

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:23:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/878
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/878 .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_284/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_284_S365_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_284/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_284_S365_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:23:02 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	47,665,270
Mapped reads	43,164,992 / 90.56%
Unmapped reads	4,500,278 / 9.44%
Mapped paired reads	43,164,992 / 90.56%
Mapped reads, first in pair	21,615,521 / 45.35%
Mapped reads, second in pair	21,549,471 / 45.21%
Mapped reads, both in pair	41,712,510 / 87.51%
Mapped reads, singletons	1,452,482 / 3.05%
Read min/max/mean length	30 / 151 / 148.11
Duplicated reads (flagged)	6,860,490 / 14.39%
Clipped reads	10,717,782 / 22.49%

2.2. ACGT Content

Number/percentage of A's	1,820,009,452 / 30.92%
Number/percentage of C's	1,120,443,795 / 19.04%
Number/percentage of T's	1,823,685,336 / 30.99%
Number/percentage of G's	1,121,358,664 / 19.05%
Number/percentage of N's	21,129 / 0%
GC Percentage	38.09%

2.3. Coverage

Mean	18.9338
Standard Deviation	194.2639

2.4. Mapping Quality

Mean Mapping Quality	44.61
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2.5. Insert size

Mean	262,763.42
Standard Deviation	2,487,020.28
P25/Median/P75	329 / 435 / 563

2.6. Mismatches and indels

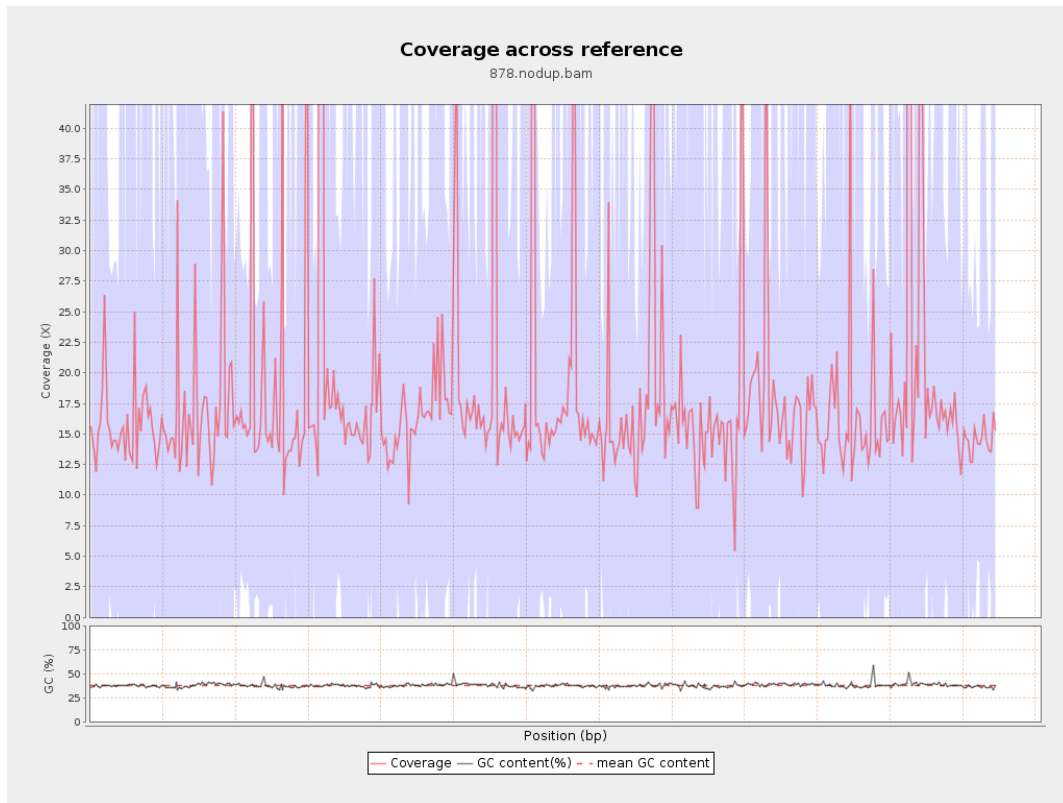
General error rate	2.41%
Mismatches	130,034,808
Insertions	4,334,670
Mapped reads with at least one insertion	8.93%
Deletions	4,042,799
Mapped reads with at least one deletion	8.31%
Homopolymer indels	57.25%

2.7. Chromosome stats

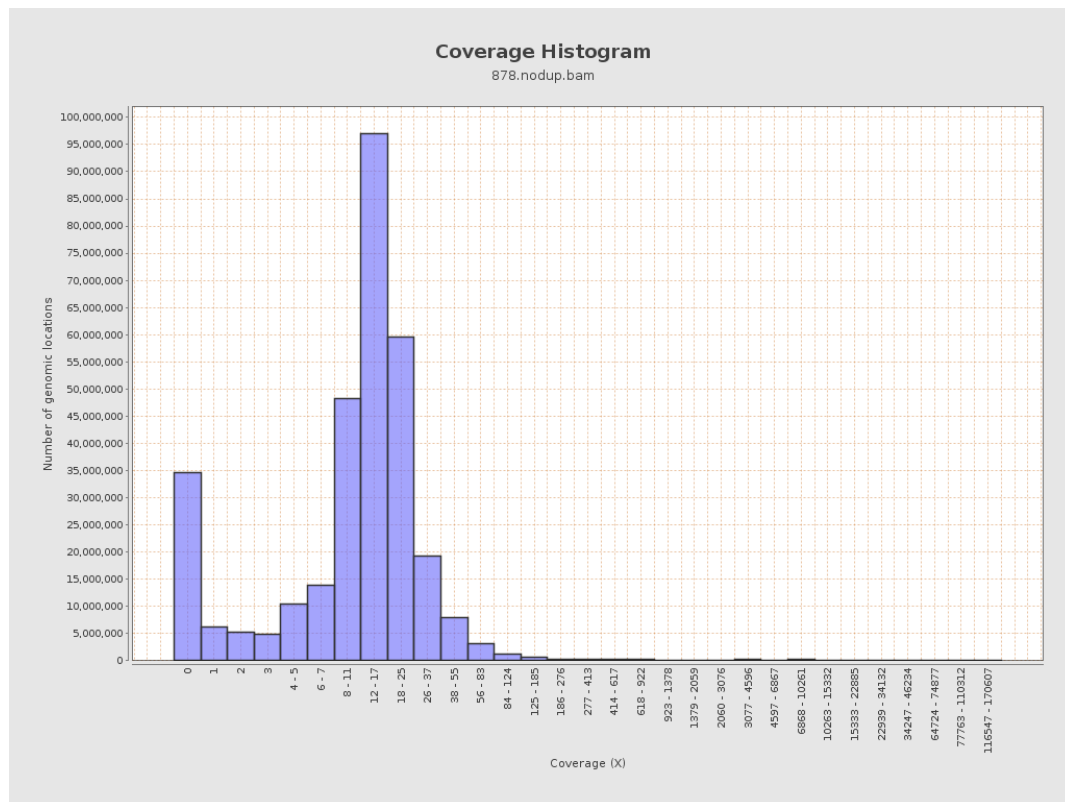
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	461906182	15.5397	82.6809

LT669789.1	36598175	679325039	18.5617	192.3243
LT669790.1	30422129	735970778	24.192	289.4373
LT669791.1	52758100	989312440	18.7519	210.8404
LT669792.1	28376109	532882793	18.7793	188.6894
LT669793.1	33388210	582917545	17.4588	155.1244
LT669794.1	50579949	889573119	17.5875	151.0732
LT669795.1	49795044	1028671786	20.6581	216.8002

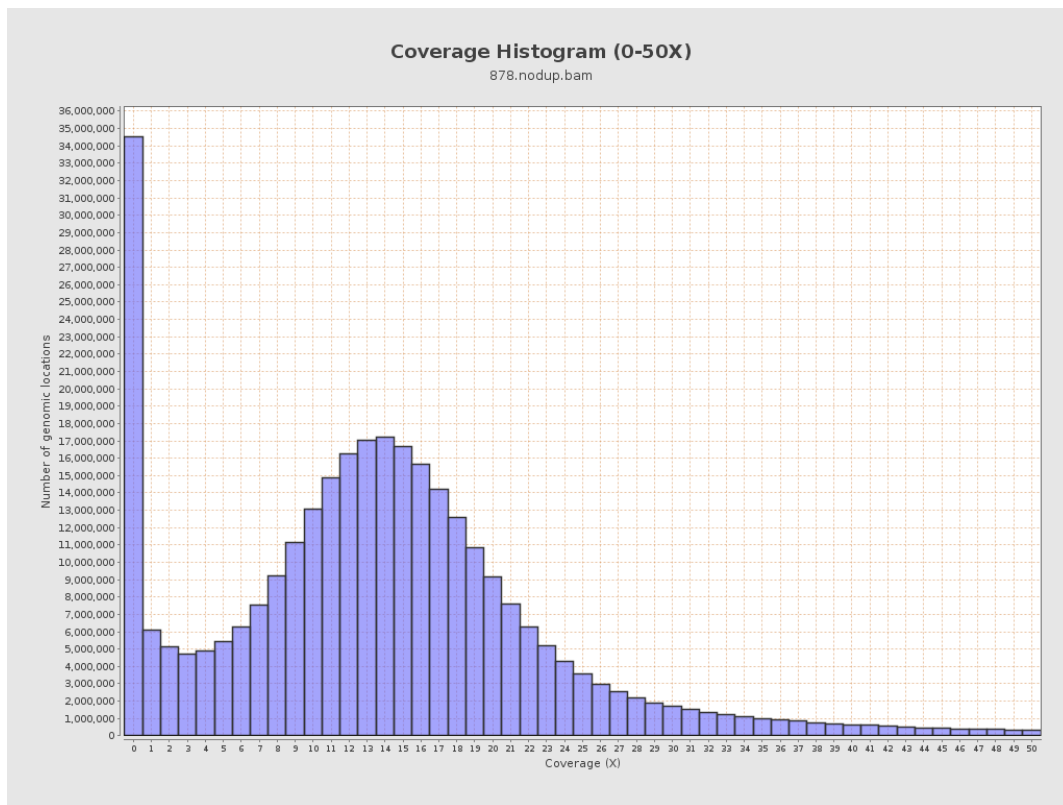
3. Results : Coverage across reference



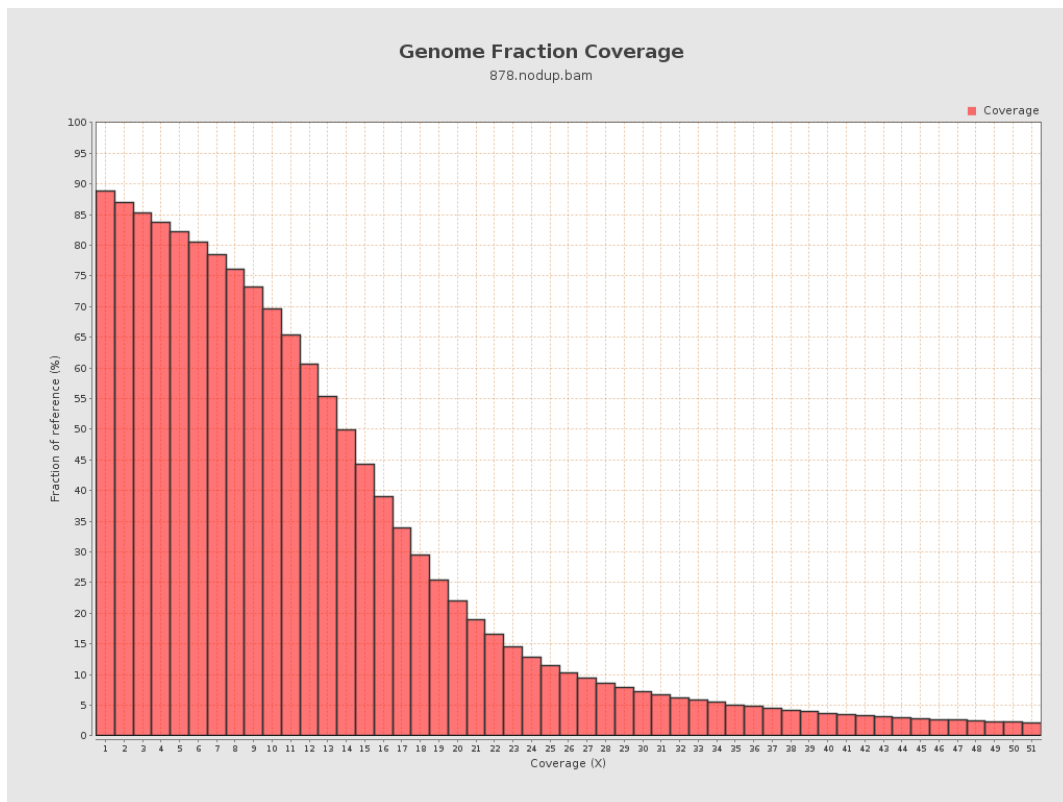
4. Results : Coverage Histogram



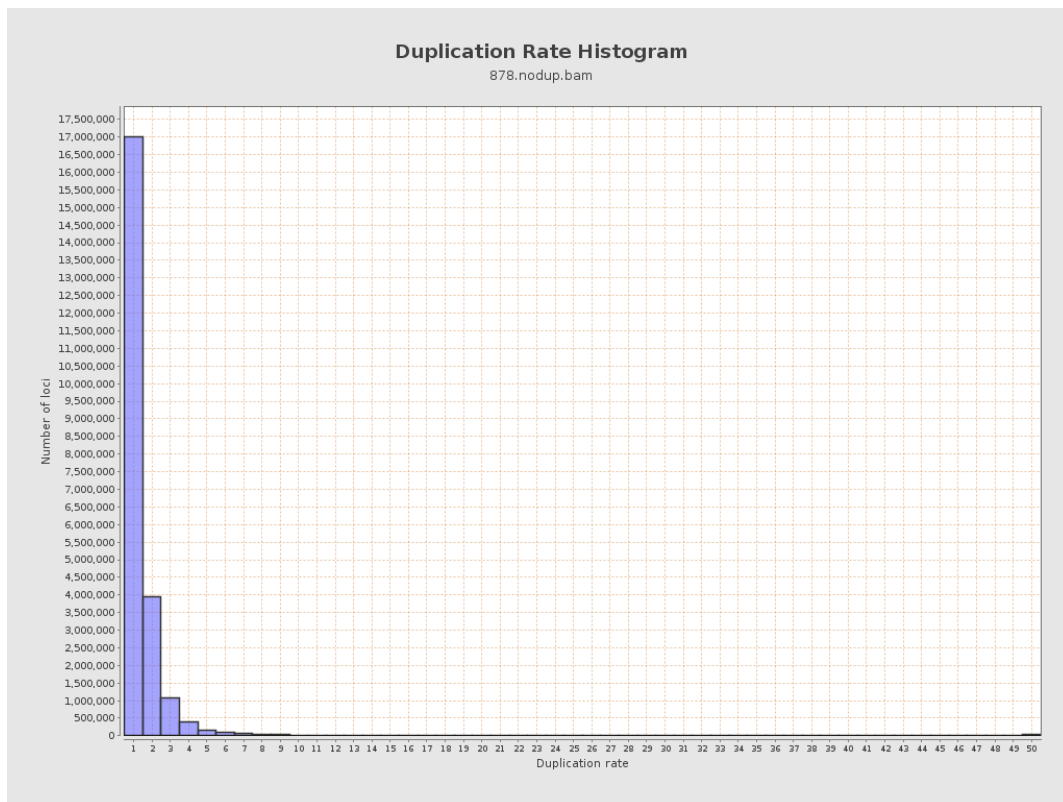
5. Results : Coverage Histogram (0-50X)



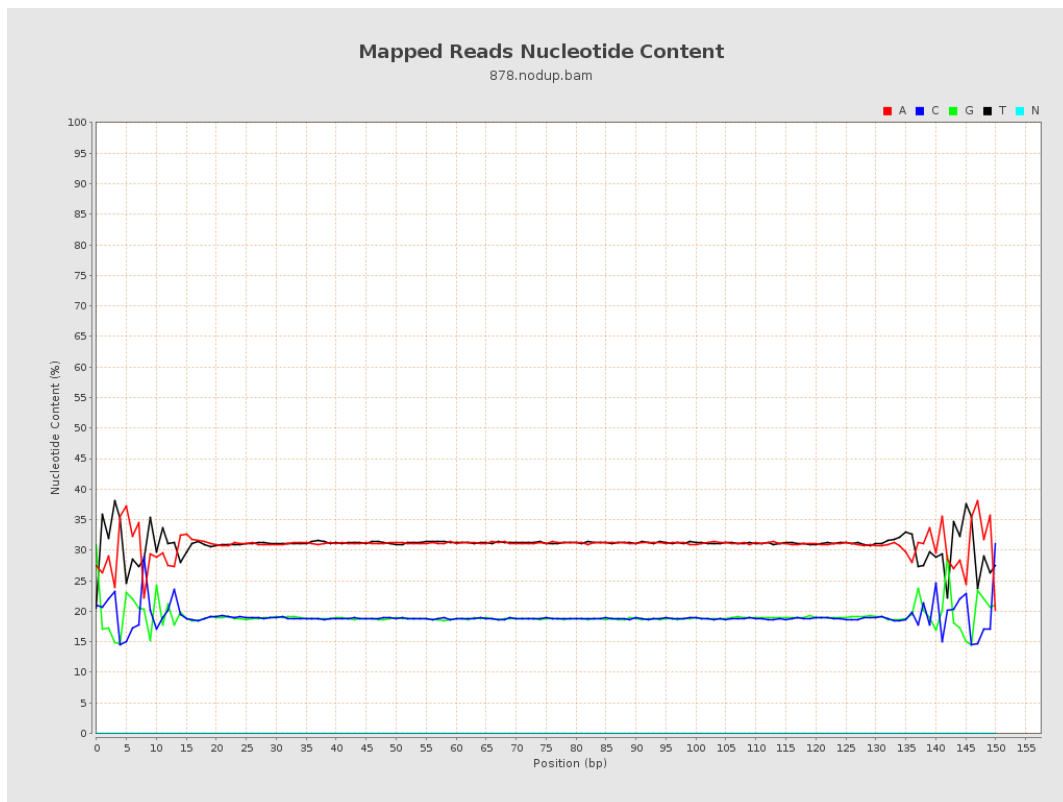
6. Results : Genome Fraction Coverage



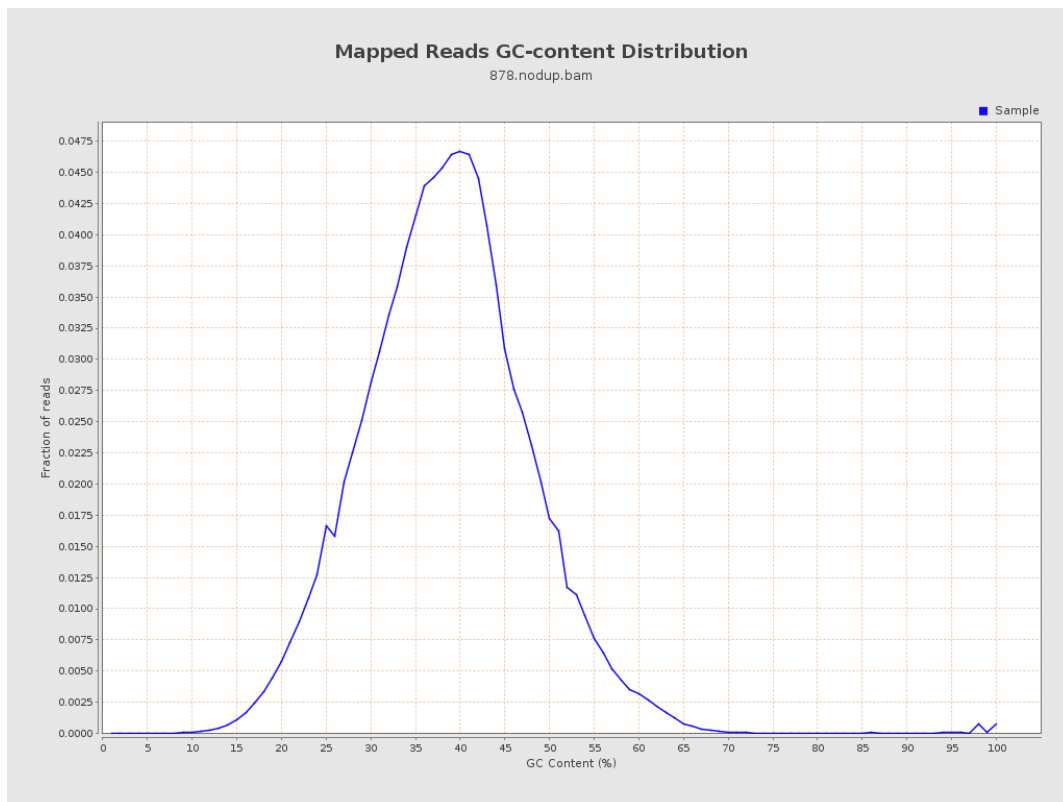
7. Results : Duplication Rate Histogram



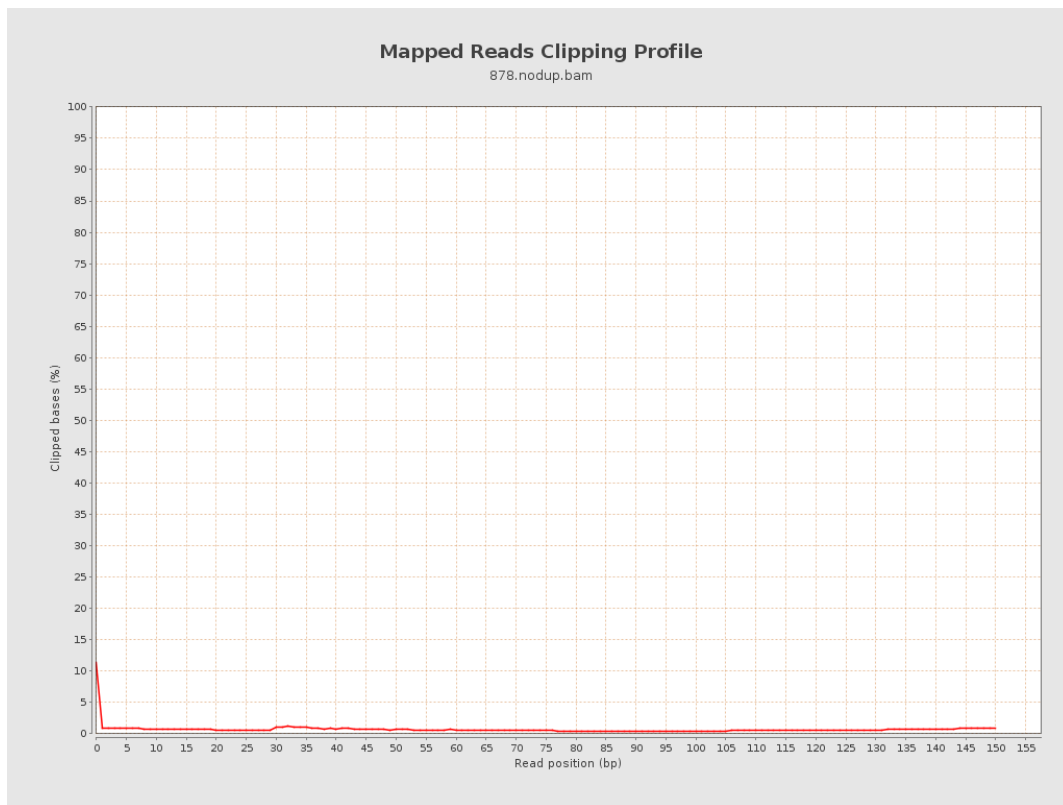
8. Results : Mapped Reads Nucleotide Content



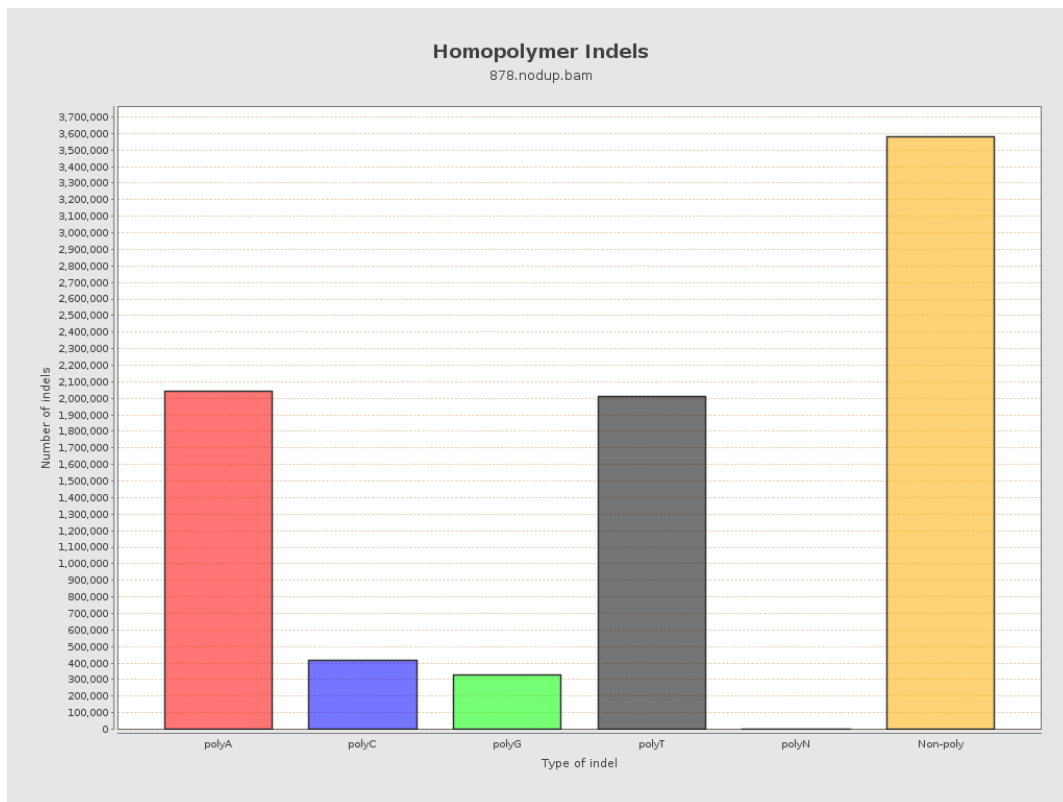
9. Results : Mapped Reads GC-content Distribution



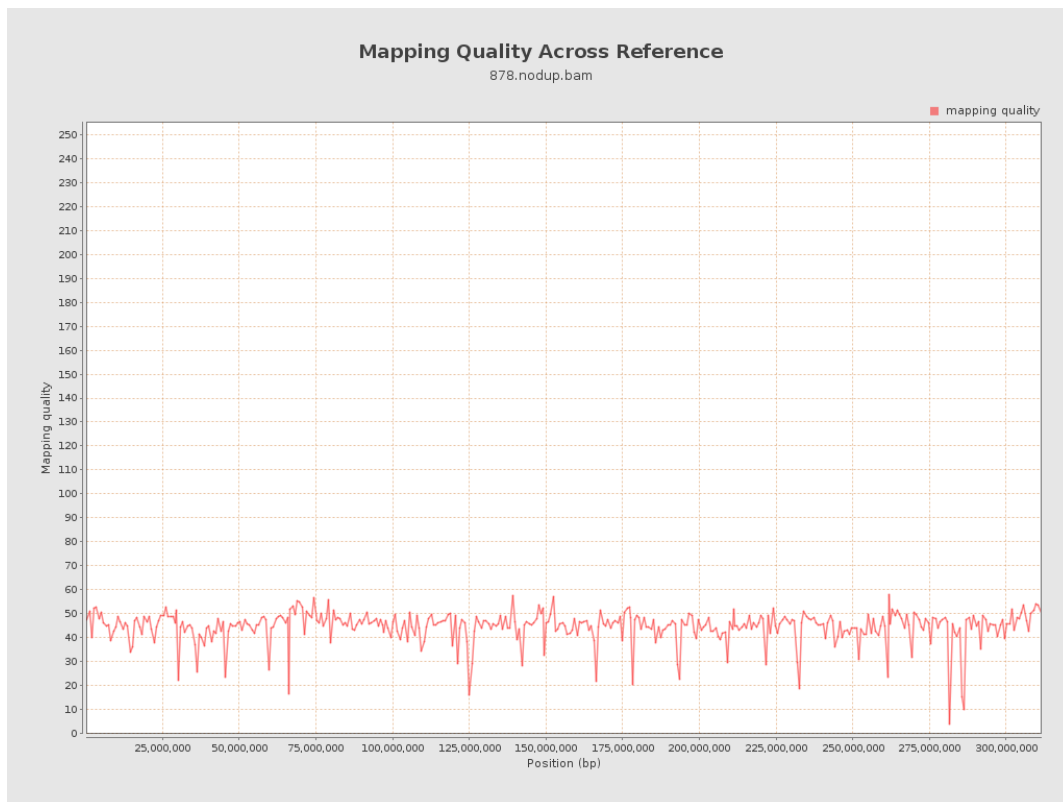
10. Results : Mapped Reads Clipping Profile



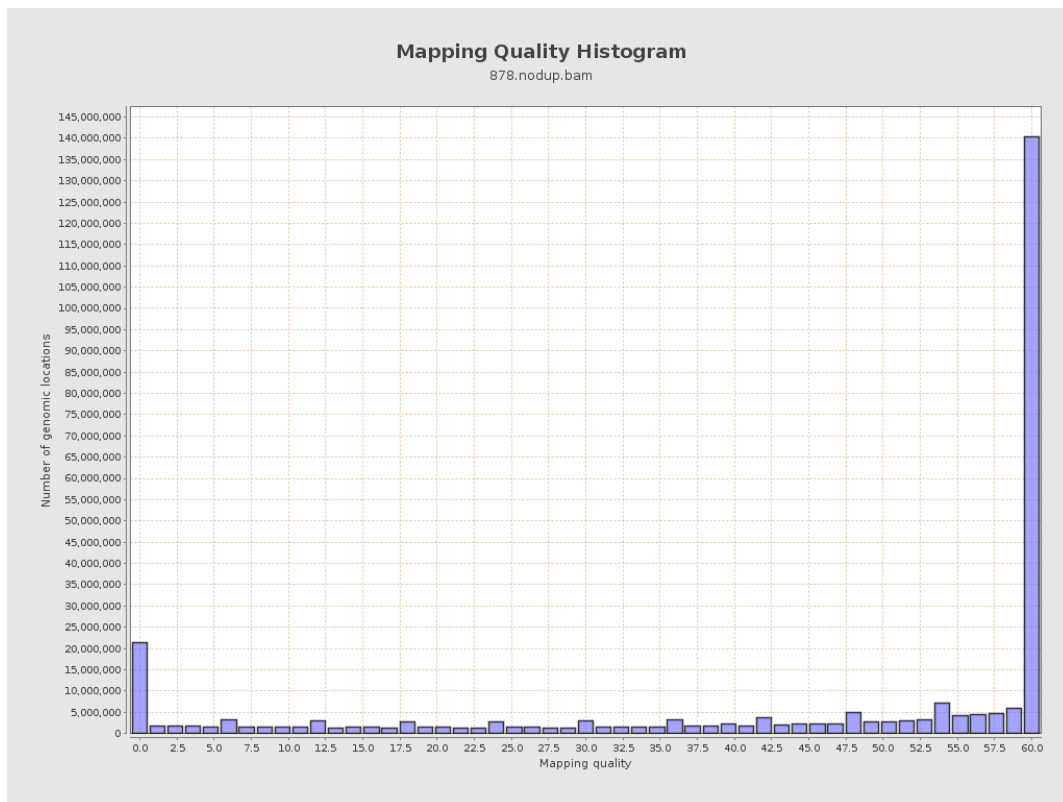
11. Results : Homopolymer Indels



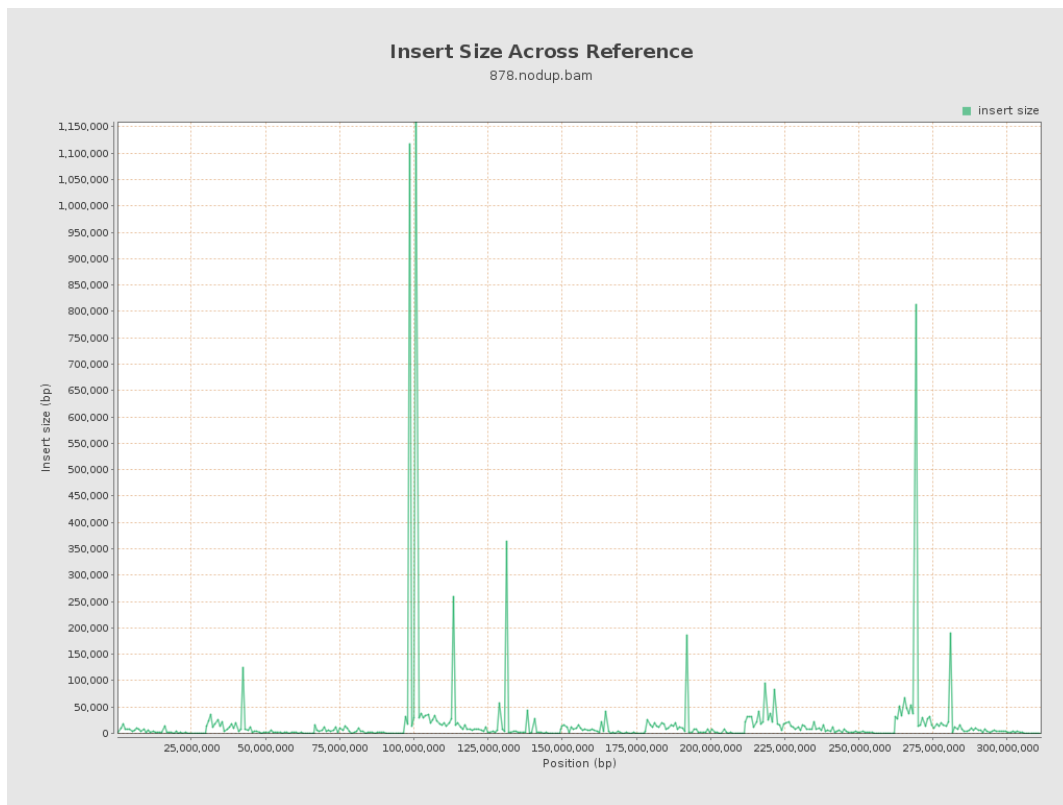
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

