Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:24:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/463.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/463.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_169/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_169_S259_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_169/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_169_S259_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:24:48 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	48,586,783
Mapped reads	45,475,064 / 93.6%
Unmapped reads	3,111,719 / 6.4%
Mapped paired reads	45,475,064 / 93.6%
Mapped reads, first in pair	22,776,121 / 46.88%
Mapped reads, second in pair	22,698,943 / 46.72%
Mapped reads, both in pair	44,557,874 / 91.71%
Mapped reads, singletons	917,190 / 1.89%
Read min/max/mean length	30 / 151 / 147.73
Duplicated reads (flagged)	7,709,304 / 15.87%
Clipped reads	11,537,132 / 23.75%

2.2. ACGT Content

Number/percentage of A's	1,910,420,214 / 30.79%
Number/percentage of C's	1,188,539,494 / 19.16%
Number/percentage of T's	1,915,652,120 / 30.88%
Number/percentage of G's	1,189,731,964 / 19.18%
Number/percentage of N's	25,617 / 0%
GC Percentage	38.33%

2.3. Coverage

Mean	19.9615
Standard Deviation	184.5014

2.4. Mapping Quality

Mean Mapping Quality	43.9

2.5. Insert size

Mean	234,638.78
Standard Deviation	2,297,746.46
P25/Median/P75	304 / 421 / 558

2.6. Mismatches and indels

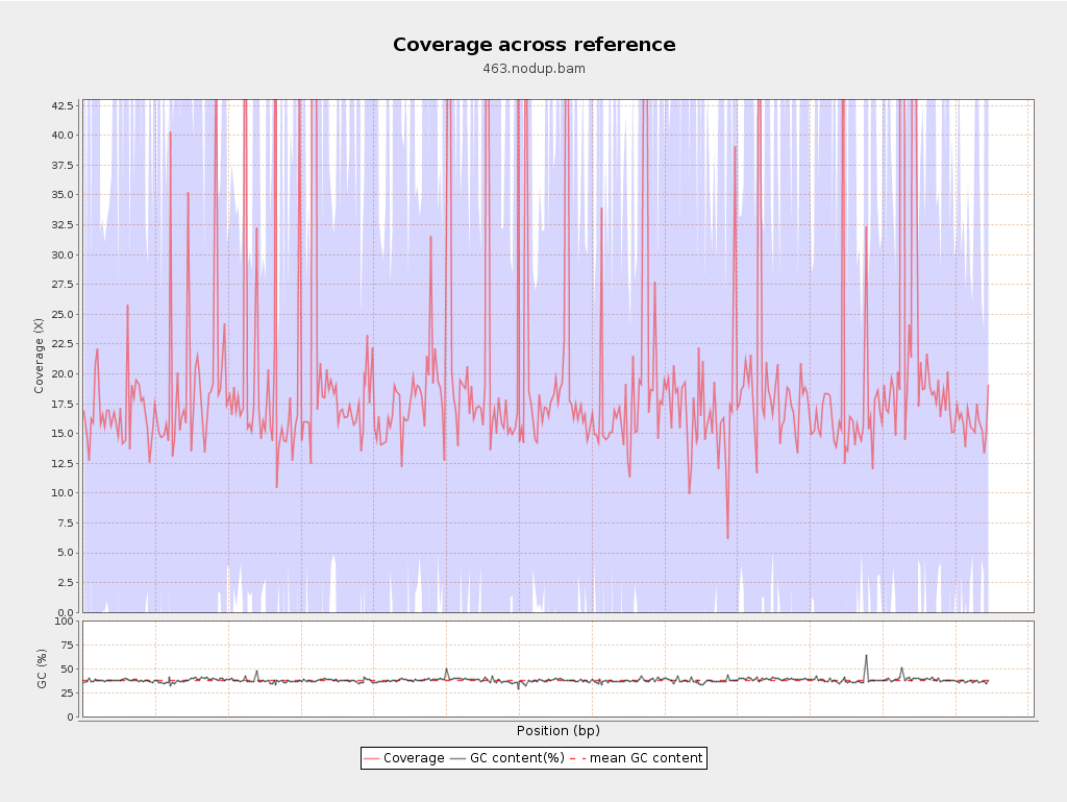
General error rate	2.34%
Mismatches	133,383,816
Insertions	4,276,617
Mapped reads with at least one insertion	8.44%
Deletions	4,360,667
Mapped reads with at least one deletion	8.49%
Homopolymer indels	55.99%

2.7. Chromosome stats

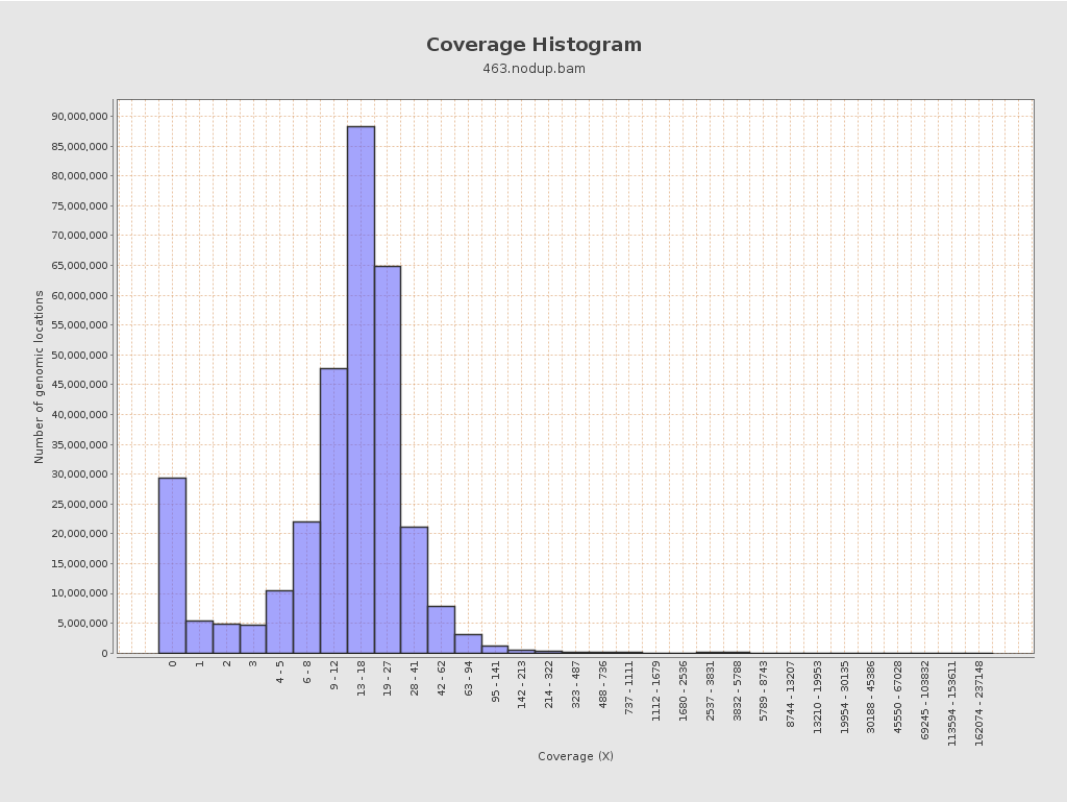
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	491961999	16.5508	60.6706

LT669789.1	36598175	751247796	20.5269	187.2783
LT669790.1	30422129	656545167	21.5812	167.021
LT669791.1	52758100	1024362500	19.4162	162.7288
LT669792.1	28376109	559746146	19.726	177.4766
LT669793.1	33388210	636505919	19.0638	163.4855
LT669794.1	50579949	946688759	18.7167	154.842
LT669795.1	49795044	1153793956	23.1709	282.3533

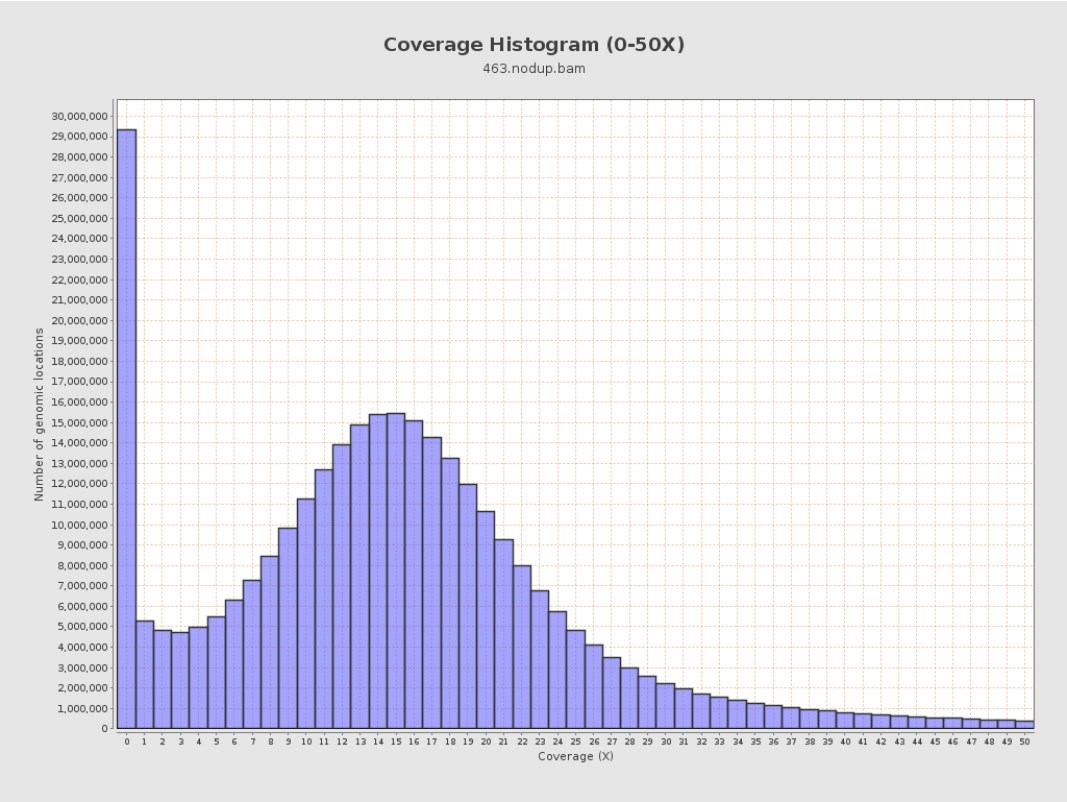
3. Results : Coverage across reference



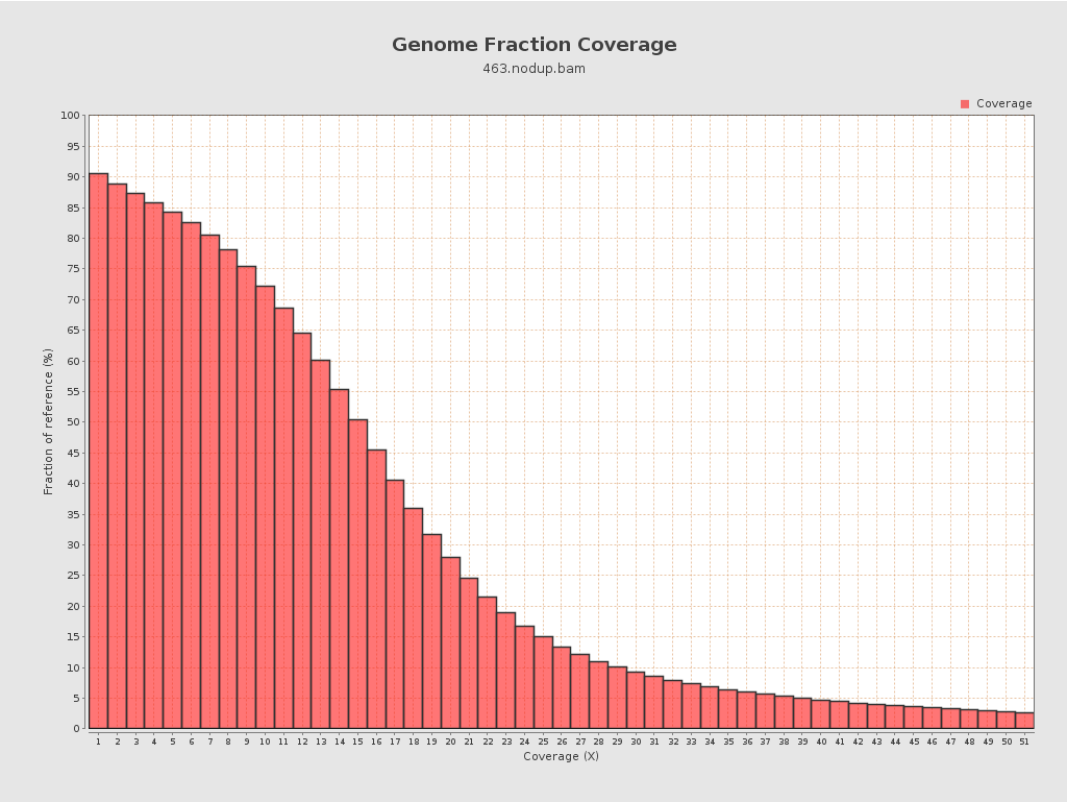
4. Results : Coverage Histogram



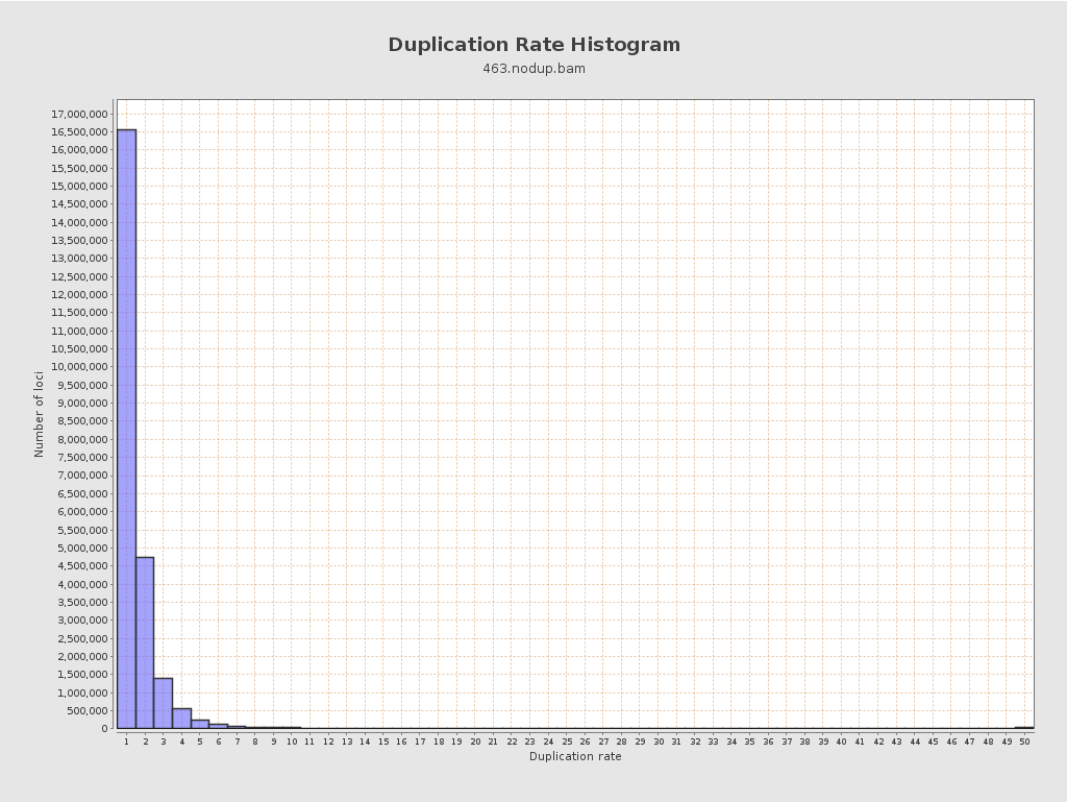
5. Results : Coverage Histogram (0-50X)



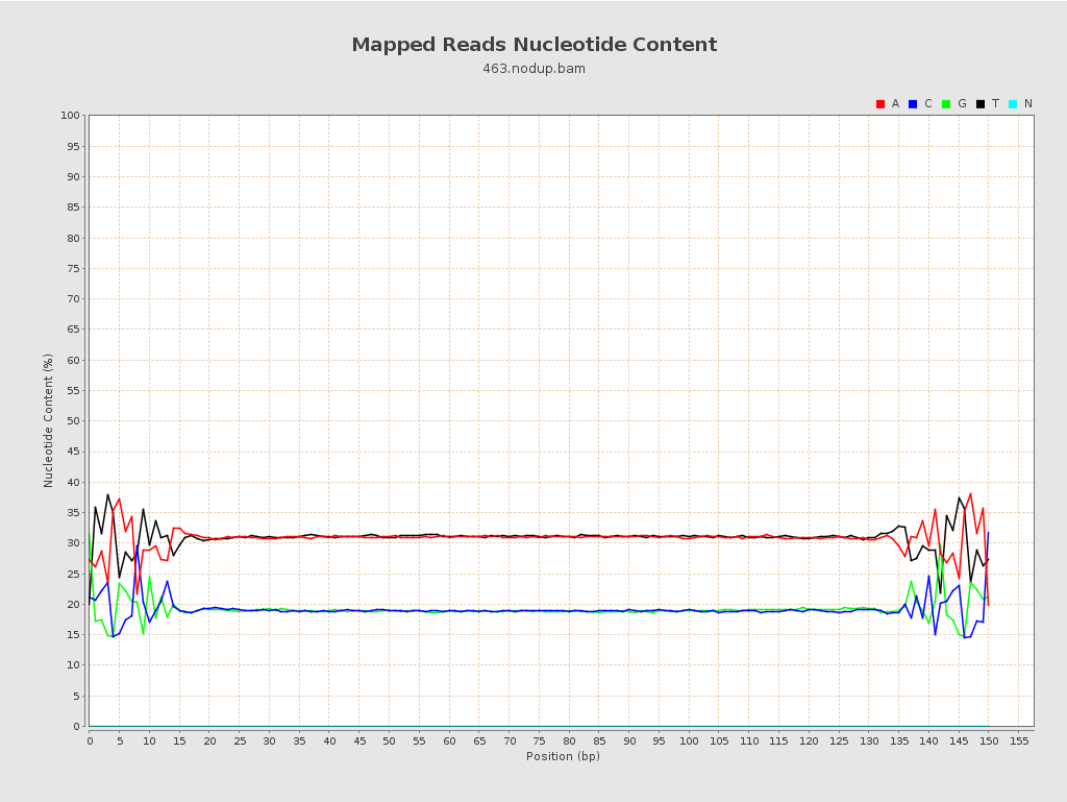
6. Results : Genome Fraction Coverage



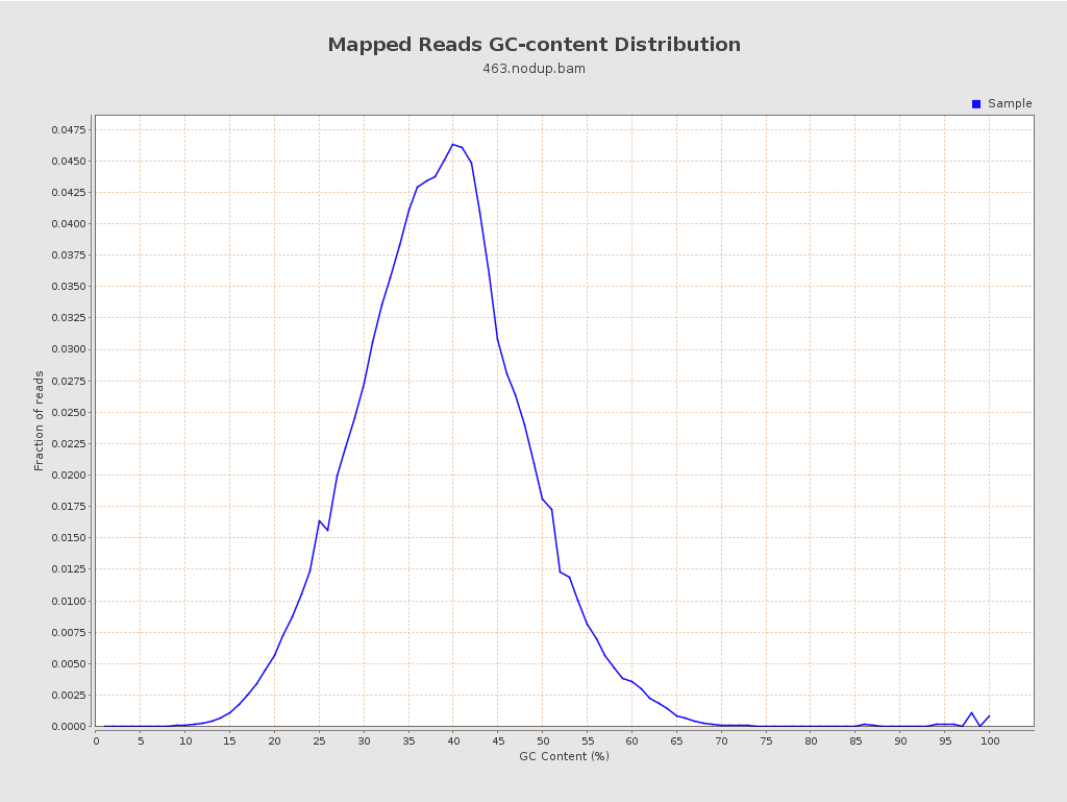
7. Results : Duplication Rate Histogram



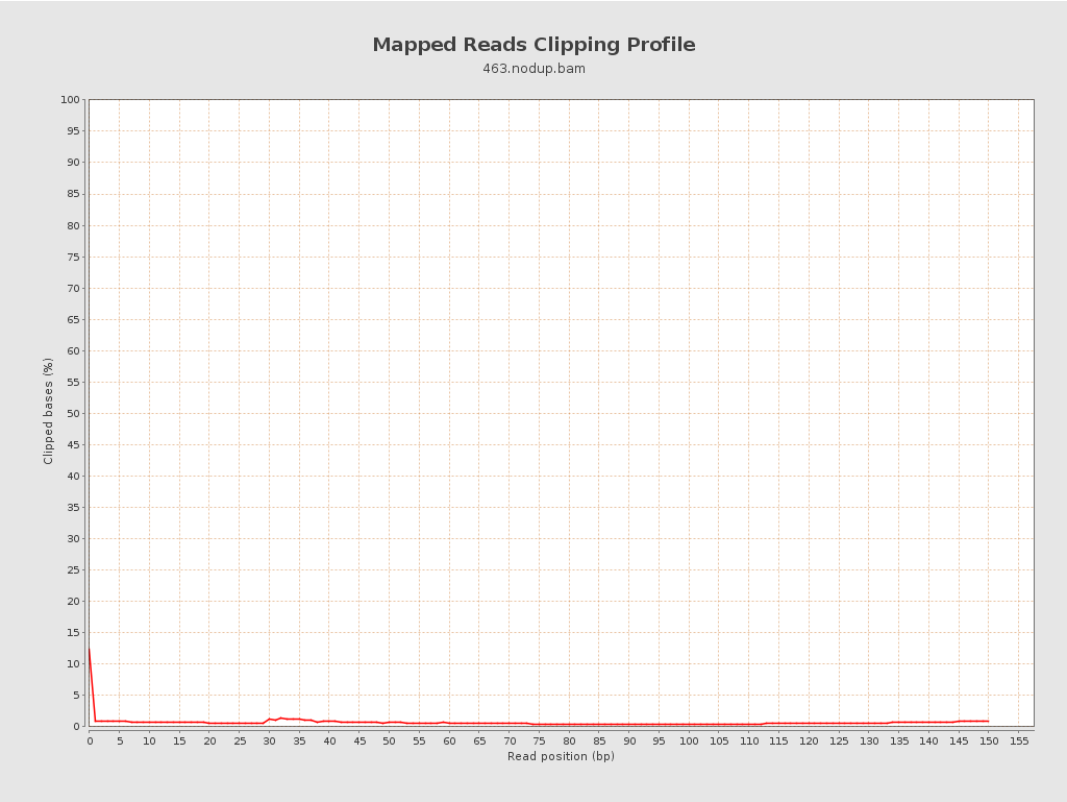
8. Results : Mapped Reads Nucleotide Content



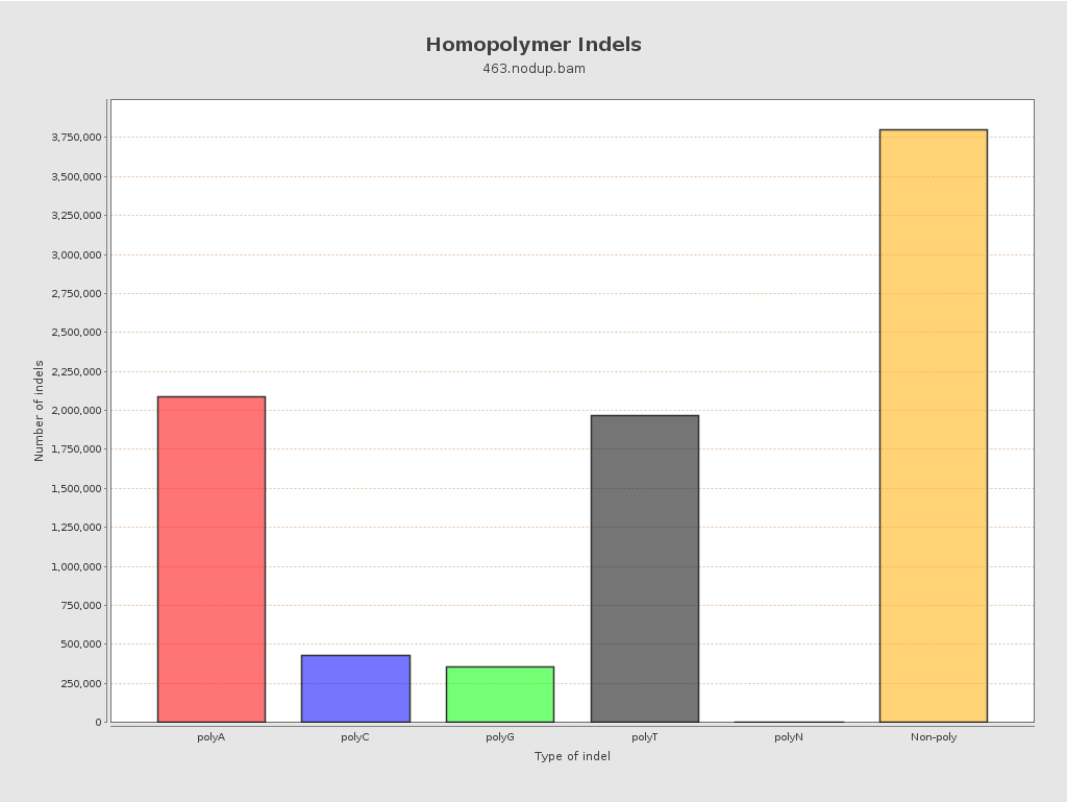
9. Results : Mapped Reads GC-content Distribution



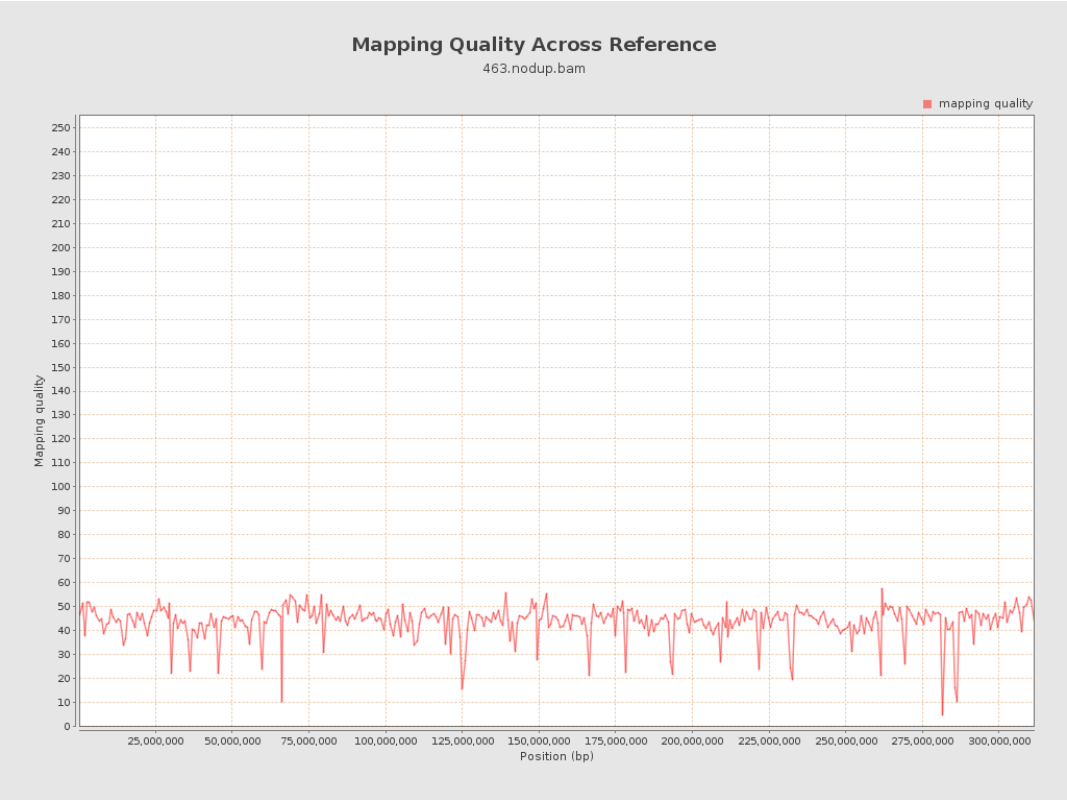
10. Results : Mapped Reads Clipping Profile



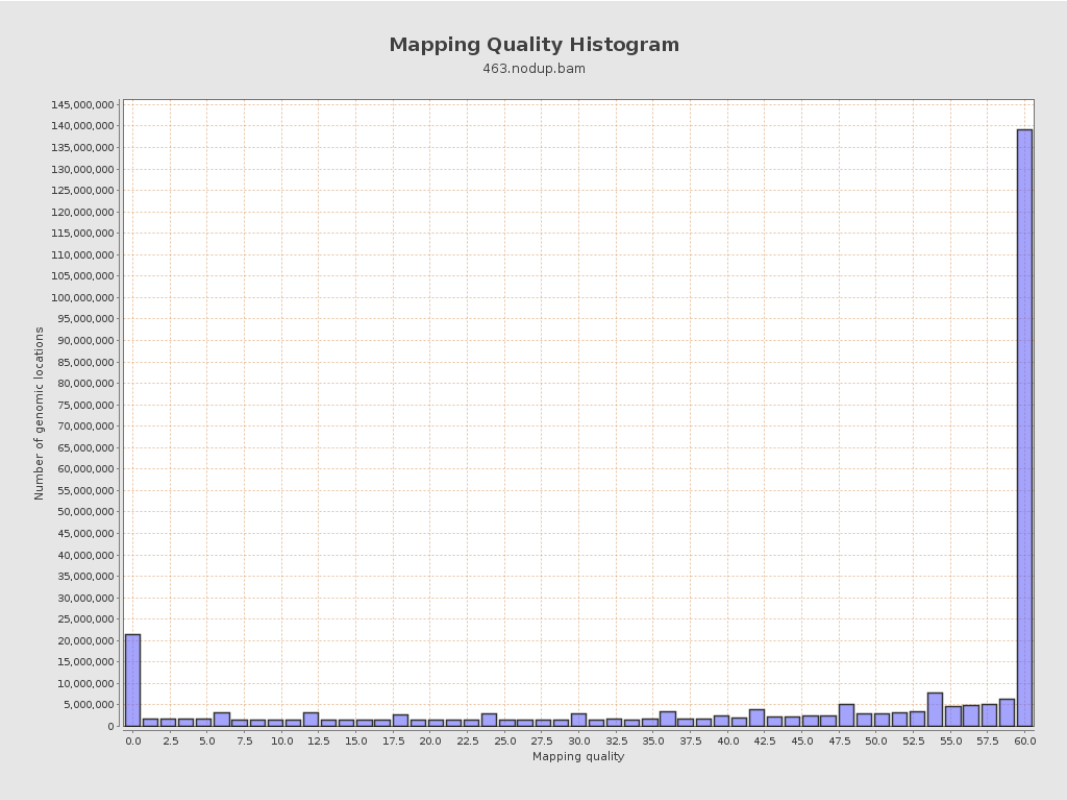
11. Results : Homopolymer Indels



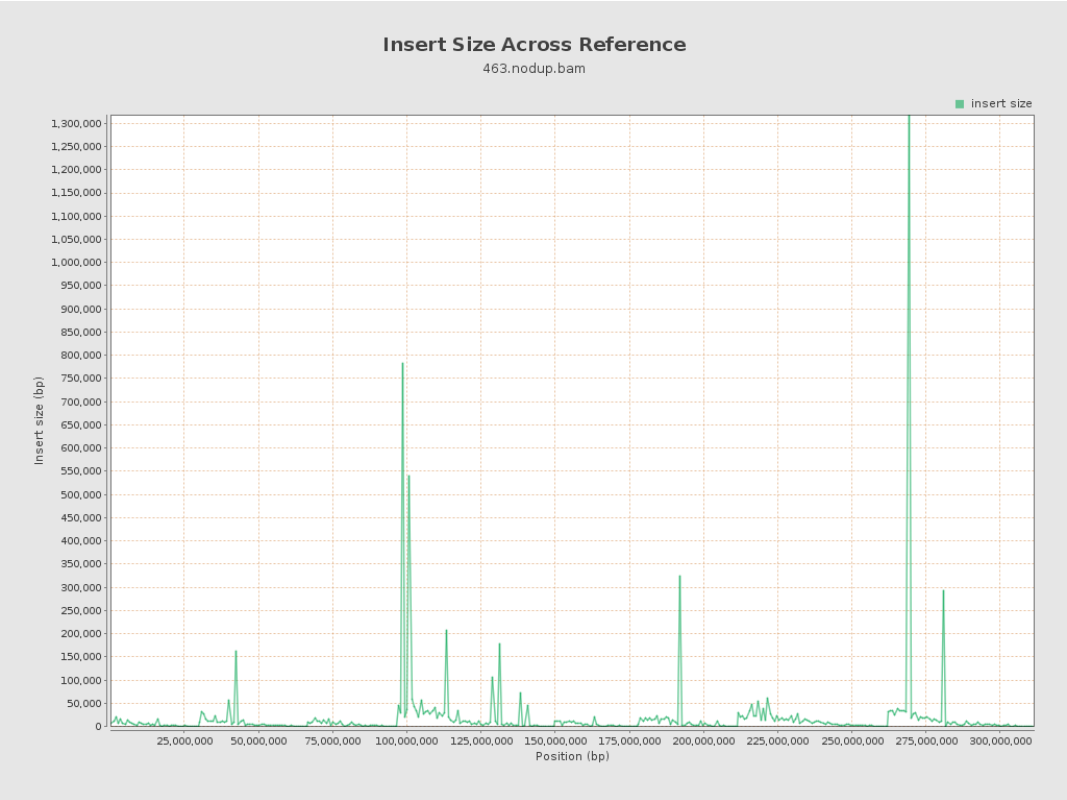
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram