

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:24:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/117
9
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1179 .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_580/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_580_S147_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_580/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_580_S147_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:24:21 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	45,245,158
Mapped reads	42,535,804 / 94.01%
Unmapped reads	2,709,354 / 5.99%
Mapped paired reads	42,535,804 / 94.01%
Mapped reads, first in pair	21,355,677 / 47.2%
Mapped reads, second in pair	21,180,127 / 46.81%
Mapped reads, both in pair	41,590,353 / 91.92%
Mapped reads, singletons	945,451 / 2.09%
Read min/max/mean length	30 / 151 / 148.05
Duplicated reads (flagged)	6,114,185 / 13.51%
Clipped reads	10,251,832 / 22.66%

2.2. ACGT Content

Number/percentage of A's	1,808,826,539 / 30.83%
Number/percentage of C's	1,124,731,221 / 19.17%
Number/percentage of T's	1,812,011,348 / 30.88%
Number/percentage of G's	1,122,240,335 / 19.13%
Number/percentage of N's	40,825 / 0%
GC Percentage	38.29%

2.3. Coverage

Mean	18.8772
Standard Deviation	160.4492

2.4. Mapping Quality

Mean Mapping Quality	43.82
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2.5. Insert size

Mean	232,411.11
Standard Deviation	2,287,956.73
P25/Median/P75	330 / 431 / 556

2.6. Mismatches and indels

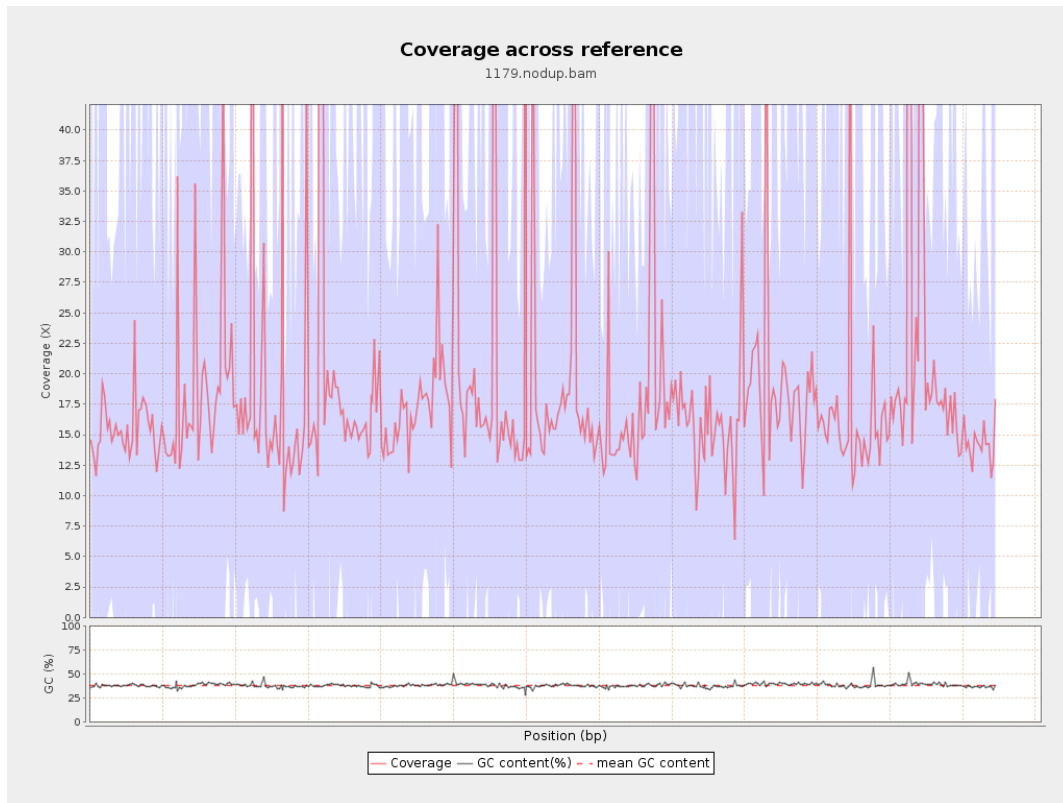
General error rate	2.61%
Mismatches	142,300,137
Insertions	4,027,333
Mapped reads with at least one insertion	8.51%
Deletions	4,028,120
Mapped reads with at least one deletion	8.42%
Homopolymer indels	55.6%

2.7. Chromosome stats

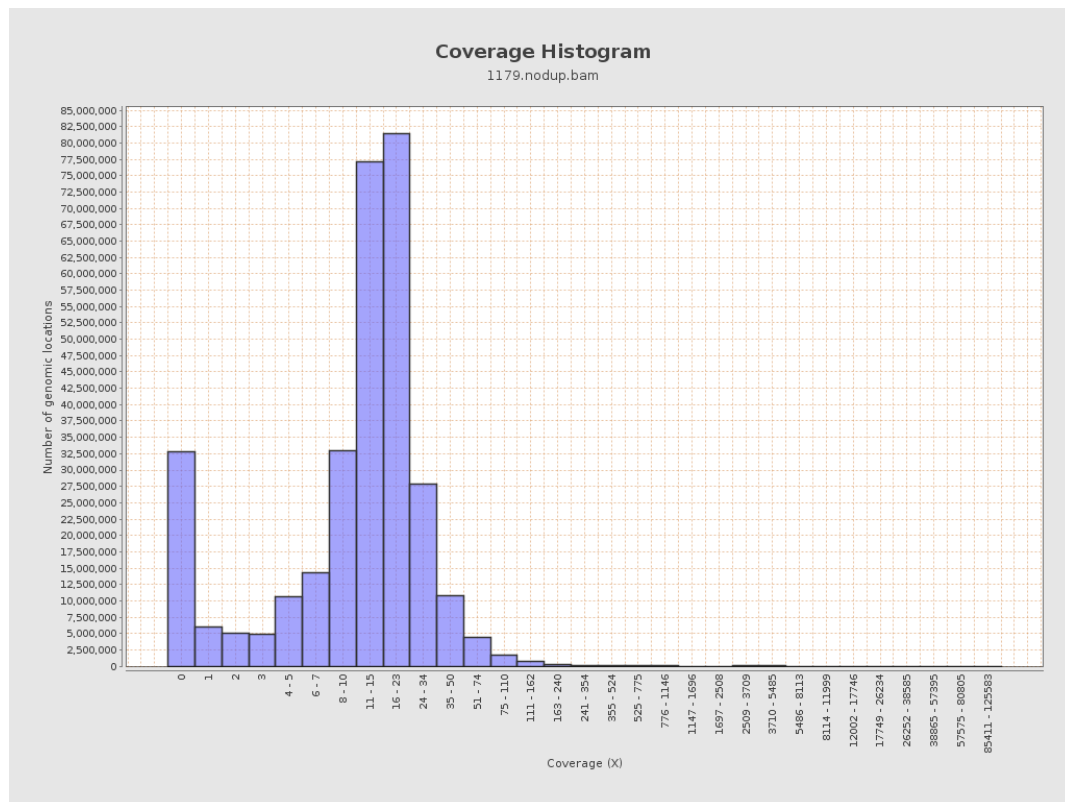
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	451126321	15.177	58.9429

LT669789.1	36598175	717745318	19.6115	178.8945
LT669790.1	30422129	615467563	20.2309	158.6134
LT669791.1	52758100	986091391	18.6908	159.2076
LT669792.1	28376109	530975440	18.7121	178.8411
LT669793.1	33388210	592565631	17.7478	112.3191
LT669794.1	50579949	917172379	18.1331	149.301
LT669795.1	49795044	1071776839	21.5238	209.6464

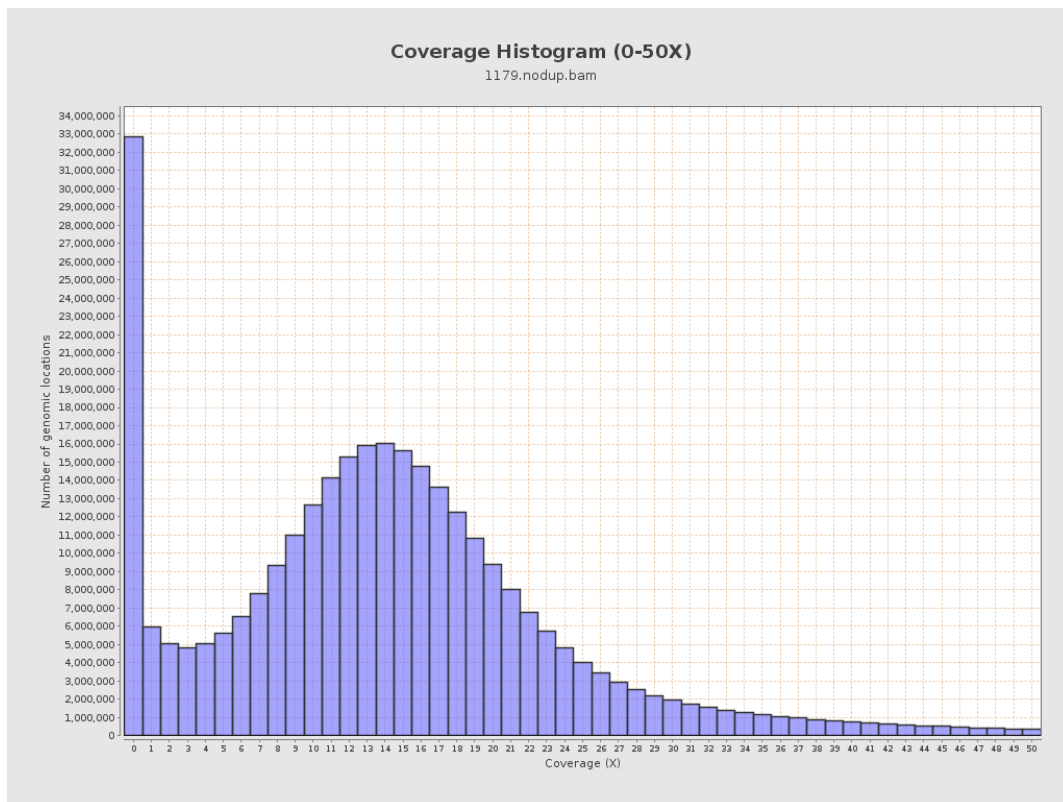
3. Results : Coverage across reference



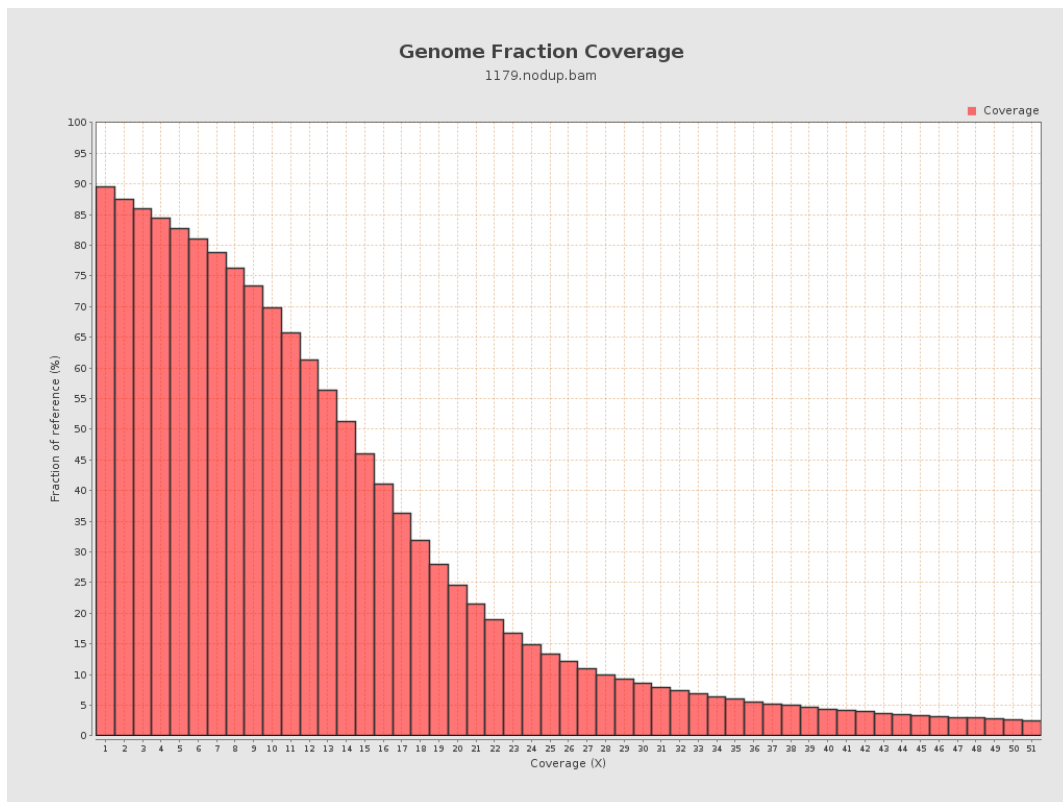
4. Results : Coverage Histogram



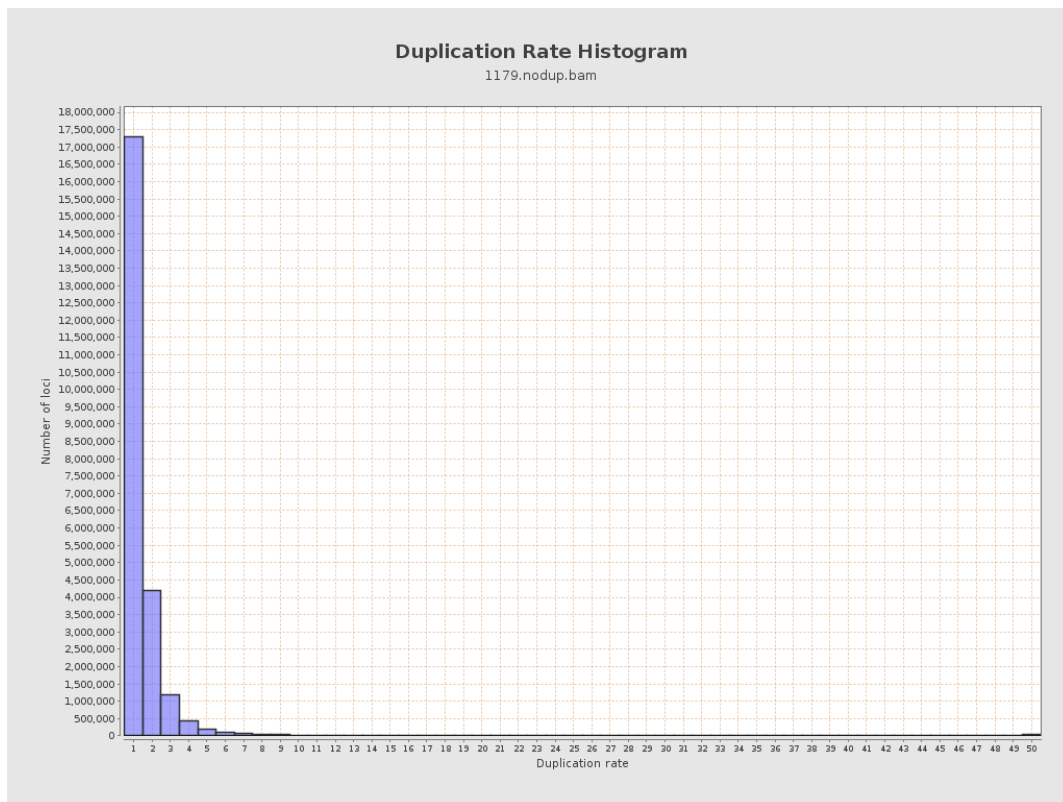
5. Results : Coverage Histogram (0-50X)



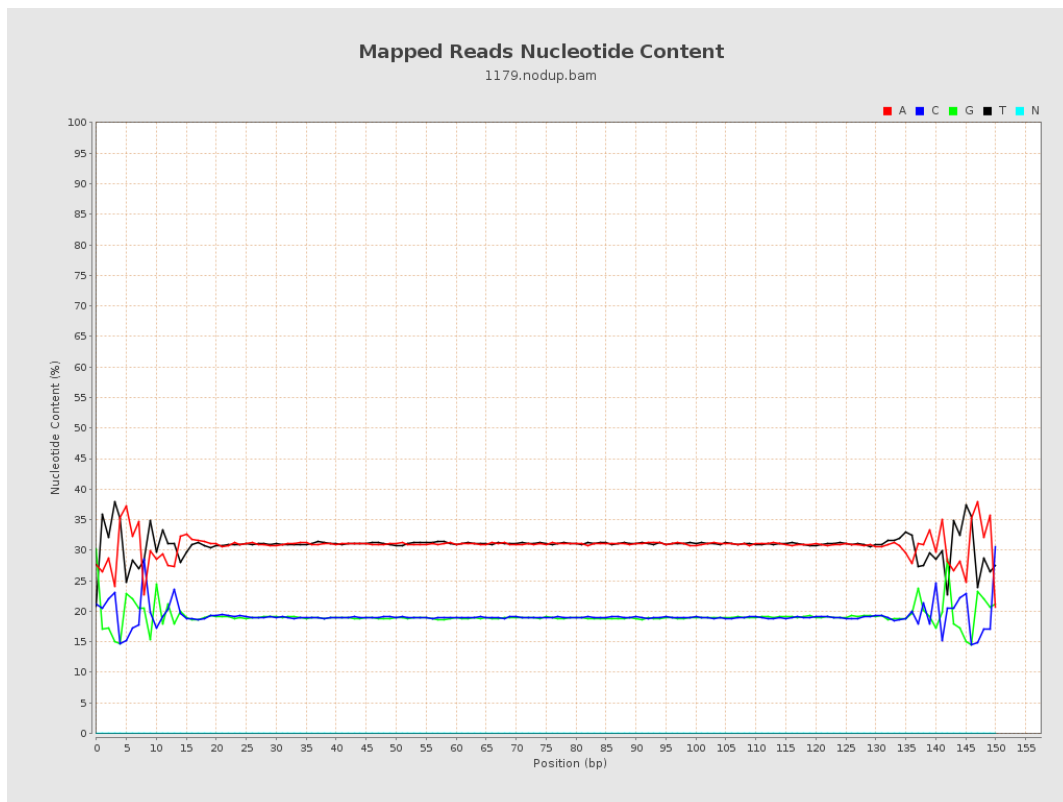
6. Results : Genome Fraction Coverage



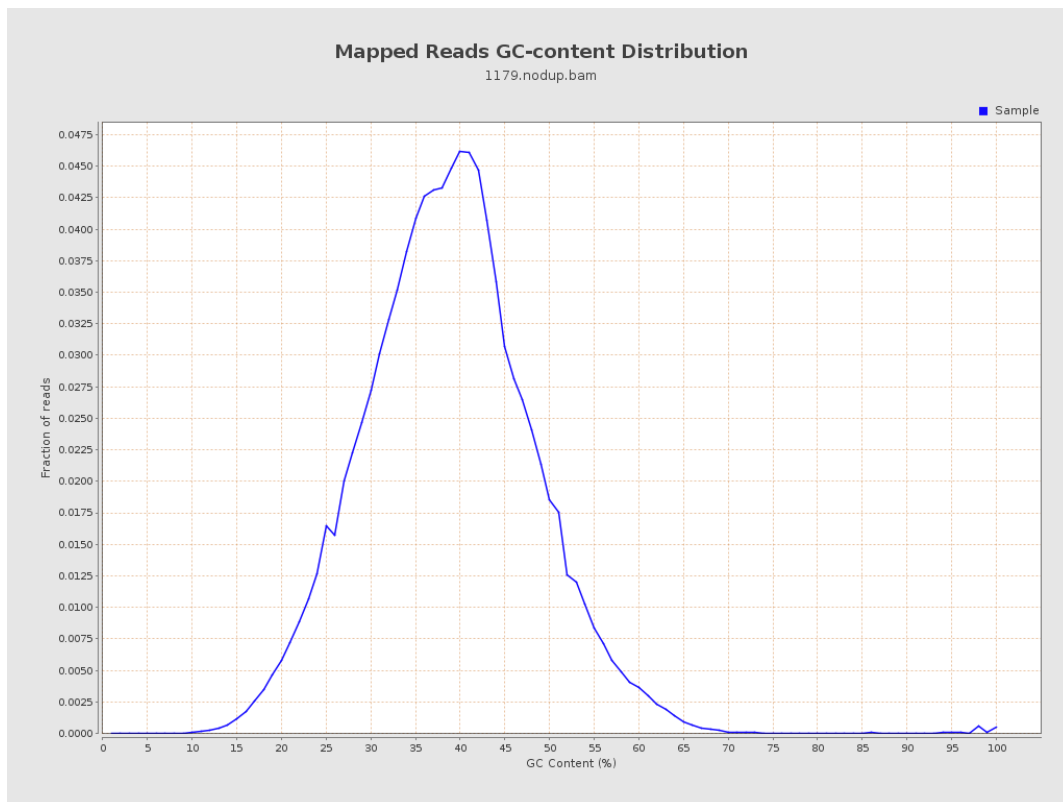
7. Results : Duplication Rate Histogram



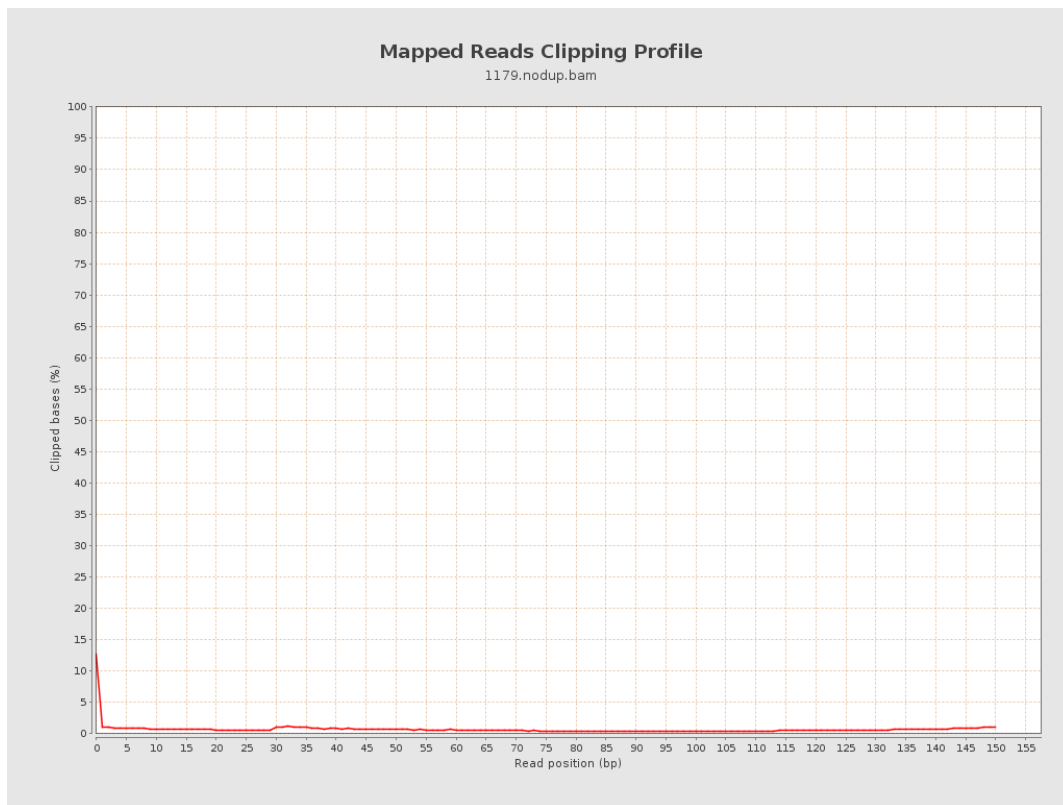
8. Results : Mapped Reads Nucleotide Content



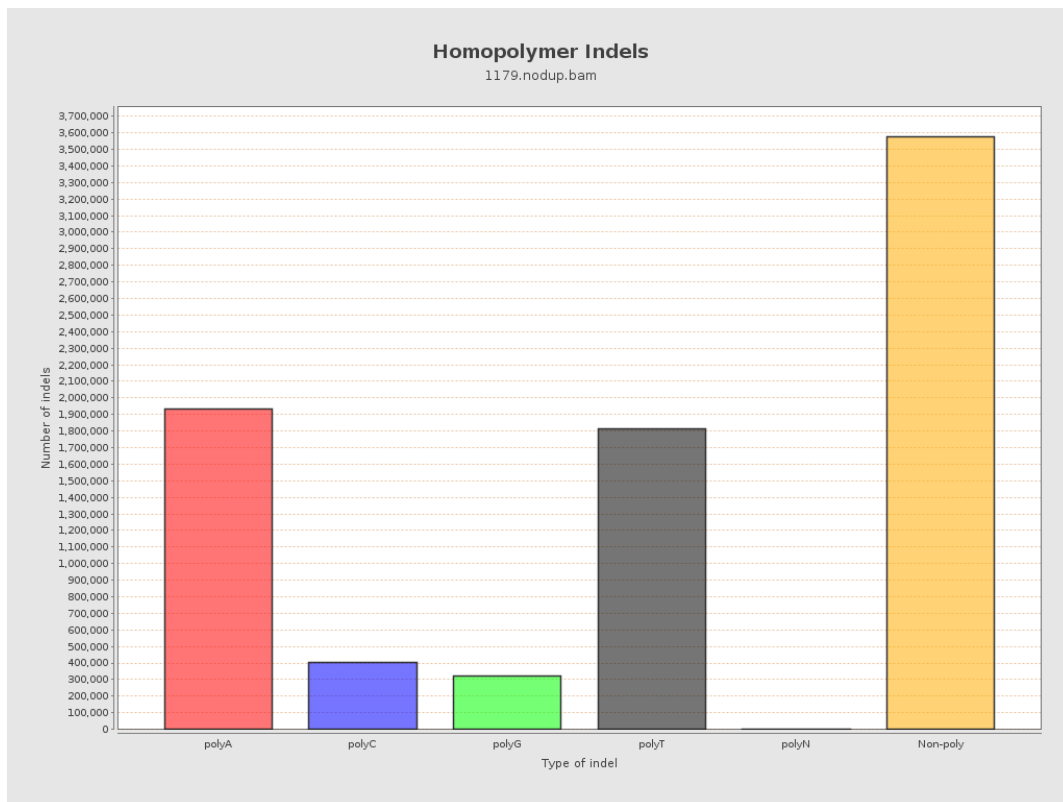
9. Results : Mapped Reads GC-content Distribution



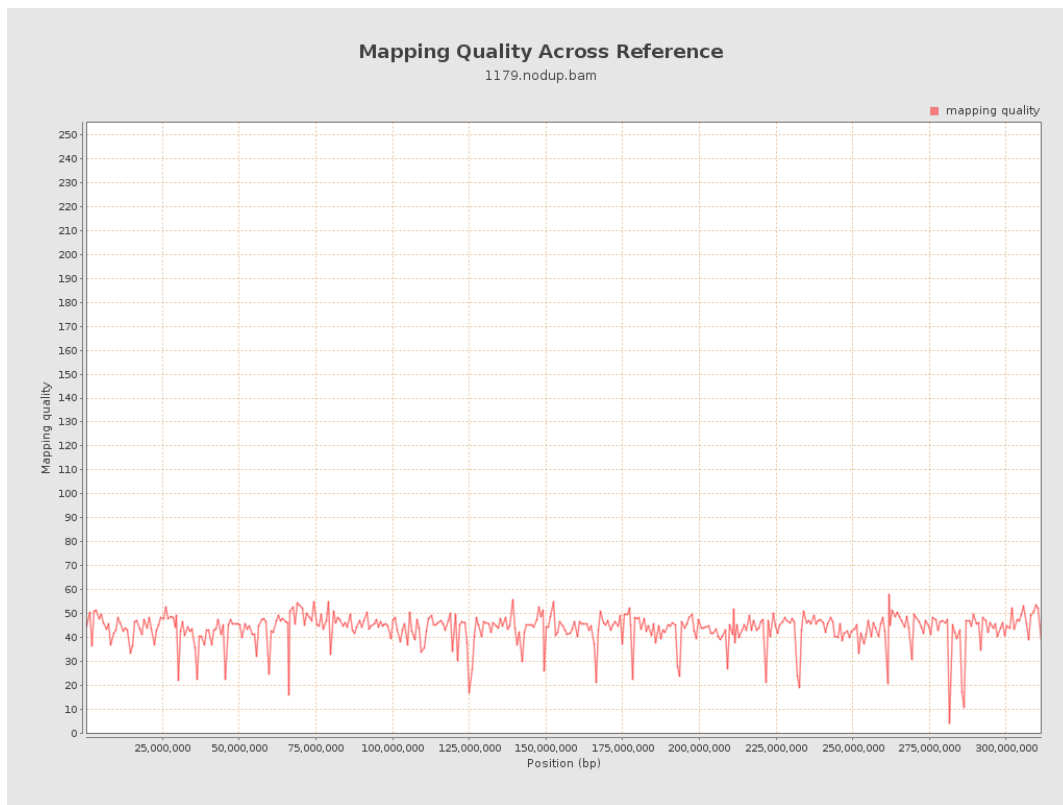
10. Results : Mapped Reads Clipping Profile



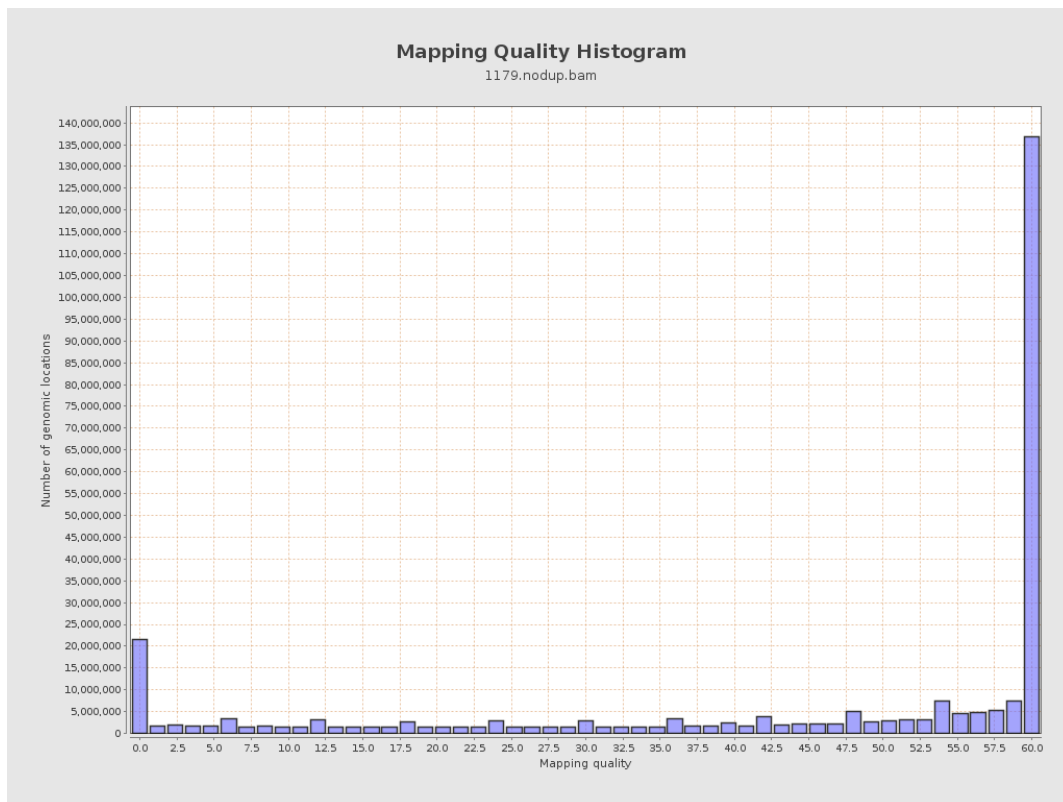
11. Results : Homopolymer Indels



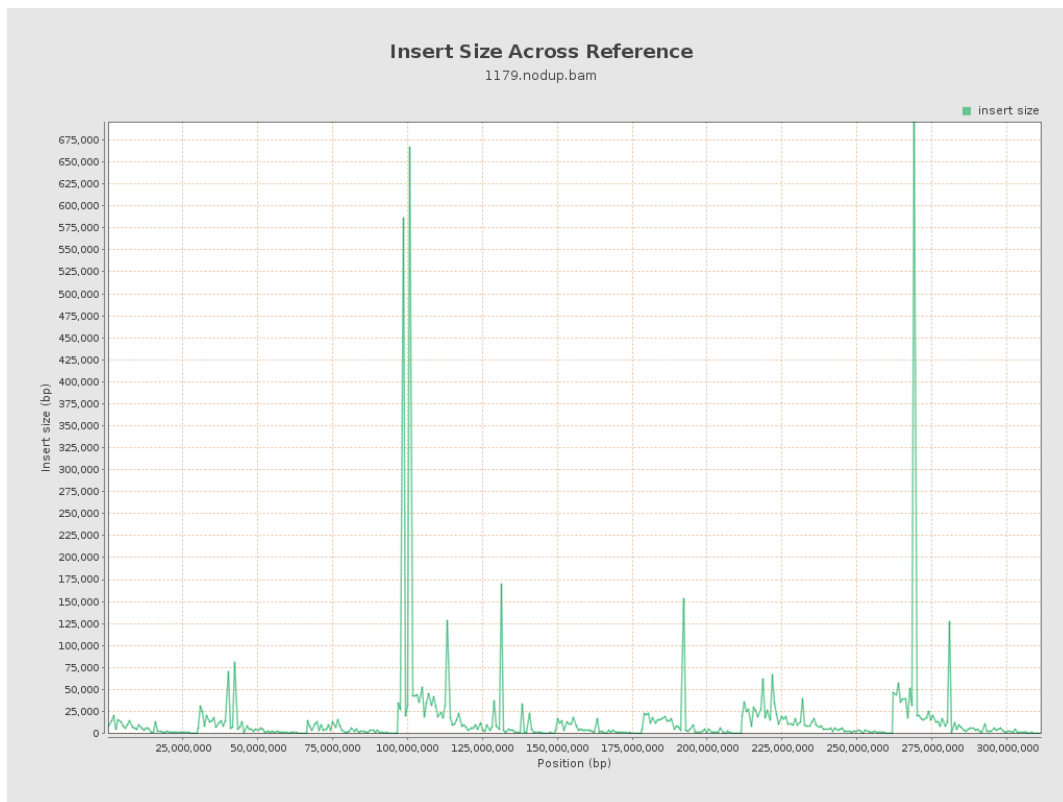
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

