

*Organ-Specific Differences in Gene Expression and UniGene Annotations Describing Source Material*

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For this paper, we analyzed data collected for Project Normal, which assessed the normal variation of gene expression in three distinct mouse organs. Our approach uncovered two difficulties with the original analysis. First, normalization using the loess method obscures a difference in the distribution of gene expression measurements between pure organ samples and the reference mixture. Second, and more importantly, it appears that the link between spot location and gene annotations was broken during data processing. We used principal components analysis to confirm that reordering the data matrices based on spot locations produced more consistent data from the reference channels. In order to recover the true gene annotations, we then introduced a model that explicitly accounted for organ-specific differences in gene expression and related those differences to UniGene annotations that describe mRNA sources. Using this model, we were able to determine which set of annotations was correct.