

Figure S2

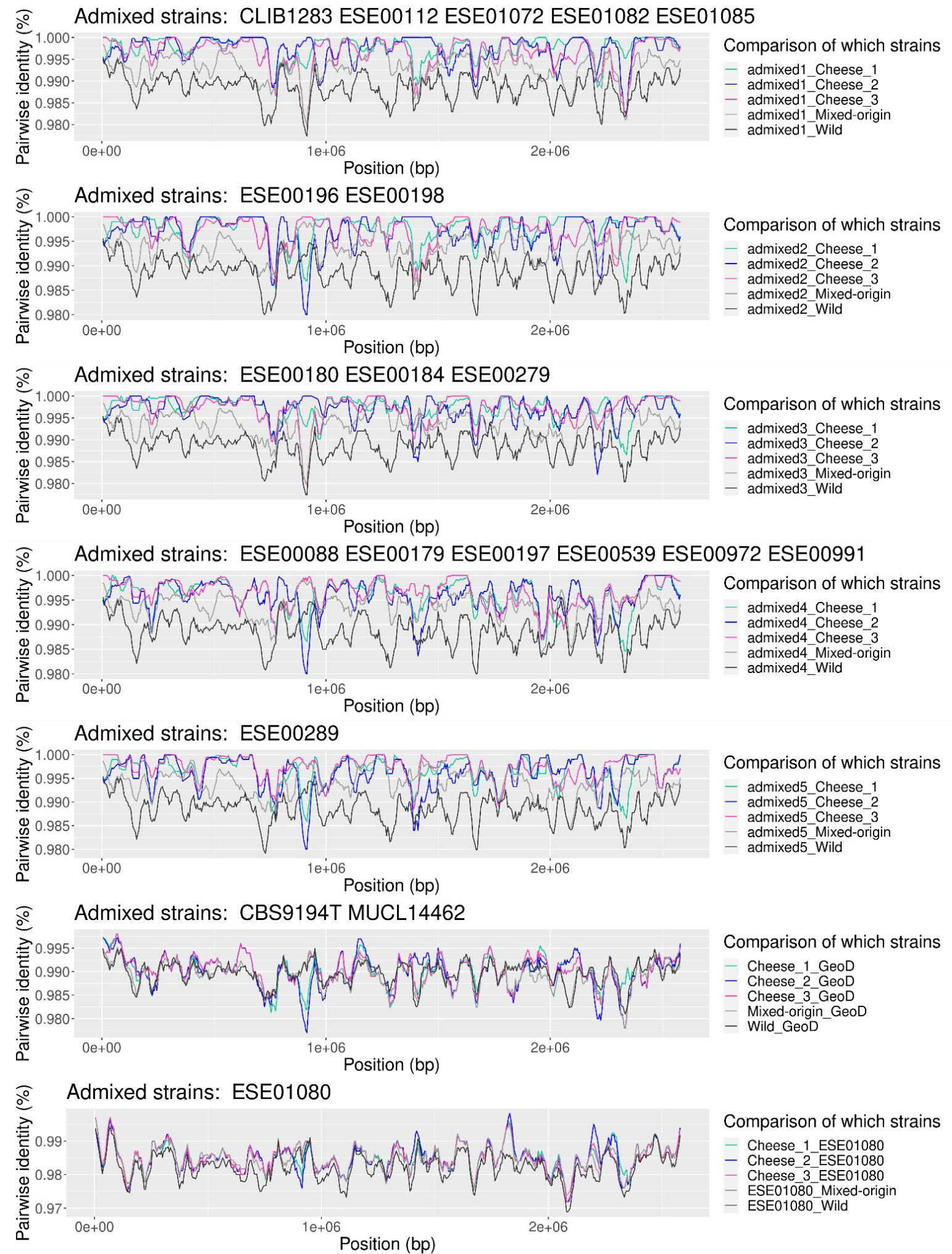


Figure S2: Pairwise identity between admixed and other strains, averaged by population of *Geotrichum candidum*.

In order to see traces of introgression from different populations of *G. candidum* in some hybrid strains we computed the pairwise identity along the genome. Only the first scaffold of the CLIB 918 genome is shown in this figure. Values were averaged by population and when admixed strains had the same genetic background (name of strains are above each subplot) across 30kb overlapping sliding windows with 5kb steps. If no introgression happened, we expect the admixed strain to be equally distant to the different populations along the genome. Introgression results in genomic regions being atypically closer to a single population. All admixed strains within the cheese clades had introgression imprints while the other three strains (CBS 9194^T, MUCL 14462 and ESE01080) did not, meaning that they were either from different genetic backgrounds or introgressed with genetic backgrounds different from the five populations of *G. candidum*.