

Supplemental Material Figure Legends

Fig. S1. Genomic organization of flagellar genes in 41 bacterial species belonging to (A) Delta- and Epsilonproteobacteria, (B) Alpha- and Betaproteobacteria, (C) Gammaproteobacteria, and (D) all other bacterial subdivisions. Homologs of the 47 flagellar genes considered in this study are depicted as black arrows (representing gene orientation), and all other spacer genes are designated with gray arrows and numbers. When the number of spacer genes between flagellar genes or operons is less than four, then each spacer gene is portrayed as a grey arrow; otherwise the actual number of genes is provided. For space considerations, neighboring flagellar genes having the same three-letter prefix and orientation are displayed as clusters in which only the first gene name contains the prefix, and all subsequent genes are labeled with the last letter and shown as an arrow. Note that these clusters need not correspond to operons. Flagellar genes of the secondary systems are boxed.

Fig. S2. Phylogenetic tree of secondary flagellar systems. This tree is based of the concatenated alignment of 14 flagellar proteins and differs from Fig. 1B in that it includes the secondary flagellar system of *E. coli* 042 (33). Numbers (“1” and “2”) after species names denote primary and secondary systems. Secondary flagellar systems are highlighted in red.