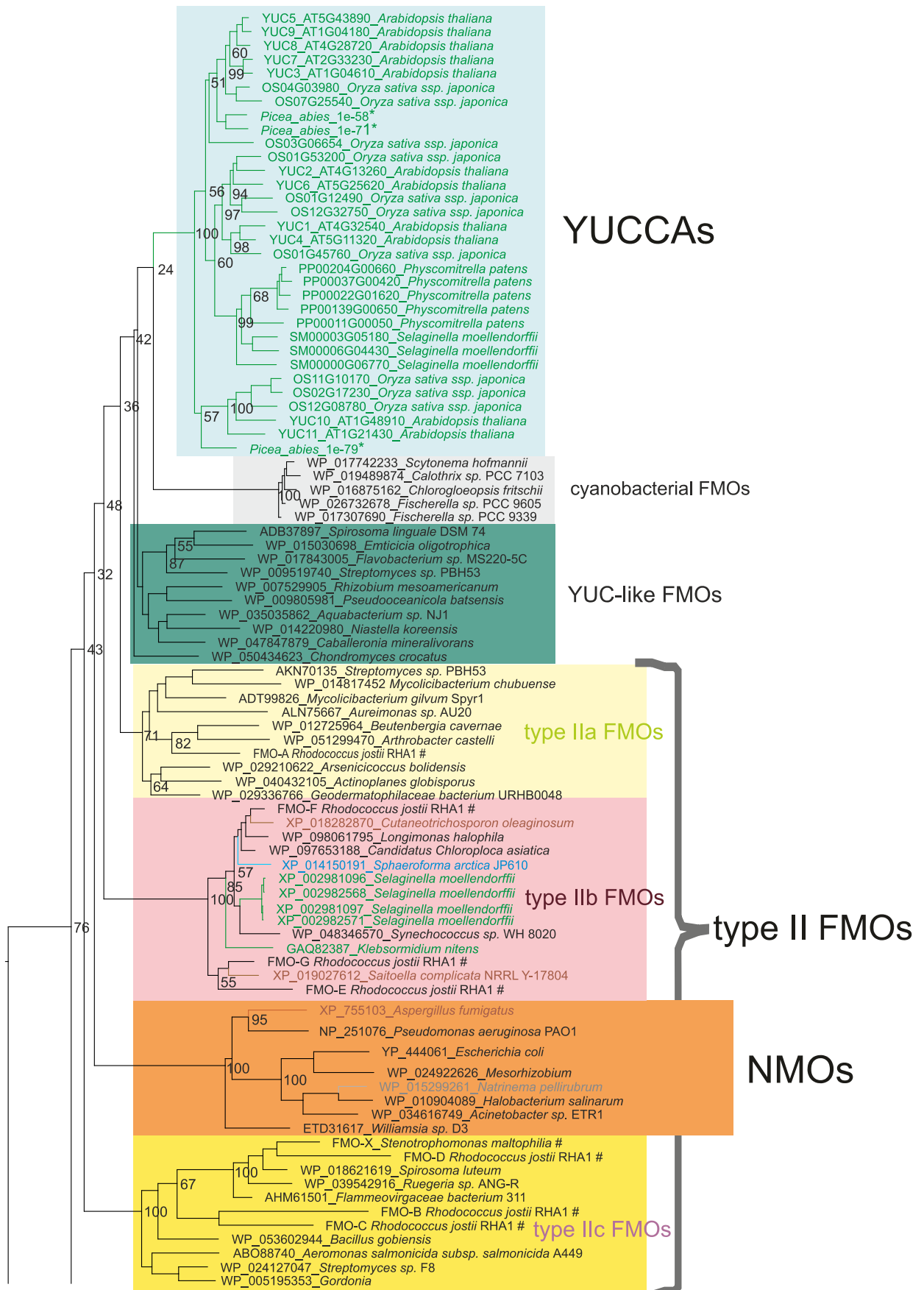
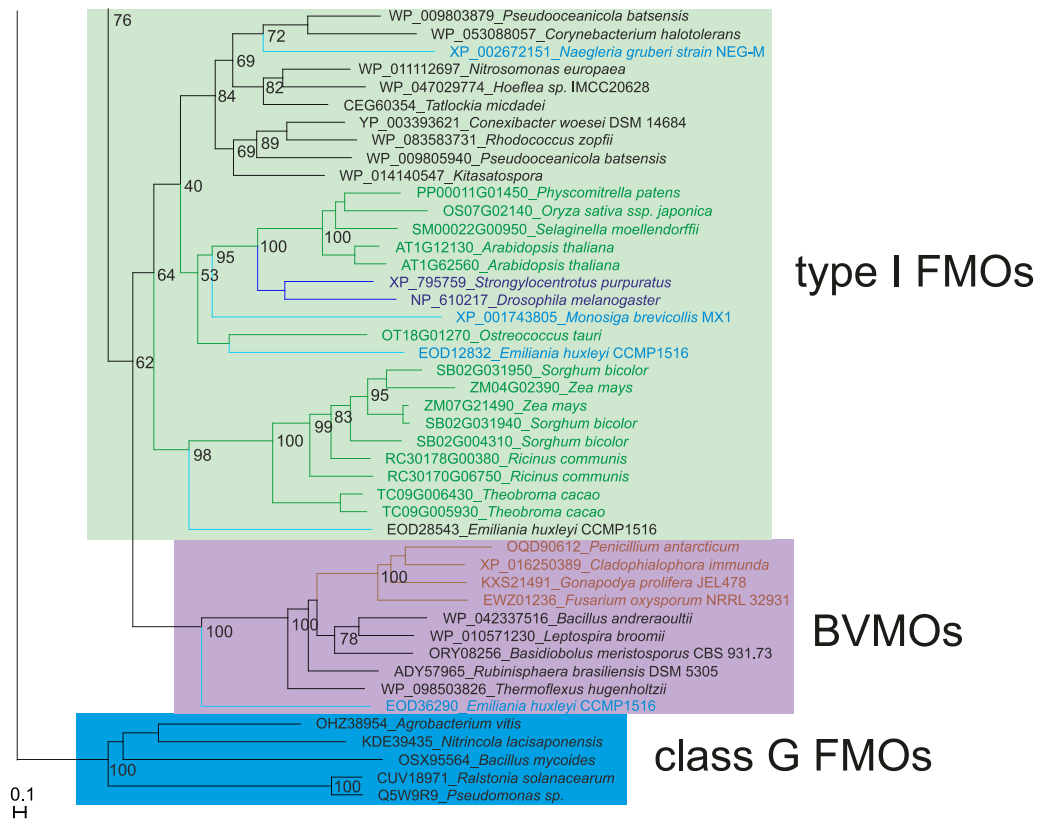


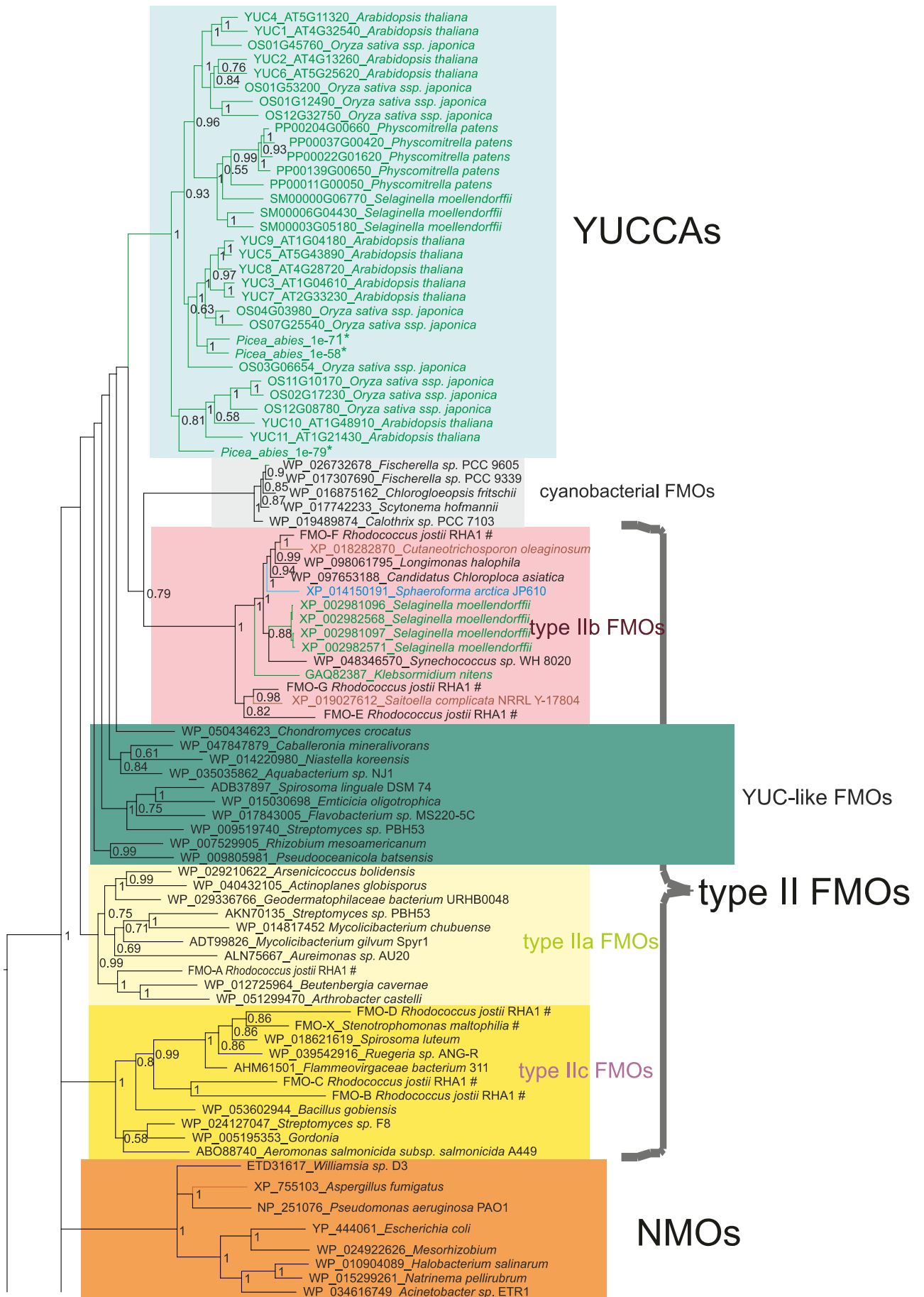
Supplementary materials for Turnaev et al. 2020
Phylogenetic trees for class B flavoprotein monooxygenases.

(a)





(b)



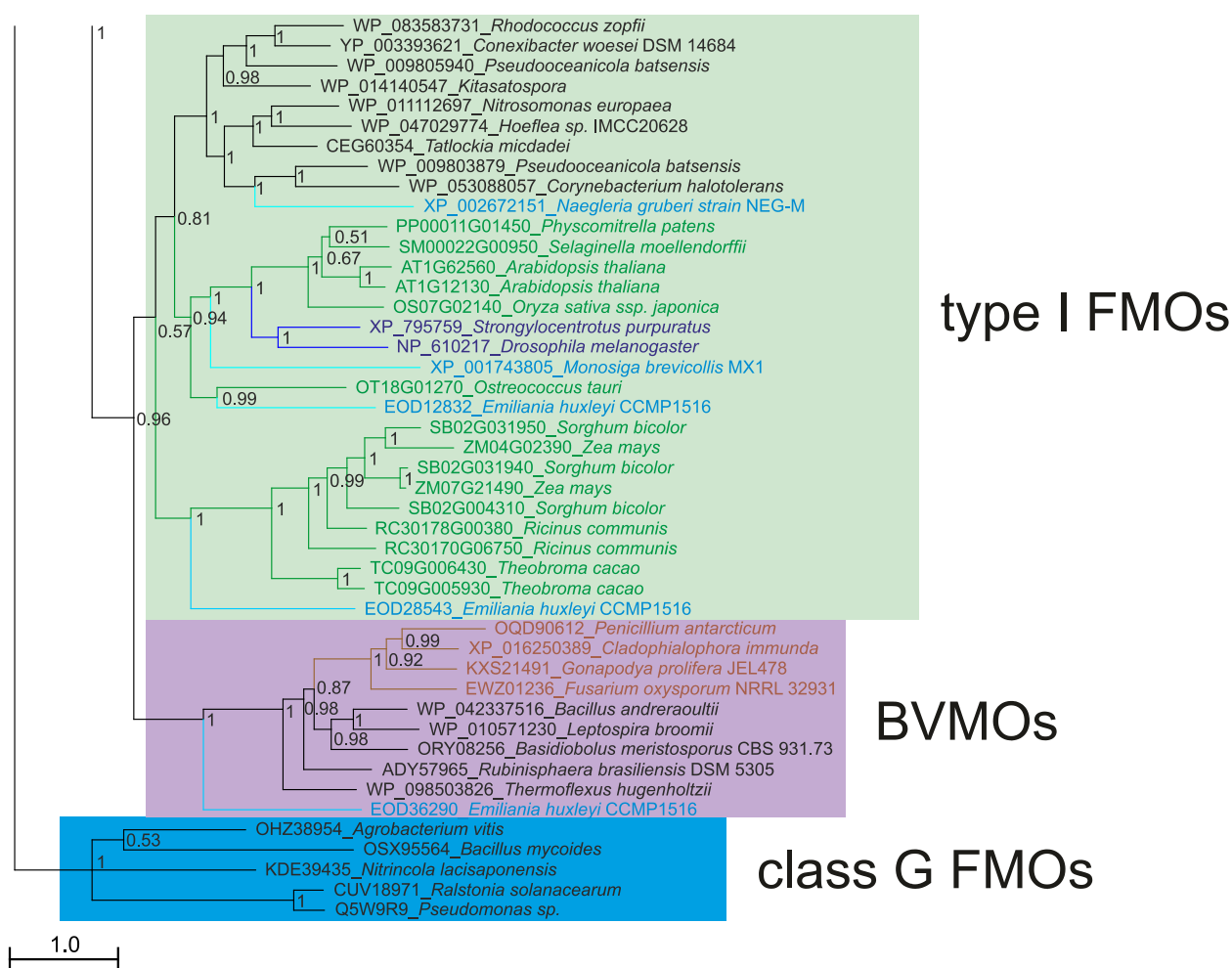
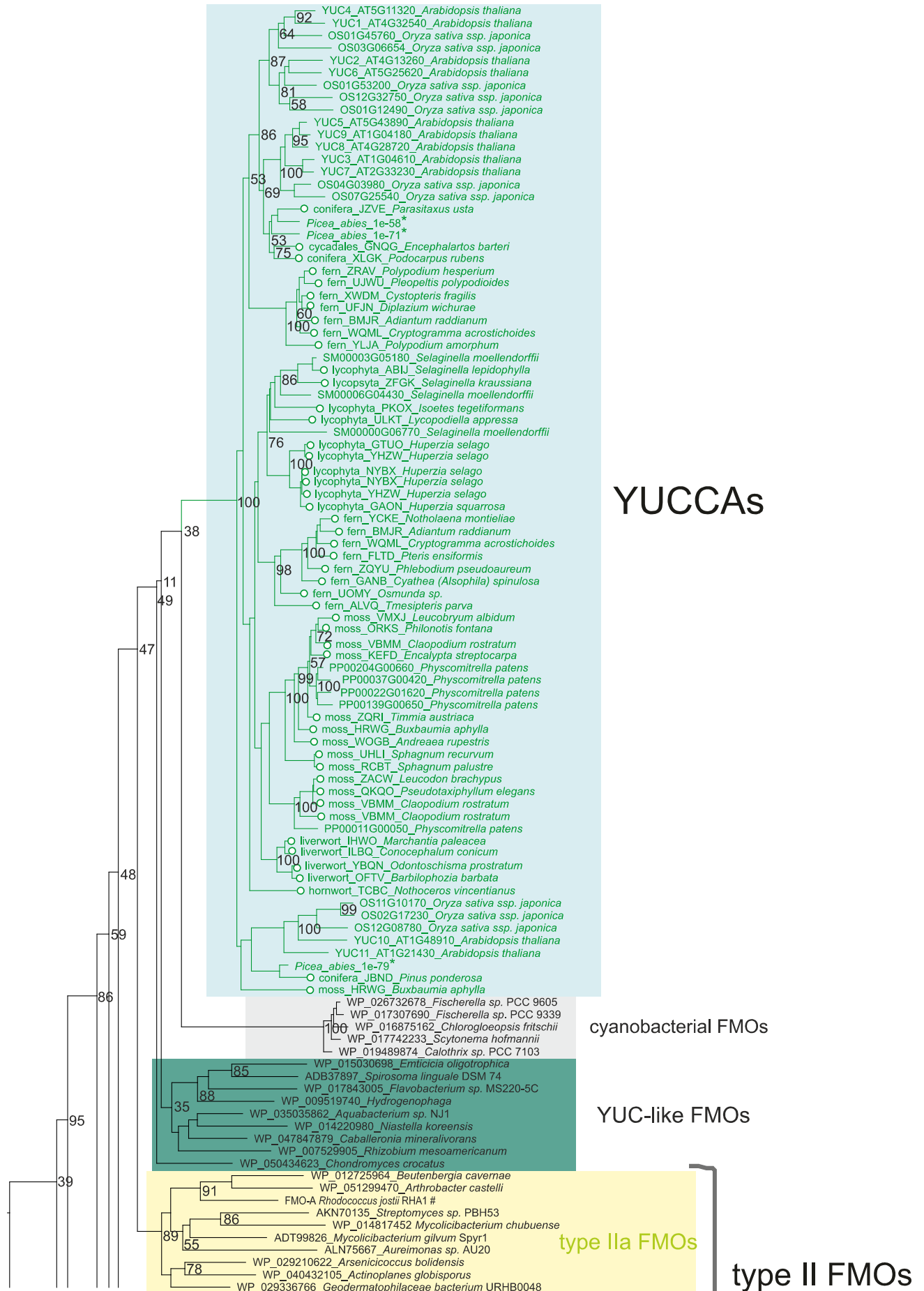
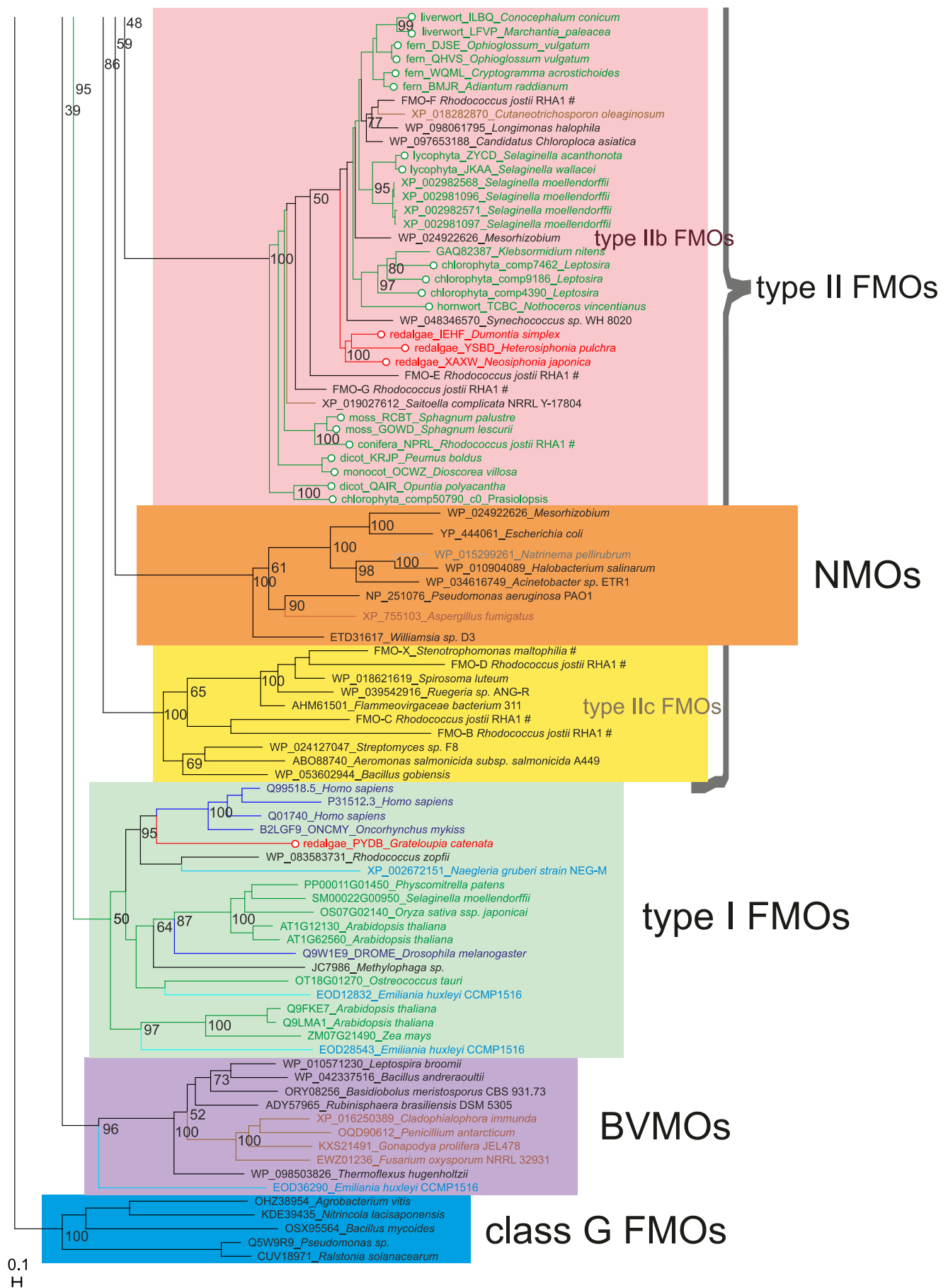


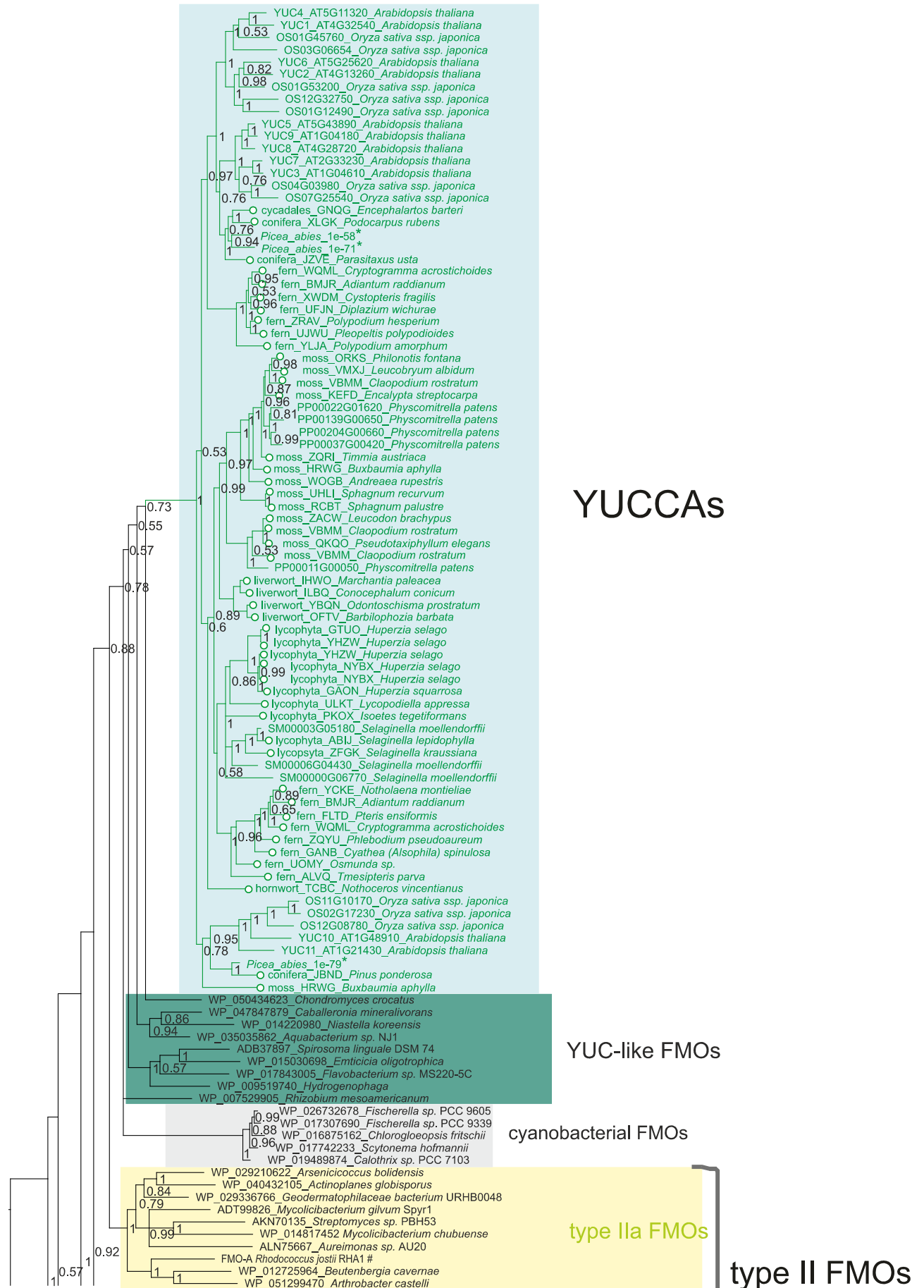
Figure S1. Phylogenetic tree of the class B flavoprotein monooxygenases, class_B_FMO_proteins sample. The branches of green alga and land plant proteins are green; of fungi, brown; of protists, cyan; of animals, blue; of bacteria, black; and of archaeobacteria, gray. The class G flavoprotein monooxygenase proteins is outgroup (dark blue background). # denotes protein sequences from Riebel et al. [ref. 40 of the main text]: FMO-A – FMO-G from *R. jostii* RHA1; FMO-X *S. maltophilia* (B2FLR2). Asterisk (*) denotes proteins identified in the Spruce Genome Project [refs. 67,68 of the main text; Congenie.org]. (a) Phylogeny reconstructed using RAxML. The numbers near the branches represent bootstrap support values. (b) Phylogeny reconstructed using mrBayes. The numbers near the branches represent posterior probability values.

(a)





(b)



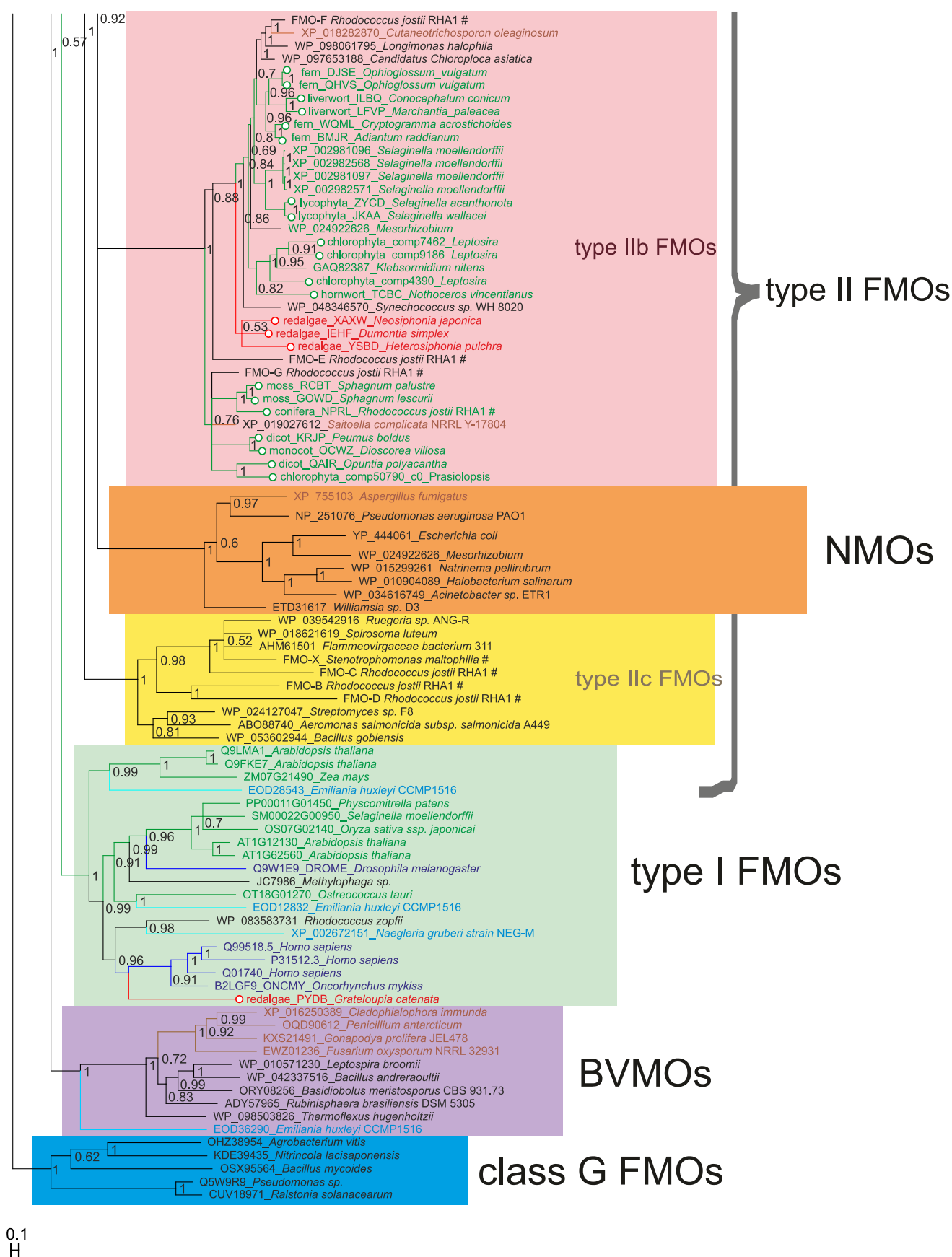
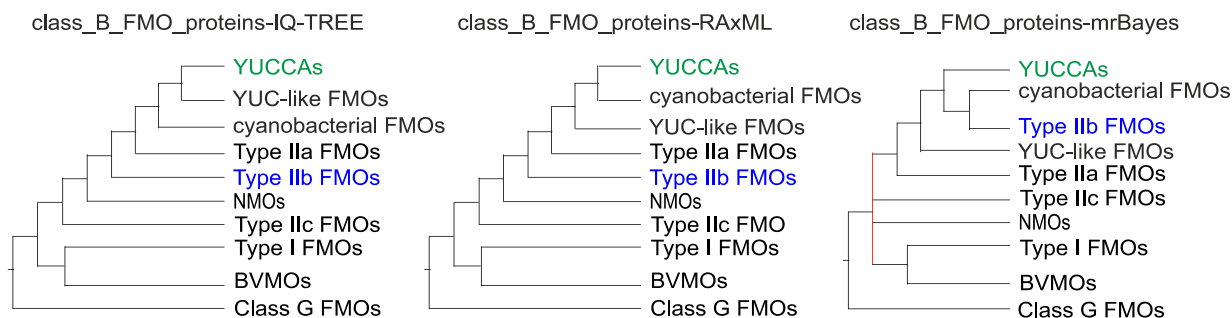


Figure S2. Phylogenetic trees of the class B flavoprotein monooxygenases, class_B_FMO_proteins_ext sample. All designations are as in Figure S1a; sequences from the 1KP project [ref. 49 of the main text] and the Green Algal Tree of Life Project [ref. 26 of the main text] are marked with a circle. The sequences of green algae and land plants are colored green; of red algae, red; of fungi, brown; of protists, cyan; of animals, blue; of bacteria, black, and of archaeobacteria, gray. The class G flavoprotein

monooxygenase proteins is outgroup (dark blue background). # denotes protein sequences from Riebel et al. [ref. 17 of the main text]: FMO-A – FMO-G from *R. jostii* RHA1; FMO-X *S. maltophilia* (B2FLR2). Asterisk (*) denotes proteins identified in the Spruce Genome Project [refs. 67,68 of the main text; Congenie.org]. (a) Phylogeny reconstructed using RAxML. The numbers near the branches represent bootstrap support values. (b) Phylogeny reconstructed using mrBayes. The numbers near the branches represent posterior probability values.

(a)



(b)

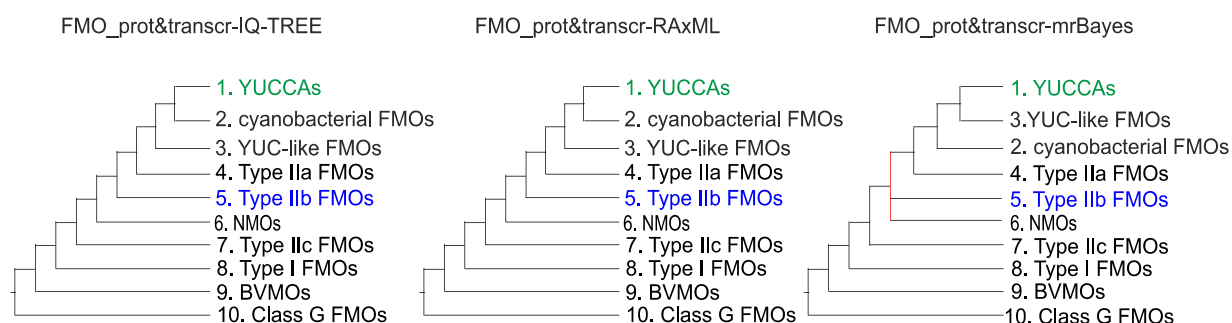


Figure S3. Simplified cladograms of the phylogenetic trees of the class B flavoprotein monooxygenases constructed by: IQ-TREE, RAxML and mrBayes. The YUCCA clade is denoted with green and type IIb FMO clade, with dark blue. Red line denotes a polyfurbations.

(a) Cladograms of the trees built using class B flavoprotein monooxygenase proteins

(class_B_FMO_proteins_ext sample).

(b) Cladograms of the trees built using extended class B flavoprotein monooxygenase proteins

(class_B_FMO_proteins_ext sample).