

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:24:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/944
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/944.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/awdata/P26207/P26207_292/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_292_S373_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_292/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_292_S373_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	47,613,858
Mapped reads	44,942,089 / 94.39%
Unmapped reads	2,671,769 / 5.61%
Mapped paired reads	44,942,089 / 94.39%
Mapped reads, first in pair	22,529,967 / 47.32%
Mapped reads, second in pair	22,412,122 / 47.07%
Mapped reads, both in pair	44,114,432 / 92.65%
Mapped reads, singletons	827,657 / 1.74%
Read min/max/mean length	30 / 151 / 148.06
Duplicated reads (flagged)	5,694,952 / 11.96%
Clipped reads	10,200,853 / 21.42%

2.2. ACGT Content

Number/percentage of A's	1,917,459,930 / 30.8%
Number/percentage of C's	1,196,613,870 / 19.22%
Number/percentage of T's	1,917,957,201 / 30.8%
Number/percentage of G's	1,194,370,107 / 19.18%
Number/percentage of N's	23,900 / 0%
GC Percentage	38.4%

2.3. Coverage

Mean	20.0305
Standard Deviation	167.2137

2.4. Mapping Quality

Mean Mapping Quality	44.27
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2.5. Insert size

Mean	217,813.67
Standard Deviation	2,188,737.12
P25/Median/P75	327 / 431 / 560

2.6. Mismatches and indels

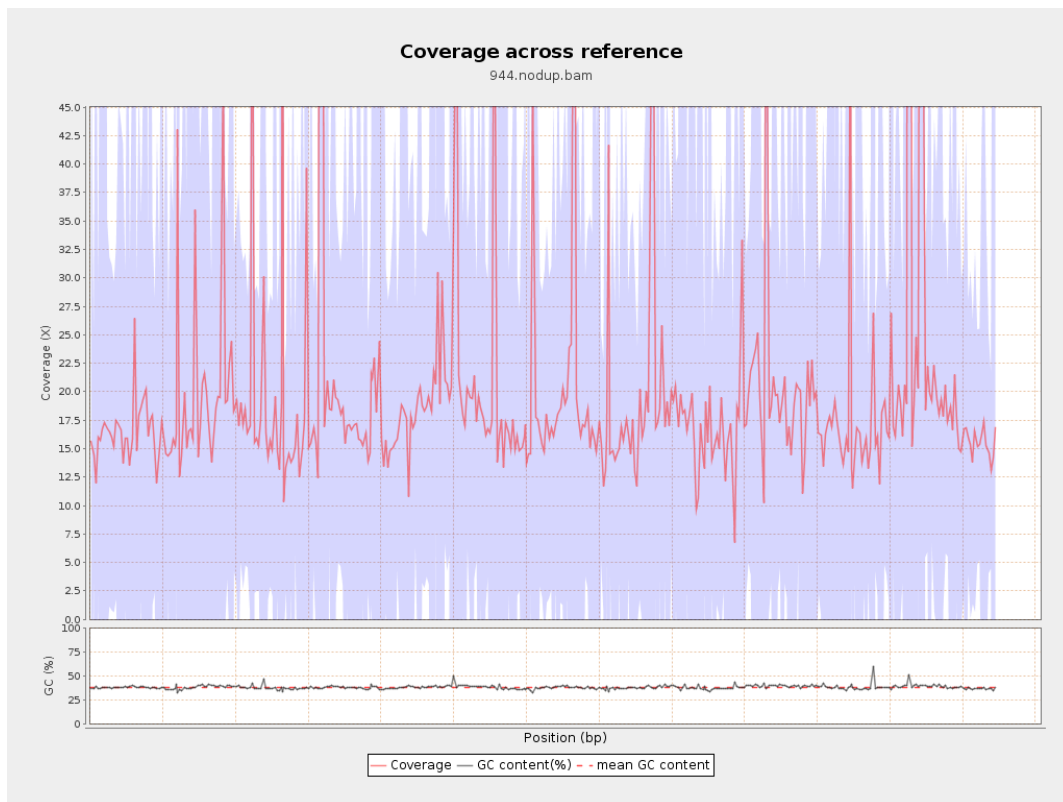
General error rate	2.29%
Mismatches	131,617,122
Insertions	4,068,480
Mapped reads with at least one insertion	8.16%
Deletions	4,221,425
Mapped reads with at least one deletion	8.36%
Homopolymer indels	56.14%

2.7. Chromosome stats

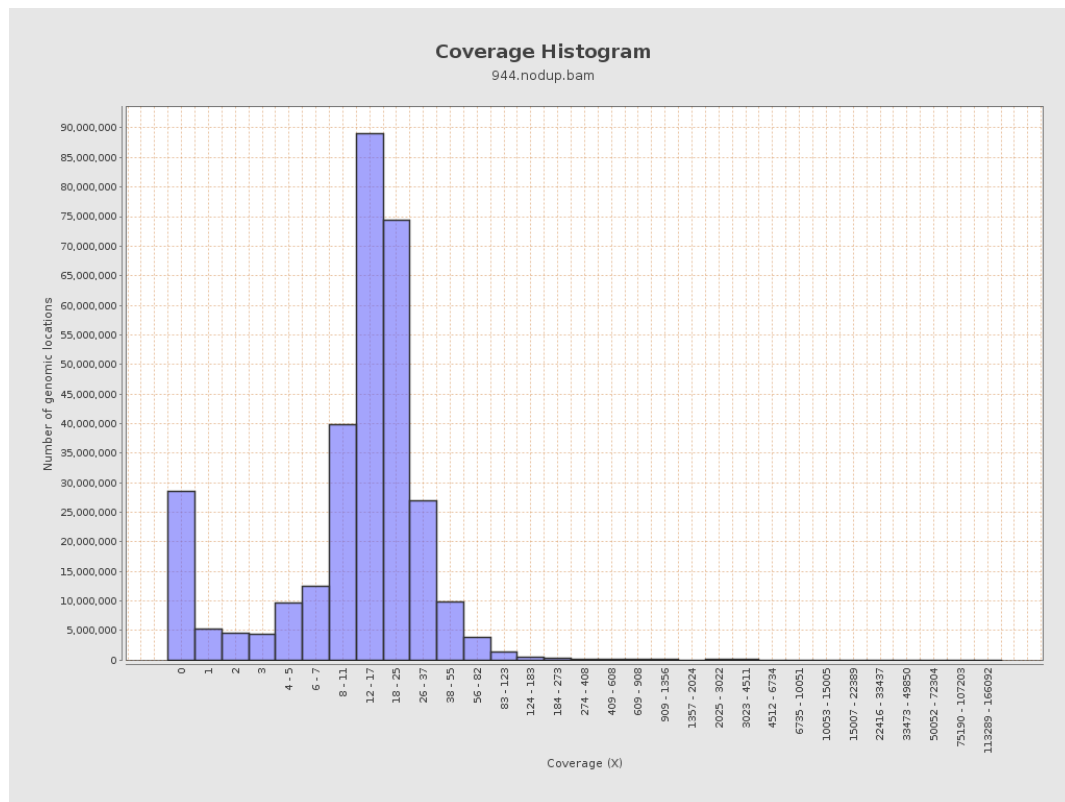
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	483287408	16.259	41.5218

LT669789.1	36598175	745794345	20.3779	165.2473
LT669790.1	30422129	635731279	20.897	152.4943
LT669791.1	52758100	1038297850	19.6803	129.4791
LT669792.1	28376109	551616654	19.4395	179.2142
LT669793.1	33388210	631334257	18.9089	117.5679
LT669794.1	50579949	968594536	19.1498	150.0748
LT669795.1	49795044	1187684425	23.8515	267.2978

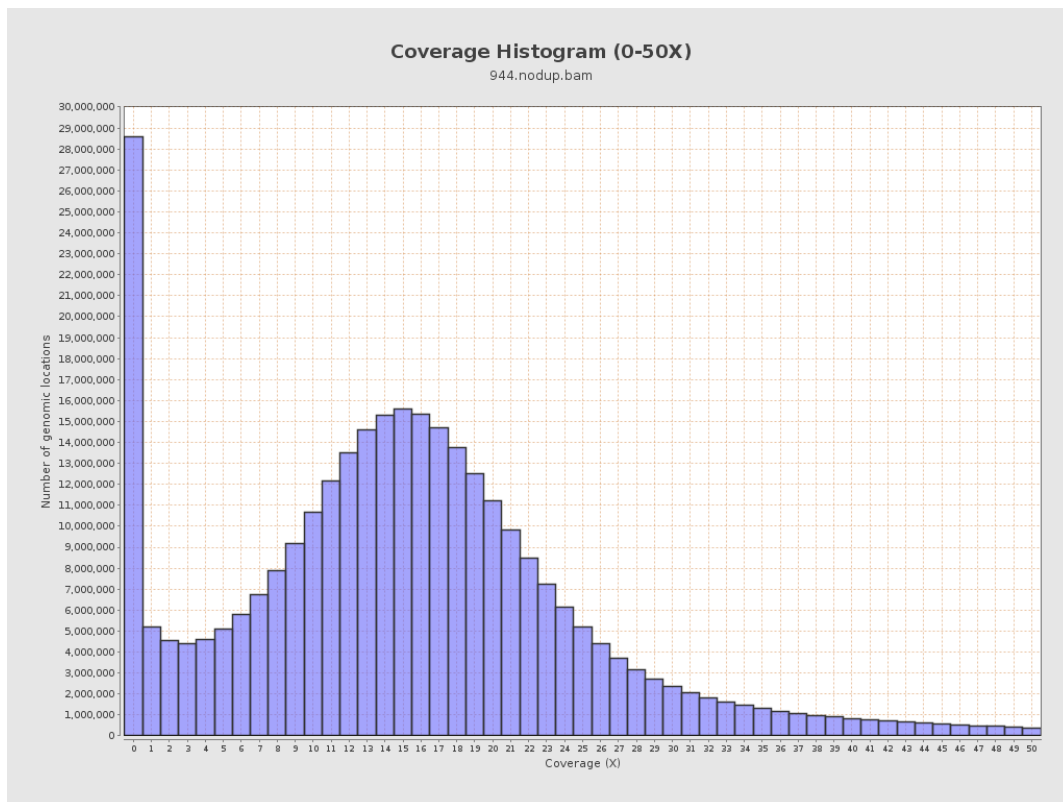
3. Results : Coverage across reference



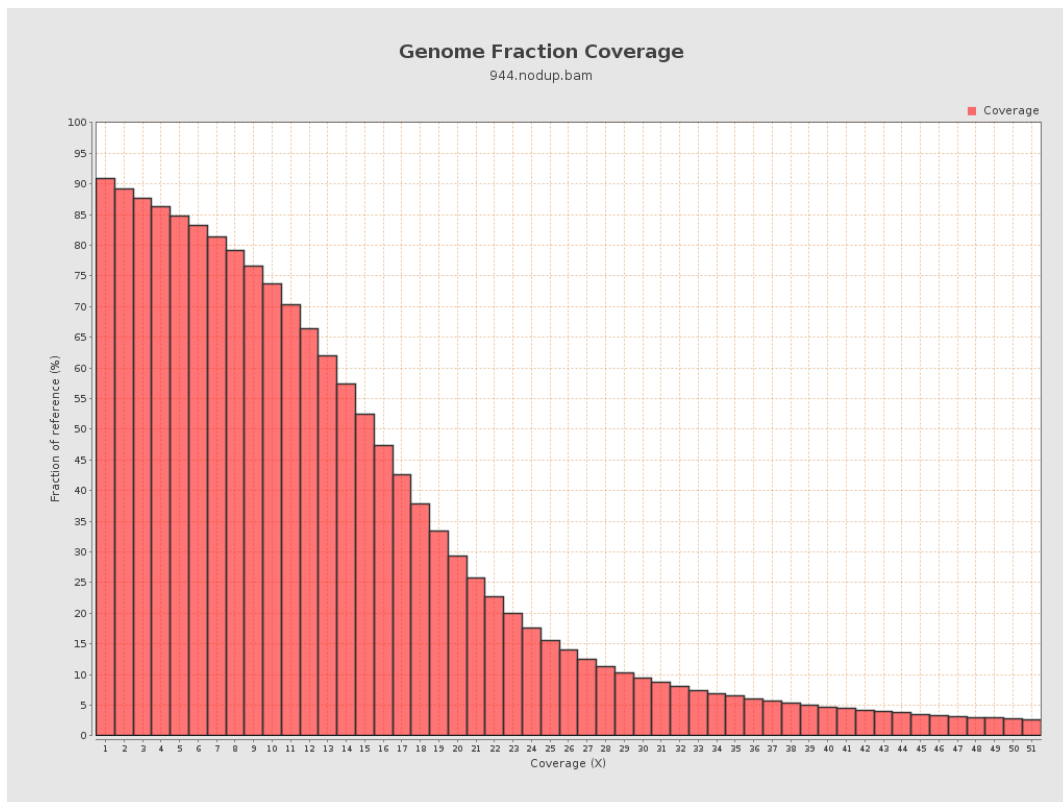
4. Results : Coverage Histogram



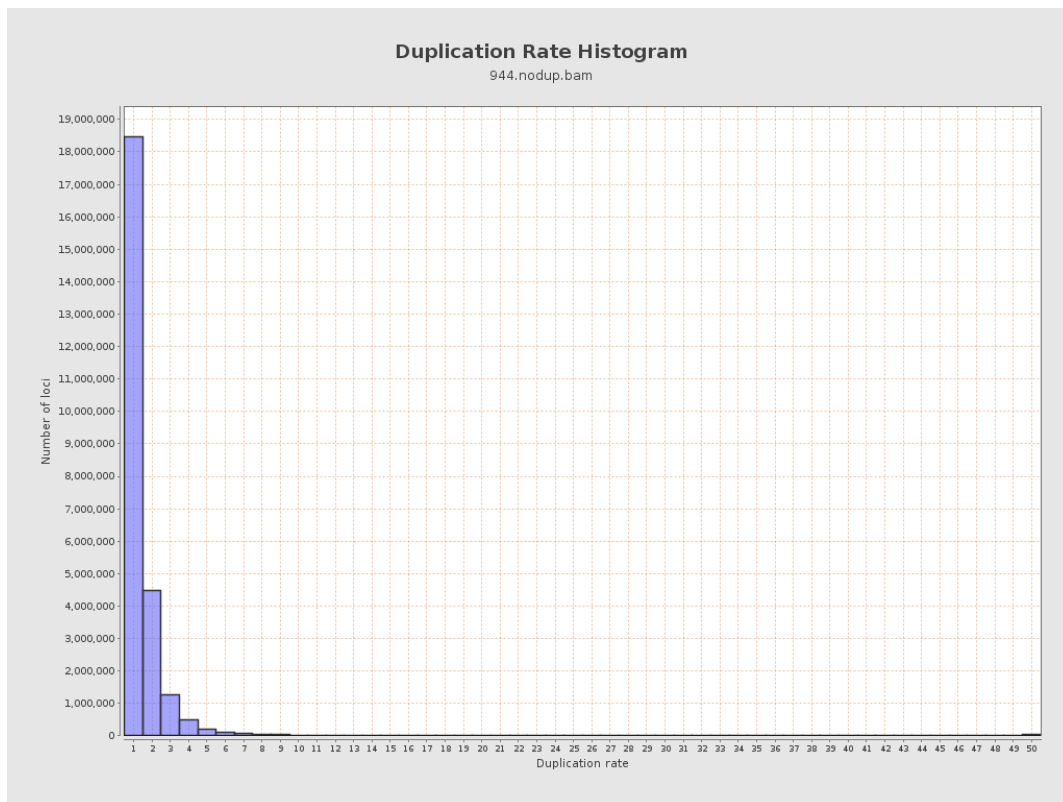
5. Results : Coverage Histogram (0-50X)



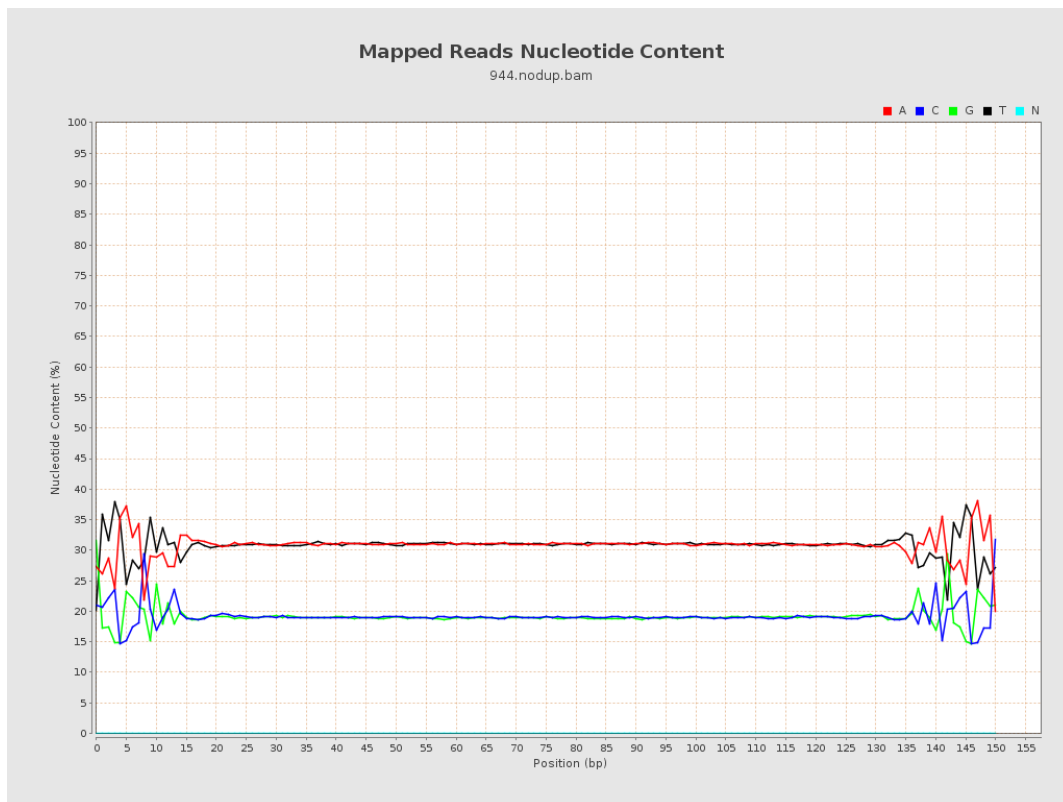
6. Results : Genome Fraction Coverage



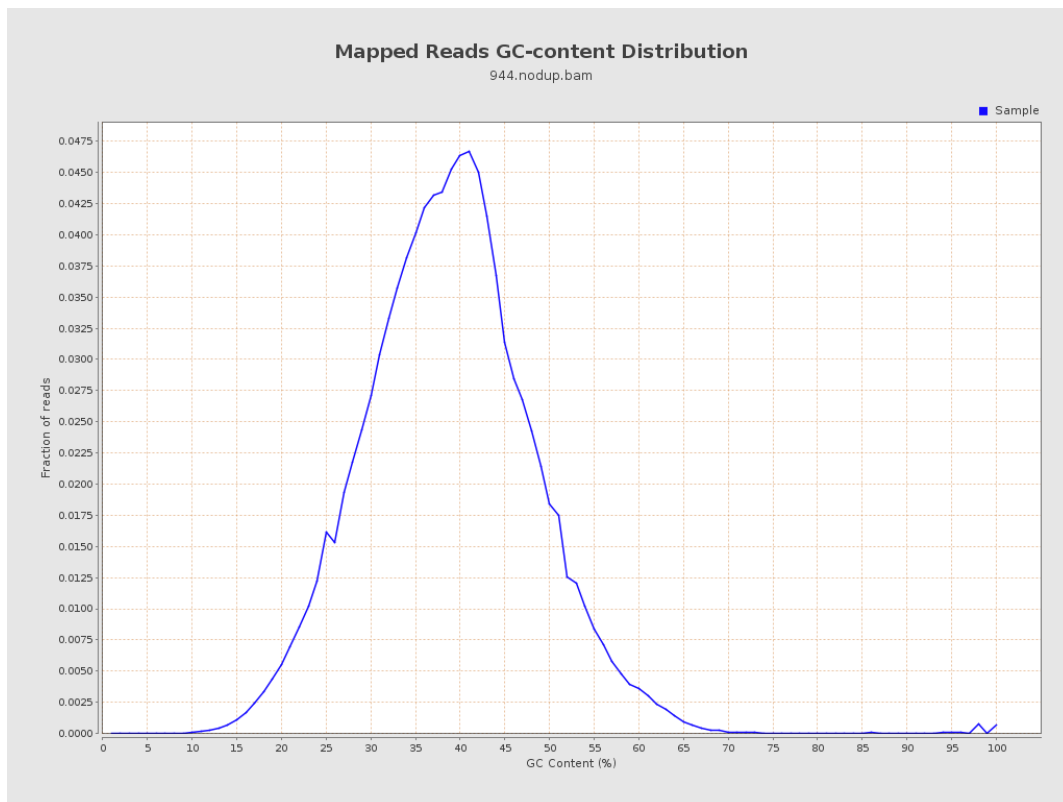
7. Results : Duplication Rate Histogram



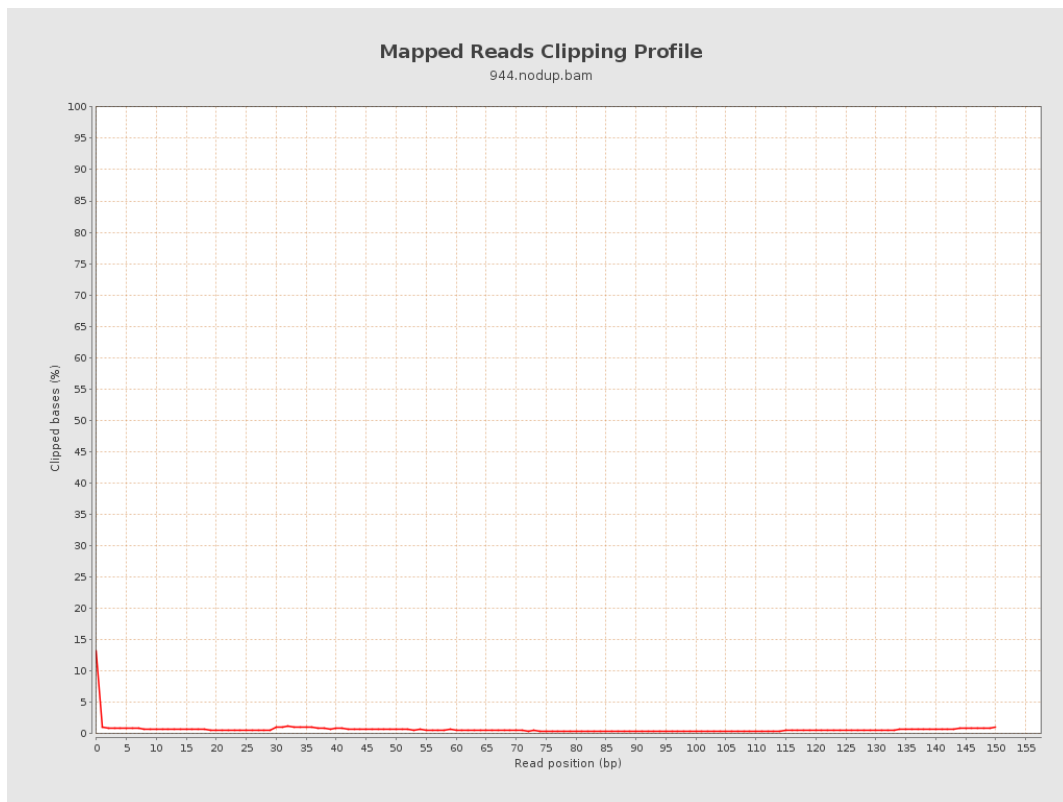
8. Results : Mapped Reads Nucleotide Content



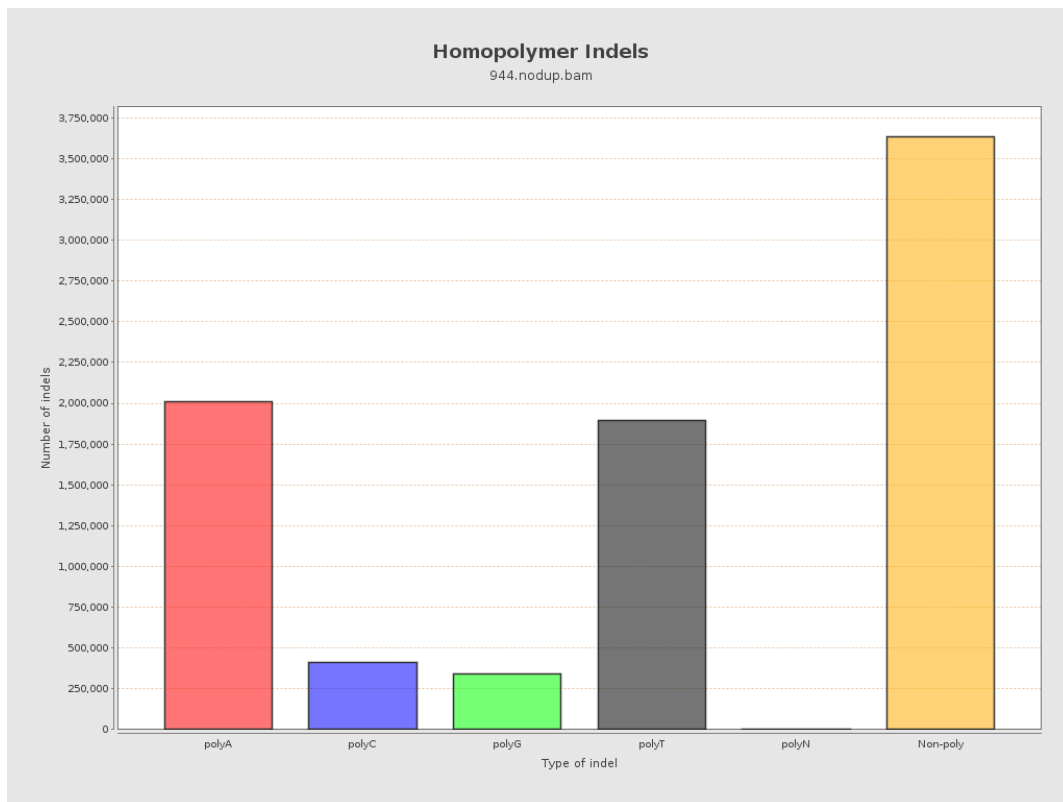
9. Results : Mapped Reads GC-content Distribution



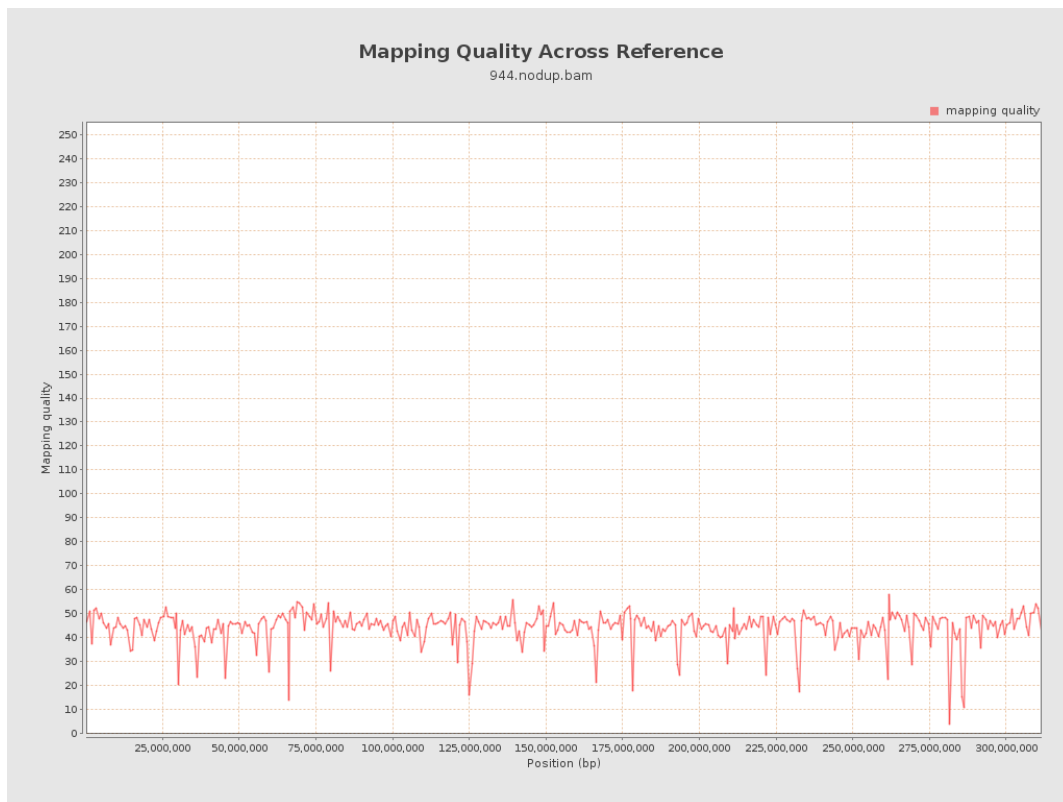
10. Results : Mapped Reads Clipping Profile



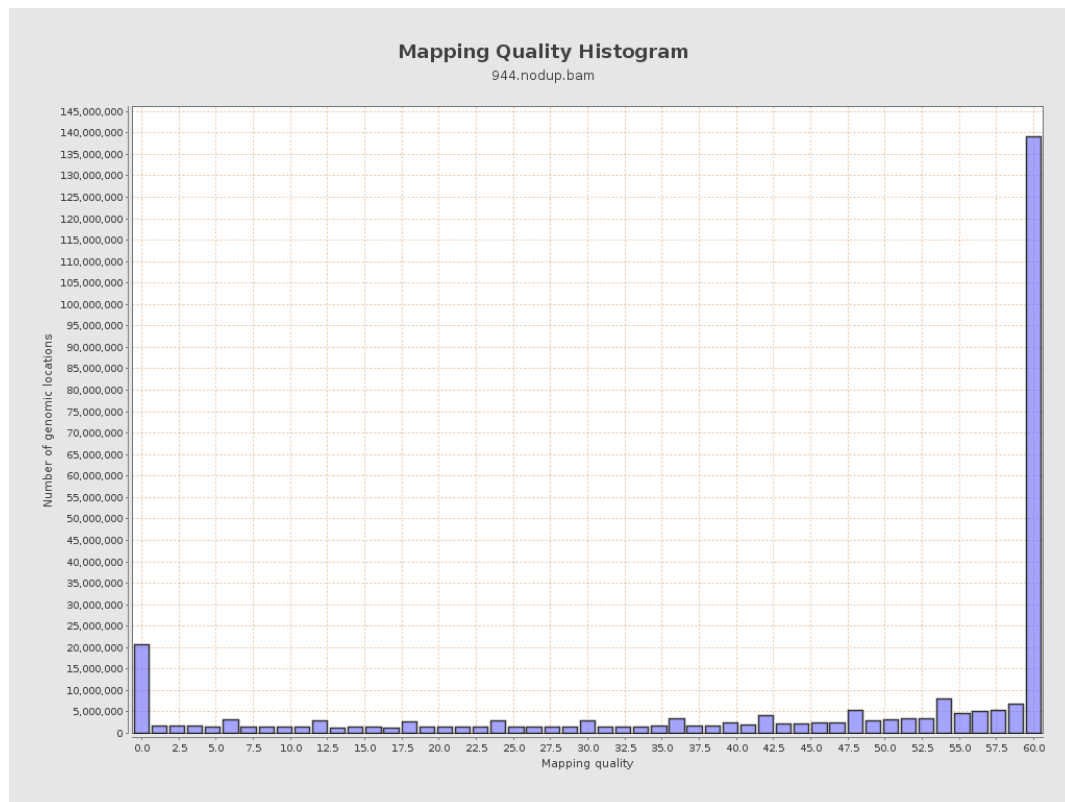
11. Results : Homopolymer Indels



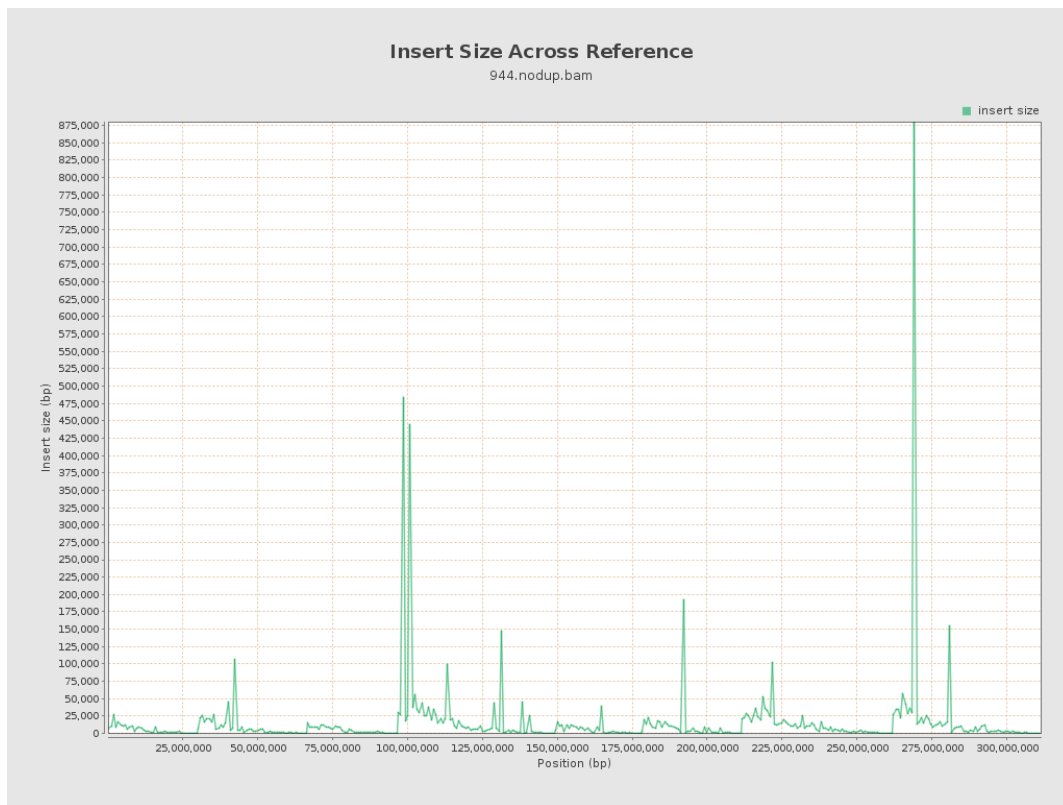
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

