



Figure S6. Test to see if transcriptomic changes due to virus used for infection are simply delayed or are qualitatively different. Differential expression analysis was run between IAV 24HPI and SCV2 48HPI infected samples at 37°C (A). Significantly differentially expressed genes ($p < 0.05$, $\log_2\text{FC} > 1.5$) were then used in pathway enrichment analysis (B). The size of the bars indicate the number of genes in that pathway identified, and the bars are colored based on p value.