



**Supplementary Figure S5.** The MFS advanced exploratory analysis for only downsampled data with unsupervised machine learning algorithms (Clustering). (A) Zoomed-in Downsampled Dendrogram image; (B) Downsampled Hierarchical Scatter plot; (C) Downsampled Hierarchical Heatmap; and (D) Downsampled K-mode cluster plot. These plots were generated using gene expression datasets from the selected experiment tissues (Fowler lab) and the selected label (“Pan-genome” genes). (B) An enlarged Dendrogram image clearly shows the three main clusters that resulted from clustering: the green cluster, the red cluster, and the blue cluster. Colors and legends on the Hierarchical Scatter plot (B) and the K-mode cluster plot (D) indicate gene clusters formed because of the clustering analysis. (C) The Hierarchical Heatmap color scale represents the measured value range of the selected data, with one end of the color scheme (yellow) representing the high-value data points and the other end (dark pink) representing the low-value data points. For details on the interpretation of the plots, see (<https://mfs.maizegdb.org/GeneExp>).