Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:28:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/627.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/627.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_184/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_184_S274_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_184/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_184_S274_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:28:43 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	59,784,944
Mapped reads	56,270,919 / 94.12%
Unmapped reads	3,514,025 / 5.88%
Mapped paired reads	56,270,919 / 94.12%
Mapped reads, first in pair	28,192,385 / 47.16%
Mapped reads, second in pair	28,078,534 / 46.97%
Mapped reads, both in pair	55,038,595 / 92.06%
Mapped reads, singletons	1,232,324 / 2.06%
Read min/max/mean length	30 / 151 / 148.06
Duplicated reads (flagged)	9,282,553 / 15.53%
Clipped reads	12,614,253 / 21.1%

2.2. ACGT Content

Number/percentage of A's	2,410,788,513 / 30.85%
Number/percentage of C's	1,497,167,204 / 19.16%
Number/percentage of T's	2,412,972,462 / 30.88%
Number/percentage of G's	1,493,436,518 / 19.11%
Number/percentage of N's	32,267 / 0%
GC Percentage	38.27%

2.3. Coverage

Mean	25.1437
Standard Deviation	211.8995

2.4. Mapping Quality

Mean Mapping Quality	43.41

2.5. Insert size

Mean	251,312.4
Standard Deviation	2,368,162.49
P25/Median/P75	348 / 452 / 588

2.6. Mismatches and indels

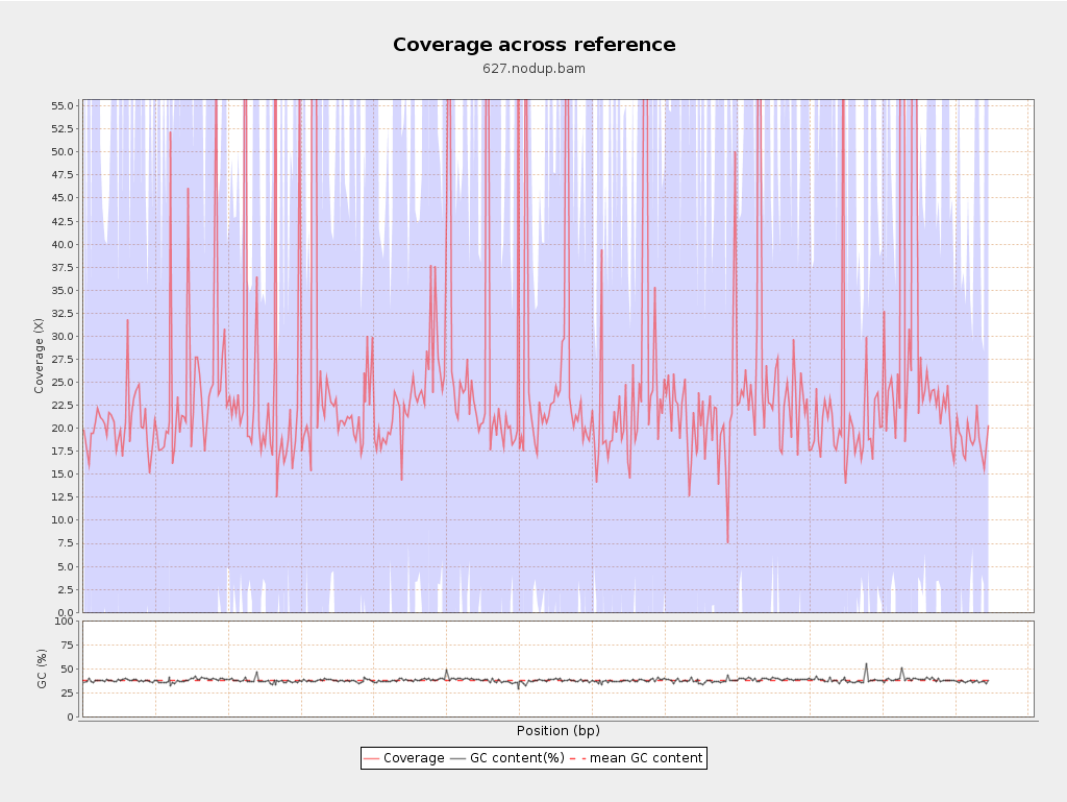
General error rate	2.42%
Mismatches	174,427,204
Insertions	5,439,559
Mapped reads with at least one insertion	8.67%
Deletions	5,614,991
Mapped reads with at least one deletion	8.85%
Homopolymer indels	56.11%

2.7. Chromosome stats

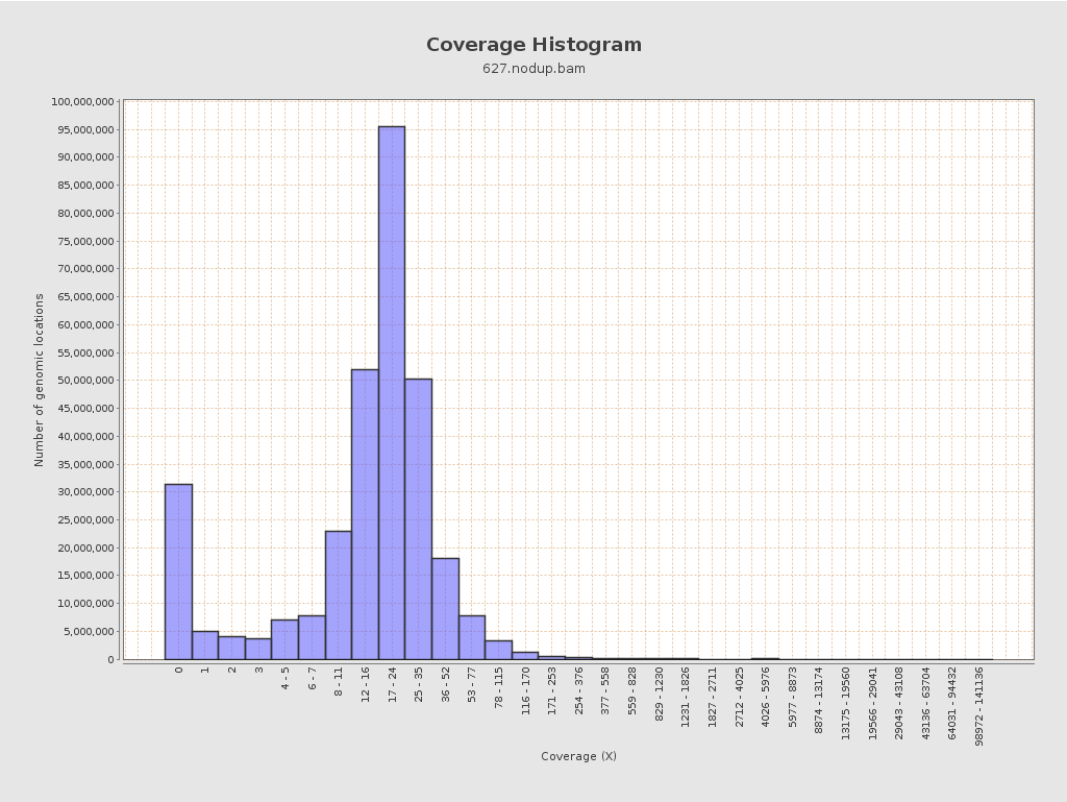
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	598868662	20.1474	61.9935

LT669789.1	36598175	943981215	25.7931	216.015
LT669790.1	30422129	822441878	27.0343	224.7774
LT669791.1	52758100	1314221833	24.9103	181.9825
LT669792.1	28376109	700458601	24.6848	226.3321
LT669793.1	33388210	803575051	24.0676	201.8992
LT669794.1	50579949	1209812328	23.9188	187.5857
LT669795.1	49795044	1442471192	28.9682	293.5429

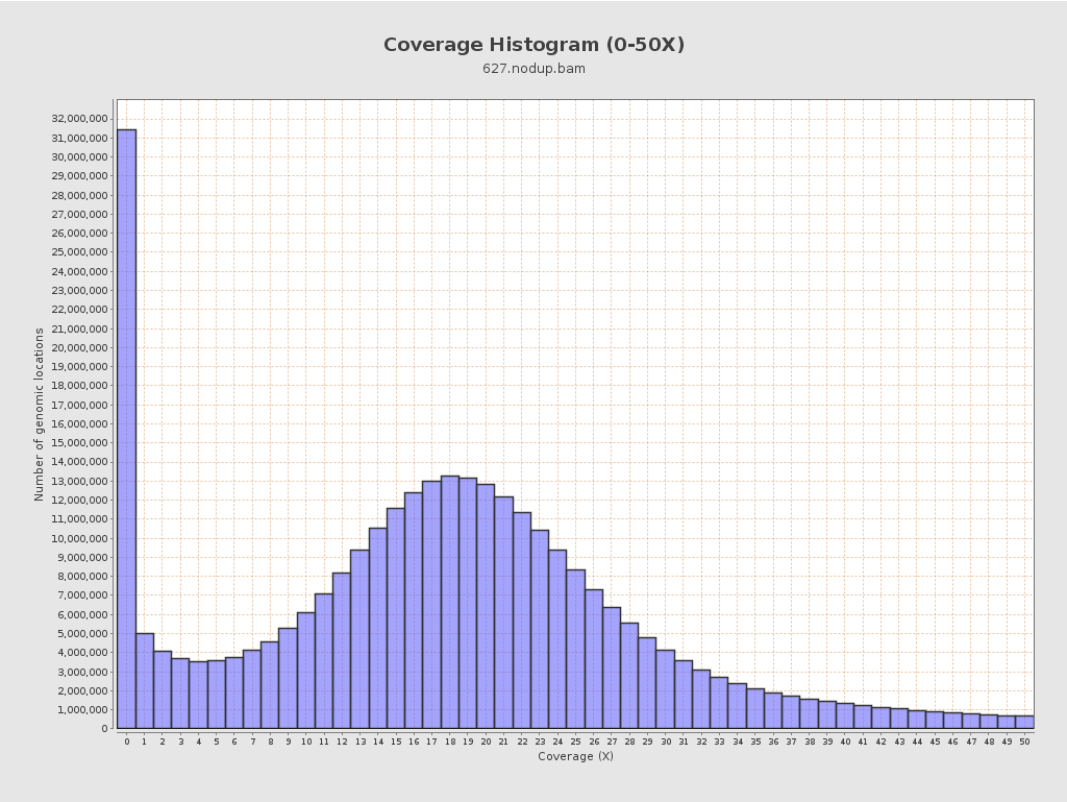
3. Results : Coverage across reference



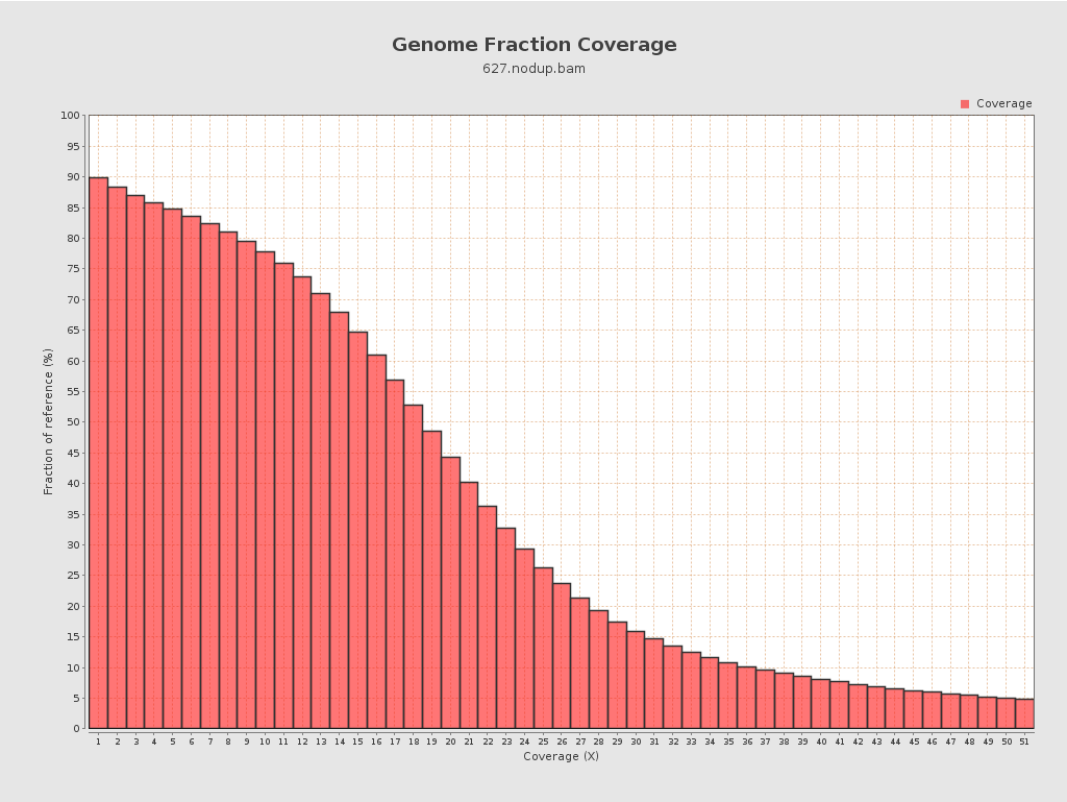
4. Results : Coverage Histogram



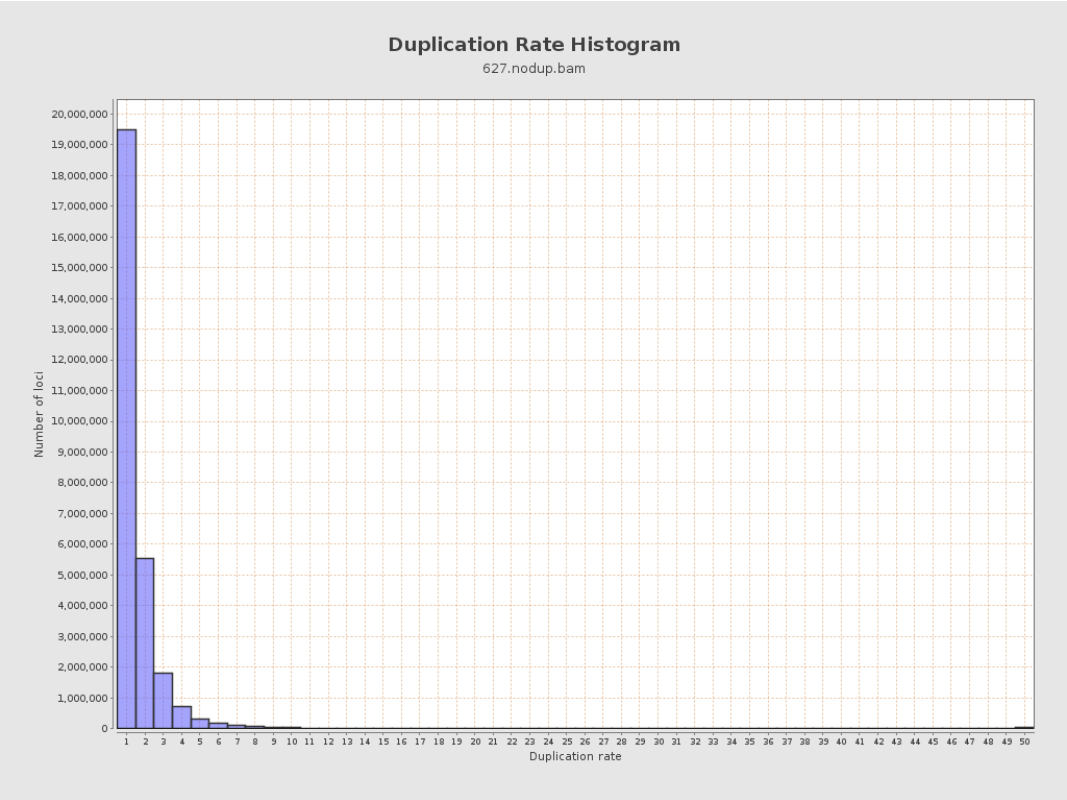
5. Results : Coverage Histogram (0-50X)



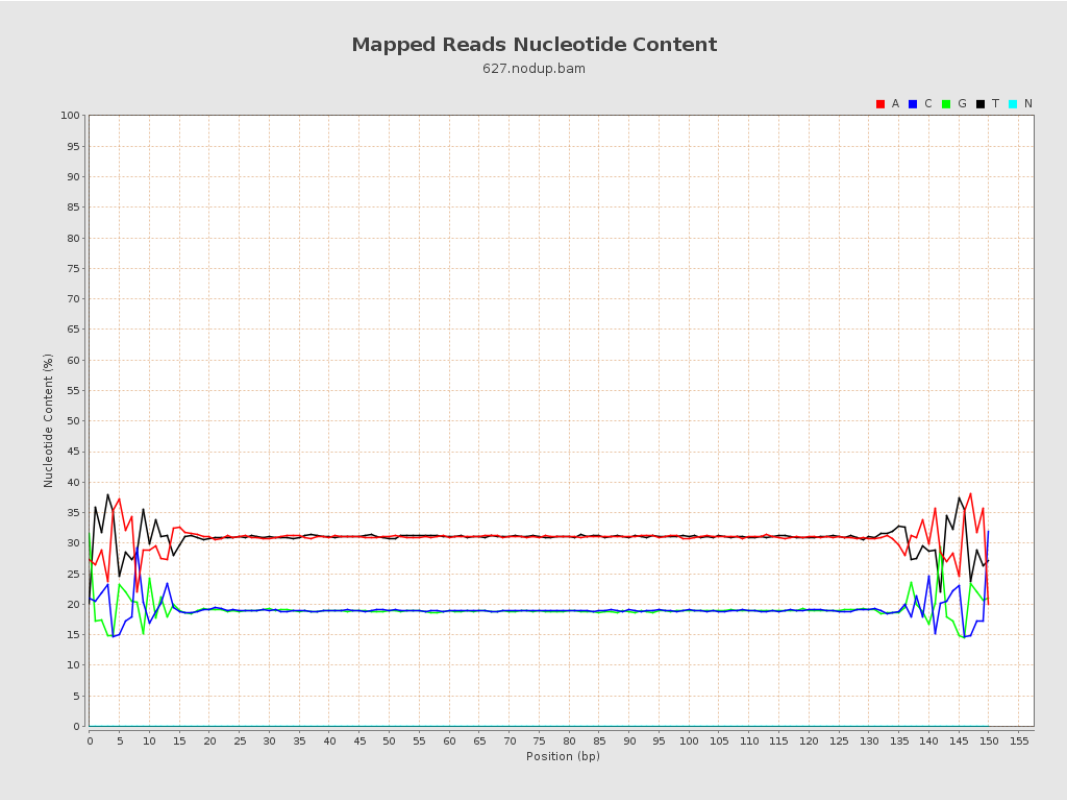
6. Results : Genome Fraction Coverage



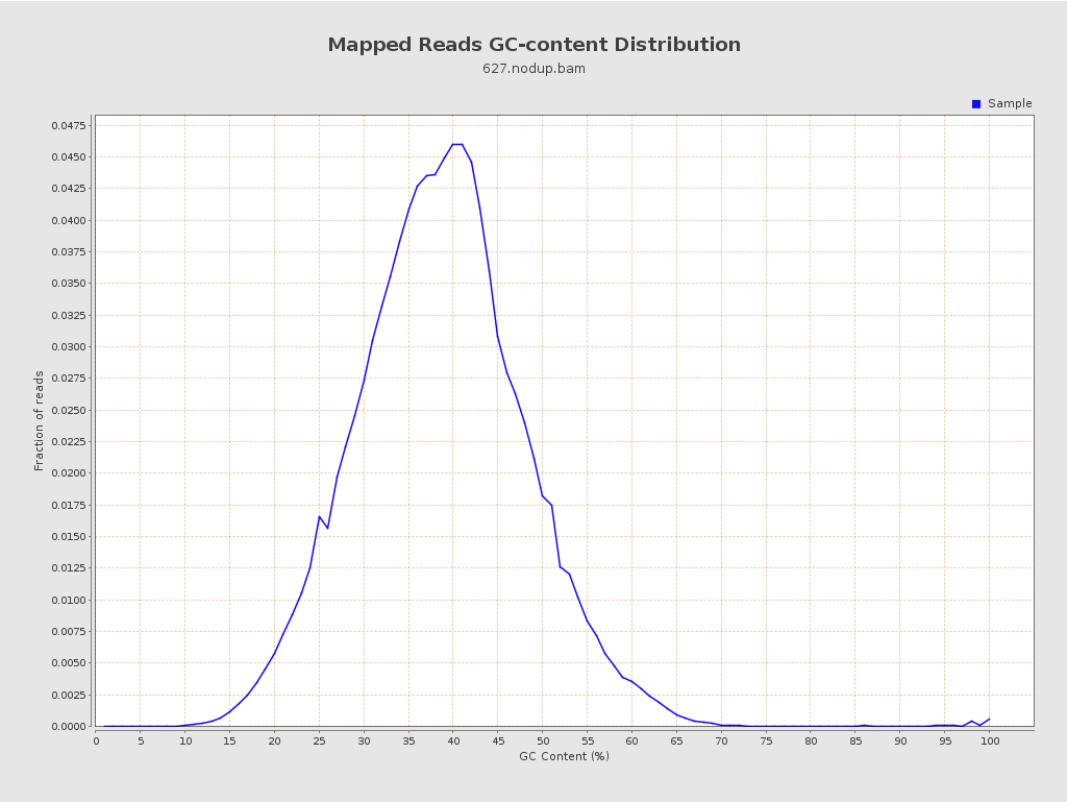
7. Results : Duplication Rate Histogram



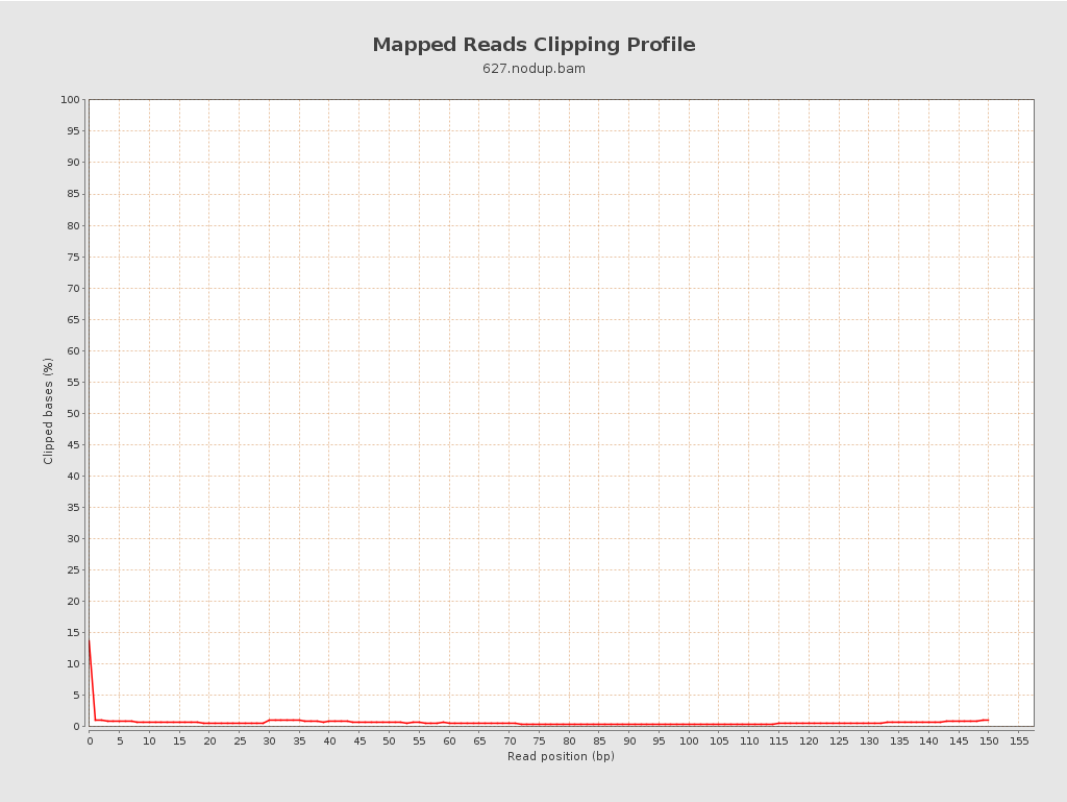
8. Results : Mapped Reads Nucleotide Content



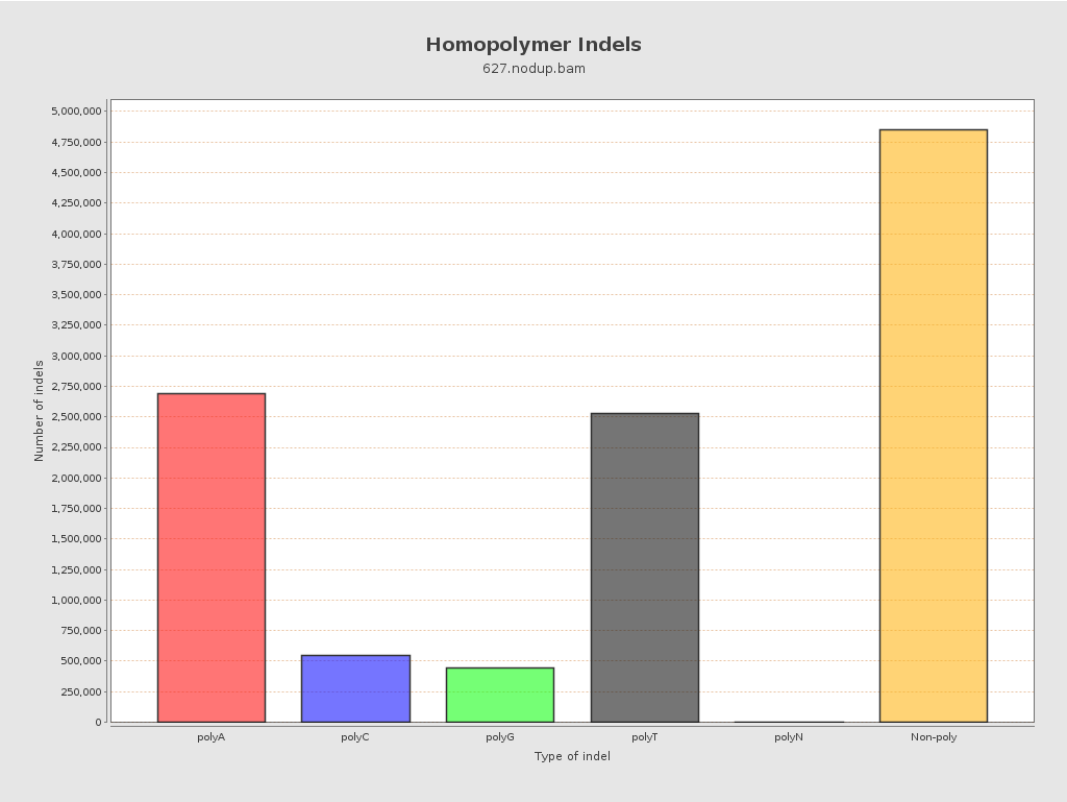
9. Results : Mapped Reads GC-content Distribution



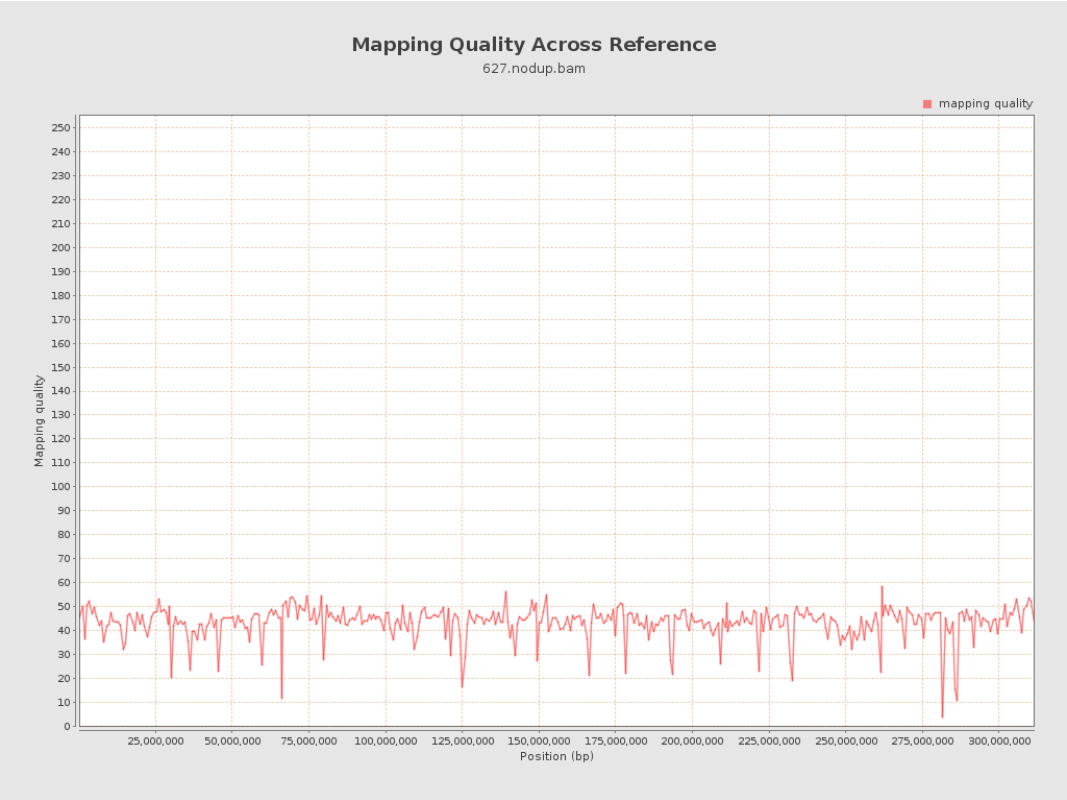
10. Results : Mapped Reads Clipping Profile



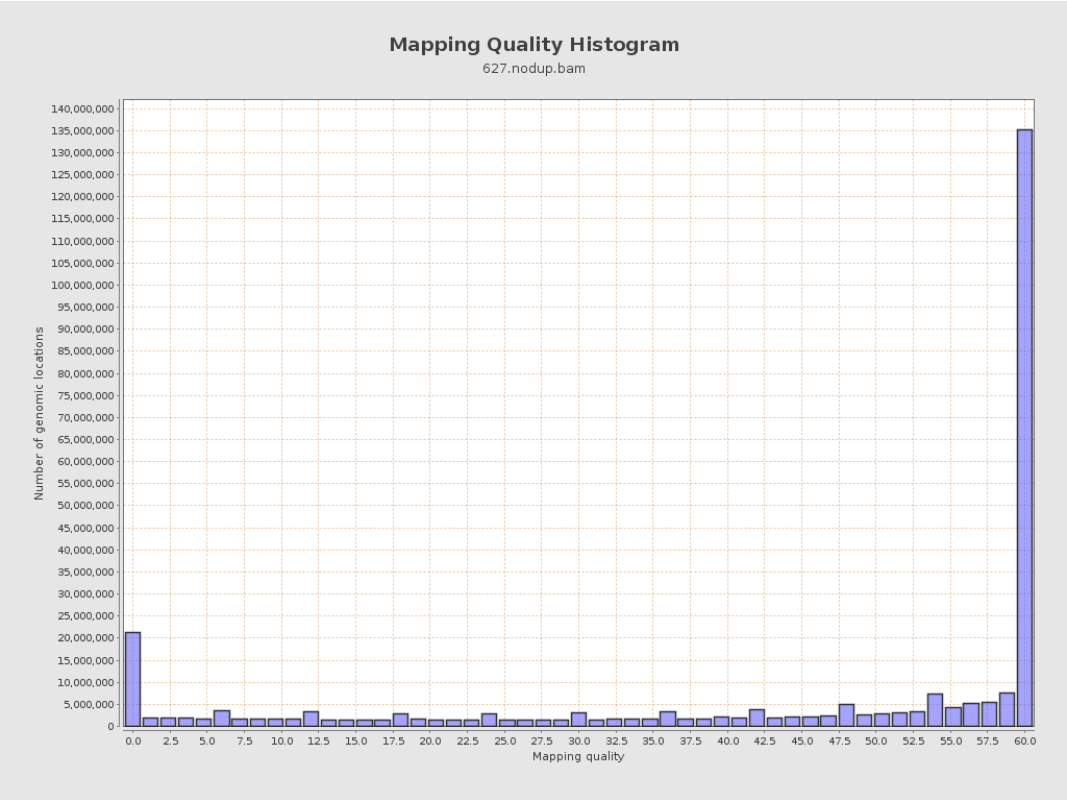
11. Results : Homopolymer Indels



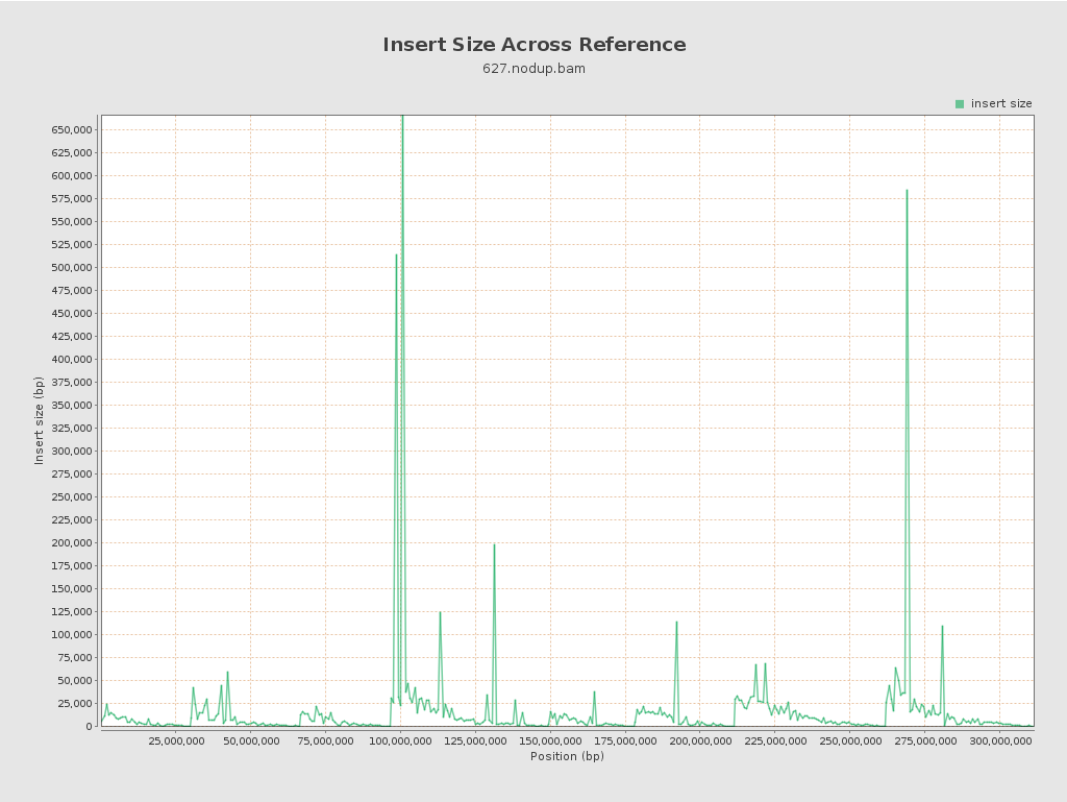
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram