Supplementary Fig. 5. Genetic diversity and mutation rates estimated for each of the *V. parahaemolyticus* ST36 sub-population groups identified by ADMIXTURE. A, bar plots representing the mean of the nucleotide diversity for each sub-population is shown in different colours according to the populations depicted in Fig 1 (Population 1: old PNW; Population 2: old PNW; Population 4: Spain; Population 3, 5 and 6: Modern US). B, mutation rates were estimated using a constant population size and fixed local clock model in BEAST. Population 1: old PNW; Population 2: old PNW; Population 4: Spain; Population 5 and 6: Modern US (Population 3 was comprised by a single isolate and was therefore not considered in this analysis).