Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:34:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/794.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/794.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_178/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_178_S268_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_178/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_178_S268_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:34:51 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	76,206,077
Mapped reads	70,925,674 / 93.07%
Unmapped reads	5,280,403 / 6.93%
Mapped paired reads	70,925,674 / 93.07%
Mapped reads, first in pair	35,503,549 / 46.59%
Mapped reads, second in pair	35,422,125 / 46.48%
Mapped reads, both in pair	69,235,066 / 90.85%
Mapped reads, singletons	1,690,608 / 2.22%
Read min/max/mean length	30 / 151 / 148.07
Duplicated reads (flagged)	12,992,657 / 17.05%
Clipped reads	16,090,742 / 21.11%

2.2. ACGT Content

Number/percentage of A's	3,024,260,823 / 30.84%
Number/percentage of C's	1,879,239,514 / 19.17%
Number/percentage of T's	3,024,484,798 / 30.85%
Number/percentage of G's	1,876,761,959 / 19.14%
Number/percentage of N's	40,195 / 0%
GC Percentage	38.31%

2.3. Coverage

Mean	31.5459
Standard Deviation	266.1485

2.4. Mapping Quality

Mean Mapping Quality	43.55

2.5. Insert size

Mean	243,370.1
Standard Deviation	2,344,118.39
P25/Median/P75	313 / 408 / 535

2.6. Mismatches and indels

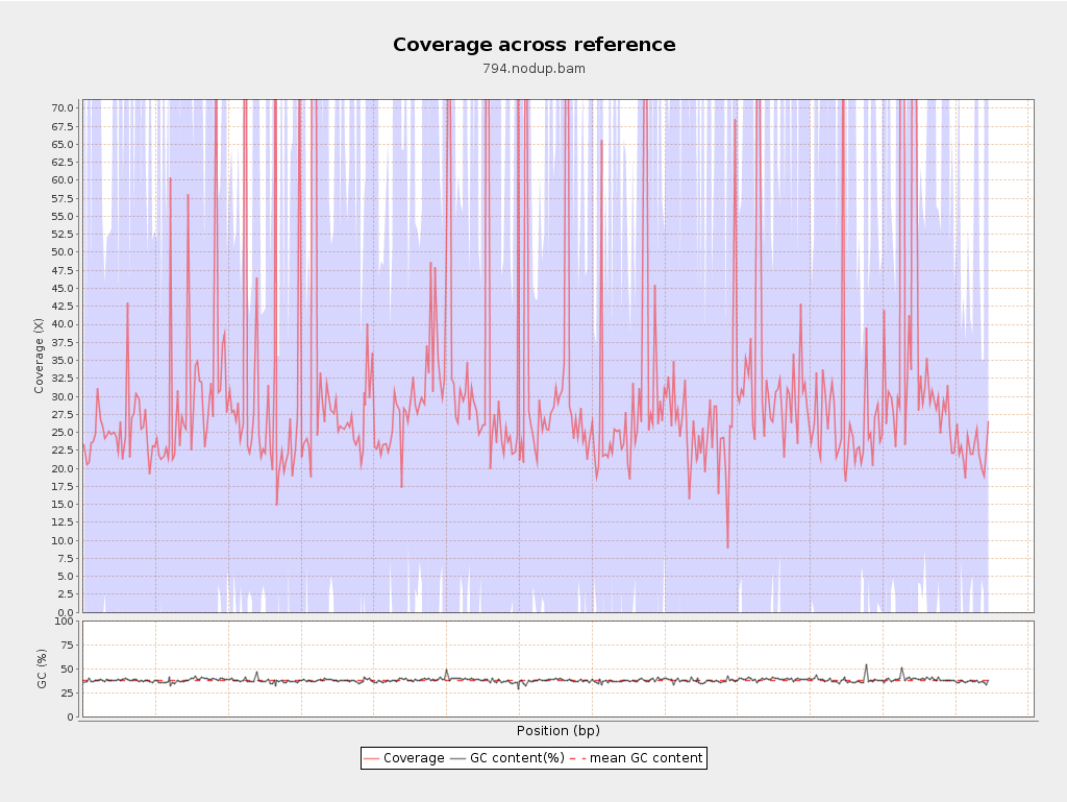
General error rate	2.35%
Mismatches	211,586,783
Insertions	6,921,902
Mapped reads with at least one insertion	8.74%
Deletions	6,947,075
Mapped reads with at least one deletion	8.7%
Homopolymer indels	56.83%

2.7. Chromosome stats

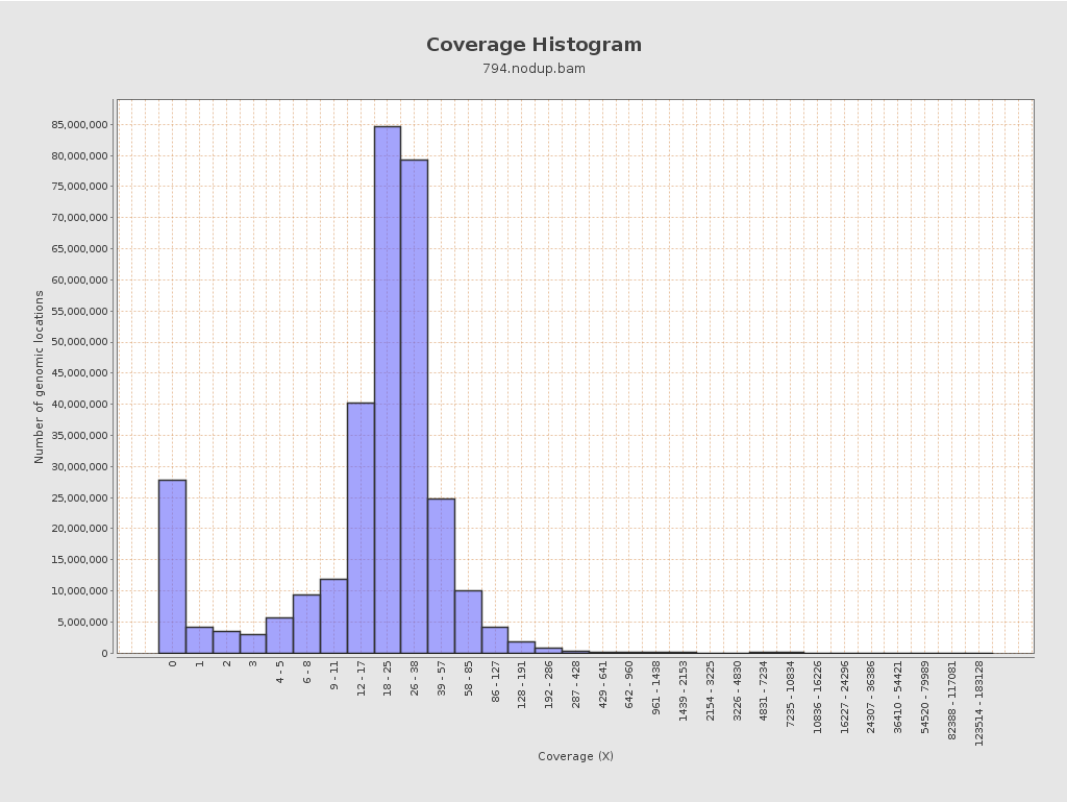
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	737739127	24.8194	90.0337

LT669789.1	36598175	1195317321	32.6606	289.8864
LT669790.1	30422129	1044163421	34.3225	314.599
LT669791.1	52758100	1660990286	31.4831	259.6376
LT669792.1	28376109	880947520	31.0454	304.5587
LT669793.1	33388210	979626737	29.3405	190.0051
LT669794.1	50579949	1557707661	30.7969	233.2756
LT669795.1	49795044	1774539871	35.6369	335.3144

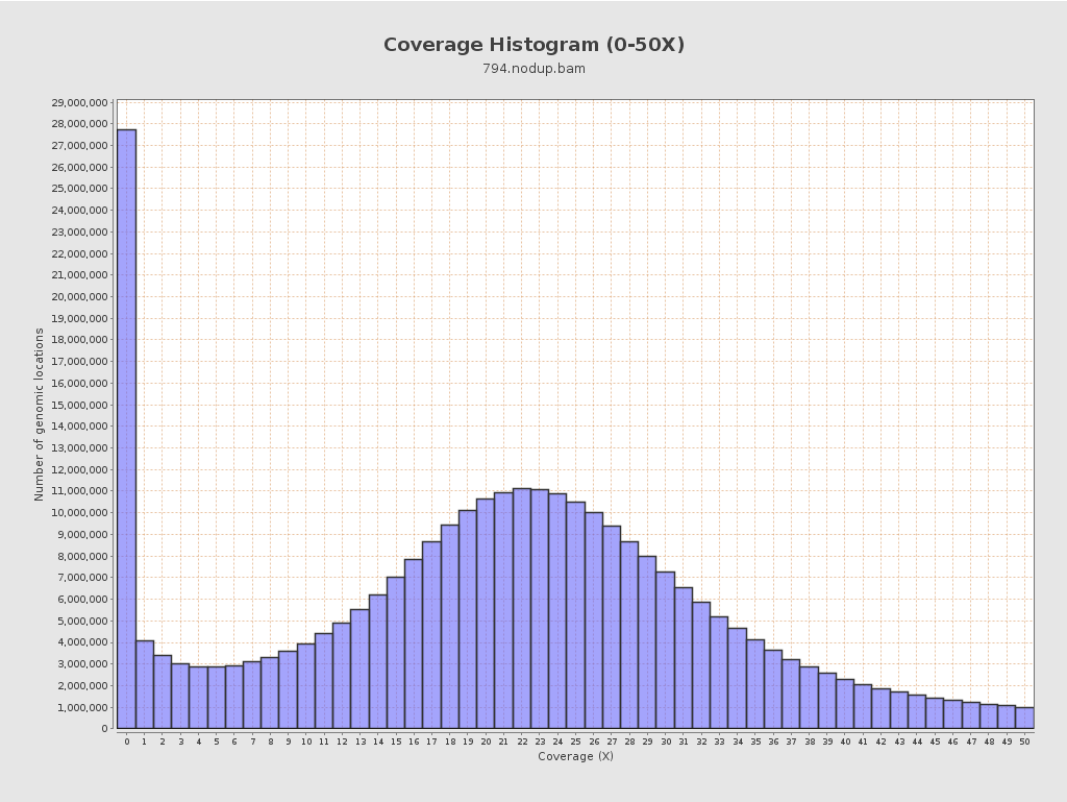
3. Results : Coverage across reference



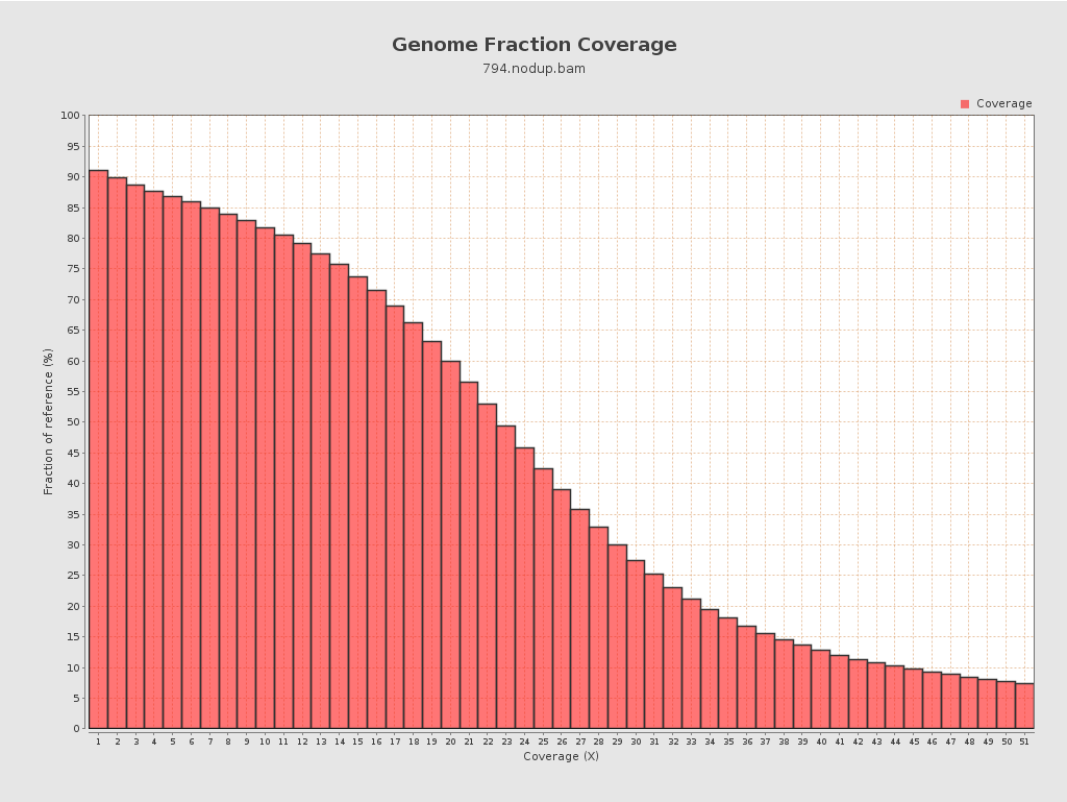
4. Results : Coverage Histogram



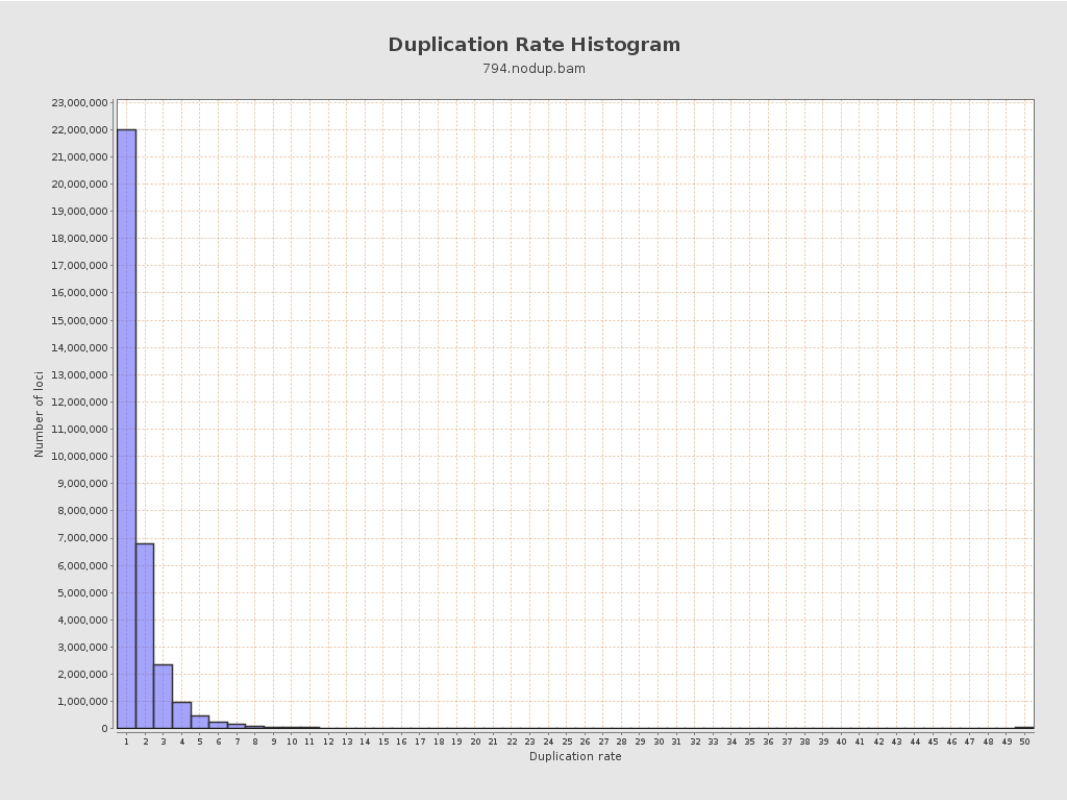
5. Results : Coverage Histogram (0-50X)



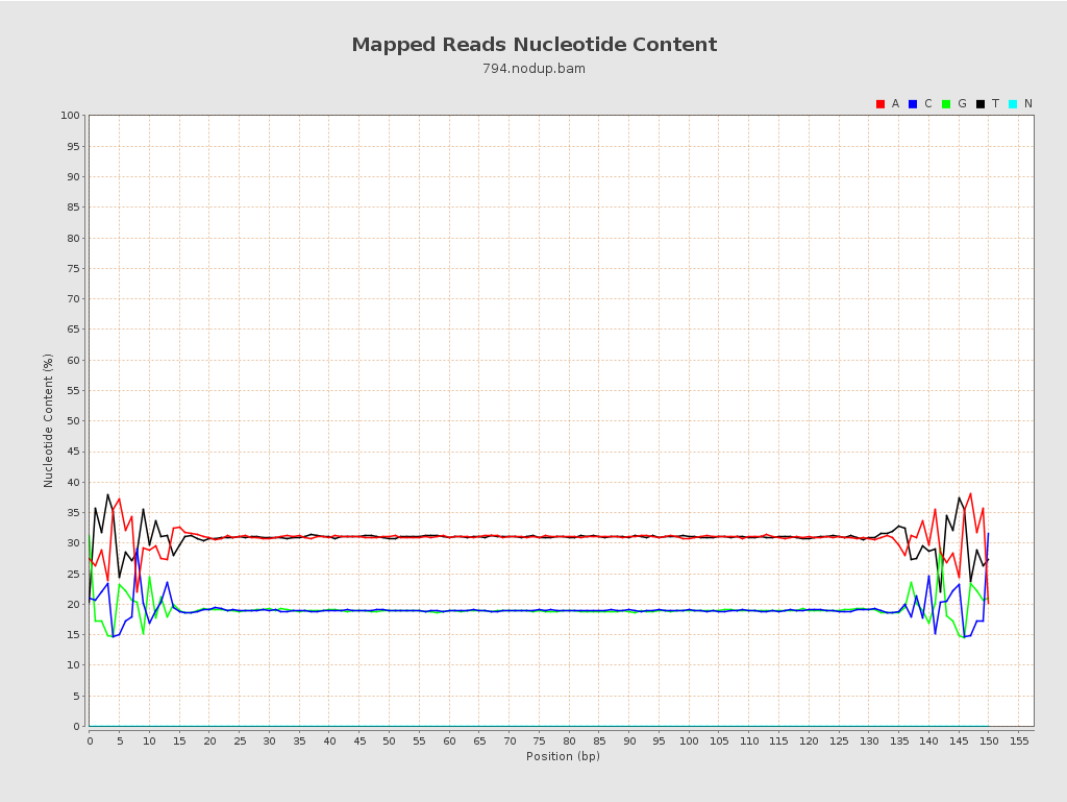
6. Results : Genome Fraction Coverage



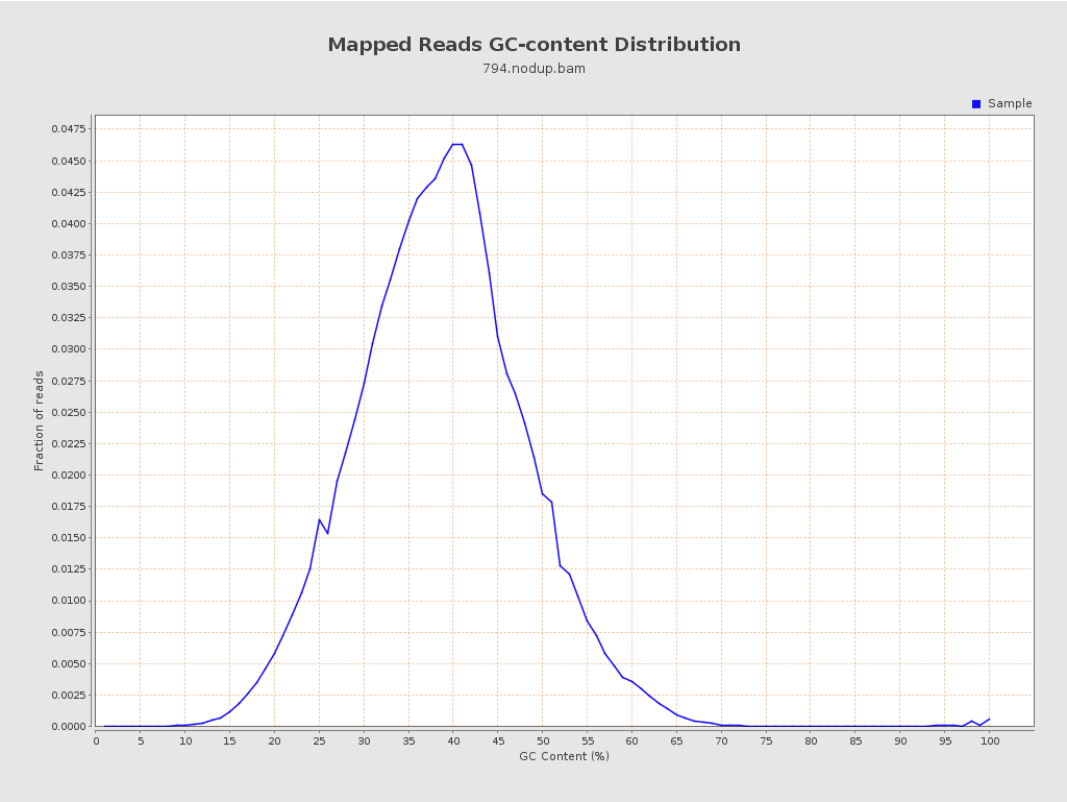
7. Results : Duplication Rate Histogram



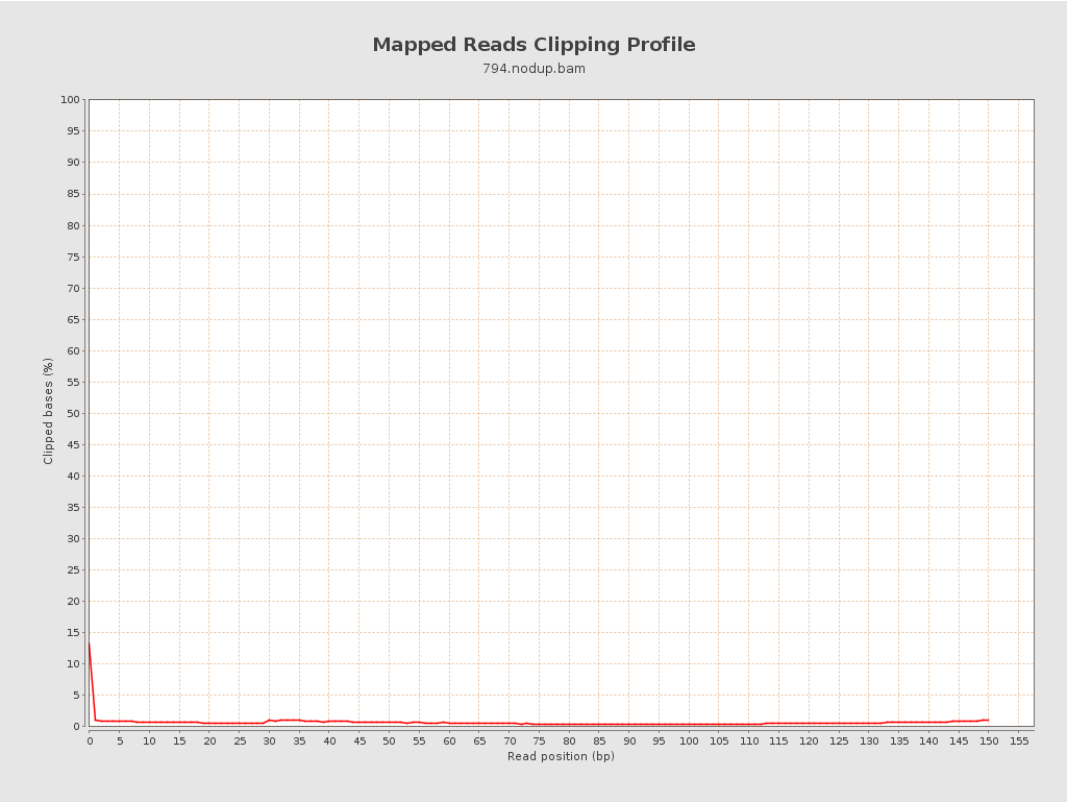
8. Results : Mapped Reads Nucleotide Content



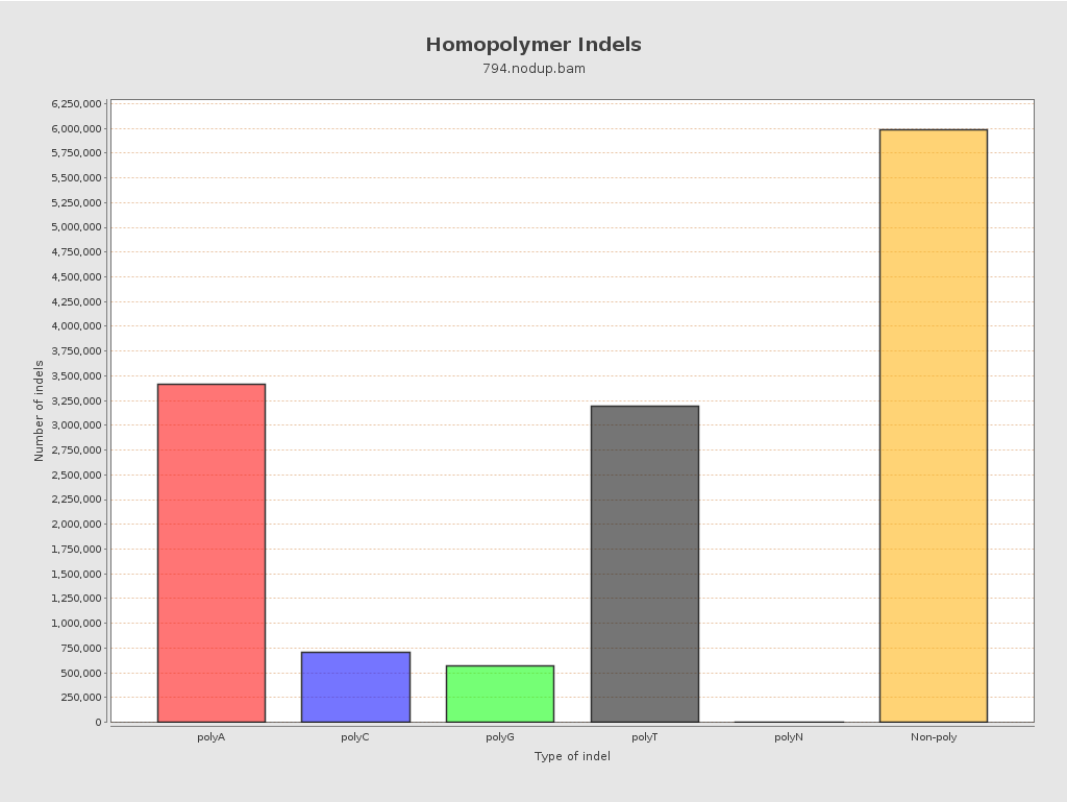
9. Results : Mapped Reads GC-content Distribution



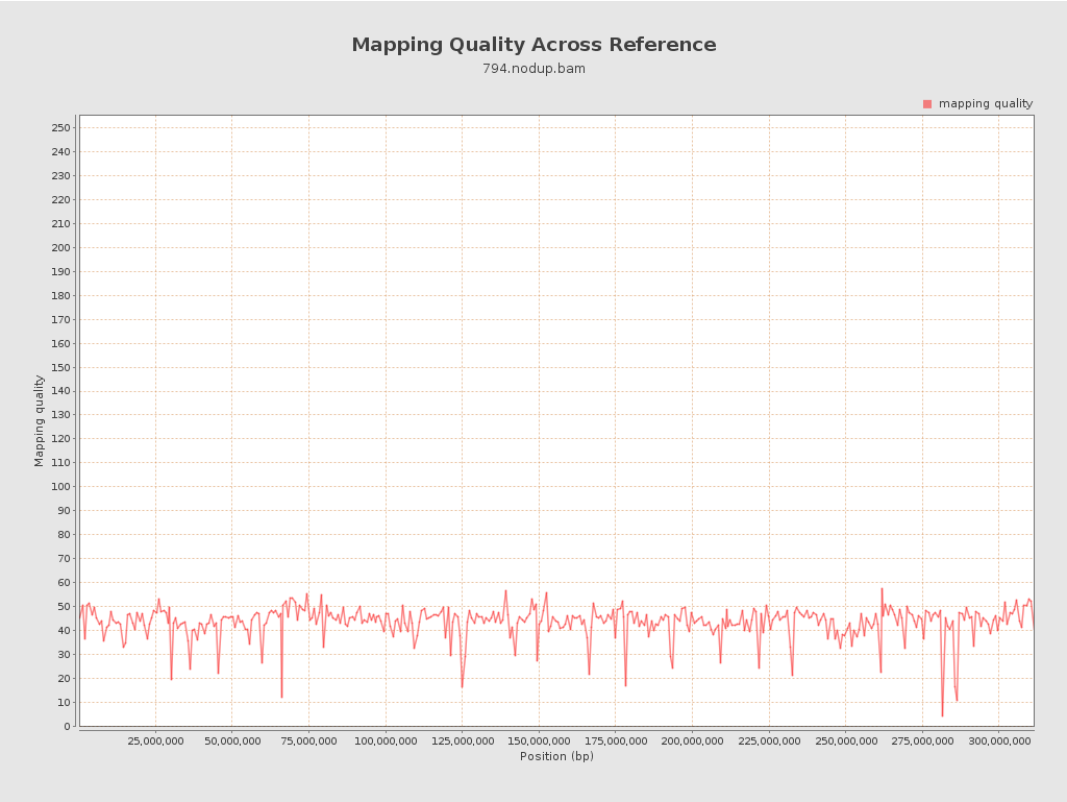
10. Results : Mapped Reads Clipping Profile



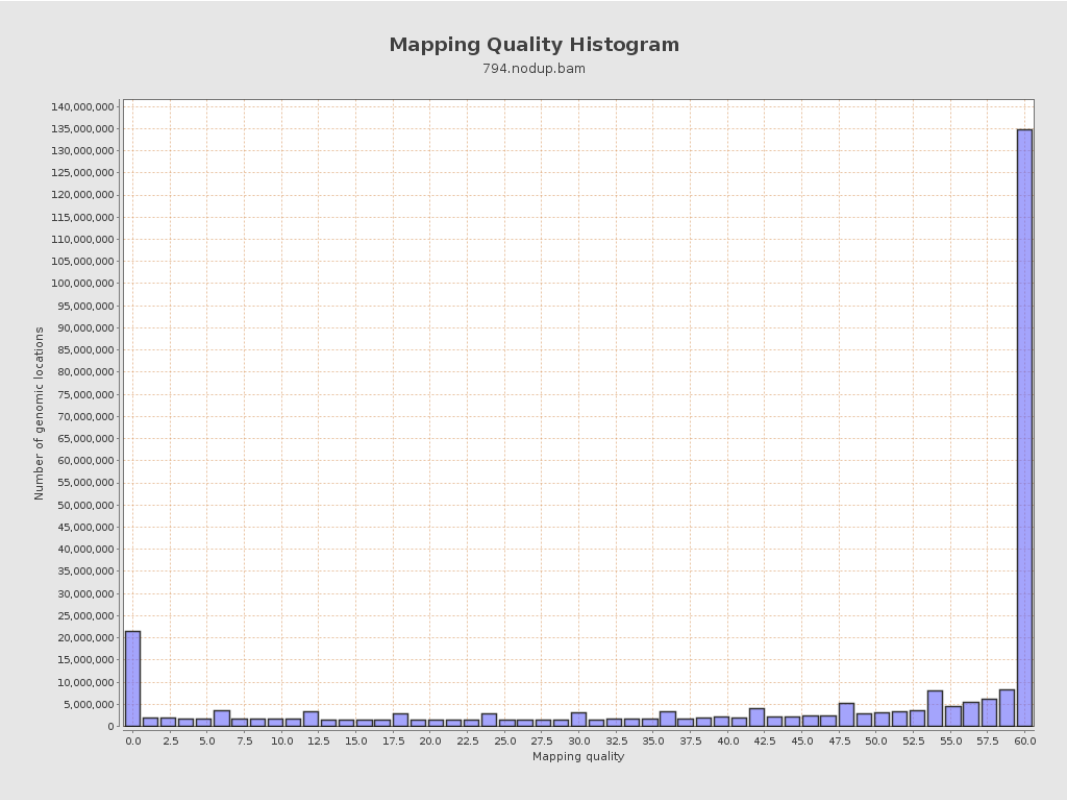
11. Results : Homopolymer Indels



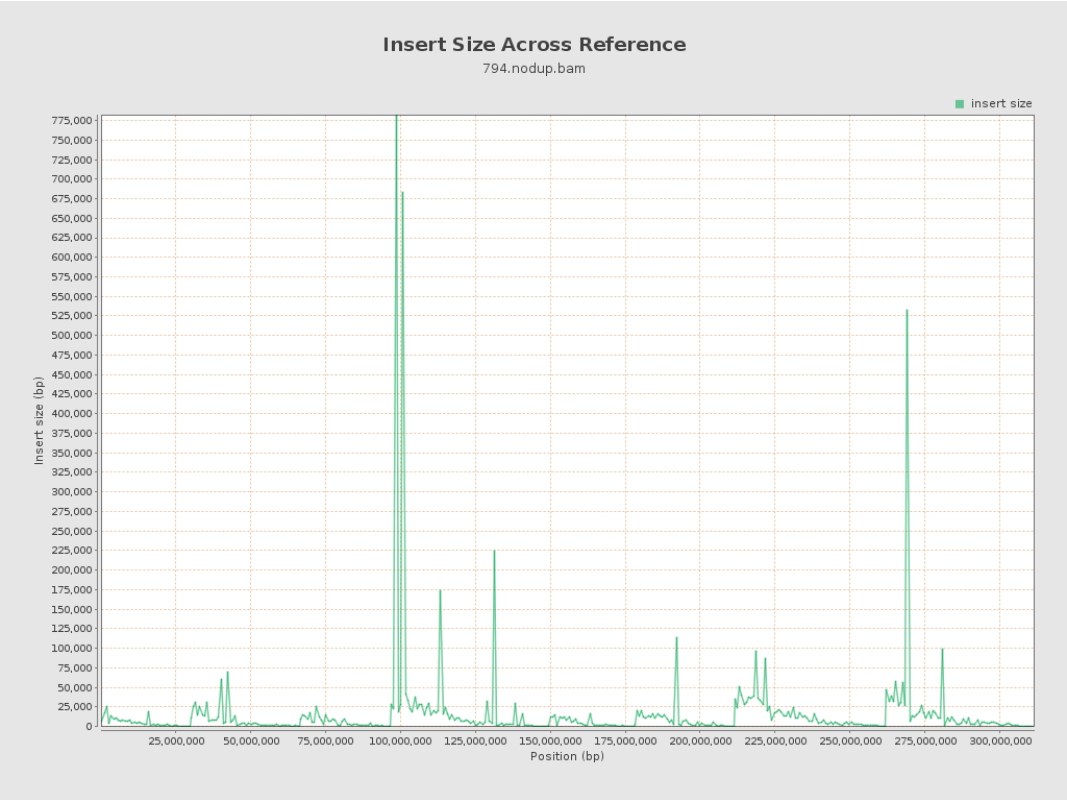
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram