Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:34:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/444.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/444.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_173/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_173_S263_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_173/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_173_S263_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:34:02 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	72,581,780
Mapped reads	67,409,108 / 92.87%
Unmapped reads	5,172,672 / 7.13%
Mapped paired reads	67,409,108 / 92.87%
Mapped reads, first in pair	33,733,864 / 46.48%
Mapped reads, second in pair	33,675,244 / 46.4%
Mapped reads, both in pair	66,009,497 / 90.94%
Mapped reads, singletons	1,399,611 / 1.93%
Read min/max/mean length	30 / 151 / 148.14
Duplicated reads (flagged)	11,556,804 / 15.92%
Clipped reads	15,017,357 / 20.69%

2.2. ACGT Content

Number/percentage of A's	2,882,794,932 / 30.86%
Number/percentage of C's	1,789,182,664 / 19.15%
Number/percentage of T's	2,883,418,807 / 30.87%
Number/percentage of G's	1,785,697,170 / 19.12%
Number/percentage of N's	38,249 / 0%
GC Percentage	38.27%

2.3. Coverage

Mean	30.0523
Standard Deviation	240.8775

2.4. Mapping Quality

Mean Mapping Quality	44.07

2.5. Insert size

Mean	225,275.88
Standard Deviation	2,251,804.66
P25/Median/P75	310 / 407 / 531

2.6. Mismatches and indels

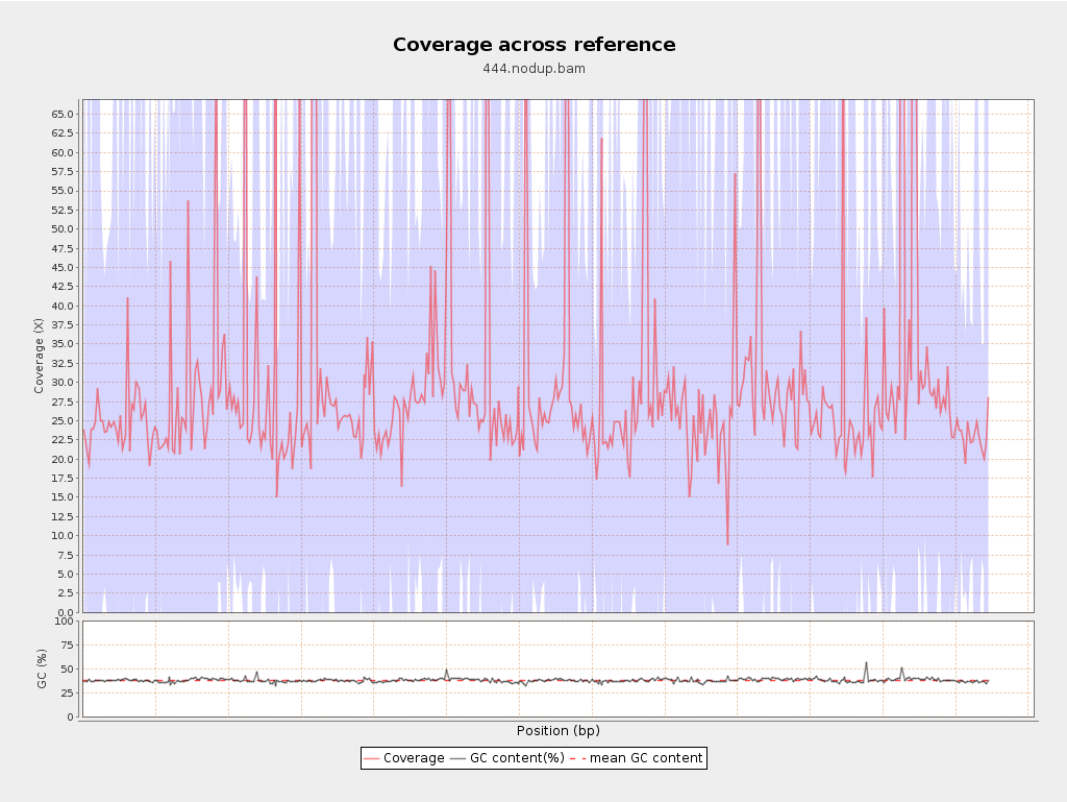
General error rate	2.3%
Mismatches	197,061,111
Insertions	6,334,137
Mapped reads with at least one insertion	8.44%
Deletions	6,503,302
Mapped reads with at least one deletion	8.58%
Homopolymer indels	56.83%

2.7. Chromosome stats

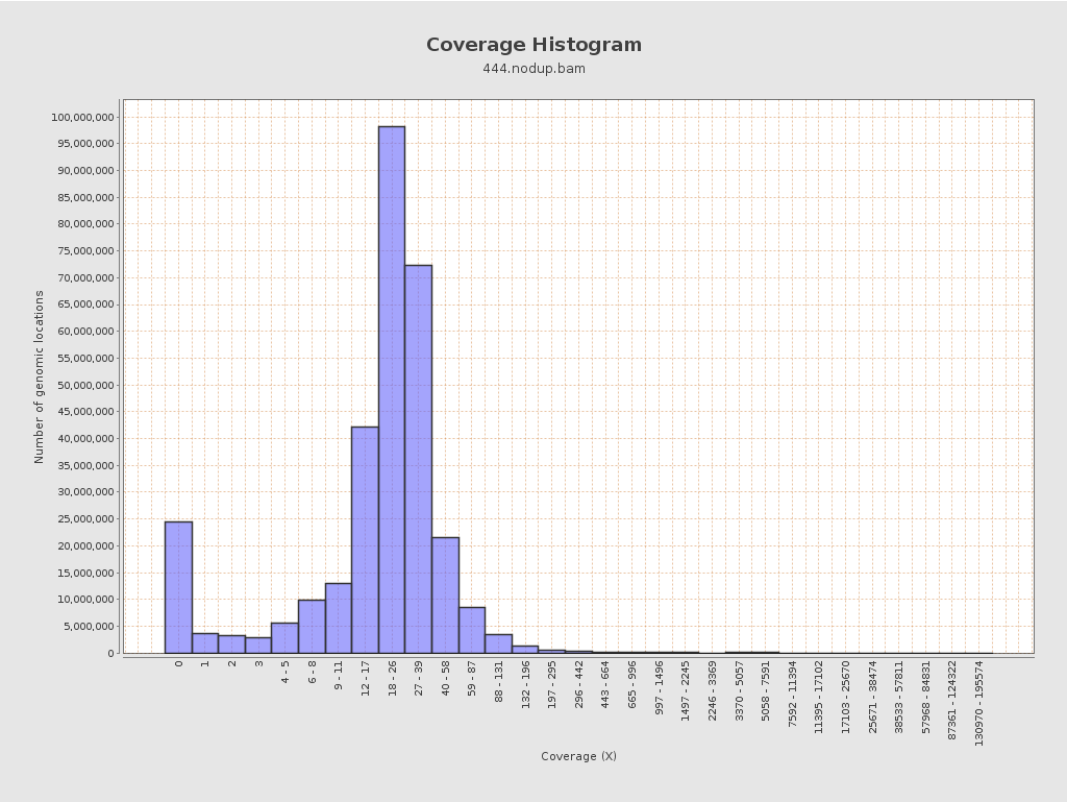
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	727234927	24.466	74.1132

LT669789.1	36598175	1127584780	30.8099	256.6311
LT669790.1	30422129	983527436	32.3293	264.847
LT669791.1	52758100	1569294019	29.7451	216.0052
LT669792.1	28376109	832915655	29.3527	278.5453
LT669793.1	33388210	944643900	28.2927	175.5591
LT669794.1	50579949	1469788732	29.0587	224.9431
LT669795.1	49795044	1710562030	34.3521	320.6814

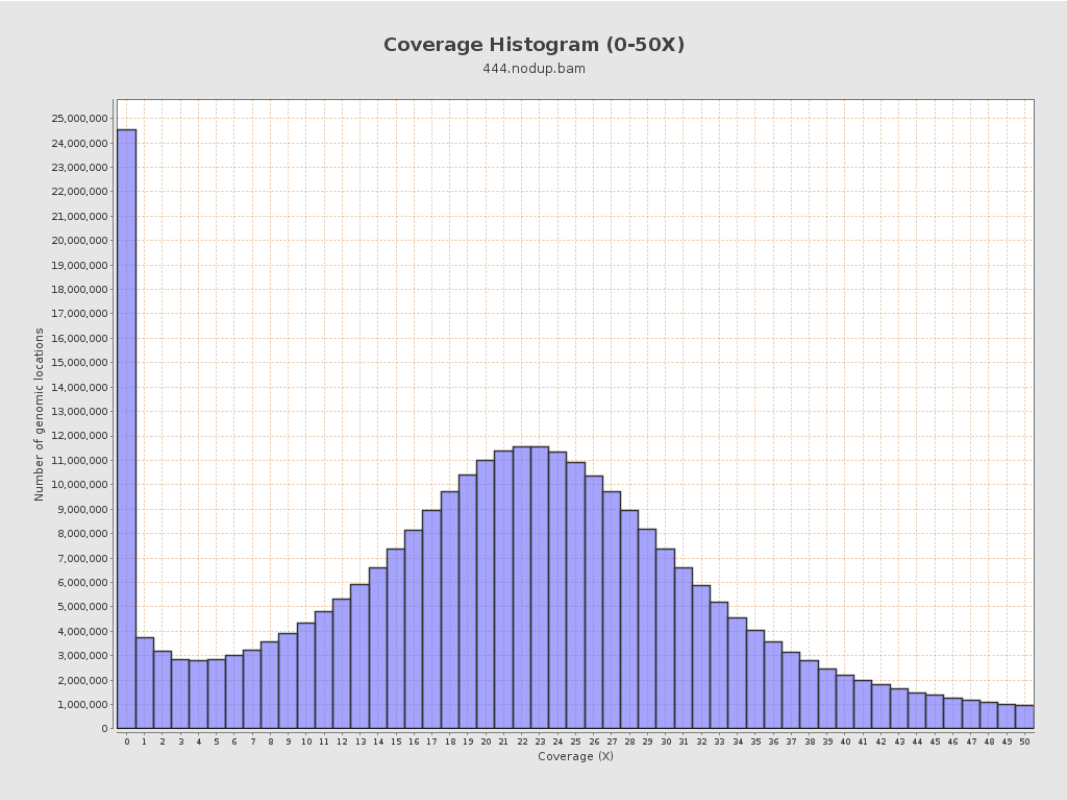
3. Results : Coverage across reference



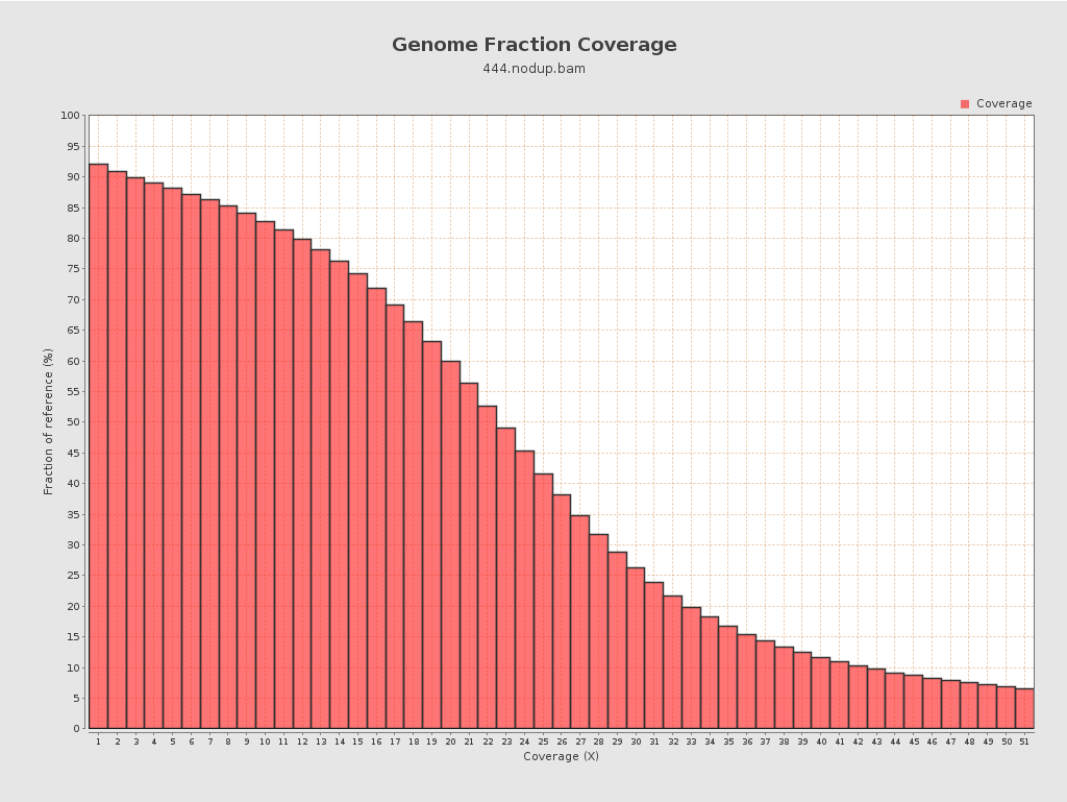
4. Results : Coverage Histogram



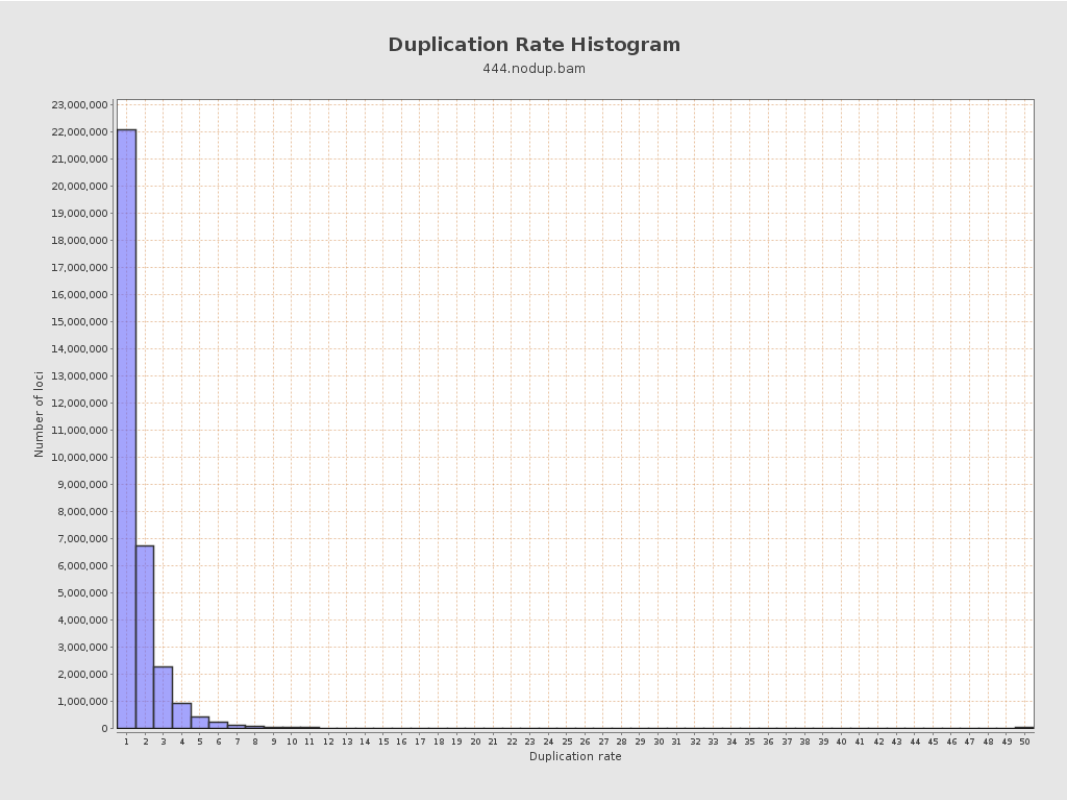
5. Results : Coverage Histogram (0-50X)



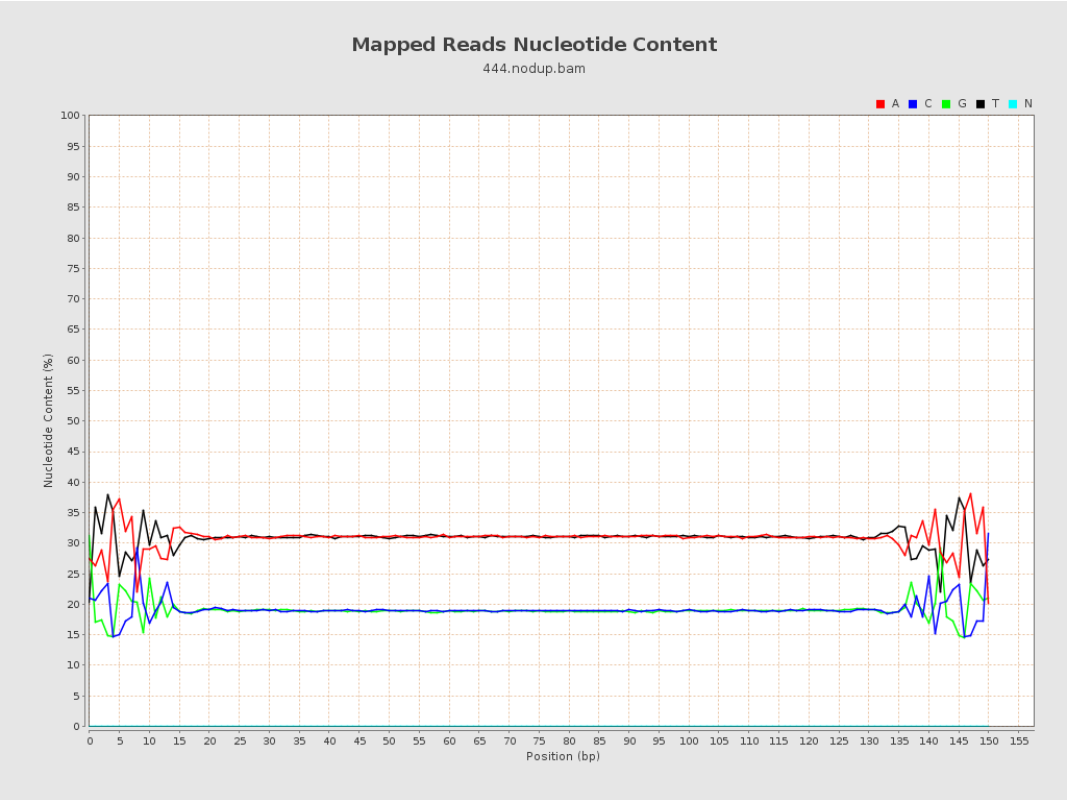
6. Results : Genome Fraction Coverage



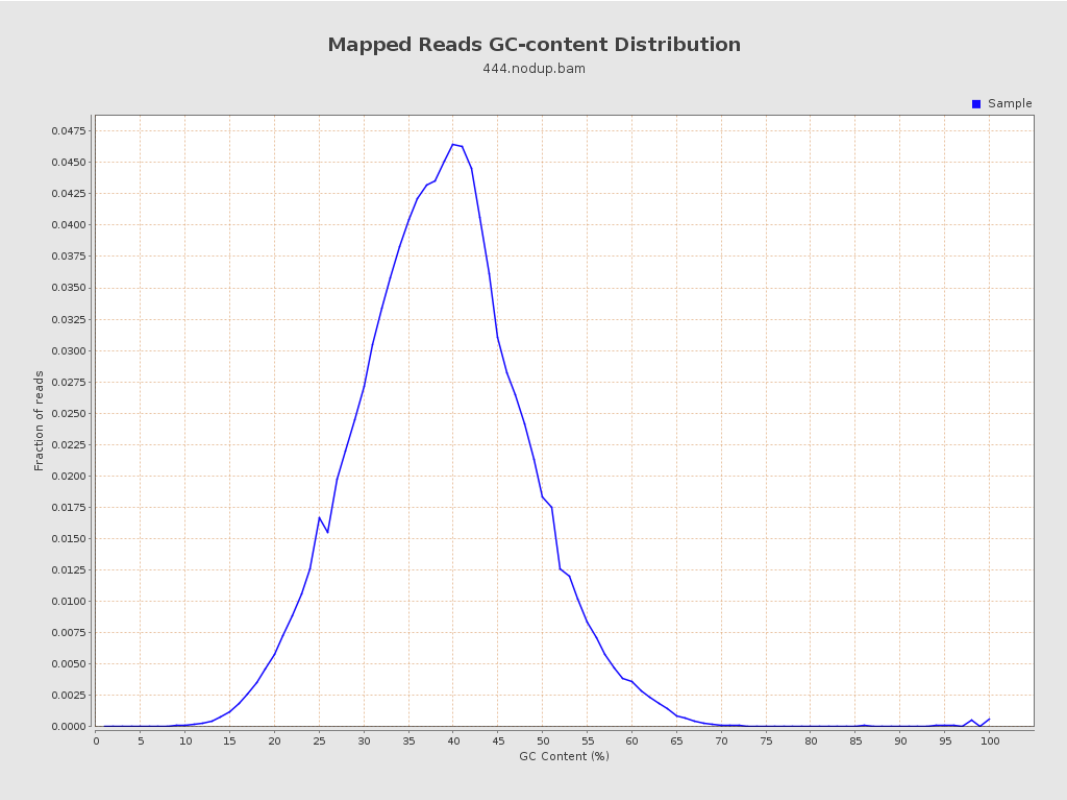
7. Results : Duplication Rate Histogram



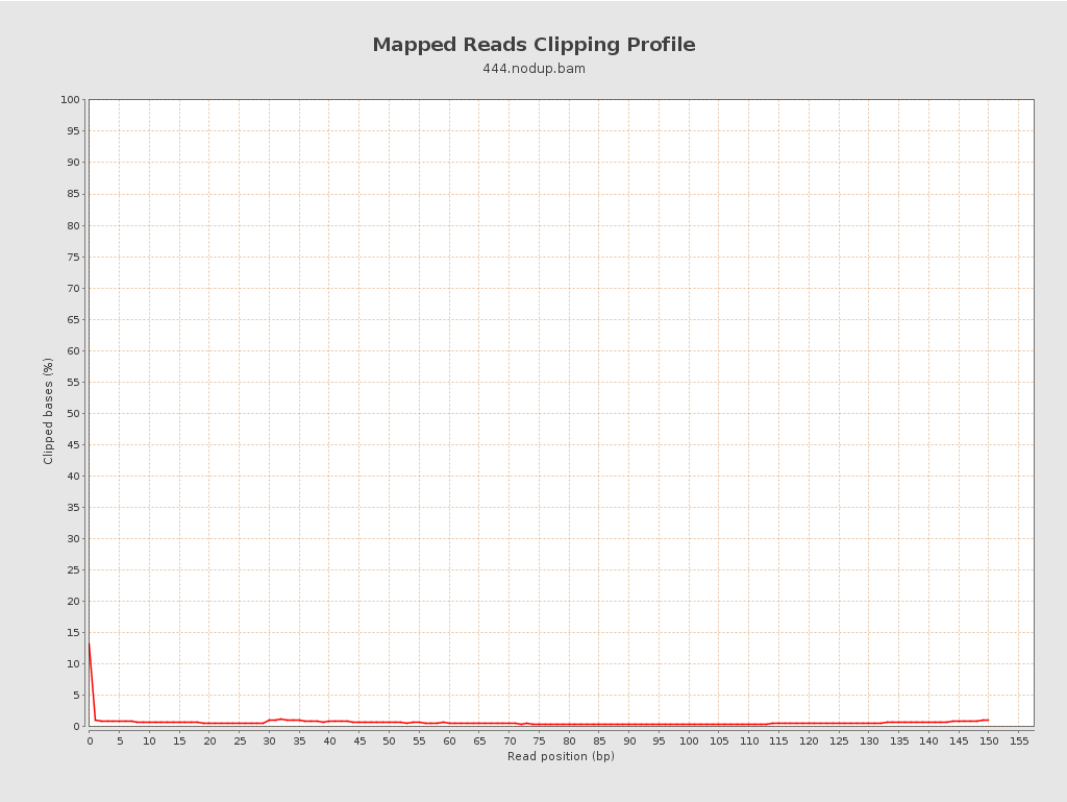
8. Results : Mapped Reads Nucleotide Content



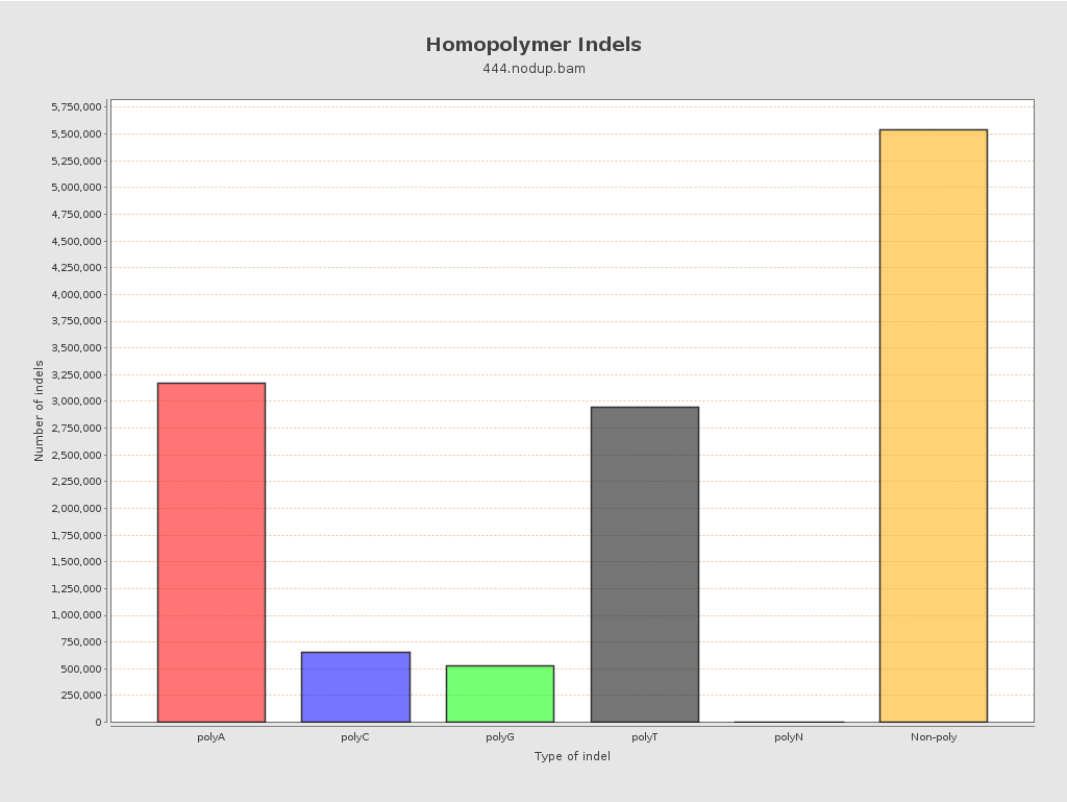
9. Results : Mapped Reads GC-content Distribution



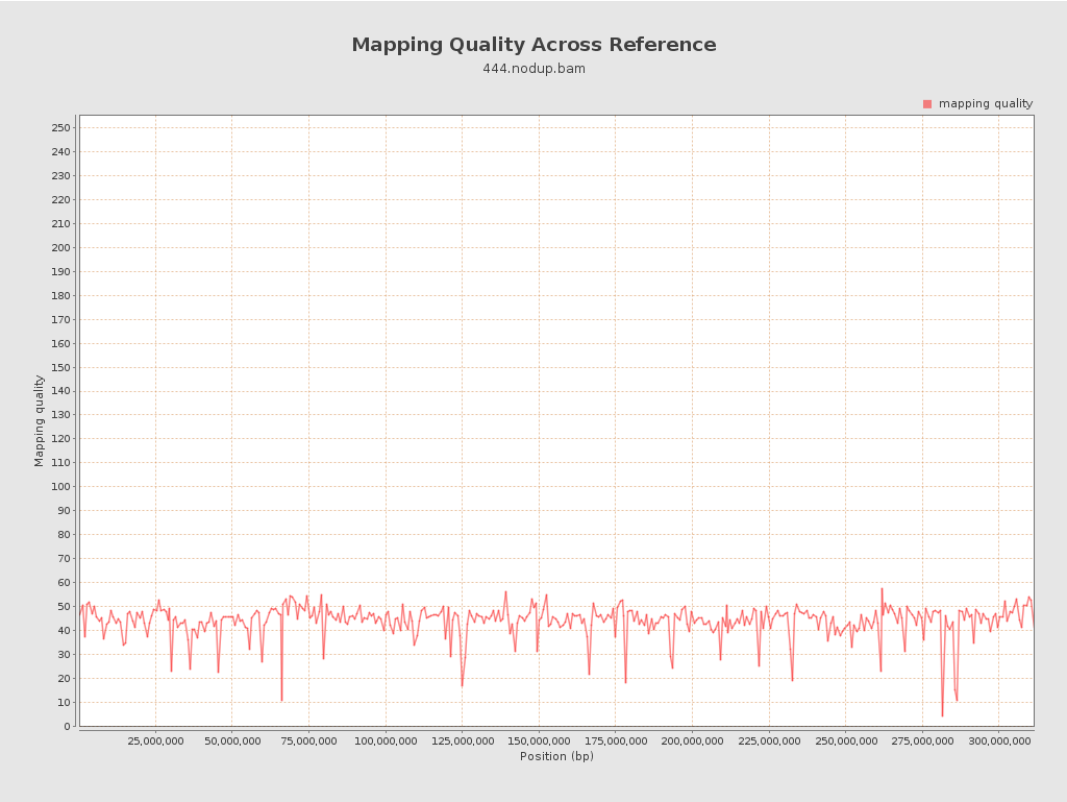
10. Results : Mapped Reads Clipping Profile



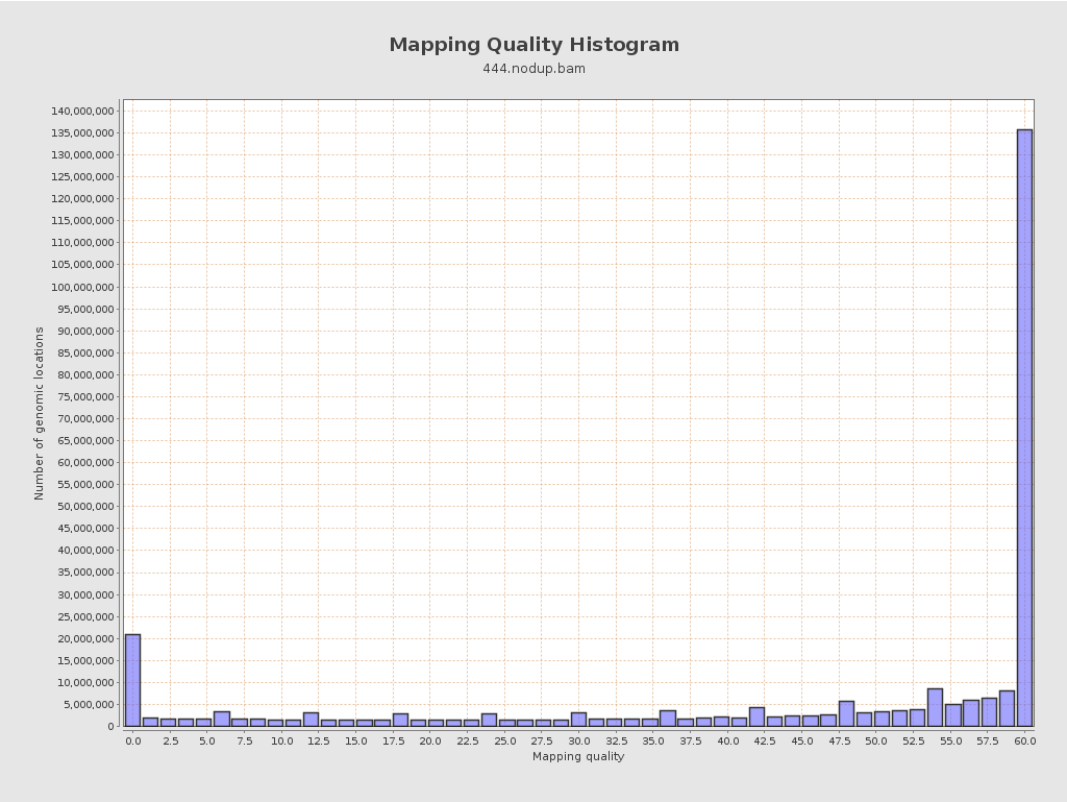
11. Results : Homopolymer Indels



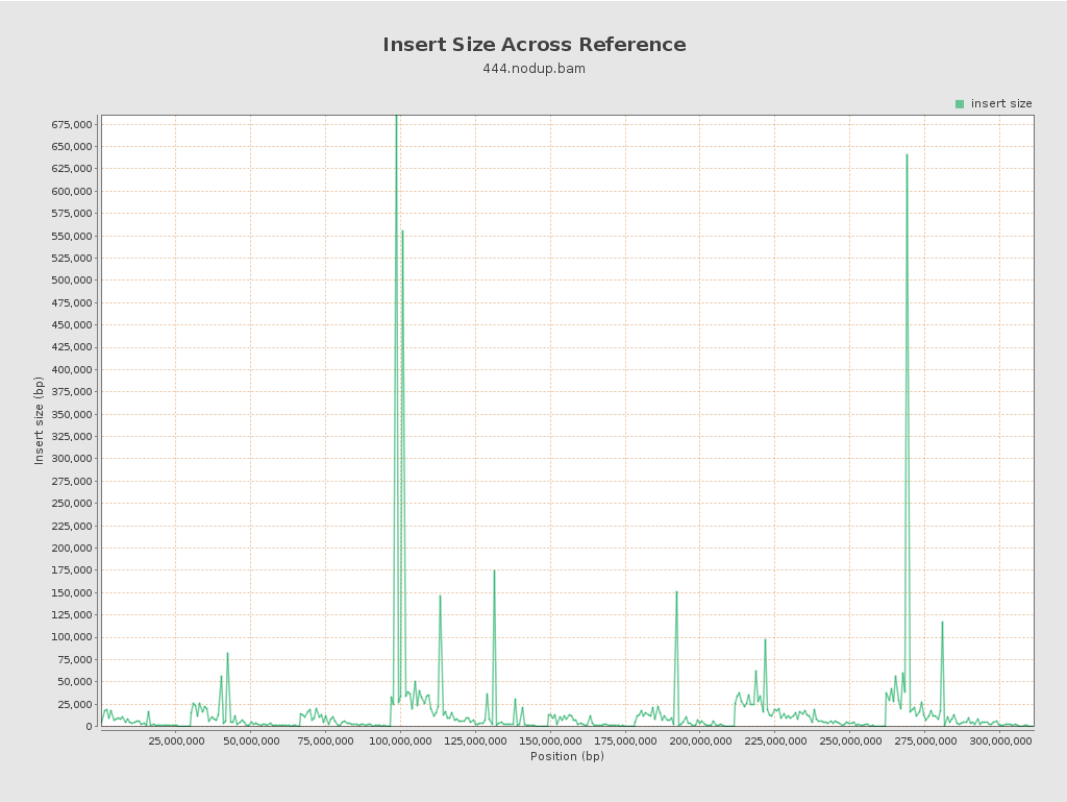
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram