Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:28:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1447
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1447 .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_102/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_102_S192_L002 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_102/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_102_S192_L002 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:28:21 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	61,794,974
Mapped reads	57,269,694 / 92.68%
Unmapped reads	4,525,280 / 7.32%
Mapped paired reads	57,269,694 / 92.68%
Mapped reads, first in pair	28,687,788 / 46.42%
Mapped reads, second in pair	28,581,906 / 46.25%
Mapped reads, both in pair	56,157,403 / 90.88%
Mapped reads, singletons	1,112,291 / 1.8%
Read min/max/mean length	30 / 151 / 148.34
Duplicated reads (flagged)	8,827,392 / 14.28%
Clipped reads	11,973,762 / 19.38%

2.2. ACGT Content

Number/percentage of A's	2,472,078,274 / 30.94%
Number/percentage of C's	1,525,013,116 / 19.08%
Number/percentage of T's	2,474,319,345 / 30.96%
Number/percentage of G's	1,519,411,617 / 19.01%
Number/percentage of N's	34,058 / 0%
GC Percentage	38.1%

2.3. Coverage

Mean	25.7067
Standard Deviation	179.7609

2.4. Mapping Quality

Mean Mapping Quality	44.62

2.5. Insert size

Mean	216,671.1
Standard Deviation	2,216,616.73
P25/Median/P75	317 / 413 / 540

2.6. Mismatches and indels

General error rate	2.2%
Mismatches	161,097,891
Insertions	5,228,006
Mapped reads with at least one insertion	8.2%
Deletions	5,365,046
Mapped reads with at least one deletion	8.31%
Homopolymer indels	57.02%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	650107448	21.8712	51.177

LT669789.1	36598175	918124996	25.0866	177.1985
LT669790.1	30422129	841490748	27.6605	185.8108
LT669791.1	52758100	1346594067	25.5239	151.5564
LT669792.1	28376109	725990472	25.5846	204.8074
LT669793.1	33388210	784178072	23.4867	93.287
LT669794.1	50579949	1215424738	24.0298	147.6648
LT669795.1	49795044	1529386012	30.7136	283.2607

3. Results : Coverage across reference

Coverage across reference
1447.nodup.bam

4. Results : Coverage Histogram

Coverage Histogram
1447.nodup.bam
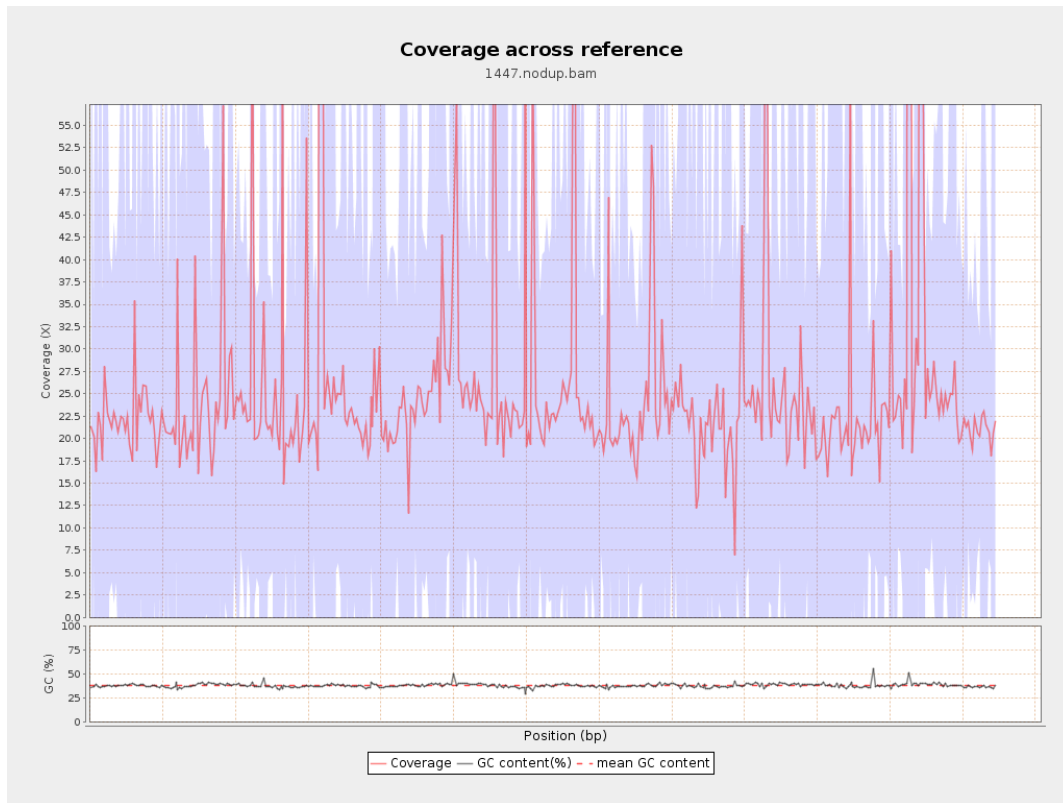
5. Results : Coverage Histogram (0-50X)
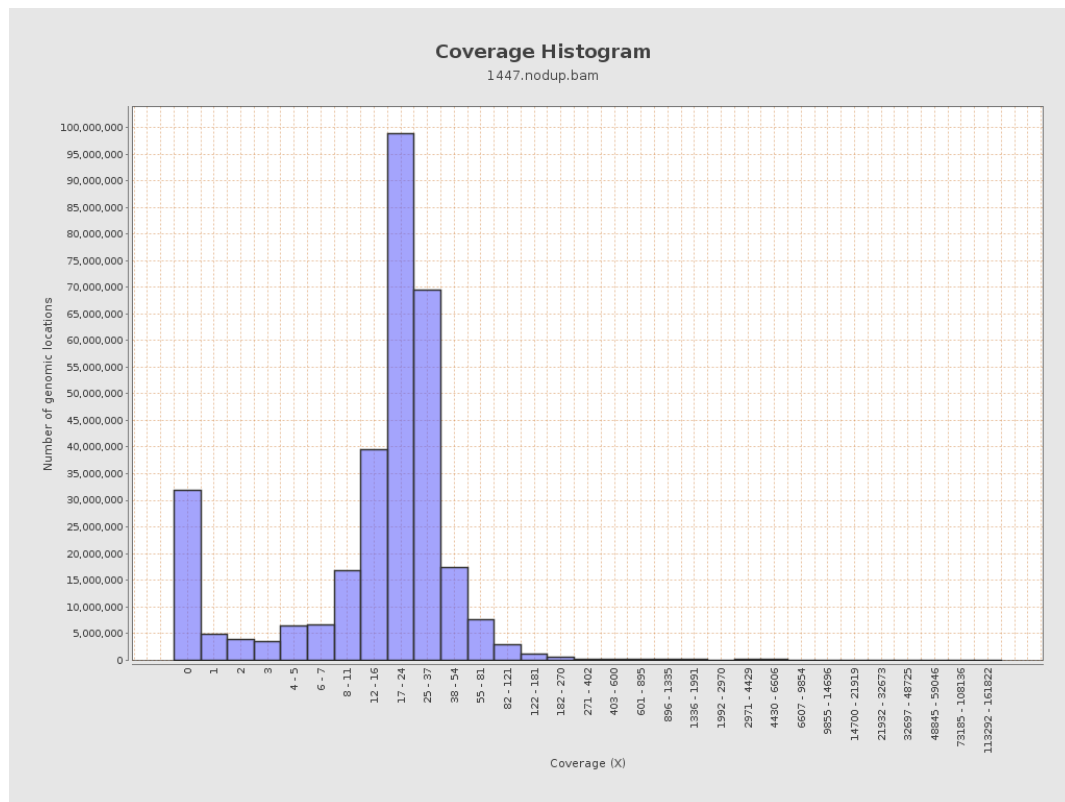
Coverage Histogram (0-50X)
1447.nodup.bam
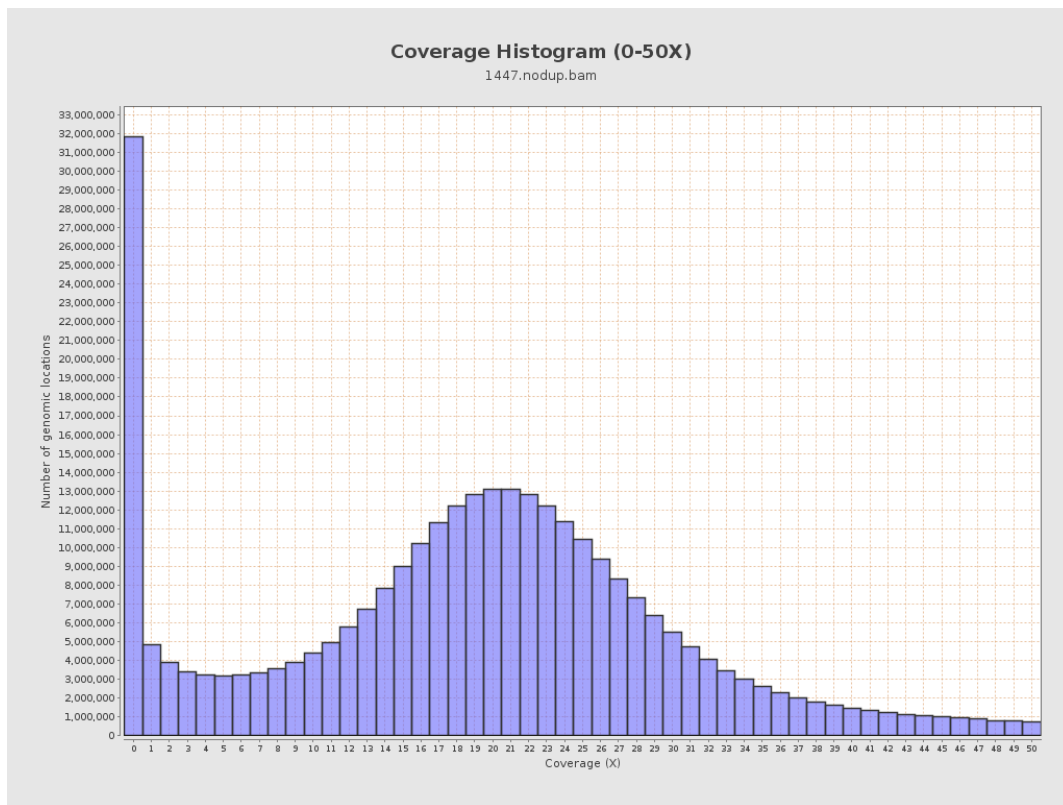
6. Results : Genome Fraction Coverage
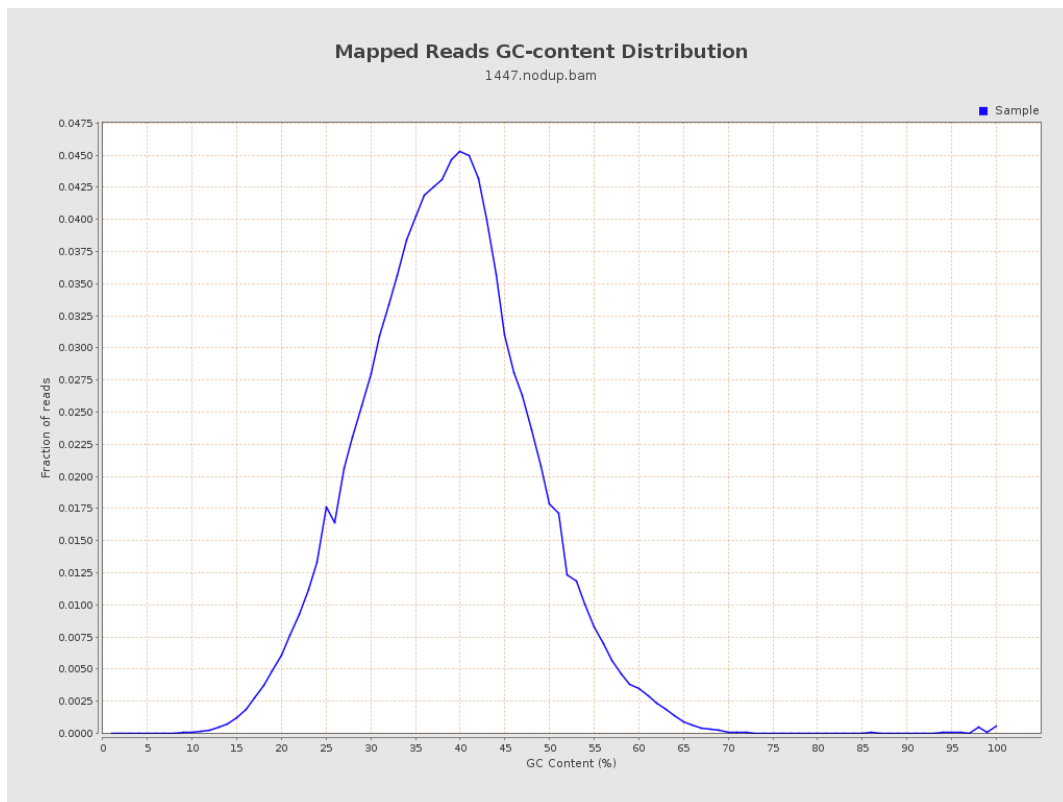

Genome Fraction Coverage
1447.nodup.bam
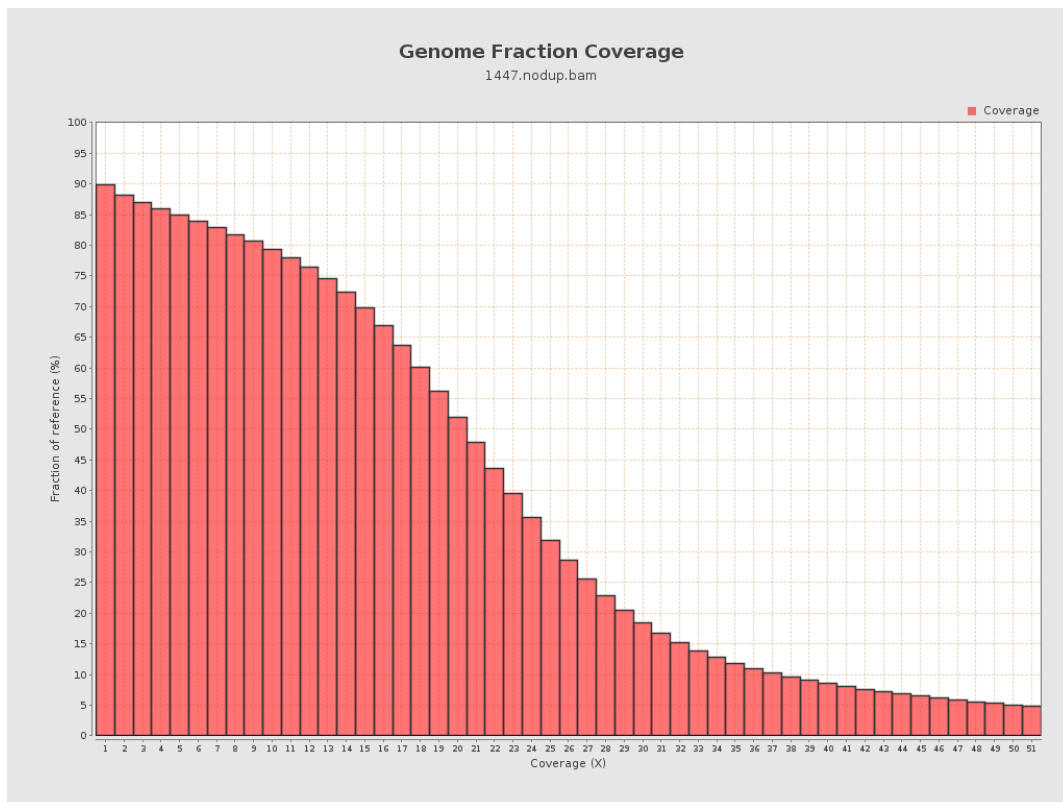
7. Results : Duplication Rate Histogram
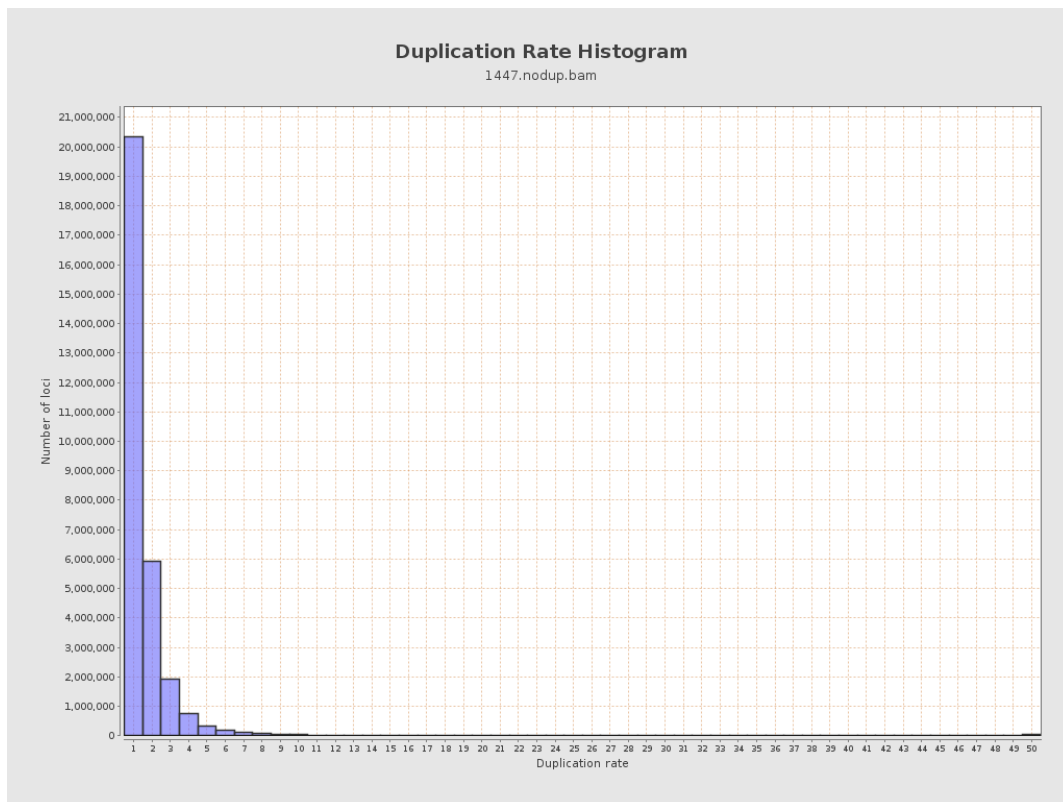
8. Results : Mapped Reads Nucleotide Content

9. Results : Mapped Reads GC-content Distribution
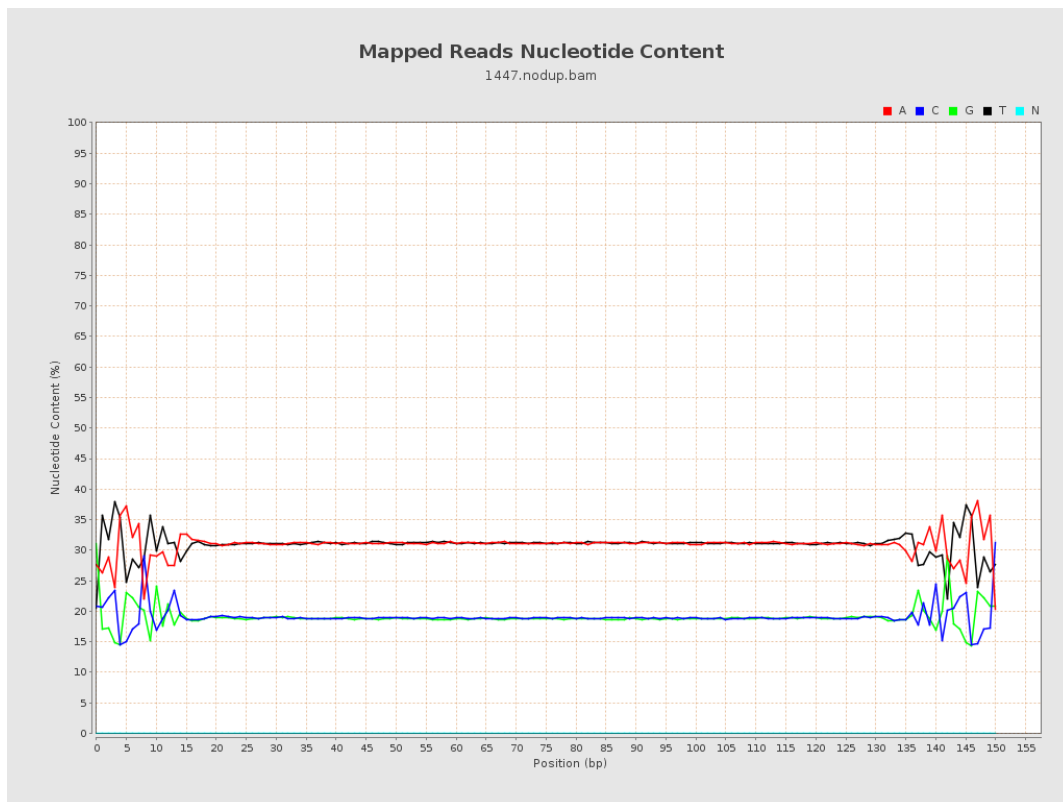
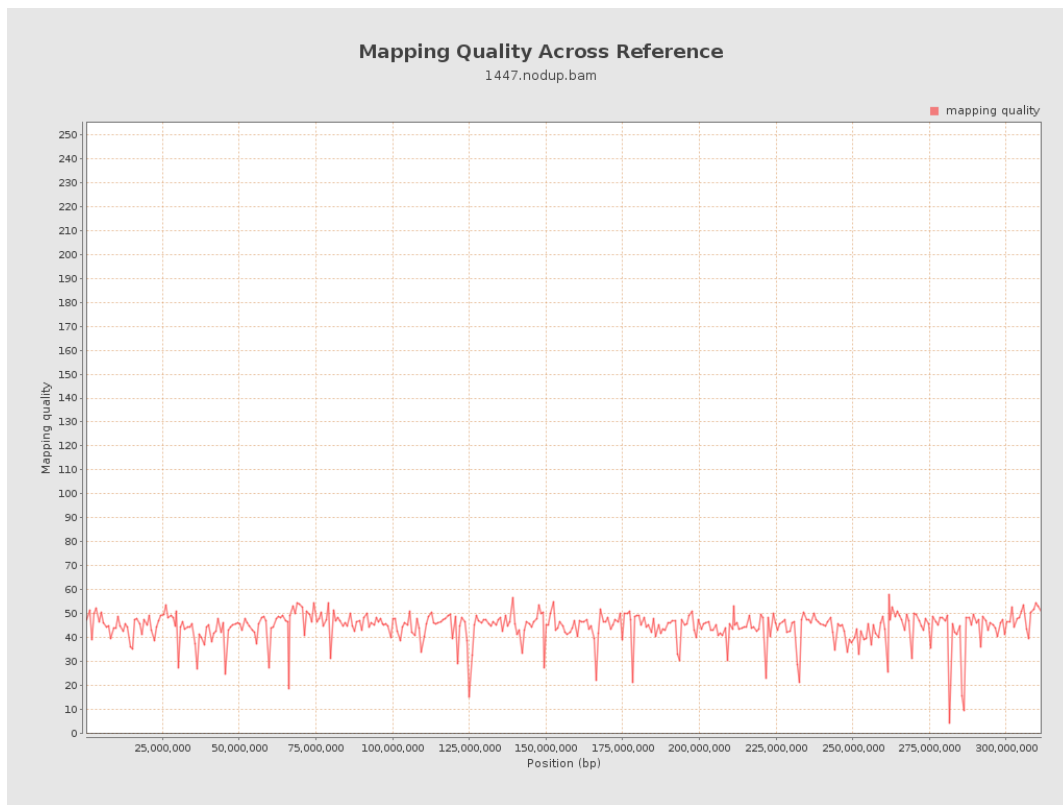Mapped Reads GC-content Distribution
1447.nodup.bam

10. Results : Mapped Reads Clipping Profile
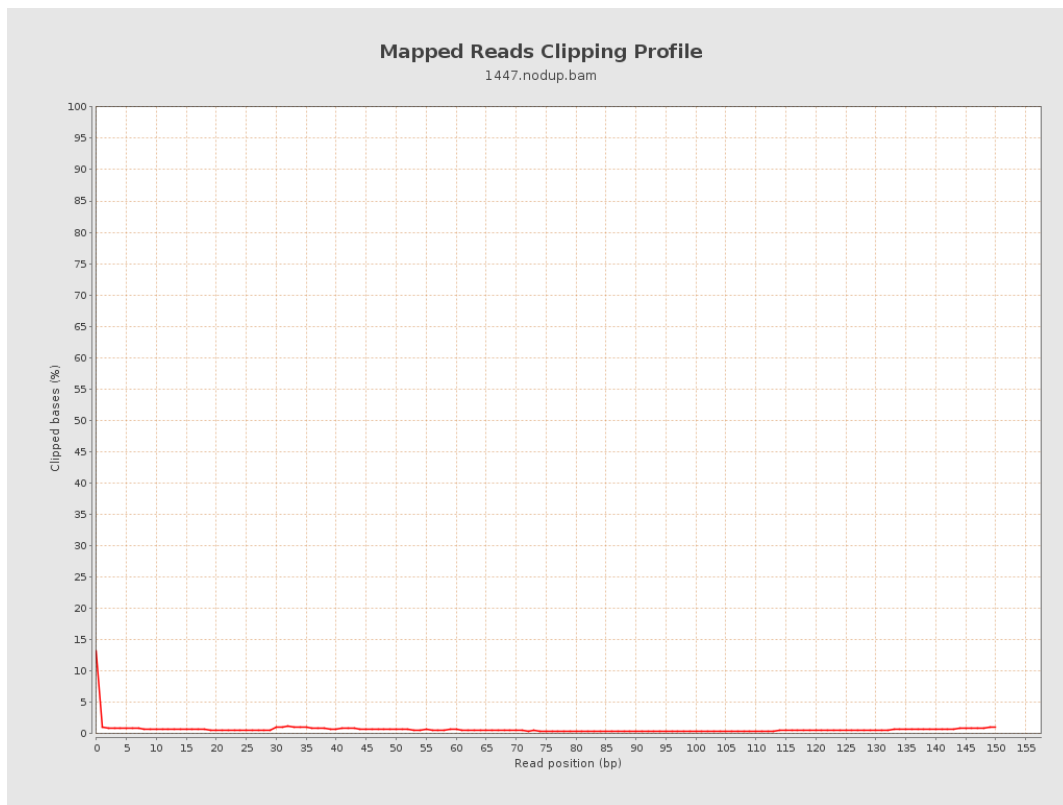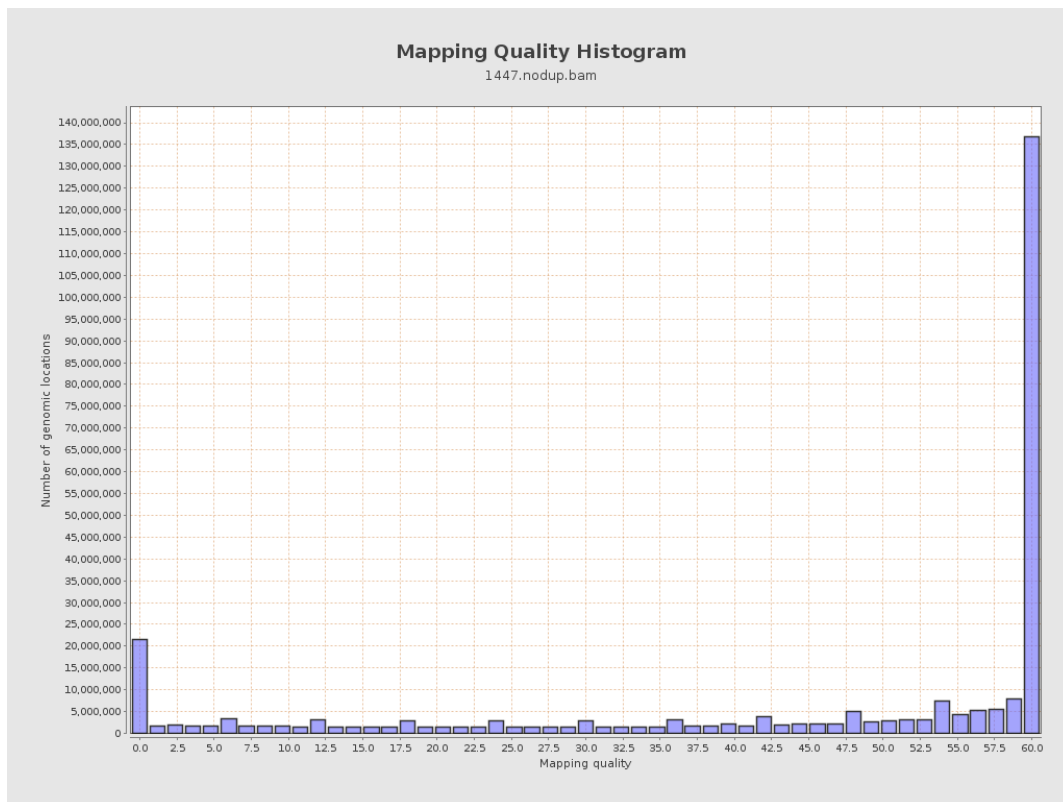
11. Results : Homopolymer Indels
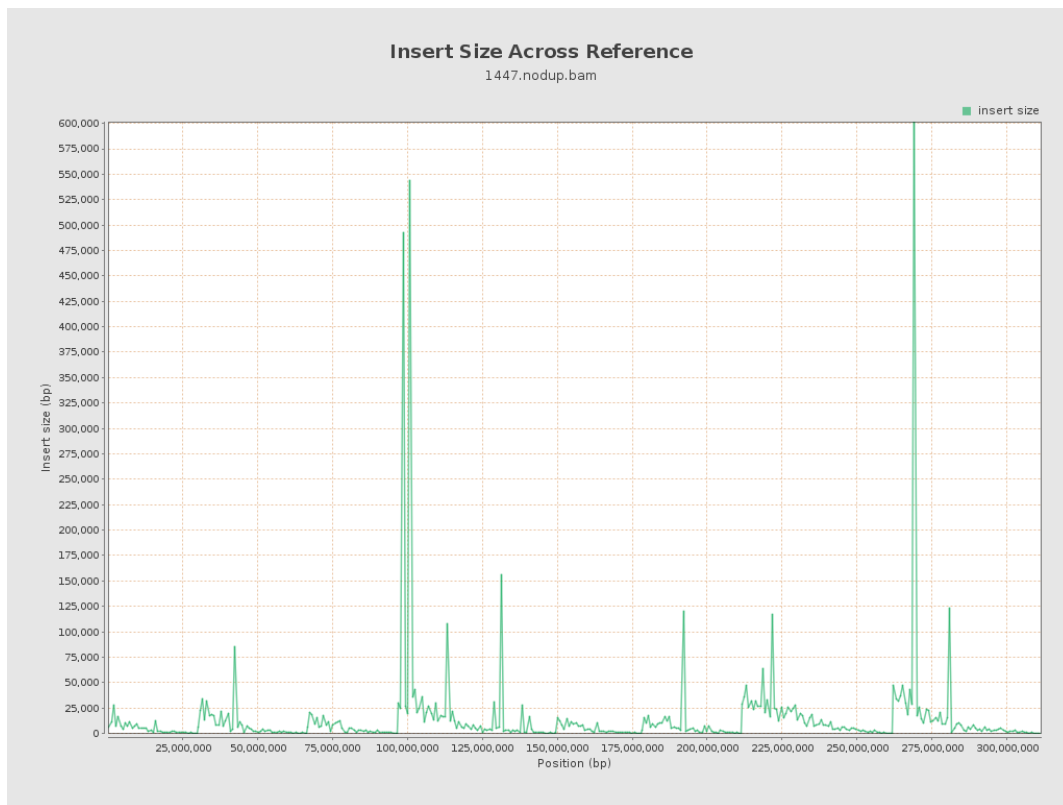

Homopolymer Indels
1447.nodup.bam
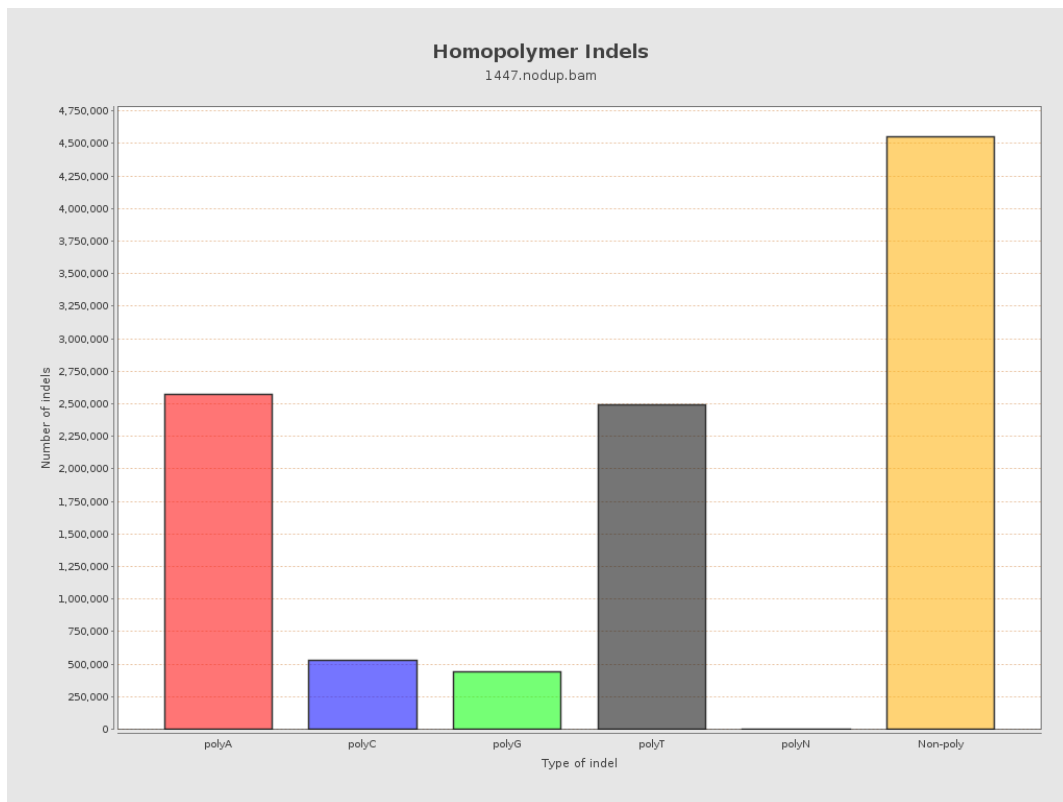
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram