

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:37:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/141
8
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1418 .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_564/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_564_S131_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_564/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_564_S131_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:37:17 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	82,266,398
Mapped reads	78,300,597 / 95.18%
Unmapped reads	3,965,801 / 4.82%
Mapped paired reads	78,300,597 / 95.18%
Mapped reads, first in pair	39,249,536 / 47.71%
Mapped reads, second in pair	39,051,061 / 47.47%
Mapped reads, both in pair	76,964,830 / 93.56%
Mapped reads, singletons	1,335,767 / 1.62%
Read min/max/mean length	30 / 151 / 148.08
Duplicated reads (flagged)	11,950,547 / 14.53%
Clipped reads	18,199,433 / 22.12%

2.2. ACGT Content

Number/percentage of A's	3,346,117,818 / 30.84%
Number/percentage of C's	2,080,114,878 / 19.17%
Number/percentage of T's	3,351,147,811 / 30.88%
Number/percentage of G's	2,073,467,303 / 19.11%
Number/percentage of N's	82,037 / 0%
GC Percentage	38.28%

2.3. Coverage

Mean	34.9094
Standard Deviation	282.2885

2.4. Mapping Quality

Mean Mapping Quality	43.84
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2.5. Insert size

Mean	210,075.31
Standard Deviation	2,164,033.79
P25/Median/P75	302 / 398 / 516

2.6. Mismatches and indels

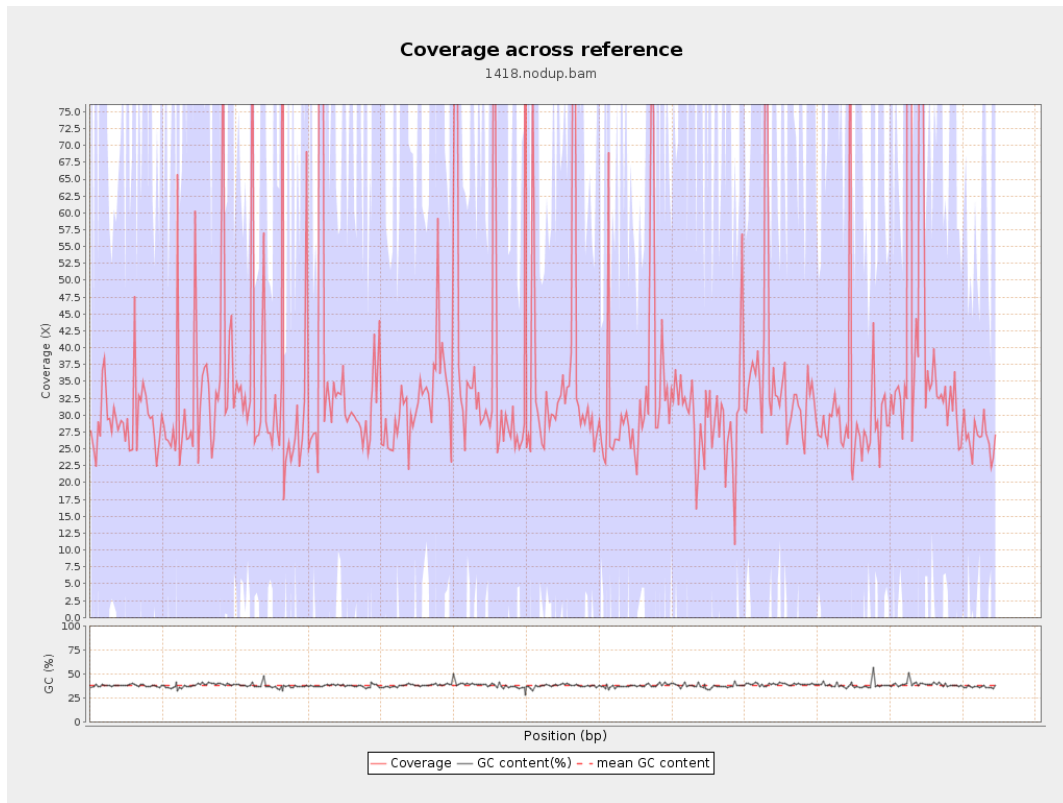
General error rate	2.49%
Mismatches	250,662,932
Insertions	7,219,050
Mapped reads with at least one insertion	8.3%
Deletions	7,512,174
Mapped reads with at least one deletion	8.5%
Homopolymer indels	55.54%

2.7. Chromosome stats

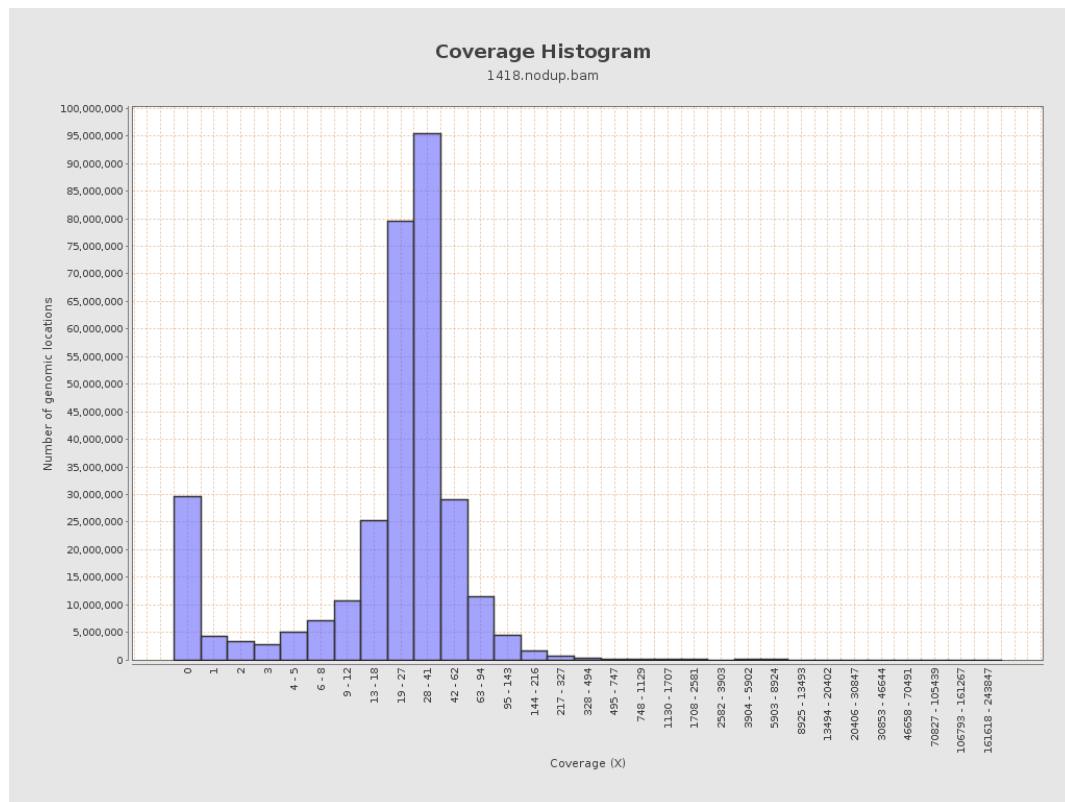
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	863191342	29.0399	100.7727

LT669789.1	36598175	1301383999	35.5587	312.8611
LT669790.1	30422129	1087378673	35.743	241.0187
LT669791.1	52758100	1812931417	34.3631	263.0038
LT669792.1	28376109	978424391	34.4806	308.651
LT669793.1	33388210	1078730916	32.3087	148.2384
LT669794.1	50579949	1704773480	33.7045	271.5706
LT669795.1	49795044	2052425350	41.2175	409.8013

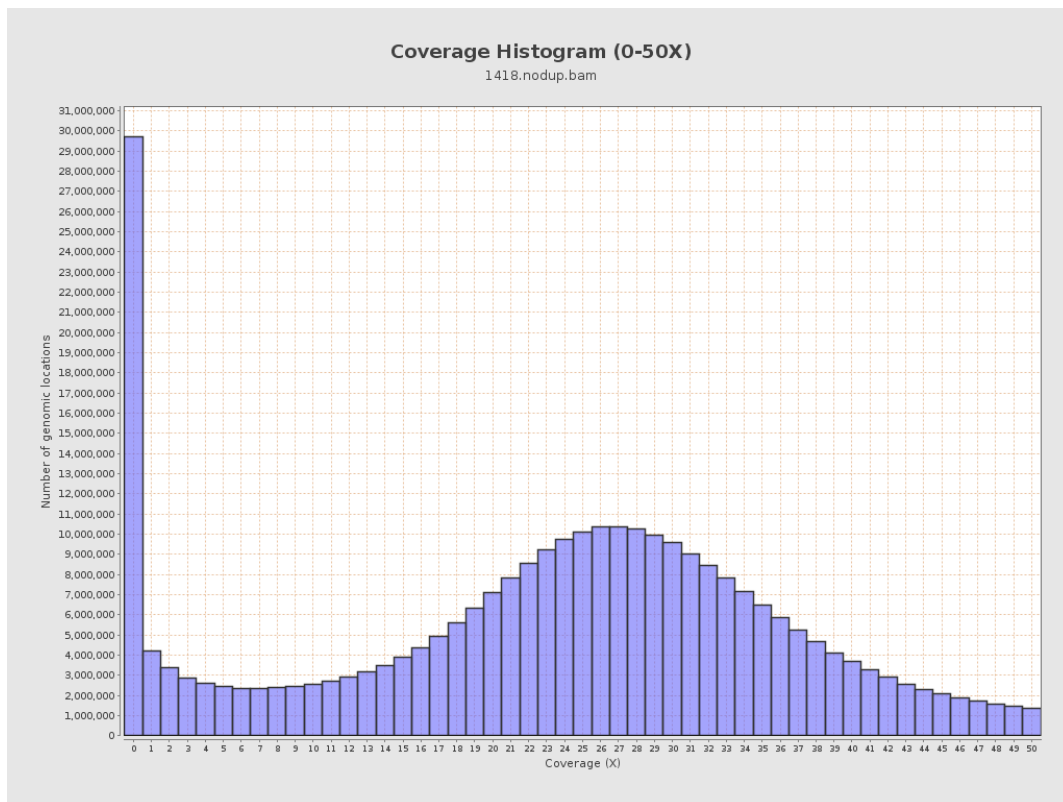
3. Results : Coverage across reference



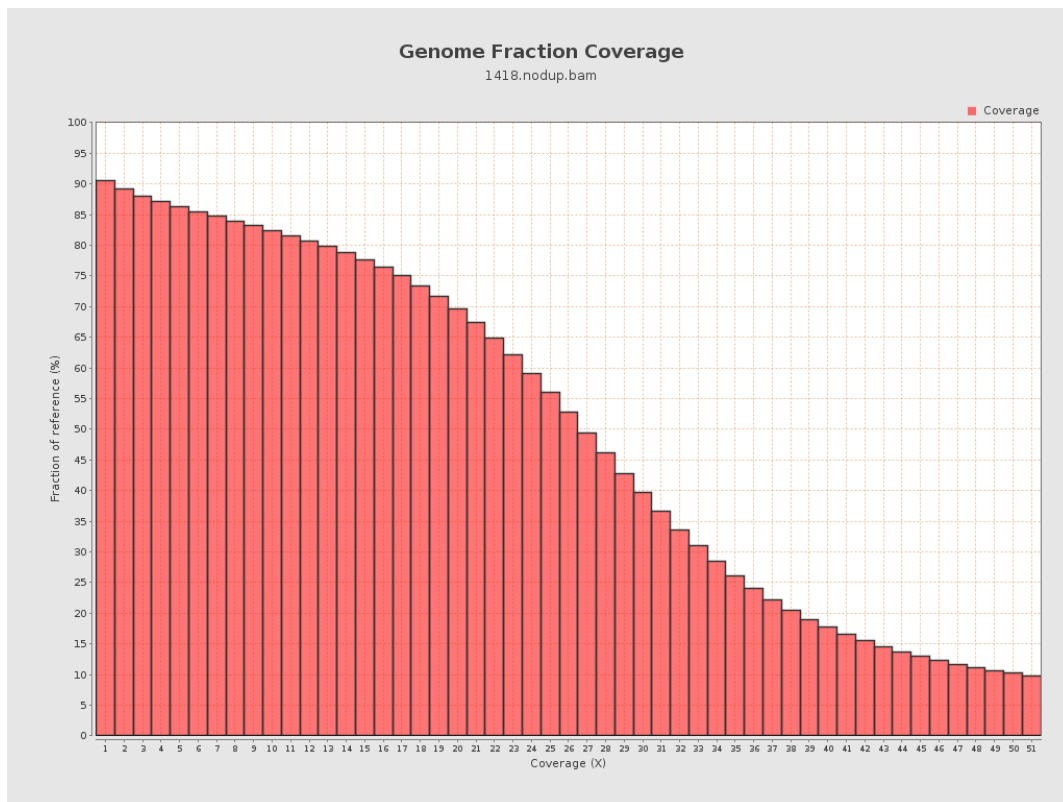
4. Results : Coverage Histogram



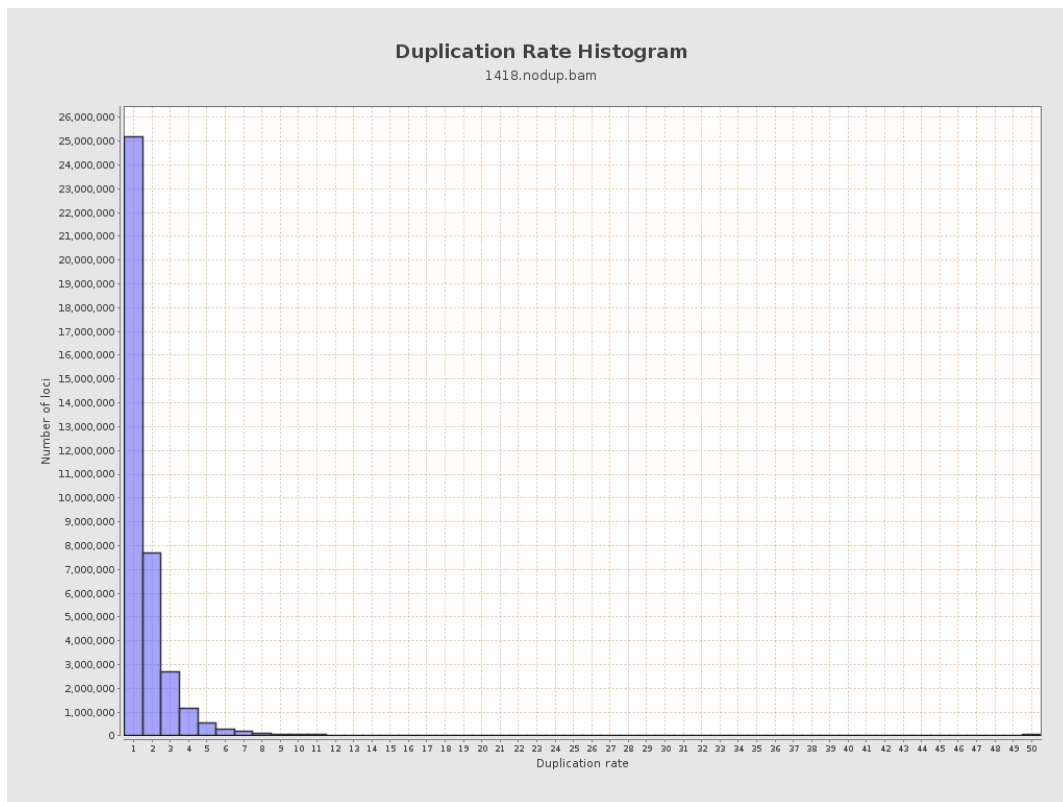
5. Results : Coverage Histogram (0-50X)



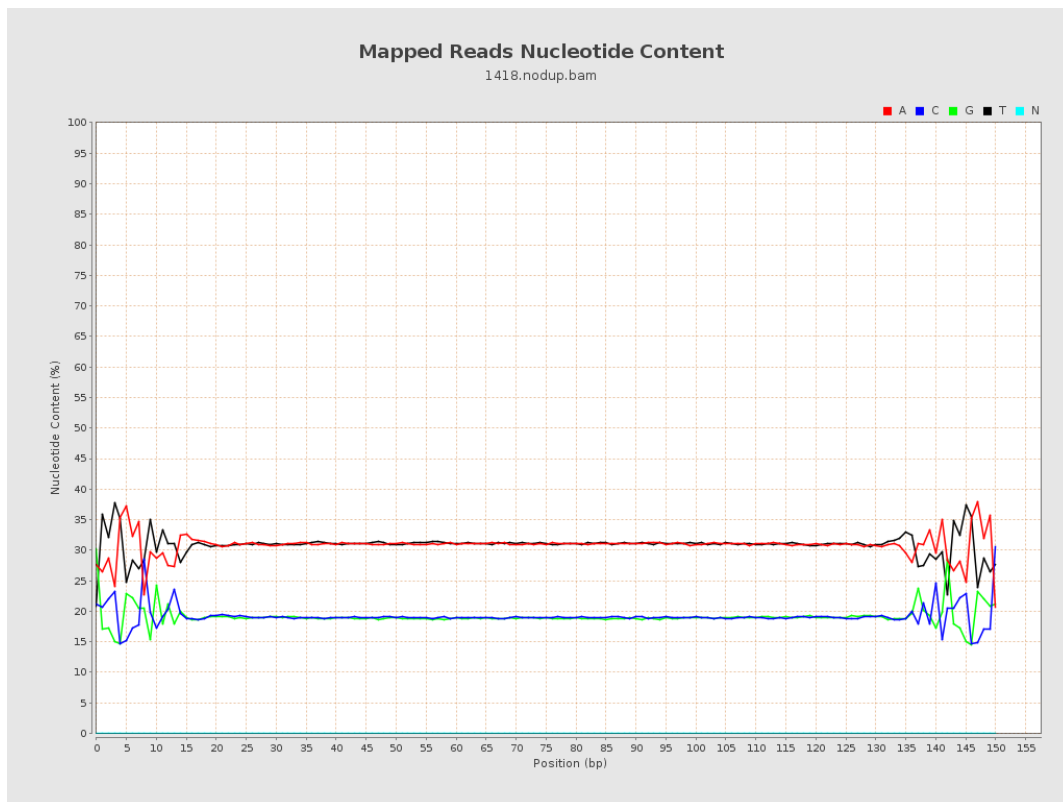
6. Results : Genome Fraction Coverage



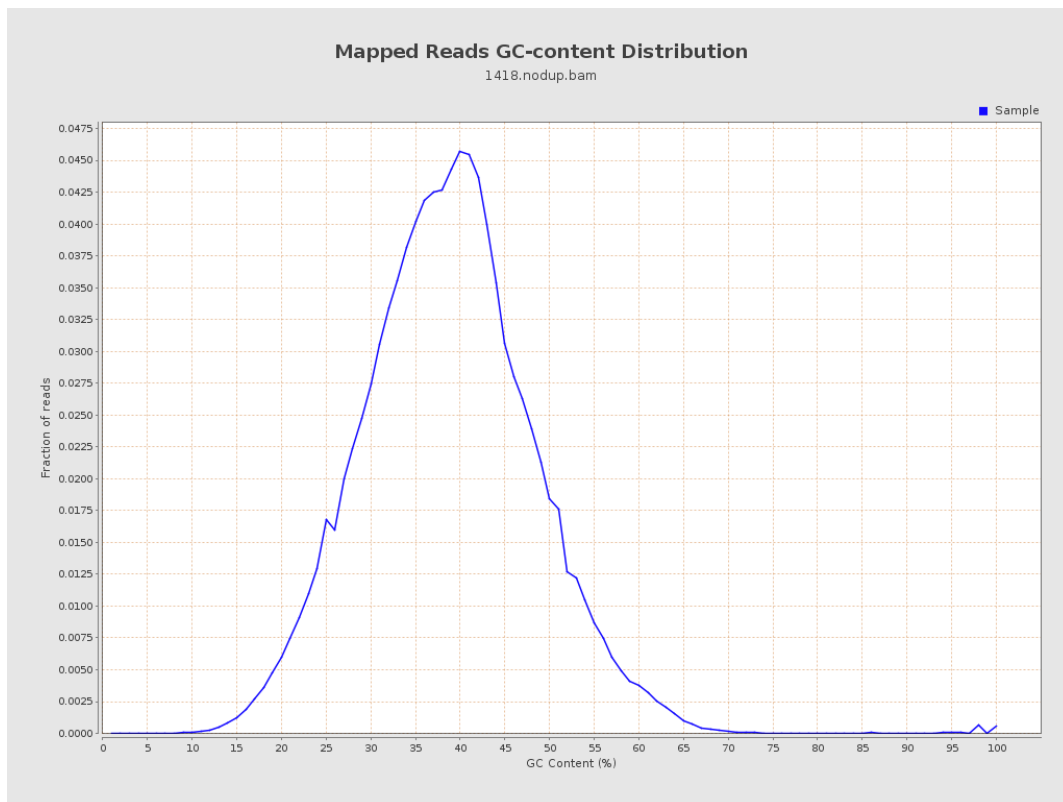
7. Results : Duplication Rate Histogram



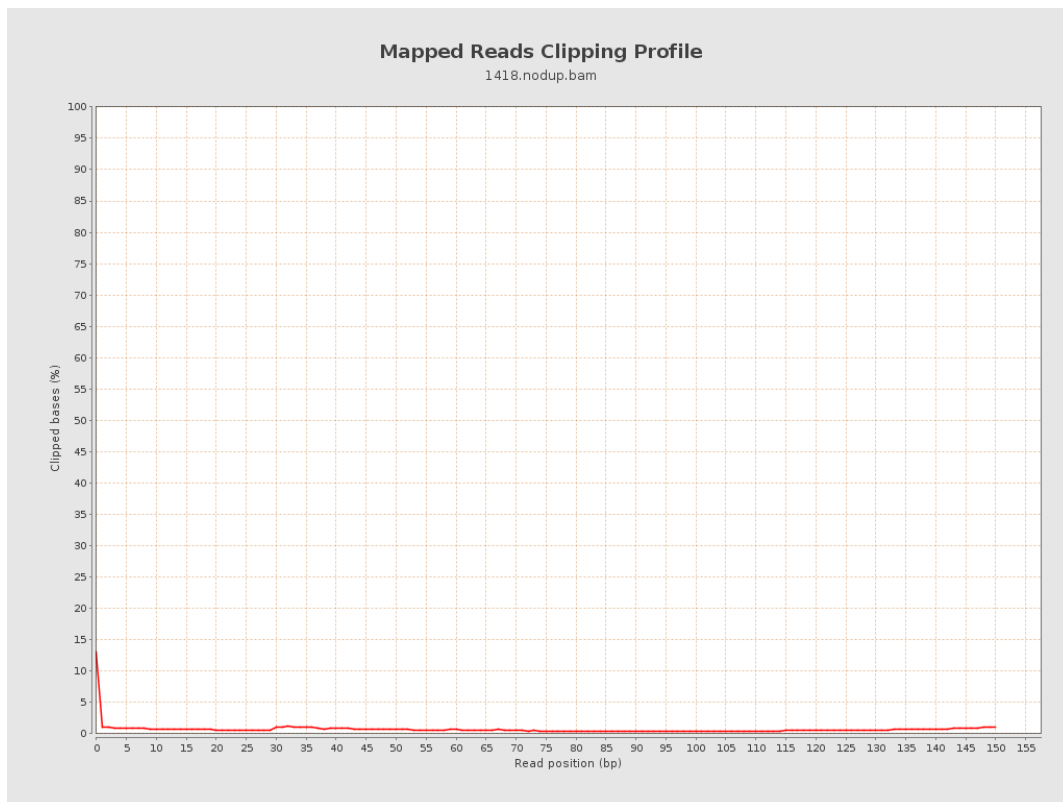
8. Results : Mapped Reads Nucleotide Content



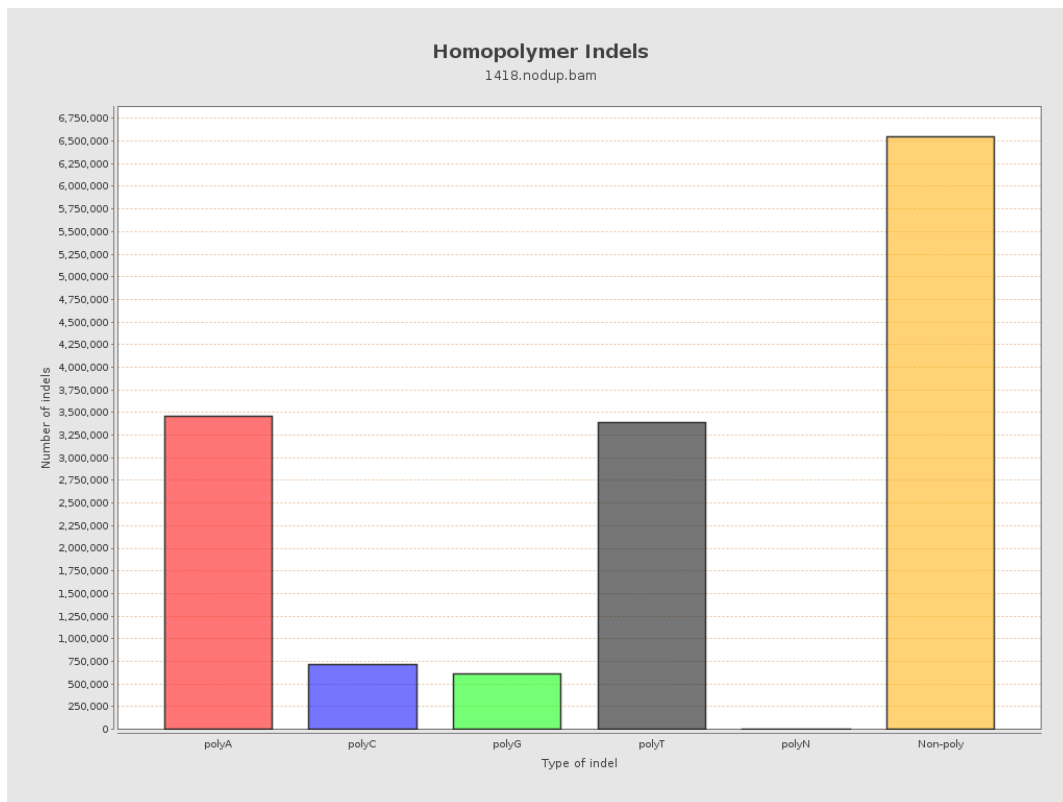
9. Results : Mapped Reads GC-content Distribution



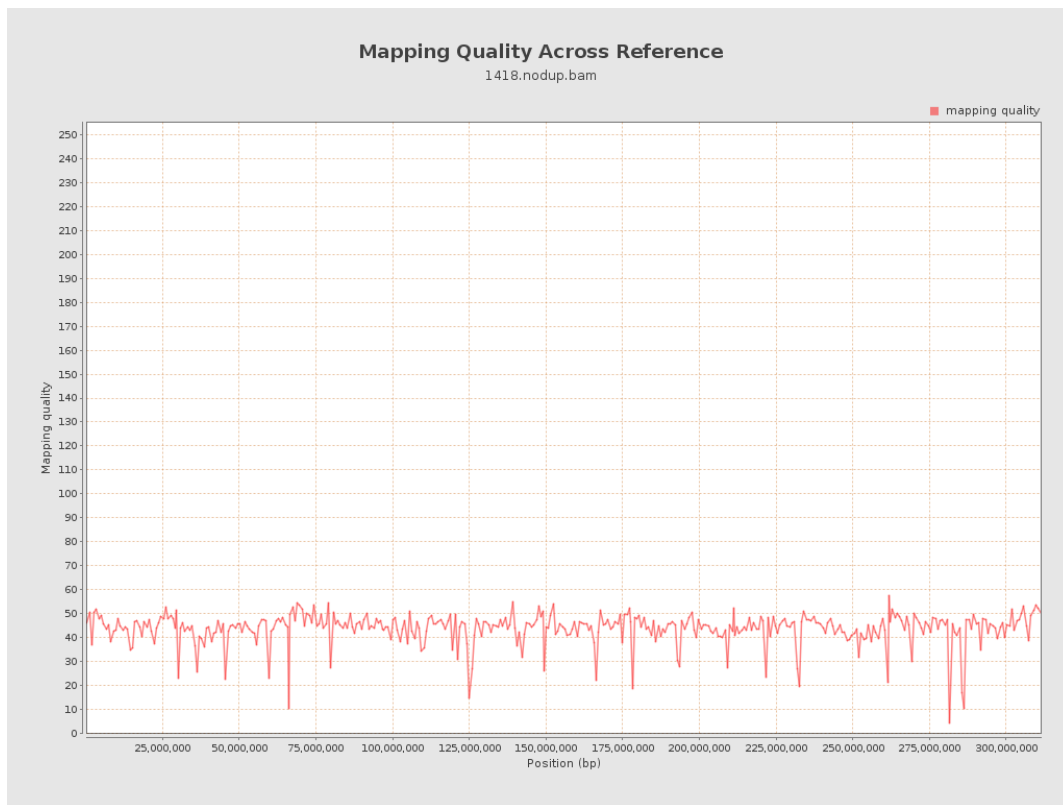
10. Results : Mapped Reads Clipping Profile



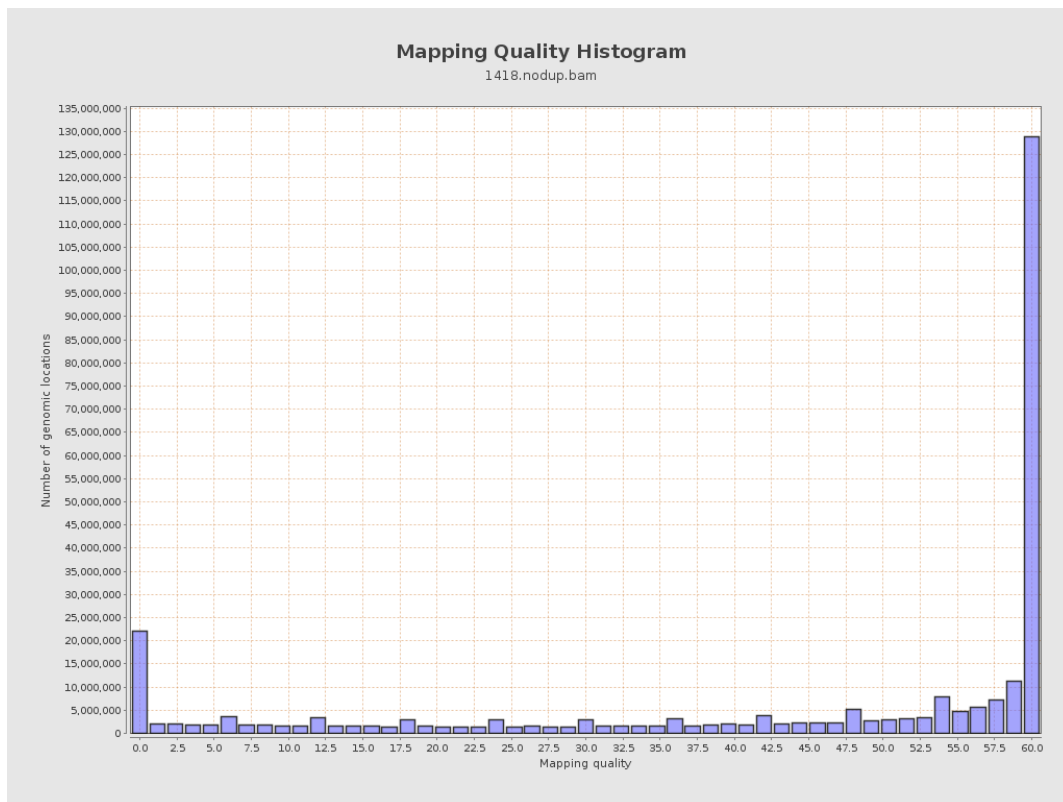
11. Results : Homopolymer Indels



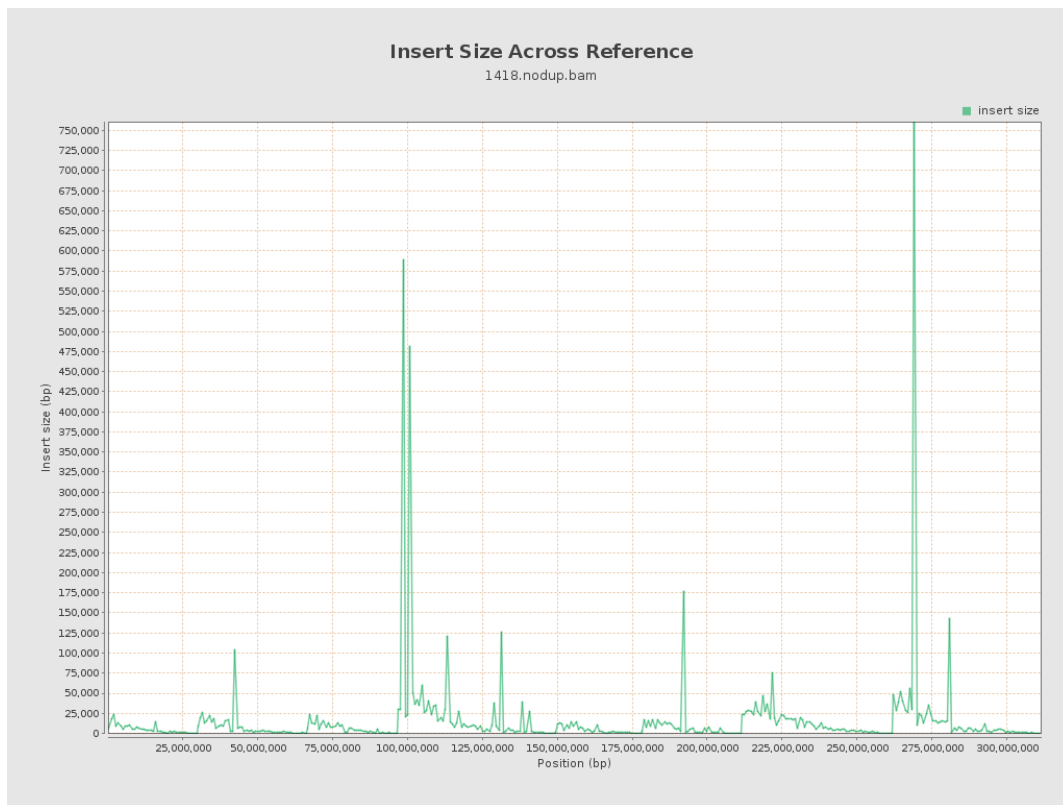
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

