Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:42:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/718.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/718.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_126/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_126_S216_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_126/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_126_S216_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:42:38 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	101,167,649
Mapped reads	91,721,066 / 90.66%
Unmapped reads	9,446,583 / 9.34%
Mapped paired reads	91,721,066 / 90.66%
Mapped reads, first in pair	46,009,197 / 45.48%
Mapped reads, second in pair	45,711,869 / 45.18%
Mapped reads, both in pair	88,716,561 / 87.69%
Mapped reads, singletons	3,004,505 / 2.97%
Read min/max/mean length	30 / 151 / 148.2
Duplicated reads (flagged)	18,748,134 / 18.53%
Clipped reads	21,675,844 / 21.43%

2.2. ACGT Content

Number/percentage of A's	3,900,938,351 / 31%
Number/percentage of C's	2,390,916,491 / 19%
Number/percentage of T's	3,904,121,879 / 31.02%
Number/percentage of G's	2,388,163,756 / 18.98%
Number/percentage of N's	52,095 / 0%
GC Percentage	37.98%

2.3. Coverage

Mean	40.4825
Standard Deviation	364.9173

2.4. Mapping Quality

Mean Mapping Quality	44.64

2.5. Insert size

Mean	250,557.13
Standard Deviation	2,412,942.14
P25/Median/P75	321 / 421 / 556

2.6. Mismatches and indels

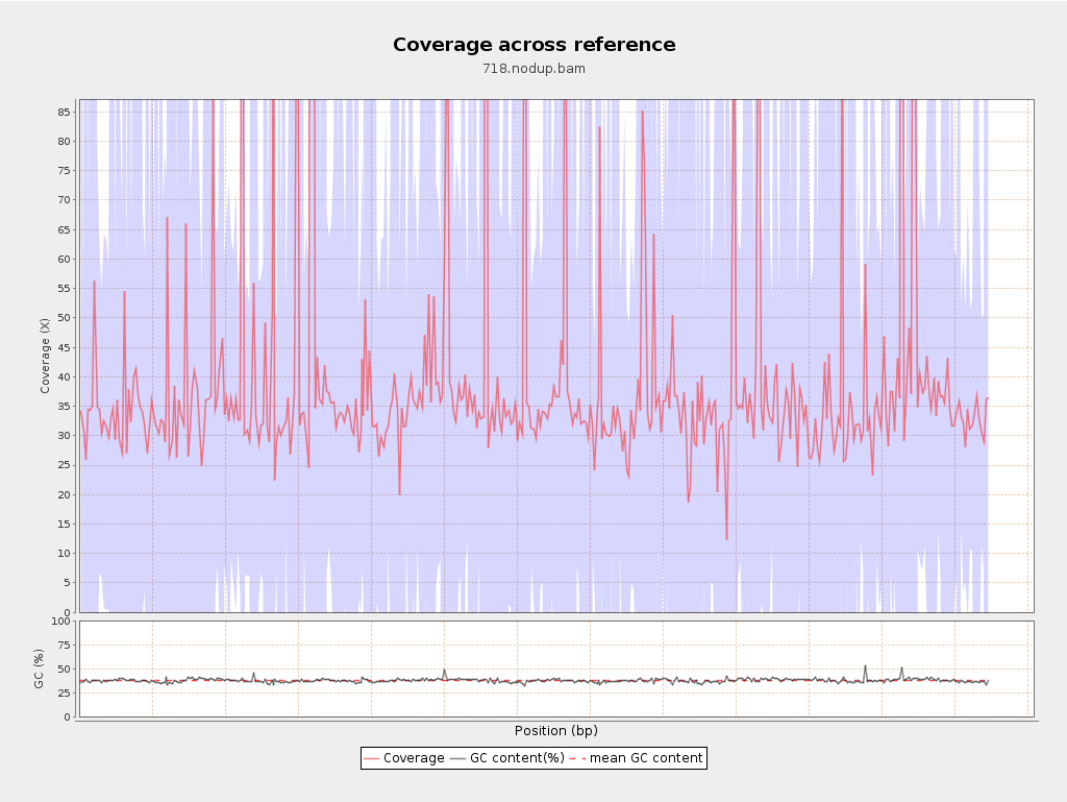
General error rate	2.38%
Mismatches	274,300,899
Insertions	9,142,462
Mapped reads with at least one insertion	8.88%
Deletions	8,648,518
Mapped reads with at least one deletion	8.35%
Homopolymer indels	57.27%

2.7. Chromosome stats

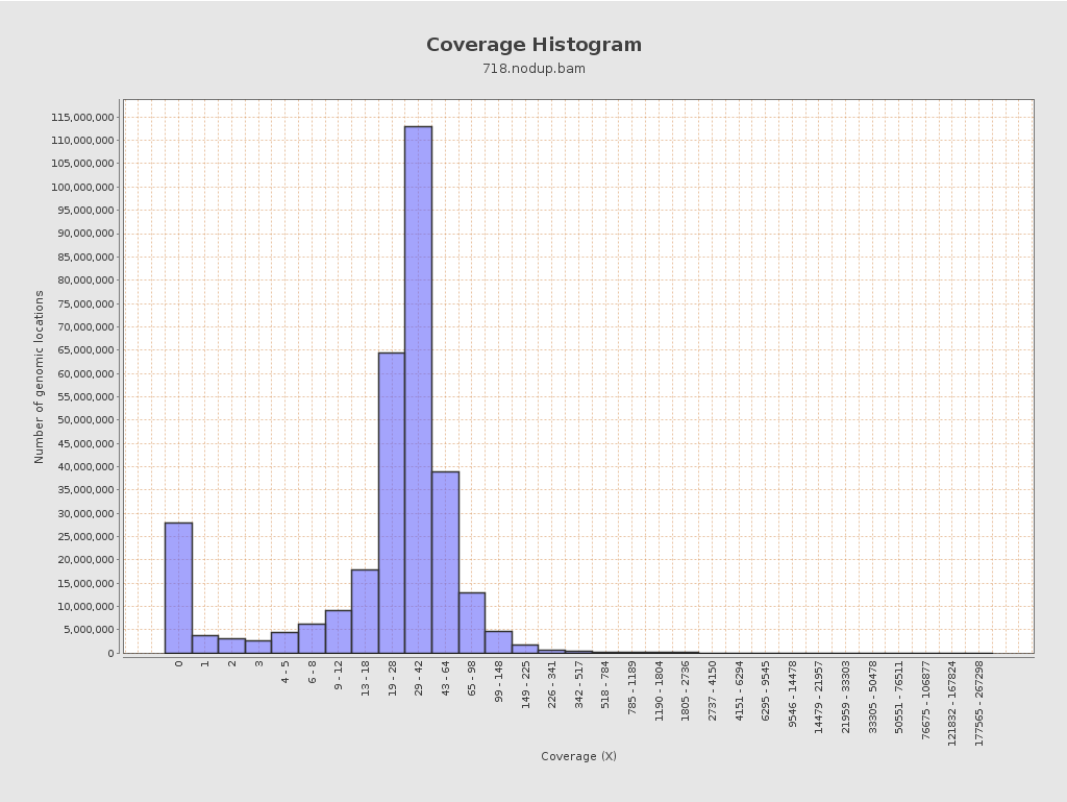
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	1008797557	33.9384	143.6786

LT669789.1	36598175	1478830235	40.4072	383.5134
LT669790.1	30422129	1519737587	49.955	544.9219
LT669791.1	52758100	2108096205	39.9578	393.2886
LT669792.1	28376109	1167854192	41.1562	398.7314
LT669793.1	33388210	1212555619	36.3169	203.549
LT669794.1	50579949	1878457189	37.1384	303.489
LT669795.1	49795044	2241723696	45.019	394.4982

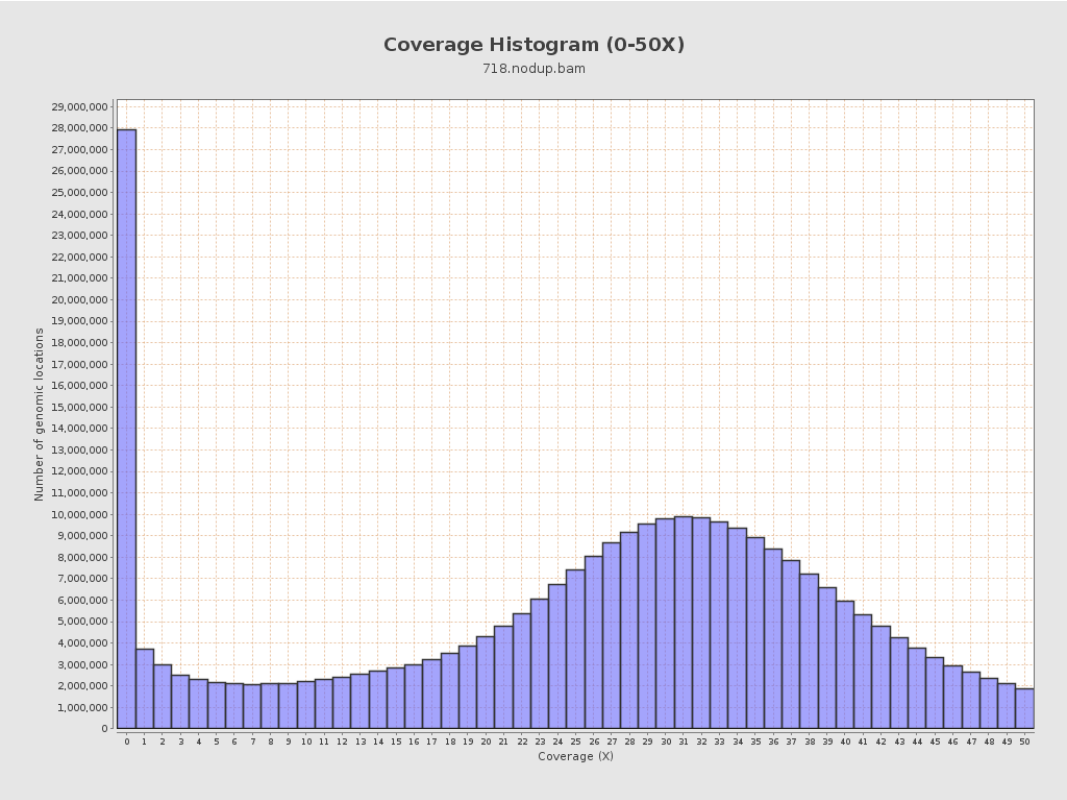
3. Results : Coverage across reference



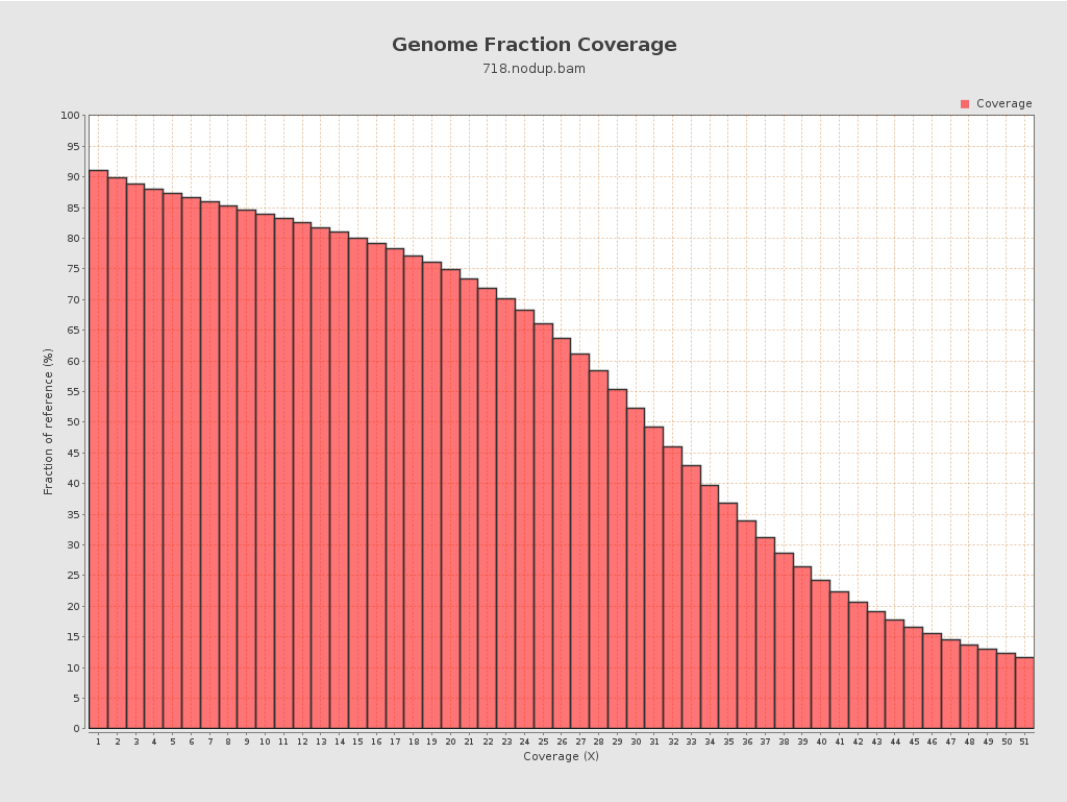
4. Results : Coverage Histogram



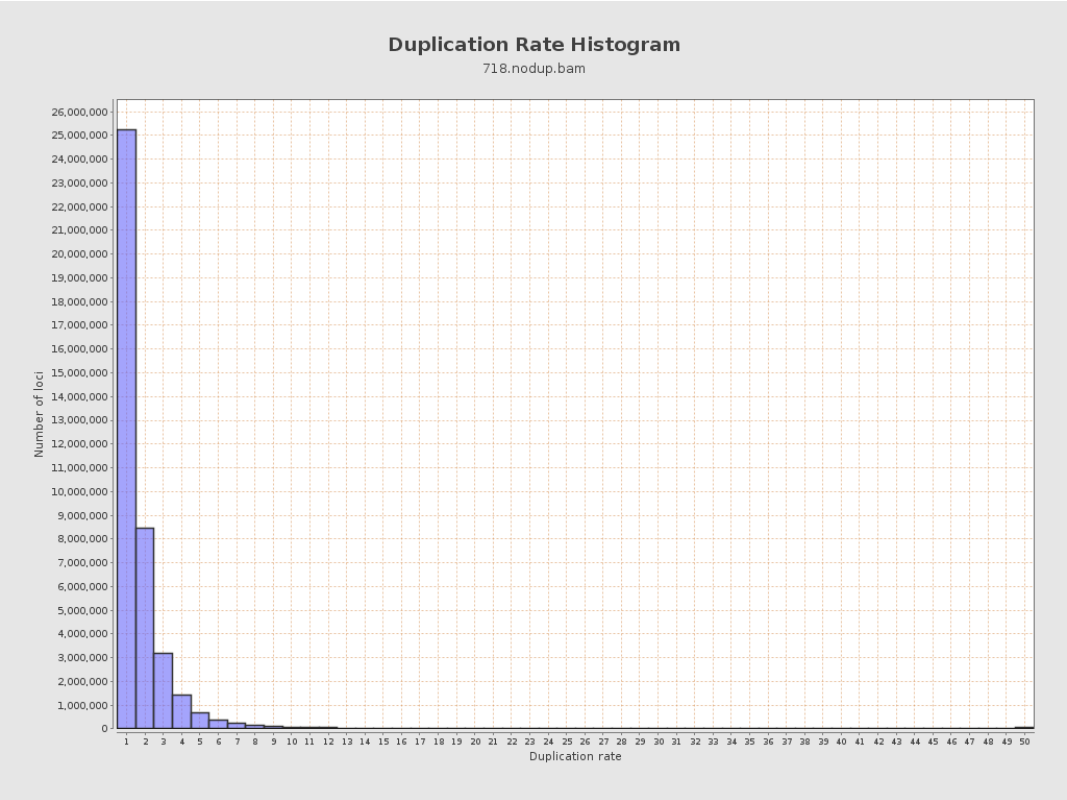
5. Results : Coverage Histogram (0-50X)



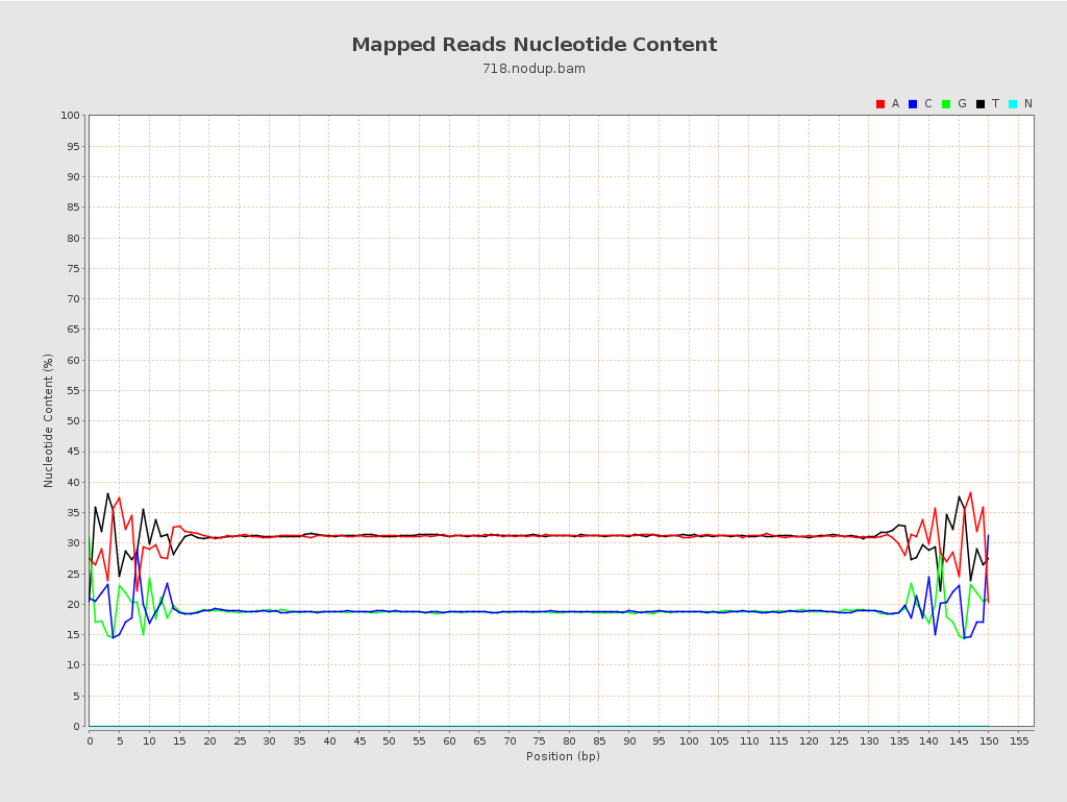
6. Results : Genome Fraction Coverage



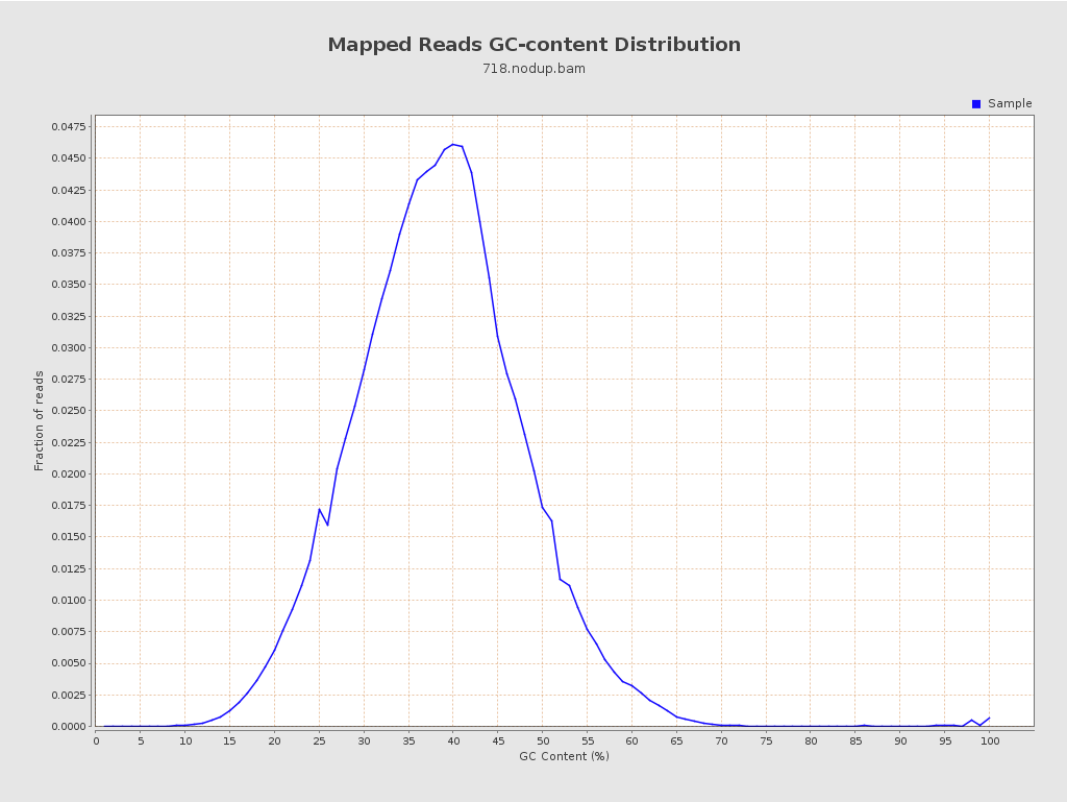
7. Results : Duplication Rate Histogram



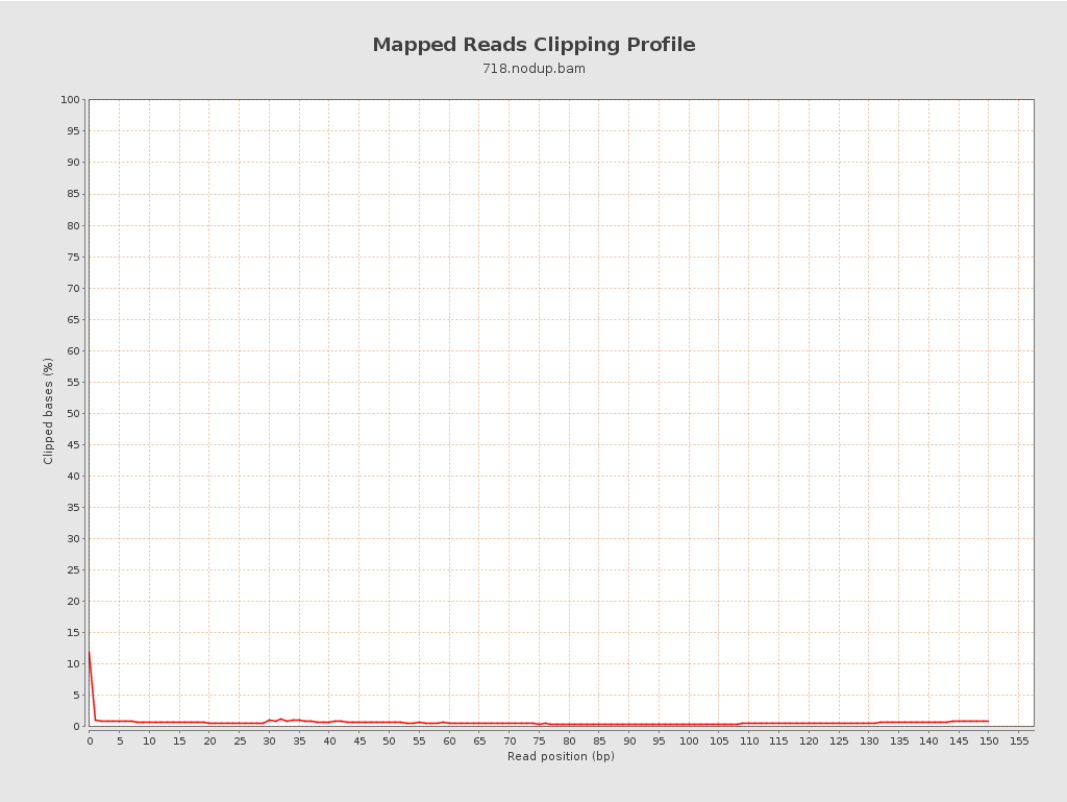
8. Results : Mapped Reads Nucleotide Content



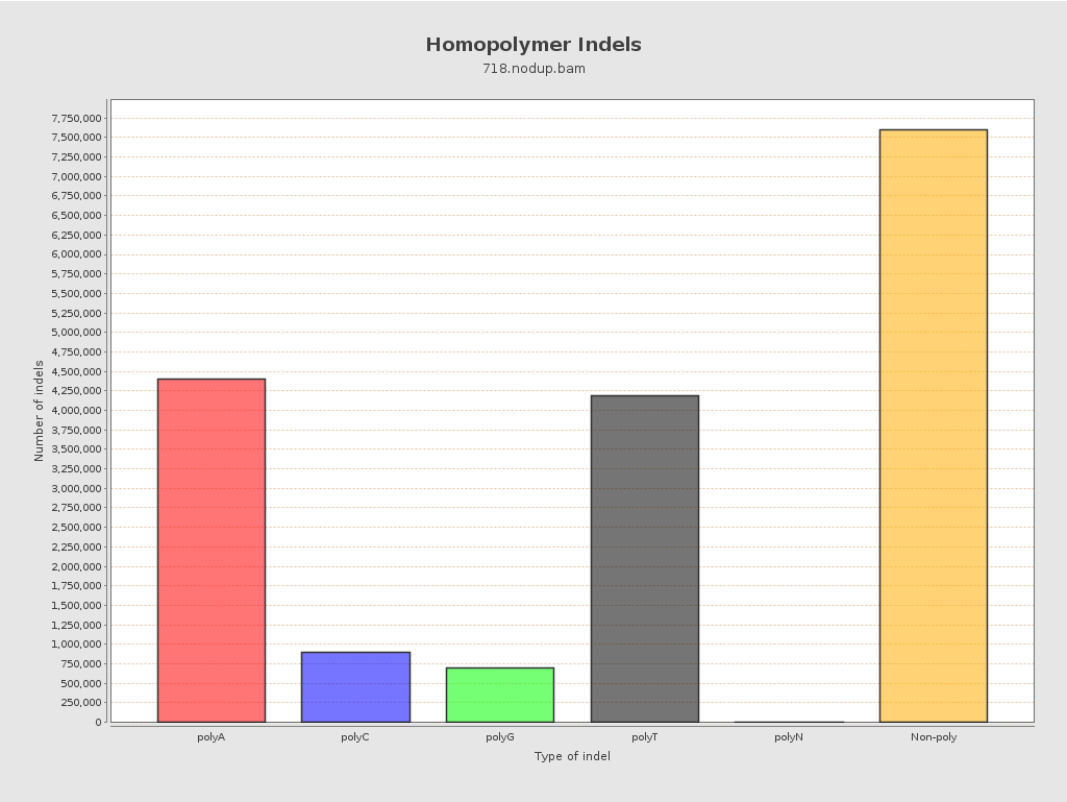
9. Results : Mapped Reads GC-content Distribution



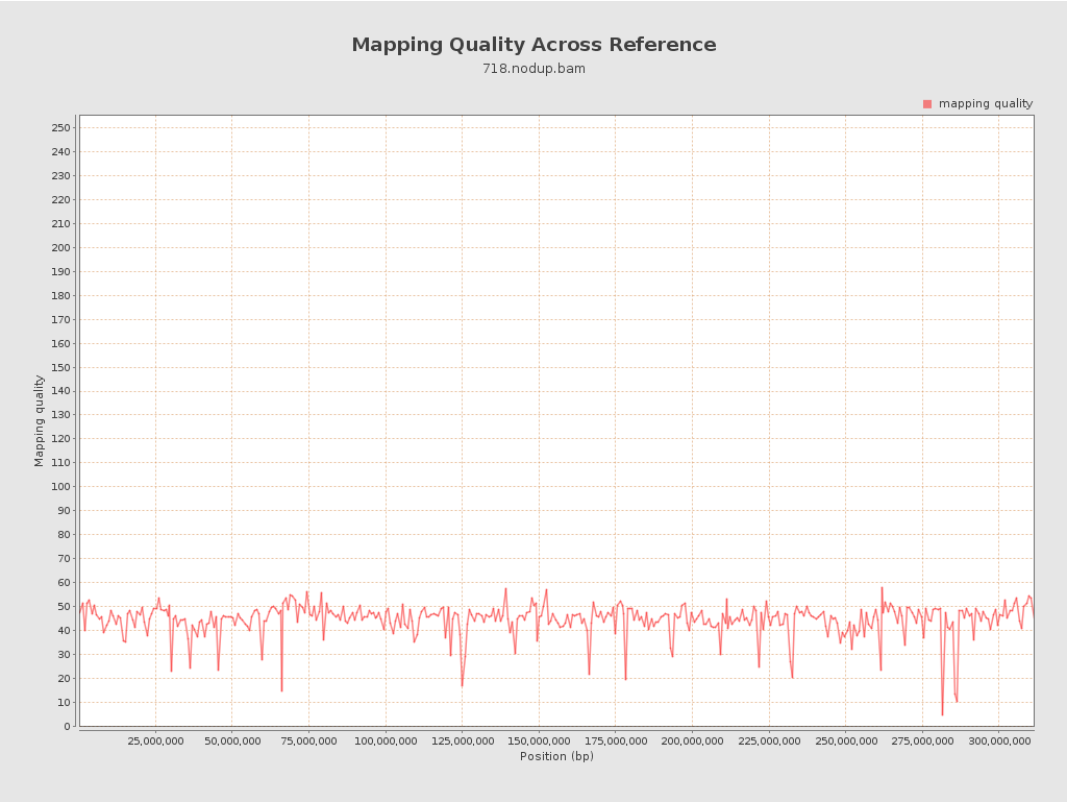
10. Results : Mapped Reads Clipping Profile



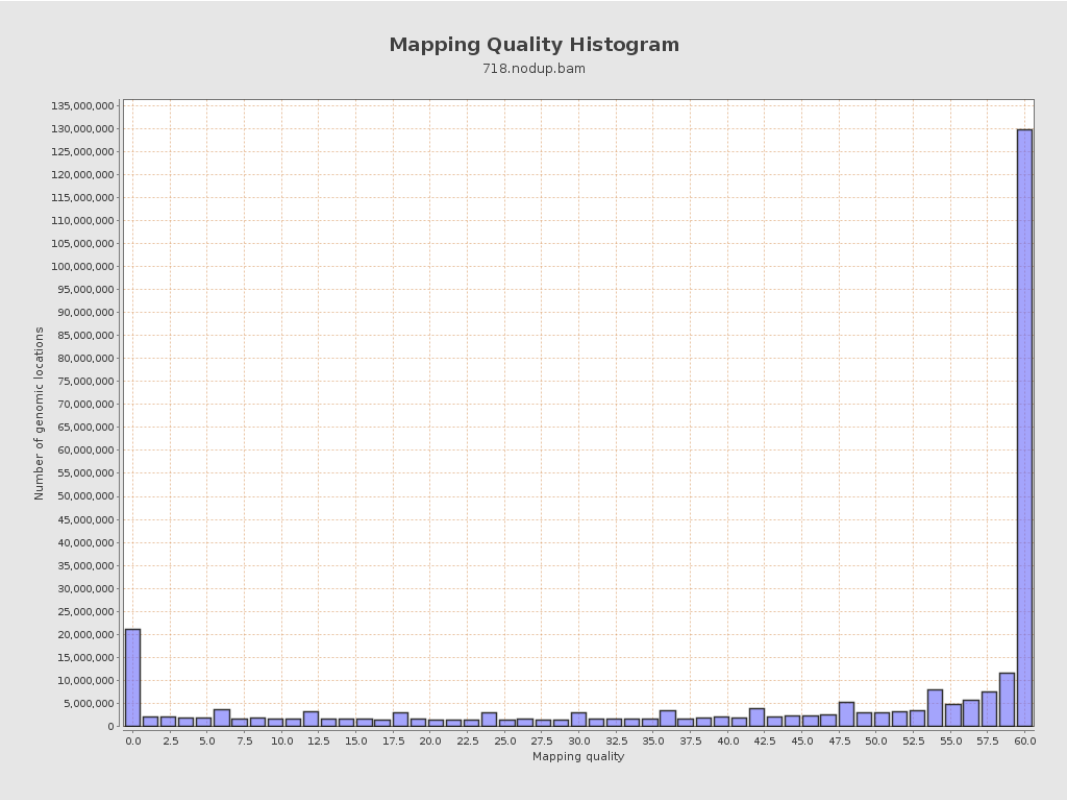
11. Results : Homopolymer Indels



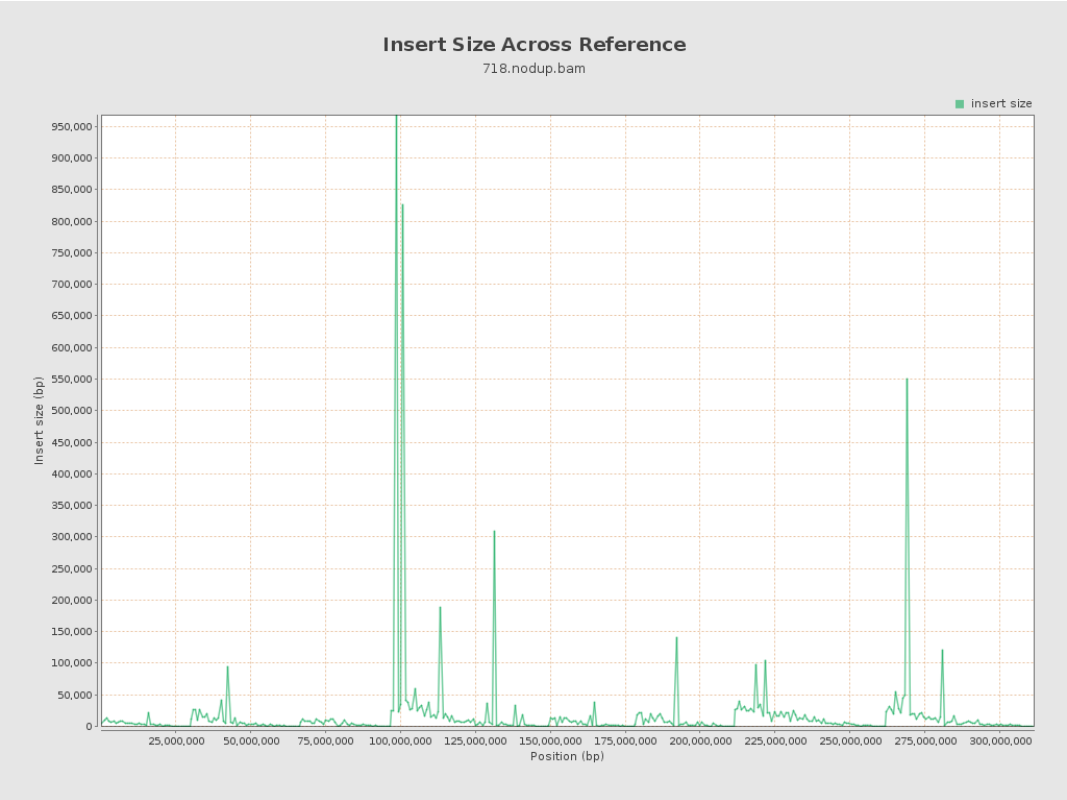
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram