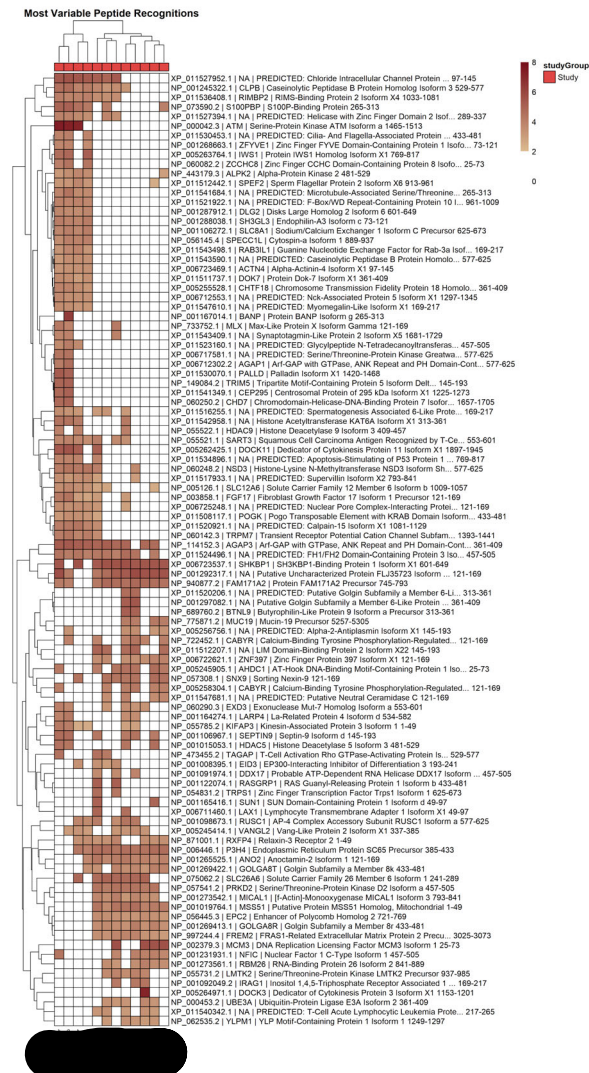


# 10 Most Variable Peptides



**Unbiased hierarchical clustering of the Top100\_Variant\_Peptides.csv output rows.** Created in R with the *pheatmap* package with default row and column clustering settings (Euclidean distance as the similarity measure and clustering samples based on the ‘complete’ method). Full resolution figure is provided in your **plots** folder. This file is often good at independently identifying and clustering sample pairs and replicates via observation of your study’s most variable semi-continuous hits data. Note: most public epitopes are unrelated with conditions of interest and this plot often will not cluster disease groups.

*plots/cohort\_top100variable\_heatmap.png*