

Supplementary Material

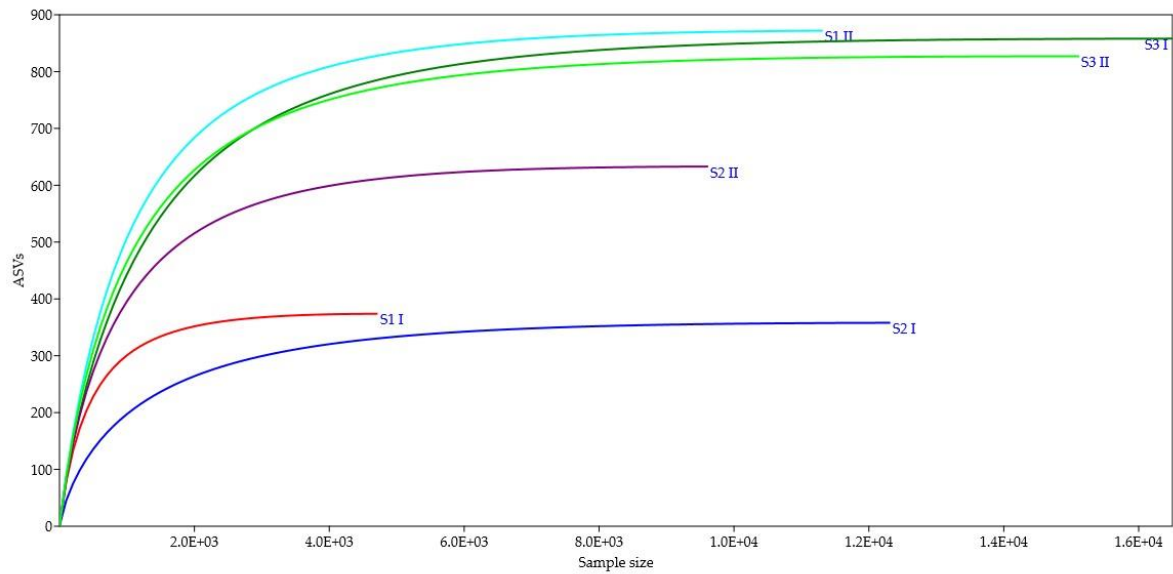


Figure S1. Species accumulation plot showing the number of amplicon sequence variants (ASVs) on sample size for each sample.

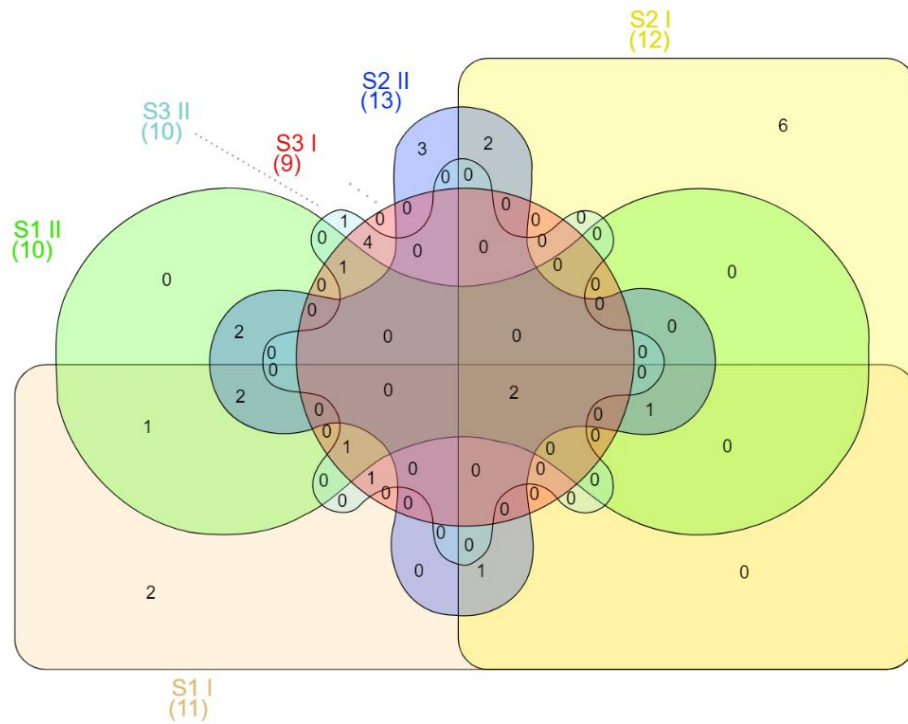


Figure S2. Venn diagram underlining the common ASVs (give in brackets) at the family level. In the Figure [S1 I]: env.OPS 17, Xanthomonadaceae; [S2 I]: Bdellovibrionaceae, Hyphomonadaceae, Ilumatobacteraceae, Rhodanobacteraceae, Rhodobacteraceae, Sporichthyaceae; [S3 II]: Pyrinomonadaceae; [S2 II]: Methylomonaceae, Methylophilaceae, Opitutaceae; [S3 I] and [S3 II]: Chthoniobacteraceae, Nocardiodaceae, Solirubrobacteraceae, Xanthobacteraceae; [S1 I] and [S1 II]: Flavobacteriaceae; [S1 II] and [S2 II]: Pedosphaeraceae, Solibacteraceae (Subgroup 3); [S1 I] and [S2 I] and [S2 II]: Burkholderiaceae; [S1 I] and [S1 II] and [S2 II]: Microscillaceae, Nitrosomonadaceae; [S1 I] and [S2 I] and [S1 II] and [S2 II]: Nitrospiraceae; [S1 I] and [S3 I] and [S1 II] and [S3 II]: Gemmatimonadaceae; [S1 I] and [S3 I] and [S3 II]: Sphingomonadaceae; [S1 I] and [S2 I] and [S3 I] and [S1 II] and [S2 II] and [S3 II]: uncultured, unknown; [S3 I] and [S1 II] and [S3 II]: TRA3-20; [S2 I] and [S2 II]: Chitinophagaceae, Gallionellaceae.

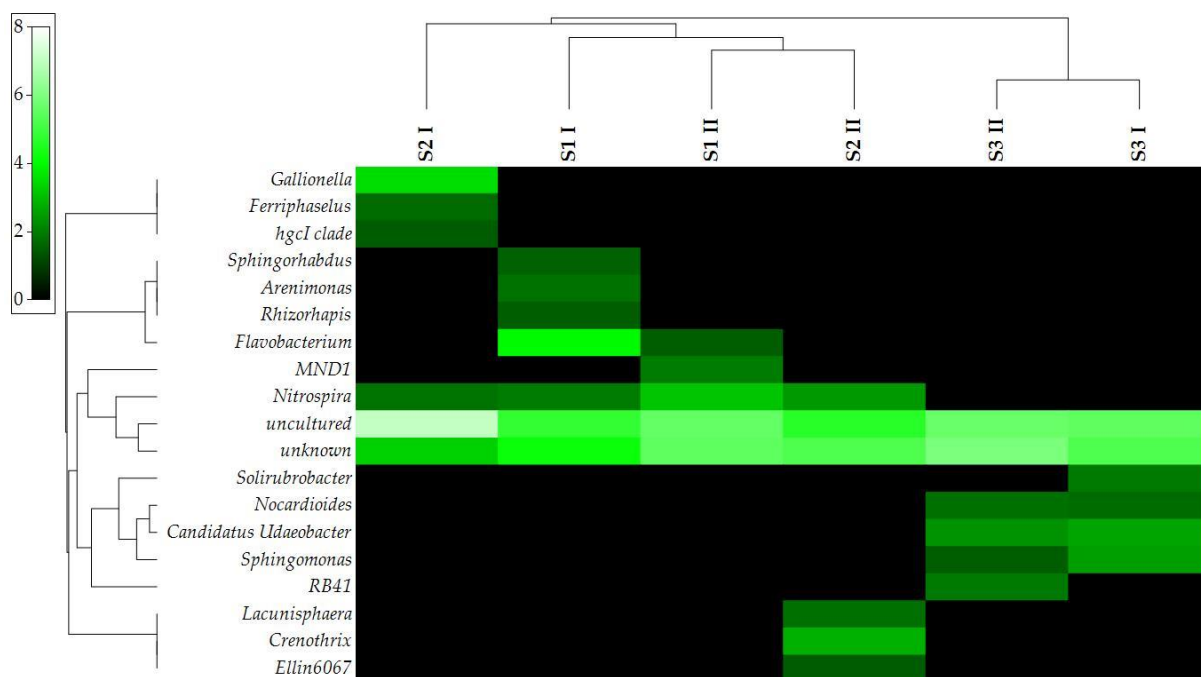


Figure S3. Heatmap of the main genera found in the samples. The upper clusterization shows the sample distribution according to taxa presence/absence and abundances. The heat map was realized based on a resemblance matrix (Analysis between variables and measure of the index of association) and hierarchical cluster analysis (Group average cluster mode).

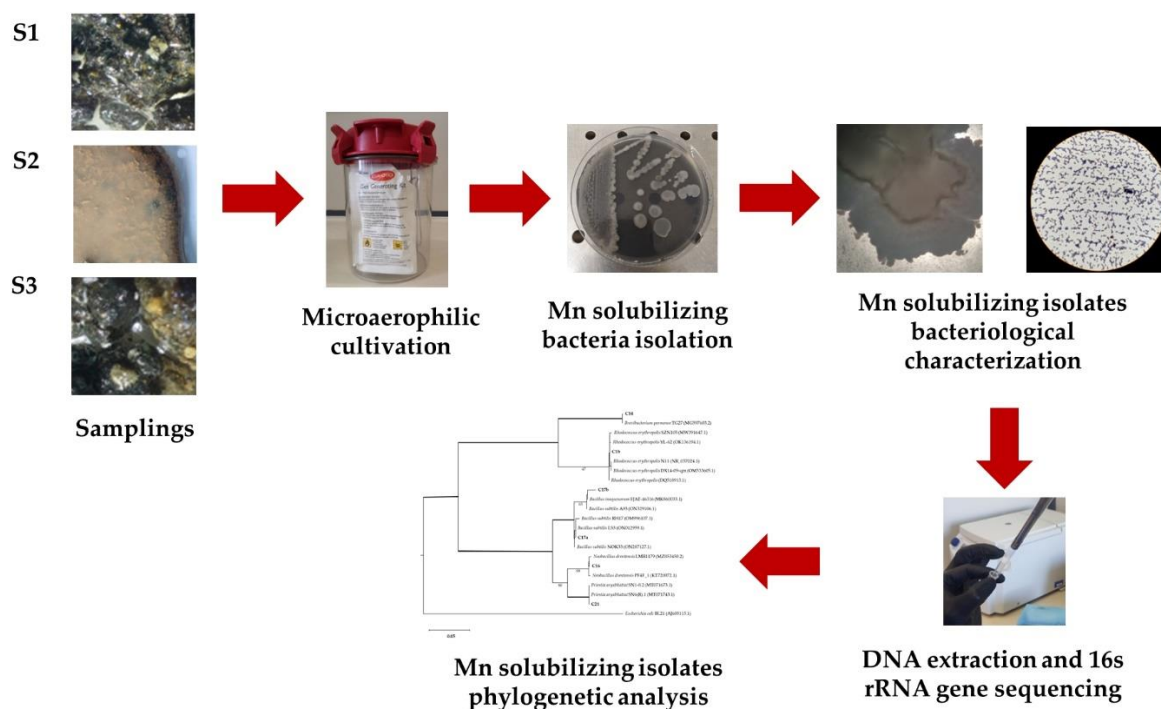
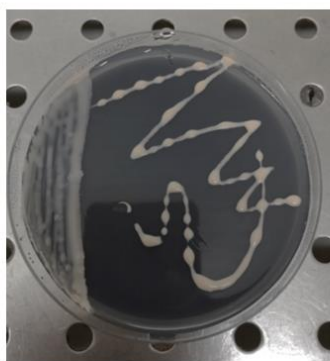
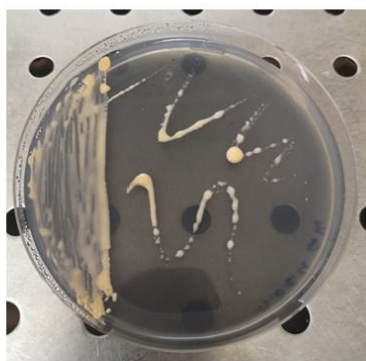


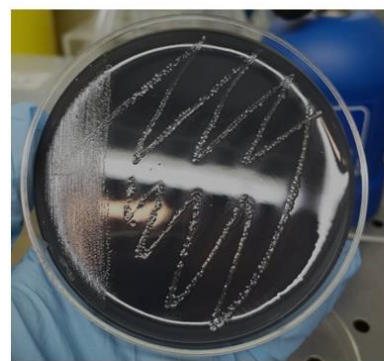
Figure S4. Summary of the experiment setup during Mn-oxide solubilizing process.



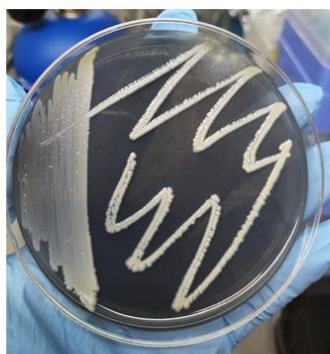
C1b



C14



C16



C17a



C17b



C21

Figure S5. Mn-oxide solubilizing isolates on manganese basal medium (MMB).