

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:31:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/443
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/443.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/awdata/P26207/P26207_240/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_240_S321_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_240/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_240_S321_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:31:06 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	67,078,900
Mapped reads	59,231,368 / 88.3%
Unmapped reads	7,847,532 / 11.7%
Mapped paired reads	59,231,368 / 88.3%
Mapped reads, first in pair	29,678,688 / 44.24%
Mapped reads, second in pair	29,552,680 / 44.06%
Mapped reads, both in pair	57,981,979 / 86.44%
Mapped reads, singletons	1,249,389 / 1.86%
Read min/max/mean length	30 / 151 / 148.47
Duplicated reads (flagged)	8,403,828 / 12.53%
Clipped reads	12,787,077 / 19.06%

2.2. ACGT Content

Number/percentage of A's	2,541,882,242 / 30.87%
Number/percentage of C's	1,577,428,476 / 19.16%
Number/percentage of T's	2,543,112,679 / 30.88%
Number/percentage of G's	1,571,764,242 / 19.09%
Number/percentage of N's	30,478 / 0%
GC Percentage	38.25%

2.3. Coverage

Mean	26.4871
Standard Deviation	203.8783

2.4. Mapping Quality

Mean Mapping Quality	44.5
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2.5. Insert size

Mean	217,392.96
Standard Deviation	2,219,556.74
P25/Median/P75	323 / 422 / 548

2.6. Mismatches and indels

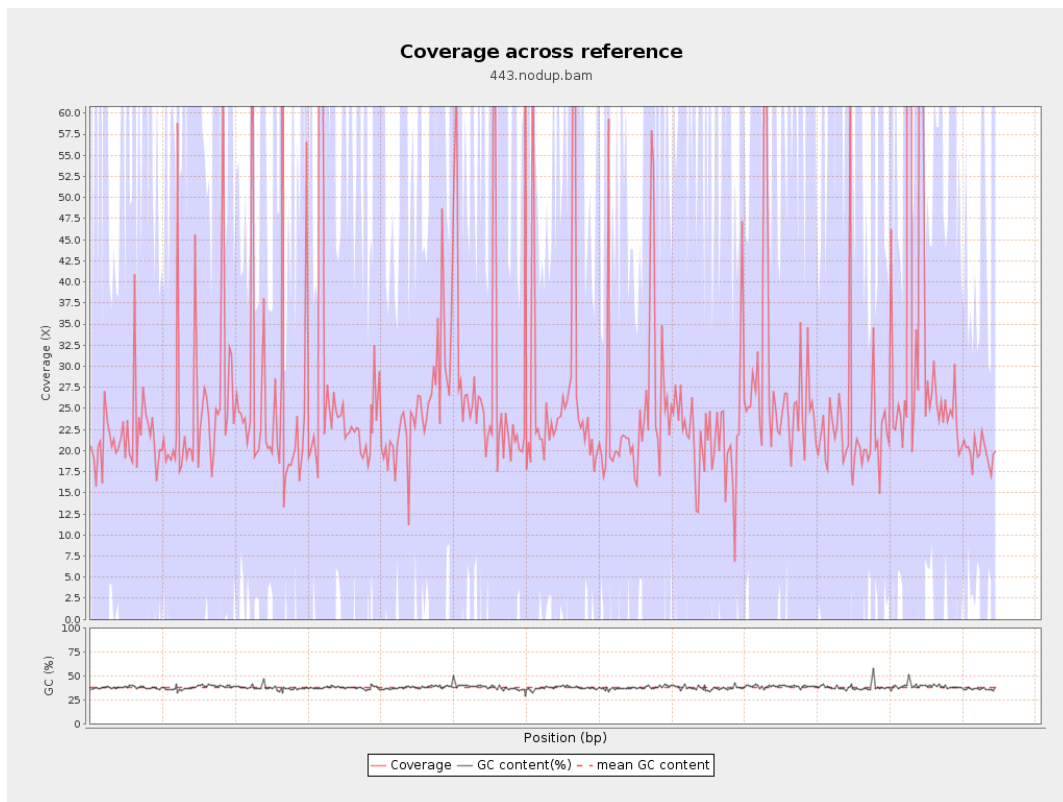
General error rate	2.21%
Mismatches	167,607,221
Insertions	5,336,395
Mapped reads with at least one insertion	8.11%
Deletions	5,396,679
Mapped reads with at least one deletion	8.13%
Homopolymer indels	57.17%

2.7. Chromosome stats

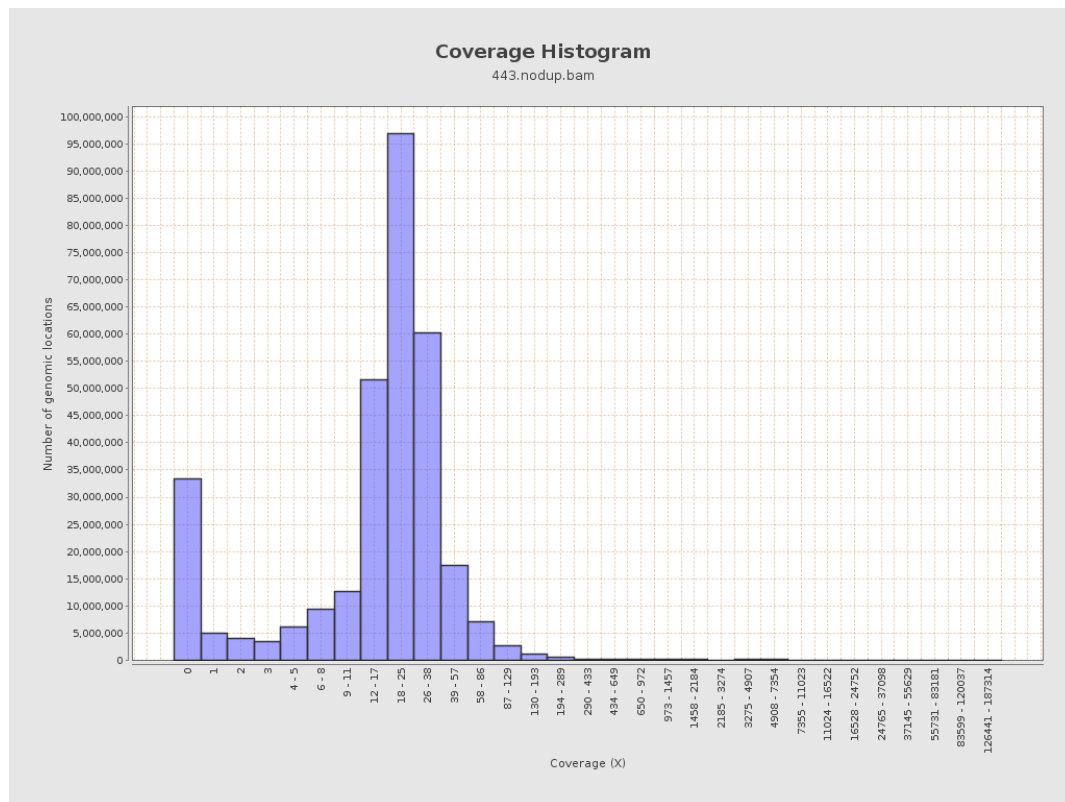
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	636059475	21.3986	56.4216

LT669789.1	36598175	978585487	26.7386	226.088
LT669790.1	30422129	843757752	27.735	206.3393
LT669791.1	52758100	1381128737	26.1785	171.2734
LT669792.1	28376109	734318160	25.878	219.2382
LT669793.1	33388210	803344182	24.0607	112.1881
LT669794.1	50579949	1292188489	25.5474	172.3706
LT669795.1	49795044	1585114664	31.8328	312.2855

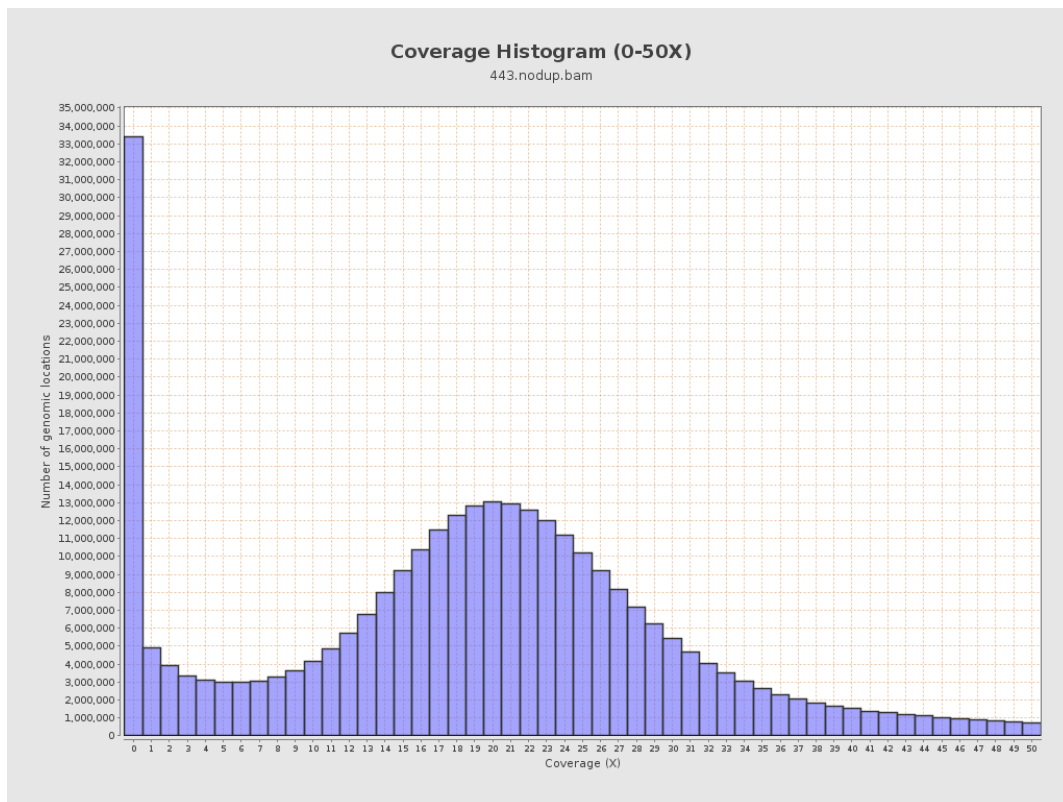
3. Results : Coverage across reference



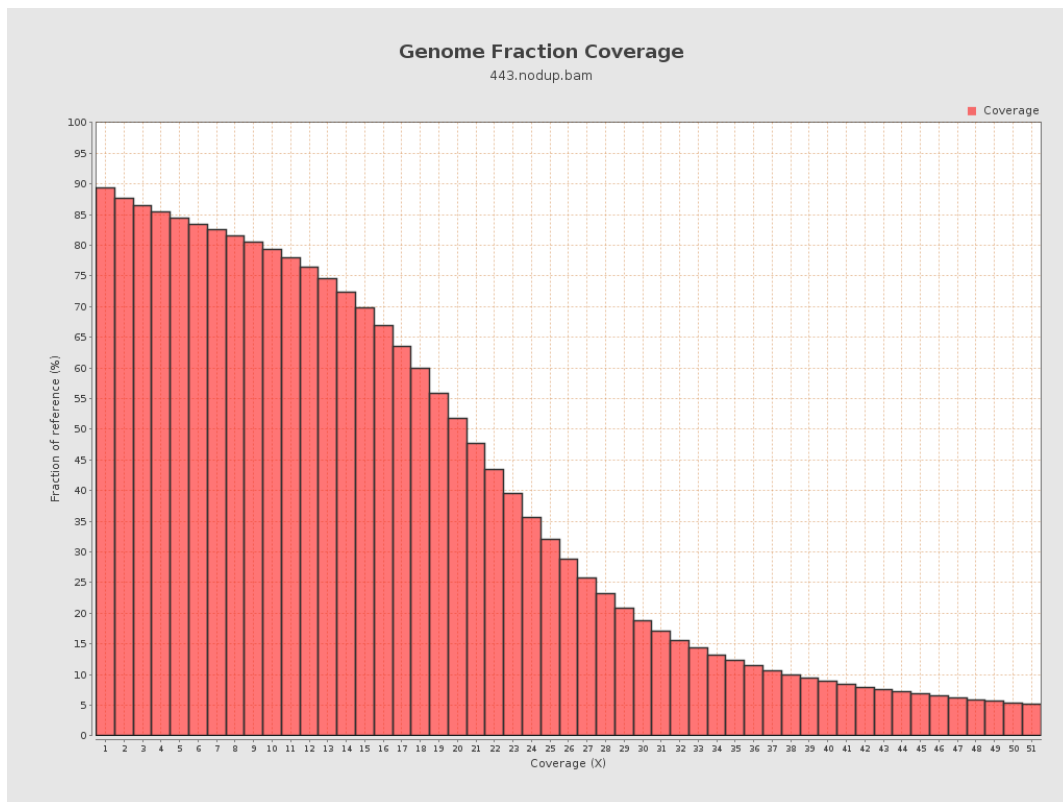
4. Results : Coverage Histogram



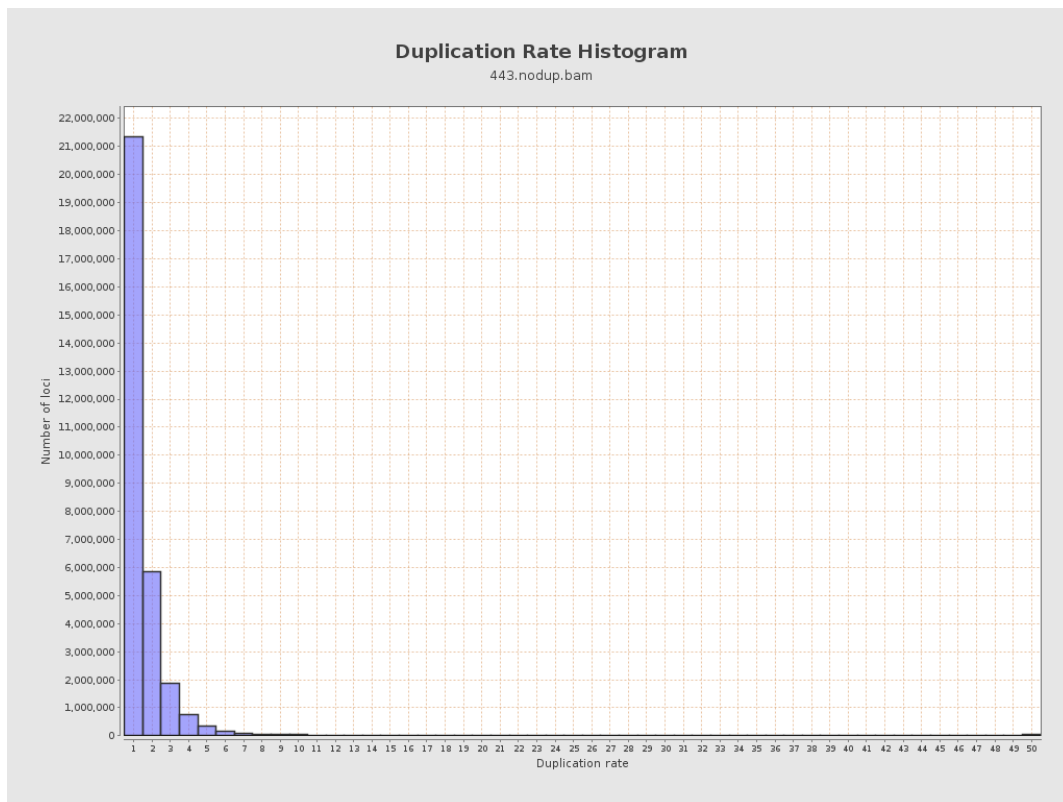
5. Results : Coverage Histogram (0-50X)



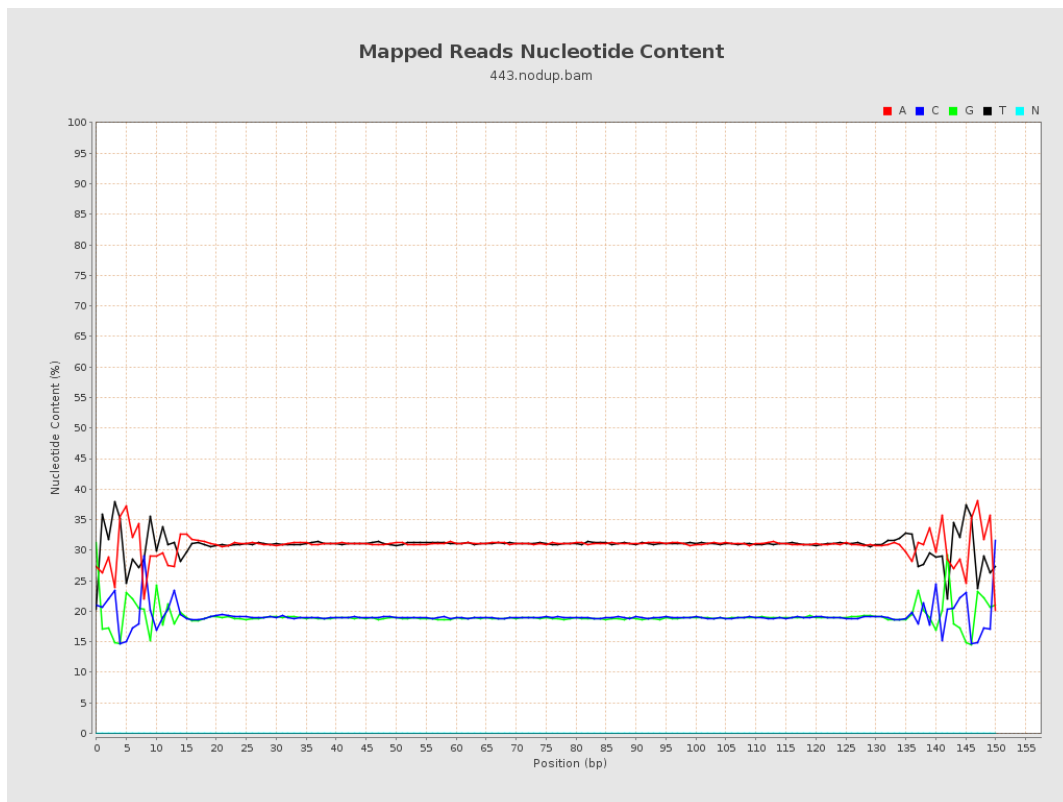
6. Results : Genome Fraction Coverage



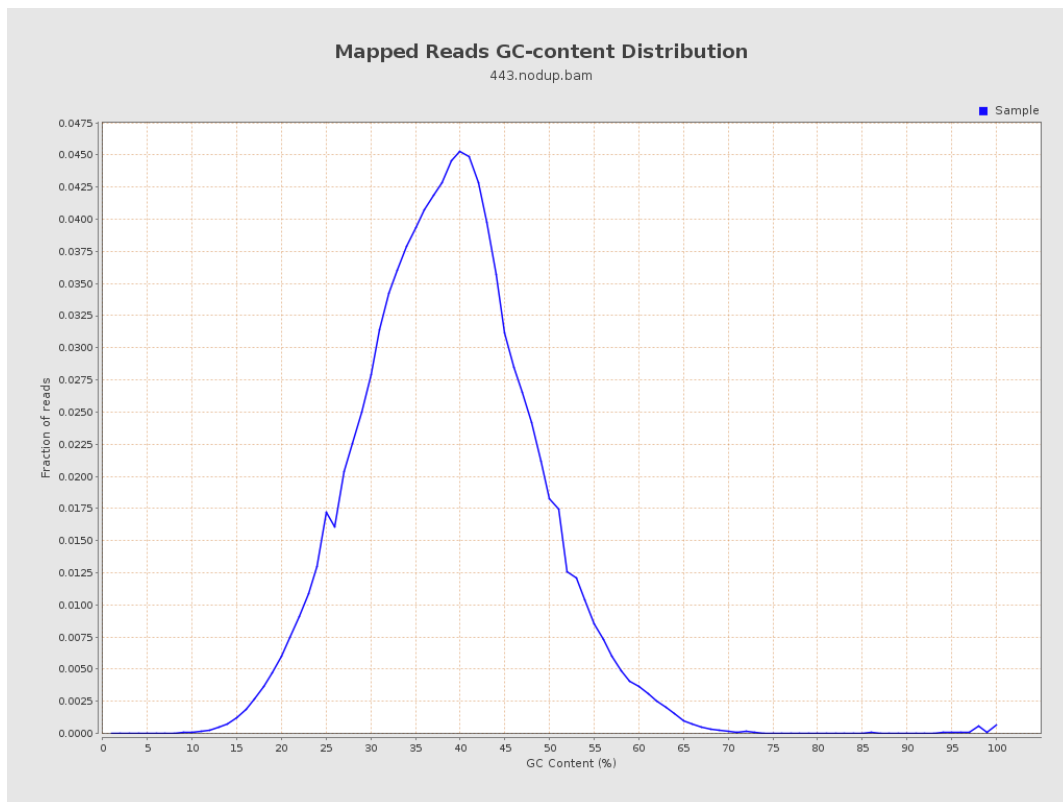
7. Results : Duplication Rate Histogram



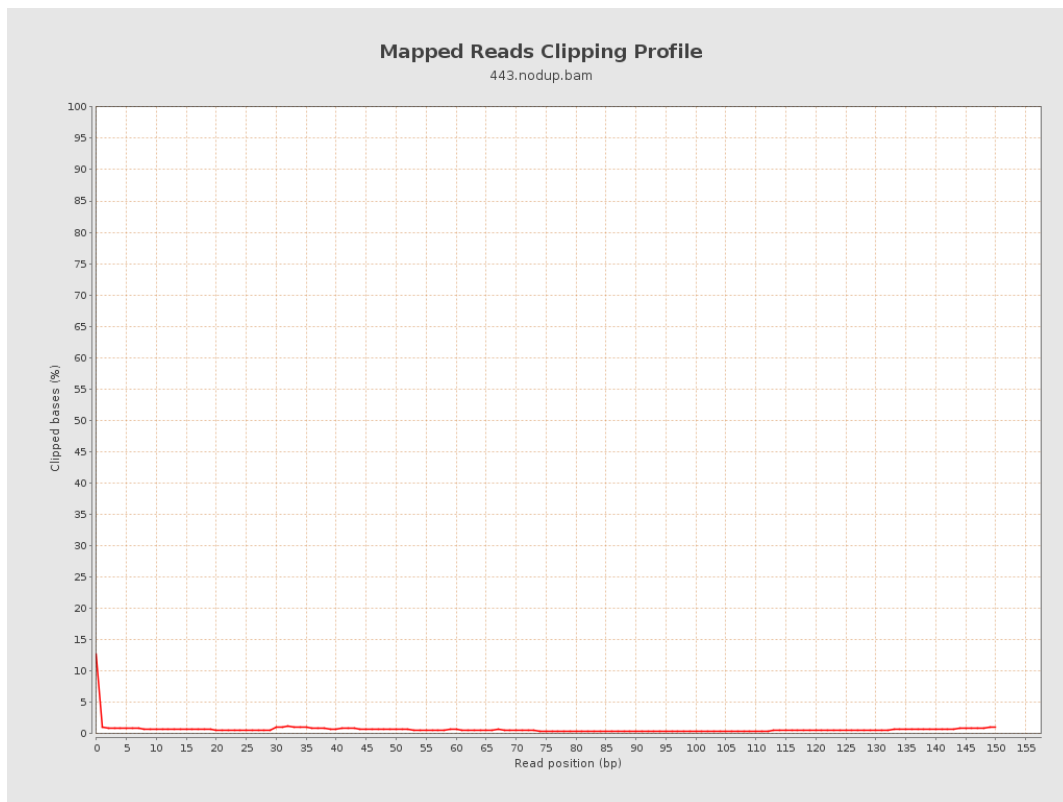
8. Results : Mapped Reads Nucleotide Content



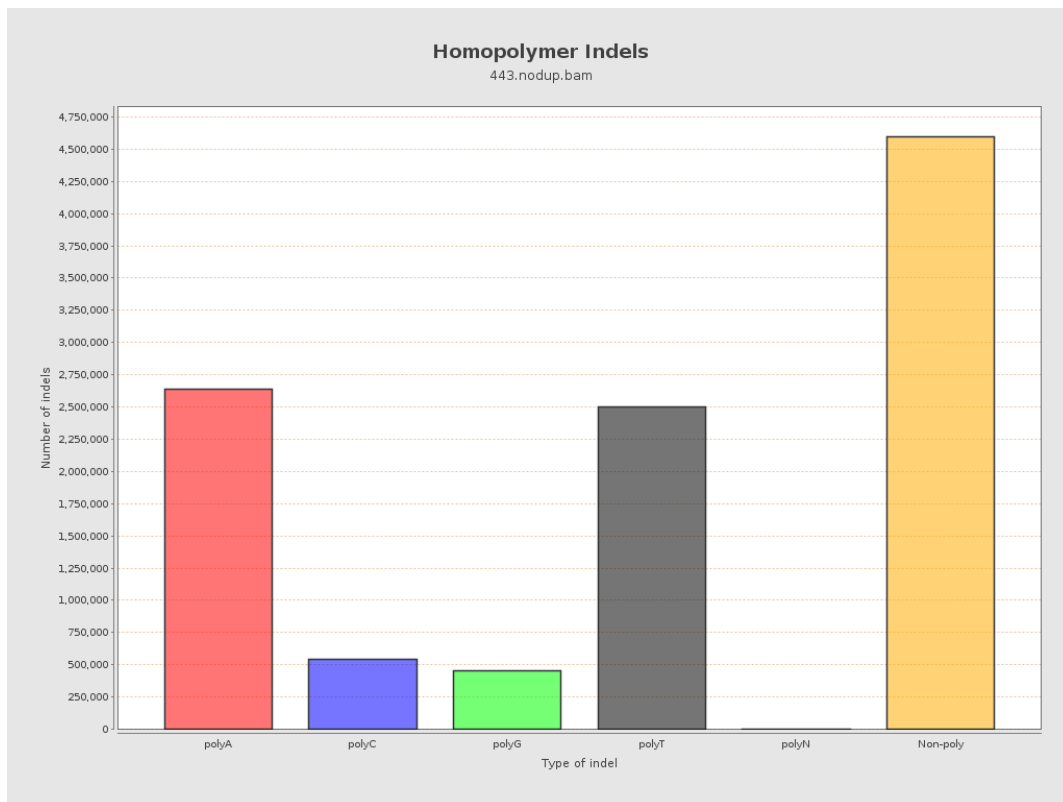
9. Results : Mapped Reads GC-content Distribution



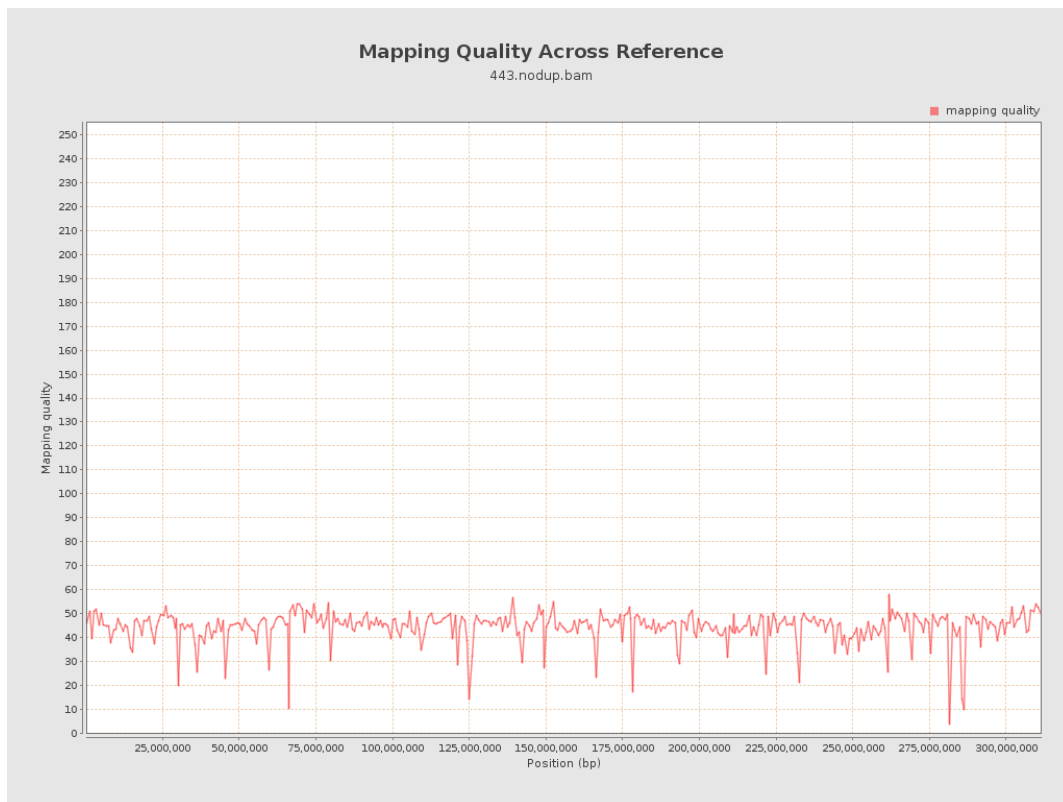
10. Results : Mapped Reads Clipping Profile



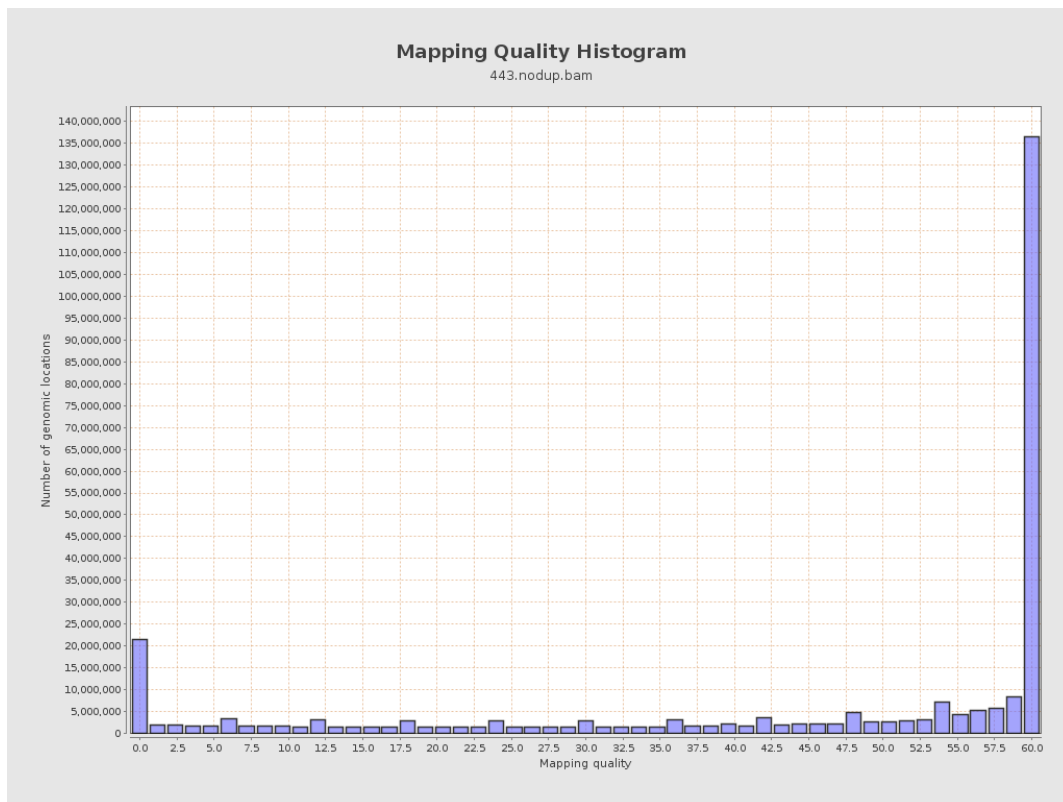
11. Results : Homopolymer Indels



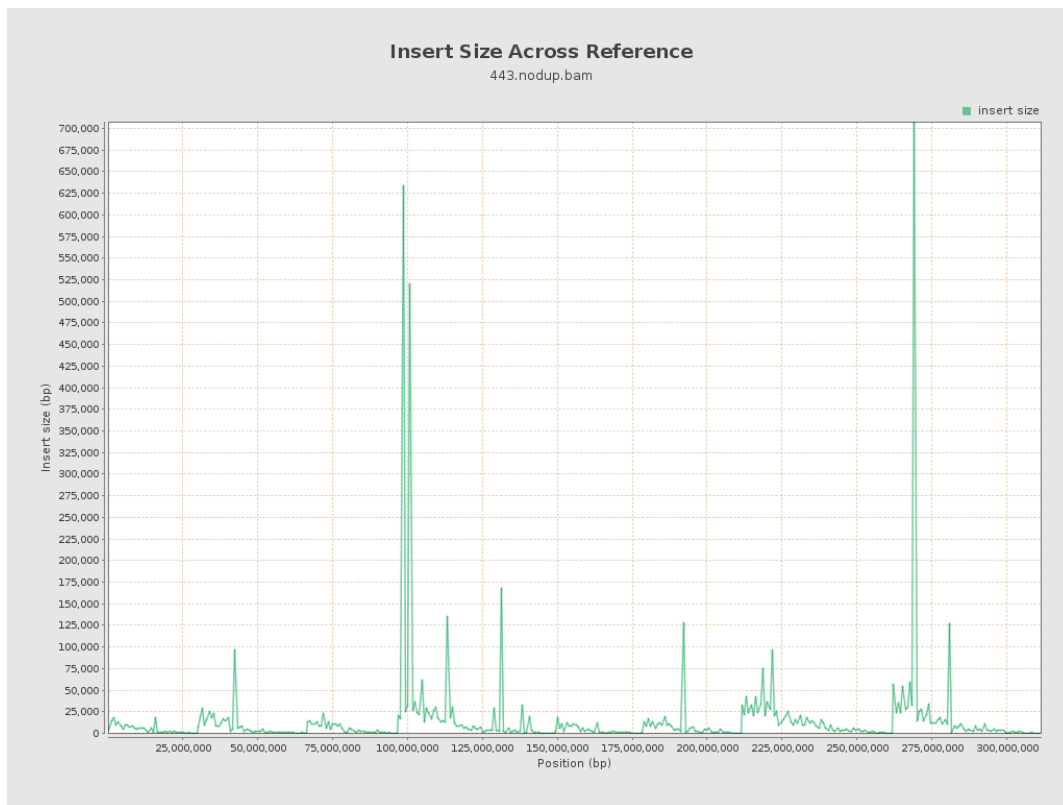
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

