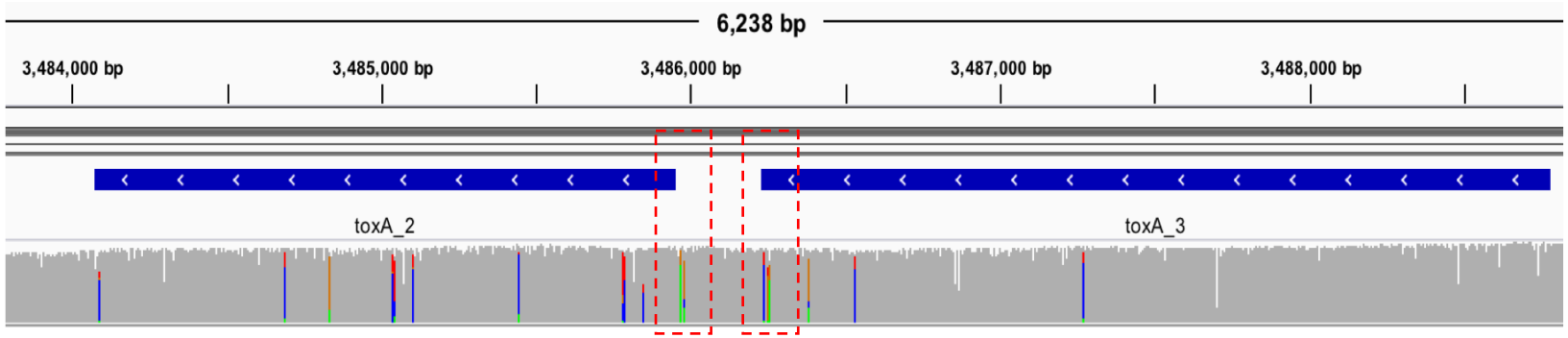
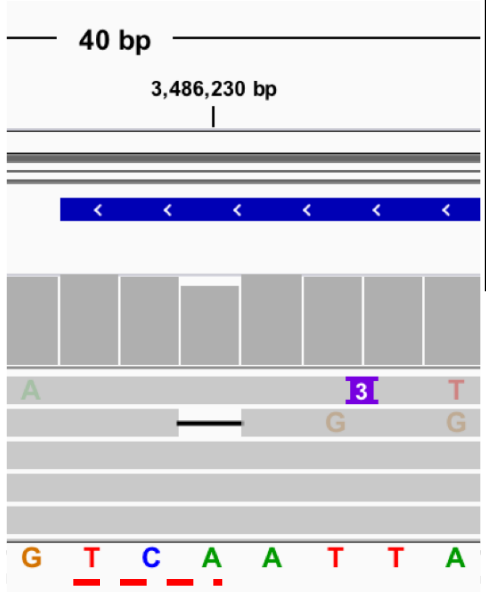
We take toxA_2 and toxA_3 as an example:



Issue: the "stop codon" so happens at the end of toxA_3



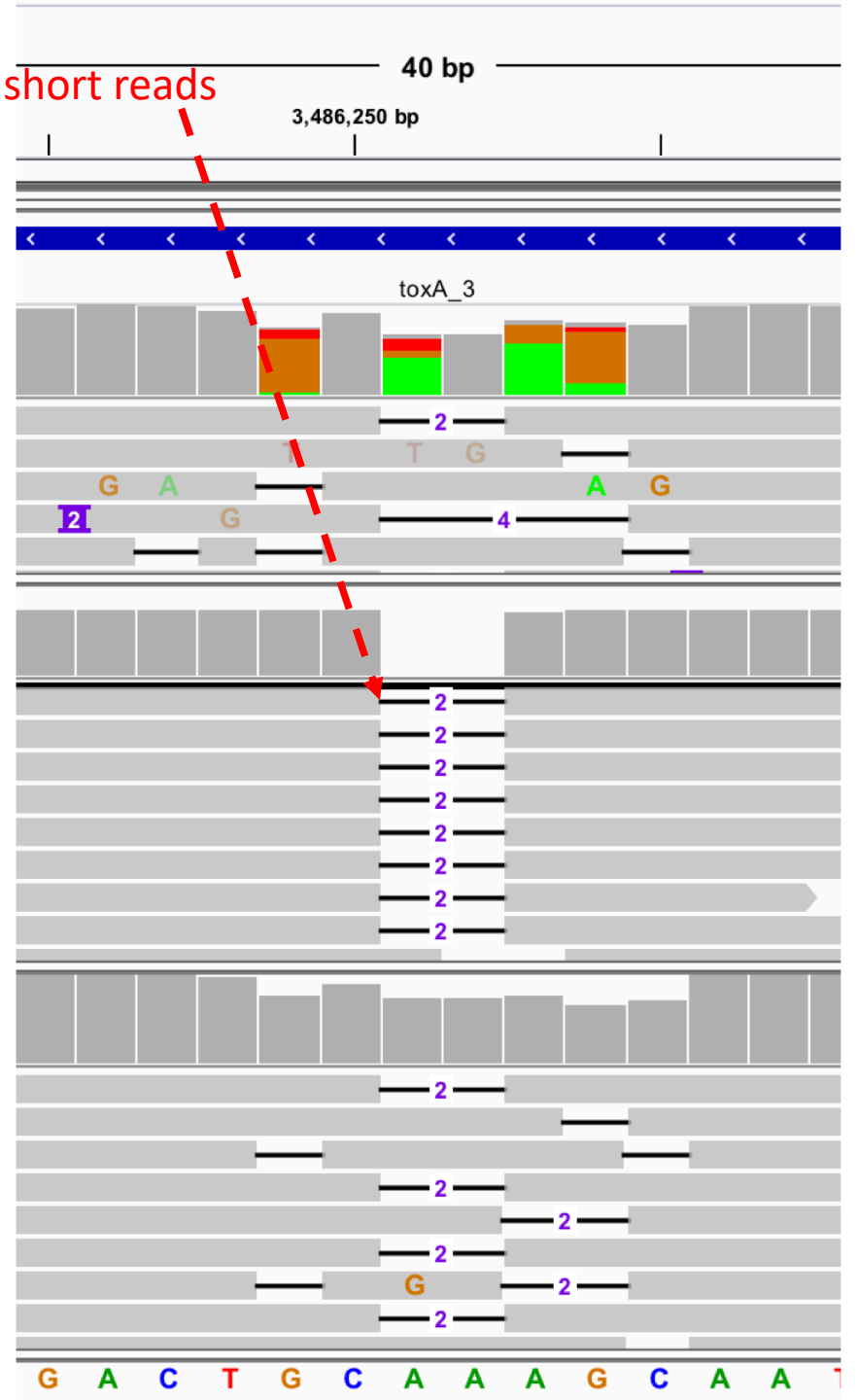
- strand: **AUG**

Method:, blastn toxA_3 to tcdA genes: AA causing the **frame shift**

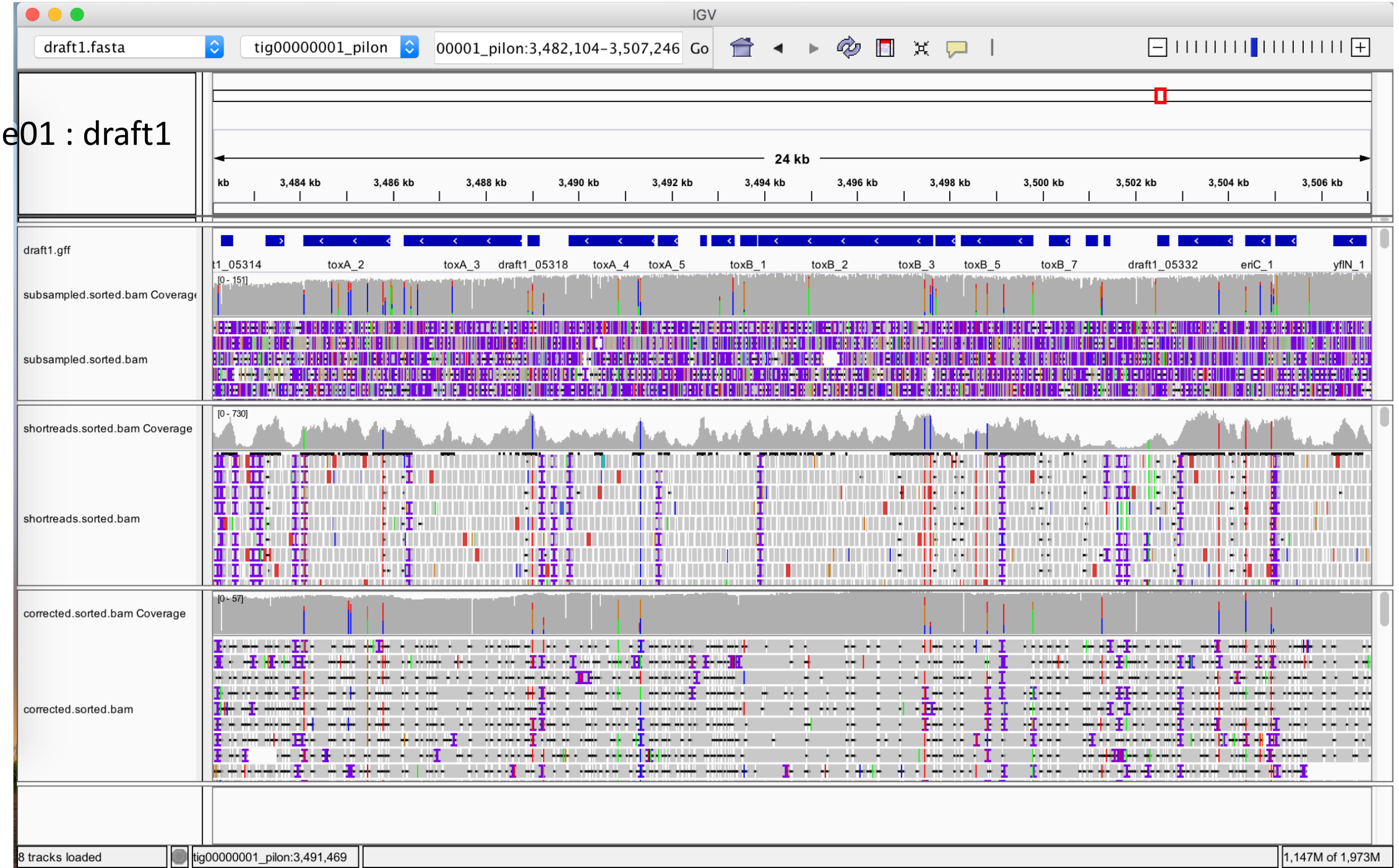
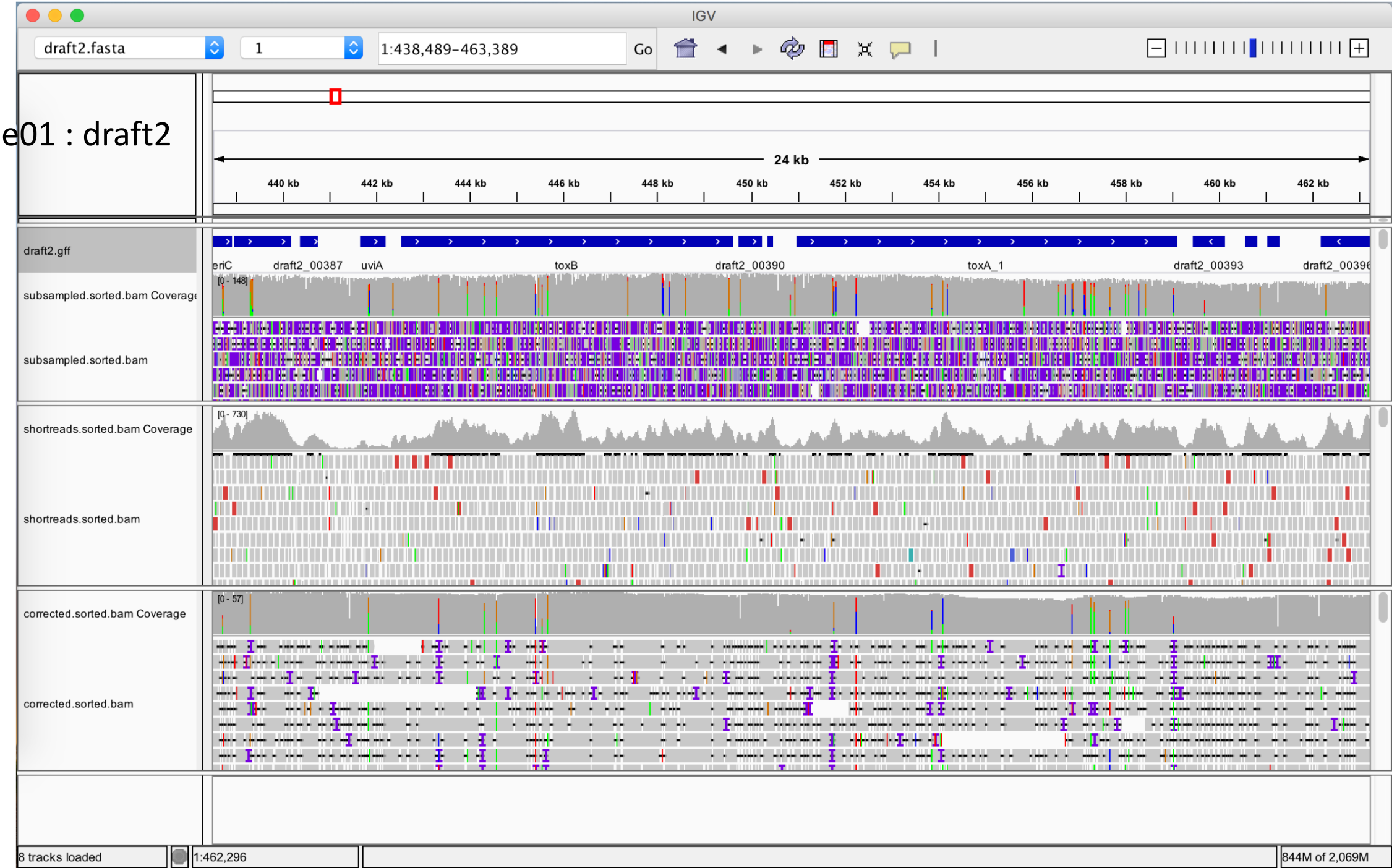
```
> NC_009089.1:795843-803975 Clostridioides difficile 630, complete
genome
Length=8133

 Score = 4680 bits (2534),  Expect = 0.0
 Identities = 2546/2551 (99%), Gaps = 3/2551 (0%)
 Strand=Plus/Minus

Query  1     TCAATTACTTGCAATCCGACTGCAAAGCAATAGCATTATTAGGATTAAAGTAATA
             ||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Sbjct  5912  TCAATTACTTGCAATCCGACTGCA--GCAATAGCATTATTAGGATTAAAGTAATA
```

Conclusion: the assembly error in the consensus sequences caused the **frame shift**, which causing "stop codon" breaks the gene. Multiple rounds of Pilon should be able to polish the (hopefully).

deletion in the short reads



barcode01 : draft1



barcode01 : draft2