

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/117
3
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1173 .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_536/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_536_S103_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_536/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_536_S103_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:35:27 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	74,881,448
Mapped reads	71,003,468 / 94.82%
Unmapped reads	3,877,980 / 5.18%
Mapped paired reads	71,003,468 / 94.82%
Mapped reads, first in pair	35,620,982 / 47.57%
Mapped reads, second in pair	35,382,486 / 47.25%
Mapped reads, both in pair	69,716,105 / 93.1%
Mapped reads, singletons	1,287,363 / 1.72%
Read min/max/mean length	30 / 151 / 148.17
Duplicated reads (flagged)	11,006,849 / 14.7%
Clipped reads	16,248,838 / 21.7%

2.2. ACGT Content

Number/percentage of A's	3,044,830,333 / 30.92%
Number/percentage of C's	1,880,735,481 / 19.1%
Number/percentage of T's	3,046,161,680 / 30.94%
Number/percentage of G's	1,874,388,684 / 19.04%
Number/percentage of N's	67,037 / 0%
GC Percentage	38.14%

2.3. Coverage

Mean	31.6741
Standard Deviation	232.4884

2.4. Mapping Quality

Mean Mapping Quality	44.58
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2.5. Insert size

Mean	208,161.54
Standard Deviation	2,160,600.66
P25/Median/P75	321 / 421 / 545

2.6. Mismatches and indels

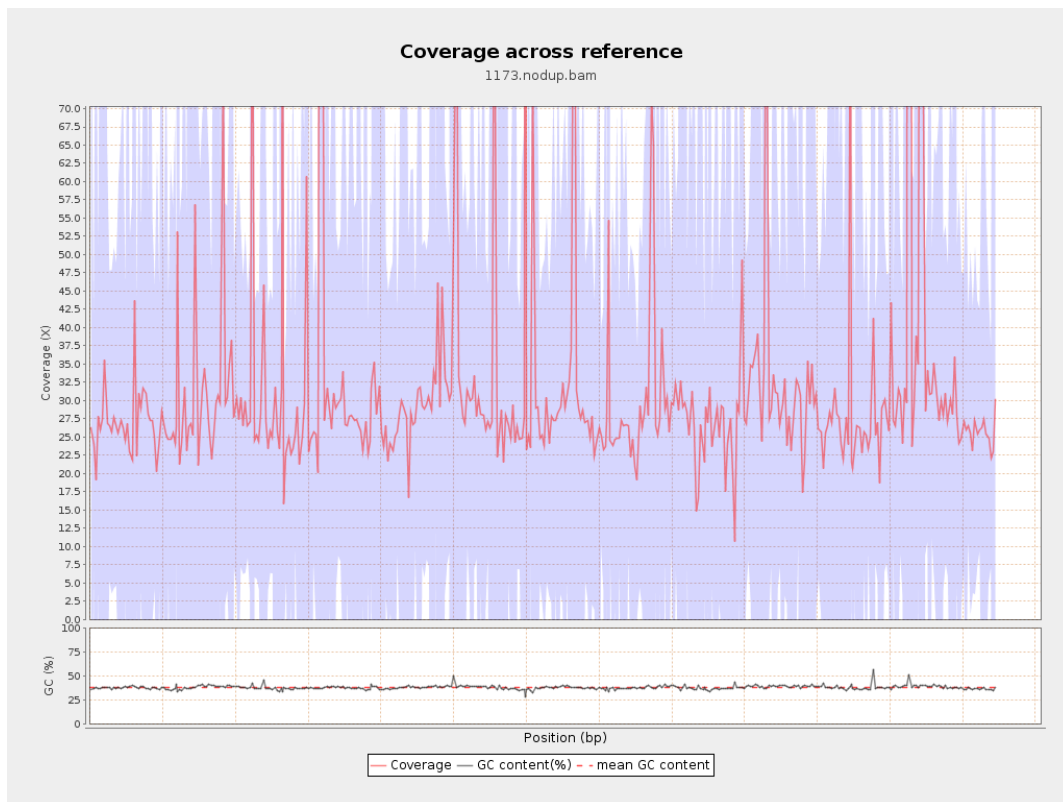
General error rate	2.44%
Mismatches	223,152,678
Insertions	6,387,307
Mapped reads with at least one insertion	8.11%
Deletions	6,598,700
Mapped reads with at least one deletion	8.27%
Homopolymer indels	56.31%

2.7. Chromosome stats

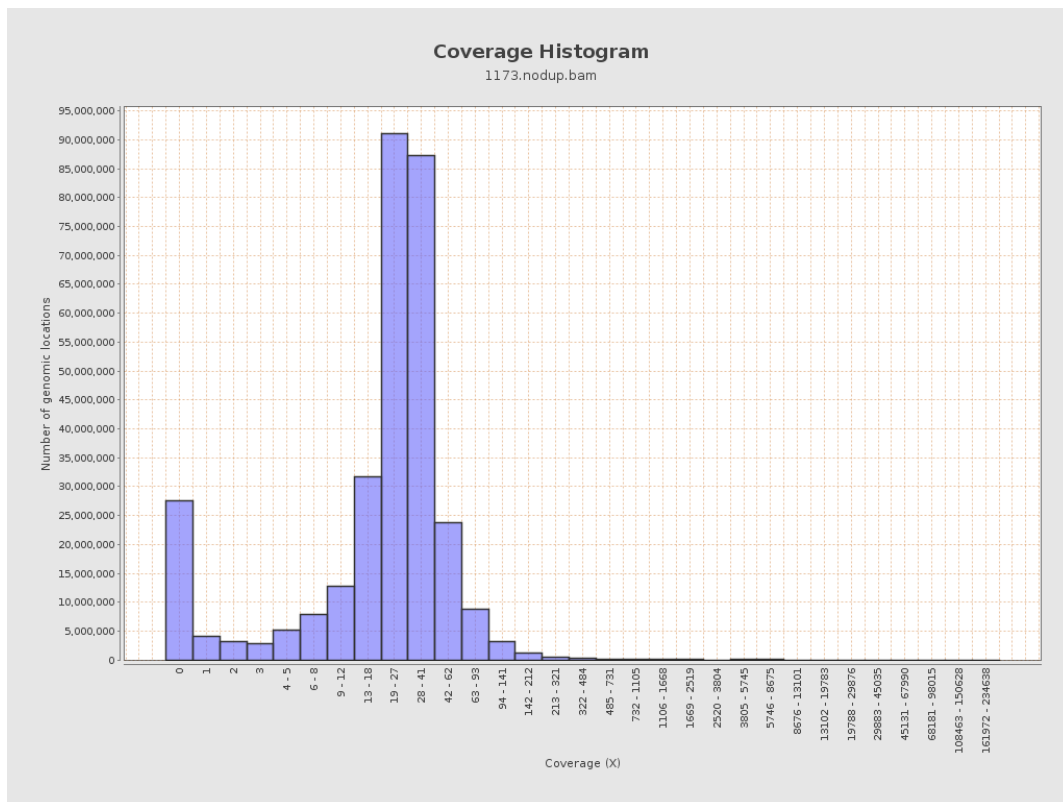
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	794955701	26.7443	65.7954

LT669789.1	36598175	1167728938	31.9068	237.5474
LT669790.1	30422129	1002141352	32.9412	221.6575
LT669791.1	52758100	1630516214	30.9055	187.8297
LT669792.1	28376109	894504336	31.5231	249.6921
LT669793.1	33388210	970397482	29.0641	125.8492
LT669794.1	50579949	1539356733	30.4341	217.0039
LT669795.1	49795044	1871370640	37.5815	364.3962

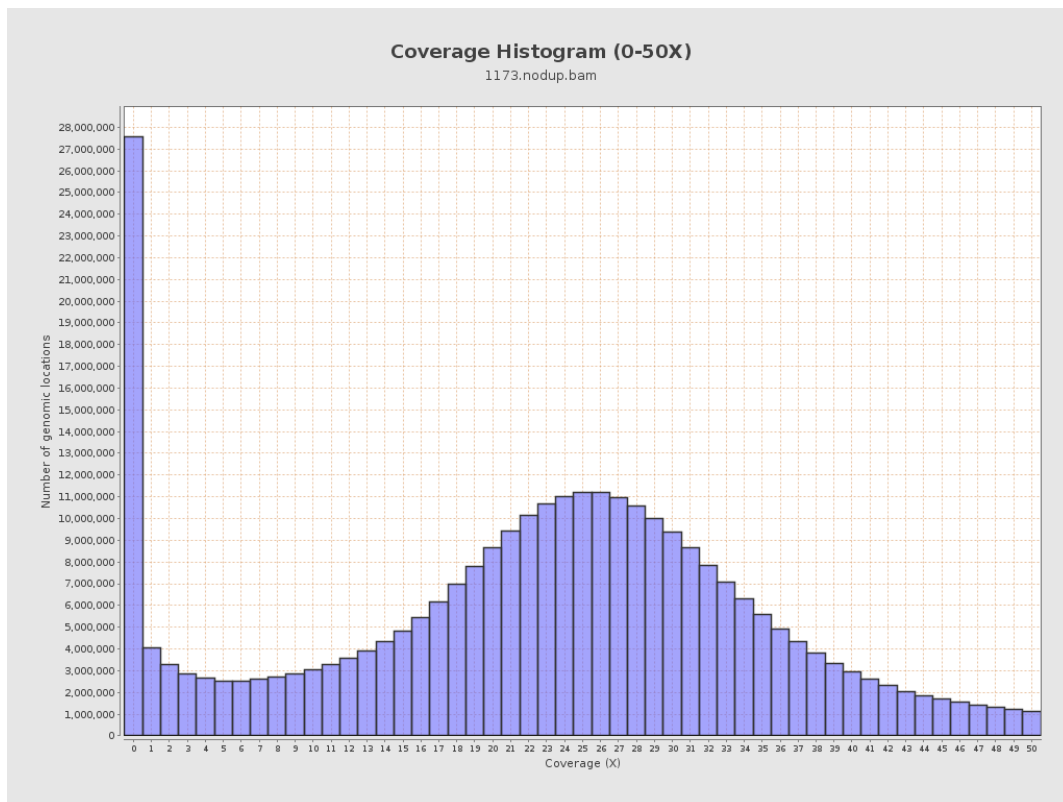
3. Results : Coverage across reference



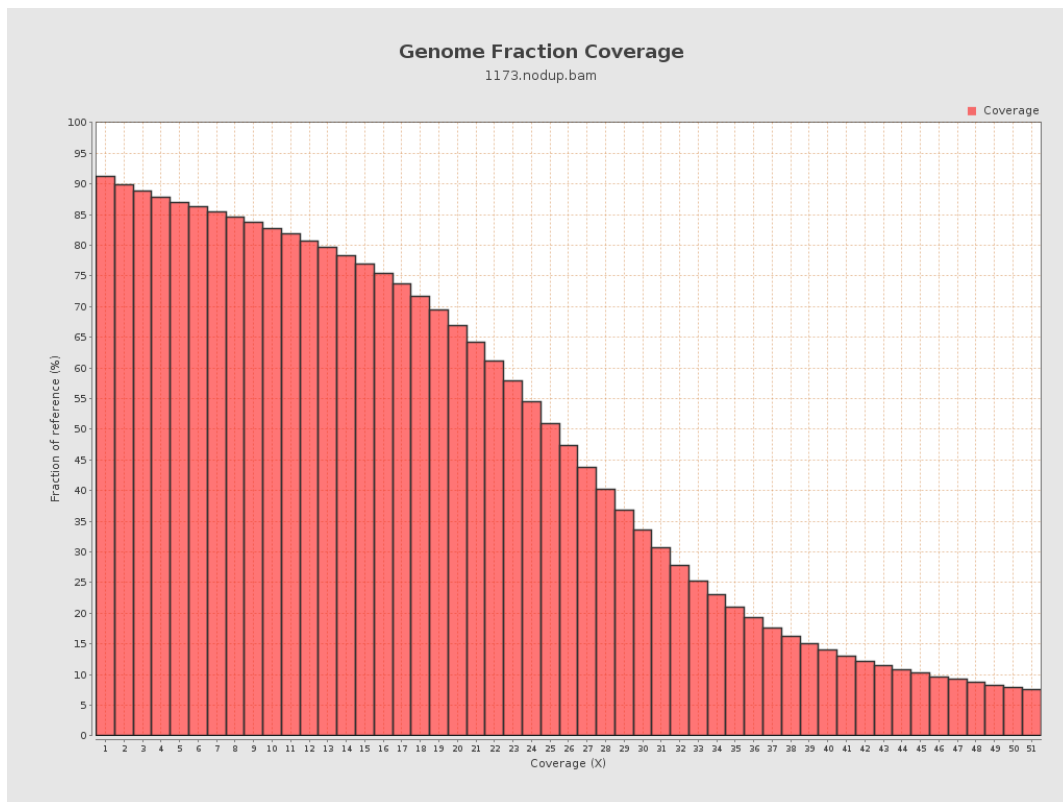
4. Results : Coverage Histogram



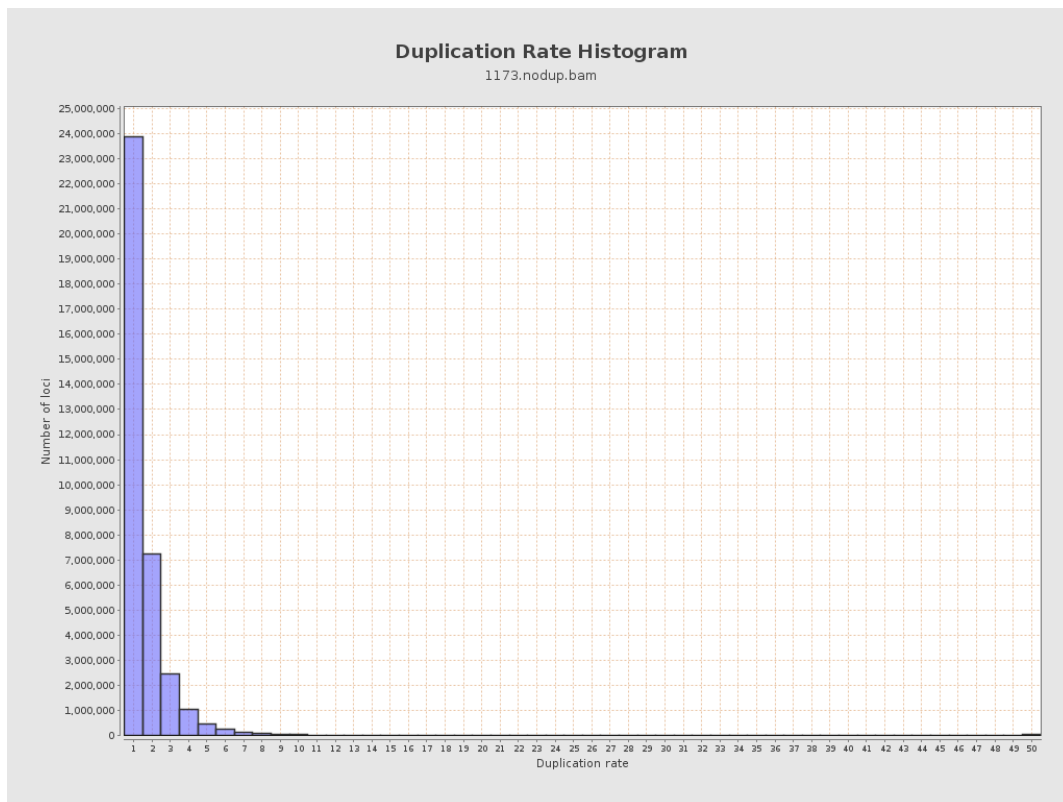
5. Results : Coverage Histogram (0-50X)



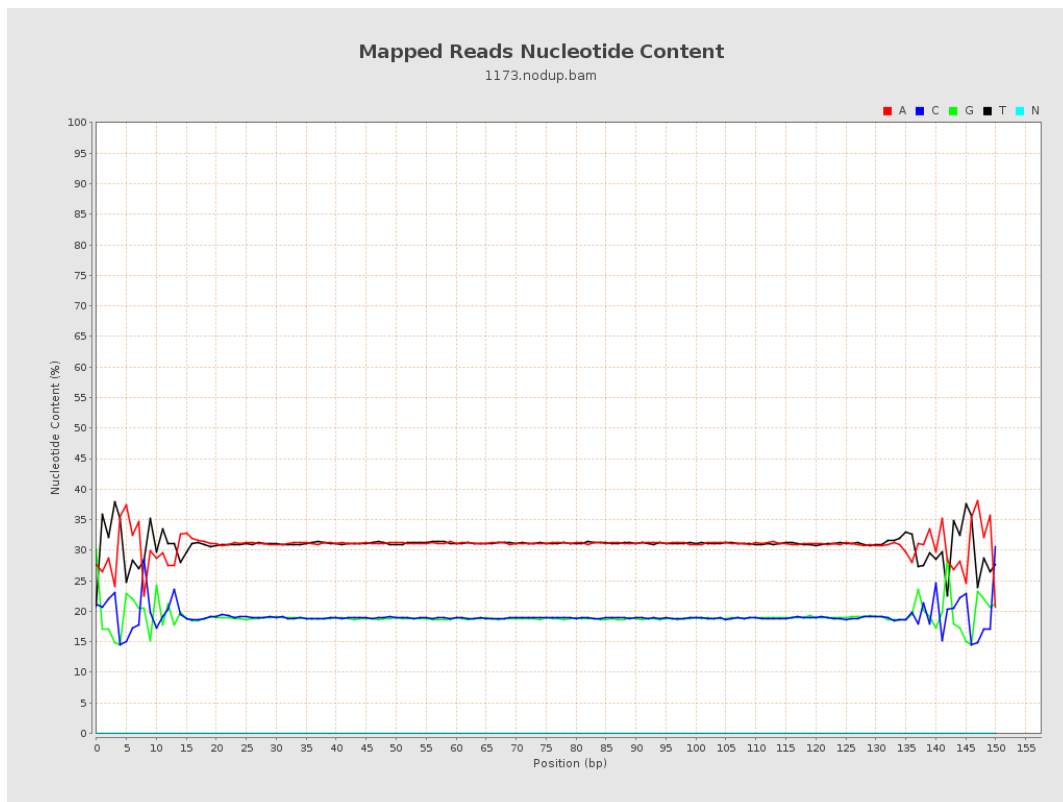
6. Results : Genome Fraction Coverage



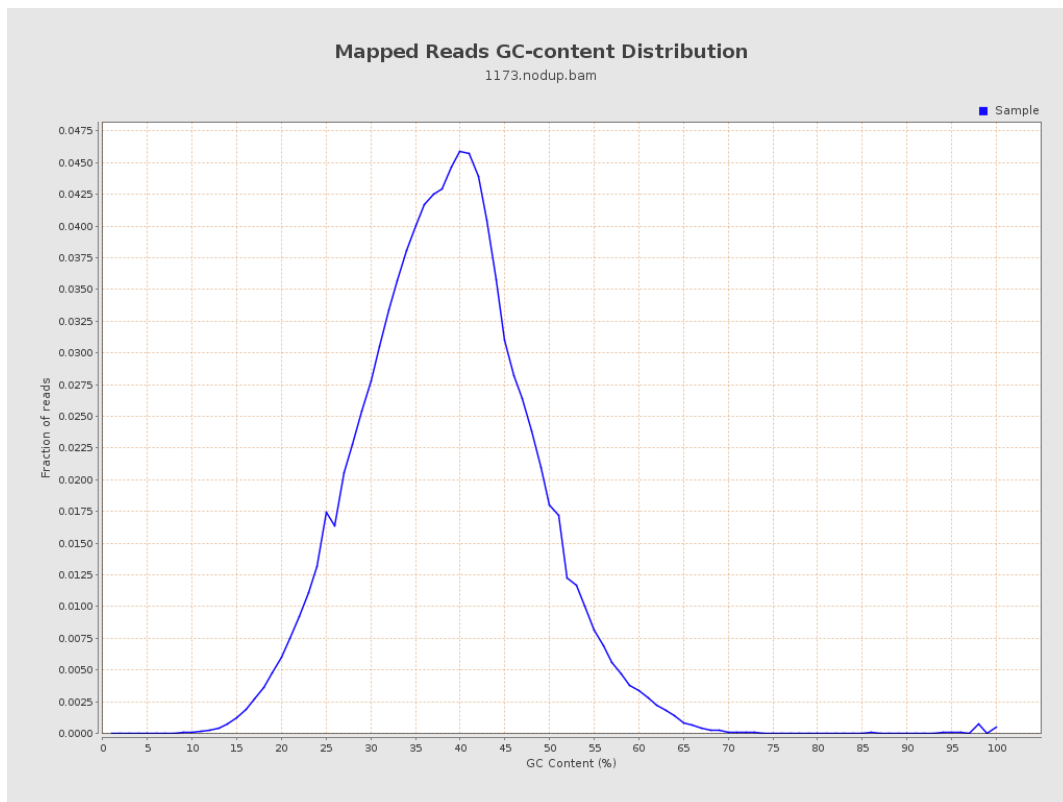
7. Results : Duplication Rate Histogram



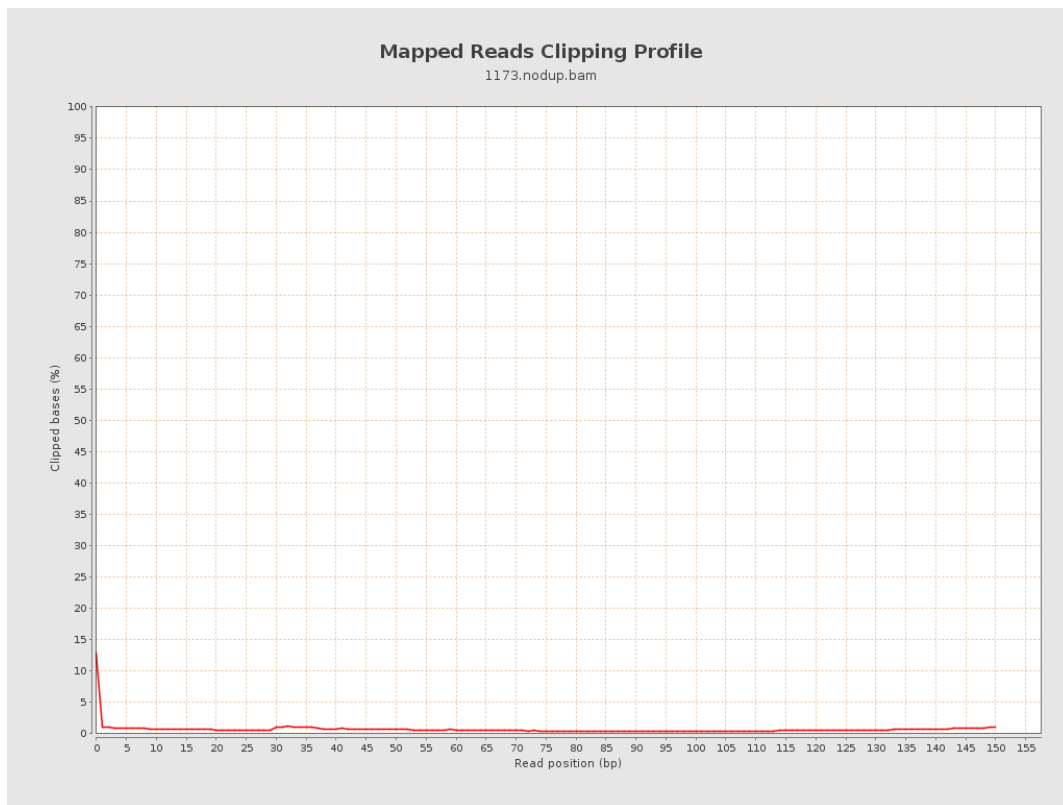
8. Results : Mapped Reads Nucleotide Content



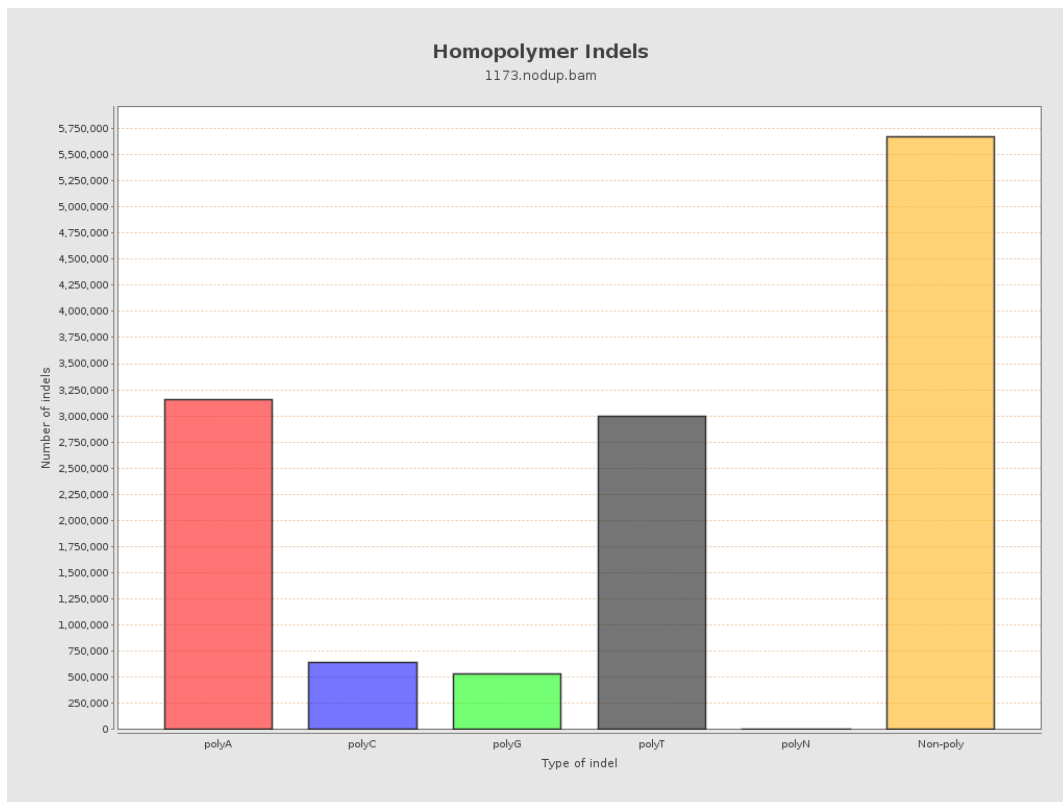
9. Results : Mapped Reads GC-content Distribution



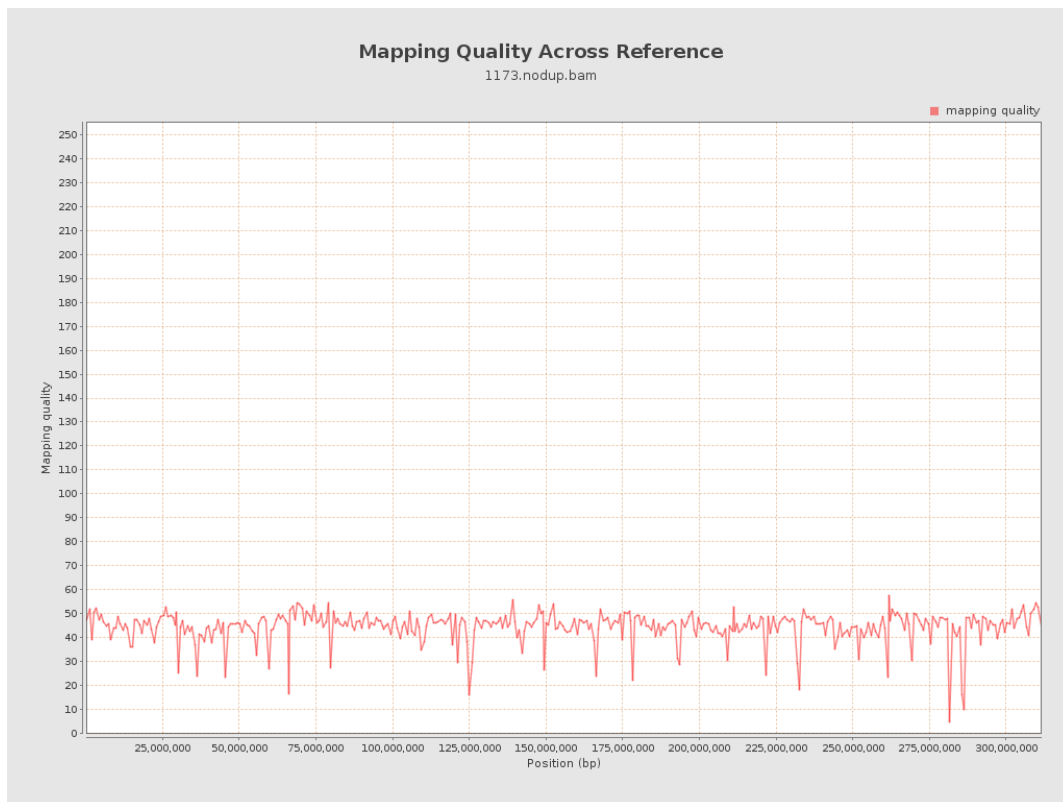
10. Results : Mapped Reads Clipping Profile



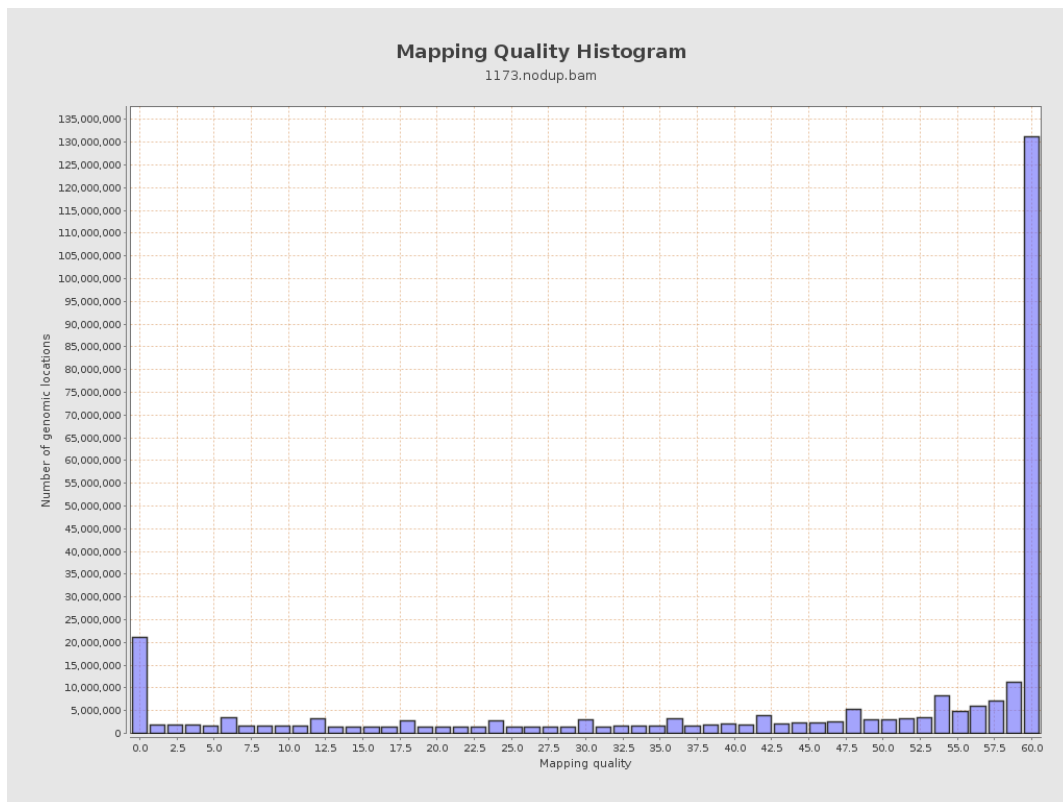
11. Results : Homopolymer Indels



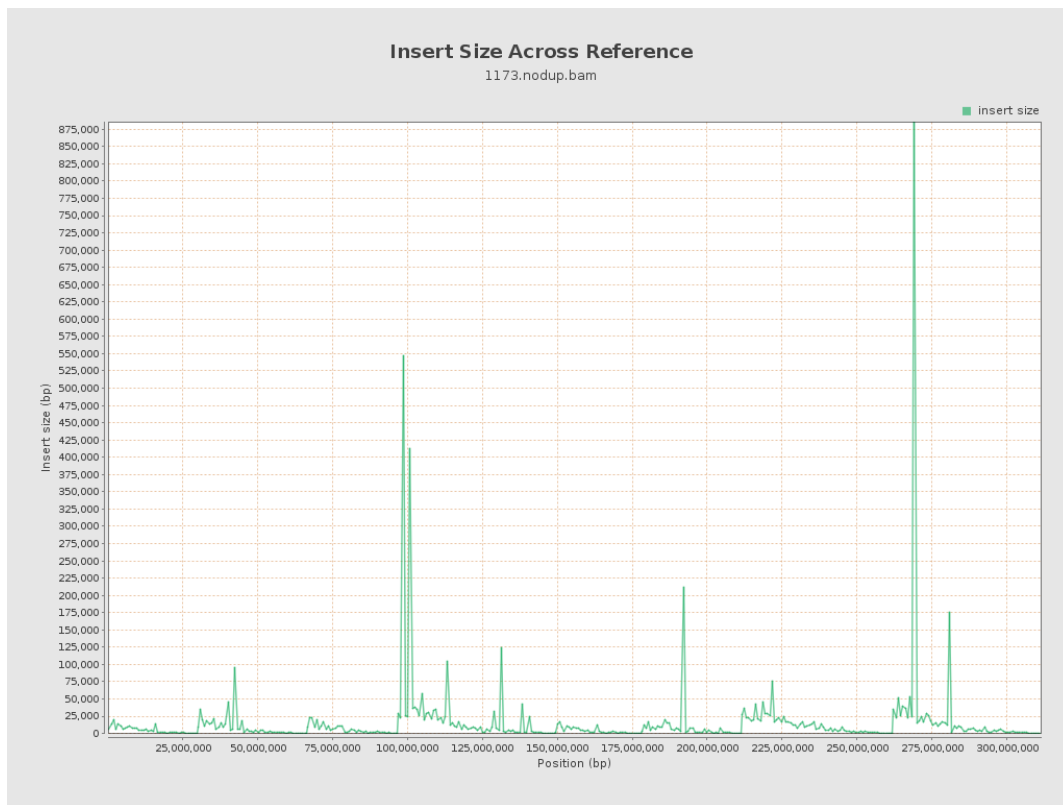
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

