

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:37:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/827
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/827 .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_136/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_136_S226_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_136/02-FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_136_S226_L002_R2_001.fastq.gz
Size of a homopolymer:	3
Number of windows:	400

Analysis date:	Mon May 29 21:37:33 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	85,226,075
Mapped reads	80,366,308 / 94.3%
Unmapped reads	4,859,767 / 5.7%
Mapped paired reads	80,366,308 / 94.3%
Mapped reads, first in pair	40,269,571 / 47.25%
Mapped reads, second in pair	40,096,737 / 47.05%
Mapped reads, both in pair	78,890,735 / 92.57%
Mapped reads, singletons	1,475,573 / 1.73%
Read min/max/mean length	30 / 151 / 148.16
Duplicated reads (flagged)	13,875,014 / 16.28%
Clipped reads	17,409,315 / 20.43%

2.2. ACGT Content

Number/percentage of A's	3,446,980,717 / 30.79%
Number/percentage of C's	2,151,776,073 / 19.22%
Number/percentage of T's	3,455,559,463 / 30.87%
Number/percentage of G's	2,140,961,189 / 19.12%
Number/percentage of N's	48,059 / 0%
GC Percentage	38.34%

2.3. Coverage

Mean	36.0169
Standard Deviation	281.8541

2.4. Mapping Quality

Mean Mapping Quality	44
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2.5. Insert size

Mean	227,408.13
Standard Deviation	2,249,370.11
P25/Median/P75	338 / 442 / 582

2.6. Mismatches and indels

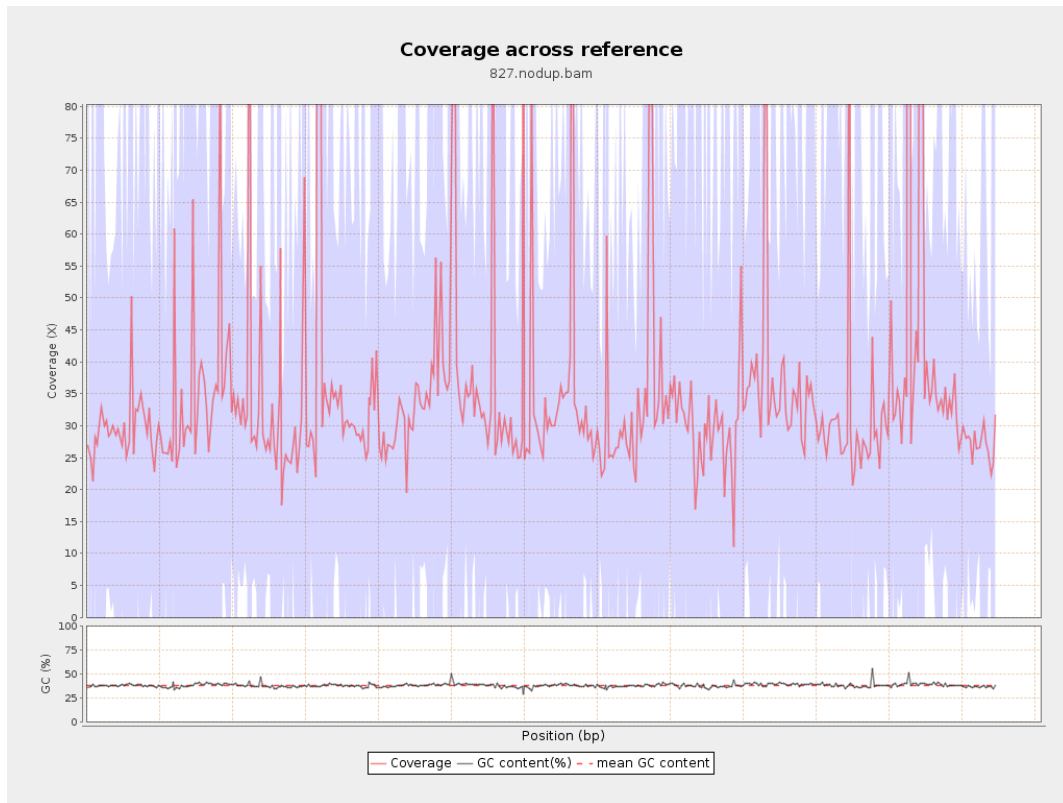
General error rate	2.3%
Mismatches	237,003,631
Insertions	7,407,232
Mapped reads with at least one insertion	8.3%
Deletions	7,667,836
Mapped reads with at least one deletion	8.47%
Homopolymer indels	56.13%

2.7. Chromosome stats

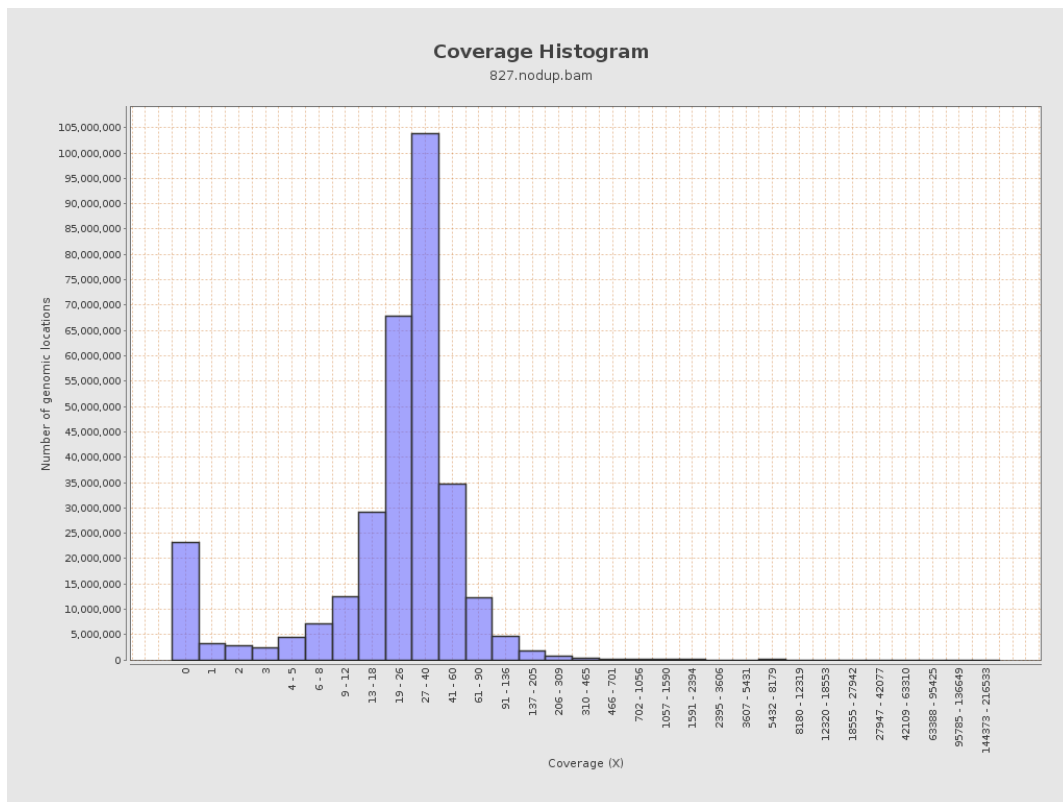
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	861505388	28.9832	74.5508

LT669789.1	36598175	1335338904	36.4865	291.9981
LT669790.1	30422129	1113431019	36.5994	240.6091
LT669791.1	52758100	1870110410	35.4469	226.9199
LT669792.1	28376109	996280706	35.1098	327.2973
LT669793.1	33388210	1120524032	33.5605	199.827
LT669794.1	50579949	1744208063	34.4842	245.1516
LT669795.1	49795044	2182988328	43.8395	438.5334

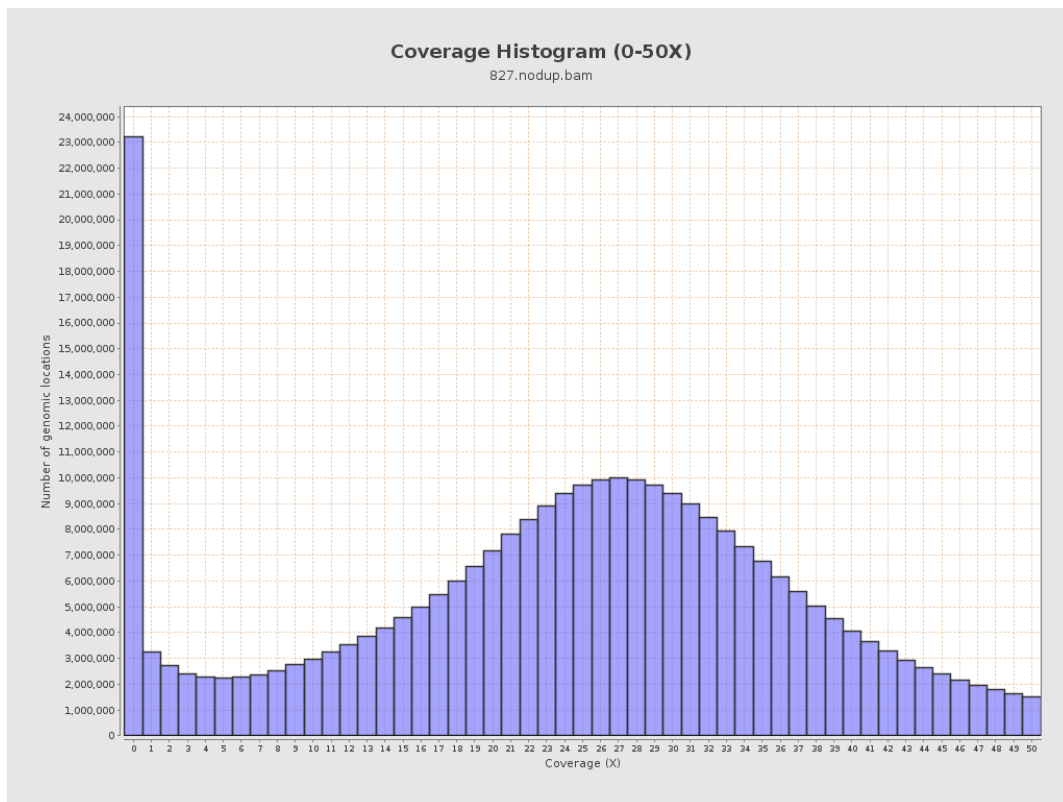
3. Results : Coverage across reference



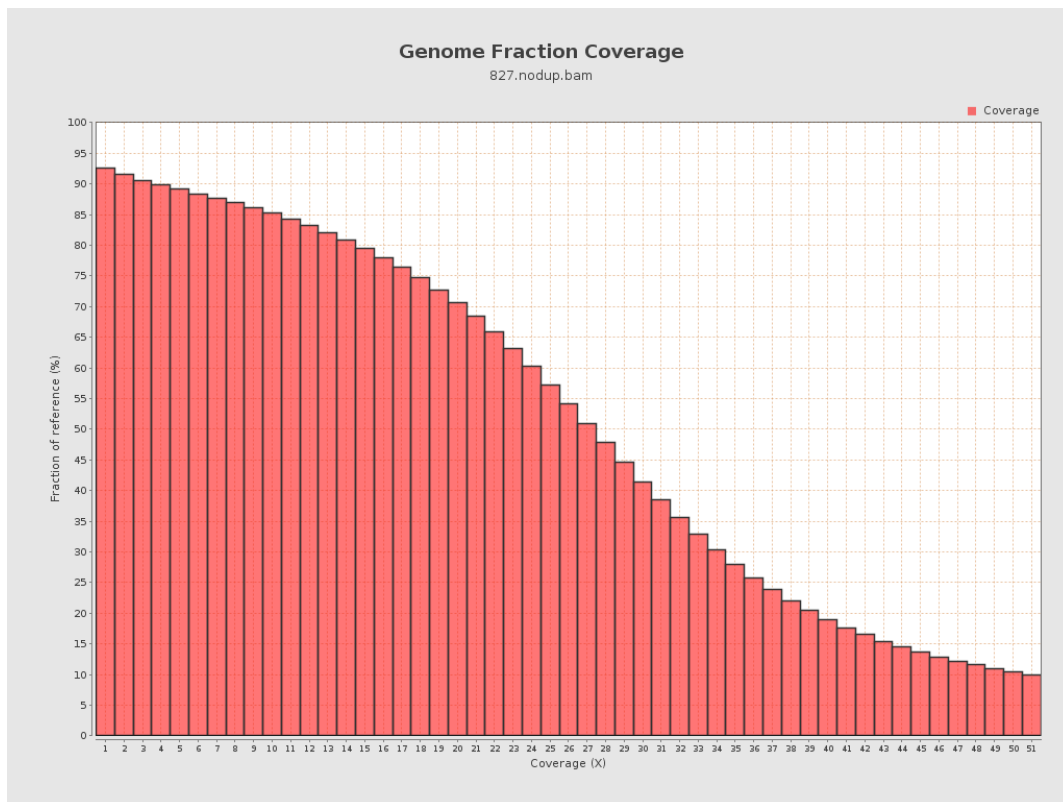
4. Results : Coverage Histogram



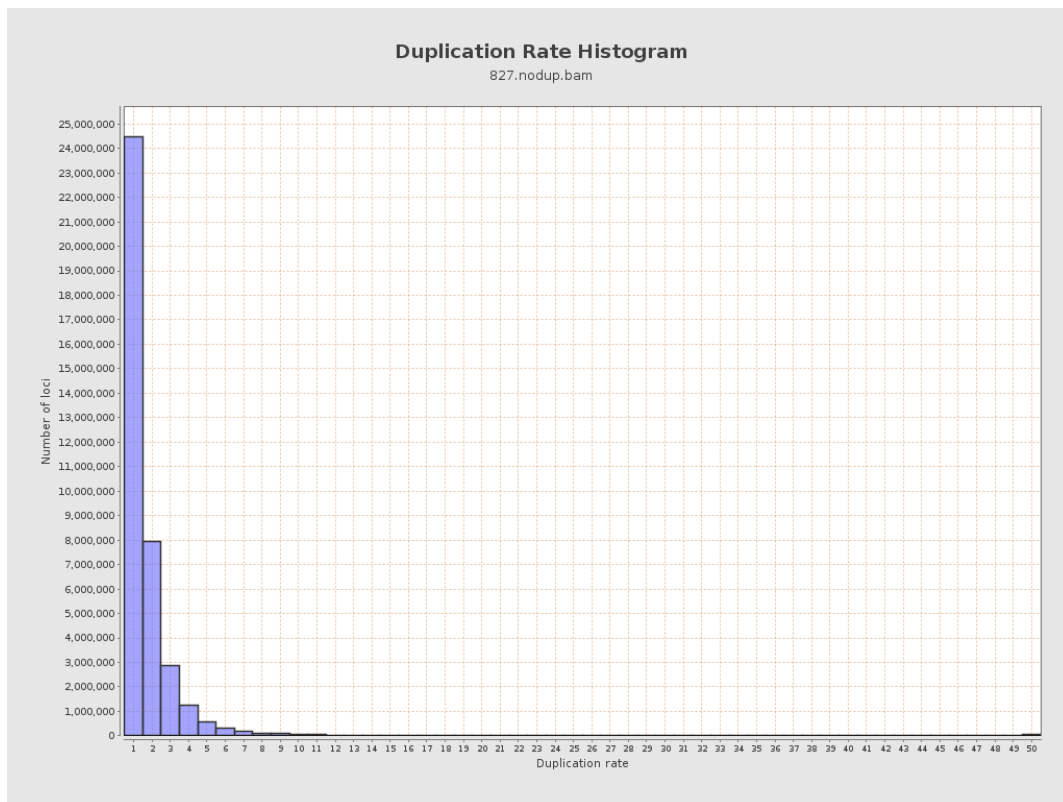
5. Results : Coverage Histogram (0-50X)



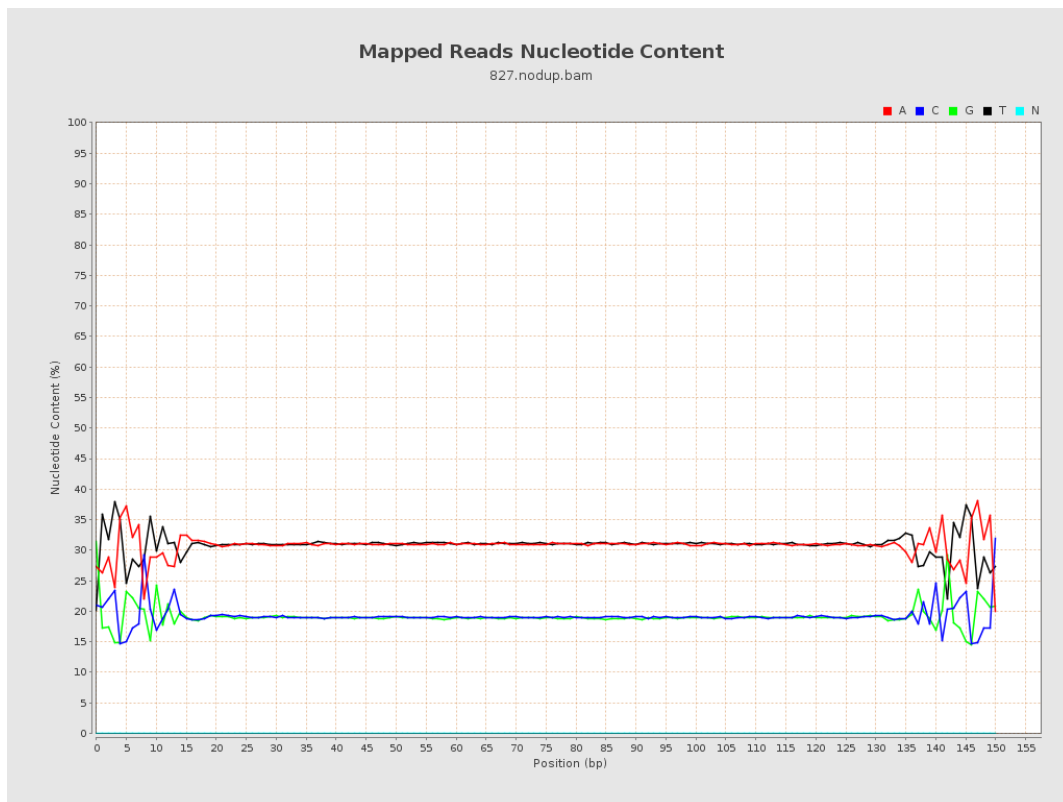
6. Results : Genome Fraction Coverage



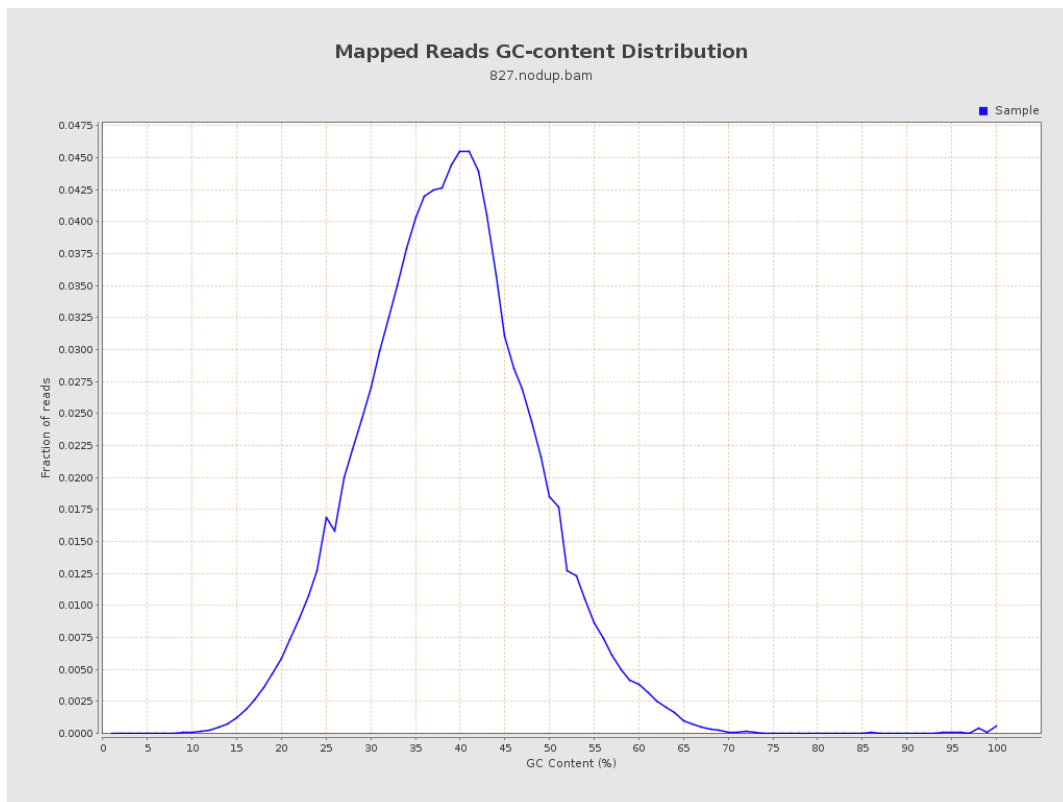
7. Results : Duplication Rate Histogram



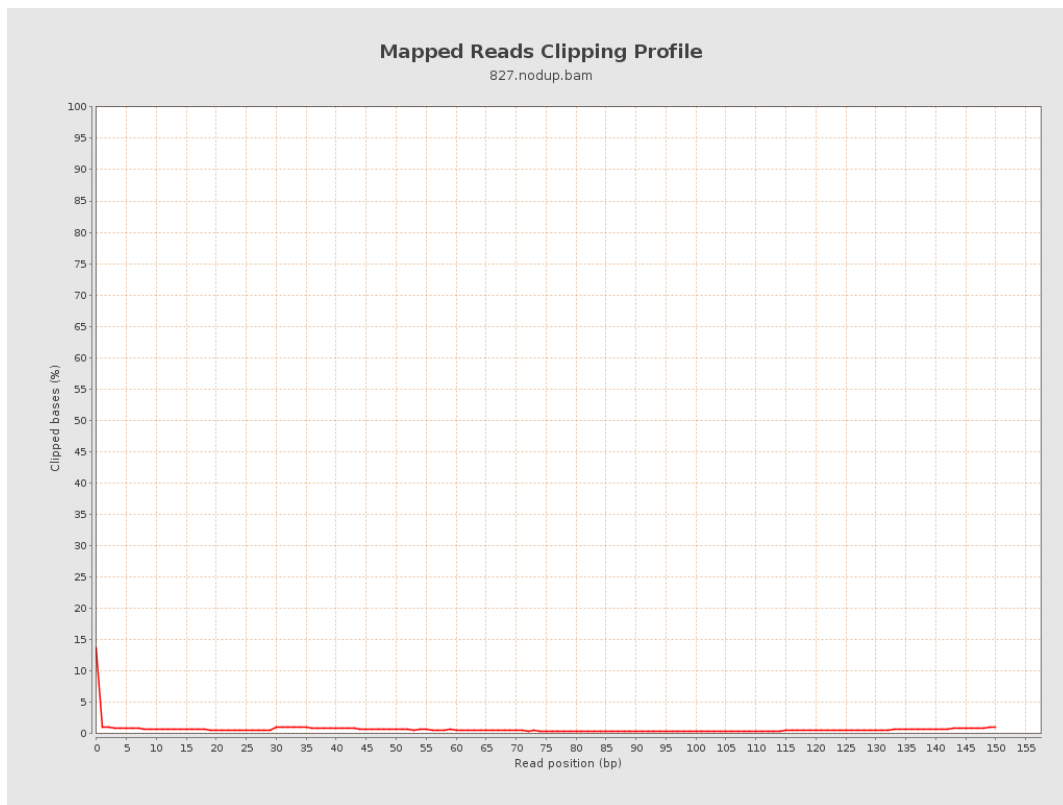
8. Results : Mapped Reads Nucleotide Content



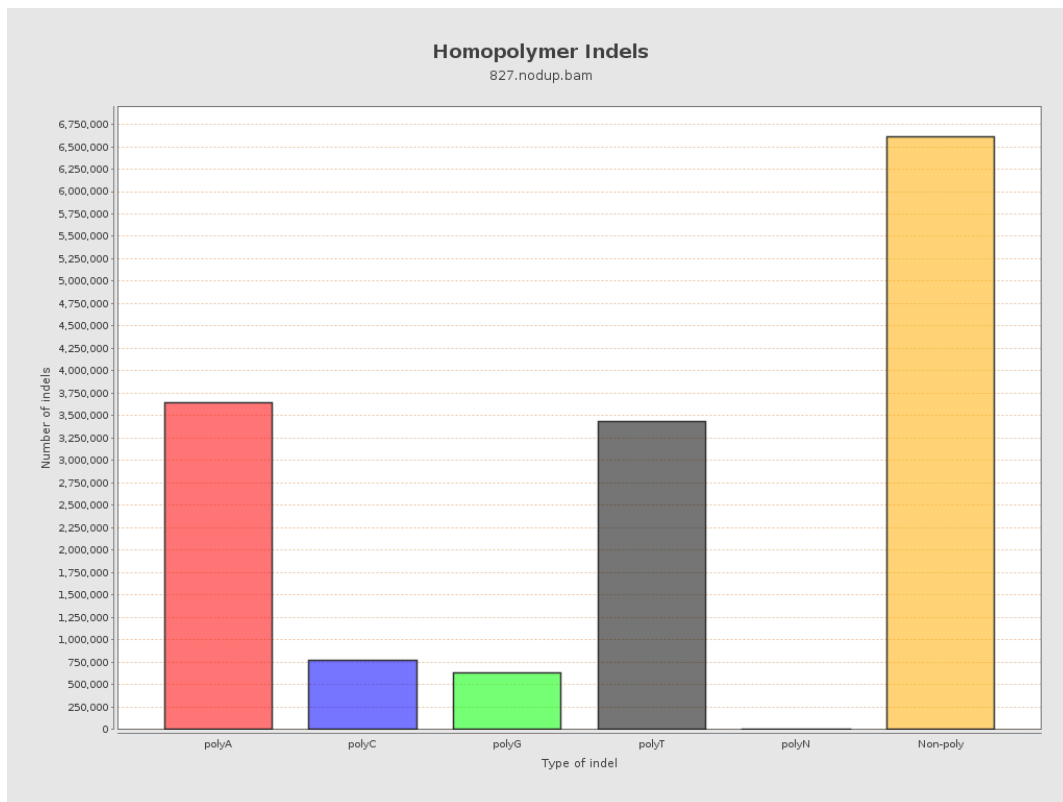
9. Results : Mapped Reads GC-content Distribution



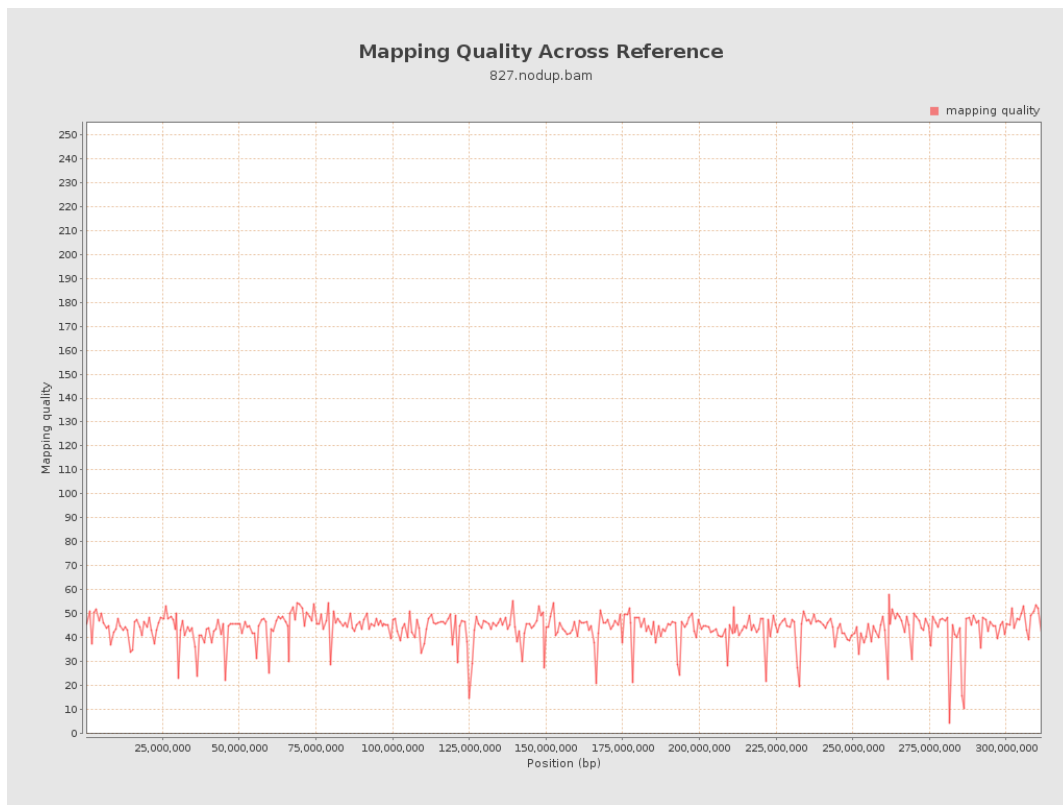
10. Results : Mapped Reads Clipping Profile



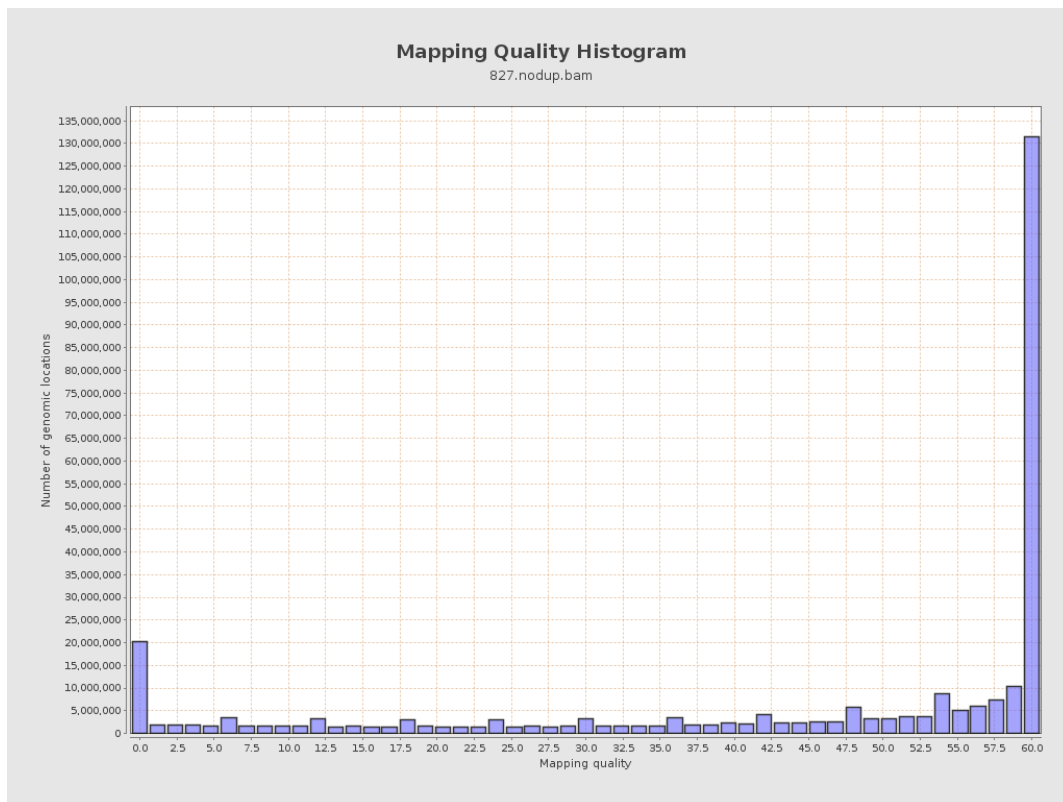
11. Results : Homopolymer Indels



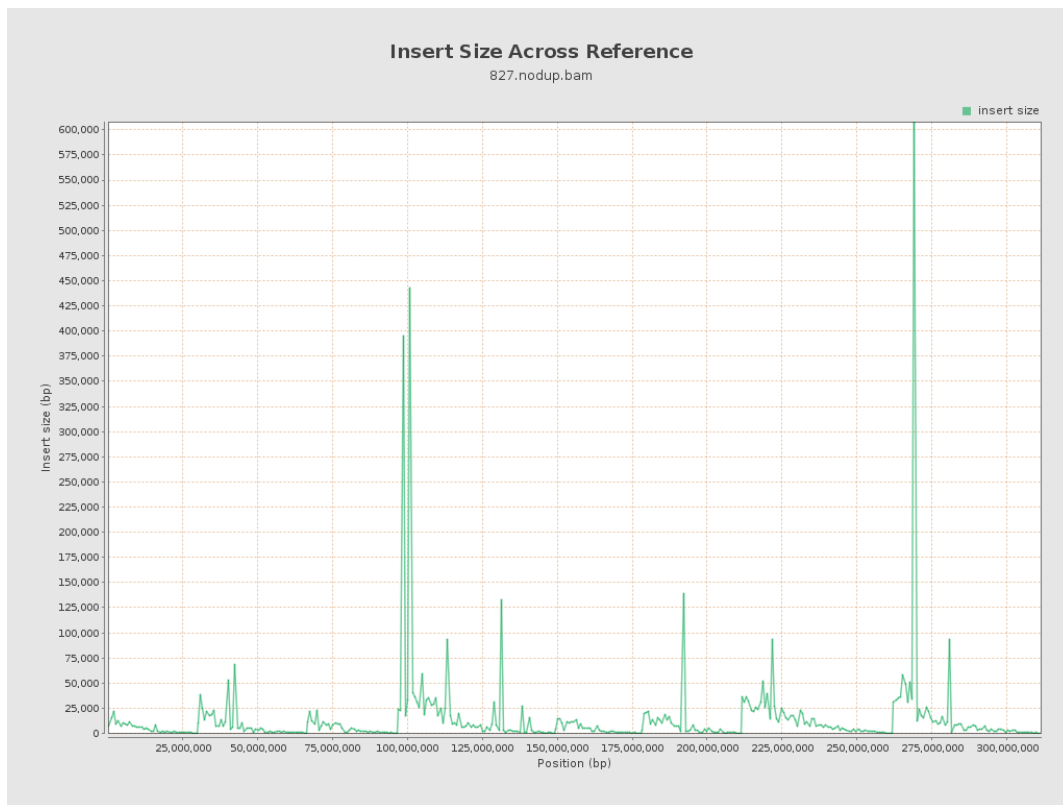
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

