The procedural steps for the independent and dependent datasets with random dependent effect at \( \pi_0 = 0.7 \) and \( \pi_0 = 0.9 \). The plots in first row show the \( \hat{\pi}_0 \) and \( e_{\hat{\pi}_0} \) at different \( k/n \). The blue curve indicates \( \hat{\pi}_0 \) and the black curve indicates \( e_{\hat{\pi}_0} \), the red horizontal line indicates the cutoff of \( e_{\hat{\pi}_0} \) (here we used 0.05), the red vertical line indicates the choice of \( k/n \) at which locally minimized \( \hat{\pi}_0 \) under \( e_{\hat{\pi}_0} < 0.05 \) is obtained. The plots in second row show the regression.
procedure. The black thick curve indicates the \((p_i, p'_i), i = 1, \ldots, k\) and the blue curve is the regression line \(h_k(.)\), and the red curve is the regression line \(f(.)\) after transformation. The plots in third and fourth row show the p-value histograms before and after applying ConReg-R and the gray horizontal line indicates the \(\pi_0\). The plots in last row show the FDR estimation errors between real FDR and the FDR estimated by p-values before (black) and after applying ConReg-R (red).

**Figure S2**

The procedure details for “Min”, “Max”, “Sqroot”, “Square” and “Prod” datasets at \(\pi_0 = 0.7\). The detail description for plots in each raw is same as Figure S1.
The procedure details for “Min”, “Max”, “Sqroot”, “Square” and “Prod” datasets at $\pi_0 = 0.9$. The detail description for plots in each raw is same as Figure S1.
The p-value density histograms for 10 stress response data sets. (CRR) indicates the re-estimated p-values after ConReg-R. The gray horizontal line indicates $\pi_0 = 0.5$ for each plot.
Figure S5

p-value density histograms for RNA-seq and Affymetrix datasets.