

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:32:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/135
9
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1359 .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_176/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_176_S266_L002 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_176/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_176_S266_L002 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:32:15 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	70,275,773
Mapped reads	64,676,265 / 92.03%
Unmapped reads	5,599,508 / 7.97%
Mapped paired reads	64,676,265 / 92.03%
Mapped reads, first in pair	32,357,964 / 46.04%
Mapped reads, second in pair	32,318,301 / 45.99%
Mapped reads, both in pair	62,843,309 / 89.42%
Mapped reads, singletons	1,832,956 / 2.61%
Read min/max/mean length	30 / 151 / 148.08
Duplicated reads (flagged)	11,588,319 / 16.49%
Clipped reads	15,159,158 / 21.57%

2.2. ACGT Content

Number/percentage of A's	2,754,185,304 / 30.94%
Number/percentage of C's	1,695,748,982 / 19.05%
Number/percentage of T's	2,759,047,572 / 30.99%
Number/percentage of G's	1,693,278,081 / 19.02%
Number/percentage of N's	36,557 / 0%
GC Percentage	38.07%

2.3. Coverage

Mean	28.6426
Standard Deviation	252.8031

2.4. Mapping Quality

Mean Mapping Quality	43.99
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2.5. Insert size

Mean	260,787.33
Standard Deviation	2,454,433.51
P25/Median/P75	329 / 432 / 570

2.6. Mismatches and indels

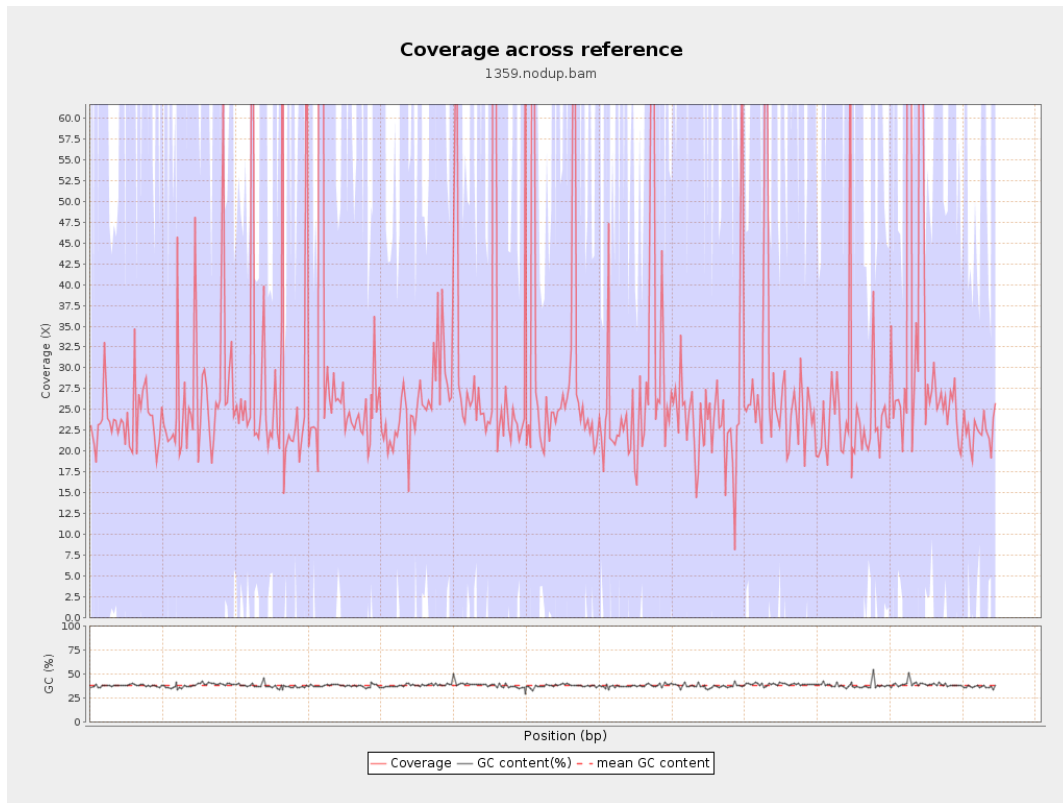
General error rate	2.41%
Mismatches	196,317,150
Insertions	6,453,241
Mapped reads with at least one insertion	8.9%
Deletions	6,326,722
Mapped reads with at least one deletion	8.66%
Homopolymer indels	56.94%

2.7. Chromosome stats

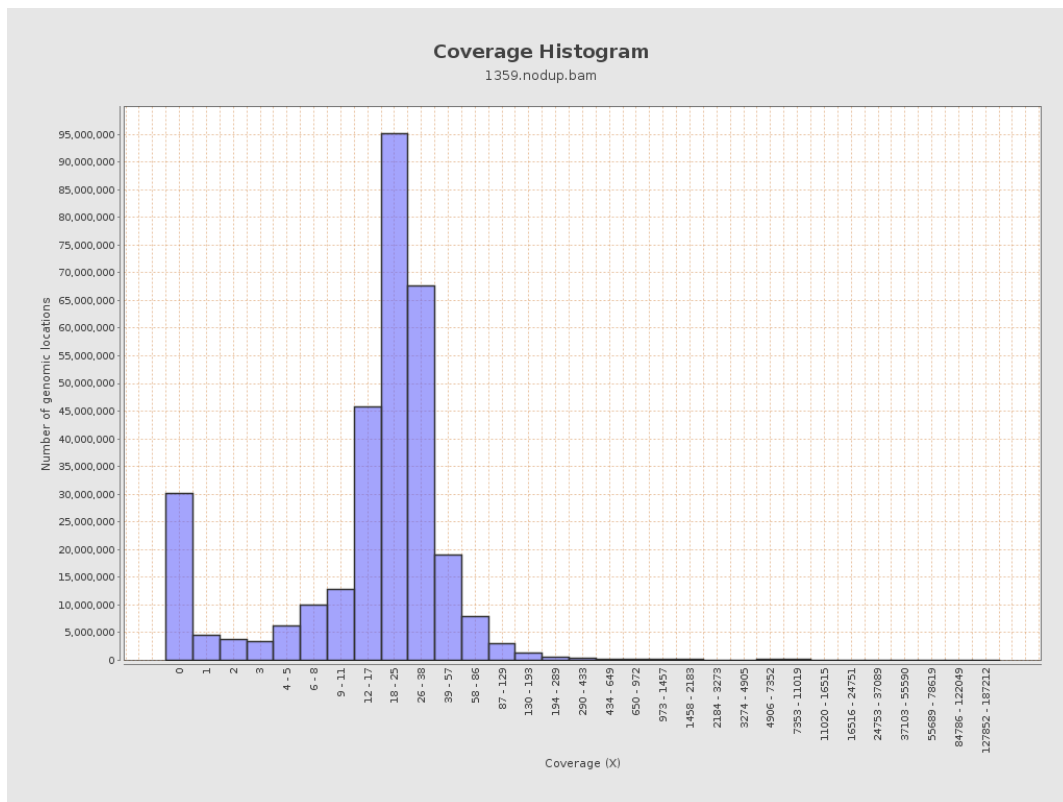
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	698177422	23.4884	94.0392

LT669789.1	36598175	1051659557	28.7353	261.7469
LT669790.1	30422129	1031127198	33.894	341.5591
LT669791.1	52758100	1486968784	28.1847	254.7516
LT669792.1	28376109	811410401	28.5948	252.848
LT669793.1	33388210	895038016	26.807	222.6488
LT669794.1	50579949	1350569222	26.7017	206.8532
LT669795.1	49795044	1601297670	32.1578	301.867

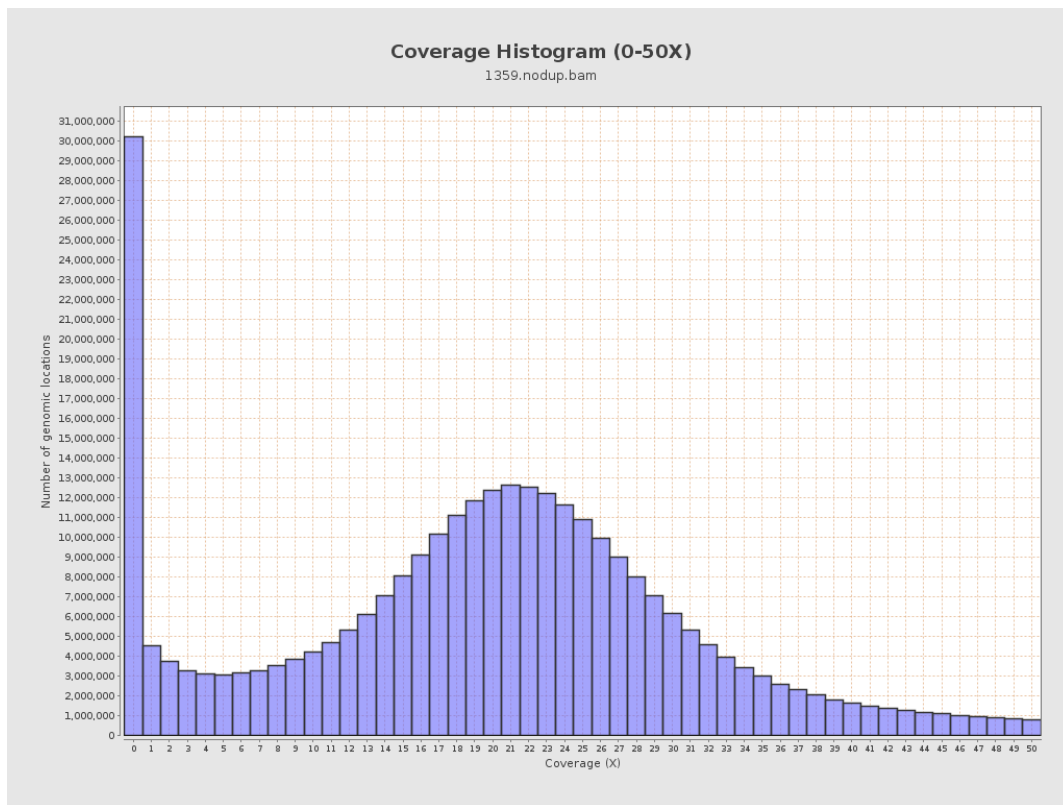
3. Results : Coverage across reference



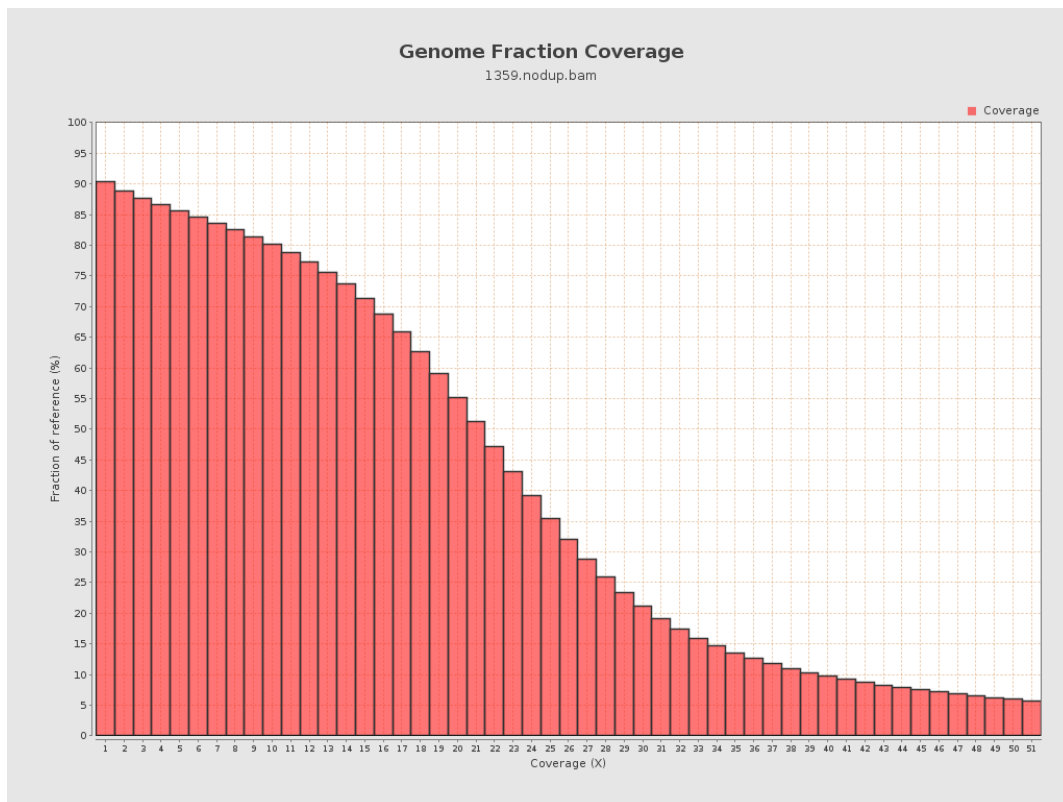
4. Results : Coverage Histogram



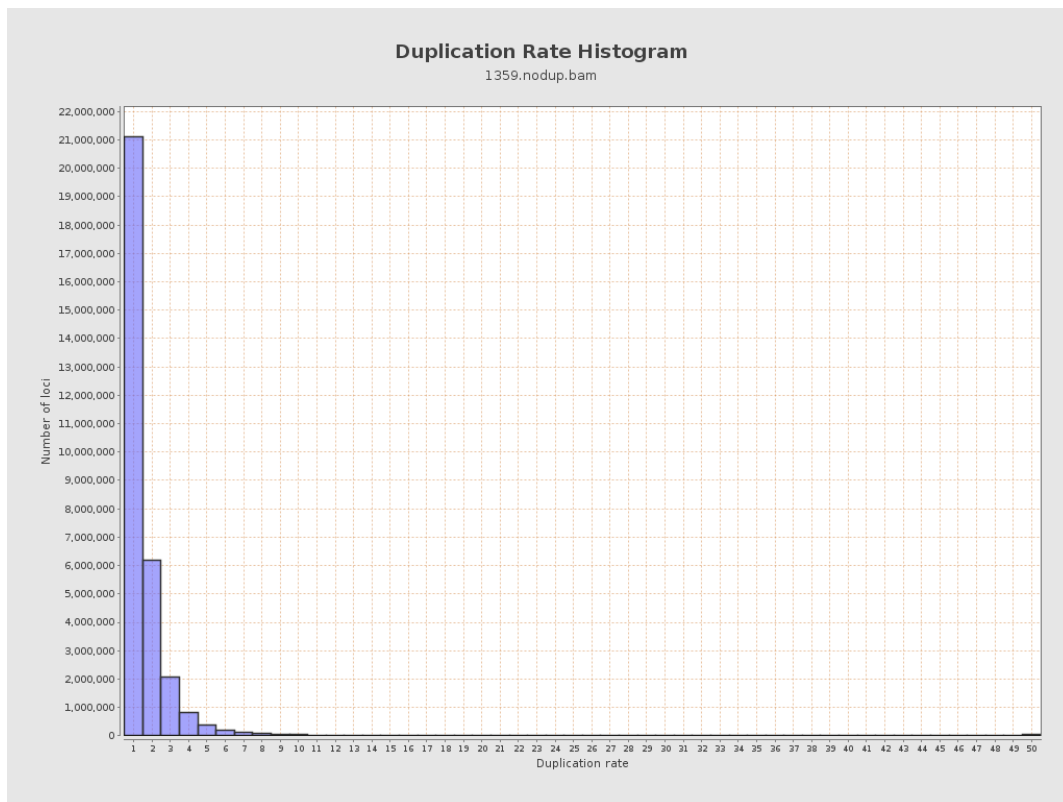
5. Results : Coverage Histogram (0-50X)



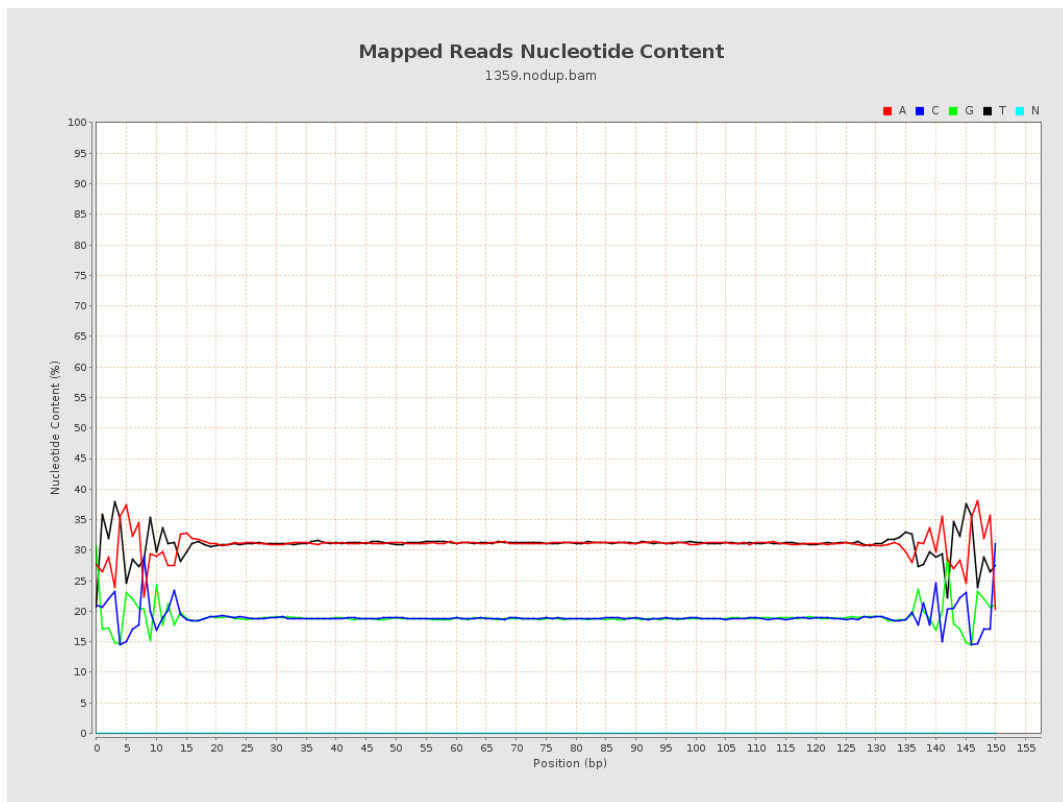
6. Results : Genome Fraction Coverage



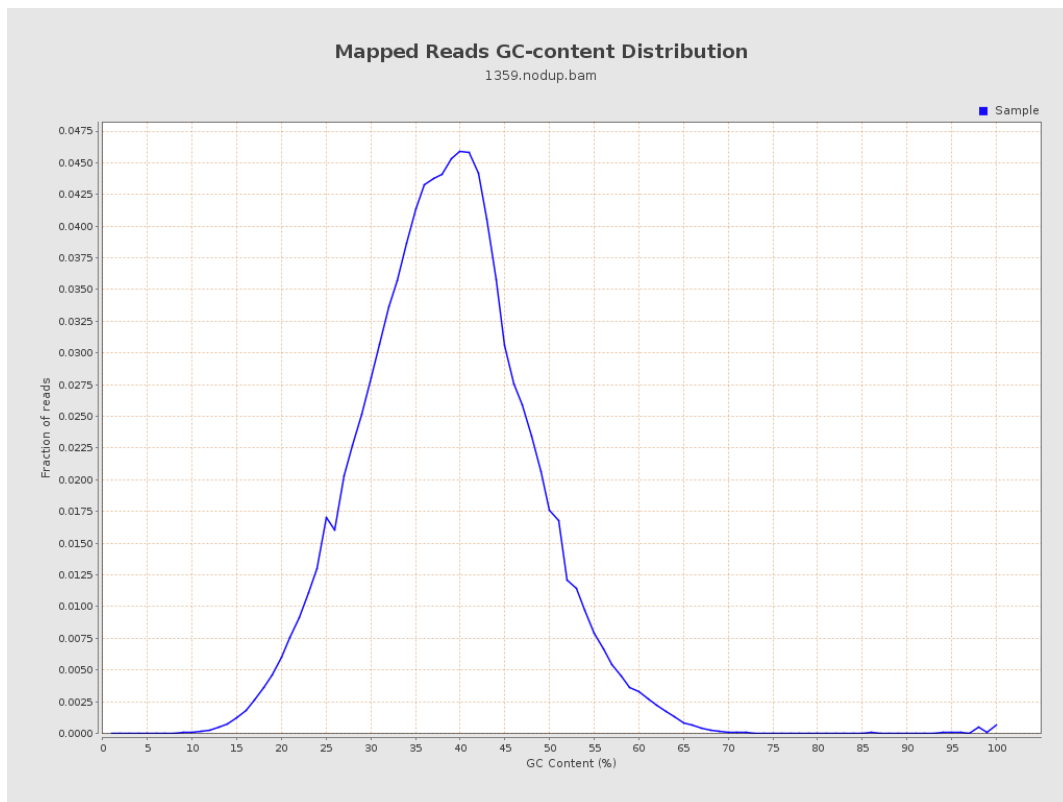
7. Results : Duplication Rate Histogram



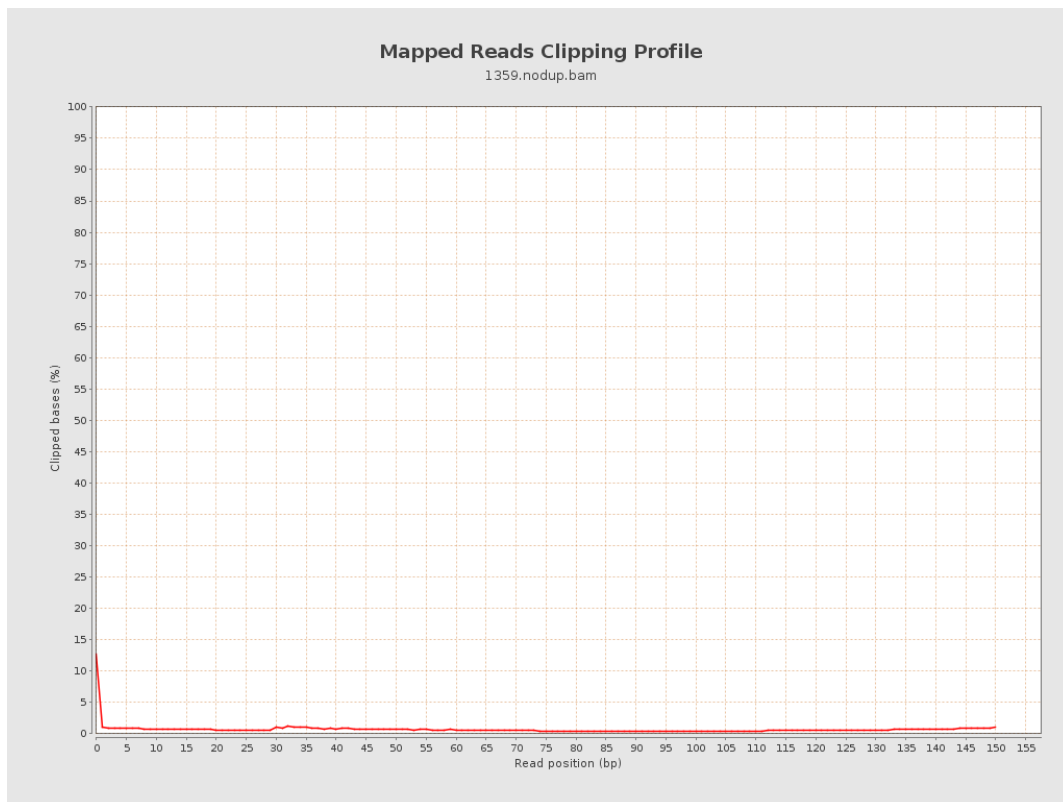
8. Results : Mapped Reads Nucleotide Content



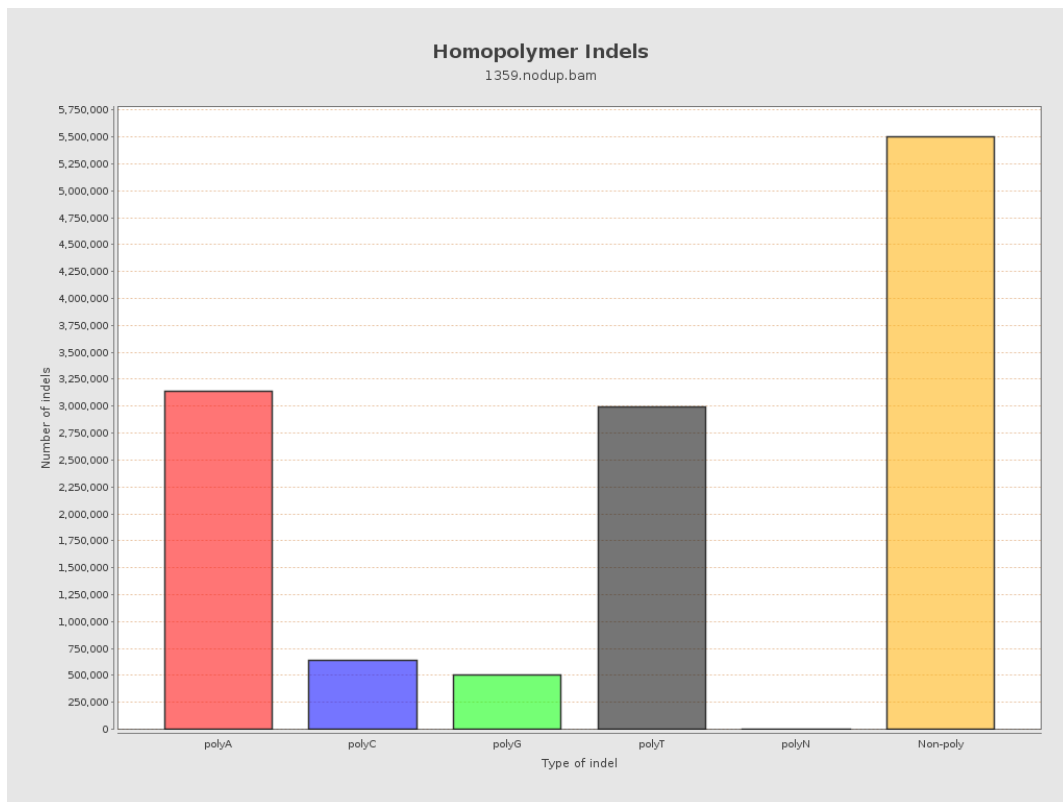
9. Results : Mapped Reads GC-content Distribution



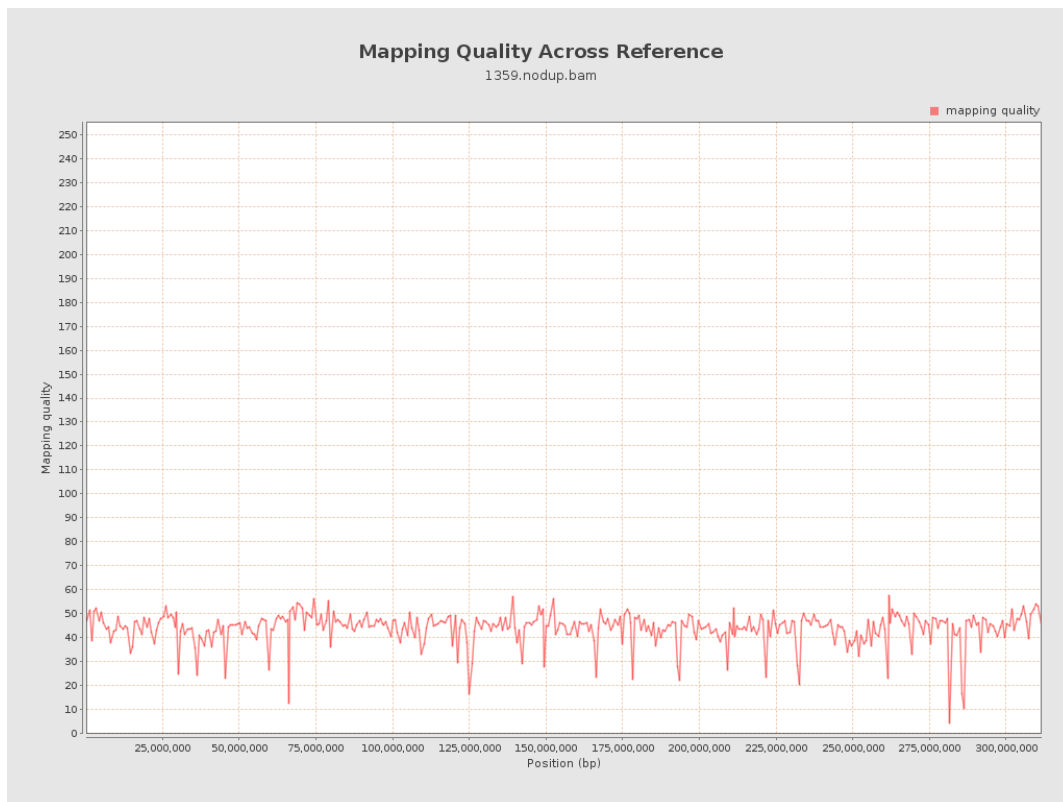
10. Results : Mapped Reads Clipping Profile



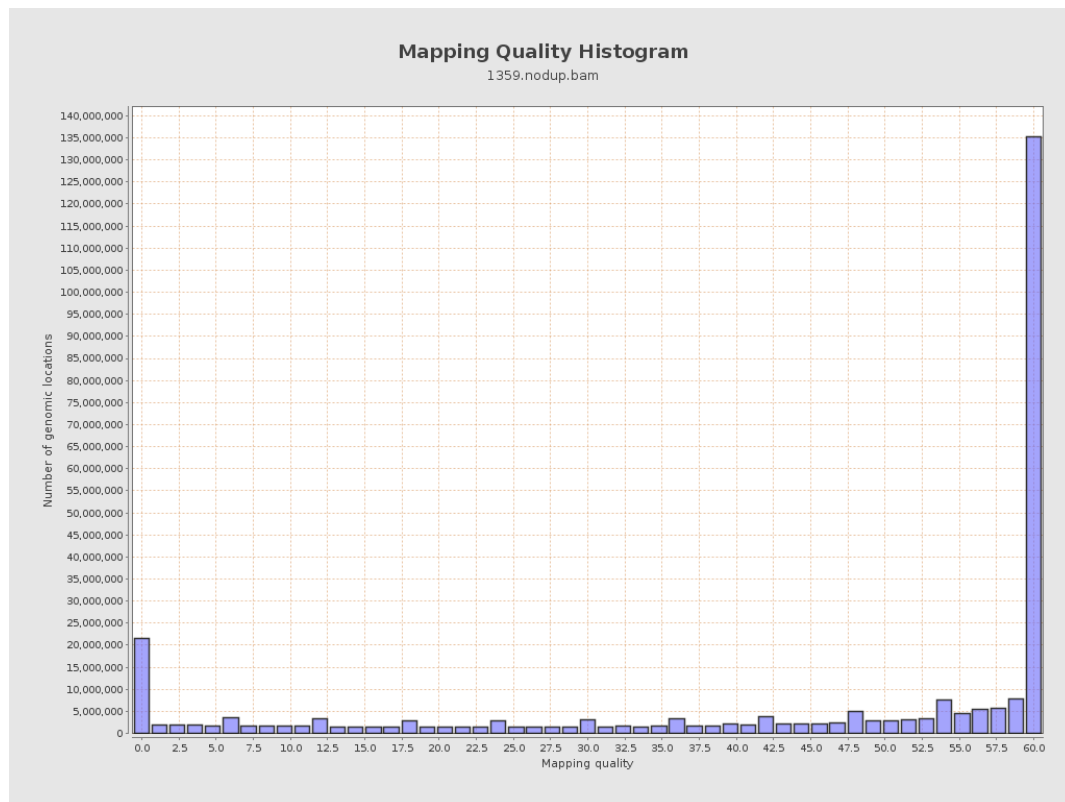
11. Results : Homopolymer Indels



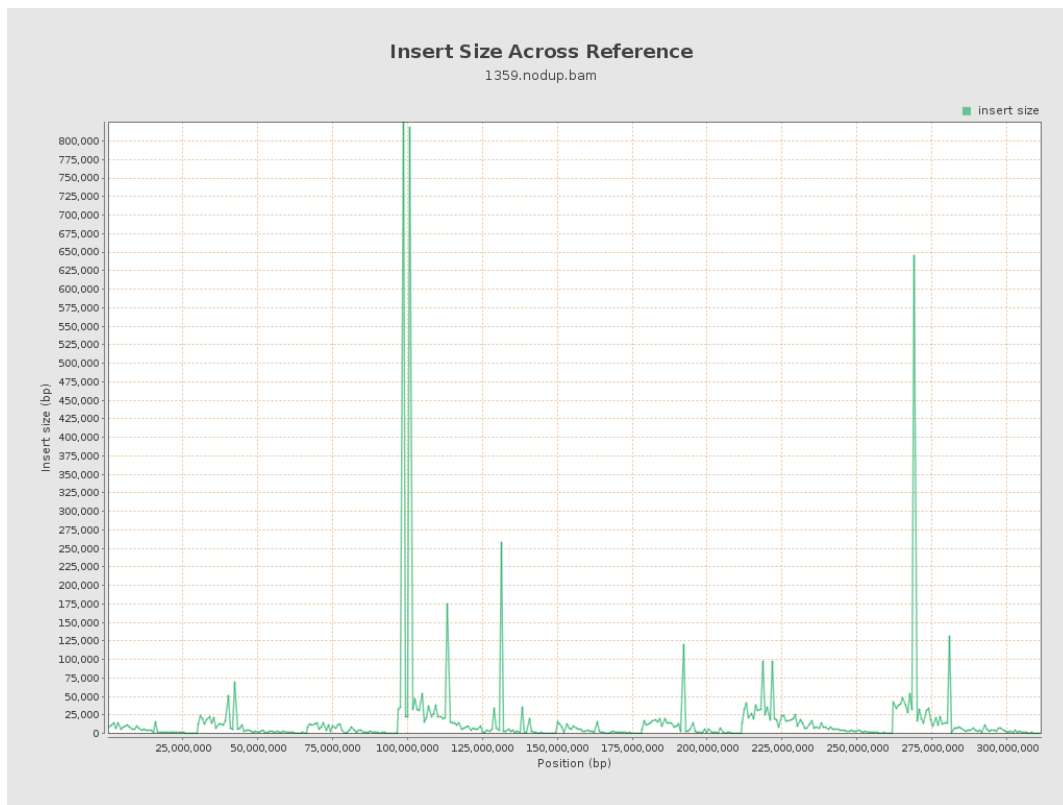
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

