Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:28:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/828.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/828.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_213/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_213_S294_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_213/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_213_S294_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:28:05 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	57,878,489
Mapped reads	54,662,638 / 94.44%
Unmapped reads	3,215,851 / 5.56%
Mapped paired reads	54,662,638 / 94.44%
Mapped reads, first in pair	27,373,282 / 47.29%
Mapped reads, second in pair	27,289,356 / 47.15%
Mapped reads, both in pair	53,609,881 / 92.62%
Mapped reads, singletons	1,052,757 / 1.82%
Read min/max/mean length	30 / 151 / 147.98
Duplicated reads (flagged)	7,362,116 / 12.72%
Clipped reads	12,579,920 / 21.74%

2.2. ACGT Content

Number/percentage of A's	2,324,809,195 / 30.74%
Number/percentage of C's	1,456,577,695 / 19.26%
Number/percentage of T's	2,328,970,589 / 30.79%
Number/percentage of G's	1,453,141,611 / 19.21%
Number/percentage of N's	28,407 / 0%
GC Percentage	38.47%

2.3. Coverage

Mean	24.3335
Standard Deviation	204.3279

2.4. Mapping Quality

Mean Mapping Quality	43.83

2.5. Insert size

Mean	234,176.32
Standard Deviation	2,288,331.54
P25/Median/P75	331 / 435 / 566

2.6. Mismatches and indels

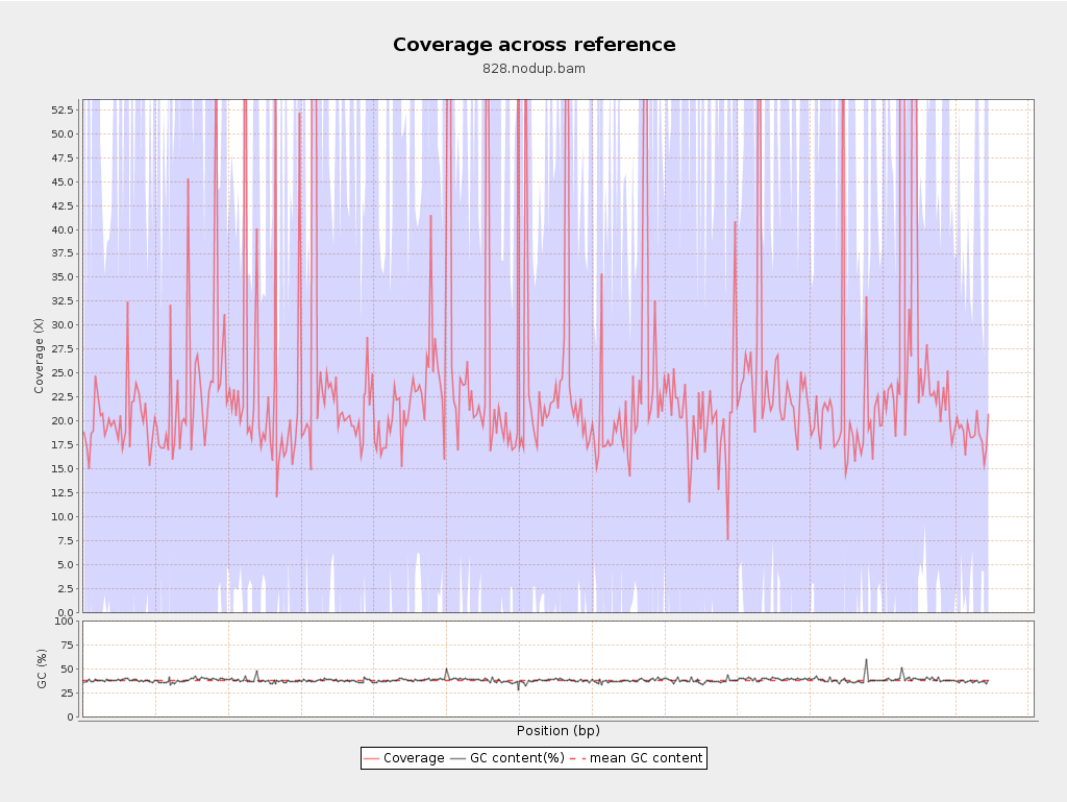
General error rate	2.35%
Mismatches	163,997,673
Insertions	5,096,813
Mapped reads with at least one insertion	8.38%
Deletions	5,231,082
Mapped reads with at least one deletion	8.48%
Homopolymer indels	55.76%

2.7. Chromosome stats

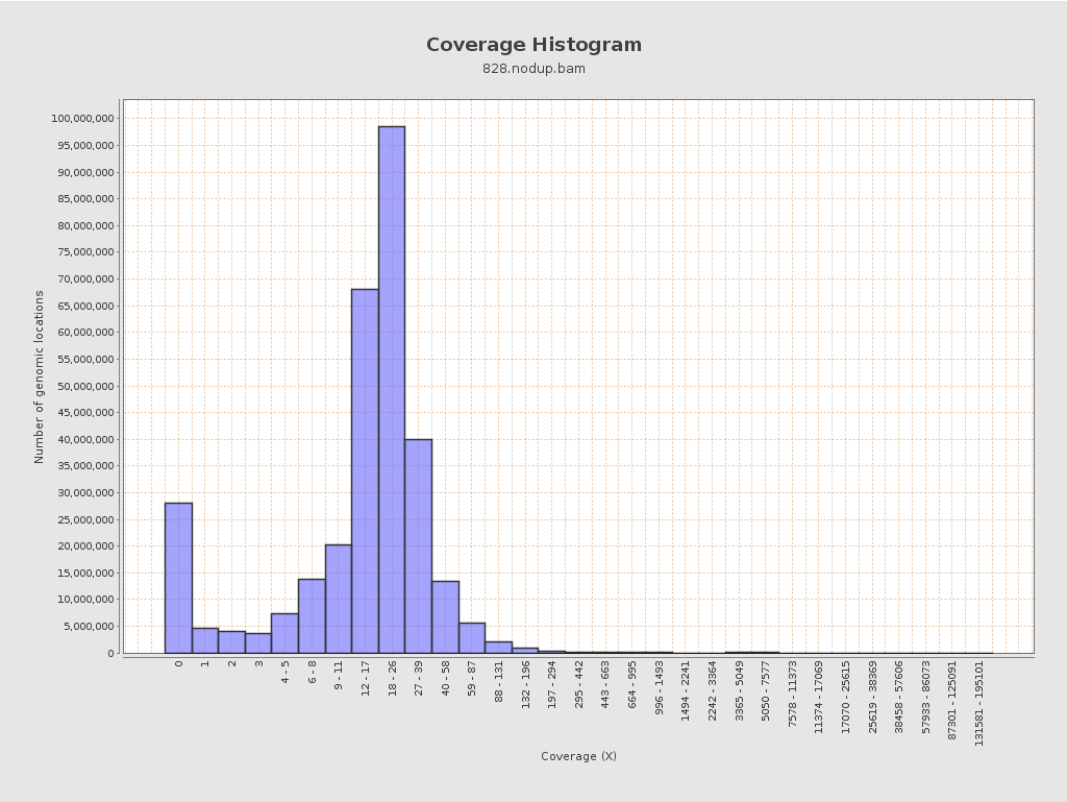
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	588154709	19.787	71.8855

LT669789.1	36598175	902944054	24.6718	216.164
LT669790.1	30422129	777879461	25.5695	185.5636
LT669791.1	52758100	1260245838	23.8872	190.0228
LT669792.1	28376109	680596025	23.9848	205.8996
LT669793.1	33388210	759856172	22.7582	139.4435
LT669794.1	50579949	1183285253	23.3944	190.9209
LT669795.1	49795044	1430392682	28.7256	300.5191

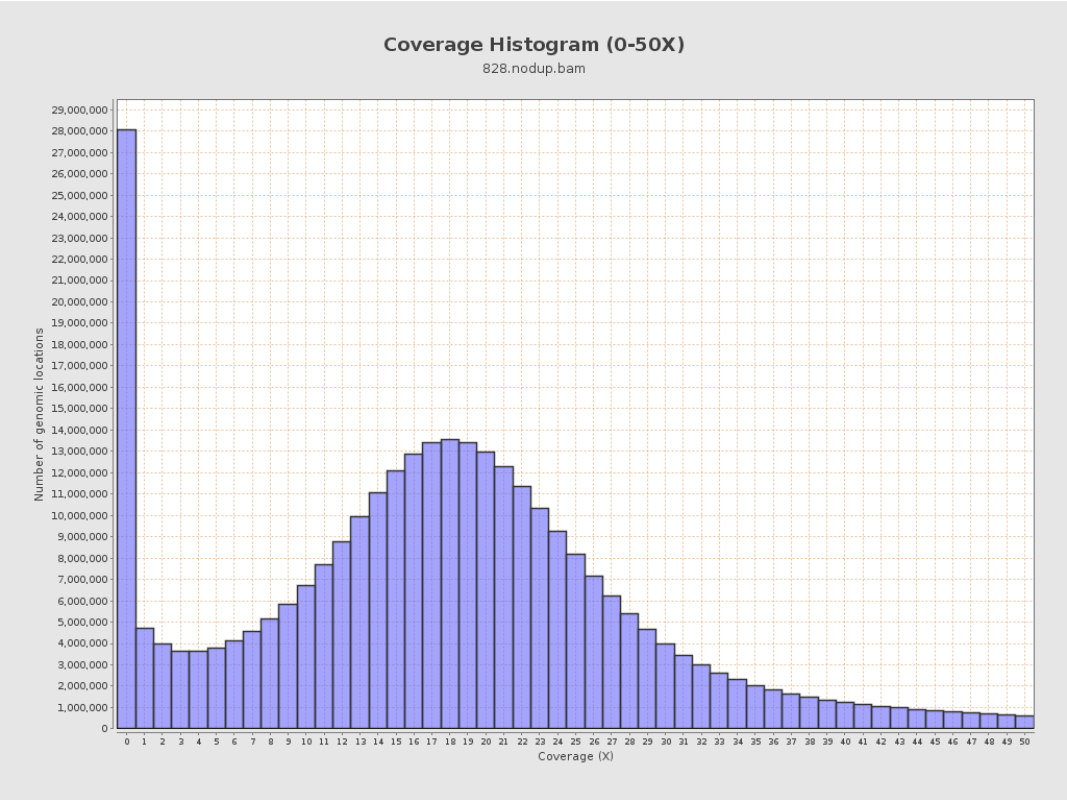
3. Results : Coverage across reference



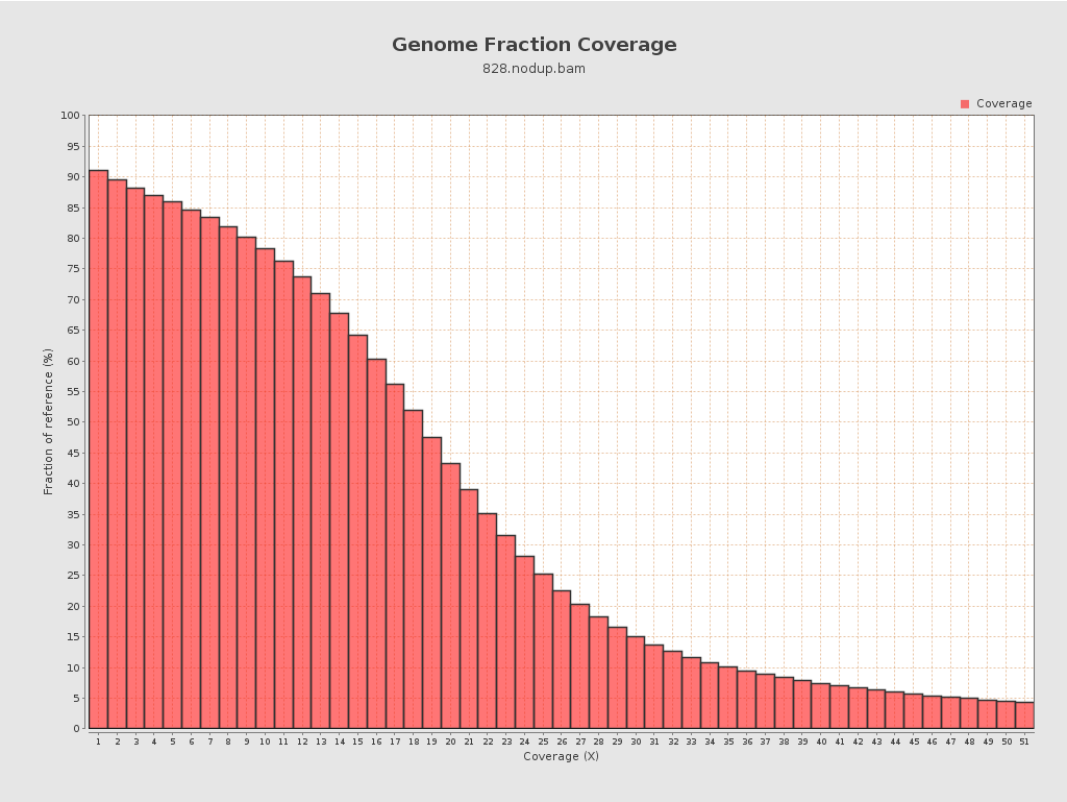
4. Results : Coverage Histogram



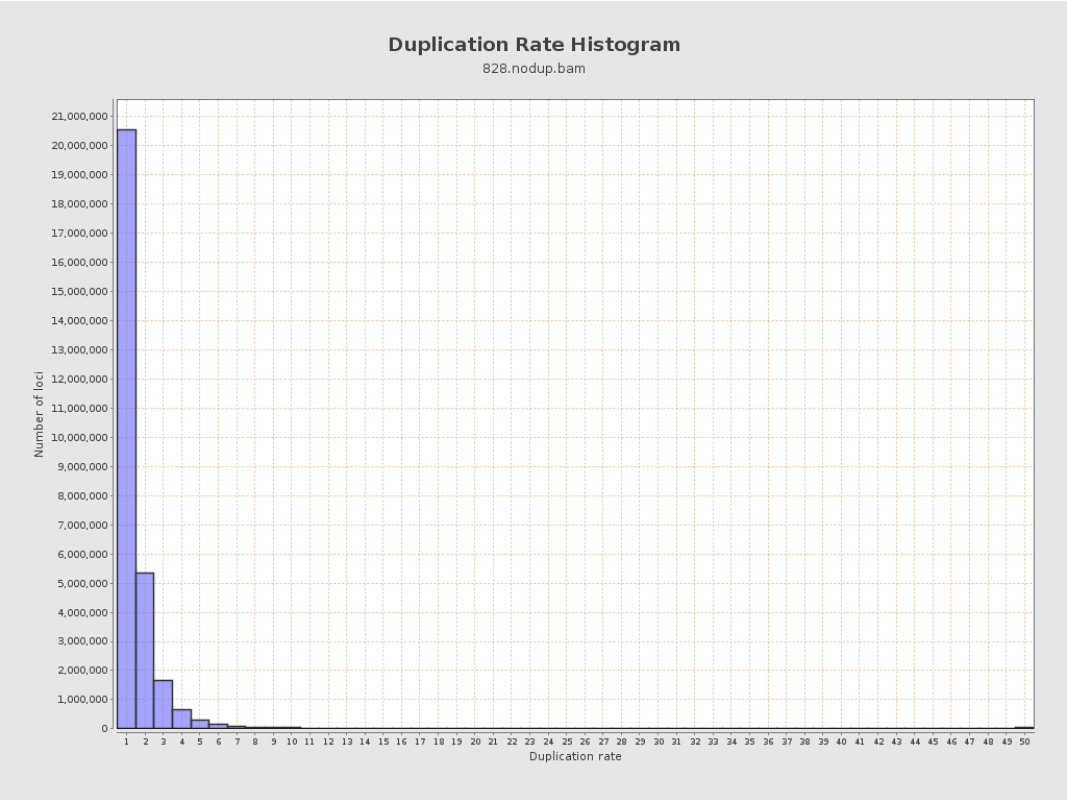
5. Results : Coverage Histogram (0-50X)



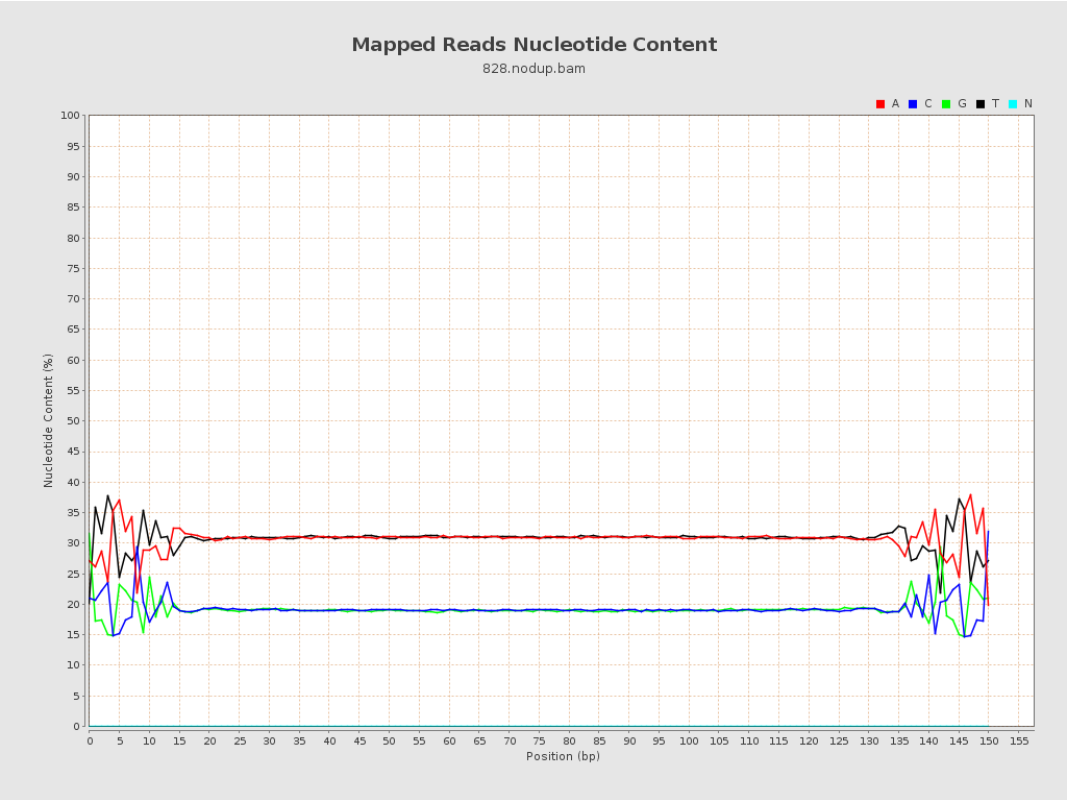
6. Results : Genome Fraction Coverage



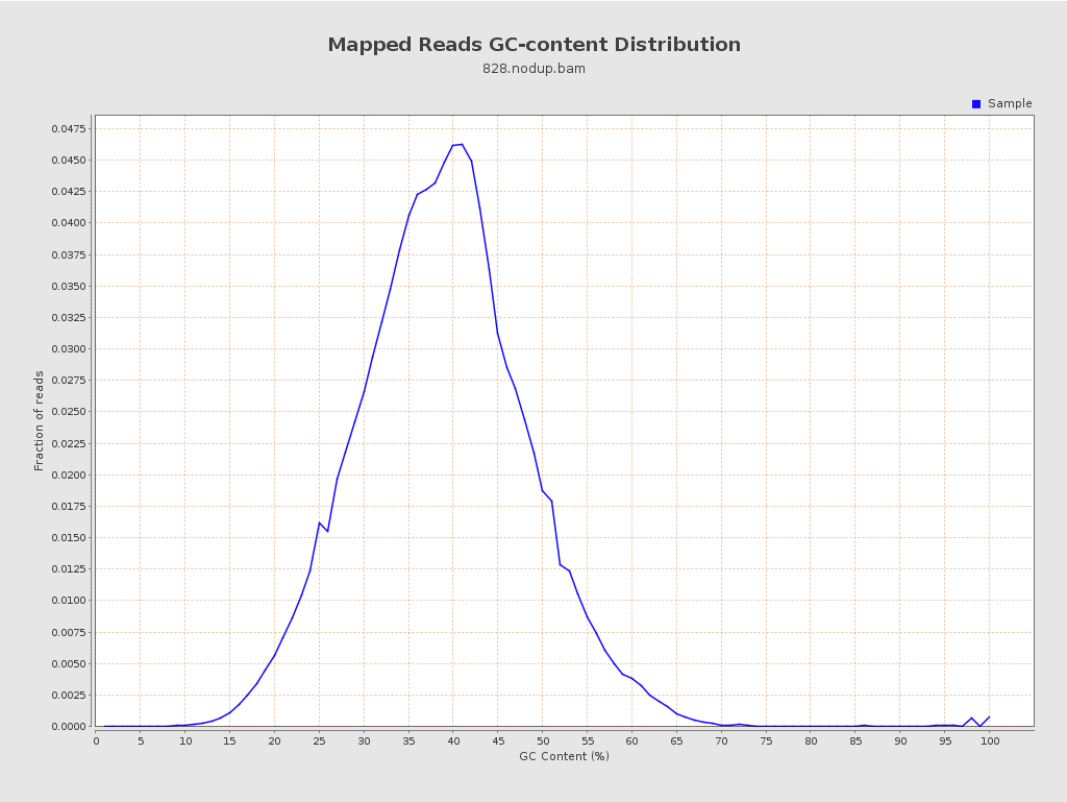
7. Results : Duplication Rate Histogram



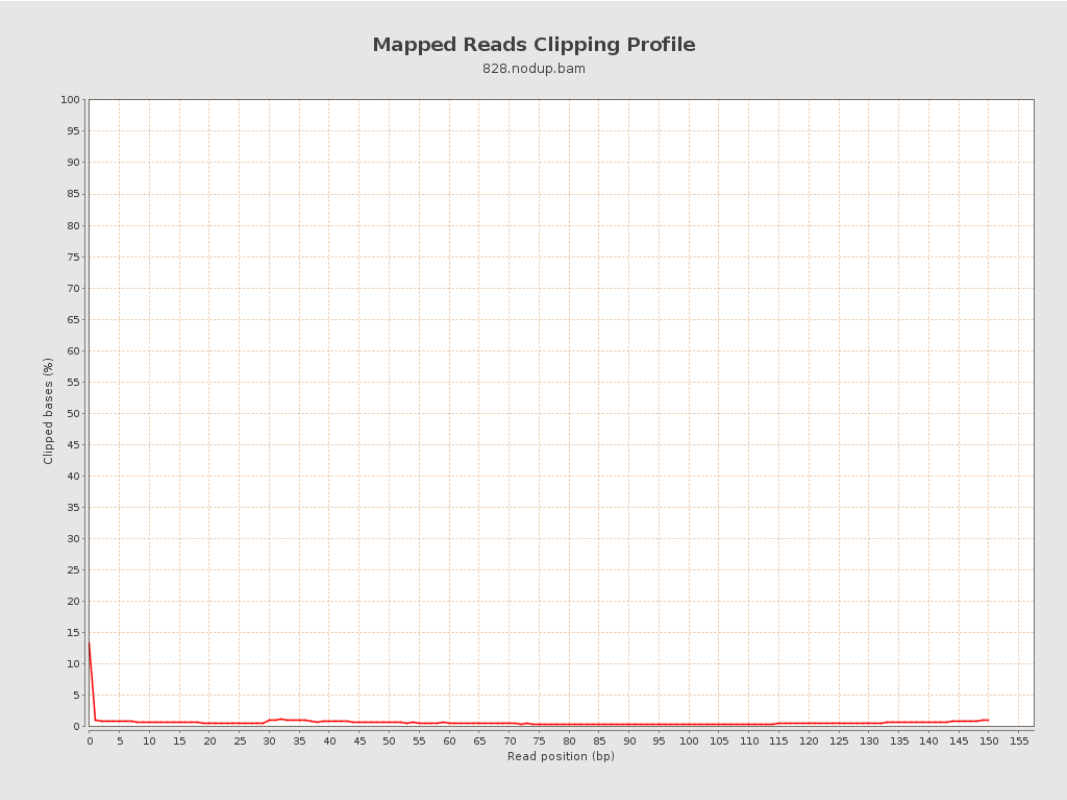
8. Results : Mapped Reads Nucleotide Content



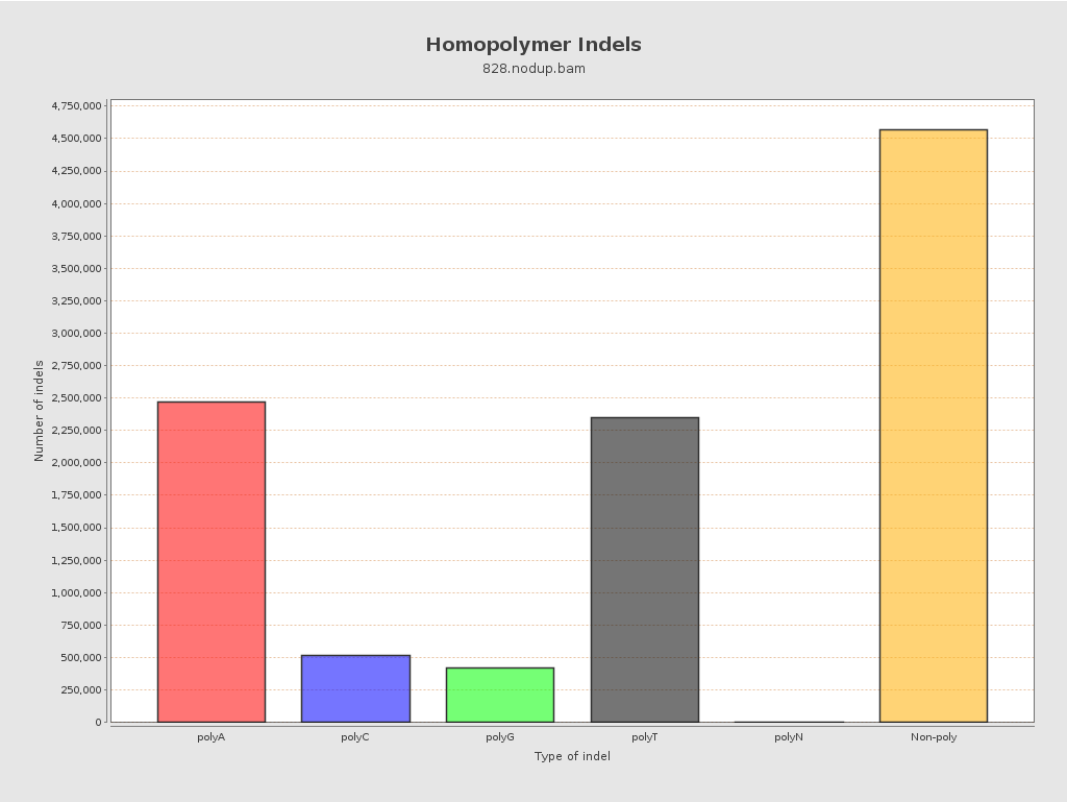
9. Results : Mapped Reads GC-content Distribution



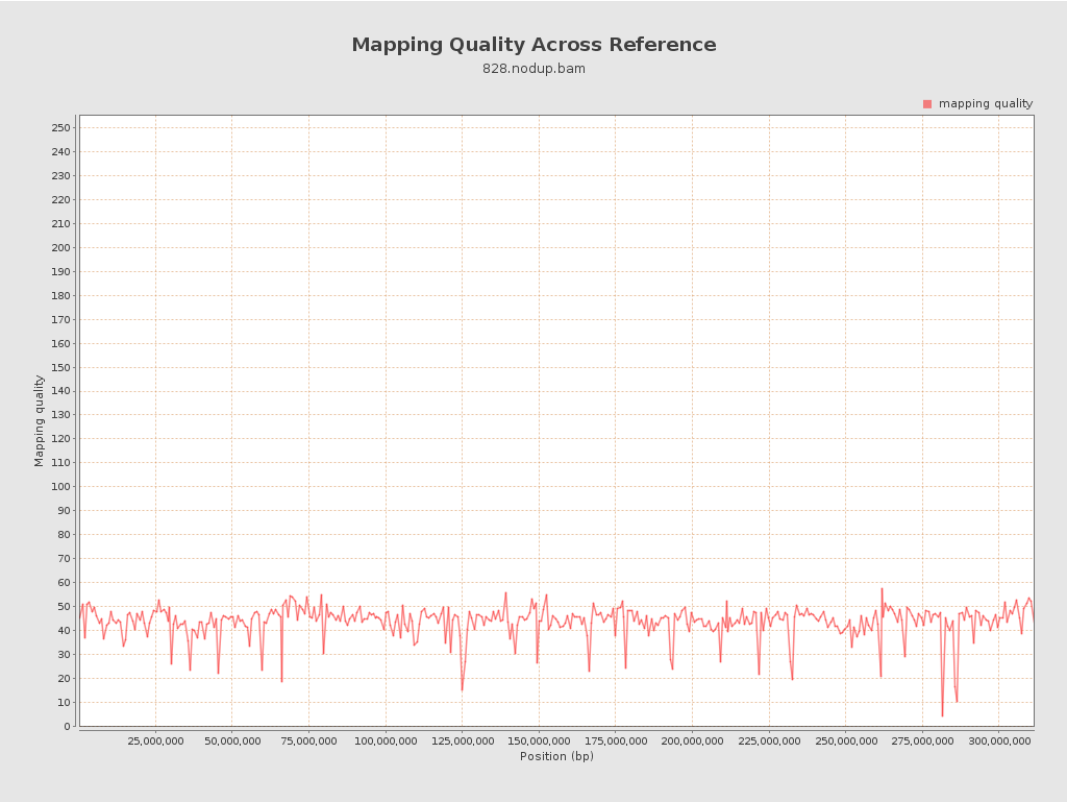
10. Results : Mapped Reads Clipping Profile



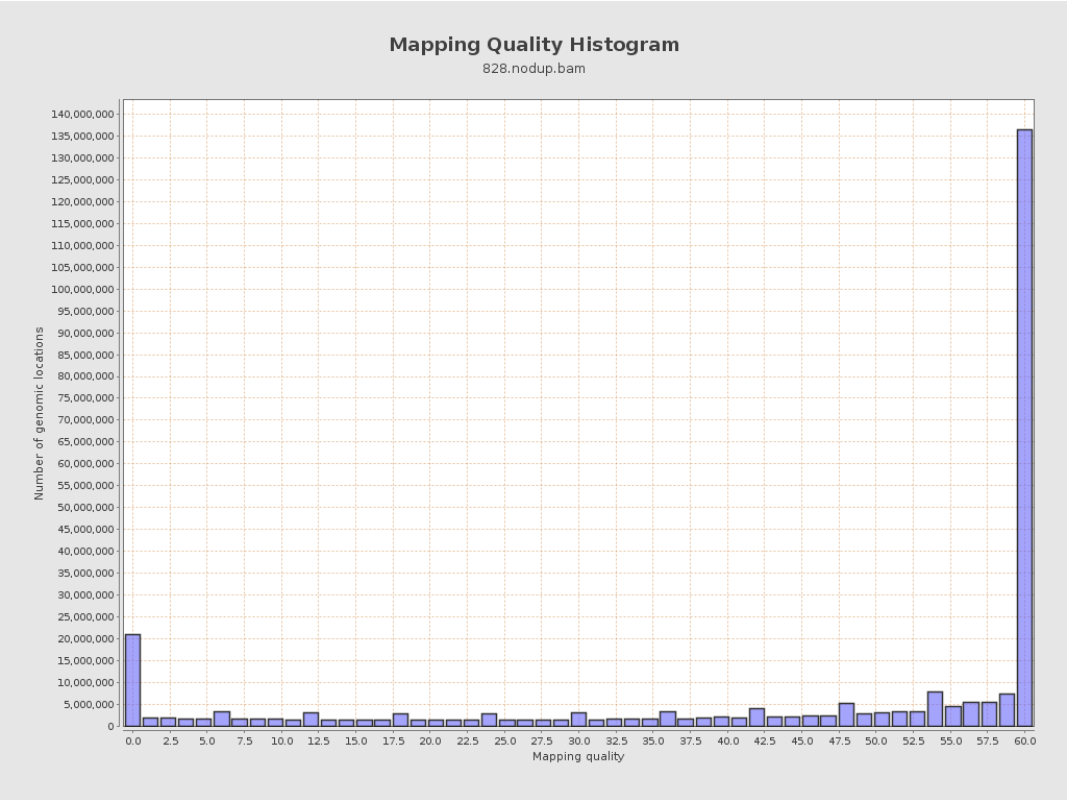
11. Results : Homopolymer Indels



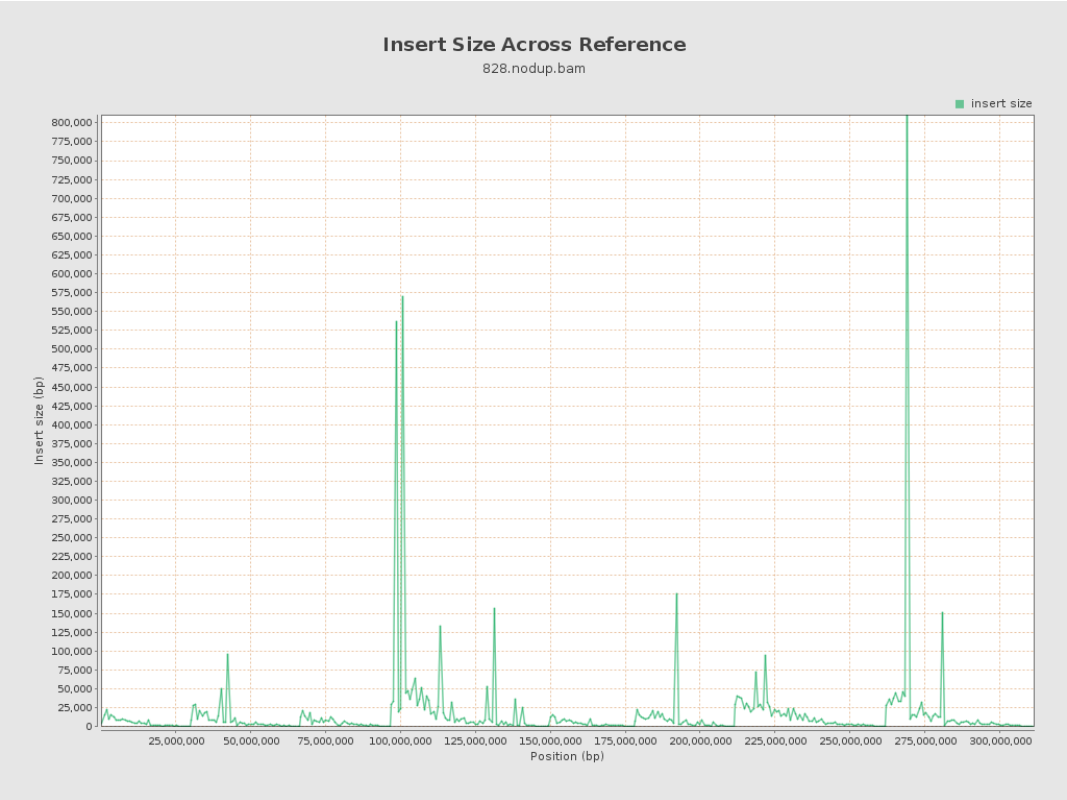
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram