

Supplementary Materials

Supplementary Figure 1. ROC curves for the posterior probability based on the proposed normalization and the two-sample t-test p-values following no or median normalizations. True array effects are non-randomized. Mean expression of under-expressed genes are -1 for the left panels and -3 for the right panels. From top to bottom, (π, λ) is (30%, 90%), (10%, 90%), and (30%, 60%).

Supplementary Figure 2. ROC curves for the posterior probability based on the proposed normalization and the two-sample t-test p-values following no or median normalizations. True array effects are non-randomized. For the left panels, data were simulated with gene effects β_g having a uniform distribution. For the right panels, data were simulated with measurement errors ϵ_{igp} having a $t(\text{df}=3)$ distribution. From top to bottom, (π, λ) is (30%, 90%), (10%, 90%), and (30%, 60%).

Supplementary Figure 3. ROC curves for the posterior probability based on the proposed normalization and the two-sample t-test p-values following no or median normalizations. True array effects are non-randomized. Measurement error is 1. Mean expression of under-expressed genes are -1 for the left panels and -2 for the right panels. From top to bottom, (π, λ) are (30%, 90%), (10%, 90%), and (30%, 60%).

Supplementary Figure 4. QQplot for the normal fat samples ($n=12$), with the observed expression on the x axis and the predicted expression on the y axis. Data from a random set of 2228 probesets are plotted. The red line indicates the diagonal.

Supplementary Figure 5. QQplot for the MRC samples ($n=8$), with the observed expression on the x axis and the predicted expression on the y axis. Data from a random set of 2228 probesets are plotted. The red line indicates the diagonal.

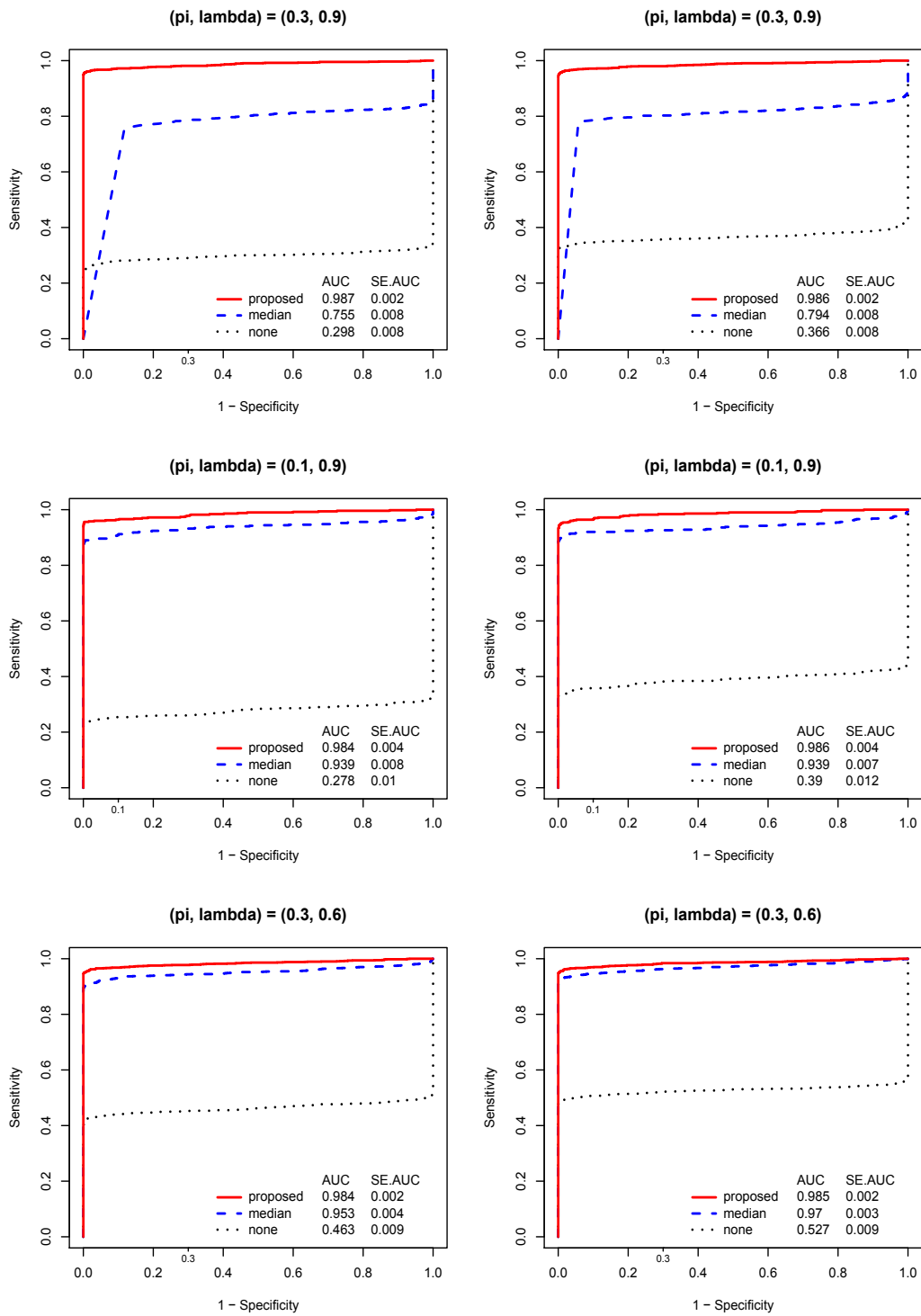


Figure 1:

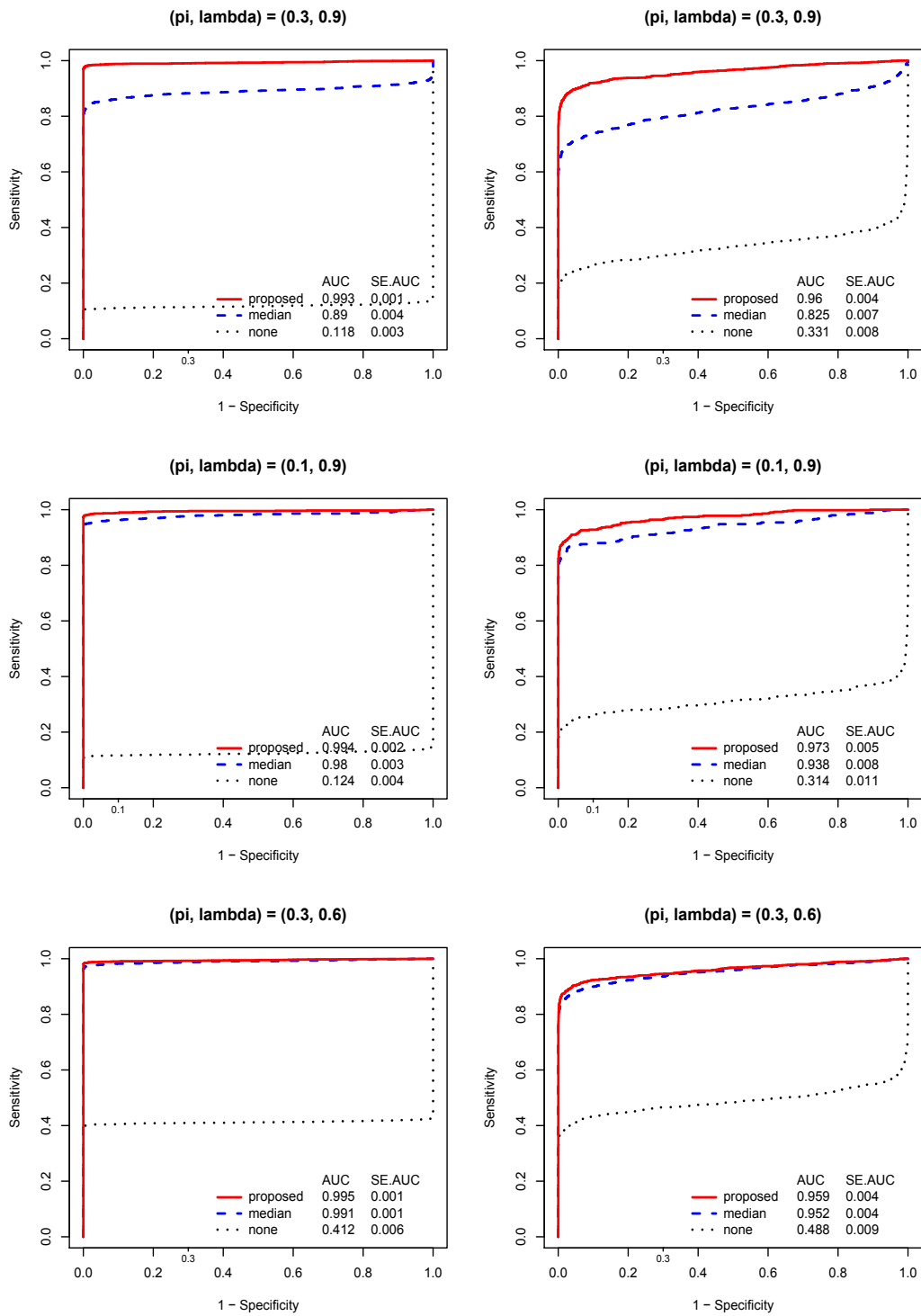


Figure 2:

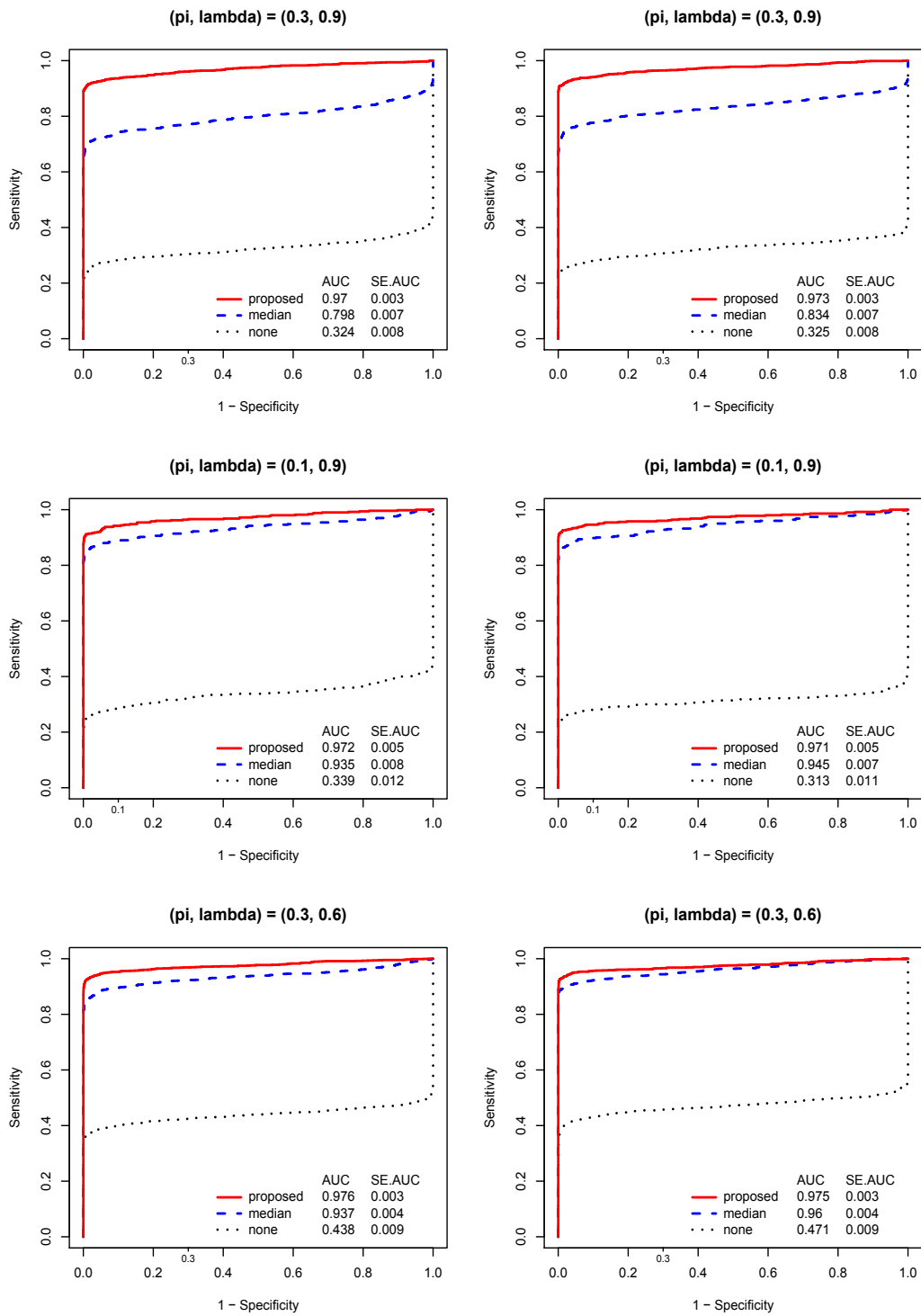


Figure 3:

Normal Fat

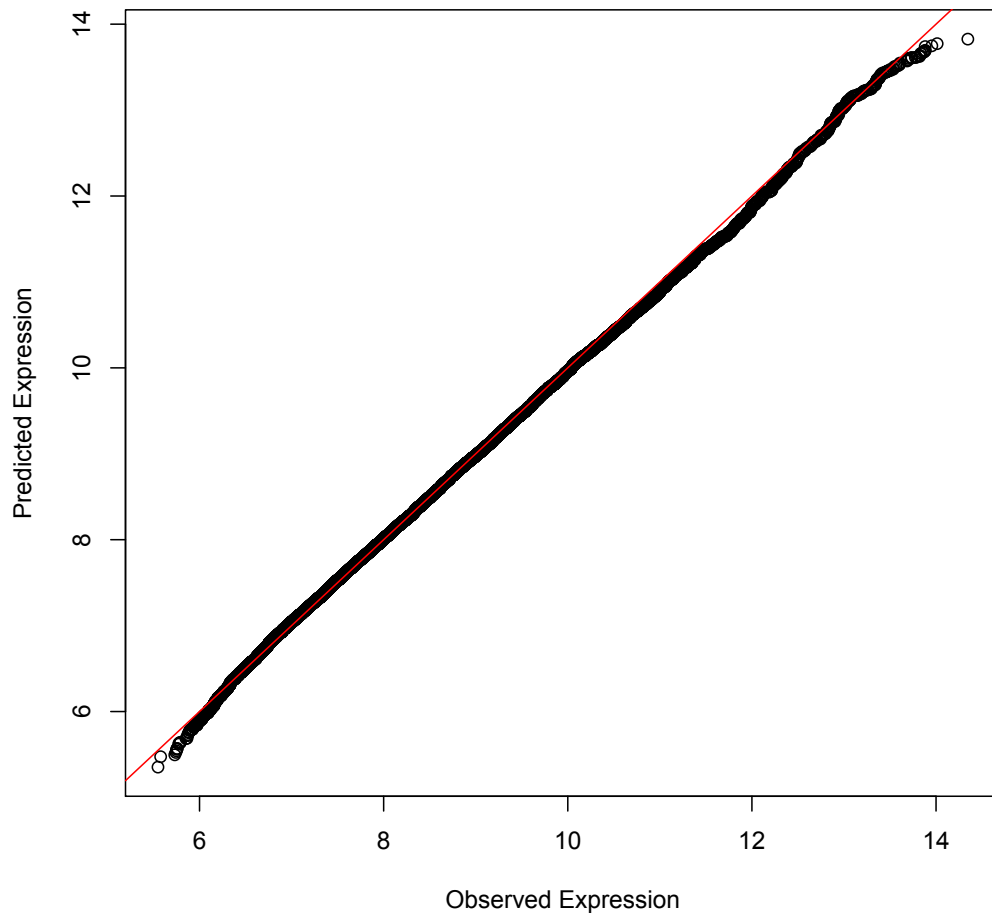


Figure 4:

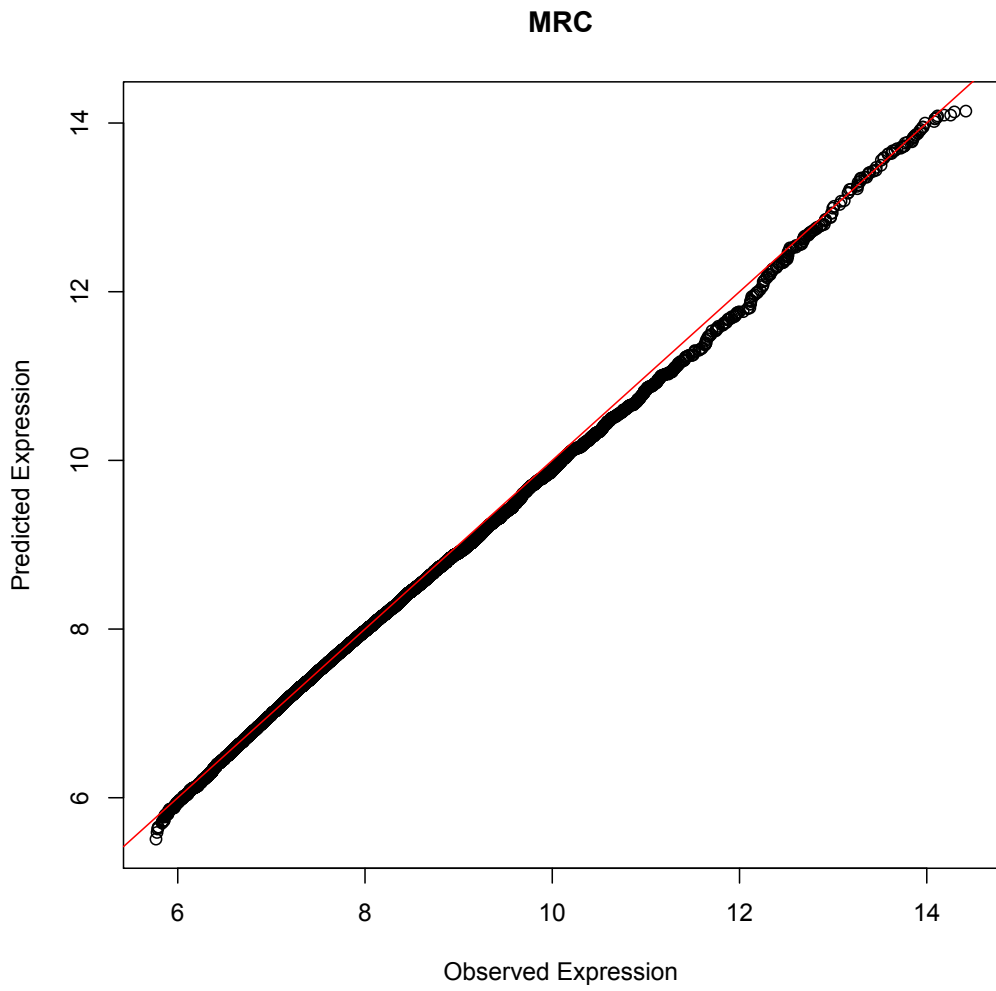


Figure 5: