

Renaming Files in a Folder from the Bash Command Line: Removing the first Eight Characters of Every File Name

Introduction:

Sometimes it is useful to be able to rename many files at once. For example, our Sanger sequencing chromatograms come back with eight characters added to the front of the sample name that represent the position of the specimen in the 96 well sequencing plate. For example, note the first eight characters in blue in the following file name:

```
A01_hvs_22-042_MiFishU-F_7267059_015.ab1  
A02_hvs_Pleco-101_MiFishU-F_7267059_016.ab1
```

These eight characters (**A01_hvs_**, **A02_hvs_**, etc.) are not helpful and should be removed. The program below does this from the BASH command line.

If working from a PC, you can open Rstudio and click on the terminal pane in the bottom left window. Then navigate to the folder with your files using the "cd" command. Once there, apply the following code:

Code:

```
# Check if it is a file  
if [ -f "$file" ]; then  
  
# Create a new filename by removing the first eight letters  
new_file="${file:8}"  
  
# Rename the file if the new filename is different  
if [ "$file" != "$new_file" ]; then  
mv "$file" "$new_file"  
echo "Renamed '$file' to '$new_file'"  
fi  
fi  
done
```

Result: The result will be something like:

```
22-042_MiFishU-F_7267059_015.ab1  
Pleco-101_MiFishU-F_7267059_016.ab1
```

And so on for the rest of the files.