Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:32:33

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/540
.nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/540 .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_170/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_170_S260_L002 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_170/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_170_S260_L002 _R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:32:32 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	69,898,889
Mapped reads	64,462,691 / 92.22%
Unmapped reads	5,436,198 / 7.78%
Mapped paired reads	64,462,691 / 92.22%
Mapped reads, first in pair	32,291,011 / 46.2%
Mapped reads, second in pair	32,171,680 / 46.03%
Mapped reads, both in pair	62,650,650 / 89.63%
Mapped reads, singletons	1,812,041 / 2.59%
Read min/max/mean length	30 / 151 / 148.11
Duplicated reads (flagged)	12,202,620 / 17.46%
Clipped reads	14,825,710 / 21.21%

2.2. ACGT Content

Number/percentage of A's	2,747,065,020 / 30.9%
Number/percentage of C's	1,697,495,584 / 19.09%
Number/percentage of T's	2,749,233,064 / 30.92%
Number/percentage of G's	1,697,029,382 / 19.09%
Number/percentage of N's	36,870 / 0%
GC Percentage	38.18%

2.3. Coverage

Mean	28.6044
Standard Deviation	257.7448

2.4. Mapping Quality

Mean Mapping Quality	44.02

2.5. Insert size

Mean	254,535.08
Standard Deviation	2,412,673.88
P25/Median/P75	331 / 431 / 563

2.6. Mismatches and indels

General error rate	2.36%
Mismatches	192,301,088
Insertions	6,358,154
Mapped reads with at least one insertion	8.81%
Deletions	6,247,417
Mapped reads with at least one deletion	8.6%
Homopolymer indels	56.95%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	693318723	23.3249	94.3173

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LT669789.1	36598175	1062753618	29.0384	273.6544
LT669790.1	30422129	1018484379	33.4784	343.9718
LT669791.1	52758100	1486003999	28.1664	258.8805
LT669792.1	28376109	810654420	28.5682	265.9949
LT669793.1	33388210	872043775	26.1183	221.2043
LT669794.1	50579949	1350845386	26.7071	213.9263
LT669795.1	49795044	1620240850	32.5382	304.0652

3. Results : Coverage across reference

Coverage across reference
540.nodup.bam
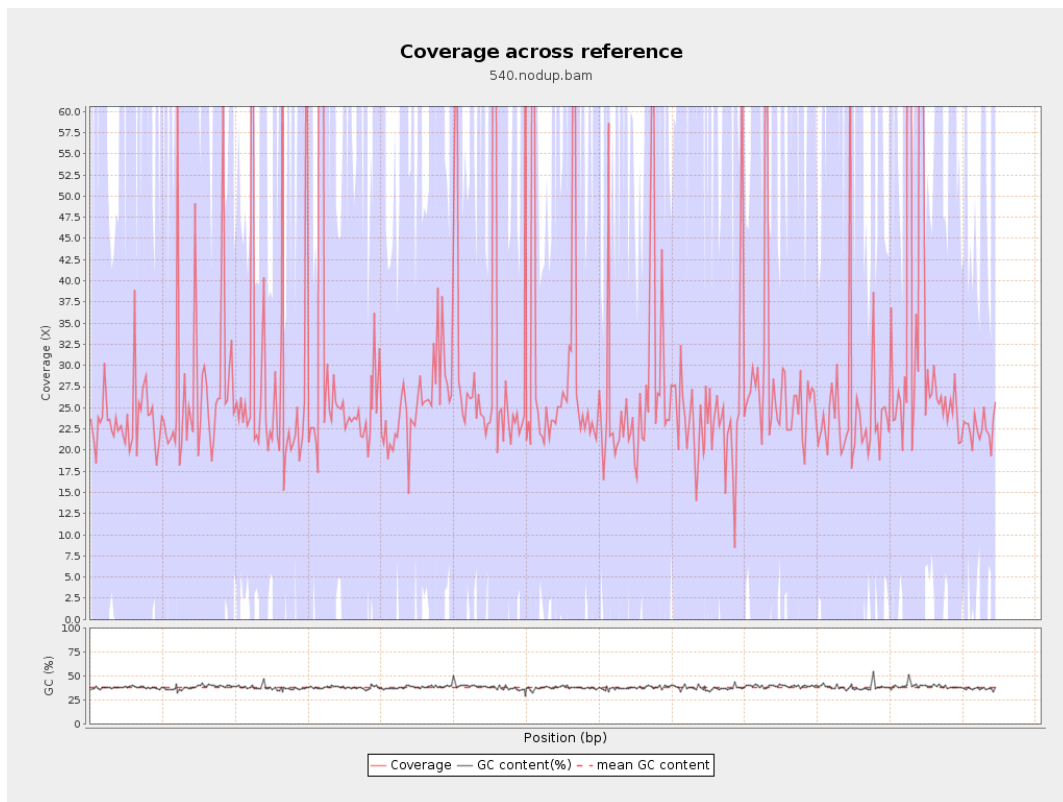
4. Results : Coverage Histogram
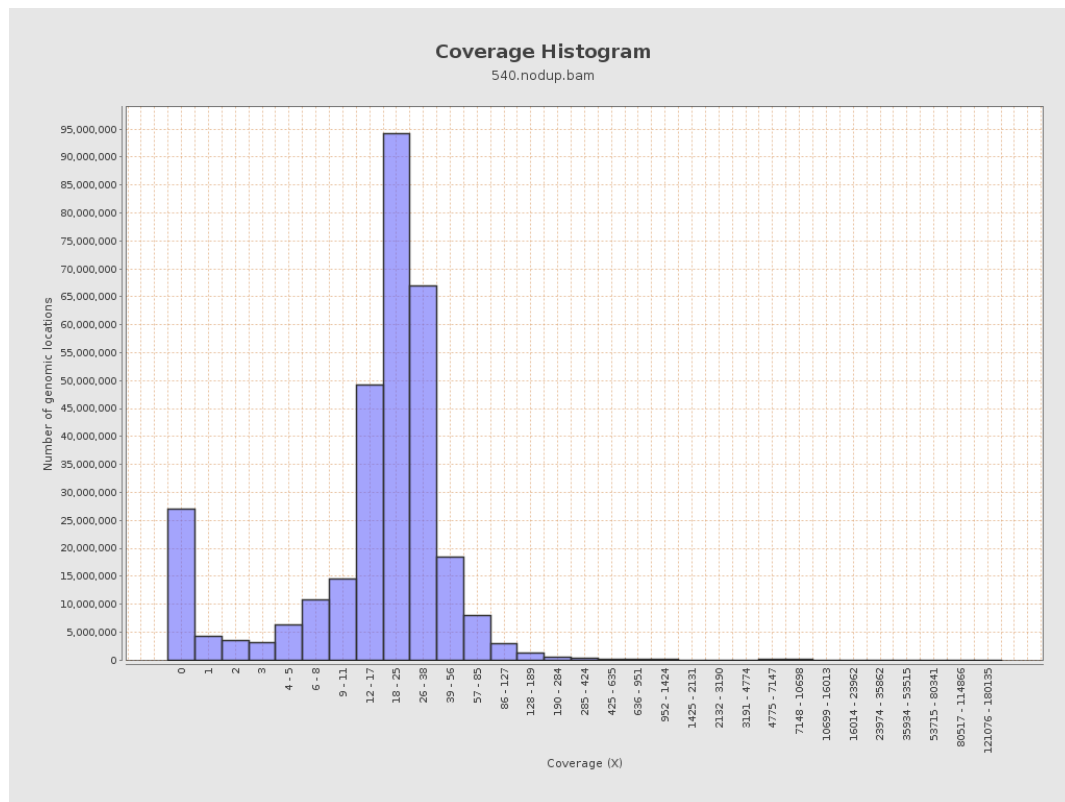
5. Results : Coverage Histogram (0-50X)
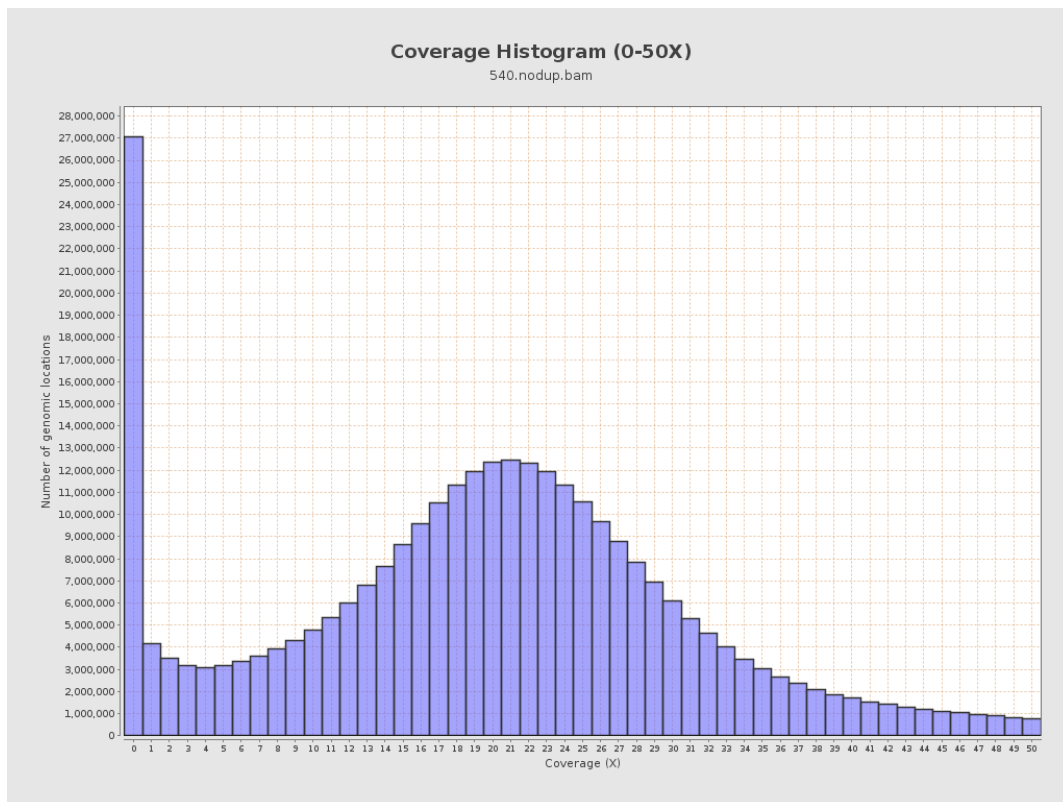
6. Results : Genome Fraction Coverage
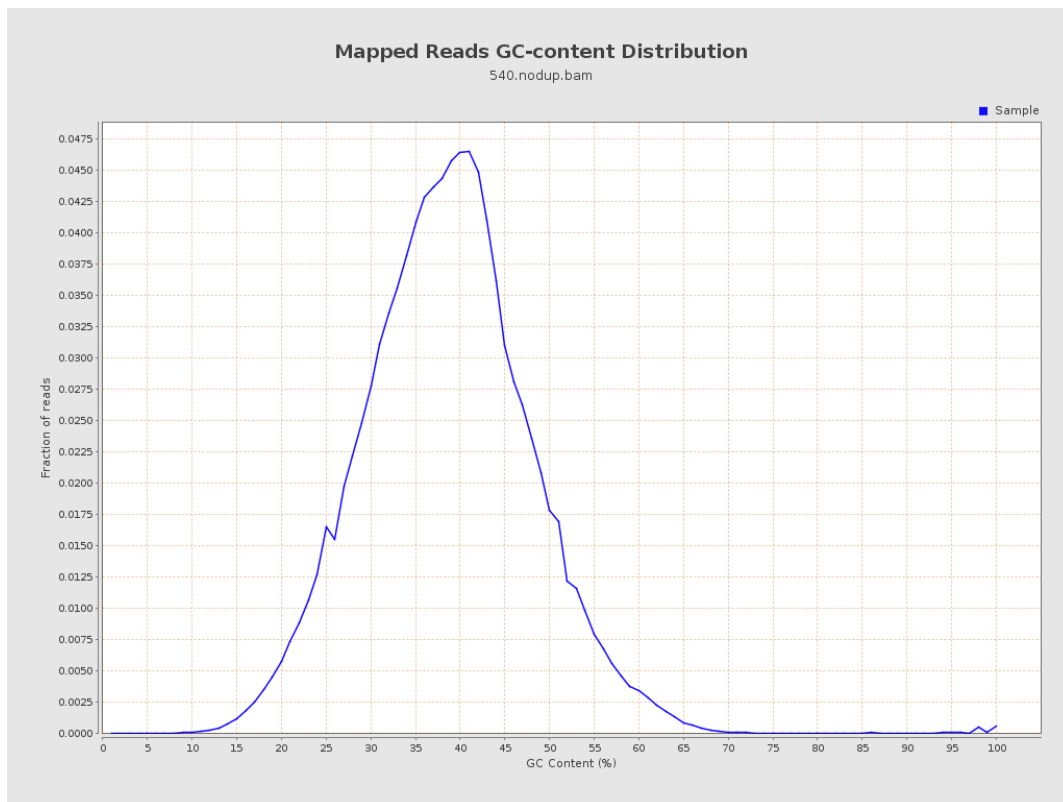

Genome Fraction Coverage
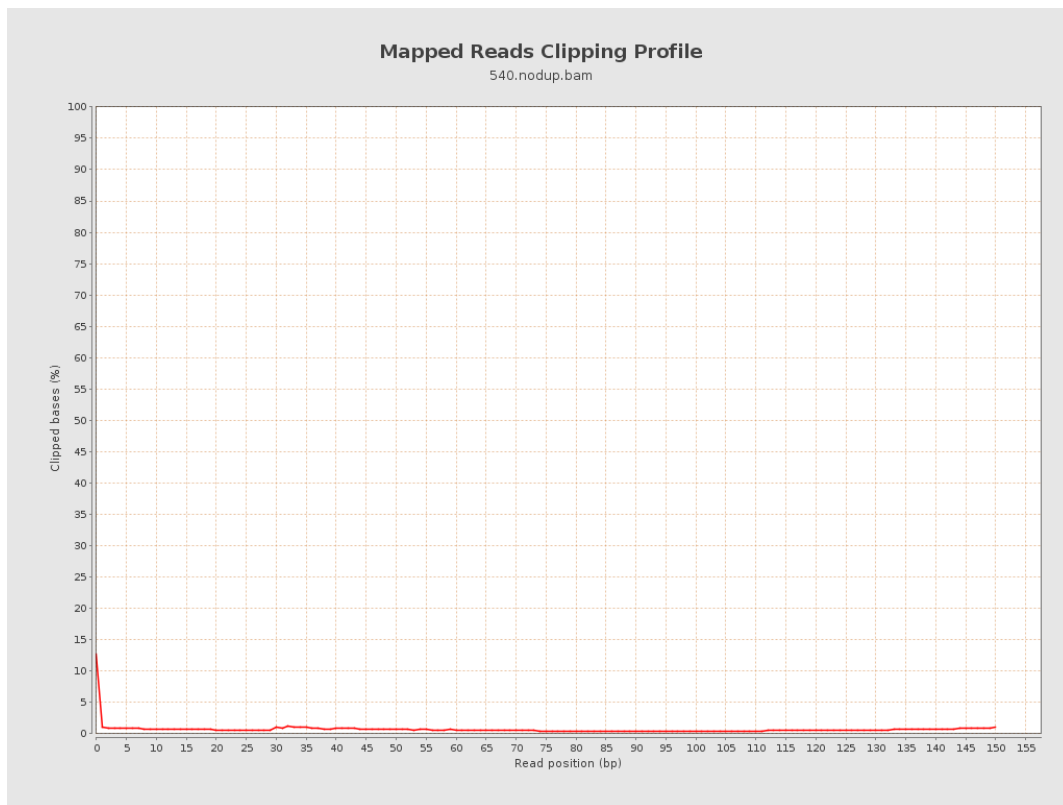540.nodup.bam
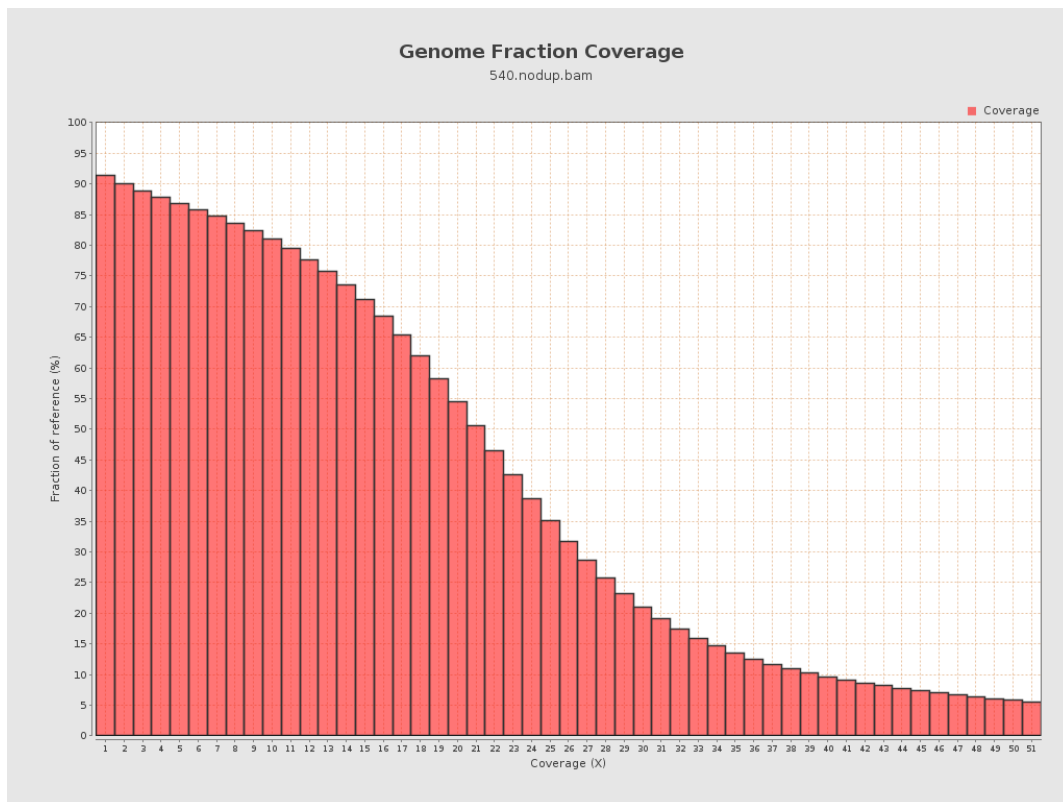
7. Results : Duplication Rate Histogram
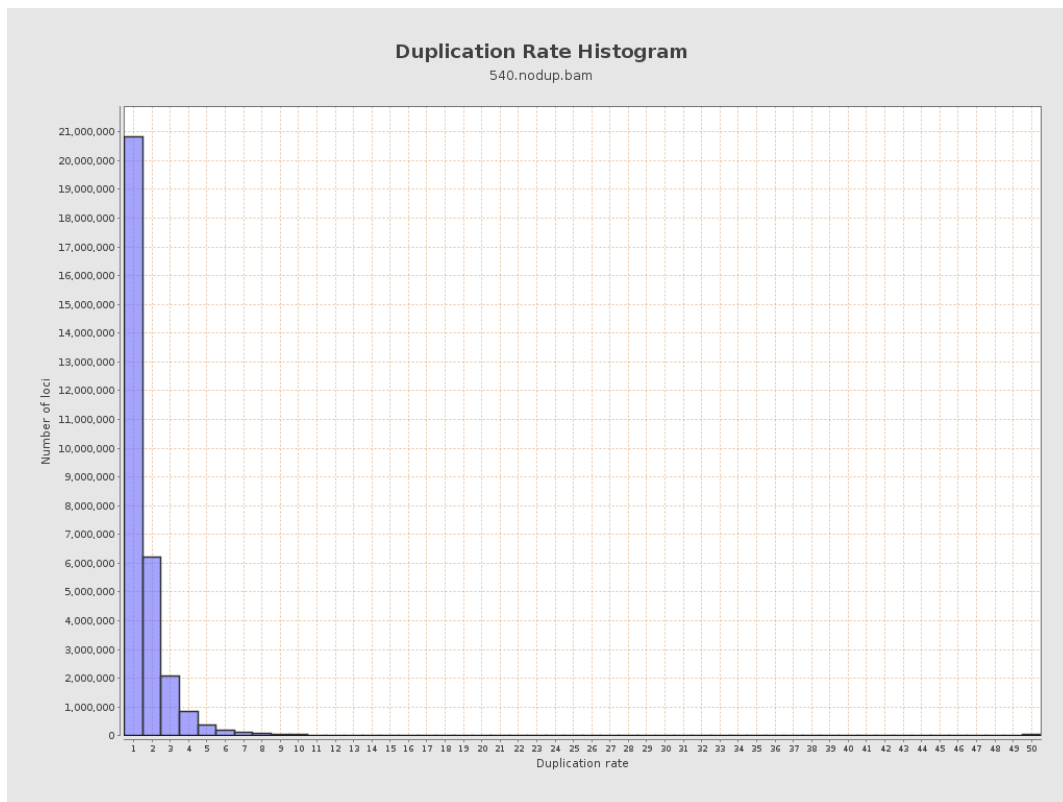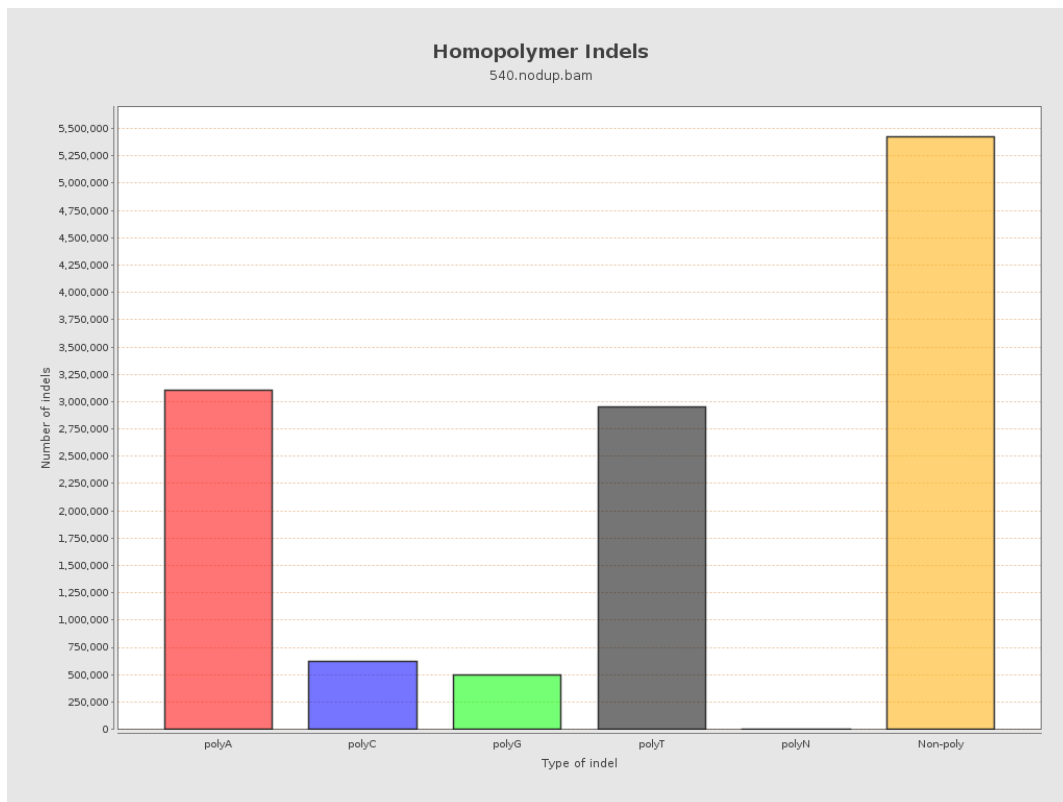
8. Results : Mapped Reads Nucleotide Content
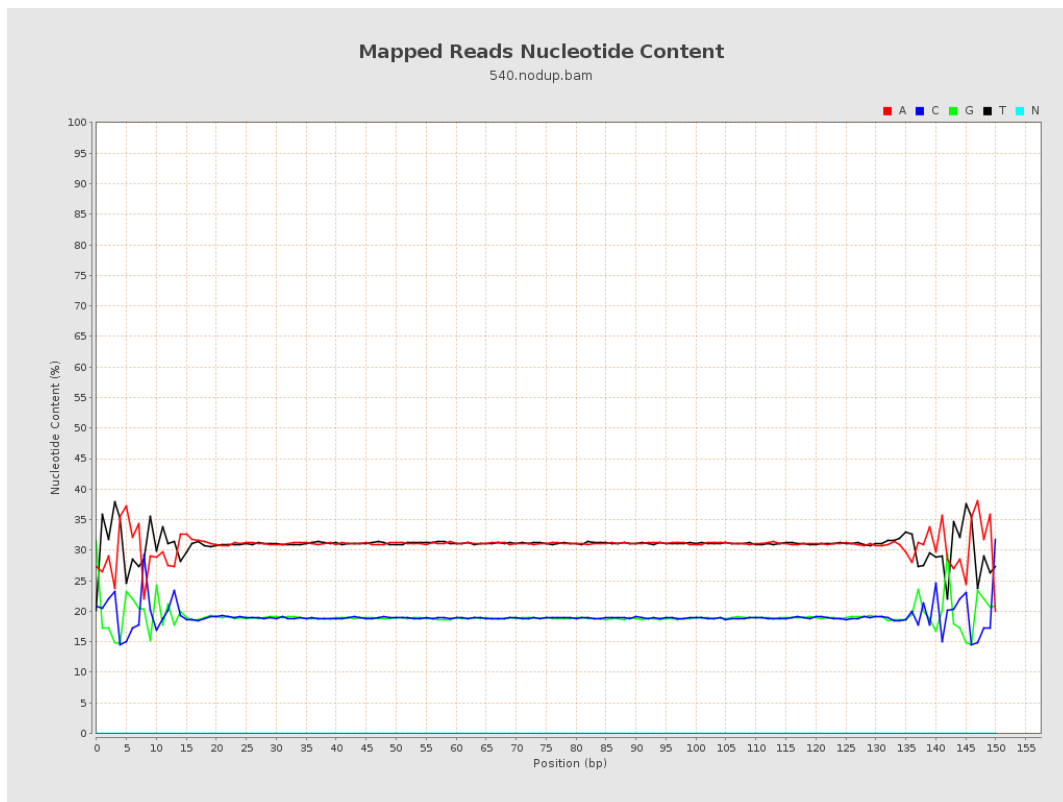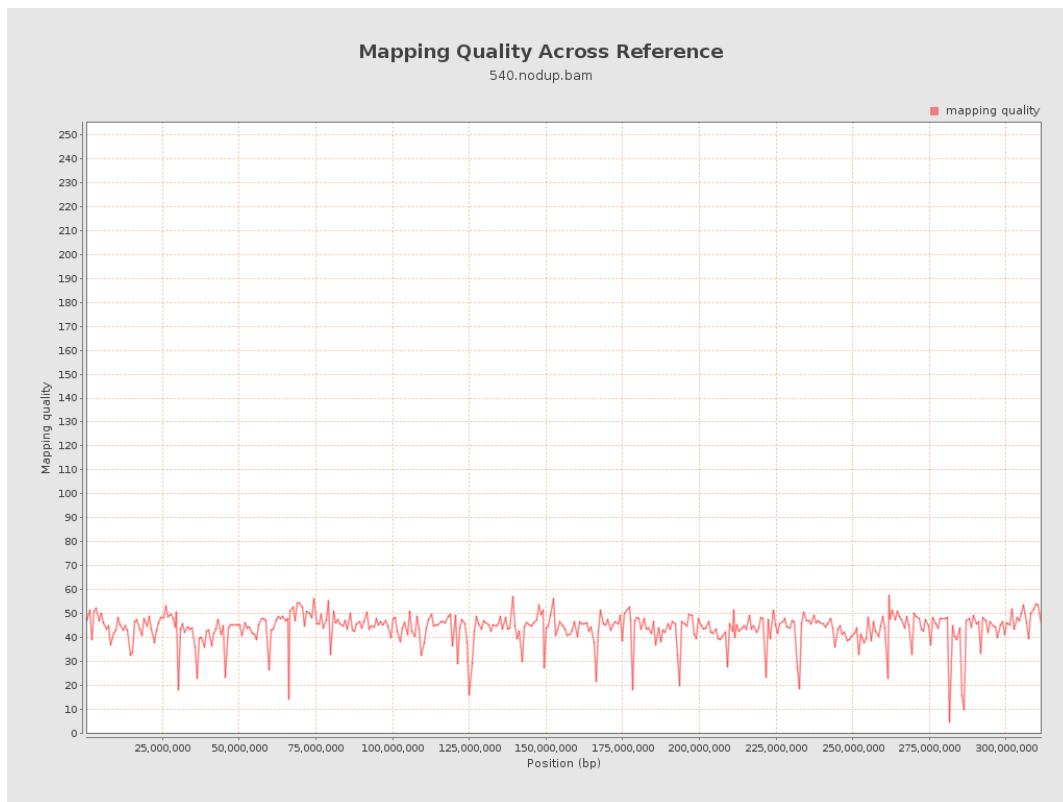
9. Results : Mapped Reads GC-content Distribution

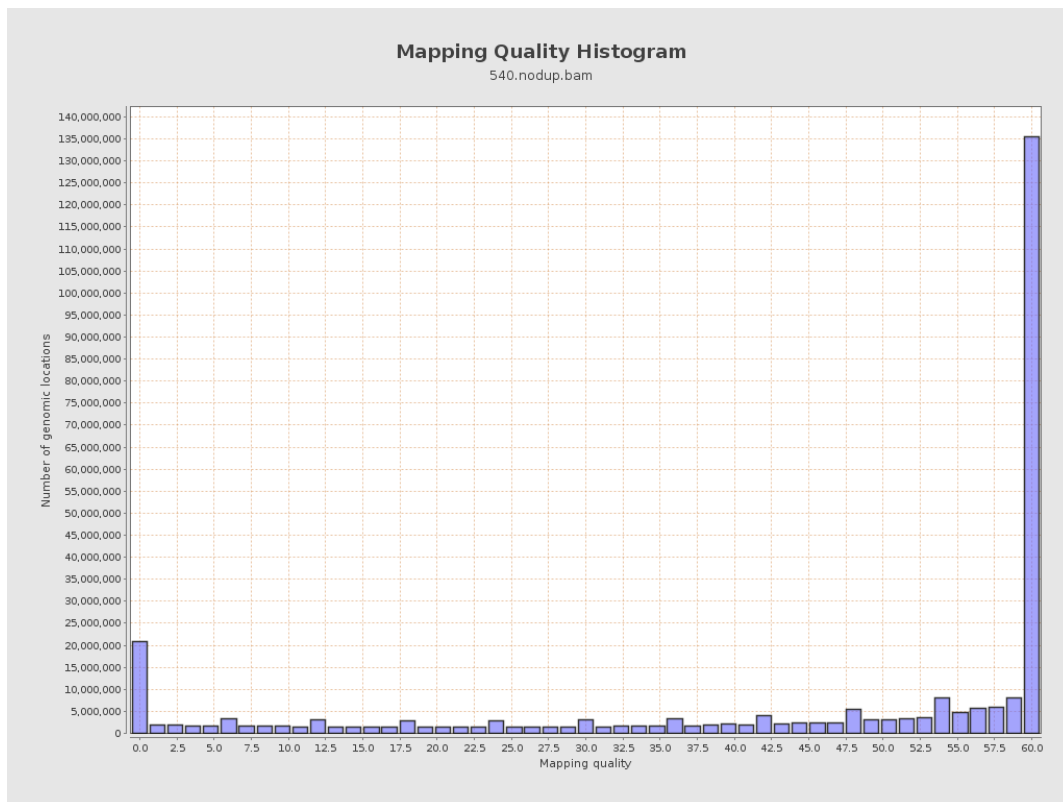# 10. Results : Mapped Reads Clipping Profile

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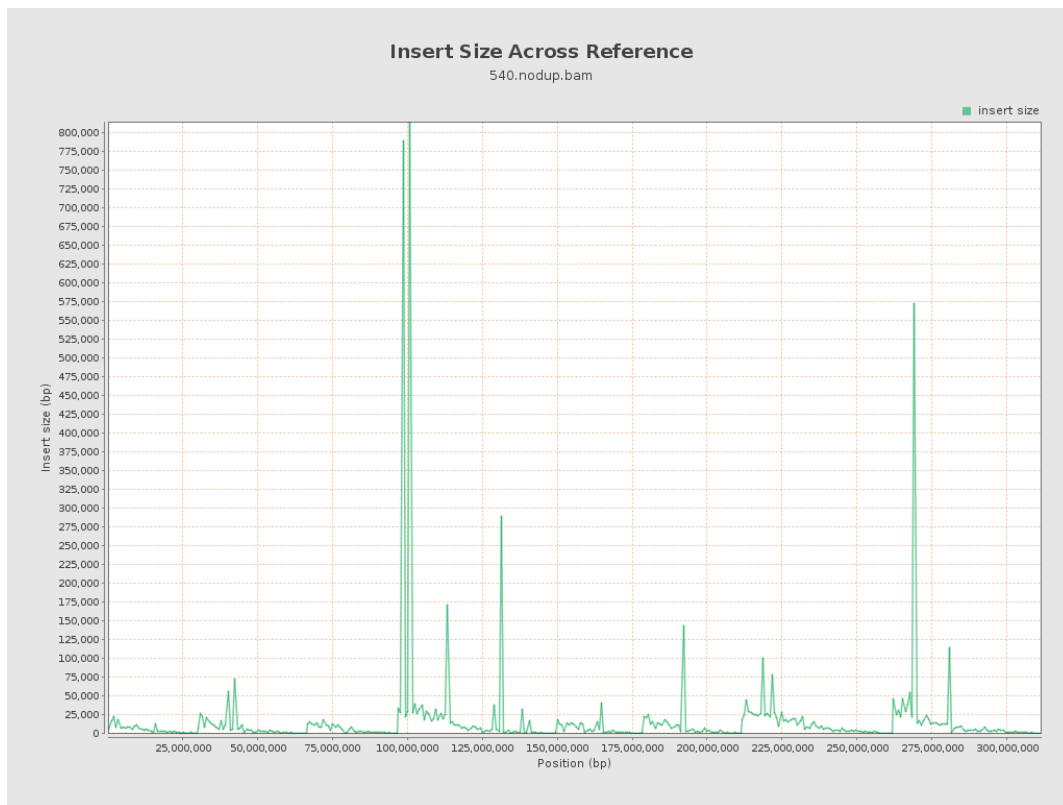
12. Results : Mapping Quality Across Reference

Mapping Quality Across Reference
540.nodup.bam

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram

Insert Size Histogram
540.nodup.bam