

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:23:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/141
9
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1419 .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_569/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_569_S136_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_569/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_569_S136_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:23:54 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	42,989,384
Mapped reads	40,678,559 / 94.62%
Unmapped reads	2,310,825 / 5.38%
Mapped paired reads	40,678,559 / 94.62%
Mapped reads, first in pair	20,399,408 / 47.45%
Mapped reads, second in pair	20,279,151 / 47.17%
Mapped reads, both in pair	39,890,383 / 92.79%
Mapped reads, singletons	788,176 / 1.83%
Read min/max/mean length	30 / 151 / 148.06
Duplicated reads (flagged)	5,188,082 / 12.07%
Clipped reads	9,464,973 / 22.02%

2.2. ACGT Content

Number/percentage of A's	1,732,875,433 / 30.77%
Number/percentage of C's	1,082,261,097 / 19.22%
Number/percentage of T's	1,736,340,024 / 30.83%
Number/percentage of G's	1,079,599,576 / 19.17%
Number/percentage of N's	40,373 / 0%
GC Percentage	38.39%

2.3. Coverage

Mean	18.1159
Standard Deviation	149.6444

2.4. Mapping Quality

Mean Mapping Quality	43.95
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2.5. Insert size

Mean	223,730.35
Standard Deviation	2,233,191.61
P25/Median/P75	329 / 428 / 548

2.6. Mismatches and indels

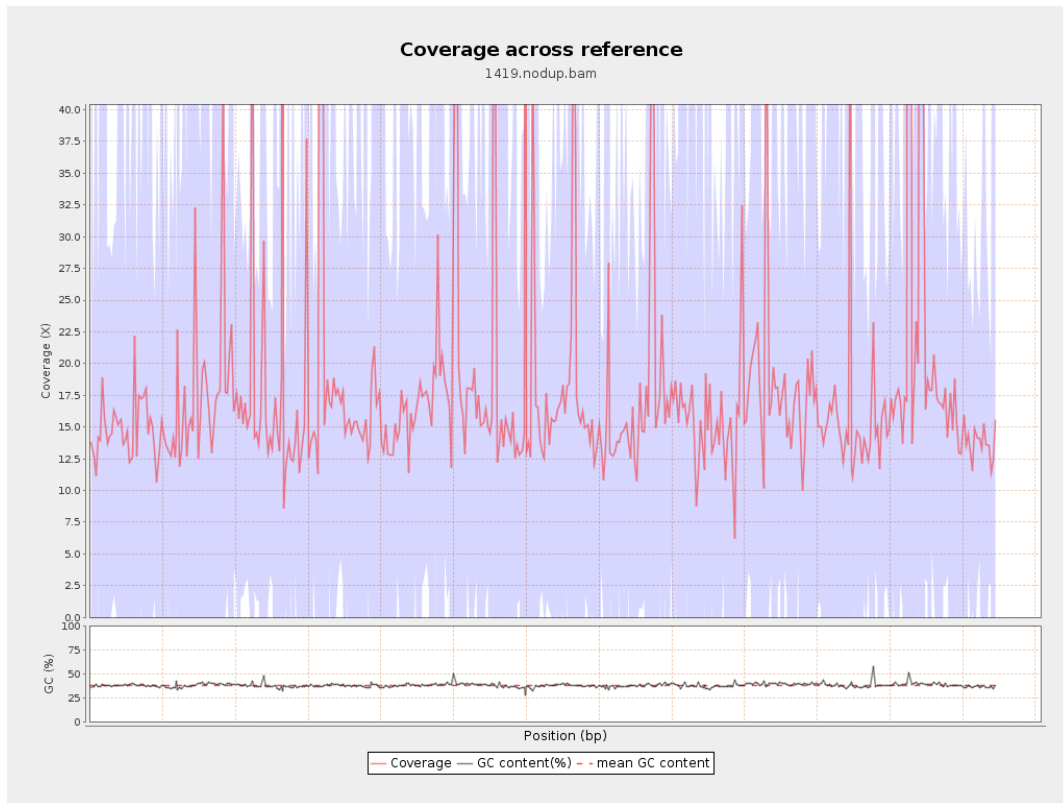
General error rate	2.51%
Mismatches	131,056,171
Insertions	3,756,149
Mapped reads with at least one insertion	8.31%
Deletions	3,863,208
Mapped reads with at least one deletion	8.44%
Homopolymer indels	55.66%

2.7. Chromosome stats

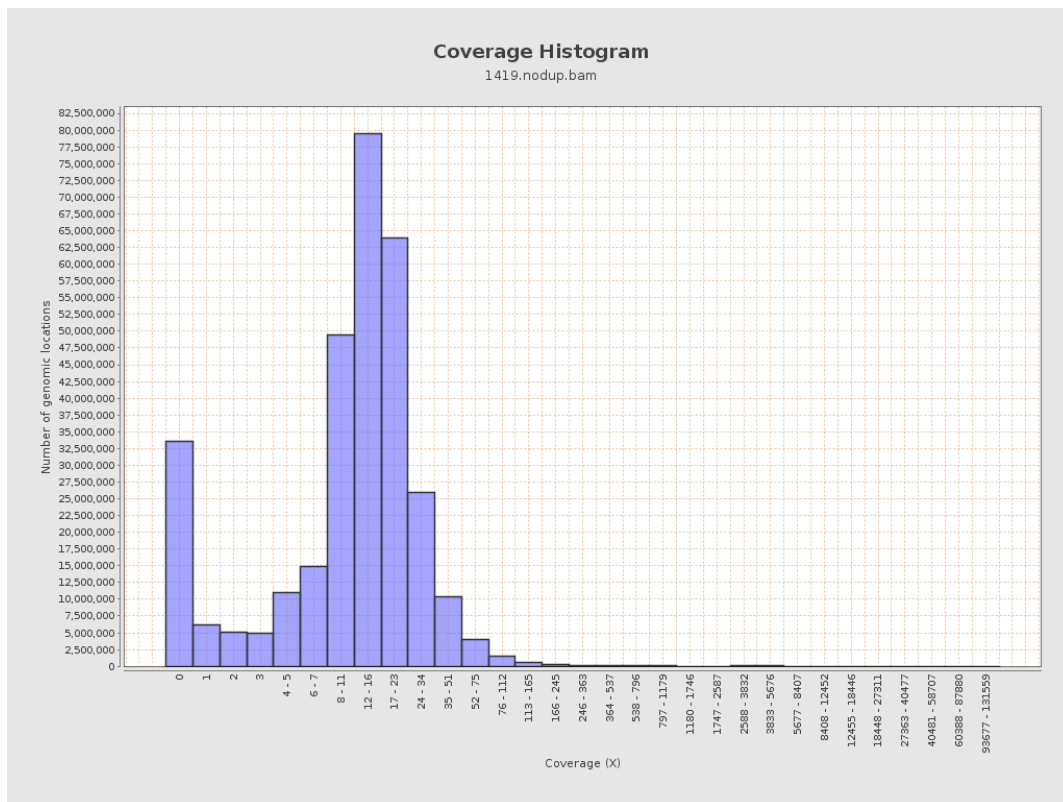
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	435242330	14.6426	54.3377

LT669789.1	36598175	678208714	18.5312	161.2827
LT669790.1	30422129	575980161	18.9329	135.7218
LT669791.1	52758100	939173784	17.8015	133.3265
LT669792.1	28376109	501943156	17.6889	140.4748
LT669793.1	33388210	566916290	16.9795	98.3452
LT669794.1	50579949	884313996	17.4835	135.2918
LT669795.1	49795044	1063898423	21.3655	229.8665

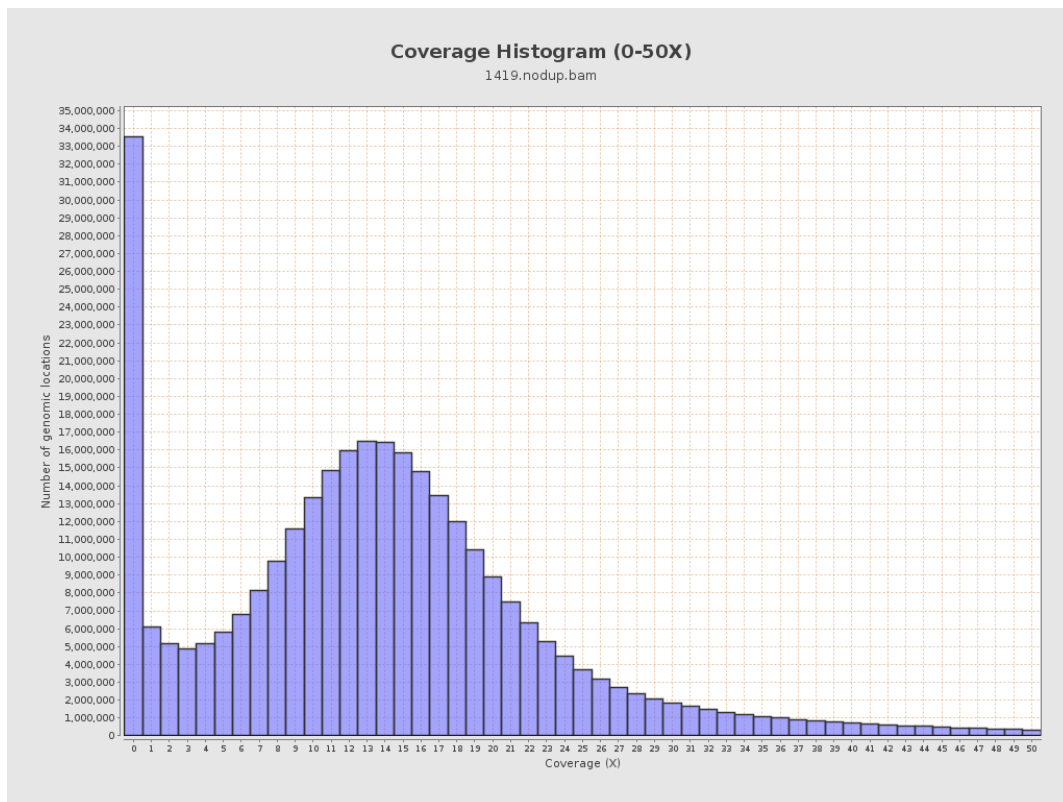
3. Results : Coverage across reference



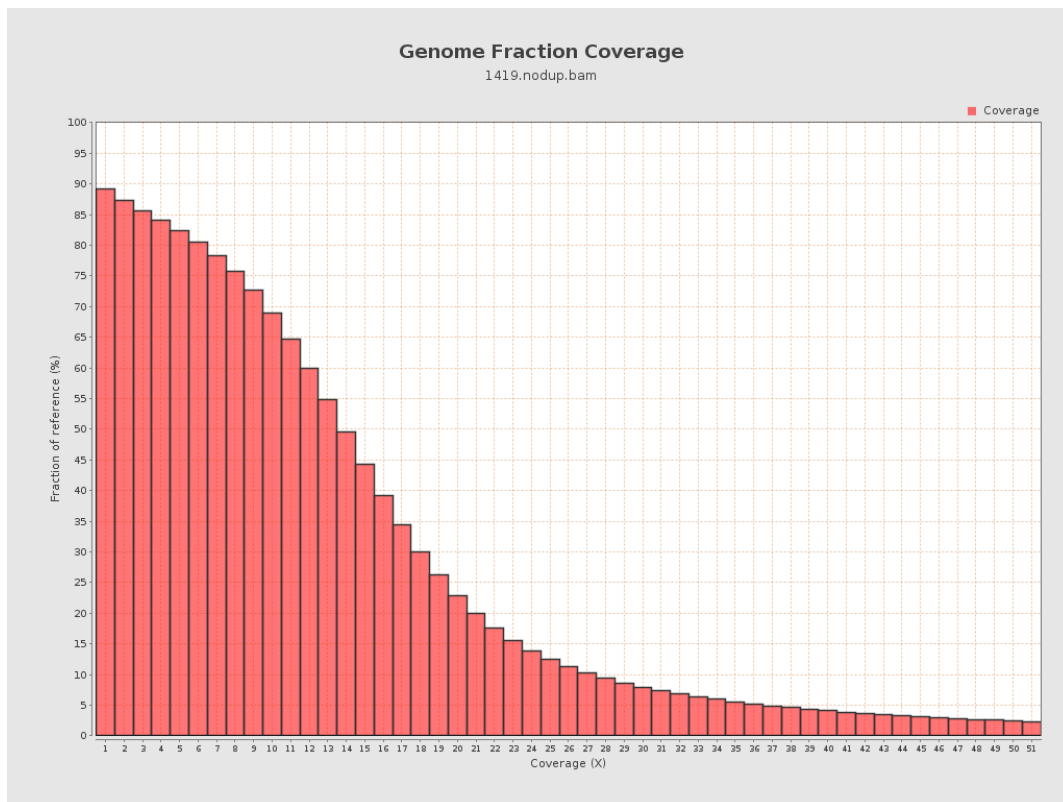
4. Results : Coverage Histogram



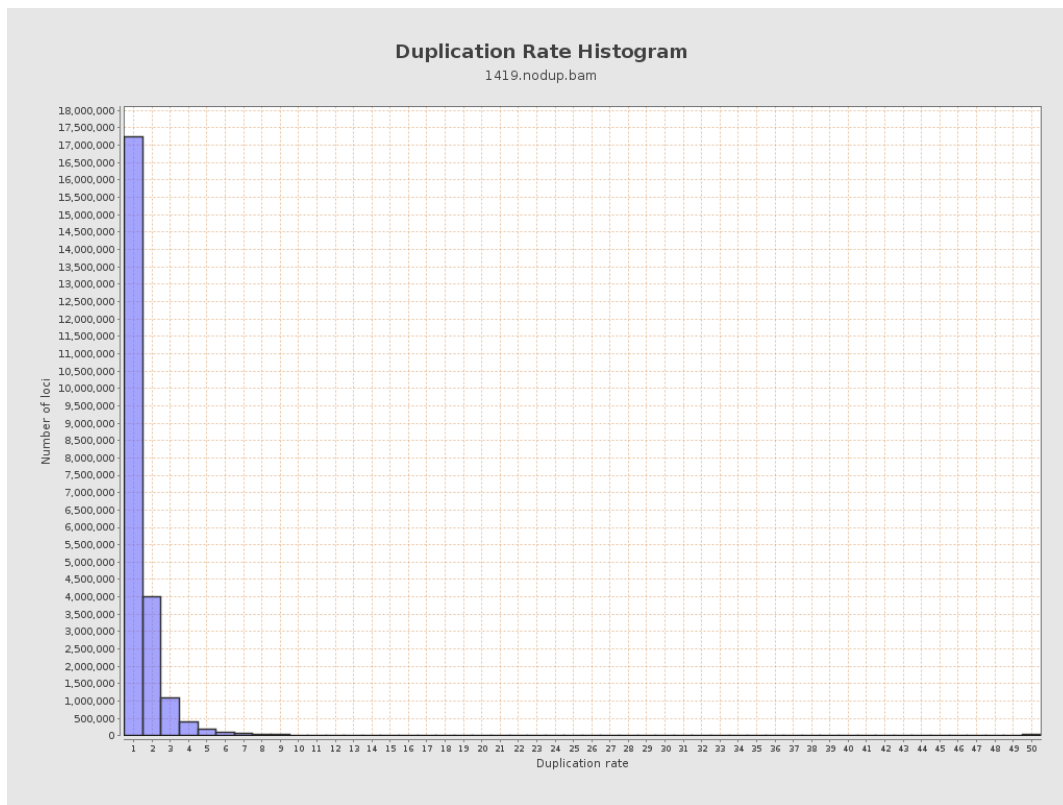
5. Results : Coverage Histogram (0-50X)



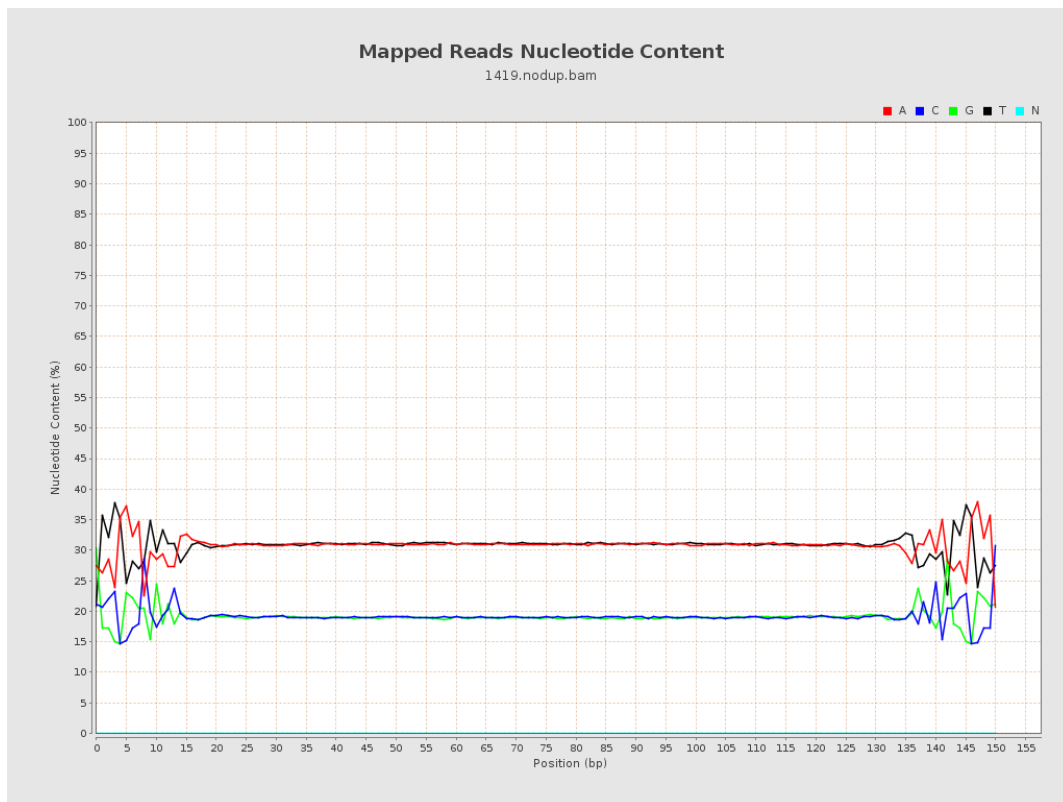
6. Results : Genome Fraction Coverage



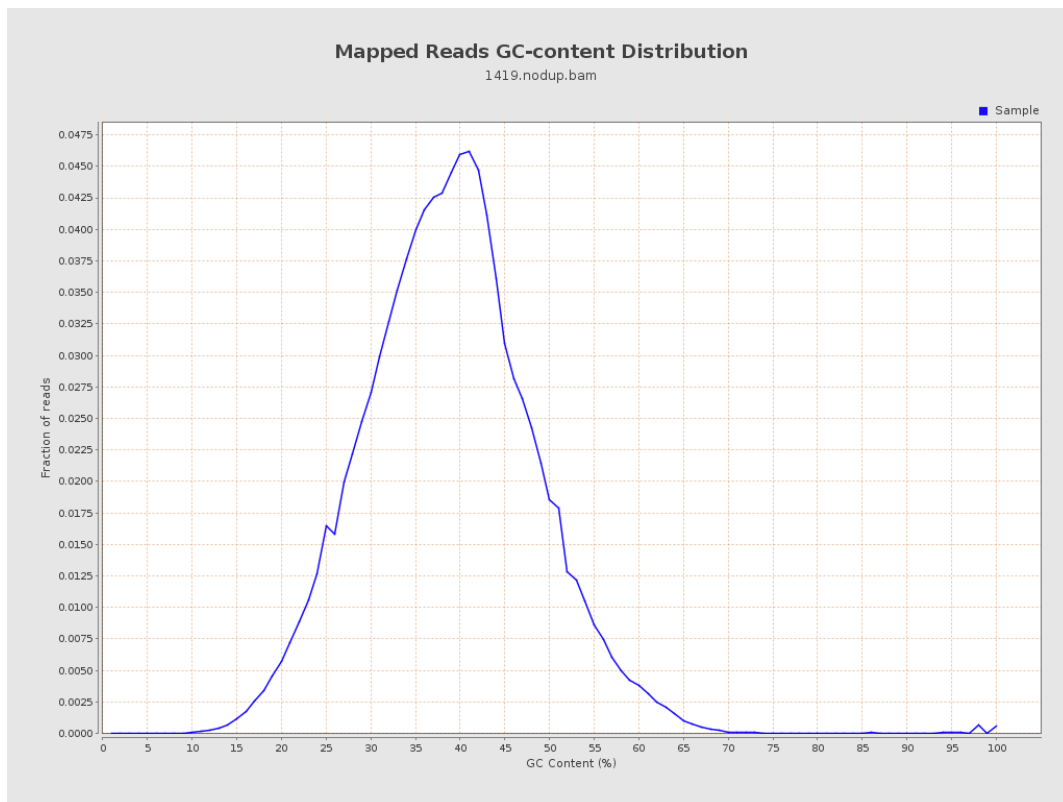
7. Results : Duplication Rate Histogram



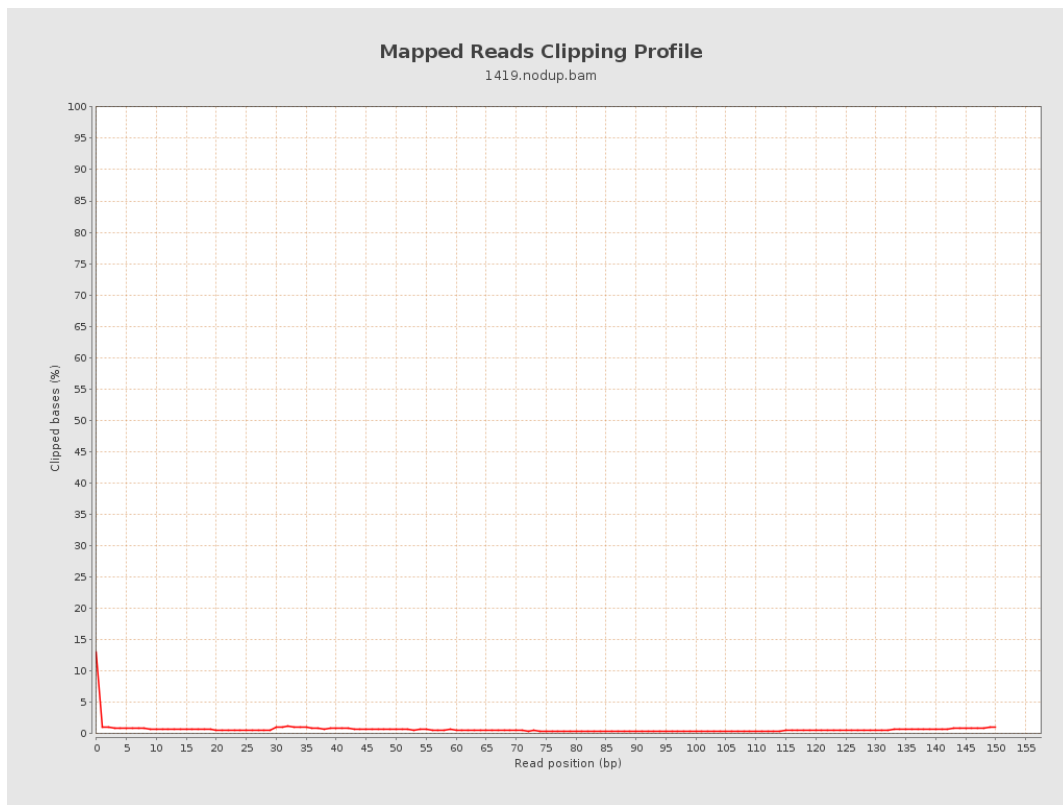
8. Results : Mapped Reads Nucleotide Content



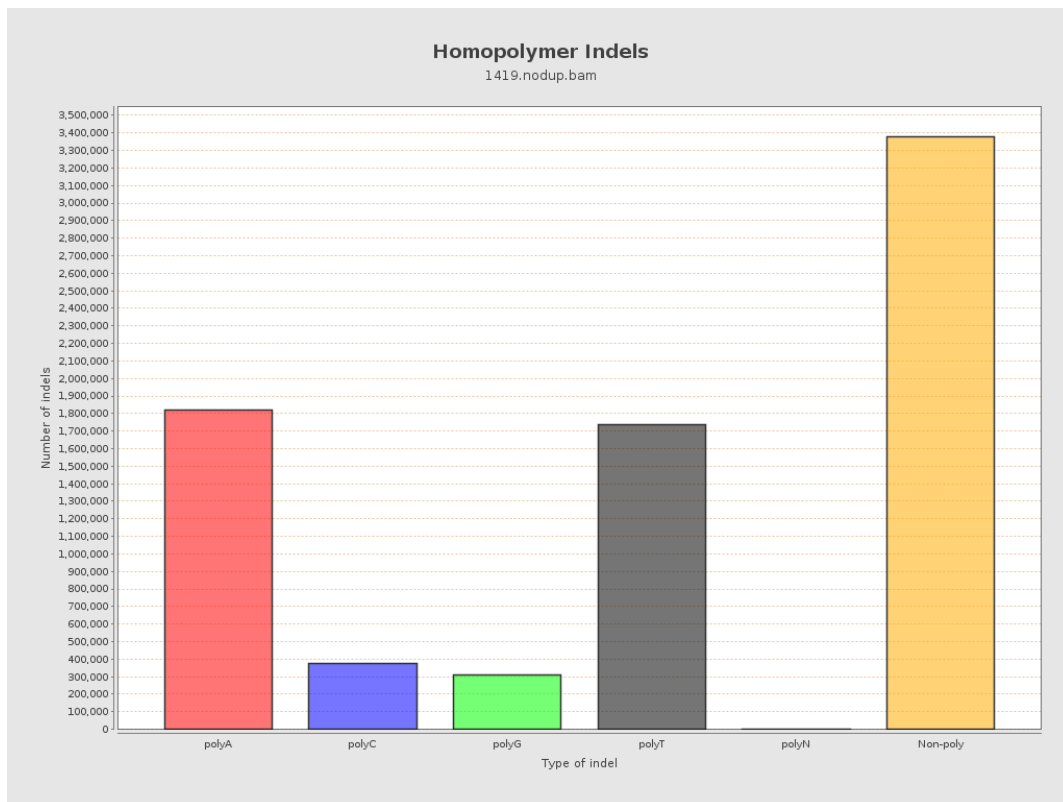
9. Results : Mapped Reads GC-content Distribution



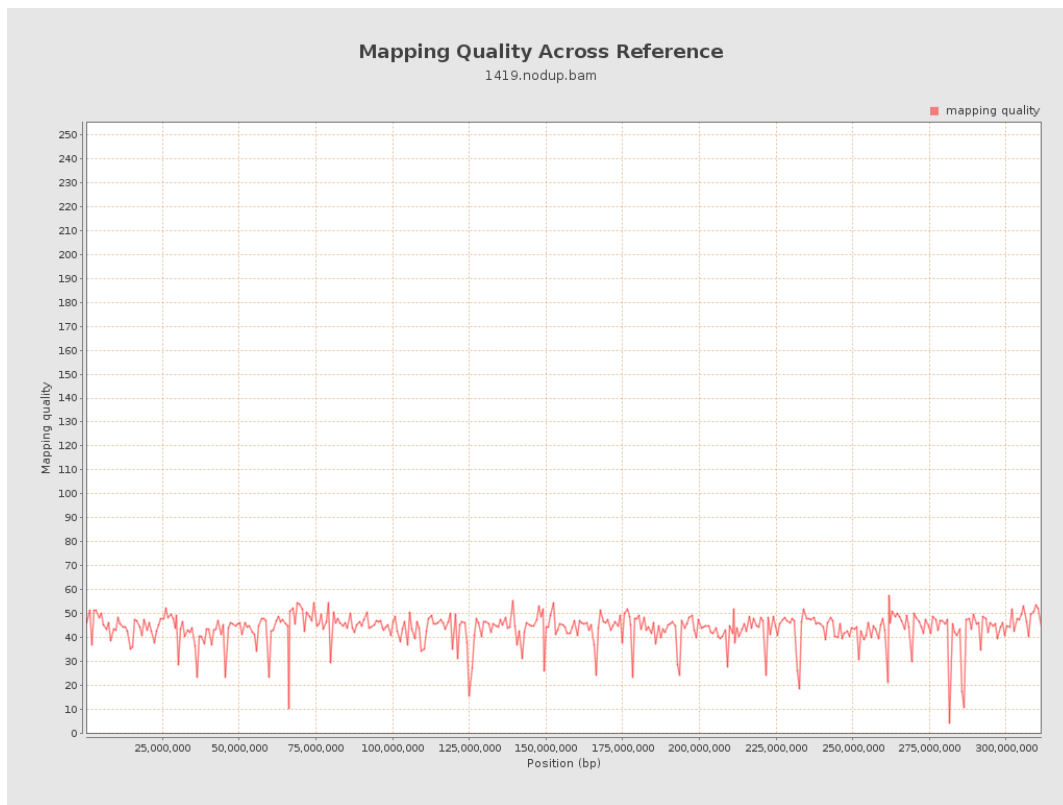
10. Results : Mapped Reads Clipping Profile



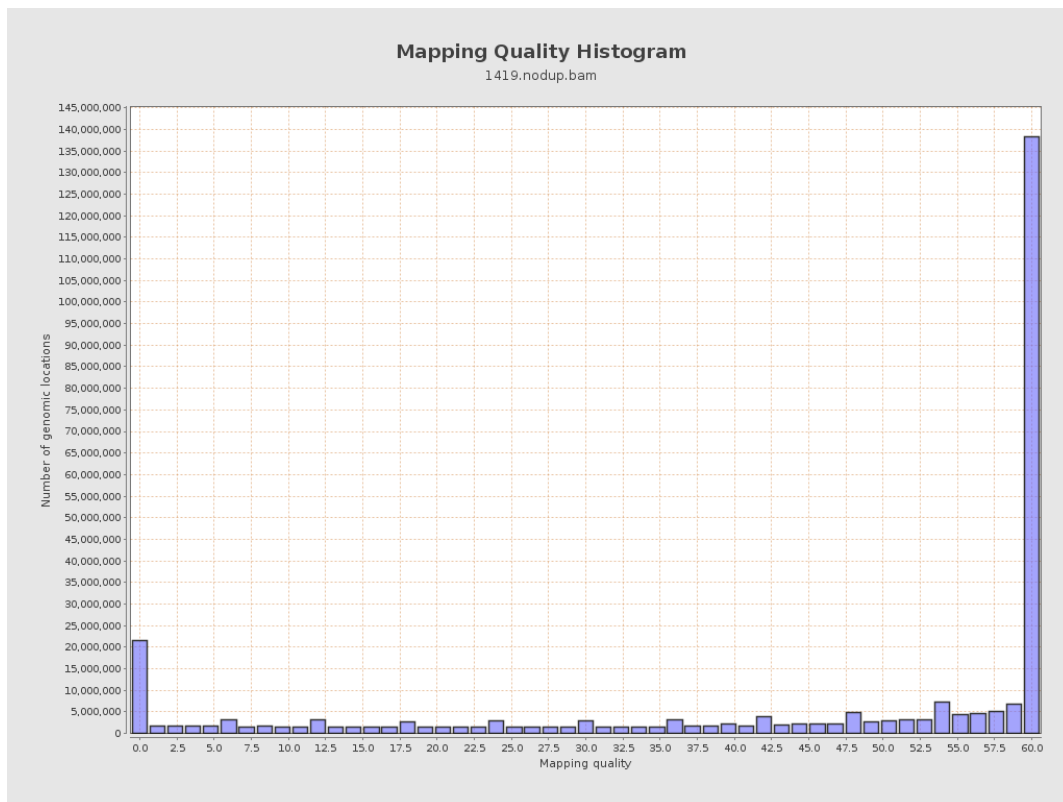
11. Results : Homopolymer Indels



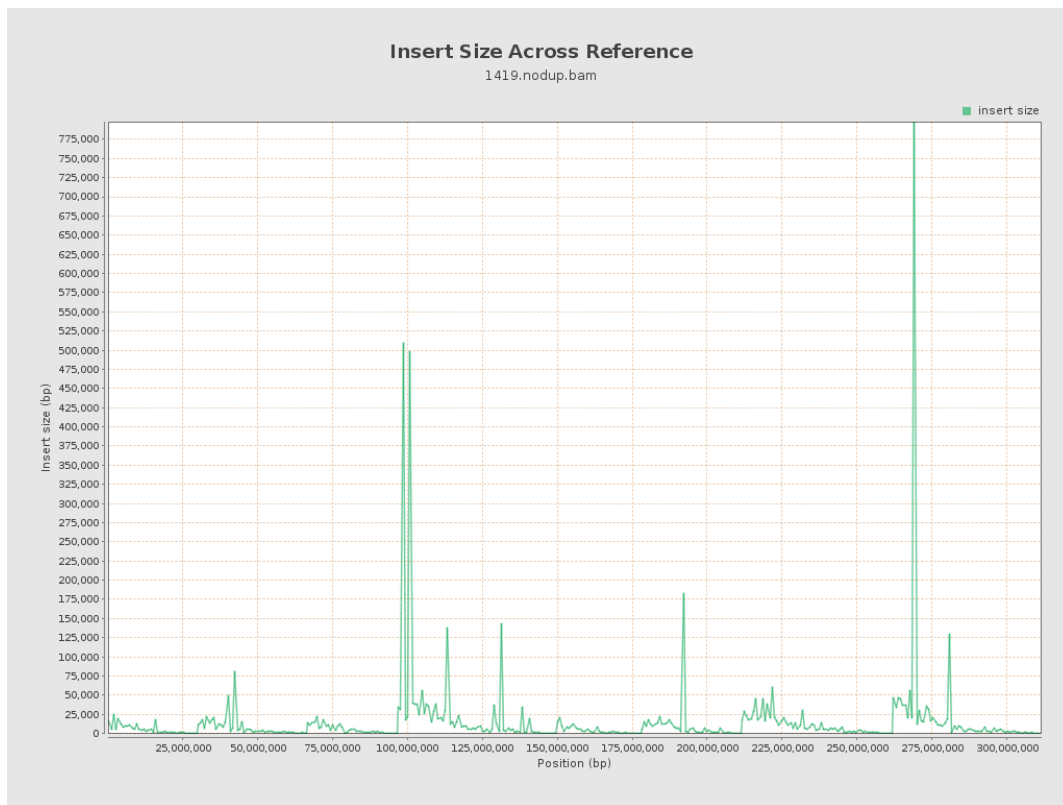
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

