



Supplementary Figure S1. Minimum Spanning Tree (MST) of STEC genomes isolated from cattle ($n = 30$). Each circle represents an isolate. Each color indicates a serotype. Numbers on lines between circles indicate allele differences among the genomes. Each circle contains the isolate identification code, the origin of the isolates (central or southern Chile), *stx* type, the sequence type (ST). Three clusters are represented by a light blue area merging two or more circles and were defined as genomes with fewer than ten allele differences. A total of 2351 genes representing the STEC core genome was used to construct the MST.