**How to generate Krona plot from ‘OTUs, reads and taxonomic assignments.tsv’ file available on the Download tab for runs on EBI Metagenomics website**

* Download and install Krona tools (<https://github.com/marbl/Krona/wiki>)
* Download the OTUs, reads and taxonomic assignments.tsv file

Its content looks like this :

# Constructed from biom file

#OTU ID ERR2042073 taxonomy

4333897 2 k\_\_Bacteria; p\_\_Proteobacteria; c\_\_Gammaproteobacteria; o\_\_Enterobacteriales; f\_\_Enterobacteriaceae; g\_\_; s\_\_

1868703 7 k\_\_Bacteria; p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_; s\_\_

364538 3 k\_\_Bacteria; p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Bacteroidales; f\_\_Porphyromonadaceae; g\_\_Dysgonomonas; s\_\_

198190 83 k\_\_Bacteria; p\_\_Bacteroidetes; c\_\_Bacteroidia; o\_\_Bacteroidales; f\_\_Porphyromonadaceae; g\_\_Parabacteroides; s\_\_distasonis

199501 2 k\_\_Bacteria; p\_\_Firmicutes; c\_\_Clostridia; o\_\_Clostridiales; f\_\_Lachnospiraceae; g\_\_Blautia; s\_\_ …

* We need to transform the file to keep the count (2nd column) and lineage (3rd column) then split the lineage with tabs and remove the k\_\_ prefix.

The resulting file should be:

# Constructed from biom file

ERR2042058 taxonomy

1.0 Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae Blautia

4.0 Bacteria Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae Dysgonomonas

117.0 Bacteria Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae Parabacteroides distasonis

This can be done using any text editor.

Using unix, this can easily be done using one line of command:

cat ERR2042058\_MERGED\_FASTQ\_otu\_table.txt | sed 's/; /;/g' | cut -f 2,3 | sed 's/;/\t/g' | sed 's/.\_\_//g' > ERR2042058\_post\_filtering.txt

* Finally run Krona to generate the html file:

KronaTools-2.3/bin/ktImportText ERR2042058\_post\_filtering.txt -o ERR2042058\_post\_filtering.html