Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:30:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/867.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/867.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_202/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_202_S283_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_202/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_202_S283_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:30:50 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	68,719,724
Mapped reads	62,626,418 / 91.13%
Unmapped reads	6,093,306 / 8.87%
Mapped paired reads	62,626,418 / 91.13%
Mapped reads, first in pair	31,369,846 / 45.65%
Mapped reads, second in pair	31,256,572 / 45.48%
Mapped reads, both in pair	60,804,971 / 88.48%
Mapped reads, singletons	1,821,447 / 2.65%
Read min/max/mean length	30 / 151 / 148.2
Duplicated reads (flagged)	10,354,087 / 15.07%
Clipped reads	14,484,244 / 21.08%

2.2. ACGT Content

Number/percentage of A's	2,663,721,375 / 30.92%
Number/percentage of C's	1,641,761,466 / 19.06%
Number/percentage of T's	2,667,403,449 / 30.96%
Number/percentage of G's	1,641,897,727 / 19.06%
Number/percentage of N's	31,946 / 0%
GC Percentage	38.12%

2.3. Coverage

Mean	27.7123
Standard Deviation	262.3021

2.4. Mapping Quality

Mean Mapping Quality	44.61

2.5. Insert size

Mean	245,763.58
Standard Deviation	2,397,059.98
P25/Median/P75	320 / 418 / 541

2.6. Mismatches and indels

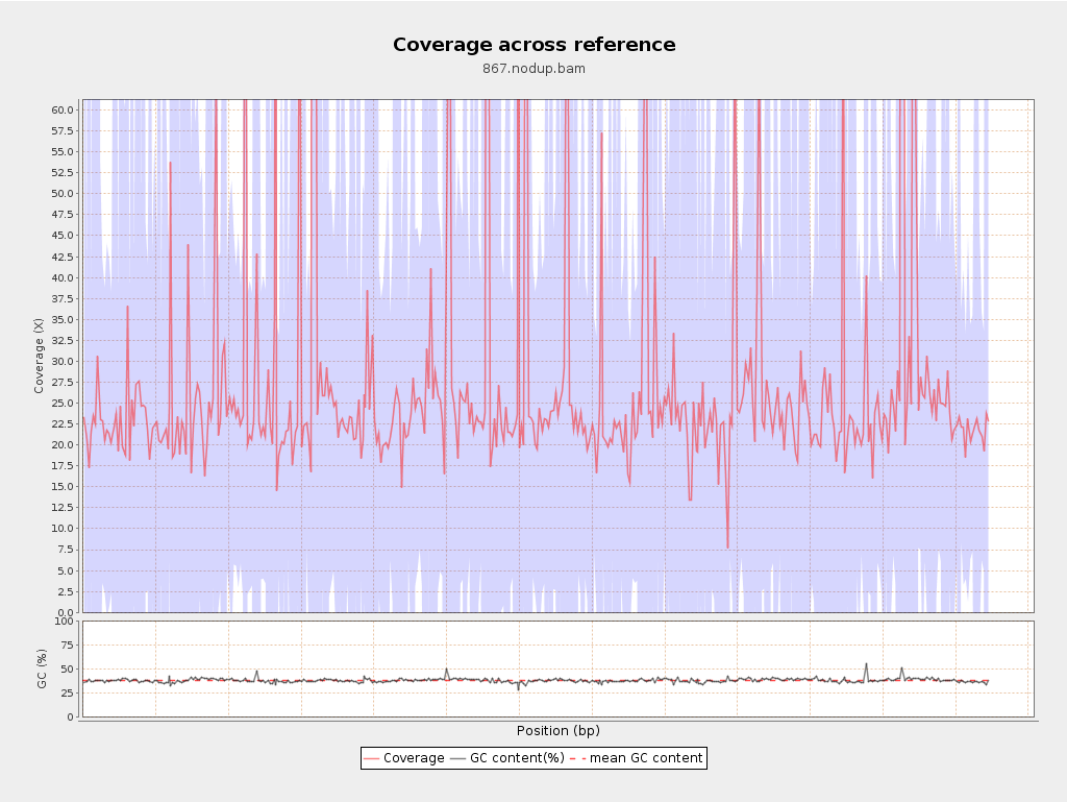
General error rate	2.3%
Mismatches	181,027,926
Insertions	6,122,375
Mapped reads with at least one insertion	8.72%
Deletions	5,820,251
Mapped reads with at least one deletion	8.24%
Homopolymer indels	57.09%

2.7. Chromosome stats

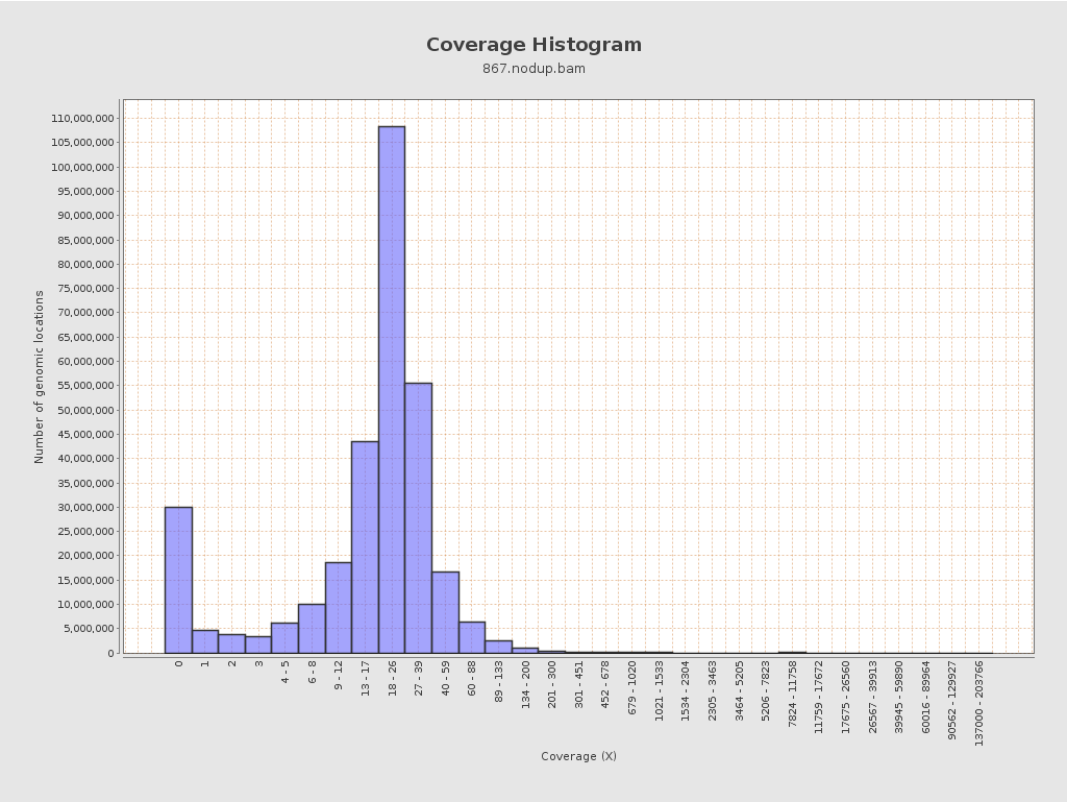
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	672586020	22.6274	99.7794

LT669789.1	36598175	1007784047	27.5365	281.6942
LT669790.1	30422129	1016973809	33.4288	358.7868
LT669791.1	52758100	1435363659	27.2065	291.0723
LT669792.1	28376109	791606263	27.8969	269.5565
LT669793.1	33388210	846899295	25.3652	171.1601
LT669794.1	50579949	1316027886	26.0188	219.326
LT669795.1	49795044	1549071434	31.1089	296.5788

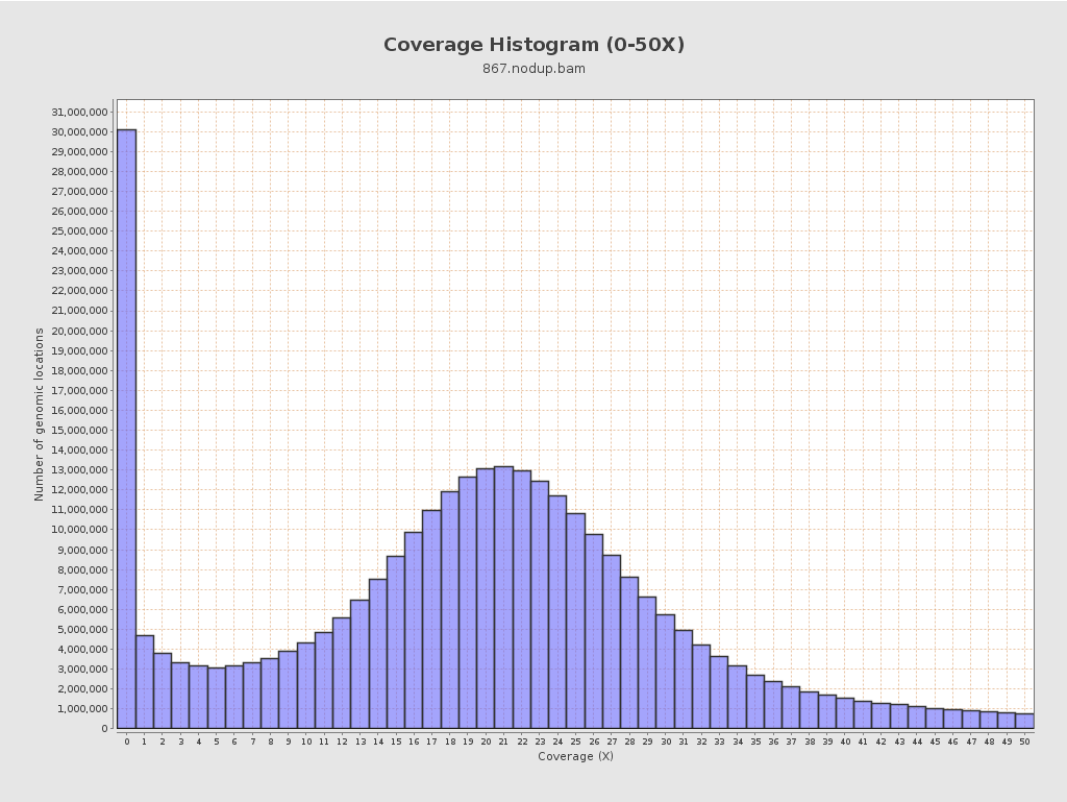
3. Results : Coverage across reference



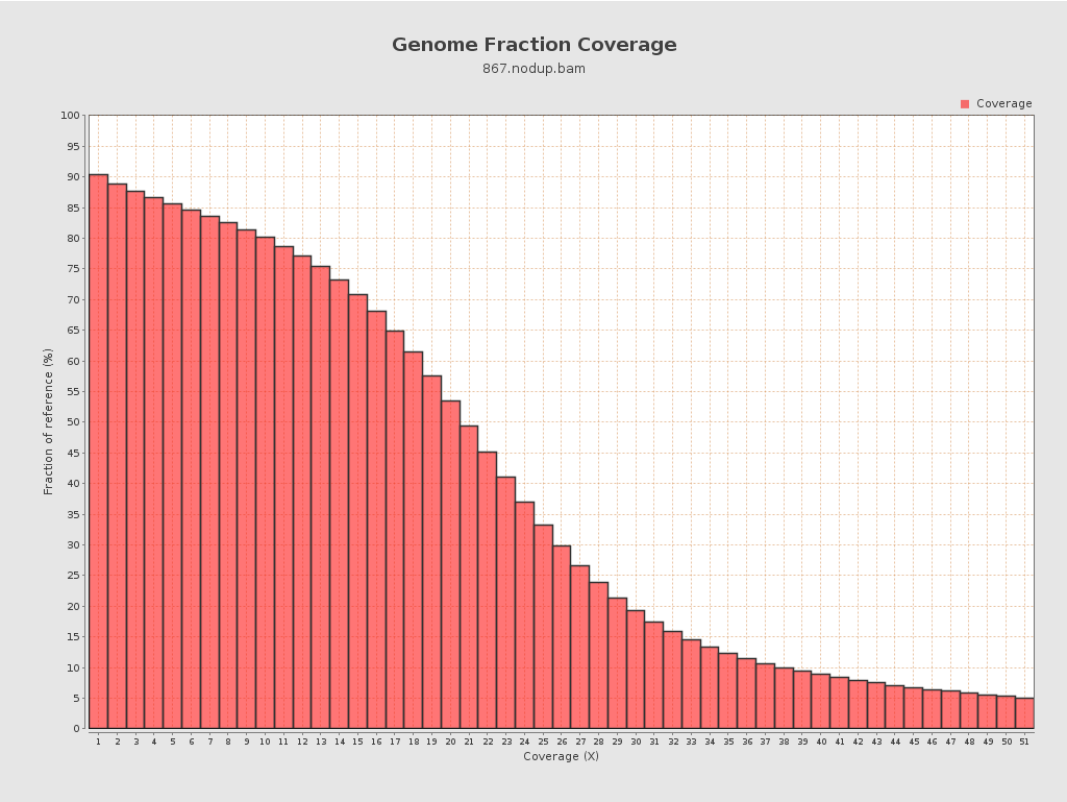
4. Results : Coverage Histogram



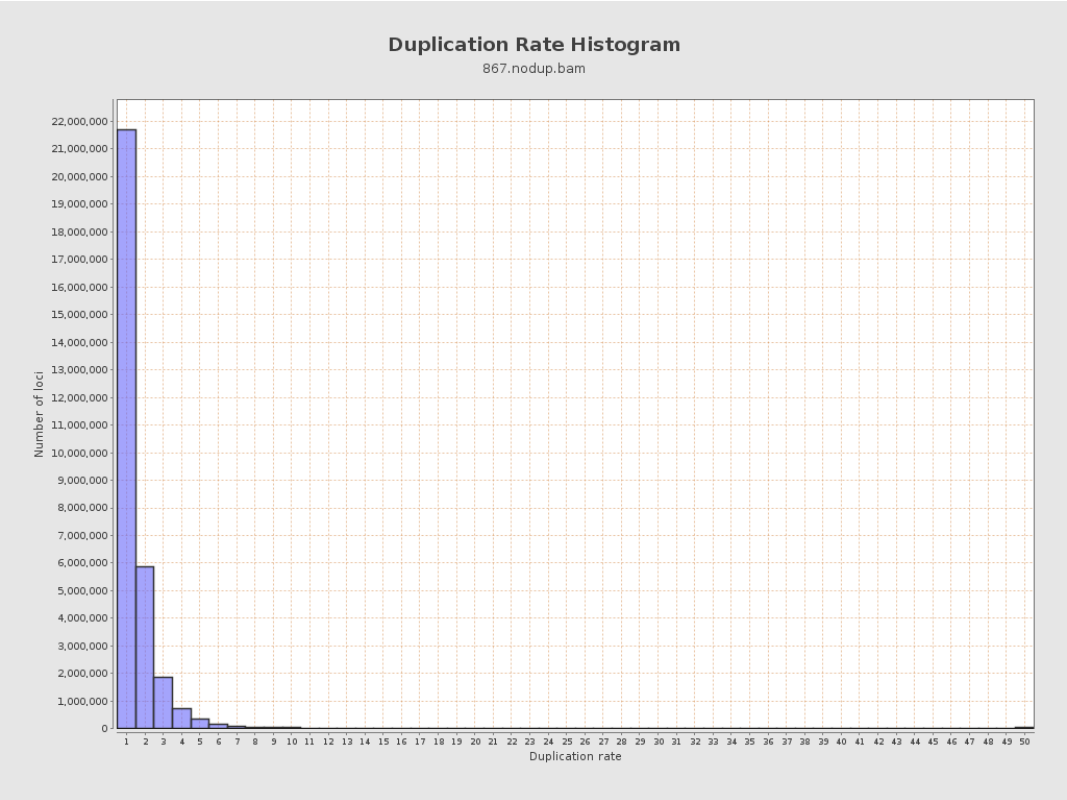
5. Results : Coverage Histogram (0-50X)



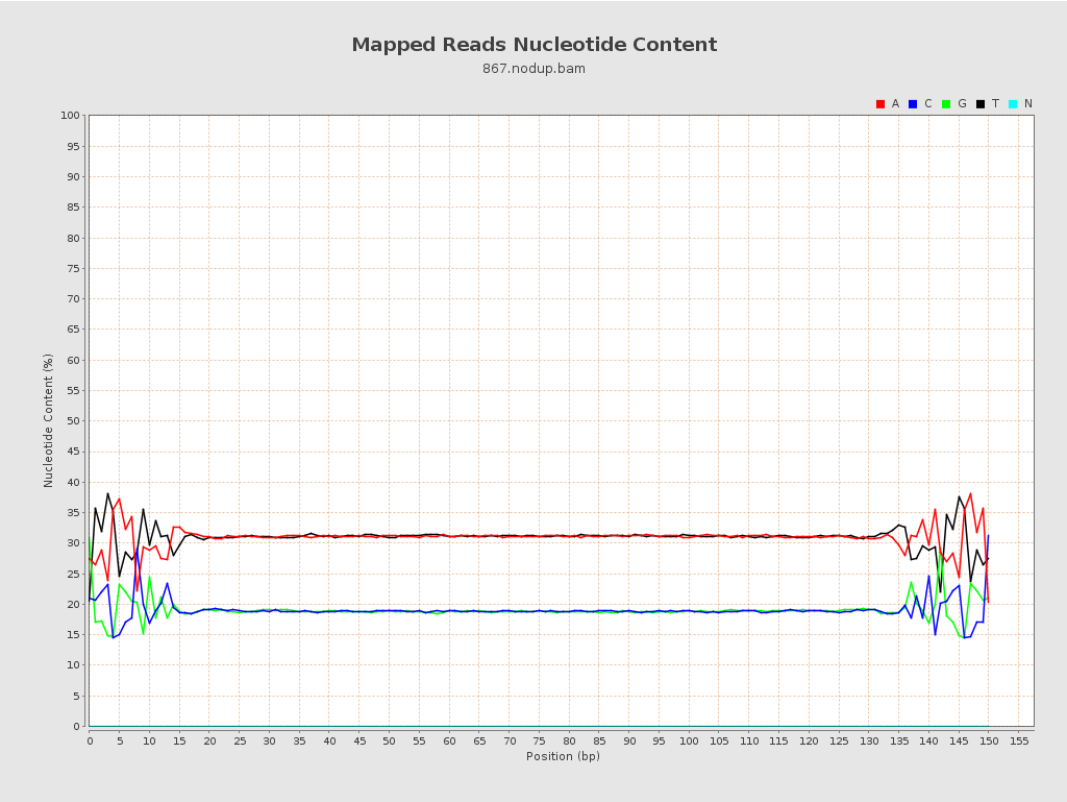
6. Results : Genome Fraction Coverage



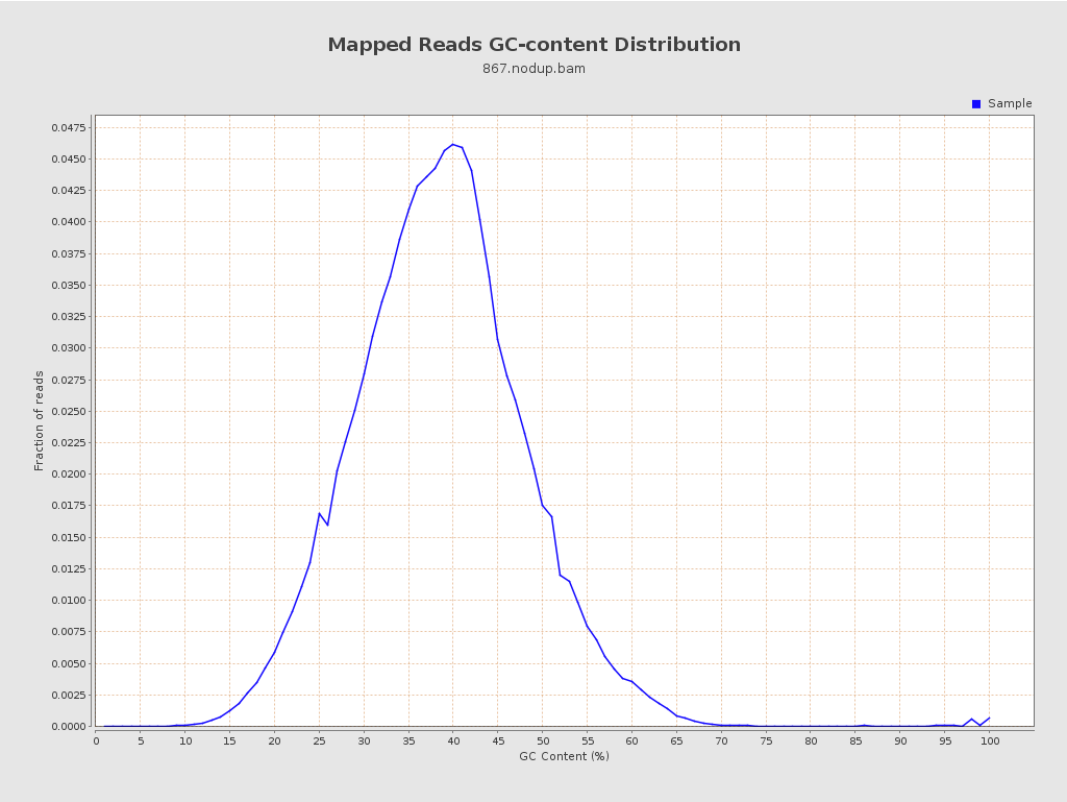
7. Results : Duplication Rate Histogram



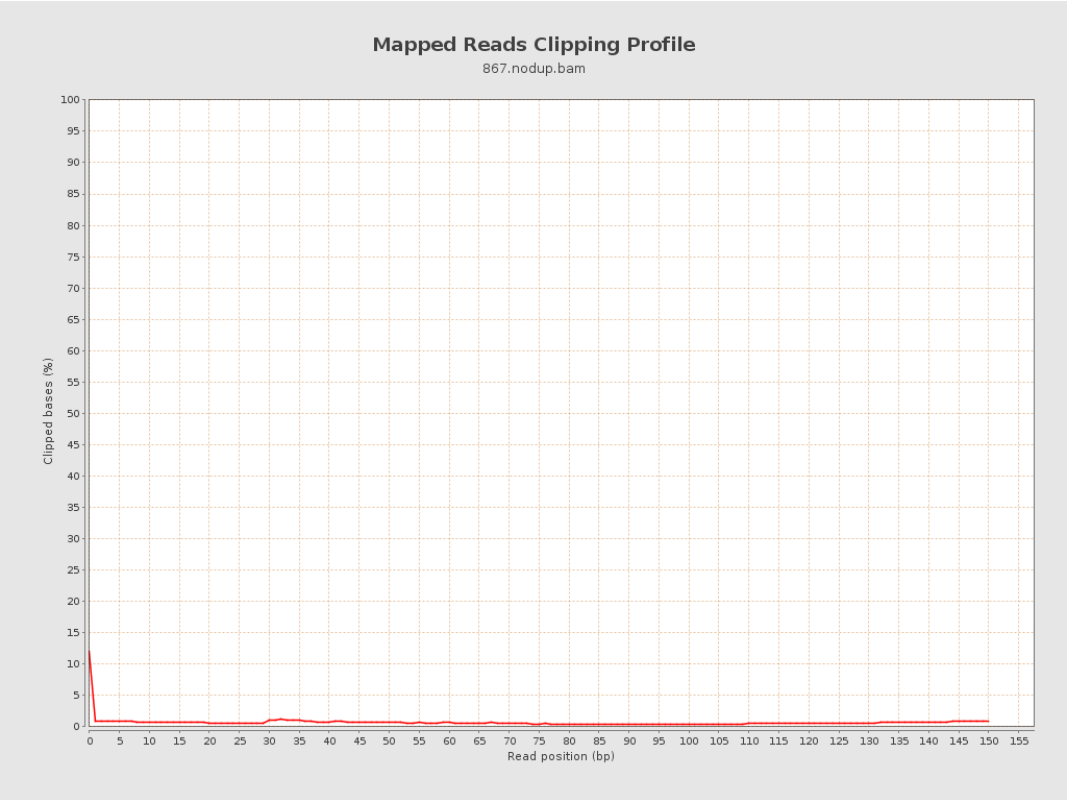
8. Results : Mapped Reads Nucleotide Content



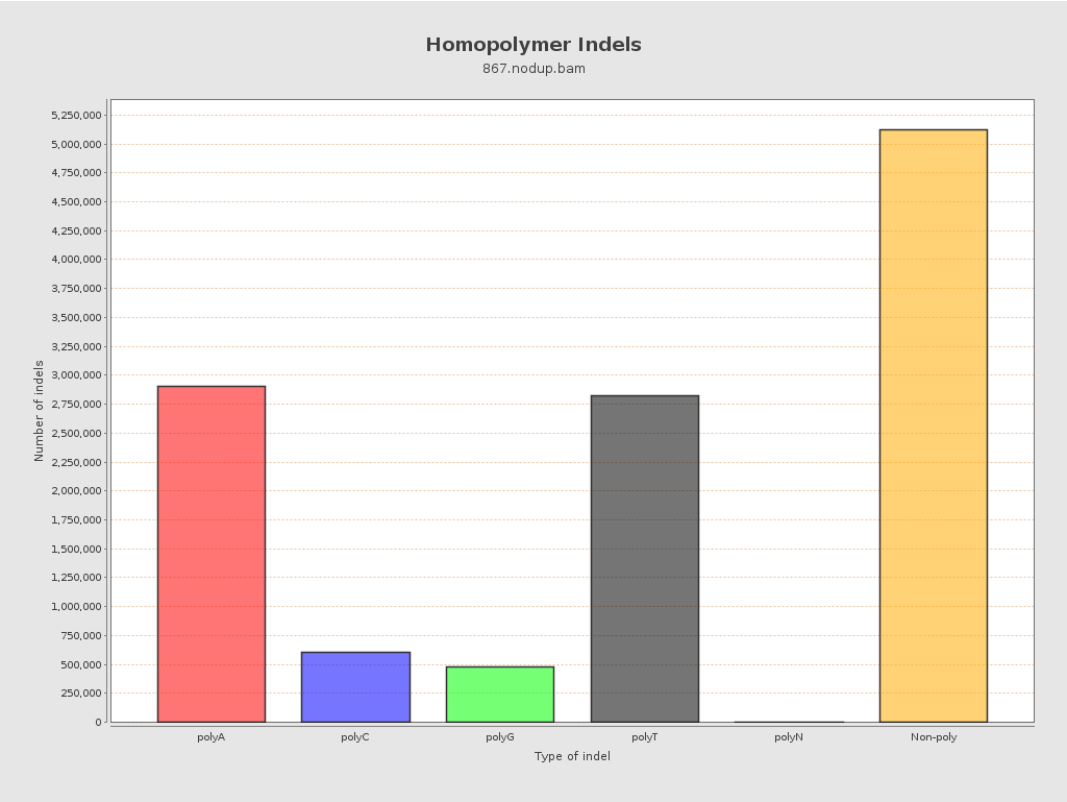
9. Results : Mapped Reads GC-content Distribution



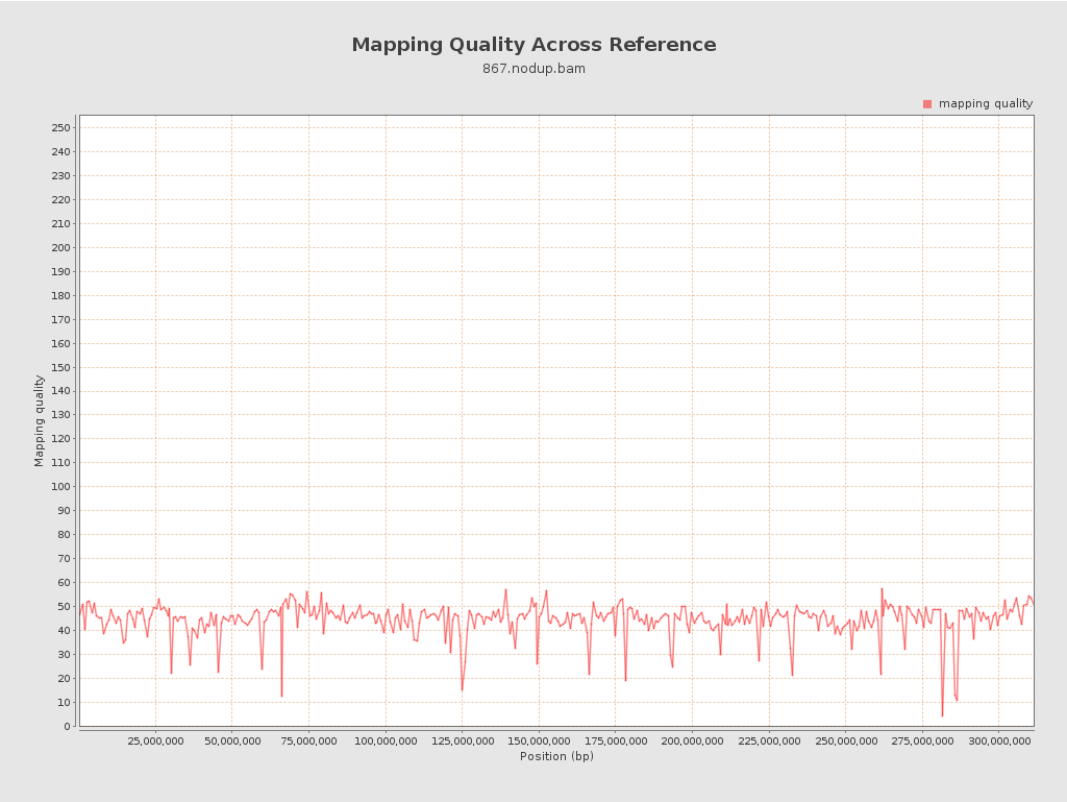
10. Results : Mapped Reads Clipping Profile



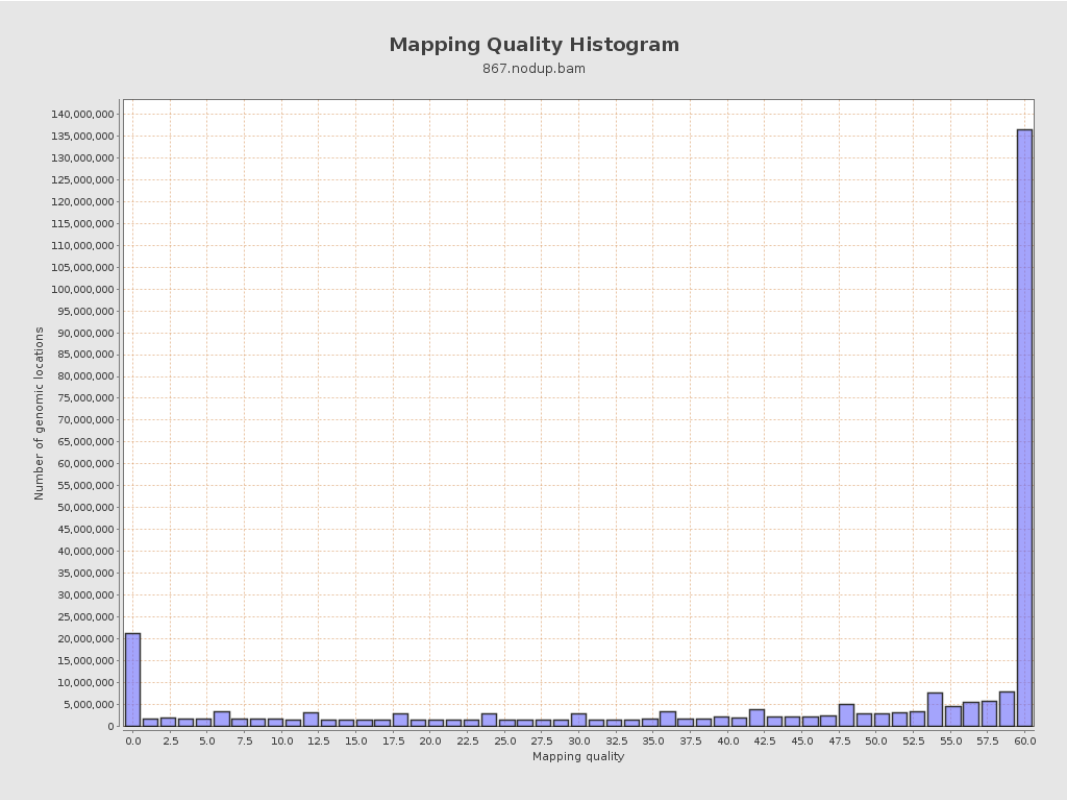
11. Results : Homopolymer Indels



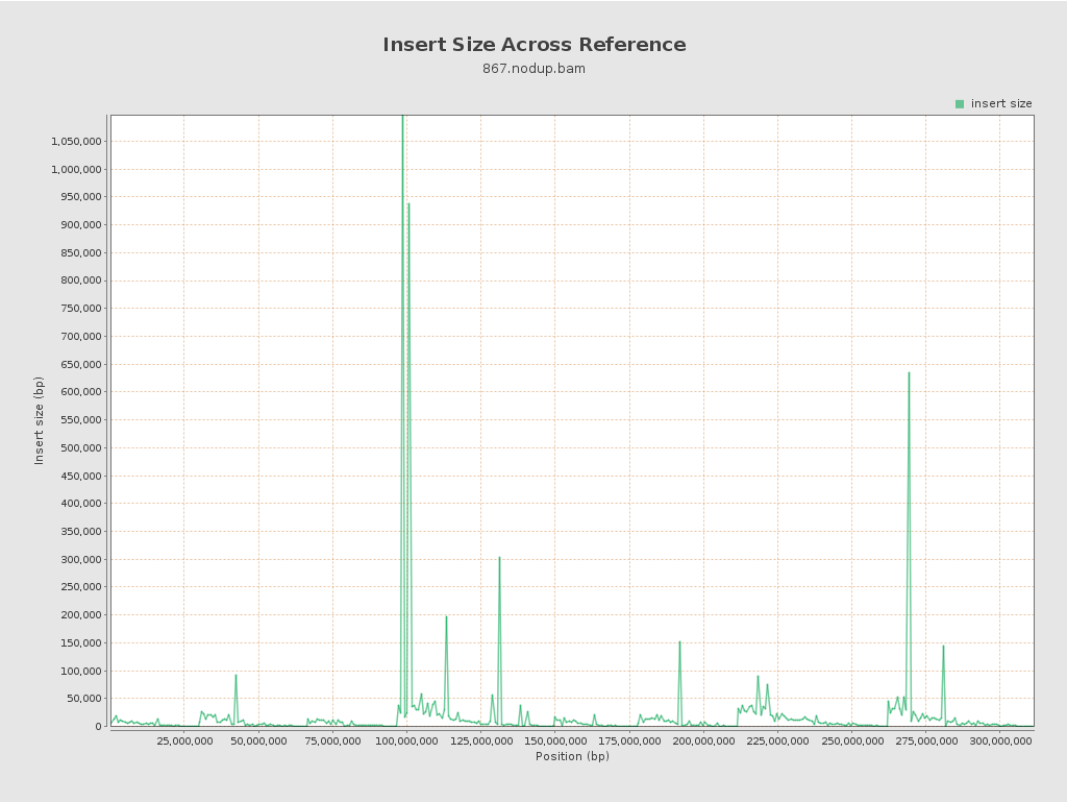
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram