



Supplementary Fig. 1. Phylogenetic positions of sequenced species among members of the family Bacillaceae. The numbers indicate the percentages of bootstrap samples, derived from 1000 samples that supported the internal branches. Bootstrap probability values less than 50 were omitted from this figure. Bar=0.01 KnuC unit. *G. kaustophilus* HTA426 sequenced in this study is colored by red. The other sequenced species are colored by blue. Abbreviations: A., *Aneurinibacillus*; Alb., *Alicyclobacillus*; Amb., *Amphibacillus*; B., *Bacillus*; Brb., *Brevibacillus*; G., *Geobacillus*; Gb., *Gracilibacillus*; H., *Halobacillus*; M., *Marinococcus*; O., *Oceanobacillus*; P., *Paenibacillus*; S., *Saccharococcus*; Sb., *Salibacillus*; T., *Thermoactinomyces*; V., *Virgibacillus*.