Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:42:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1266
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1266 .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_460/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_460_S435_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_460/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_460_S435_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:42:27 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	96,641,037
Mapped reads	91,656,462 / 94.84%
Unmapped reads	4,984,575 / 5.16%
Mapped paired reads	91,656,462 / 94.84%
Mapped reads, first in pair	45,855,803 / 47.45%
Mapped reads, second in pair	45,800,659 / 47.39%
Mapped reads, both in pair	90,032,603 / 93.16%
Mapped reads, singletons	1,623,859 / 1.68%
Read min/max/mean length	30 / 151 / 148.13
Duplicated reads (flagged)	13,501,103 / 13.97%
Clipped reads	19,714,023 / 20.4%

2.2. ACGT Content

Number/percentage of A's	3,955,939,483 / 30.96%
Number/percentage of C's	2,431,958,782 / 19.03%
Number/percentage of T's	3,962,034,327 / 31.01%
Number/percentage of G's	2,427,747,535 / 19%
Number/percentage of N's	41,652 / 0%
GC Percentage	38.03%

2.3. Coverage

Mean	41.1098
Standard Deviation	279.9399

2.4. Mapping Quality

Mean Mapping Quality	44.2

2.5. Insert size

Mean	233,721.42
Standard Deviation	2,296,571.57
P25/Median/P75	346 / 454 / 595

2.6. Mismatches and indels

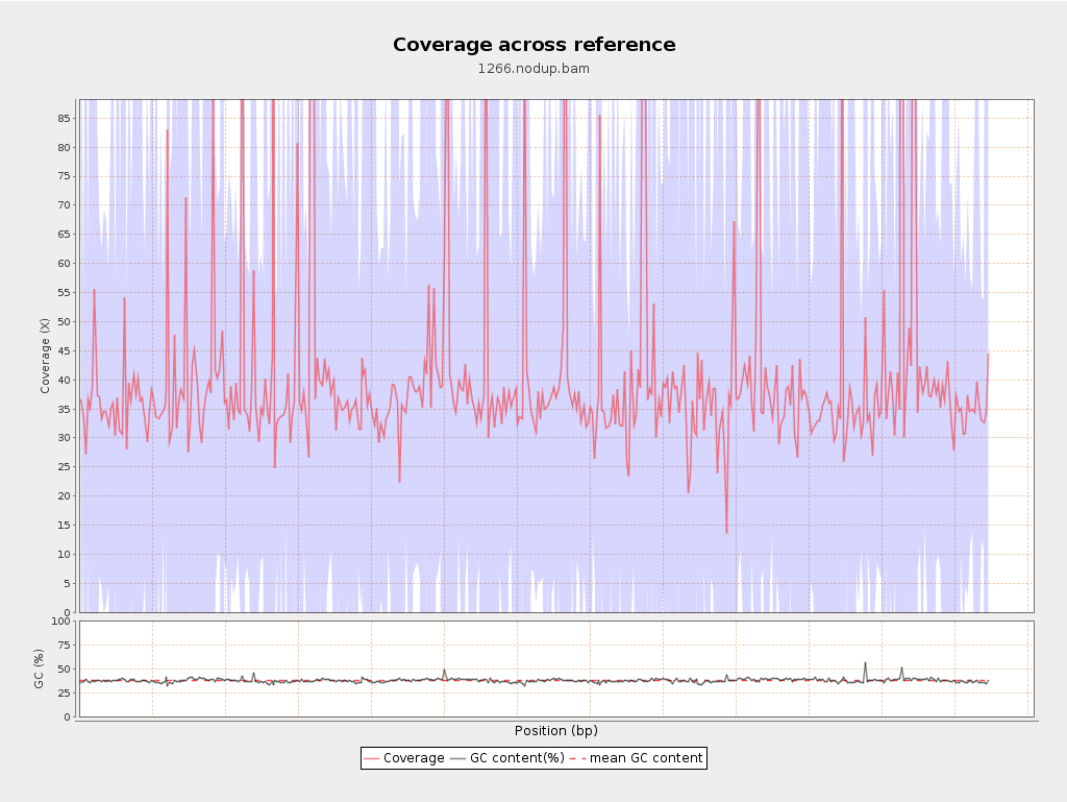
General error rate	2.3%
Mismatches	270,735,324
Insertions	8,505,257
Mapped reads with at least one insertion	8.35%
Deletions	8,828,204
Mapped reads with at least one deletion	8.54%
Homopolymer indels	56.33%

2.7. Chromosome stats

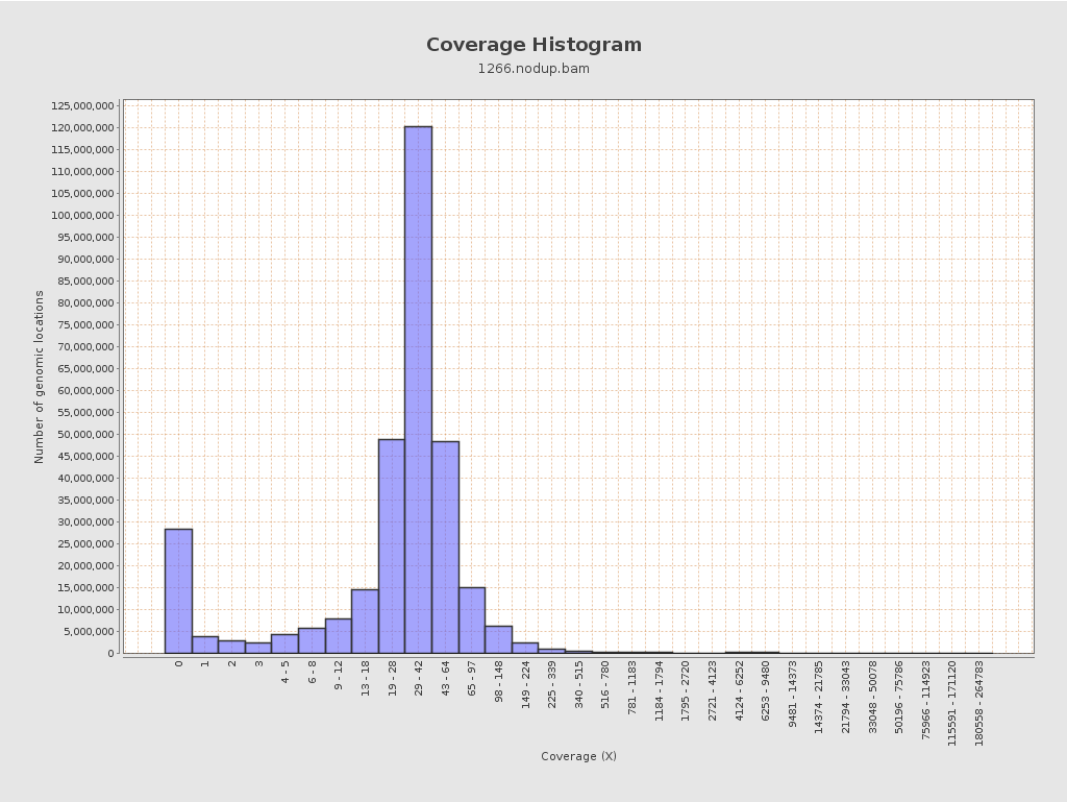
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	1068714454	35.9542	85.2717

LT669789.1	36598175	1538641698	42.0415	312.2785
LT669790.1	30422129	1342103942	44.116	265.4521
LT669791.1	52758100	2103257134	39.8661	227.7851
LT669792.1	28376109	1150852695	40.5571	287.584
LT669793.1	33388210	1327731263	39.7665	299.7608
LT669794.1	50579949	1955733801	38.6662	247.911
LT669795.1	49795044	2324511675	46.6816	382.8152

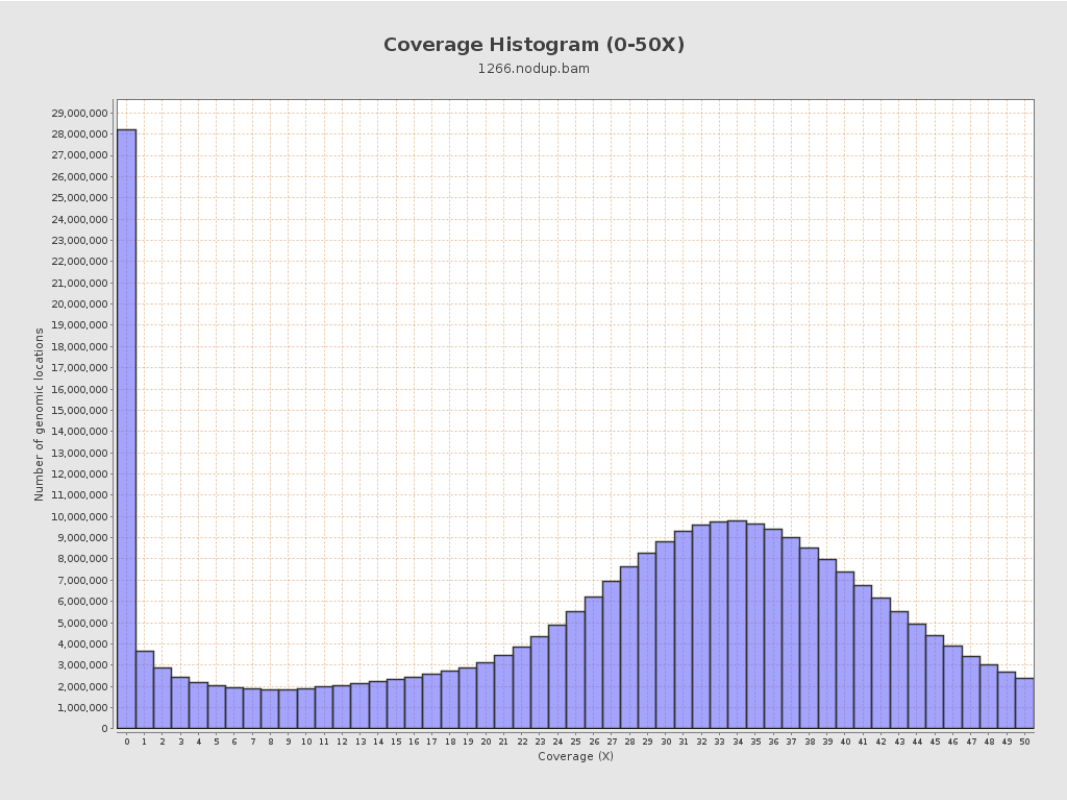
3. Results : Coverage across reference



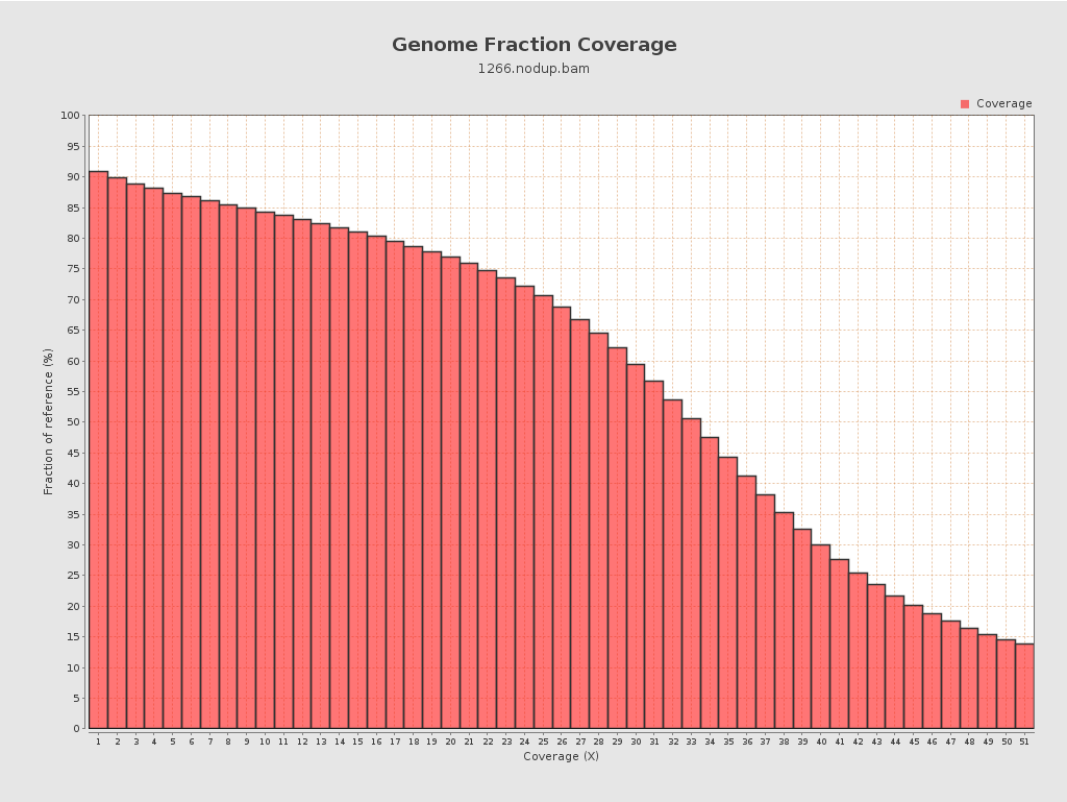
4. Results : Coverage Histogram



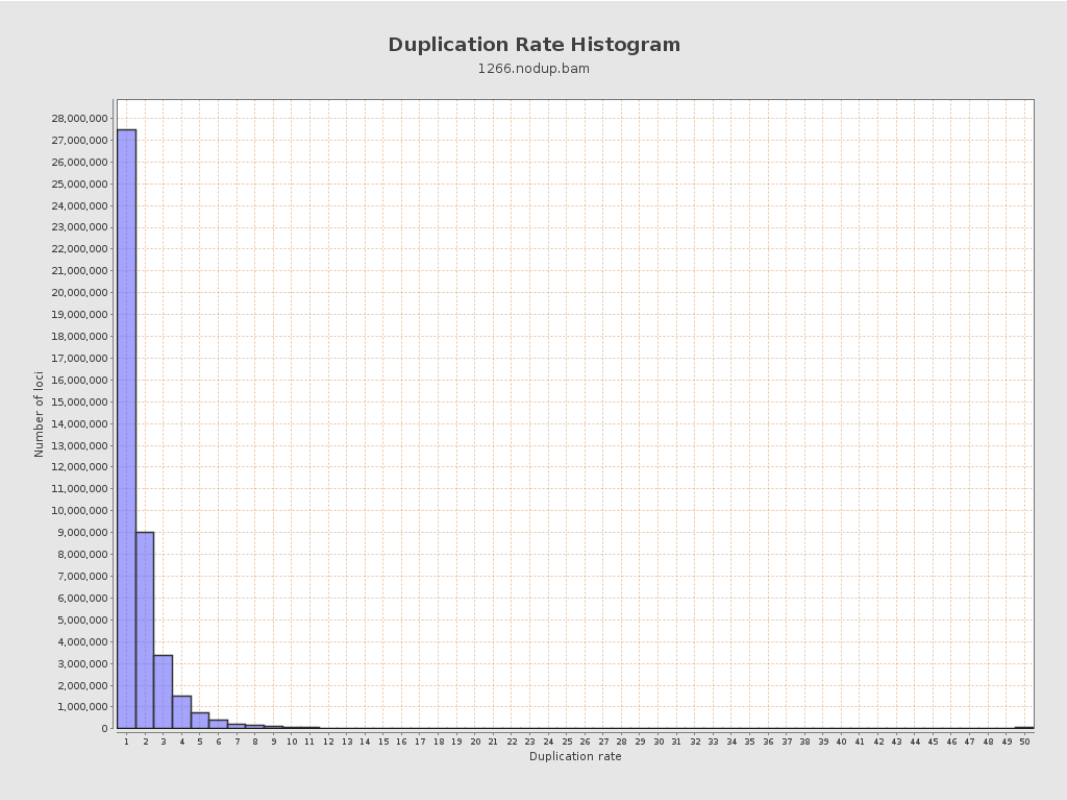
5. Results : Coverage Histogram (0-50X)



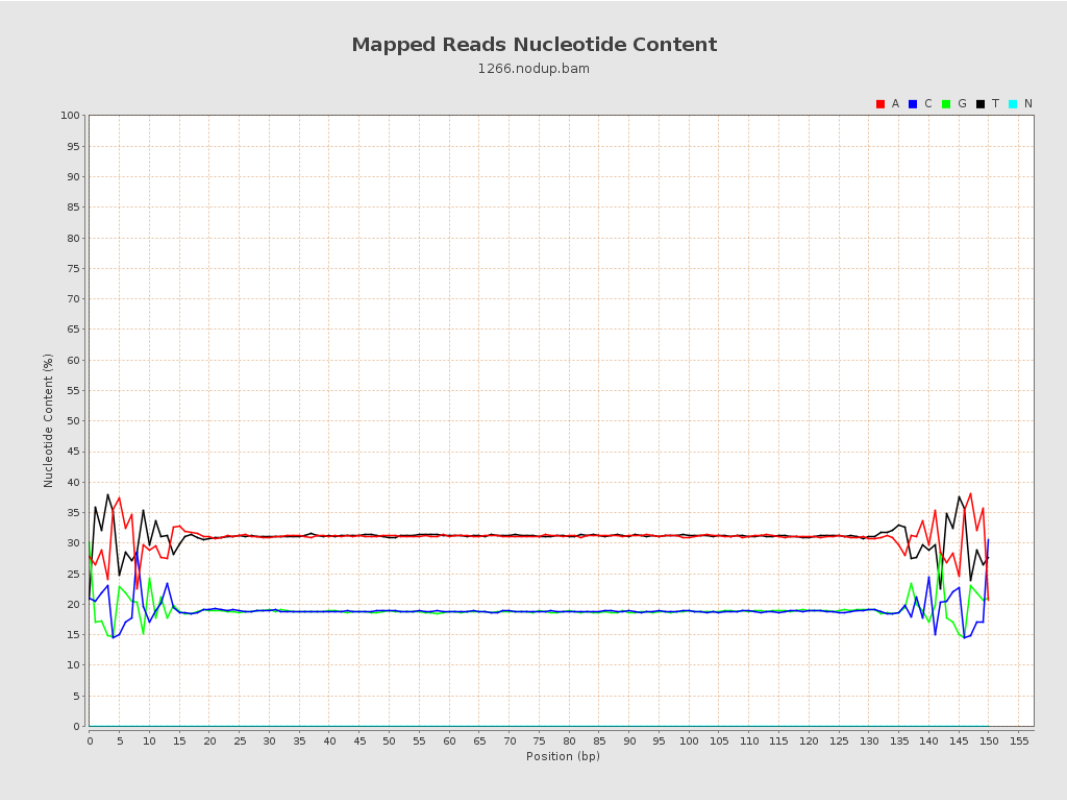
6. Results : Genome Fraction Coverage



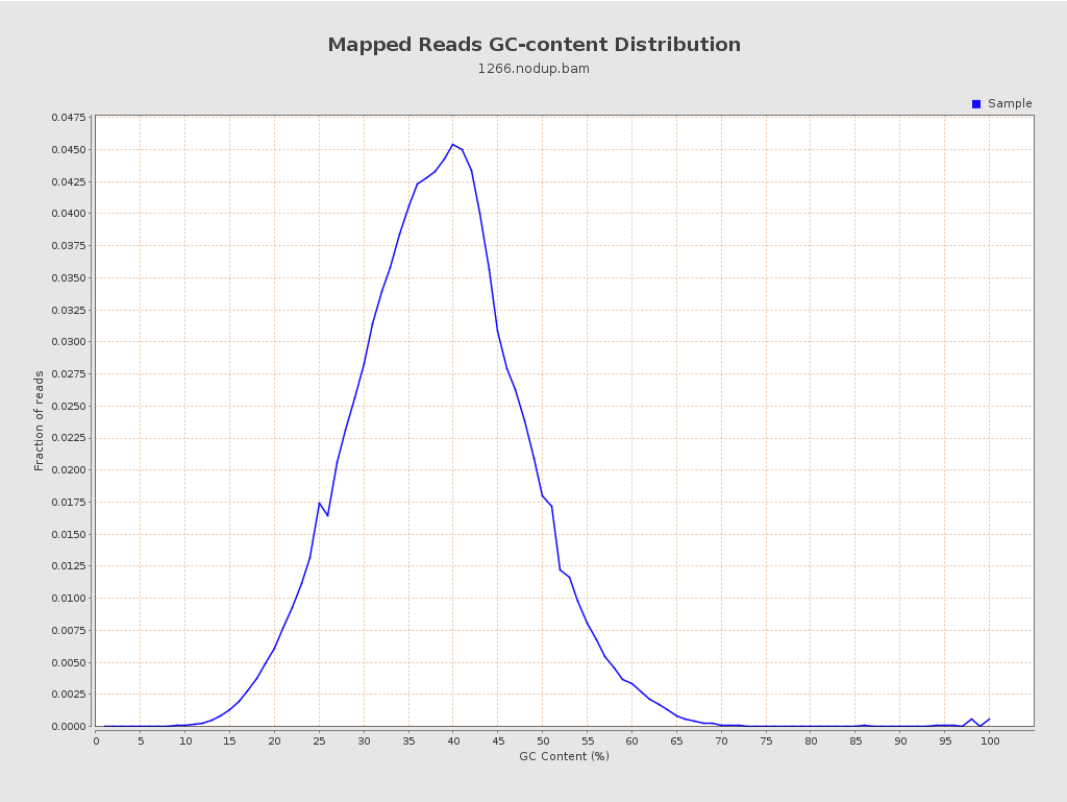
7. Results : Duplication Rate Histogram



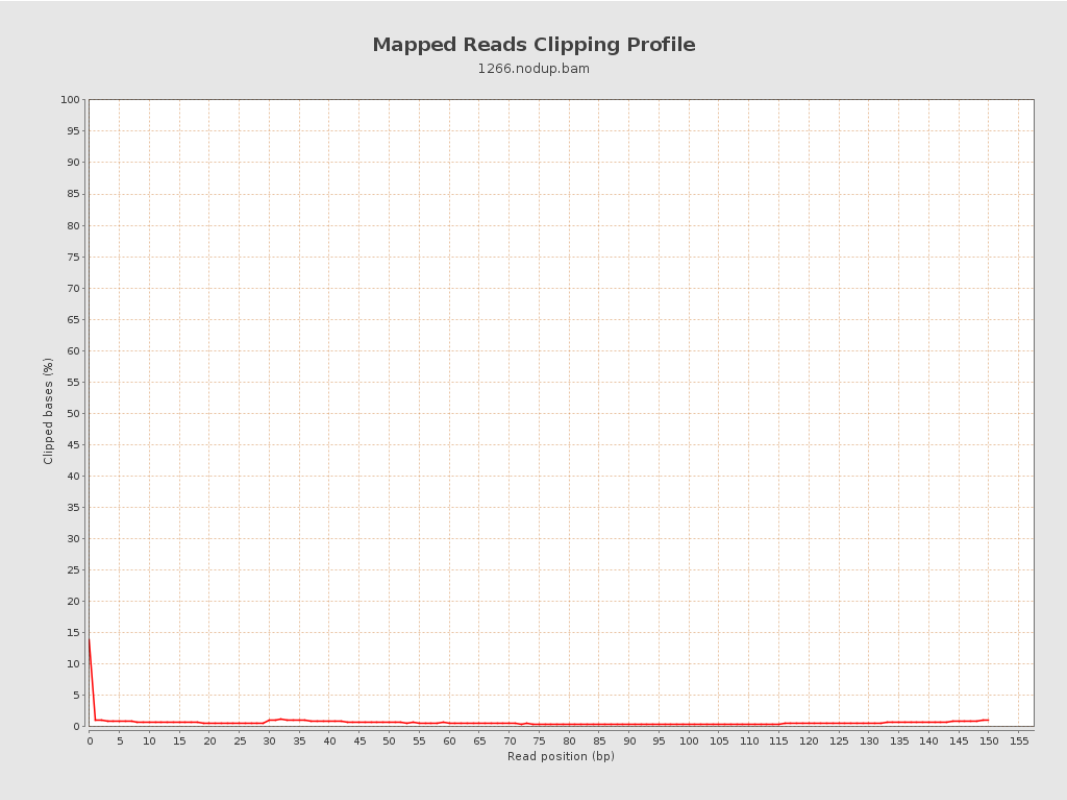
8. Results : Mapped Reads Nucleotide Content



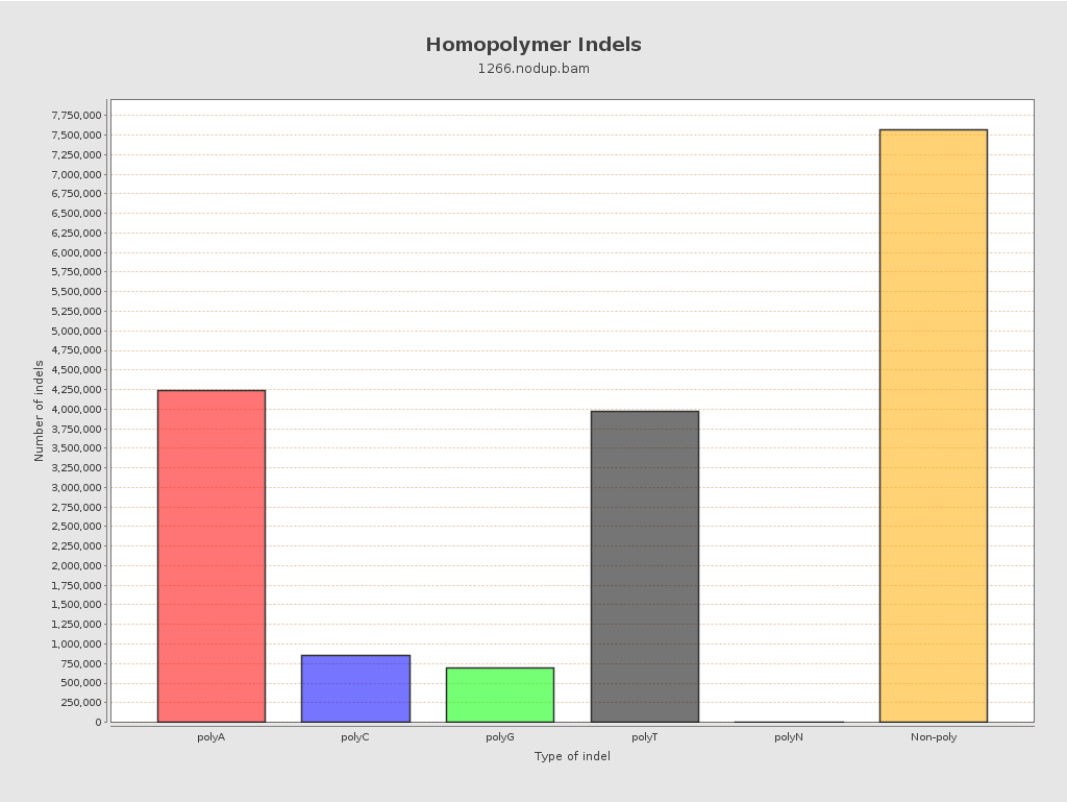
9. Results : Mapped Reads GC-content Distribution



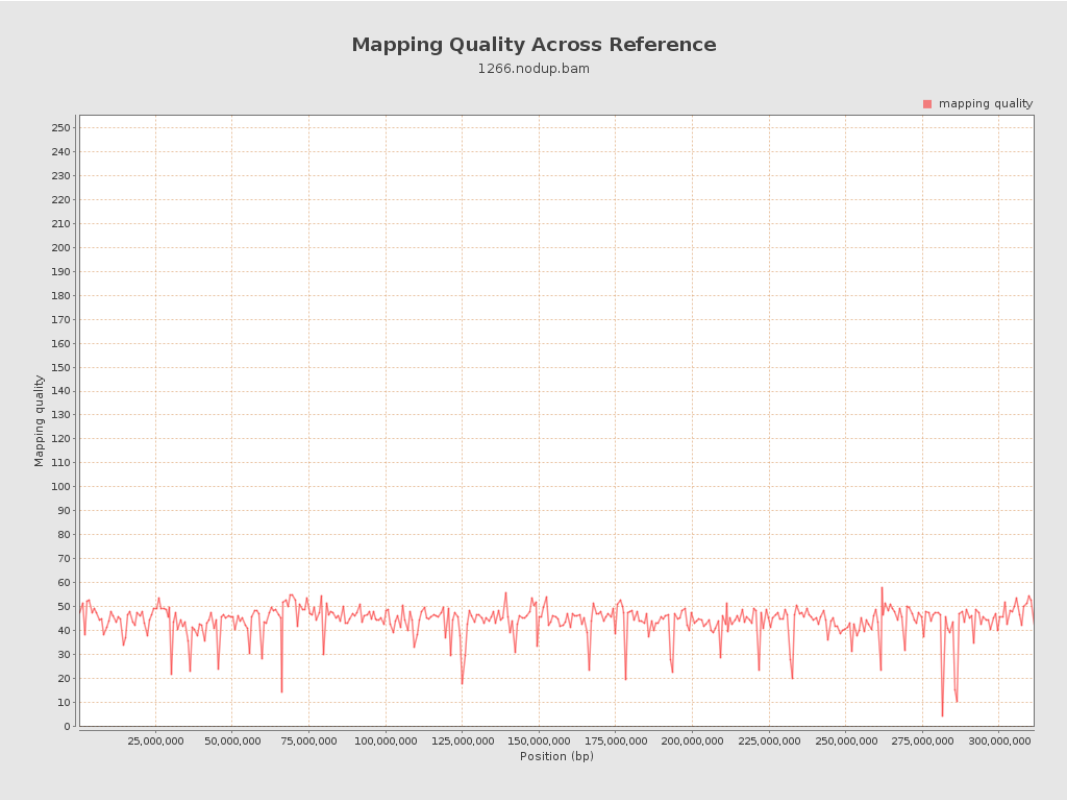
10. Results : Mapped Reads Clipping Profile



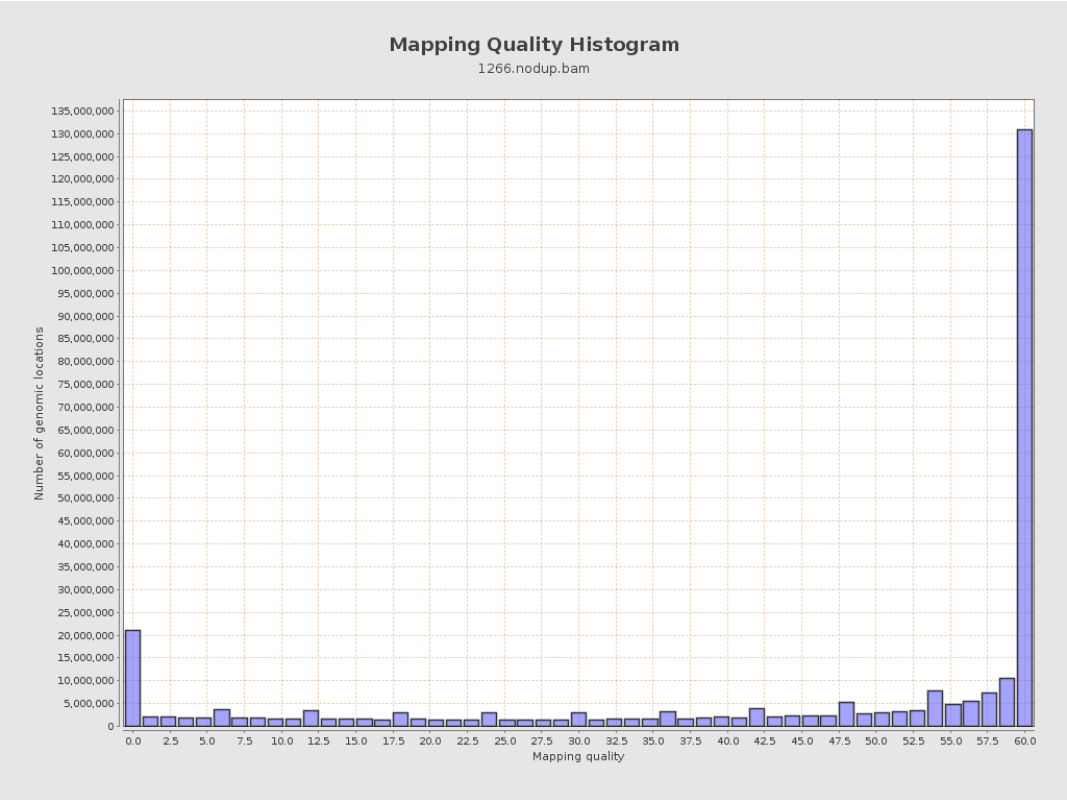
11. Results : Homopolymer Indels



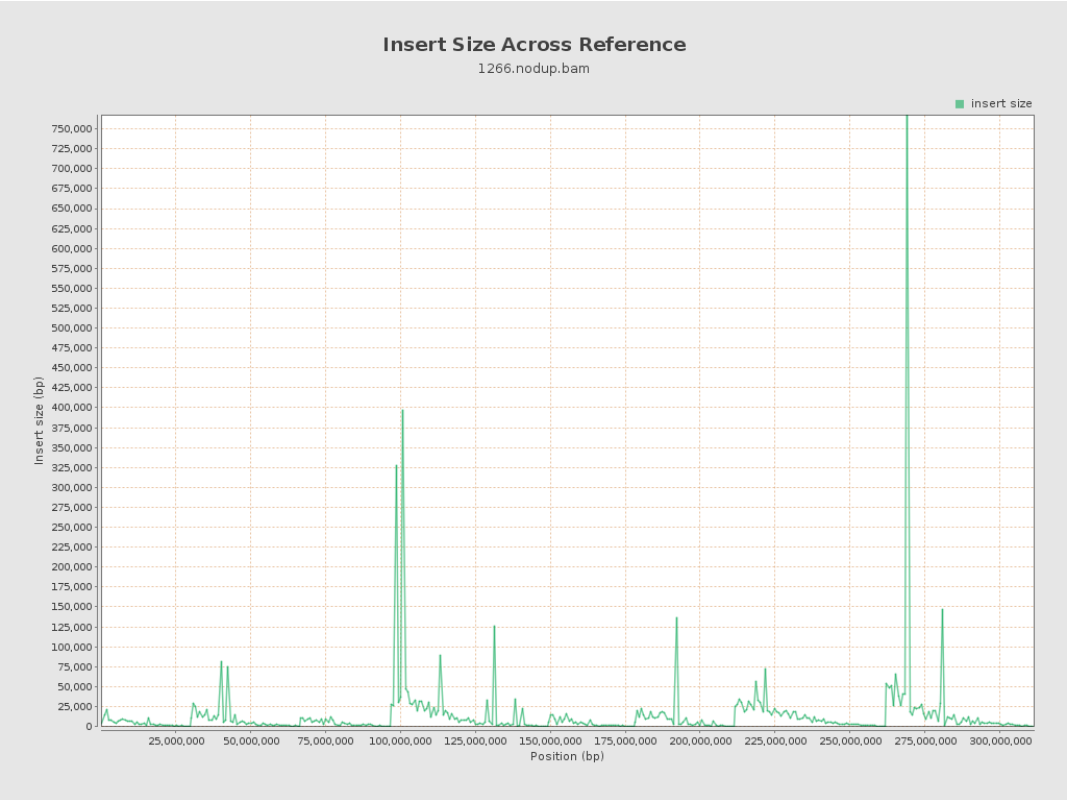
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram