Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:42:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/865.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/865.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_436/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_436_S411_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_436/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_436_S411_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:42:04 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	97,764,473
Mapped reads	90,114,521 / 92.18%
Unmapped reads	7,649,952 / 7.82%
Mapped paired reads	90,114,521 / 92.18%
Mapped reads, first in pair	45,155,283 / 46.19%
Mapped reads, second in pair	44,959,238 / 45.99%
Mapped reads, both in pair	87,590,870 / 89.59%
Mapped reads, singletons	2,523,651 / 2.58%
Read min/max/mean length	30 / 151 / 148.03
Duplicated reads (flagged)	15,633,191 / 15.99%
Clipped reads	20,751,658 / 21.23%

2.2. ACGT Content

Number/percentage of A's	3,855,007,224 / 31.06%
Number/percentage of C's	2,349,614,638 / 18.93%
Number/percentage of T's	3,856,519,032 / 31.07%
Number/percentage of G's	2,351,685,053 / 18.95%
Number/percentage of N's	43,574 / 0%
GC Percentage	37.87%

2.3. Coverage

Mean	39.9355
Standard Deviation	331.4415

2.4. Mapping Quality

Mean Mapping Quality	44.32

2.5. Insert size

Mean	261,407.96
Standard Deviation	2,457,652.26
P25/Median/P75	343 / 451 / 591

2.6. Mismatches and indels

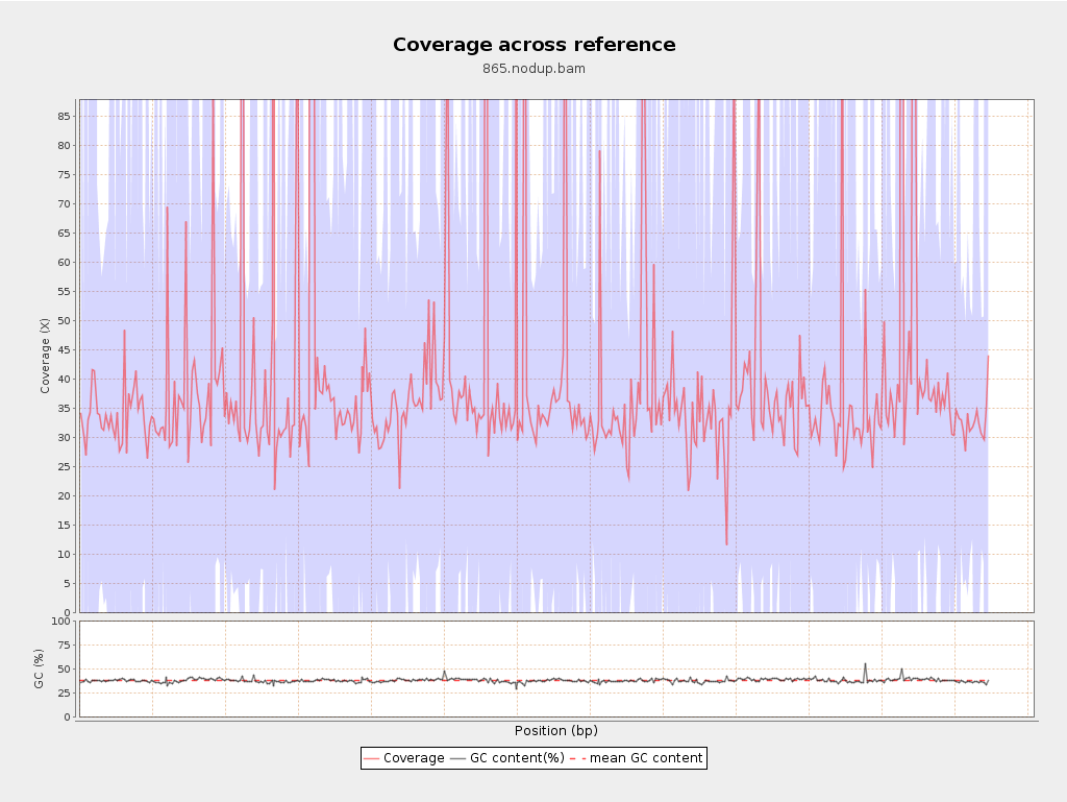
General error rate	2.32%
Mismatches	262,702,977
Insertions	8,952,908
Mapped reads with at least one insertion	8.86%
Deletions	8,765,304
Mapped reads with at least one deletion	8.62%
Homopolymer indels	57.52%

2.7. Chromosome stats

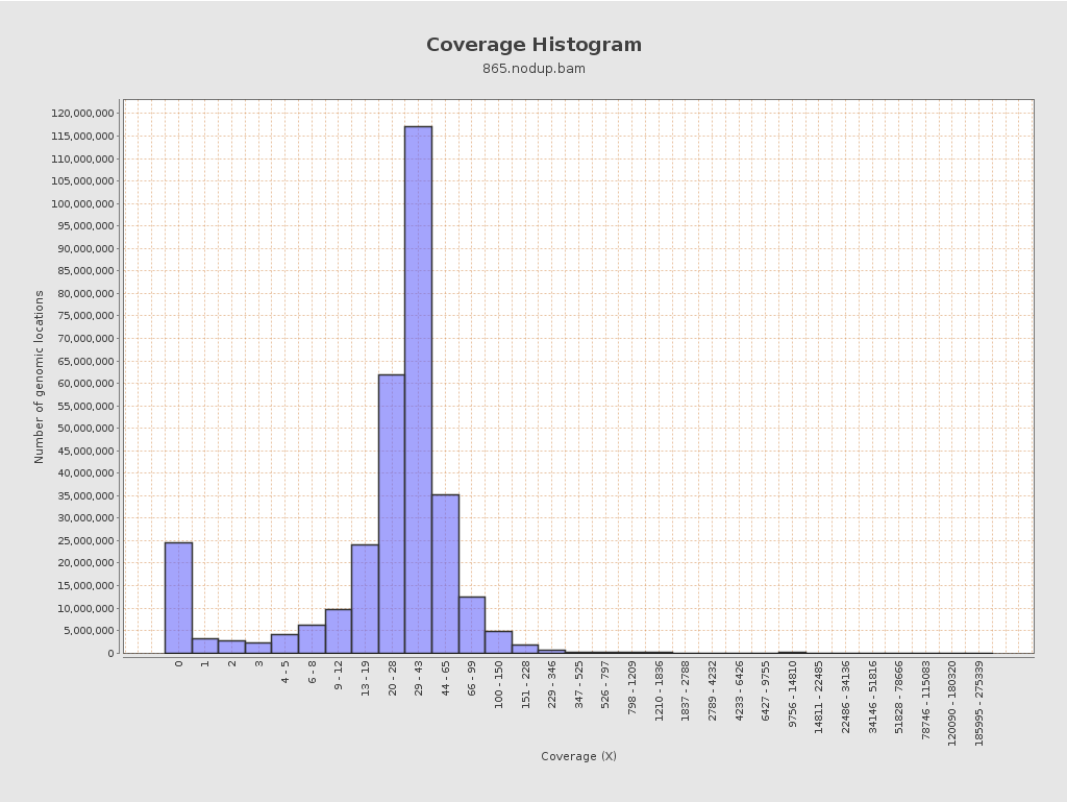
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	995304397	33.4845	143.6621

LT669789.1	36598175	1508731322	41.2242	367.1495
LT669790.1	30422129	1433705922	47.1271	453.0477
LT669791.1	52758100	2075519200	39.3403	342.4188
LT669792.1	28376109	1142858150	40.2754	362.1815
LT669793.1	33388210	1244136758	37.2628	231.4891
LT669794.1	50579949	1916703819	37.8945	271.1503
LT669795.1	49795044	2128618772	42.7476	375.5784

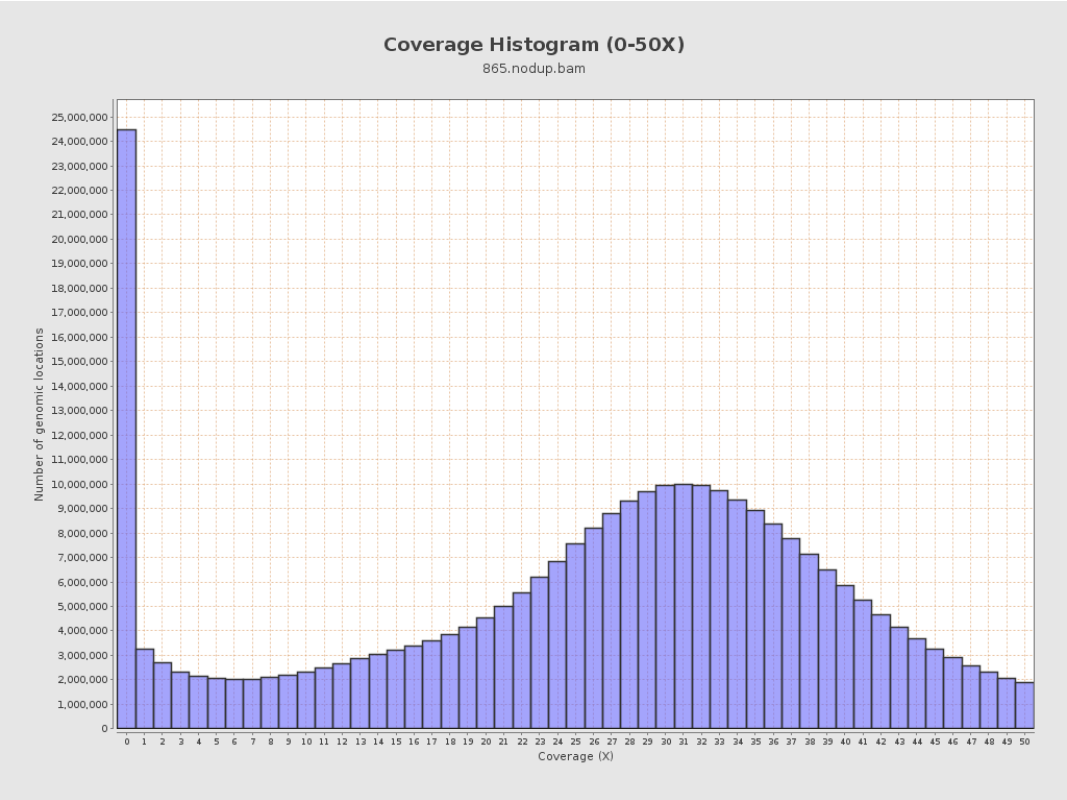
3. Results : Coverage across reference



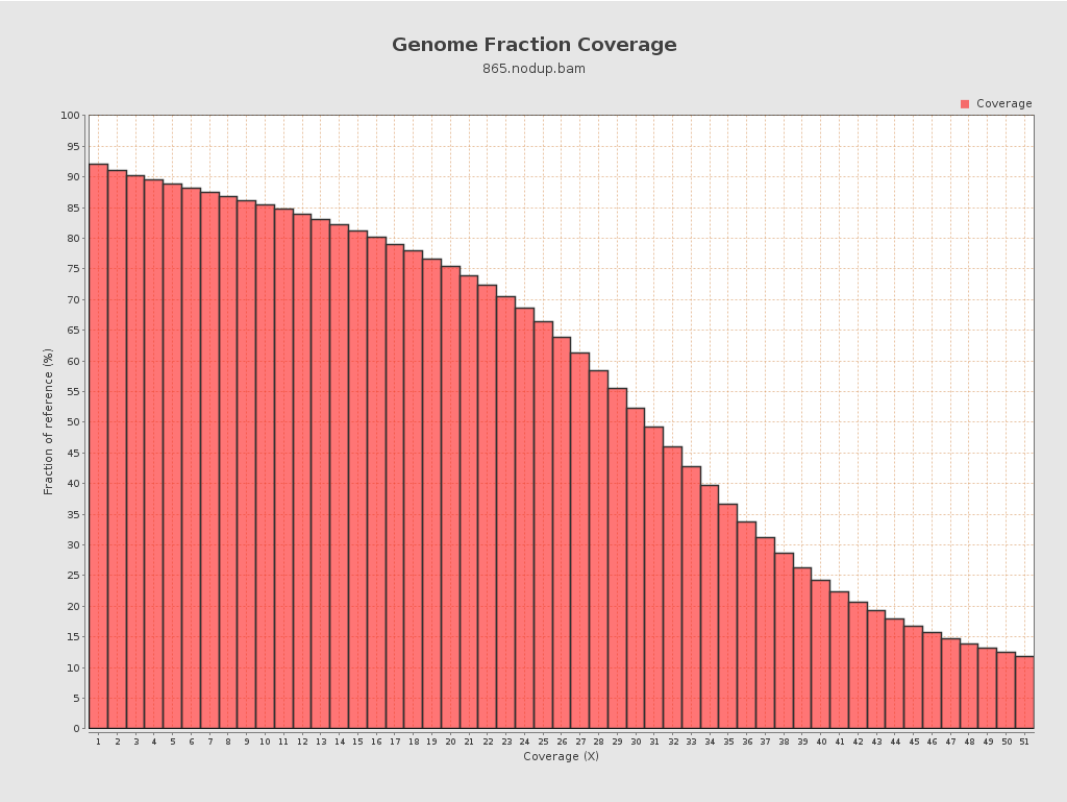
4. Results : Coverage Histogram



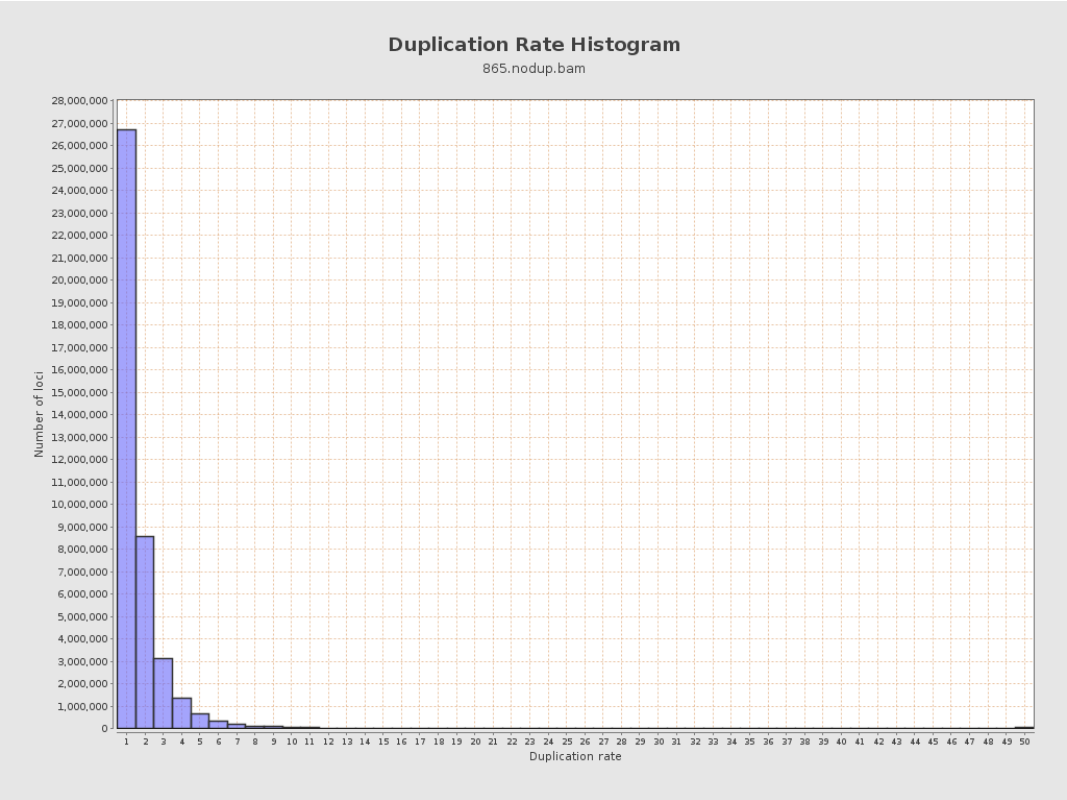
5. Results : Coverage Histogram (0-50X)



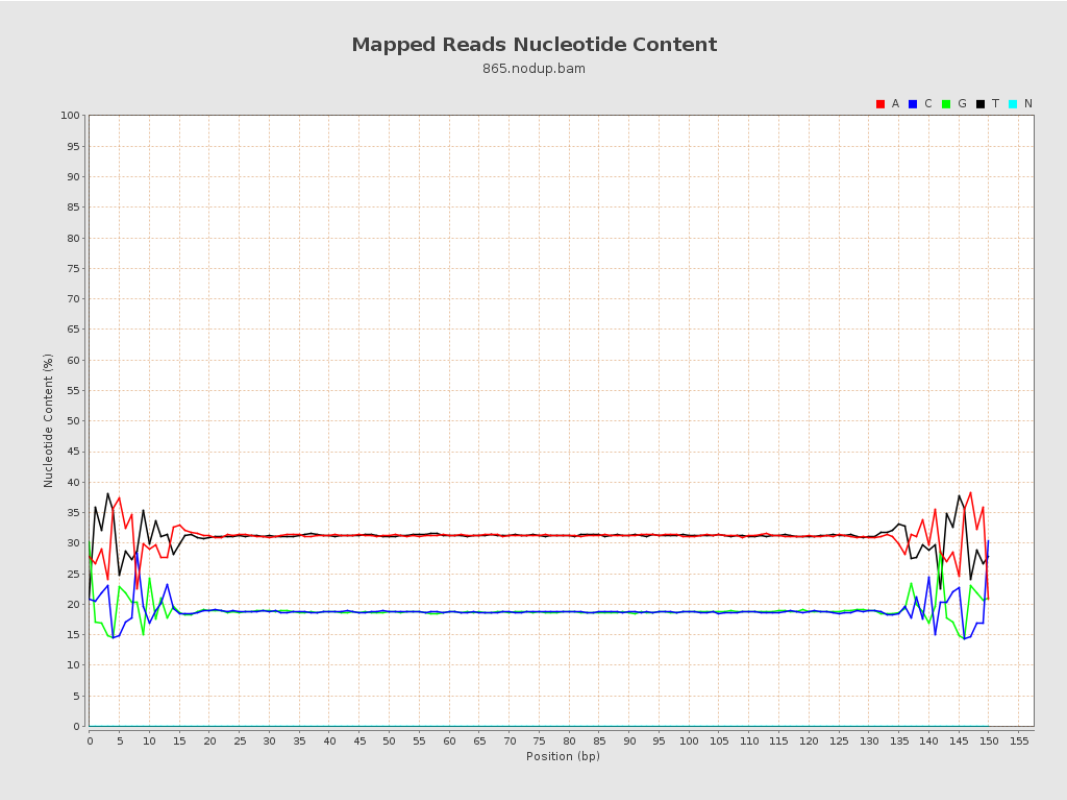
6. Results : Genome Fraction Coverage



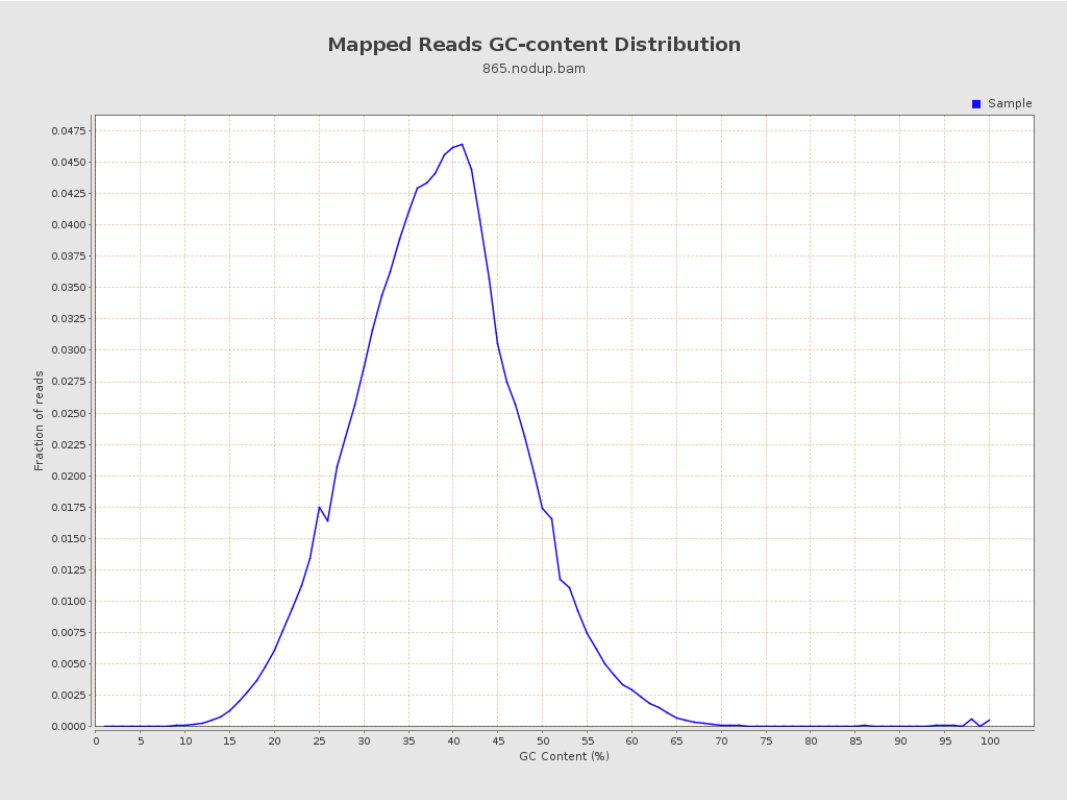
7. Results : Duplication Rate Histogram



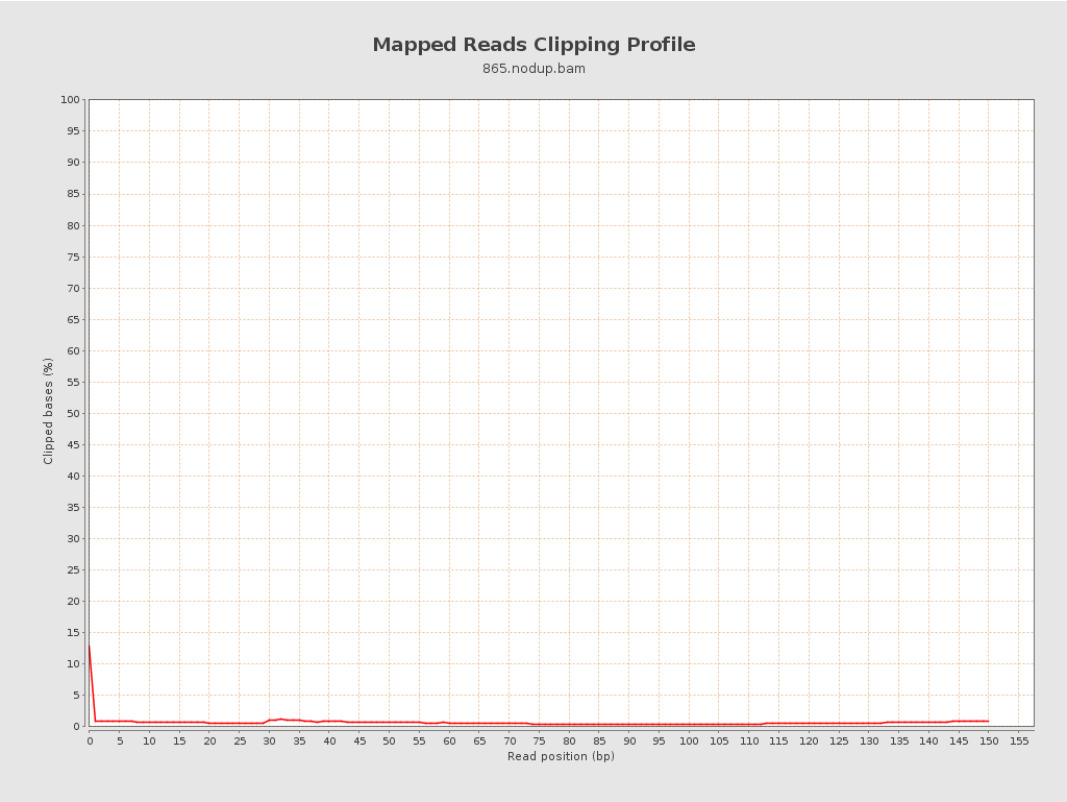
8. Results : Mapped Reads Nucleotide Content



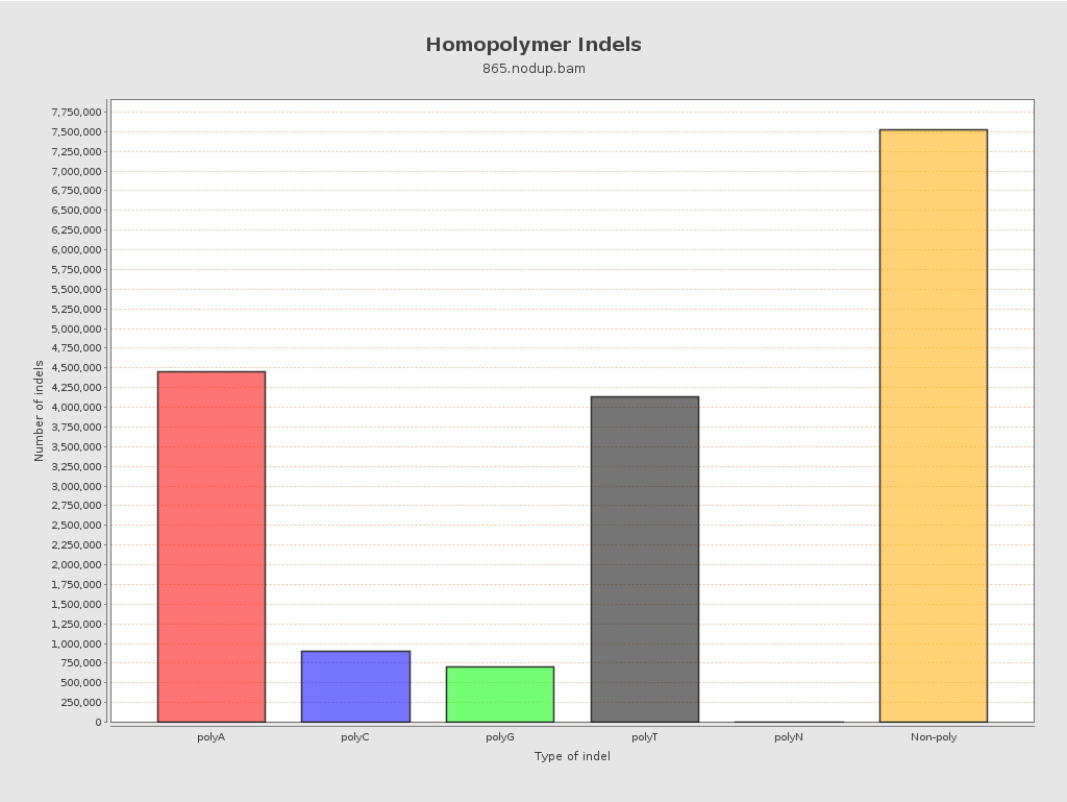
9. Results : Mapped Reads GC-content Distribution



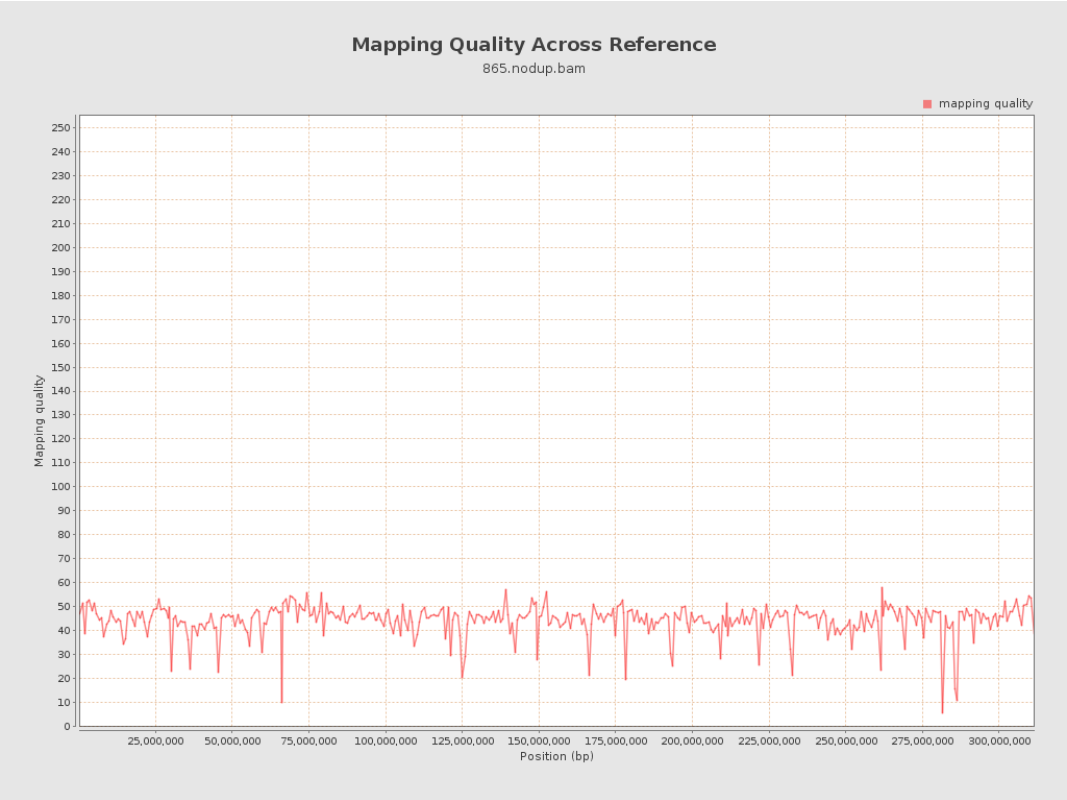
10. Results : Mapped Reads Clipping Profile



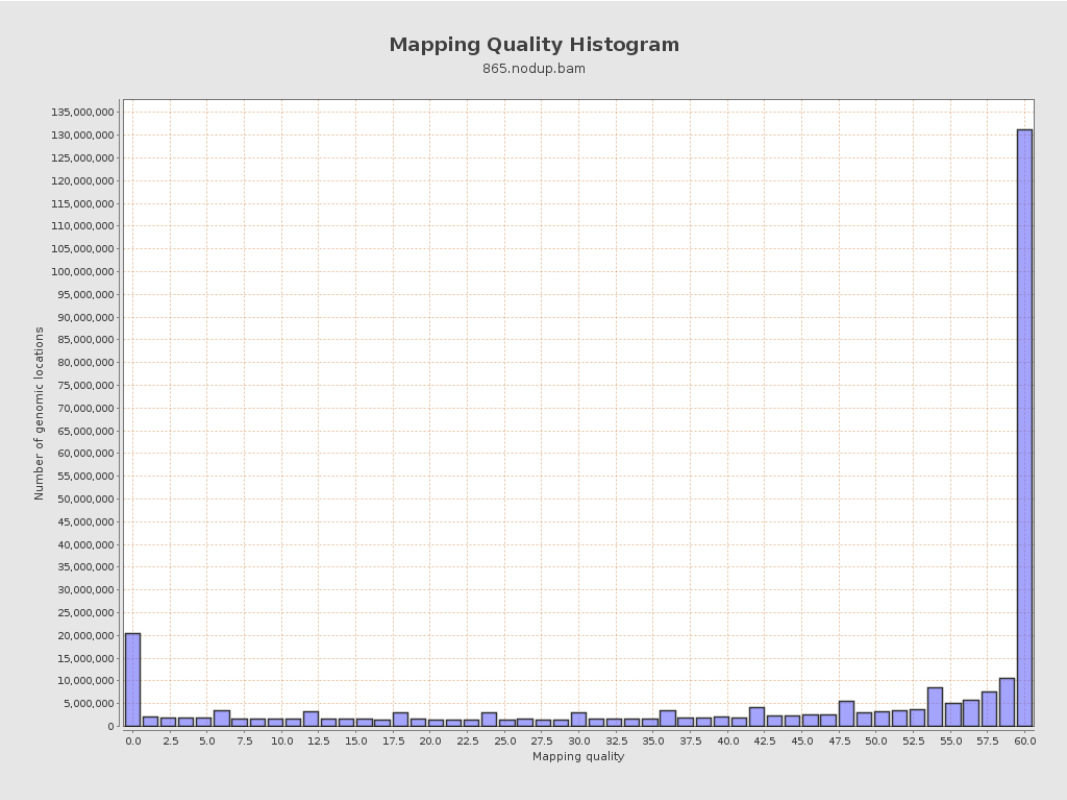
11. Results : Homopolymer Indels



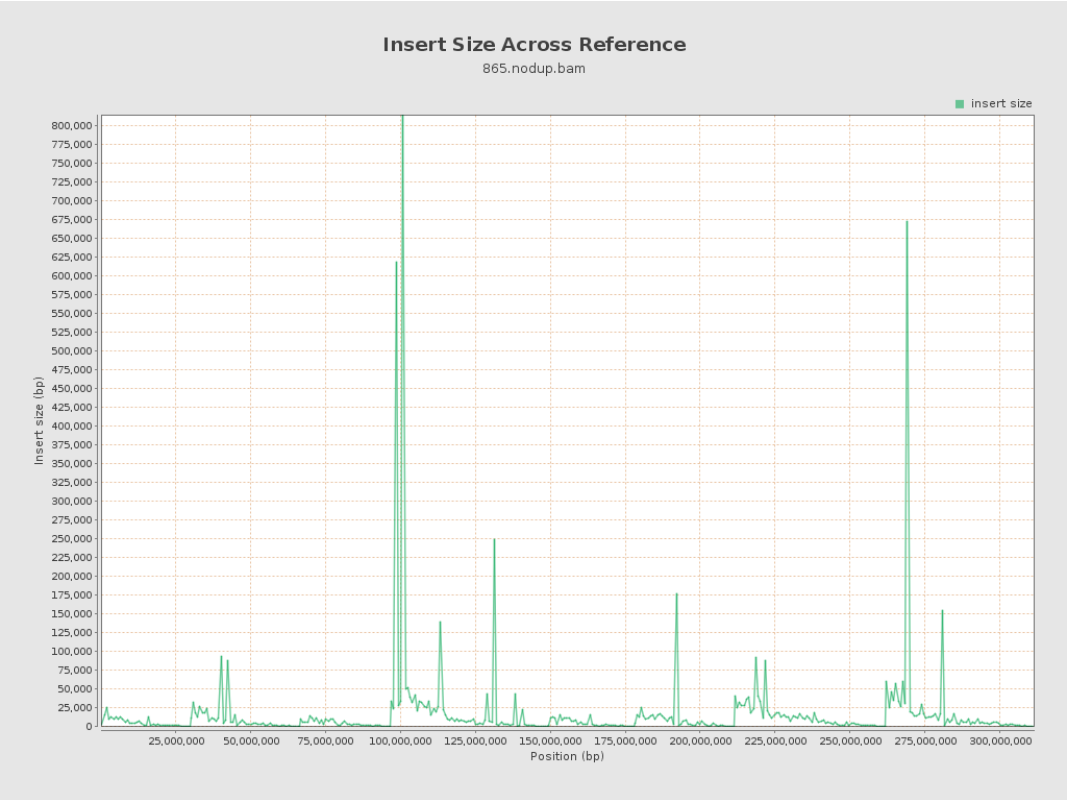
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram