

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:21:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/140
3
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1403 .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\t SM:\$sample /proj/uppstore2018210/Aalpina/data/r eference/GCA_900128785.1_MPIPZ. v5_genomic.fa /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_577/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_577_S144_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_577/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_577_S144_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:21:47 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	47,488,883
Mapped reads	35,004,317 / 73.71%
Unmapped reads	12,484,566 / 26.29%
Mapped paired reads	35,004,317 / 73.71%
Mapped reads, first in pair	17,565,952 / 36.99%
Mapped reads, second in pair	17,438,365 / 36.72%
Mapped reads, both in pair	34,260,117 / 72.14%
Mapped reads, singletons	744,200 / 1.57%
Read min/max/mean length	30 / 151 / 148.81
Duplicated reads (flagged)	4,388,289 / 9.24%
Clipped reads	9,169,603 / 19.31%

2.2. ACGT Content

Number/percentage of A's	1,457,643,719 / 30.89%
Number/percentage of C's	900,567,296 / 19.08%
Number/percentage of T's	1,460,534,053 / 30.95%
Number/percentage of G's	900,366,902 / 19.08%
Number/percentage of N's	31,322 / 0%
GC Percentage	38.16%

2.3. Coverage

Mean	15.1835
Standard Deviation	117.8005

2.4. Mapping Quality

Mean Mapping Quality	43.03
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2.5. Insert size

Mean	223,406.74
Standard Deviation	2,222,514.93
P25/Median/P75	312 / 416 / 540

2.6. Mismatches and indels

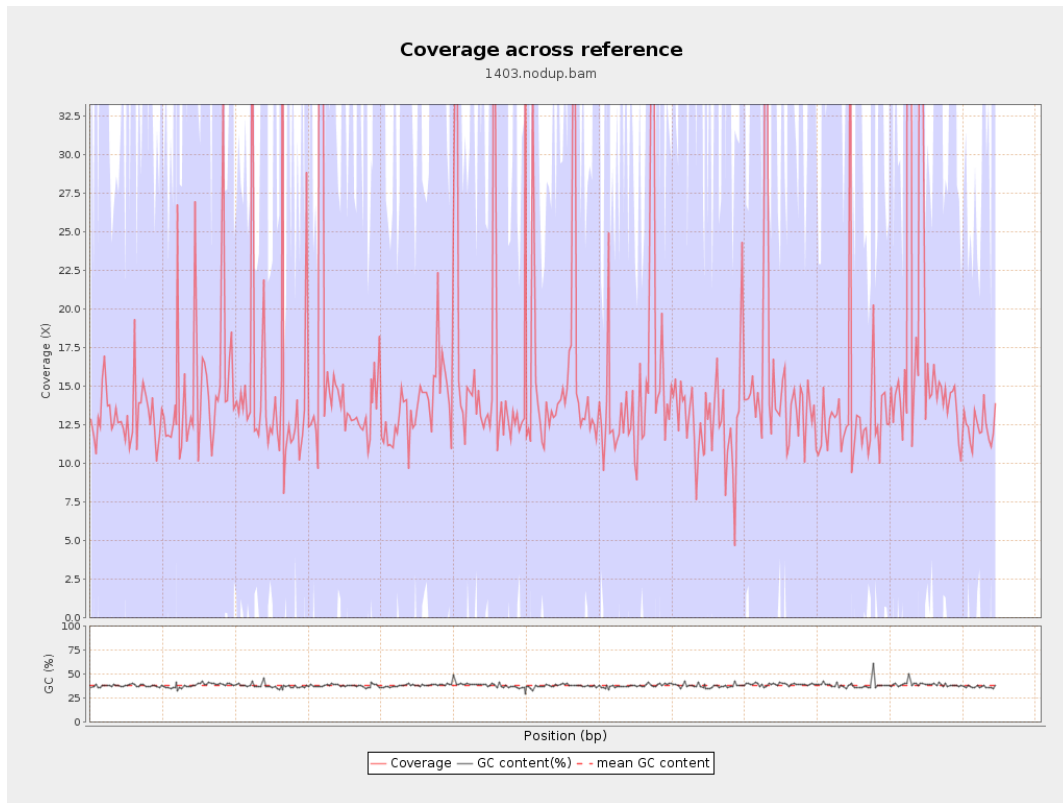
General error rate	2.63%
Mismatches	115,754,399
Insertions	3,167,117
Mapped reads with at least one insertion	8.13%
Deletions	3,328,201
Mapped reads with at least one deletion	8.42%
Homopolymer indels	55.34%

2.7. Chromosome stats

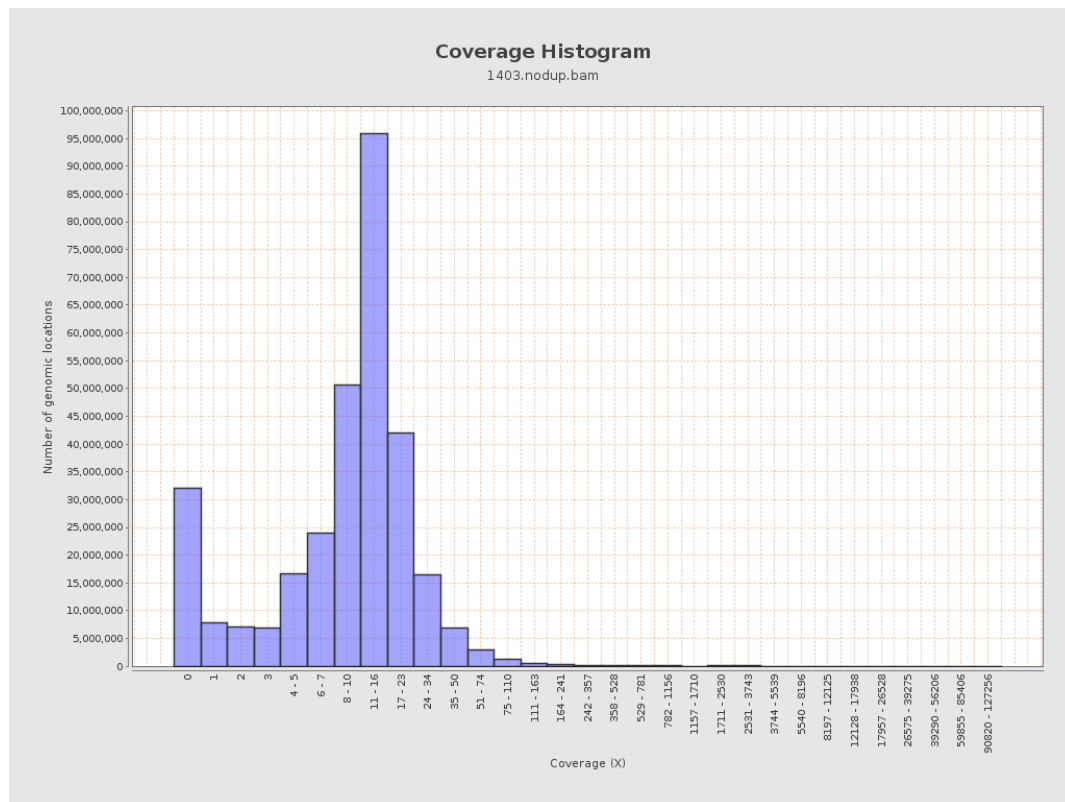
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	386303738	12.9962	38.2154

LT669789.1	36598175	560600348	15.3177	107.5447
LT669790.1	30422129	484944470	15.9405	101.2937
LT669791.1	52758100	779946329	14.7834	101.8511
LT669792.1	28376109	425789215	15.0052	118.9869
LT669793.1	33388210	485587271	14.5437	111.1781
LT669794.1	50579949	730127134	14.4351	107.2927
LT669795.1	49795044	878503470	17.6424	179.3255

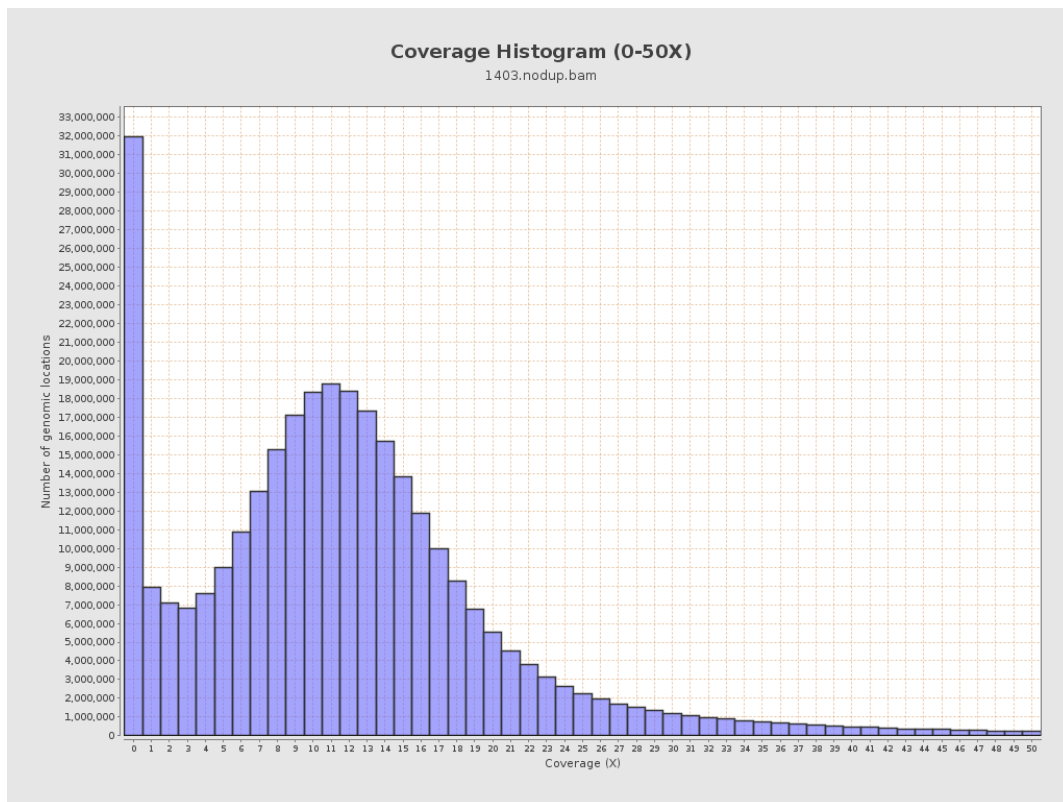
3. Results : Coverage across reference



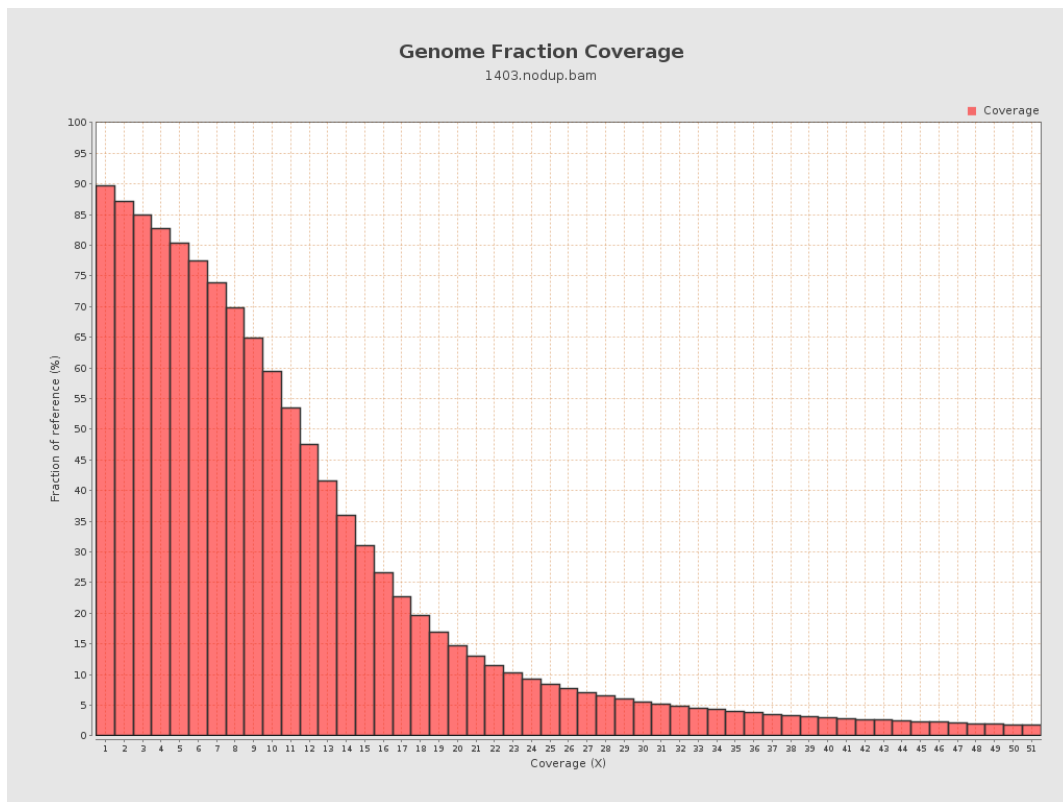
4. Results : Coverage Histogram



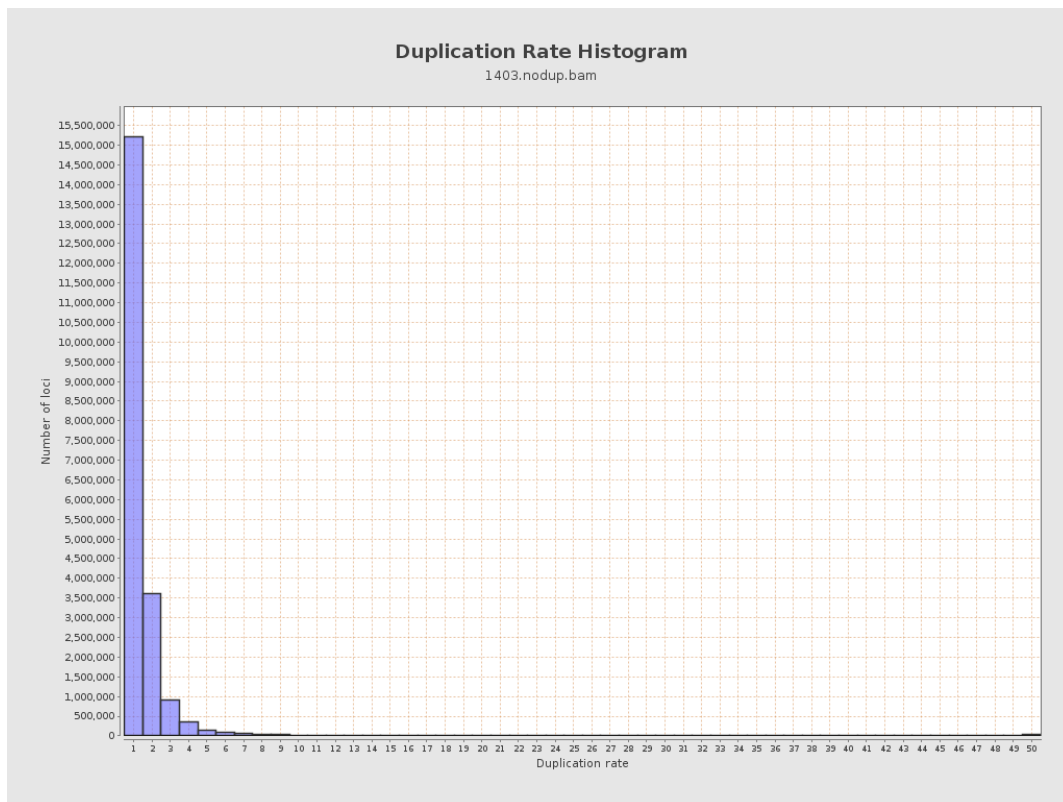
5. Results : Coverage Histogram (0-50X)



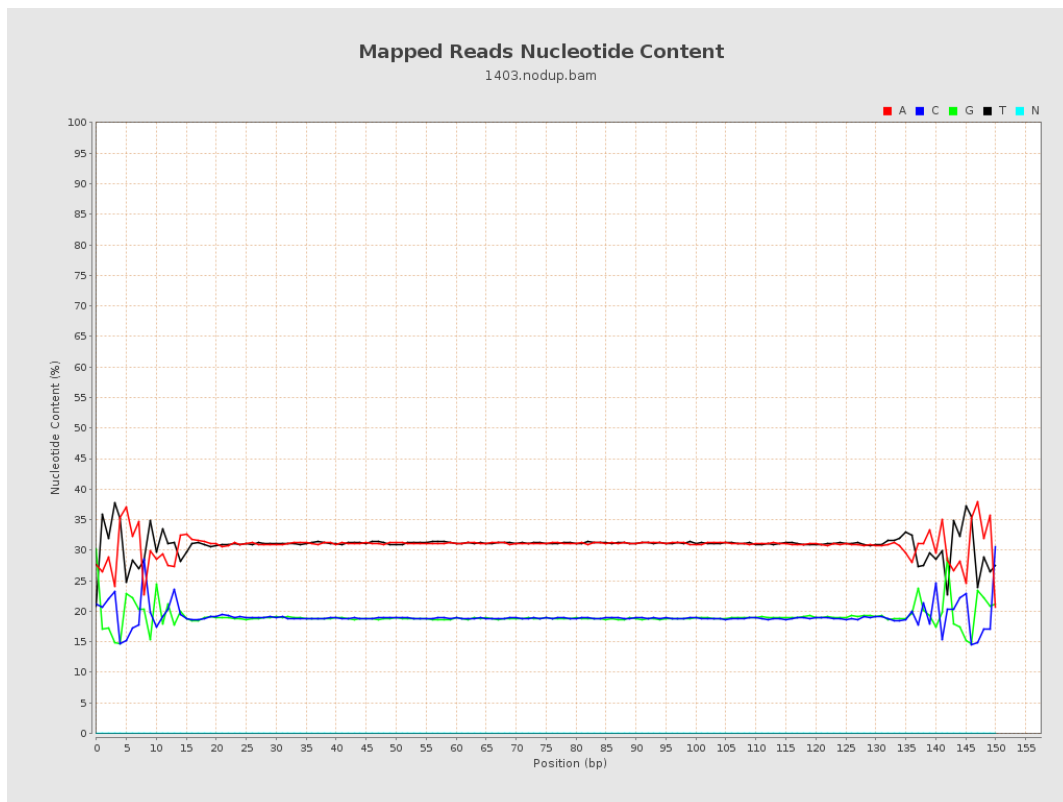
6. Results : Genome Fraction Coverage



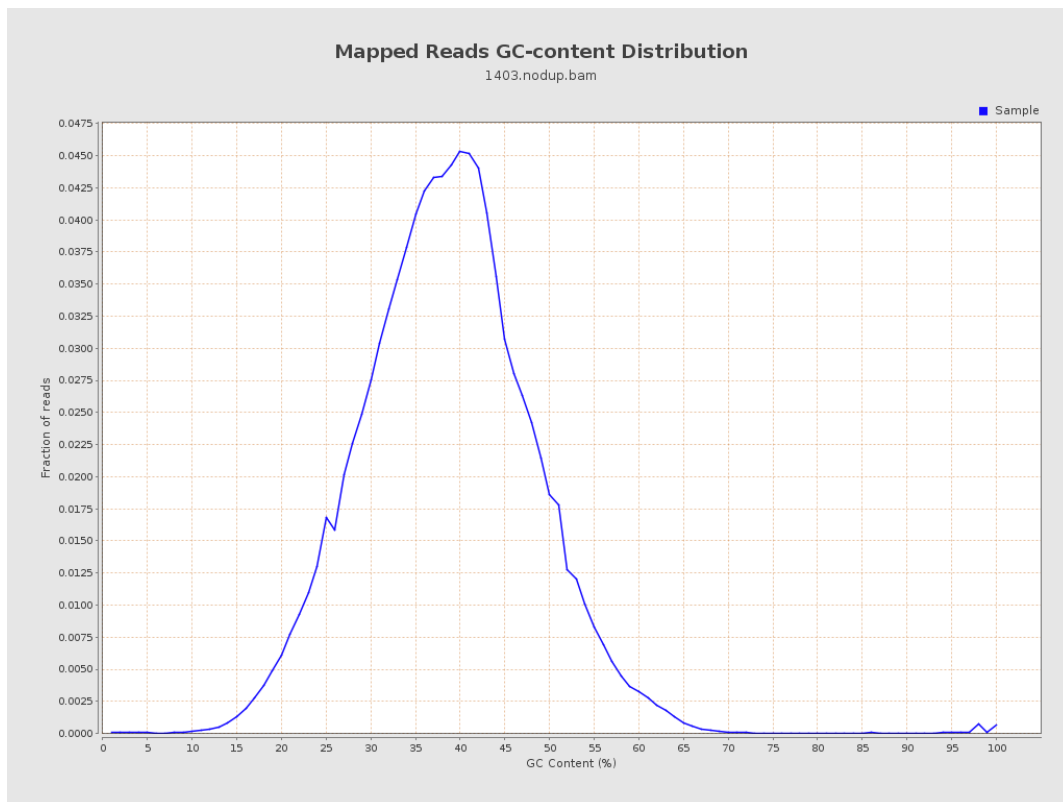
7. Results : Duplication Rate Histogram



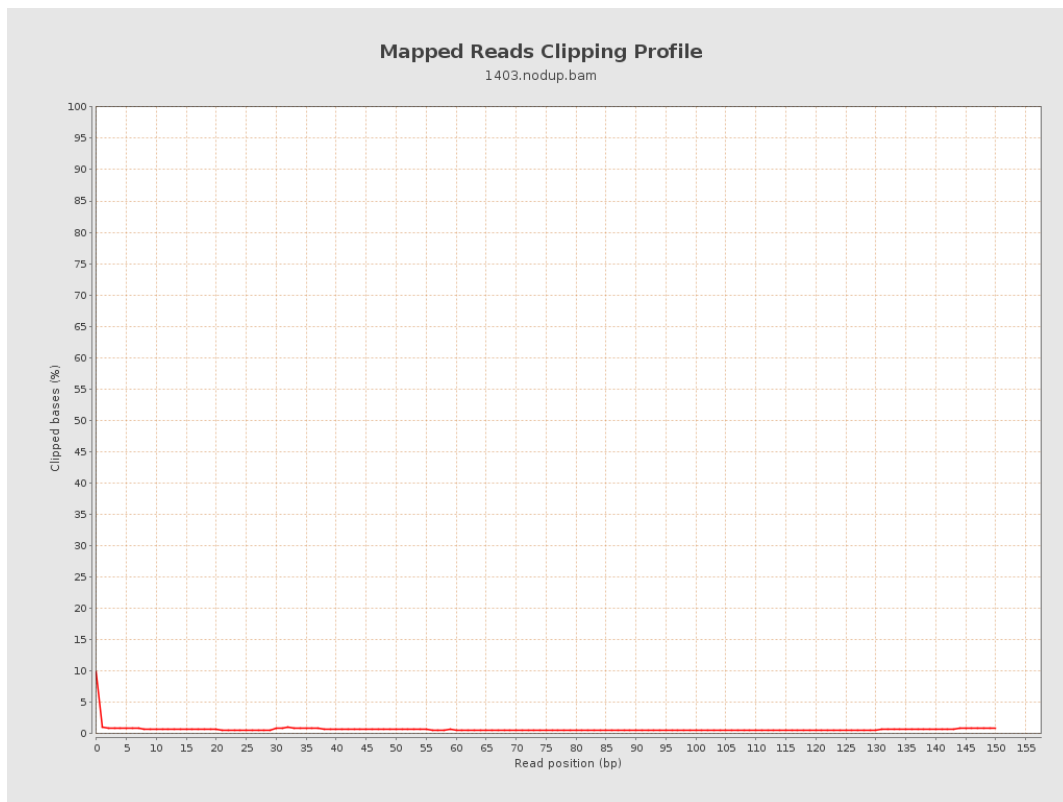
8. Results : Mapped Reads Nucleotide Content



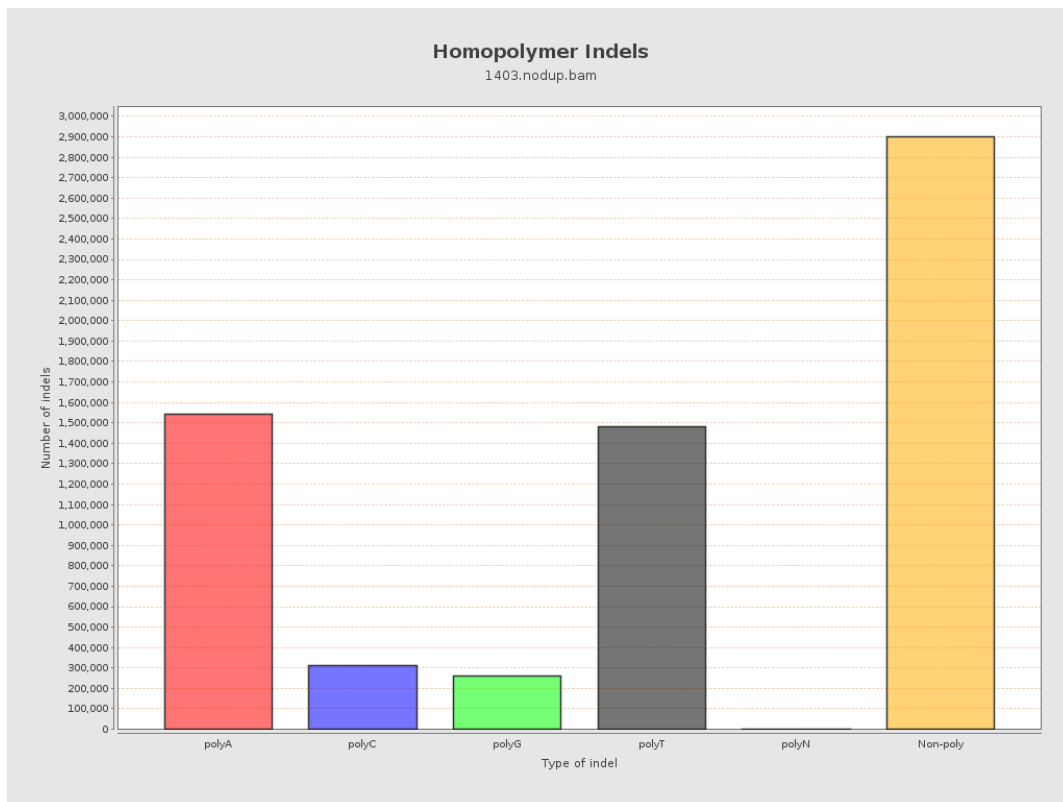
9. Results : Mapped Reads GC-content Distribution



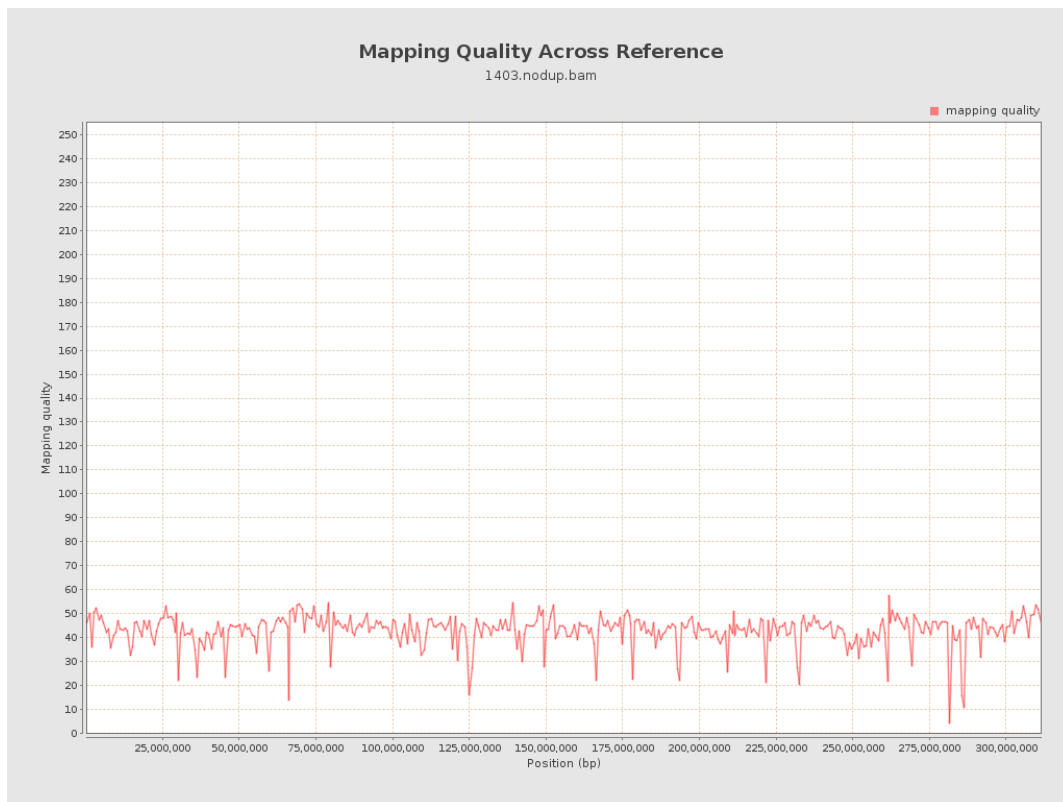
10. Results : Mapped Reads Clipping Profile



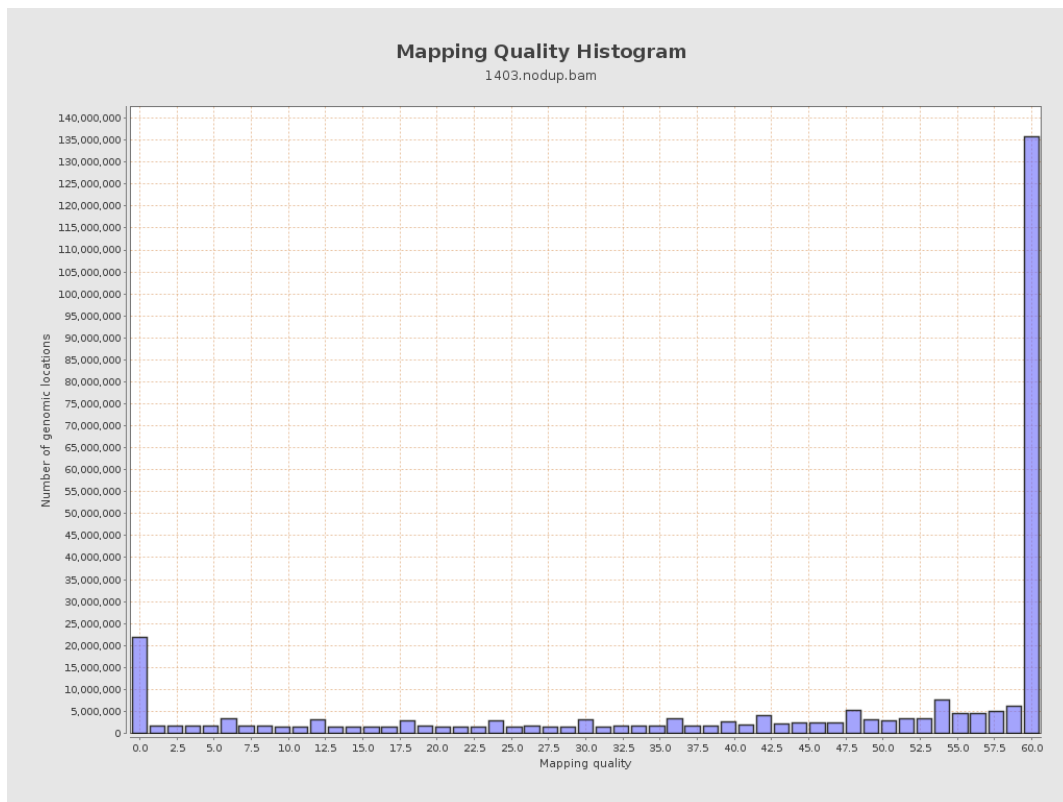
11. Results : Homopolymer Indels



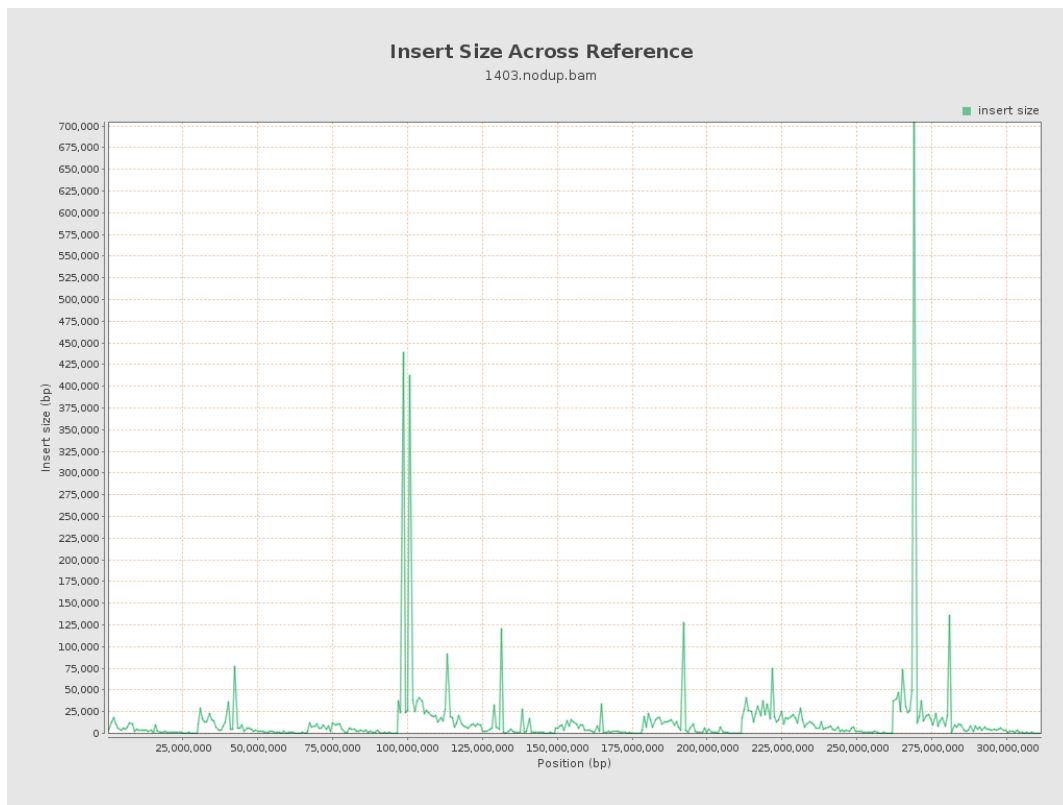
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

