

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:33:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/102
7
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1027 .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_439/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_439_S414_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_439/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_439_S414_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:33:48 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	73,282,645
Mapped reads	67,973,757 / 92.76%
Unmapped reads	5,308,888 / 7.24%
Mapped paired reads	67,973,757 / 92.76%
Mapped reads, first in pair	34,067,224 / 46.49%
Mapped reads, second in pair	33,906,533 / 46.27%
Mapped reads, both in pair	66,159,407 / 90.28%
Mapped reads, singletons	1,814,350 / 2.48%
Read min/max/mean length	30 / 151 / 148
Duplicated reads (flagged)	11,384,839 / 15.54%
Clipped reads	16,008,341 / 21.84%

2.2. ACGT Content

Number/percentage of A's	2,888,010,446 / 30.87%
Number/percentage of C's	1,786,901,170 / 19.1%
Number/percentage of T's	2,893,710,684 / 30.93%
Number/percentage of G's	1,786,456,586 / 19.1%
Number/percentage of N's	32,507 / 0%
GC Percentage	38.2%

2.3. Coverage

Mean	30.1002
Standard Deviation	260.4492

2.4. Mapping Quality

Mean Mapping Quality	43.68
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2.5. Insert size

Mean	268,567.56
Standard Deviation	2,476,336.47
P25/Median/P75	359 / 475 / 622

2.6. Mismatches and indels

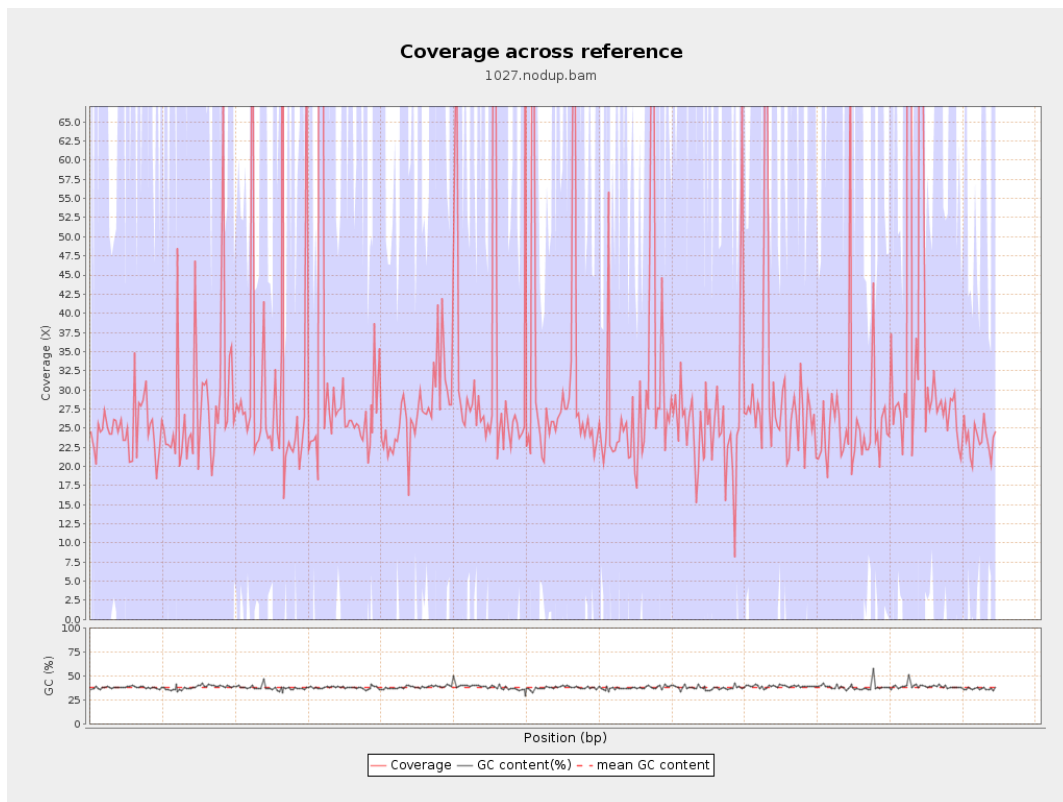
General error rate	2.39%
Mismatches	205,249,167
Insertions	6,584,969
Mapped reads with at least one insertion	8.66%
Deletions	6,627,574
Mapped reads with at least one deletion	8.64%
Homopolymer indels	56.55%

2.7. Chromosome stats

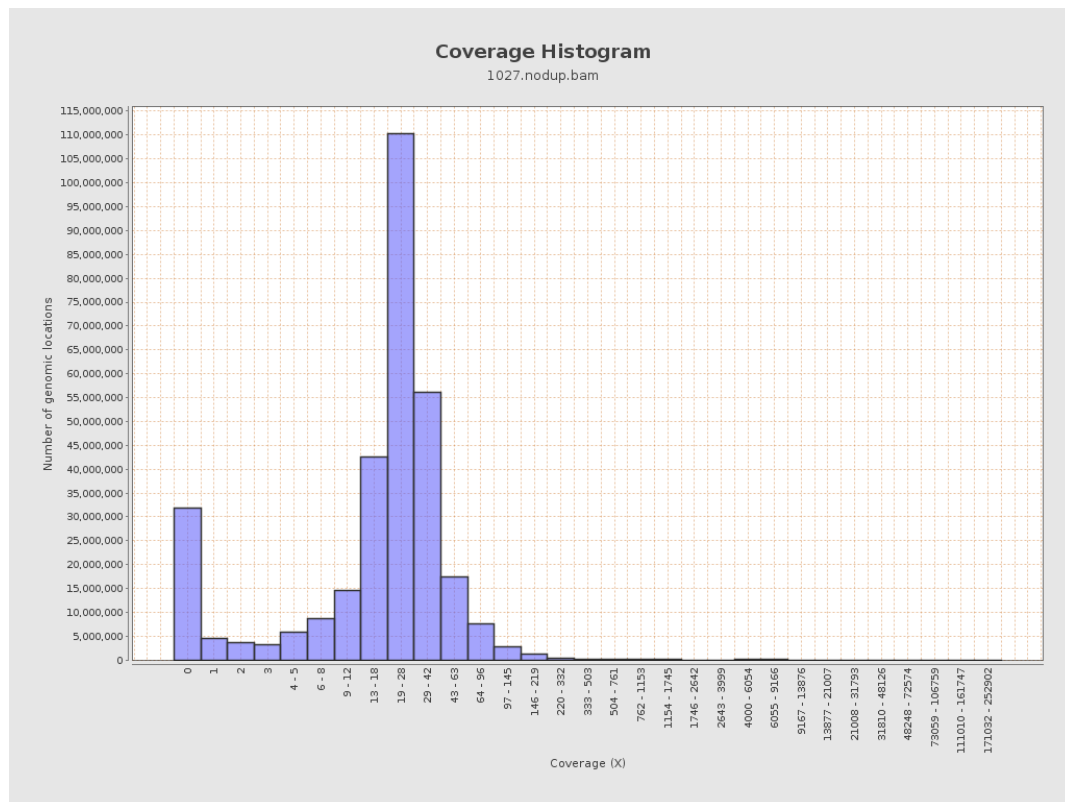
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	730994983	24.5925	84.236

LT669789.1	36598175	1097287579	29.982	253.6849
LT669790.1	30422129	1033545672	33.9735	303.3132
LT669791.1	52758100	1566139237	29.6853	236.1531
LT669792.1	28376109	853321817	30.0718	267.1729
LT669793.1	33388210	948665275	28.4132	228.983
LT669794.1	50579949	1427790413	28.2284	205.0425
LT669795.1	49795044	1722757647	34.597	372.9825

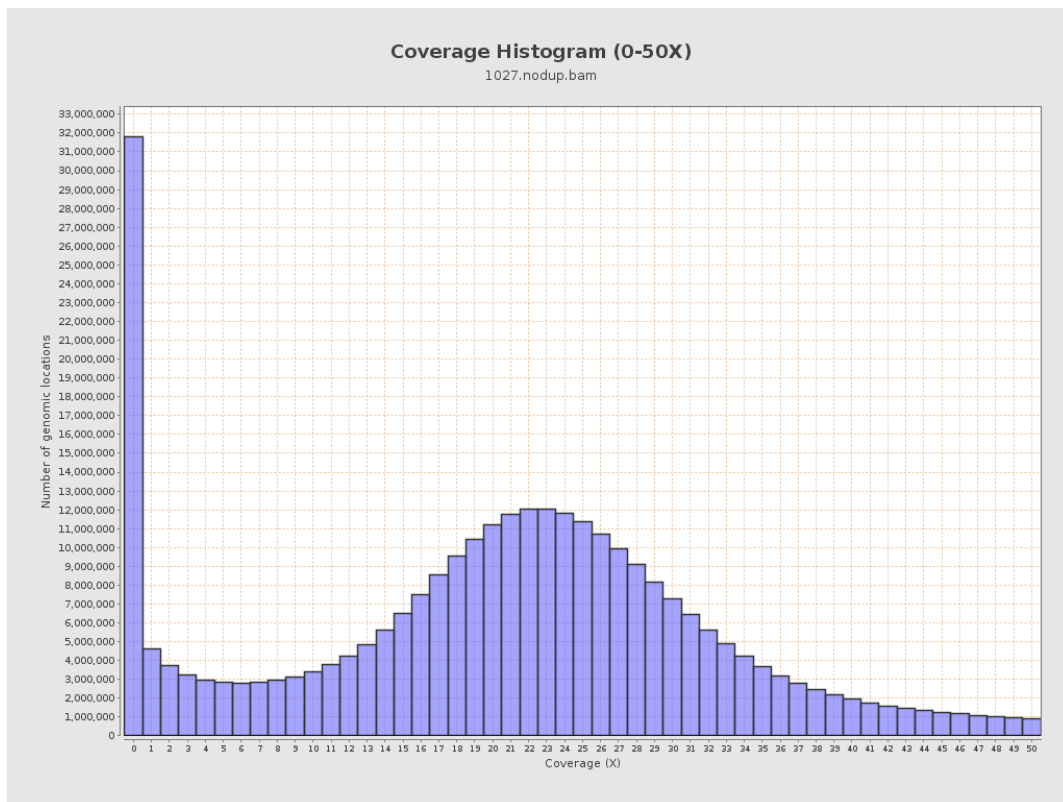
3. Results : Coverage across reference



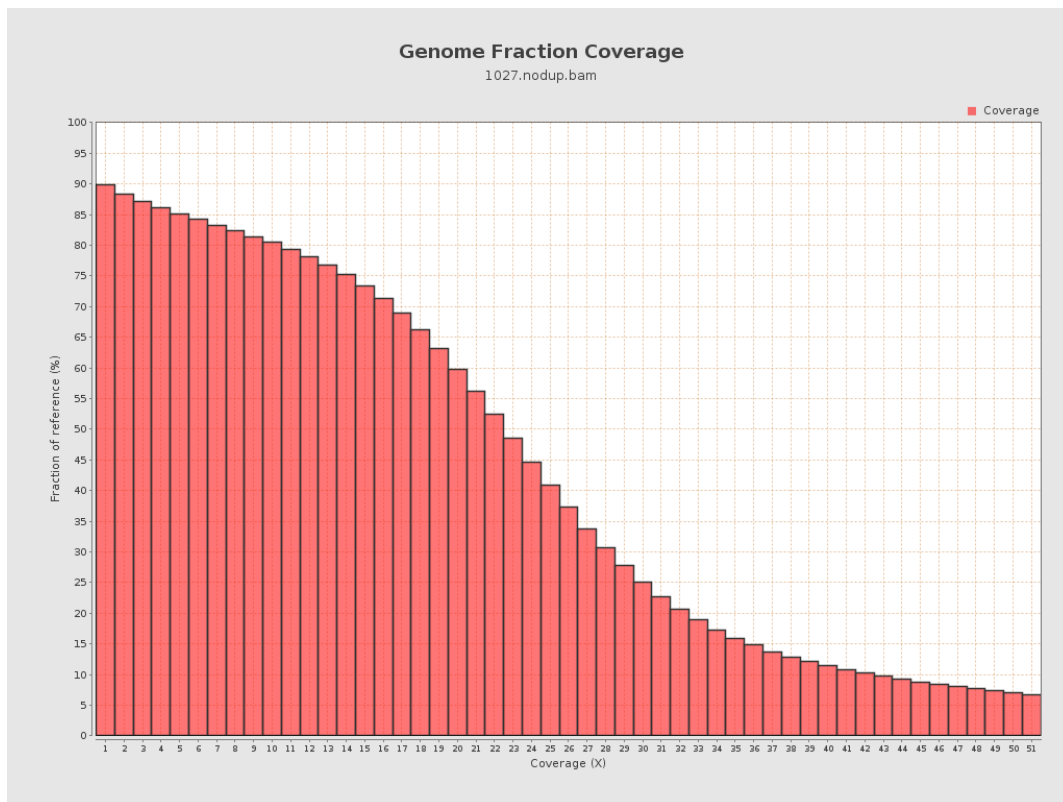
4. Results : Coverage Histogram



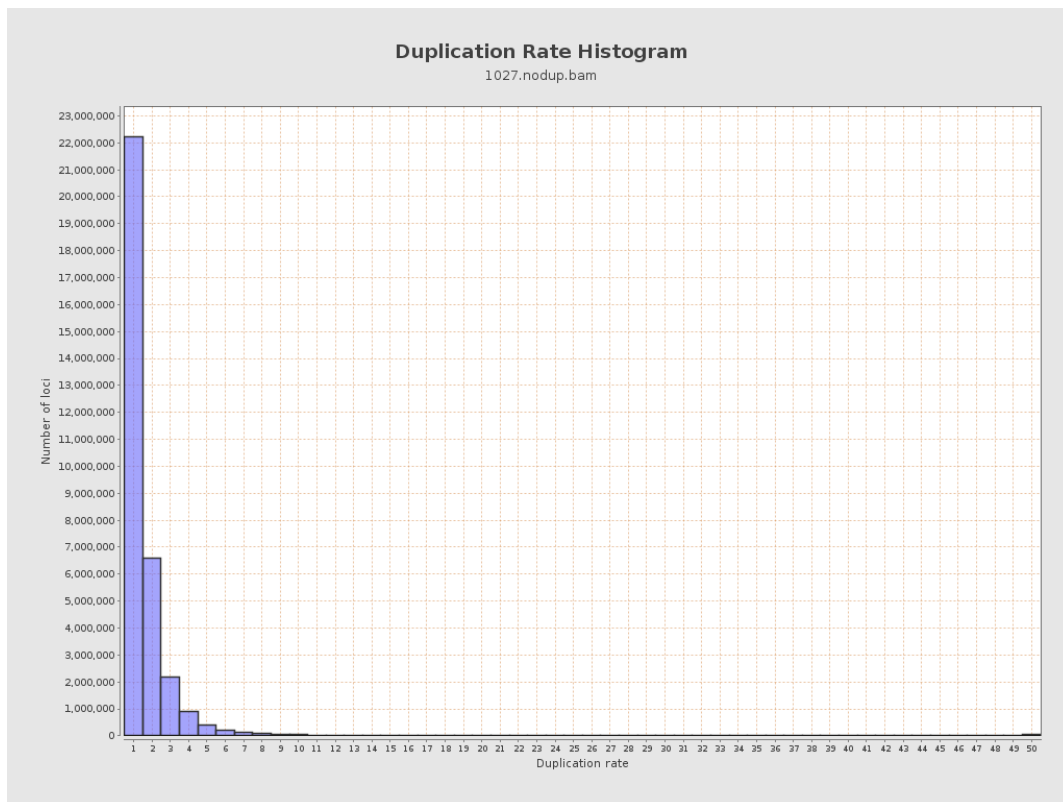
5. Results : Coverage Histogram (0-50X)



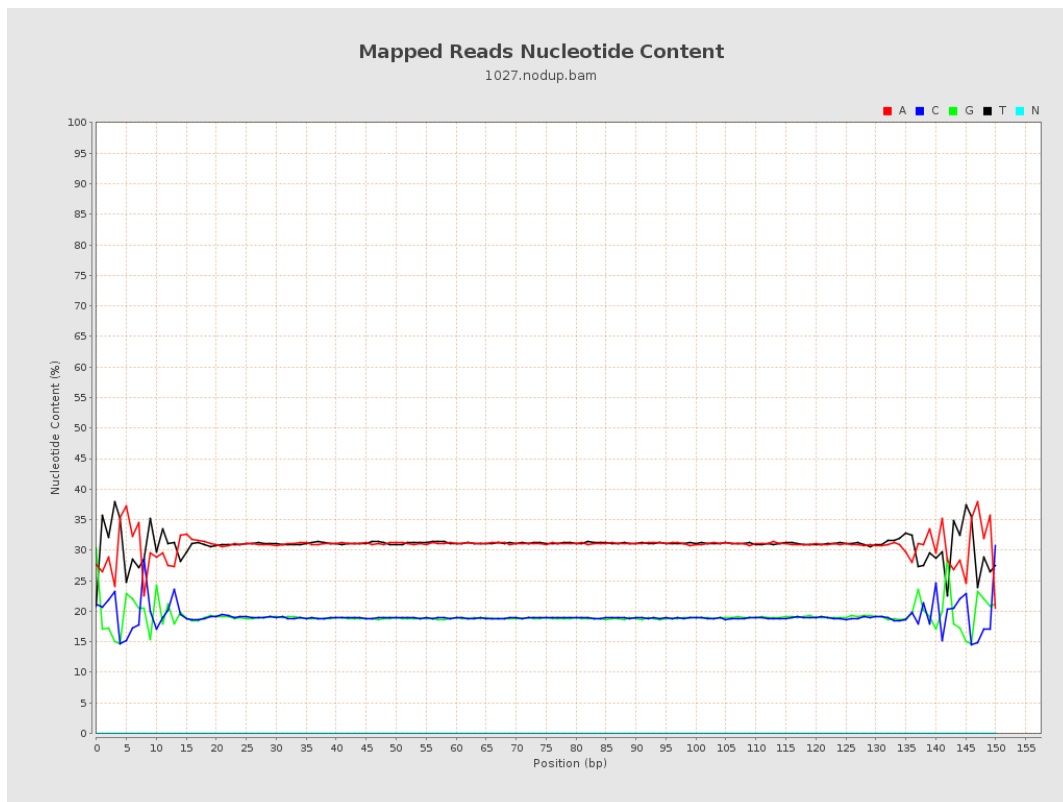
6. Results : Genome Fraction Coverage



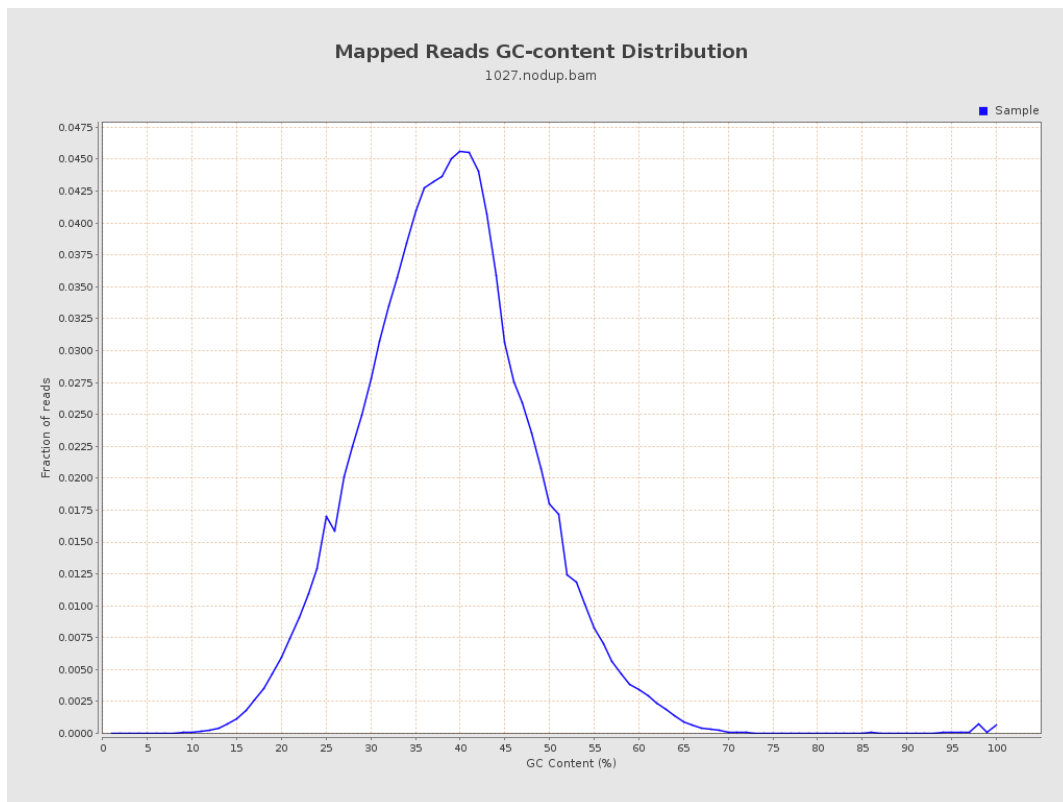
7. Results : Duplication Rate Histogram



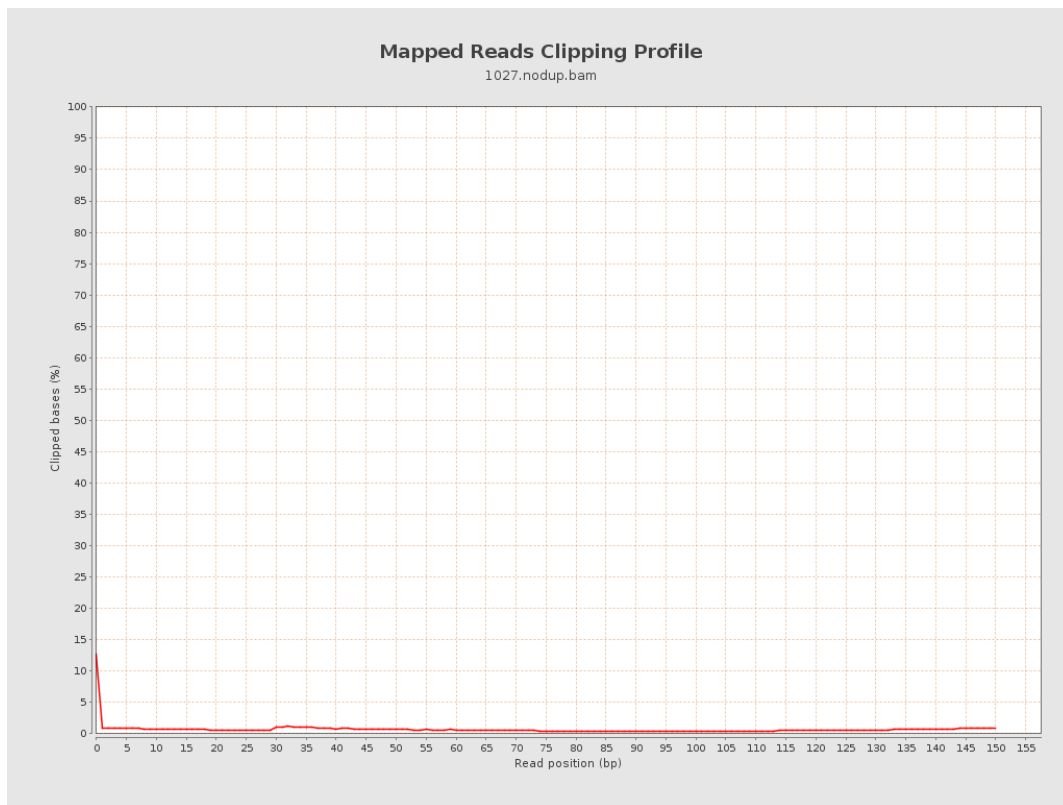
8. Results : Mapped Reads Nucleotide Content



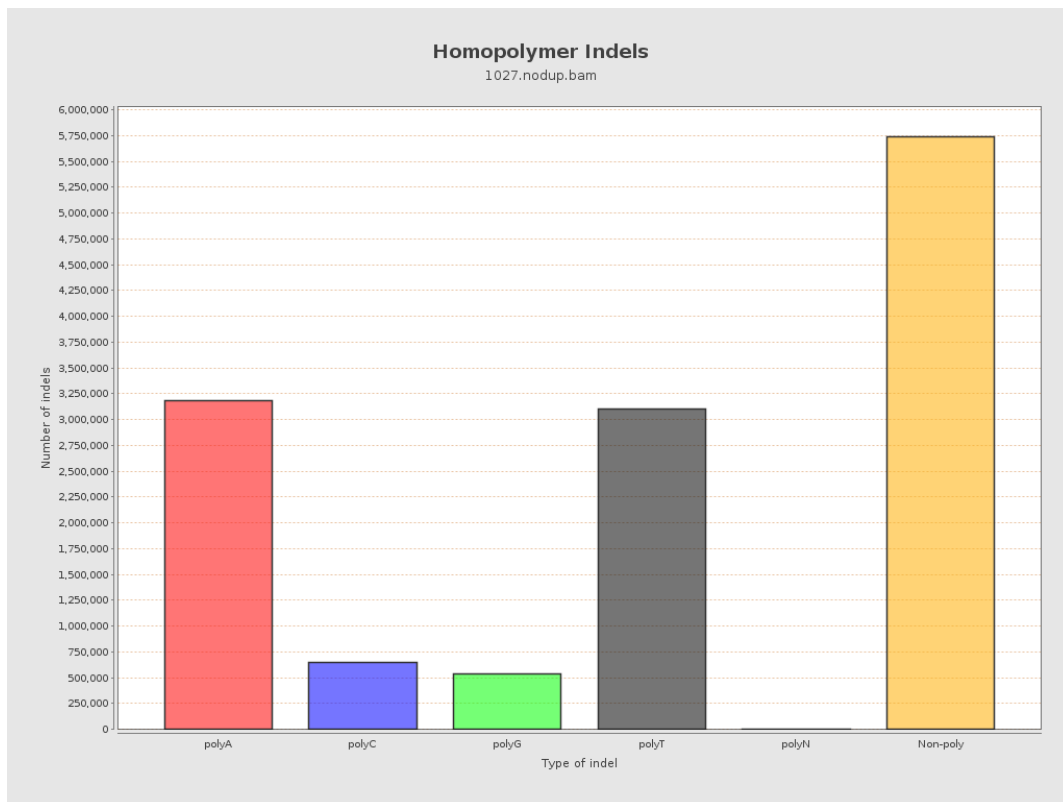
9. Results : Mapped Reads GC-content Distribution



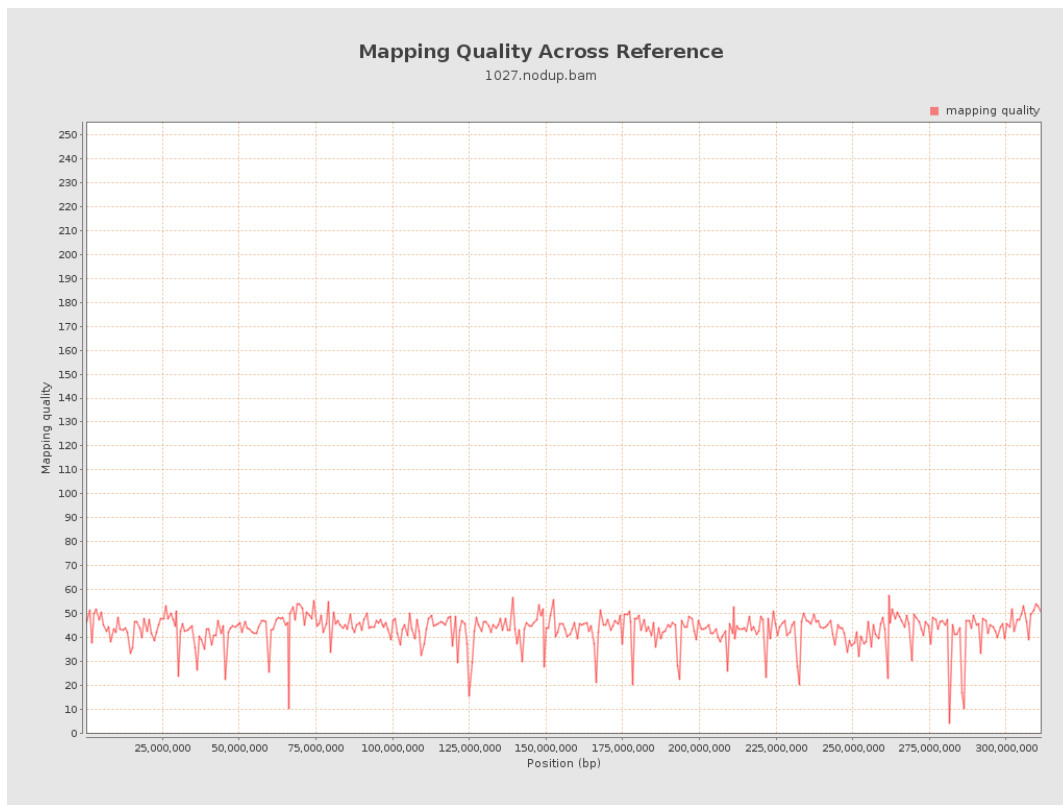
10. Results : Mapped Reads Clipping Profile



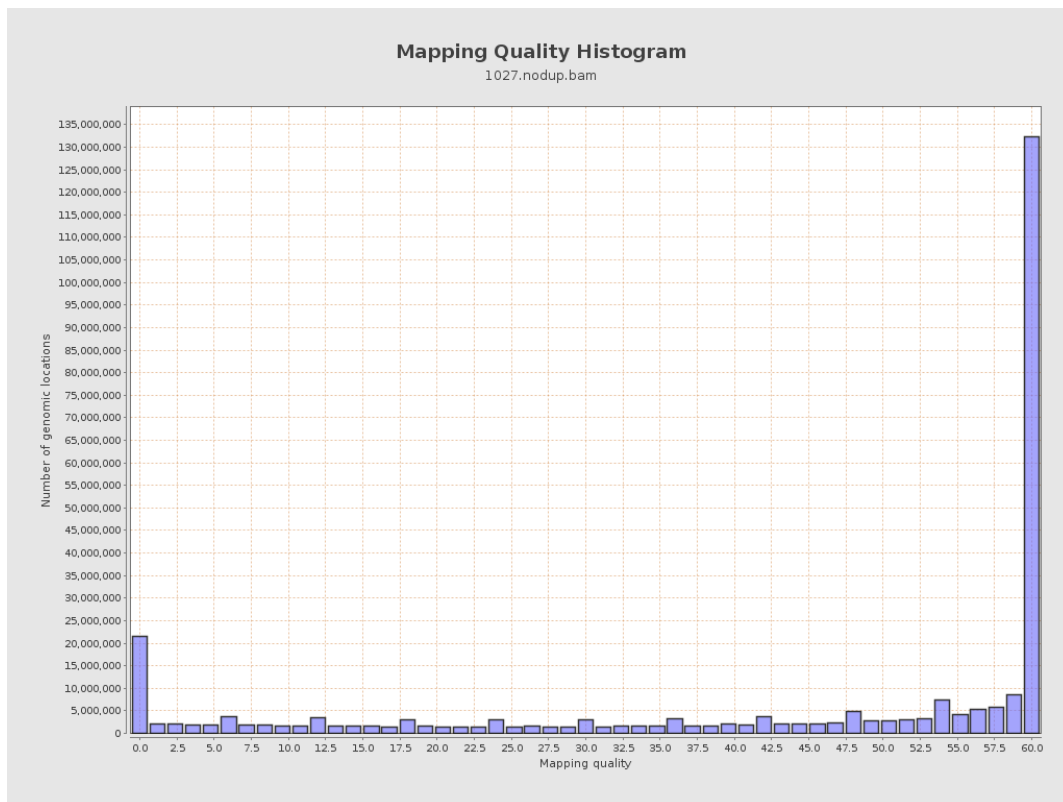
11. Results : Homopolymer Indels



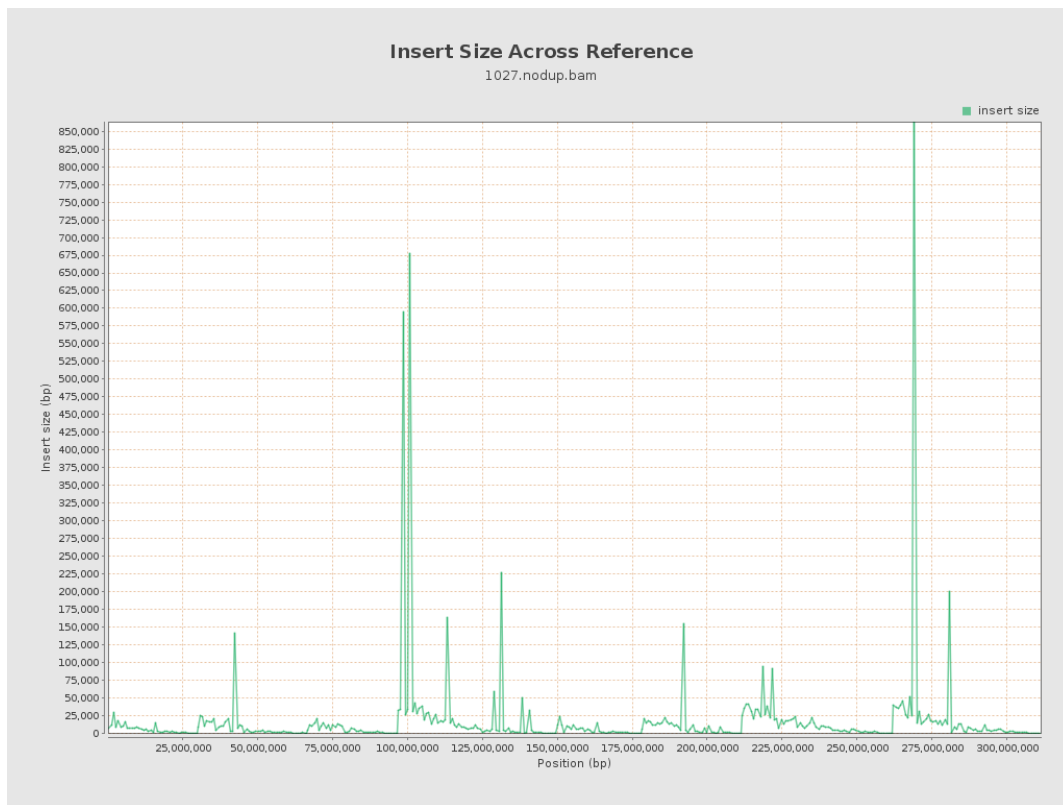
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

