



**Figure S3. Clust analysis of the *Salisipilia sapeloensis* transcriptomic dataset across all conditions.** The analysis resulted in 19 clusters and includes 2165 of the 4592 oomycete-affiliated genes. The y-axis shows the relative expression based on the  $\text{TPM}_{\text{TMM-normalized}}$  values and was normalized using a normalization step built-in in the clust analysis. The three conditions are shown on the x-axis. High values indicate a high  $\text{TPM}_{\text{TMM-normalized}}$  and low values indicate a low  $\text{TPM}_{\text{TMM-normalized}}$ . Genes with low expression in all three conditions were removed from the analysis.