

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:22:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/812
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/812.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_542/02-FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_542_S109_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_542/02-FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_542_S109_L004_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:22:44 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	40,229,899
Mapped reads	36,275,753 / 90.17%
Unmapped reads	3,954,146 / 9.83%
Mapped paired reads	36,275,753 / 90.17%
Mapped reads, first in pair	18,284,512 / 45.45%
Mapped reads, second in pair	17,991,241 / 44.72%
Mapped reads, both in pair	34,907,302 / 86.77%
Mapped reads, singletons	1,368,451 / 3.4%
Read min/max/mean length	30 / 151 / 148.32
Duplicated reads (flagged)	5,784,092 / 14.38%
Clipped reads	9,521,508 / 23.67%

2.2. ACGT Content

Number/percentage of A's	1,527,205,948 / 30.94%
Number/percentage of C's	939,995,852 / 19.04%
Number/percentage of T's	1,530,370,816 / 31.01%
Number/percentage of G's	938,291,027 / 19.01%
Number/percentage of N's	31,581 / 0%
GC Percentage	38.05%

2.3. Coverage

Mean	15.8761
Standard Deviation	158.7875

2.4. Mapping Quality

Mean Mapping Quality	44.98
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2.5. Insert size

Mean	257,479.42
Standard Deviation	2,472,206.63
P25/Median/P75	367 / 483 / 605

2.6. Mismatches and indels

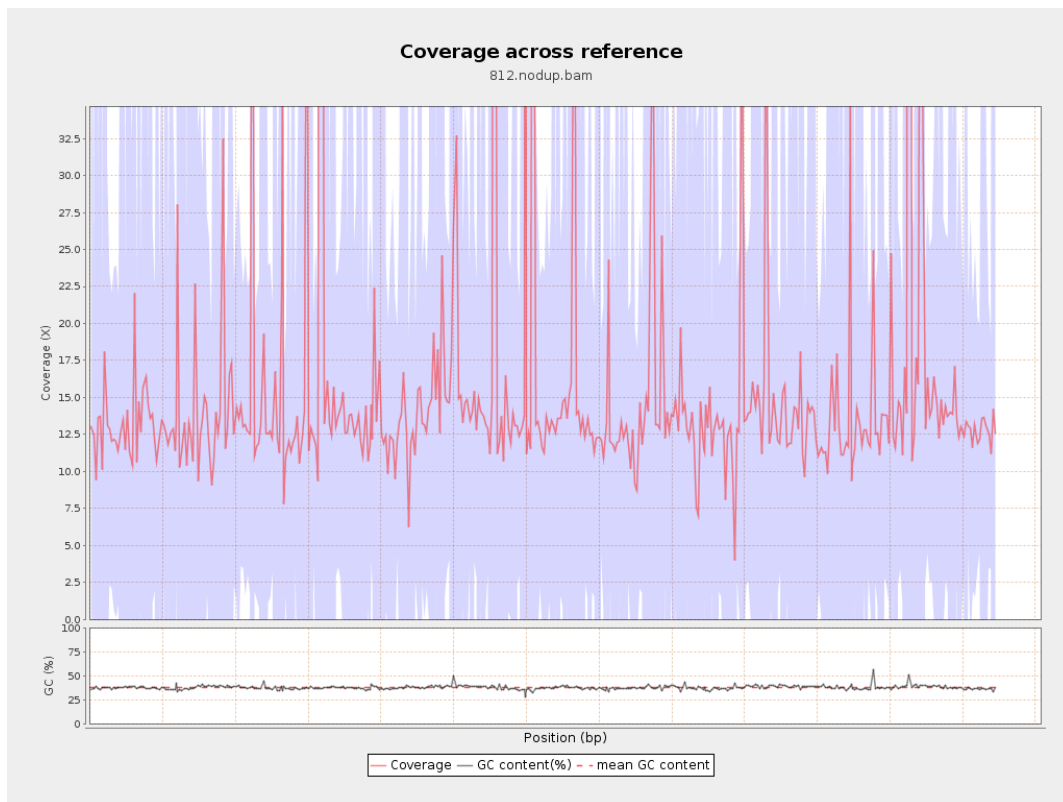
General error rate	2.75%
Mismatches	126,360,322
Insertions	3,472,564
Mapped reads with at least one insertion	8.53%
Deletions	3,214,611
Mapped reads with at least one deletion	7.9%
Homopolymer indels	57.32%

2.7. Chromosome stats

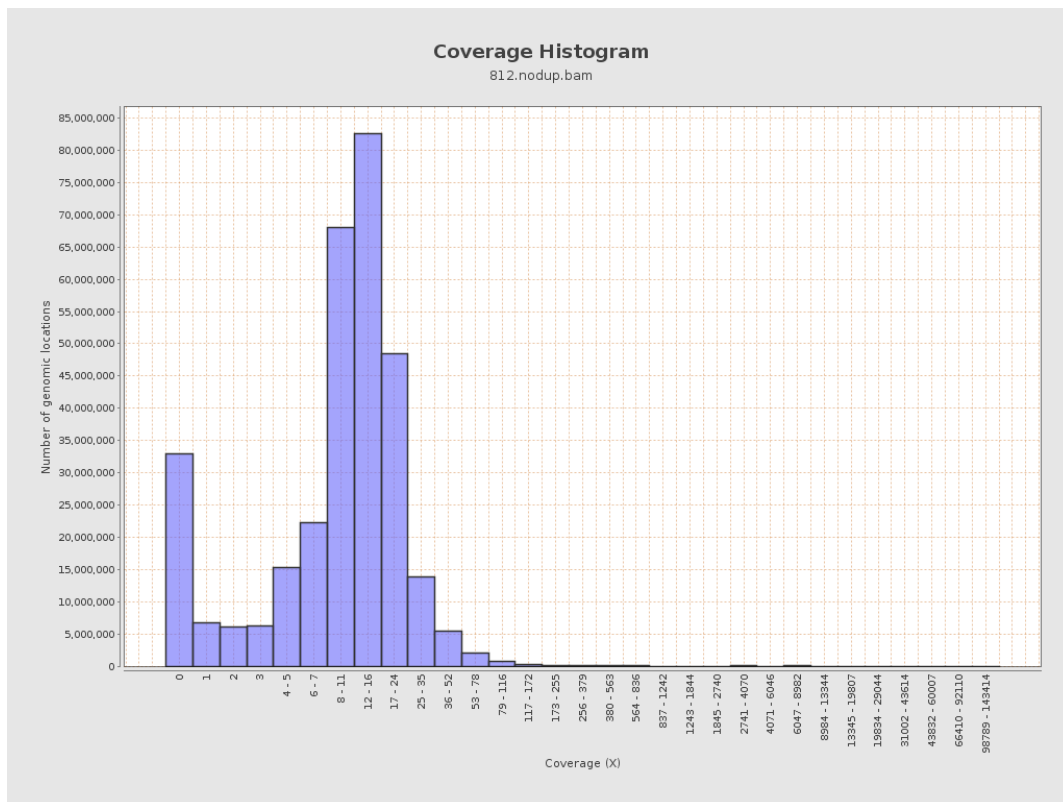
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	387496408	13.0363	61.481

LT669789.1	36598175	554887747	15.1616	153.0154
LT669790.1	30422129	600104930	19.7259	234.7807
LT669791.1	52758100	829674450	15.726	172.4878
LT669792.1	28376109	458754594	16.1669	157.2497
LT669793.1	33388210	473615800	14.1851	100.5241
LT669794.1	50579949	723800604	14.31	114.8306
LT669795.1	49795044	919324414	18.4622	197.1004

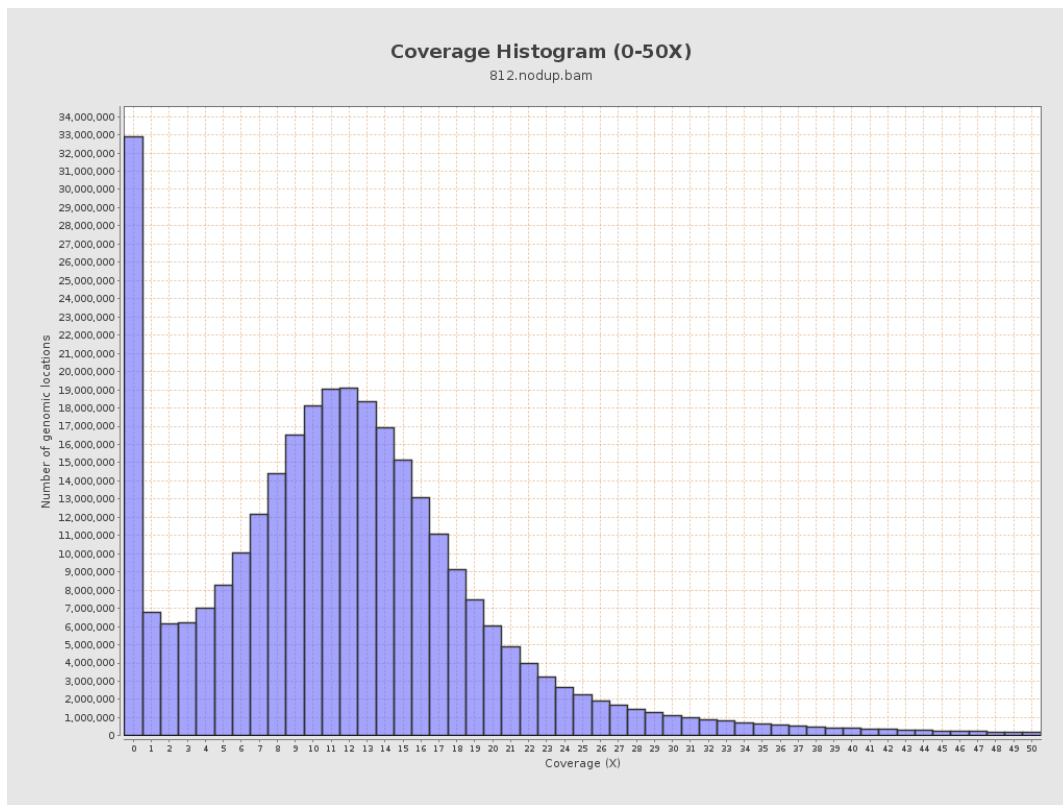
3. Results : Coverage across reference



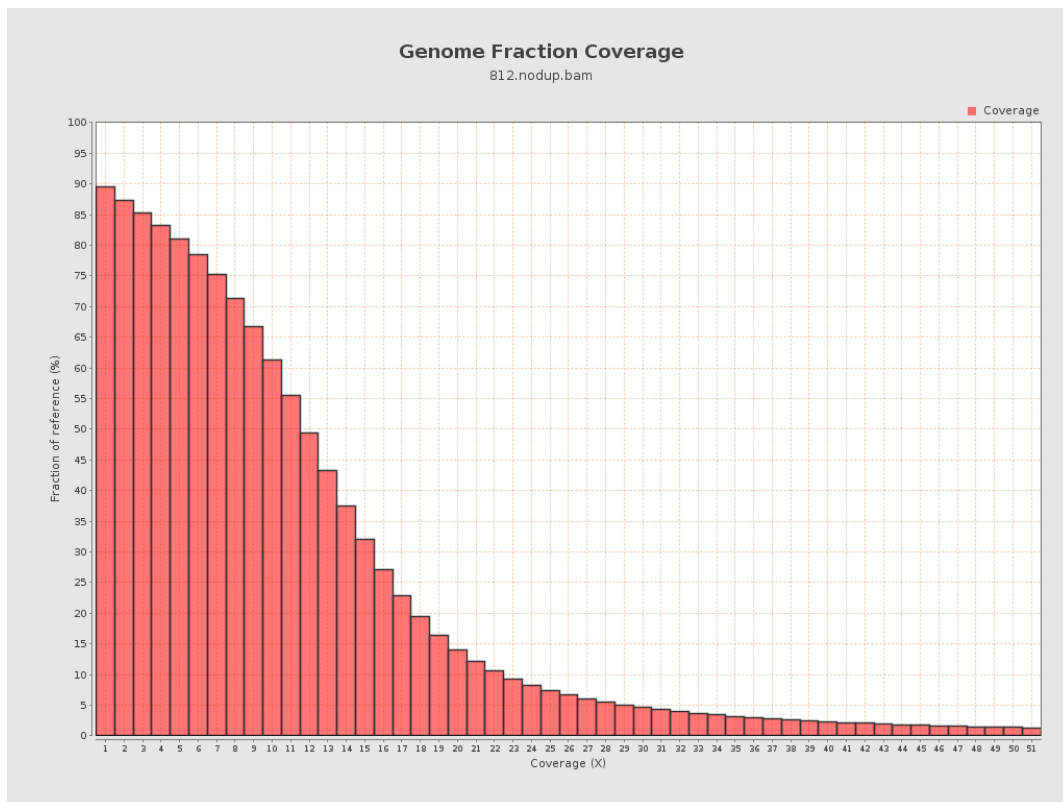
4. Results : Coverage Histogram



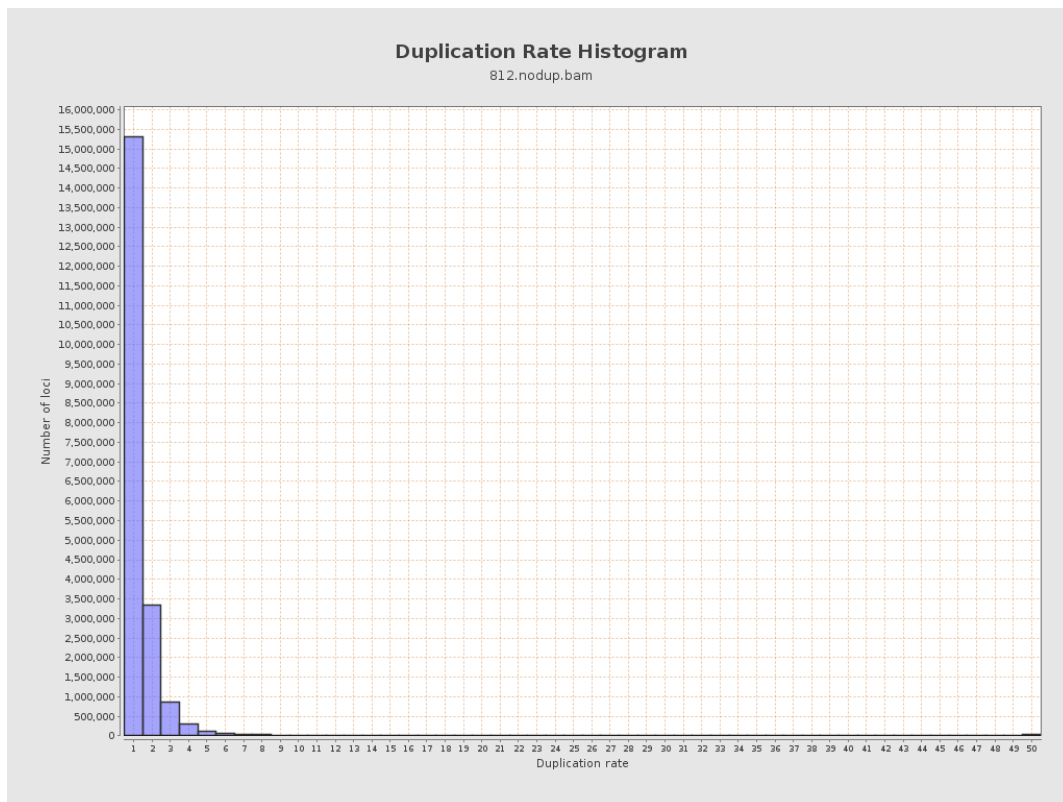
5. Results : Coverage Histogram (0-50X)



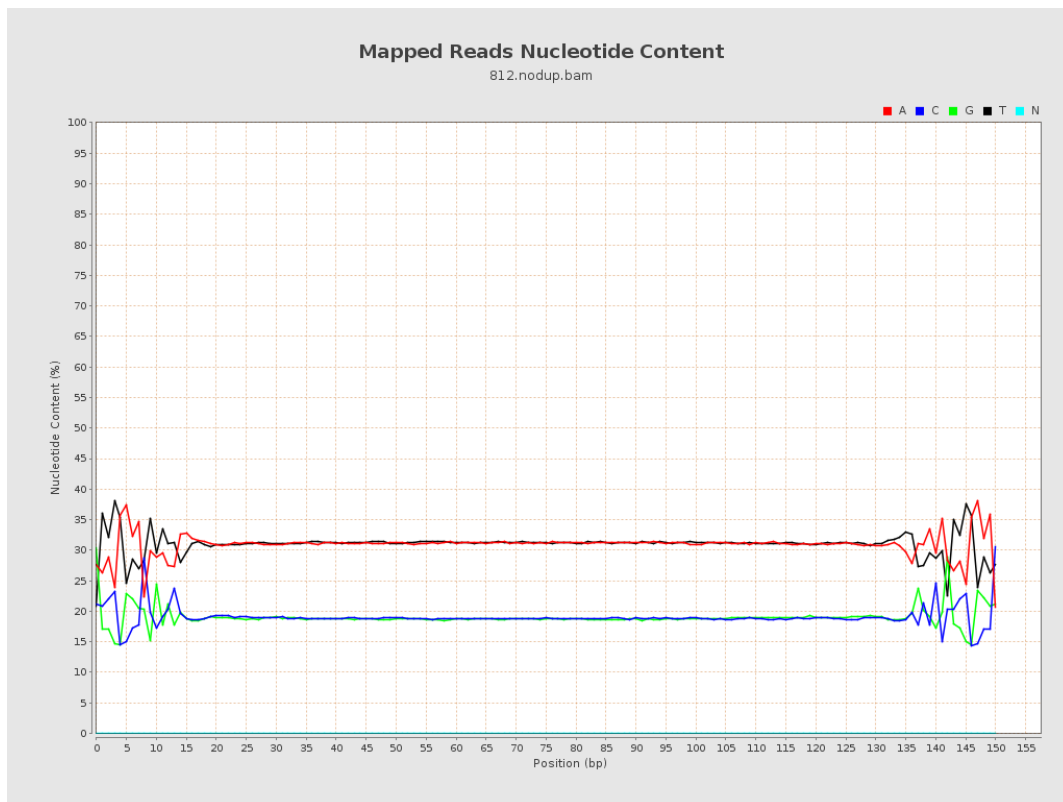
6. Results : Genome Fraction Coverage



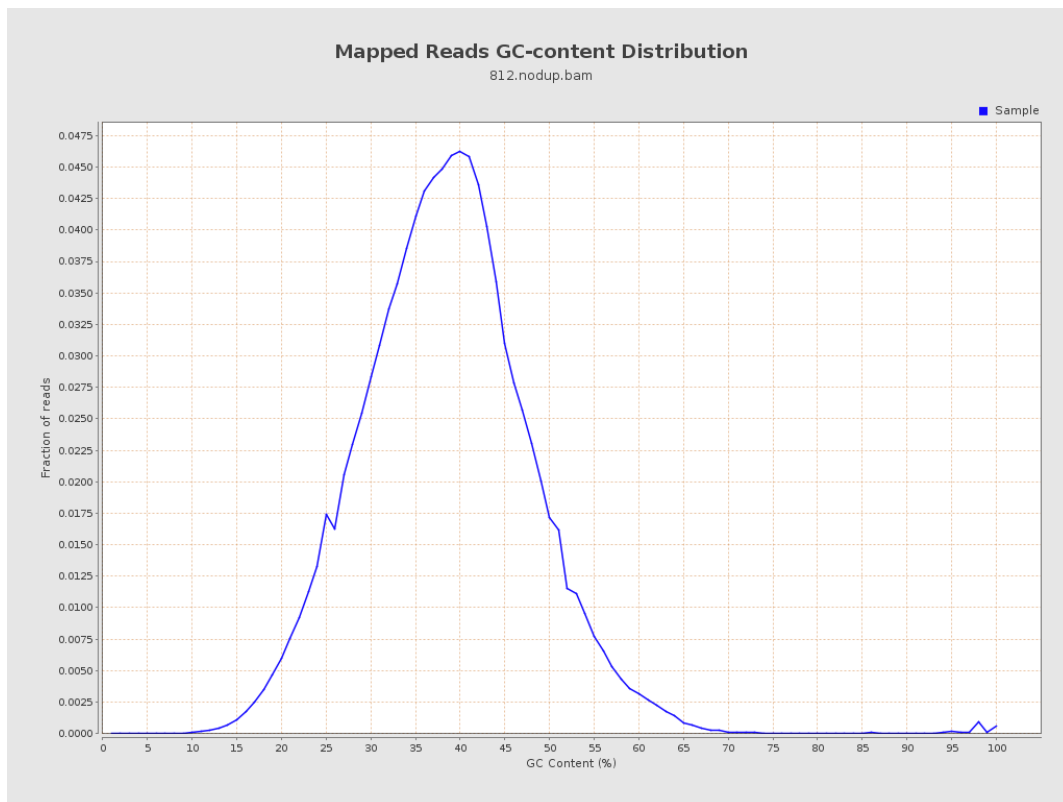
7. Results : Duplication Rate Histogram



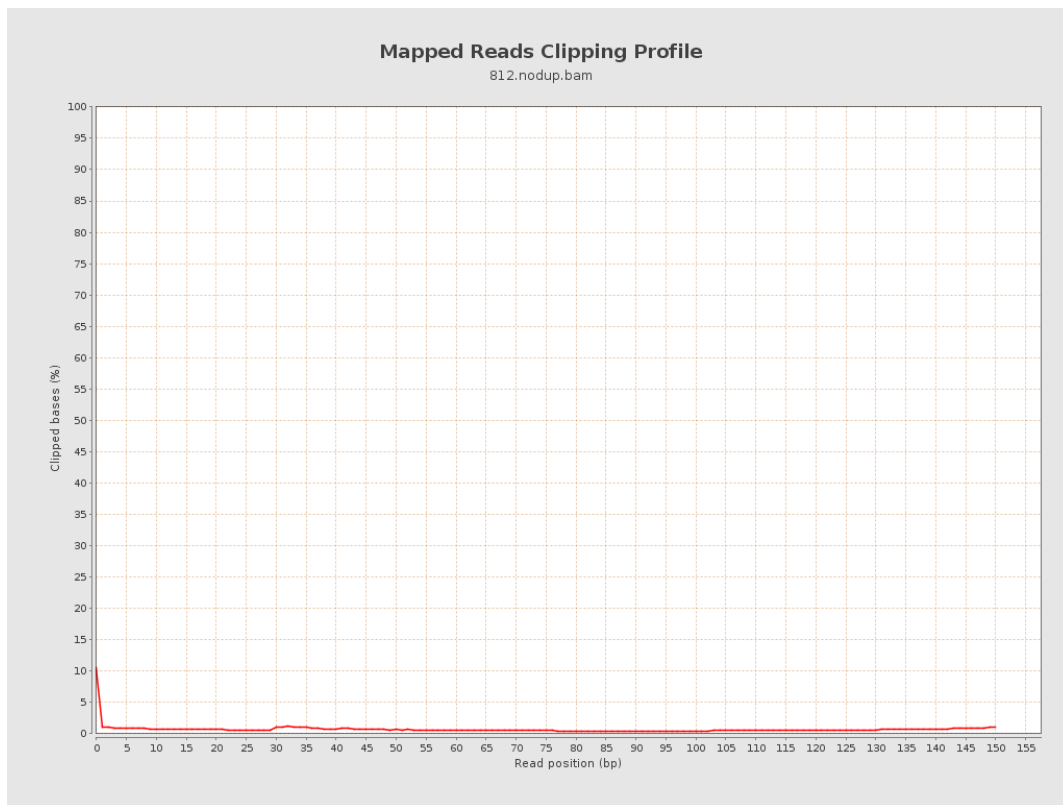
8. Results : Mapped Reads Nucleotide Content



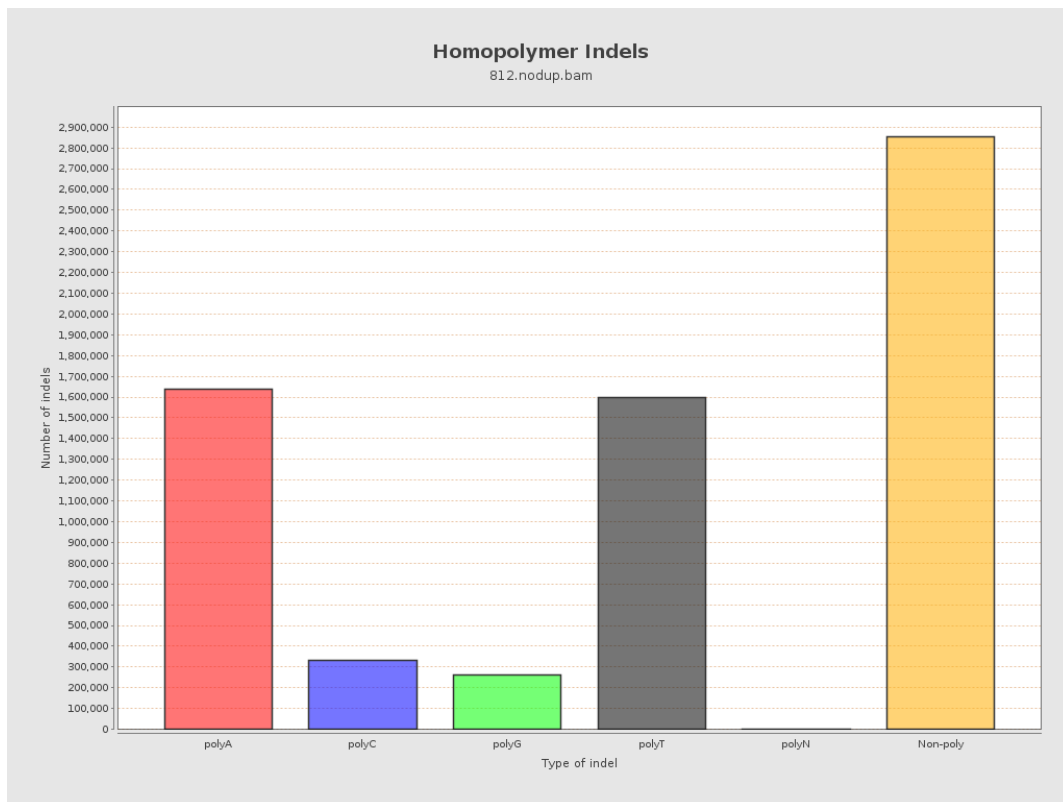
9. Results : Mapped Reads GC-content Distribution



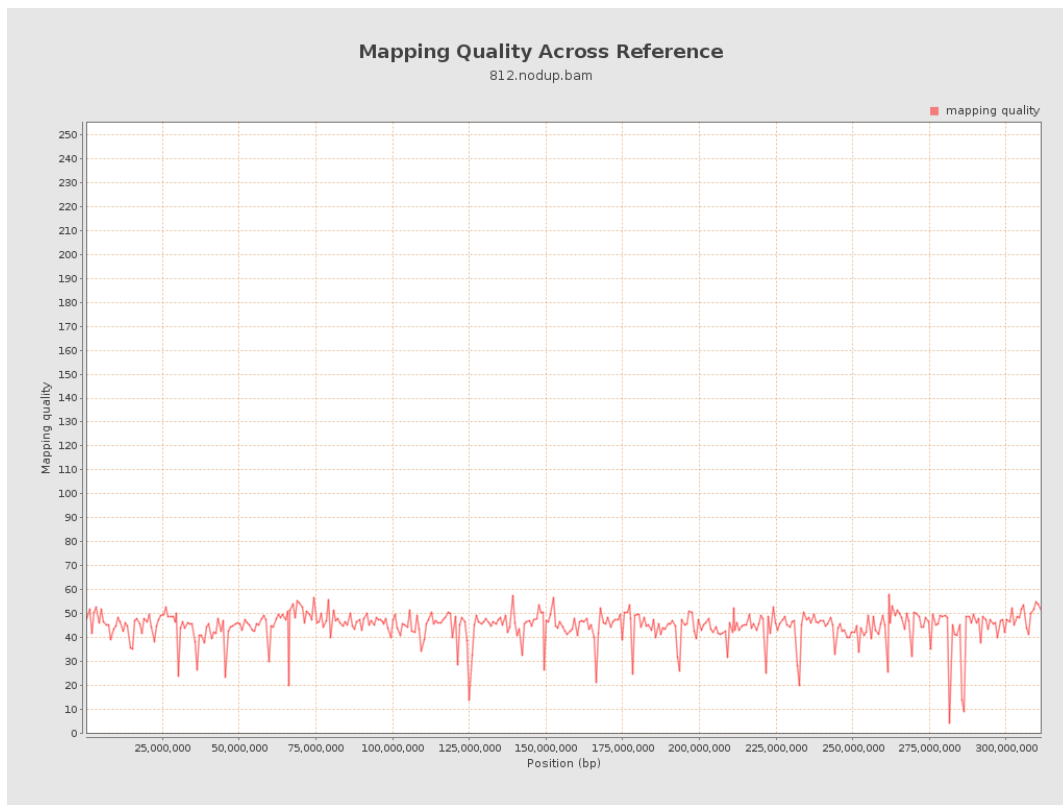
10. Results : Mapped Reads Clipping Profile



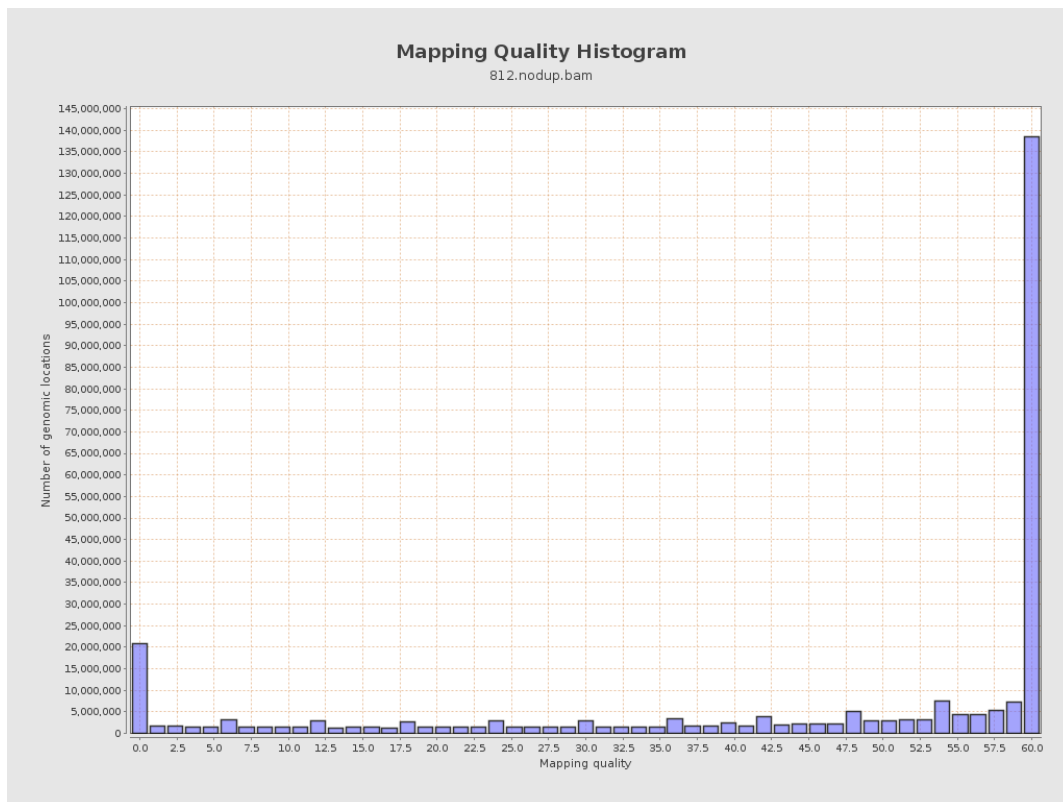
11. Results : Homopolymer Indels



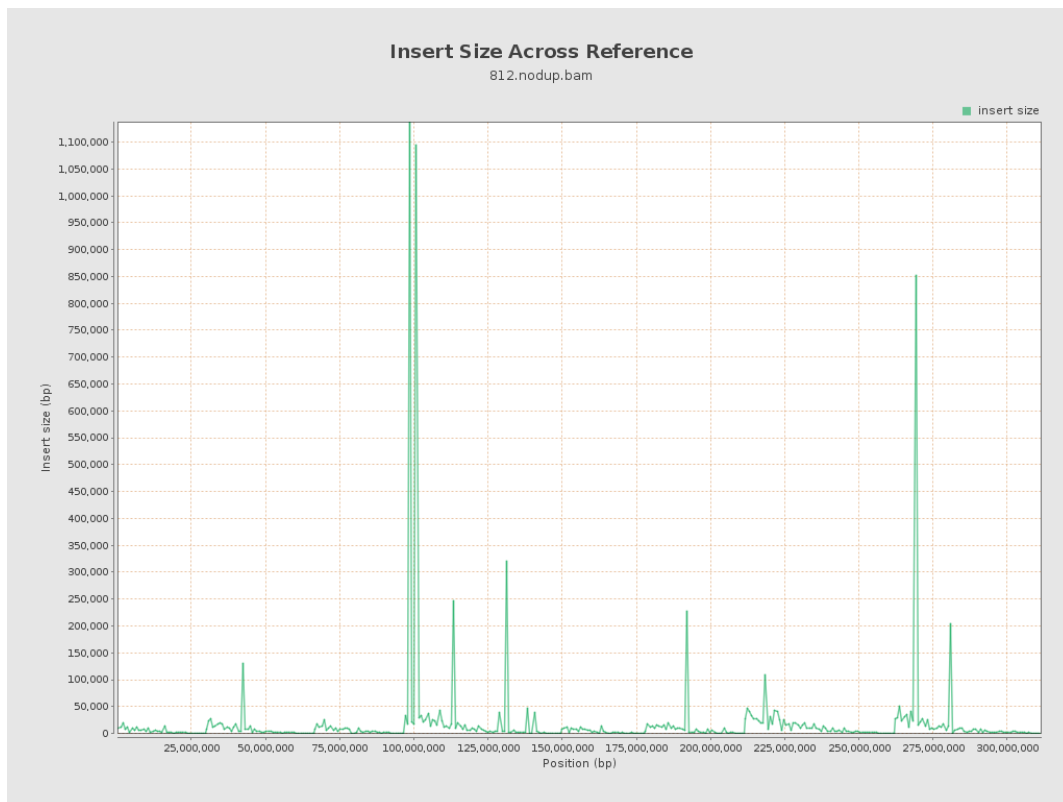
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

