

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:29:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/116
8
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1168 .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\t SM:\$sample /proj/uppstore2018210/Aalpina/data/r eference/GCA_900128785.1_MPIPZ. v5_genomic.fa /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_473/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_473_S448_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_473/02- FASTQ/220902_A00621_0737_BHM GCVDSX3/P26207_473_S448_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:29:49 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	58,812,096
Mapped reads	55,478,251 / 94.33%
Unmapped reads	3,333,845 / 5.67%
Mapped paired reads	55,478,251 / 94.33%
Mapped reads, first in pair	27,810,089 / 47.29%
Mapped reads, second in pair	27,668,162 / 47.05%
Mapped reads, both in pair	54,399,221 / 92.5%
Mapped reads, singletons	1,079,030 / 1.83%
Read min/max/mean length	30 / 151 / 148.15
Duplicated reads (flagged)	7,941,509 / 13.5%
Clipped reads	12,017,724 / 20.43%

2.2. ACGT Content

Number/percentage of A's	2,385,286,271 / 30.88%
Number/percentage of C's	1,479,203,004 / 19.15%
Number/percentage of T's	2,386,215,874 / 30.89%
Number/percentage of G's	1,474,382,120 / 19.09%
Number/percentage of N's	25,984 / 0%
GC Percentage	38.23%

2.3. Coverage

Mean	24.8529
Standard Deviation	193.6469

2.4. Mapping Quality

Mean Mapping Quality	44.13
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2.5. Insert size

Mean	235,797.01
Standard Deviation	2,280,853.48
P25/Median/P75	365 / 478 / 627

2.6. Mismatches and indels

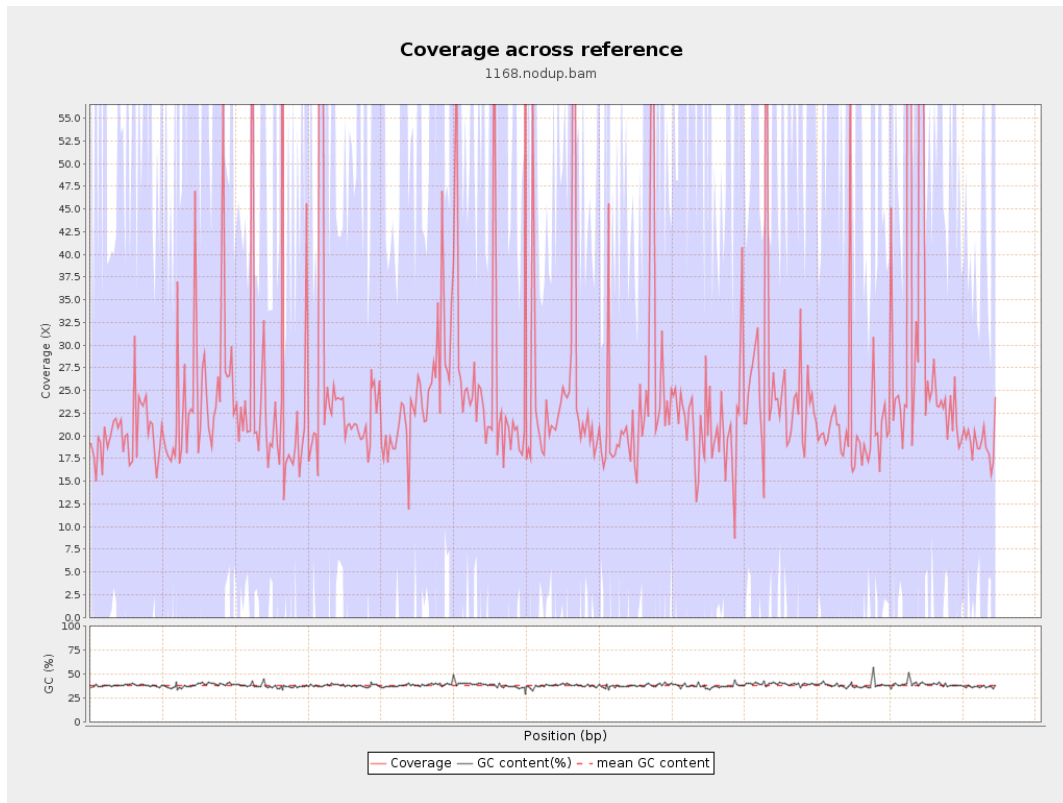
General error rate	2.28%
Mismatches	162,468,146
Insertions	5,081,219
Mapped reads with at least one insertion	8.26%
Deletions	5,267,707
Mapped reads with at least one deletion	8.46%
Homopolymer indels	56.52%

2.7. Chromosome stats

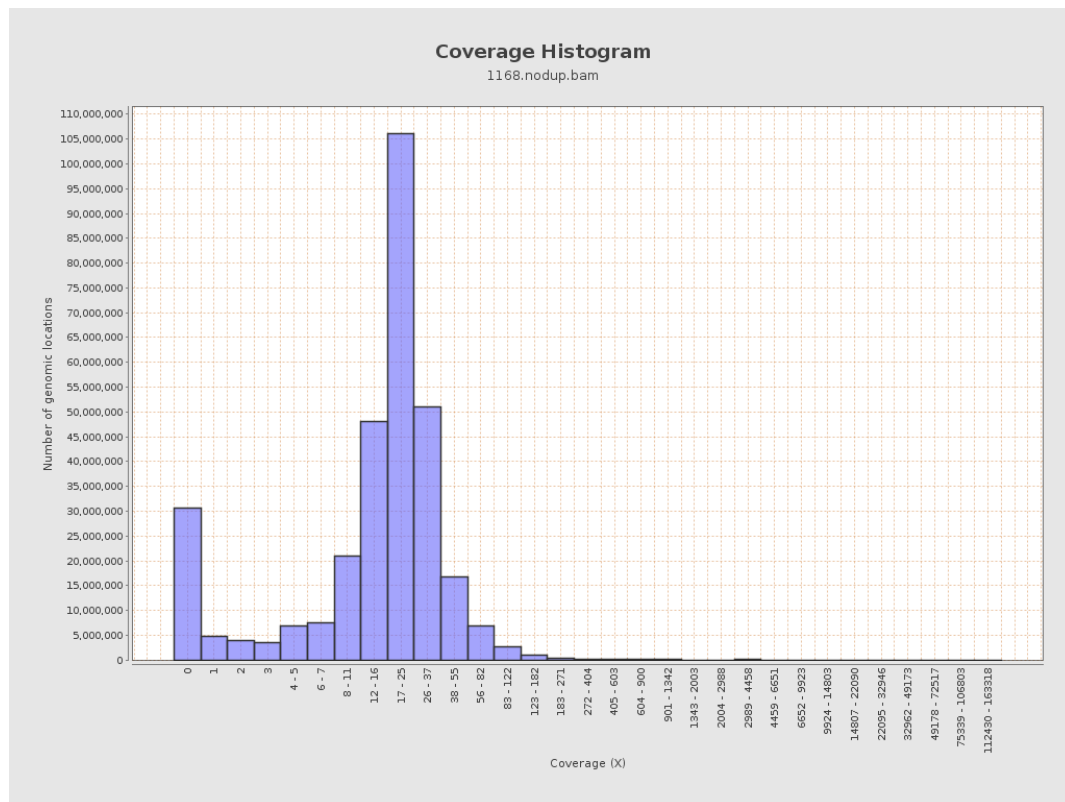
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	591096357	19.8859	43.7335

LT669789.1	36598175	937417958	25.6138	188.5497
LT669790.1	30422129	781450152	25.6869	174.9516
LT669791.1	52758100	1301180185	24.6631	139.8972
LT669792.1	28376109	693112466	24.4259	228.2448
LT669793.1	33388210	783870017	23.4774	140.6042
LT669794.1	50579949	1204726276	23.8183	167.152
LT669795.1	49795044	1452360560	29.1668	310.8406

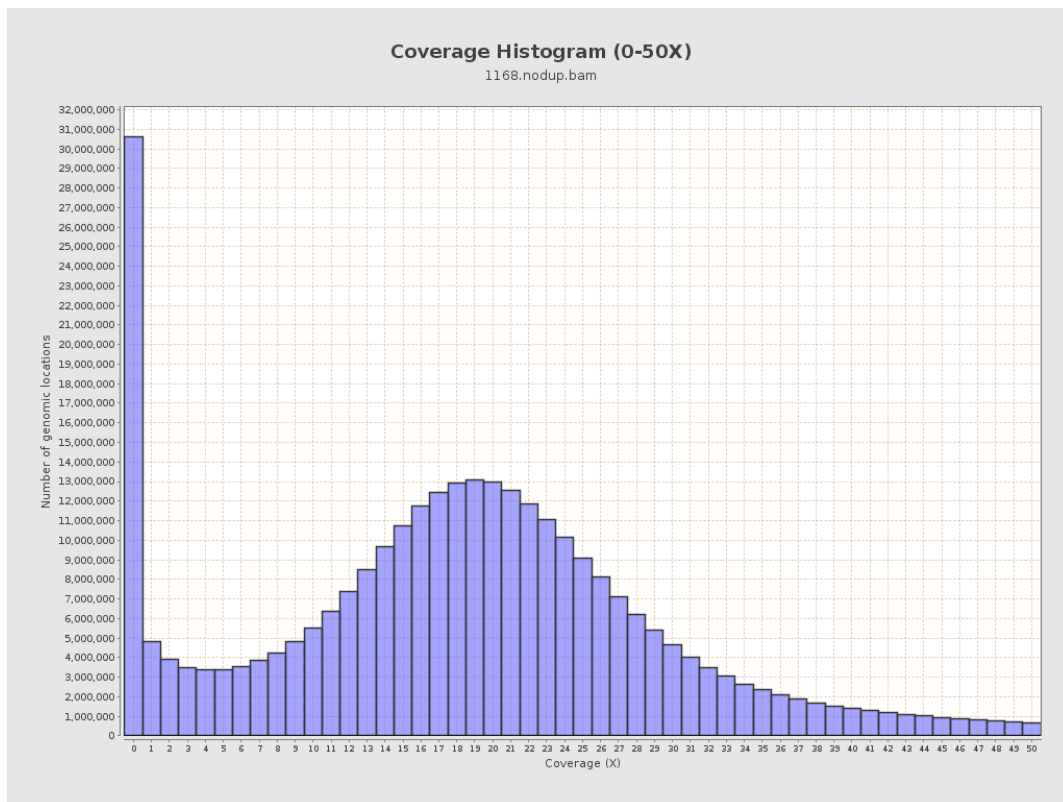
3. Results : Coverage across reference



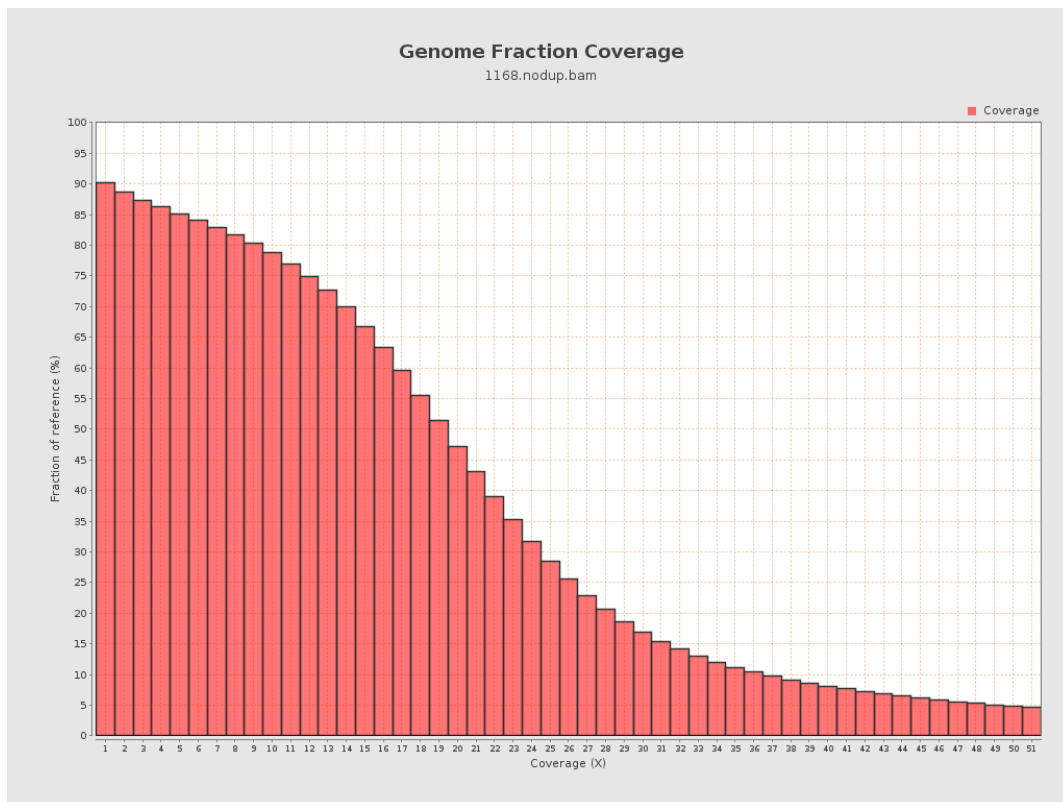
4. Results : Coverage Histogram



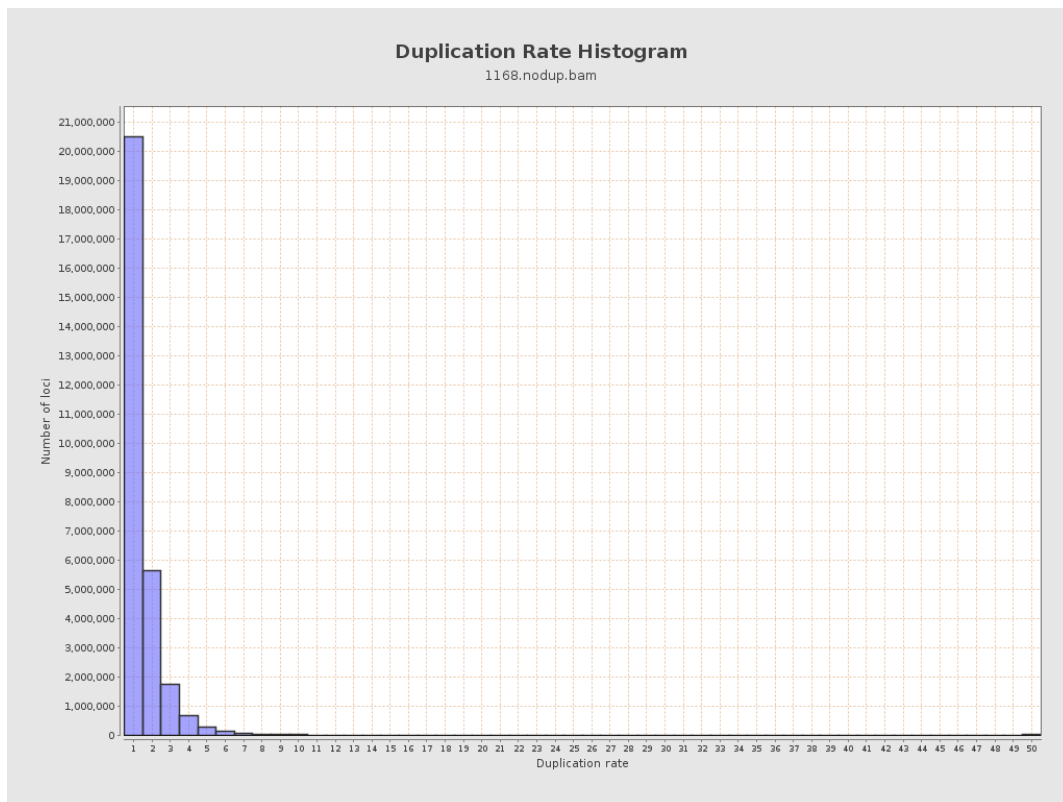
5. Results : Coverage Histogram (0-50X)



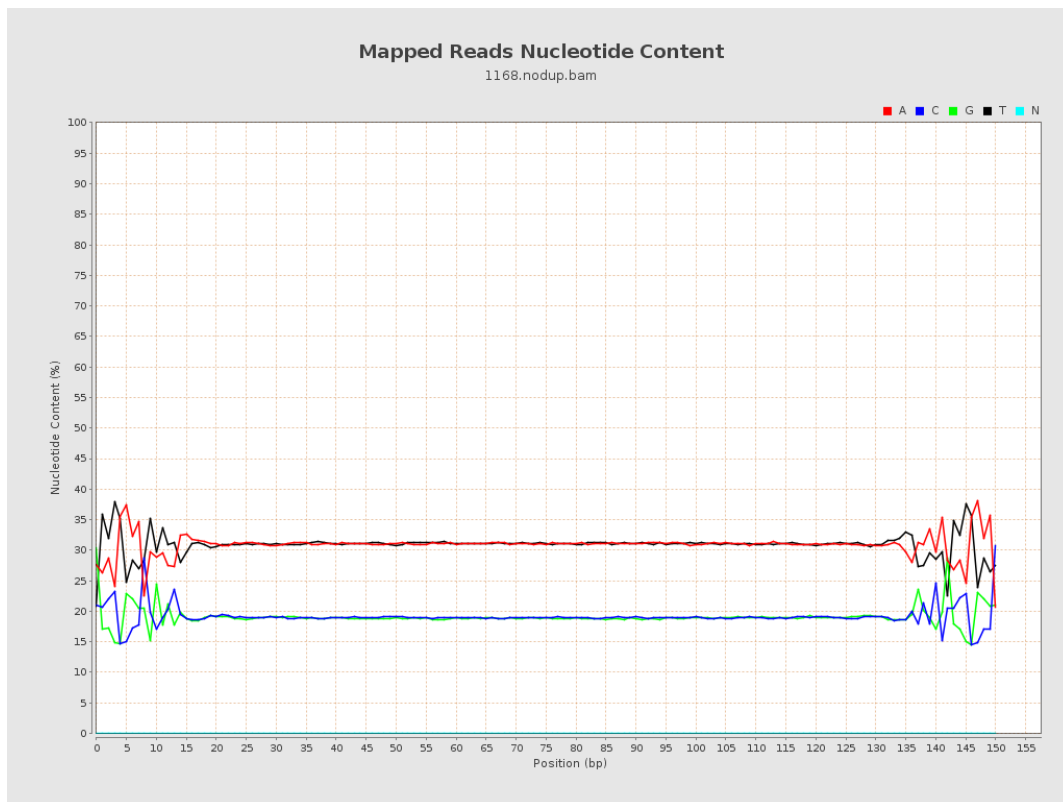
6. Results : Genome Fraction Coverage



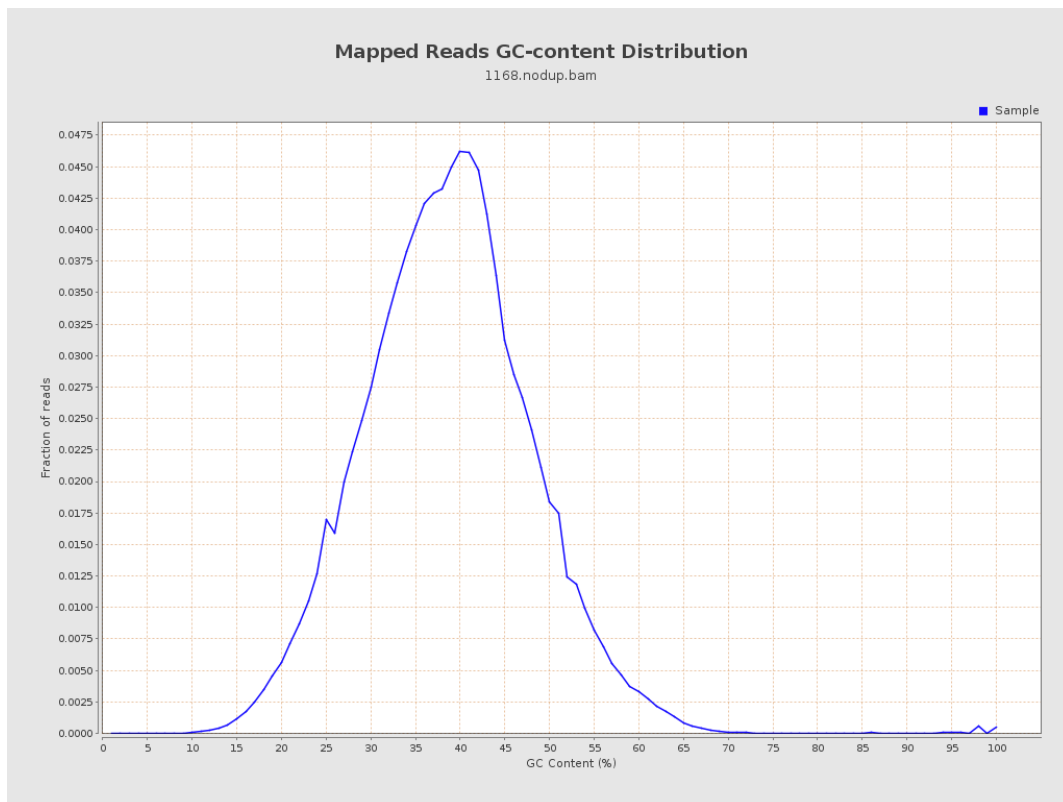
7. Results : Duplication Rate Histogram



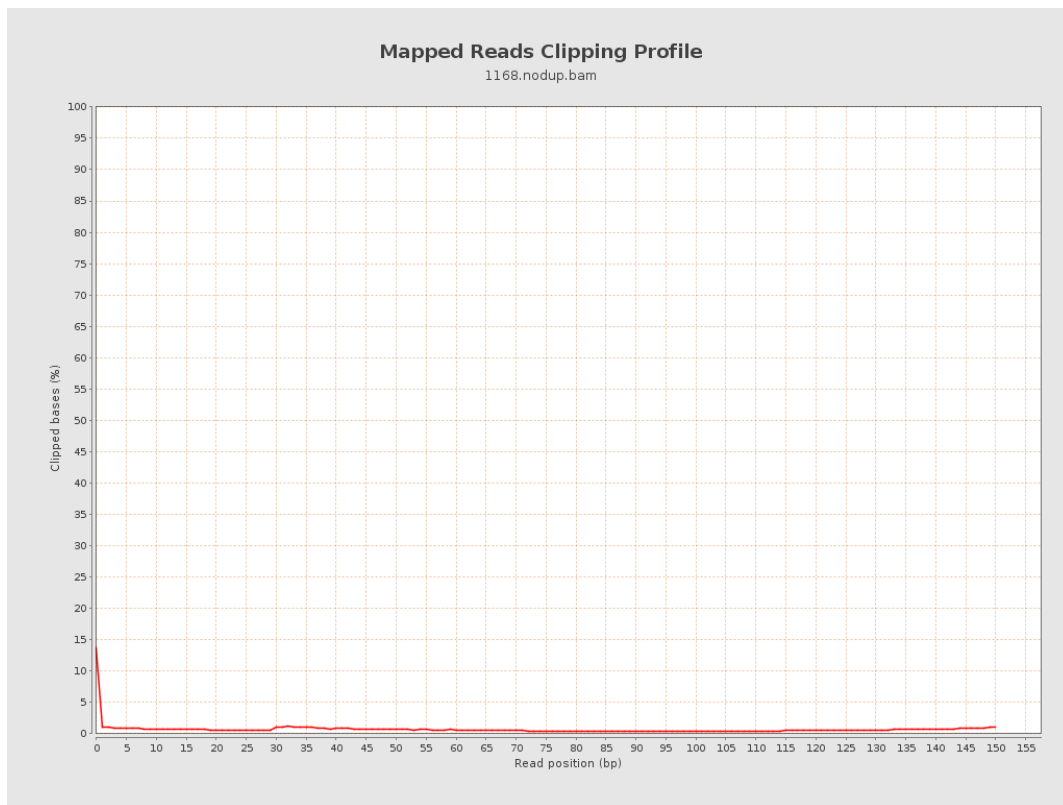
8. Results : Mapped Reads Nucleotide Content



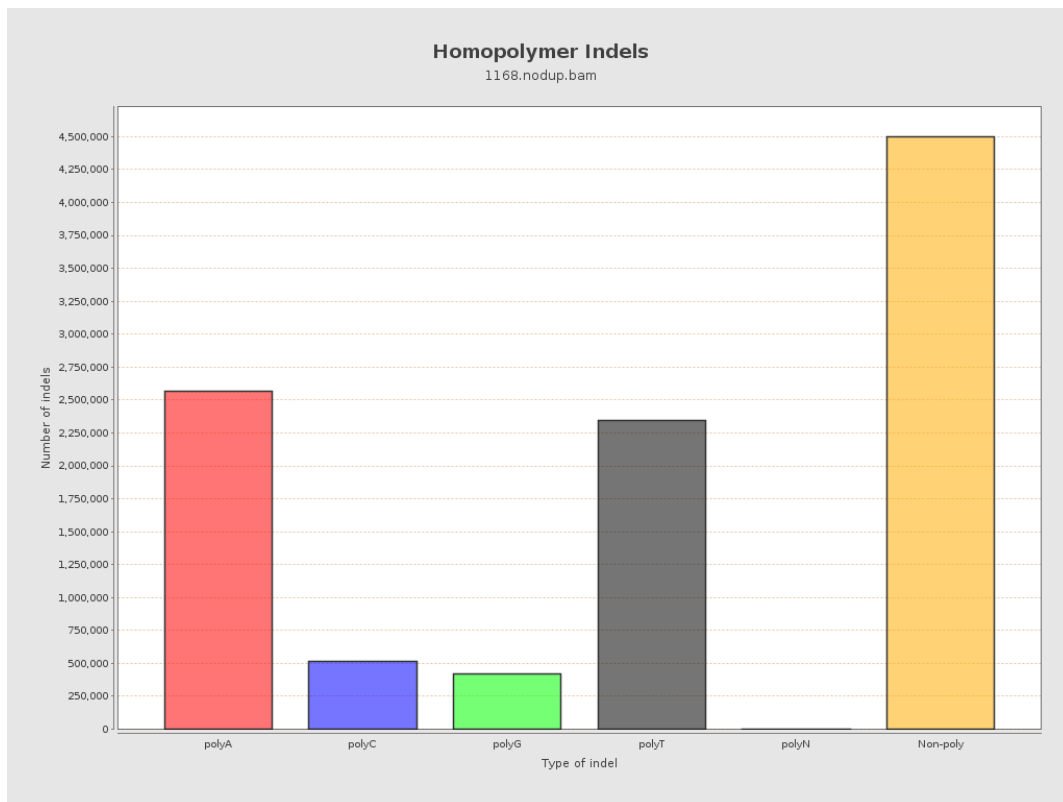
9. Results : Mapped Reads GC-content Distribution



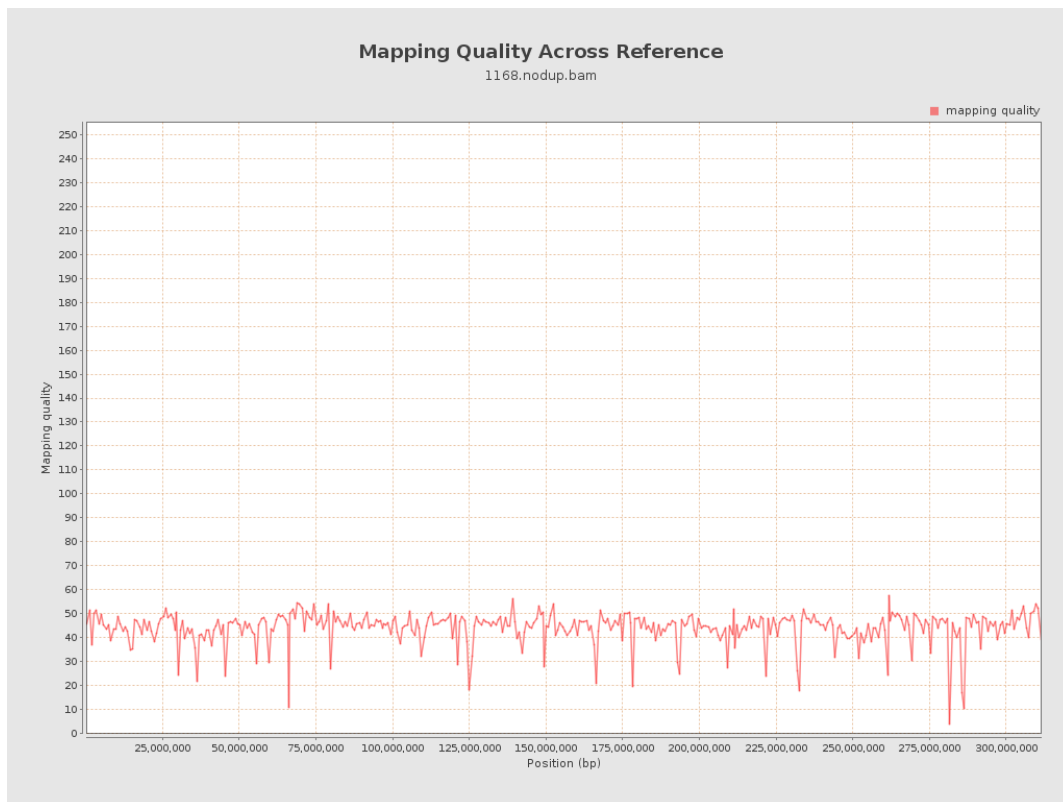
10. Results : Mapped Reads Clipping Profile



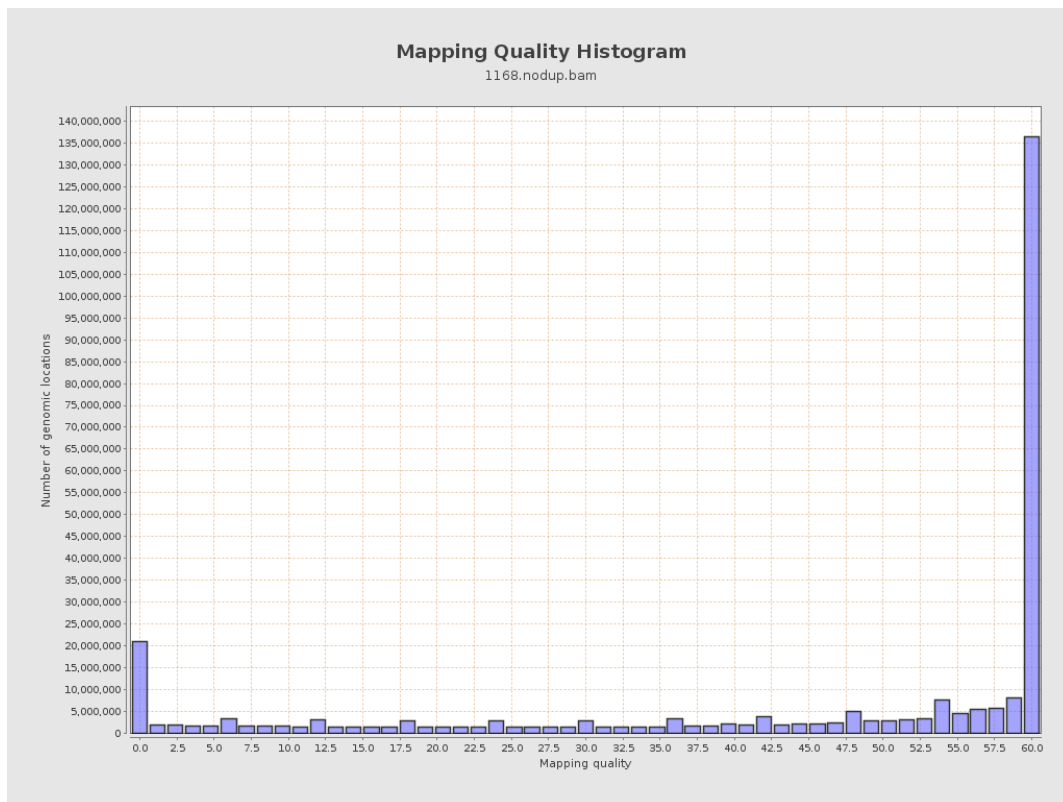
11. Results : Homopolymer Indels



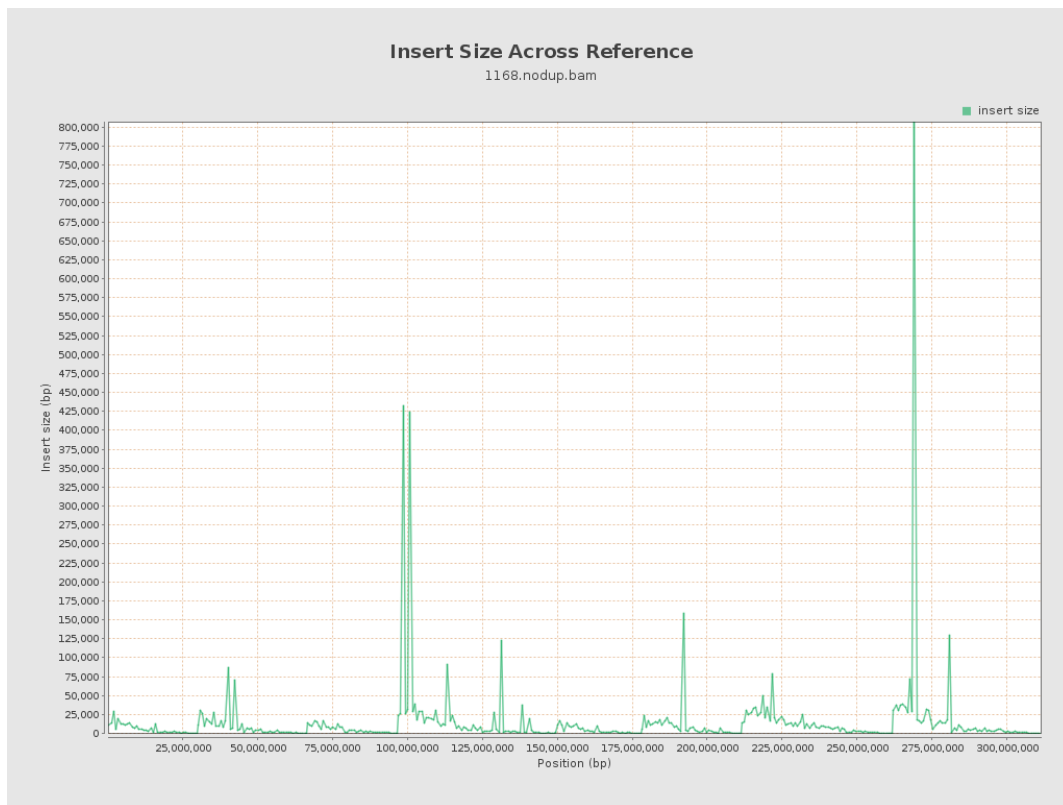
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

