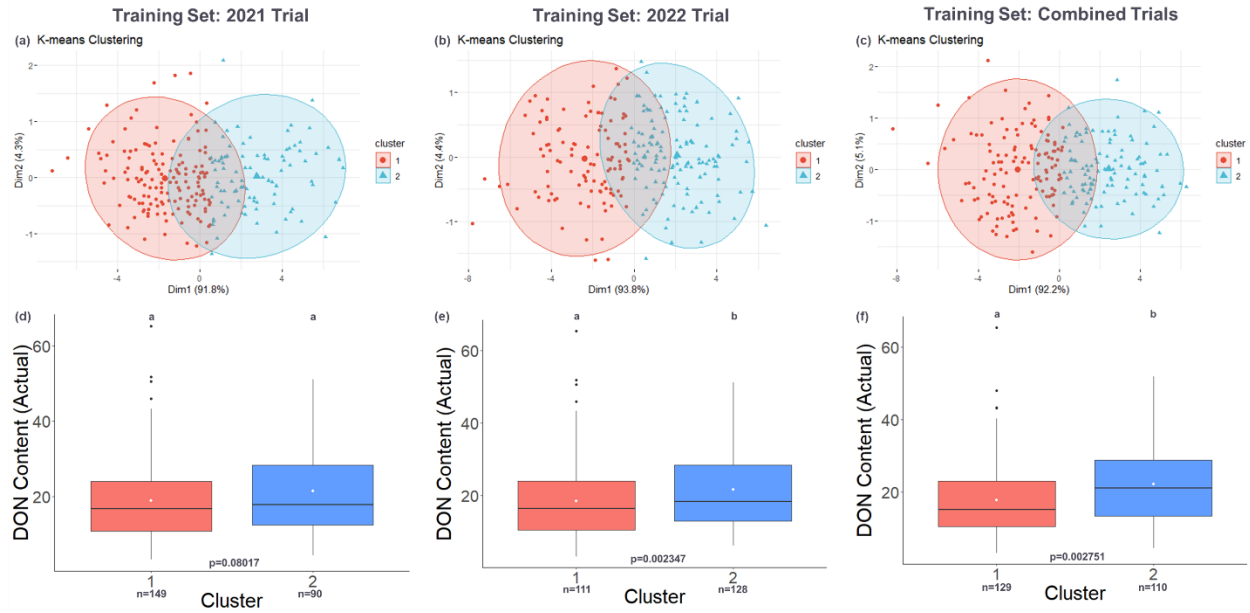




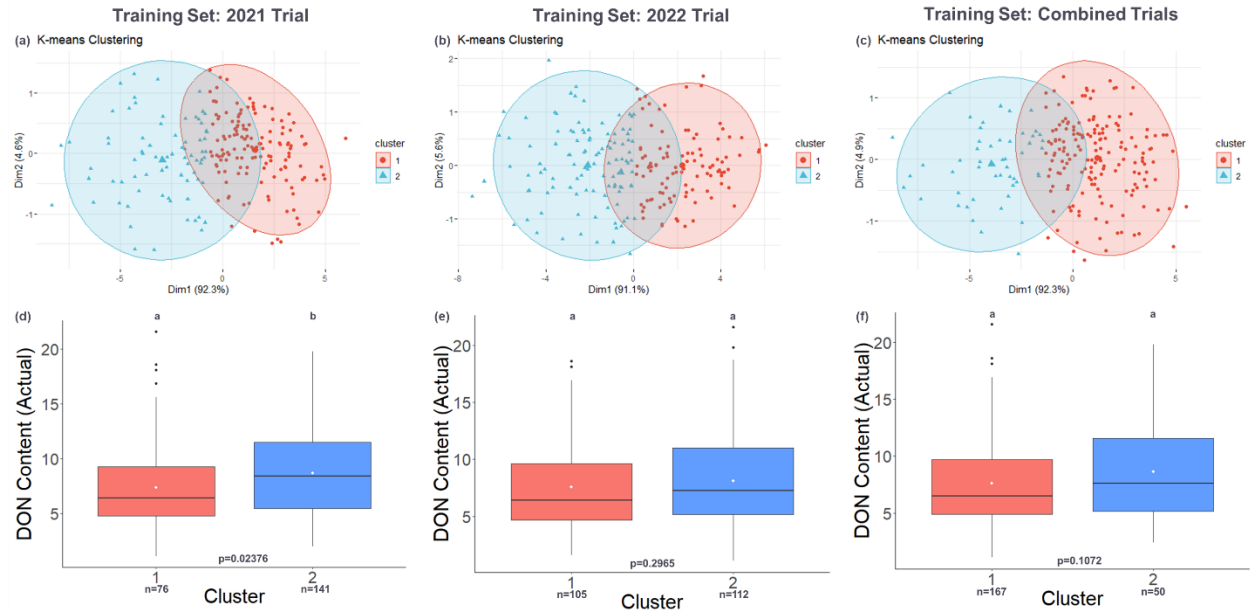
Supplementary Figure 3.1. Unsupervised K-means clustering based on blended phenomic predictions of DON content in 2022 F_{4:5} selection candidates using different training sets. (a, b, c) Clustering of 2022 F_{4:5} selection candidates using genomically and predicted values. (d,e,f) Corresponding boxplots showing the actual DON content of the genotypes in Clusters 1 and 2 grouped based on phenomically and genomically predicted values. White dot represents the mean actual DON content of genotypes belonging to Clusters 1 and 2. Means with the same letter are not significantly different at alpha 0.05



Supplementary Figure 3.2. Unsupervised K-means clustering based on blended genomic predictions of DON content in 2022 $F_{4:5}$ selection candidates using different training sets. (a, b, c) Clustering of 2022 $F_{4:5}$ selection candidates using genomically and predicted values. (d,e,f) Corresponding boxplots showing the actual DON content of the genotypes in Clusters 1 and 2 grouped based on phenomically and genomically predicted values. White dot represents the mean actual DON content of genotypes belonging to Clusters 1 and 2. Means with the same letter are not significantly different at alpha 0.05



Supplementary Figure 3.3. Unsupervised K-means clustering based on blended phenomic predictions of DON content in 2023 $F_{4:5}$ selection candidates using different training sets. (a, b, c) Clustering of 2023 $F_{4:5}$ selection candidates using genomically and predicted values. (d,e,f) Corresponding boxplots showing the actual DON content of the genotypes in Clusters 1 and 2 grouped based on phenomically and genomically predicted values. White dot represents the mean actual DON content of genotypes belonging to Clusters 1 and 2. Means with the same letter are not significantly different at alpha 0.05



Supplementary Figure 3.4. Unsupervised K-means clustering based on blended genomic predictions of DON content in 2023 $F_{4:5}$ selection candidates using different training sets. (a, b, c) Clustering of 2023 $F_{4:5}$ selection candidates using genomically and predicted values. (d,e,f) Corresponding boxplots showing the actual DON content of the genotypes in Clusters 1 and 2 grouped based on phenomically and genomically predicted values. White dot represents the mean actual DON content of genotypes belonging to Clusters 1 and 2. Means with the same letter are not significantly different at alpha 0.05