a. IWGCNA steps

1. Construct a co-expression network and modules

2. Find clinical trait related modules

3. Prioritize module genes using disease-related SNP

4. Use the integrated model to screen for genes

5. Determine causal drivers of module

b. CFS Patients analyzed in IWGCNA steps

1. Full data set: 127 CFS patients

2. Primary data set: 87 patient subset with CFS severity scores

   Exclude heterogeneous female samples

3-5. 76 samples with CFS severity scores

Repeat steps 1-5 using secondary data set (33 patients)