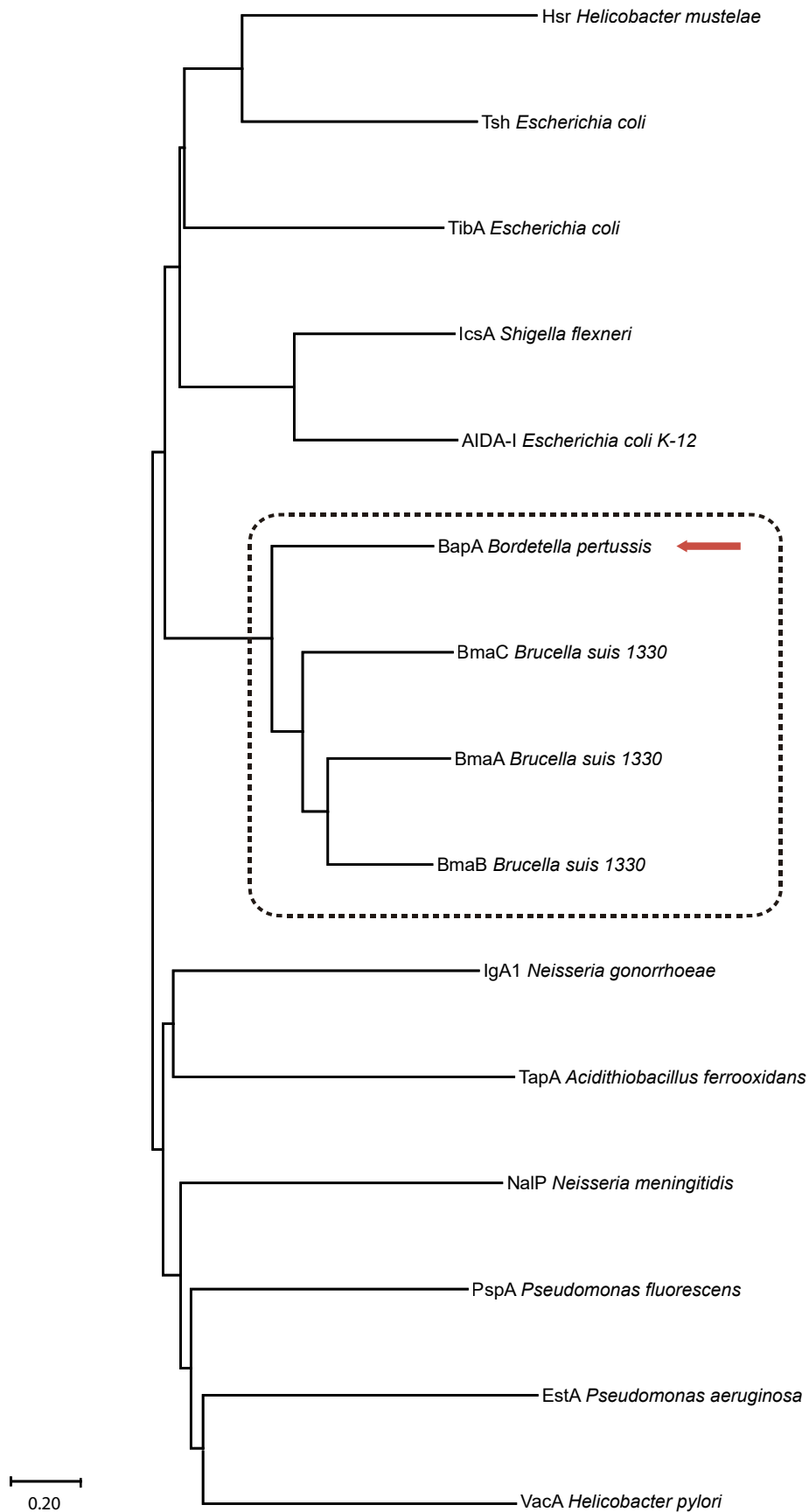Figure S1

Supplementary figure 1: Evolutionary relationships of beta barrels from type Va autotransporters. Phylogeny was inferred using the Neighbor-Joining method (Saitou & Nei, 1987). The scale bar represents the number of amino acid substitutions per site. The dotted line square highlights the position of the Bma proteins within the tree. The red arrow indicates the recognized autotransporter of the group of the barrel-domain "type" to which the Bma proteins belong (BapA).