

Temporal proteomic profiling reveals insight into critical developmental processes and temperature-influenced physiological response differences in a bivalve mollusc

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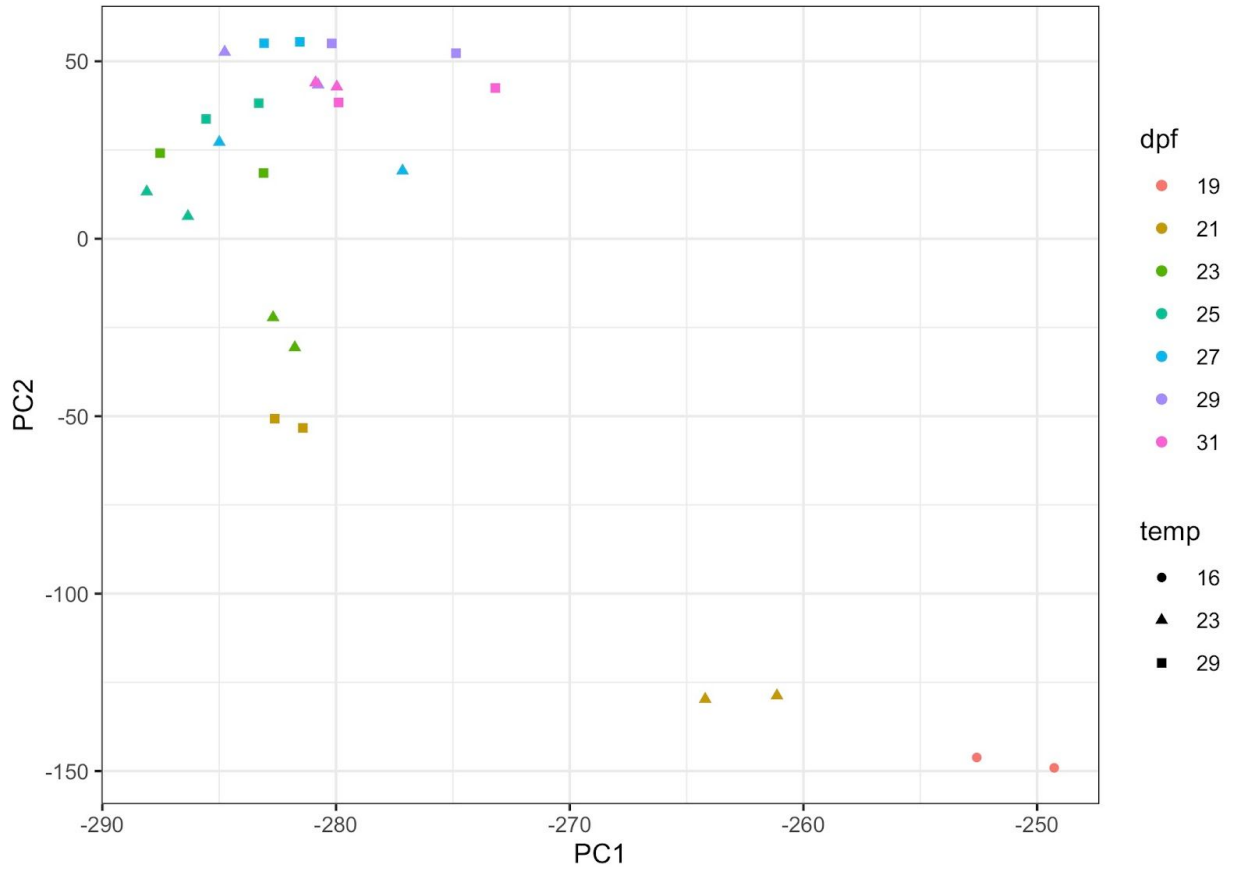
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Supplemental Figures:

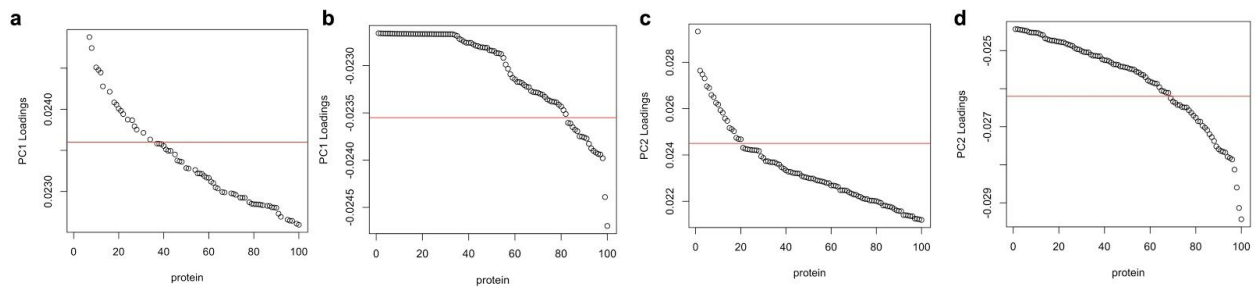
Supplemental Figure 1. PCA of all technical replicate samples. (page 2)

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

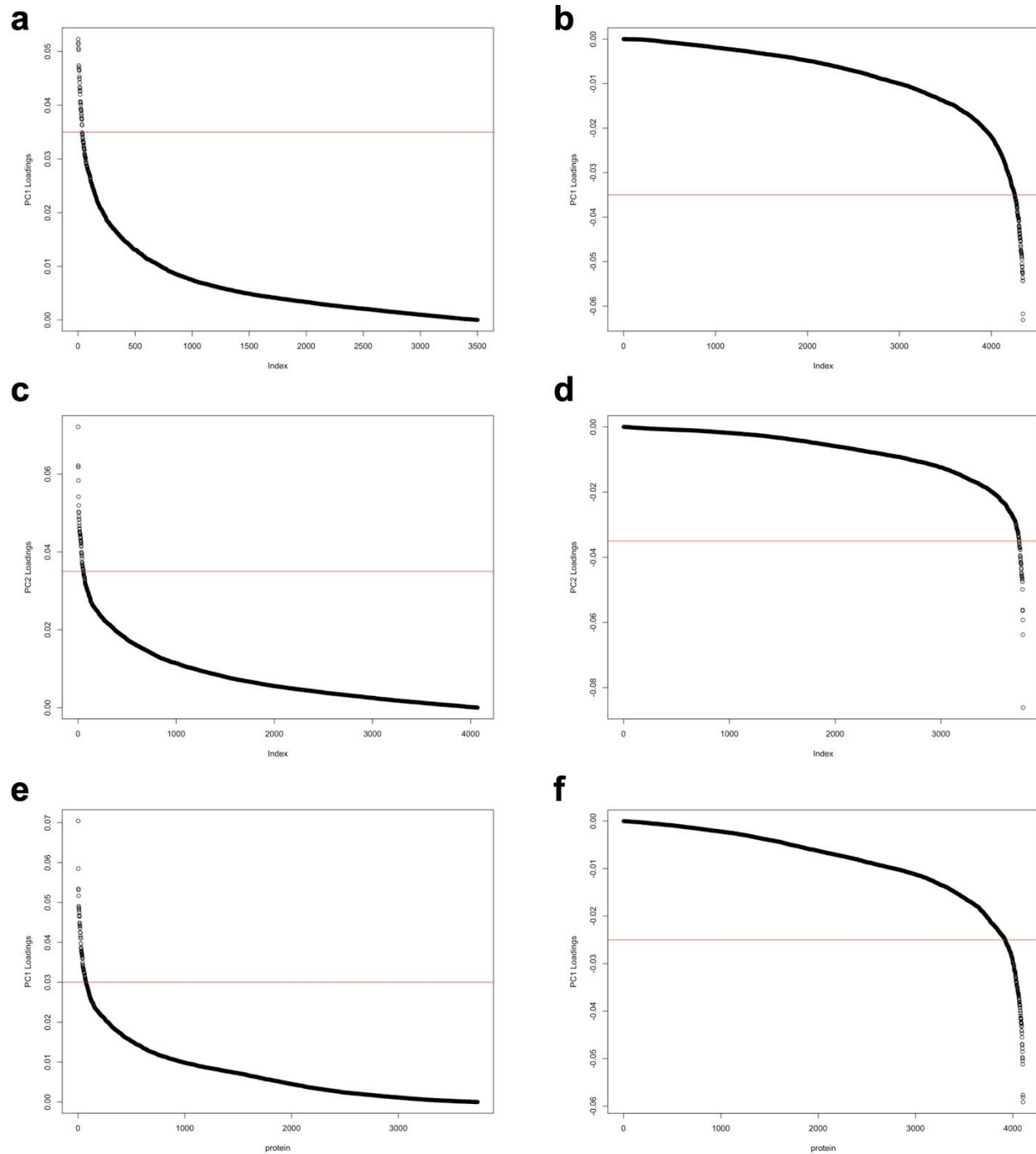
Supplemental Figure 3. ANOVA-simultaneous component analysis plots of PC loadings for all proteins. (page 3)



Supplemental Figure 1. PCA of all technical replicate samples.



Supplemental Figure 2. Preliminary principal component analysis plots of PC loadings for the top 100 ranked proteins. **(a)** Proteins with the top 100 highest positive PC1 loadings thresholded (red line) at 0.0236. **(b)** Proteins with the top 100 lowest negative PC1 loadings thresholded (red line) at -0.0235. **(c)** Proteins with the top 100 highest positive PC2 loadings thresholded (red line) at 0.0245. **(d)** Proteins with the top 100 lowest 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. **(f)** Negative 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).