Fig. S1 Effect of acclimation treatment on pectoralis size (M_p). One-way ANOVA, temperature: $F_{2,36} = 2.364$, $P = 0.133$; photoperiod: $F_{1,37} = 1.464$, $P = 0.234$.
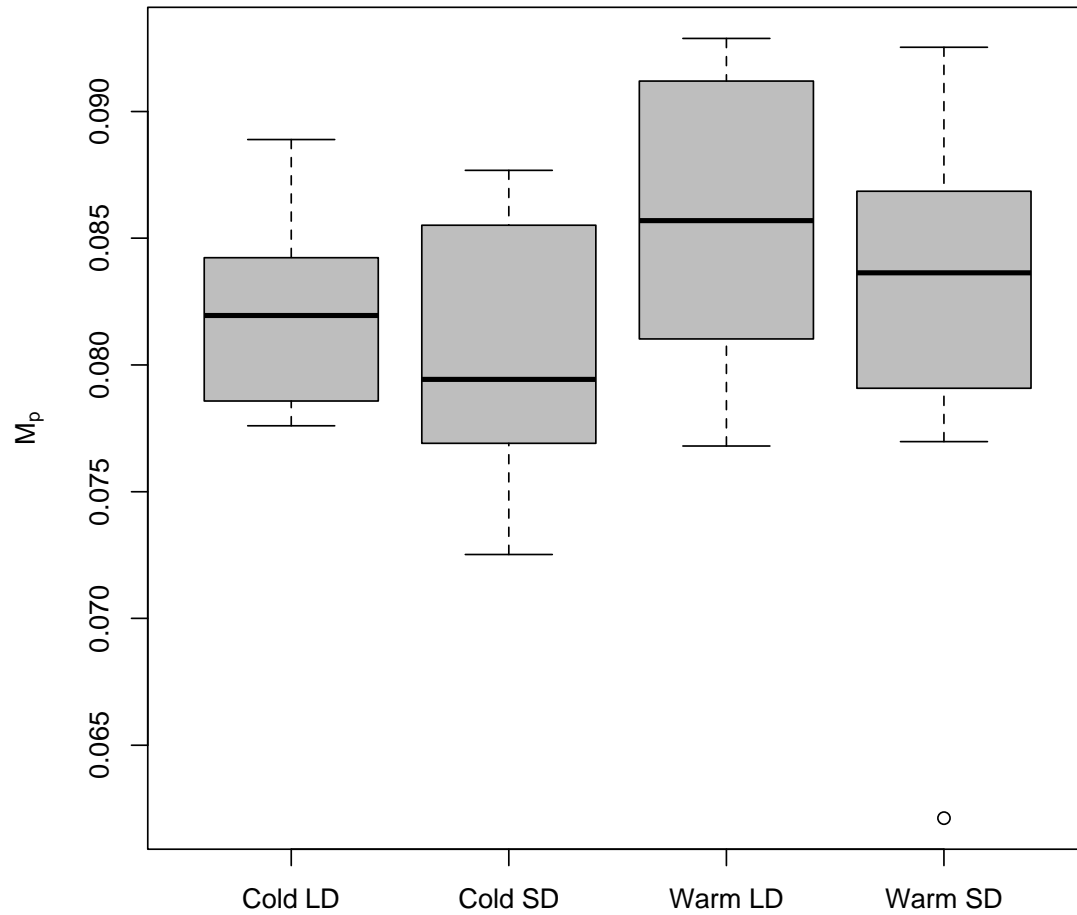
Fig. S2 Number of genes differentially expressed among photoperiod and temperature treatments.
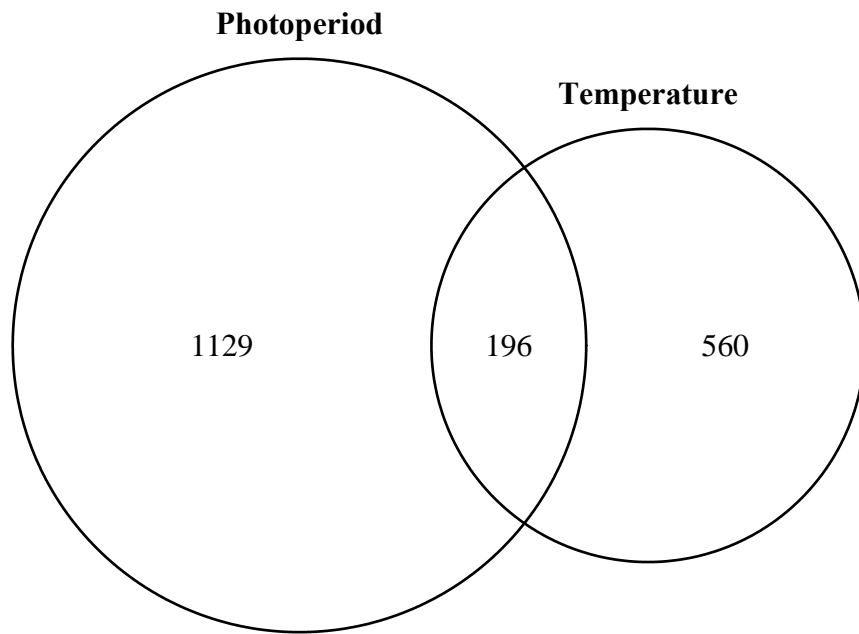
Fig. S3 Relationship between thermogenic performance (ΔM_{sum}) and pectoralis enzyme activity for (a) carnitine palmitoyl transferase, (b) citrate synthase, and (c) beta-hydroxyacyl Coenzyme-A dehydrogenase. Lines fit with linear regression for significant associations; *P*-values shown for each. This data was previously published in Swanson *et al.* 2014.
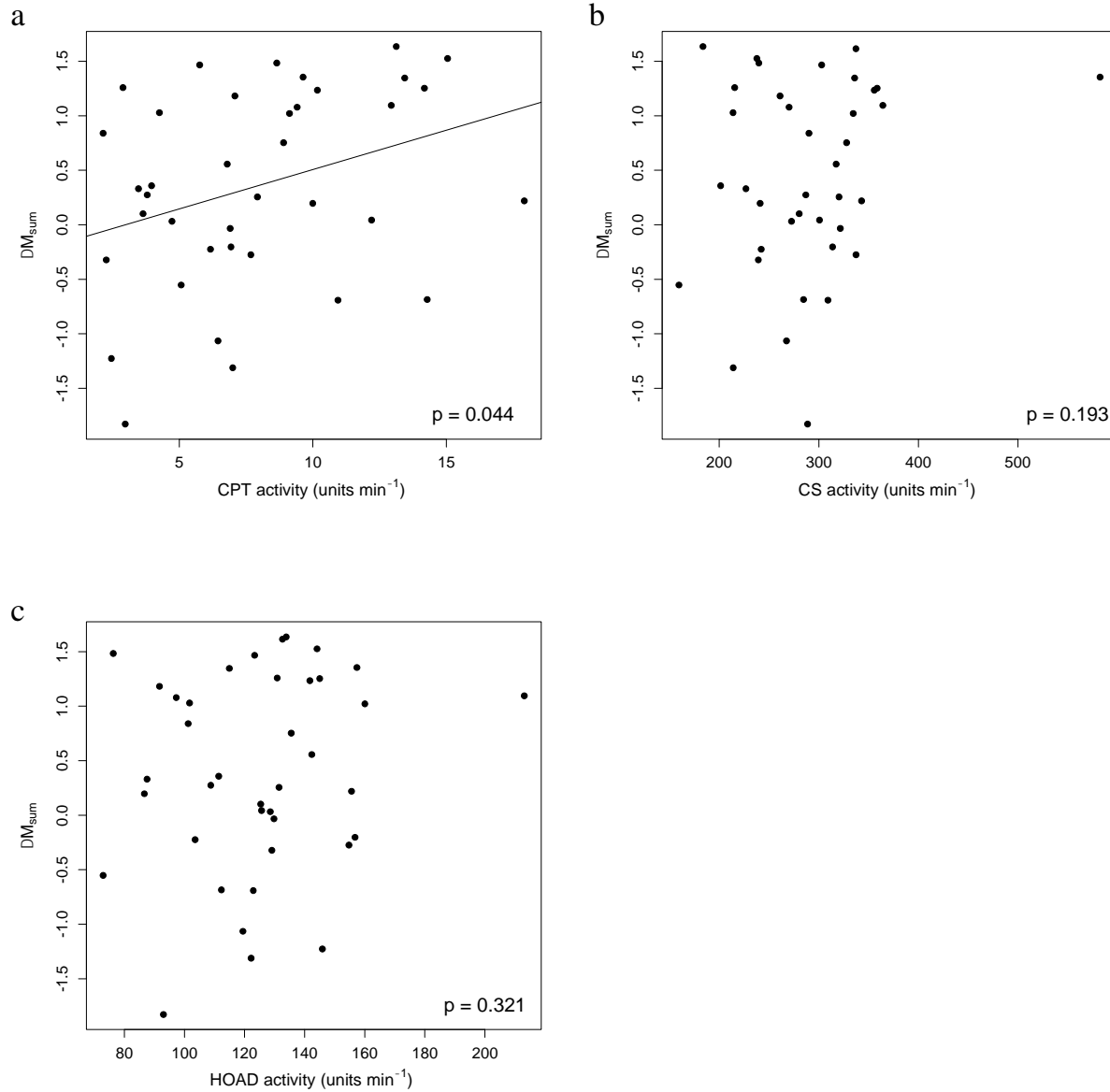
Fig. S4 Pectoralis activities of (a) carnitine palmitoyl transferase, (b) citrate synthase, and (c) beta-hydroxyacyl Coenzyme-A dehydrogenase by acclimation treatment. Asterisks indicate significant differences among treatment groups (p ≤ 0.05). This data was previously published in Swanson *et al.* 2014.
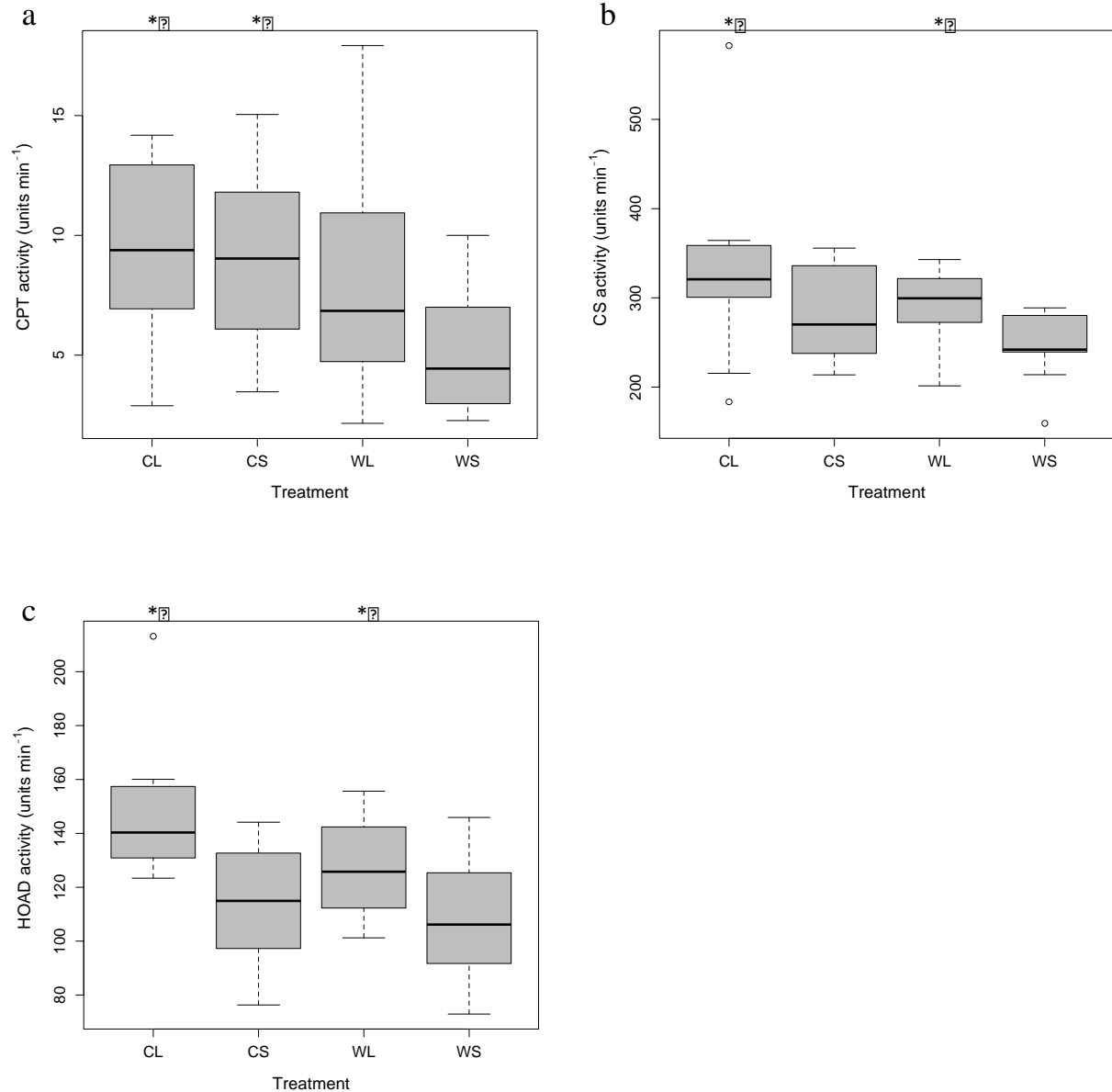
Table S1. Effect of year on phenotypes. Results from one-way ANOVA.

Phenotype	df	F	P
M_{sum0}	1	0.003	0.96
ΔM_{sum}	1	0.653	0.42
M_p	1	0.421	0.52

Table S2. Significant enrichment results for all transcriptional modules significantly associatedwith thermogenic performance or pectoralis size ($P \leq 0.05$). Modules T1 and T3 weretoo small to perform the enrichment analysis. Modules T32, T35, P41, and P50 were not enriched for any terms.

Download Table S2

Table S3. The 1325 genes with significant photoperiod treatment effects, and the associated FDR values, the module number to which the gene is assigned, the average absolute correlation between all pairs of genes in the module (Average.Degree), the average absolute correlation between the gen eand the remaining genes in its module (Degree; genes are ordered within modules by this value in decreasing order), and the PC1 loadings.

Download Table S3

Table S4. The 756 genes with significant temperature treatment effects, and the associated FDR values, the module number to which the gene is assigned, the average absolute correlation between all pairs of genes in the module (Average.Degree), the average absolute correlation between the gene and the remaining genes in its module (Degree; genes are names using gProfiler. ordered within modules by this value in decreasing order), and the PC1 loadings. TgutIDs converted to EnsemblIDs and Gene names using gProfiler.

Download Table S4