Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/29 21:33:28

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/442
.nodup.bam -nw 400 -hm 3

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/442 .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_423/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_423_S398_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_423/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_423_S398_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:33:27 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	71,666,272
Mapped reads	67,541,919 / 94.25%
Unmapped reads	4,124,353 / 5.75%
Mapped paired reads	67,541,919 / 94.25%
Mapped reads, first in pair	33,878,495 / 47.27%
Mapped reads, second in pair	33,663,424 / 46.97%
Mapped reads, both in pair	66,250,670 / 92.44%
Mapped reads, singletons	1,291,249 / 1.8%
Read min/max/mean length	30 / 151 / 148.08
Duplicated reads (flagged)	10,591,633 / 14.78%
Clipped reads	15,602,457 / 21.77%

2.2. ACGT Content

Number/percentage of A's	2,885,318,026 / 30.9%
Number/percentage of C's	1,785,294,104 / 19.12%
Number/percentage of T's	2,886,303,297 / 30.91%
Number/percentage of G's	1,782,193,715 / 19.08%
Number/percentage of N's	31,960 / 0%
GC Percentage	38.2%

2.3. Coverage

Mean	30.0446
Standard Deviation	230.7963

2.4. Mapping Quality

Mean Mapping Quality	44.1

2.5. Insert size

Mean	228,061.83
Standard Deviation	2,262,466.01
P25/Median/P75	337 / 448 / 579

2.6. Mismatches and indels

General error rate	2.33%
Mismatches	200,858,786
Insertions	6,161,280
Mapped reads with at least one insertion	8.21%
Deletions	6,378,338
Mapped reads with at least one deletion	8.42%
Homopolymer indels	56.87%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	731932820	24.624	67.4403

LT669789.1	36598175	1130915104	30.9009	235.5269
LT669790.1	30422129	957215057	31.4644	232.1944
LT669791.1	52758100	1574164657	29.8374	183.2145
LT669792.1	28376109	843424207	29.723	275.2967
LT669793.1	33388210	950490448	28.4678	177.9606
LT669794.1	50579949	1474267409	29.1473	208.2896
LT669795.1	49795044	1700748371	34.155	335.9318

3. Results : Coverage across reference

Coverage across reference
442.nodup.bam

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4. Results : Coverage Histogram

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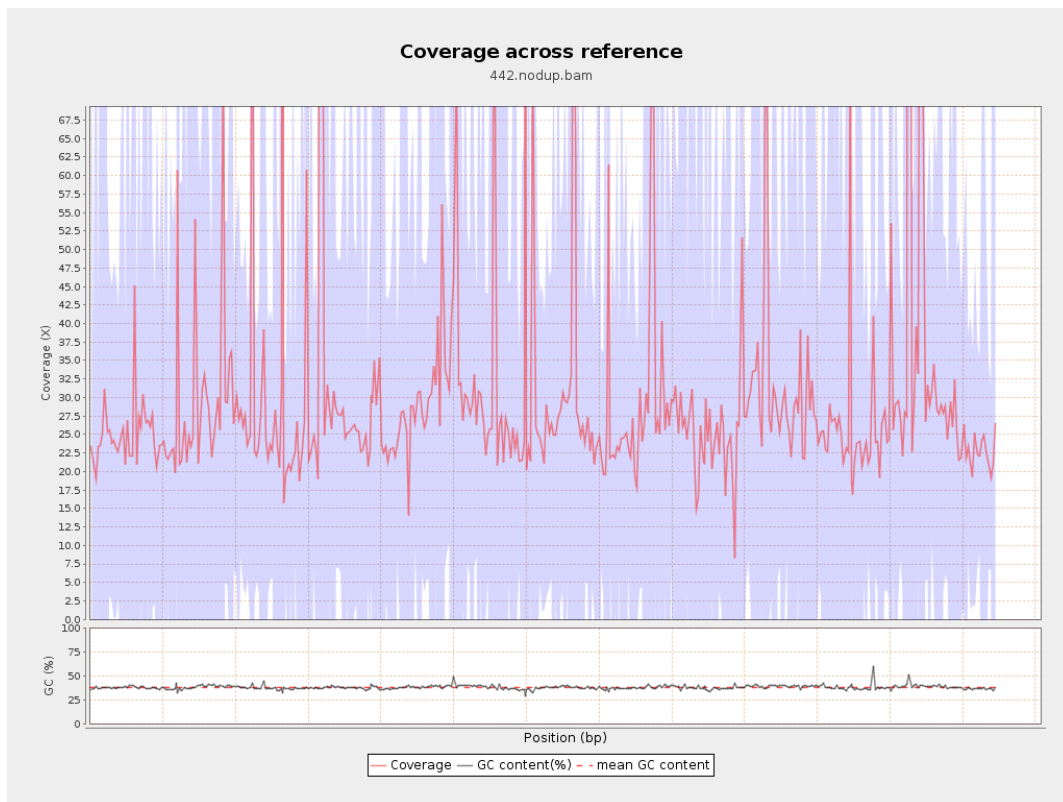
5. Results : Coverage Histogram (0-50X)
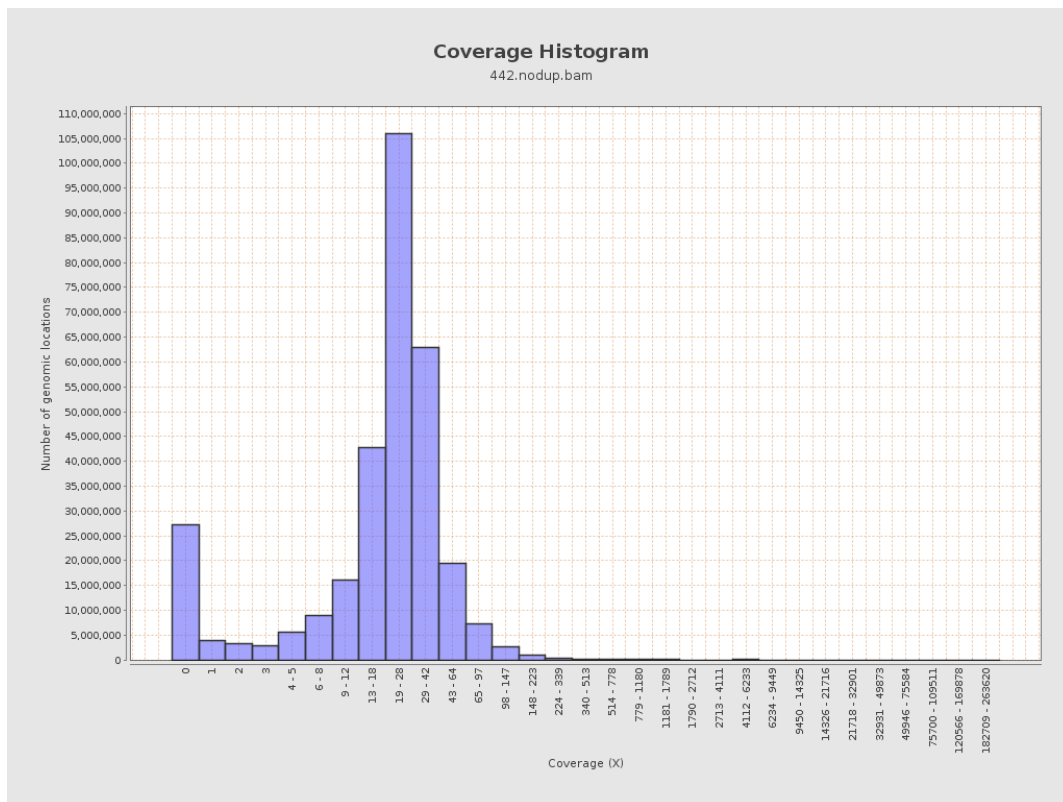
Coverage Histogram (0-50X)
442.nodup.bam
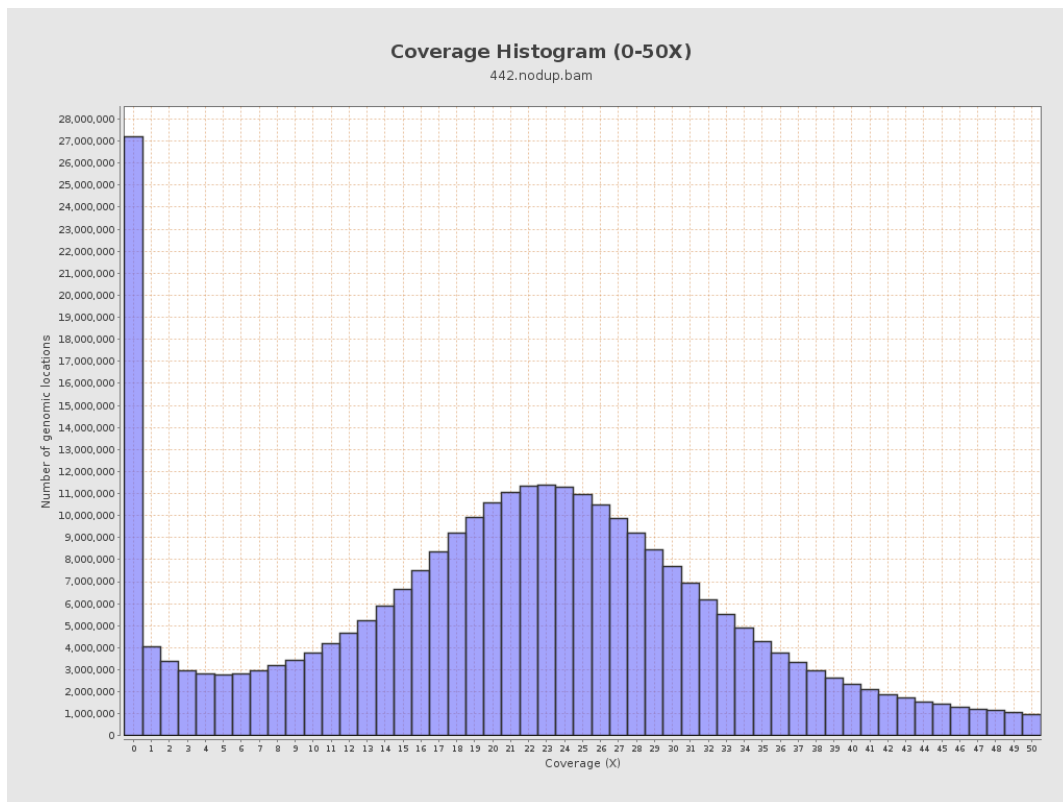
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
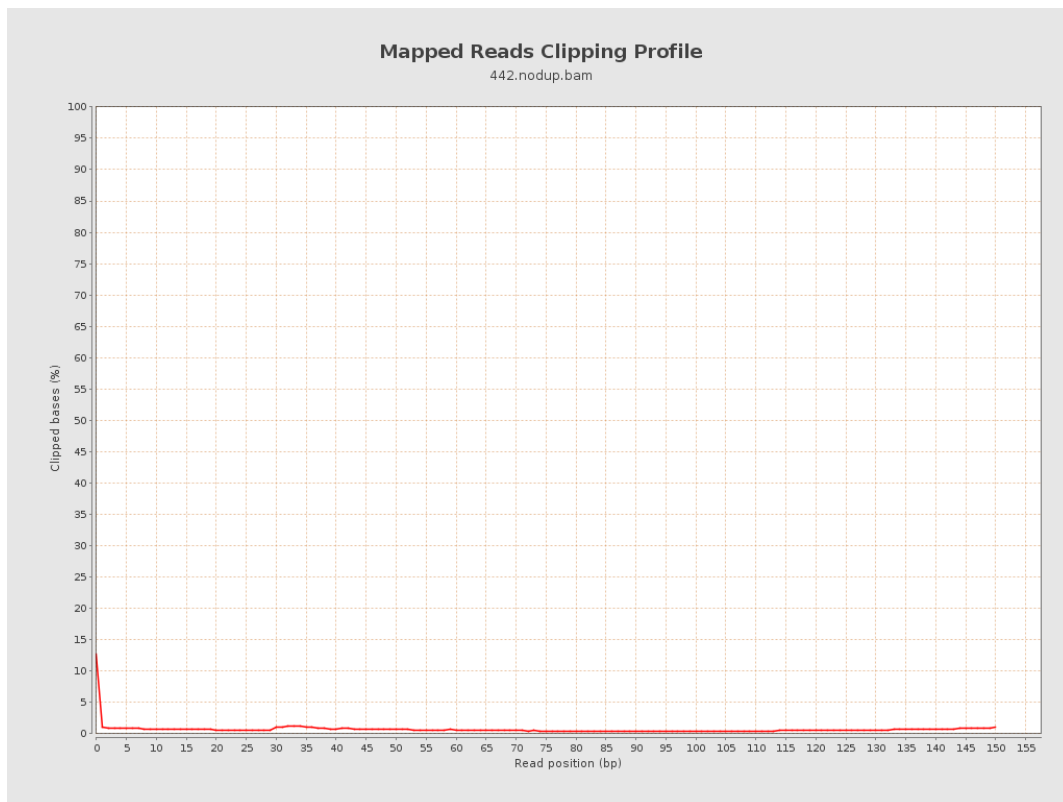442.nodup.bam
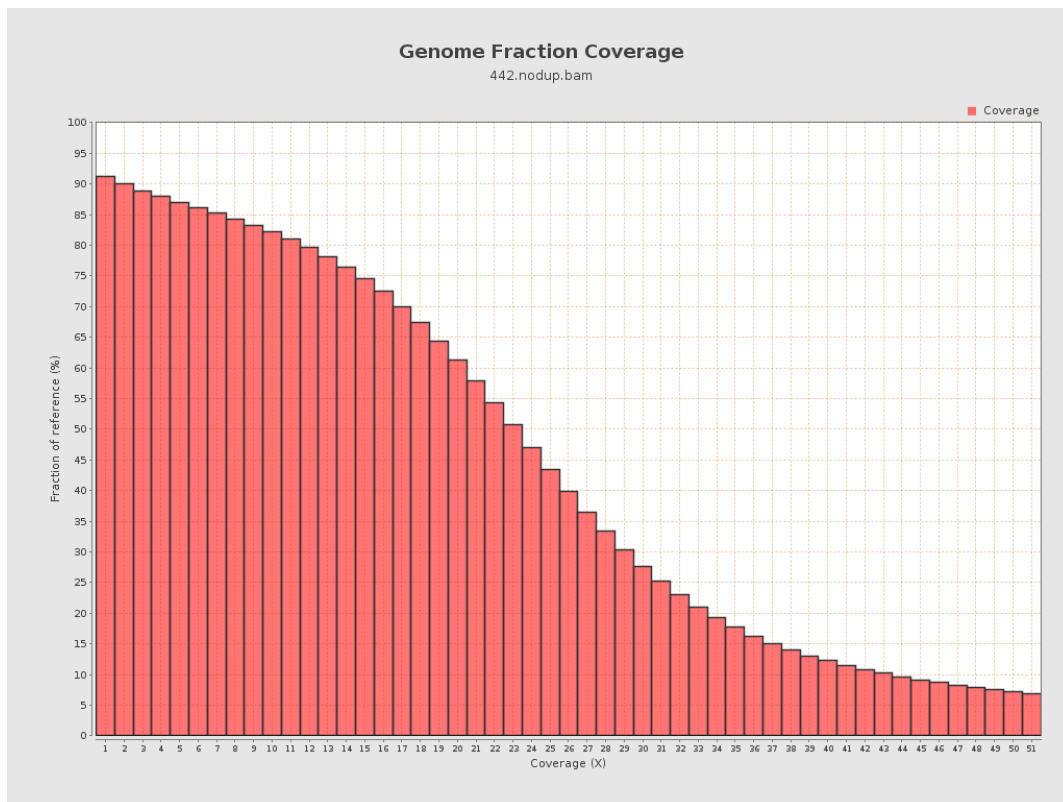
7. Results : Duplication Rate Histogram
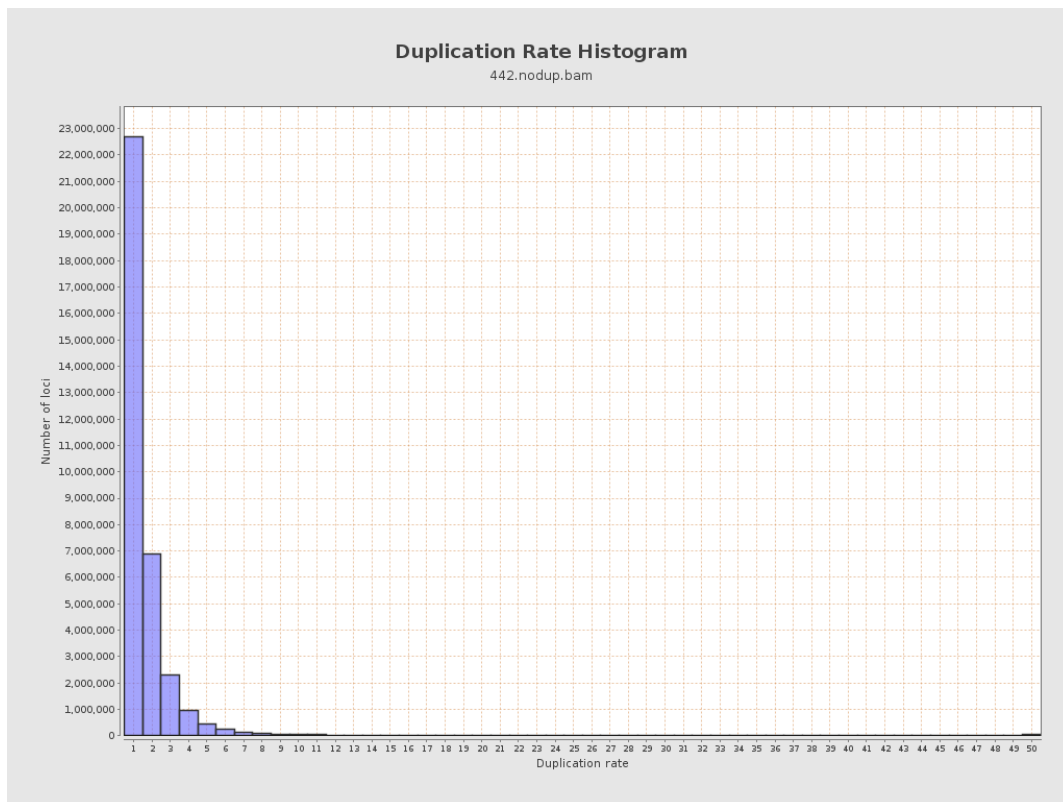
8. Results : Mapped Reads Nucleotide Content

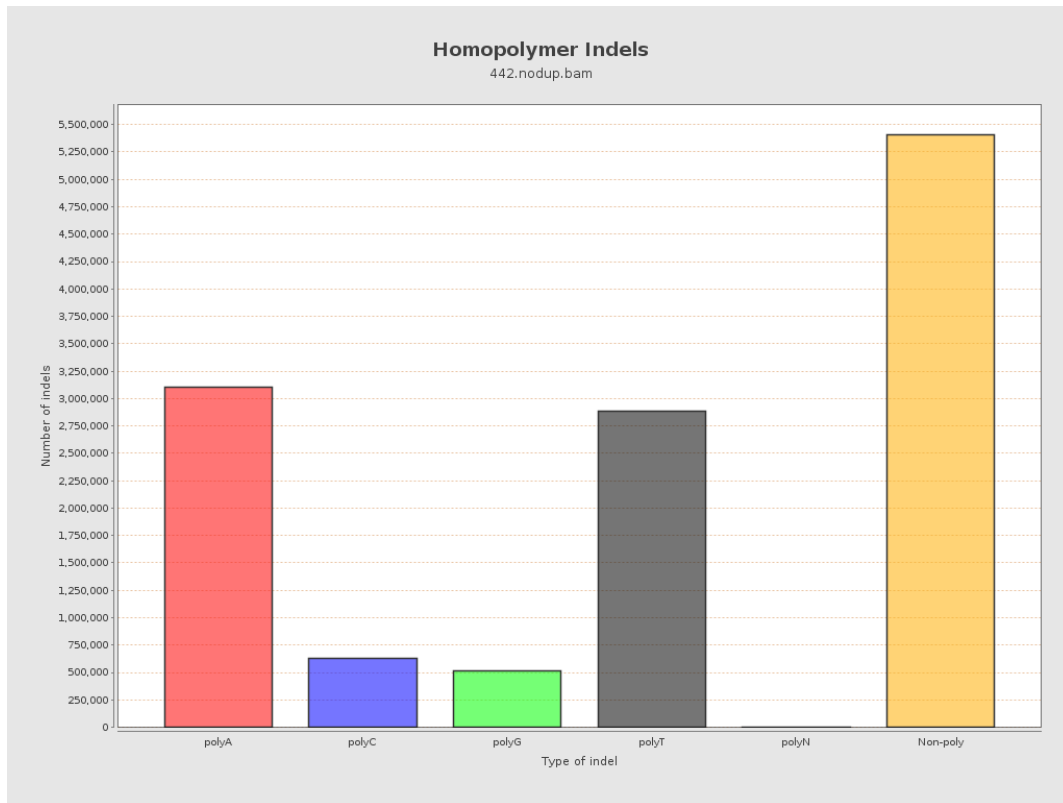# 9. Results : Mapped Reads GC-content Distribution
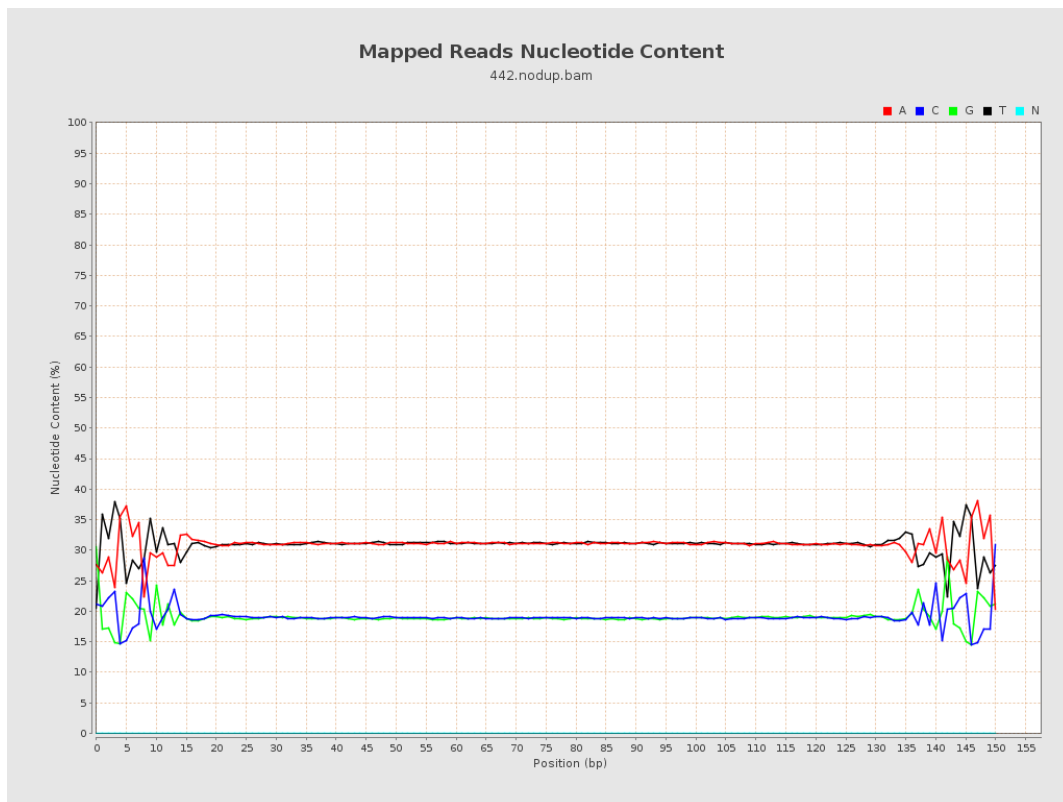
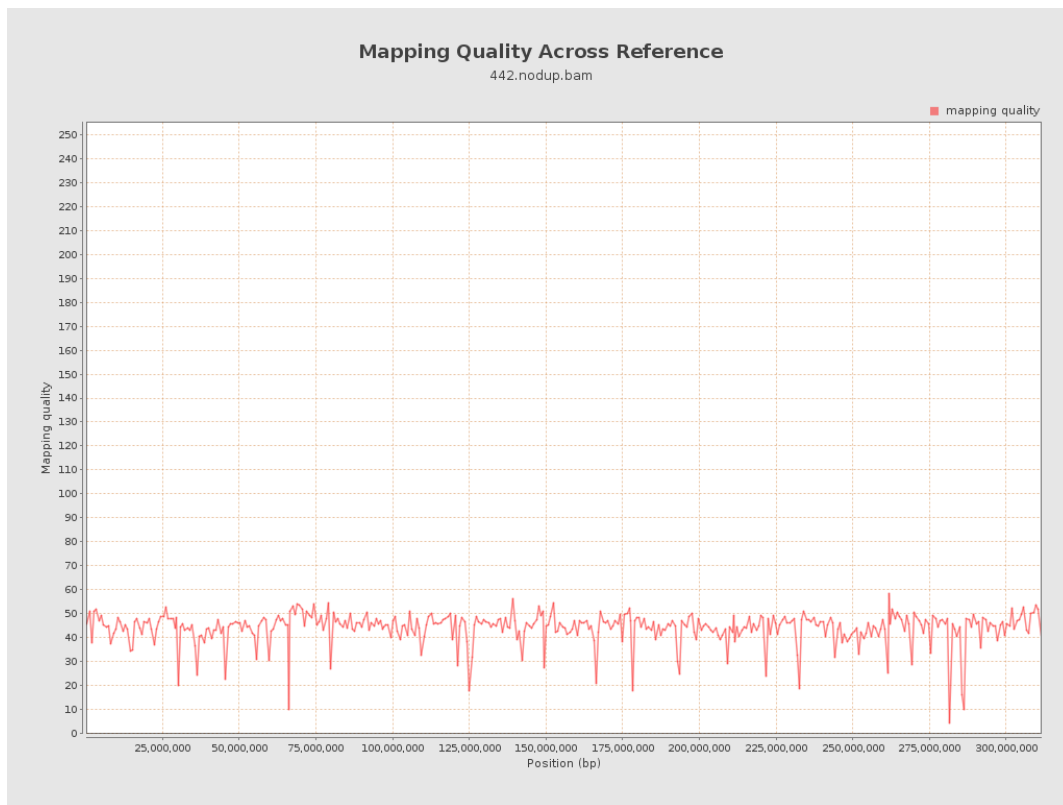Mapped Reads GC-content Distribution
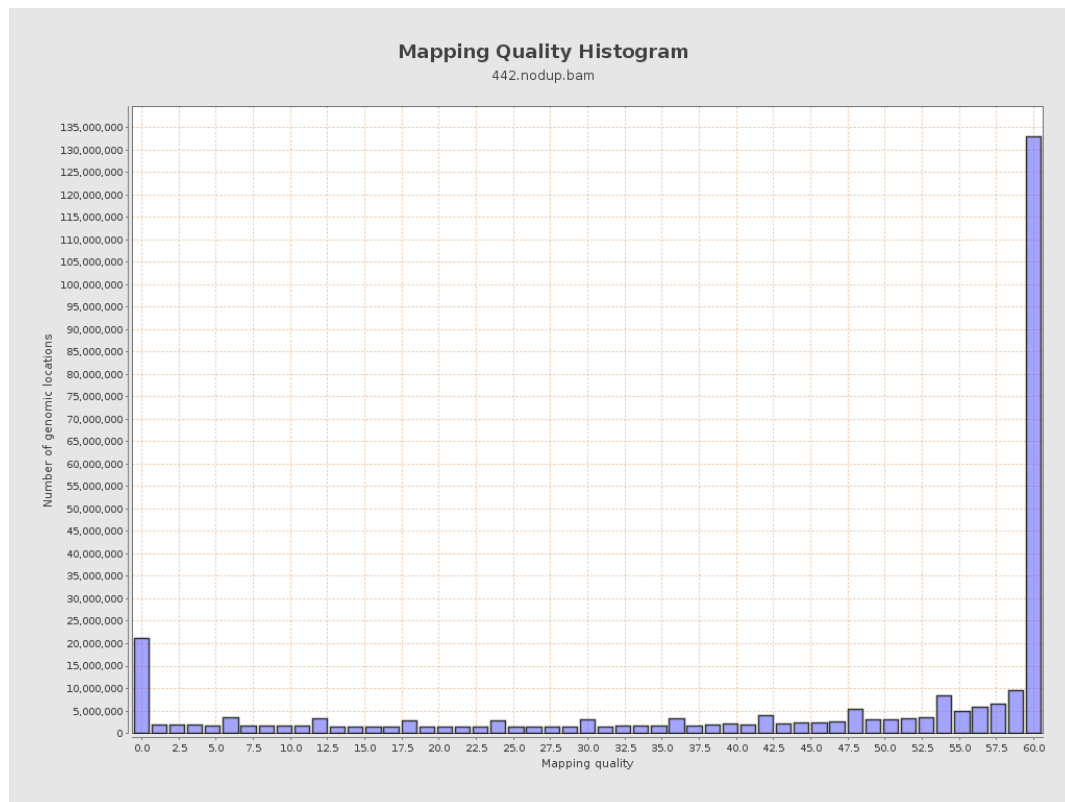442.nodup.bam
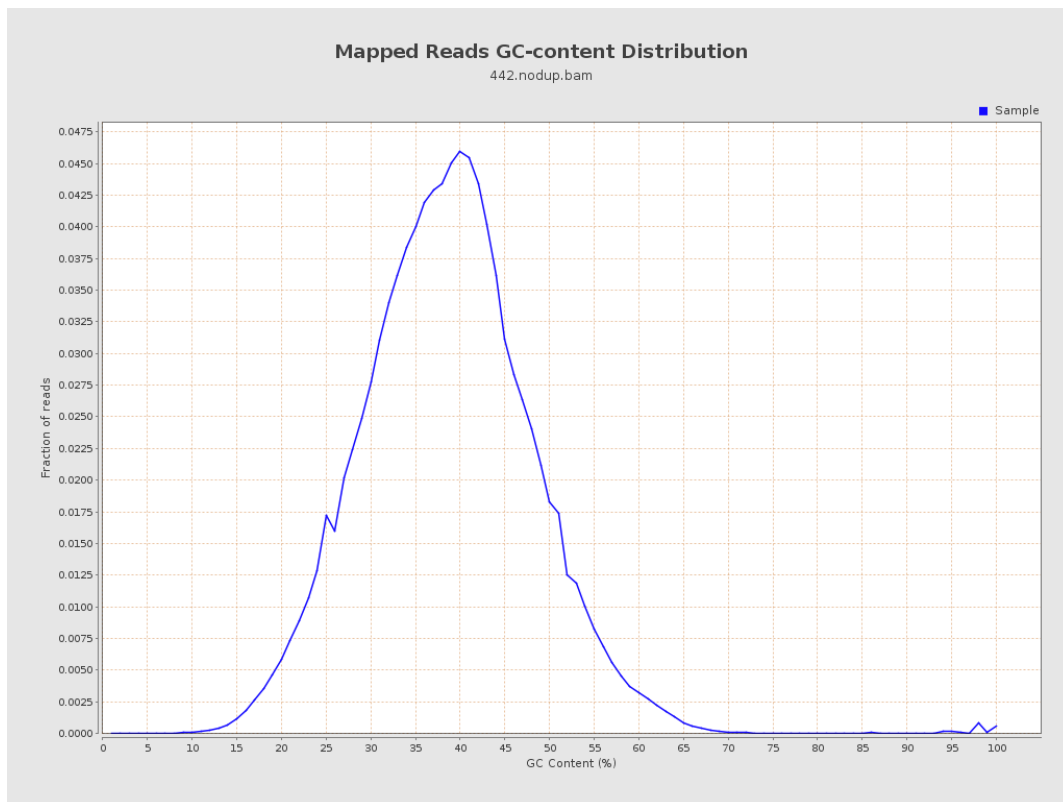
10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels

12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
442.nodup.bam

14. Results : Insert Size Across Reference

Insert Size Across Reference
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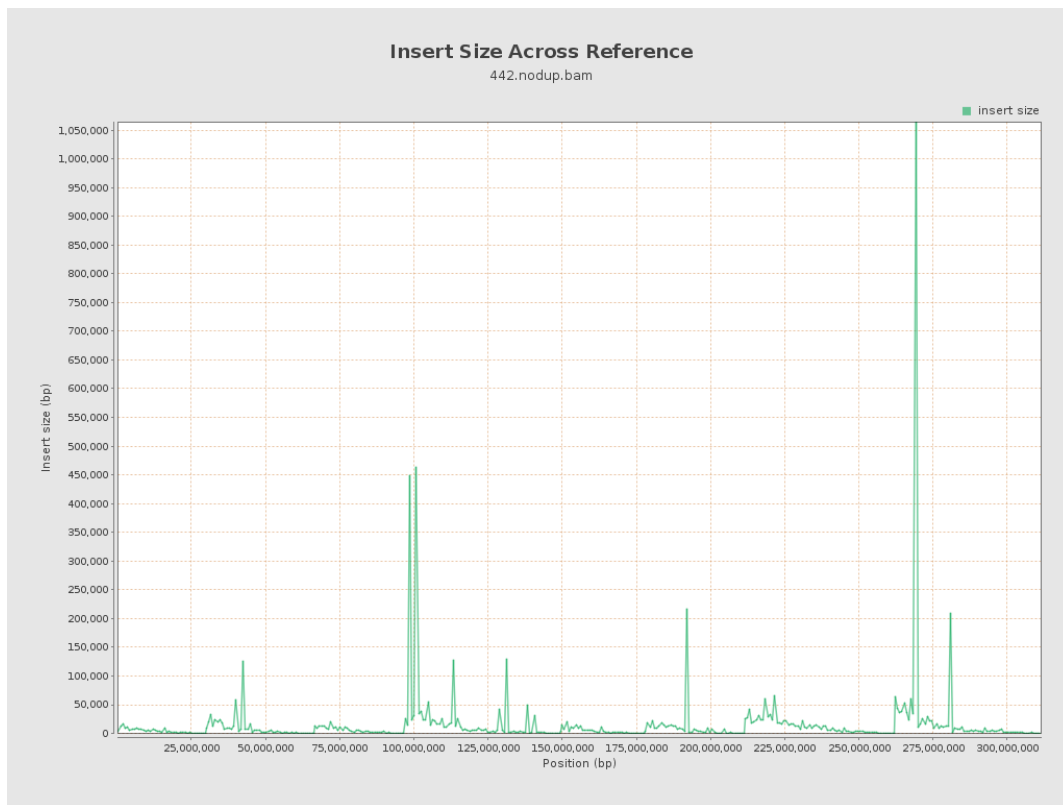
15. Results : Insert Size Histogram

Insert Size Histogram
442.nodup.bam