Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:36:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1178
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1178 .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_160/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_160_S250_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_160/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_160_S250_L002_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:36:33 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	82,076,640
Mapped reads	73,006,280 / 88.95%
Unmapped reads	9,070,360 / 11.05%
Mapped paired reads	73,006,280 / 88.95%
Mapped reads, first in pair	36,585,818 / 44.58%
Mapped reads, second in pair	36,420,462 / 44.37%
Mapped reads, both in pair	70,069,547 / 85.37%
Mapped reads, singletons	2,936,733 / 3.58%
Read min/max/mean length	30 / 151 / 148.11
Duplicated reads (flagged)	16,575,712 / 20.2%
Clipped reads	18,257,350 / 22.24%

2.2. ACGT Content

Number/percentage of A's	3,064,187,929 / 30.91%
Number/percentage of C's	1,891,660,707 / 19.08%
Number/percentage of T's	3,070,214,821 / 30.97%
Number/percentage of G's	1,888,681,980 / 19.05%
Number/percentage of N's	41,888 / 0%
GC Percentage	38.13%

2.3. Coverage

Mean	31.895
Standard Deviation	378.1353

2.4. Mapping Quality

Mean Mapping Quality	44.53

2.5. Insert size

Mean	277,346.9
Standard Deviation	2,563,029.67
P25/Median/P75	323 / 424 / 557

2.6. Mismatches and indels

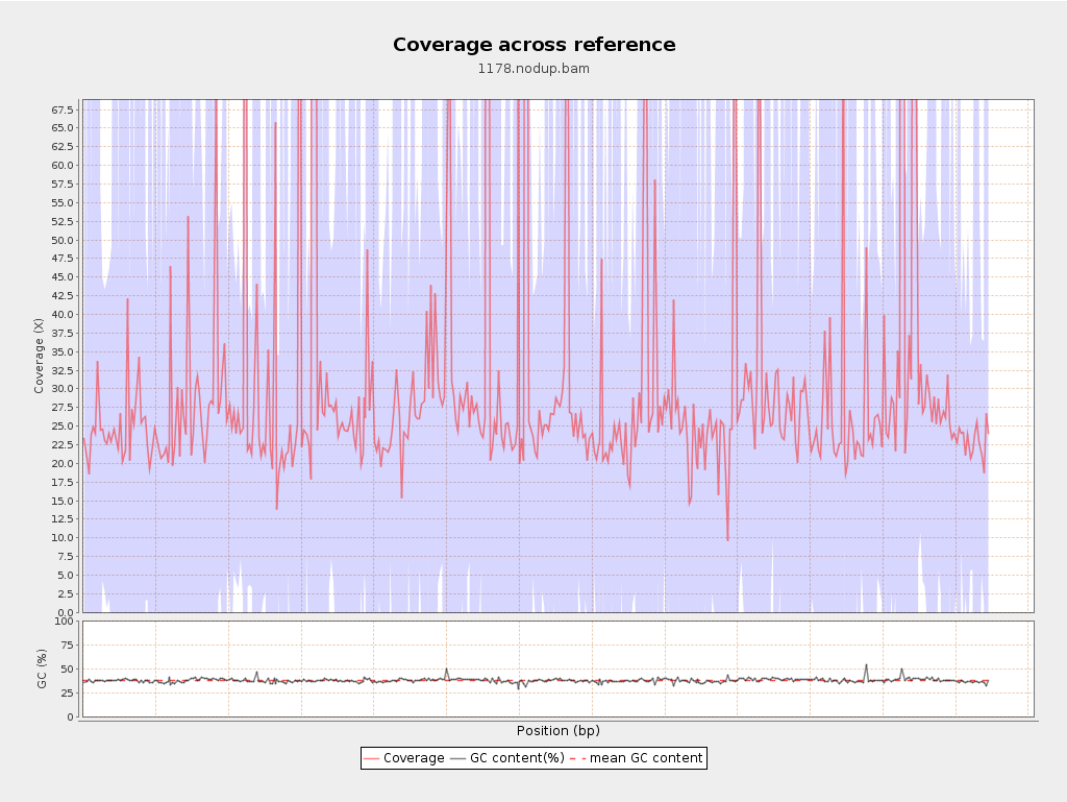
General error rate	2.42%
Mismatches	219,066,334
Insertions	7,624,739
Mapped reads with at least one insertion	9.25%
Deletions	6,865,499
Mapped reads with at least one deletion	8.33%
Homopolymer indels	58%

2.7. Chromosome stats

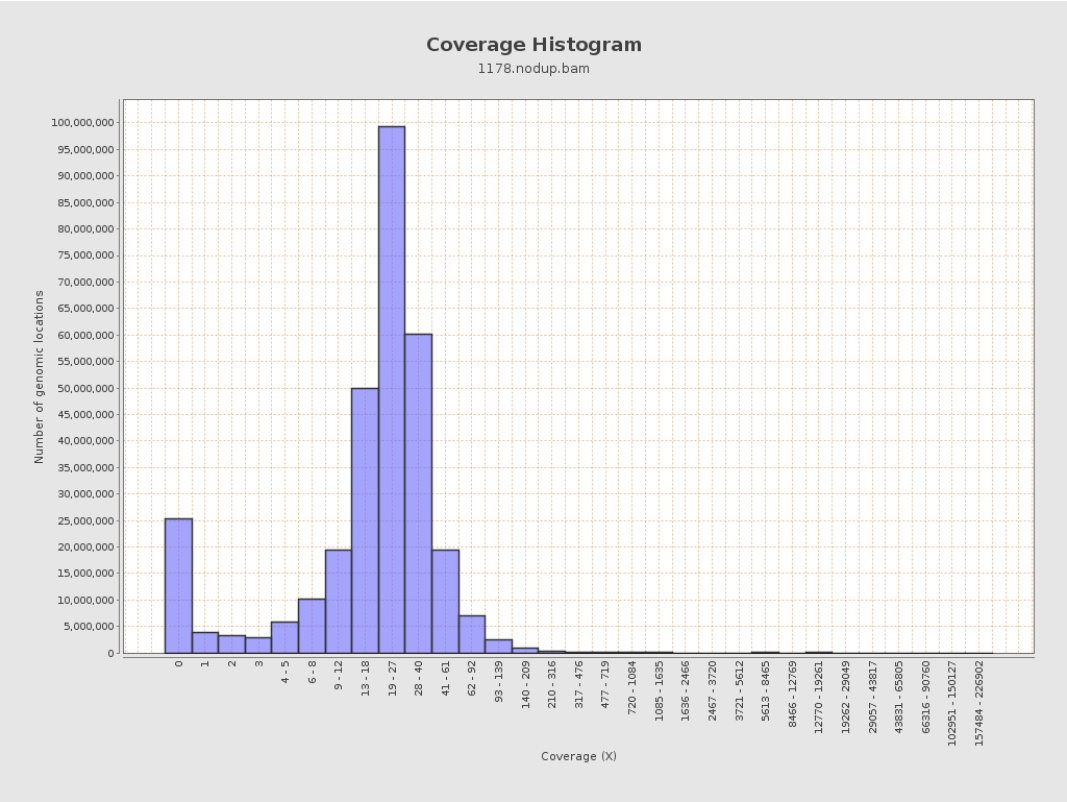
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	722157355	24.2951	157.1856

LT669789.1	36598175	1155292595	31.5669	392.4353
LT669790.1	30422129	1270404834	41.7592	591.3768
LT669791.1	52758100	1686806718	31.9725	438.1782
LT669792.1	28376109	913213167	32.1825	381.6091
LT669793.1	33388210	934850285	27.9994	223.5544
LT669794.1	50579949	1473110147	29.1244	280.8141
LT669795.1	49795044	1783993712	35.8267	391.3164

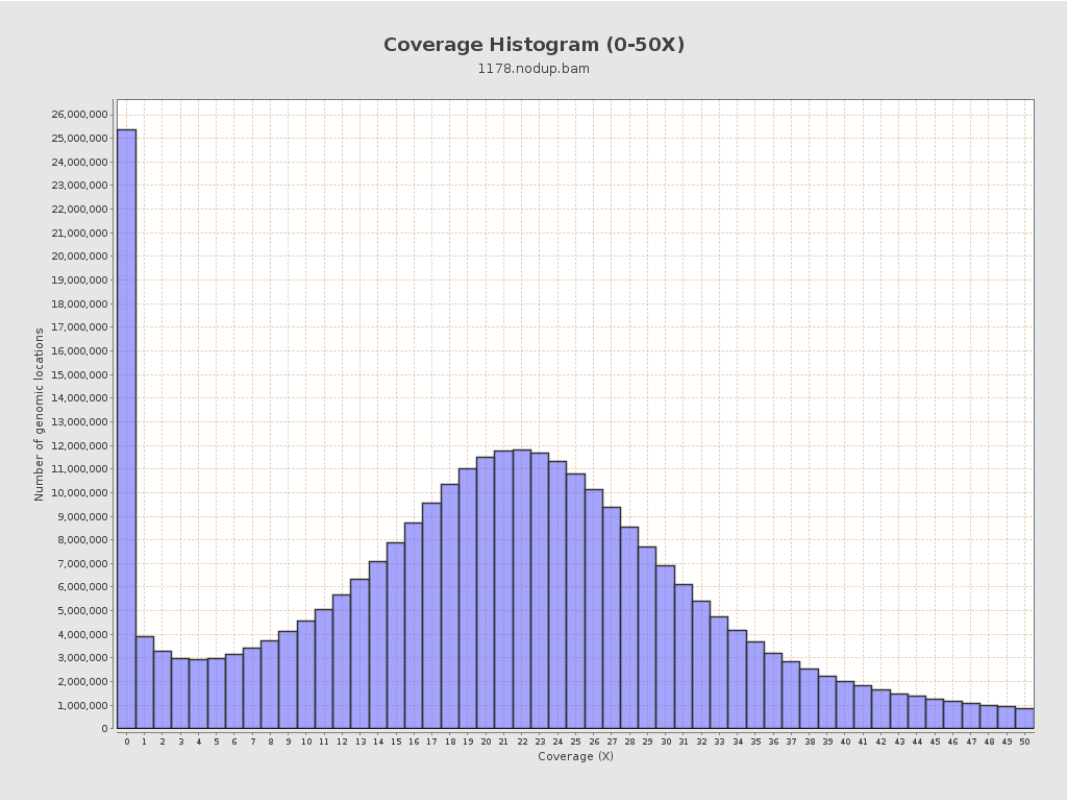
3. Results : Coverage across reference



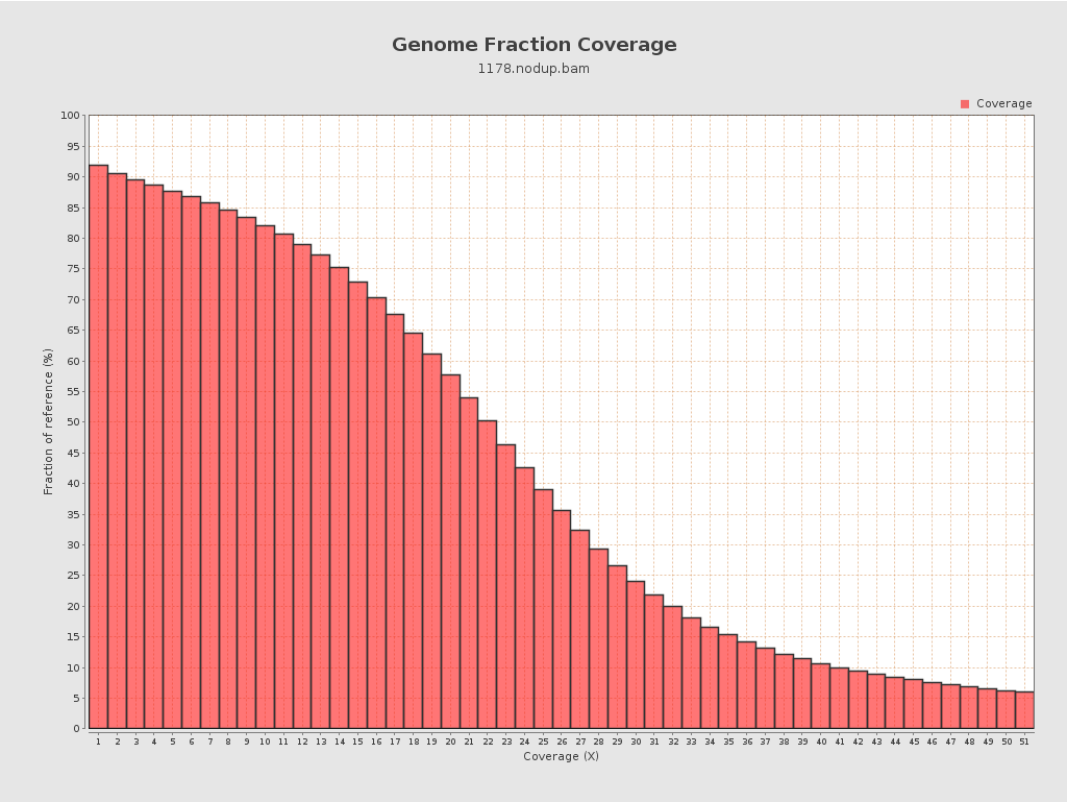
4. Results : Coverage Histogram



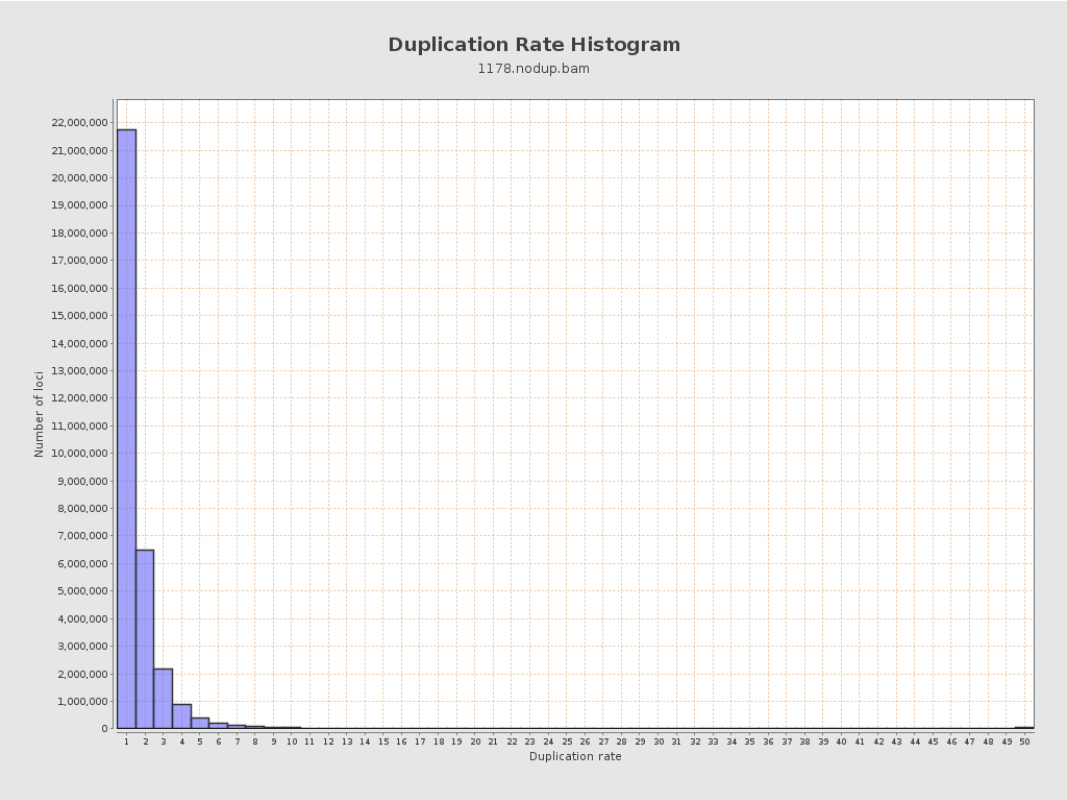
5. Results : Coverage Histogram (0-50X)



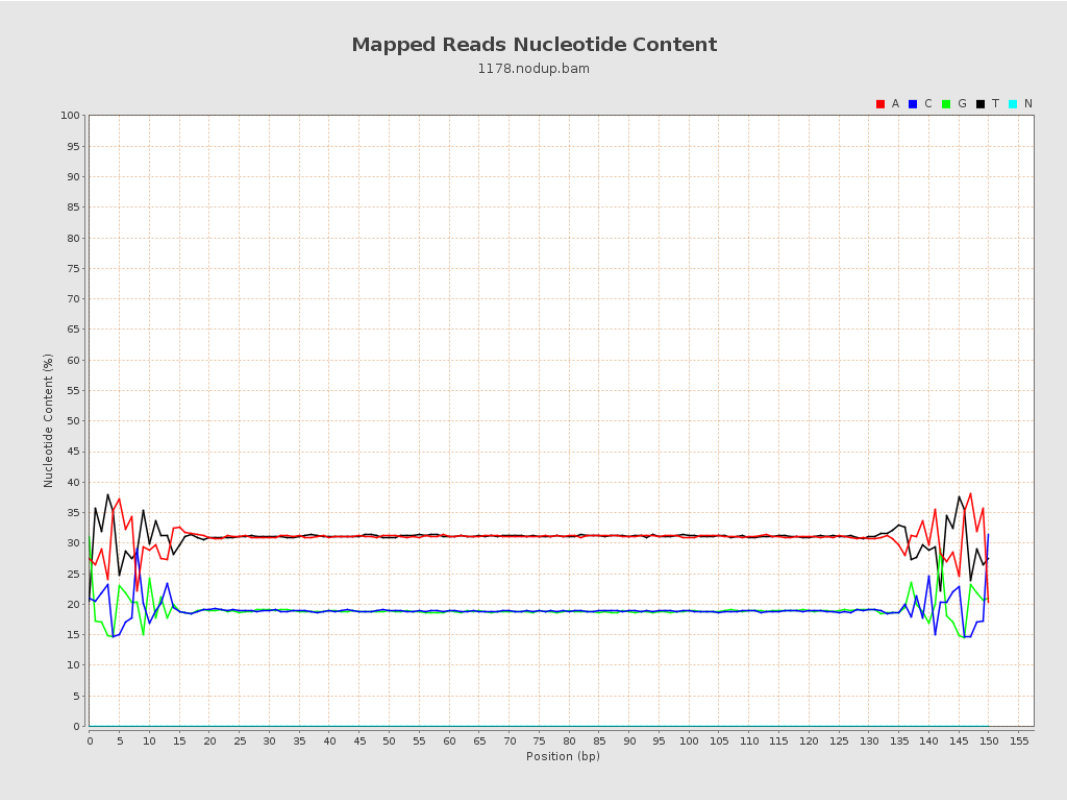
6. Results : Genome Fraction Coverage



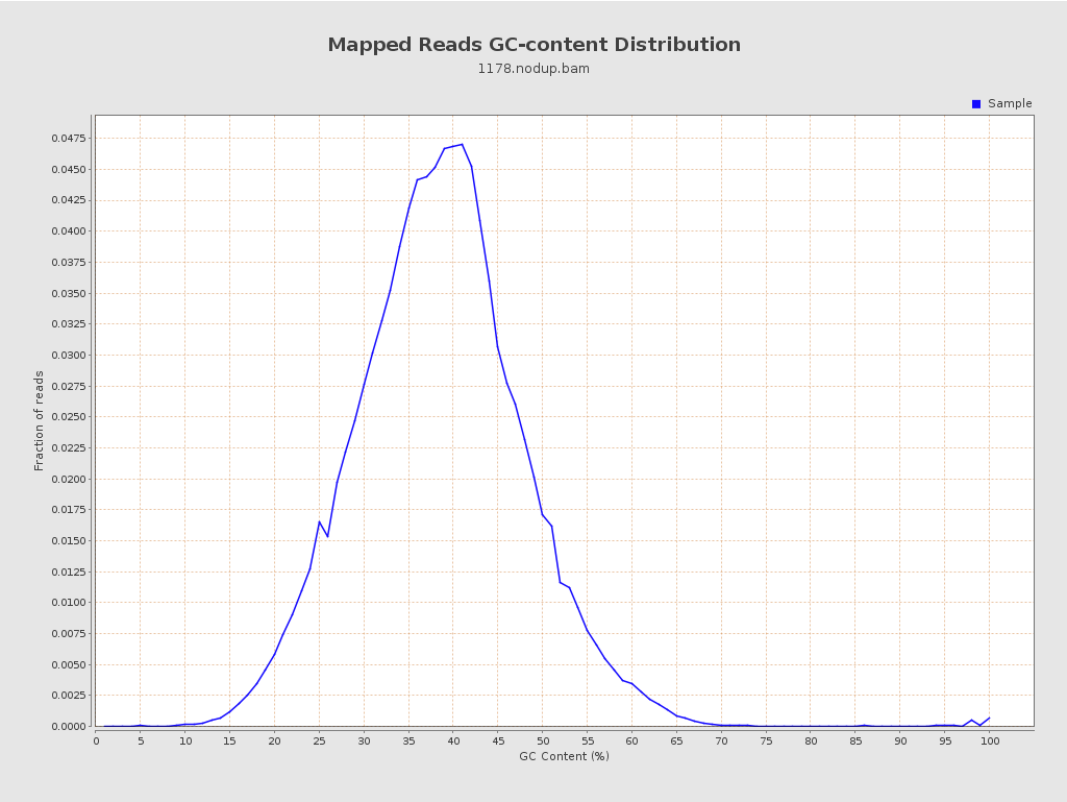
7. Results : Duplication Rate Histogram



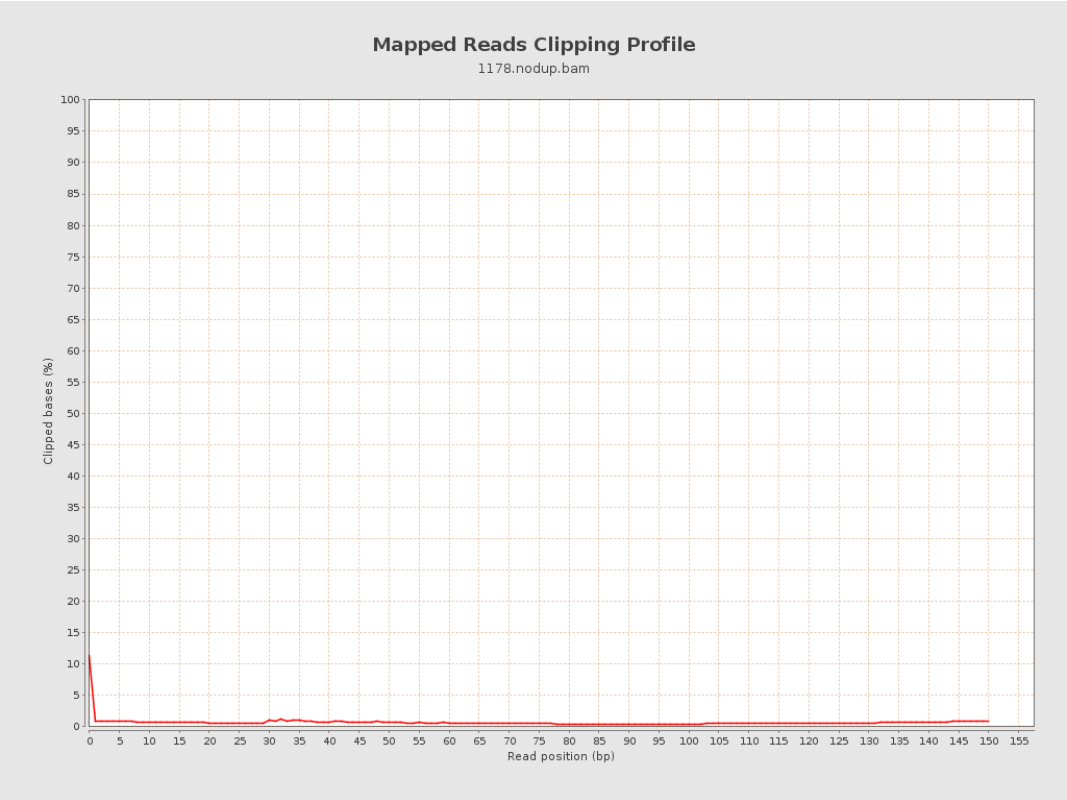
8. Results : Mapped Reads Nucleotide Content



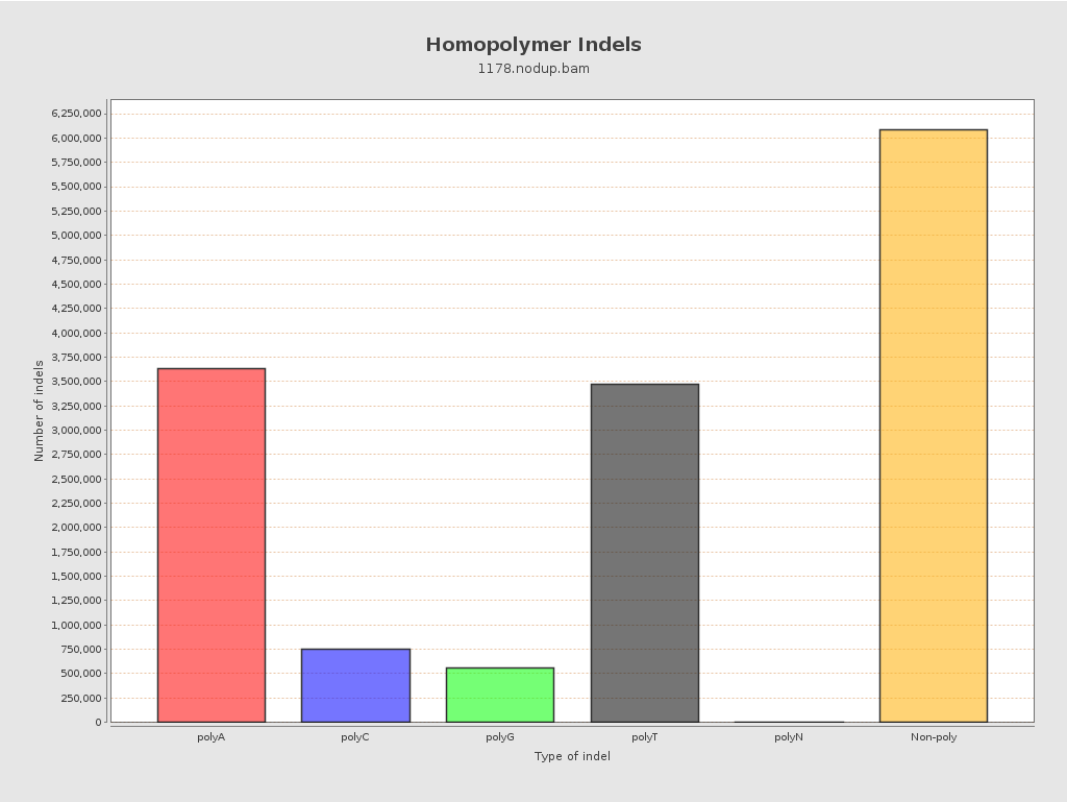
9. Results : Mapped Reads GC-content Distribution



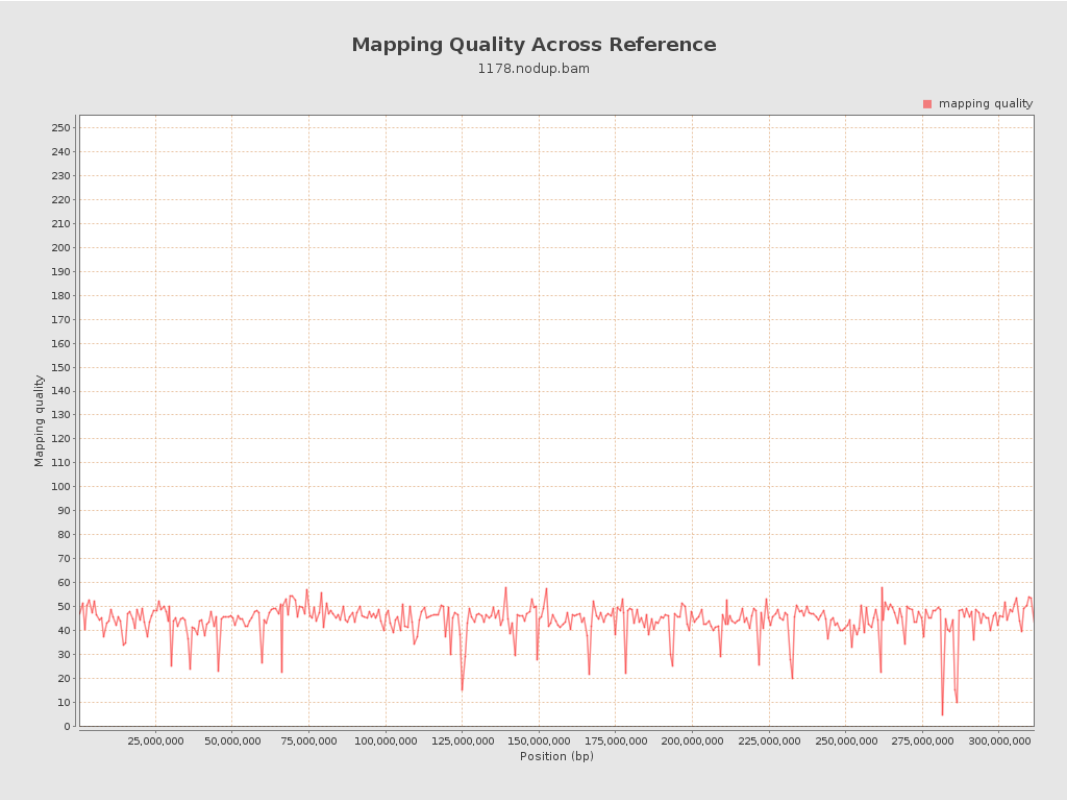
10. Results : Mapped Reads Clipping Profile



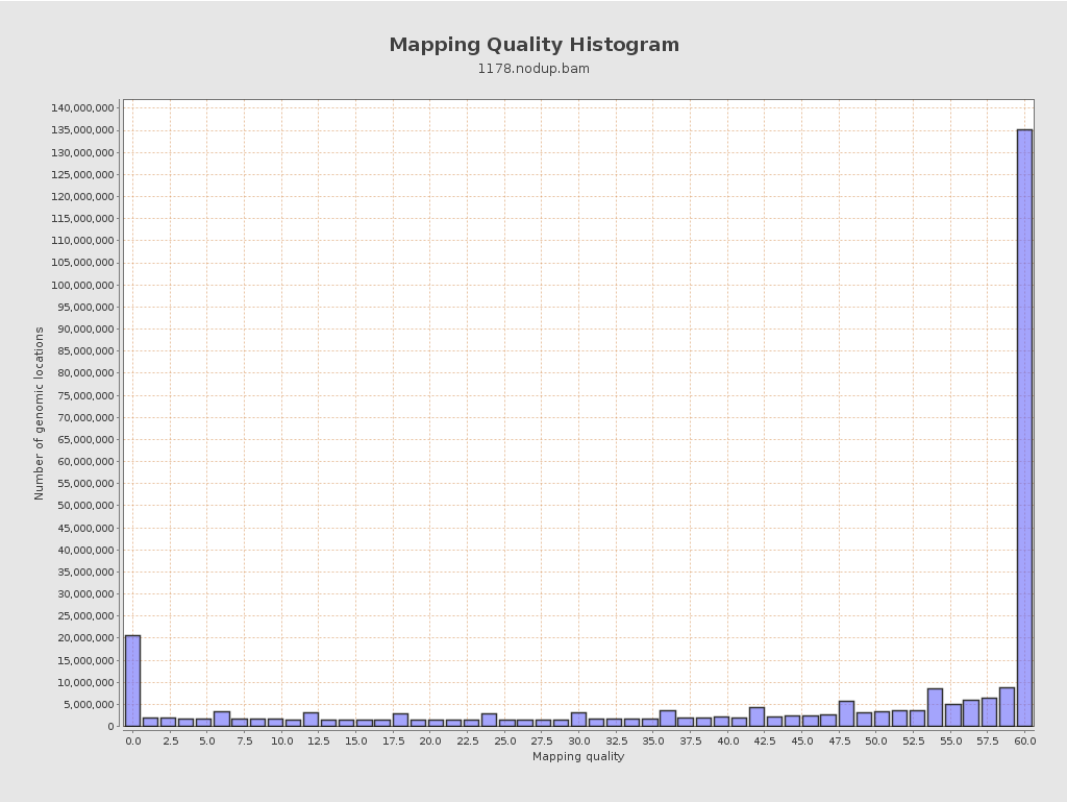
11. Results : Homopolymer Indels



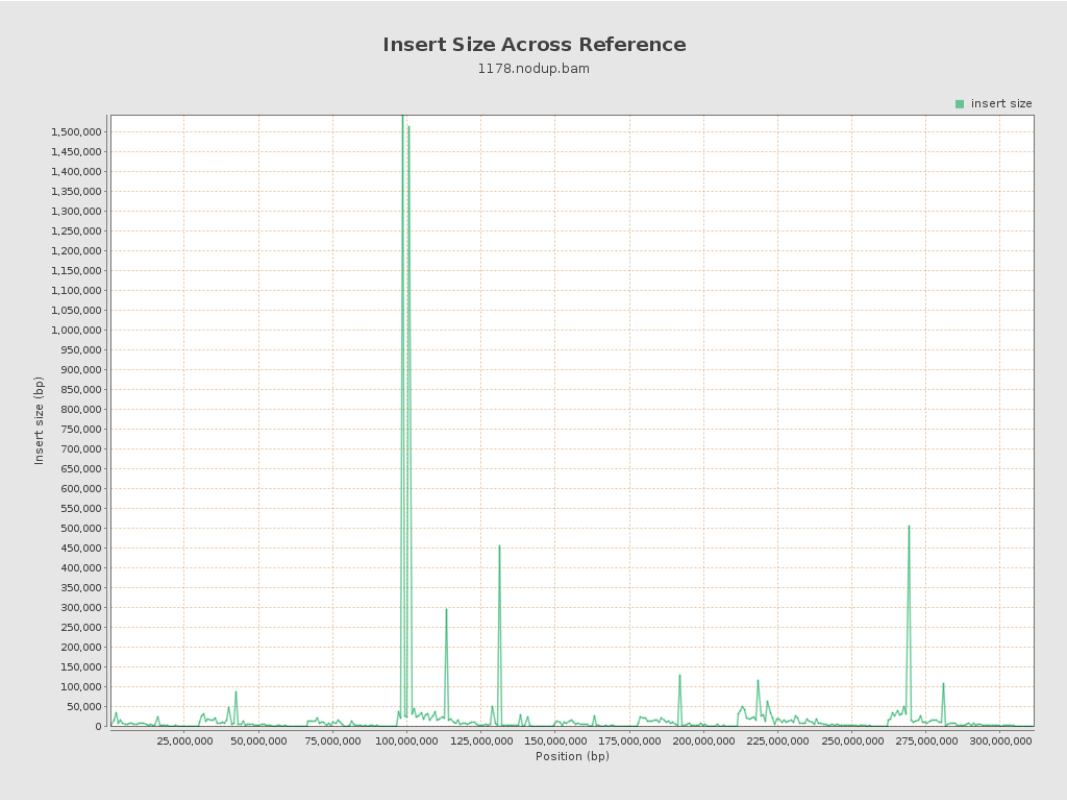
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram