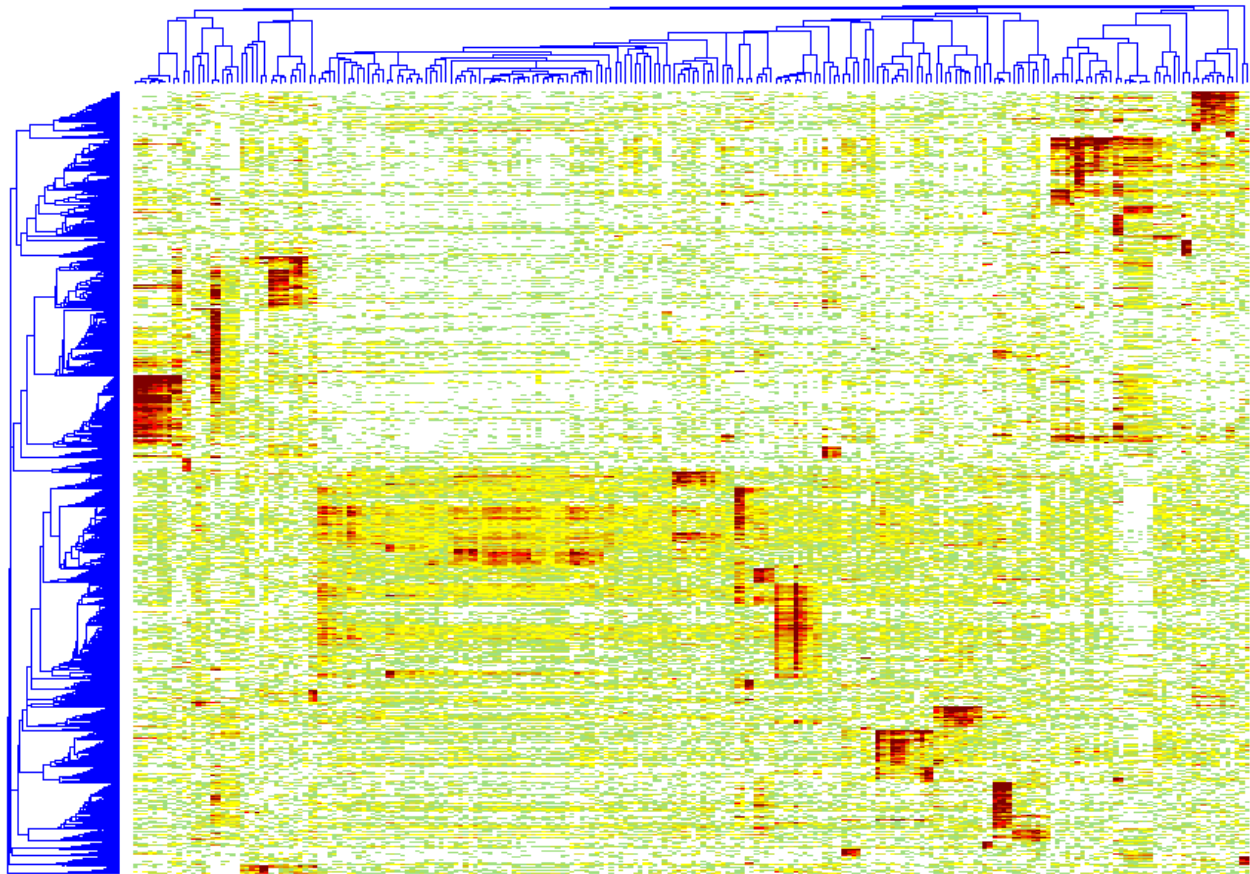
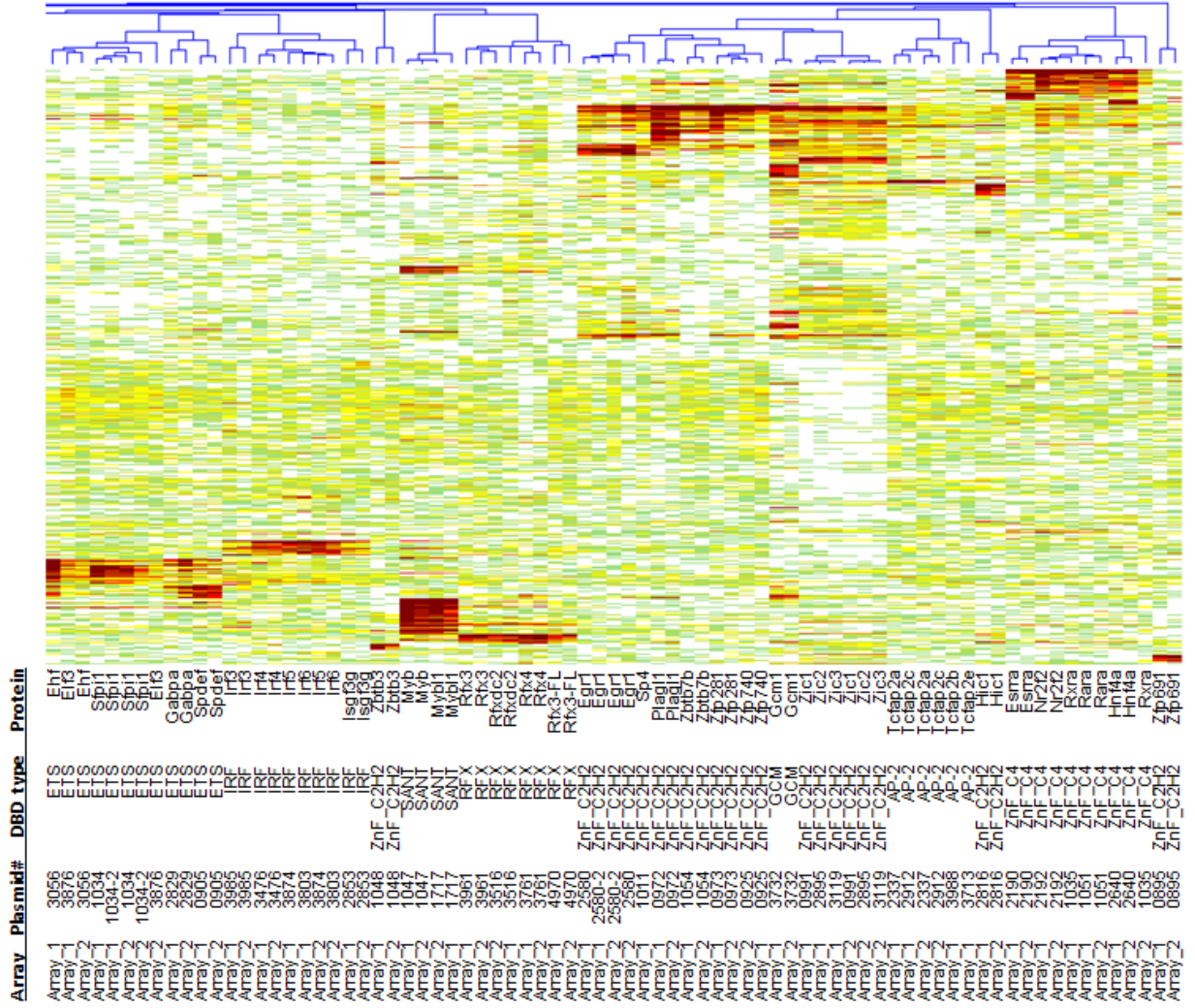


Figure S4. PBM data reproducibility. Panels **A-D** show that replicate arrays cluster together. We combined the 8-mer Z-scores from the two replicate arrays into a single file, with each replicate retained as a separate column and each 8-mer in a separate row. To minimize the impact of noise, we reduced this data structure to the 14,873 8-mers that have a Z-score of 6 or greater in at least one experiment, and set entries less than zero to zero. We clustered these data using Pearson correlations and hierarchical agglomerative linkage. Panel **A** shows the full clustering analysis. Panels **B**, **C**, and **D** show zoom-ins of the left, middle, and right of Panel **A**. Panel **E** shows the reproducibility of 8-mer E-scores (Pearson correlation coefficient $r=0.65$) and Z-scores (Pearson correlation coefficient $r=0.85$) for replicate PBMs for a single transcription factor (Esrra).

A.



D.



E.

