Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:36:34

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/663
.nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/663 .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_162/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_162_S252_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_162/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_162_S252_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:36:33 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	82,000,905
Mapped reads	77,664,056 / 94.71%
Unmapped reads	4,336,849 / 5.29%
Mapped paired reads	77,664,056 / 94.71%
Mapped reads, first in pair	38,911,579 / 47.45%
Mapped reads, second in pair	38,752,477 / 47.26%
Mapped reads, both in pair	76,172,453 / 92.89%
Mapped reads, singletons	1,491,603 / 1.82%
Read min/max/mean length	30 / 151 / 148.18
Duplicated reads (flagged)	13,179,745 / 16.07%
Clipped reads	17,117,790 / 20.88%

2.2. ACGT Content

Number/percentage of A's	3,331,490,573 / 30.83%
Number/percentage of C's	2,073,100,552 / 19.18%
Number/percentage of T's	3,337,531,165 / 30.88%
Number/percentage of G's	2,064,750,174 / 19.11%
Number/percentage of N's	45,815 / 0%
GC Percentage	38.29%

2.3. Coverage

Mean	34.7669
Standard Deviation	273.0743

2.4. Mapping Quality

Mean Mapping Quality	44.1

2.5. Insert size

Mean	224,993.29
Standard Deviation	2,252,244.75
P25/Median/P75	323 / 421 / 549

2.6. Mismatches and indels

General error rate	2.35%
Mismatches	234,193,211
Insertions	7,216,277
Mapped reads with at least one insertion	8.35%
Deletions	7,416,560
Mapped reads with at least one deletion	8.46%
Homopolymer indels	56.23%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	847058577	28.4971	81.4448

LT669789.1	36598175	1269381505	34.6843	299.5788
LT669790.1	30422129	1120440429	36.8298	267.2541
LT669791.1	52758100	1810460252	34.3163	233.6498
LT669792.1	28376109	964082746	33.9752	284.4753
LT669793.1	33388210	1078244197	32.2942	190.9926
LT669794.1	50579949	1671524796	33.0472	242.5215
LT669795.1	49795044	2073643588	41.6436	406.0711

3. Results : Coverage across reference

Coverage across reference
663.nodup.bam

4. Results : Coverage Histogram

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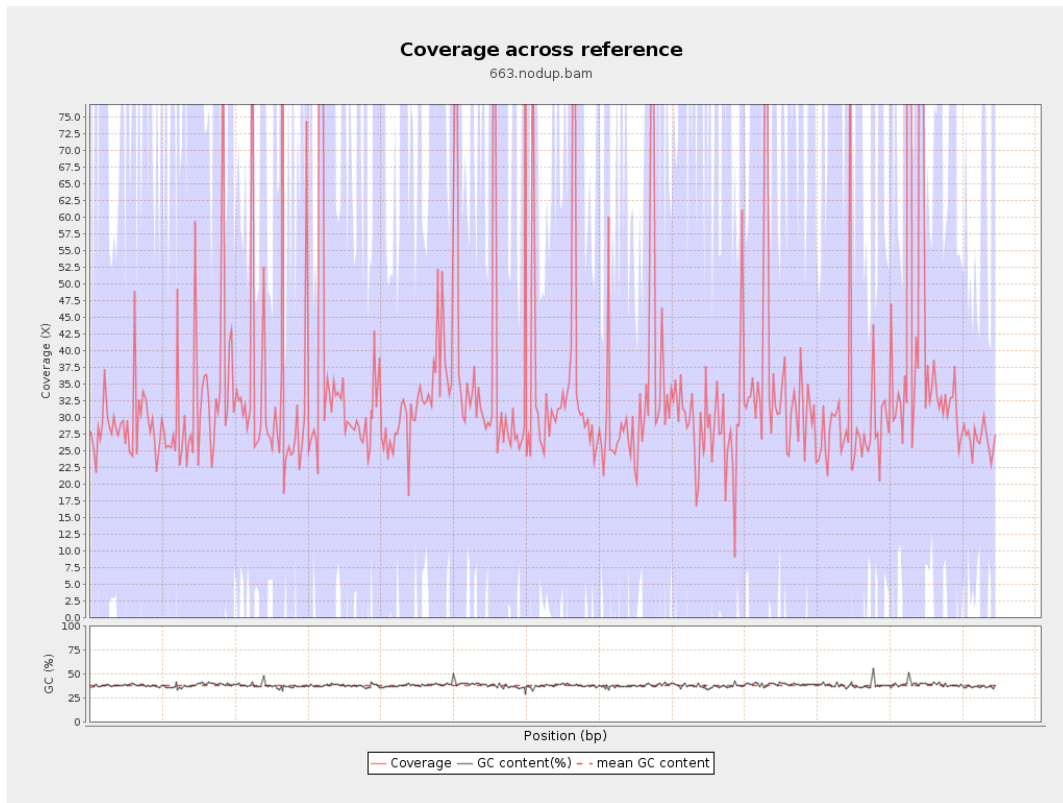
5. Results : Coverage Histogram (0-50X)
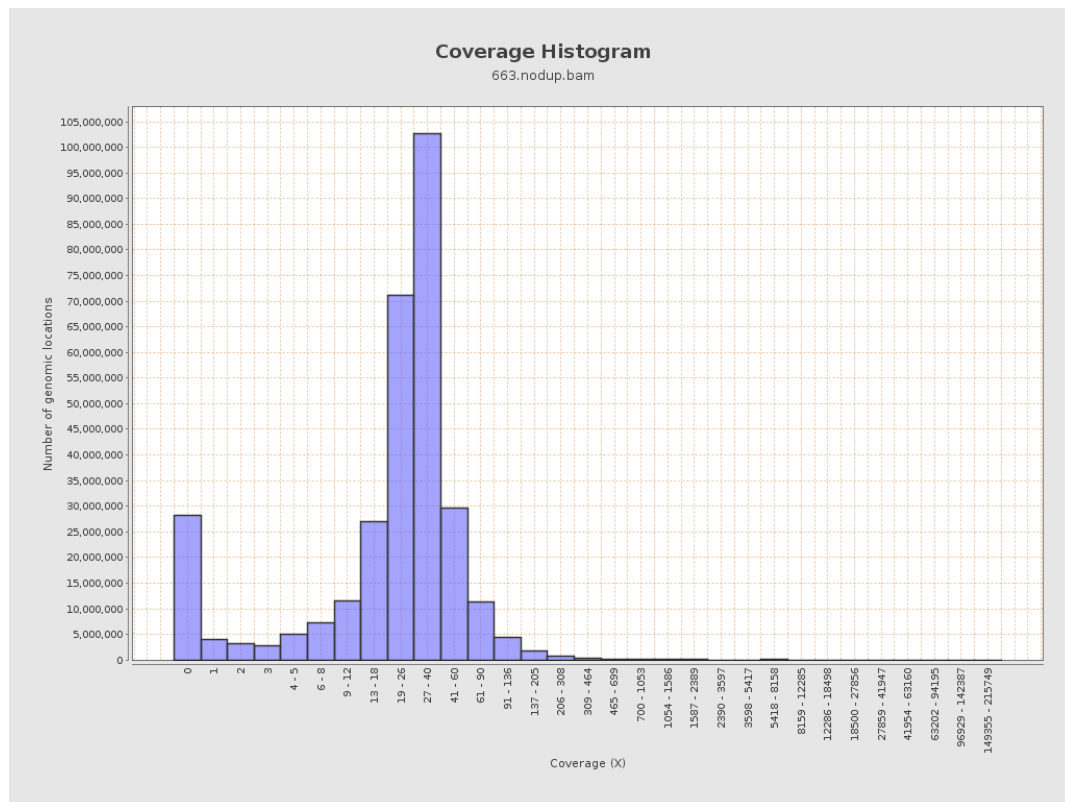
Coverage Histogram (0-50X)
663.nodup.bam
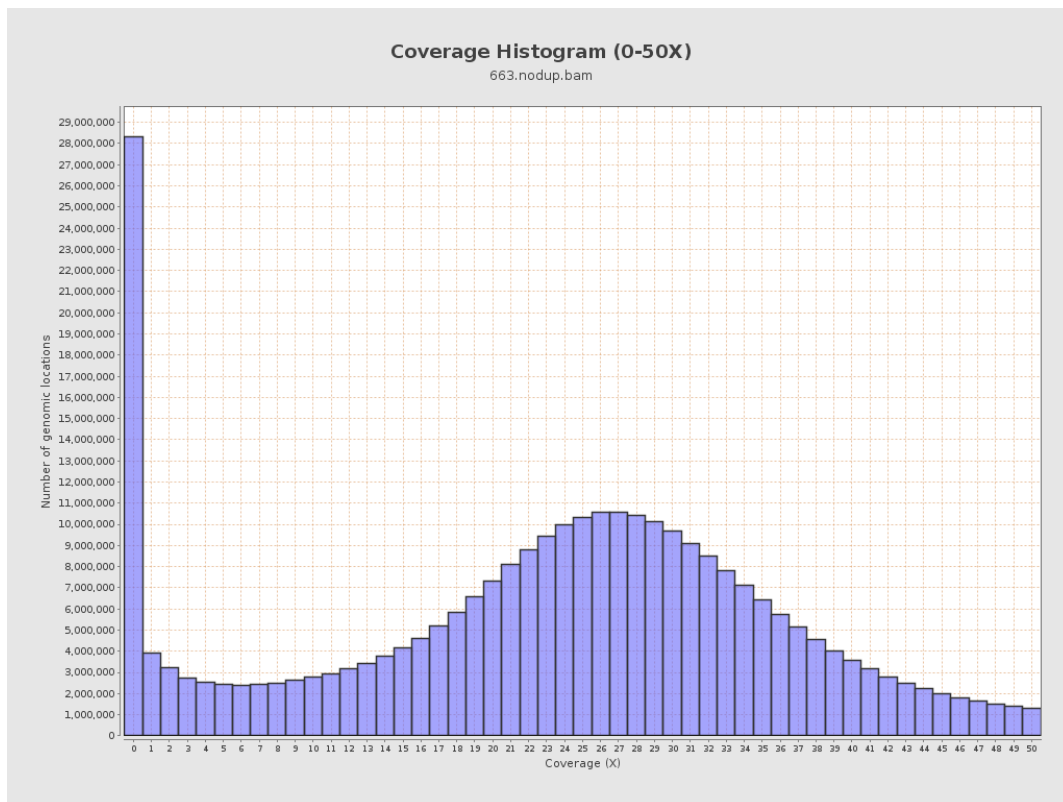
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
663.nodup.bam
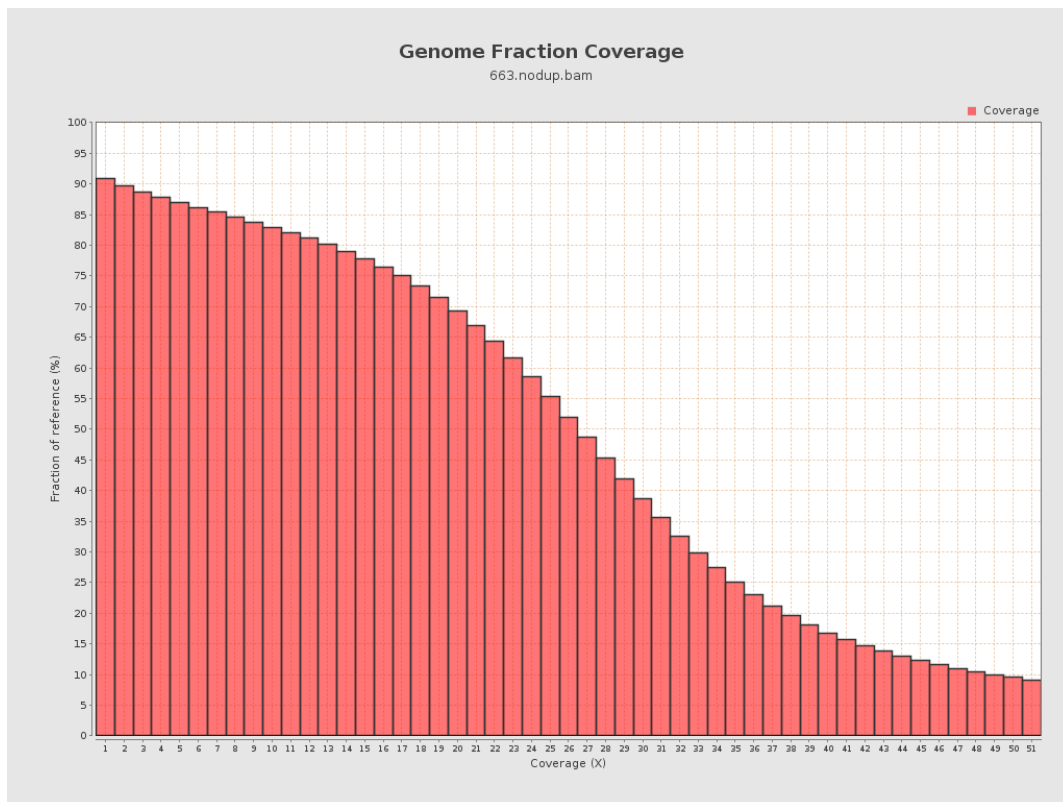
7. Results : Duplication Rate Histogram

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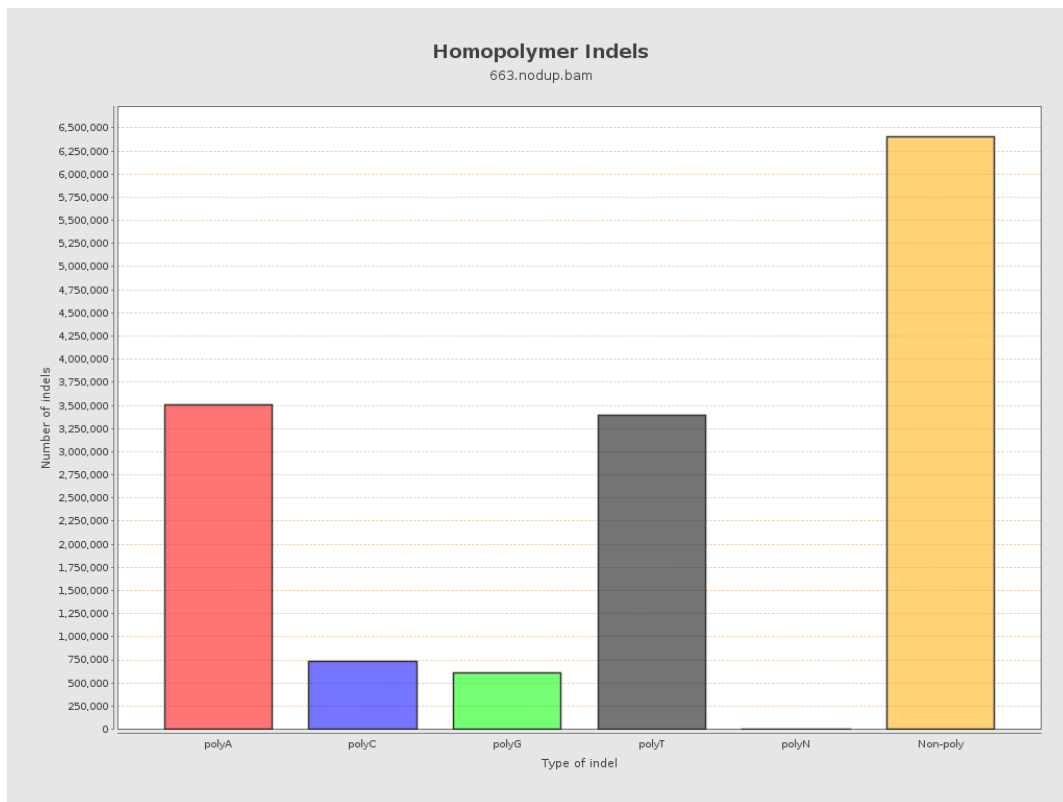663.nodup.bam
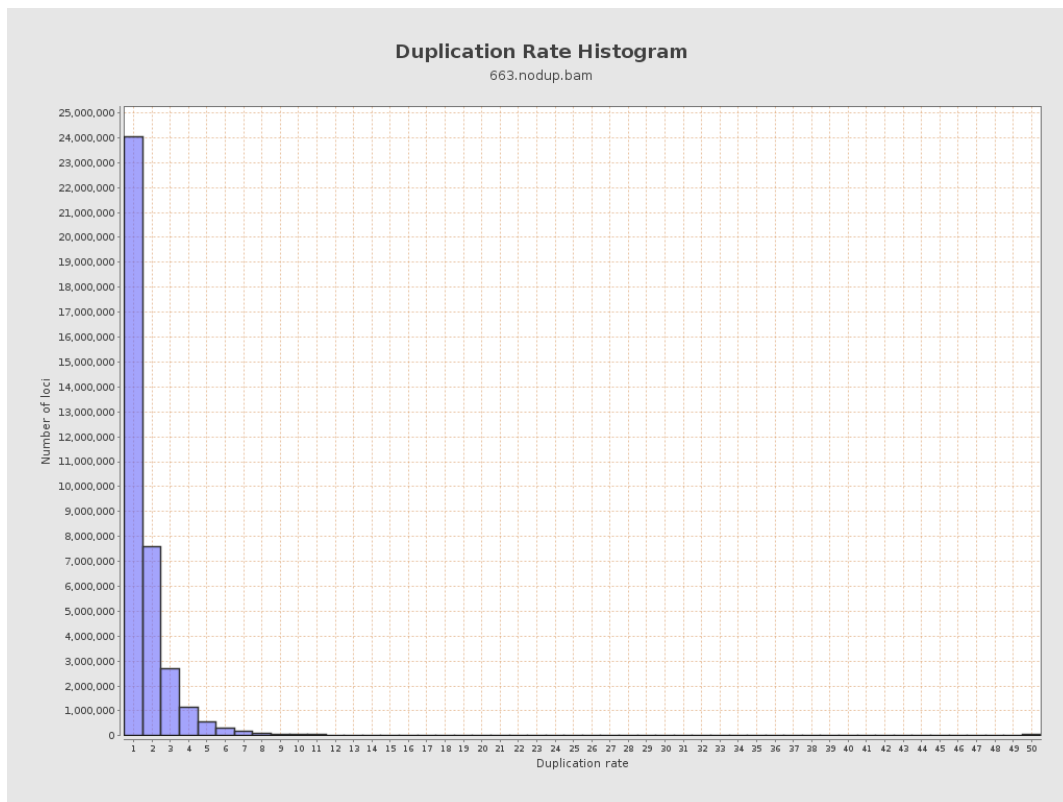
8. Results : Mapped Reads Nucleotide Content
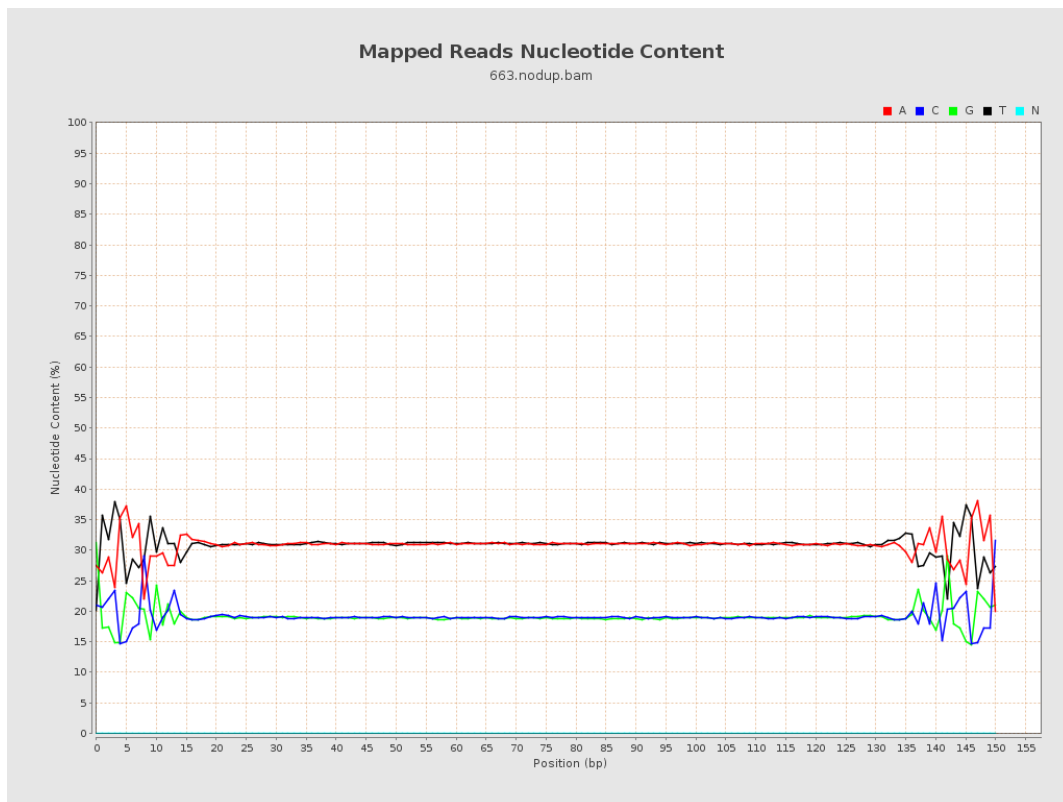
9. Results : Mapped Reads GC-content Distribution
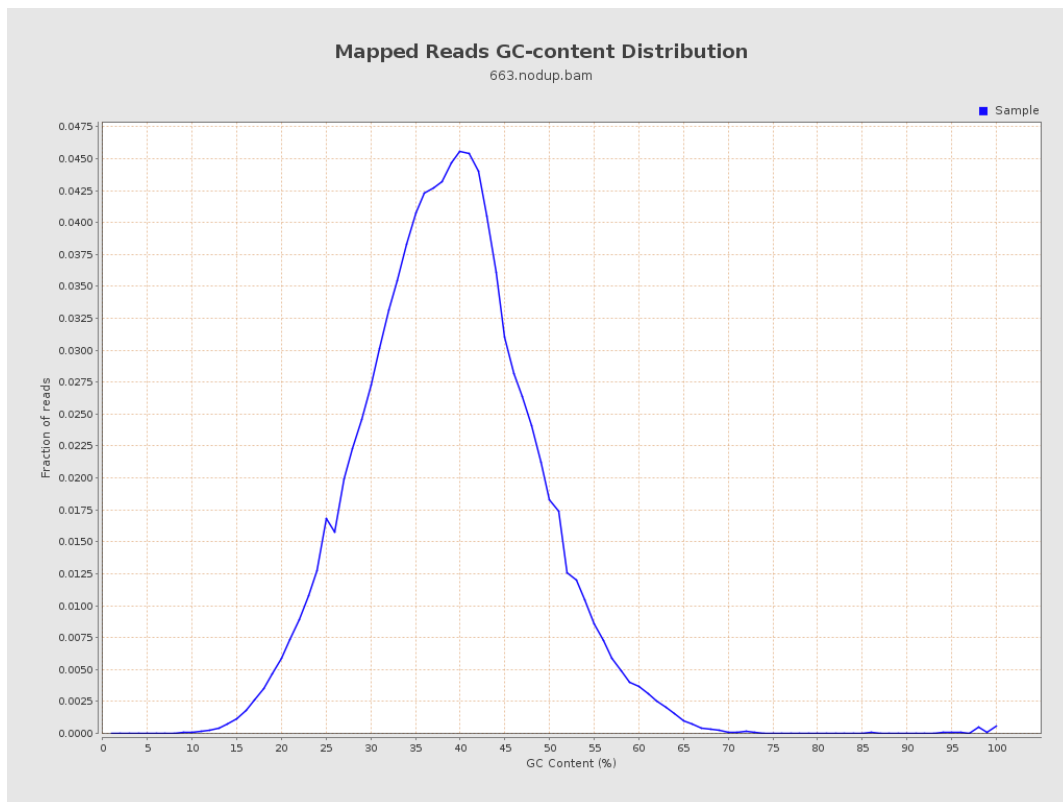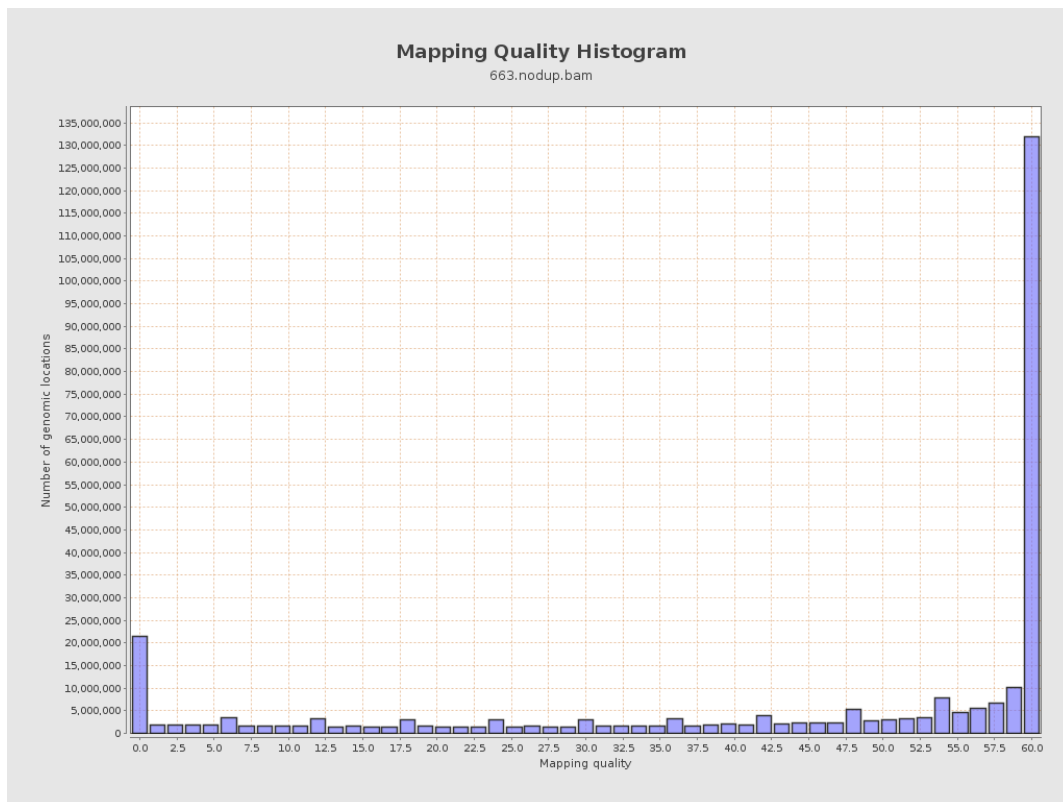
10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
663.nodup.bam
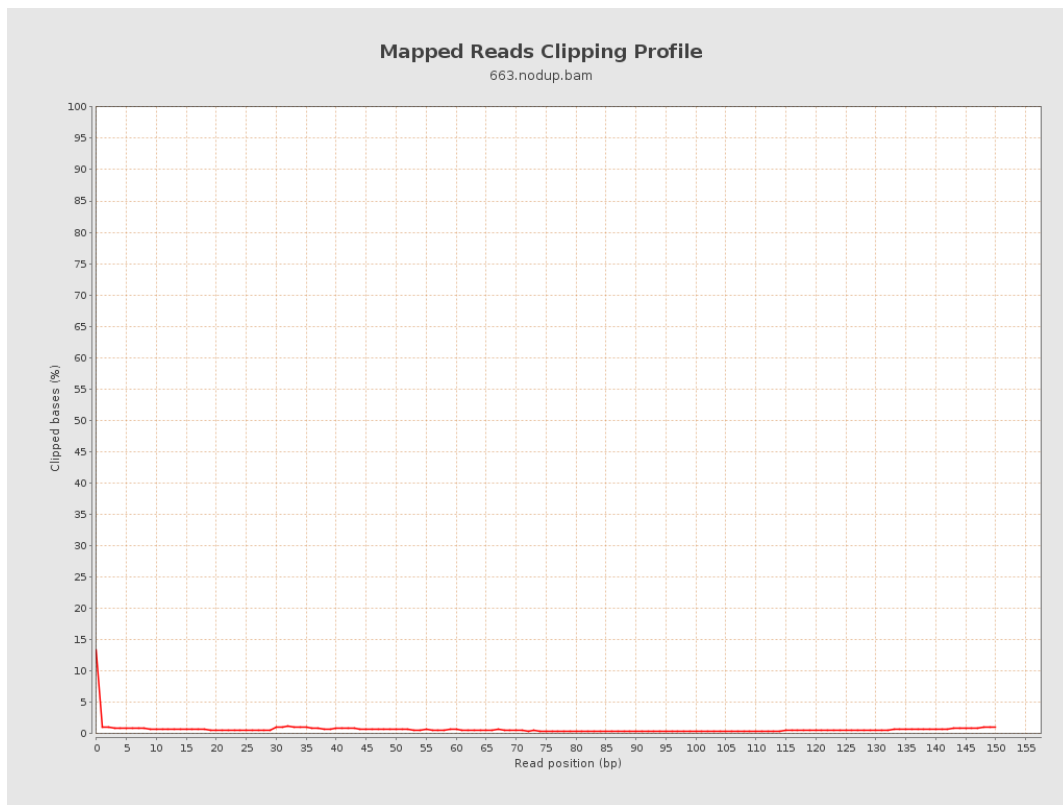
11. Results : Homopolymer Indels

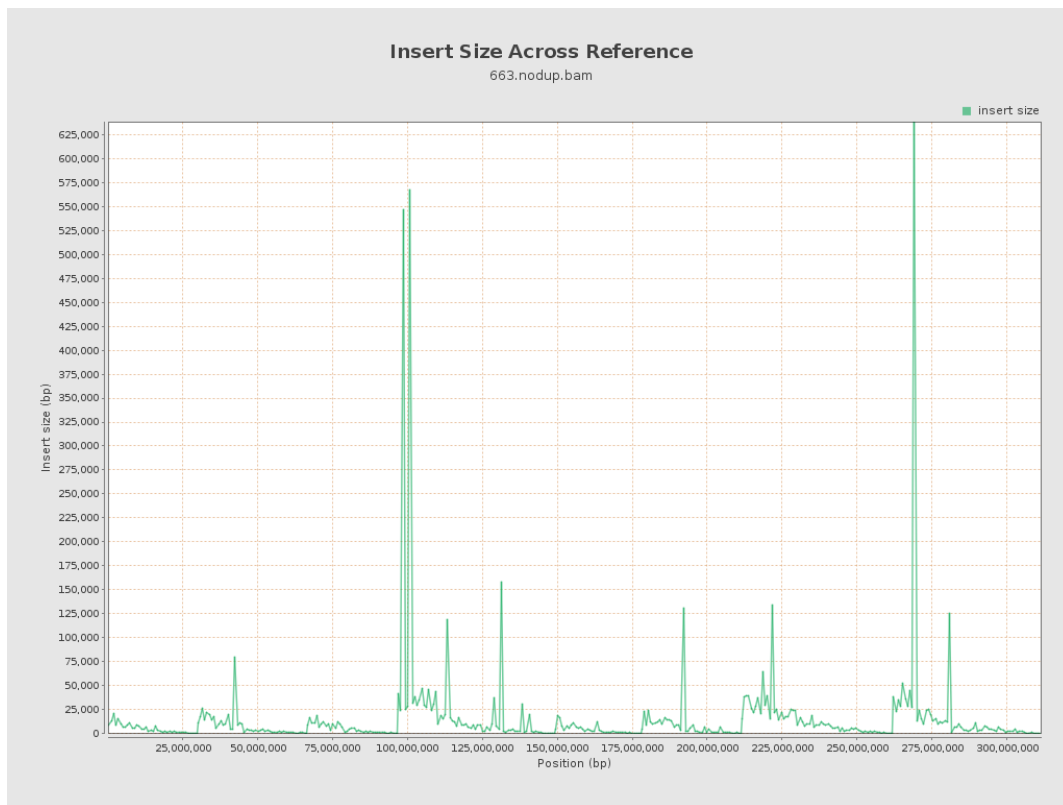Homopolymer Indels
663.nodup.bam

12. Results : Mapping Quality Across Reference
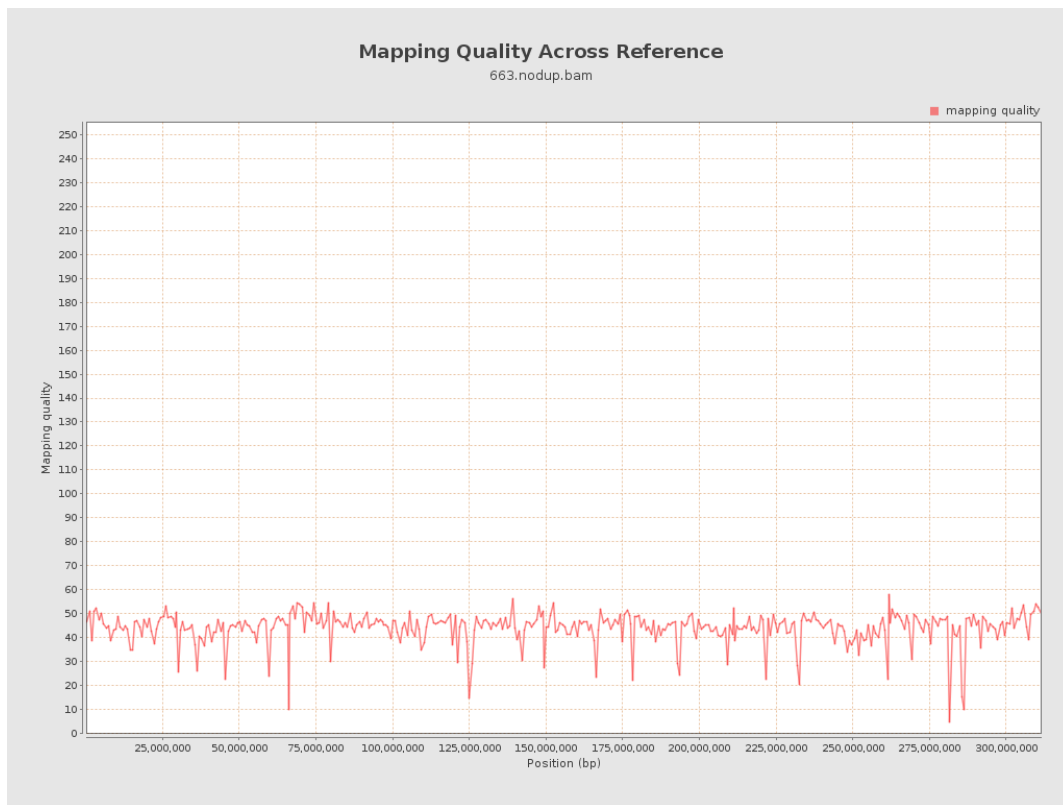
13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram