



**Supplementary Figure S6.** PCA analysis in MFS is only available for downsampled datasets. For this analysis, we used the Fowler lab gene expression data: (A) PCA 2D variables cluster plot (B) PCA 2D observation cluster plot; (C) PCA 2D biplot (D) Zoomed-in PCA 2D biplot image; (E) PCA 3D variables cluster plot, and (F) PCA 3D observation cluster plot. These plots were generated using the gene expression dataset from the selected lab tissues (Fowler lab) and the selected label (“Pan-genome” genes). (D) To visualize the relationship among the different tissues from the Fowler lab, an enlarged PCA 2D biplot image is provided. Colors and legends on the PCA variables cluster plot (2D,3D) indicate the selected lab tissues. In the PCA 2D biplot plot (C, D) colors and legends indicate the “Pan-genome” categories, and for the PCA (2D,3D) observation cluster plot (B,F), colors and legends indicate the gene models. For details on the interpretation of the plots, see (<https://mfs.maizegdb.org/GeneExp>).