Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:31:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/802.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/802.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_166/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_166_S256_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_166/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_166_S256_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:31:49 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	68,201,452
Mapped reads	62,788,968 / 92.06%
Unmapped reads	5,412,484 / 7.94%
Mapped paired reads	62,788,968 / 92.06%
Mapped reads, first in pair	31,456,166 / 46.12%
Mapped reads, second in pair	31,332,802 / 45.94%
Mapped reads, both in pair	60,979,005 / 89.41%
Mapped reads, singletons	1,809,963 / 2.65%
Read min/max/mean length	30 / 151 / 148.11
Duplicated reads (flagged)	11,486,465 / 16.84%
Clipped reads	14,445,246 / 21.18%

2.2. ACGT Content

Number/percentage of A's	2,675,734,890 / 30.93%
Number/percentage of C's	1,649,692,123 / 19.07%
Number/percentage of T's	2,679,937,228 / 30.98%
Number/percentage of G's	1,646,211,747 / 19.03%
Number/percentage of N's	36,338 / 0%
GC Percentage	38.1%

2.3. Coverage

Mean	27.8325
Standard Deviation	250.1259

2.4. Mapping Quality

Mean Mapping Quality	44.31

2.5. Insert size

Mean	257,537.36
Standard Deviation	2,434,846.84
P25/Median/P75	340 / 446 / 585

2.6. Mismatches and indels

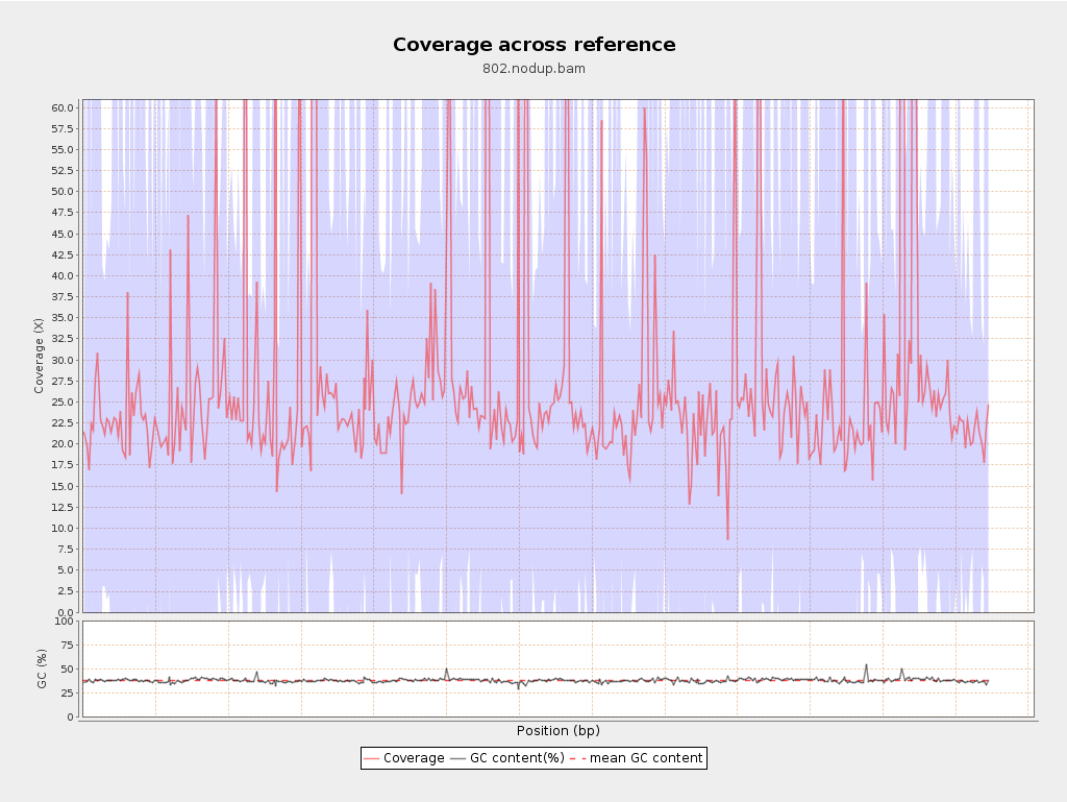
General error rate	2.33%
Mismatches	184,194,710
Insertions	6,195,148
Mapped reads with at least one insertion	8.81%
Deletions	5,980,807
Mapped reads with at least one deletion	8.42%
Homopolymer indels	57.16%

2.7. Chromosome stats

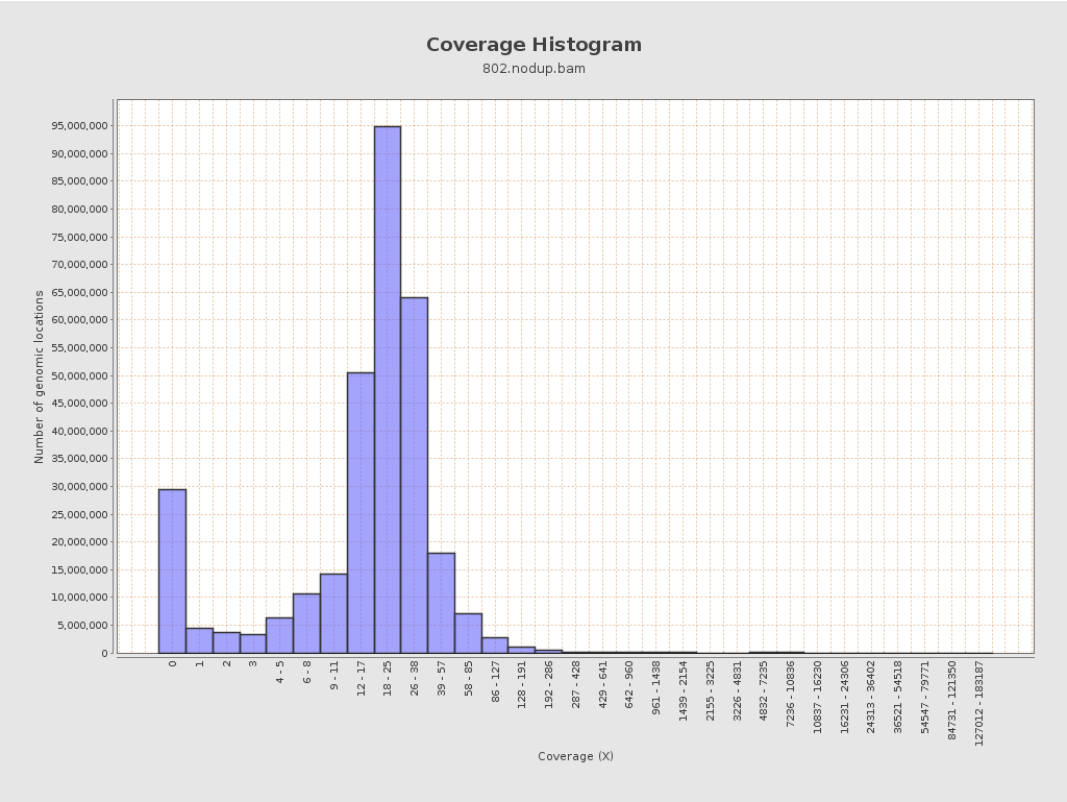
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	671520577	22.5916	103.5657

LT669789.1	36598175	1018987497	27.8426	263.1512
LT669790.1	30422129	994008546	32.6739	337.4425
LT669791.1	52758100	1455384748	27.586	256.0942
LT669792.1	28376109	790763891	27.8672	271.7647
LT669793.1	33388210	833607404	24.9671	134.5335
LT669794.1	50579949	1317348529	26.0449	204.2355
LT669795.1	49795044	1592160339	31.9743	313.9238

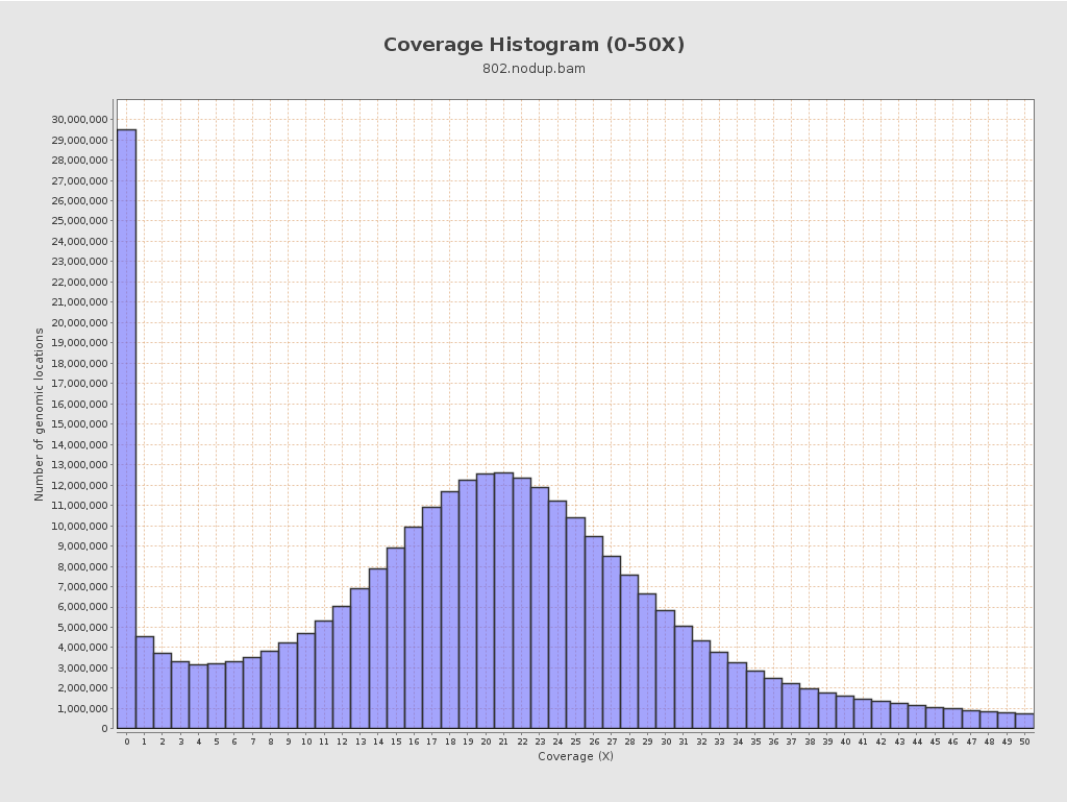
3. Results : Coverage across reference



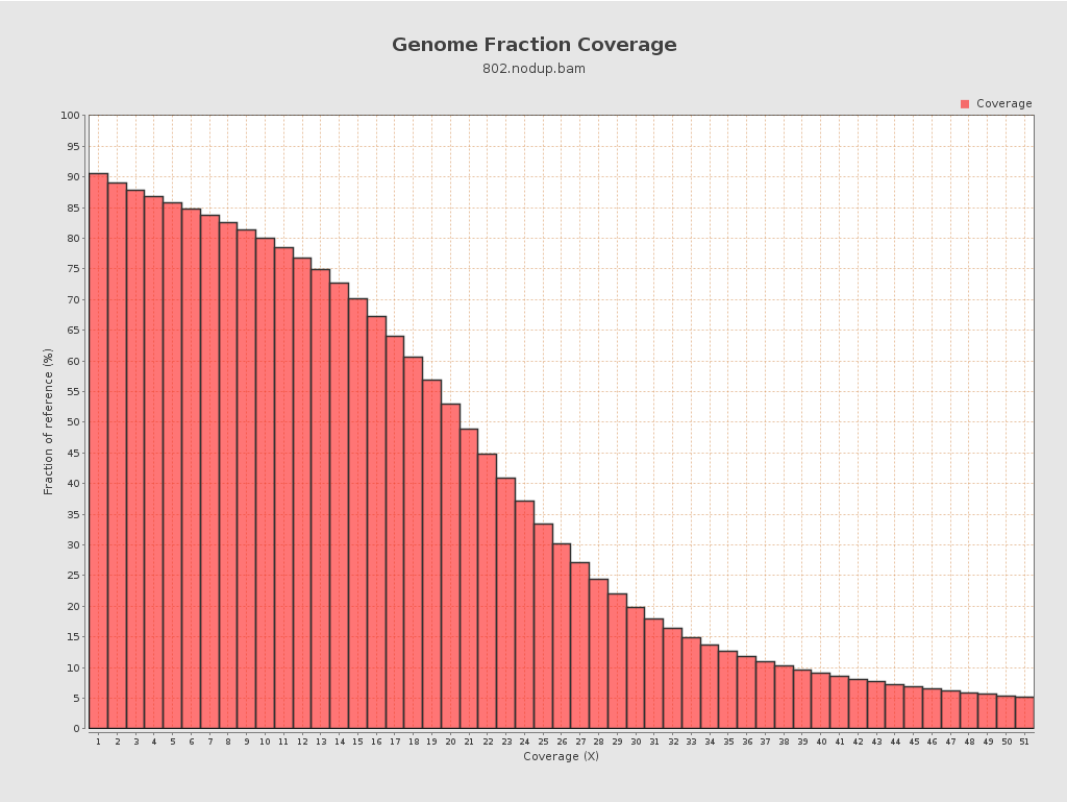
4. Results : Coverage Histogram



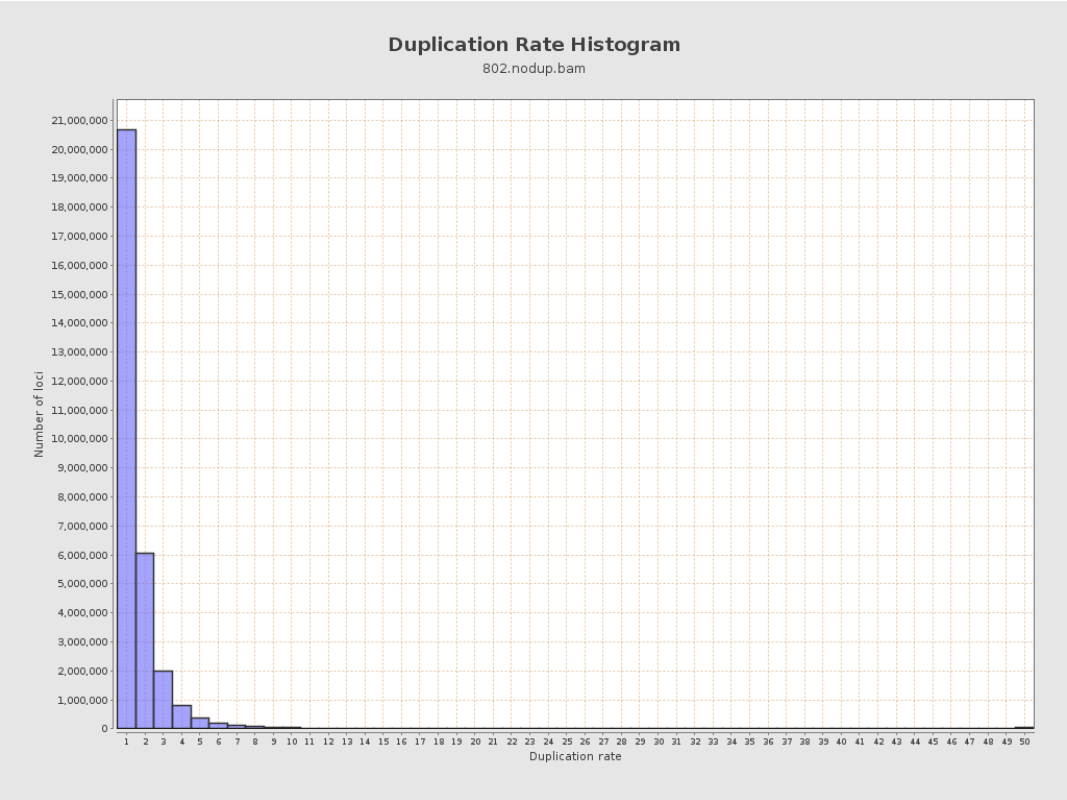
5. Results : Coverage Histogram (0-50X)



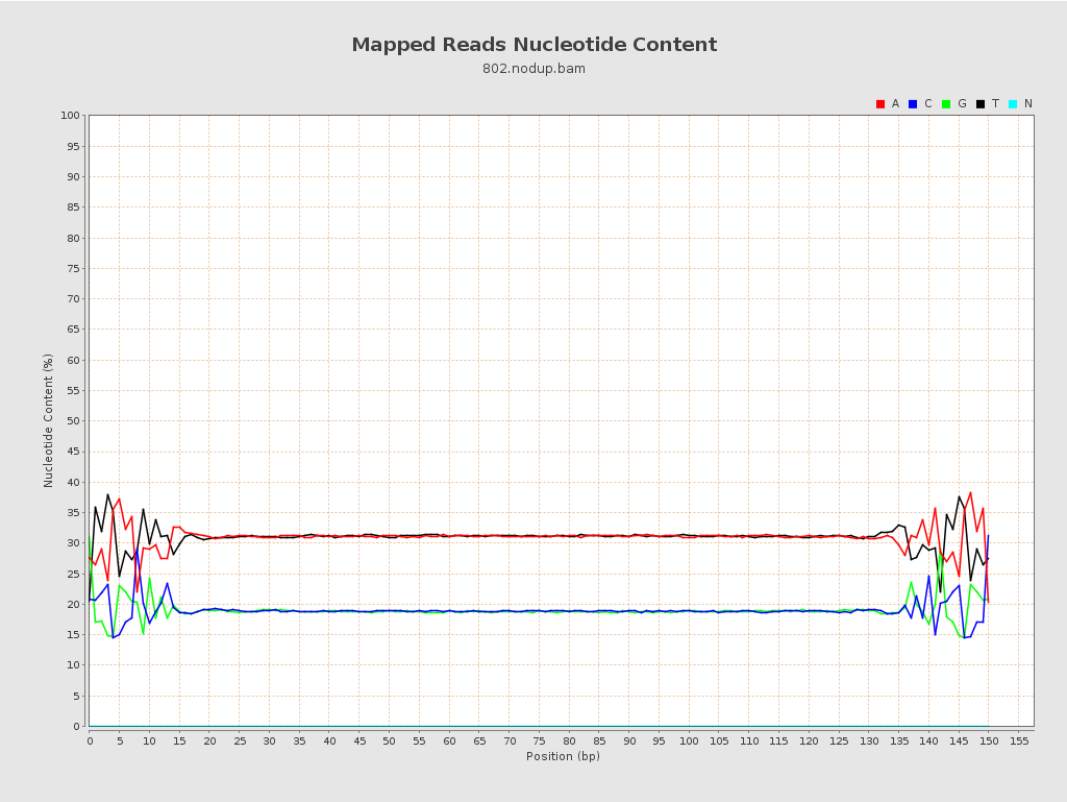
6. Results : Genome Fraction Coverage



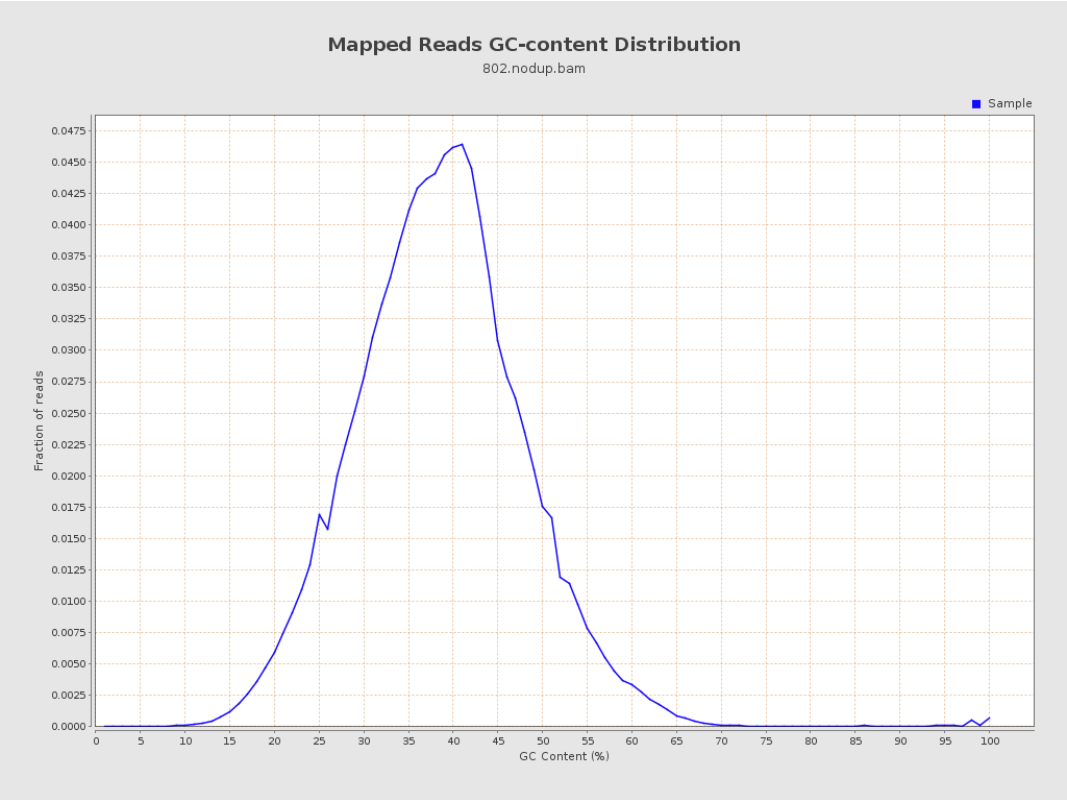
7. Results : Duplication Rate Histogram



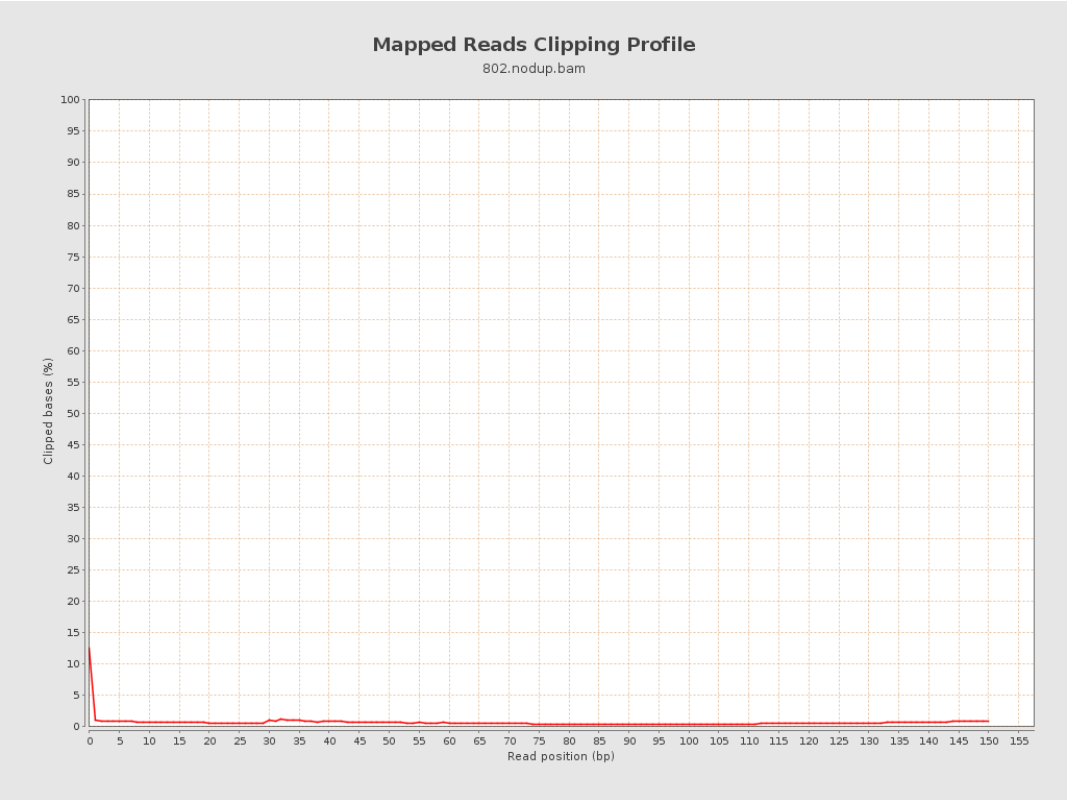
8. Results : Mapped Reads Nucleotide Content



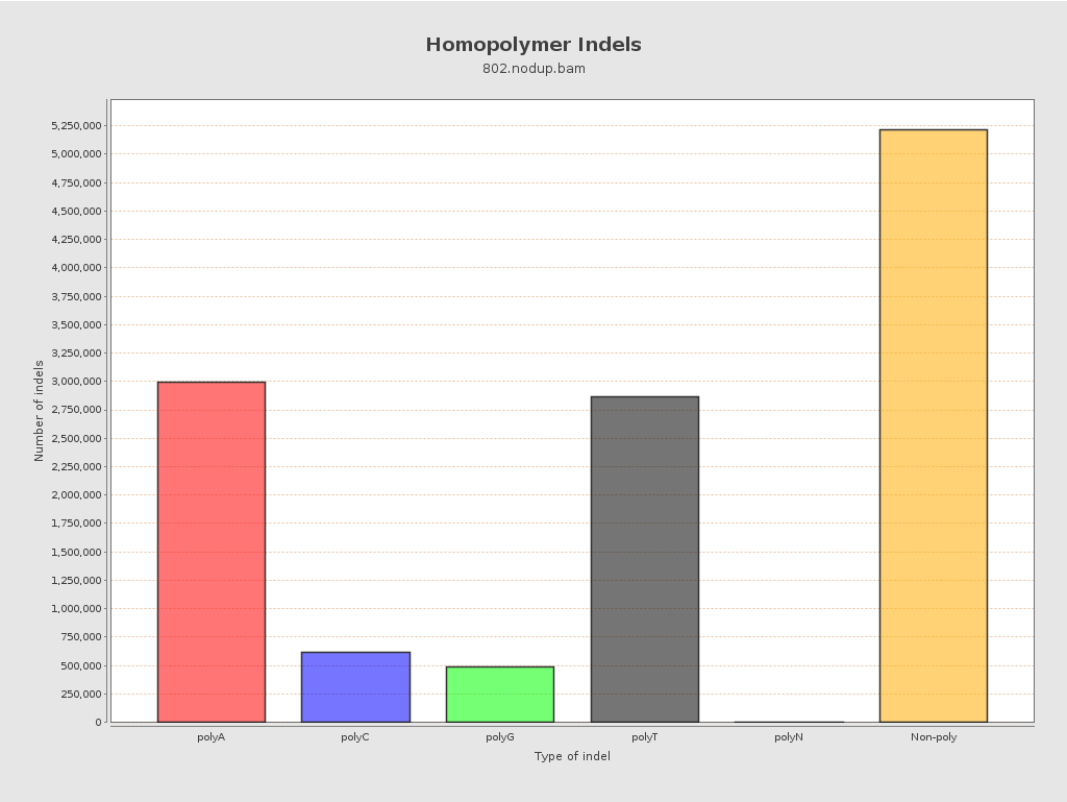
9. Results : Mapped Reads GC-content Distribution



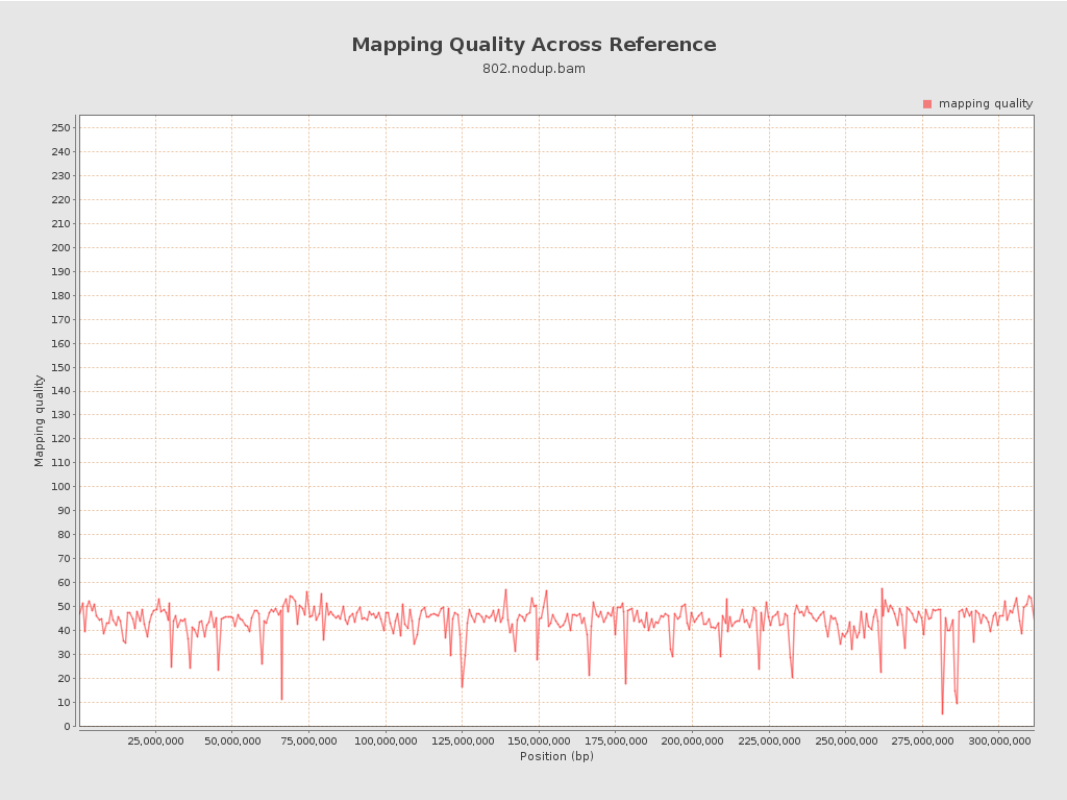
10. Results : Mapped Reads Clipping Profile



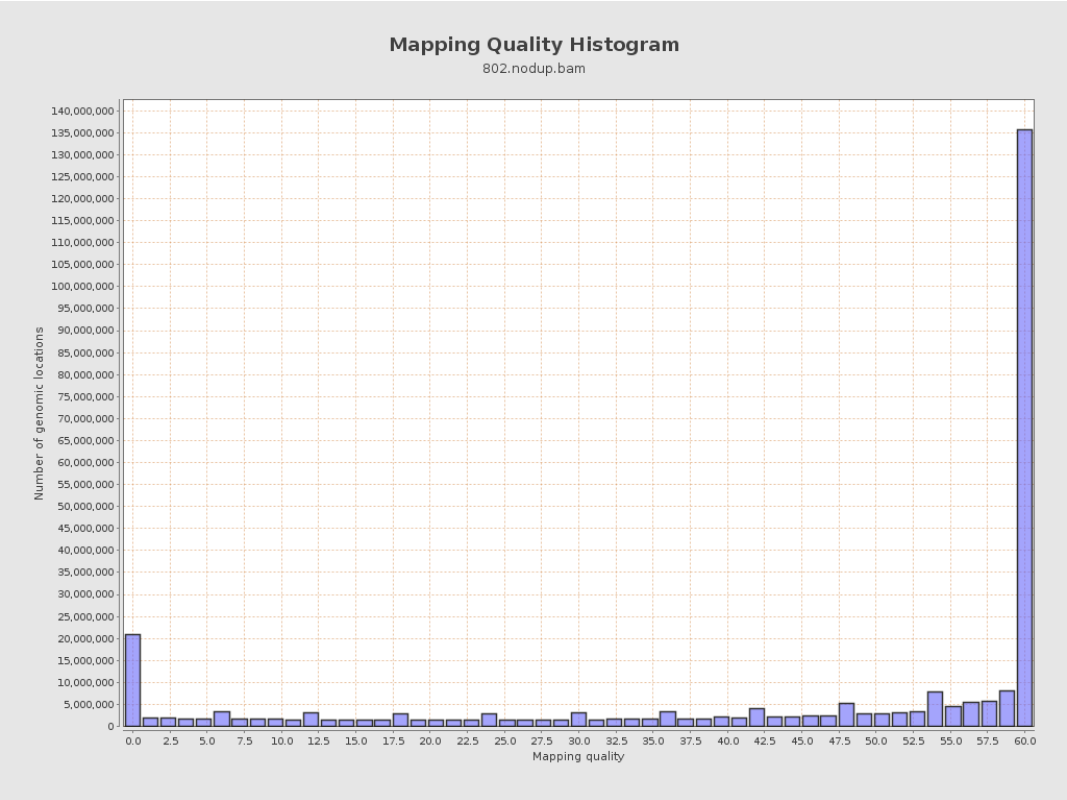
11. Results : Homopolymer Indels



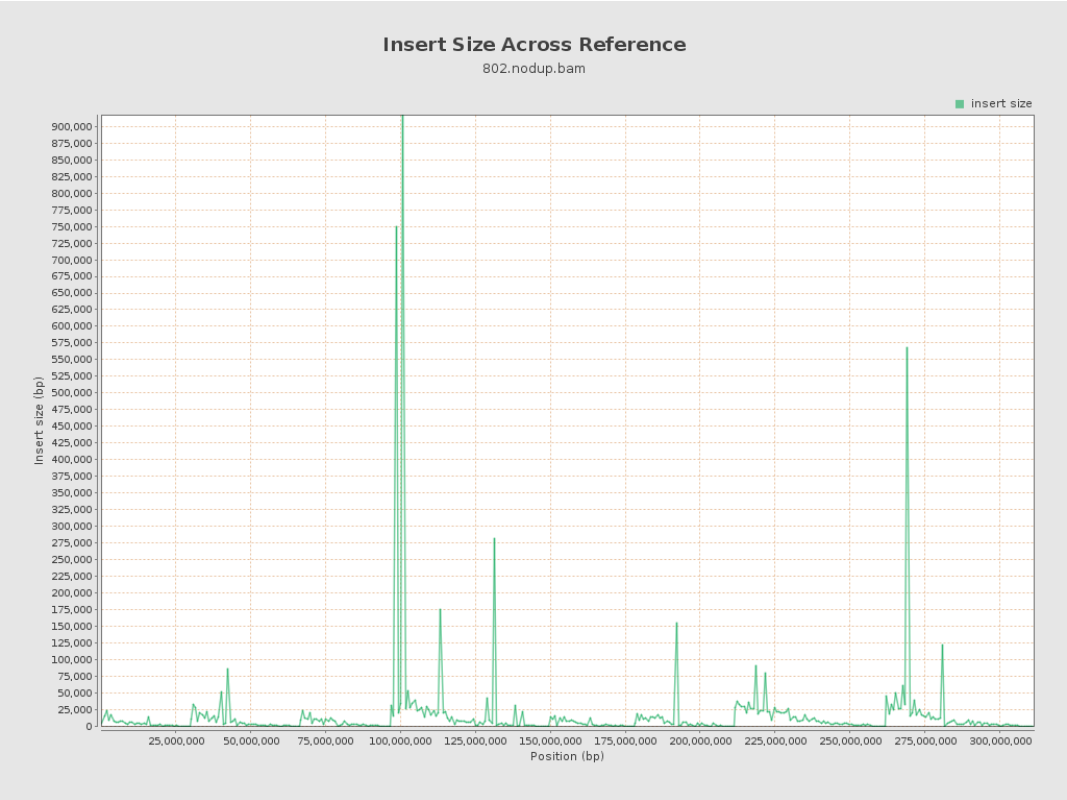
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram