Description of Additional Supplementary Files

File Name: Supplementary Data 1
Description: List of NCBI GeneBank accession numbers of the 171 assembled genomes used to create the whole-genome Multilocus sequence typing scheme.

File Name: Supplementary Data 2
Description: Characteristics of the 17,603 loci of the whole-genome Multilocus Sequence Typing scheme.

File Name: Supplementary Data 3
Description: Accession numbers and associated metadata for all 1,305 S. maltophilia isolates included in the phylogenetic analysis.

File Name: Supplementary Data 4
Description: Sequence metrics, number of consensus whole genome Multilocus sequence typing allele calls of all 1305 S. maltophilia isolates and other Stenotrophomonas species.

File Name: Supplementary Data 5
Description: Valid allele call numbers assigned by whole genome multilocus sequence typing scheme as implemented in bionumerics for all 1,305 S. maltophilia isolates.