

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:27:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/139
7
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1397 .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_273/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_273_S354_L003 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_273/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_273_S354_L003 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:27:15 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	55,043,936
Mapped reads	51,906,628 / 94.3%
Unmapped reads	3,137,308 / 5.7%
Mapped paired reads	51,906,628 / 94.3%
Mapped reads, first in pair	25,997,501 / 47.23%
Mapped reads, second in pair	25,909,127 / 47.07%
Mapped reads, both in pair	50,895,153 / 92.46%
Mapped reads, singletons	1,011,475 / 1.84%
Read min/max/mean length	30 / 151 / 147.99
Duplicated reads (flagged)	6,556,894 / 11.91%
Clipped reads	11,819,063 / 21.47%

2.2. ACGT Content

Number/percentage of A's	2,212,373,587 / 30.78%
Number/percentage of C's	1,380,906,284 / 19.21%
Number/percentage of T's	2,213,664,651 / 30.8%
Number/percentage of G's	1,381,096,987 / 19.21%
Number/percentage of N's	26,386 / 0%
GC Percentage	38.42%

2.3. Coverage

Mean	23.1268
Standard Deviation	178.4938

2.4. Mapping Quality

Mean Mapping Quality	43.58
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2.5. Insert size

Mean	242,078.9
Standard Deviation	2,326,375.9
P25/Median/P75	331 / 434 / 566

2.6. Mismatches and indels

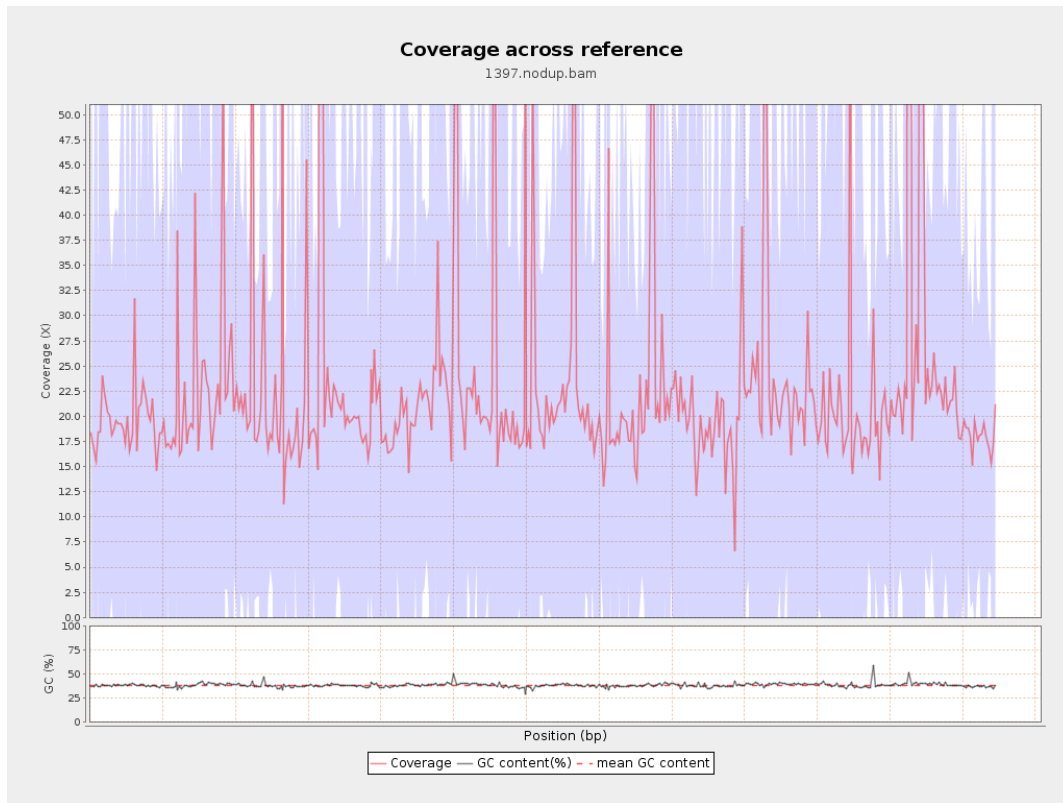
General error rate	2.34%
Mismatches	154,649,449
Insertions	4,836,191
Mapped reads with at least one insertion	8.37%
Deletions	5,043,270
Mapped reads with at least one deletion	8.62%
Homopolymer indels	56.05%

2.7. Chromosome stats

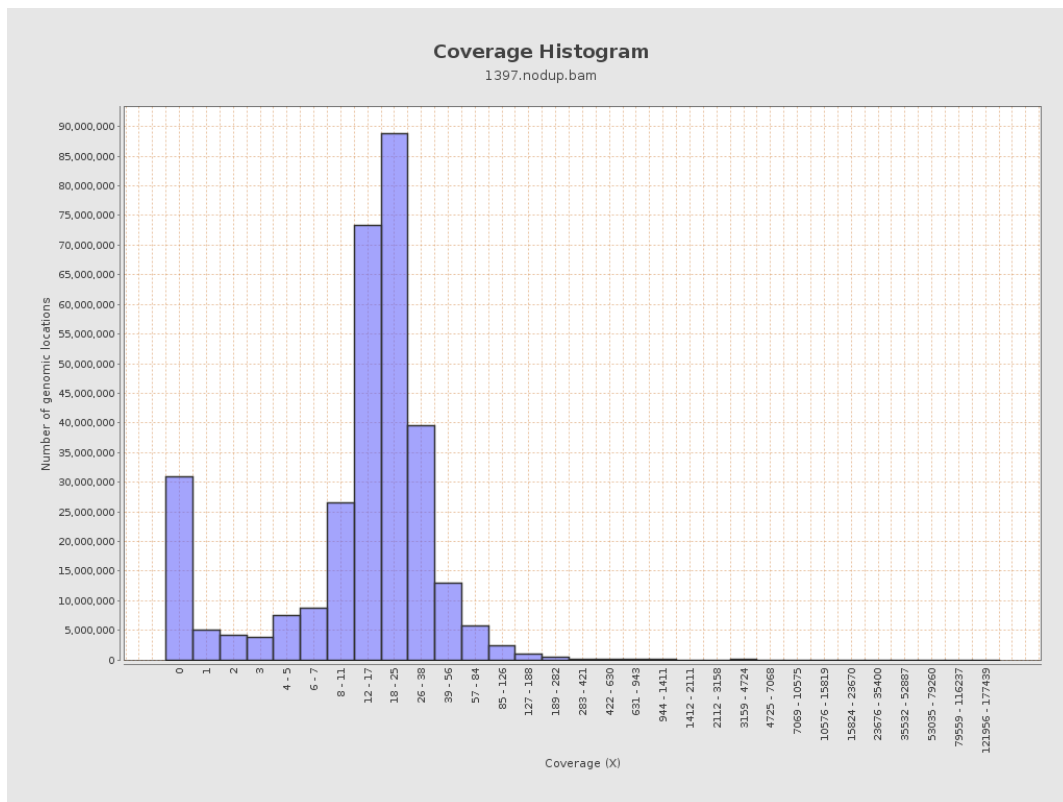
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	572962168	19.2759	66.3795

LT669789.1	36598175	868426941	23.7287	187.9168
LT669790.1	30422129	724918555	23.8287	158.7315
LT669791.1	52758100	1188588563	22.529	167.1918
LT669792.1	28376109	640754444	22.5808	175.1248
LT669793.1	33388210	733438573	21.967	125.7648
LT669794.1	50579949	1143974123	22.6171	169.3741
LT669795.1	49795044	1334215622	26.7941	261.8309

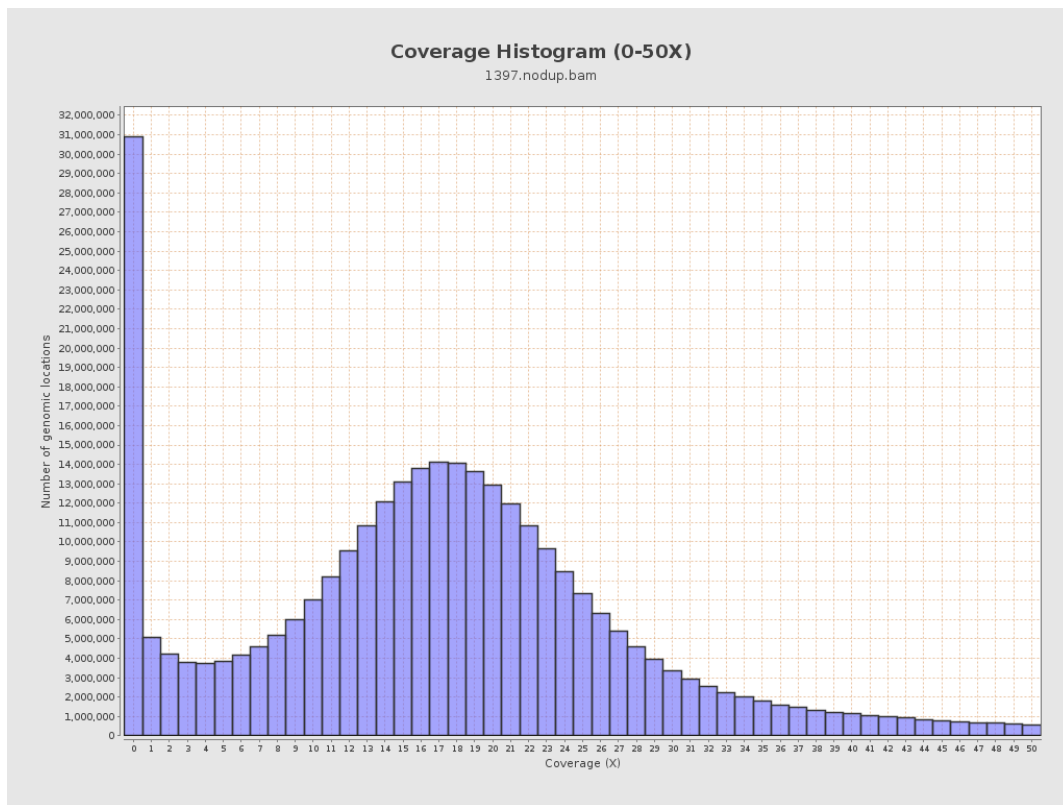
3. Results : Coverage across reference



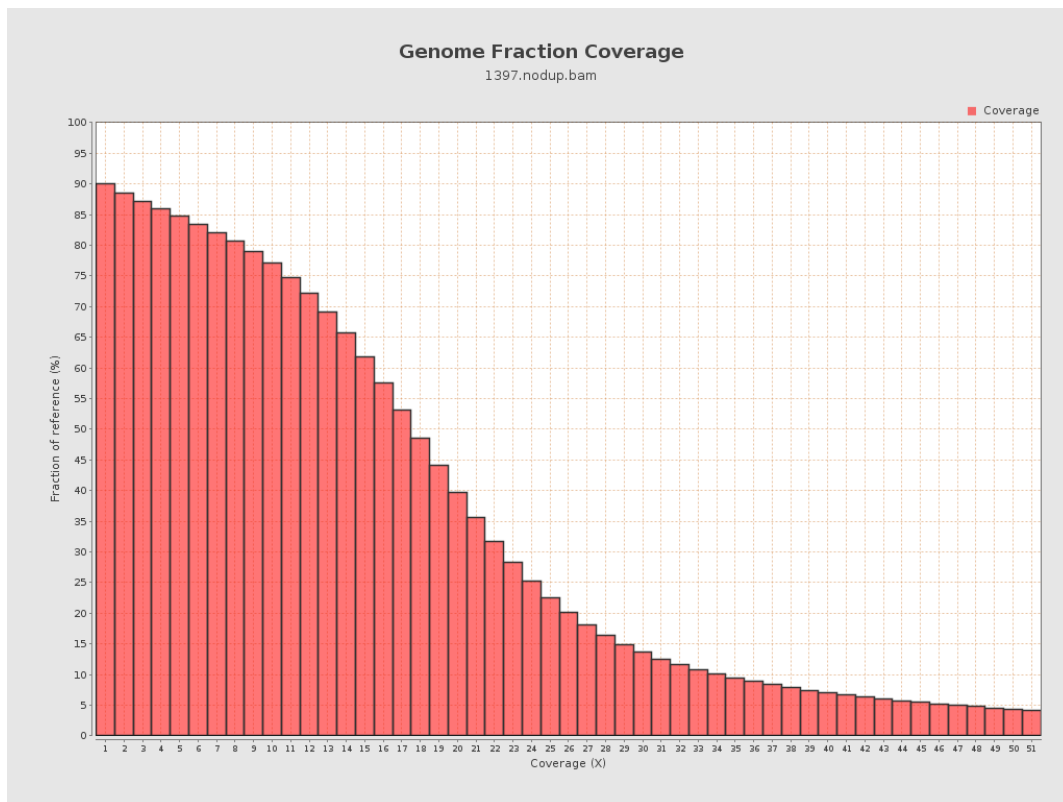
4. Results : Coverage Histogram



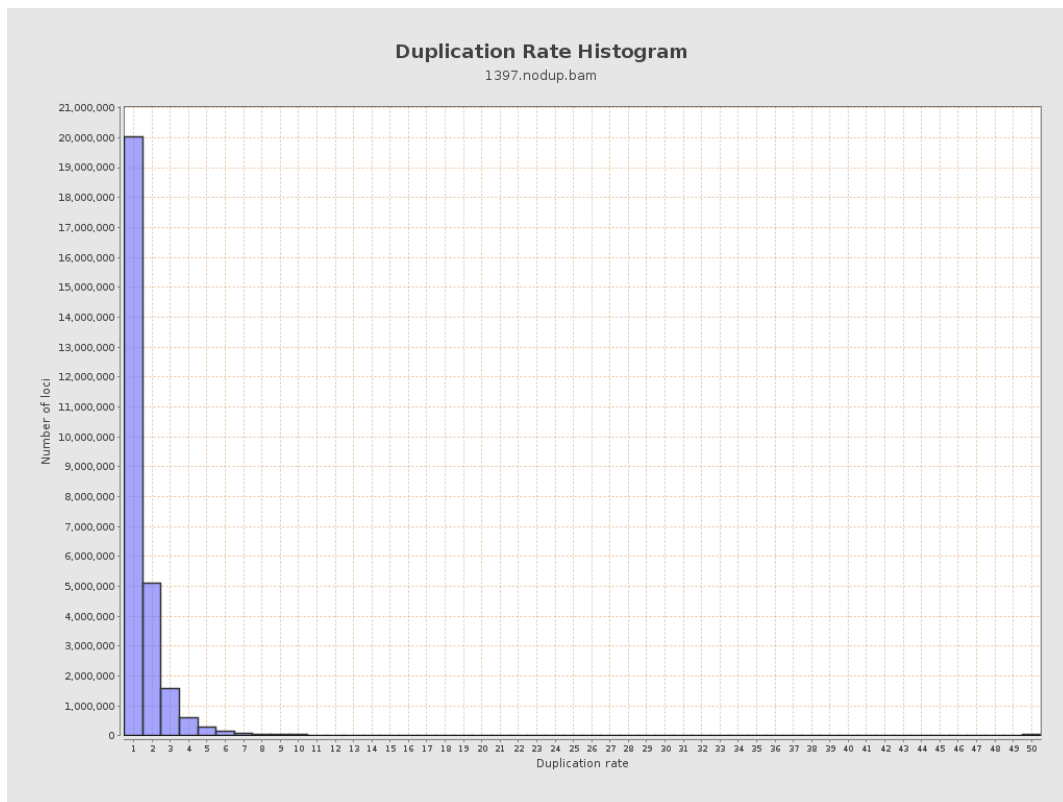
5. Results : Coverage Histogram (0-50X)



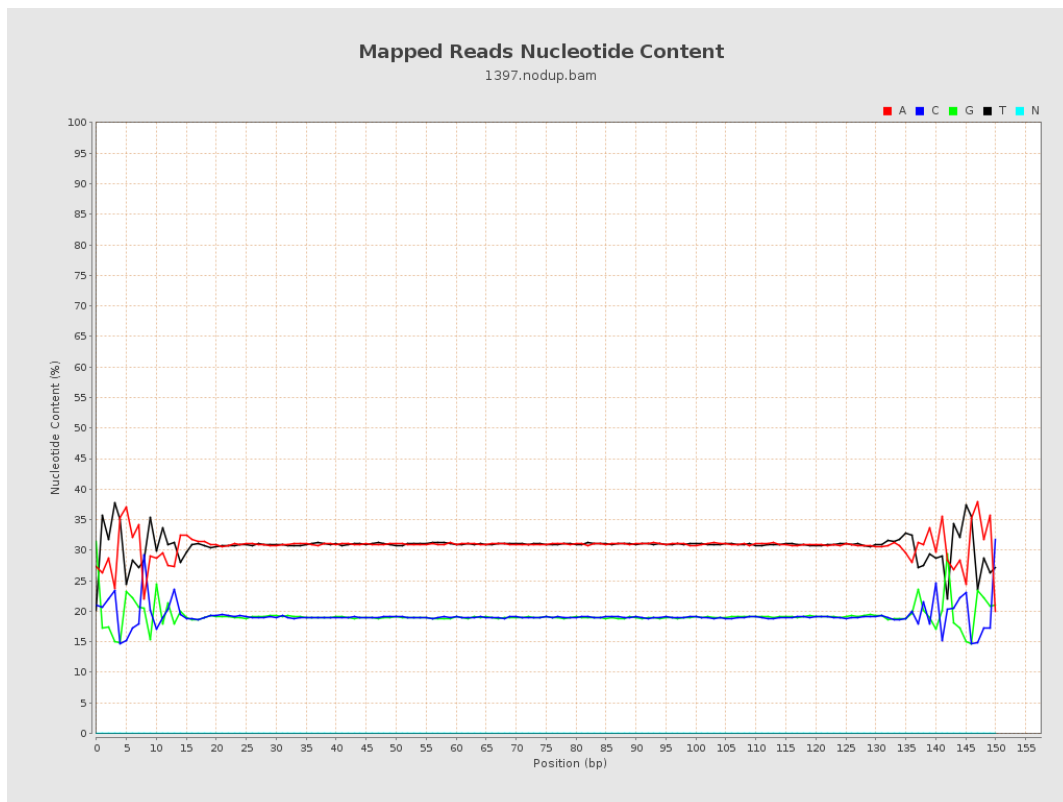
6. Results : Genome Fraction Coverage



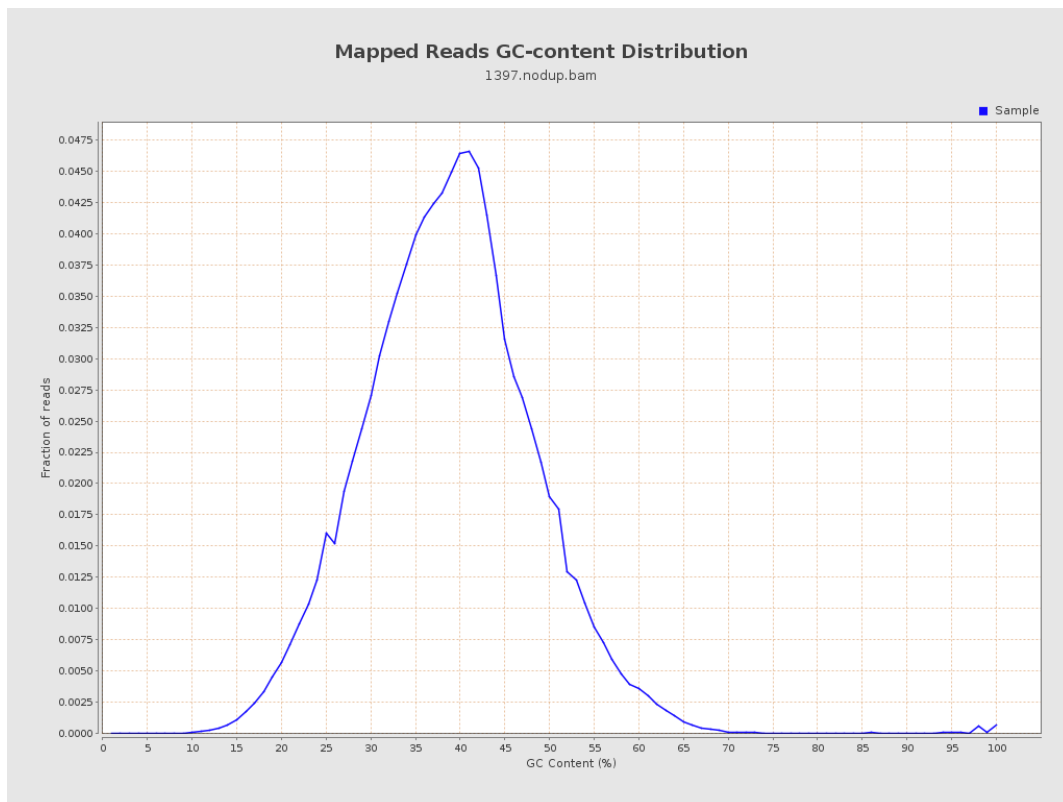
7. Results : Duplication Rate Histogram



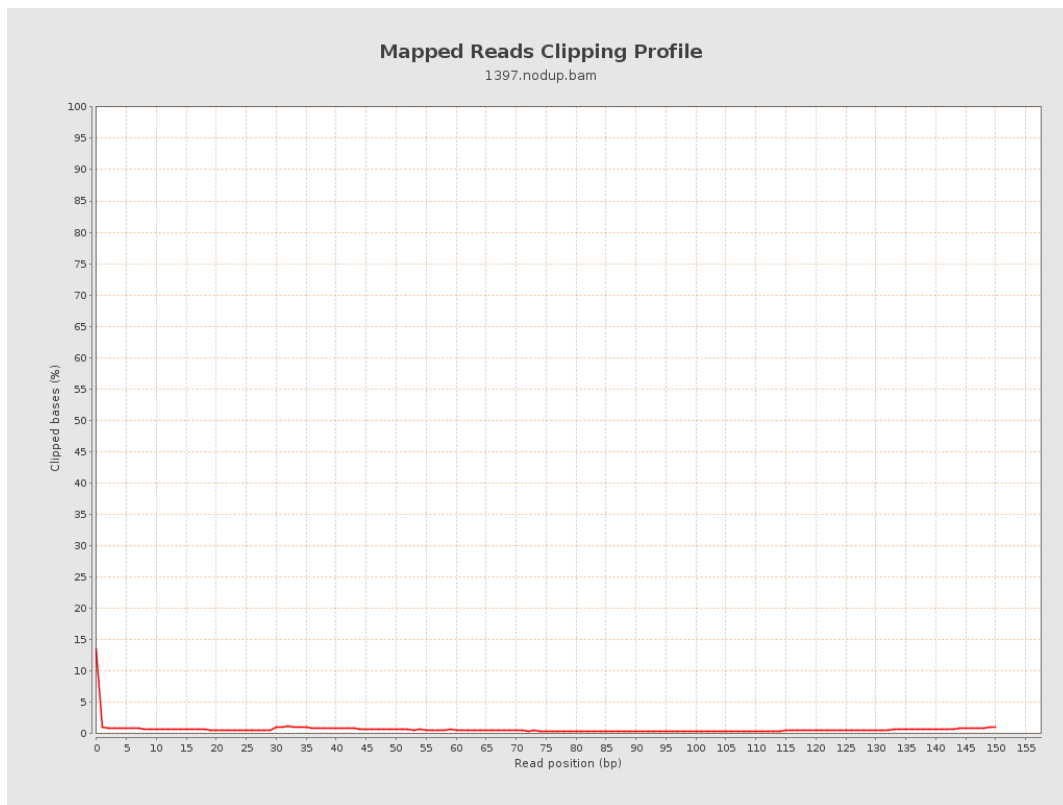
8. Results : Mapped Reads Nucleotide Content



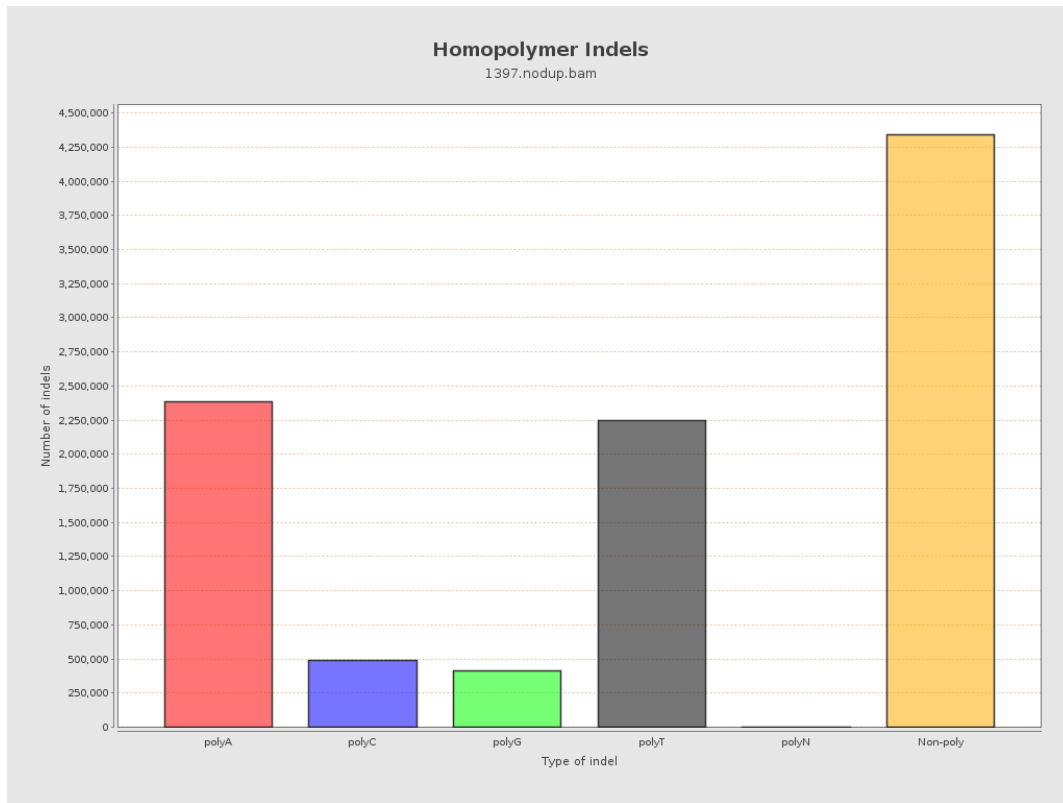
9. Results : Mapped Reads GC-content Distribution



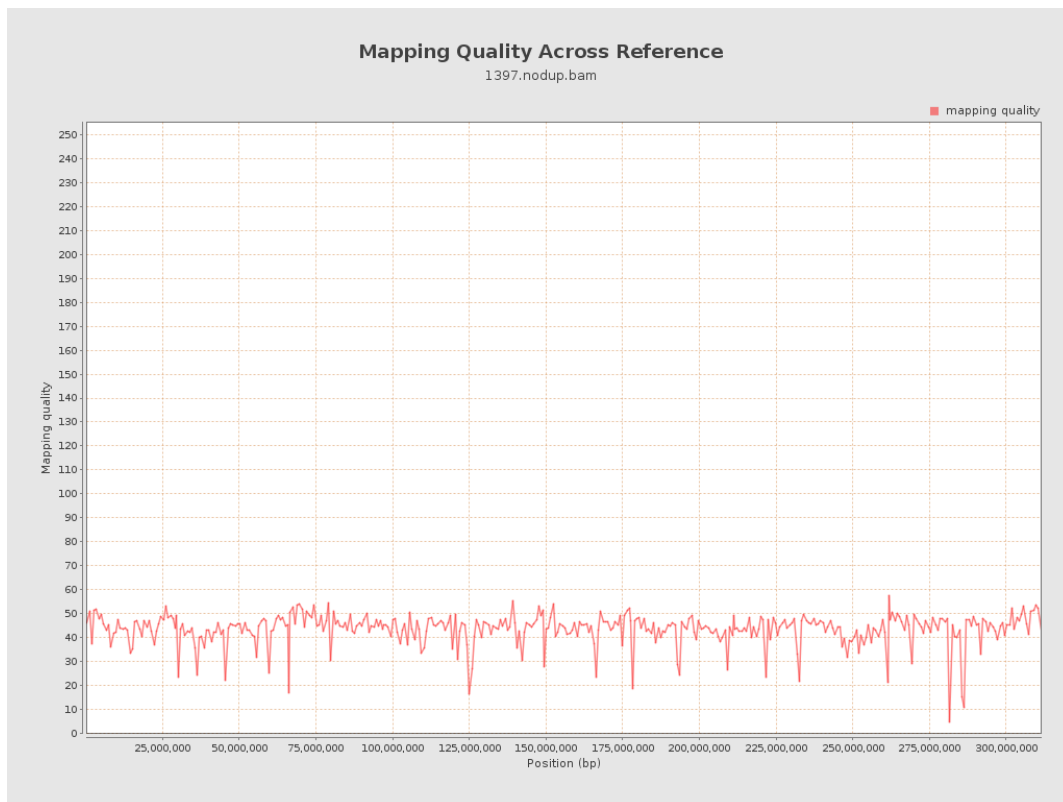
10. Results : Mapped Reads Clipping Profile



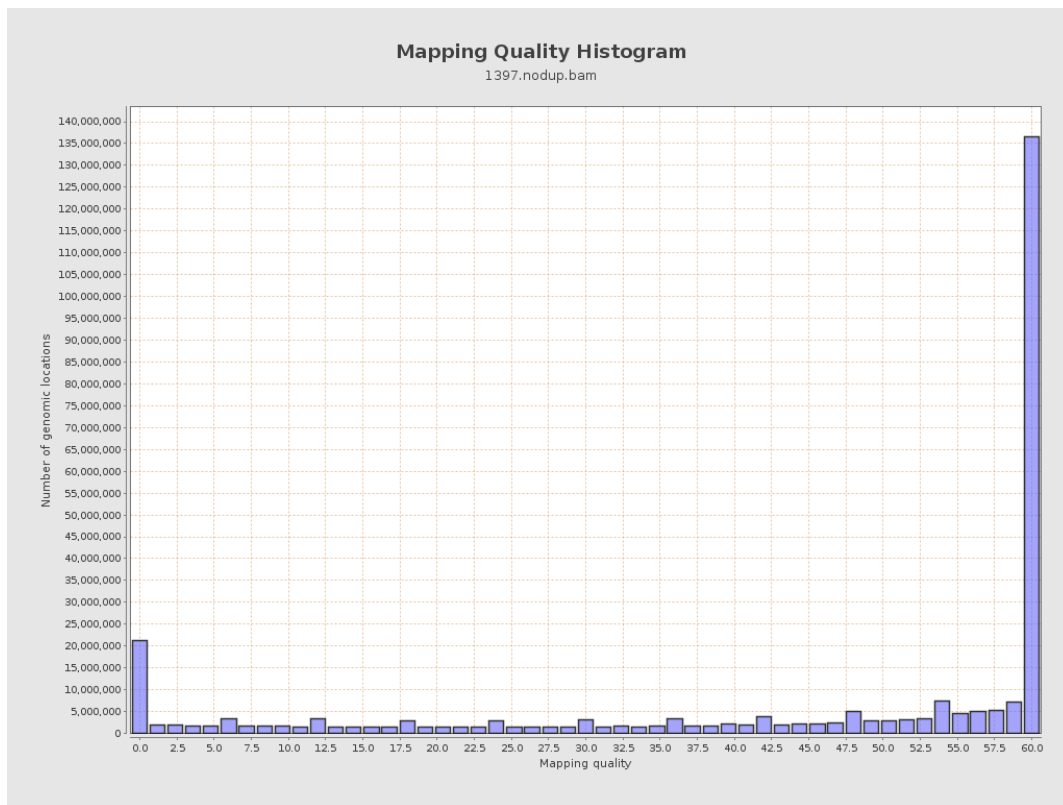
11. Results : Homopolymer Indels



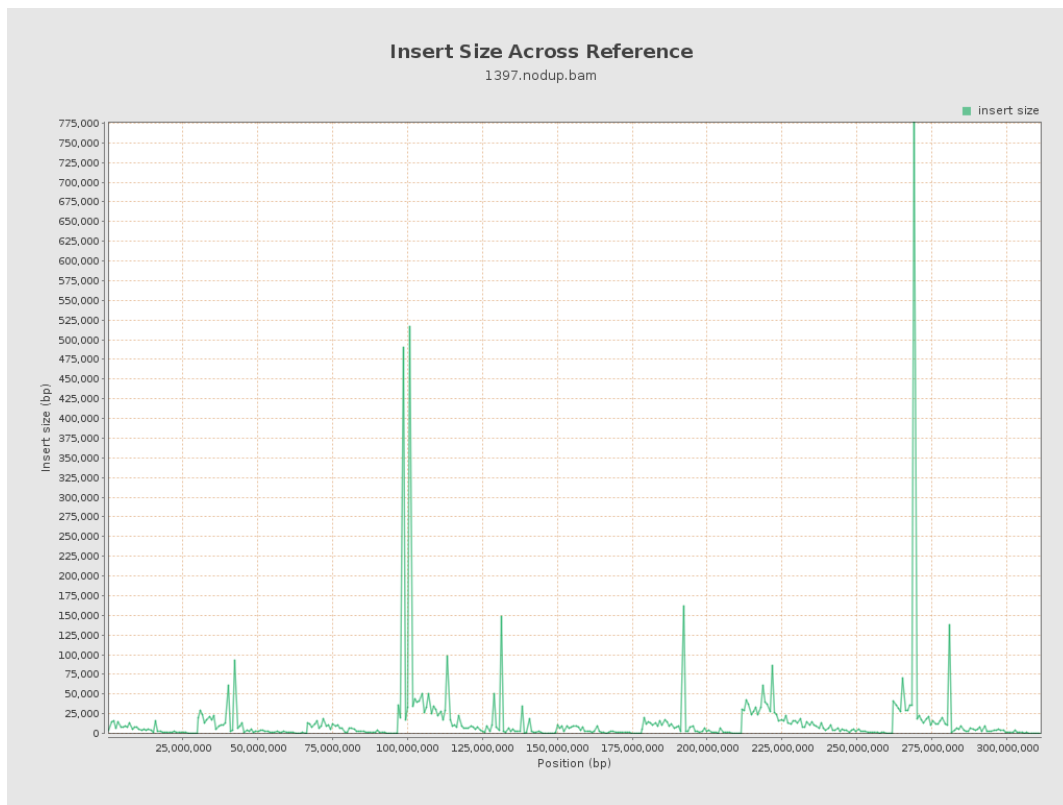
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

