SUPPLEMENTARY MATERIAL
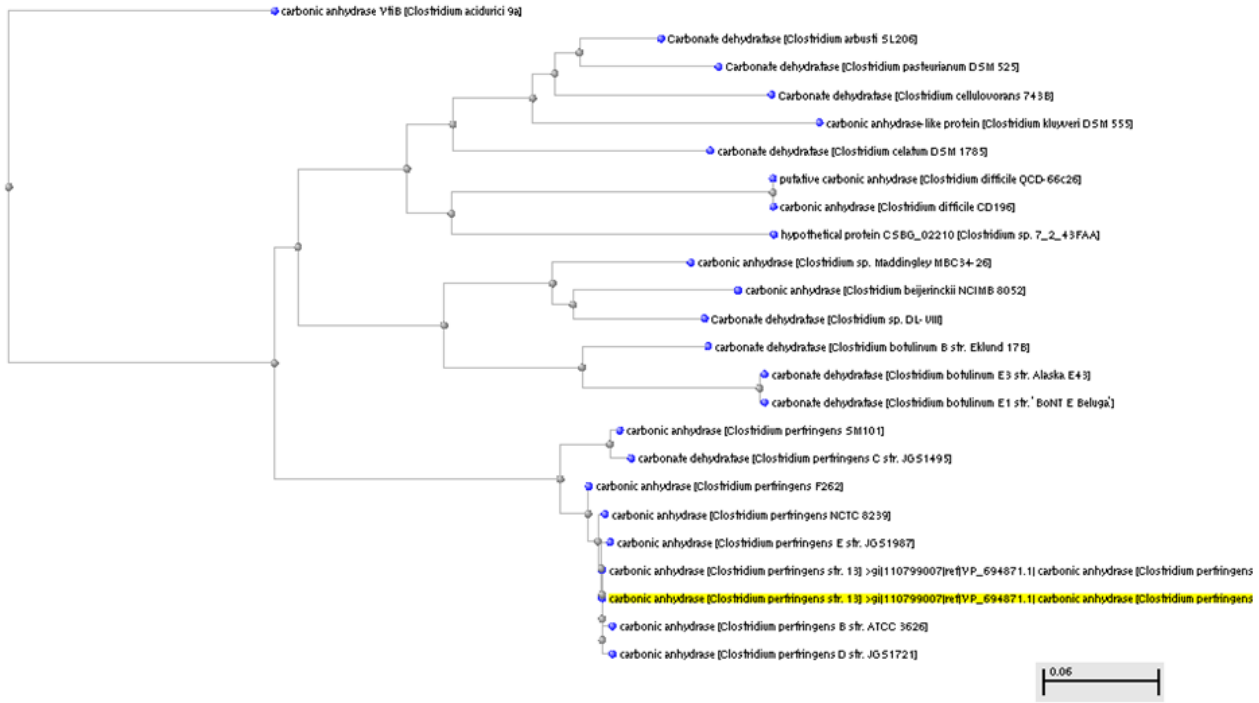
Figure S1. Phylogenetic tree showing the relationships among beta class carbonic anhydrase sequences from species of the genus *Clostridia*. The tree was produced using the Fast Minimum Evolution algorithm (Desper R and Gascuel O, Mol Biol Evol 21:587-98, 2004) with BLAST pairwise alignments obtained from all non-redundant databases available from the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). Bar indicates substitutions per site. Gene identification numbers follow. *Clostridium perfringens* str. 13 , GI:18309395; *Clostridium perfringens* E str. JGS1987, GI:168204407; *Clostridium perfringens* B str. ATCC 3626, GI:170763897; *Clostridium perfringens* NCTC 8239, GI:182420476; *Clostridium perfringens* D str. JGS1721, GI:182624627; *Clostridium perfringens* F262, GI:422872991; *Clostridium perfringens* SM101, GI:110802070; *Clostridium perfringens* C str. JGS1495, GI:169343003; *Clostridium arbusti* SL206, GI:399887674; *Clostridium* sp. DL-VIII, GI:359410832; *Clostridium beijerinckii* CIMB 8052, GI:150019236; *Clostridium cellulovorans* 743B, GI:302873277; *Clostridium* sp. Maddingley MBC34-26, GI:410729058; *Clostridium pasteurianum* DSM 525, GI:440781189; *Clostridium botulinum* B str. Eklund 17B, GI:187932534; *Clostridium celatum* DSM 1785, GI:429766678; *Clostridium difficile* QCD-66c26, GI:254975813; *Clostridium difficile* CD196, GI:260683813; *Clostridium* sp. 7_2_43FAA, GI:404370481; *Clostridium kluyveri* DSM, GI:153953171; *Clostridium botulinum* E3 str. Alaska E43, GI:188589913; *Clostridium botulinum* E1 str. 'BoNT E Beluga', GI:251780513; *Clostridium acidurici* 9a, GI:407474874.