Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:31:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/946.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/946.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_190/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_190_S280_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_190/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_190_S280_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:31:19 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	64,805,721
Mapped reads	61,168,570 / 94.39%
Unmapped reads	3,637,151 / 5.61%
Mapped paired reads	61,168,570 / 94.39%
Mapped reads, first in pair	30,641,213 / 47.28%
Mapped reads, second in pair	30,527,357 / 47.11%
Mapped reads, both in pair	59,939,743 / 92.49%
Mapped reads, singletons	1,228,827 / 1.9%
Read min/max/mean length	30 / 151 / 148.2
Duplicated reads (flagged)	9,697,315 / 14.96%
Clipped reads	13,211,440 / 20.39%

2.2. ACGT Content

Number/percentage of A's	2,625,752,198 / 30.82%
Number/percentage of C's	1,637,761,232 / 19.22%
Number/percentage of T's	2,626,975,276 / 30.83%
Number/percentage of G's	1,629,790,363 / 19.13%
Number/percentage of N's	35,509 / 0%
GC Percentage	38.35%

2.3. Coverage

Mean	27.4096
Standard Deviation	216.4775

2.4. Mapping Quality

Mean Mapping Quality	43.97

2.5. Insert size

Mean	230,972.57
Standard Deviation	2,265,482.86
P25/Median/P75	340 / 444 / 587

2.6. Mismatches and indels

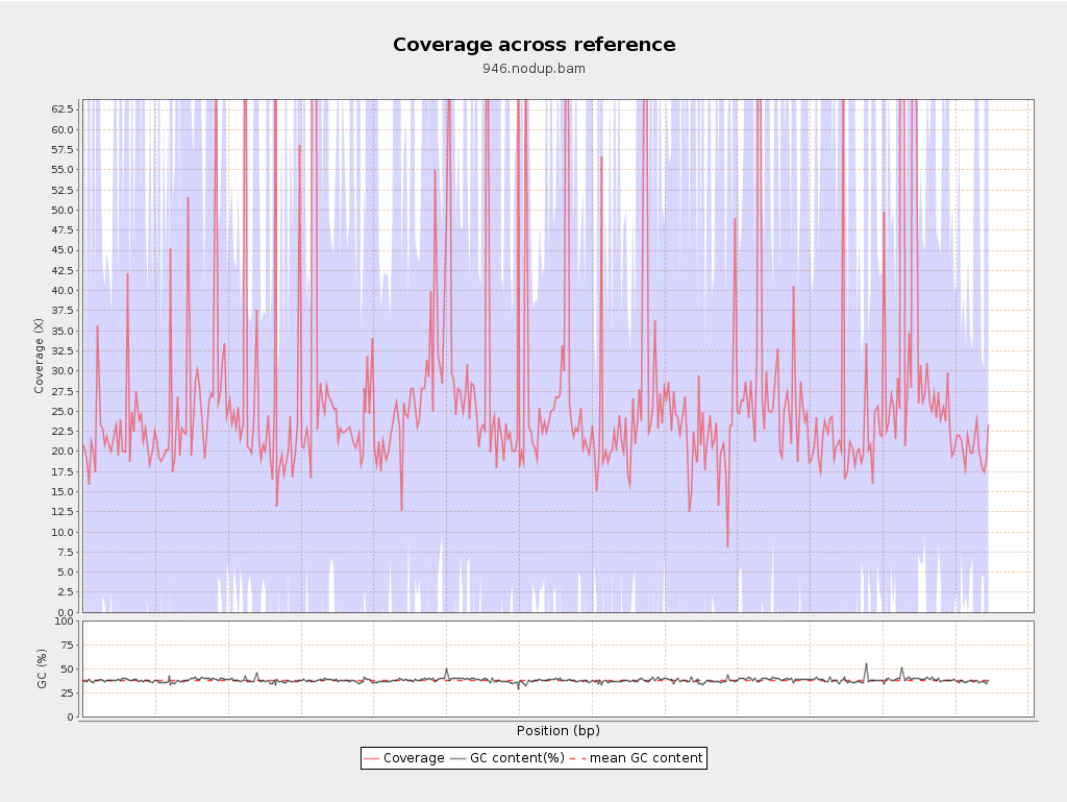
General error rate	2.3%
Mismatches	180,423,807
Insertions	5,650,391
Mapped reads with at least one insertion	8.32%
Deletions	5,758,258
Mapped reads with at least one deletion	8.36%
Homopolymer indels	56.26%

2.7. Chromosome stats

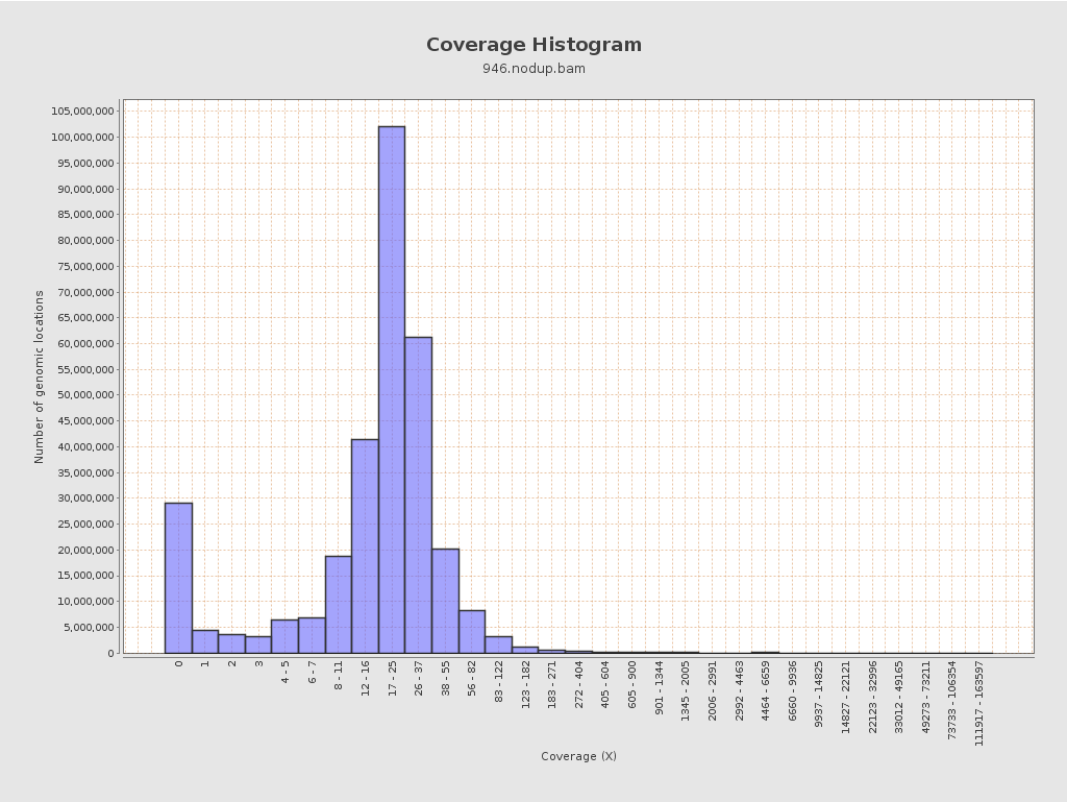
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	655530939	22.0537	56.5925

LT669789.1	36598175	1014428441	27.718	221.694
LT669790.1	30422129	880093055	28.9294	223.8392
LT669791.1	52758100	1445195795	27.3929	180.6436
LT669792.1	28376109	761559602	26.8381	268.2993
LT669793.1	33388210	859828445	25.7525	168.797
LT669794.1	50579949	1315681488	26.0119	197.7543
LT669795.1	49795044	1609672004	32.3259	300.2898

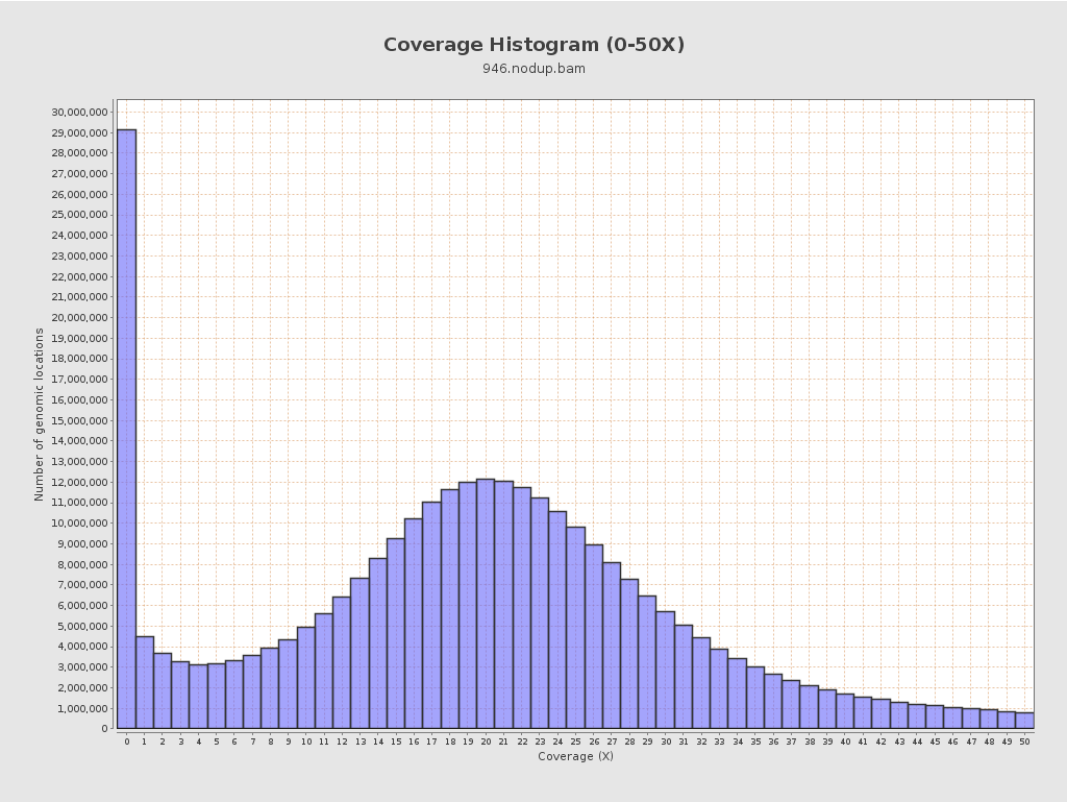
3. Results : Coverage across reference



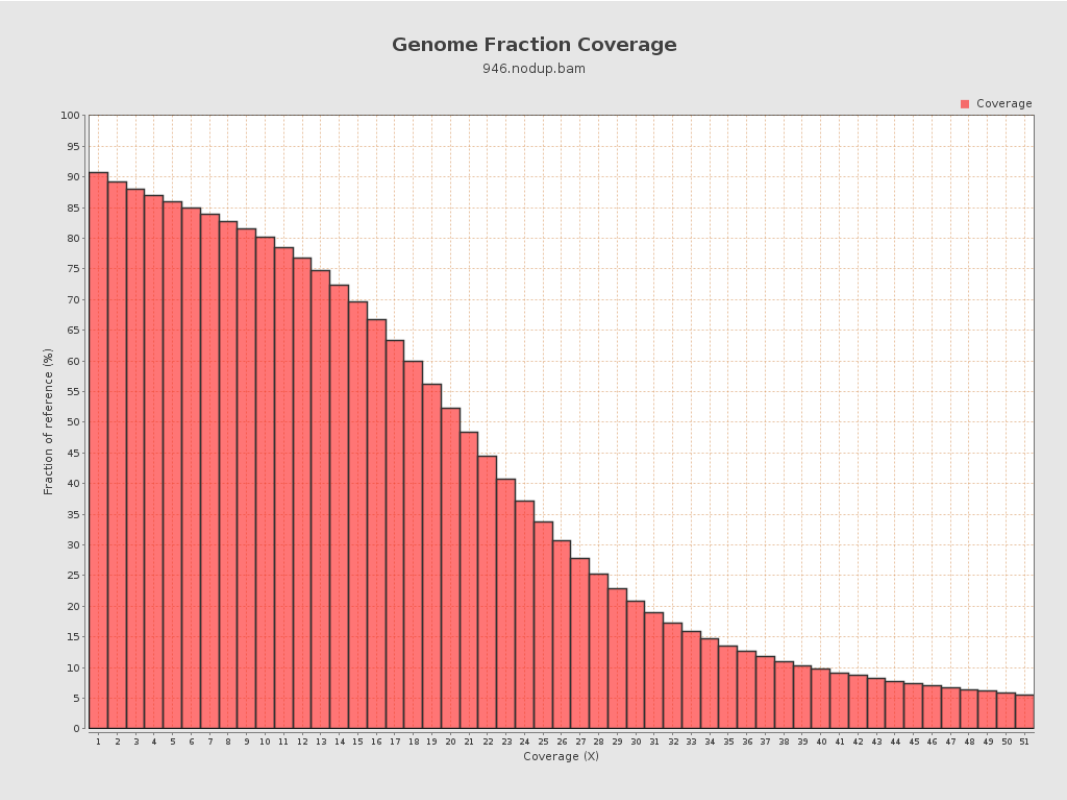
4. Results : Coverage Histogram



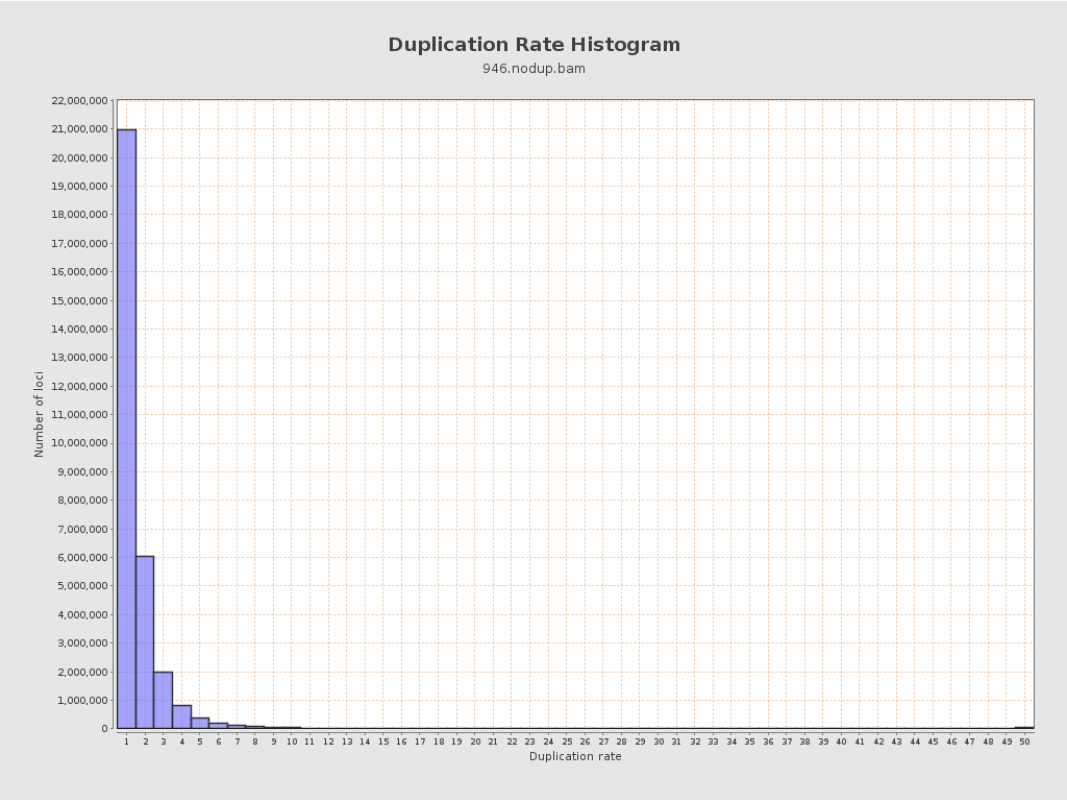
5. Results : Coverage Histogram (0-50X)



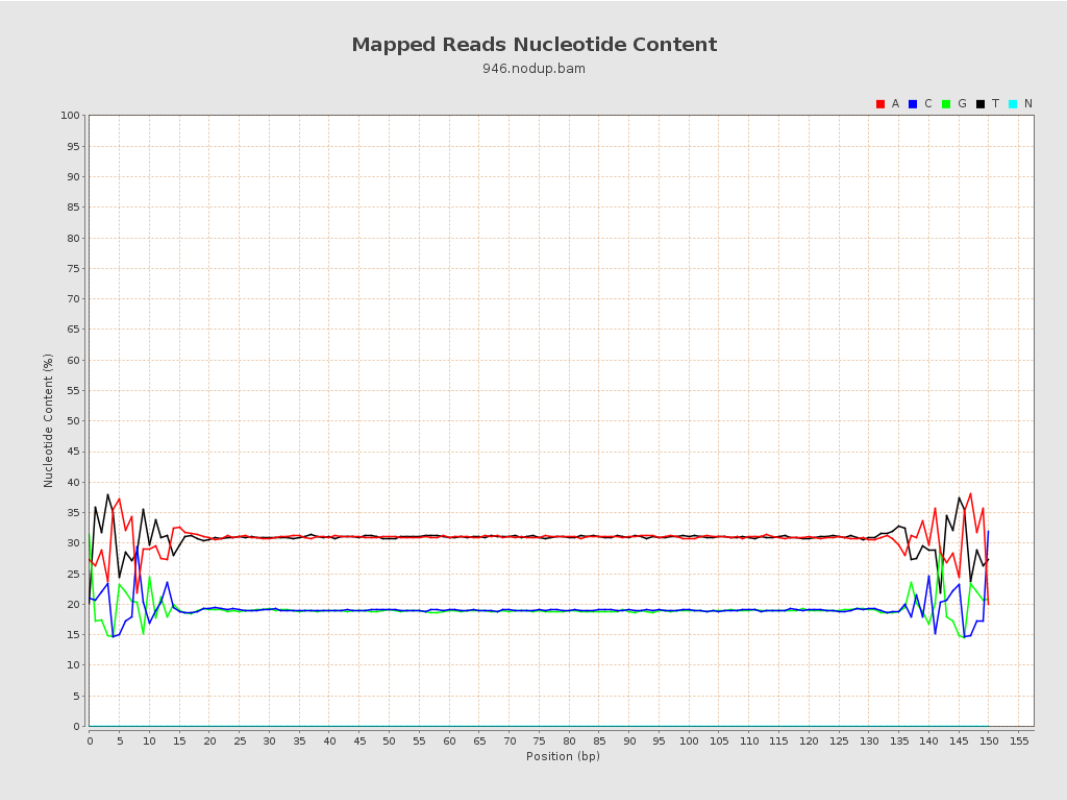
6. Results : Genome Fraction Coverage



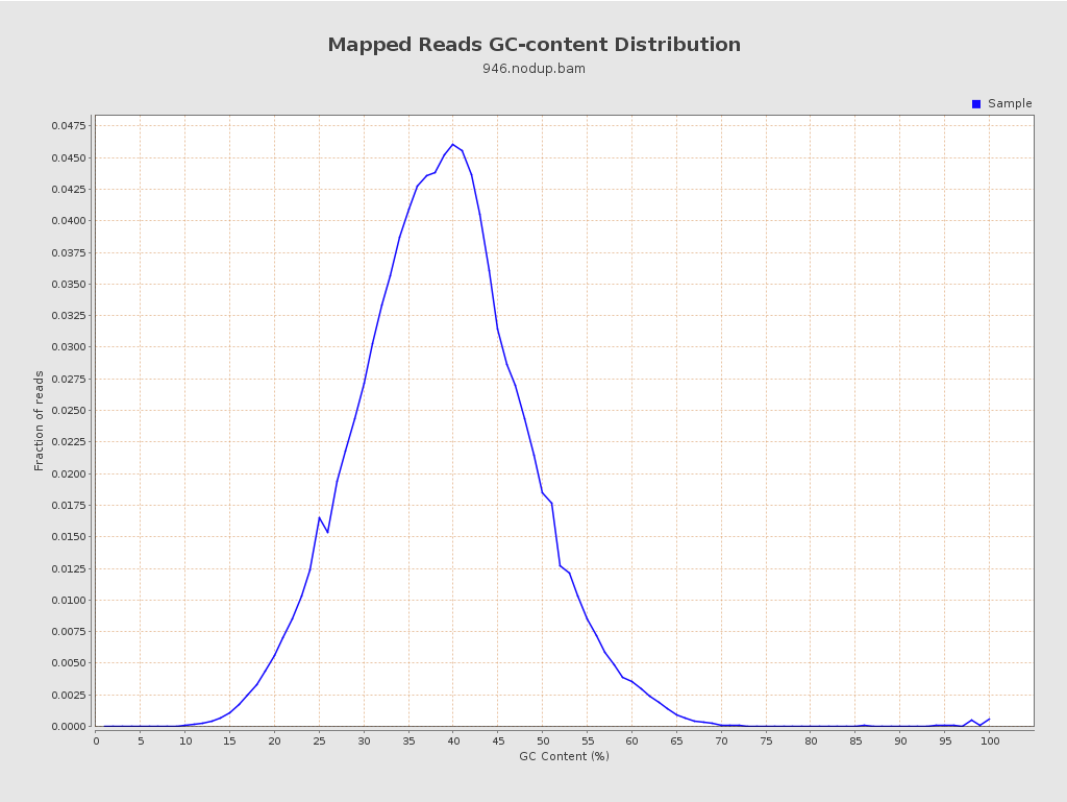
7. Results : Duplication Rate Histogram



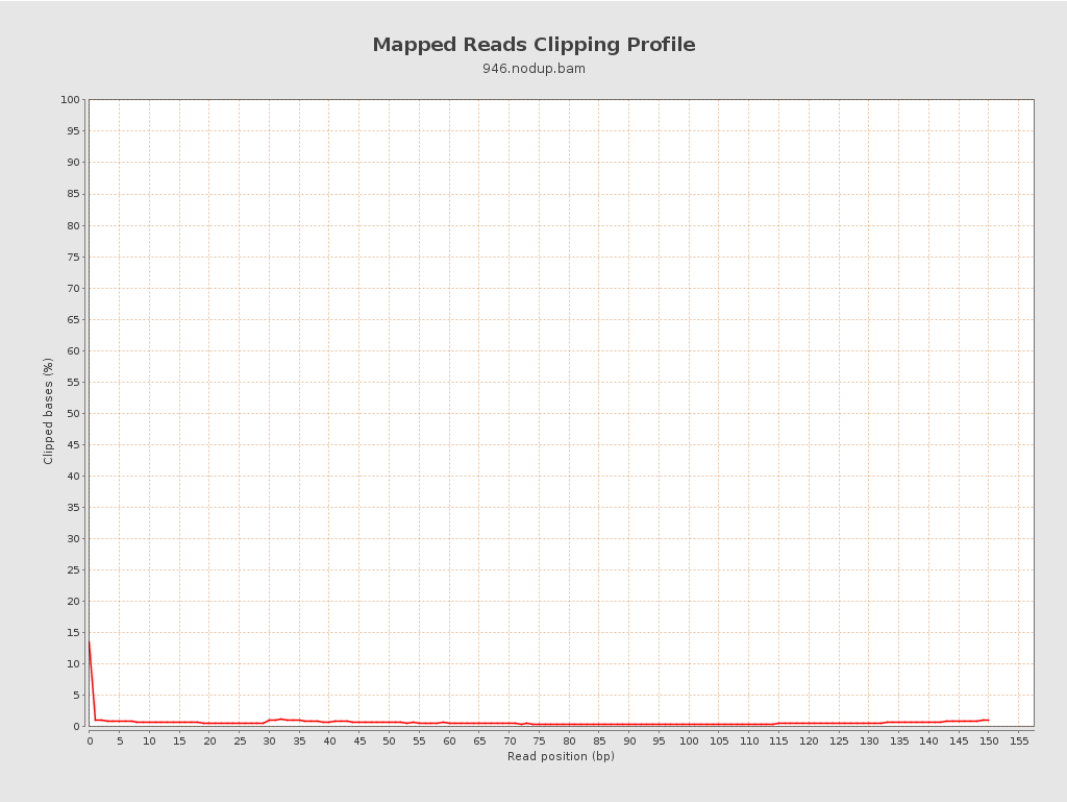
8. Results : Mapped Reads Nucleotide Content



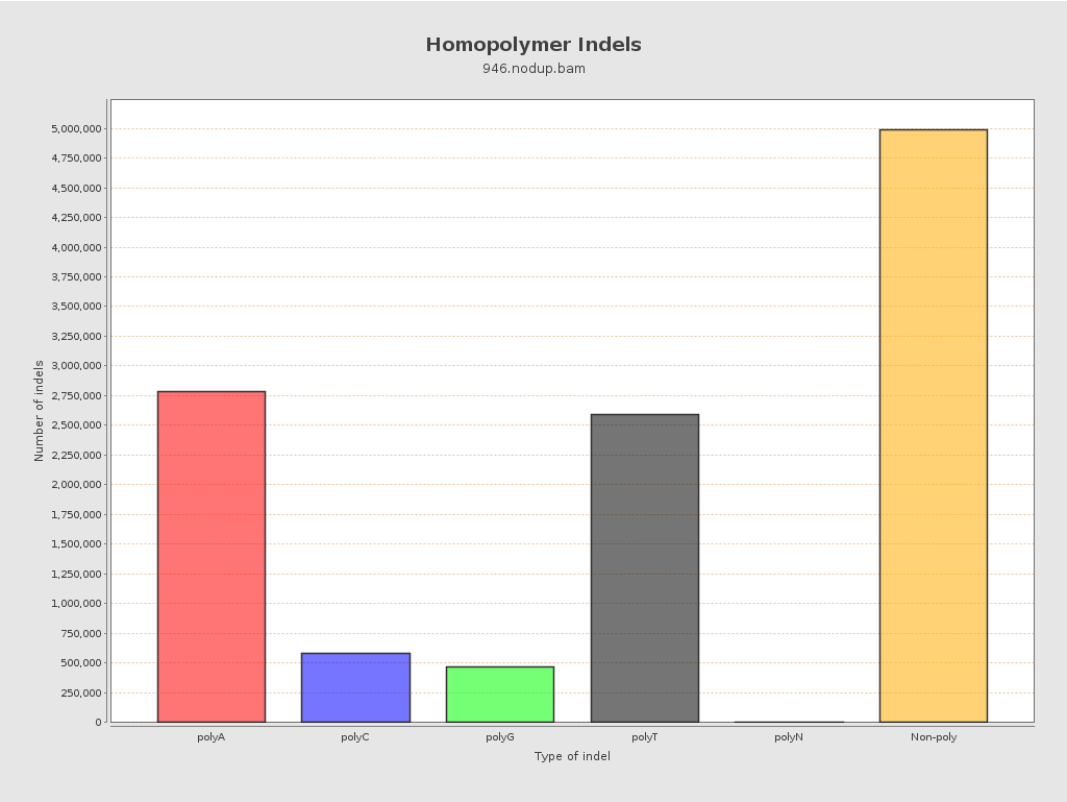
9. Results : Mapped Reads GC-content Distribution



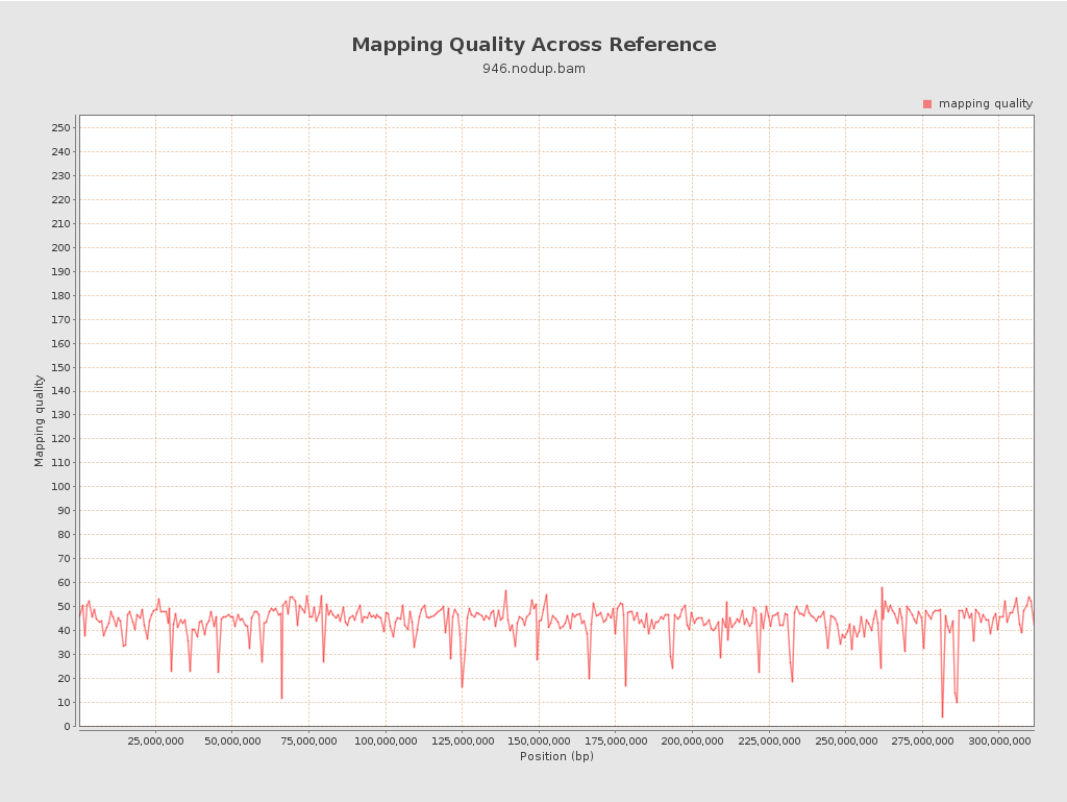
10. Results : Mapped Reads Clipping Profile



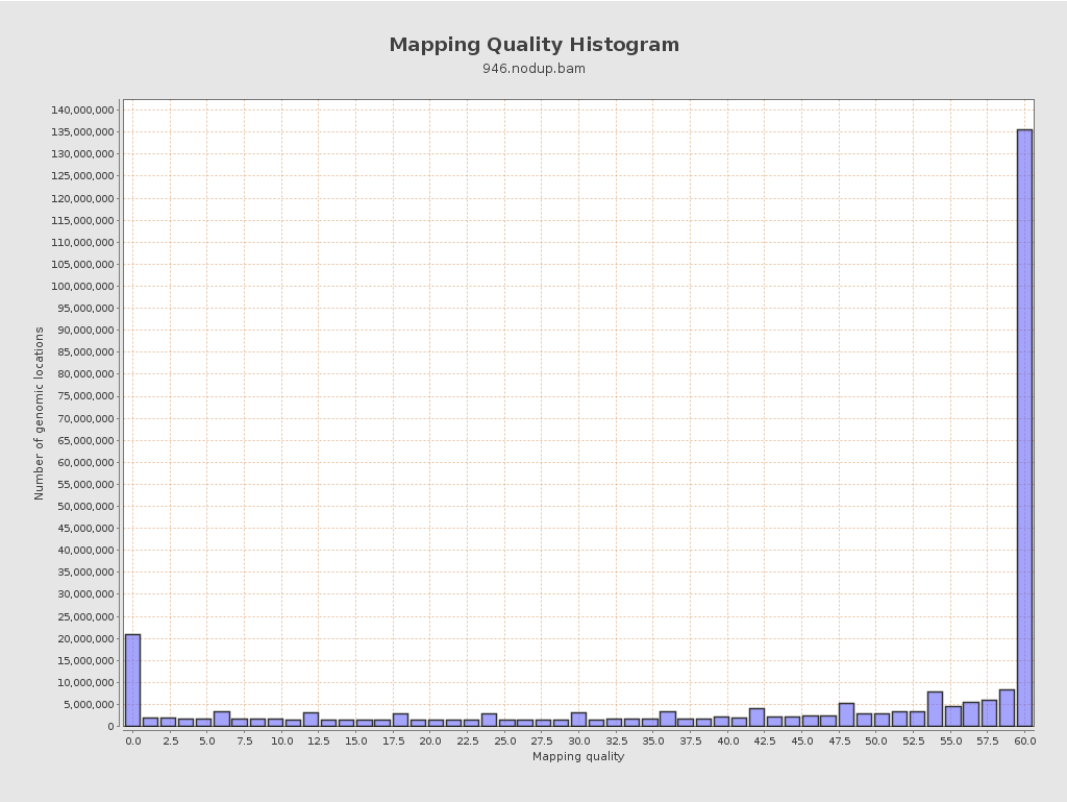
11. Results : Homopolymer Indels



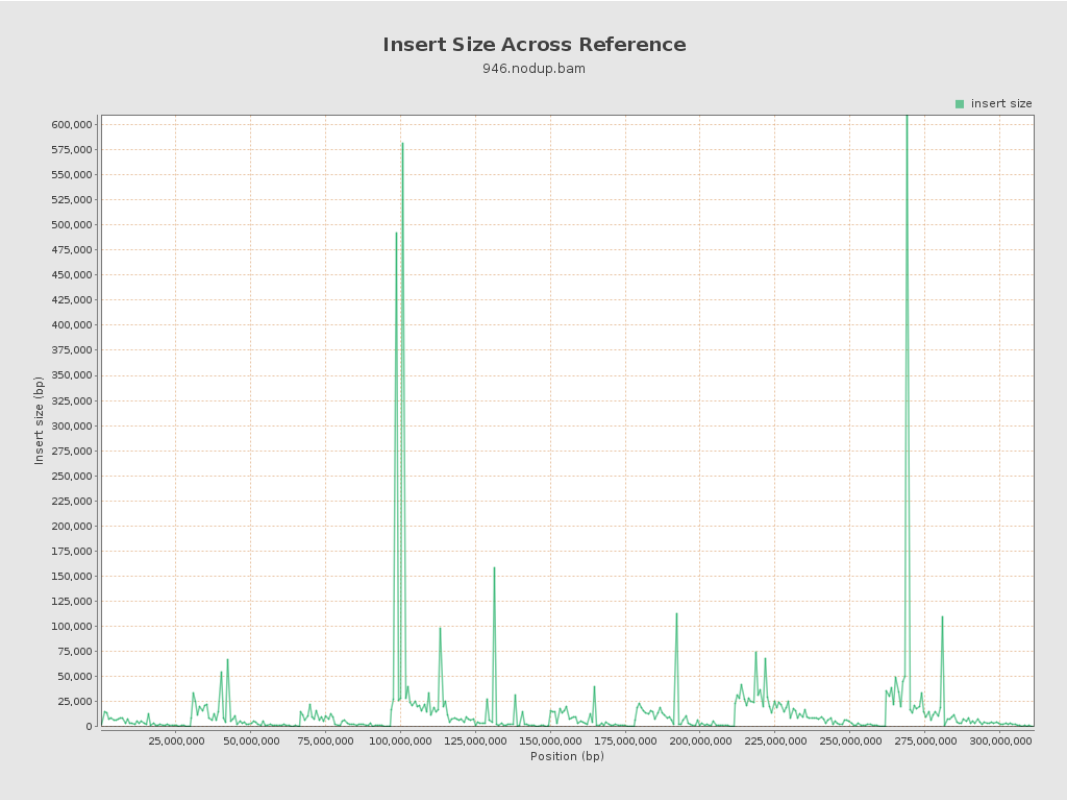
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram