Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:46:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/949.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/949.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_258/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_258_S339_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_258/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_258_S339_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:46:52 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	108,507,125
Mapped reads	103,229,826 / 95.14%
Unmapped reads	5,277,299 / 4.86%
Mapped paired reads	103,229,826 / 95.14%
Mapped reads, first in pair	51,716,793 / 47.66%
Mapped reads, second in pair	51,513,033 / 47.47%
Mapped reads, both in pair	101,621,093 / 93.65%
Mapped reads, singletons	1,608,733 / 1.48%
Read min/max/mean length	30 / 151 / 147.99
Duplicated reads (flagged)	15,725,069 / 14.49%
Clipped reads	23,197,137 / 21.38%

2.2. ACGT Content

Number/percentage of A's	4,410,581,846 / 30.79%
Number/percentage of C's	2,751,142,910 / 19.21%
Number/percentage of T's	4,416,219,922 / 30.83%
Number/percentage of G's	2,746,154,228 / 19.17%
Number/percentage of N's	54,192 / 0%
GC Percentage	38.38%

2.3. Coverage

Mean	46.0822
Standard Deviation	365.7653

2.4. Mapping Quality

Mean Mapping Quality	44.07

2.5. Insert size

Mean	213,811.57
Standard Deviation	2,182,553.85
P25/Median/P75	305 / 403 / 531

2.6. Mismatches and indels

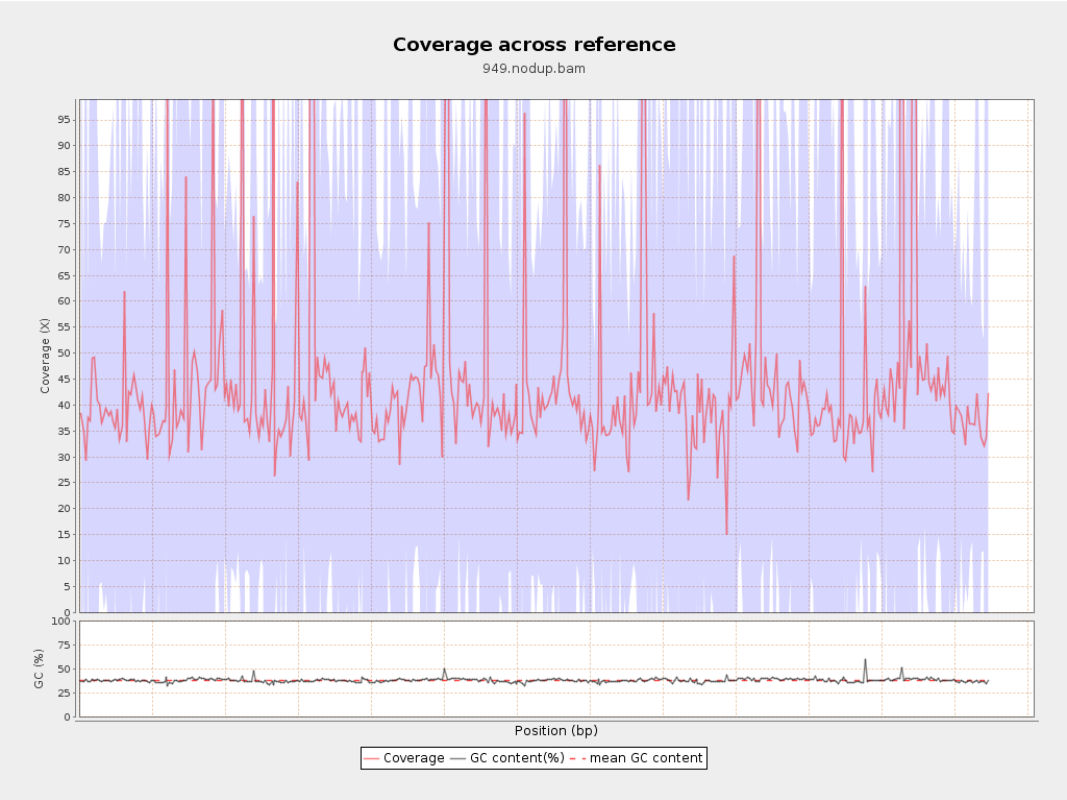
General error rate	2.27%
Mismatches	299,208,507
Insertions	9,333,435
Mapped reads with at least one insertion	8.15%
Deletions	9,786,930
Mapped reads with at least one deletion	8.39%
Homopolymer indels	55.84%

2.7. Chromosome stats

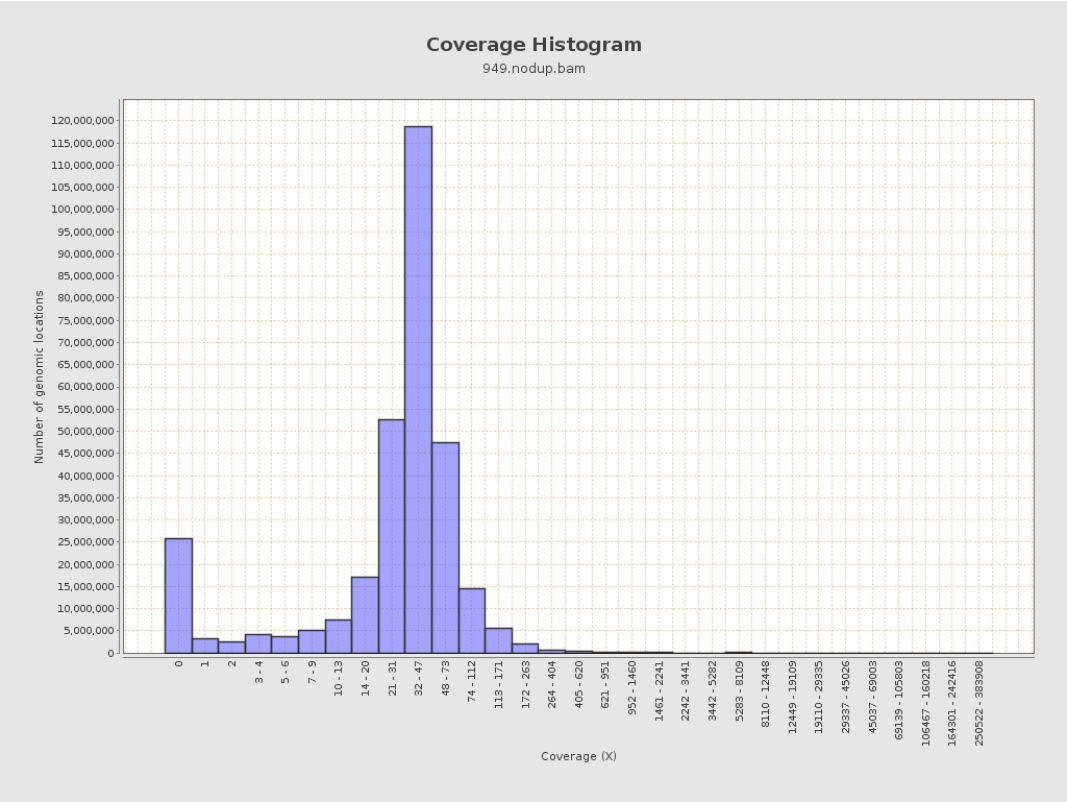
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	1155257438	38.8657	122.5233

LT669789.1	36598175	1741972888	47.5973	411.3479
LT669790.1	30422129	1448789556	47.6229	282.7632
LT669791.1	52758100	2359562085	44.7242	321.4872
LT669792.1	28376109	1265020694	44.5805	350.5453
LT669793.1	33388210	1453311759	43.5277	252.2139
LT669794.1	50579949	2222427395	43.9389	344.7246
LT669795.1	49795044	2714797756	54.5194	558.6659

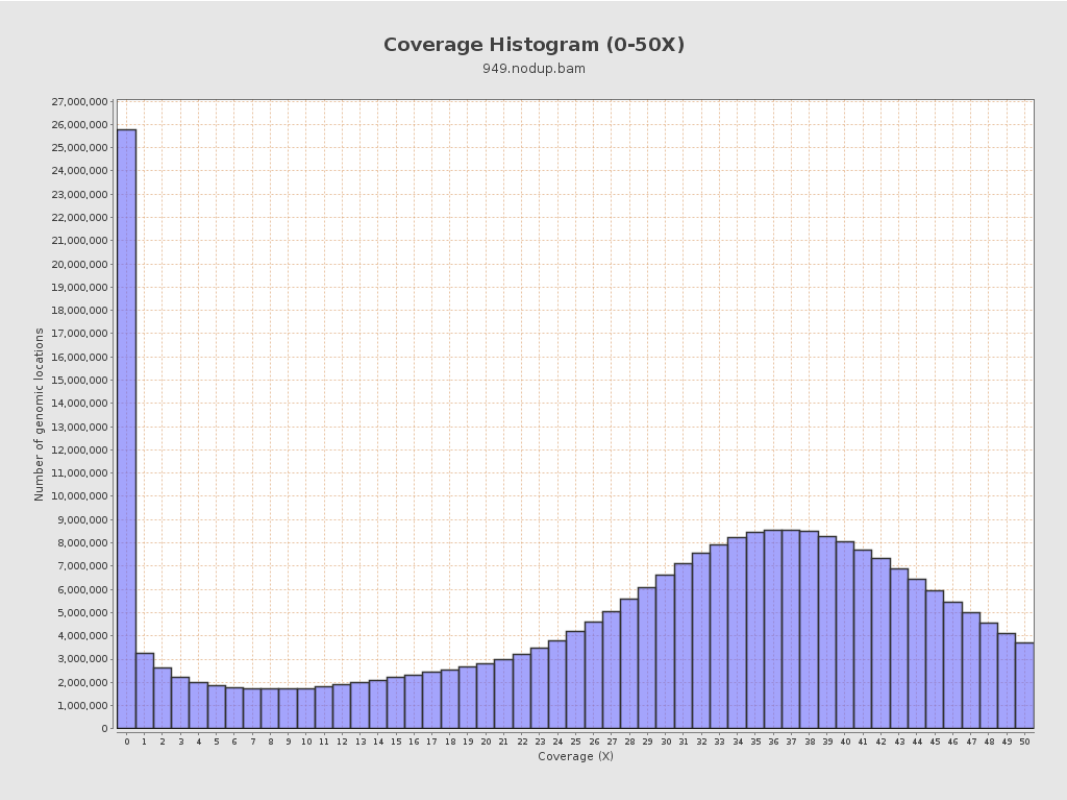
3. Results : Coverage across reference



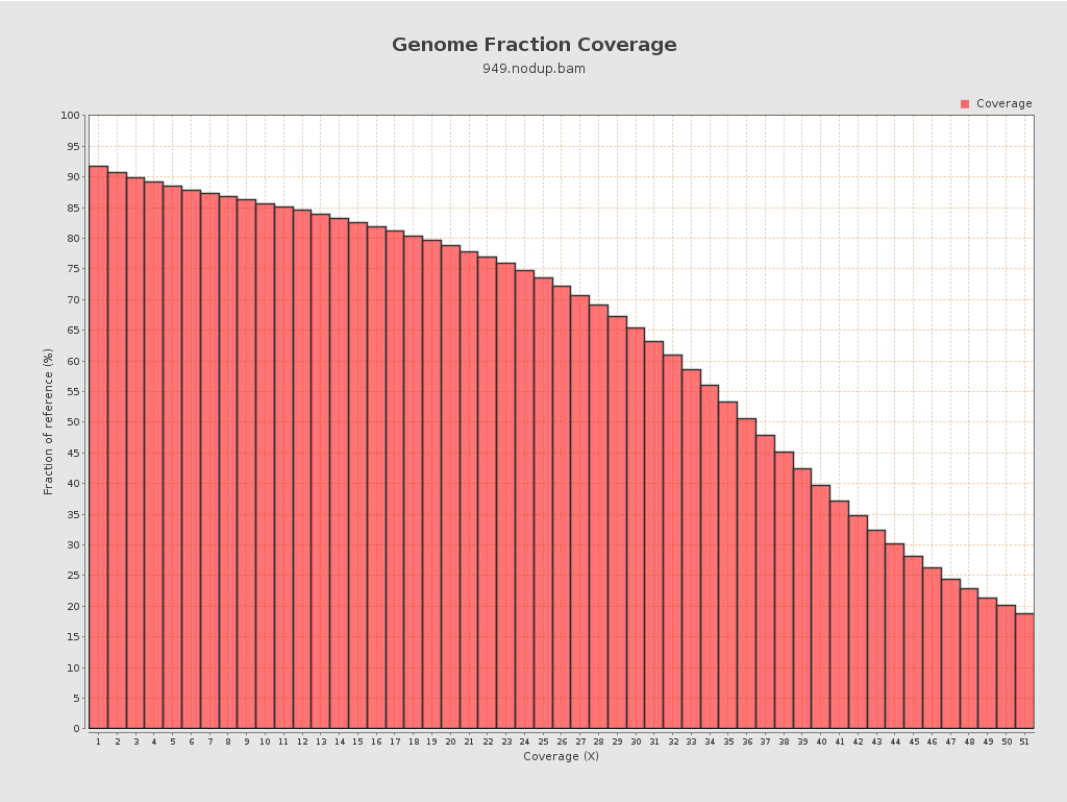
4. Results : Coverage Histogram



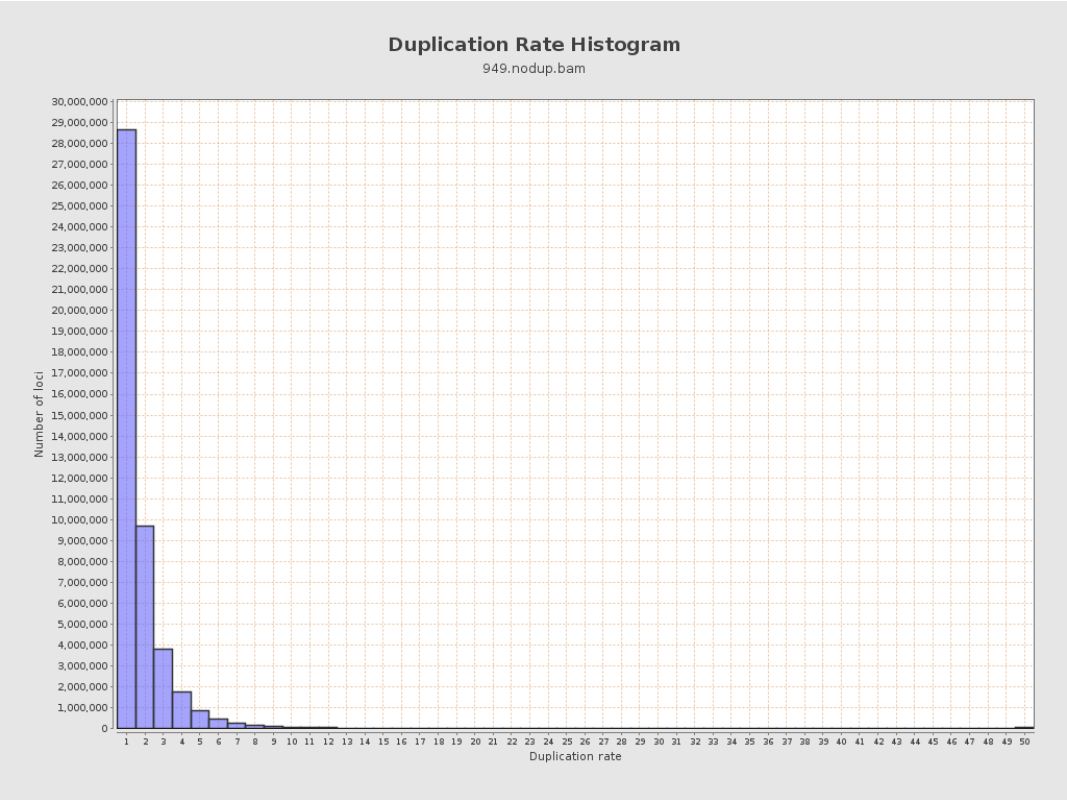
5. Results : Coverage Histogram (0-50X)



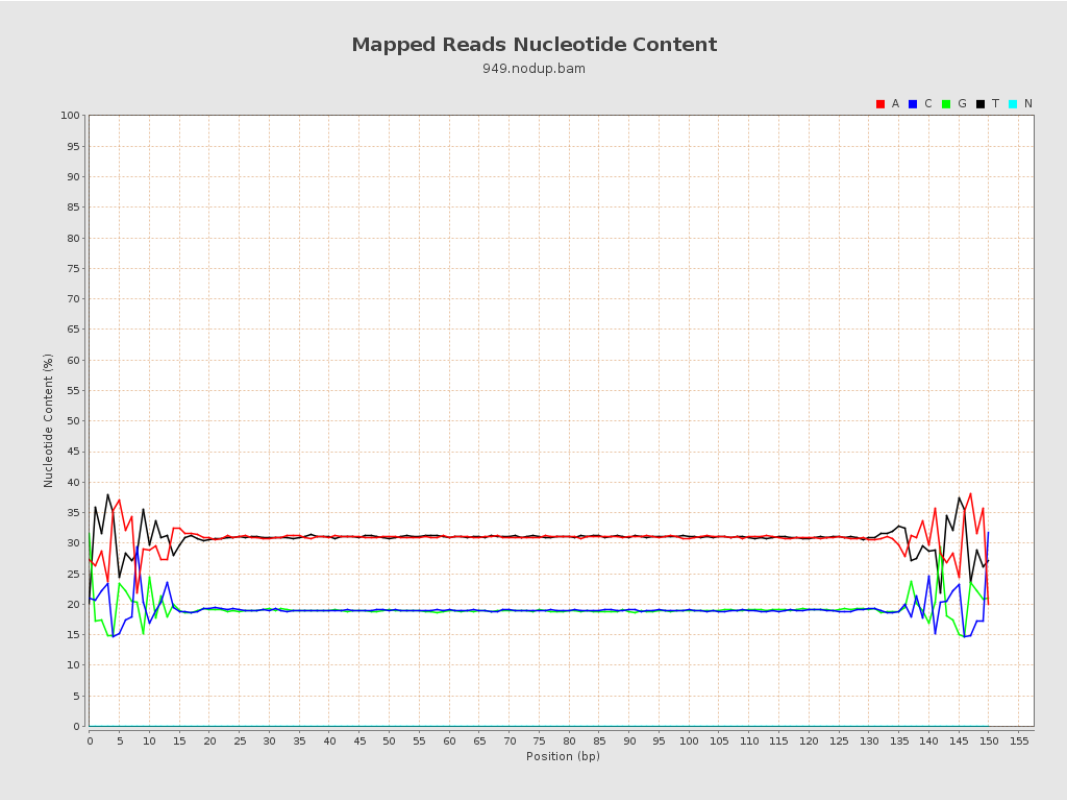
6. Results : Genome Fraction Coverage



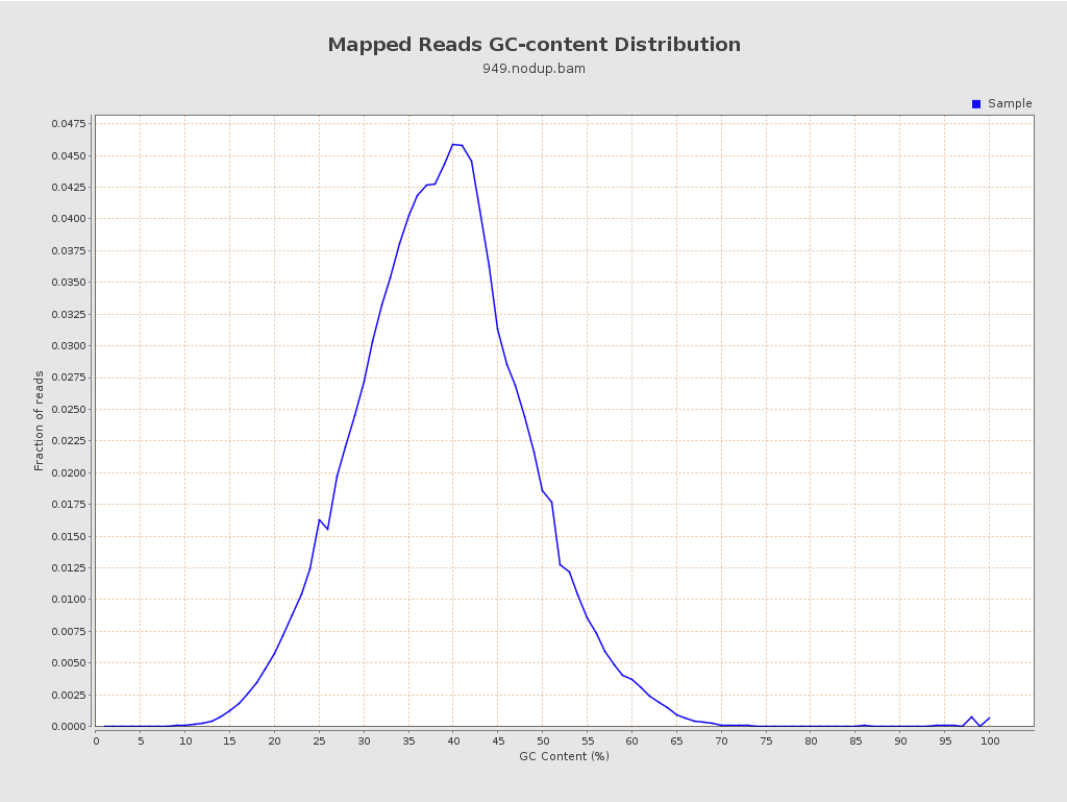
7. Results : Duplication Rate Histogram



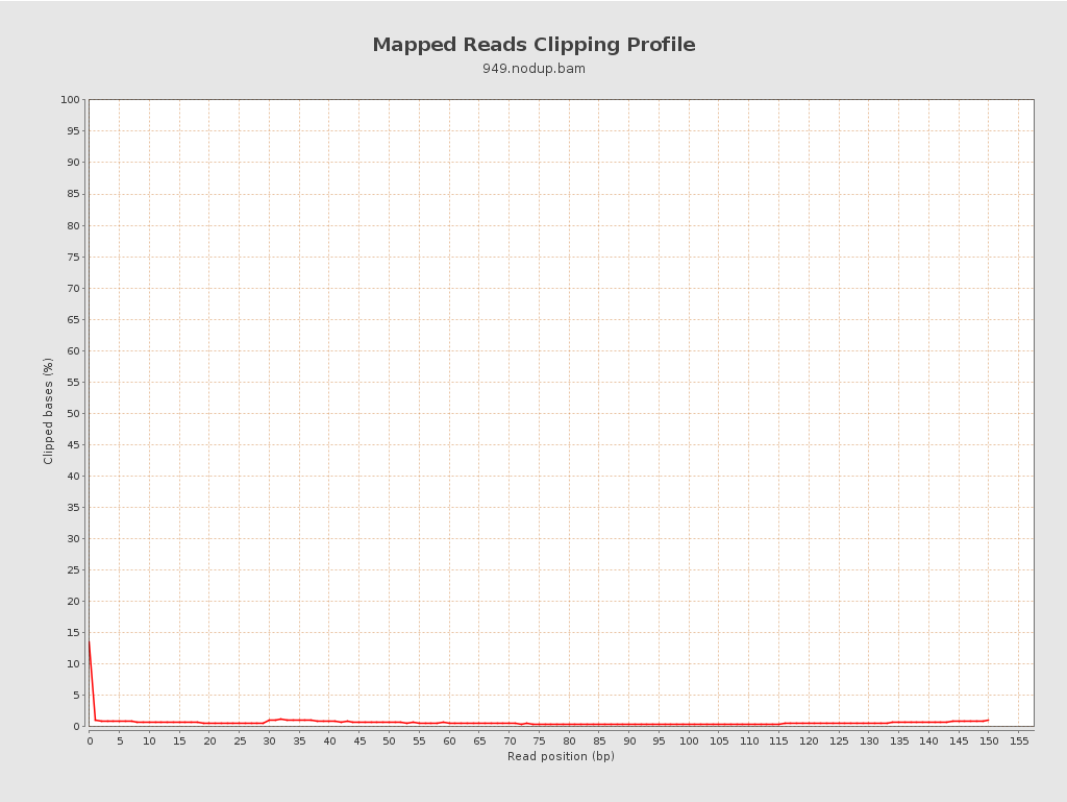
8. Results : Mapped Reads Nucleotide Content



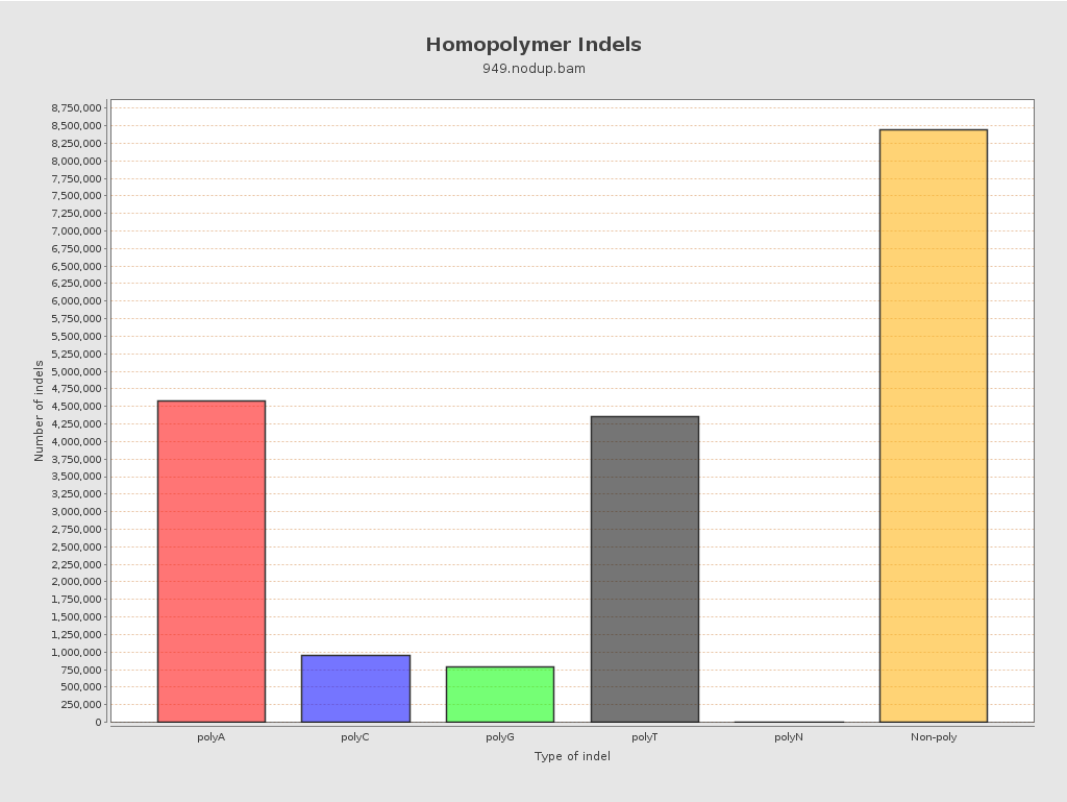
9. Results : Mapped Reads GC-content Distribution



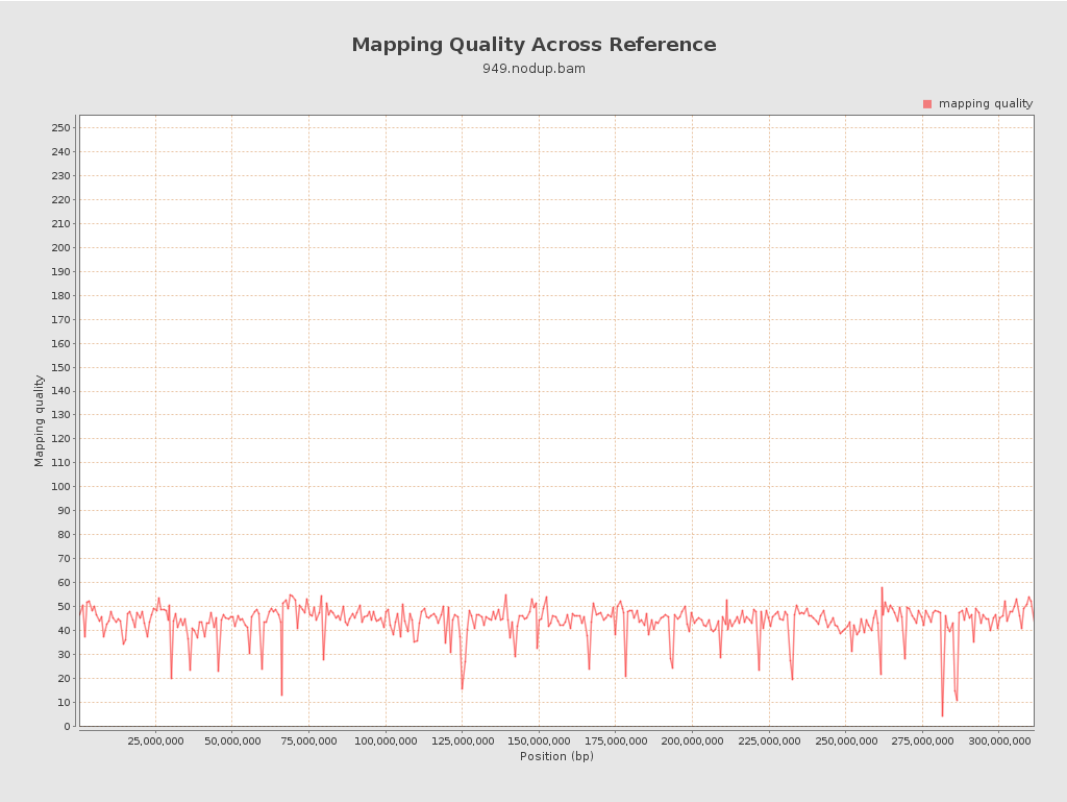
10. Results : Mapped Reads Clipping Profile



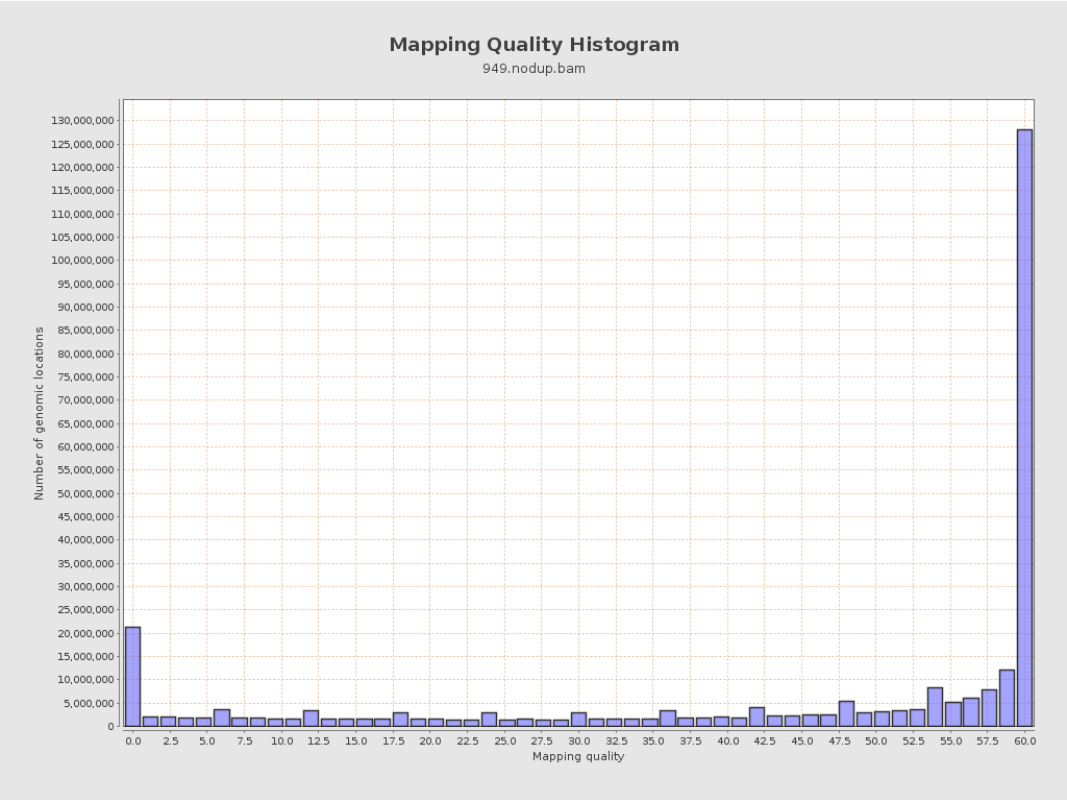
11. Results : Homopolymer Indels



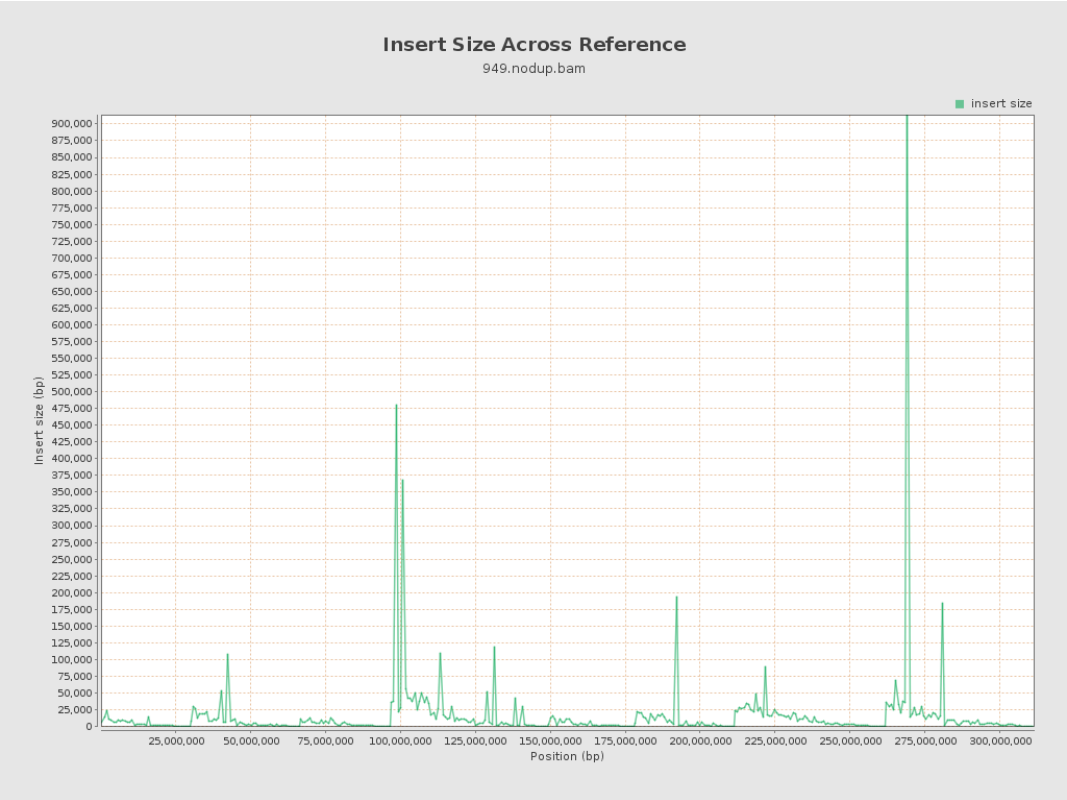
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram