Supplementary Materials and Methods

Primer Design Methods:

A lake sturgeon head kidney transcriptome was used to design primers for *TLR4*, *NF-kB*, *TNFa*, *IL-8*, and *IgM* (Thorstensen et al., 2022b). Annotated lake sturgeon sequences for *TLR4* demonstrated conserved regions with 98.3 and 94.7% identity to the sterlet sturgeon, *Acipenser ruthenus,* and the American paddlefish *Polydon spathula* (Transcripts XM_034909094.1 and XM_041234367.1, respectively). Similarly, *NF-kB* and *TNFa* transcripts shared 98 and 98.5% identity, respectively, with published transcripts from the sterlet sturgeon (Transcripts XM_034013617.2 and XM_034909934.1, respectively). Lake sturgeon head kidney transcripts annotated as *IL-8* shared 94.8 and 94.5% identity to published transcripts from the Siberian sturgeon, *Acipenser baerii*, and the sterlet sturgeon, respectively (Transcripts MK140599.1 and XM_034035867.2, respectively). Finally, transcripts annotated as *IgM* shared conserved regions of 96.4, 95.2, 95, 95, and 93.4% identity to previously annotated transcripts from the Siberian sturgeon, beluga sturgeon, *Huso huso*, sterlet sturgeon, Russian sturgeon, *Acipenser gueldenstaedtii*, and Japanese sturgeon, *Acipenser schrenckii*, respectively (Transcripts KC734558.1, DQ257633.1, DQ257636.1, DQ257634.1 and DQ257635.1, respectively).

Primers for *C3* and *TICAM-1* were designed from an annotated and published white sturgeon, liver transcriptome (Doering et al., 2016) while primers for *Lysozyme-C* were designed from a lake sturgeon liver transcriptome (Thorstensen et al., 2022b). Transcripts for both *C3* and *TICAM-1* shared conserved regions with 98% identity to previously annotated transcripts from the sterlet sturgeon (Transcripts XM_034016062.2 and XM_034911846.1, respectively). Transcripts for *Lysozyme-C* shared conserved regions with 98.6, 99.4 and 99.1% identity to previously annotated transcripts from the sterlet sturgeon, Chinese sturgeon, *Acipenser sinensis*, and Dabry's sturgeon, *Acipenser dabryanus*, respectively (Transcripts XM_034058580.2, MF280234.1, MF135537.1, respectively).

A lake sturgeon gill transcriptome was used to design primers for potential reference genes *RPL13a*, eEF*1A1*, and *RPL4* (Thorstensen et al., 2022b; Bugg et al., 2022). Transcripts for *RPL13a* shared conserved regions with both sterlet sturgeon and the American paddlefish, 98.6 and 96% identity, respectively (Transcripts XM_034908381.1 and XM_041240517.1, respectively). Similarly, transcripts for *eEF1A1* shared conserved regions with the sterlet sturgeon, American

paddlefish, and additionally Dabry's sturgeon, with identities of 96.4, 95.4, and 98.4%, respectively (Transcripts XM_034915679.1, XM_041240787.1 and MH790258.1, respectively). Finally, transcripts annotated as *RPL4* shared conserved regions with previously annotated transcripts from the Siberian sturgeon, sterlet sturgeon, and American paddlefish, with identities of 99.8, 99.4 and 97.2%, respectively (Transcripts MG722839.1, XM_034049385.2 and XM_041218712.1, respectively).

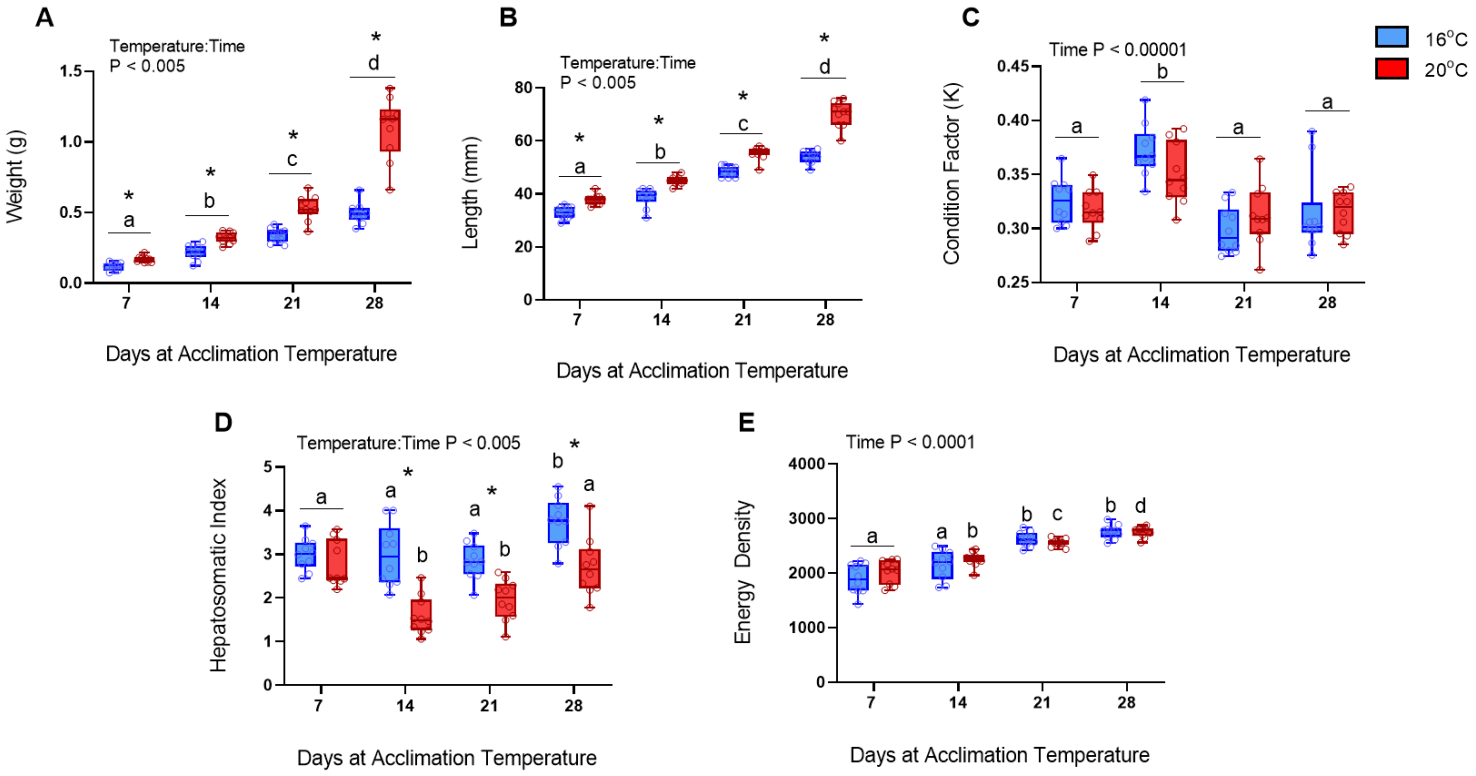

Fig. S1. A) Weight (g), B) length (mm), C) condition factor (K), D) hepatosomatic index (HSI), and E) energy density of developing lake sturgeon, *Acipenser fulvescens*, throughout 28 days acclimation to 16 and 20°C. Differences between treatments and timepoints were determined by two-factor ANOVA ($P < 0.05$) followed by Tukey's honestly significant different post-hoc test. *'s represent significance between 16 and 20°C acclimation treatments Lowercase letters a, b, c represent significance between timepoints, within an acclimation treatment. ($P < 0.05$; two-factor ANOVA). Data are expressed as mean +/- SEM (n = 10).

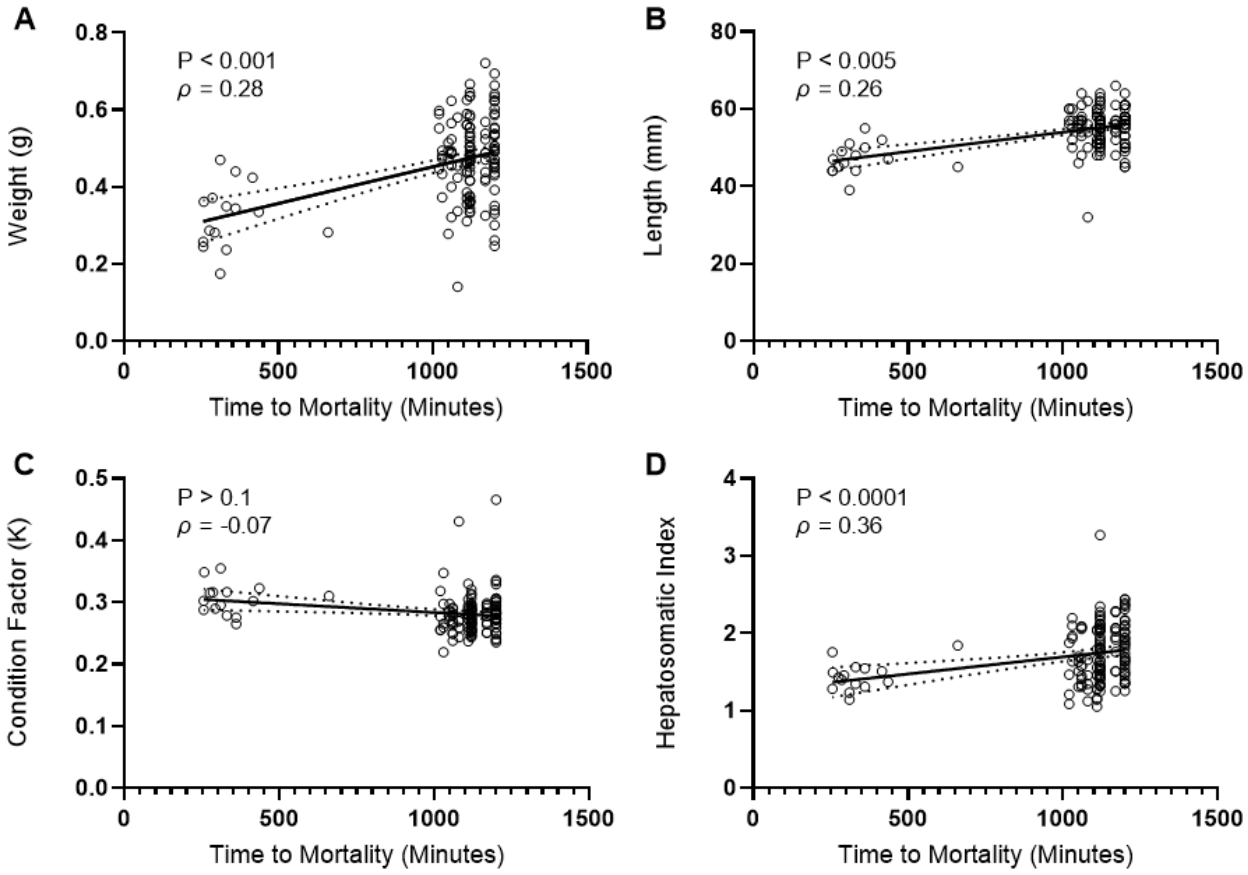

Fig. S2. The relationship between A) weight (g), B) length (mm), C) condition factor (K) and D) hepatosomatic index (HSI) and time to mortality of 20˚C acclimated developing lake sturgeon, *Acipenser fulvescens*, following exposure to 60 μg.ml^{-1} lipopolysaccharides. Significance was determined by Spearman's correlation. The solid line throughout the graph represents the best fit straight line surrounded by dotted lines representing the 95% confidence interval. Open circles represent individual lake sturgeon (n = 142).

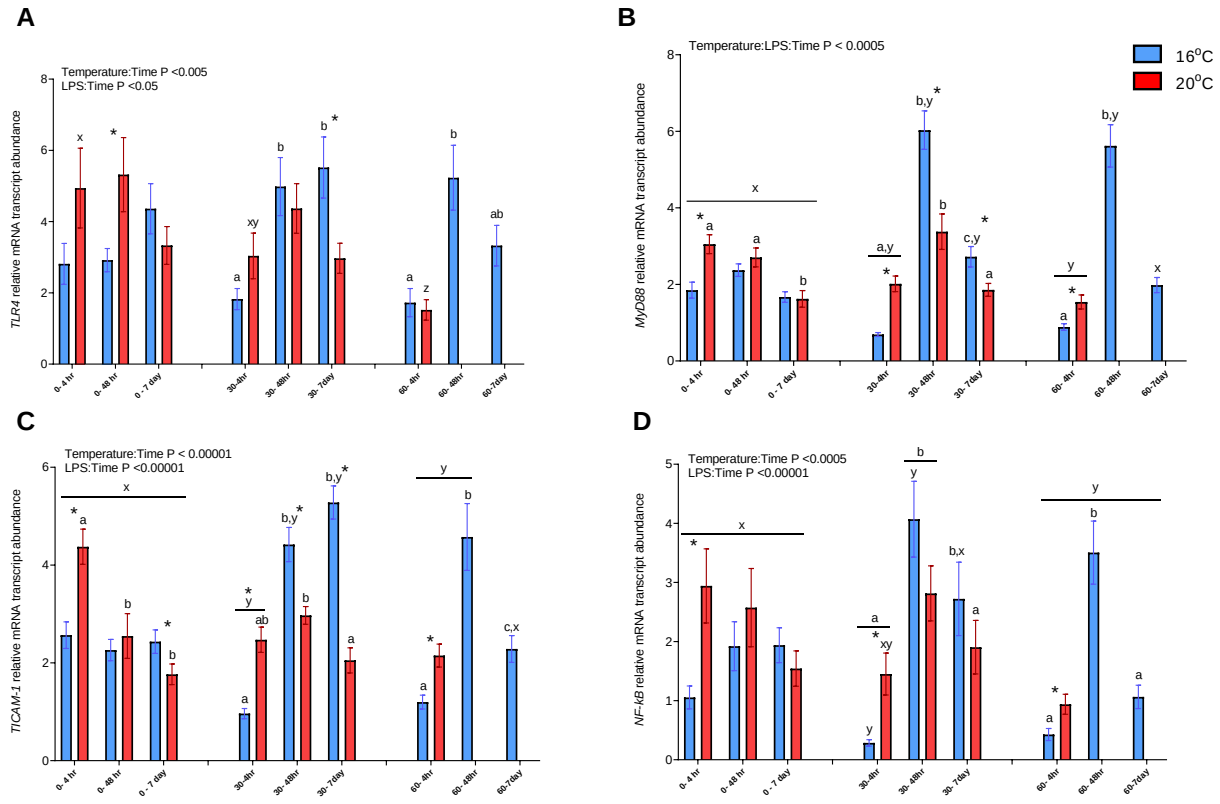

Fig. S3. Whole-body mRNA transcript abundance of genes involved in pathogen detection A) *Toll-like Receptor 4*, B) *MyD88*, C) *TICAM-1*, and D) *NF-kB* in developing lake sturgeon, *Acipenser fulvescens*, acclimated to 16 and 20°C and then exposed to 0, 30, and 60 μg.ml^{-1} of bacterial lipopolysaccharides, over a timeseries of 4 h exposure, 48 h exposure, and following a 7-day lipopolysaccharides-free recovery. Asterisks represent significance between acclimation treatments. Lowercase letters a, b, c represent significance between timepoints, within an exposure concentration and timepoint. Lowercase letters x, y, z represent significance in a given timepoint and acclimation temperature, throughout exposure concentrations ($P < 0.05$; three-factor ANOVA). Data are expressed as +/- SEM (n = 8-10).

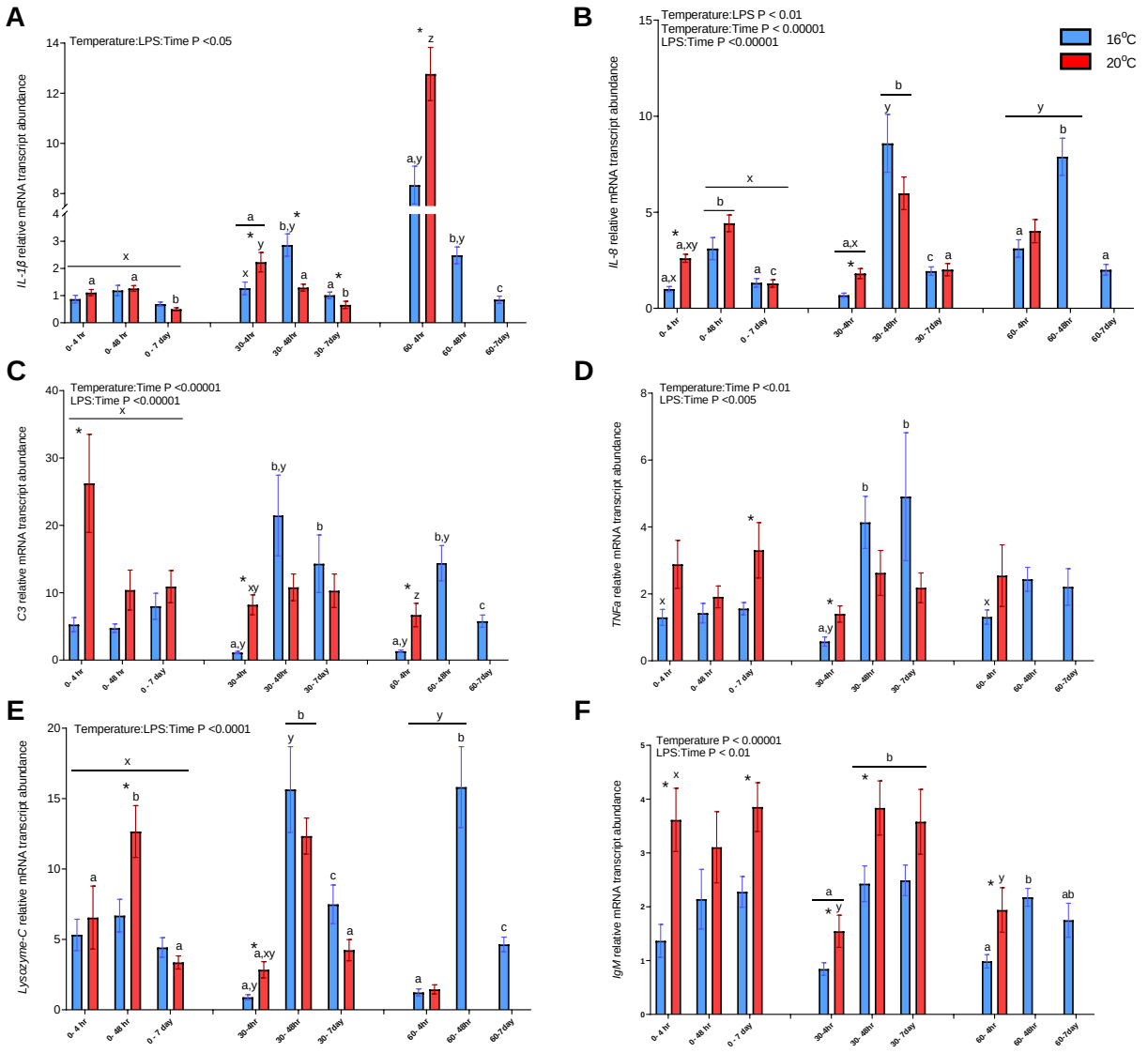

Fig. S4. Whole-body mRNA transcript abundance of genes involved in the innate immune response A) *IL-1β*, B) *IL-8*, C) *C3*, D) *TNFa*, E) *Lysozyme-C*, and F) *IgM* in developing lake sturgeon, *Acipenser fulvescens*, acclimated to 16 and 20°C and then exposed to 0, 30, and 60 μg.ml^{-1} of bacterial lipopolysaccharides, over a timeseries of 4 h exposure, 48 h exposure, and following a 7-day lipopolysaccharides-free recovery. Asterisks represent significance between acclimation treatments. Lowercase letters a, b, c represent significance between timepoints, within an exposure concentration and timepoint. Lowercase letters x, y, z represent significance in a given timepoint and acclimation temperature, throughout exposure concentrations ($P < 0.05$; three-factor ANOVA). Data are expressed as +/- SEM (n = 9-10).

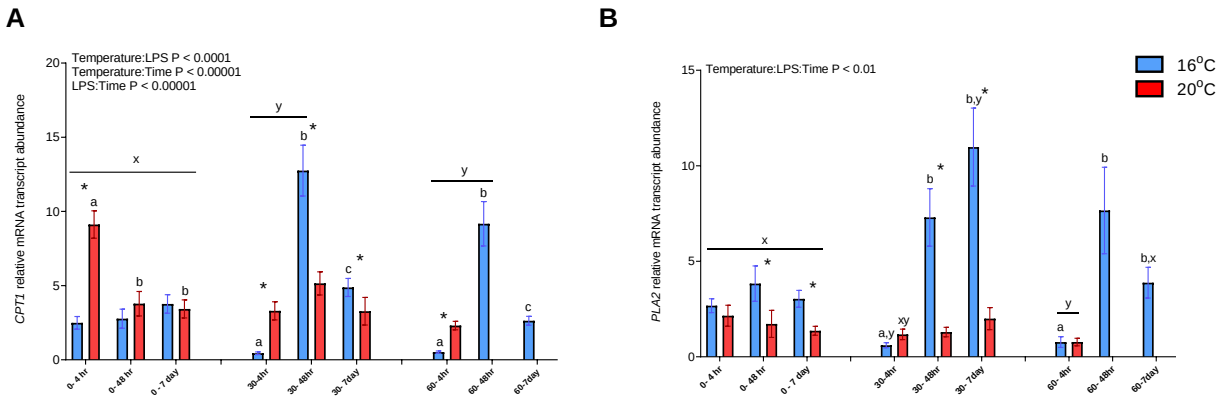

Fig. S5. Whole-body mRNA transcript abundance of genes involved in the fatty acid response A) *CPT1* and B) *PLA2* in developing lake sturgeon, *Acipenser fulvescens*, acclimated to 16 and 20°C and then exposed to 0, 30, and 60 µg.ml^{-1} of bacterial lipopolysaccharides, over a timeseries of 4 h exposure, 48 h exposure, and following a 7-day lipopolysaccharides-free recovery. Asterisks represent significance between acclimation treatments. Lowercase letters a, b, c represent significance between timepoints, within an exposure concentration and timepoint. Lowercase letters x, y, z represent significance in a given timepoint and acclimation temperature, throughout exposure concentrations ($P < 0.05$; three-factor ANOVA). Data are expressed as +/- SEM (n = 8-10).

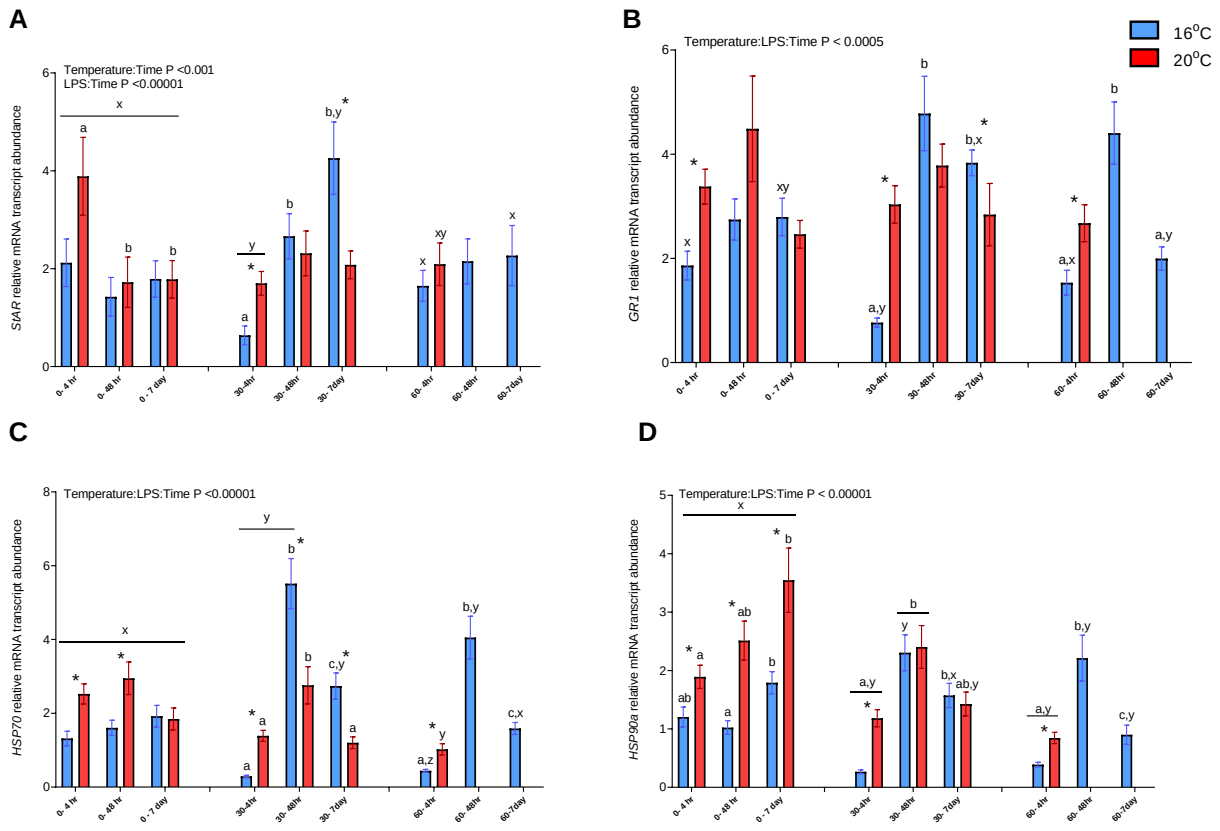

Fig. S6. Whole-body mRNA transcript abundance of genes involved in the glucocorticoid stress response A) *StAR*, B) *GR1*, C) *HSP70* , D) *HSP90a* in developing lake sturgeon, *Acipenser fulvescens*, acclimated to 16 and 20°C and then exposed to 0, 30, and 60 μg.ml^{-1} of bacterial lipopolysaccharides, over a timeseries of 4 h exposure, 48 h exposure, and following a 7 day lipopolysaccharides-free recovery. Asterisks represent significance between acclimation treatments. Lowercase letters a, b, c represent significance between timepoints, within an exposure concentration and timepoint. Lowercase letters x, y, z represent significance in a given timepoint and acclimation temperature, throughout exposure concentrations ($P < 0.05$; three-factor ANOVA). Data are expressed as +/- SEM (n = 7-10).

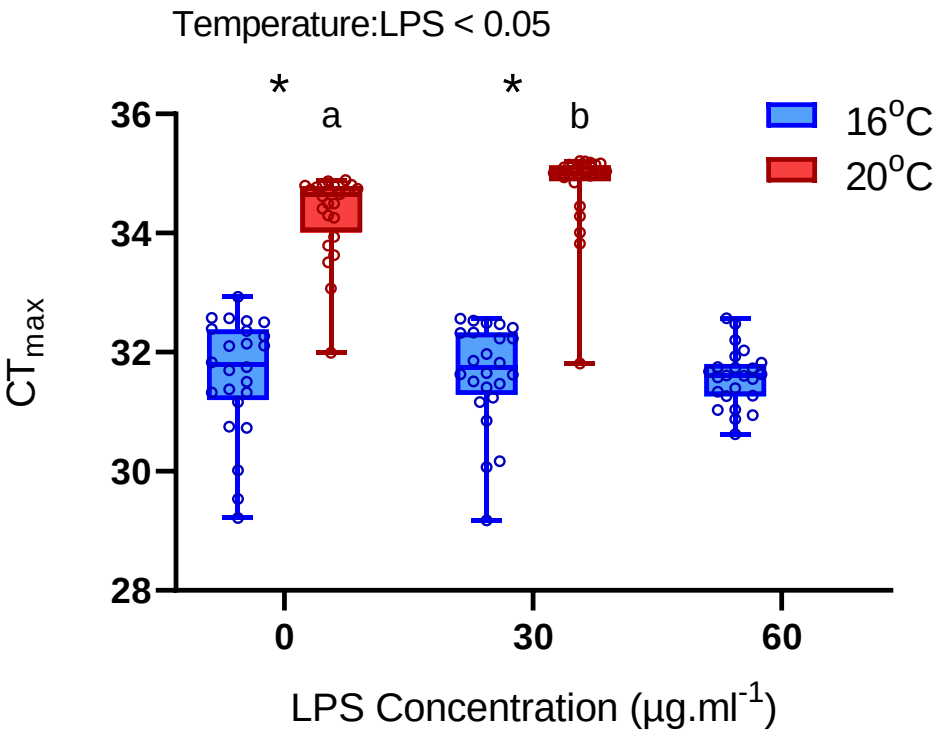

Fig. S7. Critical thermal maximum (CT_{max}) of 16 and 20°C acclimated developing lake sturgeon, *Acipenser fulvescens*, following a 7-day recovery from 48 h exposure trials in lipopolysaccharide concentrations of 0, 30, and 60 µg.ml^{-1}. Differences between treatments were determined by two-factor ANOVA ($P < 0.05$) followed by Tukey's honestly significant different post-hoc test. *'s represent significance between 16 and 20°C acclimation treatments within a lipopolysaccharide exposure concentration. Lowercase letters a and b represent significance across treatment concentrations within a single acclimation treatment (n = 24).

Table S1.

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