This repository contains the necessary files and annotated R scripts needed to carry out the various example analyses presented in the application notes of O'Connell et al.

The *project-007/cibersort_deconvolution* folder contains the files and script needed to carry out cellular deconvolution of whole blood gene expression profiles using CIBERSORTx under the same settings used in the manuscript, either via R or the java application.

The *project-007/pca_deconvolution* folder contains the files and script needed to carry out PCA-based cellular deconvolution of whole blood gene expression profiles using the WBC4.126 marker gene list under the same settings used in the manuscript.

The *project-007/deconvolution_pipeline_comparision* folder contains the files and script needed to carry out the benchmarking comparison of PCA-based and CIBERSORT-based cellular deconvolution of whole blood gene expression profiles presented in the manuscript.

The *project-007/differential_expression_analyses* folder contains the files and script needed to perform the various cell count corrected and uncorrected whole blood gene expression comparisons between Hispanic and non-Hispanic donors presented in the manuscript.

Each folder and subfolder contains a README file detailing the contents.