Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:27:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/136
1
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1361 .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_421/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_421_S396_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_421/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_421_S396_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:27:11 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	53,938,696
Mapped reads	48,989,956 / 90.83%
Unmapped reads	4,948,740 / 9.17%
Mapped paired reads	48,989,956 / 90.83%
Mapped reads, first in pair	24,564,064 / 45.54%
Mapped reads, second in pair	24,425,892 / 45.28%
Mapped reads, both in pair	47,290,701 / 87.67%
Mapped reads, singletons	1,699,255 / 3.15%
Read min/max/mean length	30 / 151 / 148.03
Duplicated reads (flagged)	8,281,988 / 15.35%
Clipped reads	11,814,993 / 21.9%

2.2. ACGT Content

Number/percentage of A's	2,075,787,553 / 30.92%
Number/percentage of C's	1,279,967,746 / 19.06%
Number/percentage of T's	2,080,610,971 / 30.99%
Number/percentage of G's	1,277,597,358 / 19.03%
Number/percentage of N's	23,362 / 0%
GC Percentage	38.09%

2.3. Coverage

Mean	21.6016
Standard Deviation	205.9445

2.4. Mapping Quality

Mean Mapping Quality	43.86

2.5. Insert size

Mean	299,815.89
Standard Deviation	2,653,907.04
P25/Median/P75	392 / 509 / 654

2.6. Mismatches and indels

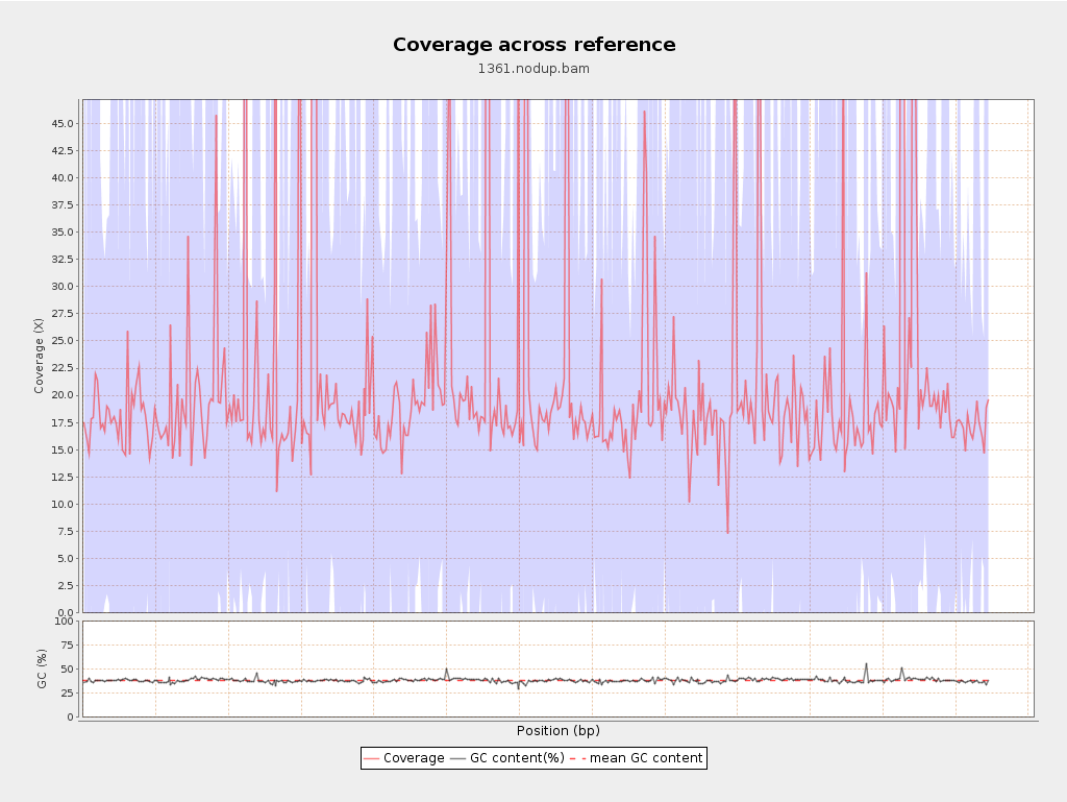
General error rate	2.46%
Mismatches	151,076,052
Insertions	5,021,783
Mapped reads with at least one insertion	9.11%
Deletions	4,794,227
Mapped reads with at least one deletion	8.65%
Homopolymer indels	57.07%

2.7. Chromosome stats

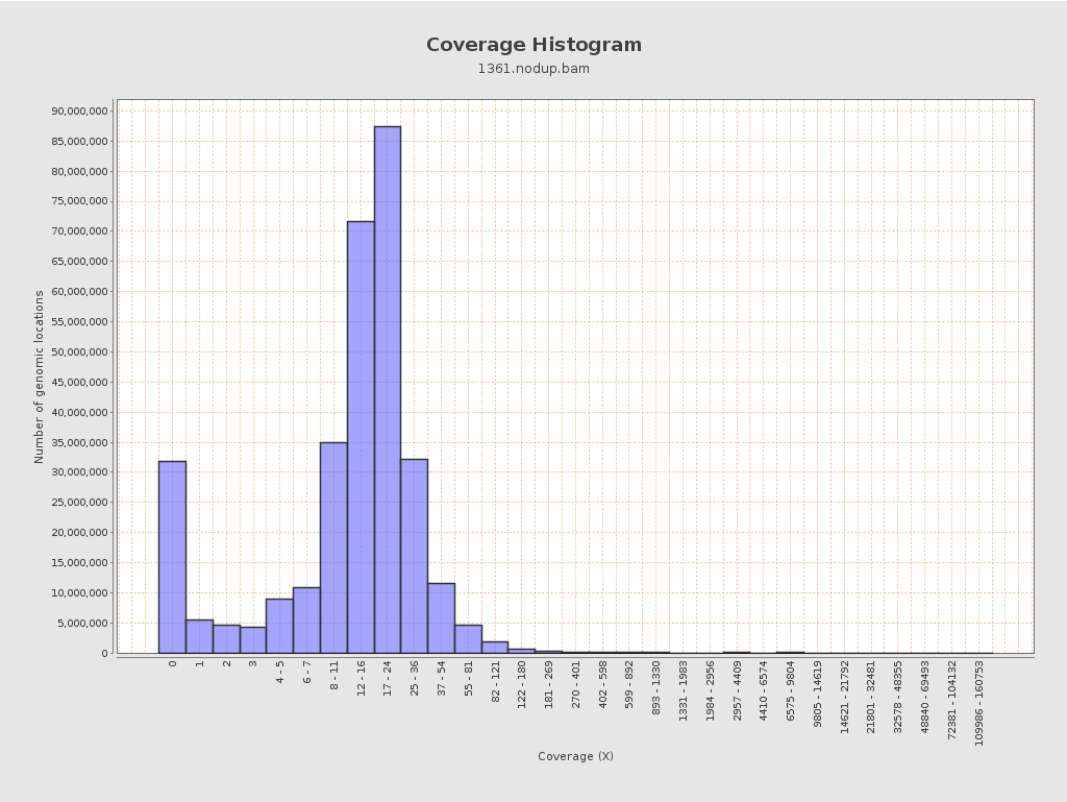
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	529733311	17.8215	89.8532

LT669789.1	36598175	794342018	21.7044	217.3911
LT669790.1	30422129	802358337	26.3742	297.7321
LT669791.1	52758100	1129584575	21.4106	222.6127
LT669792.1	28376109	624681128	22.0143	226.8284
LT669793.1	33388210	644221469	19.2949	107.6568
LT669794.1	50579949	1011930377	20.0066	162.6139
LT669795.1	49795044	1195127798	24.0009	235.0344

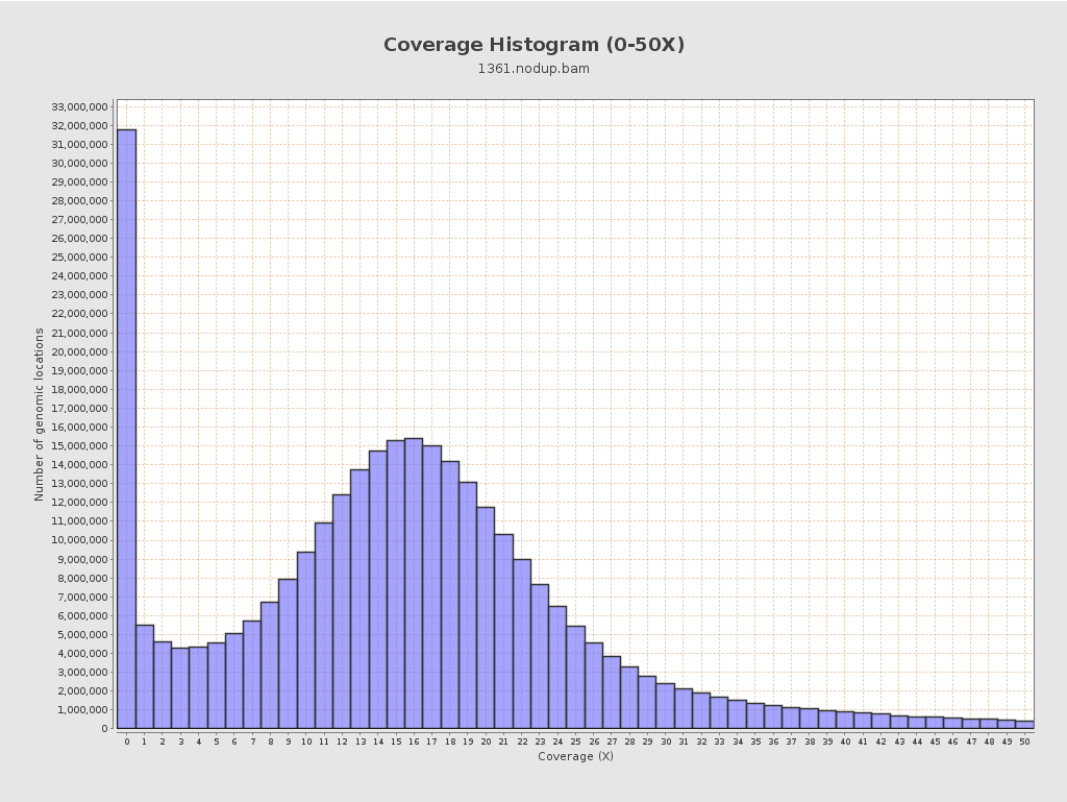
3. Results : Coverage across reference



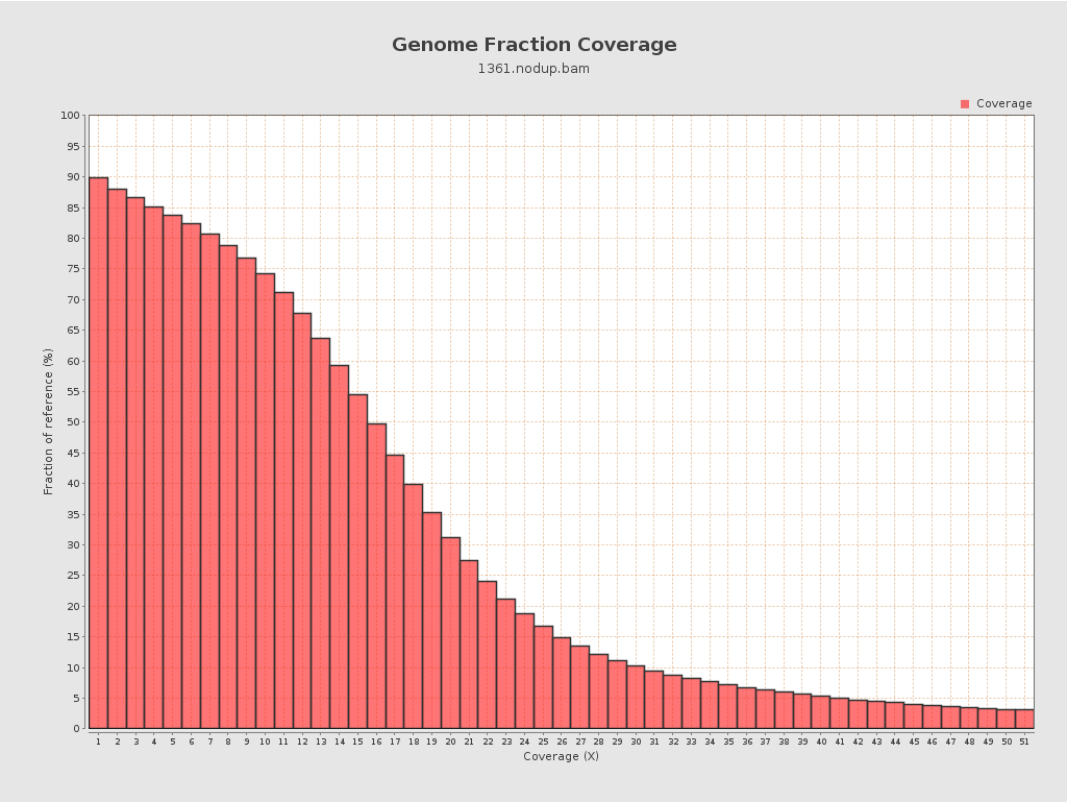
4. Results : Coverage Histogram



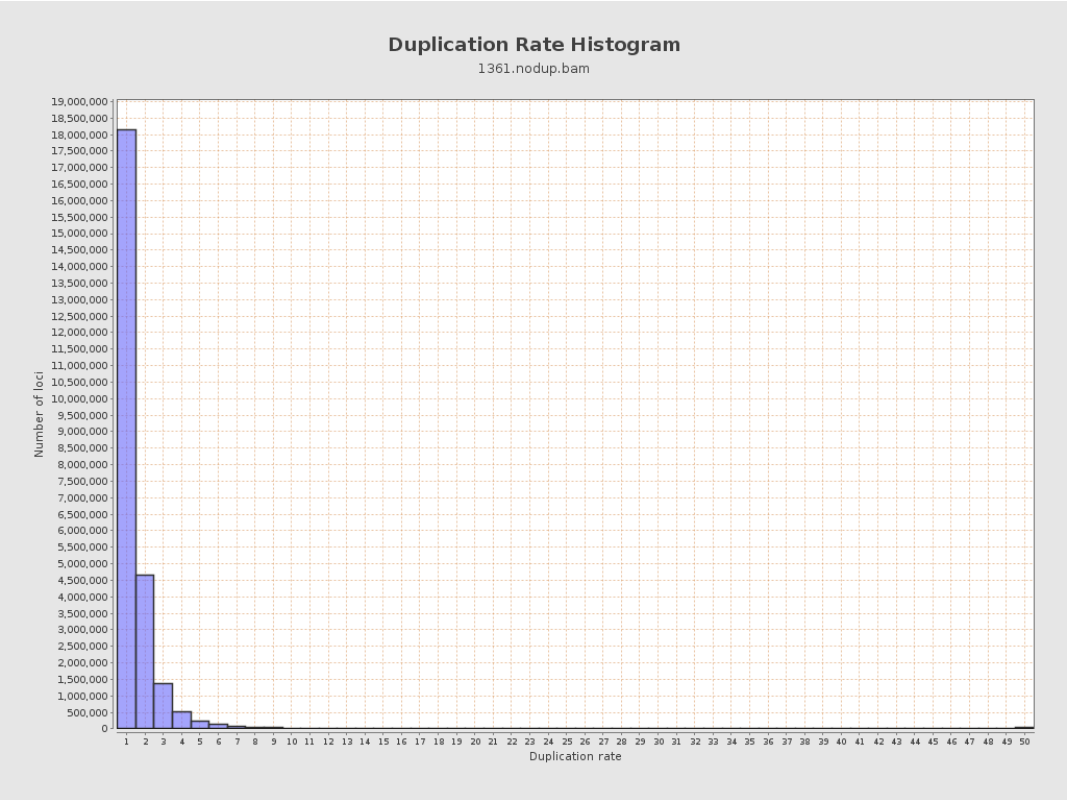
5. Results : Coverage Histogram (0-50X)



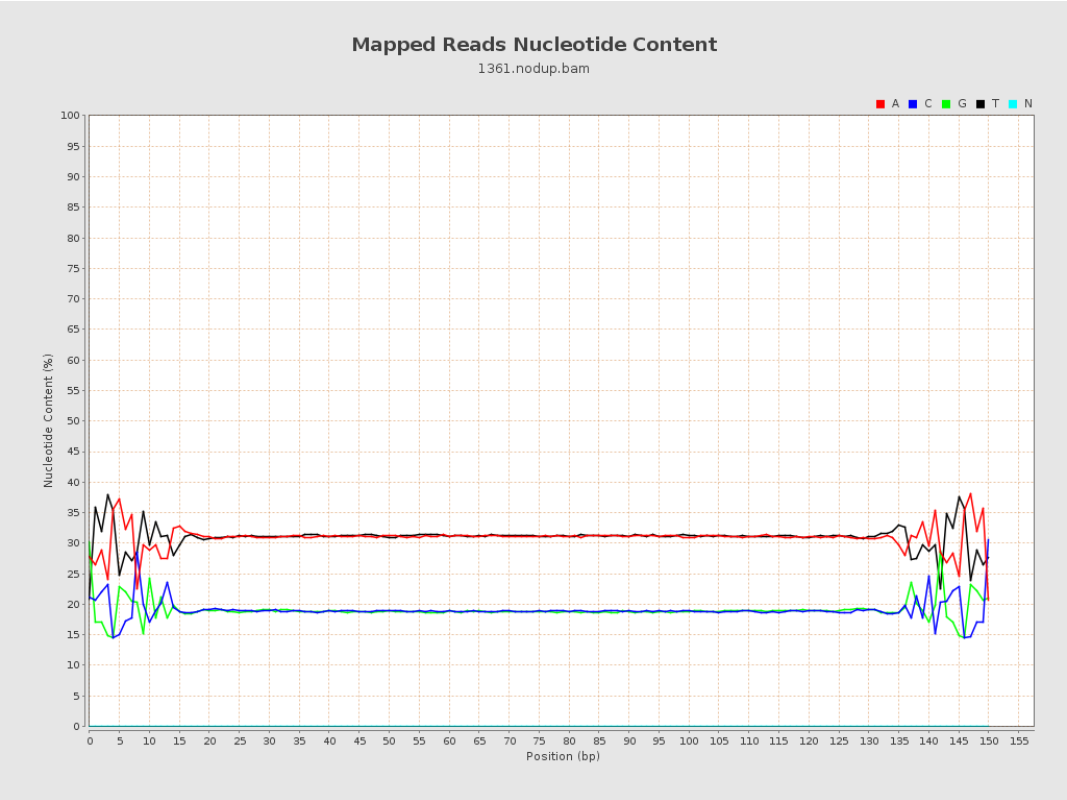
6. Results : Genome Fraction Coverage



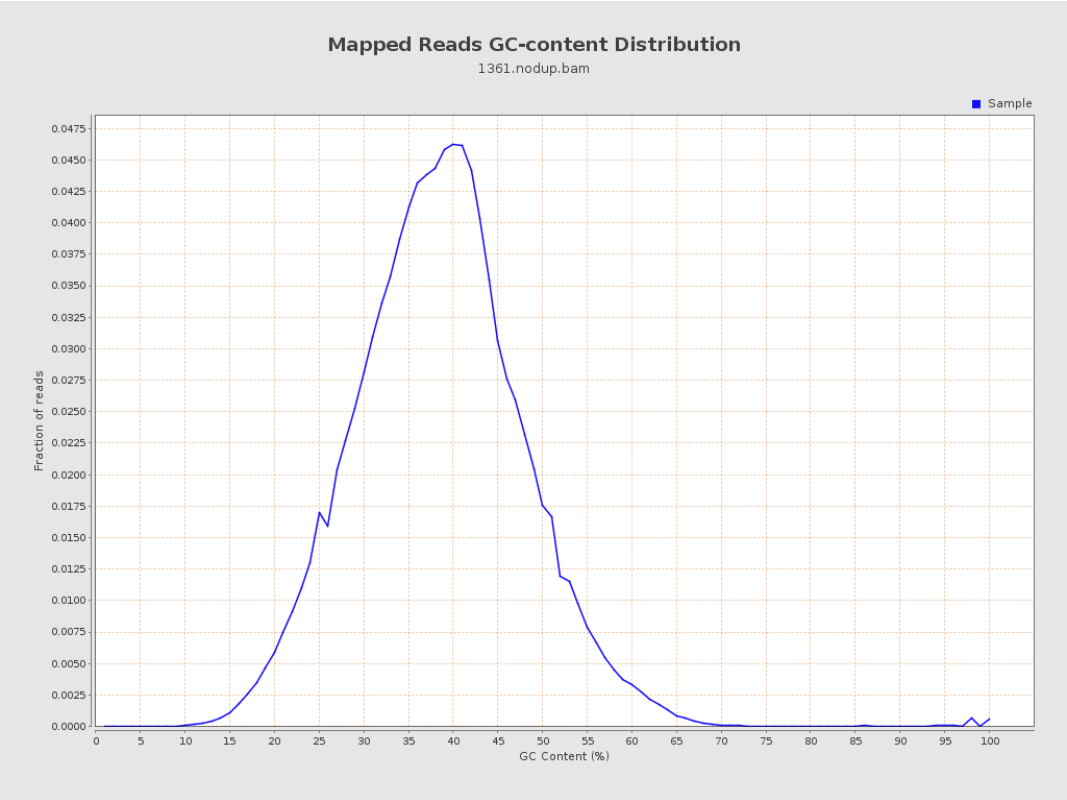
7. Results : Duplication Rate Histogram



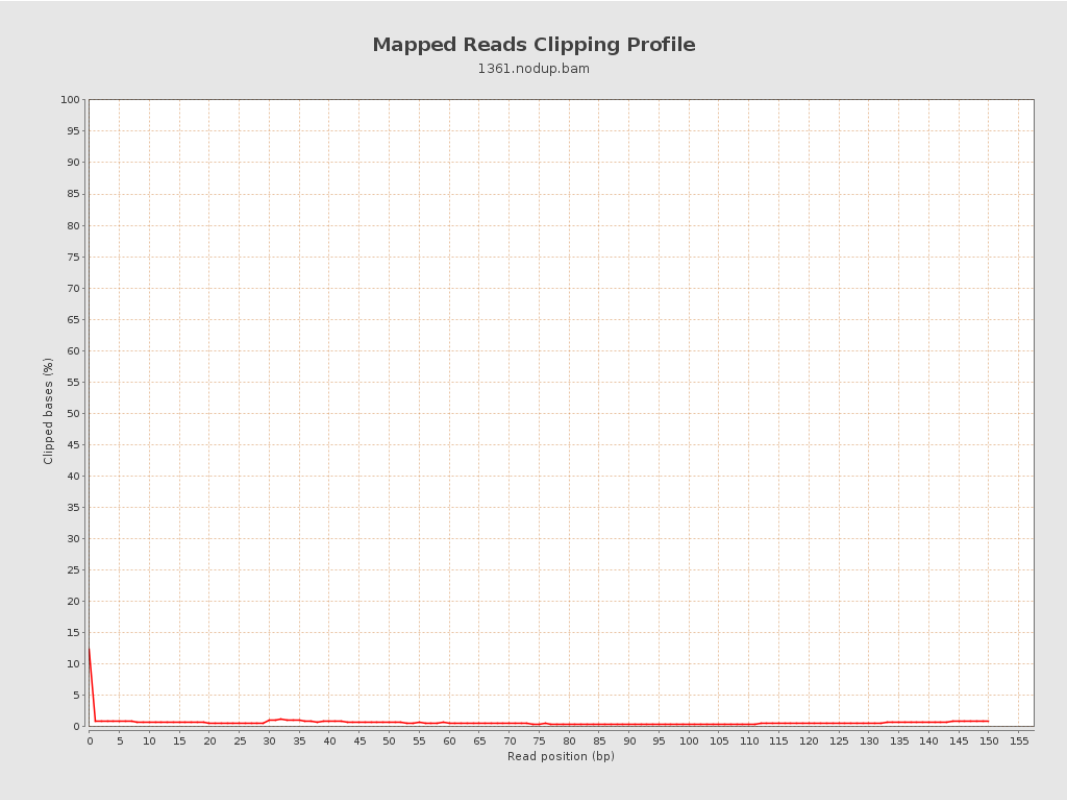
8. Results : Mapped Reads Nucleotide Content



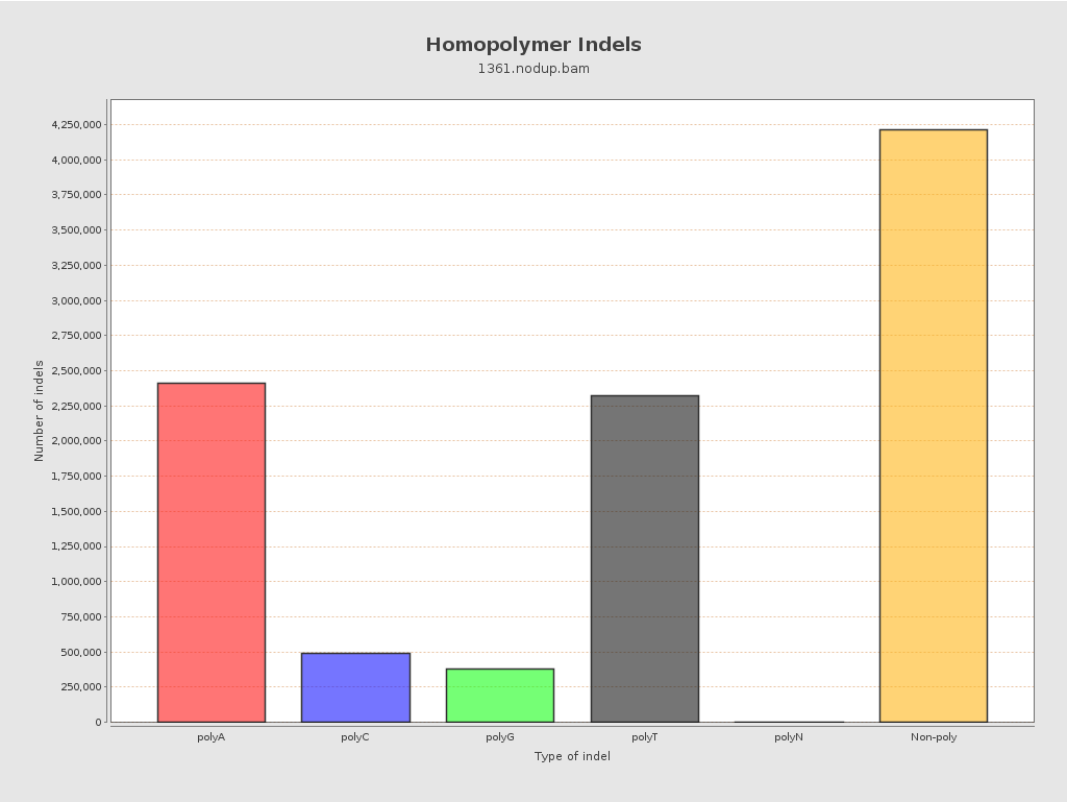
9. Results : Mapped Reads GC-content Distribution



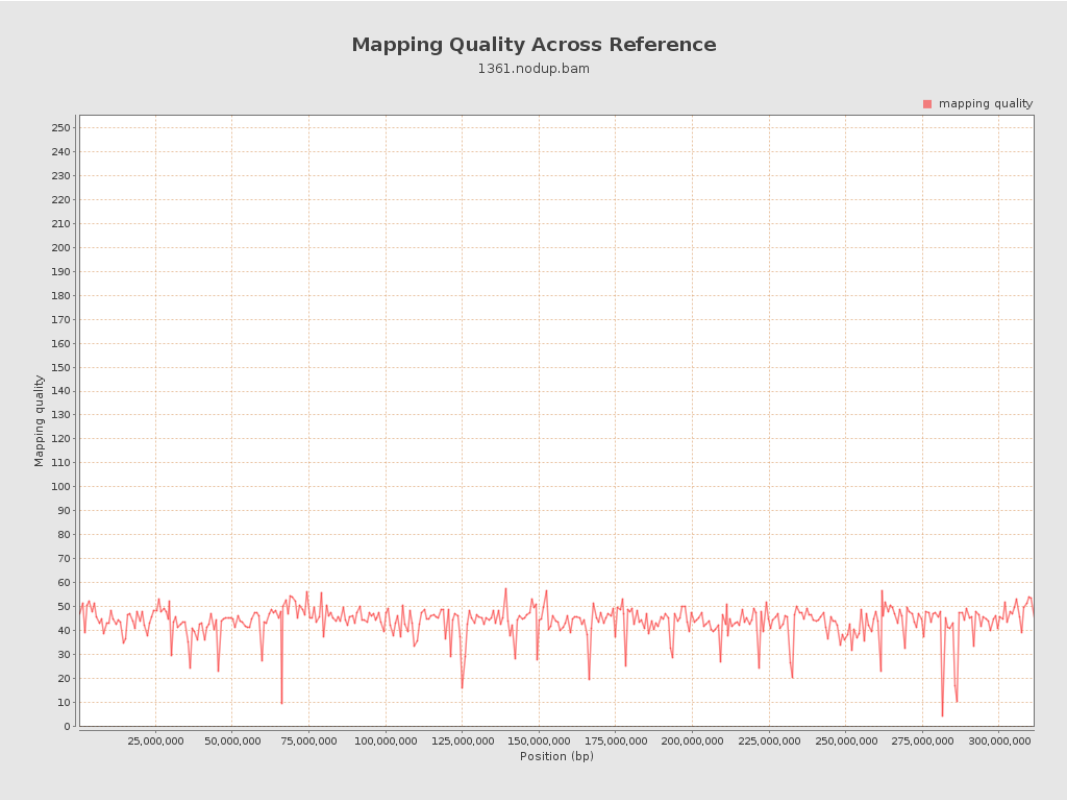
10. Results : Mapped Reads Clipping Profile



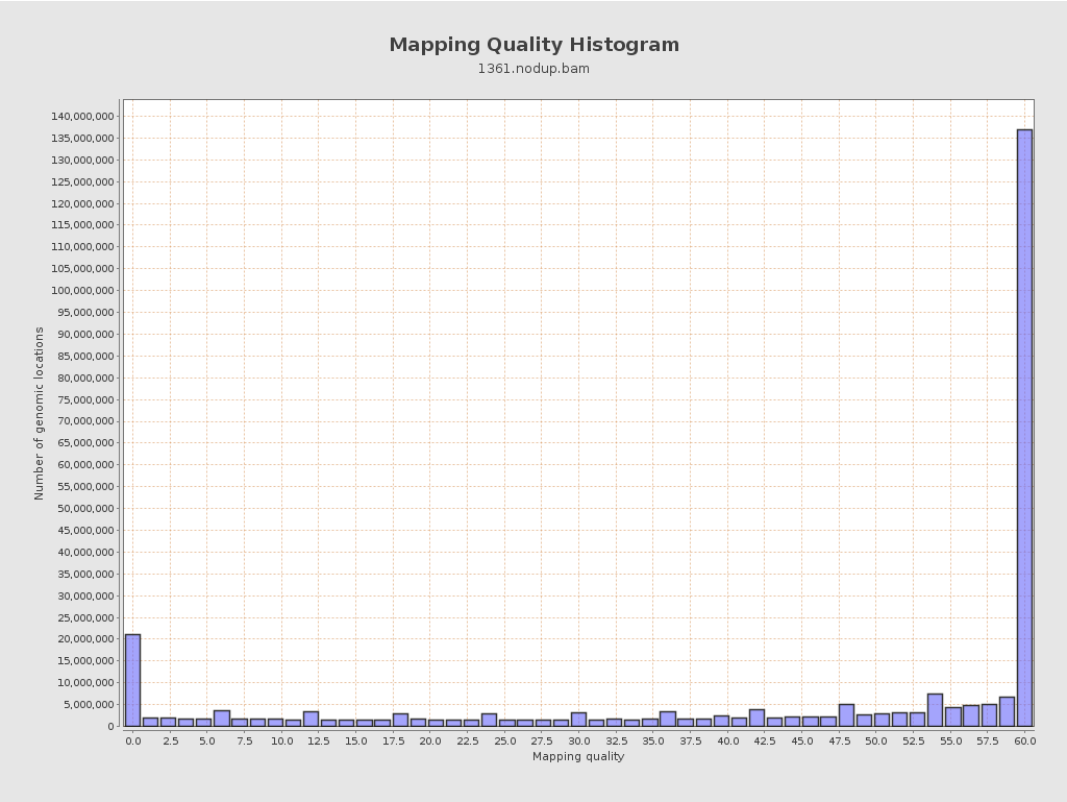
11. Results : Homopolymer Indels



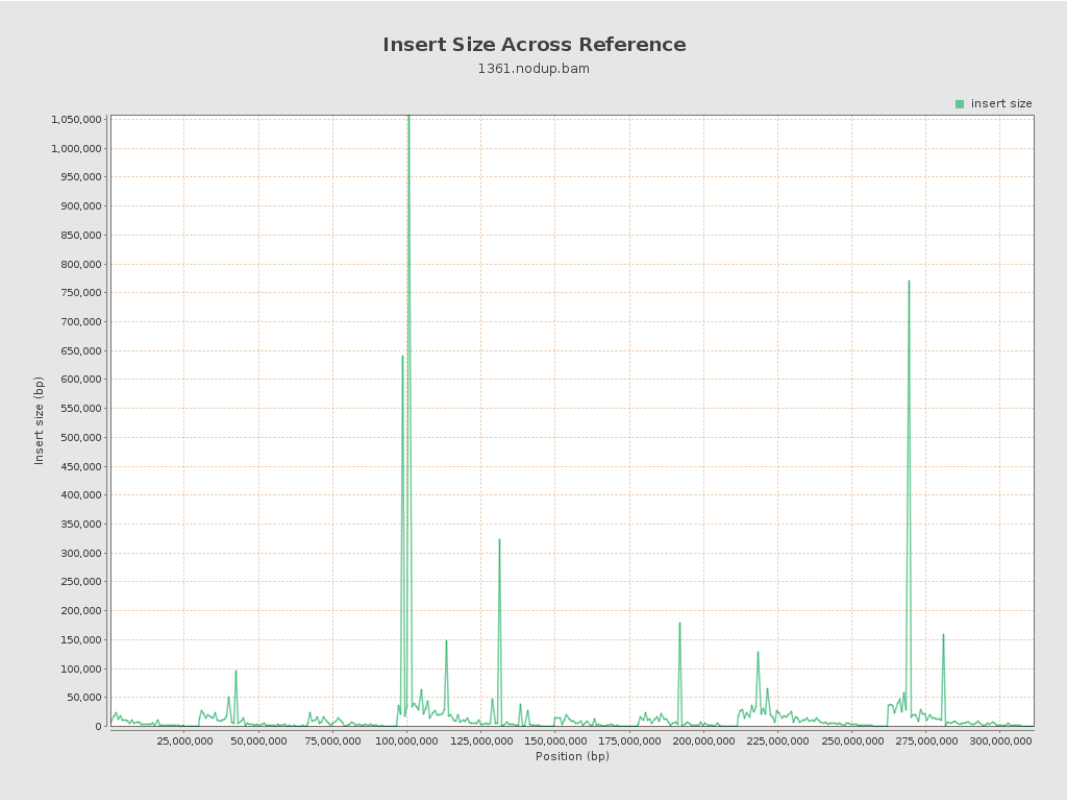
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram