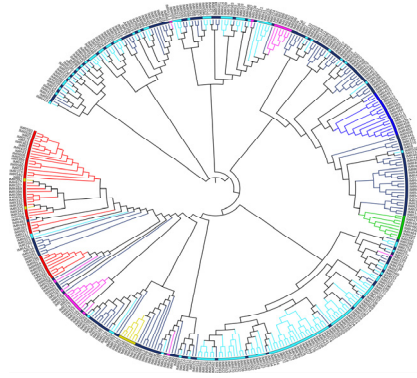
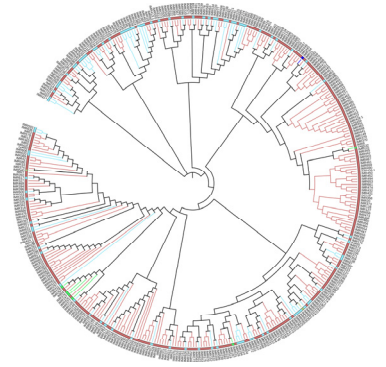


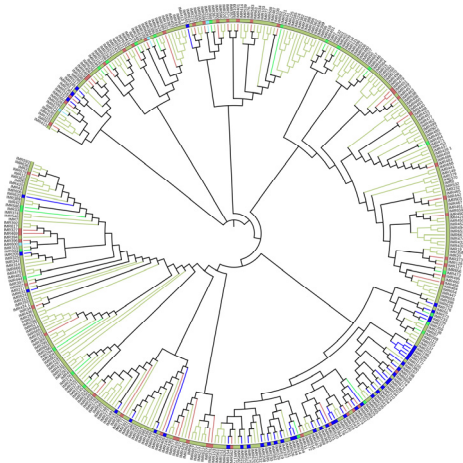
Variable 1. Clustering represented based on centers



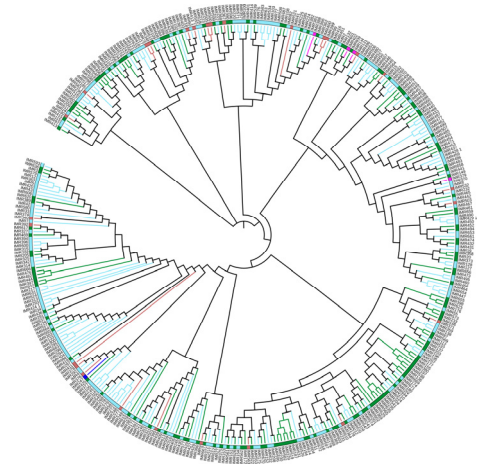
Variable 2. Clustering based on population structure



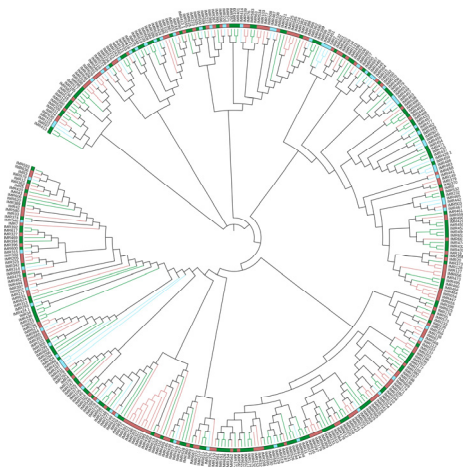
Variable 3. Clustering based on type of corn



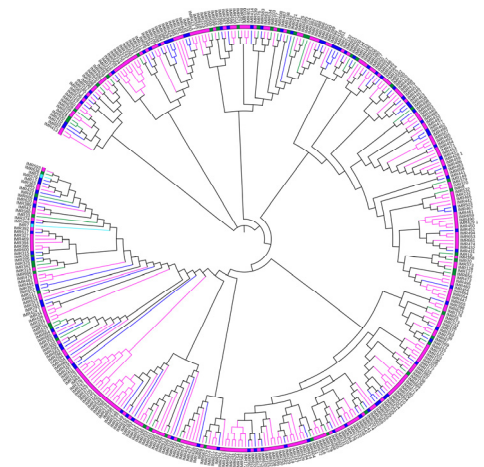
Variable 4. Clustering represented based on kernel colours



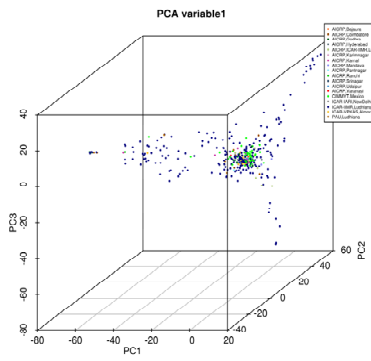
Variable 5. Clustering represented based on maturity



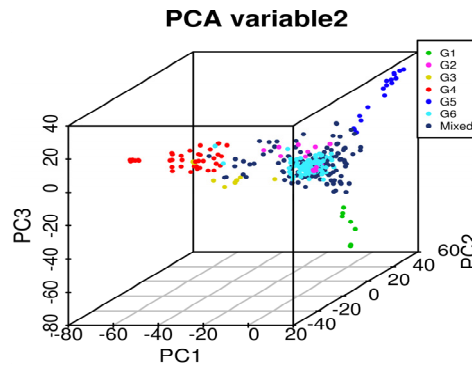
Variable 6. Clustering represented based on plant height



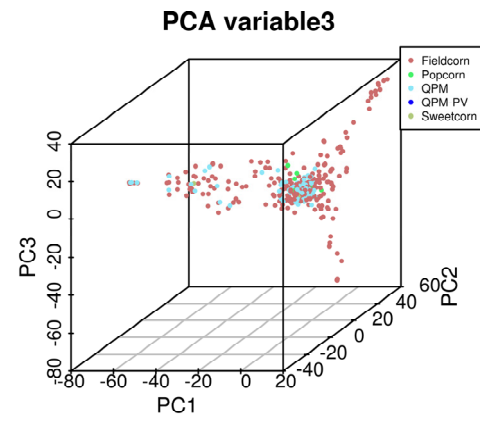
Variable 7. Clustering represented based on ear height



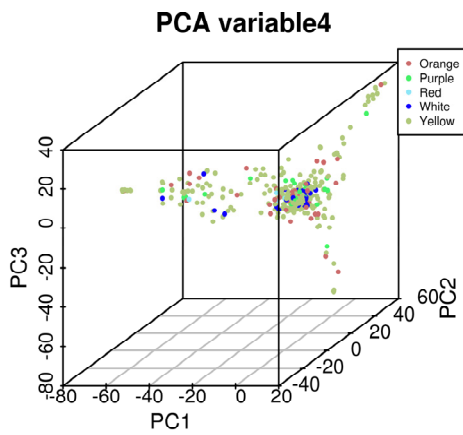
Variable 1. PCA represented based on the centers



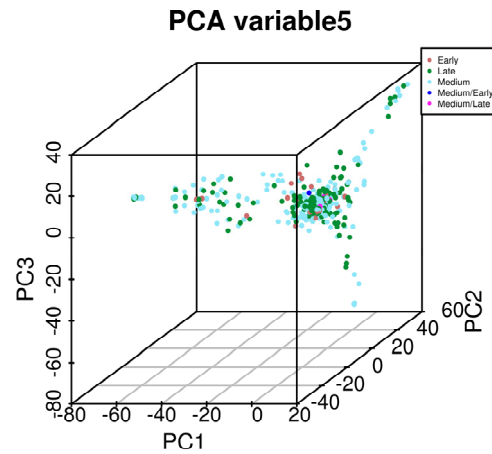
Variable 2. PCA represented based on population structure



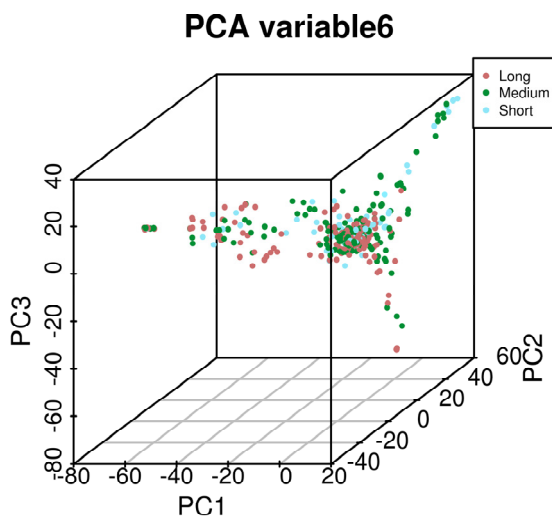
Variable 3. PCA represented based on type of corn



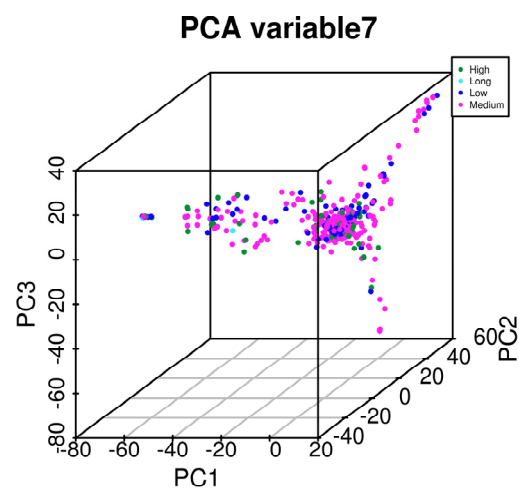
Variable 4. PCA represented based on kernel colour



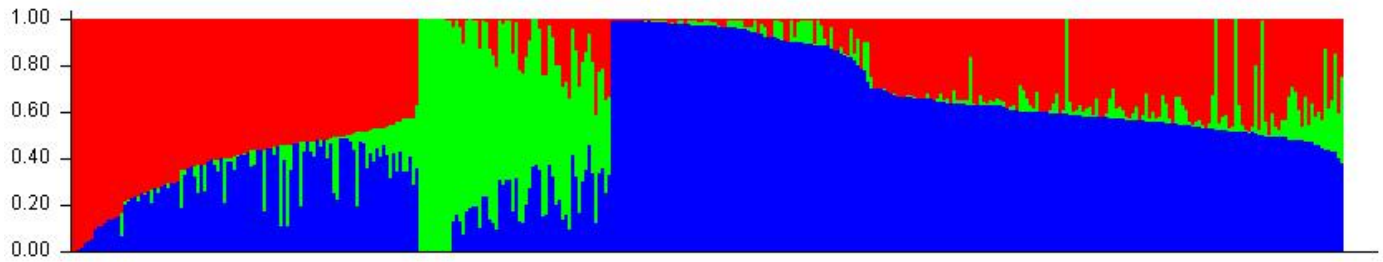
Variable 5. PCA represented based on maturity



Variable 6. PCA represented based on based plant height



Variable 7. PCA represented based on based ear height placement



Population structure of 384 maize inbred lines revealed by 60277 SNP markers.

Figure S1. Different phylogenetic trees and PCA plots for 384 lines genotyped using 60,277 SNPs and represented based on seven variables such as center, population structure, types of corn, kernel colour, maturity group, plant height and ear height placement.