



Supplementary figure 1. **Gene ontology Cytoscape maps.** Transcripts identified as differentially regulated by SAM between Δ US17 and AD169 at 12 hpi were categorized into gene ontology biological process categories using Cytoscape with the BiNGO plugin. Network maps were generated for all categories where $p < 0.0001$. Maps were clustered using the orthogonal layout option within cytoscape to group closely related gene ontology categories together. Colored boxes depict major biological themes that were quantified in Fig. 4.