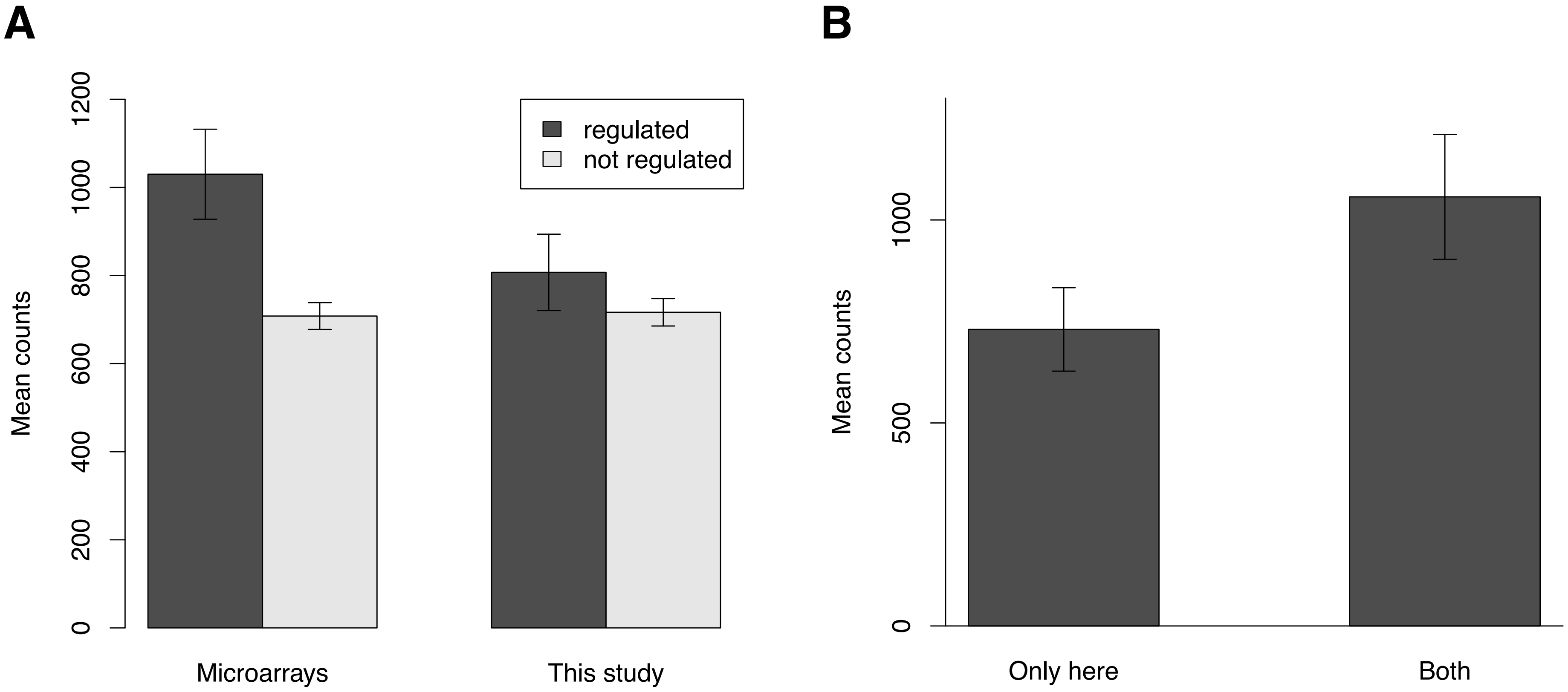

Figure S6. Genes identified as oxygen-regulated in the current RNA-seq study exhibited a lower expression level than genes identified in microarray studies. Mean counts were calculated from our RNA-seq normalized count data for each gene across the eight time points. A gene was determined to be detected by microarrays if observed in 3 or more microarray studies. Error bars represent the SEM. **(A)** Genes identified in microarrays were more highly expressed than genes identified in the current study. The expression of genes not regulated were the same between the two methods. **(B)** The genes identified as oxygen-regulated in only the current study (and not in microarray studies) exhibited a lower expression level than genes identified in both the current study and previous microarray studies.