

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:36:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/434
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/434.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/awdata/P26207/P26207_127/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_127_S217_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_127/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_127_S217_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:36:44 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	81,941,237
Mapped reads	74,984,061 / 91.51%
Unmapped reads	6,957,176 / 8.49%
Mapped paired reads	74,984,061 / 91.51%
Mapped reads, first in pair	37,550,953 / 45.83%
Mapped reads, second in pair	37,433,108 / 45.68%
Mapped reads, both in pair	72,938,595 / 89.01%
Mapped reads, singletons	2,045,466 / 2.5%
Read min/max/mean length	30 / 151 / 148.19
Duplicated reads (flagged)	13,988,195 / 17.07%
Clipped reads	16,989,653 / 20.73%

2.2. ACGT Content

Number/percentage of A's	3,205,414,481 / 31%
Number/percentage of C's	1,966,318,908 / 19.02%
Number/percentage of T's	3,204,841,768 / 30.99%
Number/percentage of G's	1,963,340,524 / 18.99%
Number/percentage of N's	44,688 / 0%
GC Percentage	38%

2.3. Coverage

Mean	33.2638
Standard Deviation	294.1569

2.4. Mapping Quality

Mean Mapping Quality	44.73
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2.5. Insert size

Mean	236,613.67
Standard Deviation	2,332,851.94
P25/Median/P75	315 / 413 / 541

2.6. Mismatches and indels

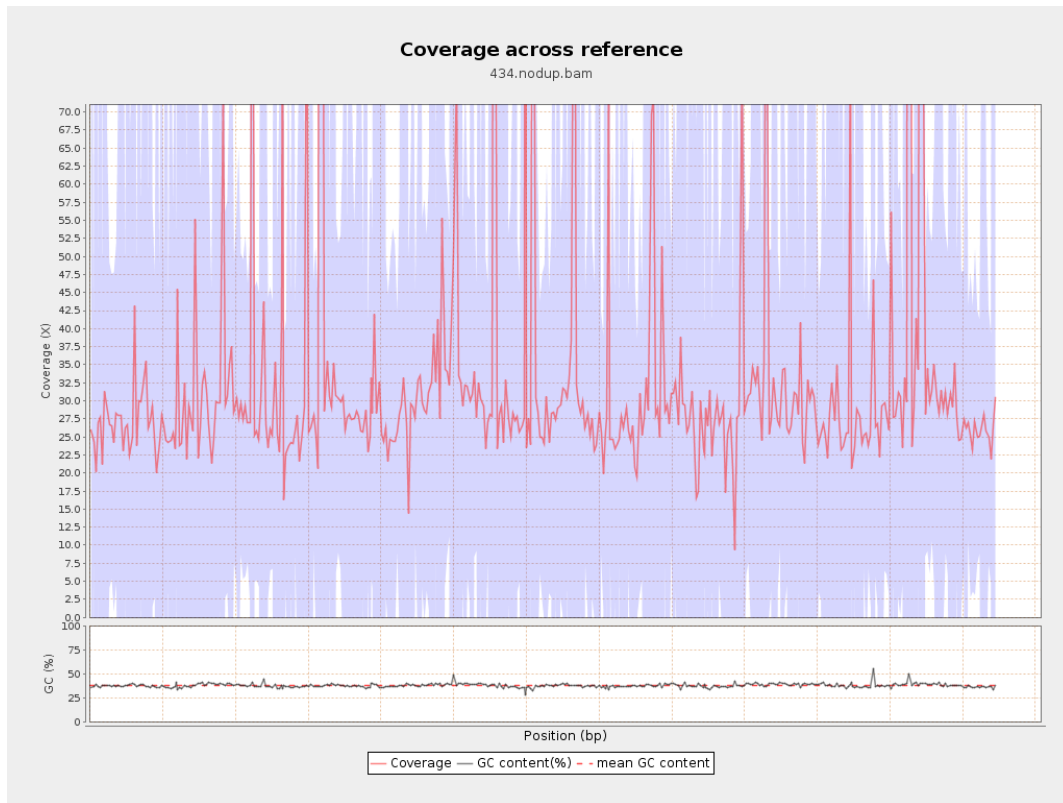
General error rate	2.26%
Mismatches	213,988,079
Insertions	7,249,177
Mapped reads with at least one insertion	8.64%
Deletions	7,040,188
Mapped reads with at least one deletion	8.35%
Homopolymer indels	57.68%

2.7. Chromosome stats

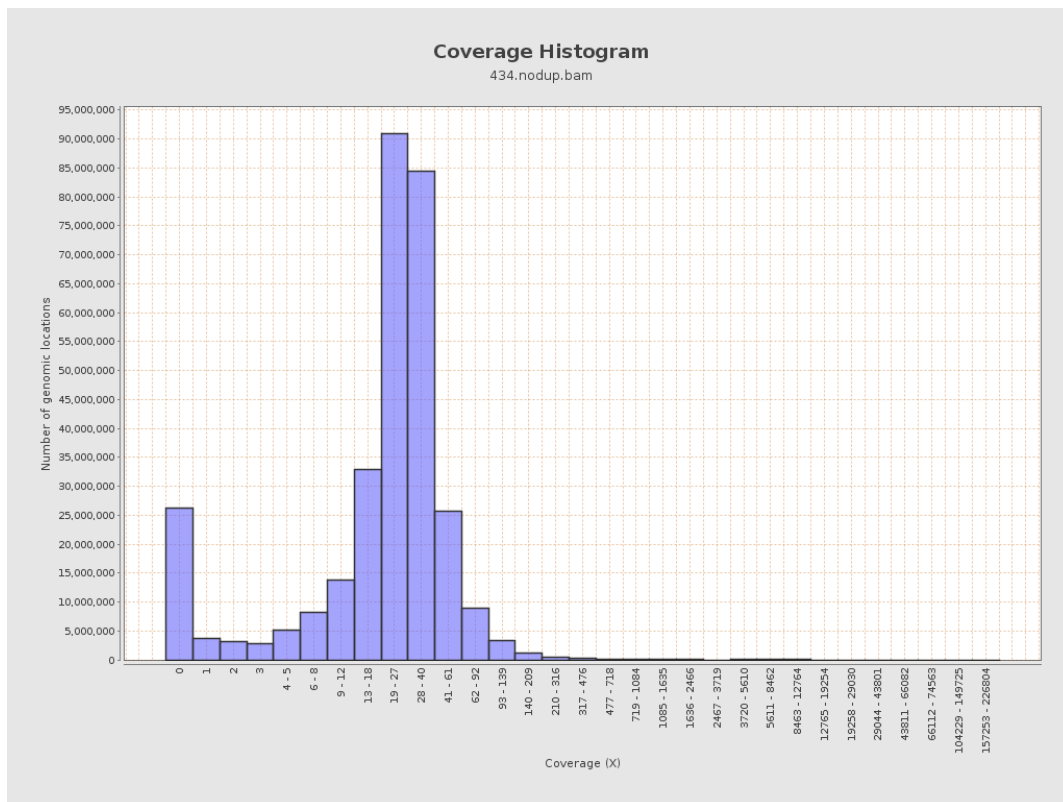
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	793870247	26.7077	102.9789

LT669789.1	36598175	1202336234	32.8524	286.6977
LT669790.1	30422129	1192929678	39.2126	390.628
LT669791.1	52758100	1735958784	32.9041	286.5094
LT669792.1	28376109	959291037	33.8063	310.6387
LT669793.1	33388210	1010654693	30.2698	200.3283
LT669794.1	50579949	1561089649	30.8638	232.798
LT669795.1	49795044	1910255914	38.3624	396.9456

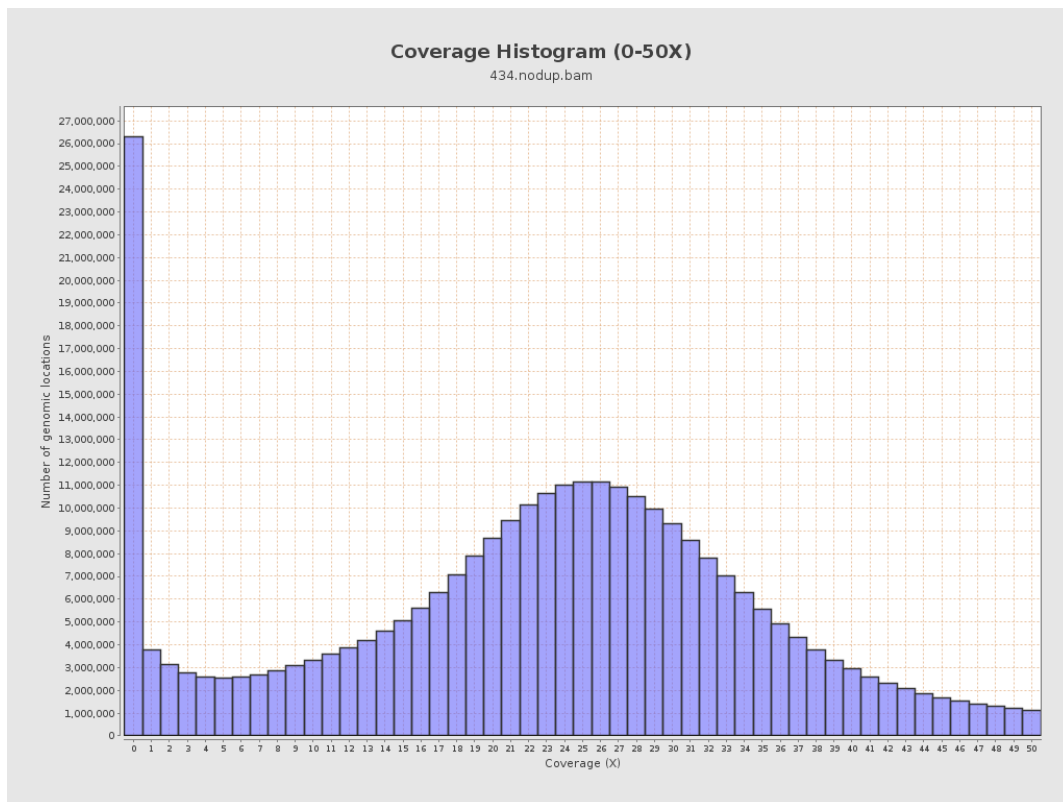
3. Results : Coverage across reference



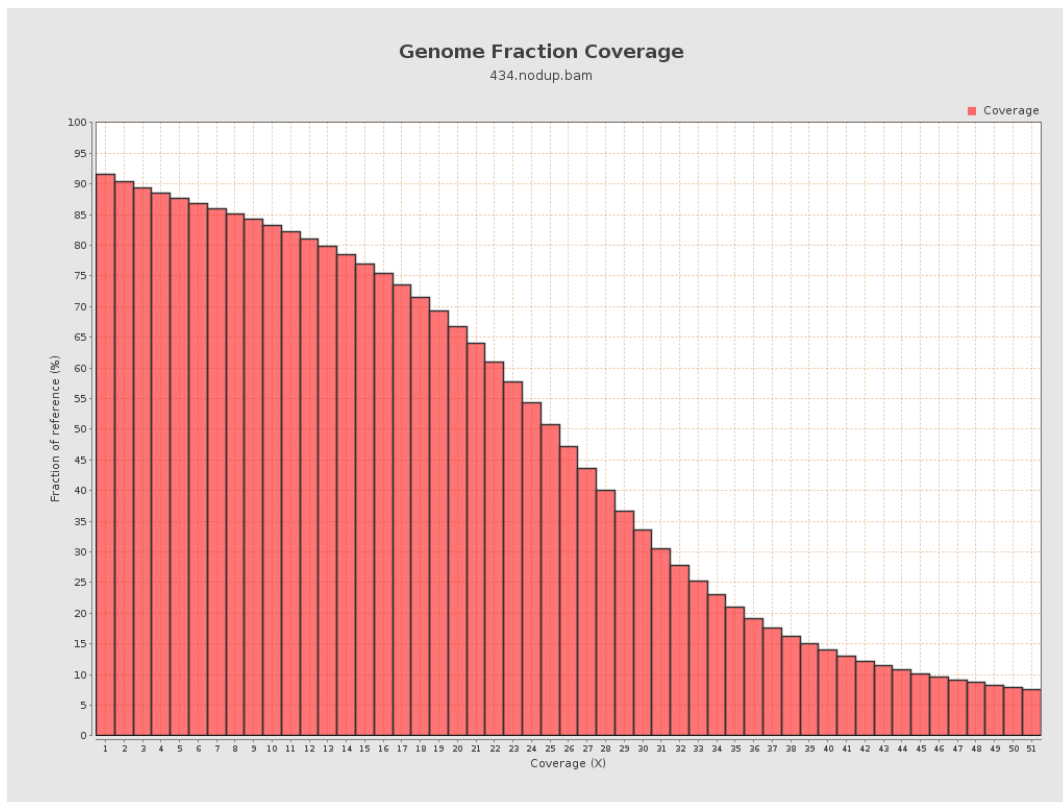
4. Results : Coverage Histogram



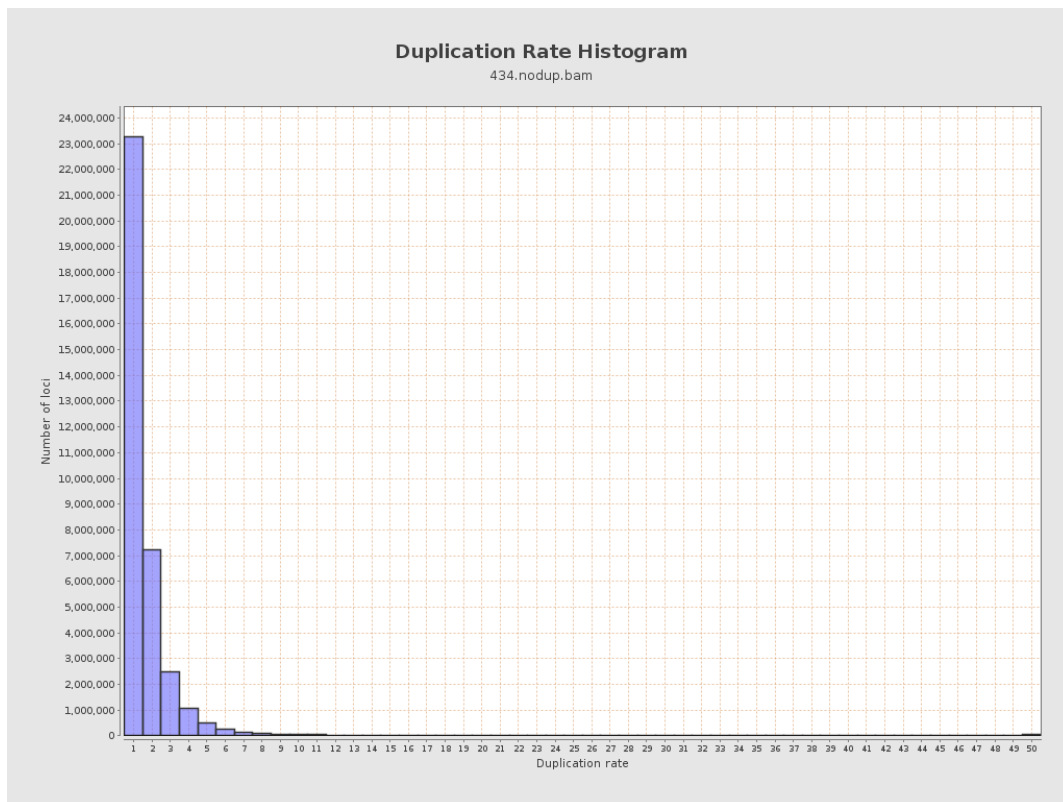
5. Results : Coverage Histogram (0-50X)



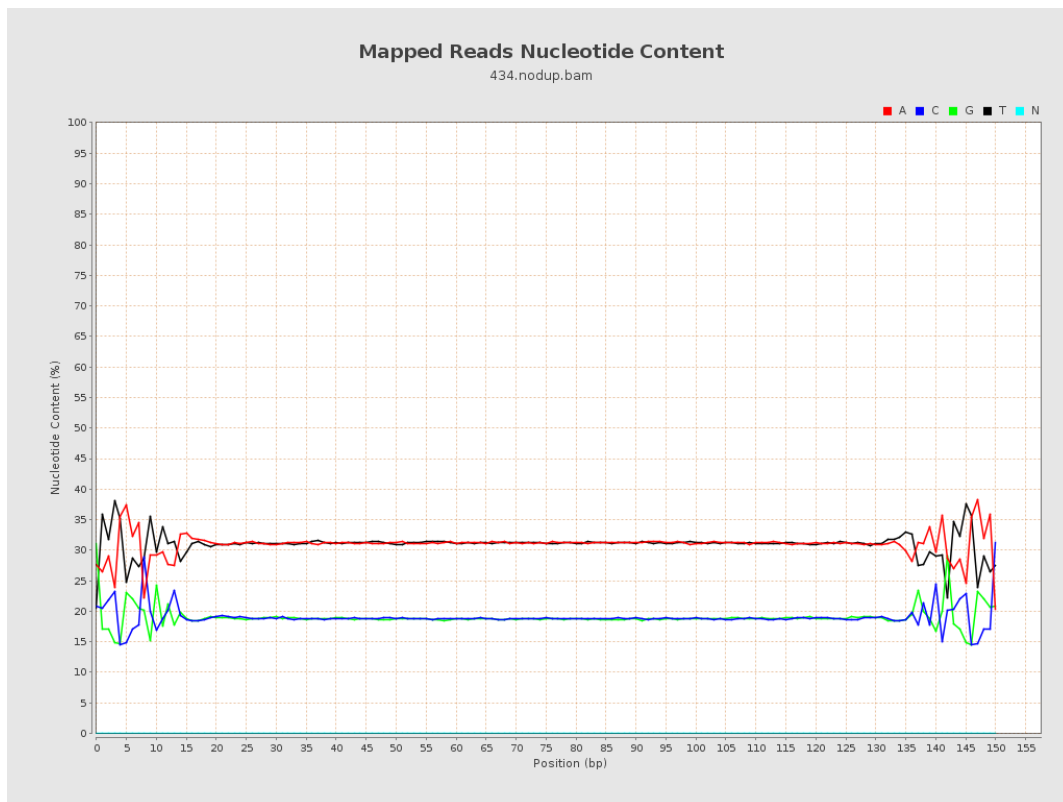
6. Results : Genome Fraction Coverage



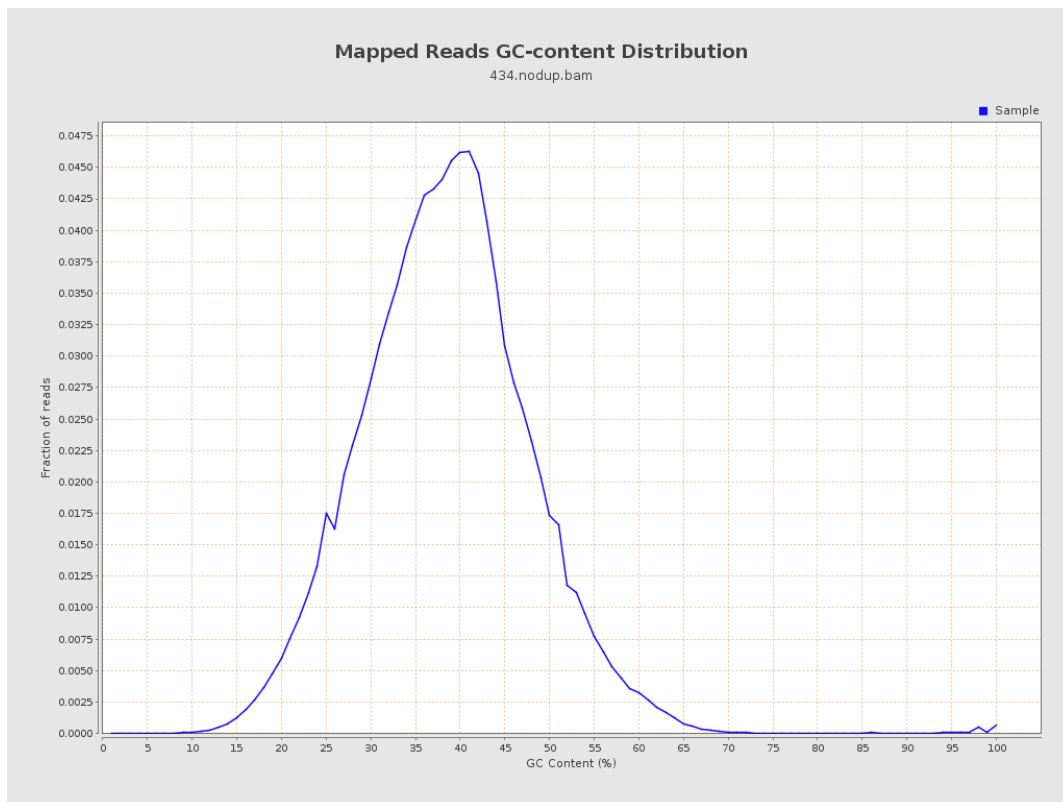
7. Results : Duplication Rate Histogram



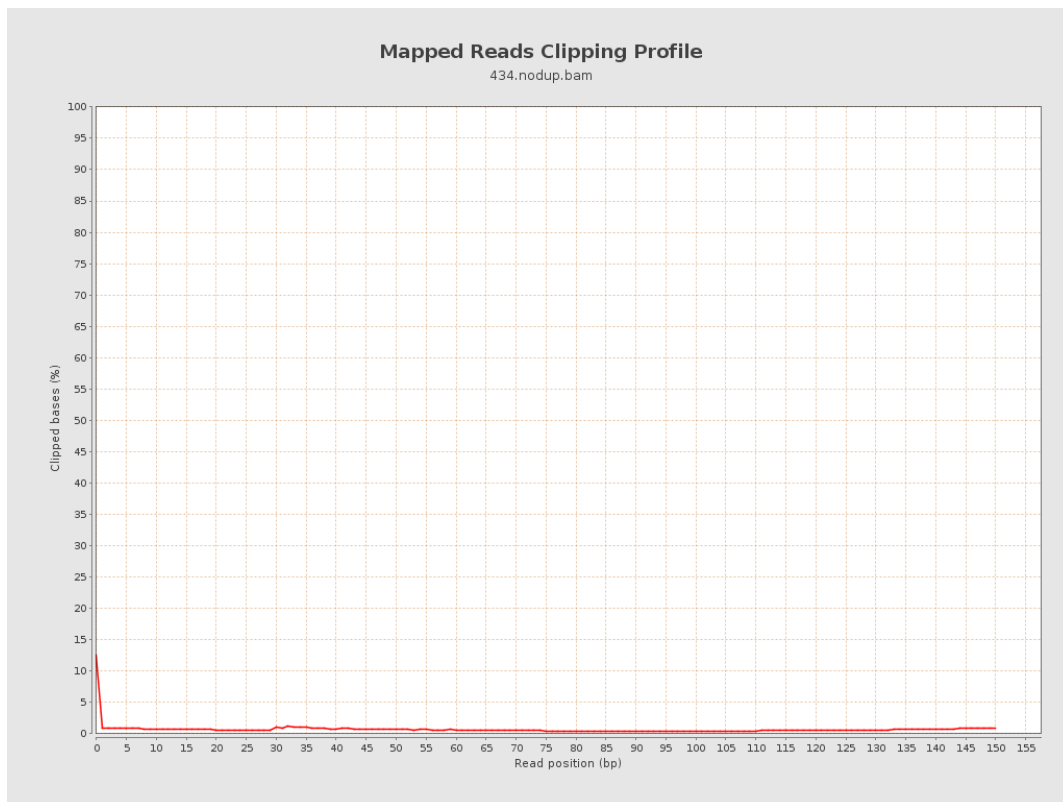
8. Results : Mapped Reads Nucleotide Content



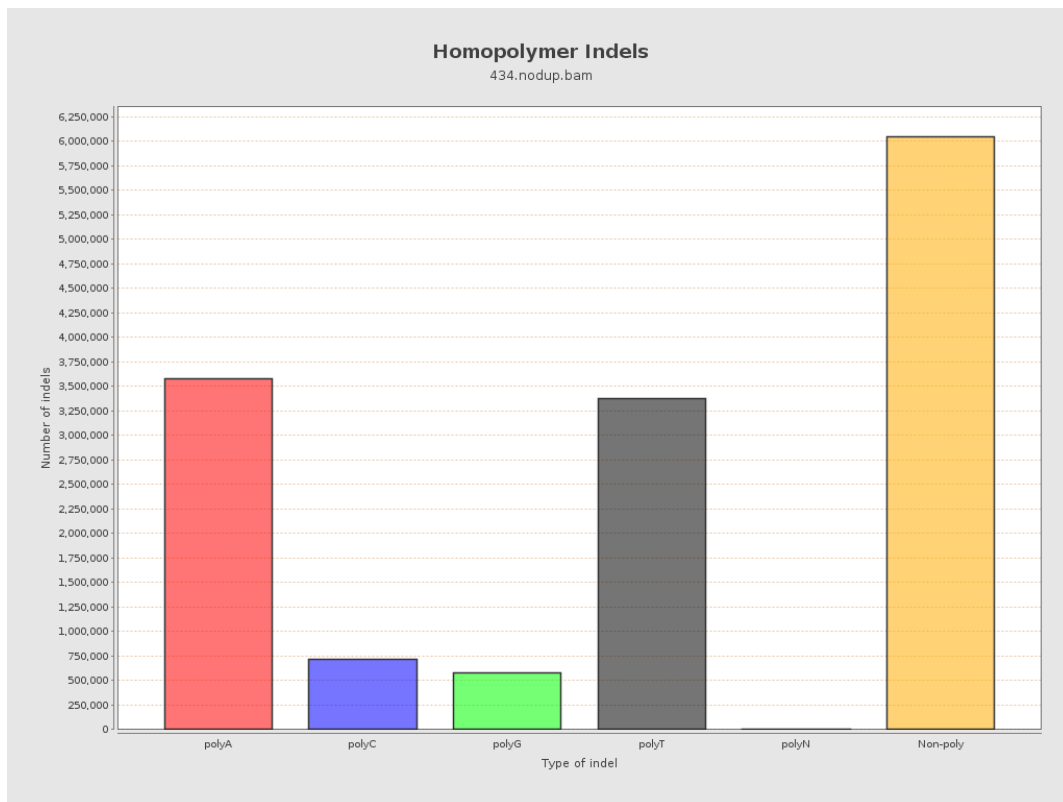
9. Results : Mapped Reads GC-content Distribution



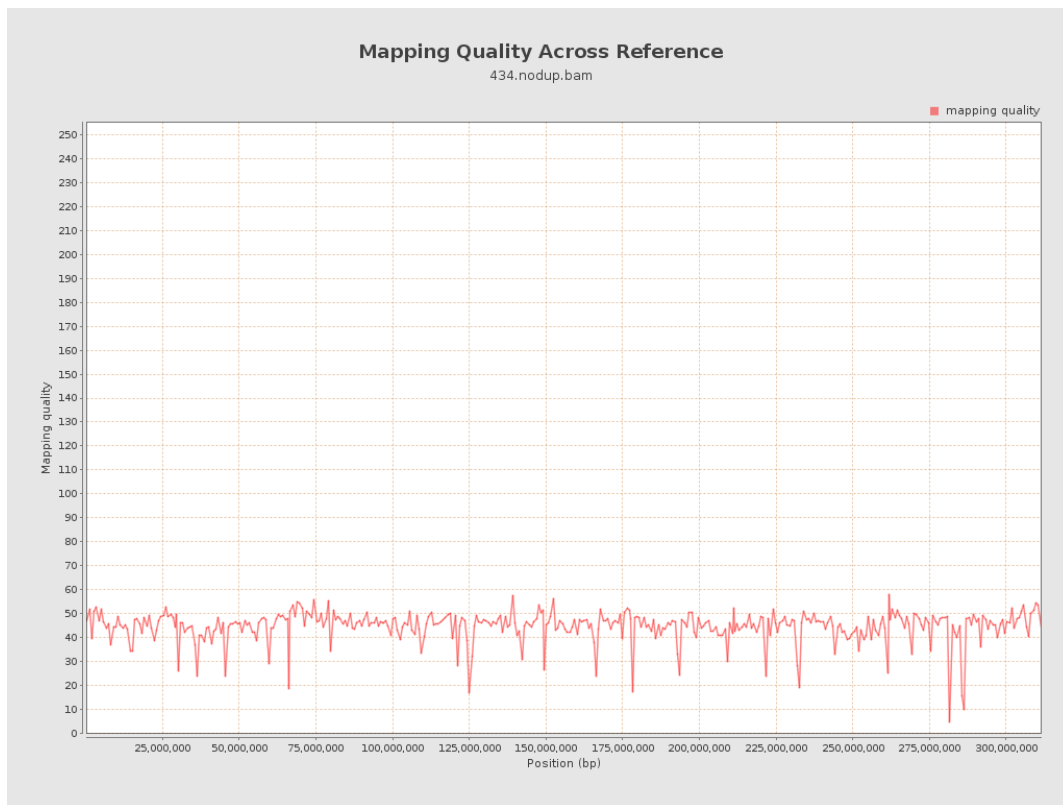
10. Results : Mapped Reads Clipping Profile



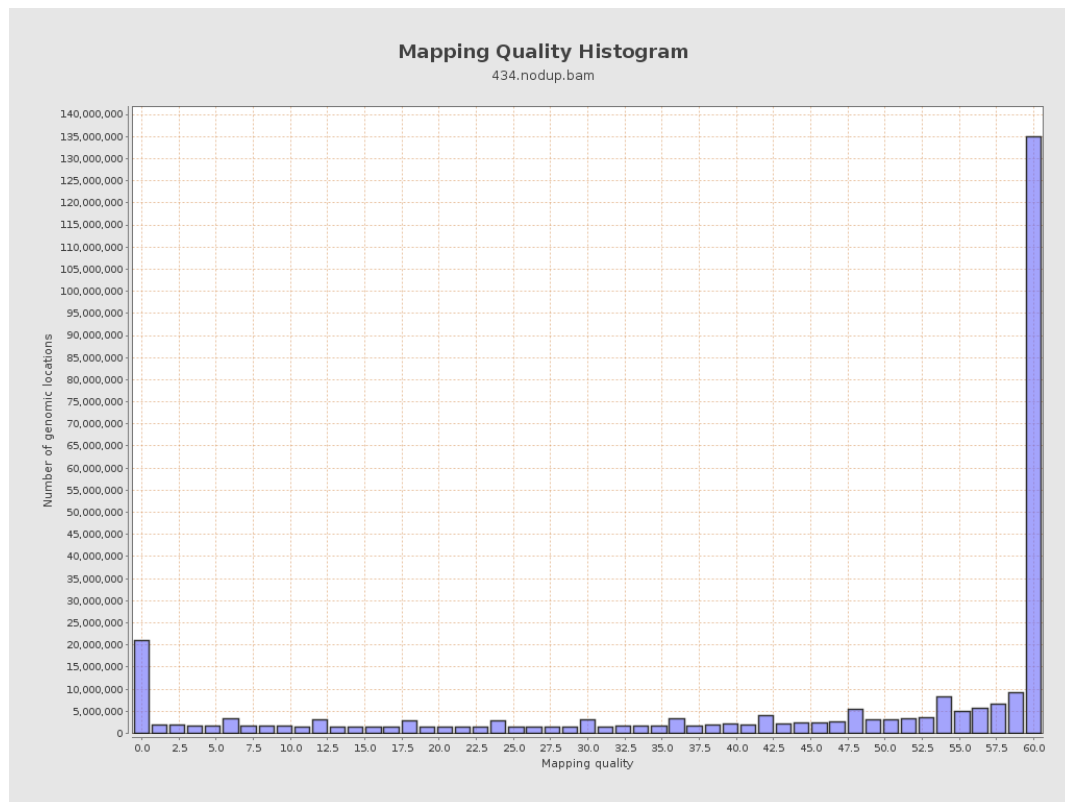
11. Results : Homopolymer Indels



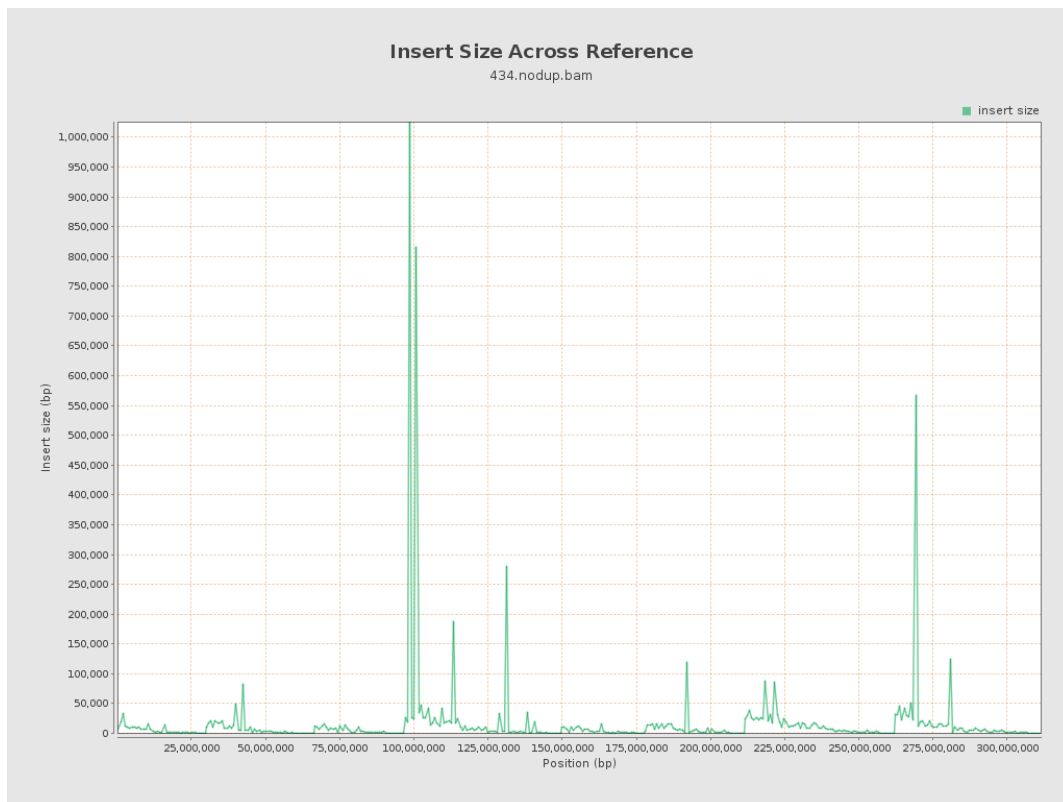
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

