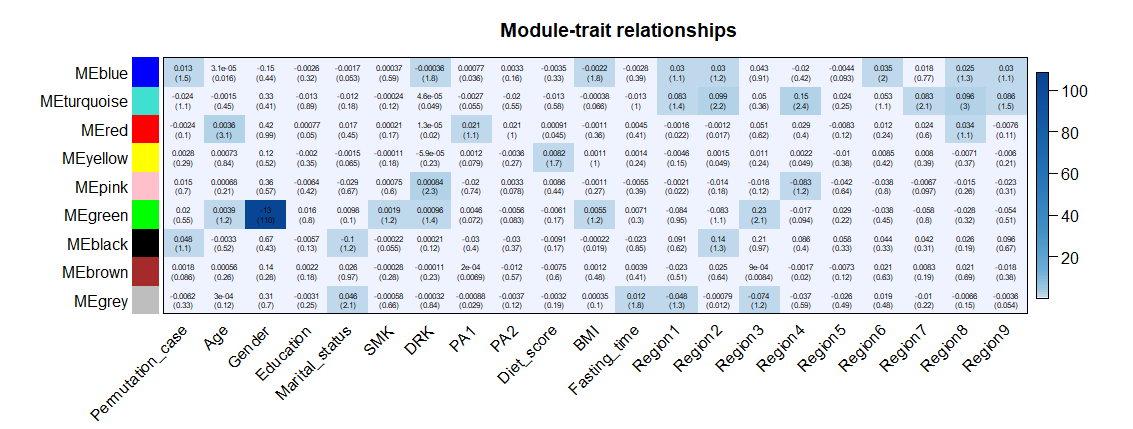
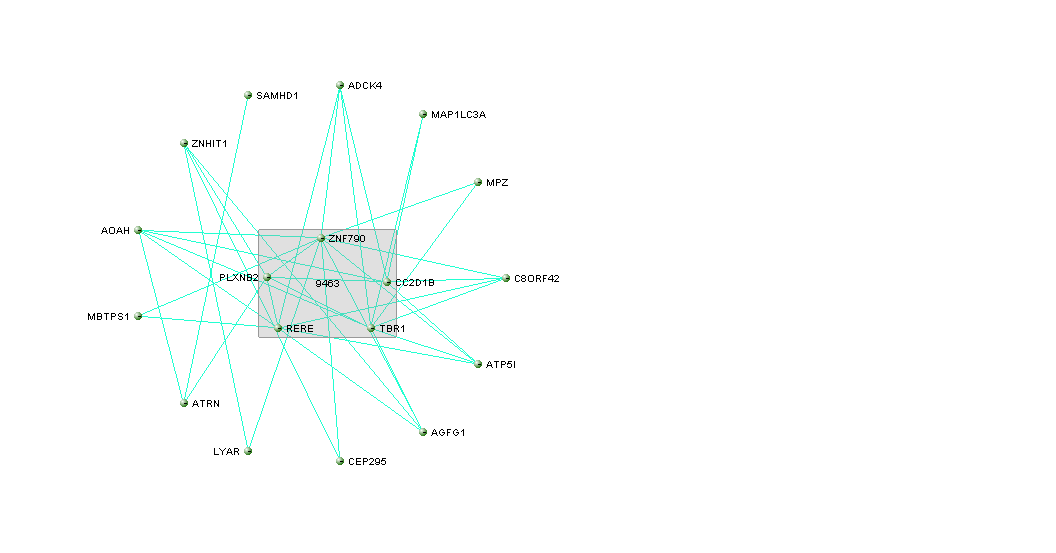
**Figure 2– figure supplement 1. Permutation test to confirm the validity of weighted gene co-methylation network analysis.**

Correlation coefficient and -log10(P) (inside the bracket) were reported; the degree of -log10(P) is illustrated with the color legend. Linear regressions were fitted with inverse normal transformed module eigengene (ME) as dependent variables; shuffled case and control status (Permutation\_case) as indicator; and age, sex, education, smoking (SMK), drinking (DRK), physical activity (PA1 and PA2 as the second and third tertile respectively), diet score, body mass index (BMI), fasting time, study area and all surrogate variables as covariates.

**Figure 2– figure supplement 2. Visualization of the brown module.**

Genes in the center are the hub genes, pairwise correlation: 0.10 to 1.