Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1109
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1109 .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_558/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_558_S125_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_558/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_558_S125_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:35:19 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	78,142,207
Mapped reads	73,377,667 / 93.9%
Unmapped reads	4,764,540 / 6.1%
Mapped paired reads	73,377,667 / 93.9%
Mapped reads, first in pair	36,795,805 / 47.09%
Mapped reads, second in pair	36,581,862 / 46.81%
Mapped reads, both in pair	71,926,985 / 92.05%
Mapped reads, singletons	1,450,682 / 1.86%
Read min/max/mean length	30 / 151 / 148.04
Duplicated reads (flagged)	10,839,078 / 13.87%
Clipped reads	17,420,081 / 22.29%

2.2. ACGT Content

Number/percentage of A's	3,136,564,464 / 30.95%
Number/percentage of C's	1,931,238,697 / 19.06%
Number/percentage of T's	3,138,653,289 / 30.97%
Number/percentage of G's	1,928,452,193 / 19.03%
Number/percentage of N's	73,814 / 0%
GC Percentage	38.08%

2.3. Coverage

Mean	32.607
Standard Deviation	255.0749

2.4. Mapping Quality

Mean Mapping Quality	44

2.5. Insert size

Mean	224,129.69
Standard Deviation	2,243,487.82
P25/Median/P75	315 / 416 / 540

2.6. Mismatches and indels

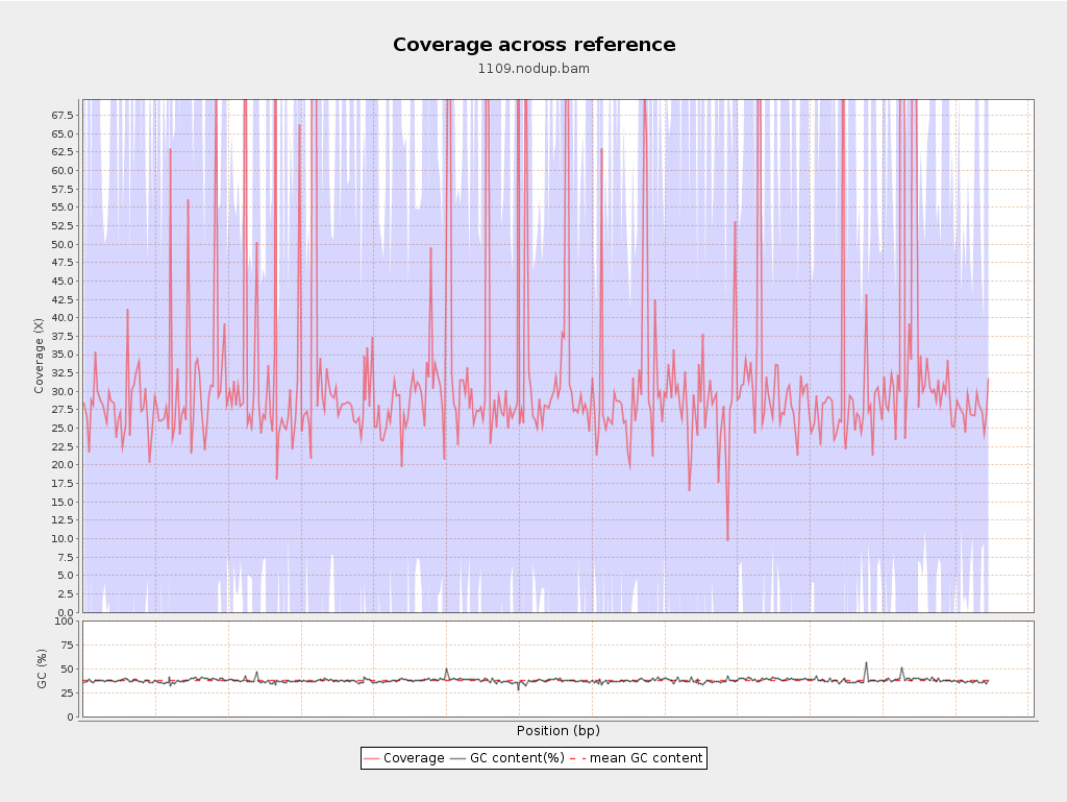
General error rate	2.51%
Mismatches	235,581,203
Insertions	6,922,741
Mapped reads with at least one insertion	8.48%
Deletions	7,105,954
Mapped reads with at least one deletion	8.59%
Homopolymer indels	55.86%

2.7. Chromosome stats

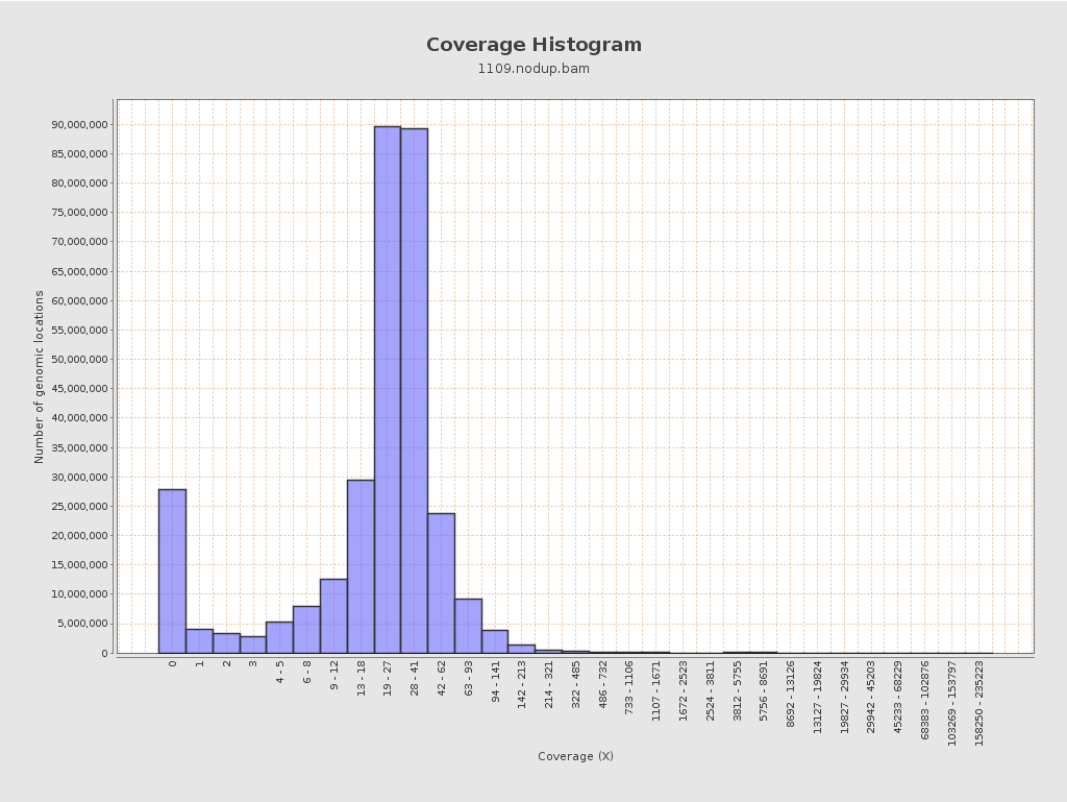
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	828600234	27.8761	93.4726

LT669789.1	36598175	1207071900	32.9818	264.1199
LT669790.1	30422129	1060466355	34.8584	246.7981
LT669791.1	52758100	1656817241	31.404	234.1509
LT669792.1	28376109	930532990	32.7928	265.6164
LT669793.1	33388210	1012244227	30.3174	134.6175
LT669794.1	50579949	1562151520	30.8848	240.1132
LT669795.1	49795044	1903843533	38.2336	380.0454

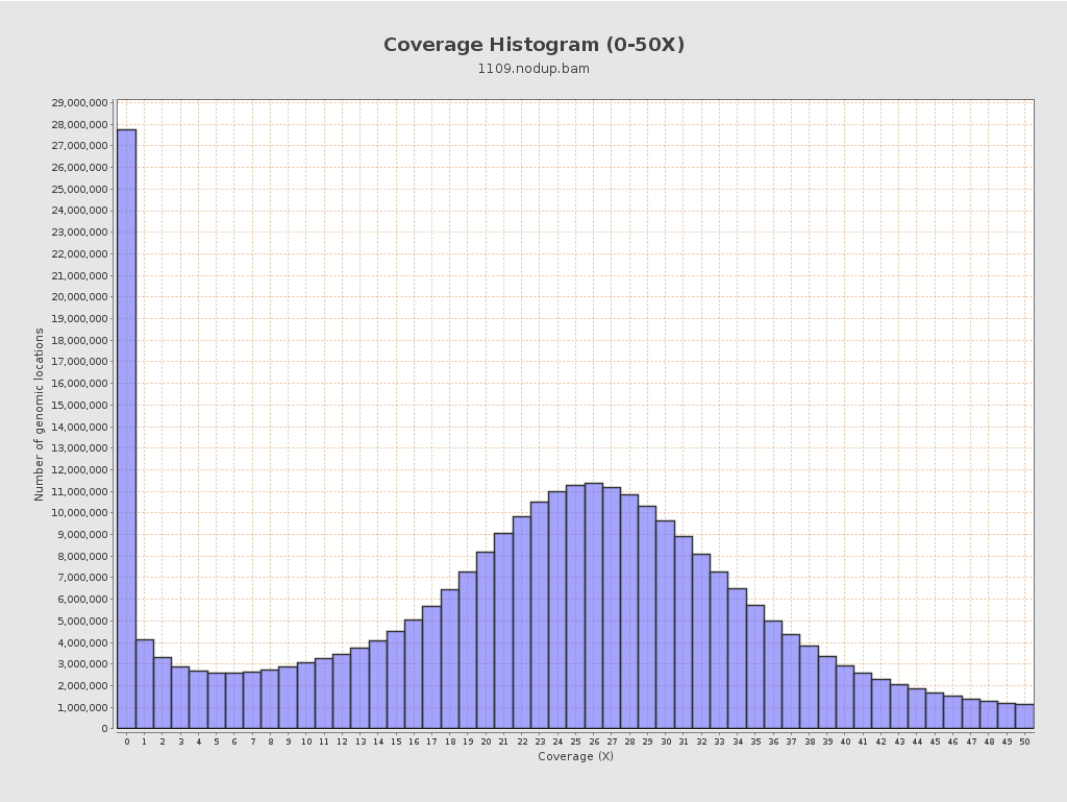
3. Results : Coverage across reference



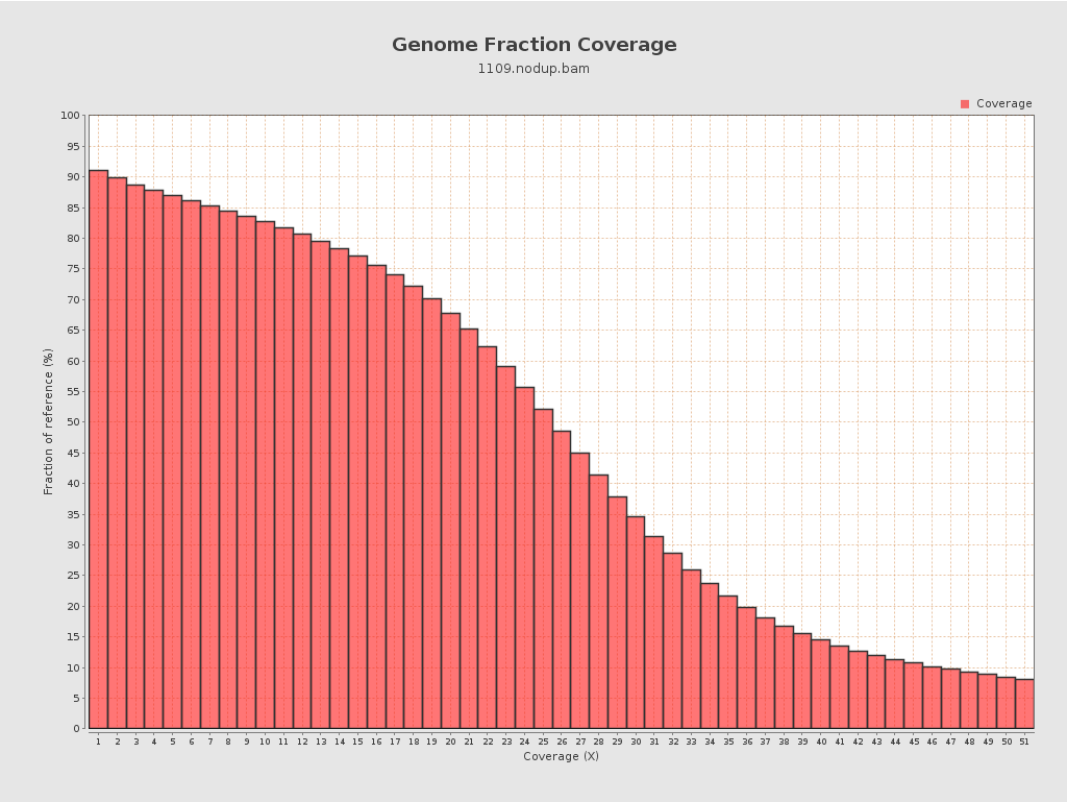
4. Results : Coverage Histogram



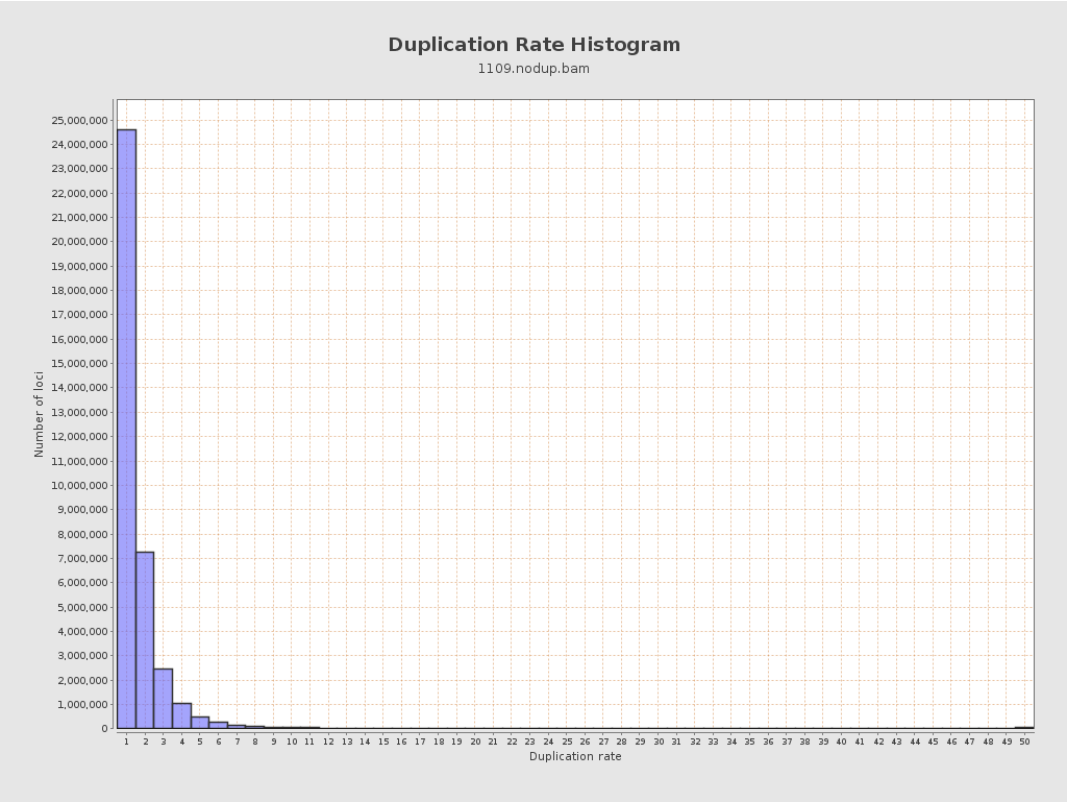
5. Results : Coverage Histogram (0-50X)



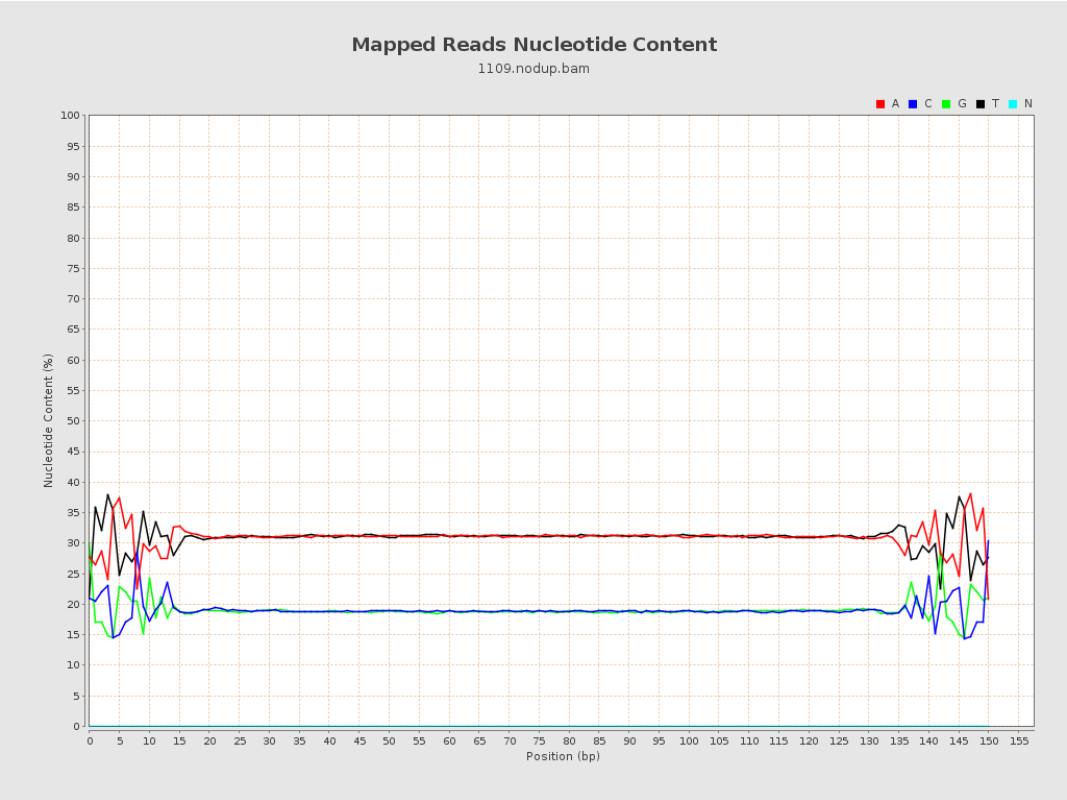
6. Results : Genome Fraction Coverage



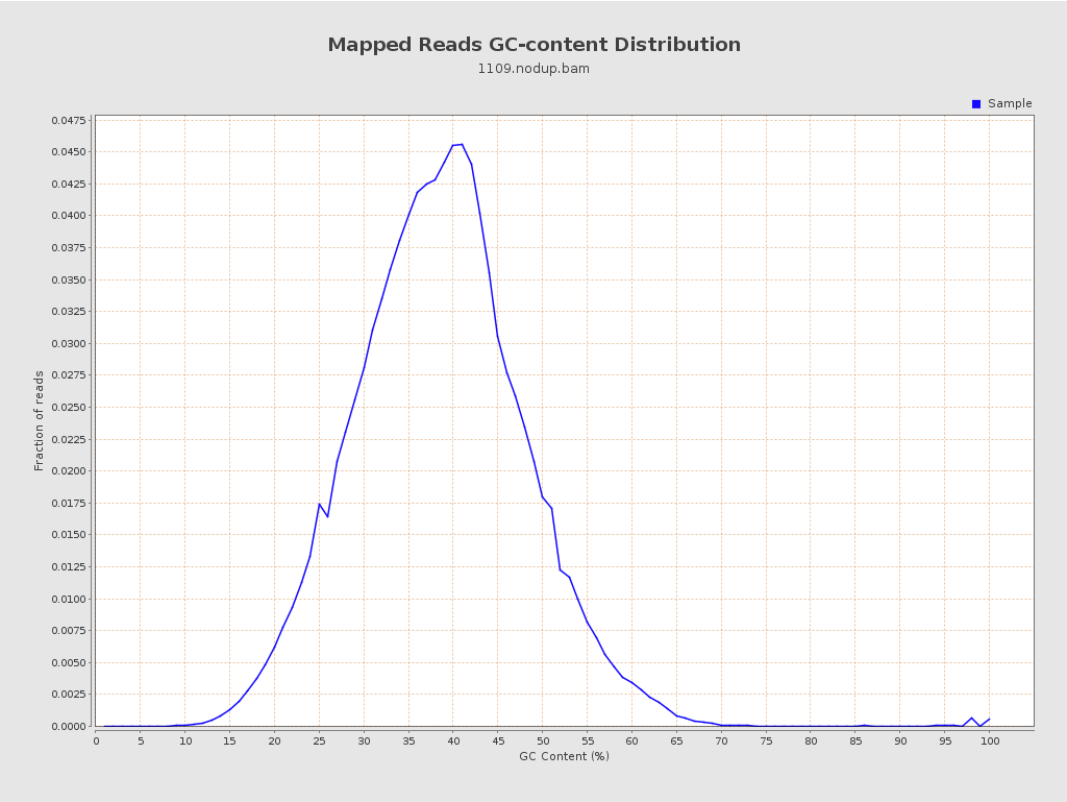
7. Results : Duplication Rate Histogram



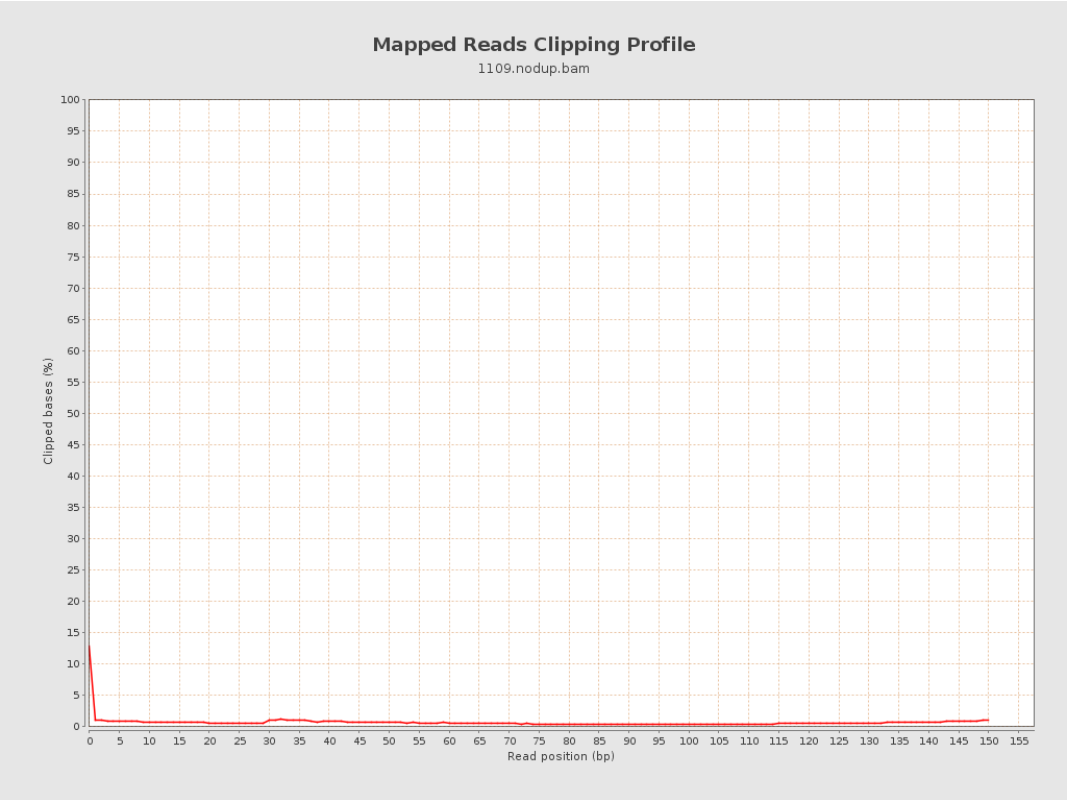
8. Results : Mapped Reads Nucleotide Content



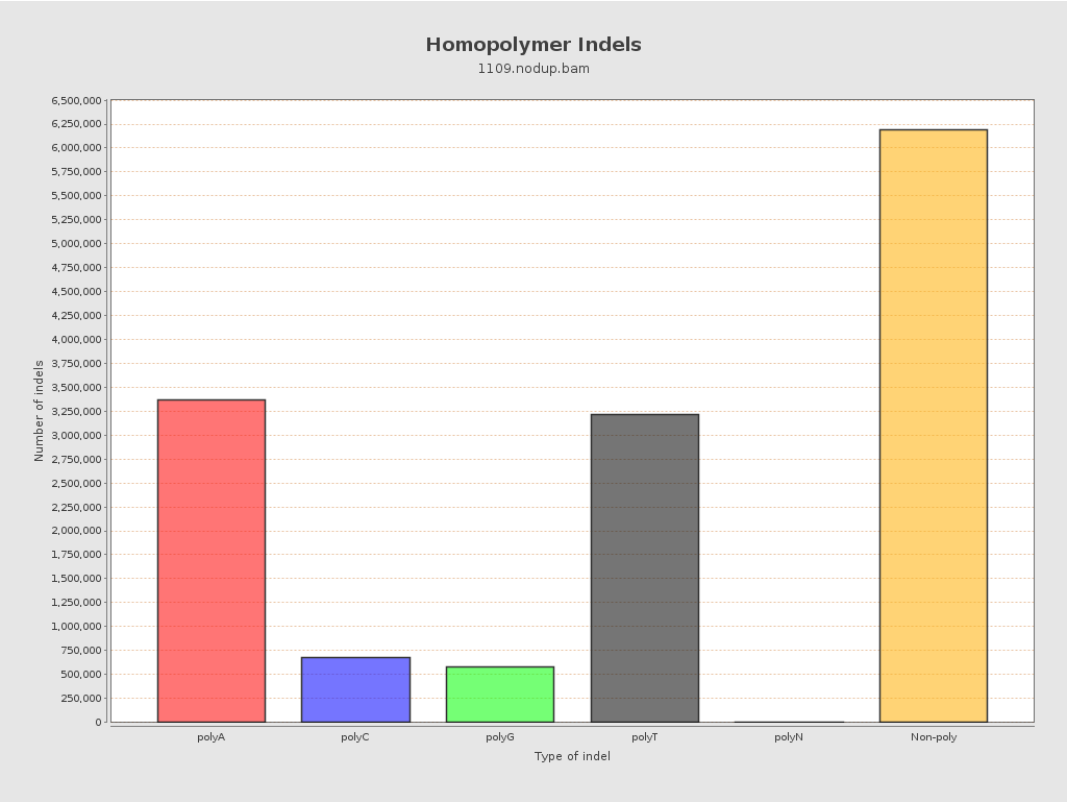
9. Results : Mapped Reads GC-content Distribution



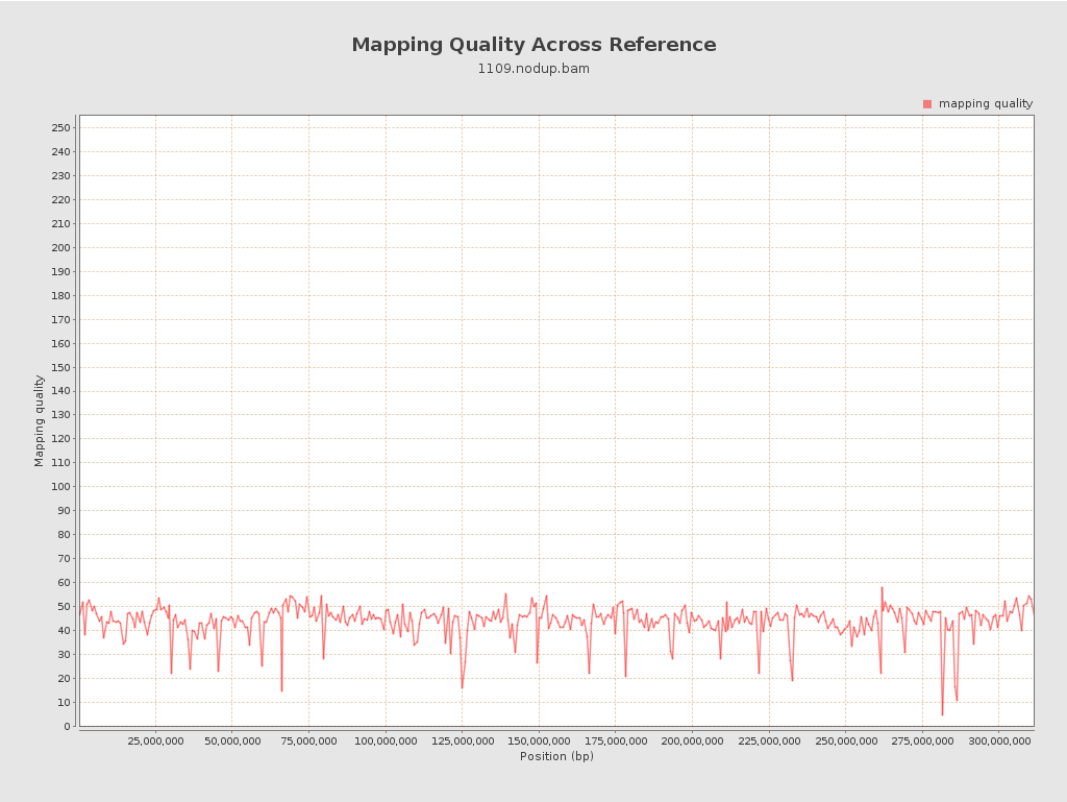
10. Results : Mapped Reads Clipping Profile



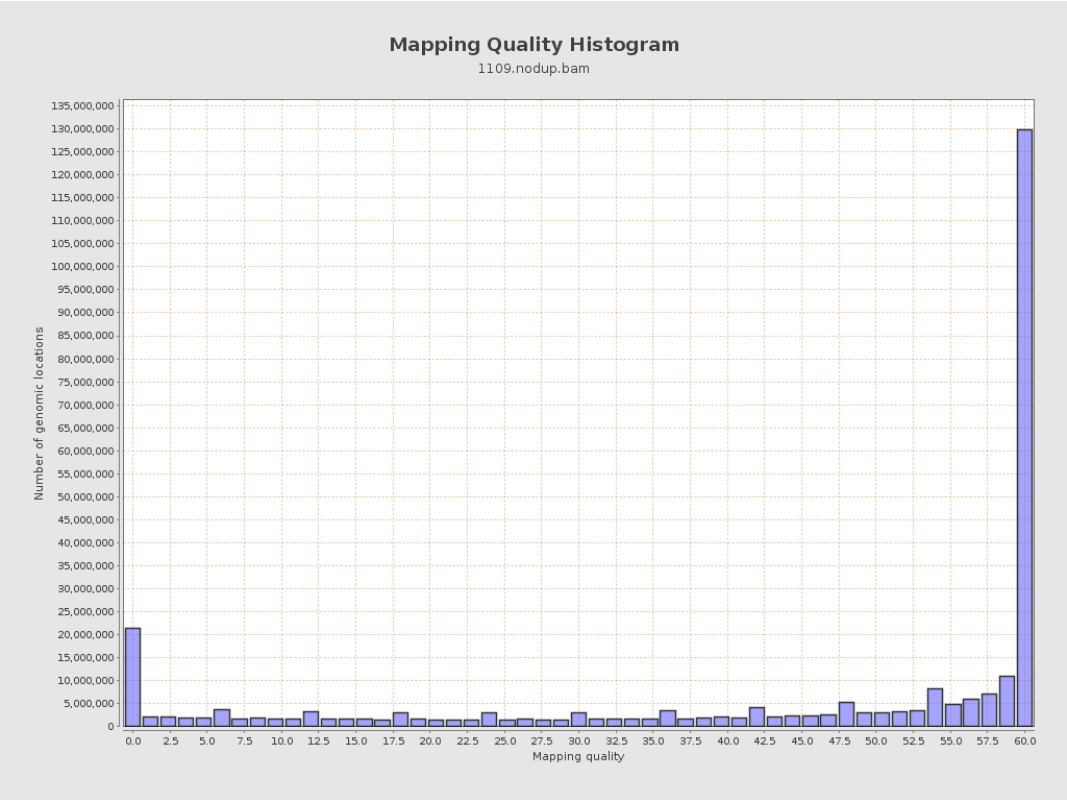
11. Results : Homopolymer Indels



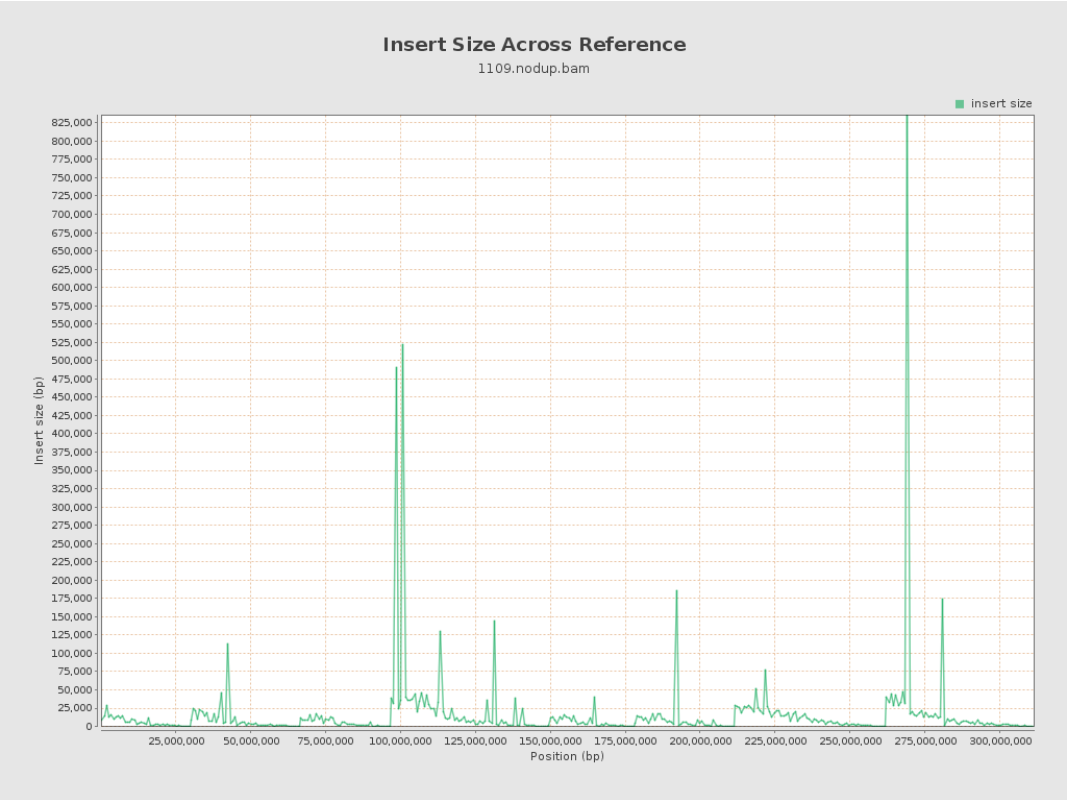
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram