The data had been already processed and filtered as explained in Eisele et al

The data is presented as a matrix with the barcode that matched the reference library list in rows and the sample in columns. The data has been renormalized per column to 10^5 reads before filtering.

The names of the samples are as follow= var.Totalreads.name of the experiment\_dose\_mouse number\_cell type\_replicate

Ex: var.Totalreads.AE4\_LOW\_1\_MPP4\_a is the data for the experiment AE4 with the lower dose of EPO for the replicate a of MPP4 in mouse 1.