

Figure S1. Phylogenetic neighbor-joining tree derived from the *gyrA* gene sequences (785 bp) showing relationships of all described *Listeria* sensu stricto species. Numbers at nodes indicate bootstrap values (percentage of 1000 replicates).

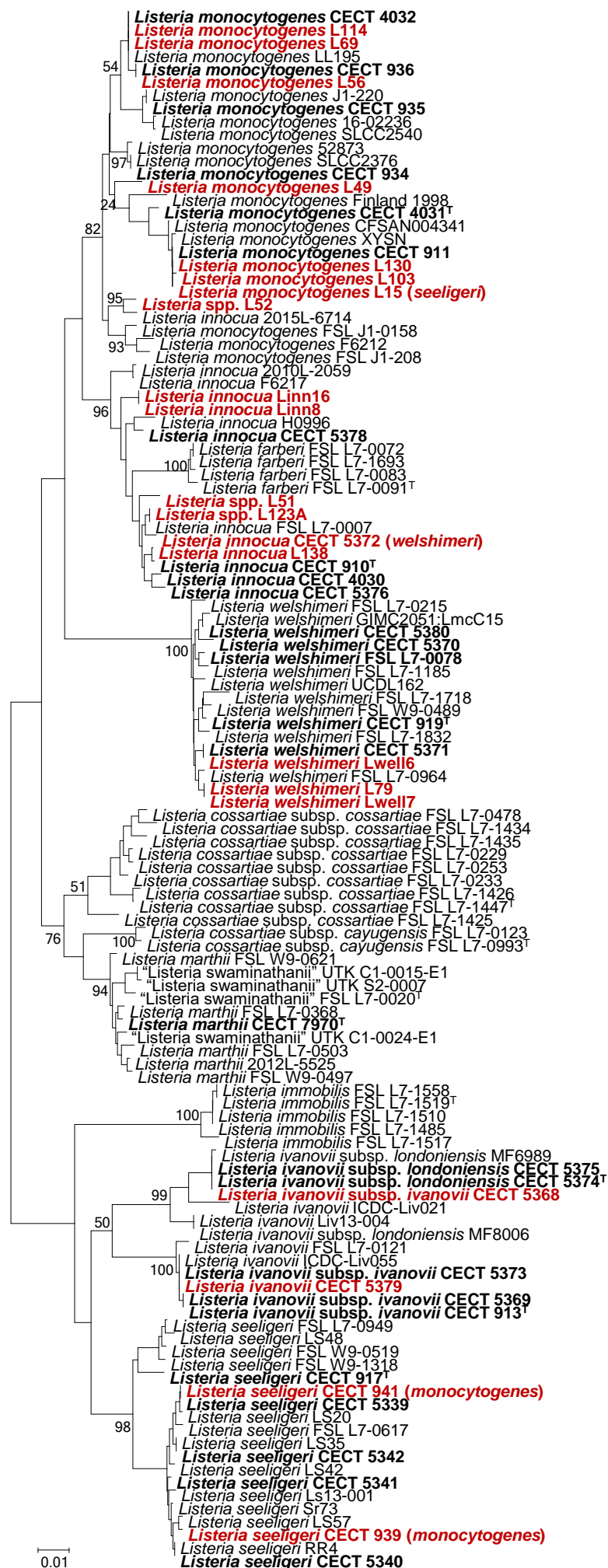


Figure S2. Phylogenetic neighbor-joining tree derived from the *cpn60* gene sequences (833 bp) showing relationships of all described *Listeria* sensu stricto species. Numbers at nodes indicate bootstrap values (percentage of 1000 replicates).

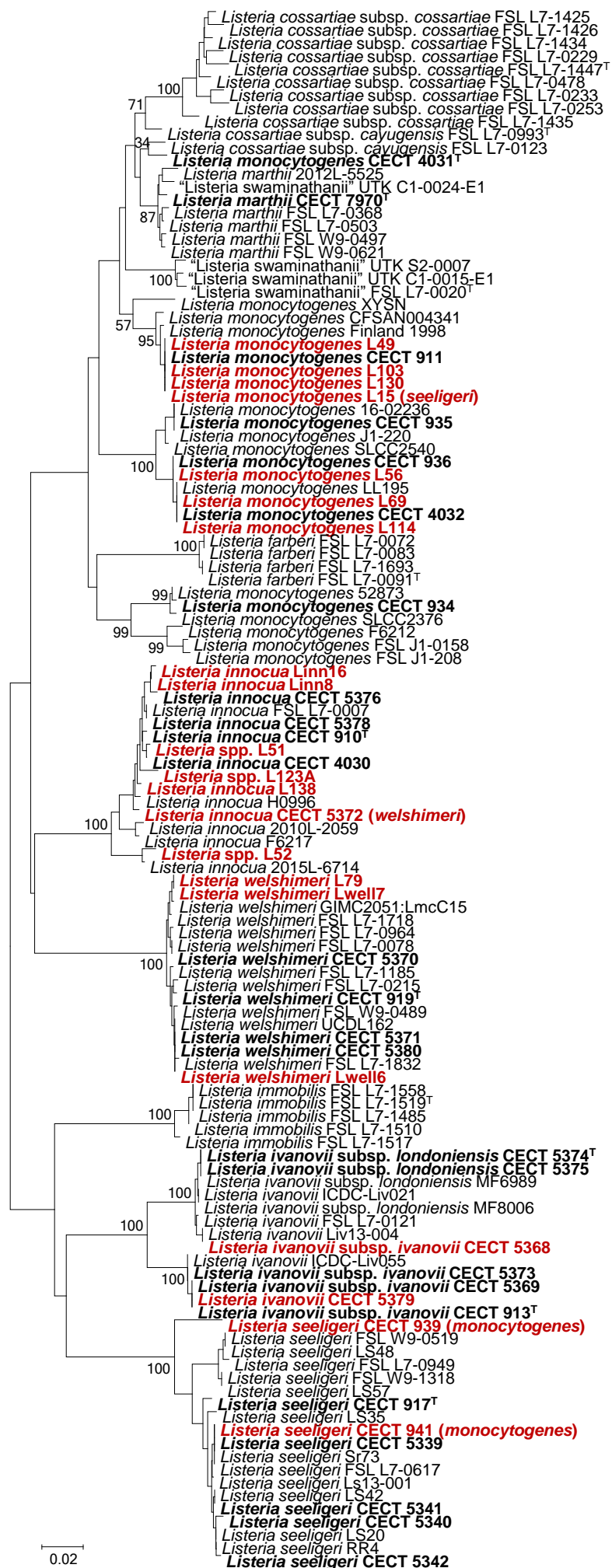


Figure S3. Phylogenetic neighbor-joining tree derived from the *parE* gene sequences (550 bp) showing relationships of all described *Listeria* sensu stricto species. Numbers at nodes indicate bootstrap values (percentage of 1000 replicates).

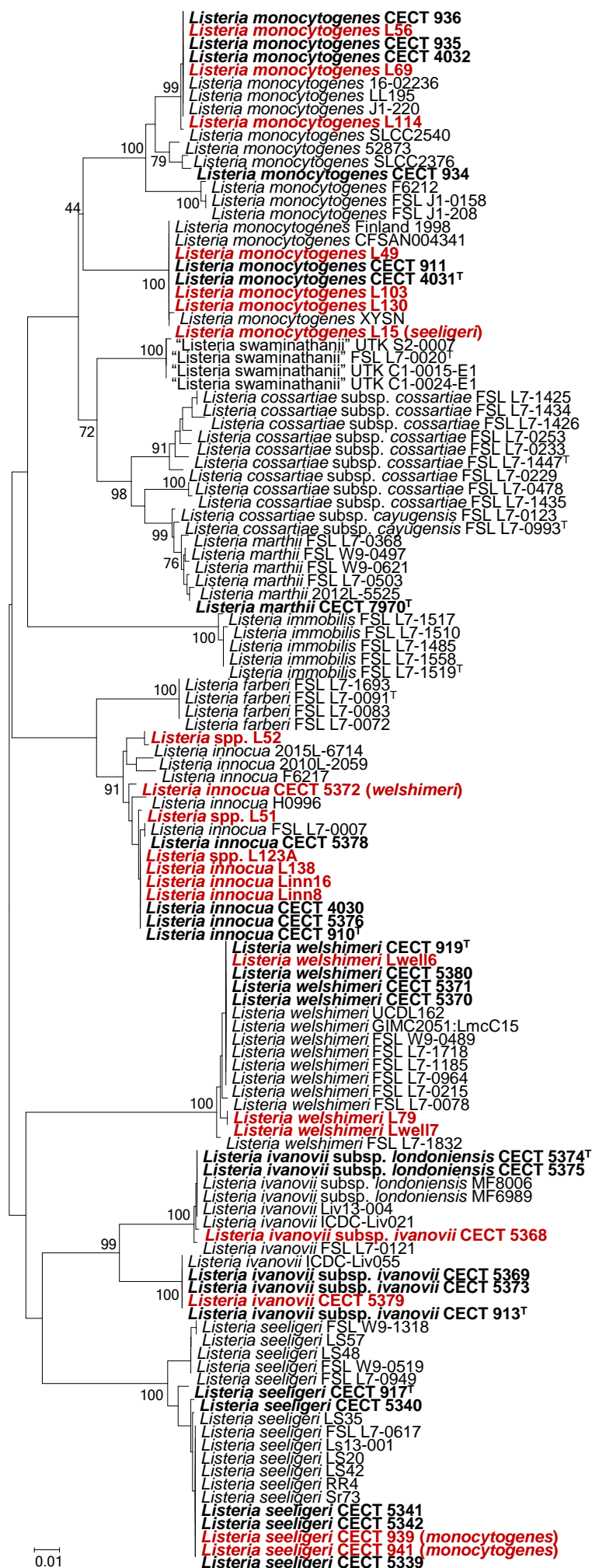


Figure S4. Phylogenetic neighbor-joining tree derived from the *recA* gene sequences (555 bp) showing relationships of all described *Listeria* sensu stricto species. Numbers at nodes indicate bootstrap values (percentage of 1000 replicates).

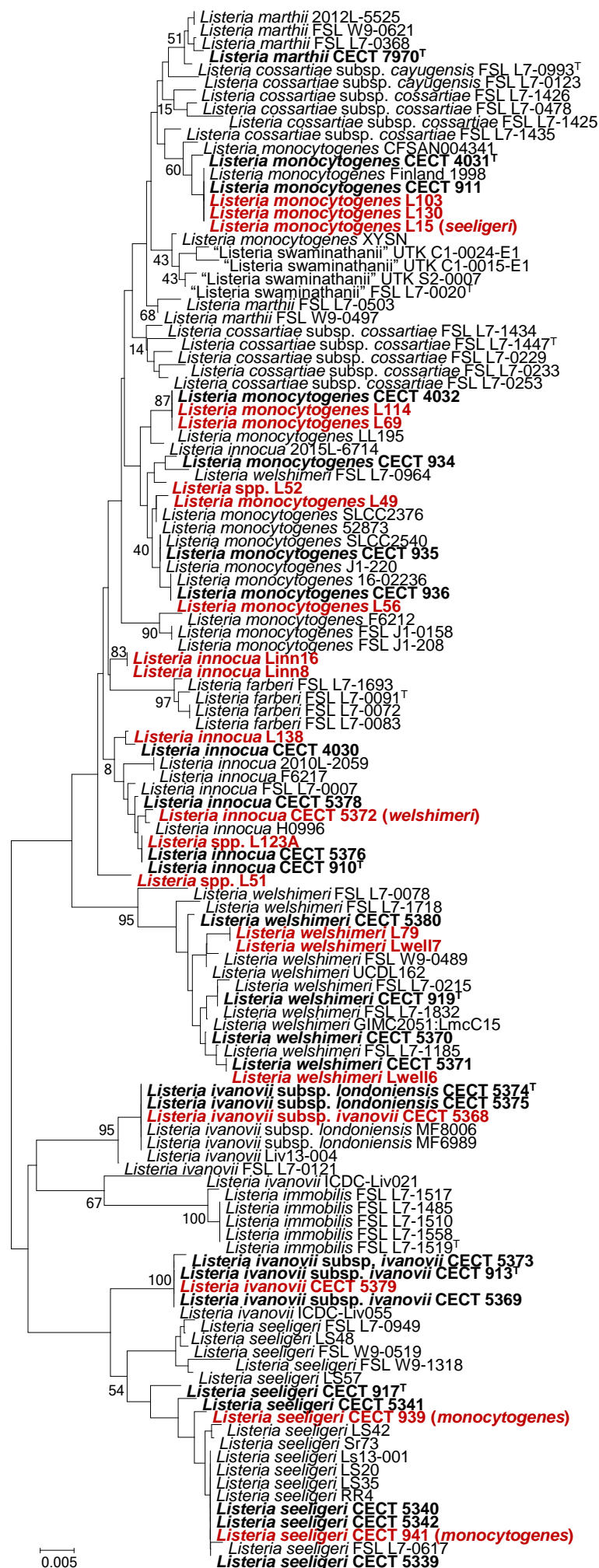


Figure S5. Phylogenetic neighbor-joining tree derived from the *rpoB* gene sequences (595 bp) showing relationships of all described *Listeria* sensu stricto species. Numbers at nodes indicate bootstrap values (percentage of 1000 replicates).

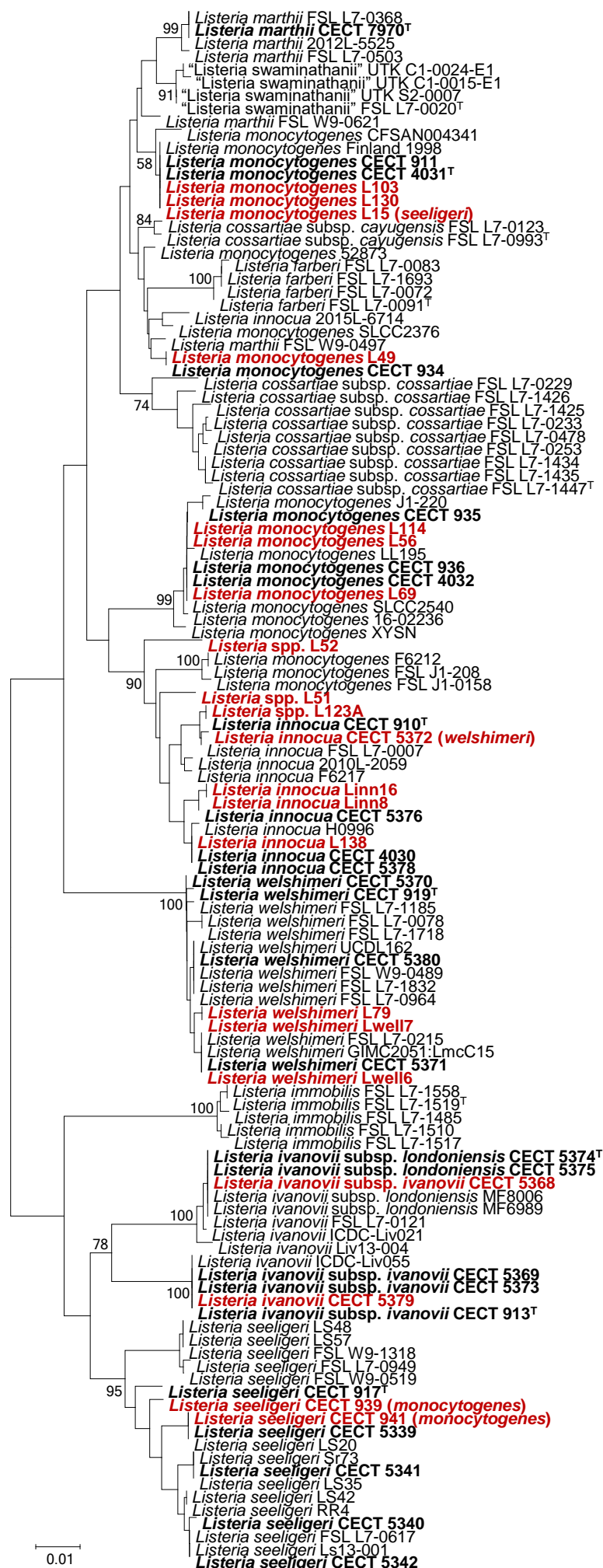


Figure S6. Phylogenetic neighbor-joining tree derived from the *atpA* gene sequences (599 bp) showing relationships of all described *Listeria* sensu stricto species. Numbers at nodes indicate bootstrap values (percentage of 1000 replicates).



Figure S7. Phylogenetic neighbor-joining tree derived from the *gyrB* gene sequences (458 bp) showing relationships of all described *Listeria* sensu stricto species. Numbers at nodes indicate bootstrap values (percentage of 1000 replicates).