

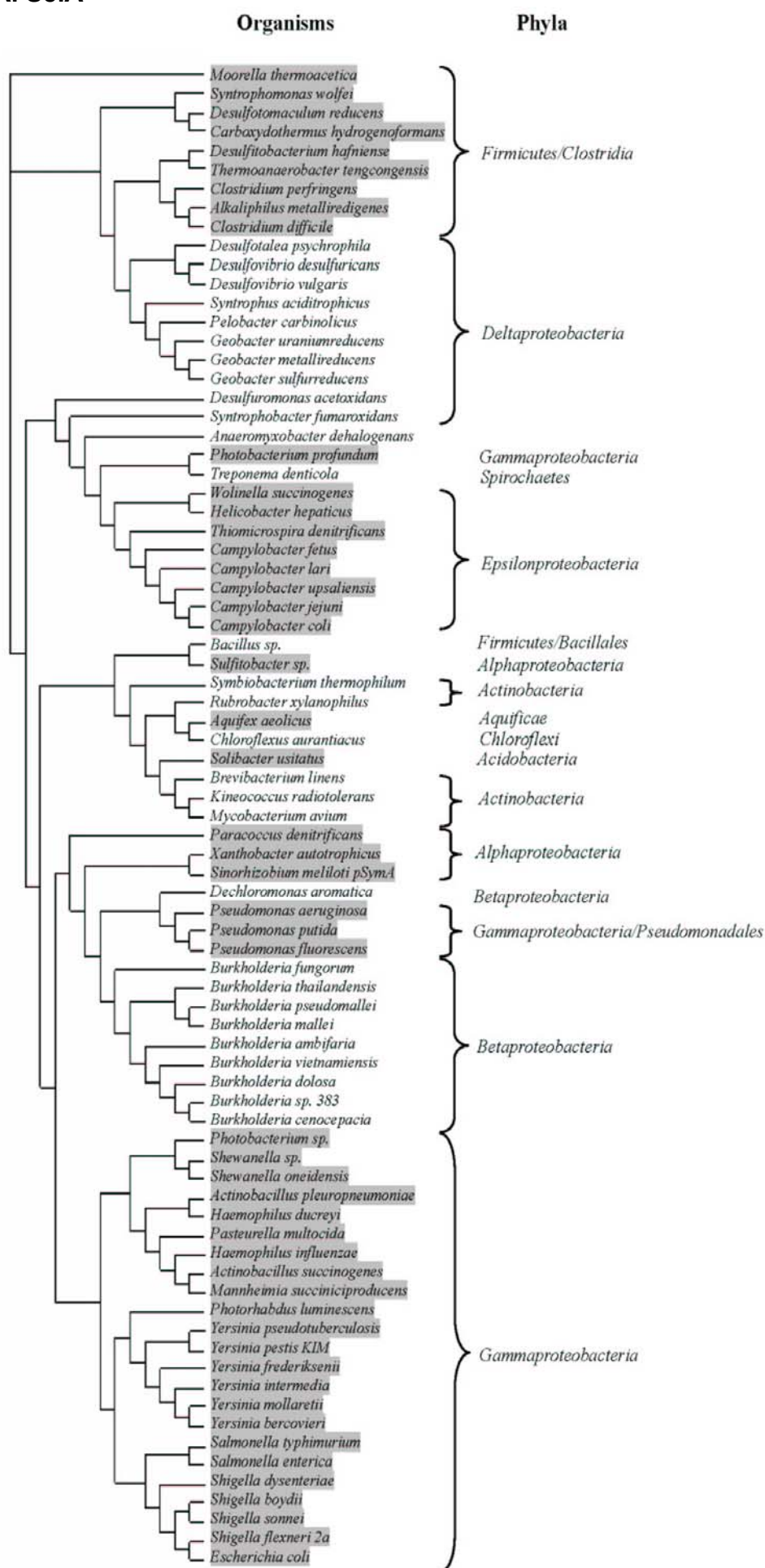
Figure Legends

Fig. S1. Phylograms of SelA, SelB, SelD and YbbB sequences. A total of 75 SelA, 75 SelB, 127 SelD and 88 YbbB sequences were identified in 349 completely and incompletely sequenced bacterial genomes. Organisms and phyla are separated using different shading patterns. In the SelD phylogram, U represents Sec-containing sequences and C represents Cys-containing sequences. A. SelA; B. SelB; C. SelD; D. YbbB.

Fig. S2. Distribution of selenoproteins and their Cys-containing homologs in organisms with and without the Sec trait. For each selenoprotein family, the occurrence of selenoproteins and their Cys homologs was determined in organisms with the Sec trait (Sec⁺) and of the Cys homologs in organisms lacking the Sec trait (Sec⁻). The data for each family are shown in three columns: (i) selenoproteins (Sec in Sec⁺, shown in red), (ii) Cys-containing homologs and the Sec trait (Cys in Sec⁺, shown in green), and (iii) Cys-containing homologs and no Sec trait (Cys in Sec⁻, shown in blue).

Fig. S3. Distribution of selenoproteins and their Cys-containing homologs in Sec-containing organisms. Two selenoprotein families (ArsC-like and DsrE-like) were excluded because the total number of both Sec- and Cys-containing sequences in Sec-containing organisms was low (less than 5). Remaining selenoprotein families were ordered based on the percentage of Sec and Cys forms of these proteins present in organisms with the Sec trait. Red, Sec in Sec⁺; Green, Cys in Sec⁺.

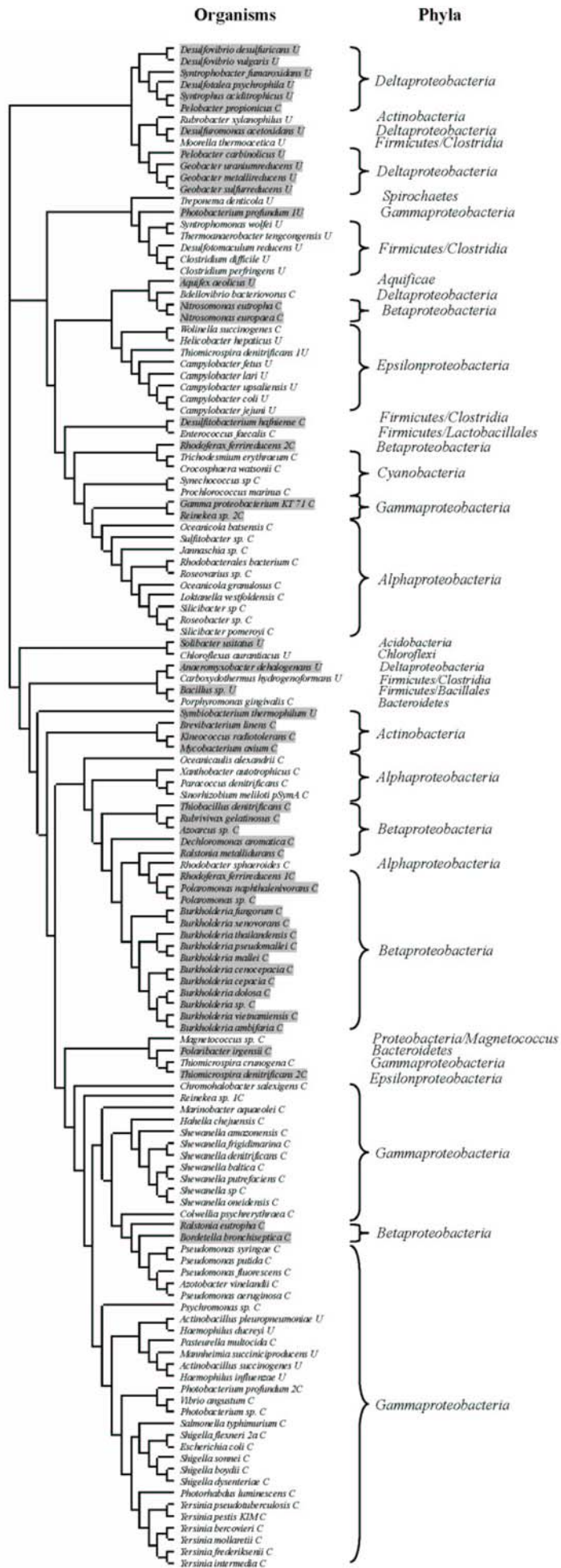
Fig. S1
A. SclA



B. SelB



C. SeID



D. YbbB

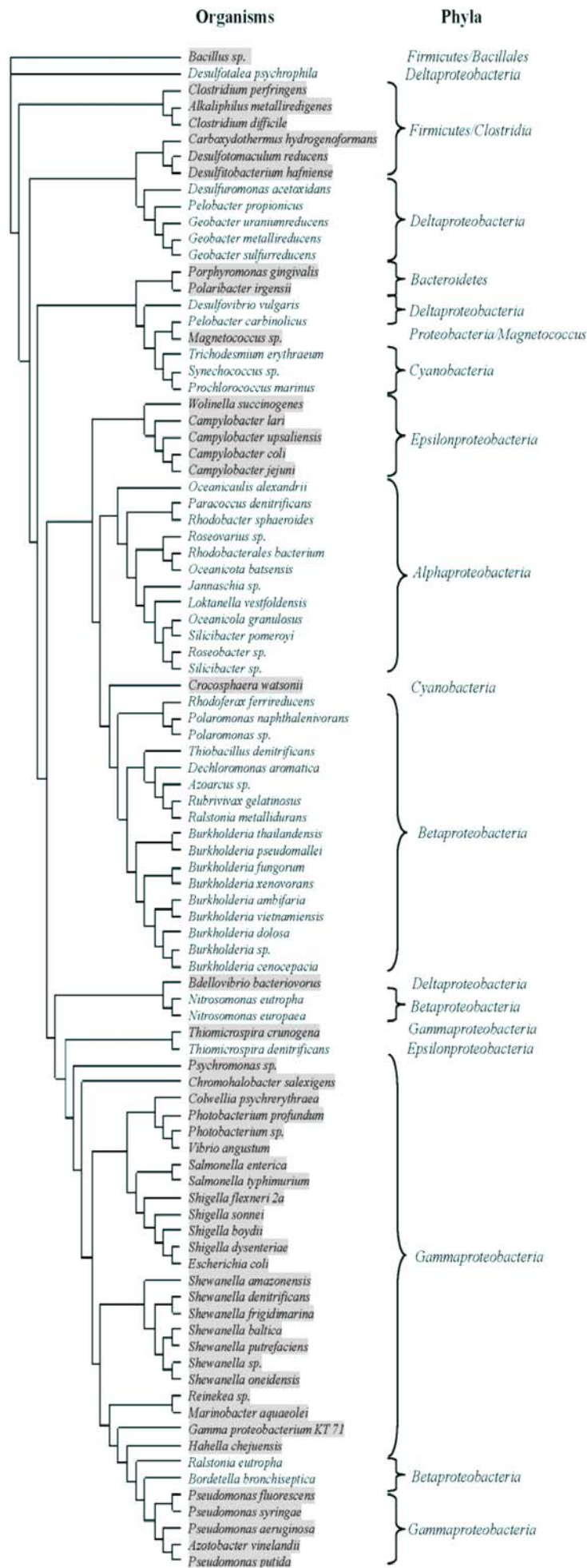


Fig. S2

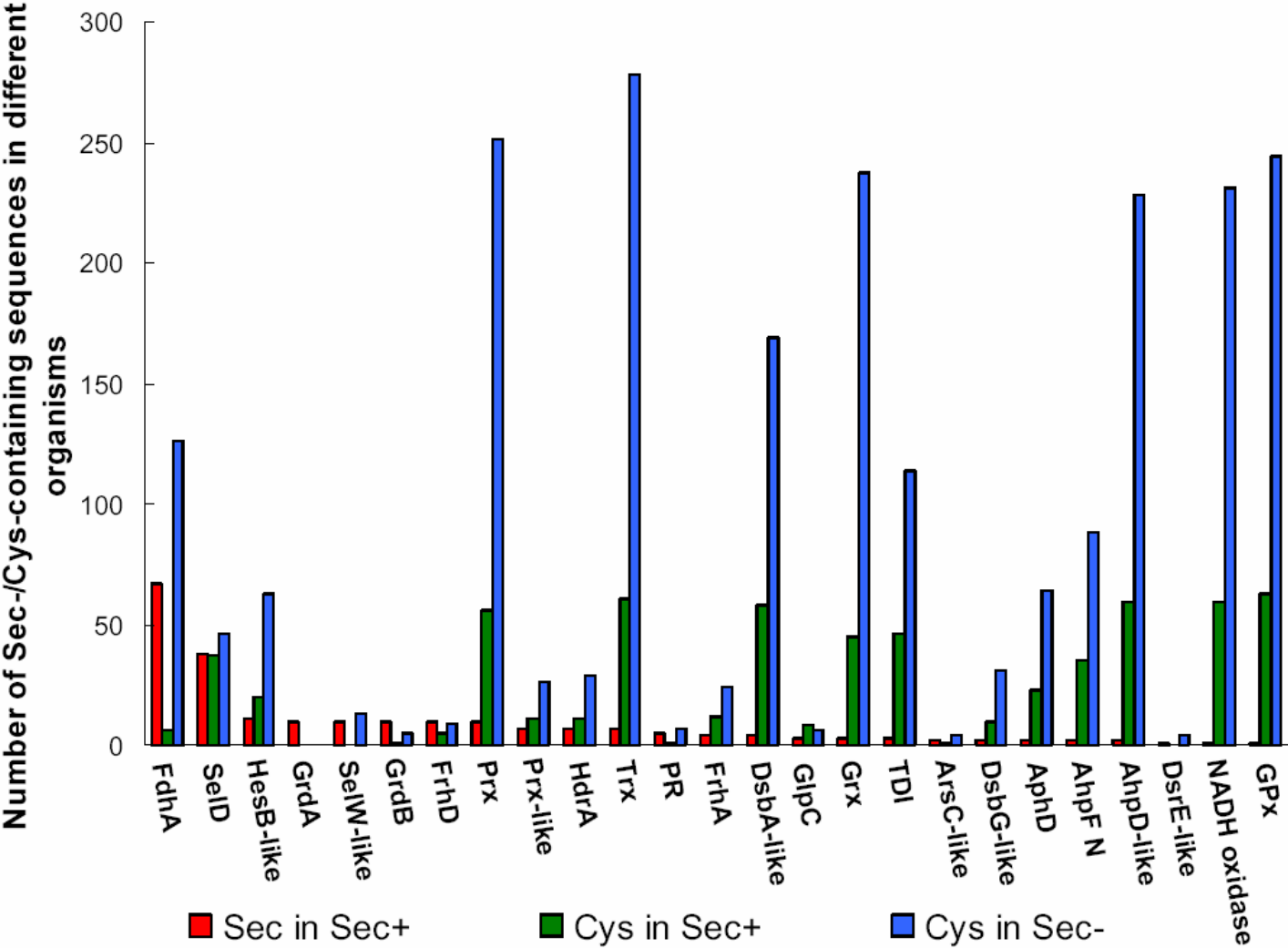


Fig. S3

