



Supplemental Figure 1. Phylogram based on Neighbor Joining phylogenetic analysis in PAUP* version 1.010b. Bootstrap values are based on 1000 bootstrap replicates. Ambiguously called SNPs were excluded from this analysis, as well as singleton SNPs, because they are not phylogenetically informative. Isolates that were designated as temporally linked to the S. Montevideo salami-related outbreak are marked with a black dot, isolates that were identified as associated with the pepper associated outbreak are marked with a circle. Names of isolates of the Lienau et al. (2011) study start with the abbreviation FDA, isolates that were newly sequenced for this study start with the abbreviation FSL.

Lienau, E. K., E. Strain, C. Wang, J. Zheng, A. R. Ottesen, C. E. Keys, T. S. Hammack, S. M. Musser, E. W. Brown, M. W. Allard, G. Cao, J. Meng, and R. Stones. 2011. Identification of a salmonellosis outbreak by means of molecular sequencing. *N Engl J Med* 364:981–982.