Supplemental Figure S3. Clusters of Orthologous Groups (COG) functional categories assigned to functionally annotated protein-encoding sequences in the genome of novel effective B. cereus group species “B. clarus” strain ATCC 21929T (n = 4,876 out of 5,328 total protein-encoding sequences). Functional annotation of the ATCC 21929T genome was performed via the eggNOG-mapper webserver (http://eggnog-mapper.embl.de/, accessed July 20, 2020), using the RefSeq protein sequences of ATCC 21929T as input. The percentage (%) of functionally annotated protein-encoding genes assigned to a particular COG or COG group is displayed on the Y-axis. COG abbreviations are displayed on the X-axis and correspond to the following: (NA), not assigned (no COG was assigned to the gene); B, chromatin structure and dynamics; C, energy production and conversion; D, cell cycle control, cell division, chromosome partitioning; E, amino acid transport and metabolism; F, nucleotide transport and metabolism; G, carbohydrate transport and metabolism; H, coenzyme transport and metabolism; I, lipid transport and metabolism; J, translation, ribosomal structure and biogenesis; K, transcription; L, replication, recombination and repair; M, cell wall/membrane/envelope biogenesis; N, cell motility; O, posttranslational modification, protein turnover, chaperones; P, inorganic ion transport and metabolism; Q, secondary metabolites biosynthesis, transport and catabolism; S, function unknown; T, signal transduction mechanisms; U, intracellular trafficking, secretion, and vesicular transport; V, defense mechanisms; W, extracellular structures.