



mapMECFS

Data Generation: Summary

Dataset Name

**ME/CFS case-control study following exercise RNA expression
GSE128078**

Submission Details

Summary about the dataset submission associated with this document.

*Submitter name	<i>RTI International</i>
*Submitter email address	<i>mapMECFS@rti.org</i>
*Submitter institution	<i>RTI International</i>
*Upload date	<i>9/16/19</i>
Version of uploaded file (default= v1.0)	<i>v1.0</i>
Reason for resubmission (if applicable)	<i>Public ME/CFS data</i>

Technical Details

Summary of the omic technology along with processes to generate the submitted data.

*Features measured in the uploaded file	<i>Normalized RNA Expression</i>
Number of Features Measured	<i>43,497 transcripts</i>
*Instrument generating raw data	<i>Illumina HiSeq 2000</i>
*Software/pipeline used to generate uploaded feature data	<i>Tophat 2/ Cufflinks 2</i>
Reference database used to generate/annotate feature data	<i>hg19 (GRCh37)</i>

* required

Enter 'N/A' or 'Unknown' for not applicable or unknown entities

Experimental Details: Study Level

Summary of the study design.

*Phenotype of interest	Females meeting Canadian 2003 criteria
Control Phenotype	controls were matched by age, gender (female only), ethnicity
*Time series /Longitudinal data?	No
*Repeated measures?	Yes, each subject contributed 4 samples at 4 different time points (days 1, 2, 3, and 7). Day 1 and day 2 were within 2 hours prior to each exercise test and day 3 and day 7 during home visits.

Experimental Details: Subject Level

Summary of the subjects in the study. Please add/modify columns to accommodate other demographics, classifications, or time series/longitudinal data.

Descriptor	Total	Cases	Controls
*Sample size	25	14	11
Age in years (median, IQR)		49 (38, 58.3)	50 (45.5, 58.5)
% Female	100%	100%	100%
Race/Ethnicity	NR	NR	NR

NR=not reported

Experimental Details: Sample Level

Summary of the samples collected and analyzed.

* required

Enter 'N/A' or 'Unknown' for not applicable or unknown entities

*Sample type	<i>Blood</i>
*Collection Method	<i>Whole blood collected with PAXgene Blood RNA Tub (QIAGEN)</i>
Isolation and or preparation method	<i>Total RNA extracted using PAX gene Blood RNA Kit (QIAGEN)</i>
*Lab performing sample isolation/preparation	<i>University of British Columbia</i>
Sample storage	<i>All samples were lyophilized in RNastable reagent (Biomatrica, San Diego, CA)</i>
Storage facility	<i>University of California, San Francisco</i>
Scan protocol	<i>NA</i>
Validation methods	<i>NA</i>
Technical Replicates	<i>NA</i>
Batch	<i>No spike-ins used but batch effects were tested via PCA. None identified.</i>

* required

Enter 'N/A' or 'Unknown' for not applicable or unknown entities



Data Generation Details

This section is intended to assist users of this dataset in understanding the protocols and analyses that have been conducted on the dataset.

All details are described in the corresponding publication (below) and GEO Accession View for GSE128078.

Bouquet J, Li T, Gardy JL, Kang X et al. [Whole blood human transcriptome and virome analysis of ME/CFS patients experiencing post-exertional malaise following cardiopulmonary exercise testing](#). *PLoS One* 2019;14(3):e0212193. PMID: [30897114](#)

* required

Enter 'N/A' or 'Unknown' for not applicable or unknown entities