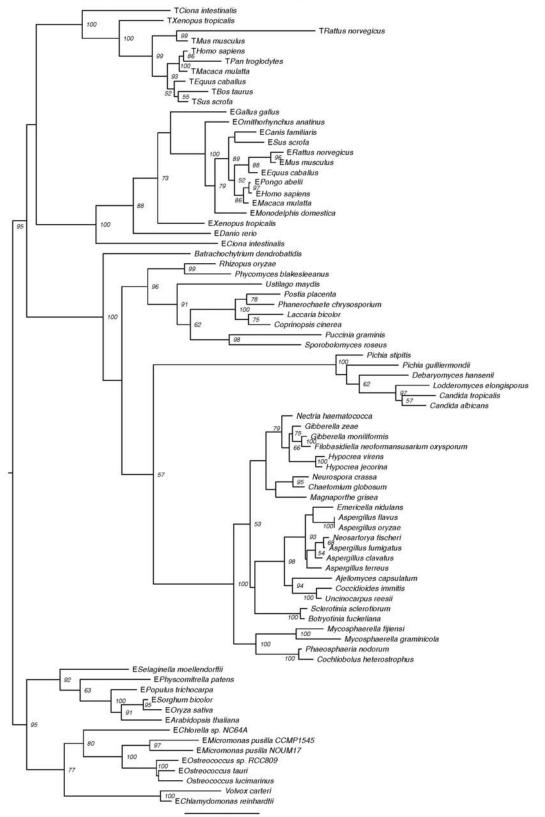
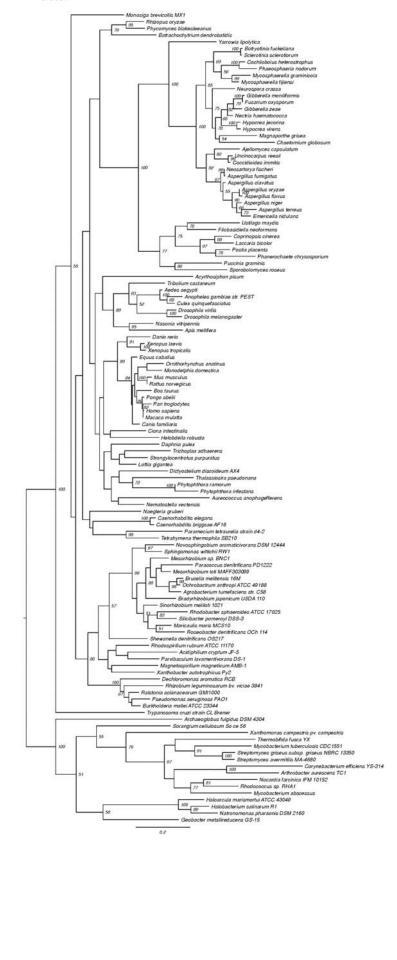
A ACD10, ACD11, and ACD11n

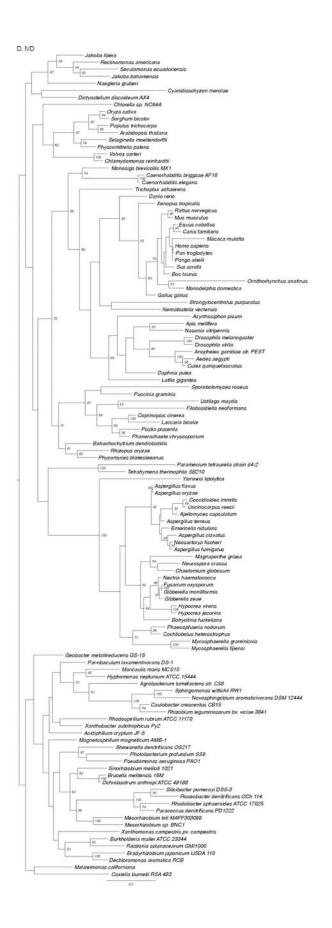




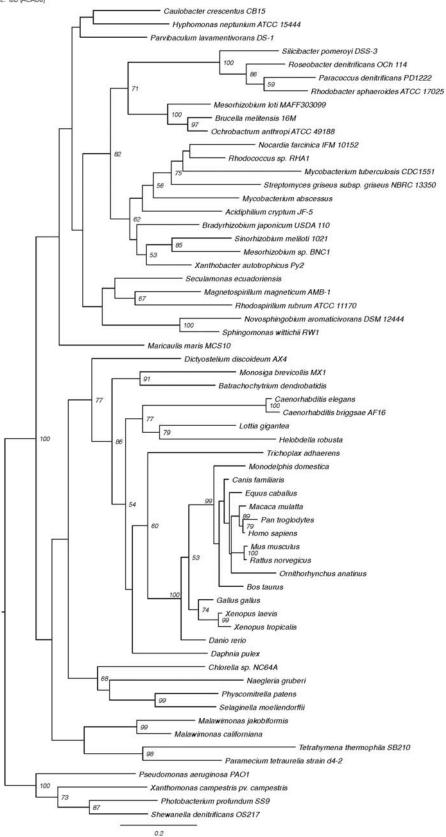
B ACD10, ACD11, and ACD11n in animals, plants, and fungi

C. GCDH

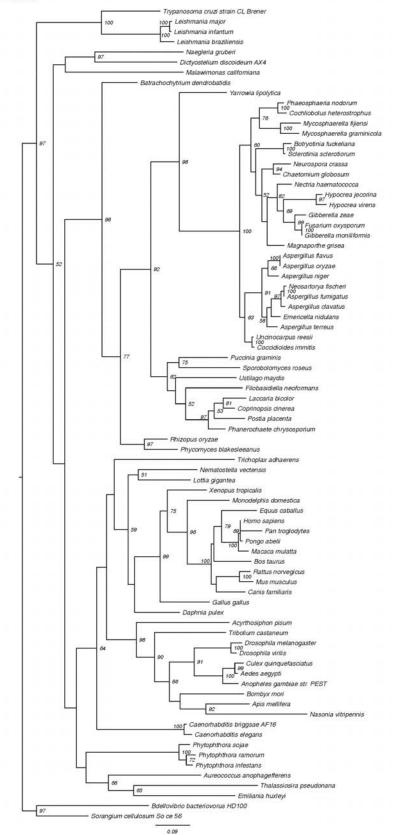




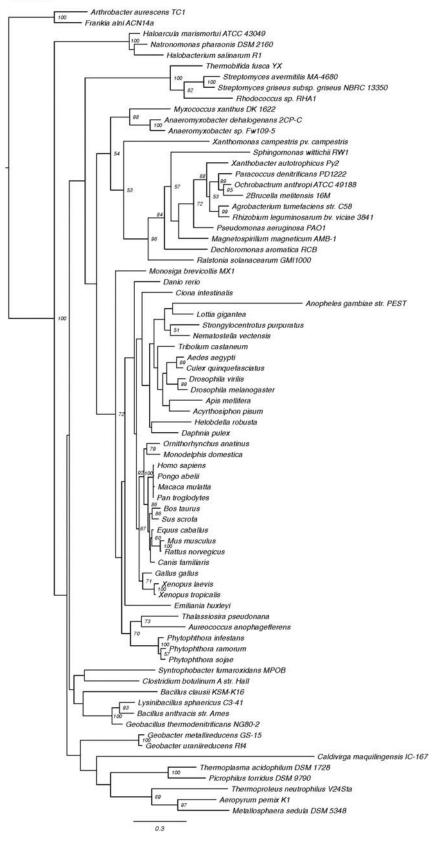


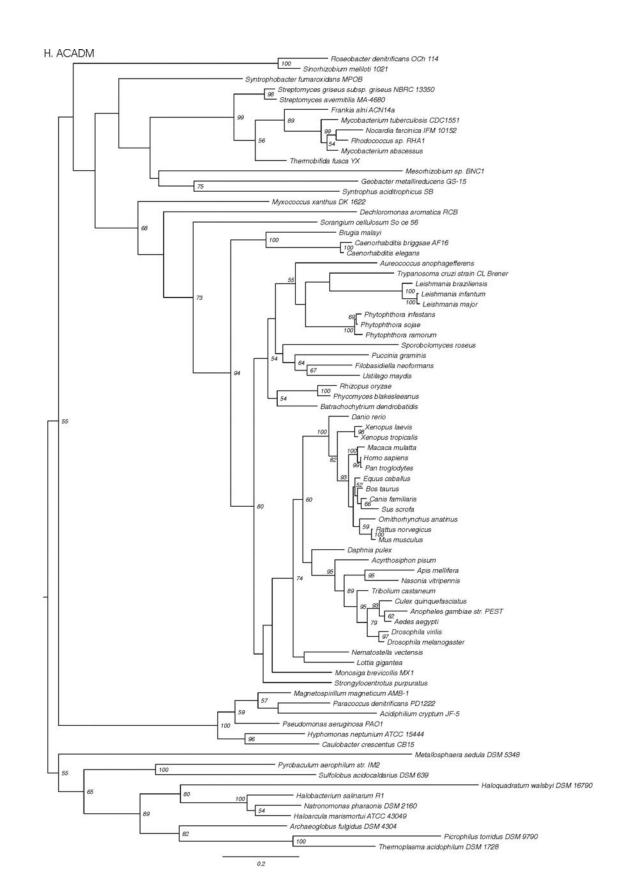


F. ACDSB

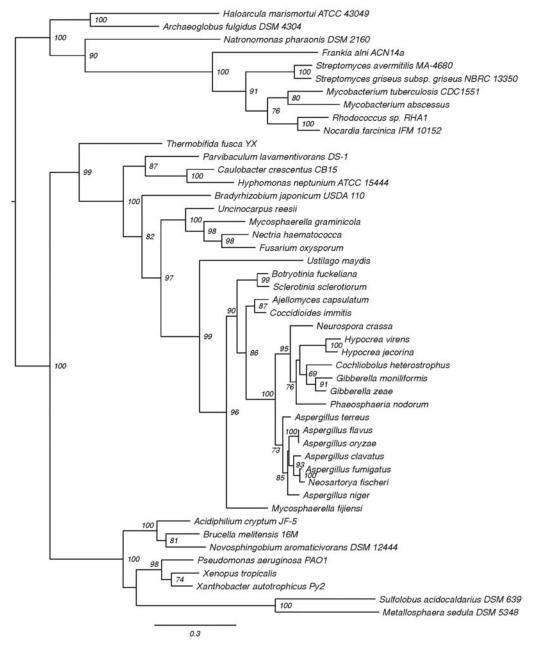


G. ACADS

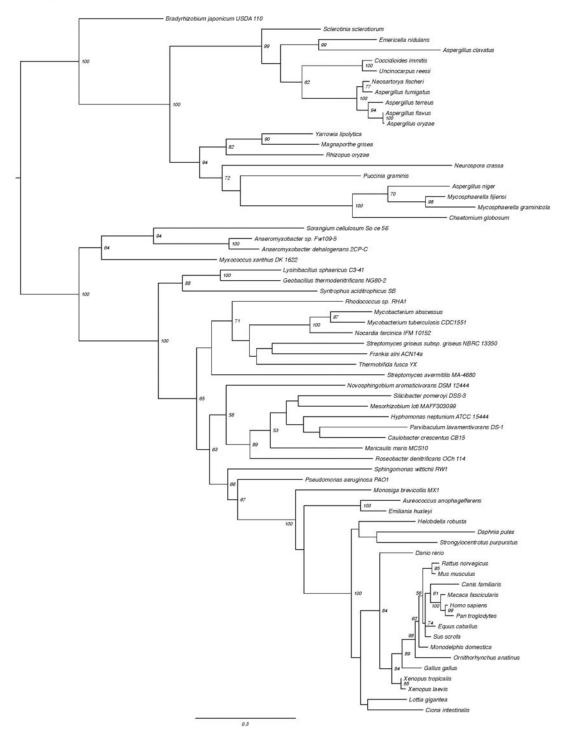




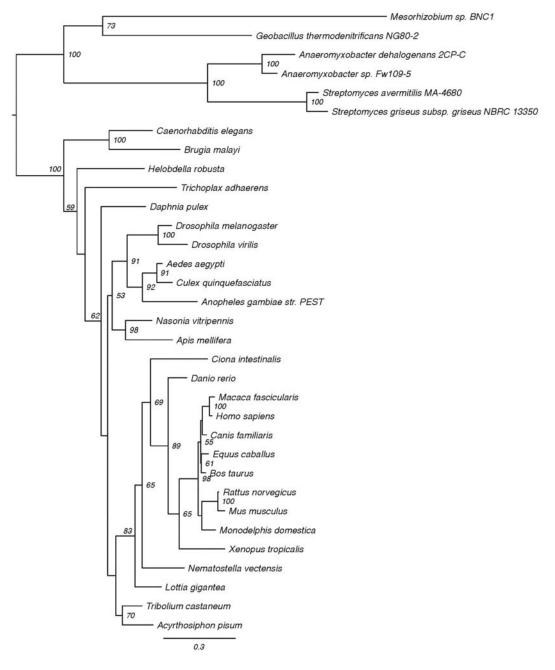
I. fadE12

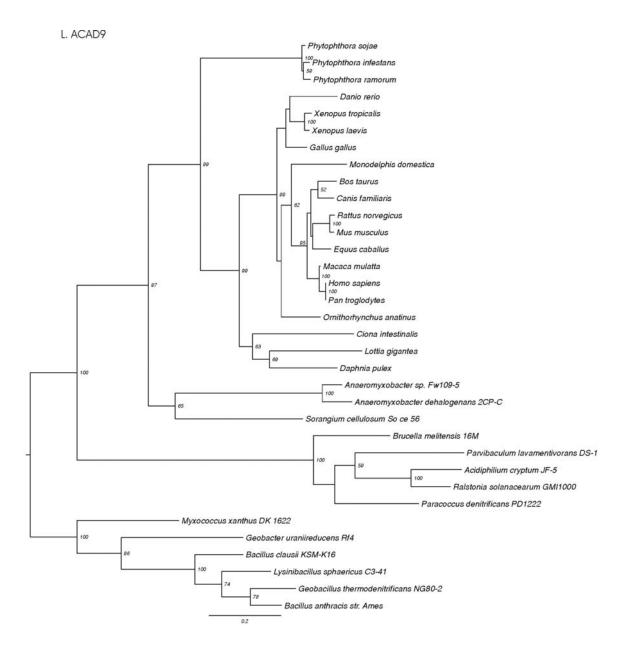


J. ACADL

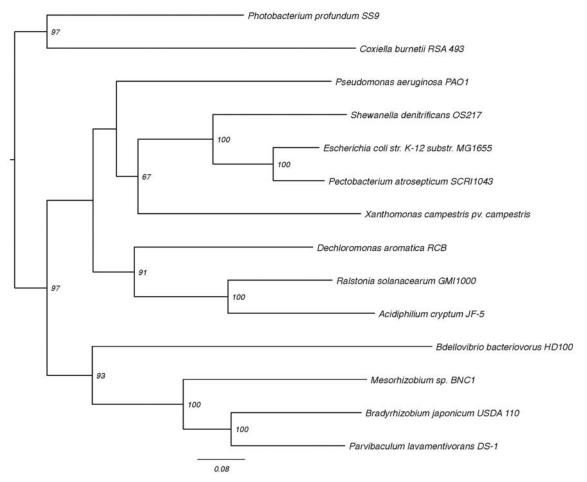


K. ACADV

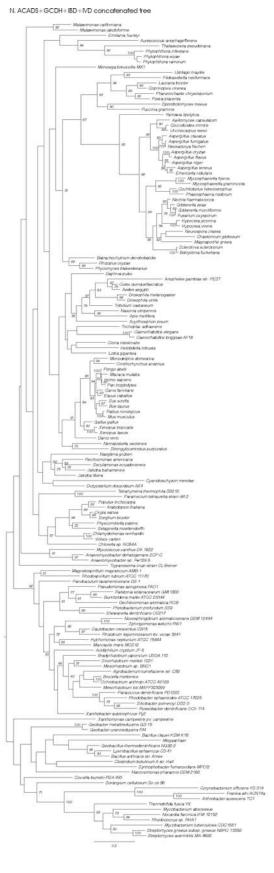




M. fadE



N. ACADS+GCDH+IBD+IVD concatenated tree



O. ACADV+ACADV2

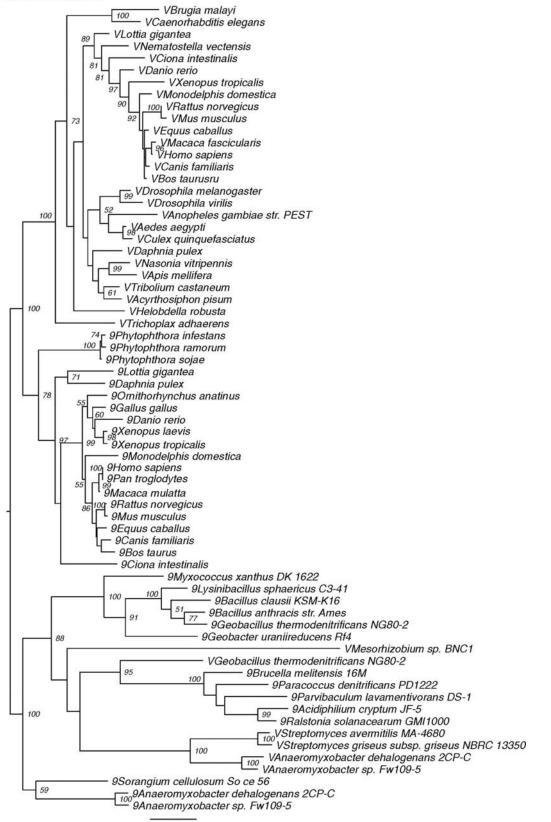


Figure S1. Phylogenetic trees of individual and combined ACAD protein subfamilies. Numbers at branches are bootstraps values. Only values >50 are shown. A: tree built with ACD10, ACD11, and ACD11n protein sequences from animals, plants, and fungi. Members of ACD11 are labeled with E ('Eleven'), and those of ACD10 with T ('Ten') preceding the species name, all others are ACD11n. Genomes of a few species encode more than one ACD11n member. These homologs are distinguished by numbers preceding the corresponding species names. The tree suggests that ACD11 is an ancestral eukaryotic gene from which ACD10 has arisen in the animal lineage by gene duplication and subsequent addition of the hydrolase domain. B: tree built with ACD10, ACD11, and ACD11n sequences from eukaryotes and bacteria. C-M: phylogenetic trees of individual subfamilies. C, GCDH; D, IVD; E, IBD; F, ACDSB; G, ACADS; H, ACADM; I, fadE12; J, ACADL; K, ACADV; L, ACADV2; M, fadE. N: phylogenetic tree built with concatenated sequences of GCDH, IVD, IBD, and ACADS, the four subfamilies considered more ancient. O: tree built with ACADV and ACADV2 sequences. Subfamily members are labeled with V (ACADV) or 9 (ACADV2, synonym ACAD9) preceding the species name. Bacterial ACADV homologs are monophyletic with strong support, but their relationships to one another are incompatible with the species tree. This indicates a single gene transfer from animals to bacteria followed by further horizontal transfer events within bacteria.