Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:29:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/806.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/806.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_201/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_201_S282_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_201/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_201_S282_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:29:39 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	60,180,812
Mapped reads	56,423,718 / 93.76%
Unmapped reads	3,757,094 / 6.24%
Mapped paired reads	56,423,718 / 93.76%
Mapped reads, first in pair	28,266,071 / 46.97%
Mapped reads, second in pair	28,157,647 / 46.79%
Mapped reads, both in pair	55,150,384 / 91.64%
Mapped reads, singletons	1,273,334 / 2.12%
Read min/max/mean length	30 / 151 / 147.96
Duplicated reads (flagged)	8,088,323 / 13.44%
Clipped reads	13,292,093 / 22.09%

2.2. ACGT Content

Number/percentage of A's	2,400,338,978 / 30.85%
Number/percentage of C's	1,489,863,475 / 19.15%
Number/percentage of T's	2,403,985,866 / 30.9%
Number/percentage of G's	1,485,513,672 / 19.09%
Number/percentage of N's	29,514 / 0%
GC Percentage	38.25%

2.3. Coverage

Mean	25.0311
Standard Deviation	214.509

2.4. Mapping Quality

Mean Mapping Quality	43.56

2.5. Insert size

Mean	246,735.91
Standard Deviation	2,352,016.02
P25/Median/P75	333 / 437 / 564

2.6. Mismatches and indels

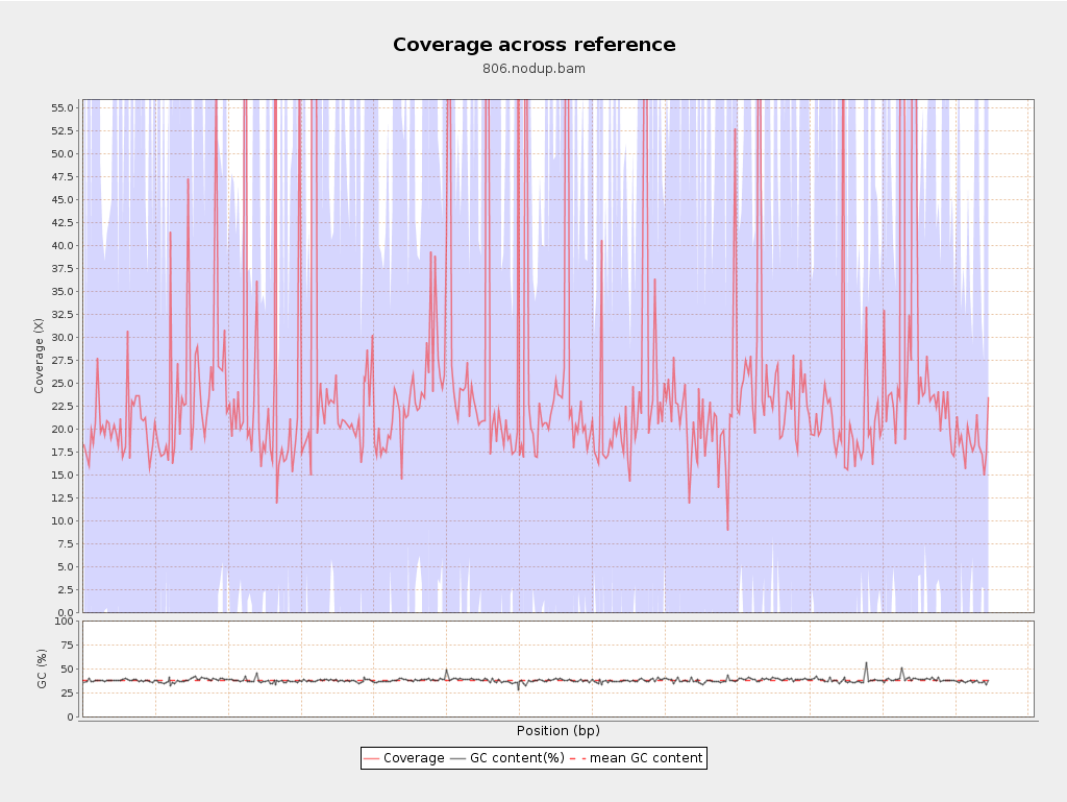
General error rate	2.39%
Mismatches	171,112,415
Insertions	5,531,468
Mapped reads with at least one insertion	8.79%
Deletions	5,555,656
Mapped reads with at least one deletion	8.73%
Homopolymer indels	56.56%

2.7. Chromosome stats

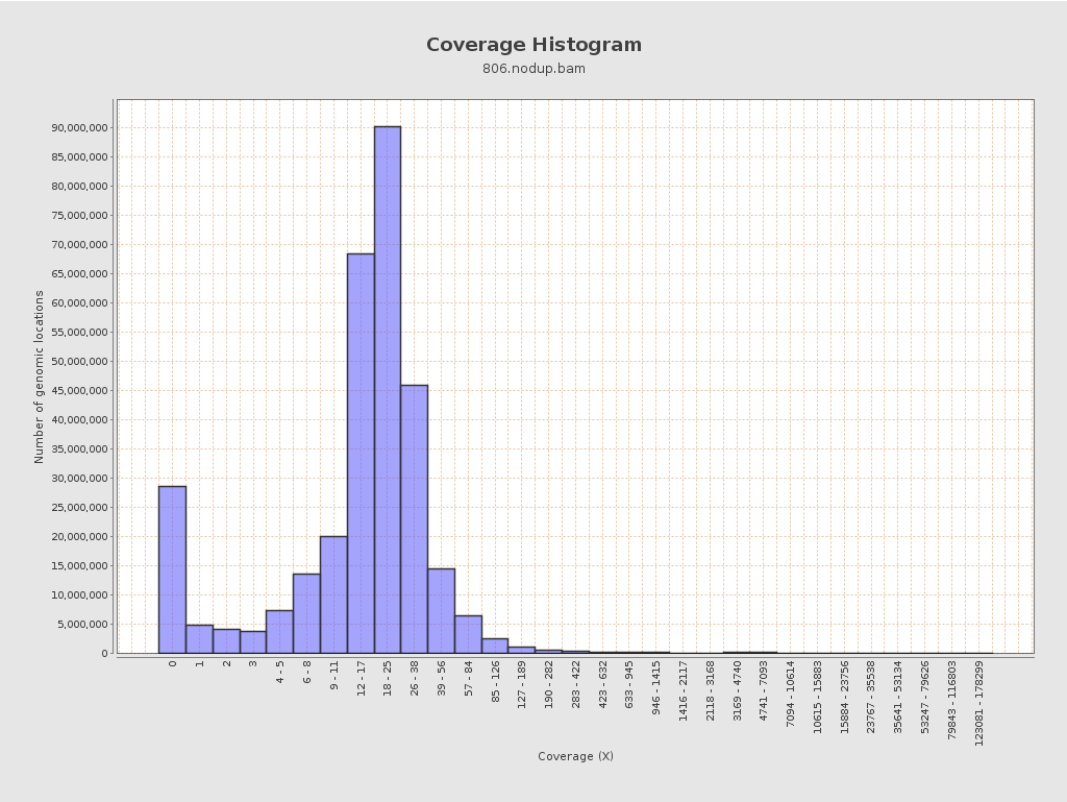
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	590698219	19.8725	65.05

LT669789.1	36598175	953494108	26.0531	231.1302
LT669790.1	30422129	828828526	27.2443	241.2584
LT669791.1	52758100	1317432110	24.9712	194.1004
LT669792.1	28376109	704276749	24.8194	263.3931
LT669793.1	33388210	777100432	23.2747	147.1569
LT669794.1	50579949	1220142480	24.123	185.6338
LT669795.1	49795044	1408776274	28.2915	285.6955

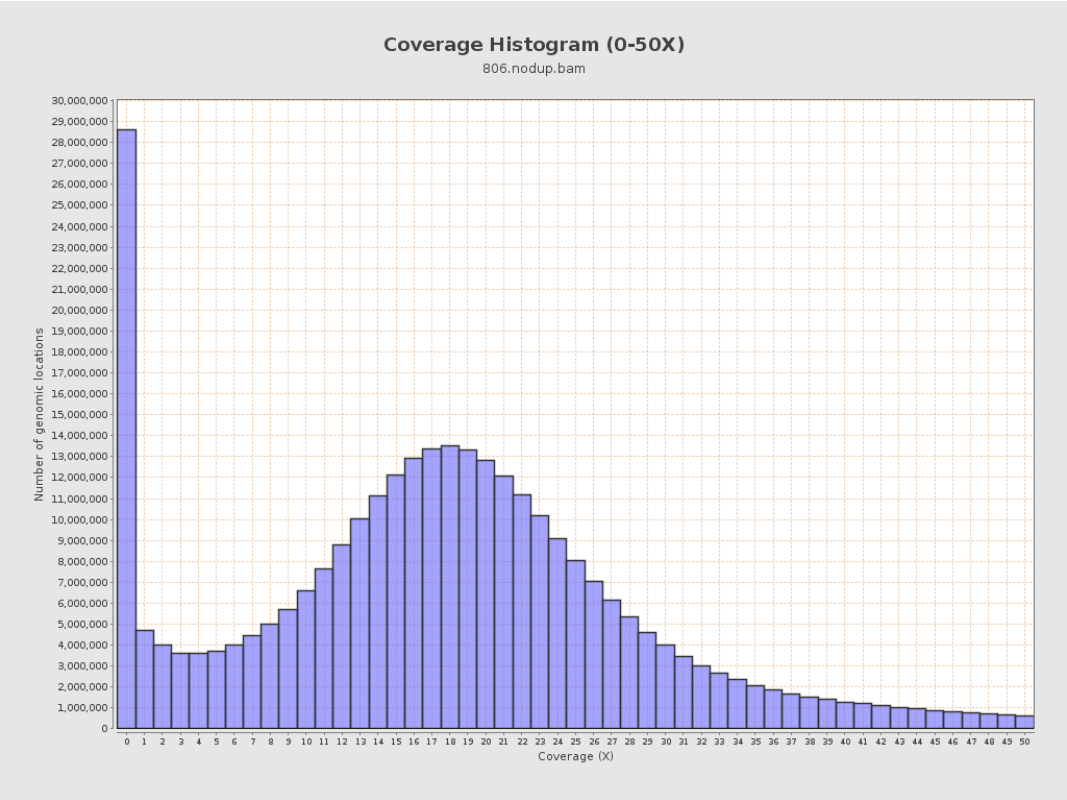
3. Results : Coverage across reference



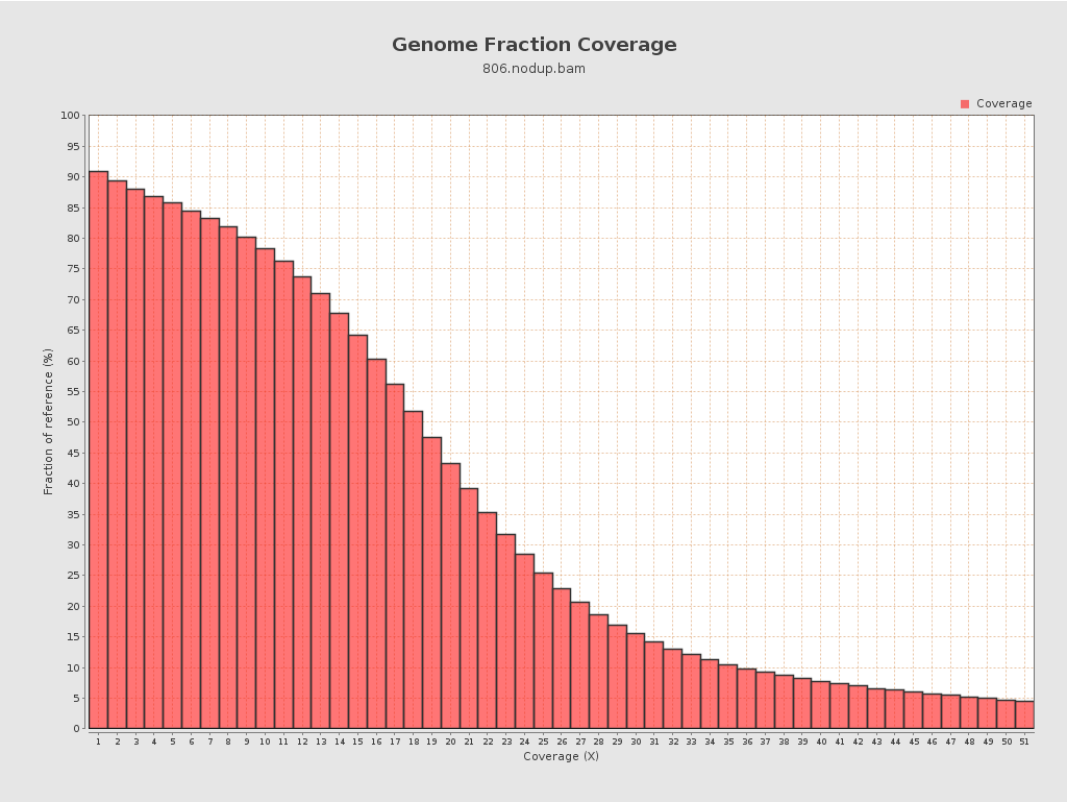
4. Results : Coverage Histogram



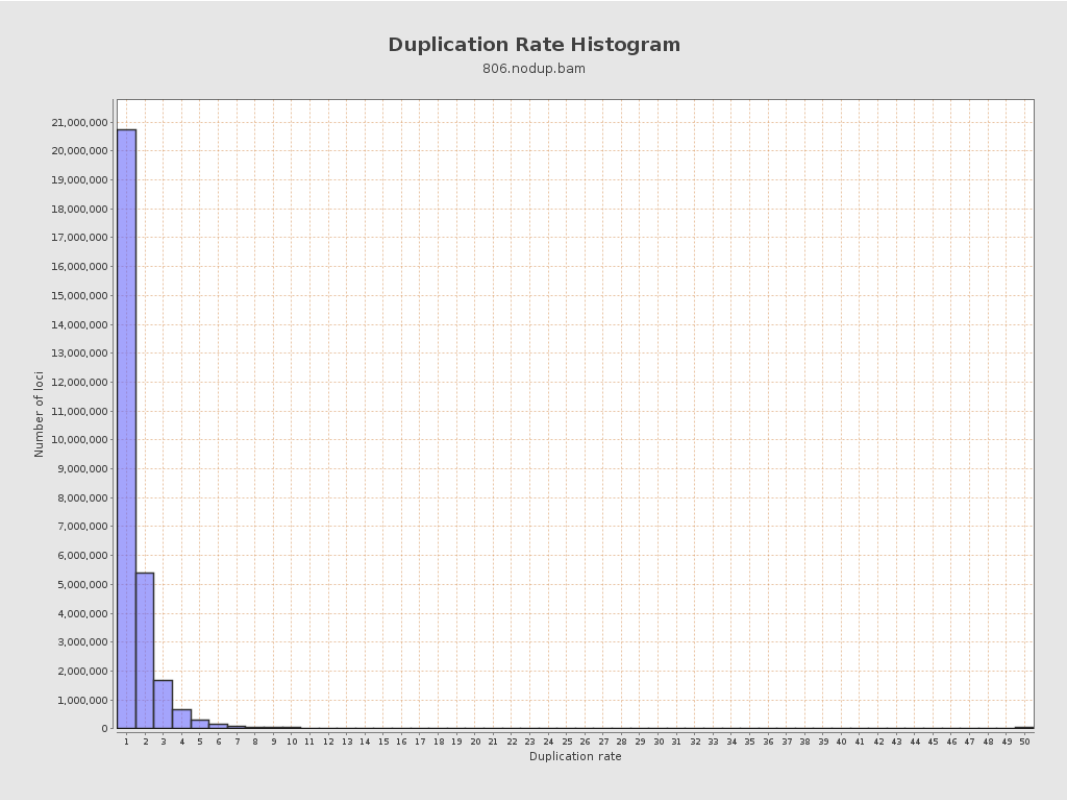
5. Results : Coverage Histogram (0-50X)



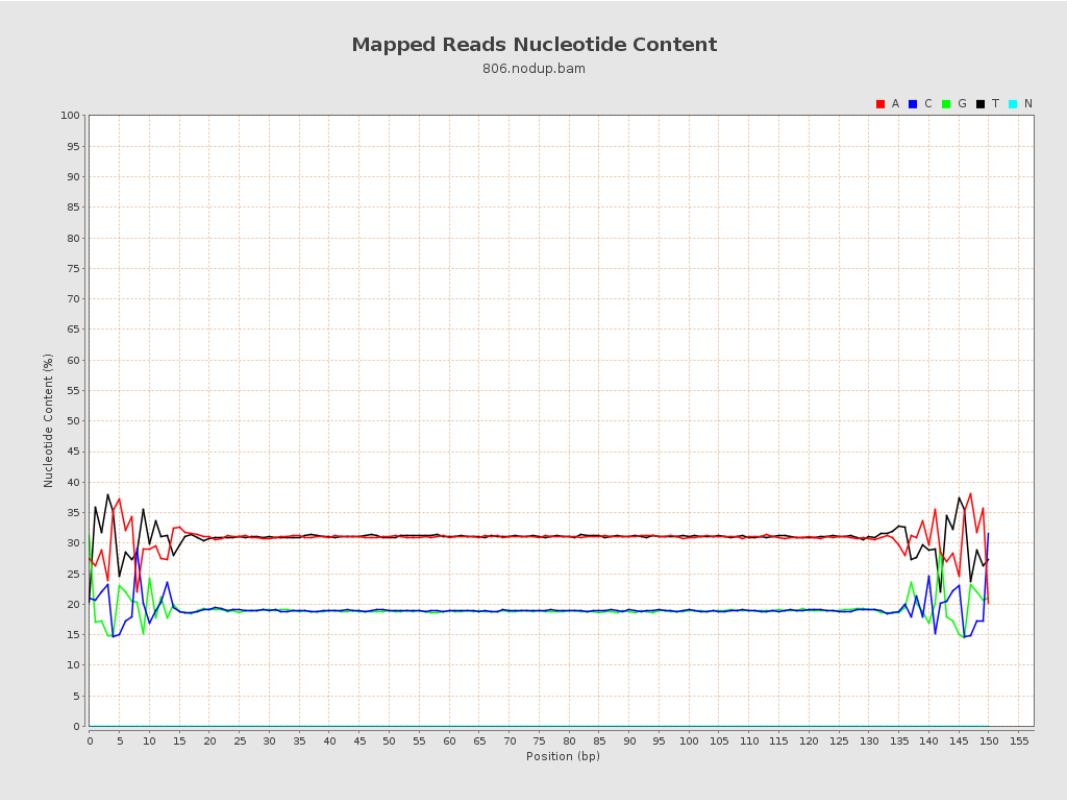
6. Results : Genome Fraction Coverage



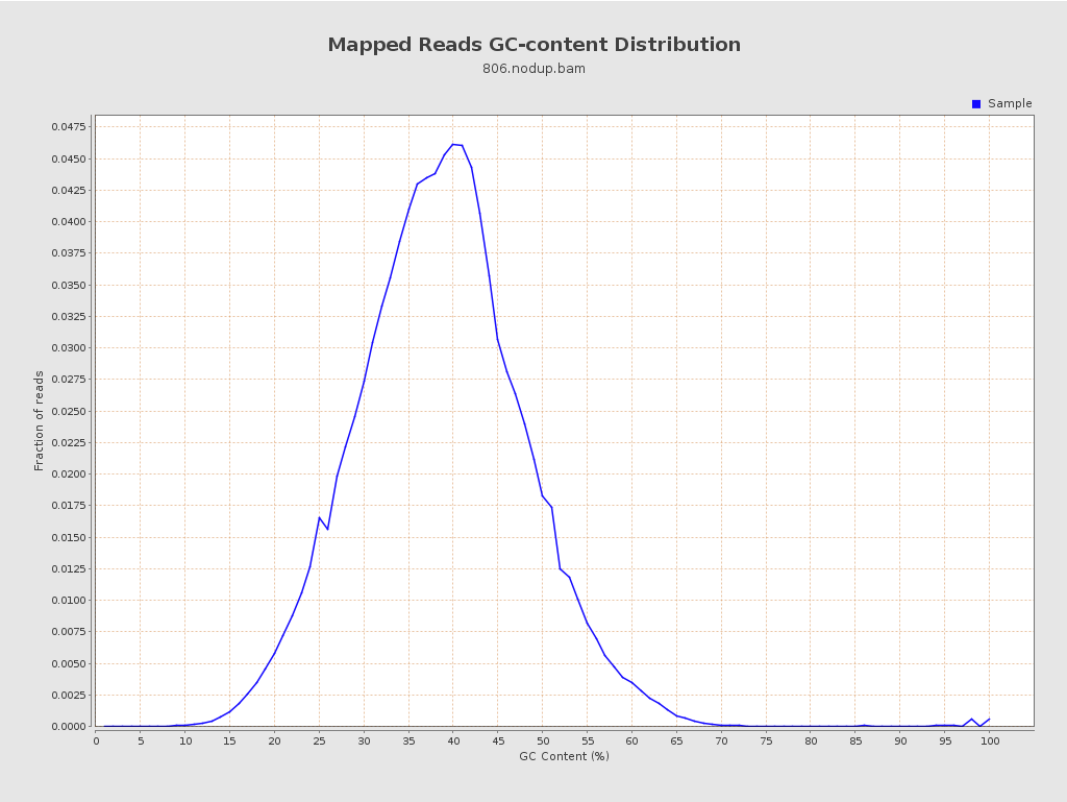
7. Results : Duplication Rate Histogram



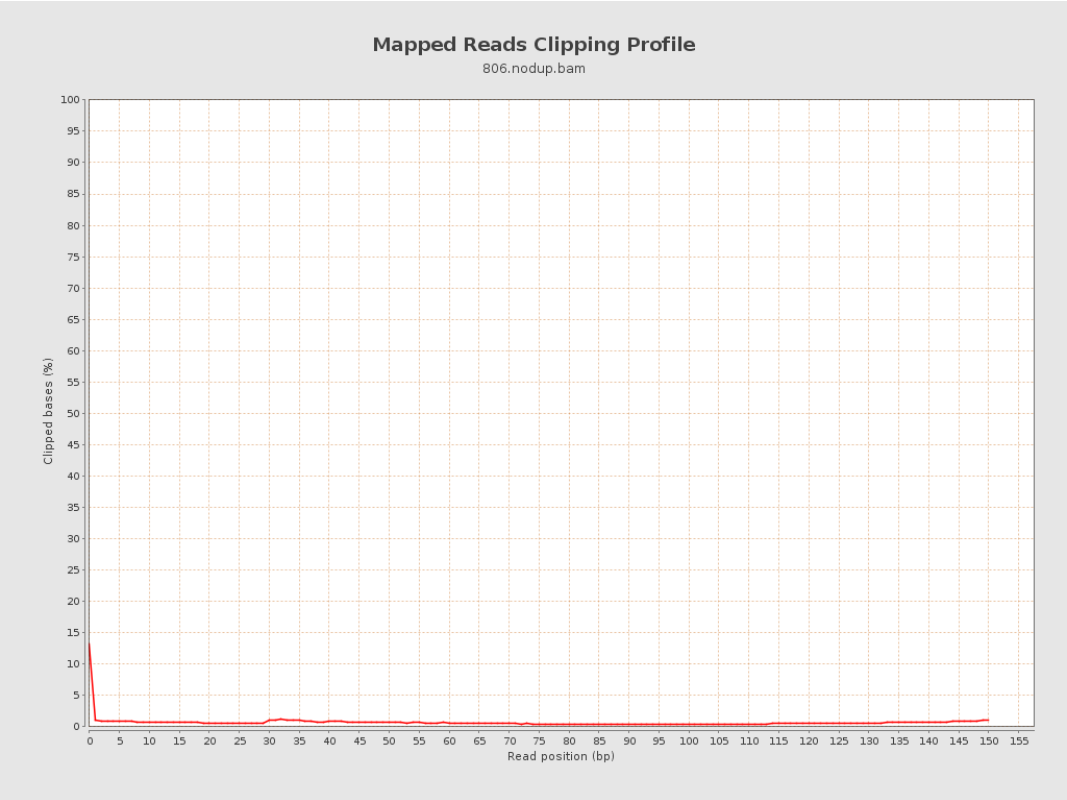
8. Results : Mapped Reads Nucleotide Content



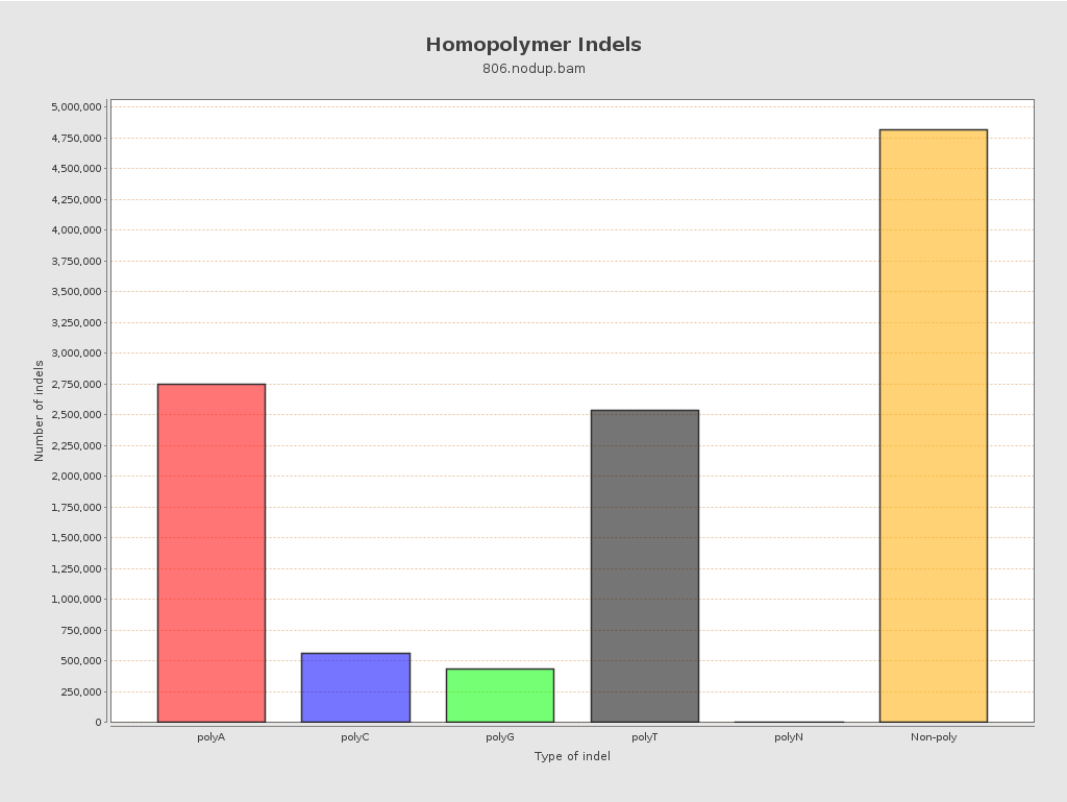
9. Results : Mapped Reads GC-content Distribution



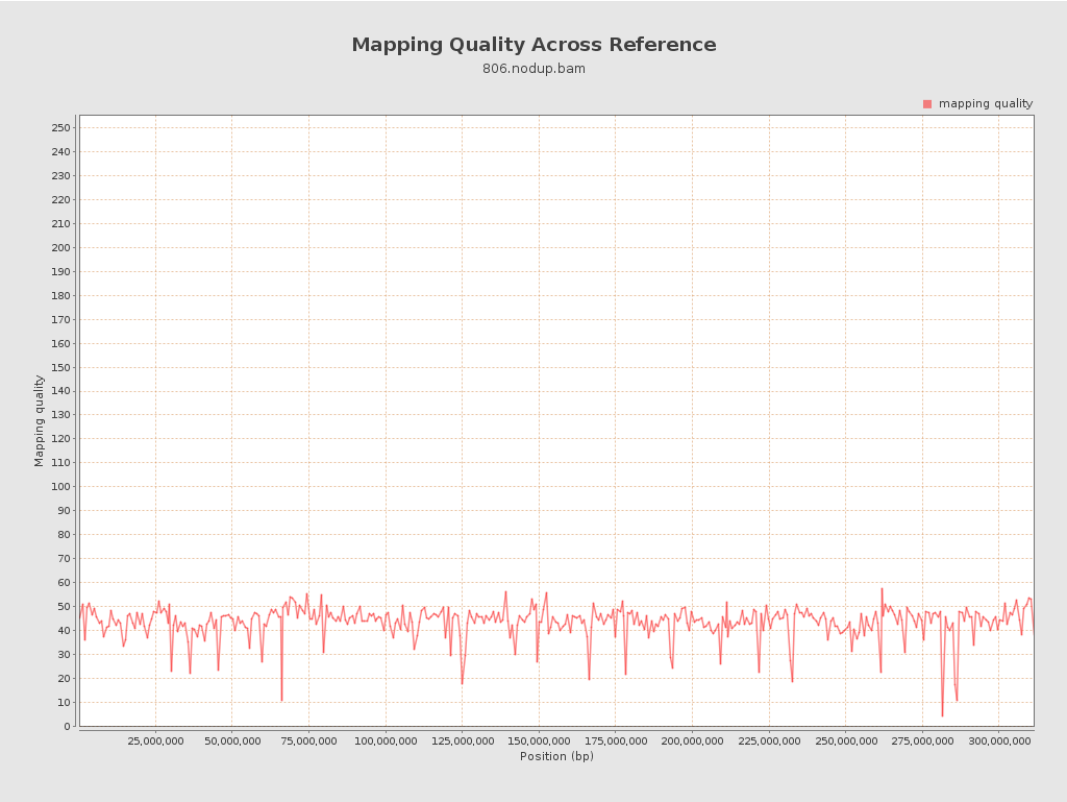
10. Results : Mapped Reads Clipping Profile



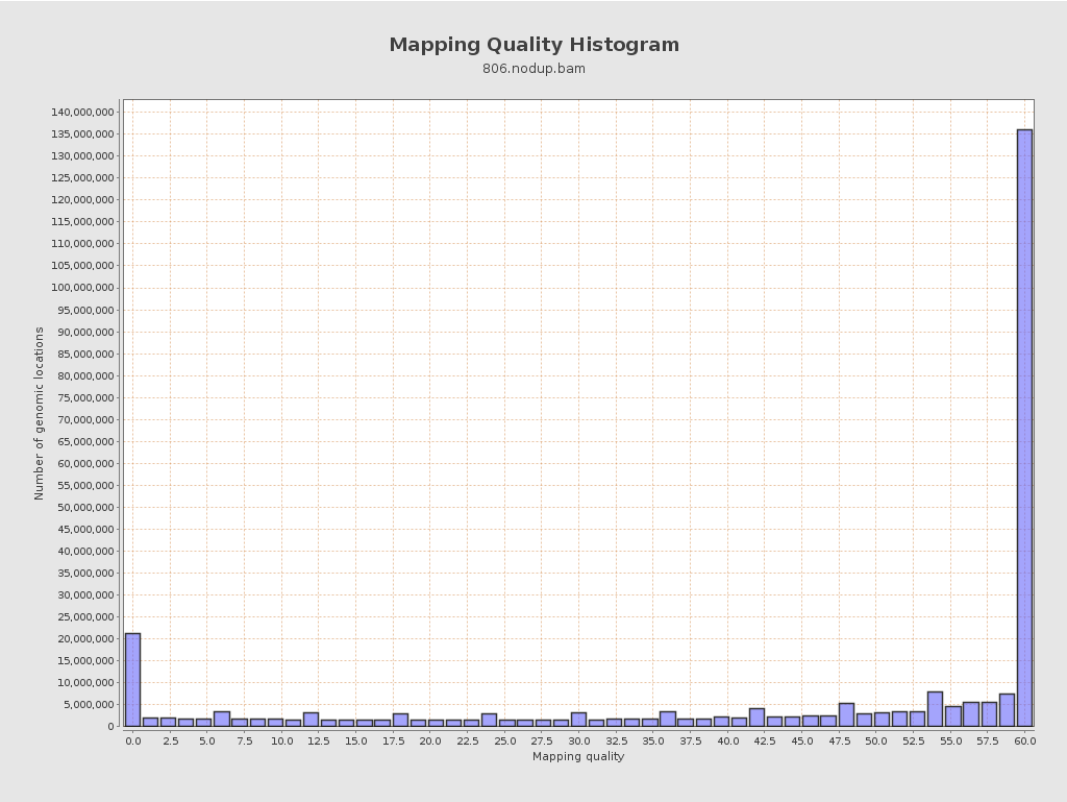
11. Results : Homopolymer Indels



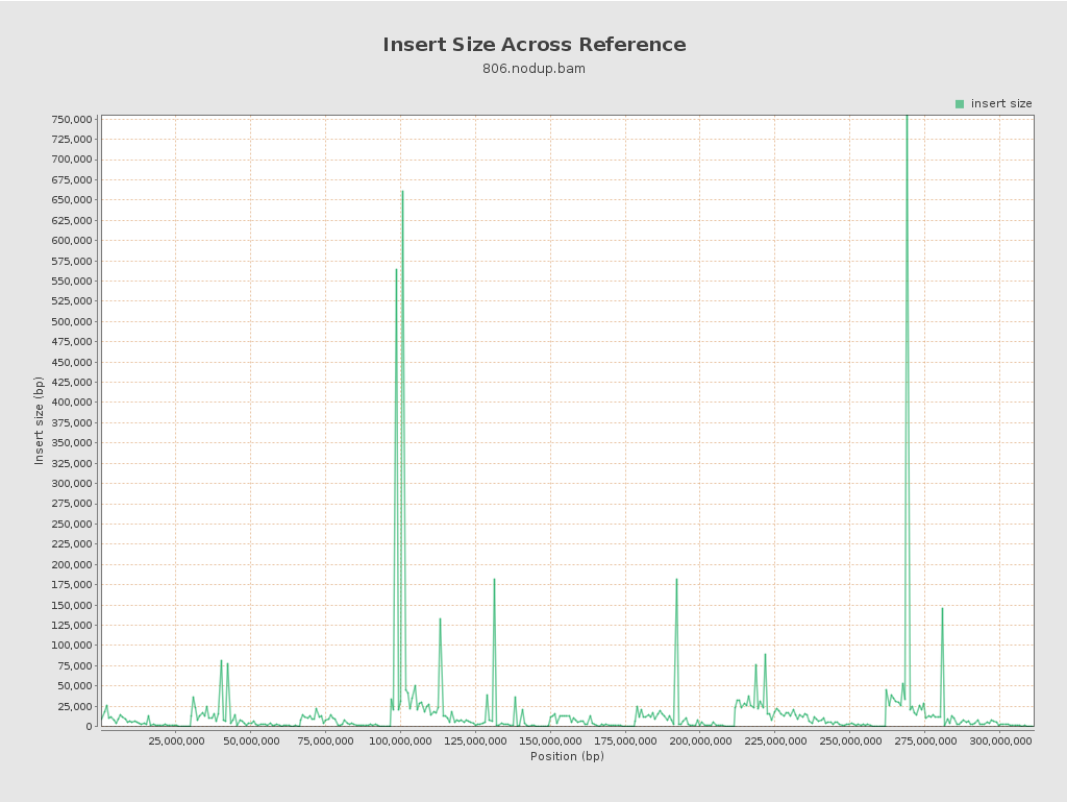
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram