



Additional File 3: Single-gene significance and agreement with operons. As in Figure 2, we divided the changers into eight groups of genes with different levels of confidence, and compare the average confidence within each group to the adjusted agreement with operon pairs. Here we compare the actual data set to additional “uncoupled” and (for *ecox*) heavy-tailed simulations. The means in the “uncoupled” simulations follow a normal distribution, while the real data sets and the other simulations have heavier tails.