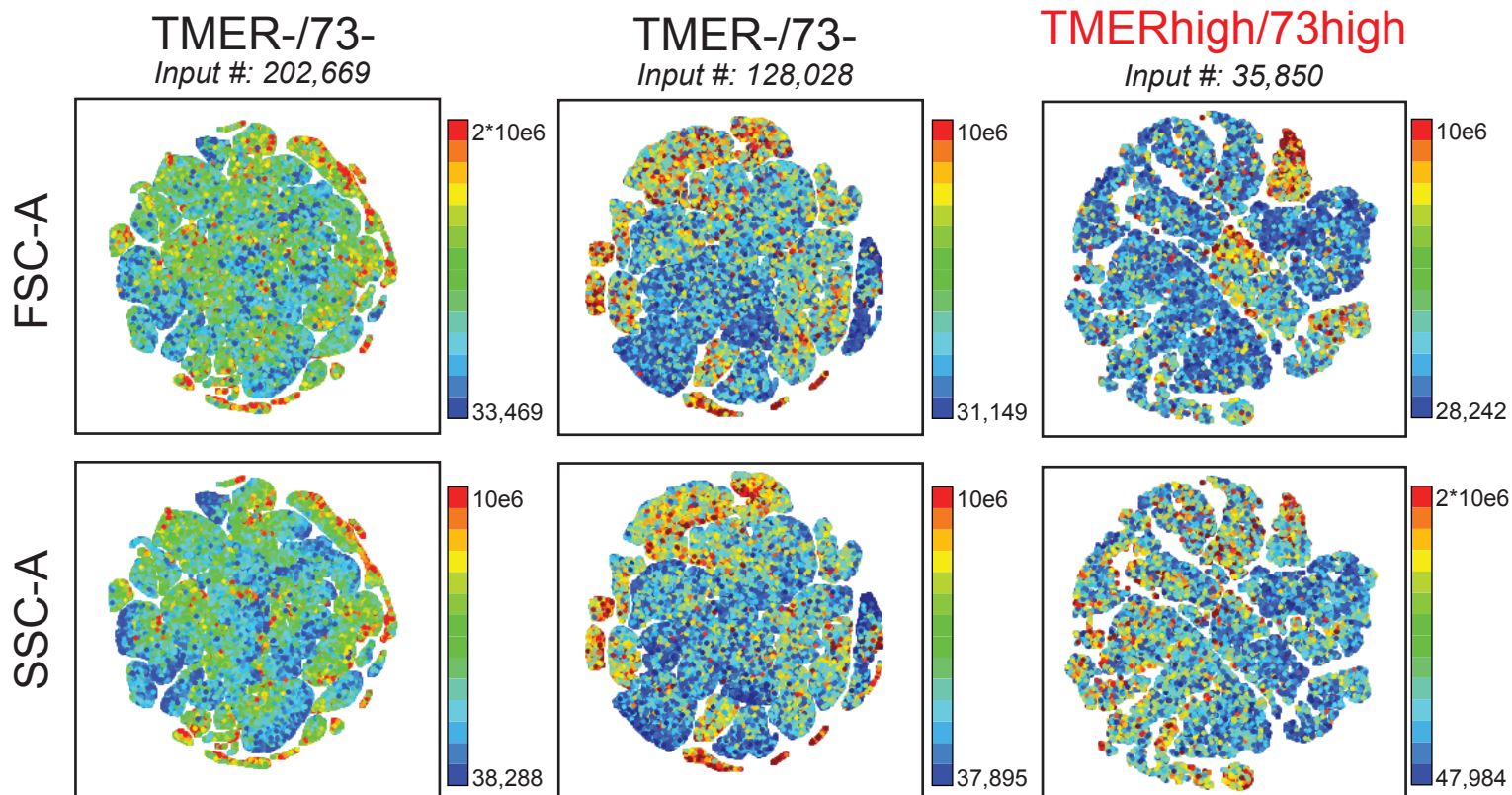


## Mock Infected

## $\gamma$ HV68 Infected



**Supplemental Figure 2. tSNE analysis of cell size and granularity as a function of infection and gene expression status.** Data show flow cytometry data using populations defined in Fig. 6. Data show all DNA+ (DAPI+) single cells (FSC-A, SSC-A) subjected to the tSNE dimensionality reduction algorithm, depicting relative expression values for cell size (FSC) and granularity (SSC) in rows relative to the defined cell populations (columns). The tSNE algorithm provides each cell with a unique coordinate, displayed on a two-dimensional plot (tSNE1 versus tSNE2), such that FSC and SSC values within cellular islands can be directly compared to the corresponding cell islands presented in Fig. 7C. The channel range was locally-defined for each individual and channel via Cytobank. Flow cytometry data shows single cells that are DNA+ (DAPI+). Data are from three independent experiments.