**SUPPLEMENTAL INFORMATION**

**Supplemental Results.** Additional results including figures and tables that support the main text.

**Additional File S1.** All enrichment analyses for Gene Ontology biological process and molecular function categories. Includes all enrichment results with five or more genes in the category and with an enrichment p ≤ 0.01 (no multiple test correction), and Swissprot identifiers within the category.

**Additional File S2.** Overview table for female and male modules, including module size, trait association, GO enrichment, preservation Zsummary and medianRank, and cross-tabulation results.

**Additional File S3.** Differential expression results for the sex-bias analysis, including log2 fold change values, p-values, identifiers and gene descriptions when available.

**Additional File S4.** Transcripts and module assignment in the female network along with Gene Significance and Module Membership values.

**Additional File S5.** Transcripts and module assignment in the male network along with Gene Significance and Module Membership values.

**Additional File S6.** Estimated counts file from eXpress used as input for network and differential expression analyses before low expression filtering and normalization.

**Additional File S7.** Interpretation file providing all phenotypes for each sample, used in the analysis pipeline.