Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:25:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1047
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1047 .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_289/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_289_S370_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_289/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_289_S370_L003_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:25:35 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	48,053,646
Mapped reads	44,270,835 / 92.13%
Unmapped reads	3,782,811 / 7.87%
Mapped paired reads	44,270,835 / 92.13%
Mapped reads, first in pair	22,186,838 / 46.17%
Mapped reads, second in pair	22,083,997 / 45.96%
Mapped reads, both in pair	43,039,373 / 89.57%
Mapped reads, singletons	1,231,462 / 2.56%
Read min/max/mean length	30 / 151 / 148.1
Duplicated reads (flagged)	6,188,957 / 12.88%
Clipped reads	10,314,628 / 21.46%

2.2. ACGT Content

Number/percentage of A's	1,886,337,884 / 30.96%
Number/percentage of C's	1,159,264,561 / 19.03%
Number/percentage of T's	1,888,348,530 / 31%
Number/percentage of G's	1,158,009,497 / 19.01%
Number/percentage of N's	22,193 / 0%
GC Percentage	38.04%

2.3. Coverage

Mean	19.5988
Standard Deviation	168.4429

2.4. Mapping Quality

Mean Mapping Quality	44.46

2.5. Insert size

Mean	250,022.82
Standard Deviation	2,395,882.65
P25/Median/P75	334 / 435 / 559

2.6. Mismatches and indels

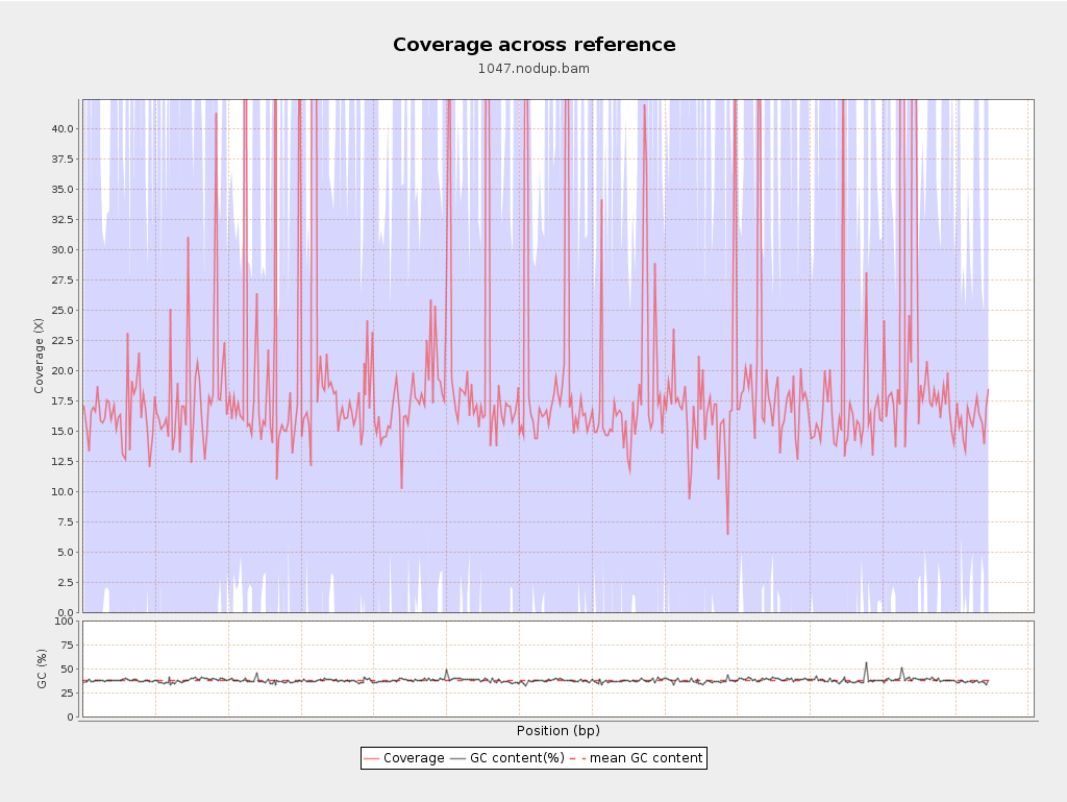
General error rate	2.33%
Mismatches	129,702,534
Insertions	4,315,004
Mapped reads with at least one insertion	8.7%
Deletions	4,212,974
Mapped reads with at least one deletion	8.43%
Homopolymer indels	57.06%

2.7. Chromosome stats

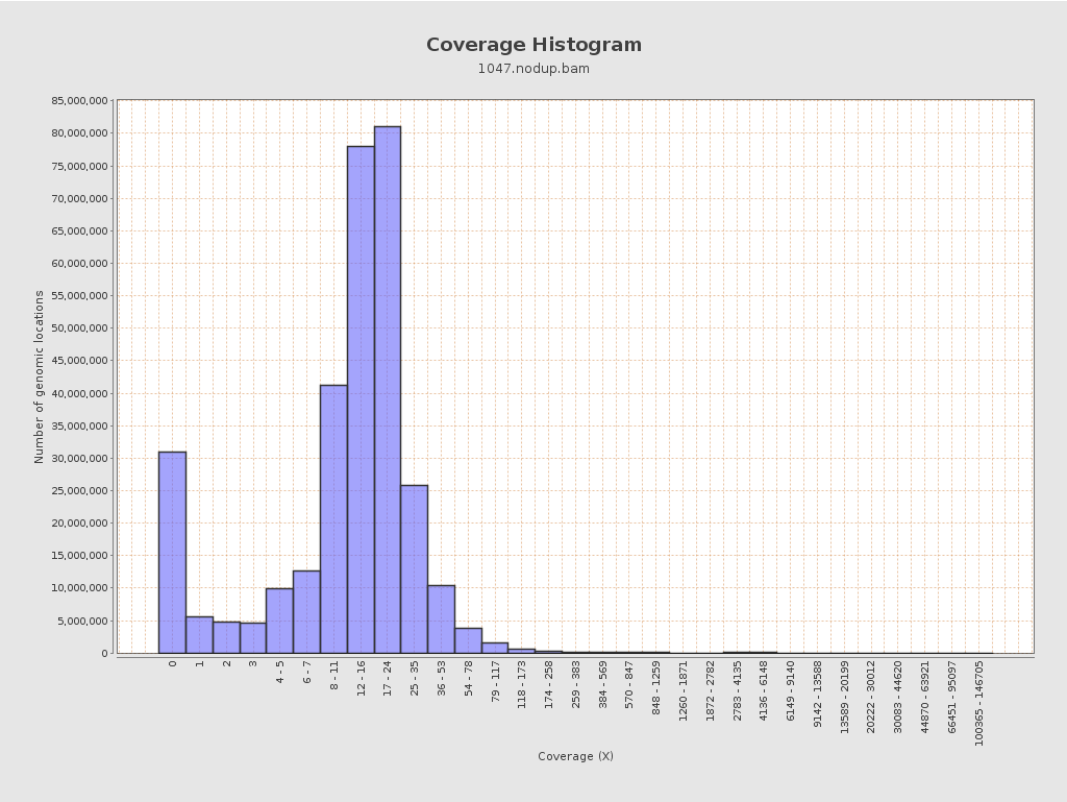
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	486496670	16.3669	60.238

LT669789.1	36598175	711120425	19.4305	165.9275
LT669790.1	30422129	711619910	23.3915	224.5582
LT669791.1	52758100	1019546832	19.3249	167.4678
LT669792.1	28376109	560630827	19.7571	191.4197
LT669793.1	33388210	592175126	17.7361	88.3
LT669794.1	50579949	926714914	18.3218	133.151
LT669795.1	49795044	1099515725	22.0808	224.7368

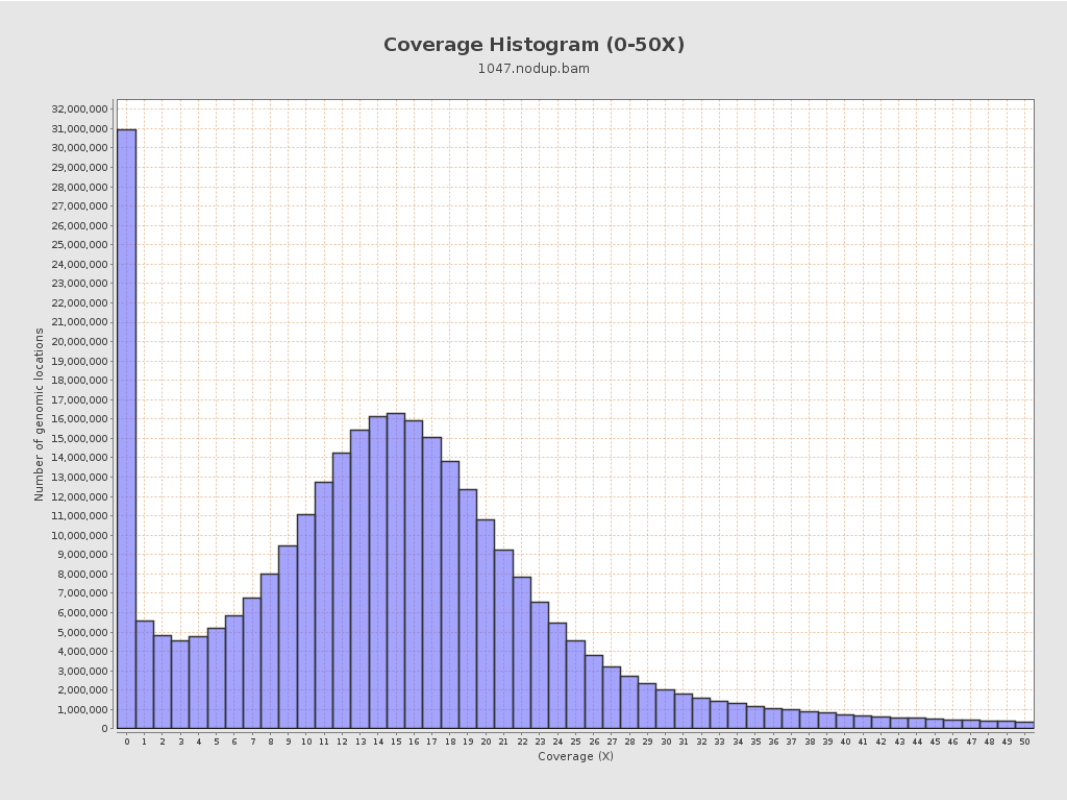
3. Results : Coverage across reference



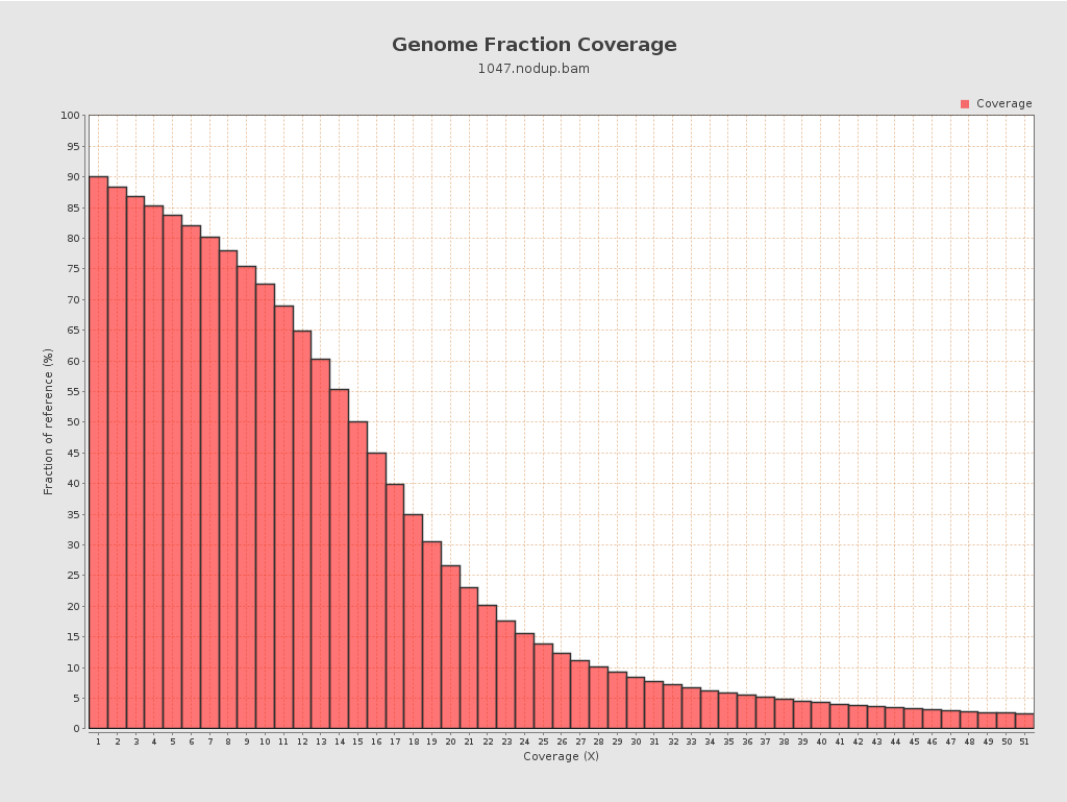
4. Results : Coverage Histogram



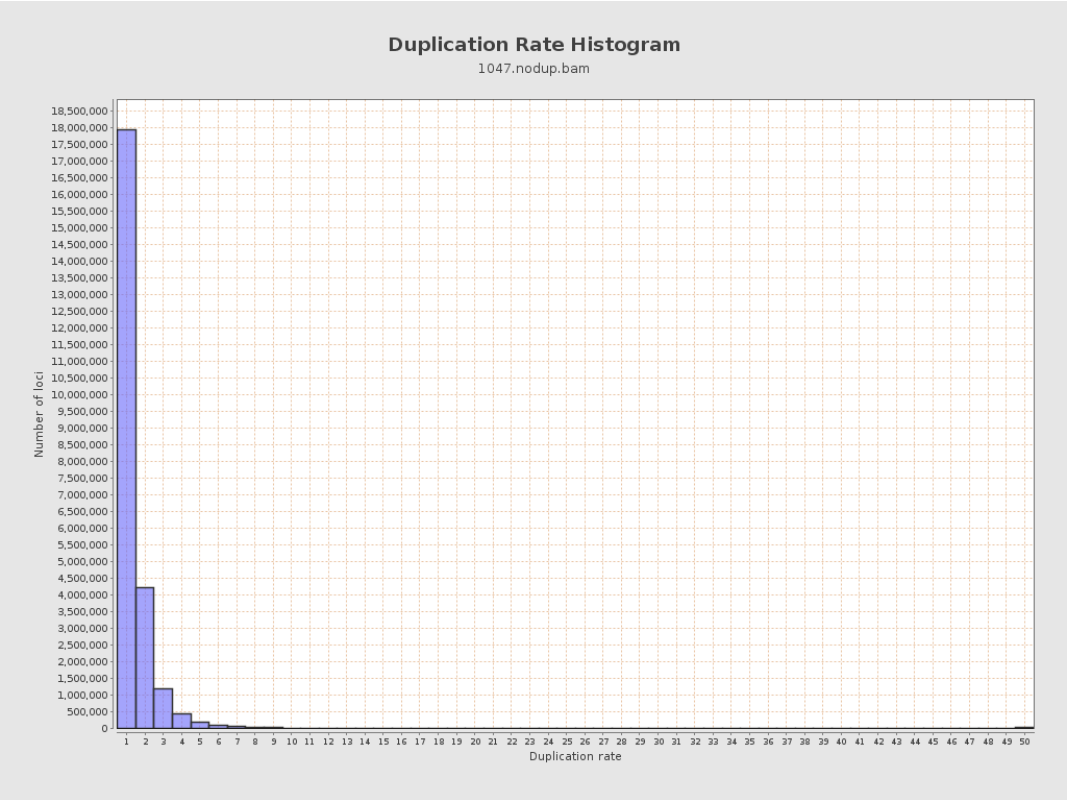
5. Results : Coverage Histogram (0-50X)



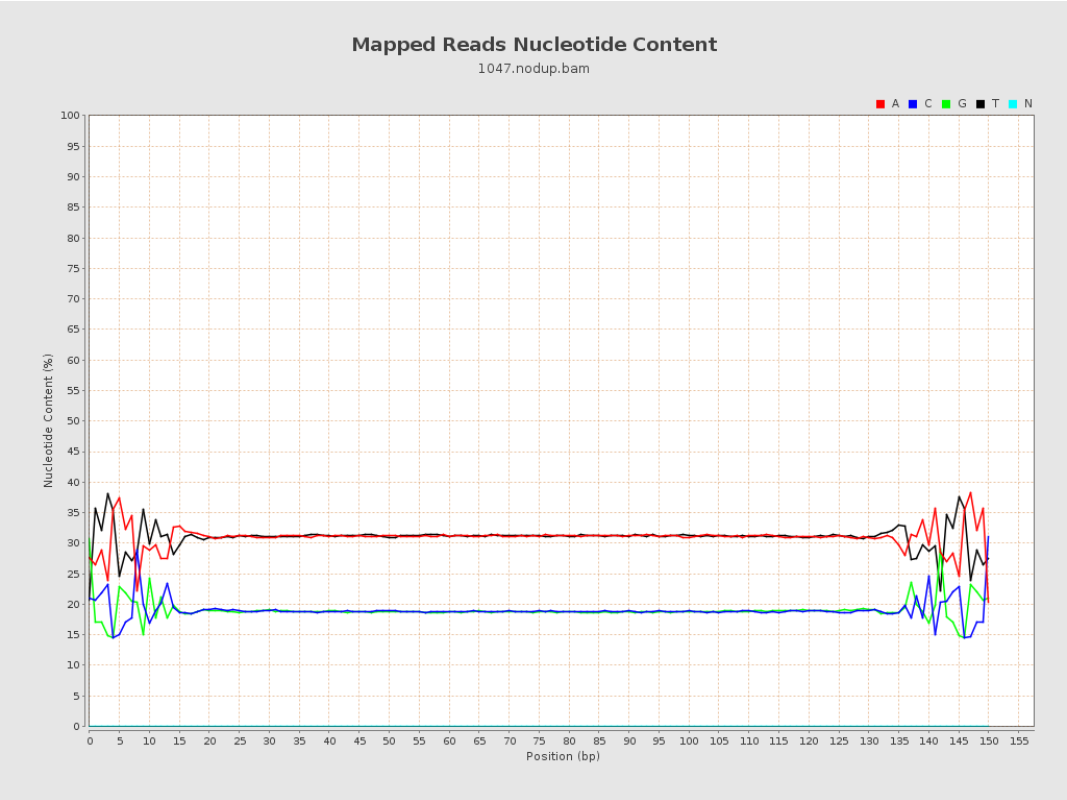
6. Results : Genome Fraction Coverage



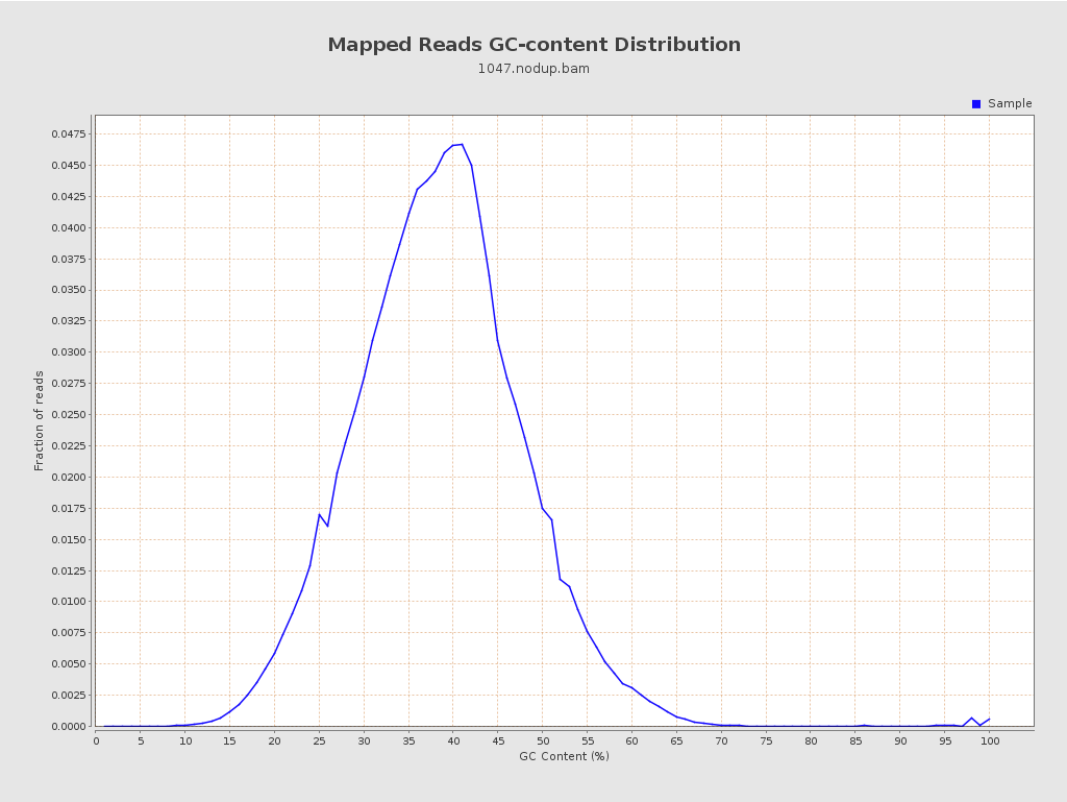
7. Results : Duplication Rate Histogram



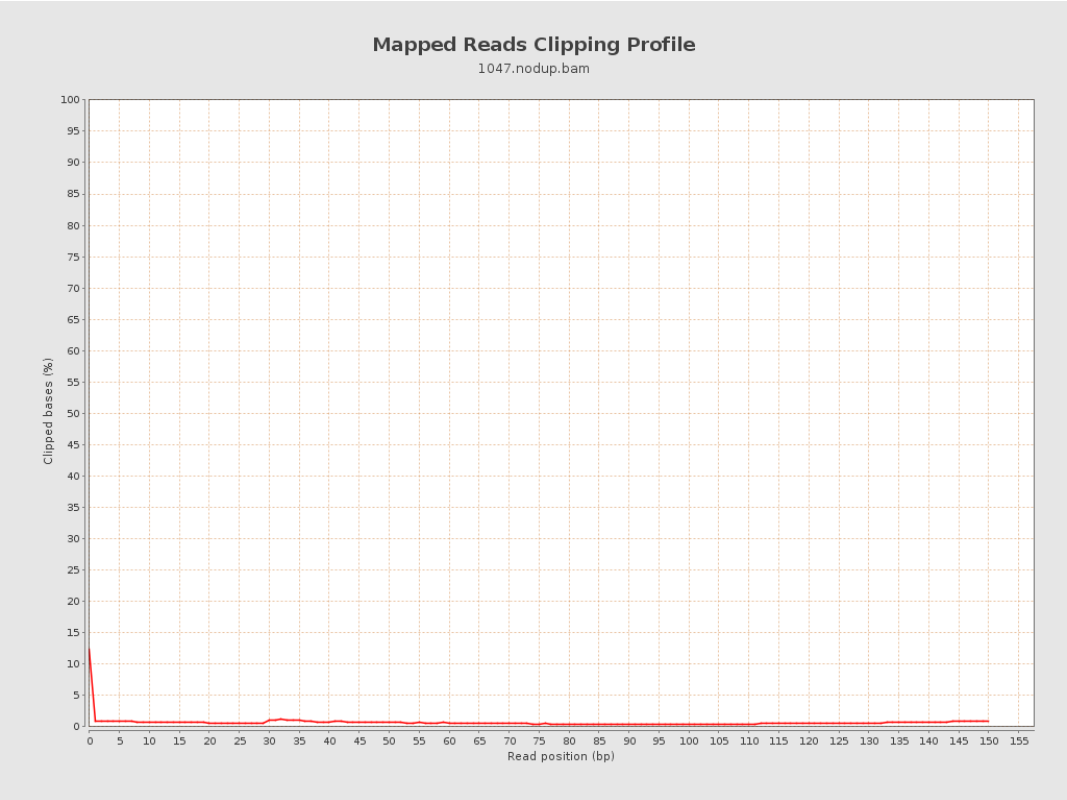
8. Results : Mapped Reads Nucleotide Content



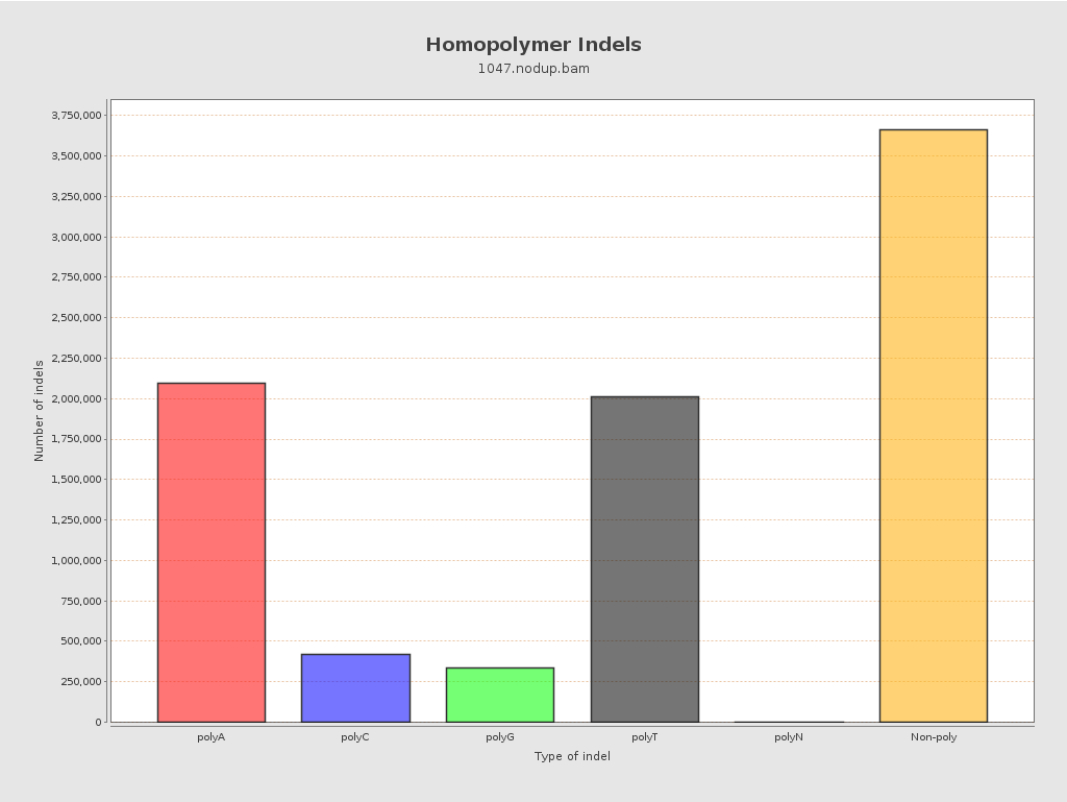
9. Results : Mapped Reads GC-content Distribution



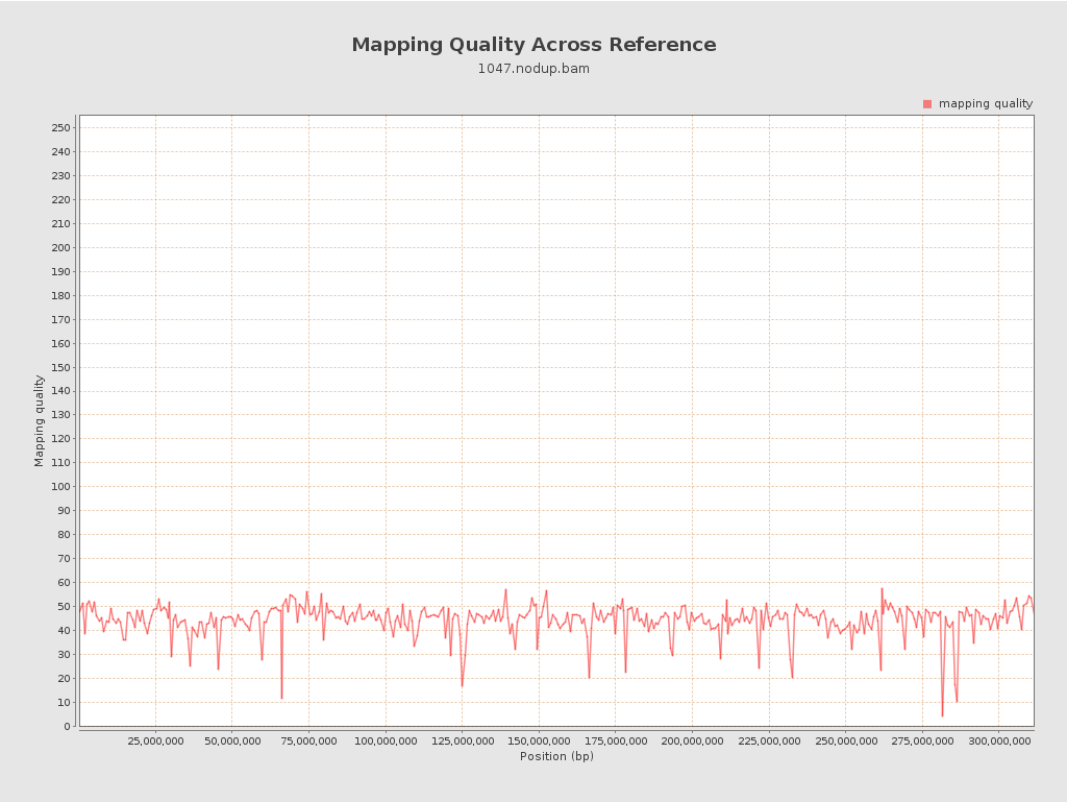
10. Results : Mapped Reads Clipping Profile



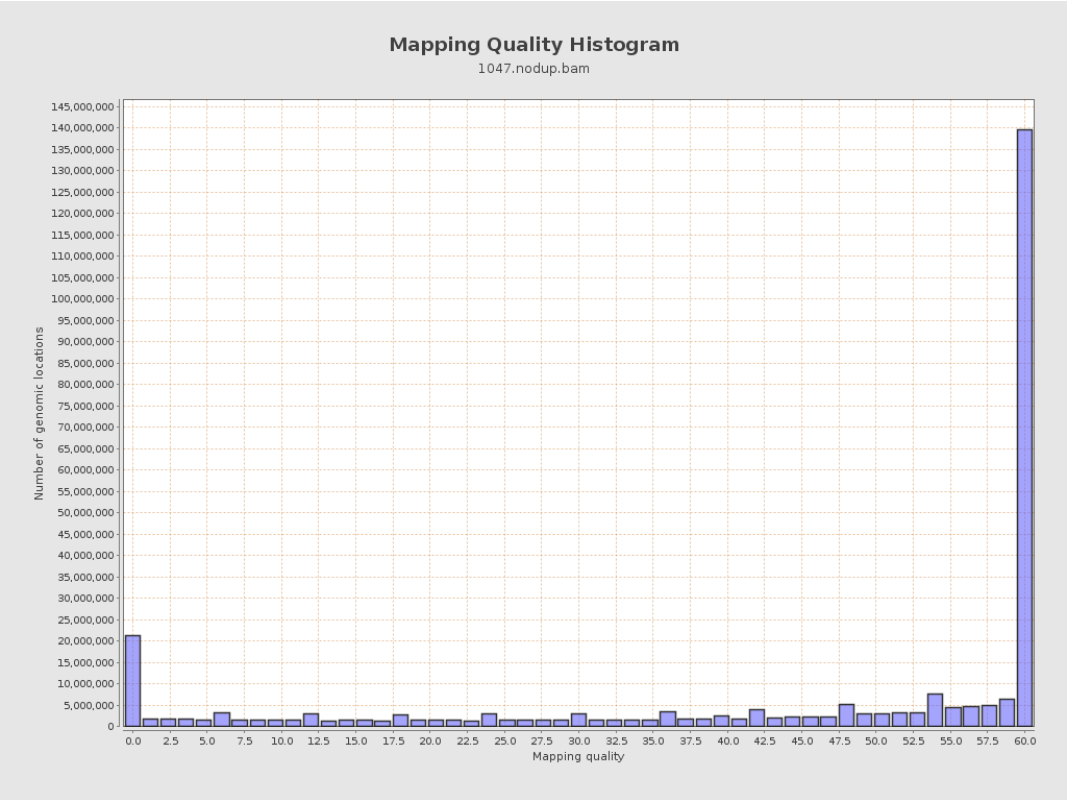
11. Results : Homopolymer Indels



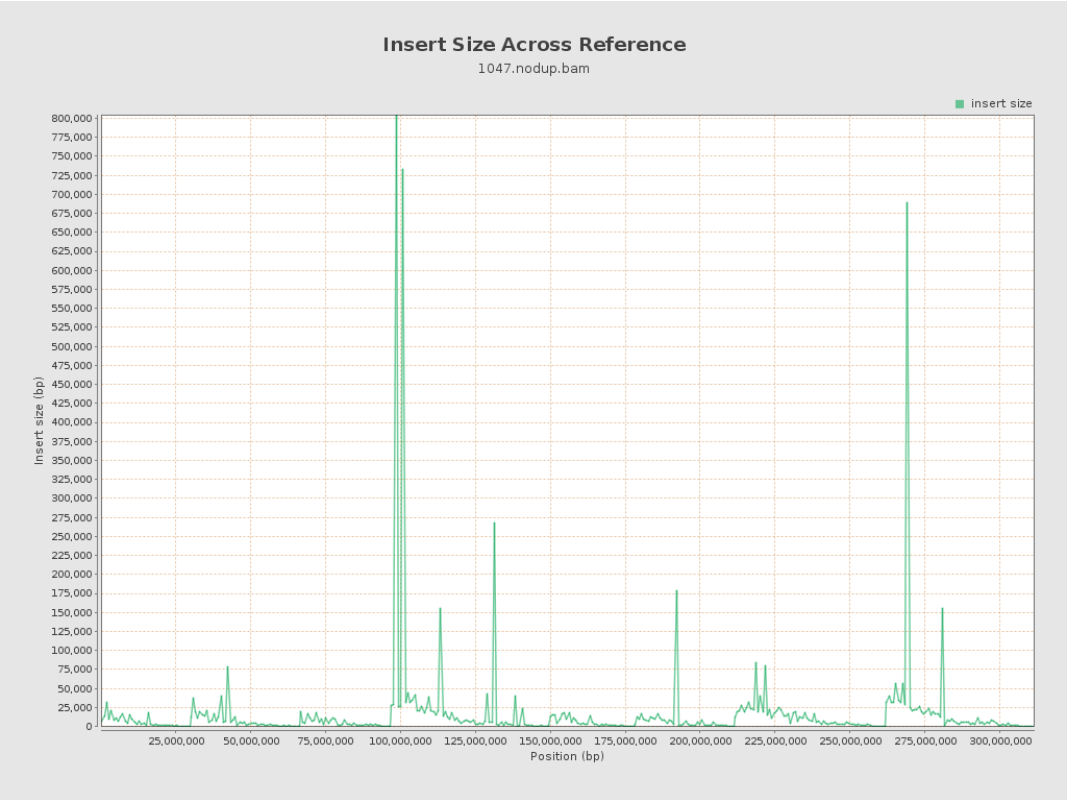
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram