Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:34:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/445.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/445.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_134/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_134_S224_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_134/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_134_S224_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:34:18 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	79,262,622
Mapped reads	72,802,379 / 91.85%
Unmapped reads	6,460,243 / 8.15%
Mapped paired reads	72,802,379 / 91.85%
Mapped reads, first in pair	36,491,434 / 46.04%
Mapped reads, second in pair	36,310,945 / 45.81%
Mapped reads, both in pair	70,750,824 / 89.26%
Mapped reads, singletons	2,051,555 / 2.59%
Read min/max/mean length	30 / 151 / 148.22
Duplicated reads (flagged)	13,683,062 / 17.26%
Clipped reads	16,530,883 / 20.86%

2.2. ACGT Content

Number/percentage of A's	3,112,638,140 / 30.95%
Number/percentage of C's	1,916,933,037 / 19.06%
Number/percentage of T's	3,113,153,108 / 30.95%
Number/percentage of G's	1,915,036,561 / 19.04%
Number/percentage of N's	41,749 / 0%
GC Percentage	38.1%

2.3. Coverage

Mean	32.3566
Standard Deviation	268.7174

2.4. Mapping Quality

Mean Mapping Quality	44.44

2.5. Insert size

Mean	246,746.36
Standard Deviation	2,378,509.98
P25/Median/P75	341 / 445 / 585

2.6. Mismatches and indels

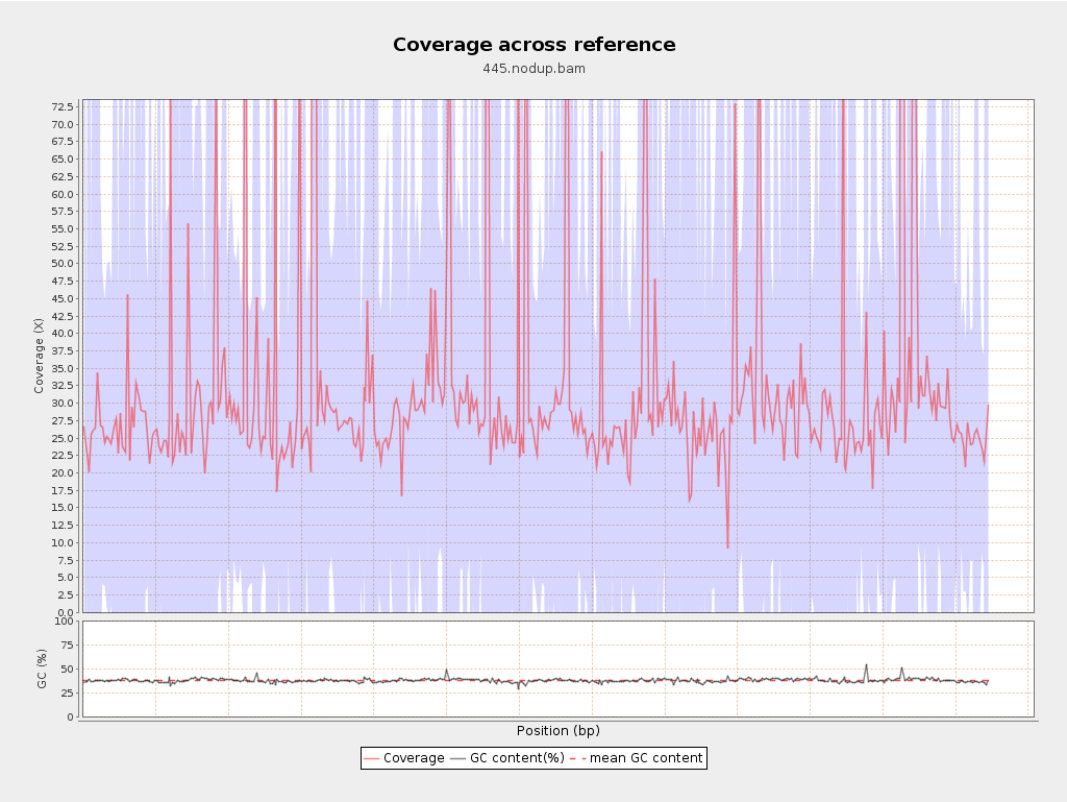
General error rate	2.35%
Mismatches	216,545,918
Insertions	7,024,004
Mapped reads with at least one insertion	8.63%
Deletions	6,952,766
Mapped reads with at least one deletion	8.49%
Homopolymer indels	57.08%

2.7. Chromosome stats

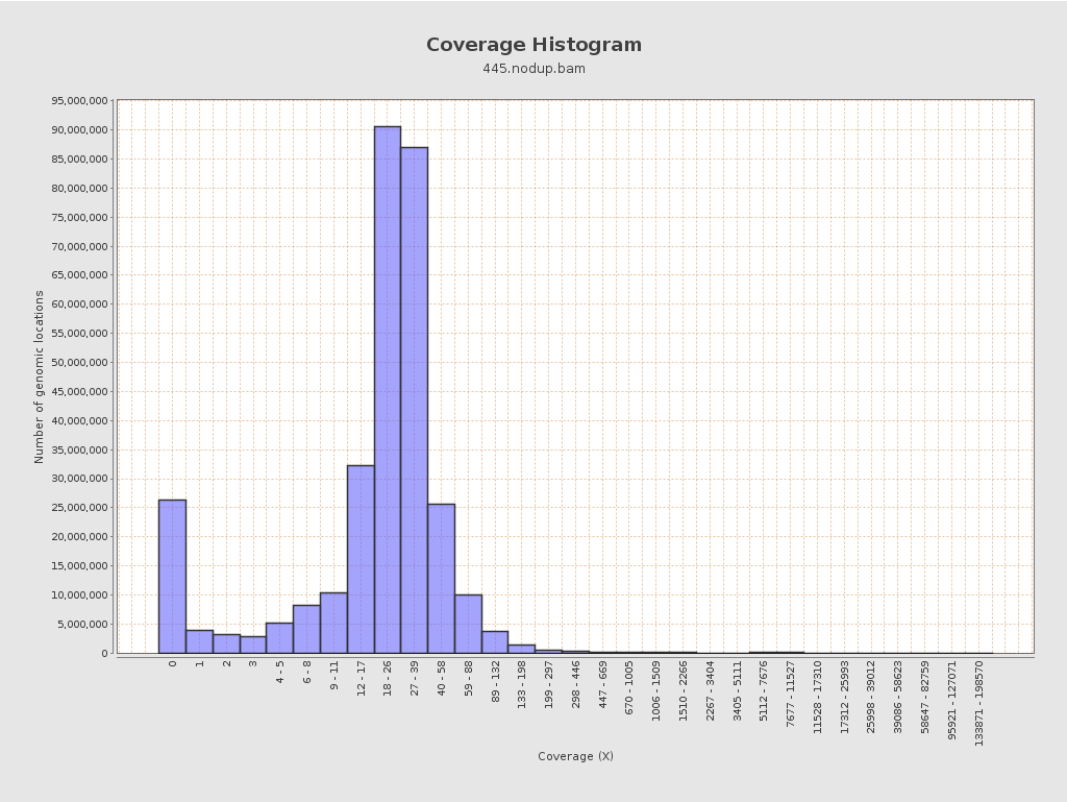
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	784550776	26.3942	94.3581

LT669789.1	36598175	1208267194	33.0144	295.1895
LT669790.1	30422129	1112386966	36.5651	343.9971
LT669791.1	52758100	1695595097	32.139	268.9857
LT669792.1	28376109	917145483	32.321	304.7443
LT669793.1	33388210	1003915508	30.068	191.4186
LT669794.1	50579949	1560160468	30.8454	244.6346
LT669795.1	49795044	1801665321	36.1816	308.6659

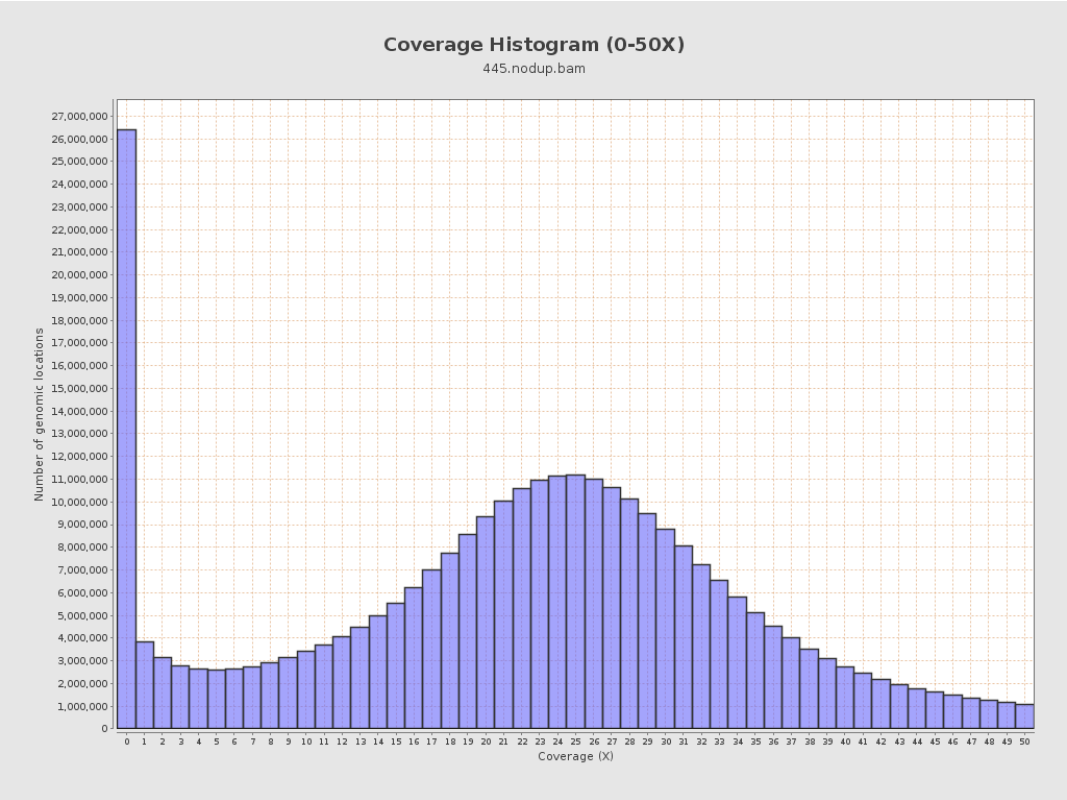
3. Results : Coverage across reference



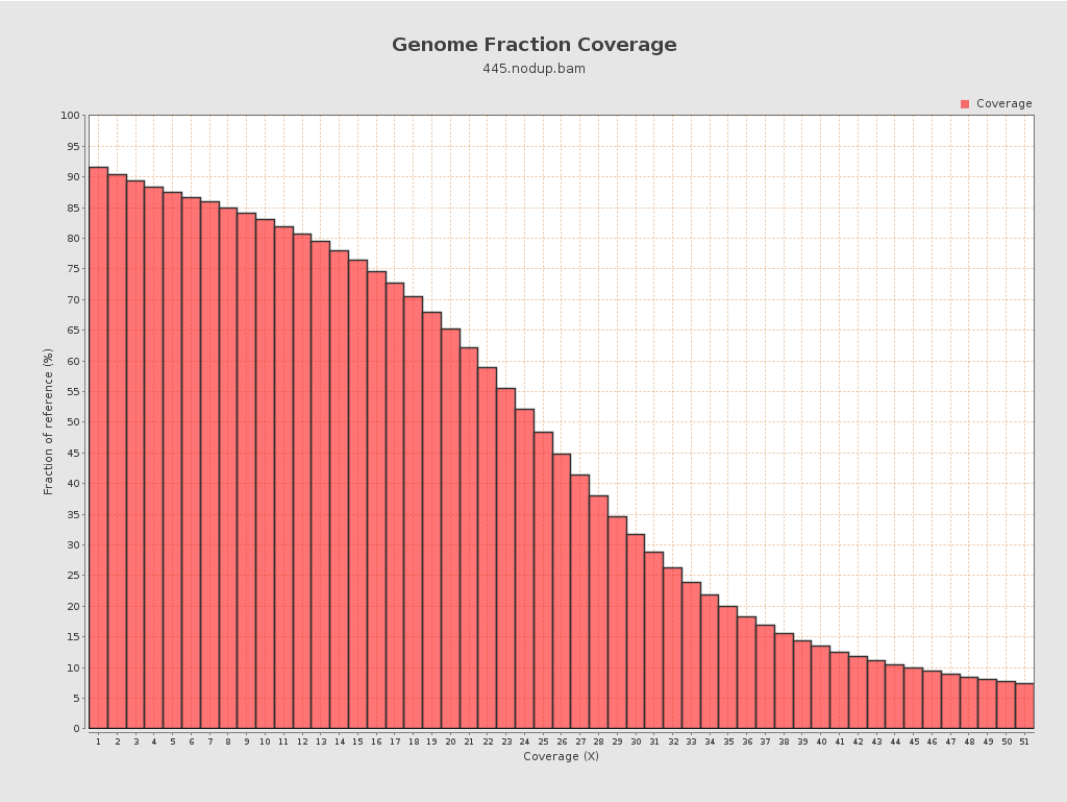
4. Results : Coverage Histogram



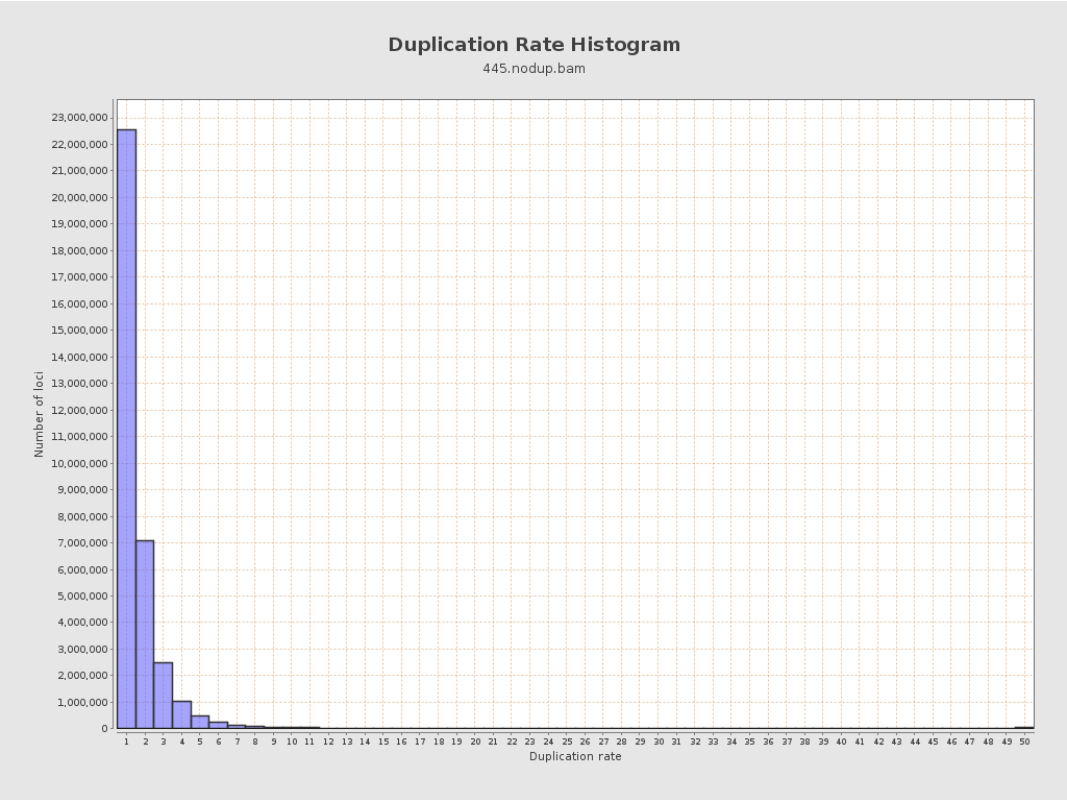
5. Results : Coverage Histogram (0-50X)



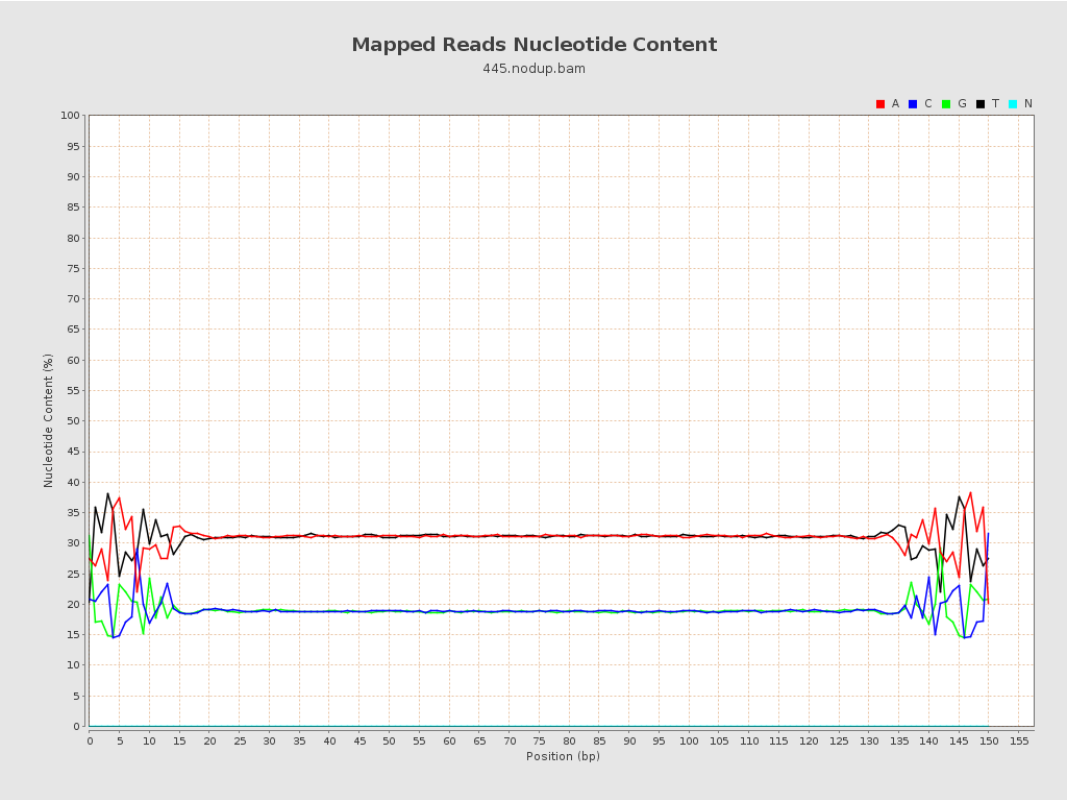
6. Results : Genome Fraction Coverage



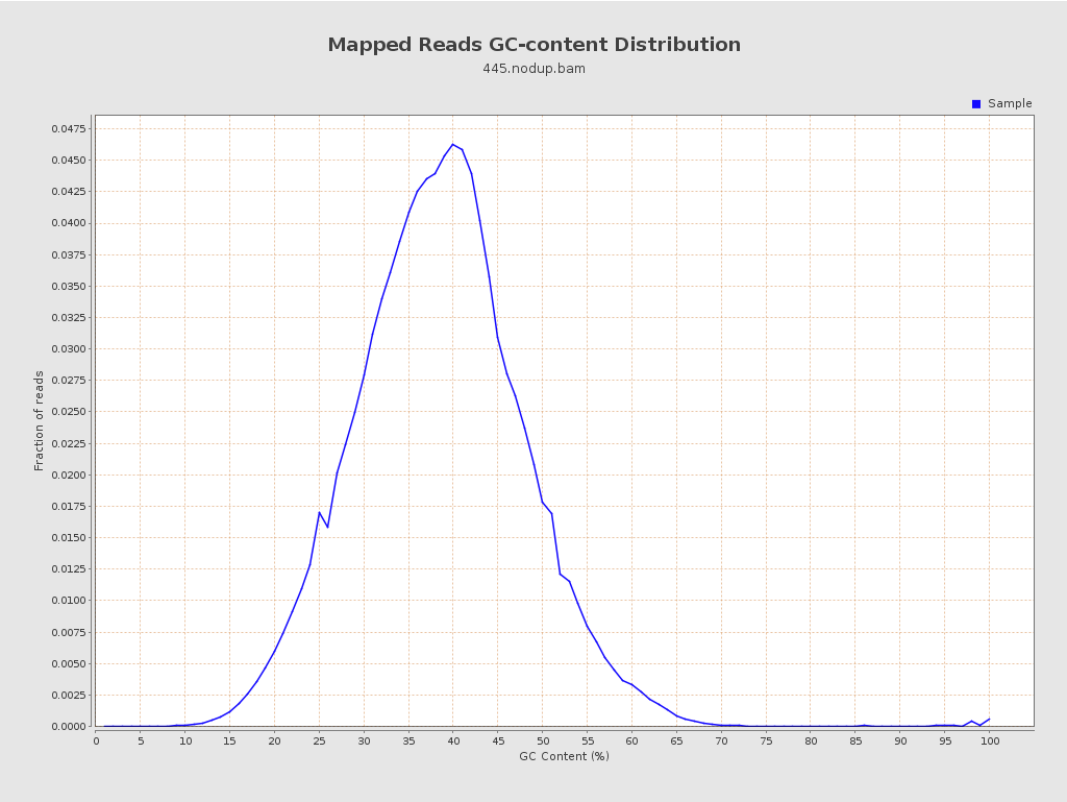
7. Results : Duplication Rate Histogram



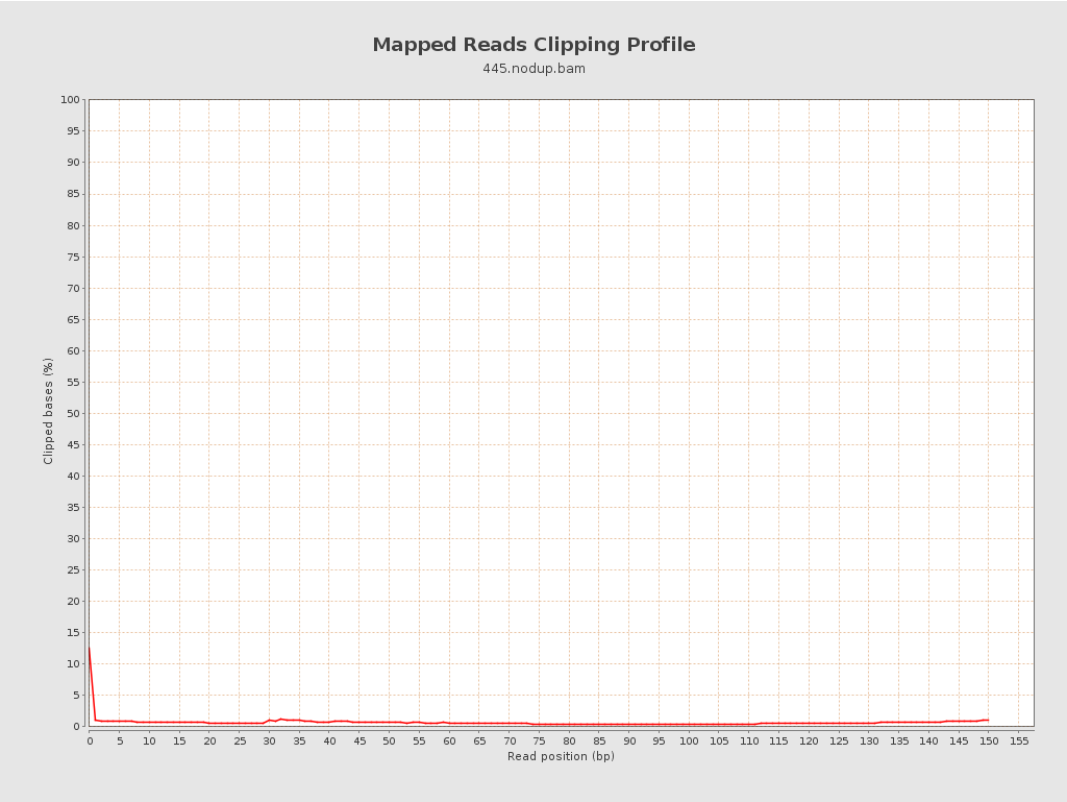
8. Results : Mapped Reads Nucleotide Content



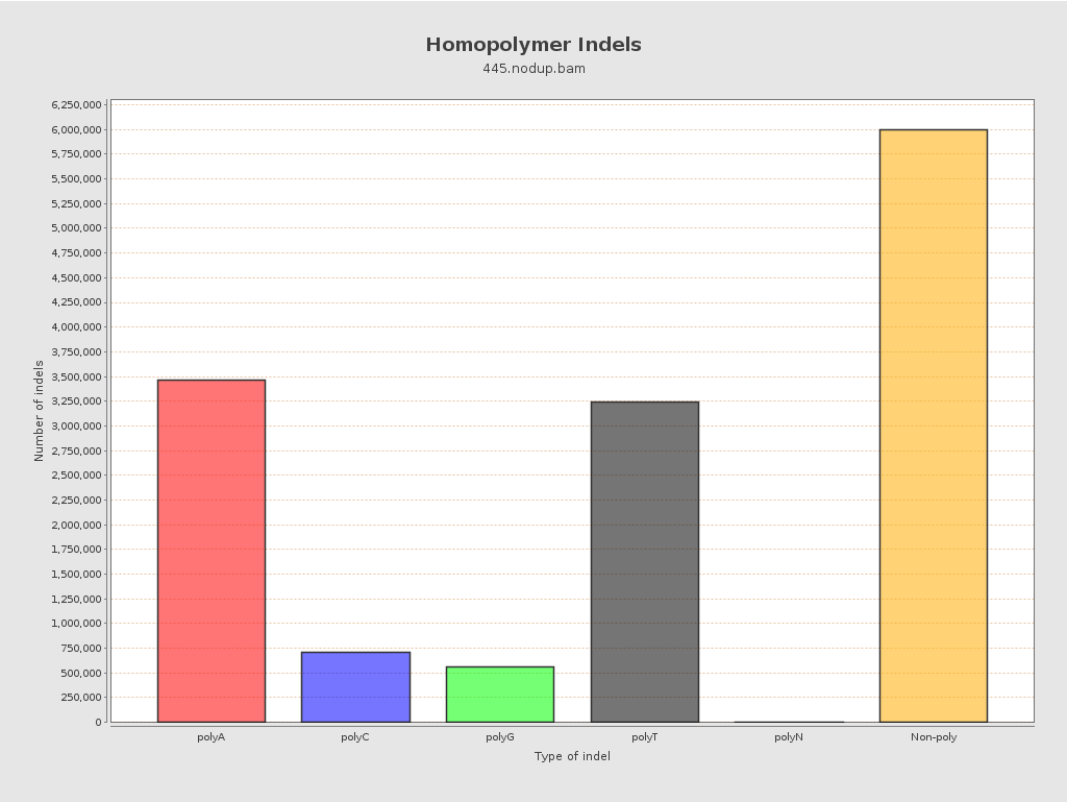
9. Results : Mapped Reads GC-content Distribution



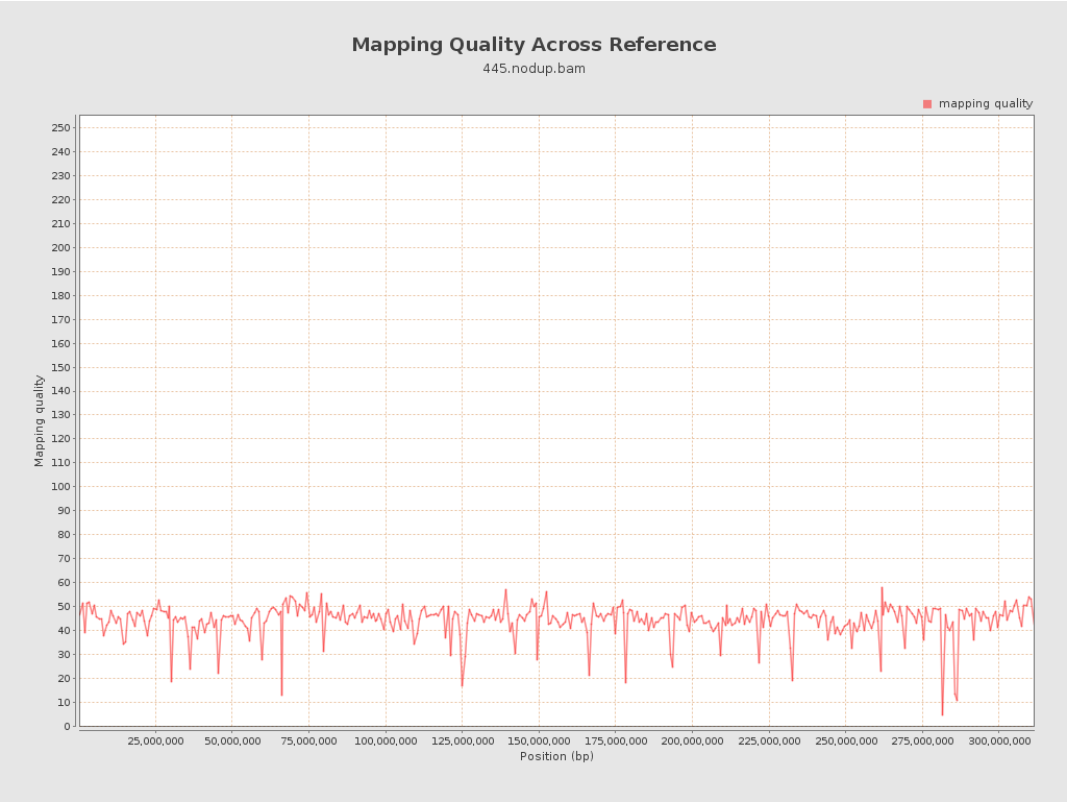
10. Results : Mapped Reads Clipping Profile



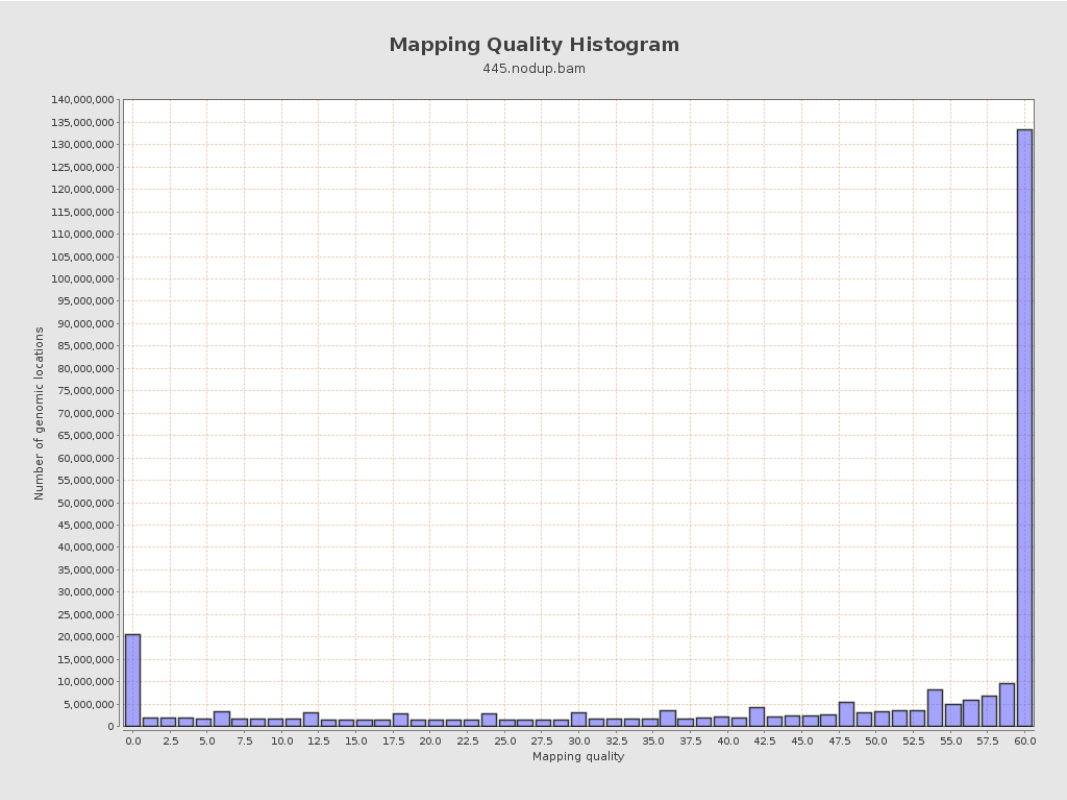
11. Results : Homopolymer Indels



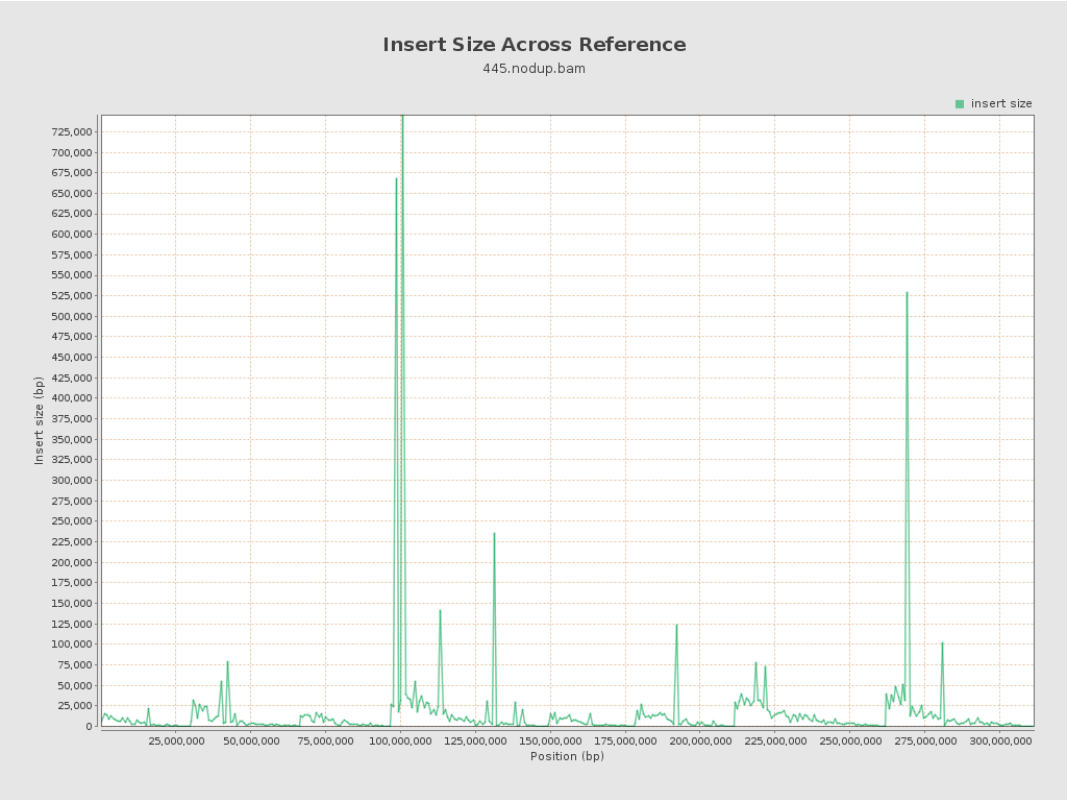
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram