

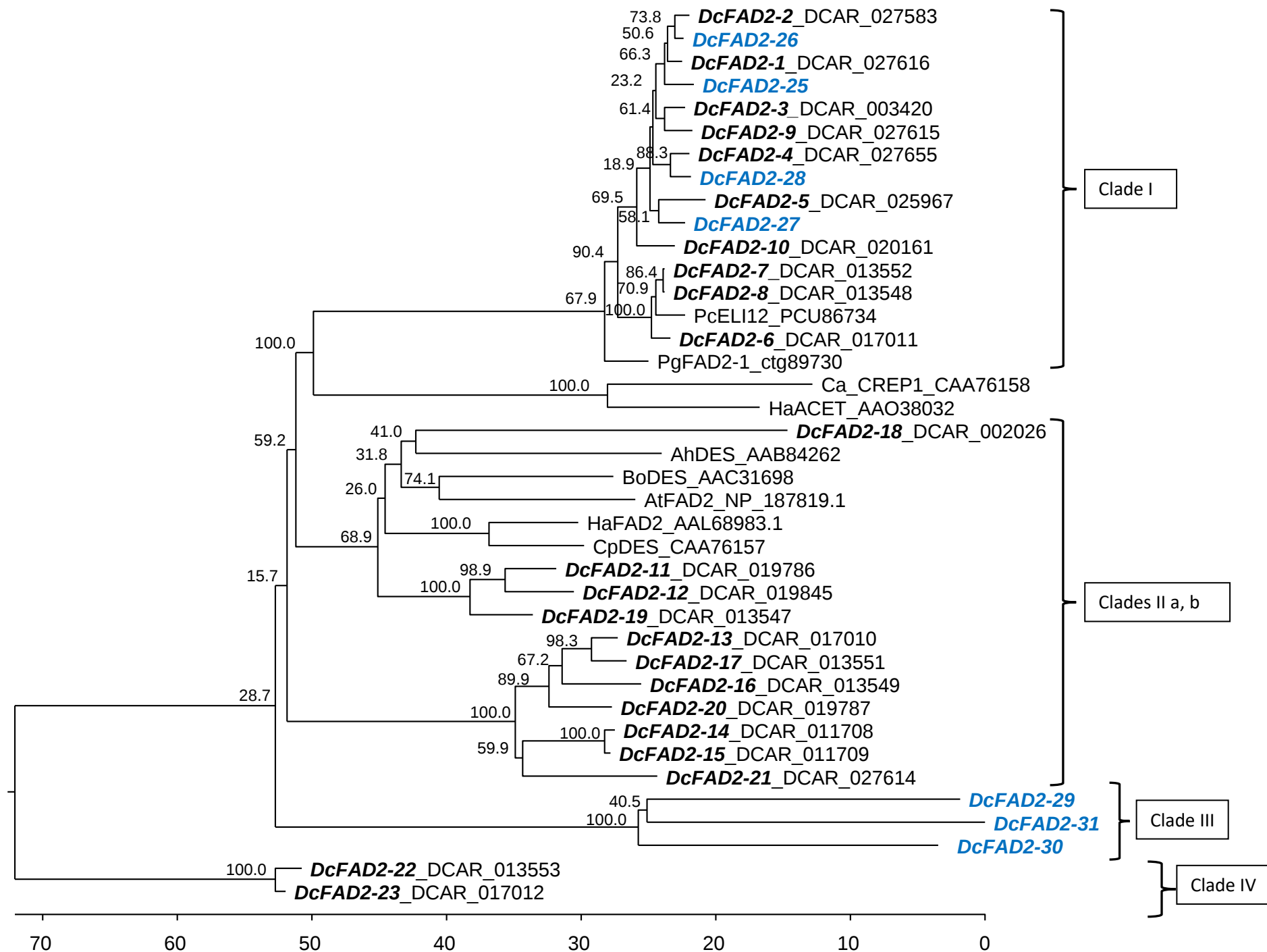


Figure S5 Phylogenetic tree of *Daucus* FAD2 proteins (DCAR numbers, [5]), the published *Petroselinum* ELI12 acetylenase [36], a *Panax ginseng* FAD2 and some other putative acetylenases and desaturases (numbers are NCBI accession numbers; Dc, *Daucus carota*; Pc, *Petroselinum crispum*; Pg, *Panax ginseng*; Ca, *Crepis alpina*; Ha, *Helianthus annuus*; At, *Arabidopsis thaliana*; Bo, *Borago officinalis*; Cp, *Crepis palaestina*; Ah, *Arachis hypogaea*). Newly identified carrot FAD2s are labeled in blue (this study). Multiple sequence alignment was performed by ClustalW using the Lasergene (DNASTAR) software package. A phylogenetic tree was constructed using the Kimura distance formula to calculate distance values and bootstrap analysis (1,000 replicates). Numbers indicate bootstrap replication, and branch length is scaled below the tree indicating the number of amino acid substitutions per 100 amino acids.