

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:36:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/144
1
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1441 .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\t SM:\$sample /proj/uppstore2018210/Aalpina/data/r eference/GCA_900128785.1_MPIPZ. v5_genomic.fa /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_128/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_128_S218_L002 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_128/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_128_S218_L002 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:36:21 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	79,664,757
Mapped reads	74,054,345 / 92.96%
Unmapped reads	5,610,412 / 7.04%
Mapped paired reads	74,054,345 / 92.96%
Mapped reads, first in pair	37,117,923 / 46.59%
Mapped reads, second in pair	36,936,422 / 46.36%
Mapped reads, both in pair	72,274,234 / 90.72%
Mapped reads, singletons	1,780,111 / 2.23%
Read min/max/mean length	30 / 151 / 148.09
Duplicated reads (flagged)	13,573,844 / 17.04%
Clipped reads	16,796,147 / 21.08%

2.2. ACGT Content

Number/percentage of A's	3,164,776,412 / 30.85%
Number/percentage of C's	1,963,460,684 / 19.14%
Number/percentage of T's	3,171,319,587 / 30.92%
Number/percentage of G's	1,957,801,160 / 19.09%
Number/percentage of N's	42,357 / 0%
GC Percentage	38.23%

2.3. Coverage

Mean	33.0024
Standard Deviation	257.1491

2.4. Mapping Quality

Mean Mapping Quality	43.76
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2.5. Insert size

Mean	256,073.43
Standard Deviation	2,419,593.27
P25/Median/P75	349 / 453 / 591

2.6. Mismatches and indels

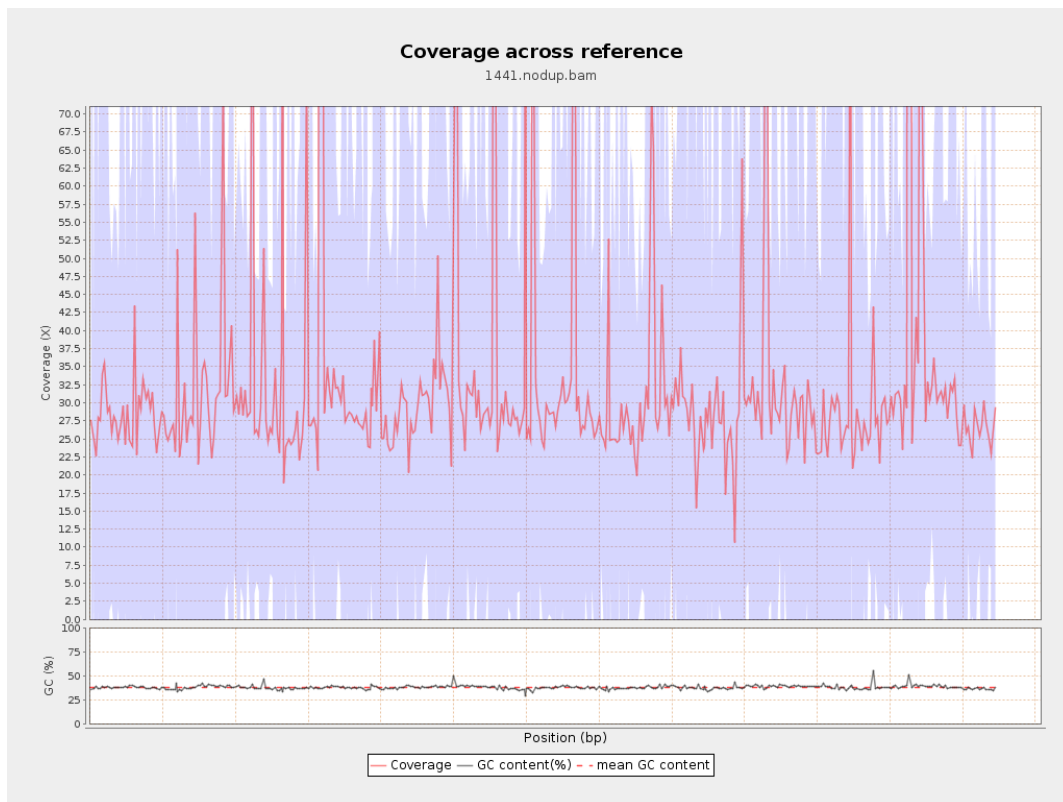
General error rate	2.4%
Mismatches	225,859,683
Insertions	7,196,107
Mapped reads with at least one insertion	8.71%
Deletions	7,281,819
Mapped reads with at least one deletion	8.69%
Homopolymer indels	56.21%

2.7. Chromosome stats

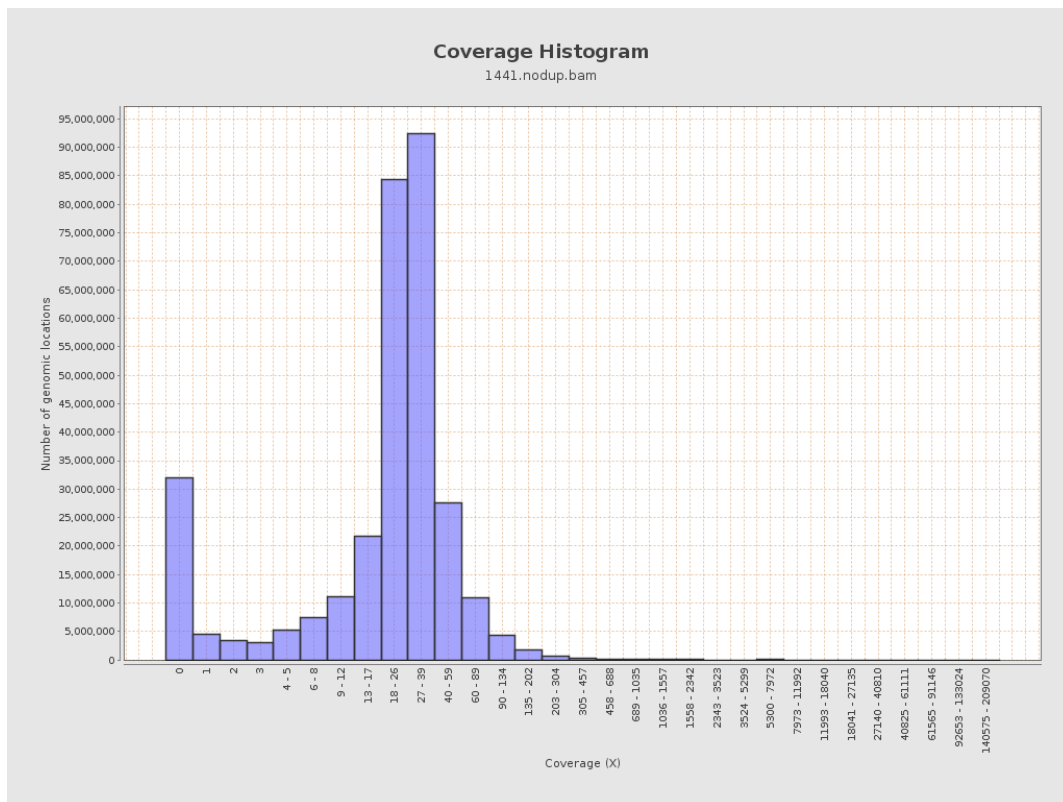
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	834156479	28.0631	99.3298

LT669789.1	36598175	1225707306	33.4909	280.0204
LT669790.1	30422129	1106423036	36.369	278.4196
LT669791.1	52758100	1715661952	32.5194	262.3956
LT669792.1	28376109	943557383	33.2518	301.9701
LT669793.1	33388210	1007356854	30.171	129.8326
LT669794.1	50579949	1581548536	31.2683	241.4823
LT669795.1	49795044	1870521909	37.5644	327.8261

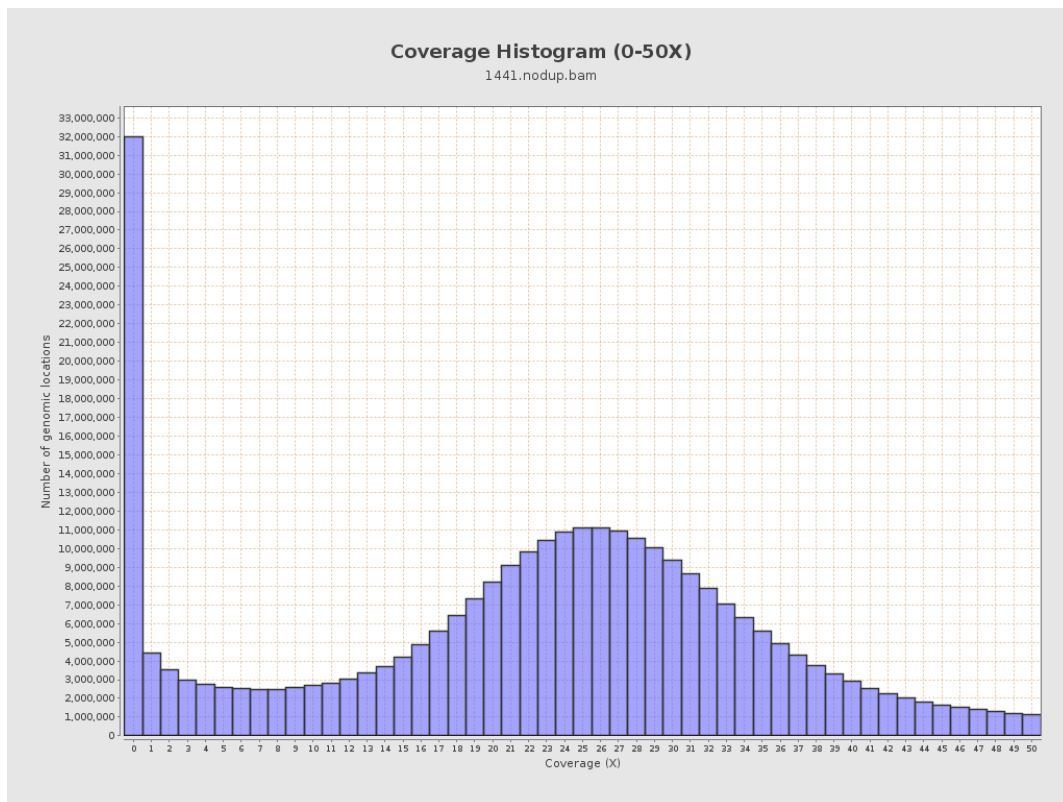
3. Results : Coverage across reference



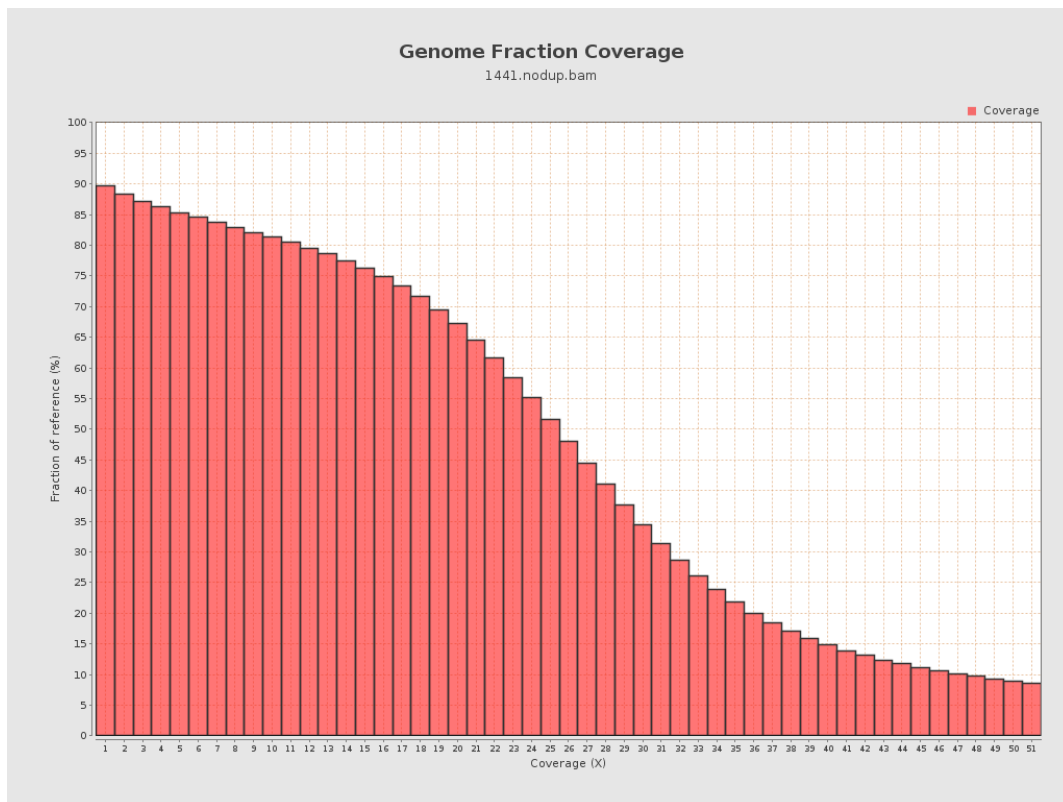
4. Results : Coverage Histogram



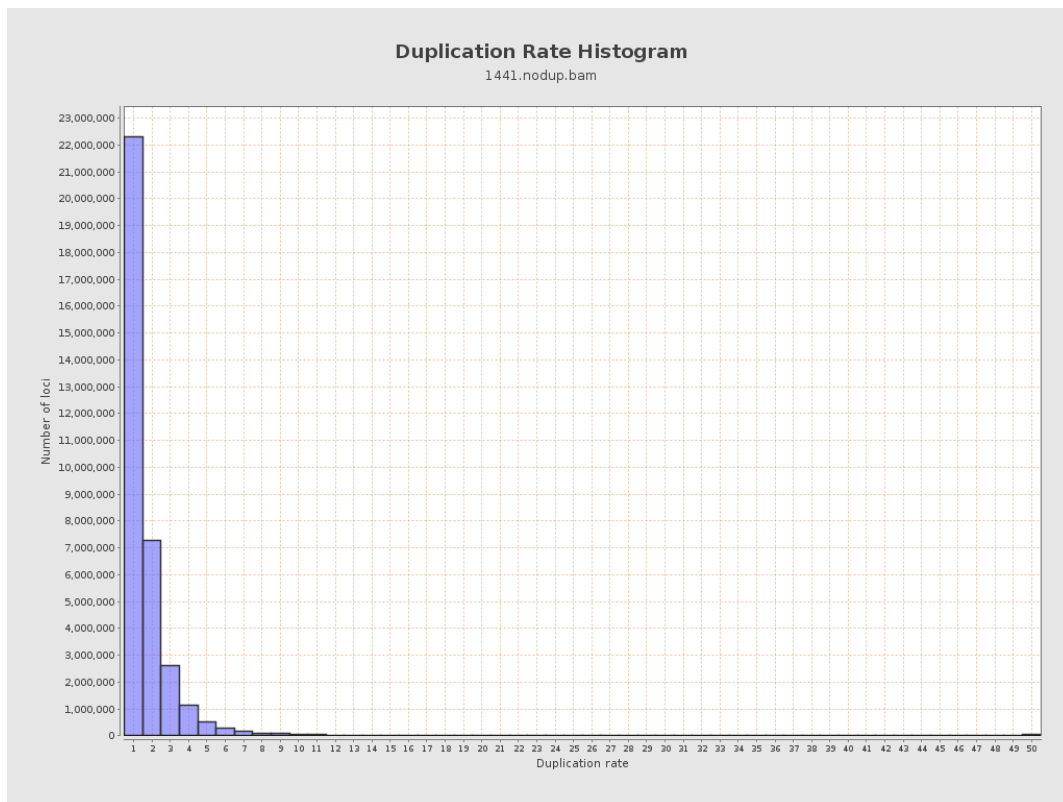
5. Results : Coverage Histogram (0-50X)



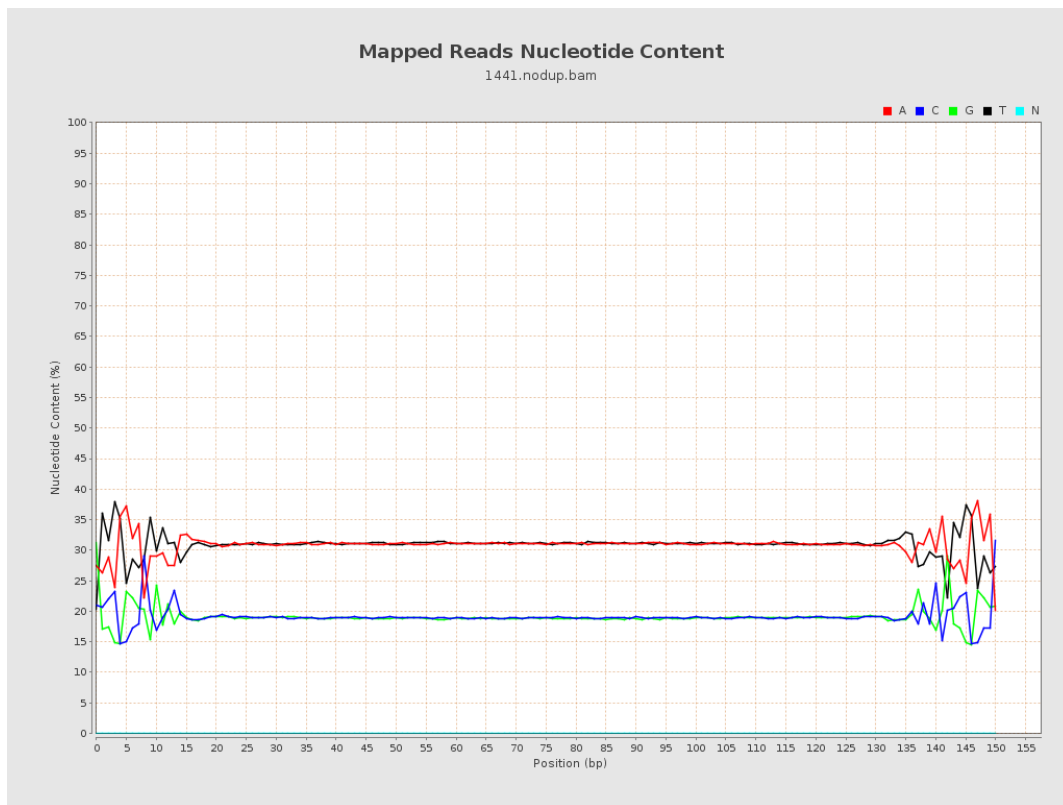
6. Results : Genome Fraction Coverage



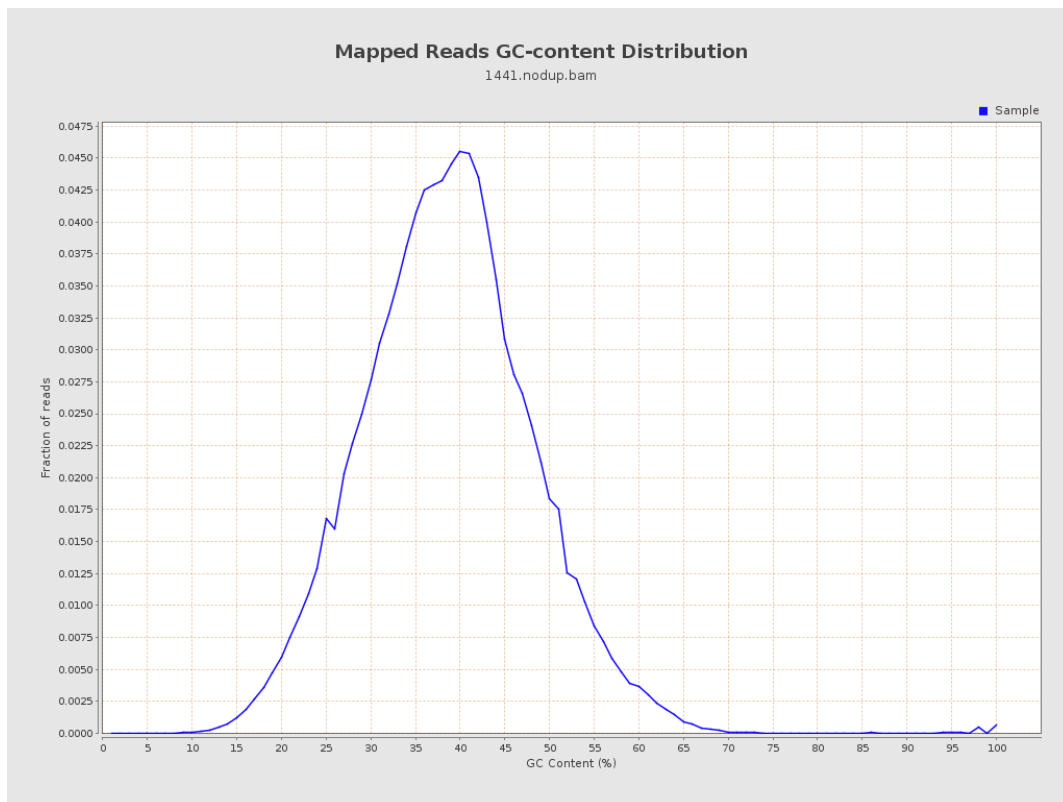
7. Results : Duplication Rate Histogram



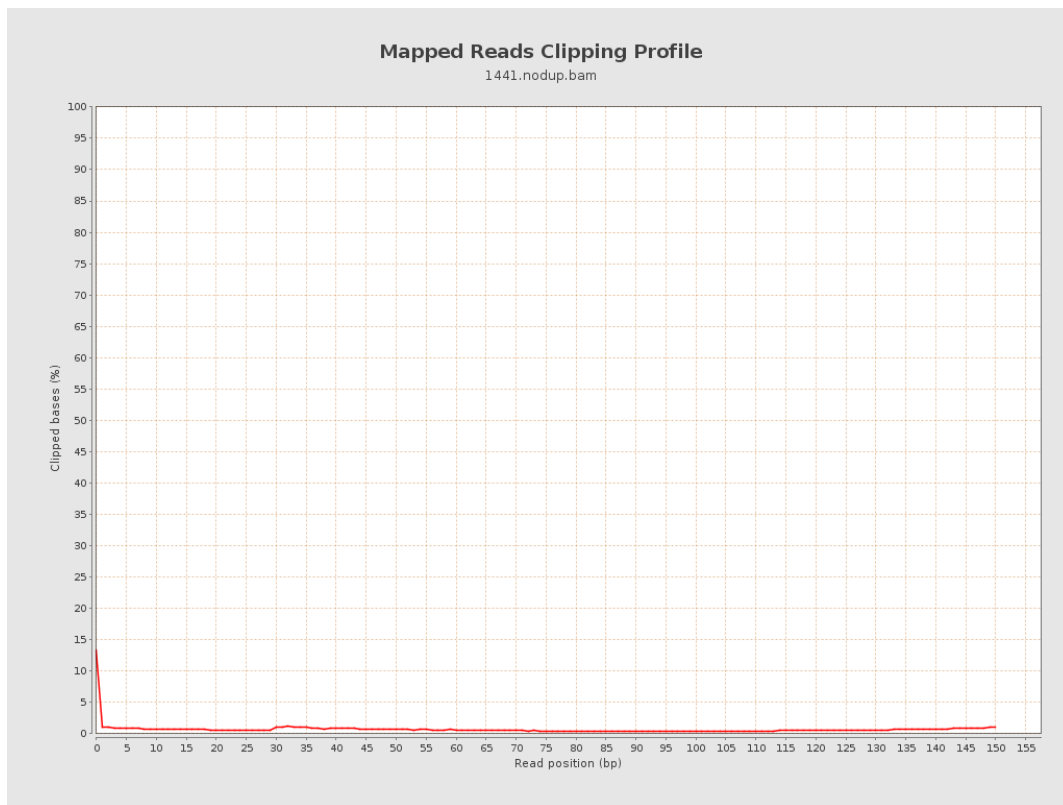
8. Results : Mapped Reads Nucleotide Content



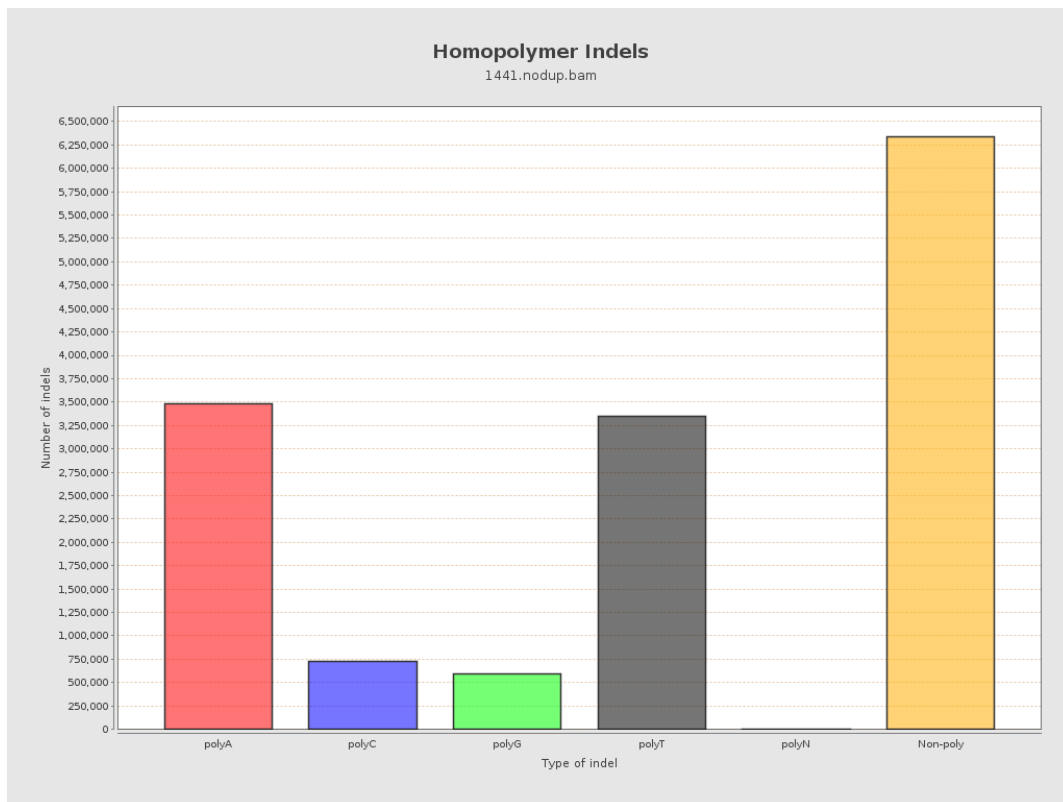
9. Results : Mapped Reads GC-content Distribution



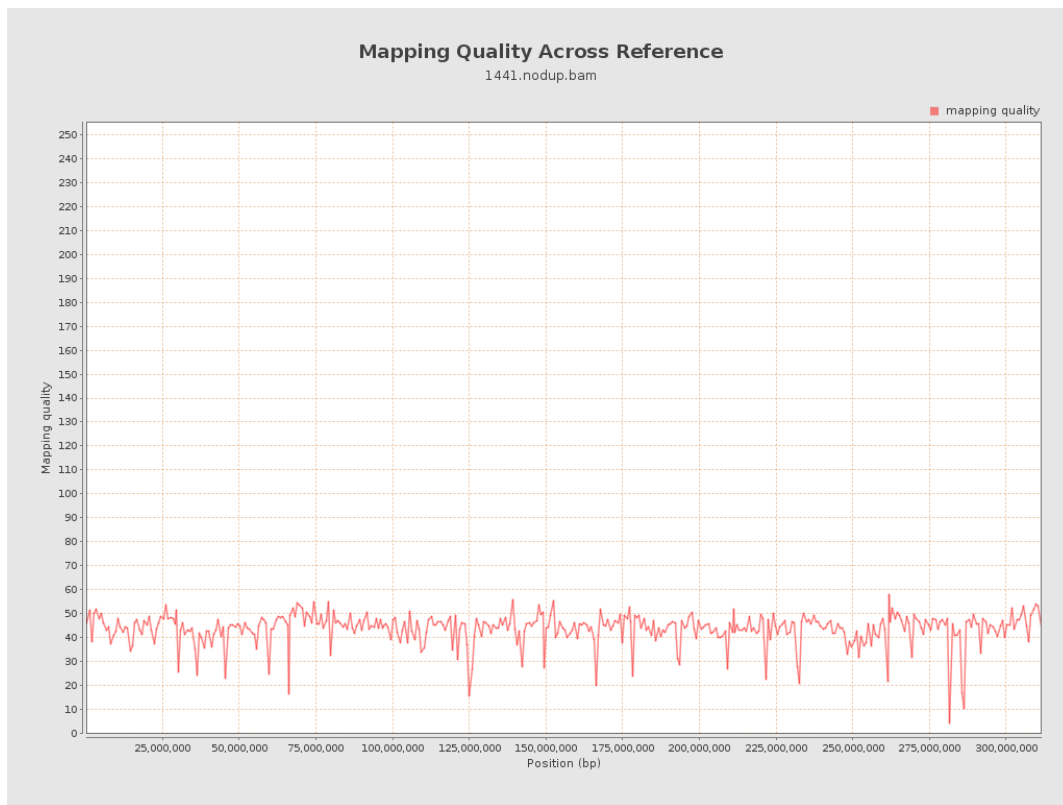
10. Results : Mapped Reads Clipping Profile



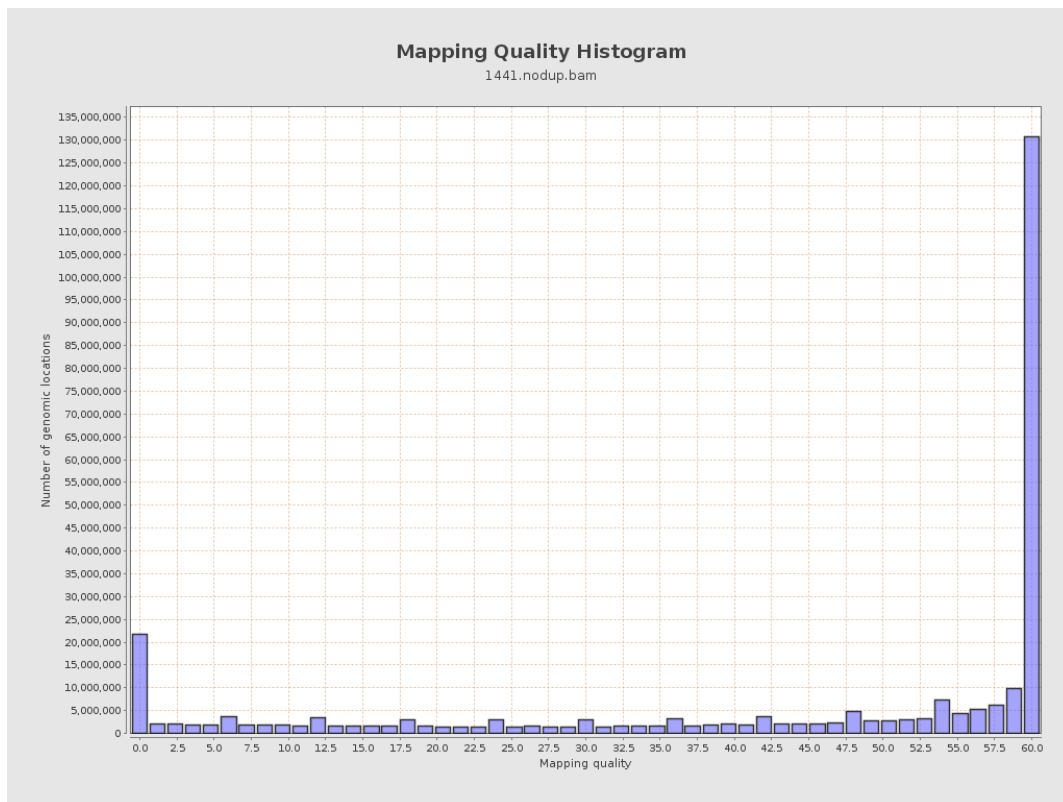
11. Results : Homopolymer Indels



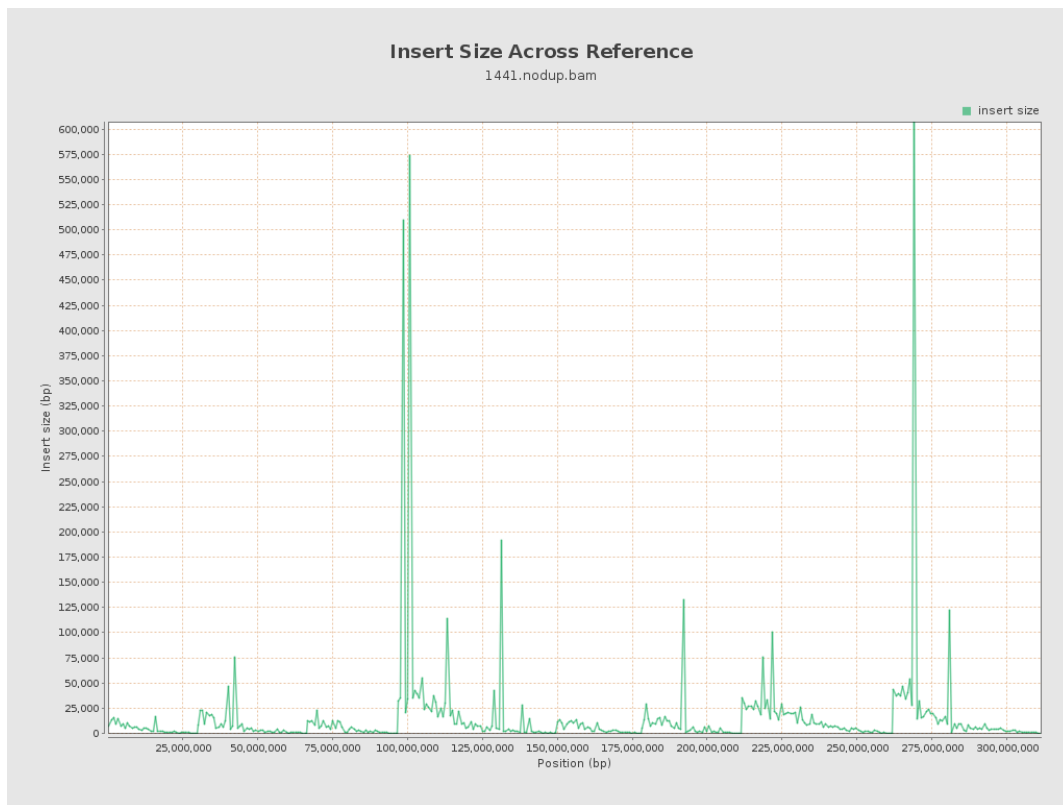
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

