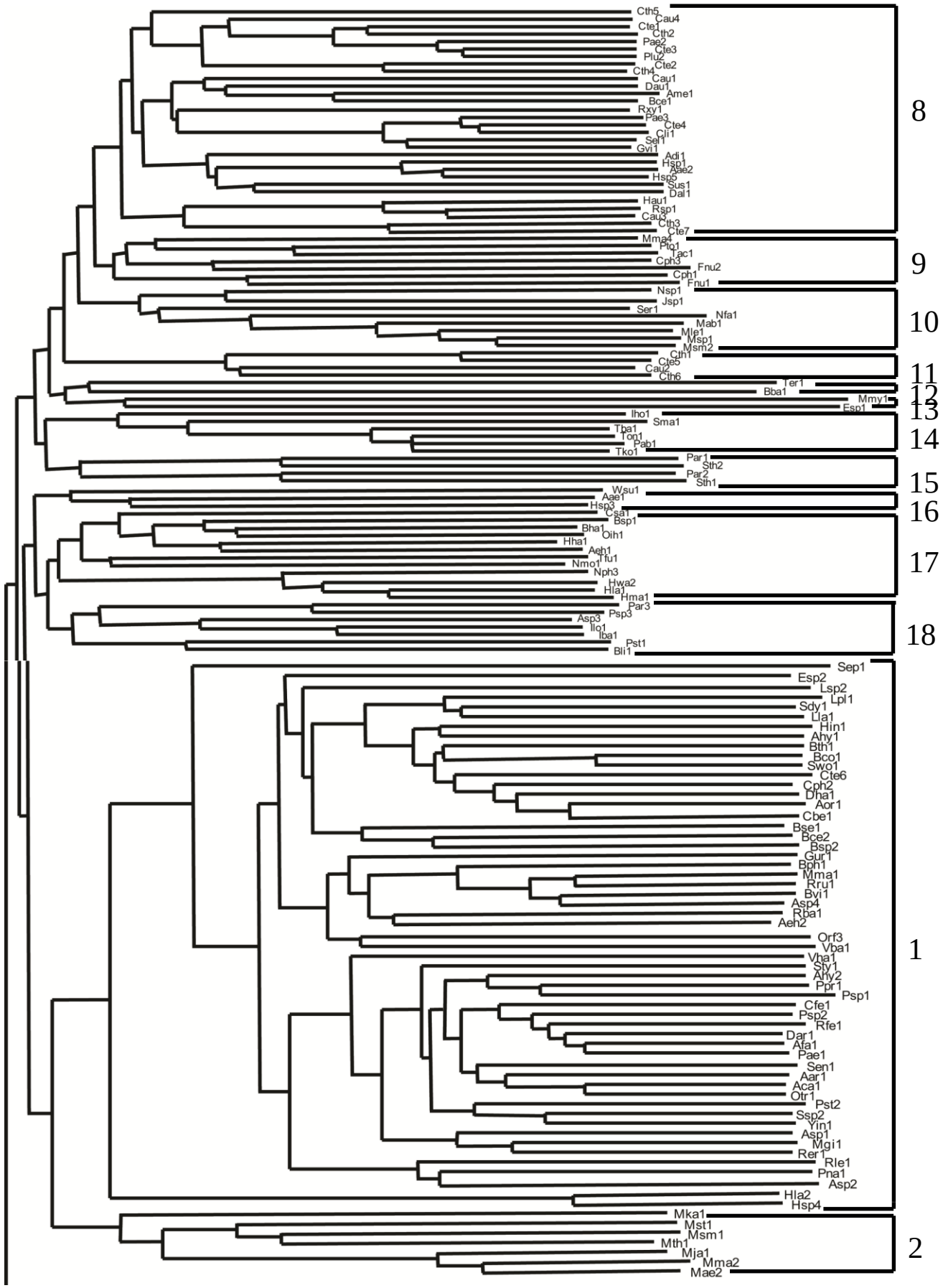
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Cth2
Pae2
Cte3
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Rxy1
Pae3
Cte4
Cli1
Sel1
Gvi1
Adi1
Hsp1
Aae2
Hsp5
Sus1
Dal1
Hau1
Rsp1
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Cth3
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Jsp1
Ser1
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Mab1
Mle1
Msp1
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Sma1
Tba1
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Tko1
Par1
Sth2
Par2
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Pst1
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Sep1
Esp2
Lsp2
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Lla1
Hin1
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Bco1
Swo1
Cte6
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Dha1
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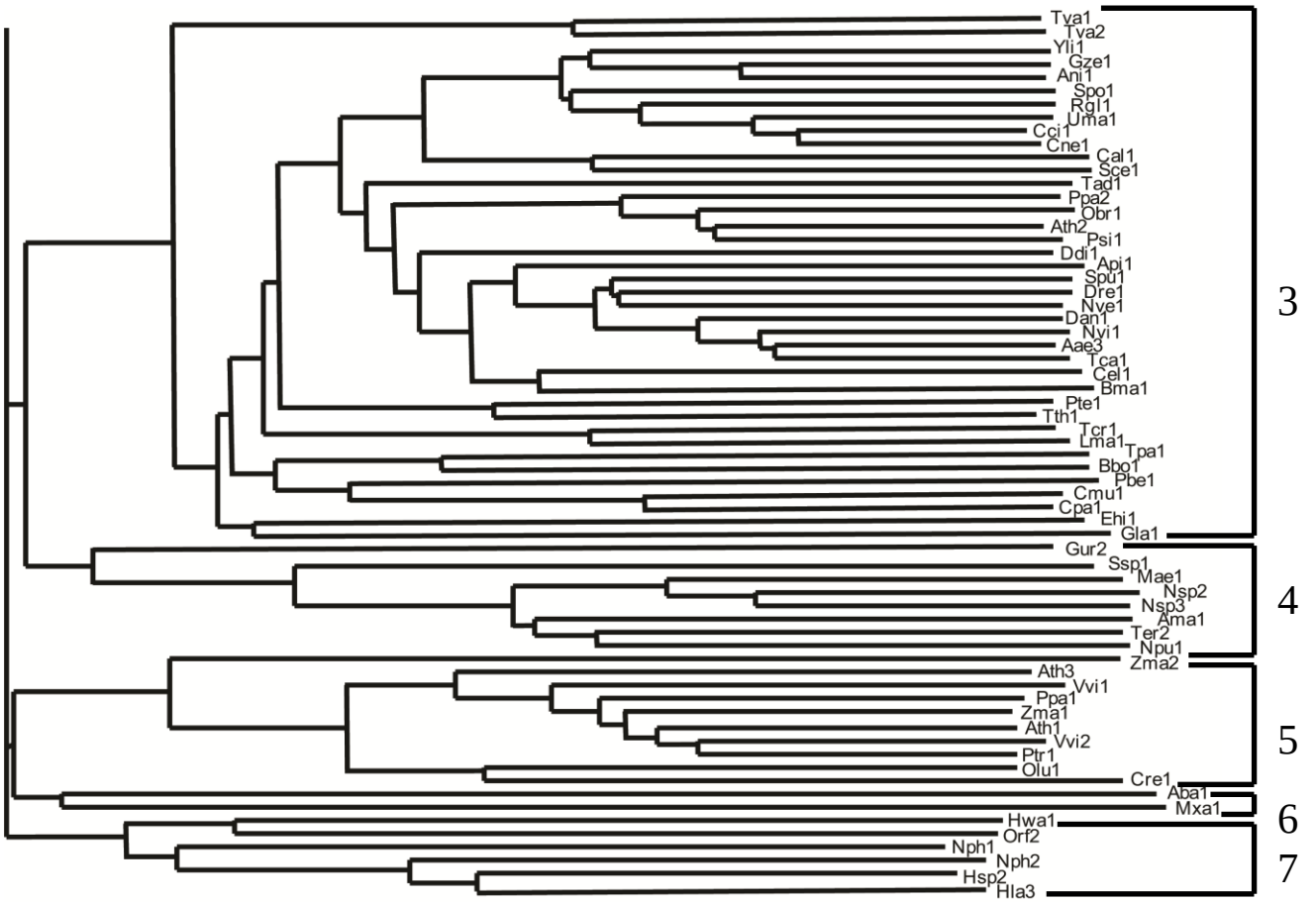
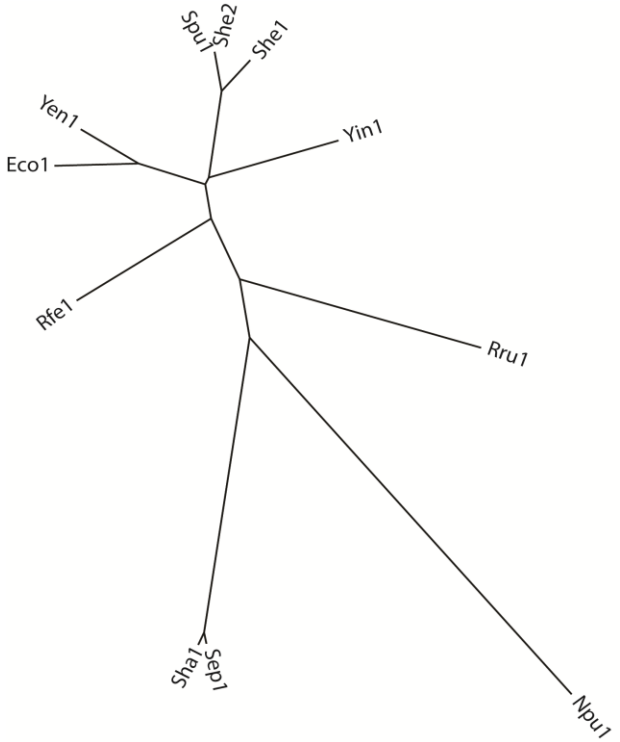
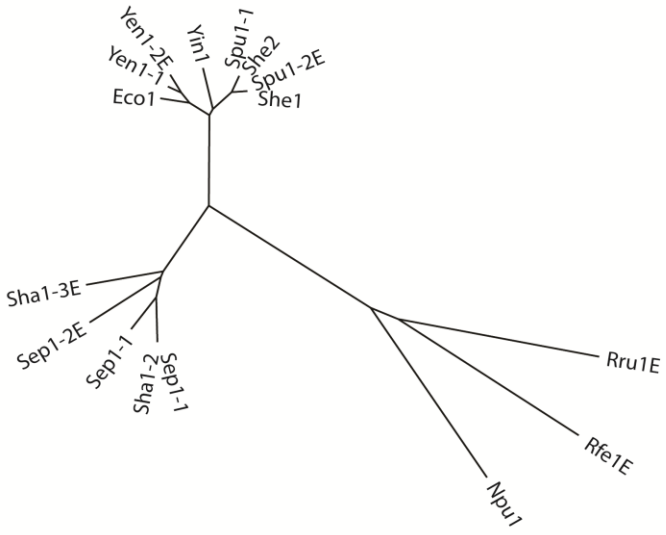



Figure S1: Dendogram of the phylogenetic tree shown in Fig. 1. Proteins are arranged according to cluster and order within the cluster as seen in Fig. 1.

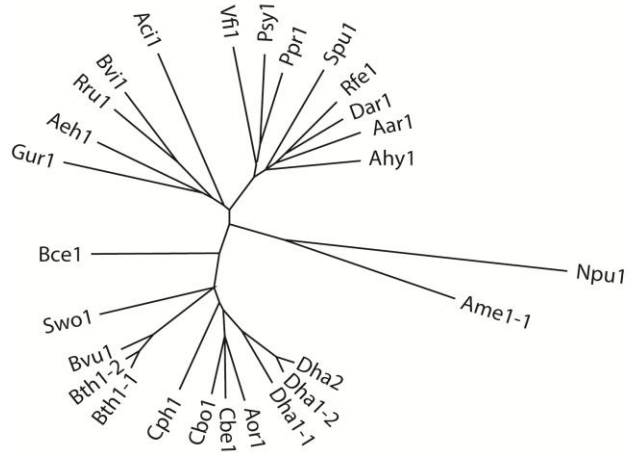
(A) ArsA



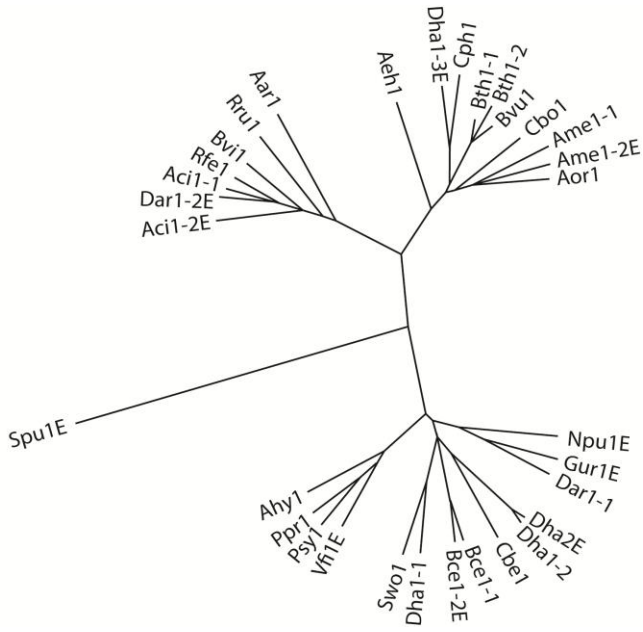

(B) ArsB




(C) ArsA




(D) Acr3



(E) ArsA (F) ArsP

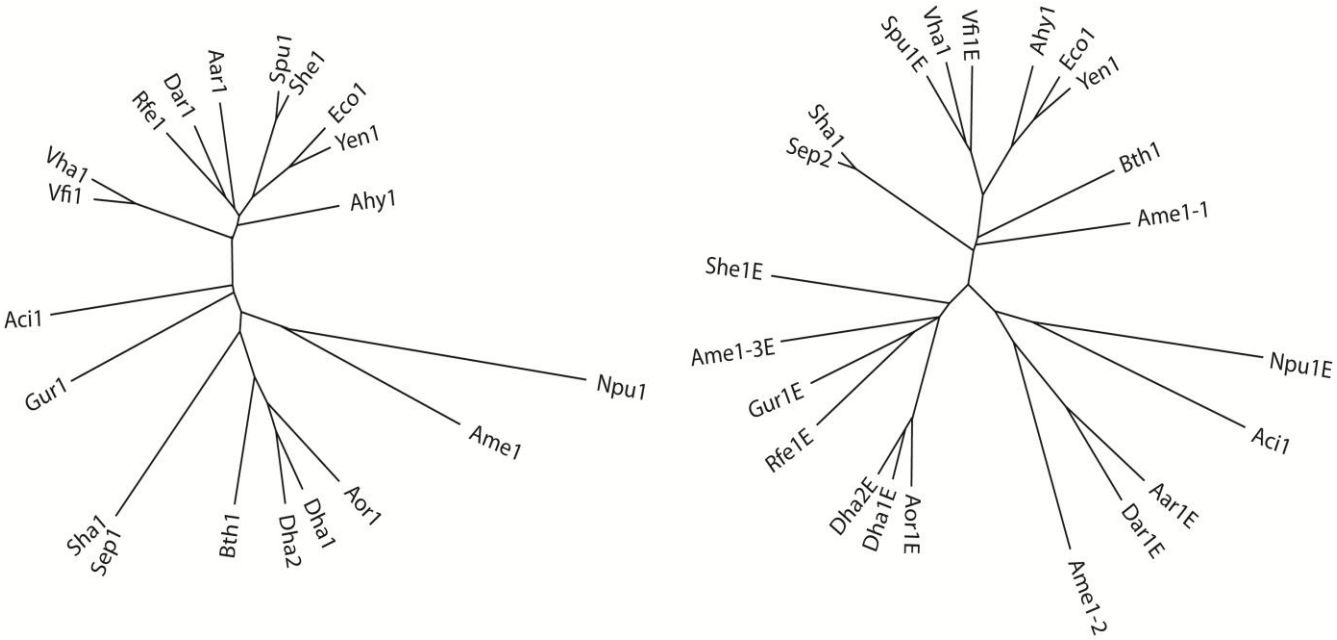



Figure S2: Phylogenetic trees showing the coevolution of (A) ArsA and (B) ArsB homologues, (C) ArsA and (D) Acr3 homologues, and (E) ArsA and (F) ArsP homologues, encoded within the same genomes. For these trees, we use the following system of nomenclature to better designate the added protein pairs not found within the same operons. The first digit indicates separate organisms with the same three letter code (ex: Aaa1, Aaa2), the second digit indicates paralogues, if present (ex: Aaa1-1, Aaa1-2). If the transporter is located within the same genome, but not the same operon as the *arsA*, the letter E, standing for elsewhere, follows the name (ex: Aaa1-3E).

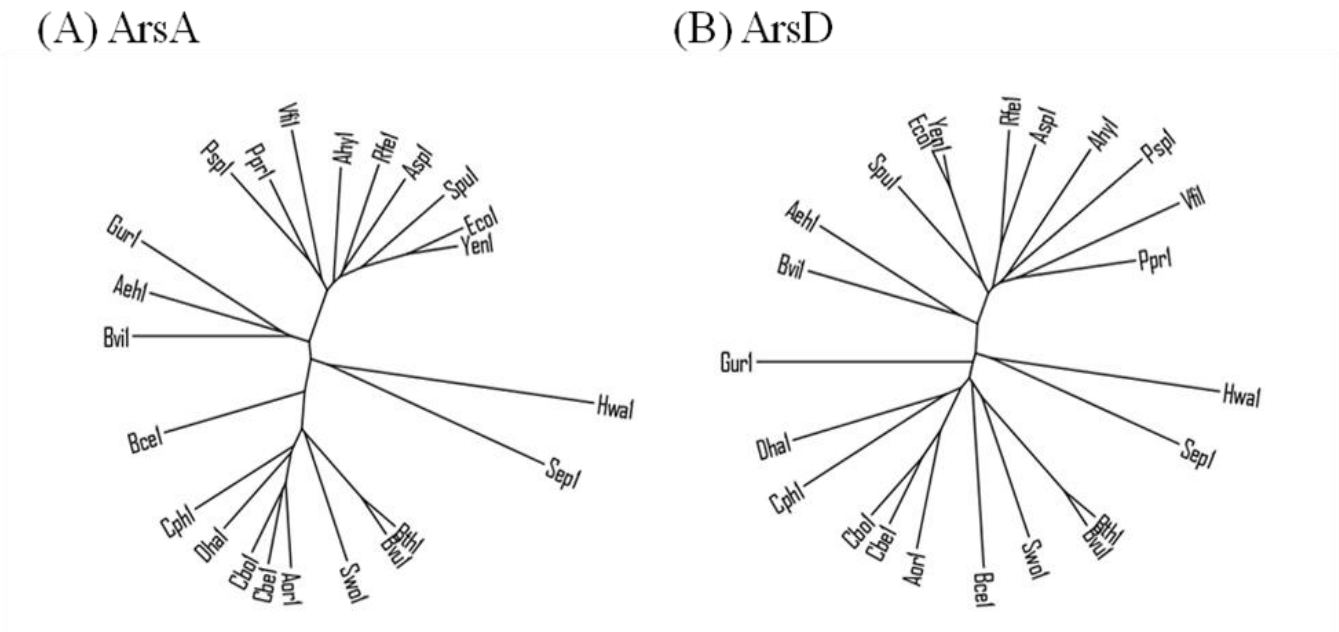



Figure S3: Phylogenetic trees showing the coevolution of (A) ArsA and (B) ArsD homologues encoded within the same operon. The methodology was as described in Fig. 1.