Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:29:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/847.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/847.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_181/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_181_S271_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_181/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_181_S271_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:29:08 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	58,274,702
Mapped reads	54,080,989 / 92.8%
Unmapped reads	4,193,713 / 7.2%
Mapped paired reads	54,080,989 / 92.8%
Mapped reads, first in pair	27,110,919 / 46.52%
Mapped reads, second in pair	26,970,070 / 46.28%
Mapped reads, both in pair	52,654,785 / 90.36%
Mapped reads, singletons	1,426,204 / 2.45%
Read min/max/mean length	30 / 151 / 148.19
Duplicated reads (flagged)	9,882,597 / 16.96%
Clipped reads	12,228,506 / 20.98%

2.2. ACGT Content

Number/percentage of A's	2,302,458,909 / 30.78%
Number/percentage of C's	1,436,825,705 / 19.21%
Number/percentage of T's	2,307,516,136 / 30.85%
Number/percentage of G's	1,433,130,714 / 19.16%
Number/percentage of N's	31,898 / 0%
GC Percentage	38.37%

2.3. Coverage

Mean	24.0626
Standard Deviation	215.7572

2.4. Mapping Quality

Mean Mapping Quality	44.25

2.5. Insert size

Mean	245,650.77
Standard Deviation	2,365,691.06
P25/Median/P75	349 / 455 / 593

2.6. Mismatches and indels

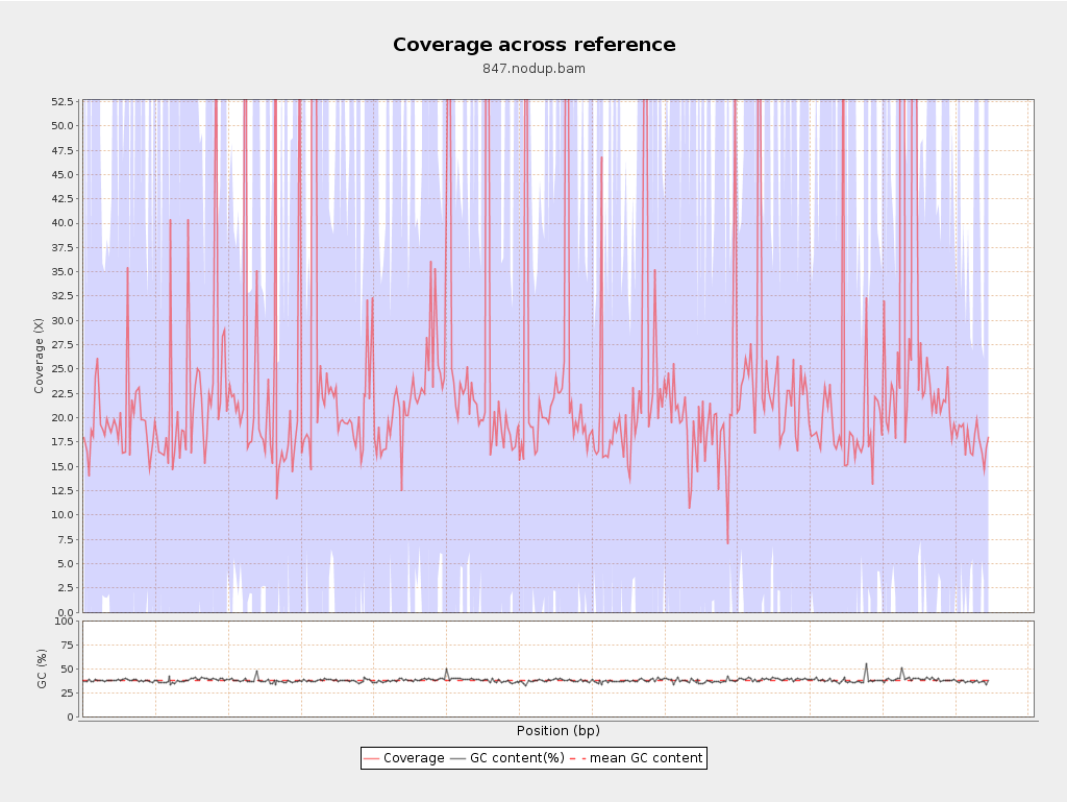
General error rate	2.35%
Mismatches	161,729,369
Insertions	5,127,471
Mapped reads with at least one insertion	8.49%
Deletions	5,074,055
Mapped reads with at least one deletion	8.32%
Homopolymer indels	56.47%

2.7. Chromosome stats

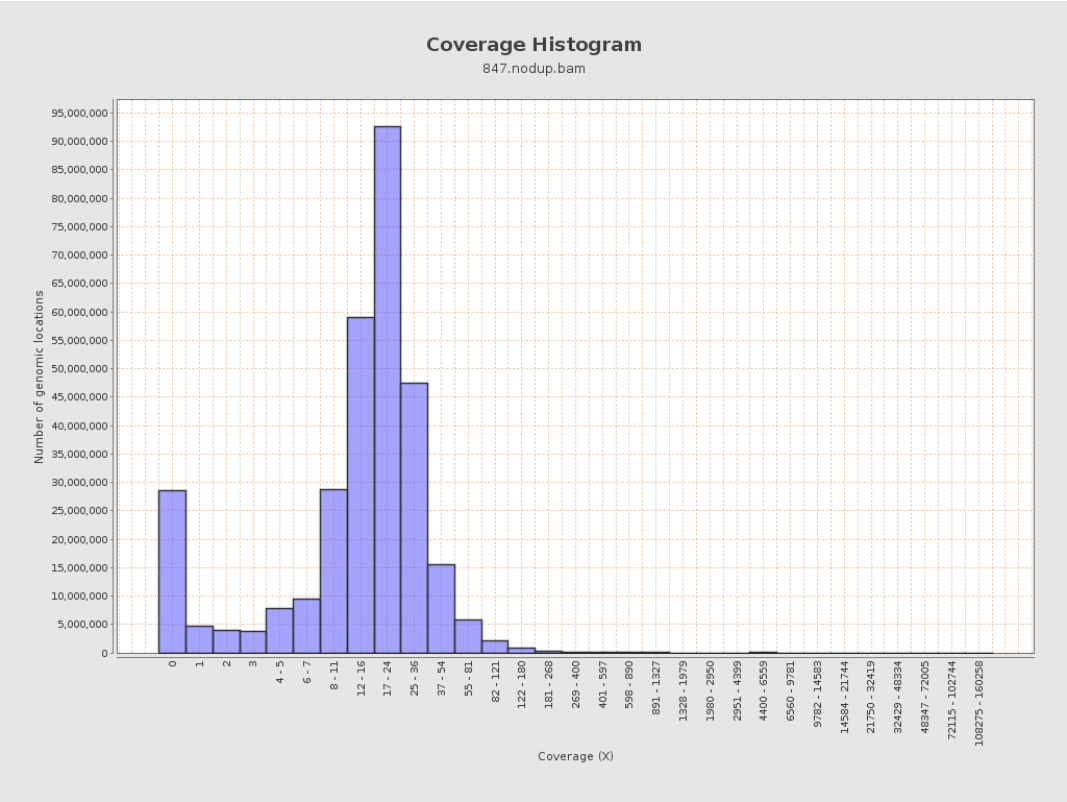
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	569963370	19.175	84.2094

LT669789.1	36598175	874050986	23.8824	219.343
LT669790.1	30422129	808703402	26.5827	247.6907
LT669791.1	52758100	1269403698	24.0608	205.7689
LT669792.1	28376109	668838049	23.5705	249.0312
LT669793.1	33388210	736793752	22.0675	142.6199
LT669794.1	50579949	1151339901	22.7628	177.4227
LT669795.1	49795044	1419838197	28.5136	297.3344

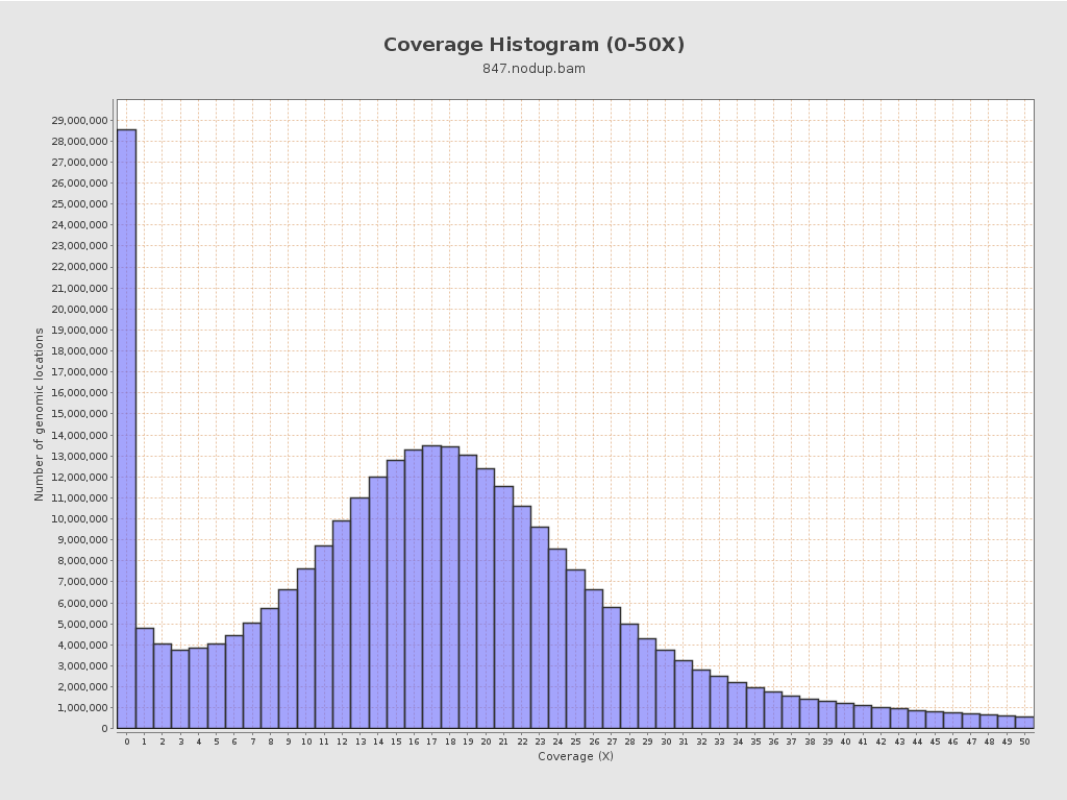
3. Results : Coverage across reference



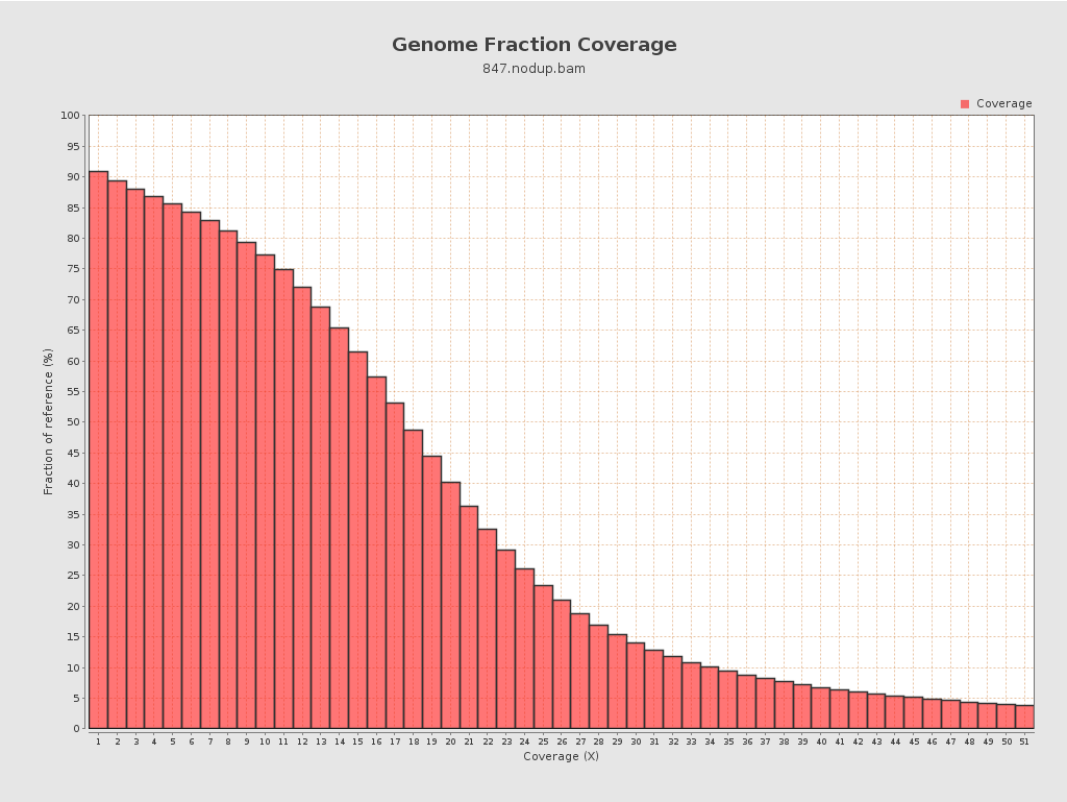
4. Results : Coverage Histogram



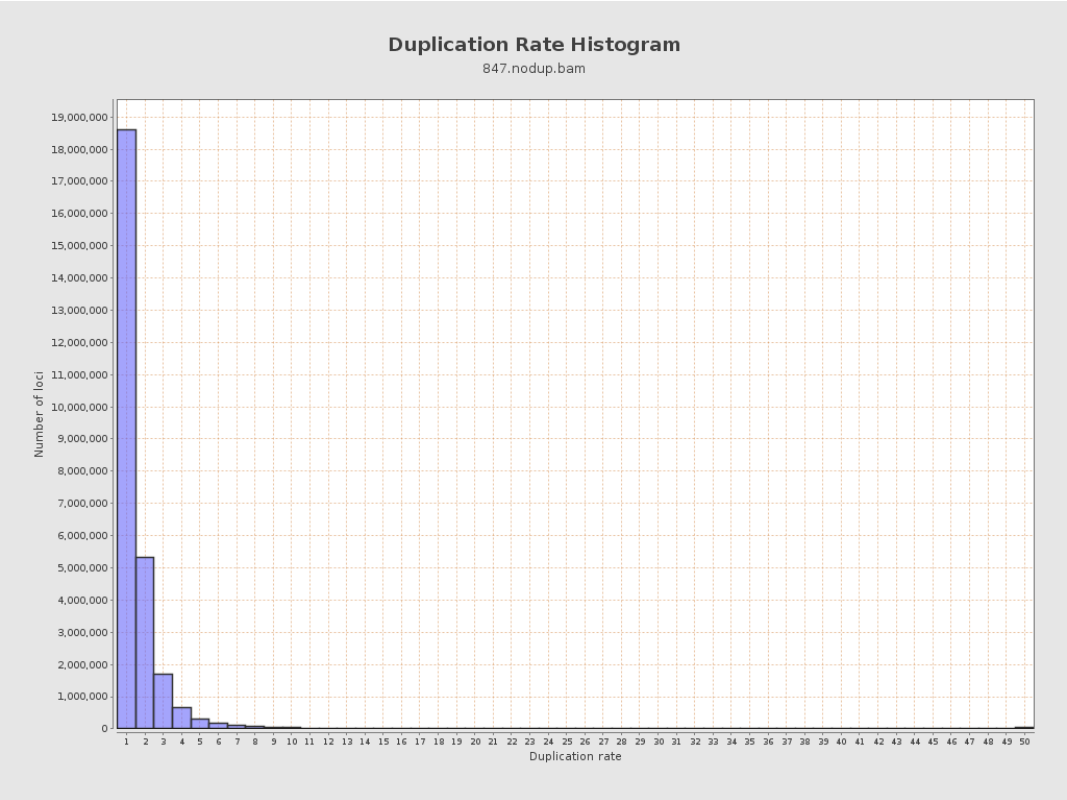
5. Results : Coverage Histogram (0-50X)



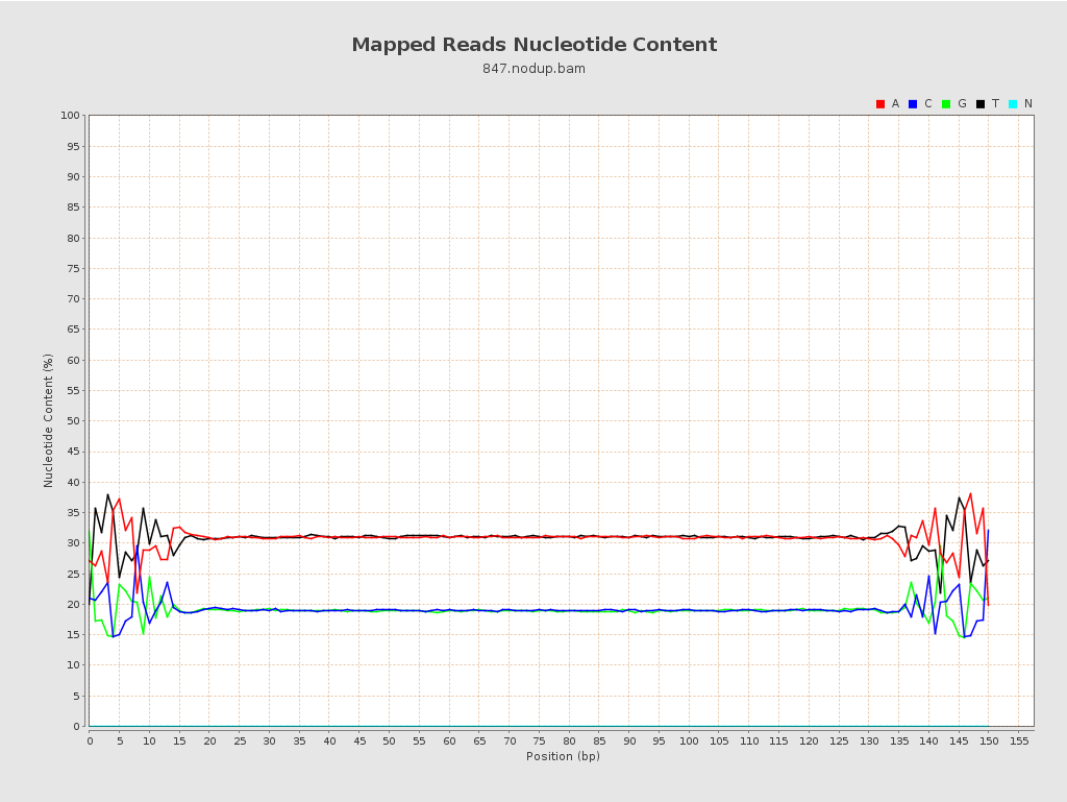
6. Results : Genome Fraction Coverage



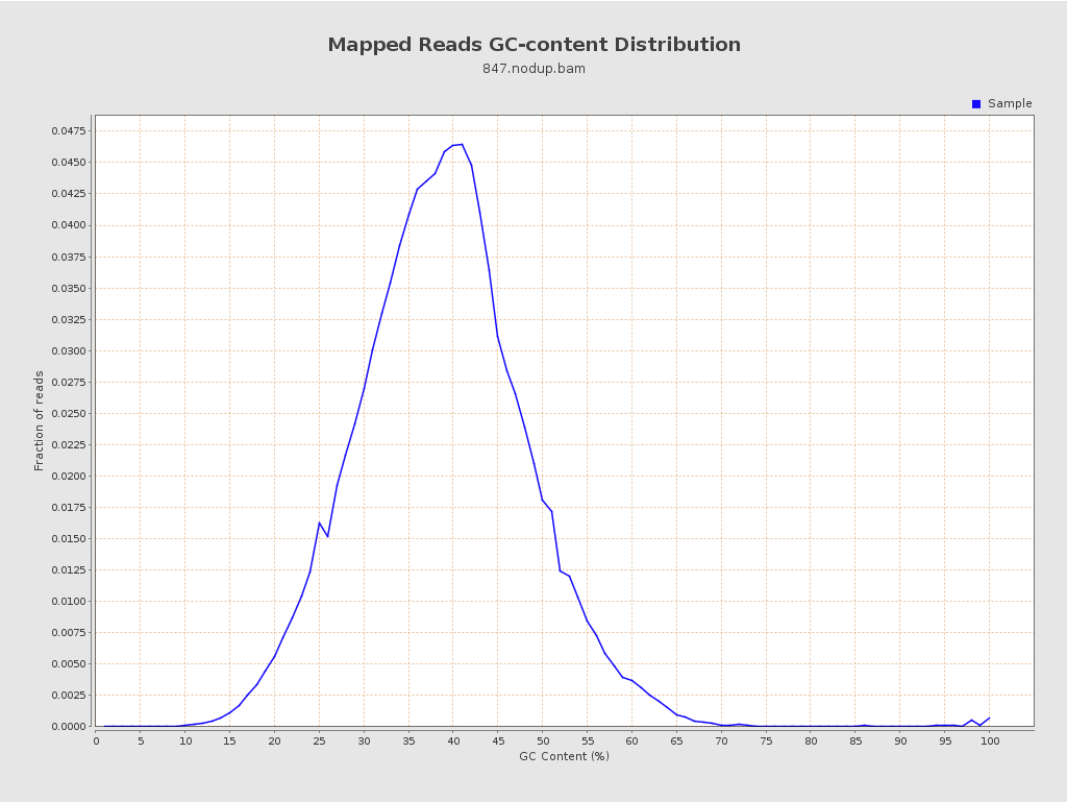
7. Results : Duplication Rate Histogram



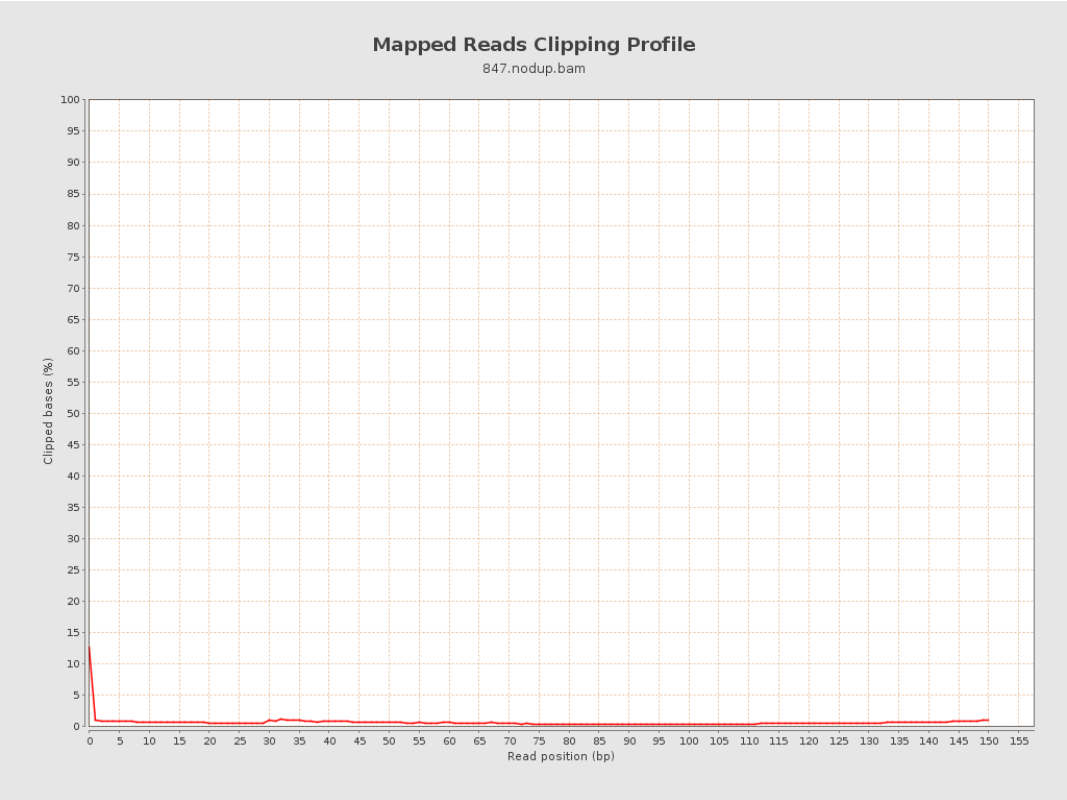
8. Results : Mapped Reads Nucleotide Content



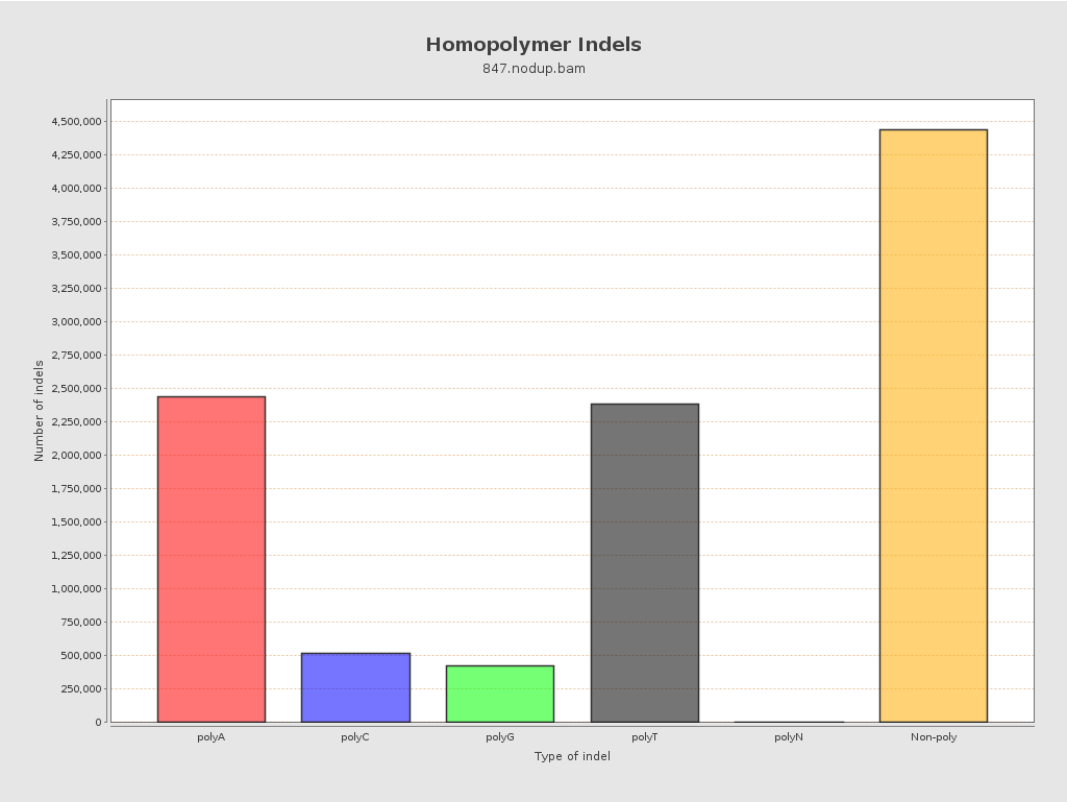
9. Results : Mapped Reads GC-content Distribution



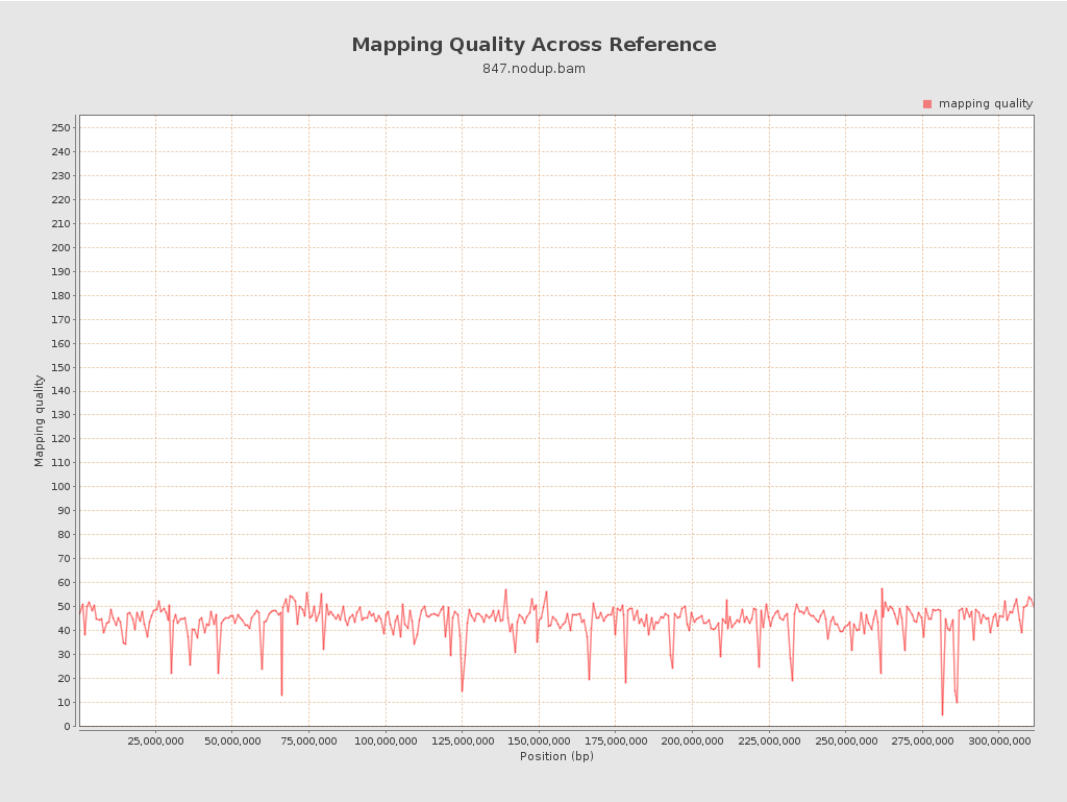
10. Results : Mapped Reads Clipping Profile



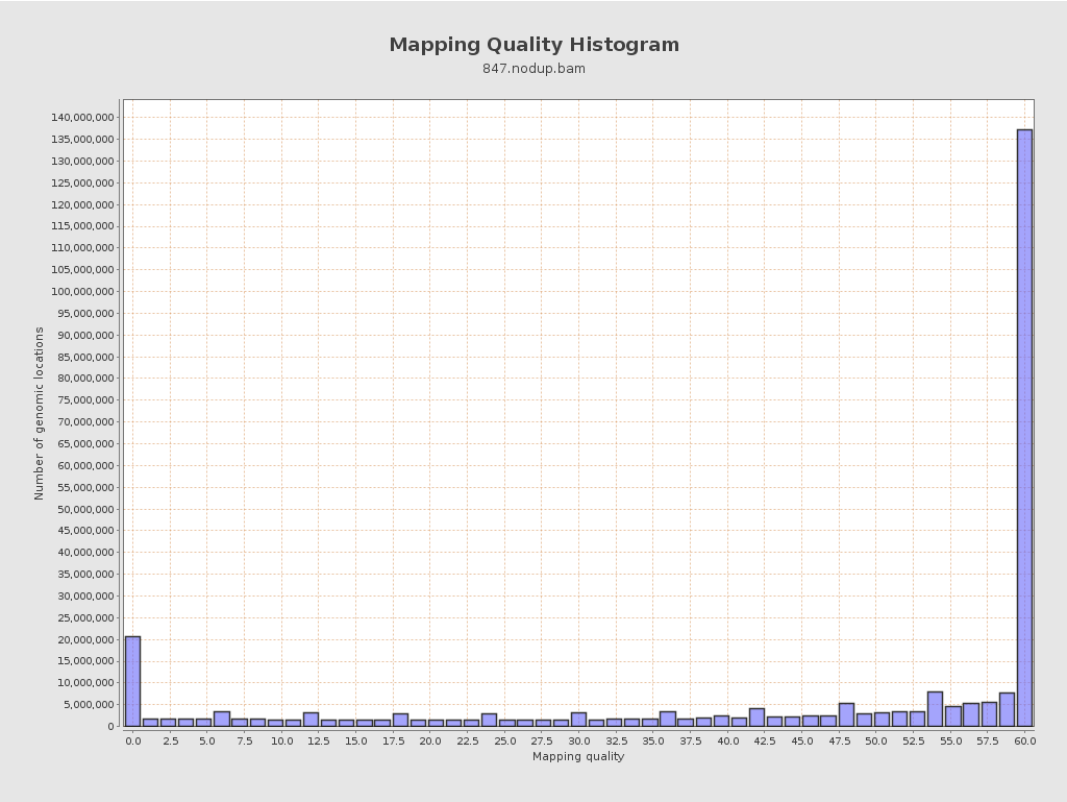
11. Results : Homopolymer Indels



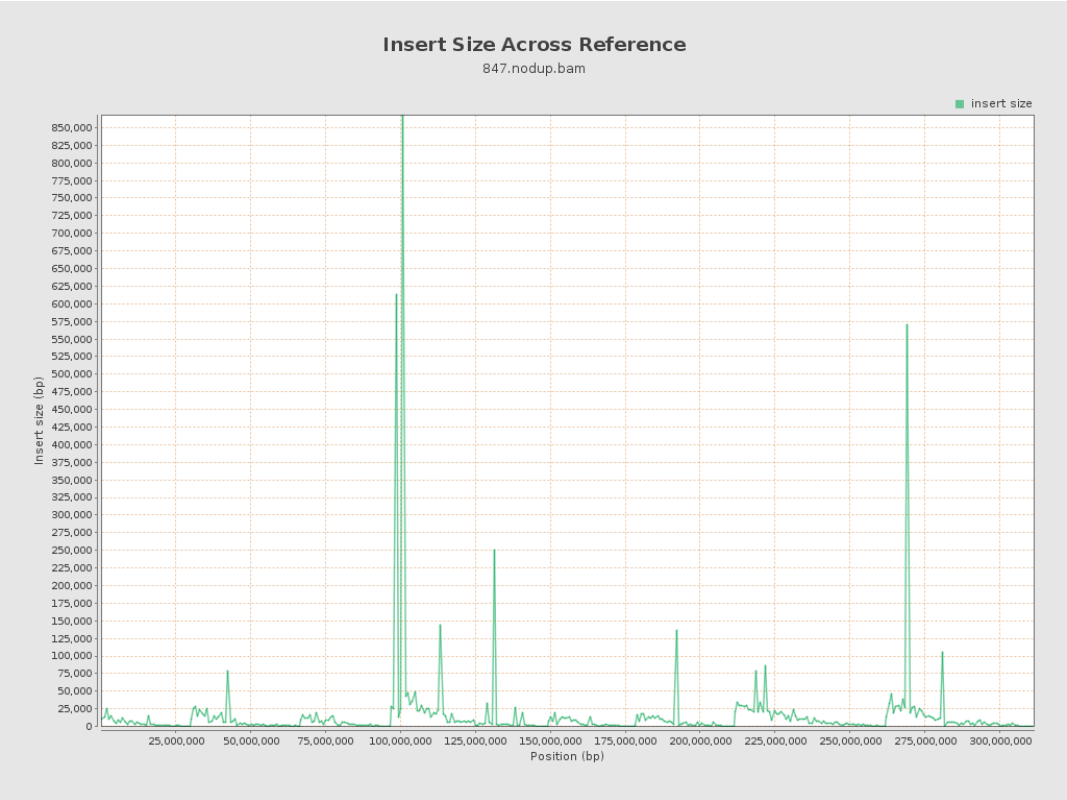
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram