**Chart, bar chart

Description automatically generated**

**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).