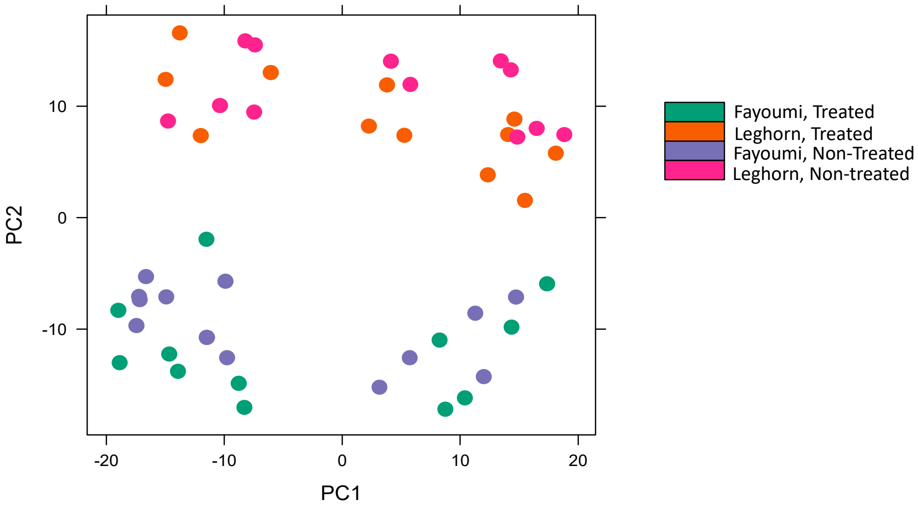

Figure S1: Principle component analysis of sample clustering of all RNA-Seq samples. Samples appear to cluster primarily due to the genetic line rather than treatment state.

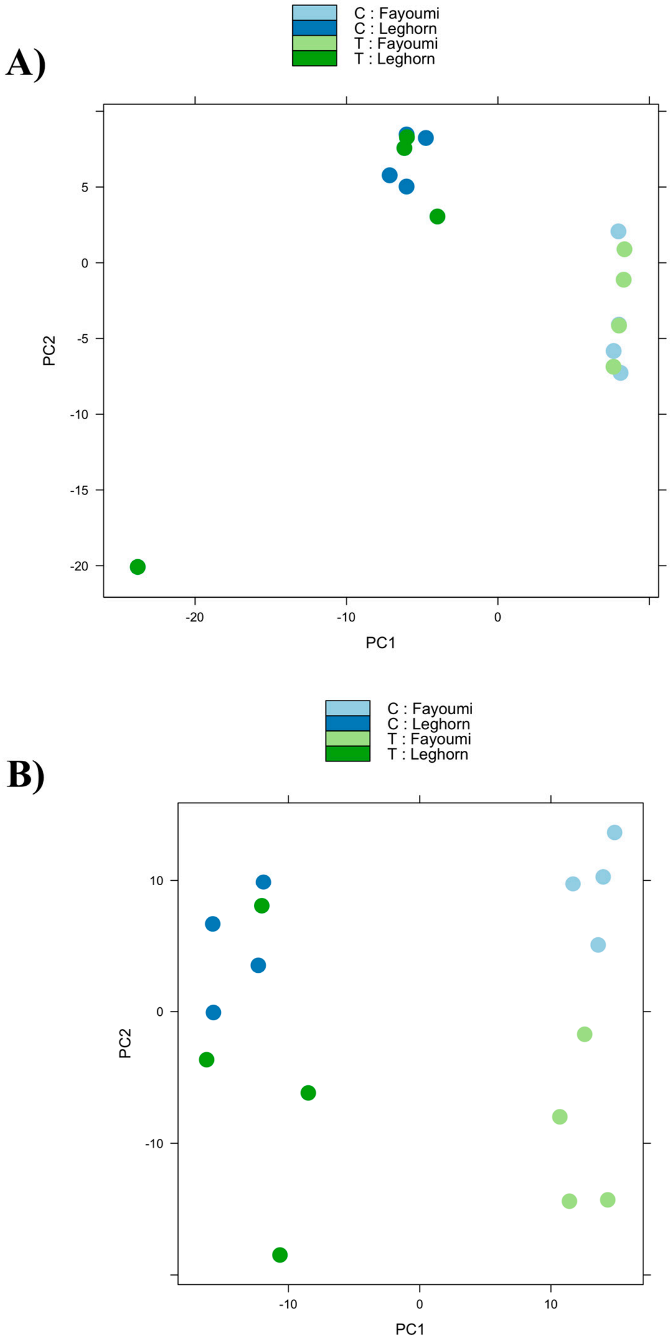

Figure S2: Principal component analysis demonstrating the clustering of proteomic samples at **A)** 2 dpi and **B)** 6 dpi.