Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/860.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/860.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_251/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_251_S332_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_251/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_251_S332_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:35:52 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	76,108,853
Mapped reads	71,643,068 / 94.13%
Unmapped reads	4,465,785 / 5.87%
Mapped paired reads	71,643,068 / 94.13%
Mapped reads, first in pair	35,877,532 / 47.14%
Mapped reads, second in pair	35,765,536 / 46.99%
Mapped reads, both in pair	70,291,472 / 92.36%
Mapped reads, singletons	1,351,596 / 1.78%
Read min/max/mean length	30 / 151 / 148.03
Duplicated reads (flagged)	10,242,443 / 13.46%
Clipped reads	16,420,119 / 21.57%

2.2. ACGT Content

Number/percentage of A's	3,056,429,075 / 30.85%
Number/percentage of C's	1,899,740,733 / 19.18%
Number/percentage of T's	3,053,336,534 / 30.82%
Number/percentage of G's	1,897,173,698 / 19.15%
Number/percentage of N's	37,339 / 0%
GC Percentage	38.33%

2.3. Coverage

Mean	31.8714
Standard Deviation	263.2884

2.4. Mapping Quality

Mean Mapping Quality	44.15

2.5. Insert size

Mean	219,141.23
Standard Deviation	2,210,378.45
P25/Median/P75	303 / 400 / 525

2.6. Mismatches and indels

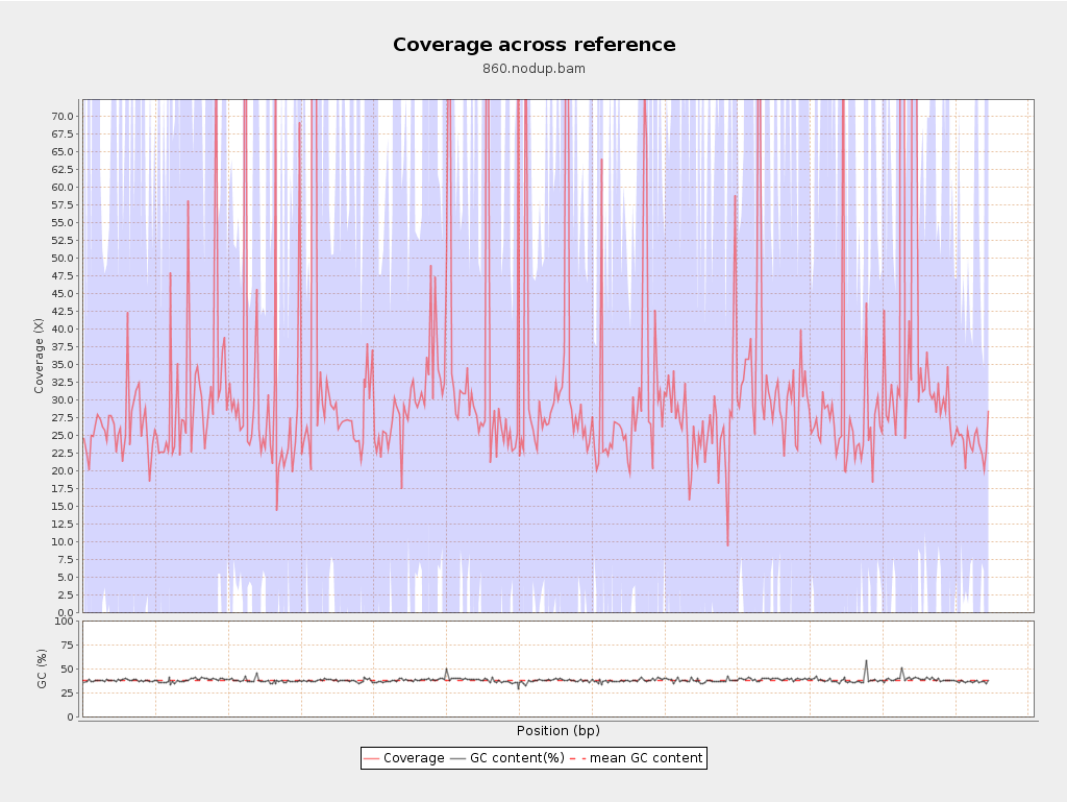
General error rate	2.3%
Mismatches	209,925,614
Insertions	6,646,704
Mapped reads with at least one insertion	8.34%
Deletions	6,854,187
Mapped reads with at least one deletion	8.51%
Homopolymer indels	56.76%

2.7. Chromosome stats

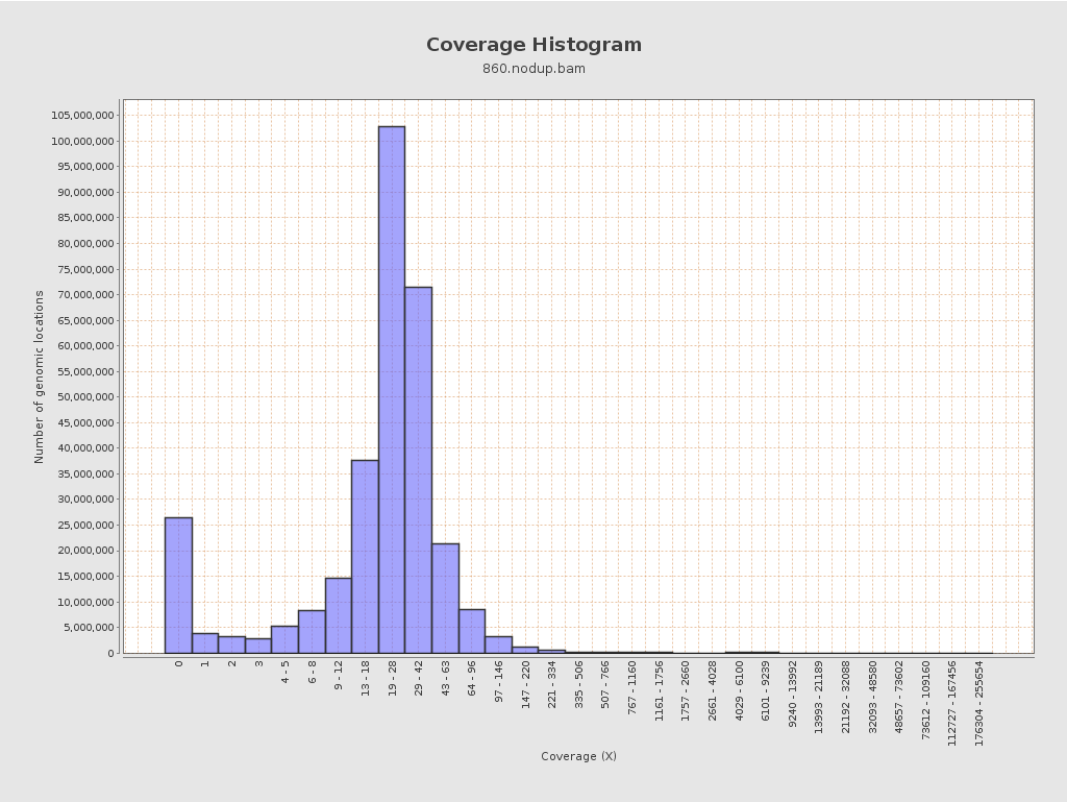
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	764462916	25.7184	74.608

LT669789.1	36598175	1189141437	32.4918	254.7313
LT669790.1	30422129	1028230601	33.7988	269.5555
LT669791.1	52758100	1666245671	31.5827	221.6146
LT669792.1	28376109	896918712	31.6082	301.0351
LT669793.1	33388210	977481445	29.2762	138.9082
LT669794.1	50579949	1566825281	30.9772	239.0738
LT669795.1	49795044	1843177574	37.0153	404.61

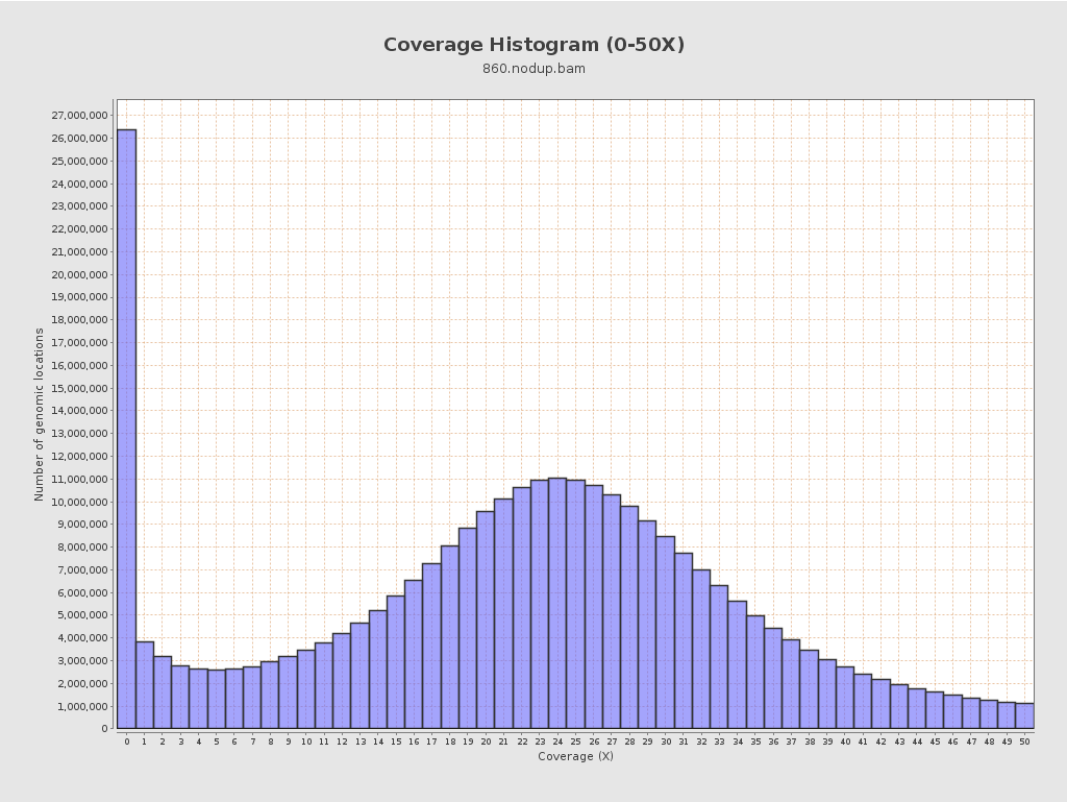
3. Results : Coverage across reference



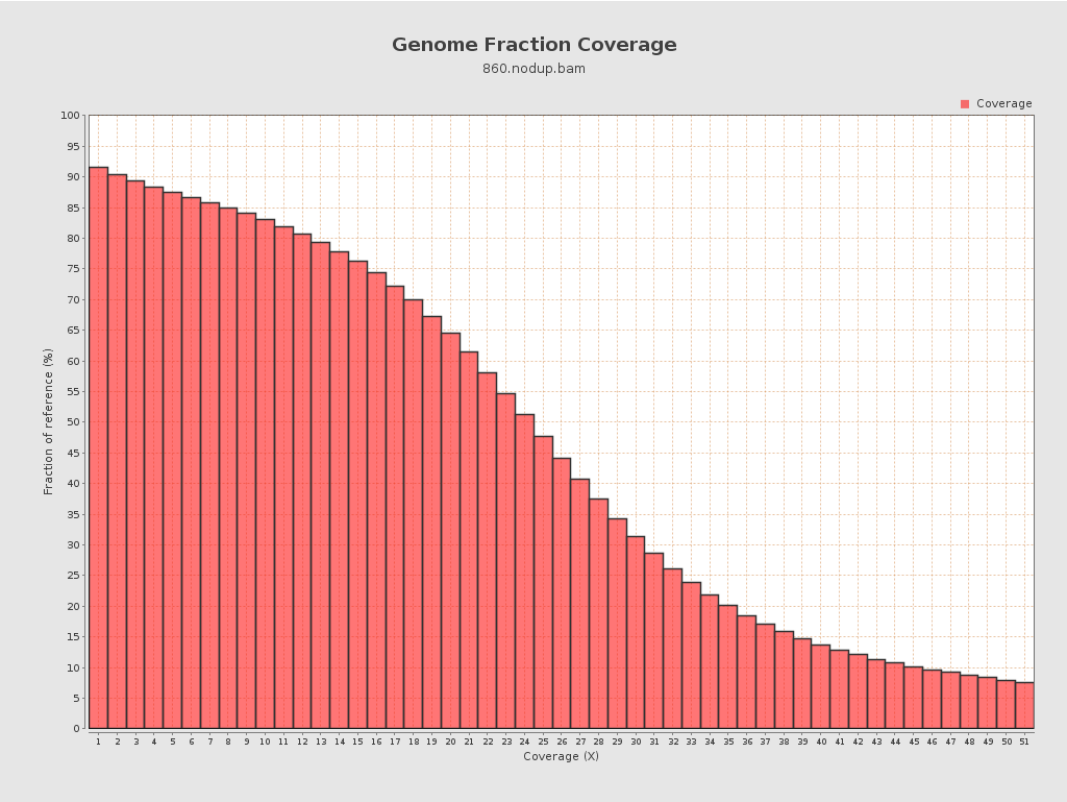
4. Results : Coverage Histogram



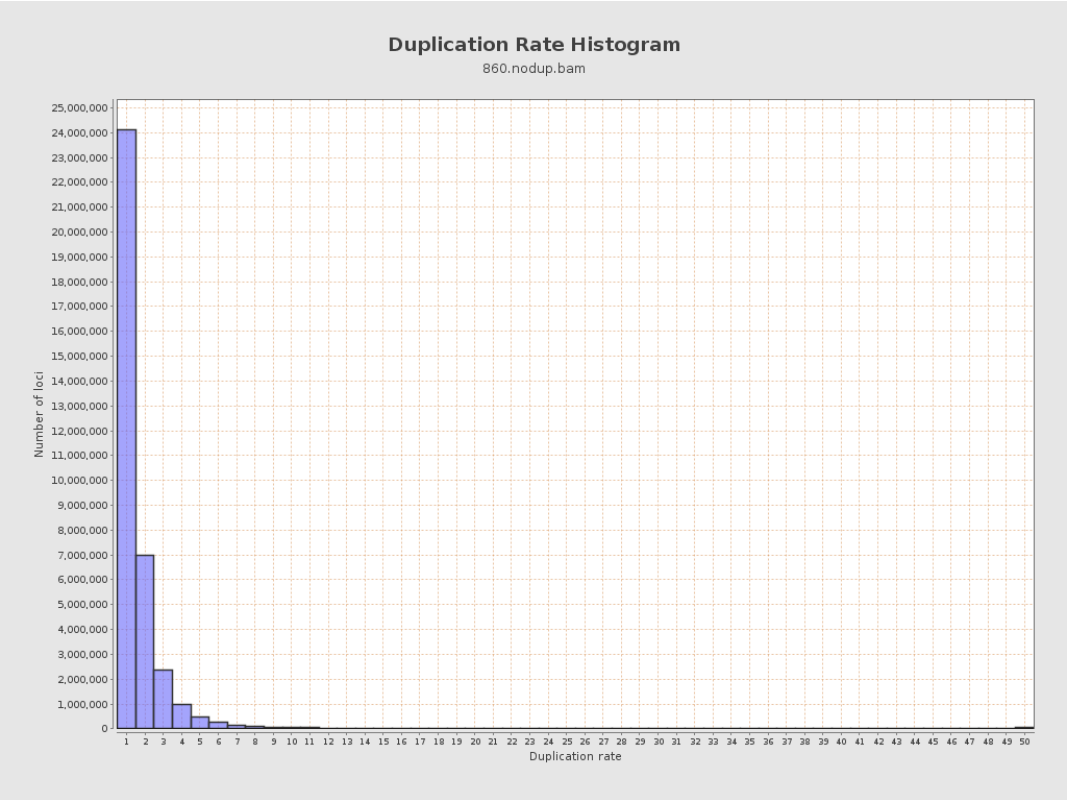
5. Results : Coverage Histogram (0-50X)



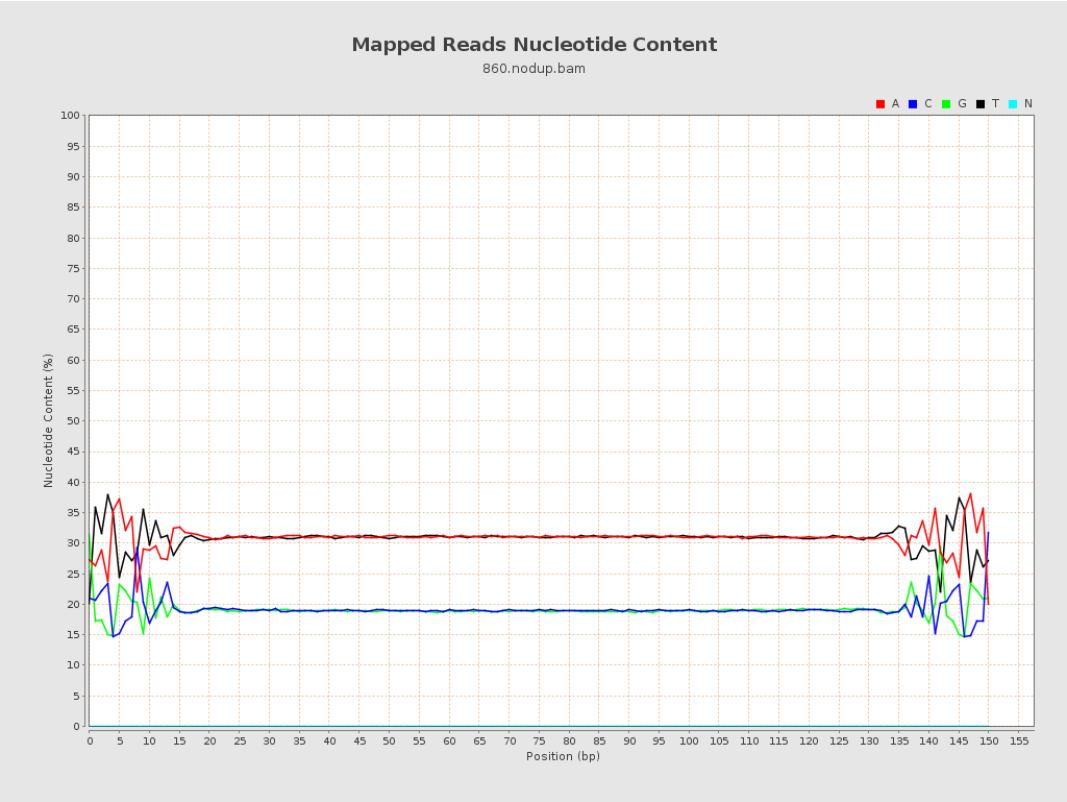
6. Results : Genome Fraction Coverage



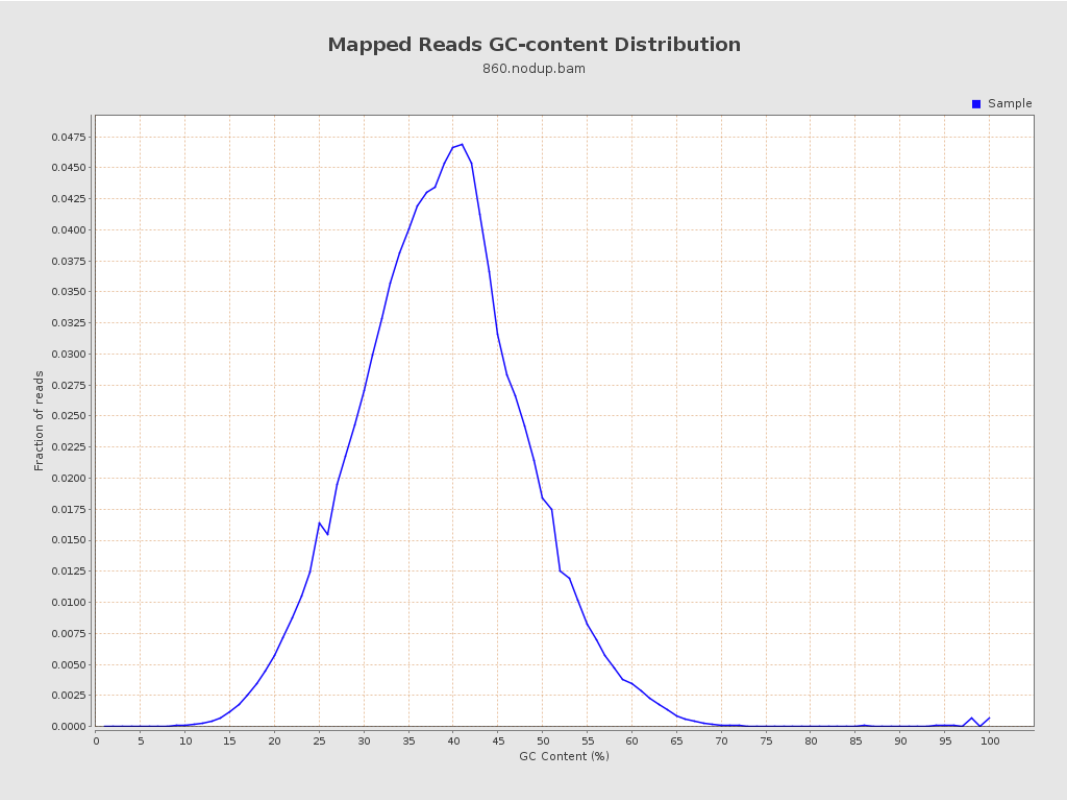
7. Results : Duplication Rate Histogram



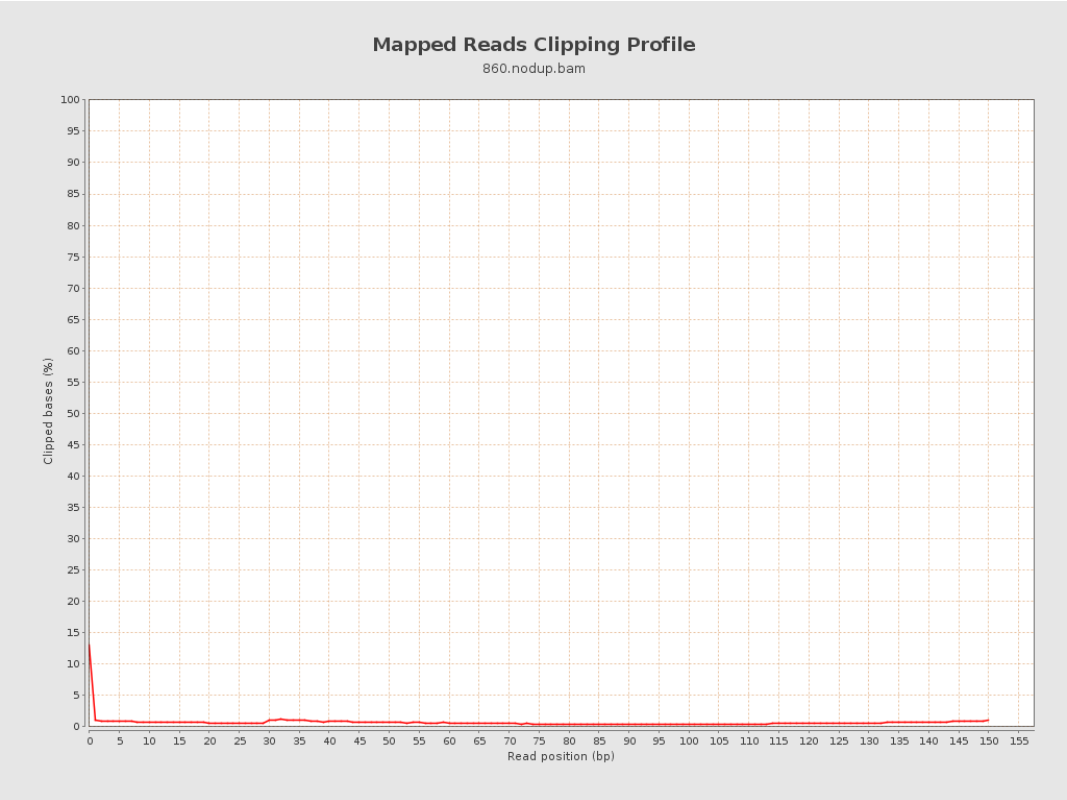
8. Results : Mapped Reads Nucleotide Content



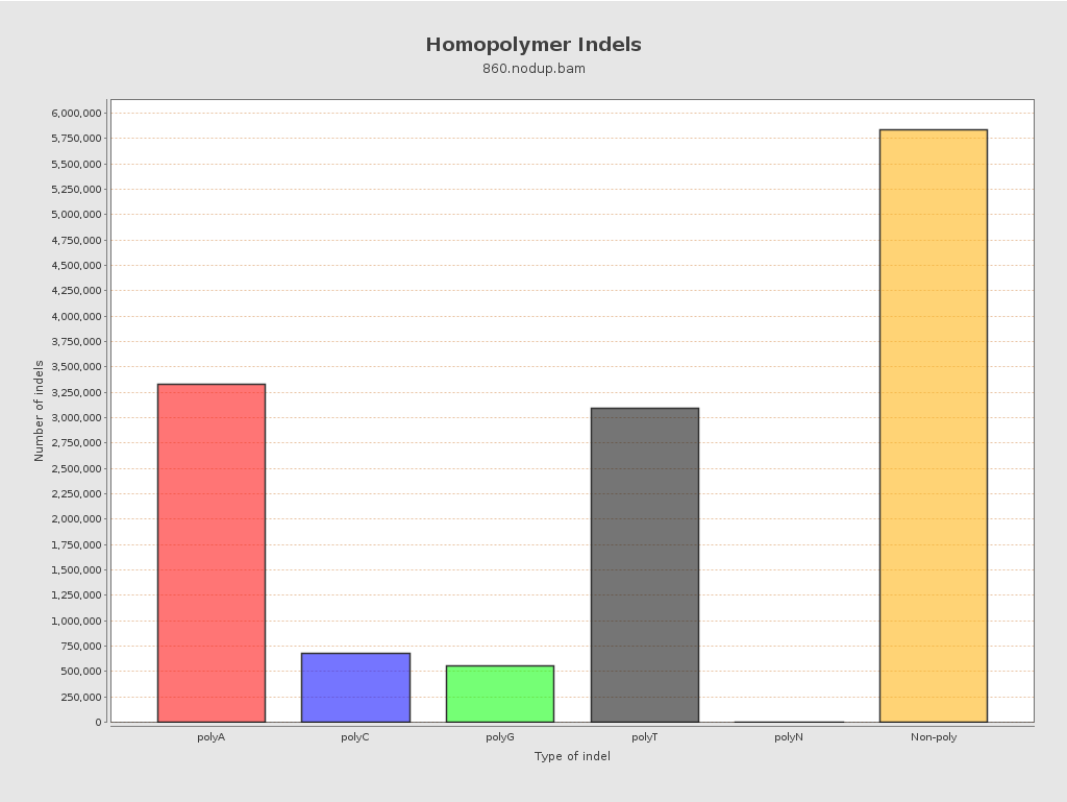
9. Results : Mapped Reads GC-content Distribution



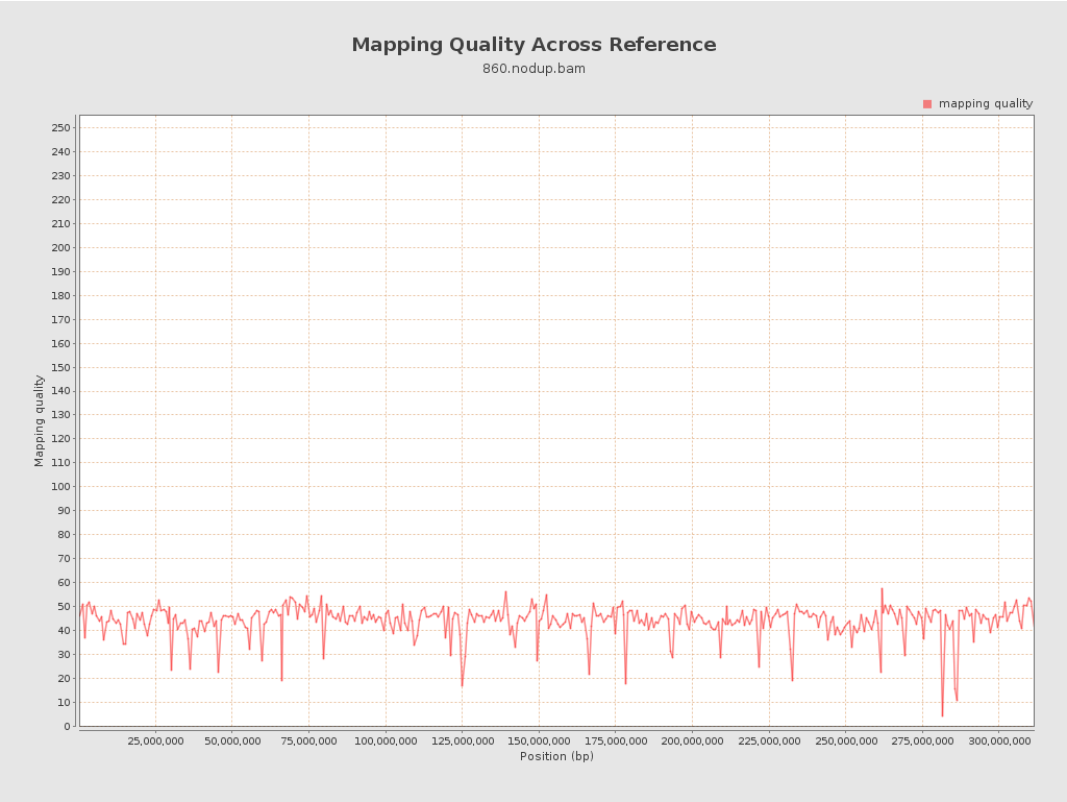
10. Results : Mapped Reads Clipping Profile



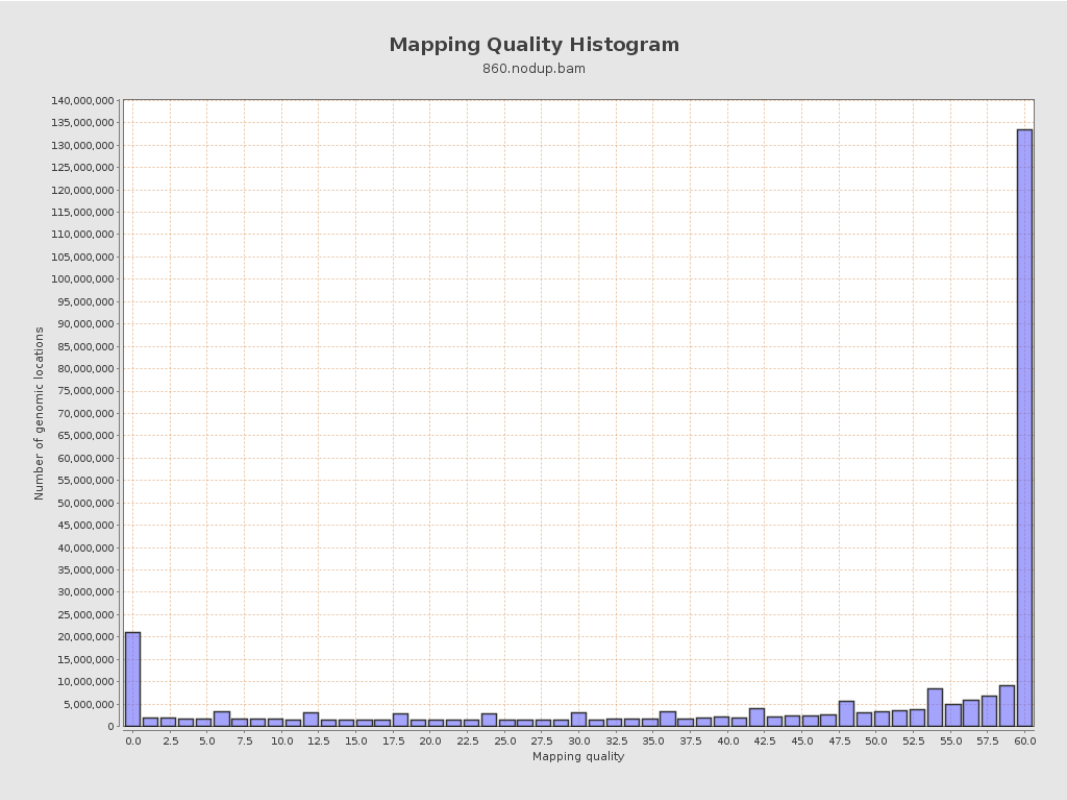
11. Results : Homopolymer Indels



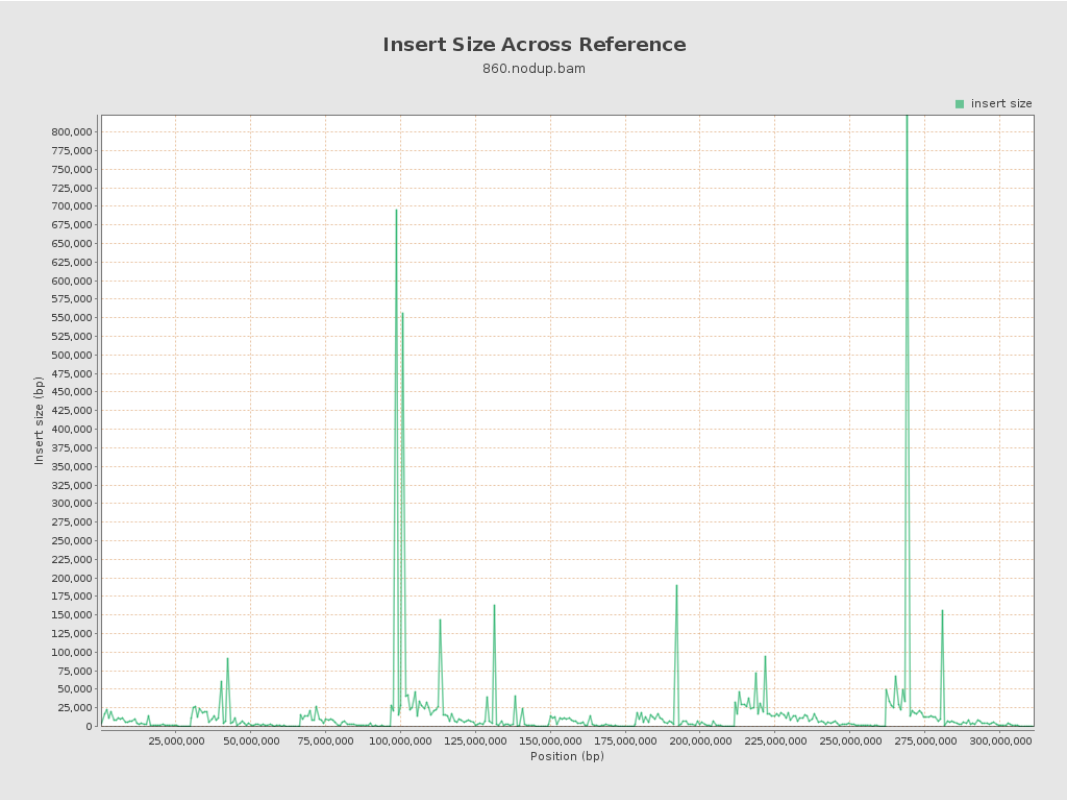
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram