

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:24:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/138
8
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1388 .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_588/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_588_S155_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_588/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_588_S155_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:24:34 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	42,914,731
Mapped reads	40,760,263 / 94.98%
Unmapped reads	2,154,468 / 5.02%
Mapped paired reads	40,760,263 / 94.98%
Mapped reads, first in pair	20,451,023 / 47.66%
Mapped reads, second in pair	20,309,240 / 47.32%
Mapped reads, both in pair	40,034,820 / 93.29%
Mapped reads, singletons	725,443 / 1.69%
Read min/max/mean length	30 / 151 / 148.3
Duplicated reads (flagged)	5,007,937 / 11.67%
Clipped reads	8,995,225 / 20.96%

2.2. ACGT Content

Number/percentage of A's	1,755,219,454 / 30.87%
Number/percentage of C's	1,089,874,403 / 19.17%
Number/percentage of T's	1,755,090,760 / 30.87%
Number/percentage of G's	1,084,940,387 / 19.08%
Number/percentage of N's	39,627 / 0%
GC Percentage	38.25%

2.3. Coverage

Mean	18.2887
Standard Deviation	136.3191

2.4. Mapping Quality

Mean Mapping Quality	44.23
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2.5. Insert size

Mean	206,589.94
Standard Deviation	2,137,672.57
P25/Median/P75	324 / 421 / 546

2.6. Mismatches and indels

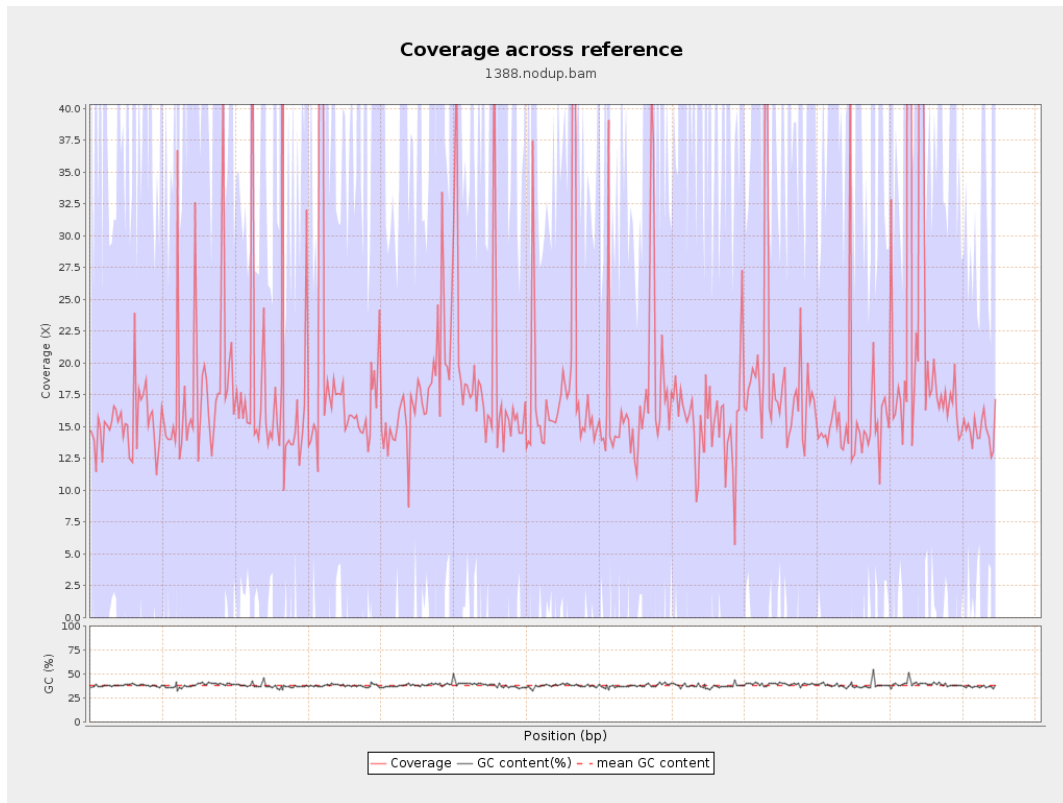
General error rate	2.47%
Mismatches	130,276,347
Insertions	3,627,888
Mapped reads with at least one insertion	8.04%
Deletions	3,779,701
Mapped reads with at least one deletion	8.26%
Homopolymer indels	56.09%

2.7. Chromosome stats

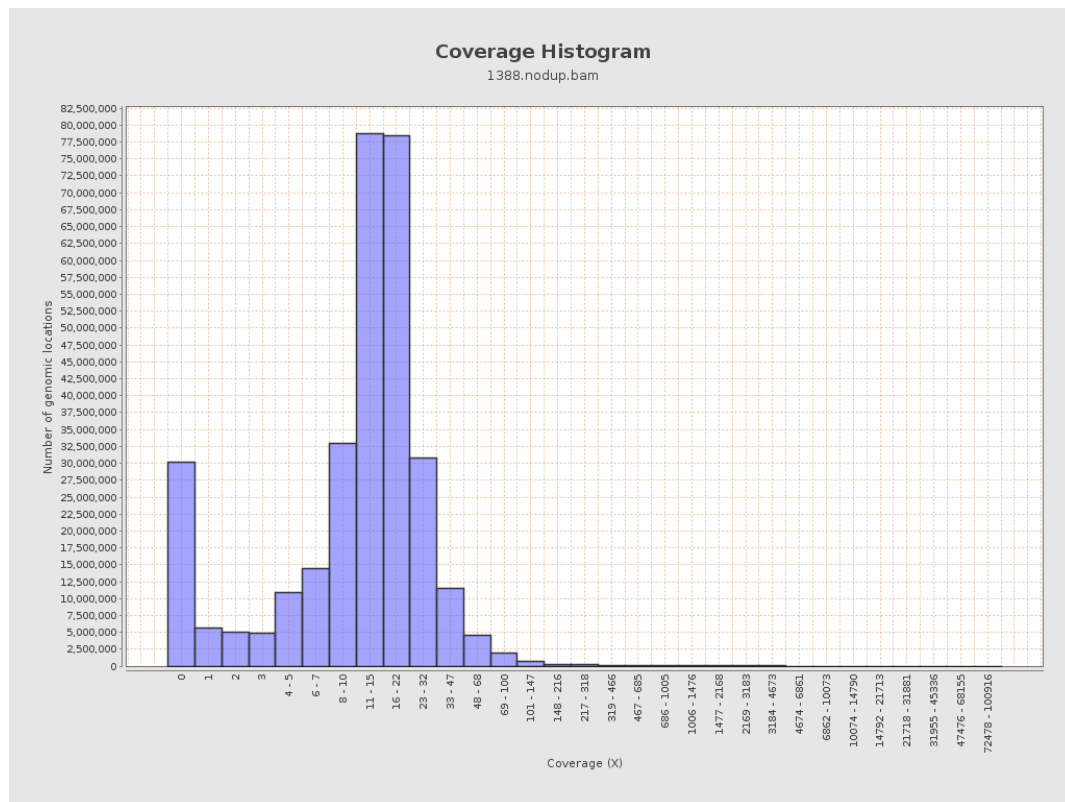
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	449900014	15.1357	29.8932

LT669789.1	36598175	679670654	18.5712	133.4703
LT669790.1	30422129	569575913	18.7224	113.4019
LT669791.1	52758100	953923344	18.0811	100.2001
LT669792.1	28376109	510159912	17.9785	177.6722
LT669793.1	33388210	563026675	16.863	72.0837
LT669794.1	50579949	880391996	17.4059	113.7688
LT669795.1	49795044	1092869349	21.9474	222.5716

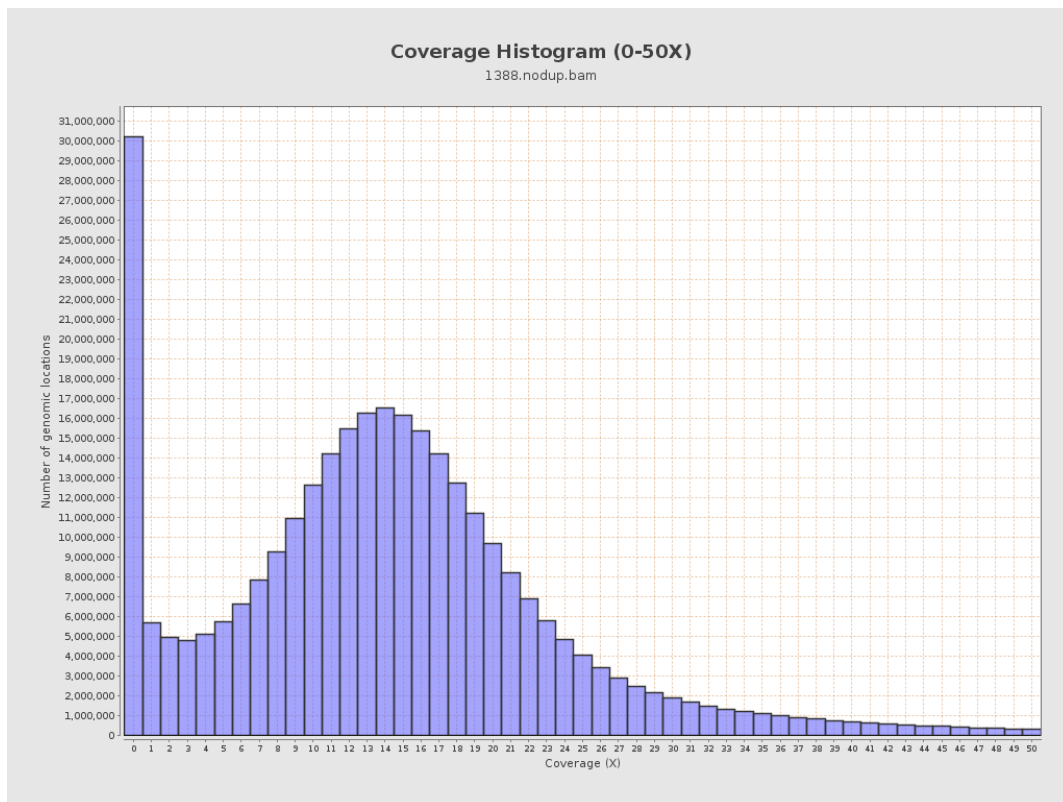
3. Results : Coverage across reference



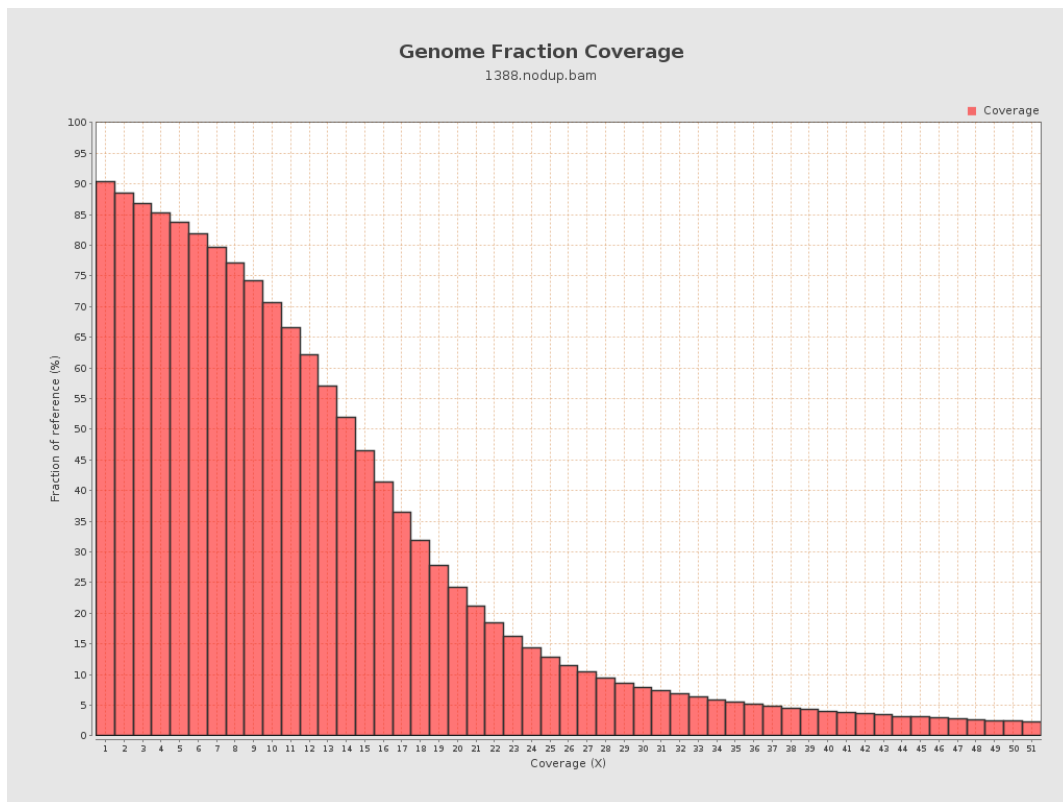
4. Results : Coverage Histogram



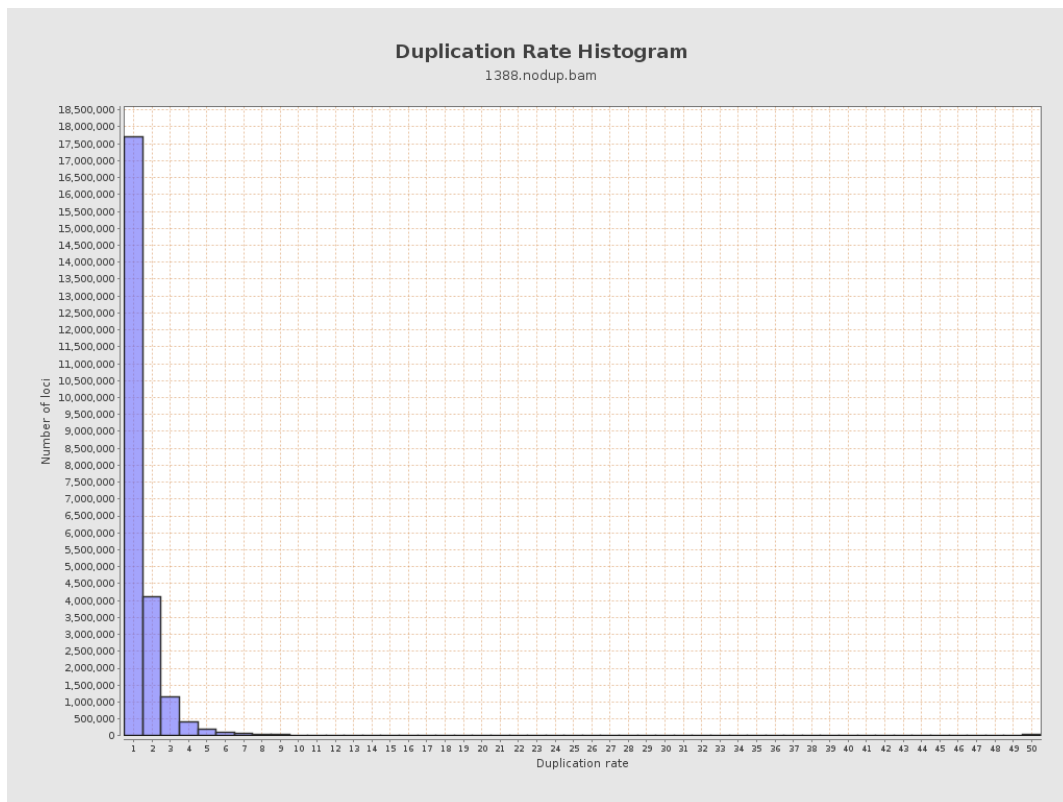
5. Results : Coverage Histogram (0-50X)



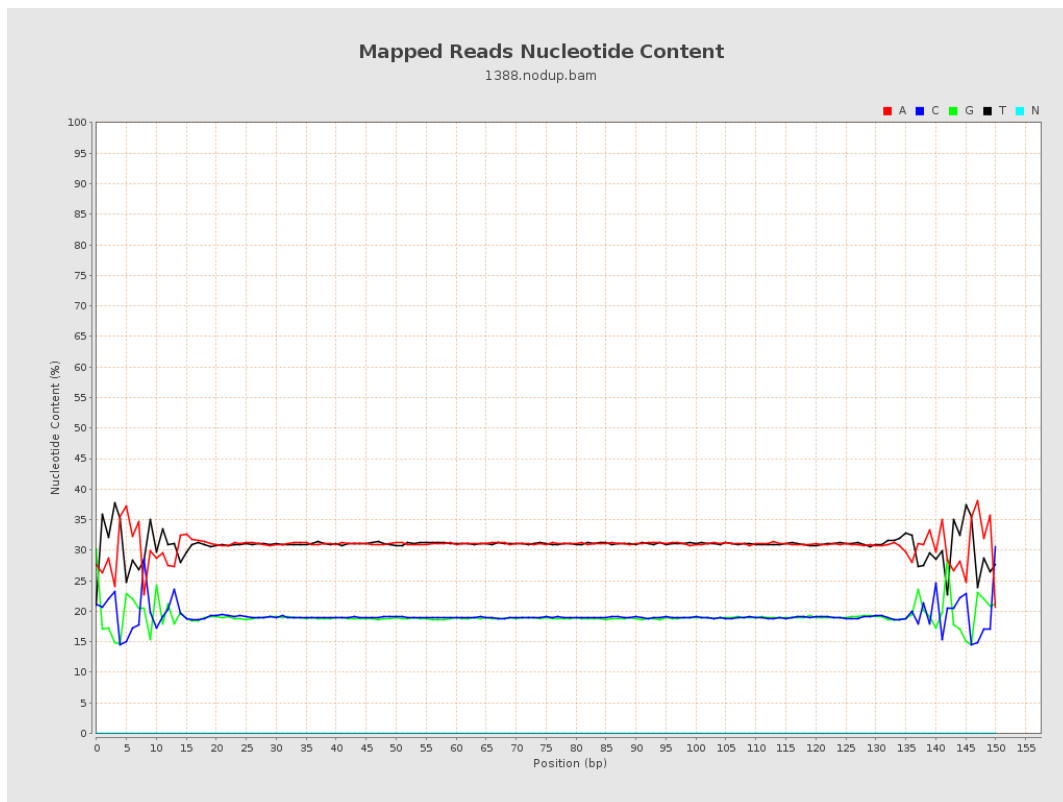
6. Results : Genome Fraction Coverage



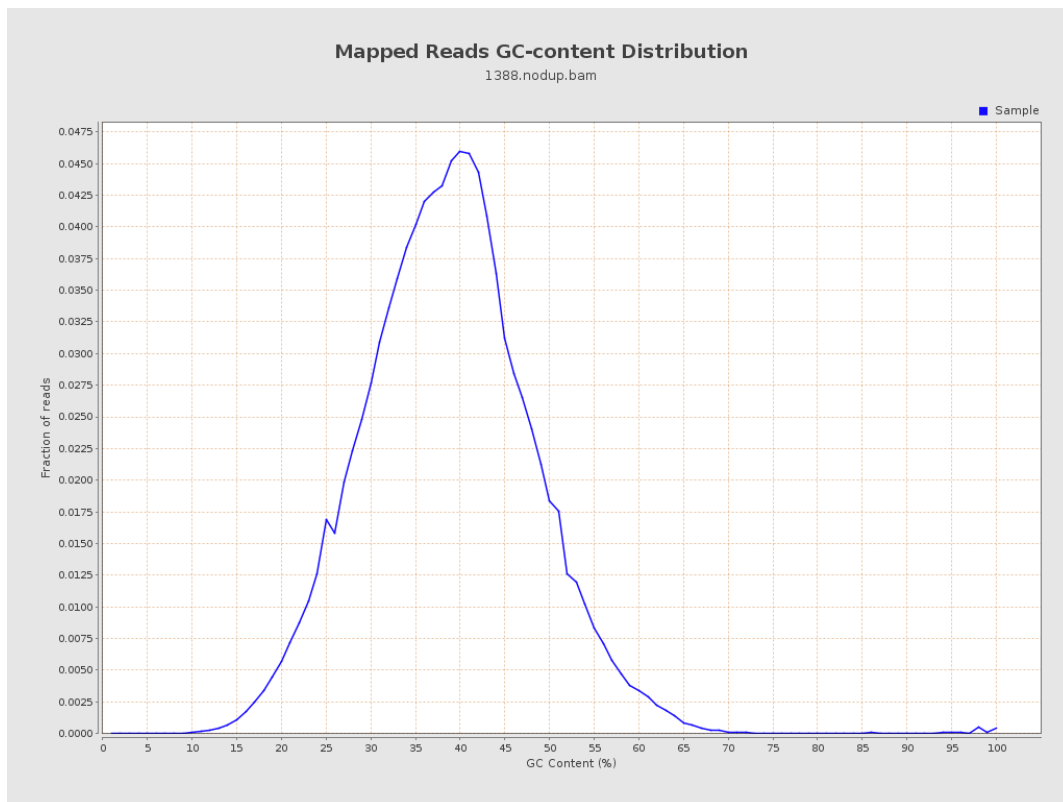
7. Results : Duplication Rate Histogram



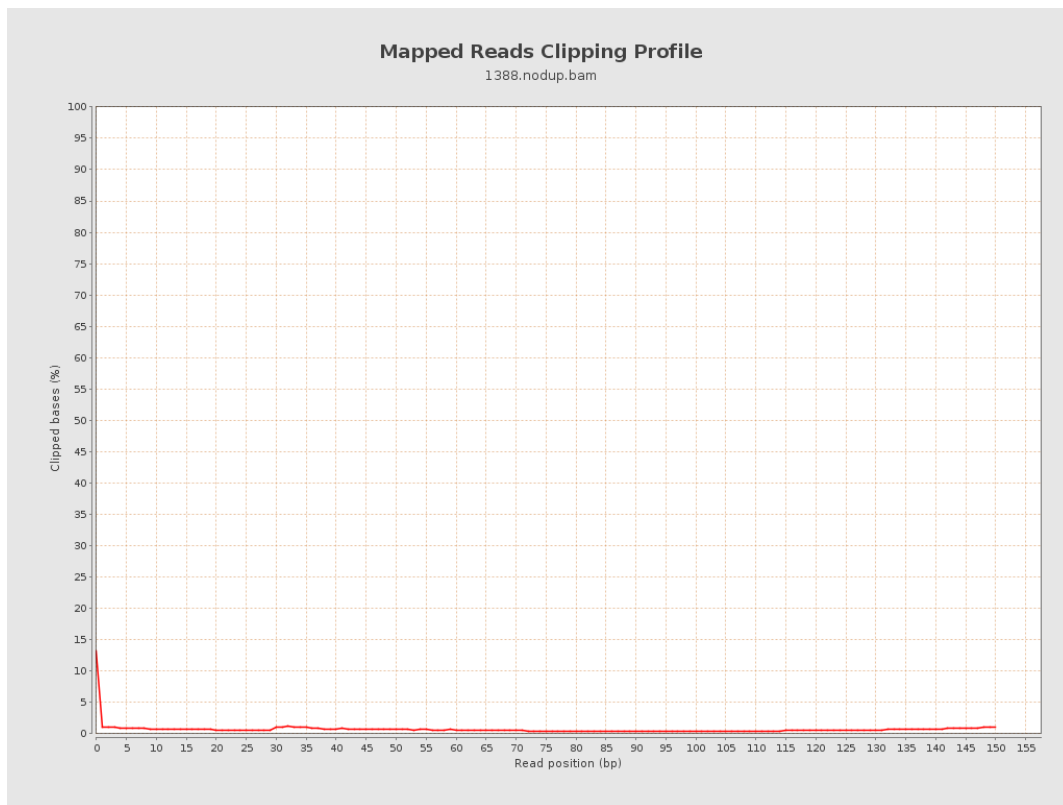
8. Results : Mapped Reads Nucleotide Content



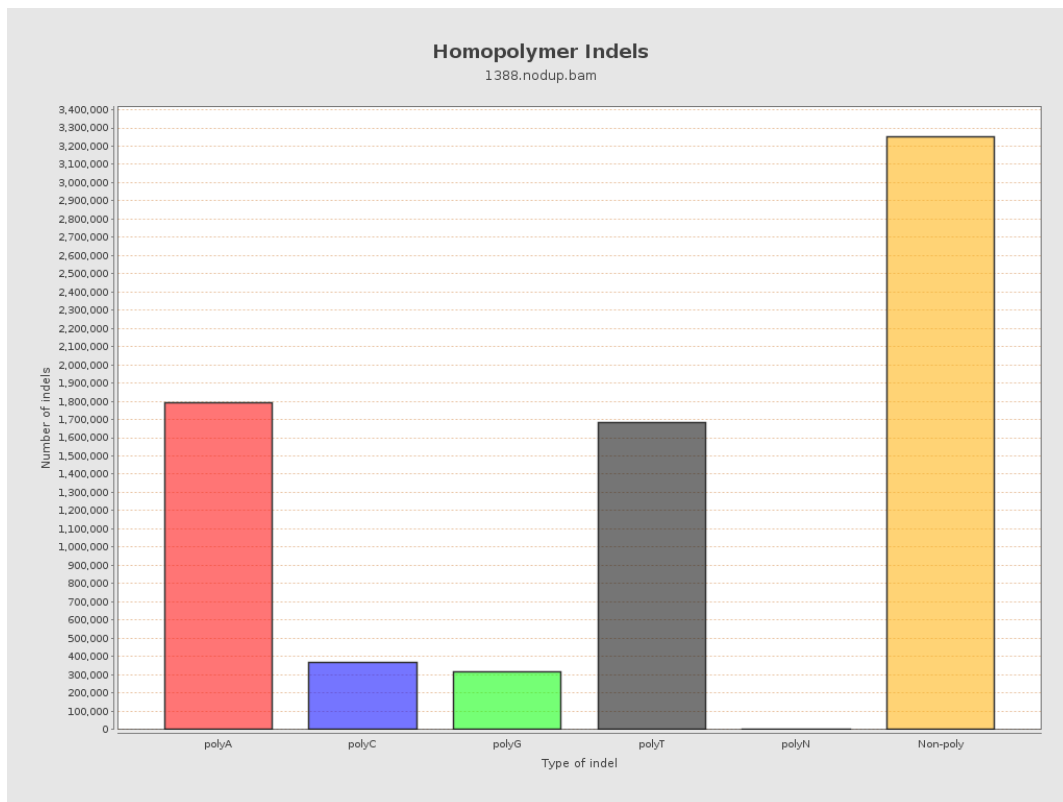
9. Results : Mapped Reads GC-content Distribution



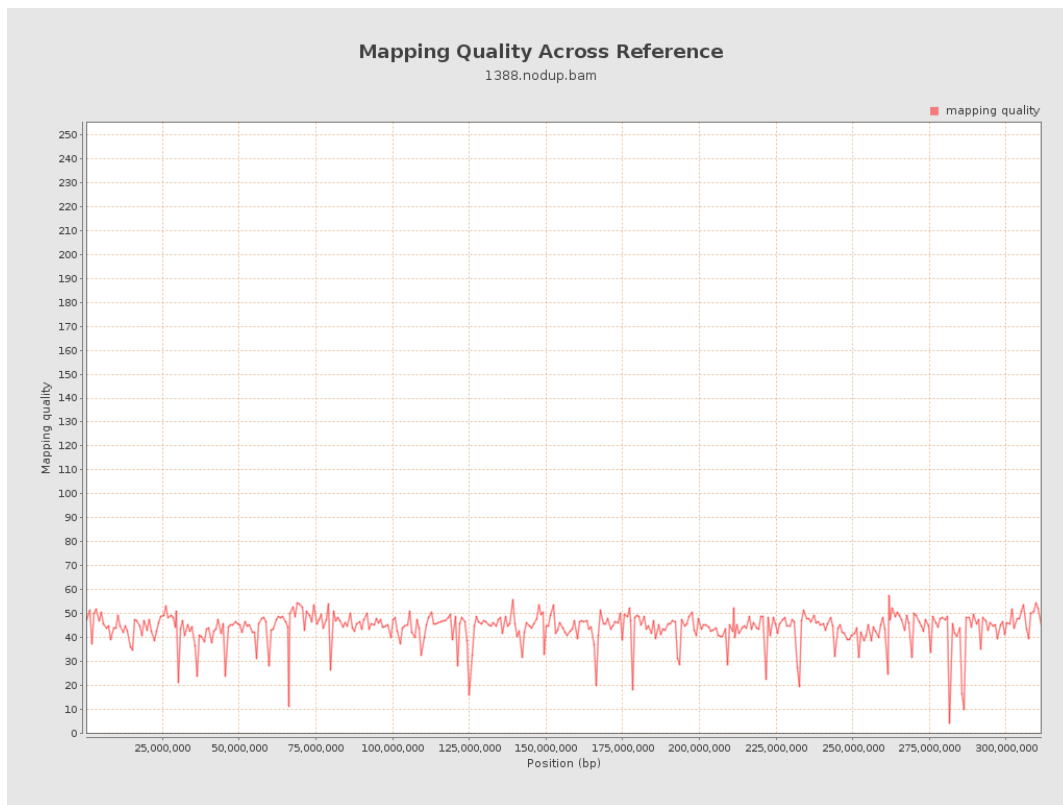
10. Results : Mapped Reads Clipping Profile



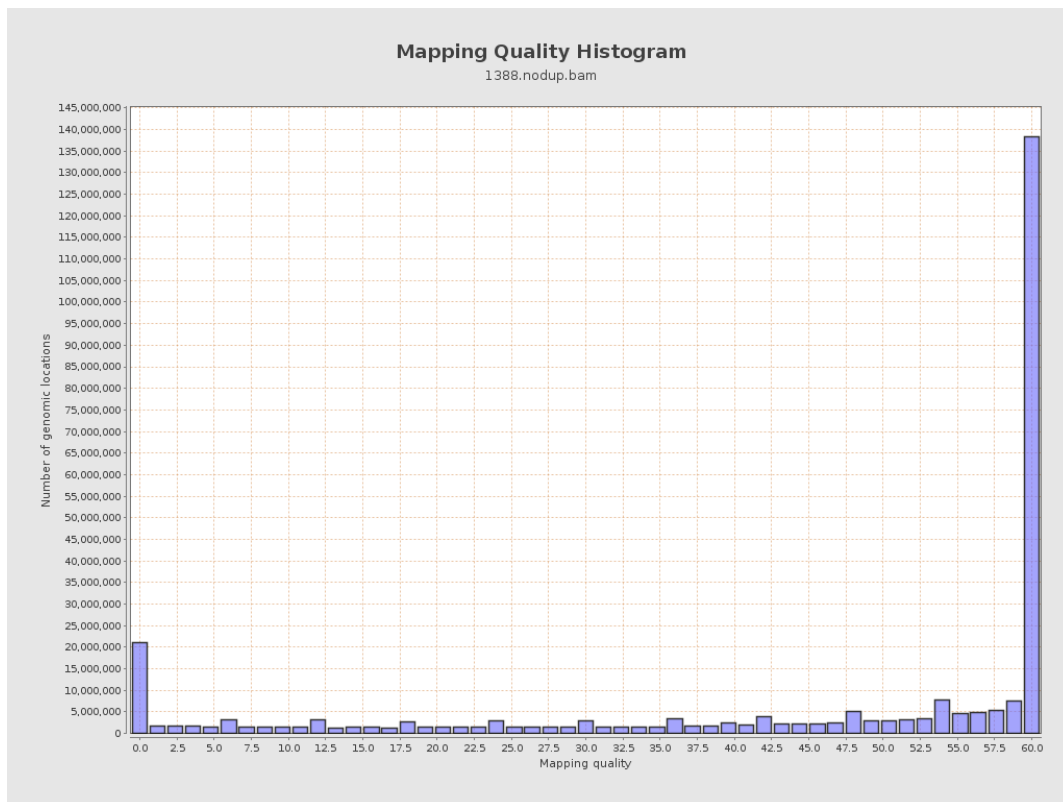
11. Results : Homopolymer Indels



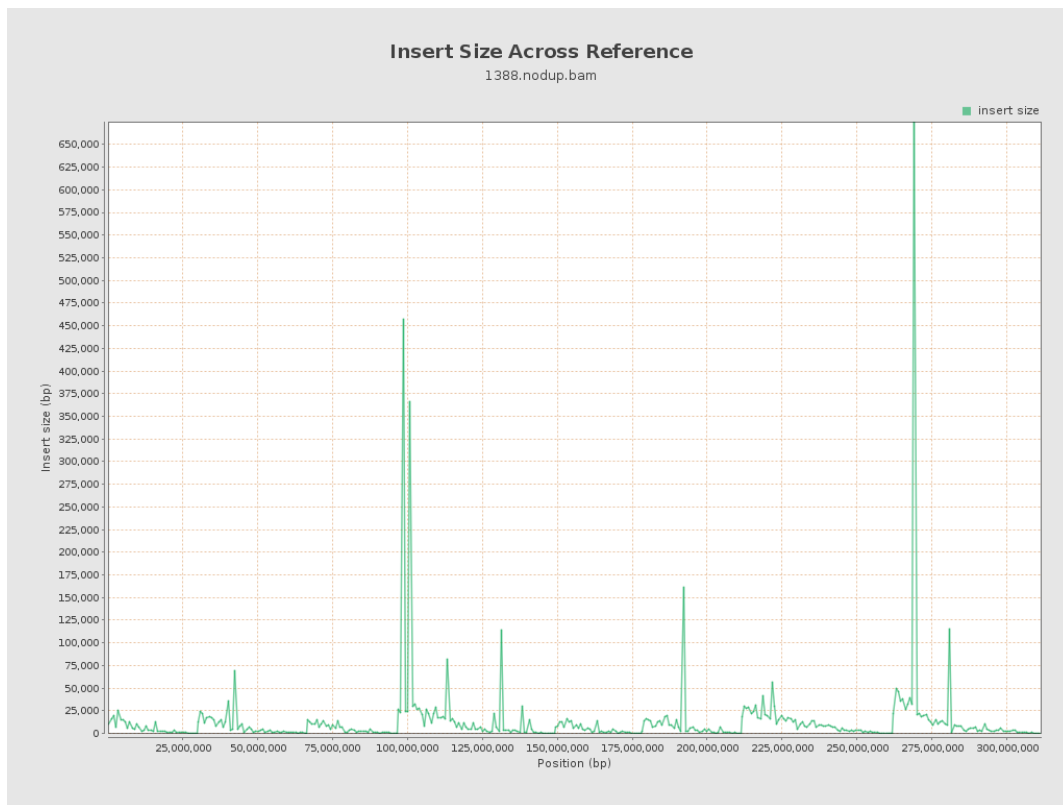
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

