

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:30:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/112
2
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1122 .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\tSM:\$sample /proj/uppstore2018210/Aalpina/data/reference/GCA_900128785.1_MPIPZ.v5_genomic.fa /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_540/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_540_S107_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_540/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_540_S107_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:30:29 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	66,112,458
Mapped reads	60,344,532 / 91.28%
Unmapped reads	5,767,926 / 8.72%
Mapped paired reads	60,344,532 / 91.28%
Mapped reads, first in pair	30,266,013 / 45.78%
Mapped reads, second in pair	30,078,519 / 45.5%
Mapped reads, both in pair	58,443,536 / 88.4%
Mapped reads, singletons	1,900,996 / 2.88%
Read min/max/mean length	30 / 151 / 148.19
Duplicated reads (flagged)	10,591,132 / 16.02%
Clipped reads	14,918,396 / 22.57%

2.2. ACGT Content

Number/percentage of A's	2,556,171,918 / 30.97%
Number/percentage of C's	1,569,990,849 / 19.02%
Number/percentage of T's	2,560,070,032 / 31.02%
Number/percentage of G's	1,567,775,957 / 18.99%
Number/percentage of N's	59,278 / 0%
GC Percentage	38.02%

2.3. Coverage

Mean	26.5532
Standard Deviation	263.5727

2.4. Mapping Quality

Mean Mapping Quality	44.35
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2.5. Insert size

Mean	246,325.56
Standard Deviation	2,390,088.19
P25/Median/P75	312 / 410 / 529

2.6. Mismatches and indels

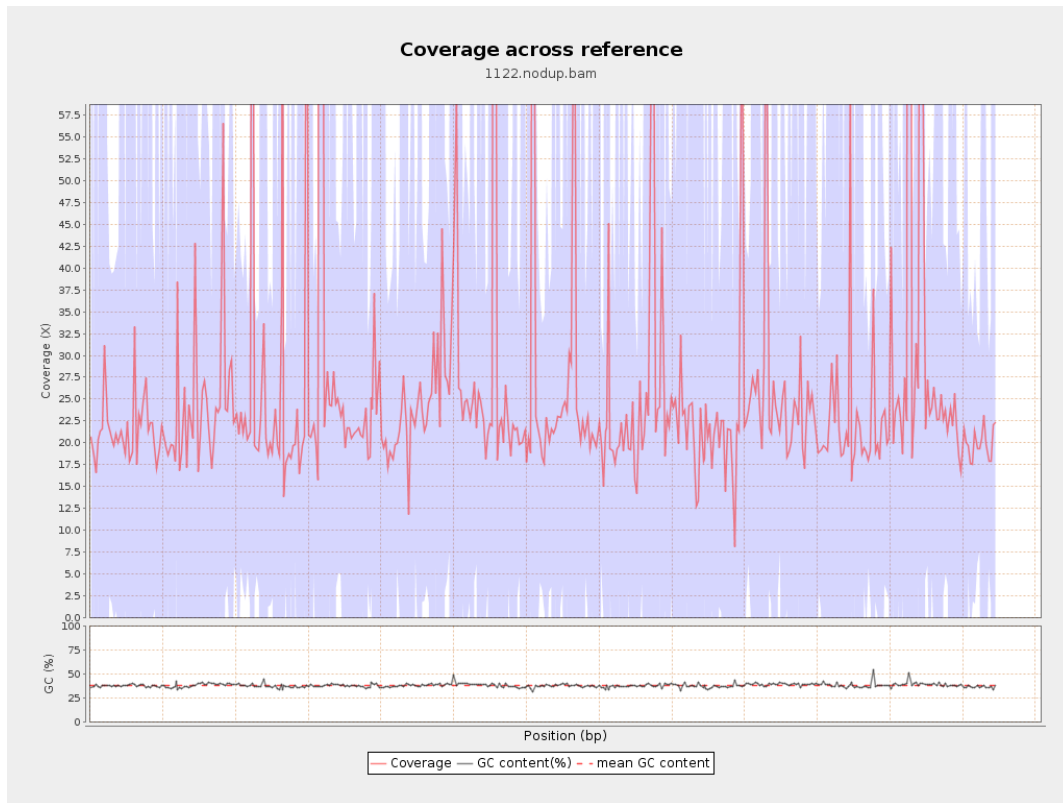
General error rate	2.57%
Mismatches	195,517,373
Insertions	6,022,675
Mapped reads with at least one insertion	8.89%
Deletions	5,664,161
Mapped reads with at least one deletion	8.34%
Homopolymer indels	57.37%

2.7. Chromosome stats

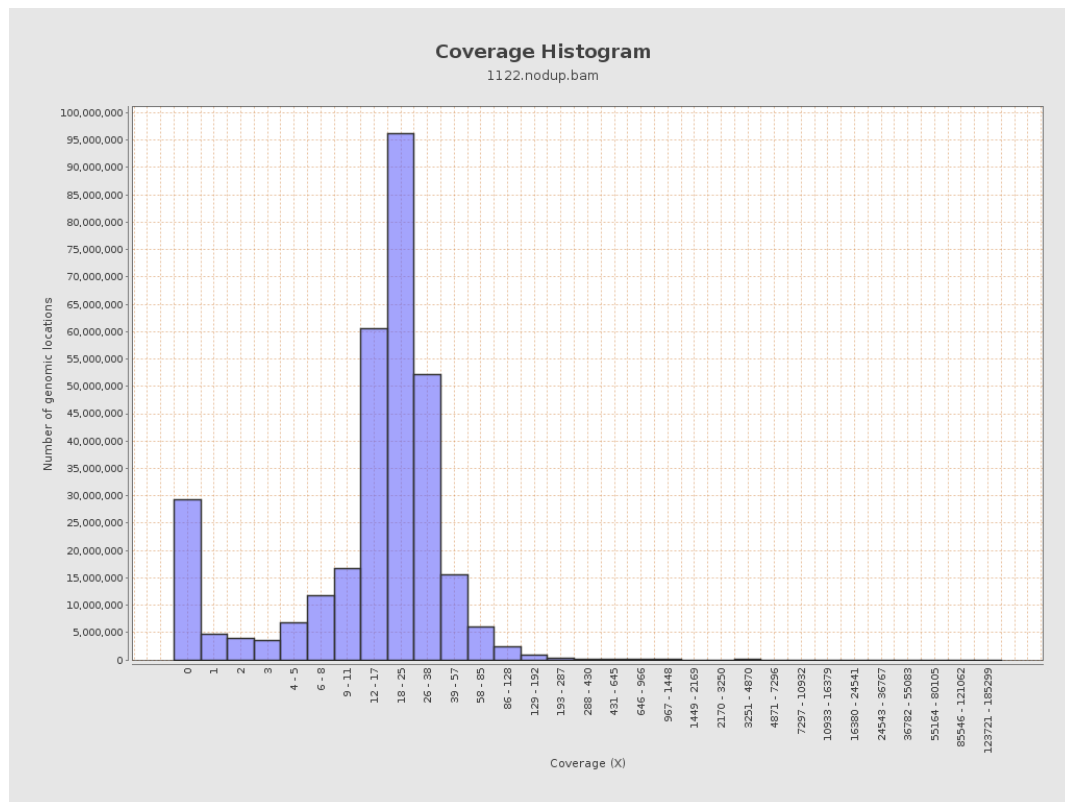
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	628042874	21.1289	103.814

LT669789.1	36598175	956819482	26.1439	260.6902
LT669790.1	30422129	1008755619	33.1586	390.0465
LT669791.1	52758100	1402662766	26.5867	281.205
LT669792.1	28376109	751369155	26.4789	270.1792
LT669793.1	33388210	821635717	24.6086	219.8876
LT669794.1	50579949	1240561211	24.5267	198.2531
LT669795.1	49795044	1465259298	29.4258	296.091

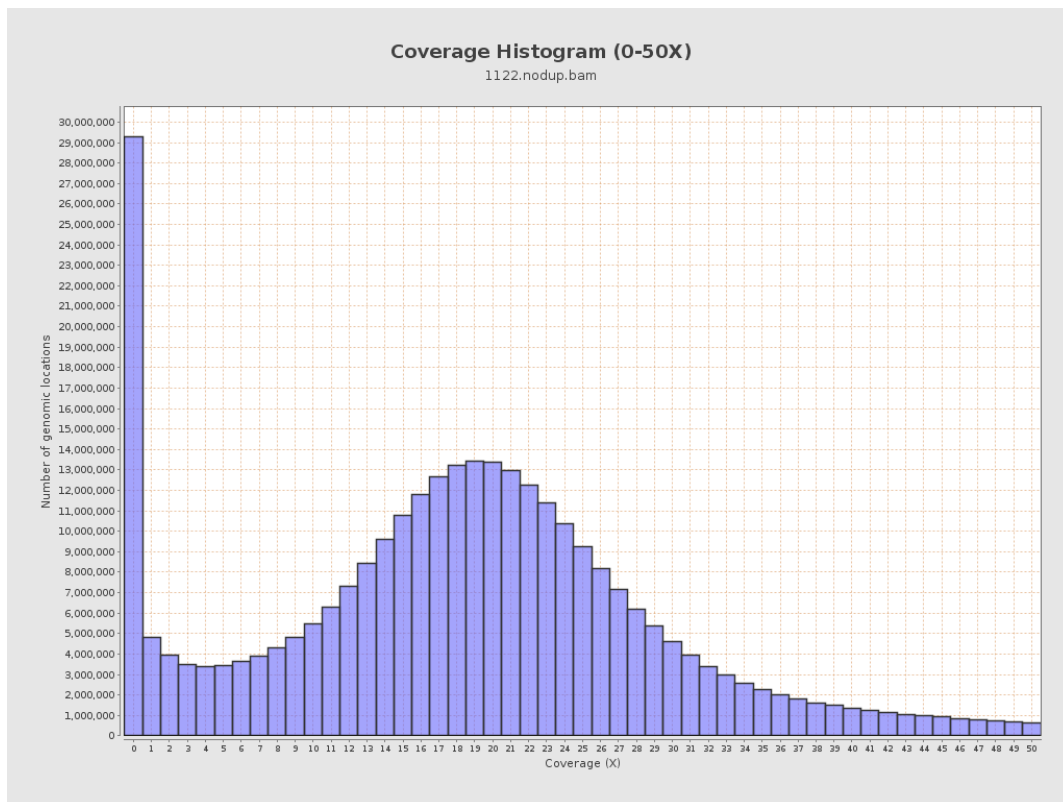
3. Results : Coverage across reference



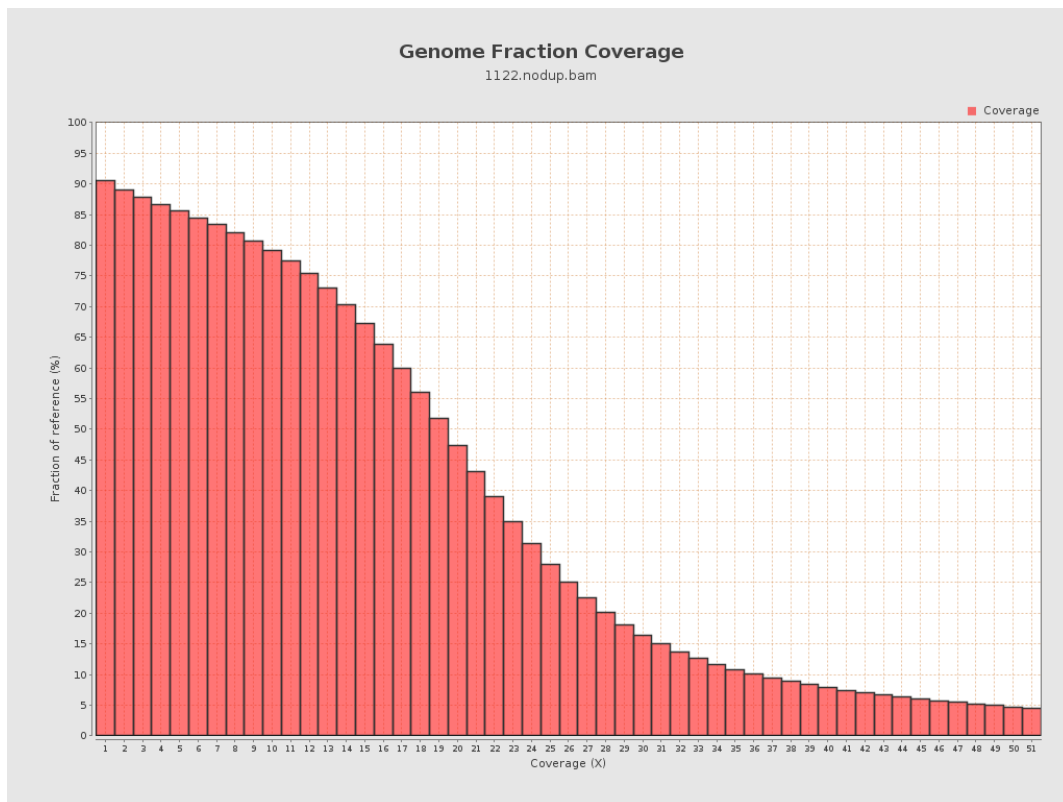
4. Results : Coverage Histogram



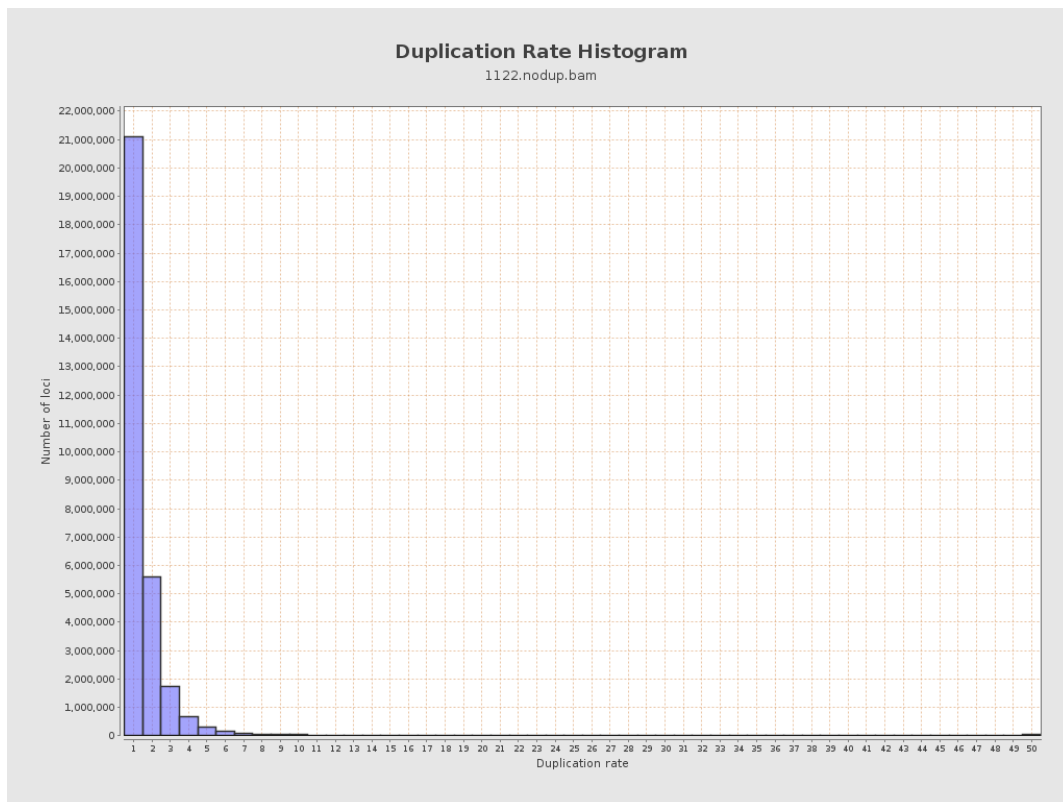
5. Results : Coverage Histogram (0-50X)



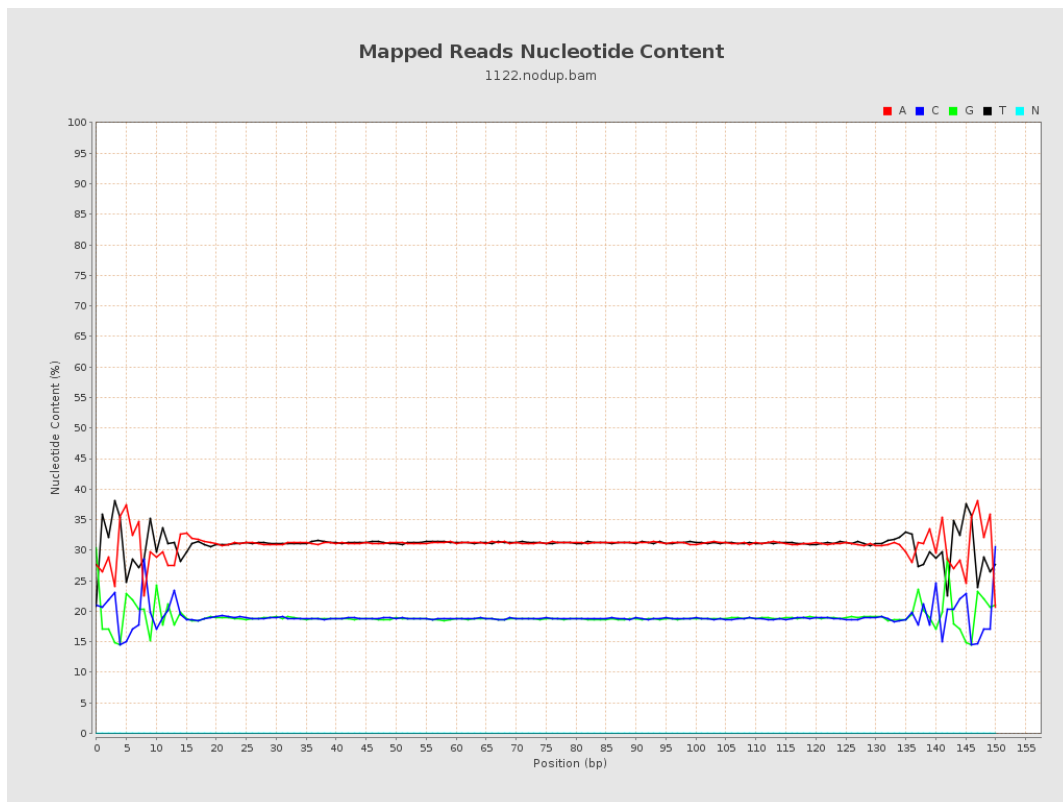
6. Results : Genome Fraction Coverage



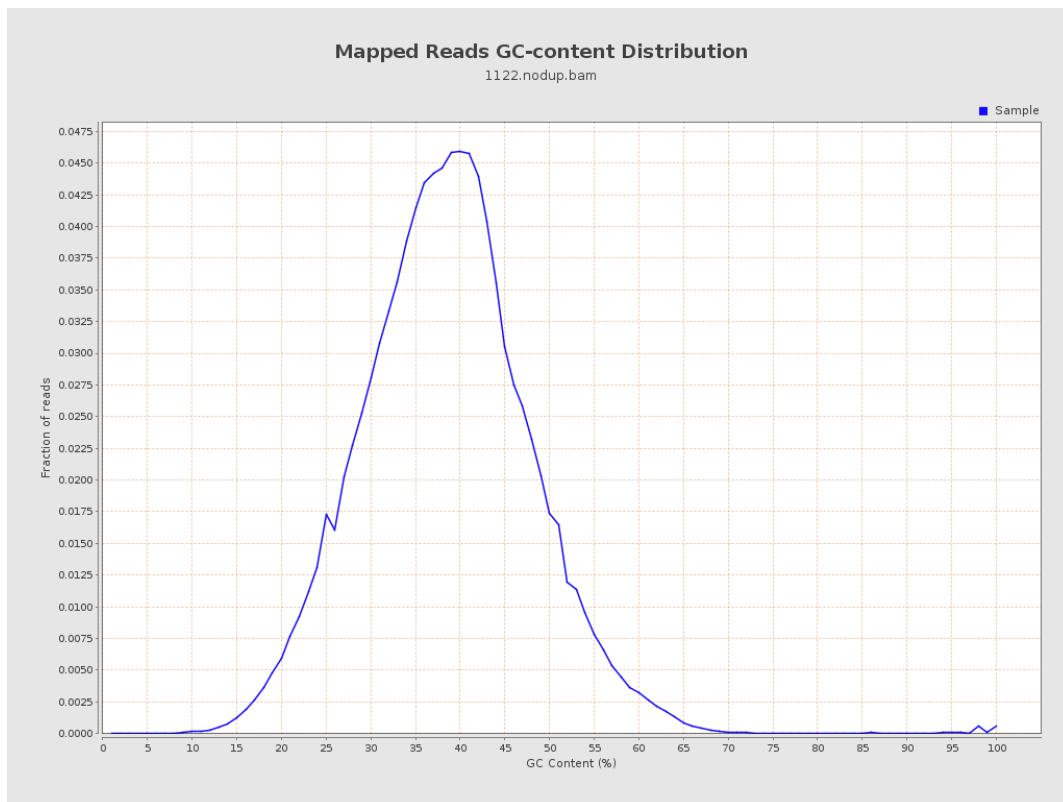
7. Results : Duplication Rate Histogram



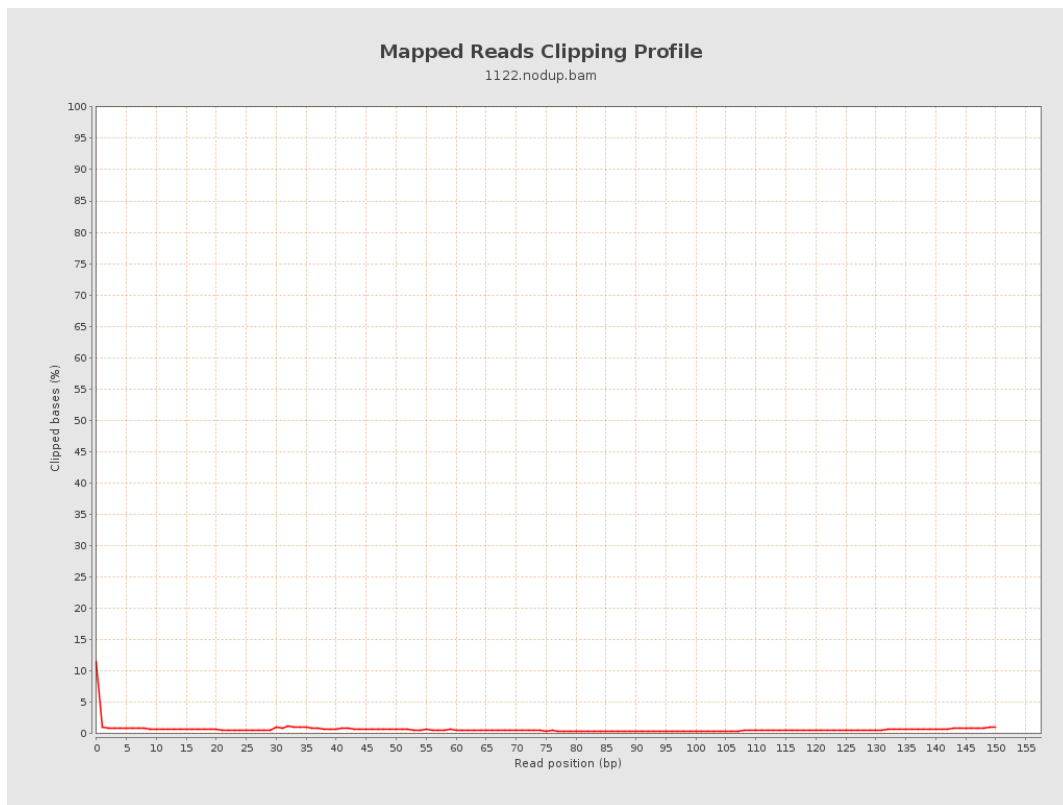
8. Results : Mapped Reads Nucleotide Content



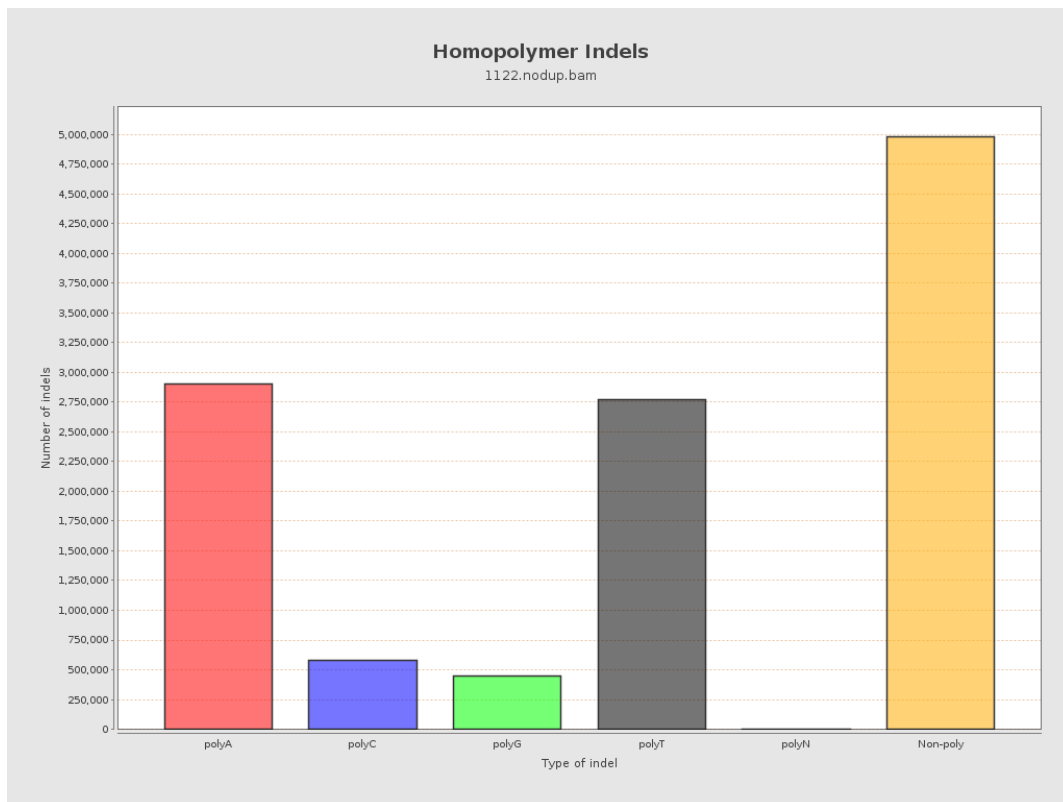
9. Results : Mapped Reads GC-content Distribution



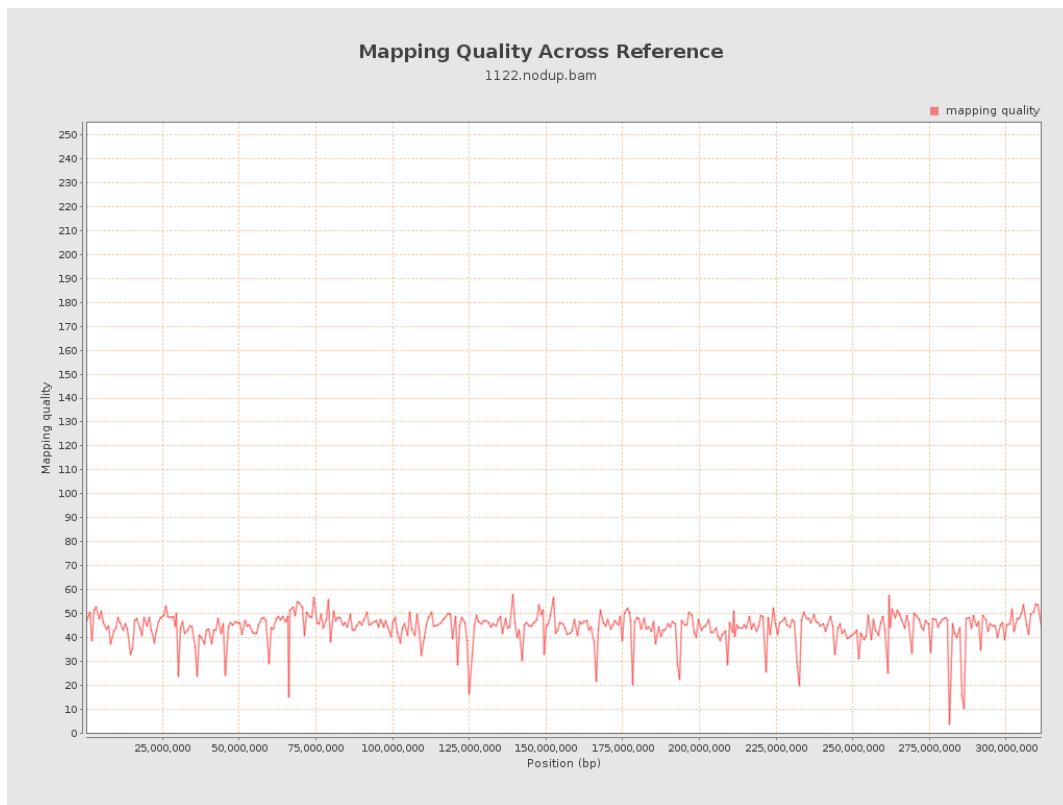
10. Results : Mapped Reads Clipping Profile



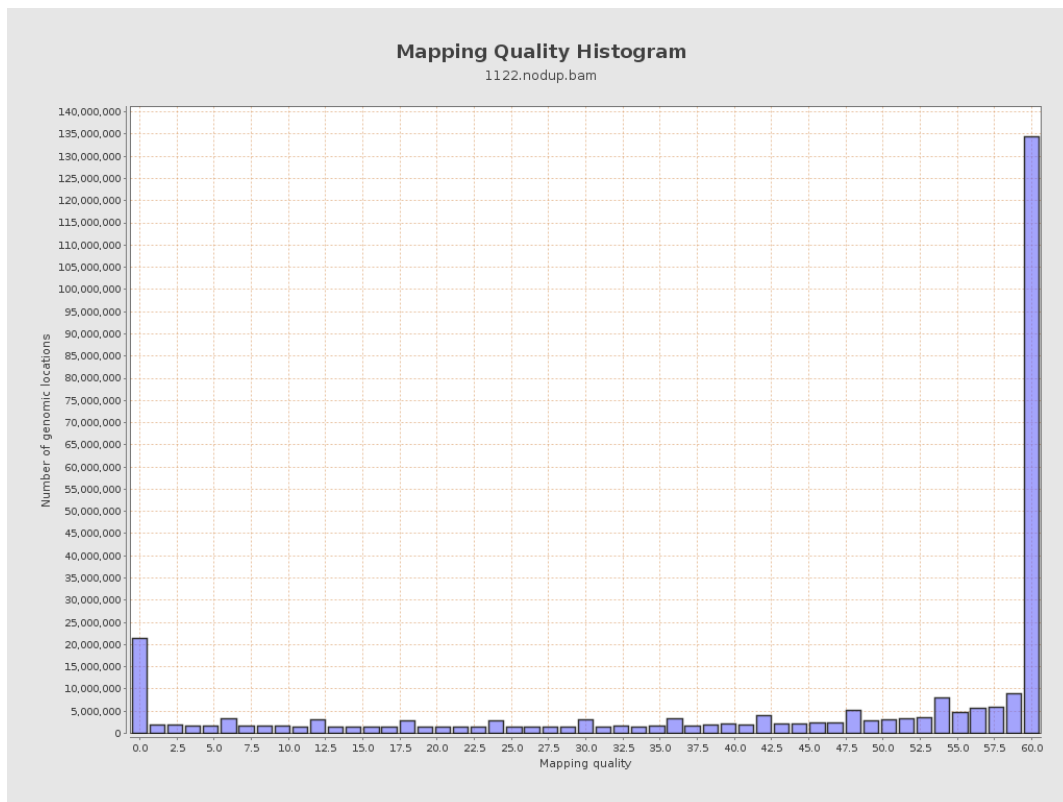
11. Results : Homopolymer Indels



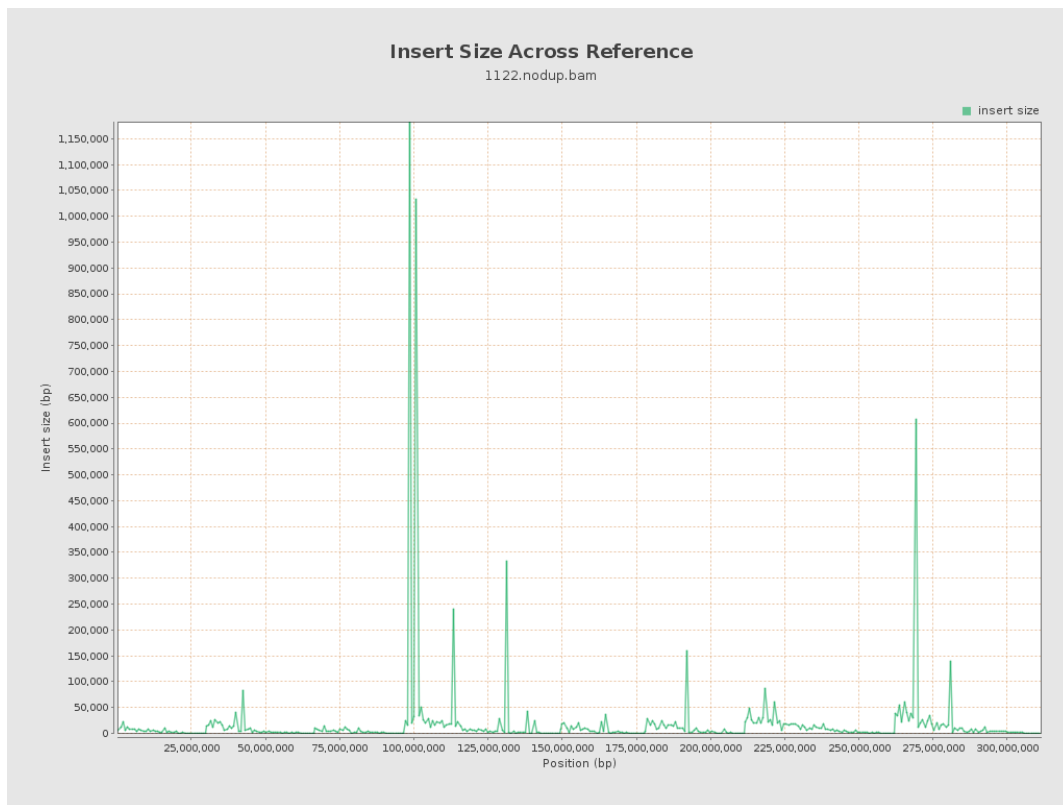
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

