Using 4Peaks software to trim sequences

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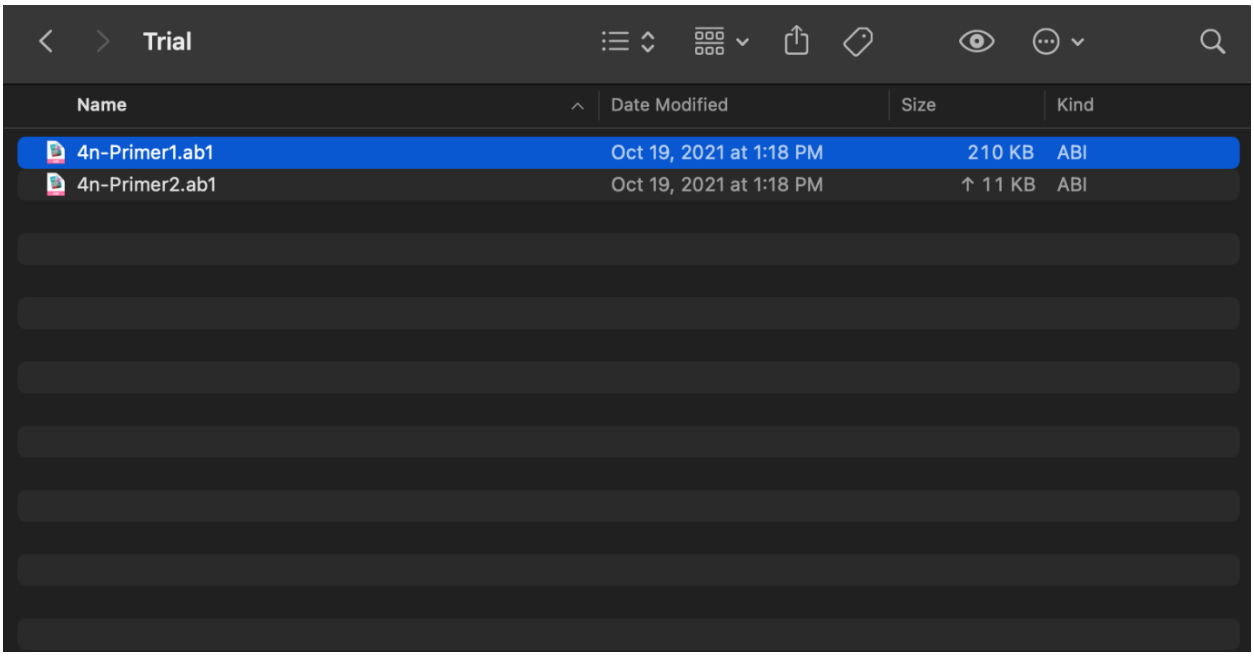
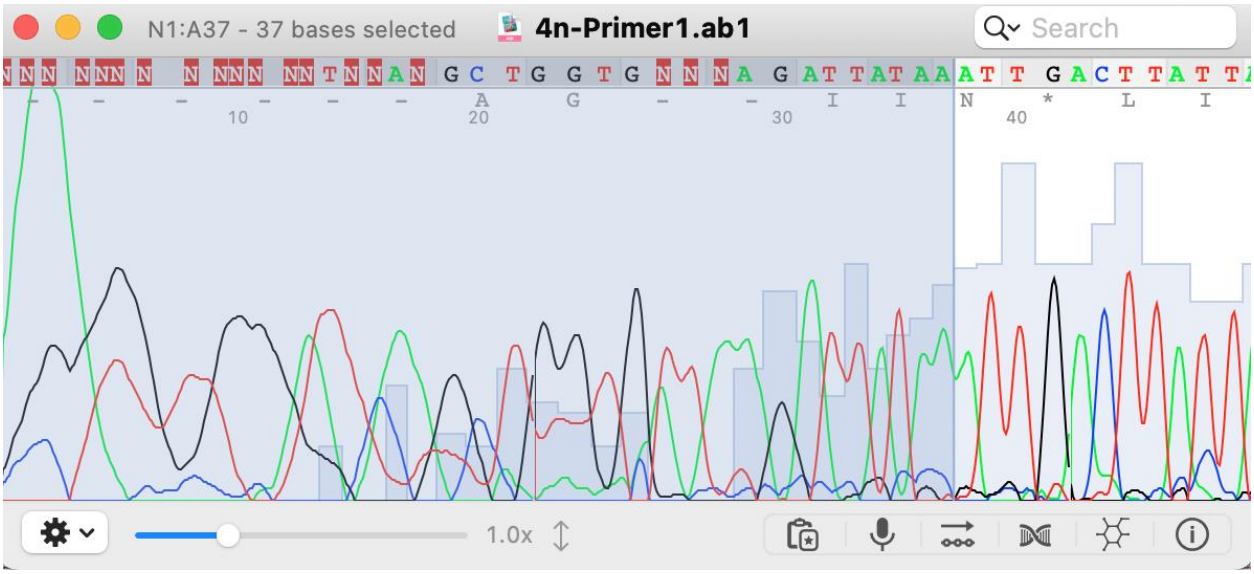
First open Primer1 which corresponds to the forward sequence

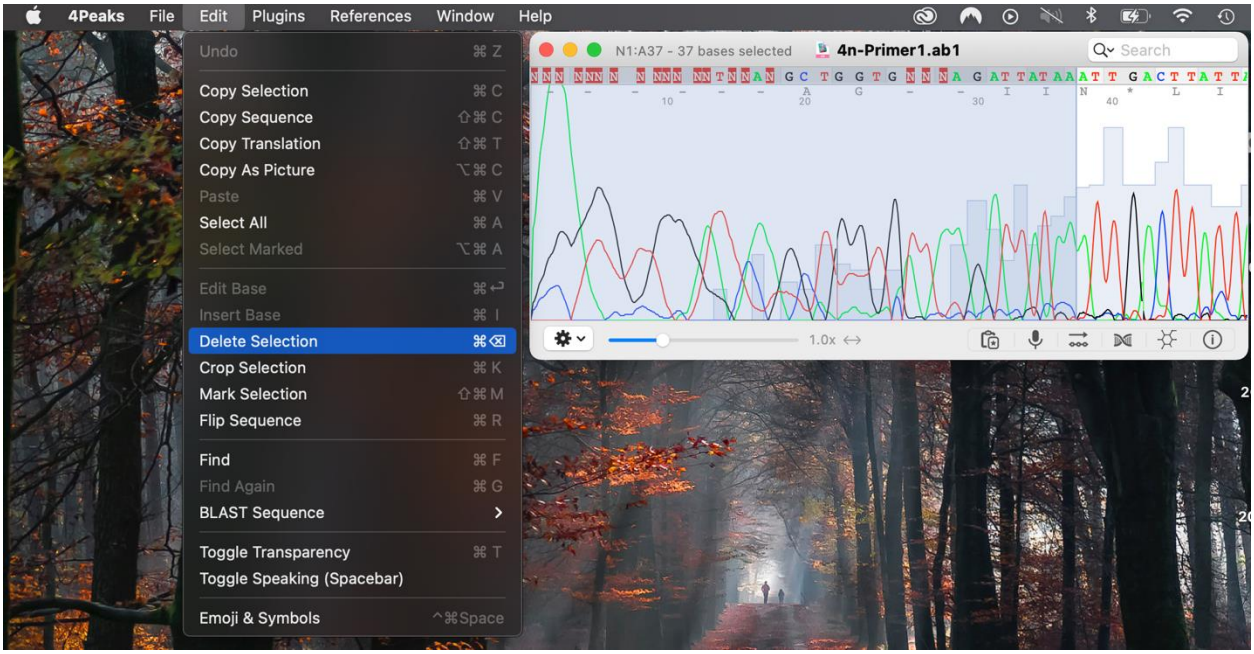


The first ~30 base pairs highlighted below will be messy as they correspond to the location the primer interacted with the DNA sequence and need to be trimmed



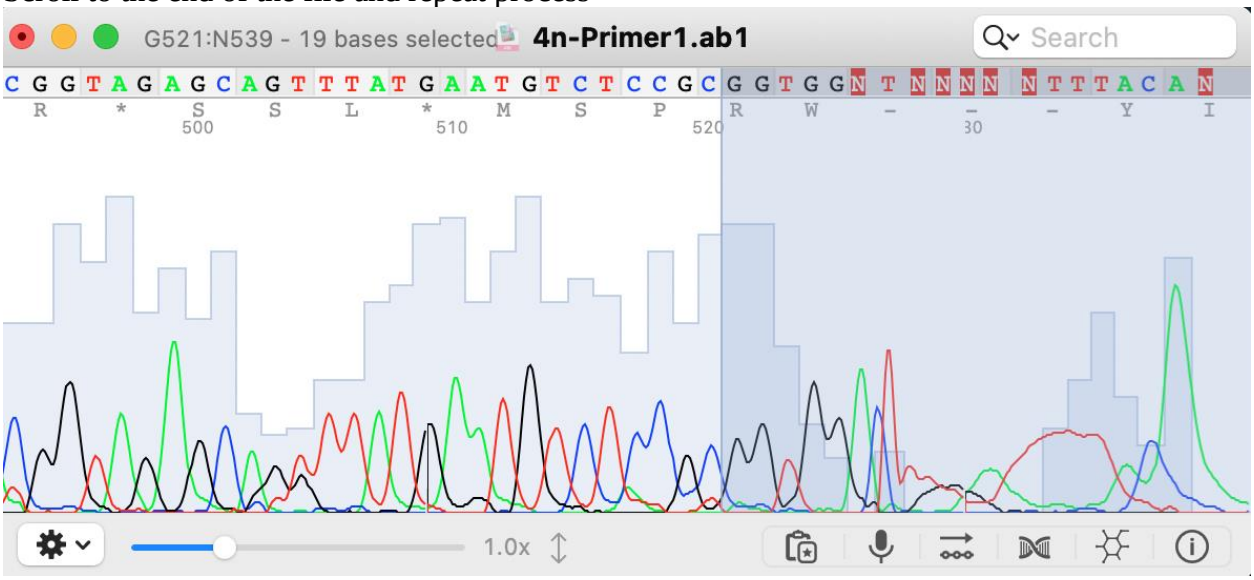
Scroll to the 50 base pair mark and check to see if the nucleotide peaks are more defined

Once you have defined a region to delete go to Edit→ Delete Selection



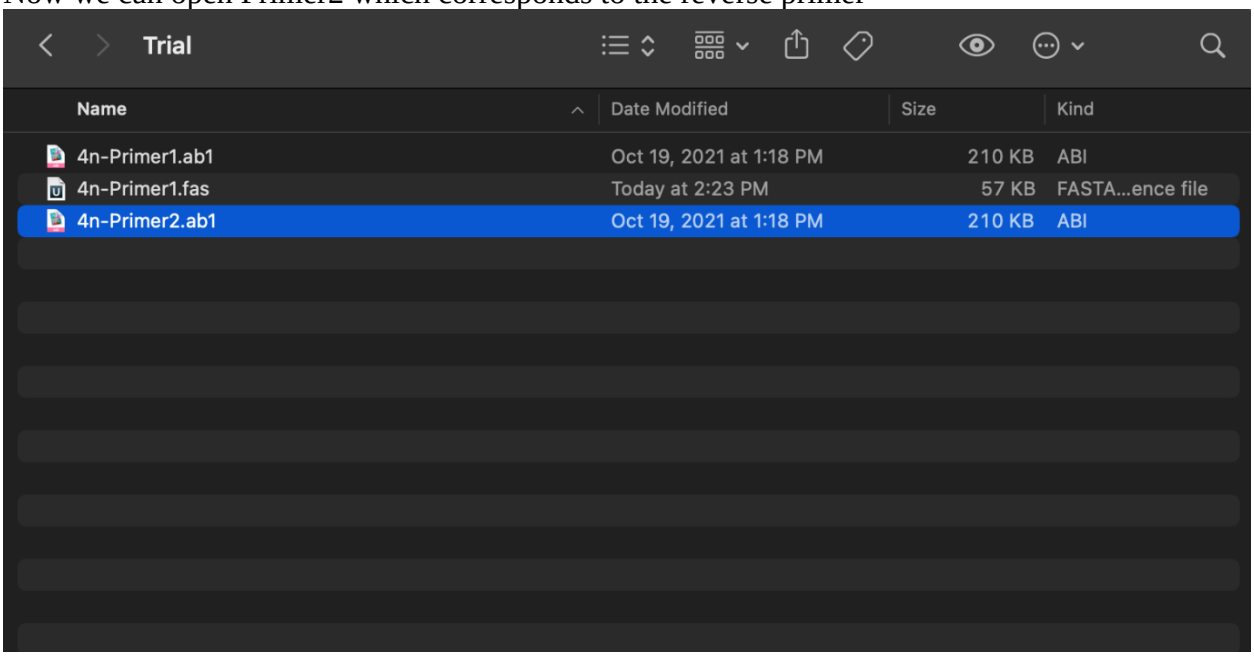
Section to be deleted

Scroll to the end of the file and repeat process

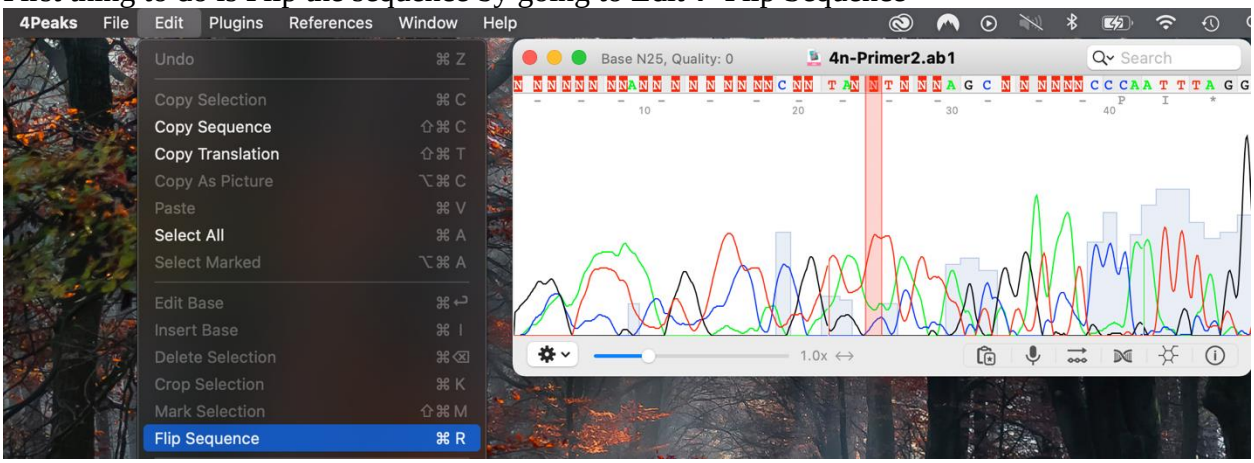


After trimming both the beginning and end of the sequence you can save as a ".fas" file

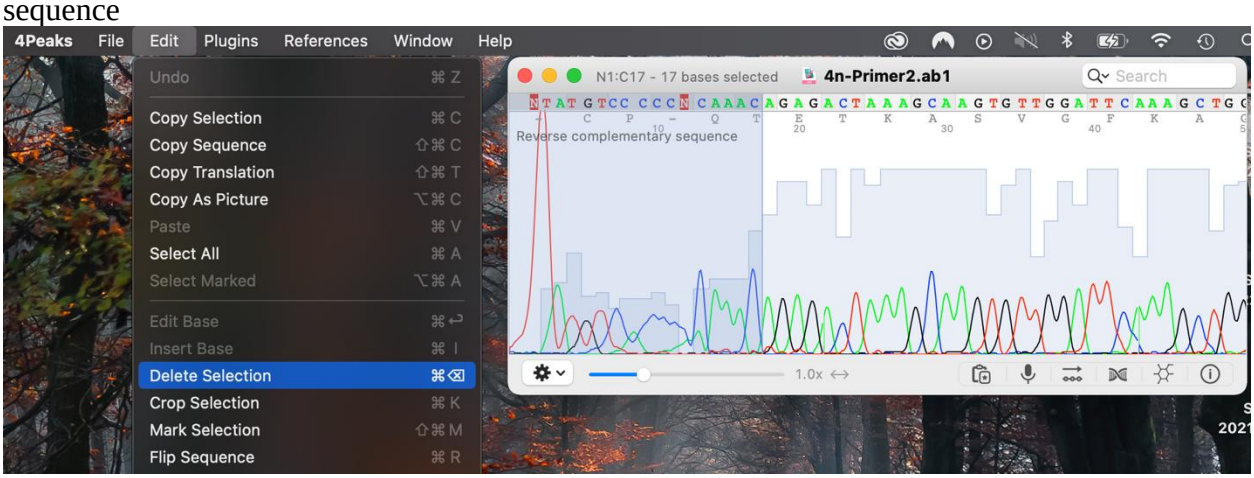
Now we can open Primer2 which corresponds to the reverse primer



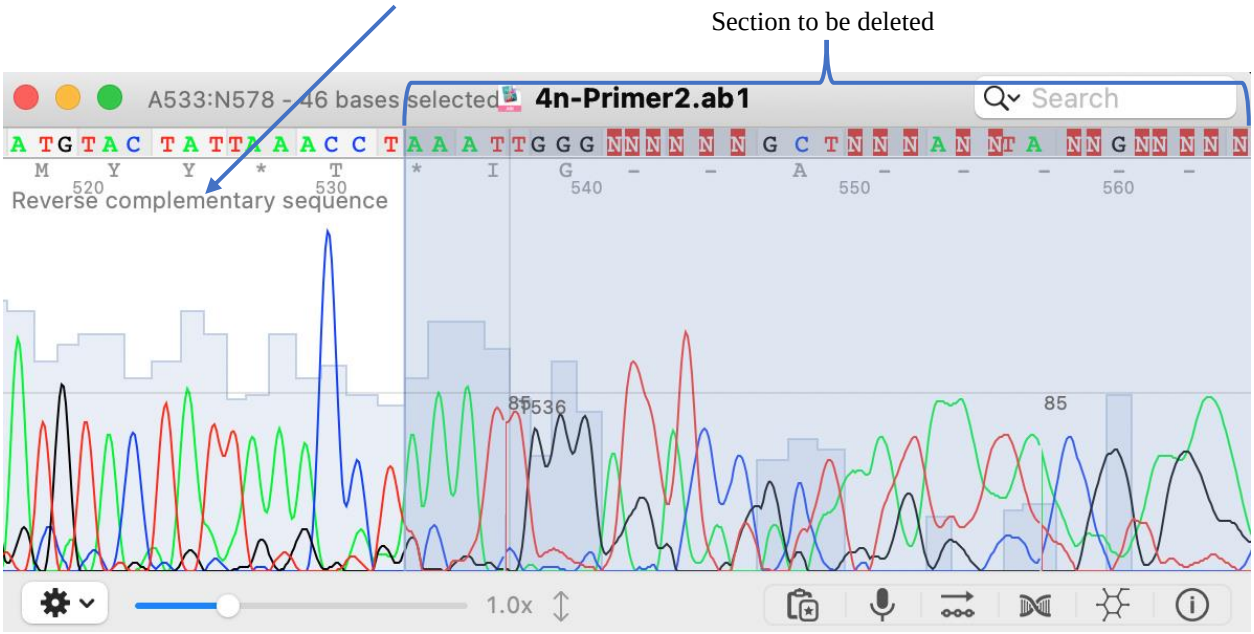
First thing to do is Flip the sequence by going to Edit→ Flip Sequence



Next you repeat the steps above to delete the section with poor quality for both sides of the sequence



You will also notice the software tells you after you have flipped the sequence that it is the reverse complementary sequence



After trimming you can also save this file in the ".fas" format.