Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:30:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/879.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/879.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_121/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_121_S211_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_121/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_121_S211_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:30:48 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	69,914,759
Mapped reads	62,779,356 / 89.79%
Unmapped reads	7,135,403 / 10.21%
Mapped paired reads	62,779,356 / 89.79%
Mapped reads, first in pair	31,439,979 / 44.97%
Mapped reads, second in pair	31,339,377 / 44.83%
Mapped reads, both in pair	60,440,333 / 86.45%
Mapped reads, singletons	2,339,023 / 3.35%
Read min/max/mean length	30 / 151 / 148.02
Duplicated reads (flagged)	12,923,320 / 18.48%
Clipped reads	15,593,962 / 22.3%

2.2. ACGT Content

Number/percentage of A's	2,646,182,301 / 30.97%
Number/percentage of C's	1,624,800,233 / 19.02%
Number/percentage of T's	2,649,395,478 / 31.01%
Number/percentage of G's	1,624,002,466 / 19.01%
Number/percentage of N's	35,815 / 0%
GC Percentage	38.02%

2.3. Coverage

Mean	27.4881
Standard Deviation	307.116

2.4. Mapping Quality

Mean Mapping Quality	44.32

2.5. Insert size

Mean	282,796.74
Standard Deviation	2,595,289.14
P25/Median/P75	323 / 425 / 559

2.6. Mismatches and indels

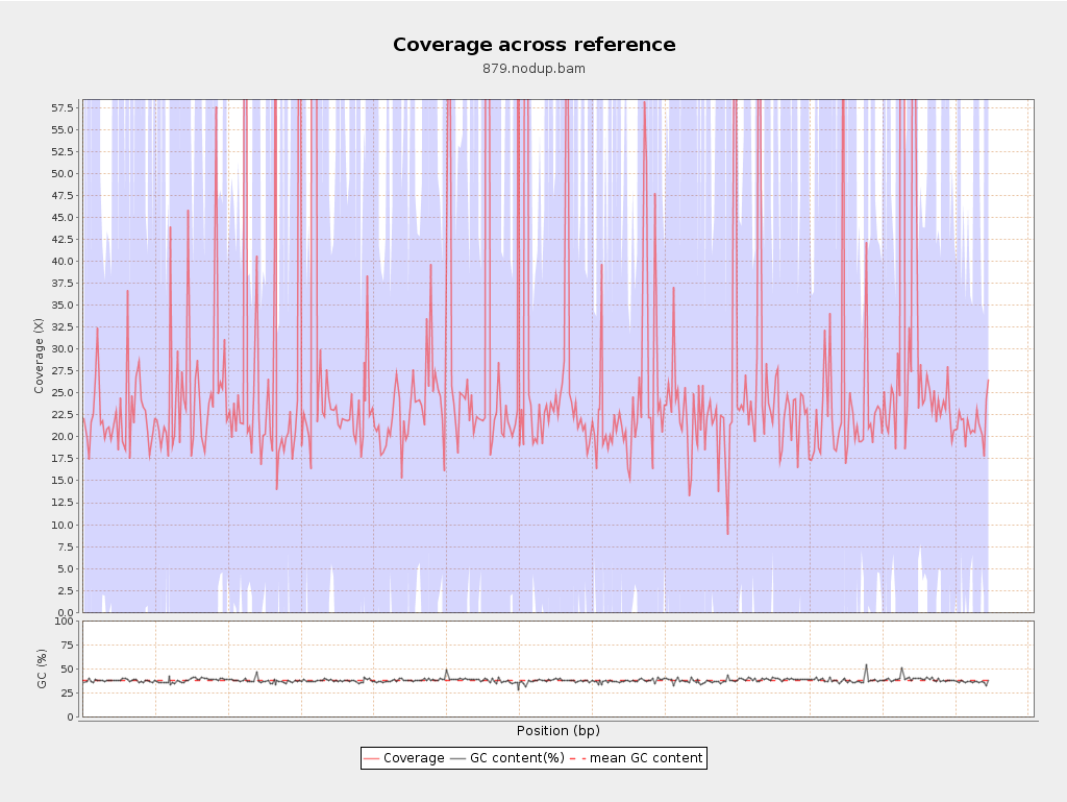
General error rate	2.43%
Mismatches	189,472,725
Insertions	6,621,911
Mapped reads with at least one insertion	9.36%
Deletions	6,067,292
Mapped reads with at least one deletion	8.54%
Homopolymer indels	57.79%

2.7. Chromosome stats

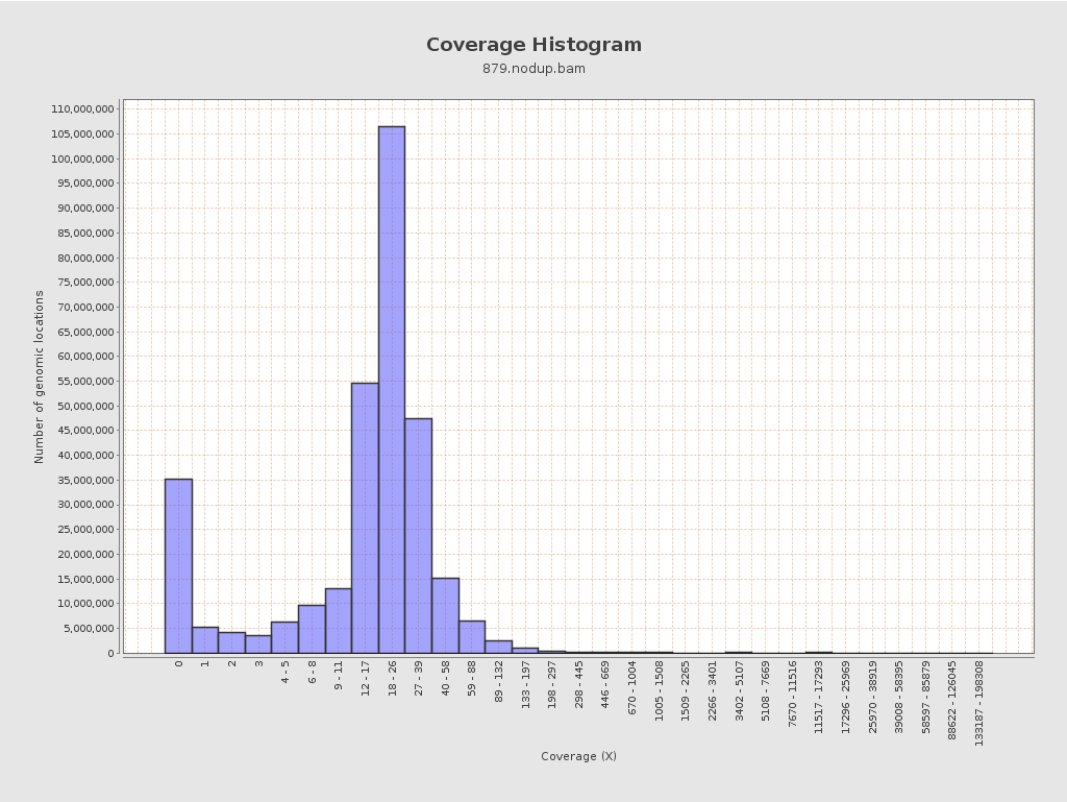
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	658259163	22.1455	137.9073

LT669789.1	36598175	1021667142	27.9158	337.3517
LT669790.1	30422129	1093760272	35.9528	481.2749
LT669791.1	52758100	1437634707	27.2496	366.2794
LT669792.1	28376109	794581399	28.0018	290.7219
LT669793.1	33388210	804746248	24.1027	159.5333
LT669794.1	50579949	1278967831	25.2861	252.0832
LT669795.1	49795044	1476831473	29.6582	285.9999

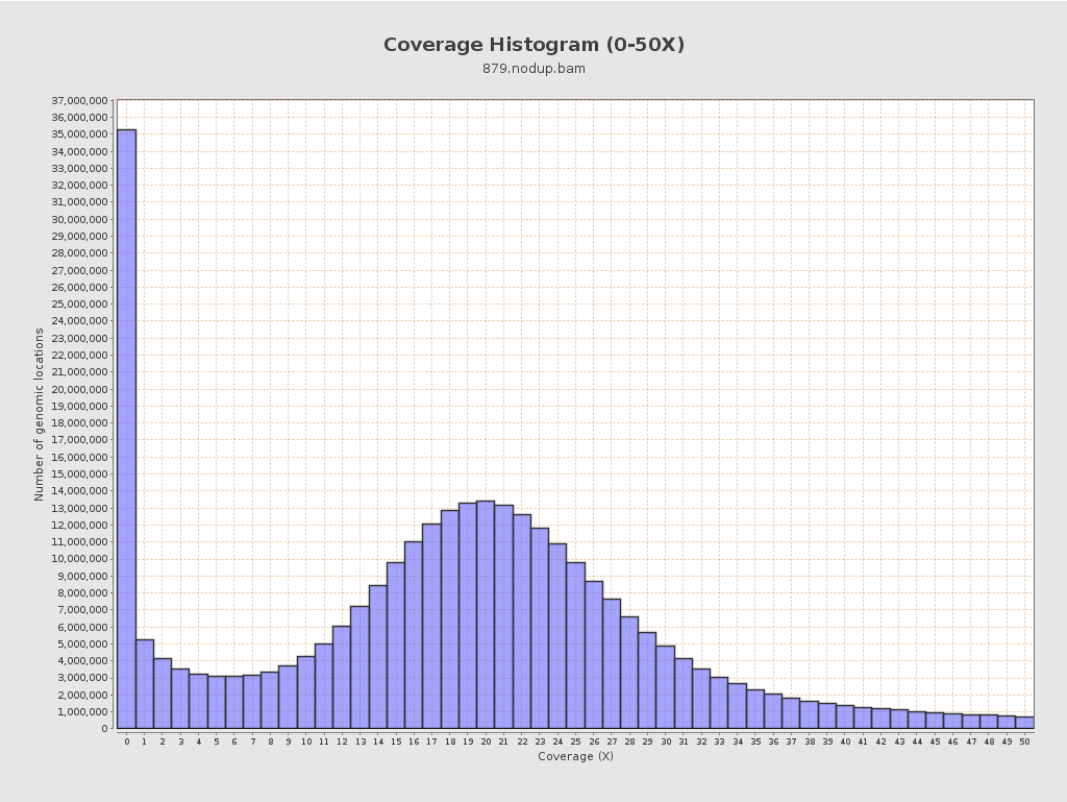
3. Results : Coverage across reference



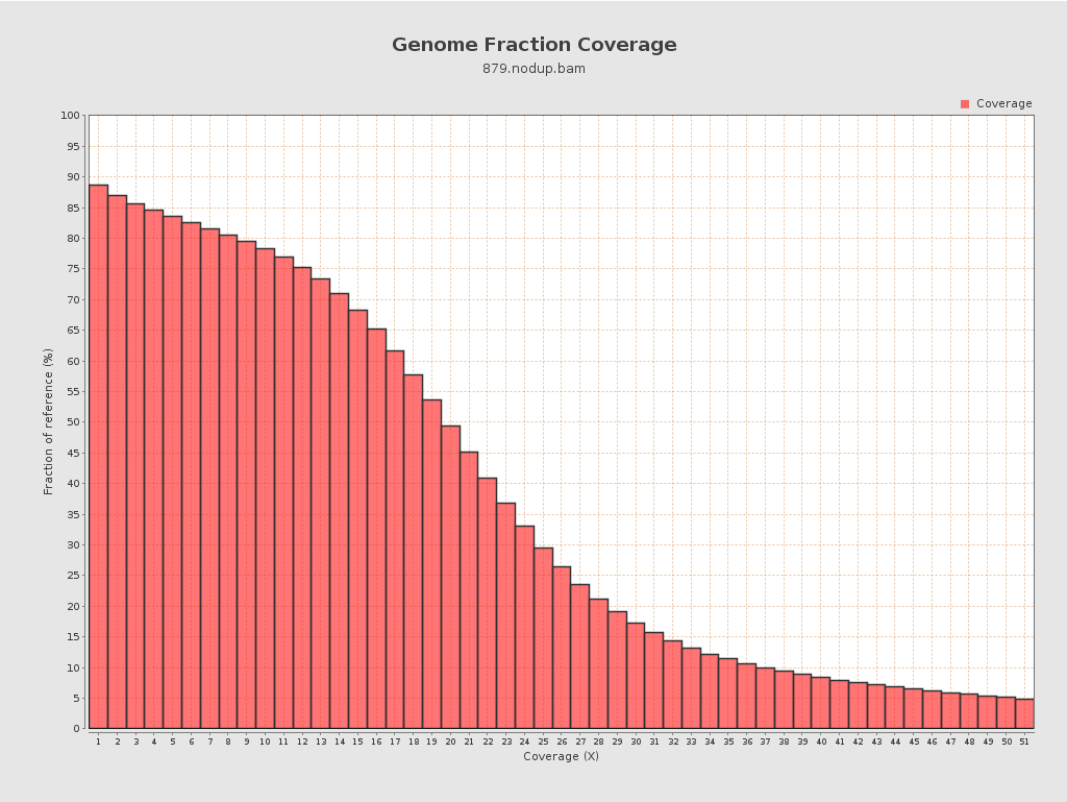
4. Results : Coverage Histogram



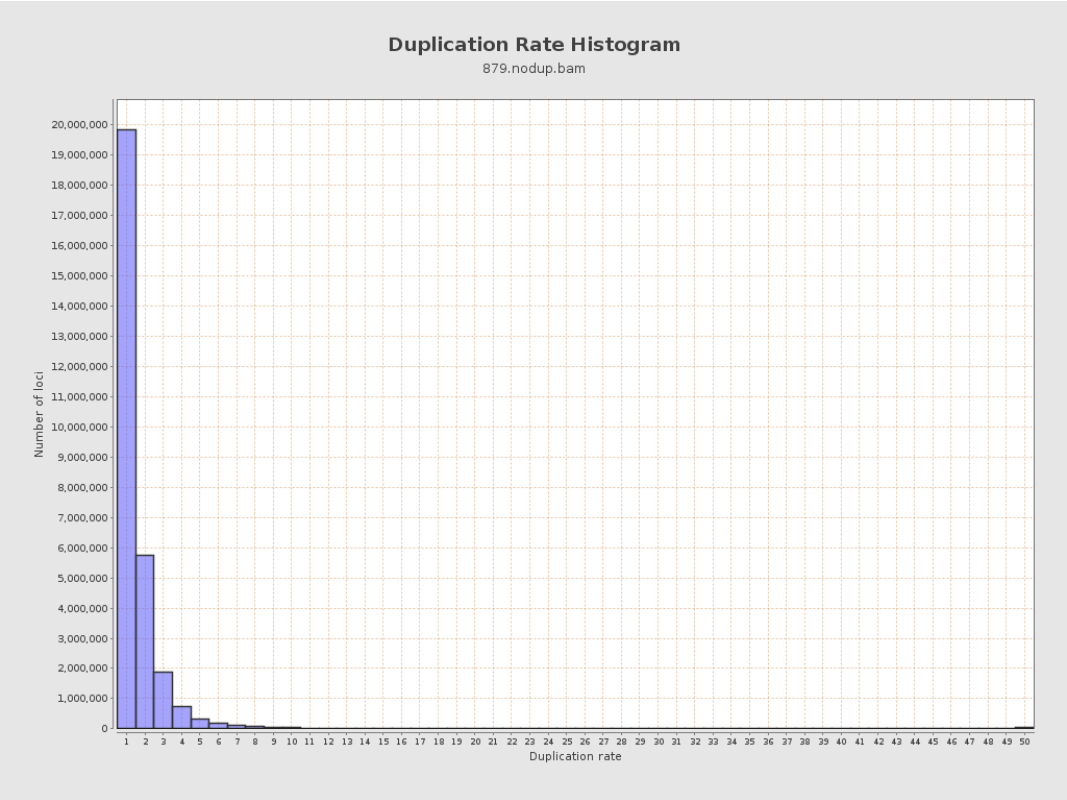
5. Results : Coverage Histogram (0-50X)



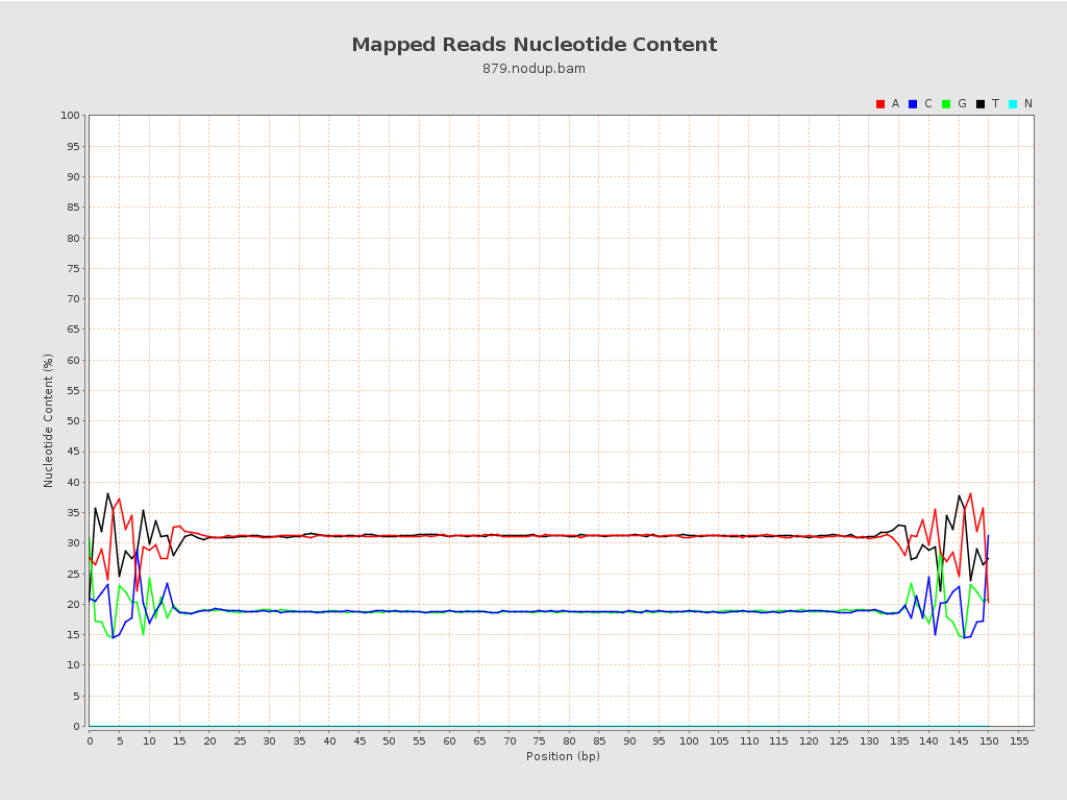
6. Results : Genome Fraction Coverage



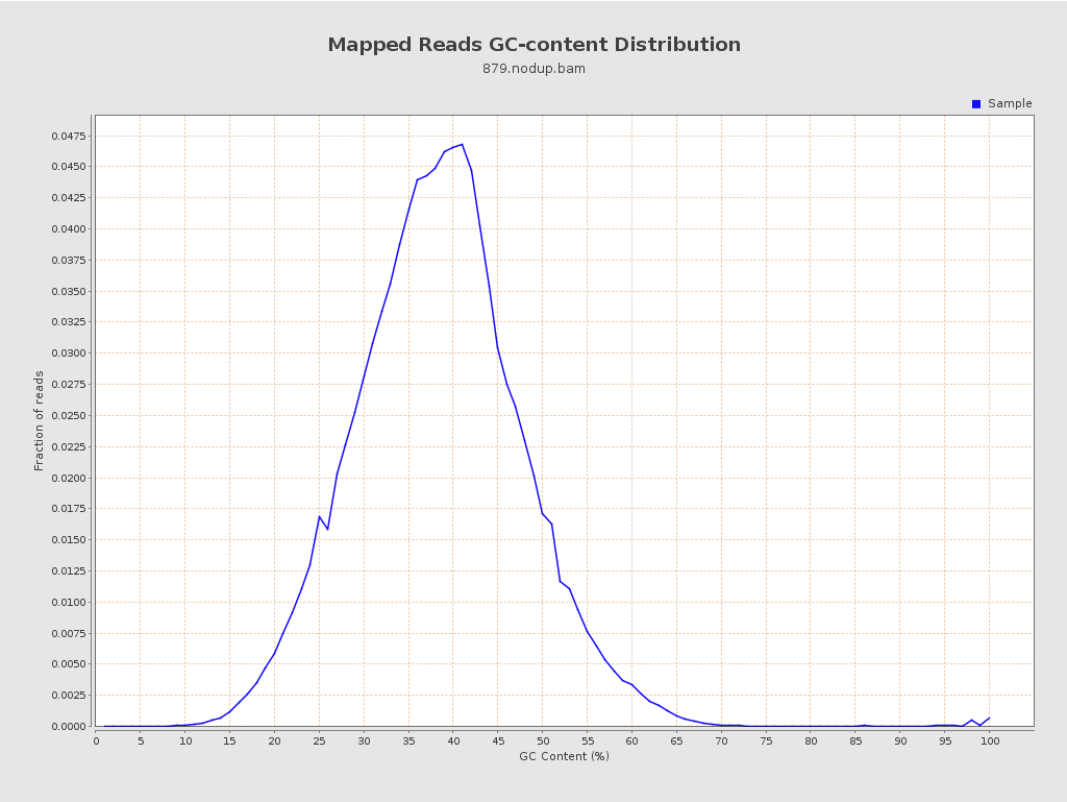
7. Results : Duplication Rate Histogram



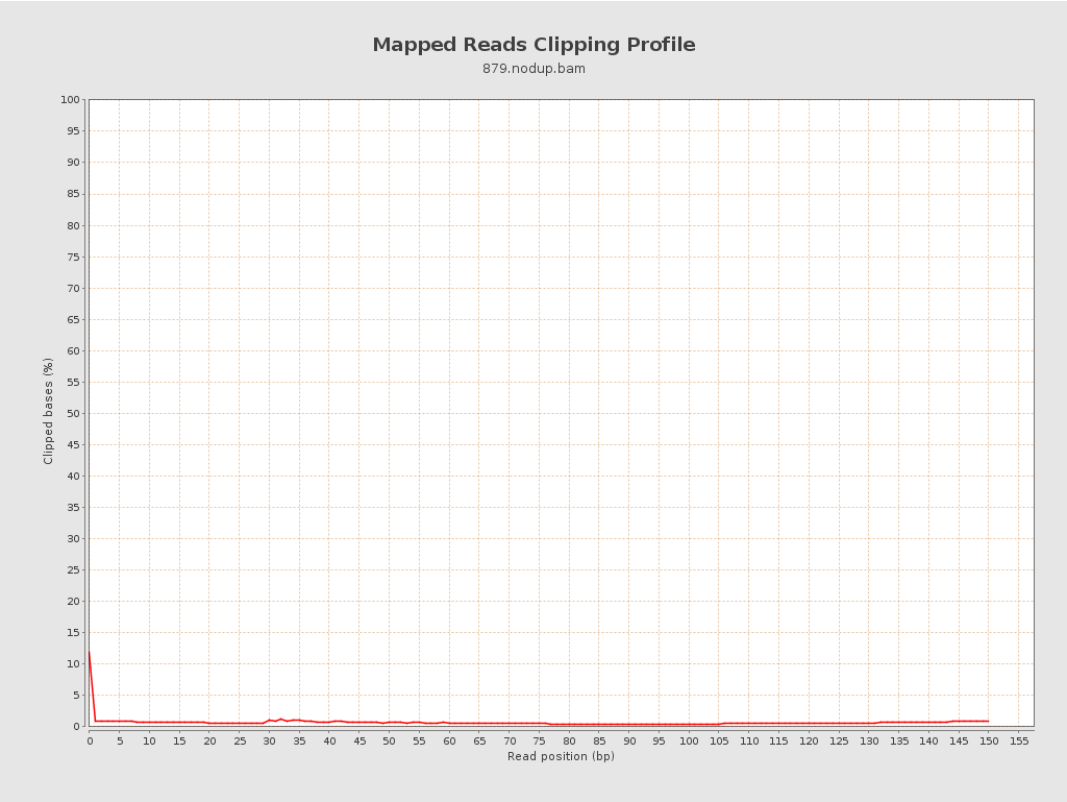
8. Results : Mapped Reads Nucleotide Content



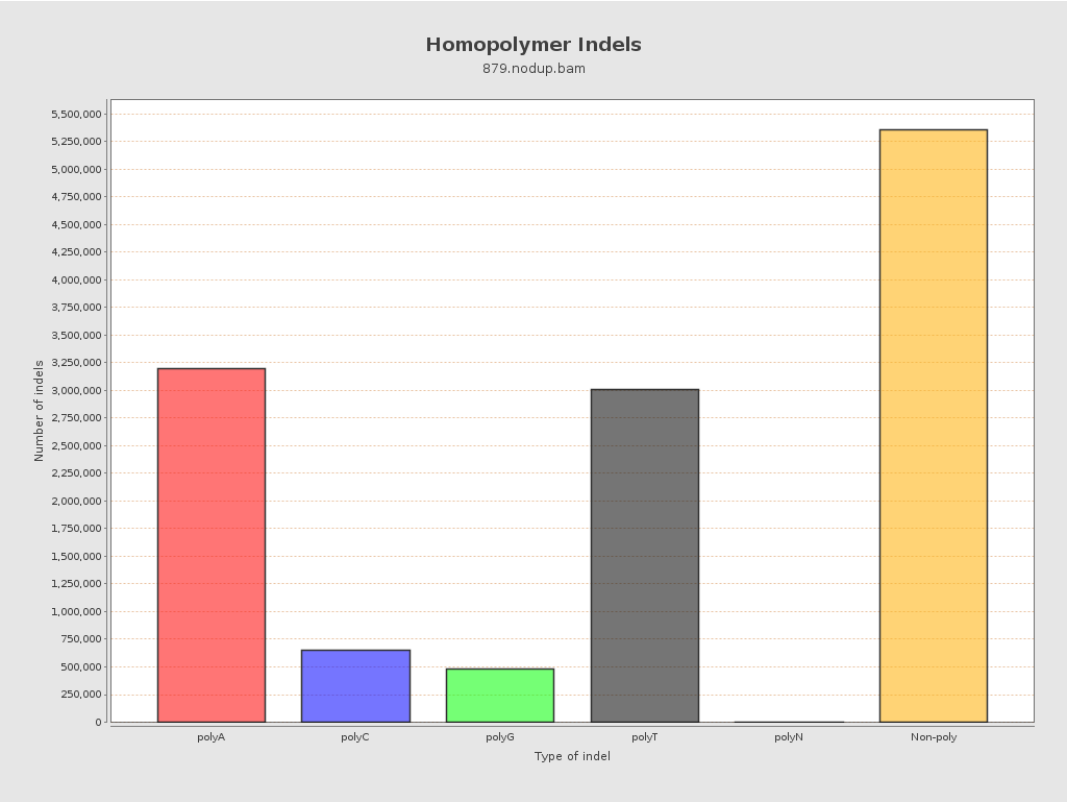
9. Results : Mapped Reads GC-content Distribution



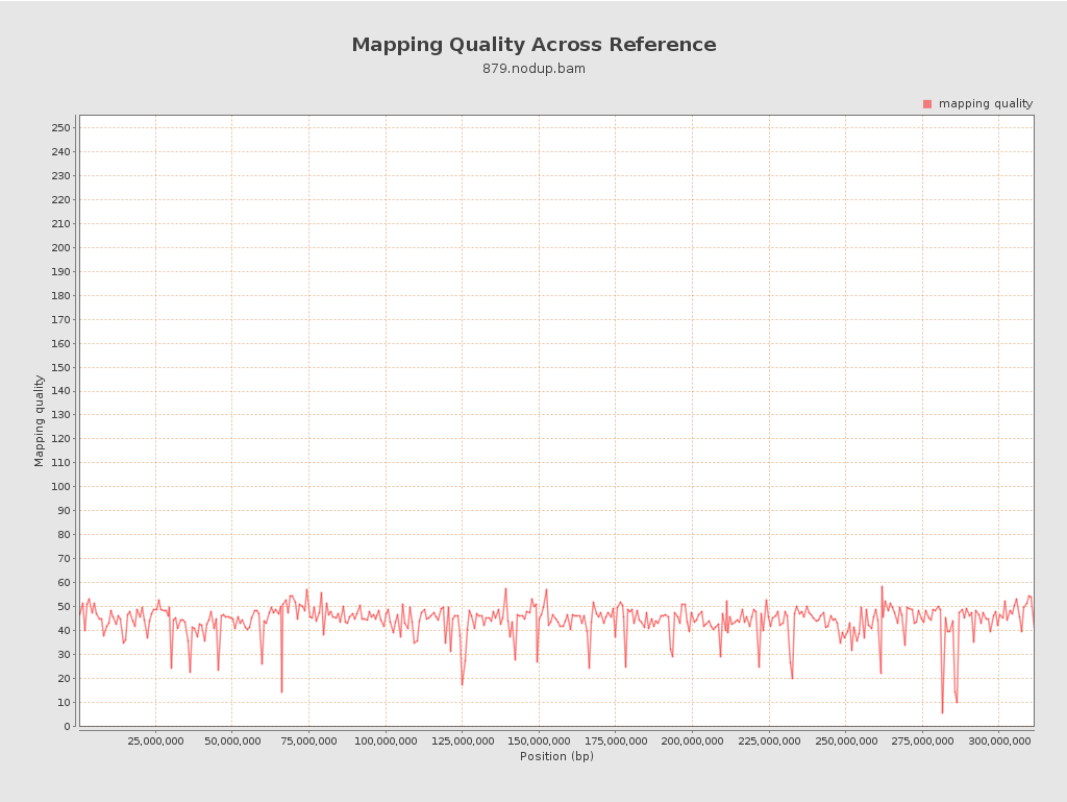
10. Results : Mapped Reads Clipping Profile



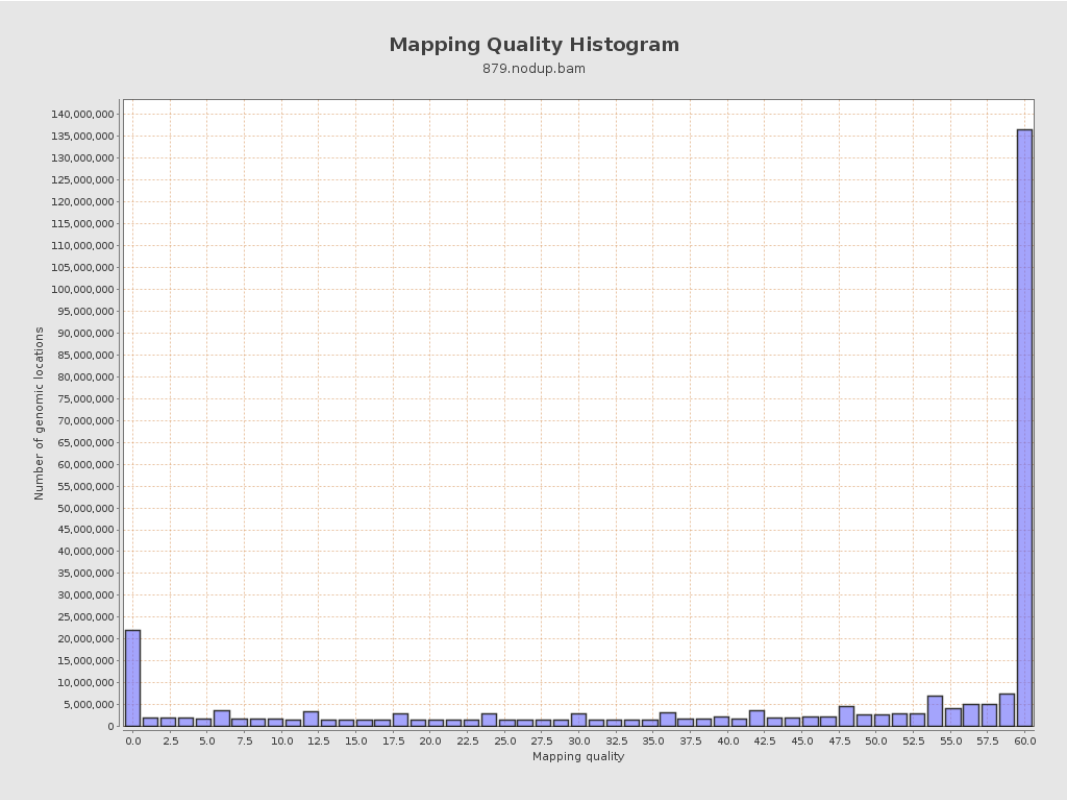
11. Results : Homopolymer Indels



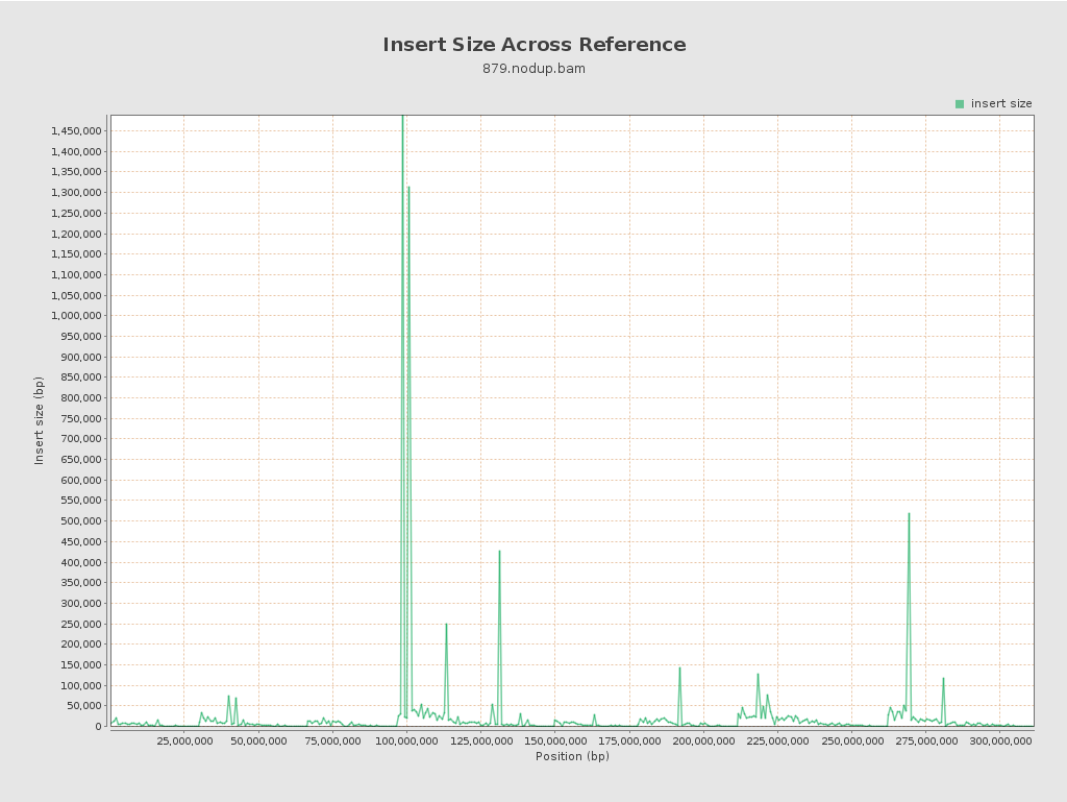
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram