

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2019/07/15 18:59:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /home/mianlee/Downloads/IndA.bam -nw 400 -hm 3
```

1.2. Alignment

Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Analysis date:	Mon Jul 15 18:59:08 EDT 2019
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/mianlee/Downloads/IndA.bam

2. Summary

2.1. Globals

Reference size	16,569
Number of reads	16,662
Mapped reads	16,662 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Read min/max/mean length	30 / 288 / 77.09
Duplicated reads (estimated)	5,788 / 34.74%
Duplication rate	38.48%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	397,796 / 30.97%
Number/percentage of C's	393,455 / 30.63%
Number/percentage of T's	327,784 / 25.52%
Number/percentage of G's	165,432 / 12.88%
Number/percentage of N's	0 / 0%
GC Percentage	43.51%

2.3. Coverage

Mean	77.5356
Standard Deviation	13.6399

2.4. Mapping Quality

Mean Mapping Quality	36.99
----------------------	-------

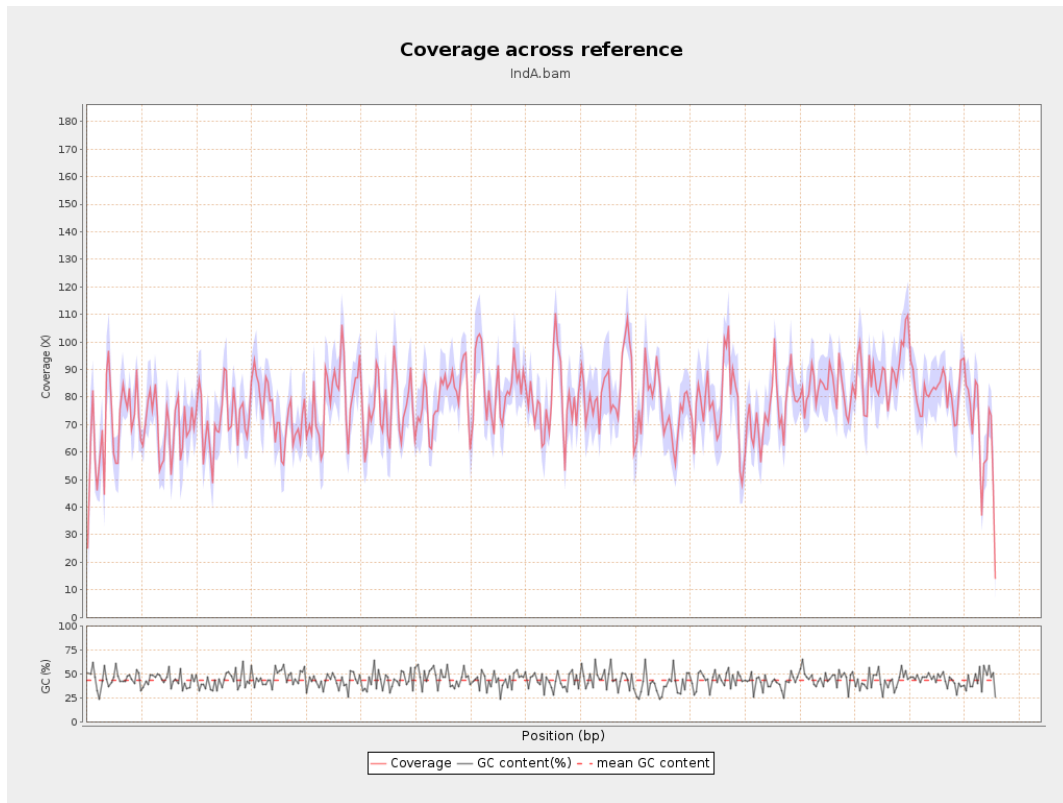
2.5. Mismatches and indels

General error rate	1.49%
Mismatches	19,110
Insertions	34
Mapped reads with at least one insertion	0.19%
Deletions	171
Mapped reads with at least one deletion	1.03%
Homopolymer indels	29.76%

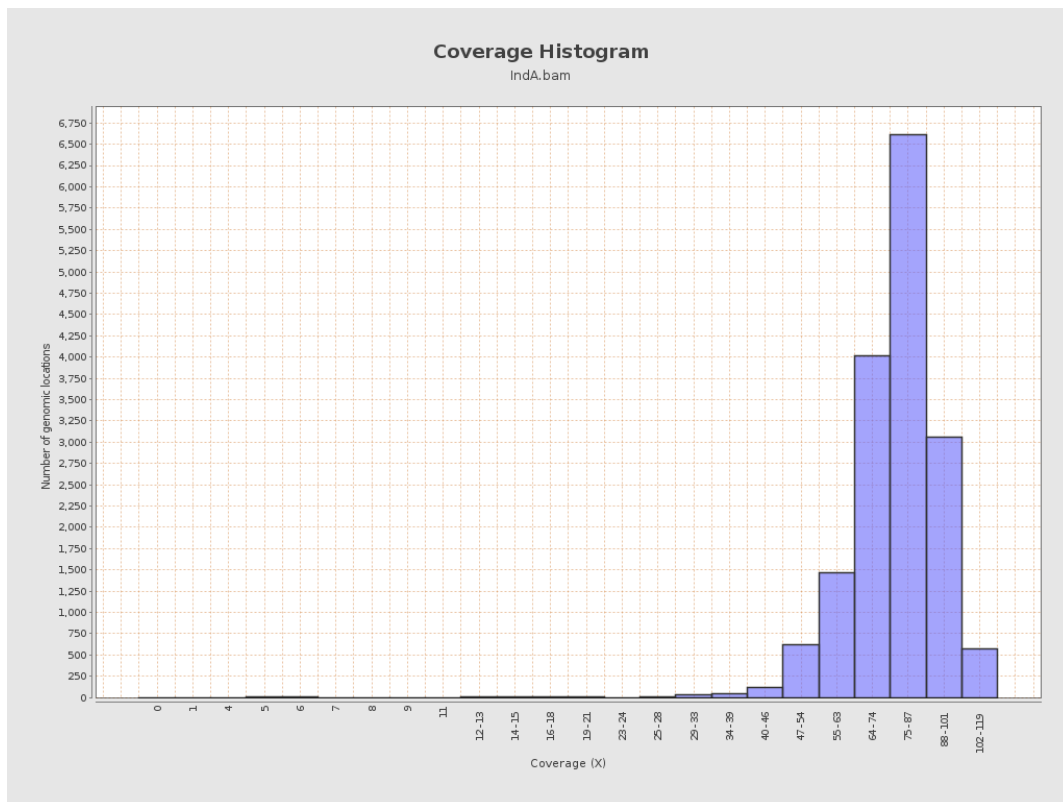
2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
gi 251831106 ref NC_012920.1	16569	1284688	77.5356	13.6399

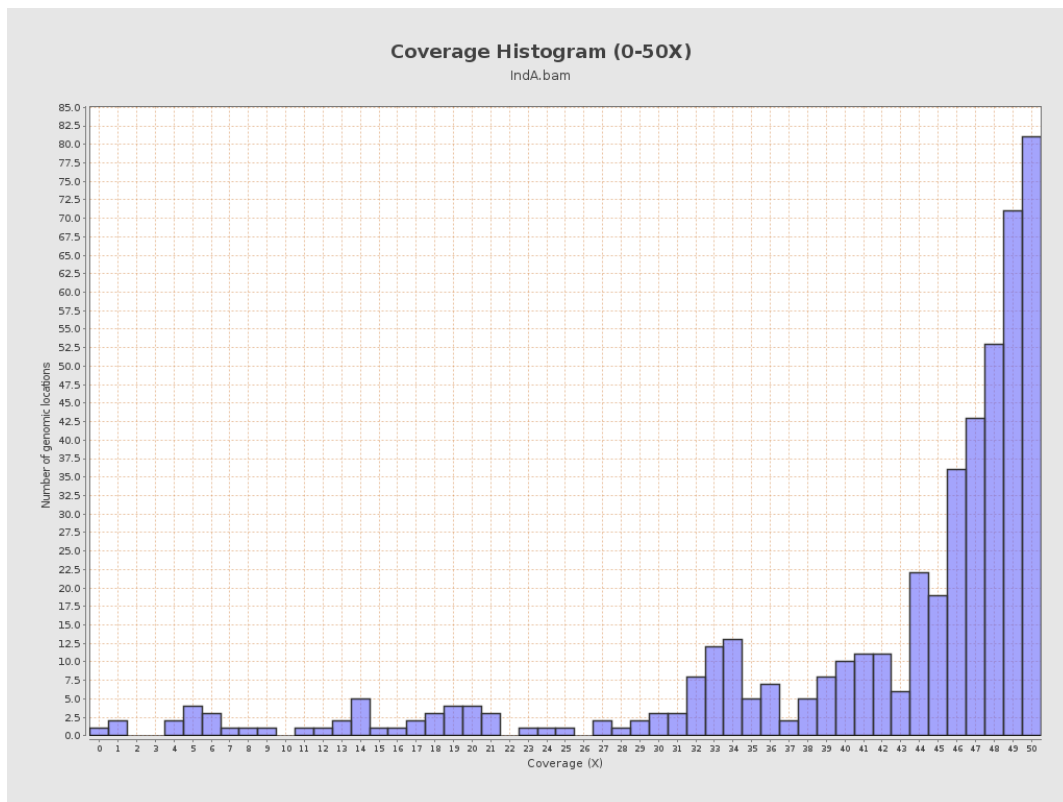
3. Results : Coverage across reference



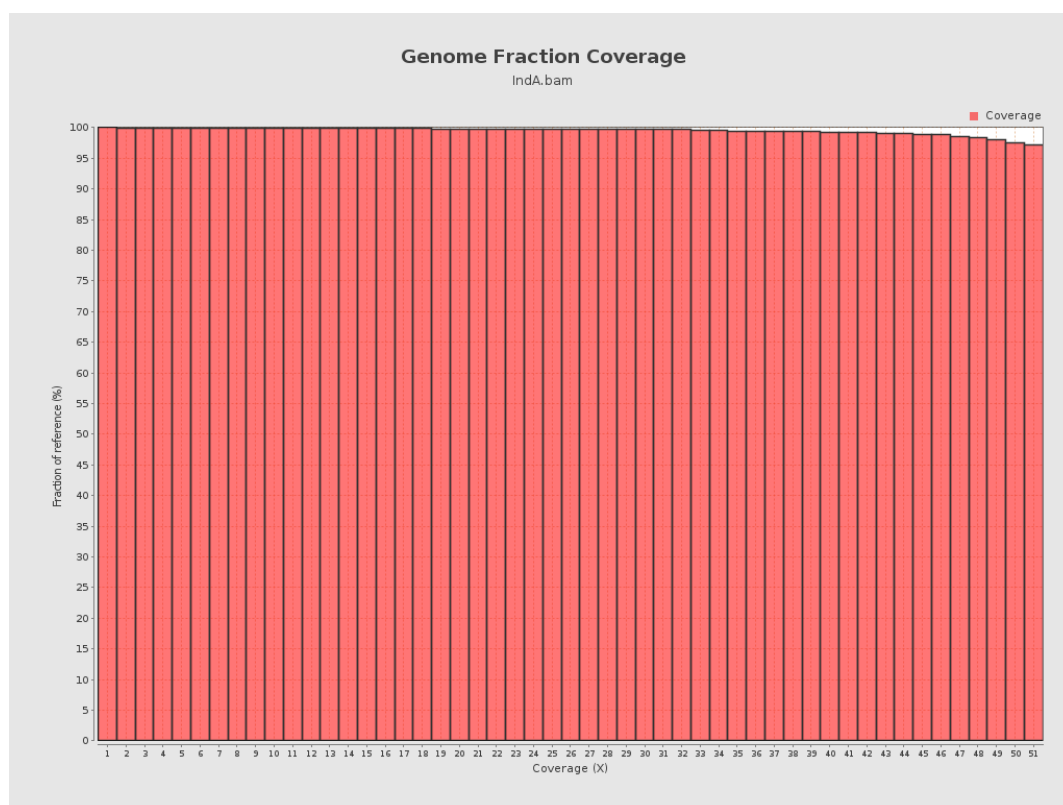
4. Results : Coverage Histogram



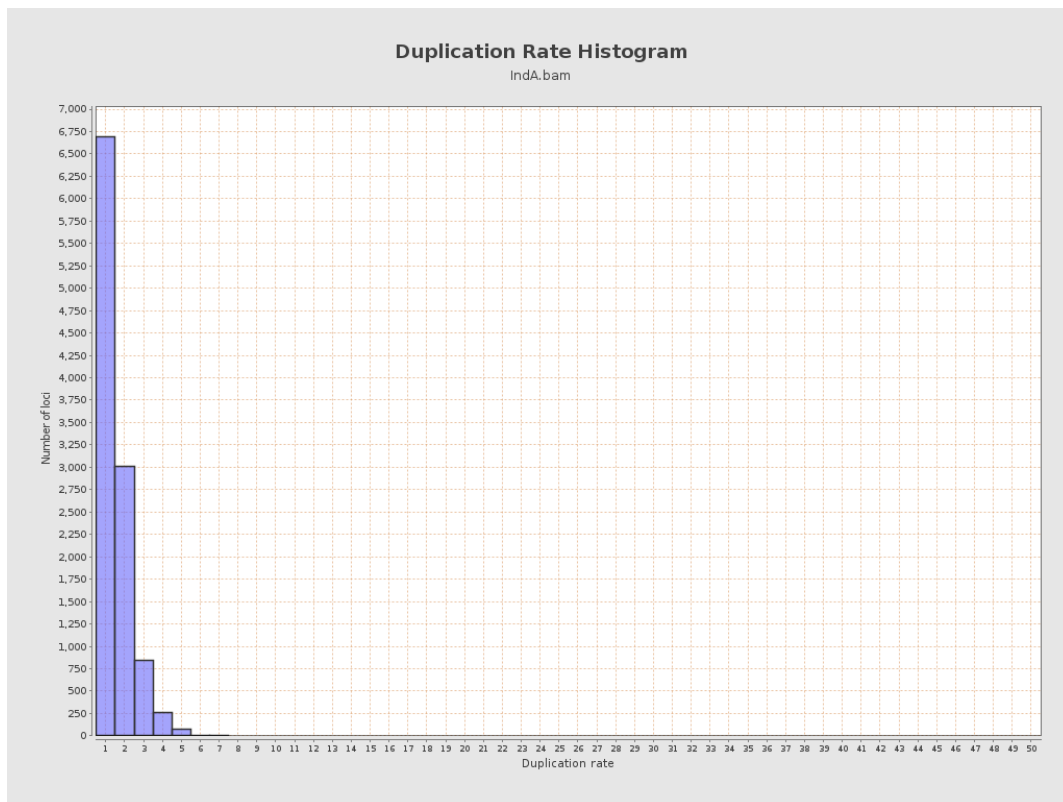
5. Results : Coverage Histogram (0-50X)



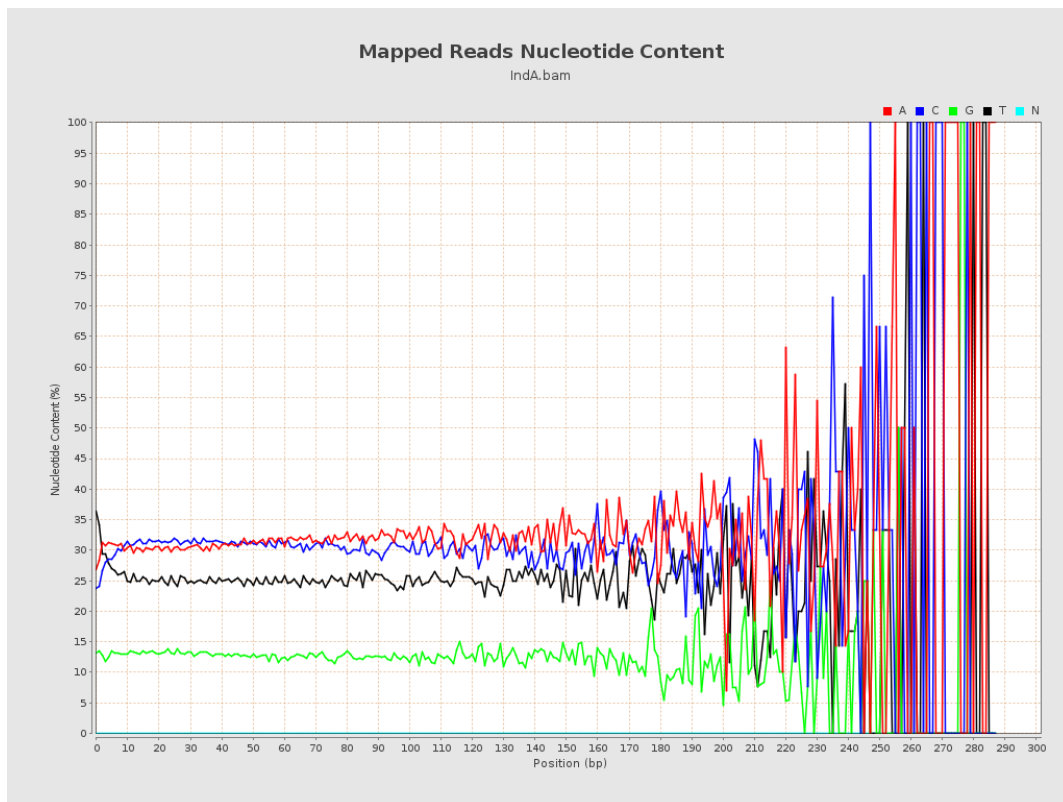
6. Results : Genome Fraction Coverage



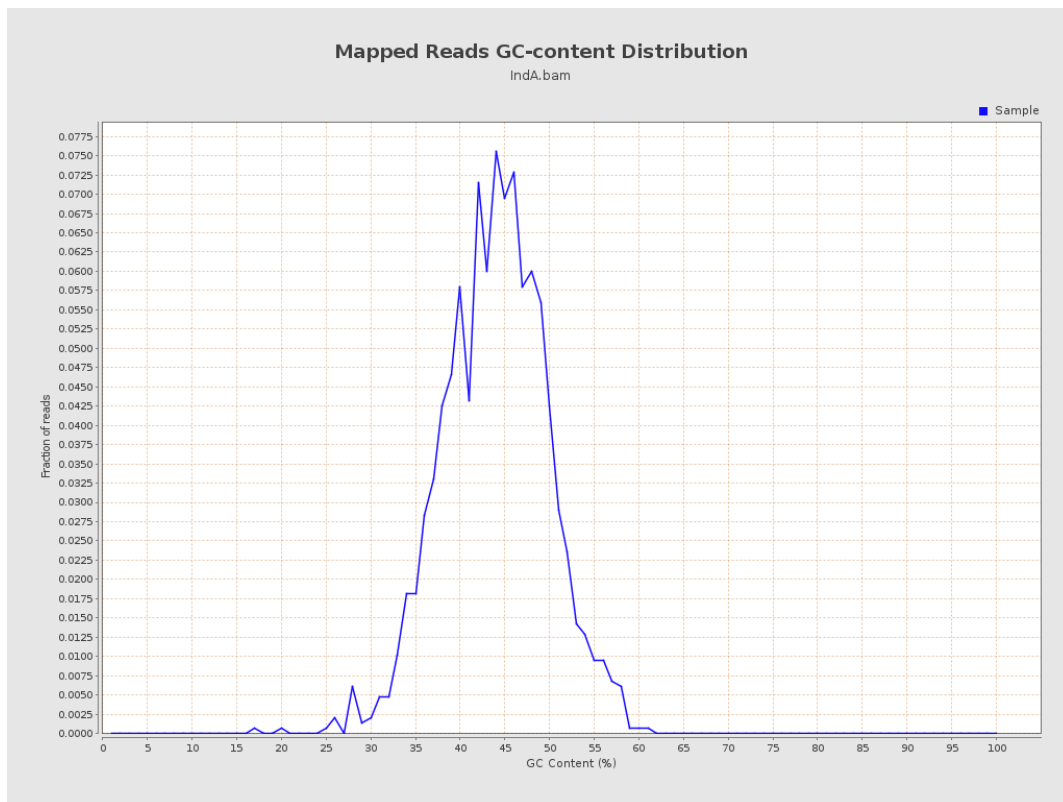
7. Results : Duplication Rate Histogram



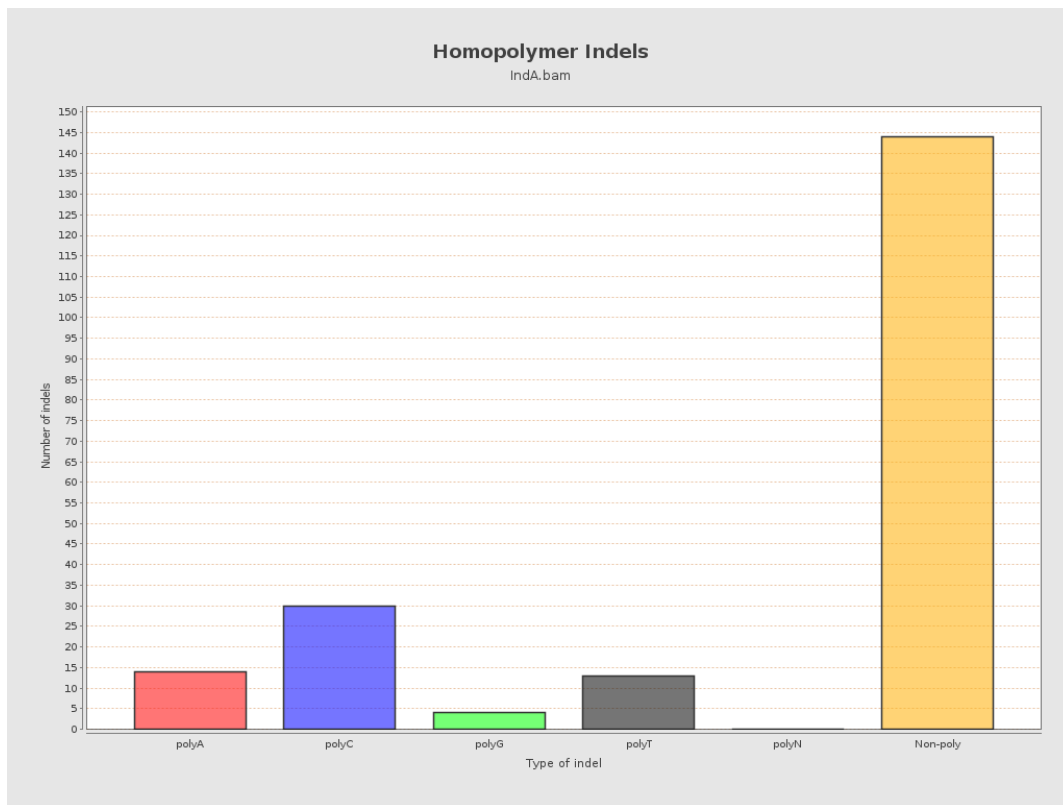
8. Results : Mapped Reads Nucleotide Content



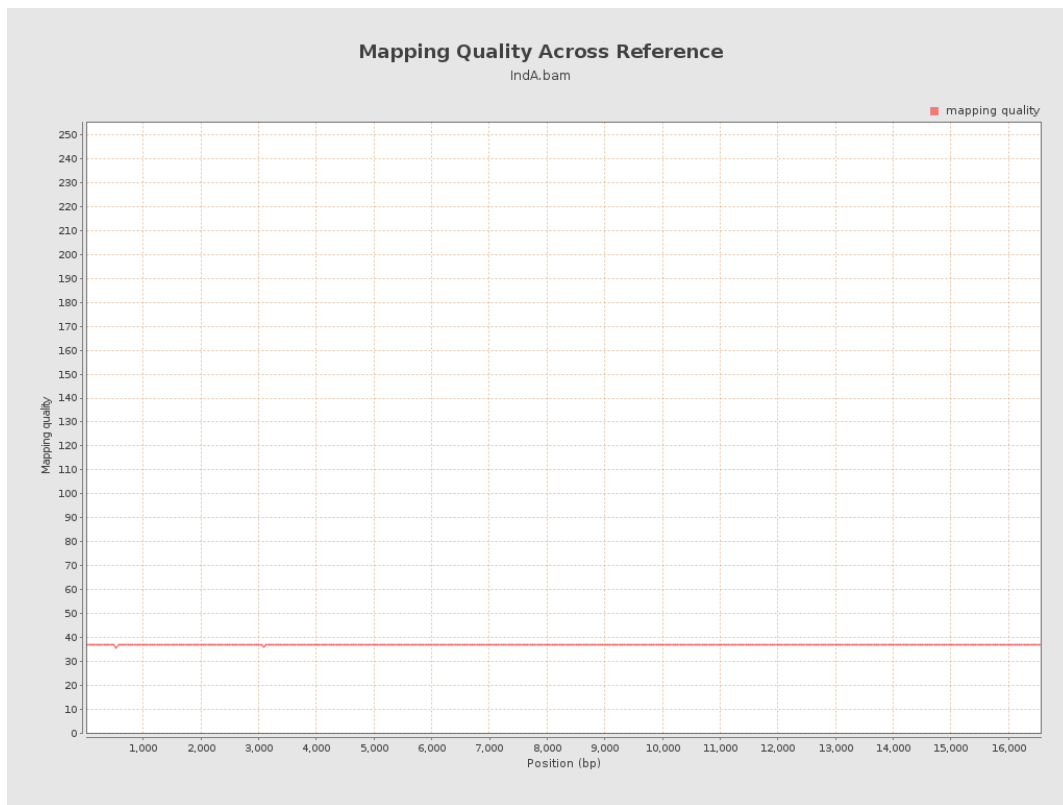
9. Results : Mapped Reads GC-content Distribution



10. Results : Homopolymer Indels



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

