

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/144
4
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1444 .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\t SM:\$sample /proj/uppstore2018210/Aalpina/data/r eference/GCA_900128785.1_MPIPZ. v5_genomic.fa /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_545/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_545_S112_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_545/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_545_S112_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:35:35 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	84,516,246
Mapped reads	72,337,089 / 85.59%
Unmapped reads	12,179,157 / 14.41%
Mapped paired reads	72,337,089 / 85.59%
Mapped reads, first in pair	36,265,475 / 42.91%
Mapped reads, second in pair	36,071,614 / 42.68%
Mapped reads, both in pair	70,969,163 / 83.97%
Mapped reads, singletons	1,367,926 / 1.62%
Read min/max/mean length	30 / 151 / 148.54
Duplicated reads (flagged)	11,193,921 / 13.24%
Clipped reads	16,935,946 / 20.04%

2.2. ACGT Content

Number/percentage of A's	3,073,125,939 / 30.94%
Number/percentage of C's	1,894,638,899 / 19.07%
Number/percentage of T's	3,075,764,475 / 30.96%
Number/percentage of G's	1,889,568,903 / 19.02%
Number/percentage of N's	72,405 / 0%
GC Percentage	38.1%

2.3. Coverage

Mean	31.9534
Standard Deviation	235.463

2.4. Mapping Quality

Mean Mapping Quality	44.45
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2.5. Insert size

Mean	201,456.44
Standard Deviation	2,132,027.72
P25/Median/P75	297 / 392 / 508

2.6. Mismatches and indels

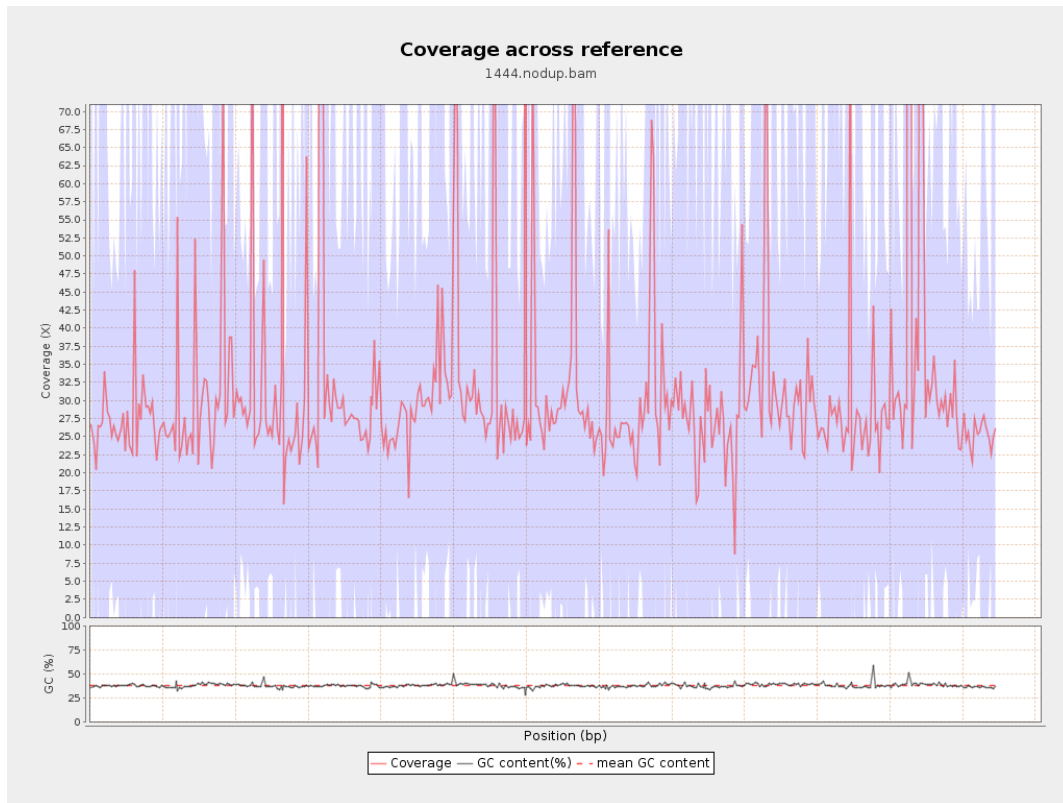
General error rate	2.39%
Mismatches	220,124,480
Insertions	6,425,149
Mapped reads with at least one insertion	8%
Deletions	6,608,979
Mapped reads with at least one deletion	8.14%
Homopolymer indels	56.48%

2.7. Chromosome stats

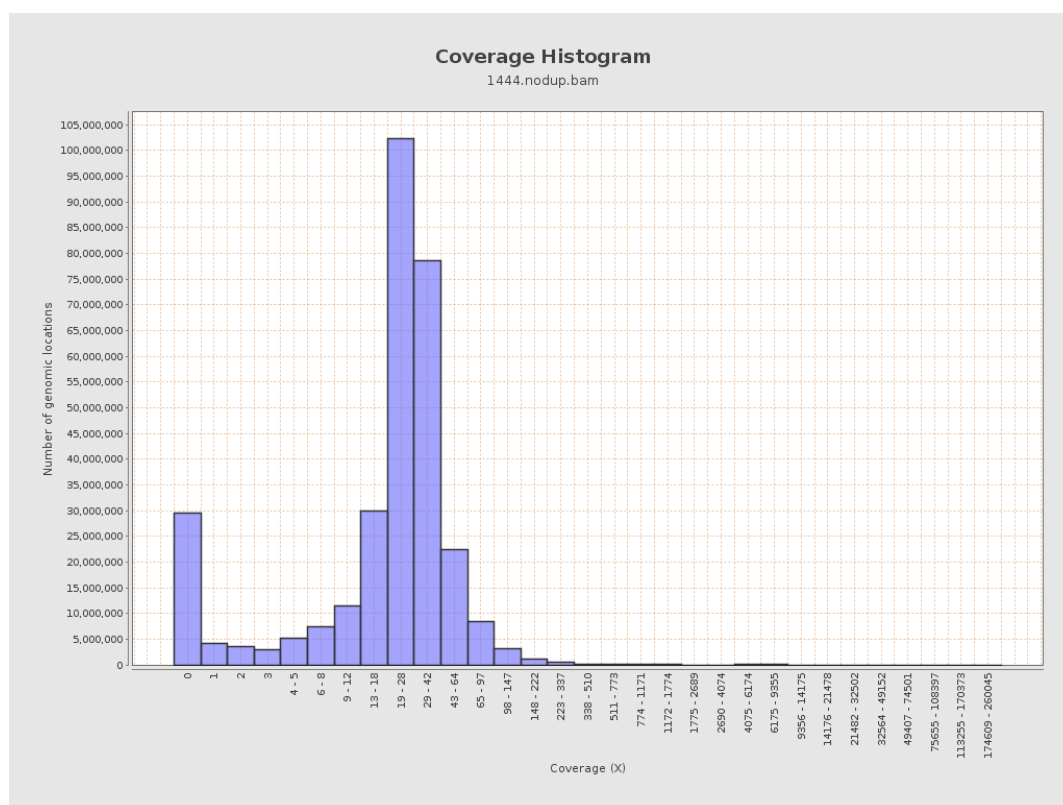
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	801602038	26.9679	68.3943

LT669789.1	36598175	1170577529	31.9846	253.324
LT669790.1	30422129	1017199556	33.4362	233.6824
LT669791.1	52758100	1652858320	31.329	196.6997
LT669792.1	28376109	899256586	31.6906	242.1159
LT669793.1	33388210	973857265	29.1677	124.6316
LT669794.1	50579949	1559706853	30.8365	215.214
LT669795.1	49795044	1882979565	37.8146	362.975

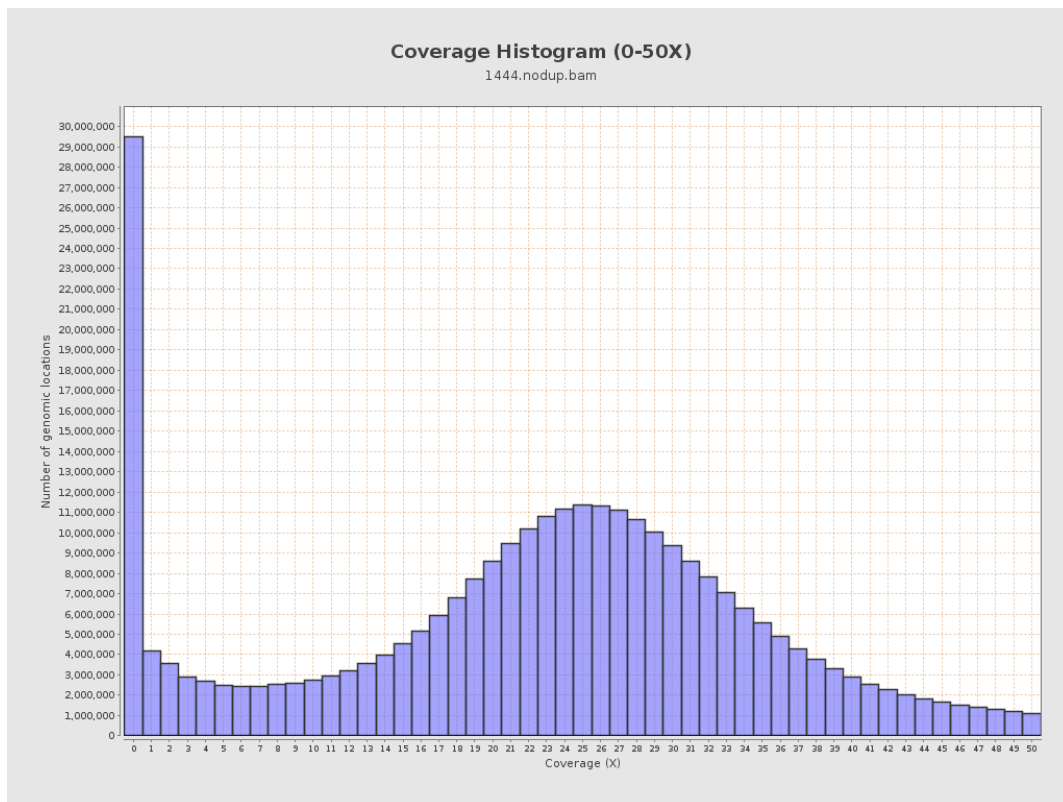
3. Results : Coverage across reference



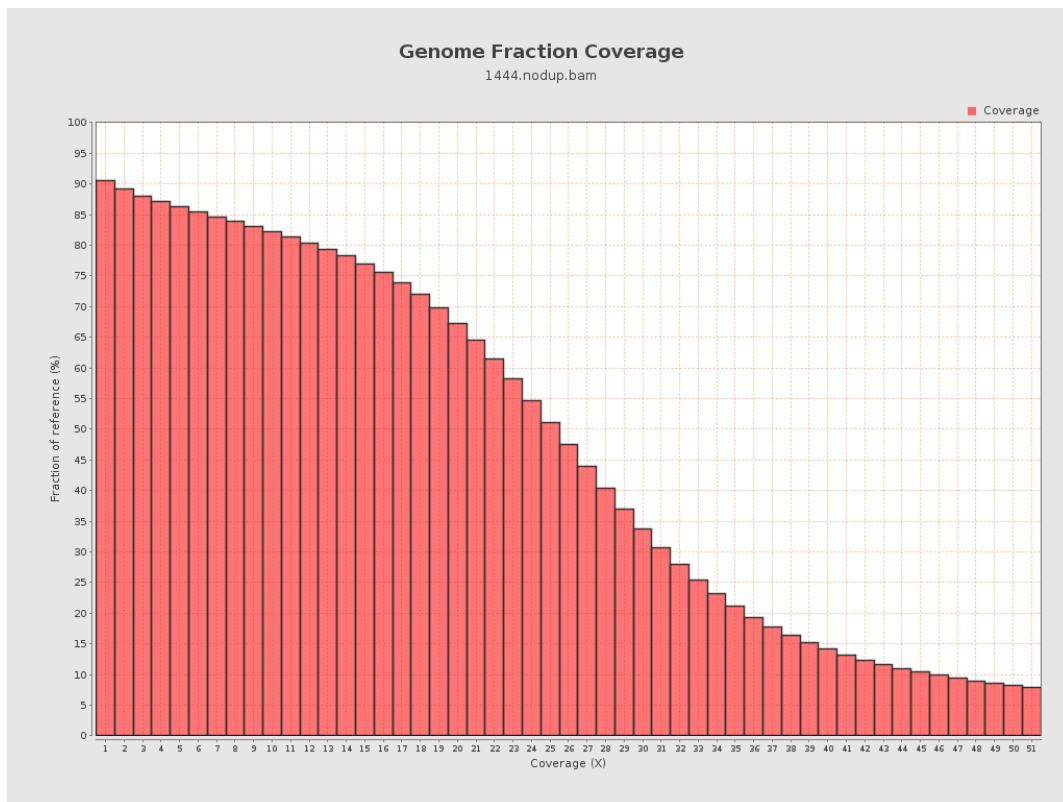
4. Results : Coverage Histogram



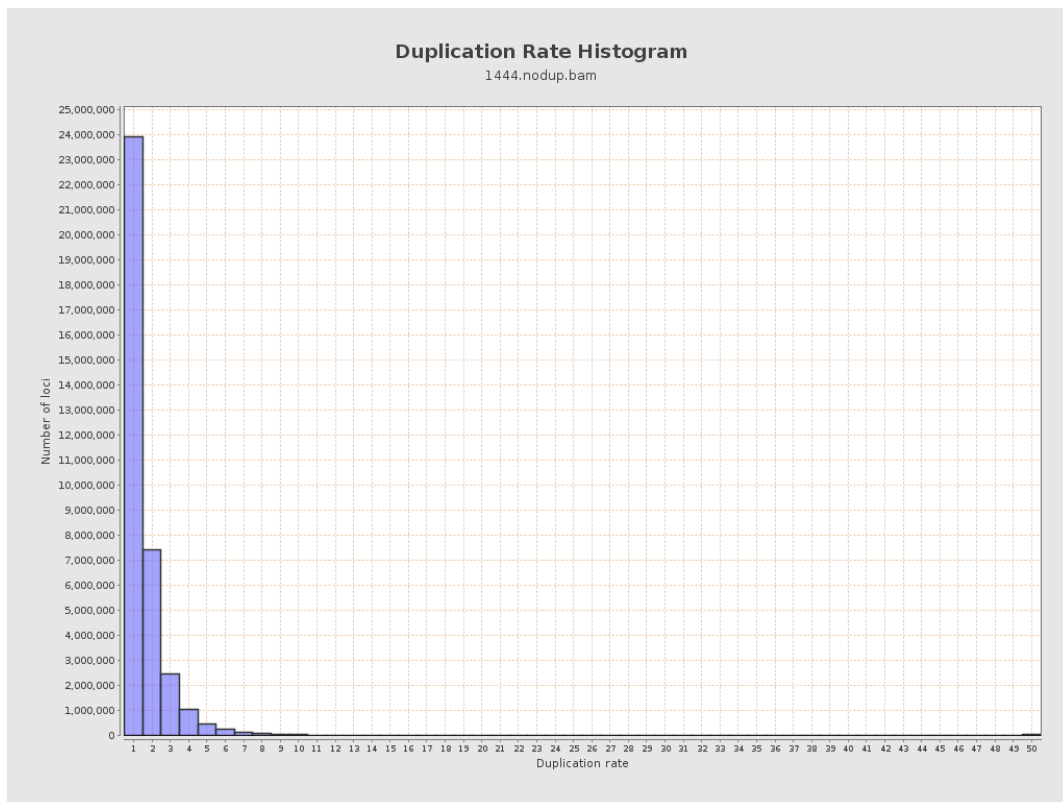
5. Results : Coverage Histogram (0-50X)



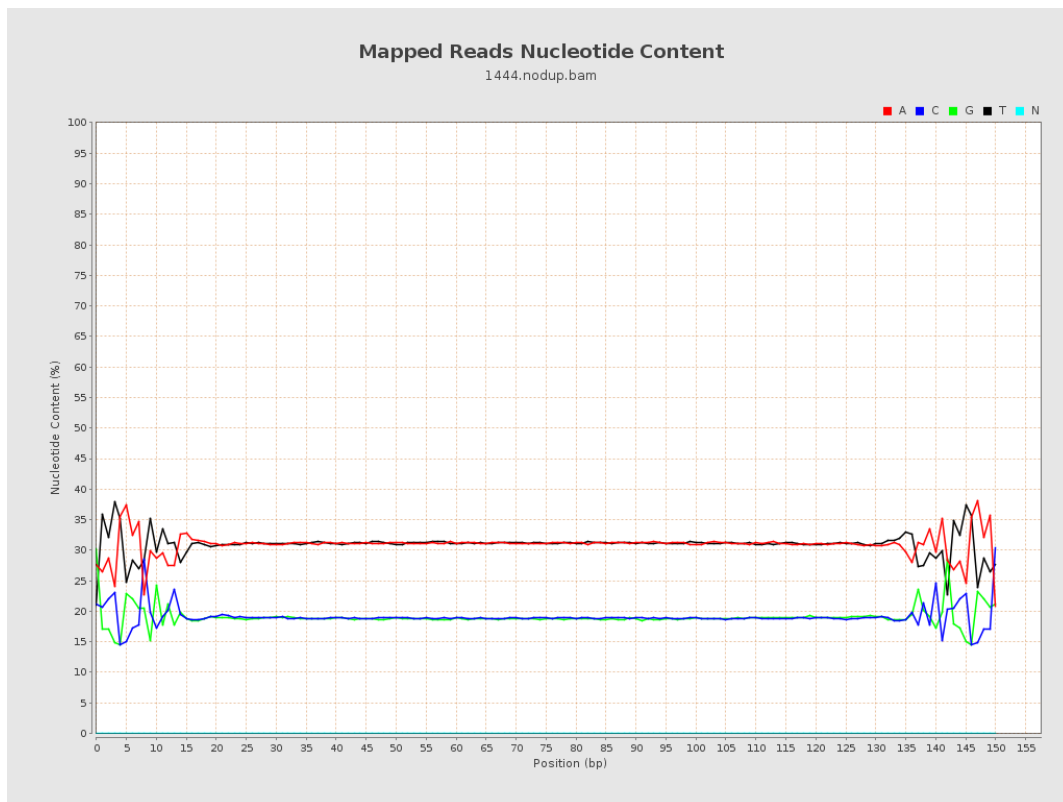
6. Results : Genome Fraction Coverage



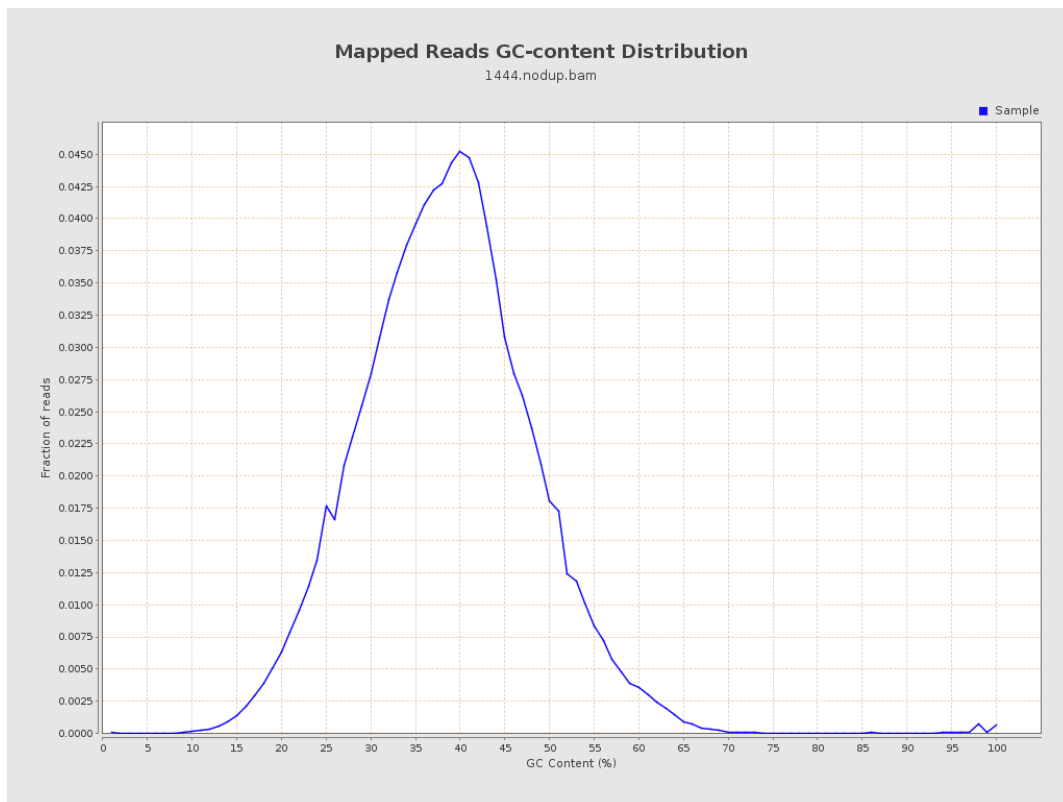
7. Results : Duplication Rate Histogram



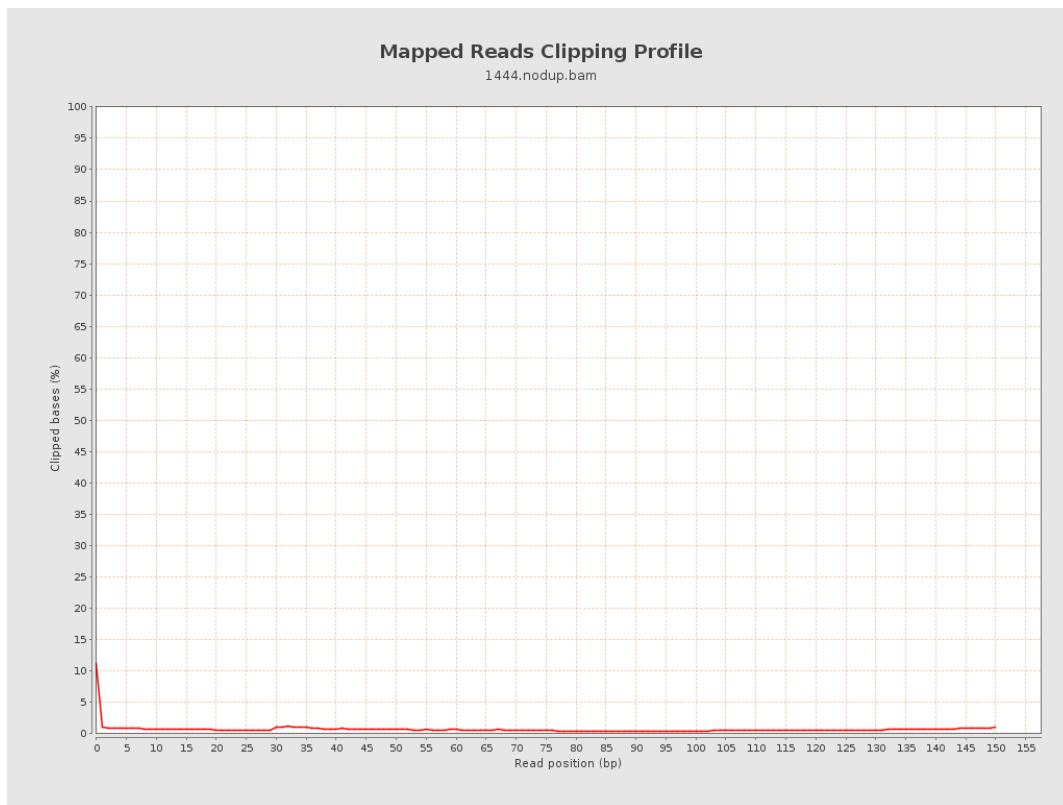
8. Results : Mapped Reads Nucleotide Content



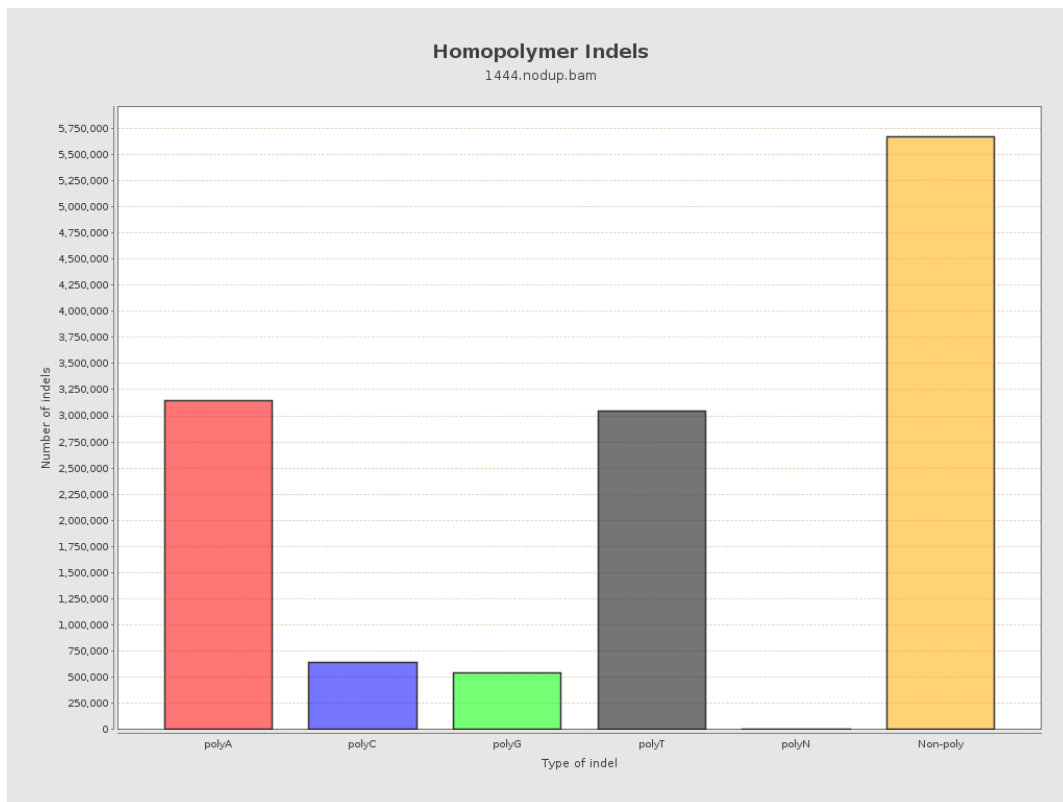
9. Results : Mapped Reads GC-content Distribution



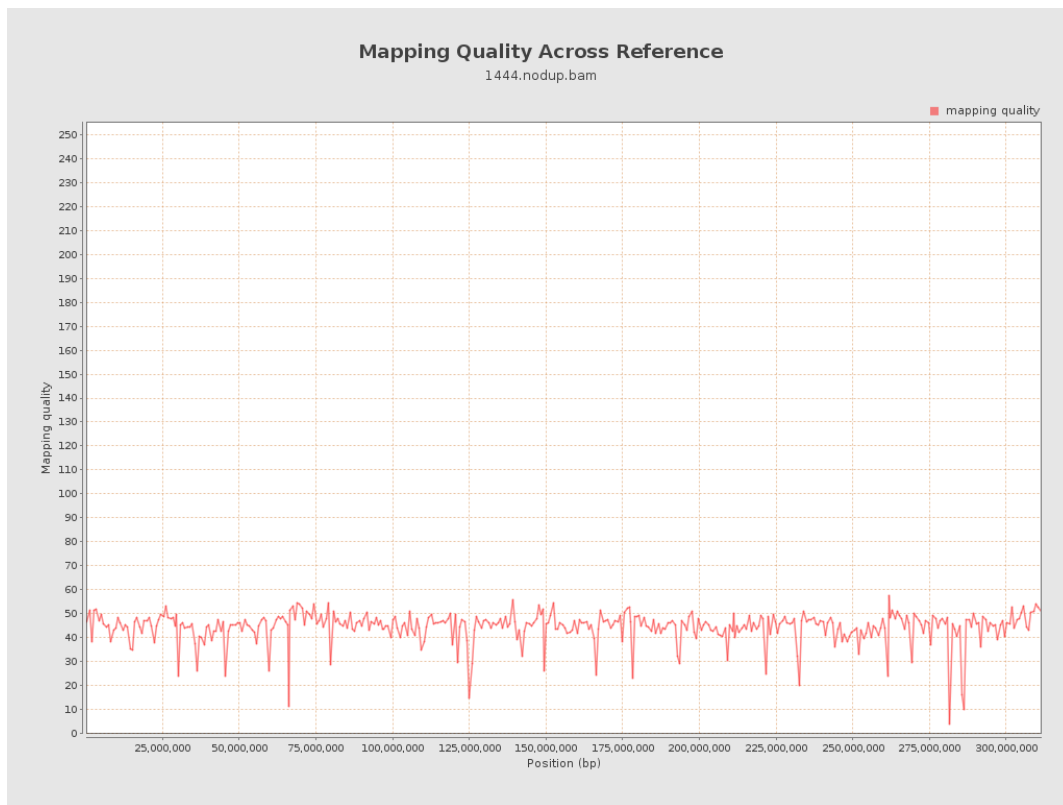
10. Results : Mapped Reads Clipping Profile



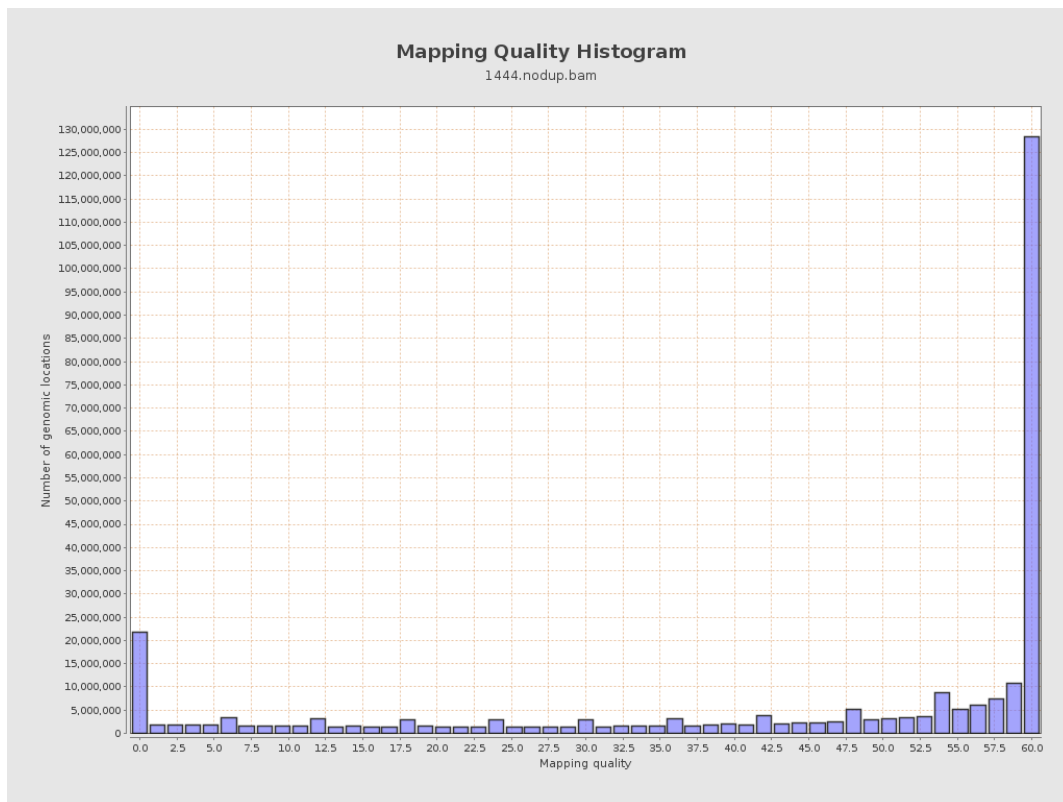
11. Results : Homopolymer Indels



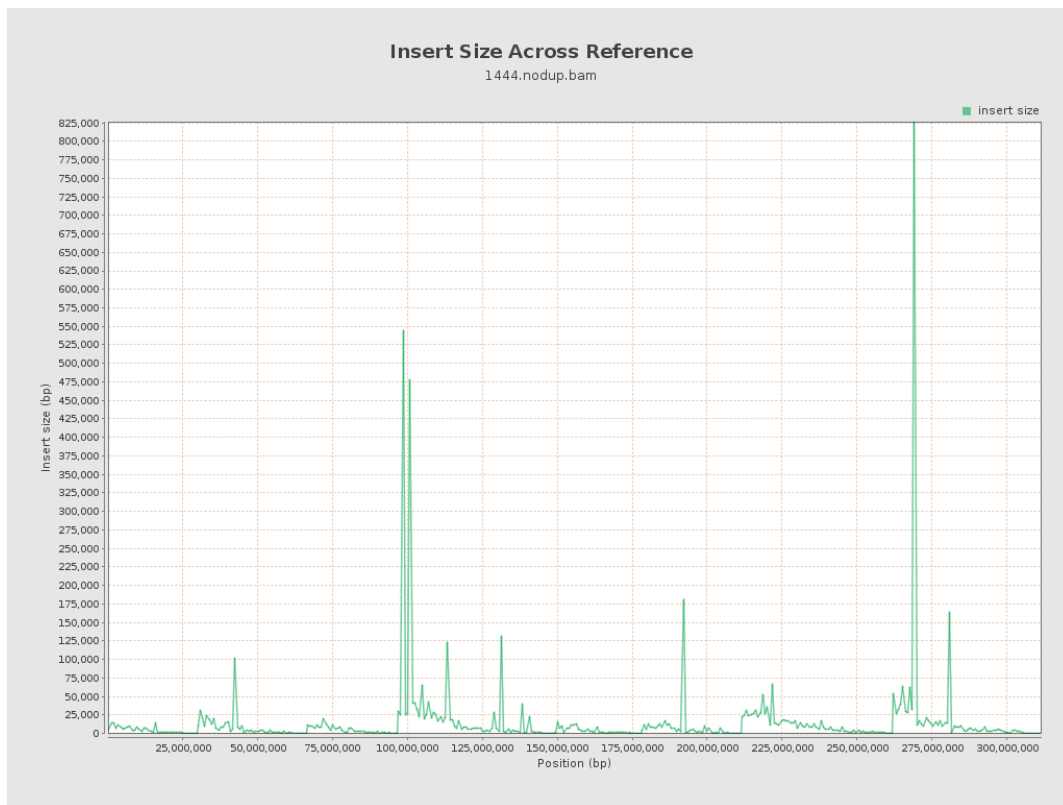
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

