Developmental proteomes of a metamorphosing mollusc at different temperatures

Shelly A. Trigg¹, Kaitlyn R. Mitchell¹, Rhonda Elliot Thompson¹, Benoit Eudeline², Brent Vadopalas³, Emma B. Timmins-Schiffman⁴, and Steven B. Roberts¹

¹School of Aquatic and Fishery Sciences, University of Washington, Seattle, Washington, USA

Supplemental Figures:

Supplemental Figure 1. PCA of all technical replicate samples. (page 2)

Supplemental Figure 2. Principal component analysis plots of PC loadings for the top 100 ranked proteins. (page 2)

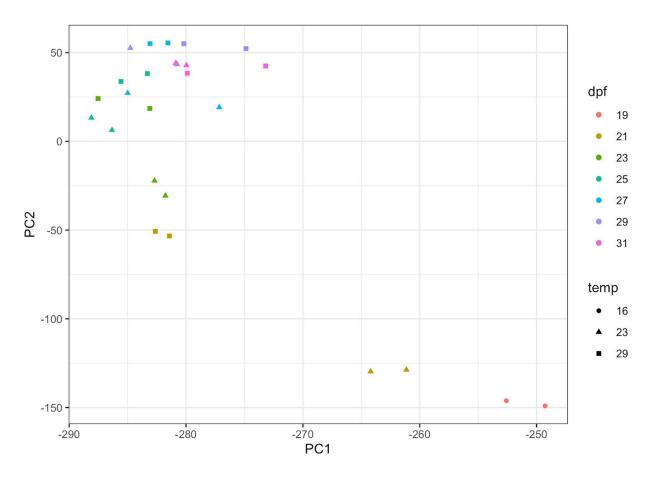
Supplemental Figure 3. ANOVA-simultaneous component analysis plots of PC loadings for all proteins. (page 3)

²Taylor Shellfish Hatchery, Quilcene, Washington, USA

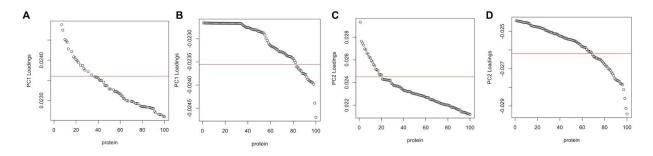
³Washington Sea Grant, University of Washington, Seattle, Washington, USA

⁴Department of Genome Sciences, University of Washington, Seattle, Washington, USA

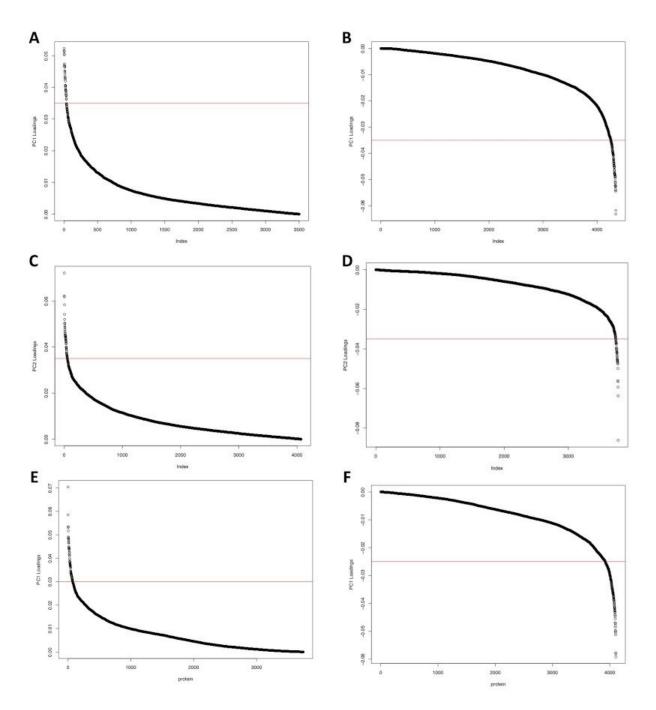
Trigg, SA et al. - Supplemental Figures



Supplemental Figure 1. PCA of all technical replicate samples.



Supplemental Figure 2. Principal component analysis plots of PC loadings for the top 100 ranked proteins. (**A**) Proteins with the top 100 most positive PC1 loadings thresholded (red line) at 0.0236. (**B**) Proteins with the top 100 most negative PC1 loadings thresholded (red line) at -0.02355. (**C**) Proteins with the top 100 most positive PC2 loadings thresholded (red line) at 0.0245. (**D**) Proteins with the top 100 most negative PC2 loadings thresholded (red line) at -0.0262.



Supplemental Figure 3. ANOVA-simultaneous component analysis plots of PC loadings for all proteins. **(a)** Positive PC1 loadings for time effect. **(b)** Negative PC1 loadings for time effect. **(c)** Positive PC2 loadings for time effect. **(d)** Negative PC2 loadings for time effect. **(e)** Positive PC1 loadings for temperature effect. Red line indicates the significance threshold loadings value set at the point of diminishing returns (0.035, -0.035, 0.035, -0.035, 0.03, and -0.025, respectively).