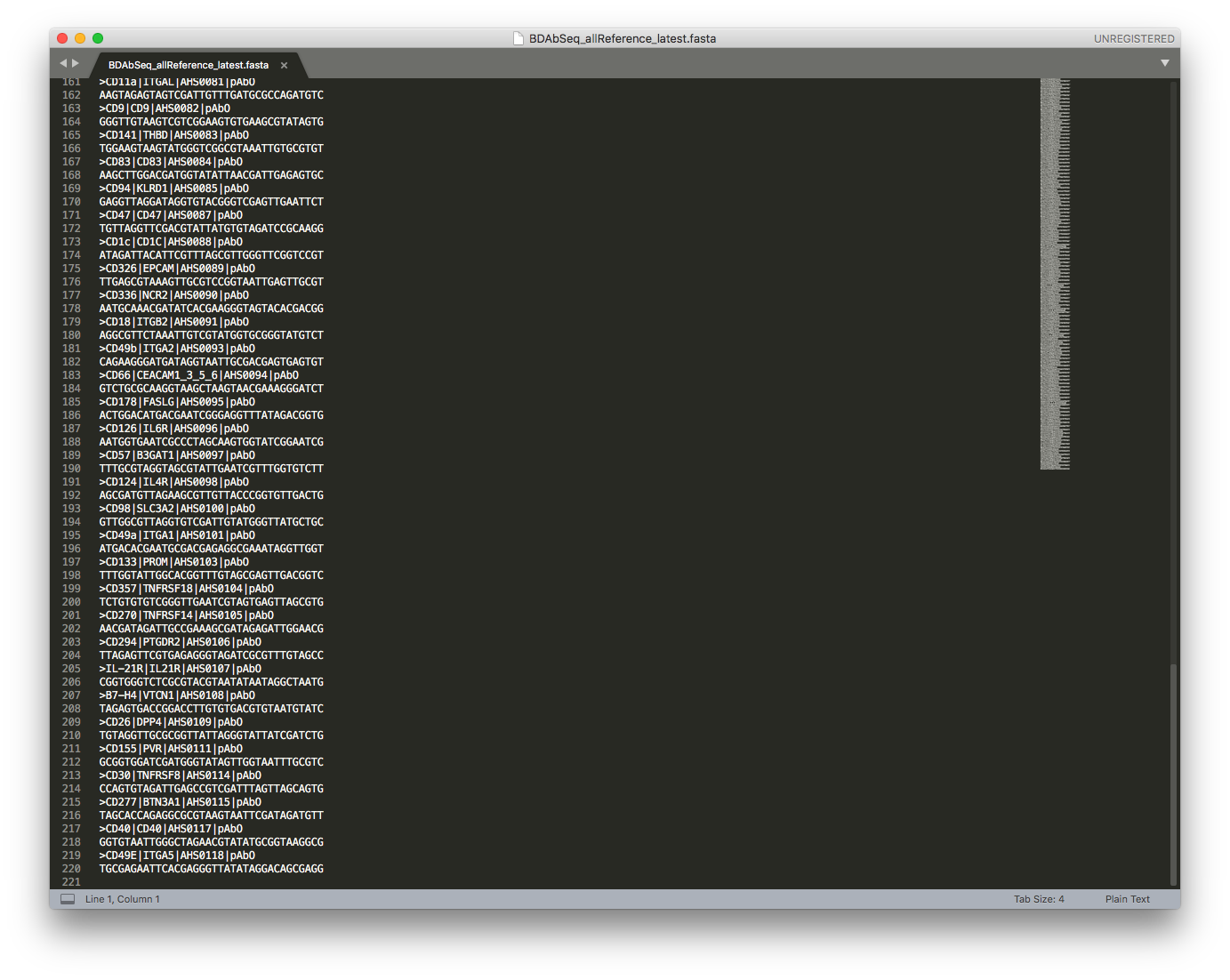
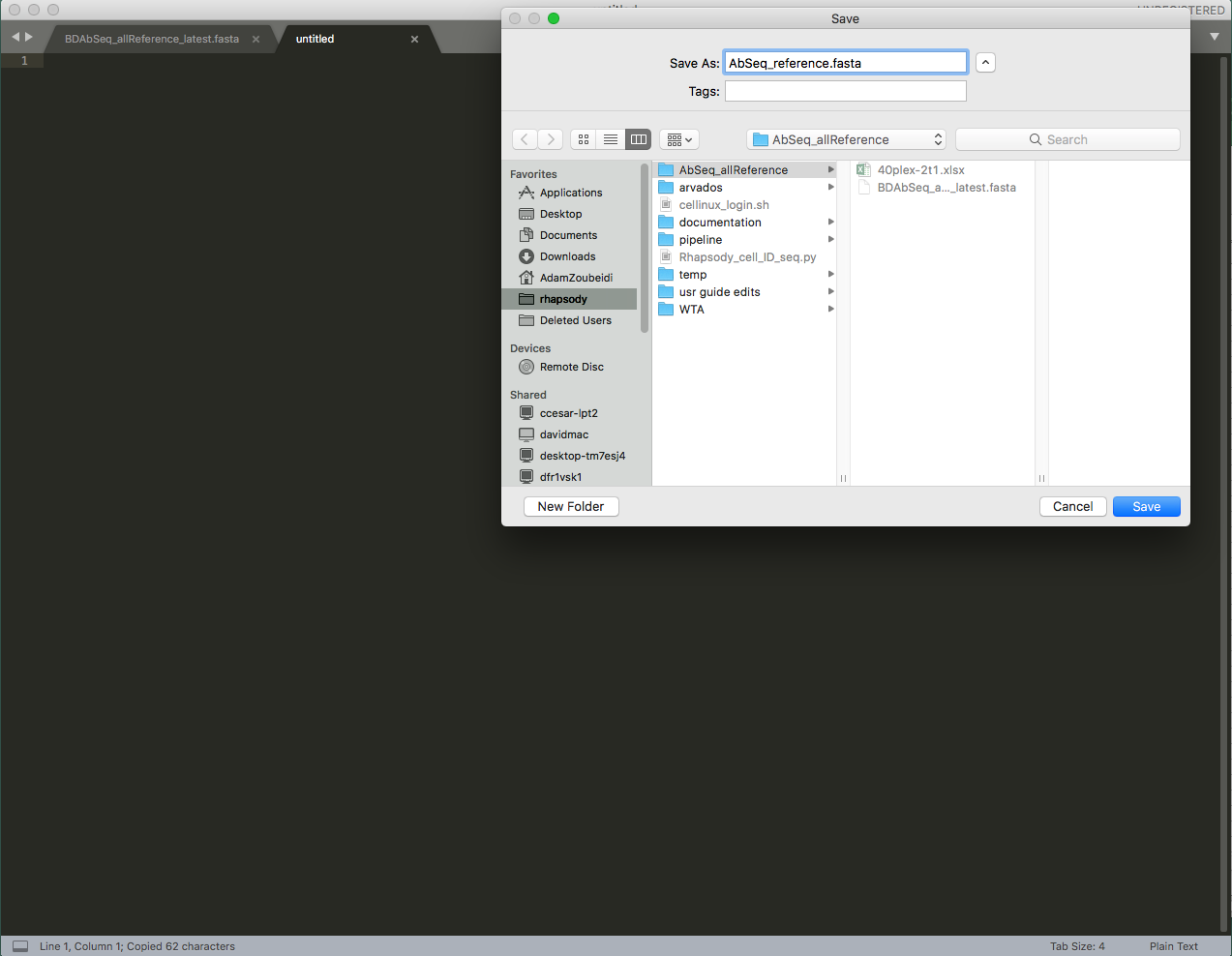
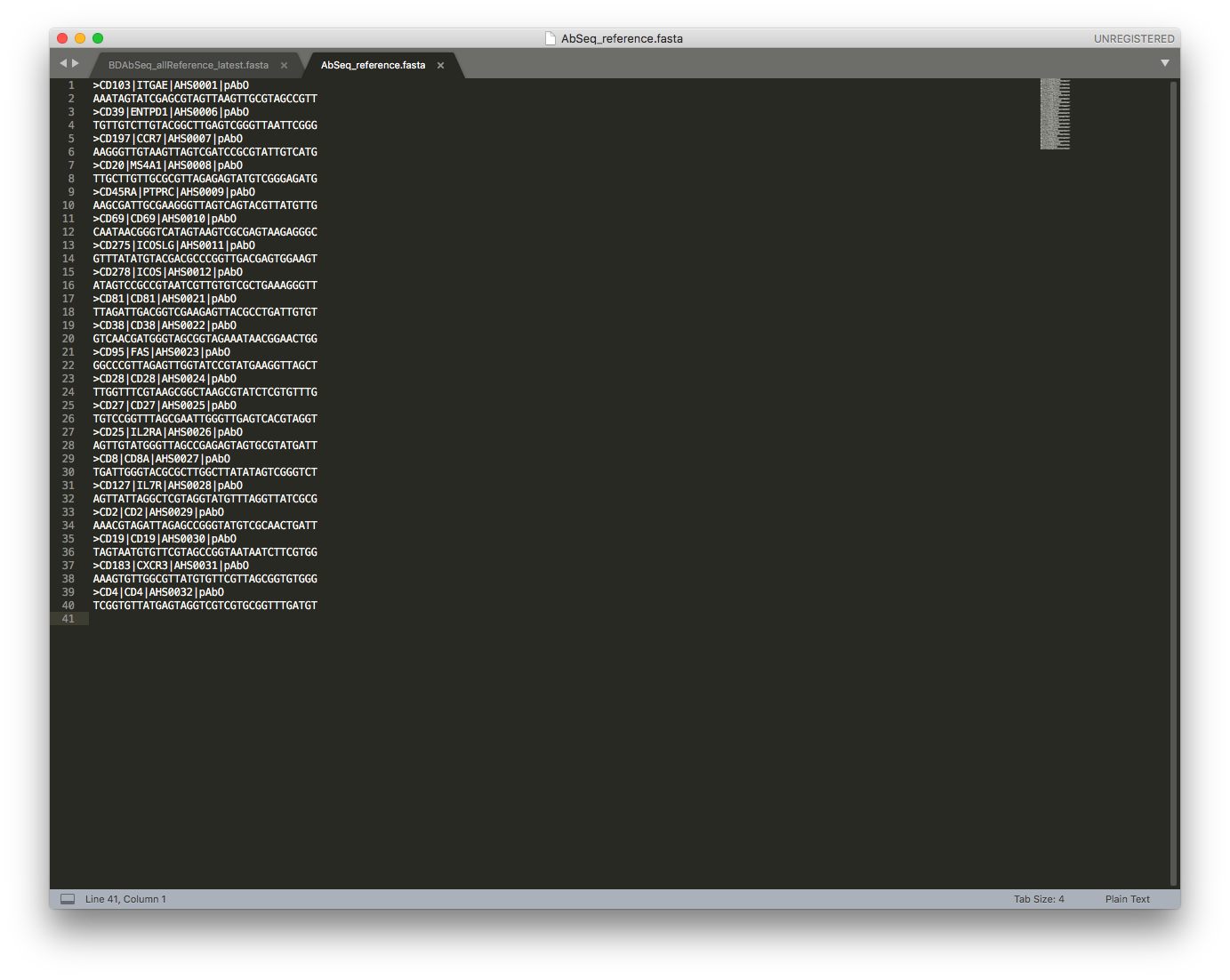


**Creating a BD™ AbSeq assay reference file**

1. Using a text editor, such as Notepad on Microsoft® Windows®, TextEdit on macOS®, or Sublime Text, open the BD AbSeq master reference file. Do not use Microsoft Word or any other word processor.

The master reference file can be downloaded from this [link](http://bd-rhapsody-public.s3-website-us-east-1.amazonaws.com/%20AbSeq-references/BDAbSeq_allReference_latest.fasta.), or from the *BD Single Cell Genomics Analysis Setup User Guide*, Doc ID 47383. Contact us at [SCOMIX@bd.com](mailto:SCOMIX@bd.com) for a copy of the file if you run into any issues with the download. The following is an example of the master file opened in Sublime Text editor.

1. Open a new file in the text editor and save it with the extension .fasta. The following screenshot shows a sample title of *AbSeq\_reference.fasta*. 
2. Locate each BD AbSeq file used in the experiment within the master list. Copy the full header line (starting with >) and its barcode sequence from the master list into the newly created .fasta file. The following example shows 20 AbOligos used. 
3. If custom sequences were used, add the antibody name to the header of the custom sequence to correspond with your targets.

The custom sequence in the reference file has no target associated with it and looks like this:

>ACU7001|pAbO

TTGCGATAGGTTACCAGGATGTGCGGATAGTTACTT

Add the target immediately after the “>” character and insert a vertical bar, “|” immediately after like this:

>CD1234|ACU7001|pAbO

TTGCGATAGGTTACCAGGATGTGCGGATAGTTACTT

This ensures that CD1234 will show up in the output files of the pipeline.

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