Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:37:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/861.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/861.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_552/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_552_S119_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_552/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_552_S119_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:37:13 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	80,551,421
Mapped reads	75,236,112 / 93.4%
Unmapped reads	5,315,309 / 6.6%
Mapped paired reads	75,236,112 / 93.4%
Mapped reads, first in pair	37,765,086 / 46.88%
Mapped reads, second in pair	37,471,026 / 46.52%
Mapped reads, both in pair	73,602,840 / 91.37%
Mapped reads, singletons	1,633,272 / 2.03%
Read min/max/mean length	30 / 151 / 148.01
Duplicated reads (flagged)	11,602,124 / 14.4%
Clipped reads	18,476,580 / 22.94%

2.2. ACGT Content

Number/percentage of A's	3,211,323,105 / 31.06%
Number/percentage of C's	1,957,658,119 / 18.94%
Number/percentage of T's	3,207,517,801 / 31.03%
Number/percentage of G's	1,961,144,937 / 18.97%
Number/percentage of N's	70,210 / 0%
GC Percentage	37.91%

2.3. Coverage

Mean	33.2574
Standard Deviation	249.9098

2.4. Mapping Quality

Mean Mapping Quality	44.06

2.5. Insert size

Mean	229,157.48
Standard Deviation	2,276,928.37
P25/Median/P75	310 / 412 / 536

2.6. Mismatches and indels

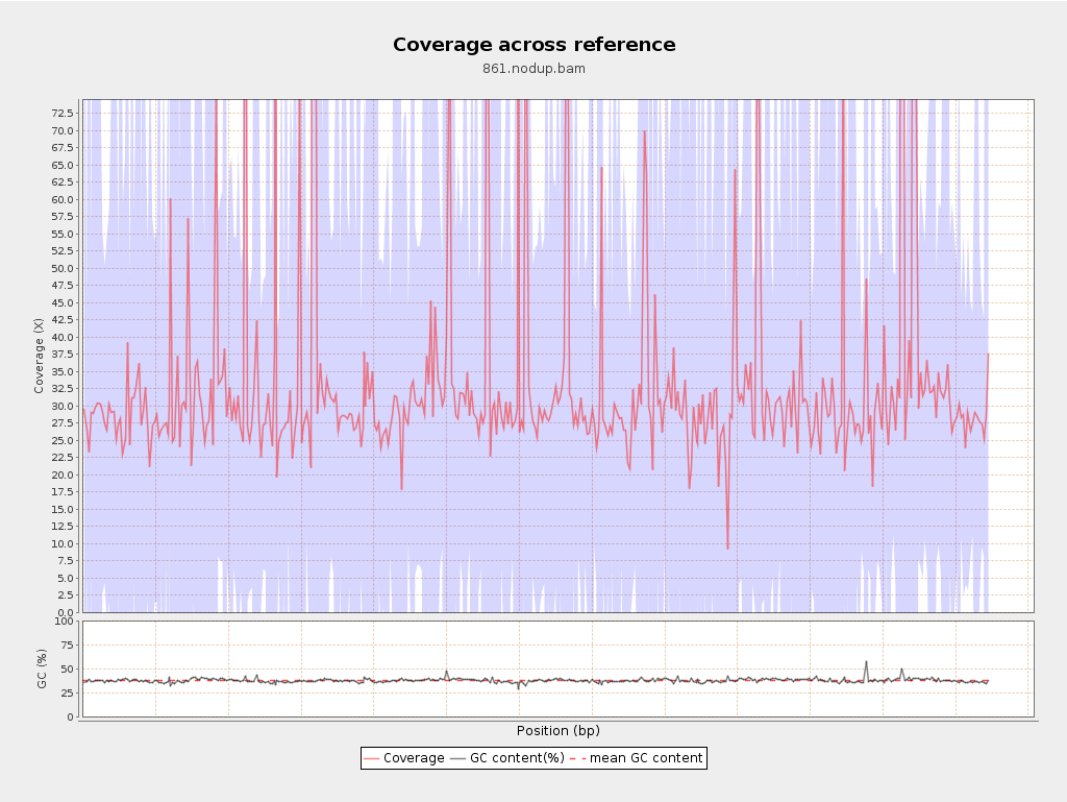
General error rate	2.54%
Mismatches	243,454,686
Insertions	7,058,830
Mapped reads with at least one insertion	8.41%
Deletions	7,170,515
Mapped reads with at least one deletion	8.47%
Homopolymer indels	56.93%

2.7. Chromosome stats

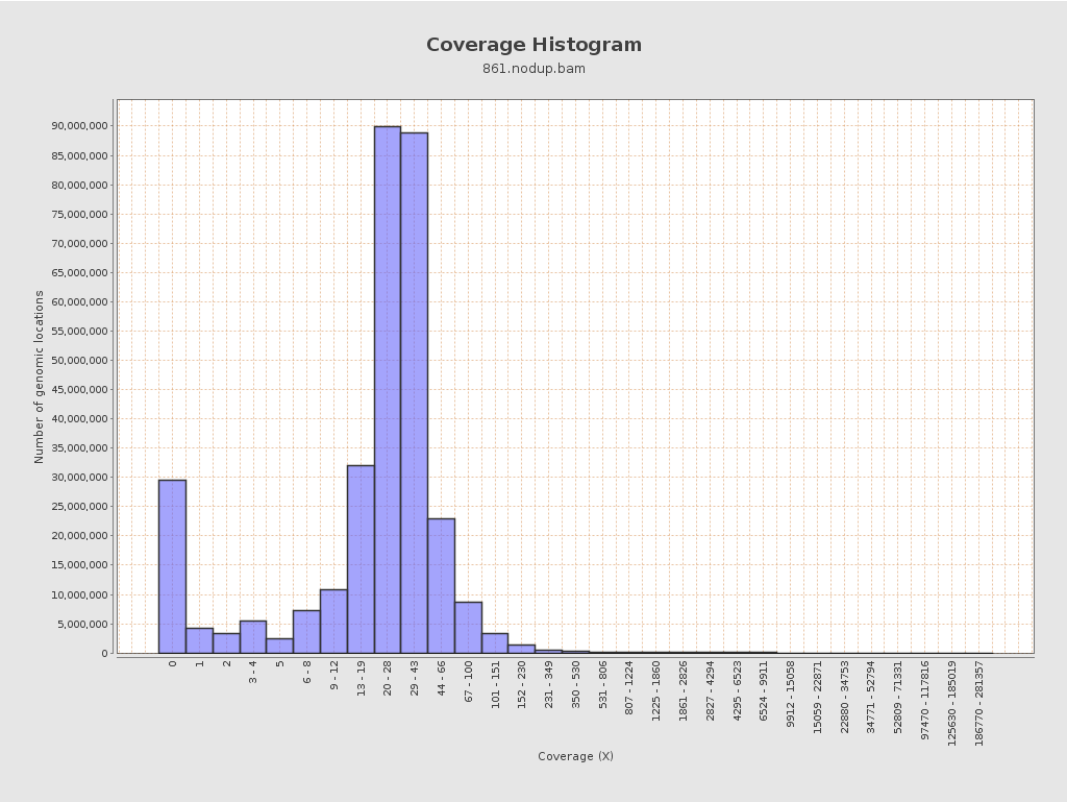
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	842717044	28.3511	80.5144

LT669789.1	36598175	1251163692	34.1865	258.7438
LT669790.1	30422129	1111091219	36.5225	269.1373
LT669791.1	52758100	1712814399	32.4654	224.5203
LT669792.1	28376109	959424441	33.811	282.0947
LT669793.1	33388210	1035186519	31.0046	146.4433
LT669794.1	50579949	1612893790	31.888	206.1132
LT669795.1	49795044	1839114979	36.9337	370.4253

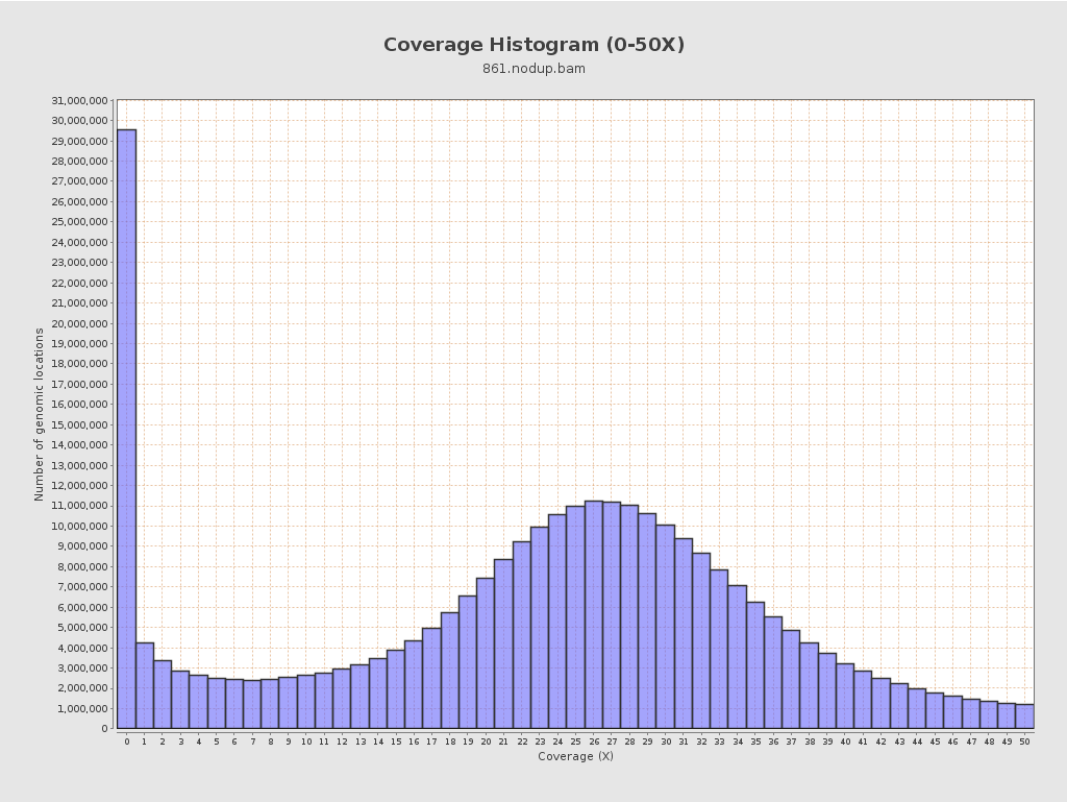
3. Results : Coverage across reference



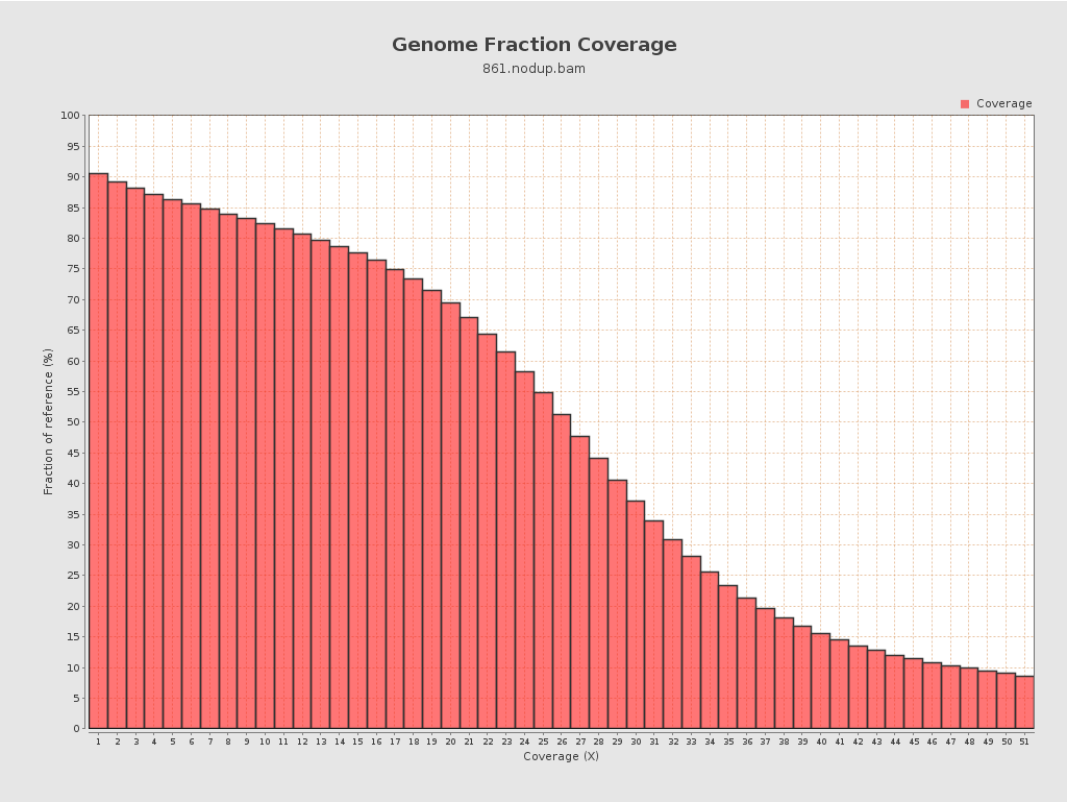
4. Results : Coverage Histogram



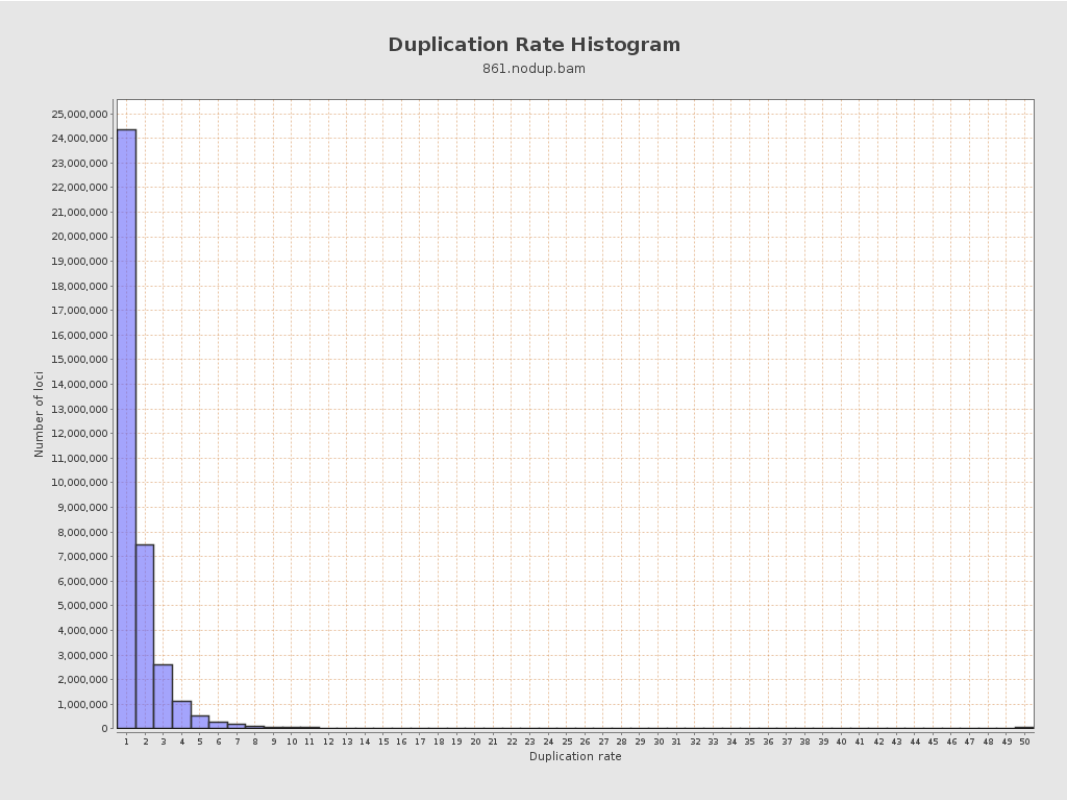
5. Results : Coverage Histogram (0-50X)



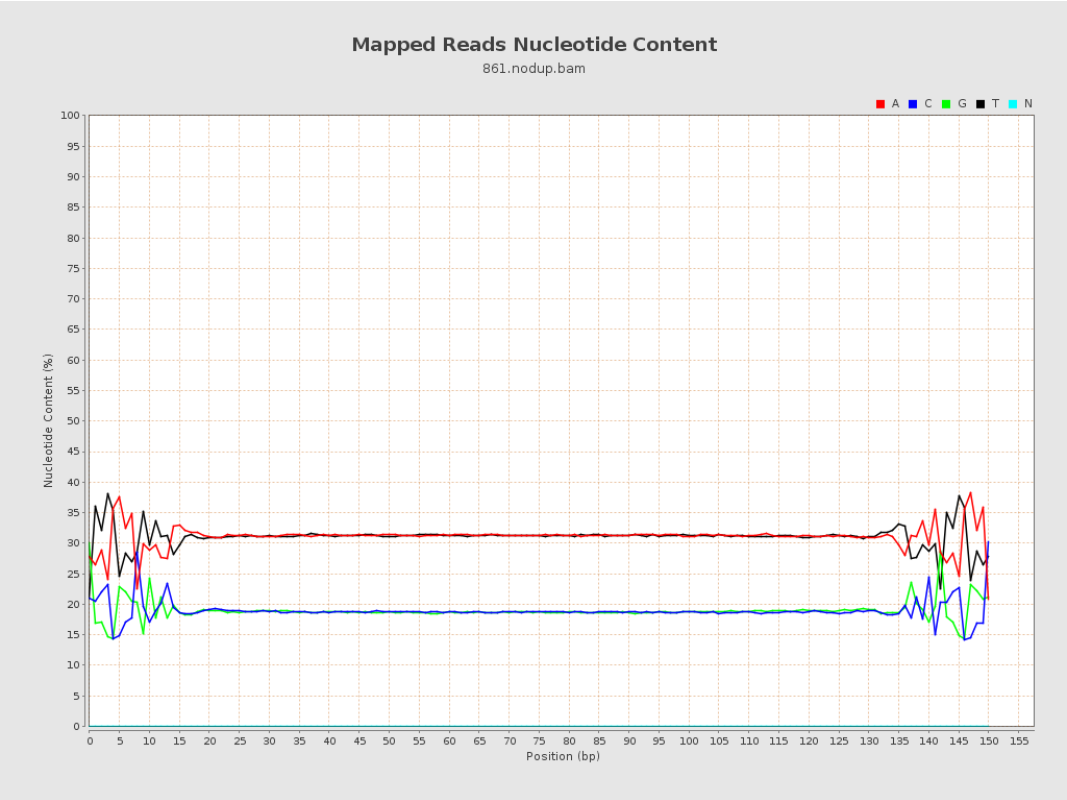
6. Results : Genome Fraction Coverage



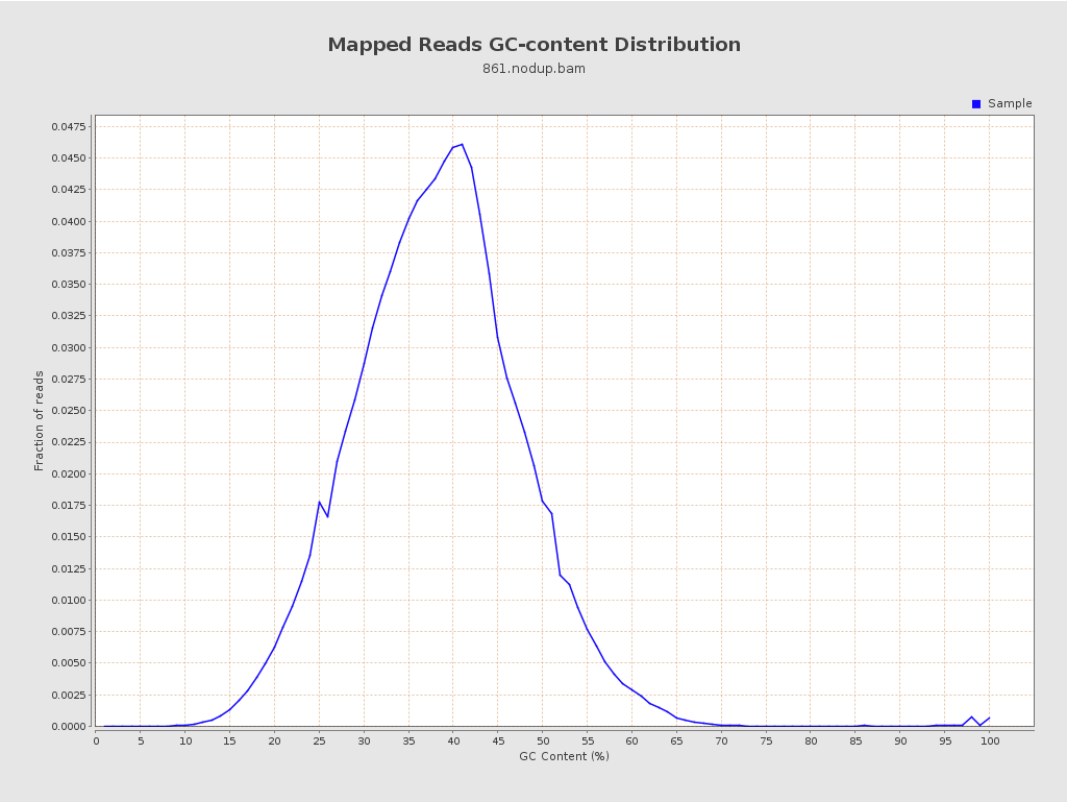
7. Results : Duplication Rate Histogram



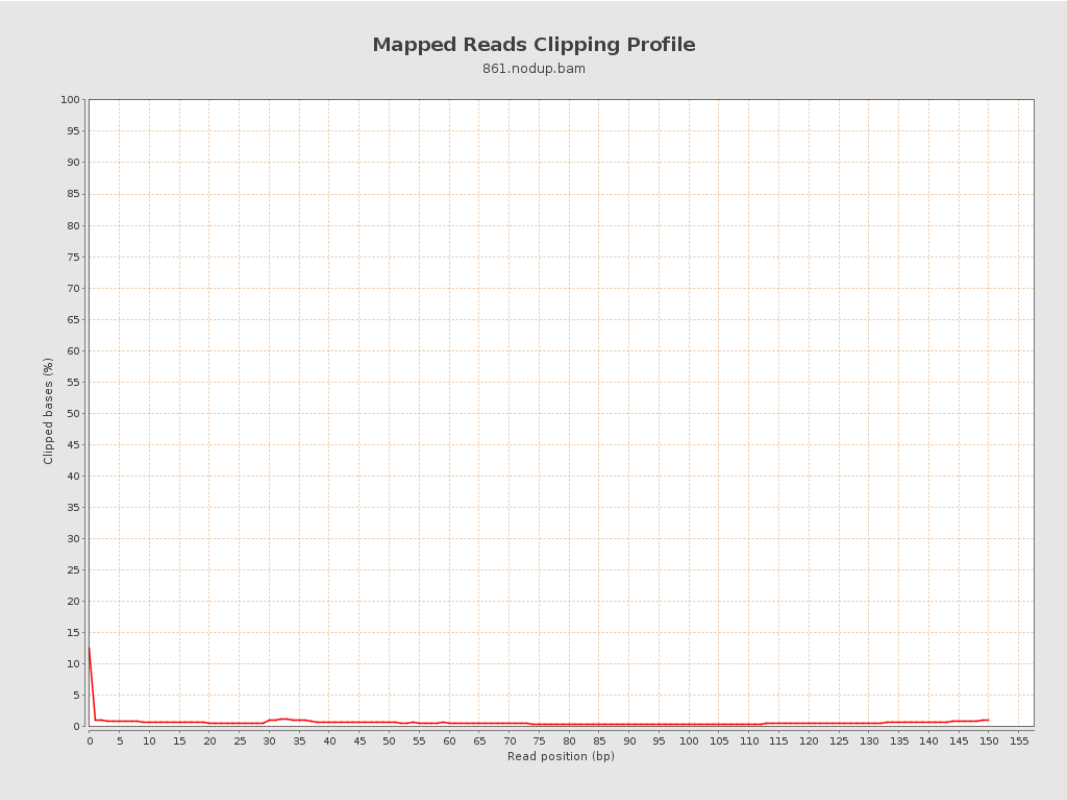
8. Results : Mapped Reads Nucleotide Content



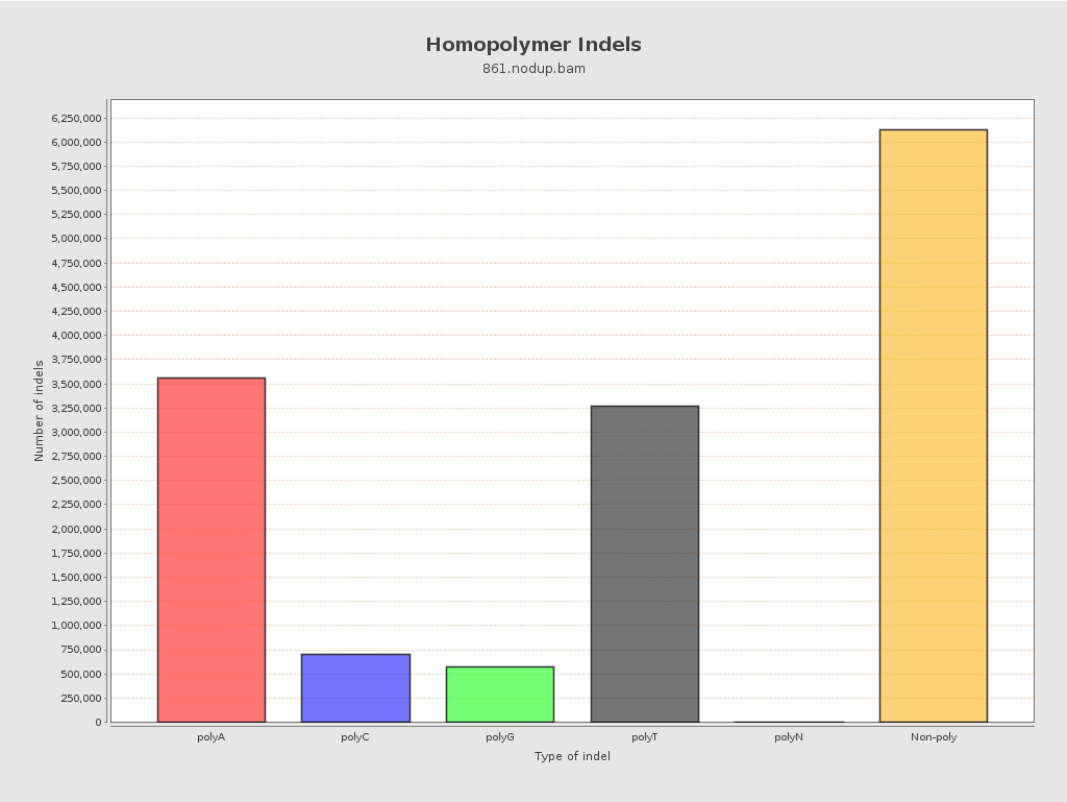
9. Results : Mapped Reads GC-content Distribution



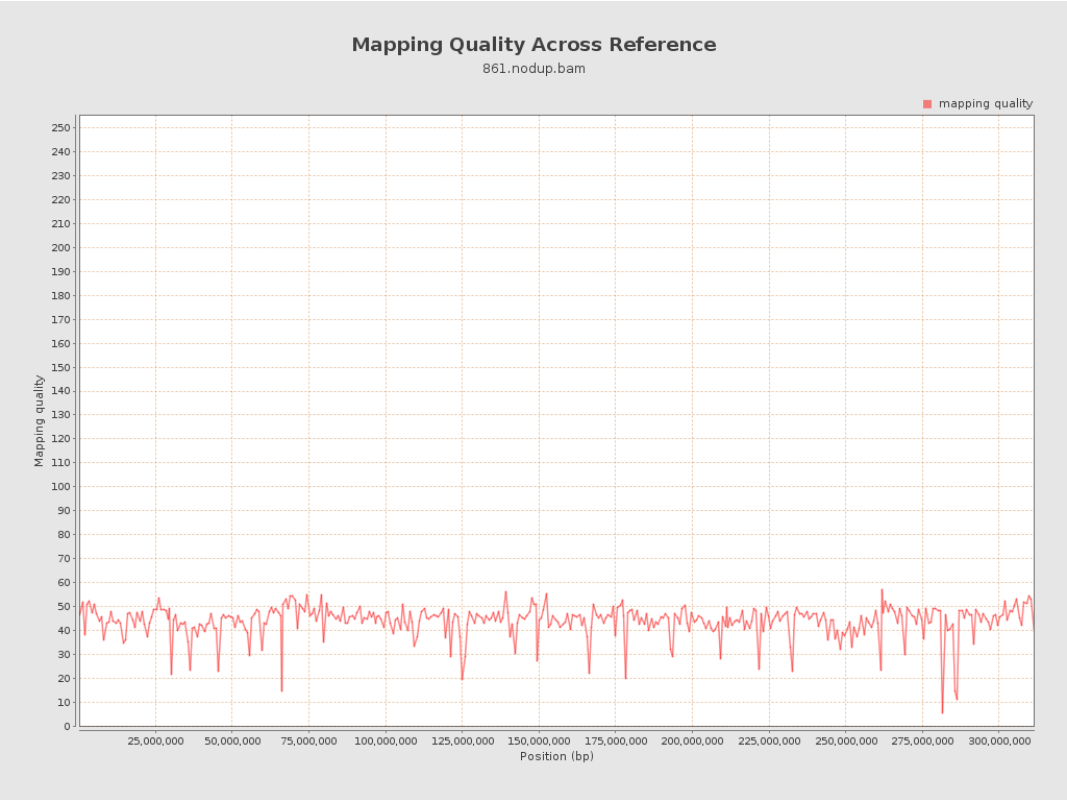
10. Results : Mapped Reads Clipping Profile



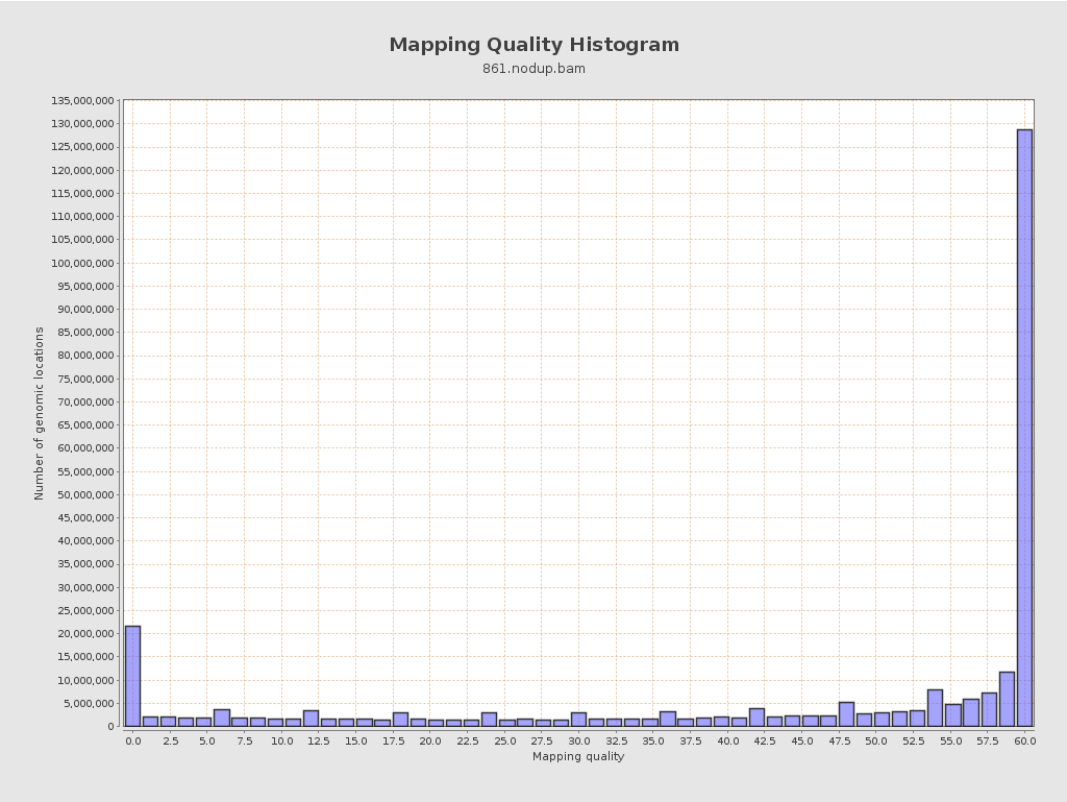
11. Results : Homopolymer Indels



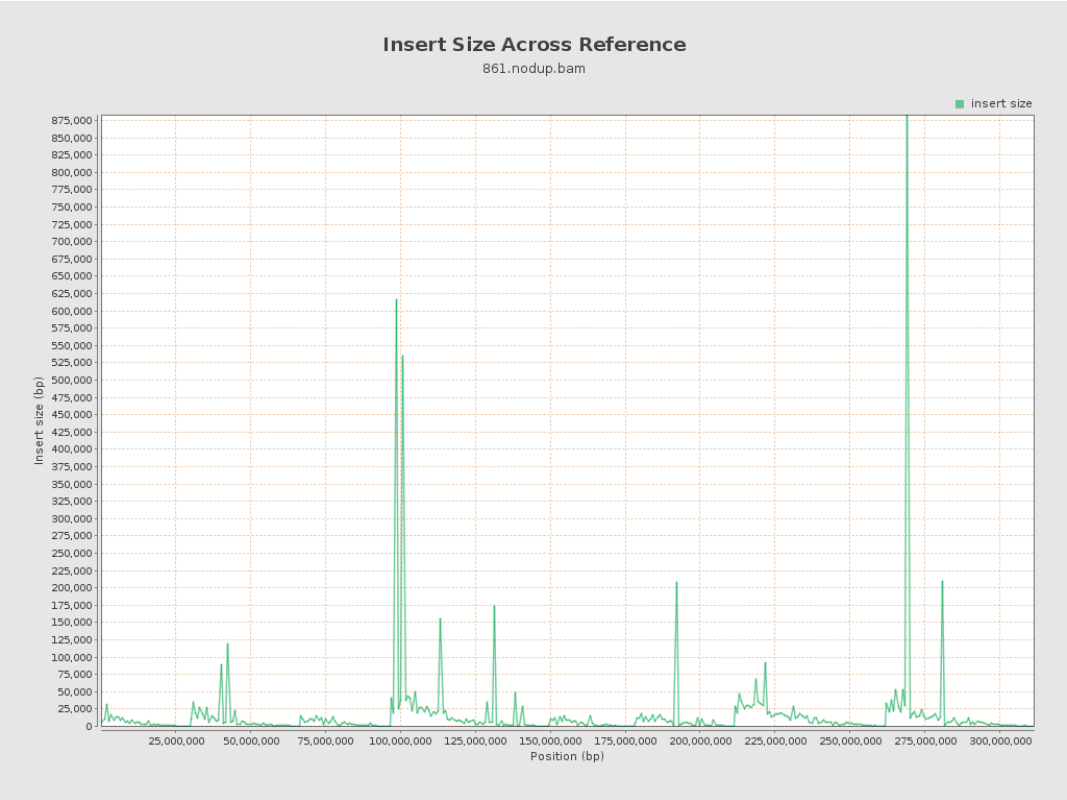
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram