Supplementary Figure 1a. Scatterplots of LogRatios computed from the data without background-adjustment (noBA) and with background-adjustment (w/BA) for the arrays involving the Placenta Test pair. Intensity normalization was done in both cases. The S-shape to the plots shows that the noBA LogRatios are usually smaller, in absolute value, compared to the w/BA LogRatios.
Supplementary Figure 1b. Scatterplots of LogRatios computed from the data without background-adjustment (noBA) and with background-adjustment (w/BA) for the arrays involving the Kidney Test pair. Intensity normalization was done in both cases. The S-shape to the plots shows that the noBA LogRatios are usually smaller, in absolute value, compared to the w/BA LogRatios.
Supplementary Figure 1c. Scatterplots of LogRatios computed from the data without background-adjustment (noBA) and with background-adjustment (w/BA) for the arrays involving the Lung Test pair. Intensity normalization was done in both cases. The S-shape to the plots shows that the noBA LogRatios are usually smaller, in absolute value, compared to the w/BA LogRatios.
Supplementary Figure 2a. This is the same as Figure 2 in the paper. Agreement between the direct log$_2$ ratios and the indirect log$_2$ ratios for the placenta test-pair. Highlighted genes are placenta-specific genes. Data version: intensity normalization, no background-adjustment.
Supplementary Figure 2b. Agreement between the direct log\(_2\) ratios and the indirect log\(_2\) ratios for the placenta test-pair. Highlighted genes are placenta-specific genes. Data version: no normalization, no background-adjustment.
Supplementary Figure 2c. Agreement between the direct log$_2$-ratios and the indirect log$_2$-ratios for the placenta test-pair. Highlighted genes are placenta-specific genes. Data version: intensity-normalization, with background-adjustment.
Supplementary Figure 2d. Agreement between the direct log$_2$ ratios and the indirect log$_2$ ratios for the placenta test-pair. Highlighted genes are placenta-specific genes. Data version: no normalization, with background-adjustment.
Supplementary Figure 3a. This is the same as Figure 3 in the paper. Agreement between the direct log$_2$ ratios and the indirect log$_2$ ratios for the kidney test-pair. Highlighted genes are kidney-specific genes. Data version: intensity normalization, no background-adjustment.
Supplementary Figure 3b. Agreement between the direct log₂-ratios and the indirect log₂-ratios for the kidney test-pair. Highlighted genes are kidney-specific genes. Data version: no normalization, no background-adjustment.
Supplementary Figure 3c. Agreement between the direct log$_2$-ratios and the indirect log$_2$-ratios for the kidney test-pair. Highlighted genes are kidney-specific genes. Data version: intensity-normalization, with background-adjustment.
Supplementary Figure 3d. Agreement between the direct log$_2$ratios and the indirect log$_2$ratios for the kidney test-pair. Highlighted genes are kidney-specific genes. Data version: no normalization, with background-adjustment.
Supplementary Figure 4a. This is the same as Figure 4 in the paper. Agreement between the direct log₂ ratios and the indirect log₂ ratios for the lung test-pair. Highlighted genes are lung-specific genes. Data version: intensity normalization, no background-adjustment.
Supplementary Figure 4b. Agreement between the direct log$_2$ratios and the indirect log$_2$ratios for the lung test-pair. Highlighted genes are lung-specific genes. Data version: no normalization, no background-adjustment.
Supplementary Figure 4c. Agreement between the direct log$_2$-ratios and the indirect log$_2$-ratios for the lung test-pair. Highlighted genes are lung-specific genes. Data version: intensity-normalization, with background-adjustment.
Supplementary Figure 4d. Agreement between the direct log₂-ratios and the indirect log₂-ratios for the lung test-pair. Highlighted genes are lung-specific genes. Data version: no normalization, with background-adjustment.
Supplementary Figure 5. Proposed filter illustrated on the Placenta test pair and the Pool reference. A. Genes with suspect measurements are those with small LogRatios but larger skewness. B. The genes that are highlighted in panel A are highlighted in the scatterplot of the direct and indirect logratios. C. For comparison, the genes flagged for non-uniform feature by the Feature Extractor software.
Supplementary Figure 6. Proposed filter illustrated on the Placenta test pair and the Placenta reference. A. Genes with suspect measurements are those with small LogRatios but larger skewness. B. The genes that are highlighted in panel A are highlighted in the scatterplot of the direct and indirect logratios. C. For comparison, the genes flagged for non-uniform feature by the Feature Extractor software.
Supplementary Figure 7. Proposed filter illustrated on the Placenta test pair and the Commercial reference. A. Genes with suspect measurements are those with small LogRatios but larger skewness. B. The genes that are highlighted in panel A are highlighted in the scatterplot of the direct and indirect logratios. C. For comparison, the genes flagged for non-uniform feature by the Feature Extractor software.
Supplementary Figure 8. Proposed filter illustrated on the Kidney test pair and the Pool reference. A. Genes with suspect measurements are those with small LogRatios but larger skewness. B. The genes that are highlighted in panel A are highlighted in the scatterplot of the direct and indirect logratios. C. For comparison, the genes flagged for non-uniform feature by the Feature Extractor software.
Supplementary Figure 9. Proposed filter illustrated on the Kidney test pair and the Placenta reference. A. Genes with suspect measurements are those with small LogRatios but larger skewness. B. The genes that are highlighted in panel A are highlighted in the scatterplot of the direct and indirect logratios. C. For comparison, the genes flagged for non-uniform feature by the Feature Extractor software.
Supplementary Figure 10. Proposed filter illustrated on the Kidney test pair and the Commercial reference. A. Genes with suspect measurements are those with small LogRatios but larger skewness. B. The genes that are highlighted in panel A are highlighted in the scatterplot of the direct and indirect logratios. C. For comparison, the genes flagged for non-uniform feature by the Feature Extractor software.
Supplementary Figure 11. Proposed filter illustrated on the Lung test pair and the Pool reference.  A. Genes with suspect measurements are those with small LogRatios but larger skewness.  B. The genes that are highlighted in panel A are highlighted in the scatterplot of the direct and indirect logratios.  C. For comparison, the genes flagged for non-uniform feature by the Feature Extractor software.
Supplementary Figure 12. Proposed filter illustrated on the Lung test pair and the Placenta reference. A. Genes with suspect measurements are those with small LogRatios but larger skewness. B. The genes that are highlighted in panel A are highlighted in the scatterplot of the direct and indirect logratios. C. For comparison, the genes flagged for non-uniform feature by the Feature Extractor software.
Supplementary Figure 13. Proposed filter illustrated on the Lung test pair and the Commercial reference. A. Genes with suspect measurements are those with small LogRatios but larger skewness. B. The genes that are highlighted in panel A are highlighted in the scatterplot of the direct and indirect logratios. C. For comparison, the genes flagged for non-uniform feature by the Feature Extractor software.