Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:31:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1123
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1123 .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_561/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_561_S128_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_561/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_561_S128_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:31:42 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	68,703,290
Mapped reads	60,842,192 / 88.56%
Unmapped reads	7,861,098 / 11.44%
Mapped paired reads	60,842,192 / 88.56%
Mapped reads, first in pair	30,491,355 / 44.38%
Mapped reads, second in pair	30,350,837 / 44.18%
Mapped reads, both in pair	58,299,987 / 84.86%
Mapped reads, singletons	2,542,205 / 3.7%
Read min/max/mean length	30 / 151 / 148.08
Duplicated reads (flagged)	13,146,815 / 19.14%
Clipped reads	16,625,977 / 24.2%

2.2. ACGT Content

Number/percentage of A's	2,538,296,457 / 31%
Number/percentage of C's	1,552,773,157 / 18.96%
Number/percentage of T's	2,543,760,032 / 31.06%
Number/percentage of G's	1,554,503,612 / 18.98%
Number/percentage of N's	56,518 / 0%
GC Percentage	37.94%

2.3. Coverage

Mean	26.3476
Standard Deviation	344.3598

2.4. Mapping Quality

Mean Mapping Quality	43.96

2.5. Insert size

Mean	277,722.28
Standard Deviation	2,565,215.89
P25/Median/P75	302 / 400 / 520

2.6. Mismatches and indels

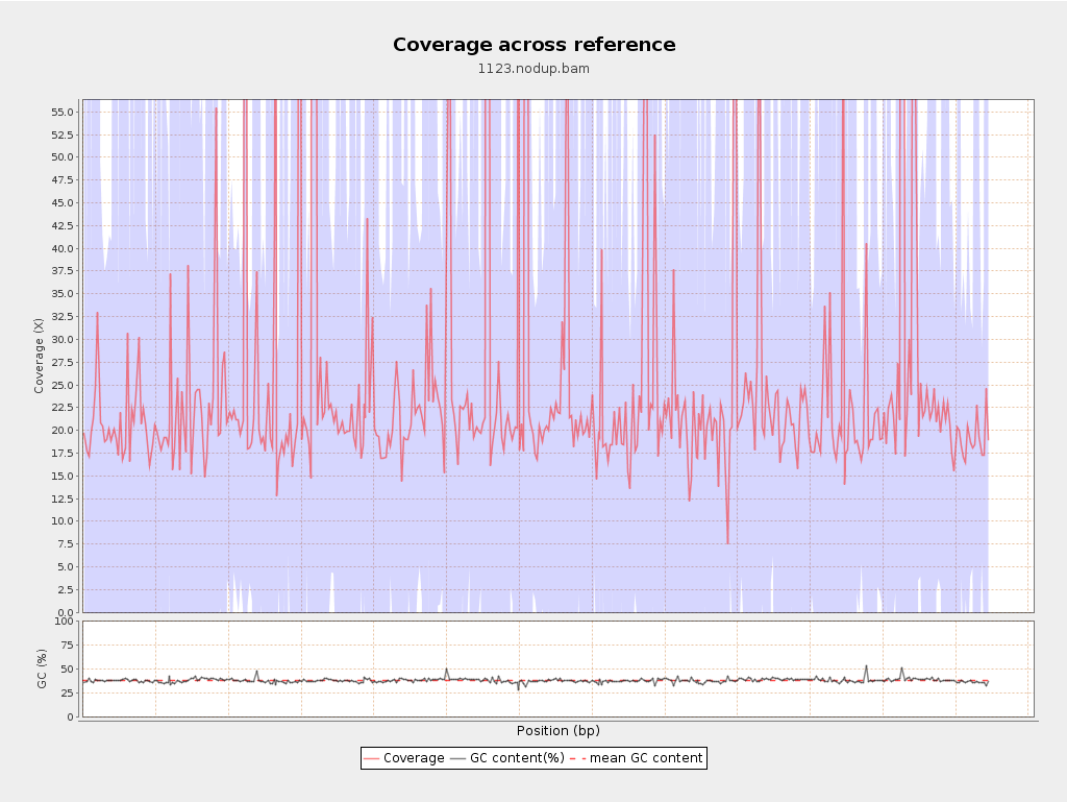
General error rate	2.75%
Mismatches	206,853,345
Insertions	6,709,911
Mapped reads with at least one insertion	9.74%
Deletions	5,930,173
Mapped reads with at least one deletion	8.63%
Homopolymer indels	57.39%

2.7. Chromosome stats

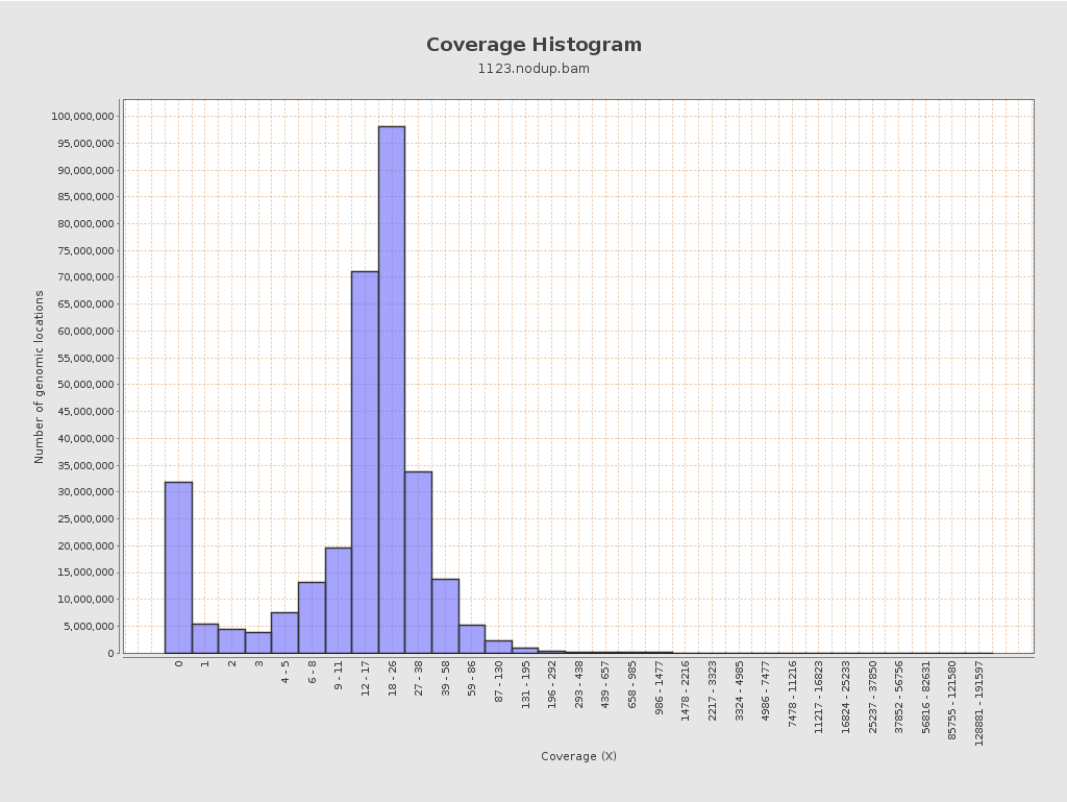
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	610435668	20.5366	151.4976

LT669789.1	36598175	936346063	25.5845	349.5789
LT669790.1	30422129	1132493874	37.226	571.4194
LT669791.1	52758100	1382234277	26.1995	404.4433
LT669792.1	28376109	772855070	27.2361	348.0716
LT669793.1	33388210	788691120	23.6218	237.9102
LT669794.1	50579949	1215345221	24.0282	265.2313
LT669795.1	49795044	1372626863	27.5655	295.4465

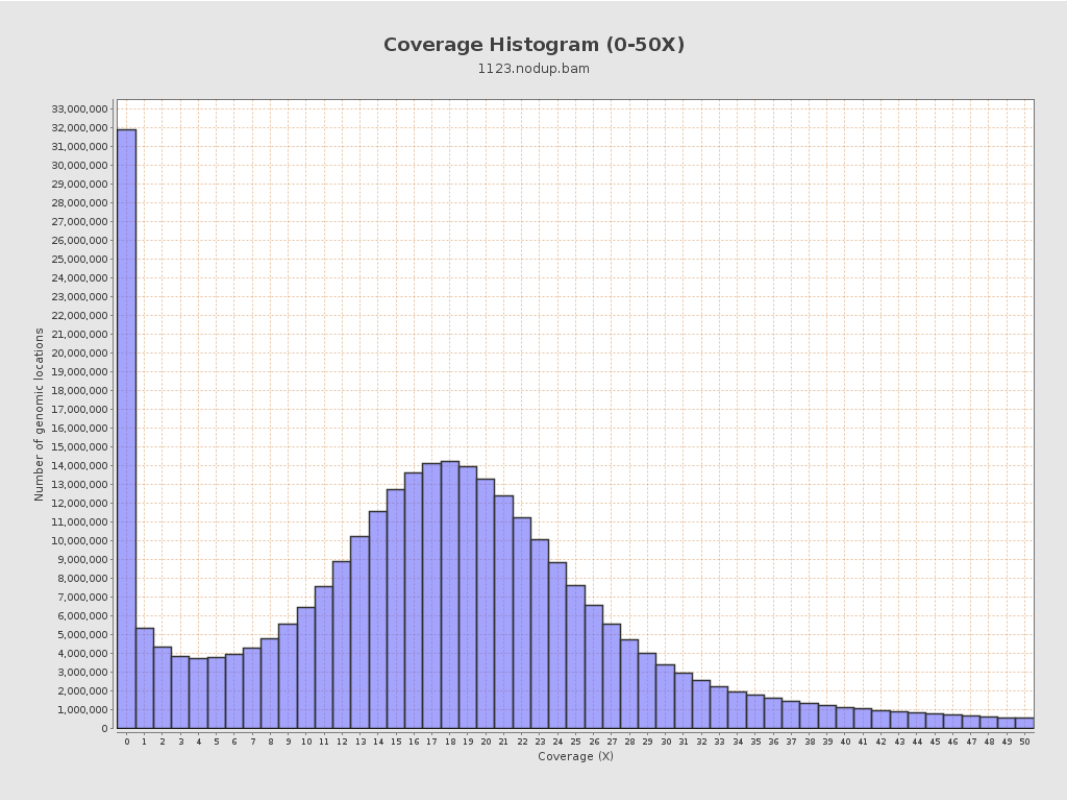
3. Results : Coverage across reference



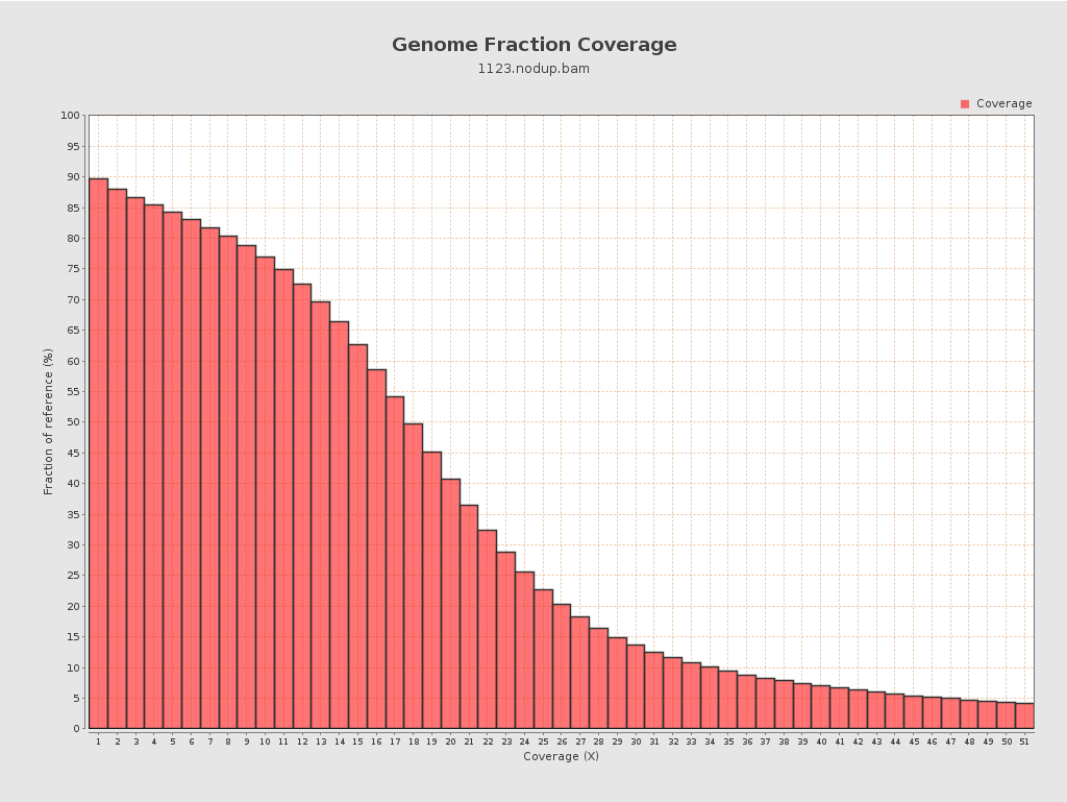
4. Results : Coverage Histogram



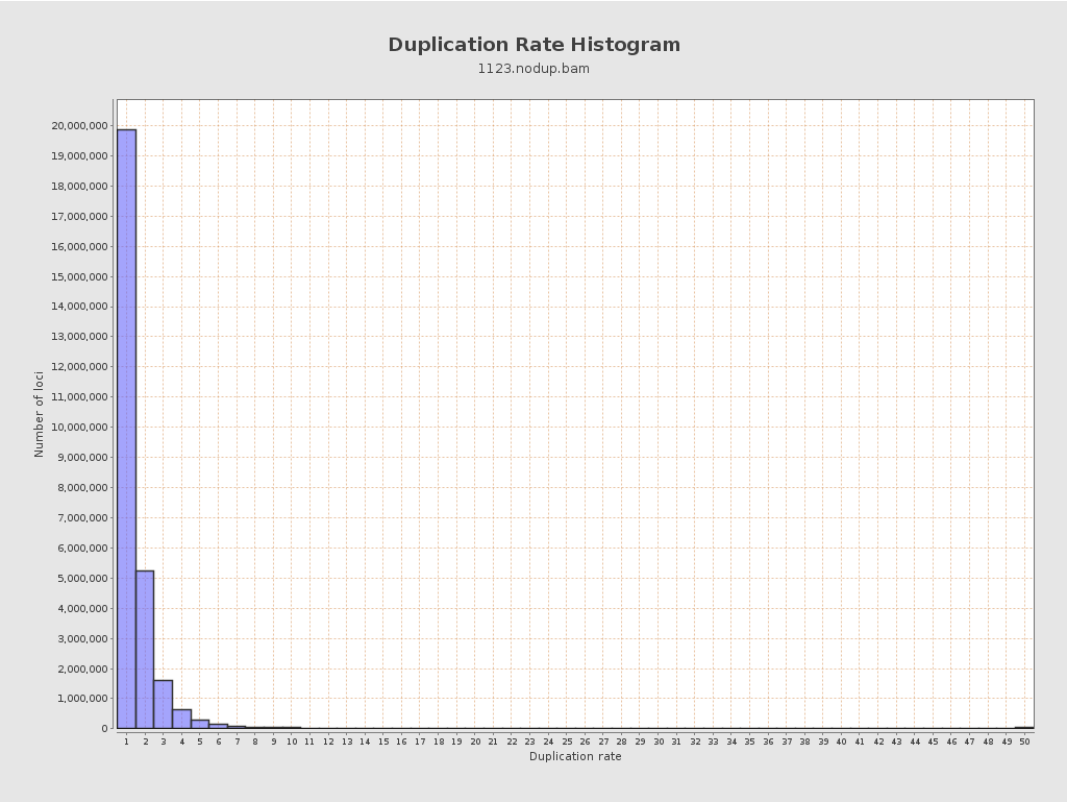
5. Results : Coverage Histogram (0-50X)



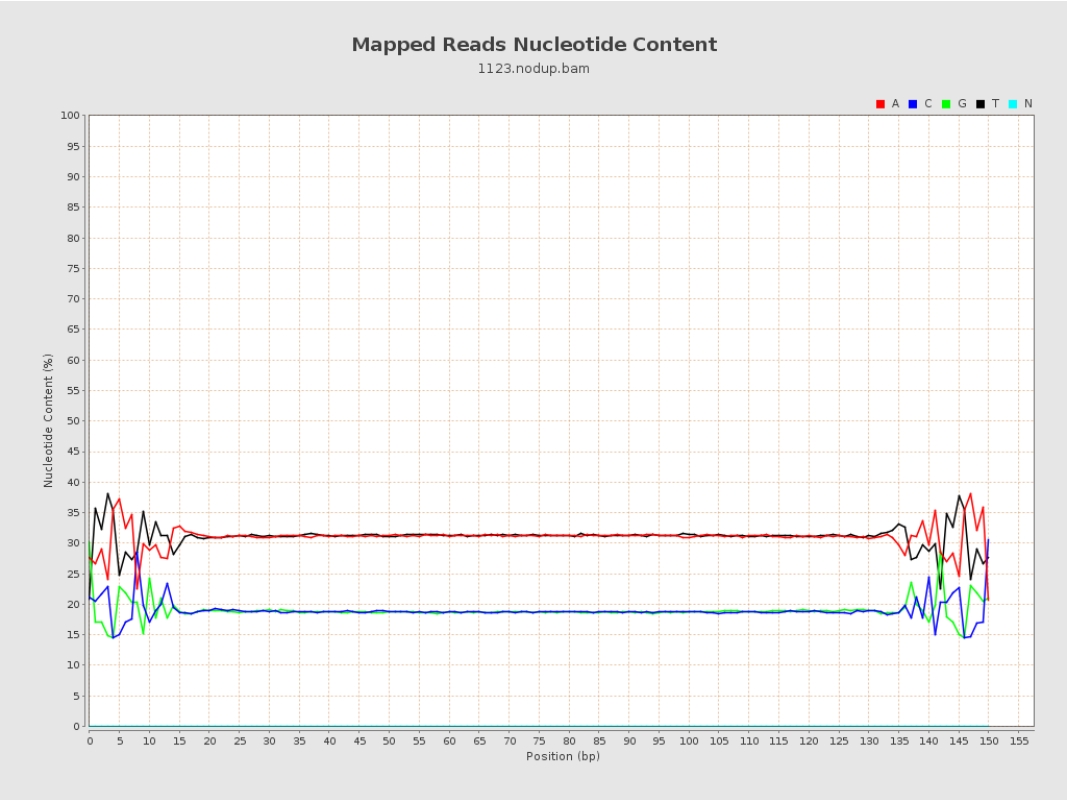
6. Results : Genome Fraction Coverage



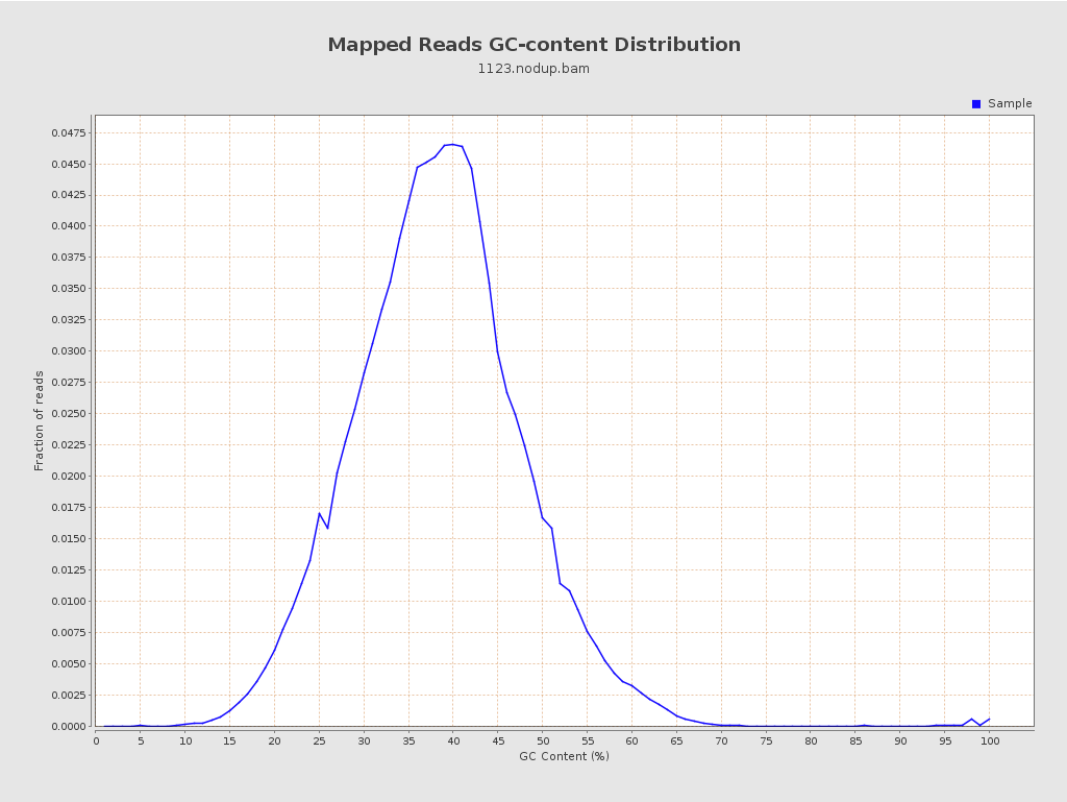
7. Results : Duplication Rate Histogram



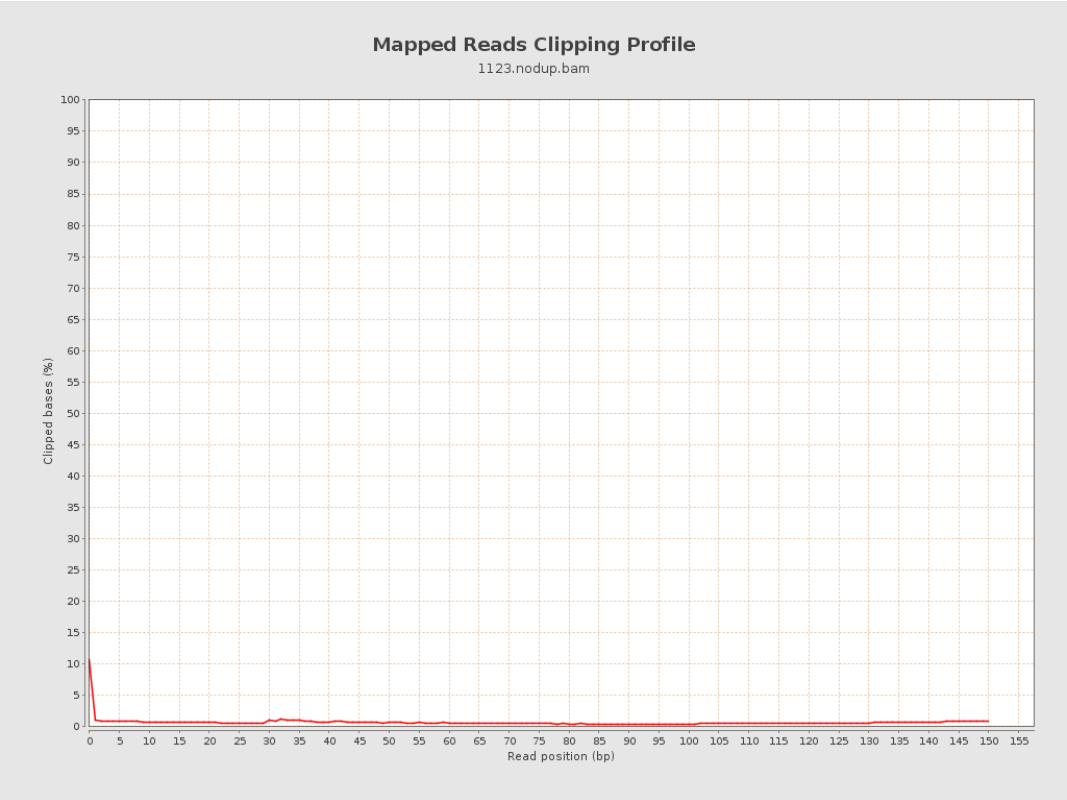
8. Results : Mapped Reads Nucleotide Content



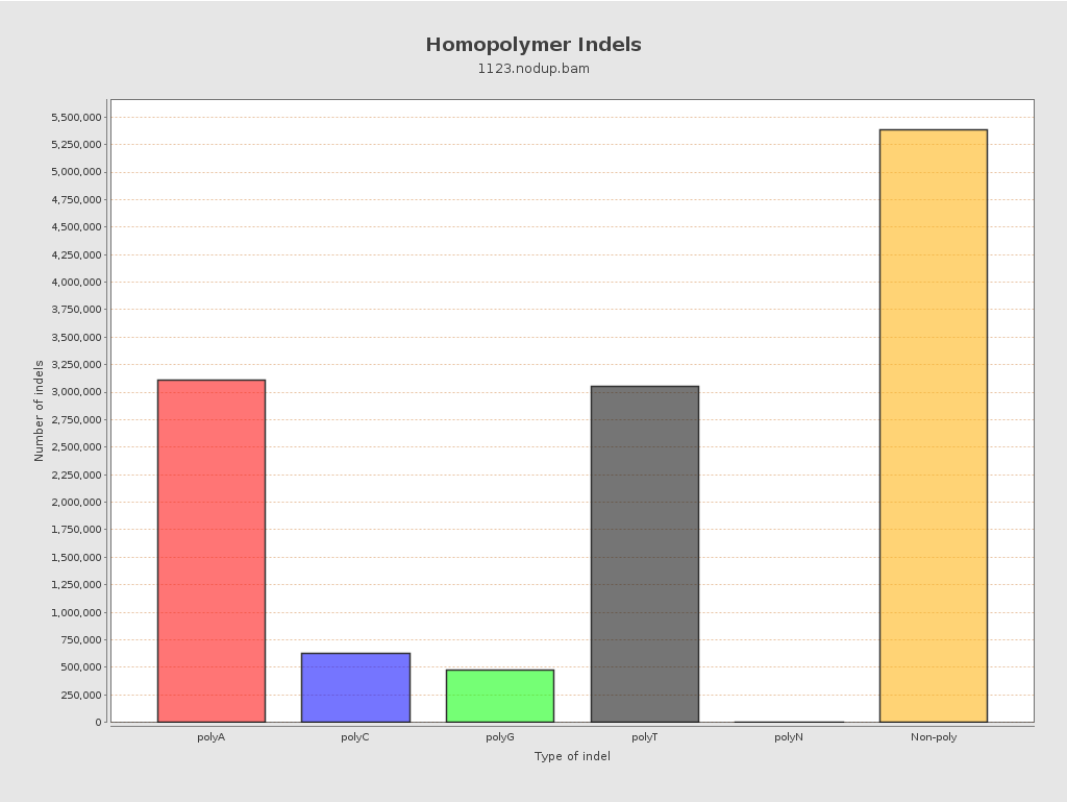
9. Results : Mapped Reads GC-content Distribution



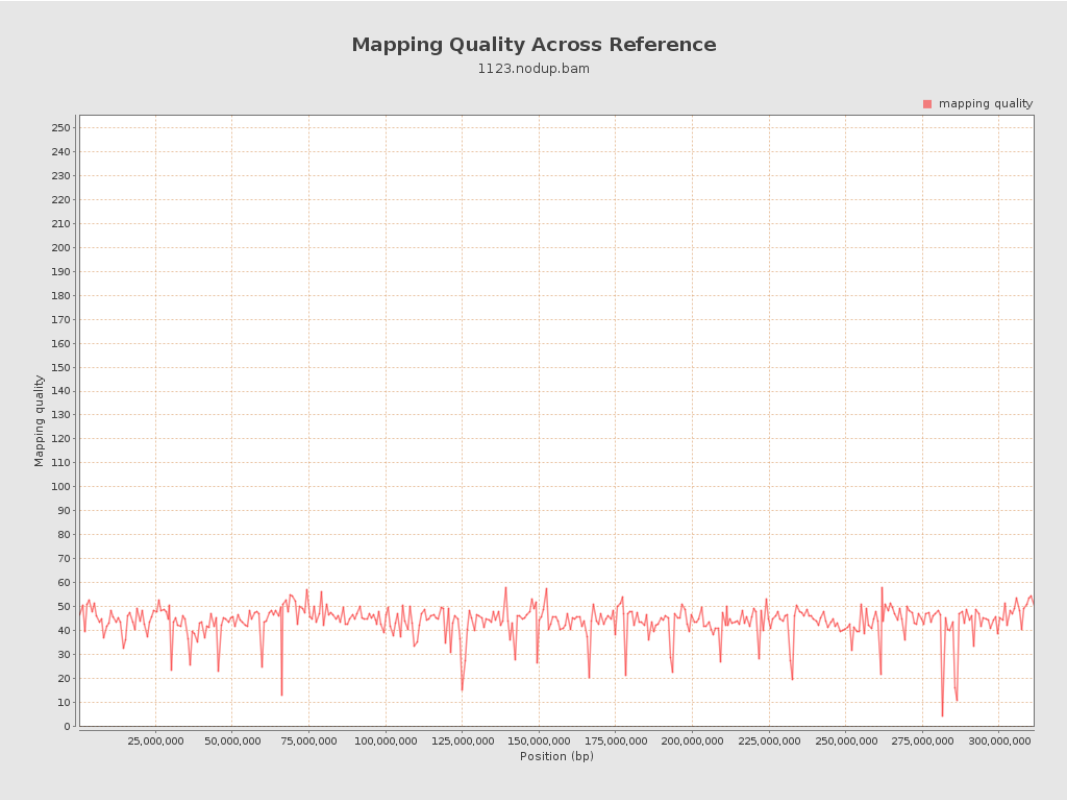
10. Results : Mapped Reads Clipping Profile



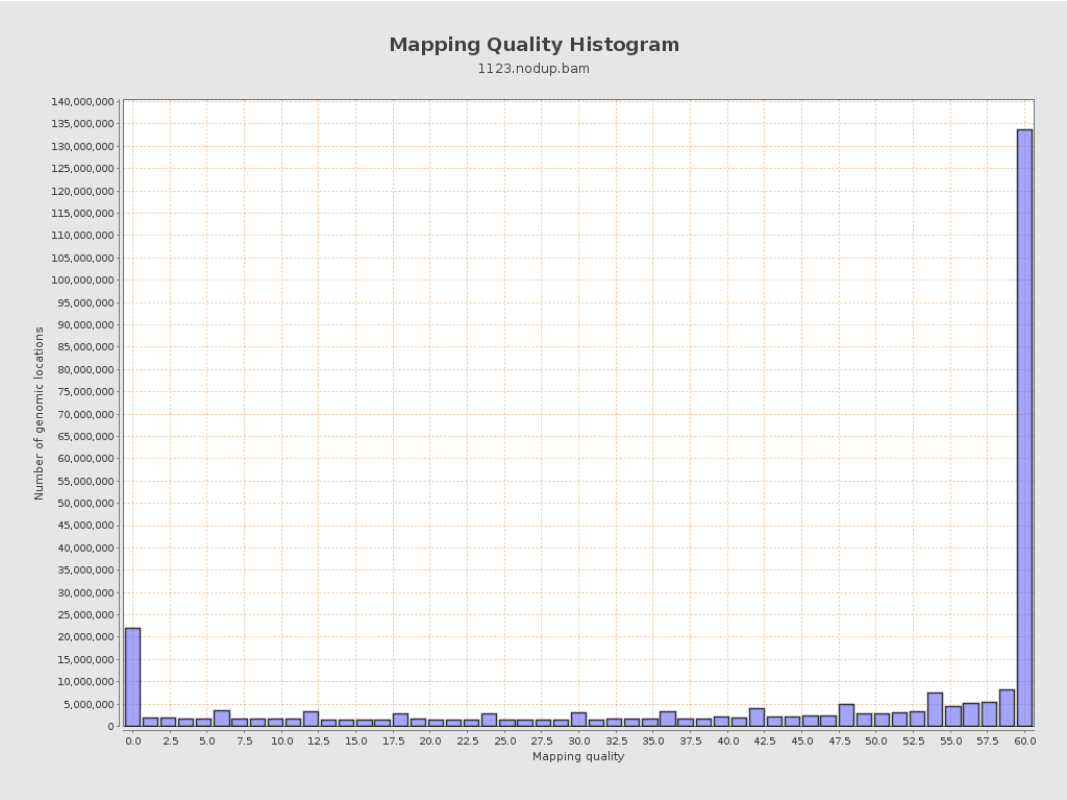
11. Results : Homopolymer Indels



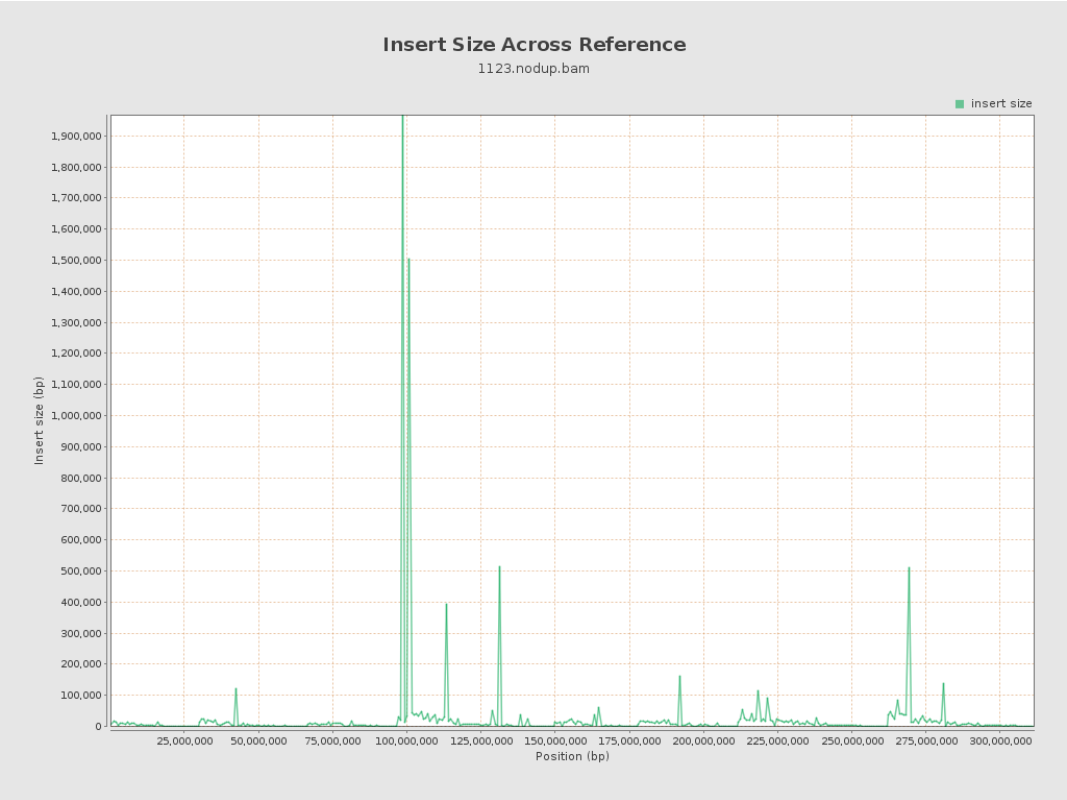
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram