Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:25:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/787.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/787.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_191/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_191_S281_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_191/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_191_S281_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:25:17 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	49,056,629
Mapped reads	45,585,429 / 92.92%
Unmapped reads	3,471,200 / 7.08%
Mapped paired reads	45,585,429 / 92.92%
Mapped reads, first in pair	22,840,146 / 46.56%
Mapped reads, second in pair	22,745,283 / 46.37%
Mapped reads, both in pair	44,430,398 / 90.57%
Mapped reads, singletons	1,155,031 / 2.35%
Read min/max/mean length	30 / 151 / 148.17
Duplicated reads (flagged)	7,170,195 / 14.62%
Clipped reads	10,119,430 / 20.63%

2.2. ACGT Content

Number/percentage of A's	1,944,414,007 / 30.79%
Number/percentage of C's	1,213,304,708 / 19.21%
Number/percentage of T's	1,948,035,059 / 30.85%
Number/percentage of G's	1,209,606,313 / 19.15%
Number/percentage of N's	27,414 / 0%
GC Percentage	38.37%

2.3. Coverage

Mean	20.3162
Standard Deviation	176.7597

2.4. Mapping Quality

Mean Mapping Quality	44.5

2.5. Insert size

Mean	238,430.62
Standard Deviation	2,329,068.31
P25/Median/P75	340 / 443 / 581

2.6. Mismatches and indels

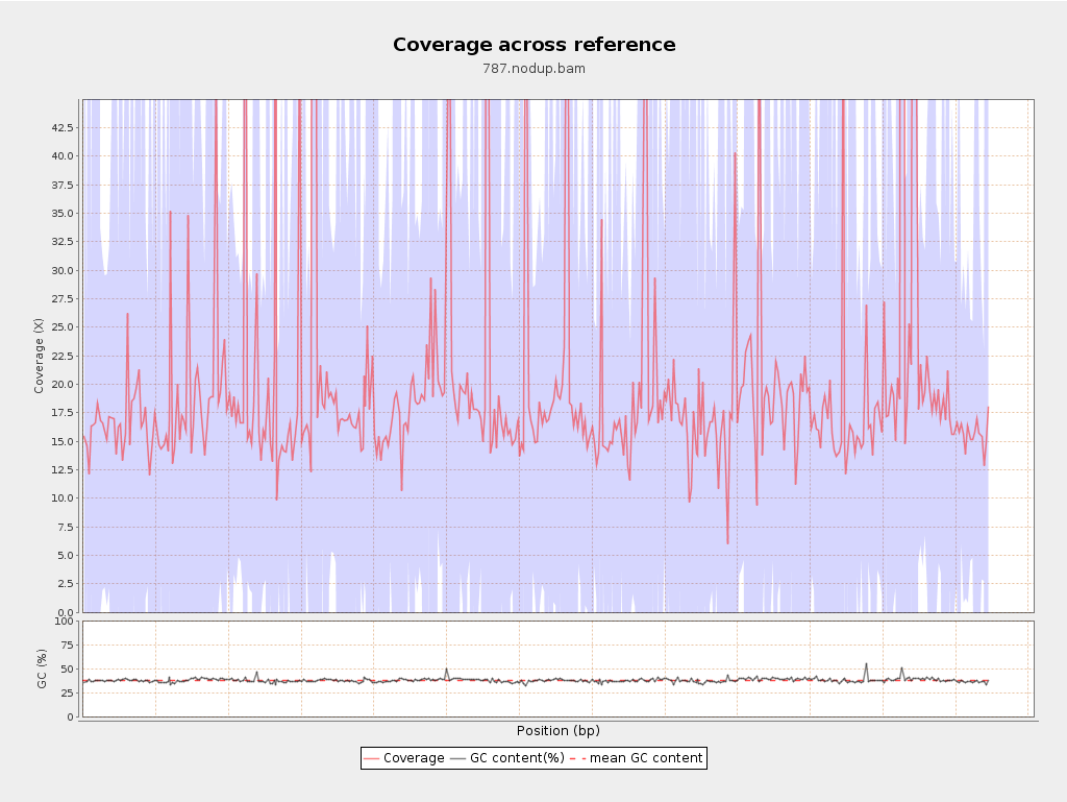
General error rate	2.3%
Mismatches	133,625,584
Insertions	4,294,943
Mapped reads with at least one insertion	8.44%
Deletions	4,240,923
Mapped reads with at least one deletion	8.28%
Homopolymer indels	56.78%

2.7. Chromosome stats

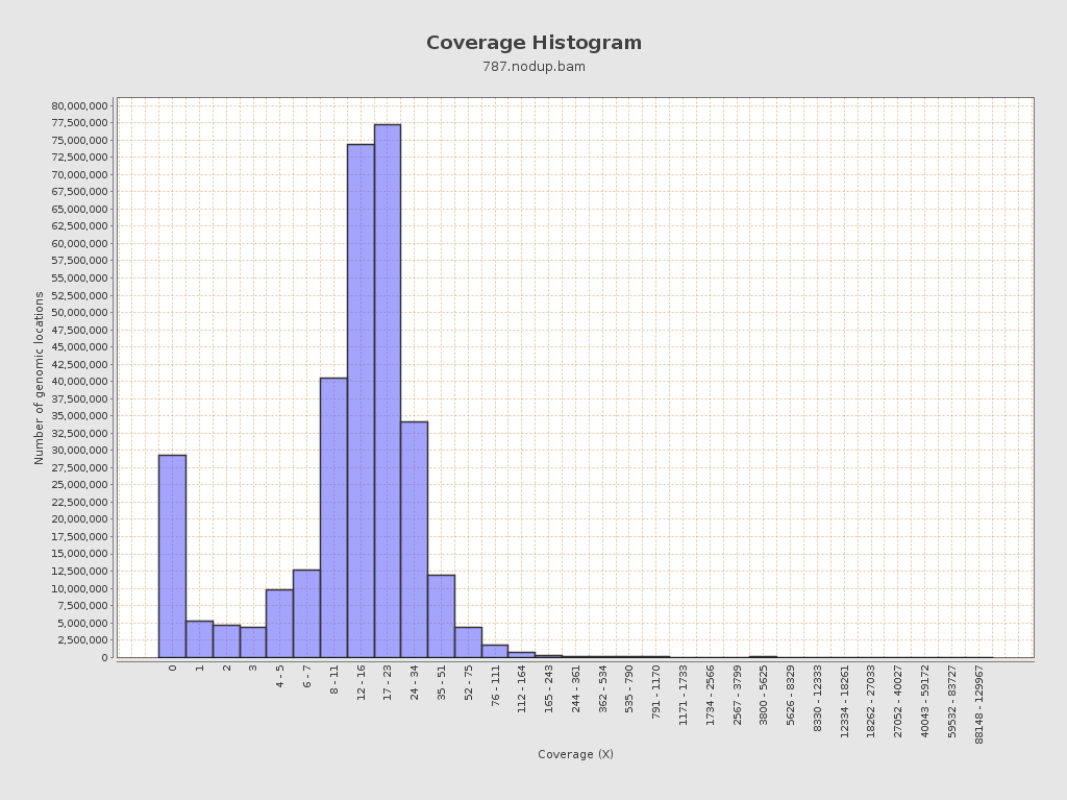
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	485306080	16.3269	57.4858

LT669789.1	36598175	748060751	20.4398	180.6552
LT669790.1	30422129	687251173	22.5905	200.0856
LT669791.1	52758100	1057004359	20.0349	165.0122
LT669792.1	28376109	565011177	19.9115	186.4208
LT669793.1	33388210	622701340	18.6503	113.9786
LT669794.1	50579949	958579047	18.9518	138.6567
LT669795.1	49795044	1207475199	24.2489	261.1461

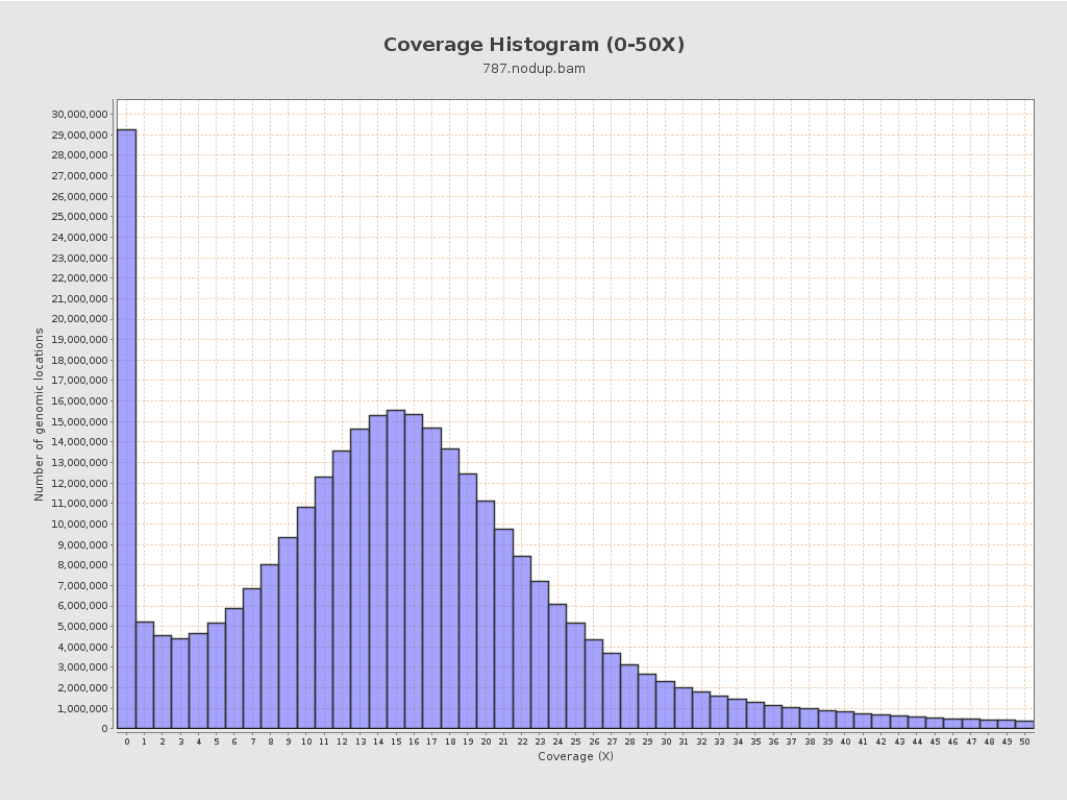
3. Results : Coverage across reference



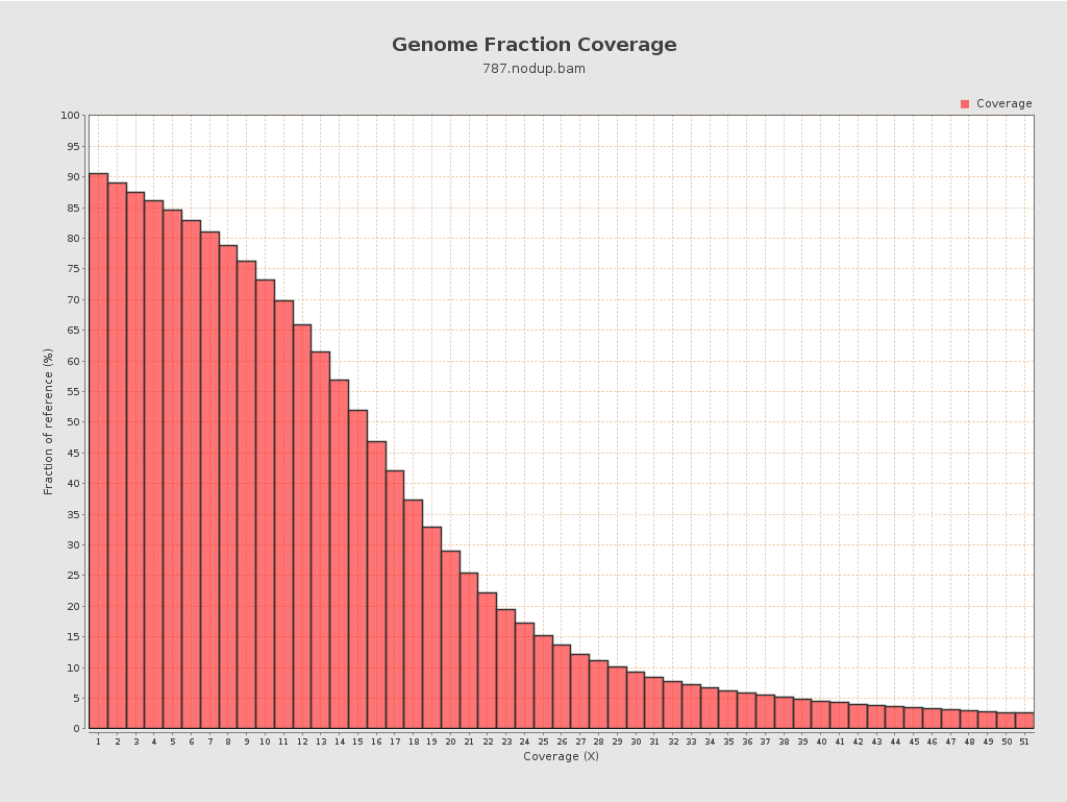
4. Results : Coverage Histogram



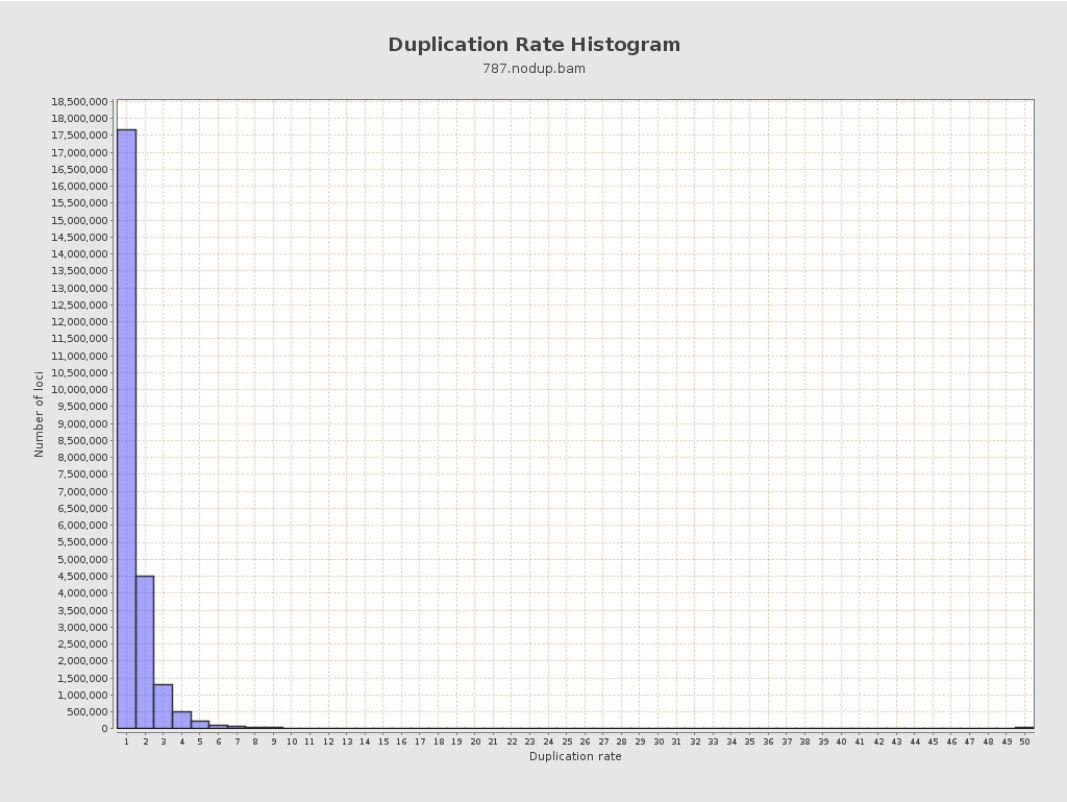
5. Results : Coverage Histogram (0-50X)



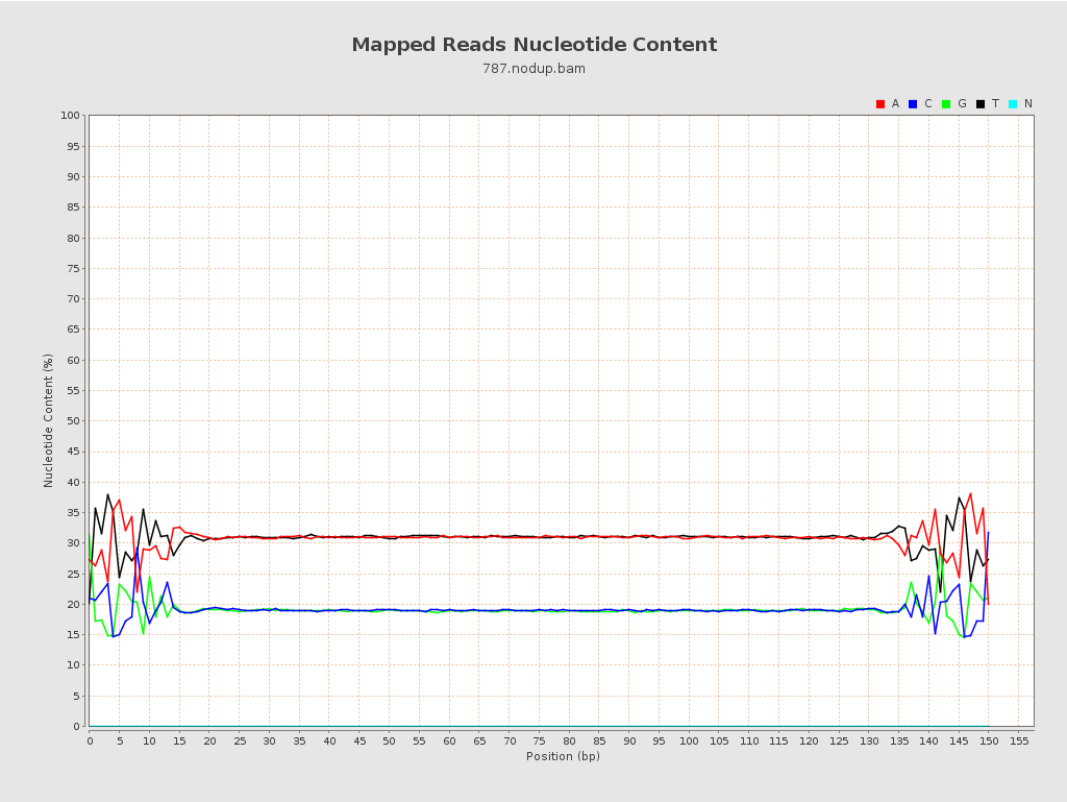
6. Results : Genome Fraction Coverage



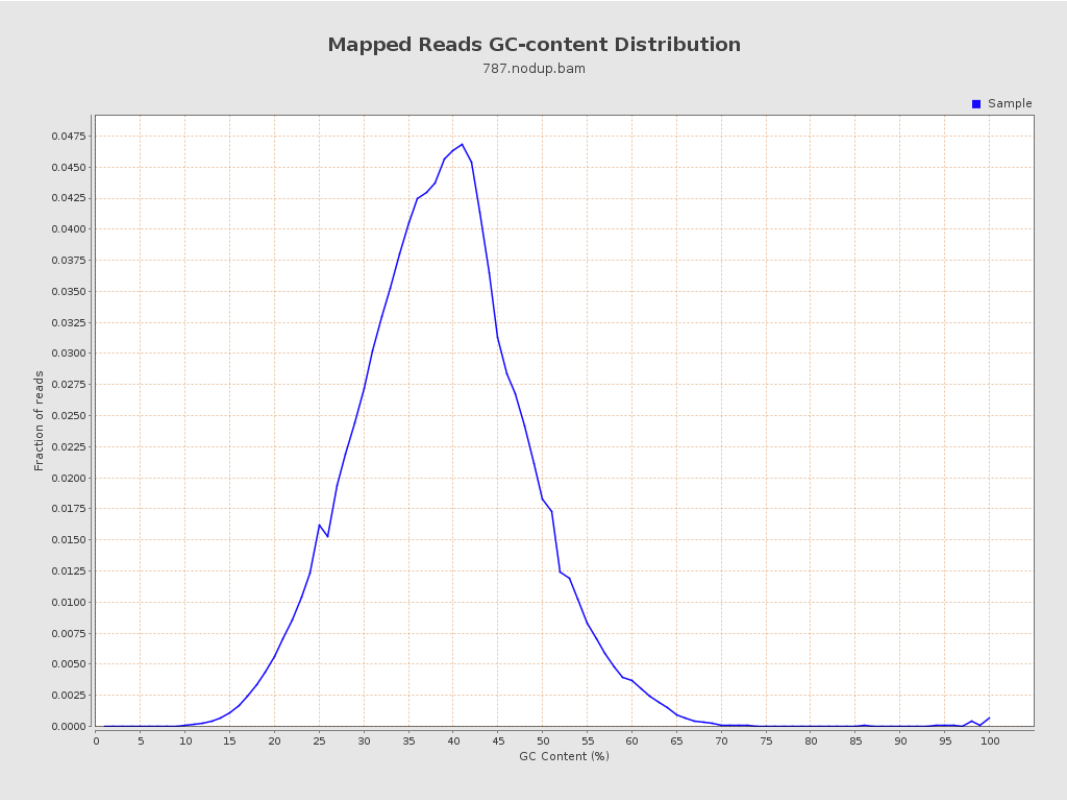
7. Results : Duplication Rate Histogram



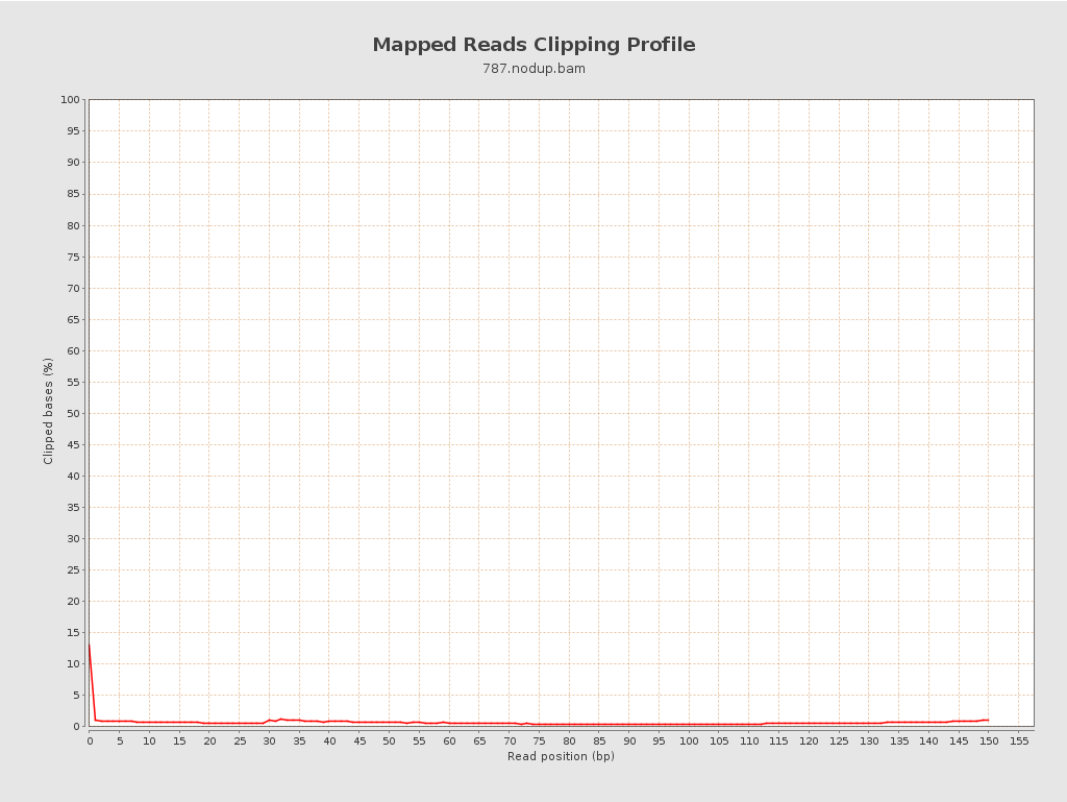
8. Results : Mapped Reads Nucleotide Content



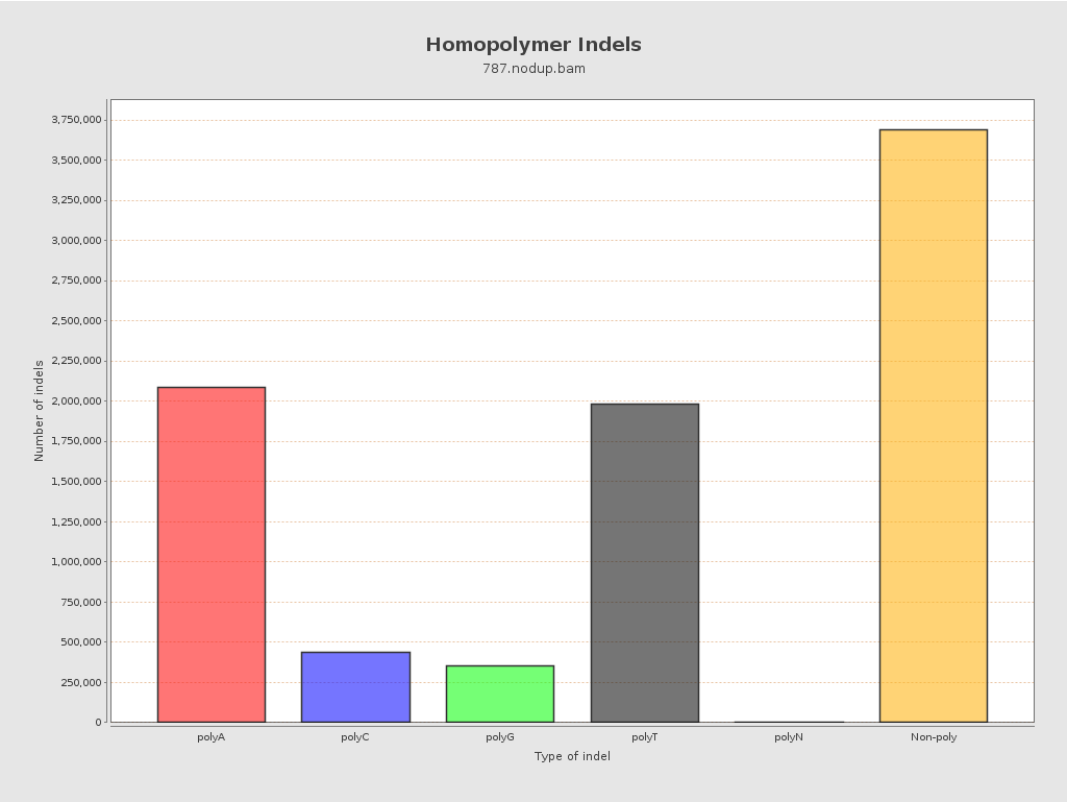
9. Results : Mapped Reads GC-content Distribution



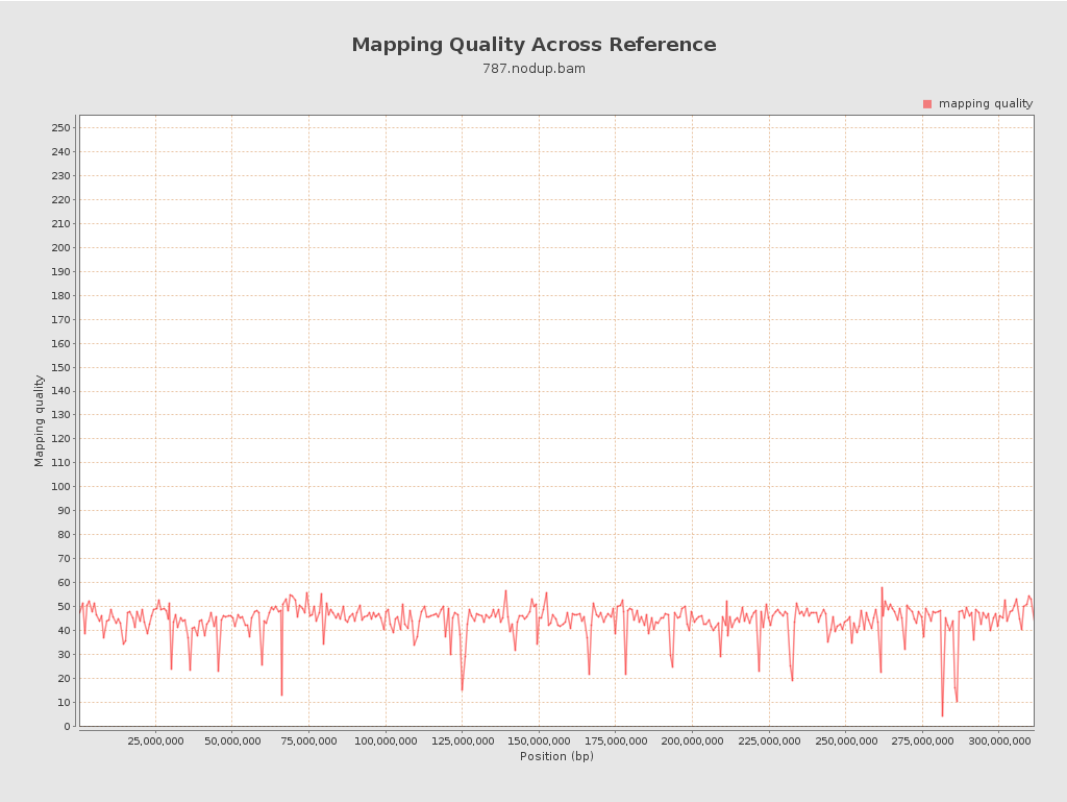
10. Results : Mapped Reads Clipping Profile



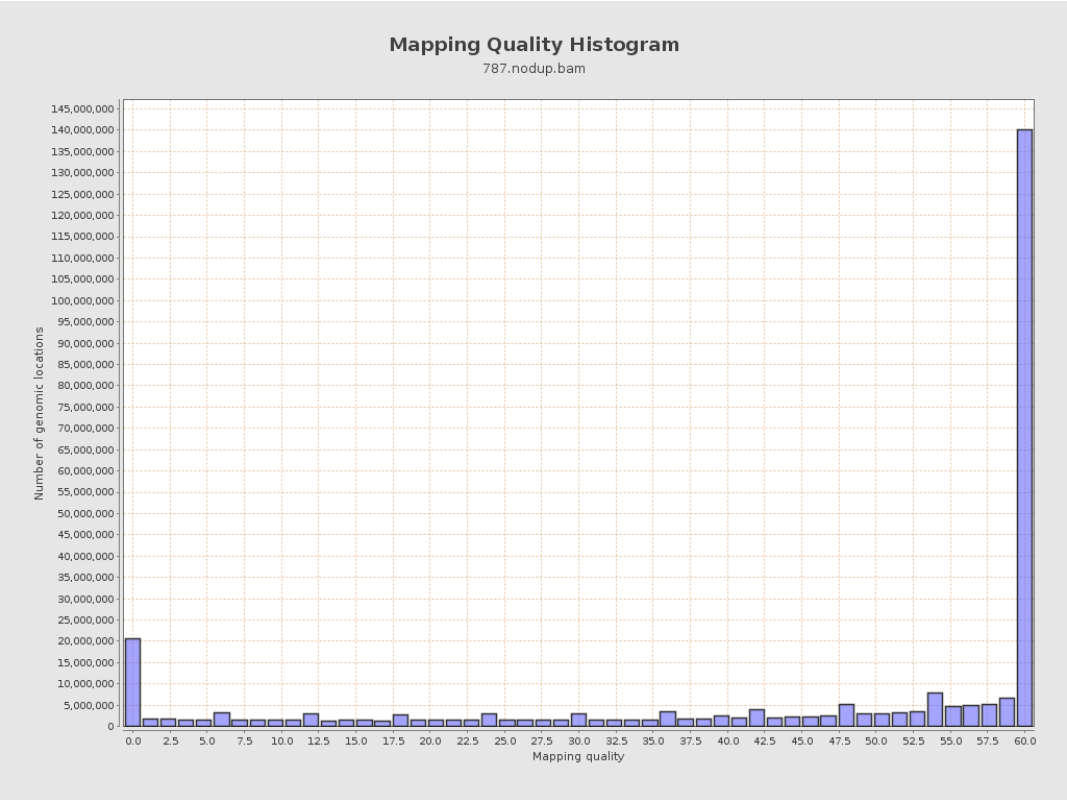
11. Results : Homopolymer Indels



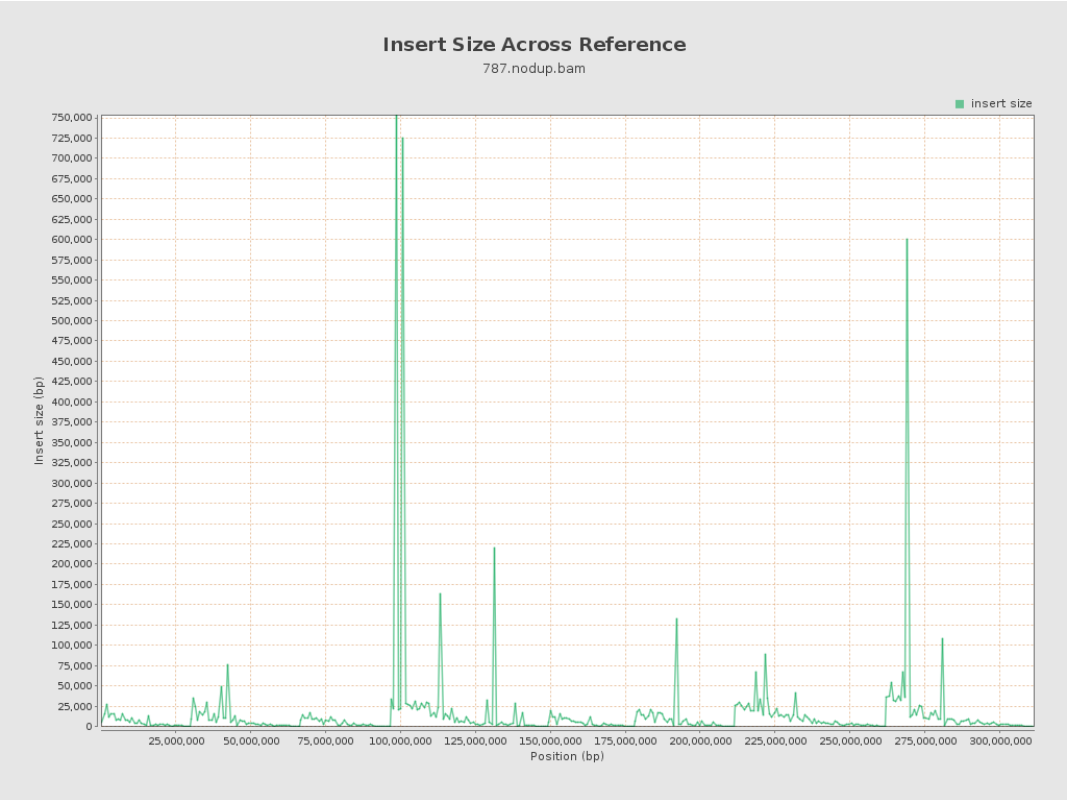
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram