

## **Supplementary Figures**

### **Rethinking sesquiterpenoids: A widespread hormone in animals**

**So and Kai et al**

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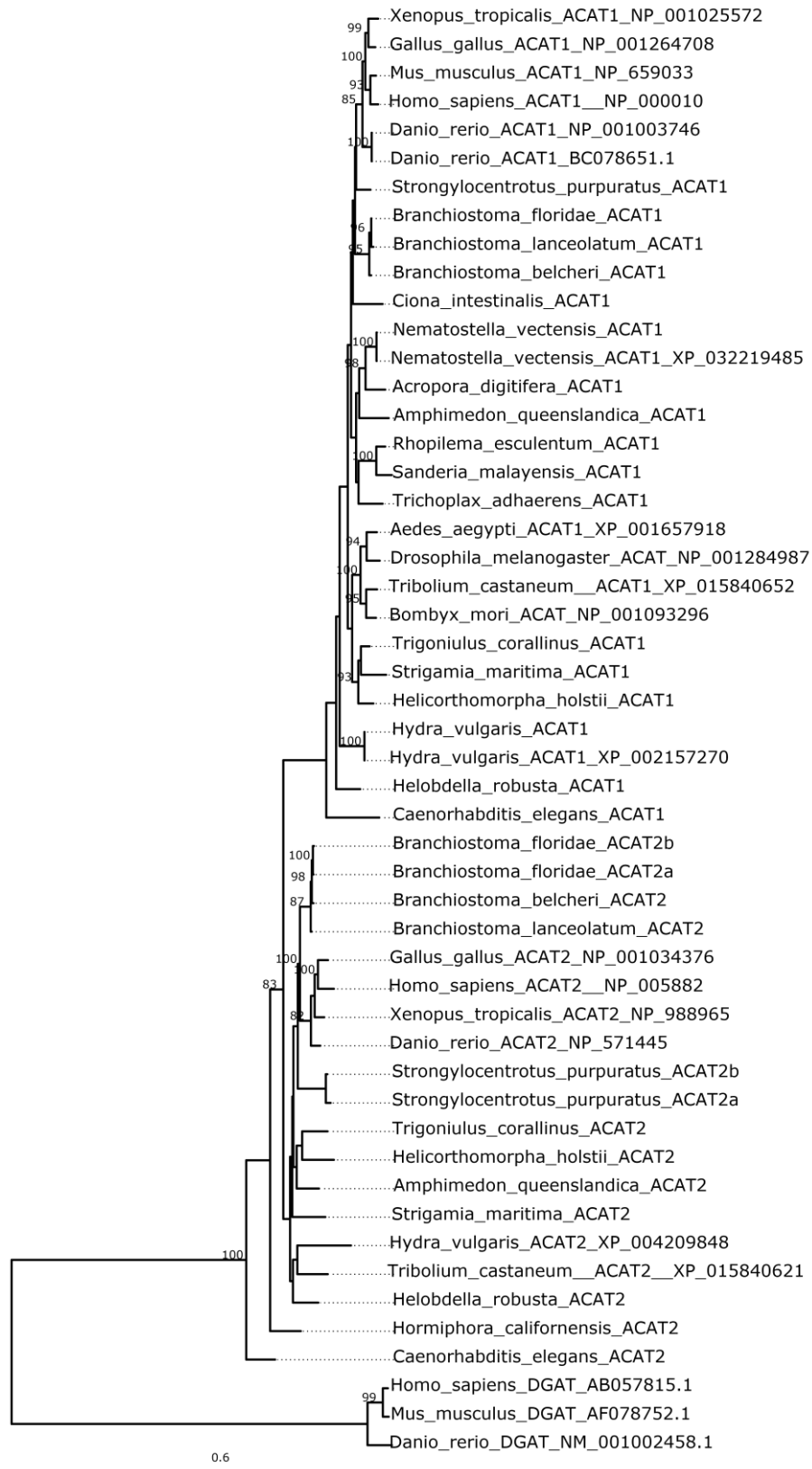
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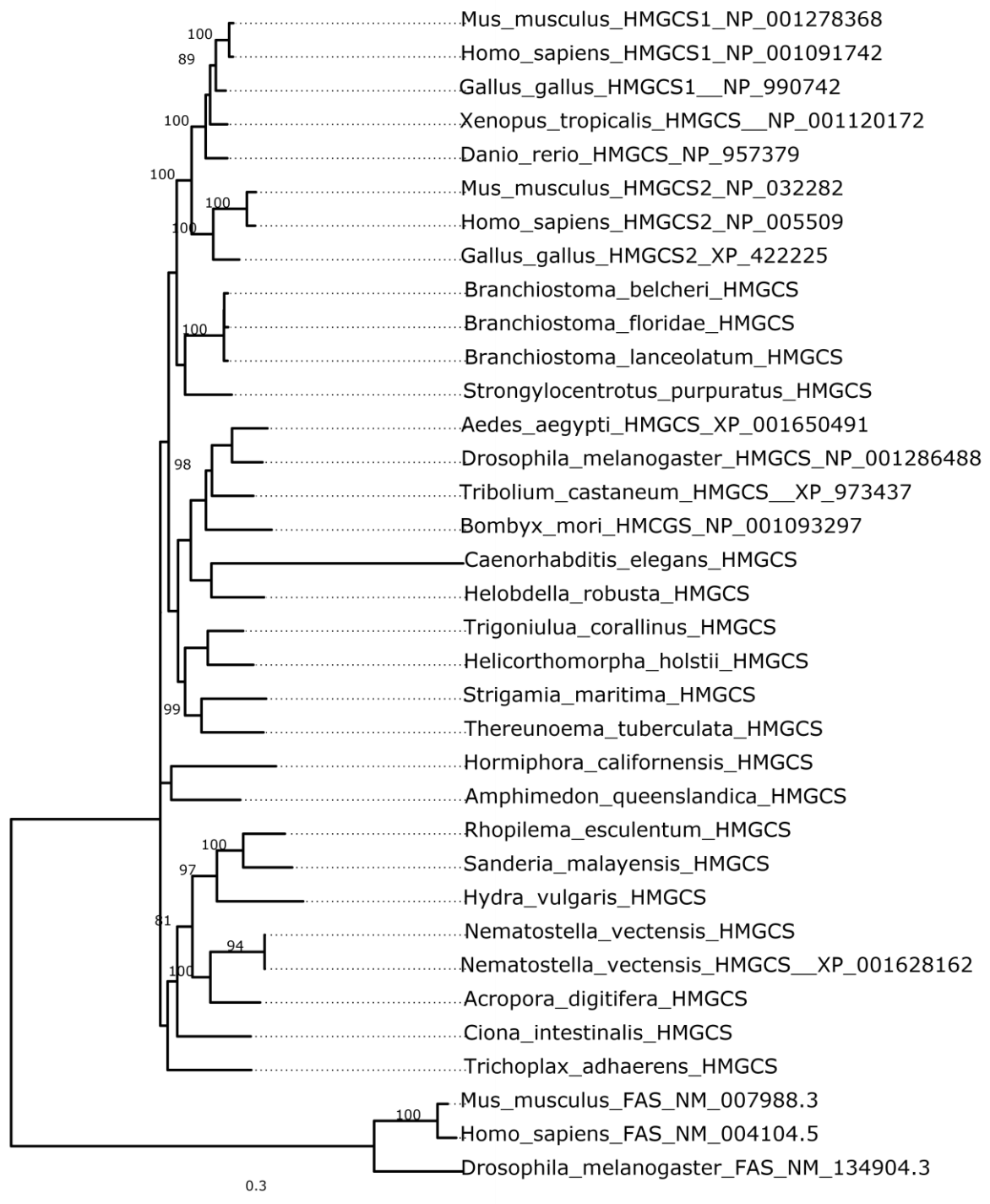
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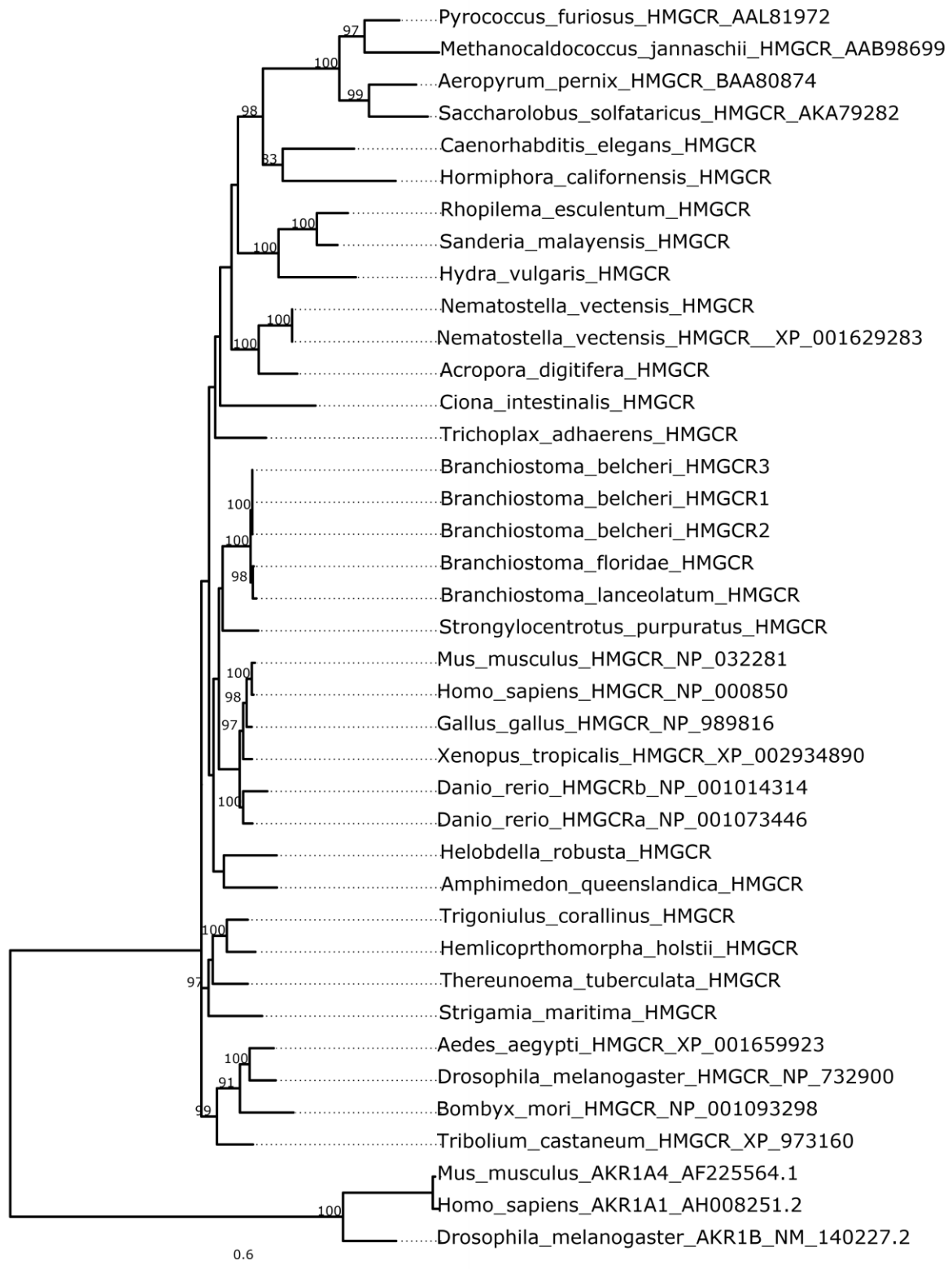


**Supplementary Figure S1. Phylogenetic tree of acetyl-CoA C-acetyltransferase (ACAT).**

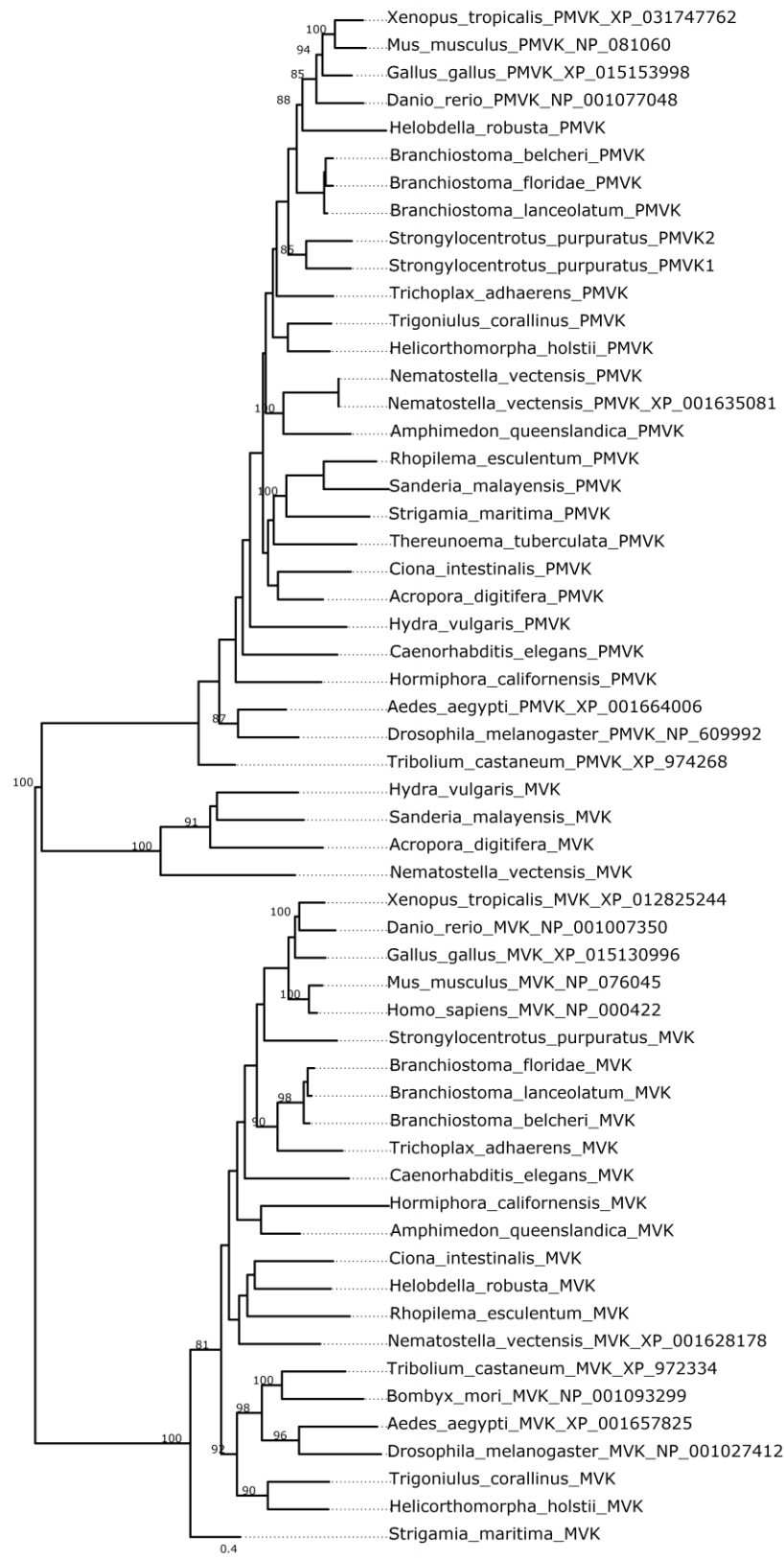
Tree is constructed with the maximum likelihood (ML) method (LG+G4) with 1000 bootstrap replicates. Only bootstrap values larger than 80% are indicated for clarity. Tree rooted using metazoan diglyceride acyltransferase (DGAT).



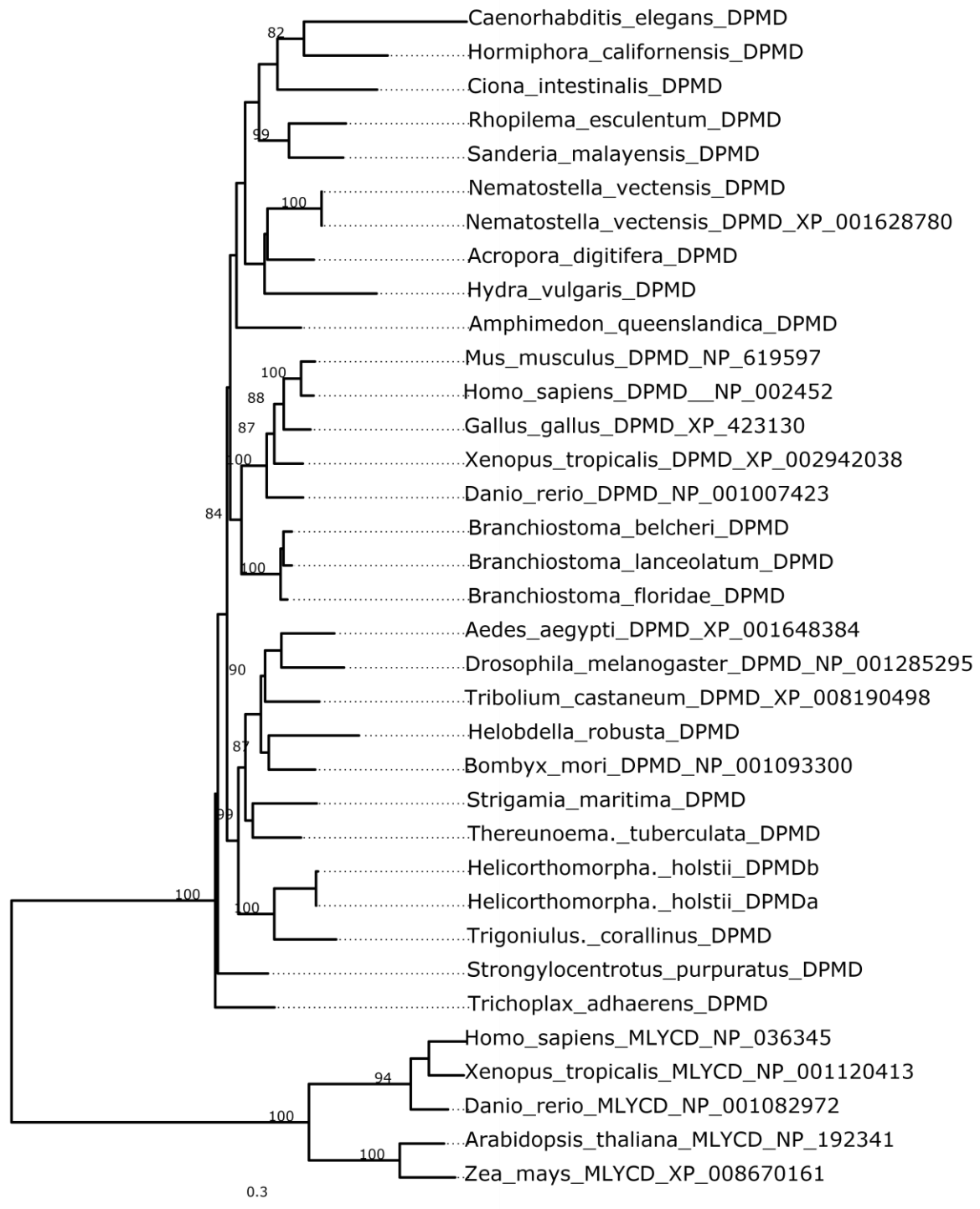
**Supplementary Figure S2. Phylogenetic tree of hydroxymethylglutaryl-CoA synthase (HMGCS).** Tree is constructed with the maximum likelihood (ML) method (LG+G4) with 1000 bootstrap replicates. Only bootstrap values larger than 80% are indicated for clarity. Tree rooted using metazoan fatty acid synthase (FAS).



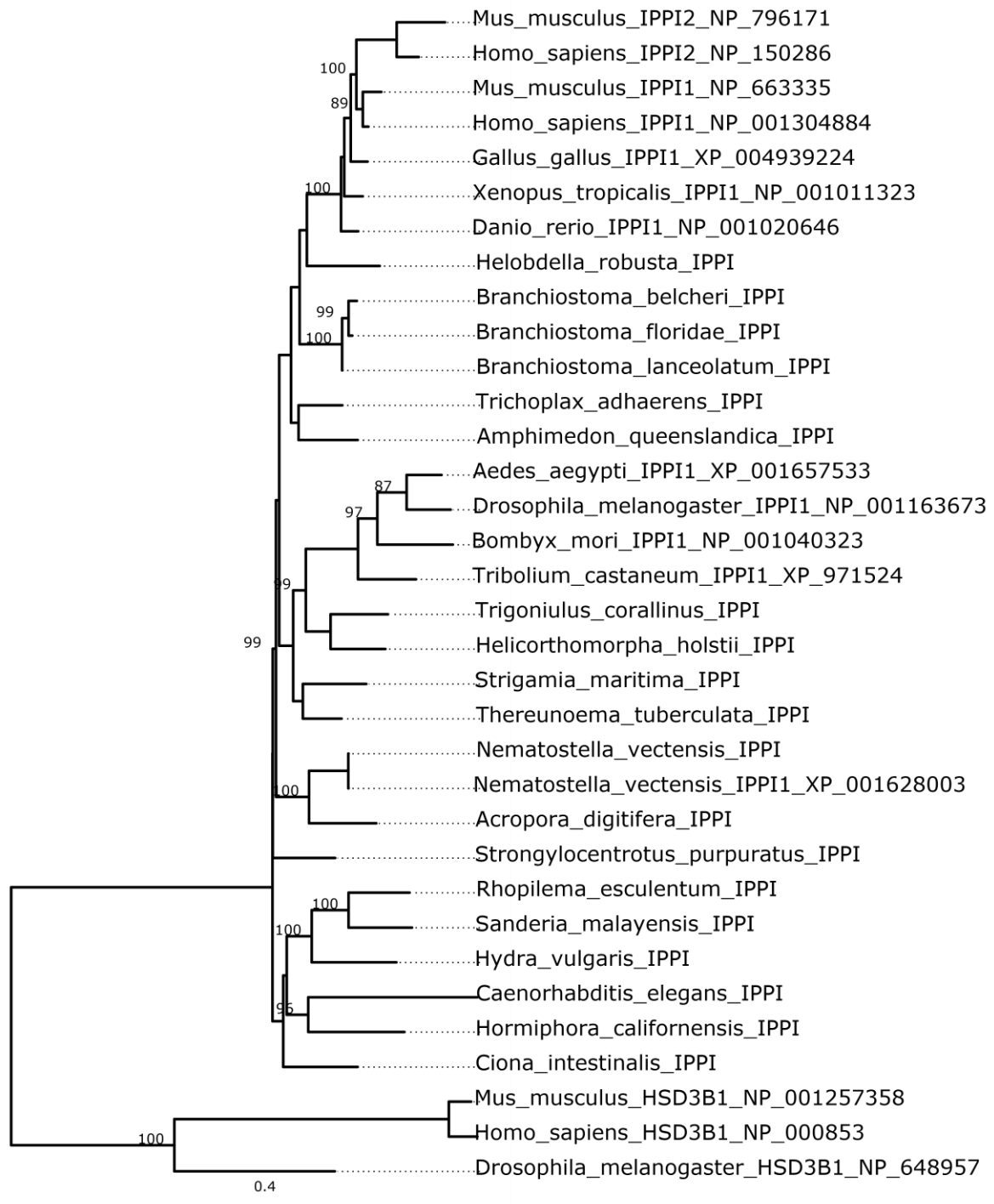
**Supplementary Figure S3. Phylogenetic tree of hydroxymethylglutaryl-CoA reductase (HMGCR).** Tree is constructed with the maximum likelihood (ML) method (LG+R5) with 1000 bootstrap replicates. Only bootstrap values larger than 80% are indicated for clarity. Tree rooted using metazoan aldo-keto reductase (AKR1).



**Supplementary Figure S4. Phylogenetic tree of mevalonate kinase (MVK) and phosphomevalonate kinase (PMVK).** Tree is constructed with the maximum likelihood (ML) method (LG+R4) with 1000 bootstrap replicates. Only bootstrap values larger than 80% are indicated for clarity.

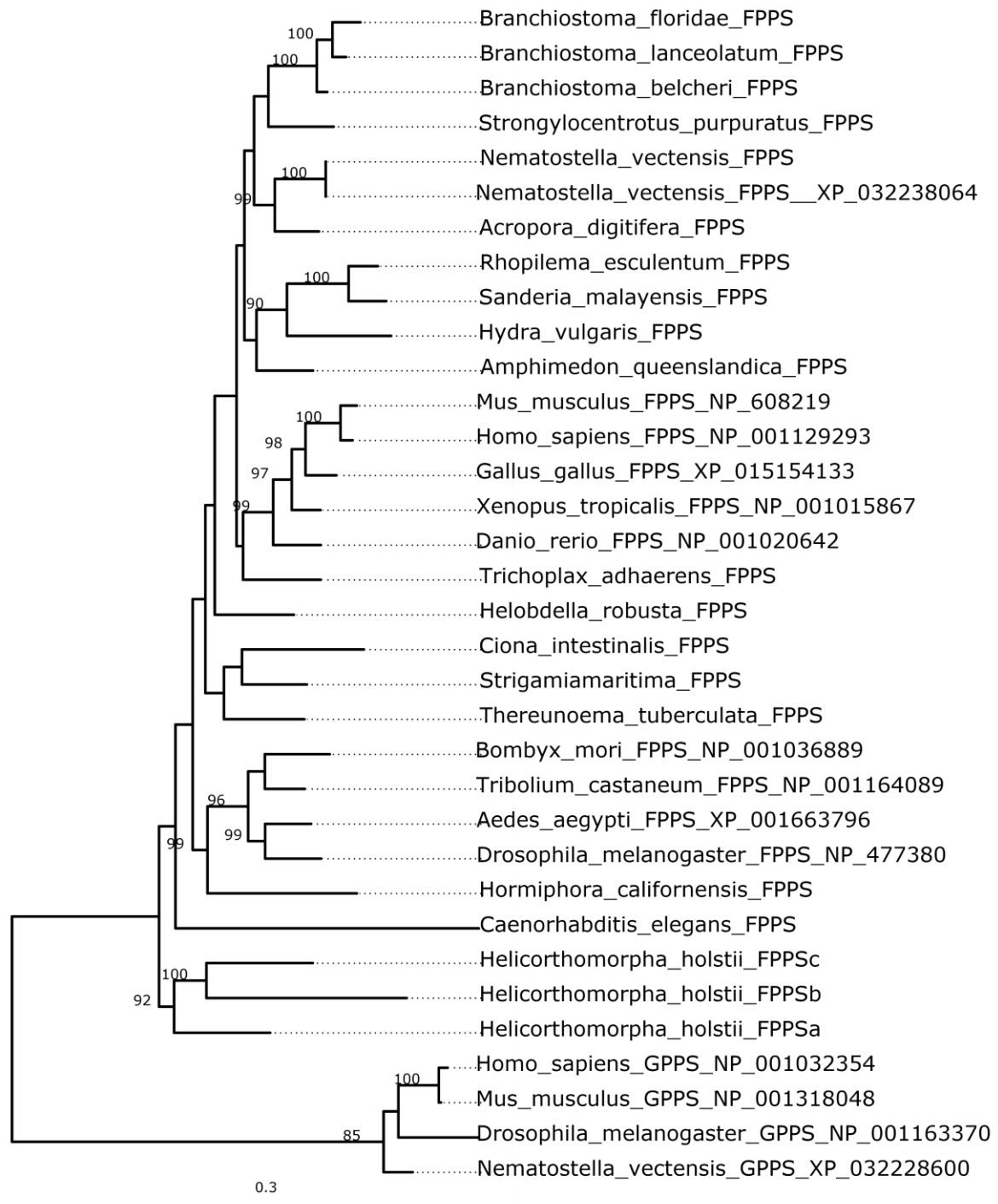


**Supplementary Figure S5. Phylogenetic tree of diphosphomevalonate decarboxylase (DPMD).** Tree is constructed with the maximum likelihood (ML) method (LG+G4) with 1000 bootstrap replicates. Only bootstrap values larger than 80% are indicated for clarity. Tree rooted using malonyl-CoA decarboxylase (MLYCD).

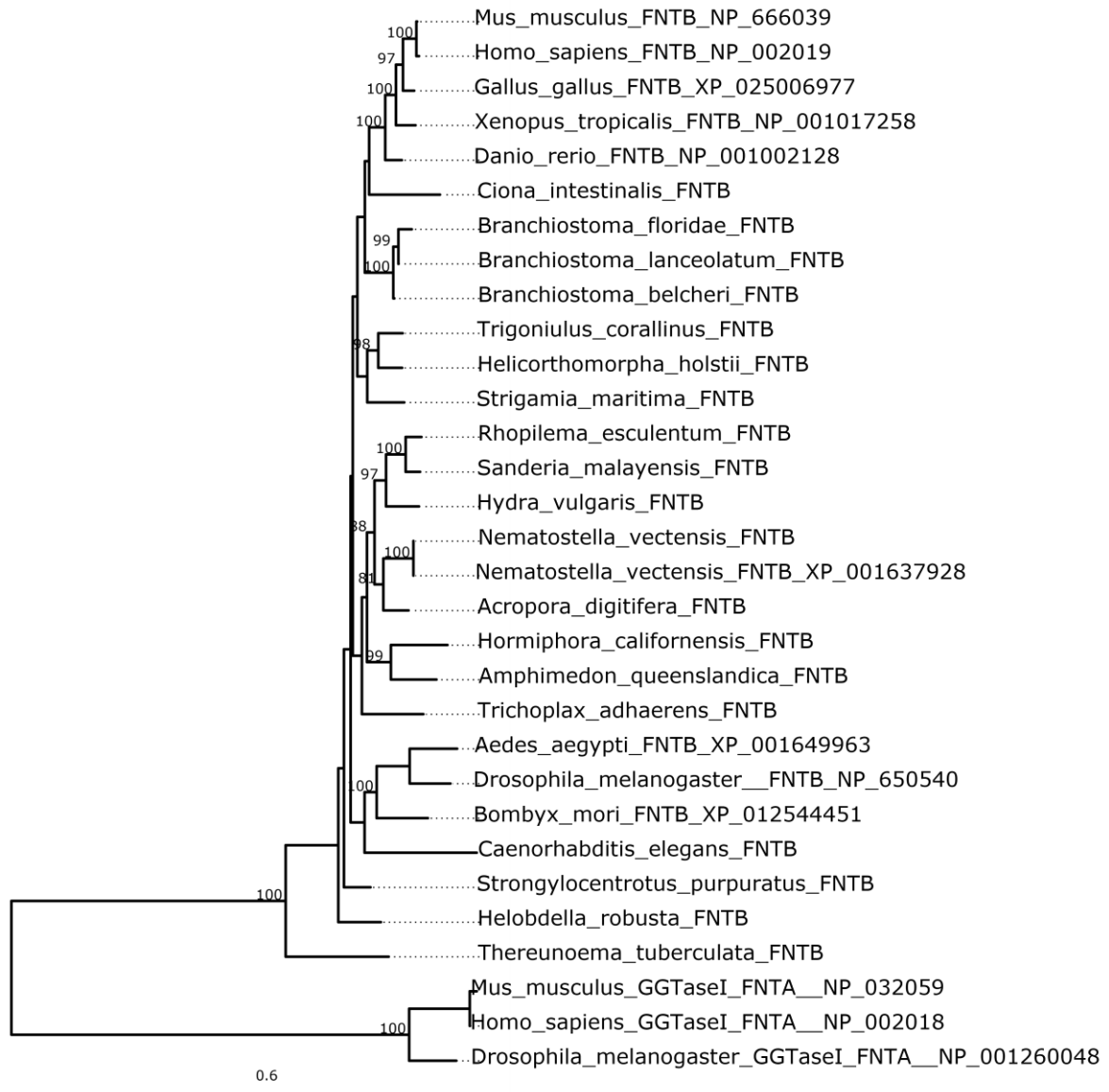


**Supplementary Figure S6. Phylogenetic tree of isopentenyl-diphosphate delta-isomerase (IPPI).** Tree is constructed with the maximum likelihood (ML) method (LG+I+G4) with 1000 bootstrap replicates. Only bootstrap values larger than 80% are indicated for clarity. Tree rooted using metazoan hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1 (HSD3B1).

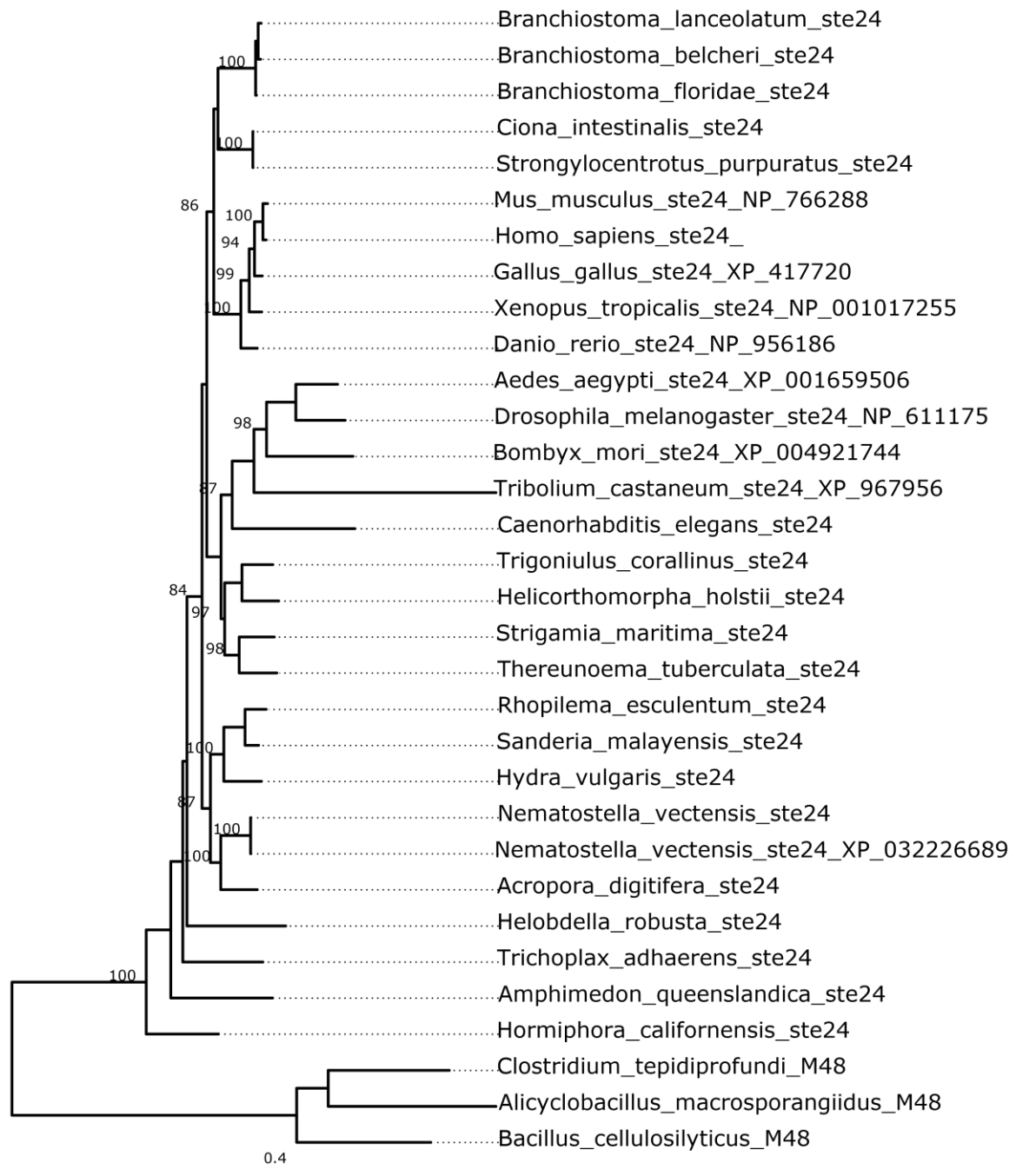


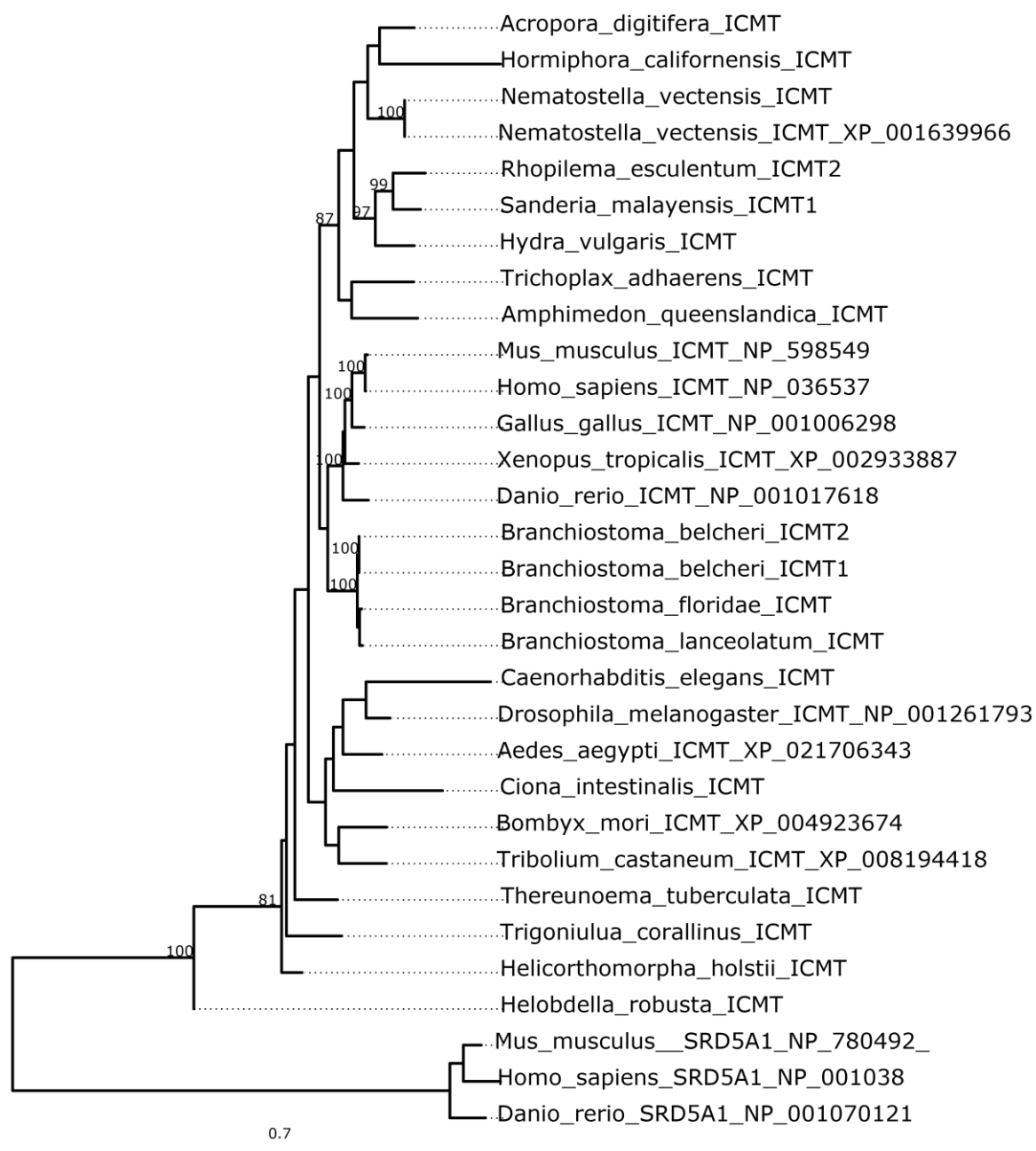


**Supplementary Figure S7. Phylogenetic tree of farnesyl pyrophosphate synthase (FPPS).** Tree is constructed with the maximum likelihood (ML) method (LG+I+G4) with 1000 bootstrap replicates. Only bootstrap values larger than 80% are indicated for clarity. Tree rooted using metazoan geranyl diphosphate synthase (GPPS).

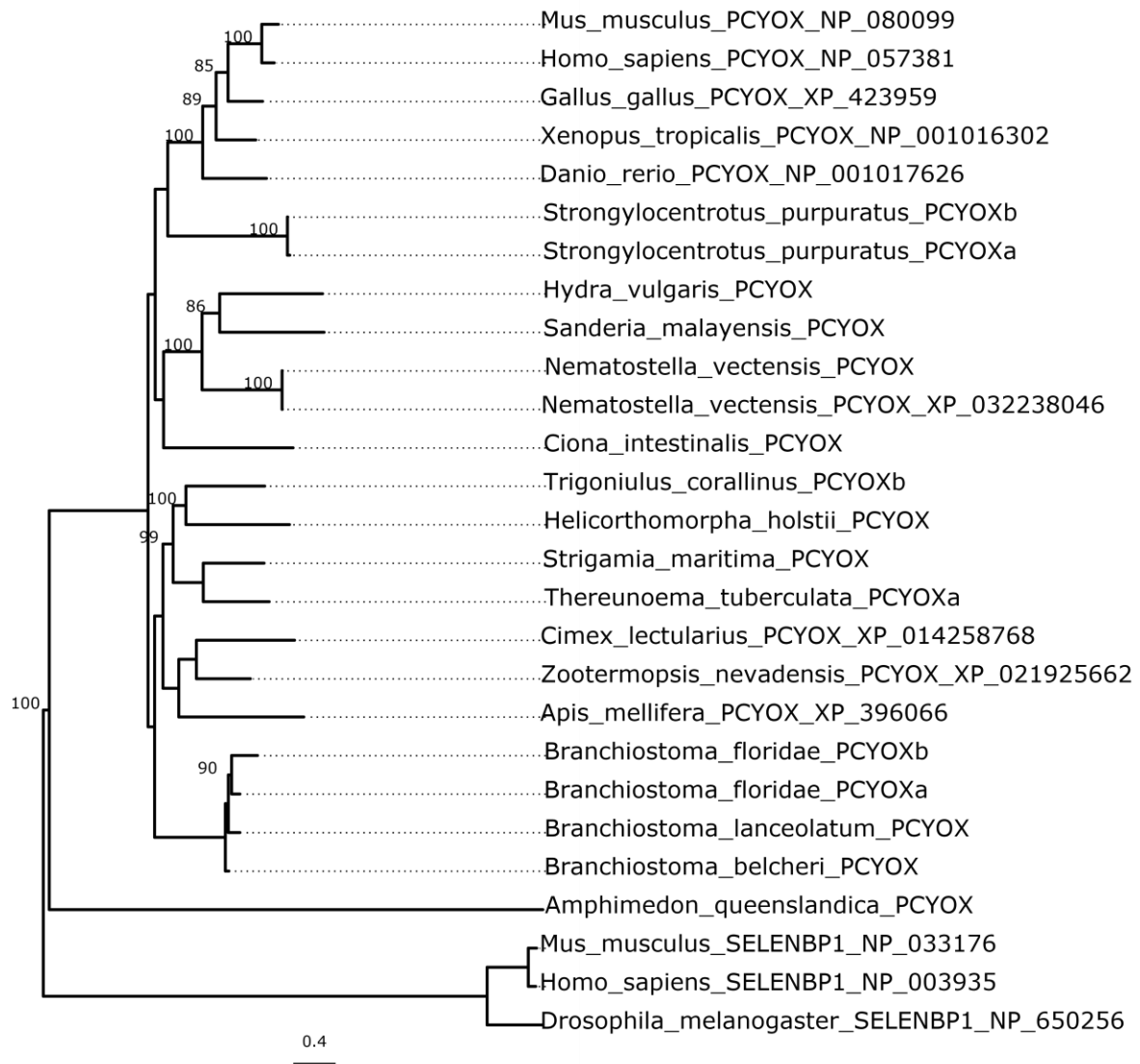


**Supplementary Figure S8. Phylogenetic tree of farnesyltransferase beta (FNTB).** Tree is constructed with the maximum likelihood (ML) method (LG+G4) with 1000 bootstrap replicates. Only bootstrap values larger than 80% are indicated for clarity. Tree rooted using metazoan geranylgeranyltransferase (FNTA).

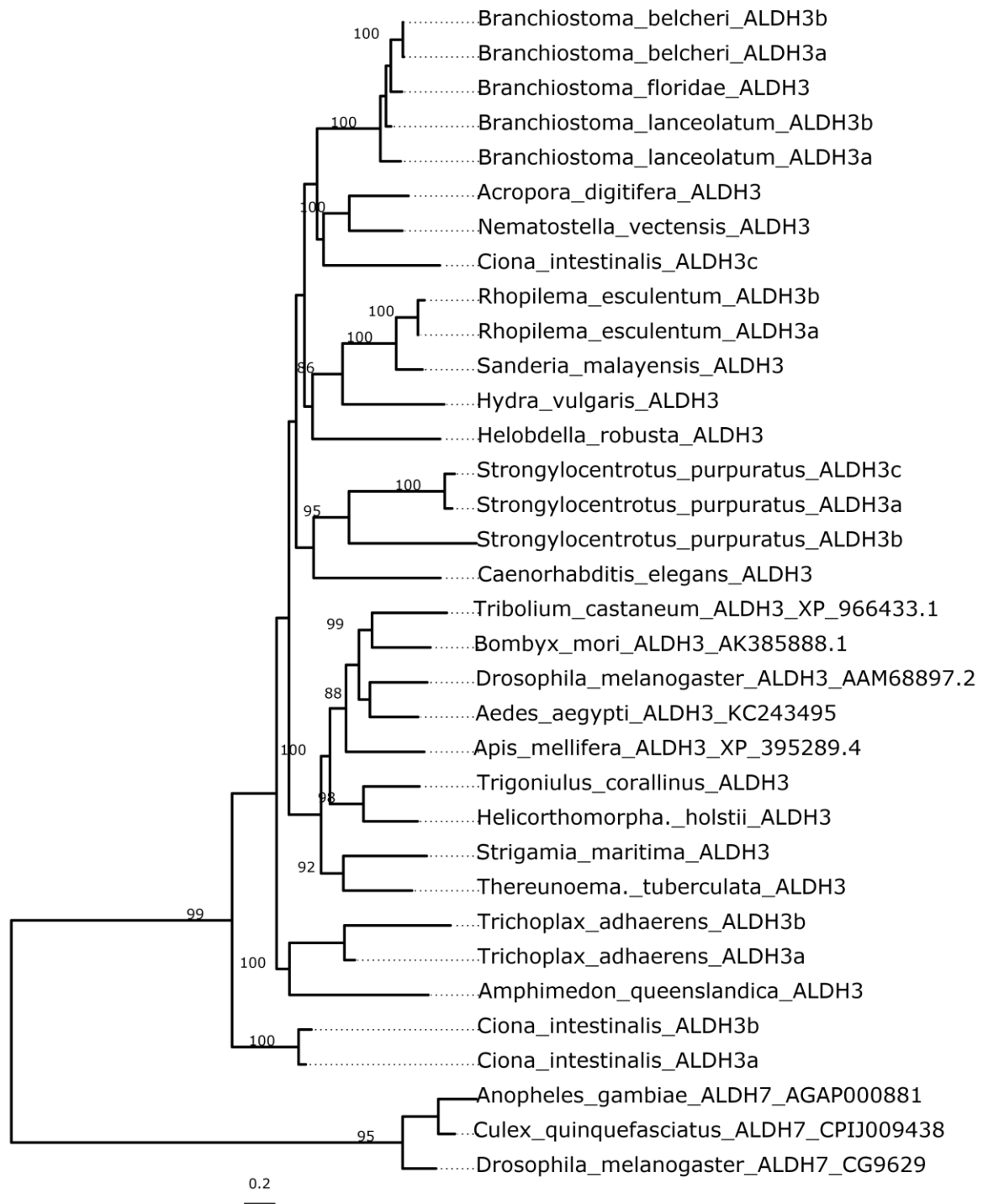




**Supplementary Figure S10. Phylogenetic tree of protein-S-isoprenylcysteine O-methyltransferase (ICMT).** Tree is constructed with the maximum likelihood (ML) method (LG+F+G4) with 1000 bootstrap replicates. Only bootstrap values larger than 80% are indicated for clarity. Tree rooted using metazoan steroid 5 alpha-reductase 1 (SRD5A1).



**Supplementary Figure S11. Phylogenetic tree of prenylcysteine oxidase (PCYOX).** Tree is constructed with the maximum likelihood (ML) method (LG+G4) with 1000 bootstrap replicates. Only bootstrap values larger than 80% are indicated for clarity. Tree rooted using metazoan selenium binding protein 1 (SELENBP1).



**Supplementary Figure S12. Phylogenetic tree of aldehyde dehydrogenase 3 (ALDH3).**

Tree is constructed with the maximum likelihood (ML) method with 1000 bootstrap replicates. Only bootstrap values larger than 80% are indicated for clarity. Tree rooted using arthropod aldehyde dehydrogenase 7 (ALDH7).