Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:27:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/869.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/869.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_568/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_568_S135_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_568/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_568_S135_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:26:59 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	52,103,289
Mapped reads	48,722,787 / 93.51%
Unmapped reads	3,380,502 / 6.49%
Mapped paired reads	48,722,787 / 93.51%
Mapped reads, first in pair	24,455,336 / 46.94%
Mapped reads, second in pair	24,267,451 / 46.58%
Mapped reads, both in pair	47,676,097 / 91.5%
Mapped reads, singletons	1,046,690 / 2.01%
Read min/max/mean length	30 / 151 / 148
Duplicated reads (flagged)	6,556,996 / 12.58%
Clipped reads	11,977,932 / 22.99%

2.2. ACGT Content

Number/percentage of A's	2,069,269,723 / 30.86%
Number/percentage of C's	1,283,365,637 / 19.14%
Number/percentage of T's	2,071,387,336 / 30.89%
Number/percentage of G's	1,281,269,825 / 19.11%
Number/percentage of N's	45,612 / 0%
GC Percentage	38.25%

2.3. Coverage

Mean	21.5746
Standard Deviation	172.0153

2.4. Mapping Quality

Mean Mapping Quality	43.47

2.5. Insert size

Mean	231,158.33
Standard Deviation	2,281,229.45
P25/Median/P75	308 / 406 / 528

2.6. Mismatches and indels

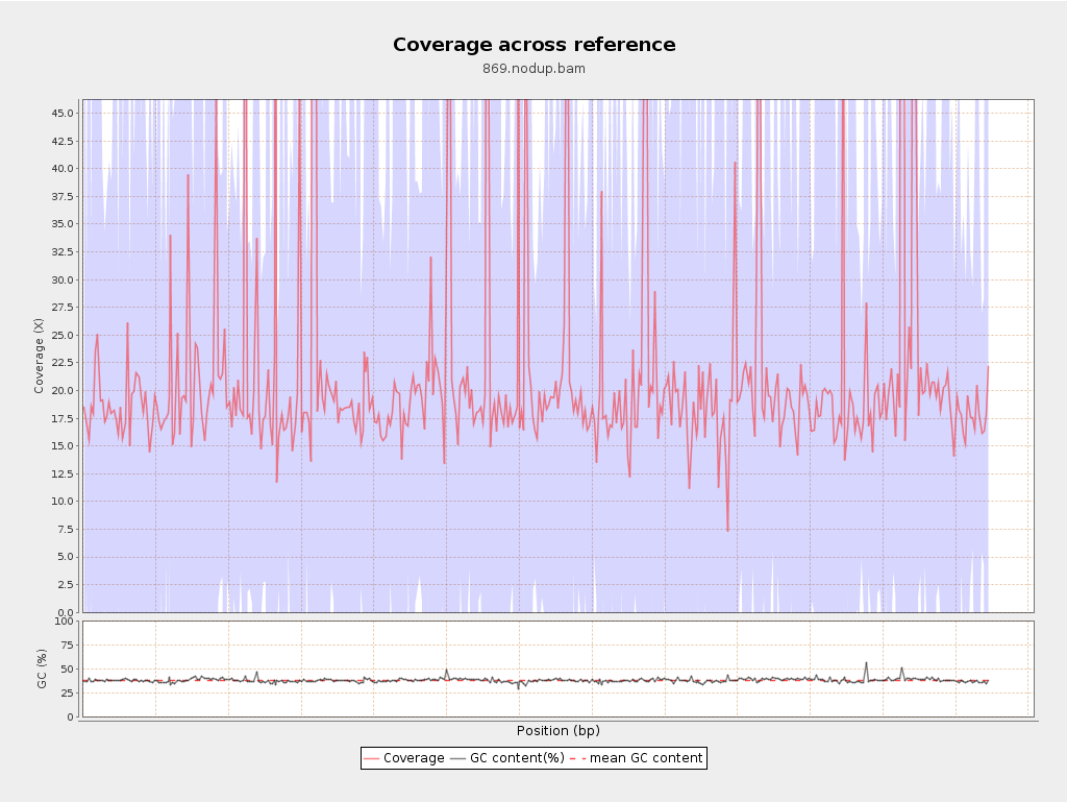
General error rate	2.63%
Mismatches	163,858,969
Insertions	4,669,120
Mapped reads with at least one insertion	8.6%
Deletions	4,803,342
Mapped reads with at least one deletion	8.74%
Homopolymer indels	55.91%

2.7. Chromosome stats

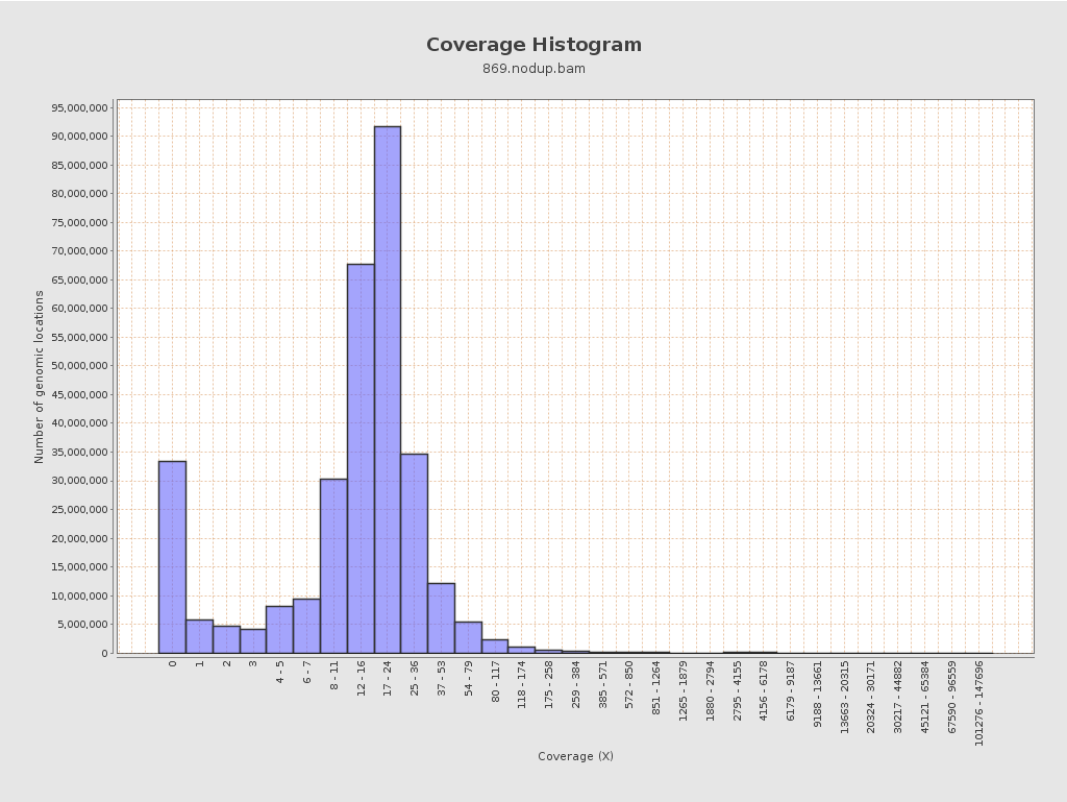
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	550444627	18.5183	63.8937

LT669789.1	36598175	807853795	22.0736	188.4424
LT669790.1	30422129	717848865	23.5963	183.8927
LT669791.1	52758100	1097712371	20.8065	162.2367
LT669792.1	28376109	609026128	21.4626	161.683
LT669793.1	33388210	690497347	20.6809	159.628
LT669794.1	50579949	1043588402	20.6325	167.2235
LT669795.1	49795044	1206592547	24.2312	218.3962

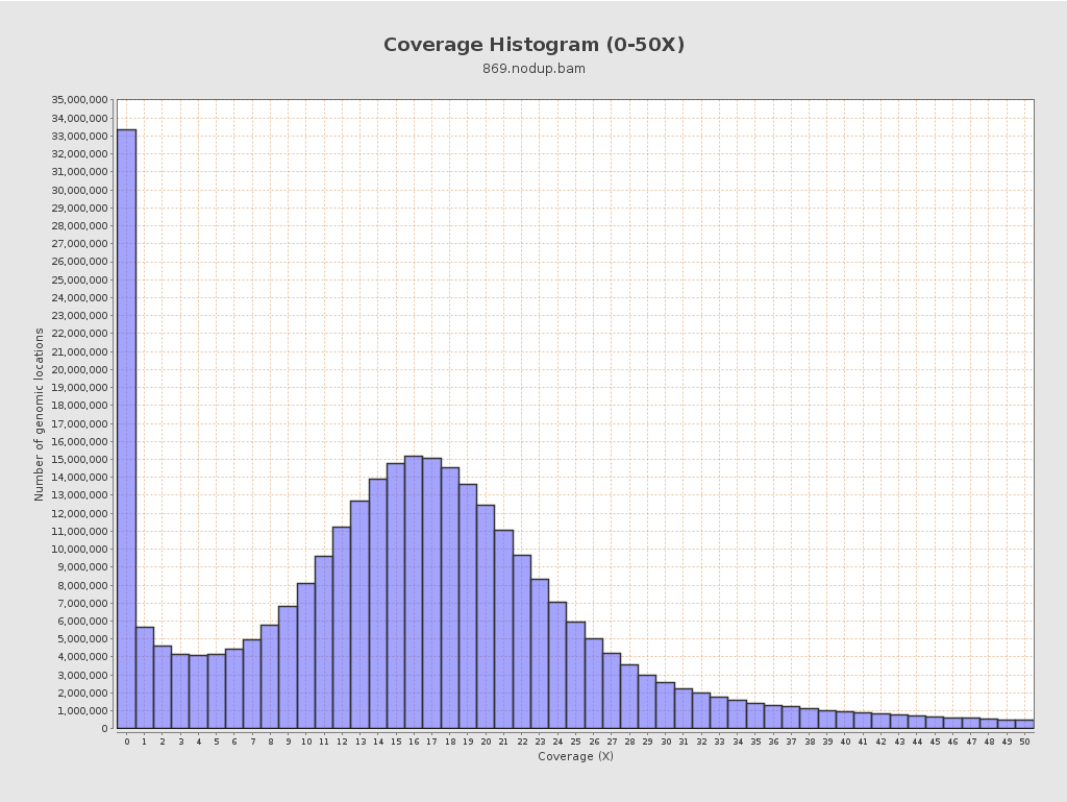
3. Results : Coverage across reference



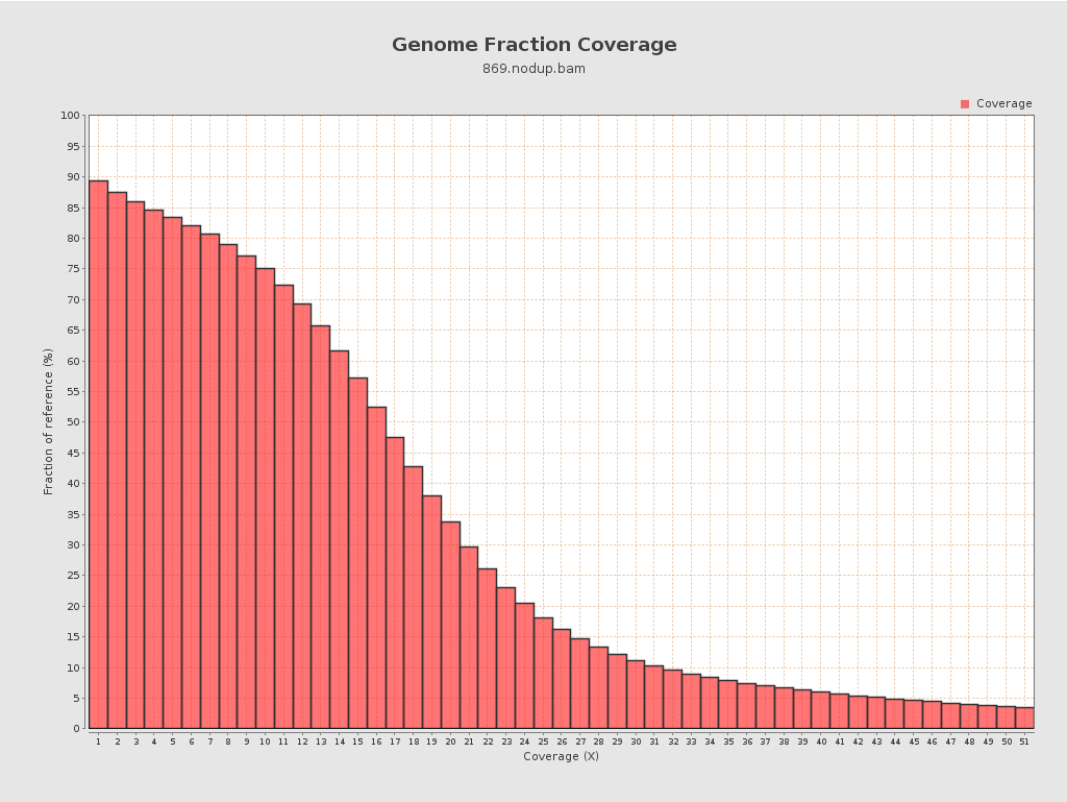
4. Results : Coverage Histogram



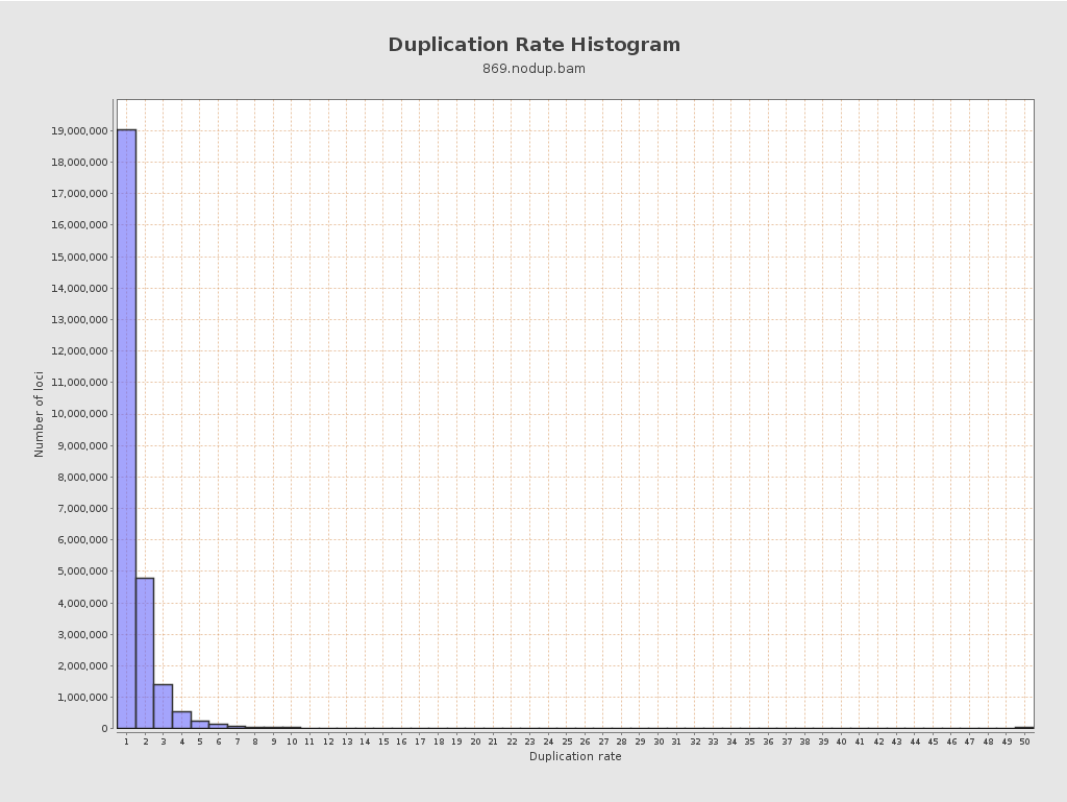
5. Results : Coverage Histogram (0-50X)



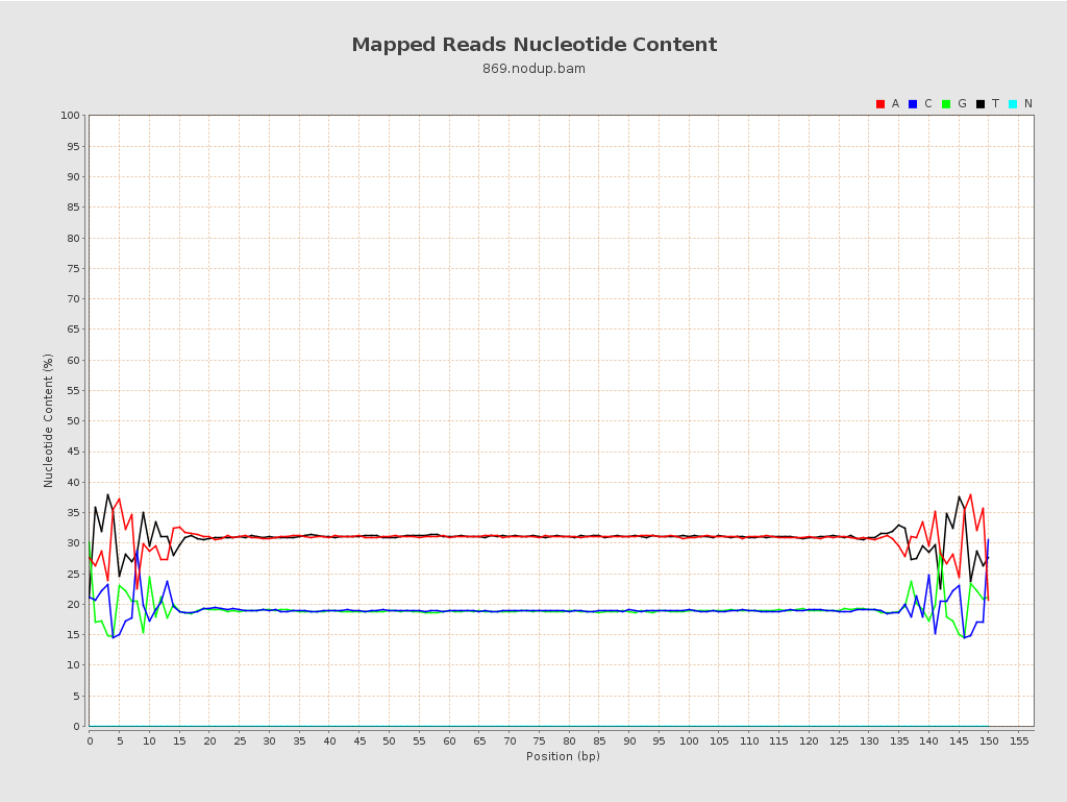
6. Results : Genome Fraction Coverage



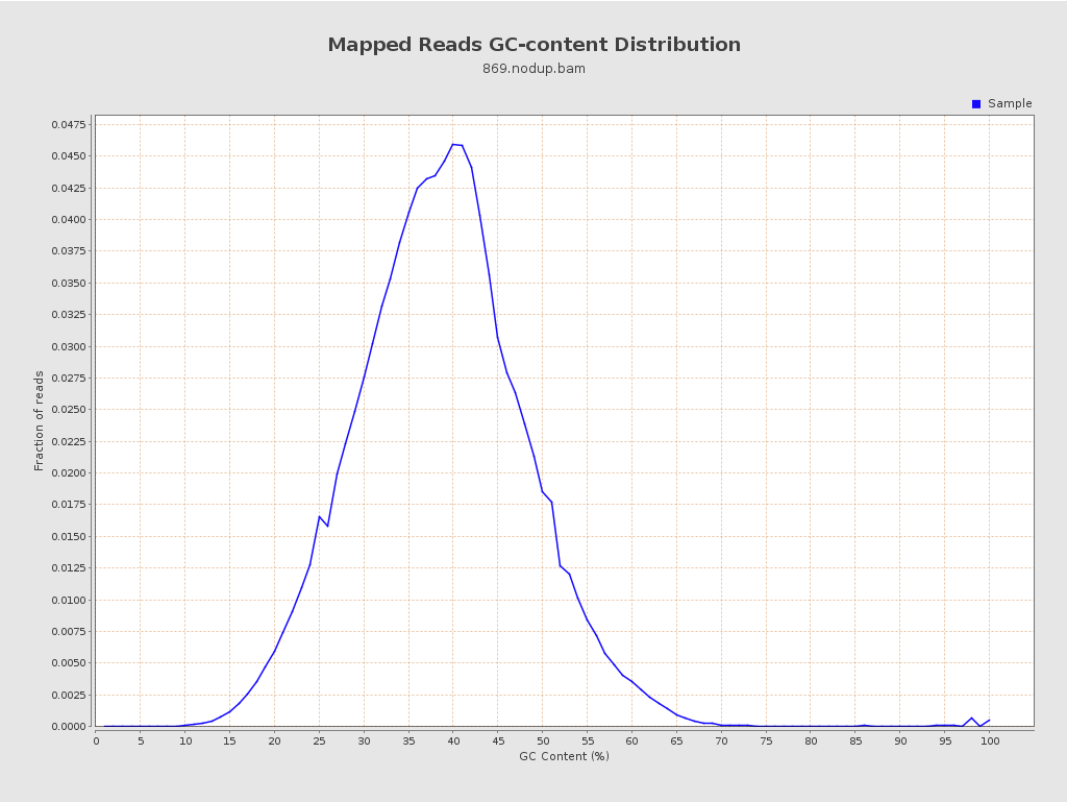
7. Results : Duplication Rate Histogram



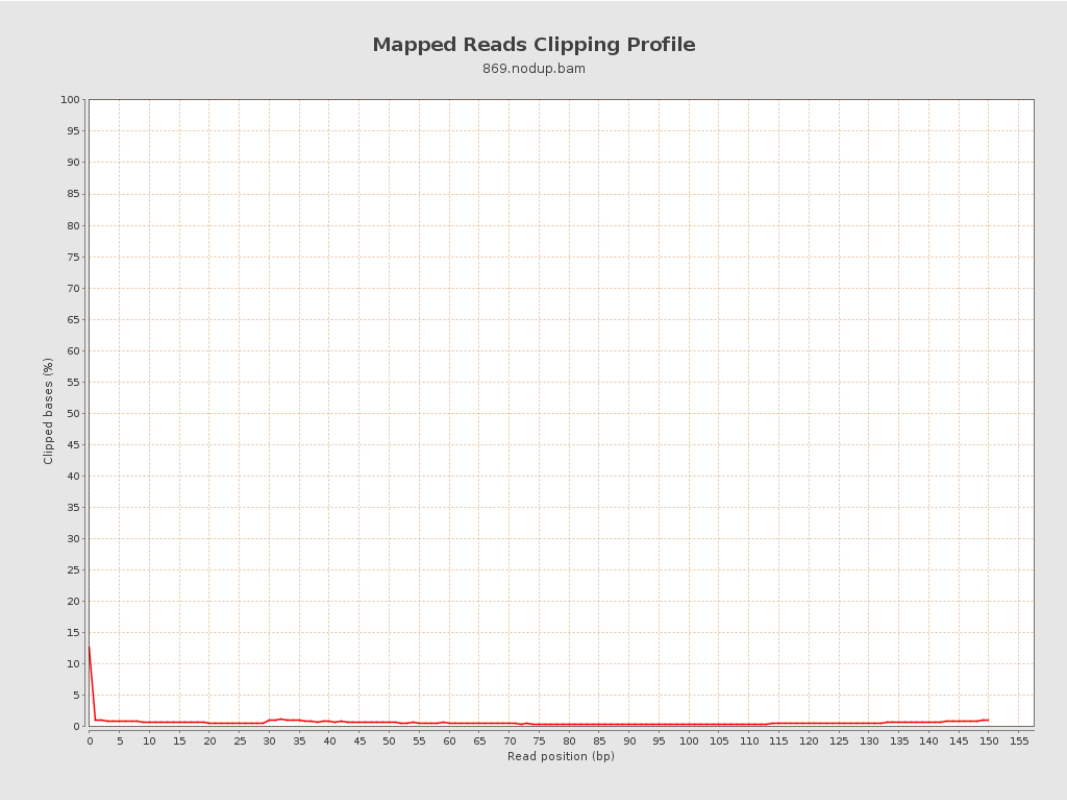
8. Results : Mapped Reads Nucleotide Content



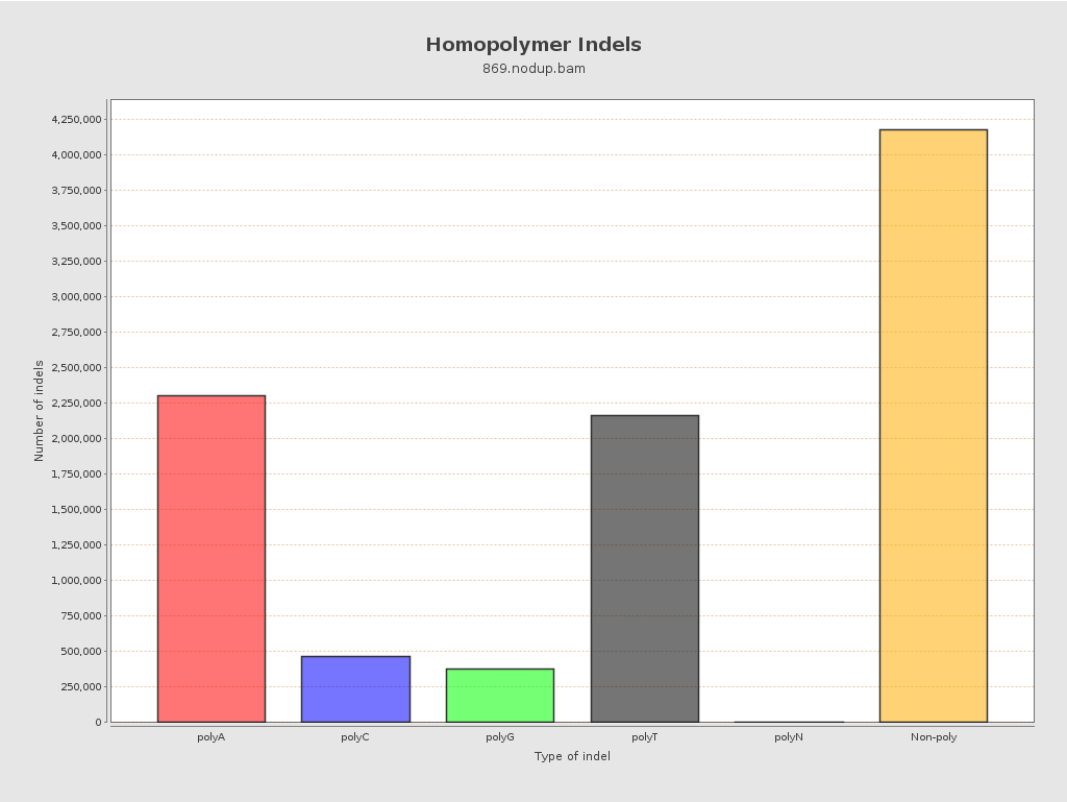
9. Results : Mapped Reads GC-content Distribution



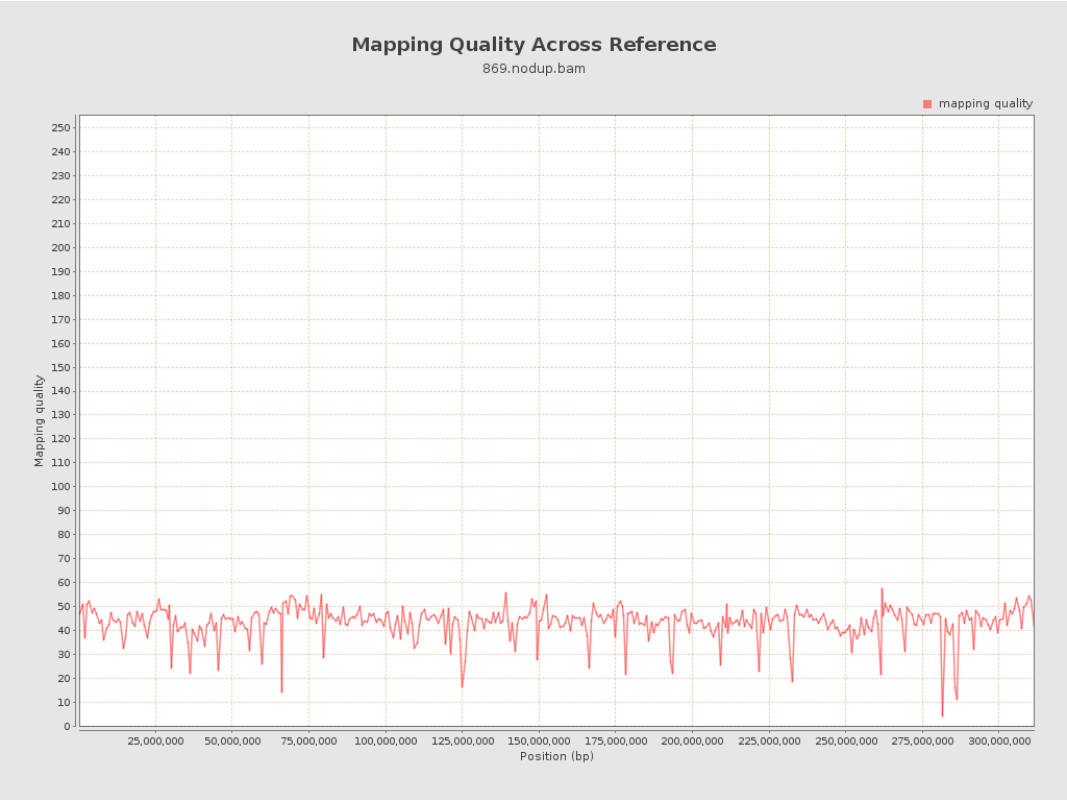
10. Results : Mapped Reads Clipping Profile



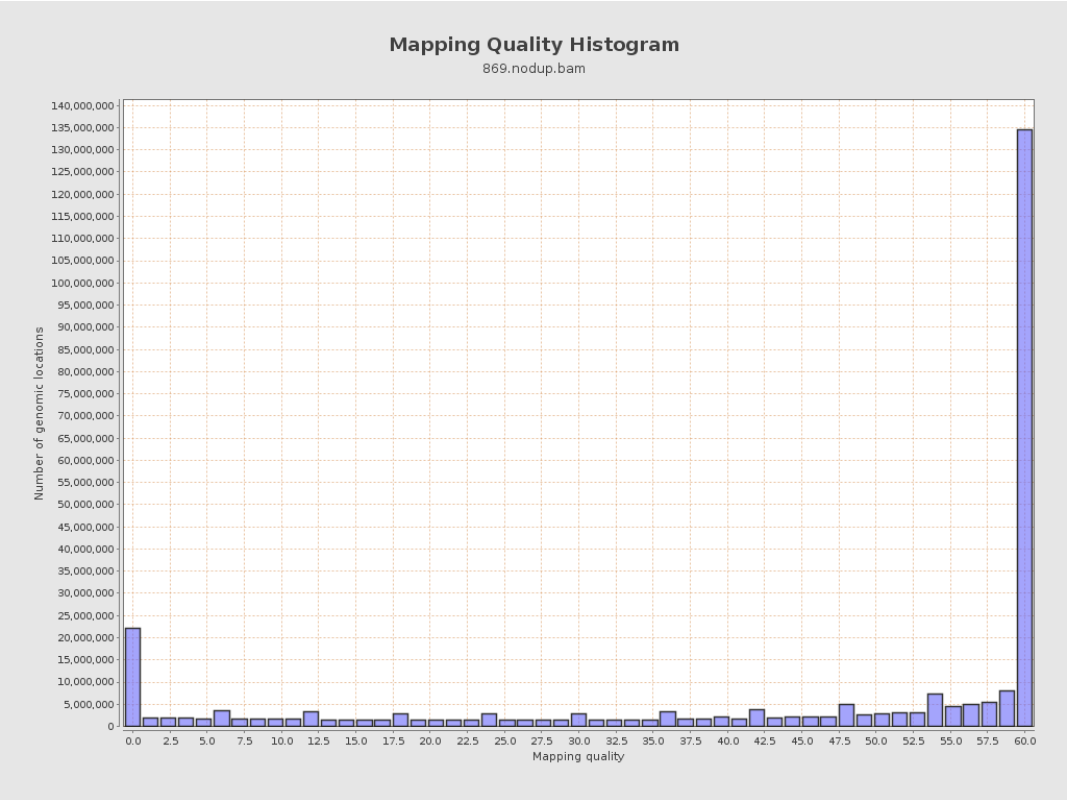
11. Results : Homopolymer Indels



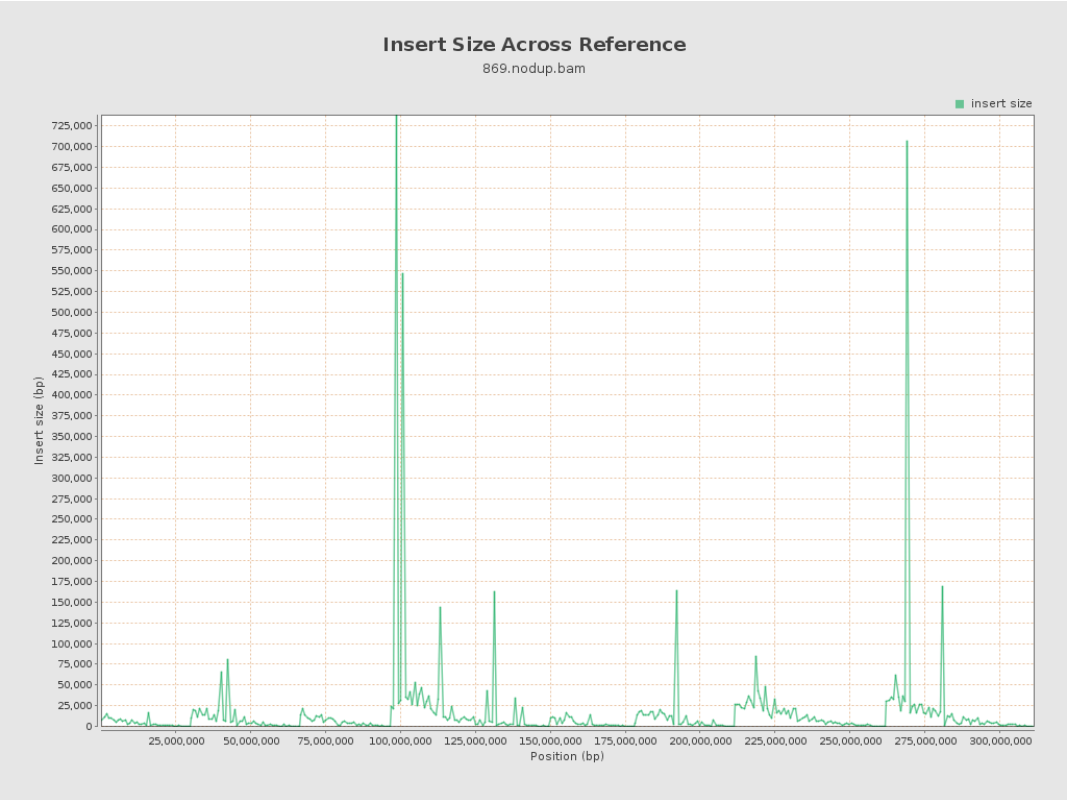
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram