Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:16:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1377
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1377 .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_471/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_471_S446_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_471/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_471_S446_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:16:42 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	21,523,371
Mapped reads	20,413,651 / 94.84%
Unmapped reads	1,109,720 / 5.16%
Mapped paired reads	20,413,651 / 94.84%
Mapped reads, first in pair	10,280,242 / 47.76%
Mapped reads, second in pair	10,133,409 / 47.08%
Mapped reads, both in pair	19,923,937 / 92.57%
Mapped reads, singletons	489,714 / 2.28%
Read min/max/mean length	30 / 151 / 148.14
Duplicated reads (flagged)	2,613,521 / 12.14%
Clipped reads	4,909,771 / 22.81%

2.2. ACGT Content

Number/percentage of A's	862,462,176 / 30.55%
Number/percentage of C's	548,801,720 / 19.44%
Number/percentage of T's	865,911,937 / 30.68%
Number/percentage of G's	545,608,527 / 19.33%
Number/percentage of N's	9,640 / 0%
GC Percentage	38.77%

2.3. Coverage

Mean	9.0803
Standard Deviation	85.2785

2.4. Mapping Quality

Mean Mapping Quality	43.31

2.5. Insert size

Mean	275,989.24
Standard Deviation	2,487,424.14
P25/Median/P75	485 / 636 / 798

2.6. Mismatches and indels

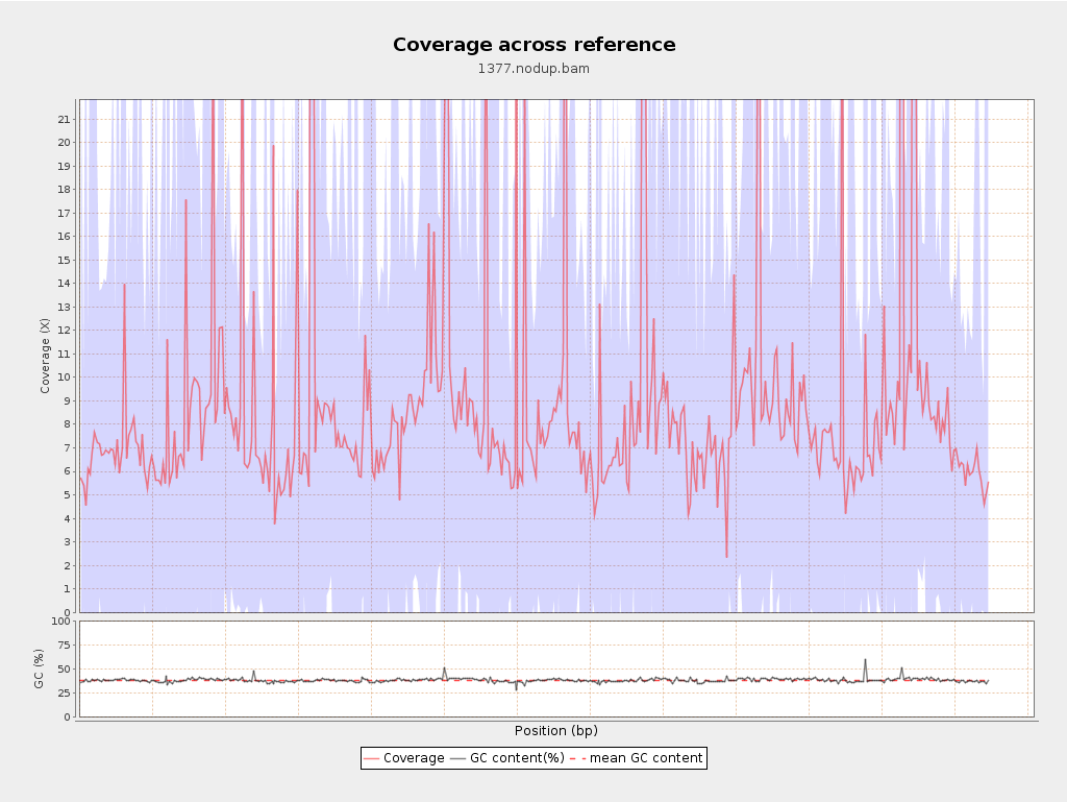
General error rate	2.56%
Mismatches	67,361,050
Insertions	1,803,595
Mapped reads with at least one insertion	7.97%
Deletions	1,875,211
Mapped reads with at least one deletion	8.19%
Homopolymer indels	55.21%

2.7. Chromosome stats

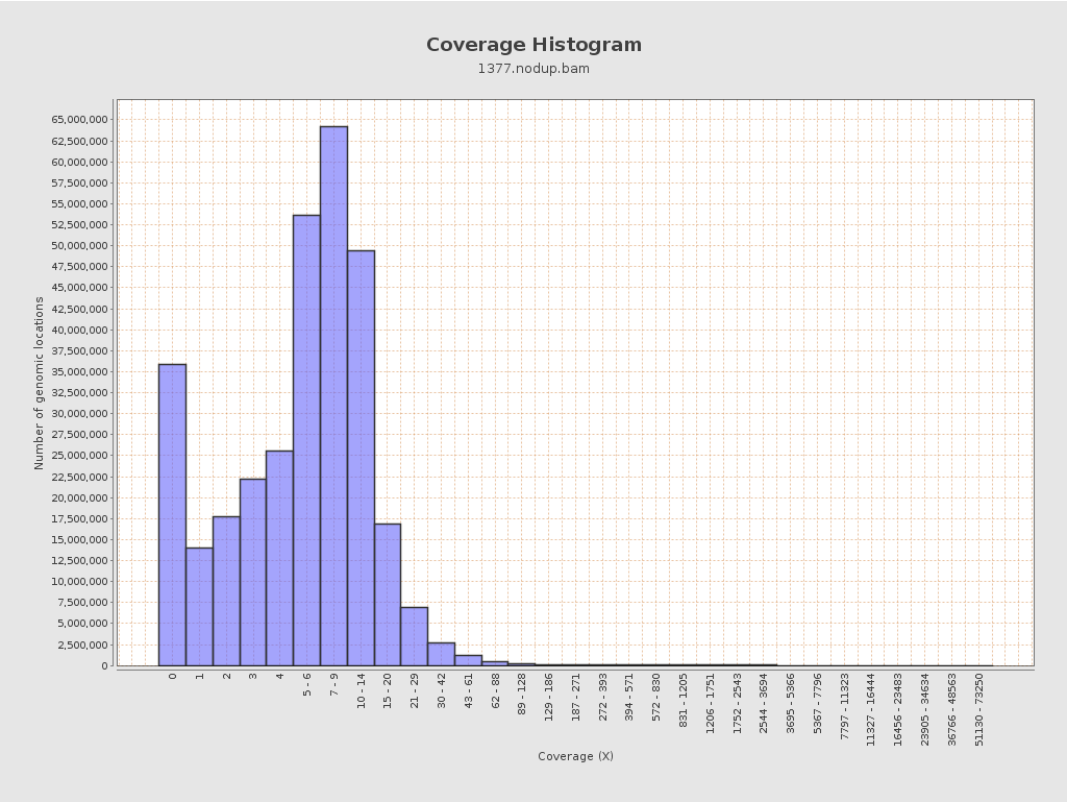
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	199727472	6.7193	20.6195

LT669789.1	36598175	329786162	9.011	79.344
LT669790.1	30422129	268753850	8.8342	64.3682
LT669791.1	52758100	481884416	9.1338	65.2348
LT669792.1	28376109	241749608	8.5195	85.7102
LT669793.1	33388210	290460264	8.6995	87.472
LT669794.1	50579949	446649837	8.8306	75.6363
LT669795.1	49795044	570791938	11.4628	135.8546

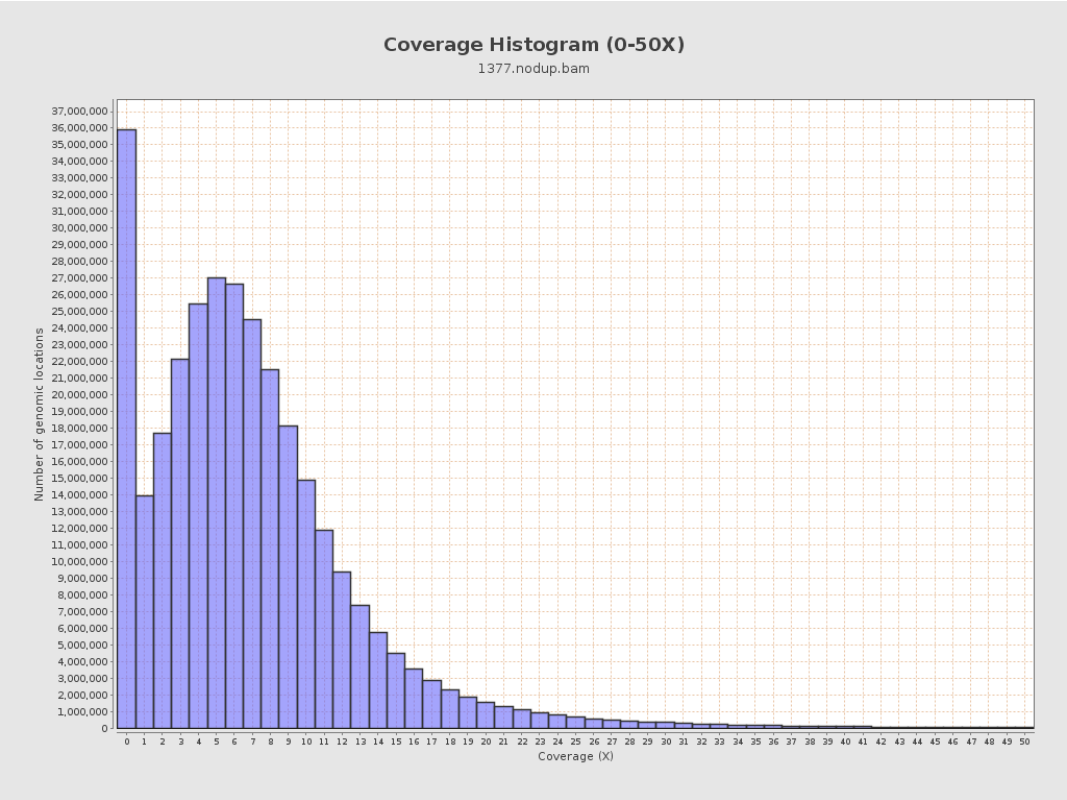
3. Results : Coverage across reference



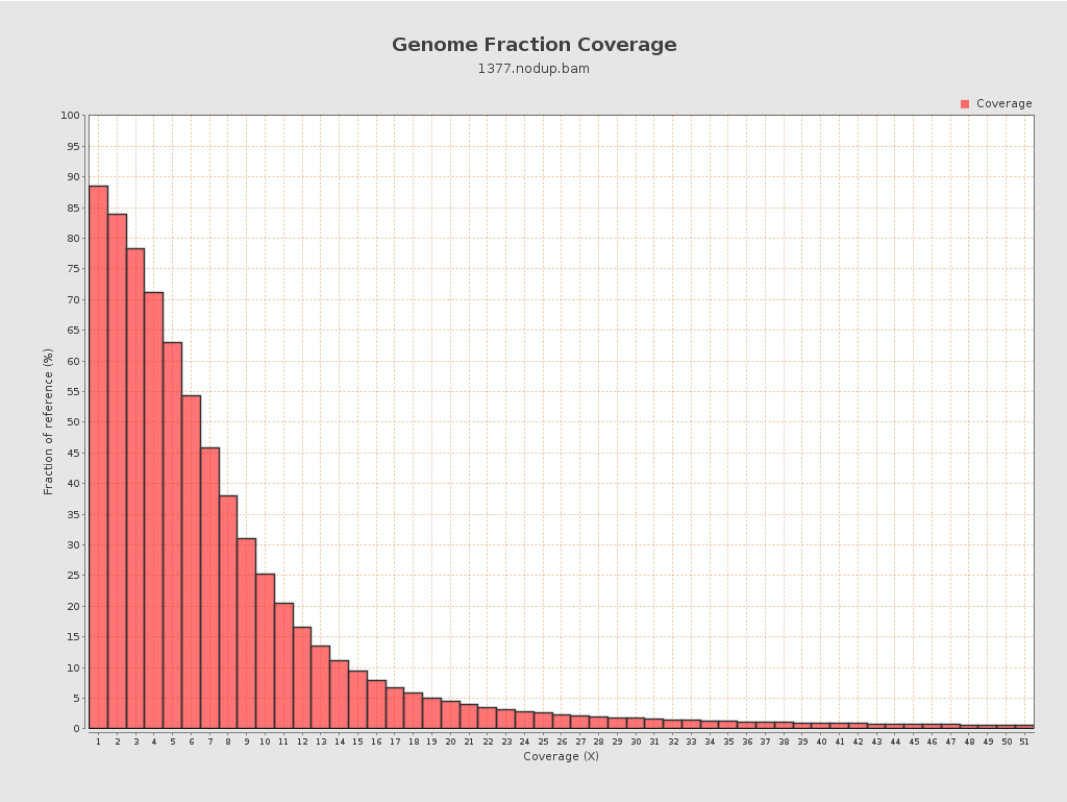
4. Results : Coverage Histogram



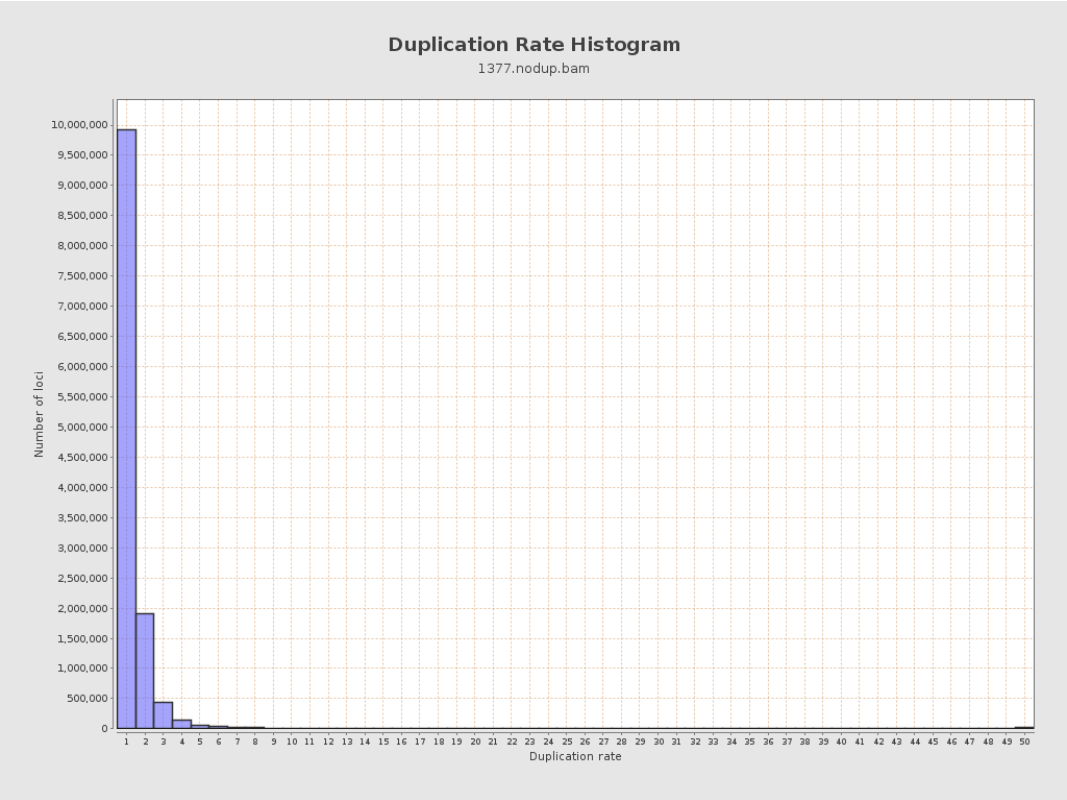
5. Results : Coverage Histogram (0-50X)



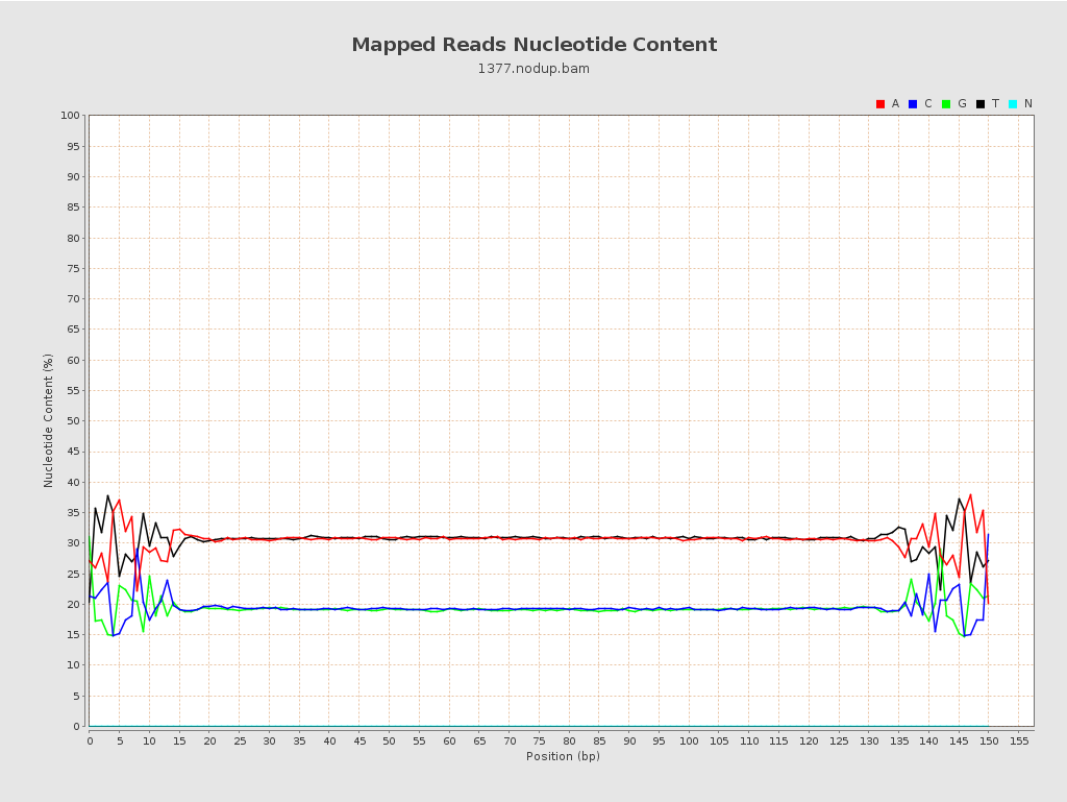
6. Results : Genome Fraction Coverage



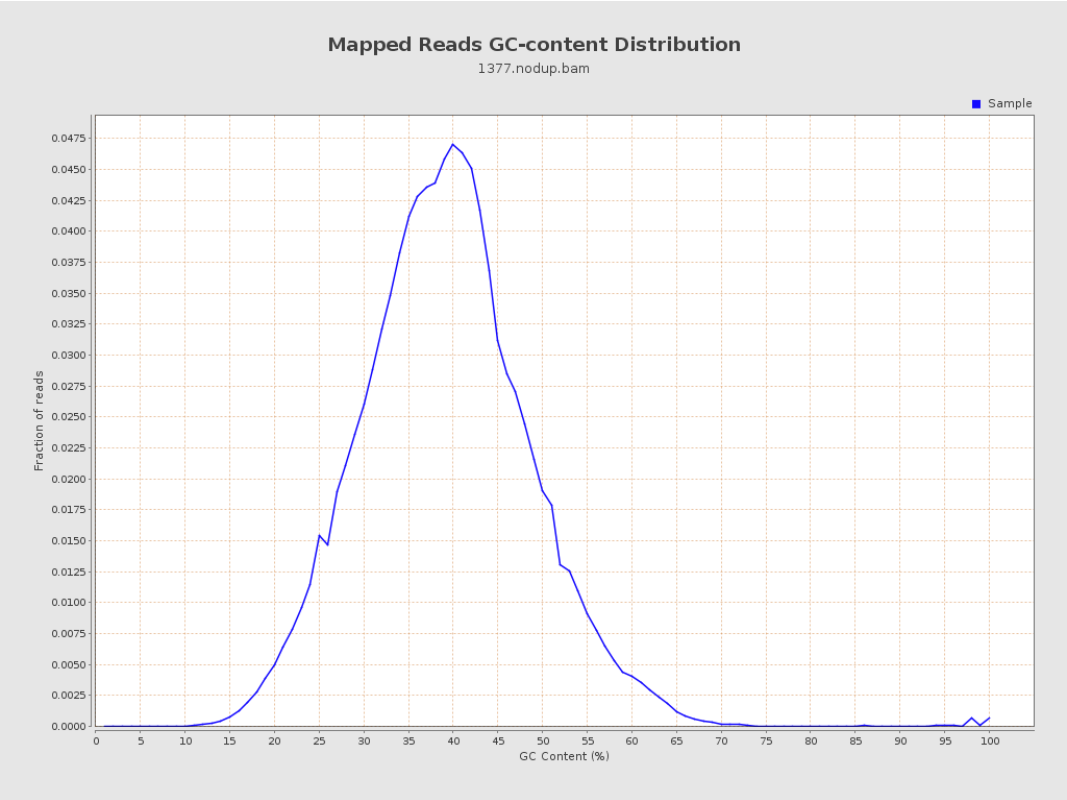
7. Results : Duplication Rate Histogram



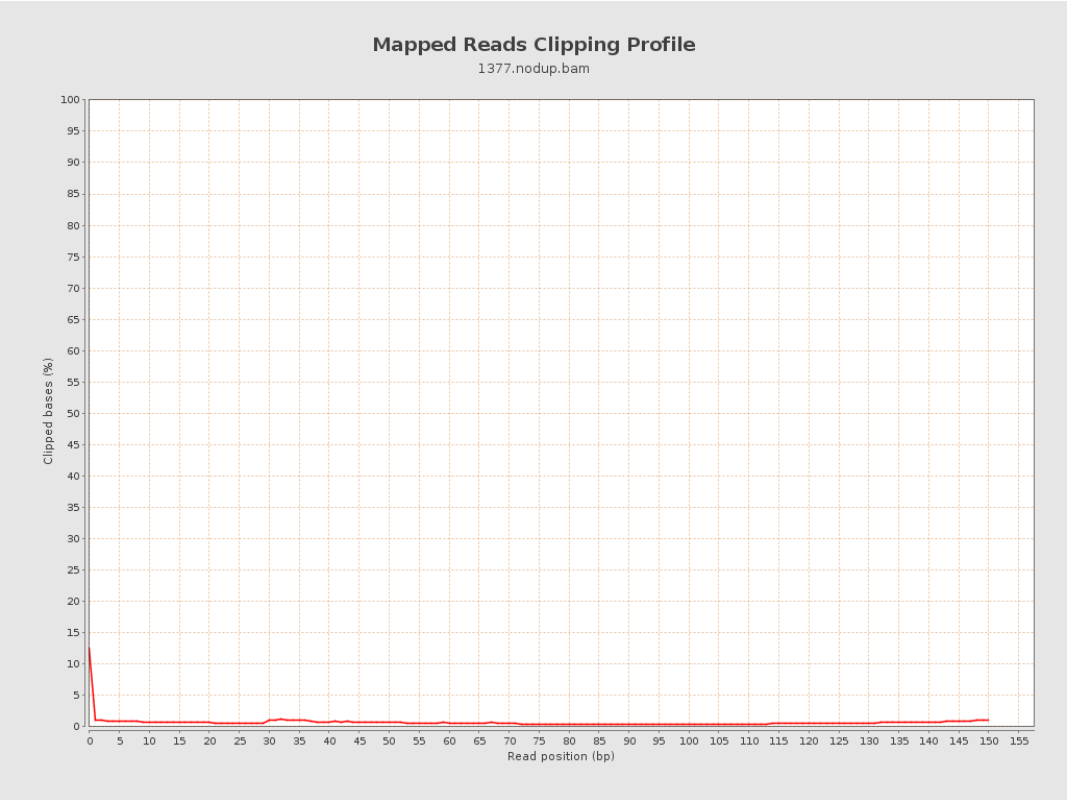
8. Results : Mapped Reads Nucleotide Content



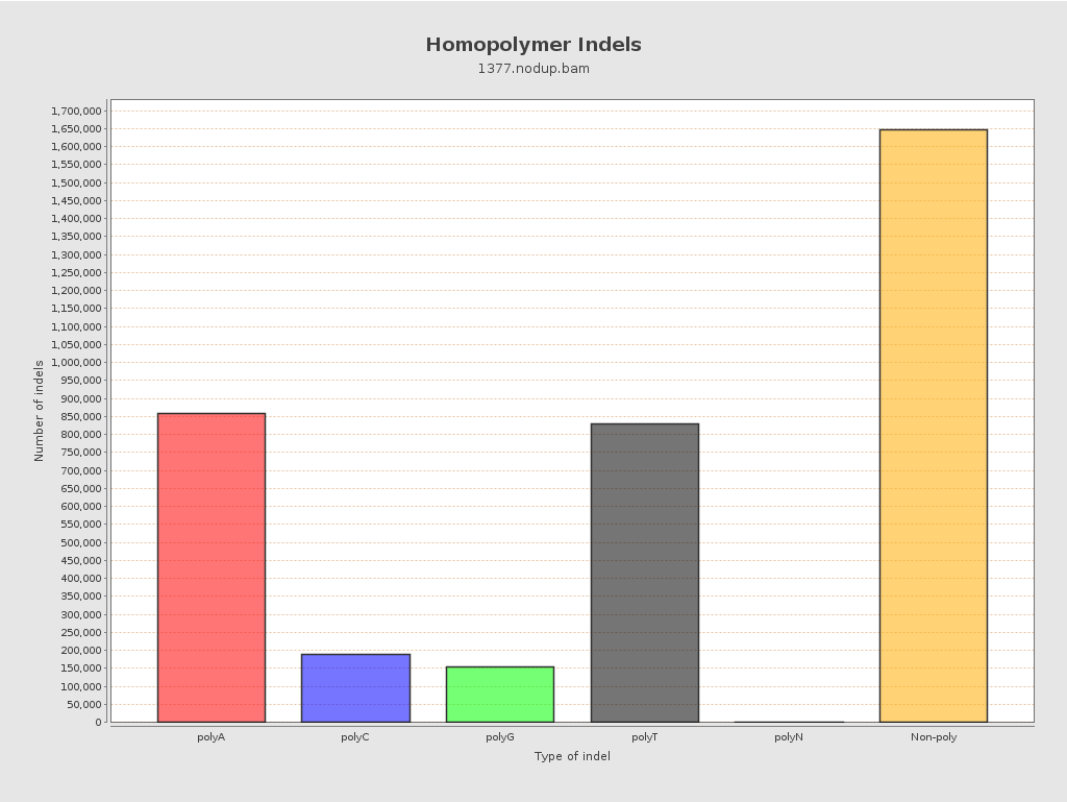
9. Results : Mapped Reads GC-content Distribution



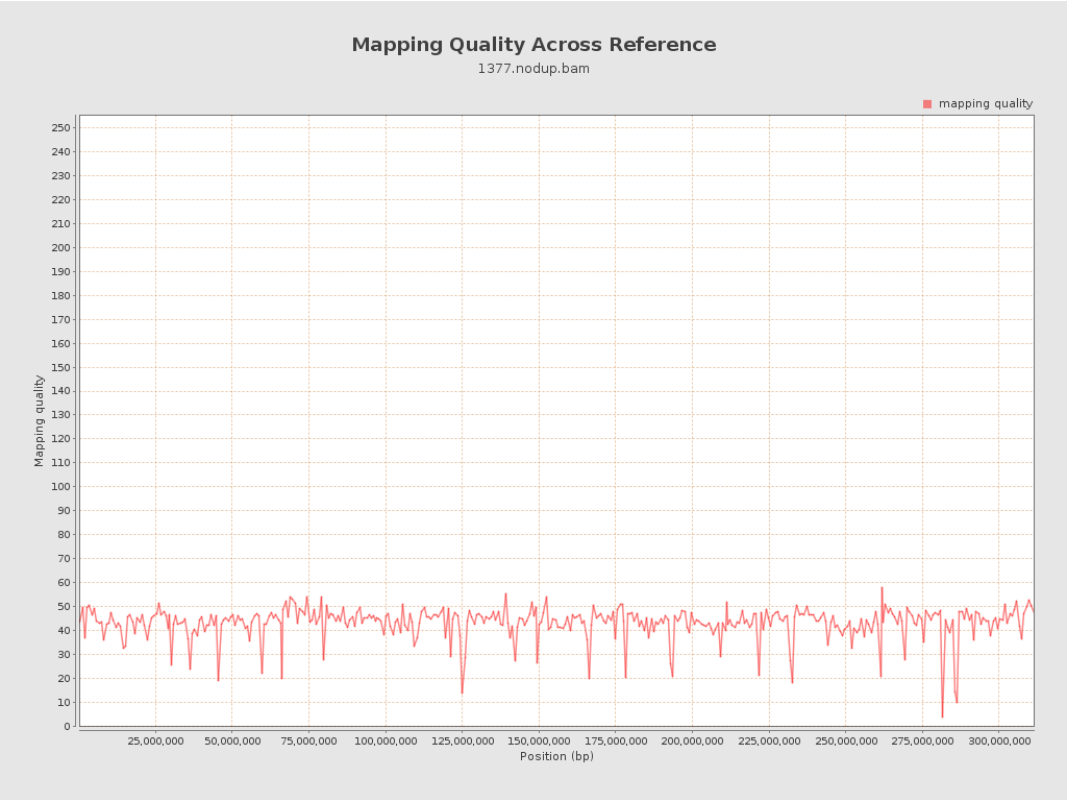
10. Results : Mapped Reads Clipping Profile



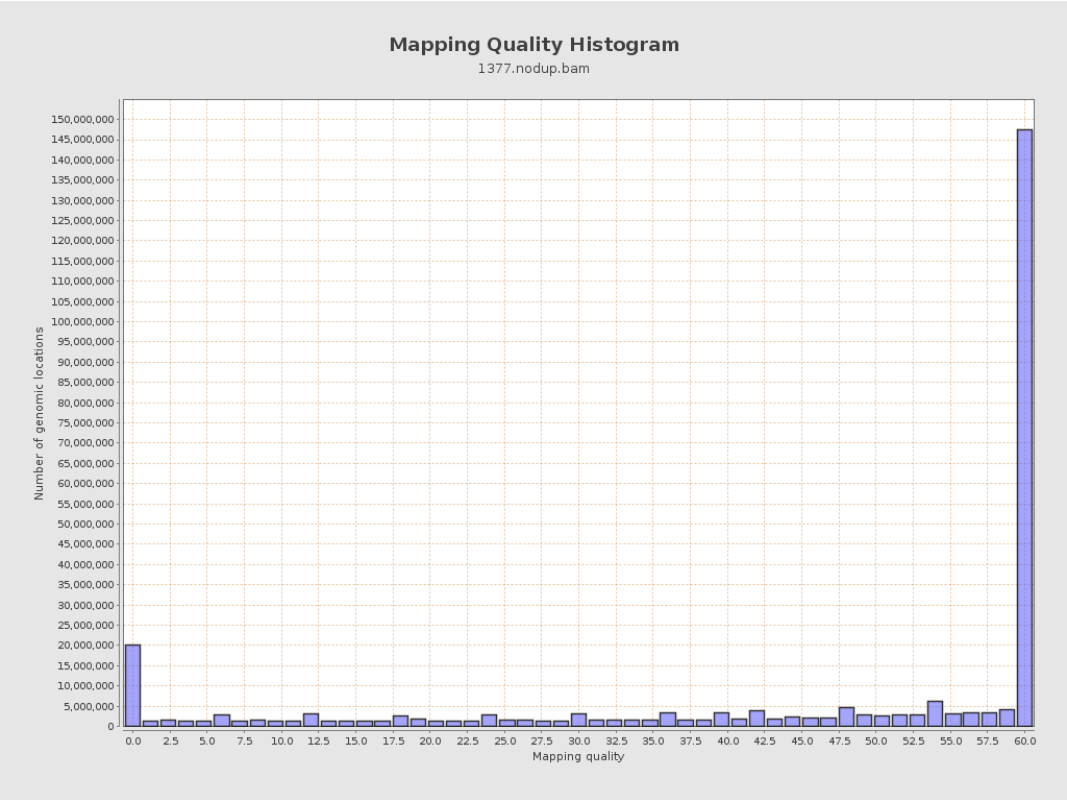
11. Results : Homopolymer Indels



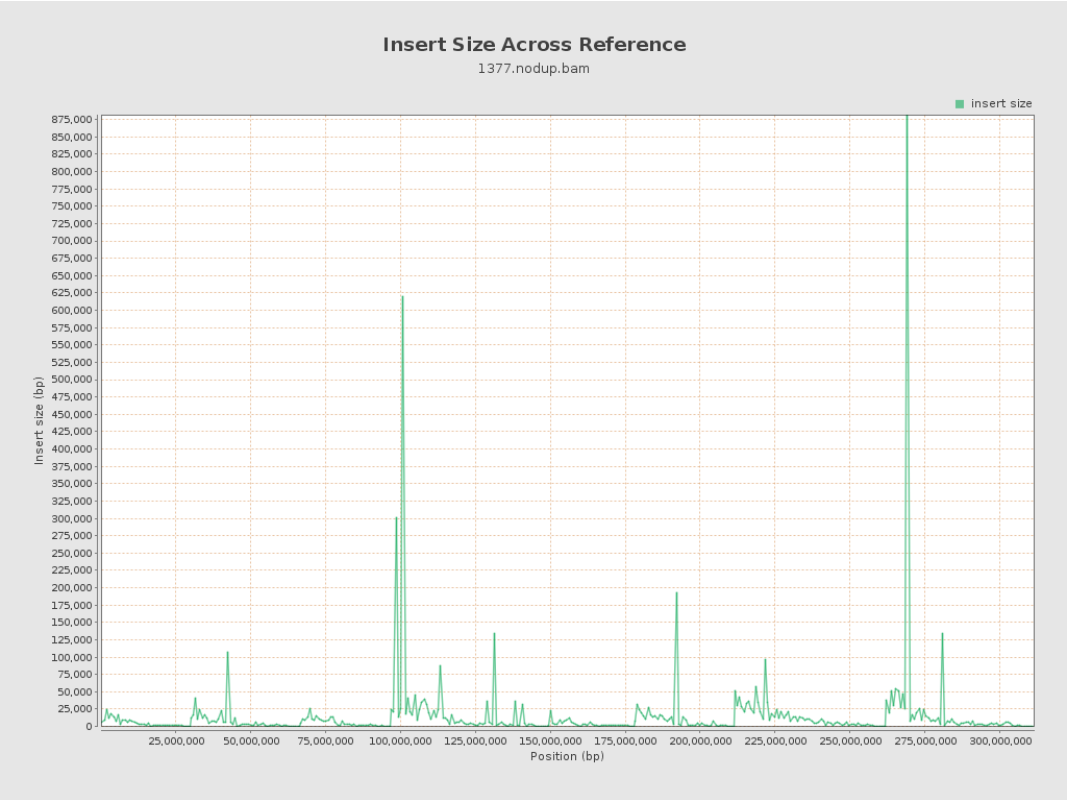
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram