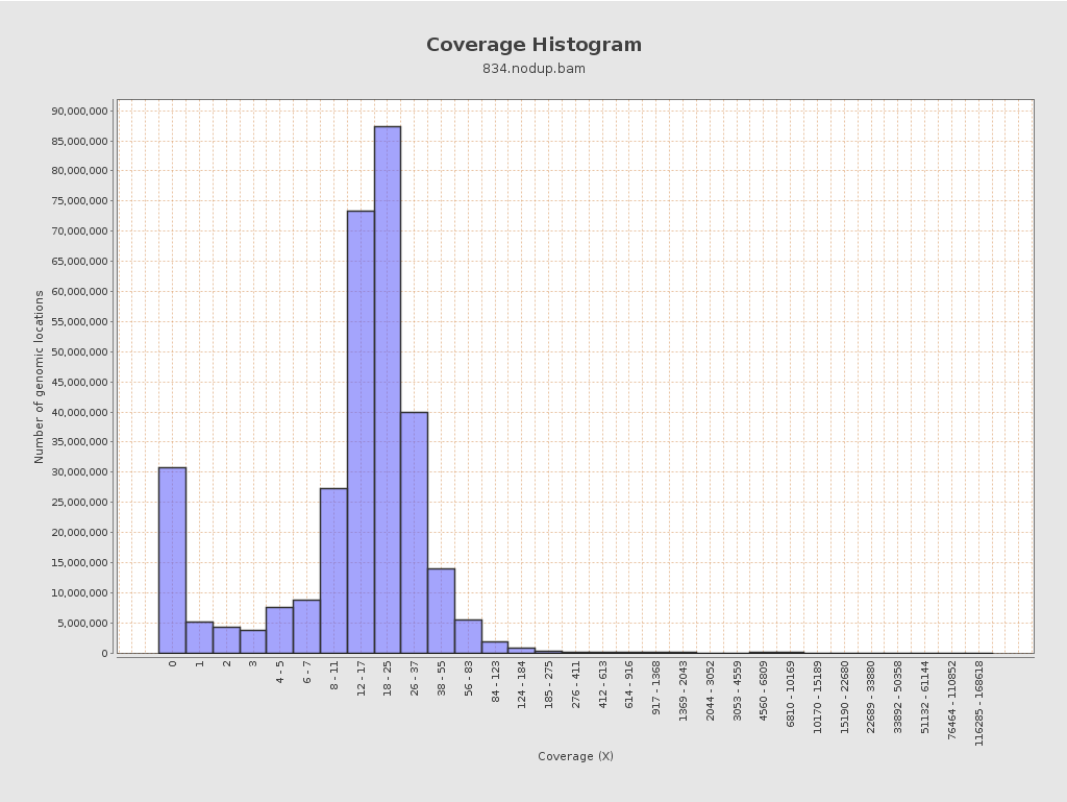
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	554498179	18.6547	72.1402

LT669789.1	36598175	862312602	23.5616	223.7086
LT669790.1	30422129	837990584	27.5454	282.6611
LT669791.1	52758100	1277116693	24.207	212.241
LT669792.1	28376109	664925889	23.4326	248.1122
LT669793.1	33388210	727471473	21.7883	149.6124
LT669794.1	50579949	1149607225	22.7285	176.4247
LT669795.1	49795044	1392538084	27.9654	283.8151

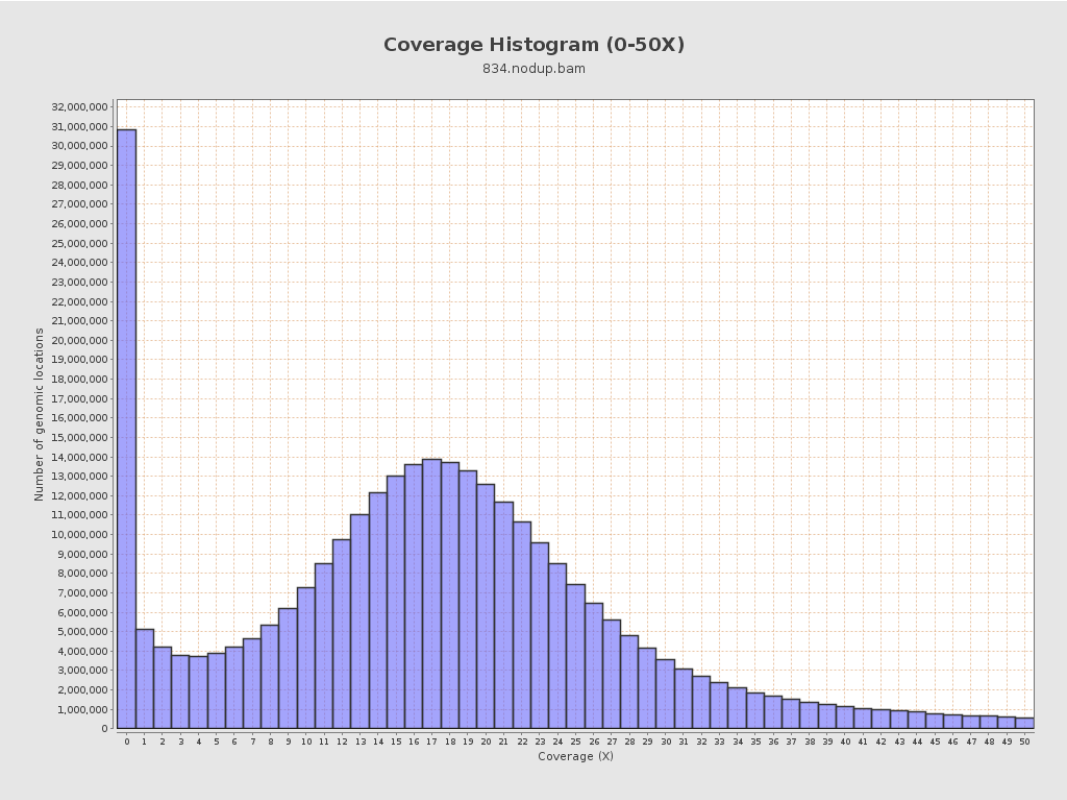
3. Results : Coverage across reference



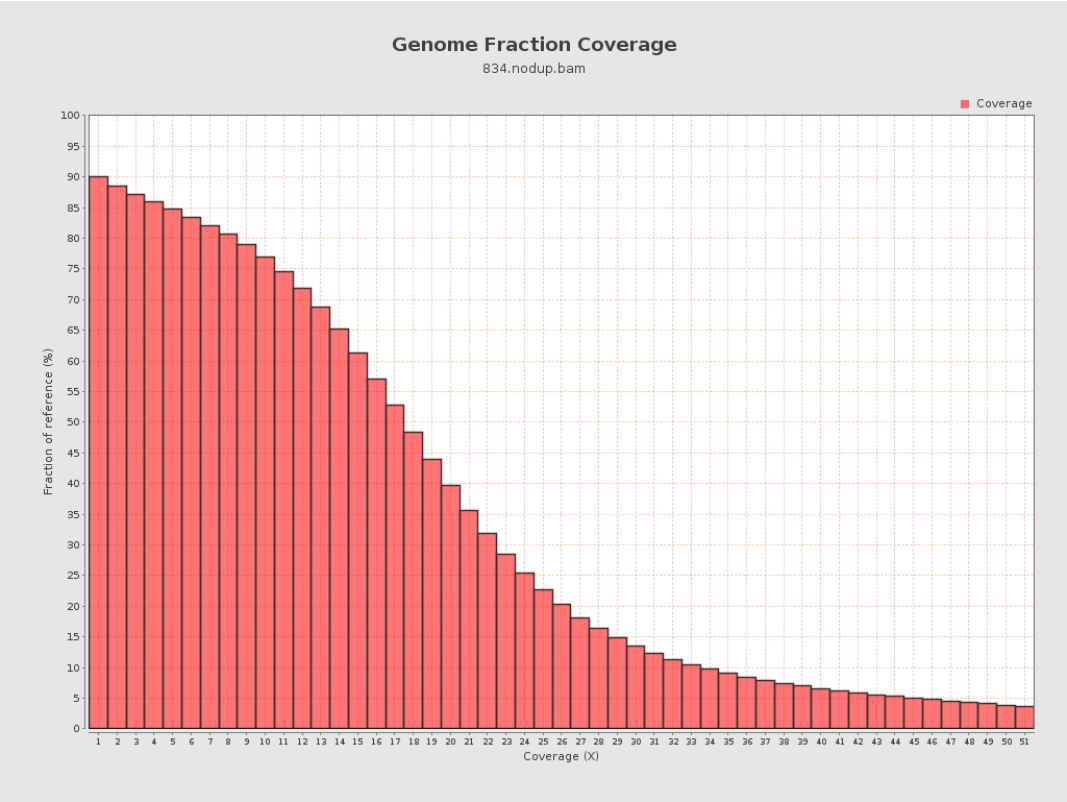
4. Results : Coverage Histogram



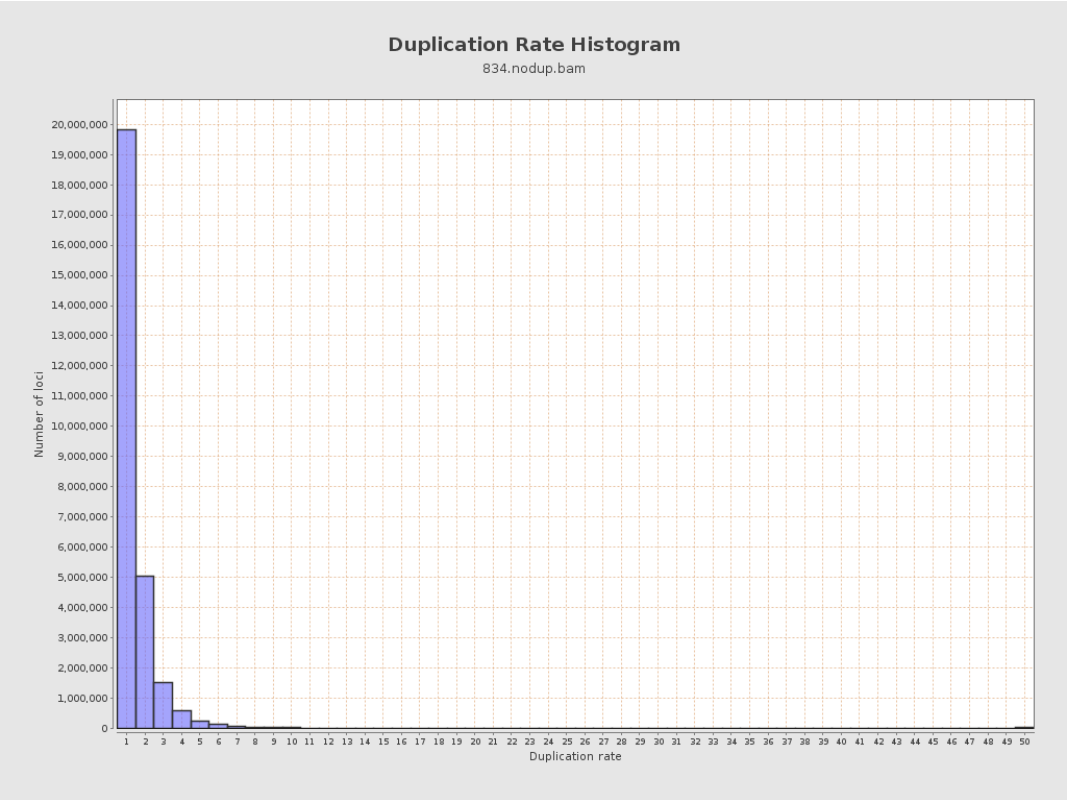
5. Results : Coverage Histogram (0-50X)



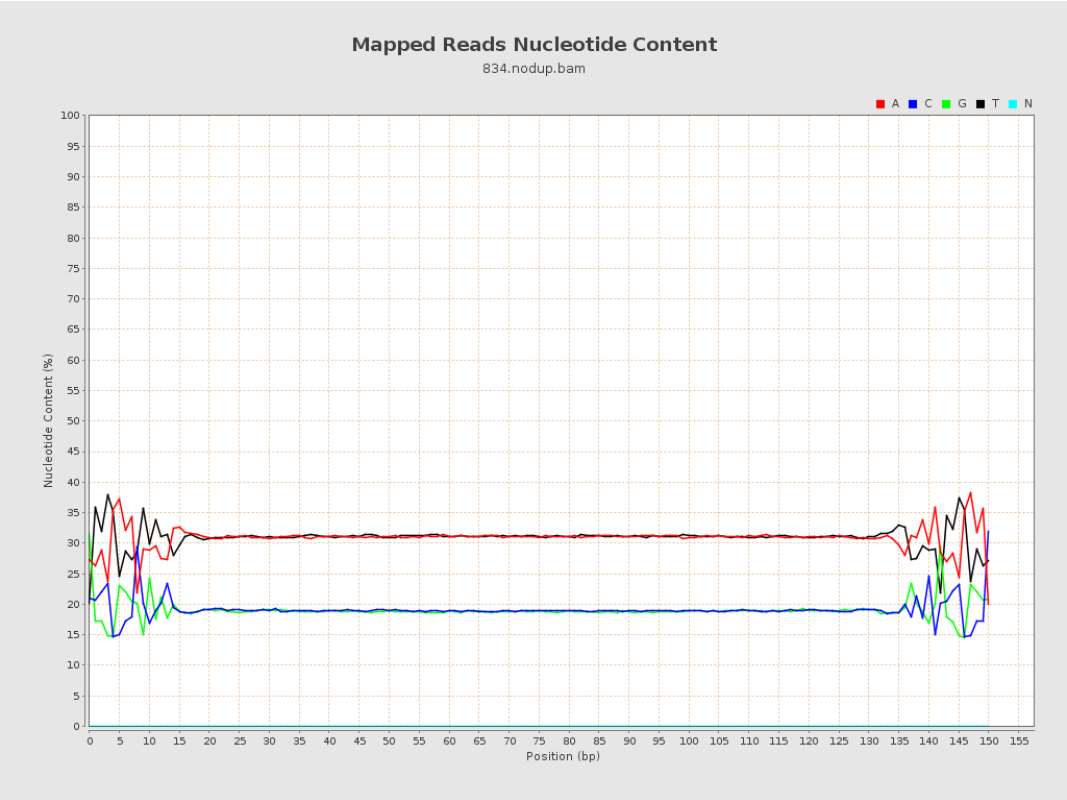
6. Results : Genome Fraction Coverage



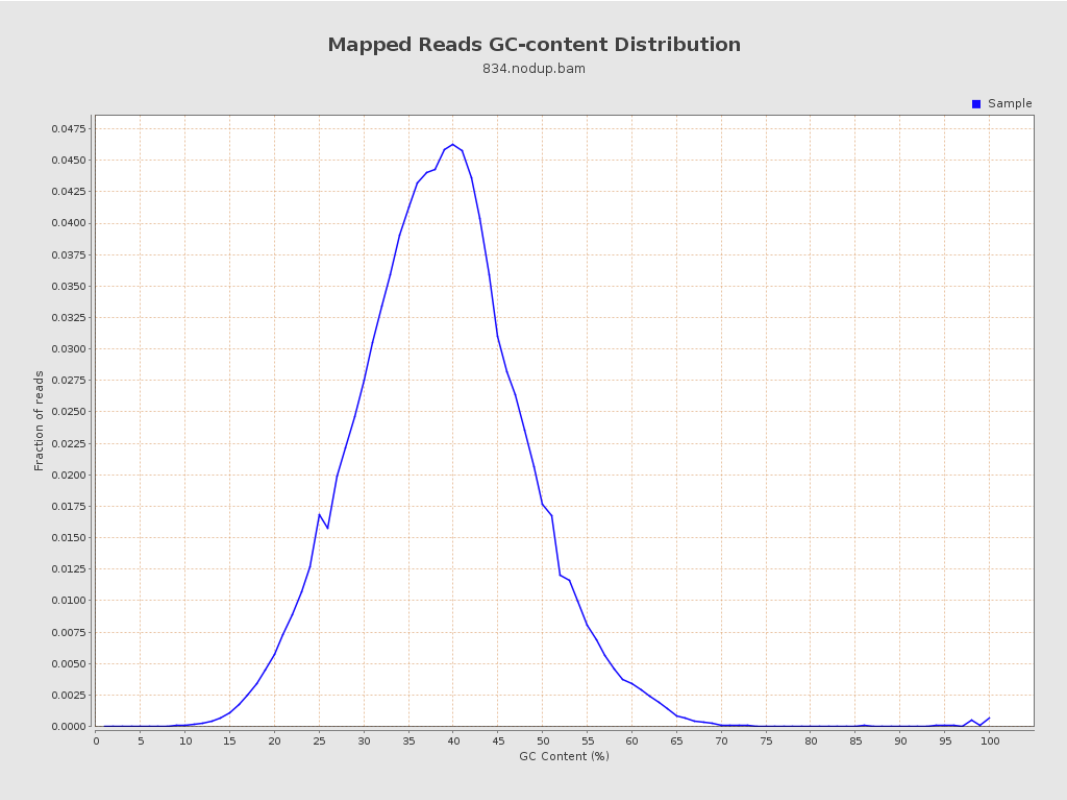
7. Results : Duplication Rate Histogram



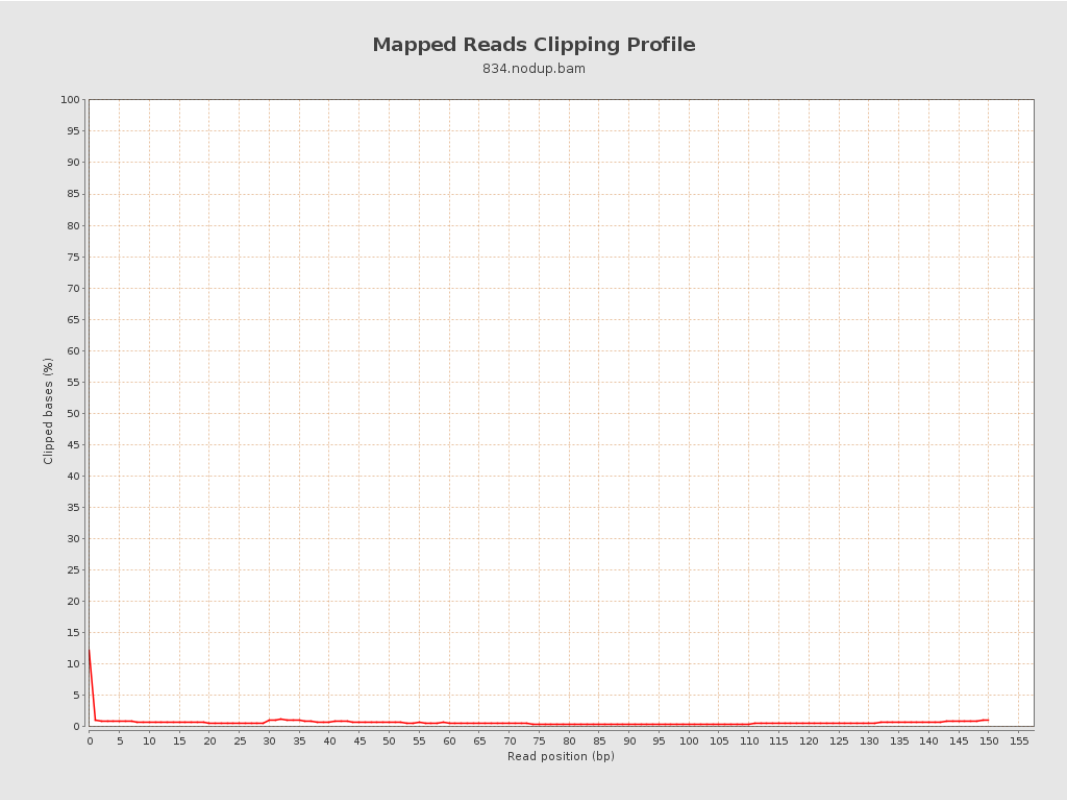
8. Results : Mapped Reads Nucleotide Content



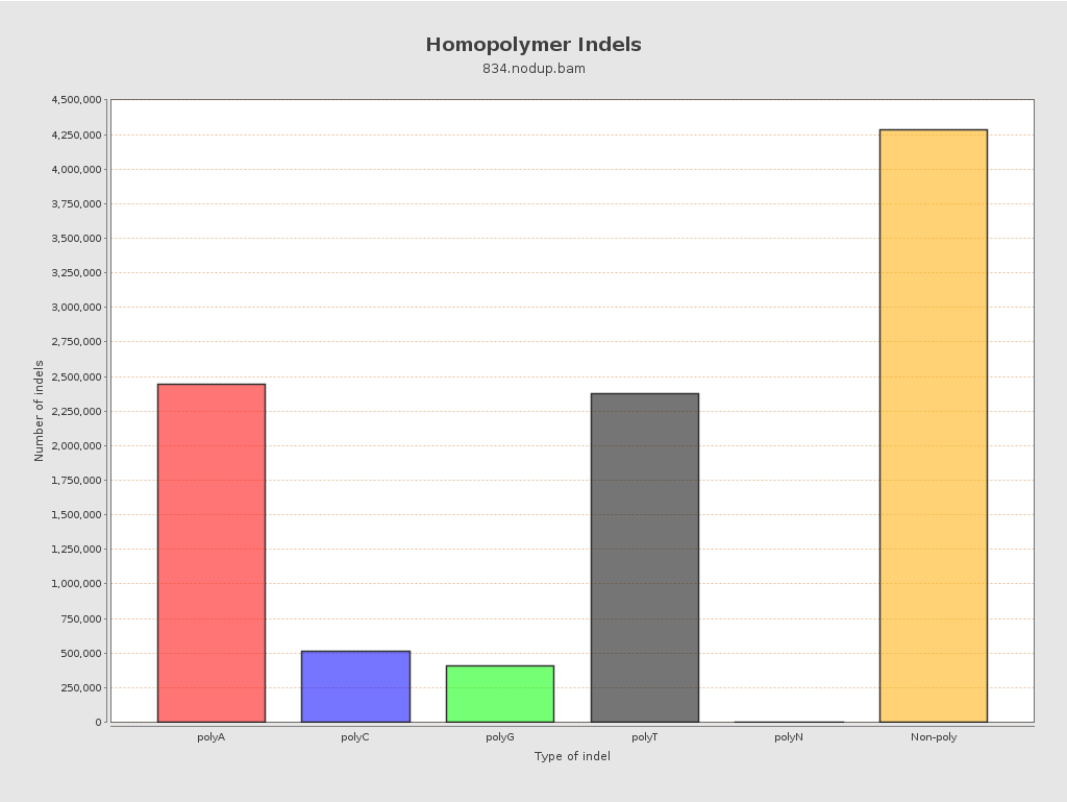
9. Results : Mapped Reads GC-content Distribution



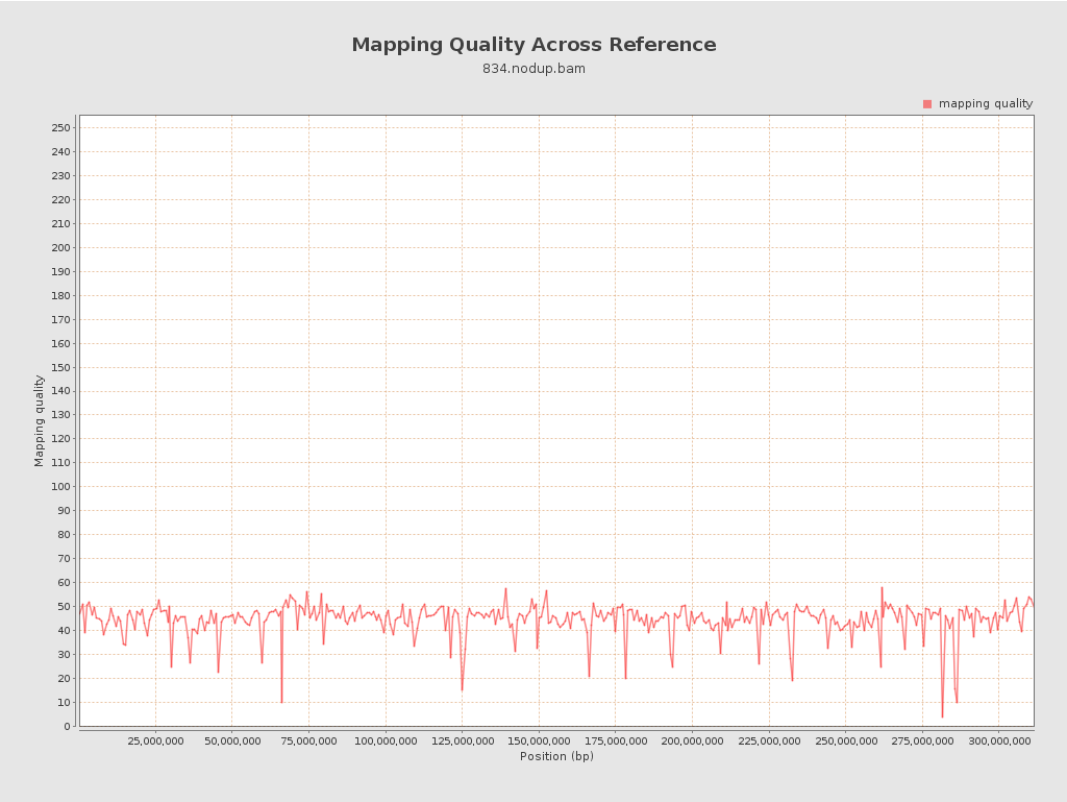
10. Results : Mapped Reads Clipping Profile



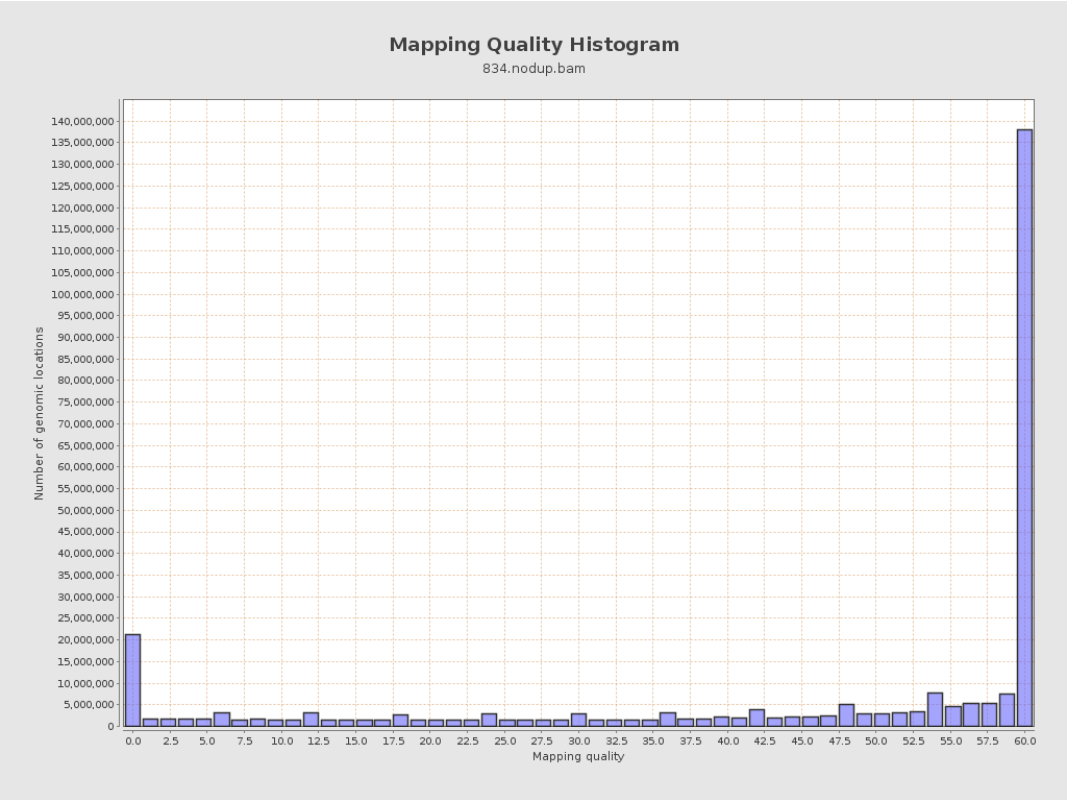
11. Results : Homopolymer Indels



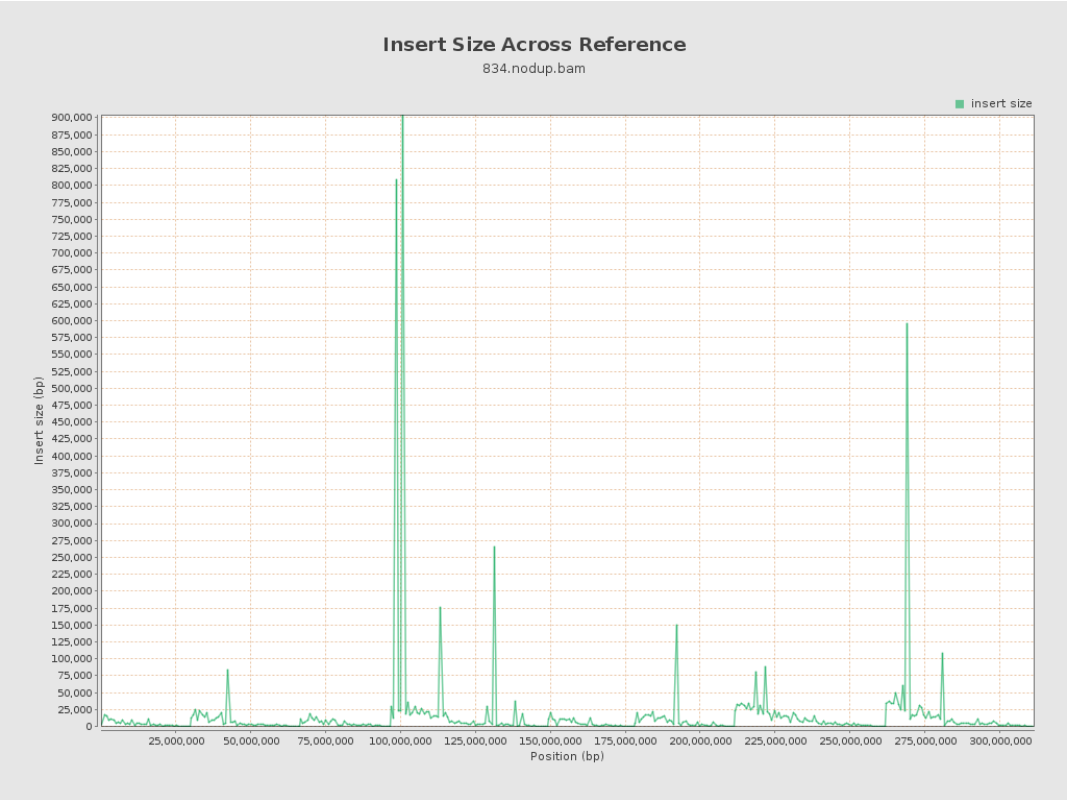
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram