



Supplementary Fig. S2. Neighbour-joining tree based on almost full-length 16S rRNA gene sequences (*E. coli* positions 47–1465). The tree reconstructs the phylogenetic relationships between the novel candidate species and environmental sequences of uncultured actinobacteria. The phylogenetic group presented in the tree represents almost the entire Luna-1 cluster (Hahn *et al.*, 2003) and the major part of the acII group (Warnecke *et al.*, 2004). Sequences that contain the diagnostic oligonucleotide sequences for discrimination of the candidate species from other taxa are shown in bold, and sequence similarities within the respective groups are presented (as percentage identity). Bootstrap values represent percentage support of nodes based on 1000 resamplings (only values $\geq 60\%$ are shown). Bar, 1 % estimated sequence divergence. The sequence of *Brevibacterium linens* DSM 20425^T (GenBank accession no. X77451) served as an outgroup (not shown). References cited are given in the main paper.