Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:28:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/825.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/825.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_204/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_204_S285_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_204/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_204_S285_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:28:27 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	59,395,201
Mapped reads	55,630,160 / 93.66%
Unmapped reads	3,765,041 / 6.34%
Mapped paired reads	55,630,160 / 93.66%
Mapped reads, first in pair	27,856,741 / 46.9%
Mapped reads, second in pair	27,773,419 / 46.76%
Mapped reads, both in pair	54,473,216 / 91.71%
Mapped reads, singletons	1,156,944 / 1.95%
Read min/max/mean length	30 / 151 / 148.21
Duplicated reads (flagged)	7,625,112 / 12.84%
Clipped reads	12,342,526 / 20.78%

2.2. ACGT Content

Number/percentage of A's	2,375,547,467 / 30.77%
Number/percentage of C's	1,485,235,263 / 19.24%
Number/percentage of T's	2,379,593,154 / 30.82%
Number/percentage of G's	1,479,366,200 / 19.16%
Number/percentage of N's	28,476 / 0%
GC Percentage	38.4%

2.3. Coverage

Mean	24.8333
Standard Deviation	194.1005

2.4. Mapping Quality

Mean Mapping Quality	44.71

2.5. Insert size

Mean	213,345.21
Standard Deviation	2,198,821.89
P25/Median/P75	314 / 412 / 537

2.6. Mismatches and indels

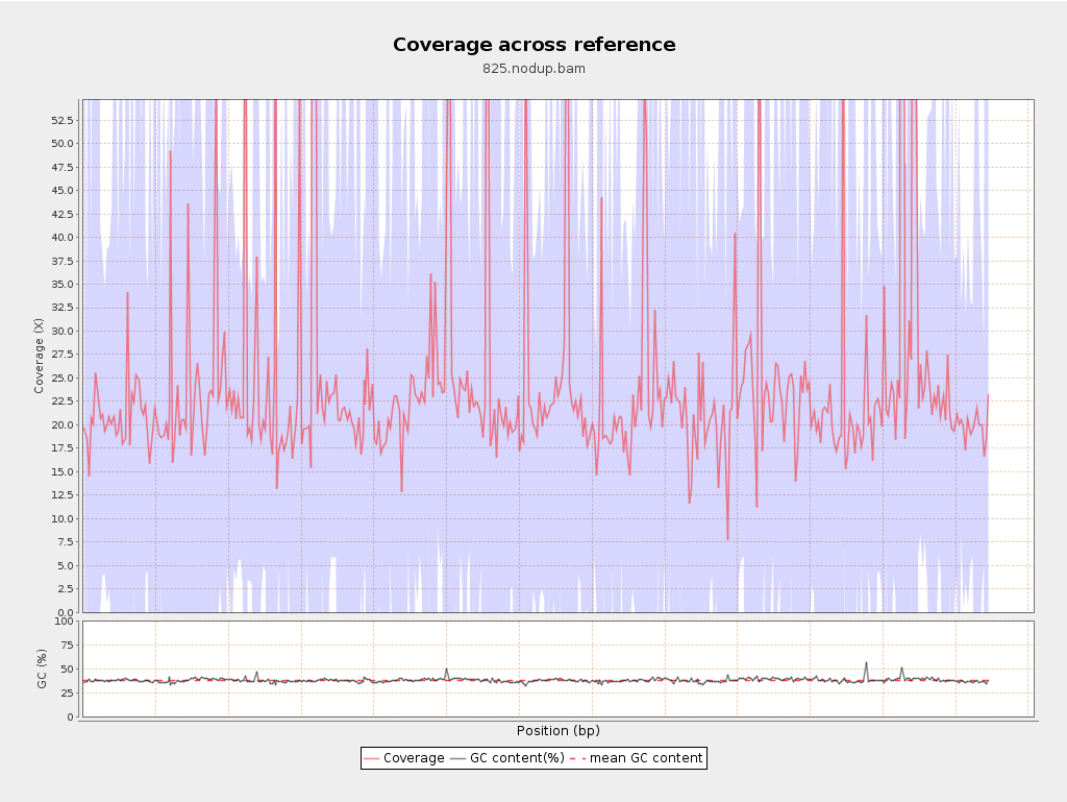
General error rate	2.28%
Mismatches	161,672,235
Insertions	5,084,419
Mapped reads with at least one insertion	8.22%
Deletions	5,122,567
Mapped reads with at least one deletion	8.19%
Homopolymer indels	56.57%

2.7. Chromosome stats

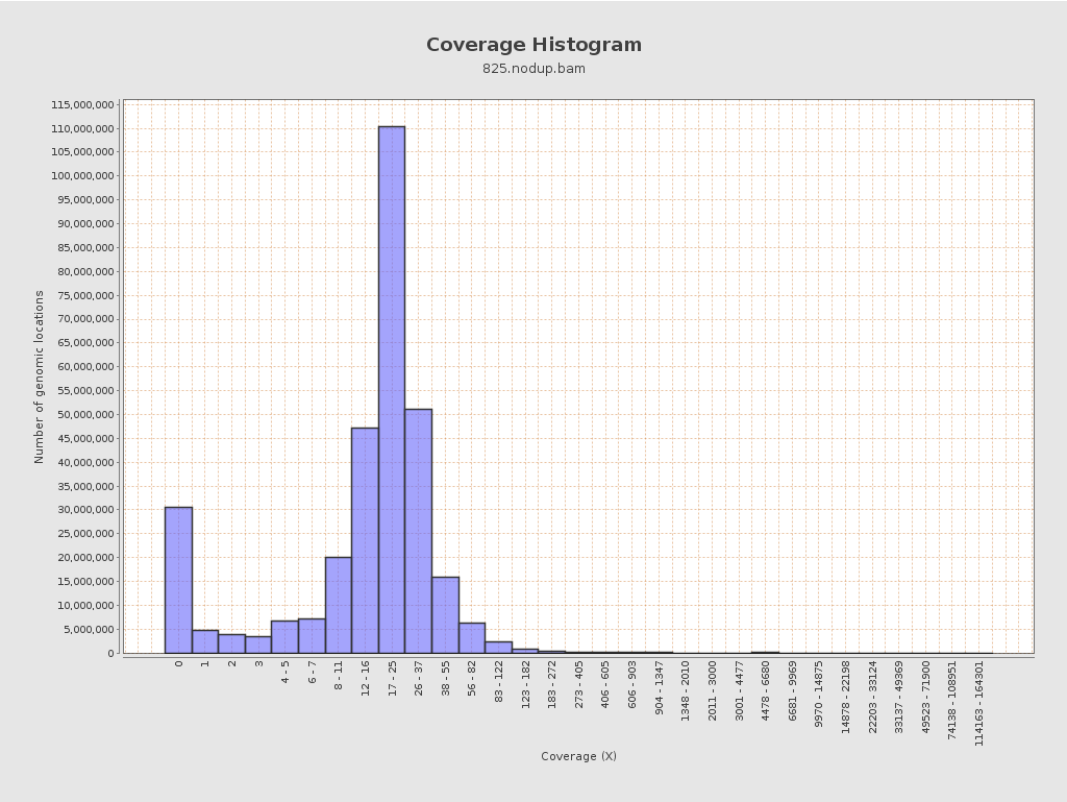
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	615481066	20.7063	73.9015

LT669789.1	36598175	922627006	25.2096	211.0968
LT669790.1	30422129	802057016	26.3643	196.6637
LT669791.1	52758100	1284231346	24.3419	171.1187
LT669792.1	28376109	688825449	24.2748	202.9119
LT669793.1	33388210	754544362	22.5991	100.0534
LT669794.1	50579949	1182013946	23.3692	166.723
LT669795.1	49795044	1489311557	29.9088	294.3982

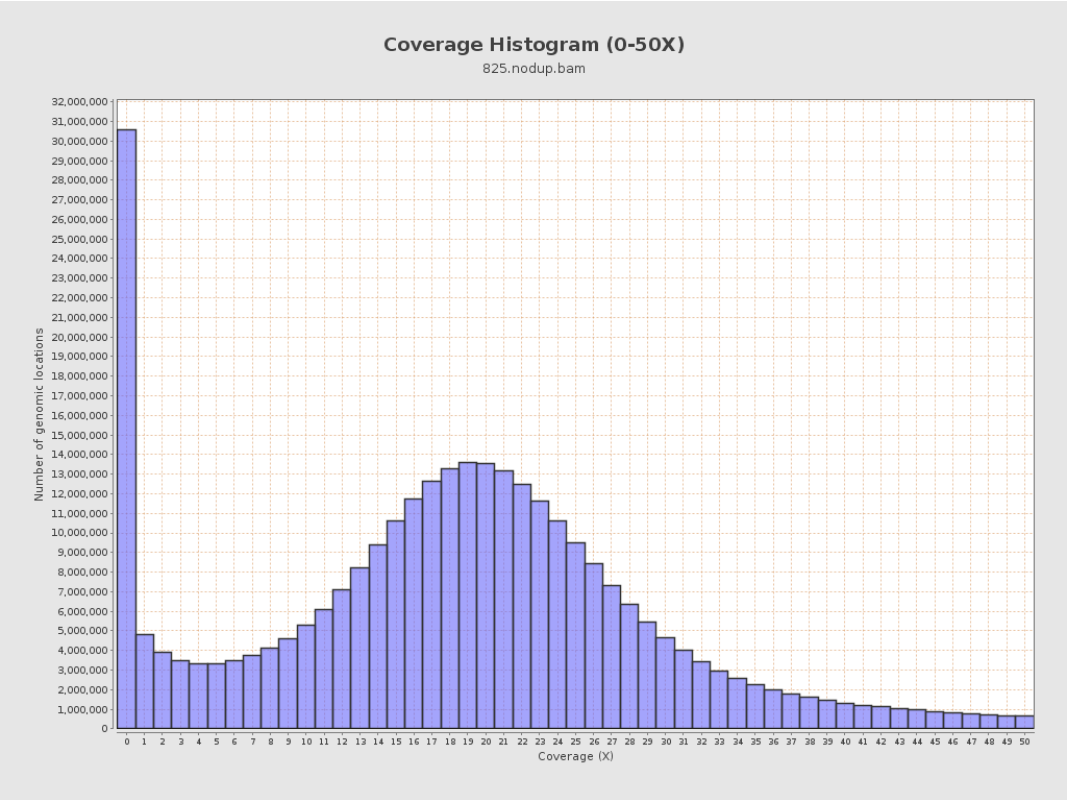
3. Results : Coverage across reference



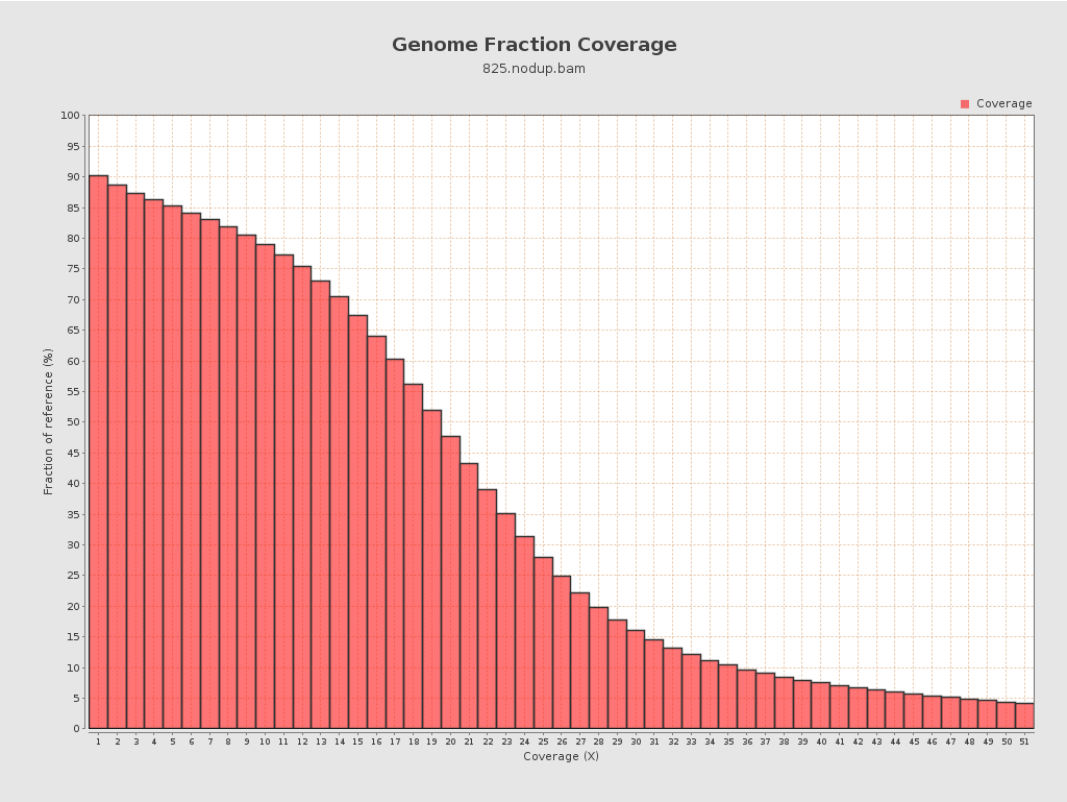
4. Results : Coverage Histogram



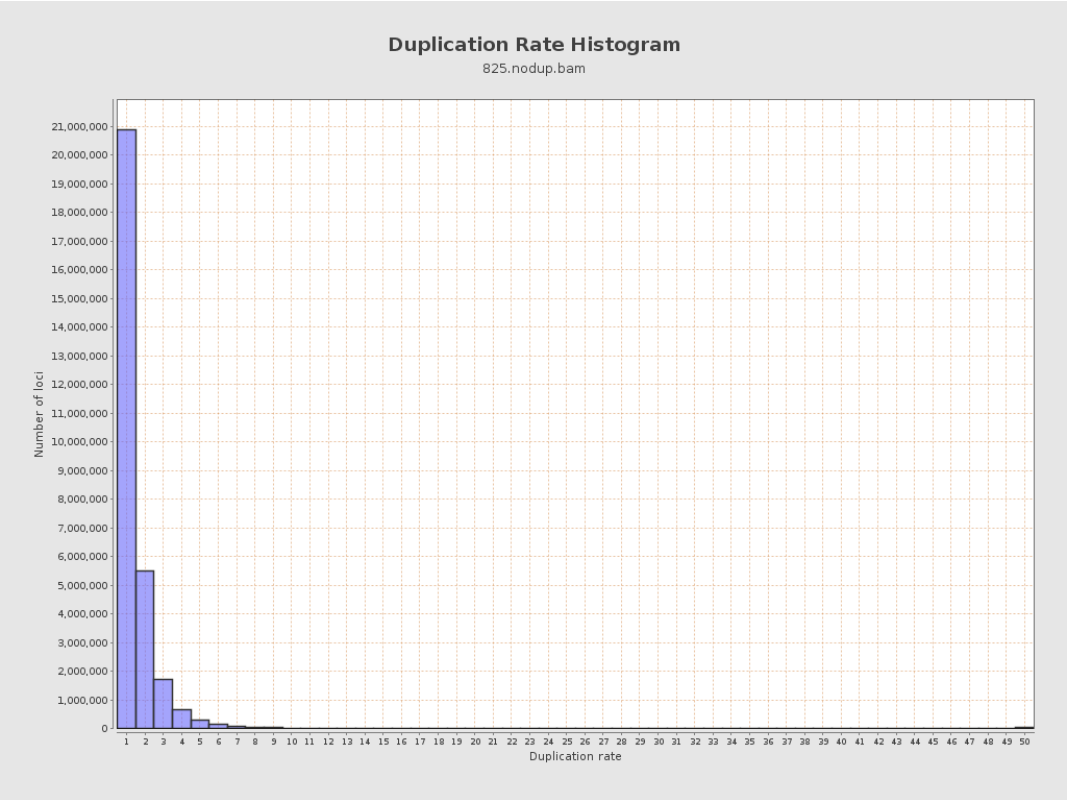
5. Results : Coverage Histogram (0-50X)



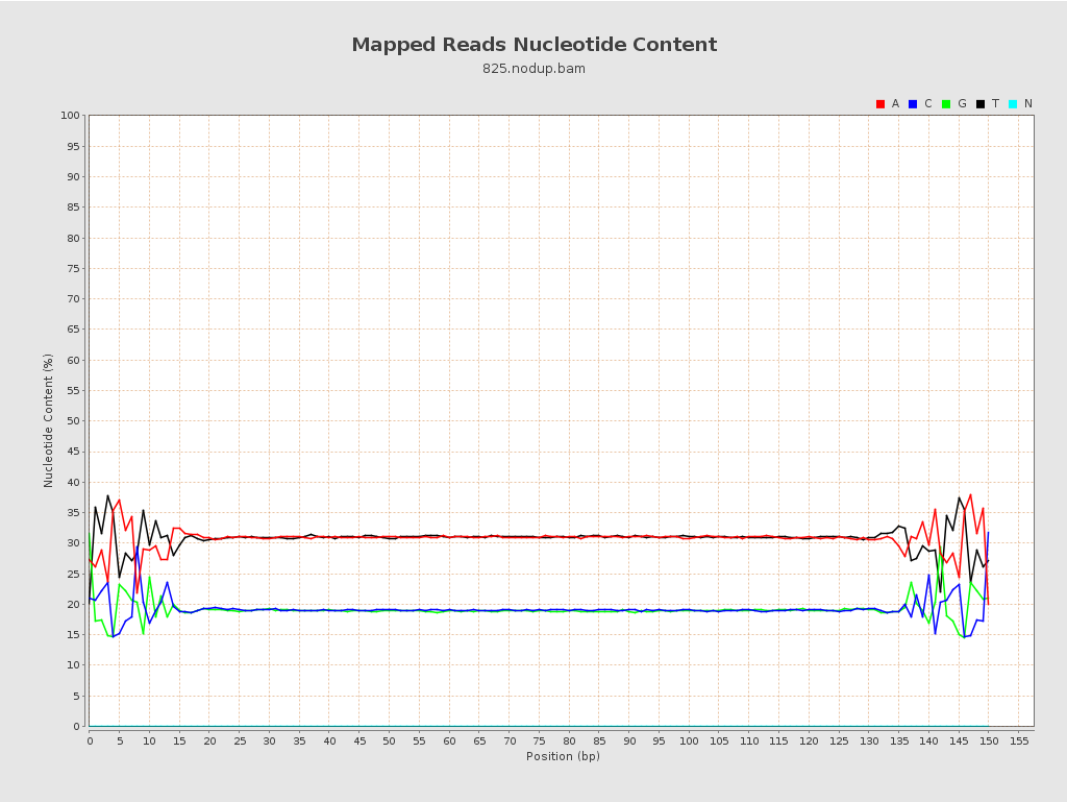
6. Results : Genome Fraction Coverage



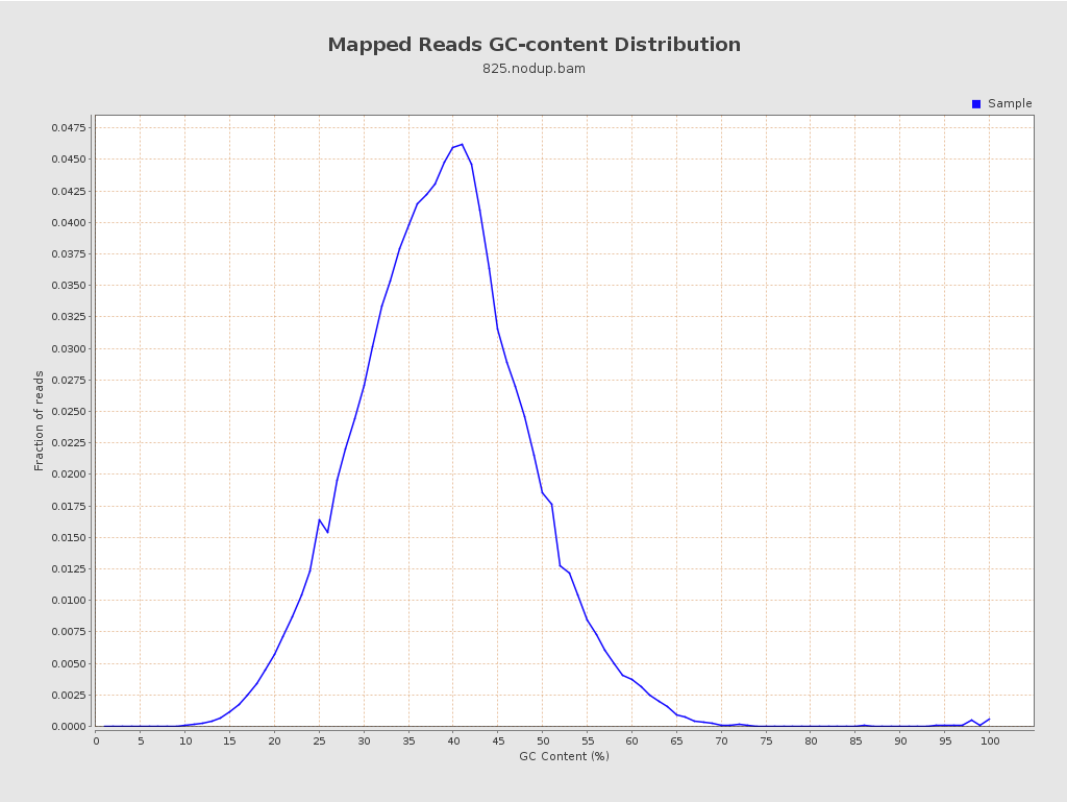
7. Results : Duplication Rate Histogram



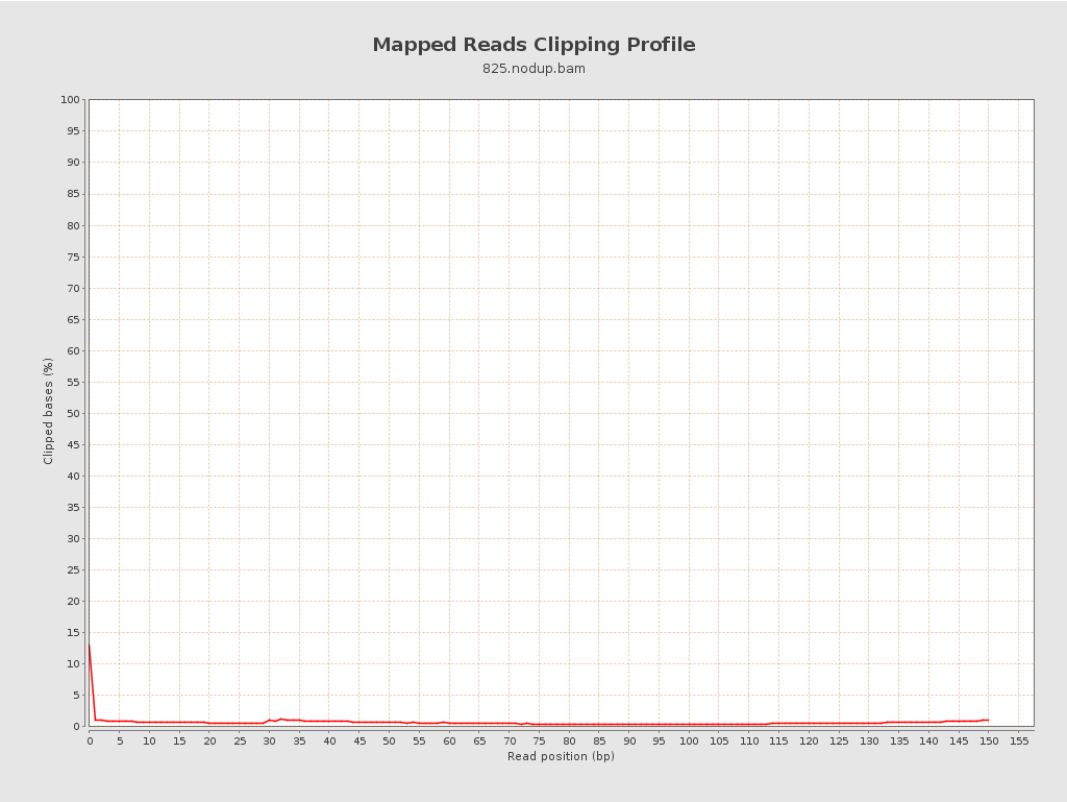
8. Results : Mapped Reads Nucleotide Content



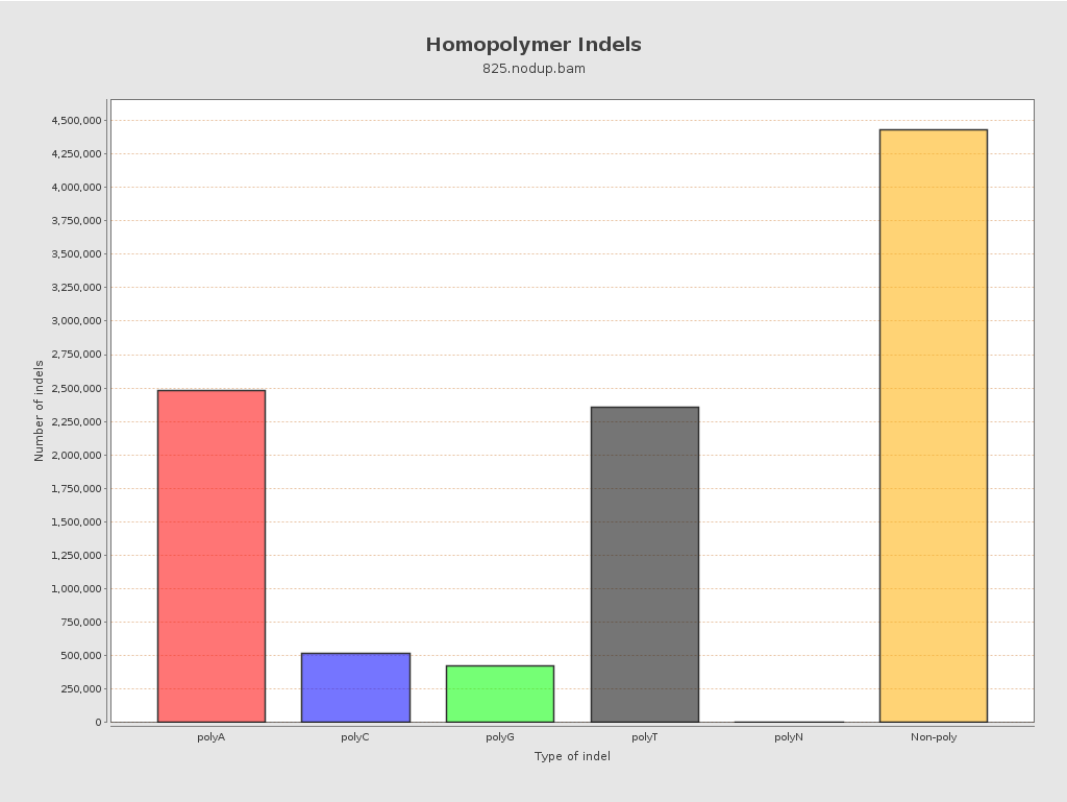
9. Results : Mapped Reads GC-content Distribution



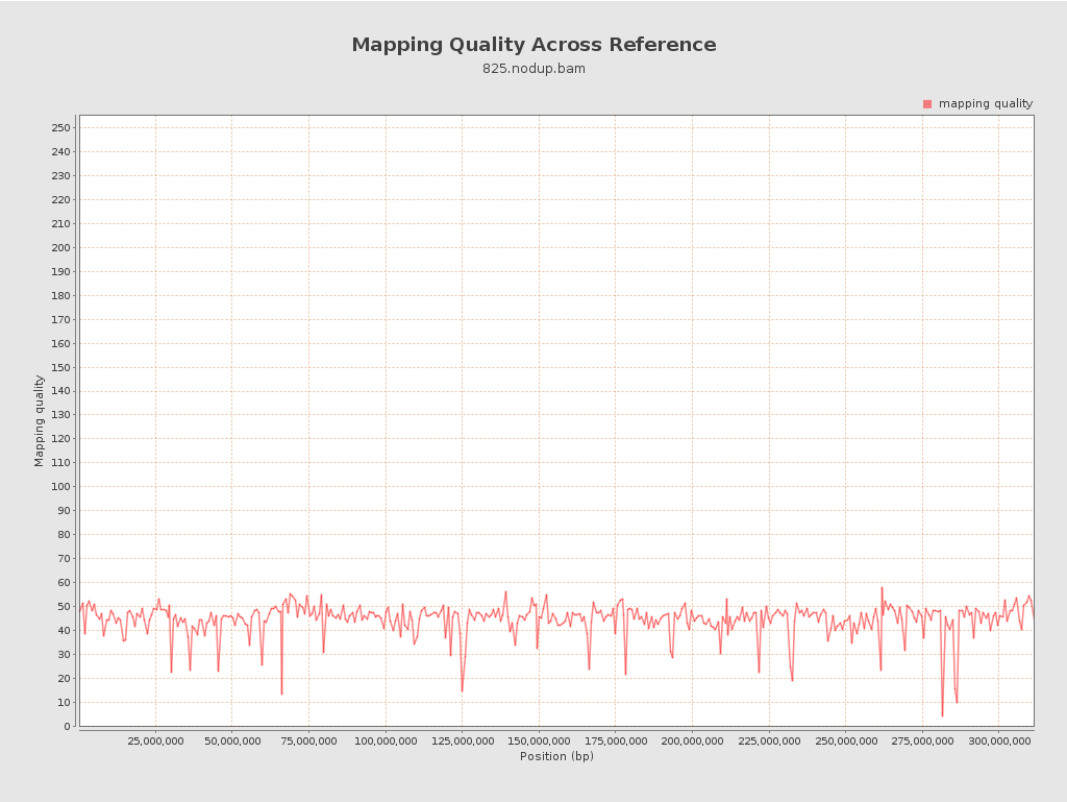
10. Results : Mapped Reads Clipping Profile



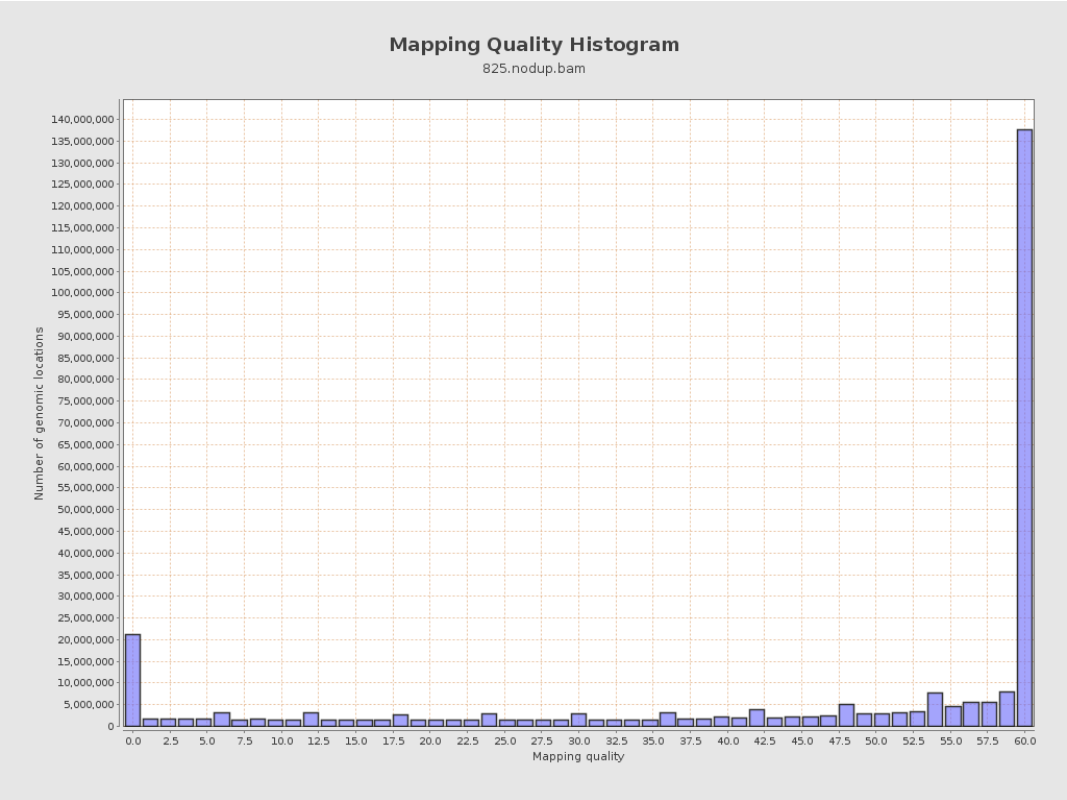
11. Results : Homopolymer Indels



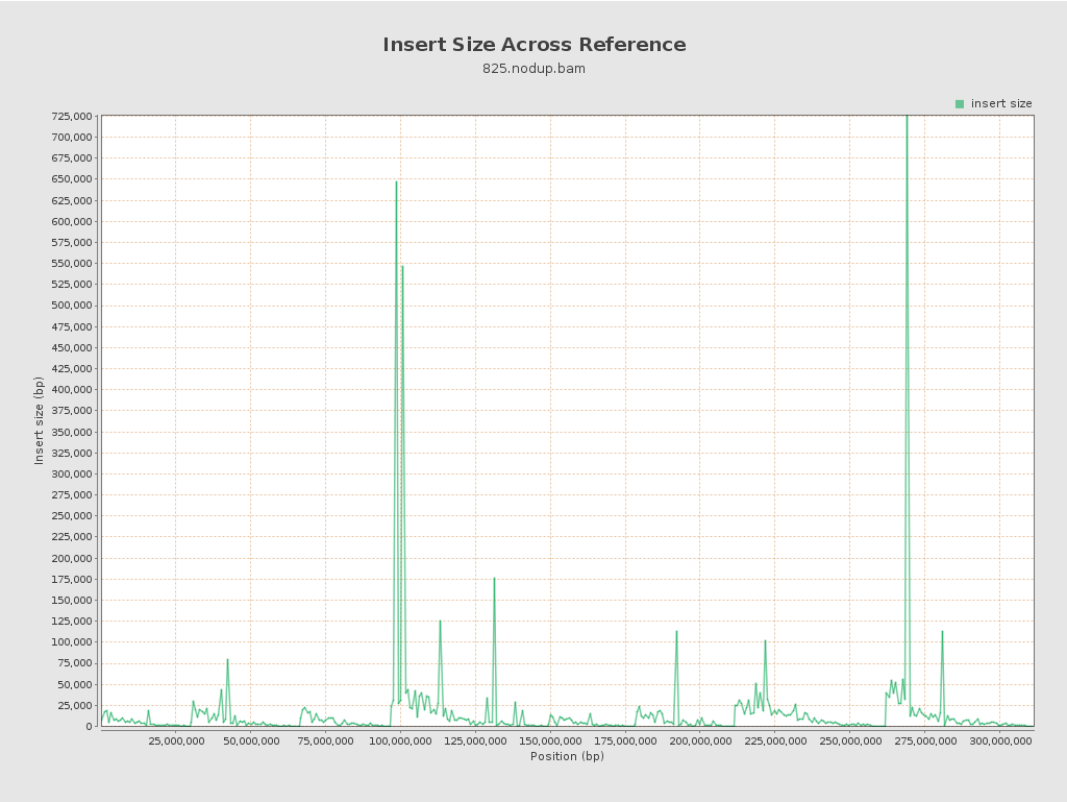
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram