SUPPLEMENTARY FIGURES for the research article

Omics signatures of tissue injury and hemorrhagic shock in swine

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Running title: ***Omics signature of TI/HS in swine***

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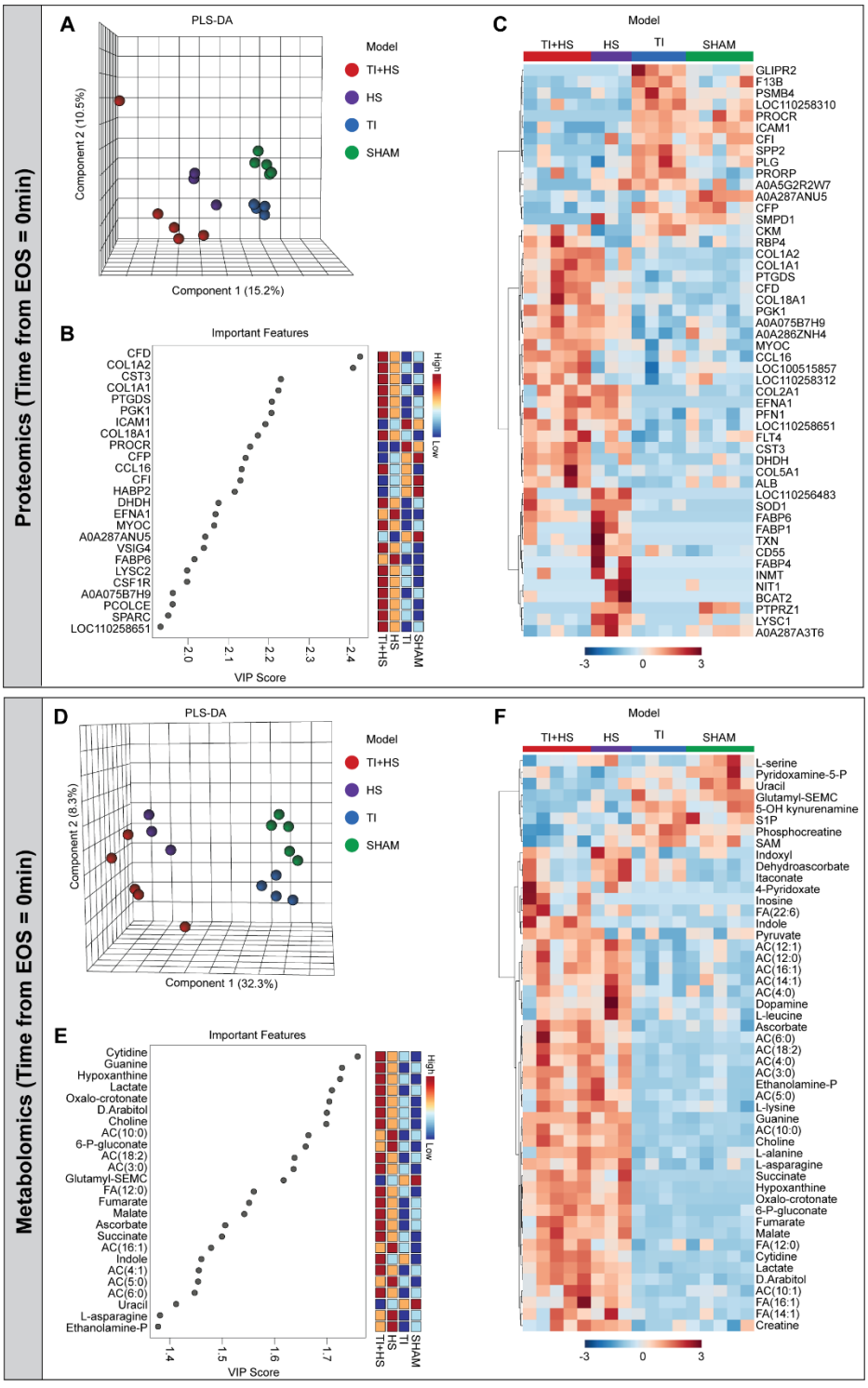
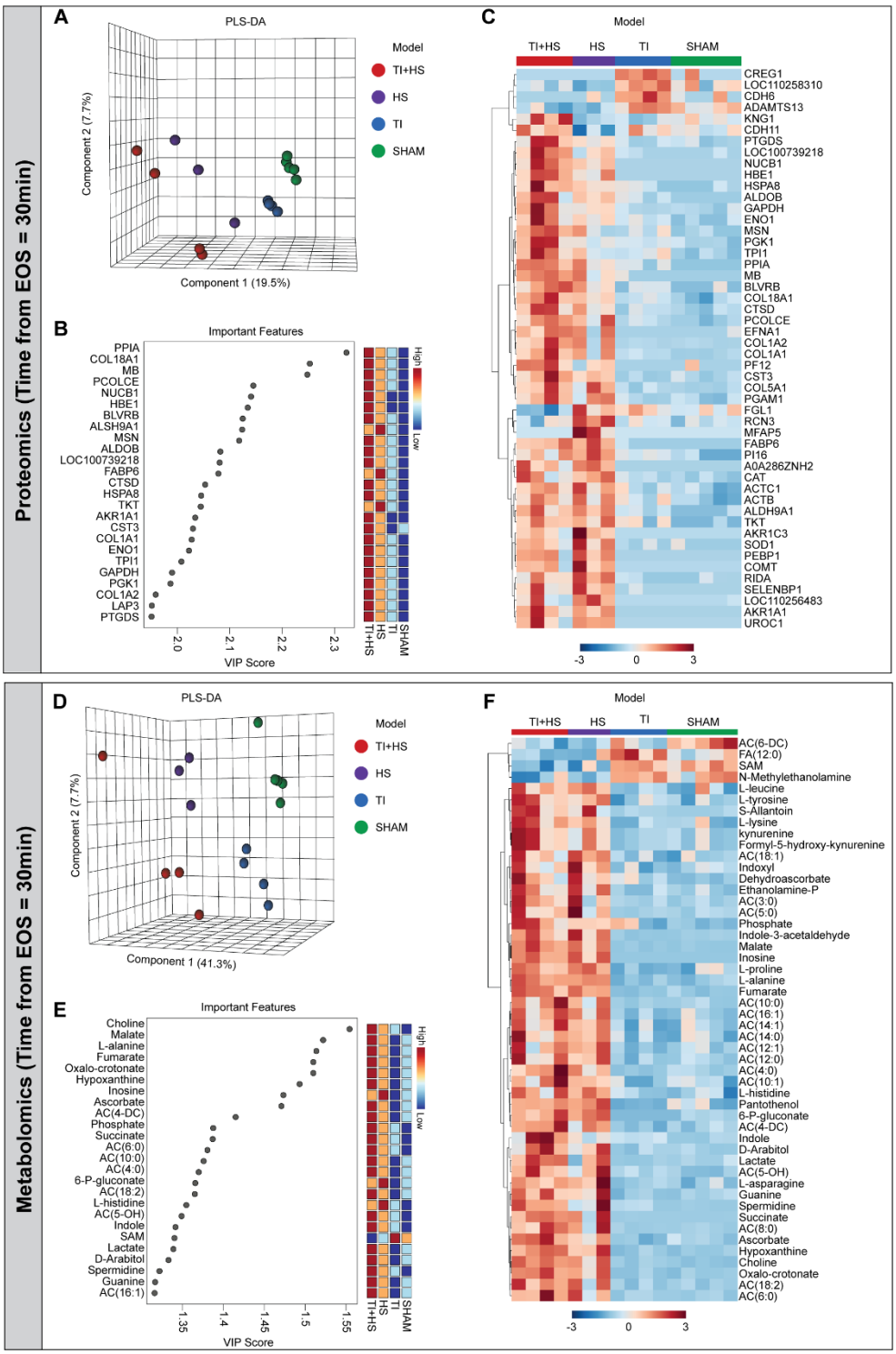
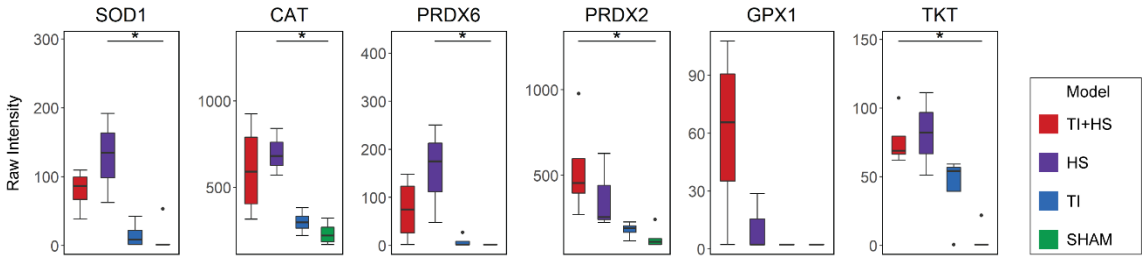


Supplementary Figure 1. Breakdown of omics data 0min from EOS. **A)** PLS-DA of swine proteomes clustered by experiment model and component 1 explained 15.2% of the variance. **B)** The proteins with top 25 VIP scores. Relative abundance per model was represented using row side colors. **C)** Heat map of the top 50 most significantly different proteins across the swine models as measured by ANOVA. **D)** PLS-DA of swine metabolomes clustered by experiment model and component 1 explained 32.2% of the variance. **E)** The metabolites with top 25 VIP scores. Relative abundance per model was represented using row side colors. **F)** Heat map of the top 50 most significantly different metabolites across the swine models as measured by ANOVA.

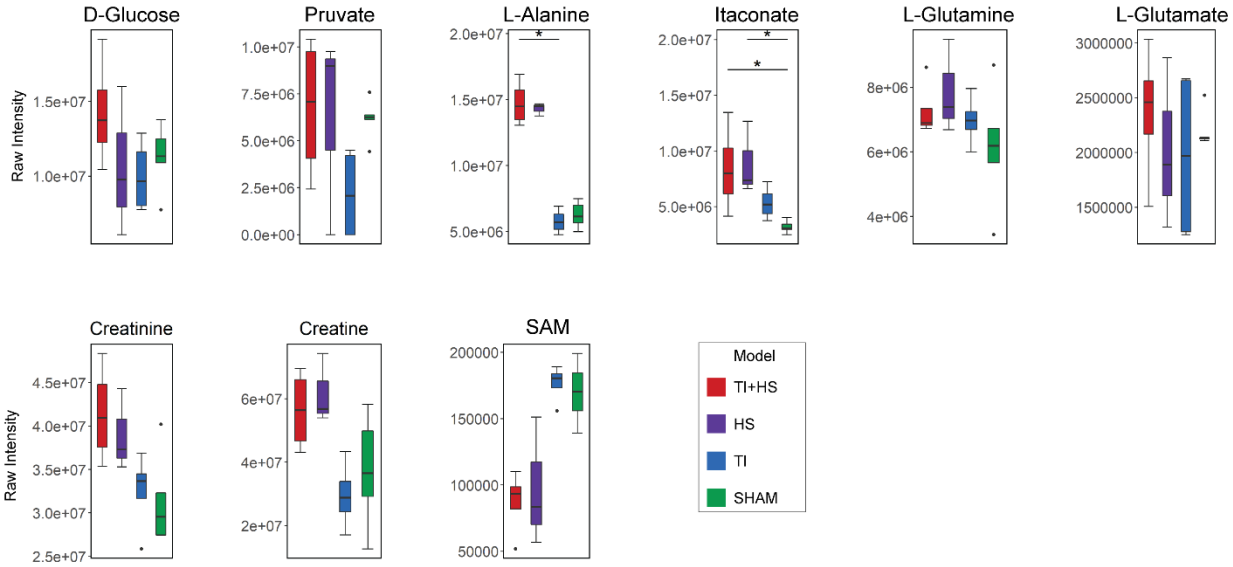


Supplementary Figure 2. Breakdown of omics data 30min from EOS. Proteomics and metabolomics data for the time point 30min from EOS was selected for further elaboration. Raw proteomics and metabolomics data was auto scale normalized separately prior to analysis. **A)** Proteomes were distinguished by swine model as measured by PLS-DA. Component 1 explained 19.5% of the variance observed in the PLS-DA model. **B)** The top 25 proteins driving separation between the swine models in the PLS-DA model at 30m from EOS as measured by VIP. Row side colors reflect protein abundance relative to each swine model. **C)** Heat map of top 50 proteins significantly different between swine models as measured by ANOVA. **D)** PLS-DA of swine metabolomes showed separation dependent upon model, where component 1 explained 41.3% of the variance. **E)** VIP scores for the top 25 metabolites driving separation

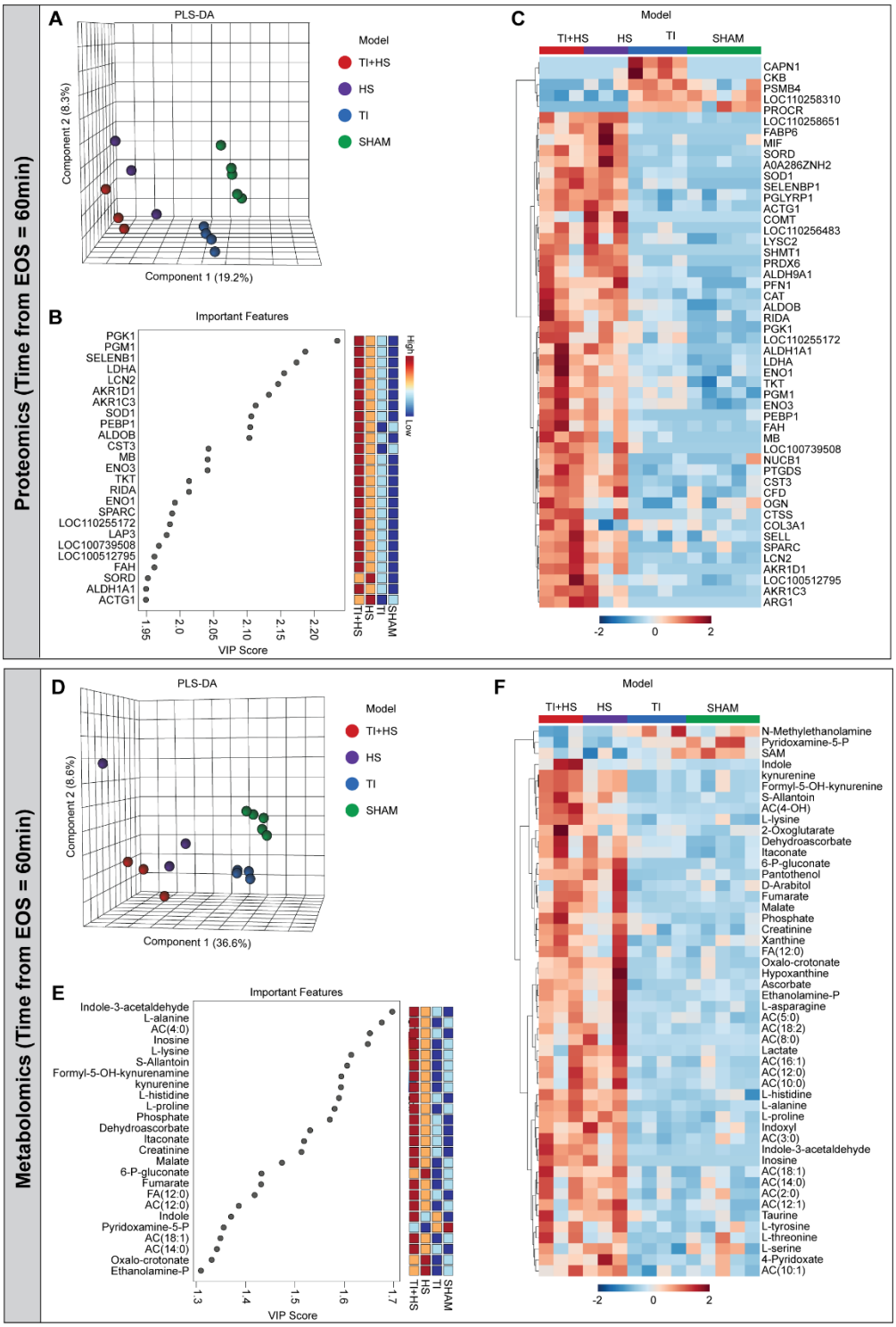
between the swine models in the PLS-DA model at 30m from EOS. Row side colors reflect protein abundance relative to each swine model. **F)** Heat map of top 50 proteins significantly different between swine models as measured by ANOVA.



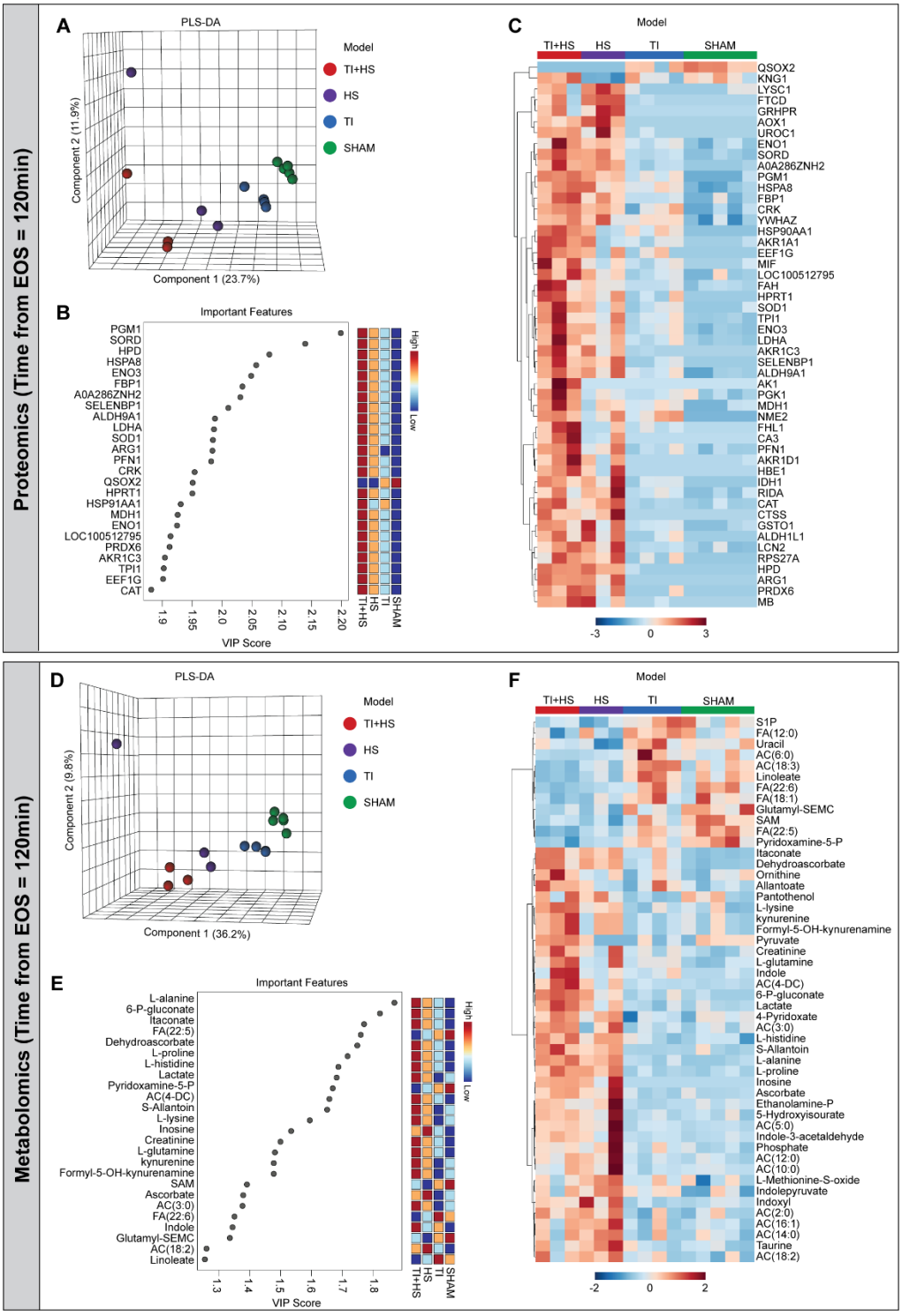
Supplementary Figure 3. Protein markers of inflammation. Proteins significantly different between swine models at 30min from EOS as measured by ANOVA were selected for further analysis using the Dunn's Test for multiple pairwise comparisons. Raw proteins values were used in the comparisons between swine models and significance was represented with: * P < 0.01



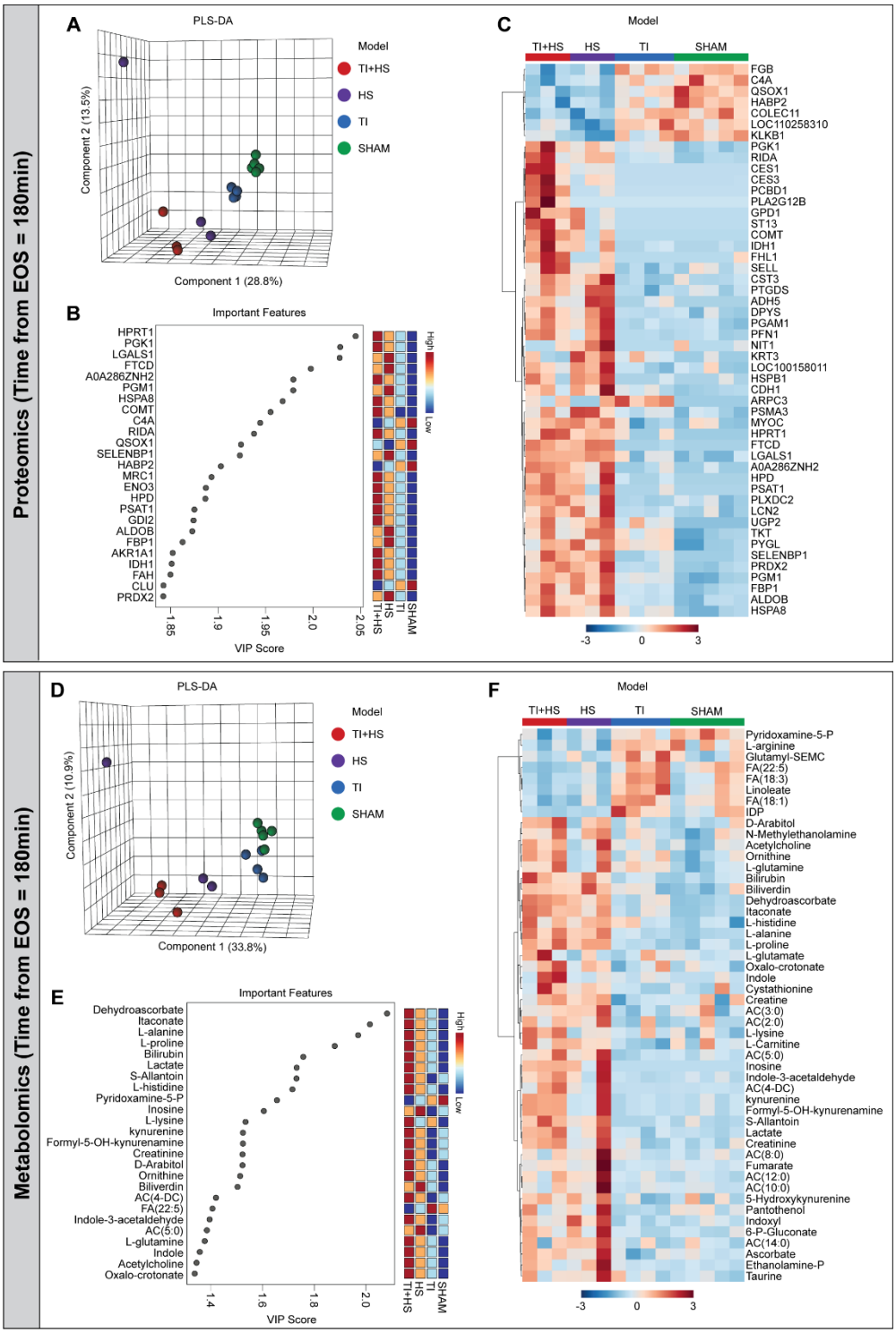
Supplementary Figure 4. Metabolic markers of dysregulated energy metabolism and mitochondrial dysfunction. Metabolites significantly different between swine models at 30min from EOS as measured by ANOVA were selected for further analysis using the Dunn's Test for multiple pairwise comparisons. Raw metabolite values were used in the comparisons between swine models and significance was represented with: * P < 0.01



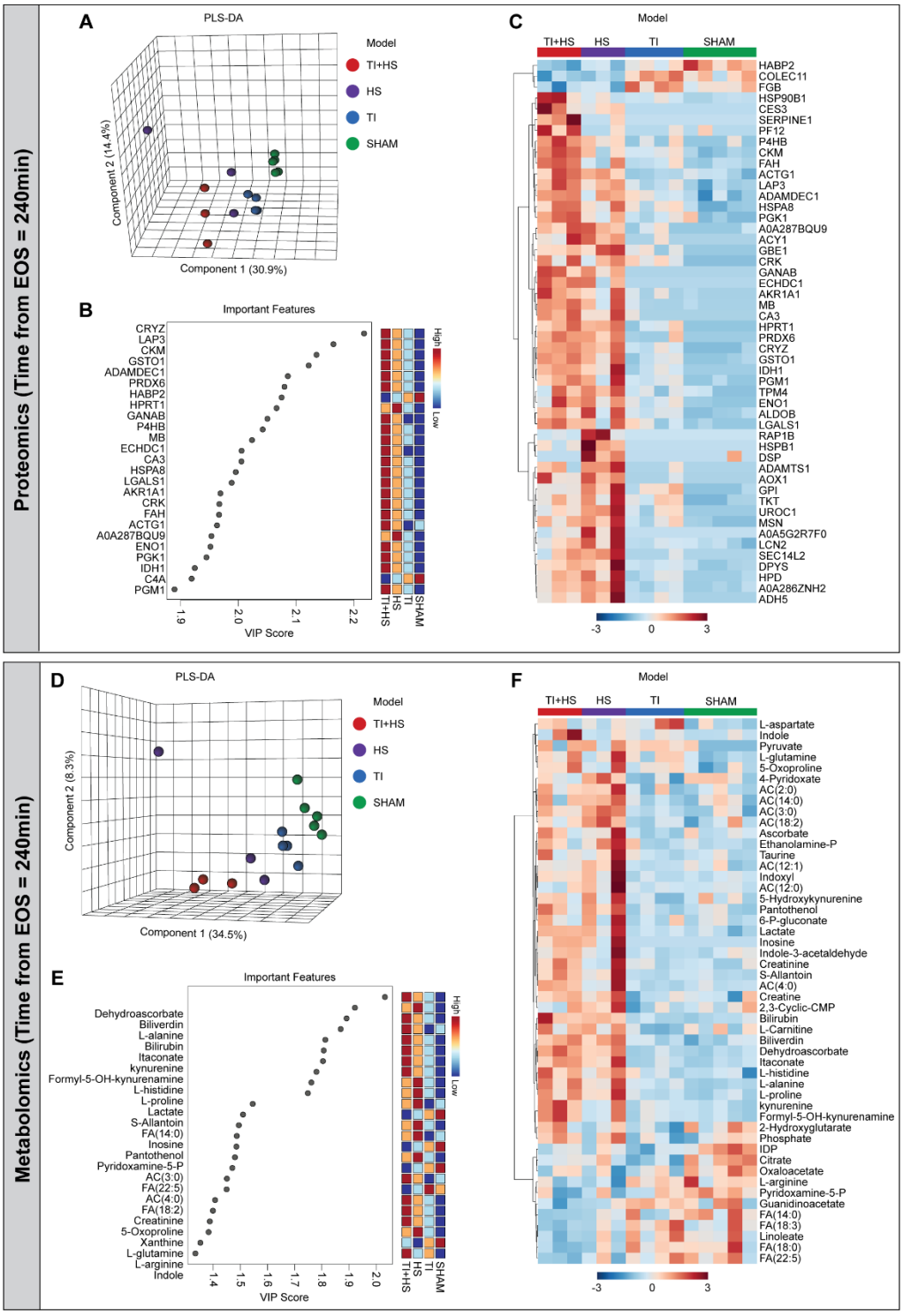
Supplementary Figure 5. Breakdown of omics data 60min from EOS. **A)** PLS-DA of swine proteomes clustered by experiment model and component 1 explained 19.2% of the variance. **B)** The proteins with top 25 VIP scores. Relative abundance per model was represented using row side colors. **C)** Heat map of the top 50 most significantly different proteins across the swine models as measured by ANOVA. **D)** PLS-DA of swine metabolomes clustered by experiment model and component 1 explained 36.6% of the variance. **E)** The metabolites with top 25 VIP scores. Relative abundance per model was represented using row side colors. **F)** Heat map of the top 50 most significantly different metabolites across the swine models as measured by ANOVA.



Supplementary Figure 6. Breakdown of omics data 120min from EOS. A) PLS-DA of swine proteomes clustered by experiment model and component 1 explained 23.7% of the variance. **B)** The proteins with top 25 VIP scores. Relative abundance per model was represented using row side colors. **C)** Heat map of the top 50 most significantly different proteins across the swine models as measured by ANOVA. **D)** PLS-DA of swine metabolomes clustered by experiment model and component 1 explained 36.2% of the variance. **E)** The metabolites with top 25 VIP scores. Relative abundance per model was represented using row side colors. **F)** Heat map of the top 50 most significantly different metabolites across the swine models as measured by ANOVA.



Supplementary Figure 7. Breakdown of omics data 180min from EOS. **A)** PLS-DA of swine proteomes clustered by experiment model and component 1 explained 28.8% of the variance. **B)** The proteins with top 25 VIP scores. Relative abundance per model was represented using row side colors. **C)** Heat map of the top 50 most significantly different proteins across the swine models as measured by ANOVA. **D)** PLS-DA of swine metabolomes clustered by experiment model and component 1 explained 33.8% of the variance. **E)** The metabolites with top 25 VIP scores. Relative abundance per model was represented using row side colors. **F)** Heat map of the top 50 most significantly different metabolites across the swine models as measured by ANOVA.



Supplementary Figure 8. Breakdown of omics data 240min from EOS. **A)** PLS-DA of swine proteomes clustered by experiment model and component 1 explained 30.9% of the variance. **B)** The proteins with top 25 VIP scores. Relative abundance per model was represented using row side colors. **C)** Heat map of the top 50 most significantly different proteins across the swine models as measured by ANOVA. **D)** PLS-DA of swine metabolomes clustered by experiment model and component 1 explained 34.5% of the variance. **E)** The metabolites with top 25 VIP scores. Relative abundance per model was represented using row side colors. **F)** Heat map of the top 50 most significantly different metabolites across the swine models as measured by ANOVA.