RNA-seq hands-on tutorial using Chipster: Convert read count table to Chipster format
Eija Korpelainen and Maria Lehtivaara, CSC – IT Center for Science, chipster@csc.fi

In this tutorial you learn how to
-import a read count table
-convert it to Chipster format and create a phenodata for it

The read count table is available here:
https://drive.google.com/drive/folders/1nxttUDKPdFLbQxEV7JtxPLN3I4PJt3tF.
It contains RNA-seq counts from 7 samples from two human cell lines.
-3 GM12892 samples (marked with GM)
-4 H1-hESC samples (marked with hESC)
Download the table to your computer.

1. Create a new session
Click the **Sessions info** tab and then the button **New session**. Give your session a name and click **Create**.

2. Import the count table
Click **Add file** and select **Upload file(s).** Select the count table file from your computer. Wait that the upload is completed. Click **Close**. Click on the file to view it as a **Spreadsheet**. Can you see the identifier column and the sample count columns? Are there some additional columns?

3. Convert table to Chipster format and create a phenodata to describe the experiment
Select the file and click on the **three dots** next to the file name. From the menu, select **Convert to Chipster format**.
-Click on the **Identifier column** text box and select the correct column by ticking the box.
-Click on the **Sample columns** text box and press the button **Select all**. Remove then the columns that do NOT contain read counts (chr, start, end, length, sequence).
Scroll in the preview above to make sure that the correct columns were selected. Click **Convert**.

4. Check the new file and fill in the phenodata for it
Select the new file **countsFrom7samples-converted.tsv** and inspect it in the **Spreadsheet** view. How does it differ from the original one?
Indicate the experimental groups in the **Phenodata**:
-sort phenodata by clicking on the Description column
-type 1 in some text editor (e.g. Notepad) and it for all the GM samples. Enter 2 for all the hESC samples in the same way.