

## Online Supplementary Material to

### Comparative genomic analysis of *Periweissella* and the characterization of novel motile species

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**Figure S1.** Box plot of the intra-genus and inter-genus average amino acid identity of core proteins (cAAI) values in the genus *Periweissella* and *Weissella*.

**Figure S2.** Heatmap of the presence and absence of 45 flagellar-related genes in motile *Lactobacillaceae* strains. Red indicates the gene is present and white indicates the gene is absent in the strains. Strains used for the graph are provided in the Supplementary Table S4.

#### Supplementary Tables provided as excel files:

**Table S1.** Genomes used for the IQ-TREE phylogenetic analysis of species previously classified in the *Leuconostocaceae* with *Lactiplantibacillus plantarum* and type species of each of the heterofermentative rod-shaped lactobacilli as the outgroup.

**Table S2.** Additional genomes of *Furfurilactobacillus* species used for Roary and Scoary analysis. Because the genus includes only three genome sequences of type strains, all genomes available on NCBI were used in the analysis.

**Table S3.** Genes used for analysis of genus-level metabolic traits of *Lactobacillaceae*.

**Table S4.** Genomes of *Lactobacillaceae* which were used for the BLAST analysis but are not shown in Tables S1 and S2.

**Table S5.** Strains and genomes used for the identification of flagellar-related genes by BLASTp.

**Table S6.** Pairwise comparison of average amino acid identity (AAI) values of heterofermentative *Lactobacillaceae* and the outgroup.

**Table S7.** Pairwise comparison of average amino acid identity of core proteins (cAAI) values of heterofermentative *Lactobacillaceae* and the outgroup.

**Table S8.** Preliminary screened results from Roary and Scoary between the group of *Periweissella* and *Furfurilactobacillus*.

**Table S9.** Preliminary screened results from Roary and Scoary between the group of *Periweissella* and *Weissella*.

Figure S1



