Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:33:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/864.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/864.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_164/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_164_S254_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_164/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_164_S254_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:33:43 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	73,135,780
Mapped reads	67,012,712 / 91.63%
Unmapped reads	6,123,068 / 8.37%
Mapped paired reads	67,012,712 / 91.63%
Mapped reads, first in pair	33,570,491 / 45.9%
Mapped reads, second in pair	33,442,221 / 45.73%
Mapped reads, both in pair	65,273,240 / 89.25%
Mapped reads, singletons	1,739,472 / 2.38%
Read min/max/mean length	30 / 151 / 148.16
Duplicated reads (flagged)	11,717,182 / 16.02%
Clipped reads	15,155,042 / 20.72%

2.2. ACGT Content

Number/percentage of A's	2,859,888,395 / 30.9%
Number/percentage of C's	1,767,609,683 / 19.1%
Number/percentage of T's	2,860,901,405 / 30.92%
Number/percentage of G's	1,765,671,817 / 19.08%
Number/percentage of N's	39,871 / 0%
GC Percentage	38.18%

2.3. Coverage

Mean	29.7707
Standard Deviation	249.2649

2.4. Mapping Quality

Mean Mapping Quality	44.1

2.5. Insert size

Mean	247,997.7
Standard Deviation	2,381,880.72
P25/Median/P75	329 / 431 / 565

2.6. Mismatches and indels

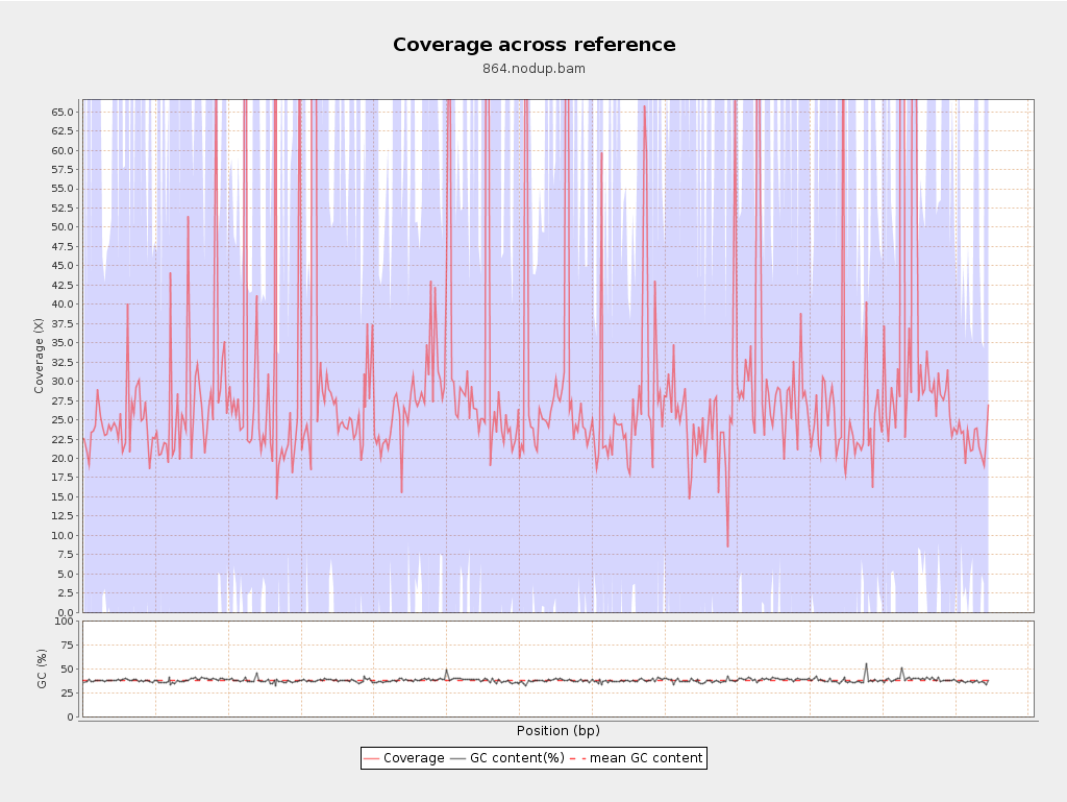
General error rate	2.3%
Mismatches	194,634,376
Insertions	6,456,850
Mapped reads with at least one insertion	8.62%
Deletions	6,356,053
Mapped reads with at least one deletion	8.42%
Homopolymer indels	57.12%

2.7. Chromosome stats

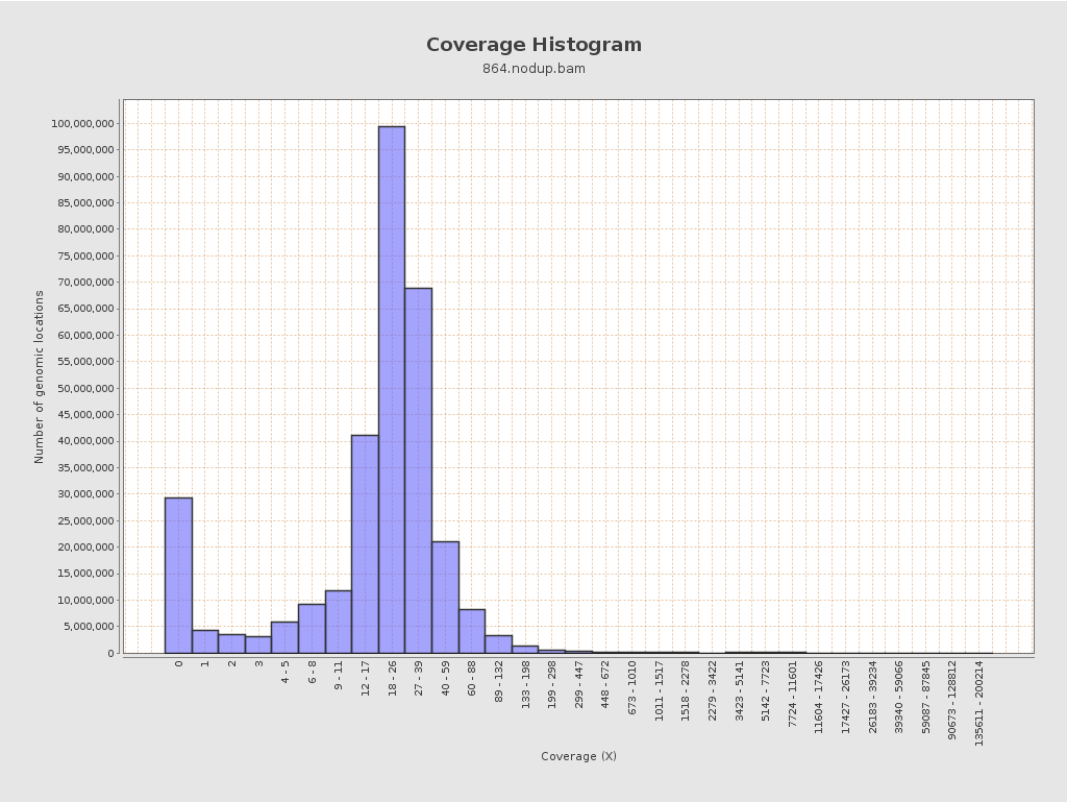
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	713369291	23.9995	88.1421

LT669789.1	36598175	1110354827	30.3391	264.053
LT669790.1	30422129	1017127314	33.4338	306.2562
LT669791.1	52758100	1565293823	29.6693	249.5172
LT669792.1	28376109	838696782	29.5564	306.5636
LT669793.1	33388210	904509248	27.0907	133.8064
LT669794.1	50579949	1456863468	28.8032	207.9082
LT669795.1	49795044	1671594881	33.5695	316.5335

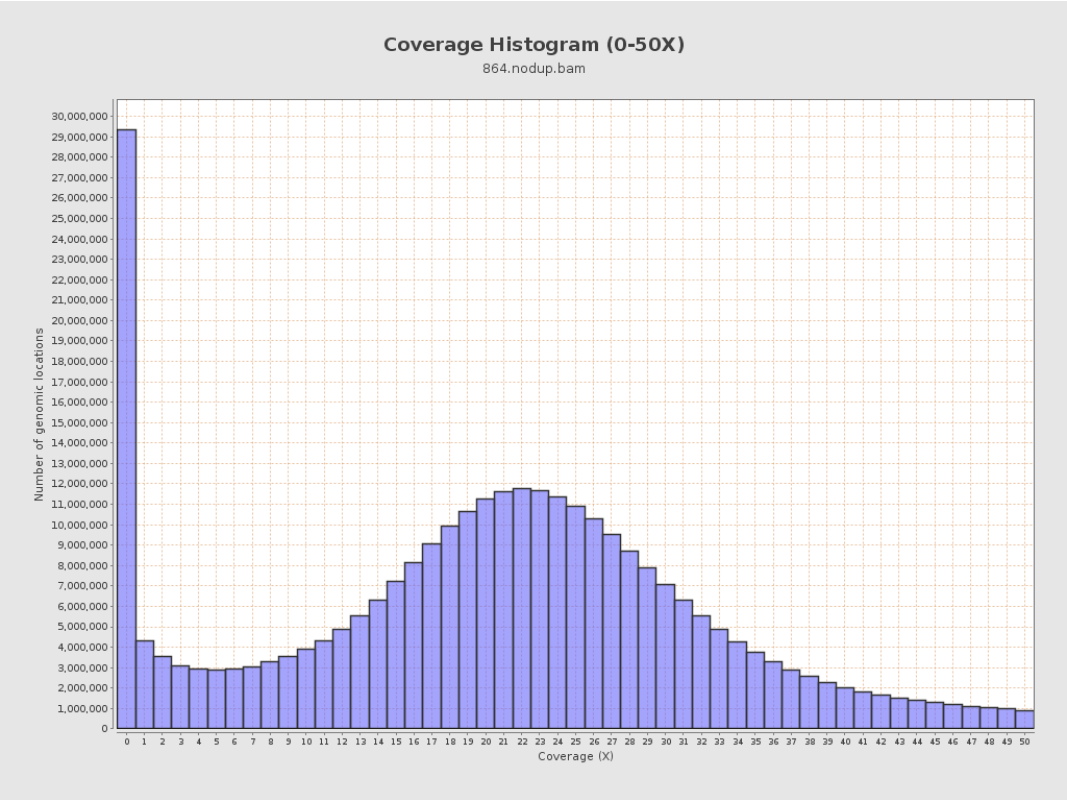
3. Results : Coverage across reference



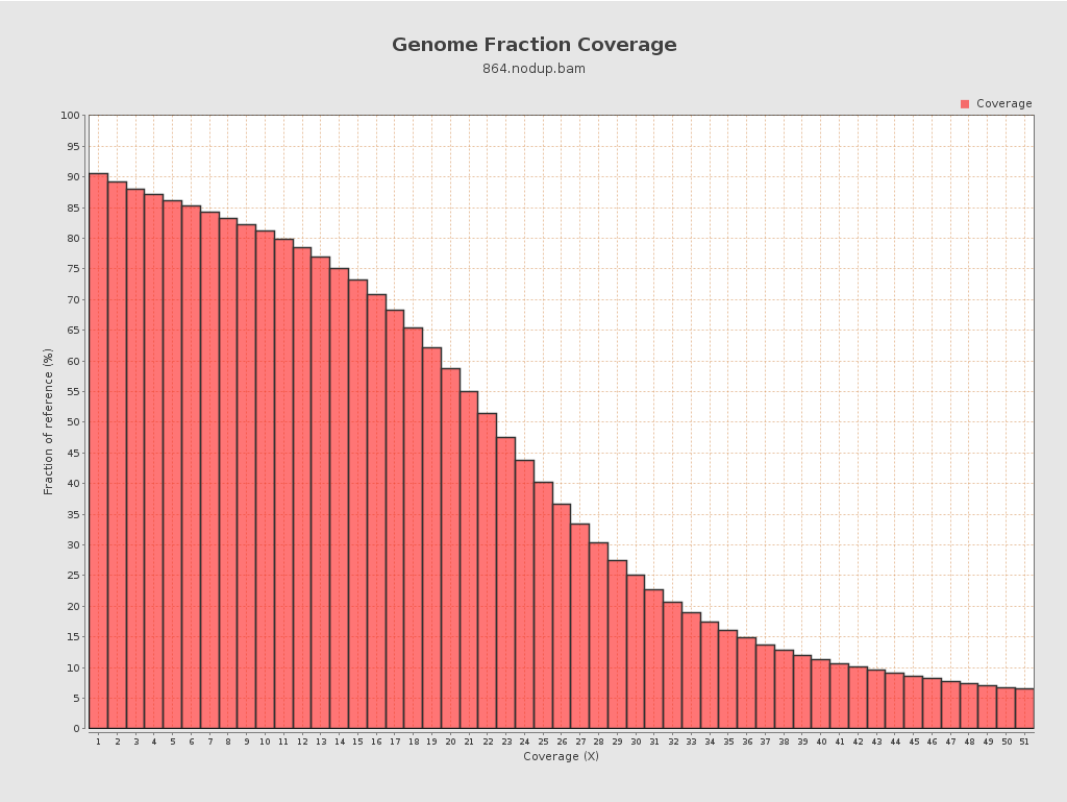
4. Results : Coverage Histogram



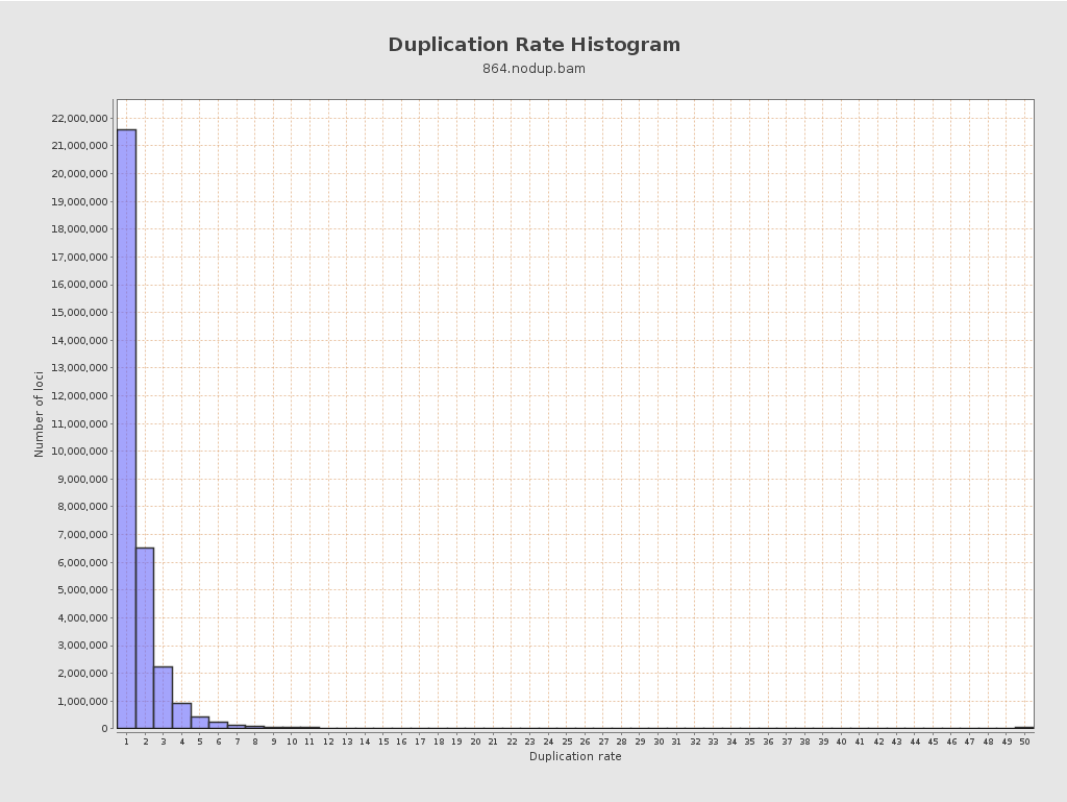
5. Results : Coverage Histogram (0-50X)



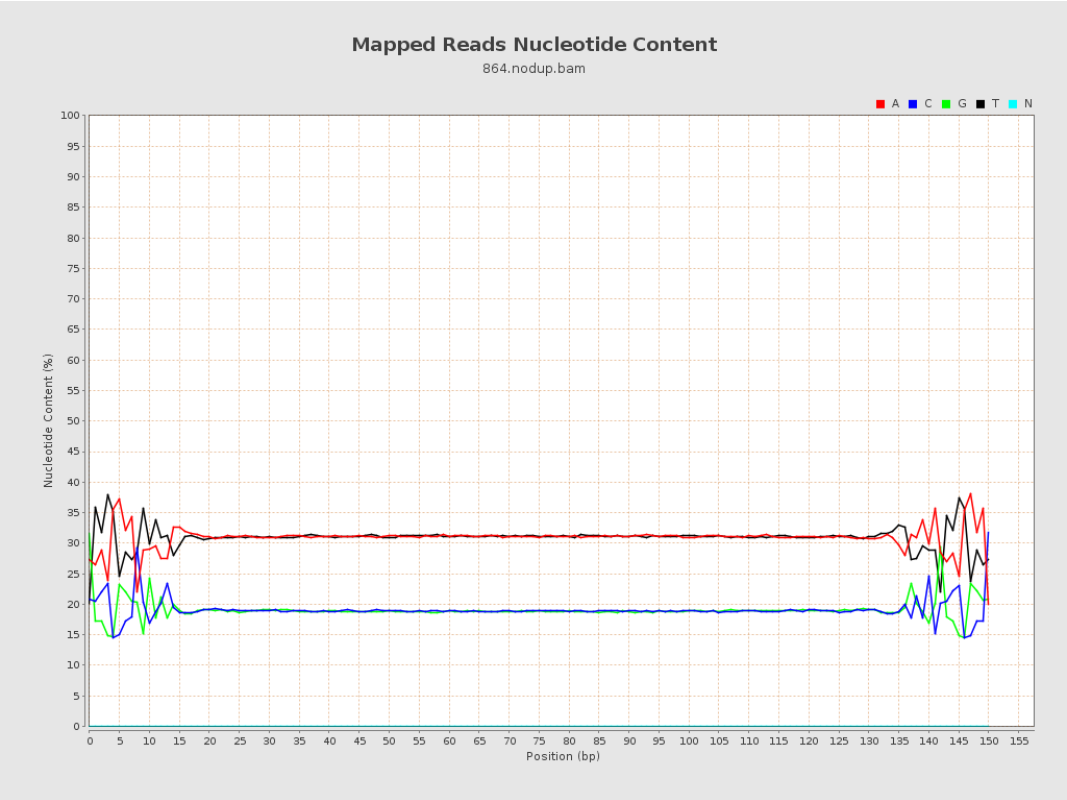
6. Results : Genome Fraction Coverage



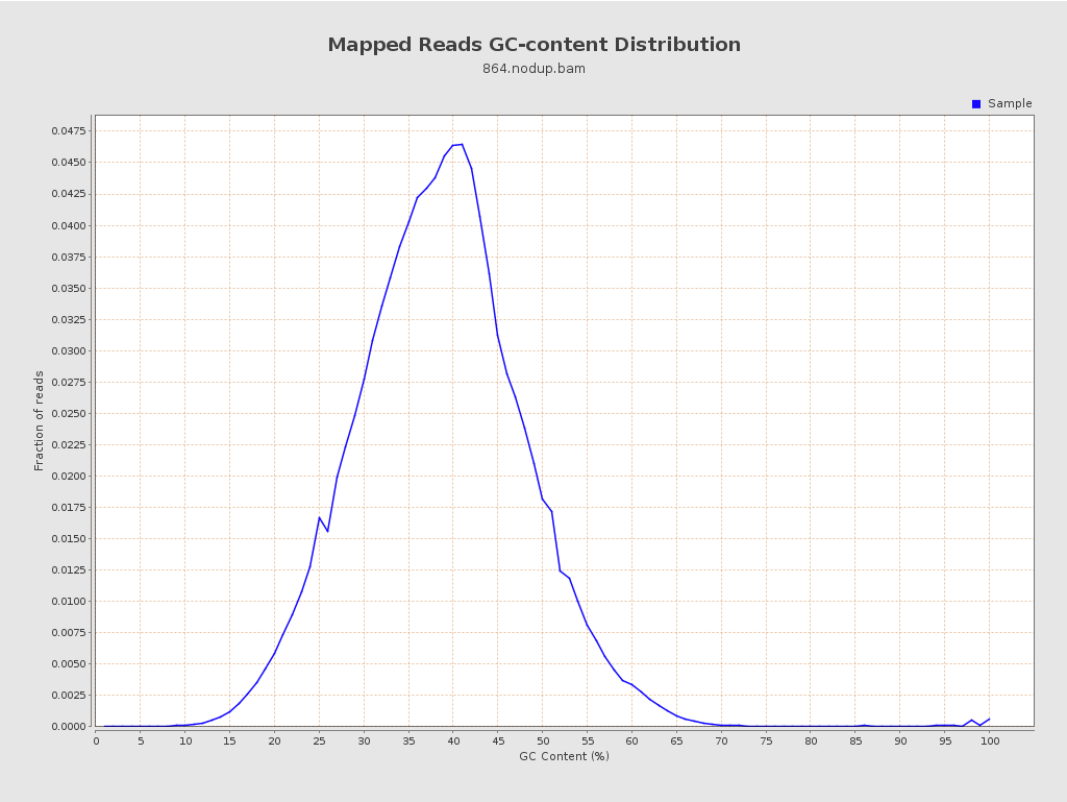
7. Results : Duplication Rate Histogram



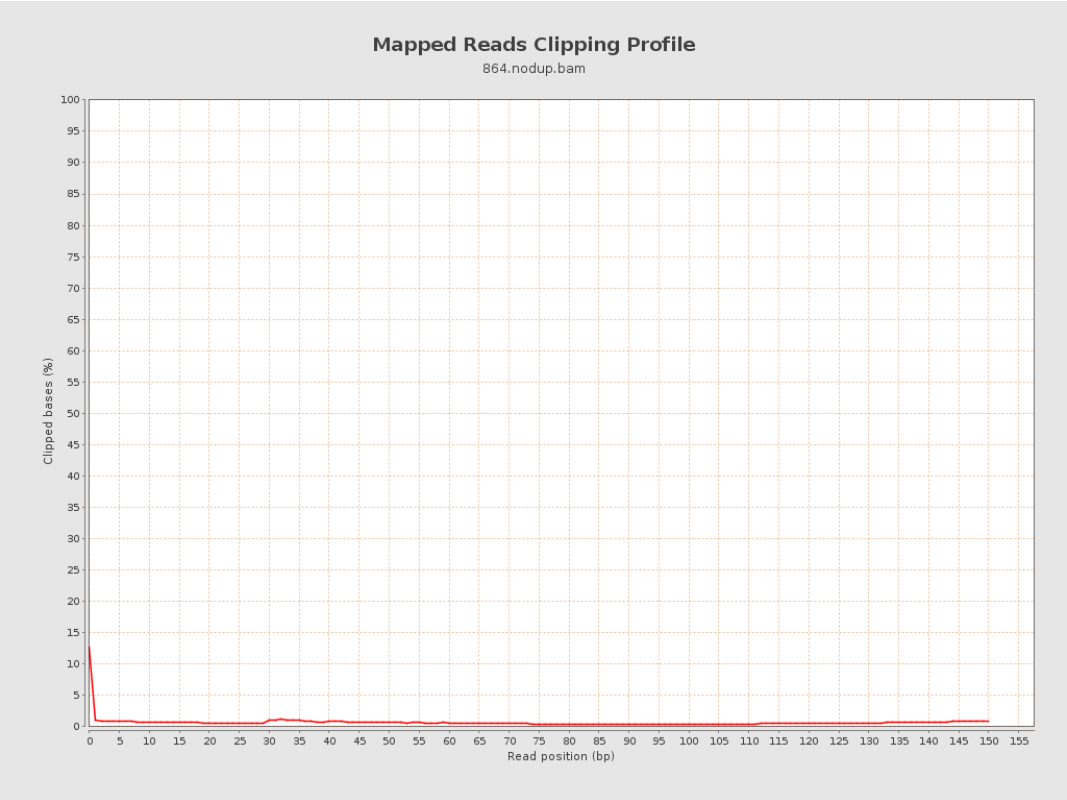
8. Results : Mapped Reads Nucleotide Content



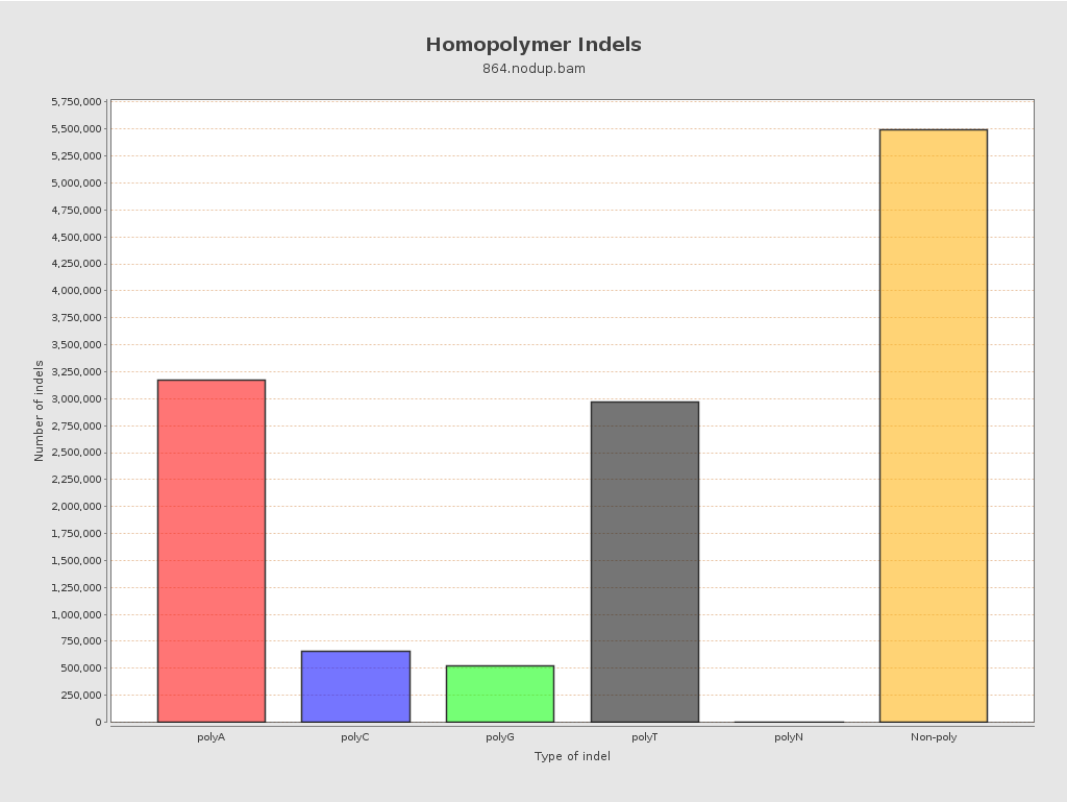
9. Results : Mapped Reads GC-content Distribution



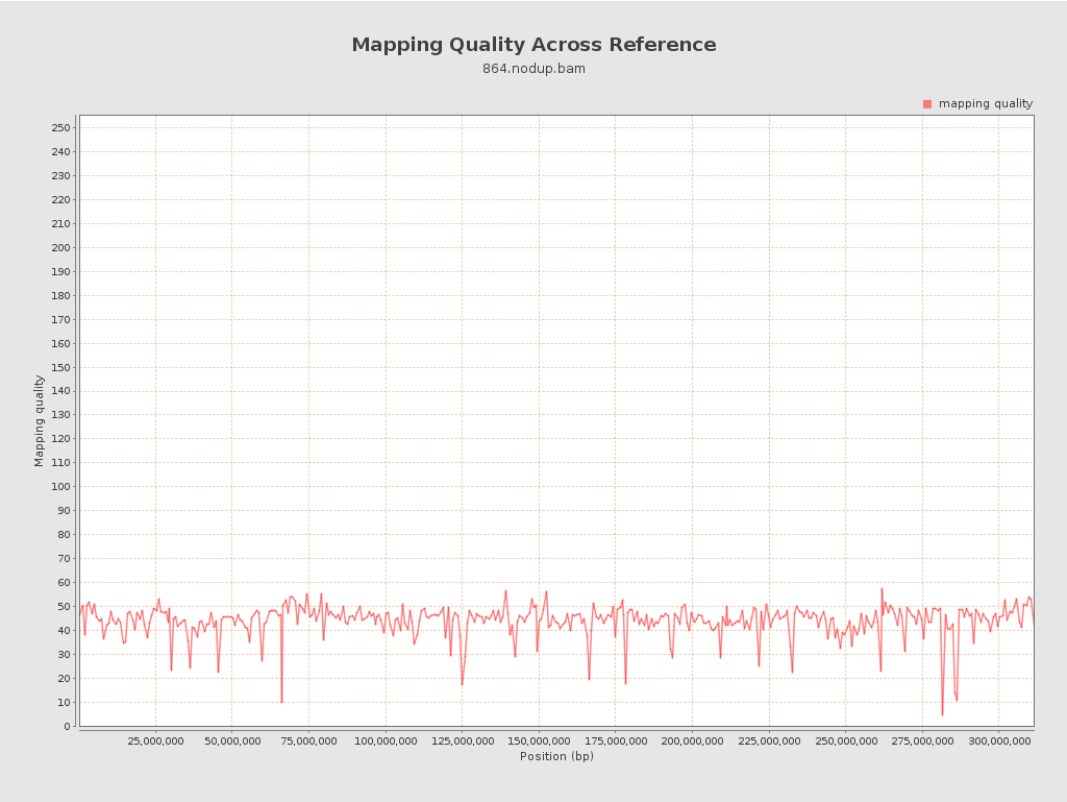
10. Results : Mapped Reads Clipping Profile



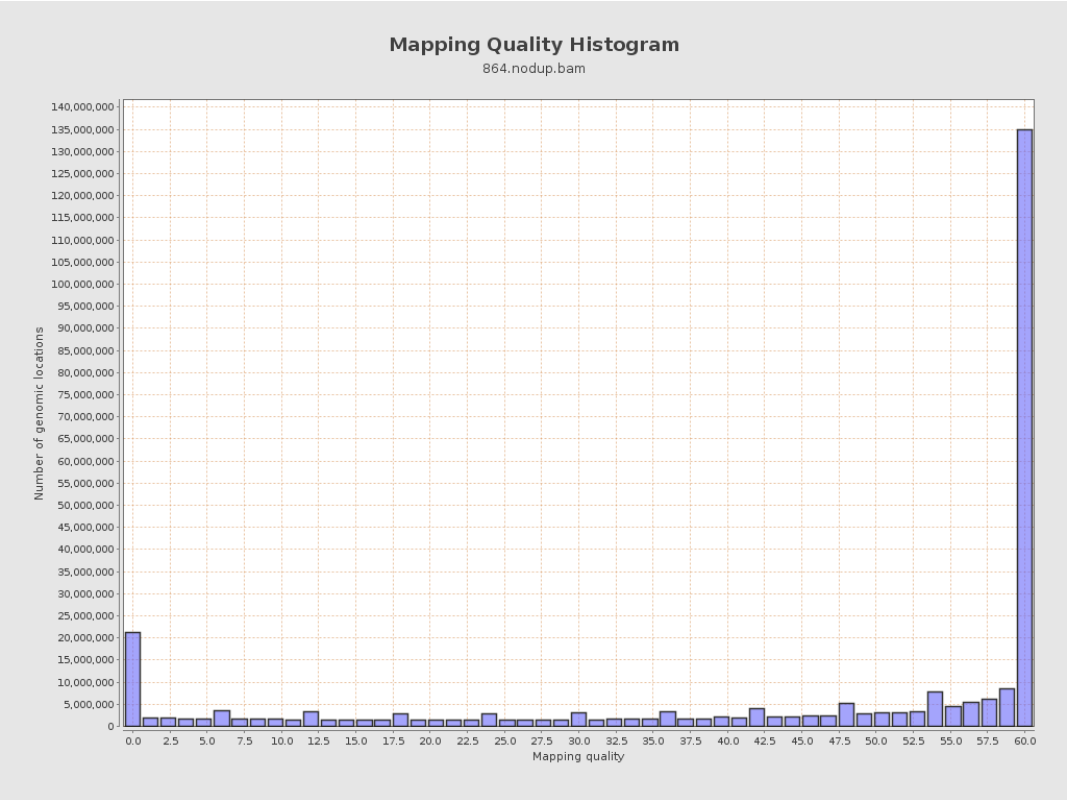
11. Results : Homopolymer Indels



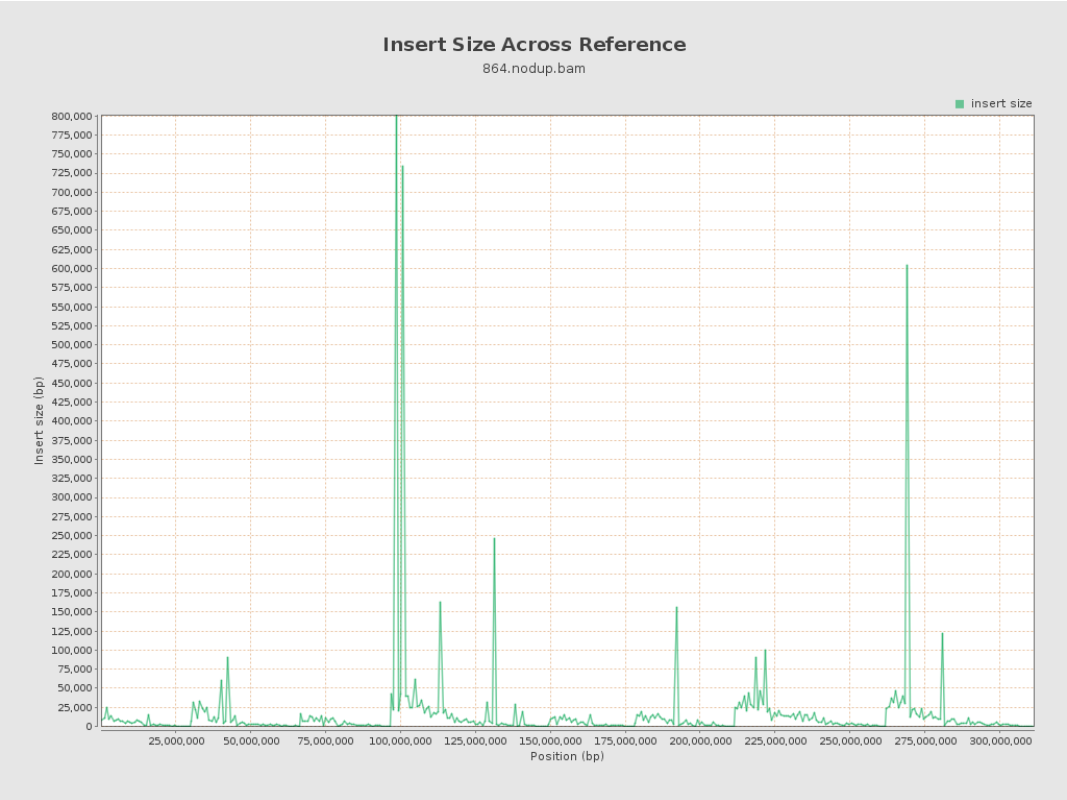
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram