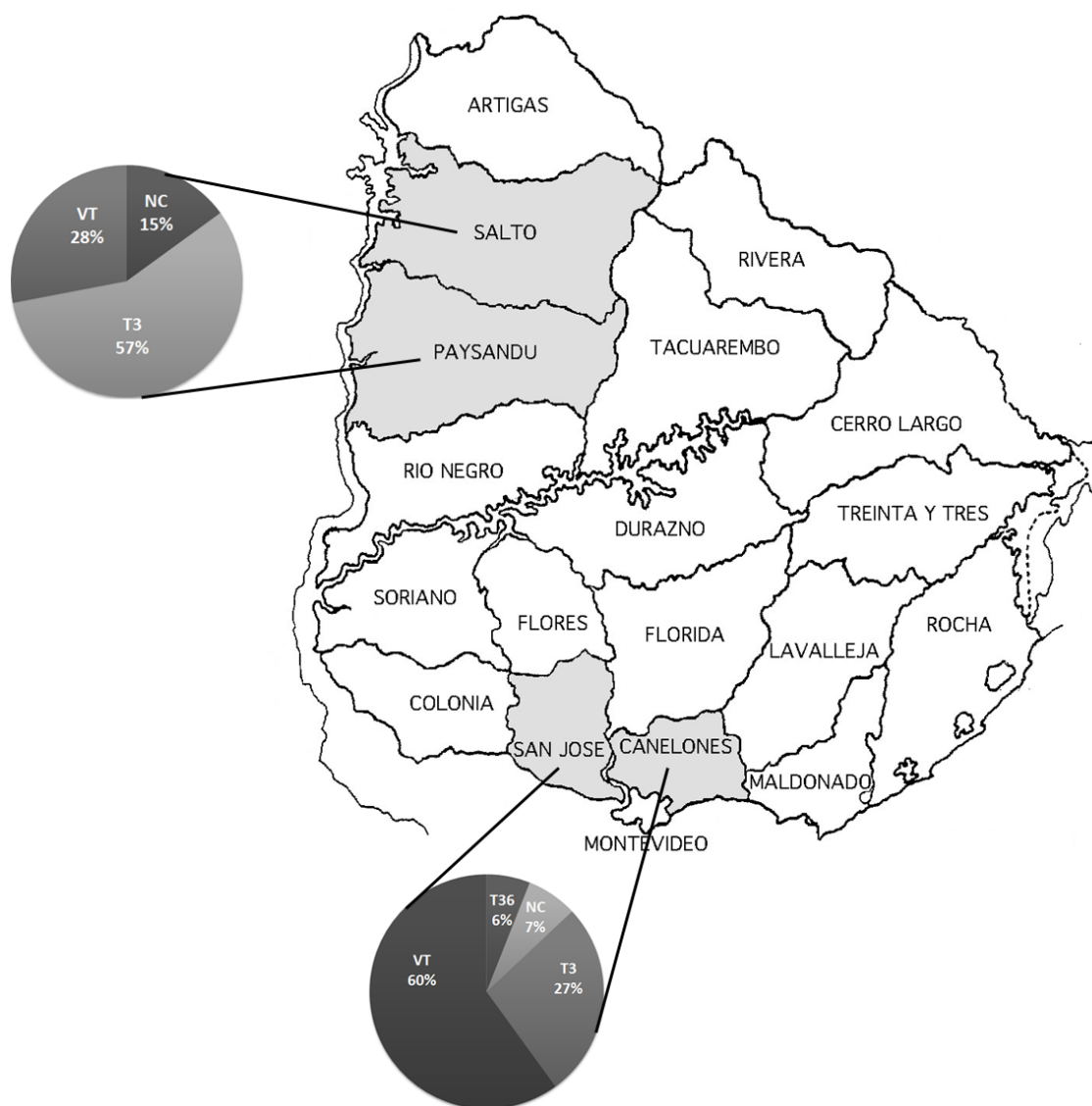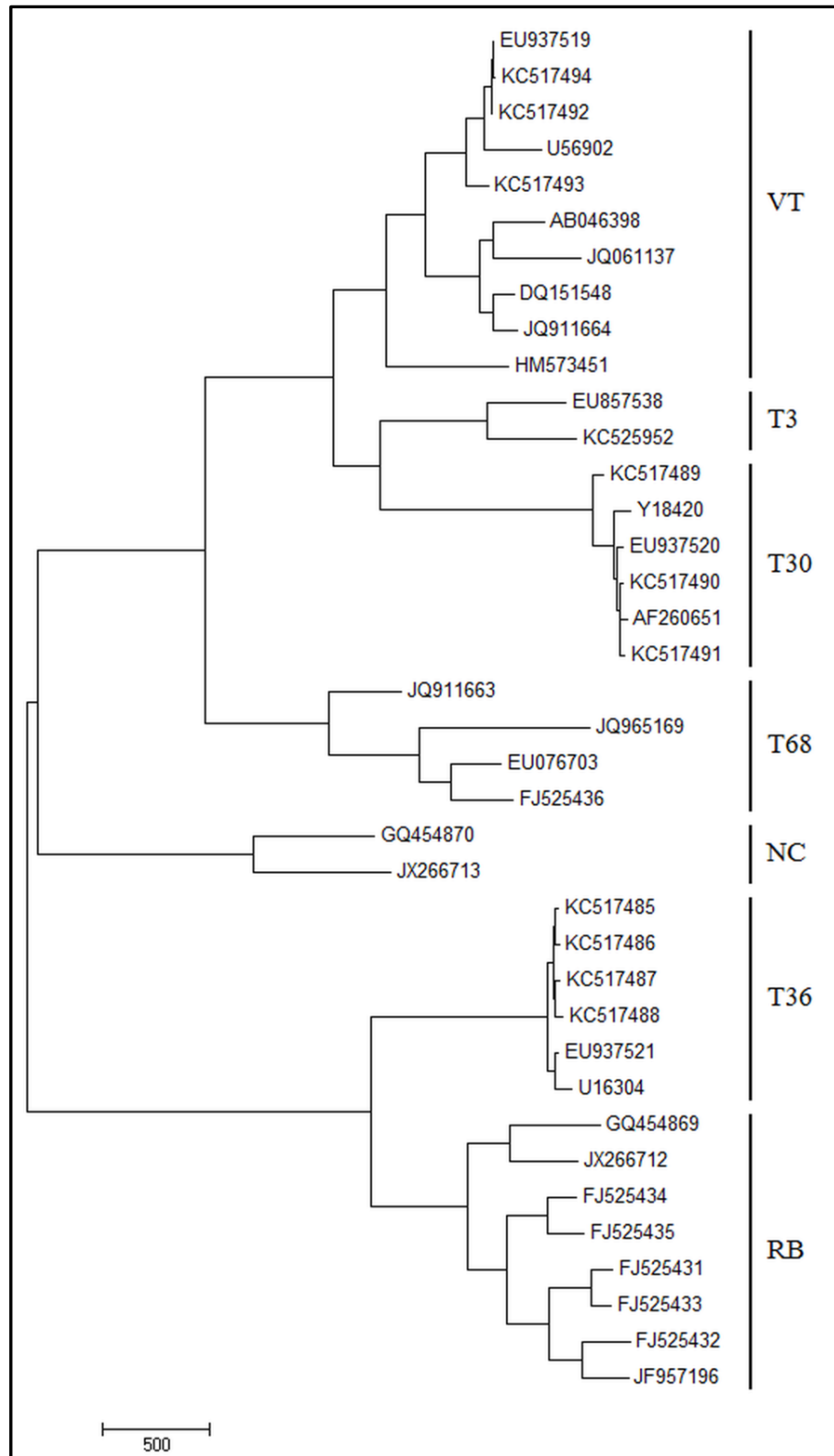# Supplementary Materials
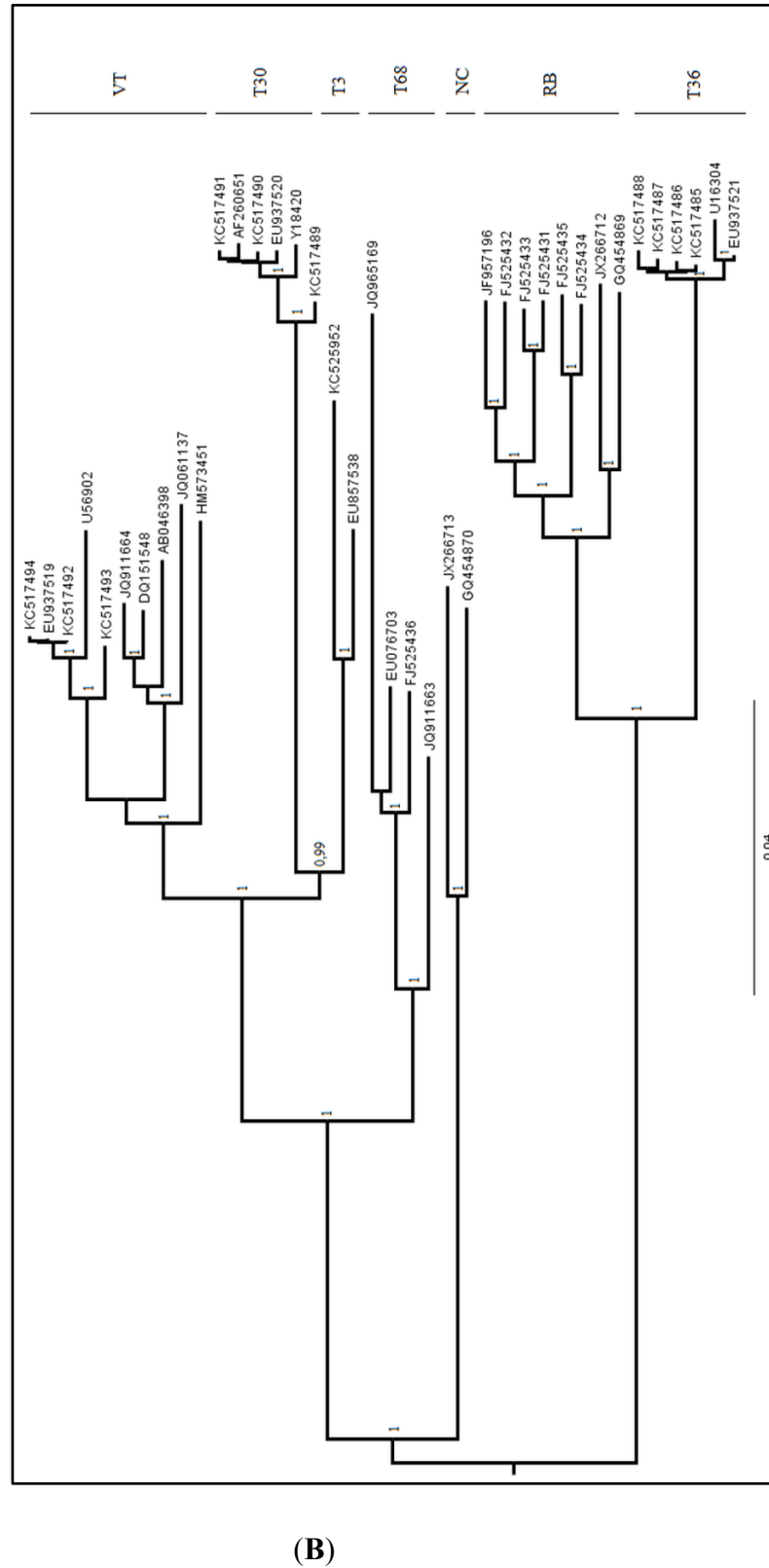

Figure S1. Genotype geographic distribution. Percentage of DNA clones per genotype, for p20 gene in the citrus growing areas of Uruguay.

(A)

Figure S2._Cont._

(**B**)

Figure S2. Complete genomes phylogenetic trees of *Citrus Tristeza Virus* isolates. Dataset was composed by isolates from Harper (2013) and Taiwanese strains JX266712-JX266713. (**A**) Maximum Parsimony method was used in the analysis. (**B**) Maximum Likelihood method with HKY nucleotide substitution model and aLRT test to estimate nodes support where used. aLRT values are shown. GenBank accession numbers of strains used are given.