T-SNE Clustering and C5.0 Analysis

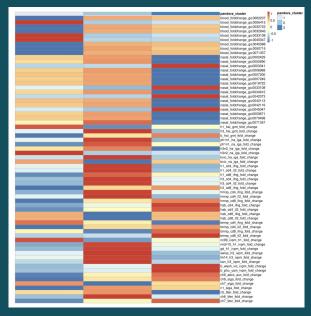
Research Question: By clustering patients with similar profiles together, can baseline measurements predict how a patient responds to the LAIV vaccine?

Method:

- Cluster patient response via t-SNE
 - a. Use fold change data only to prevent overfitting
- 2. Apply predictive C5.0 analysis on clusters using baseline data
 - a. Decisions trees seemed to give best AUCs

Results:

- Training AUC: 0.8678
- Predictive AUC: 0.8758
- Model allows us to predict response to LAIV based on patient baselines → useful in understanding what kind of immunity the patient will have



Cluster 1: high gene response in the blood, drop in flu antibody response

Cluster 2: increase in CD4+ and CD8+ IFN-γ and IL-2 for h1/h3 strains, increased antibody response for h1/h3

Cluster 3: high gene response in nasal, increase in IFN-γ and IL-2 for hab/bmnp strains, increased ADCC and secretory IgA response