Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:28:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/646.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/646.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_118/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_118_S208_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_118/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_118_S208_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

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

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	59,652,283
Mapped reads	56,067,098 / 93.99%
Unmapped reads	3,585,185 / 6.01%
Mapped paired reads	56,067,098 / 93.99%
Mapped reads, first in pair	28,097,918 / 47.1%
Mapped reads, second in pair	27,969,180 / 46.89%
Mapped reads, both in pair	54,891,190 / 92.02%
Mapped reads, singletons	1,175,908 / 1.97%
Read min/max/mean length	30 / 151 / 148.05
Duplicated reads (flagged)	8,150,929 / 13.66%
Clipped reads	12,487,910 / 20.93%

2.2. ACGT Content

Number/percentage of A's	2,404,055,506 / 30.88%
Number/percentage of C's	1,488,313,385 / 19.12%
Number/percentage of T's	2,406,930,801 / 30.92%
Number/percentage of G's	1,485,521,854 / 19.08%
Number/percentage of N's	32,540 / 0%
GC Percentage	38.2%

2.3. Coverage

Mean	25.048
Standard Deviation	182.6532

2.4. Mapping Quality

Mean Mapping Quality	43.56

2.5. Insert size

Mean	244,449.41
Standard Deviation	2,339,533.25
P25/Median/P75	334 / 435 / 570

2.6. Mismatches and indels

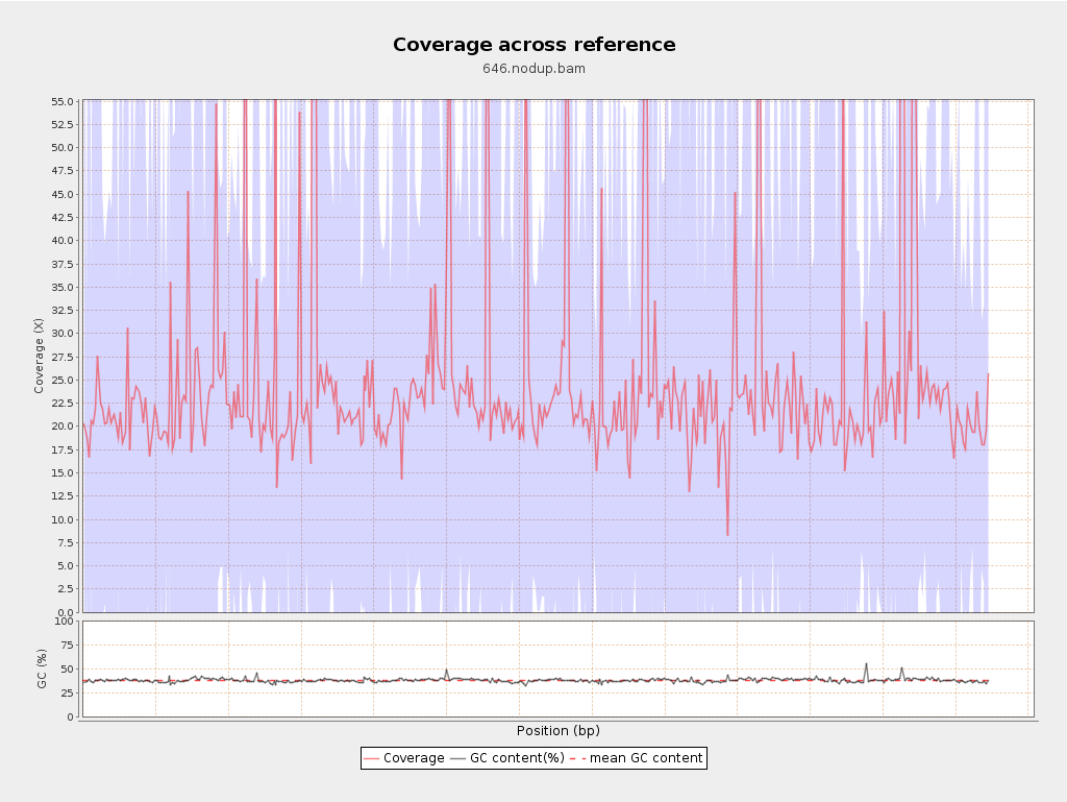
General error rate	2.36%
Mismatches	168,653,450
Insertions	5,365,506
Mapped reads with at least one insertion	8.59%
Deletions	5,517,247
Mapped reads with at least one deletion	8.71%
Homopolymer indels	56.23%

2.7. Chromosome stats

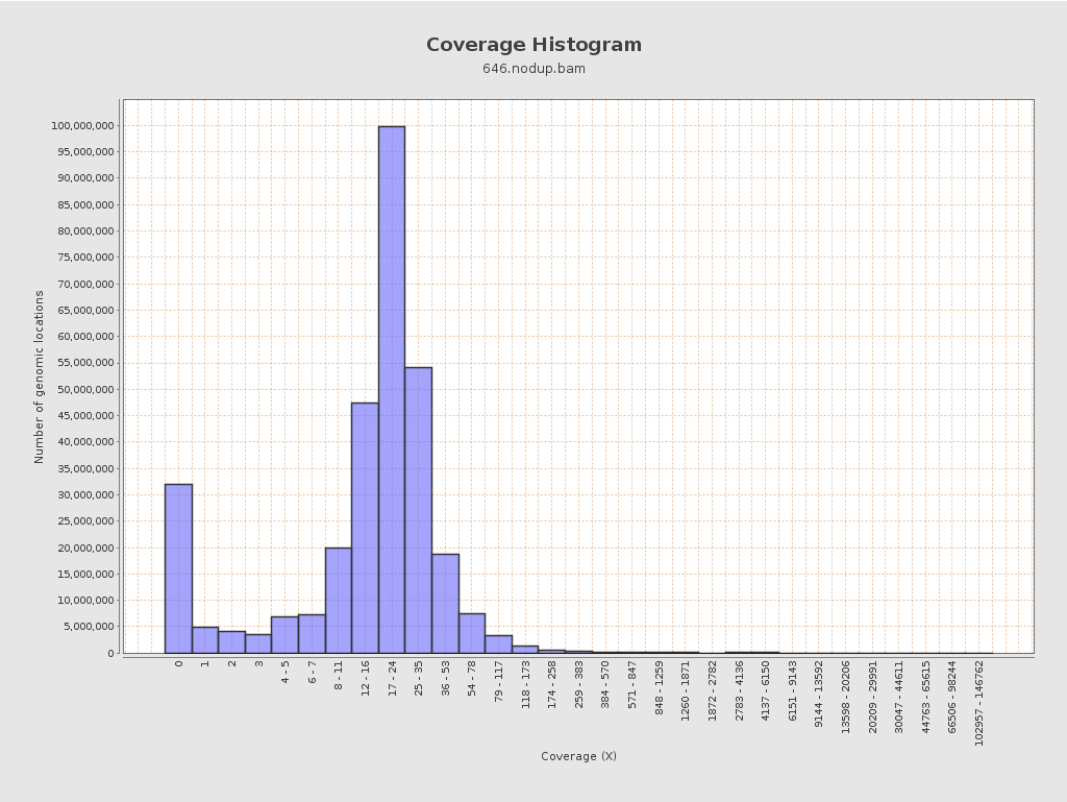
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	622722406	20.9499	57.3871

LT669789.1	36598175	942736759	25.7591	198.4629
LT669790.1	30422129	828340714	27.2282	188.3818
LT669791.1	52758100	1301891550	24.6766	158.8345
LT669792.1	28376109	698558881	24.6179	199.0284
LT669793.1	33388210	805100420	24.1133	182.6987
LT669794.1	50579949	1203012857	23.7844	156.8736
LT669795.1	49795044	1403640738	28.1884	243.9152

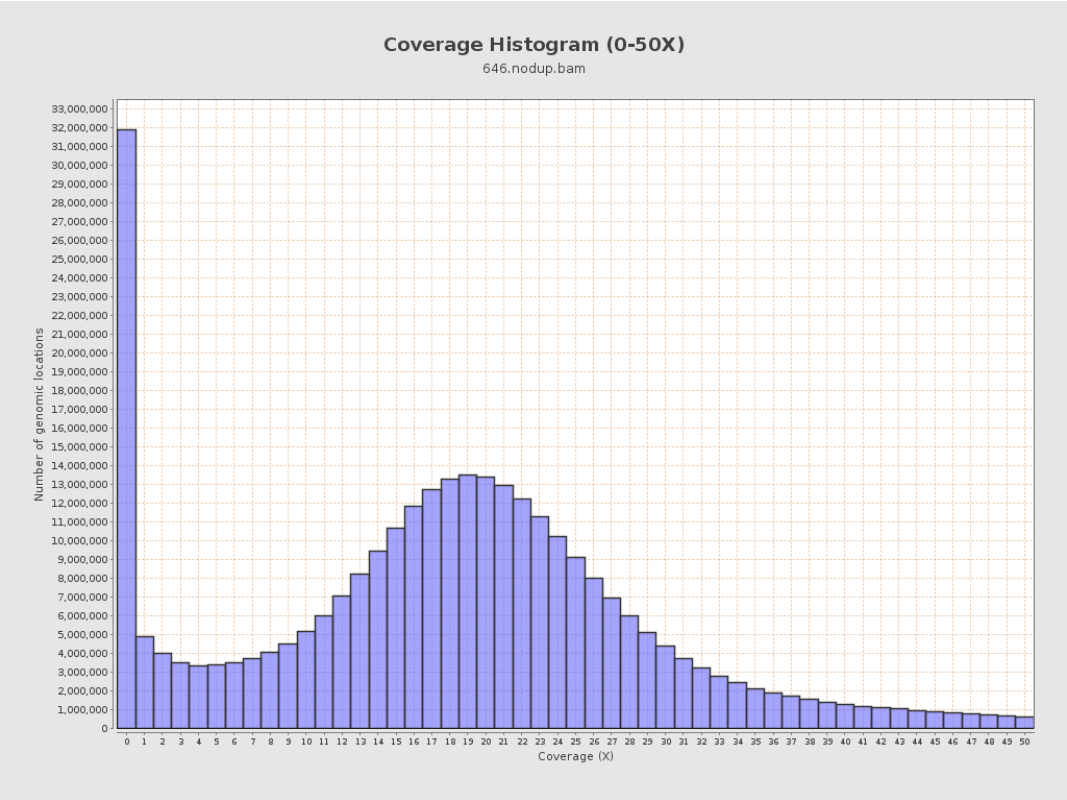
3. Results : Coverage across reference



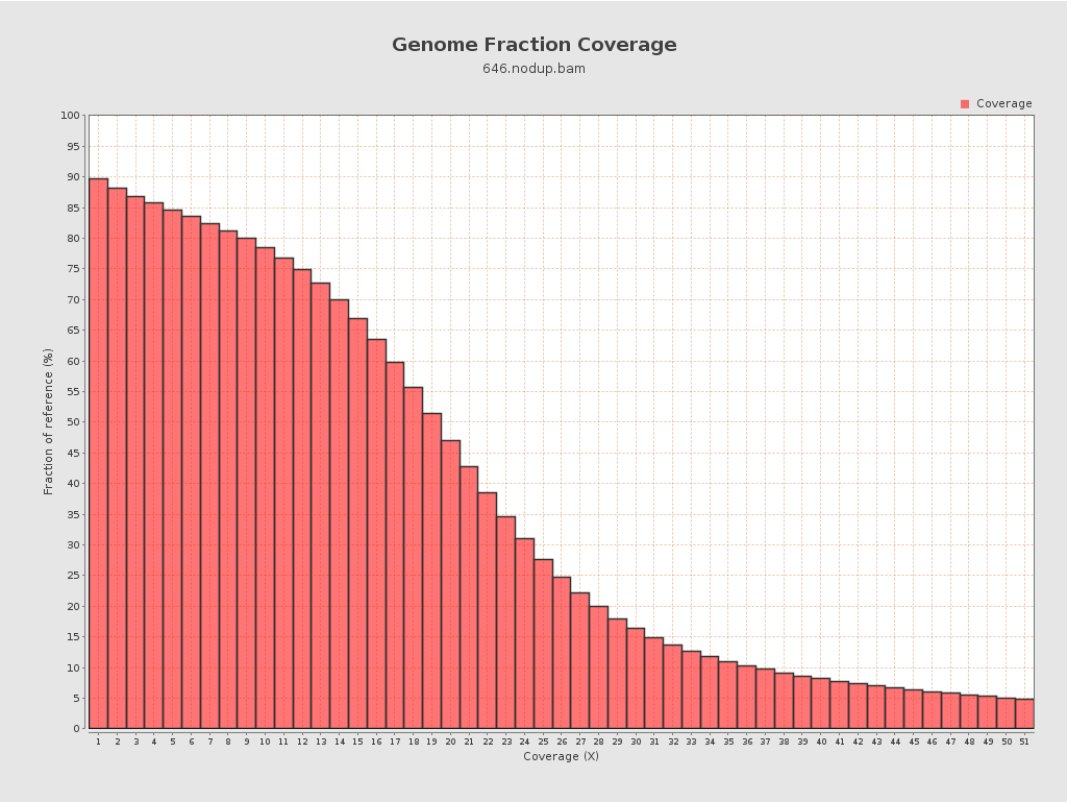
4. Results : Coverage Histogram



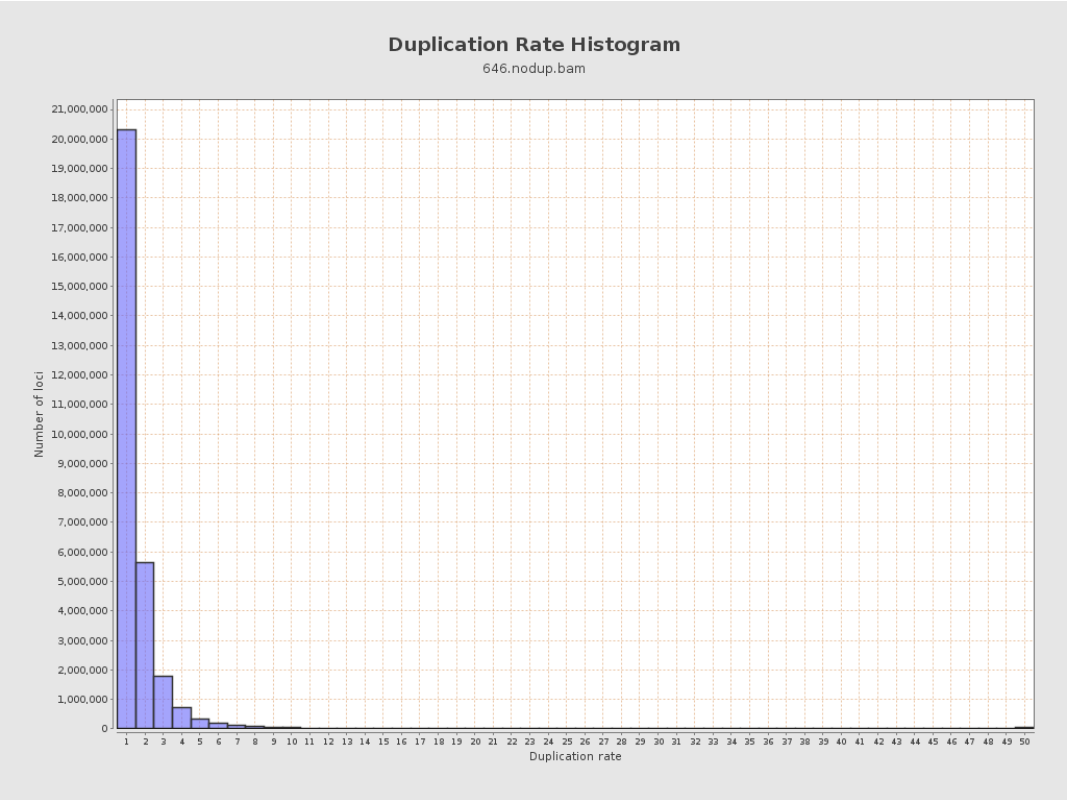
5. Results : Coverage Histogram (0-50X)



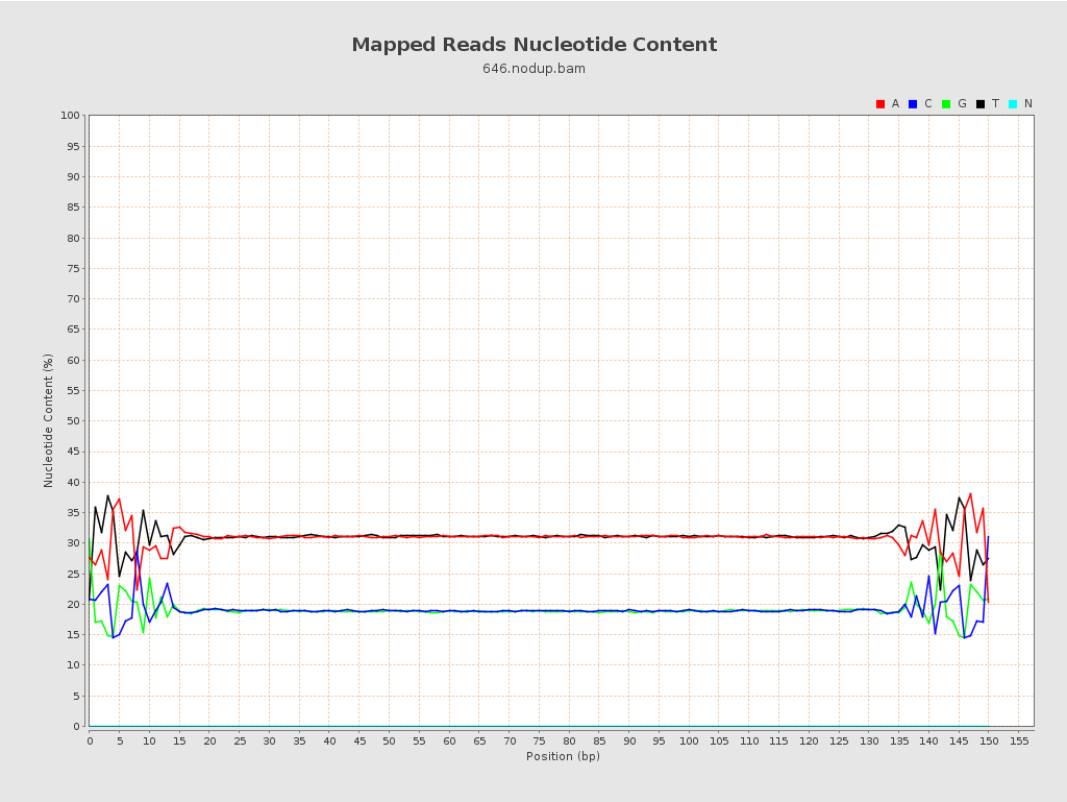
6. Results : Genome Fraction Coverage



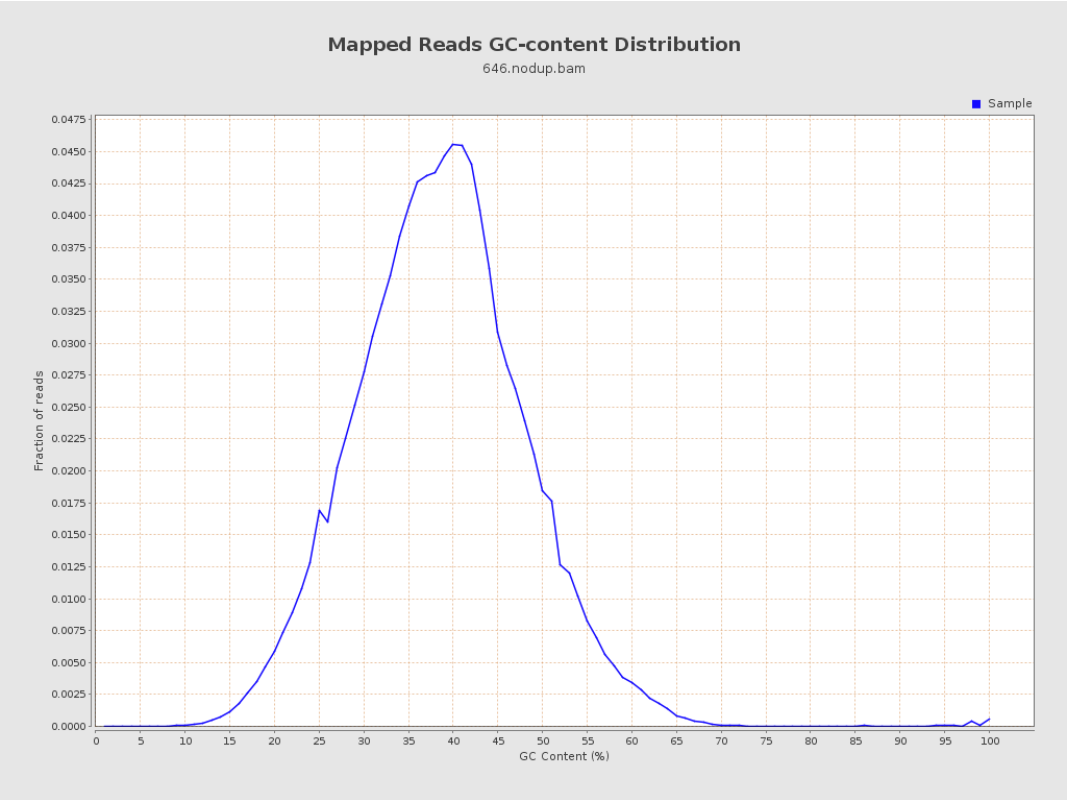
7. Results : Duplication Rate Histogram



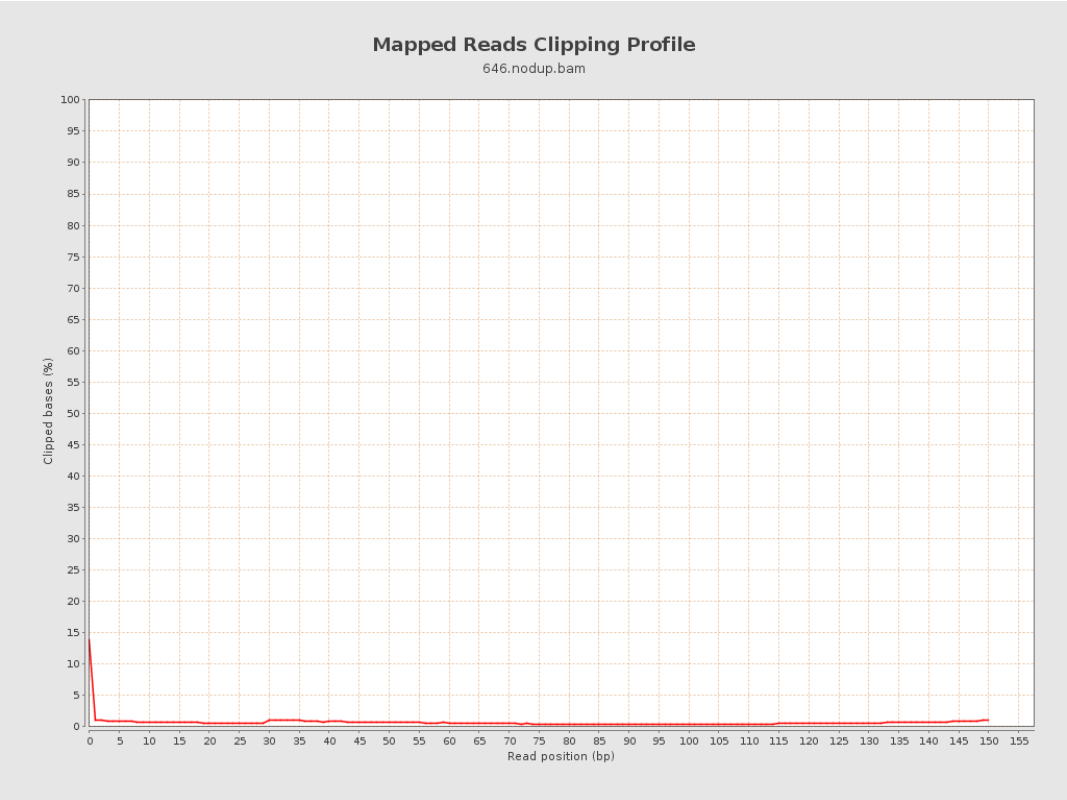
8. Results : Mapped Reads Nucleotide Content



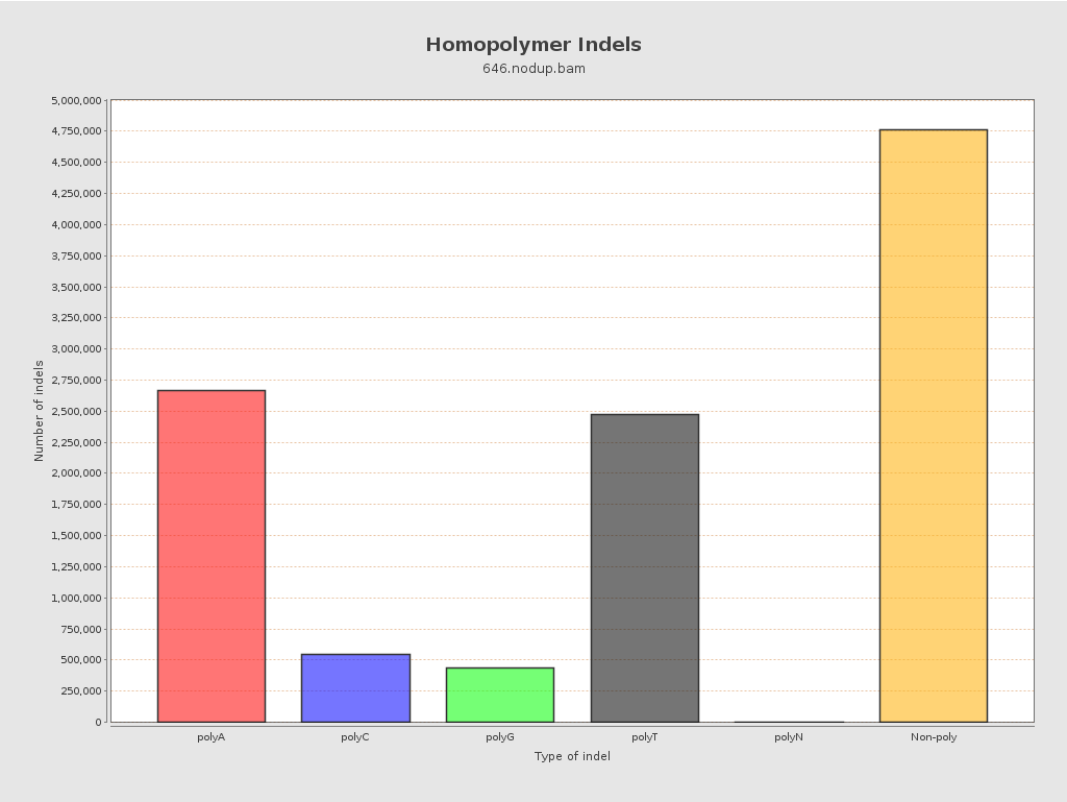
9. Results : Mapped Reads GC-content Distribution



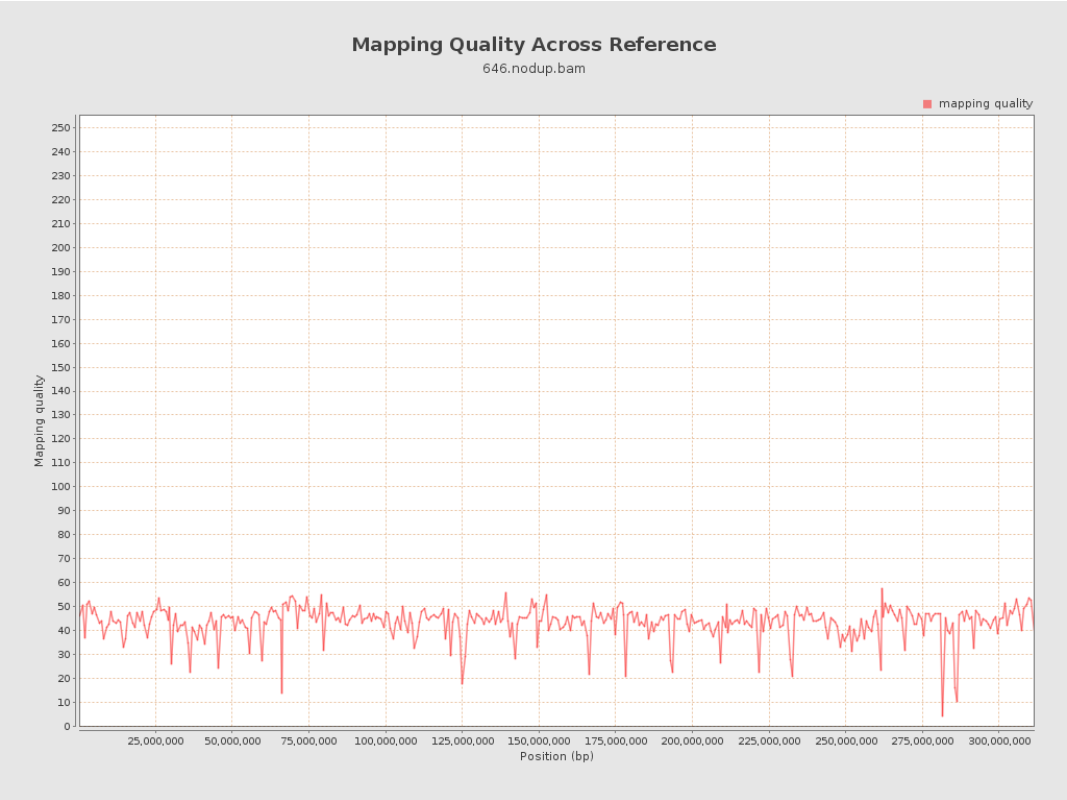
10. Results : Mapped Reads Clipping Profile



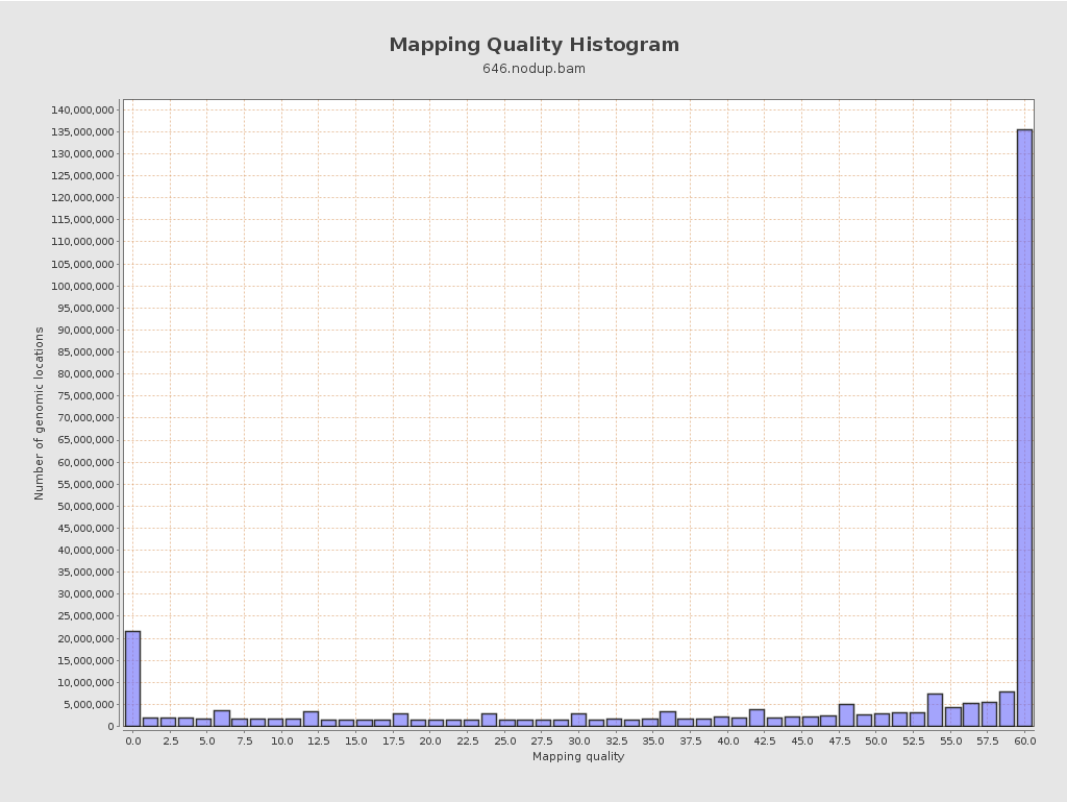
11. Results : Homopolymer Indels



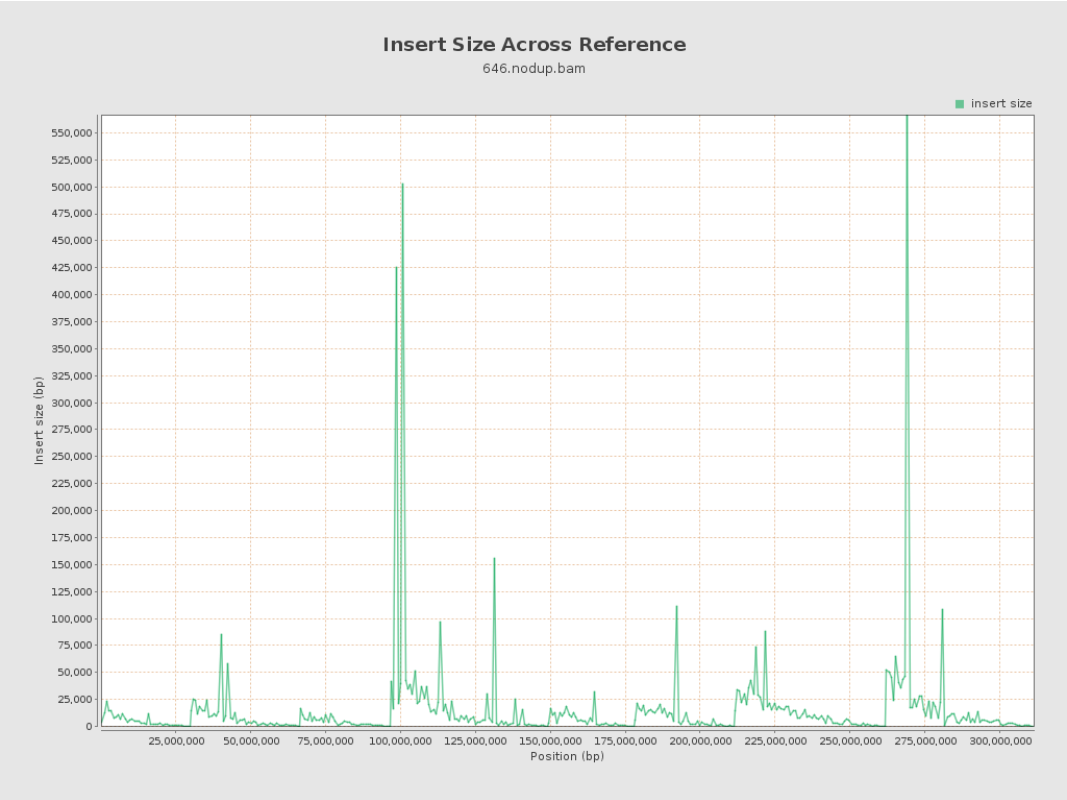
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram