



Figure S3. Heatmaps representing the Euclidian distance between samples. The \log_2 transformed normalized expression values were input into the *dist* function in R. The darker colors indicate more closely-related samples, with red indicating identity. **(A)** Euclidian distance was determined between each pair of samples using expression of all genes. **(B)** Euclidian distance was determined between each pair of samples using expression of only the 816 oxygen-regulated genes.