

Fig. S1. Sunfish transcriptome homologies. Distribution of species containing the most closely related homologue for the unigenes in the bluegill sunfish (left panels) and redear sunfish (right panels).

Supplemental Figure 2

A – Cellular Processes
 B – Environmental Information Processing
 C – Genetic Information Processing
 D – Metabolism
 E – Organismal Systems

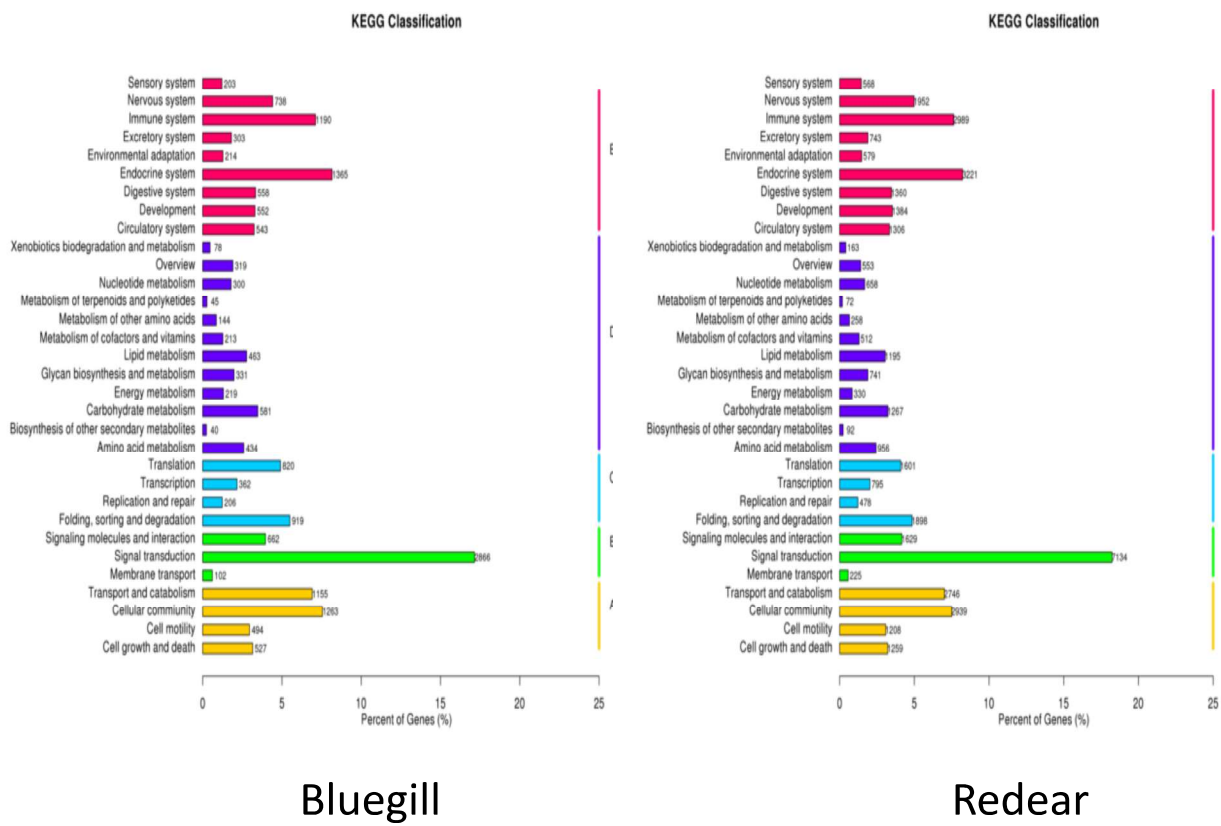


Fig. S2. Sunfish transcriptome annotations. Distribution of functional classes of unigene annotation using the KEGG database organized by the following: A = cellular processes (yellow), B = environmental information processing (green), C = genetic information processing (blue), D = metabolism (purple), and E = organismal systems (red). Bluegill are on the left and redear on the right.

Supplemental Figure 3

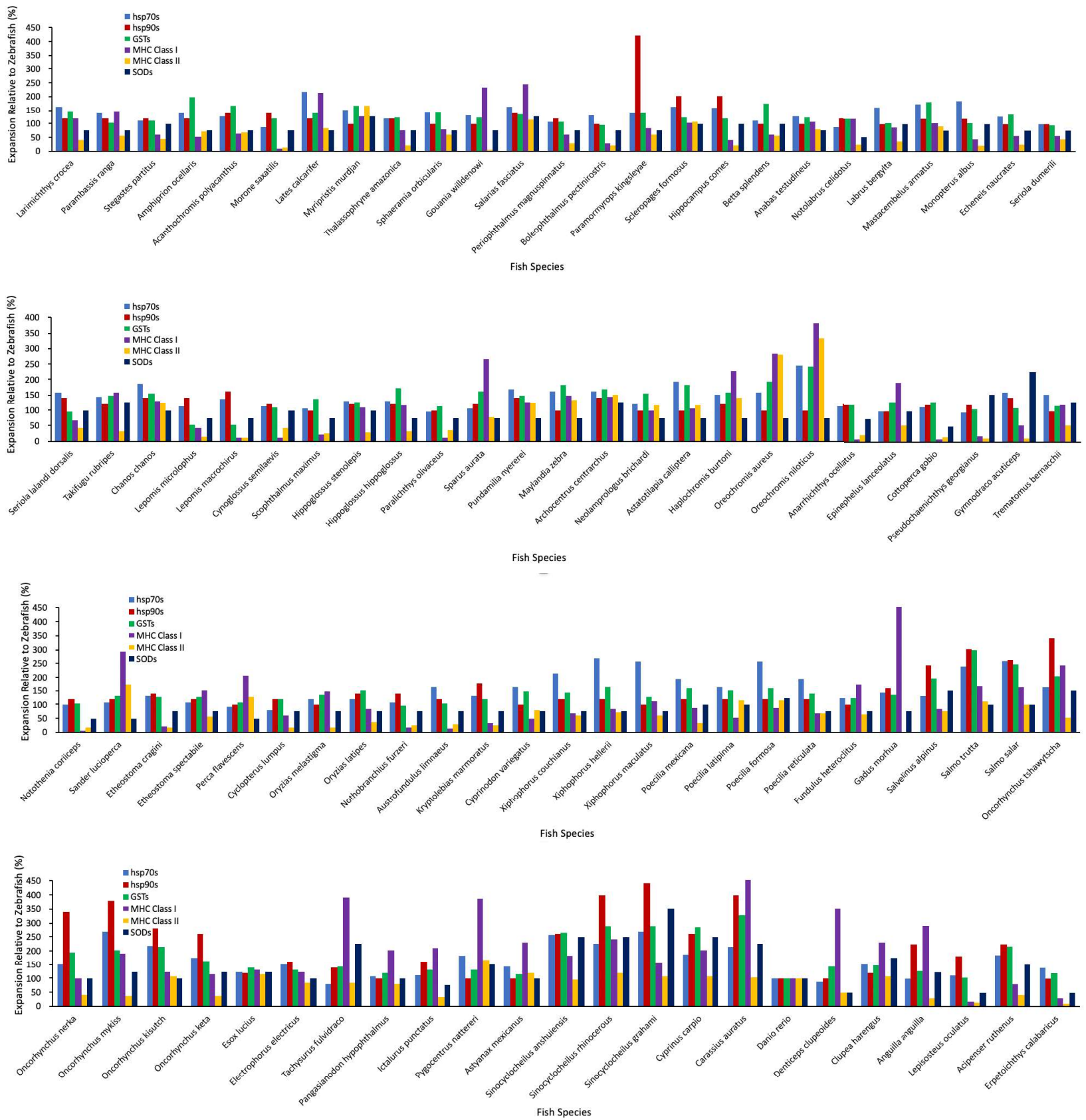


Fig. S3. Identification of stress response gene expansions in well-annotated fish genomes. BLAST searches were conducted starting with zebrafish coding regions for selected stress response gene families (HSP70, HSP90, GST, MHC, and SOD) across all fish in the RefSeq database. Data are plotted as a percentage relative to zebrafish.

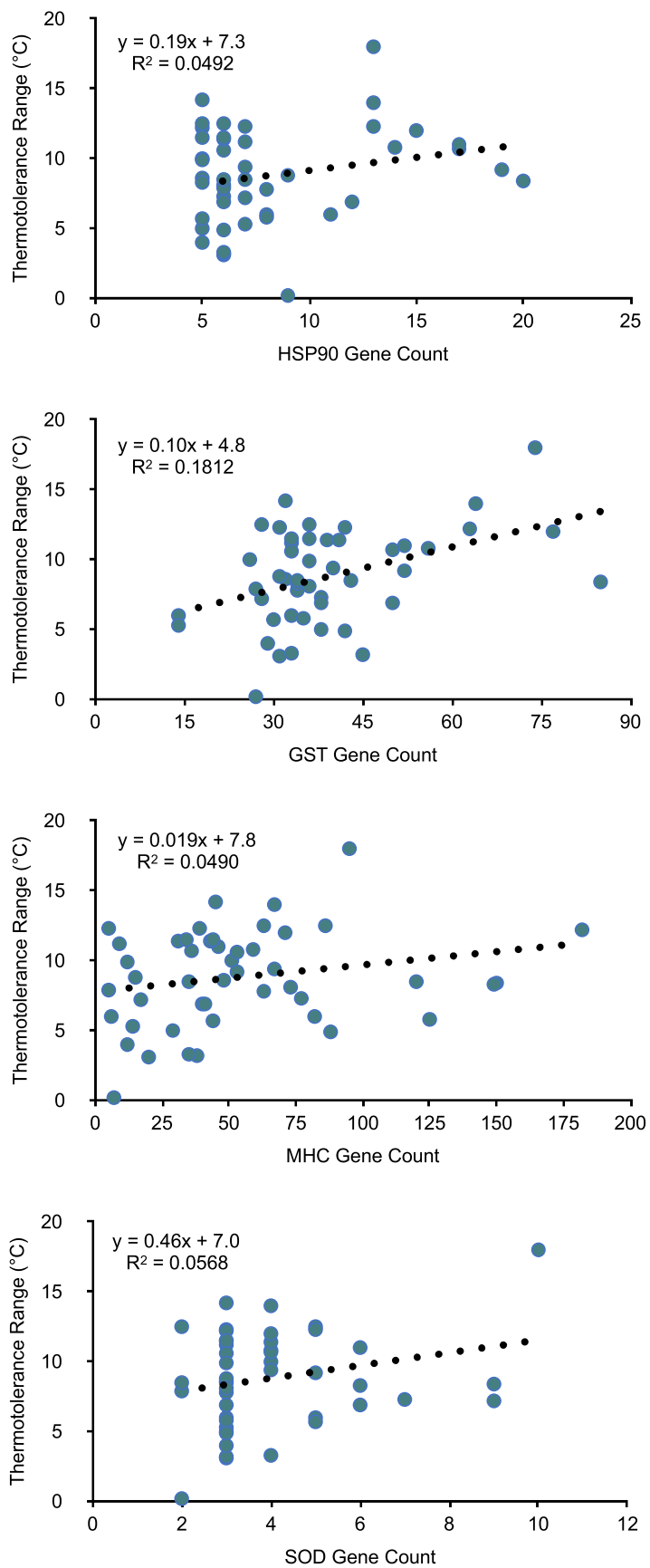


Fig. S4. Little correlation between HSP90, MHC, GST and SOD gene counts and thermotolerance range. The number of gene family paralogs identified in the RefSeq genome was plotted relative to the thermotolerance range for all fish included in both databases. Line represents a least squares linear regression of the data. The equation describing the line and the R^2 correlation are included.

Table S1. Stress response genes in sunfish.

[Click here to download Table S1](#)

Table S2. Stress response genes in teleost fish.

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Table S3. Correlation between stress response genes, thermotolerance and invasive classification.

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