Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:31:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/619.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/619.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_183/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_183_S273_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_183/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_183_S273_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:31:10 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	64,703,630
Mapped reads	60,084,897 / 92.86%
Unmapped reads	4,618,733 / 7.14%
Mapped paired reads	60,084,897 / 92.86%
Mapped reads, first in pair	30,091,774 / 46.51%
Mapped reads, second in pair	29,993,123 / 46.35%
Mapped reads, both in pair	58,535,153 / 90.47%
Mapped reads, singletons	1,549,744 / 2.4%
Read min/max/mean length	30 / 151 / 147.92
Duplicated reads (flagged)	10,351,824 / 16%
Clipped reads	14,078,882 / 21.76%

2.2. ACGT Content

Number/percentage of A's	2,559,042,210 / 30.91%
Number/percentage of C's	1,579,785,672 / 19.08%
Number/percentage of T's	2,557,698,792 / 30.9%
Number/percentage of G's	1,581,732,540 / 19.11%
Number/percentage of N's	34,691 / 0%
GC Percentage	38.19%

2.3. Coverage

Mean	26.6368
Standard Deviation	232.7925

2.4. Mapping Quality

Mean Mapping Quality	43.28

2.5. Insert size

Mean	265,564.18
Standard Deviation	2,449,443.85
P25/Median/P75	332 / 432 / 563

2.6. Mismatches and indels

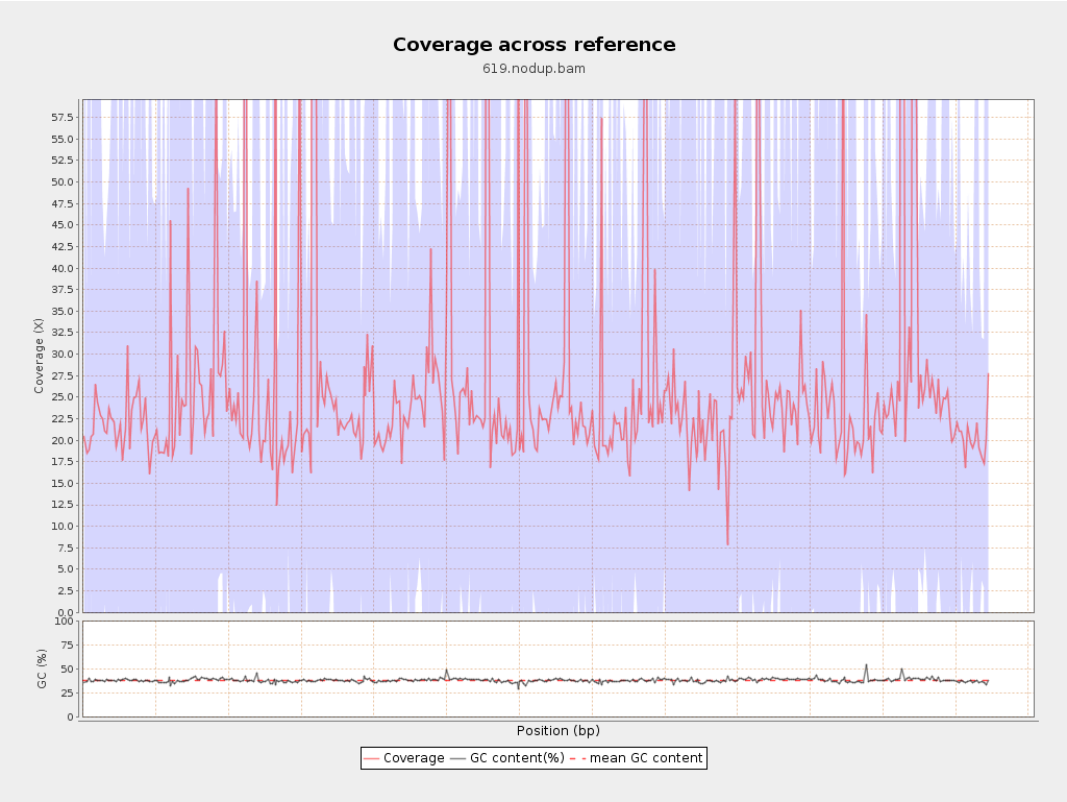
General error rate	2.42%
Mismatches	183,565,298
Insertions	6,046,569
Mapped reads with at least one insertion	8.99%
Deletions	6,056,066
Mapped reads with at least one deletion	8.92%
Homopolymer indels	56.78%

2.7. Chromosome stats

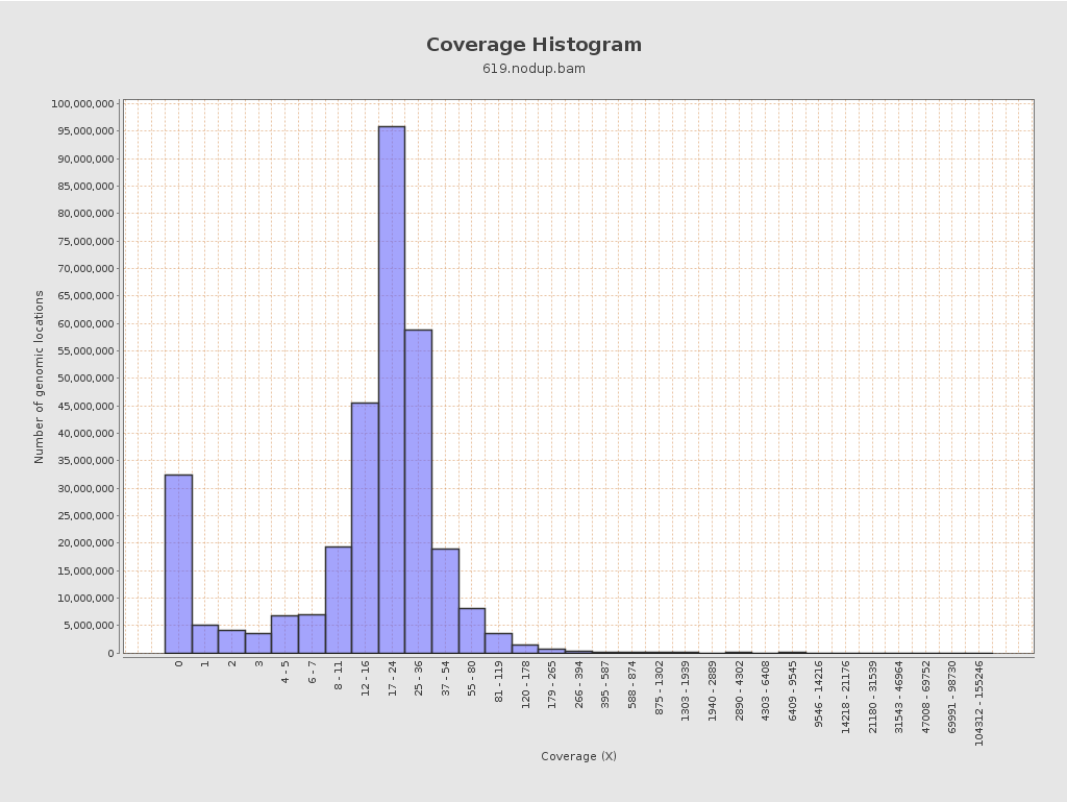
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	639024265	21.4983	90.0497

LT669789.1	36598175	1024270865	27.9869	250.5139
LT669790.1	30422129	898853780	29.5461	266.3325
LT669791.1	52758100	1390492965	26.356	244.2204
LT669792.1	28376109	758196062	26.7195	271.0566
LT669793.1	33388210	837342570	25.079	157.9513
LT669794.1	50579949	1315873153	26.0157	206.3955
LT669795.1	49795044	1437093899	28.8602	282.4381

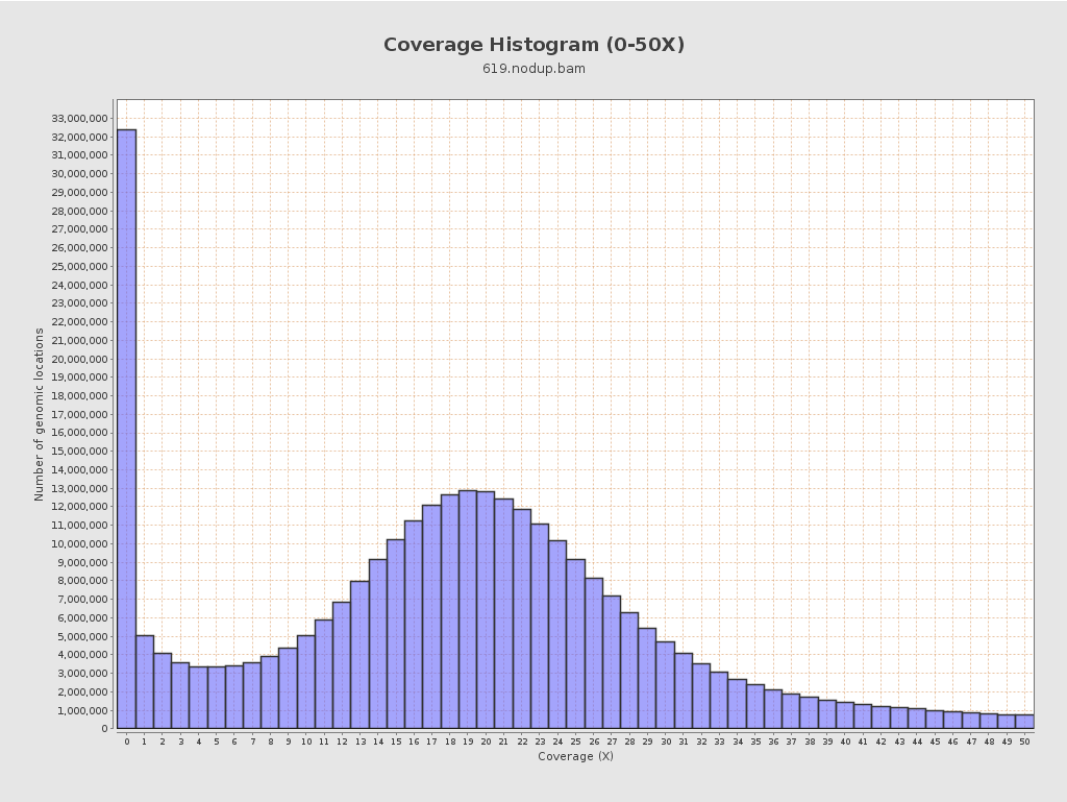
3. Results : Coverage across reference



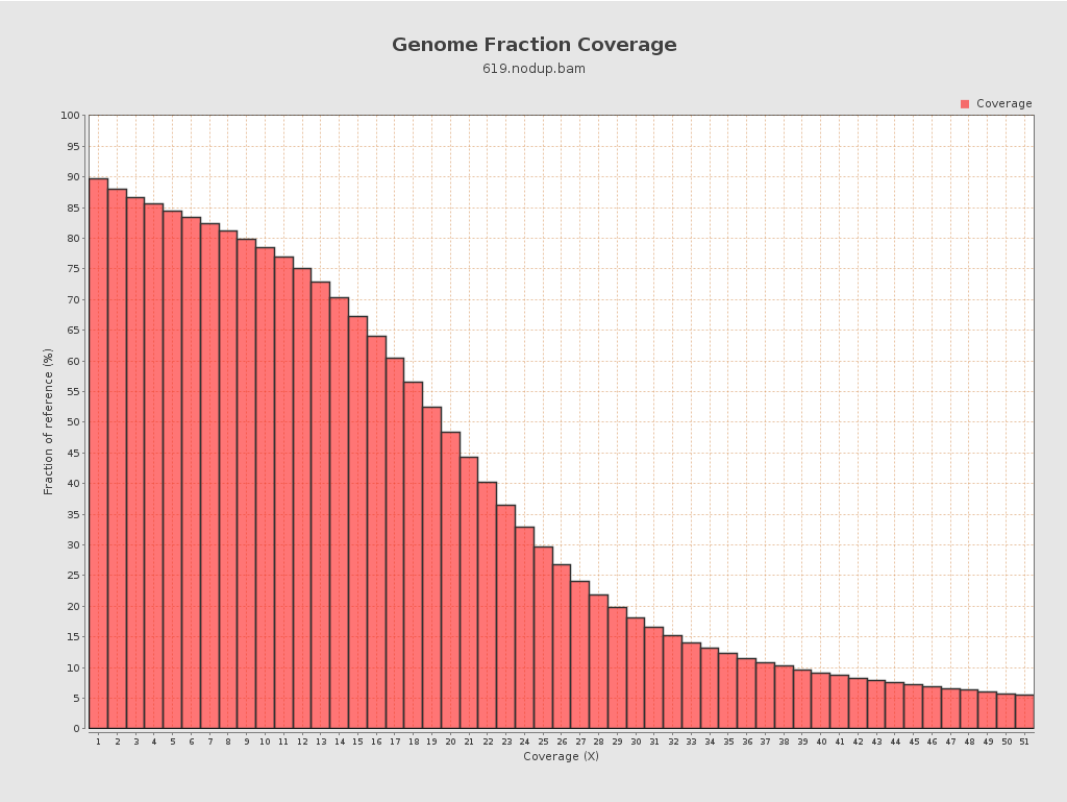
4. Results : Coverage Histogram



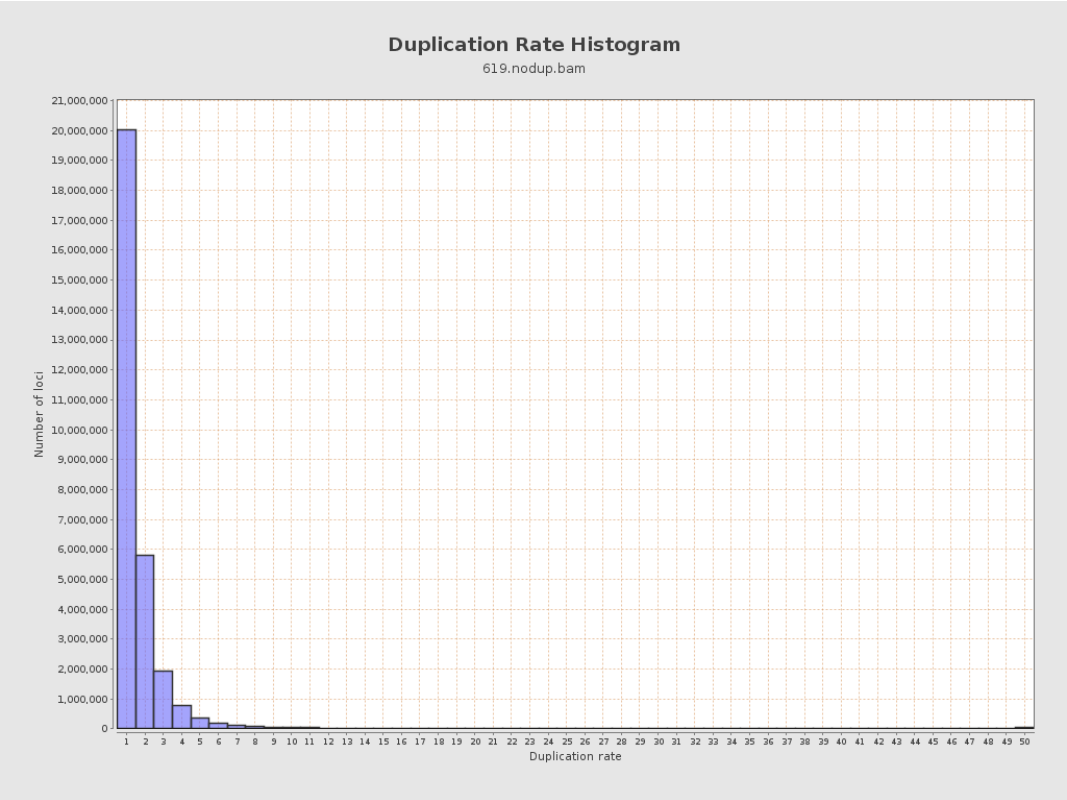
5. Results : Coverage Histogram (0-50X)



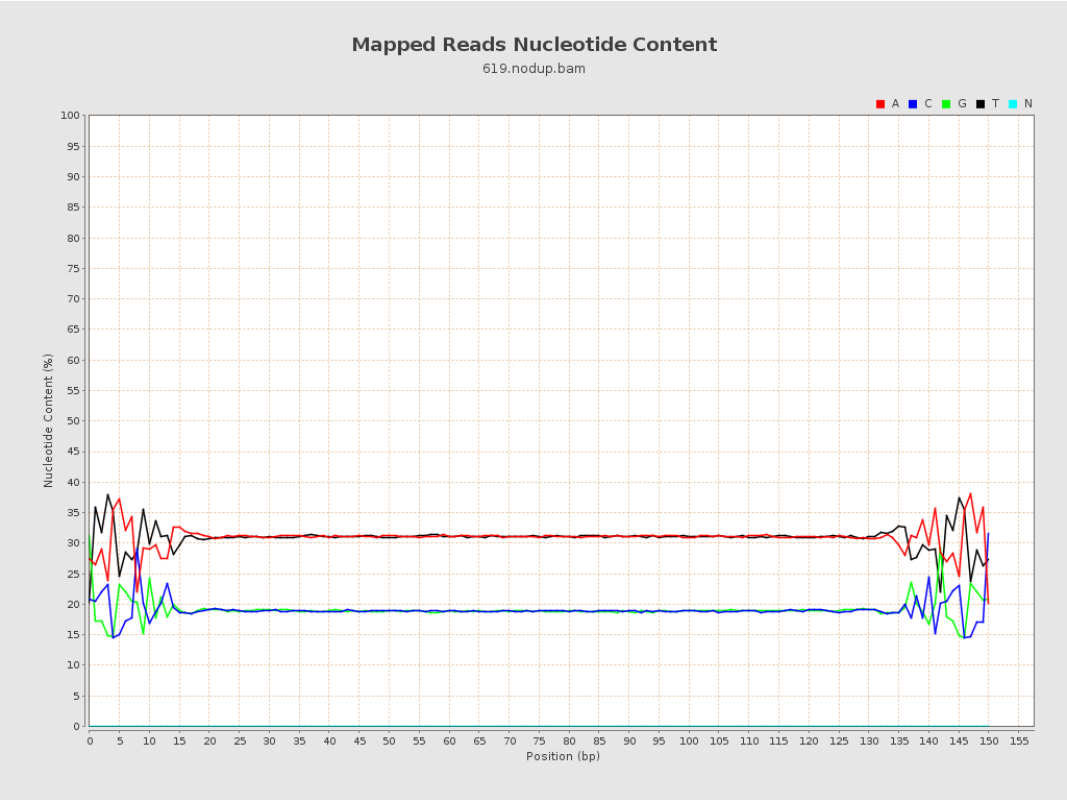
6. Results : Genome Fraction Coverage



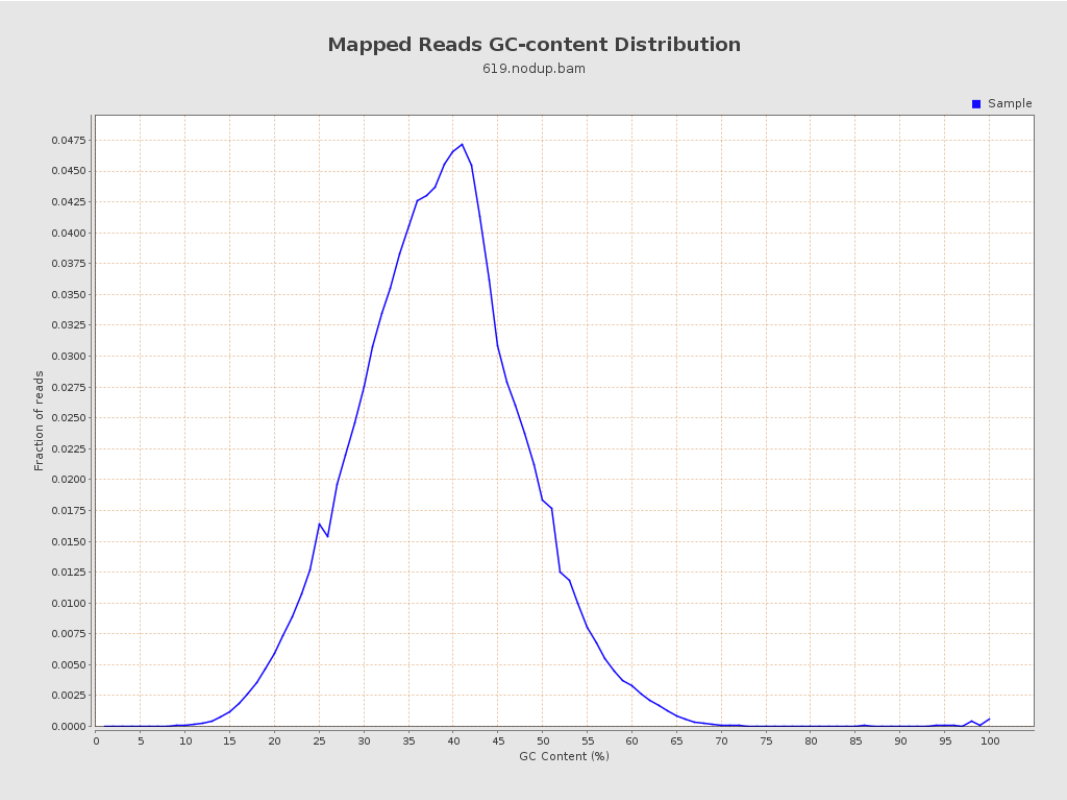
7. Results : Duplication Rate Histogram



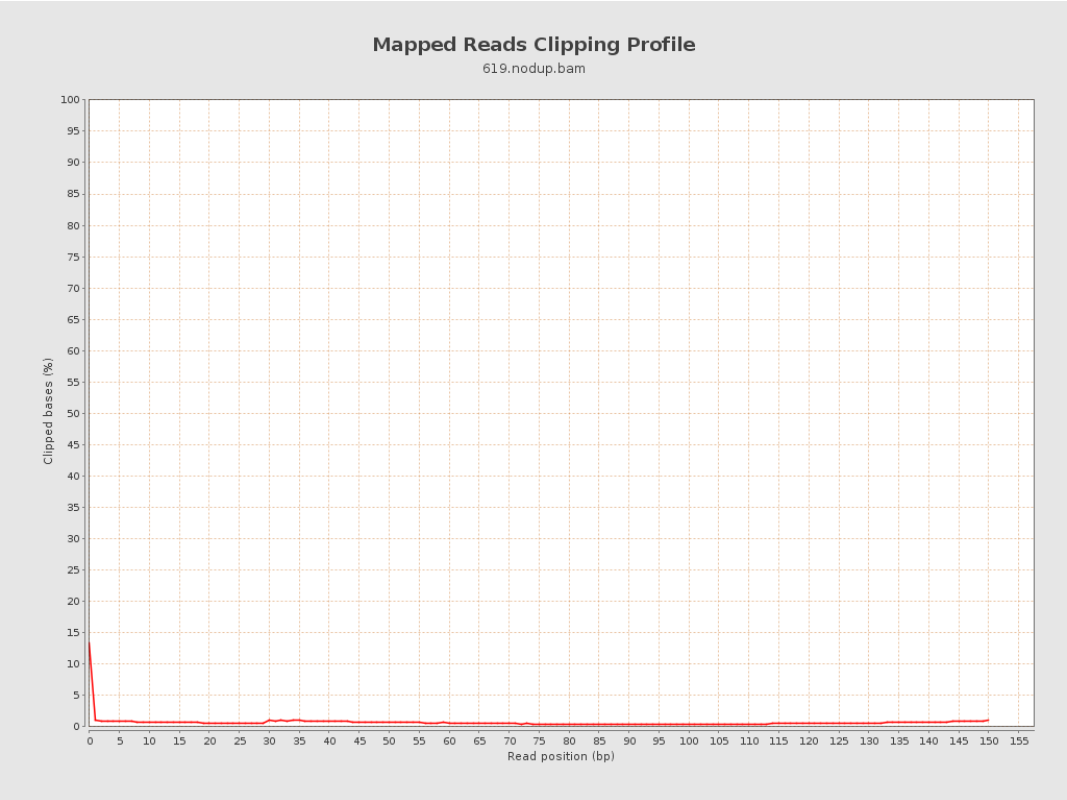
8. Results : Mapped Reads Nucleotide Content



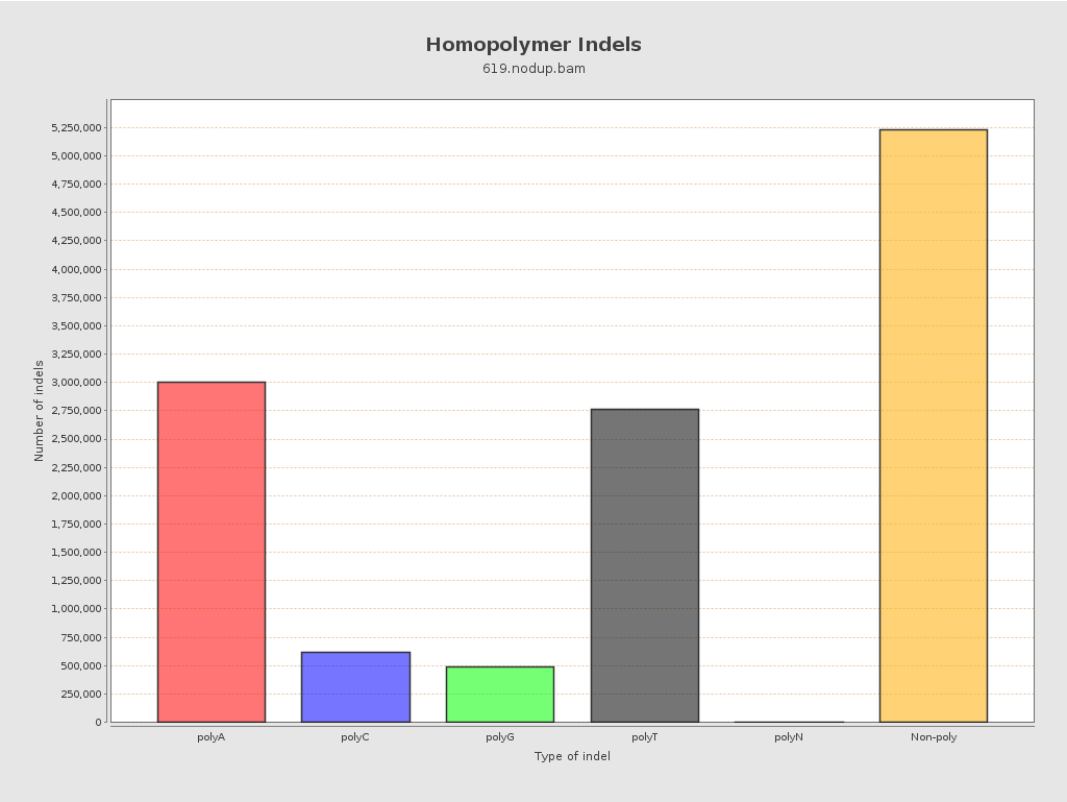
9. Results : Mapped Reads GC-content Distribution



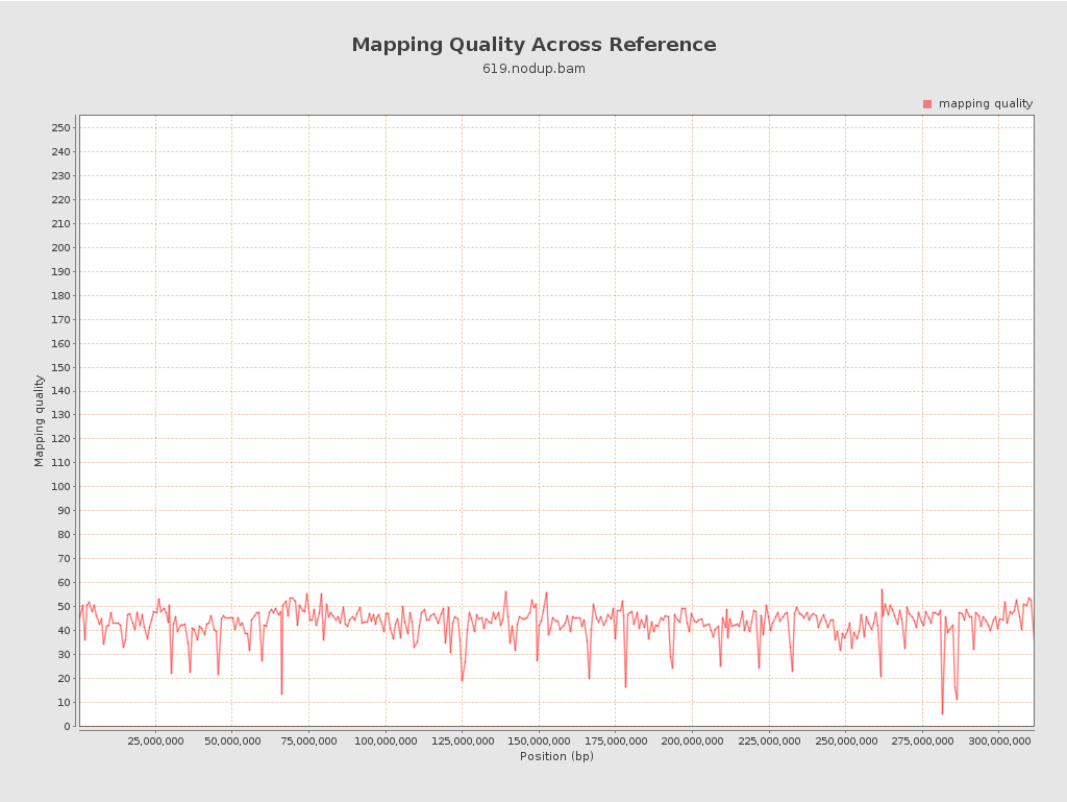
10. Results : Mapped Reads Clipping Profile



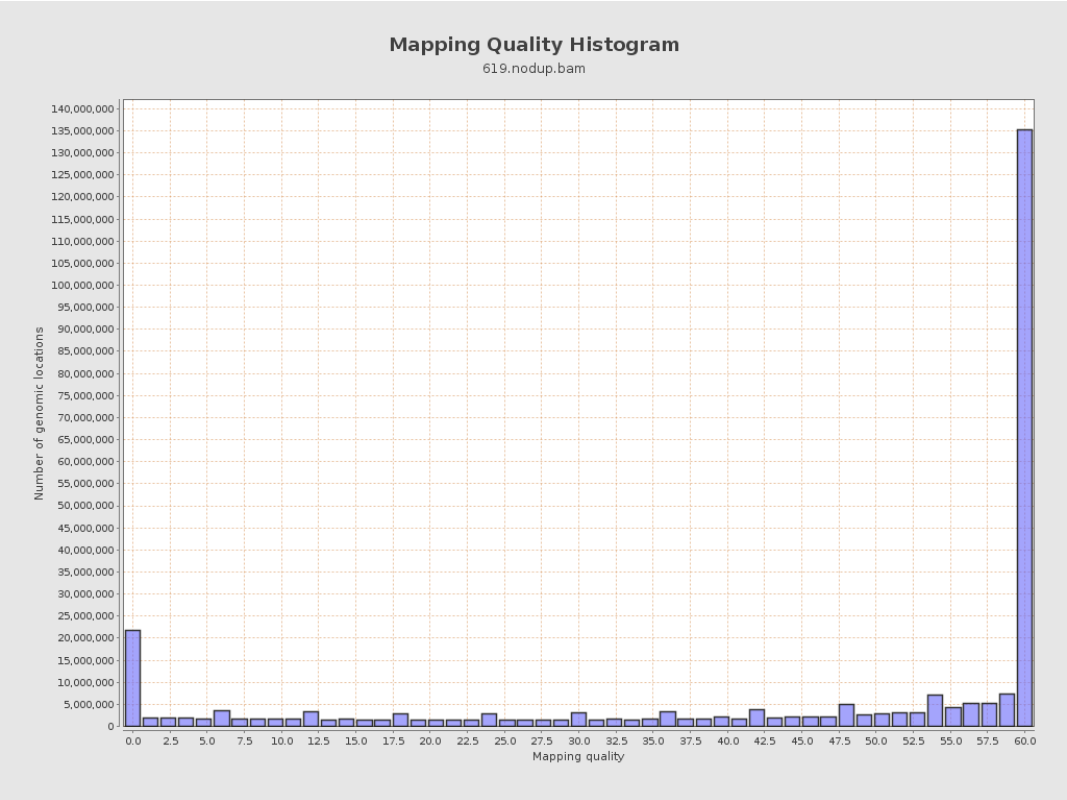
11. Results : Homopolymer Indels



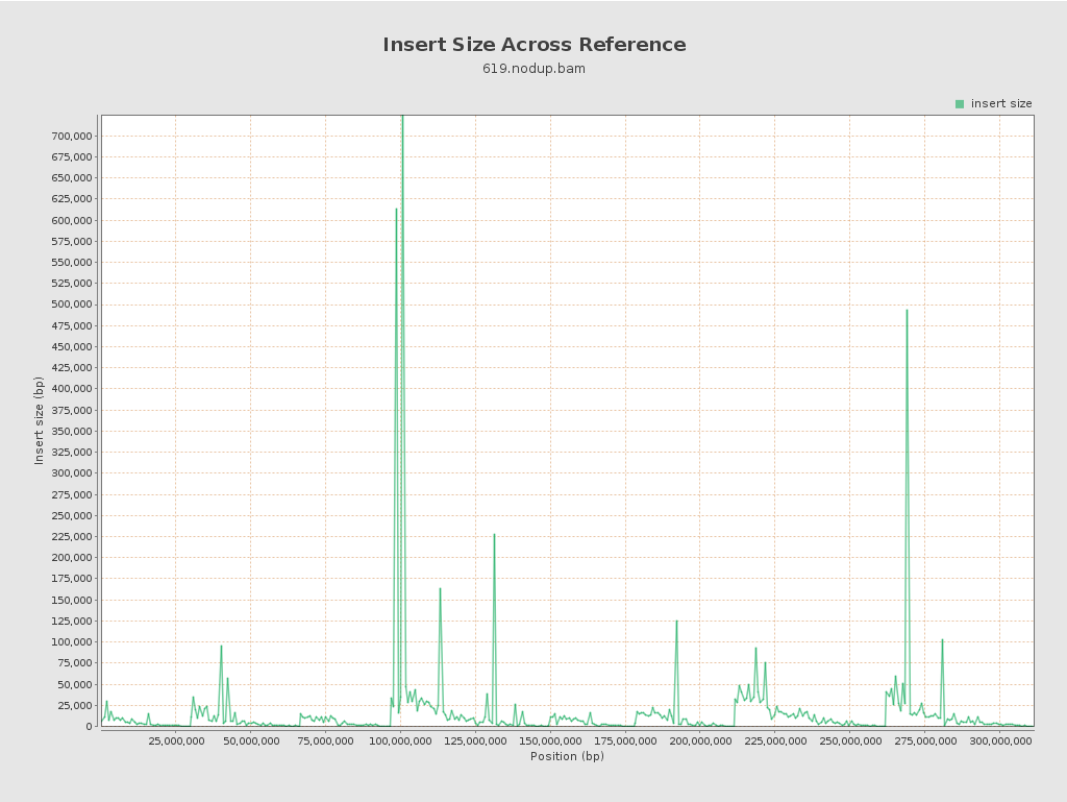
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram