SUPPLEMENT FIGURES
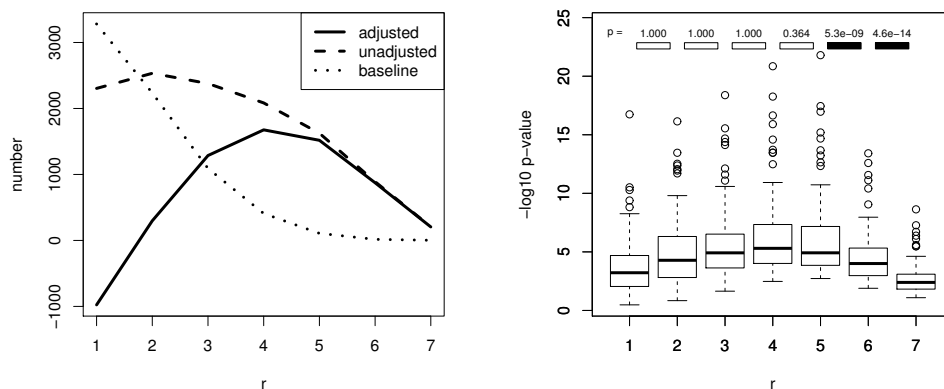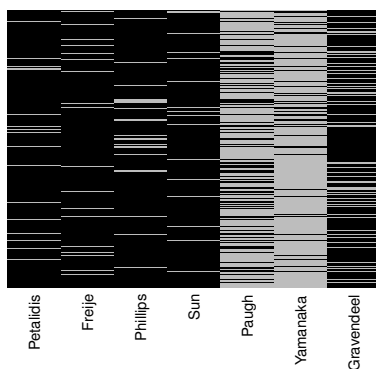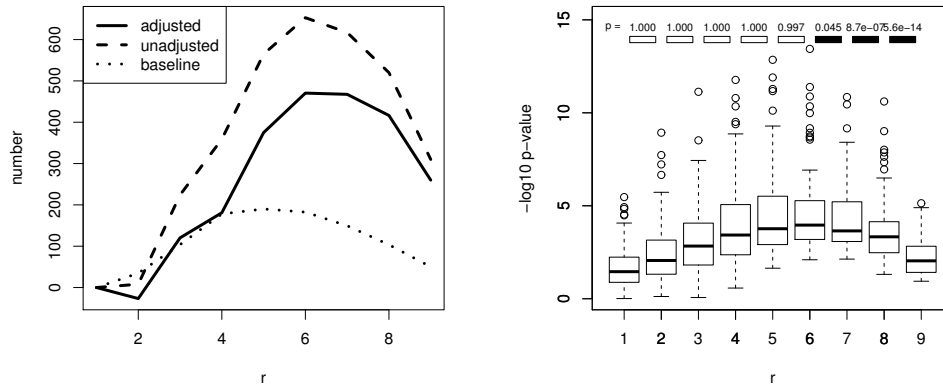

(a) Adjusted and unadjusted number of detected DE genes.

(b) Boxplots of $-\log(p)$ for the biological association evaluation.
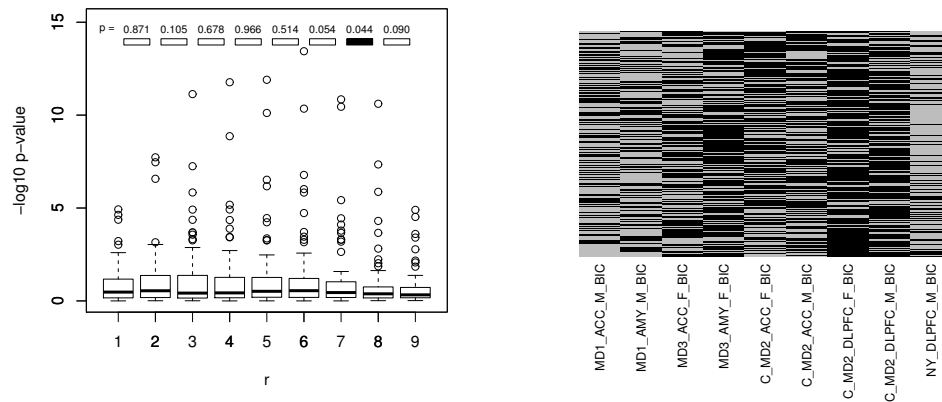

(c) Heatmap to show effective studies of rOP in each gene.

SUPPLEMENT FIGURE 1. Similar to Figure 1, results of brain cancer dataset using one-sided corrected rOP are shown.
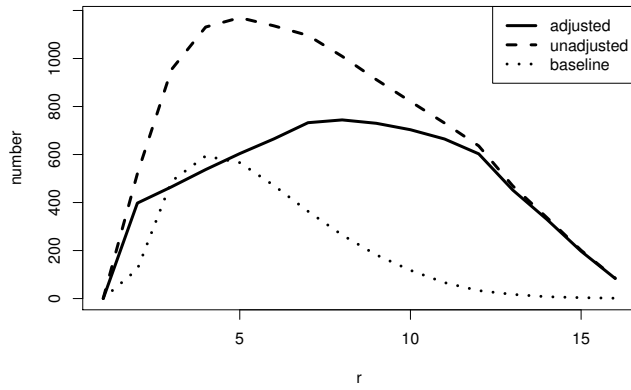
(a) Adjusted and unadjusted number of detected DE genes.

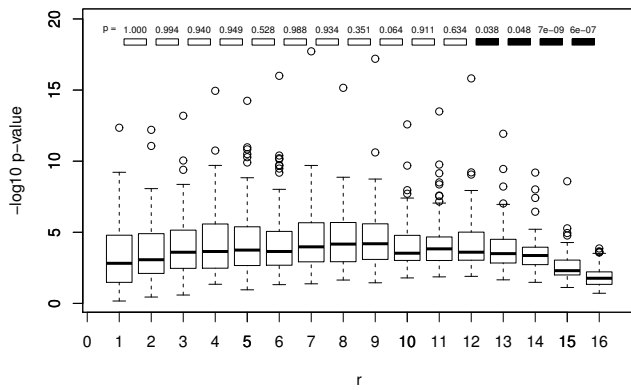(b) Boxplots of $-\log(p)$ for the biological association evaluation.

(c) Boxplots of $-\log(p)$ for the biological association evaluation using potentially related pathways.

(d) Heatmap to show effective studies of rOP in each gene.
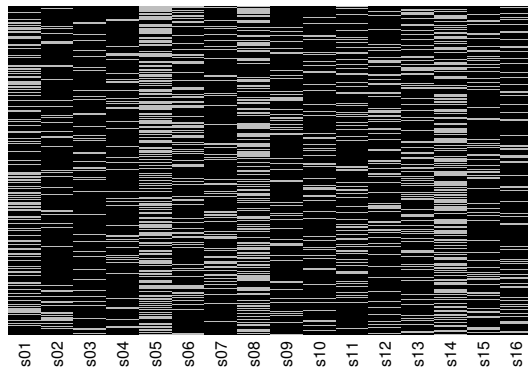
SUPPLEMENT FIGURE 2. Results of MDD dataset applying rOP.

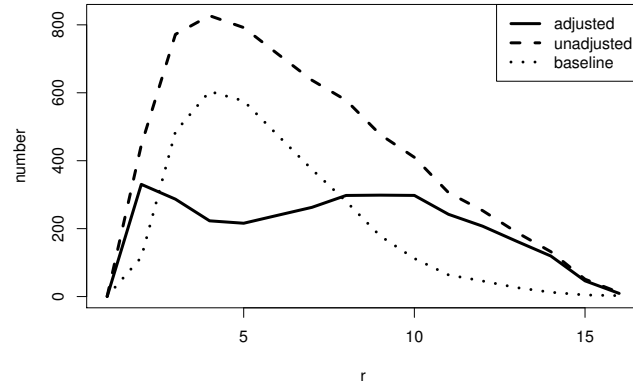(a) Adjusted and unadjusted number of detected DE genes.

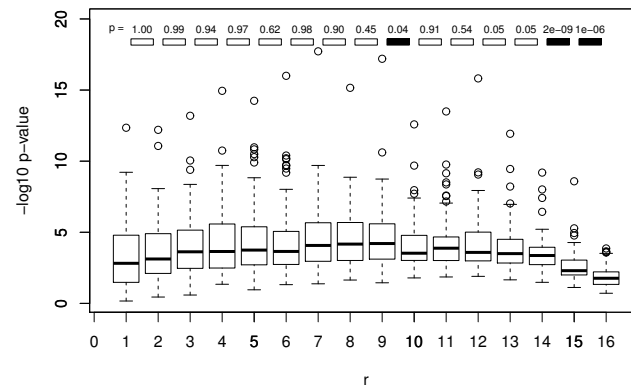(b) Boxplots of $-\log(p)$ for the biological association evaluation.

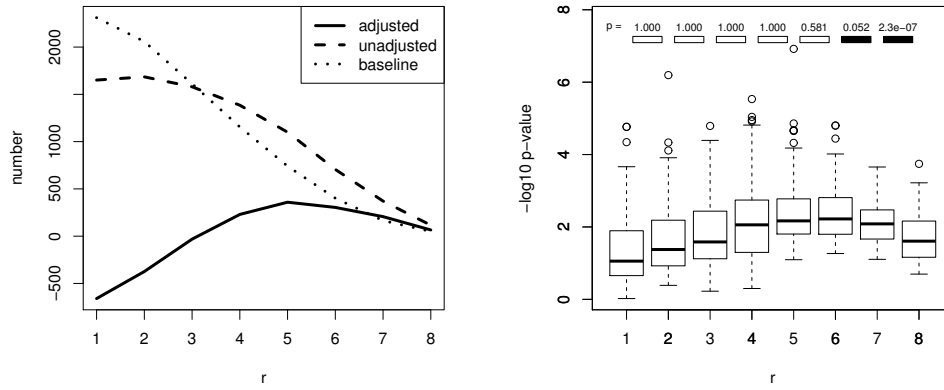(c) Heatmap to show effective studies of rOP in each gene.

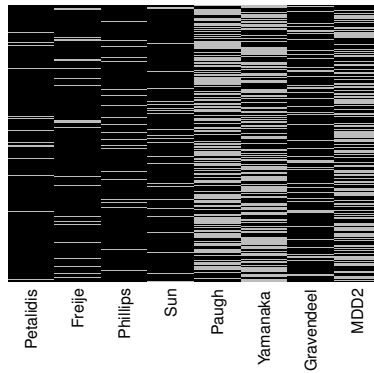SUPPLEMENT FIGURE 3. Results of diabetes dataset applying rOP.

(a) Adjusted and unadjusted number of detected DE genes.

(b) Boxplots of $-\log(p)$ for the biological association evaluation.

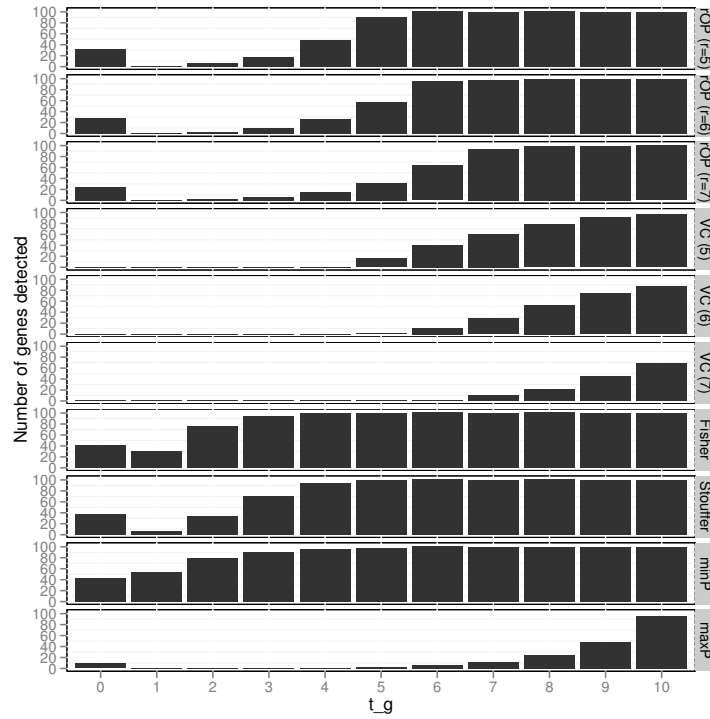SUPPLEMENT FIGURE 4. Permutation results of diabetes dataset

(a) Adjusted and unadjusted number of detected DE genes.

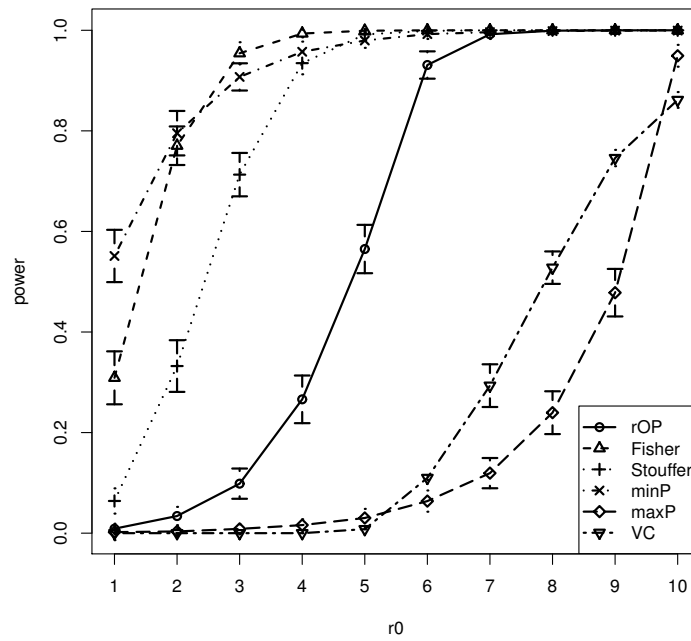(b) Boxplots of $-\log(p)$ for the biological association evaluation.

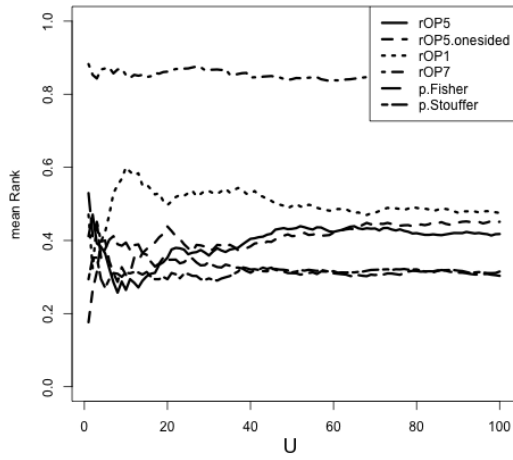(c) Heatmap to show effective studies of rOP in each gene.

SUPPLEMENT FIGURE 5. Results of Brain Cancer and 1 random MDD dataset applying rOP.
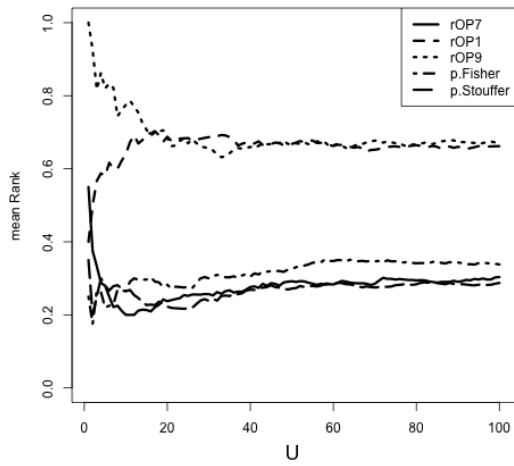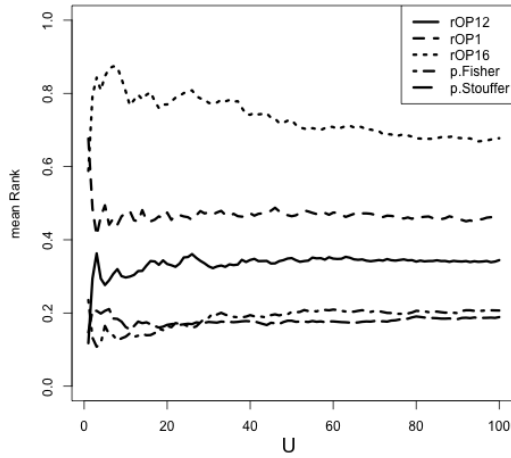
(a) Number of genes detected

(b) Power

SUPPLEMENT FIGURE 6. Simulation result without correlated genes

(a) Brain cancer

(b) MDD

(c) Diabetes

SUPPLEMENT FIGURE 7. Mean rank of different methods for the top U pathways