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File	Description
LM22 (txt)	LM22 Signature genes file
LM22 ref (txt)	LM22 Reference sample file
LM22 classes (txt)	LM22 Phenotype classes file
Tutorial Example Mixtures (txt)	Example mixtures file used in the tutorial.
Tutorial Example Ground Truth (txt)	Ground truth of the cell subset fractions in the example mixtures used in the tutorial.
R script - convert CEL to mixture file	For Affymetrix data, this R script can be used to convert raw CEL files into a custom CDF normalized expression dataset that is compatible with CIBERSORT.

> Notes on usage....
> - customCDF should be downloaded from BrainArray (http://brainarray.mbni.med.umich.edu/Brainarray/Dat
>   (Entrez Gene Identifiers Only). Entrez v12.1.0 for HGU133A, along with
>   v18 for HGU133A and HGU133Plus2.0 are provided above.
> - To install, do not gunzip. Use following command
>   (using hgu133plus2.0 v18 as an example, in a Linux environment):
>
>   ```
>   sudo R CMD INSTALL hgu133plus2hsentrezgcdf_18.0.0.tar.gz
>   ```
>
> - Change cdfname in the provided R script if chipset is different
> - Choose mas5 or rma normalization
>   (mas5 is default and rma is commented out)
> - Make sure Bioconductor is installed in R
>   (need affy, annotate, and org.Hs.eg.db packages)
> - Navigate to directory containing CEL files and run R script

File	Description
CustomCDF v12.1.0 (gzipped tar)	BrainArray CustomCDF Entrez v12.1.0 for HGU133A (used in Newman et al.)
CustomCDF v18.0.0 (gzipped tar)	BrainArray CustomCDF Entrez v18 for HGU133A
CustomCDF v18.0.0 (gzipped tar)	BrainArray CustomCDF Entrez v18 for HGU133Plus2.0
Download CIBERSORT software package (zip) Access expires in: 13 day(s) 6 hr 3 min	The CIBERSORT software package which includes the java executable for CIBERSORT, software license, documentation and example files (also available separately below). Note: requires R. Linux environment strongly recommended. Details in documentation.
Download CIBERSORT source code Access expires in: 13 day(s) 6 hr 3 min	The CIBERSORT software source code in R, available to academic users and subject to the software license. Commercial users should email (mailto: cibersort@gmail.com) the CIBERSORT team to inquire commercial licensing options.
GSE11103 Matrix (pure) (txt)	Example Abbas et al. (GSE11103) pure file
GSE11103 Matrix (mixture) (txt)	Example Abbas et al. (GSE11103) mixture file
GSE11103 Matrix (classes) (txt)	Example Abbas et al. (GSE11103) class file
GSE11103 Matrix (sig genes) (txt)	Example Abbas et al. (GSE11103) signature genes file
Abbas tumor + noise (txt)	Example Abbas et al. mixtures with added tumor content and noise
Abbas Jurkat spike (txt)	Example Abbas et al. mixtures with Jurkat spike and added tumor content
Fig 3a PBMCs Gene Expression	Illumina PBMC transcriptomes as described in Figure 3a of the CIBERSORT manuscript.
Fig 3a PBMCs Flow Cytometry	Accompanying Flow Cytometry data for the Illumina PBMC transcriptomes as described in Figure 3a of the CIBERSORT manuscript.

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