

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)

