

**Supplemental Figure S1** Clustered and hierarchical ordered heatmap based on 45 target genes. The heatmap illustrates the cluster structure based on transcript expression similarities between the means of the Control (CT), Warm Normoxic (WN) and Warm Hypoxic (WH) groups at 12°C, 16°C-3d, 18°C-3d, 20°C-3d and 20°C-4wks. The Pearson correlation and average UPGMA agglomerative (bottom-up) cluster structure is reflected by the dendrogram and spacing. The integrated color code shows the up-regulated genes in red and down-regulated genes in blue color tones (log2 RQ-values were used to generate the heatmap).