

Supplementary Materials

Whole genome-based characterization of *Listeria monocytogenes* Isolates recovered from the Food Chain in South Africa.

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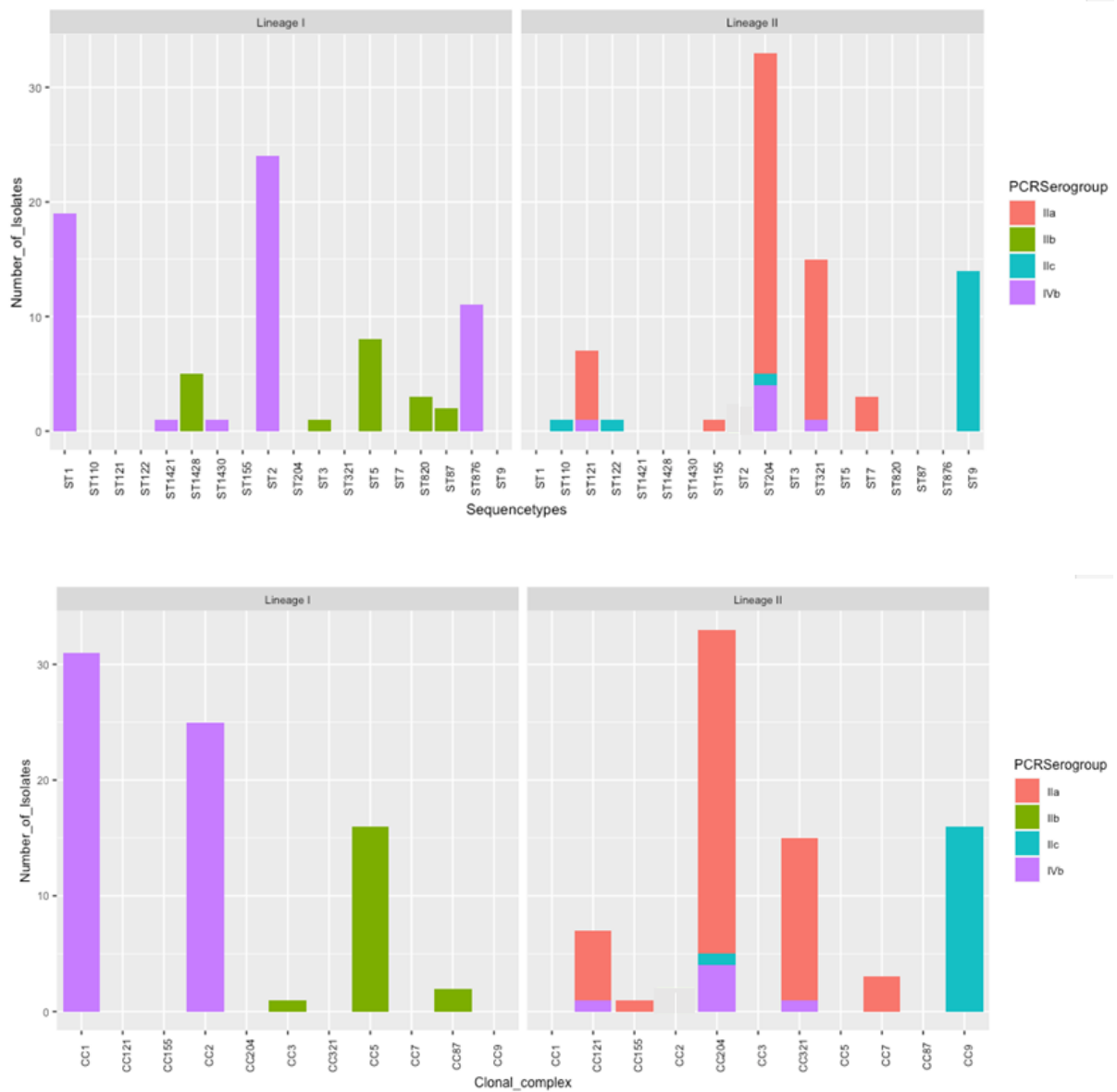


Figure S1. Distribution of *Listeria monocytogenes* serogroups, STs and CCs per study isolates. The coloured bar graph on lineage I indicate serogroups, sequences types and clonal complexes that belong to lineage I. The coloured bar graph on lineage II indicates serogroups, sequence types and clonal complexes that belong to lineage II.

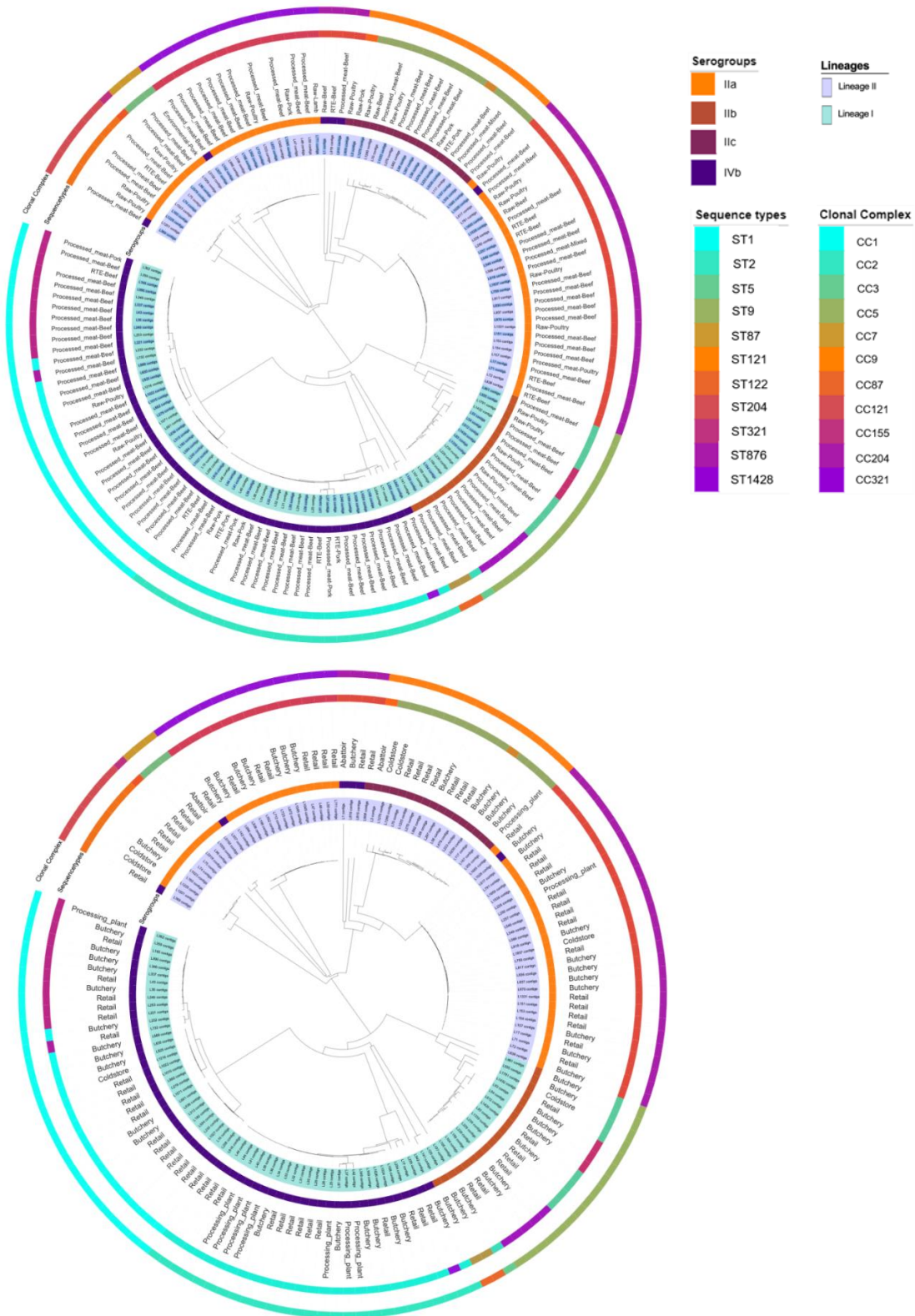


Figure S2. Core genome MLST phylogenetic analysis of *Listeria monocytogenes* isolates showing the association between MLST typing and isolation source isolates, **(A)** Meat category and **(B)** Establishment category isolates.

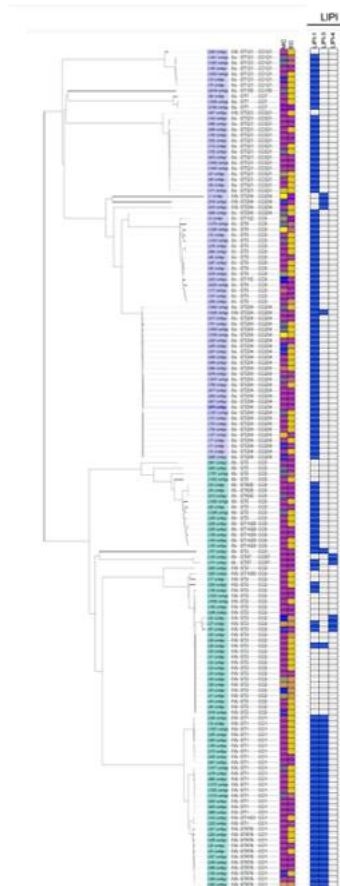


Figure S3. Core-genome MLST phylogenetic grouping of *Listeria* pathogenicity island across the *L. monocytogenes* isolates. The heat map shows the presence (blue) or absence (white) of genes involved in *L. monocytogenes* virulence. The isolation source MC and EC labelling on the heat map indicate the Meat category and Establishment category, respectively.