

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2019/04/10 15:59:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam  
/Users/Maria/Desktop/ENAH_course/Ex1_aDNA_BAM/IndC.bam -c -nw 400  
-hm 3
```

1.2. Alignment

Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Analysis date:	Wed Apr 10 15:59:34 CDT 2019
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/Users/Maria/Desktop/ENAH_course/ Ex1_aDNA_BAM/IndC.bam

2. Summary

2.1. Globals

Reference size	16,569
Number of reads	2,696
Mapped reads	2,696 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Read min/max/mean length	30 / 291 / 103.28
Duplicated reads (estimated)	220 / 8.16%
Duplication rate	8.32%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	85,736 / 30.8%
Number/percentage of C's	87,788 / 31.54%
Number/percentage of T's	68,327 / 24.55%
Number/percentage of G's	36,520 / 13.12%
Number/percentage of N's	0 / 0%
GC Percentage	44.66%

2.3. Coverage

Mean	16.8024
Standard Deviation	4.2491

2.4. Mapping Quality

Mean Mapping Quality	37
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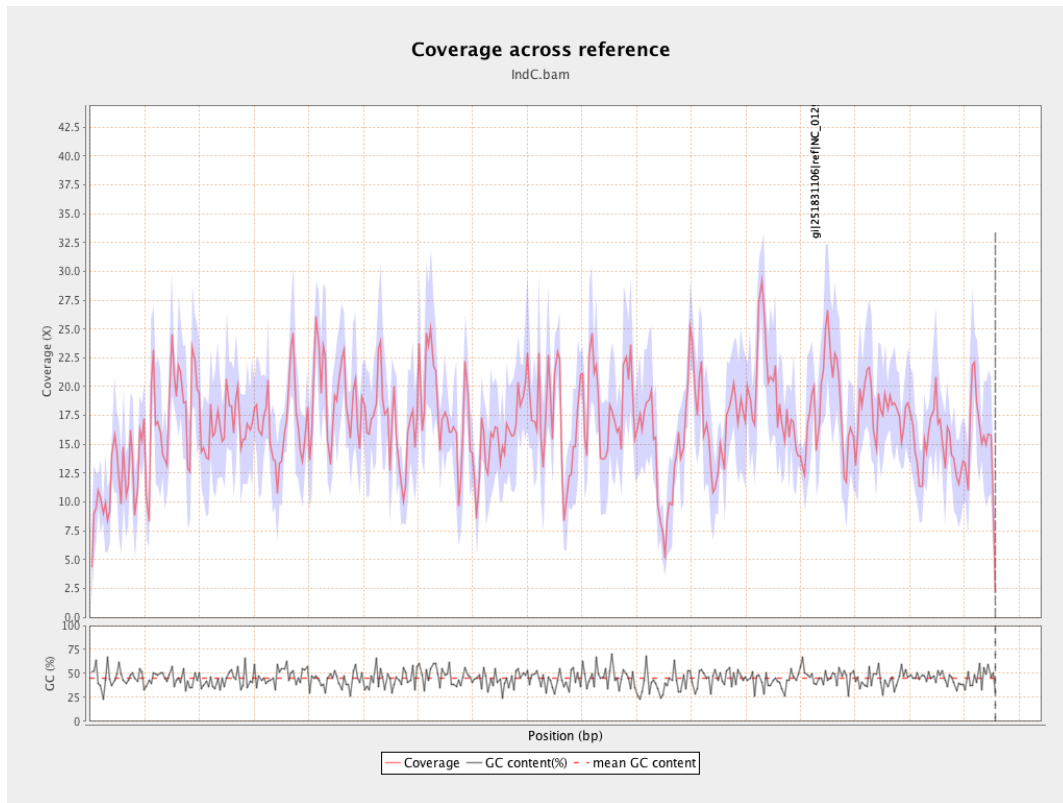
2.5. Mismatches and indels

General error rate	0.51%
Mismatches	1,358
Insertions	63
Mapped reads with at least one insertion	2.34%
Deletions	24
Mapped reads with at least one deletion	0.89%
Homopolymer indels	66.67%

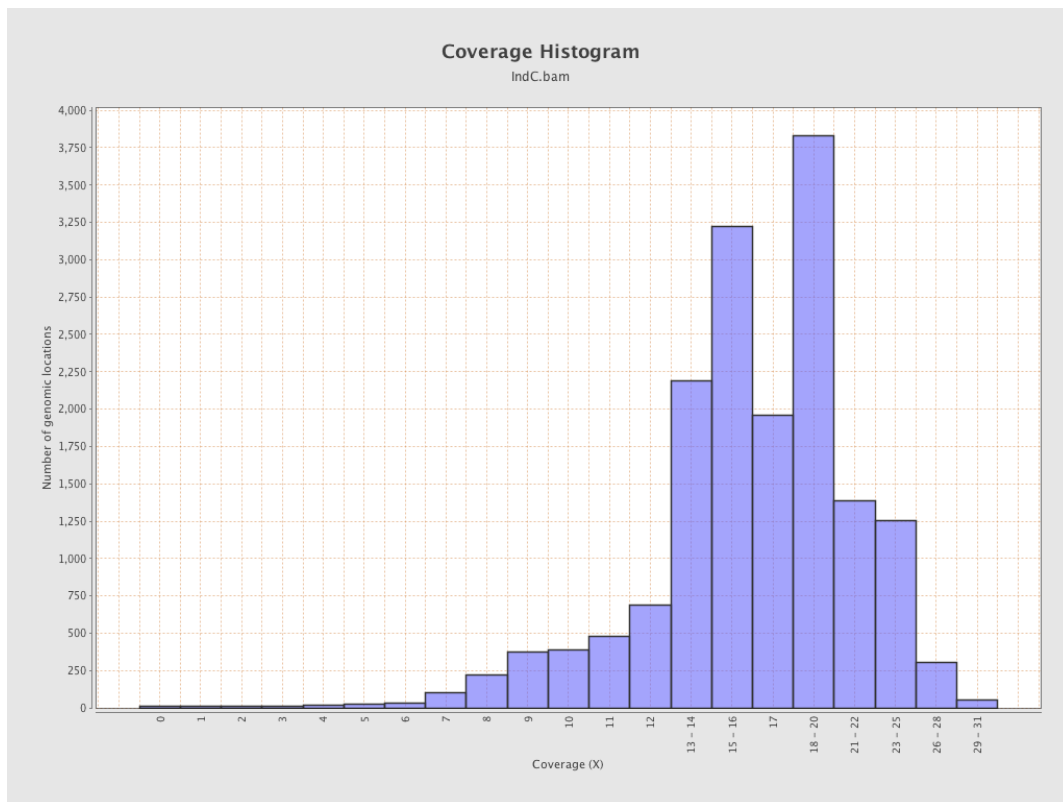
2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
gi 251831106 ref NC_012920.1	16569	278399	16.8024	4.2491

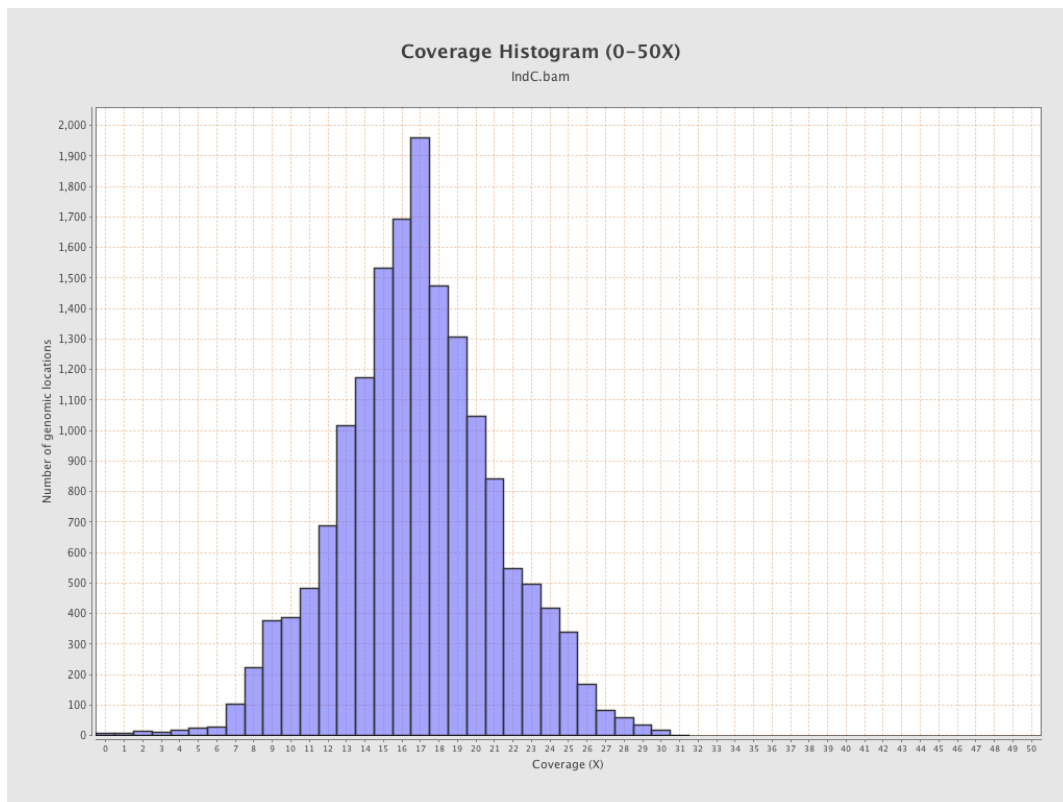
3. Results : Coverage across reference



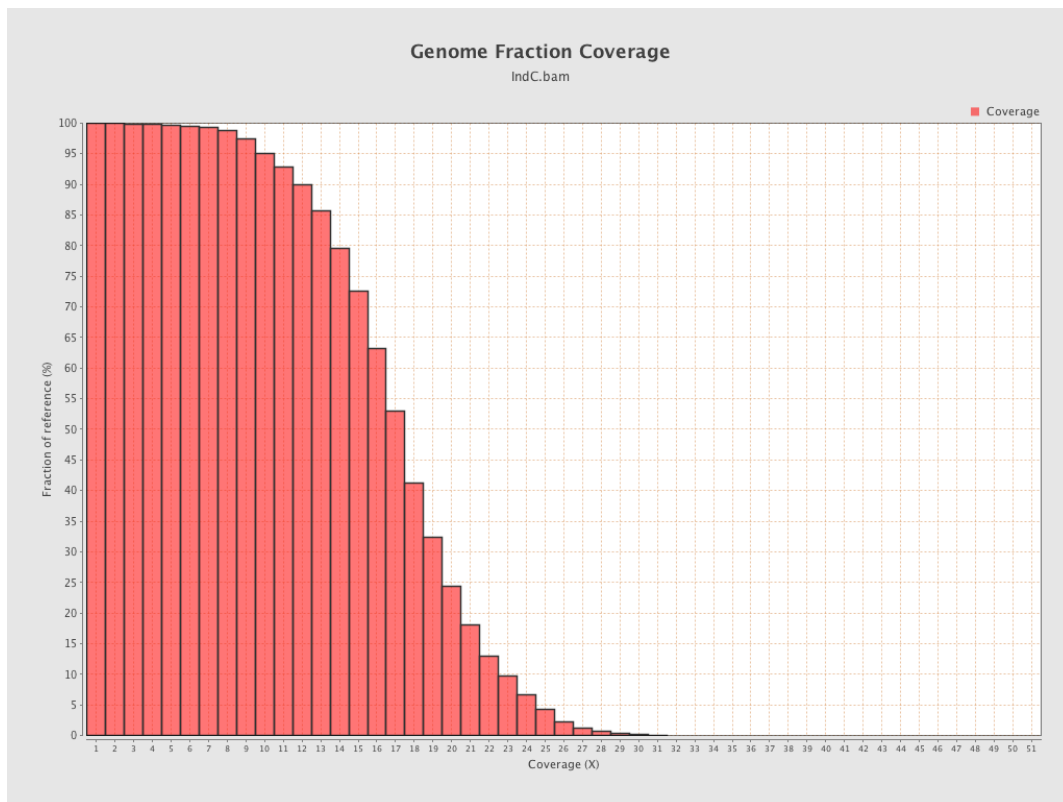
4. Results : Coverage Histogram



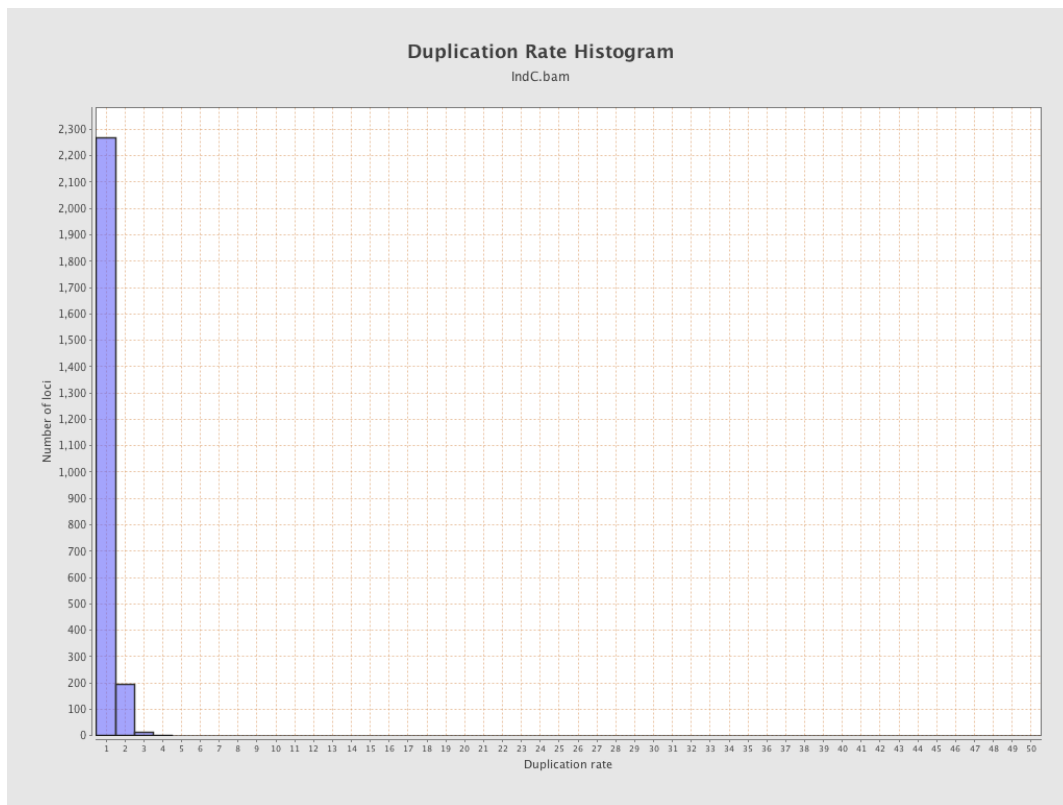
5. Results : Coverage Histogram (0-50X)



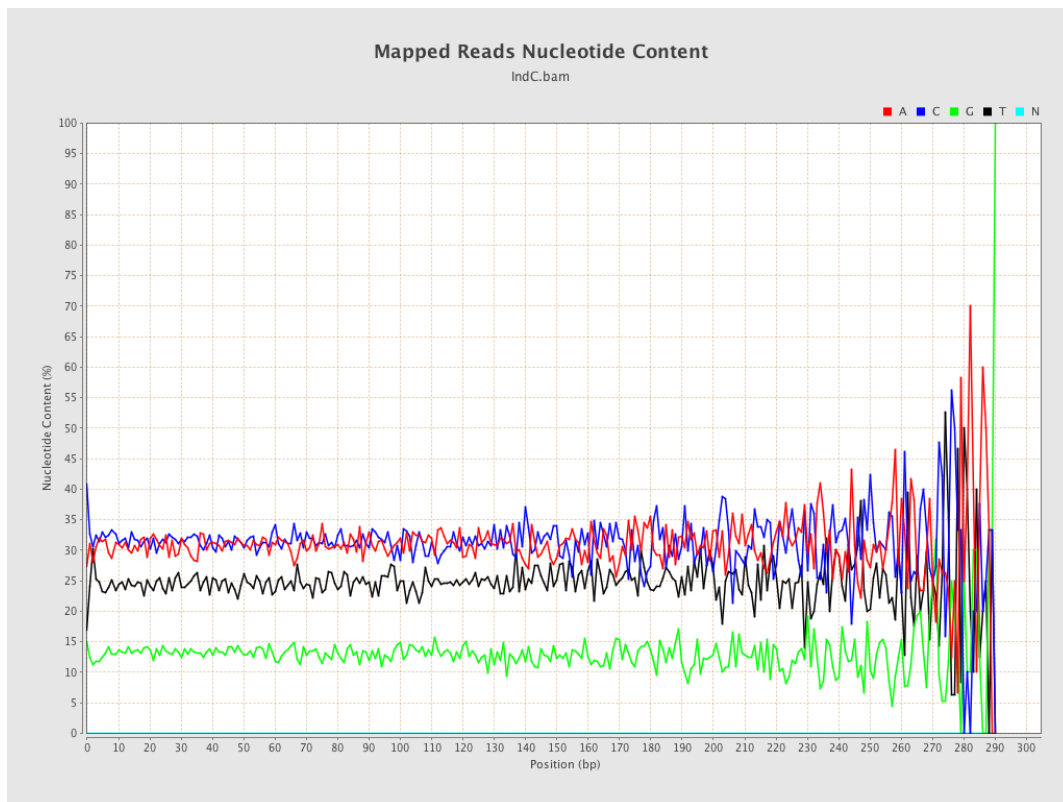
6. Results : Genome Fraction Coverage



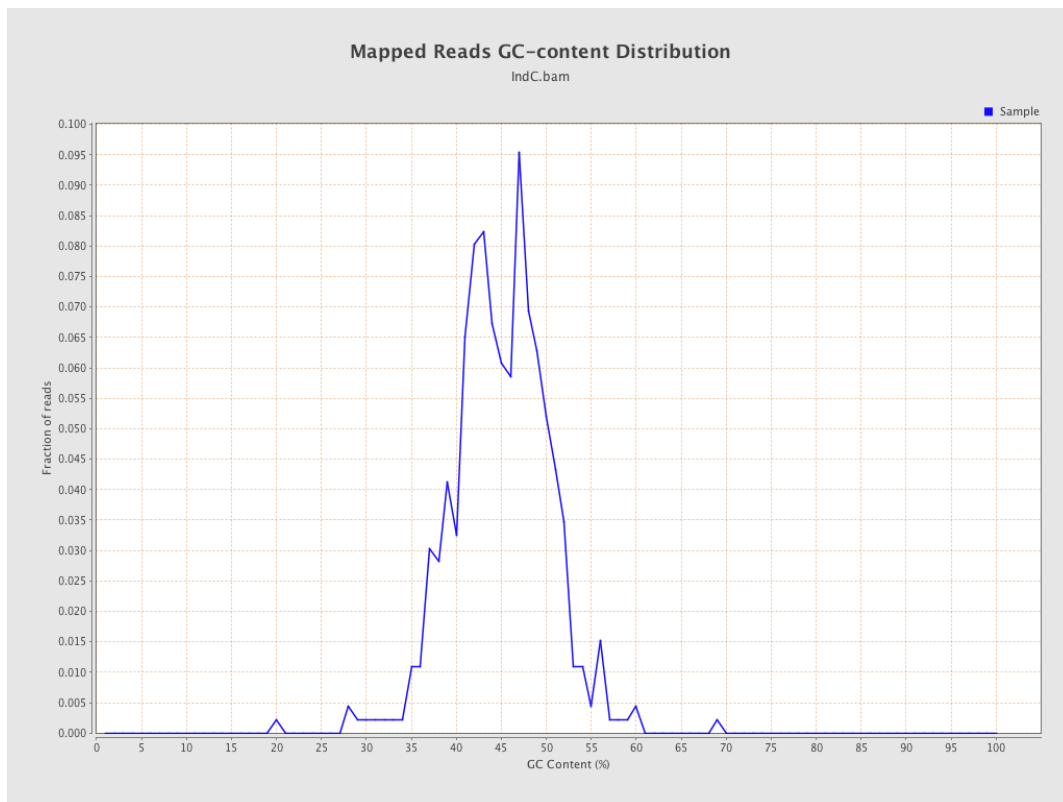
7. Results : Duplication Rate Histogram



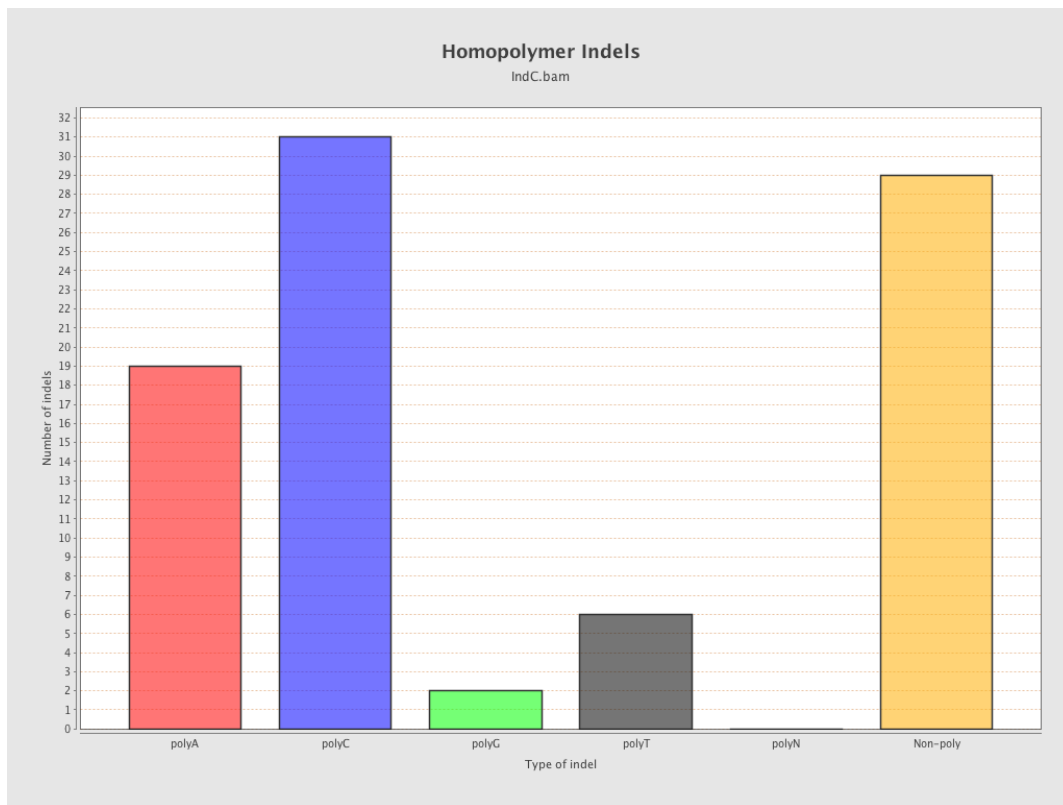
8. Results : Mapped Reads Nucleotide Content



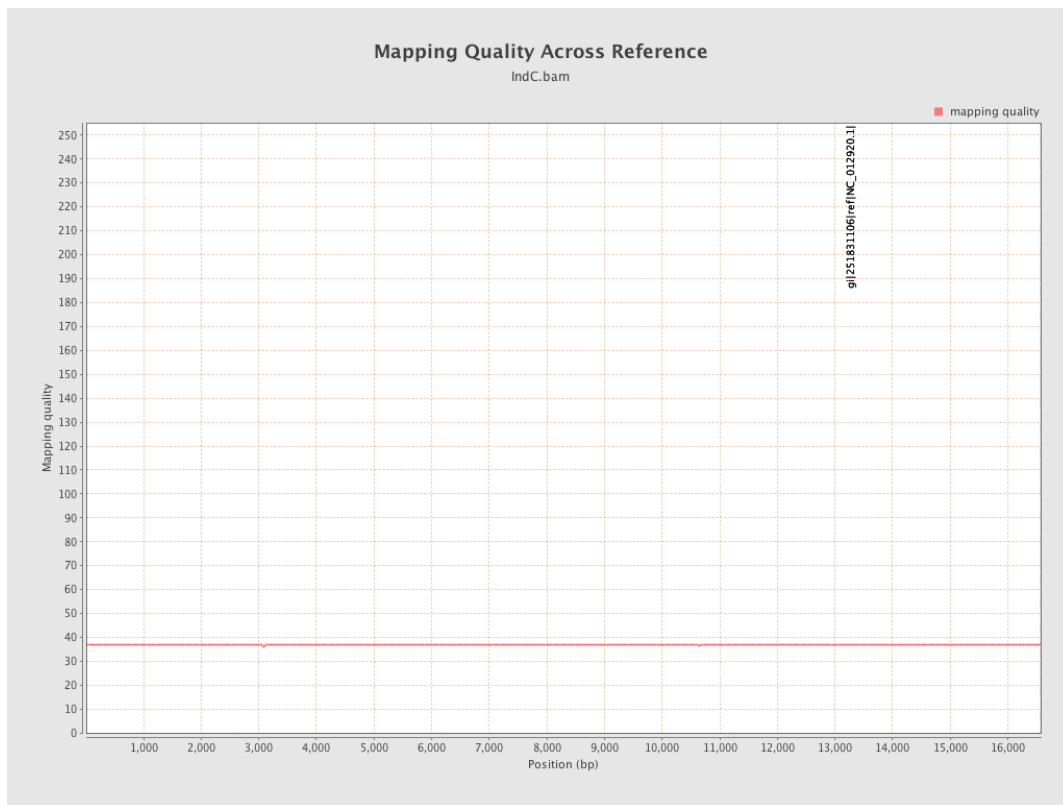
9. Results : Mapped Reads GC-content Distribution



10. Results : Homopolymer Indels



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

