8 Supplementary Materials

Figure 5. (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%).

Figure 6. (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(df=3) distribution. From top to bottom, (π, λ) is (30%, 90%), (10%, 90%), and (30%, 60%).

Figure 7. (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%).

Figure 8. (Supplementary Figure 4a.) 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.

Figure 9. (Supplementary Figure 4b.) 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.

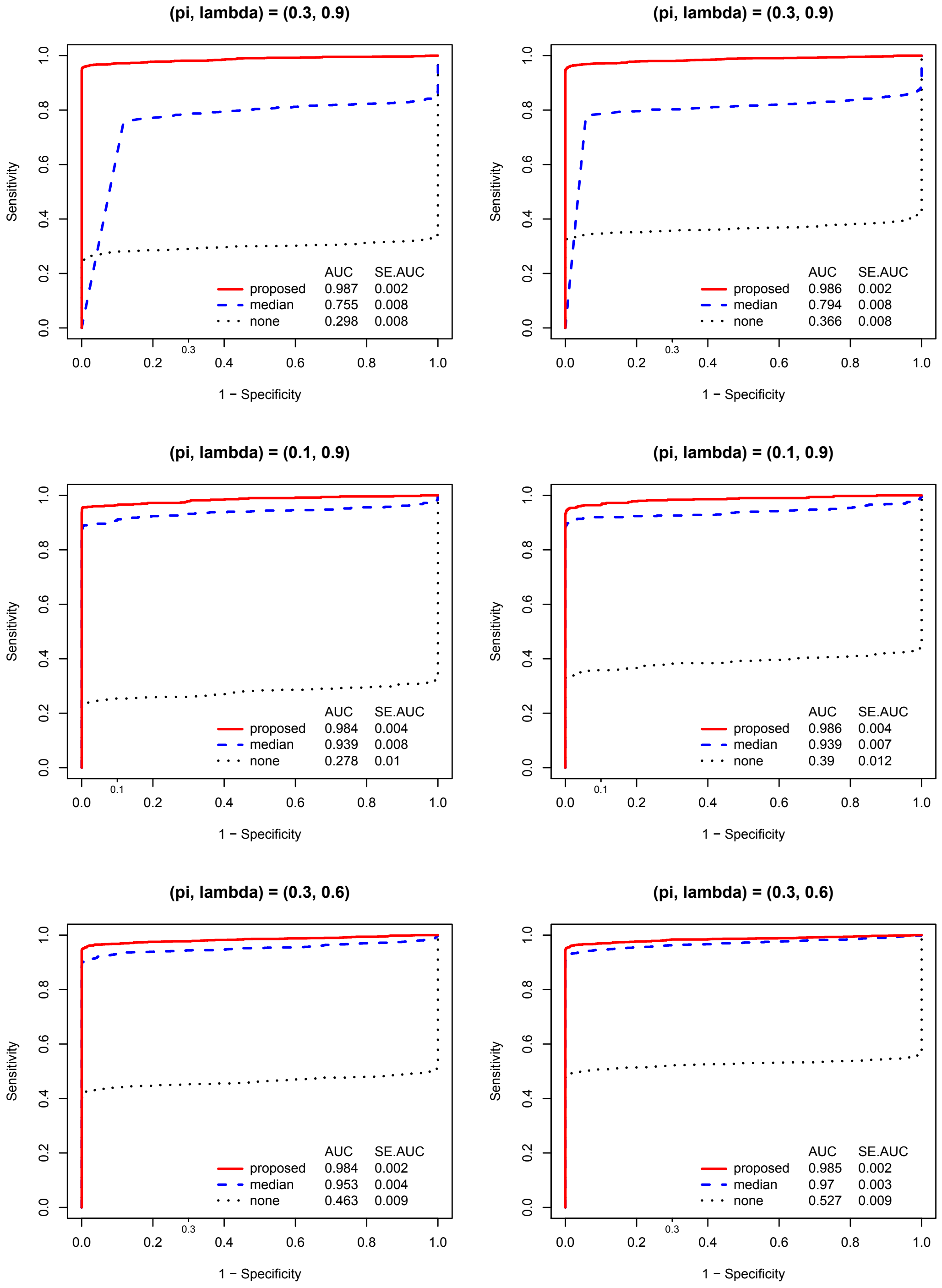

Figure 5: ROC curves for the posterior probability based on the proposed normalization and the two-sample t-test p-values following no or median normalizations. True array effects are non-randomized. Mean expression of under-expressed genes are -1 for the left panels and -3 for the right panels. From top to bottom, the proportion of differential expression and the proportion of over-expression (π, λ) are (30%, 90%), (10%, 90%), and (30%, 60%).

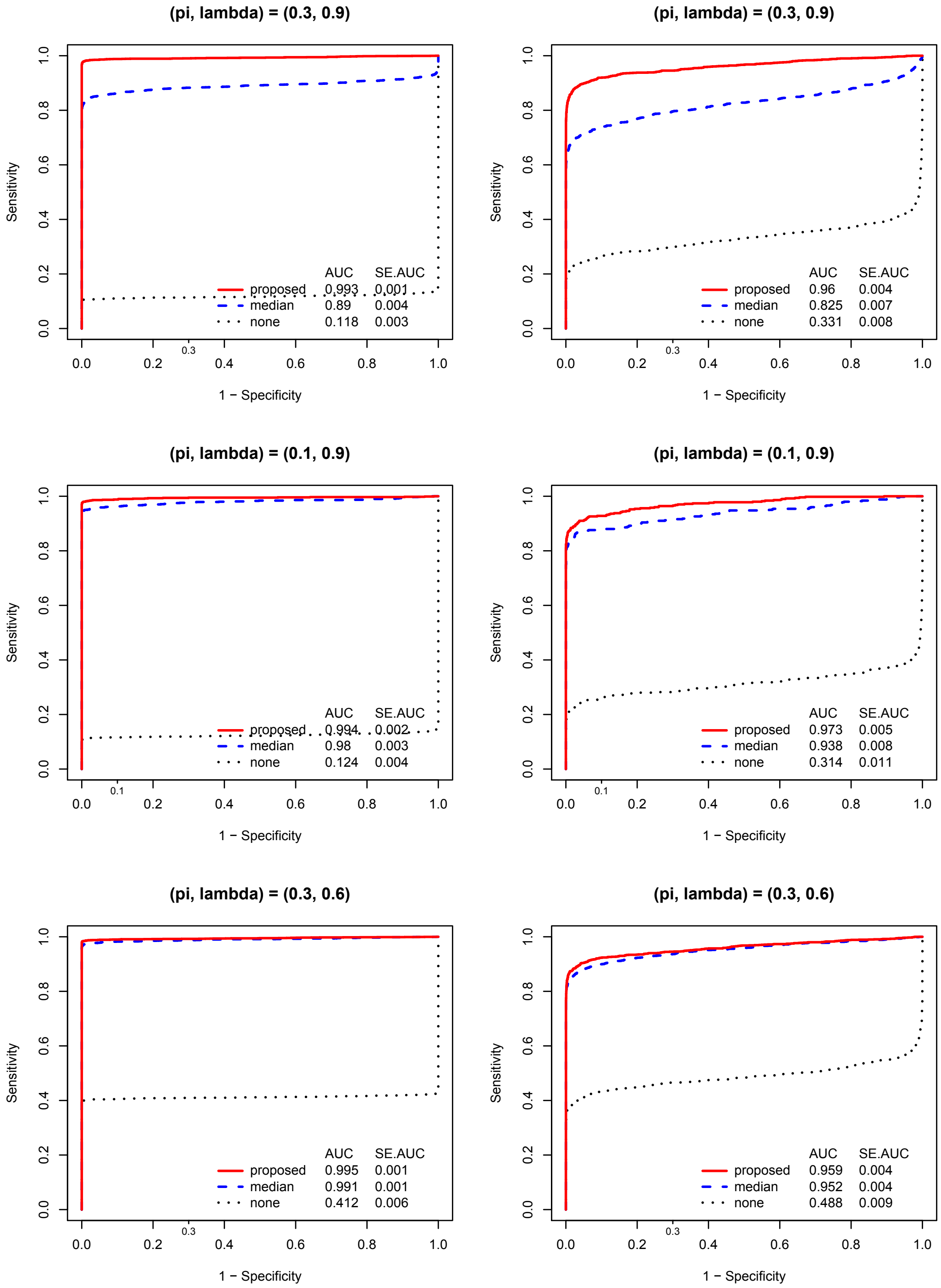

Figure 6: ROC curves for the posterior probability based on the proposed normalization and the two-sample t-test p-values following no or median normalizations. True array effects are non-randomized. Gene effects have a uniform distribution for the left panels and measurement errors have a t(df=3) distribution for the right panels. From top to bottom, (π, λ) are (30%, 90%), (10%, 90%), and (30%, 60%).

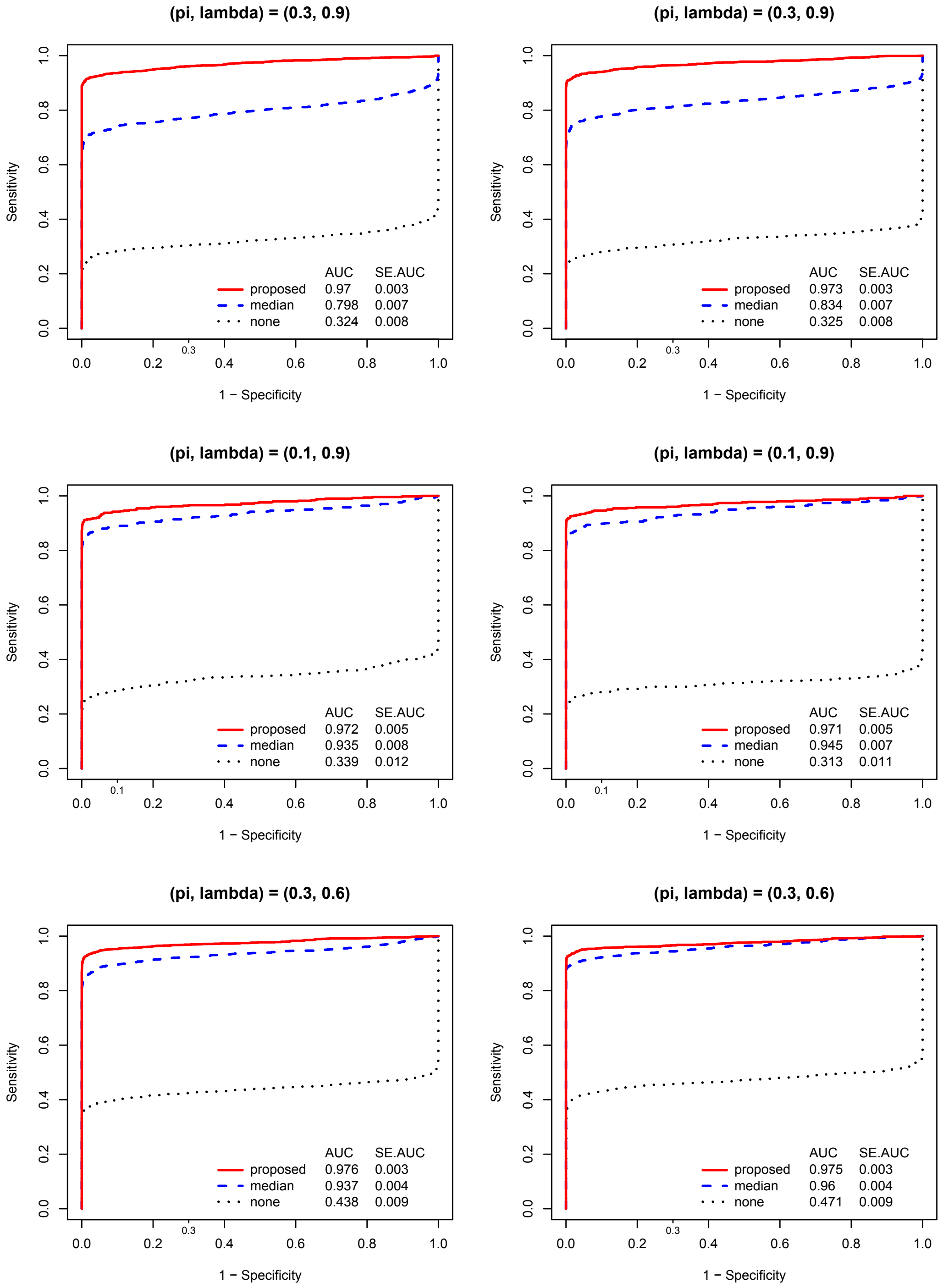

Figure 7: ROC curves for the posterior probability based on the proposed normalization and the two-sample t-test p-values following no or median normalizations. True array effects are non-randomized. Measurement error is 1. Mean expression of under-expressed genes are -1 for the left panels and -2 for the right panels. From top to bottom, (π, λ) are (30%, 90%), (10%, 90%), and (30%, 60%).

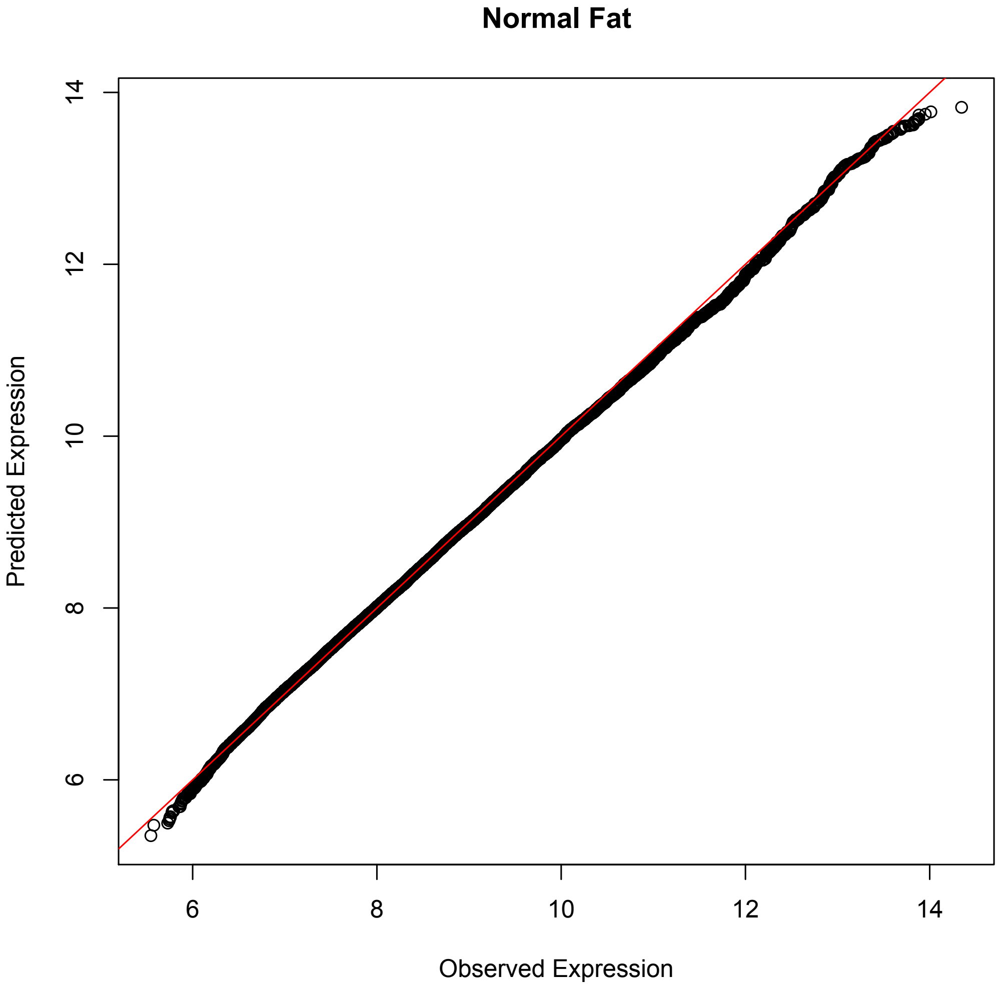

Figure 8: QQplot for the normal fat samples (n=12), with the observed expression on the x axis and the predicted expression on the y axis. Data from a set of randomly selected 2228 probesets are plotted. The red line indicates the diagonal.

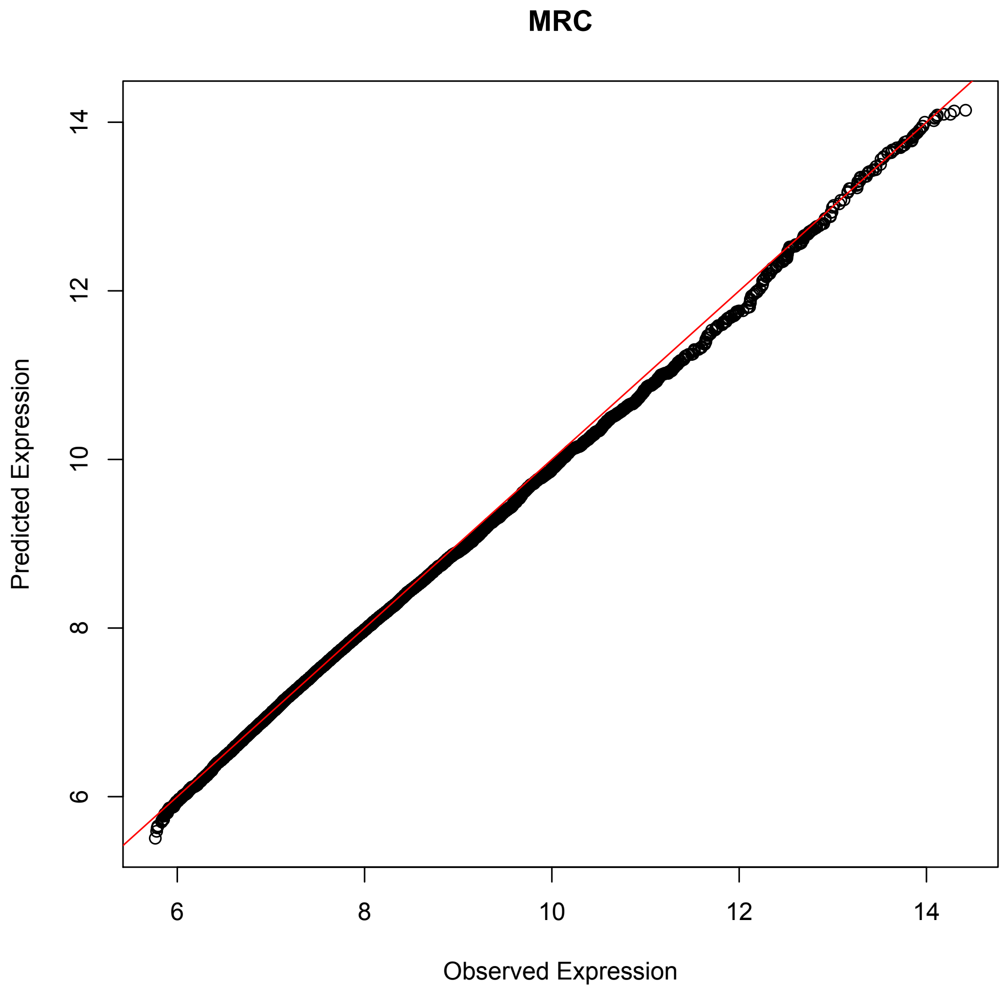

Figure 9: QQplot for the MRC samples (n=8), with the observed expression on the x axis and the predicted expression on the y axis. Data from a set of randomly selected 2228 probesets are plotted. The red line indicates the diagonal.