Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:30:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1229
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1229 .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_117/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_117_S207_L002_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_117/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_117_S207_L002_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:30:01 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	68,784,847
Mapped reads	61,487,833 / 89.39%
Unmapped reads	7,297,014 / 10.61%
Mapped paired reads	61,487,833 / 89.39%
Mapped reads, first in pair	30,807,815 / 44.79%
Mapped reads, second in pair	30,680,018 / 44.6%
Mapped reads, both in pair	59,271,851 / 86.17%
Mapped reads, singletons	2,215,982 / 3.22%
Read min/max/mean length	30 / 151 / 148.18
Duplicated reads (flagged)	12,655,677 / 18.4%
Clipped reads	14,675,612 / 21.34%

2.2. ACGT Content

Number/percentage of A's	2,592,670,598 / 30.84%
Number/percentage of C's	1,611,585,814 / 19.17%
Number/percentage of T's	2,593,802,809 / 30.85%
Number/percentage of G's	1,609,002,135 / 19.14%
Number/percentage of N's	34,379 / 0%
GC Percentage	38.31%

2.3. Coverage

Mean	27.0442
Standard Deviation	276.7817

2.4. Mapping Quality

Mean Mapping Quality	44.67

2.5. Insert size

Mean	258,106.69
Standard Deviation	2,456,705.69
P25/Median/P75	322 / 421 / 553

2.6. Mismatches and indels

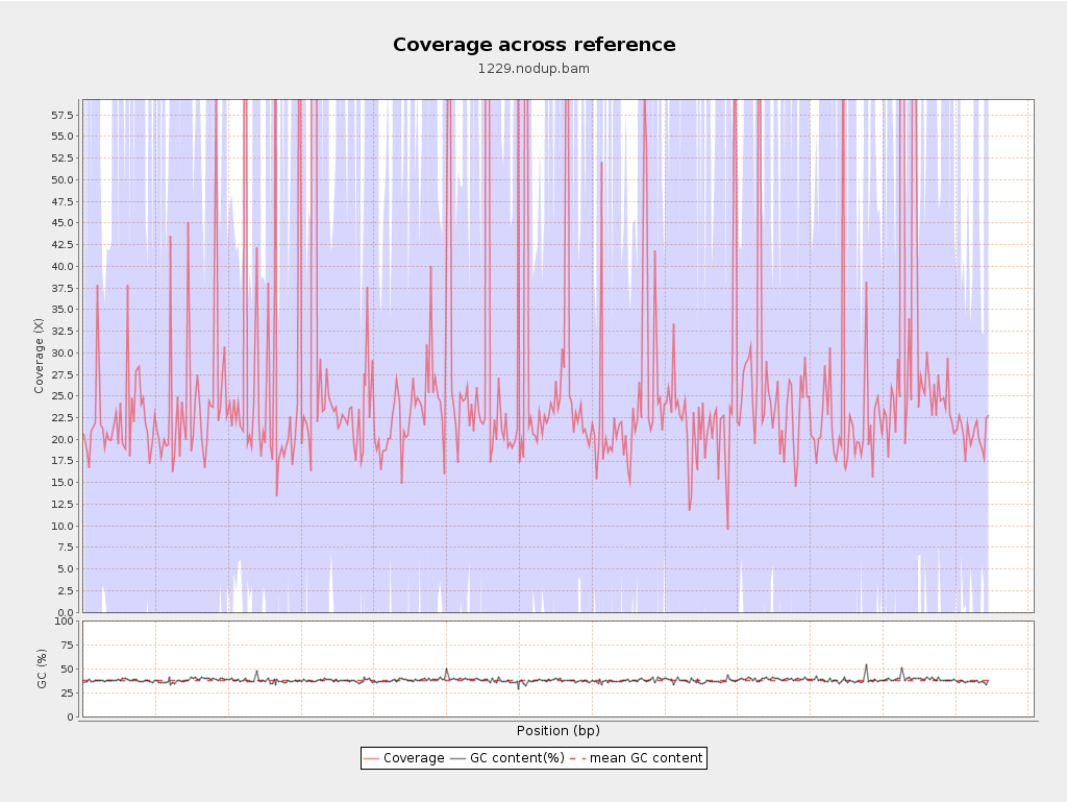
General error rate	2.34%
Mismatches	179,707,144
Insertions	6,150,127
Mapped reads with at least one insertion	8.92%
Deletions	5,755,502
Mapped reads with at least one deletion	8.3%
Homopolymer indels	57.27%

2.7. Chromosome stats

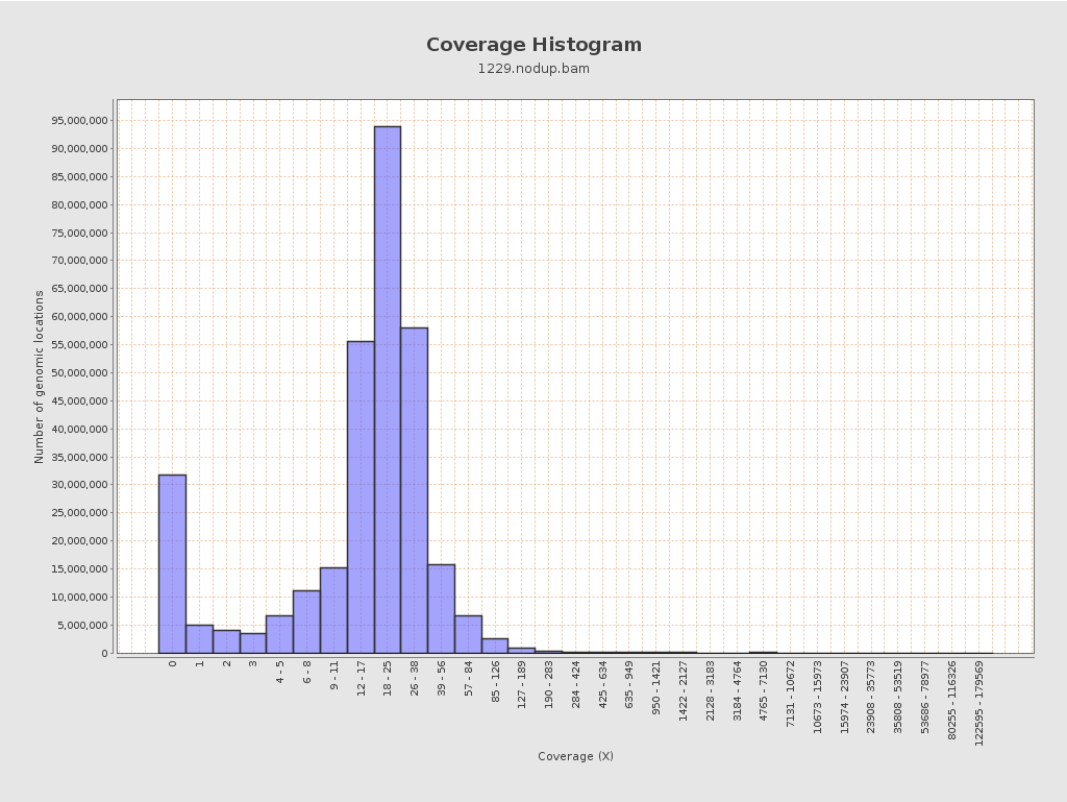
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	653841340	21.9968	112.5239

LT669789.1	36598175	991846249	27.101	300.2699
LT669790.1	30422129	1029243571	33.8321	405.8413
LT669791.1	52758100	1404825518	26.6277	321.3193
LT669792.1	28376109	762521618	26.872	266.3332
LT669793.1	33388210	802867786	24.0464	140.0829
LT669794.1	50579949	1279756659	25.3017	248.0181
LT669795.1	49795044	1503208384	30.1879	281.9312

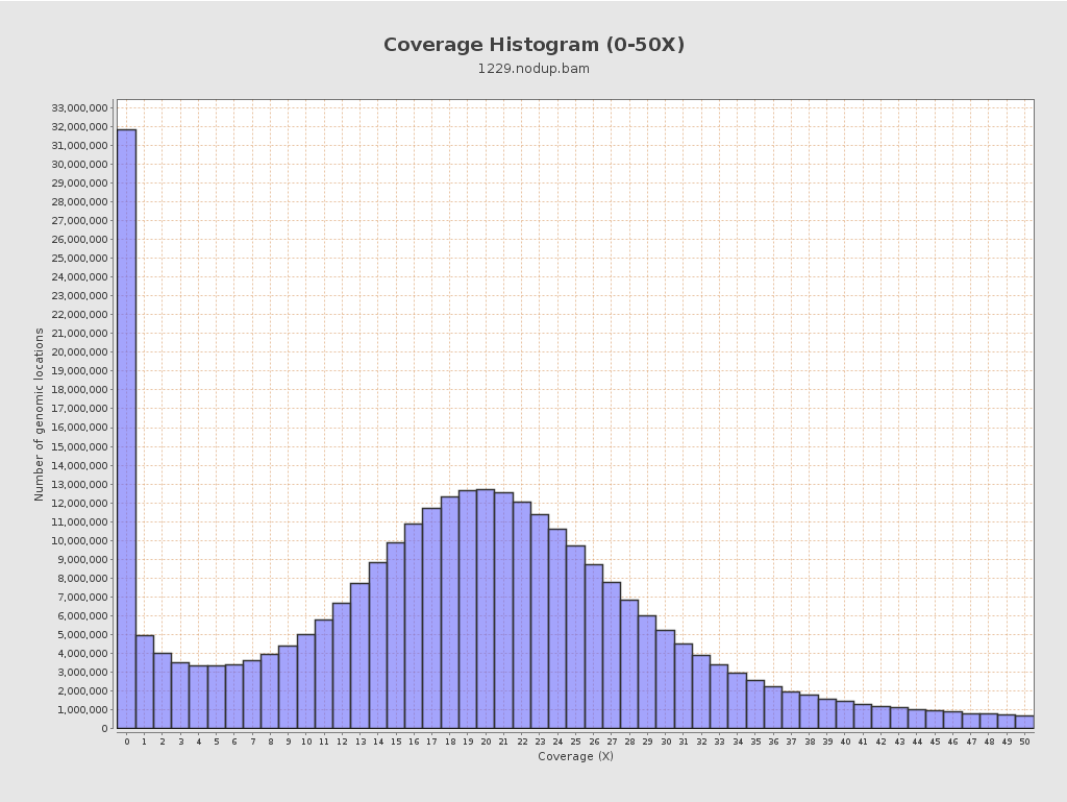
3. Results : Coverage across reference



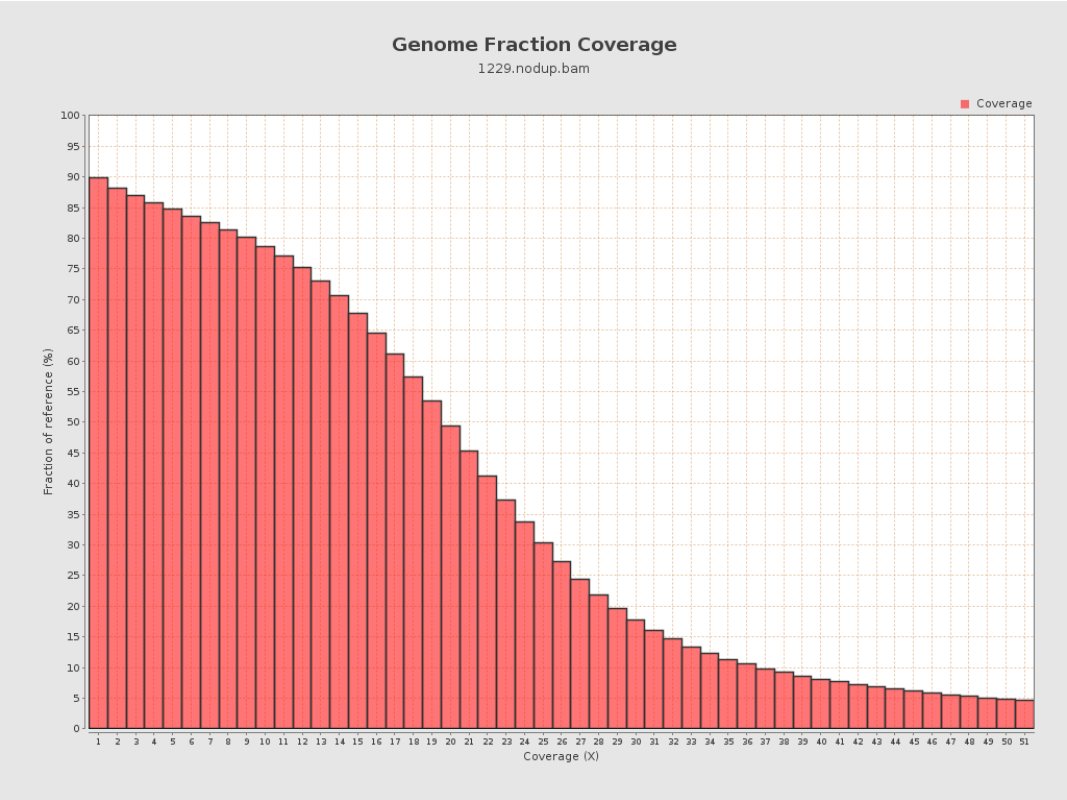
4. Results : Coverage Histogram



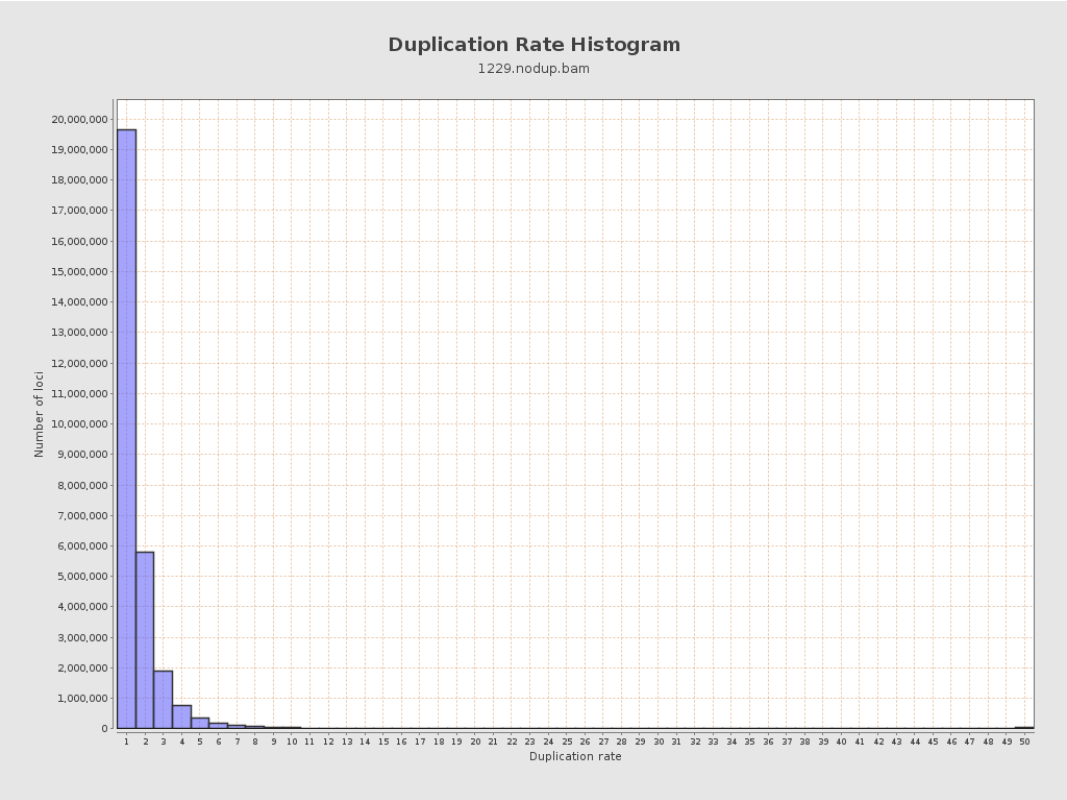
5. Results : Coverage Histogram (0-50X)



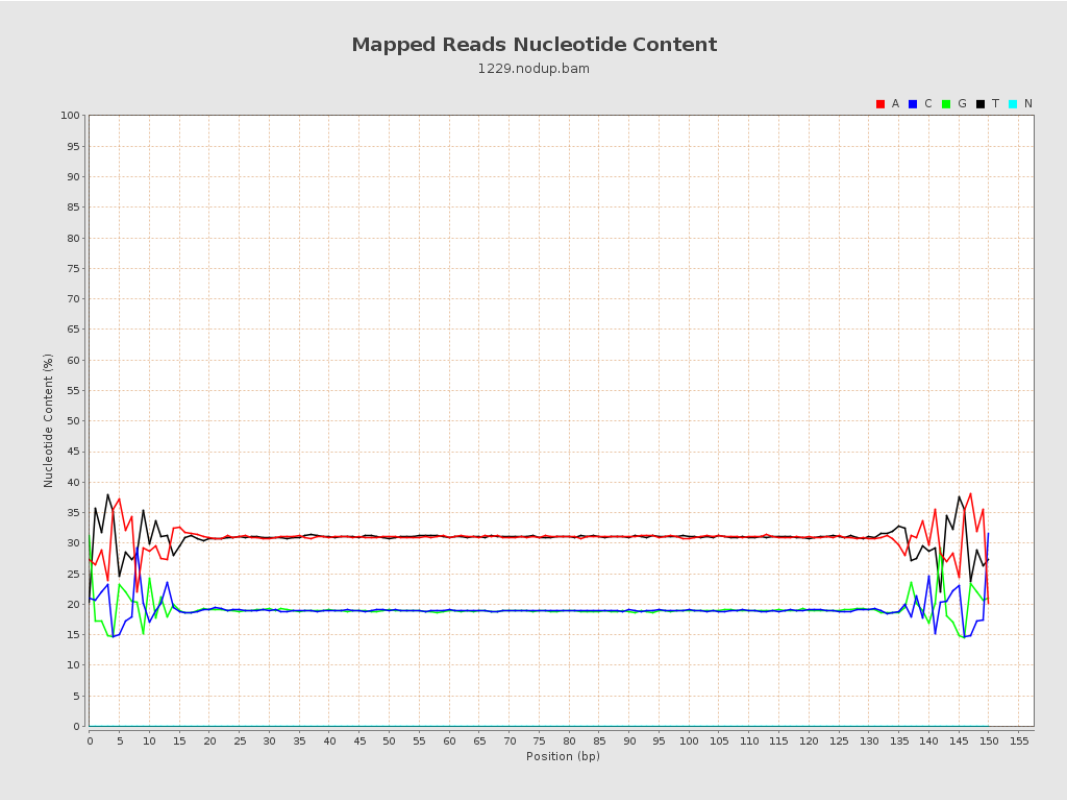
6. Results : Genome Fraction Coverage



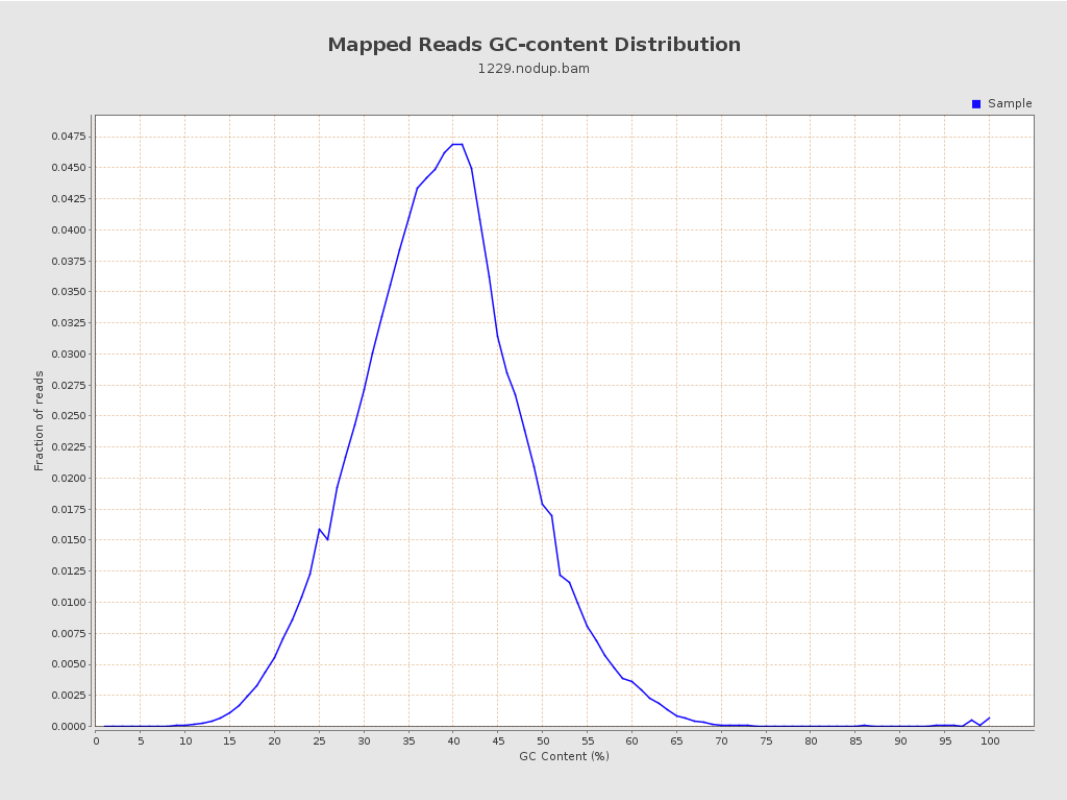
7. Results : Duplication Rate Histogram



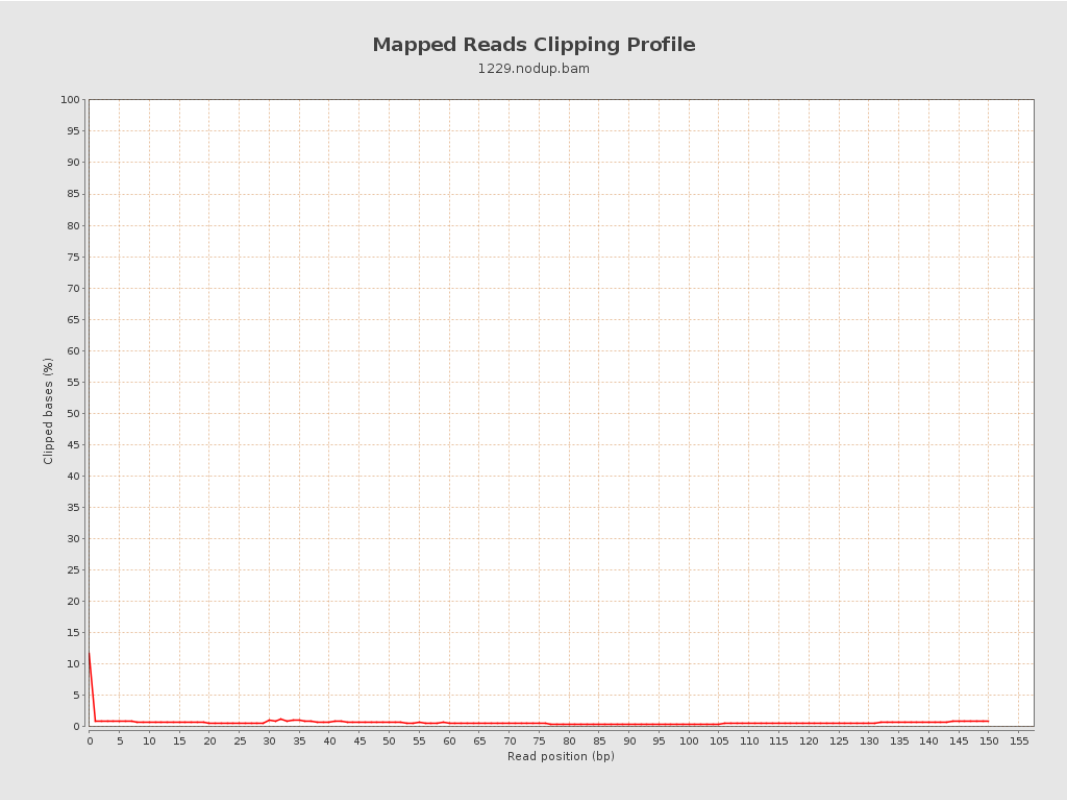
8. Results : Mapped Reads Nucleotide Content



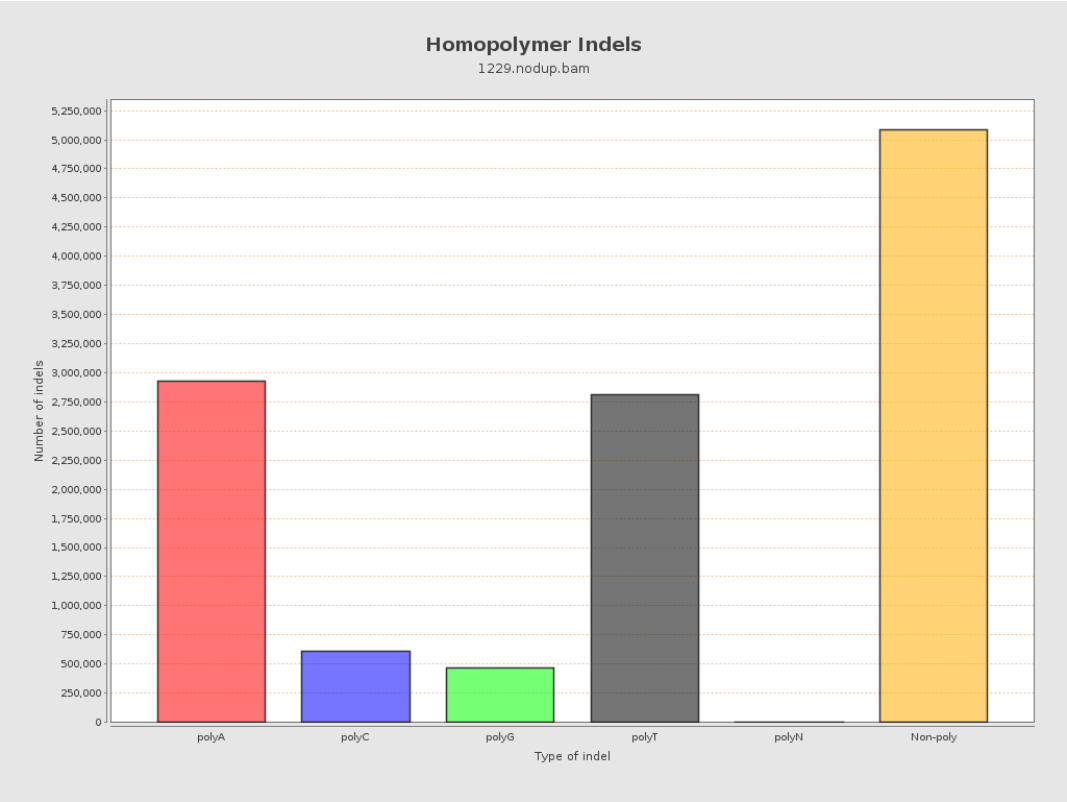
9. Results : Mapped Reads GC-content Distribution



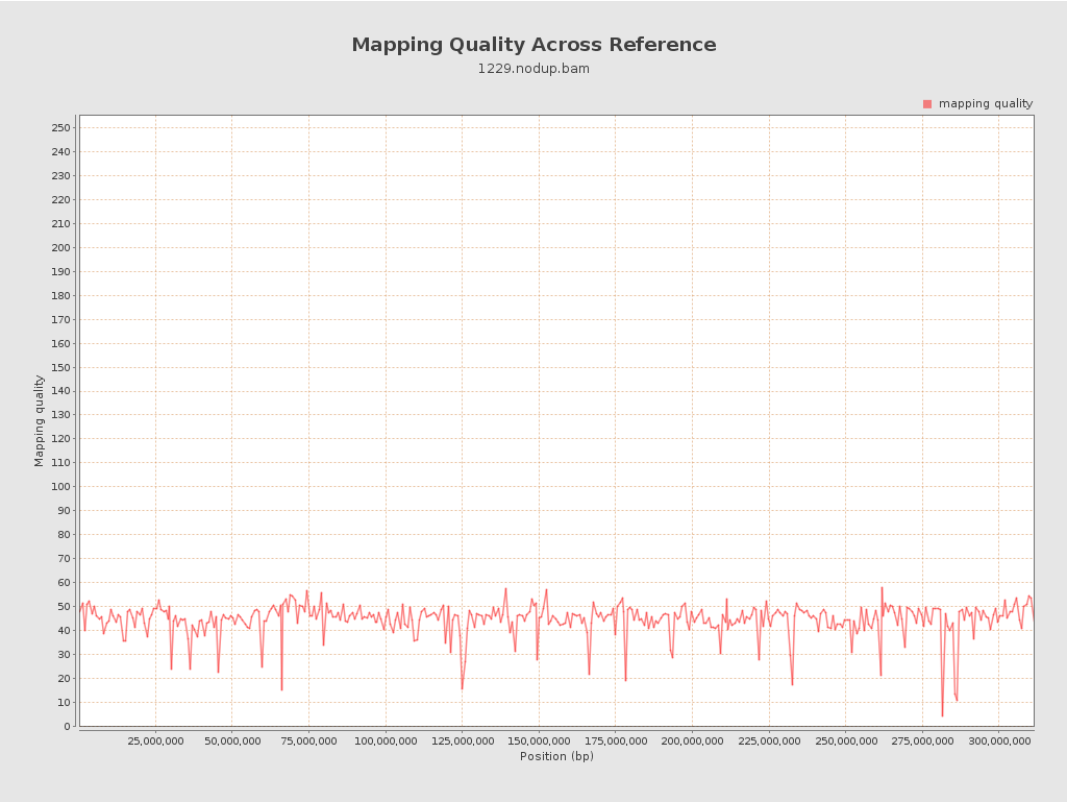
10. Results : Mapped Reads Clipping Profile



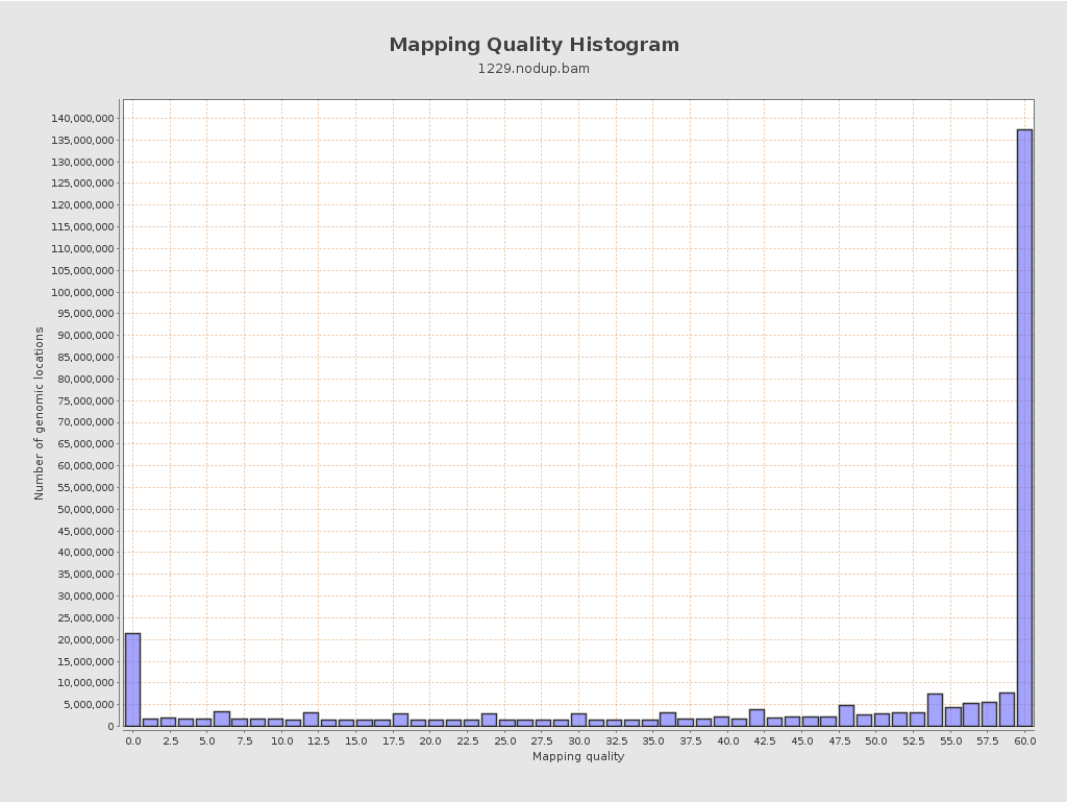
11. Results : Homopolymer Indels



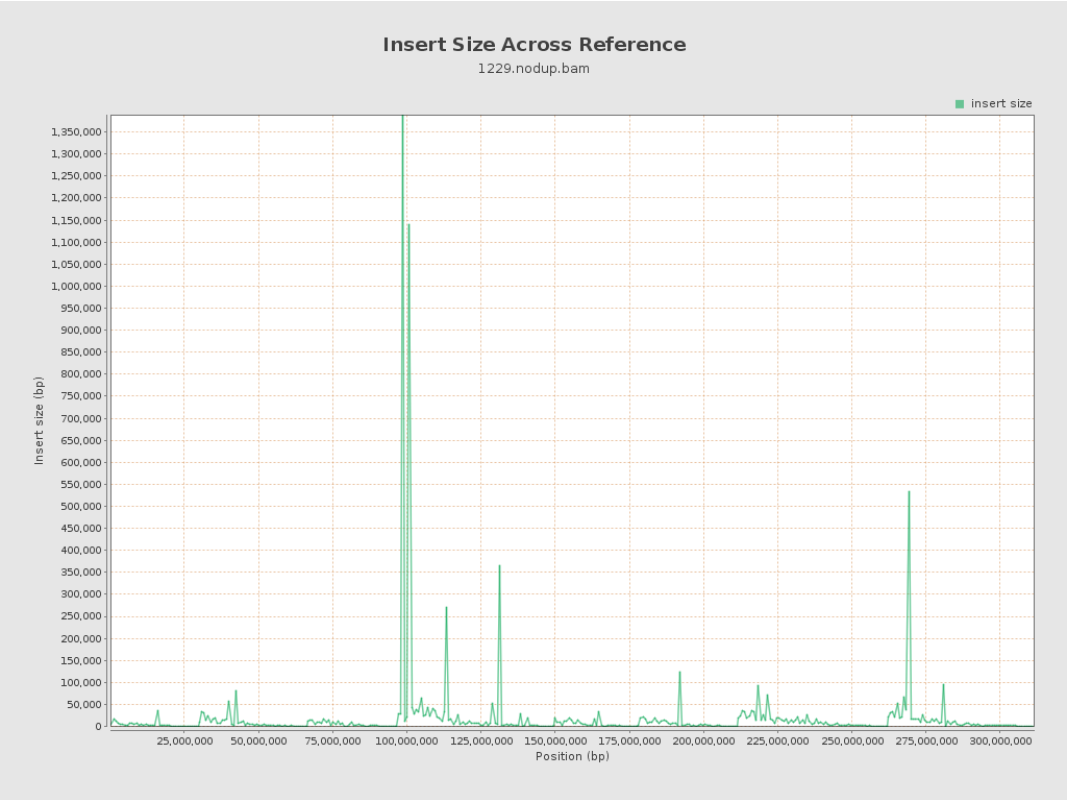
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram