

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:49:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/397
P
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 397P .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_592/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_592_S159_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_592/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_592_S159_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:49:41 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	117,757,241
Mapped reads	111,093,975 / 94.34%
Unmapped reads	6,663,266 / 5.66%
Mapped paired reads	111,093,975 / 94.34%
Mapped reads, first in pair	55,677,595 / 47.28%
Mapped reads, second in pair	55,416,380 / 47.06%
Mapped reads, both in pair	109,245,085 / 92.77%
Mapped reads, singletons	1,848,890 / 1.57%
Read min/max/mean length	30 / 151 / 148.11
Duplicated reads (flagged)	17,699,959 / 15.03%
Clipped reads	24,622,419 / 20.91%

2.2. ACGT Content

Number/percentage of A's	4,765,393,988 / 30.85%
Number/percentage of C's	2,961,364,105 / 19.17%
Number/percentage of T's	4,769,995,559 / 30.88%
Number/percentage of G's	2,952,566,605 / 19.11%
Number/percentage of N's	79,213 / 0%
GC Percentage	38.28%

2.3. Coverage

Mean	49.7024
Standard Deviation	360.8459

2.4. Mapping Quality

Mean Mapping Quality	44.02
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2.5. Insert size

Mean	221,337.51
Standard Deviation	2,210,886.53
P25/Median/P75	334 / 441 / 574

2.6. Mismatches and indels

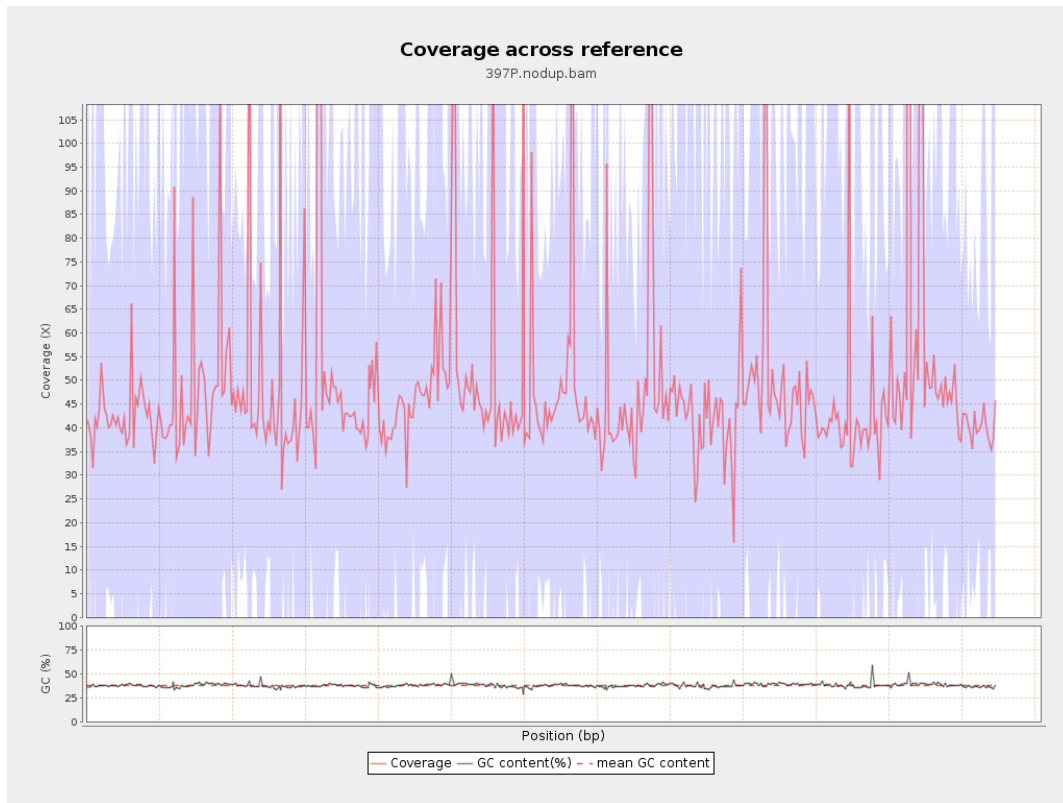
General error rate	2.35%
Mismatches	335,862,292
Insertions	10,049,913
Mapped reads with at least one insertion	8.16%
Deletions	10,546,256
Mapped reads with at least one deletion	8.43%
Homopolymer indels	55.95%

2.7. Chromosome stats

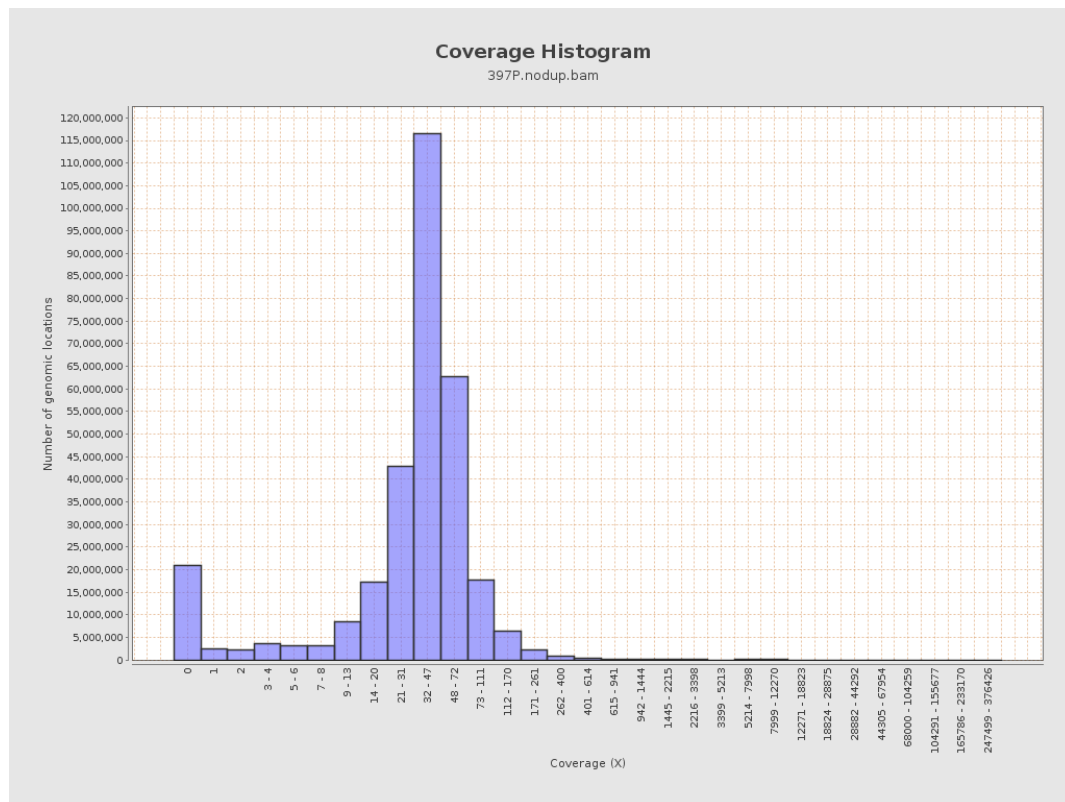
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	1248040874	41.9872	92.2672

LT669789.1	36598175	1859542514	50.8097	382.4447
LT669790.1	30422129	1540644559	50.6422	299.8504
LT669791.1	52758100	2576513040	48.8364	283.194
LT669792.1	28376109	1382394363	48.7168	392.6127
LT669793.1	33388210	1565482882	46.8873	261.6946
LT669794.1	50579949	2396055406	47.3716	329.3261
LT669795.1	49795044	2920699534	58.6544	564.2509

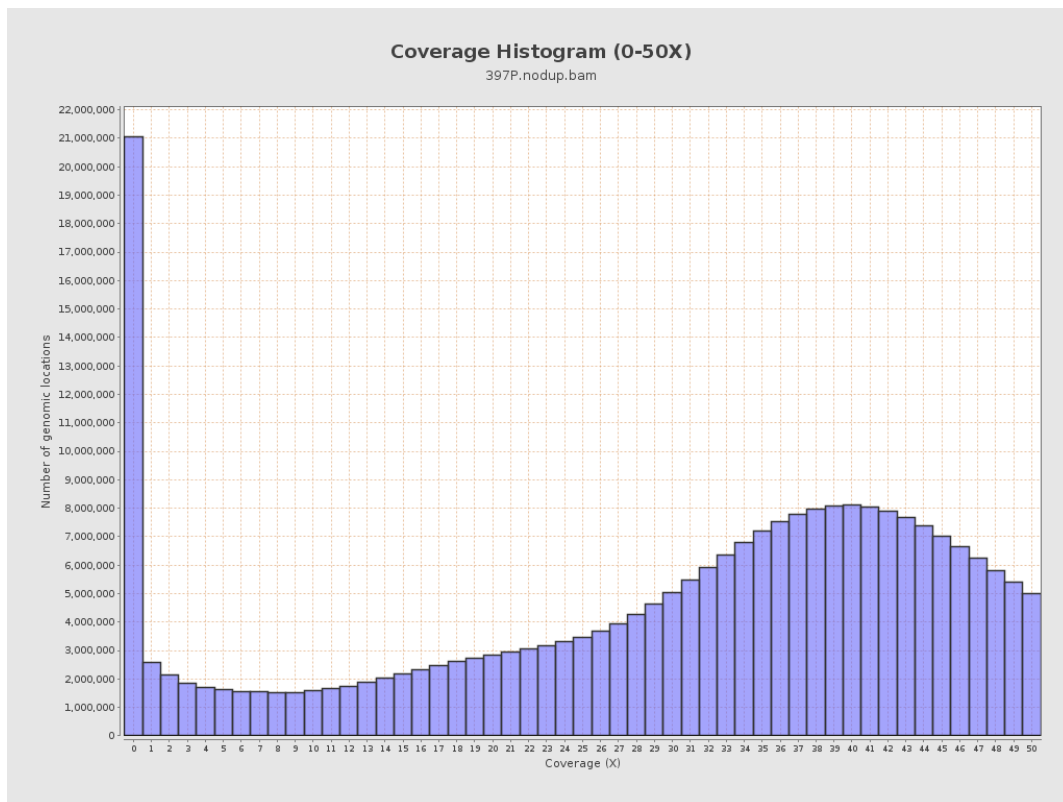
3. Results : Coverage across reference



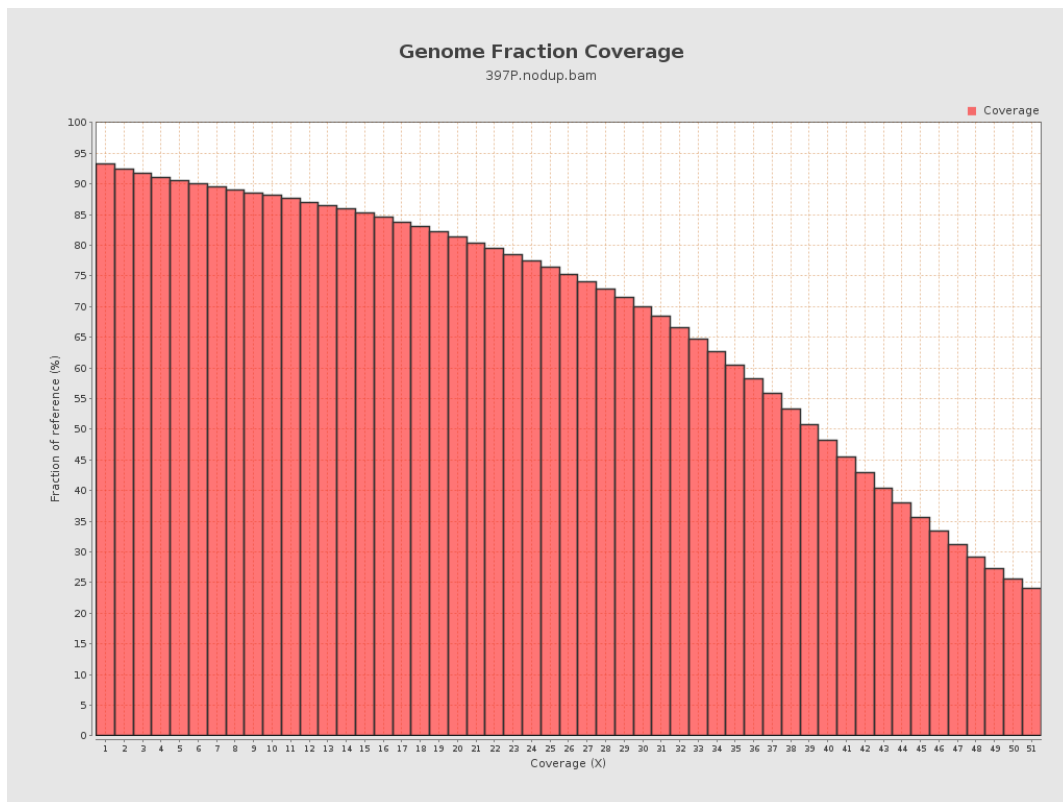
4. Results : Coverage Histogram



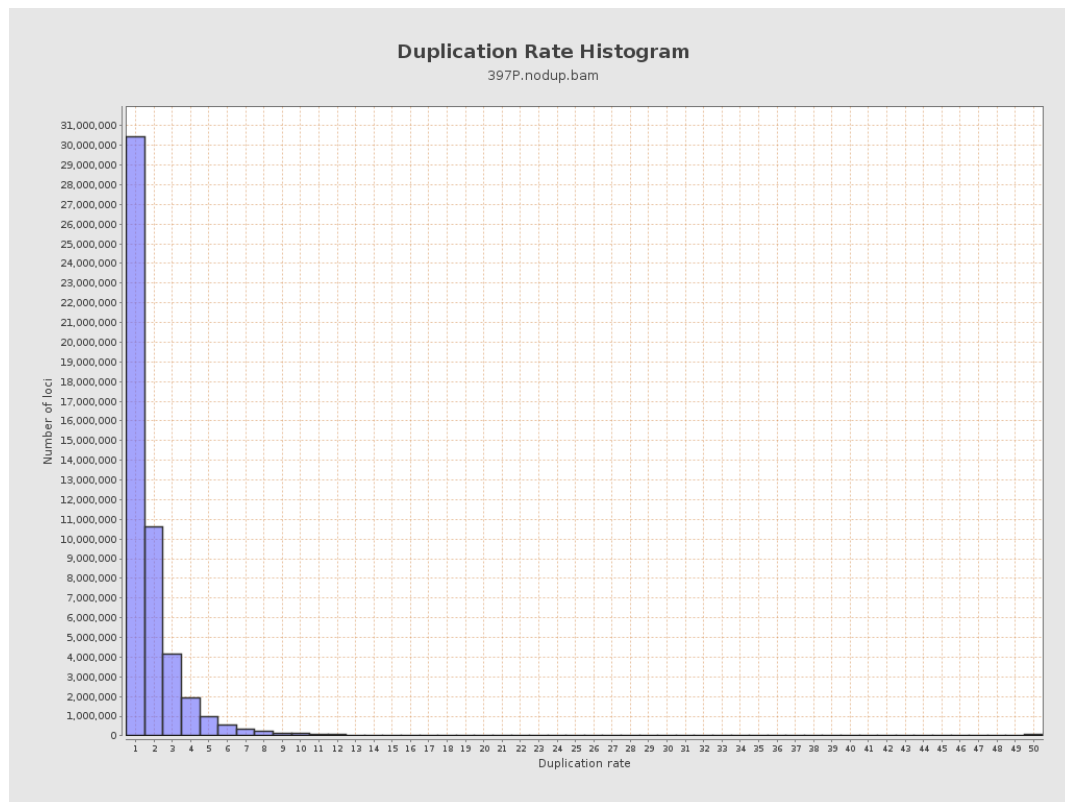
5. Results : Coverage Histogram (0-50X)



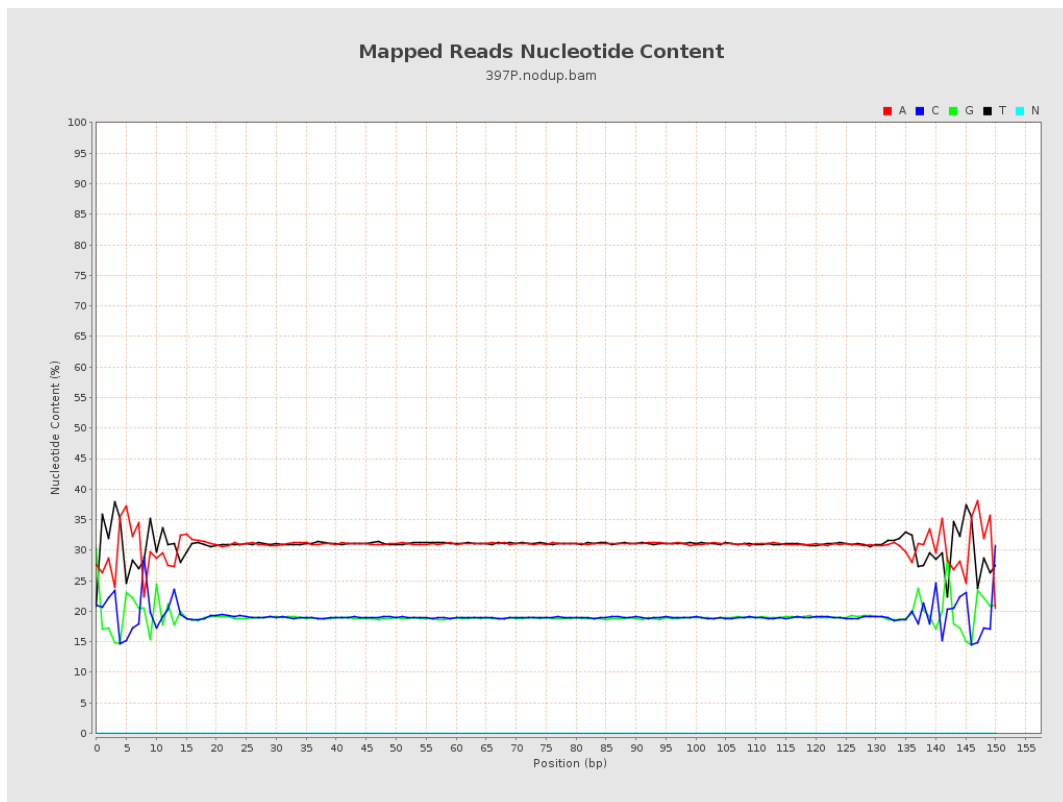
6. Results : Genome Fraction Coverage



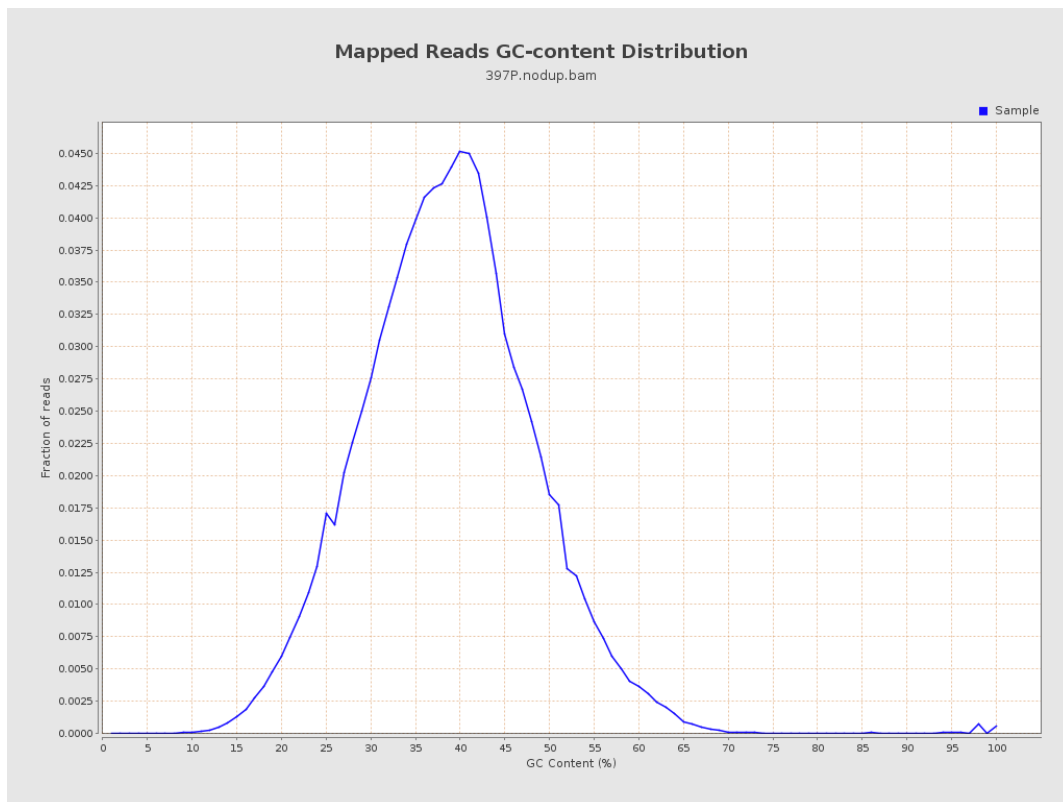
7. Results : Duplication Rate Histogram



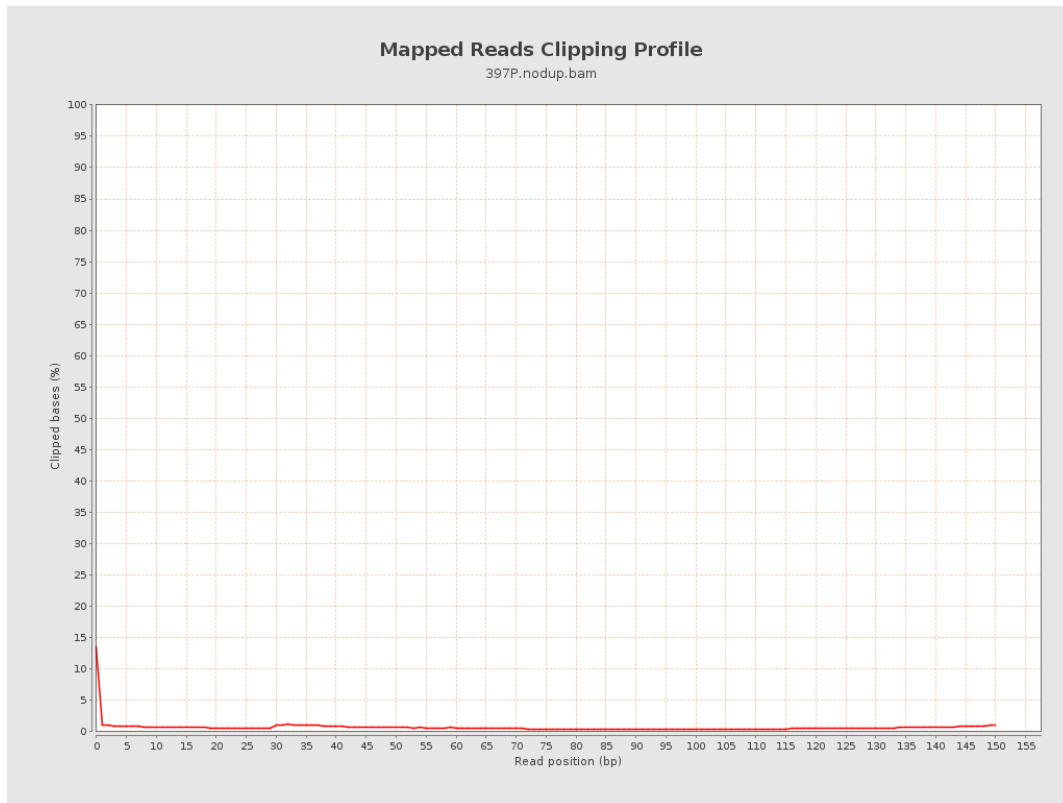
8. Results : Mapped Reads Nucleotide Content



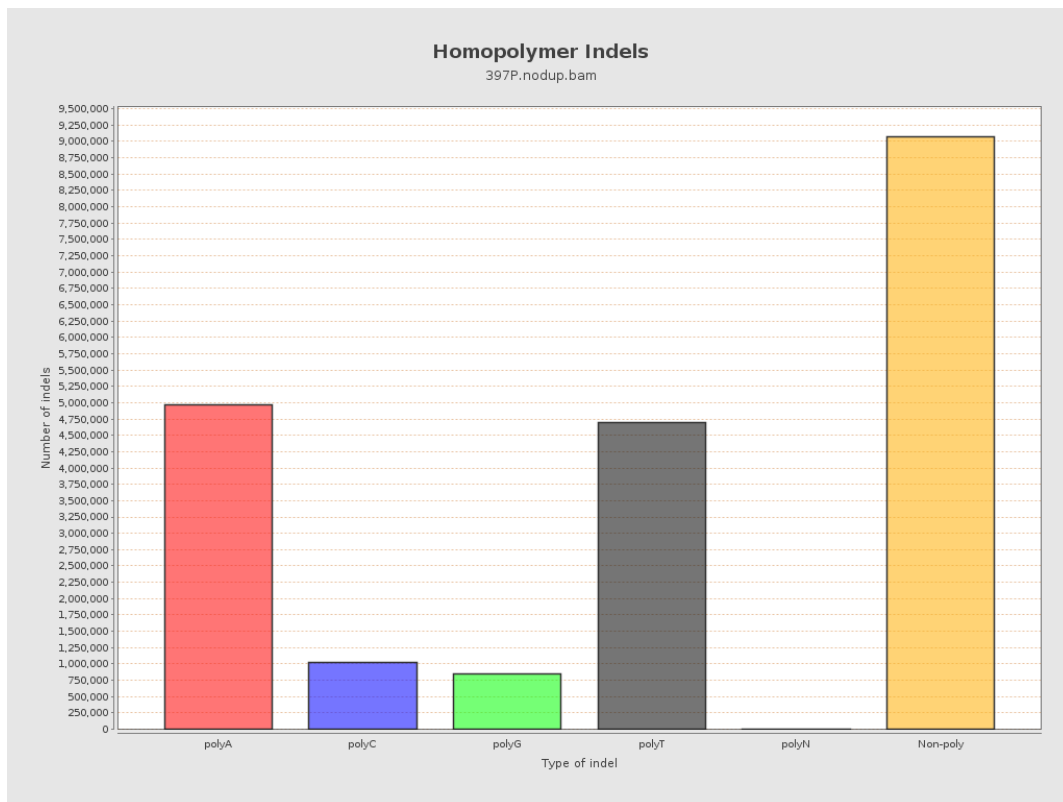
9. Results : Mapped Reads GC-content Distribution



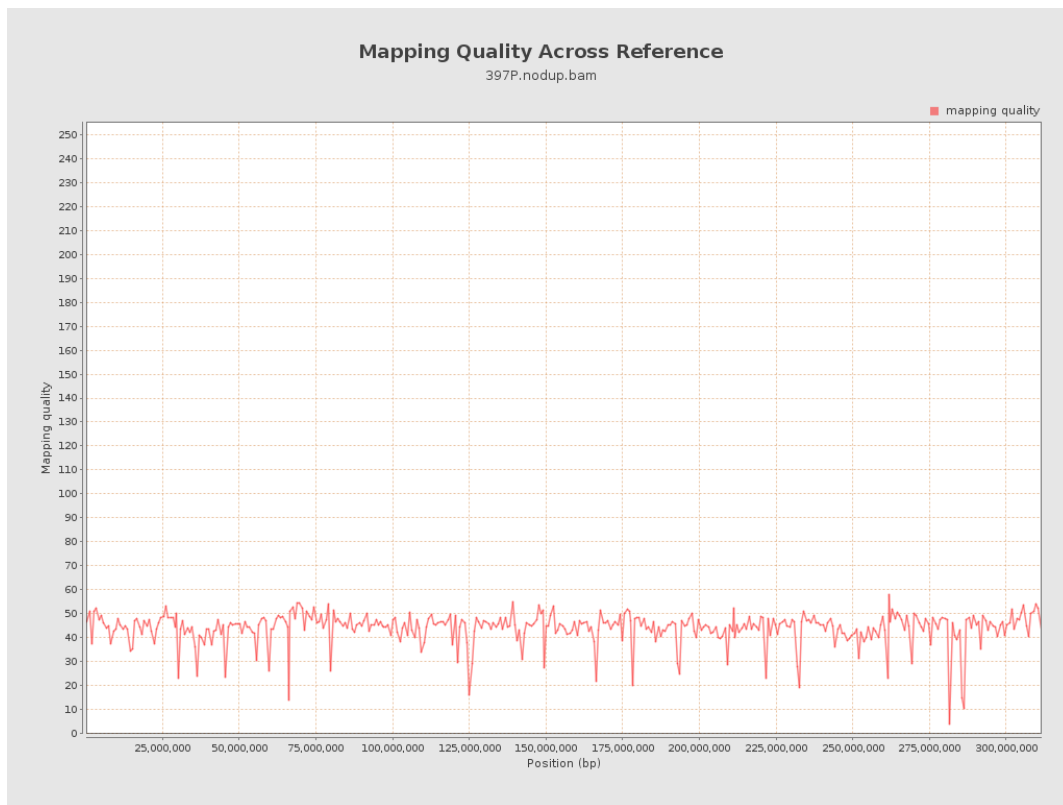
10. Results : Mapped Reads Clipping Profile



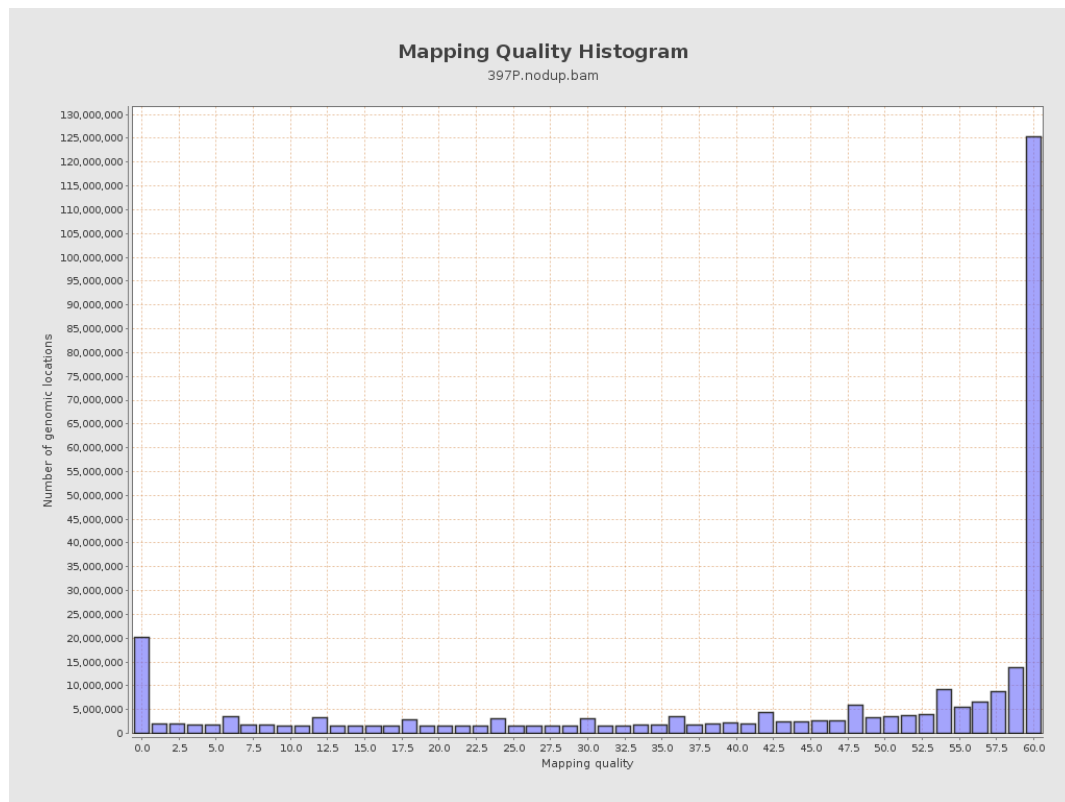
11. Results : Homopolymer Indels



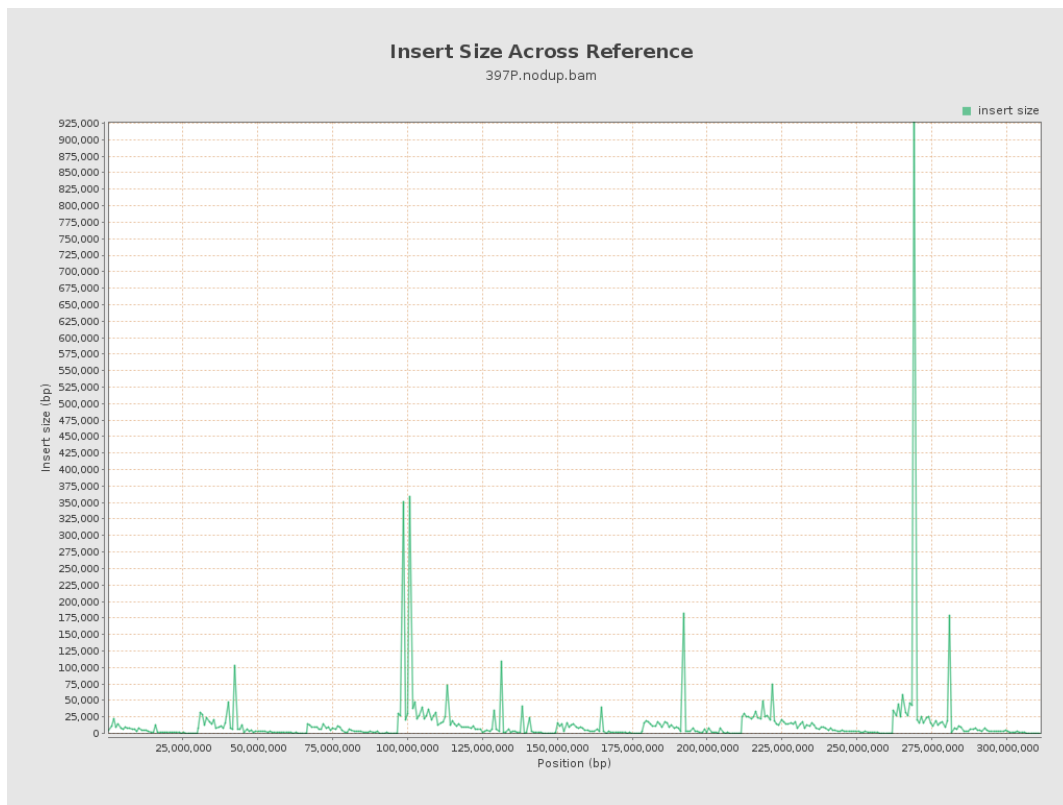
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

