Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:32:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/440.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/440.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_223/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_223_S304_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_223/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_223_S304_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:32:58 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	68,824,939
Mapped reads	64,067,091 / 93.09%
Unmapped reads	4,757,848 / 6.91%
Mapped paired reads	64,067,091 / 93.09%
Mapped reads, first in pair	32,094,433 / 46.63%
Mapped reads, second in pair	31,972,658 / 46.46%
Mapped reads, both in pair	62,651,402 / 91.03%
Mapped reads, singletons	1,415,689 / 2.06%
Read min/max/mean length	30 / 151 / 148.21
Duplicated reads (flagged)	9,576,883 / 13.91%
Clipped reads	14,254,650 / 20.71%

2.2. ACGT Content

Number/percentage of A's	2,742,519,868 / 30.87%
Number/percentage of C's	1,702,278,619 / 19.16%
Number/percentage of T's	2,742,290,400 / 30.86%
Number/percentage of G's	1,698,110,751 / 19.11%
Number/percentage of N's	33,569 / 0%
GC Percentage	38.27%

2.3. Coverage

Mean	28.5846
Standard Deviation	233.5608

2.4. Mapping Quality

Mean Mapping Quality	44.36

2.5. Insert size

Mean	227,107.5
Standard Deviation	2,261,713.03
P25/Median/P75	322 / 421 / 545

2.6. Mismatches and indels

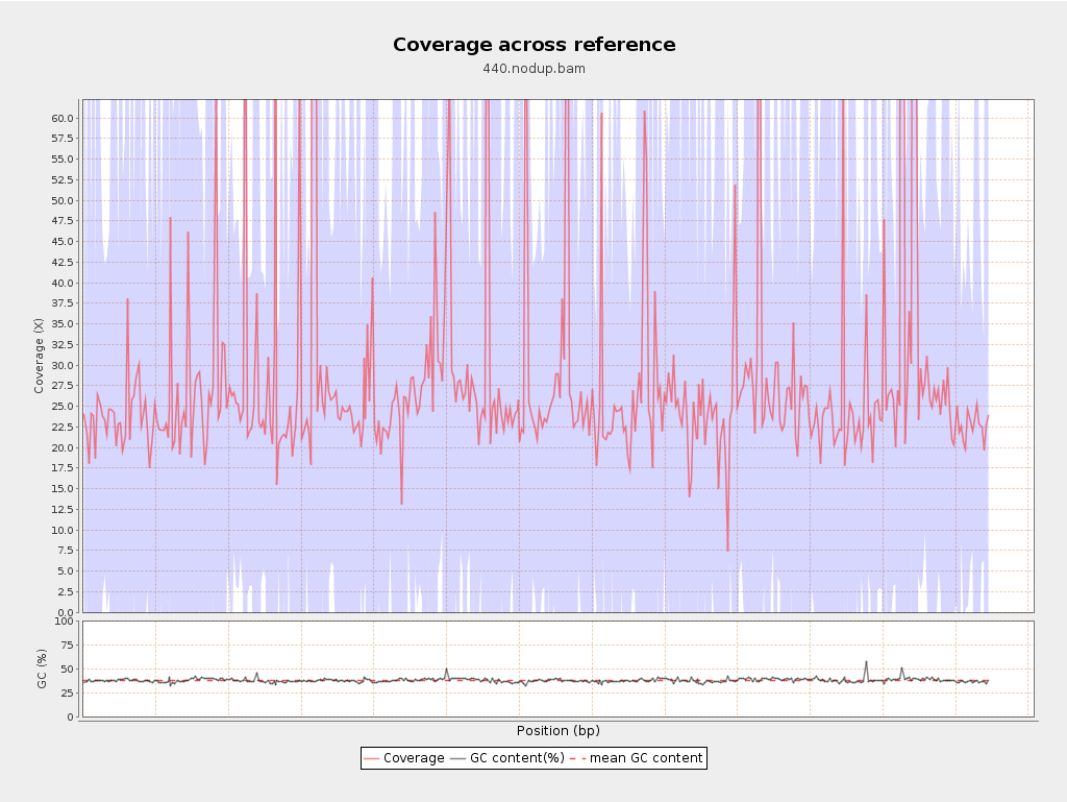
General error rate	2.29%
Mismatches	186,578,696
Insertions	5,973,391
Mapped reads with at least one insertion	8.37%
Deletions	6,039,463
Mapped reads with at least one deletion	8.39%
Homopolymer indels	56.71%

2.7. Chromosome stats

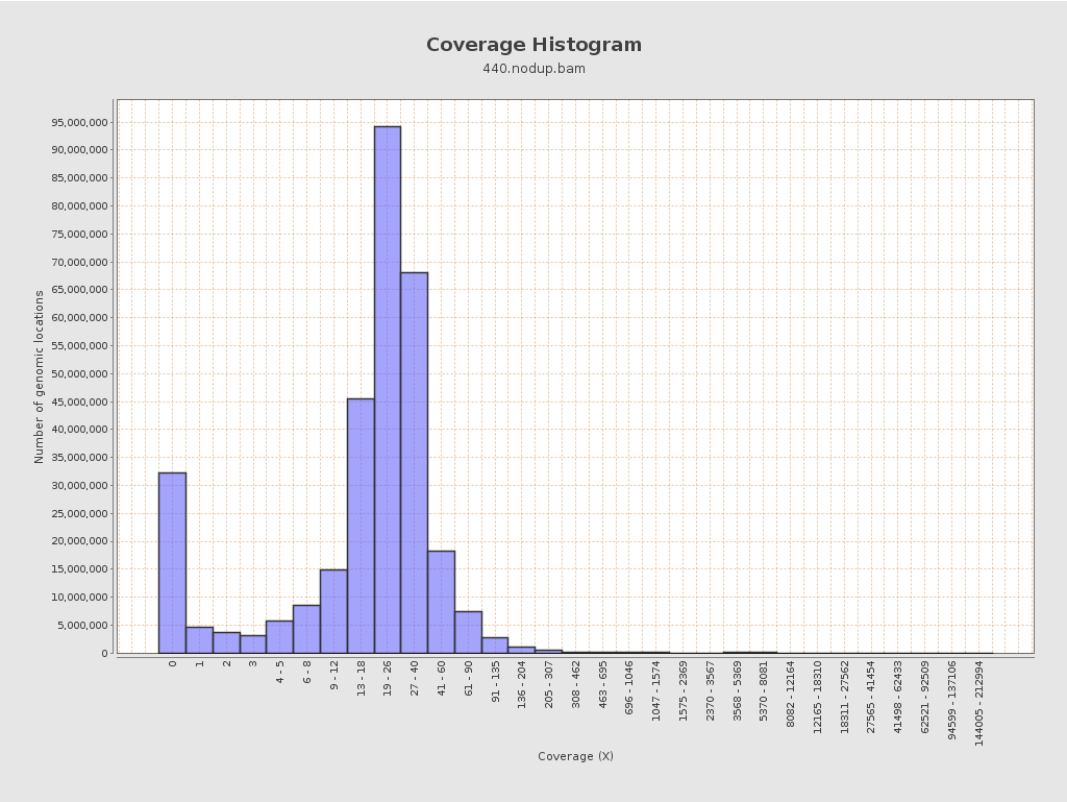
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	699377154	23.5288	65.5576

LT669789.1	36598175	1034554686	28.2679	214.8938
LT669790.1	30422129	955844105	31.4194	256.0546
LT669791.1	52758100	1495295148	28.3425	200.9973
LT669792.1	28376109	804376735	28.347	274.3667
LT669793.1	33388210	872311896	26.1263	119.8897
LT669794.1	50579949	1352959912	26.7489	189.7451
LT669795.1	49795044	1693450354	34.0084	364.5217

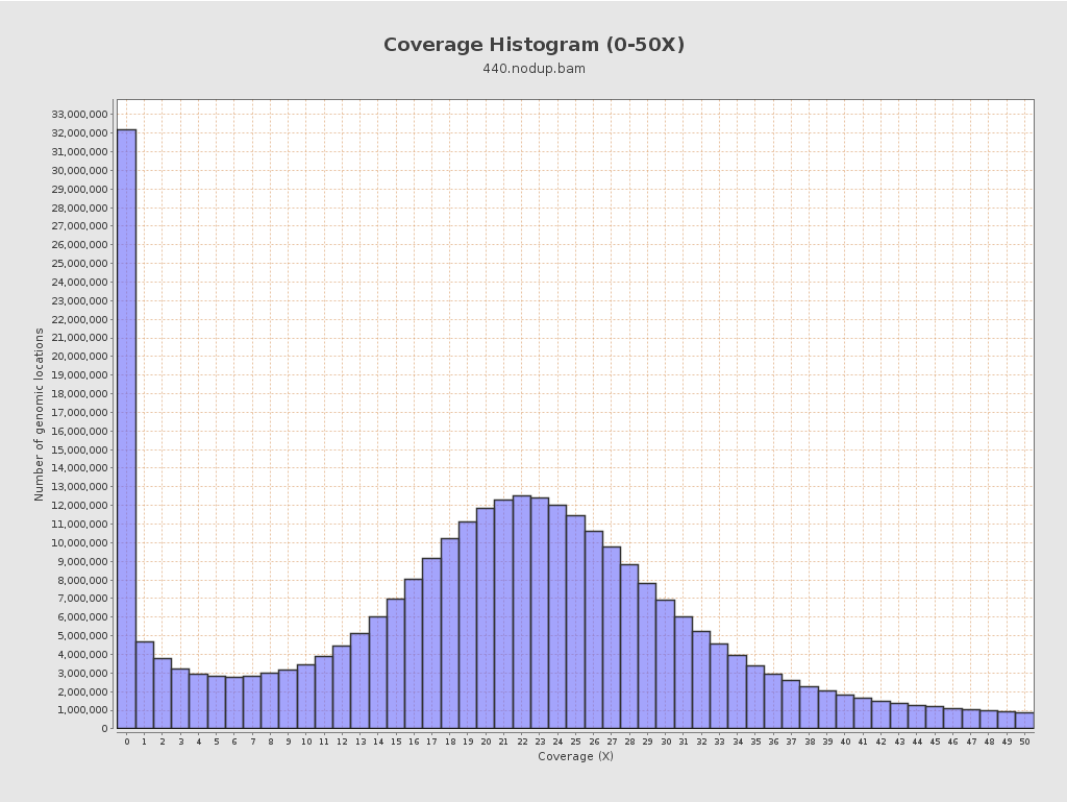
3. Results : Coverage across reference



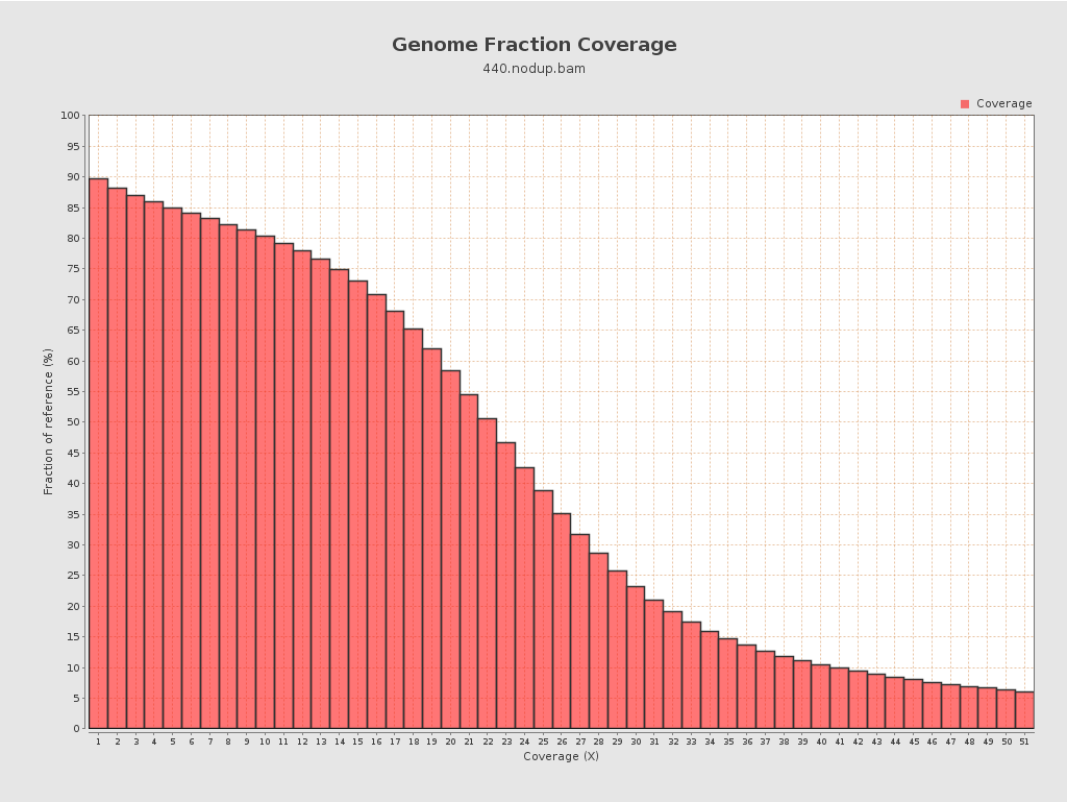
4. Results : Coverage Histogram



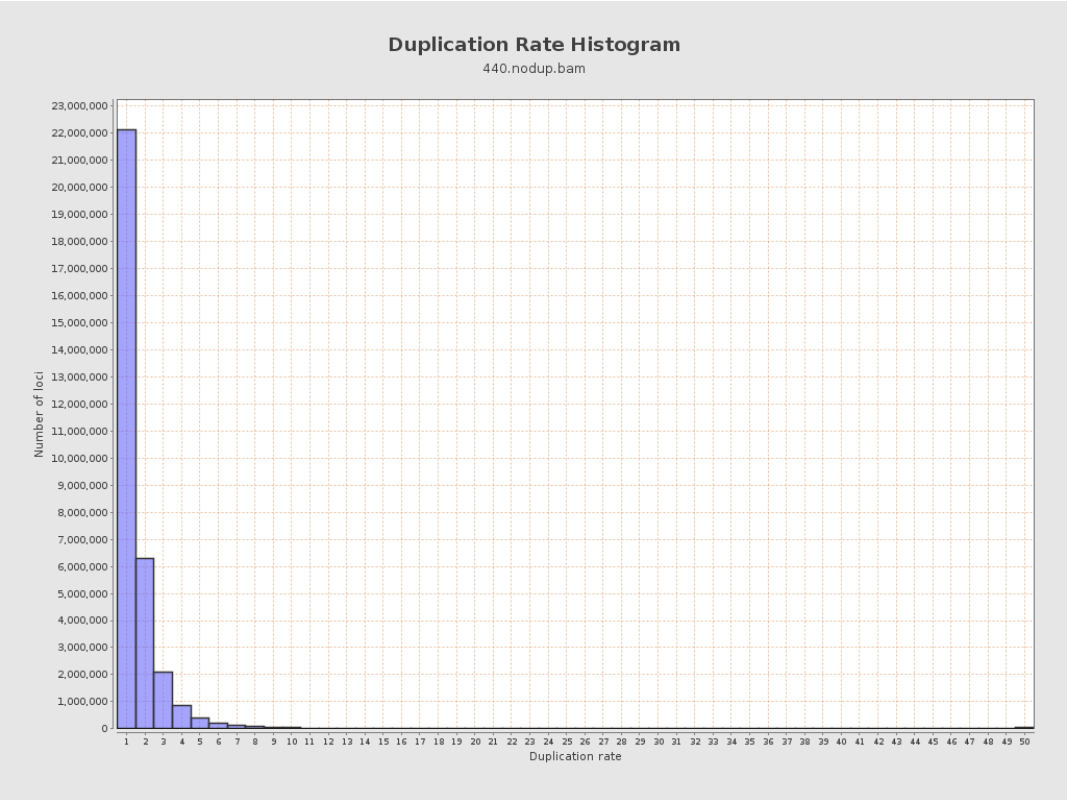
5. Results : Coverage Histogram (0-50X)



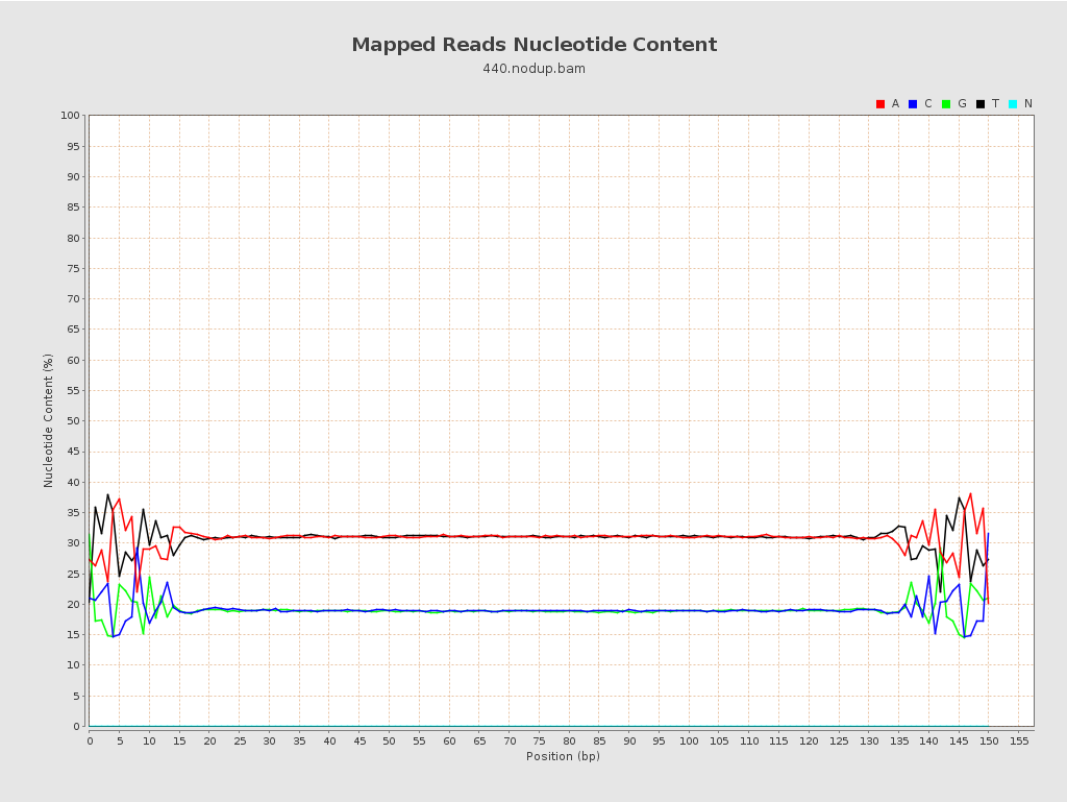
6. Results : Genome Fraction Coverage



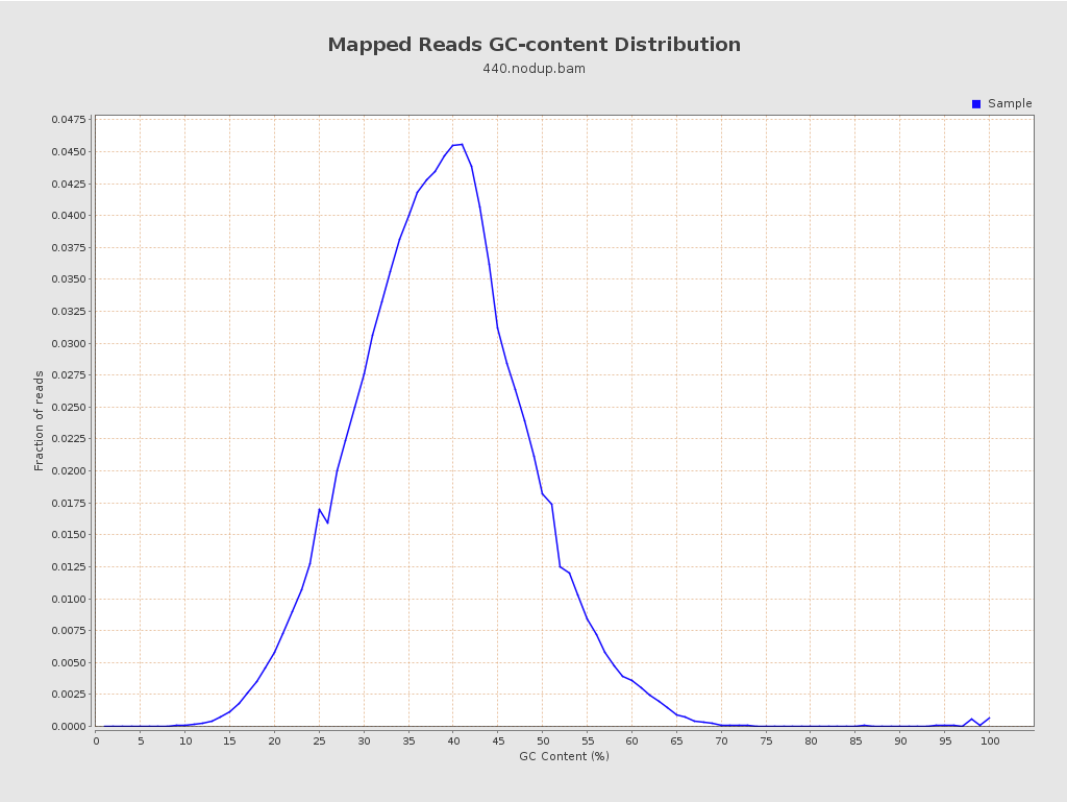
7. Results : Duplication Rate Histogram



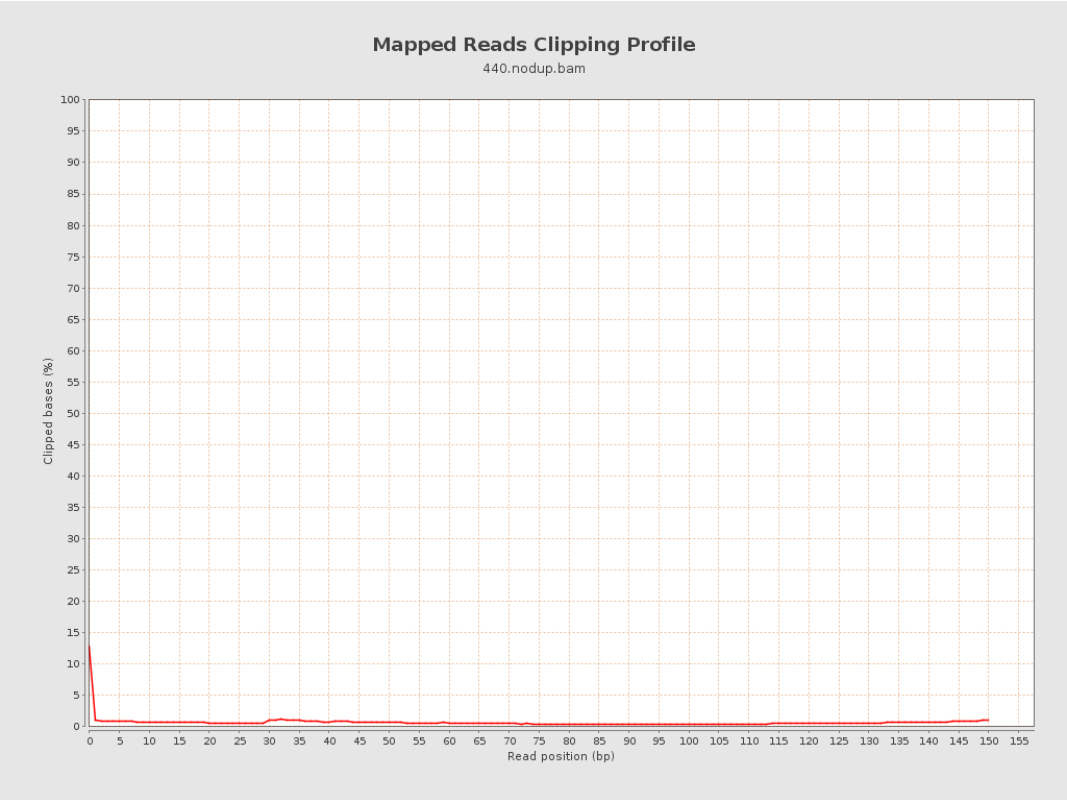
8. Results : Mapped Reads Nucleotide Content



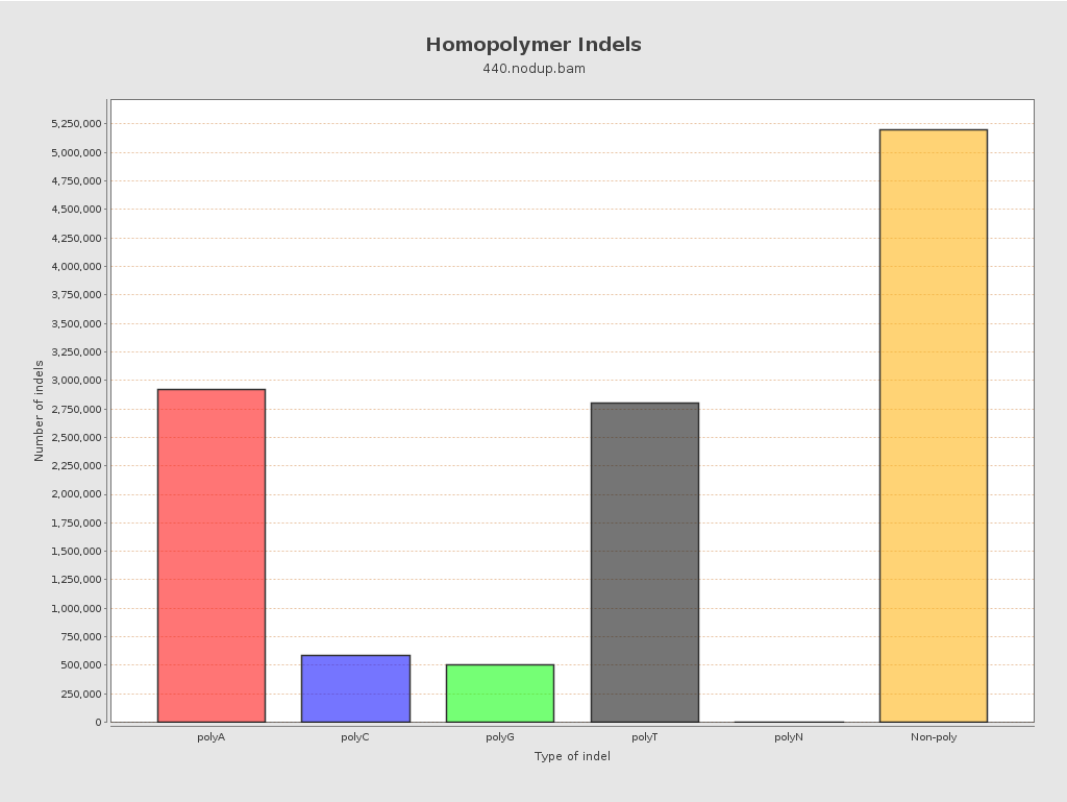
9. Results : Mapped Reads GC-content Distribution



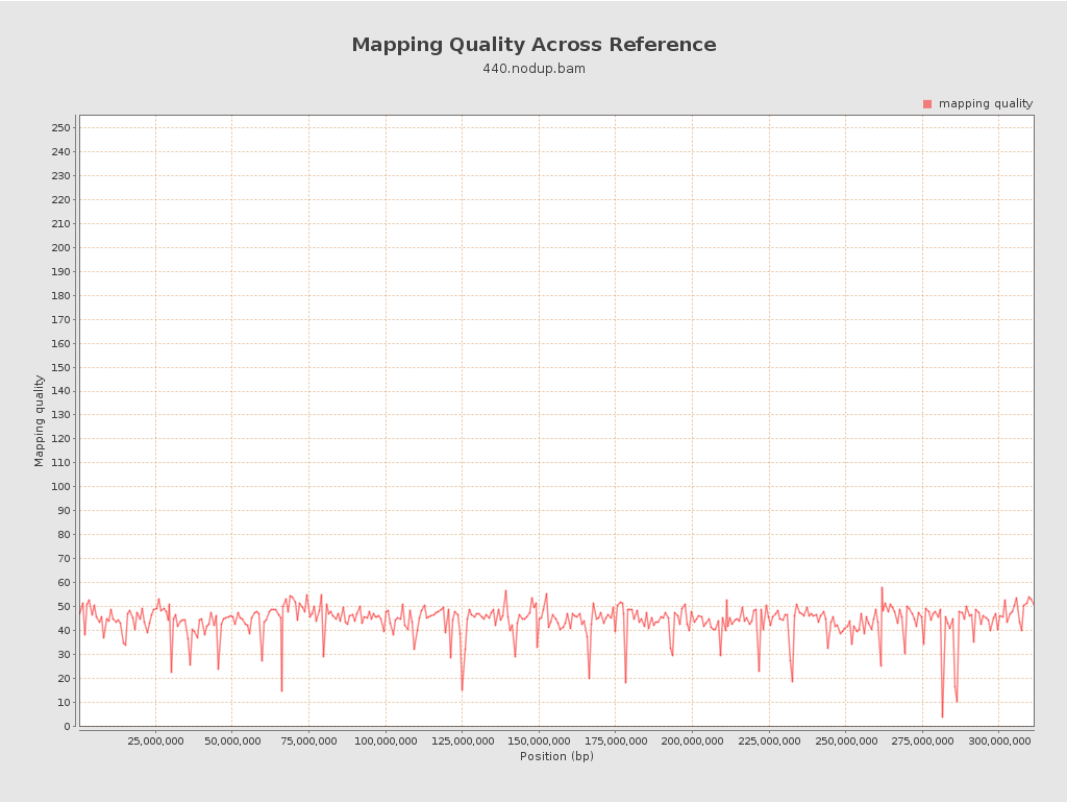
10. Results : Mapped Reads Clipping Profile



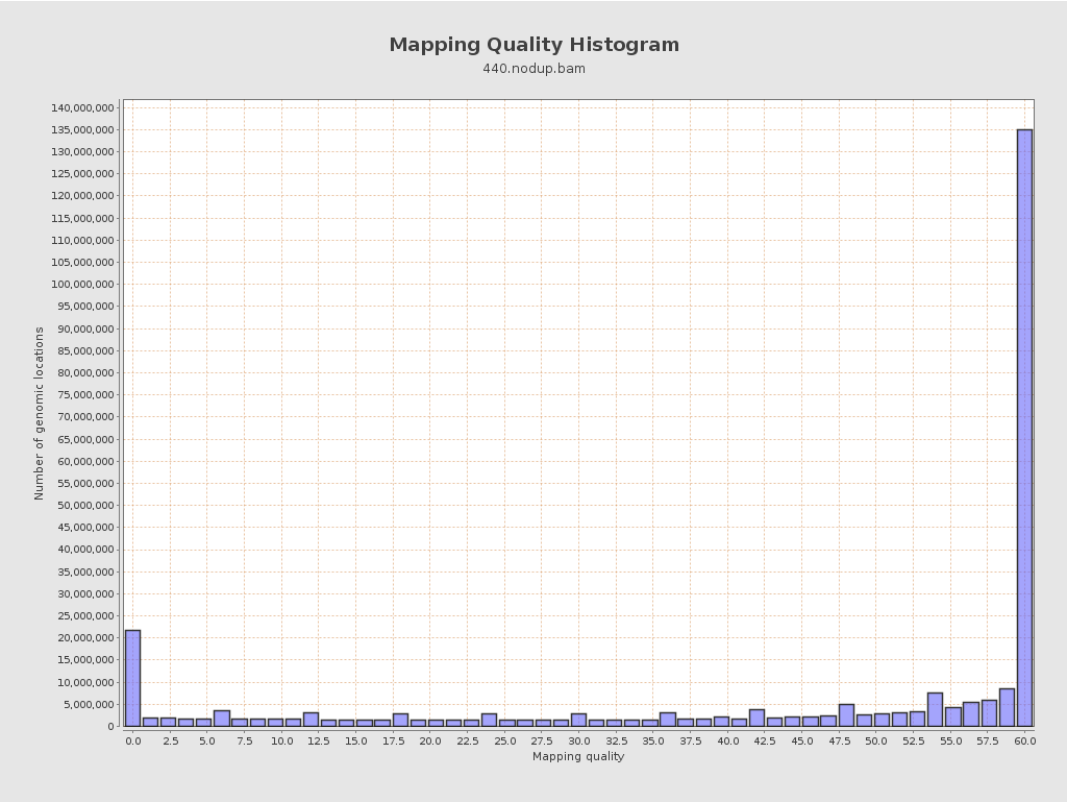
11. Results : Homopolymer Indels



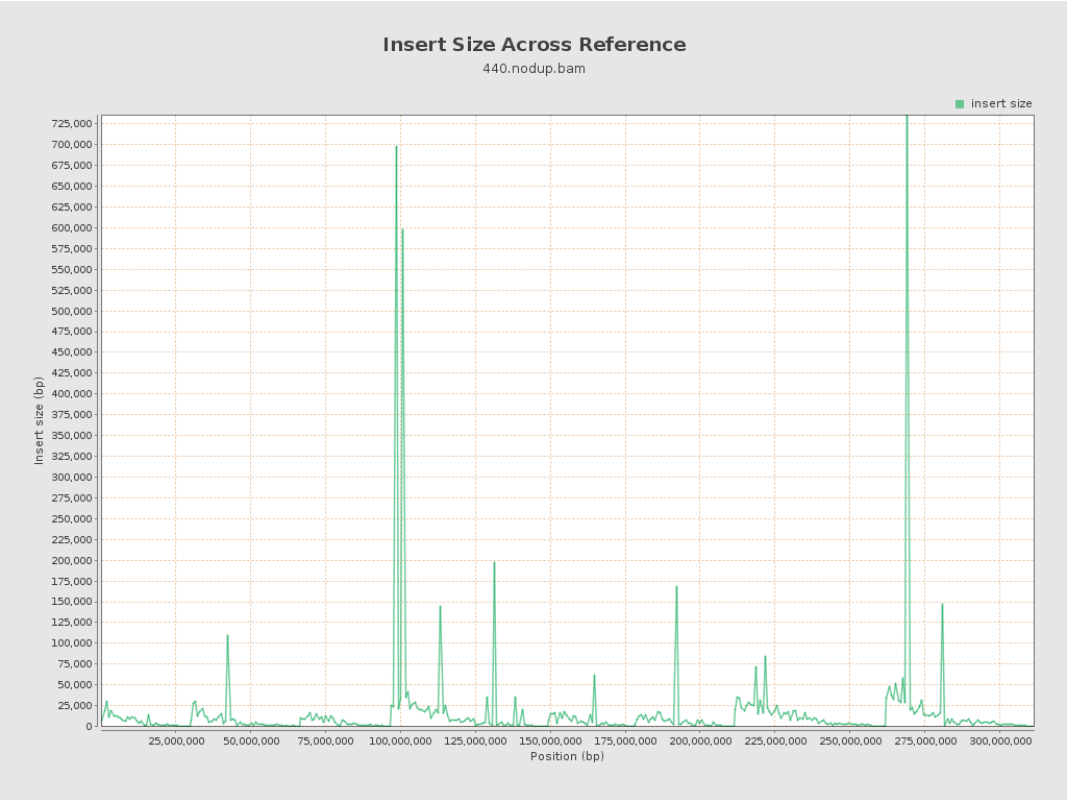
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram