Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:40:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/877.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/877.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_159/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_159_S249_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_159/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_159_S249_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:40:00 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	94,464,462
Mapped reads	83,299,339 / 88.18%
Unmapped reads	11,165,123 / 11.82%
Mapped paired reads	83,299,339 / 88.18%
Mapped reads, first in pair	41,738,064 / 44.18%
Mapped reads, second in pair	41,561,275 / 44%
Mapped reads, both in pair	79,818,501 / 84.5%
Mapped reads, singletons	3,480,838 / 3.68%
Read min/max/mean length	30 / 151 / 147.96
Duplicated reads (flagged)	19,305,000 / 20.44%
Clipped reads	21,882,873 / 23.17%

2.2. ACGT Content

Number/percentage of A's	3,485,301,998 / 31.02%
Number/percentage of C's	2,127,872,358 / 18.94%
Number/percentage of T's	3,492,136,738 / 31.08%
Number/percentage of G's	2,131,889,700 / 18.97%
Number/percentage of N's	47,474 / 0%
GC Percentage	37.91%

2.3. Coverage

Mean	36.1567
Standard Deviation	437.0578

2.4. Mapping Quality

Mean Mapping Quality	43.98

2.5. Insert size

Mean	295,284.45
Standard Deviation	2,644,979.55
P25/Median/P75	317 / 422 / 556

2.6. Mismatches and indels

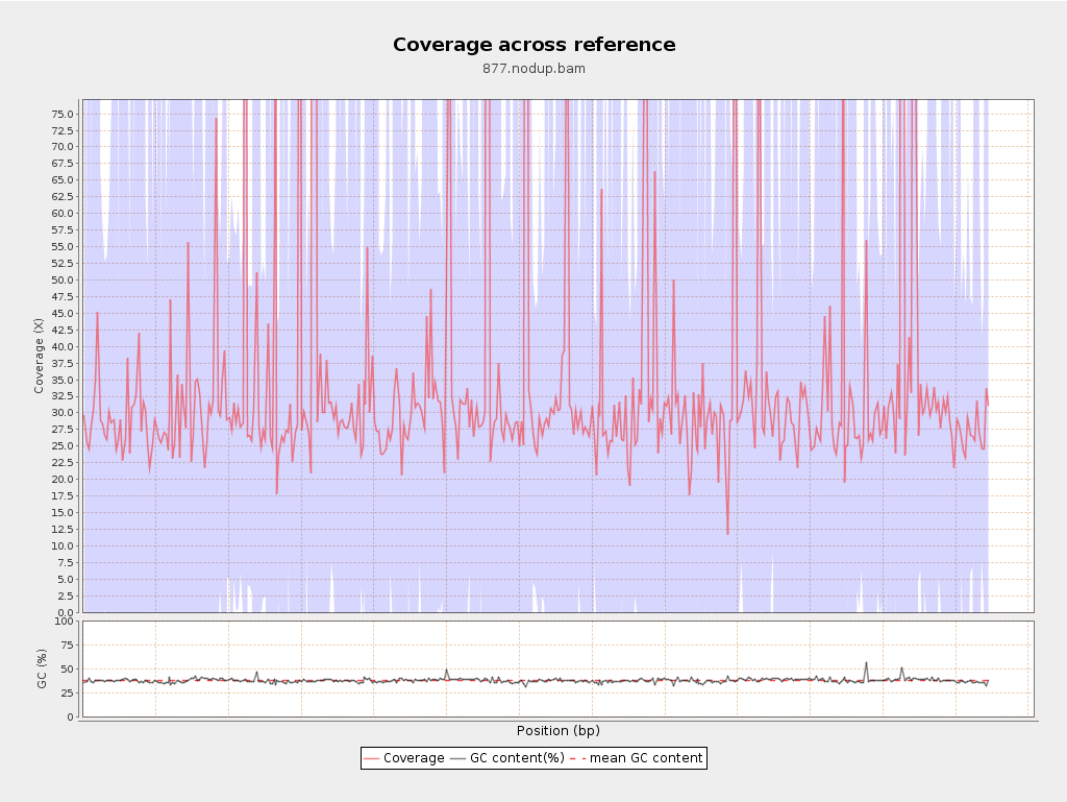
General error rate	2.48%
Mismatches	253,962,254
Insertions	9,106,474
Mapped reads with at least one insertion	9.66%
Deletions	8,280,596
Mapped reads with at least one deletion	8.78%
Homopolymer indels	57.74%

2.7. Chromosome stats

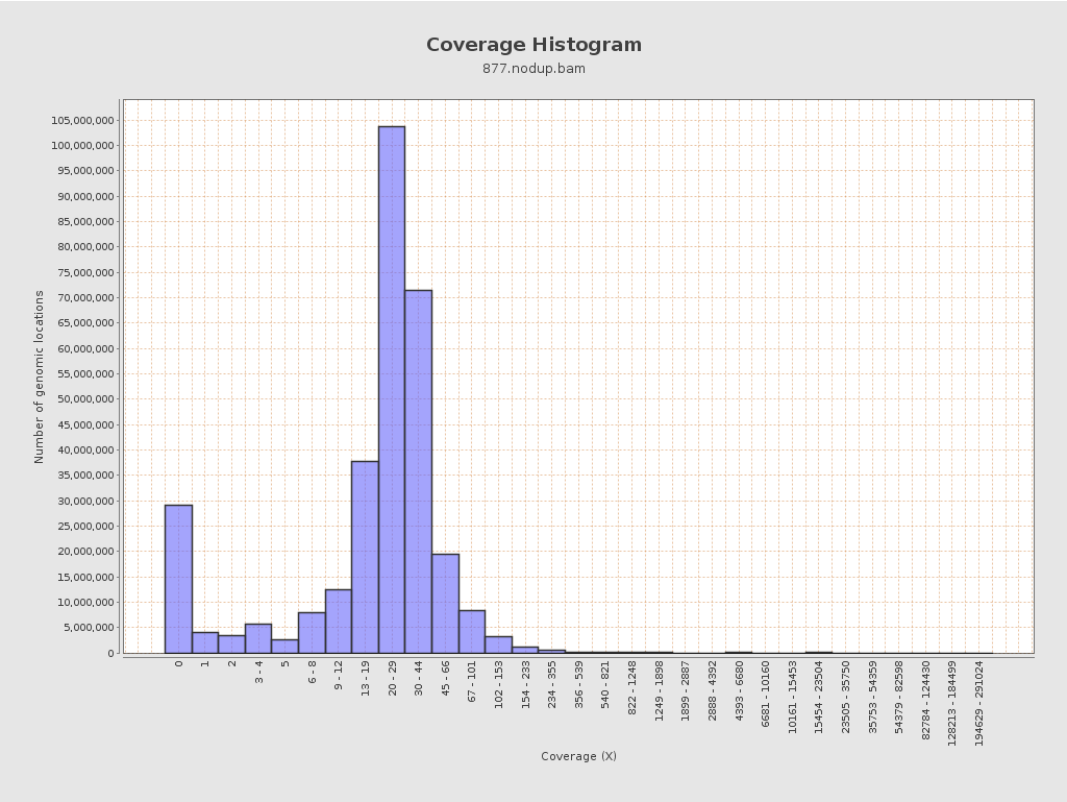
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	853821231	28.7246	193.0016

LT669789.1	36598175	1307154896	35.7164	439.2021
LT669790.1	30422129	1503607024	49.4248	699.9144
LT669791.1	52758100	1884867964	35.7266	506.6364
LT669792.1	28376109	1039910112	36.6474	415.0205
LT669793.1	33388210	1099750344	32.9383	305.8712
LT669794.1	50579949	1679713310	33.2091	337.9018
LT669795.1	49795044	1899111051	38.1386	428.0379

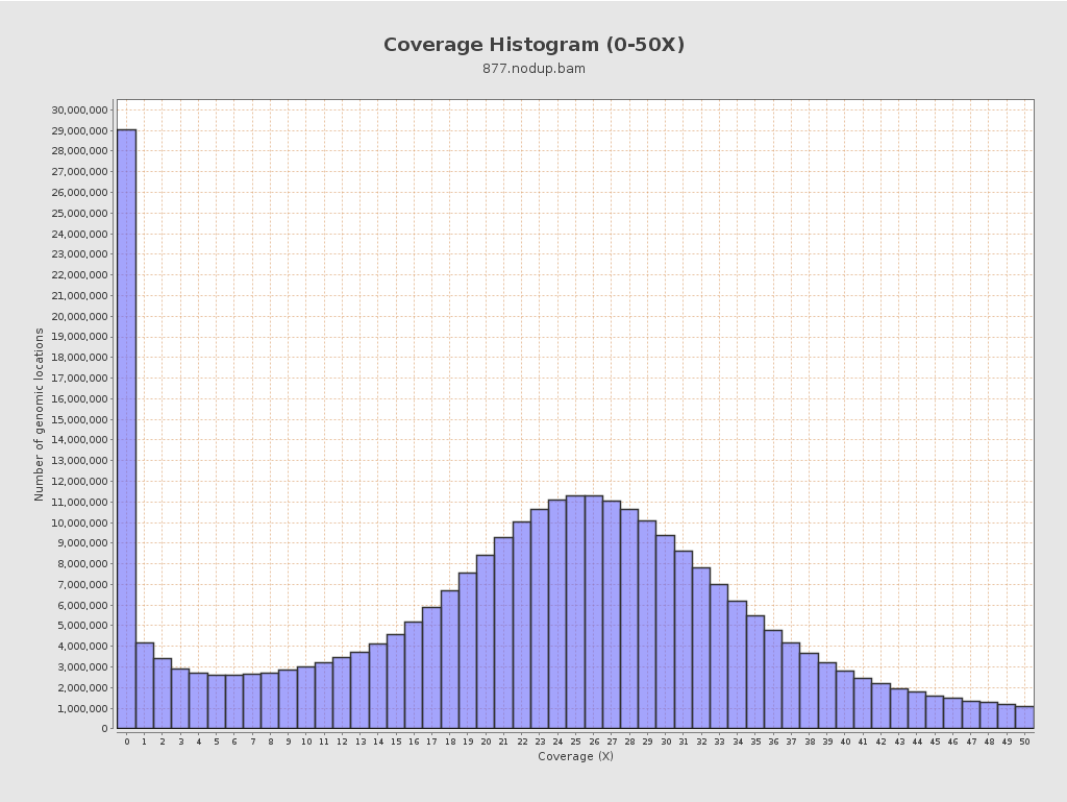
3. Results : Coverage across reference



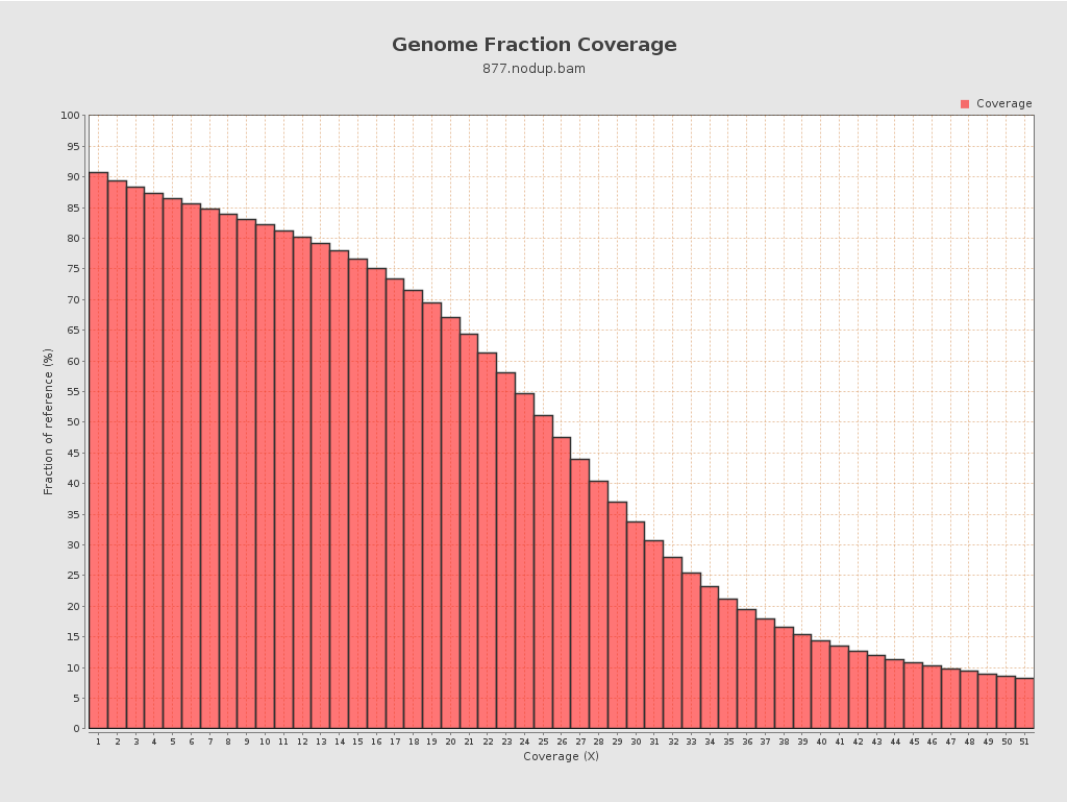
4. Results : Coverage Histogram



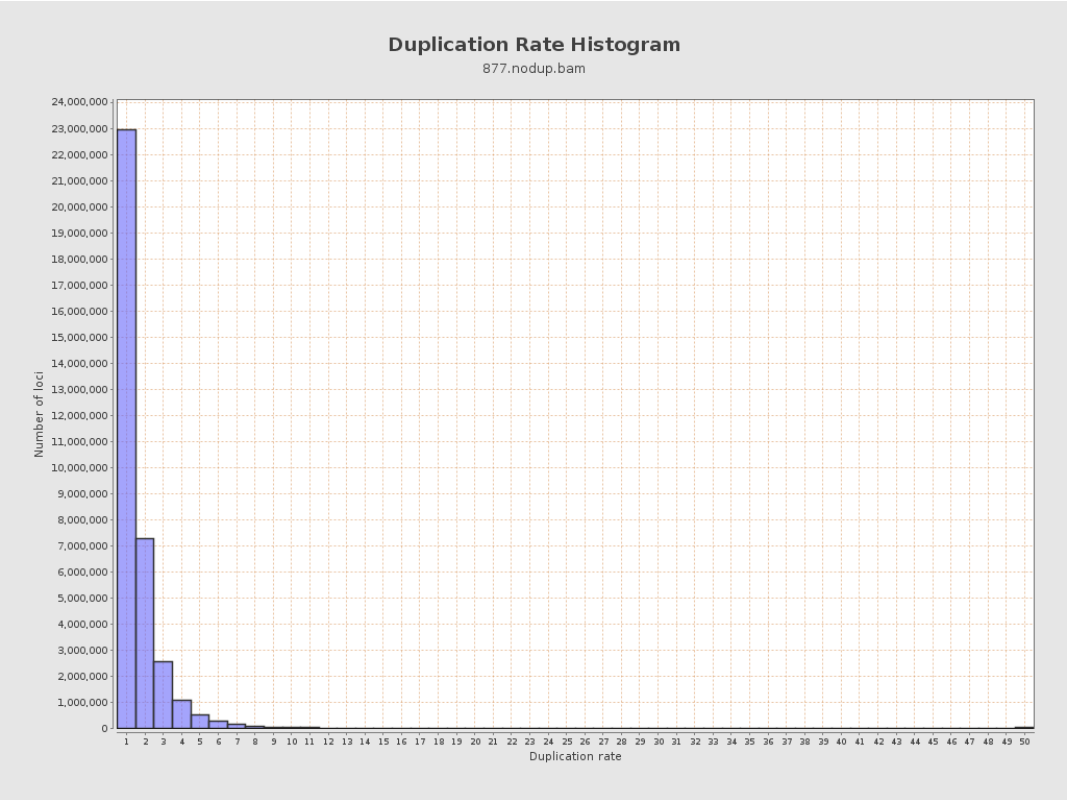
5. Results : Coverage Histogram (0-50X)



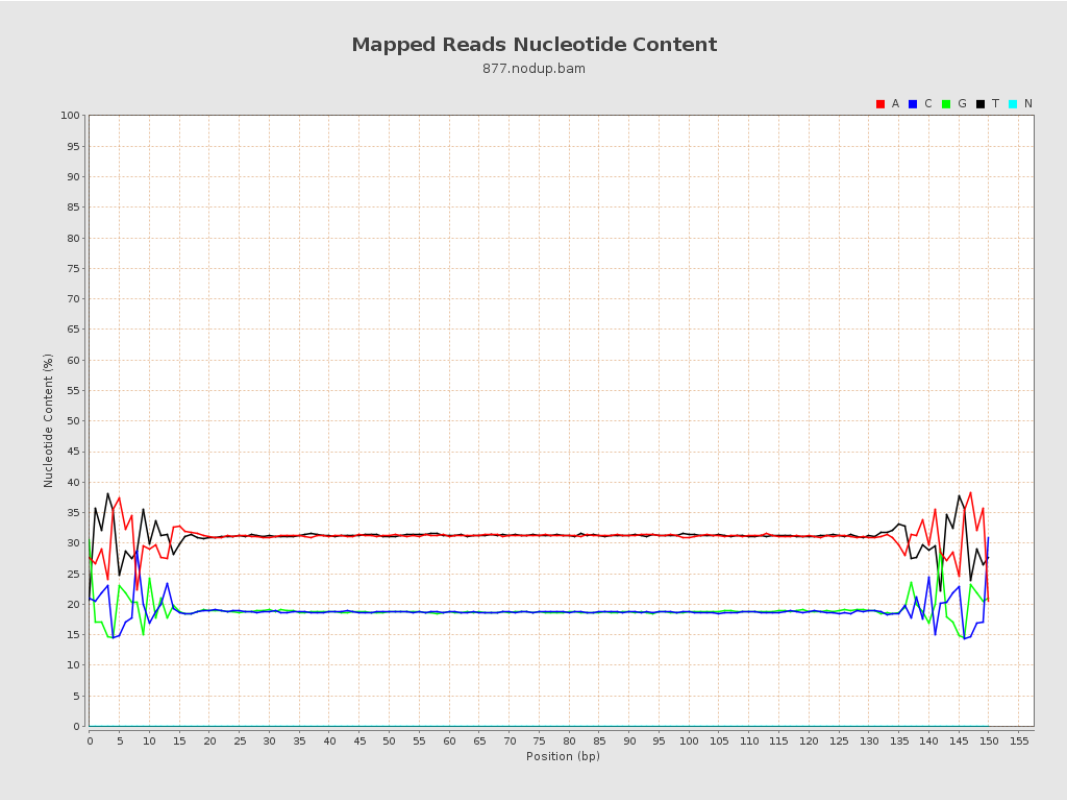
6. Results : Genome Fraction Coverage



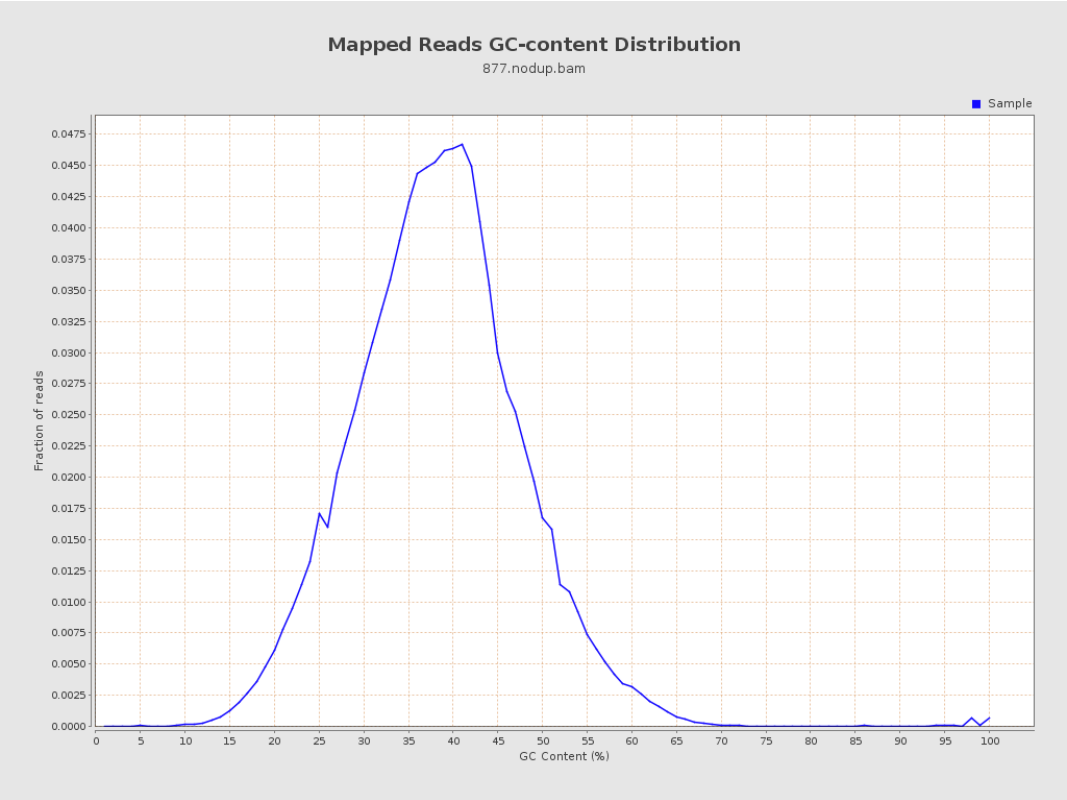
7. Results : Duplication Rate Histogram



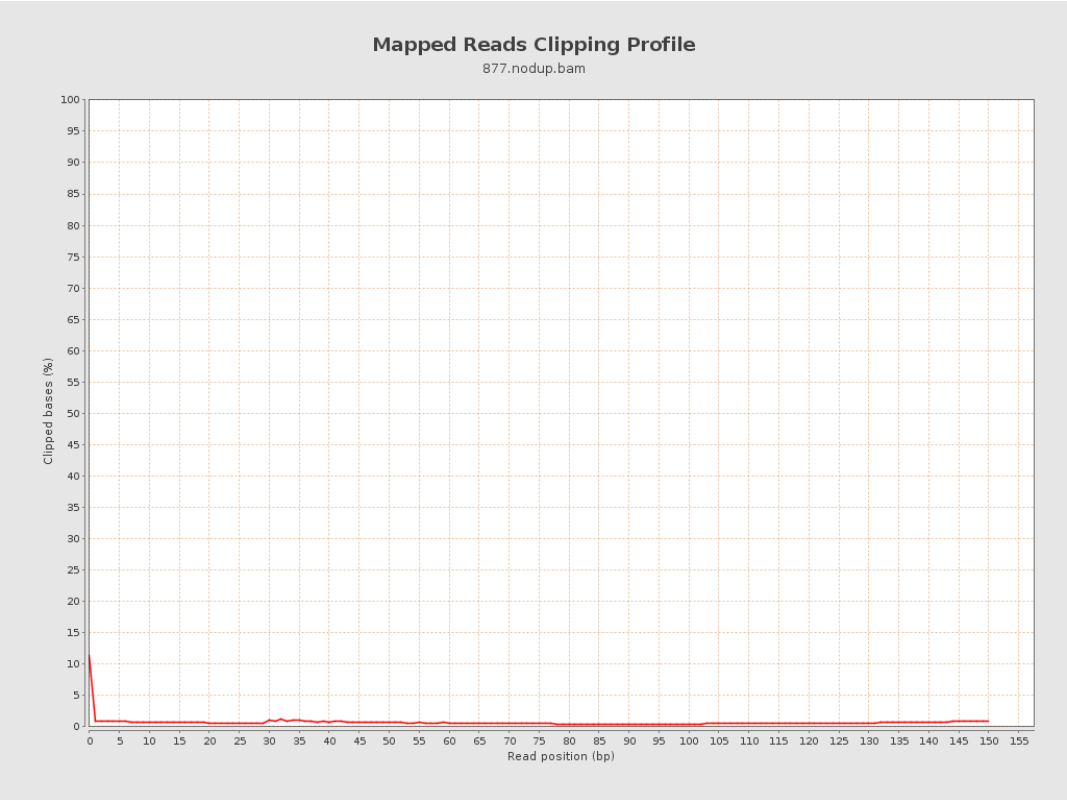
8. Results : Mapped Reads Nucleotide Content



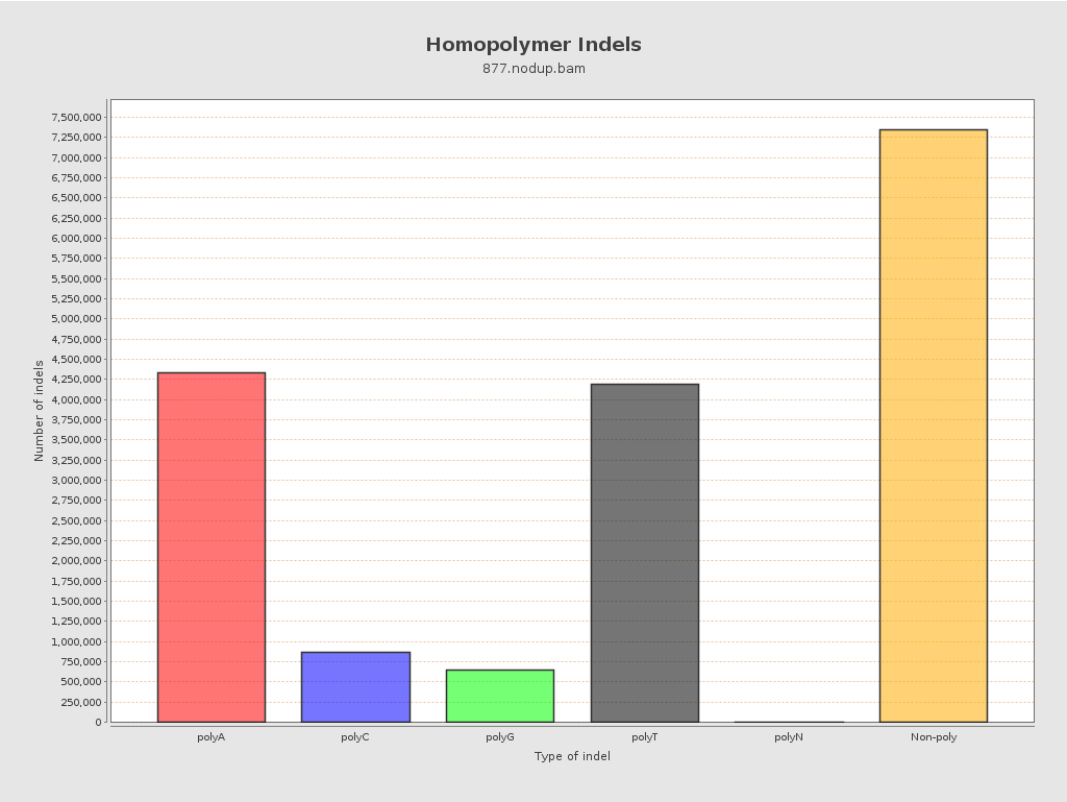
9. Results : Mapped Reads GC-content Distribution



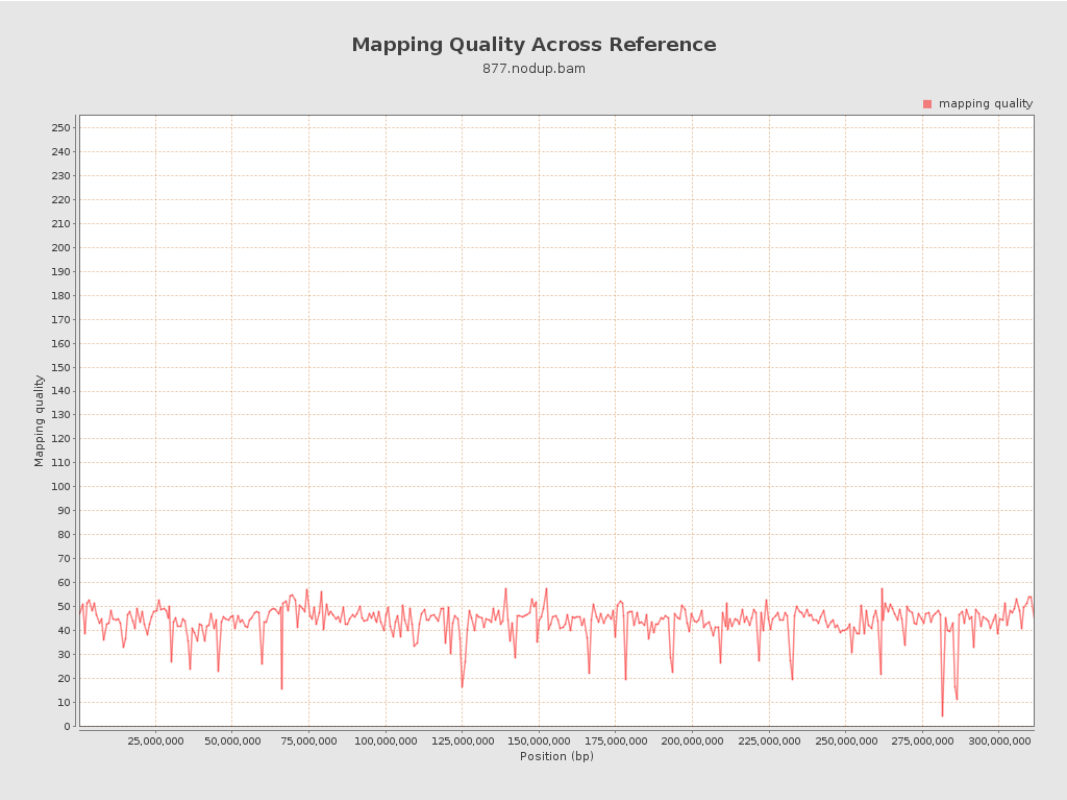
10. Results : Mapped Reads Clipping Profile



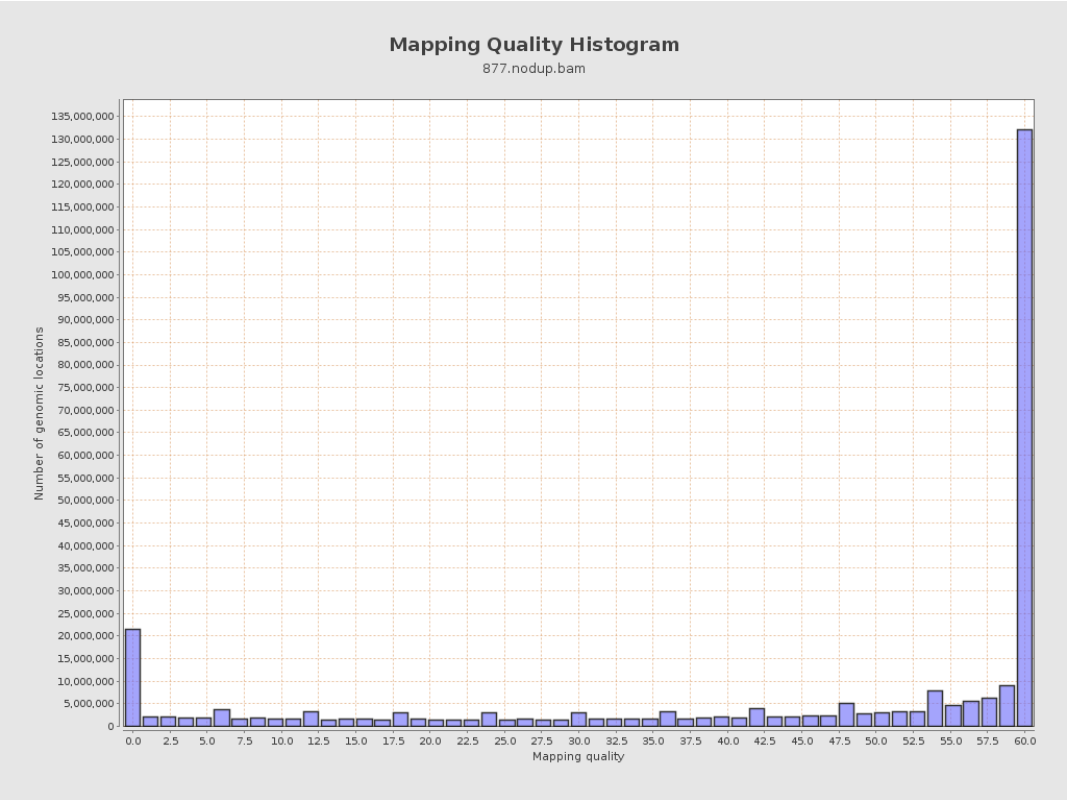
11. Results : Homopolymer Indels



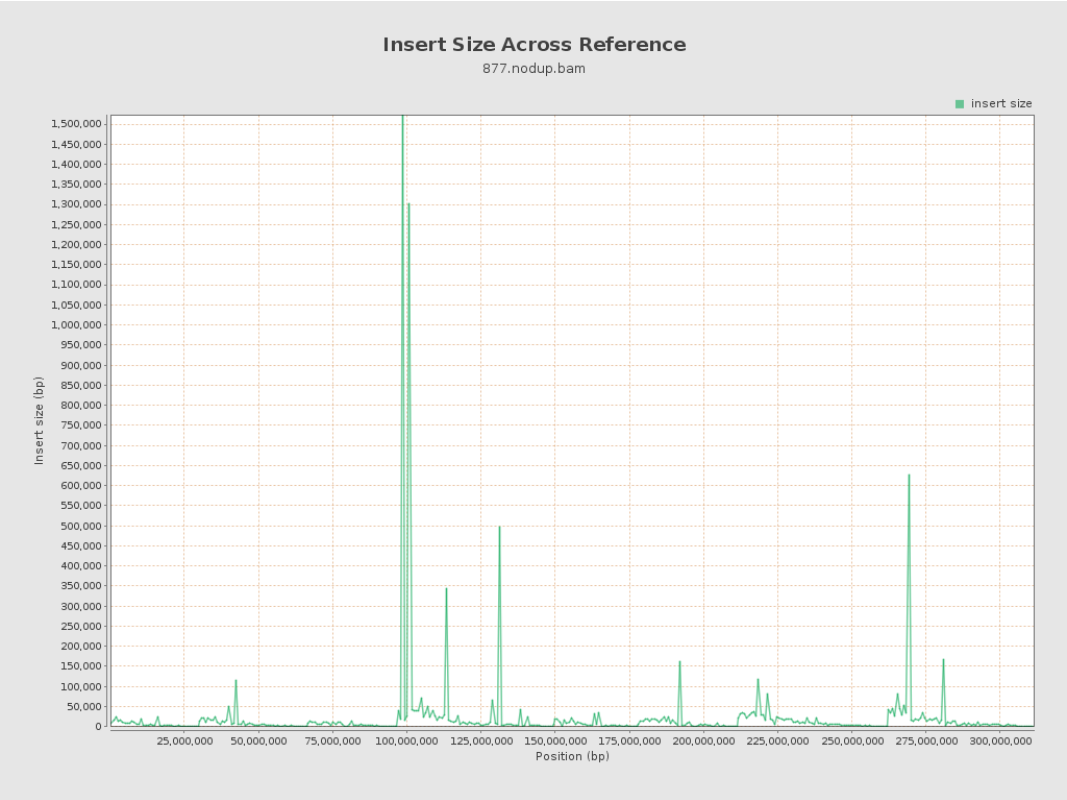
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram