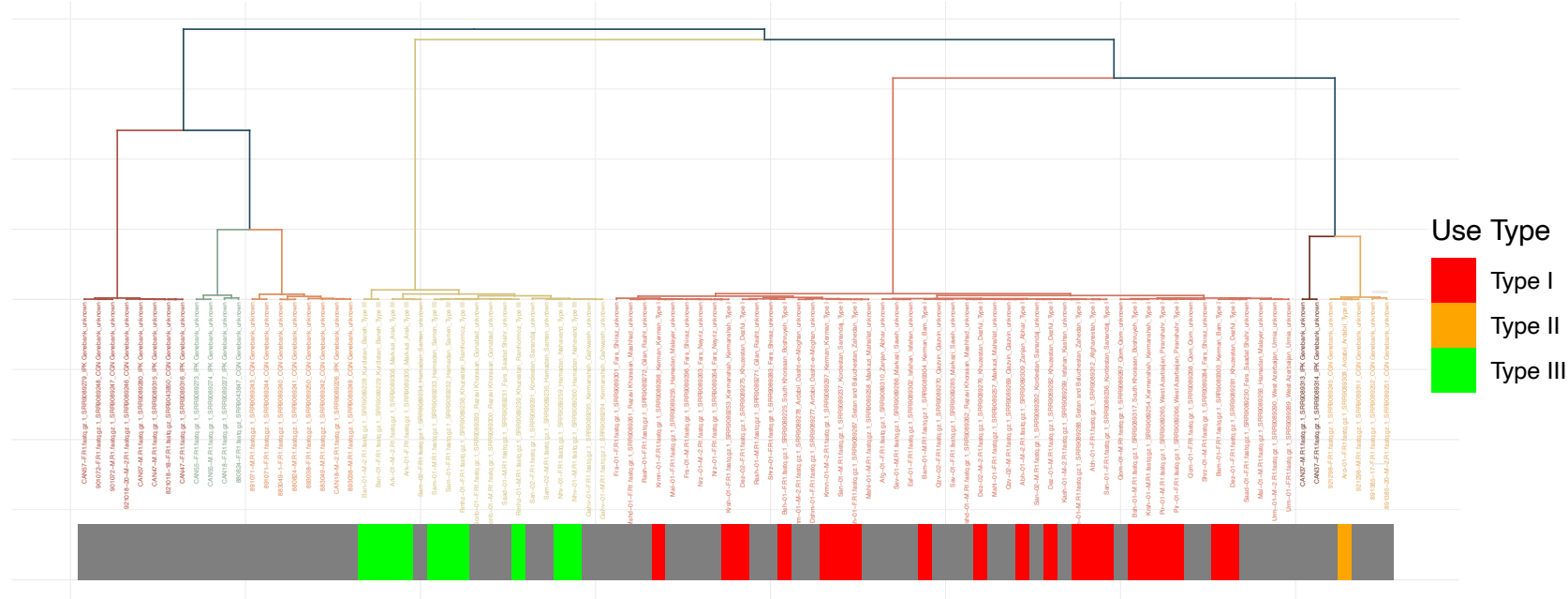
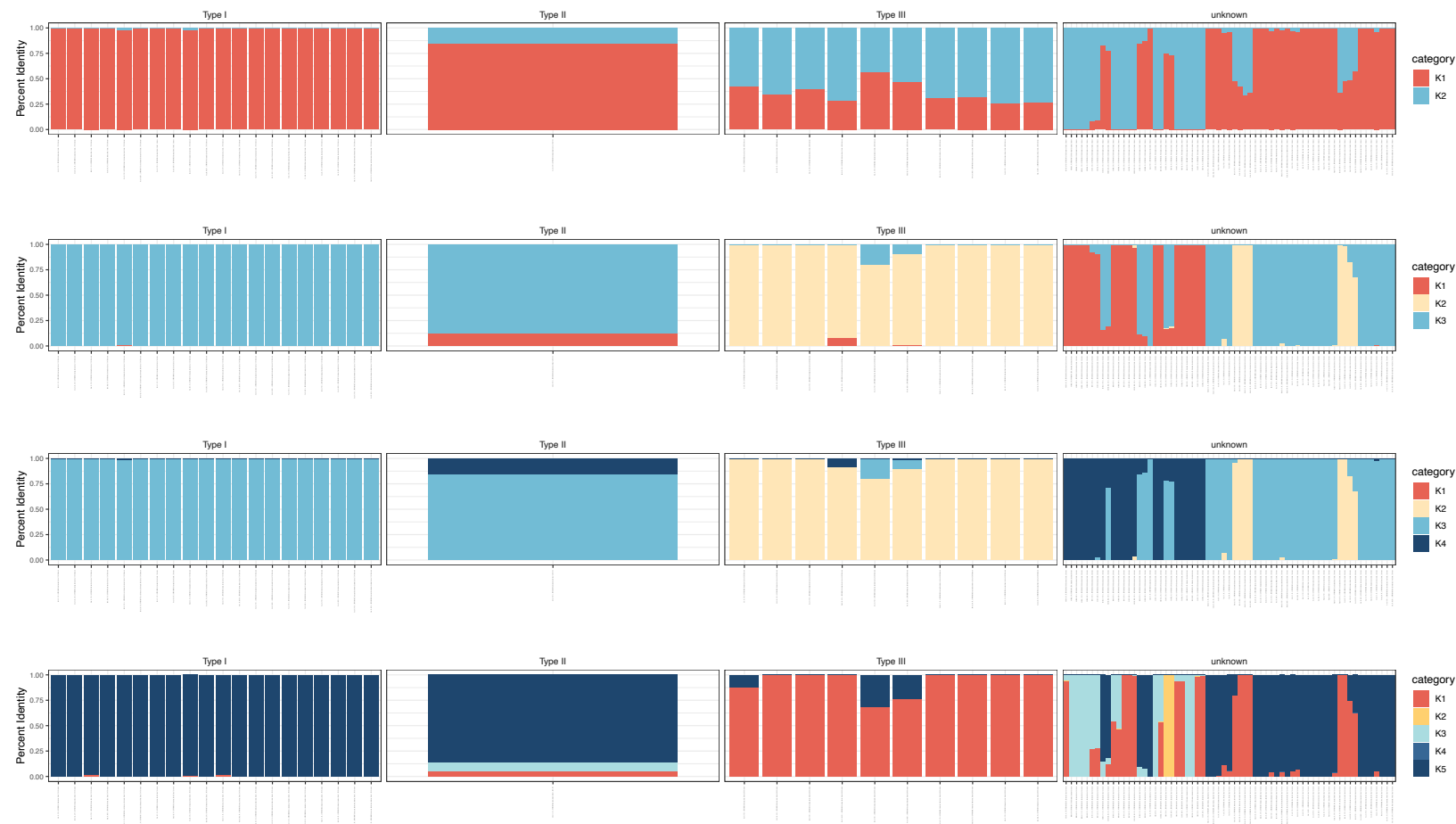


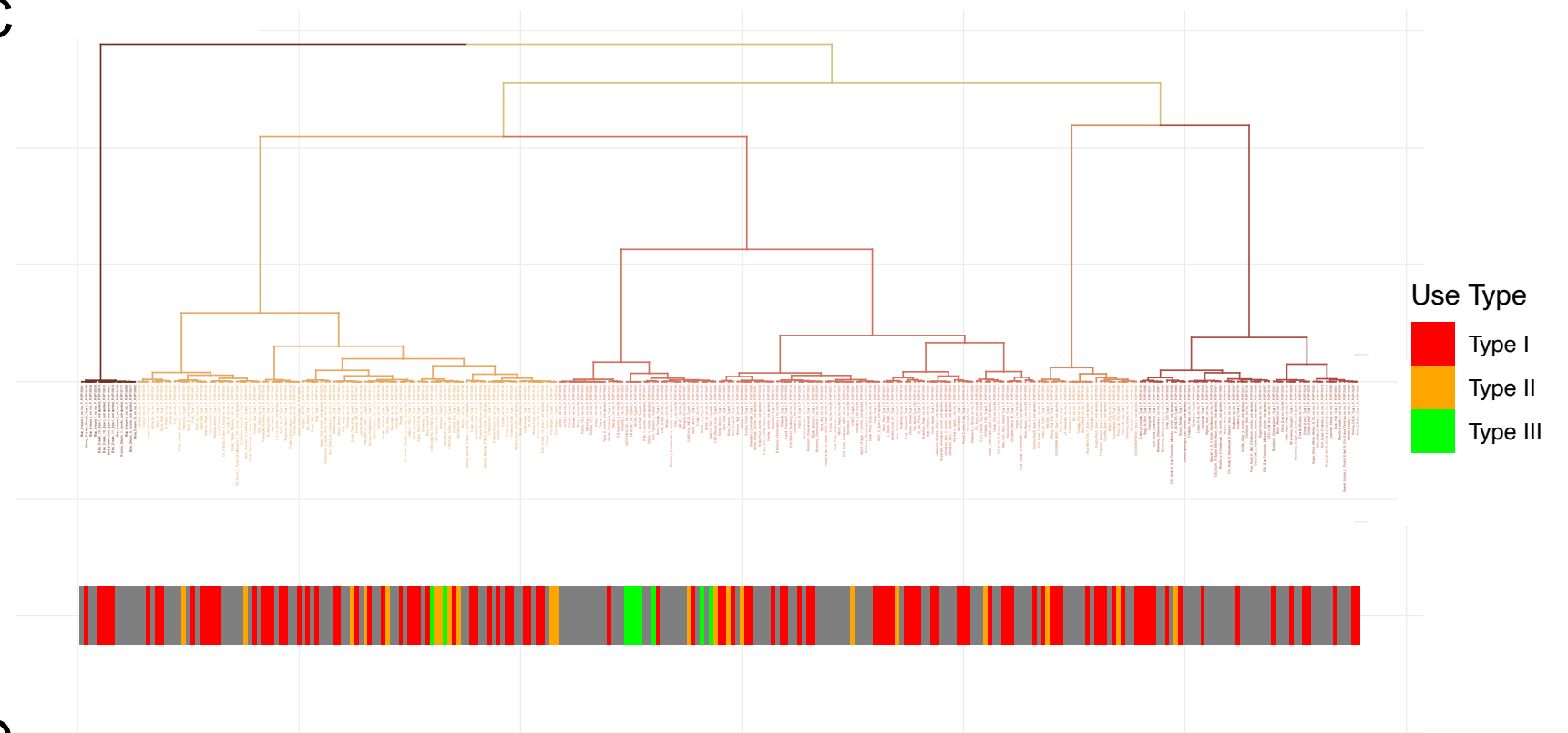
A



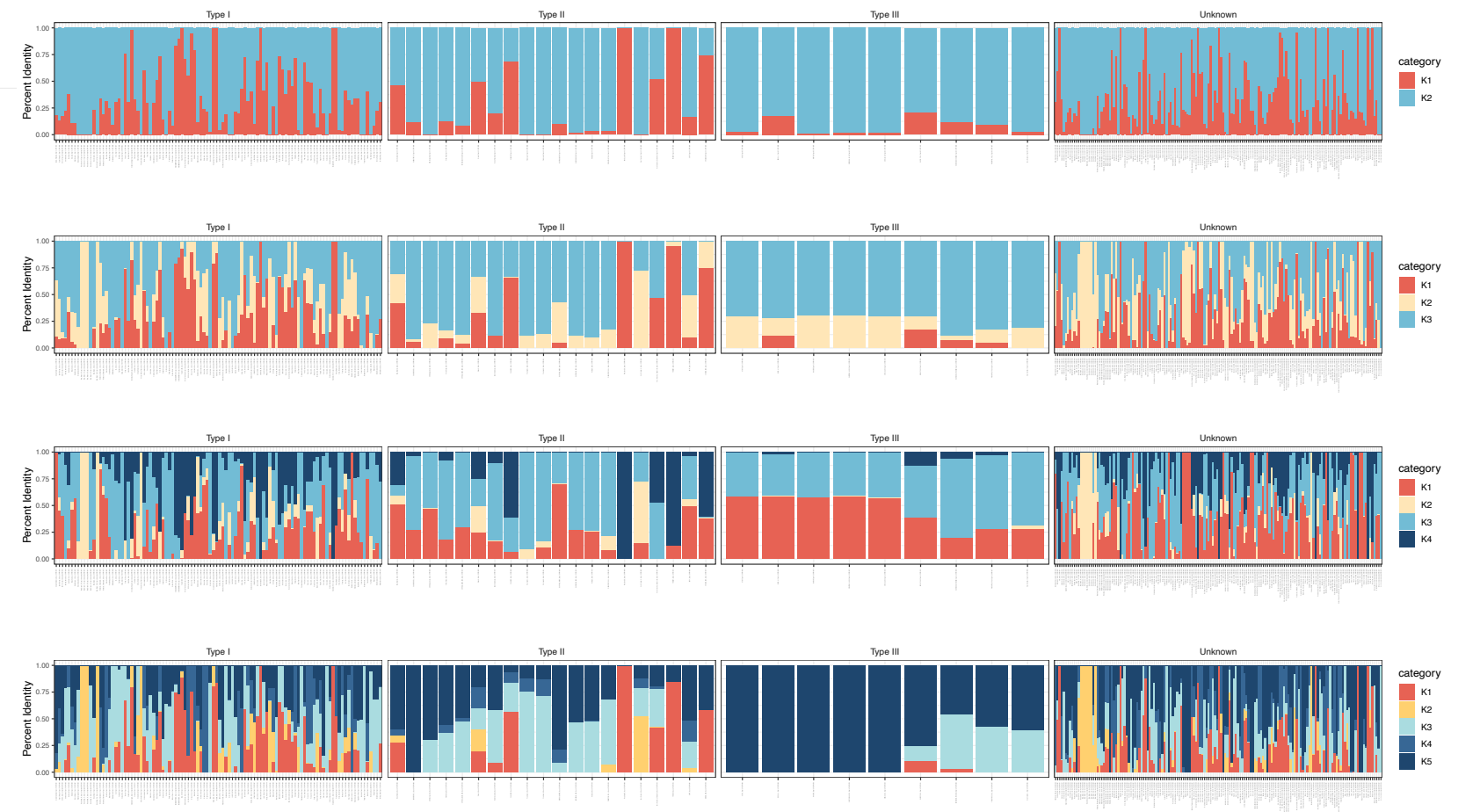
B



C



D



**Figure 2** Examining hierarchical clustering and population structure in the Soorni et al., 2017 (n=94) and the Medicinal Genomics StrainSEEK V1 (n=289) datasets. In each case clustering was conducted based on nuclear genetic SNPs while reported use-type within the dataset is below in solid bars to facilitate interpretation based upon community standards **(A)** Hierarchical cluster dendrogram from 6,865 nuclear SNPs for the Soorni et al., 2017 dataset with use-type of each accession indicated below. Use-type are pictured below (Type I=20, Type III=10, Type II=1, Landrace=78 and Unknown=63) **(B)** Visualization of population structure and admixture from 33,629 nuclear SNPs for the Soorni et al., 2017 dataset using the fastSTRUCTURE software (k=2-5) with the optimal number of K being 3 using the silhouette method **(Fig. S9-10)** **(C)** Hierarchical cluster dendrogram from 5,045 nuclear SNPs for the Medicinal Genomics StrainSEEK V1 dataset with use-type indicated below. Use-type of accessions include Type I=108, Type III=9, Type II=17 and Unknown=155 **(D)** Visualization of population structure and admixture from 20,566 nuclear SNPs for the Medicinal Genomics StrainSEEK V1 dataset using the fastSTRUCTURE software (k=2-5) with the optimal number of K being 3 using the silhouette method **(Fig. S9-10).**