



**Supplementary Figure S3.** The MFS Bivariate analysis for both the total and downsampled omics data: (A) Total Joint plot (B) Downsampled Joint plot; (C) Total Scatter plot (D) Downsampled Scatter plot. Due to the nature of the bivariate plots, these can be generated from any two features at a time: Gene Structures such as three-prime UTR length and five-prime UTR length were selected. The plot's colors and legends indicate the multiple “Pan-genome” categories (core/near-core/dispensable/private). In addition, the scatter plot comes with a simple linear regression that explains the strength of the relationship between the two variables using  $R^2$ , the squared correlation coefficient. For details on the interpretation of the plots, see (<https://mfs.maizegdb.org/Structure>).