Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:30:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/423.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/423.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_225/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_225_S306_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_225/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_225_S306_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:30:57 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	65,831,894
Mapped reads	60,233,629 / 91.5%
Unmapped reads	5,598,265 / 8.5%
Mapped paired reads	60,233,629 / 91.5%
Mapped reads, first in pair	30,177,311 / 45.84%
Mapped reads, second in pair	30,056,318 / 45.66%
Mapped reads, both in pair	58,862,737 / 89.41%
Mapped reads, singletons	1,370,892 / 2.08%
Read min/max/mean length	30 / 151 / 148.23
Duplicated reads (flagged)	8,798,047 / 13.36%
Clipped reads	13,601,771 / 20.66%

2.2. ACGT Content

Number/percentage of A's	2,564,165,944 / 30.76%
Number/percentage of C's	1,603,781,704 / 19.24%
Number/percentage of T's	2,566,807,970 / 30.79%
Number/percentage of G's	1,600,450,234 / 19.2%
Number/percentage of N's	31,788 / 0%
GC Percentage	38.44%

2.3. Coverage

Mean	26.8147
Standard Deviation	227.1704

2.4. Mapping Quality

Mean Mapping Quality	44.15

2.5. Insert size

Mean	229,328.68
Standard Deviation	2,276,257.3
P25/Median/P75	321 / 422 / 548

2.6. Mismatches and indels

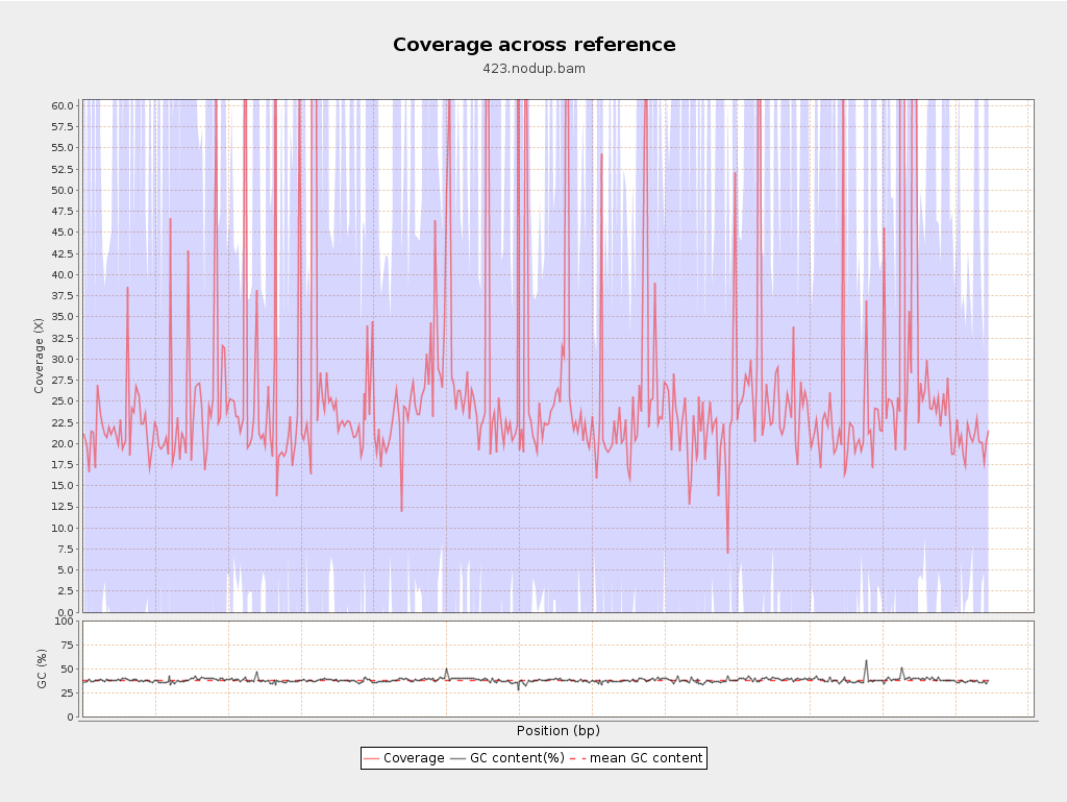
General error rate	2.29%
Mismatches	175,910,268
Insertions	5,573,099
Mapped reads with at least one insertion	8.3%
Deletions	5,613,280
Mapped reads with at least one deletion	8.3%
Homopolymer indels	56.67%

2.7. Chromosome stats

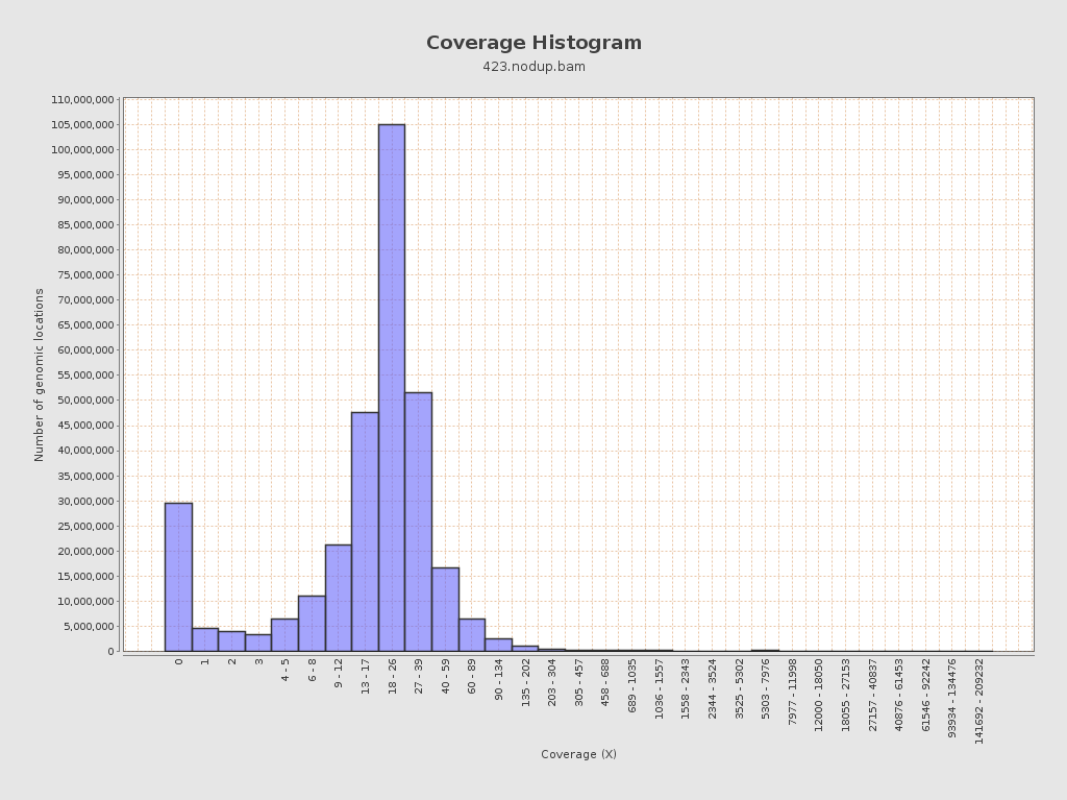
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	645871904	21.7287	68.3167

LT669789.1	36598175	966210117	26.4005	217.489
LT669790.1	30422129	903499740	29.6988	251.2519
LT669791.1	52758100	1403963413	26.6113	197.0576
LT669792.1	28376109	758565836	26.7326	242.3758
LT669793.1	33388210	822486114	24.634	213.3971
LT669794.1	50579949	1264888971	25.0077	174.7193
LT669795.1	49795044	1591102222	31.953	332.6327

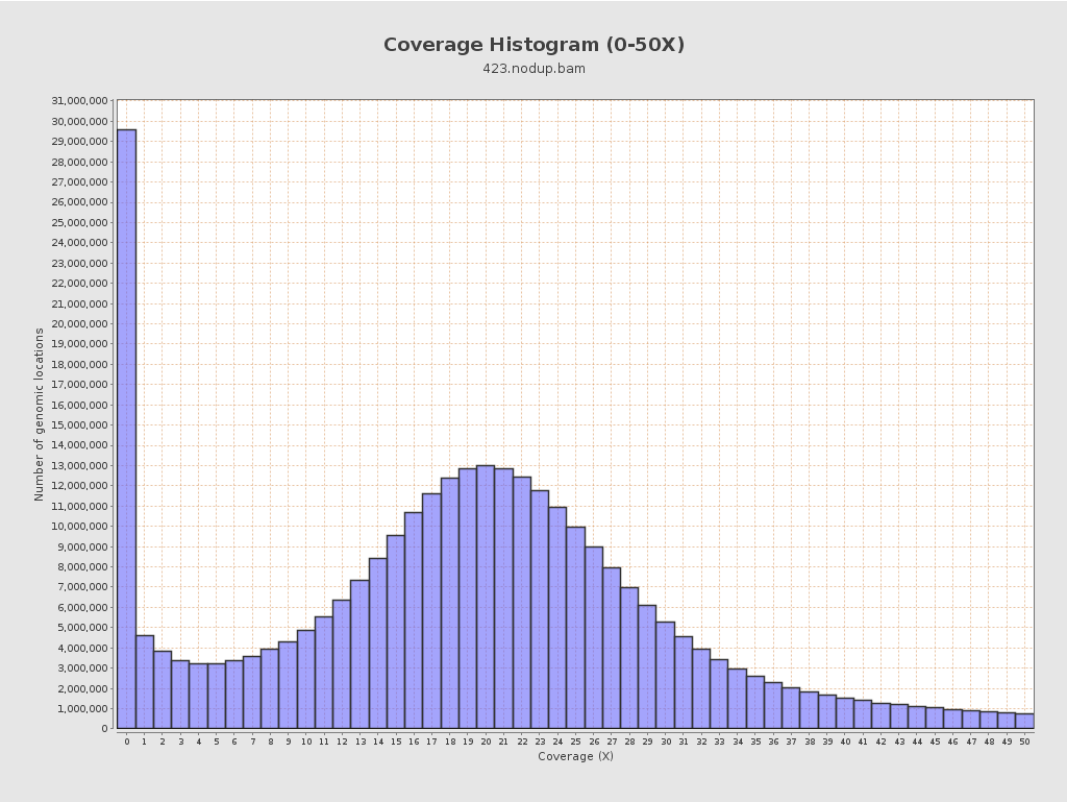
3. Results : Coverage across reference



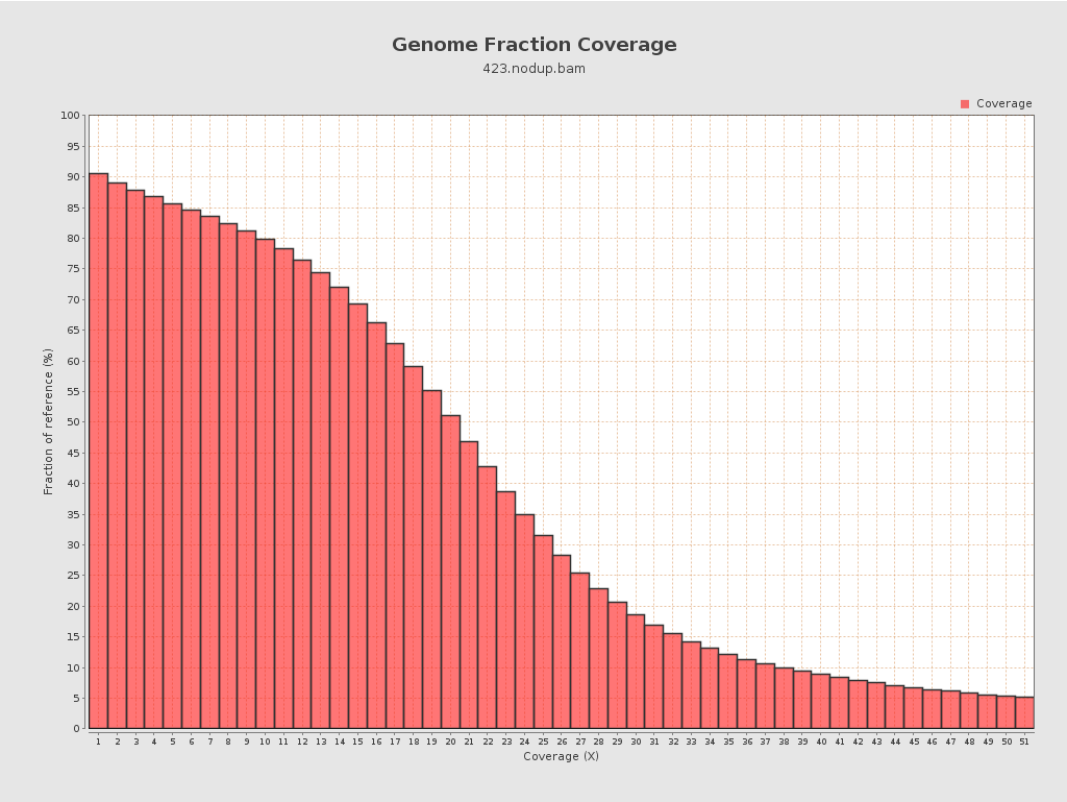
4. Results : Coverage Histogram



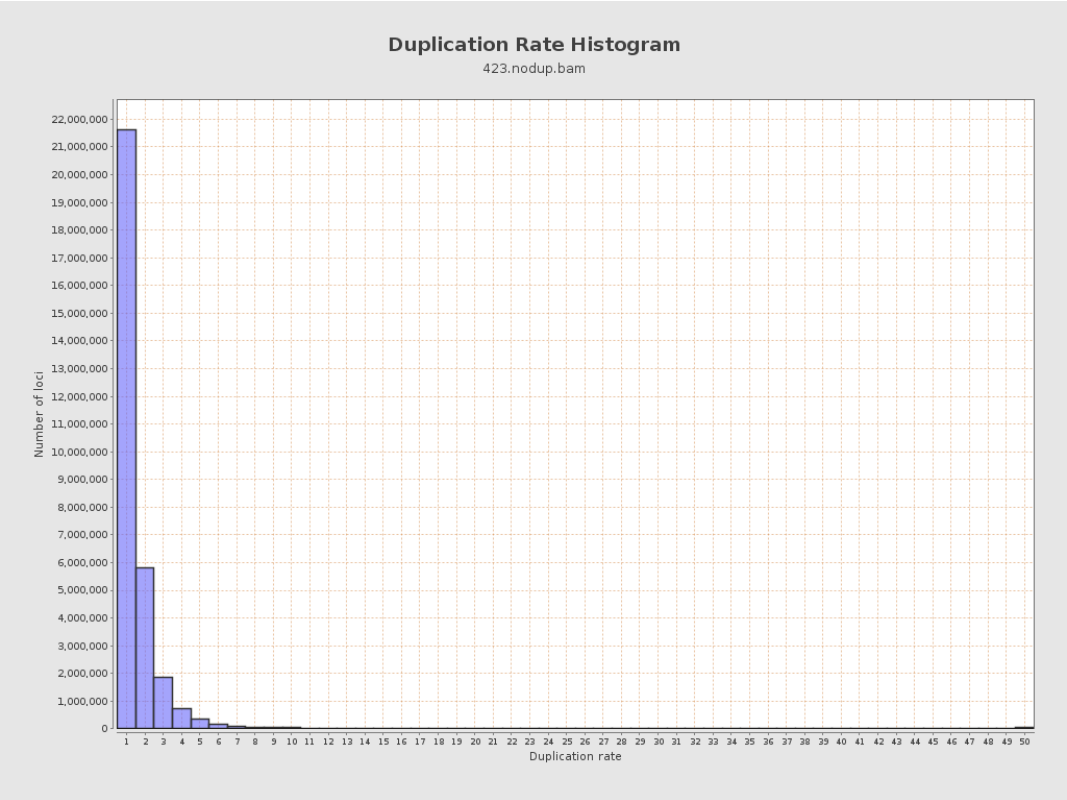
5. Results : Coverage Histogram (0-50X)



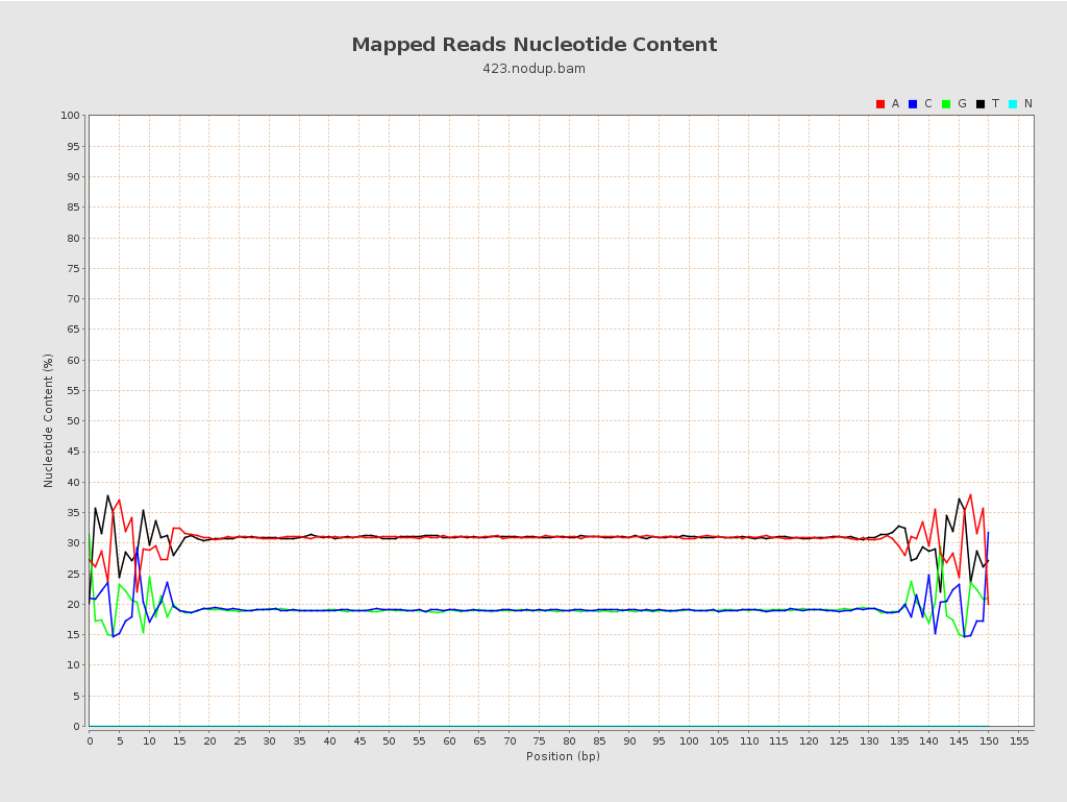
6. Results : Genome Fraction Coverage



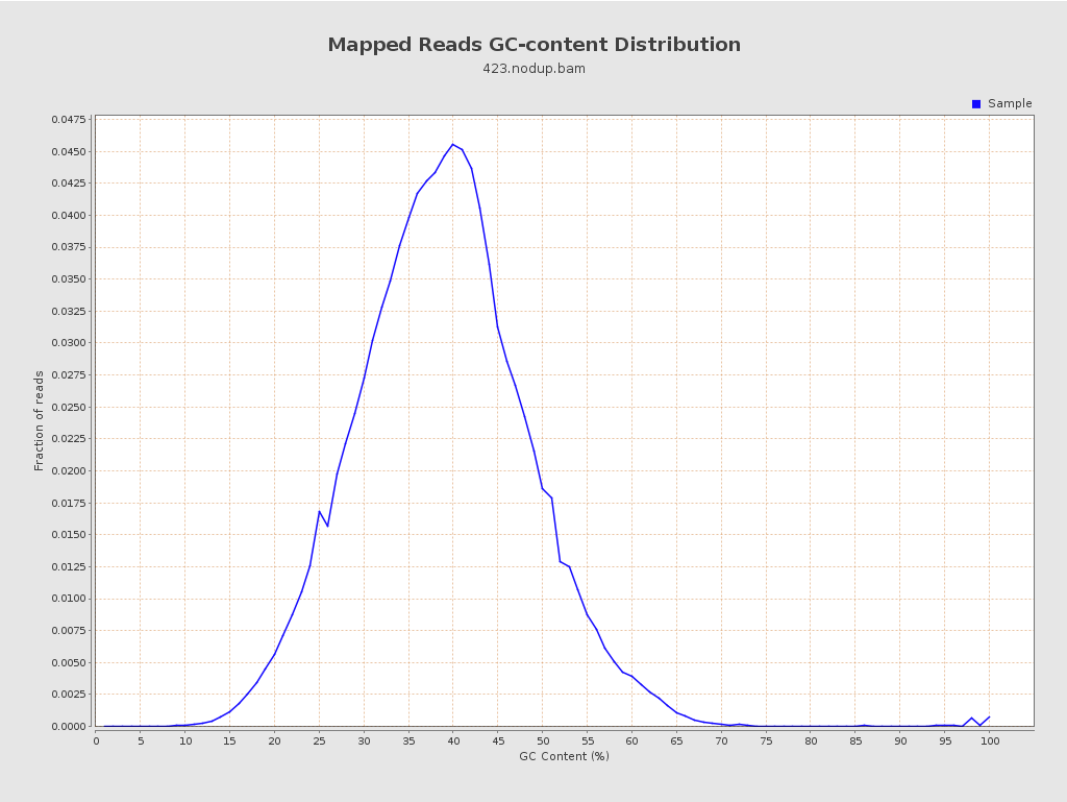
7. Results : Duplication Rate Histogram



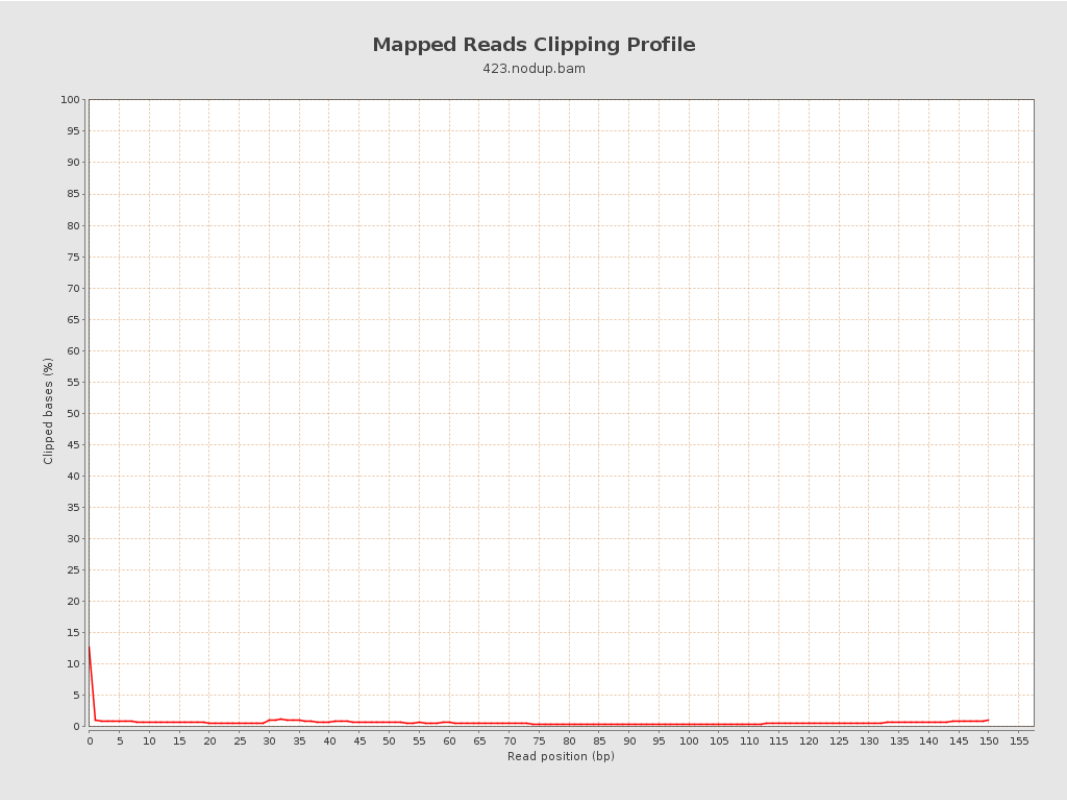
8. Results : Mapped Reads Nucleotide Content



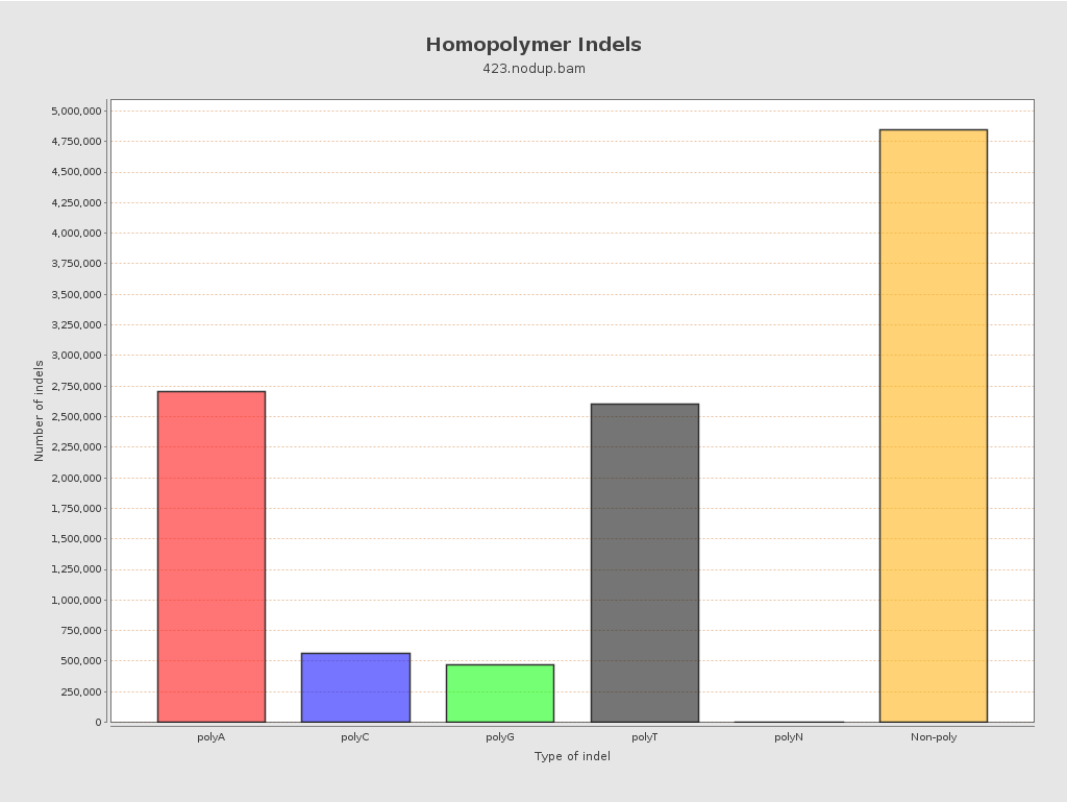
9. Results : Mapped Reads GC-content Distribution



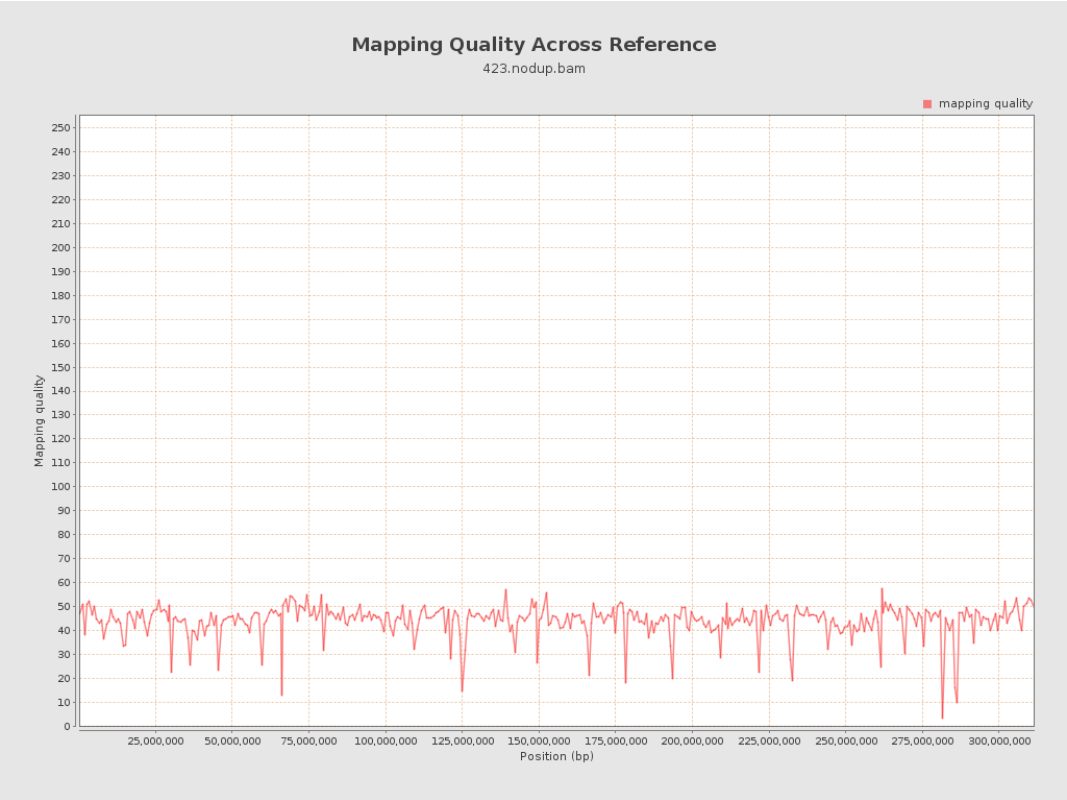
10. Results : Mapped Reads Clipping Profile



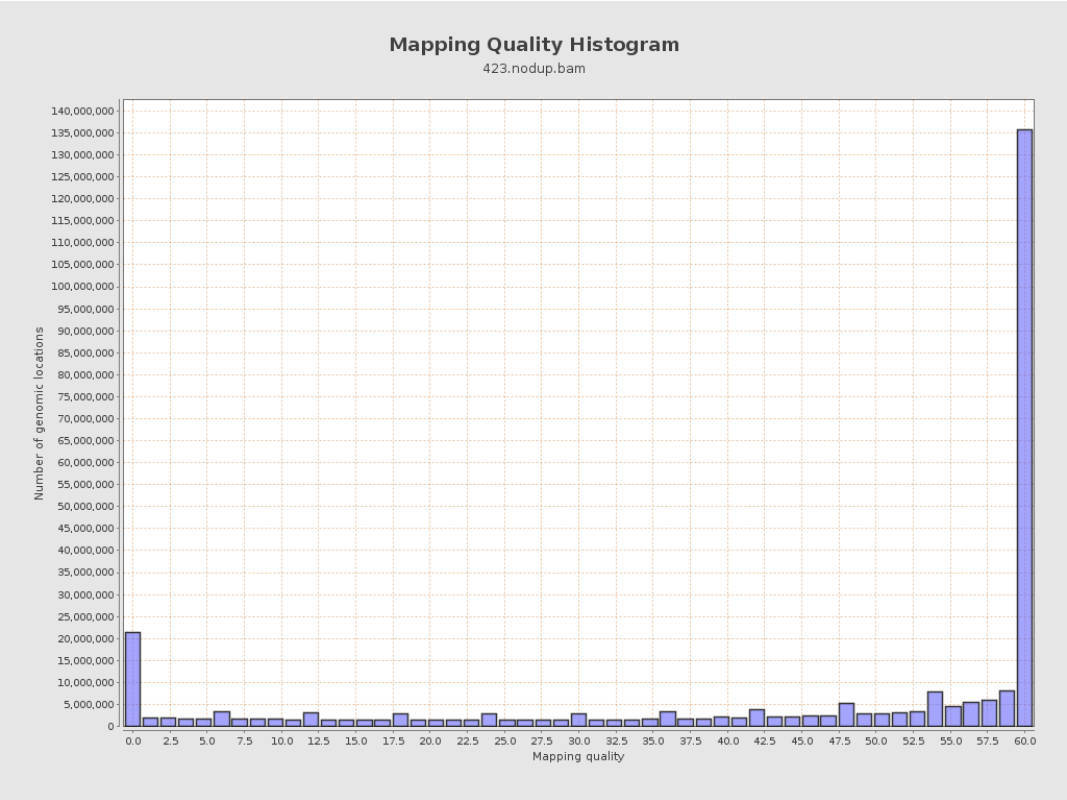
11. Results : Homopolymer Indels



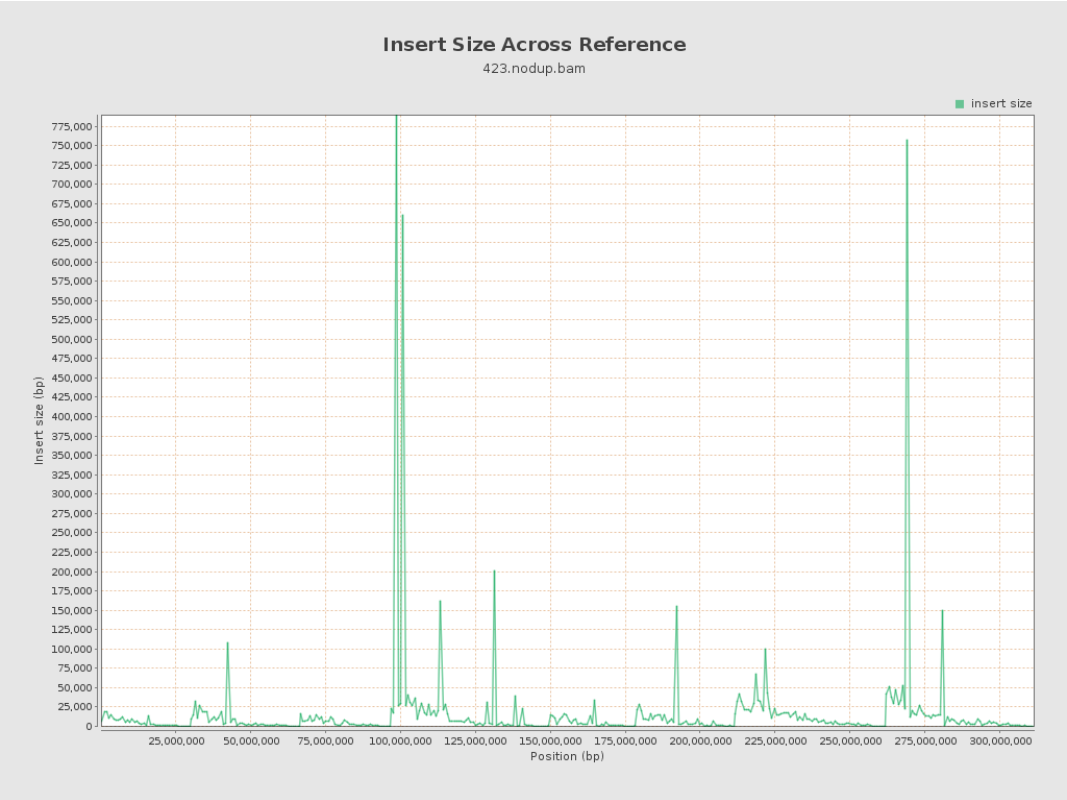
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram