Figure S3. Epigenome-wide association *p*-value distribution

A

All clinical traits
EWAS *p*-value distribution

B

OGTT insulin area under the curve
EWAS *p*-value distribution

C

OGTT insulin AUC
qq-plot

D

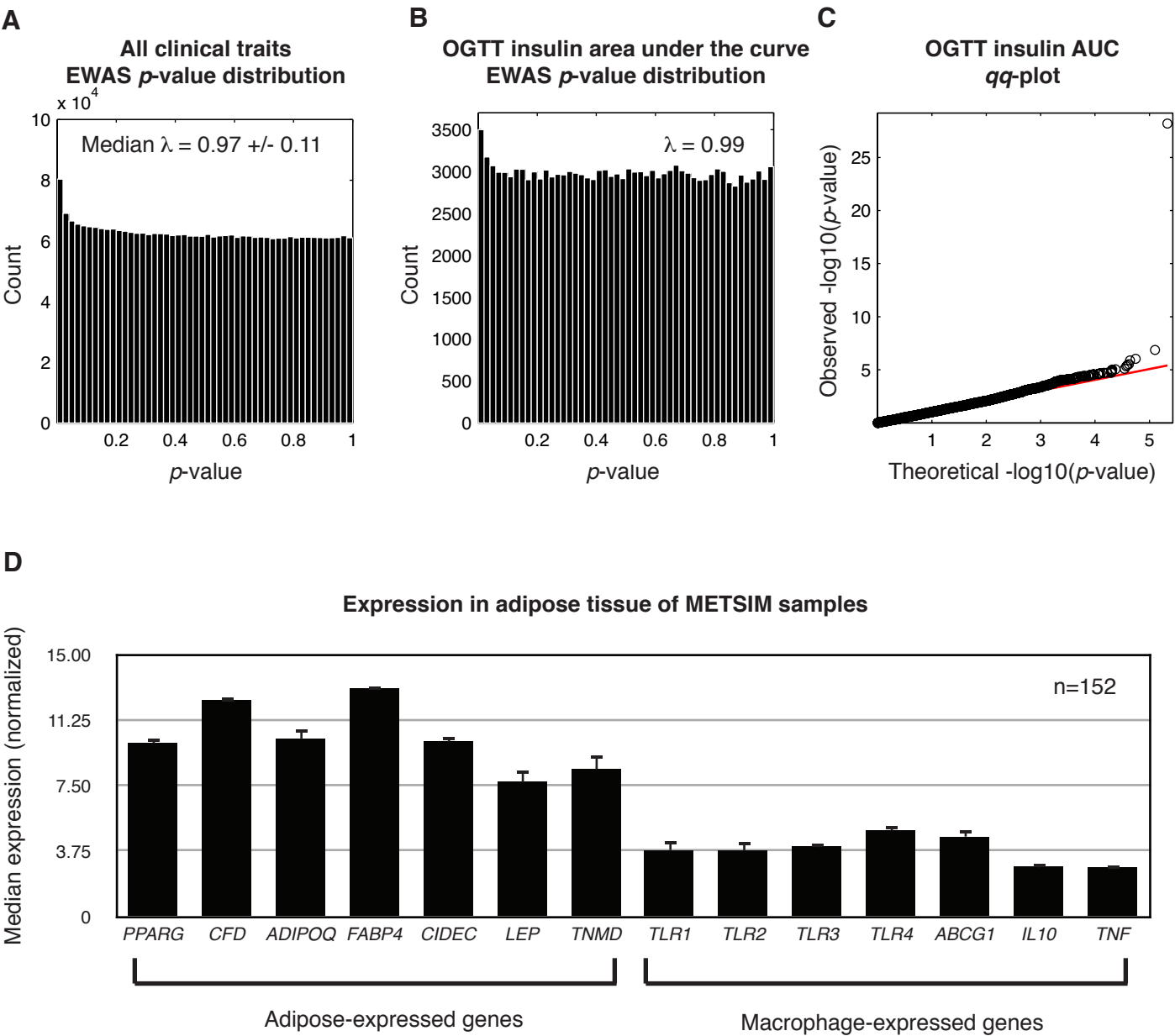### Expression in adipose tissue of METSIM samples

Figure S3. EWAS p-value distributions and expression of tissue specific genes. Histogram of the p-value distributions in the EWAS for (A) all clinical traits, and (B) oral glucose tolerance test area under the curve. (C) Q-Q plot between the theoretical uniform distribution (red) and the EWAS p-value distribution (black) for the trait oral glucose tolerance test area under the curve. (D) Expression levels in adipose tissue biopsies for samples where we have both methylation and expression data. The y-axis is the median expression across individuals, and the x-axis are genes known to be expressed in adipocytes or macrophages.