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Please refer to **output logs.txt** for output logs of the data requested.

What can be learned about the first 10 hits having length at least 50 nucleotides:

- 1. The algorithm converged after the 4th iteration, so the first 10 hits having length at least 50 nucleotides stayed the same for the following iterations.
- 2. Overlapping results from genome annotation
 - a. Start: 97326, End: 97541, Length: 216
 - i. tRNA complement(join(97426..97464,97500..97537))
 - b. Start: 97627, End: 97823, Length: 197
 - i. tRNA 97629..97716
 - c. Start: 111764, End: 111856, Length: 93
 - i. tRNA 111768..111852
 - d. Start: 118079, End: 118179, Length: 101
 - i. None overlapping
 - e. Start: 138345, End: 138419, Length: 75
 - i. tRNA complement(138344..138419)
 - f. Start: 154610, End: 157697, Length: 3088
 - i. rRNA complement(154662..157639)
 - g. Start: 157782, End: 159591, Length: 1810
 - i. tRNA complement(157847..157919) and rRNA complement(157984..159463)
 - h. Start: 186974, End: 187067, Length: 94
 - i. tRNA 186978..187066
 - i. Start: 190831, End: 190907, Length: 77
 - i. tRNA 190832..190908
 - j. Start: 215200, End: 215296, Length: 97
 - i. tRNA 215210..215297