

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:29:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/138
9
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1389 .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_571/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_571_S138_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_571/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_571_S138_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:29:16 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	61,885,525
Mapped reads	57,297,057 / 92.59%
Unmapped reads	4,588,468 / 7.41%
Mapped paired reads	57,297,057 / 92.59%
Mapped reads, first in pair	28,765,948 / 46.48%
Mapped reads, second in pair	28,531,109 / 46.1%
Mapped reads, both in pair	55,934,128 / 90.38%
Mapped reads, singletons	1,362,929 / 2.2%
Read min/max/mean length	30 / 151 / 148.37
Duplicated reads (flagged)	9,817,136 / 15.86%
Clipped reads	13,630,459 / 22.03%

2.2. ACGT Content

Number/percentage of A's	2,436,900,766 / 30.76%
Number/percentage of C's	1,523,959,200 / 19.24%
Number/percentage of T's	2,442,534,648 / 30.83%
Number/percentage of G's	1,518,298,769 / 19.17%
Number/percentage of N's	53,232 / 0%
GC Percentage	38.4%

2.3. Coverage

Mean	25.4821
Standard Deviation	207.5678

2.4. Mapping Quality

Mean Mapping Quality	44.41
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2.5. Insert size

Mean	209,391.92
Standard Deviation	2,185,490.21
P25/Median/P75	306 / 398 / 513

2.6. Mismatches and indels

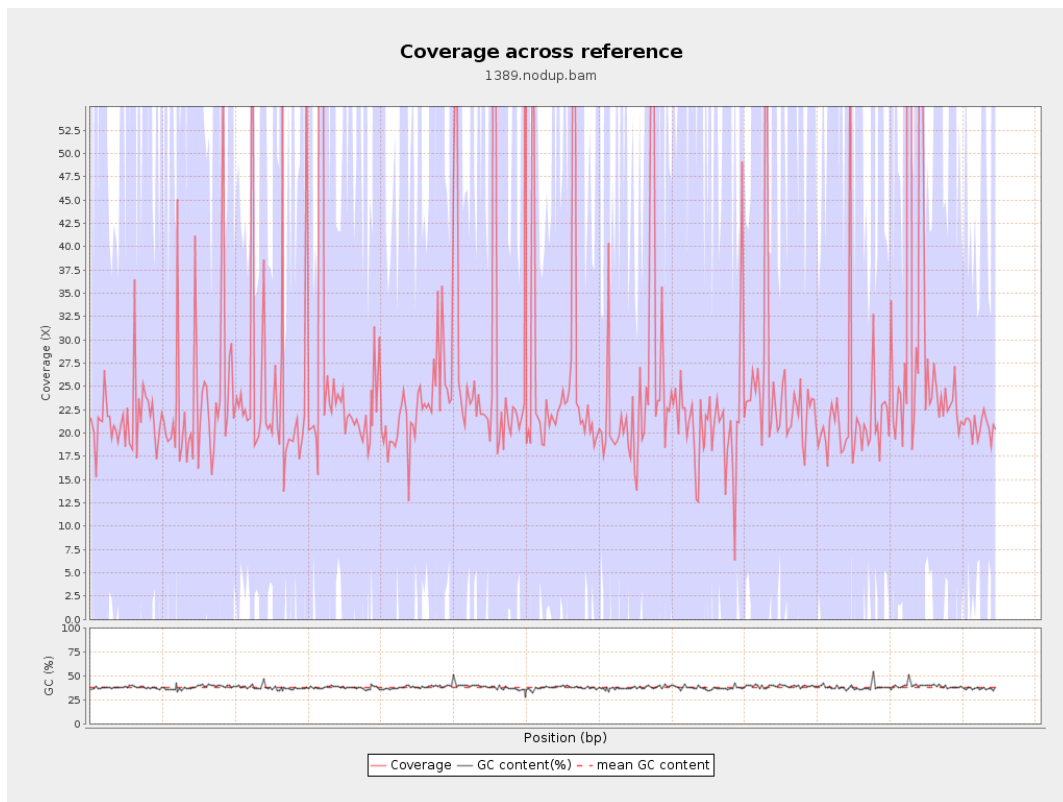
General error rate	2.62%
Mismatches	193,161,175
Insertions	5,234,108
Mapped reads with at least one insertion	8.21%
Deletions	5,229,996
Mapped reads with at least one deletion	8.12%
Homopolymer indels	55.99%

2.7. Chromosome stats

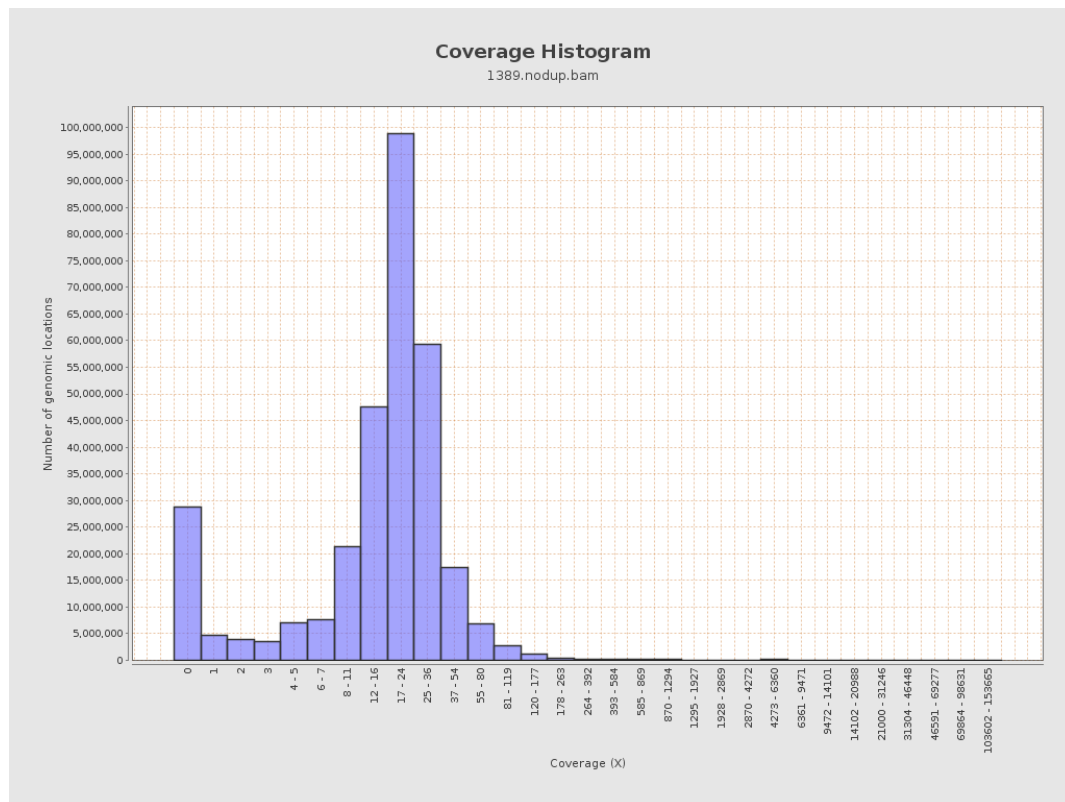
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	632613160	21.2827	67.6338

LT669789.1	36598175	911631632	24.9092	211.9645
LT669790.1	30422129	852955952	28.0374	228.9674
LT669791.1	52758100	1320434067	25.0281	193.1513
LT669792.1	28376109	721830438	25.438	226.5444
LT669793.1	33388210	795807996	23.835	197.1286
LT669794.1	50579949	1189388721	23.515	167.9188
LT669795.1	49795044	1516620374	30.4573	279.902

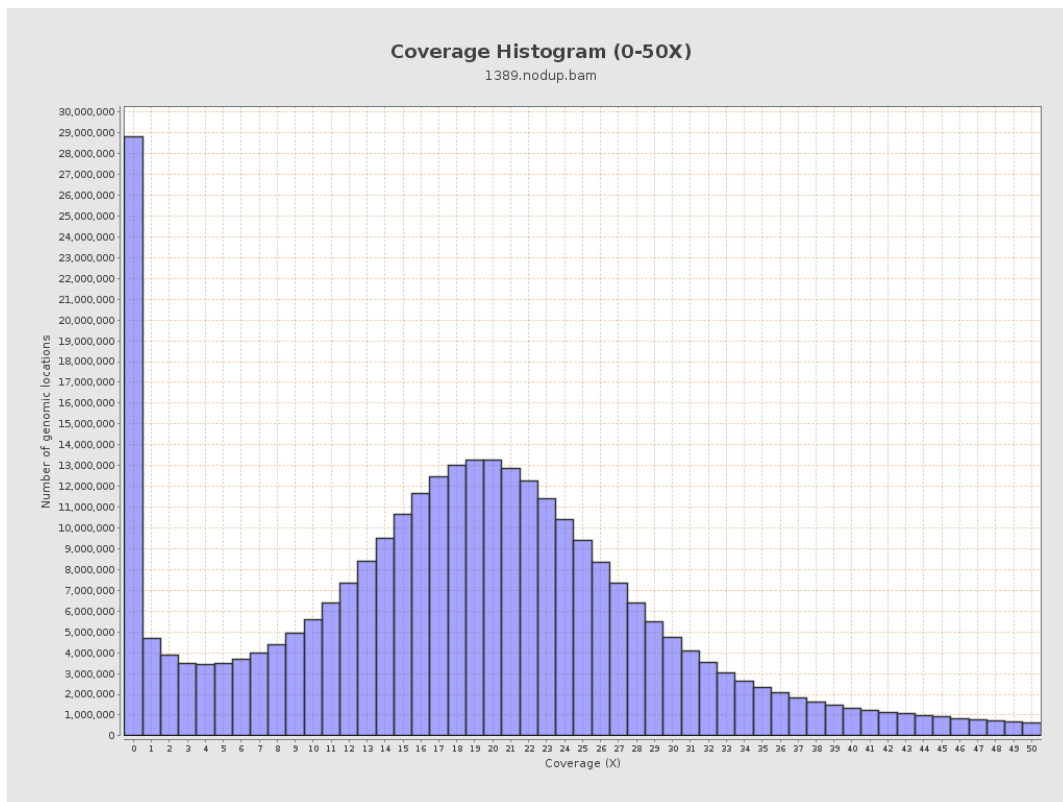
3. Results : Coverage across reference



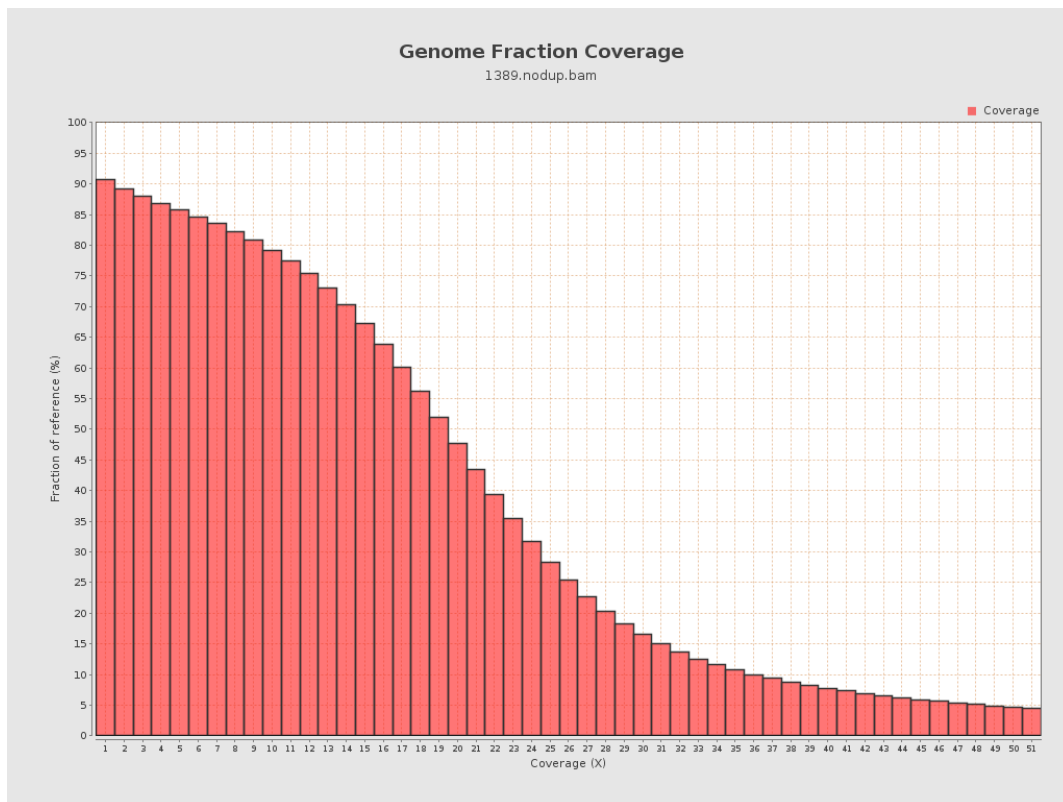
4. Results : Coverage Histogram



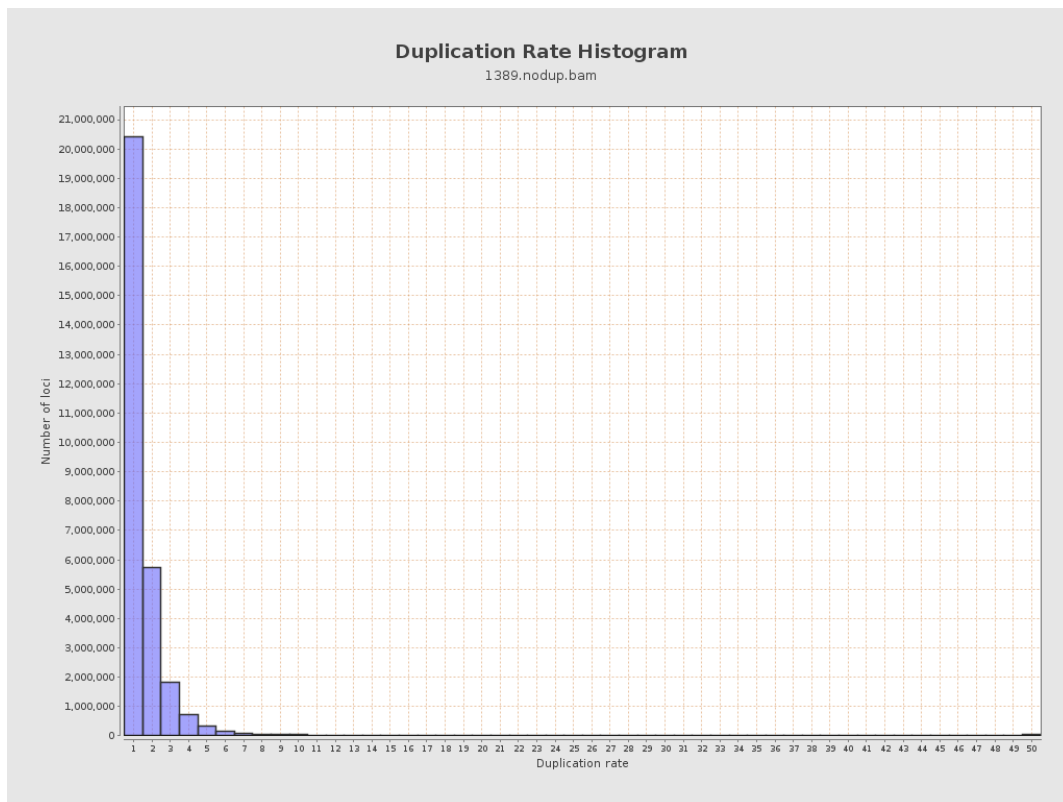
5. Results : Coverage Histogram (0-50X)



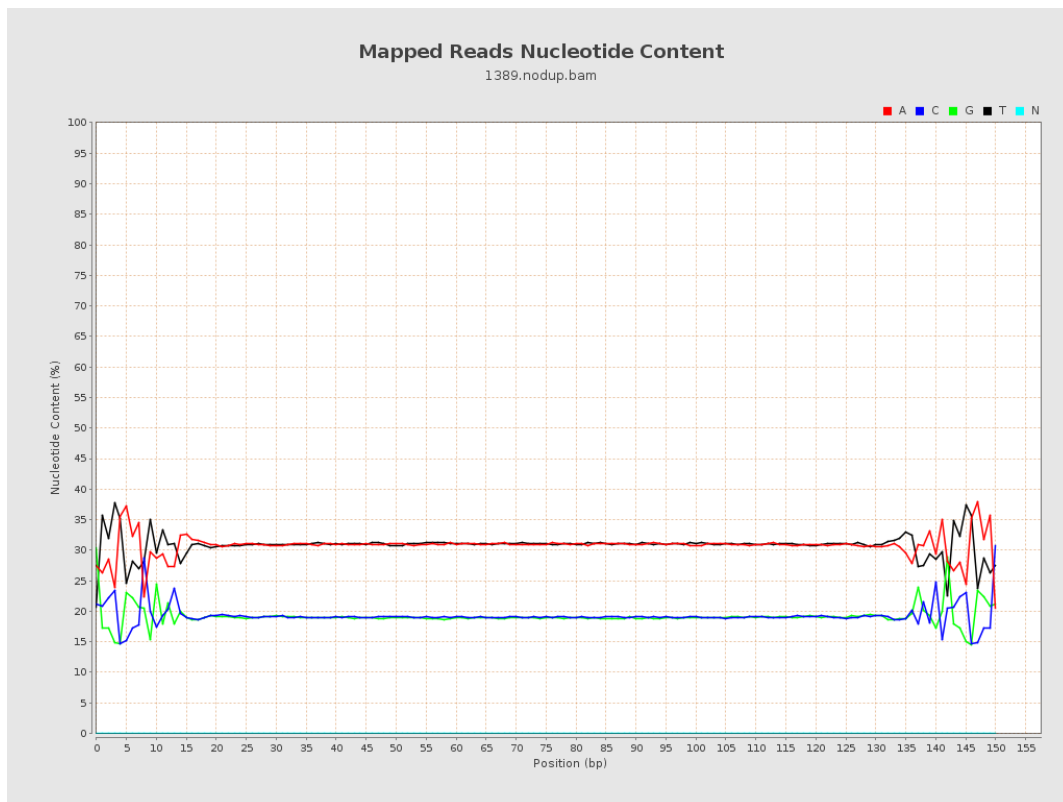
6. Results : Genome Fraction Coverage



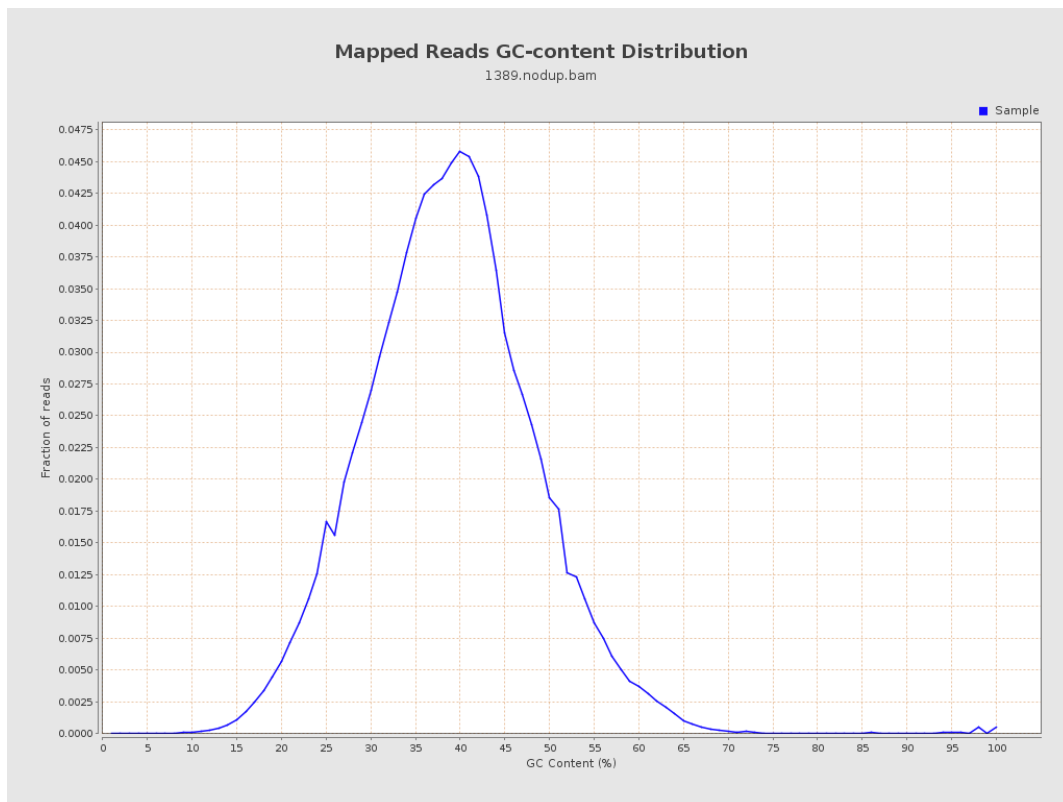
7. Results : Duplication Rate Histogram



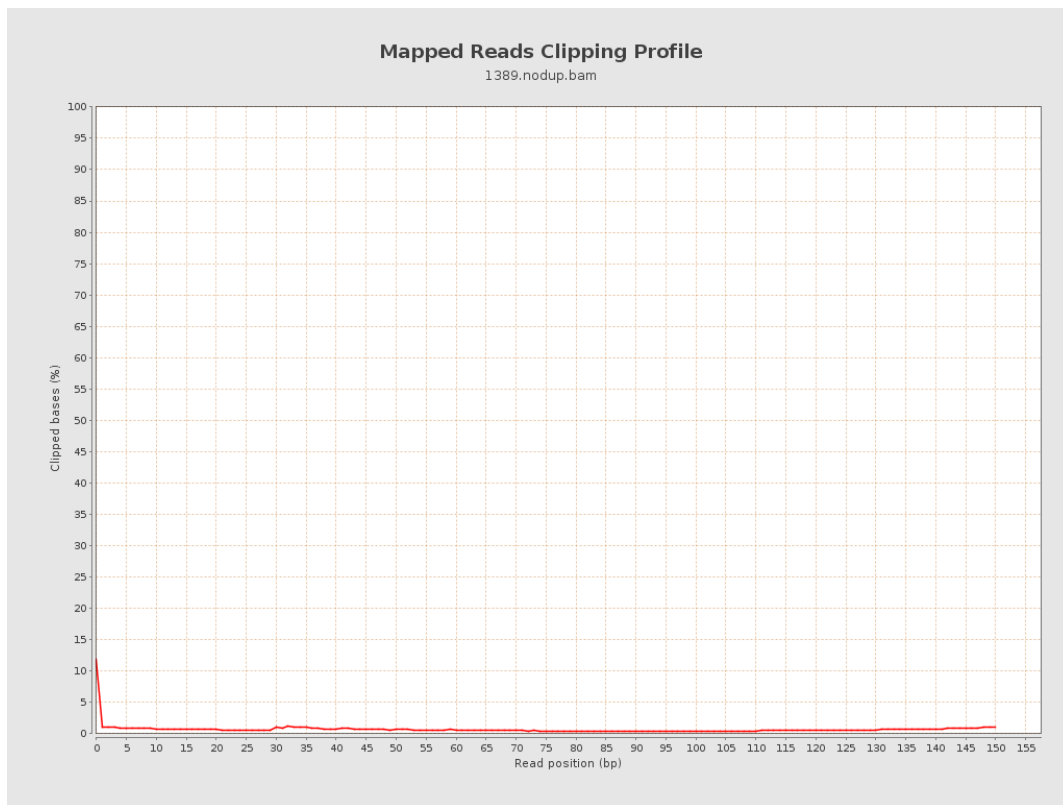
8. Results : Mapped Reads Nucleotide Content



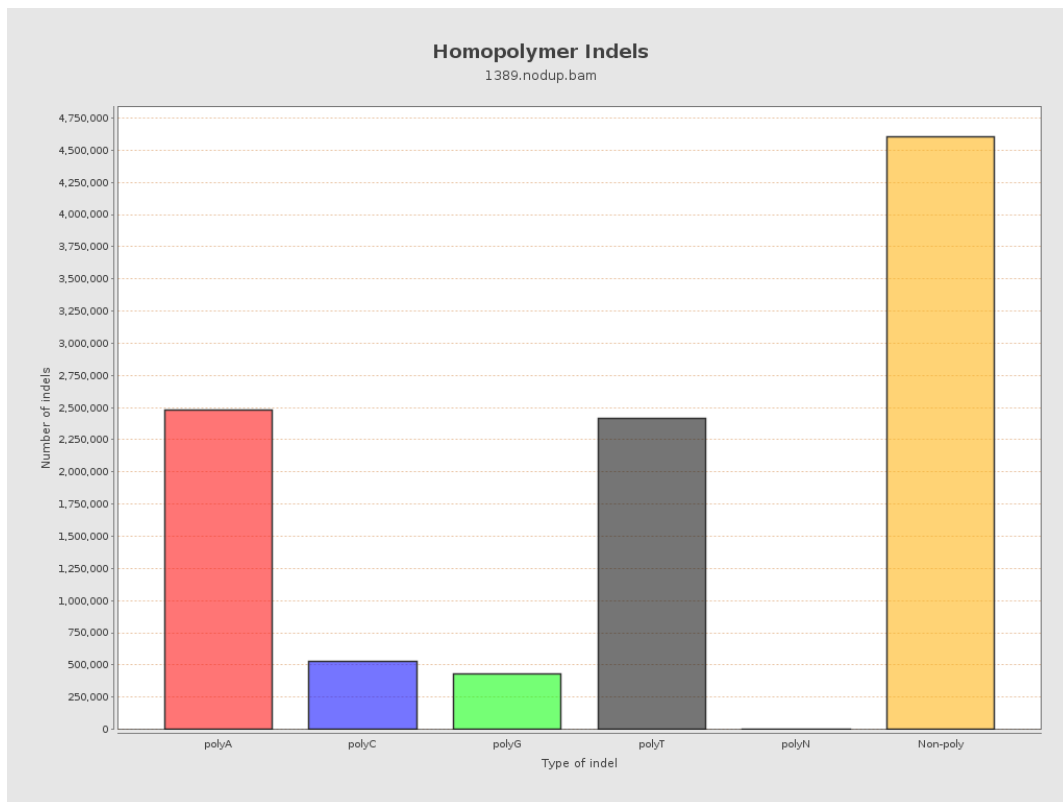
9. Results : Mapped Reads GC-content Distribution



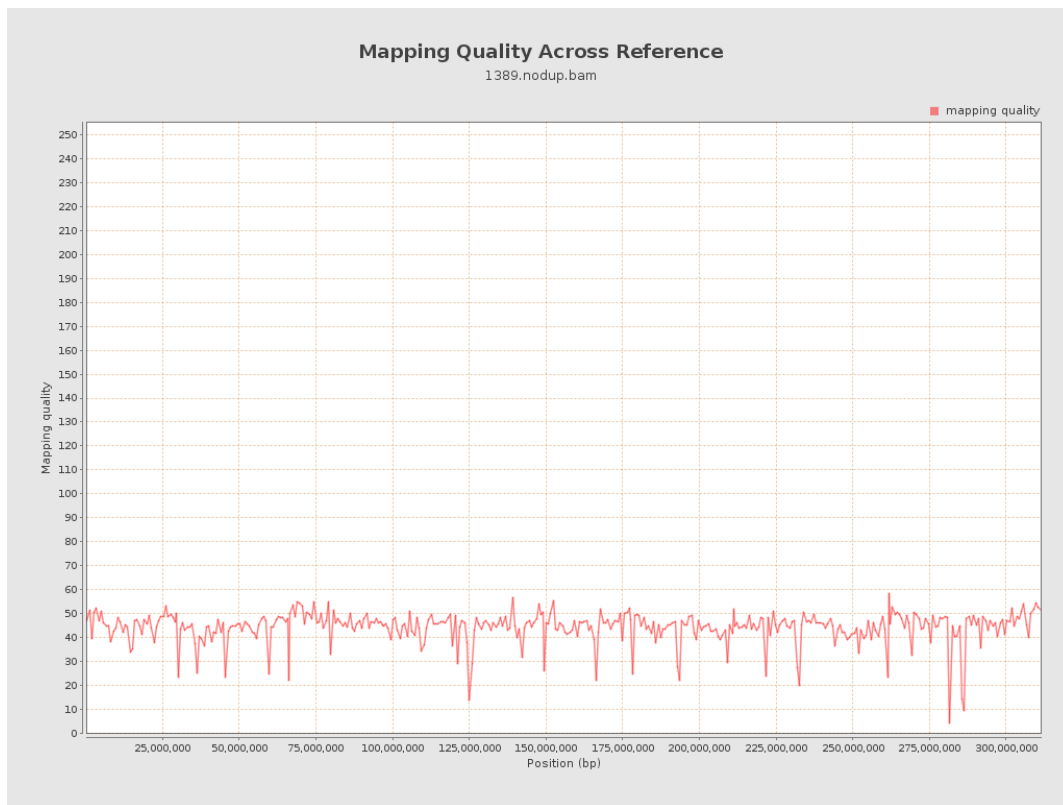
10. Results : Mapped Reads Clipping Profile



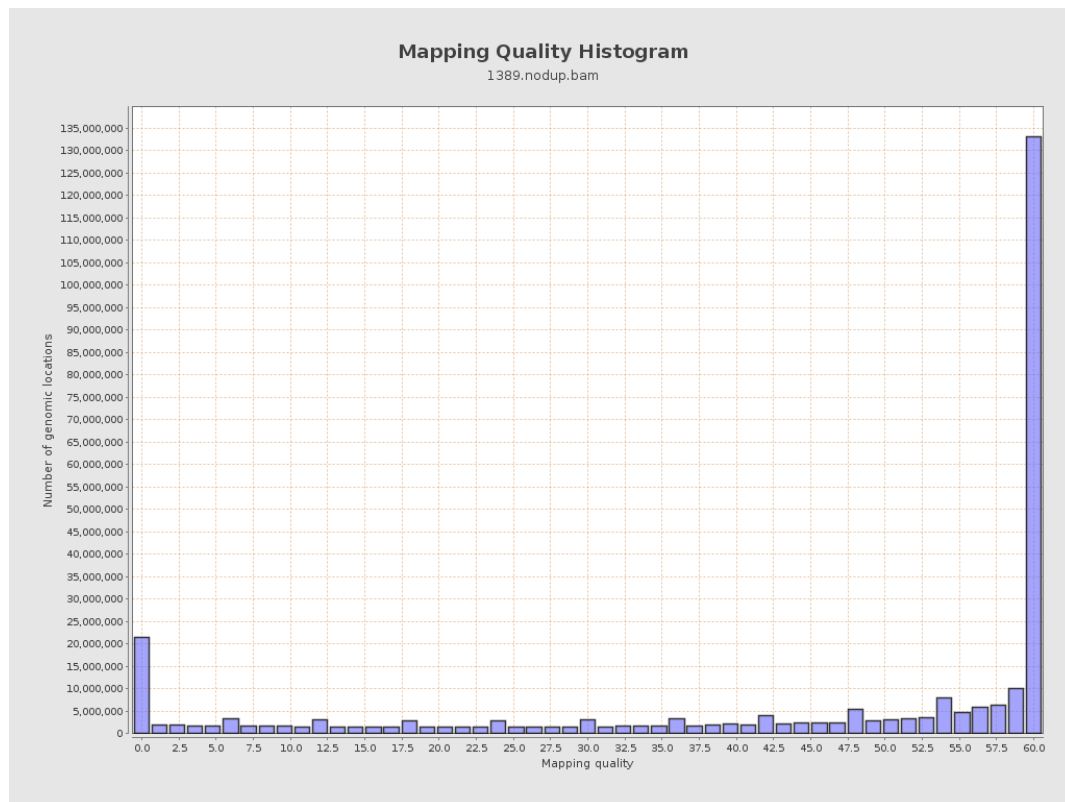
11. Results : Homopolymer Indels



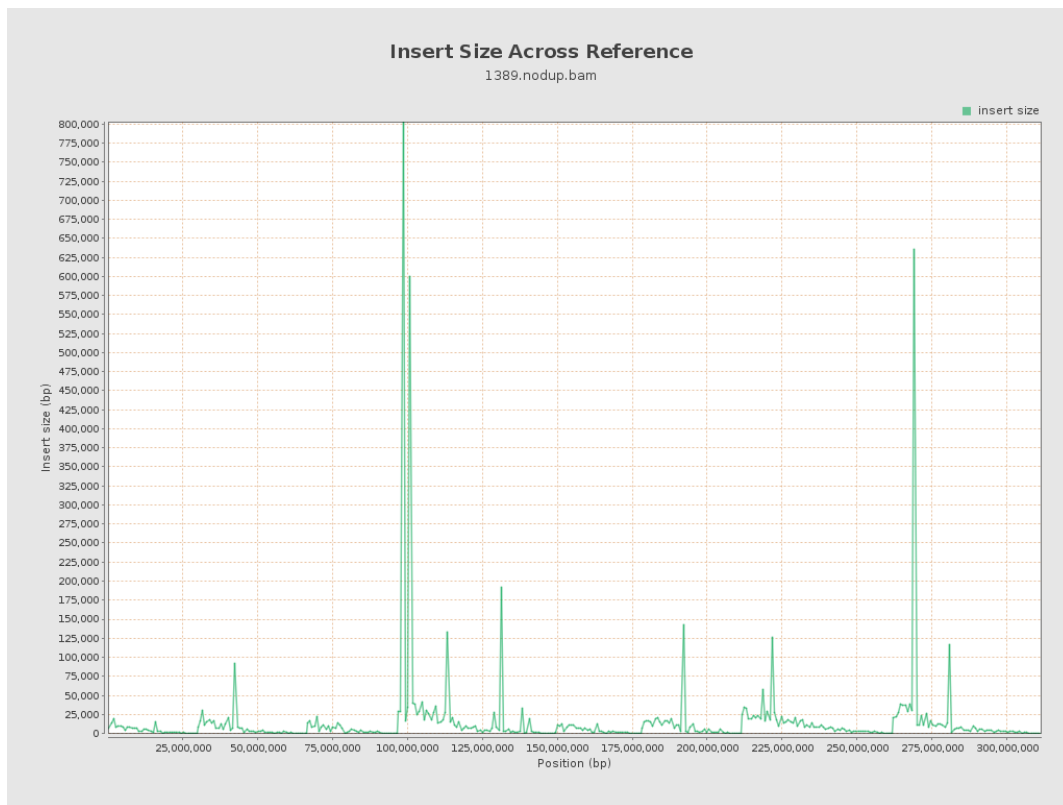
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

