

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:35:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/714
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/714.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_143/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_143_S233_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_143/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_143_S233_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:35:10 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	77,122,377
Mapped reads	70,748,666 / 91.74%
Unmapped reads	6,373,711 / 8.26%
Mapped paired reads	70,748,666 / 91.74%
Mapped reads, first in pair	35,413,766 / 45.92%
Mapped reads, second in pair	35,334,900 / 45.82%
Mapped reads, both in pair	68,652,573 / 89.02%
Mapped reads, singletons	2,096,093 / 2.72%
Read min/max/mean length	30 / 151 / 148.14
Duplicated reads (flagged)	13,624,561 / 17.67%
Clipped reads	16,908,537 / 21.92%

2.2. ACGT Content

Number/percentage of A's	3,005,054,204 / 30.92%
Number/percentage of C's	1,852,498,946 / 19.06%
Number/percentage of T's	3,008,628,191 / 30.96%
Number/percentage of G's	1,851,834,954 / 19.06%
Number/percentage of N's	38,985 / 0%
GC Percentage	38.12%

2.3. Coverage

Mean	31.2648
Standard Deviation	301.1629

2.4. Mapping Quality

Mean Mapping Quality	44.28
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2.5. Insert size

Mean	256,265.49
Standard Deviation	2,422,029.33
P25/Median/P75	336 / 445 / 590

2.6. Mismatches and indels

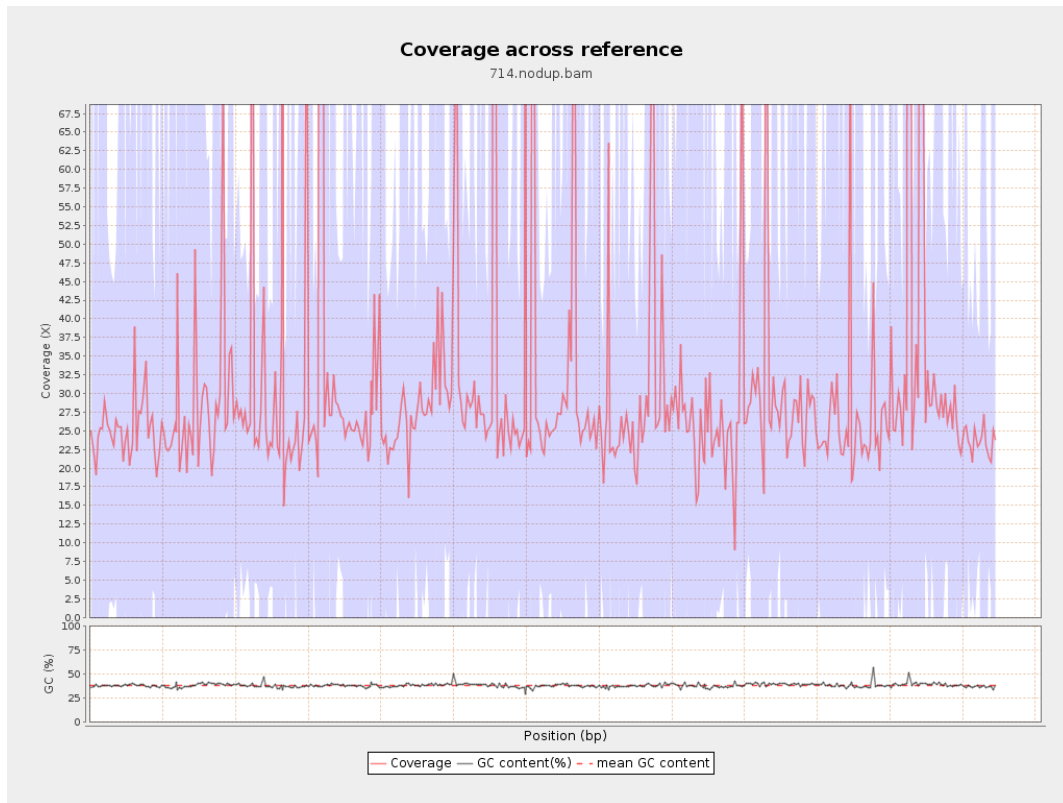
General error rate	2.45%
Mismatches	218,614,384
Insertions	7,085,769
Mapped reads with at least one insertion	8.93%
Deletions	6,798,334
Mapped reads with at least one deletion	8.53%
Homopolymer indels	56.64%

2.7. Chromosome stats

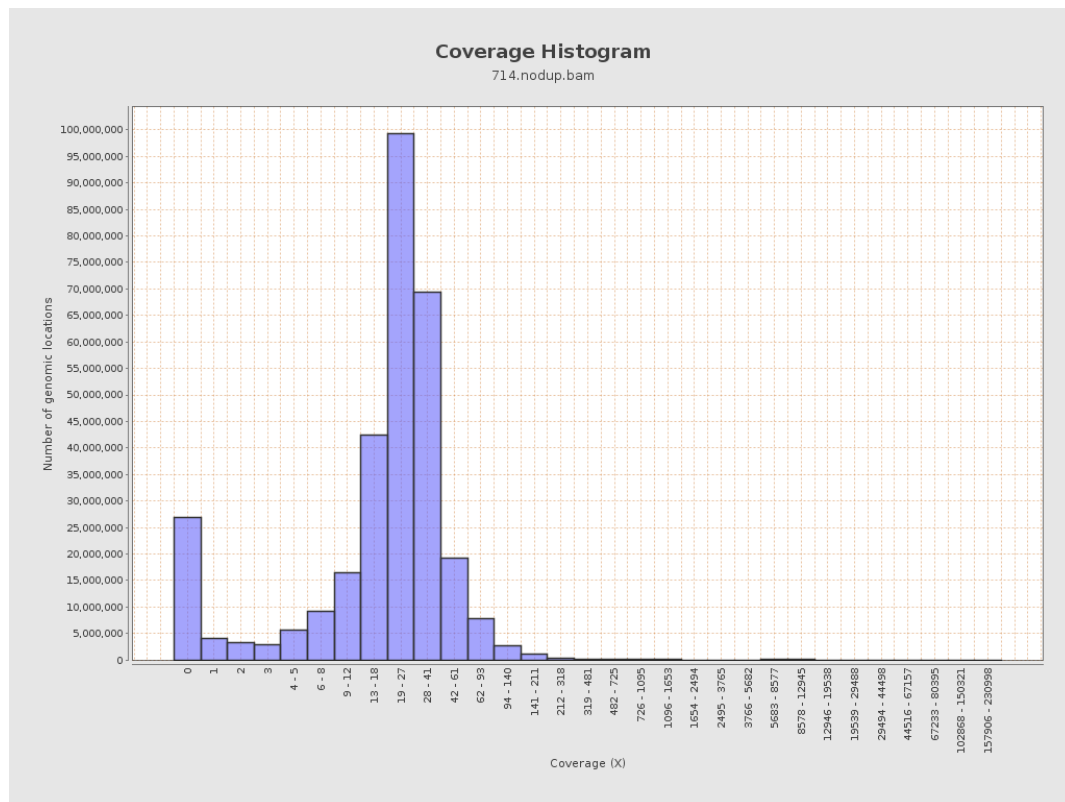
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	742144420	24.9676	105.3742

LT669789.1	36598175	1121930763	30.6554	290.7341
LT669790.1	30422129	1143777710	37.5969	407.1774
LT669791.1	52758100	1638148646	31.0502	300.2251
LT669792.1	28376109	897952510	31.6447	343.377
LT669793.1	33388210	961079462	28.785	195.766
LT669794.1	50579949	1468320428	29.0297	245.8243
LT669795.1	49795044	1770063298	35.547	384.3845

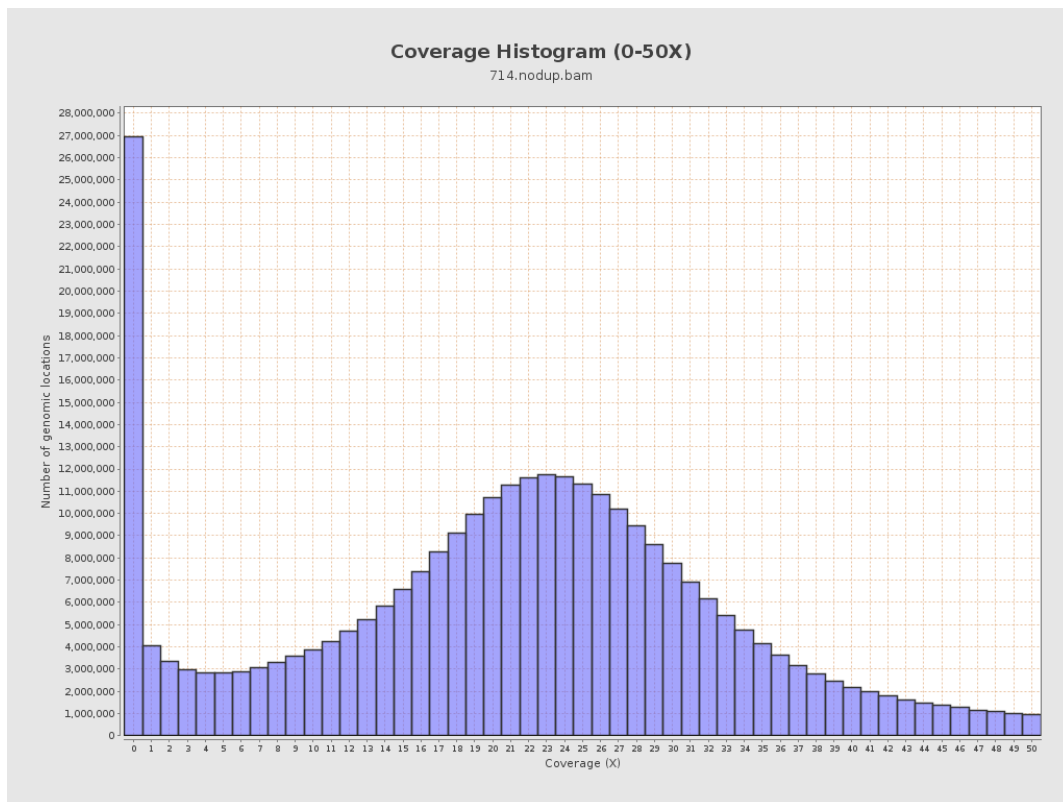
3. Results : Coverage across reference



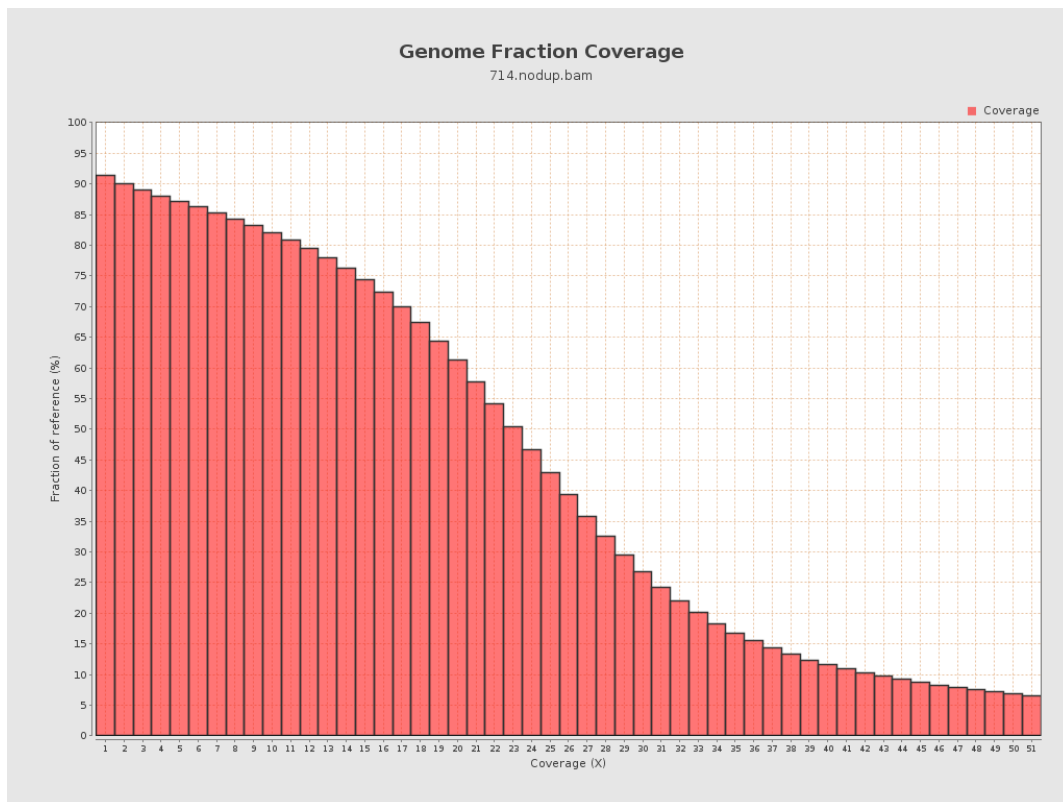
4. Results : Coverage Histogram



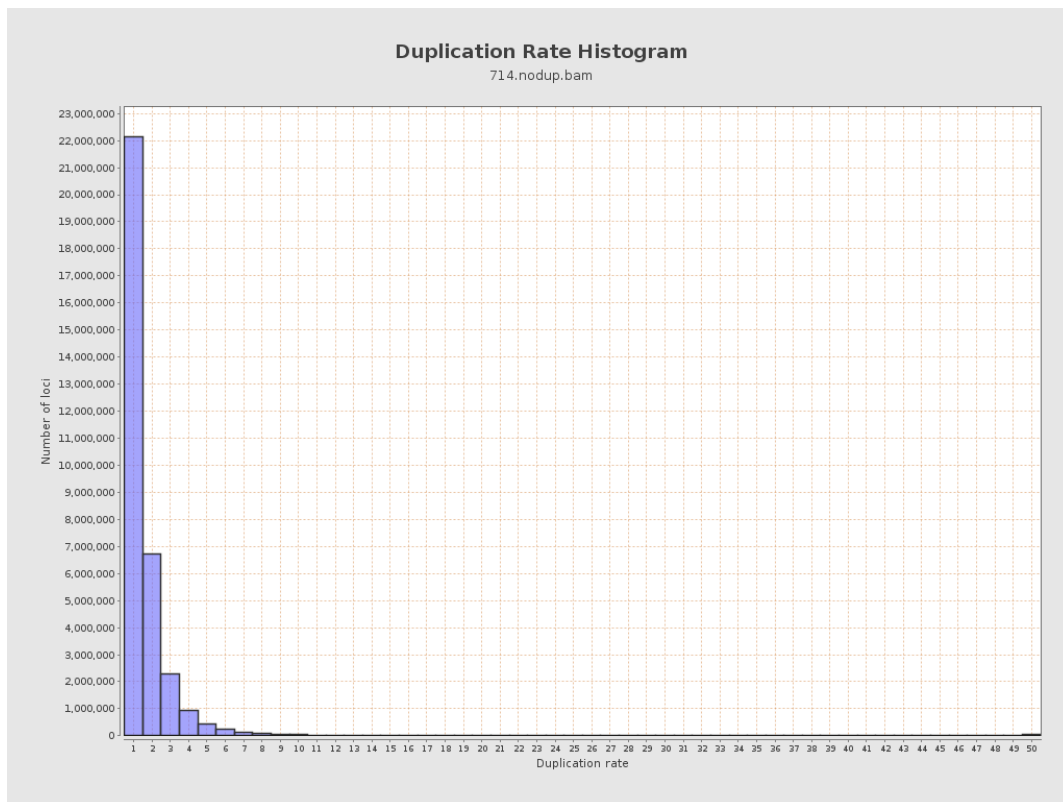
5. Results : Coverage Histogram (0-50X)



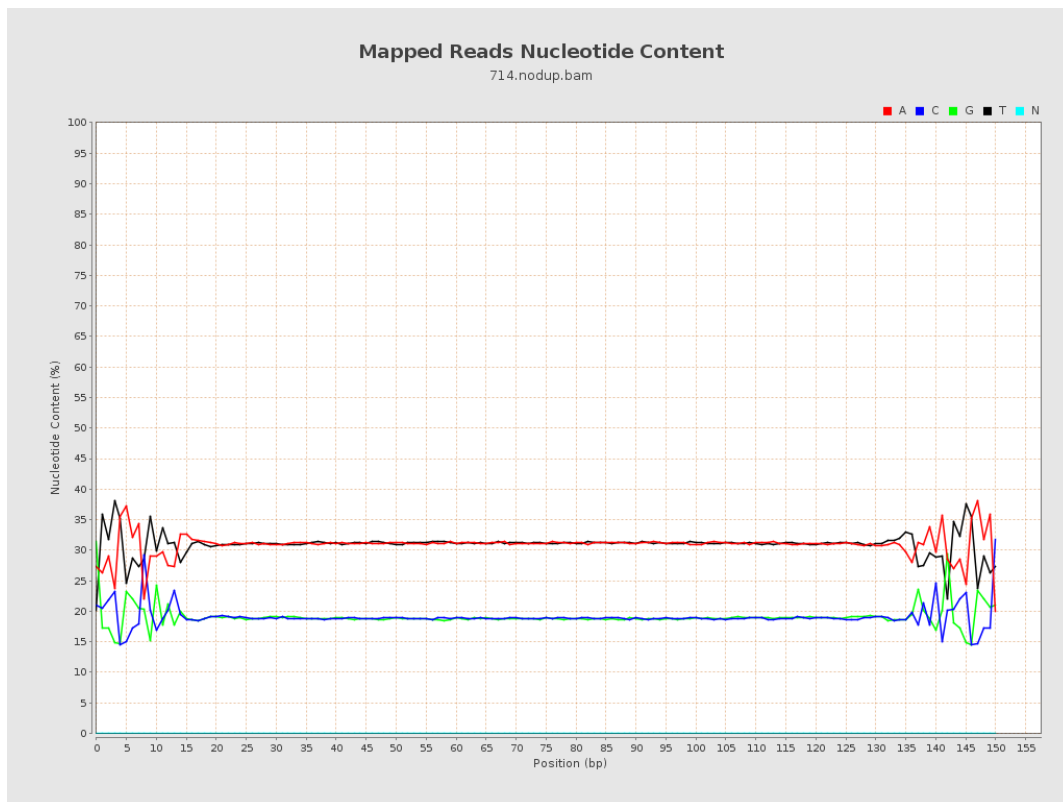
6. Results : Genome Fraction Coverage



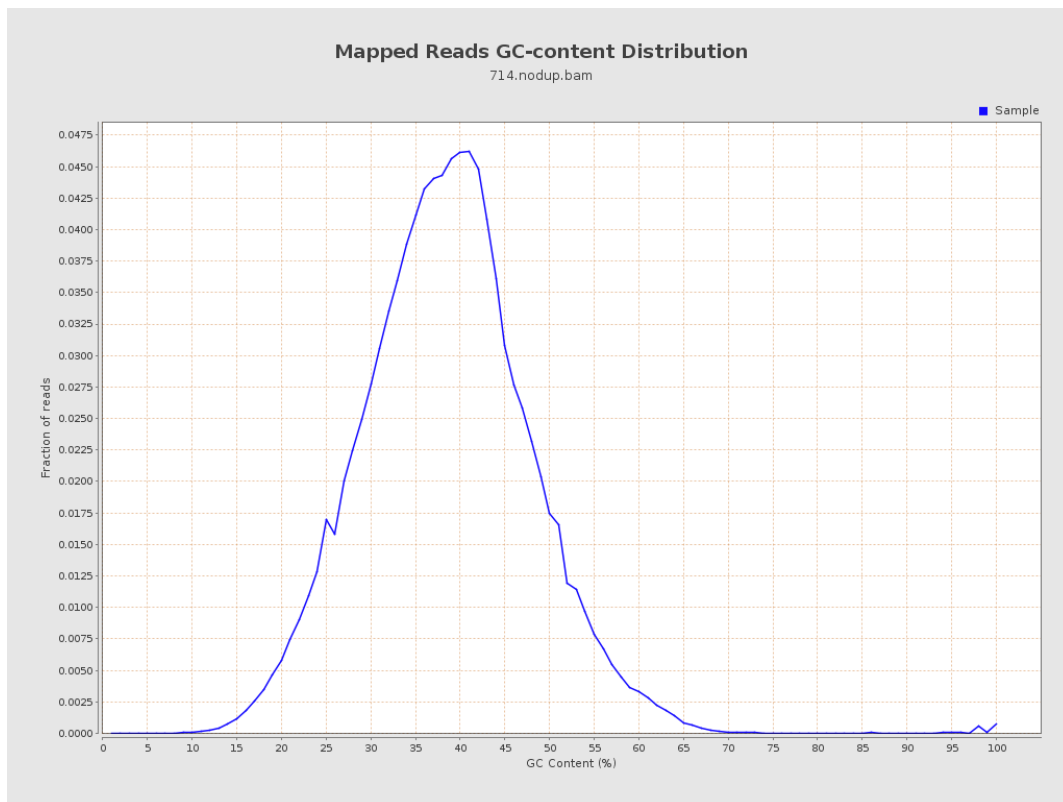
7. Results : Duplication Rate Histogram



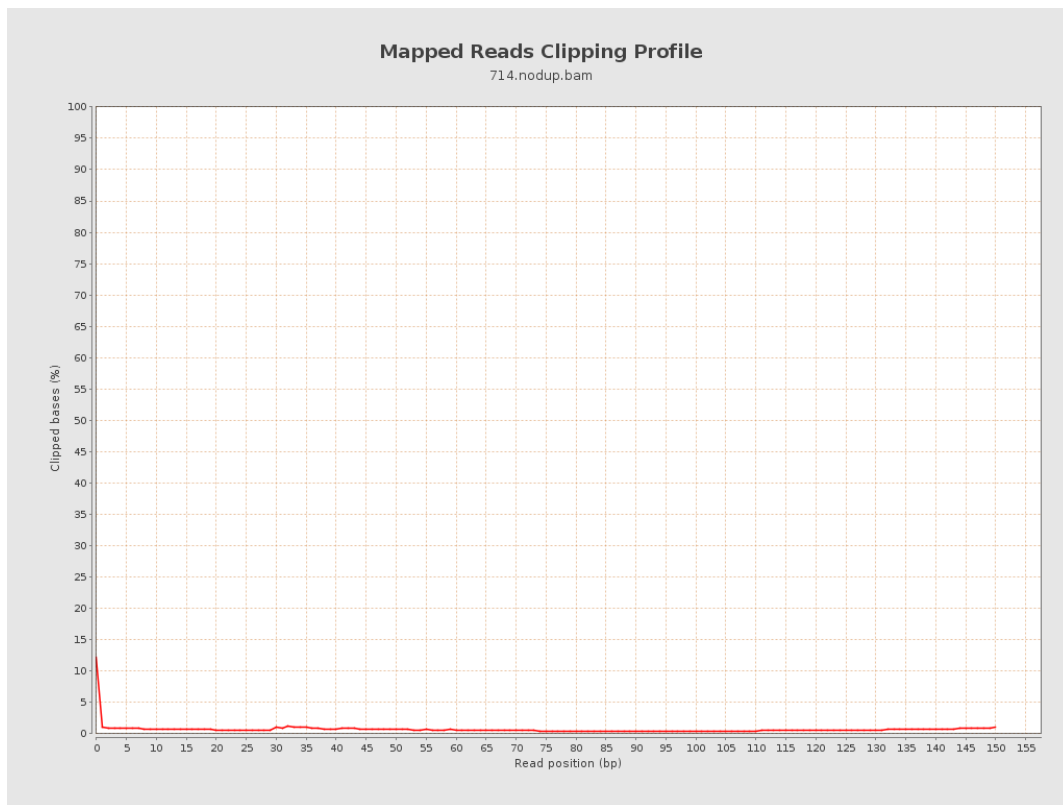
8. Results : Mapped Reads Nucleotide Content



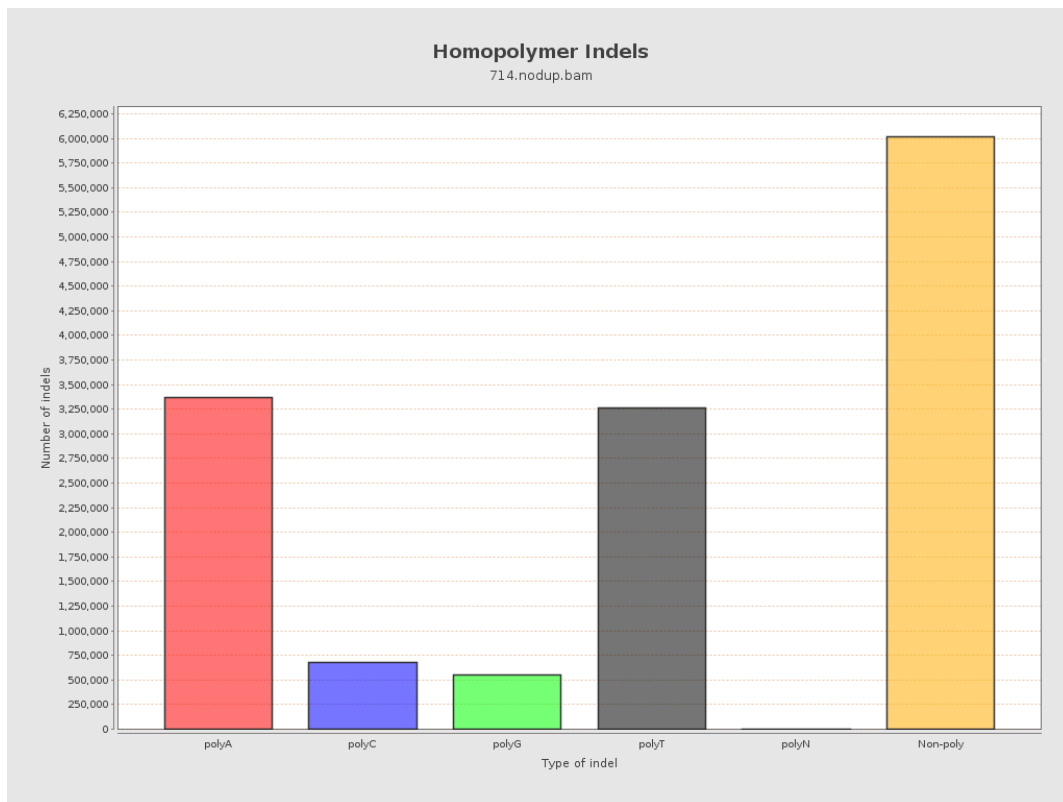
9. Results : Mapped Reads GC-content Distribution



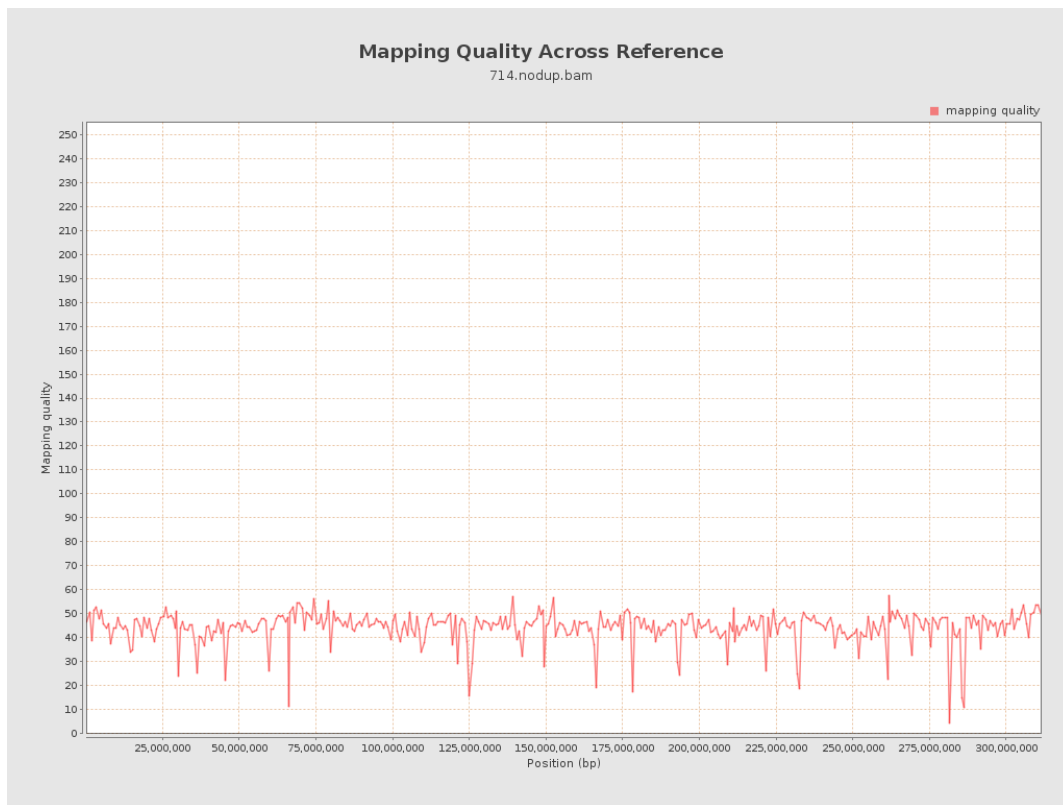
10. Results : Mapped Reads Clipping Profile



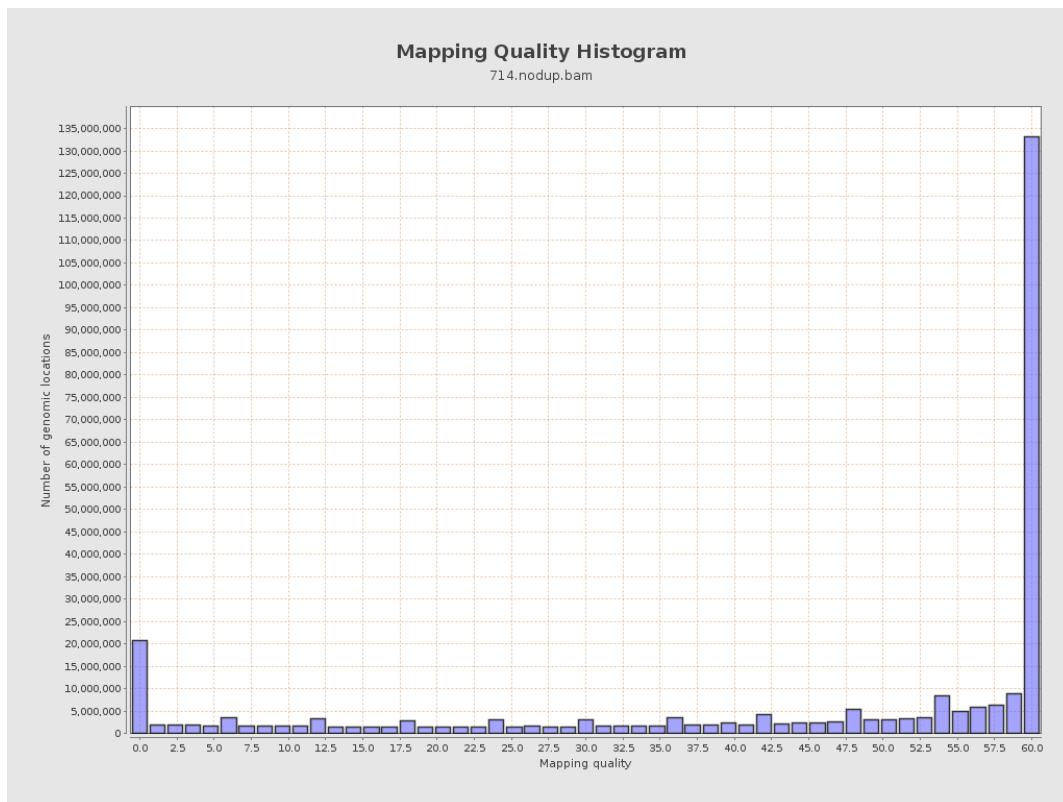
11. Results : Homopolymer Indels



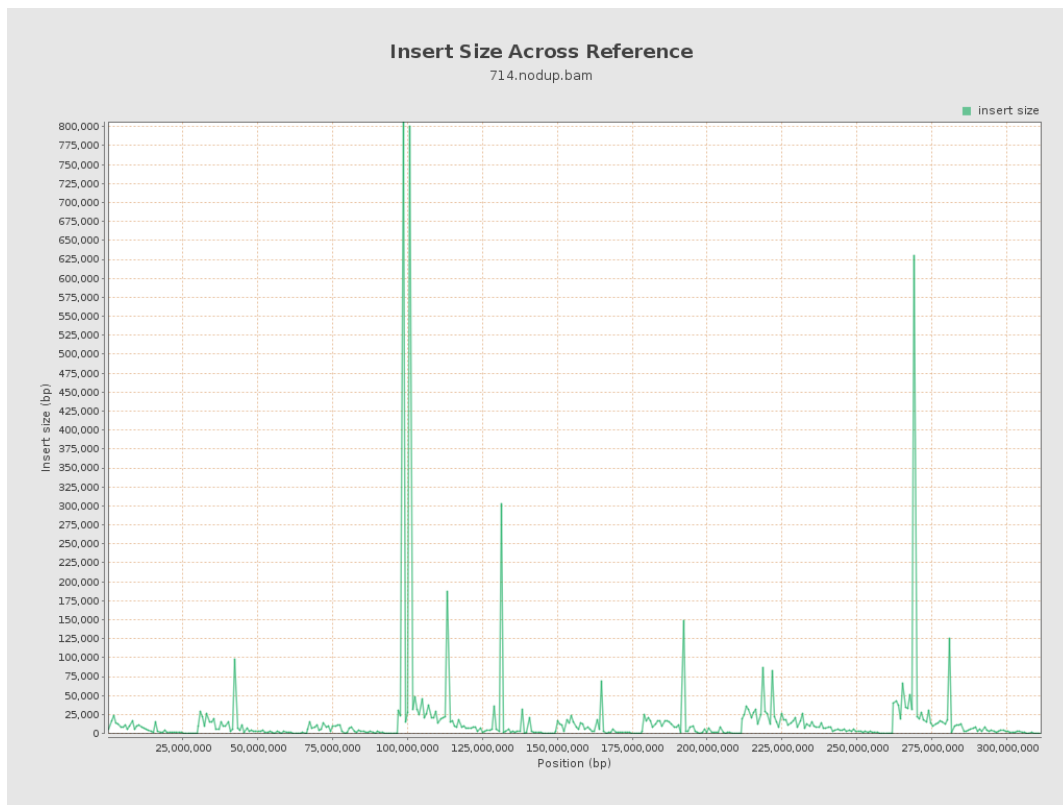
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

