Figure S17 Phylogenetic tree of 84 16S rDNA sequences of ‘novel’ *Clostridium* species. A neighbor – joining analysis with Jukes–Cantor correction and bootstrap support was performed on the gene sequences. Bootstrap values are given at nodes. Sequences marked by filled square are the ones considered as representative (56) of the 12 clusters. Values in parentheses are accession numbers (RDP and NCBI) (http://rdp.cme.msu.edu/ and http://www.ncbi.nlm.nih.gov/).