Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:38:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/986.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/986.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_477/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_477_S452_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_477/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_477_S452_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:38:02 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	82,477,377
Mapped reads	77,317,975 / 93.74%
Unmapped reads	5,159,402 / 6.26%
Mapped paired reads	77,317,975 / 93.74%
Mapped reads, first in pair	38,752,022 / 46.99%
Mapped reads, second in pair	38,565,953 / 46.76%
Mapped reads, both in pair	75,673,433 / 91.75%
Mapped reads, singletons	1,644,542 / 1.99%
Read min/max/mean length	30 / 151 / 148.22
Duplicated reads (flagged)	13,693,677 / 16.6%
Clipped reads	16,720,342 / 20.27%

2.2. ACGT Content

Number/percentage of A's	3,309,337,447 / 30.74%
Number/percentage of C's	2,075,171,372 / 19.28%
Number/percentage of T's	3,313,299,005 / 30.78%
Number/percentage of G's	2,067,412,335 / 19.2%
Number/percentage of N's	36,875 / 0%
GC Percentage	38.48%

2.3. Coverage

Mean	34.6322
Standard Deviation	276.1653

2.4. Mapping Quality

Mean Mapping Quality	43.74

2.5. Insert size

Mean	244,801.73
Standard Deviation	2,350,412.4
P25/Median/P75	356 / 465 / 610

2.6. Mismatches and indels

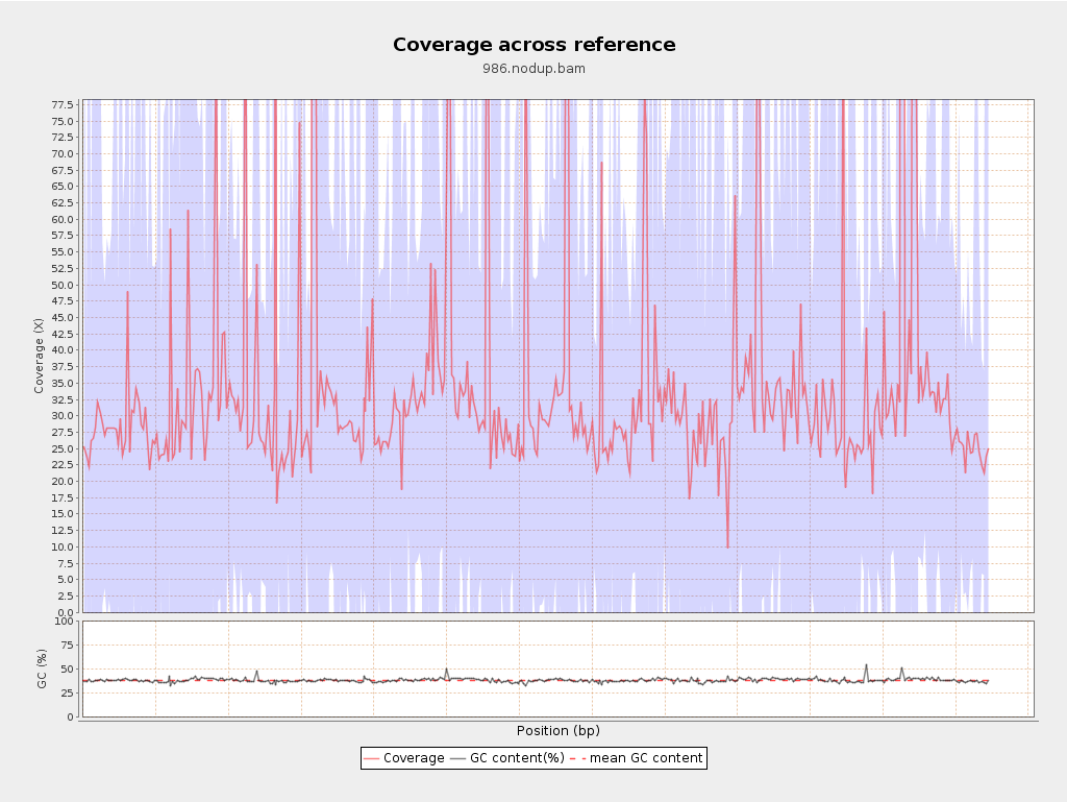
General error rate	2.31%
Mismatches	228,957,388
Insertions	7,186,837
Mapped reads with at least one insertion	8.35%
Deletions	7,295,431
Mapped reads with at least one deletion	8.38%
Homopolymer indels	56.23%

2.7. Chromosome stats

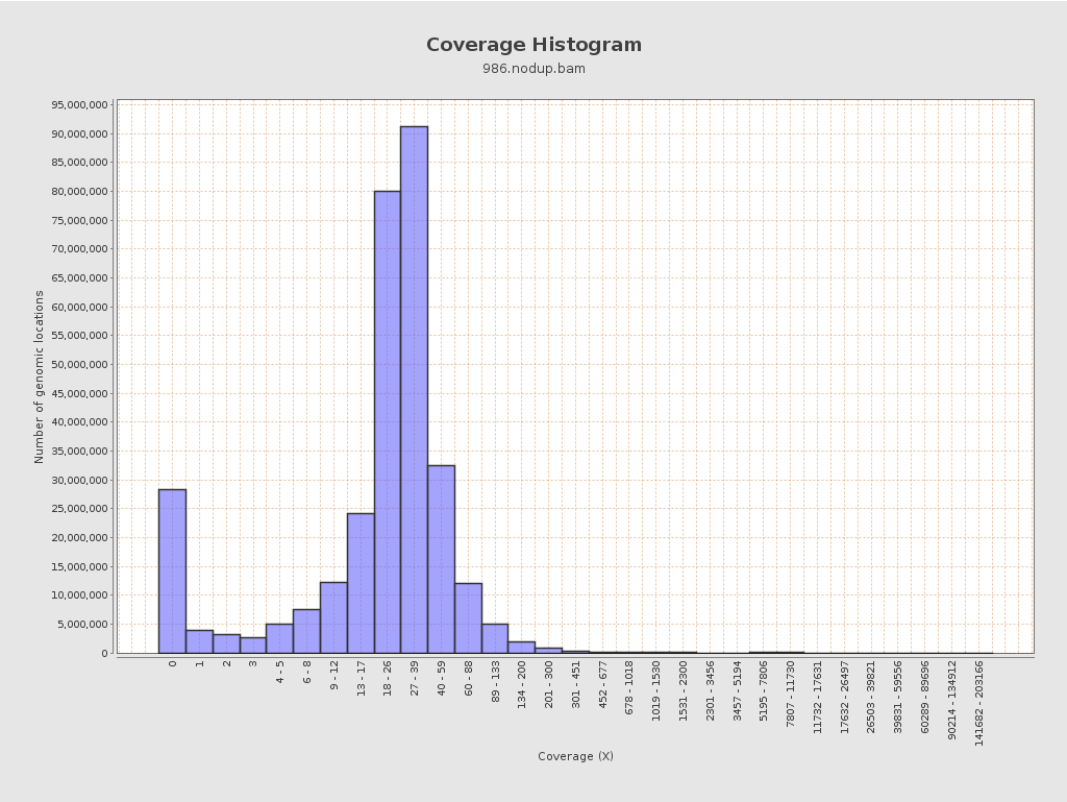
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	823756168	27.7132	82.9132

LT669789.1	36598175	1280911027	34.9993	293.3352
LT669790.1	30422129	1091354555	35.8737	263.4403
LT669791.1	52758100	1817345655	34.4468	247.2375
LT669792.1	28376109	961603926	33.8878	351.9931
LT669793.1	33388210	1054449096	31.5815	143.2442
LT669794.1	50579949	1718794290	33.9817	234.6508
LT669795.1	49795044	2044621366	41.0607	403.0376

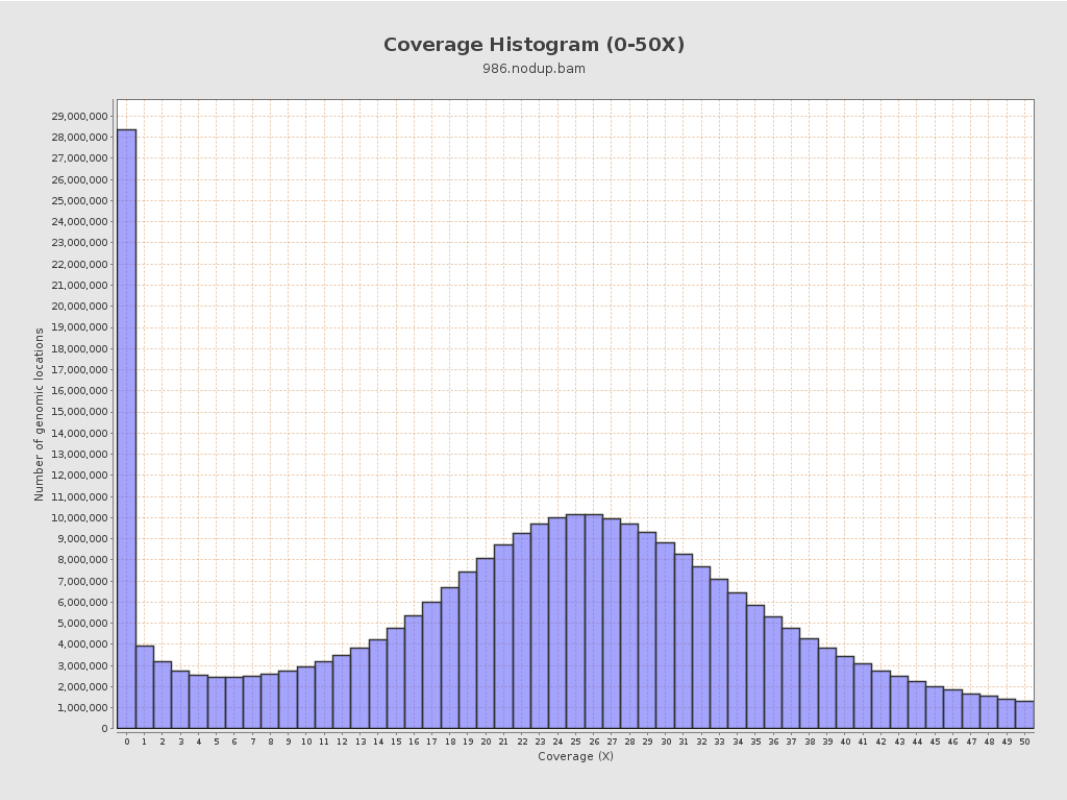
3. Results : Coverage across reference



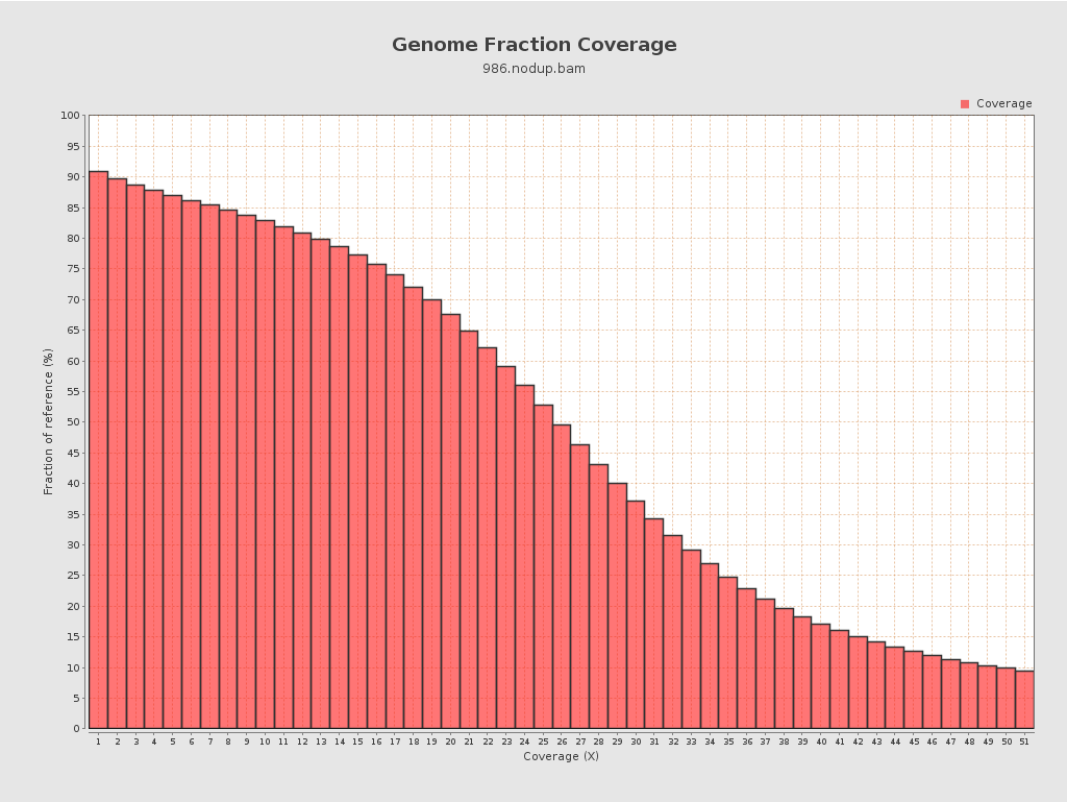
4. Results : Coverage Histogram



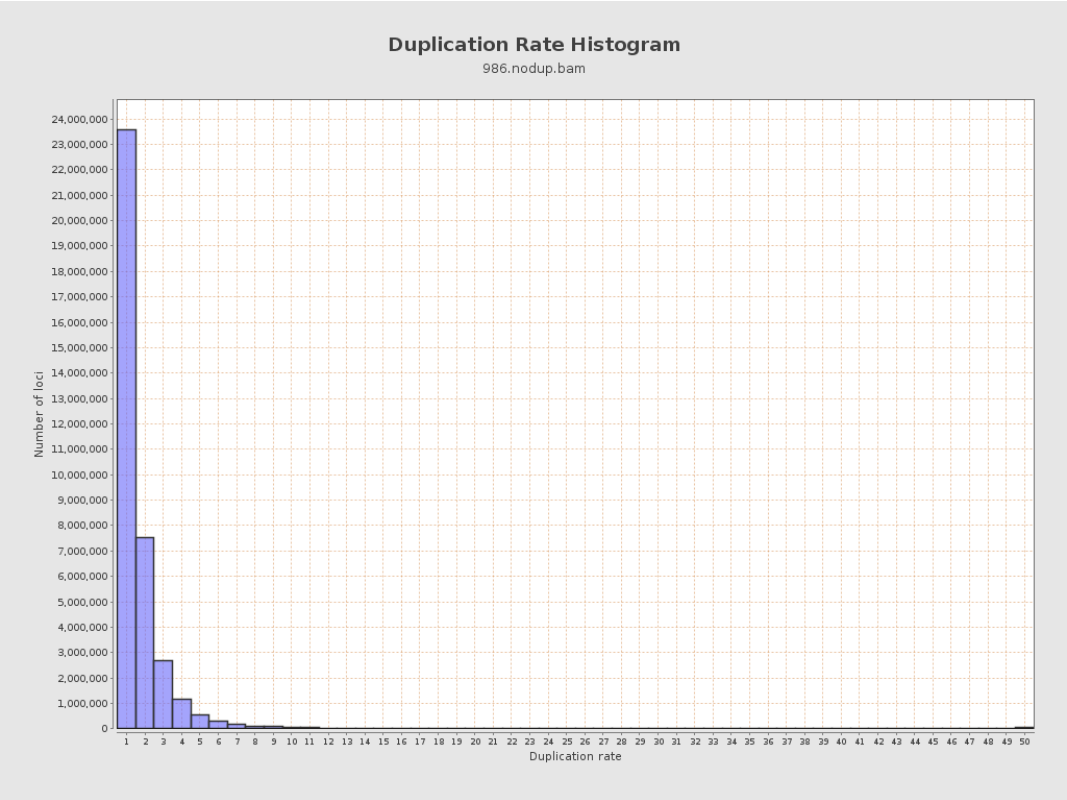
5. Results : Coverage Histogram (0-50X)



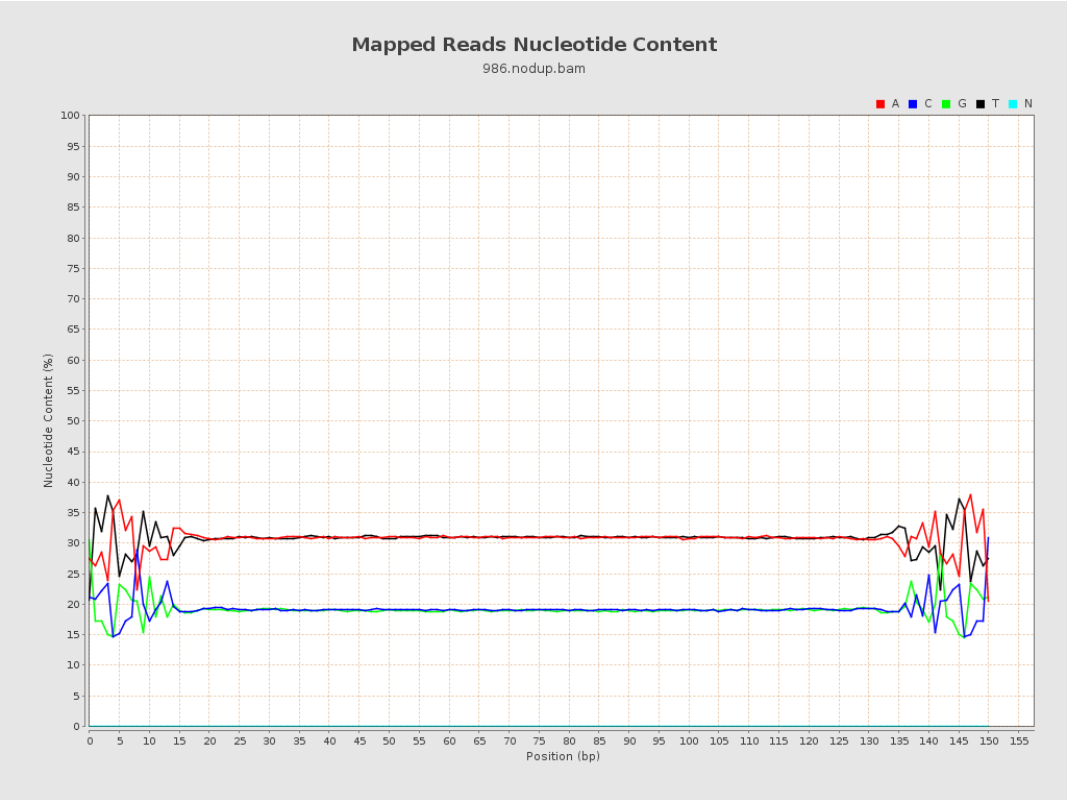
6. Results : Genome Fraction Coverage



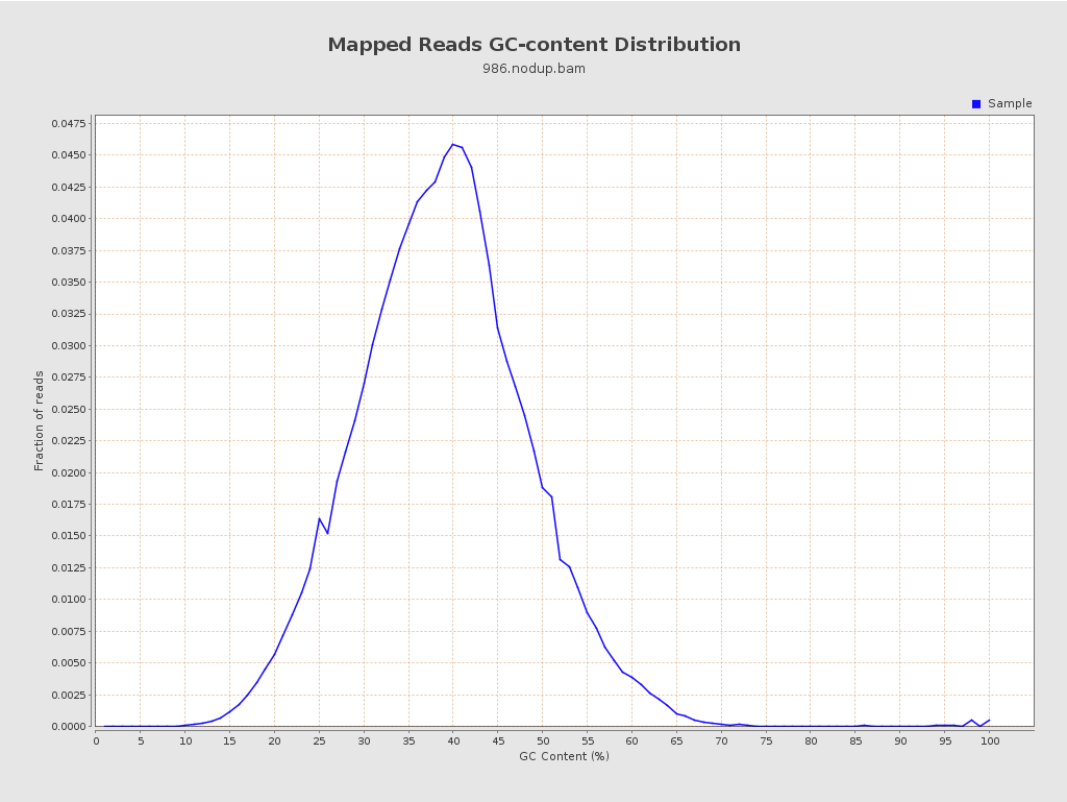
7. Results : Duplication Rate Histogram



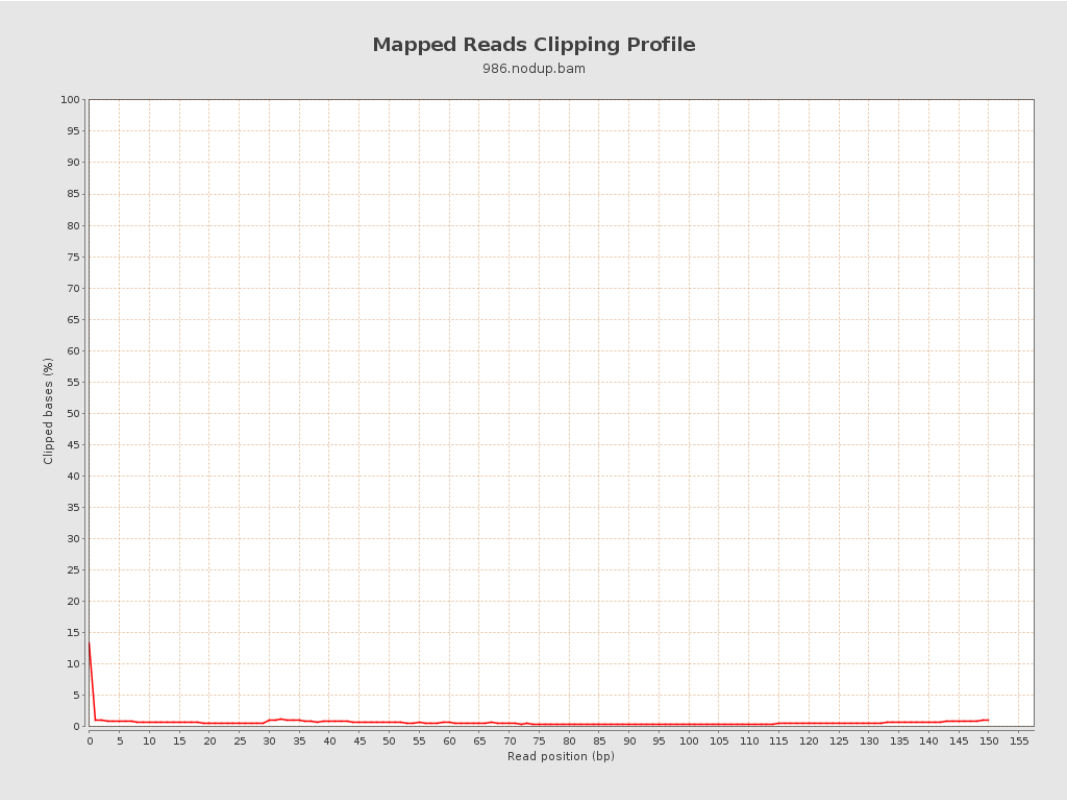
8. Results : Mapped Reads Nucleotide Content



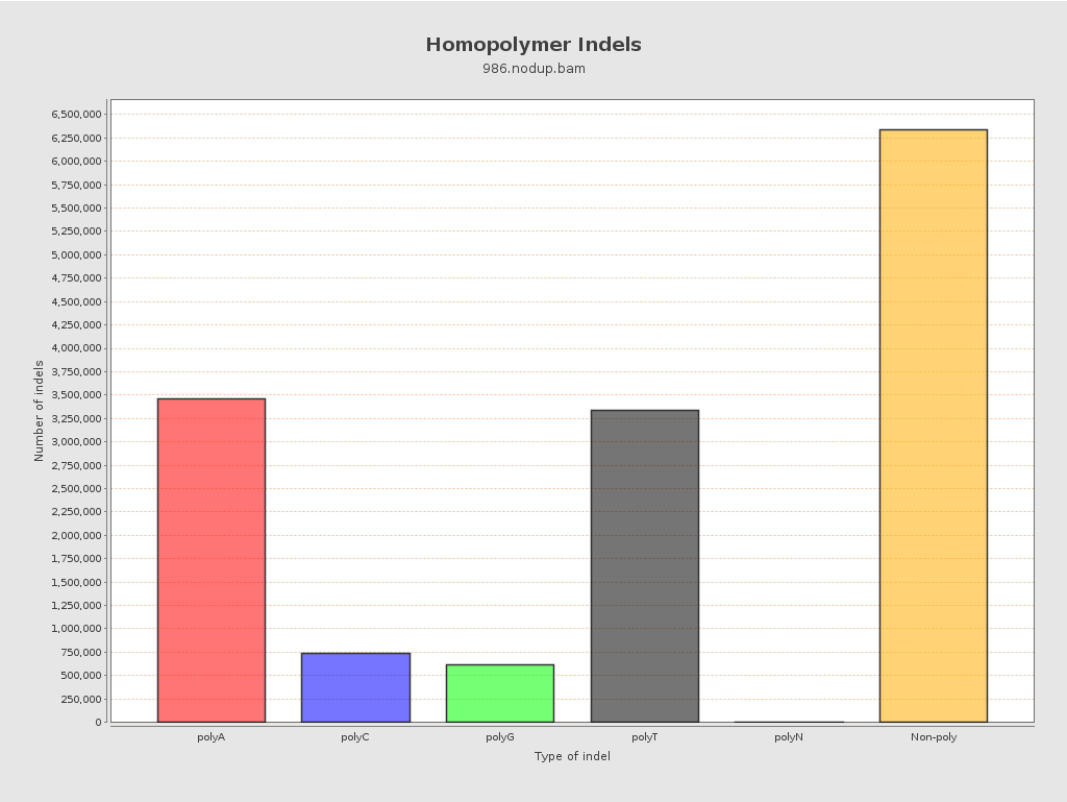
9. Results : Mapped Reads GC-content Distribution



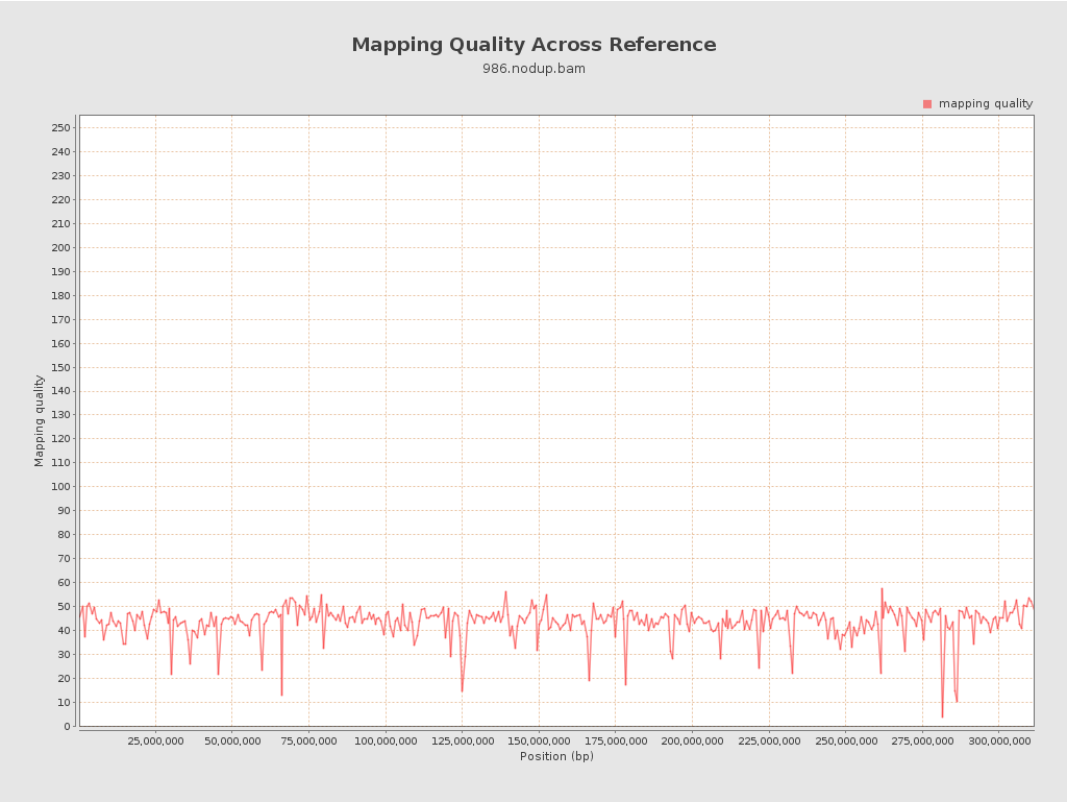
10. Results : Mapped Reads Clipping Profile



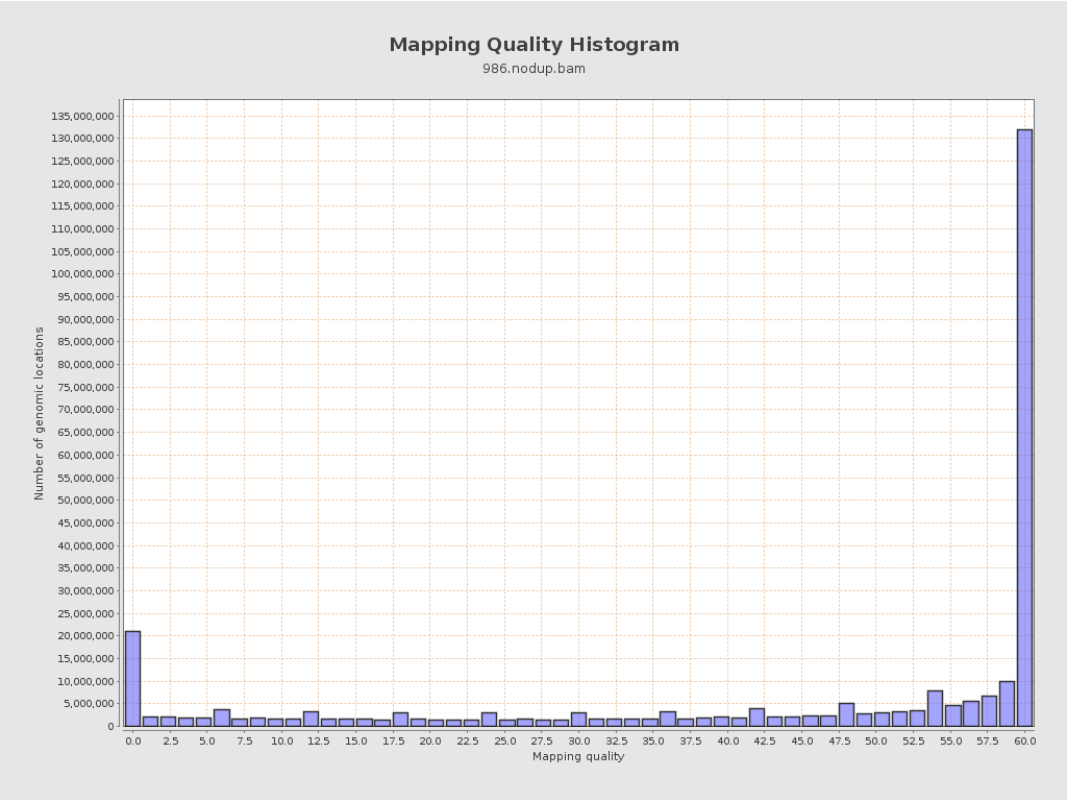
11. Results : Homopolymer Indels



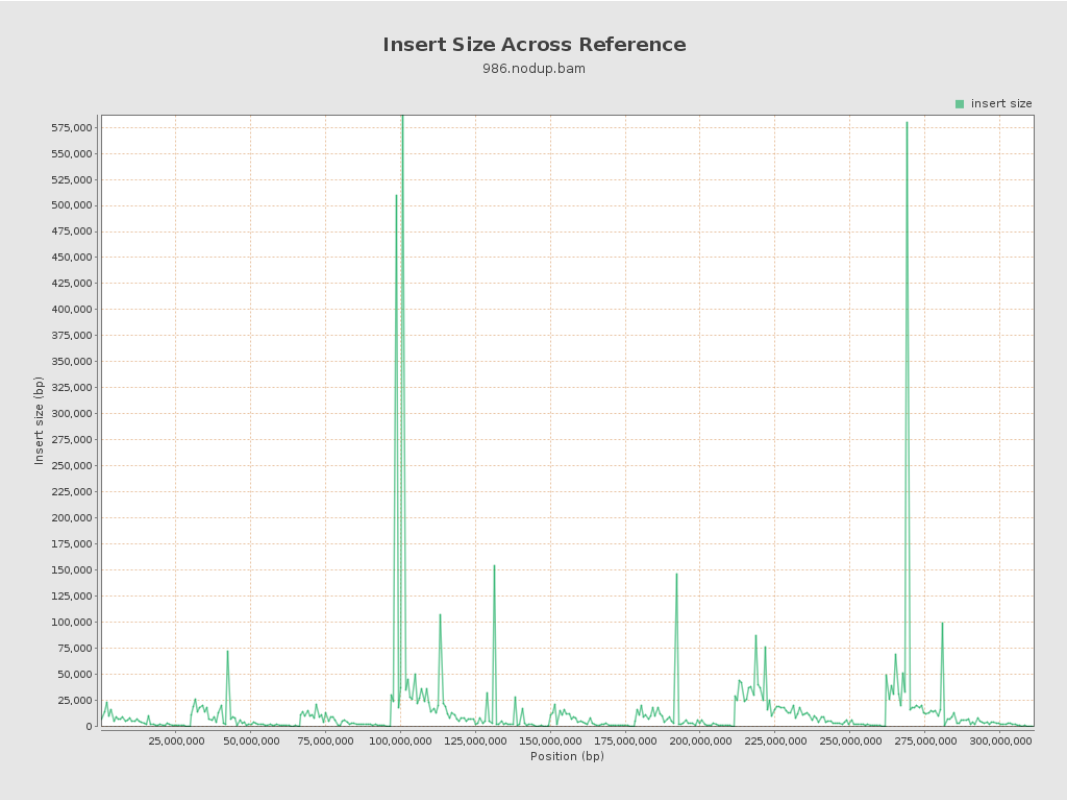
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram