Figure S2. Neighbor-joining rooted phylogenetic tree based on multiple alignments of the 16S rRNA gene sequences of bacterial OTUs and their respective best sequence matches from the NCBI database. Values in parentheses indicate the frequency (%) of sequences in the clone libraries BT-M, IC1-M and IC2-M, respectively. The scale bar represents change per nucleotide position. Bootstrap values >50% (1,000 replications) are indicated at the nodes.