

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/29 21:40:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/103
6
.nodup.bam -nw 400 -hm 3
```

1.2. Alignment

BAM file:	/proj/uppstore2018210/Aalpina/worki ng/Kate/Working/F2/MarkDuplicates/ 1036 .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_556/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_556_S123_L004 _R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/r awdata/P26207/P26207_556/02- FASTQ/220906_A00187_0838_AHM G3KDSX3/P26207_556_S123_L004 _R2_001.fastq.gz
Size of a homopolymer:	3

Number of windows:	400
Analysis date:	Mon May 29 21:40:24 CEST 2023
Draw chromosome limits:	no
Skip duplicate alignments:	no

2. Summary

2.1. Globals

Reference size	311,642,060
Number of reads	93,286,487
Mapped reads	87,004,136 / 93.27%
Unmapped reads	6,282,351 / 6.73%
Mapped paired reads	87,004,136 / 93.27%
Mapped reads, first in pair	43,615,076 / 46.75%
Mapped reads, second in pair	43,389,060 / 46.51%
Mapped reads, both in pair	85,098,620 / 91.22%
Mapped reads, singletons	1,905,516 / 2.04%
Read min/max/mean length	30 / 151 / 148.19
Duplicated reads (flagged)	14,410,105 / 15.45%
Clipped reads	20,260,129 / 21.72%

2.2. ACGT Content

Number/percentage of A's	3,719,287,351 / 30.97%
Number/percentage of C's	2,286,139,286 / 19.04%
Number/percentage of T's	3,722,379,506 / 31%
Number/percentage of G's	2,280,571,866 / 18.99%
Number/percentage of N's	86,953 / 0%
GC Percentage	38.03%

2.3. Coverage

Mean	38.6299
Standard Deviation	309.6901

2.4. Mapping Quality

Mean Mapping Quality	44.84
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2.5. Insert size

Mean	210,970.99
Standard Deviation	2,205,975.05
P25/Median/P75	297 / 392 / 507

2.6. Mismatches and indels

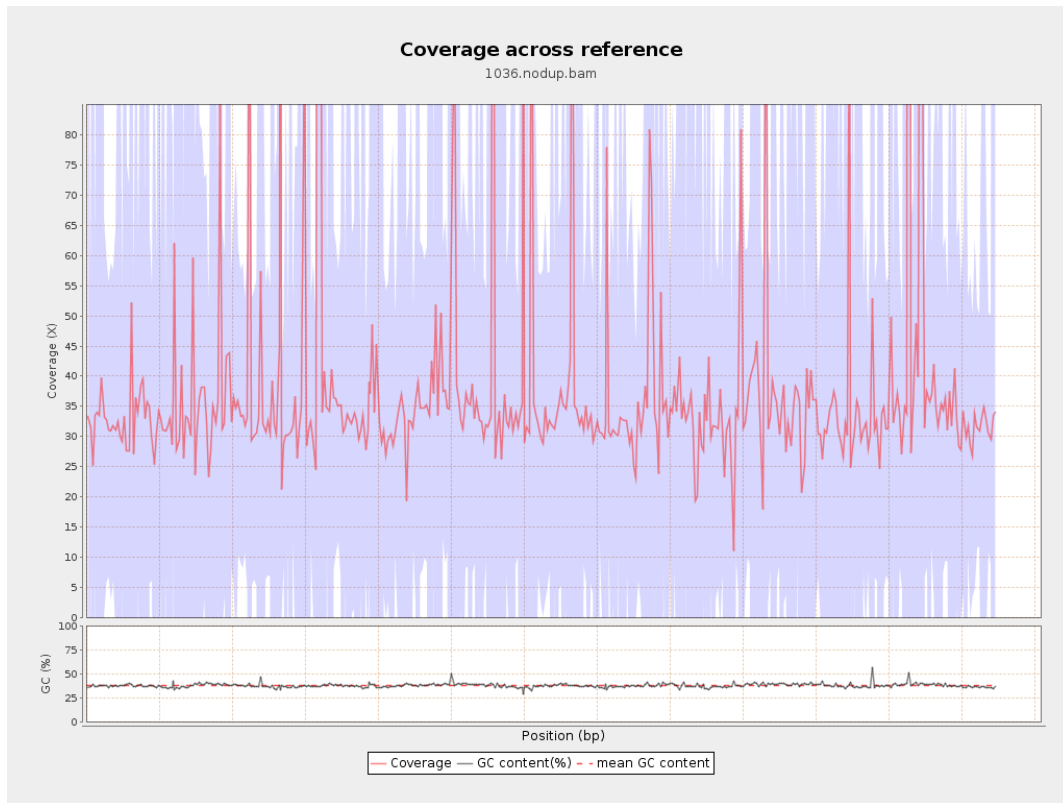
General error rate	2.42%
Mismatches	267,758,875
Insertions	8,099,453
Mapped reads with at least one insertion	8.35%
Deletions	8,069,232
Mapped reads with at least one deletion	8.25%
Homopolymer indels	56.77%

2.7. Chromosome stats

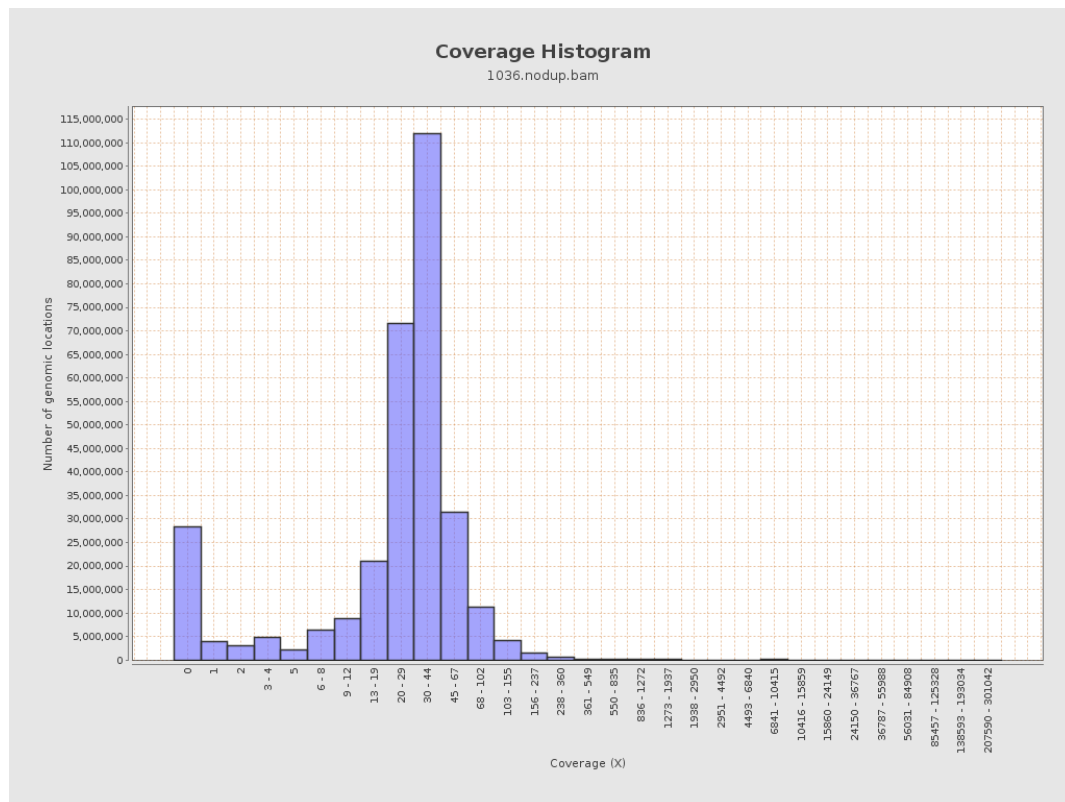
Name	Length	Mapped bases	Mean coverage	Standard deviation
LT669788.1	29724344	972509669	32.7176	104.4063

LT669789.1	36598175	1401138154	38.2844	318.2258
LT669790.1	30422129	1329498544	43.7017	370.3395
LT669791.1	52758100	1993594111	37.7875	291.8066
LT669792.1	28376109	1098856815	38.7247	325.2057
LT669793.1	33388210	1175782904	35.2155	170.7873
LT669794.1	50579949	1828841147	36.1574	267.7526
LT669795.1	49795044	2238491740	44.9541	438.8115

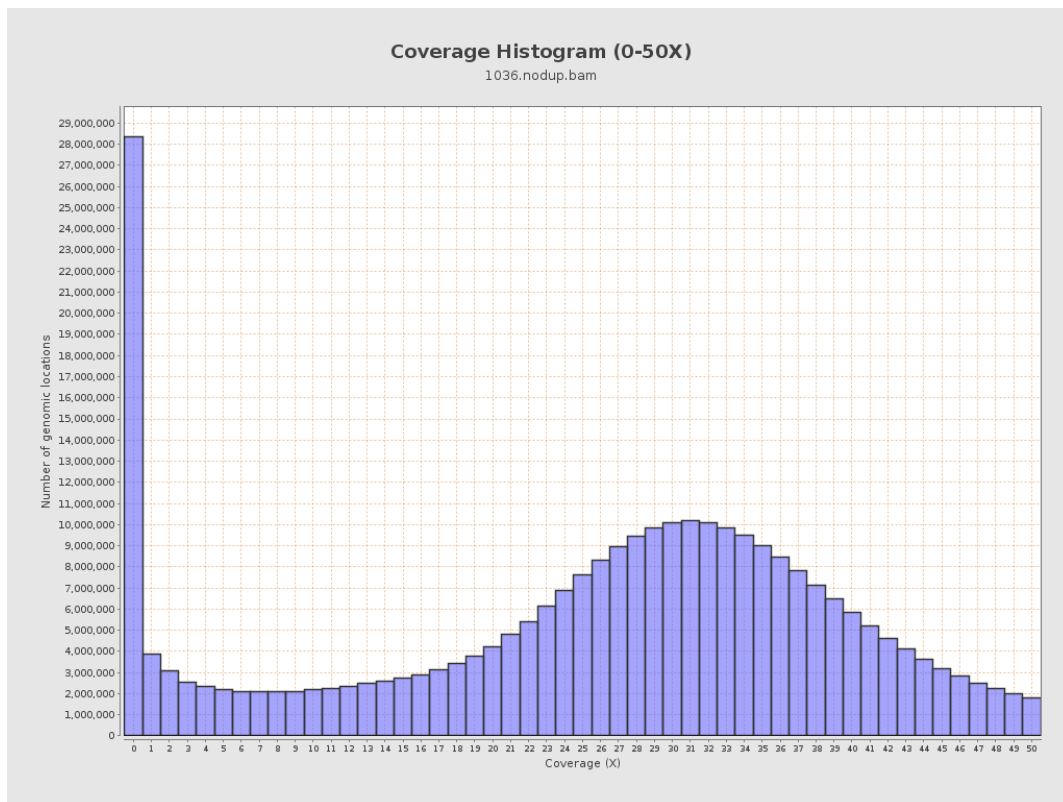
3. Results : Coverage across reference



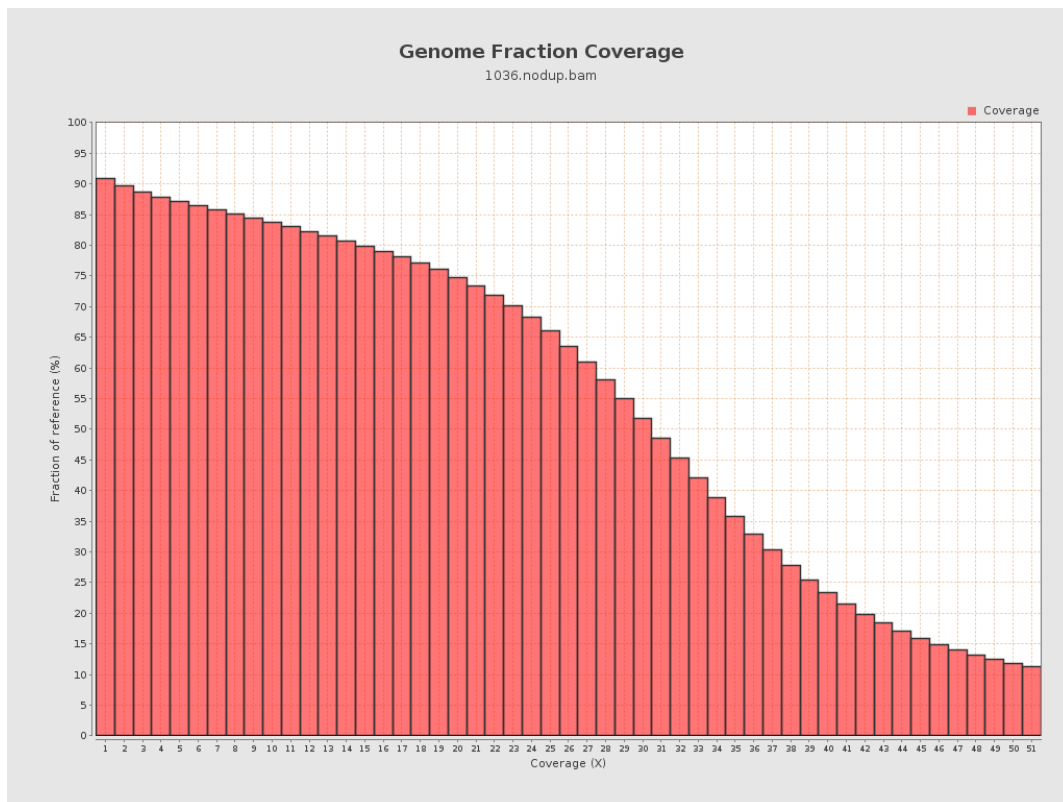
4. Results : Coverage Histogram



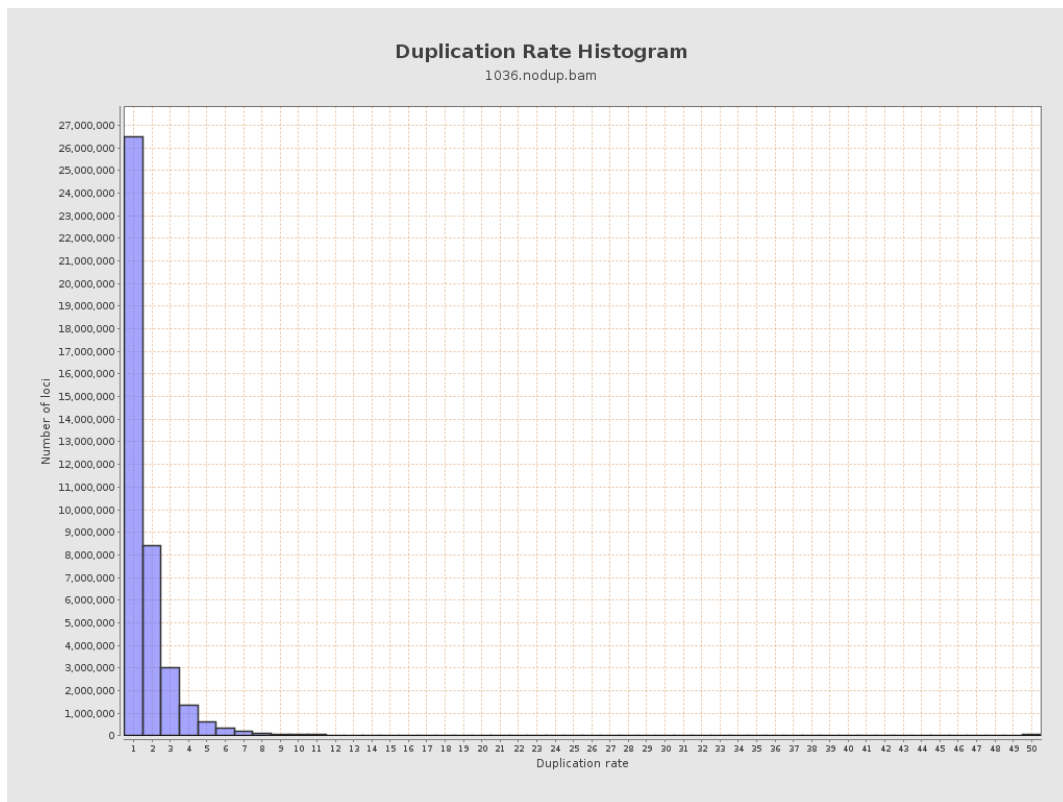
5. Results : Coverage Histogram (0-50X)



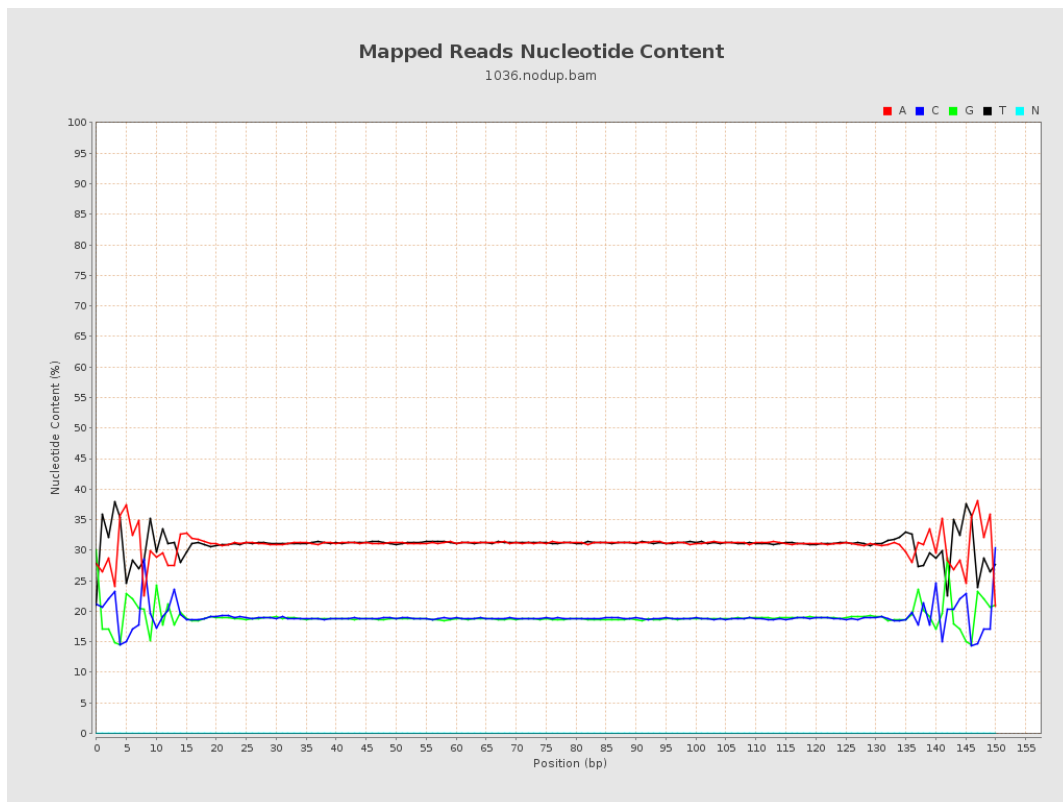
6. Results : Genome Fraction Coverage



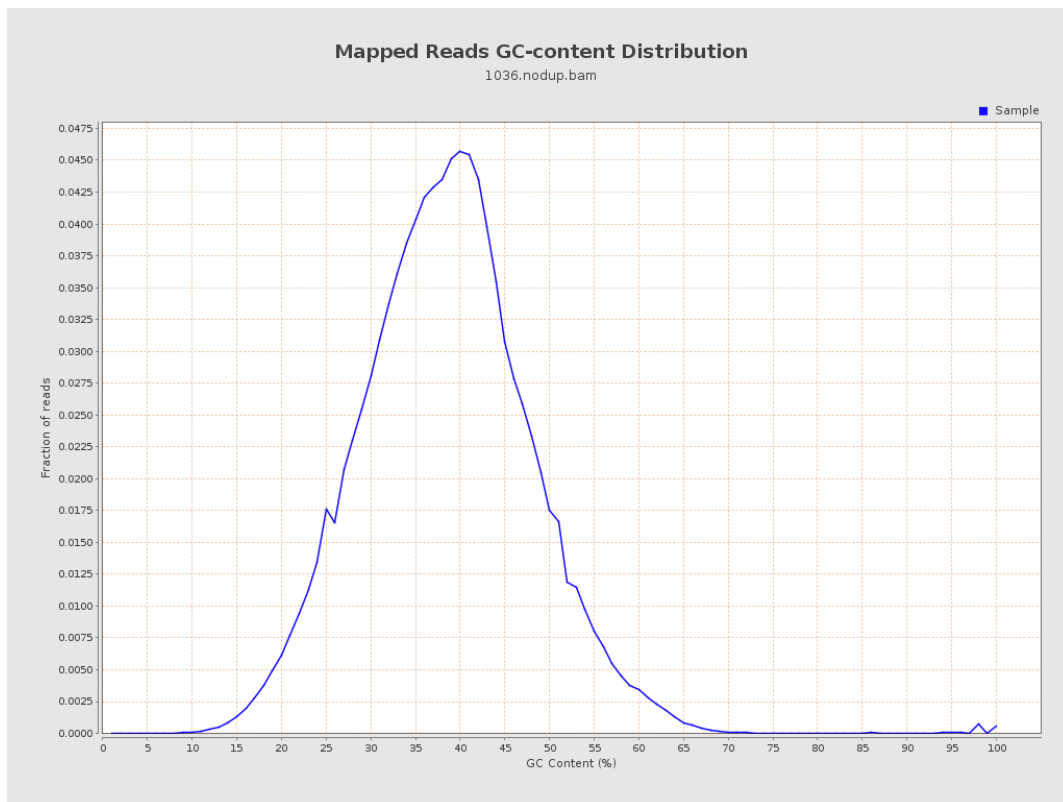
7. Results : Duplication Rate Histogram



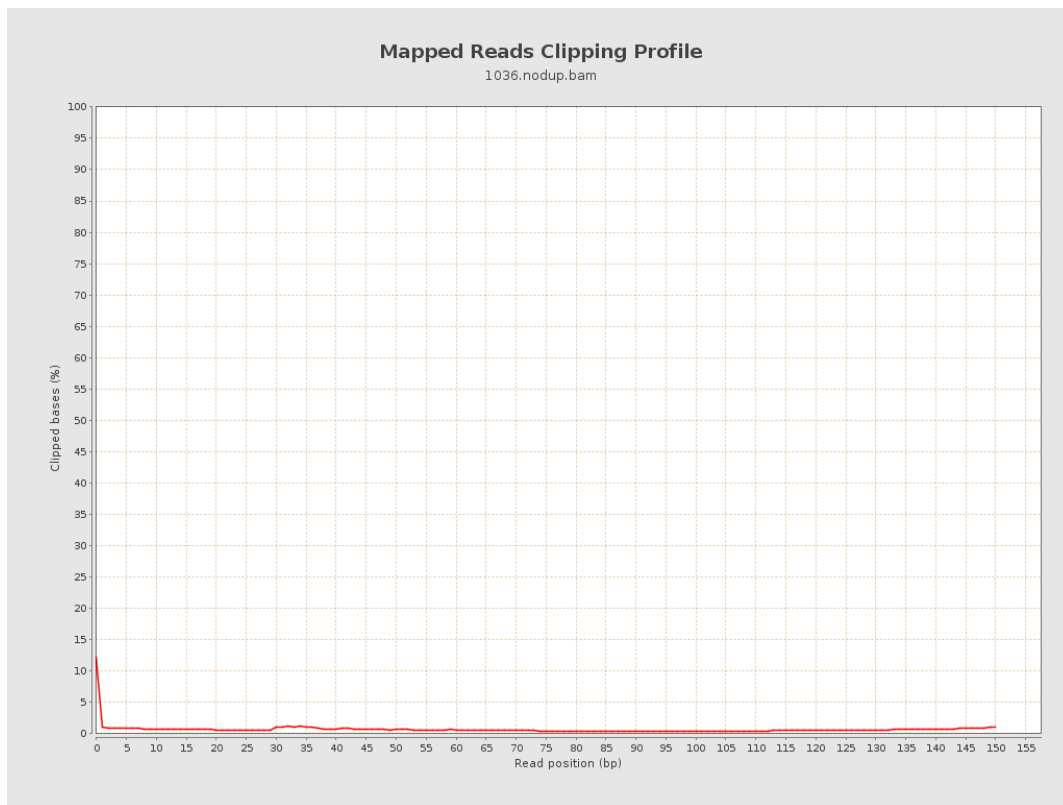
8. Results : Mapped Reads Nucleotide Content



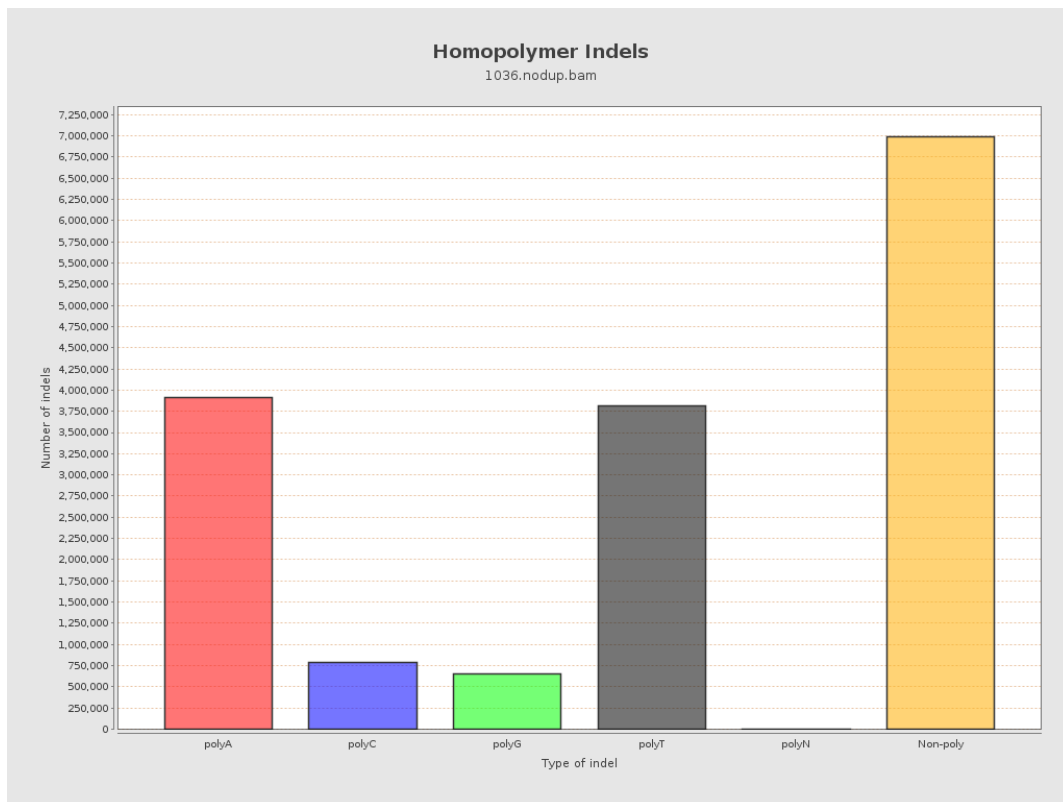
9. Results : Mapped Reads GC-content Distribution



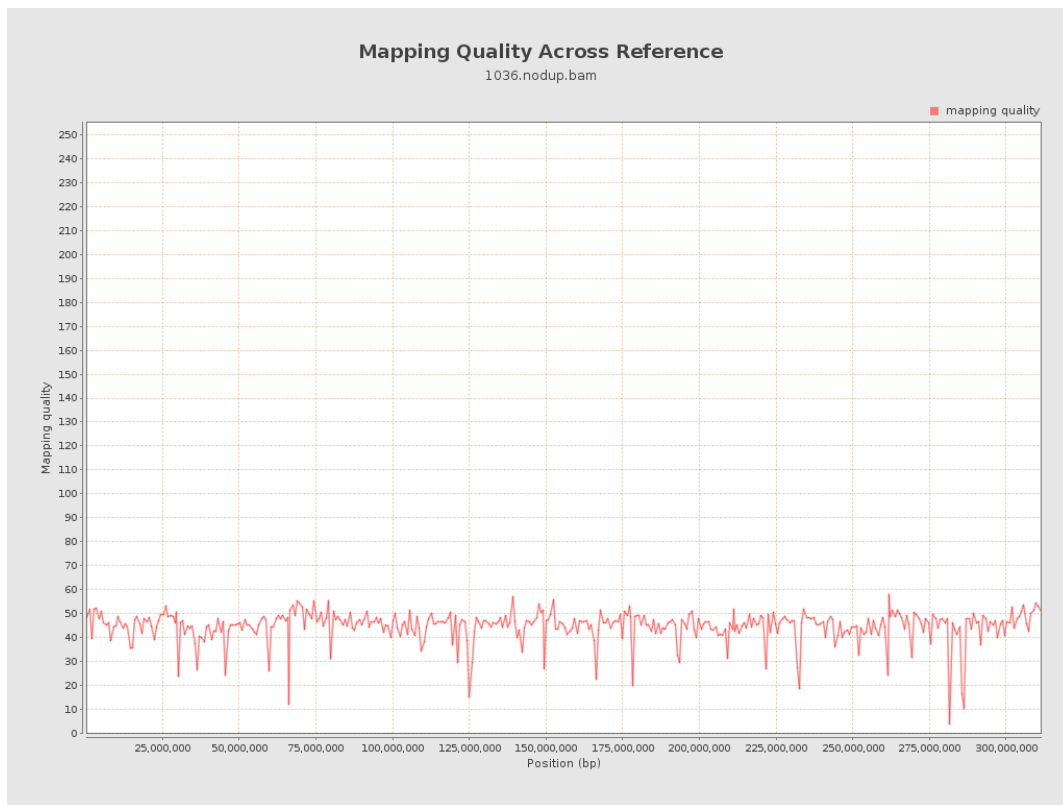
10. Results : Mapped Reads Clipping Profile



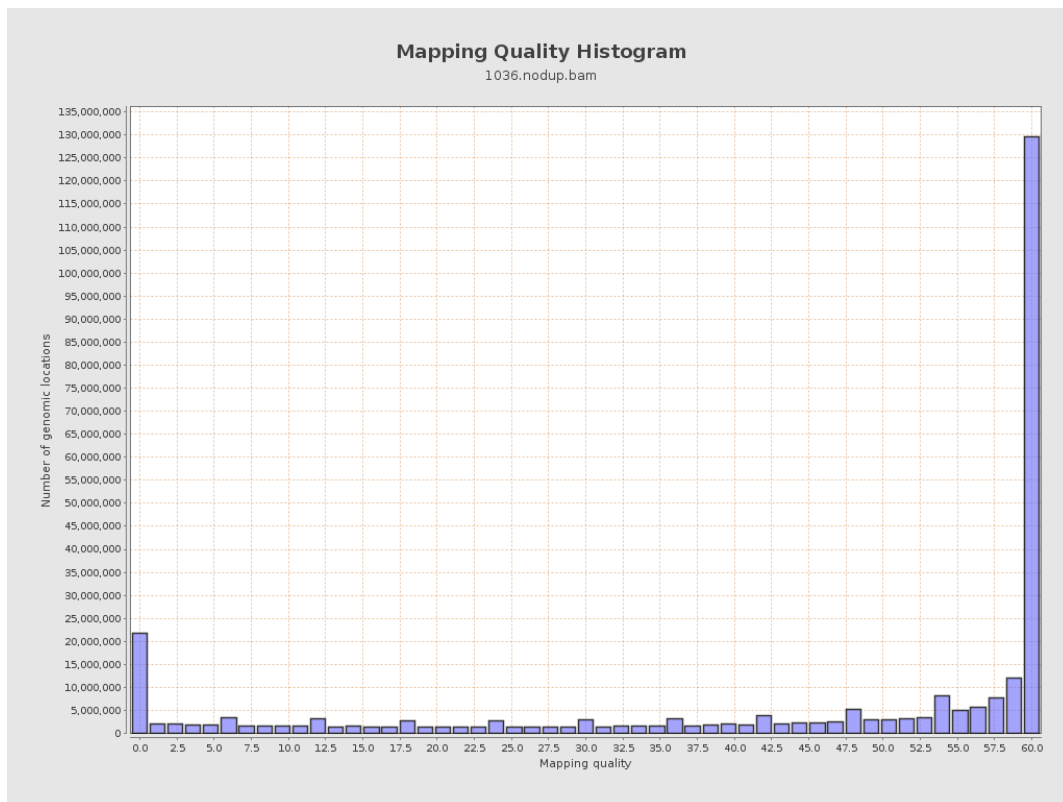
11. Results : Homopolymer Indels



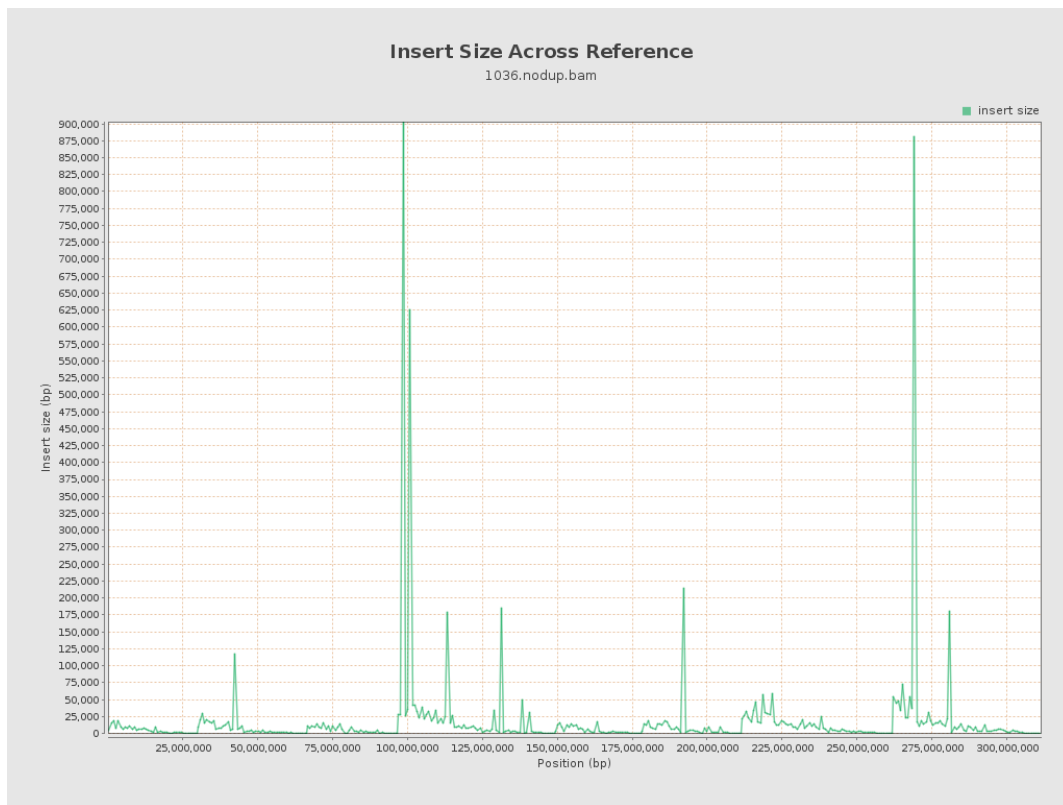
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

