

Description of Additional Supplementary Files

Supplementary Data 1: Sampling timepoints and industrial metadata.

Description: Overview of industrial samples and their corresponding metadata.

Supplementary Data 2: Sequencing info and mapping stats of metagenomes.

Description: Overview of the sequencing quality and mapping stats of metagenomes from analysed industrial samples.

Supplementary Data 3: Metrics for genome and metagenome assemblies.

Description: Quality parameters from genome and metagenome assemblies.

Supplementary Data 4: MAGs taxonomy analysis and quality metrics.

Description: Metagenome Assembled Genomes (MAGs) from metagenomics samples, and subsequent taxonomic profiling from MAGs, showing *L. fermentum* and *L. amylovorus* as most abundant bacterial species for the majority of the industrial samples.

Supplementary Data 5: Sequences used for microbial community profiling

Description: Overview of sequences used for the microbial community profiling, including base length, identity to SILVA database sequence and SINA alignment score (in percentages).