Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:22:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/840.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/840.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_269/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_269_S350_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_269/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_269_S350_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:22:45 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	42,330,064
Mapped reads	39,644,097 / 93.65%
Unmapped reads	2,685,967 / 6.35%
Mapped paired reads	39,644,097 / 93.65%
Mapped reads, first in pair	19,843,430 / 46.88%
Mapped reads, second in pair	19,800,667 / 46.78%
Mapped reads, both in pair	38,710,211 / 91.45%
Mapped reads, singletons	933,886 / 2.21%
Read min/max/mean length	30 / 151 / 148.08
Duplicated reads (flagged)	5,167,943 / 12.21%
Clipped reads	9,113,388 / 21.53%

2.2. ACGT Content

Number/percentage of A's	1,693,344,223 / 30.86%
Number/percentage of C's	1,050,965,972 / 19.15%
Number/percentage of T's	1,695,886,763 / 30.9%
Number/percentage of G's	1,047,288,756 / 19.09%
Number/percentage of N's	19,203 / 0%
GC Percentage	38.24%

2.3. Coverage

Mean	17.6549
Standard Deviation	145.2698

2.4. Mapping Quality

Mean Mapping Quality	43.62

2.5. Insert size

Mean	256,700.59
Standard Deviation	2,409,182.63
P25/Median/P75	363 / 468 / 592

2.6. Mismatches and indels

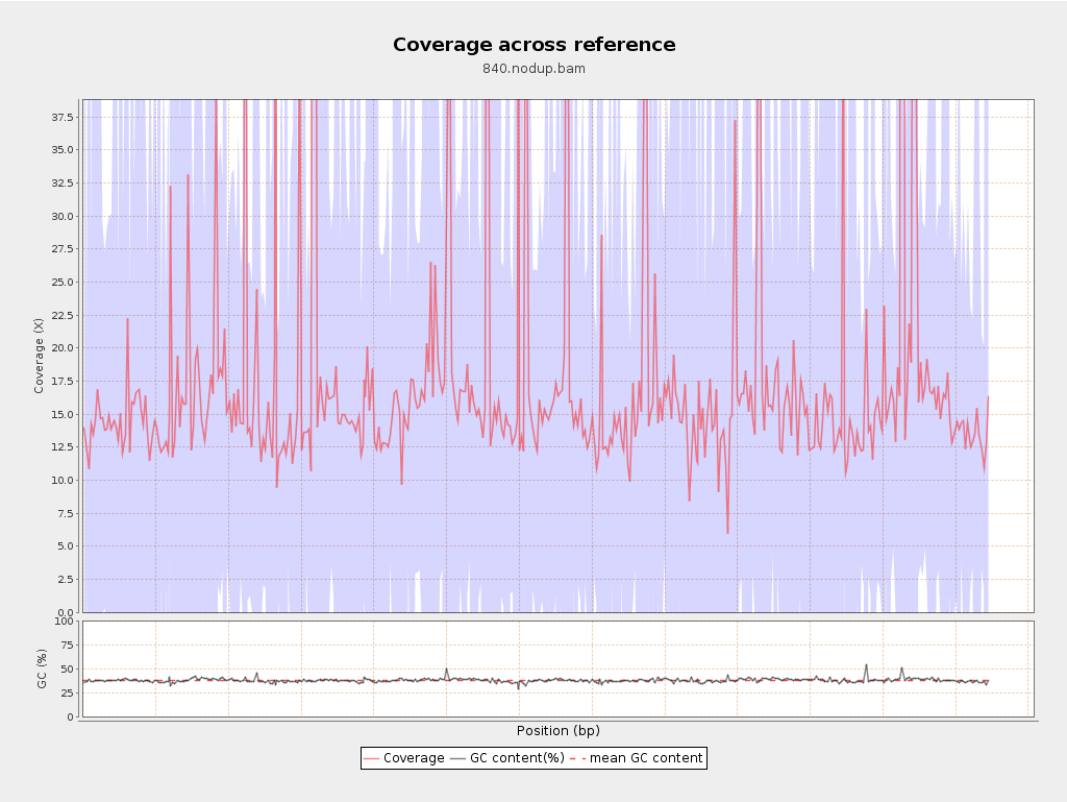
General error rate	2.41%
Mismatches	121,785,938
Insertions	3,835,785
Mapped reads with at least one insertion	8.67%
Deletions	3,854,747
Mapped reads with at least one deletion	8.62%
Homopolymer indels	56.64%

2.7. Chromosome stats

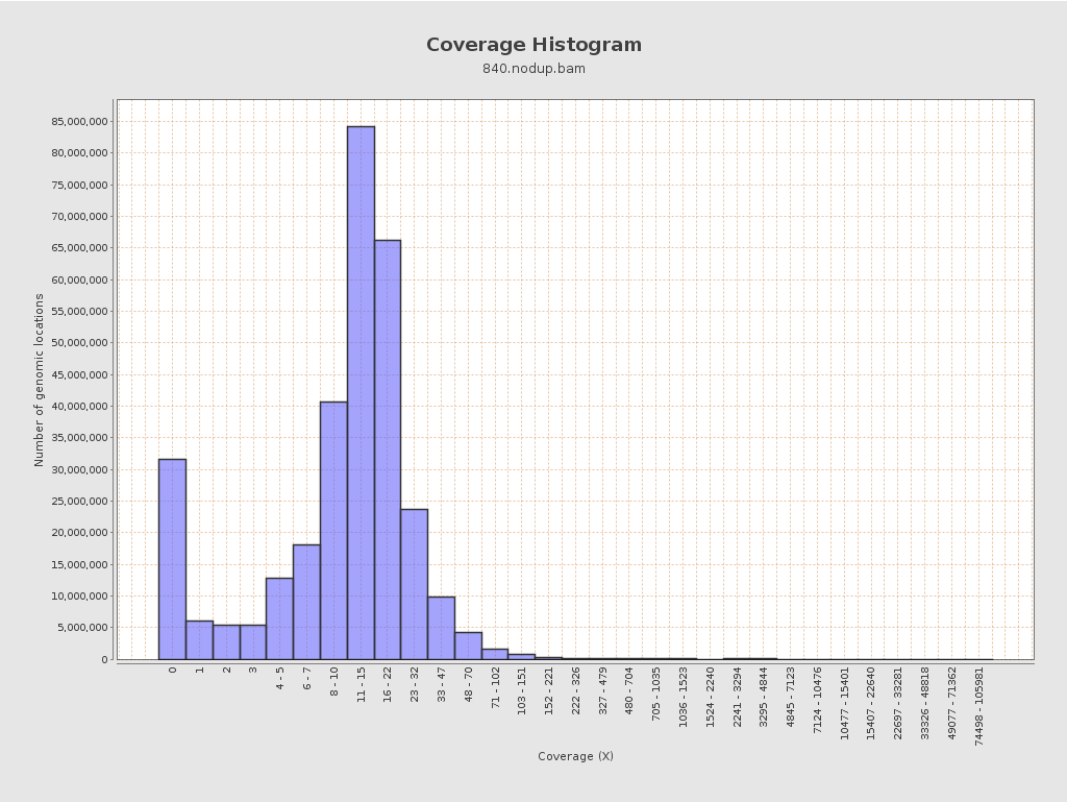
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	421670888	14.186	46.012

LT669789.1	36598175	662486585	18.1016	153.6658
LT669790.1	30422129	589979878	19.3931	168.2959
LT669791.1	52758100	918175802	17.4035	133.7862
LT669792.1	28376109	498864266	17.5804	167.4661
LT669793.1	33388210	544107913	16.2964	100.6722
LT669794.1	50579949	850423898	16.8135	127.7799
LT669795.1	49795044	1016290224	20.4095	194.4407

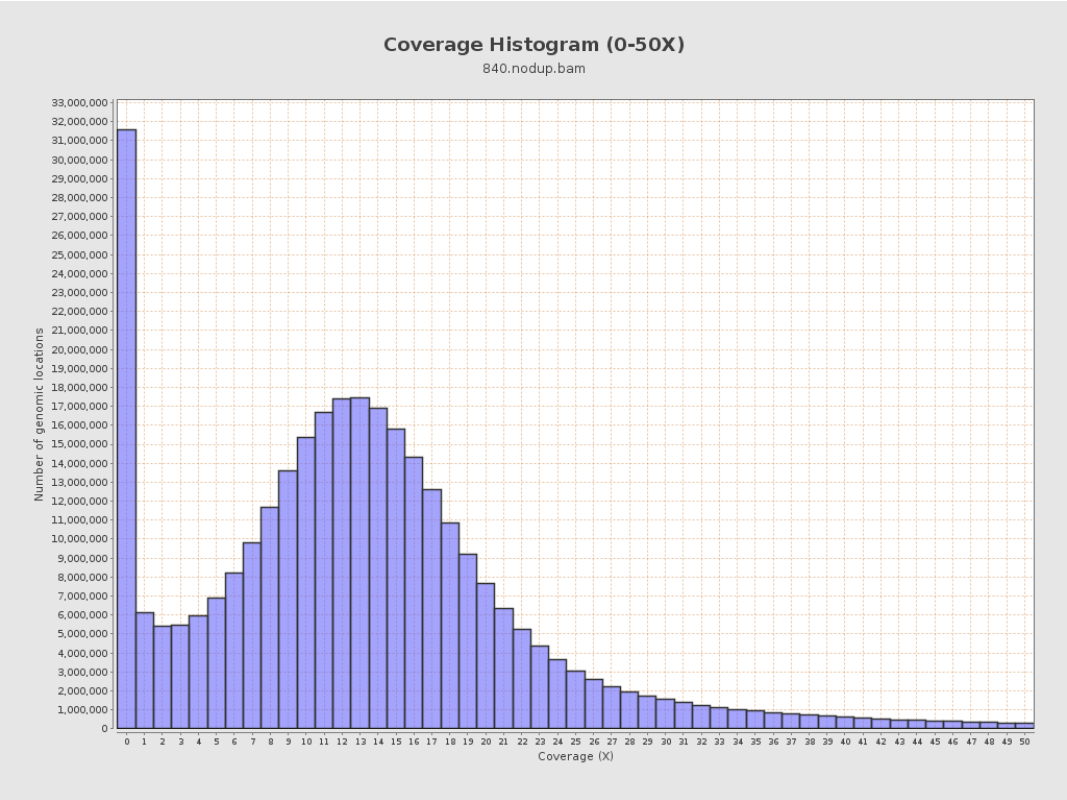
3. Results : Coverage across reference



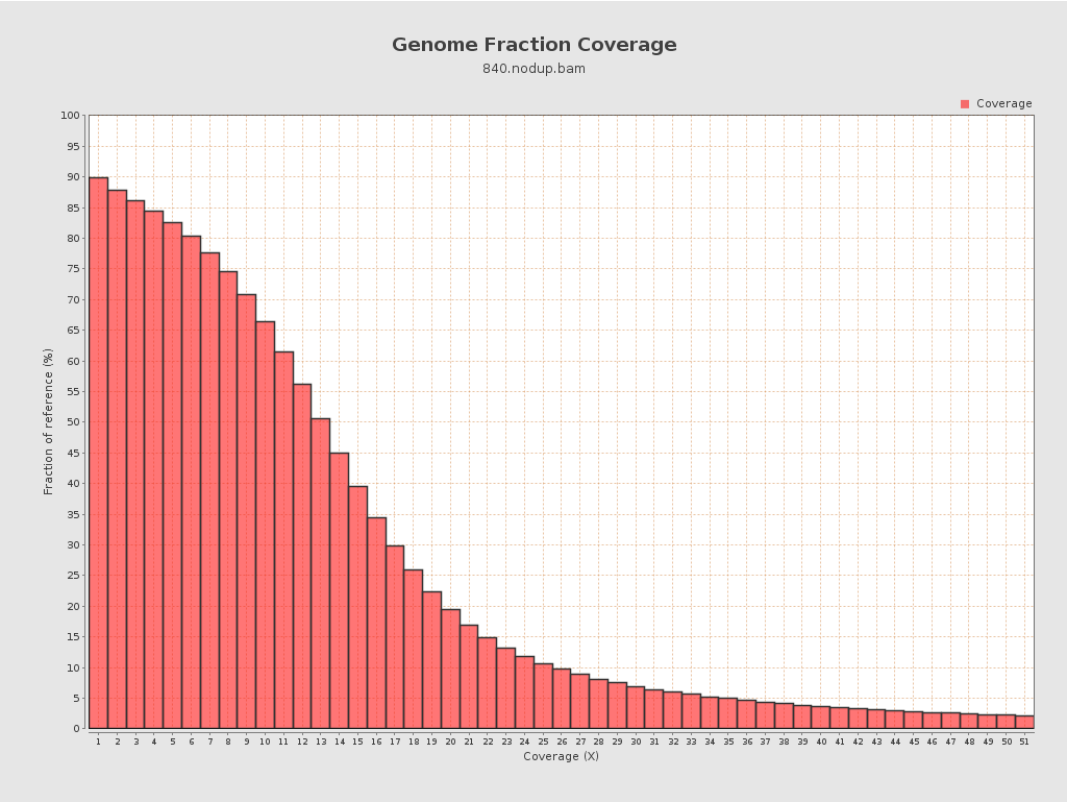
4. Results : Coverage Histogram



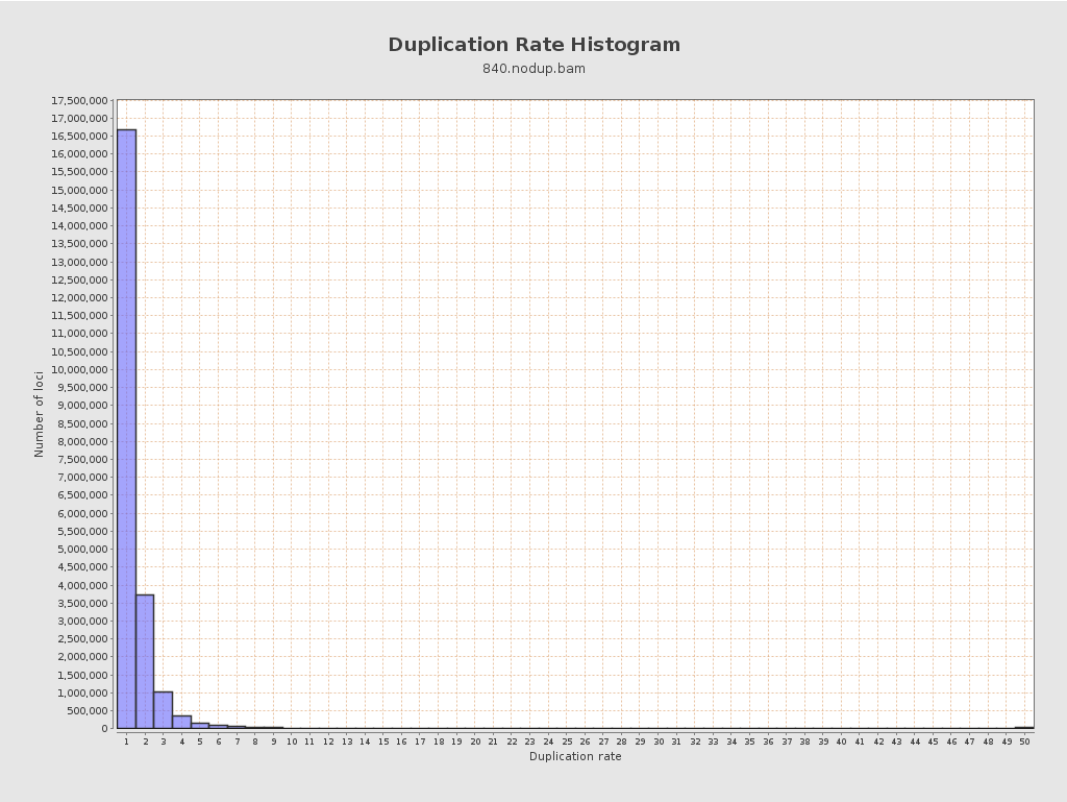
5. Results : Coverage Histogram (0-50X)



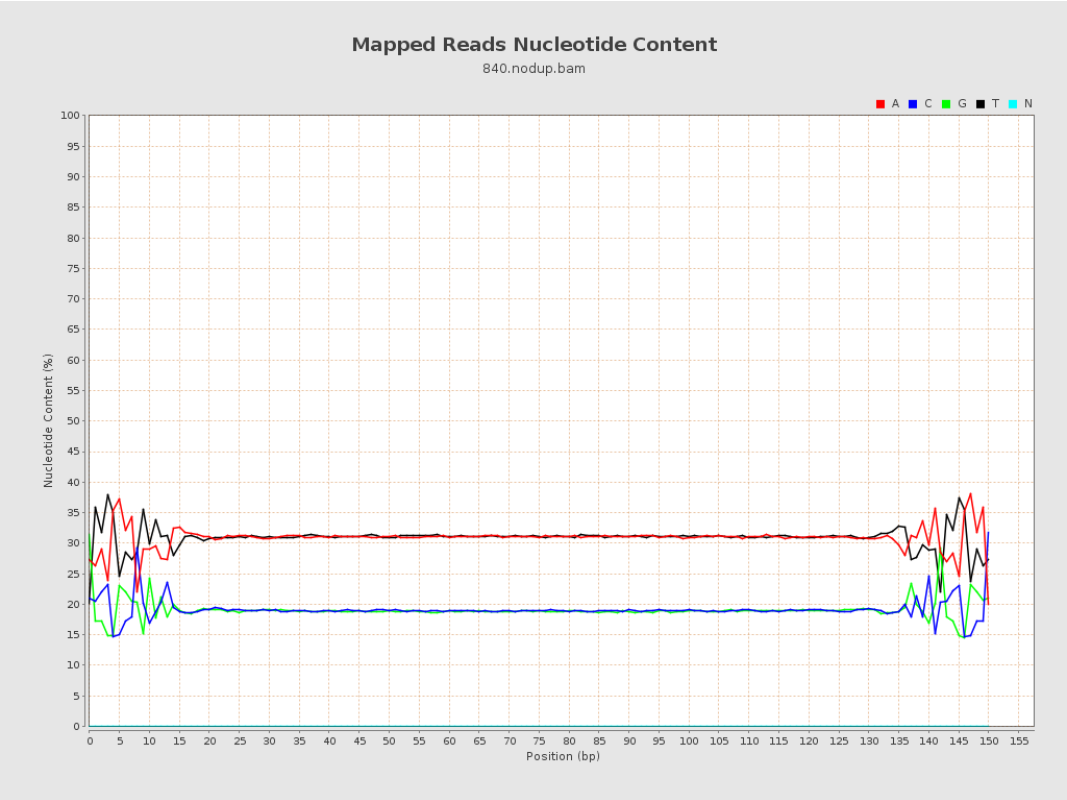
6. Results : Genome Fraction Coverage



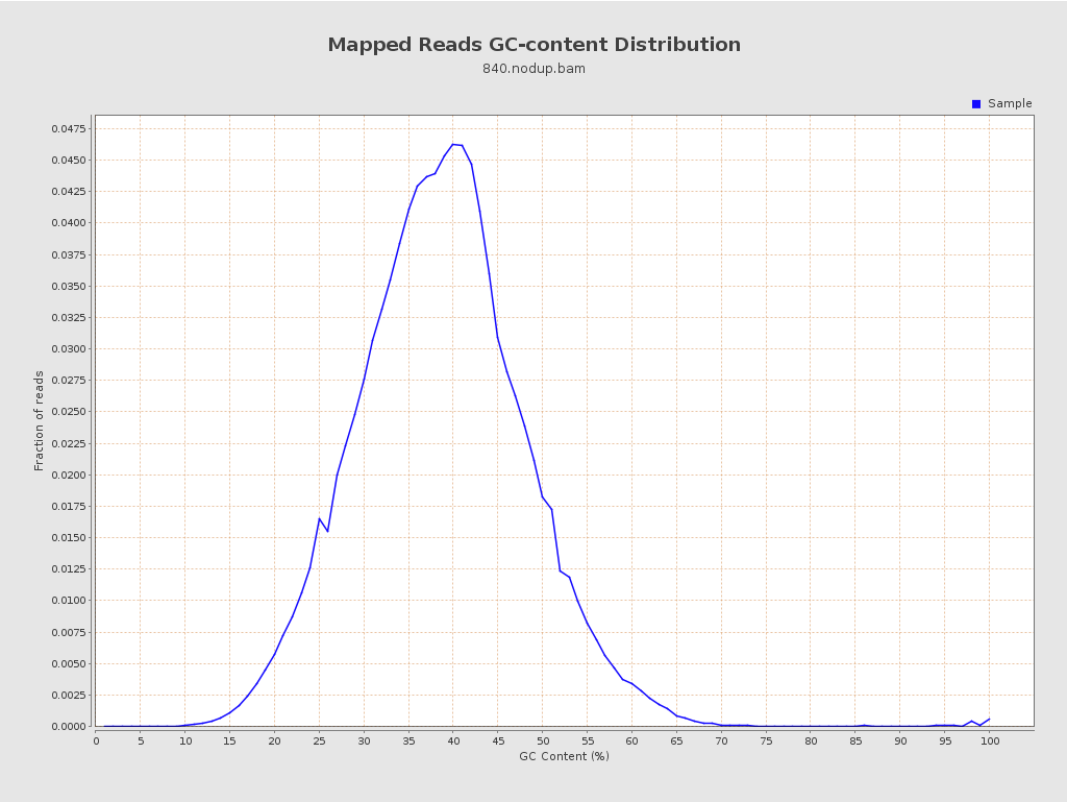
7. Results : Duplication Rate Histogram



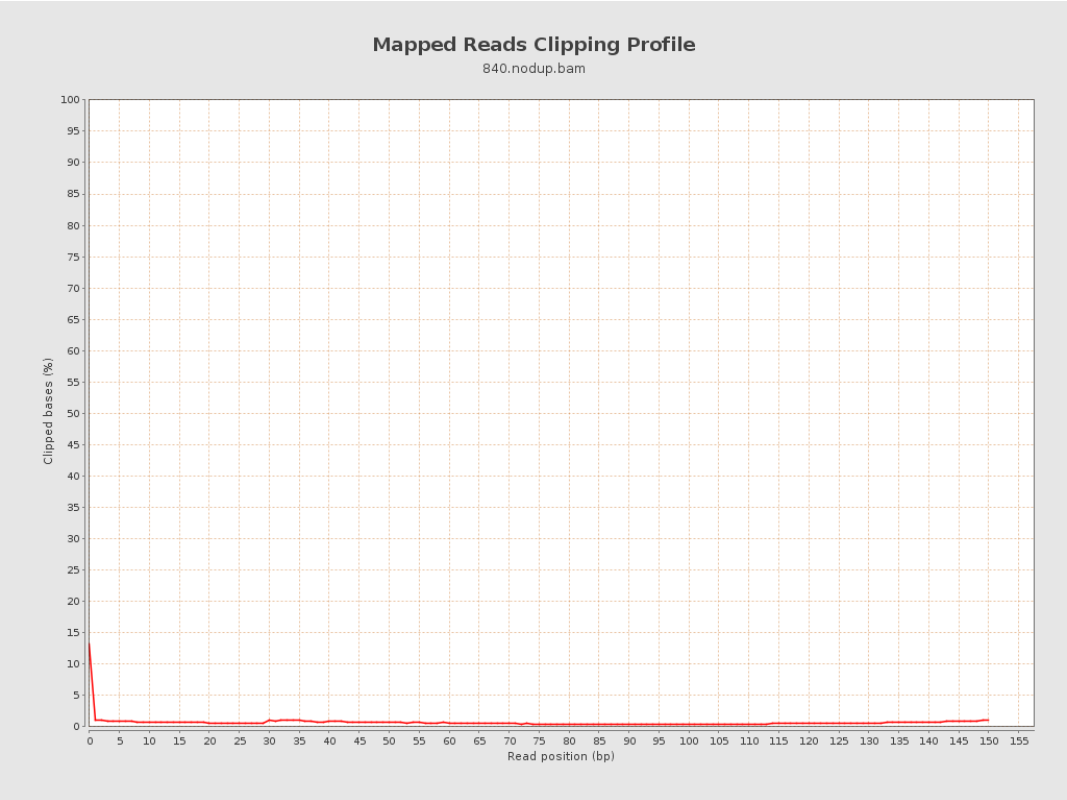
8. Results : Mapped Reads Nucleotide Content



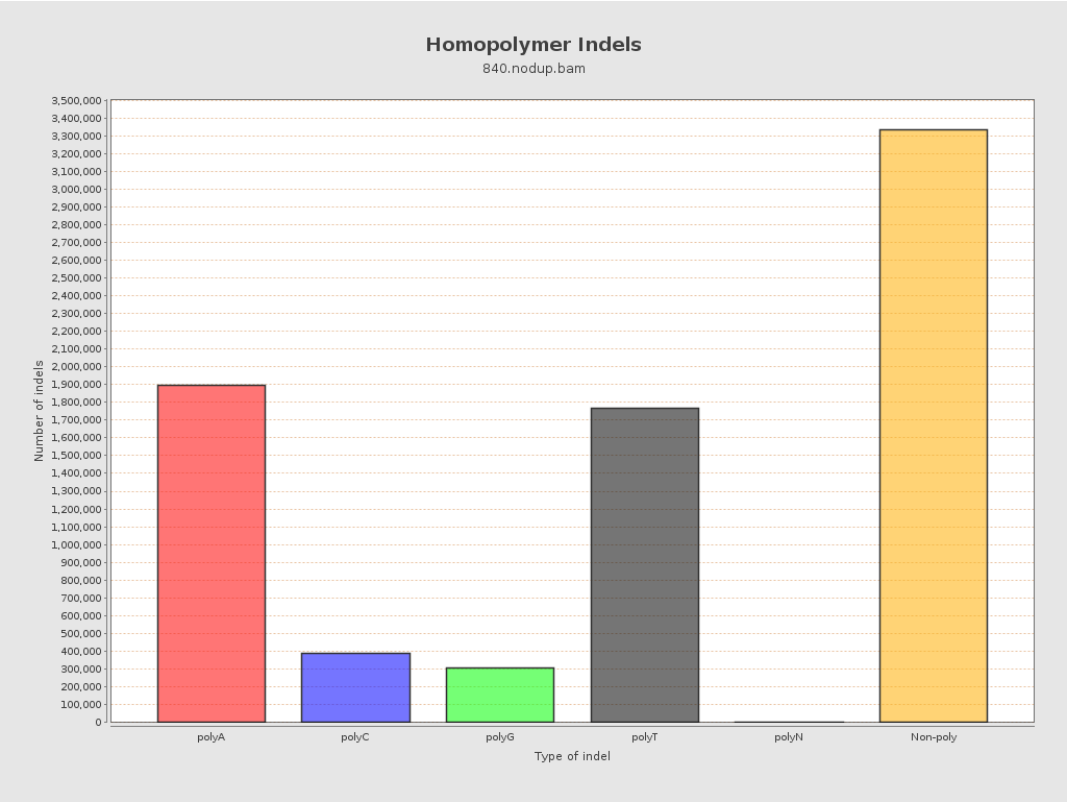
9. Results : Mapped Reads GC-content Distribution



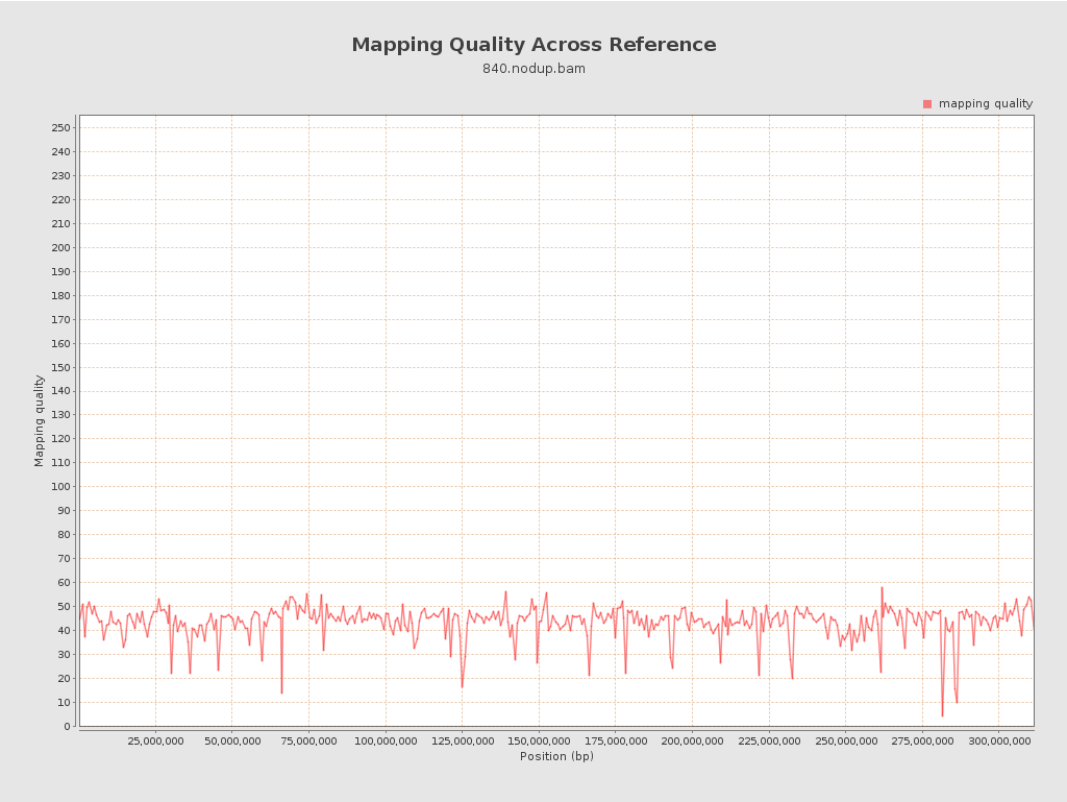
10. Results : Mapped Reads Clipping Profile



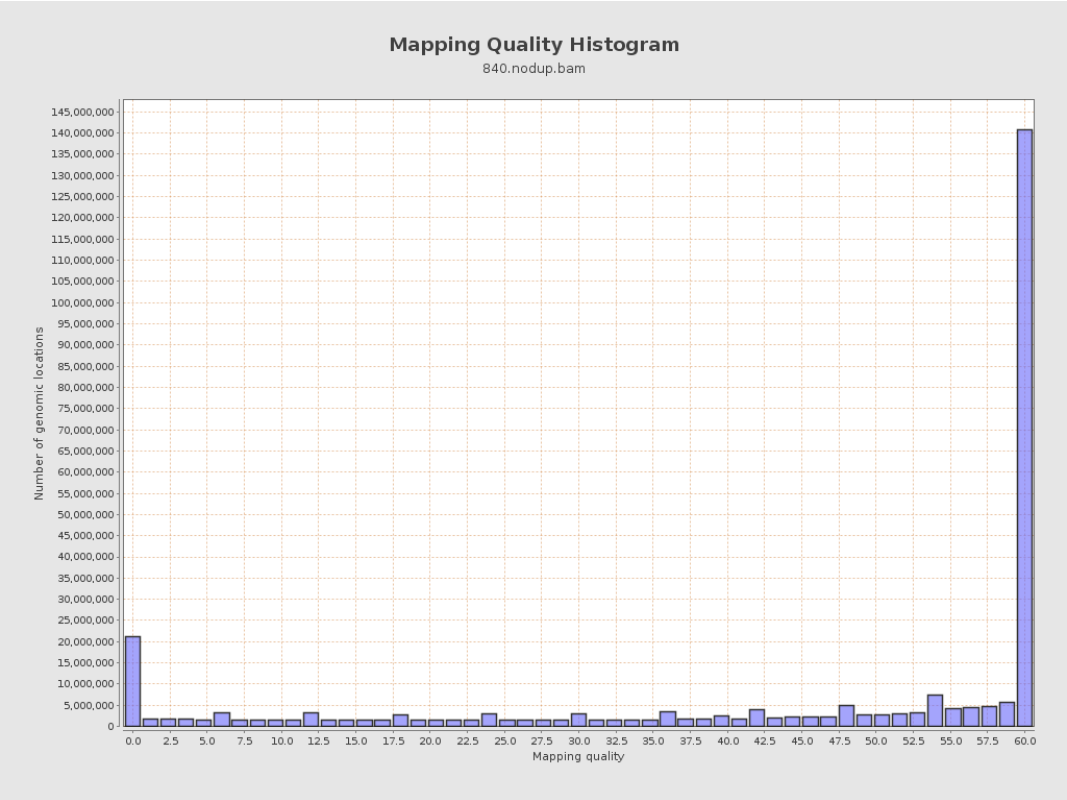
11. Results : Homopolymer Indels



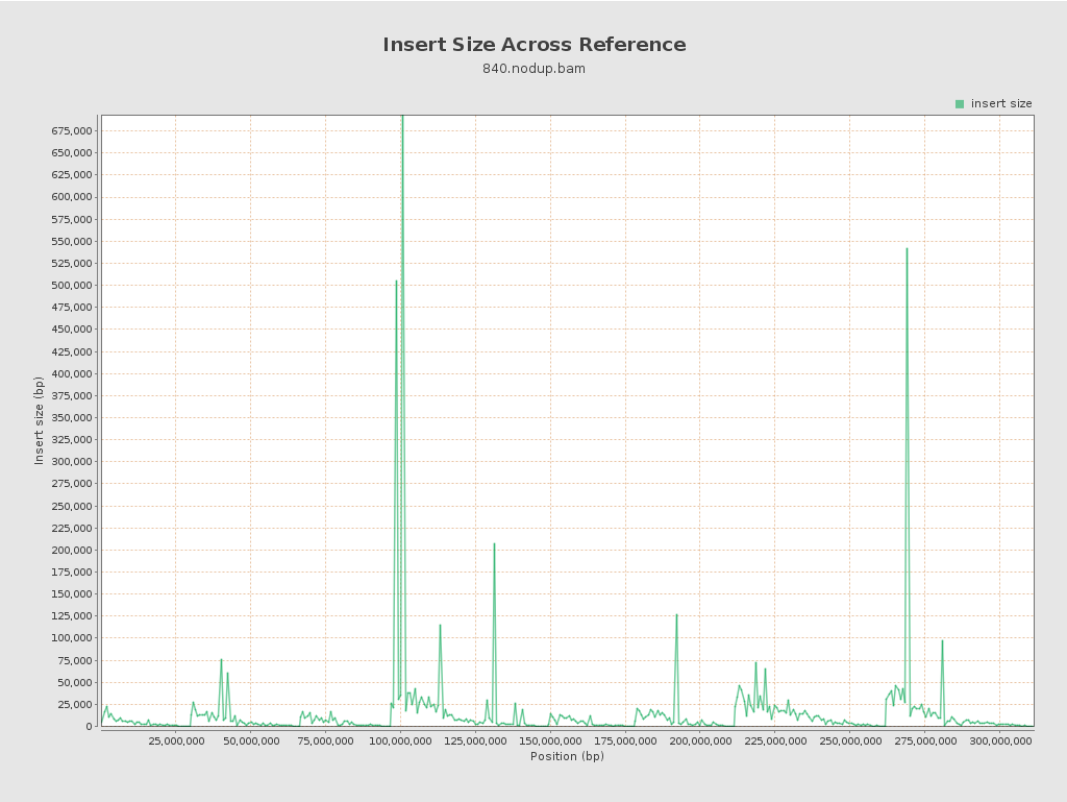
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram