

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:34:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/116
9
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1169 .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_535/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_535_S102_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_535/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_535_S102_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:34:30 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	71,537,074
Mapped reads	67,132,623 / 93.84%
Unmapped reads	4,404,451 / 6.16%
Mapped paired reads	67,132,623 / 93.84%
Mapped reads, first in pair	33,662,991 / 47.06%
Mapped reads, second in pair	33,469,632 / 46.79%
Mapped reads, both in pair	65,698,647 / 91.84%
Mapped reads, singletons	1,433,976 / 2%
Read min/max/mean length	30 / 151 / 148.29
Duplicated reads (flagged)	10,021,640 / 14.01%
Clipped reads	15,176,521 / 21.21%

2.2. ACGT Content

Number/percentage of A's	2,889,482,887 / 31.03%
Number/percentage of C's	1,768,201,924 / 18.99%
Number/percentage of T's	2,891,150,505 / 31.05%
Number/percentage of G's	1,762,789,299 / 18.93%
Number/percentage of N's	66,758 / 0%
GC Percentage	37.92%

2.3. Coverage

Mean	29.9535
Standard Deviation	212.5459

2.4. Mapping Quality

Mean Mapping Quality	44.74
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2.5. Insert size

Mean	214,926.43
Standard Deviation	2,213,018.66
P25/Median/P75	319 / 416 / 534

2.6. Mismatches and indels

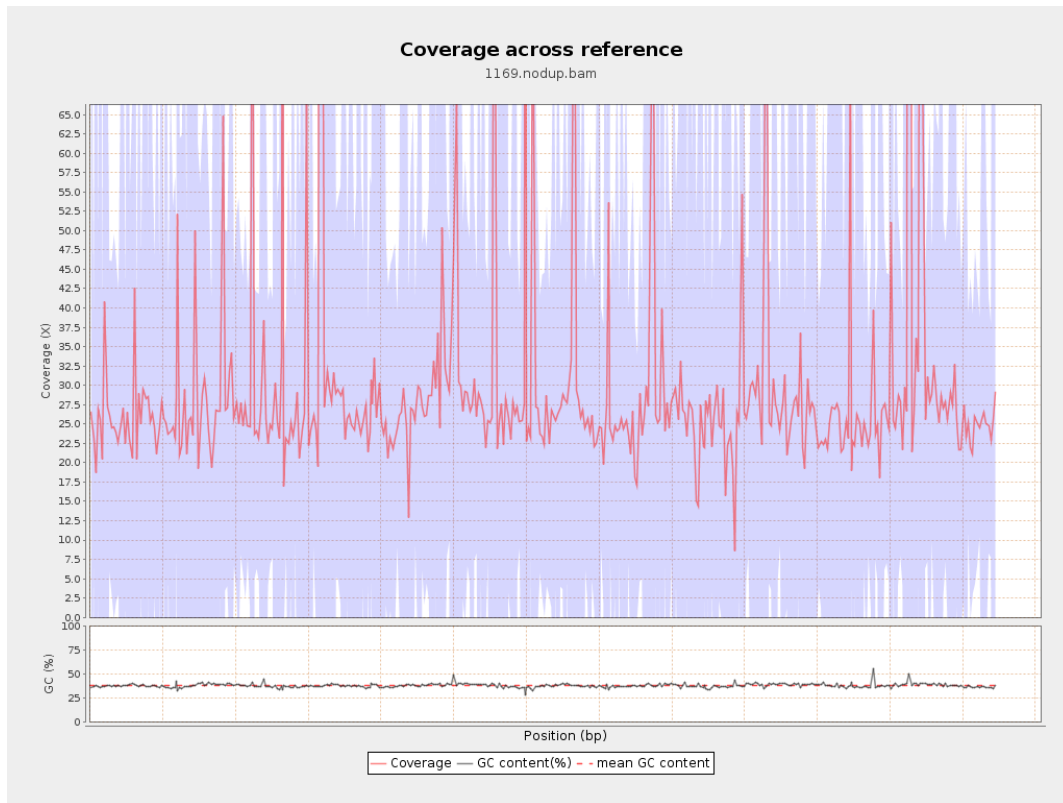
General error rate	2.43%
Mismatches	209,400,965
Insertions	6,099,534
Mapped reads with at least one insertion	8.17%
Deletions	6,149,876
Mapped reads with at least one deletion	8.15%
Homopolymer indels	56.83%

2.7. Chromosome stats

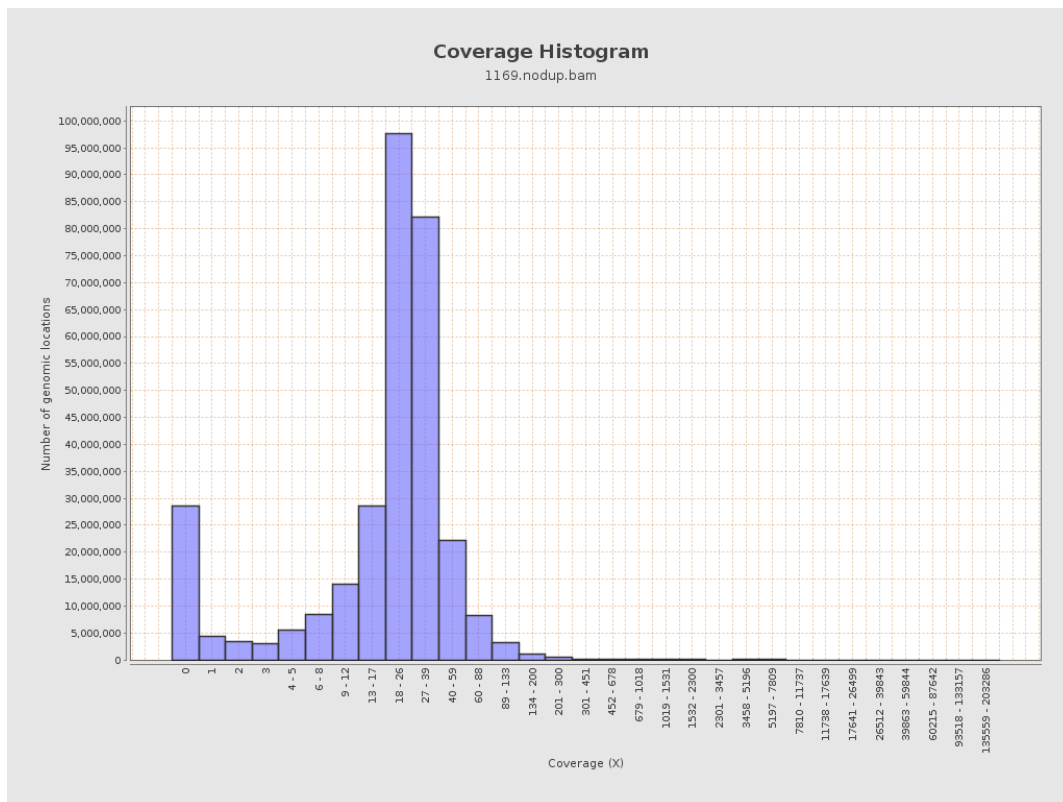
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	763551594	25.6878	65.8115

LT669789.1	36598175	1086373755	29.6838	214.9207
LT669790.1	30422129	1010188677	33.2057	242.9422
LT669791.1	52758100	1548554794	29.352	185.4133
LT669792.1	28376109	849895386	29.9511	230.2347
LT669793.1	33388210	928996949	27.8241	160.397
LT669794.1	50579949	1421885068	28.1116	183.1103
LT669795.1	49795044	1725322806	34.6485	303.5685

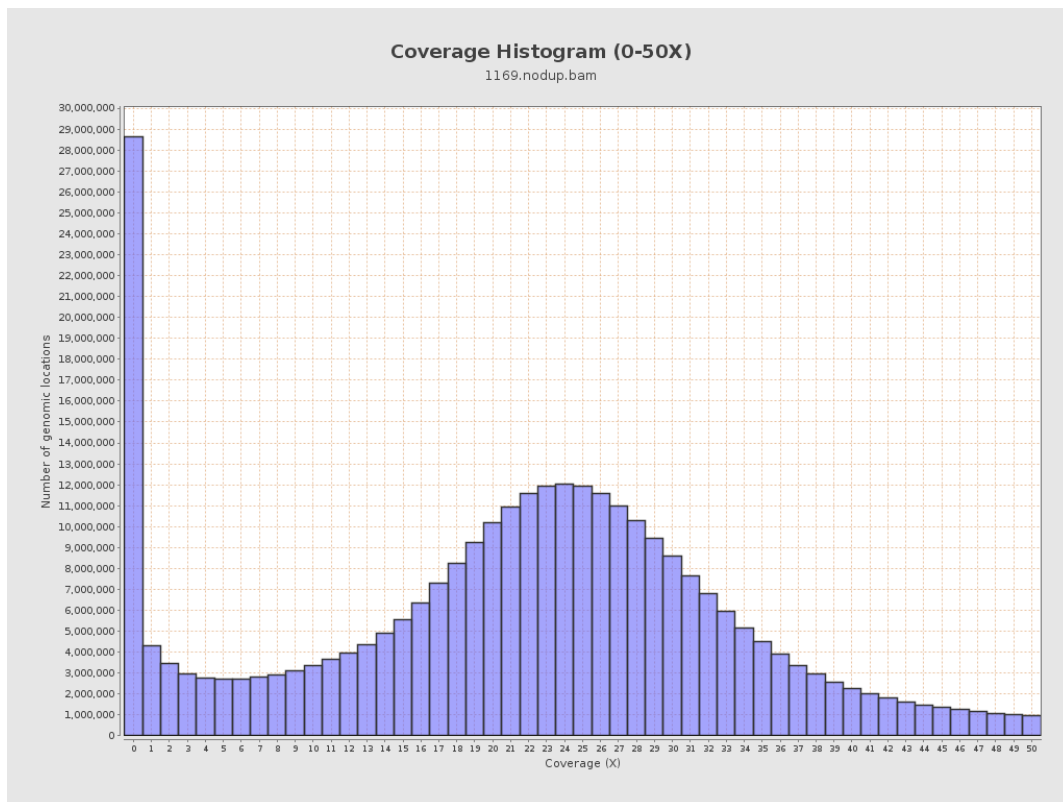
3. Results : Coverage across reference



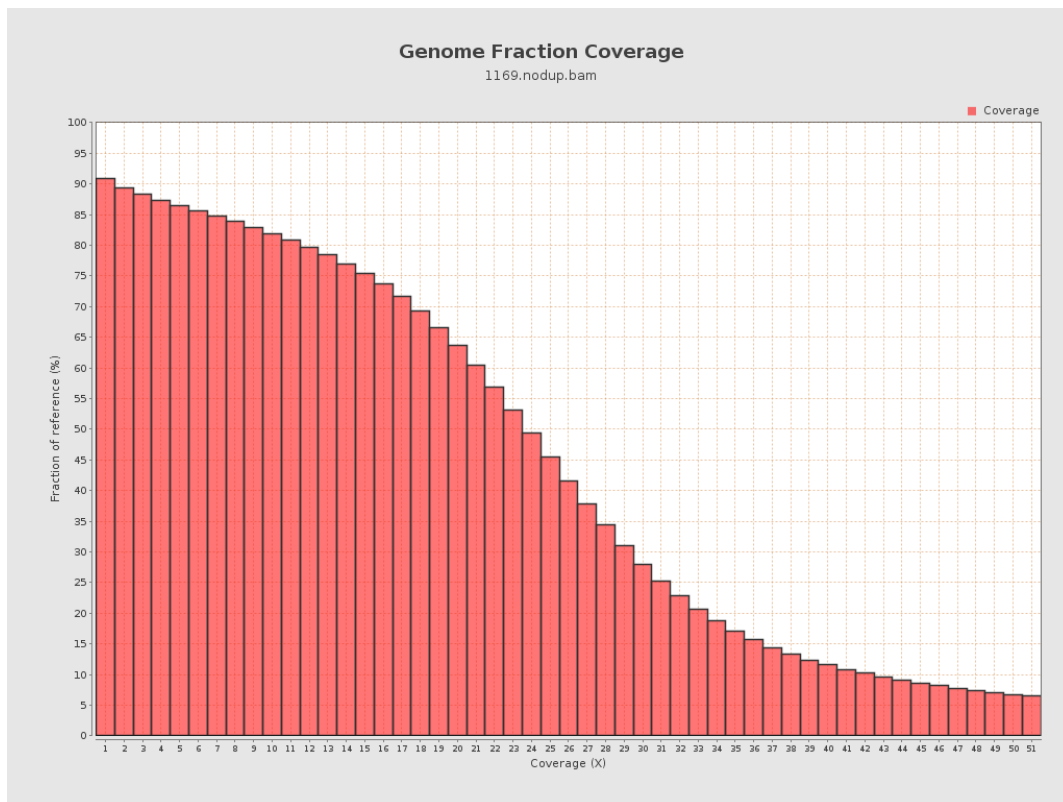
4. Results : Coverage Histogram



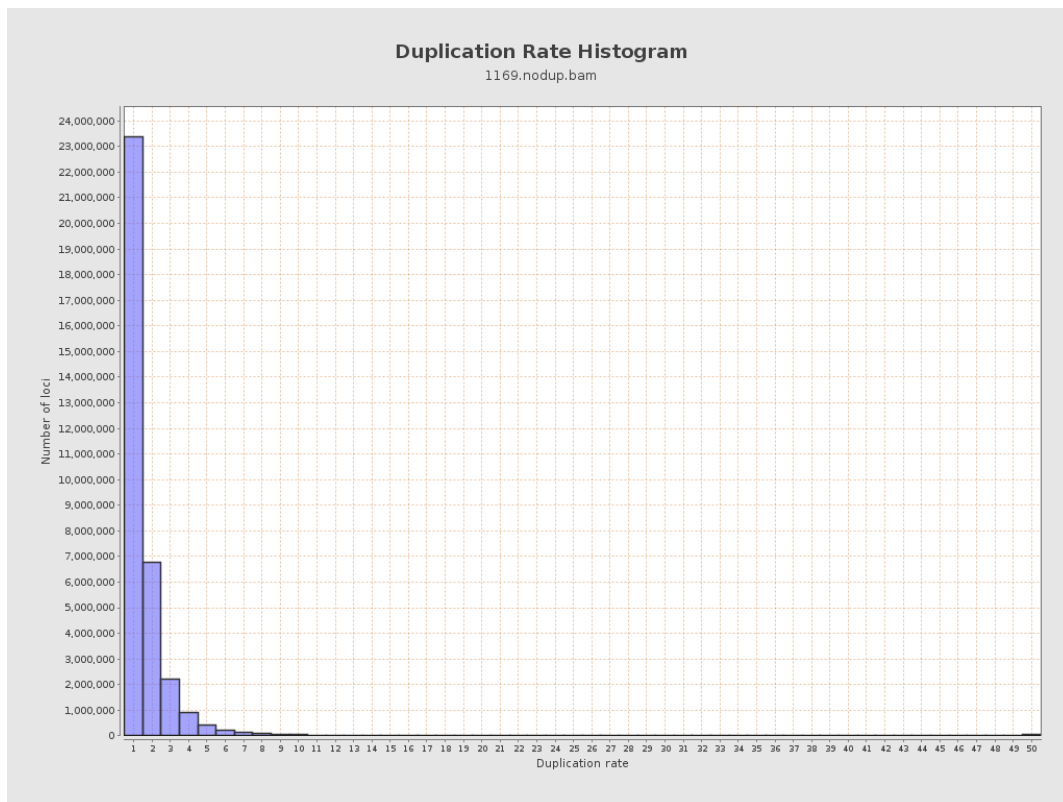
5. Results : Coverage Histogram (0-50X)



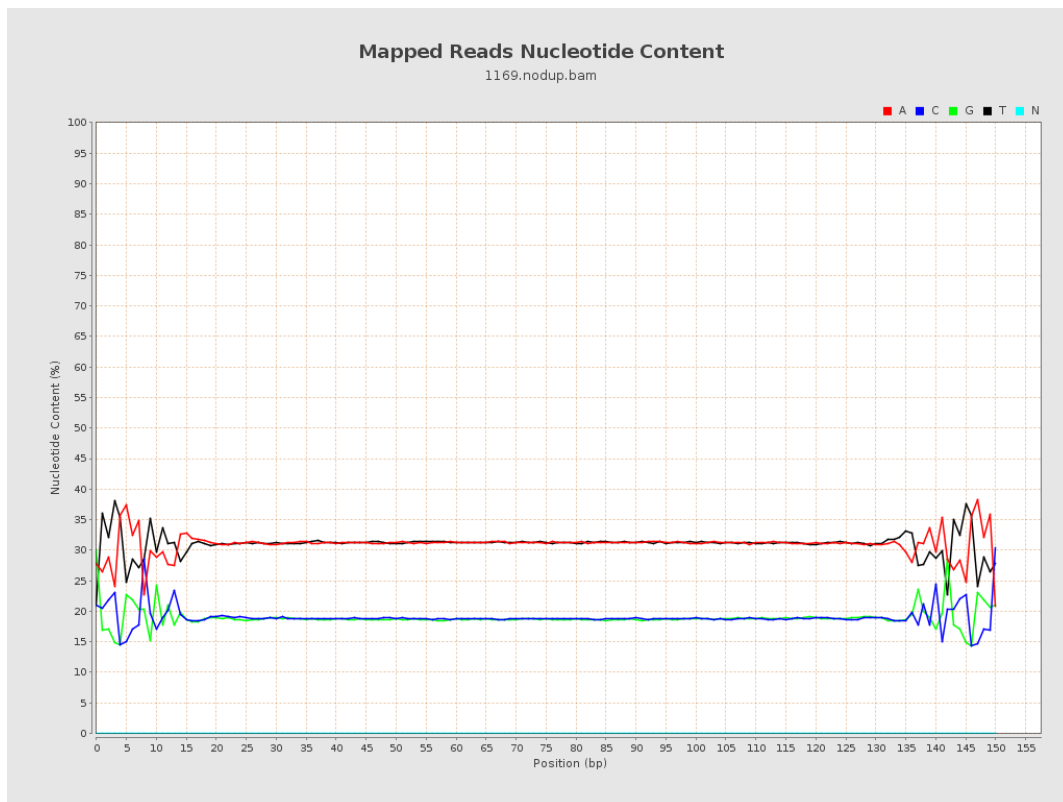
6. Results : Genome Fraction Coverage



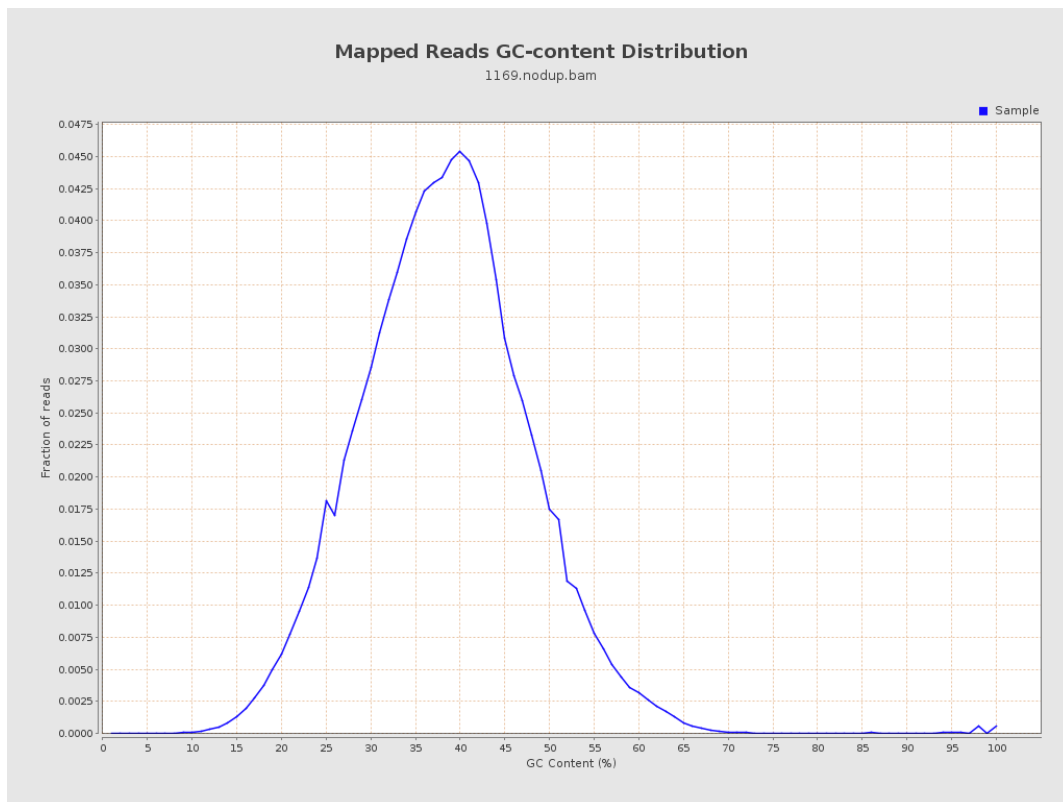
7. Results : Duplication Rate Histogram



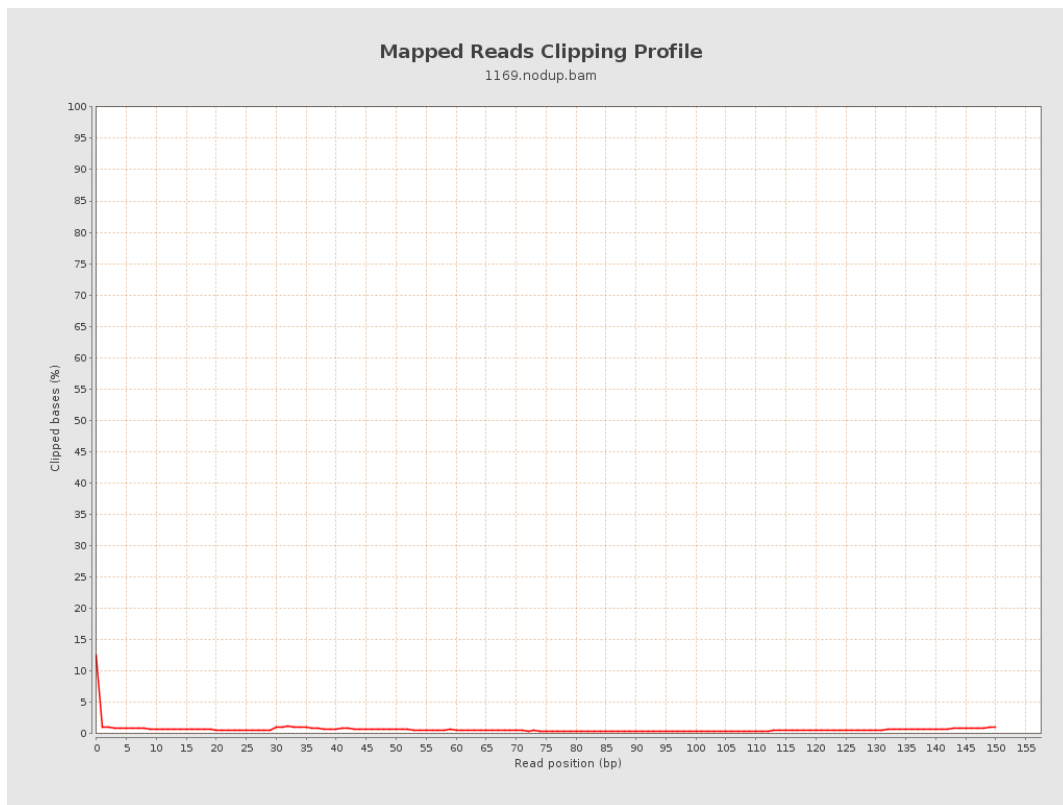
8. Results : Mapped Reads Nucleotide Content



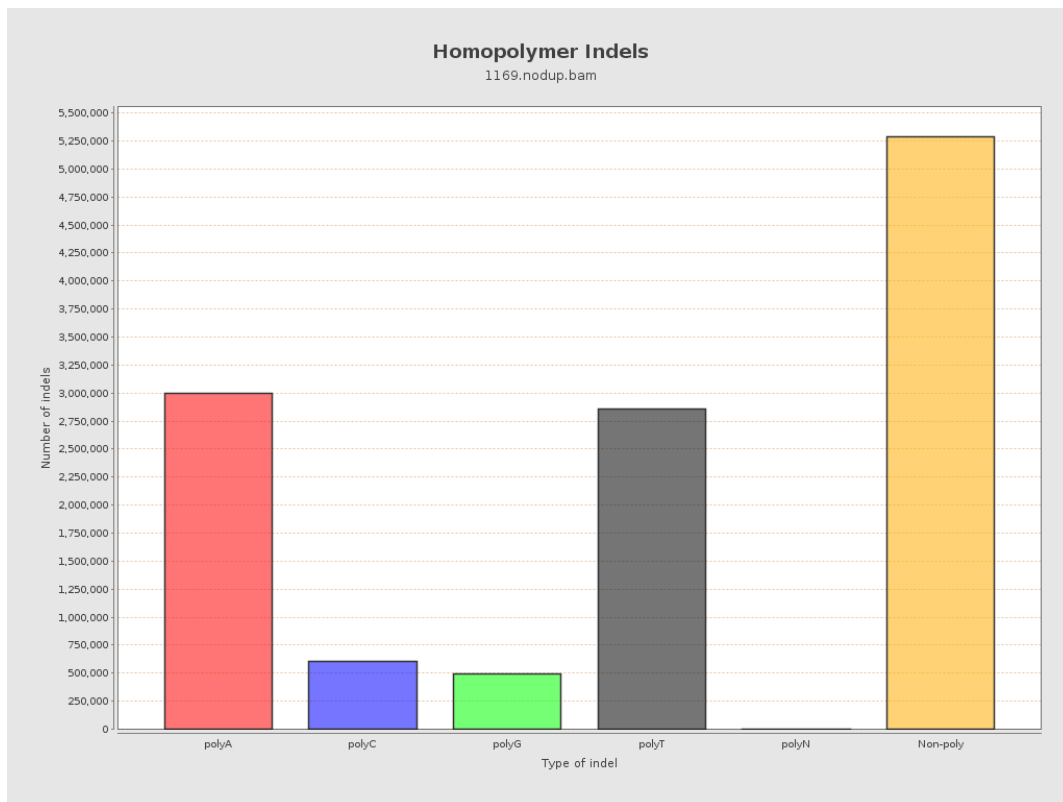
9. Results : Mapped Reads GC-content Distribution



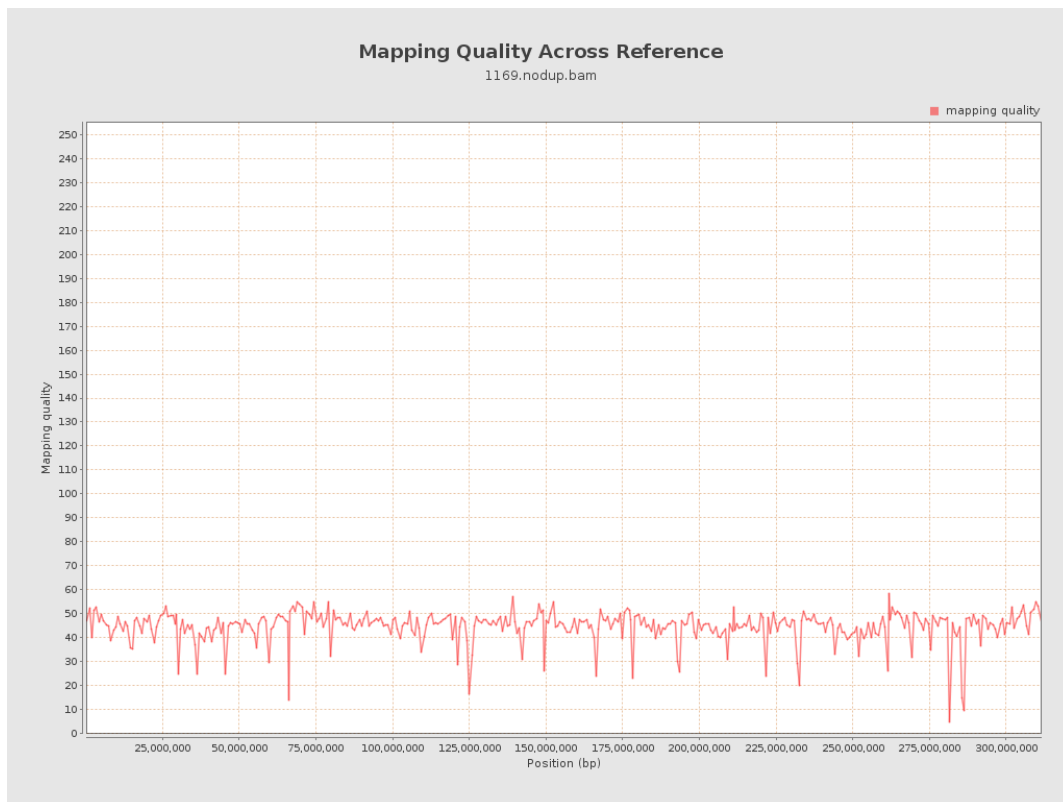
10. Results : Mapped Reads Clipping Profile



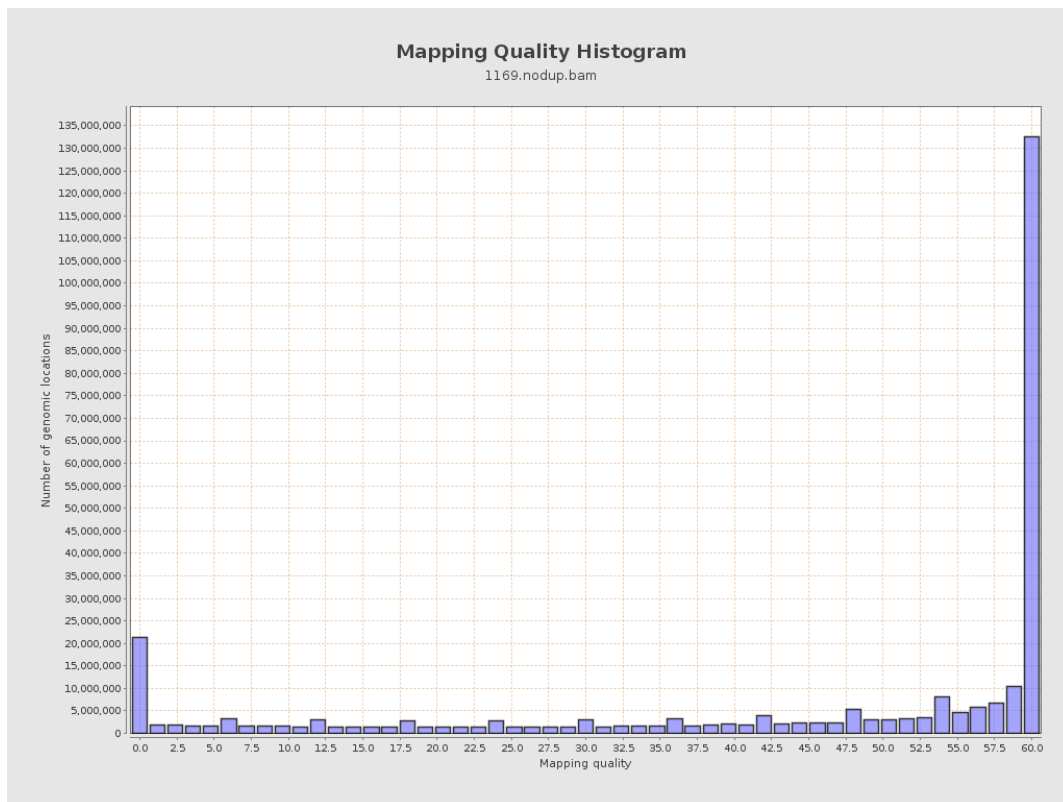
11. Results : Homopolymer Indels



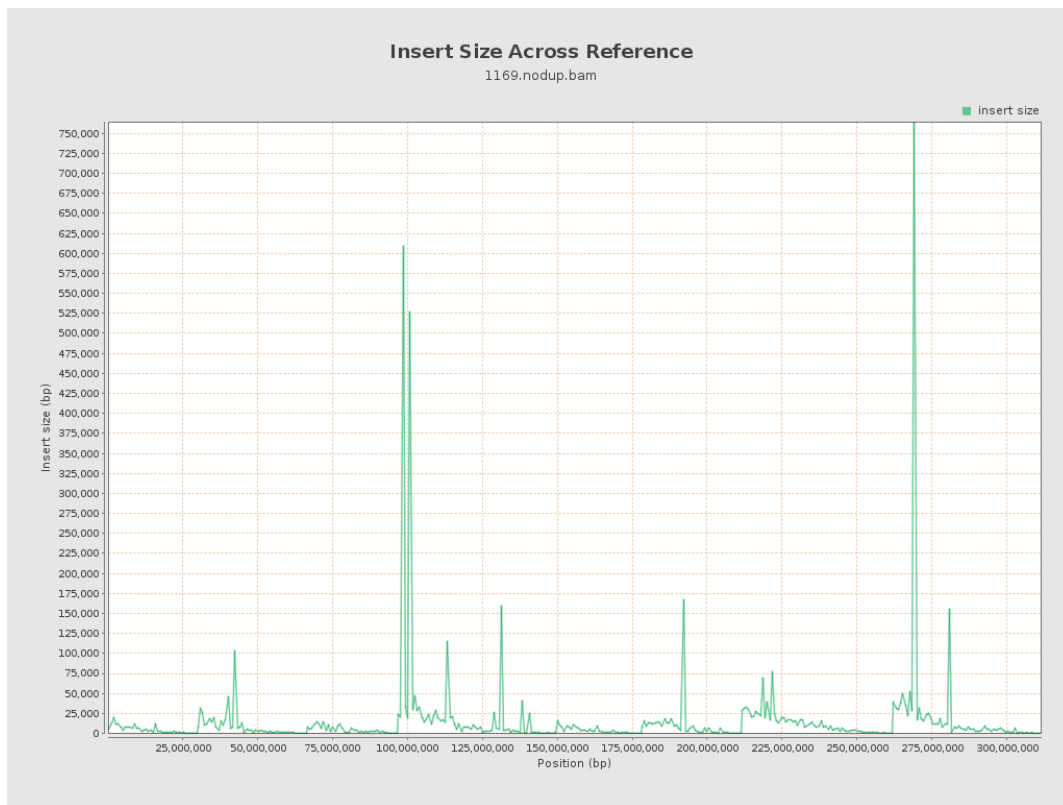
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

