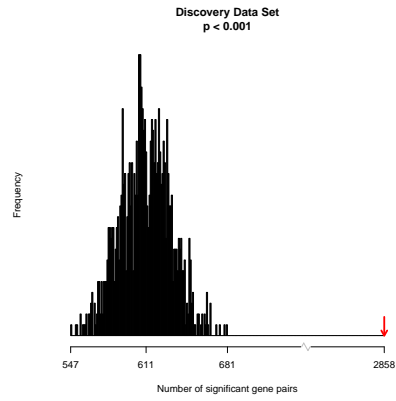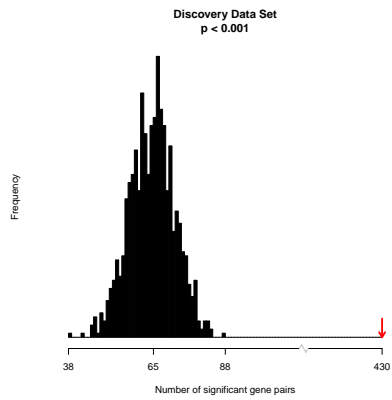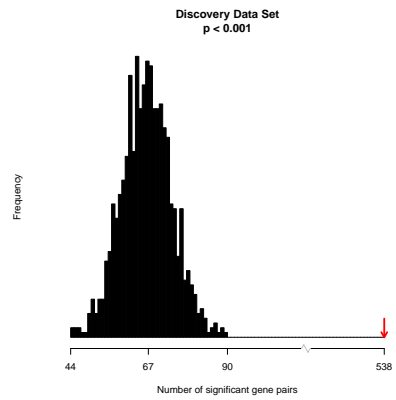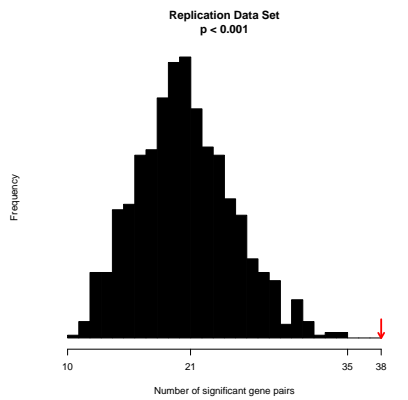(a) Pre-Tx (1044 genes)

(b) Post-Tx (1044 genes)
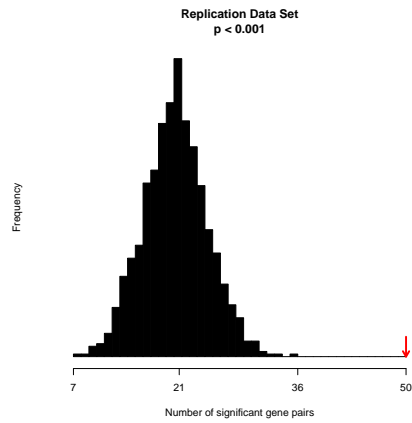
(c) Pre-Tx (263 genes)

(d) Post-Tx (263 genes)

(e) Pre-Tx (263 genes)

(f) Post-Tx (263 genes)

Additional file 1 — **Permutation testing for coexpression.** Permutation tests were designed to randomize the expression values for each gene, across samples, within each time point. After randomization, we calculated coexpression by the 1st-order Spearman's correlation coefficient. We counted the number of significant results ($\alpha = 0.001$) then repeated 1000 times to generate a null distribution. Arrows indicate the number of observed coexpression relationships for a given data set.