Supplemental Figure 1. Phylogram inferred by neighbor joining from a concatenated sequence containing \textit{gap}, \textit{prs}, and \textit{sigB} for unique \textit{L. monocytogenes} sequence types and \textit{L. innocua}. Phylogram was constructed using one representative isolate for each unique \textit{L. monocytogenes} sequence type. \textit{L. monocytogenes} isolate labels include the name (e.g., F2655, representing isolate FSL F2-655), ribotype (e.g., 44A represents DUP-1044A) and source (e.g., human isolate from NYSDOH [HS], human isolate from NYCDOH [HC], animal isolate [AN], and food isolate [FD]). A concatenated \textit{gap}, \textit{prs}, and \textit{sigB} sequence for \textit{L. innocua} (CLIP 11262) was also included (http://genolist.pasteur.fr/ListiList/). The phylogram was rooted using a concatenated \textit{gap}, \textit{prs}, and \textit{sigB} sequence from \textit{Bacillus subtilis} as an outgroup (http://genolist.pasteur.fr/SubtiList/). The branch length of the outgroup was collapsed (indicated by “//”) to best view the topology of the tree. Neighbor joining bootstrap support values (if >70) are shown as node labels. Genetic lineages assigned by EcoRI ribotyping are designated by different colors; lineage I isolates are in red, lineage II isolates in green and lineage III isolates in blue.