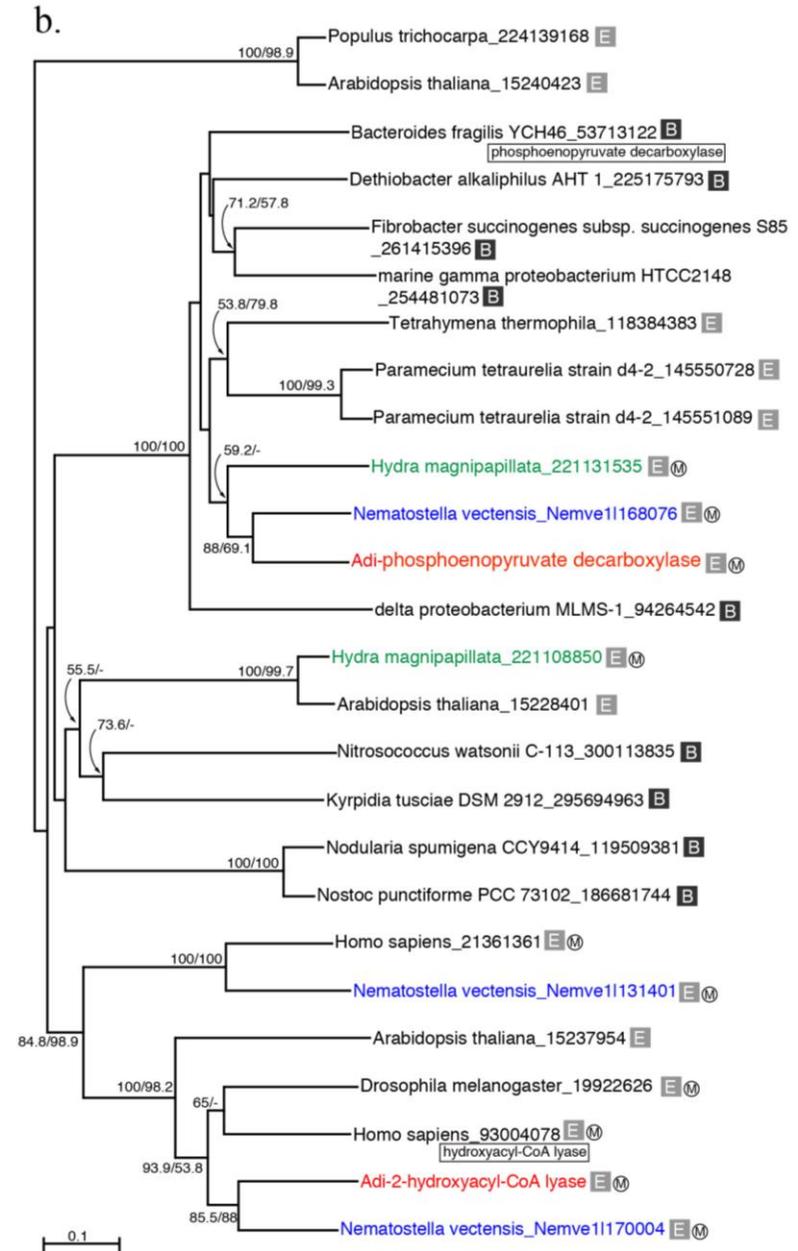
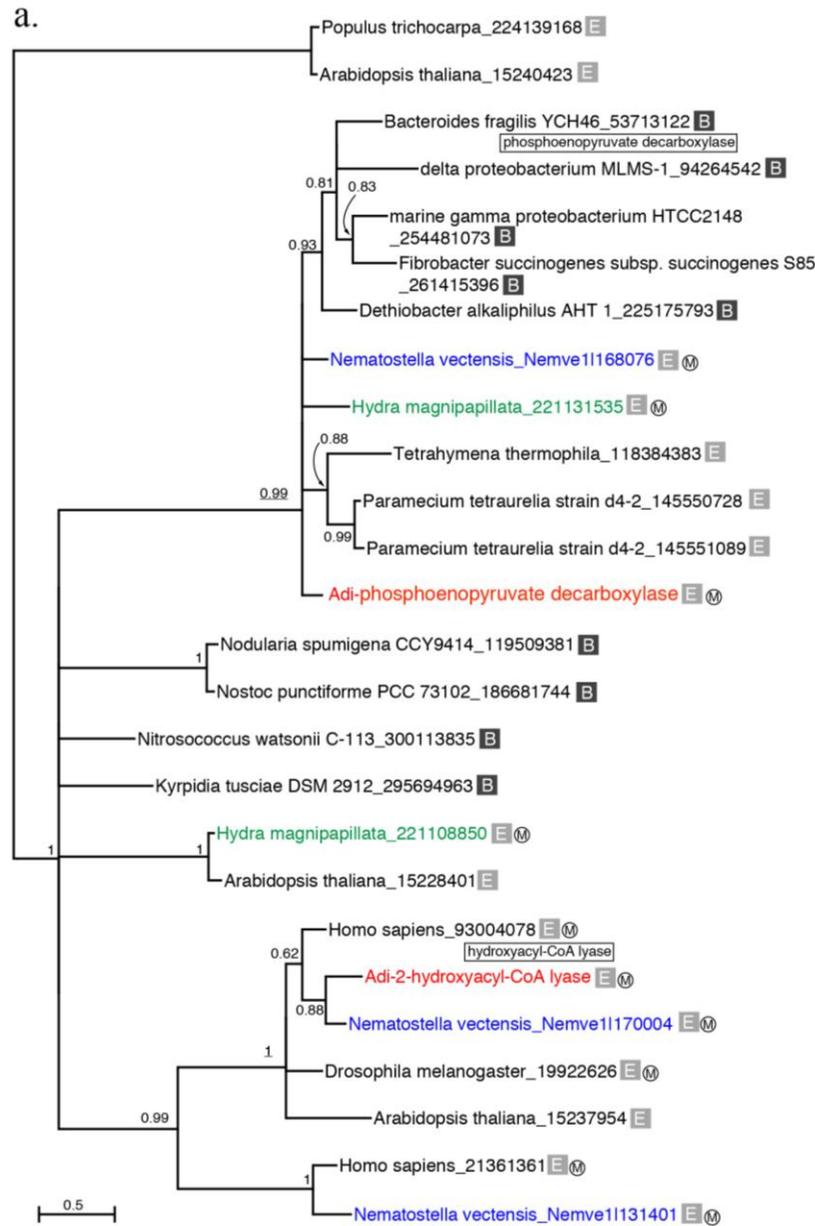


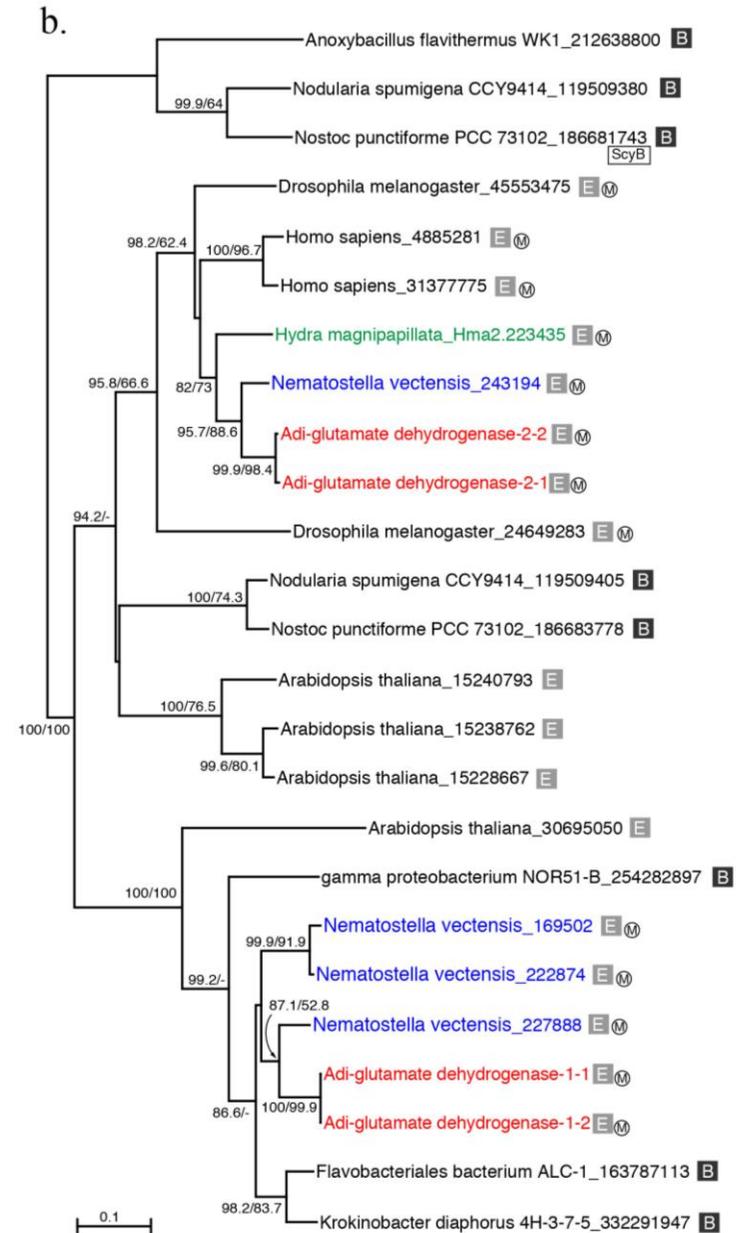
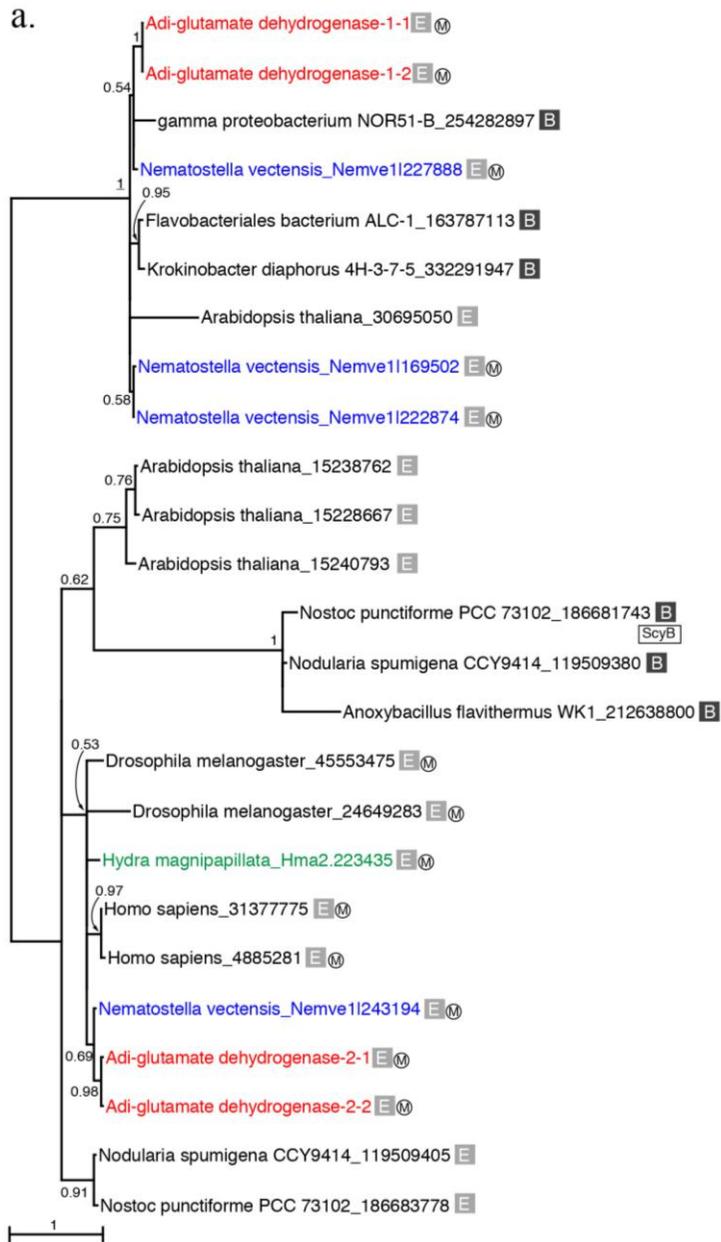
## Supplementary Information

**Figure S1. (a)** Molecular phylogenetic tree of thiamine pyrophosphate (TPP) domain-containing enzymes, including *scyA*, phosphonolpyruvate decarboxylase, and 2-hydroxyacyl-CoA lyase, constructed using the Bayesian inference (BI) method. 2-hydroxyacyl-CoA lyase of *A. digitifera* forms a clade with the *N. vectensis* homolog. No thiamine pyrophosphate (TPP) domain-containing genes in Anthozoa form a clade with *scyA* (GI: 186681744) of cyanobacteria. Numbers at the nodes indicate a BI posterior probability greater than 0.5. The scale bar represents 0.5 expected substitutions per site in the aligned region. Species names are followed by NCBI gene ID numbers. For *N. vectensis*, protein ID numbers from the JGI genome browser are shown. The highlighted B indicates bacterial proteins; E indicates eukaryotic proteins; and a circled M denotes metazoan proteins. Putative proteins of *A. digitifera* are shown in red, *Nematostella* proteins in blue, and *Hydra* in green.

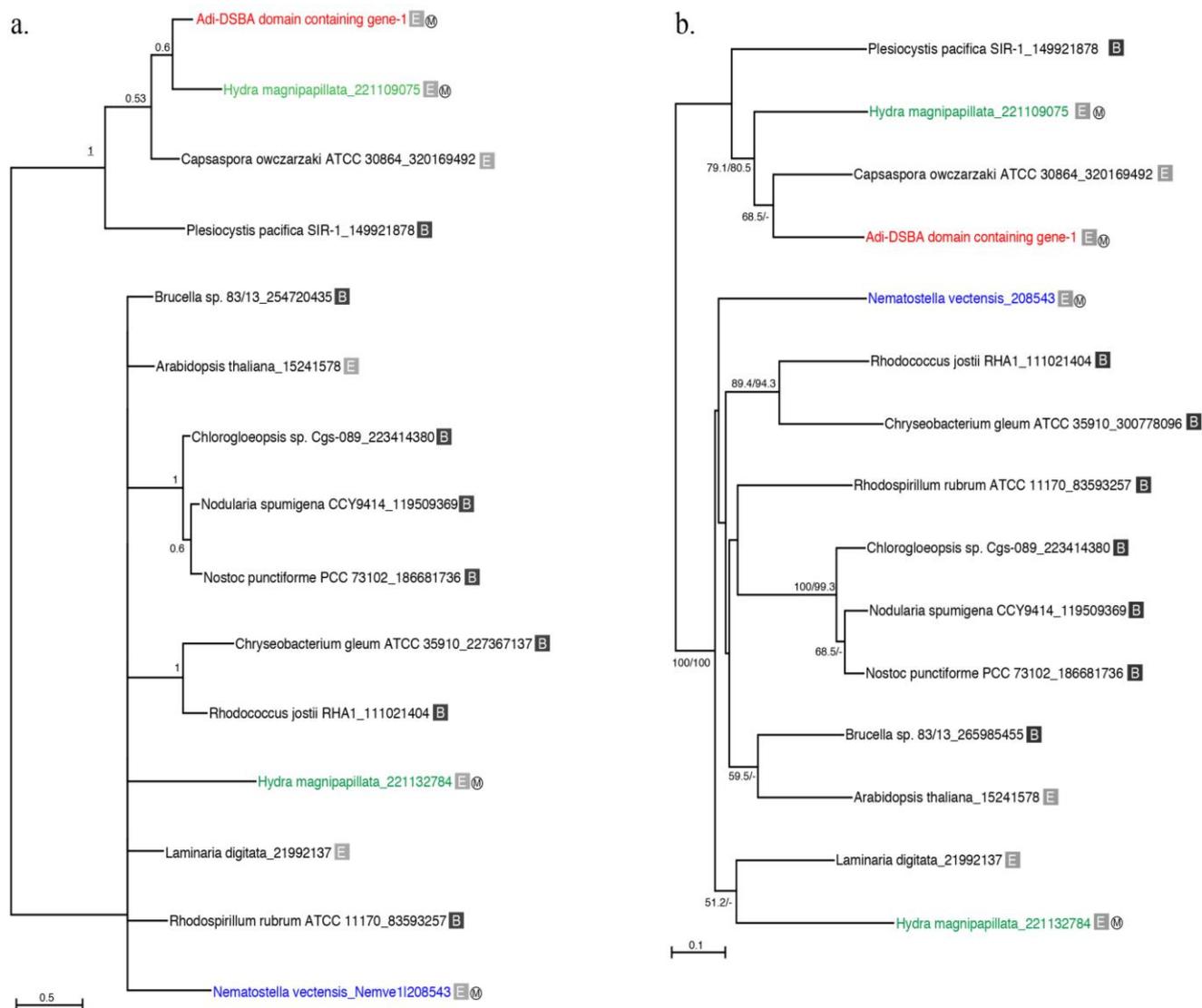
**(b)** Molecular phylogenetic tree of thiamine pyrophosphate (TPP) domain-containing enzymes, including *scyA* and 2-hydroxyacyl-CoA lyase, constructed using the neighbor-joining (NJ) method. Both enzymes of *A. digitifera* form a clade with *N. vectensis* homologs. Numbers at the nodes indicate bootstrap supports greater than 50% (NJ, left; ML, right). The scale bar represents 0.1 expected substitutions per site in the aligned region. Species names are followed by NCBI gene ID numbers. For *N. vectensis*, protein ID numbers from the JGI genome browser are shown. The highlighted B indicates bacterial proteins; E indicates eukaryotic proteins; and a circled M denotes metazoan proteins. Putative proteins of *A. digitifera* are shown in red, *Nematostella* proteins in blue and *Hydra* in green.



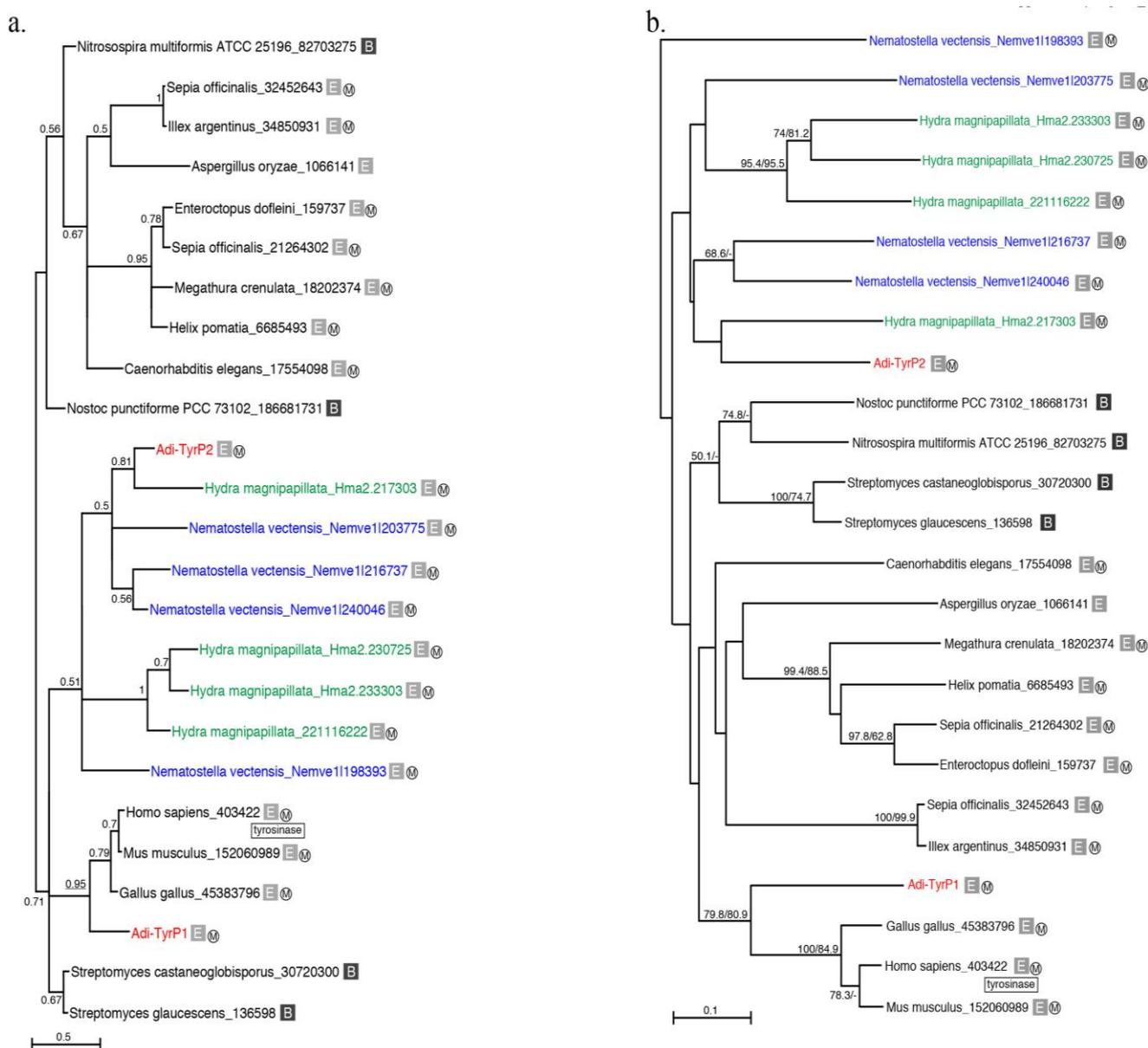
**Figure S2.** (a) BI molecular phylogenetic tree of homologs of glutamate dehydrogenase (GDH), including scyB. The *A. digitifera* genome contains four candidates; pairwise (1-1 and 1-2, and 2-1 and 2-2), these form clades with *Nematostella* and/or *Hydra*. No *A. digitifera* ortholog to cyanobacterium scyB (GI: 186681743) was found. Interestingly, two of the anthozoan glutamate dehydrogenases, including Adi-gdh-1-1 and Adi-gdh-1-2, form a clade with bacterial GDH. Details for gene ID, number, and scale bars are shown in Figure S1a. The highlighted B indicates bacterial proteins; E indicates eukaryotic proteins; and a circled M denotes metazoan proteins. Putative proteins in *A. digitifera* are shown in red, *Nematostella* proteins in blue, and *Hydra* in green. (b) NJ molecular phylogenetic tree of homologs of glutamate dehydrogenase (GDH), including scyB. The *A. digitifera* genome contains four candidates; pairwise (1-1 and 1-2, and 2-1 and 2-2), these form clades with *Nematostella* and *Hydra*. No *A. digitifera* ortholog to cyanobacterium scyB (GI: 186681743) was found. Interestingly, five of the anthozoan glutamate dehydrogenases, including Adi-gdh-1-1 and Adi-gdh-1-2, form a clade with bacterial GDH. The details for gene ID, number, and scale bars are shown in Figure S1b.



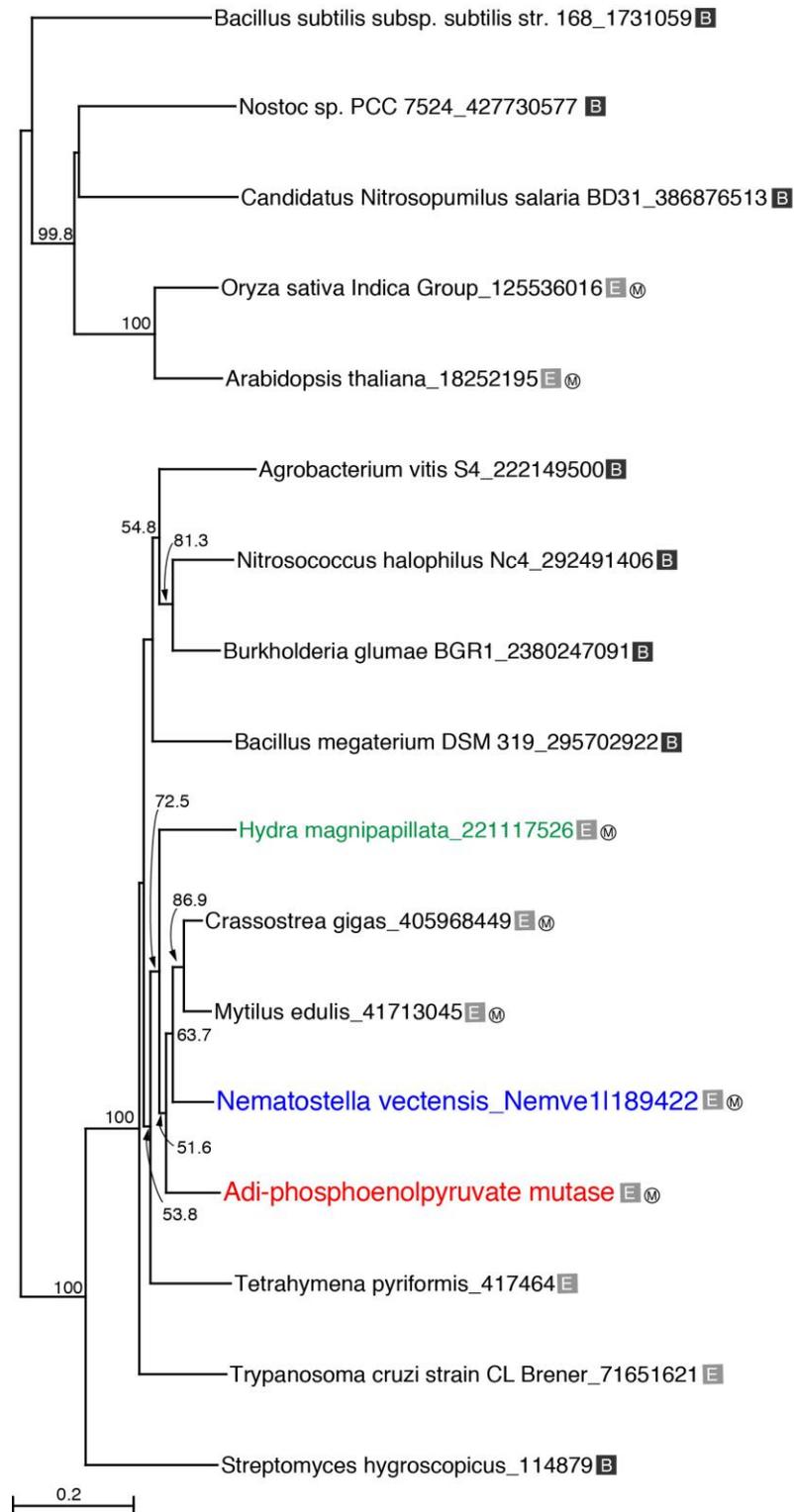
**Figure S3.** (a) BI molecular phylogeny of putative proteins from DSBA domain-containing genes. No *A. digitifera* ortholog to cyanobacterium DsbA (GI: 186681736) was found, although the *Nematostella* protein is more similar to cyanobacterium DsbA. Gene IDs, numbers, and scale bars are as in Figure S1a. The highlighted B indicates bacterial proteins; E indicates eukaryotic proteins; and a circled M denotes metazoan proteins. Enzymes of *A. digitifera* are shown in red, *Nematostella* proteins in blue, and *Hydra* in green. (b) NJ molecular phylogeny of putative proteins from DSBA domain-containing genes. No *A. digitifera* ortholog to cyanobacterium DsbA (GI: 186681736) was found; although the *Nematostella* protein is more similar to cyanobacterium DsbA. Gene IDs, numbers, and scale bars are as in Figure S1b.



**Figure S4.** (a) Molecular phylogeny of TyrP, constructed by the BI method. The tree indicates the presence of two candidate genes for *tyrP* in the *Acropora* genome, although the *Nematostella* and *Hydra* genomes contain more candidate genes. *Acropora* TyrP1 is at a basal position among vertebrate tyrosinases. Details for gene ID, number, and scale bar are shown in Figure S1a. The highlighted B indicates bacterial proteins; E indicates eukaryotic proteins; and a circled M denotes metazoan proteins. Enzymes of *A. digitifera* are shown in red, *Nematostella* proteins in blue, and *Hydra* in green. (b) Molecular phylogeny of TyrP, constructed by the NJ method. The tree indicates the presence of two candidate genes for *tyrP* in the coral genome, although the *Nematostella* and *Hydra* genomes contain more candidate genes. Adi-TyrP1 is at a basal position among vertebrate tyrosinases. Details for gene ID, number, and scale bar are shown in Figure S1b.



**Figure S5.** Molecular phylogenetic tree of PEP mutase, constructed by the NJ method. The tree indicates the presence of orthologous genes for *PEP mutase* in the coral genome. Details for gene ID, number, and scale bar are shown in Figure S1b.



**Figure S6.** Molecular phylogenetic tree of Ppyr decarboxylase, constructed by the NJ method. The tree indicates the presence of orthologous genes for *Ppyr decarboxylase* in the coral genome. *Ppyr decarboxylase* orthologs were not found in *Drosophila*, *Homo*, and *Arabidopsis*. Details for gene ID, number, and scale bar are shown in Figure S1b.

