Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:24:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/544.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/544.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_287/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_287_S368_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_287/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_287_S368_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:24:53 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	45,868,131
Mapped reads	42,641,843 / 92.97%
Unmapped reads	3,226,288 / 7.03%
Mapped paired reads	42,641,843 / 92.97%
Mapped reads, first in pair	21,354,638 / 46.56%
Mapped reads, second in pair	21,287,205 / 46.41%
Mapped reads, both in pair	41,584,282 / 90.66%
Mapped reads, singletons	1,057,561 / 2.31%
Read min/max/mean length	30 / 151 / 148.08
Duplicated reads (flagged)	5,763,189 / 12.56%
Clipped reads	9,925,297 / 21.64%

2.2. ACGT Content

Number/percentage of A's	1,811,491,379 / 30.84%
Number/percentage of C's	1,125,643,872 / 19.16%
Number/percentage of T's	1,811,946,334 / 30.85%
Number/percentage of G's	1,124,770,743 / 19.15%
Number/percentage of N's	21,646 / 0%
GC Percentage	38.31%

2.3. Coverage

Mean	18.895
Standard Deviation	163.1834

2.4. Mapping Quality

Mean Mapping Quality	44.48

2.5. Insert size

Mean	236,345.09
Standard Deviation	2,331,995.19
P25/Median/P75	325 / 426 / 553

2.6. Mismatches and indels

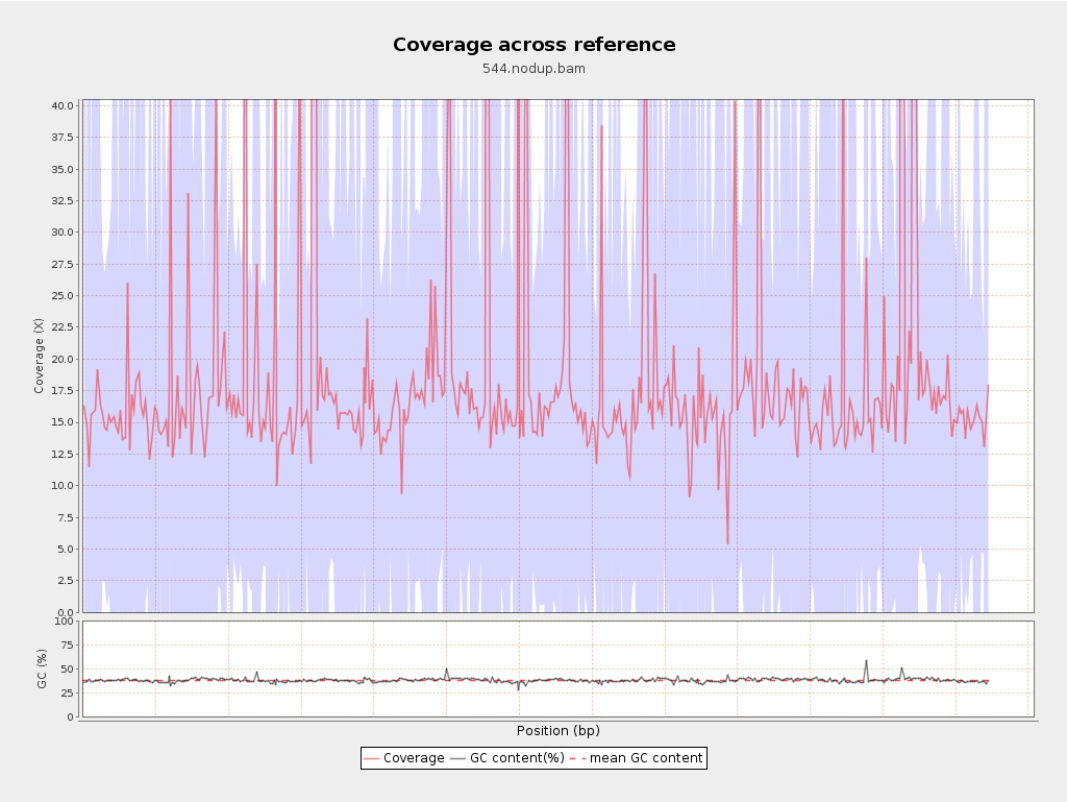
General error rate	2.3%
Mismatches	123,986,206
Insertions	3,992,142
Mapped reads with at least one insertion	8.4%
Deletions	3,931,516
Mapped reads with at least one deletion	8.19%
Homopolymer indels	56.94%

2.7. Chromosome stats

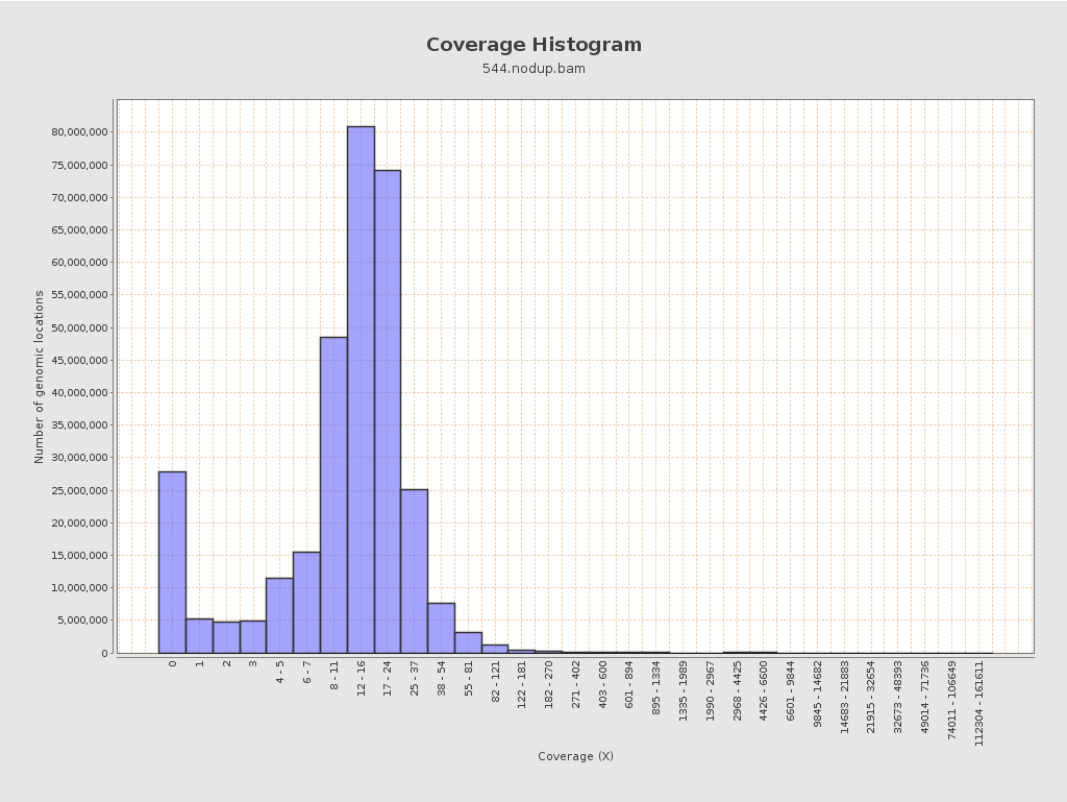
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	461734970	15.5339	56.2386

LT669789.1	36598175	699420987	19.1108	172.3327
LT669790.1	30422129	656298928	21.5731	199.0108
LT669791.1	52758100	972176630	18.4271	154.4776
LT669792.1	28376109	535522726	18.8723	162.7626
LT669793.1	33388210	572552080	17.1483	109.114
LT669794.1	50579949	891140241	17.6184	133.7931
LT669795.1	49795044	1099645079	22.0834	228.4145

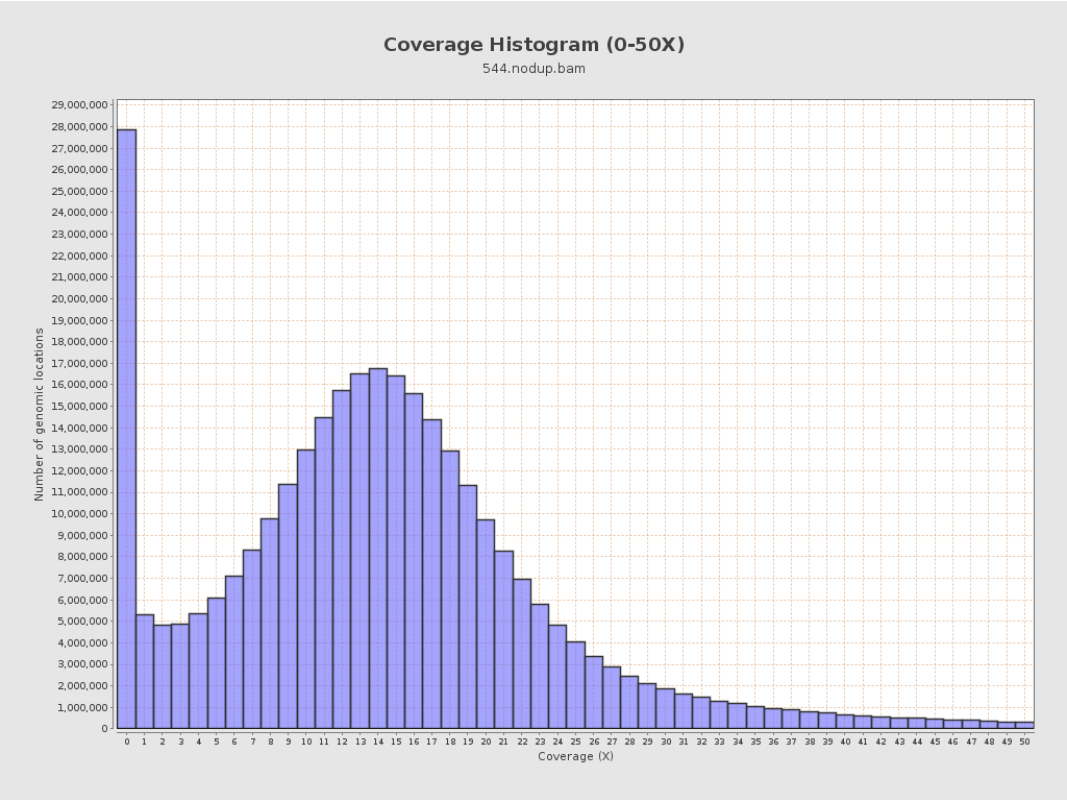
3. Results : Coverage across reference



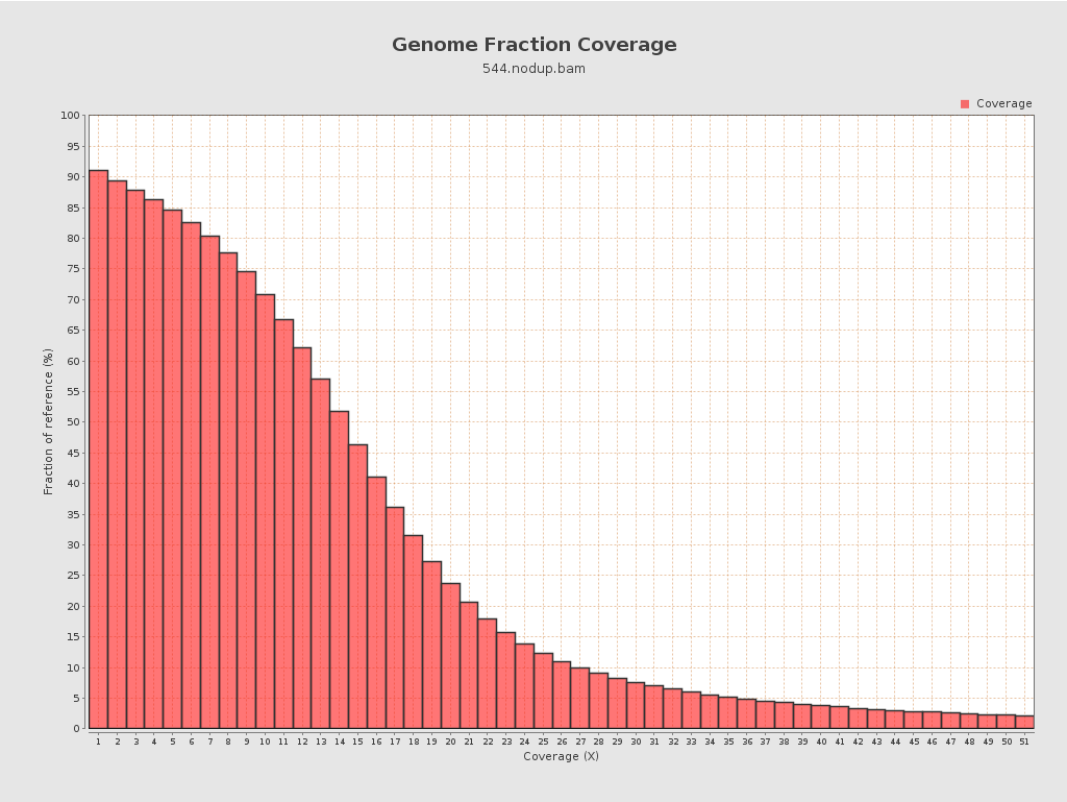
4. Results : Coverage Histogram



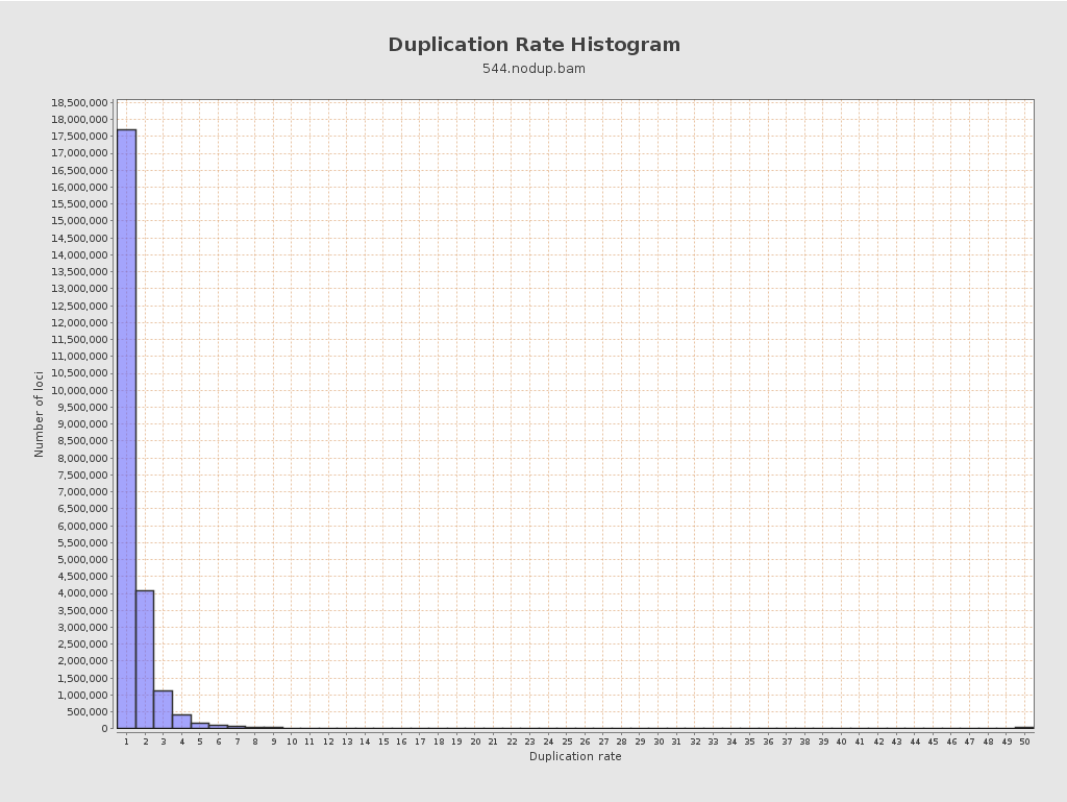
5. Results : Coverage Histogram (0-50X)



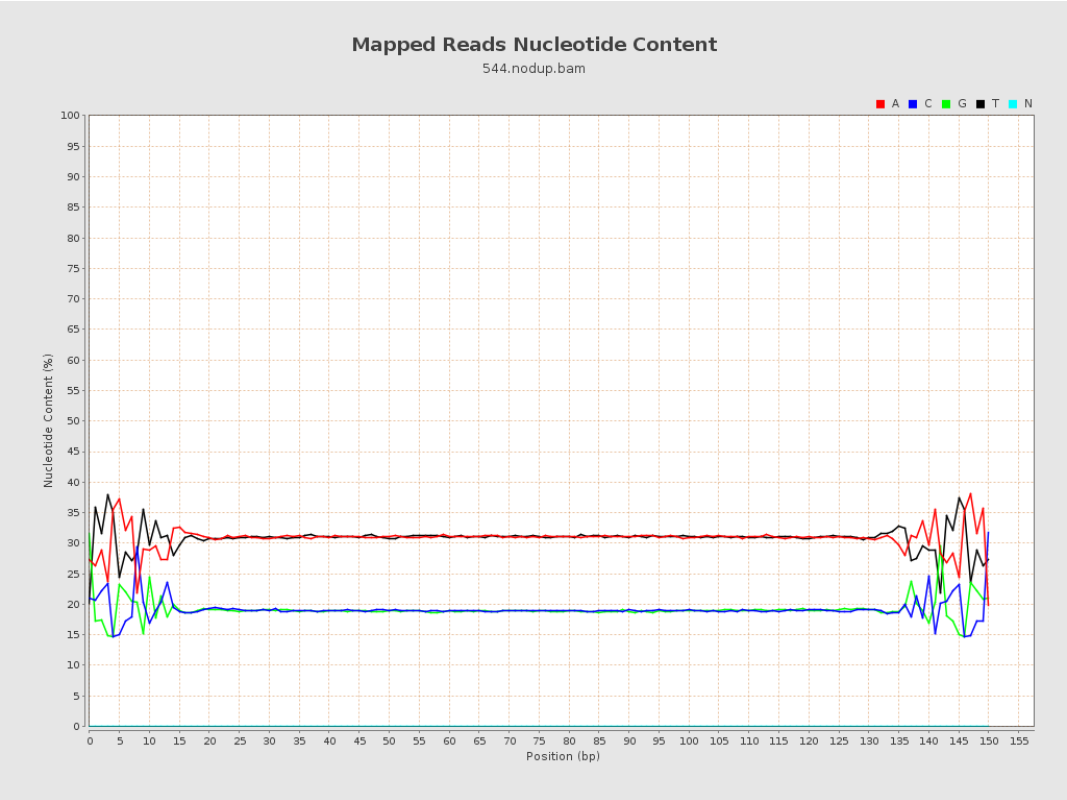
6. Results : Genome Fraction Coverage



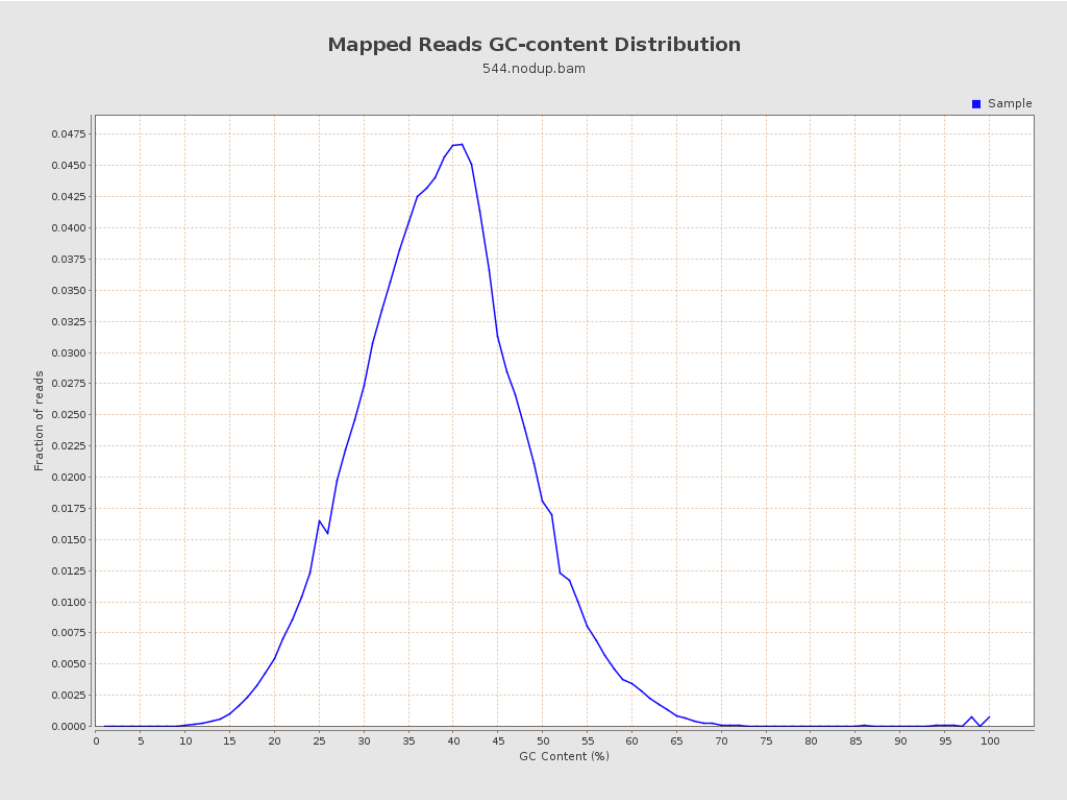
7. Results : Duplication Rate Histogram



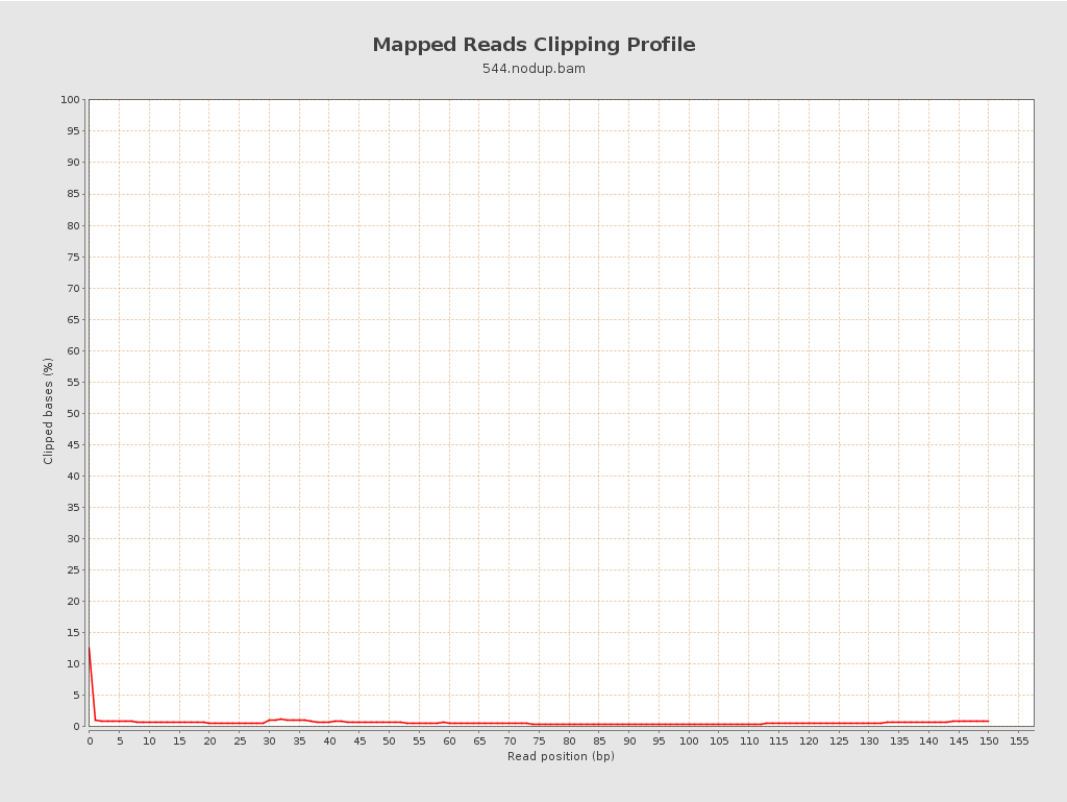
8. Results : Mapped Reads Nucleotide Content



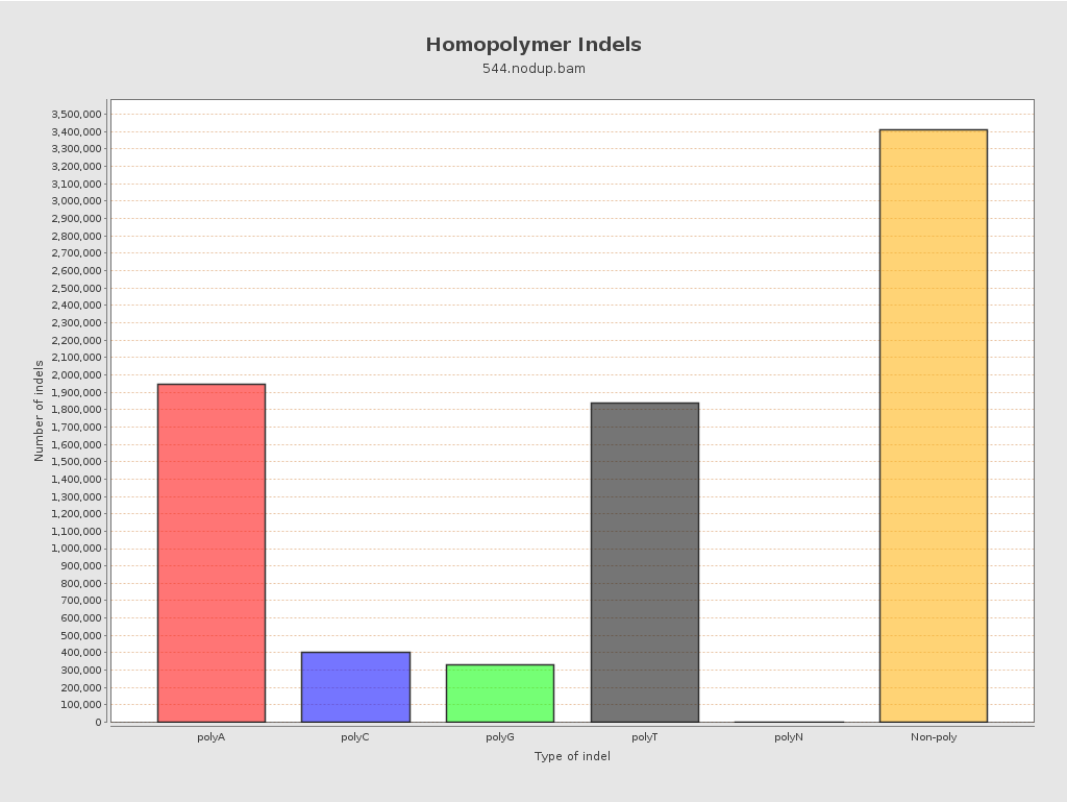
9. Results : Mapped Reads GC-content Distribution



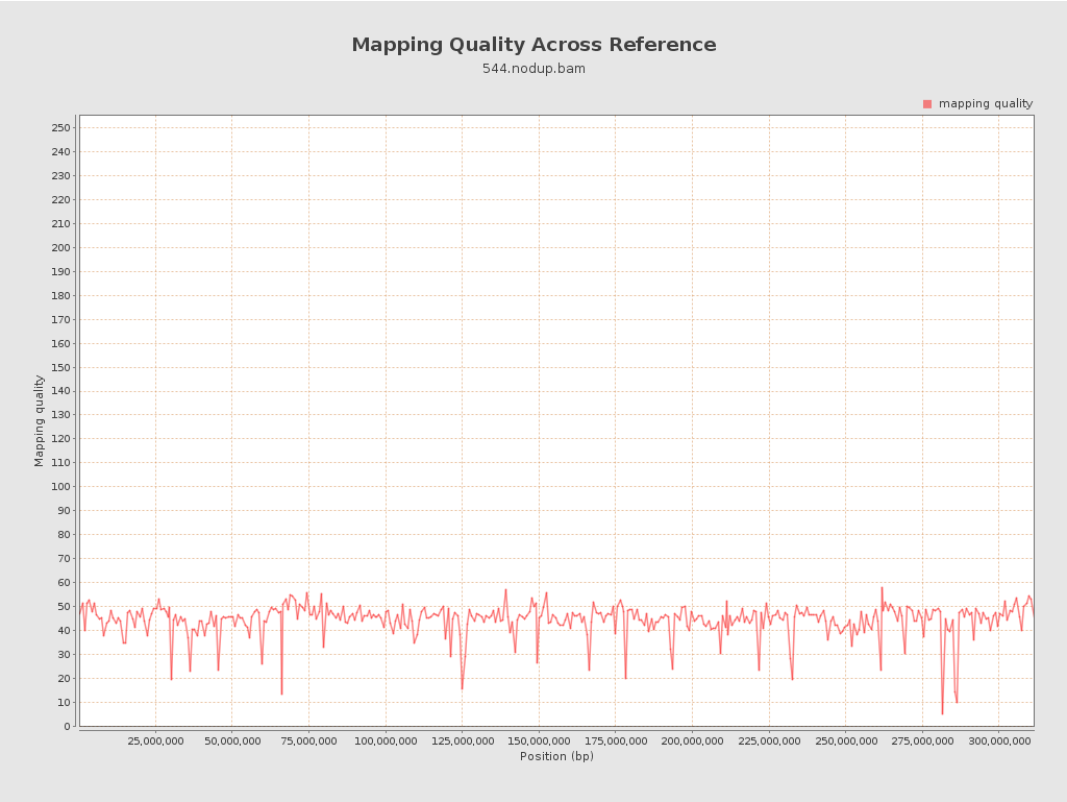
10. Results : Mapped Reads Clipping Profile



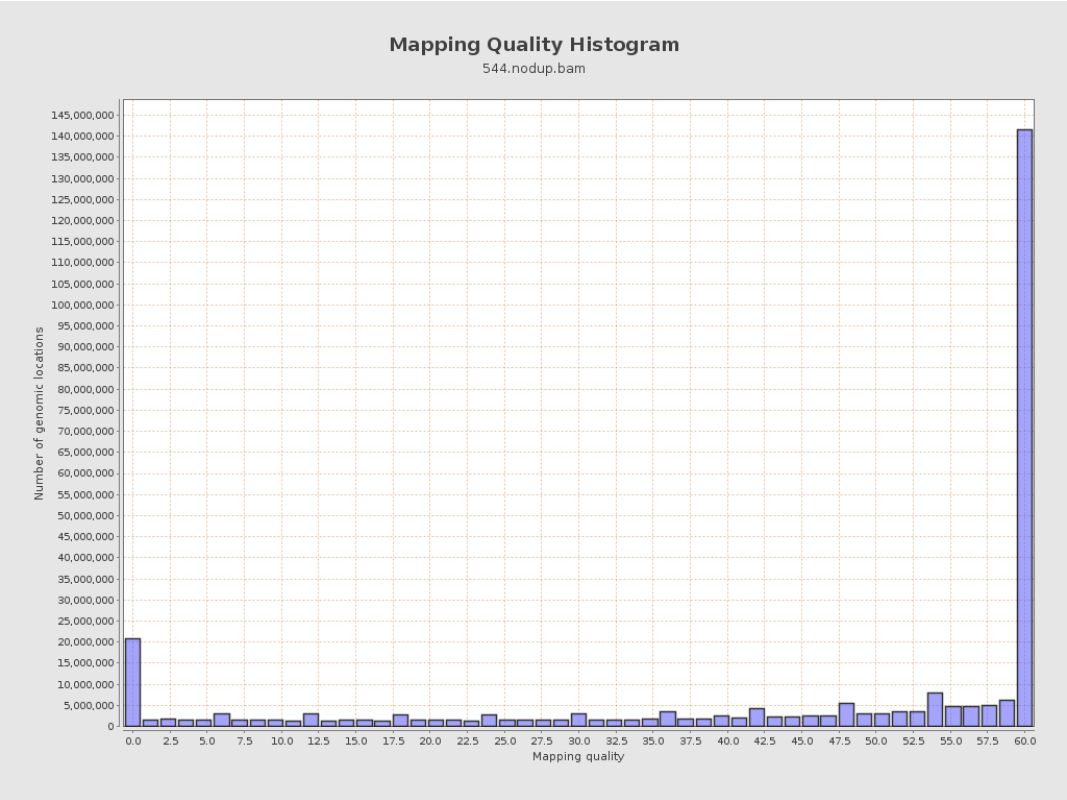
11. Results : Homopolymer Indels



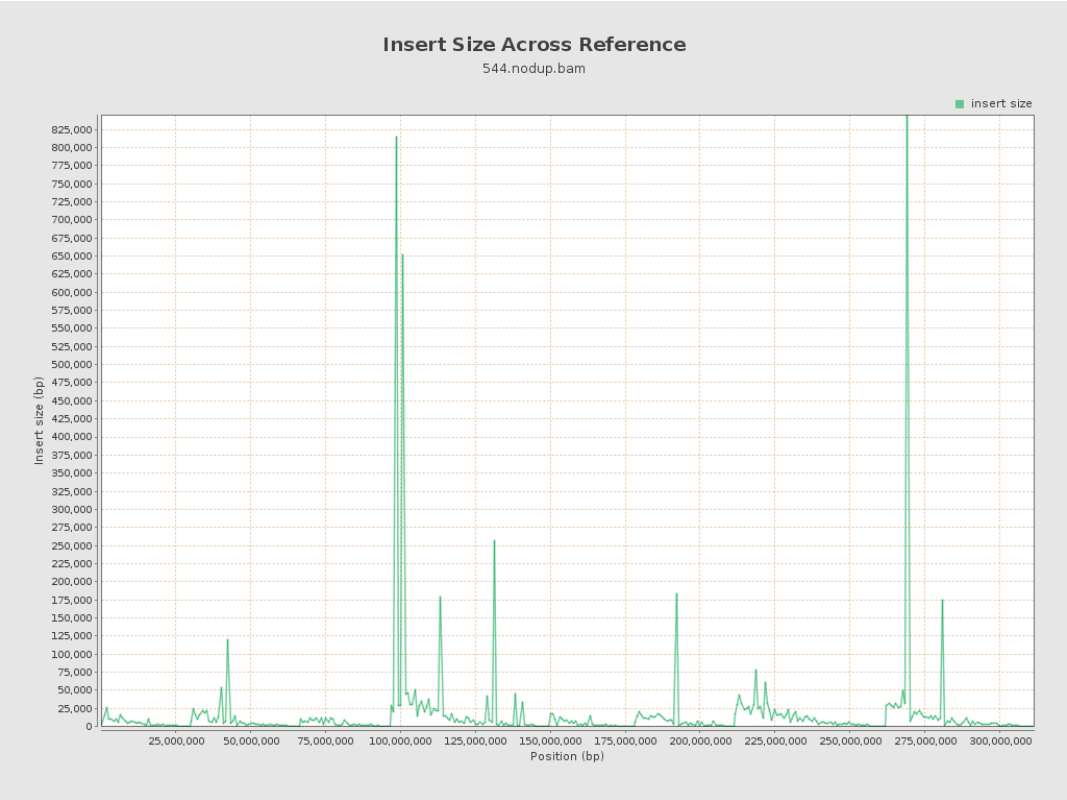
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram