



**Supplementary Figure S2.** The MFS provides users with options to carry out four different univariate analyses for both the total and downsampled omics data: (A) Total Histogram; (B) Downsampled Histogram; (C) Total Count and Distribution plots; (D) Downsampled Count and Distribution plots; (E) Total Box plots; (F) Downsampled Box plots; (G) Total Violin Plots; (H) Downsampled Violin Plots. These plots were generated from the selected Gene Structures such as Gene length, Exon number, three-prime UTR length, five-prime UTR length, and the selected label (Pan-genome: core/near-core/dispensable/private). The colors and the legends in the plot indicate the multiple “Pan-genome” categories. In addition to the graph, to increase the interpretability of the data, we have also included p-values, mean and standard deviations of the selected datasets. For details on the interpretation of the plots, see (<https://mfs.maizegdb.org/Structure>).