Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:25:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1156
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1156 .nodup.bam
Program:	bwa (0.7.17-r1188)
Analyze overlapping paired-end reads:	no
Command line:	bwa mem -M -t 8 -R @RG\tID:$unit\tPL:Illumina\tLB:LibA\tSM:$sample /proj/uppstore2018210/Aalpina/data/reference/GCA_900128785.1_MPIPZ.v5_genomic.fa /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_442/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_442_S417_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_442/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_442_S417_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:25:24 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	46,836,314
Mapped reads	44,153,085 / 94.27%
Unmapped reads	2,683,229 / 5.73%
Mapped paired reads	44,153,085 / 94.27%
Mapped reads, first in pair	22,131,088 / 47.25%
Mapped reads, second in pair	22,021,997 / 47.02%
Mapped reads, both in pair	43,185,619 / 92.21%
Mapped reads, singletons	967,466 / 2.07%
Read min/max/mean length	30 / 151 / 148.02
Duplicated reads (flagged)	6,126,761 / 13.08%
Clipped reads	9,910,069 / 21.16%

2.2. ACGT Content

Number/percentage of A's	1,892,993,391 / 30.93%
Number/percentage of C's	1,166,681,102 / 19.07%
Number/percentage of T's	1,893,914,331 / 30.95%
Number/percentage of G's	1,165,814,504 / 19.05%
Number/percentage of N's	20,867 / 0%
GC Percentage	38.12%

2.3. Coverage

Mean	19.6888
Standard Deviation	151.4683

2.4. Mapping Quality

Mean Mapping Quality	43.85

2.5. Insert size

Mean	263,375.53
Standard Deviation	2,437,171.05
P25/Median/P75	397 / 515 / 654

2.6. Mismatches and indels

General error rate	2.33%
Mismatches	130,869,494
Insertions	4,170,800
Mapped reads with at least one insertion	8.48%
Deletions	4,308,834
Mapped reads with at least one deletion	8.68%
Homopolymer indels	56.6%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	484889837	16.3129	45.0693

LT669789.1	36598175	739142635	20.1962	154.989
LT669790.1	30422129	636655756	20.9274	157.0363
LT669791.1	52758100	1022006202	19.3716	129.5987
LT669792.1	28376109	554774952	19.5508	170.6812
LT669793.1	33388210	620281603	18.5779	111.3998
LT669794.1	50579949	964809474	19.0749	141.8965
LT669795.1	49795044	1113294173	22.3575	215.5612

3. Results : Coverage across reference

Coverage across reference
1156.nodup.bam
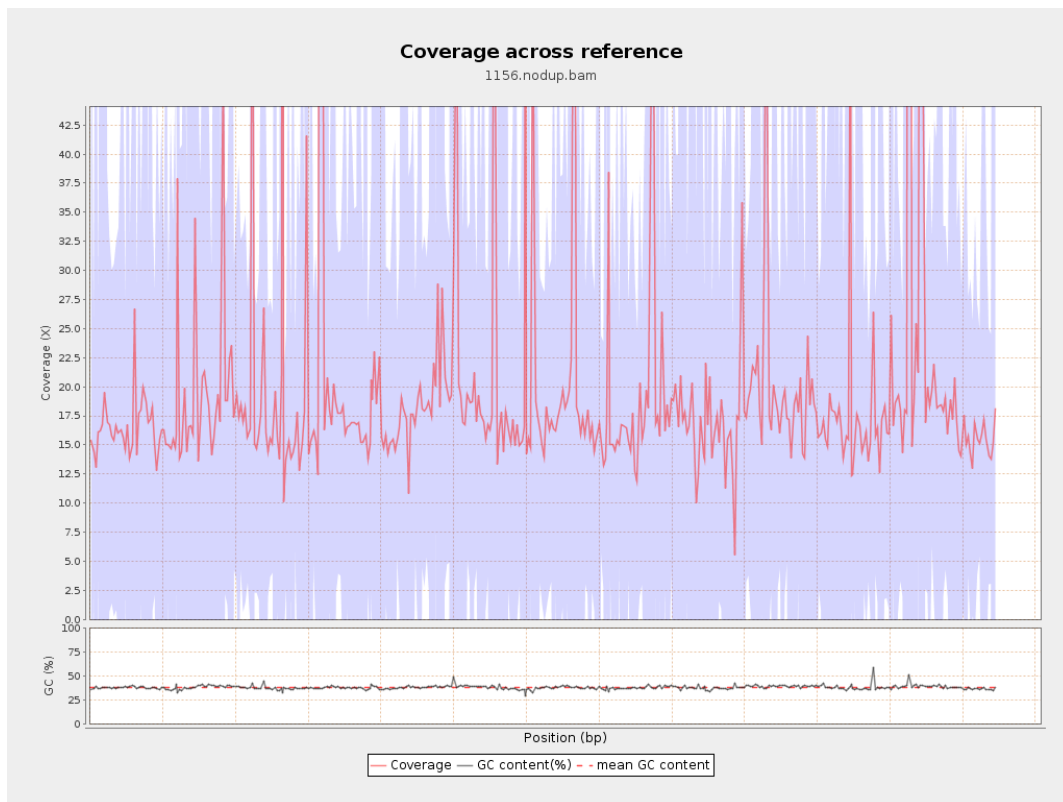
4. Results : Coverage Histogram

5. Results : Coverage Histogram (0-50X)
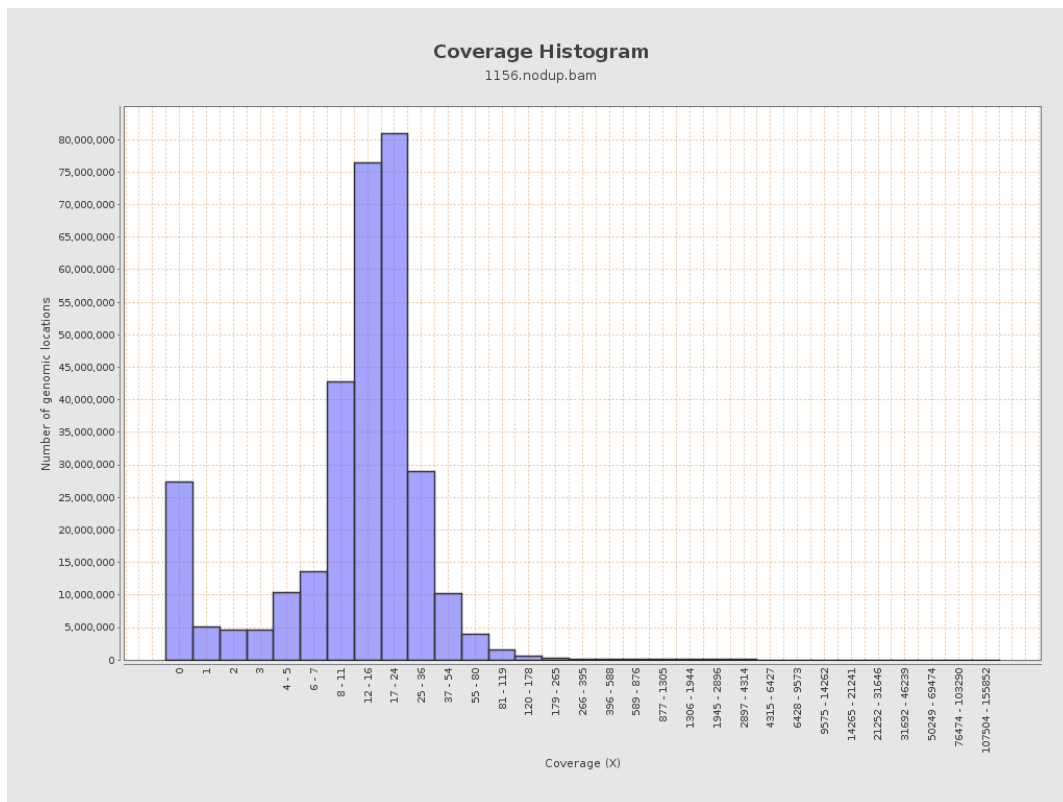
Coverage Histogram (0-50X)
1156.nodup.bam
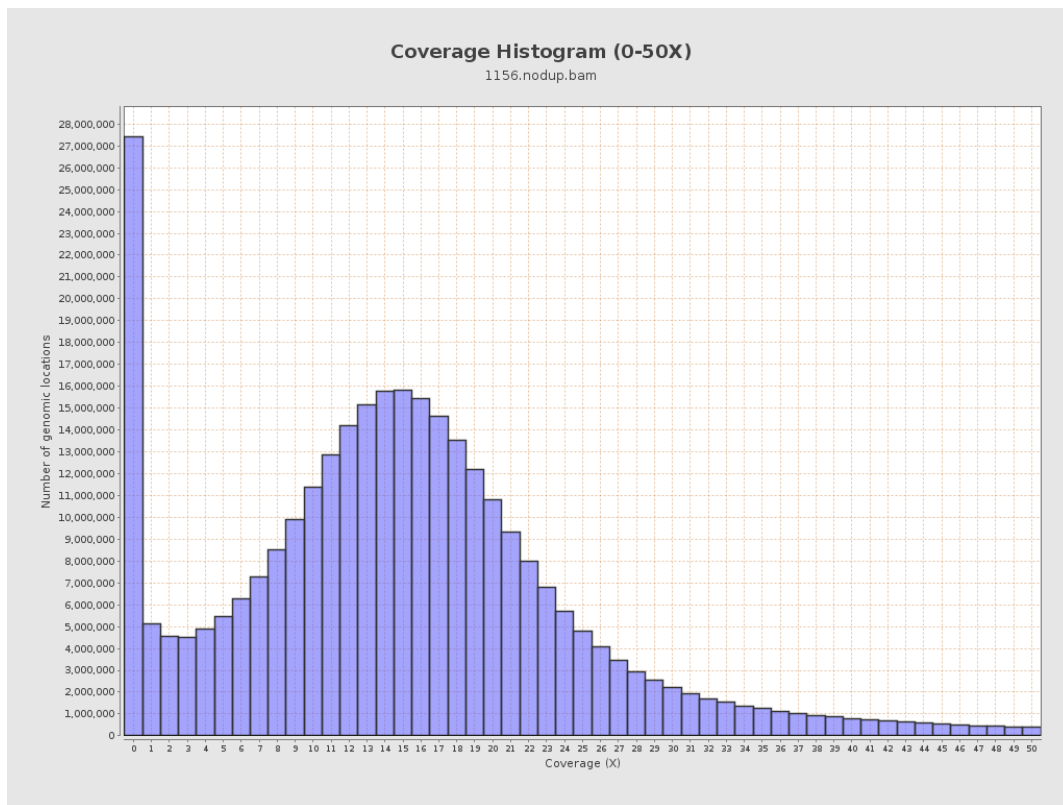
6. Results : Genome Fraction Coverage
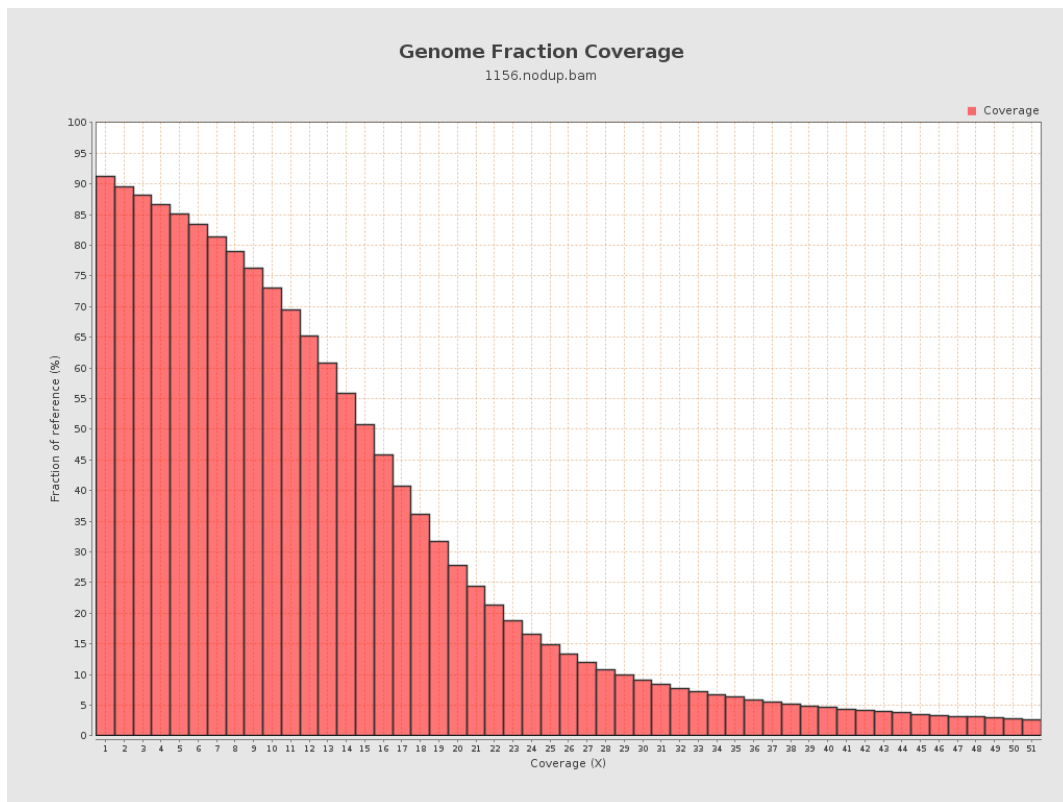
7. Results : Duplication Rate Histogram
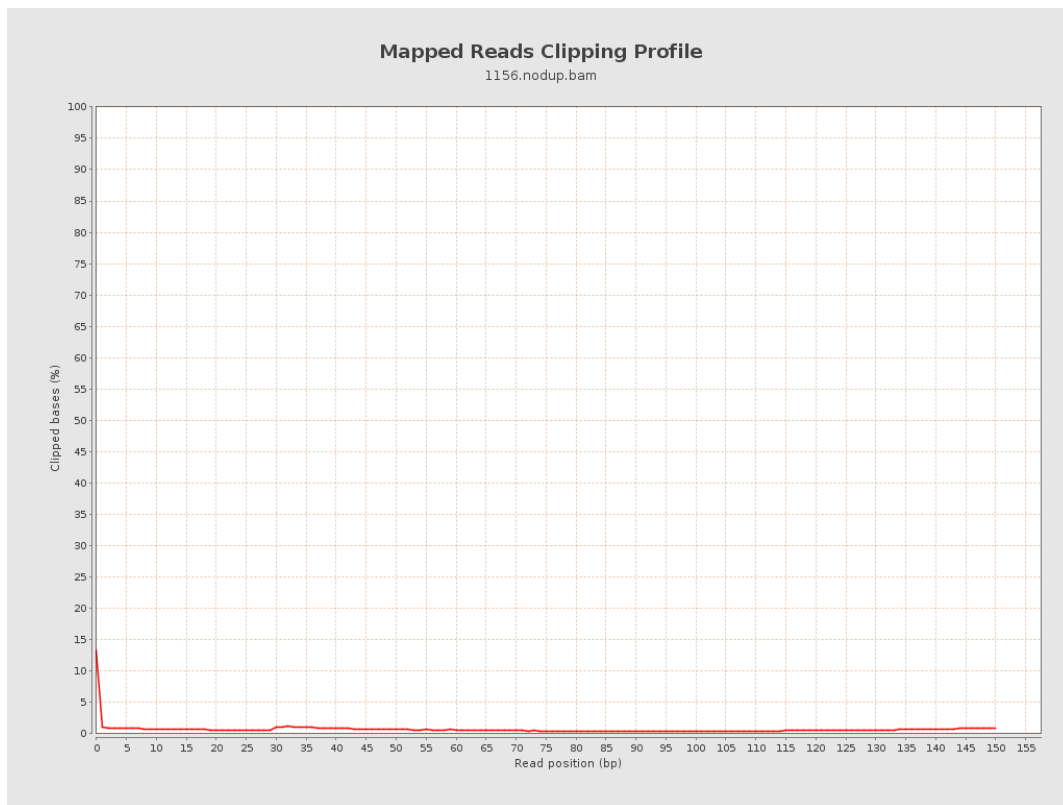

Duplication Rate Histogram
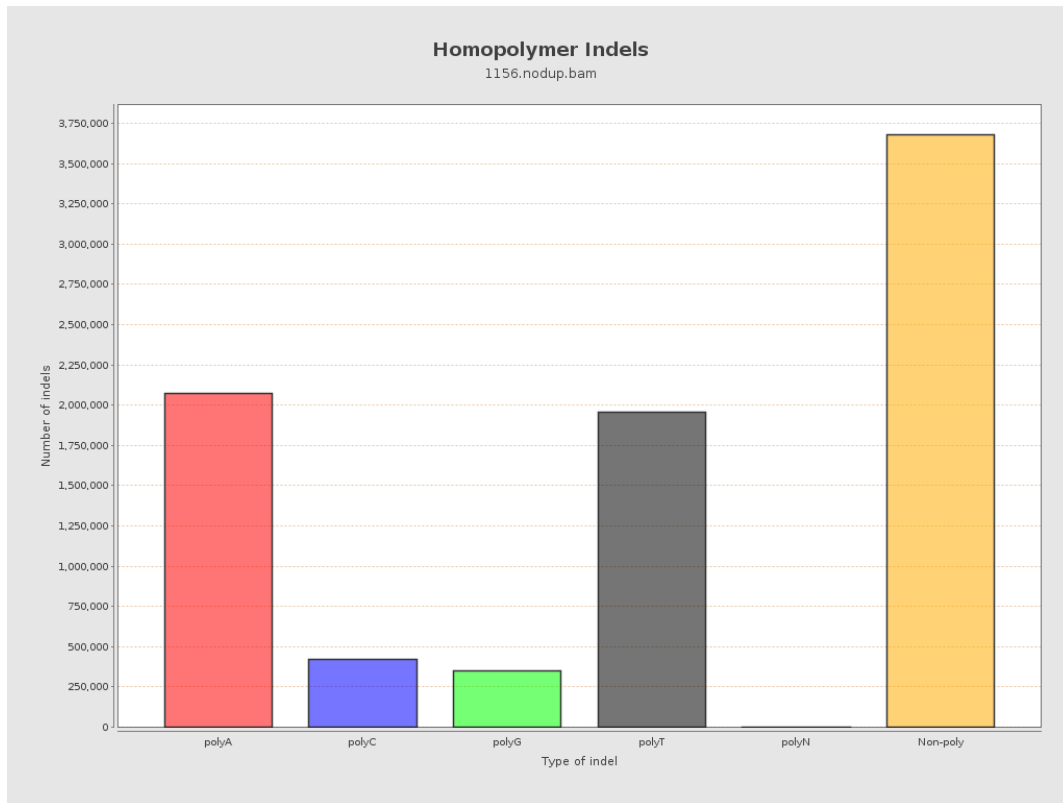1156.nodup.bam
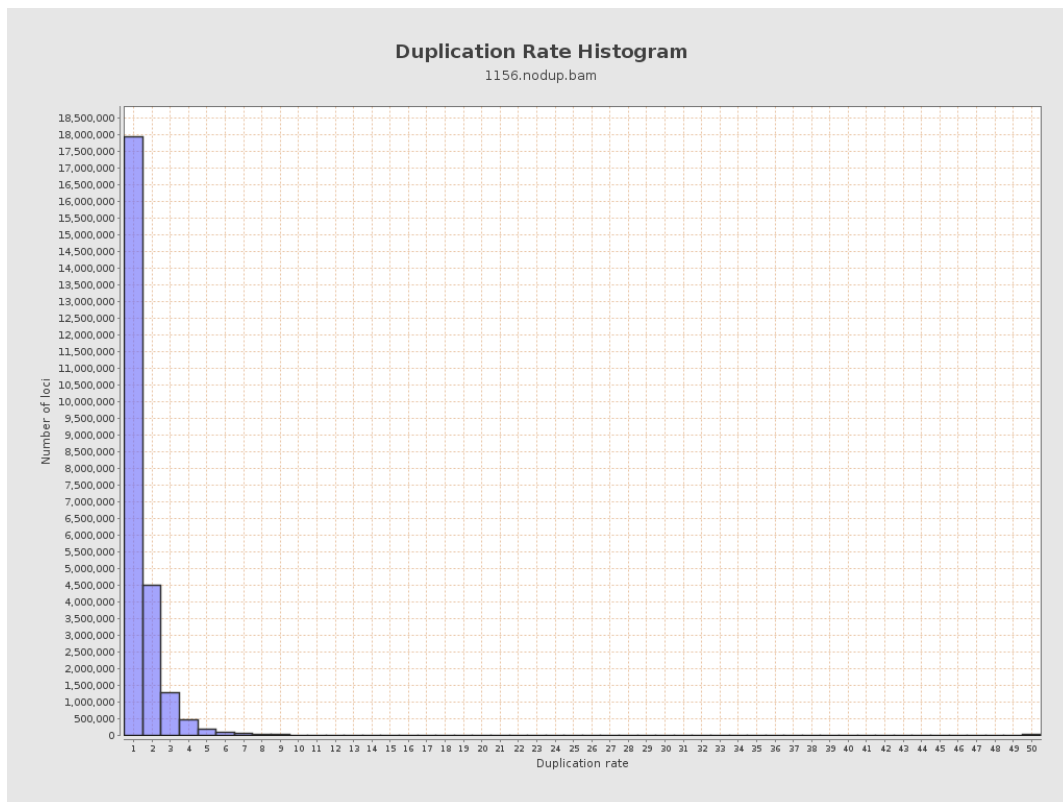
8. Results : Mapped Reads Nucleotide Content
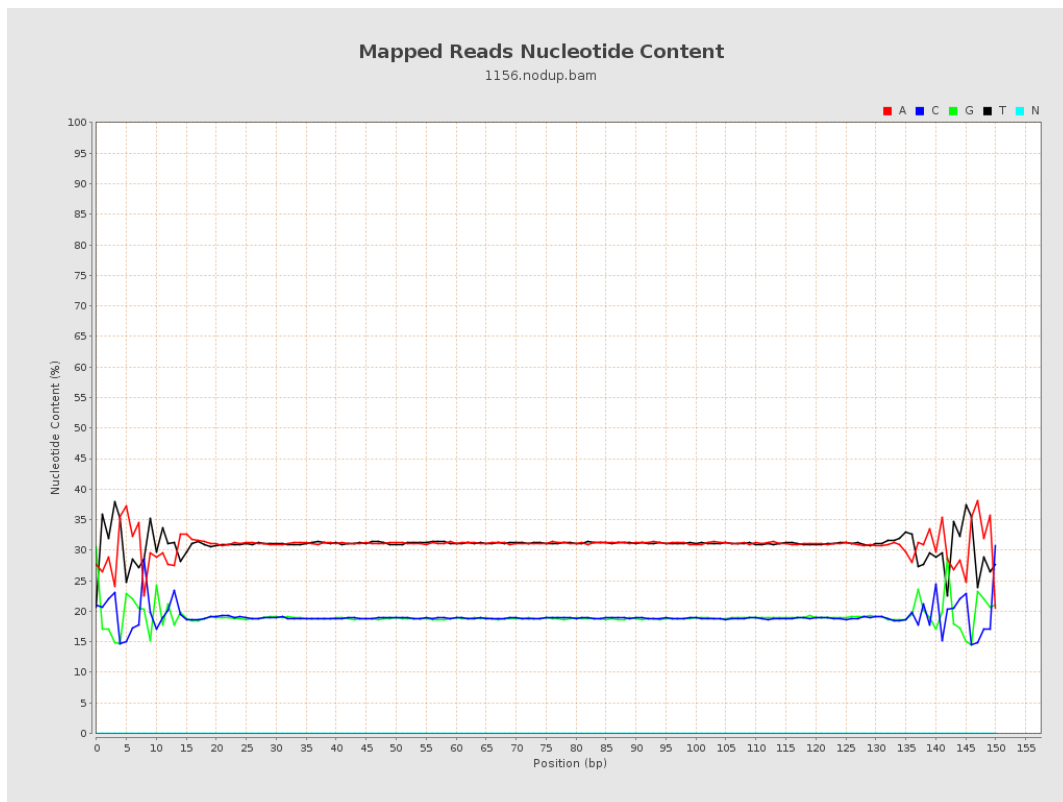
9. Results : Mapped Reads GC-content Distribution
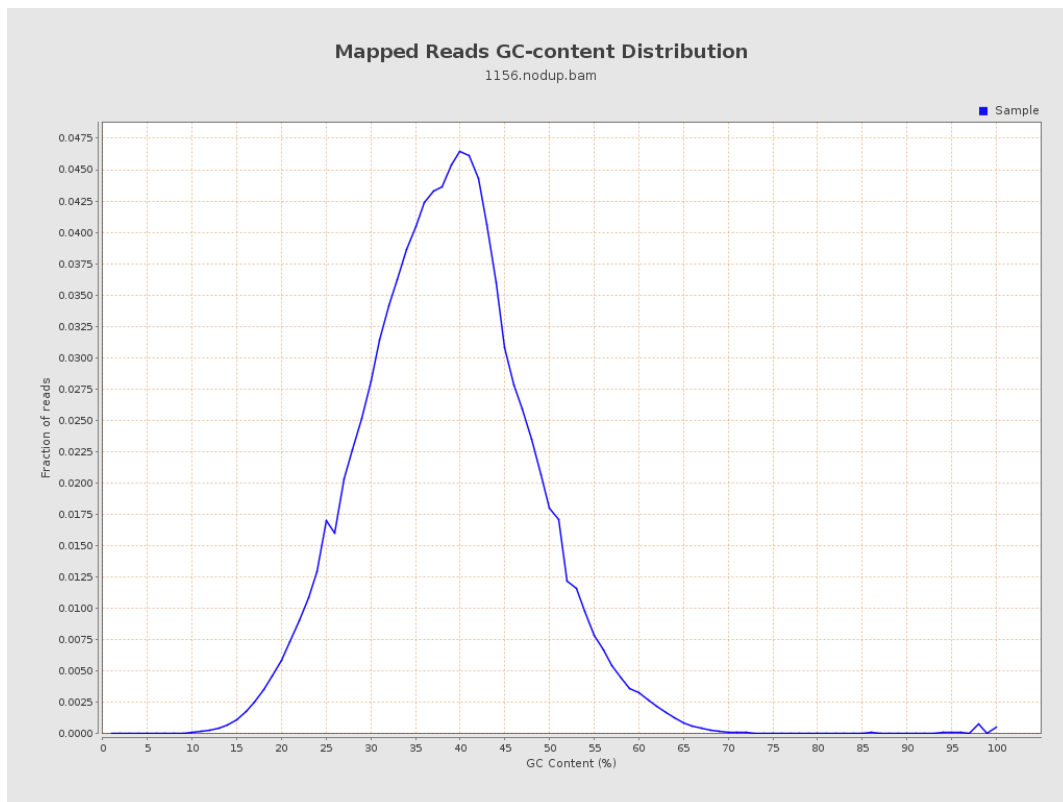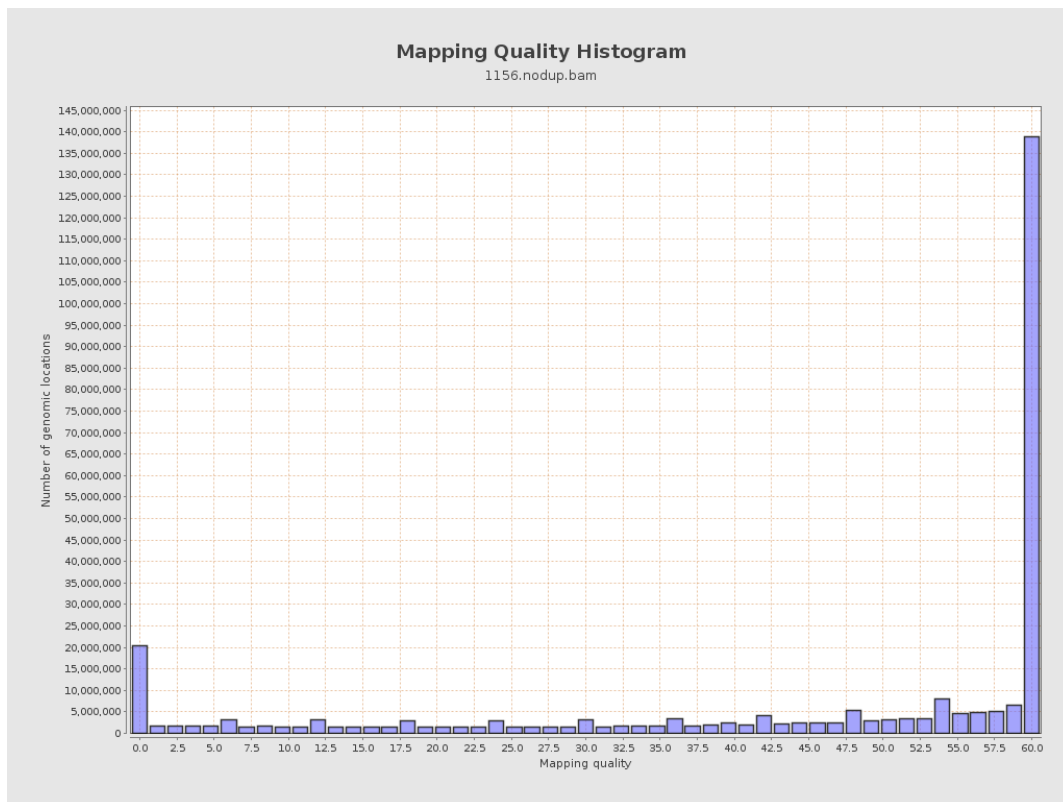
10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
1156.nodup.bam

11. Results : Homopolymer Indels

12. Results : Mapping Quality Across Reference

Mapping Quality Across Reference
1156.nodup.bam
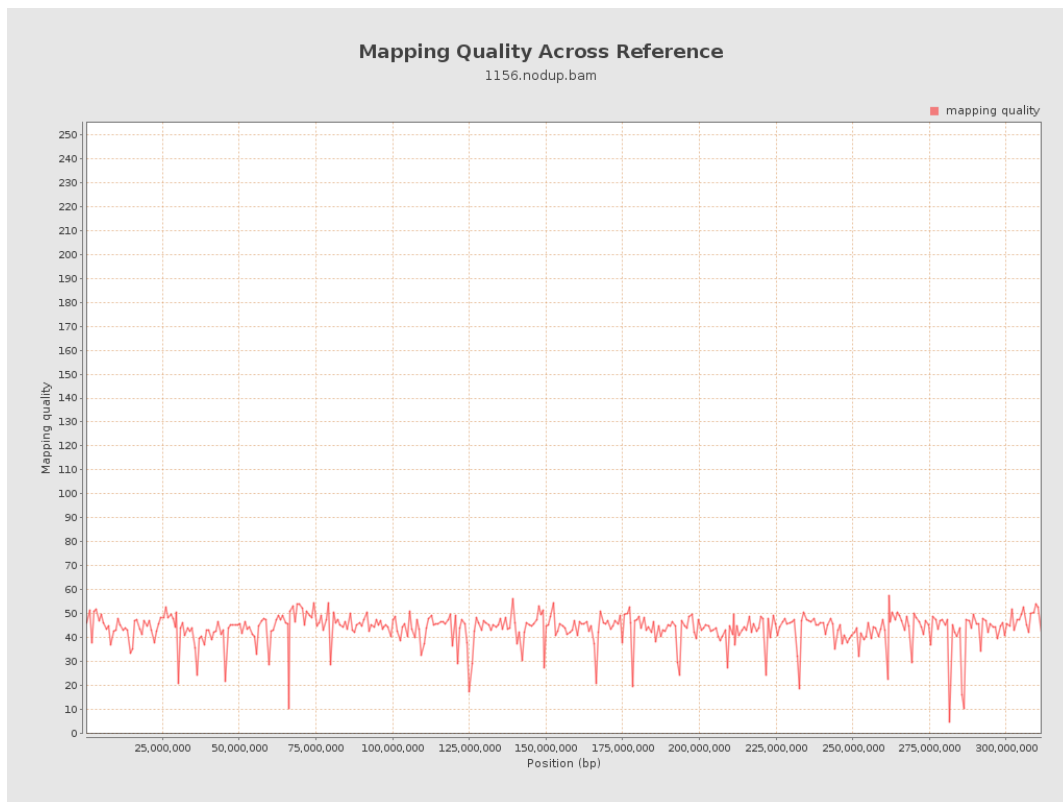
13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

Insert Size Across Reference
1156.nodup.bam
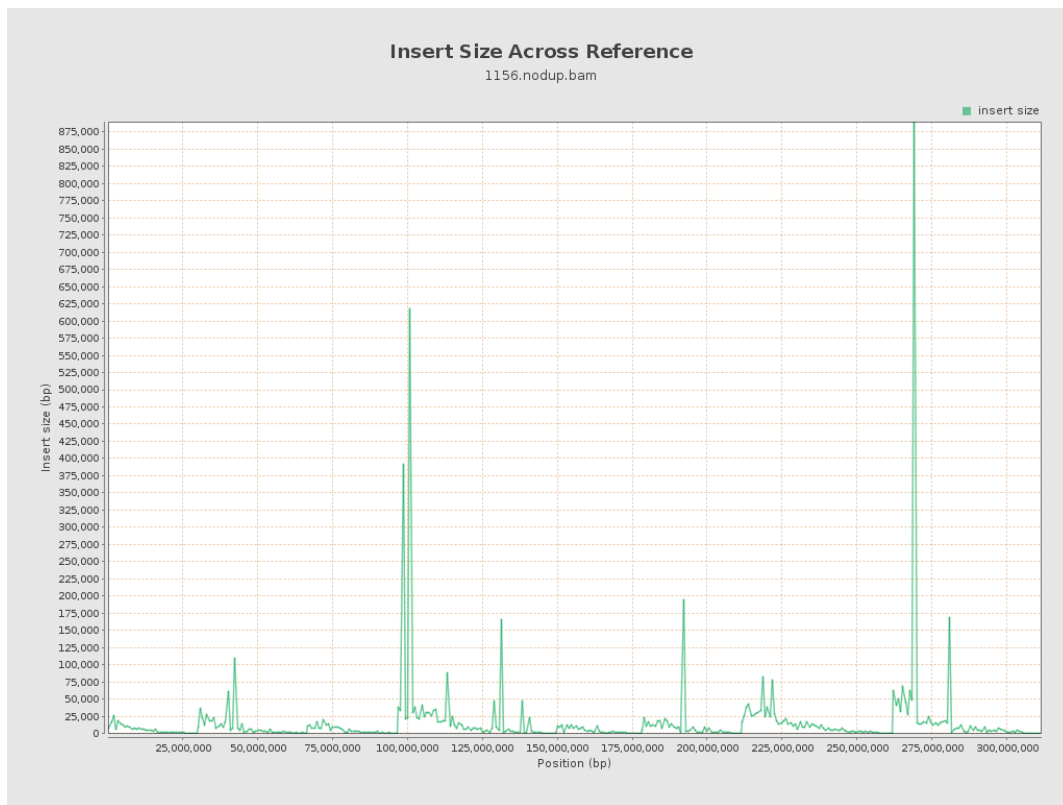
15. Results : Insert Size Histogram