## Using 4Peaks software to trim sequences

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First open Primer1 which corresponds to the forward sequence

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Name	A Date Modified	Size Kind
🧕 4n-Primer1.ab1	Oct 19, 2021 at 1:18 PM	210 KB ABI
🧕 4n-Primer2.ab1	Oct 19, 2021 at 1:18 PM	↑ 11 KB ABI

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  $\text{Edit} \rightarrow$  Delete Selection





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

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🧕 4n-Primer1.ab1	Oct 19, 2021 at 1:18 PM	210 KB ABI
😈 4n-Primer1.fas	Today at 2:23 PM	57 KB FASTAence file
4n-Primer2.ab1	Oct 19, 2021 at 1:18 PM	210 KB ABI

## First thing to do is Flip the sequence by going to $Edit \rightarrow Flip$ Sequence

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

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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.