

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:32:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/100
7
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1007 .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_445/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_445_S420_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_445/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_445_S420_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:32:02 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	66,712,491
Mapped reads	63,024,182 / 94.47%
Unmapped reads	3,688,309 / 5.53%
Mapped paired reads	63,024,182 / 94.47%
Mapped reads, first in pair	31,592,438 / 47.36%
Mapped reads, second in pair	31,431,744 / 47.12%
Mapped reads, both in pair	61,723,596 / 92.52%
Mapped reads, singletons	1,300,586 / 1.95%
Read min/max/mean length	30 / 151 / 148.16
Duplicated reads (flagged)	9,205,346 / 13.8%
Clipped reads	13,742,575 / 20.6%

2.2. ACGT Content

Number/percentage of A's	2,703,577,534 / 30.86%
Number/percentage of C's	1,679,471,198 / 19.17%
Number/percentage of T's	2,703,320,647 / 30.86%
Number/percentage of G's	1,674,840,443 / 19.12%
Number/percentage of N's	30,285 / 0%
GC Percentage	38.29%

2.3. Coverage

Mean	28.1823
Standard Deviation	228.8737

2.4. Mapping Quality

Mean Mapping Quality	44.69
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2.5. Insert size

Mean	230,803.02
Standard Deviation	2,277,801.82
P25/Median/P75	365 / 484 / 641

2.6. Mismatches and indels

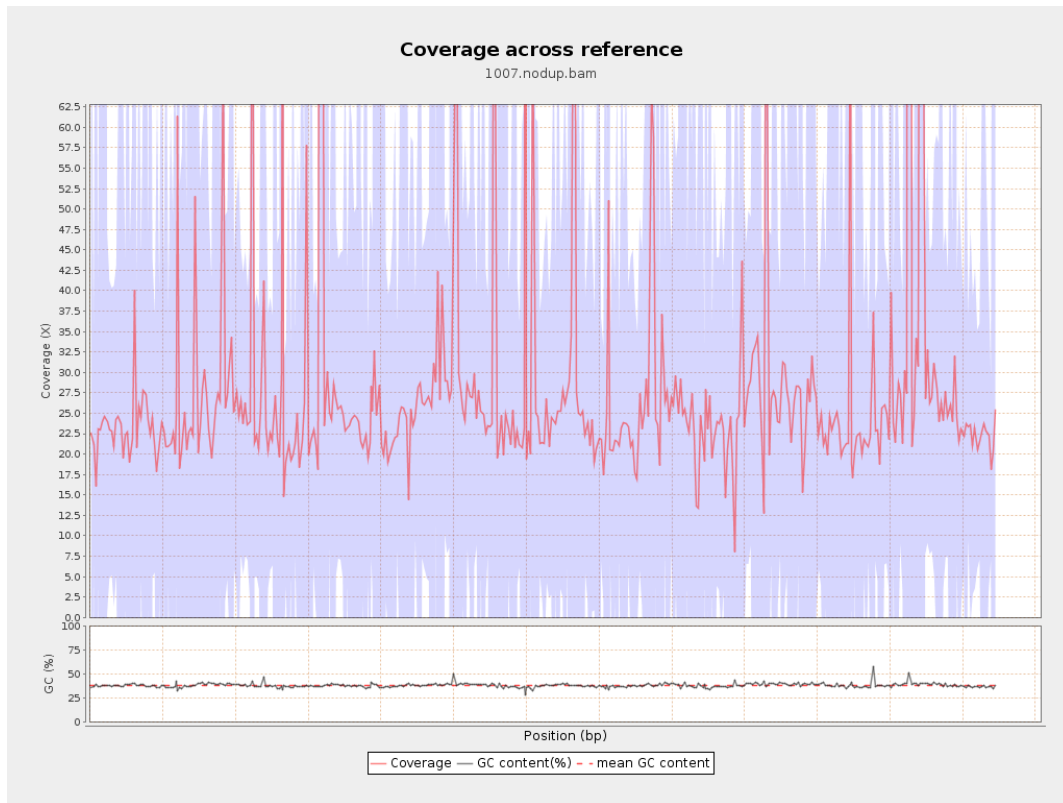
General error rate	2.25%
Mismatches	181,610,007
Insertions	5,682,590
Mapped reads with at least one insertion	8.13%
Deletions	5,785,602
Mapped reads with at least one deletion	8.18%
Homopolymer indels	56.62%

2.7. Chromosome stats

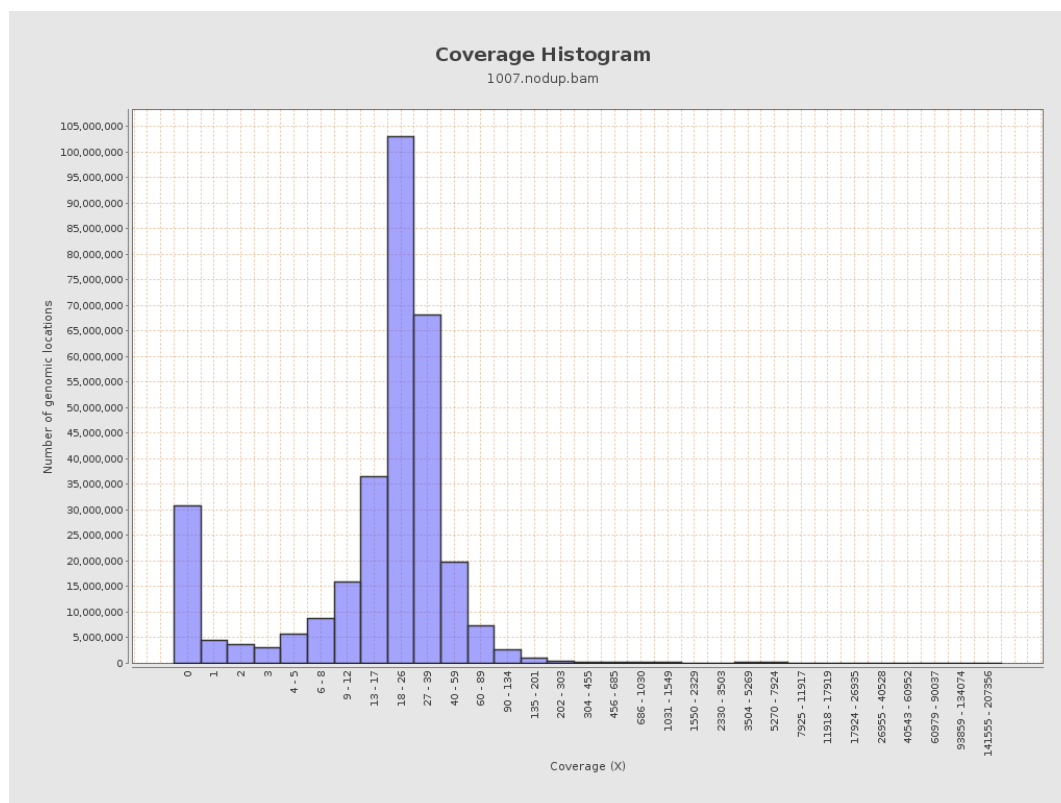
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	683713408	23.0018	65.7628

LT669789.1	36598175	1048648331	28.653	232.7931
LT669790.1	30422129	901735513	29.6408	223.1734
LT669791.1	52758100	1454828910	27.5755	183.7154
LT669792.1	28376109	788534864	27.7887	236.9123
LT669793.1	33388210	860597649	25.7755	112.5386
LT669794.1	50579949	1349176798	26.6741	208.3501
LT669795.1	49795044	1695546506	34.0505	366.8926

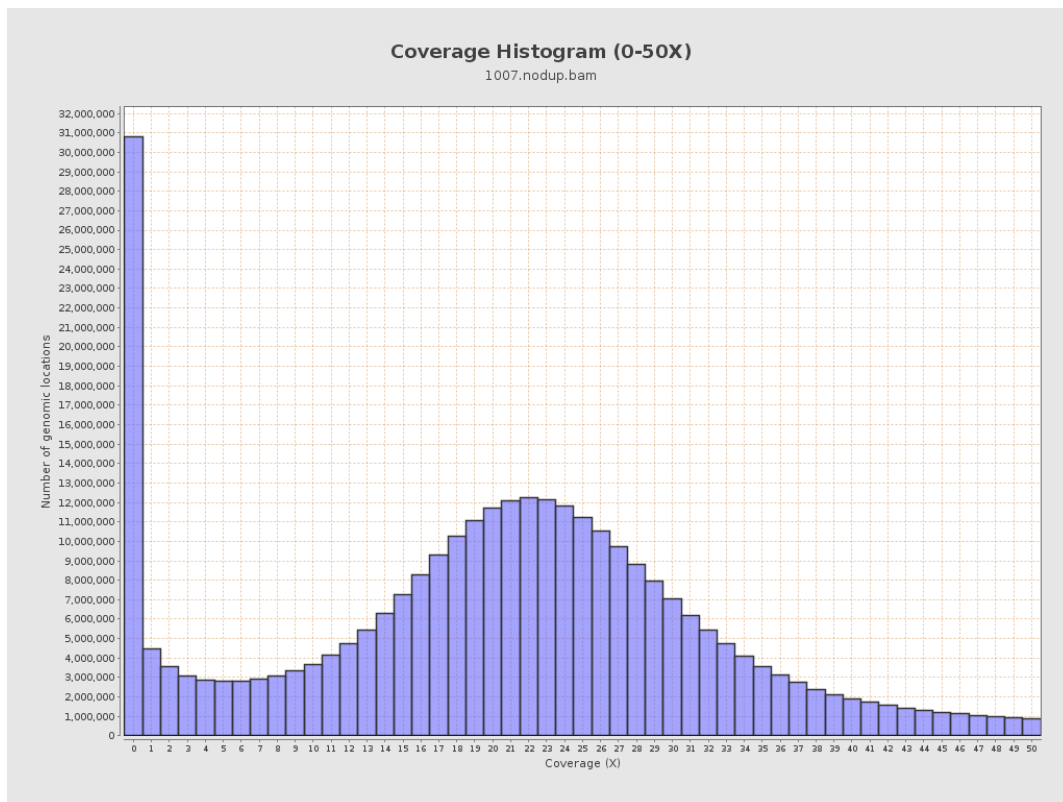
3. Results : Coverage across reference



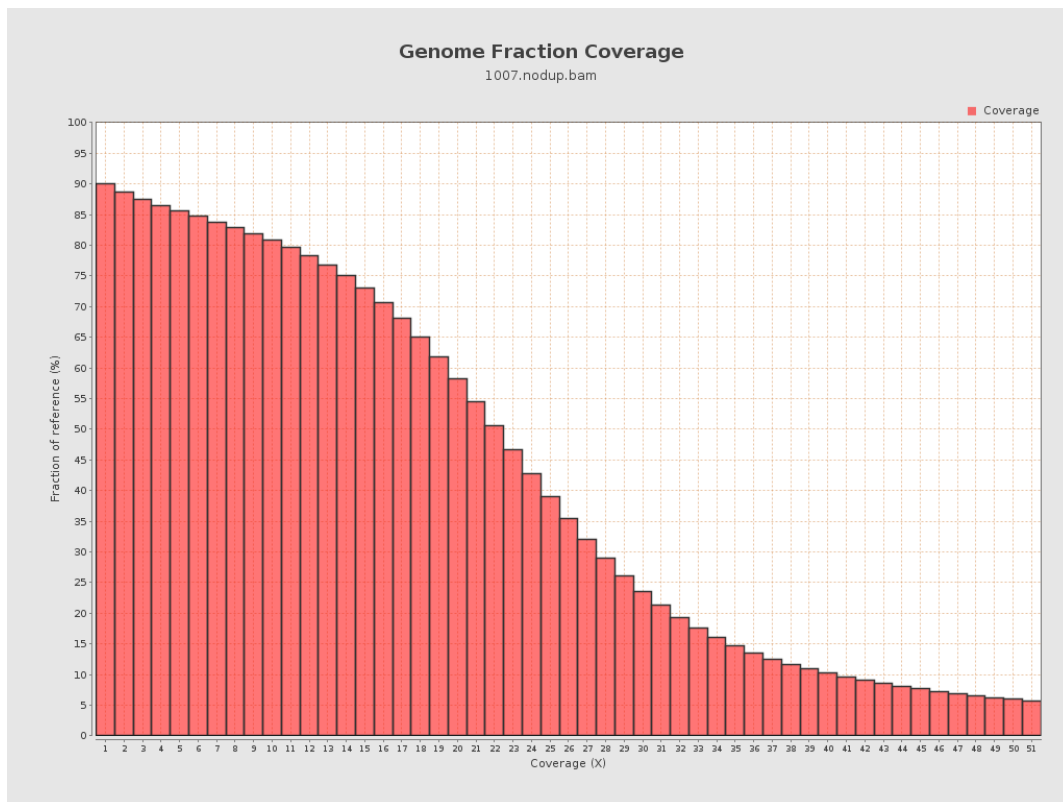
4. Results : Coverage Histogram



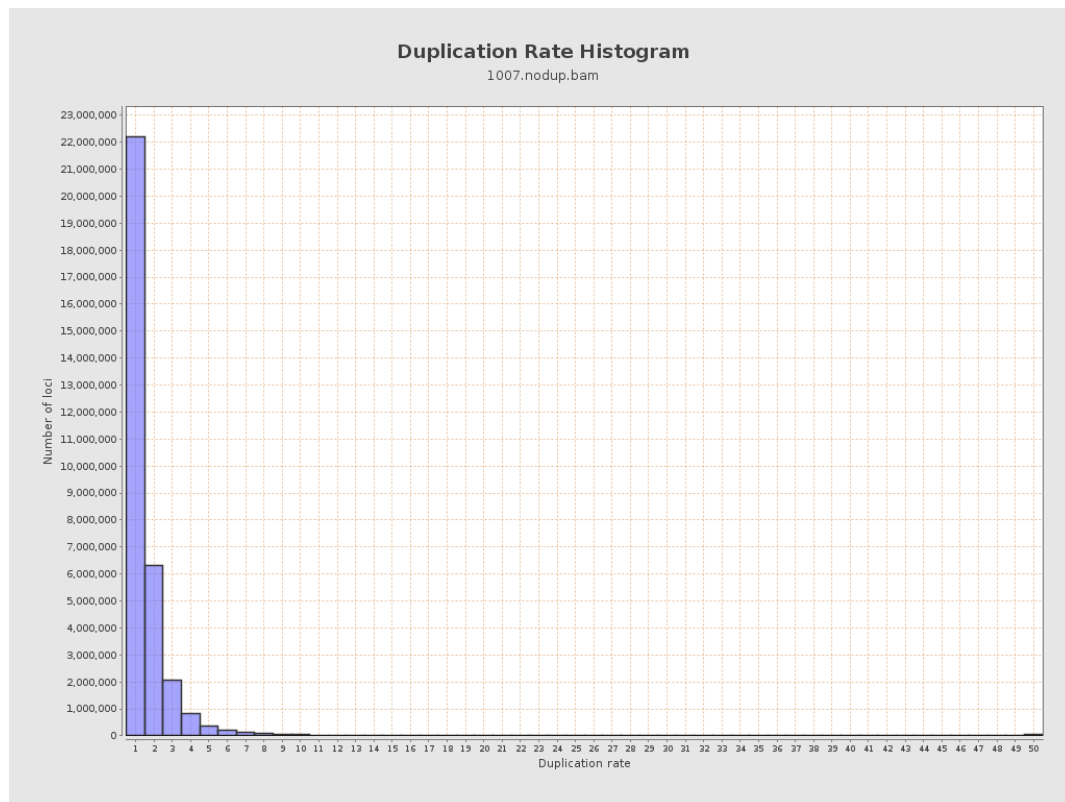
5. Results : Coverage Histogram (0-50X)



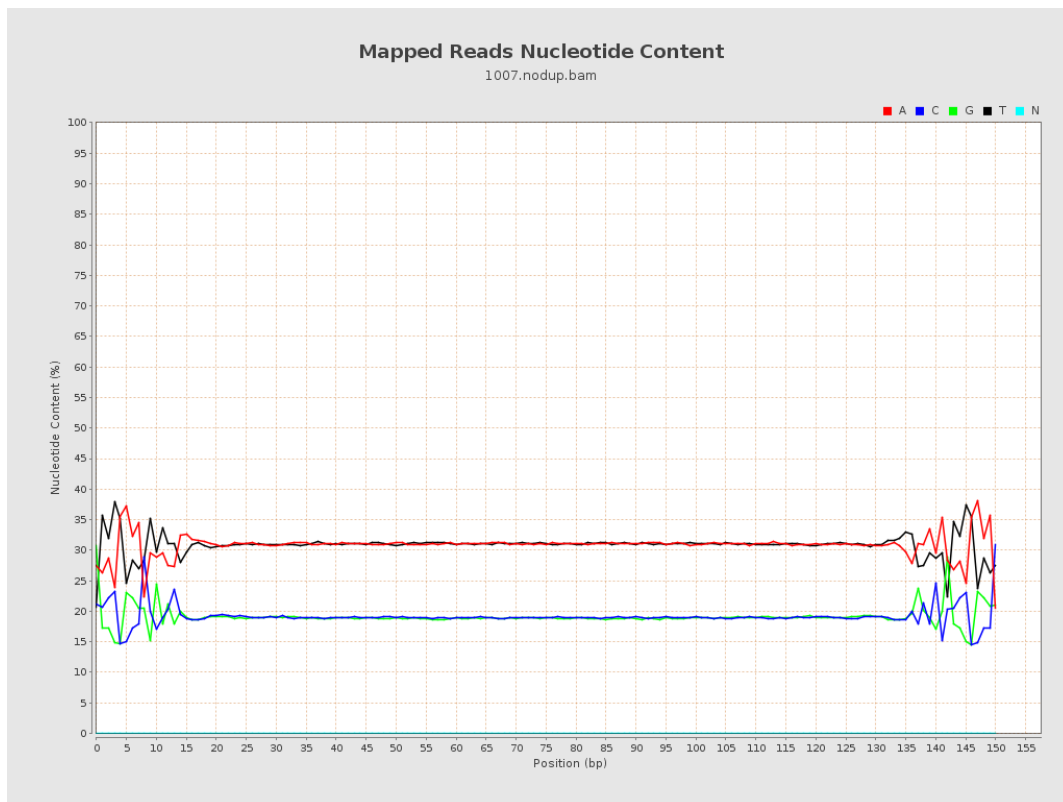
6. Results : Genome Fraction Coverage



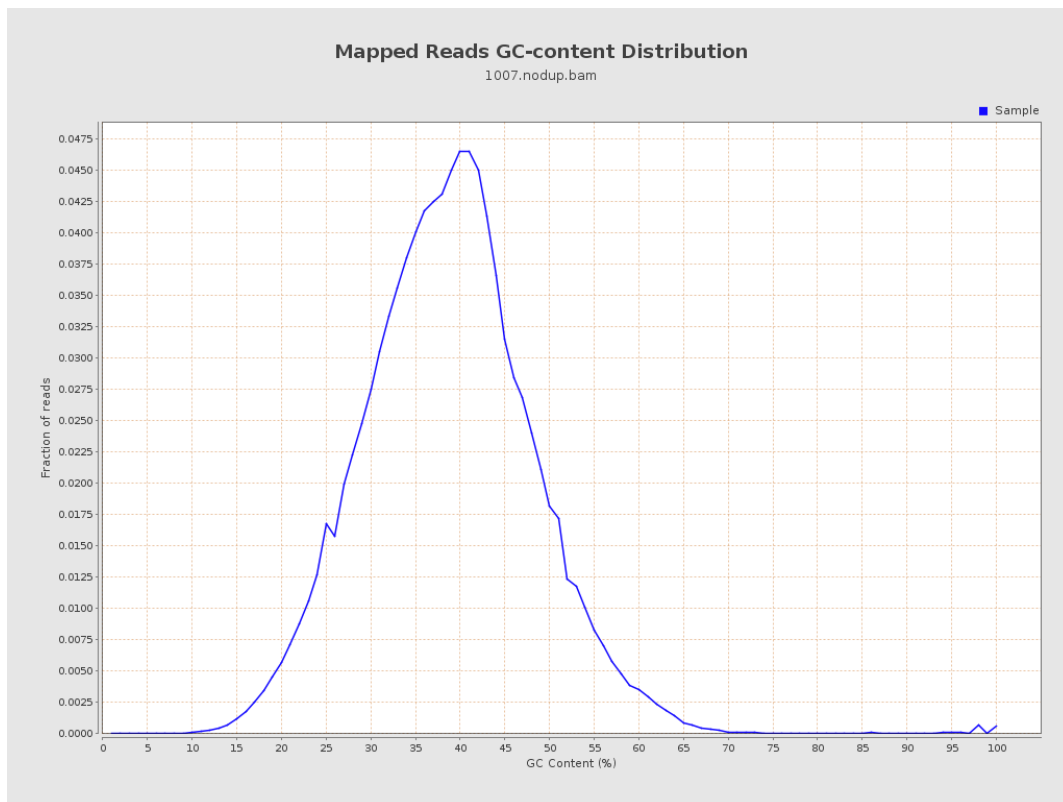
7. Results : Duplication Rate Histogram



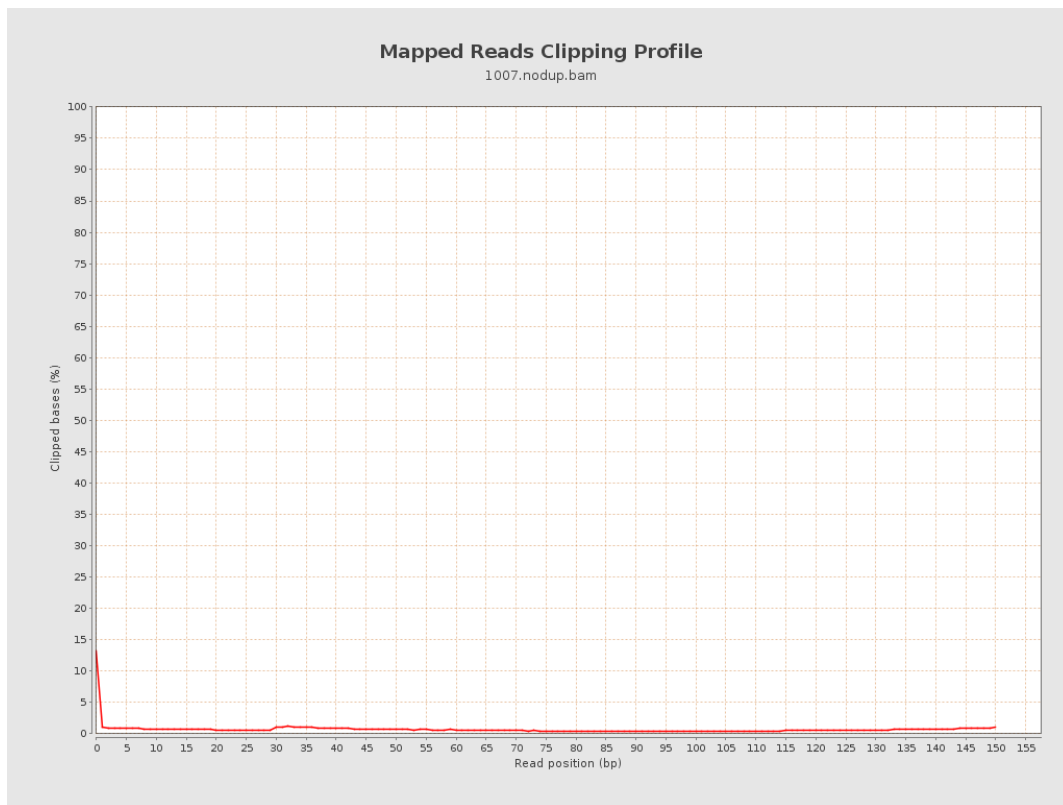
8. Results : Mapped Reads Nucleotide Content



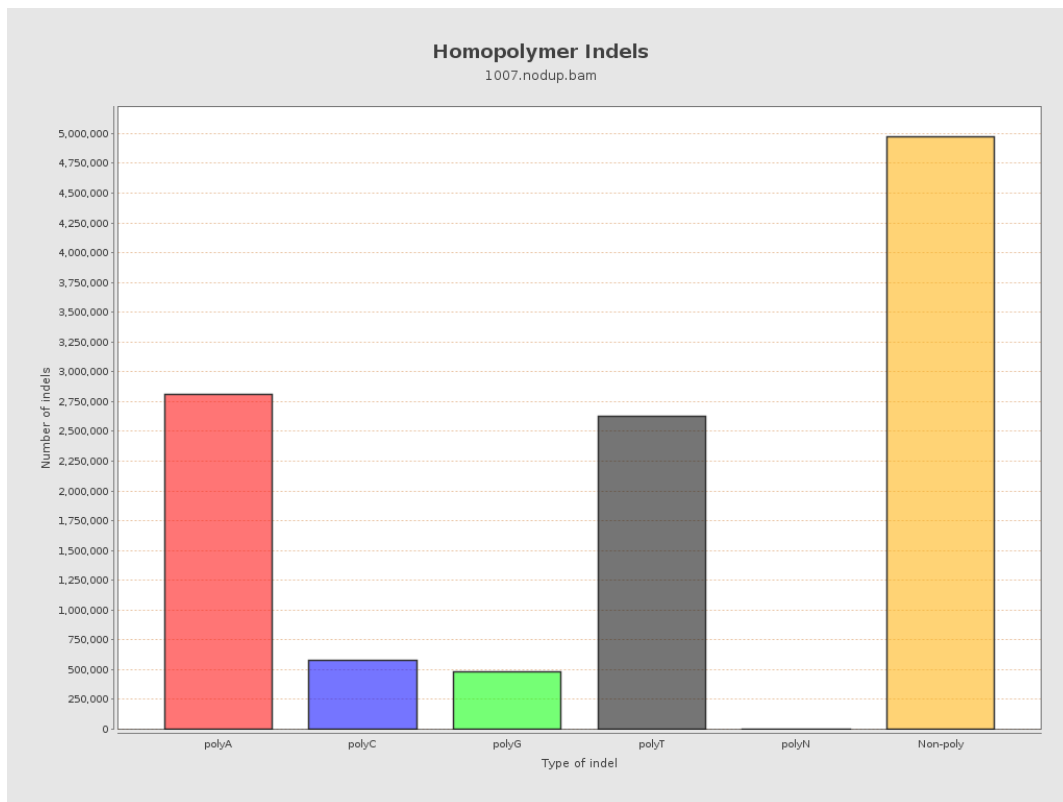
9. Results : Mapped Reads GC-content Distribution



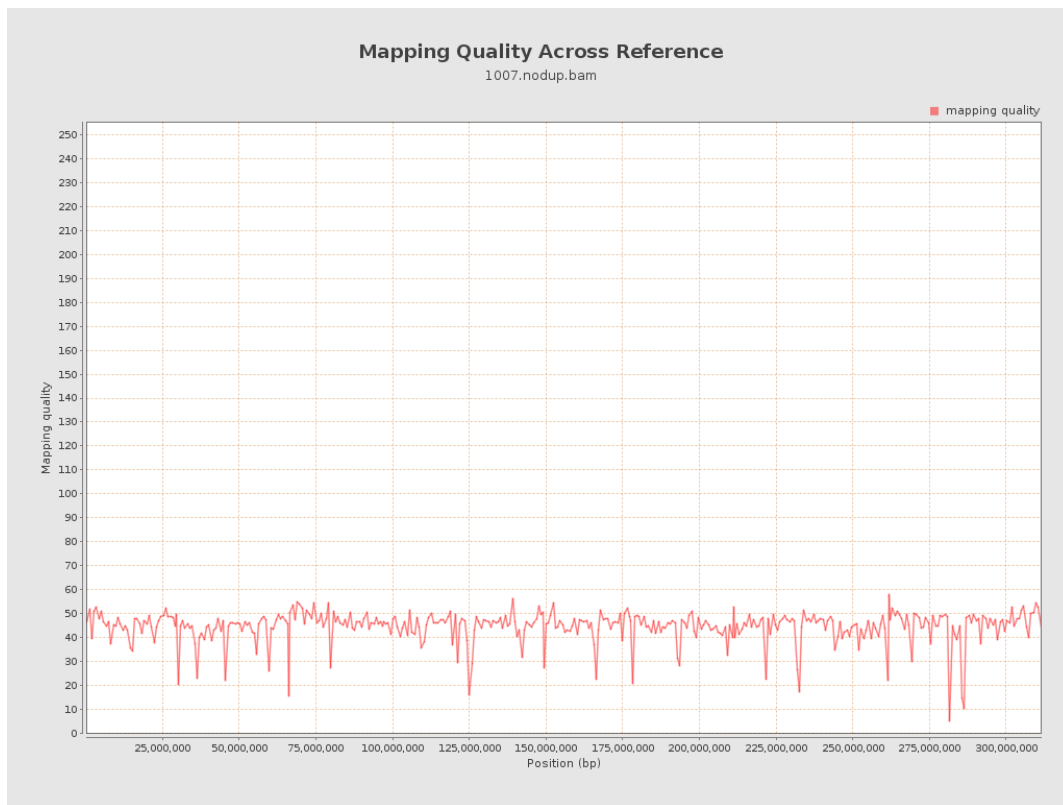
10. Results : Mapped Reads Clipping Profile



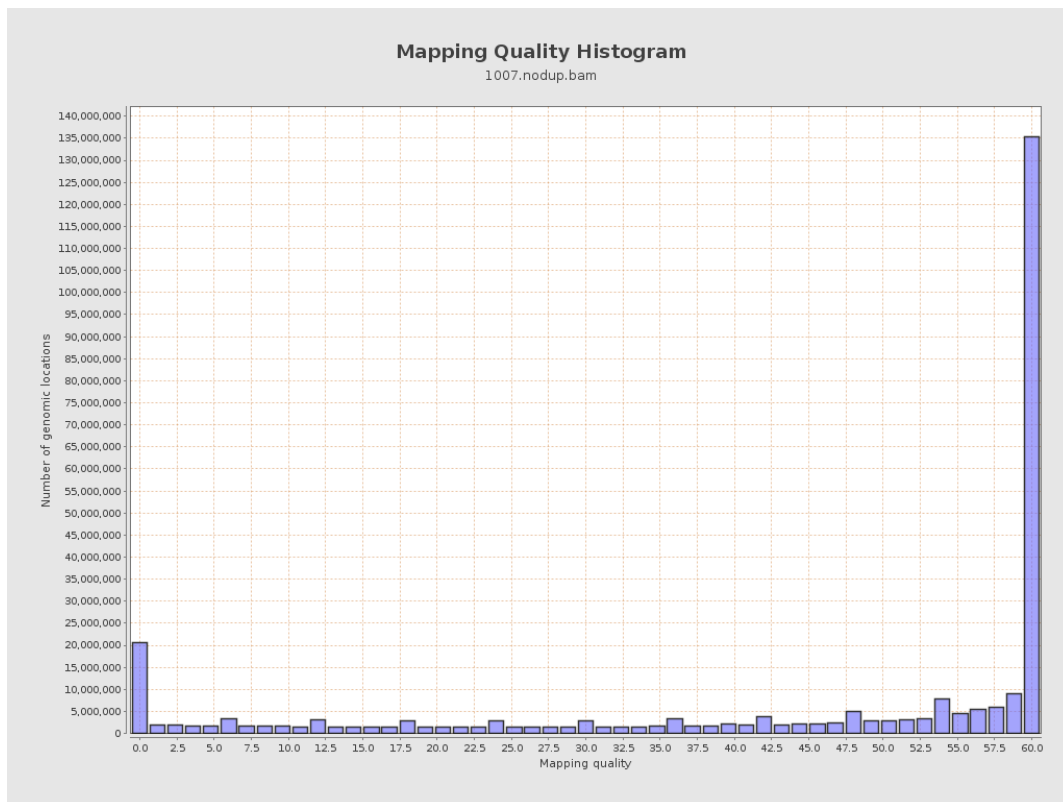
11. Results : Homopolymer Indels



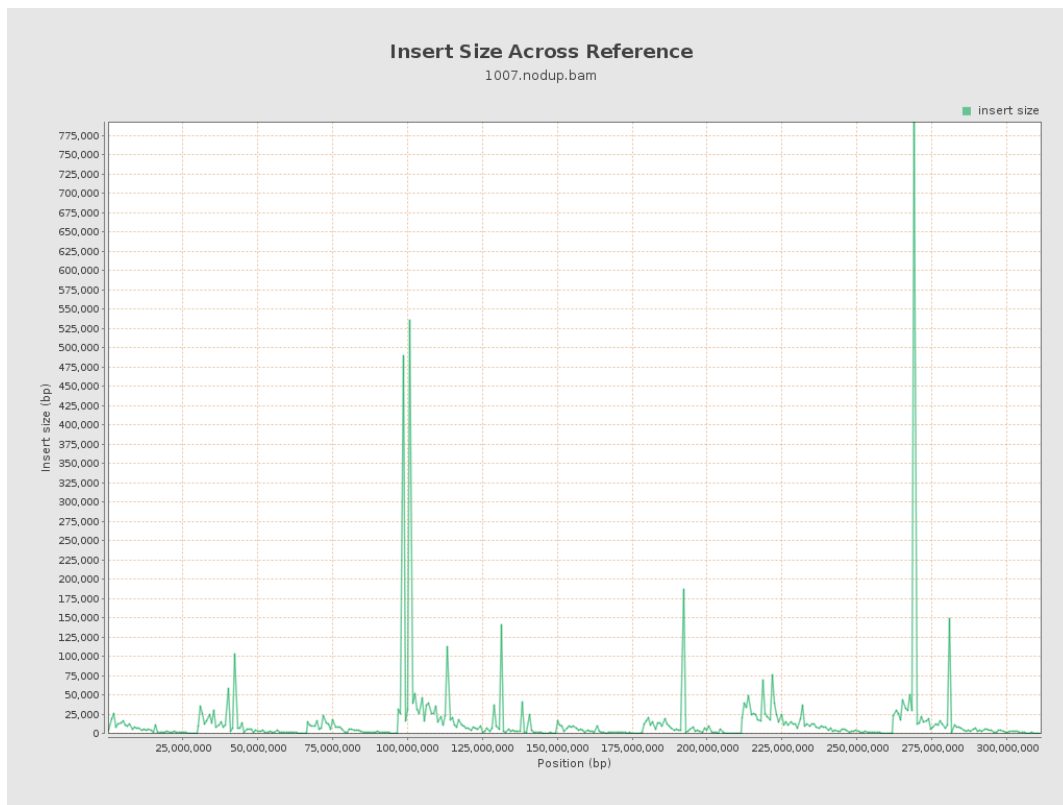
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

