



Supplementary Figure S1: Chromosomal positions of the 128 and 400 protein-coding genes used for the construction of the maximum likelihood phylogenies (Figure 1 and Supplementary Figure S2) distributed on the chromosome, using the type species *B. japonicum* USDA 6^T as reference. Genes are a representation of shared genes of respective taxa investigated in this study. For more information see Supplementary Table S3.