Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:35:01

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/513
.nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/513 .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_438/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_438_S413_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_438/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_438_S413_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:35:00 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	75,306,721
Mapped reads	70,025,068 / 92.99%
Unmapped reads	5,281,653 / 7.01%
Mapped paired reads	70,025,068 / 92.99%
Mapped reads, first in pair	35,078,568 / 46.58%
Mapped reads, second in pair	34,946,500 / 46.41%
Mapped reads, both in pair	68,246,026 / 90.62%
Mapped reads, singletons	1,779,042 / 2.36%
Read min/max/mean length	30 / 151 / 148.17
Duplicated reads (flagged)	11,675,032 / 15.5%
Clipped reads	15,503,025 / 20.59%

2.2. ACGT Content

Number/percentage of A's	2,994,926,166 / 30.89%
Number/percentage of C's	1,854,652,439 / 19.13%
Number/percentage of T's	2,999,313,808 / 30.94%
Number/percentage of G's	1,846,261,626 / 19.04%
Number/percentage of N's	32,754 / 0%
GC Percentage	38.17%

2.3. Coverage

Mean	31.1894
Standard Deviation	273.5052

2.4. Mapping Quality

Mean Mapping Quality	44.48

2.5. Insert size

Mean	240,783.28
Standard Deviation	2,344,044.27
P25/Median/P75	342 / 447 / 582

2.6. Mismatches and indels

General error rate	2.29%
Mismatches	203,343,133
Insertions	6,805,214
Mapped reads with at least one insertion	8.7%
Deletions	6,658,323
Mapped reads with at least one deletion	8.45%
Homopolymer indels	57.07%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	735118107	24.7312	91.8256

LT669789.1	36598175	1167225260	31.893	297.8895
LT669790.1	30422129	1060615775	34.8633	341.2209
LT669791.1	52758100	1645951124	31.1981	266.4186
LT669792.1	28376109	879089810	30.9799	310.5269
LT669793.1	33388210	932752979	27.9366	139.0193
LT669794.1	50579949	1505109523	29.757	241.616
LT669795.1	49795044	1794074166	36.0292	352.569

3. Results : Coverage across reference

Coverage across reference
513.nodup.bam

4. Results : Coverage Histogram

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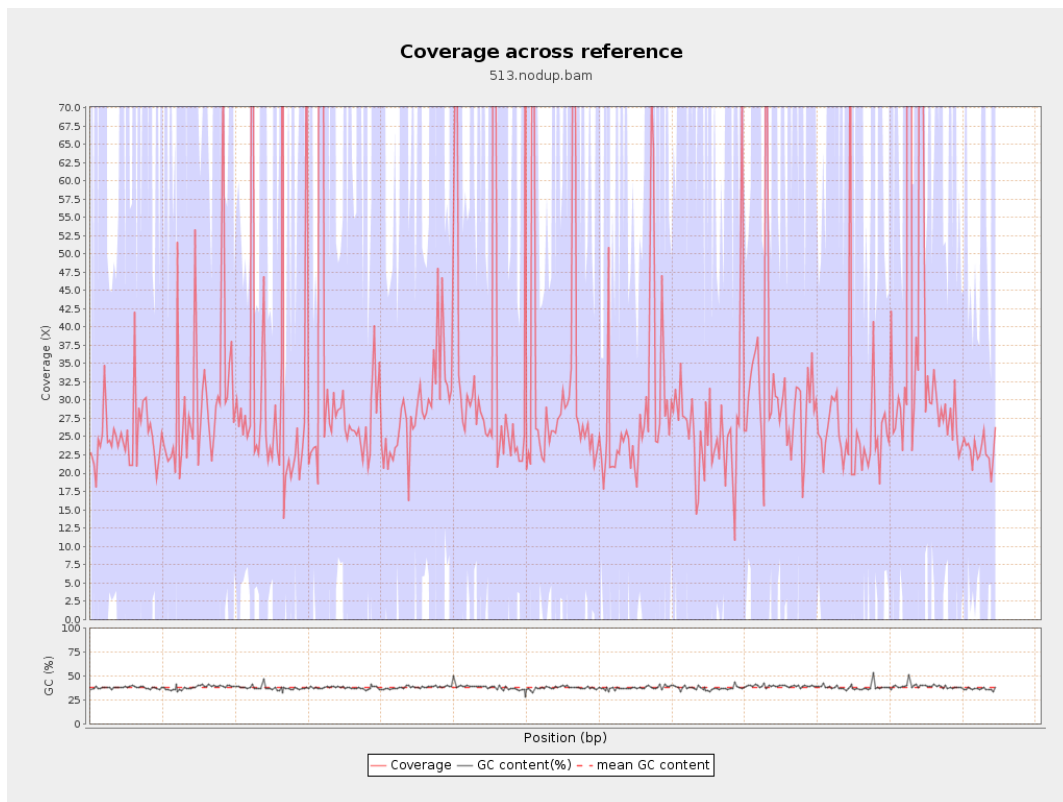
5. Results : Coverage Histogram (0-50X)
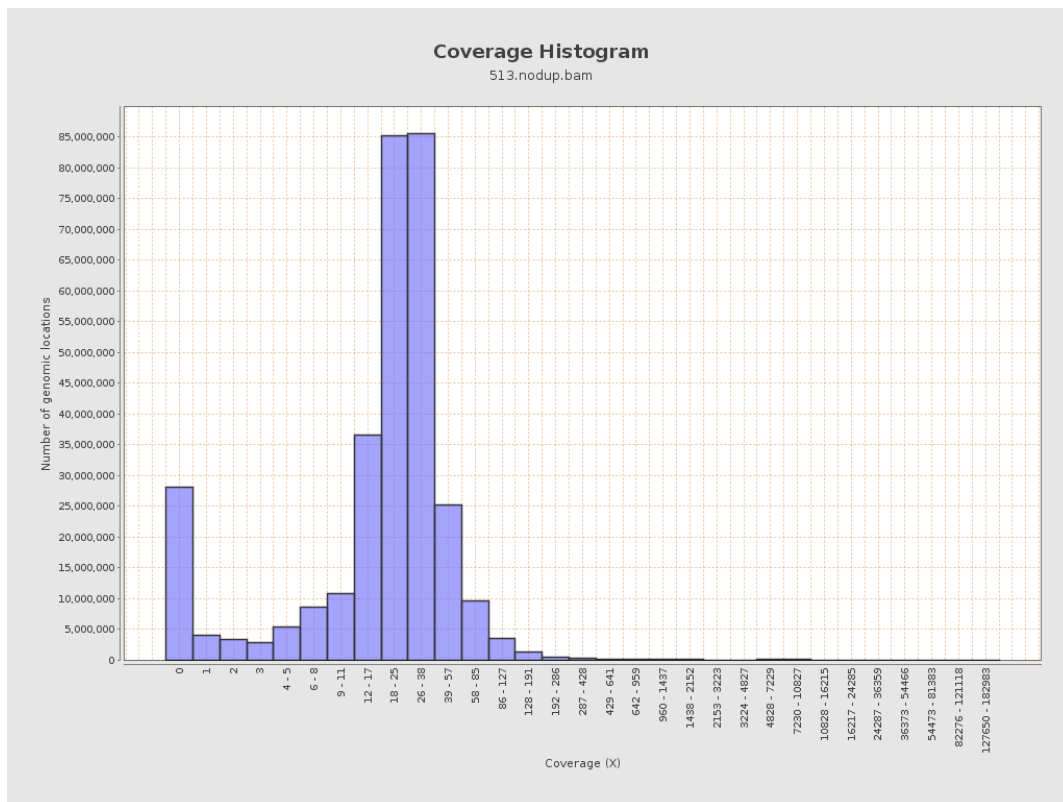
Coverage Histogram (0-50X)
513.nodup.bam
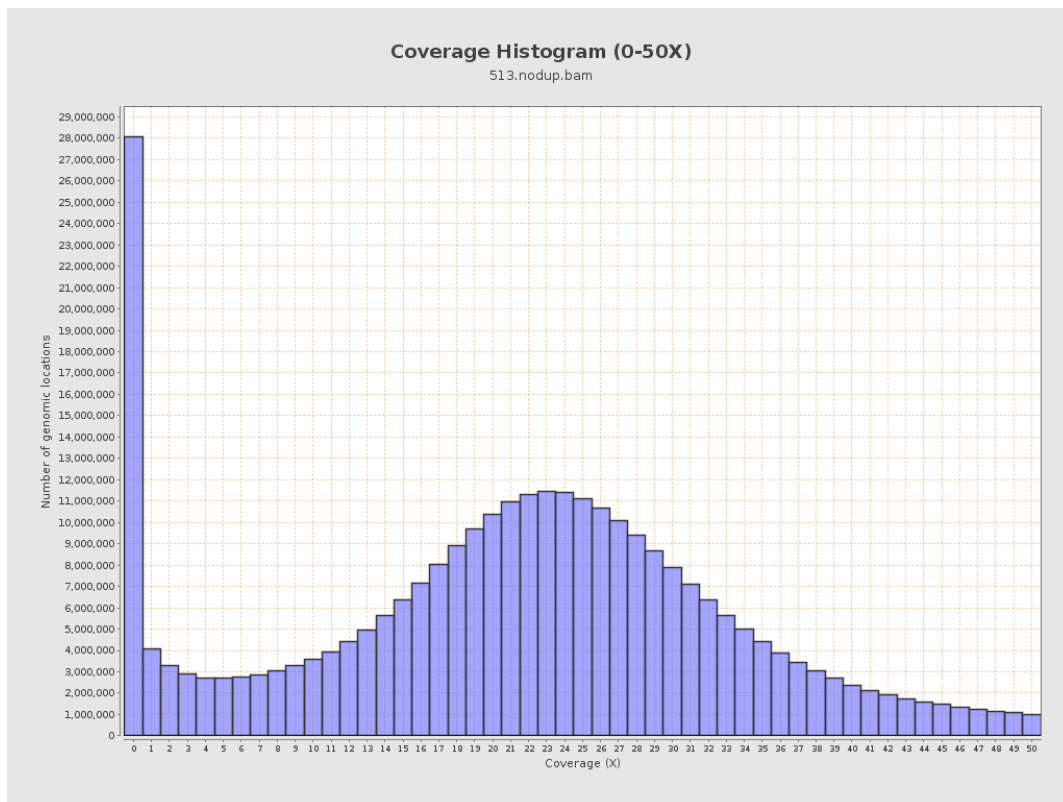
6. Results : Genome Fraction Coverage
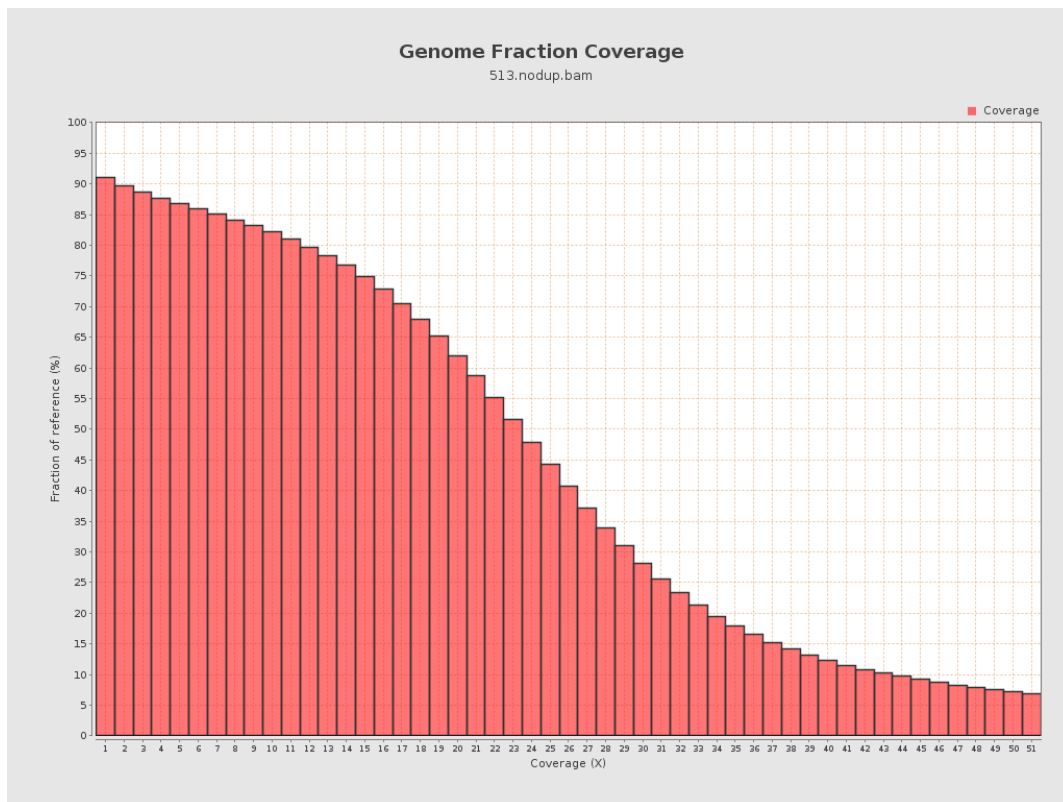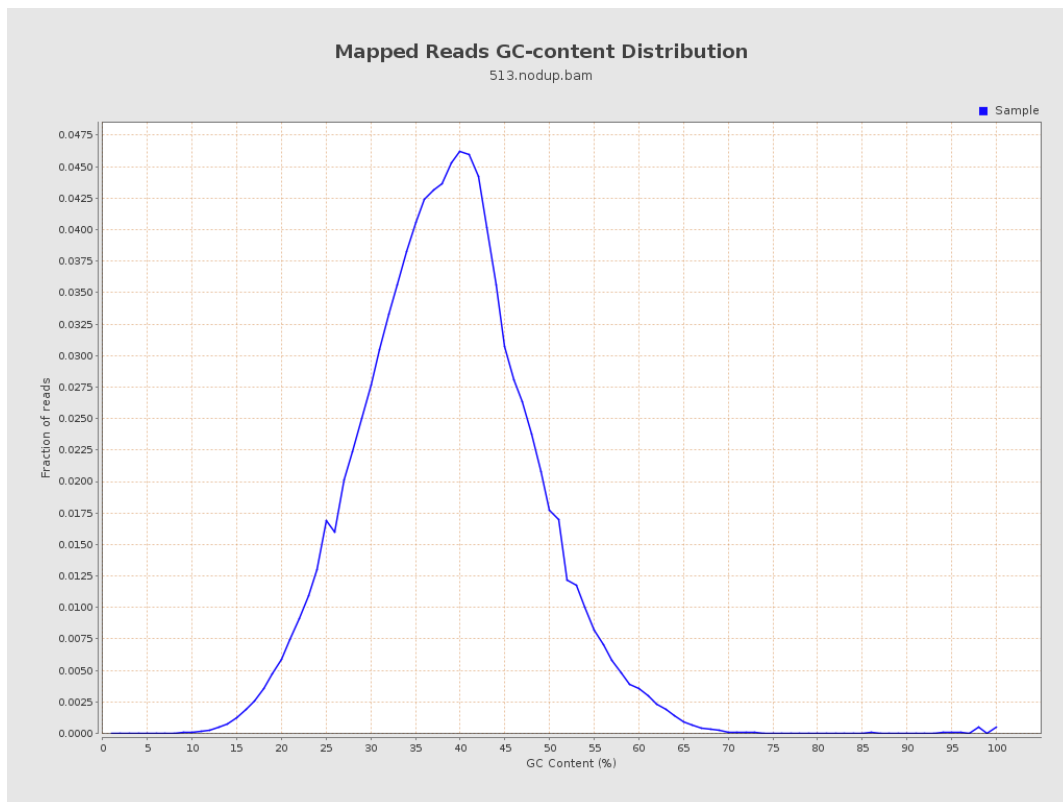
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
513.nodup.bam
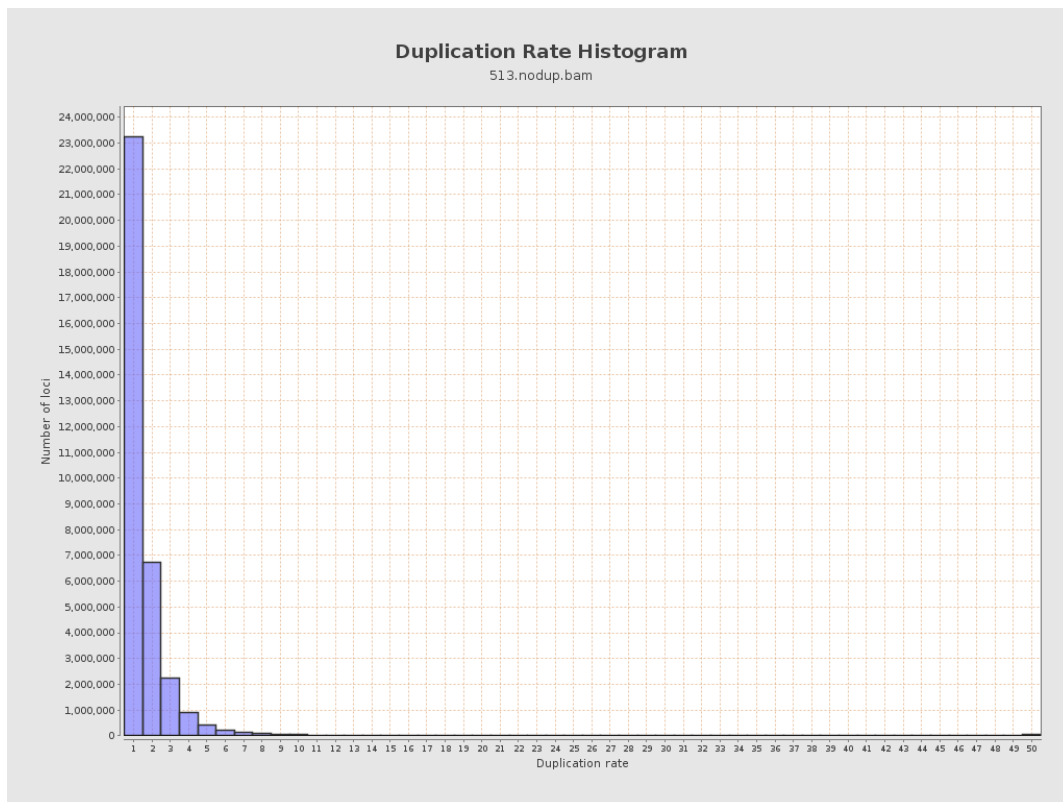
8. Results : Mapped Reads Nucleotide Content

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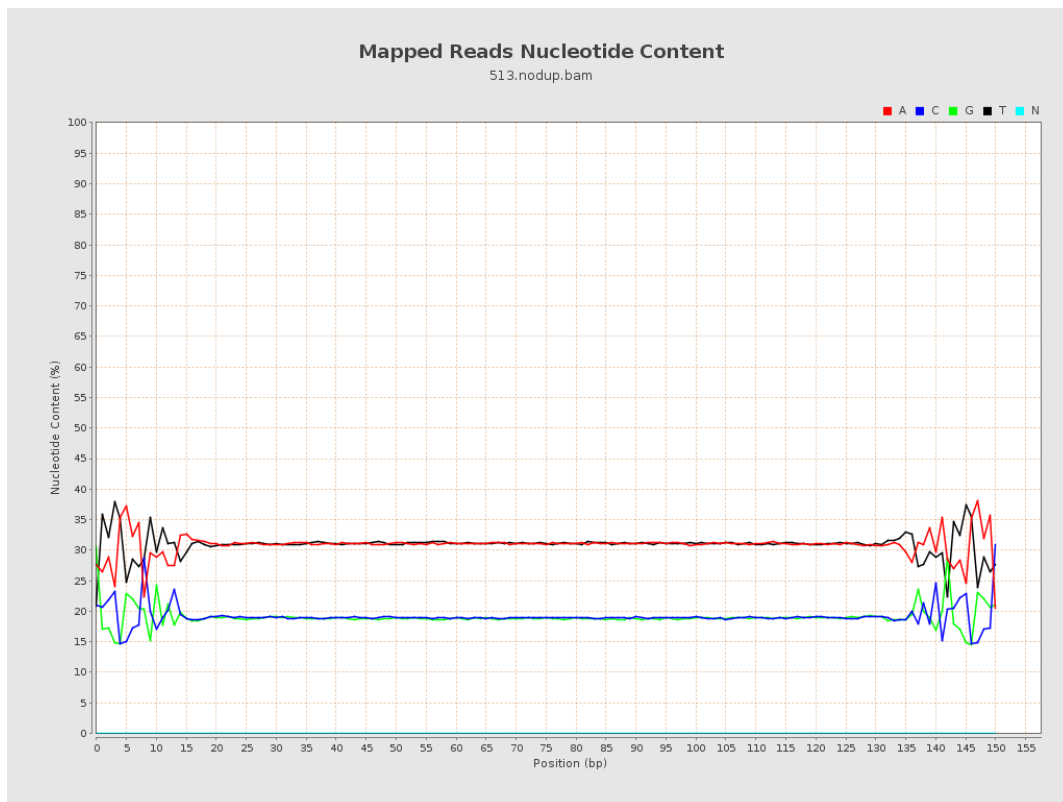
Mapped Reads GC-content Distribution
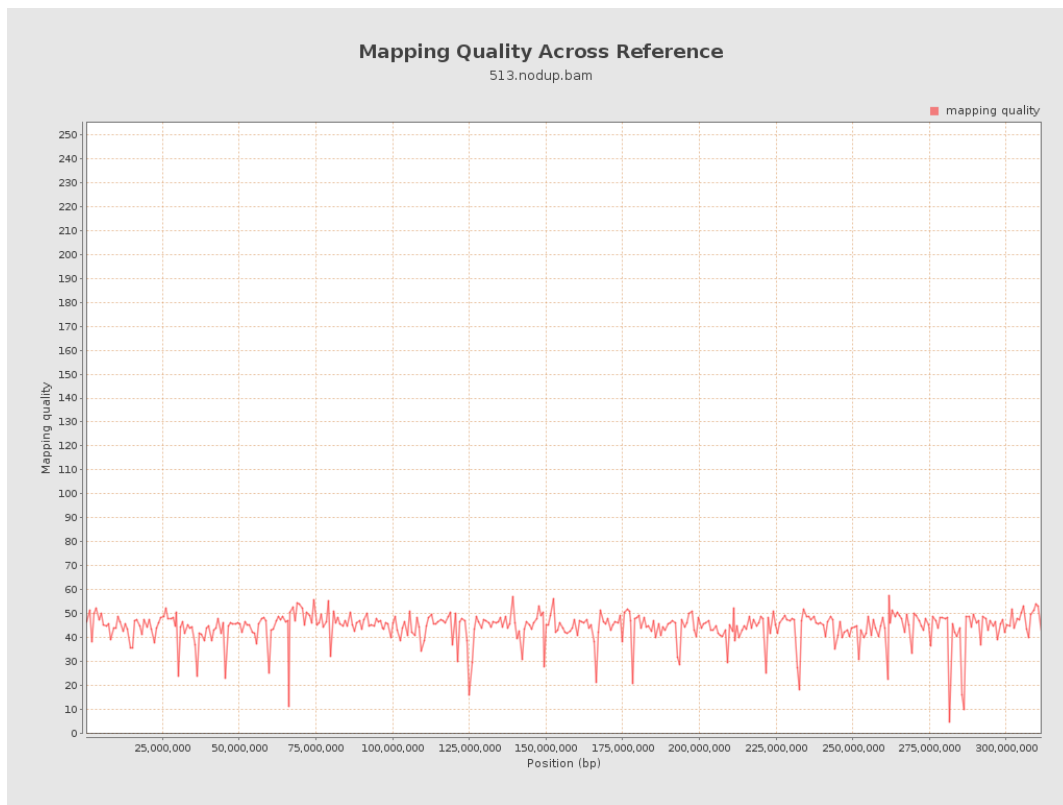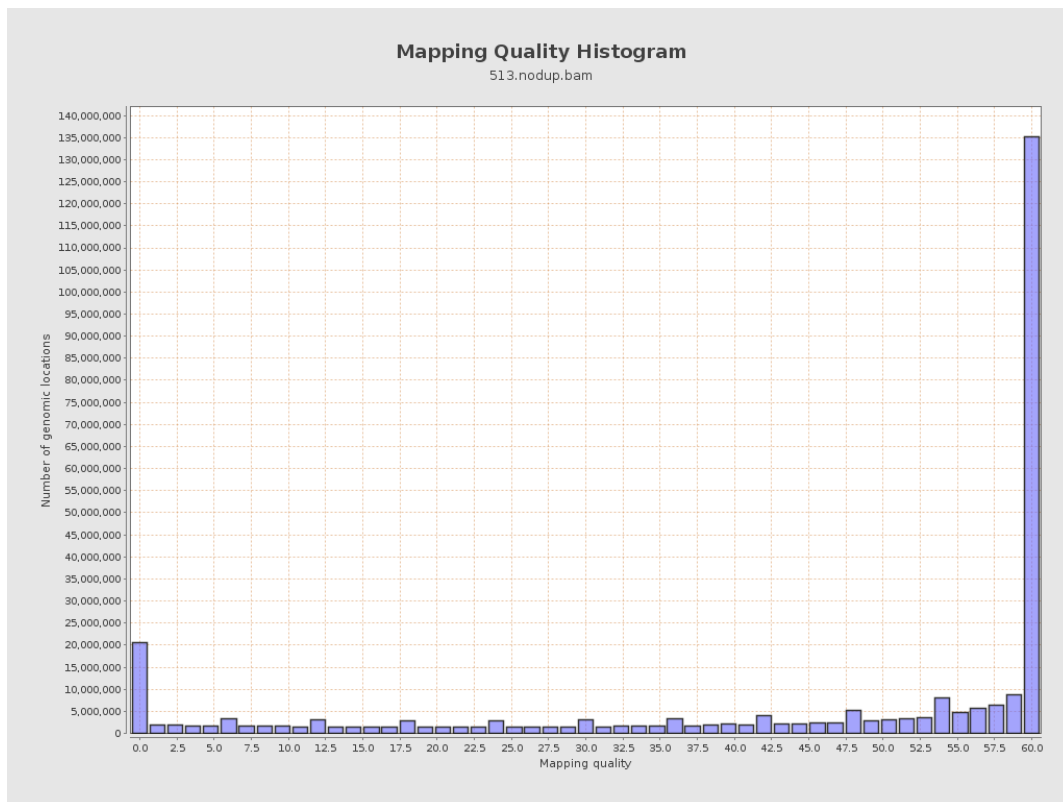513.nodup.bam

10. Results : Mapped Reads Clipping Profile
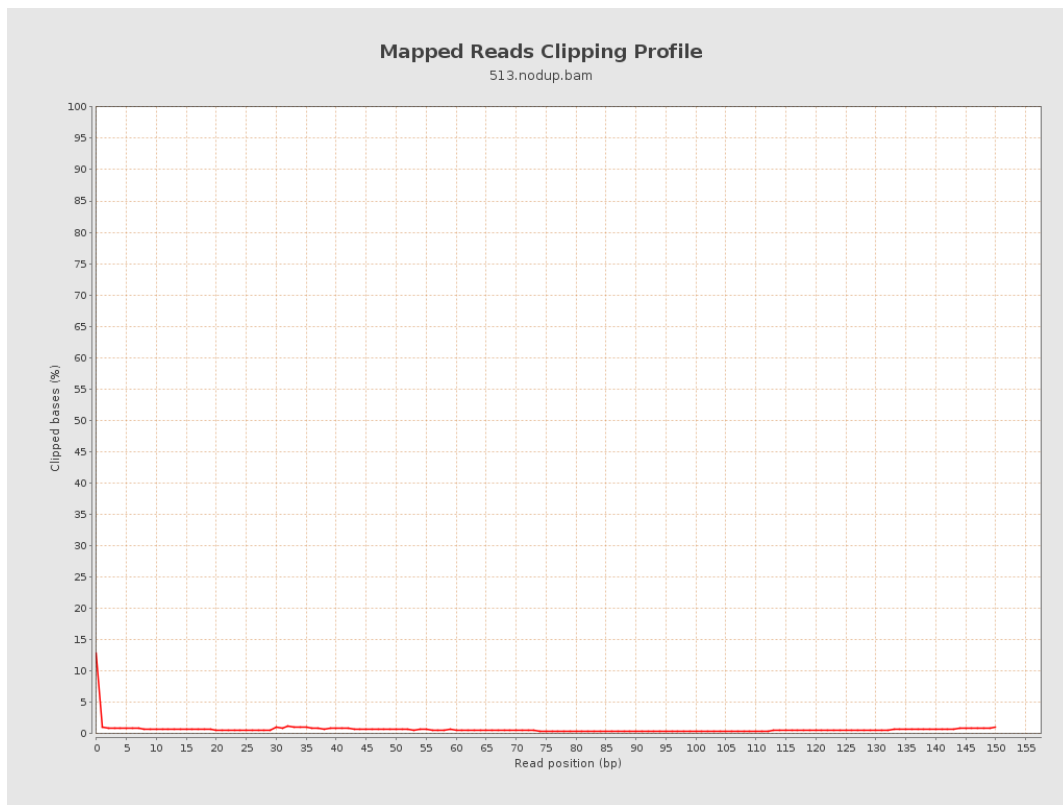
11. Results : Homopolymer Indels
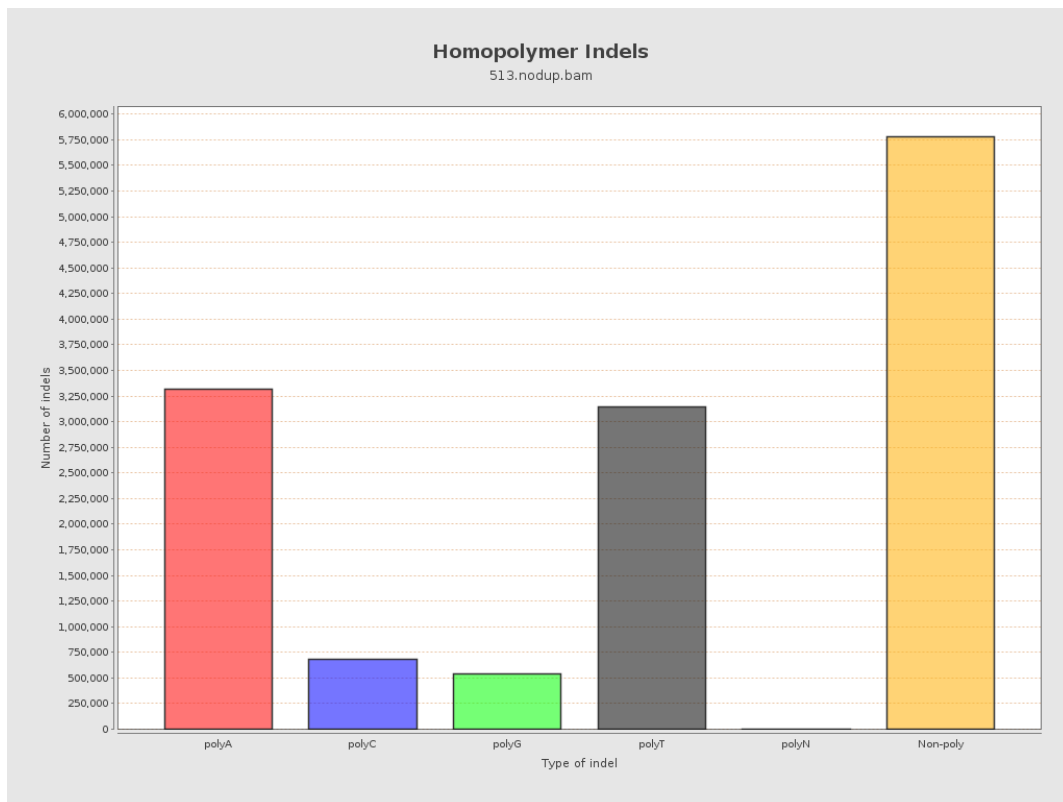
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
513.nodup.bam

14. Results : Insert Size Across Reference
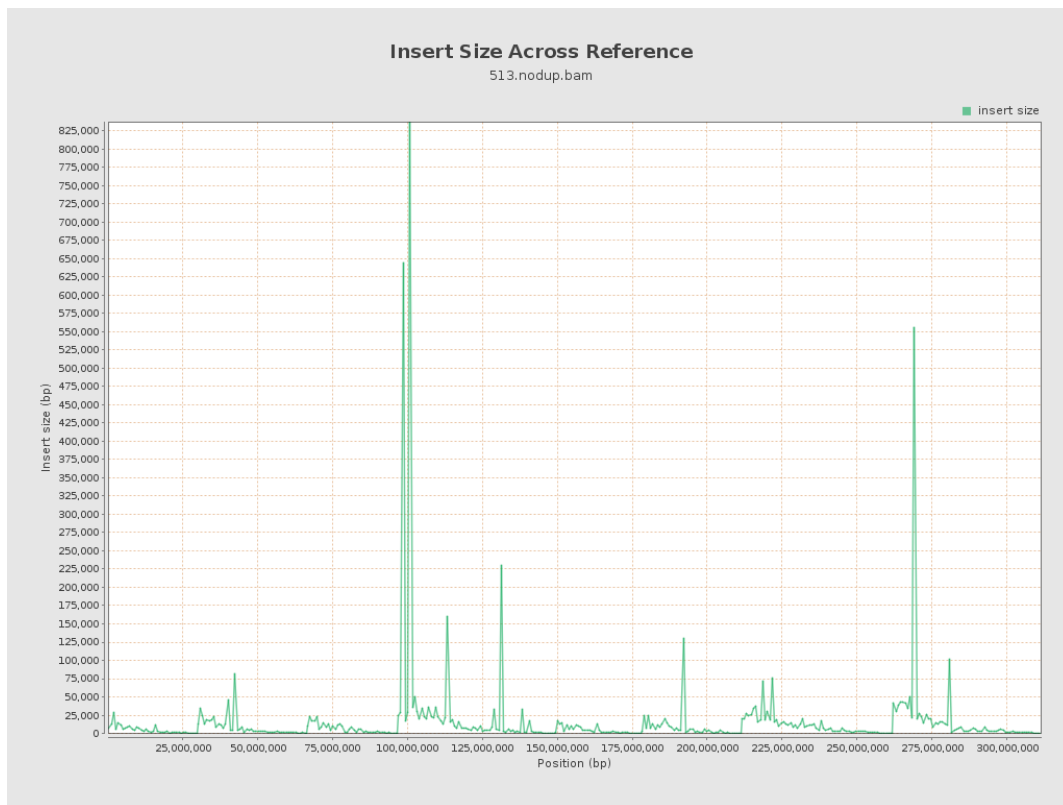
15. Results : Insert Size Histogram

Insert Size Histogram
513.nodup.bam