Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:32:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1167
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1167 .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_484/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_484_S459_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_484/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_484_S459_L004_R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:32:33 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	68,582,778
Mapped reads	63,131,982 / 92.05%
Unmapped reads	5,450,796 / 7.95%
Mapped paired reads	63,131,982 / 92.05%
Mapped reads, first in pair	31,632,327 / 46.12%
Mapped reads, second in pair	31,499,655 / 45.93%
Mapped reads, both in pair	61,779,989 / 90.08%
Mapped reads, singletons	1,351,993 / 1.97%
Read min/max/mean length	30 / 151 / 148.32
Duplicated reads (flagged)	9,901,847 / 14.44%
Clipped reads	13,341,175 / 19.45%

2.2. ACGT Content

Number/percentage of A's	2,720,094,710 / 30.88%
Number/percentage of C's	1,685,878,378 / 19.14%
Number/percentage of T's	2,723,924,438 / 30.92%
Number/percentage of G's	1,678,276,609 / 19.05%
Number/percentage of N's	31,043 / 0%
GC Percentage	38.19%

2.3. Coverage

Mean	28.3346
Standard Deviation	208.9262

2.4. Mapping Quality

Mean Mapping Quality	44.39

2.5. Insert size

Mean	238,790.63
Standard Deviation	2,327,325.6
P25/Median/P75	372 / 484 / 636

2.6. Mismatches and indels

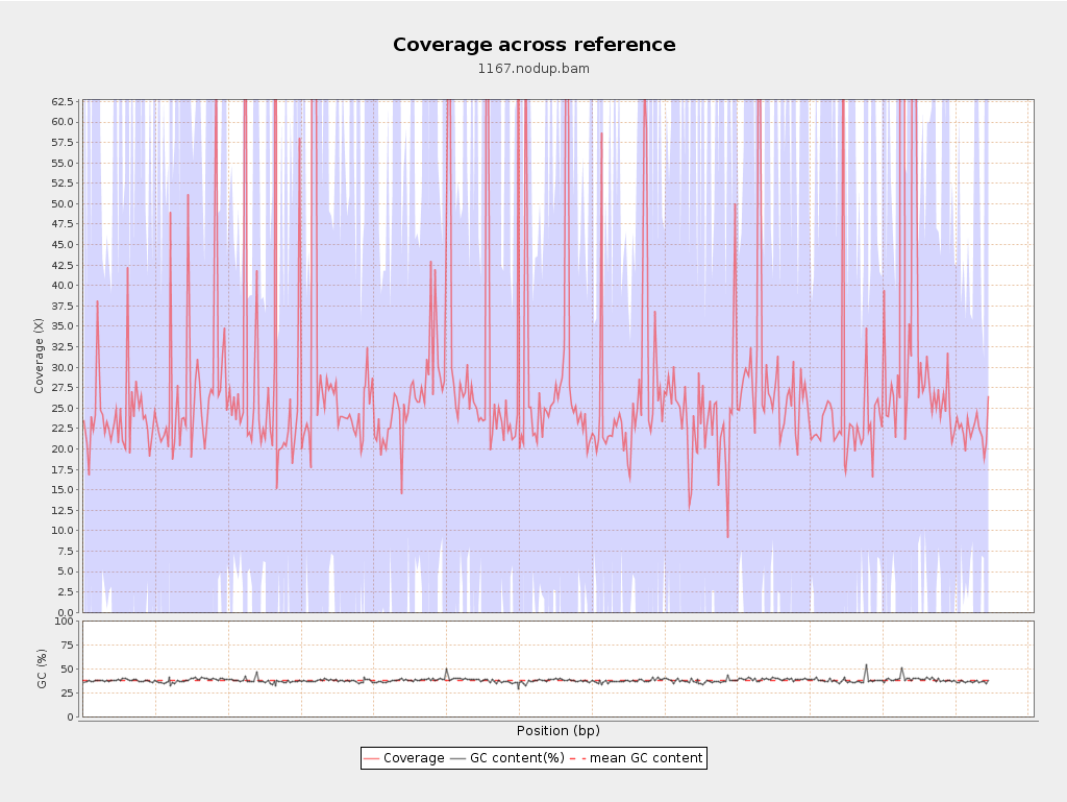
General error rate	2.27%
Mismatches	184,304,894
Insertions	5,820,735
Mapped reads with at least one insertion	8.3%
Deletions	5,902,171
Mapped reads with at least one deletion	8.3%
Homopolymer indels	56.47%

2.7. Chromosome stats

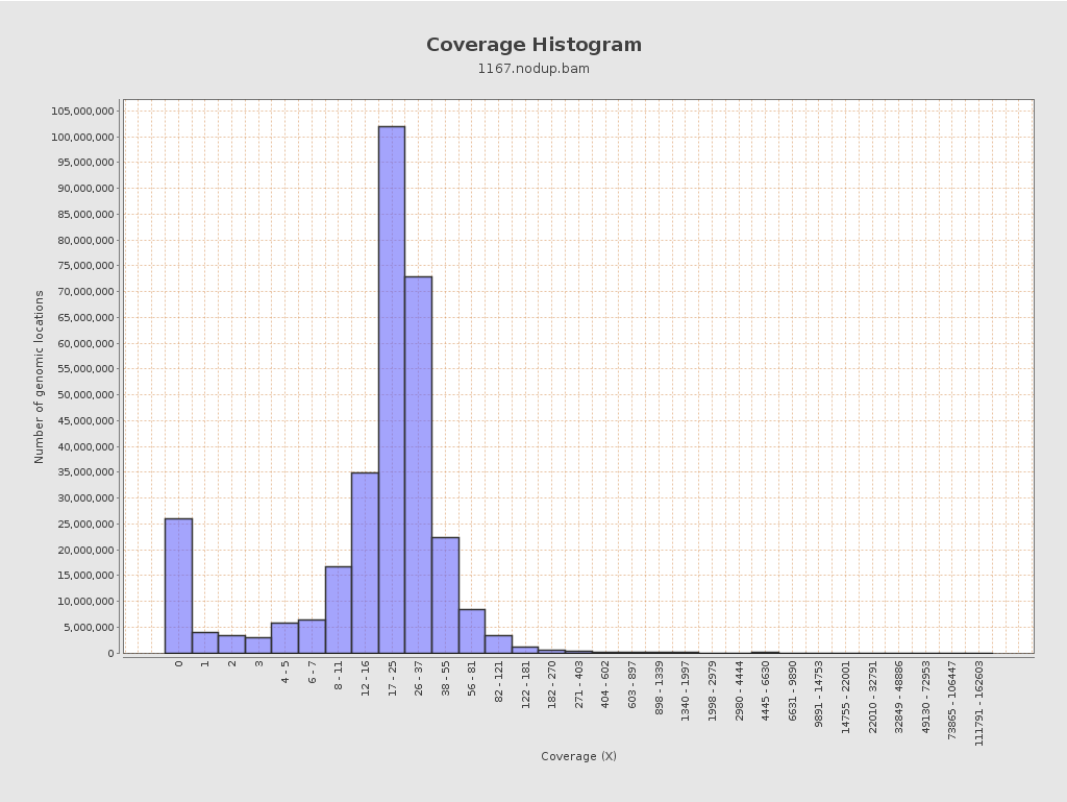
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	704661733	23.7066	65.9208

LT669789.1	36598175	1061831177	29.0132	246.8461
LT669790.1	30422129	913688176	30.0337	215.681
LT669791.1	52758100	1468666434	27.8377	181.4708
LT669792.1	28376109	787781868	27.7622	227.9389
LT669793.1	33388210	866611036	25.9556	113.9528
LT669794.1	50579949	1366813207	27.0228	197.2872
LT669795.1	49795044	1660203880	33.3407	290.8585

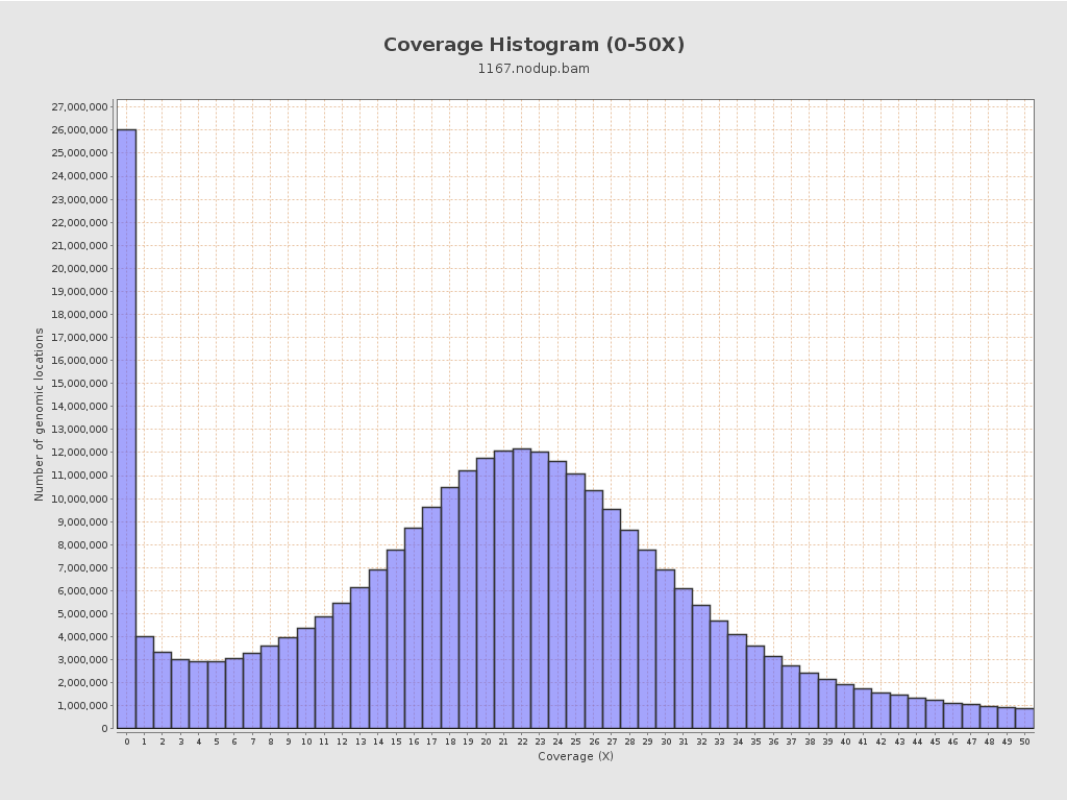
3. Results : Coverage across reference



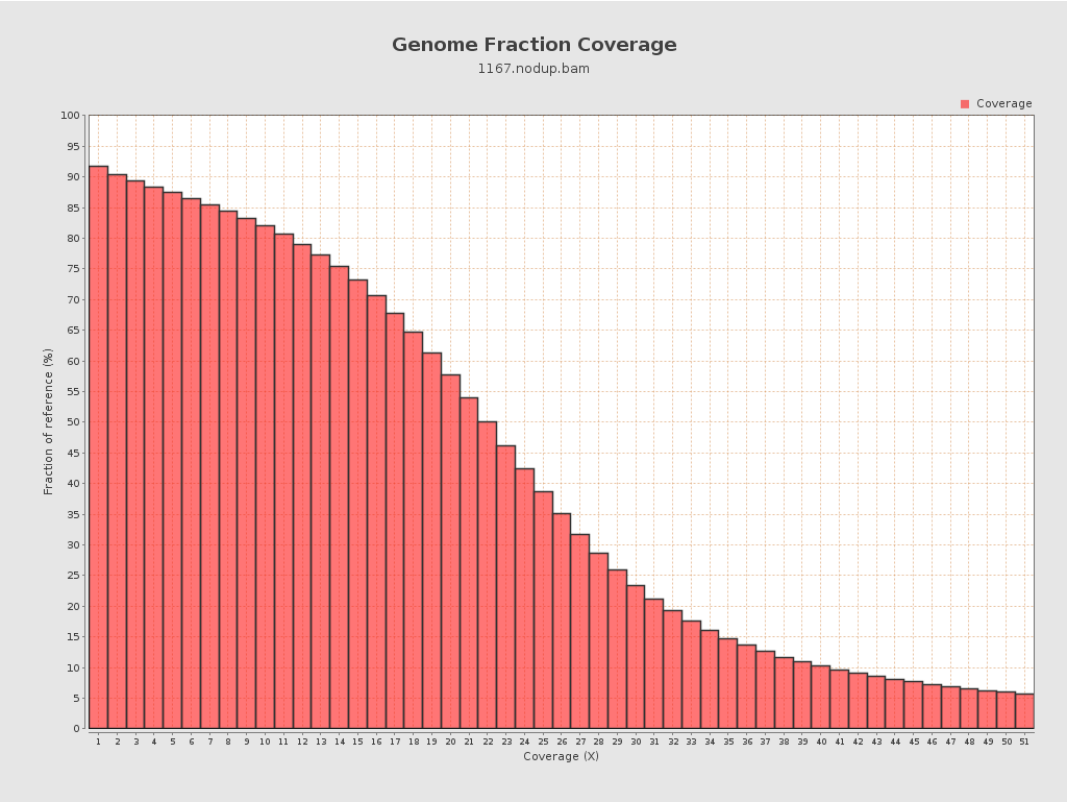
4. Results : Coverage Histogram



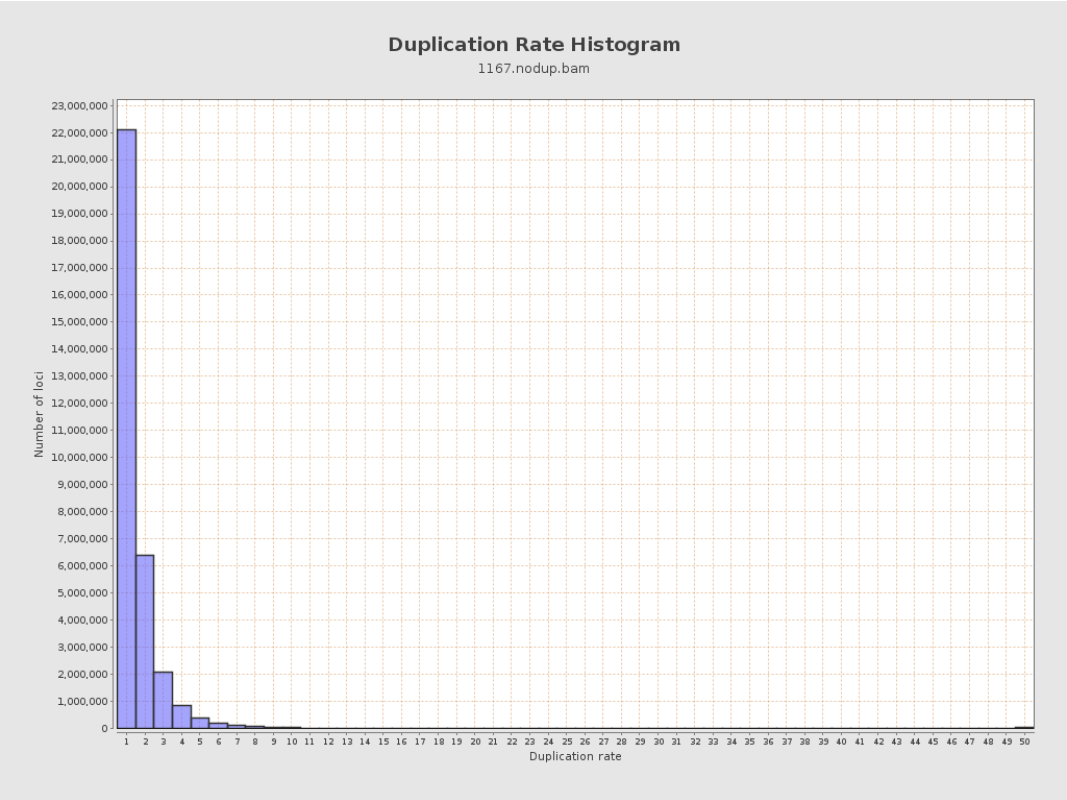
5. Results : Coverage Histogram (0-50X)



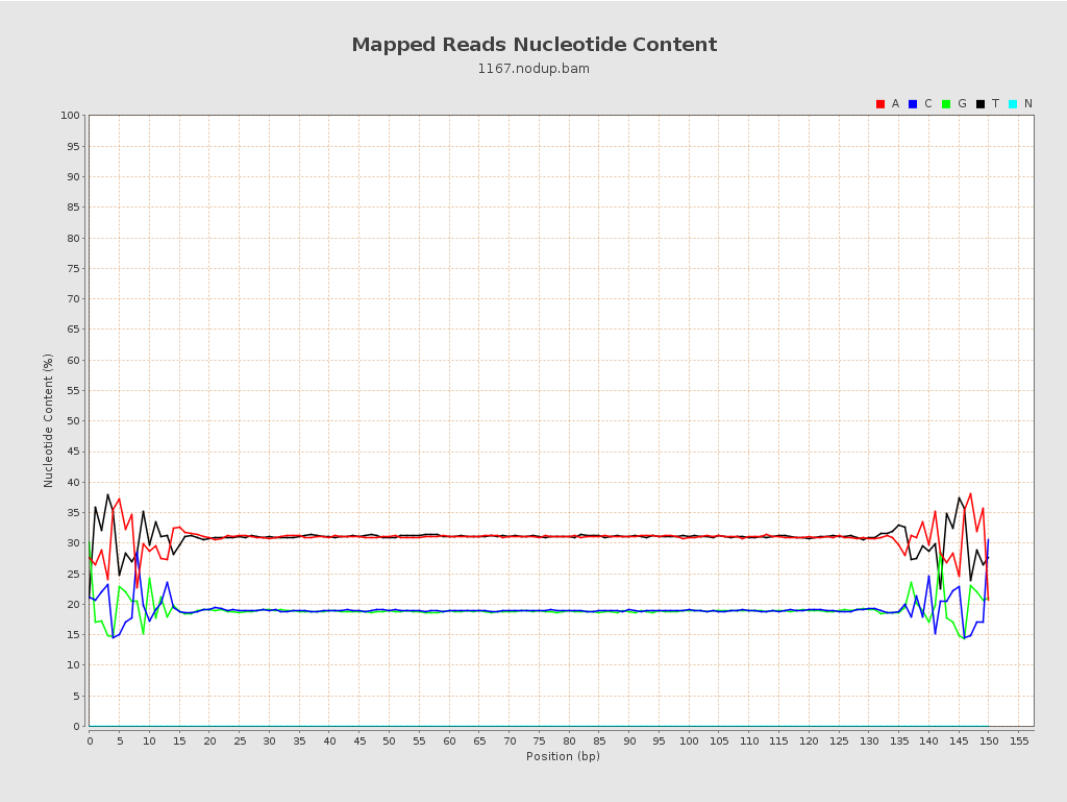
6. Results : Genome Fraction Coverage



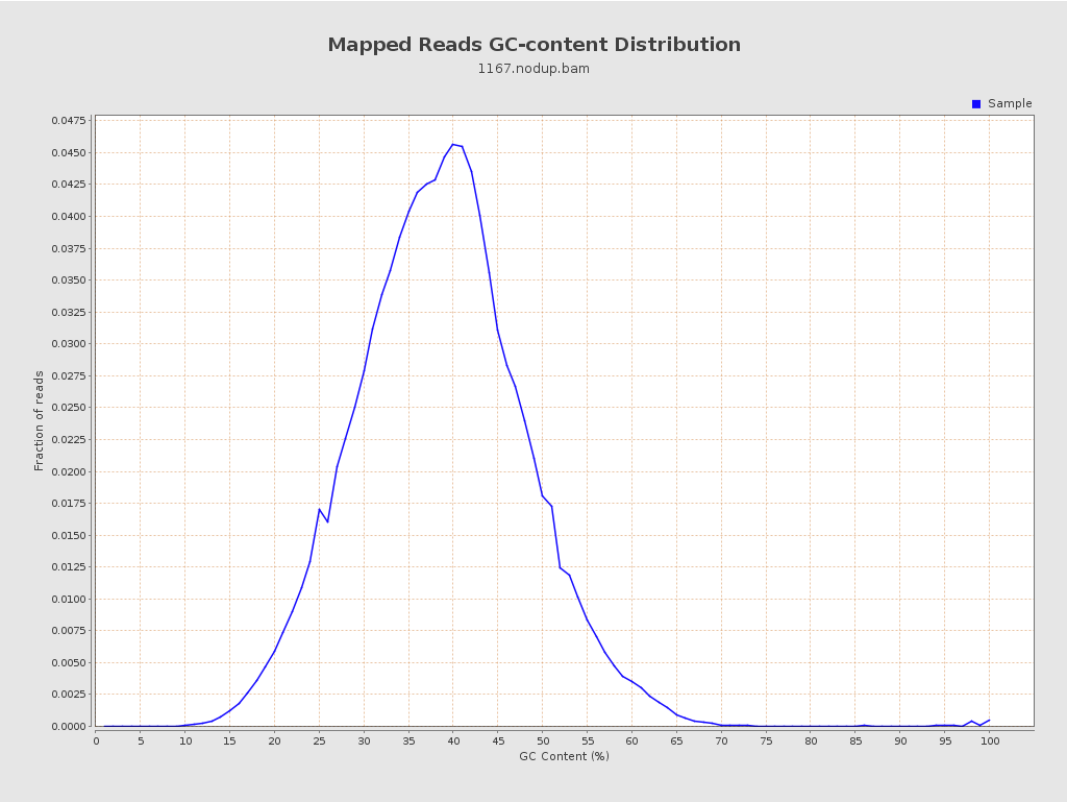
7. Results : Duplication Rate Histogram



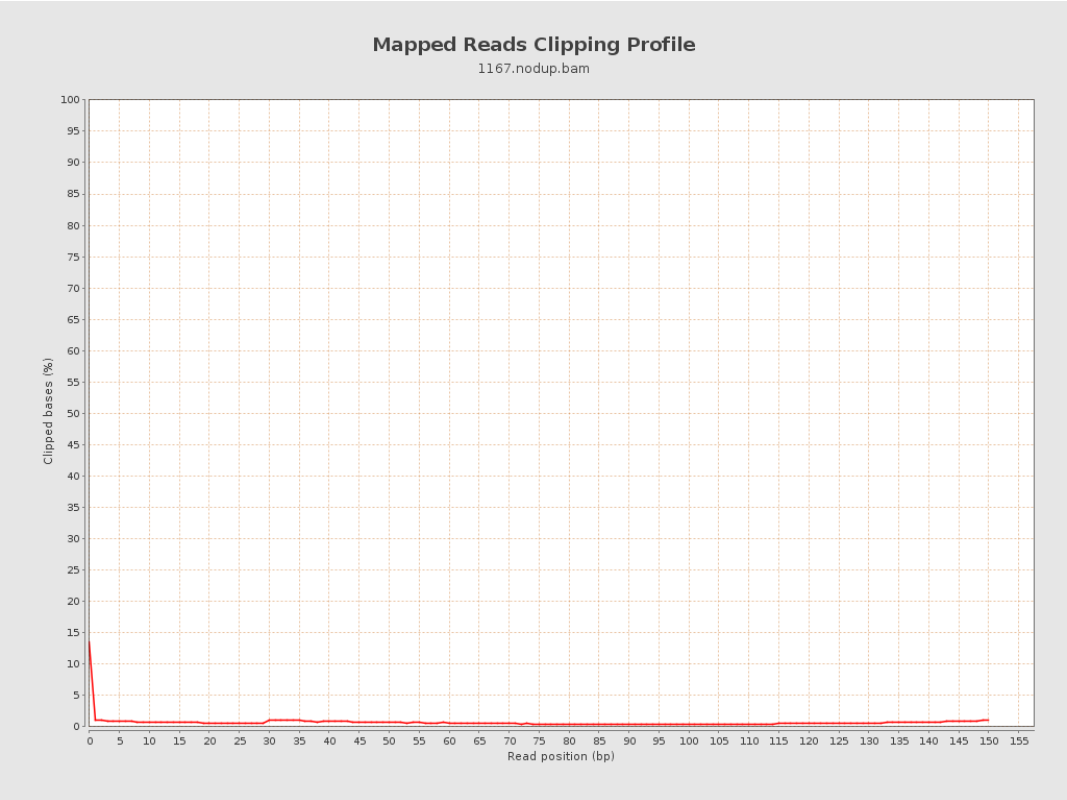
8. Results : Mapped Reads Nucleotide Content



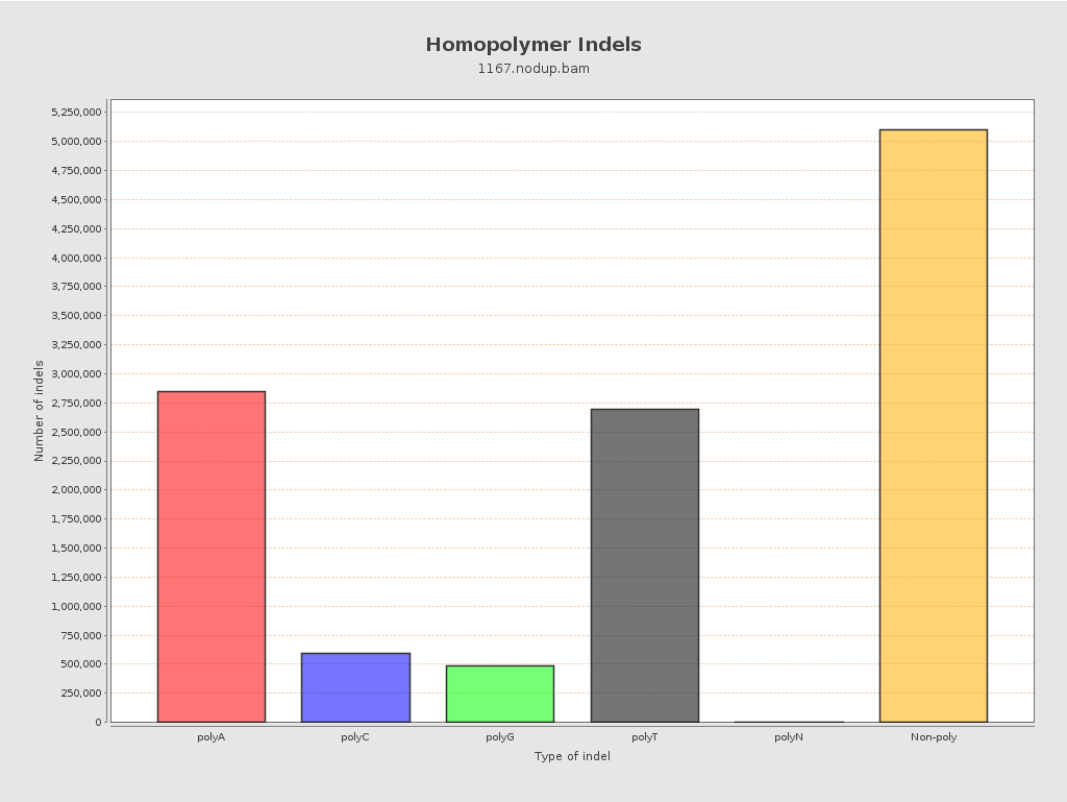
9. Results : Mapped Reads GC-content Distribution



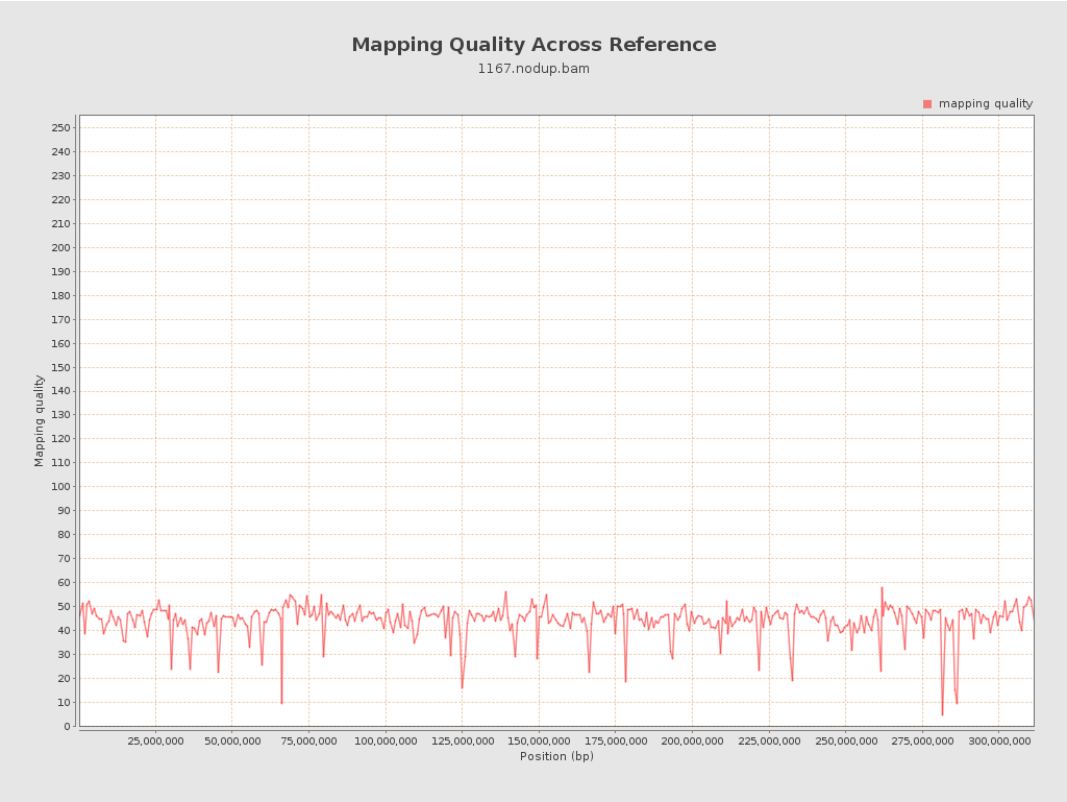
10. Results : Mapped Reads Clipping Profile



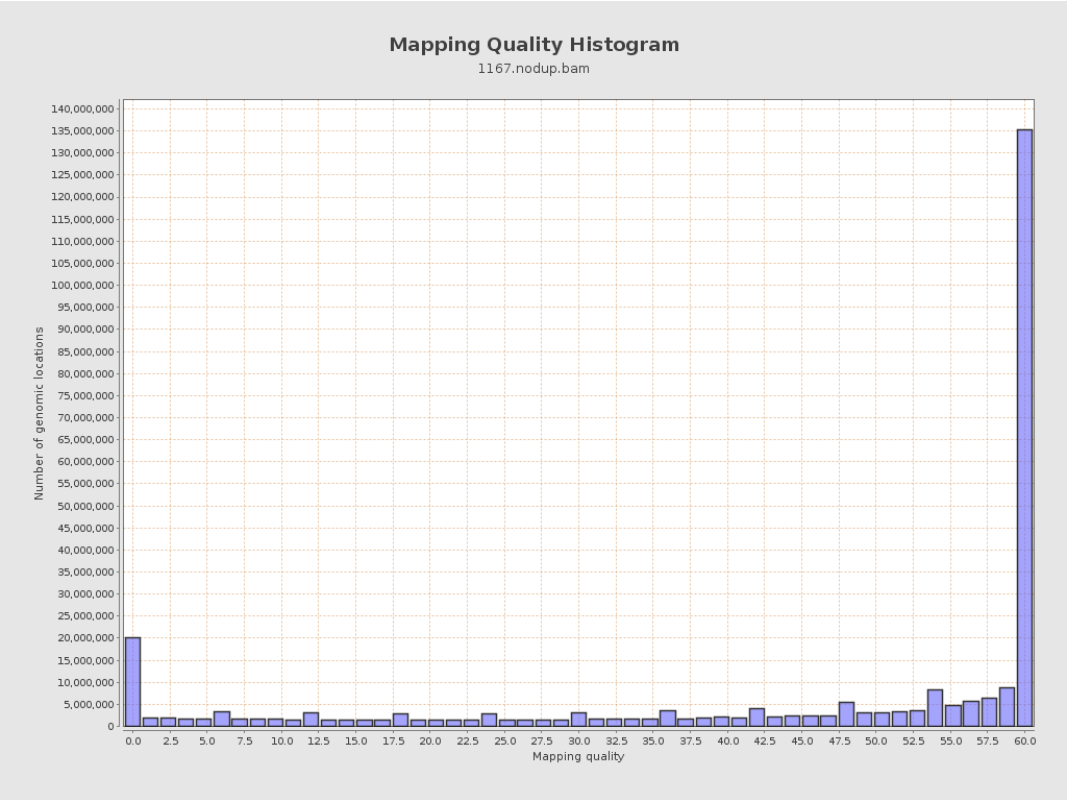
11. Results : Homopolymer Indels



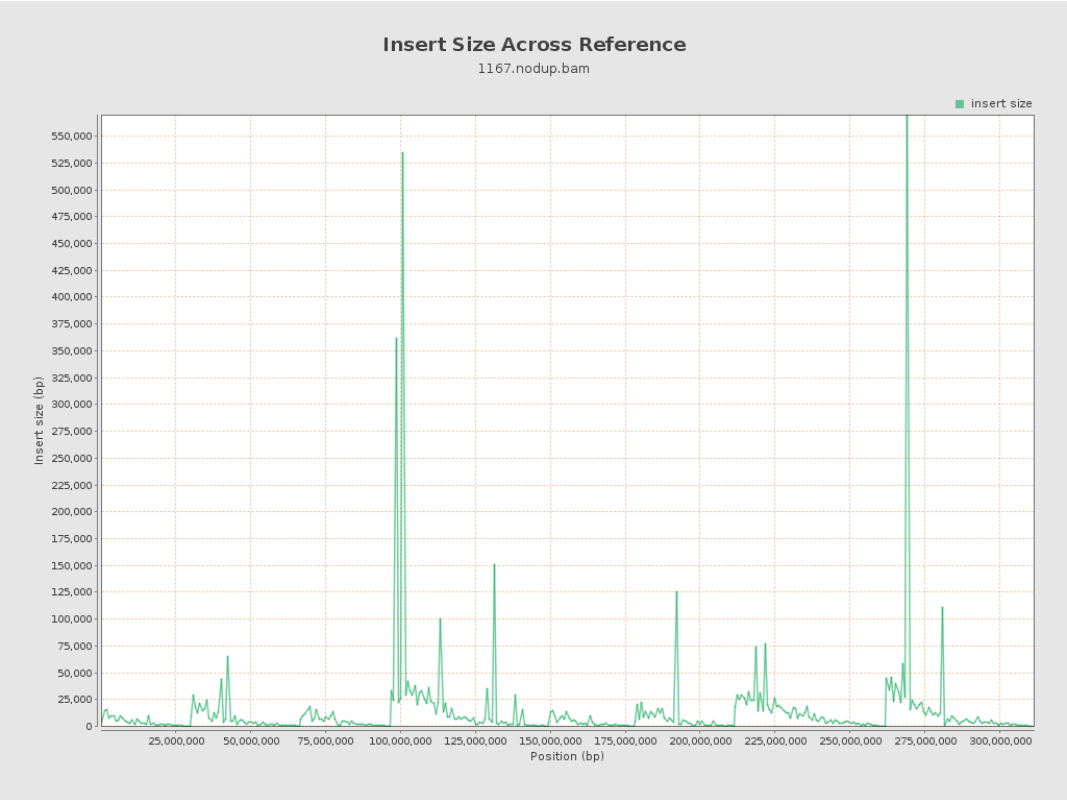
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram