EUTOS CF Spreadsheet v030322 Instructions for use

The spreadsheet has been produced to help laboratories calculate conversion factors using either sample exchange methods or secondary reference materials. The calculation is based on the linear regression approach suggested by the NIBSC (https://www.nibsc.org/documents/ifu/09-138.pdf; pdf document attached as supplementary material).

PLEASE NOTE THAT THE SPREADSHEET IS NOT CE MARKED OR OTHERWISE CERTIFIED. IF YOU USE IT TO DERIVE CONVERSION FACTORS FOR CLINICAL USE THEN YOU ARE RESPONSIBLE FOR ENSURING THAT THE RESULTS ARE CORRECT.

1. Enter the known BCR::ABL1^{IS} value of the reference sample into column A starting in cell A2. The data can be pasted from another spreadsheet

2. Add the corresponding **unconverted** %BCR::ABL1/reference gene value obtained from your analysis of the reference sample into column B starting in cell B2. The data can be pasted in from another spreadsheet

IMPORTANT: these values should be calculated with NO conversion factor applied.

3. The spreadsheet allows you to add up to 180 paired values.

Do not edit or move the data once they have been added to the sheet. If you need to delete or move data then start a new spreadsheet.

Do not manipulate the sheet in any way.

Once all the data are added the **conversion factor** will be displayed in **cell I1**

Three quality parameters are also shown:

1) Lower 95% confidence interval of the slope (I11).

2) Upper 95% confidence interval of the slope (I12).

3) R^2 (I14).

Cells I11, I12 and I14 will appear green if the data are linear and show no bias. The 95% confidence interval of the slope must be fully contained within the range 0.83 - 1.20 and the R^2 should be >0.97. If the cells appear red then it may be helpful to visualise your data to see where any issues are occurring. For a visual representation of the data the log10 transformed BCR::ABL1^{IS} reference values can be plotted against the corresponding log10 transformed %*BCR::ABL1* / reference gene (laboratory derived non-IS) using the Chart function in Excel.

If you have an existing CF the newly derived CF can be validated using the following criteria:

Optimal (+/- 1.2 fold):   Old CF / New CF = 0.83 – 1.2

Satisfactory (+/- 1.6 fold):   Old CF / New CF = 0.63 – 1.58

Unvalidated: Old CF / New CF <0.63 or >1.58

White HE et al. Standardization of molecular monitoring of CML: results and recommendations from the European Treatment and Outcome Study. Leukemia 2022