Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:25:18

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1153
.nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1153 .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_407/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_407_S382_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_407/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_407_S382_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:25:18 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	51,339,530
Mapped reads	46,592,687 / 90.75%
Unmapped reads	4,746,843 / 9.25%
Mapped paired reads	46,592,687 / 90.75%
Mapped reads, first in pair	23,349,645 / 45.48%
Mapped reads, second in pair	23,243,042 / 45.27%
Mapped reads, both in pair	45,010,198 / 87.67%
Mapped reads, singletons	1,582,489 / 3.08%
Read min/max/mean length	30 / 151 / 148.18
Duplicated reads (flagged)	8,744,504 / 17.03%
Clipped reads	10,878,075 / 21.19%

2.2. ACGT Content

Number/percentage of A's	1,969,298,166 / 30.74%
Number/percentage of C's	1,234,204,571 / 19.27%
Number/percentage of T's	1,971,983,184 / 30.79%
Number/percentage of G's	1,230,165,675 / 19.2%
Number/percentage of N's	21,556 / 0%
GC Percentage	38.47%

2.3. Coverage

| Mean | 20.6073 |
| Standard Deviation | 212.2009 |

2.4. Mapping Quality

| Mean Mapping Quality | 43.84 |

2.5. Insert size

| Mean | 277,553.63 |
| Standard Deviation | 2,539,186.97 |
| P25/Median/P75 | 367 / 477 / 624 |

2.6. Mismatches and indels

| General error rate | 2.4% |
Mismatches	141,079,023
Insertions	4,615,964
Mapped reads with at least one insertion	8.84%
Deletions	4,421,247
Mapped reads with at least one deletion	8.44%
Homopolymer indels	56.99%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	460193755	15.482	76.3951

| LT669789.1 | 36598175 | 763386685 | 20.8586 | 225.3035 |
LT669790.1	30422129	735696744	24.1829	287.5075
LT669791.1	52758100	1096579832	20.7851	224.812
LT669792.1	28376109	569763145	20.079	234.9998
LT669793.1	33388210	622094636	18.6322	130.389
LT669794.1	50579949	995079193	19.6734	173.0827
LT669795.1	49795044	1179297829	23.683	252.2644

3. Results : Coverage across reference

Coverage across reference
1153.nodup.bam

4. Results : Coverage Histogram

Coverage Histogram
1153.nodup.bam
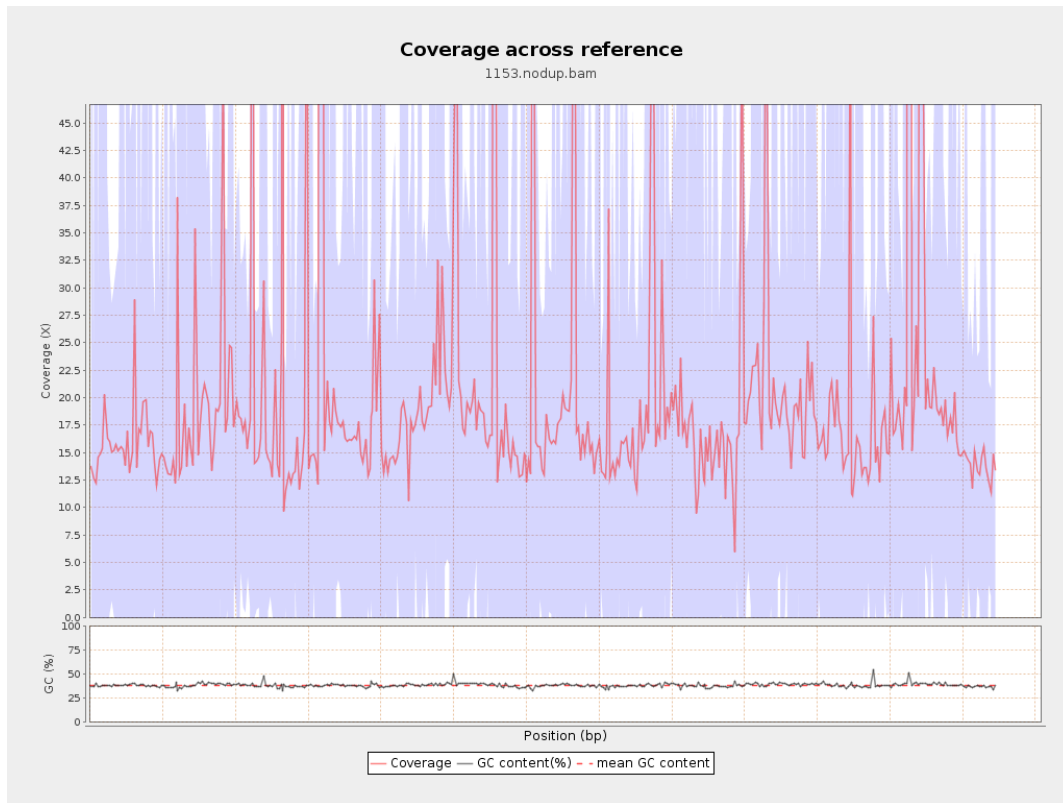
5. Results : Coverage Histogram (0-50X)
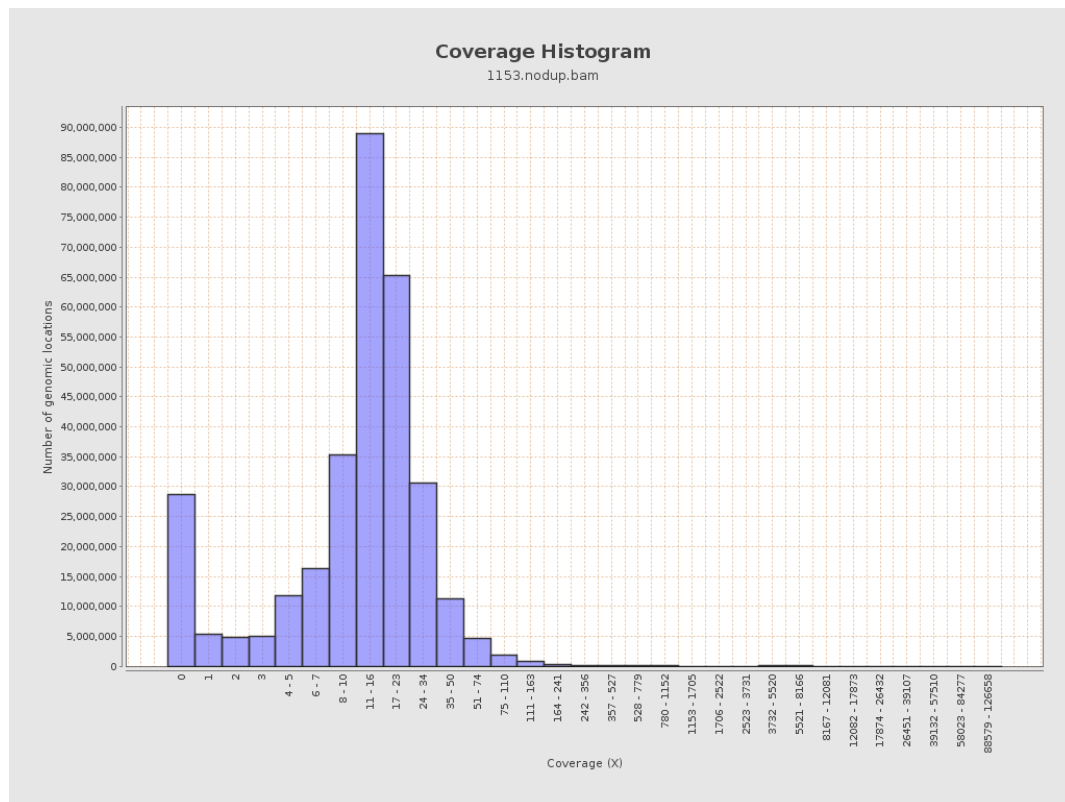
Coverage Histogram (0-50X)
1153.nodup.bam
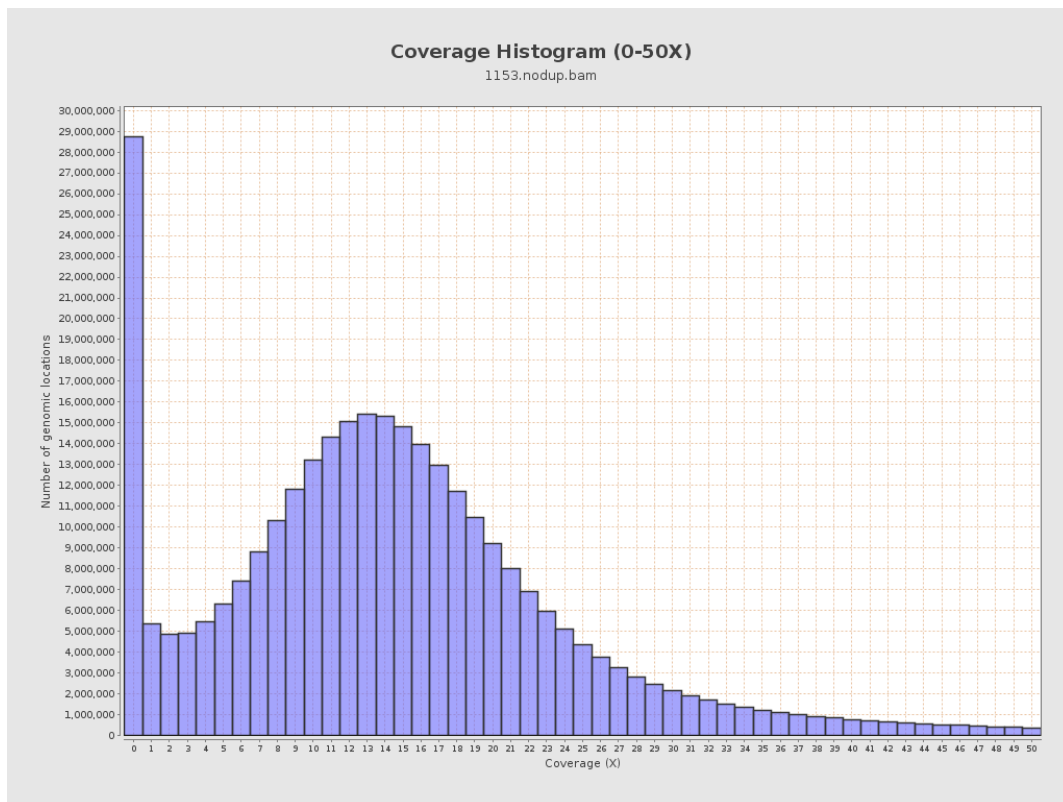
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
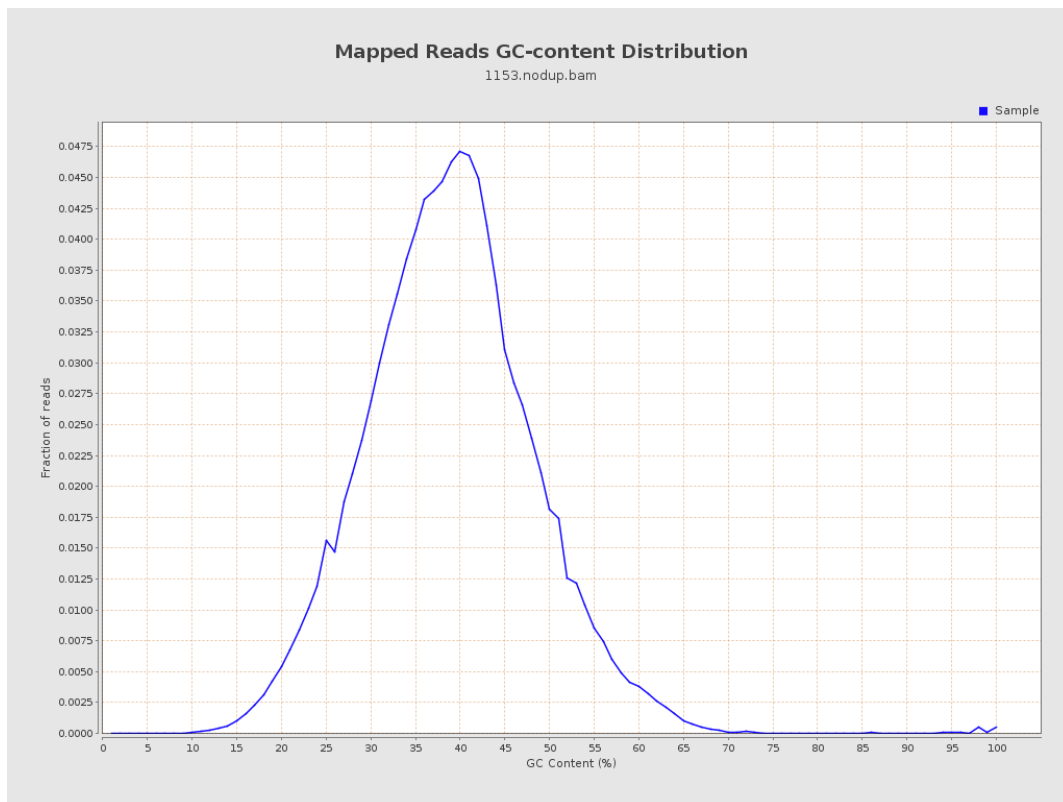1153.nodup.bam
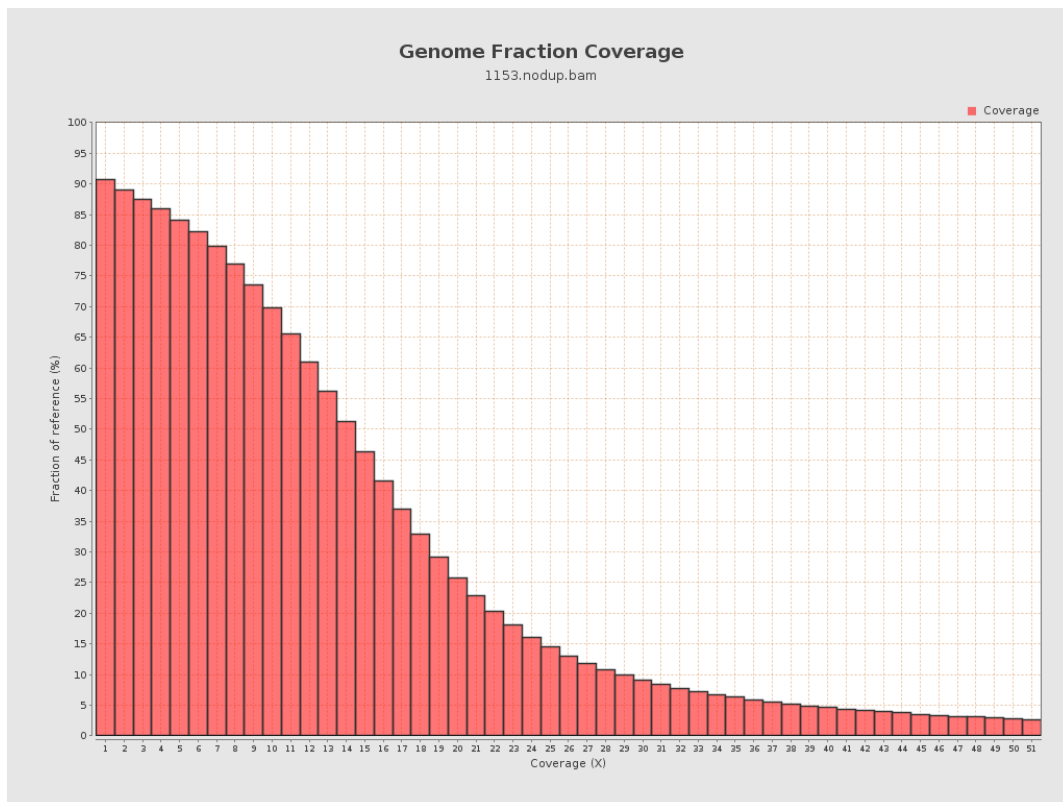
7. Results : Duplication Rate Histogram
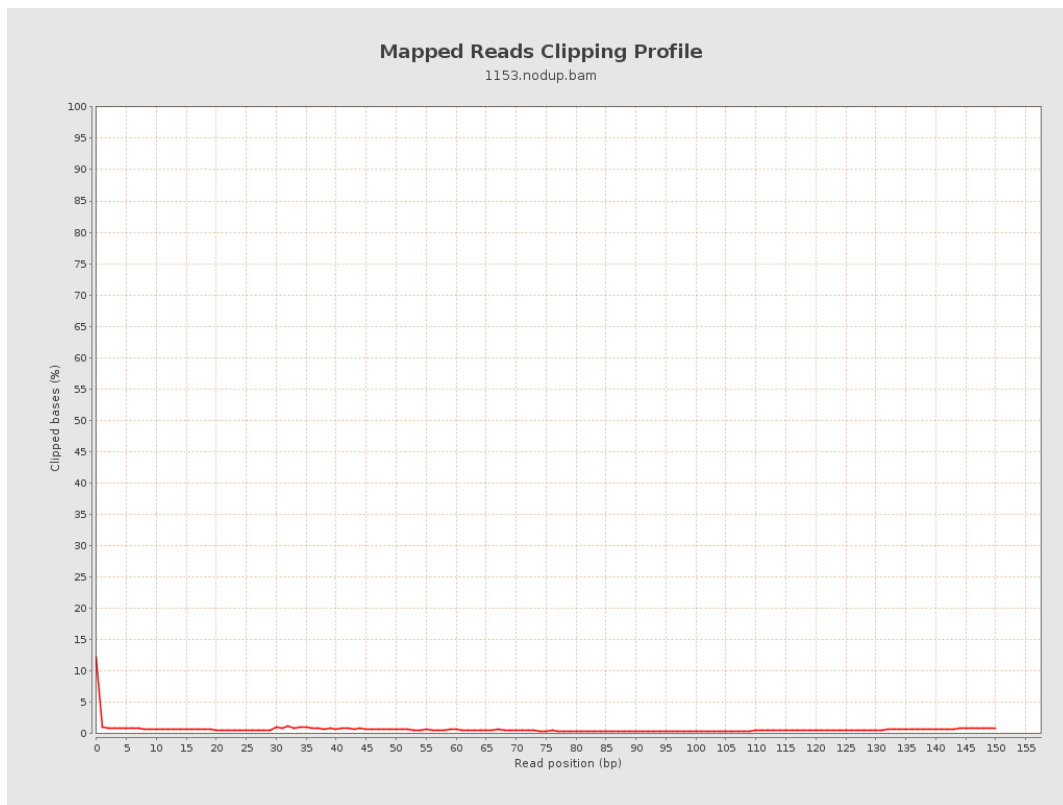

Duplication Rate Histogram
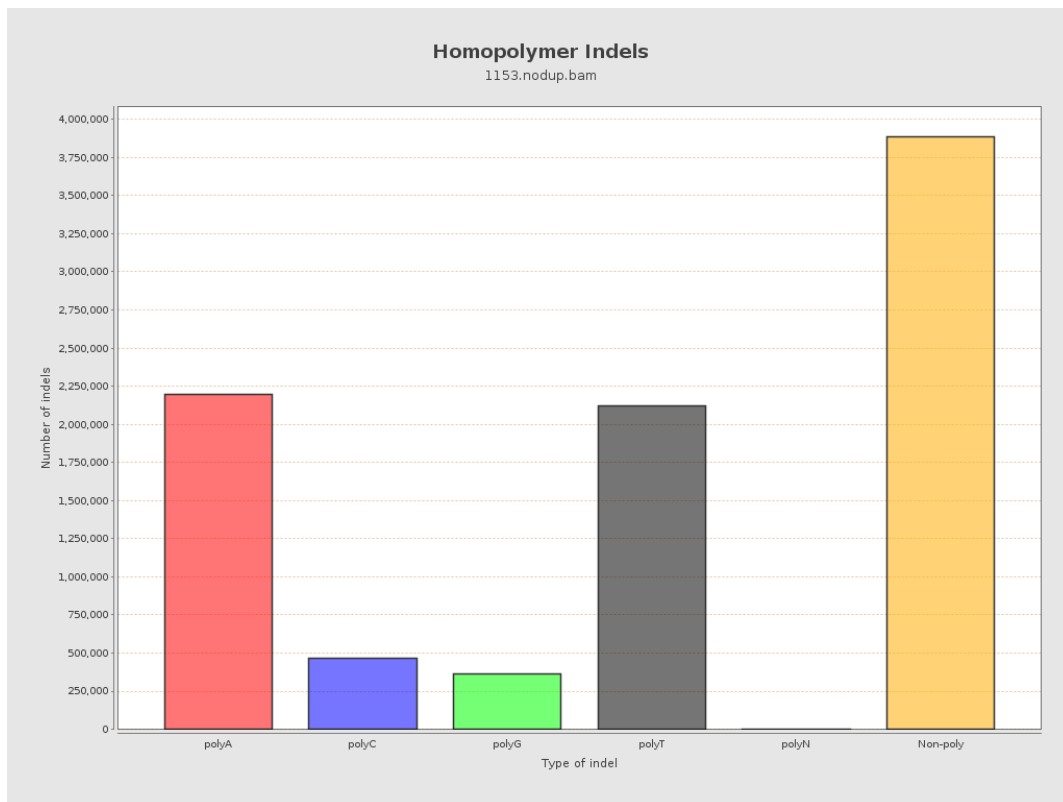1153.nodup.bam
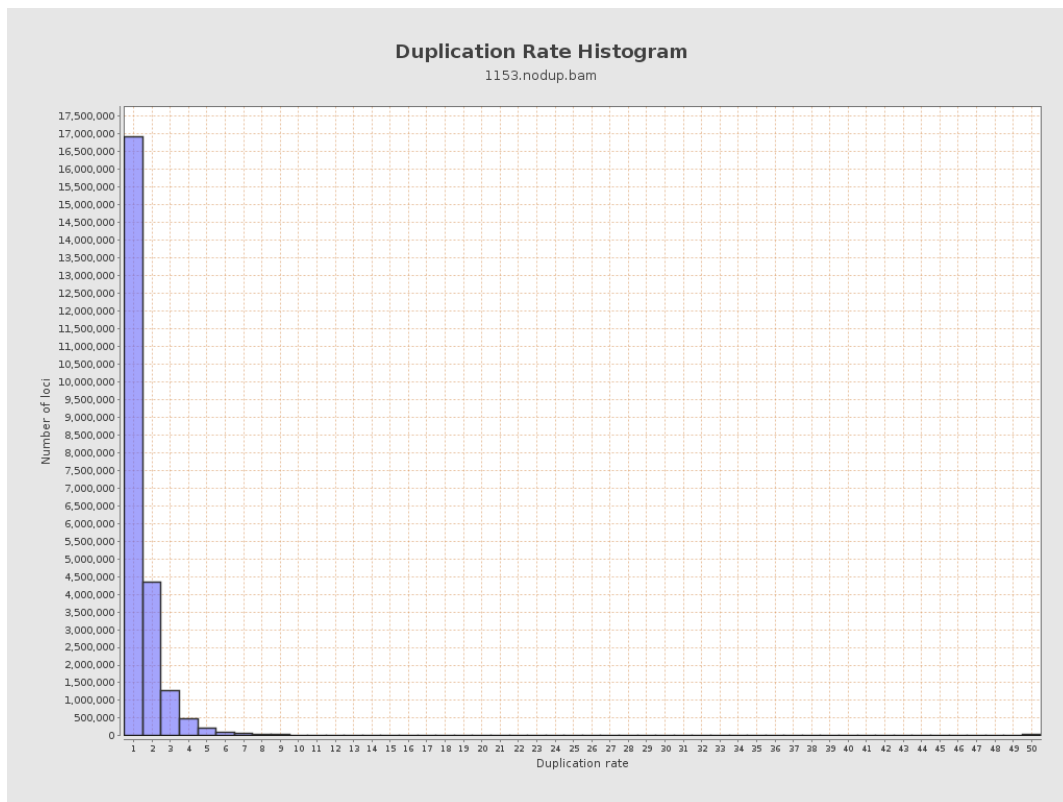
8. Results : Mapped Reads Nucleotide Content
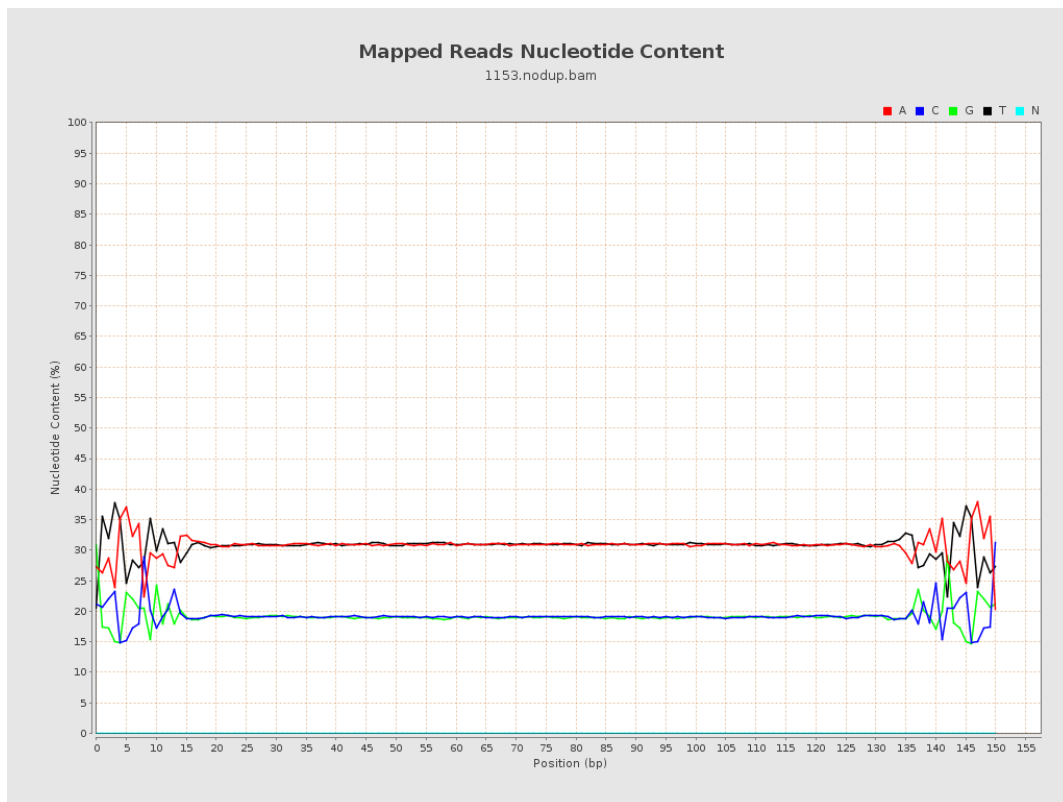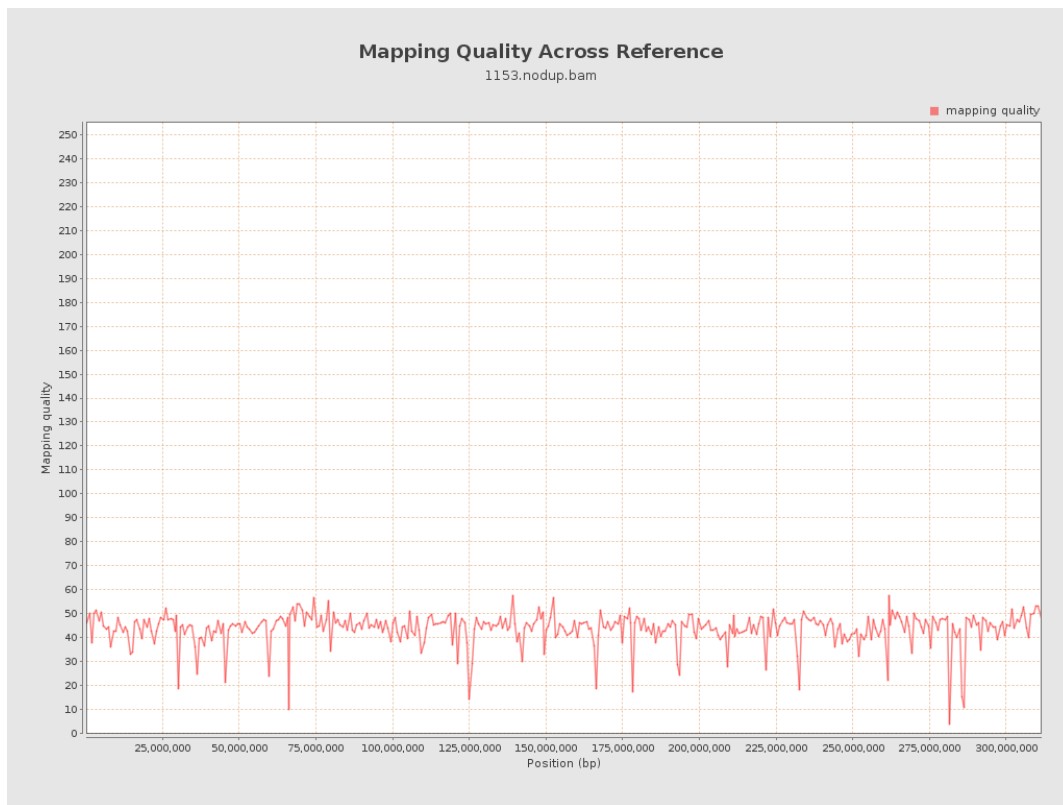
9. Results : Mapped Reads GC-content Distribution

10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels
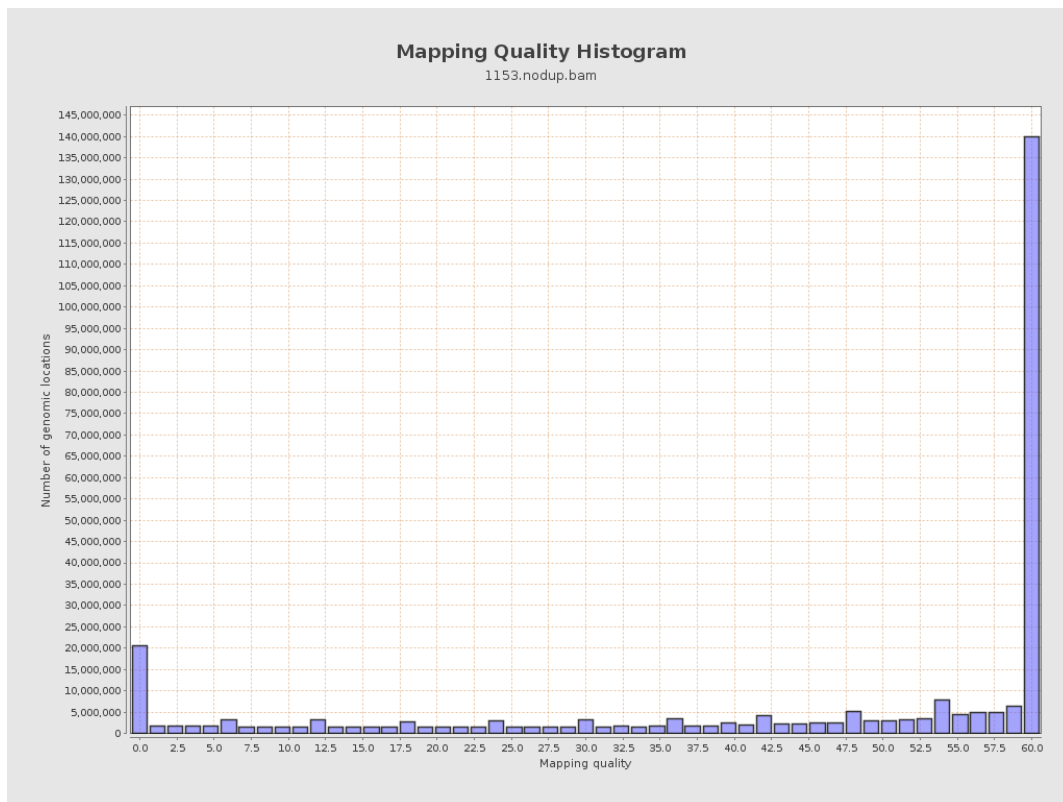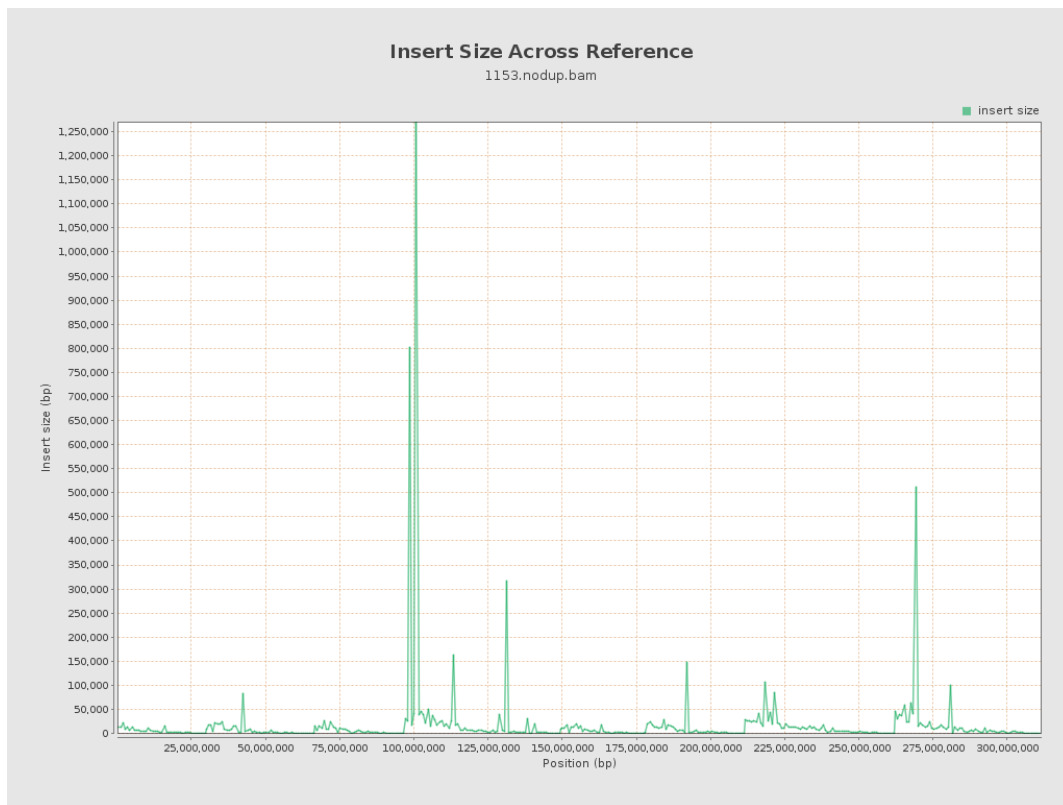
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
1153.nodup.bam

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram