SUPPLEMENTAL MATERIAL

Title: Redefinition and unification of the SXT/R391 family of integrative and conjugative elements

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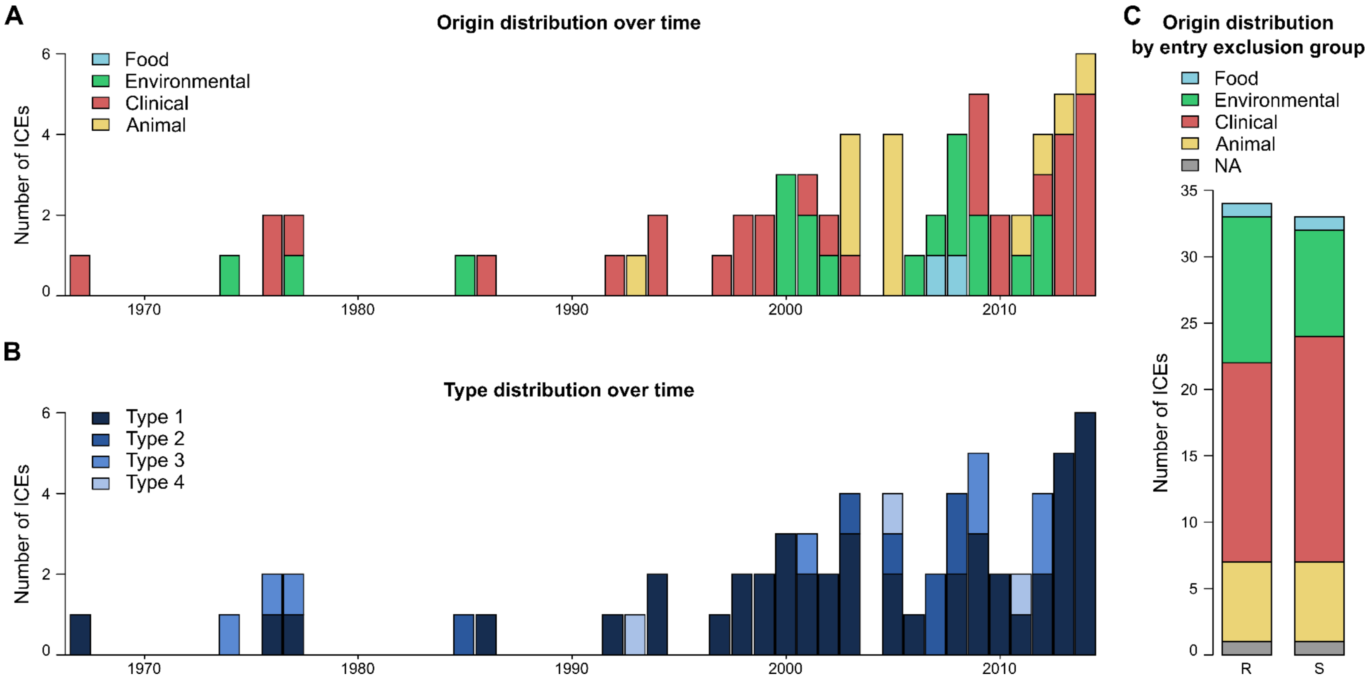

Figure S1. Distribution of ICEs. (A) Distribution of isolation niches and **(B)** ICE types over time. **(C)** Distribution of isolation niches according to exclusion group.

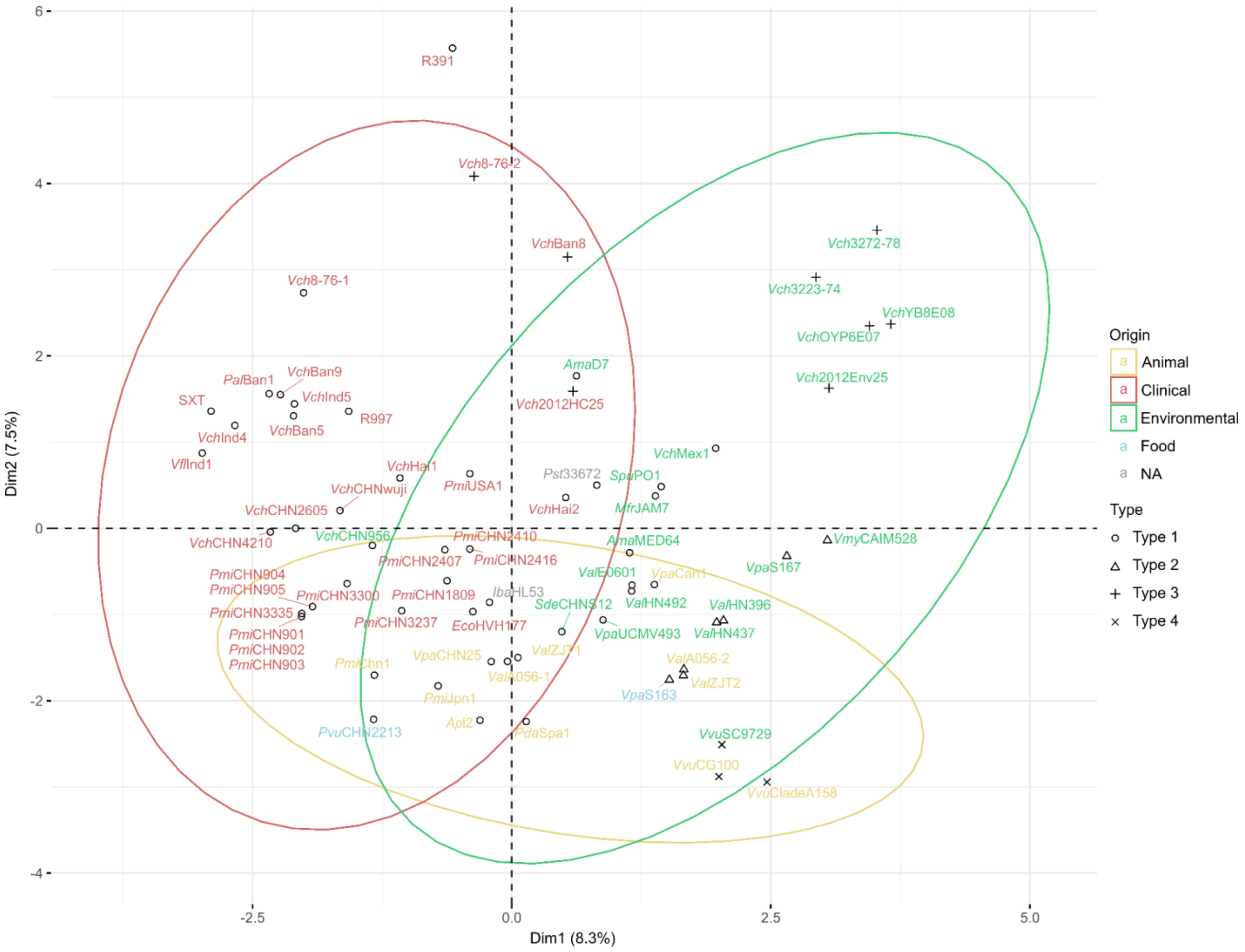

Figure S2. Factorial Analysis of Mixed-Data. Dimensions 1 and 2 explain 8.3 % and 7.5 % of the variance, respectively. Ellipses were drawn with a probability level of 0.95 except when they were too few points.

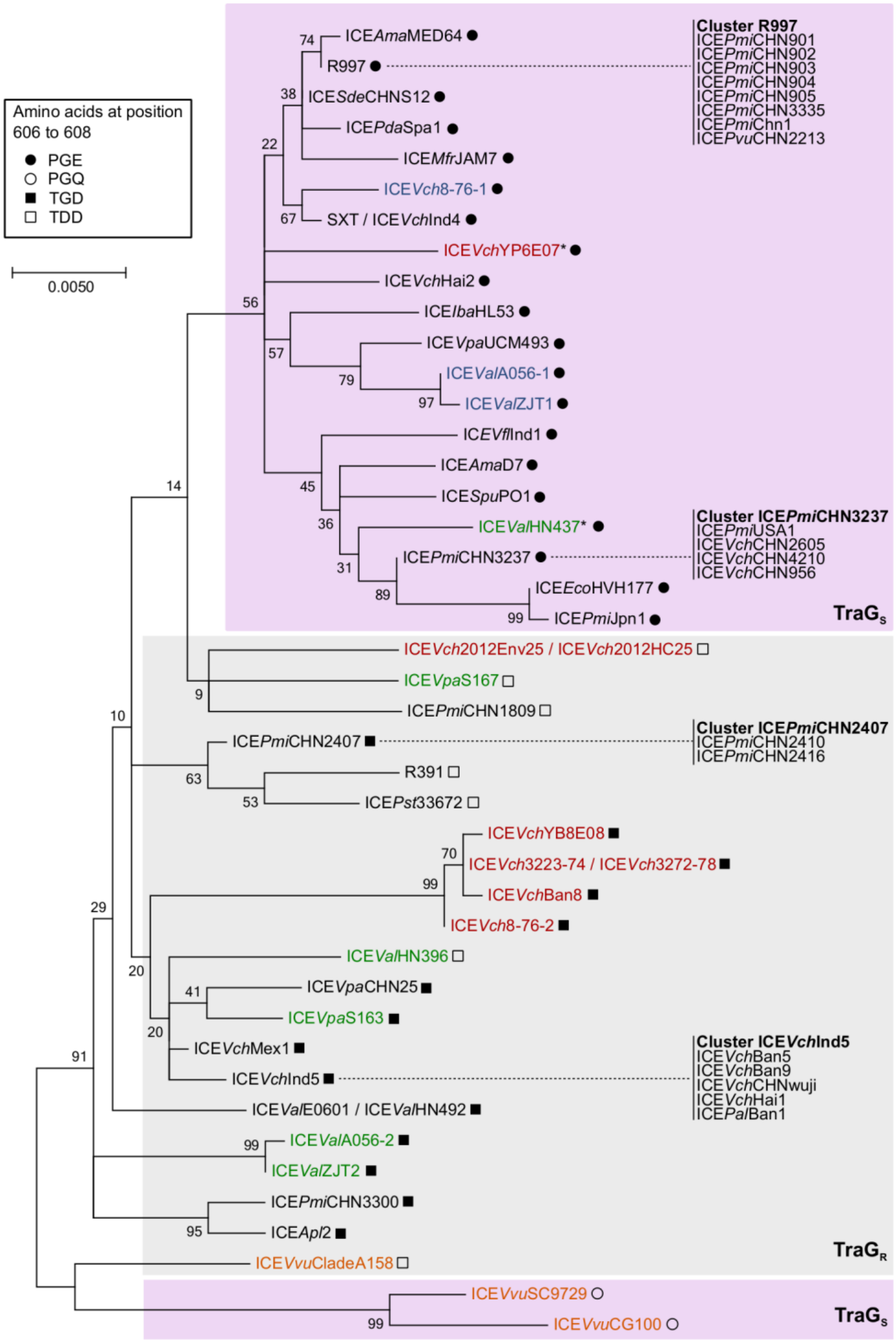

Figure S3. Maximum likelihood phylogenetic analysis of 43 TraG orthologue proteins. Bootstrap supports, as percentage, are indicated at the branching points. Branch length represents the number of substitutions per site over 1189 amino acid positions. Taxa corresponding to type 2, 3 and 4 ICEs are shown in green, dark red and orange, respectively. Taxa highlighted in blue correspond to type 1 ICEs found in strains also bearing a co-resident type 2 or 3 ICE. Asterisks indicate ICEs with an ambiguous entry exclusion group. Circles and squares indicate that the amino acid residues at positions 606 to 608 define either the S (PG[E/Q] or R (T[G/D]D exclusion group.