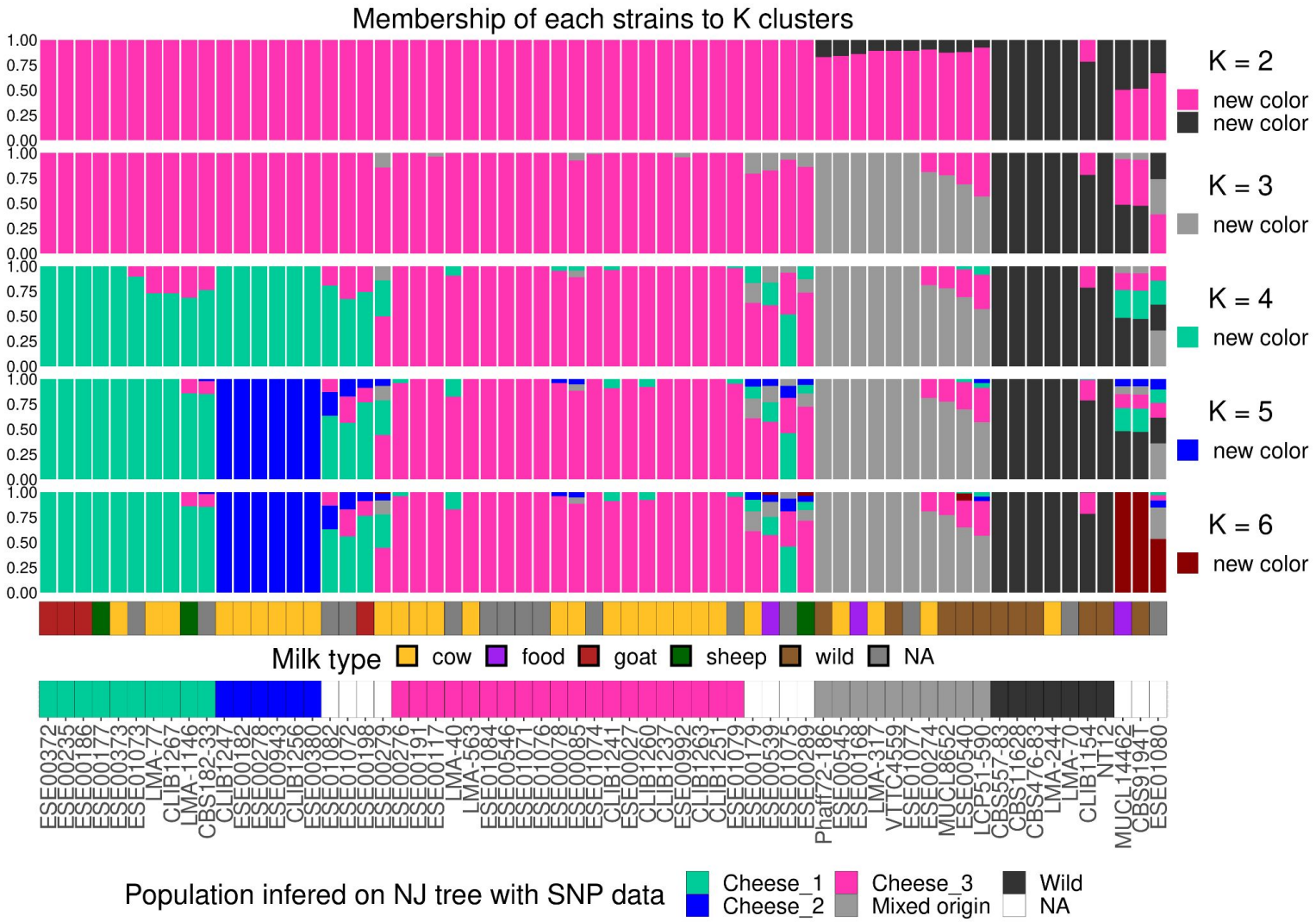

Figure S1: Population structure of *Geotrichum candidum*.

Population subdivision inferred for *K* population ranging from two to six. Colored bars represent the coefficients of membership in the K gene pools based on genomic data. Each bar represents a strain, its name being indicated at the bottom of the figure. The new color for each *K* increment is indicated on the right part. The second order rate of change in the likelihood (ΔK) peaked at *K*=6. However the additional population distinguished at *K*=6 only encompassed two strains that were not that differentiated in the splistree (MUCL 14462 and CBS 9194; ; FIGURE 1).

Therefore, we chose to set the number of populations to five, the *K* value at which the structure was the strongest and the clearest, with three cheese populations, several admixed or hybrid cheese strains, a population of mixed origins and a wild population. These populations are indicated on the last rows.

Below the admixture plot, two rows are indicating milk from which the strains was sampled and the population delineation.