Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:24:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1028
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1028 .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_566/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_566_S133_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_566/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_566_S133_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:24:52 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	44,532,804
Mapped reads	41,701,286 / 93.64%
Unmapped reads	2,831,518 / 6.36%
Mapped paired reads	41,701,286 / 93.64%
Mapped reads, first in pair	21,007,107 / 47.17%
Mapped reads, second in pair	20,694,179 / 46.47%
Mapped reads, both in pair	40,707,667 / 91.41%
Mapped reads, singletons	993,619 / 2.23%
Read min/max/mean length	30 / 151 / 148.36
Duplicated reads (flagged)	5,788,308 / 13%
Clipped reads	10,037,821 / 22.54%

2.2. ACGT Content

Number/percentage of A's	1,780,113,159 / 30.85%
Number/percentage of C's	1,104,742,166 / 19.15%
Number/percentage of T's	1,782,861,662 / 30.9%
Number/percentage of G's	1,101,642,541 / 19.09%
Number/percentage of N's	37,153 / 0%
GC Percentage	38.24%

2.3. Coverage

Mean	18.5588
Standard Deviation	142.1303

2.4. Mapping Quality

Mean Mapping Quality	44.21

2.5. Insert size

Mean	211,850.89
Standard Deviation	2,191,560.03
P25/Median/P75	322 / 418 / 536

2.6. Mismatches and indels

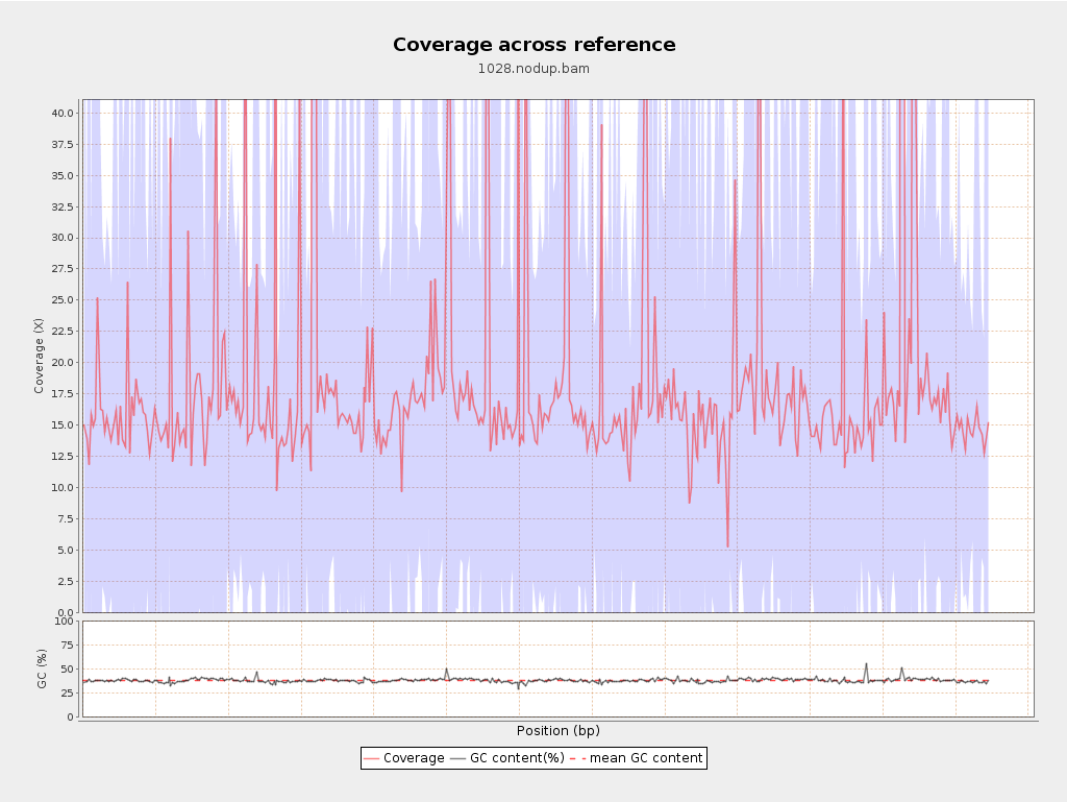
General error rate	2.76%
Mismatches	149,236,308
Insertions	3,789,003
Mapped reads with at least one insertion	8.18%
Deletions	3,822,737
Mapped reads with at least one deletion	8.16%
Homopolymer indels	55.72%

2.7. Chromosome stats

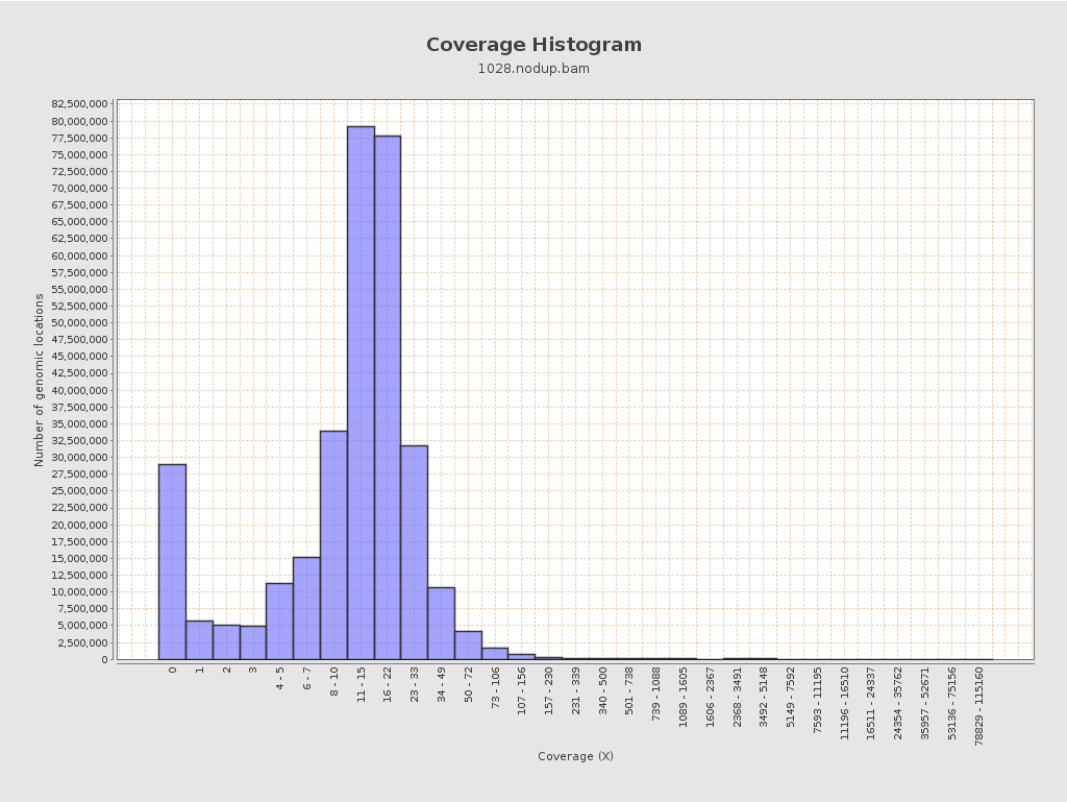
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	463497131	15.5932	44.9613

LT669789.1	36598175	679811692	18.575	155.167
LT669790.1	30422129	610256592	20.0596	153.3862
LT669791.1	52758100	965445873	18.2995	128.1106
LT669792.1	28376109	519225467	18.298	159.6702
LT669793.1	33388210	577252313	17.2891	103.895
LT669794.1	50579949	884495973	17.4871	123.577
LT669795.1	49795044	1083713901	21.7635	196.1263

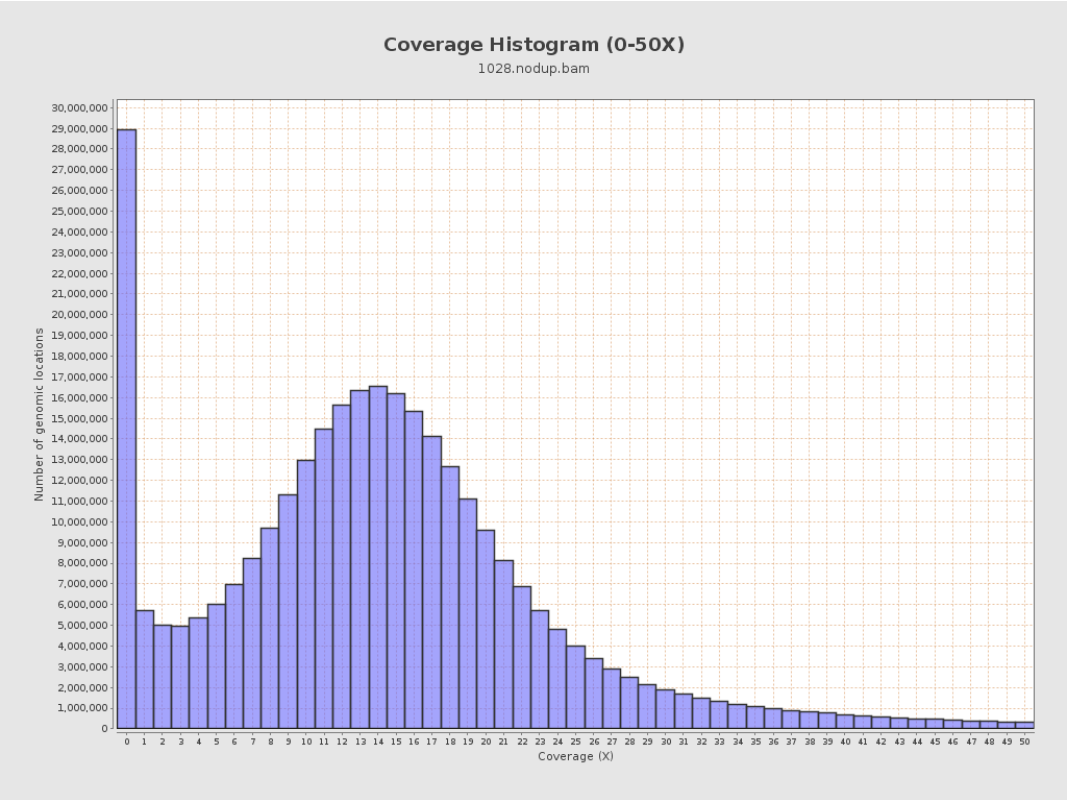
3. Results : Coverage across reference



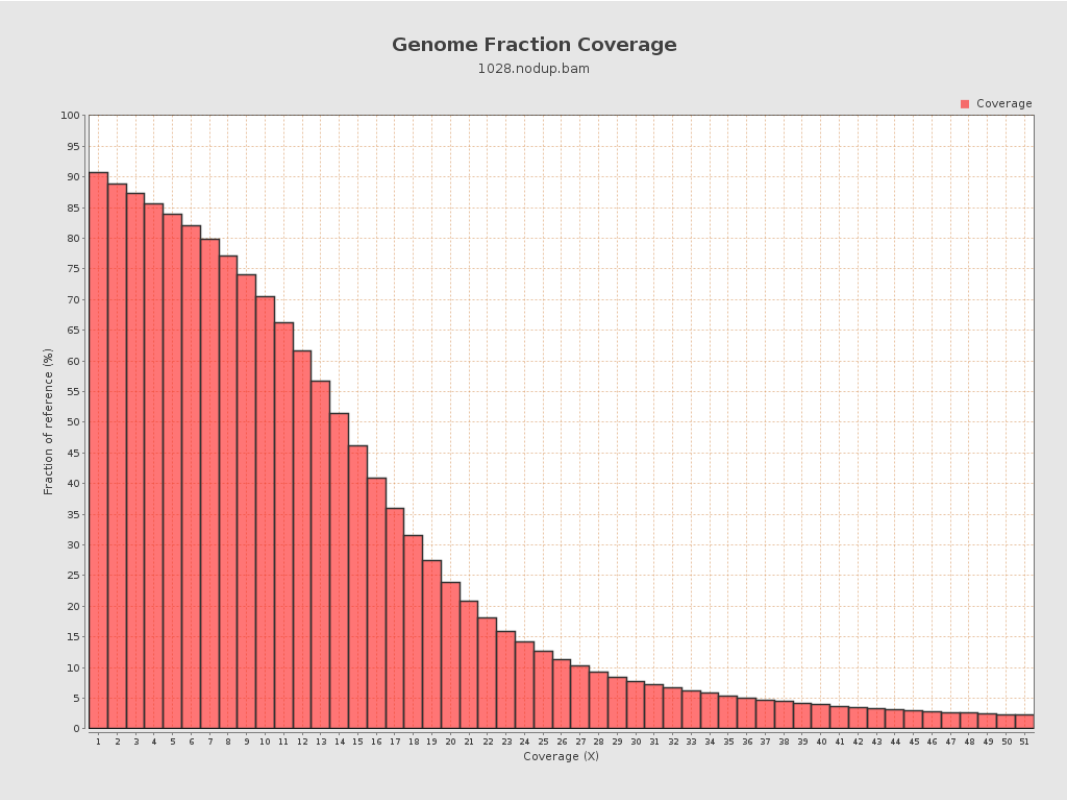
4. Results : Coverage Histogram



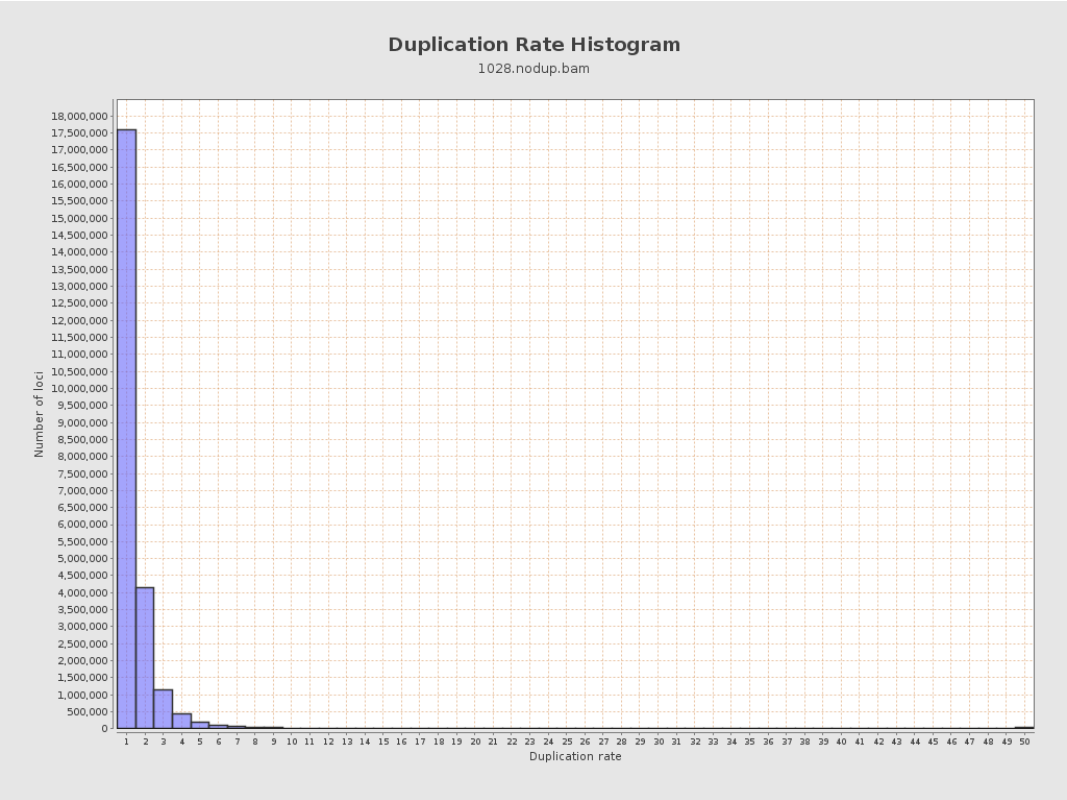
5. Results : Coverage Histogram (0-50X)



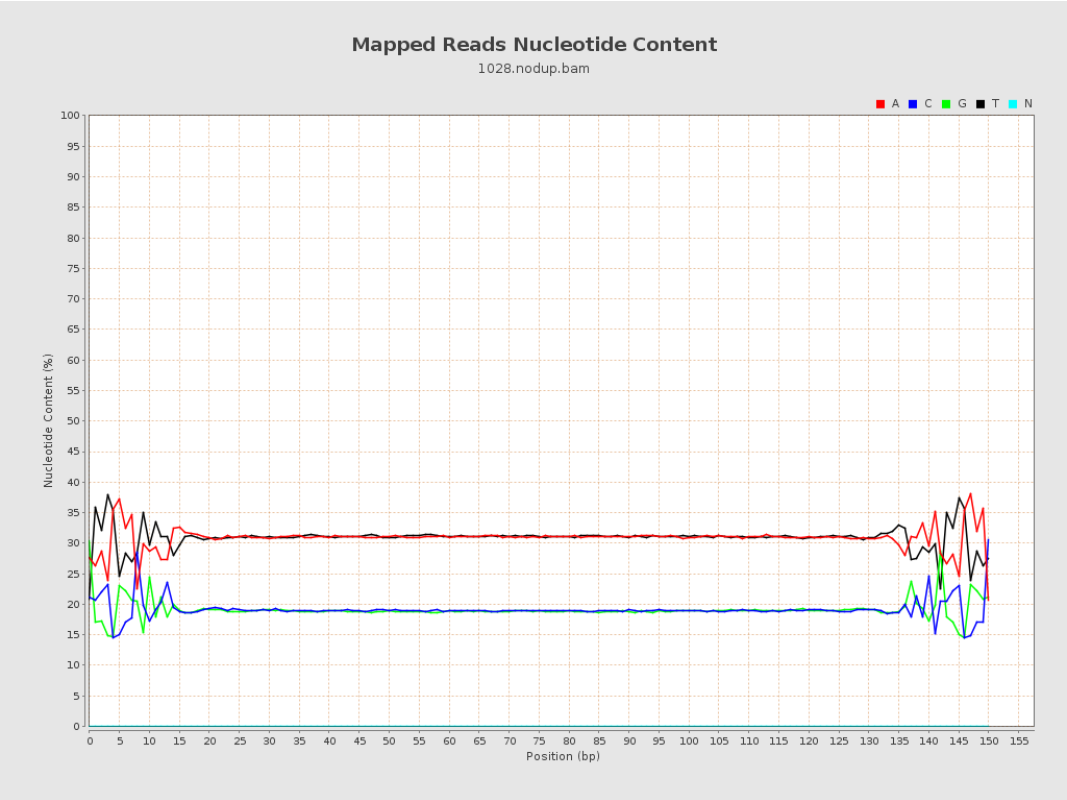
6. Results : Genome Fraction Coverage



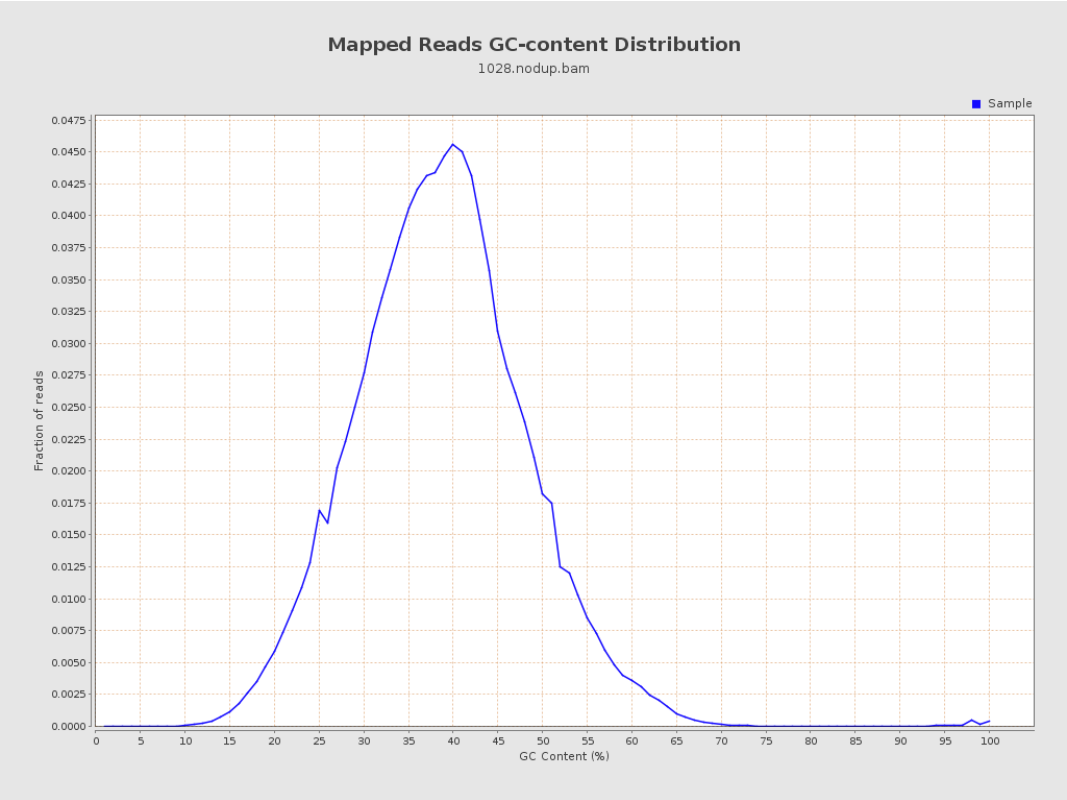
7. Results : Duplication Rate Histogram



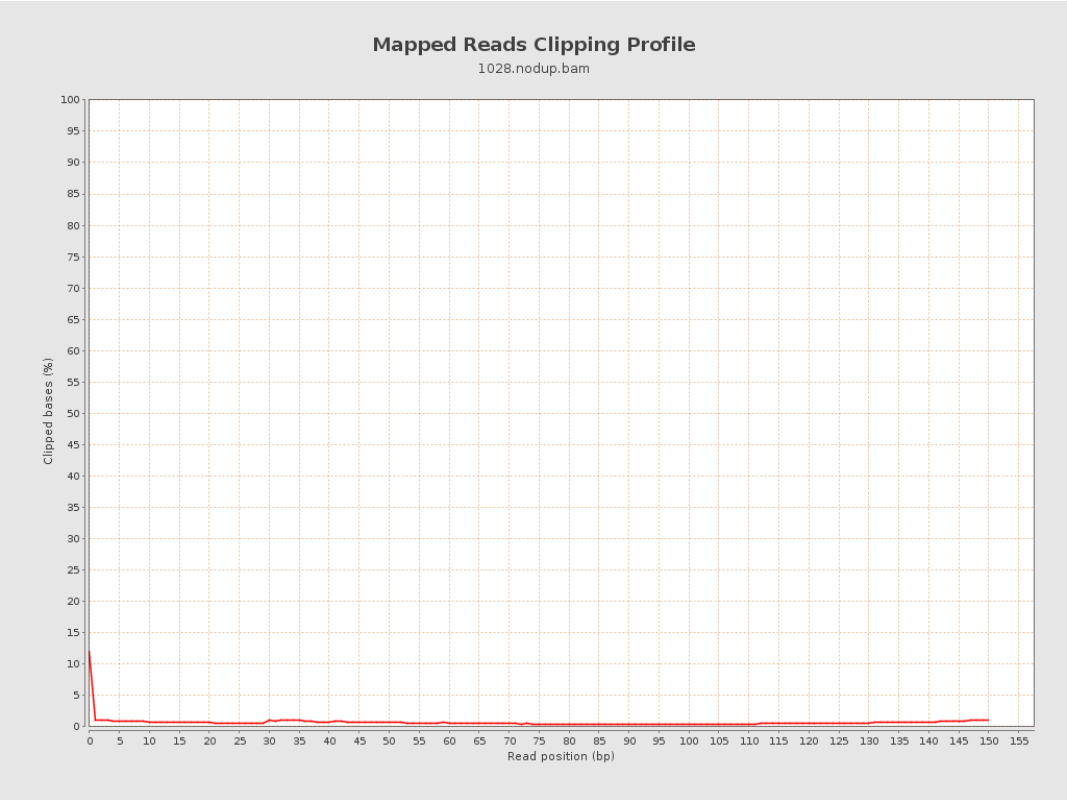
8. Results : Mapped Reads Nucleotide Content



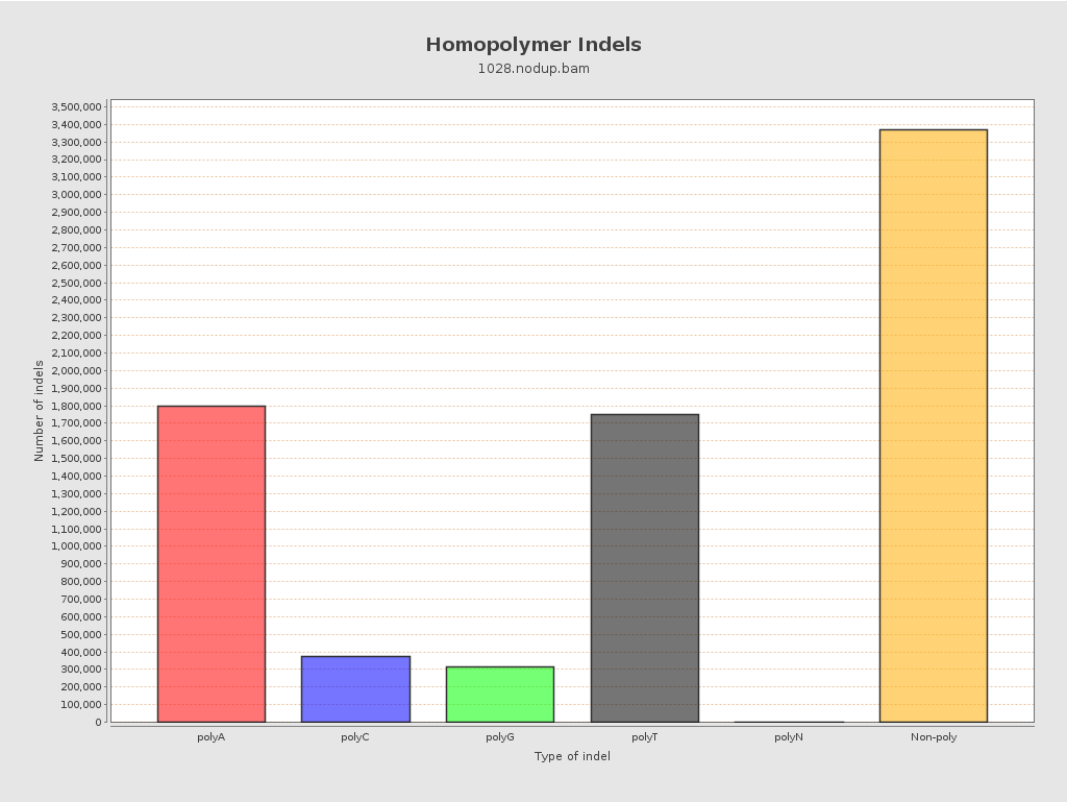
9. Results : Mapped Reads GC-content Distribution



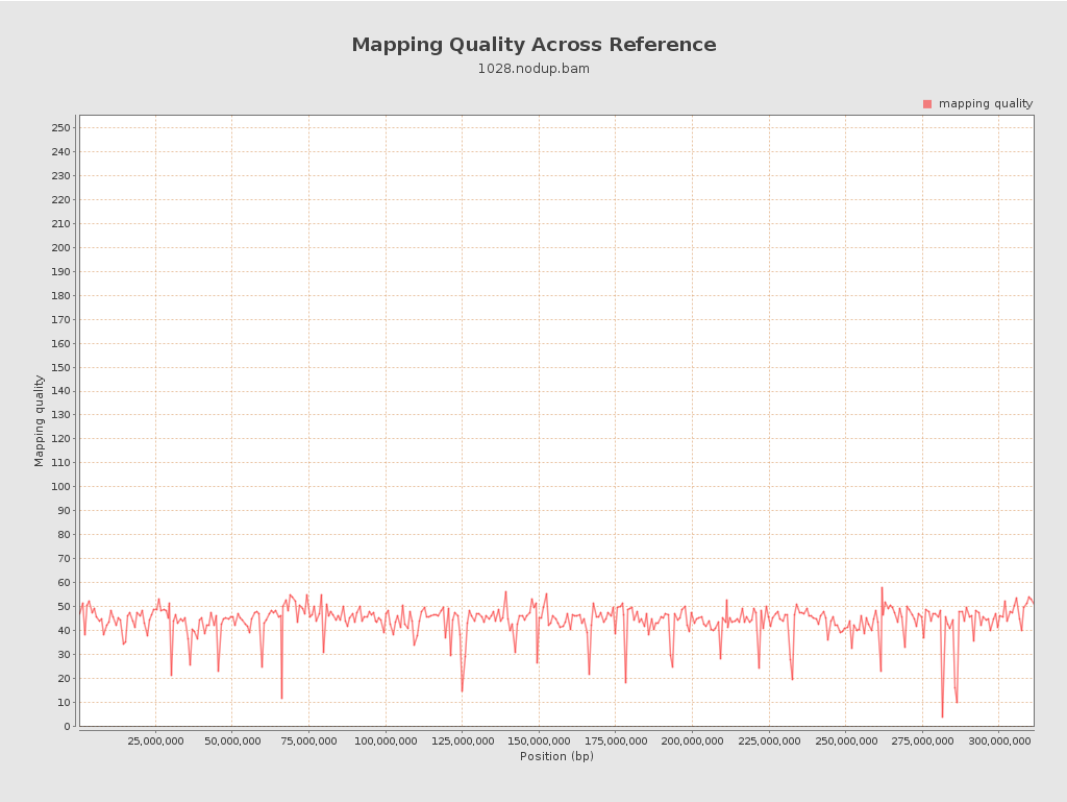
10. Results : Mapped Reads Clipping Profile



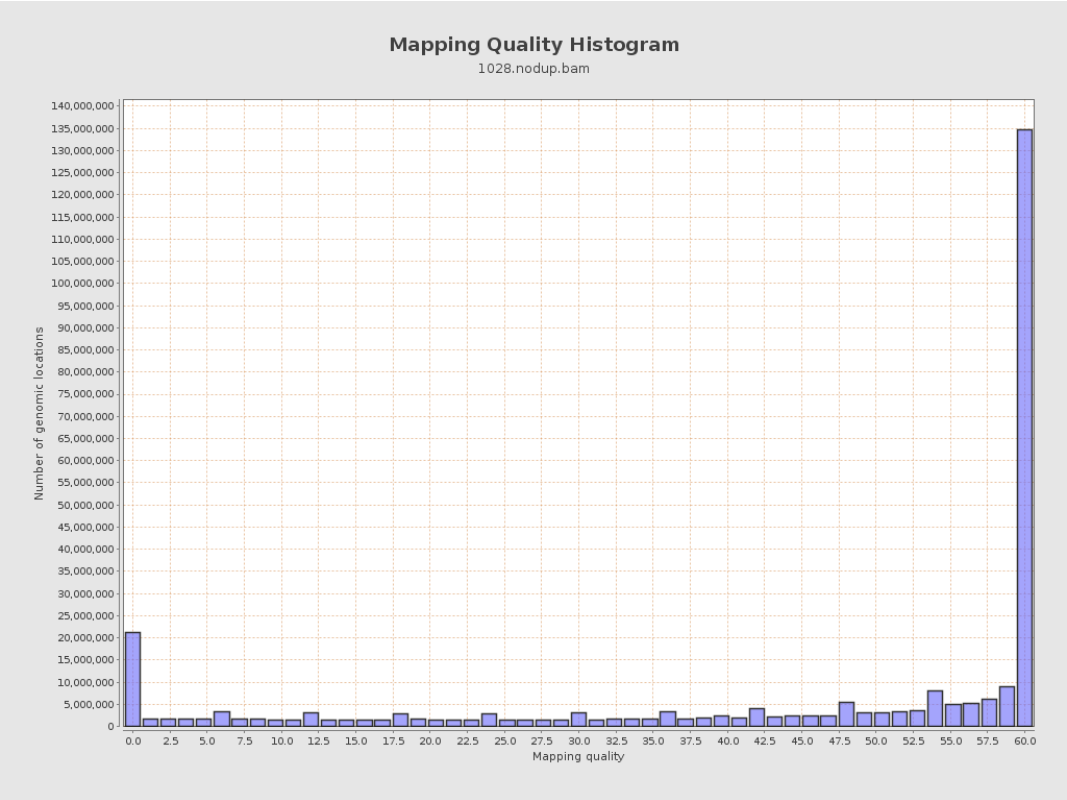
11. Results : Homopolymer Indels



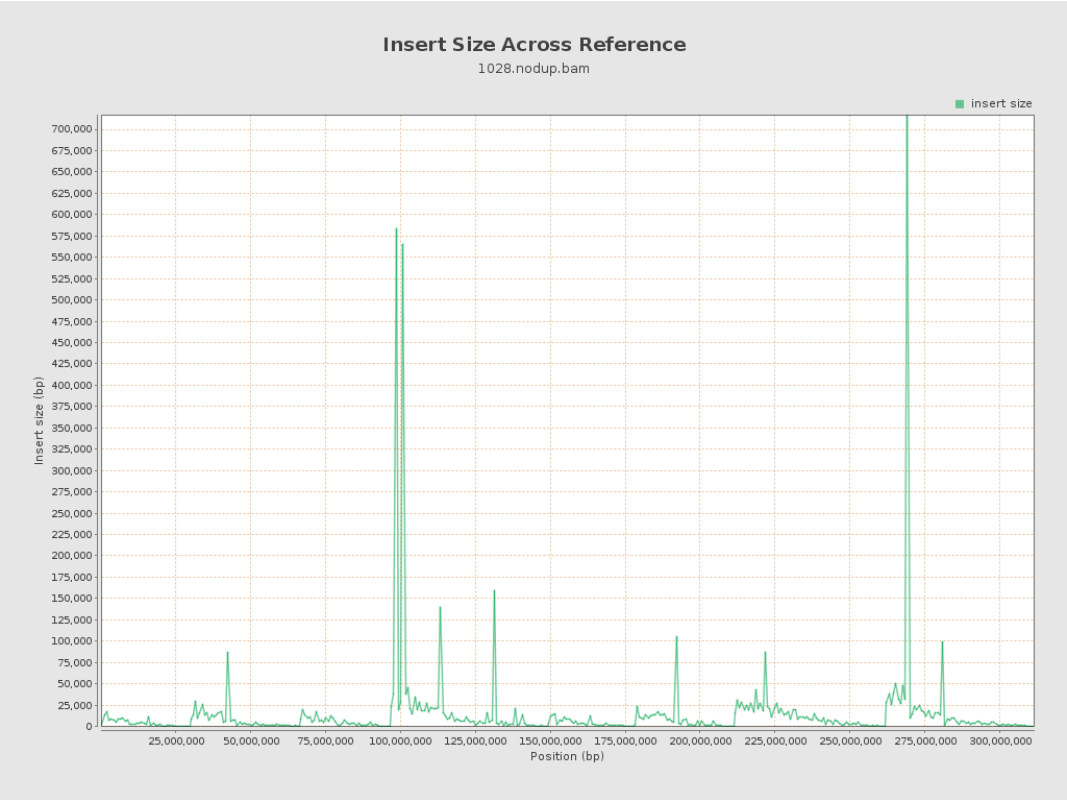
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram