Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/857.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/857.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_551/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_551_S118_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_551/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_551_S118_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:35:29 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	78,431,182
Mapped reads	73,382,746 / 93.56%
Unmapped reads	5,048,436 / 6.44%
Mapped paired reads	73,382,746 / 93.56%
Mapped reads, first in pair	36,799,729 / 46.92%
Mapped reads, second in pair	36,583,017 / 46.64%
Mapped reads, both in pair	71,781,695 / 91.52%
Mapped reads, singletons	1,601,051 / 2.04%
Read min/max/mean length	30 / 151 / 148.05
Duplicated reads (flagged)	11,411,451 / 14.55%
Clipped reads	17,538,958 / 22.36%

2.2. ACGT Content

Number/percentage of A's	3,127,659,301 / 30.95%
Number/percentage of C's	1,925,437,688 / 19.05%
Number/percentage of T's	3,128,670,666 / 30.96%
Number/percentage of G's	1,925,064,334 / 19.05%
Number/percentage of N's	73,618 / 0%
GC Percentage	38.1%

2.3. Coverage

Mean	32.5155
Standard Deviation	254.6169

2.4. Mapping Quality

Mean Mapping Quality	44.19

2.5. Insert size

Mean	226,321.32
Standard Deviation	2,268,143.72
P25/Median/P75	308 / 407 / 531

2.6. Mismatches and indels

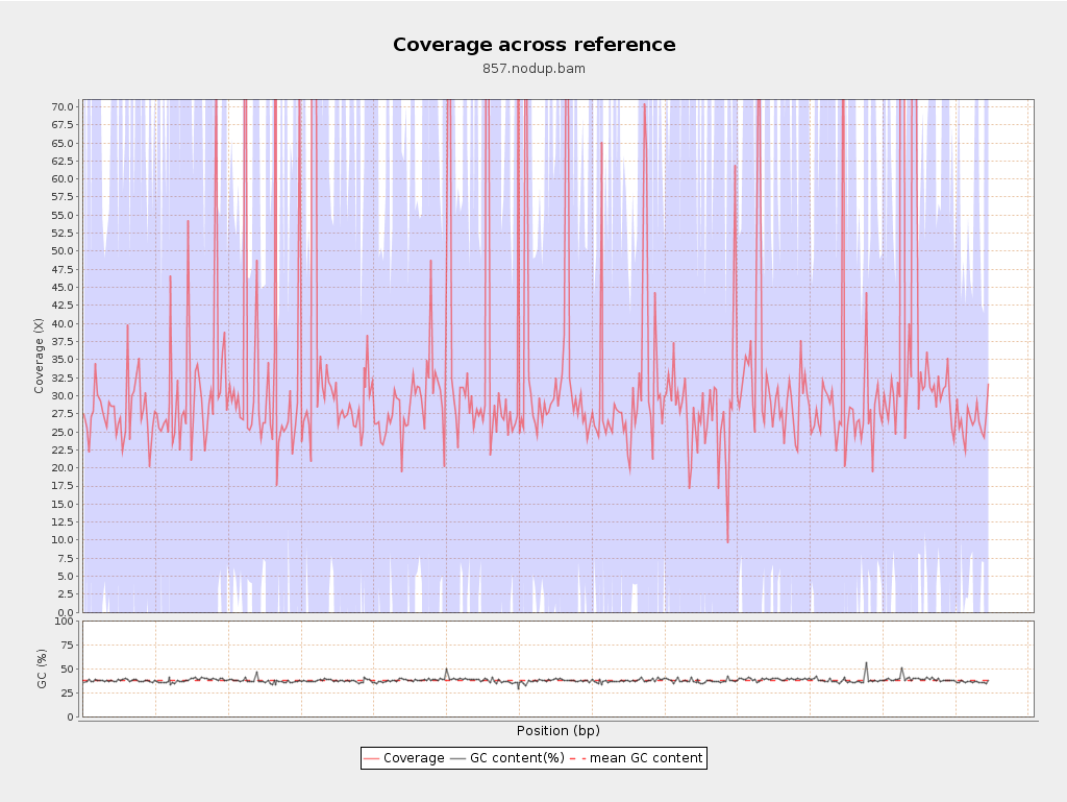
General error rate	2.48%
Mismatches	232,195,361
Insertions	6,911,396
Mapped reads with at least one insertion	8.44%
Deletions	7,018,554
Mapped reads with at least one deletion	8.48%
Homopolymer indels	56.46%

2.7. Chromosome stats

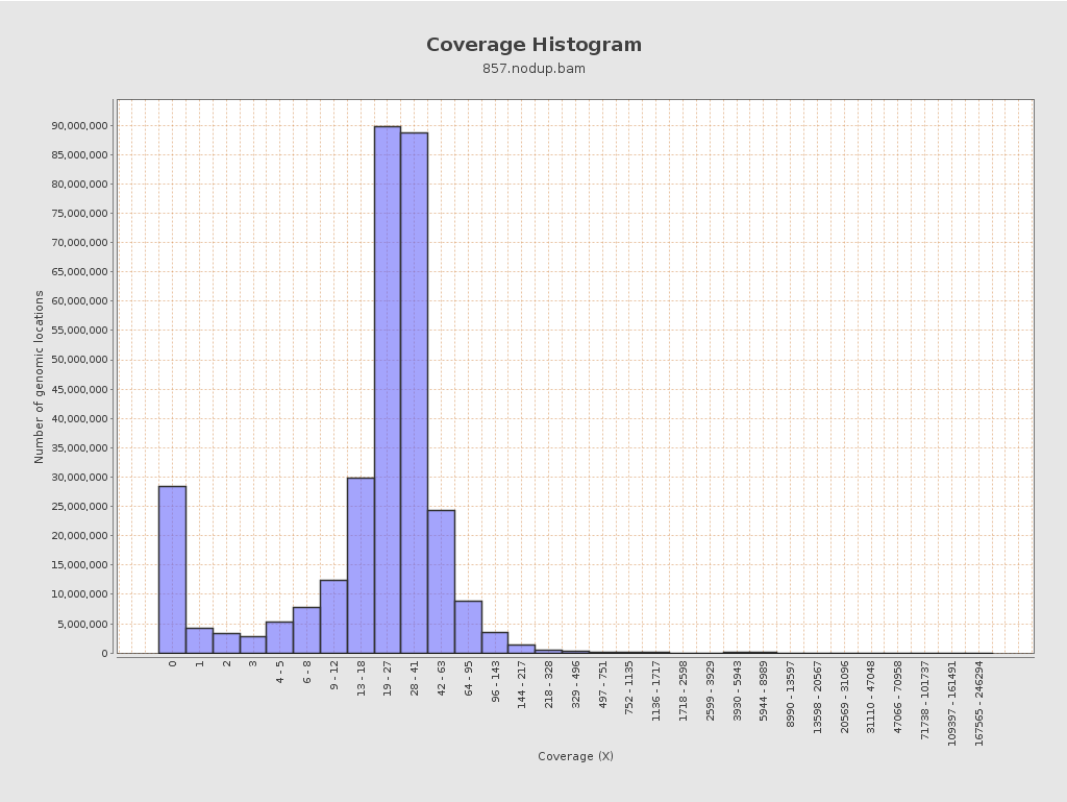
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	820080540	27.5895	99.4962

LT669789.1	36598175	1200402089	32.7995	260.8704
LT669790.1	30422129	1092269317	35.9038	274.2205
LT669791.1	52758100	1663758028	31.5356	248.3347
LT669792.1	28376109	926126667	32.6375	248.7205
LT669793.1	33388210	1009205419	30.2264	140.1032
LT669794.1	50579949	1575687762	31.1524	233.3514
LT669795.1	49795044	1845680689	37.0655	367.0899

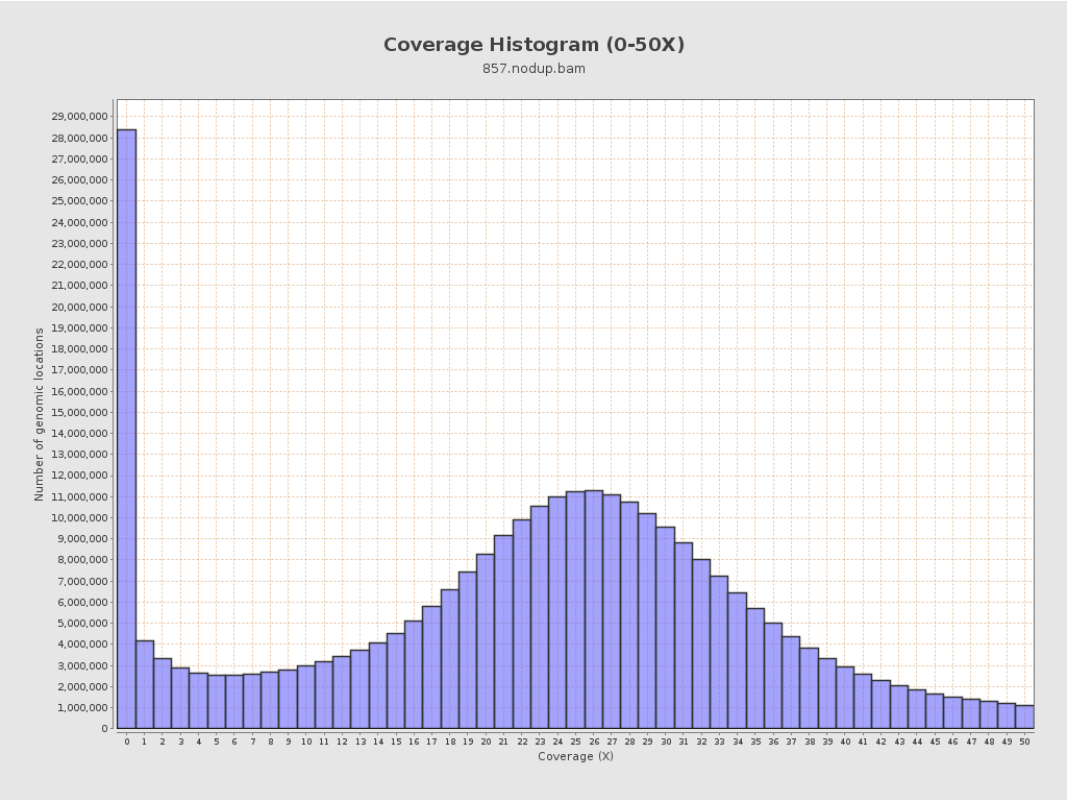
3. Results : Coverage across reference



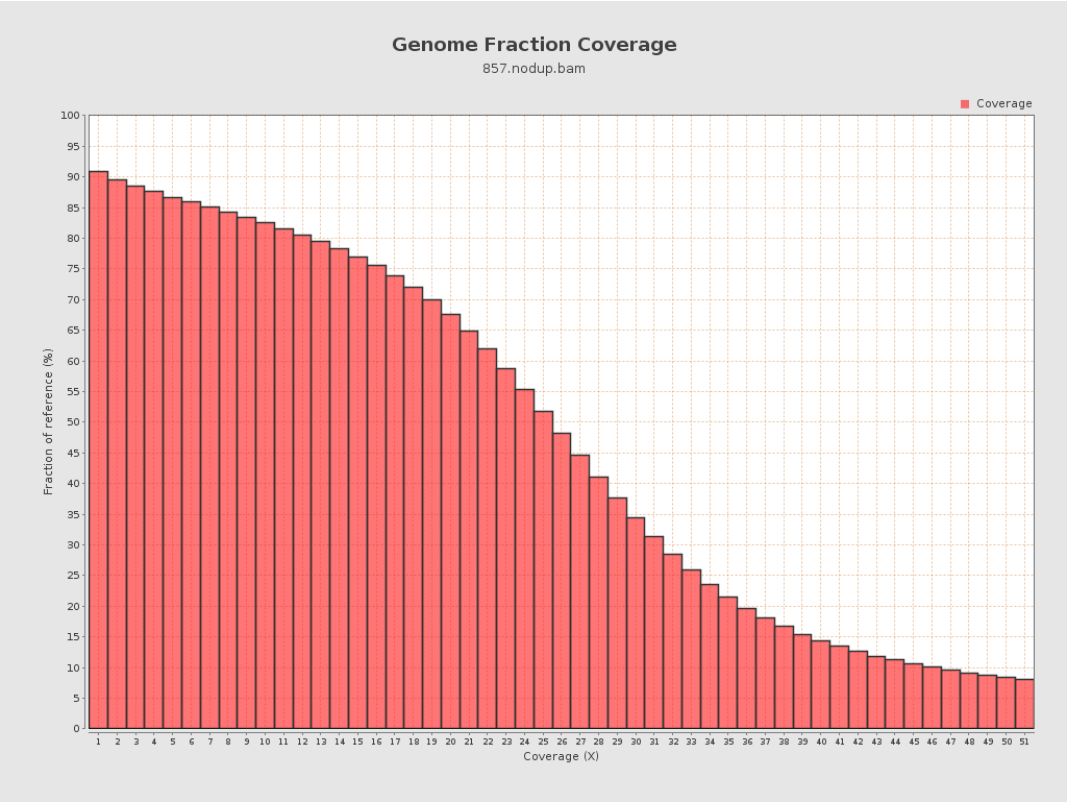
4. Results : Coverage Histogram



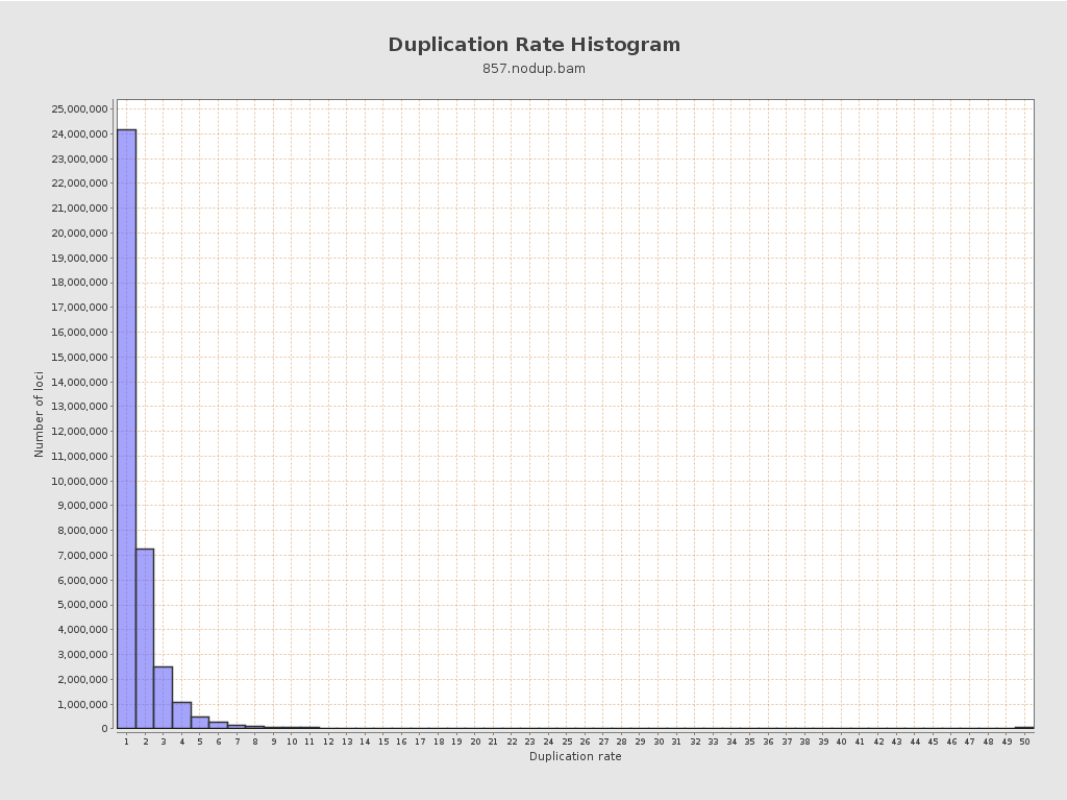
5. Results : Coverage Histogram (0-50X)



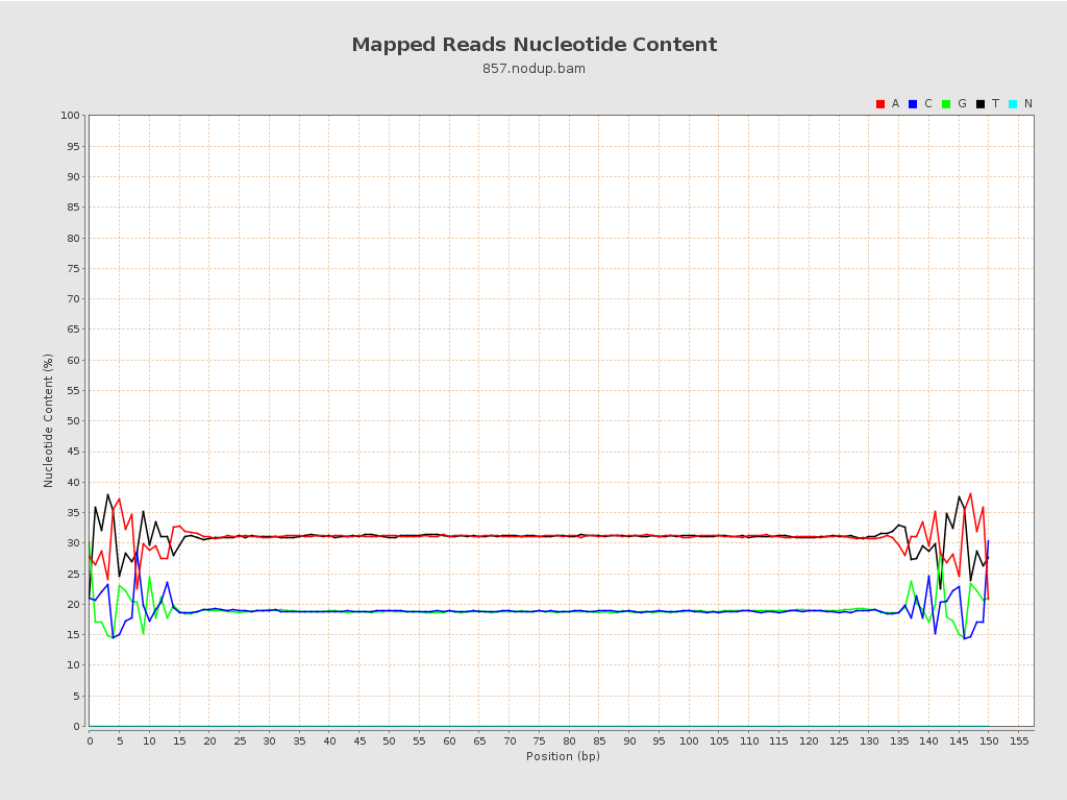
6. Results : Genome Fraction Coverage



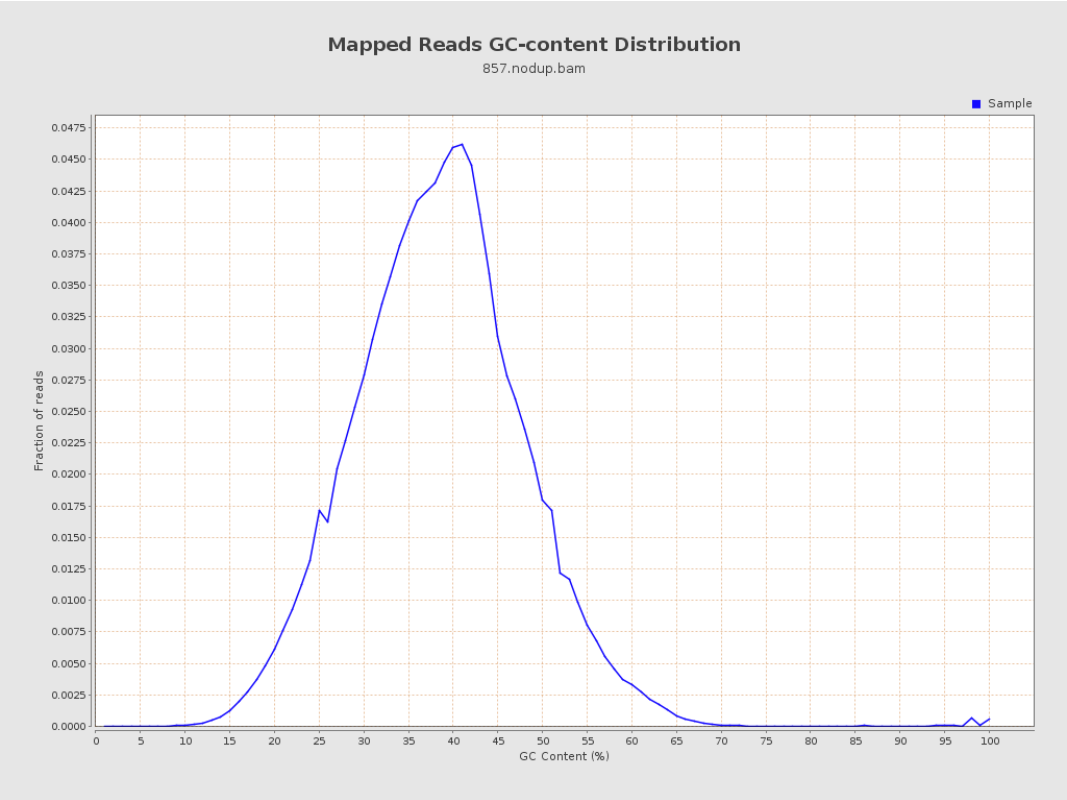
7. Results : Duplication Rate Histogram



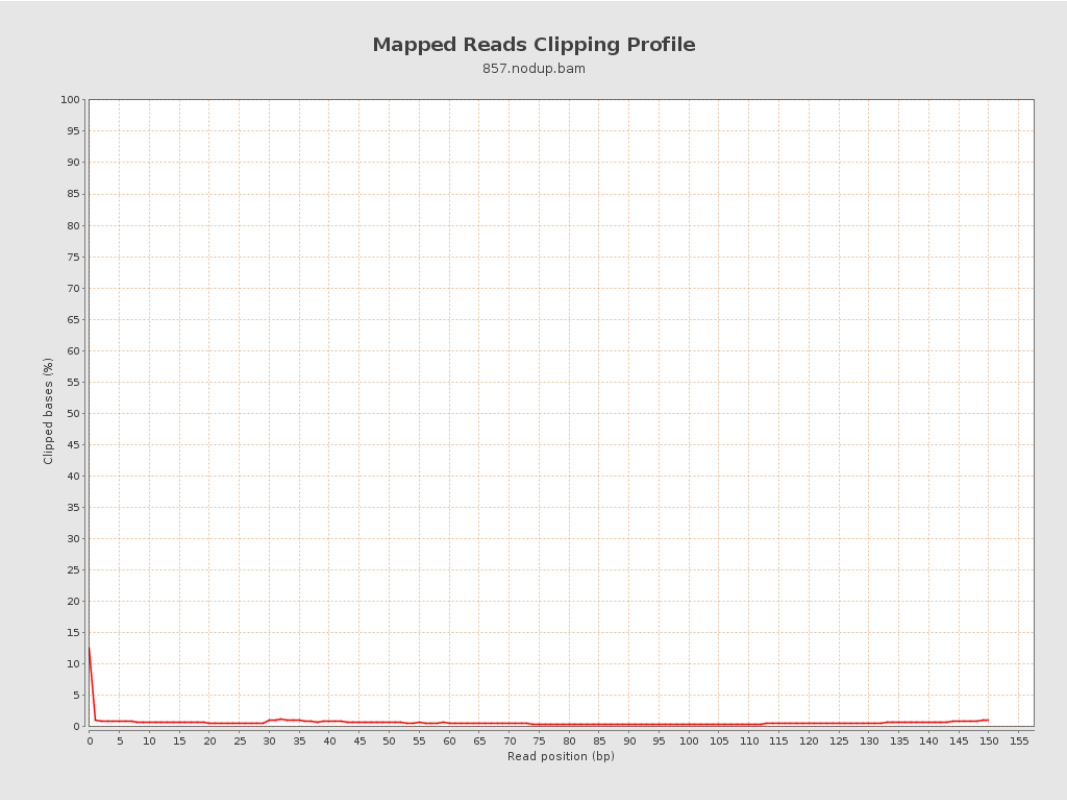
8. Results : Mapped Reads Nucleotide Content



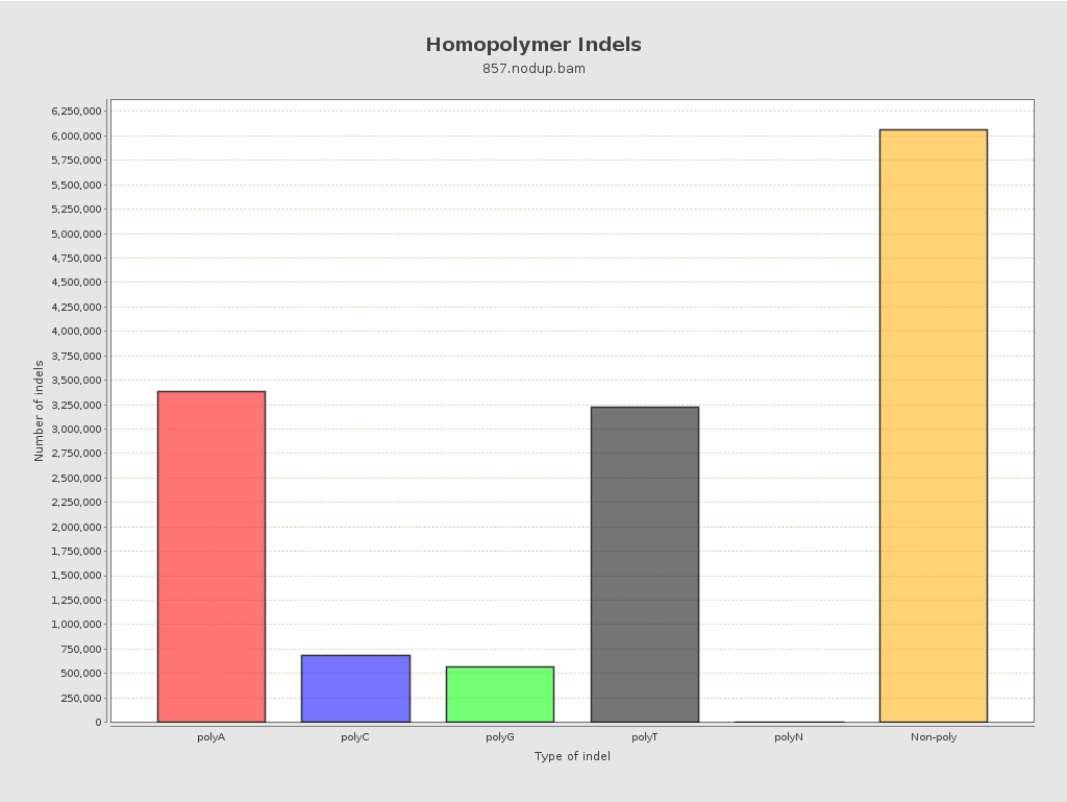
9. Results : Mapped Reads GC-content Distribution



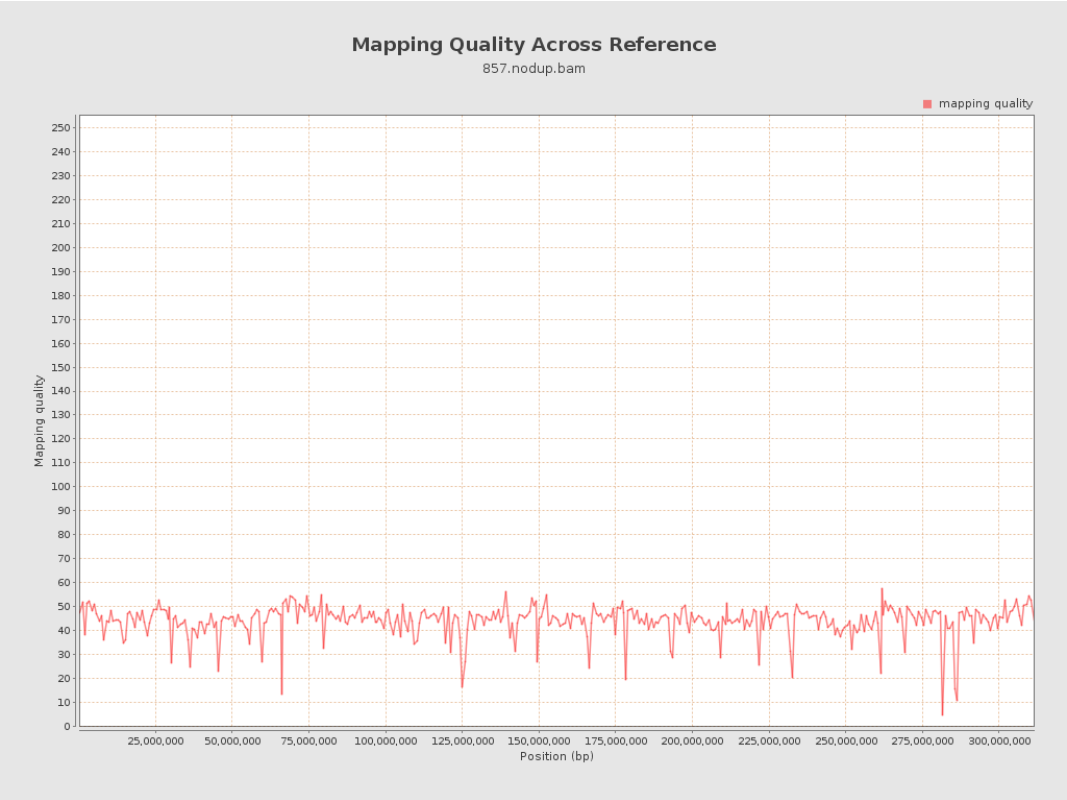
10. Results : Mapped Reads Clipping Profile



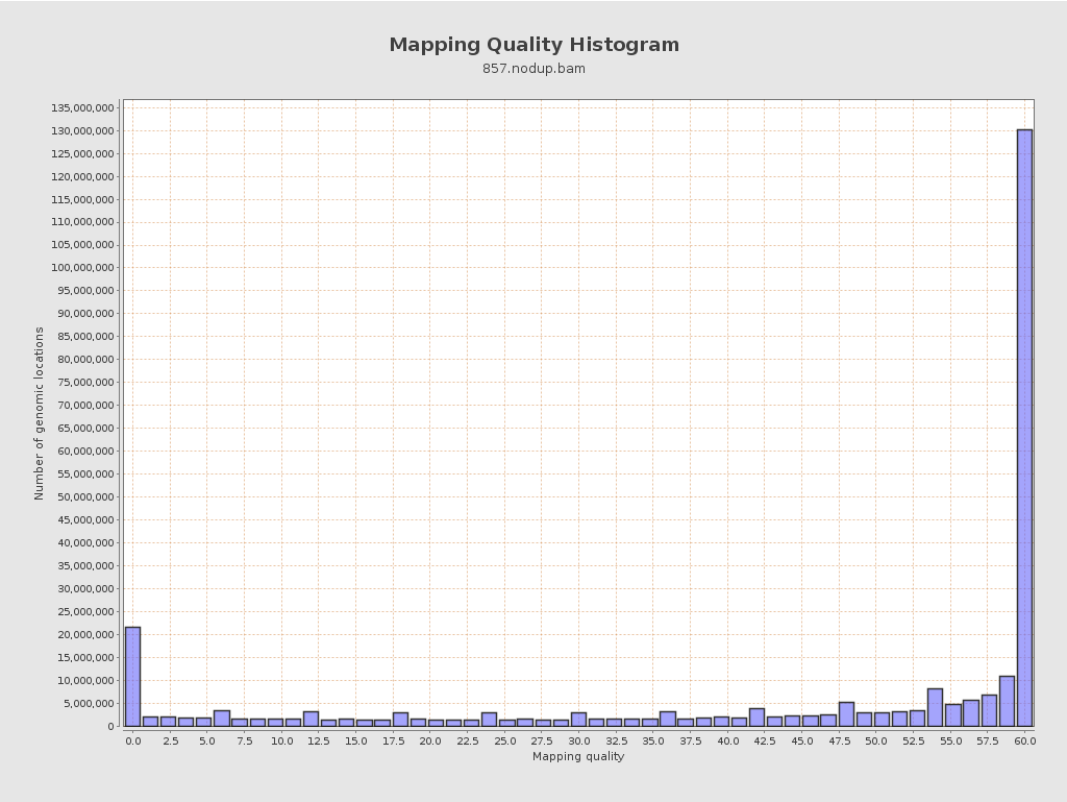
11. Results : Homopolymer Indels



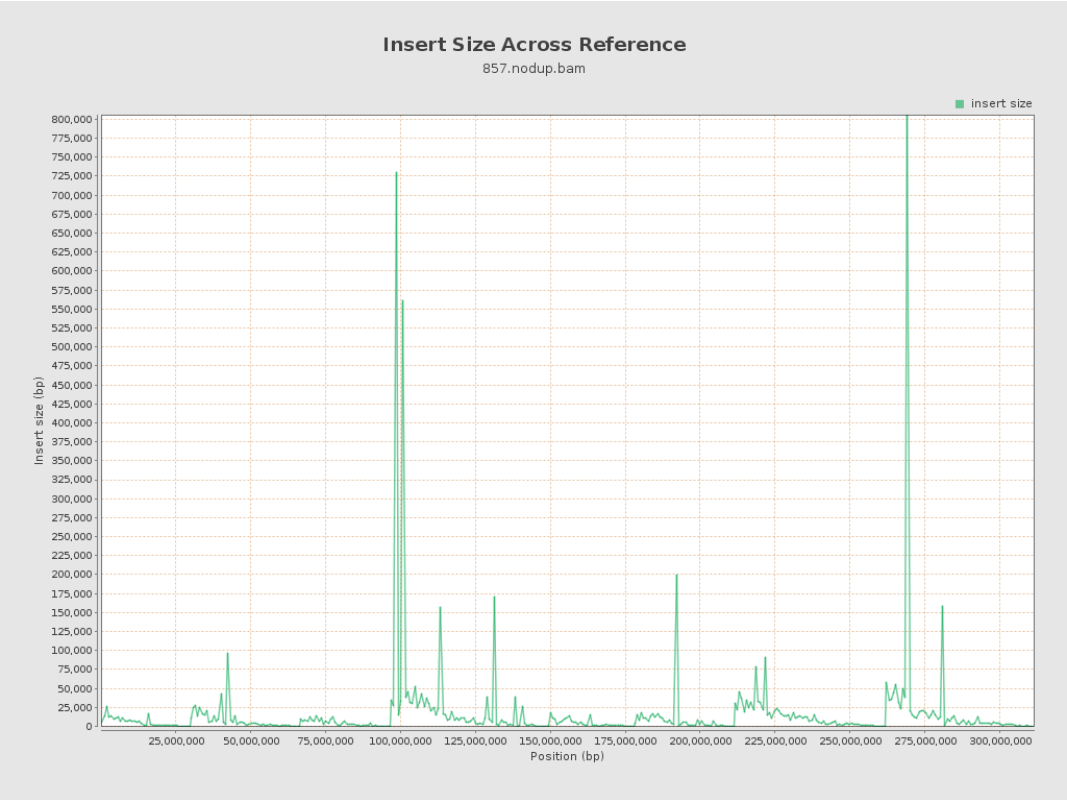
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram