

This folder contains the necessary files and R scripts needed to carry out cellular deconvolution of whole blood gene expression profiles to generate inferred neutrophil, lymphocyte, monocyte, and eosinophil counts using the CIBERSORTx source code under the same settings used in the Technical Validation section of O'Connell et al. Note that the CIBERSORTx source code is the property of Stanford University, and thus, we cannot share it here. However, it can be directly requested from its authors at <https://cibersortx.stanford.edu>.

We slightly modified the CIBERSORTx source code for use in our analyses to allow for the direct passage of matrix objects to the CIBERSORT() function as input, as opposed to reading in .txt files as originally written. *cibersort\_source\_code\_modification.r* contains the lines of modified code.

*cibersort\_deconvolution\_script.r* contains the R script used to carry out deconvolution using the modified CIBERSORTx source code. *cibersort\_reference\_signature\_matrix.csv* is the reference signature matrix used for deconvolution, which was originally generated via the CIBERSORTx java application as described in the *project-007/cibersort\_deconvolution/java\_application* folder of this repository. *whole\_blood\_raw\_counts.csv* is an abbreviated example input file illustrating the format whole blood RNA sequencing data should be provided in. Data should be in the form of gene-level summarized read counts. The exact RNA sequencing data used for the analyses presented in the manuscript can be retrieved from the National Center for Biotechnology Information via BioProject accession number PRJNA949611.