Figure S1. Weighted gene co-expression analysis (WGCNA). a) Cluster dendrogram showing how genes with similar expression levels cluster together. 11 modules were identified and assigned different colors. **b)** Heat map showing correlations between individual modules and clinical characteristics of depression measured in the TRD sample. The clinical features included are: age of illness onset, chronicity of illness (current episode lasting > 2yrs) (Yes/No), recurrence of major depressive episodes (Yes/No), psychiatric comorbidities (Yes/No), psychiatric hospitalizations (Yes/No), suicide attempts (Yes/No), baseline MADRS score. On the Y axis WGCNA modules by color (numbers in parenthesis indicating the number of genes per each module). * *p* < 0.01, *** *p* < 0.001.

Fig. S1