Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:29:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1069
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1069 .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_468/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_468_S443_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_468/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_468_S443_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:29:06 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	58,508,243
Mapped reads	54,711,270 / 93.51%
Unmapped reads	3,796,973 / 6.49%
Mapped paired reads	54,711,270 / 93.51%
Mapped reads, first in pair	27,409,851 / 46.85%
Mapped reads, second in pair	27,301,419 / 46.66%
Mapped reads, both in pair	53,351,015 / 91.19%
Mapped reads, singletons	1,360,255 / 2.32%
Read min/max/mean length	30 / 151 / 148.15
Duplicated reads (flagged)	9,045,044 / 15.46%
Clipped reads	12,149,122 / 20.76%

2.2. ACGT Content

Number/percentage of A's	2,341,673,689 / 30.86%
Number/percentage of C's	1,453,820,190 / 19.16%
Number/percentage of T's	2,343,832,038 / 30.89%
Number/percentage of G's	1,447,888,063 / 19.08%
Number/percentage of N's	25,519 / 0%
GC Percentage	38.24%

2.3. Coverage

Mean	24.4087
Standard Deviation	211.5023

2.4. Mapping Quality

Mean Mapping Quality	43.83

2.5. Insert size

Mean	255,931.62
Standard Deviation	2,403,589.55
P25/Median/P75	366 / 475 / 617

2.6. Mismatches and indels

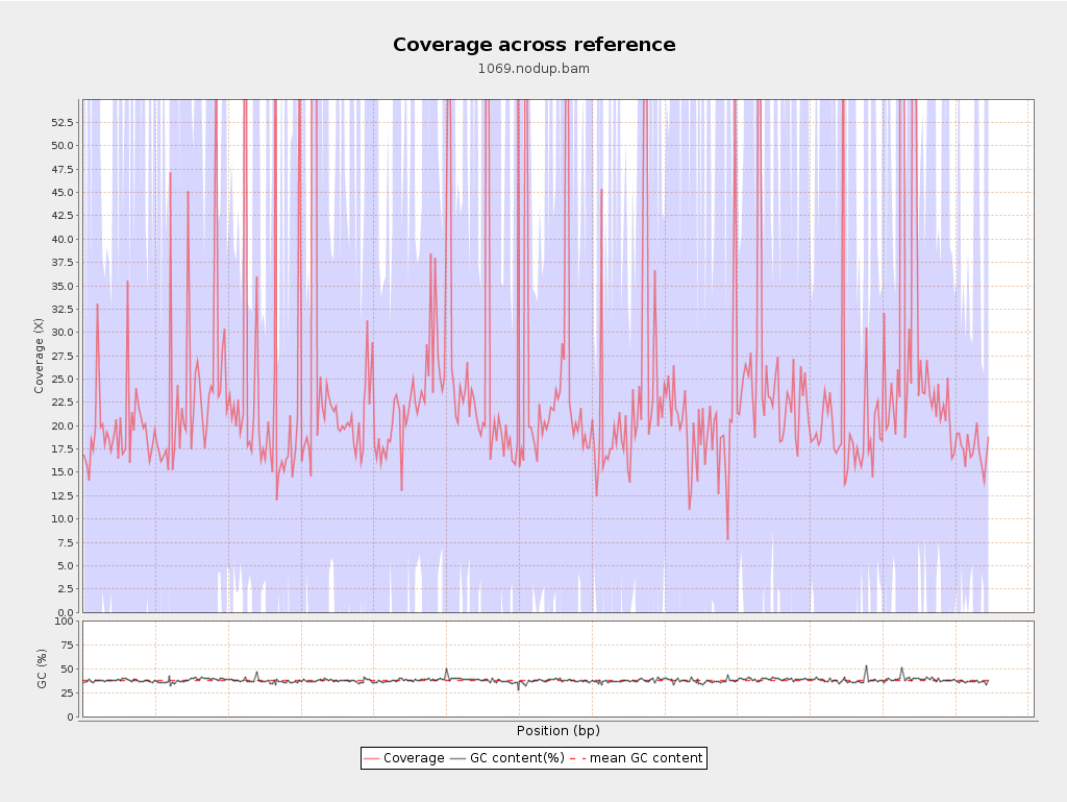
General error rate	2.35%
Mismatches	164,078,348
Insertions	5,301,022
Mapped reads with at least one insertion	8.69%
Deletions	5,264,913
Mapped reads with at least one deletion	8.55%
Homopolymer indels	56.63%

2.7. Chromosome stats

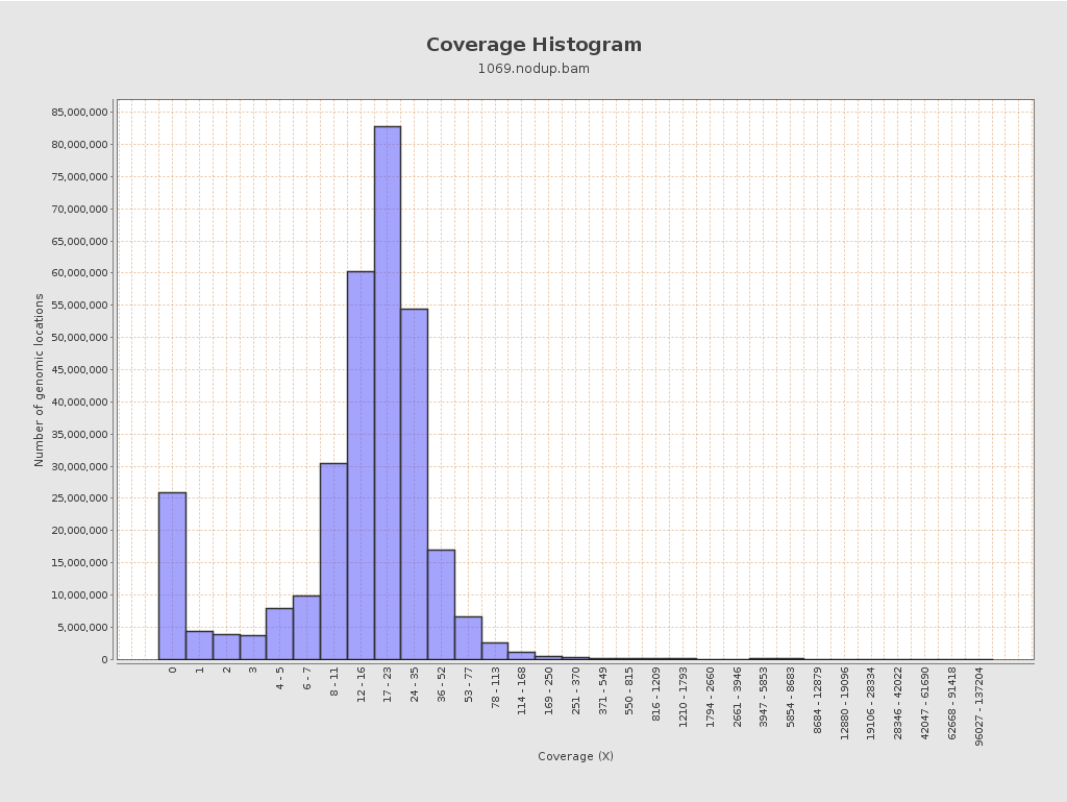
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	572623972	19.2645	68.7746

LT669789.1	36598175	917397699	25.0668	228.4929
LT669790.1	30422129	826848399	27.1792	266.4498
LT669791.1	52758100	1286692615	24.3885	203.8413
LT669792.1	28376109	681516585	24.0173	239.6697
LT669793.1	33388210	754981106	22.6122	148.2167
LT669794.1	50579949	1188269509	23.4929	201.4146
LT669795.1	49795044	1378456745	27.6826	250.3263

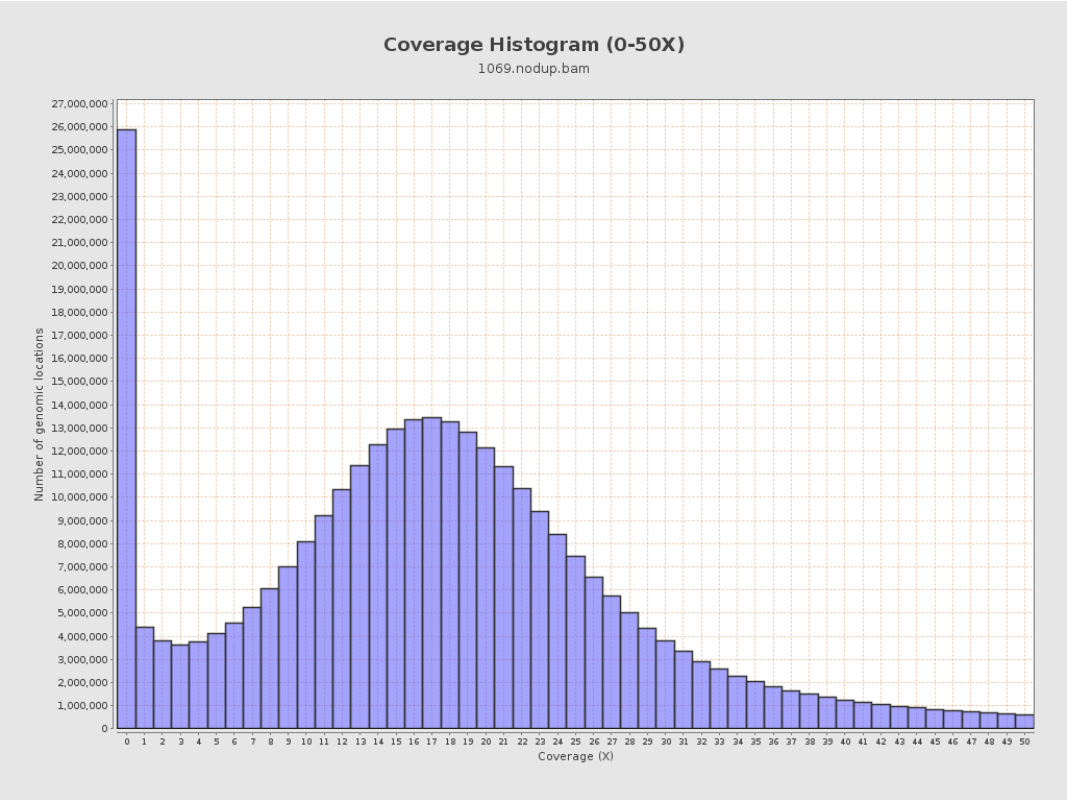
3. Results : Coverage across reference



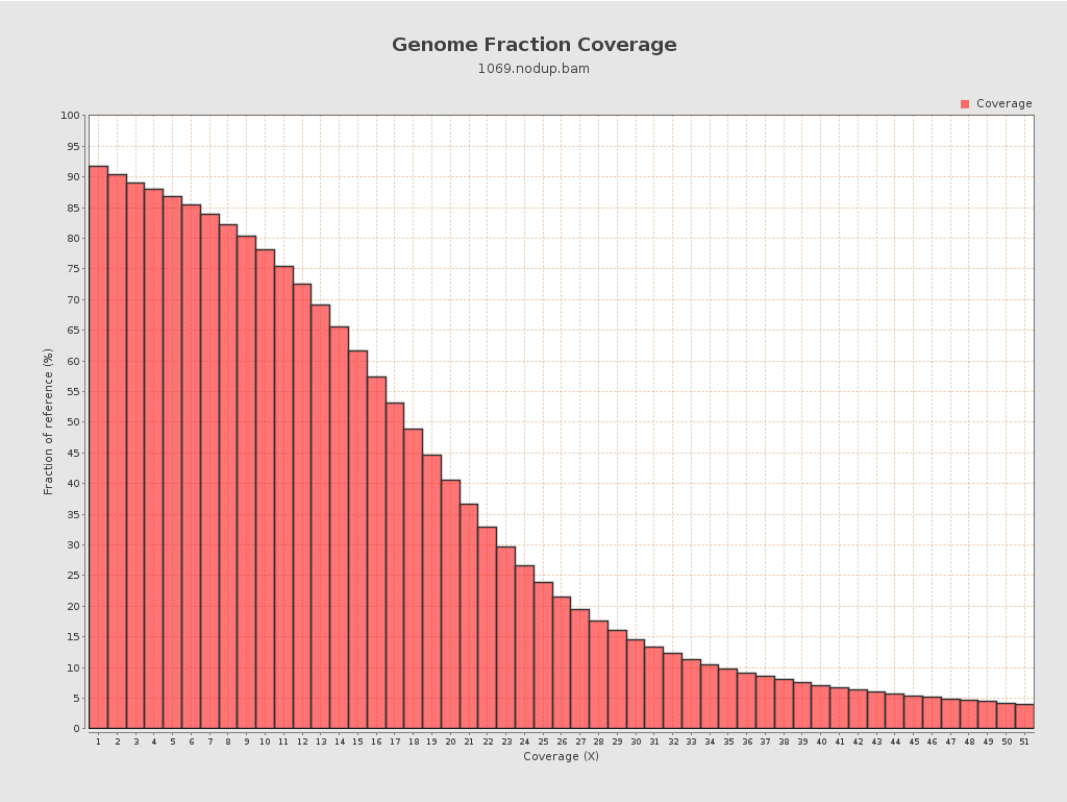
4. Results : Coverage Histogram



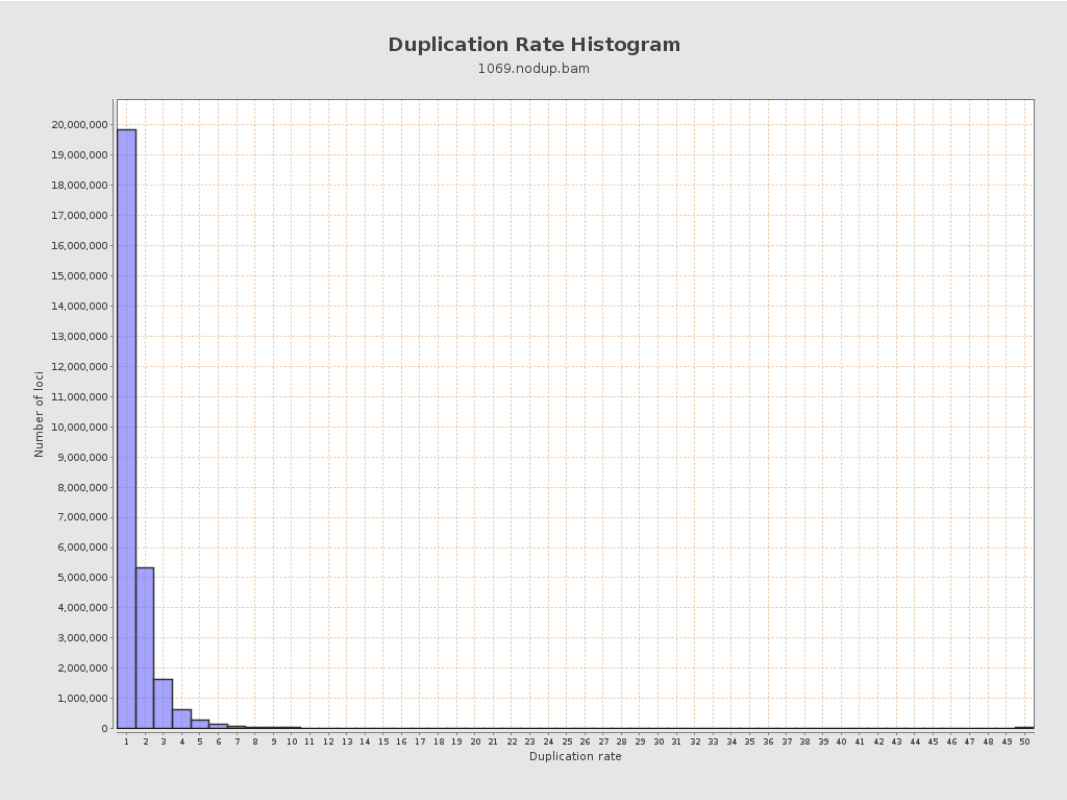
5. Results : Coverage Histogram (0-50X)



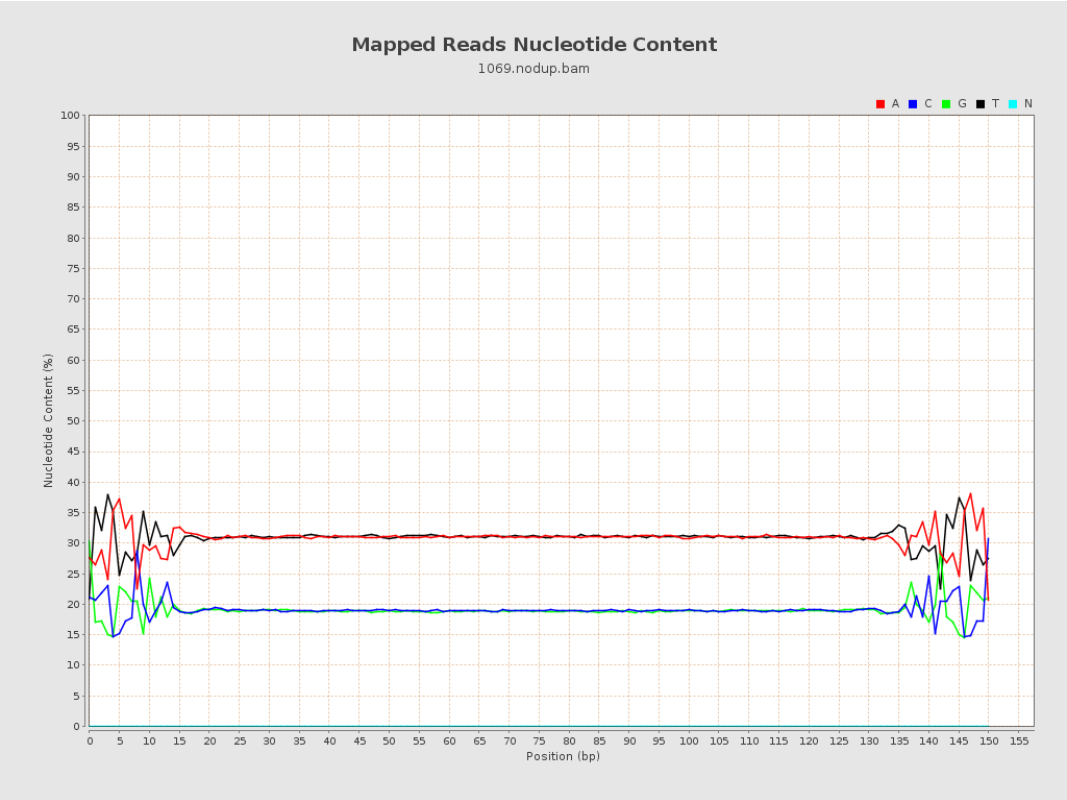
6. Results : Genome Fraction Coverage



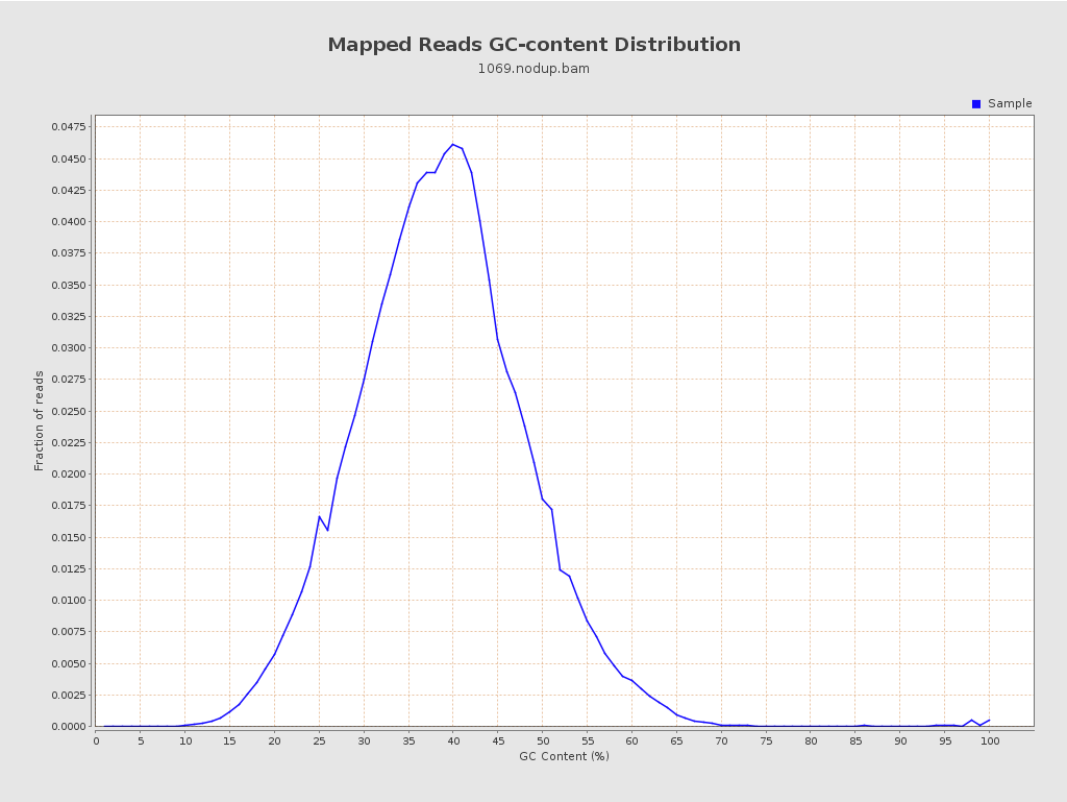
7. Results : Duplication Rate Histogram



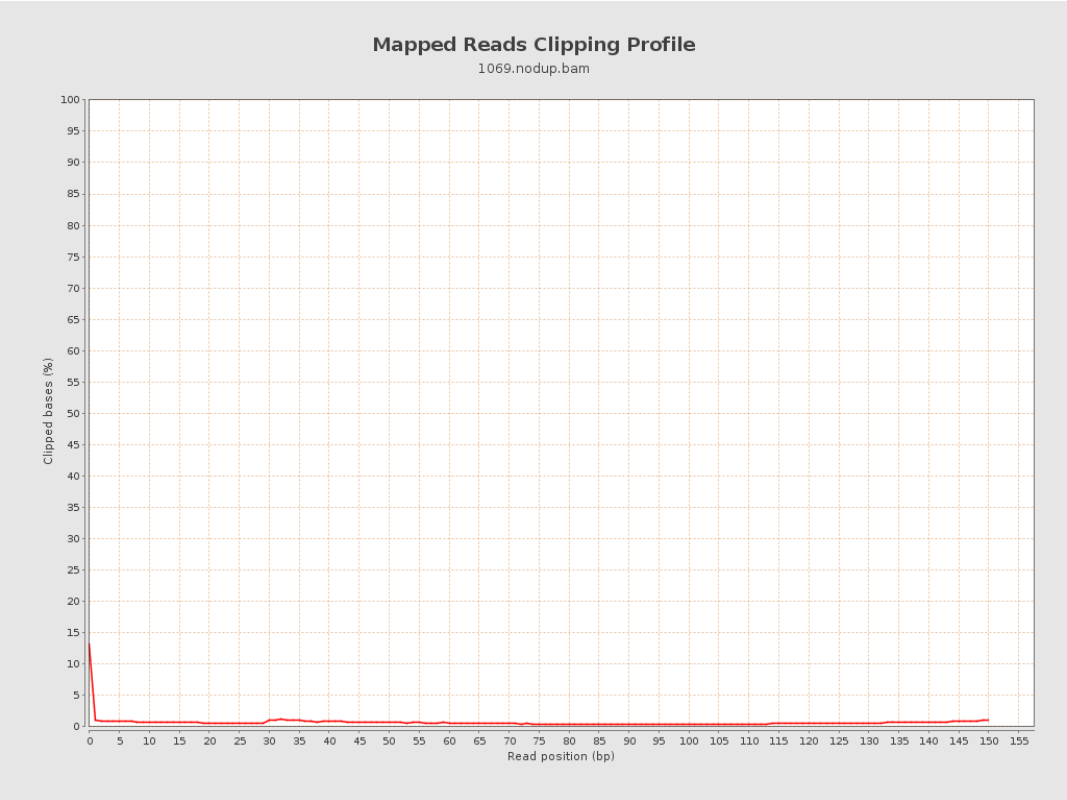
8. Results : Mapped Reads Nucleotide Content



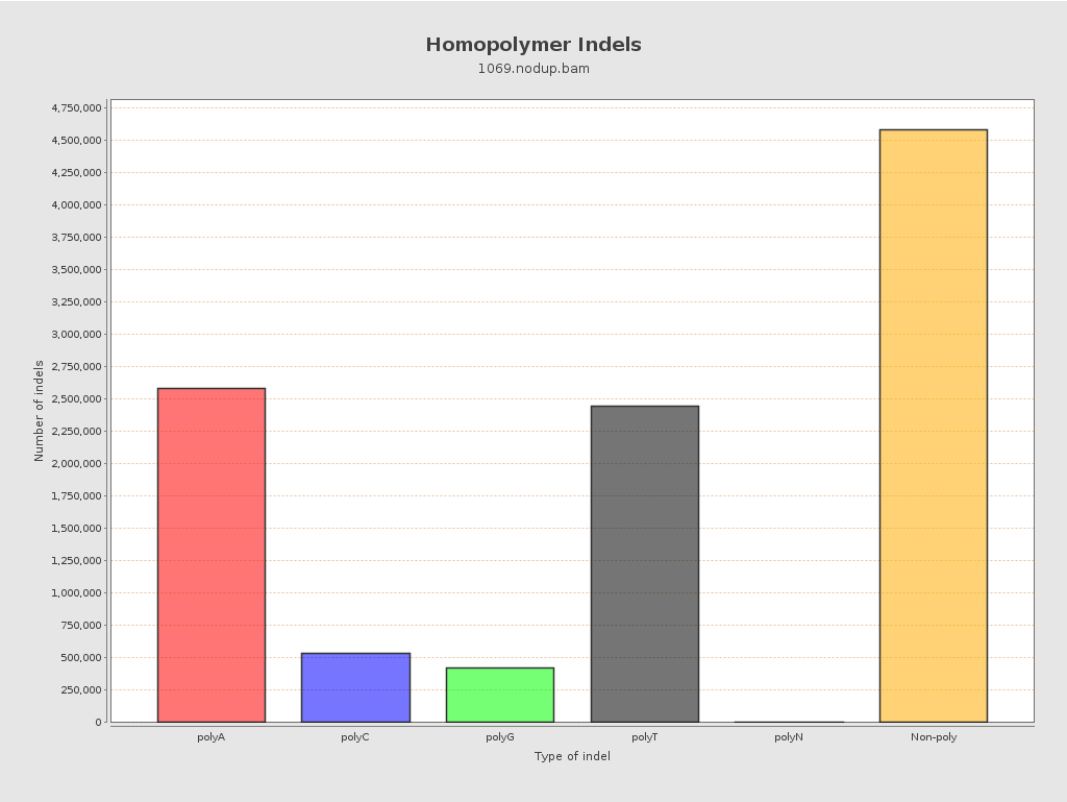
9. Results : Mapped Reads GC-content Distribution



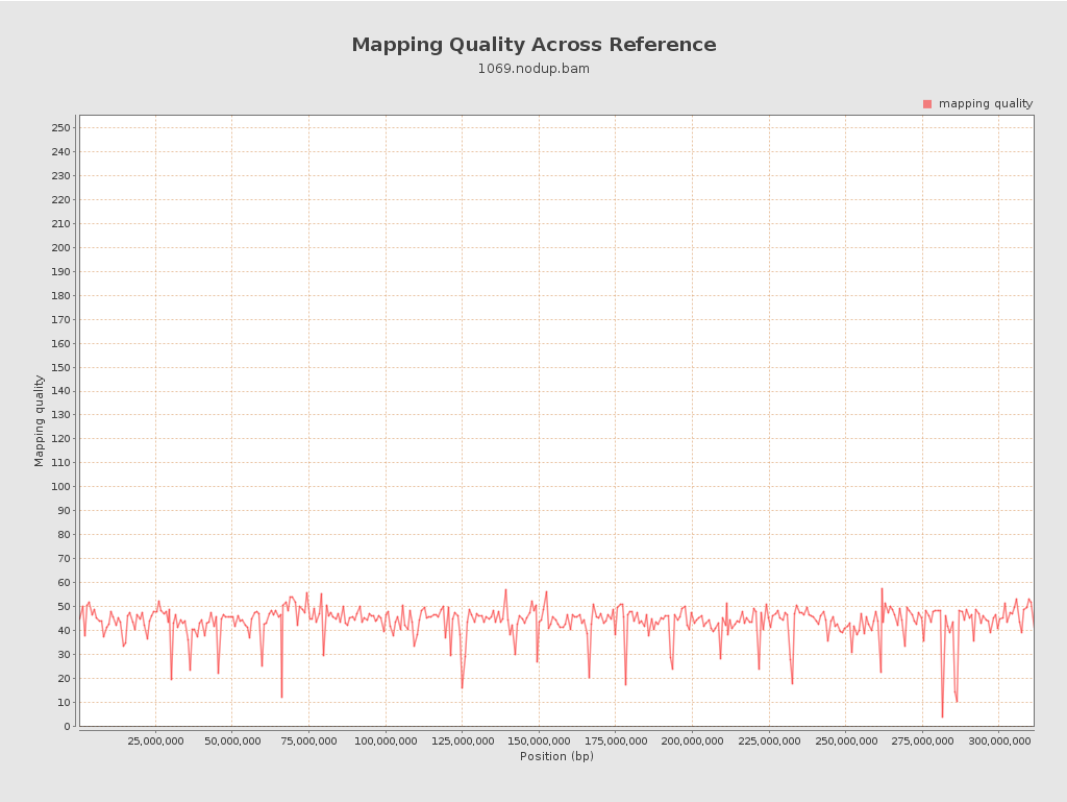
10. Results : Mapped Reads Clipping Profile



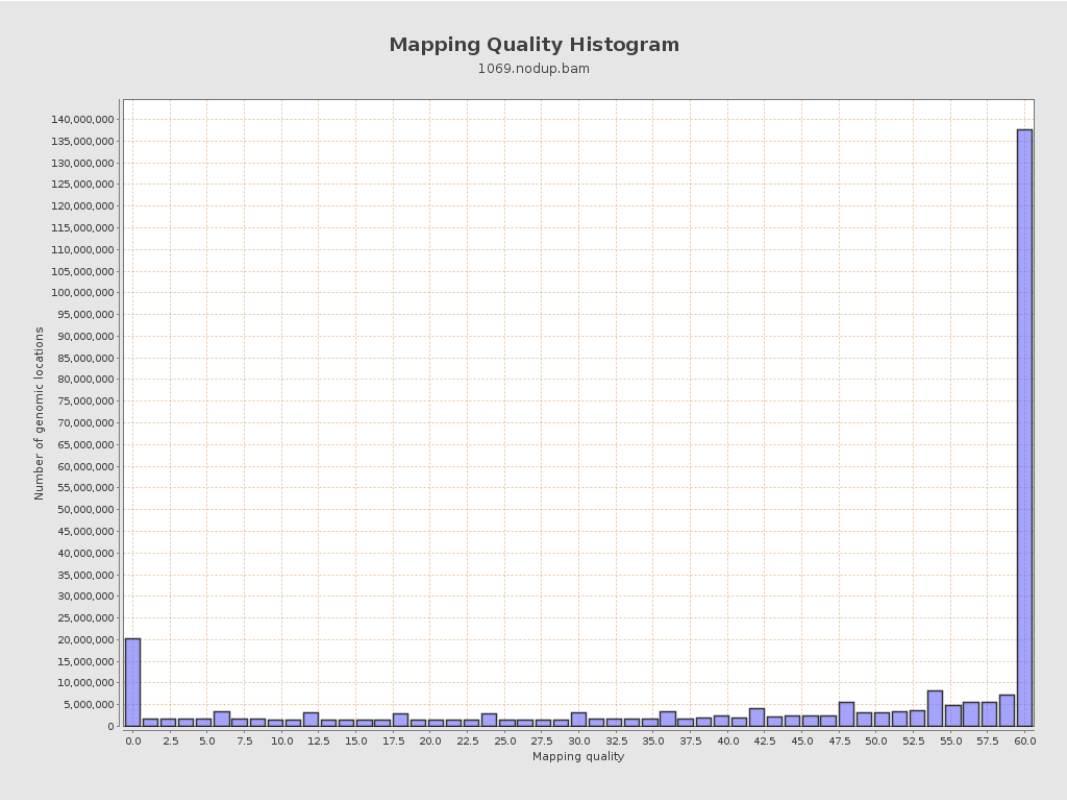
11. Results : Homopolymer Indels



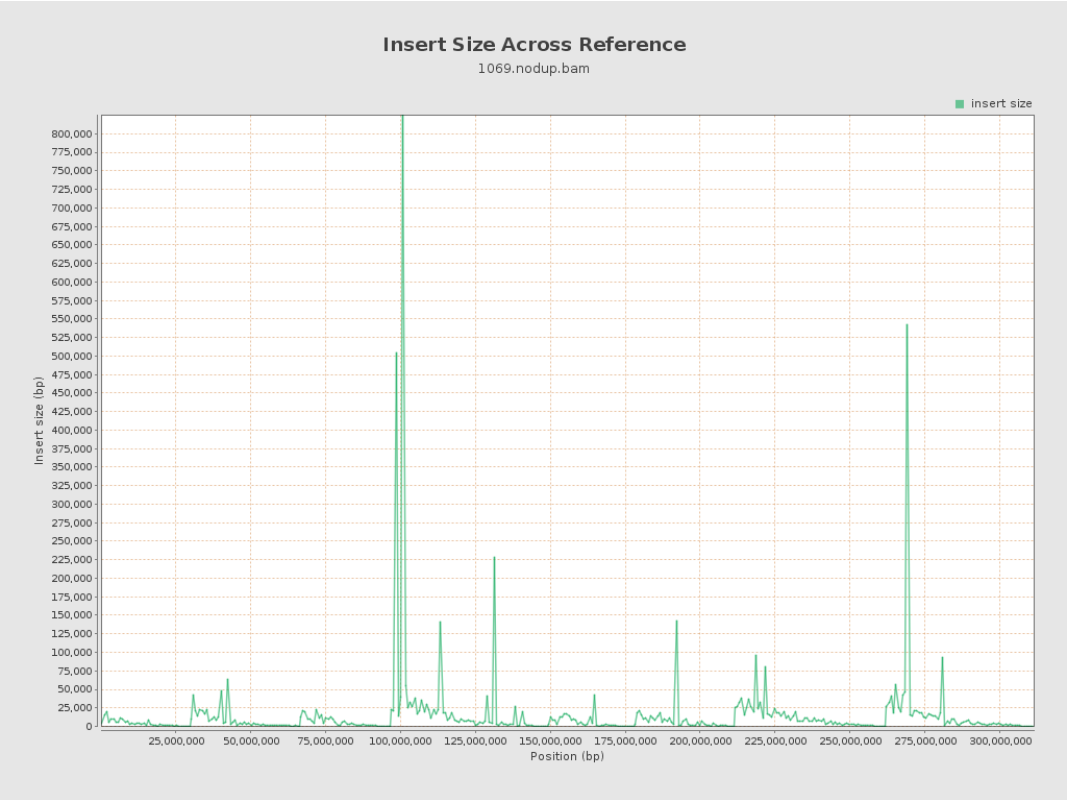
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram