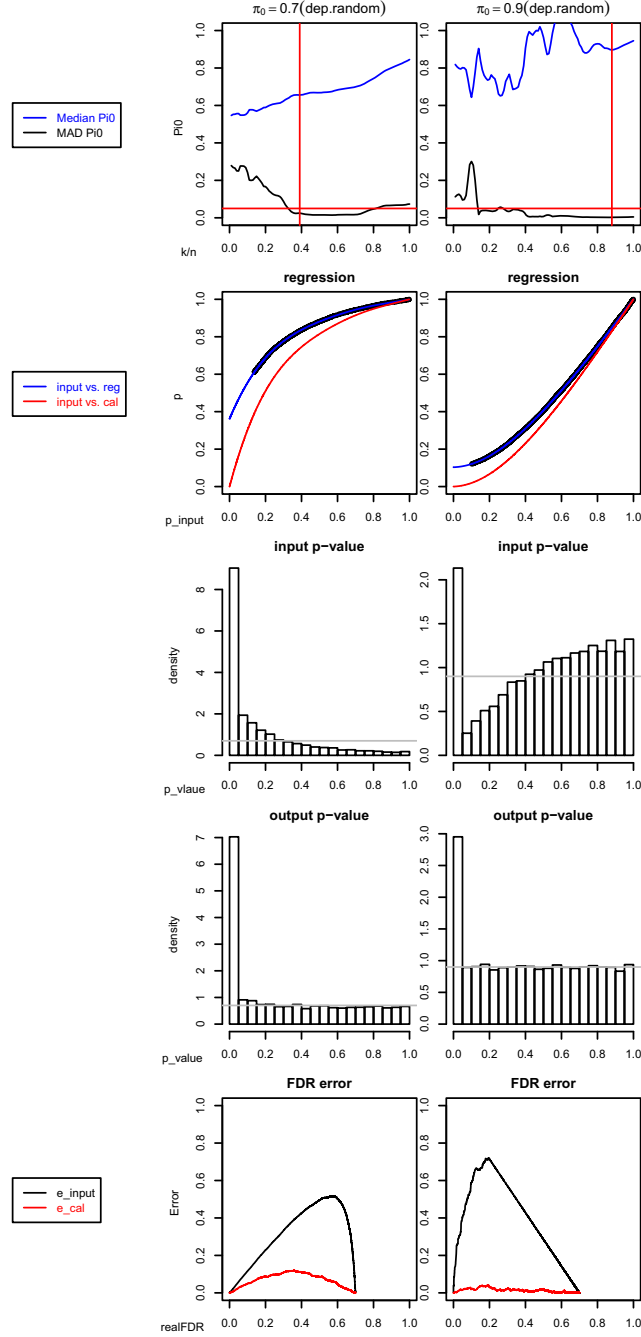


Supplementary figures

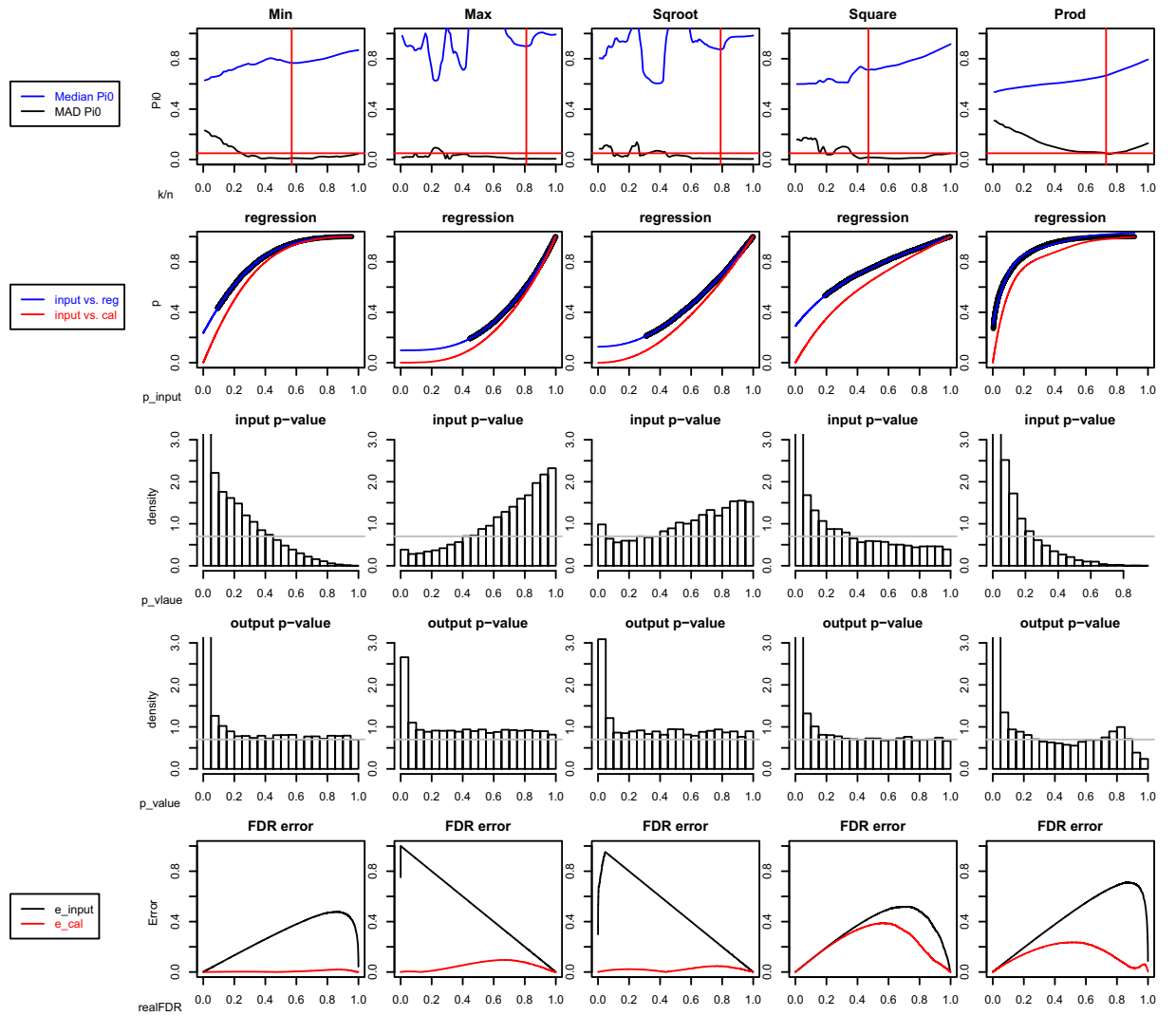
Figure S1



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

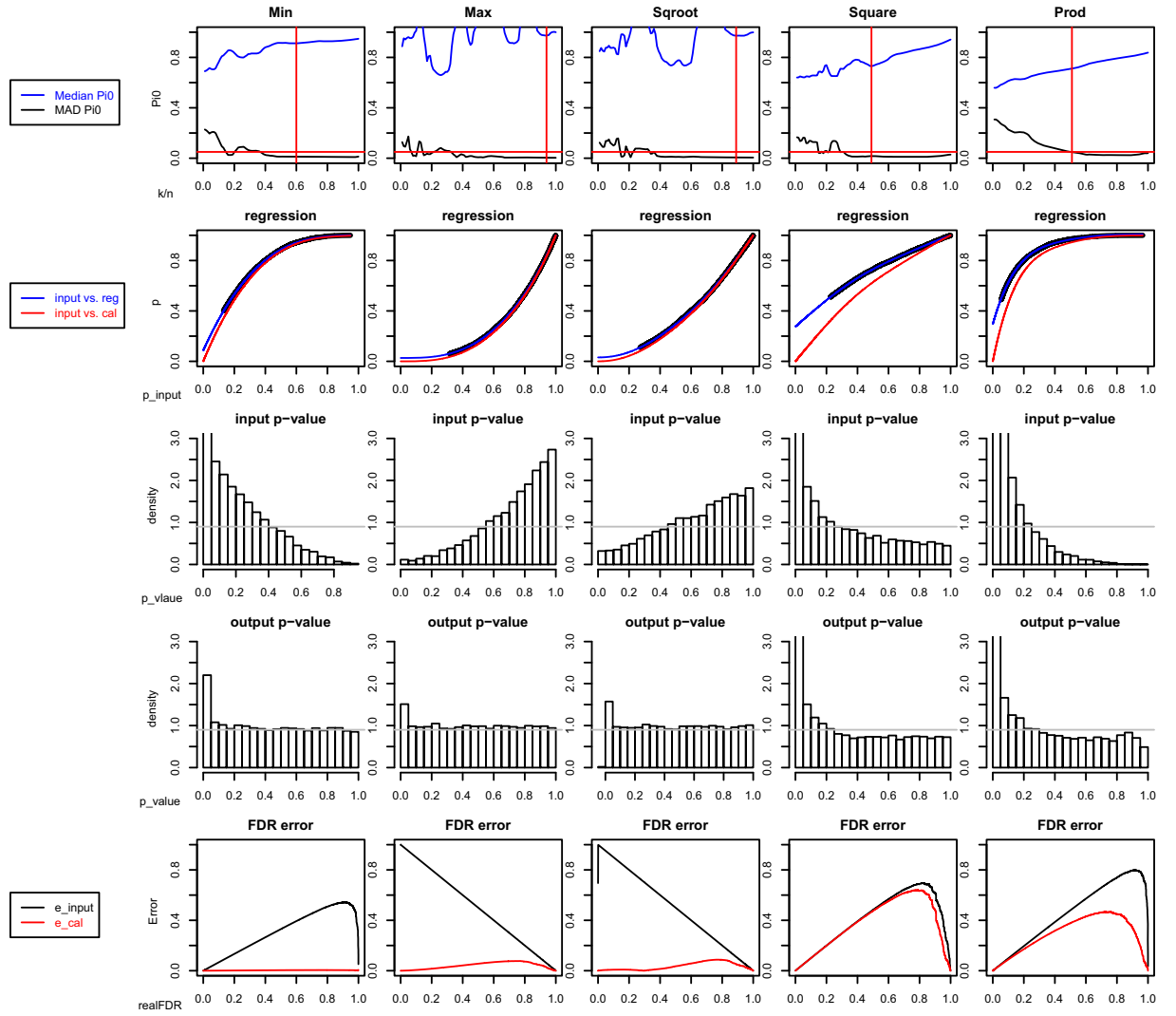
procedure. The black thick curve indicates the $(p_i, p'_i), i = 1, \dots, k$ and the blue curve is the regression line $h_k(\cdot)$, and the red curve is the regression line $f(\cdot)$ after transformation. The plots in third and fourth row show the p-value histograms before and after applying ConReg-R and the gray horizontal line indicates the π_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



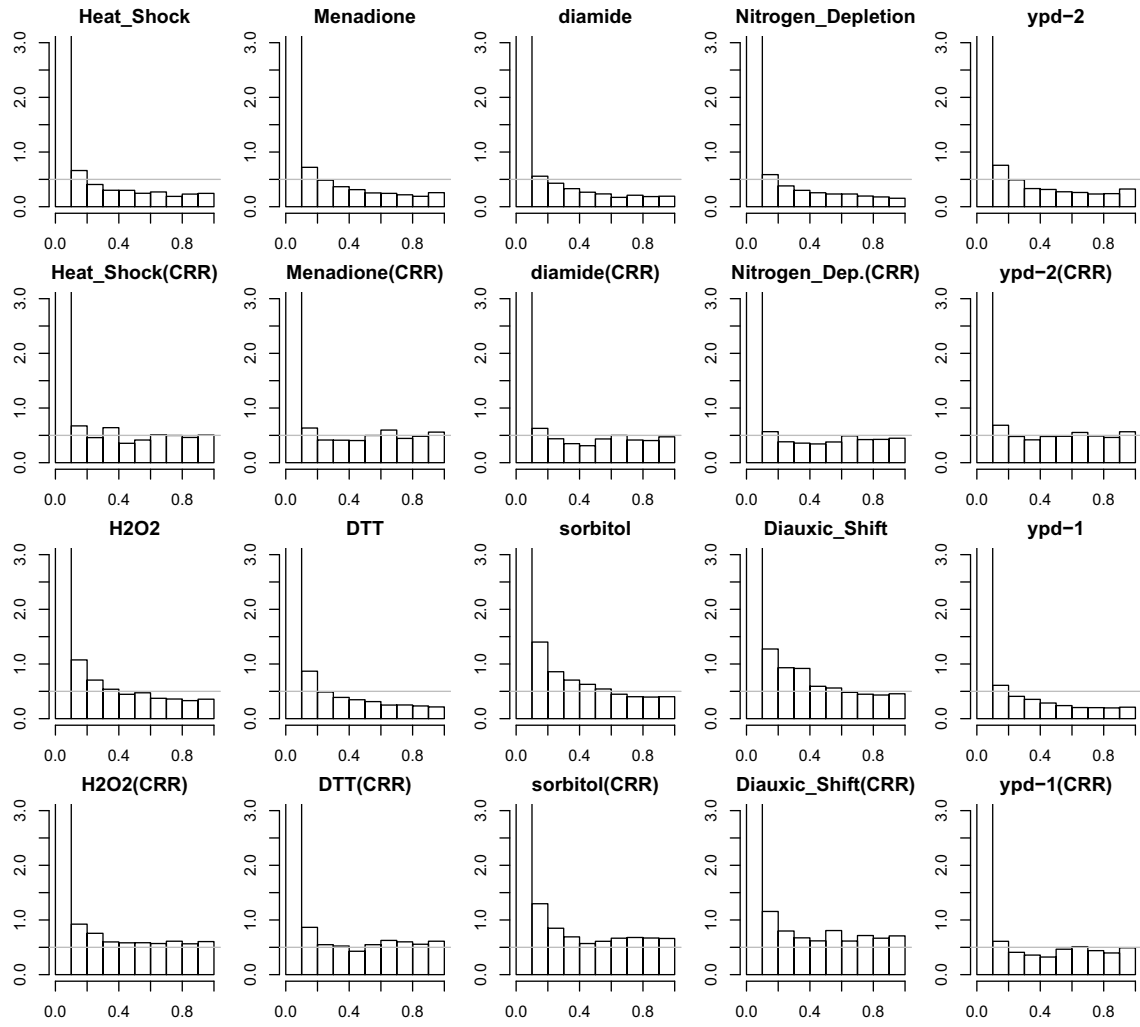
The procedure details for “Min”, “Max”, “Sqroot”, “Square” and “Prod” datasets at $\pi_0 = 0.7$. The detail description for plots in each row is same as Figure S1.

Figure S3



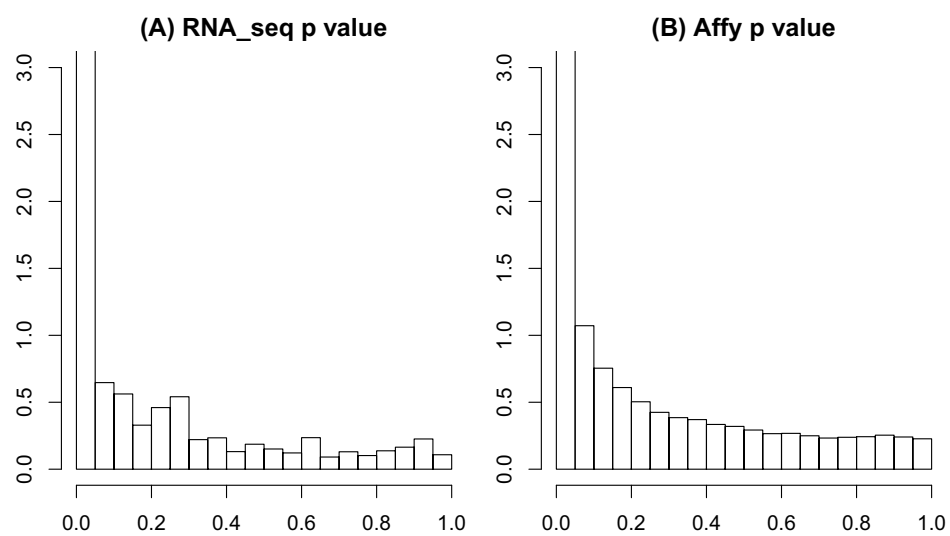
The procedure details for “Min”, “Max”, “Sqroot”, “Square” and “Prod” datasets at $\pi_0 = 0.9$. The detail description for plots in each row is same as Figure S1.

Figure S4



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.