



Supplementary Figure S4. The MFS Multivariate analysis for both the total and downsampled omics data: (A) Total Pair plot; (B) Downsampled Pair plot; (C) Total Correlation plot; (D) Downsampled Correlation plot; and (E) Downsampled Heatmap plot. Each of these plots were generated from the selected Gene Structures such as gene length, exon number, CDS length, three-prime UTR length, five-prime UTR length, and the selected label (“Pan-genome”: core/near-core/dispensable/private). Colors and legends on the Pair plot indicate “Pan-genome” categories. Correlation plot scales range from -1 to +1, with values closer to -1 indicating a poor correlation, whereas values closer to +1 suggest a stronger correlation. The 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 purple) representing the low-value data points. For details on the interpretation of the plots, see (<https://mfs.maizegdb.org/Structure>).