

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2019/04/10 15:59:21

1. Input data & parameters

1.1. QualiMap command line

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

1.2. Alignment

Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Analysis date:	Wed Apr 10 15:59:02 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/IndB.bam

2. Summary

2.1. Globals

Reference size	16,569
Number of reads	234
Mapped reads	234 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Read min/max/mean length	30 / 183 / 53.36
Duplicated reads (estimated)	2 / 0.85%
Duplication rate	0.86%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	3,871 / 31%
Number/percentage of C's	3,839 / 30.75%
Number/percentage of T's	3,070 / 24.59%
Number/percentage of G's	1,706 / 13.66%
Number/percentage of N's	0 / 0%
GC Percentage	44.41%

2.3. Coverage

Mean	0.7539
Standard Deviation	0.9171

2.4. Mapping Quality

Mean Mapping Quality	25.84
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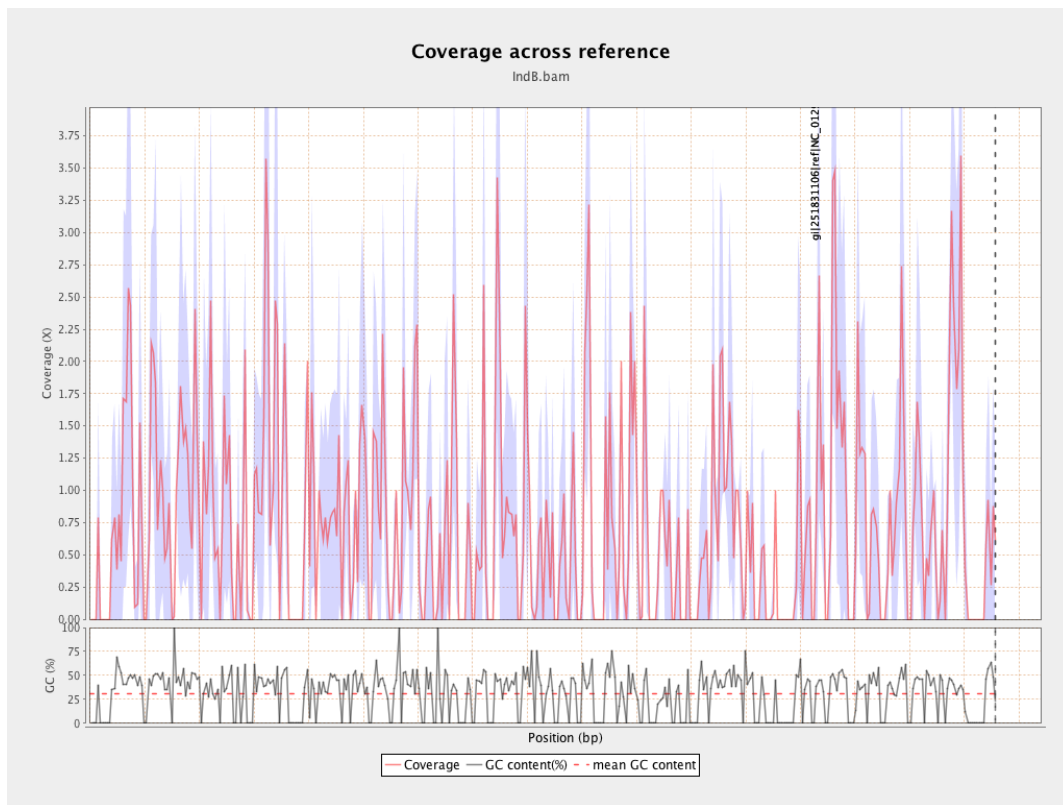
2.5. Mismatches and indels

General error rate	1.37%
Mismatches	171
Insertions	0
Mapped reads with at least one insertion	0%
Deletions	3
Mapped reads with at least one deletion	1.28%
Homopolymer indels	33.33%

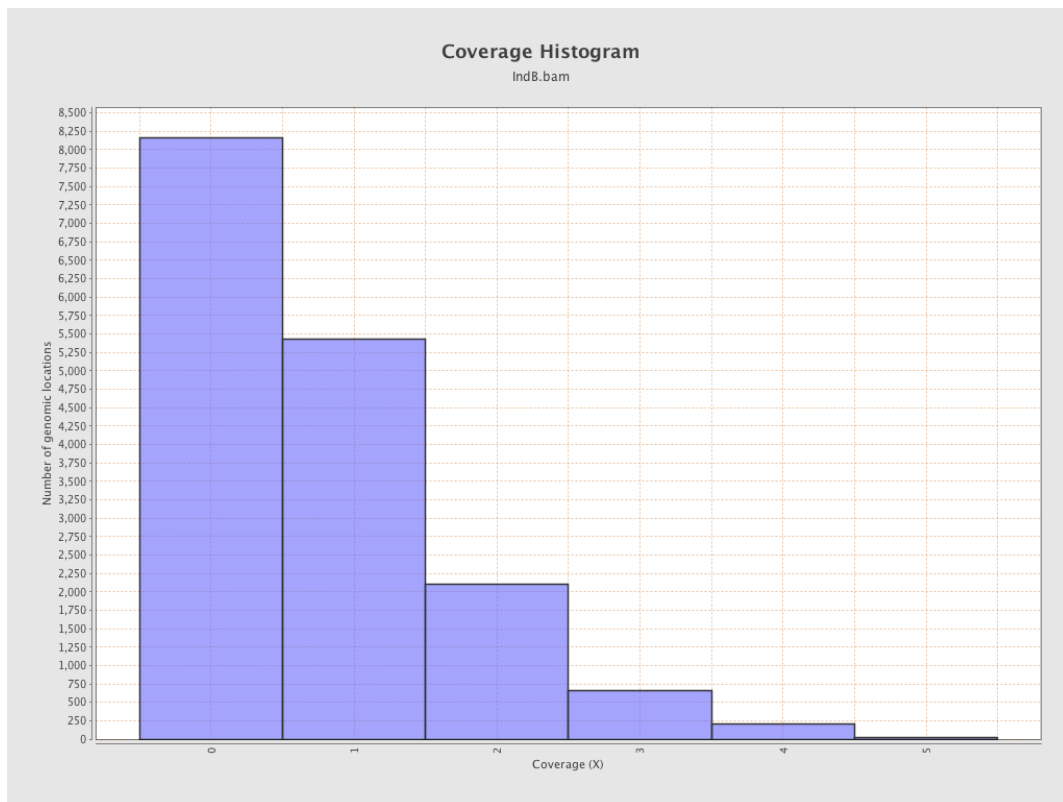
2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
gi 251831106 ref NC_012920.1	16569	12491	0.7539	0.9171

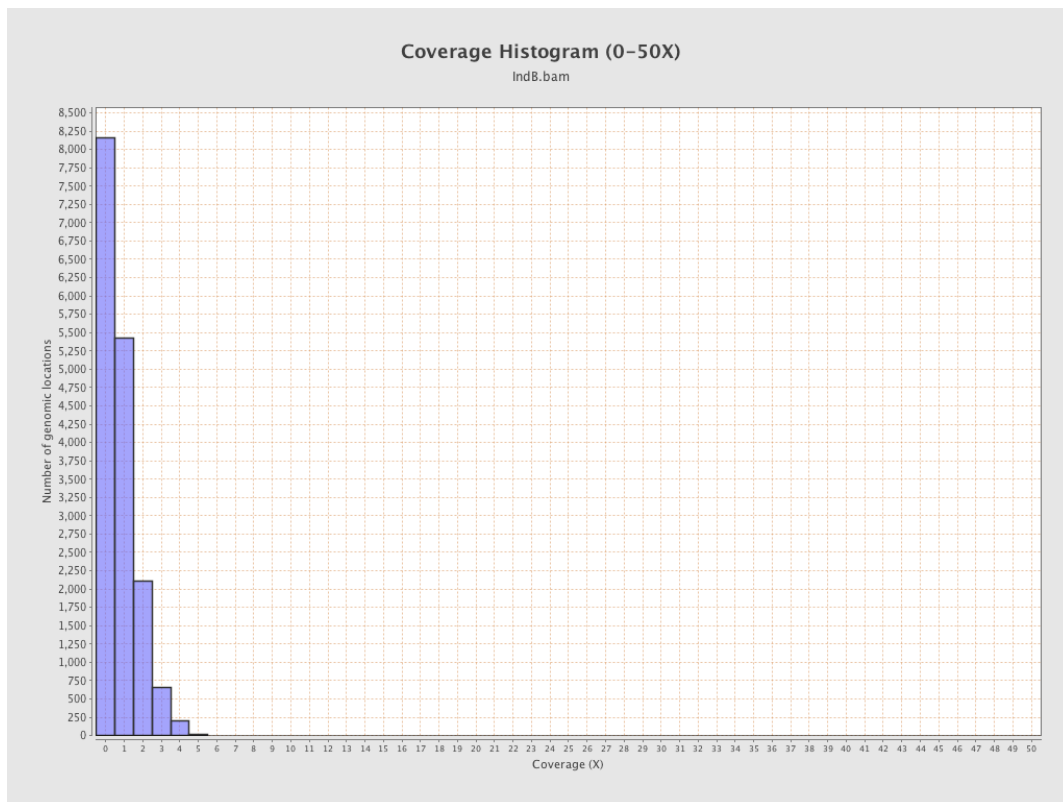
3. Results : Coverage across reference



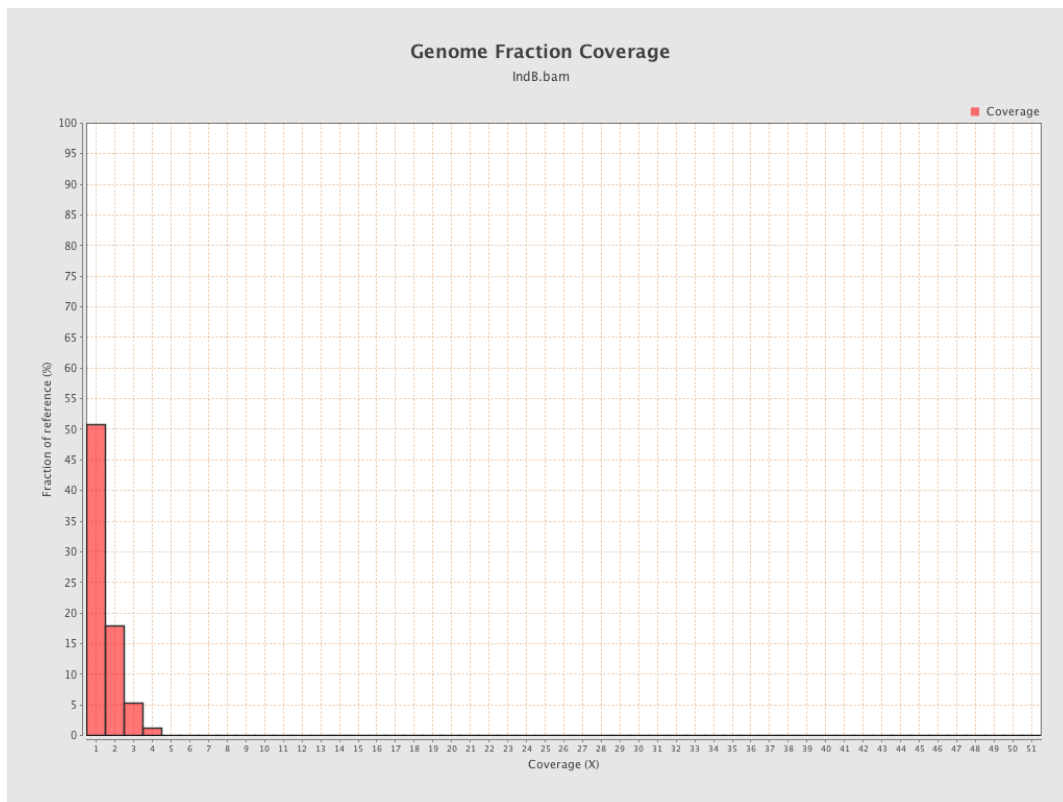
4. Results : Coverage Histogram



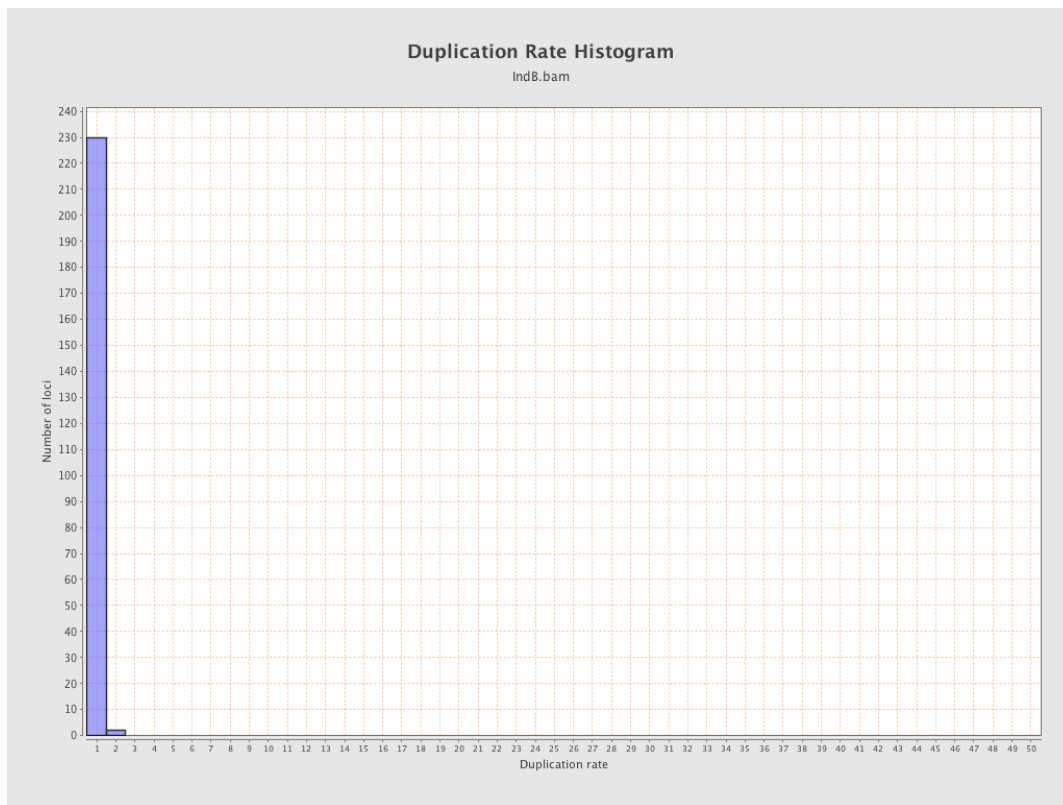
5. Results : Coverage Histogram (0-50X)



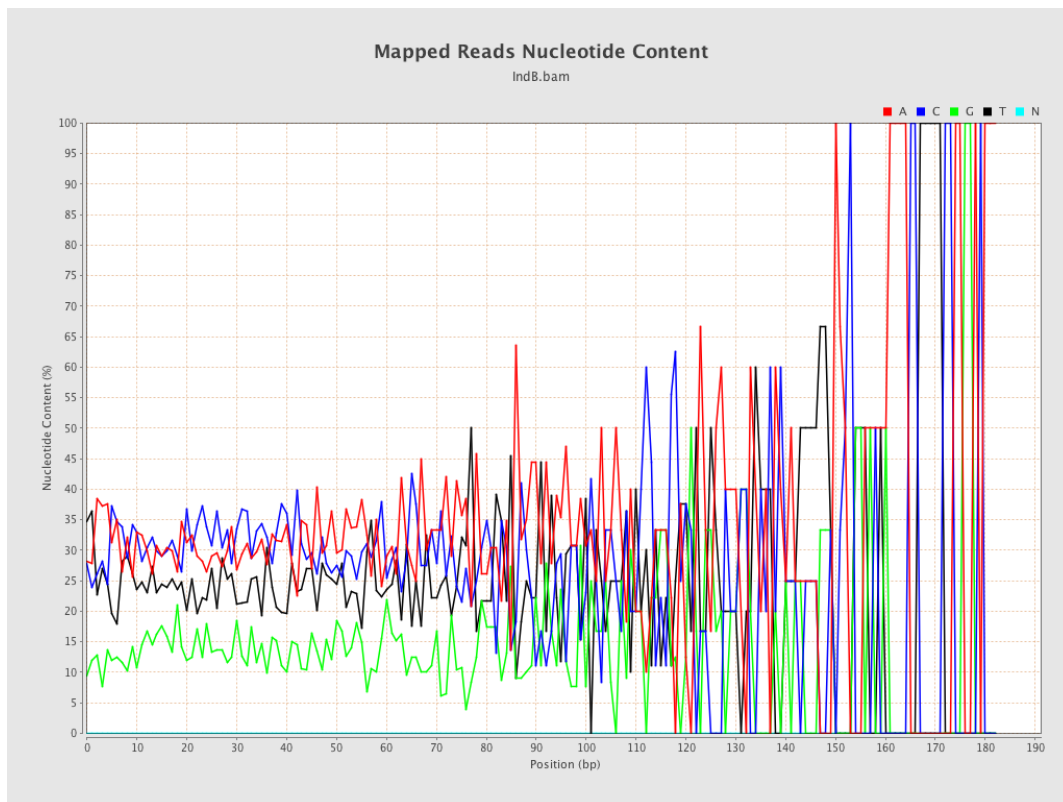
6. Results : Genome Fraction Coverage



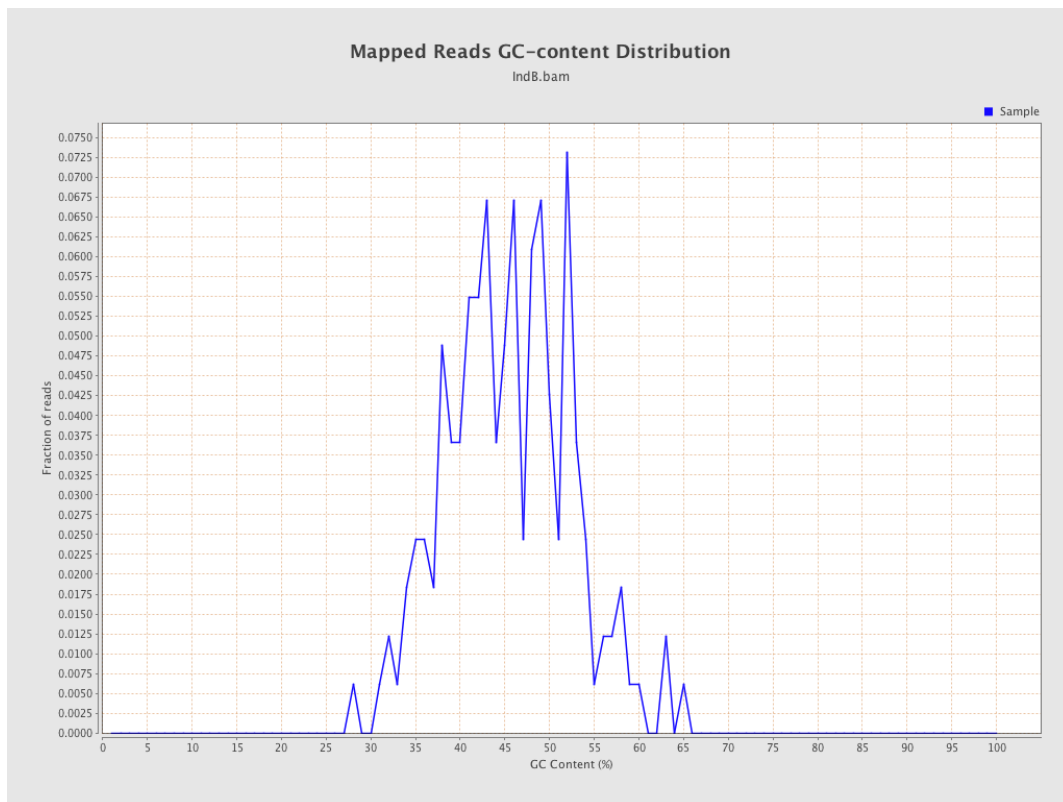
7. Results : Duplication Rate Histogram



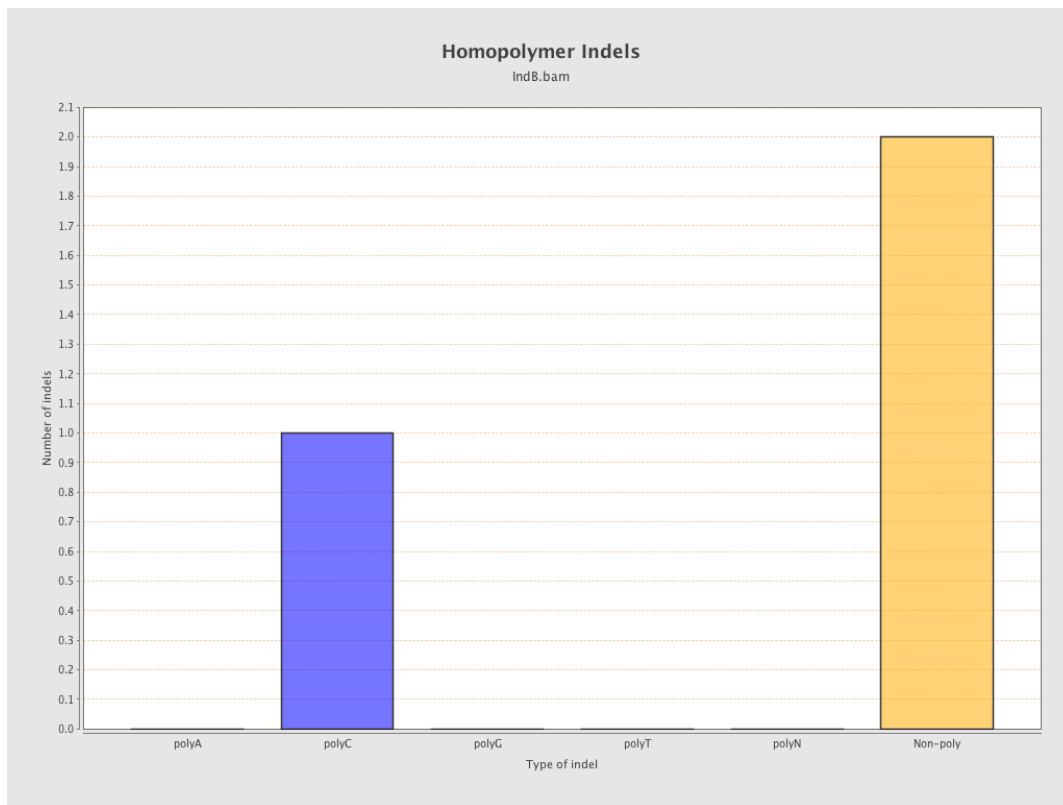
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



10. Results : Homopolymer Indels



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

