Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:39:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/427.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/427.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_256/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_256_S337_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_256/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_256_S337_L003_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:39:44 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	88,195,174
Mapped reads	82,074,490 / 93.06%
Unmapped reads	6,120,684 / 6.94%
Mapped paired reads	82,074,490 / 93.06%
Mapped reads, first in pair	41,144,446 / 46.65%
Mapped reads, second in pair	40,930,044 / 46.41%
Mapped reads, both in pair	80,159,685 / 90.89%
Mapped reads, singletons	1,914,805 / 2.17%
Read min/max/mean length	30 / 151 / 147.95
Duplicated reads (flagged)	12,937,547 / 14.67%
Clipped reads	19,592,365 / 22.21%

2.2. ACGT Content

Number/percentage of A's	3,479,716,985 / 30.84%
Number/percentage of C's	2,159,313,003 / 19.14%
Number/percentage of T's	3,484,926,062 / 30.89%
Number/percentage of G's	2,158,126,653 / 19.13%
Number/percentage of N's	41,587 / 0%
GC Percentage	38.27%

2.3. Coverage

Mean	36.2988
Standard Deviation	304.5207

2.4. Mapping Quality

Mean Mapping Quality	43.94

2.5. Insert size

Mean	240,404.68
Standard Deviation	2,331,984.35
P25/Median/P75	313 / 415 / 544

2.6. Mismatches and indels

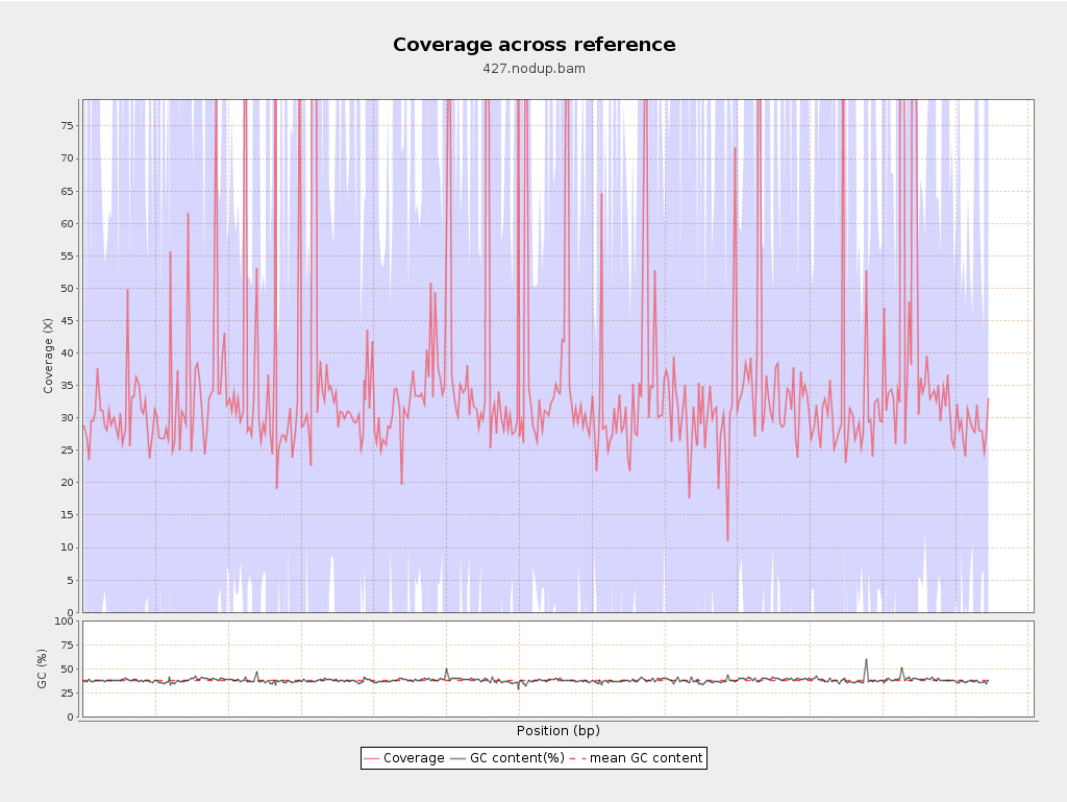
General error rate	2.34%
Mismatches	242,732,727
Insertions	7,835,592
Mapped reads with at least one insertion	8.55%
Deletions	7,906,643
Mapped reads with at least one deletion	8.55%
Homopolymer indels	56.42%

2.7. Chromosome stats

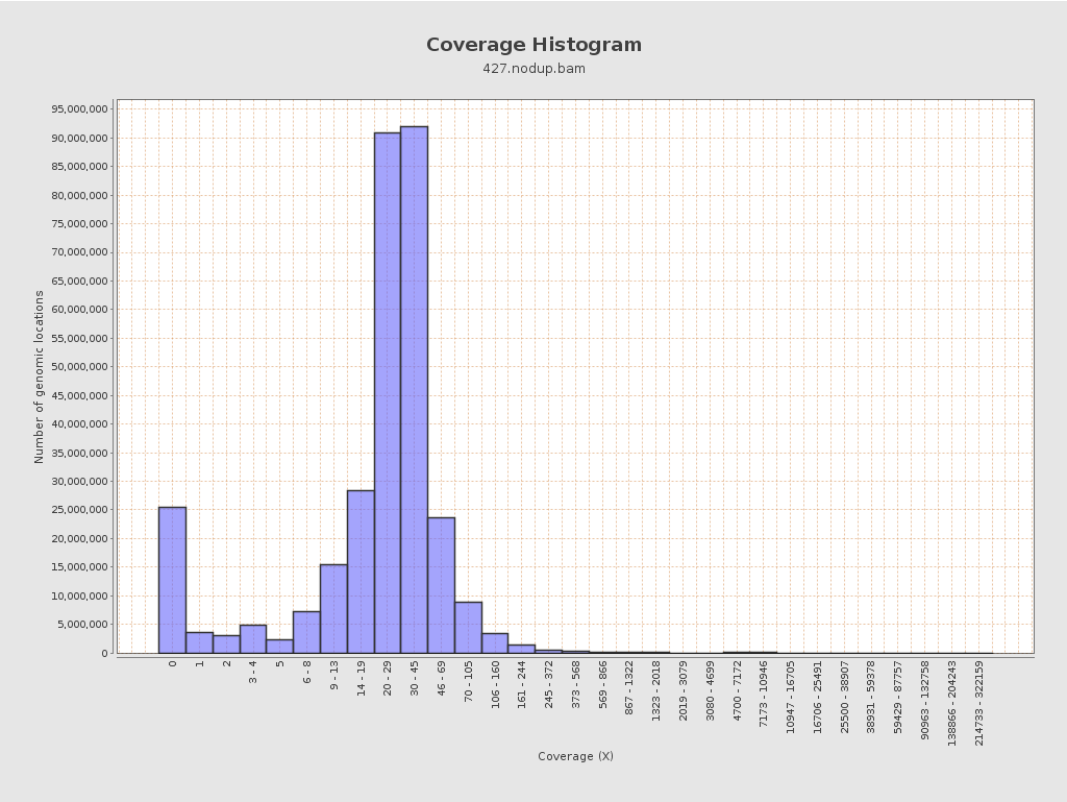
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	893341422	30.0542	98.8683

LT669789.1	36598175	1331628709	36.3851	301.1313
LT669790.1	30422129	1235226133	40.6029	339.1872
LT669791.1	52758100	1885558997	35.7397	277.0909
LT669792.1	28376109	1026234319	36.1654	311.702
LT669793.1	33388210	1122484044	33.6192	277.0065
LT669794.1	50579949	1727555479	34.1549	245.3379
LT669795.1	49795044	2090207523	41.9762	433.8397

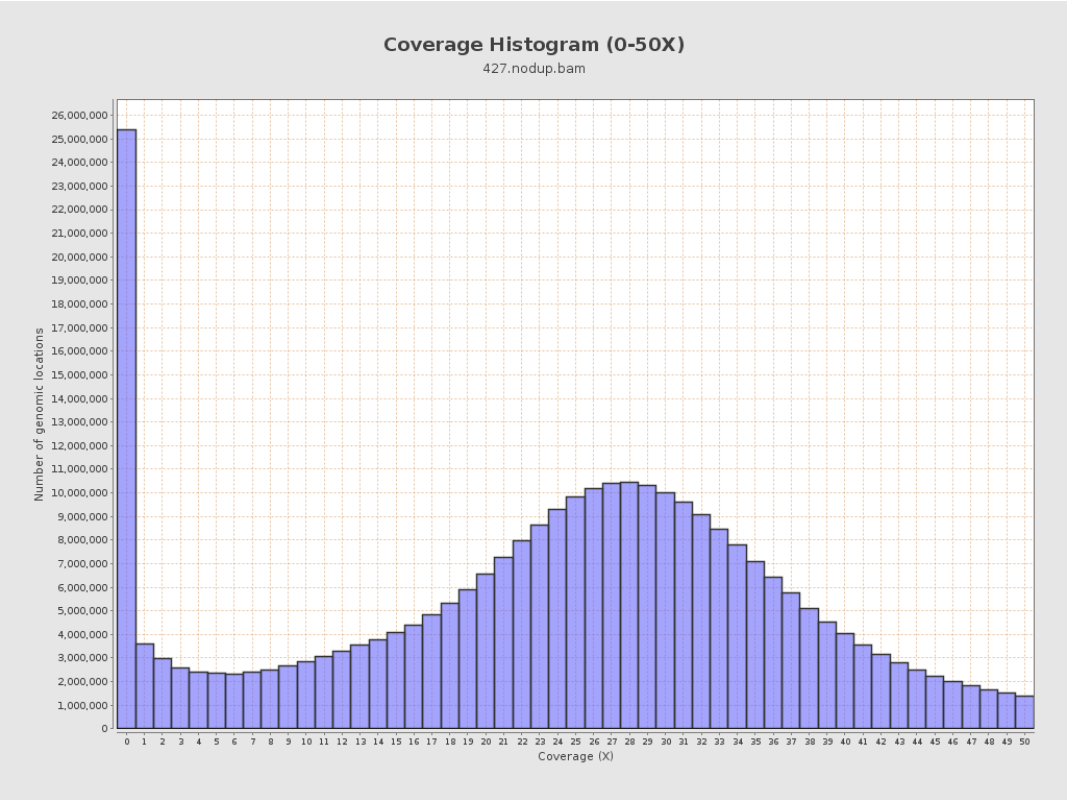
3. Results : Coverage across reference



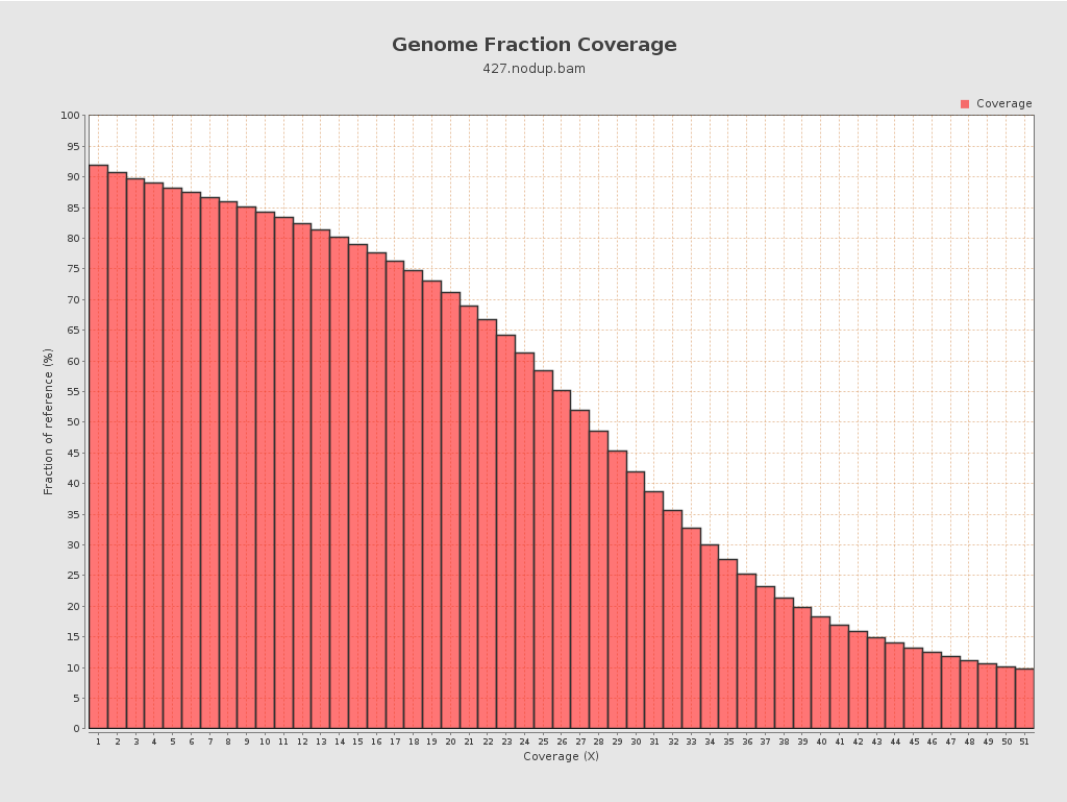
4. Results : Coverage Histogram



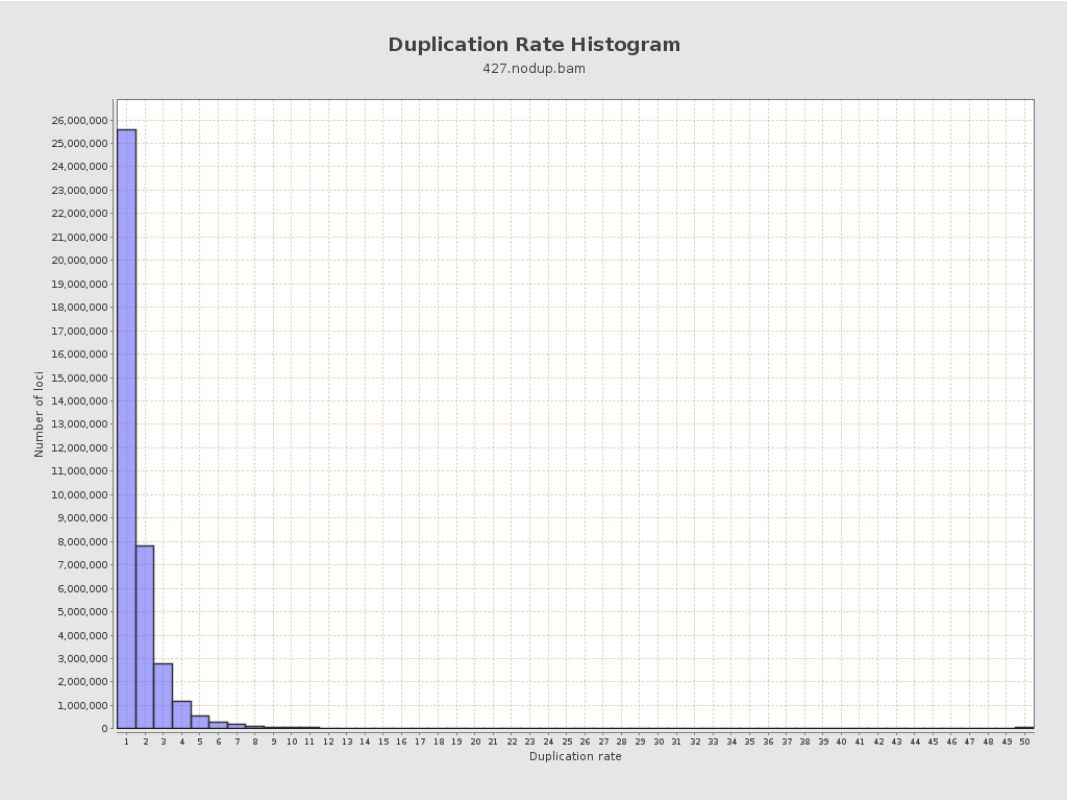
5. Results : Coverage Histogram (0-50X)



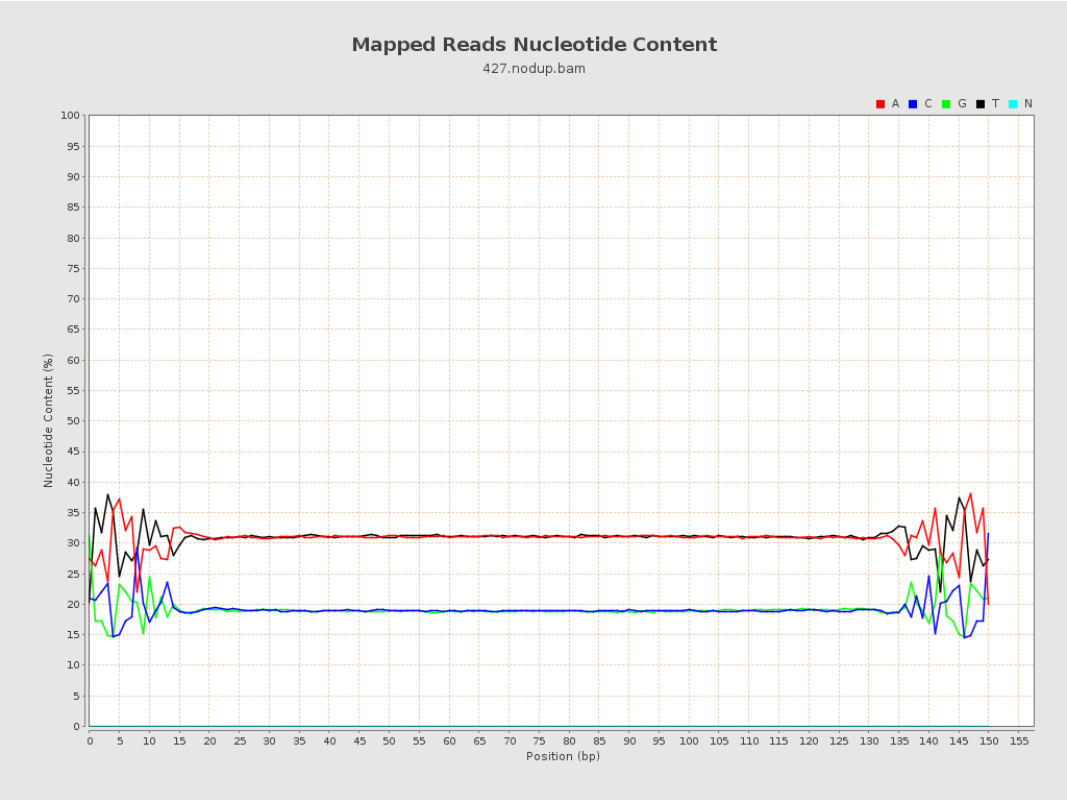
6. Results : Genome Fraction Coverage



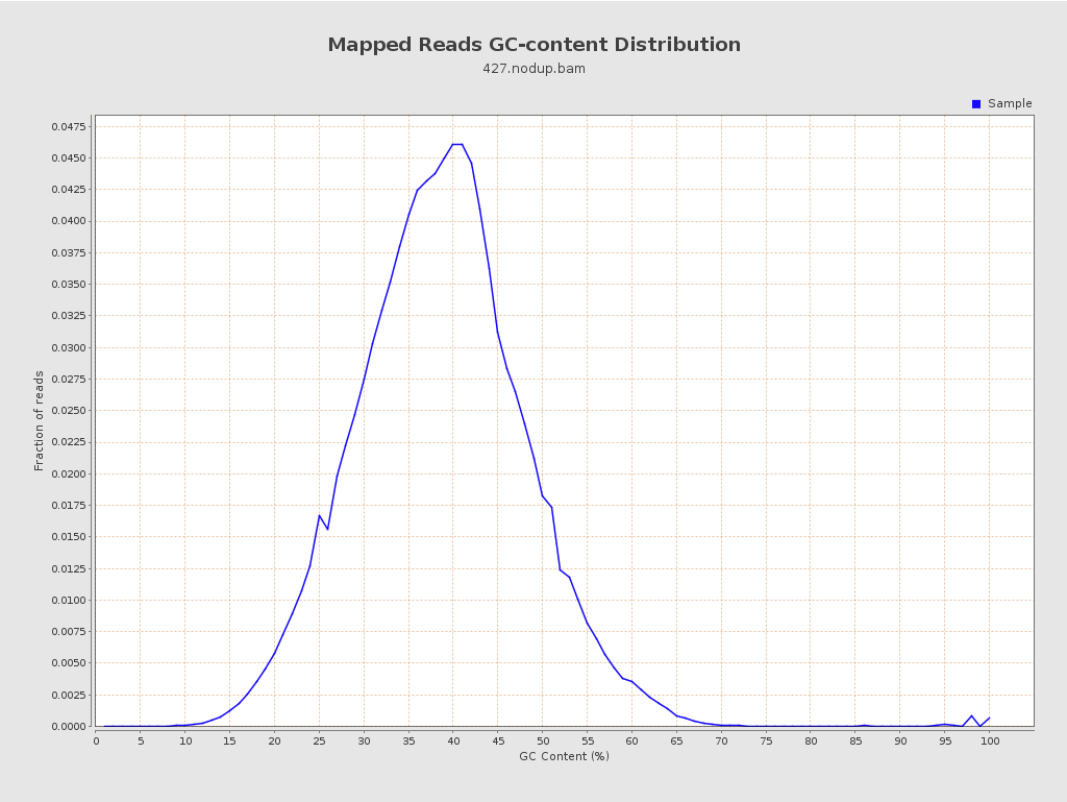
7. Results : Duplication Rate Histogram



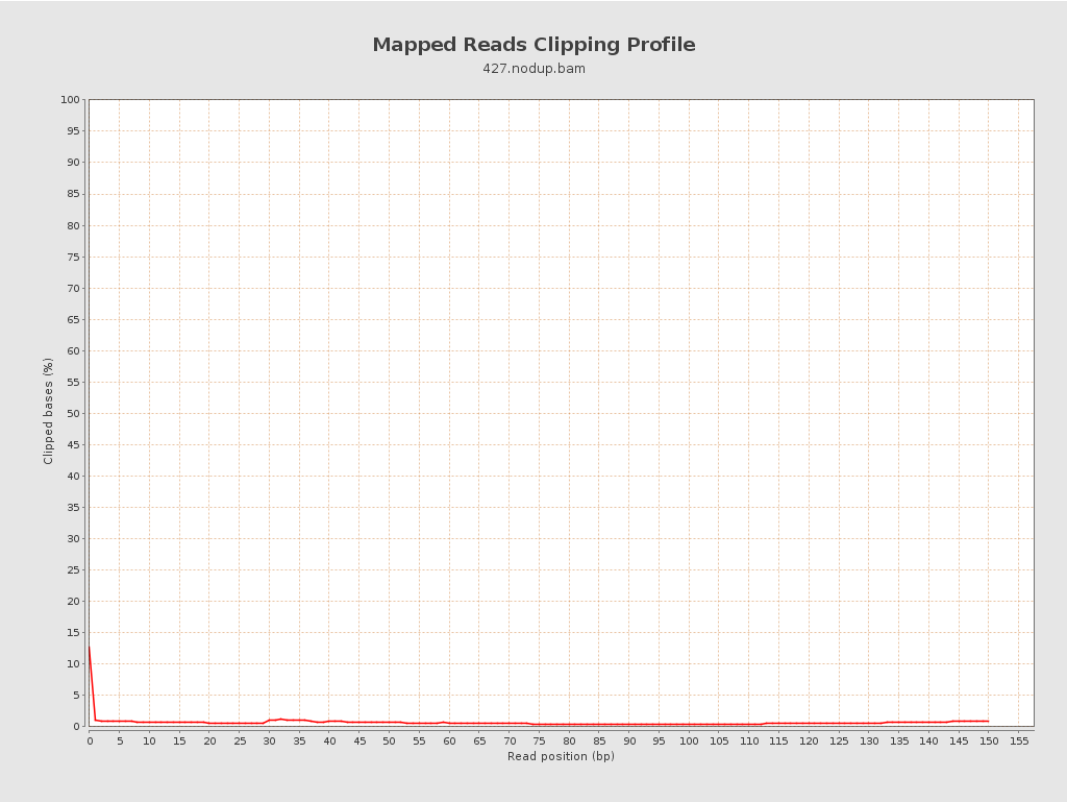
8. Results : Mapped Reads Nucleotide Content



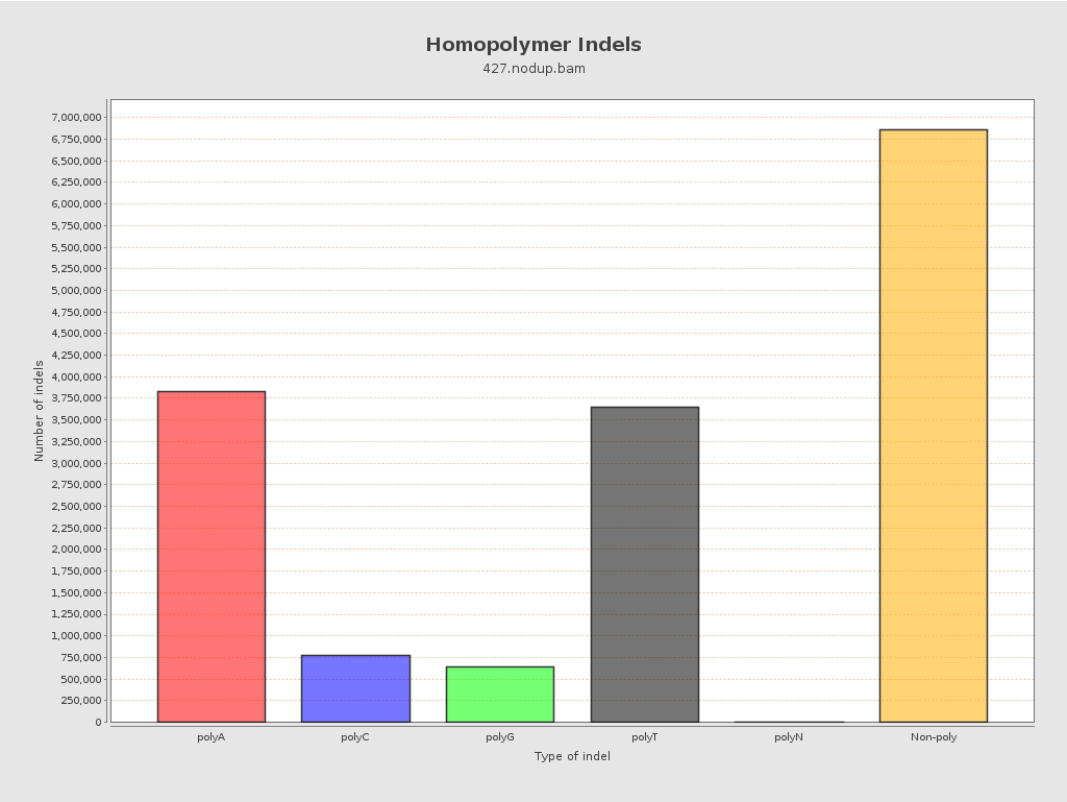
9. Results : Mapped Reads GC-content Distribution



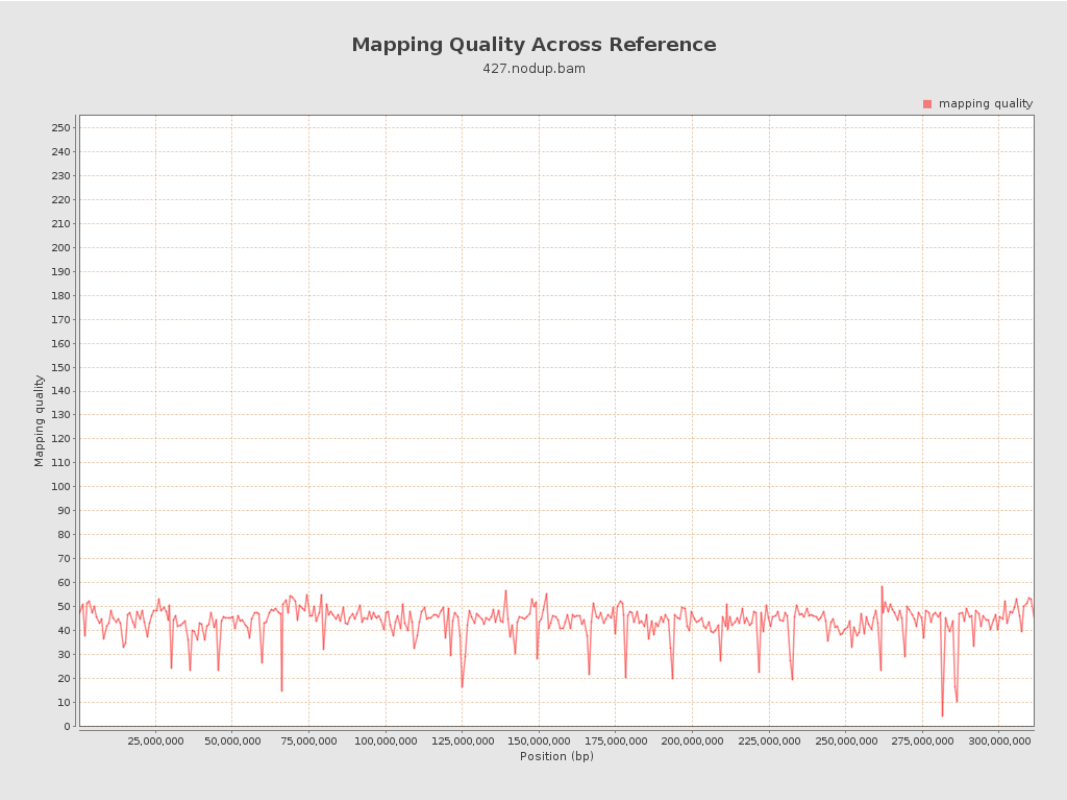
10. Results : Mapped Reads Clipping Profile



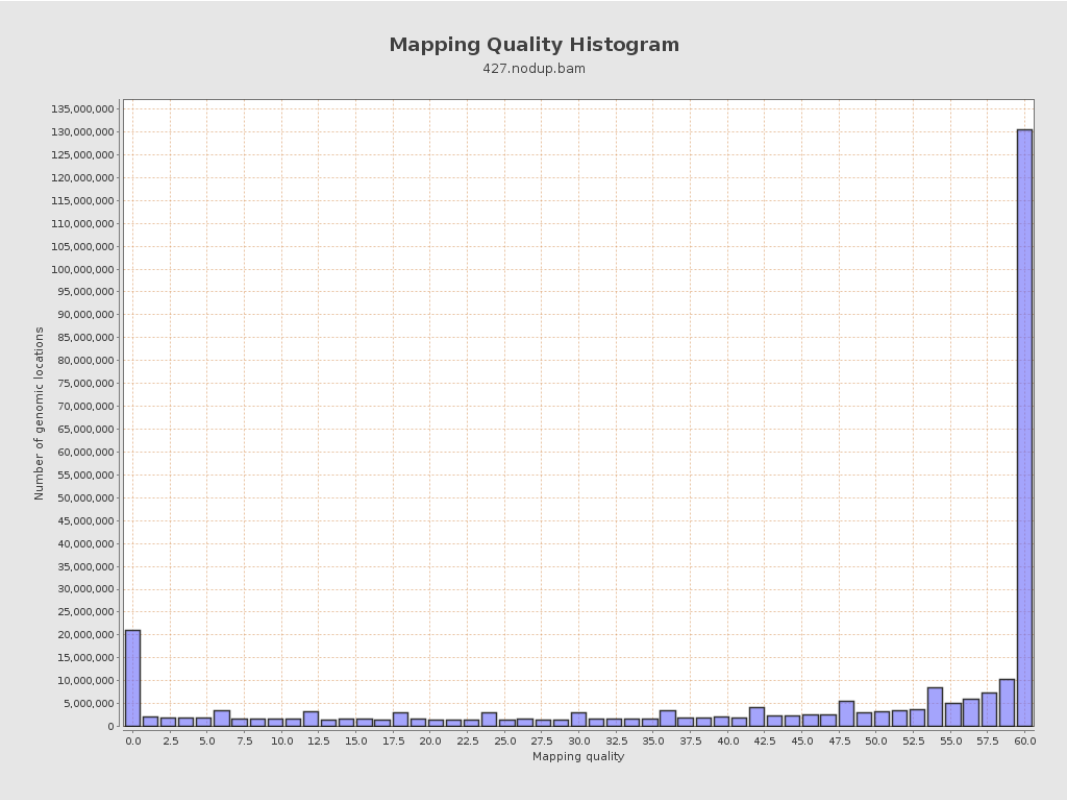
11. Results : Homopolymer Indels



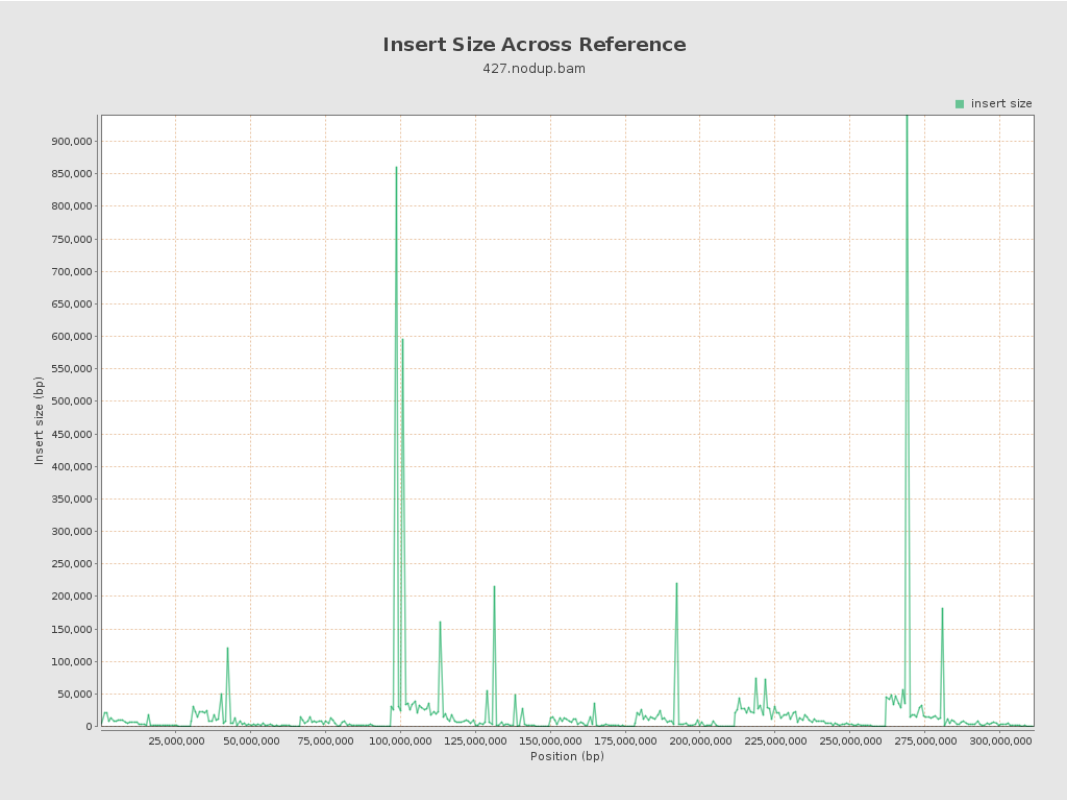
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram