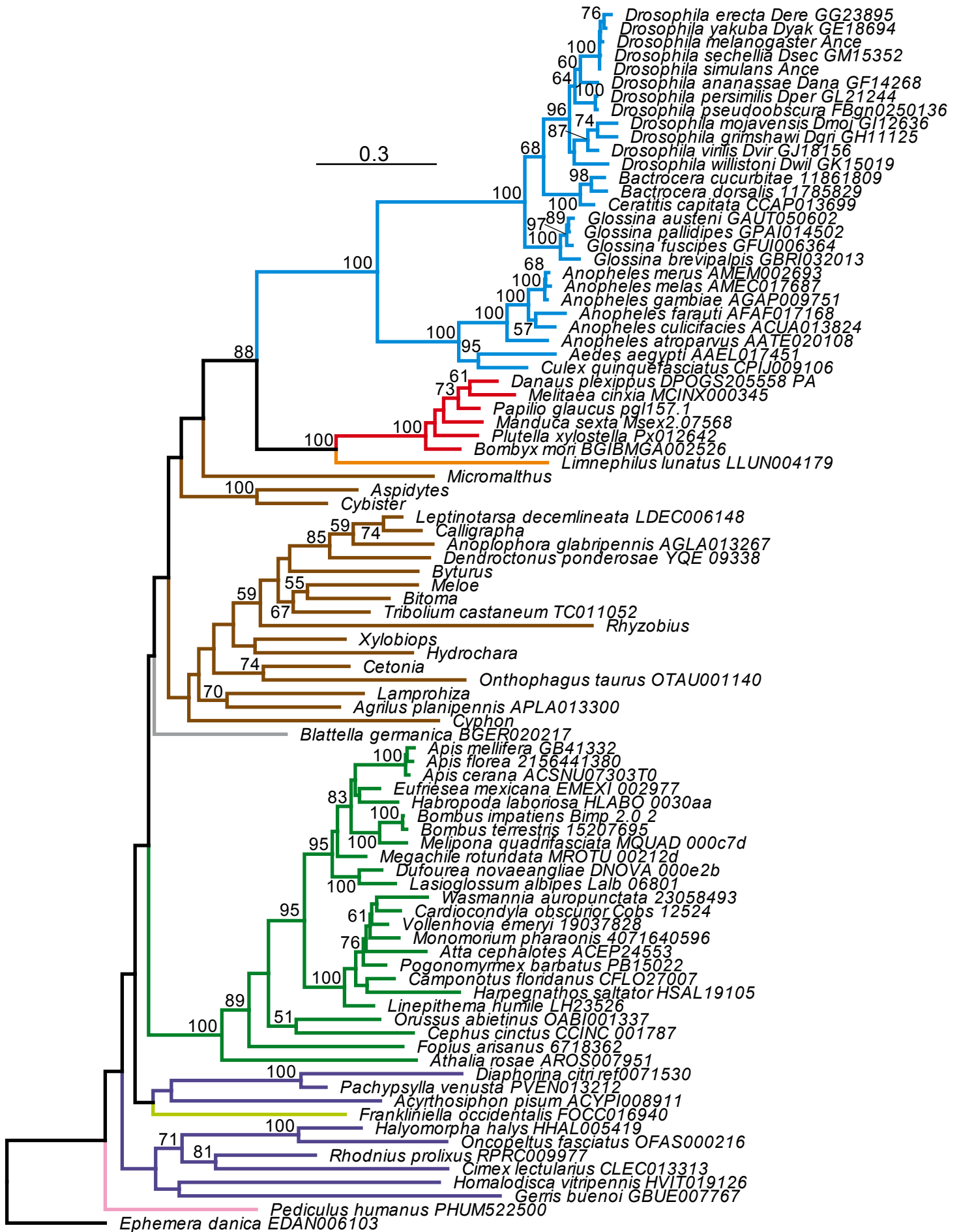


File S1. Maximum likelihood trees based on the amino acid alignments of different sperm individualization proteins in insects.

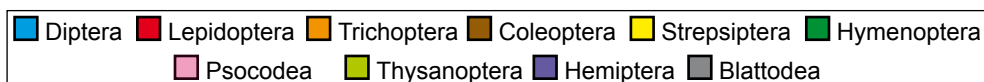
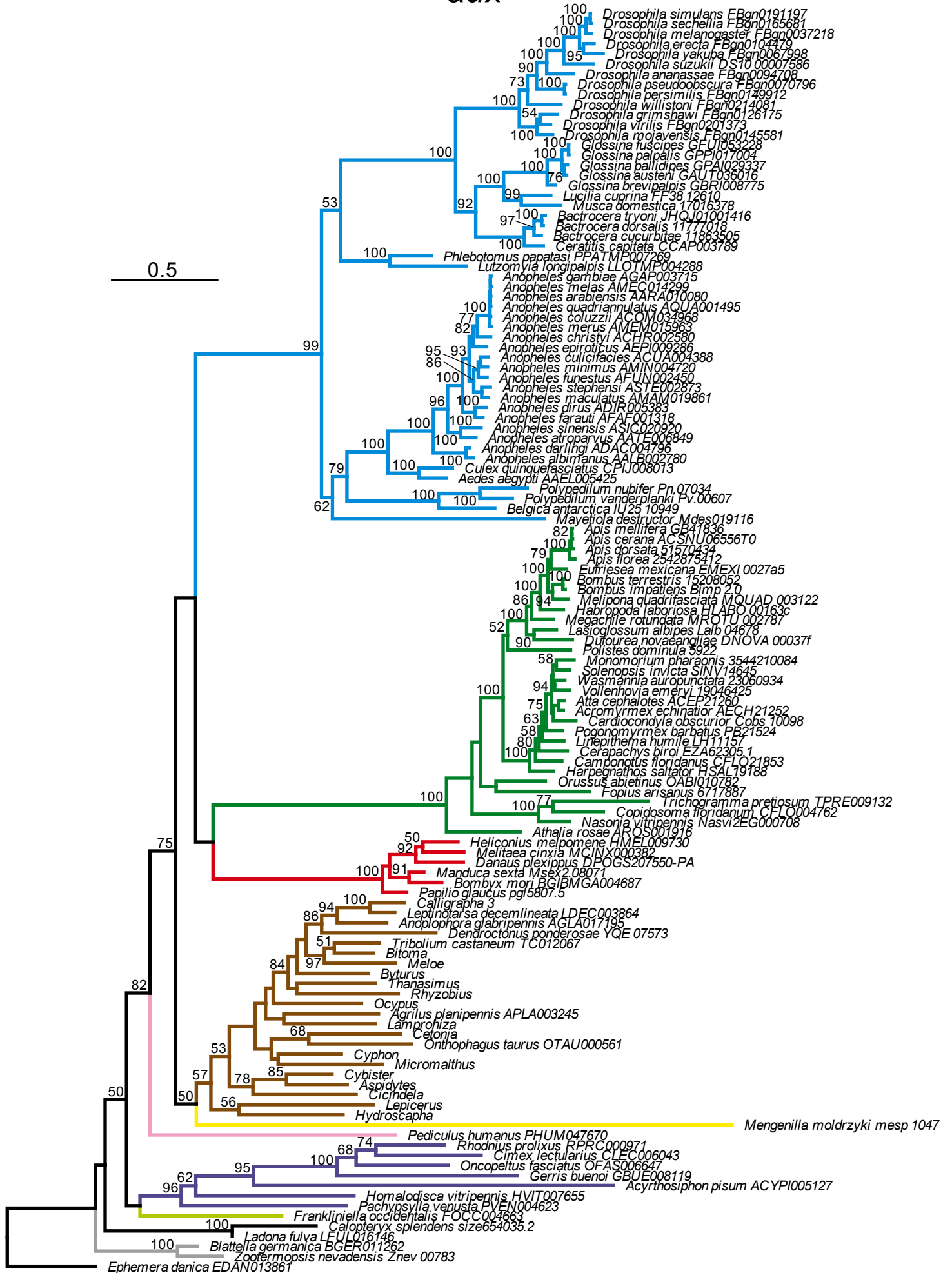
Tree	Gene	Model	Gamma	Invariant	Log likelihood
1	<i>Ance*</i>	LG	0.975	0.075	-36264.30406
2	<i>aux</i>	LG	0.861	0.042	-101341.43324
3	<i>blanks</i>	JTT	1.000	0.006	-51030.51327
4	<i>Bug22*</i>	LG	0.970	0.076	-11344.29415
5	<i>CdsA</i>	JTT	0.662	0.164	-20188.93347
6	<i>Chc</i>	JTT	0.646	0.429	-27341.73092
7	<i>Cul3*</i>	JTT	0.617	0.203	-21620.12771
8	<i>Dark</i>	JTT	1.873	0.003	-175174.99008
9	<i>didum</i>	LG	0.896	0.094	-118892.32085
10	<i>Dredd*</i>	JTT	1.420	0.006	-57705.56572
11	<i>Dronc</i>	WAG	1.405	0.013	-53433.37737
12	<i>Duba</i>	JTT	0.992	0.055	-43655.01217
13	<i>EcR</i>	JTT	0.663	0.140	-13958.07538
14	<i>eIF3m</i>	JTT	0.817	0.145	-15809.34033
15	<i>Fadd</i>	JTT	1.307	0.004	-30734.15211
16	<i>gish</i>	JTT	0.678	0.335	-7663.02559
17	<i>gudu</i>	LG	0.921	0.038	-38783.13178
18	<i>heph</i>	JTT	0.965	0.170	-15480.89741
19	<i>hmw</i>	JTT	1.149	0.007	-35247.66673
20	<i>jar</i>	LG	0.857	0.181	-62829.80003
21	<i>klhl10*</i>	LG	0.913	0.017	-35556.78931
22	<i>Lasp</i>	JTT	0.844	0.249	-9432.56476
23	<i>Mer</i>	JTT	0.699	0.123	-21840.64371
24	<i>mlt</i>	LG	0.628	0.095	-34633.21523
25	<i>nes</i>	LG	1.073	0.040	-42646.95754
26	<i>Npcla*</i>	LG	0.833	0.156	-85235.55965
27	<i>nsr*</i>	JTT	0.854	0.036	-28961.01227
28	<i>orb2</i>	JTT	0.489	0.214	-3222.50637
29	<i>Osbp</i>	JTT	0.863	0.082	-51127.87538
30	<i>oys</i>	LG	0.984	0.066	-29099.88610
31	<i>Past1</i>	LG	0.711	0.302	-16096.65909
32	<i>Pen*</i>	LG	0.930	0.090	-38161.29725
33	<i>poe</i>	JTT	0.769	0.060	-163837.44235
34	<i>porin</i>	LG	1.341	0.028	-15895.84791
35	<i>Prosalpha6T</i>	LG	0.792	0.197	-15675.74518
36	<i>scat</i>	JTT	0.939	0.037	-72098.82783
37	<i>shi</i>	LG	0.650	0.287	-23338.29850
38	<i>skap*</i>	LG	0.831	0.257	-19572.71029
39	<i>sw</i>	JTT	0.960	0.066	-27022.45452
40	<i>Taz</i>	LG	1.034	0.157	-17370.63510
41	<i>Vps28</i>	LG	0.720	0.100	-6256.72767

*Orthologs to the *Drosophila* paralog with sperm individualization function.

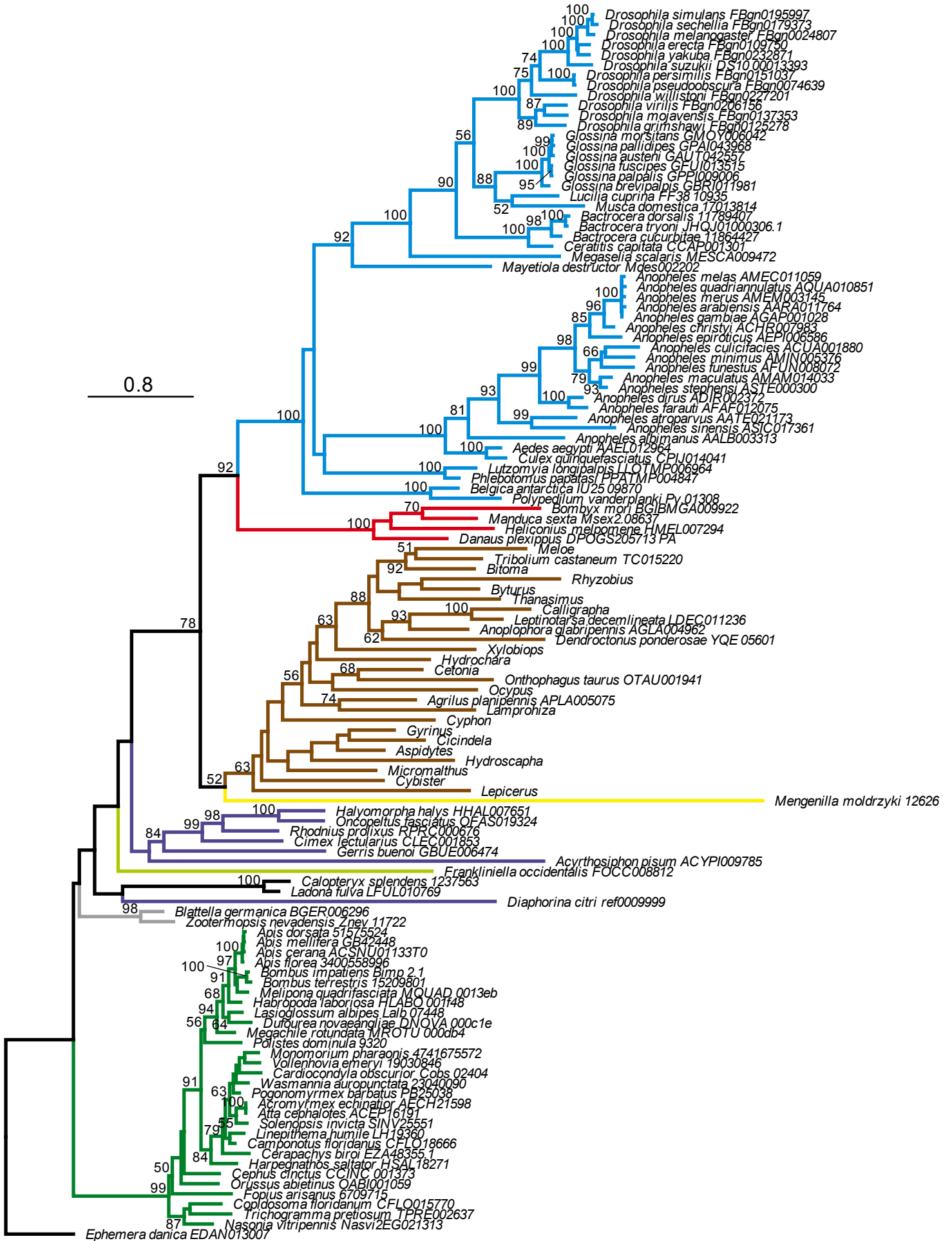
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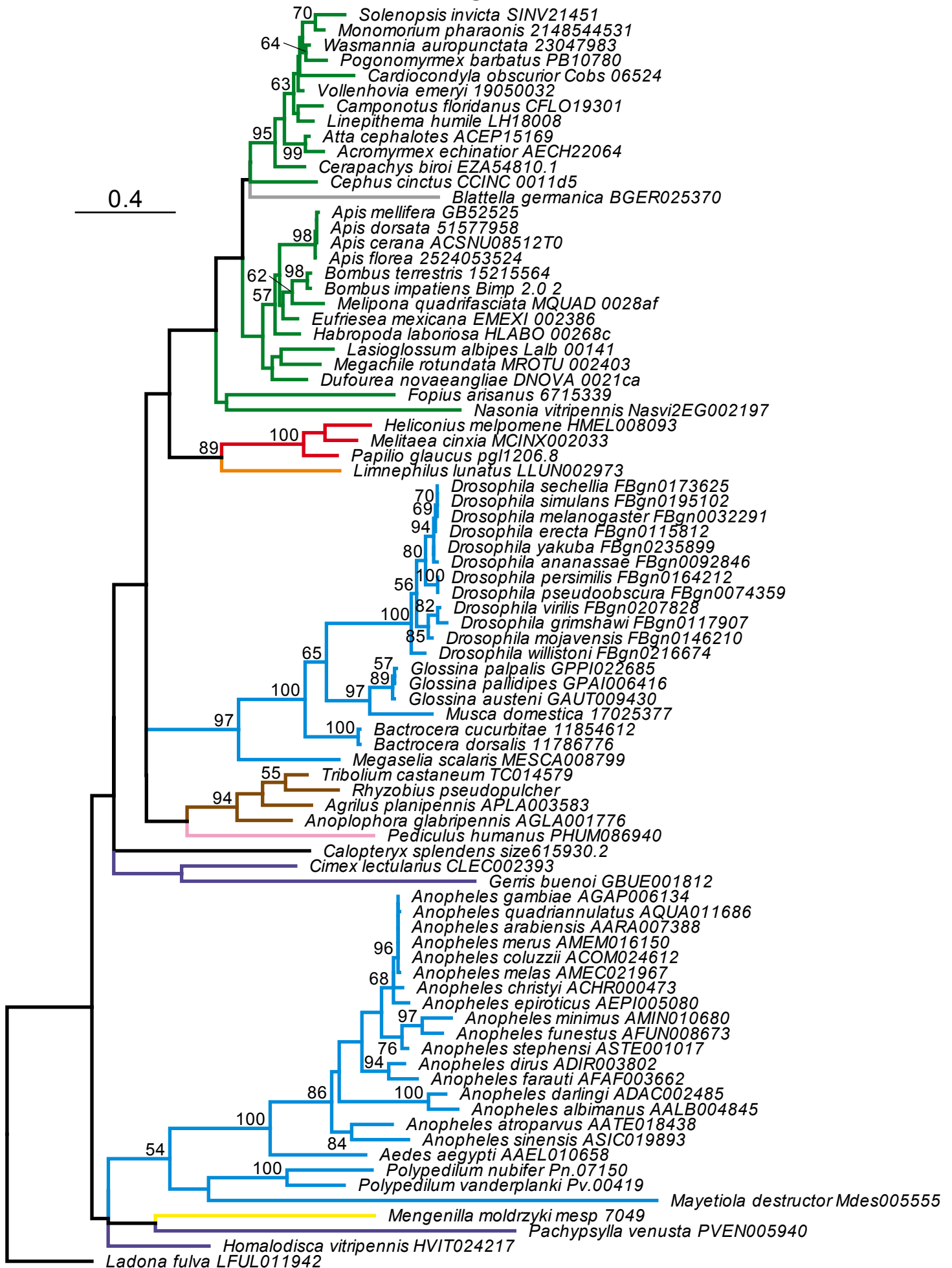
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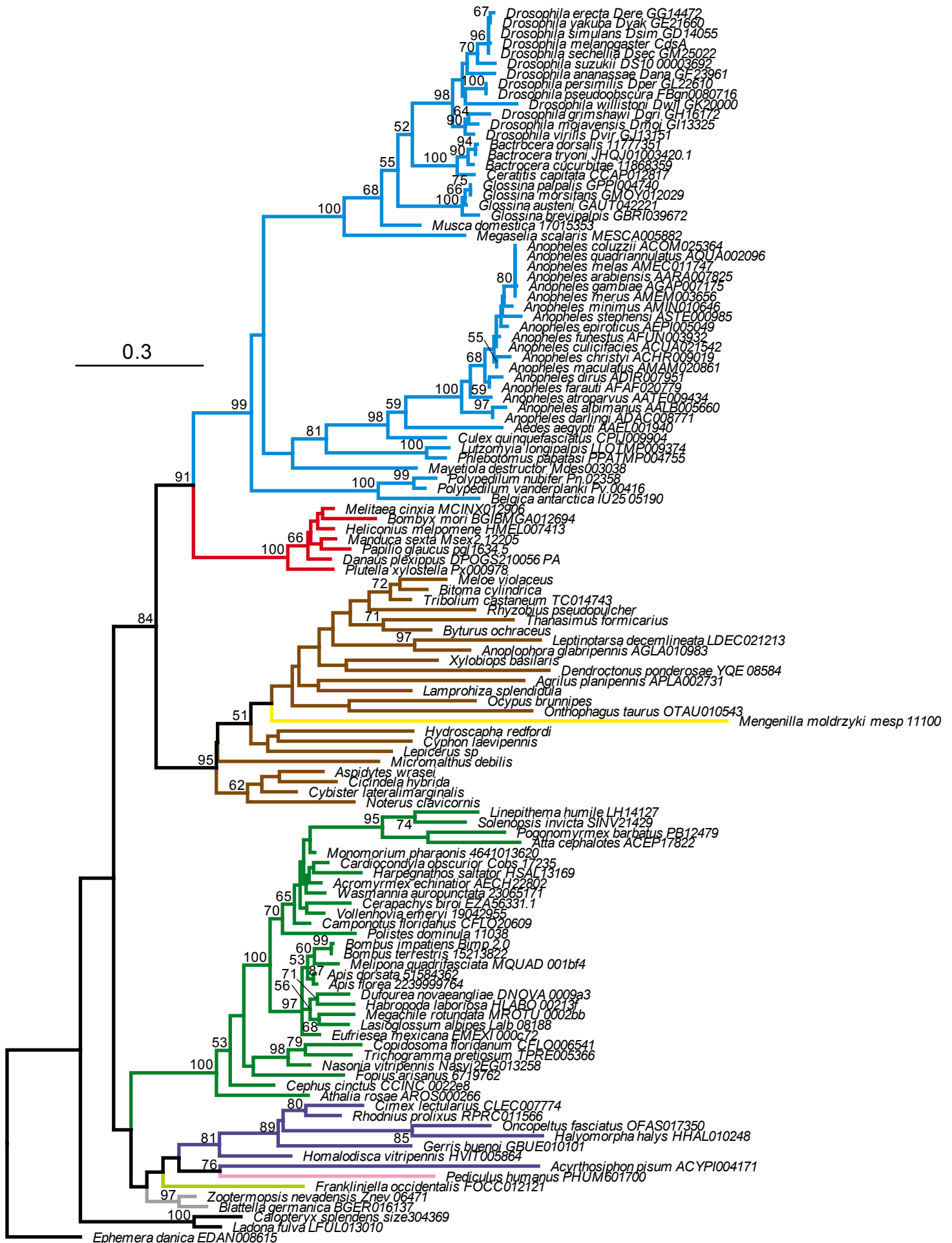
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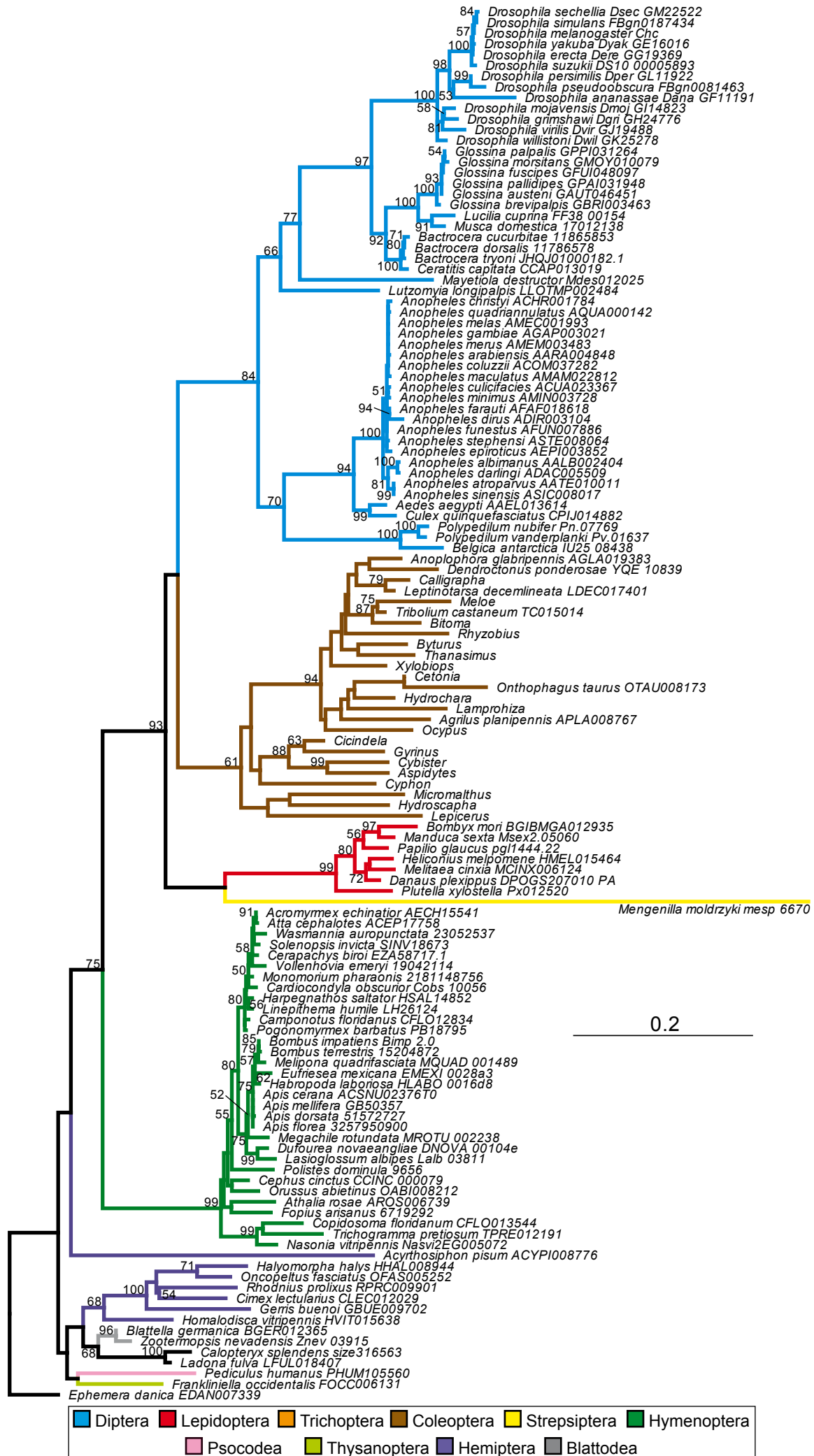
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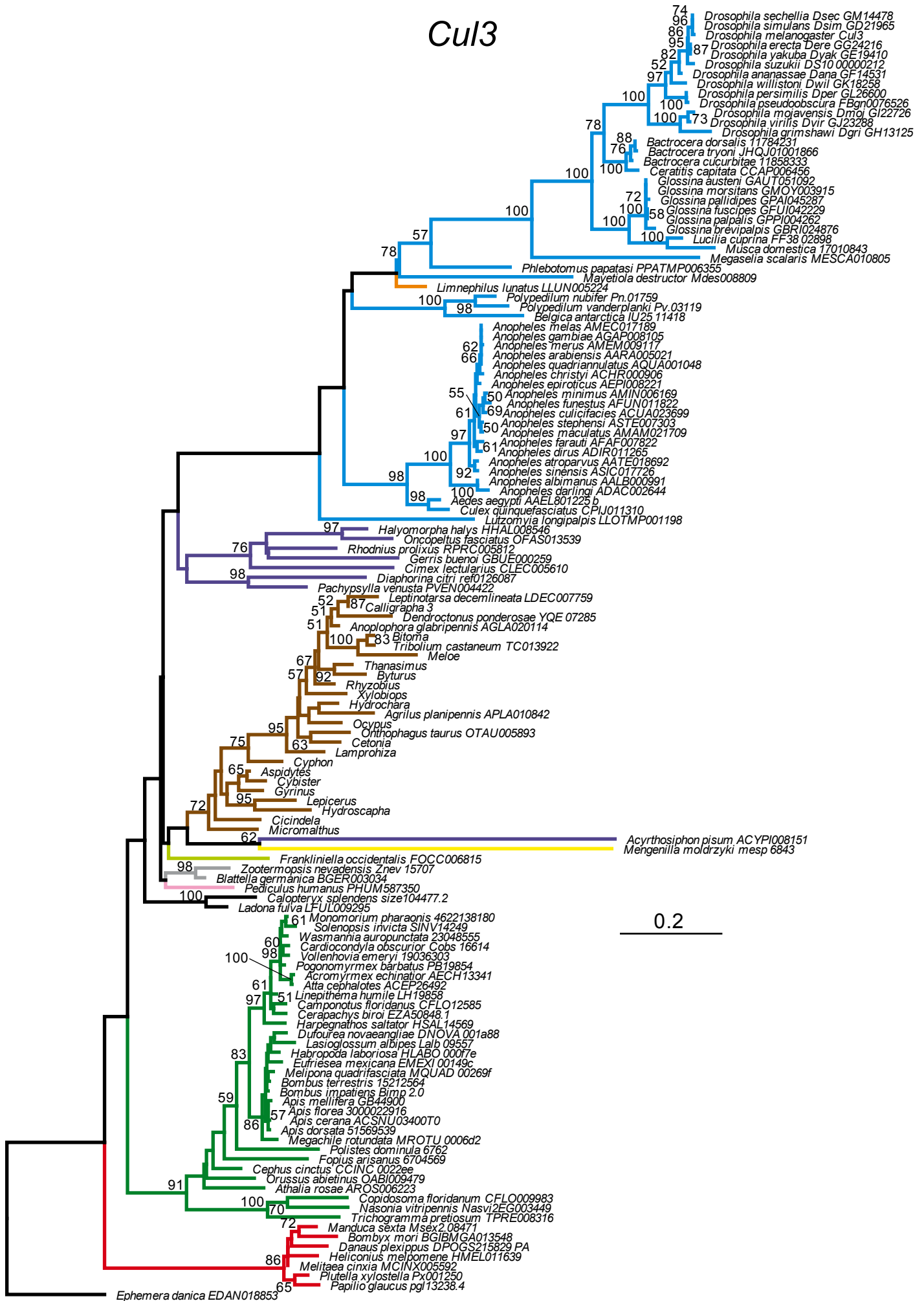
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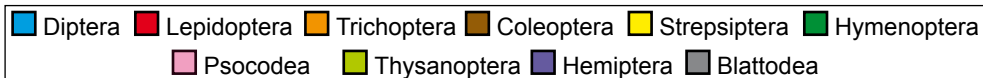
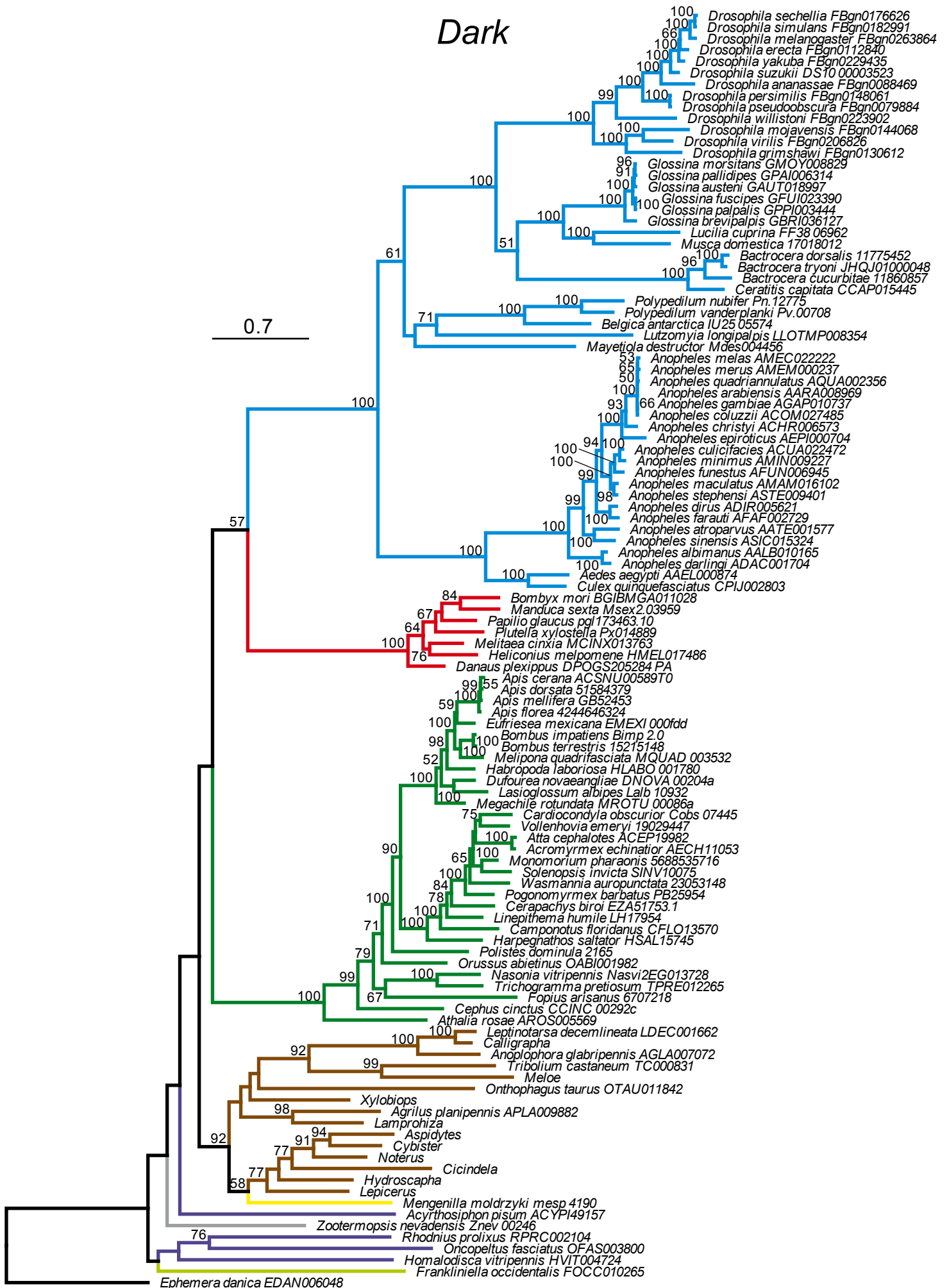
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Cul3

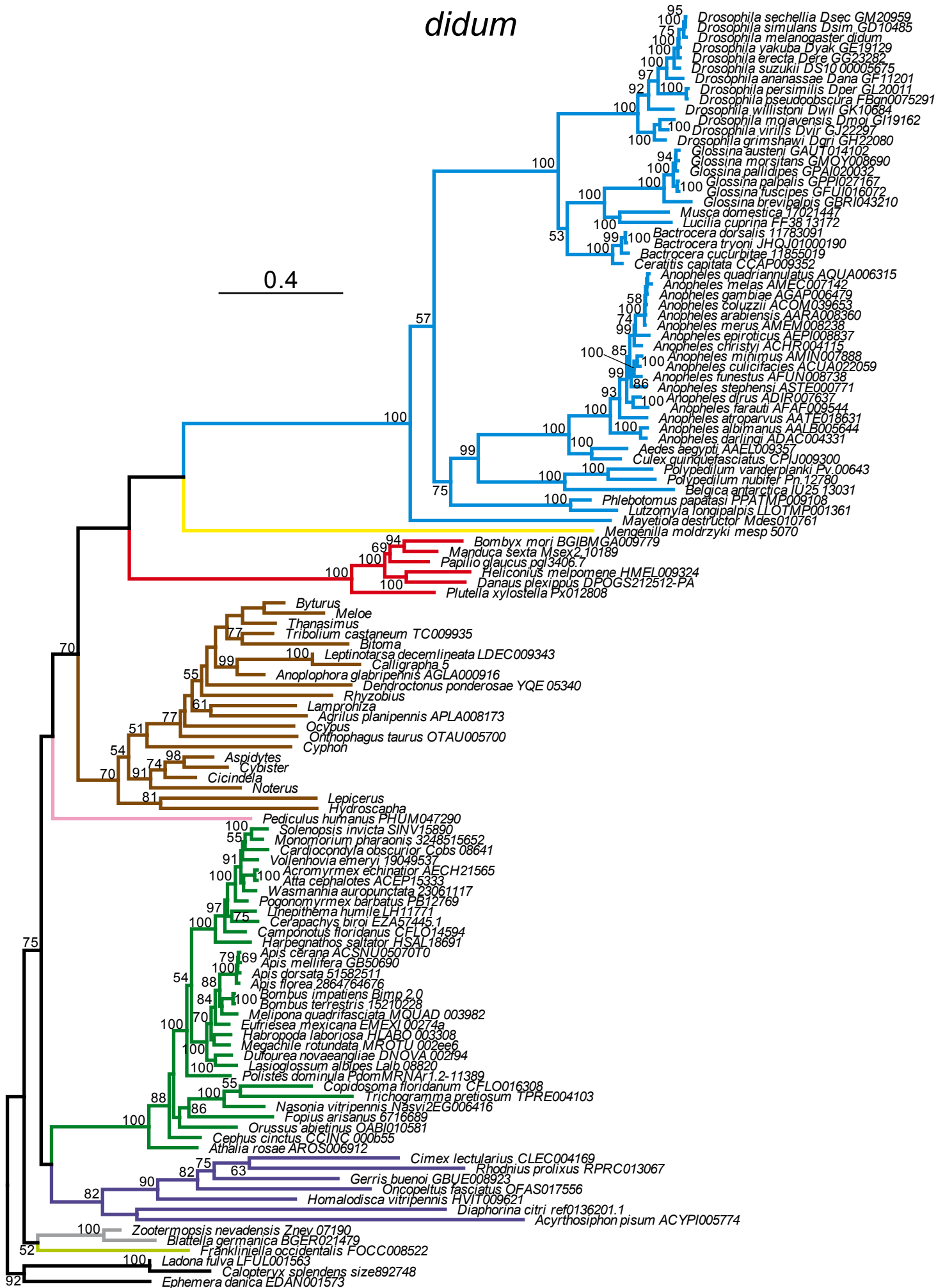


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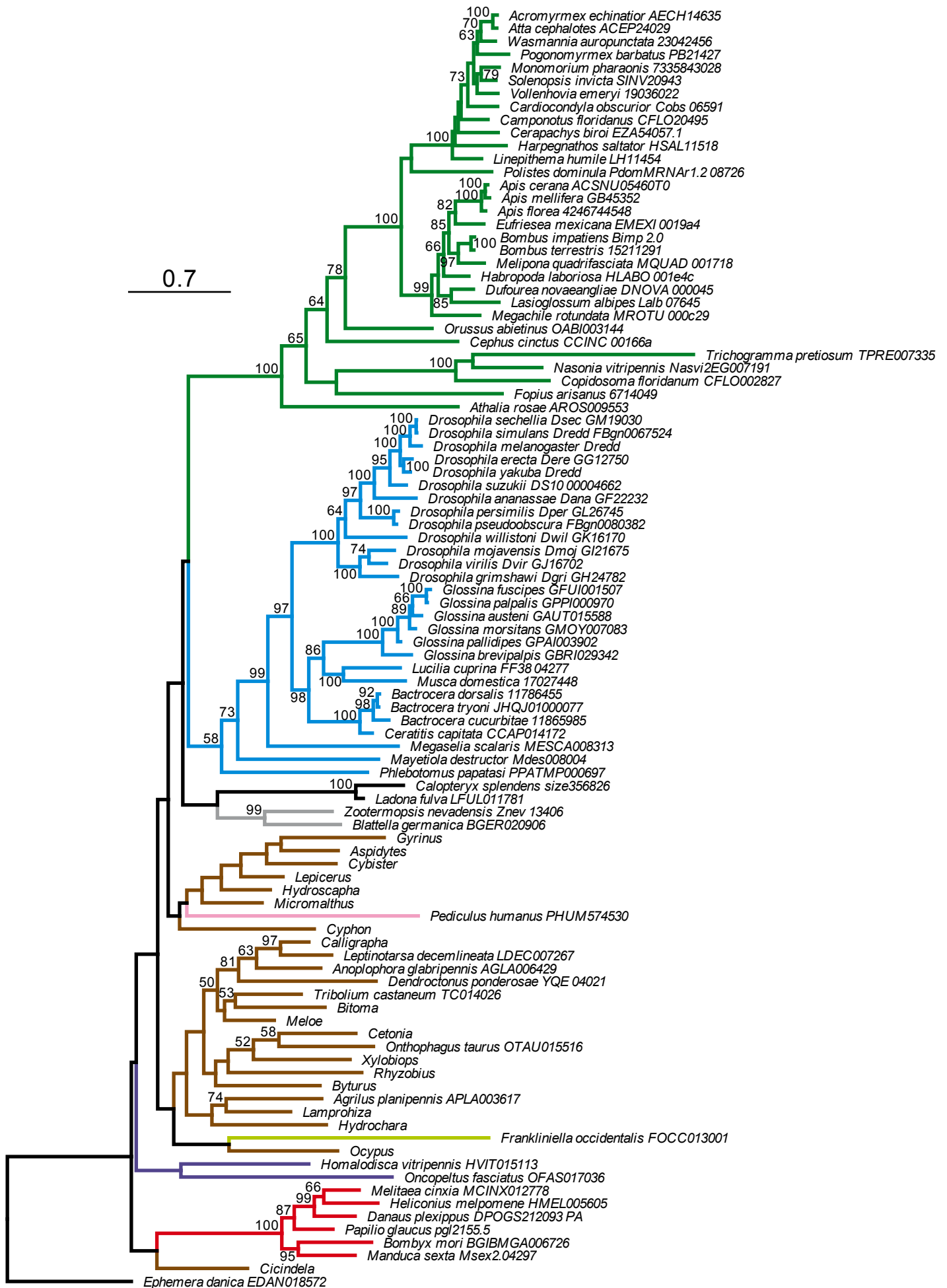


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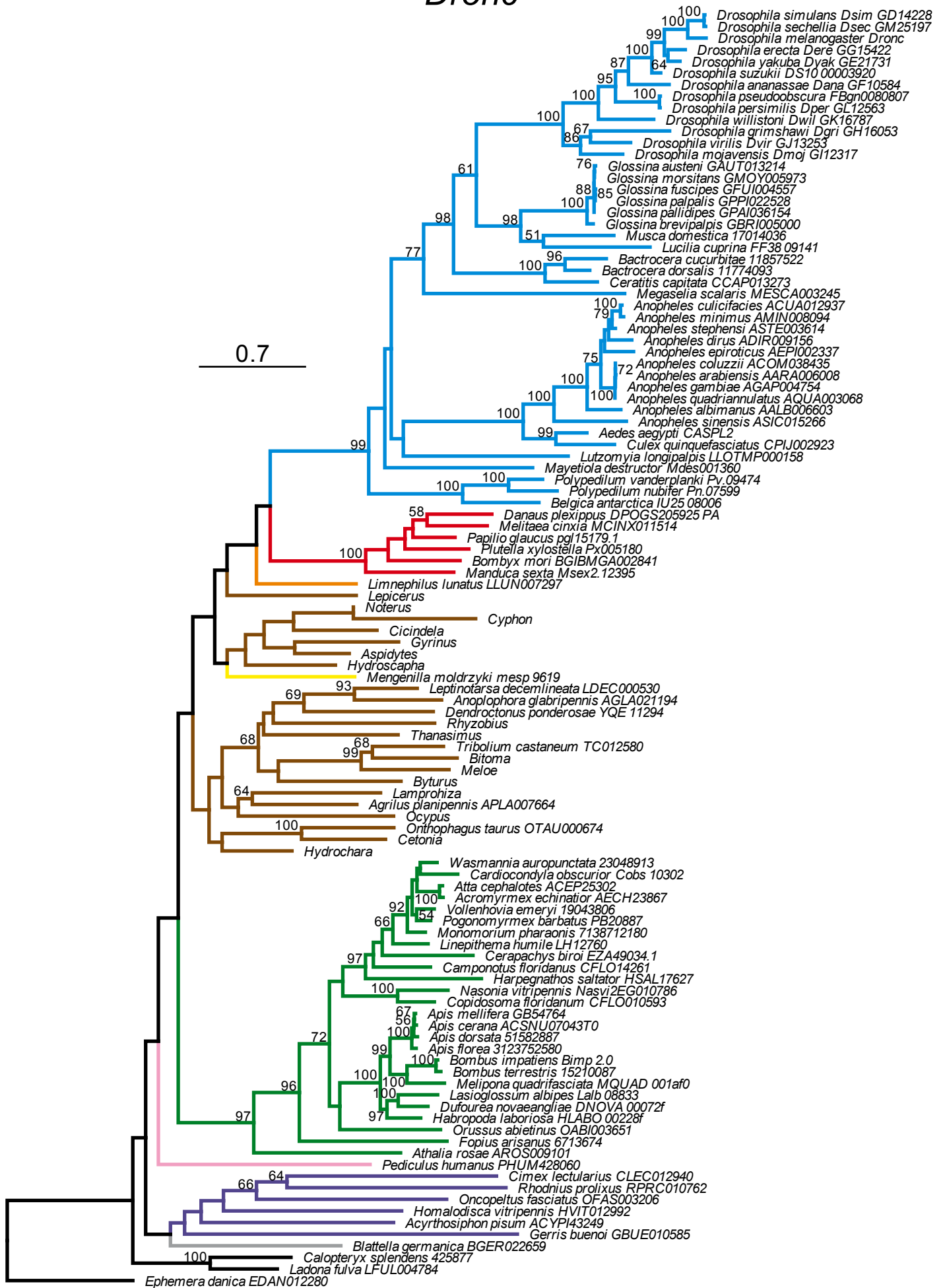
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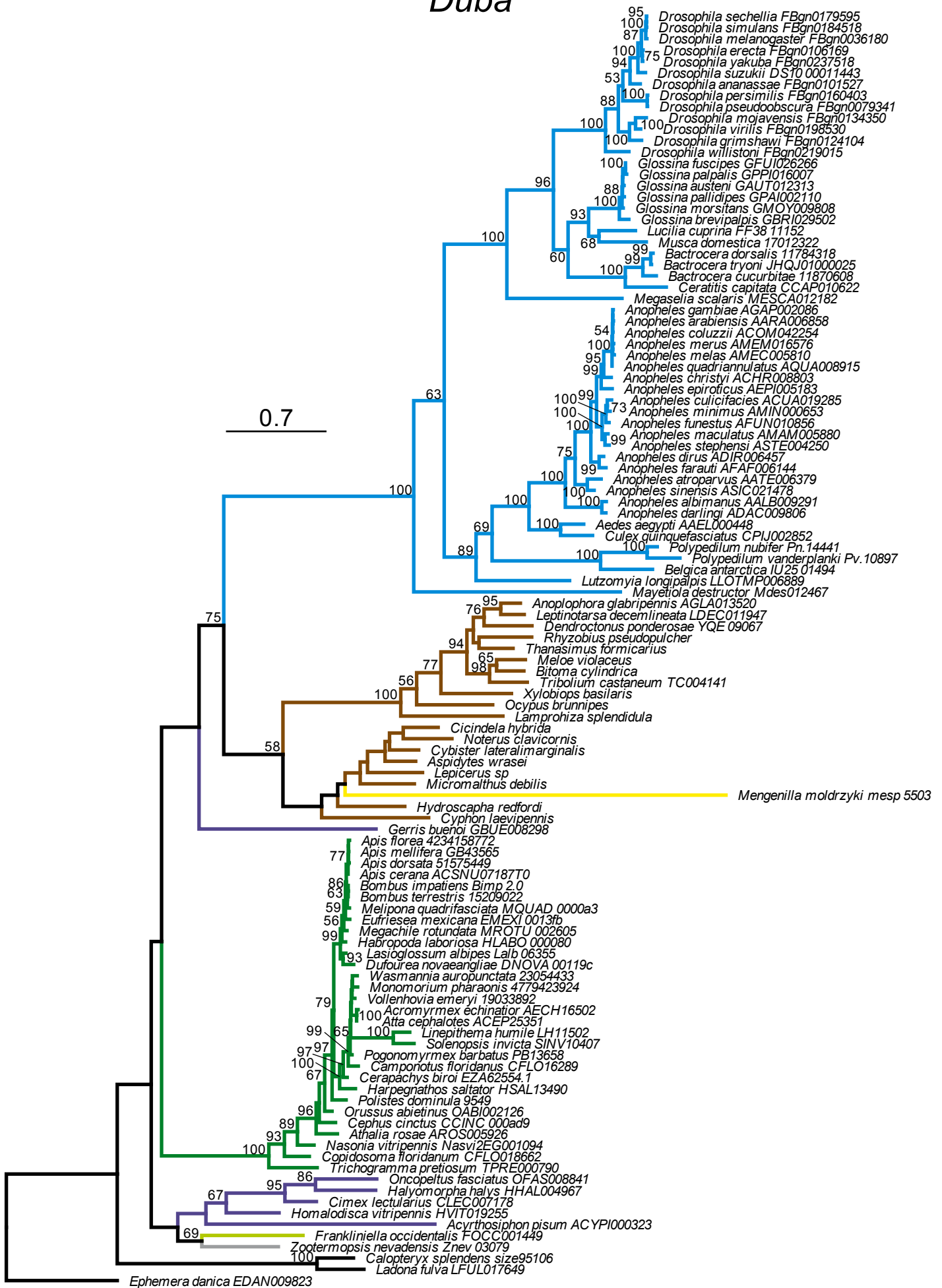
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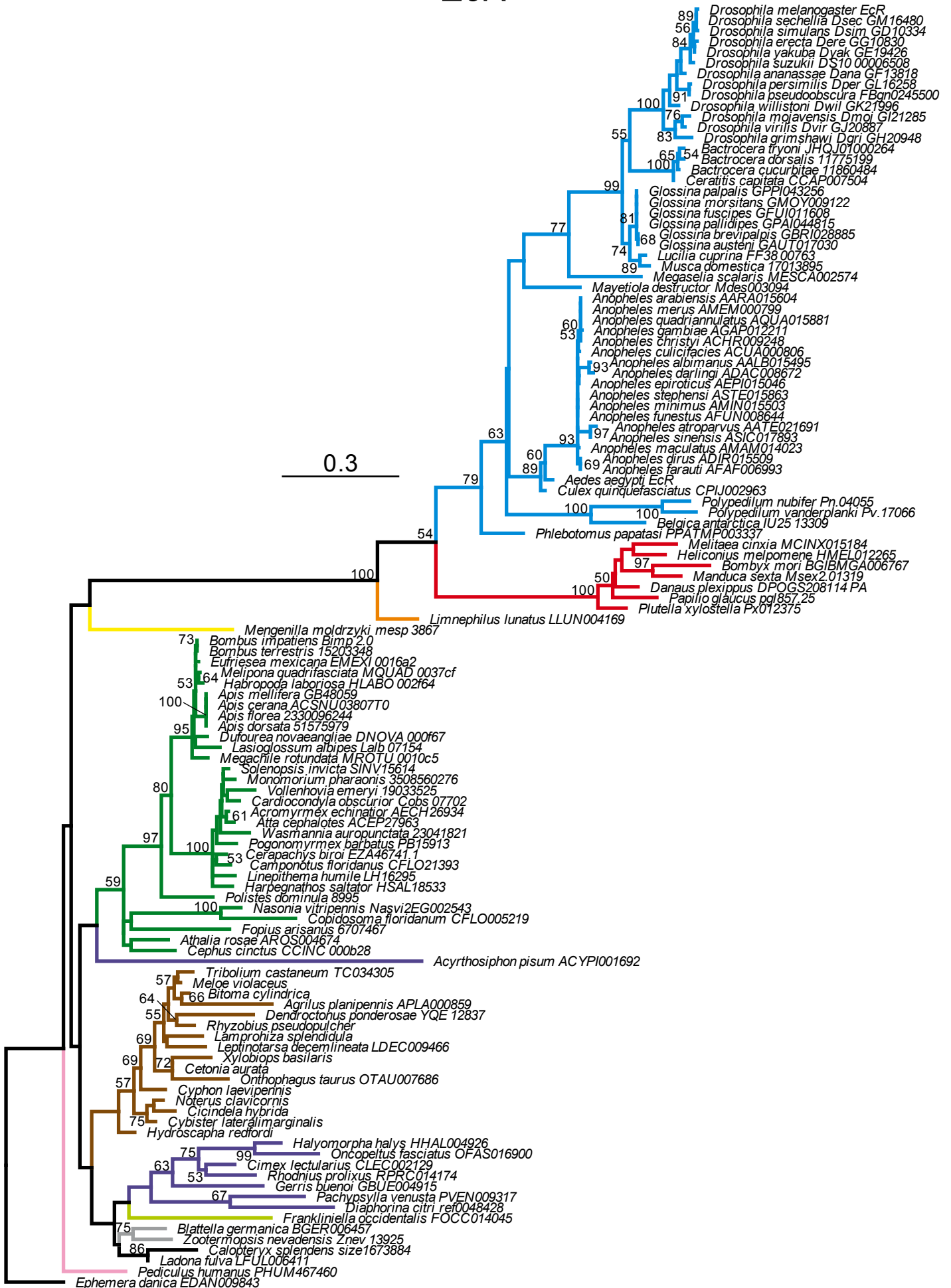
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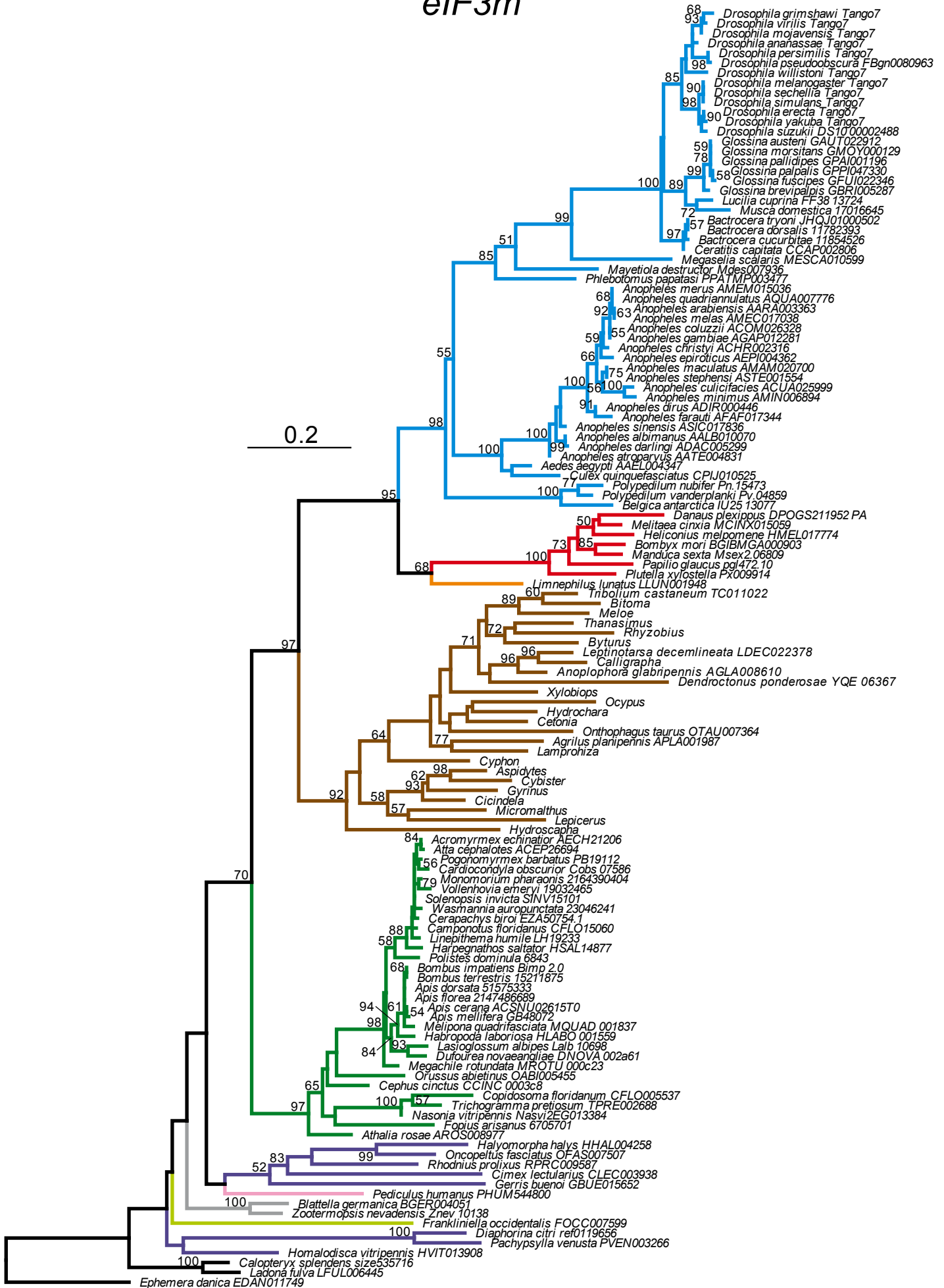
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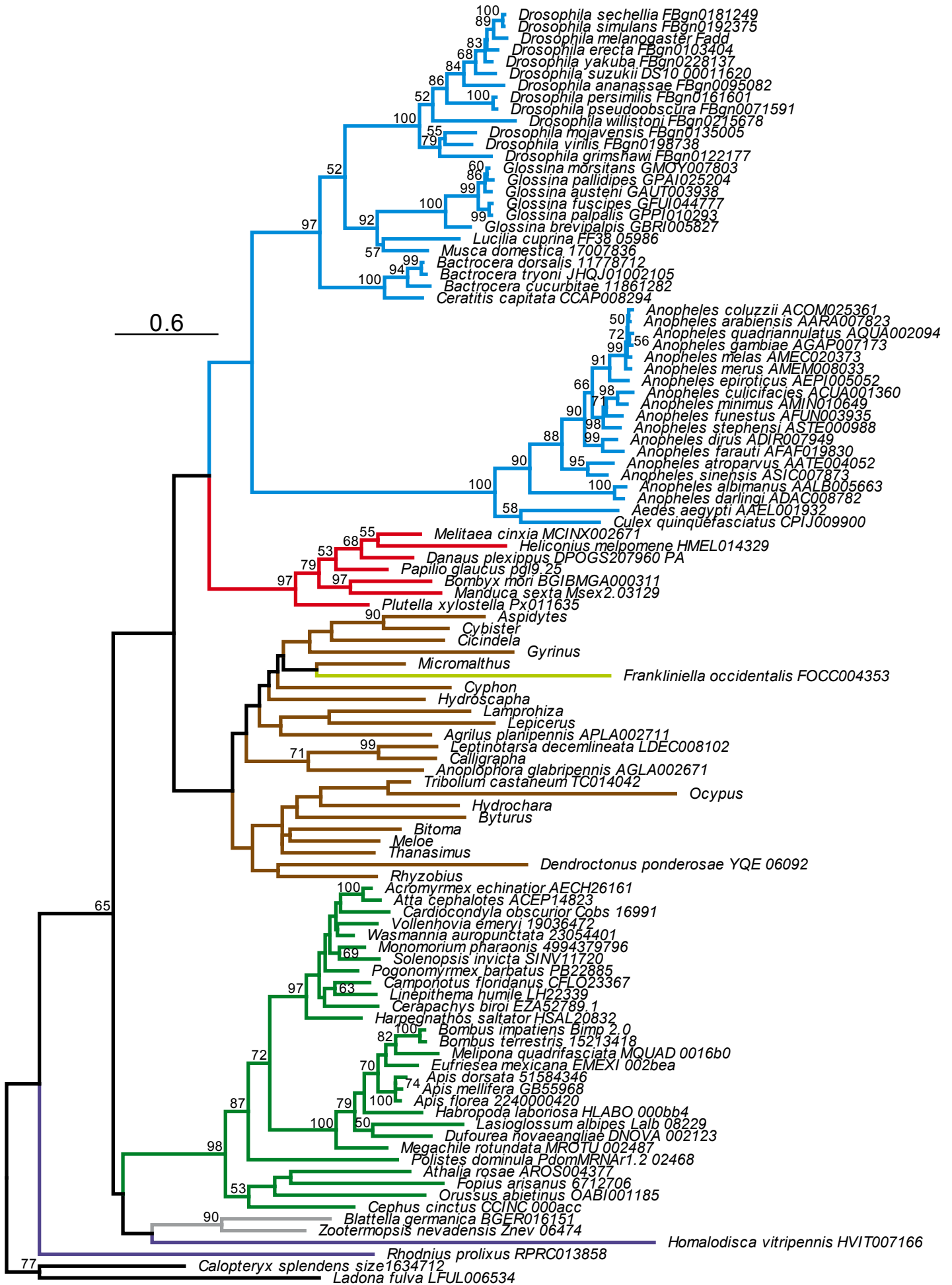
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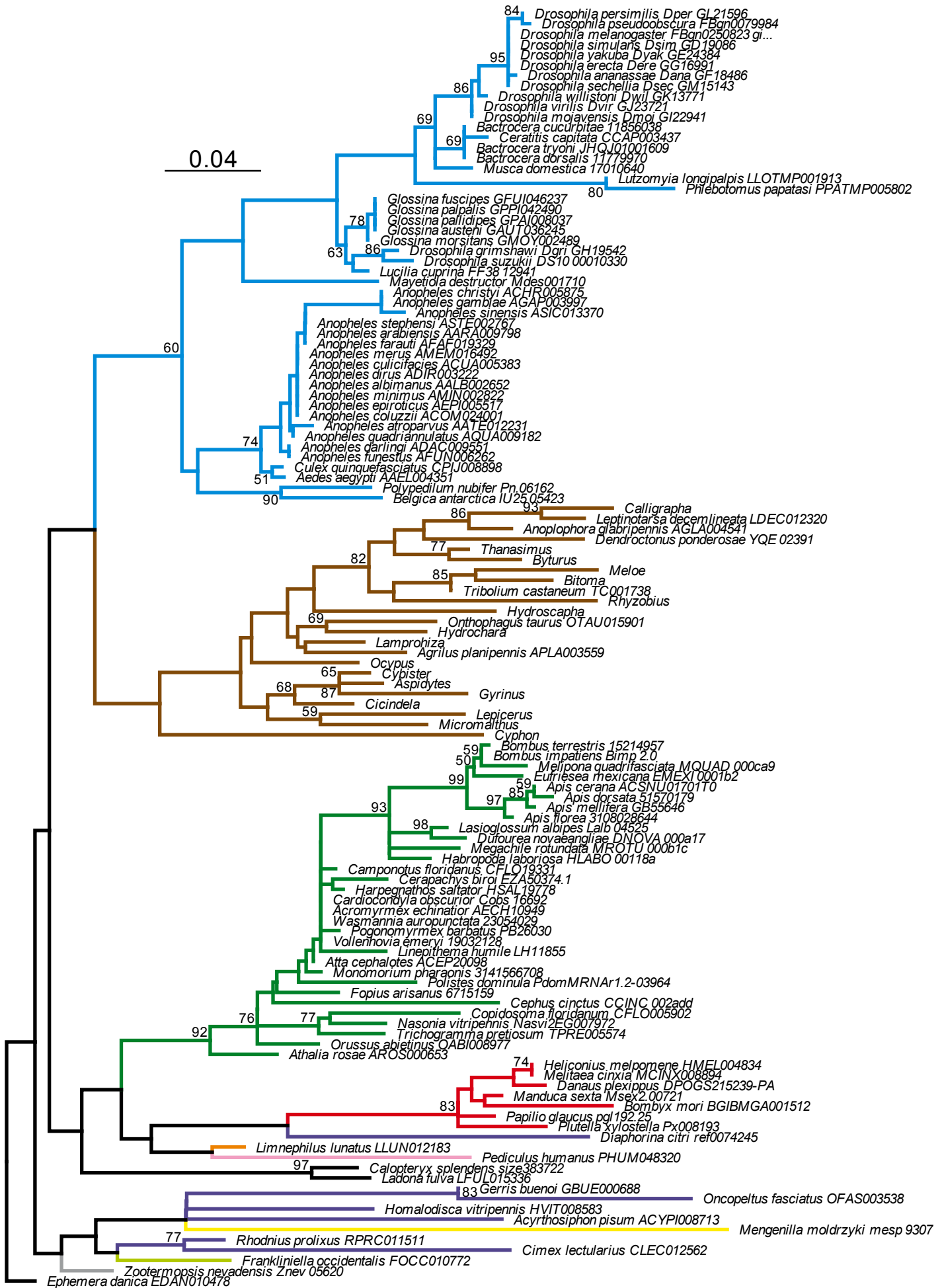
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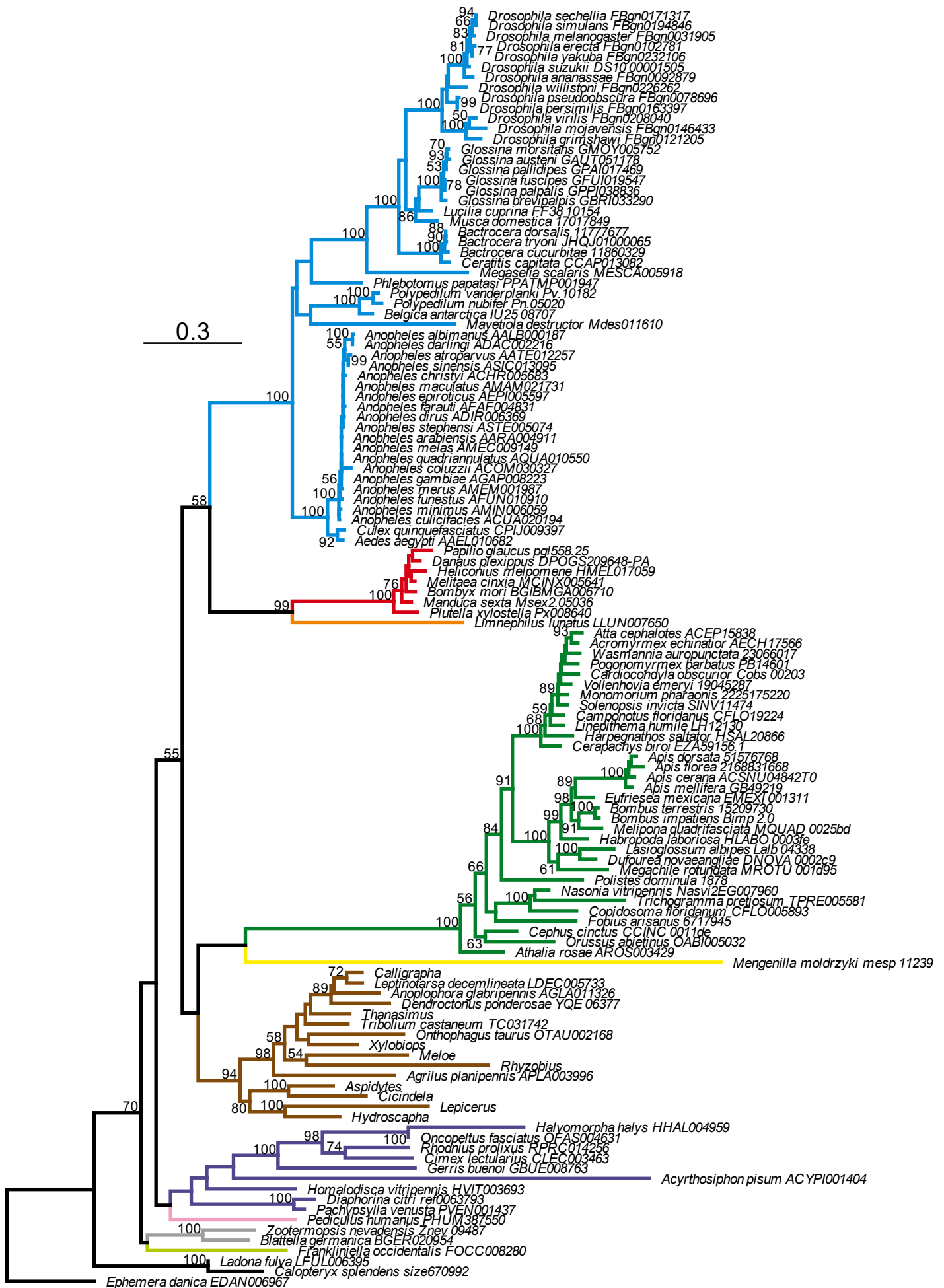
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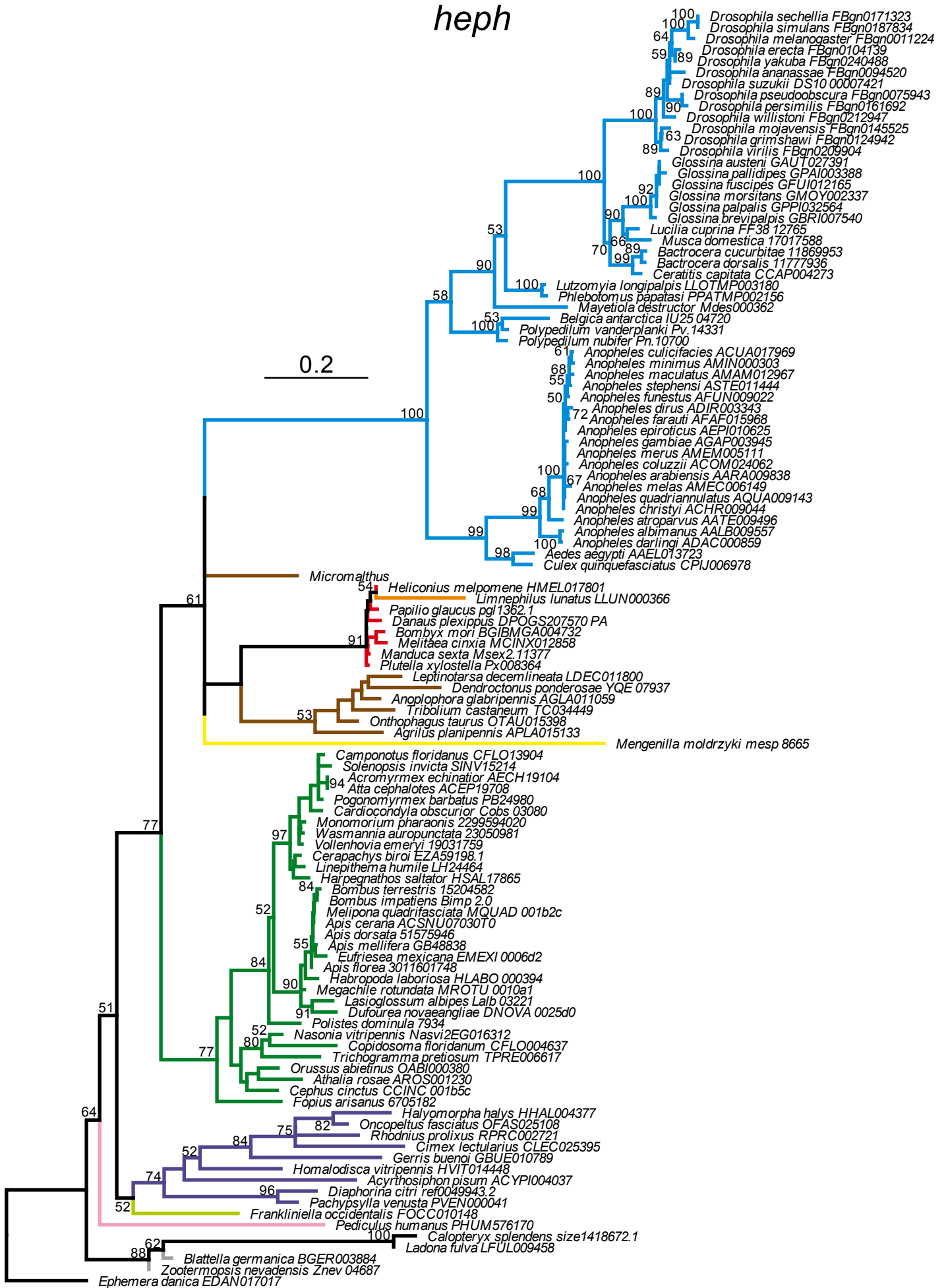
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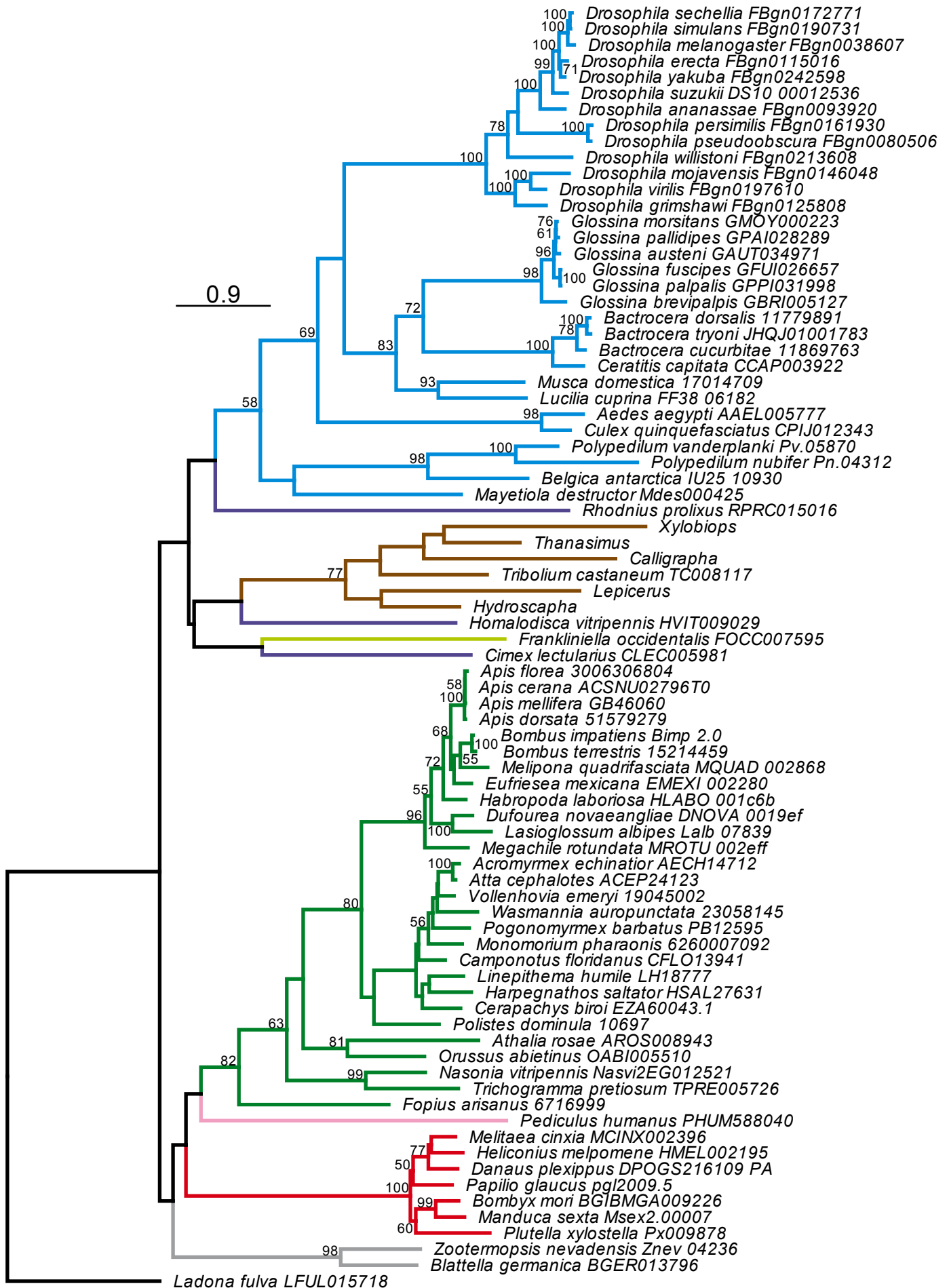
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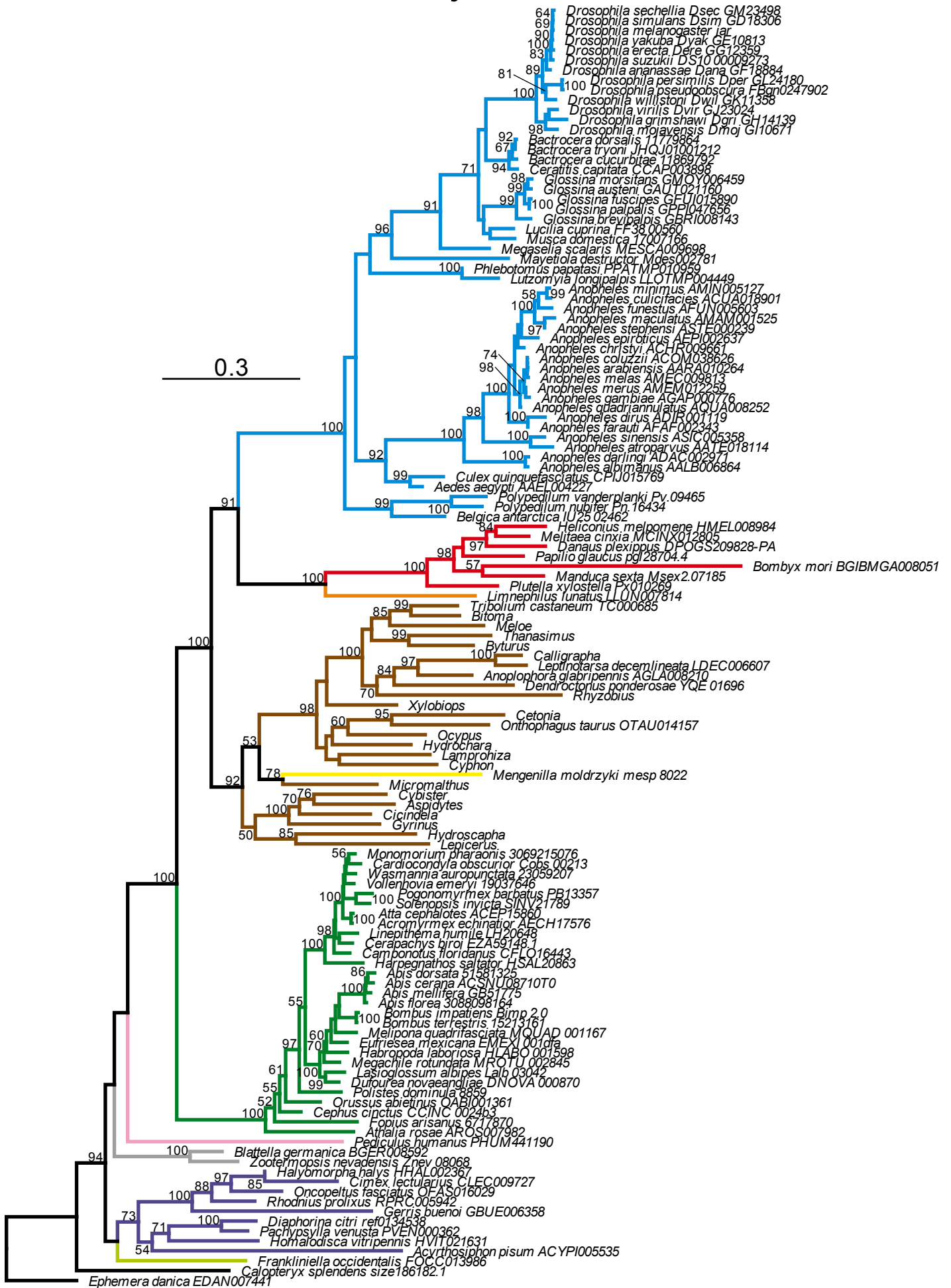
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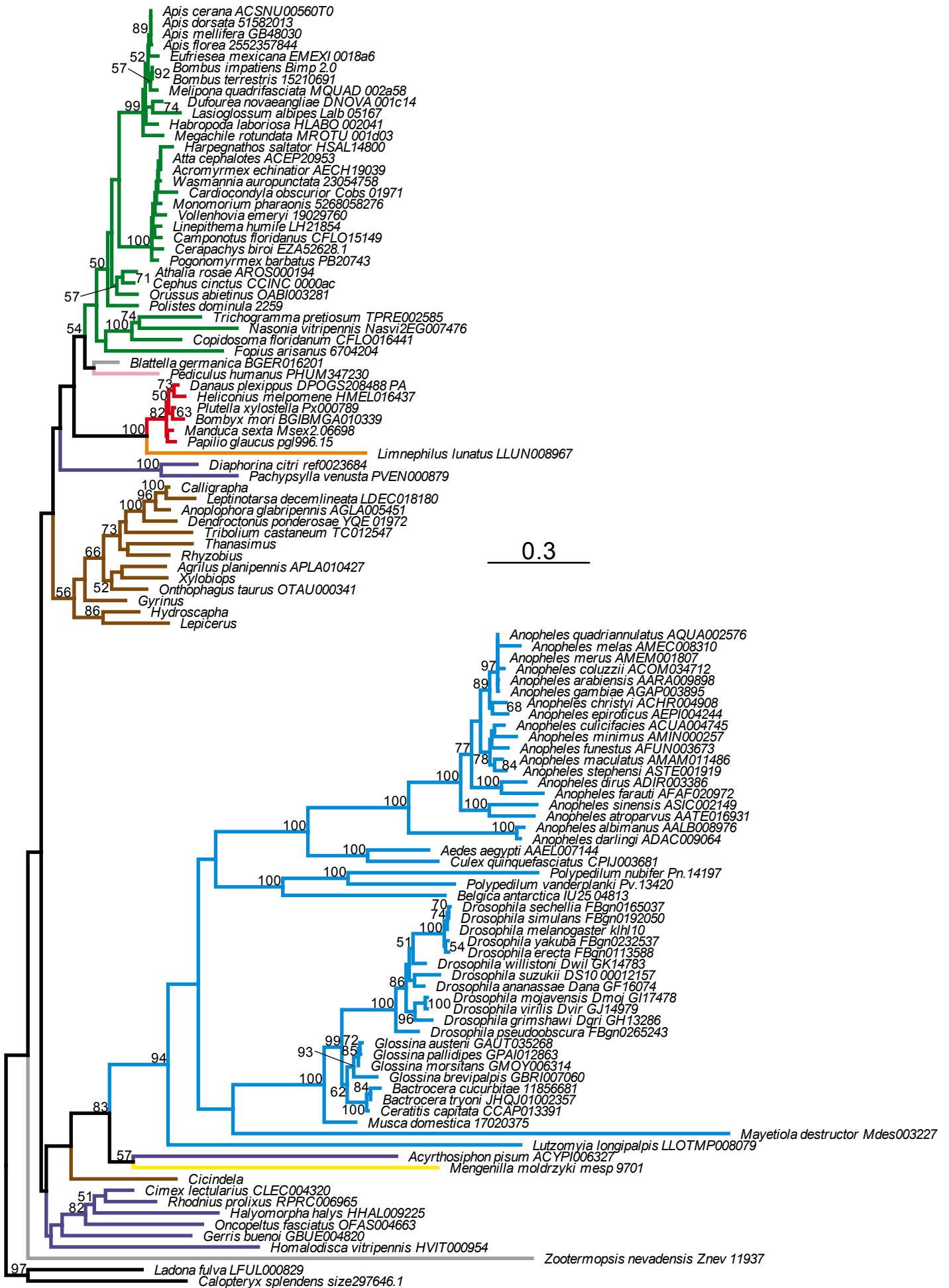
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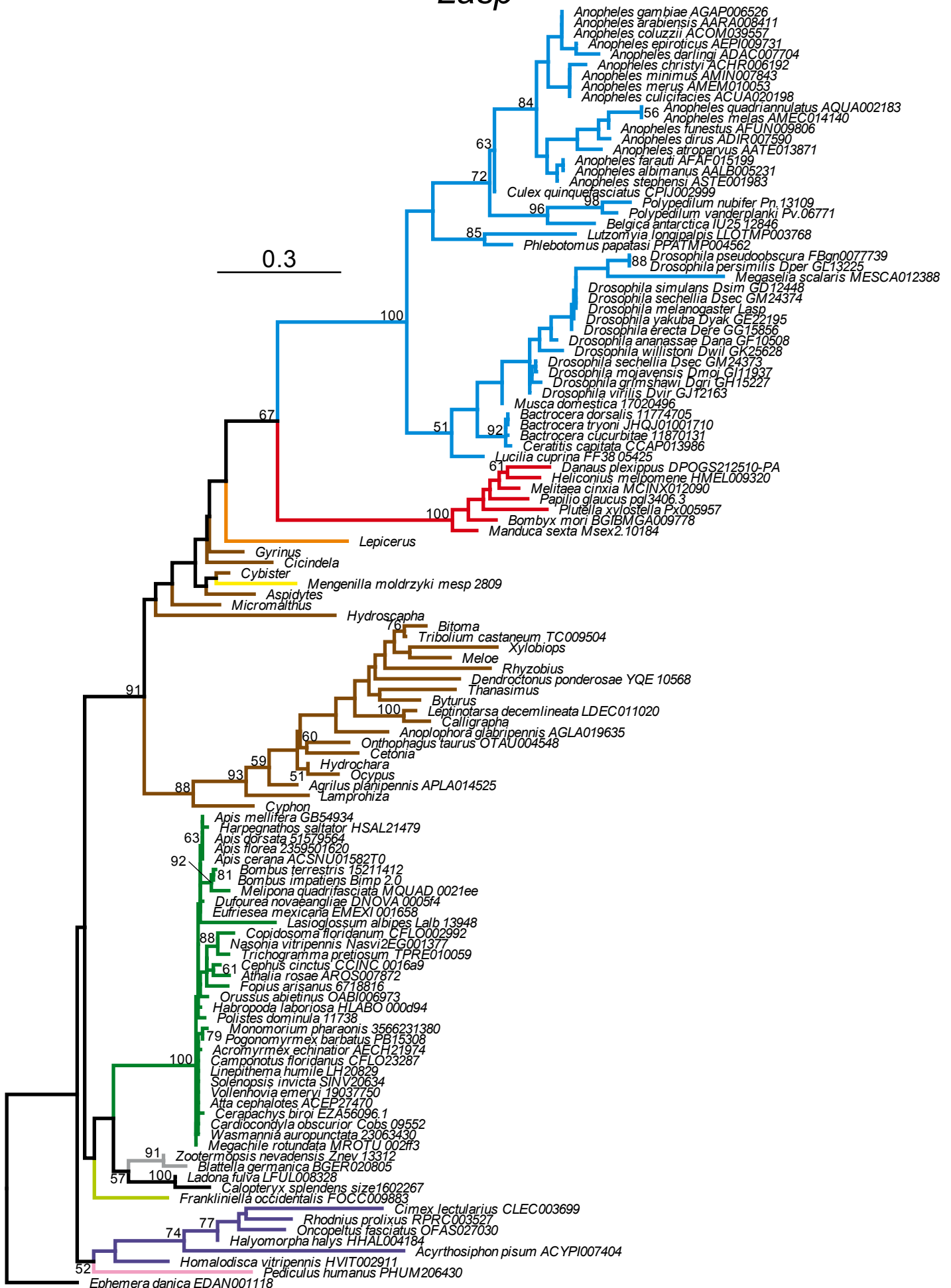
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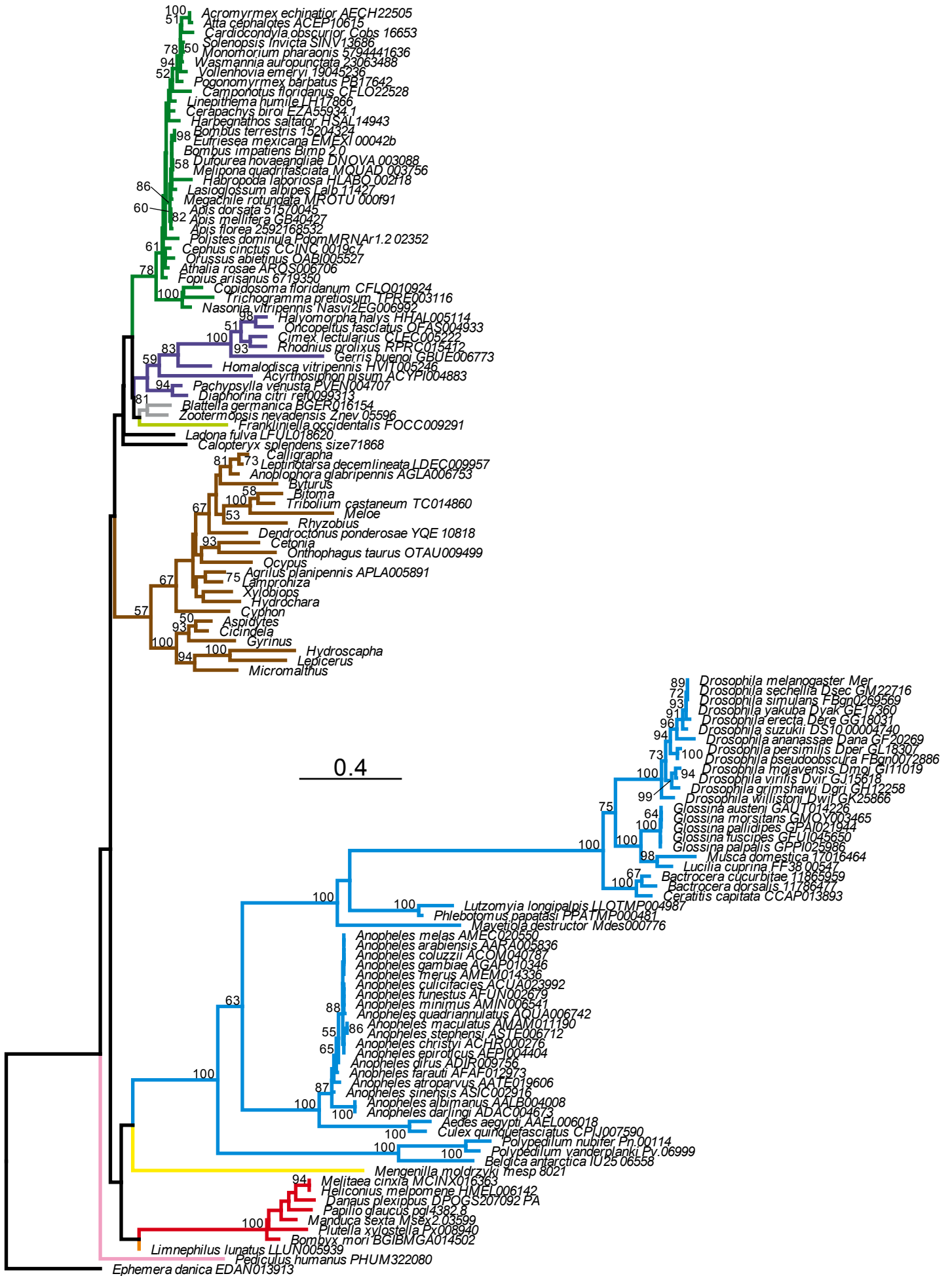
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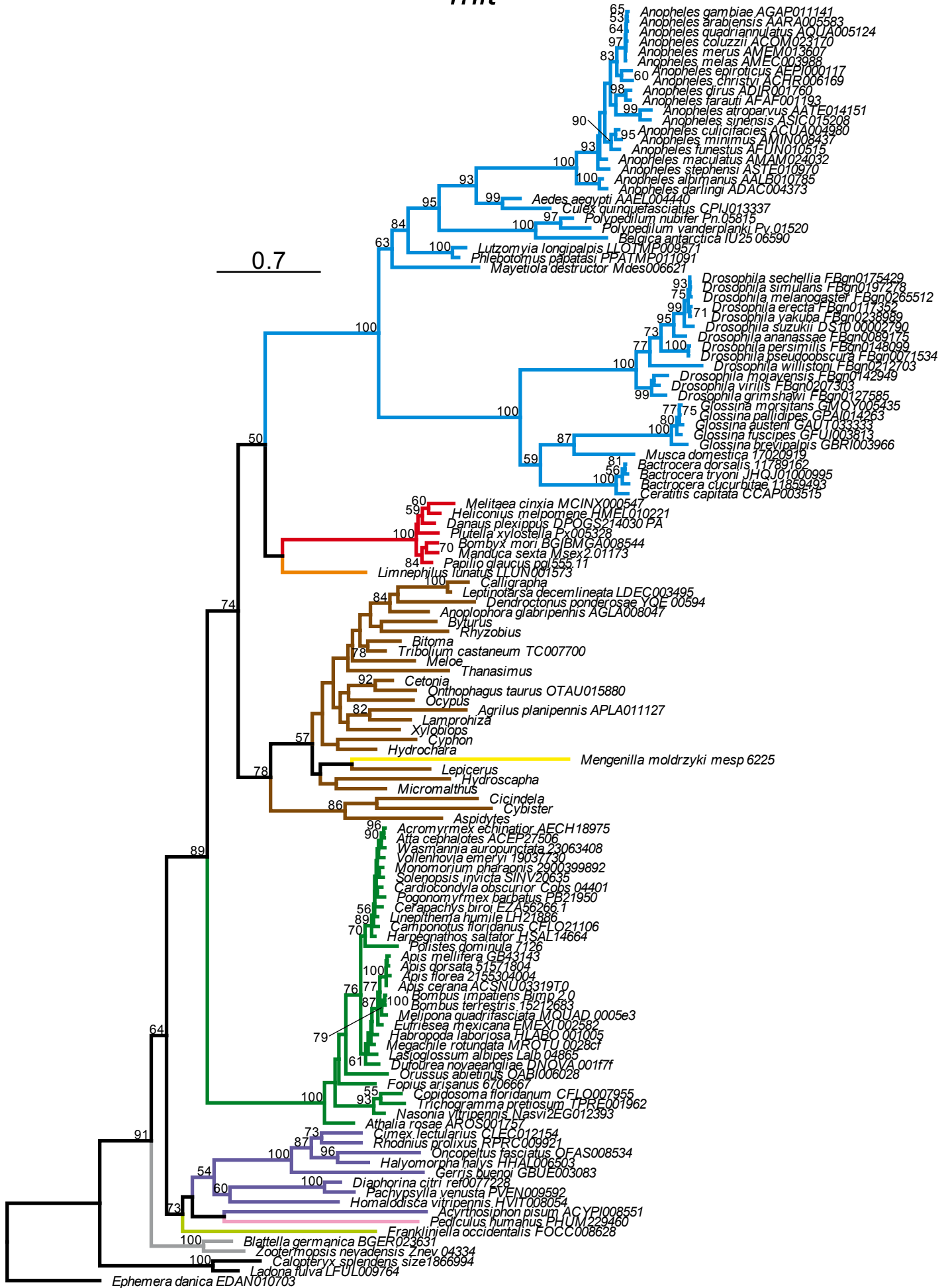
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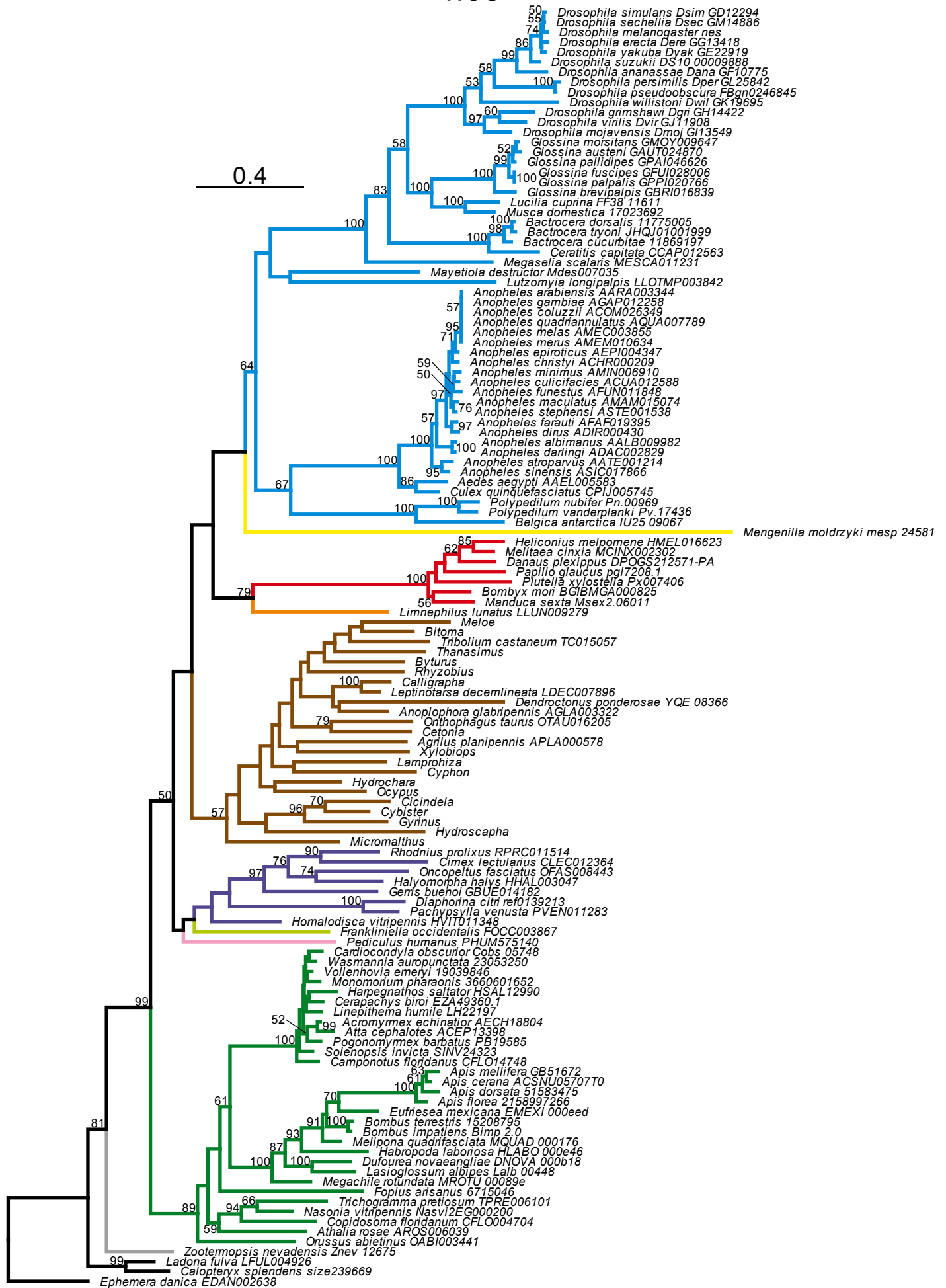
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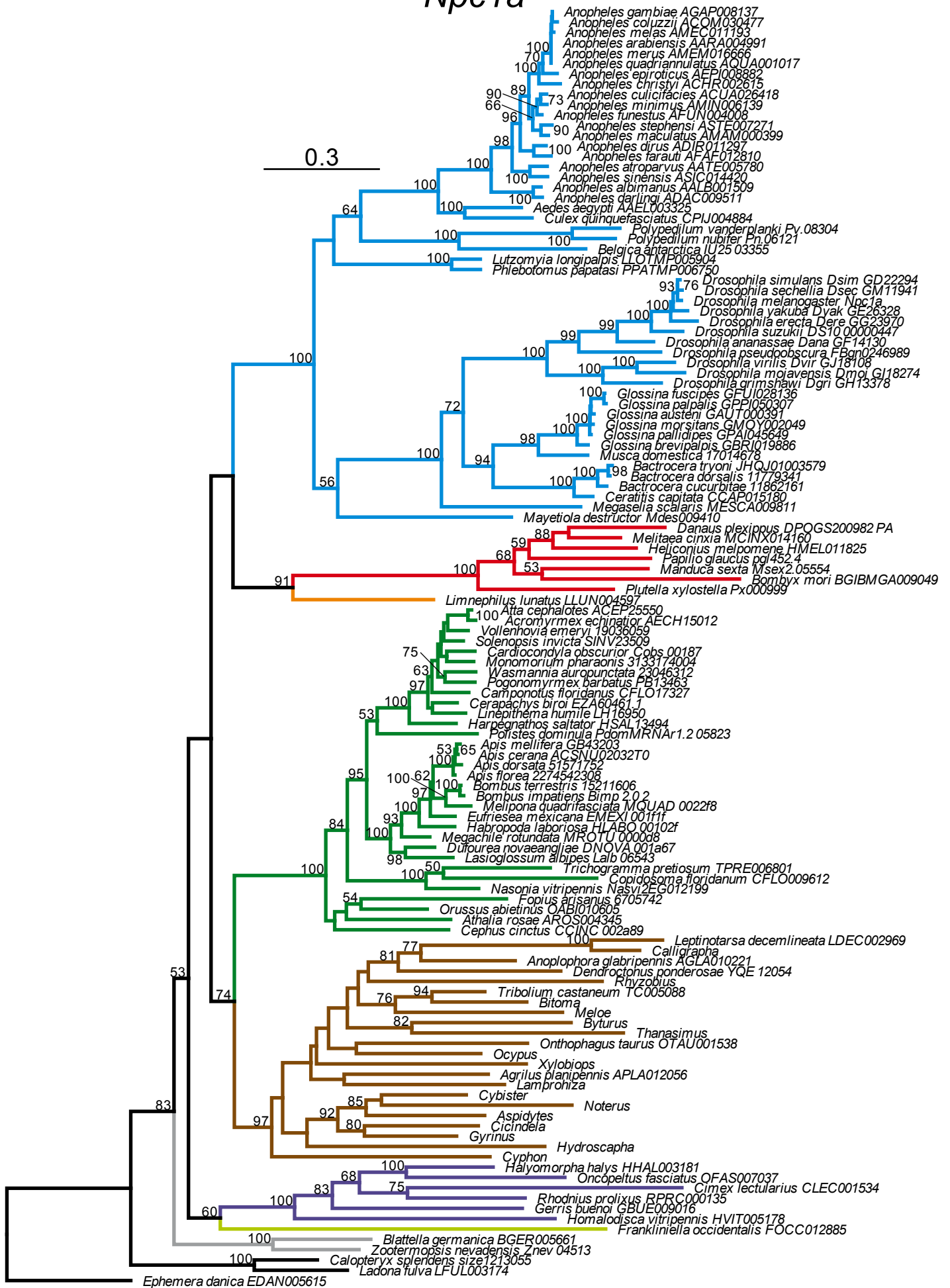
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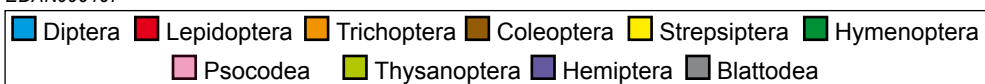
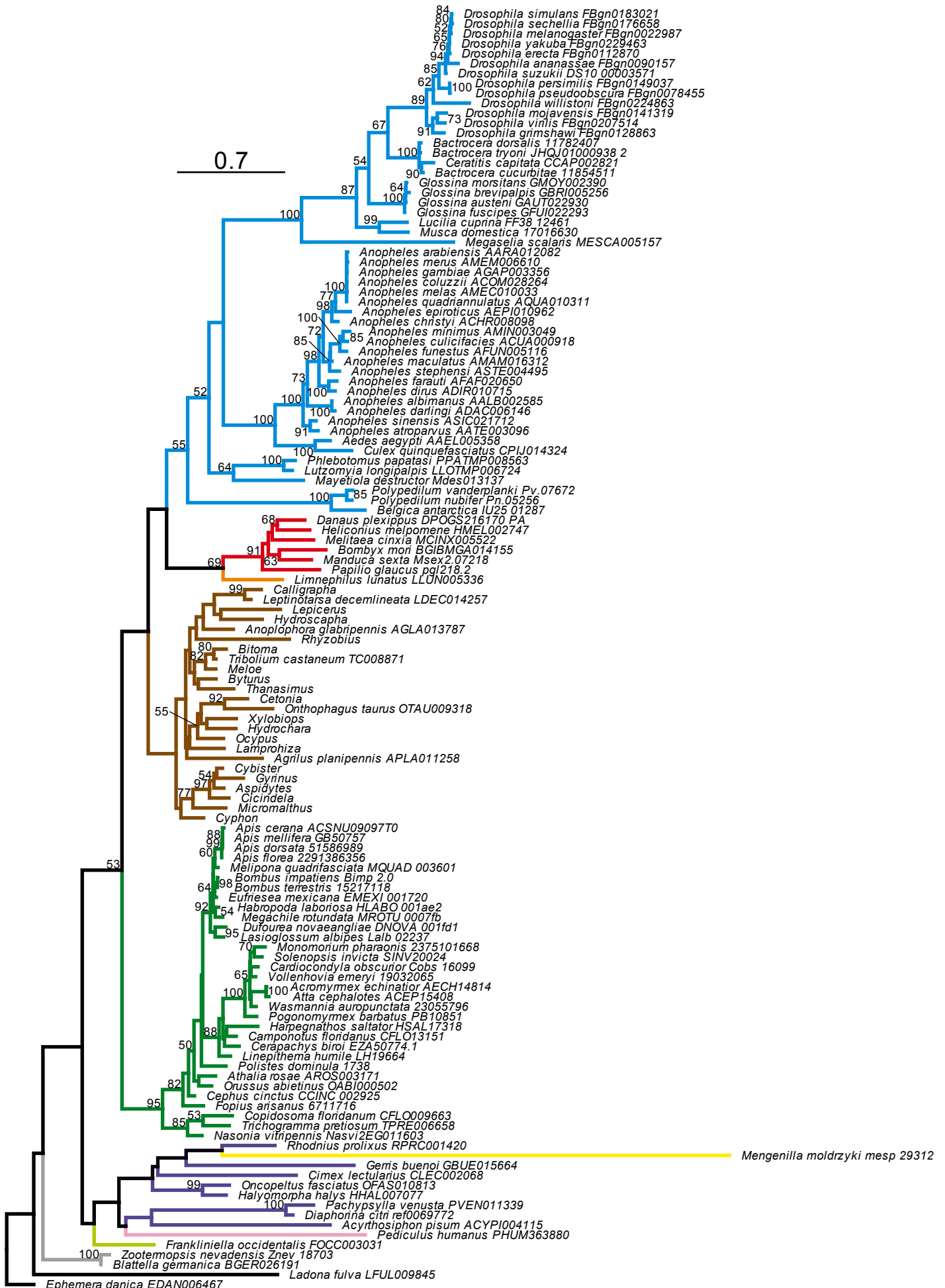
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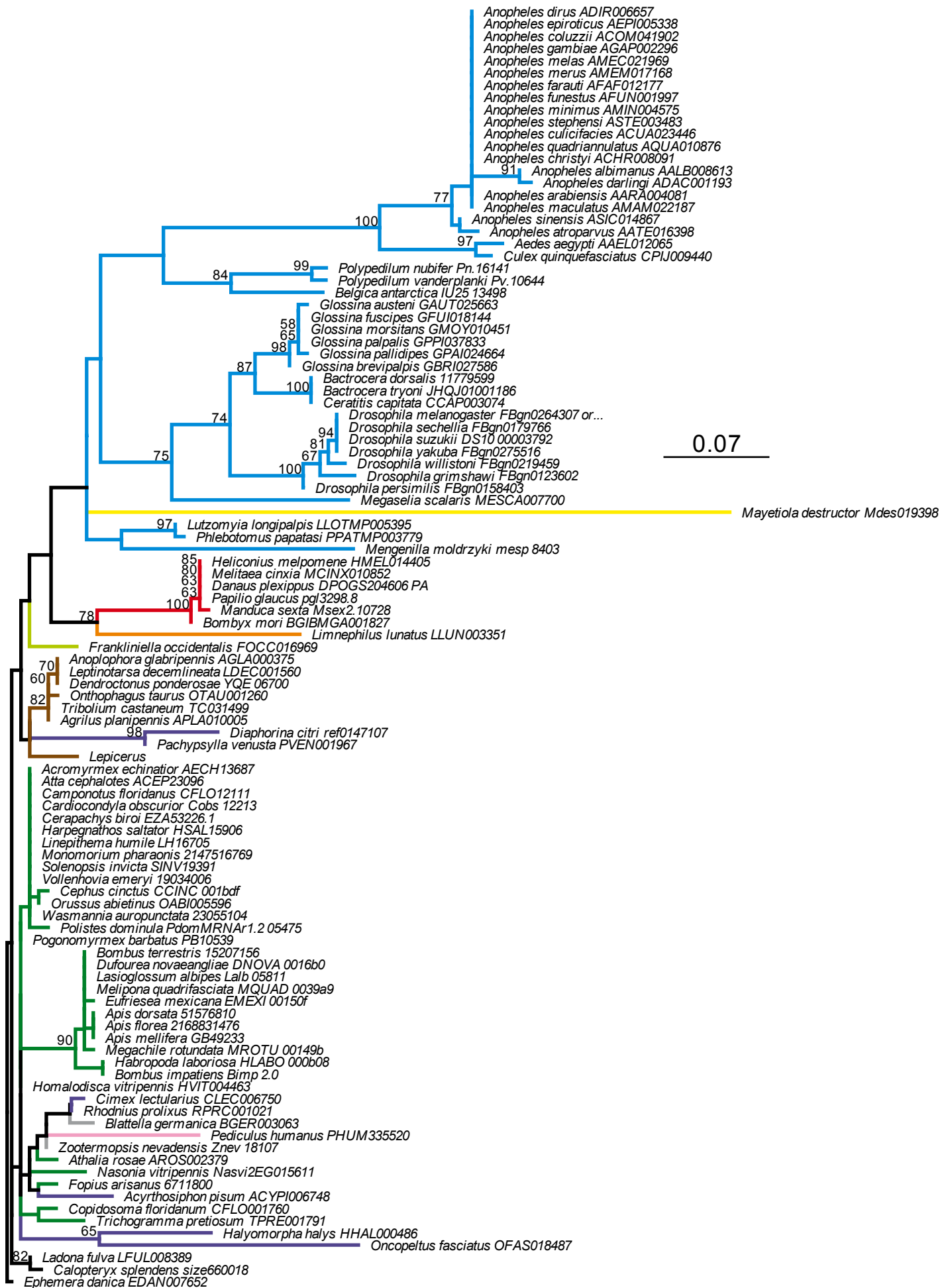
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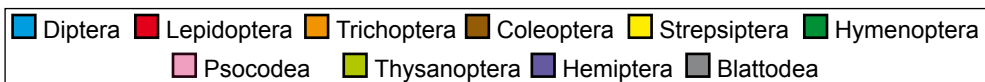
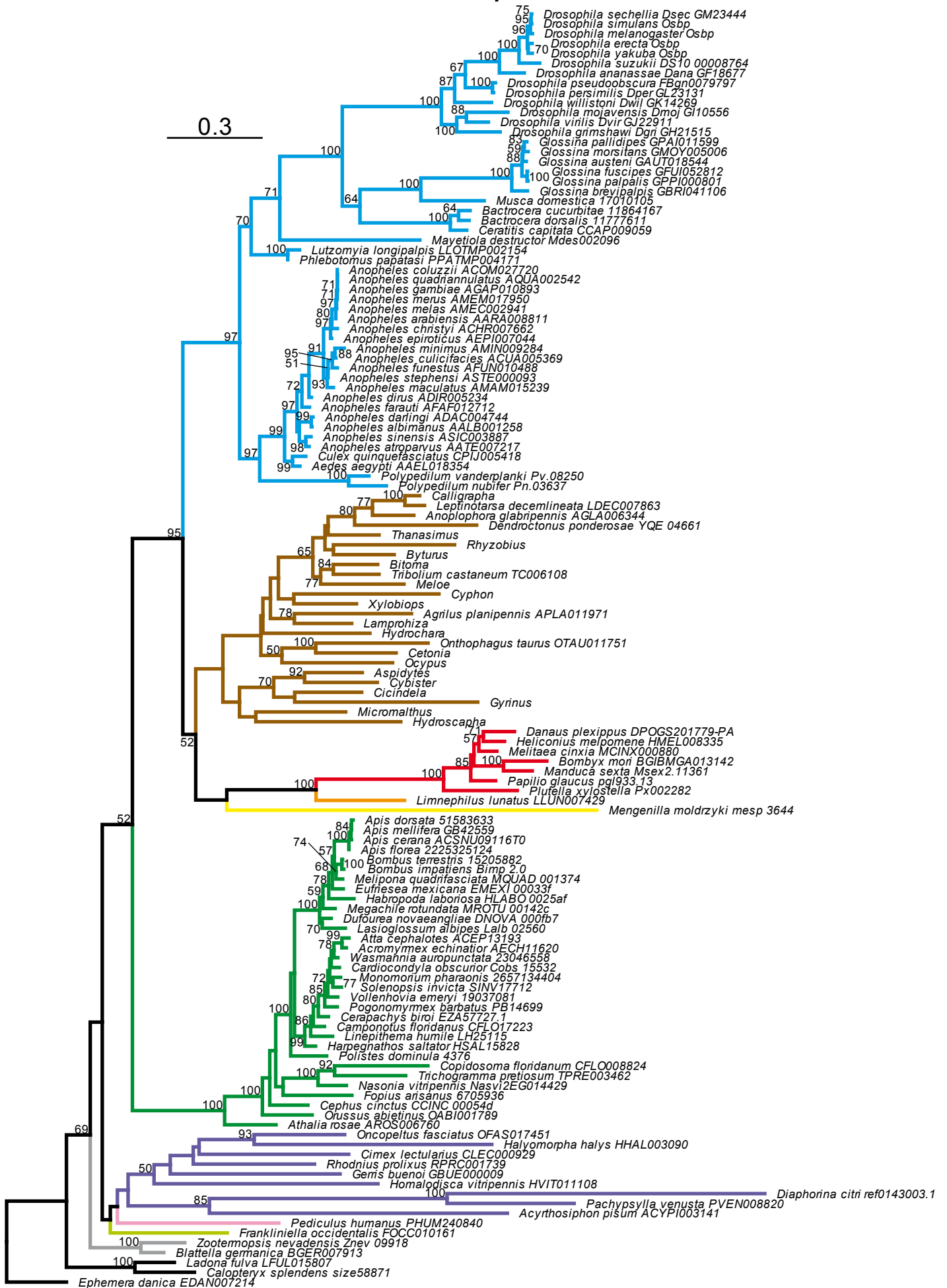
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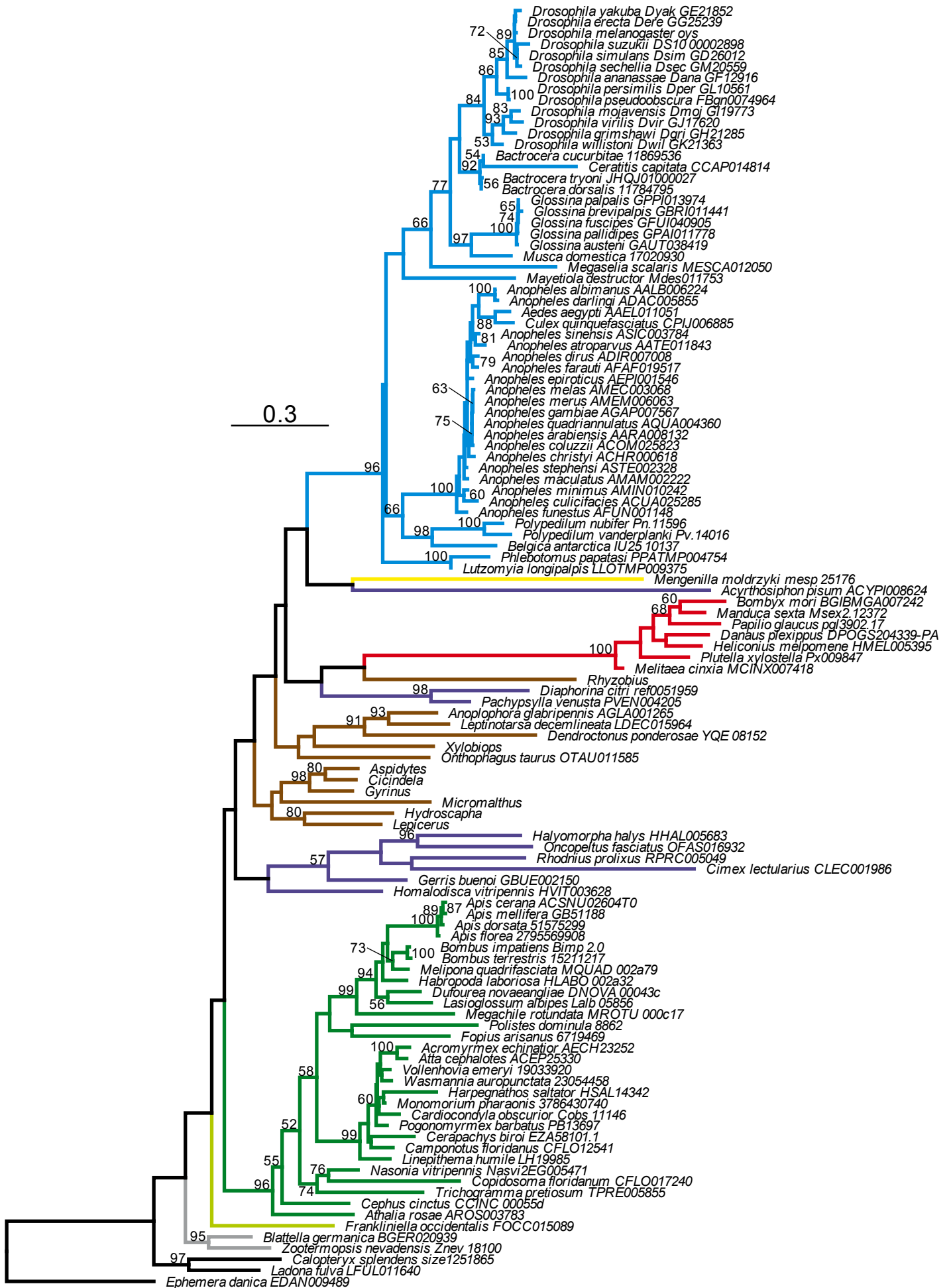
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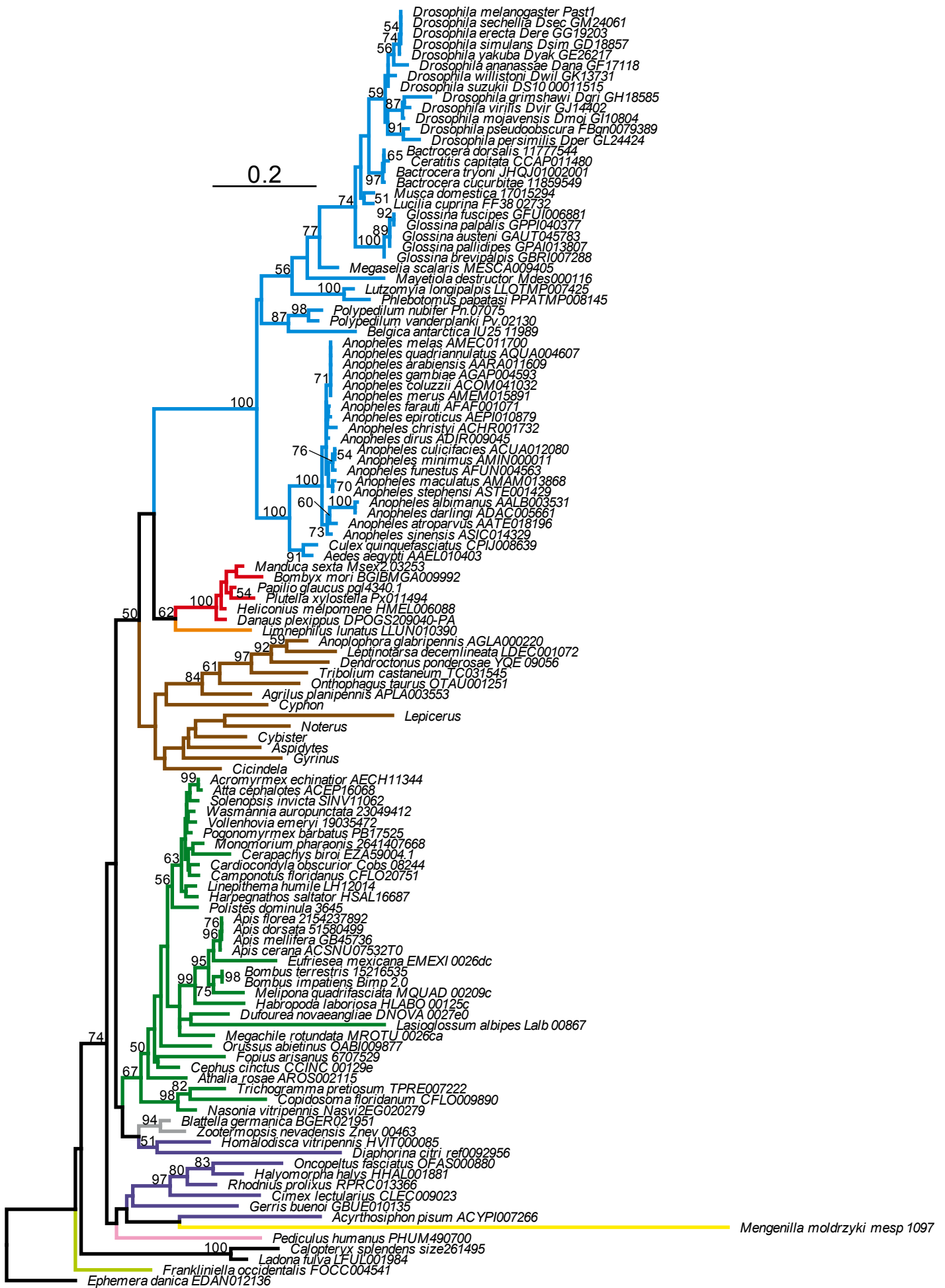
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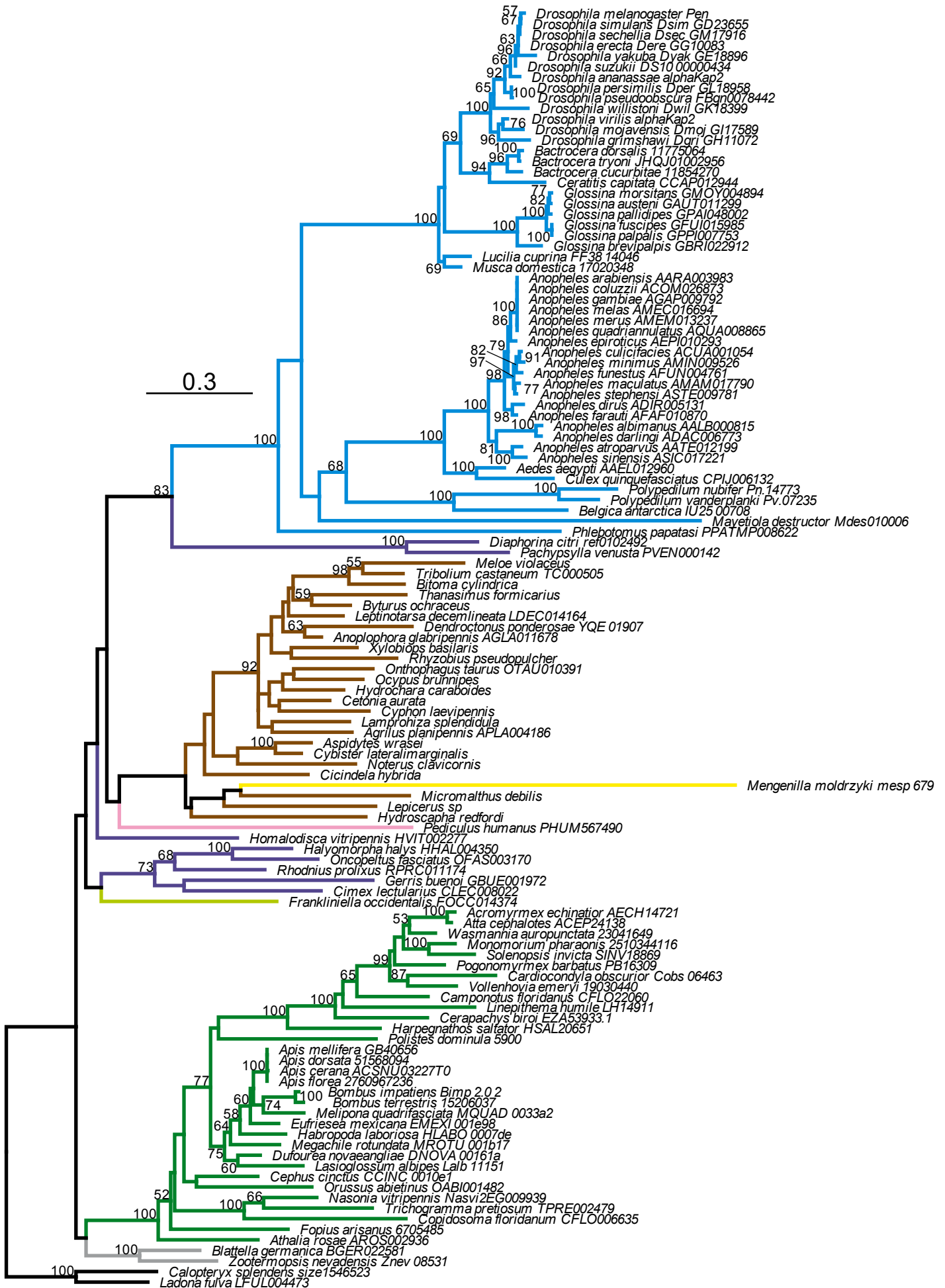
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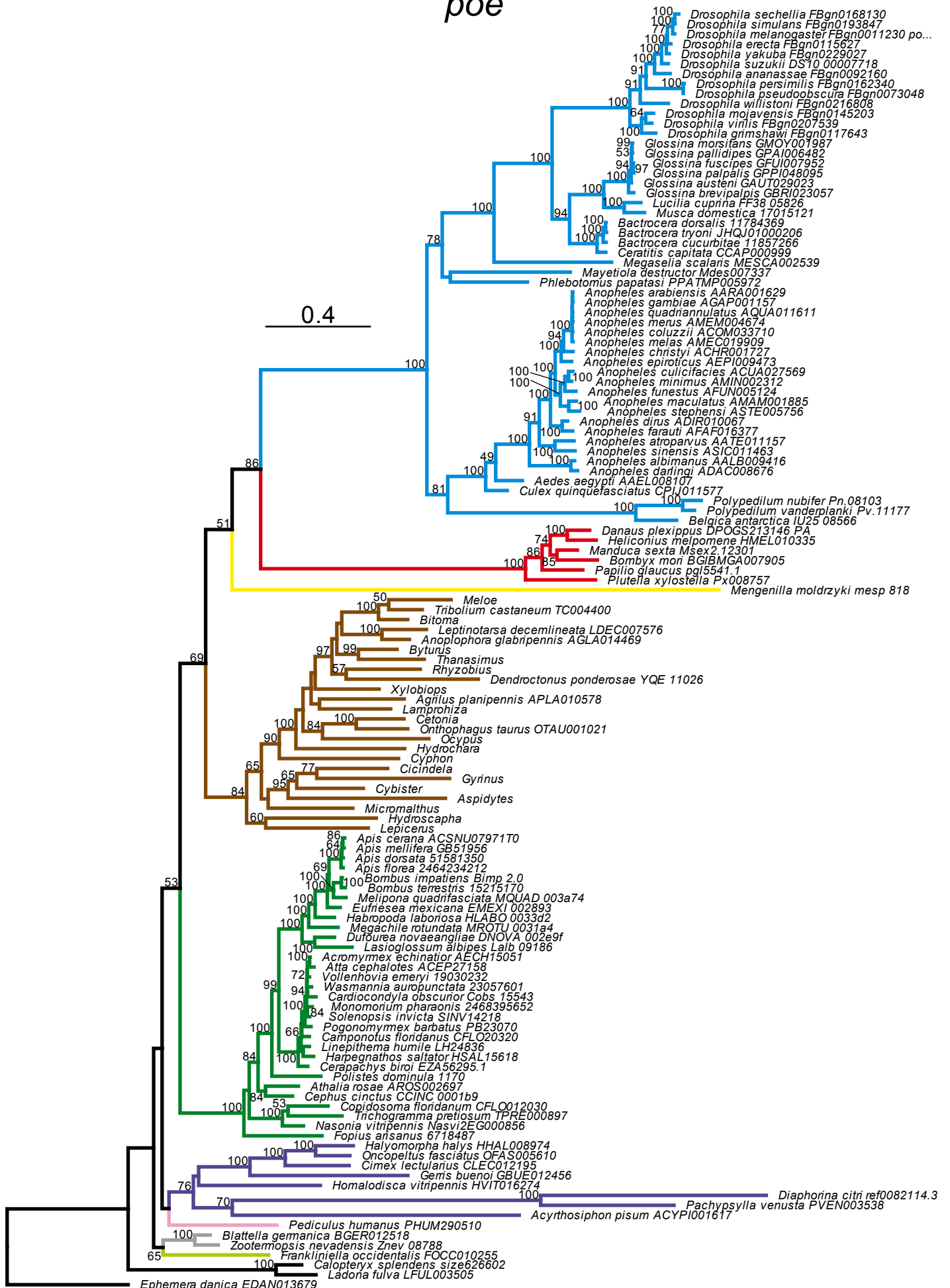
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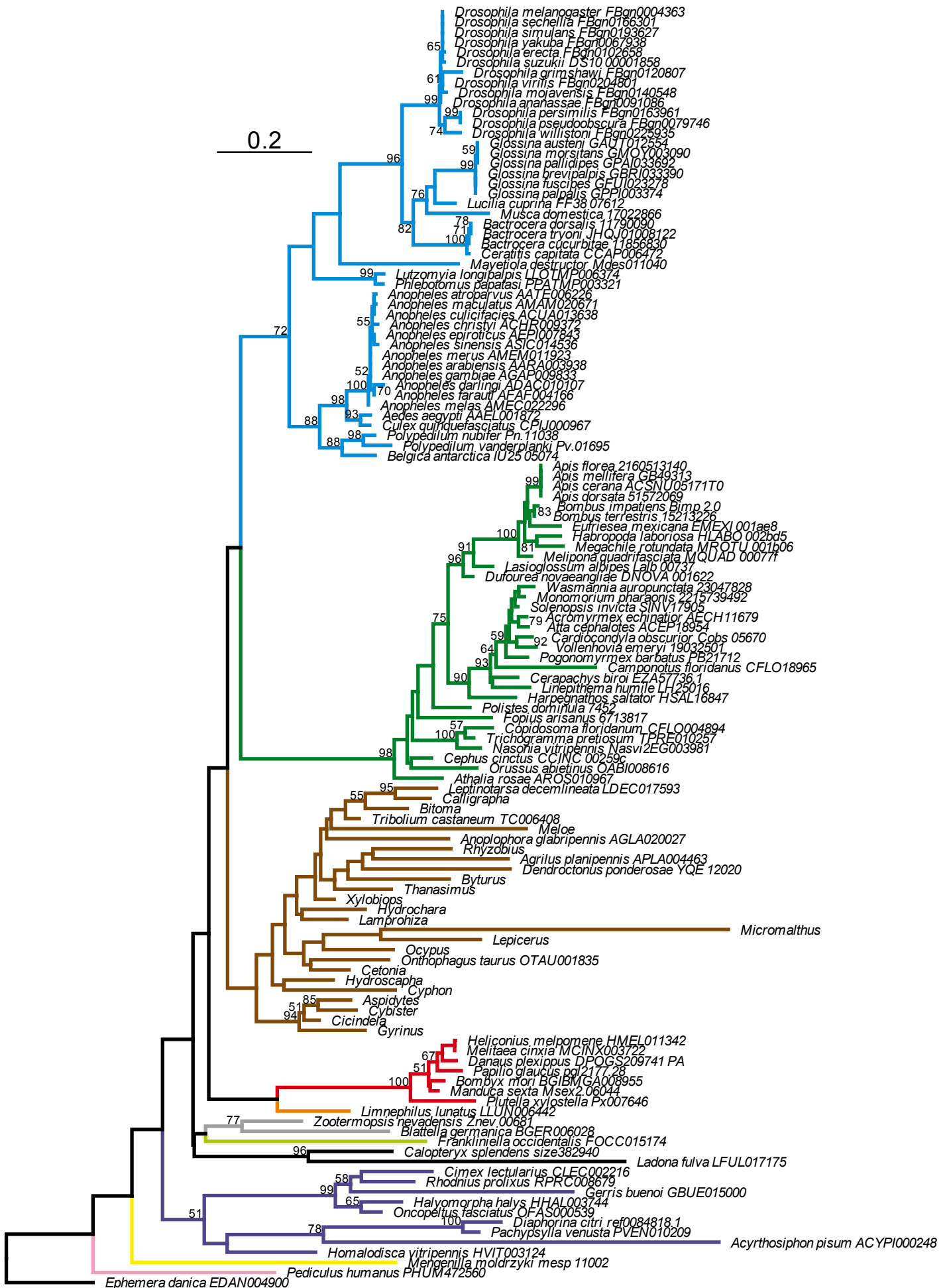
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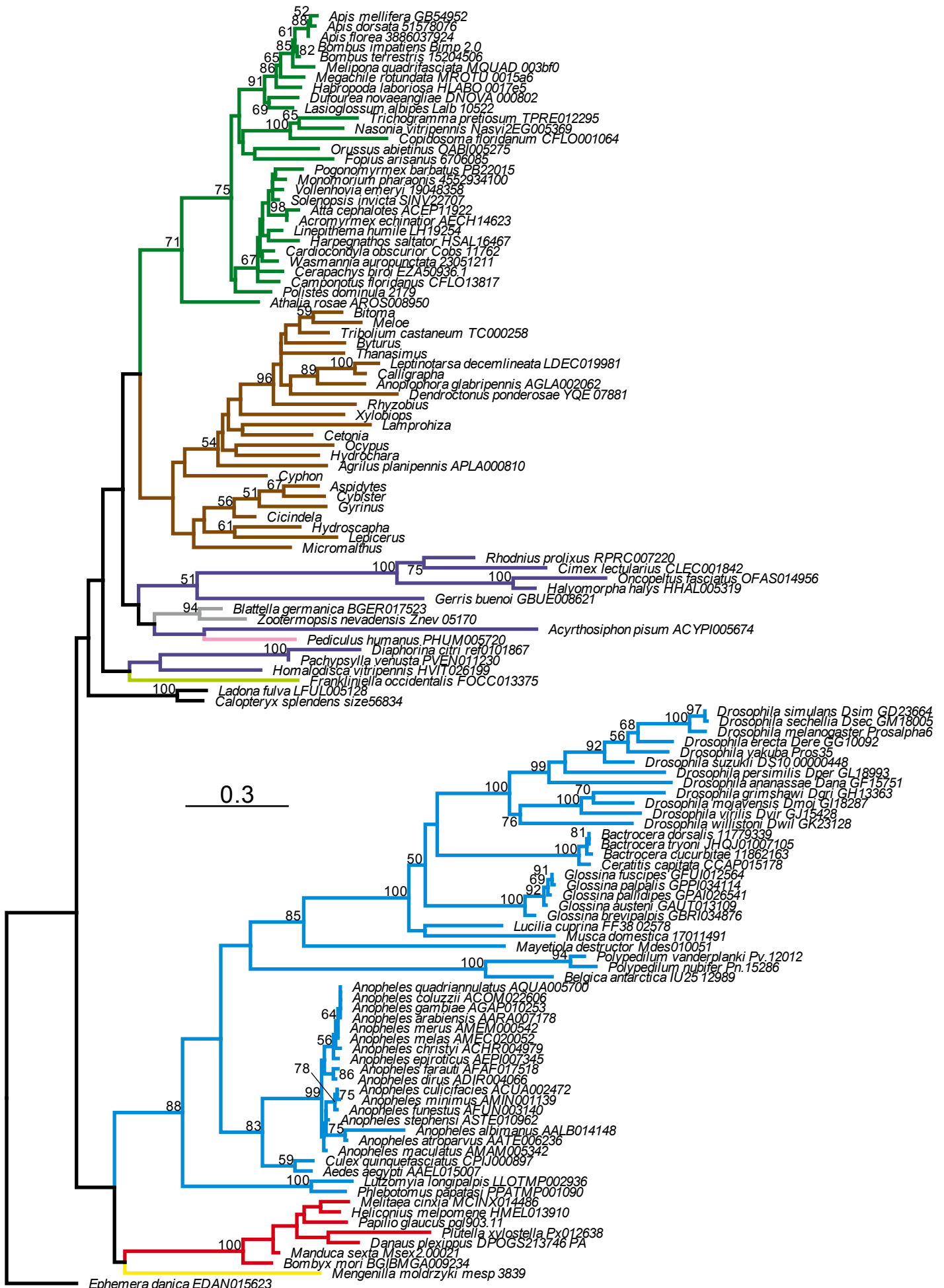
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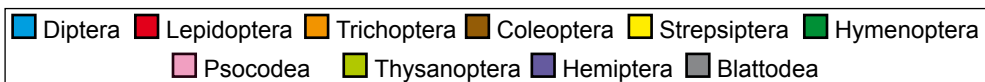
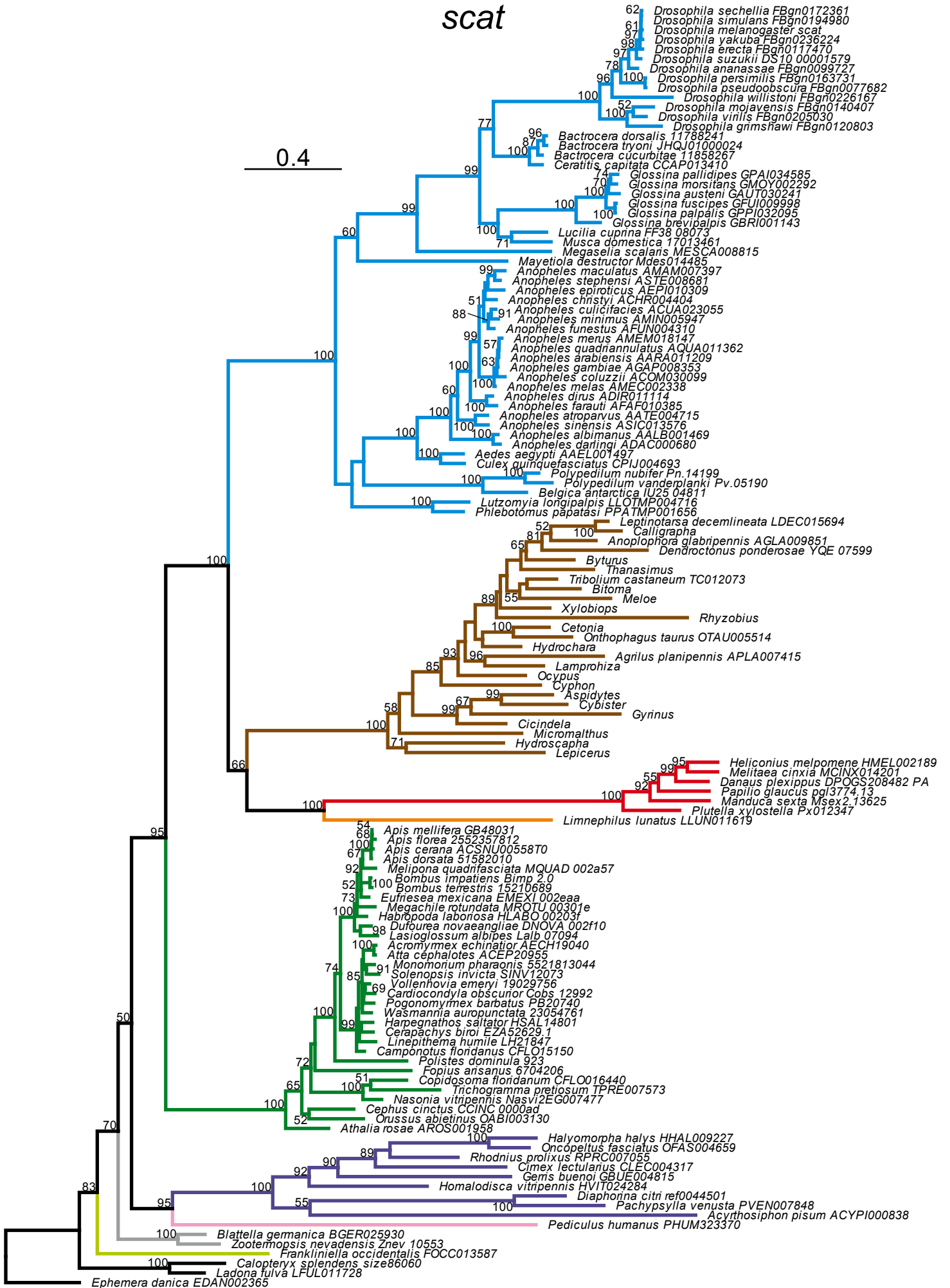


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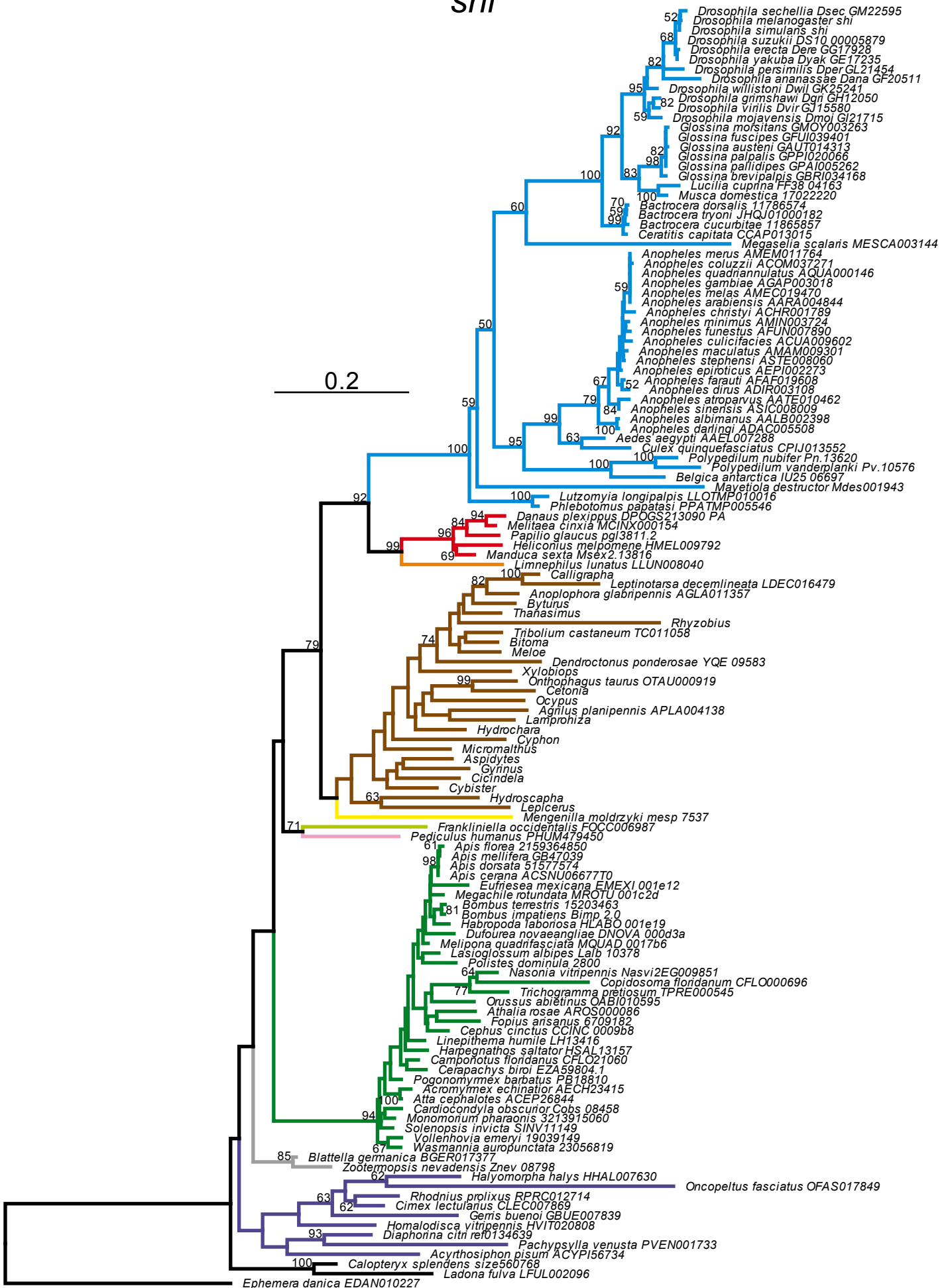


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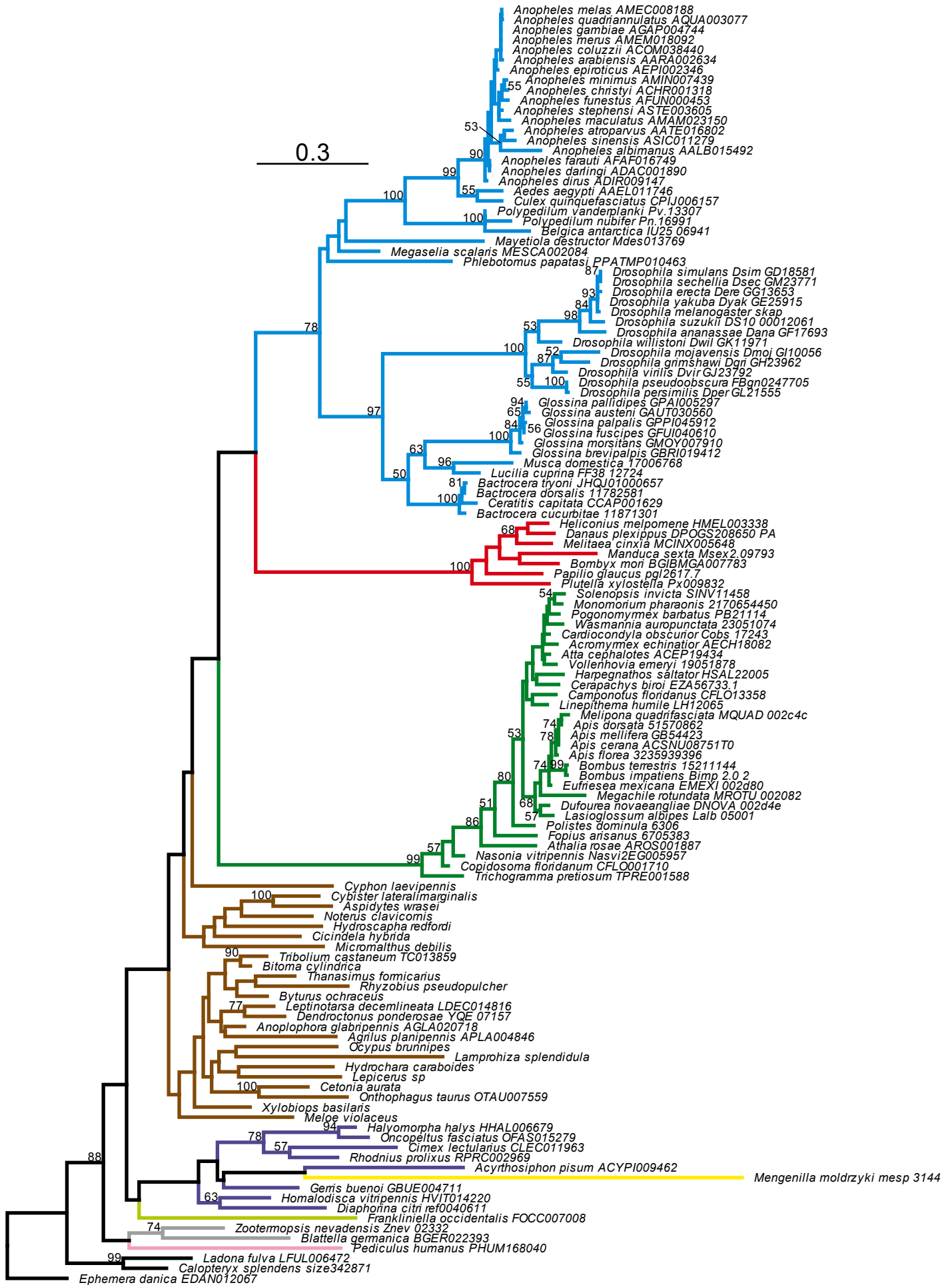
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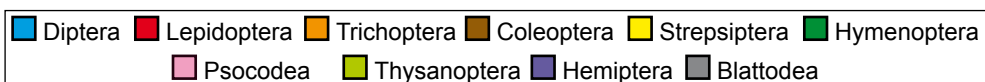
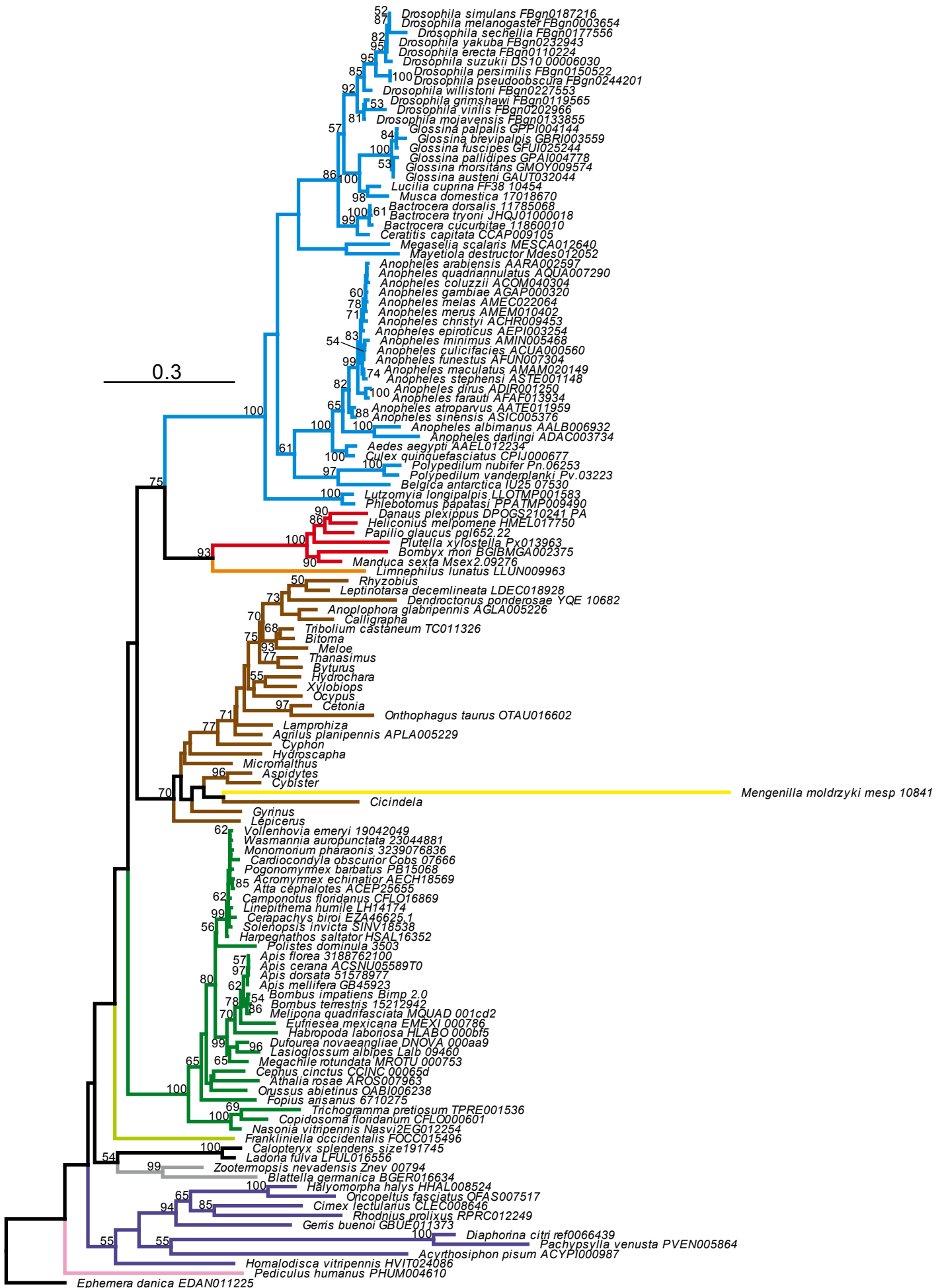
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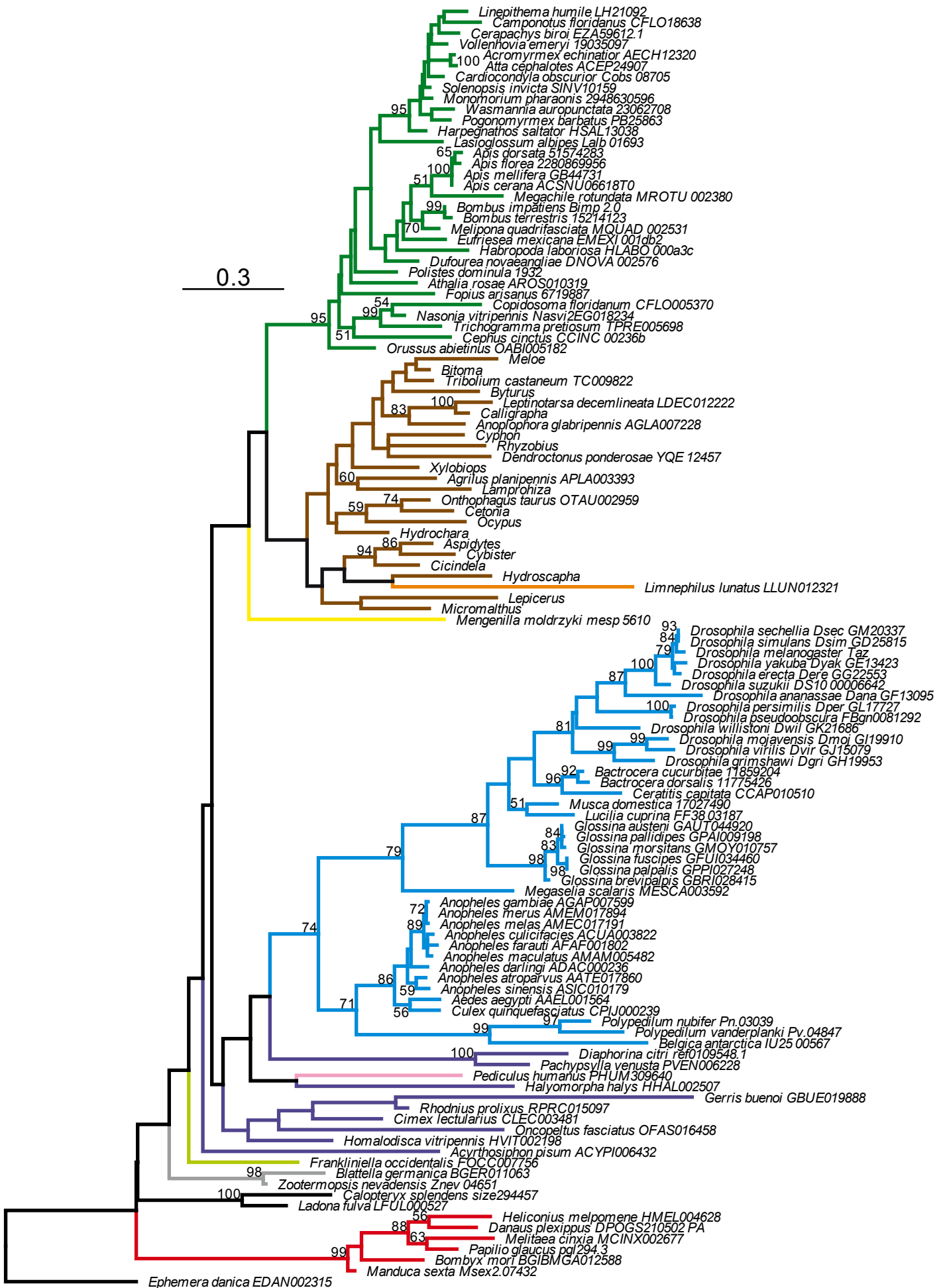
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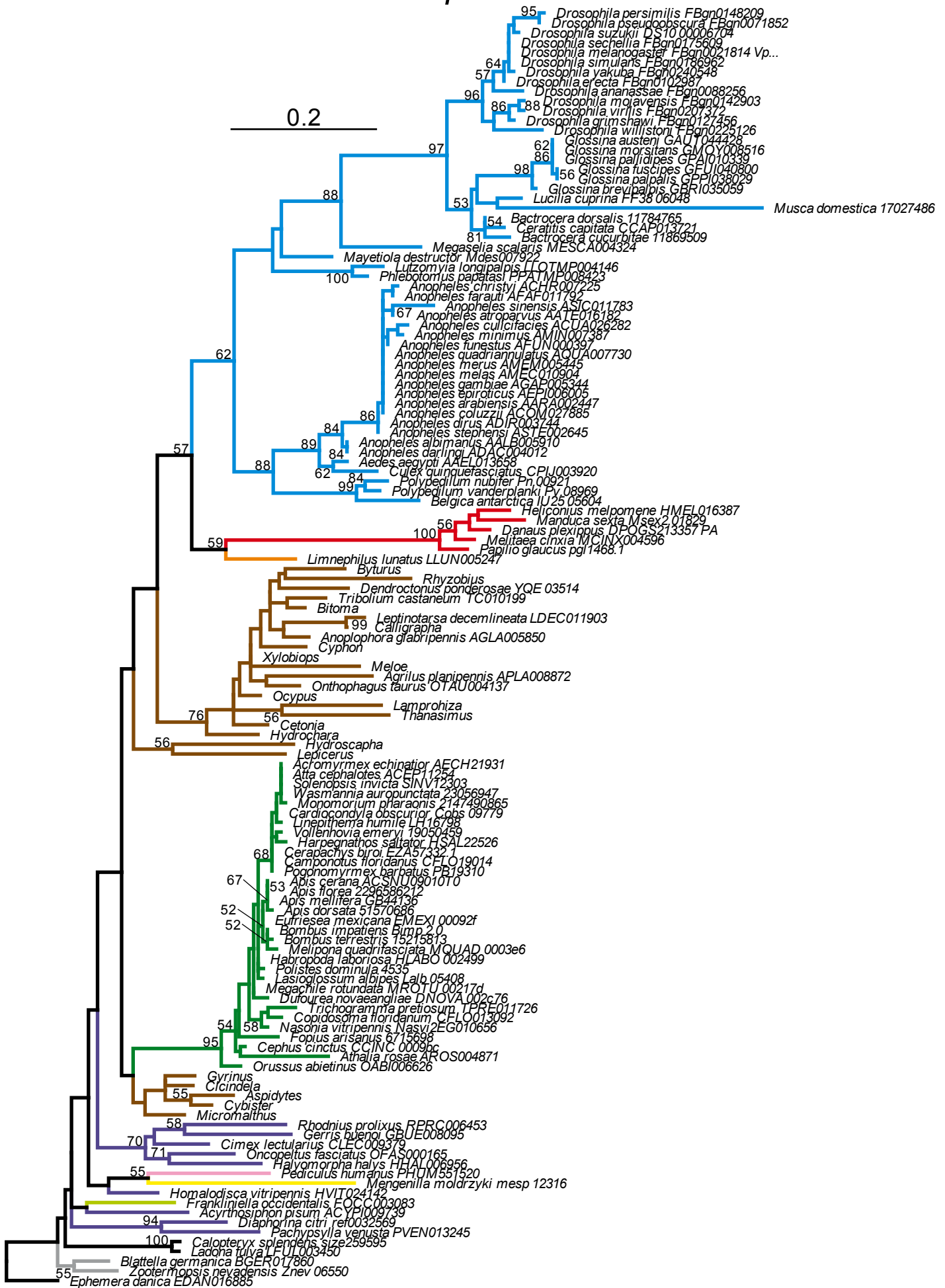
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Taz

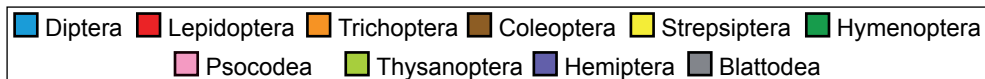
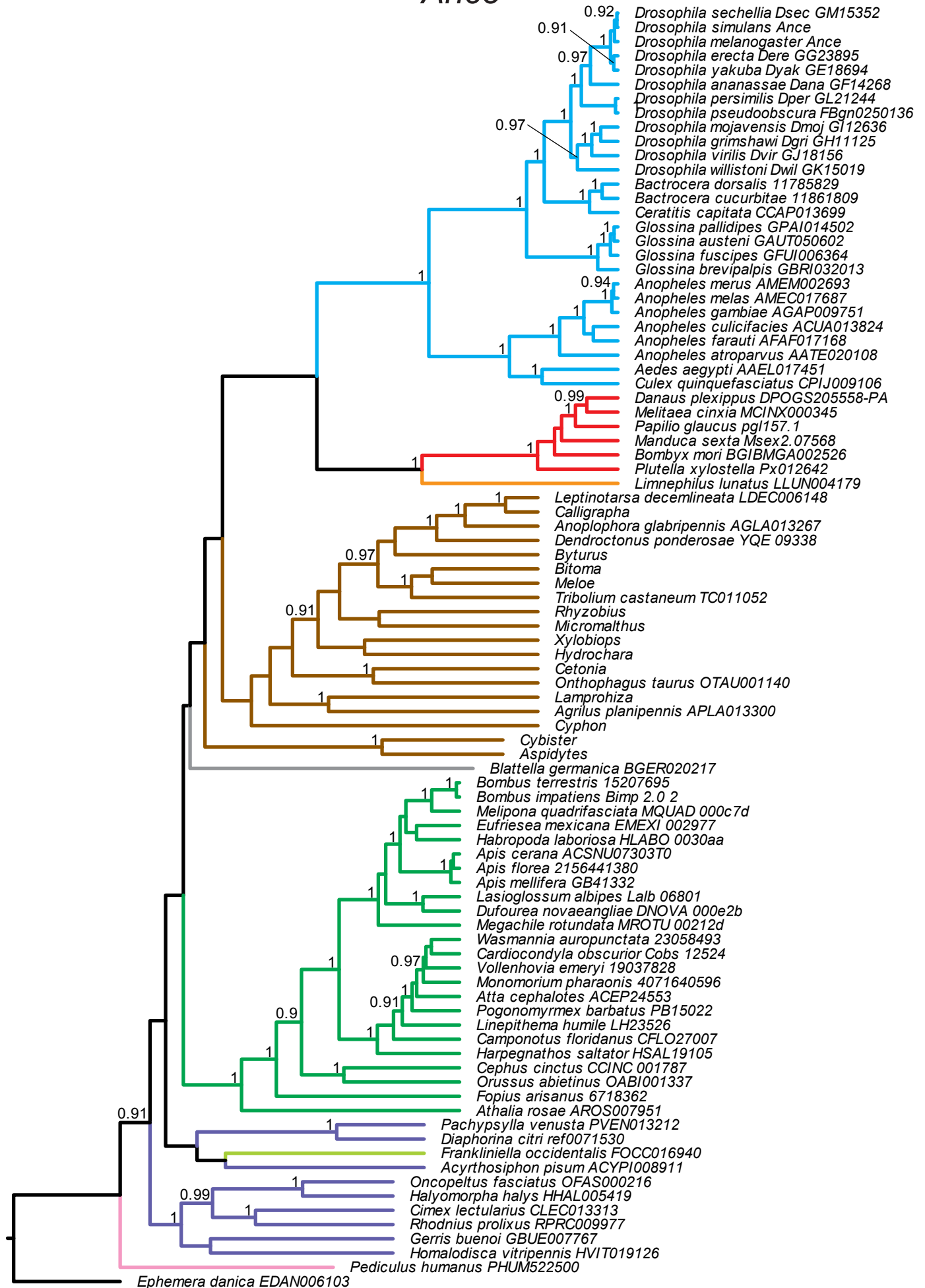


Vps28

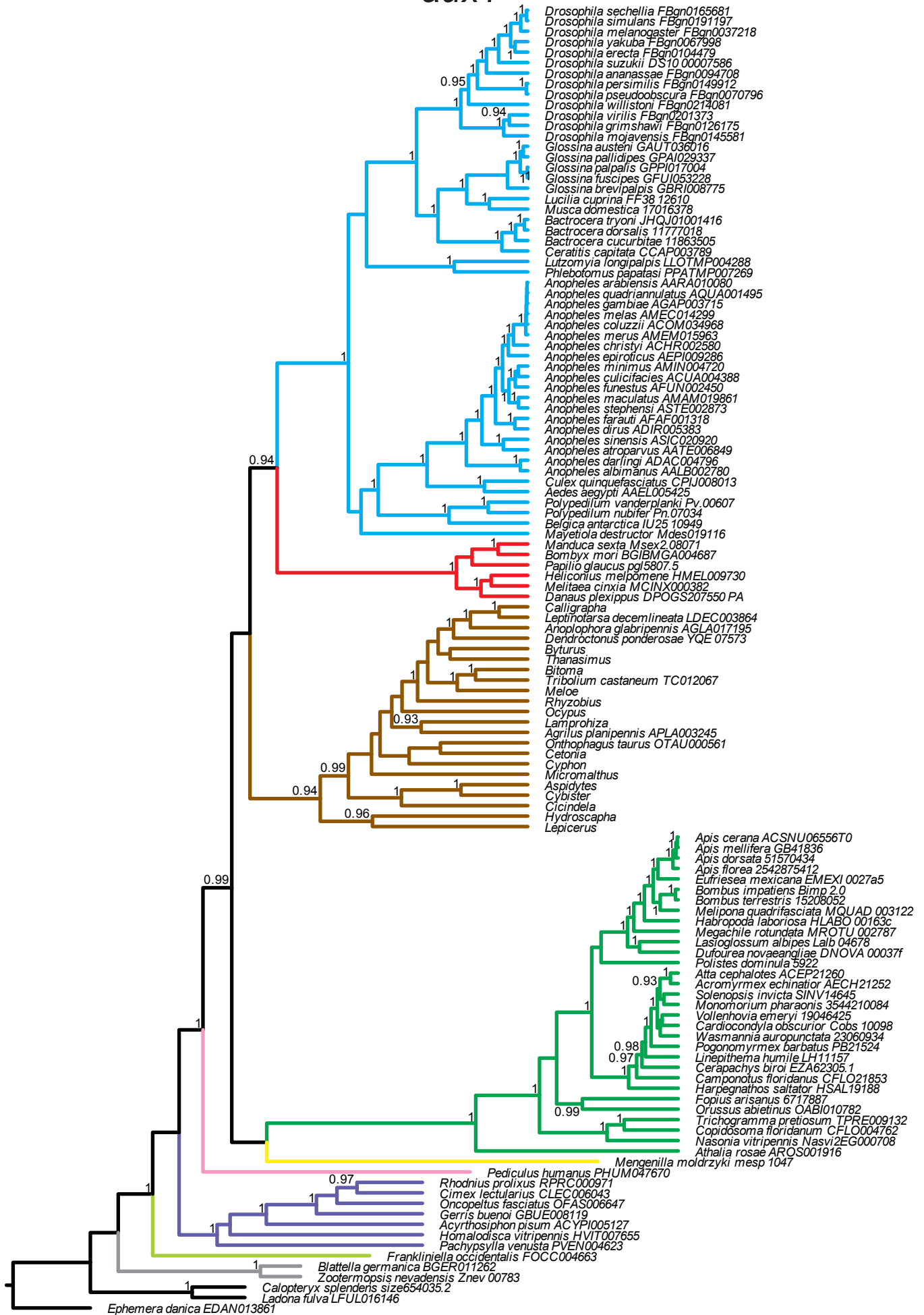


File S2. Bayesian inference trees based on the amino acid alignments of different sperm individualization proteins in insects.

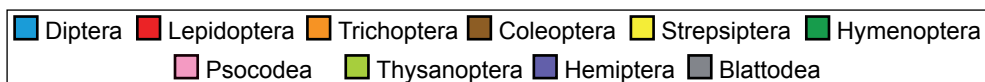
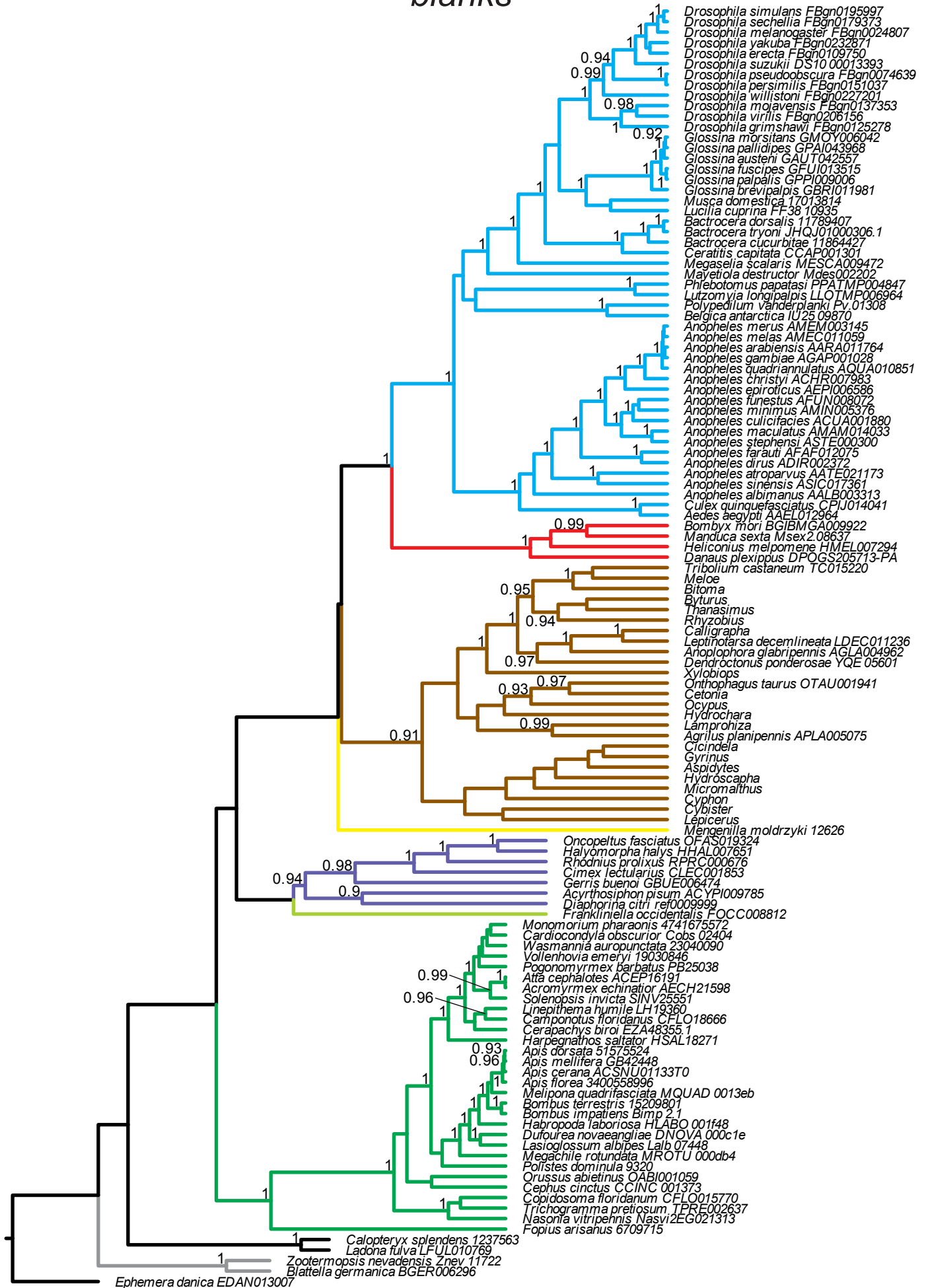
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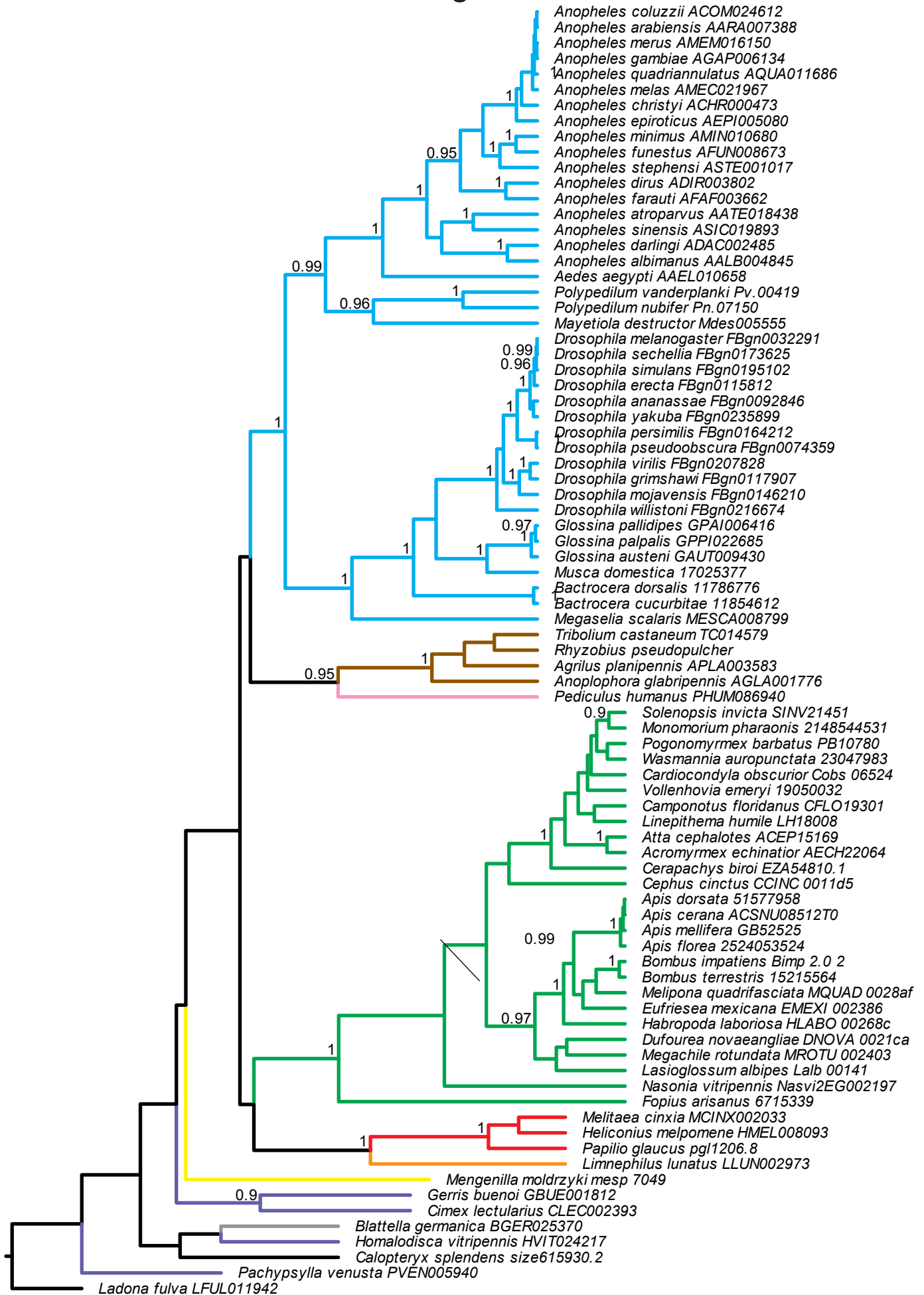
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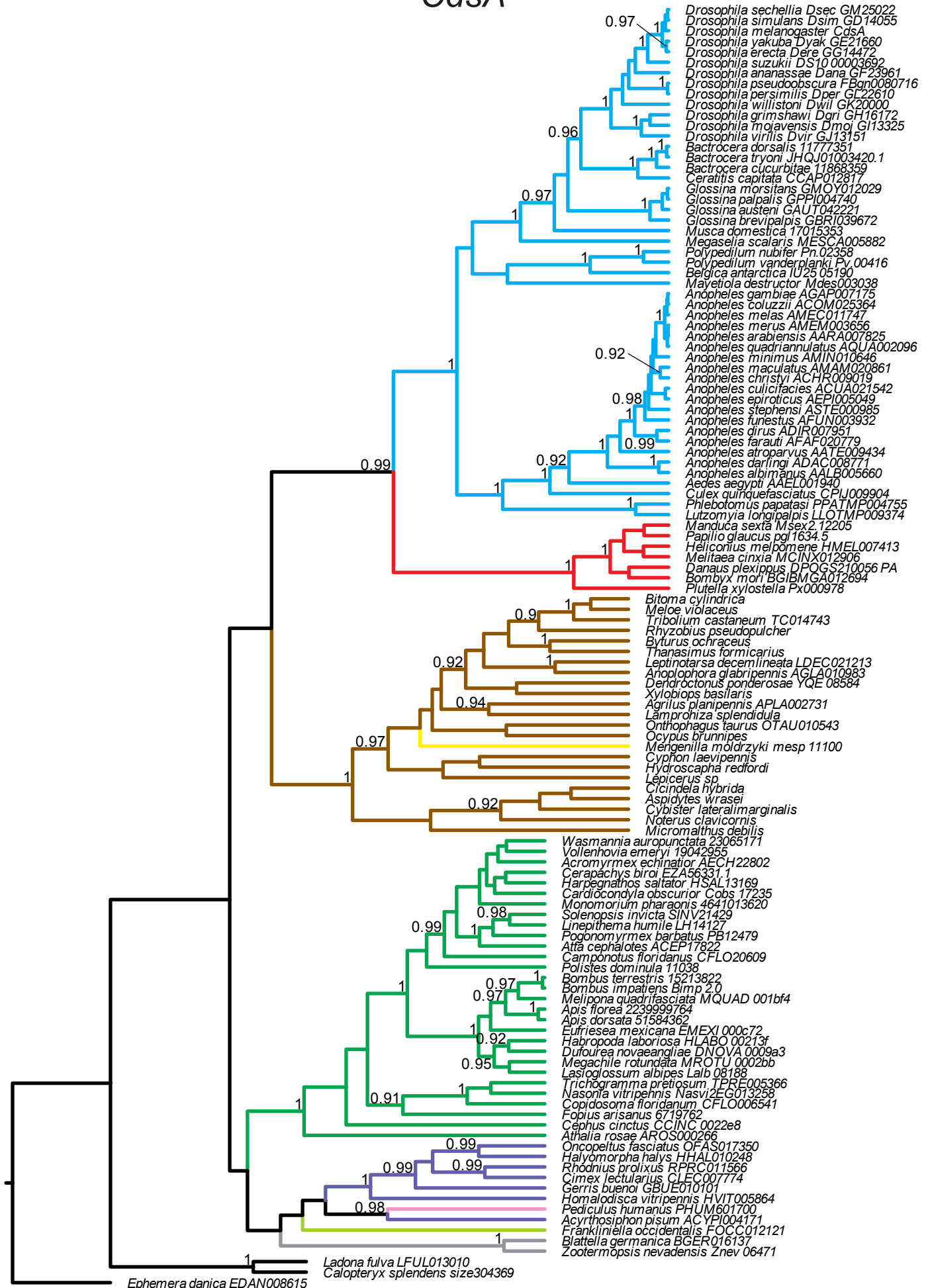
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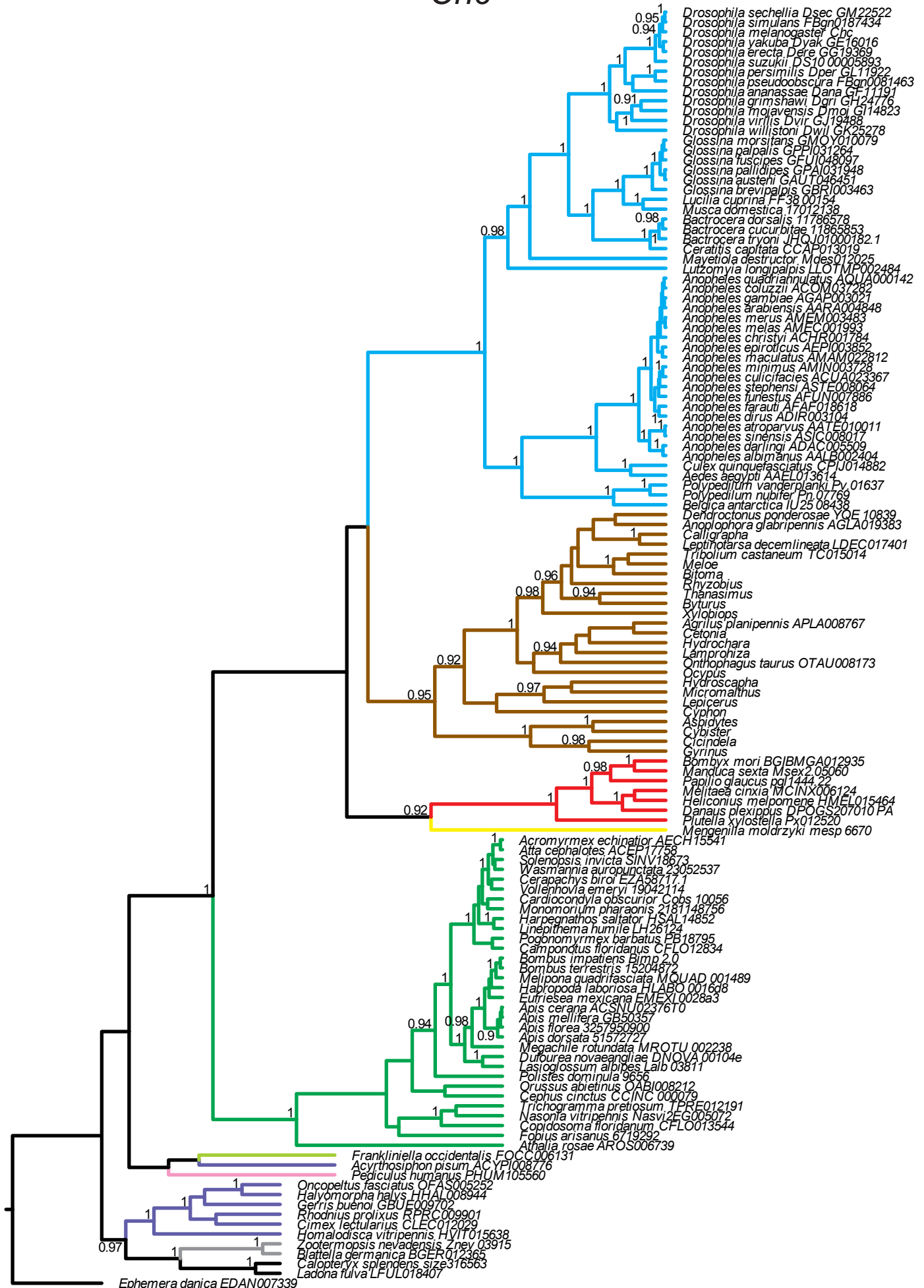
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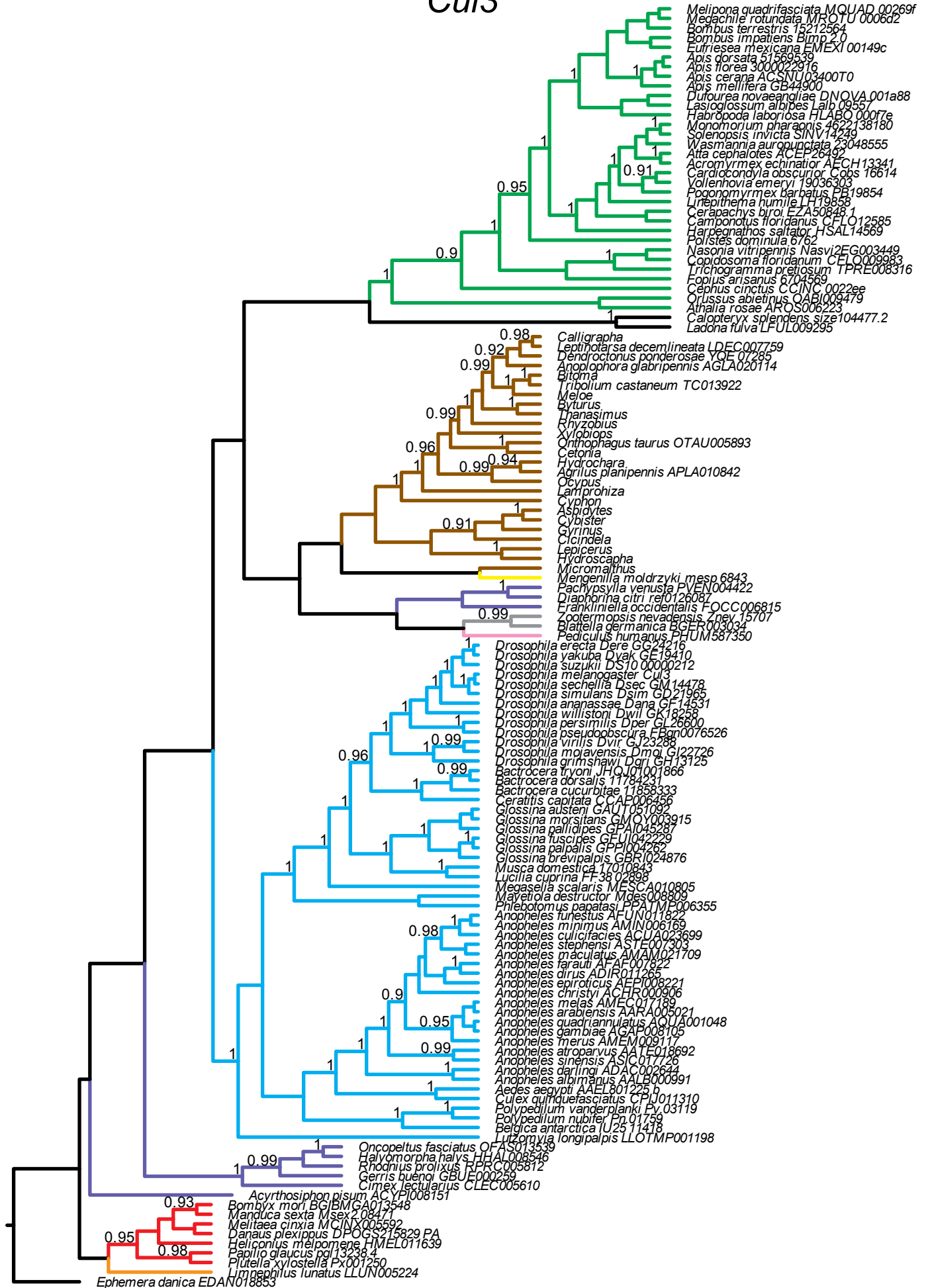
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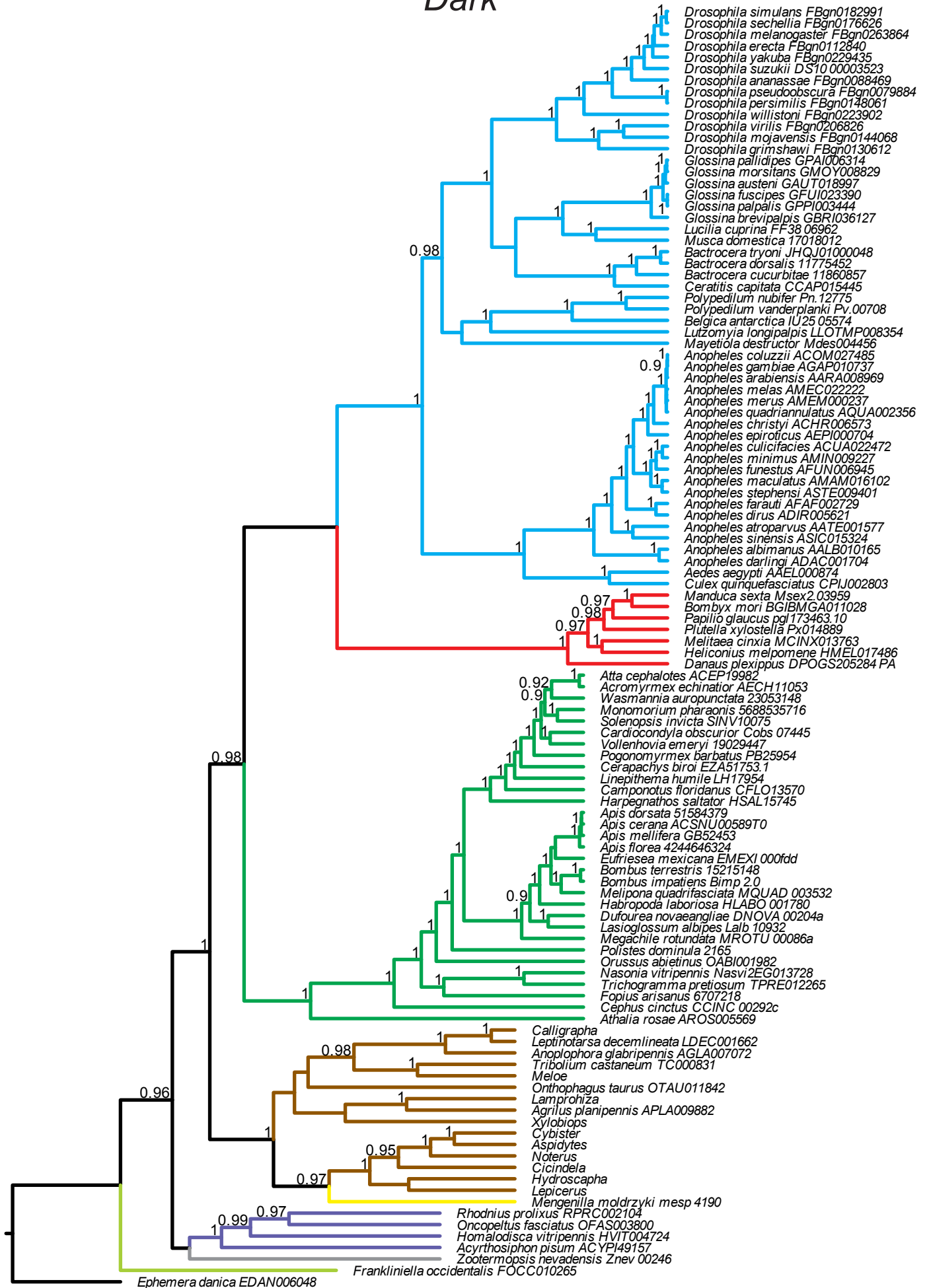
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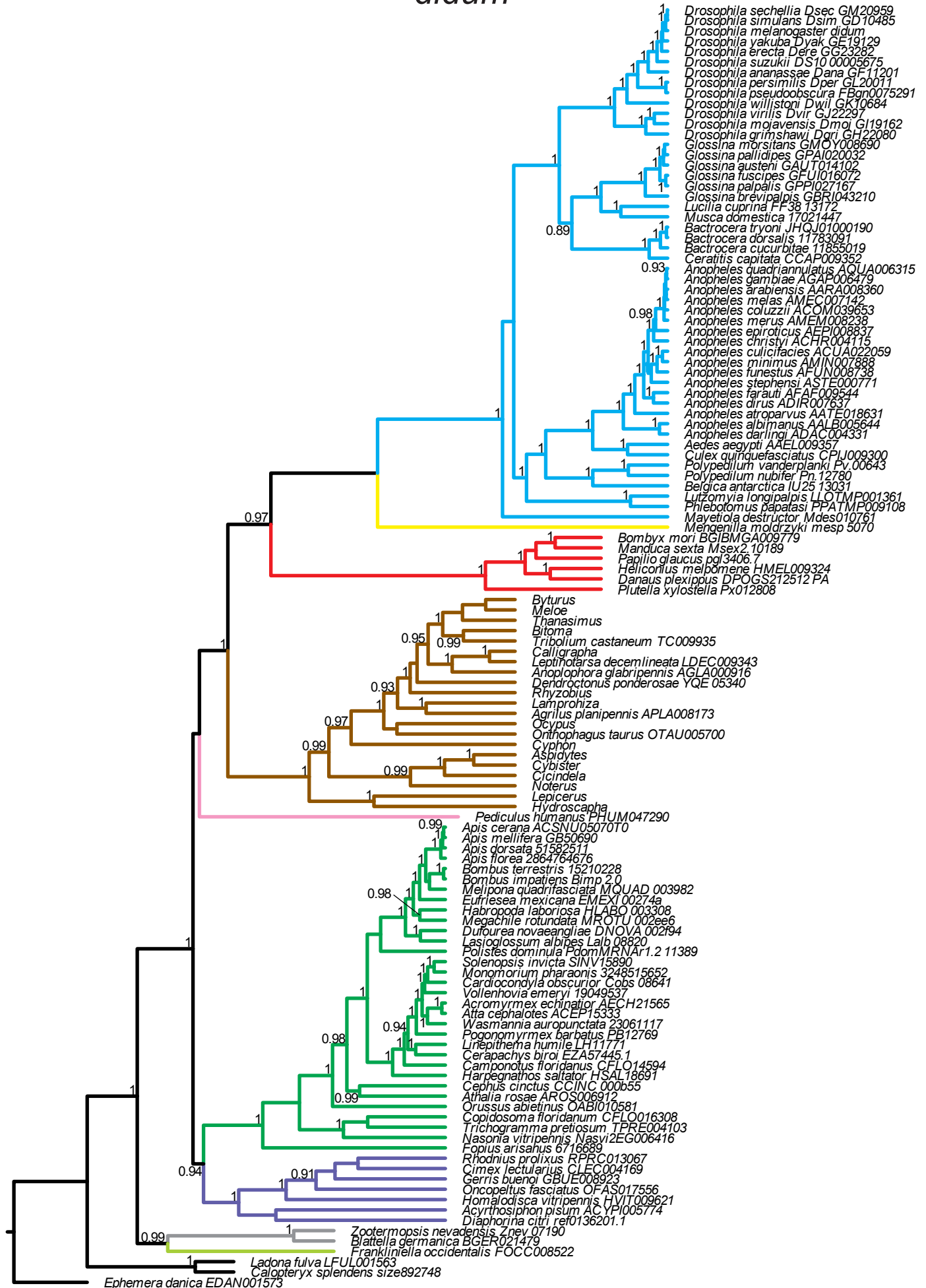
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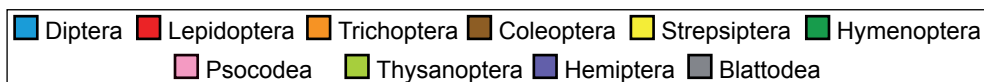
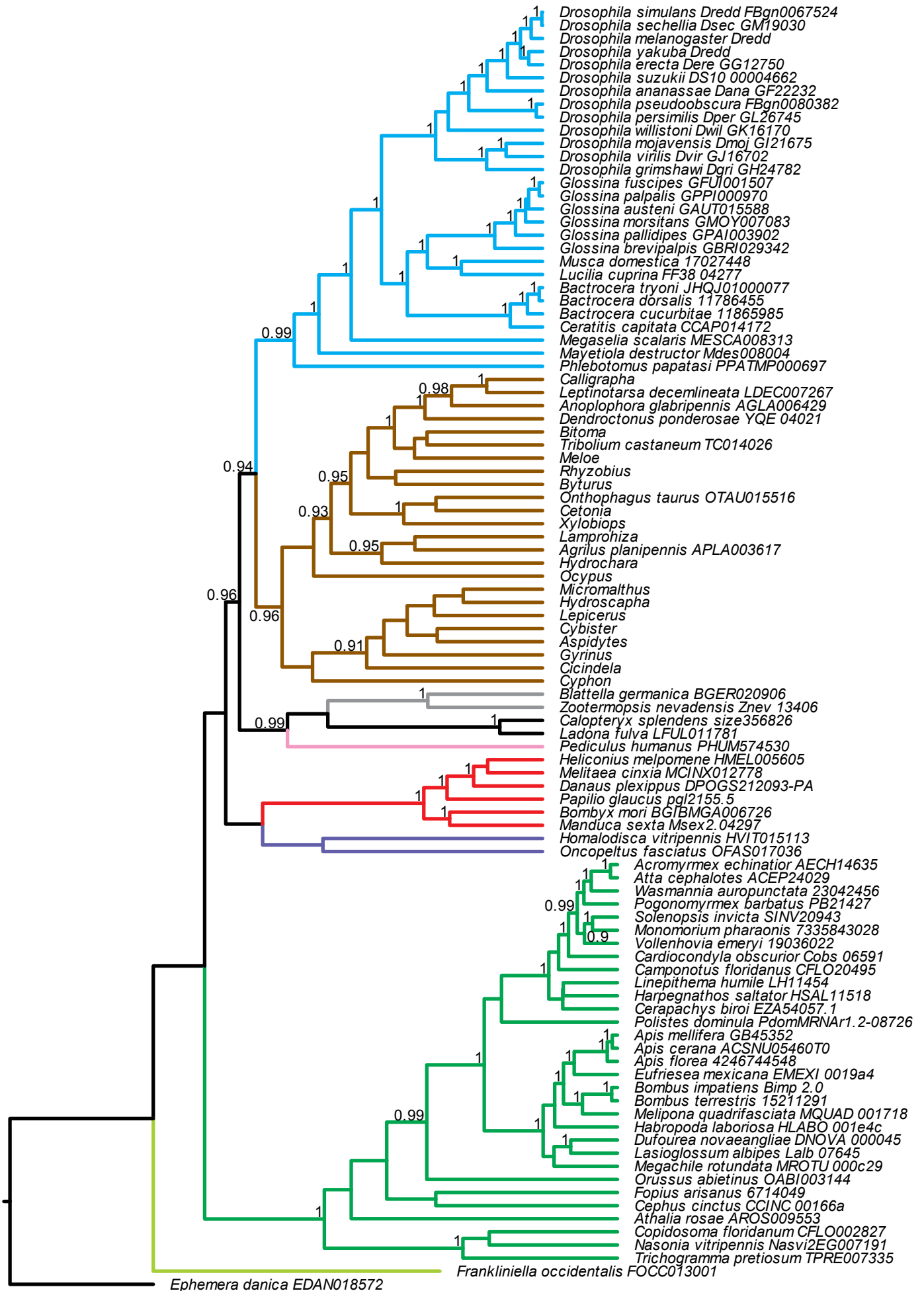
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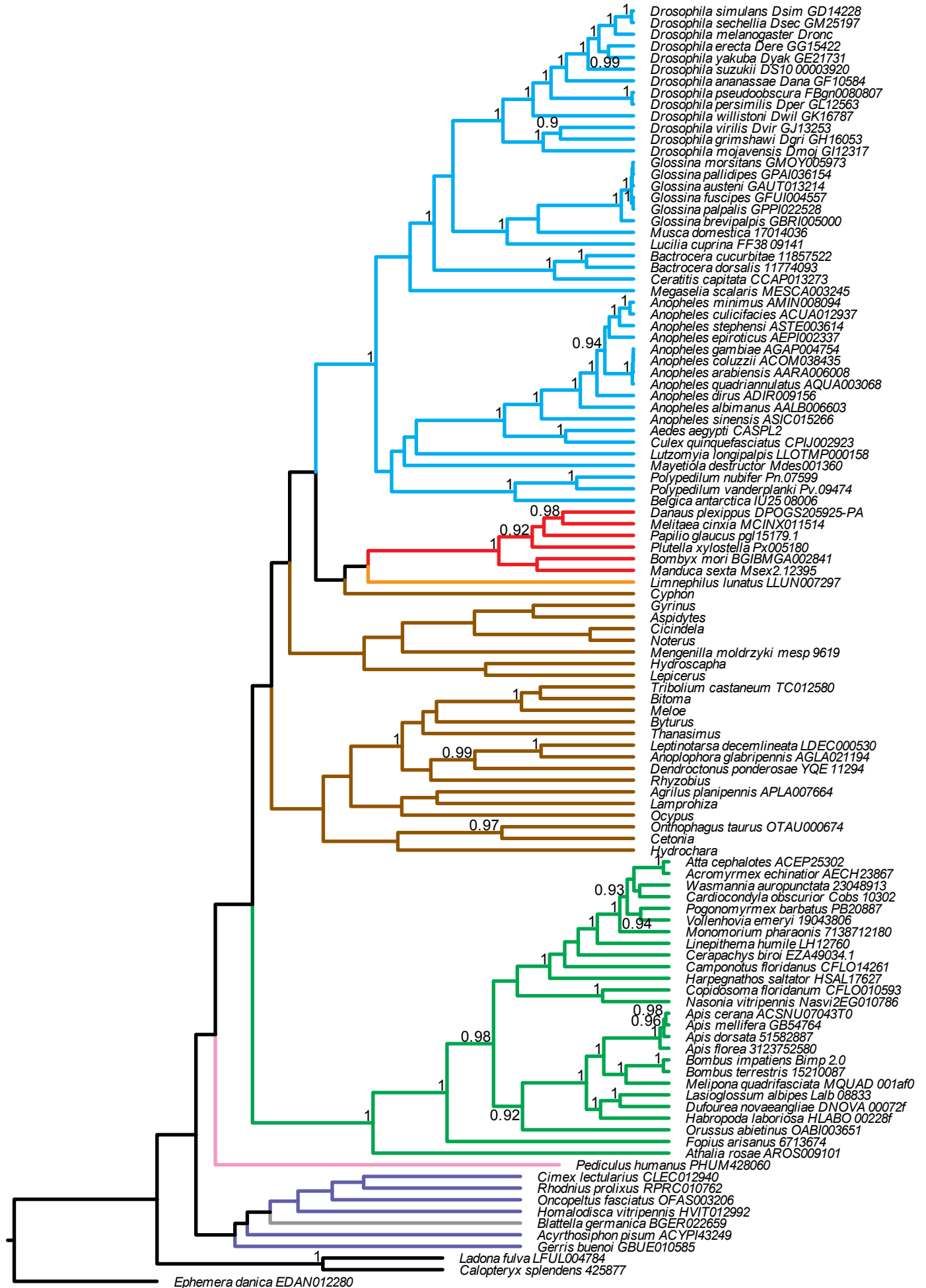
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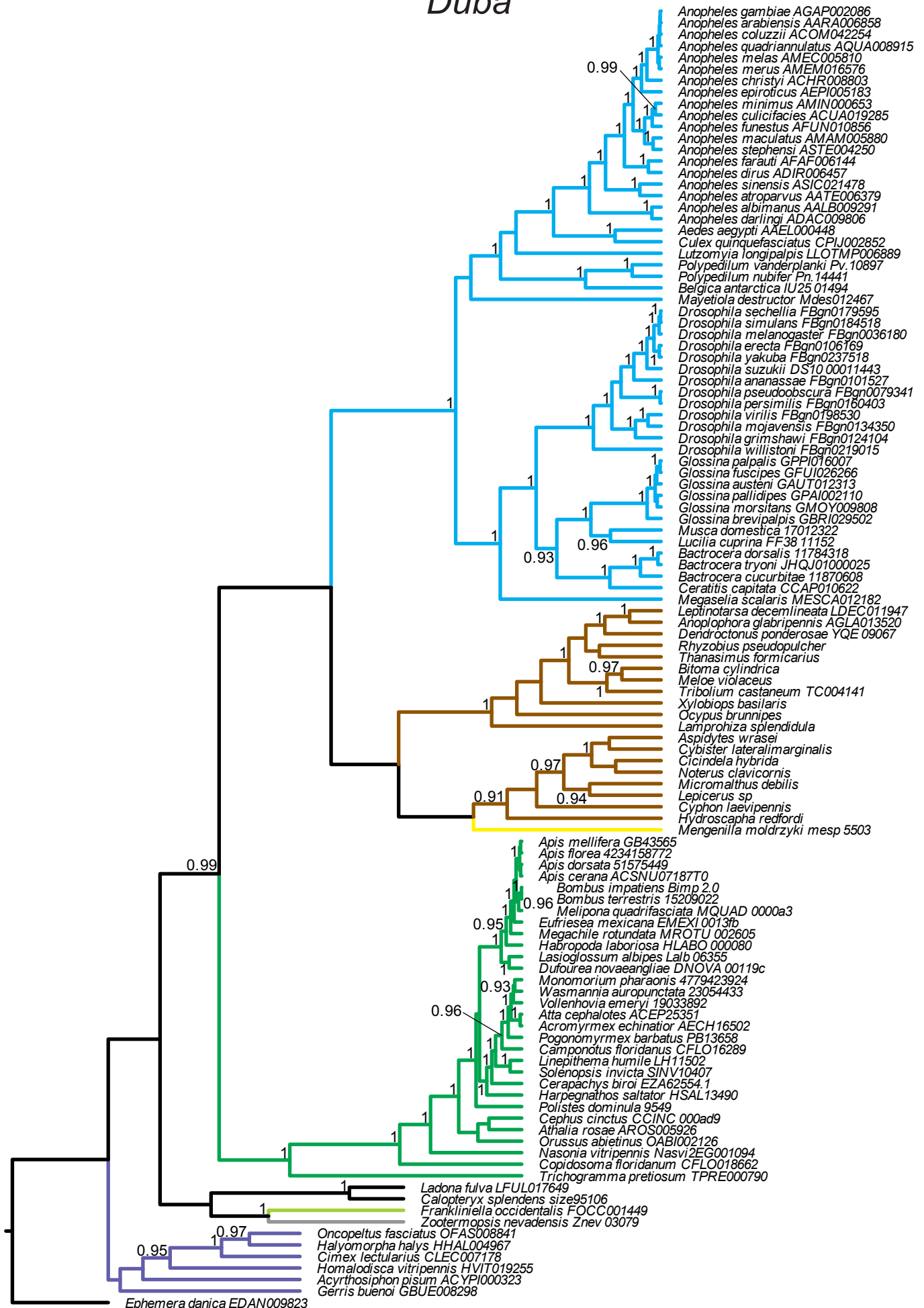
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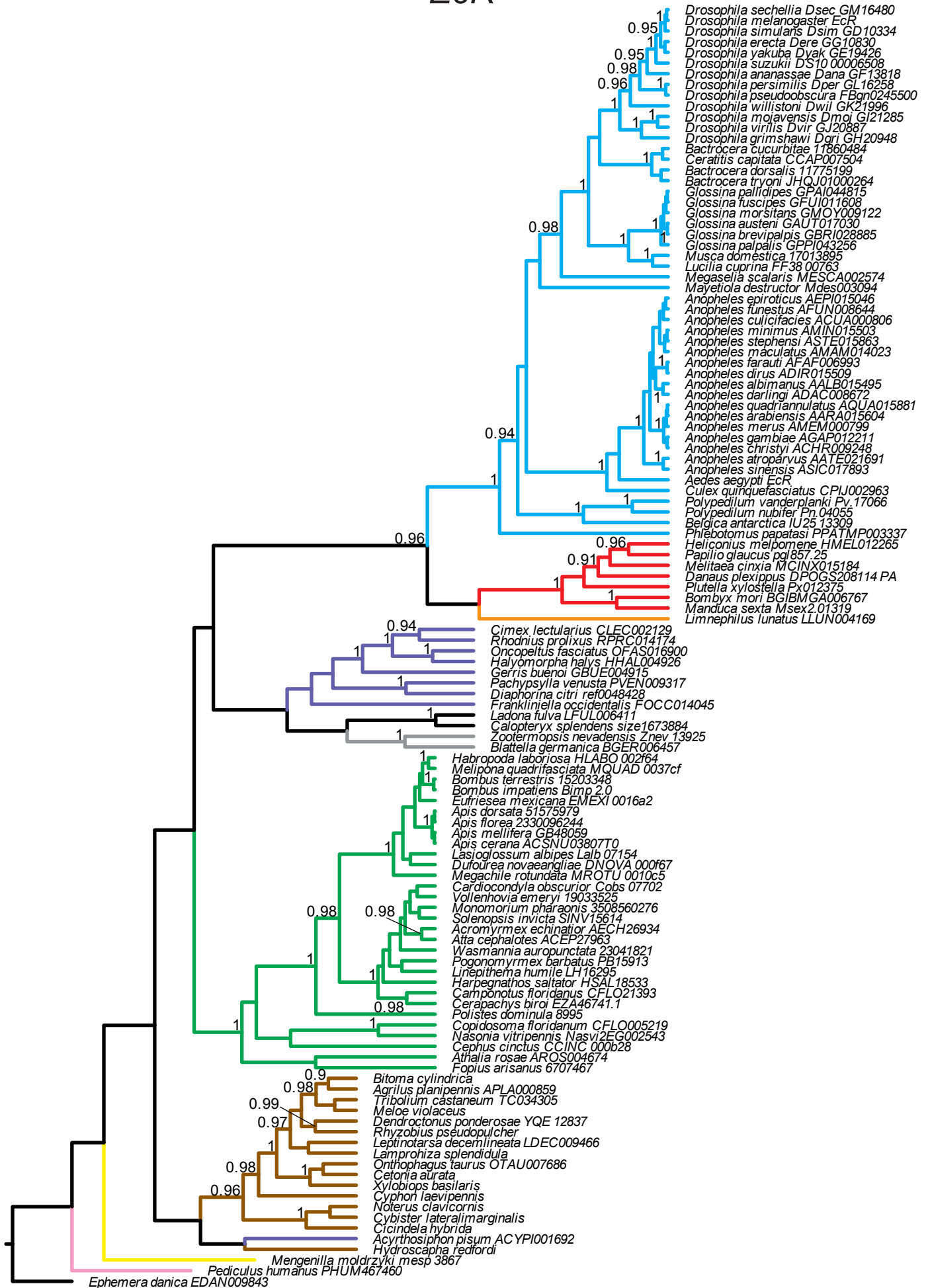
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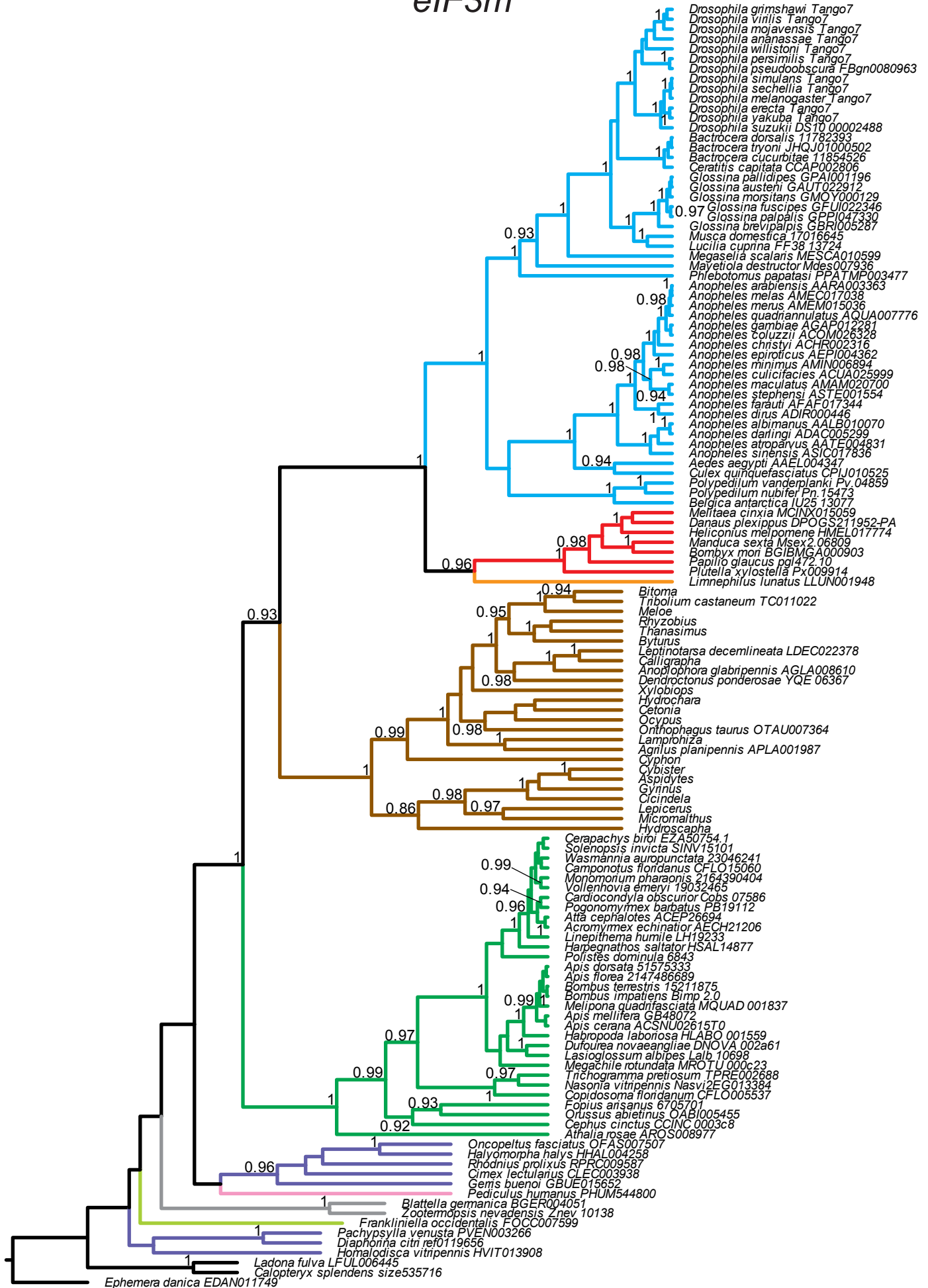
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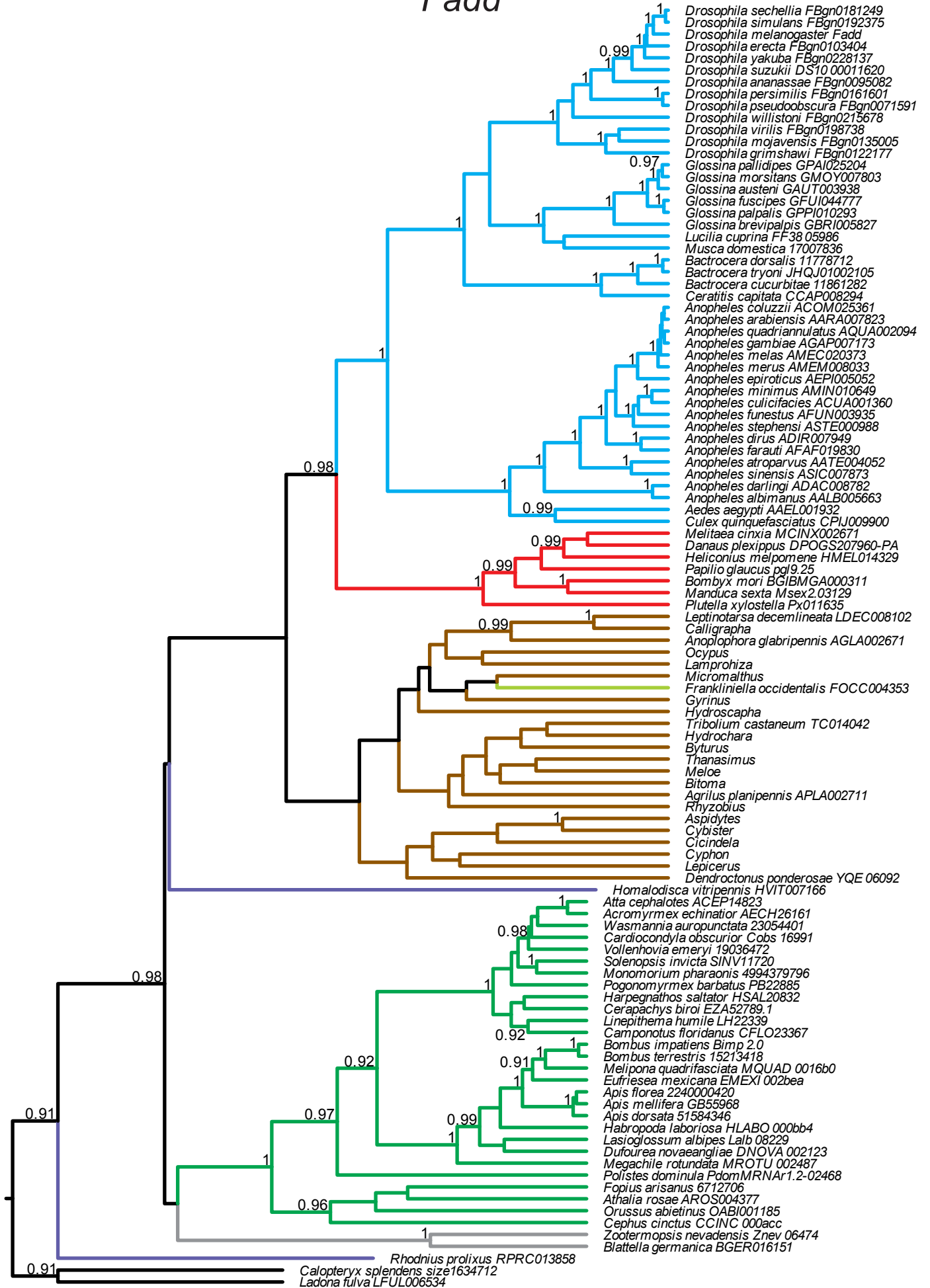
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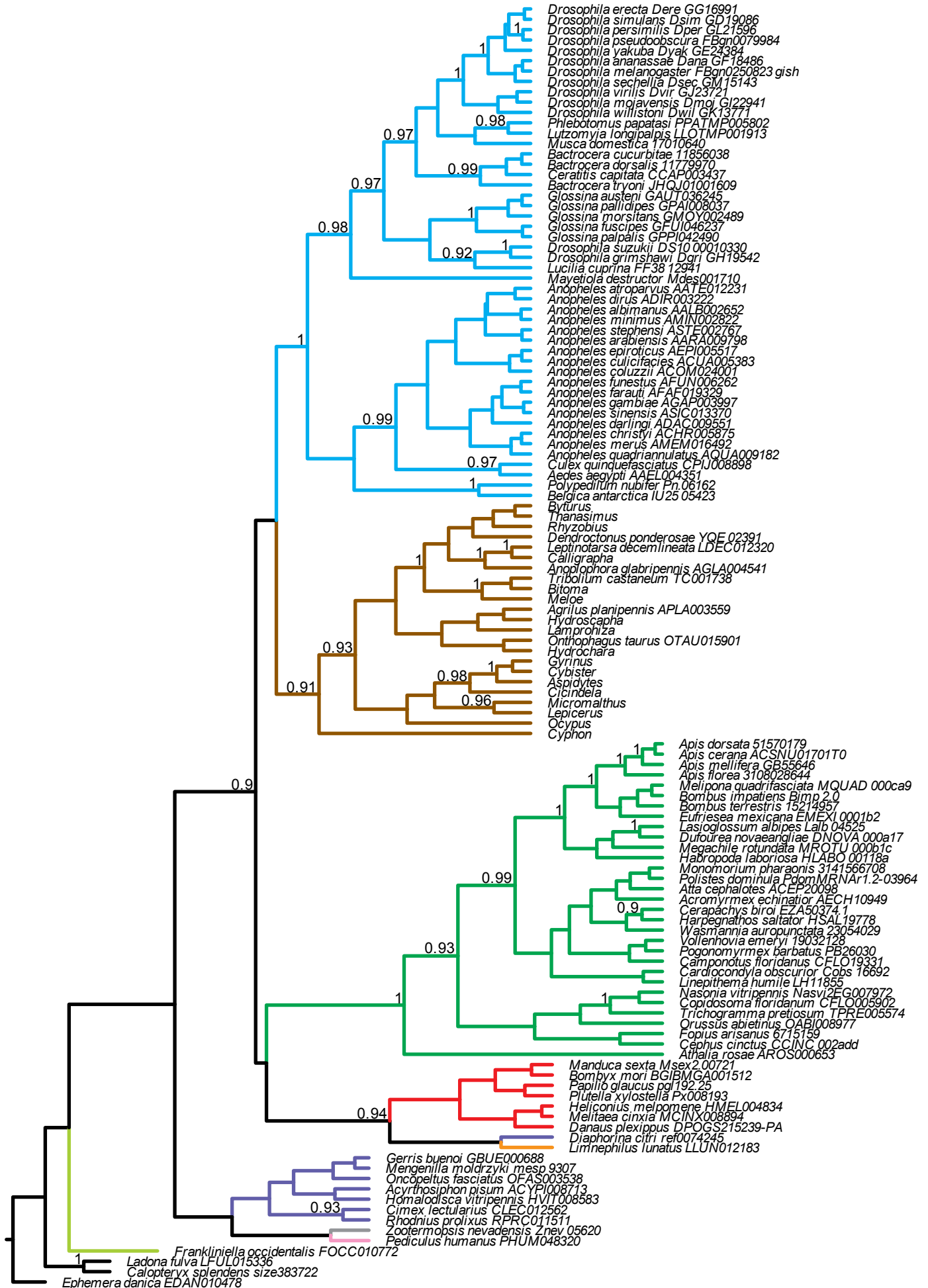
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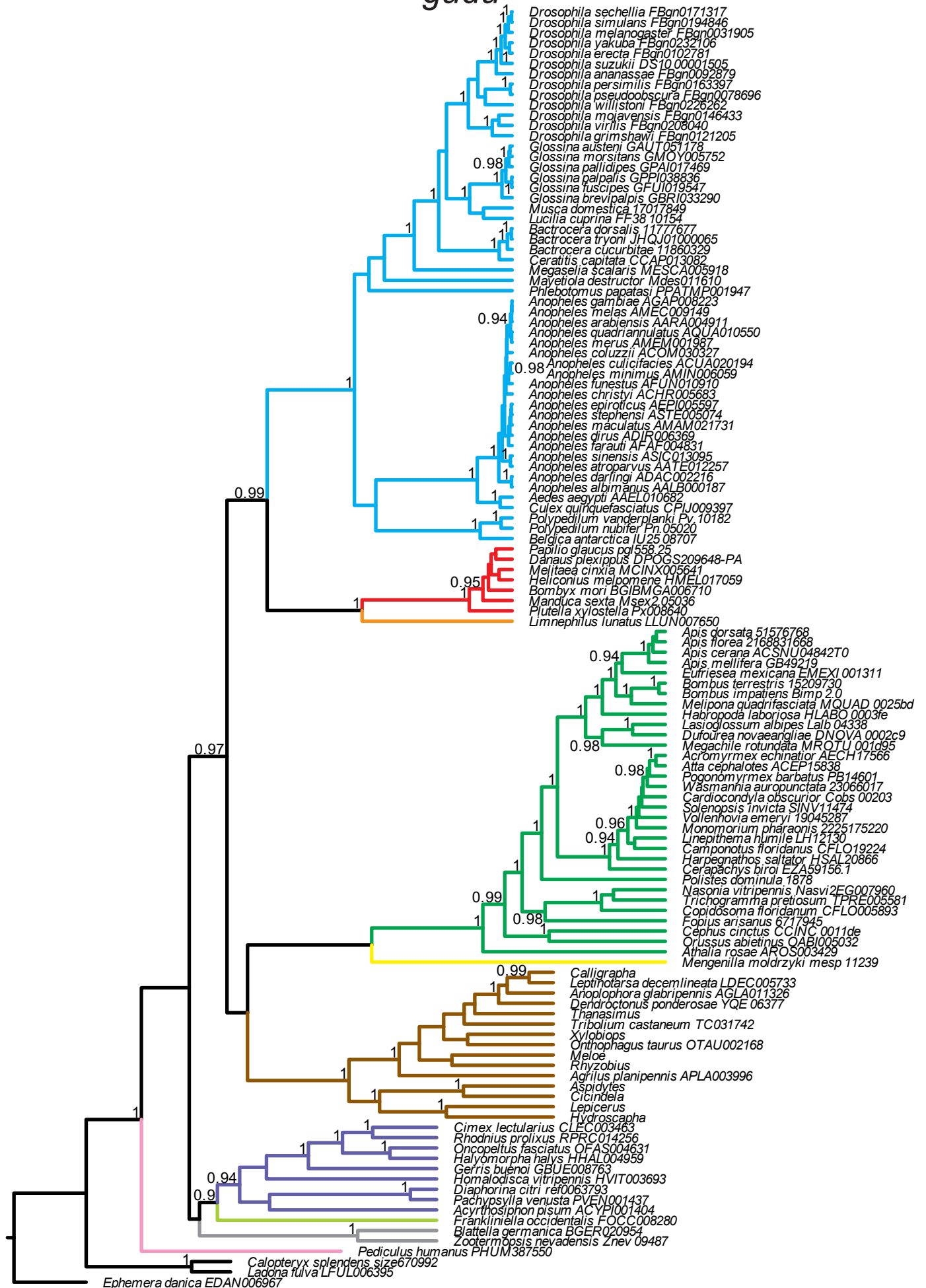
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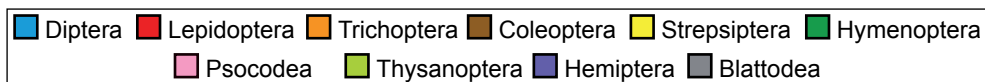
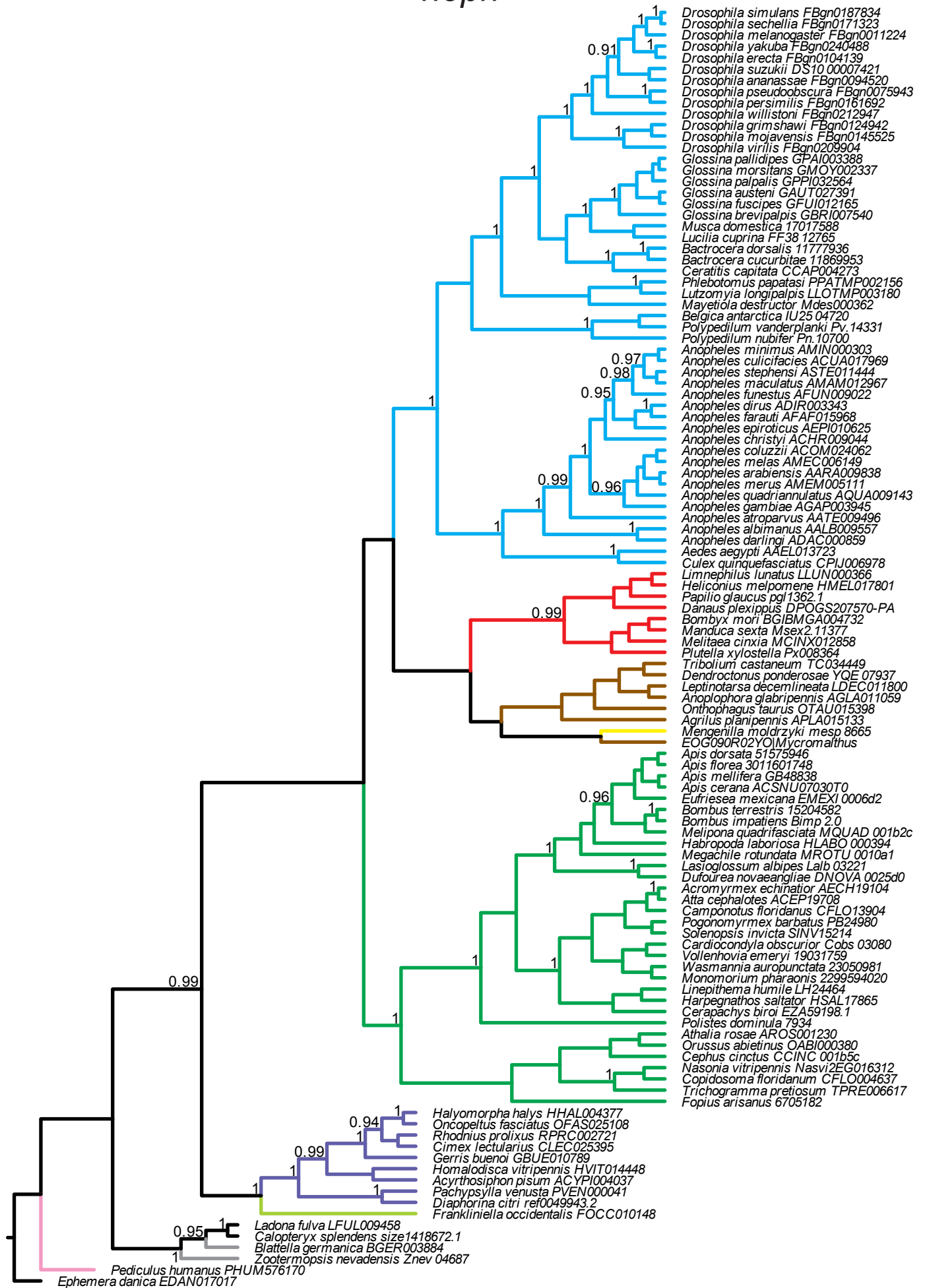
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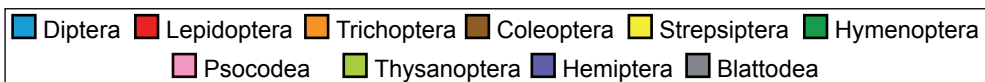
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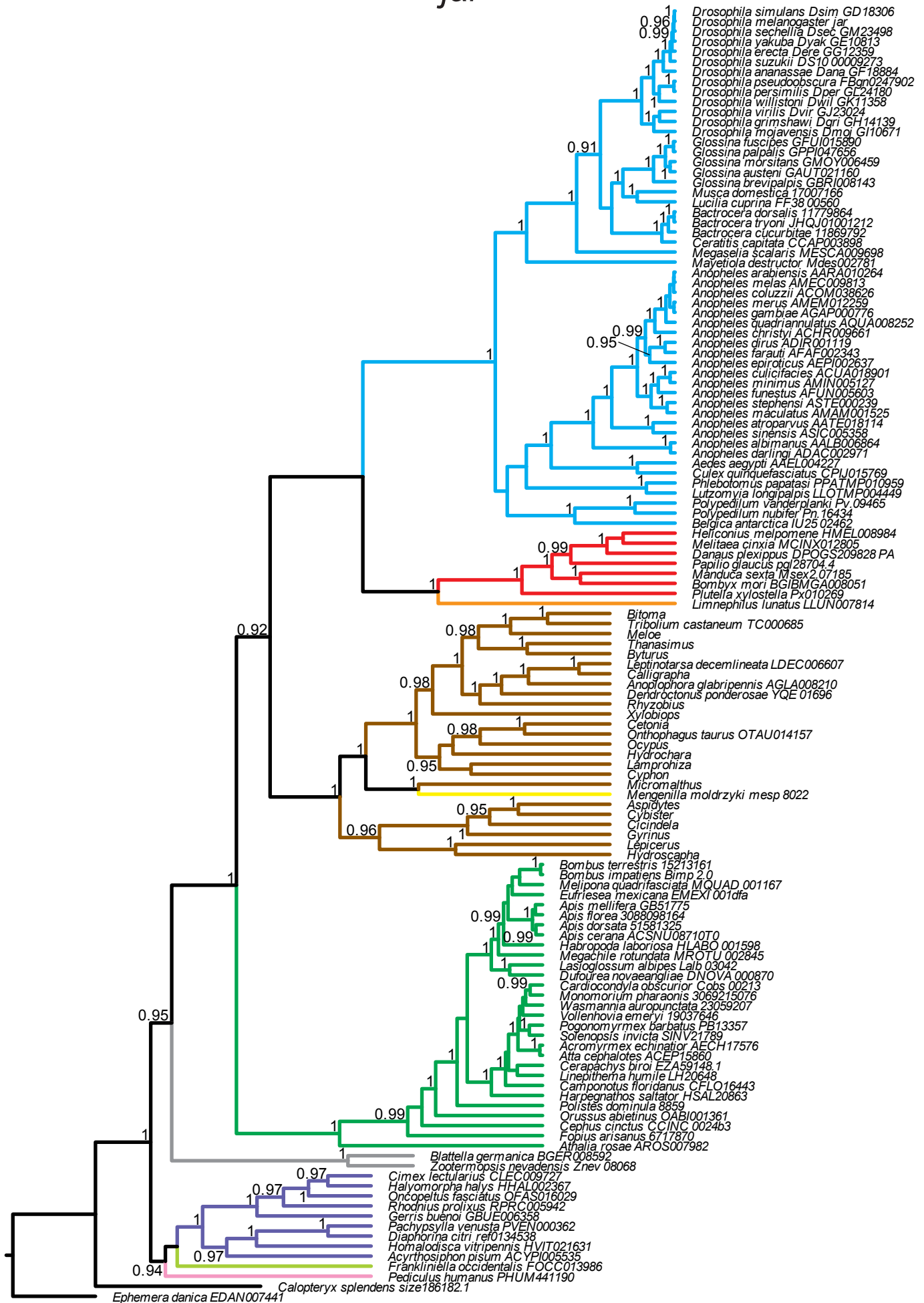
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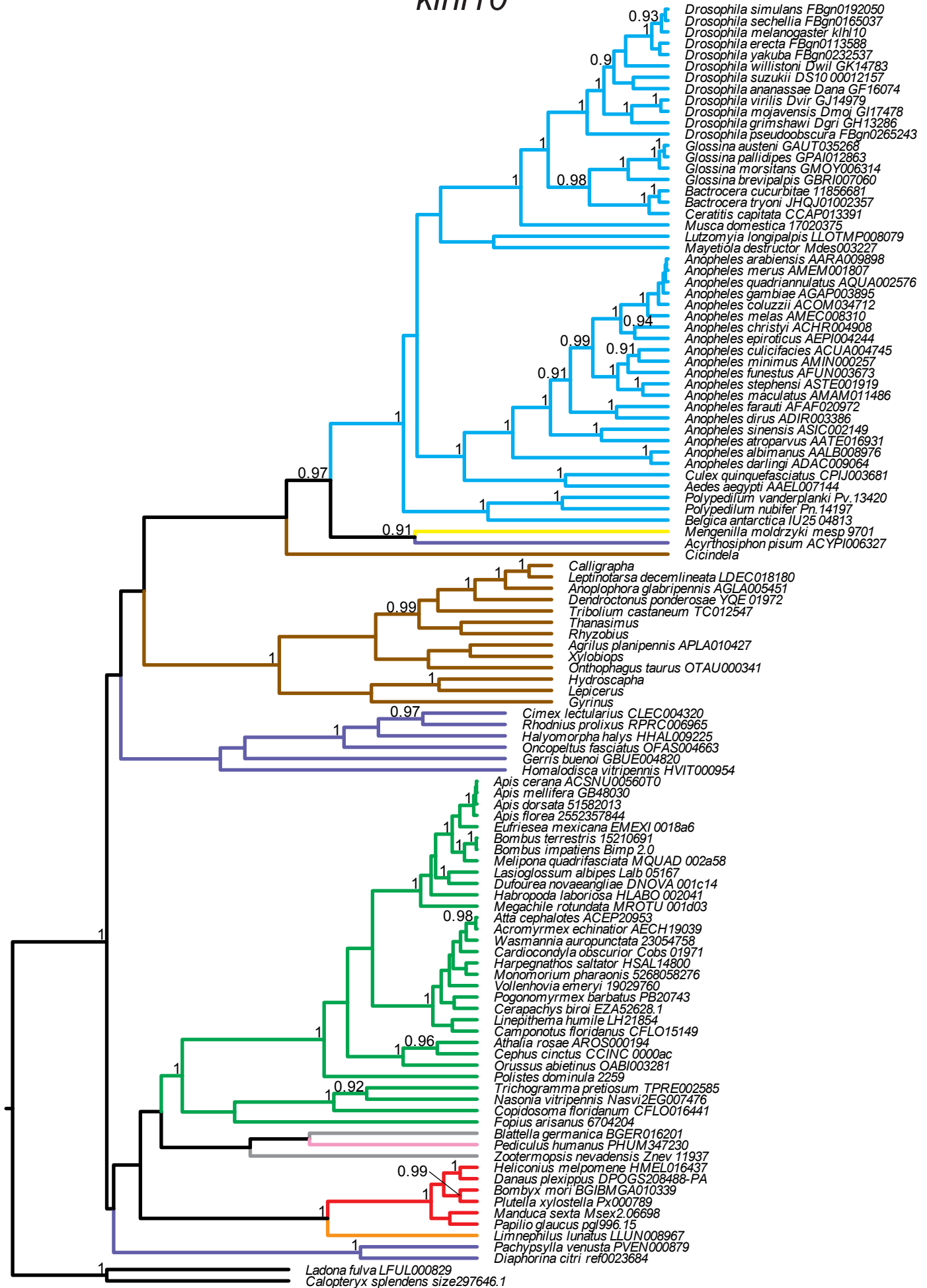
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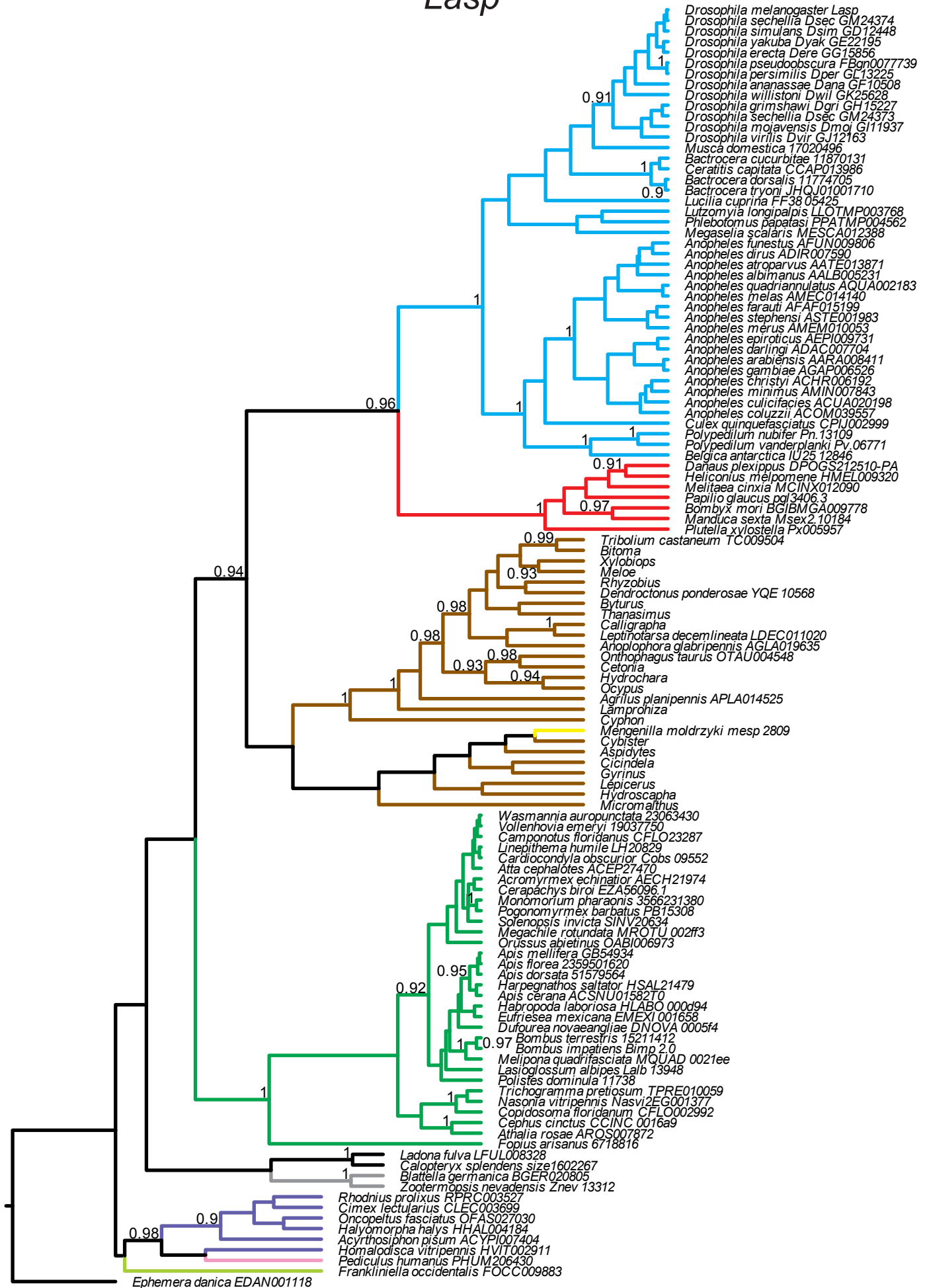
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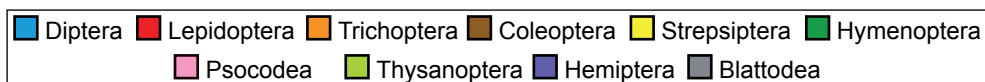
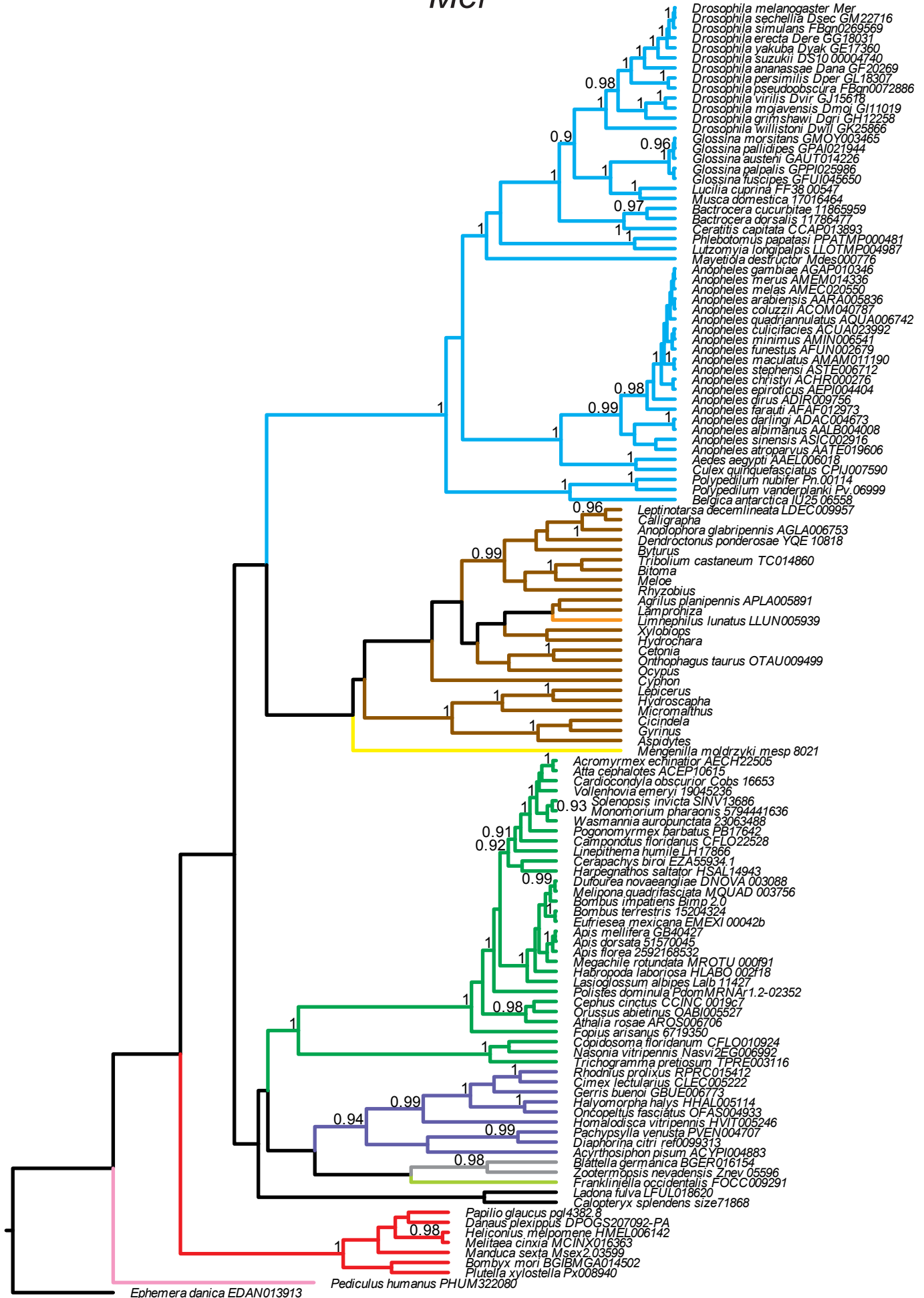
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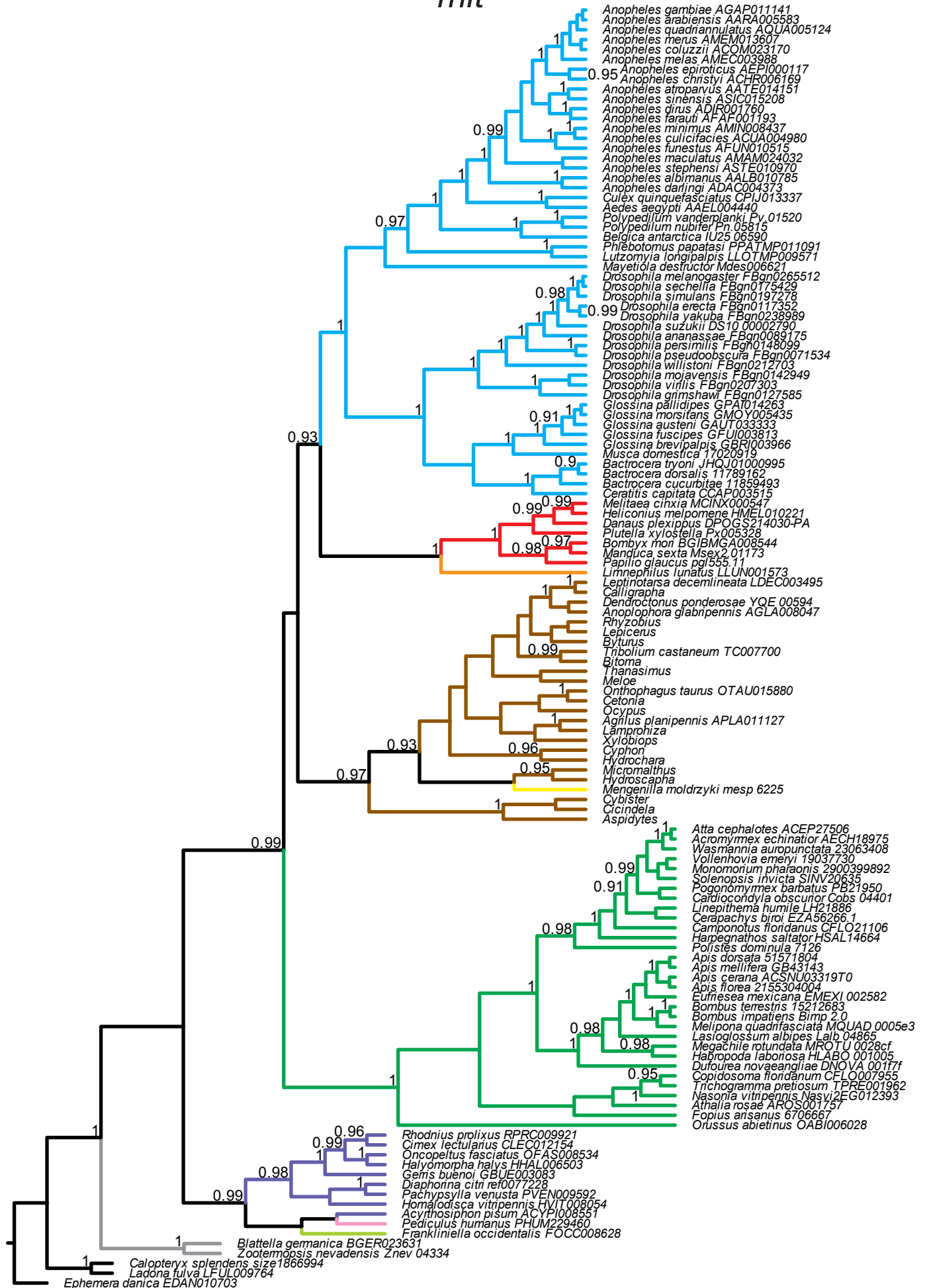
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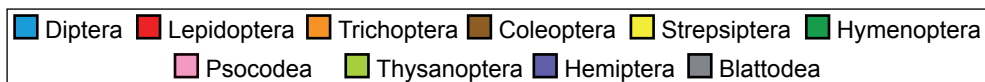
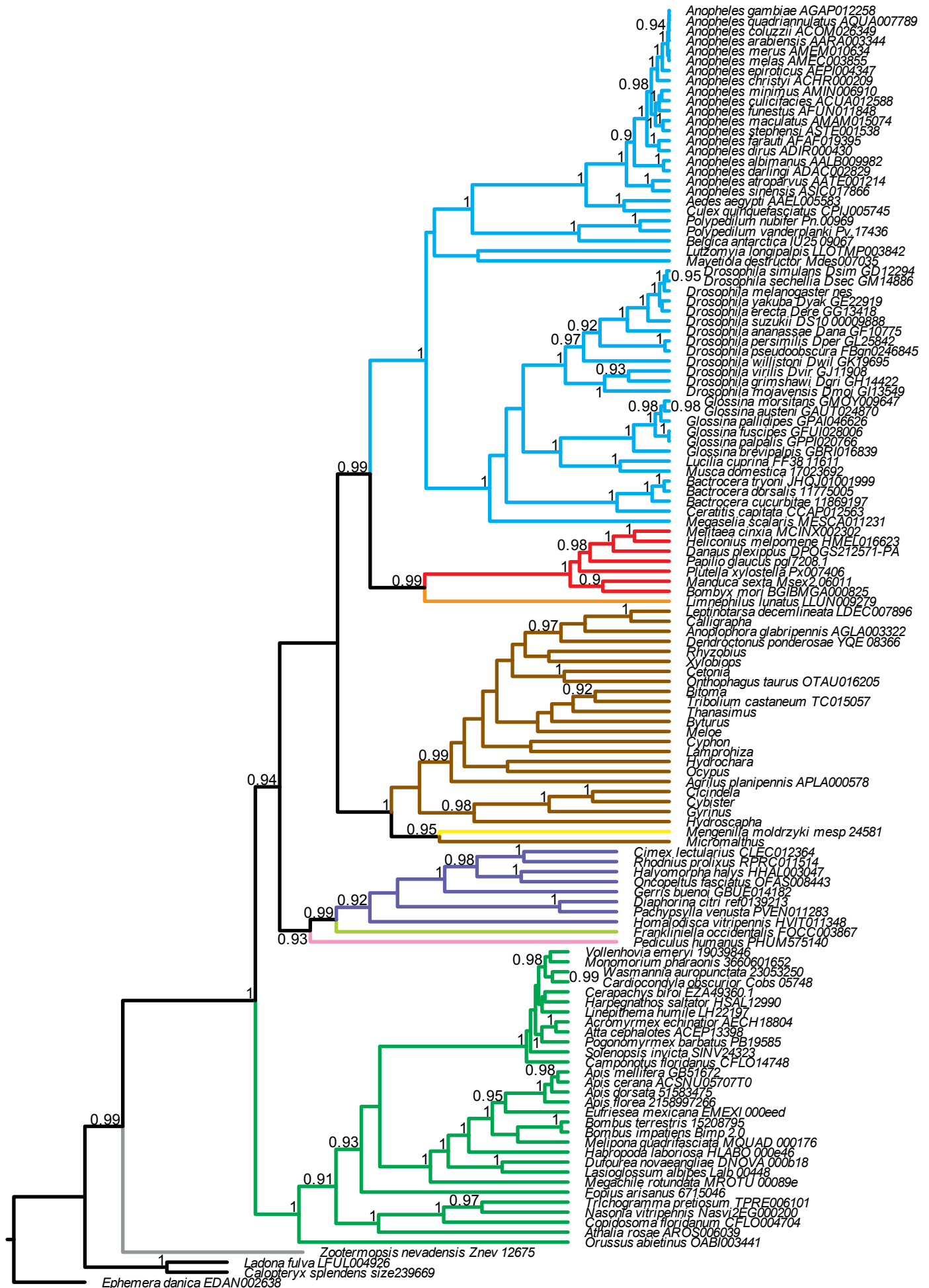
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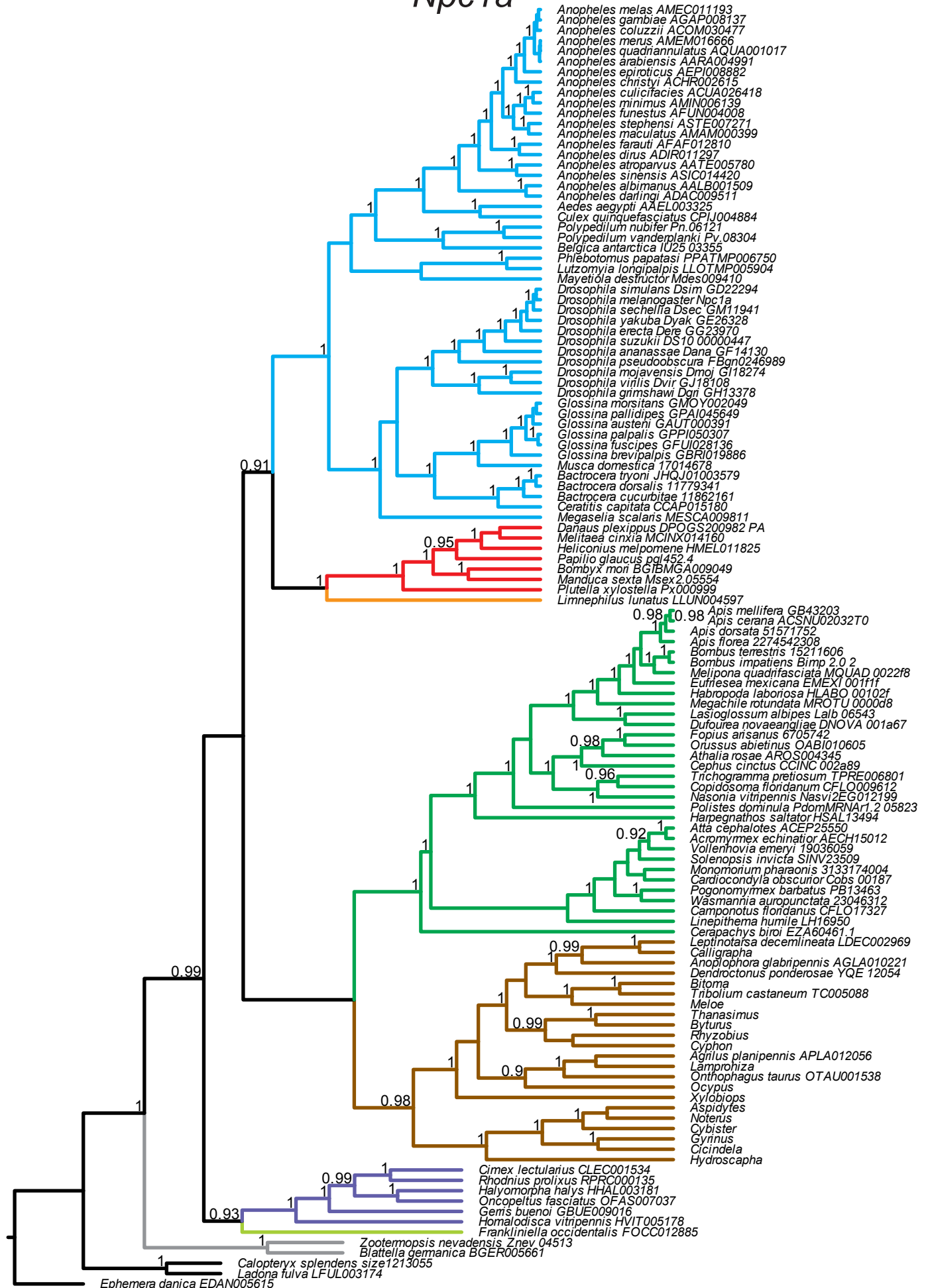
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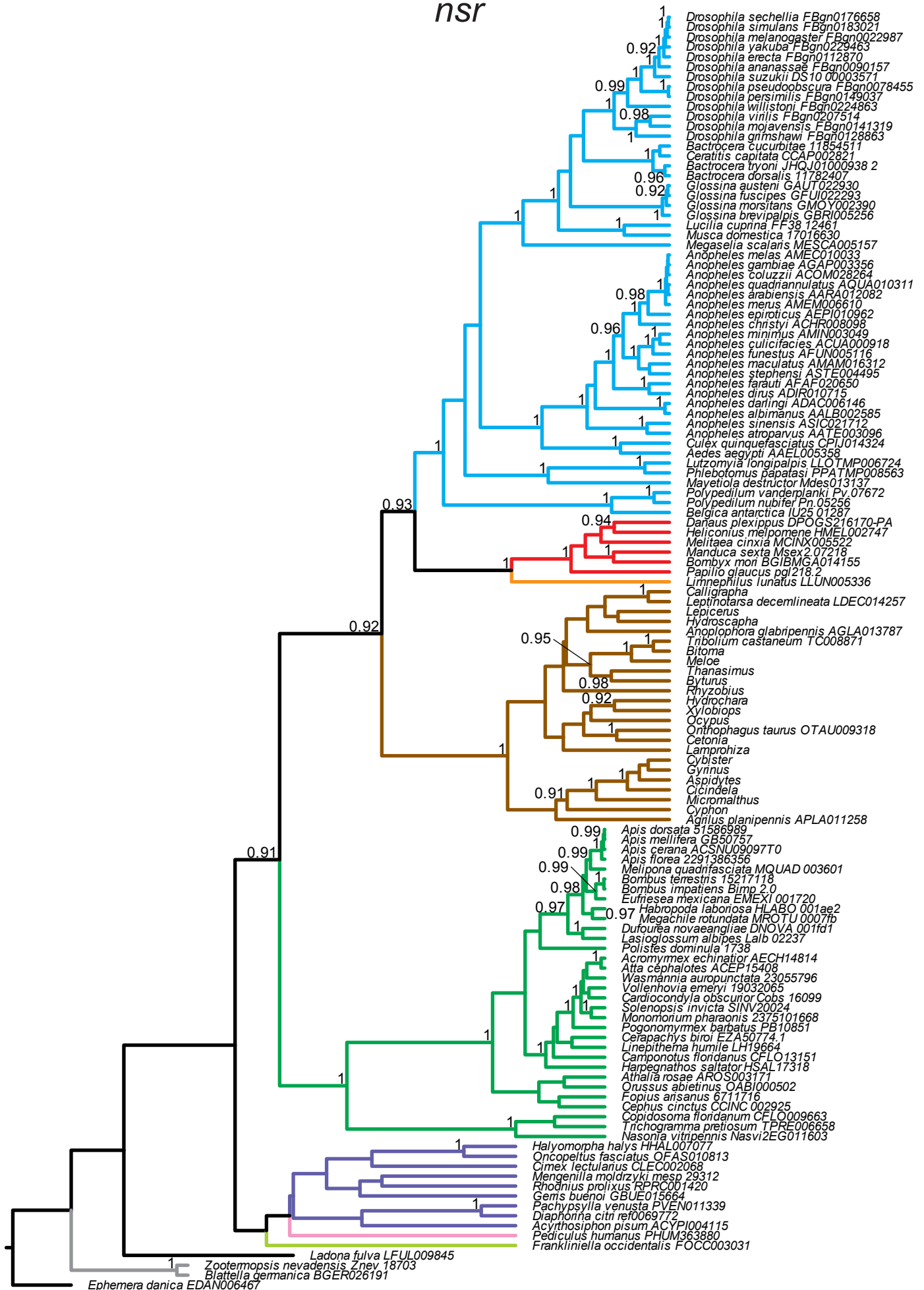
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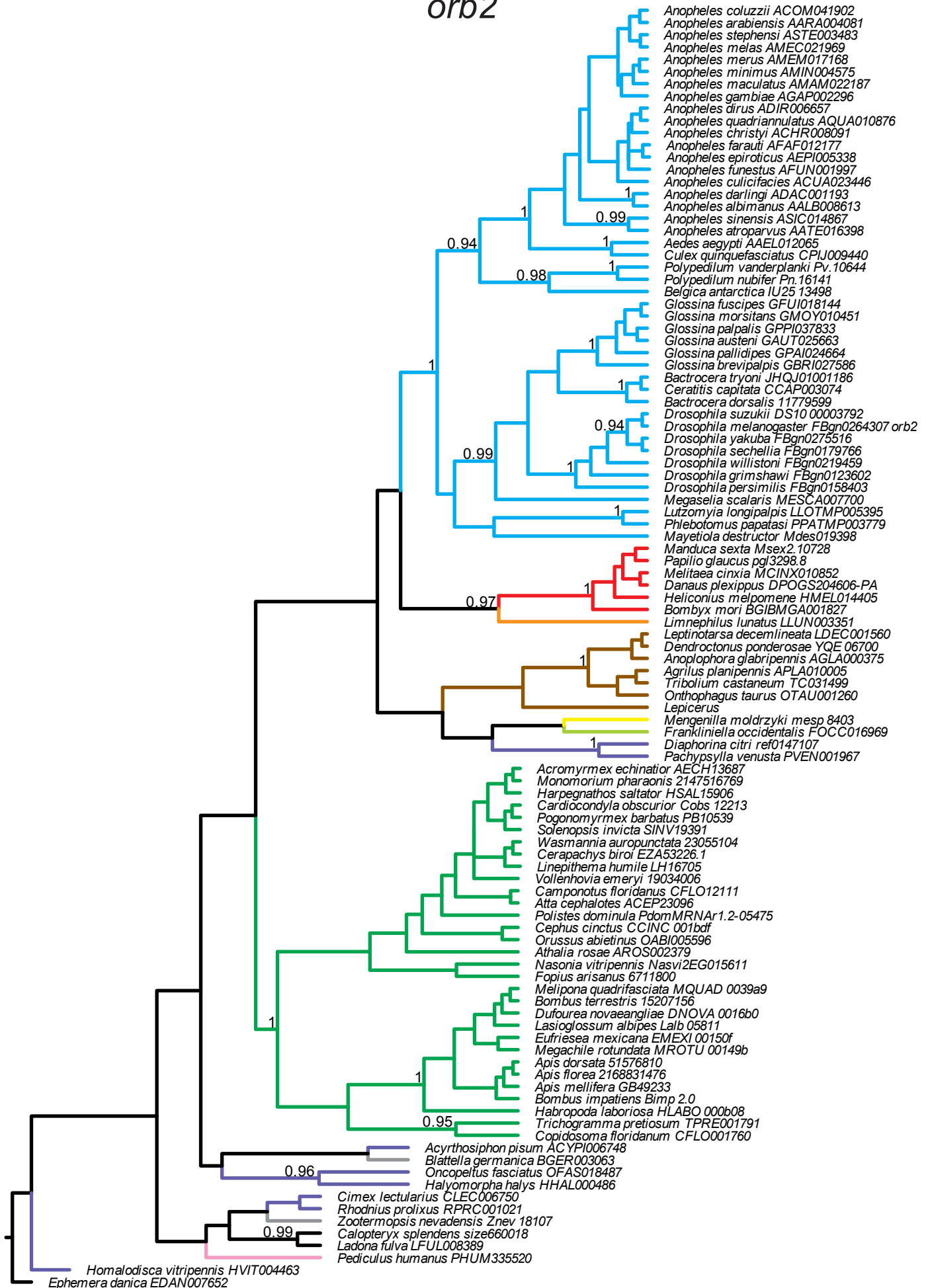
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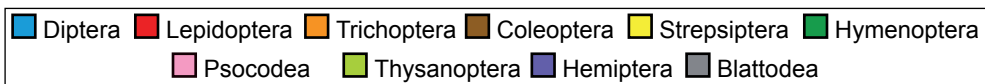
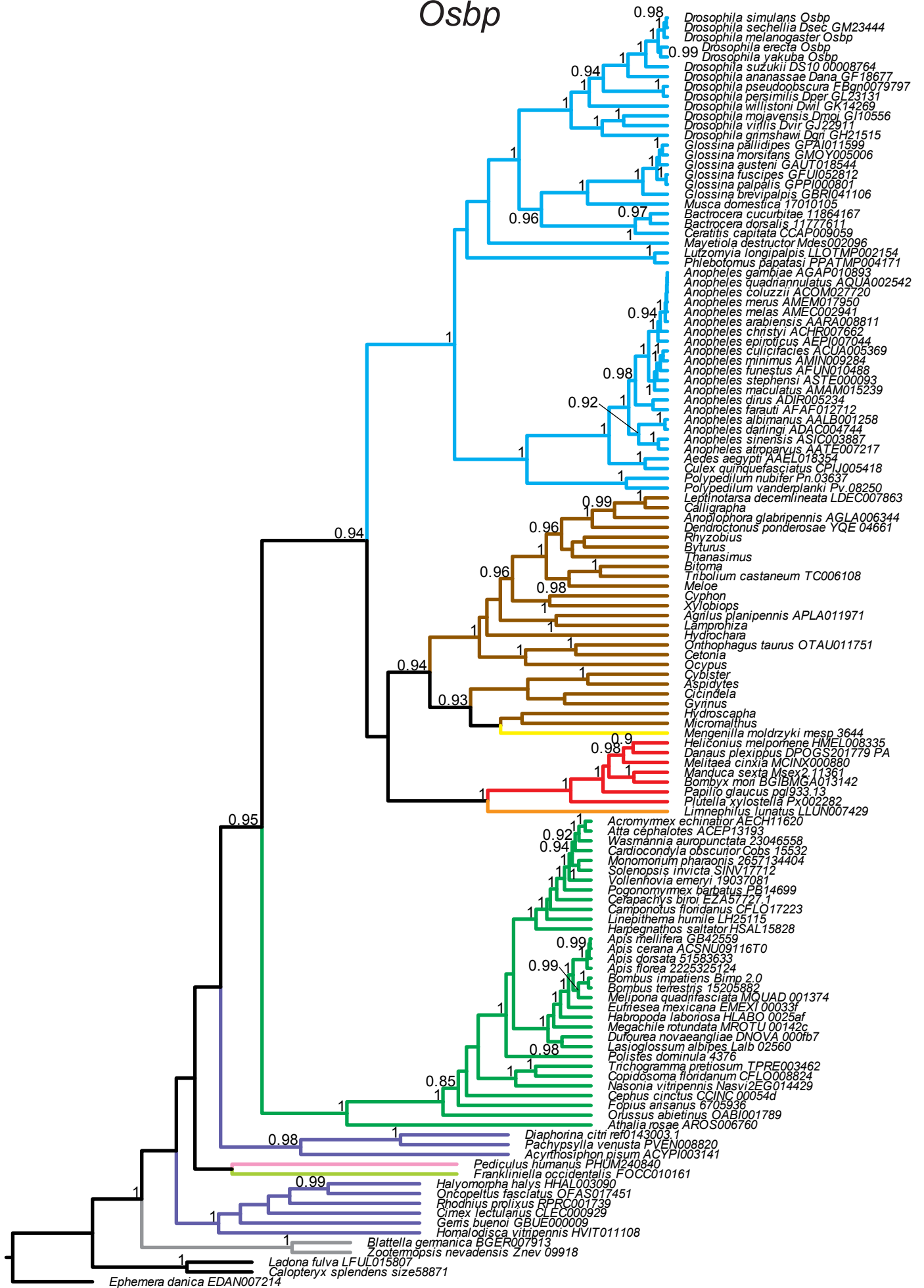
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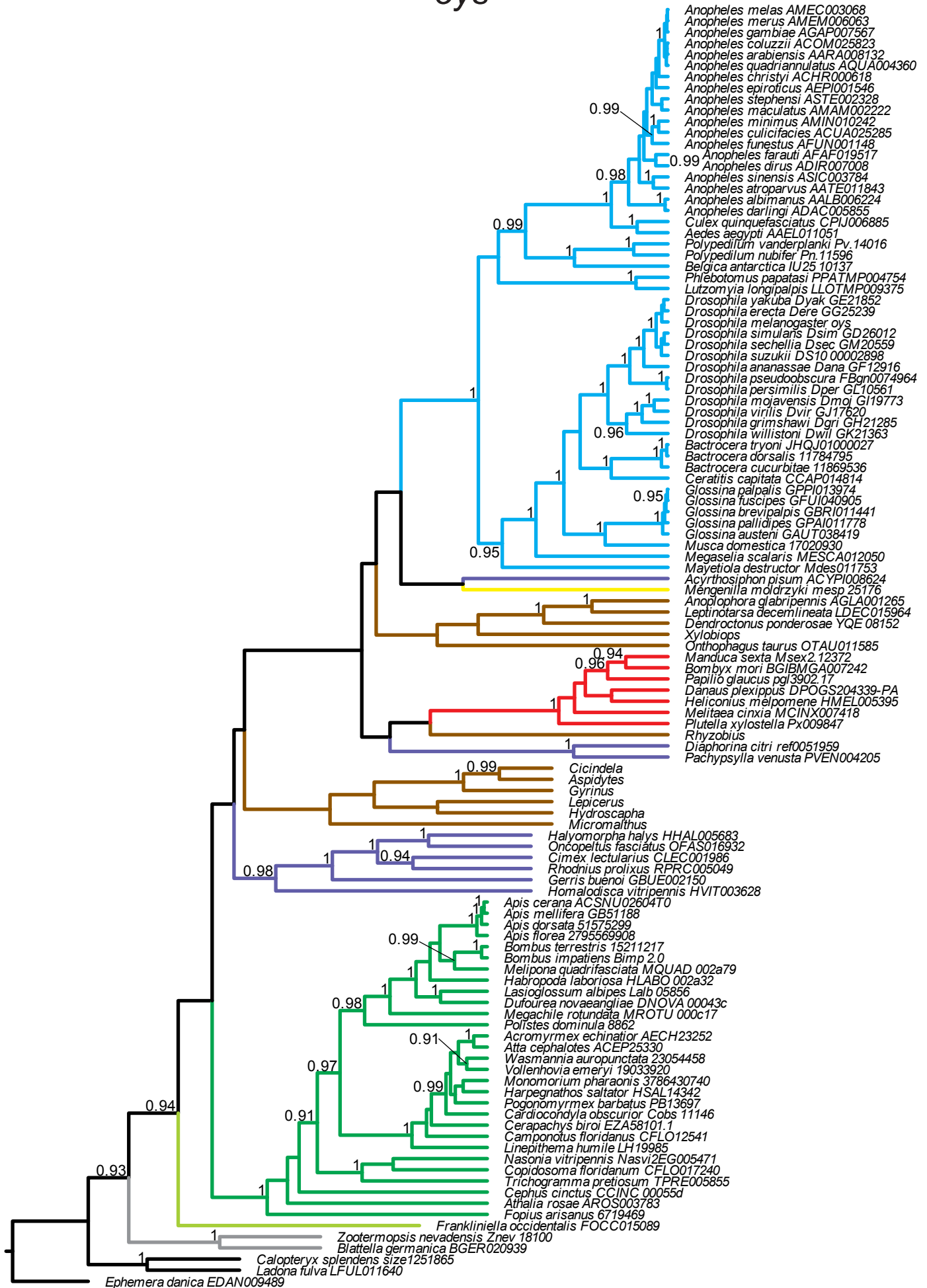
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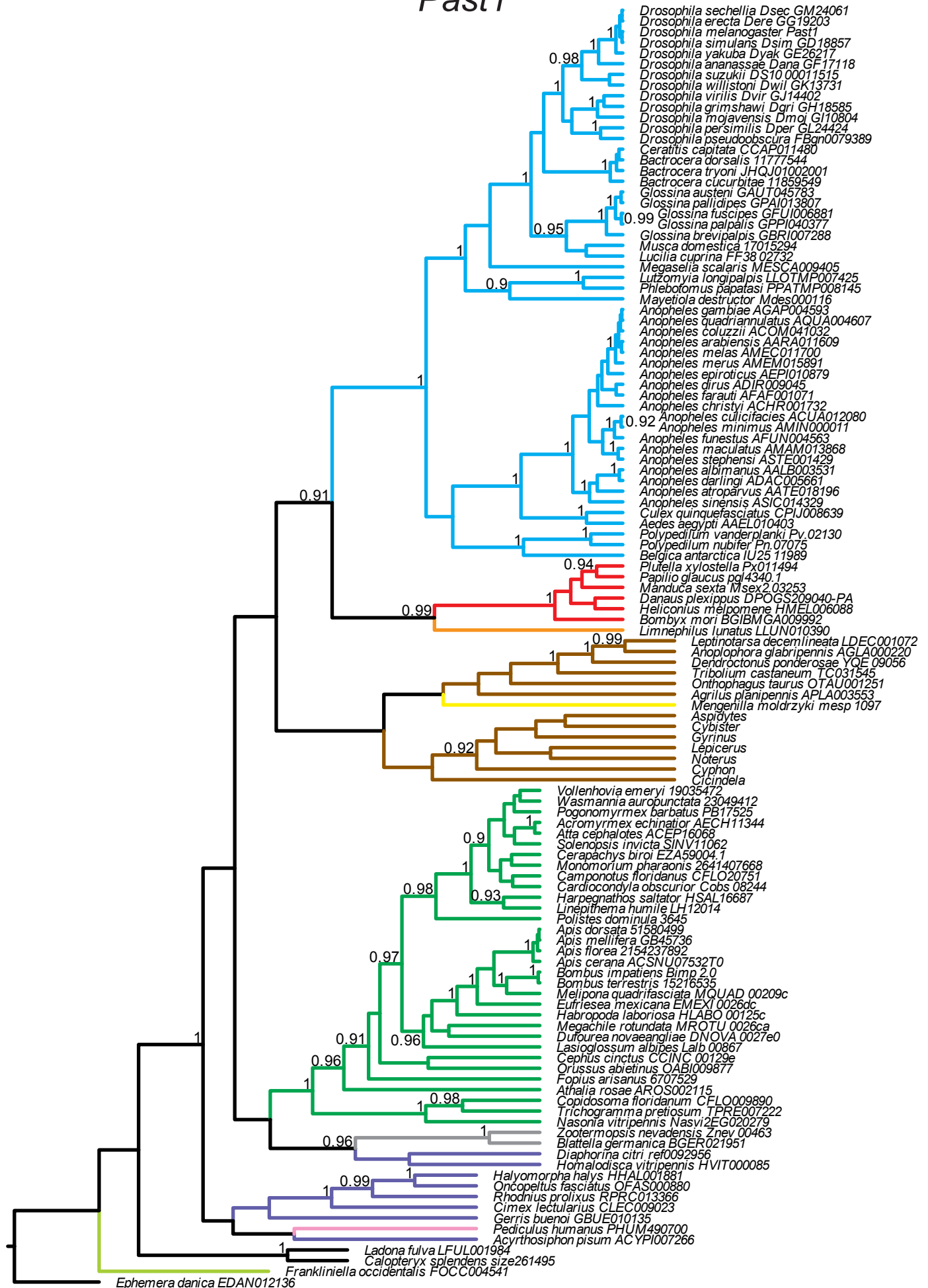
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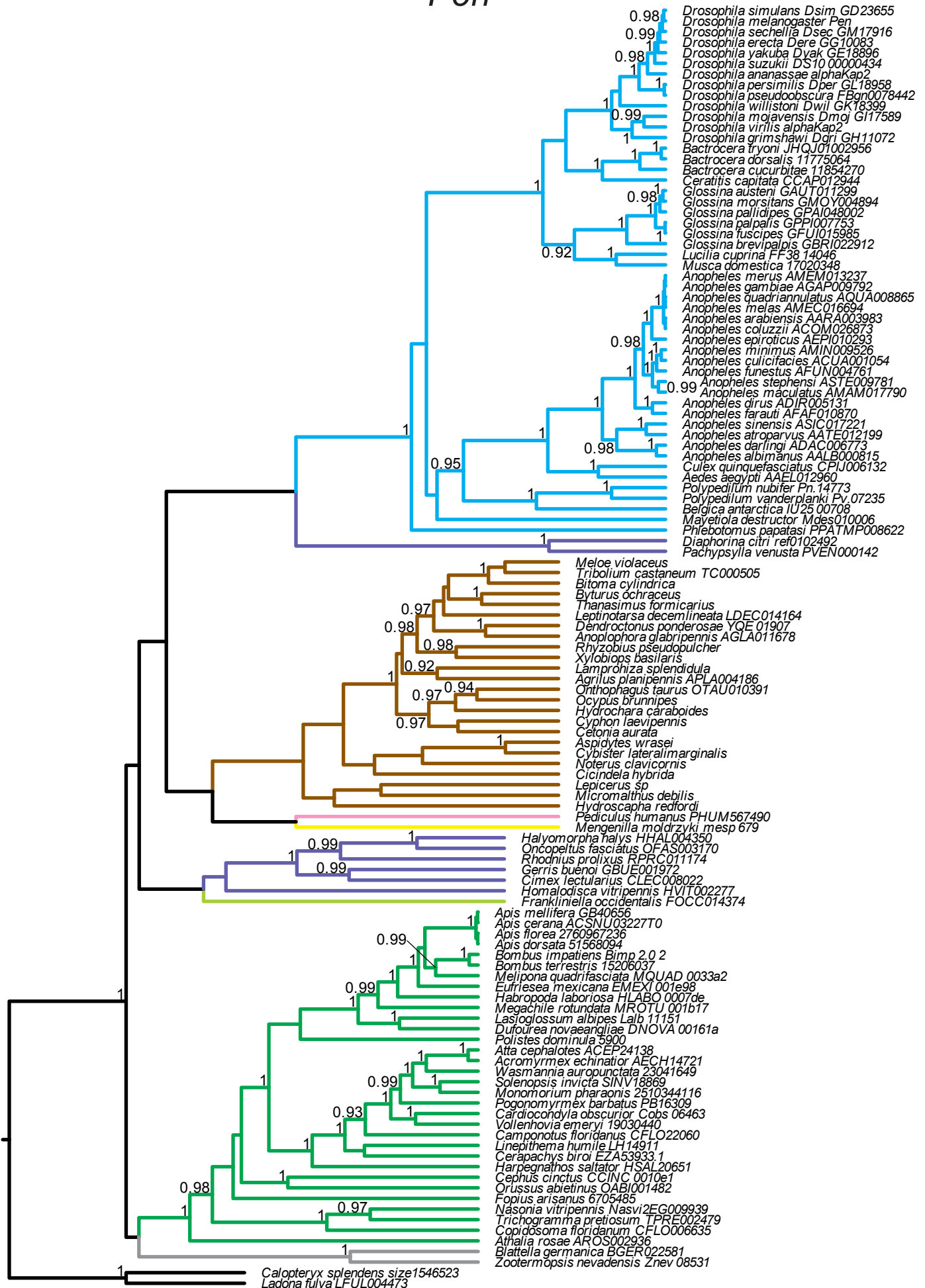
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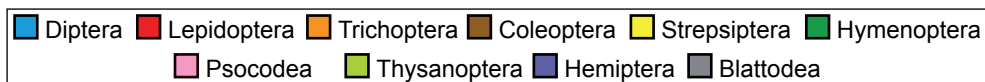
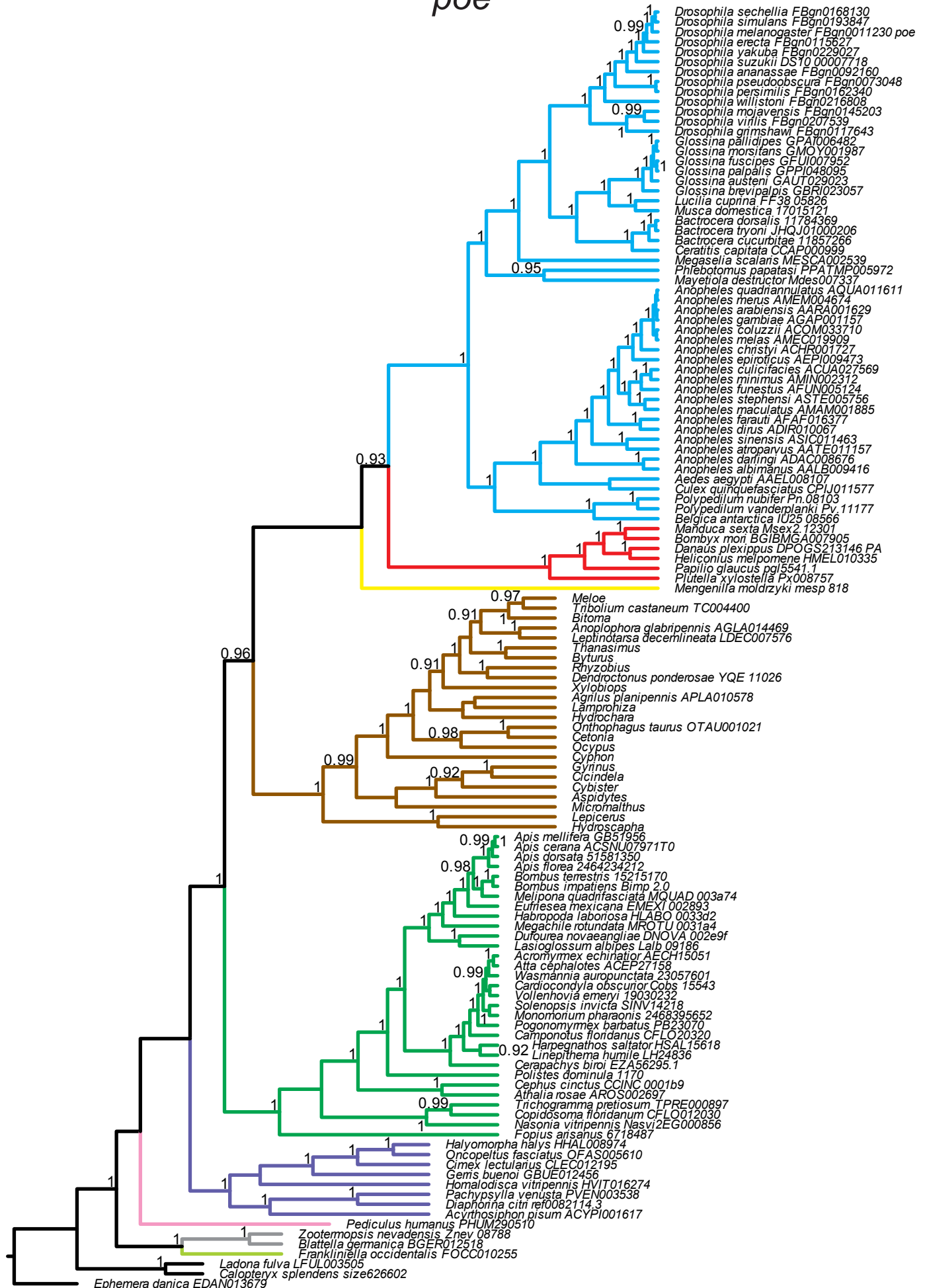
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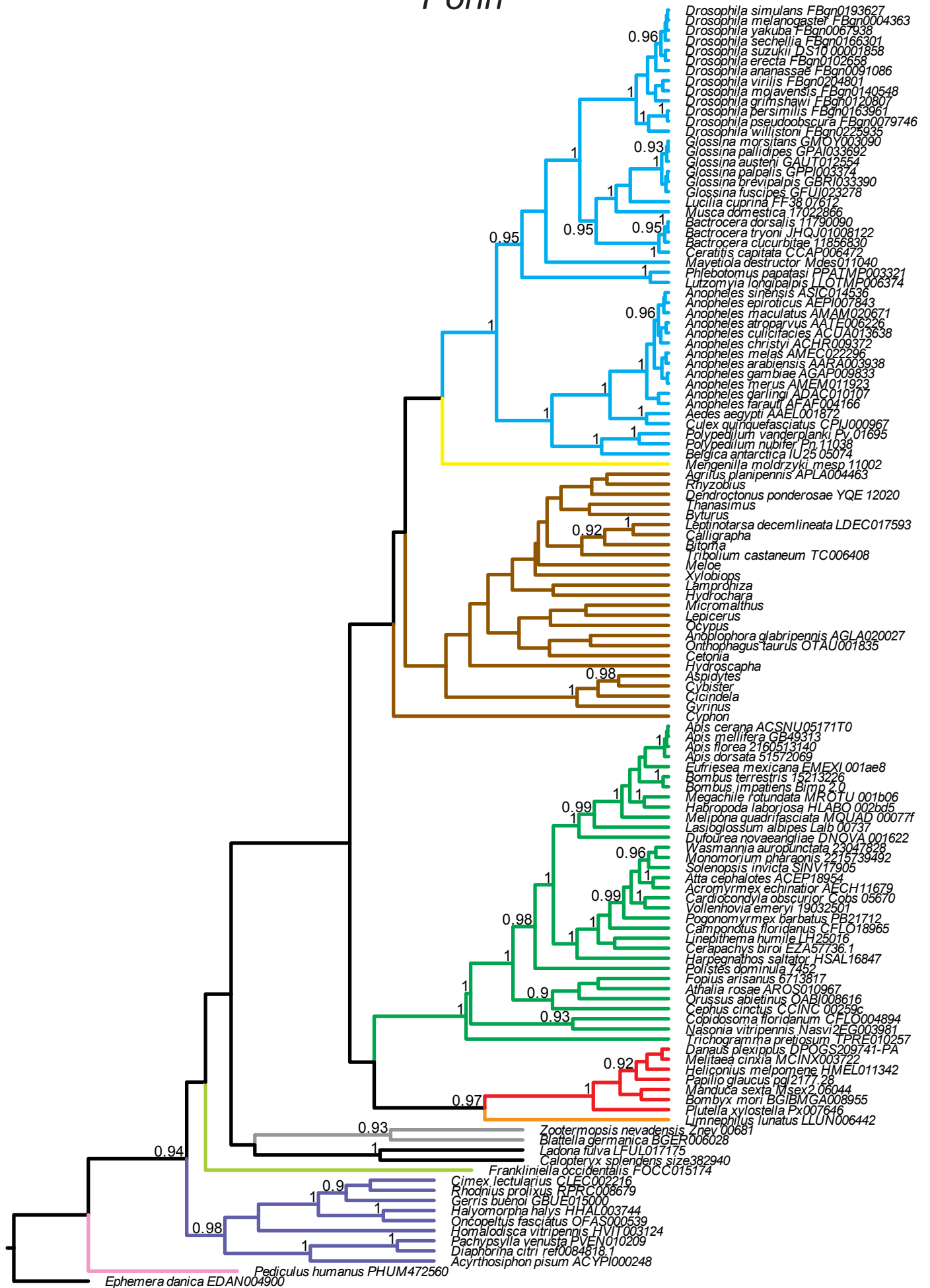
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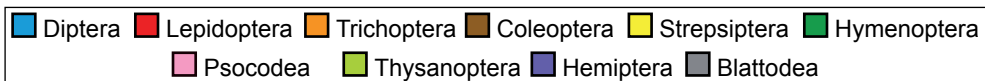
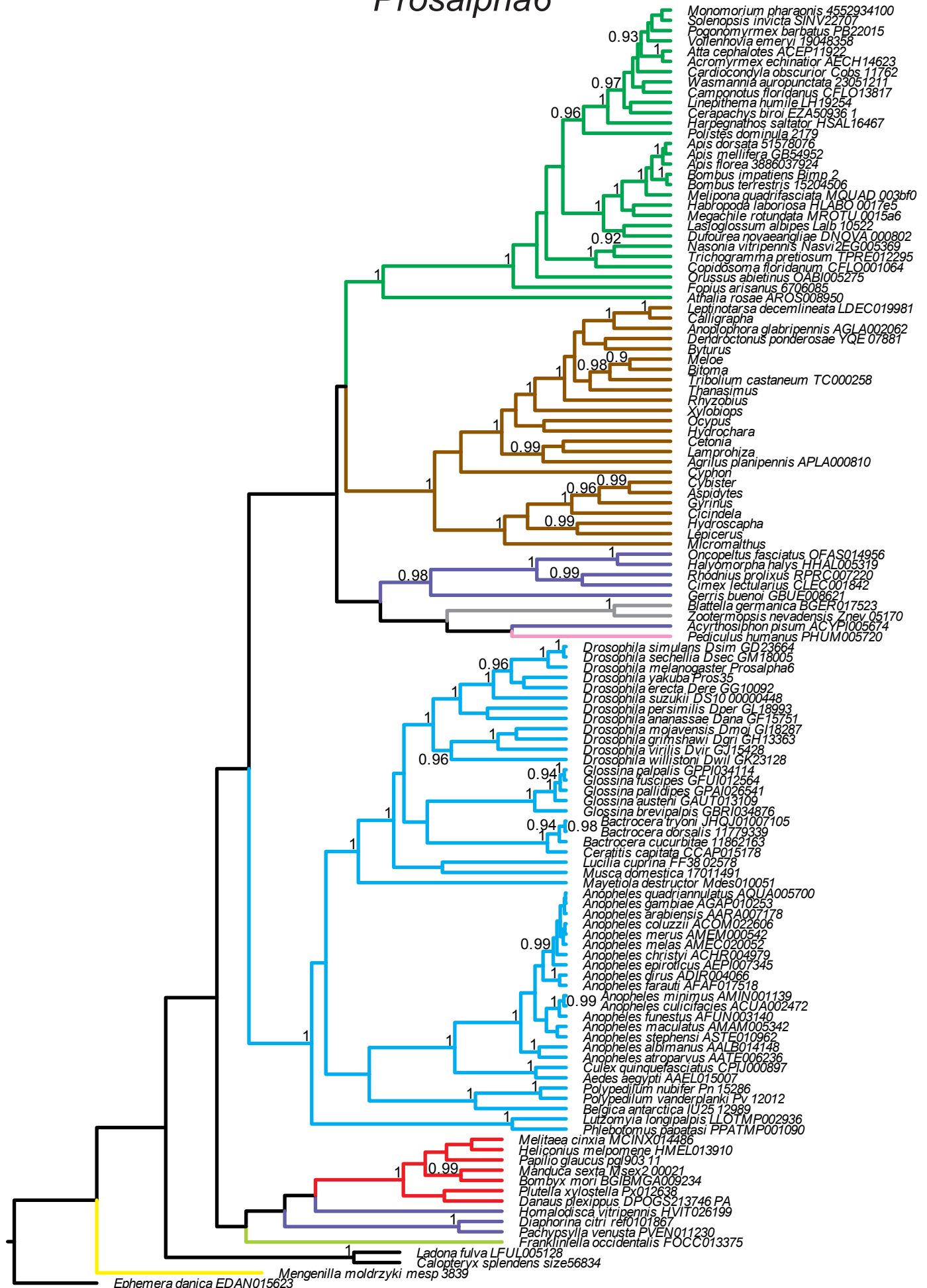
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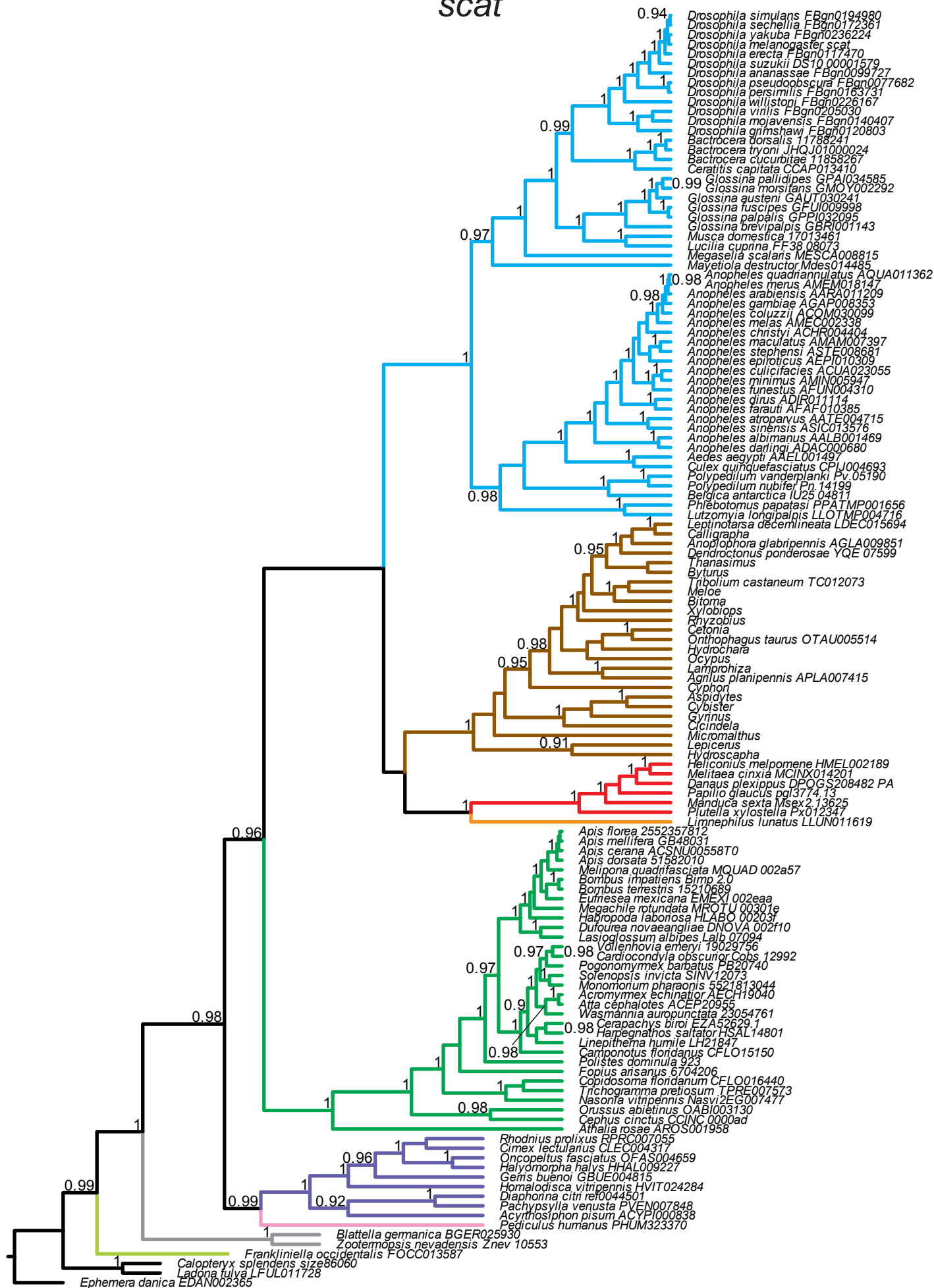
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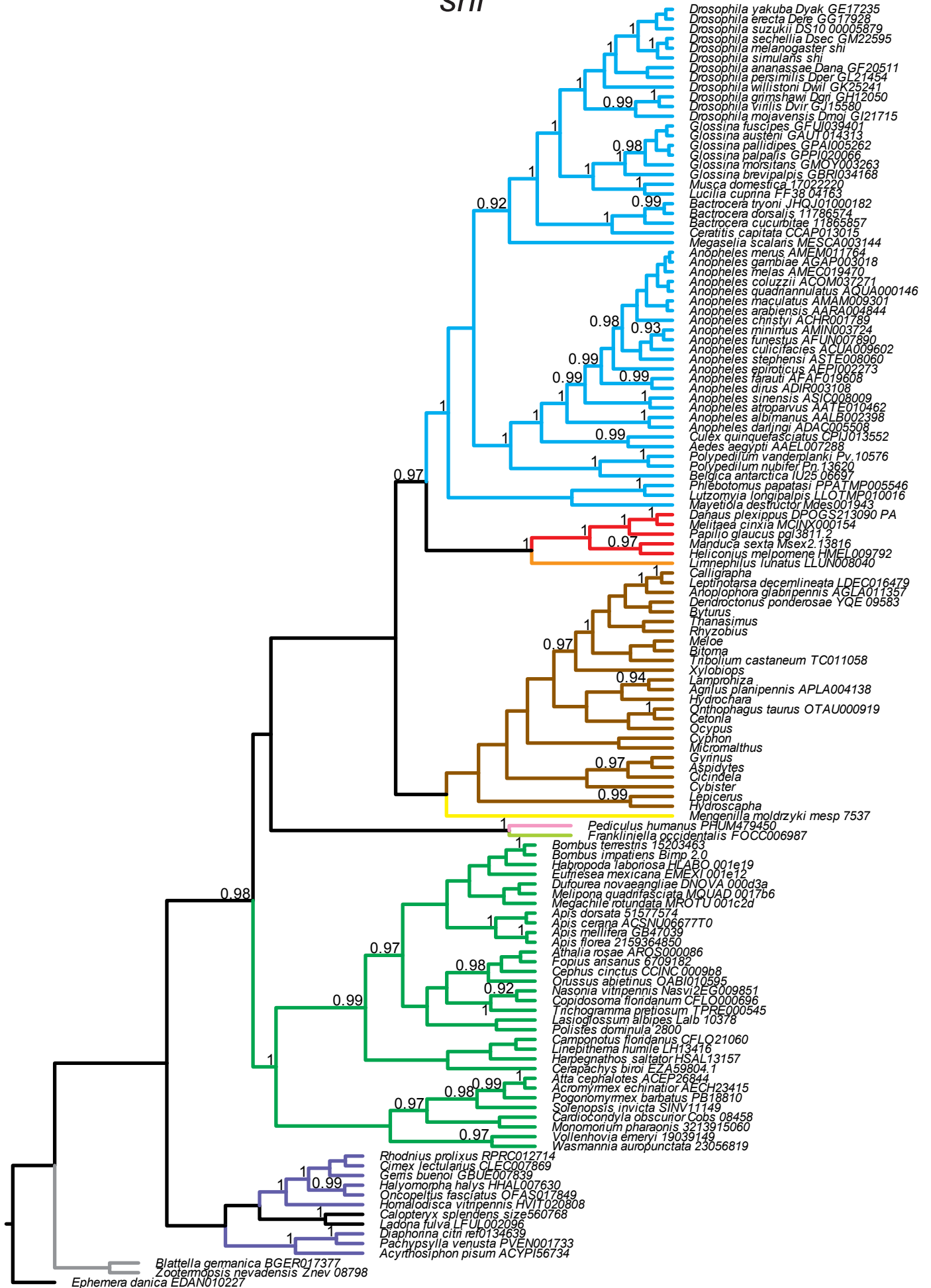
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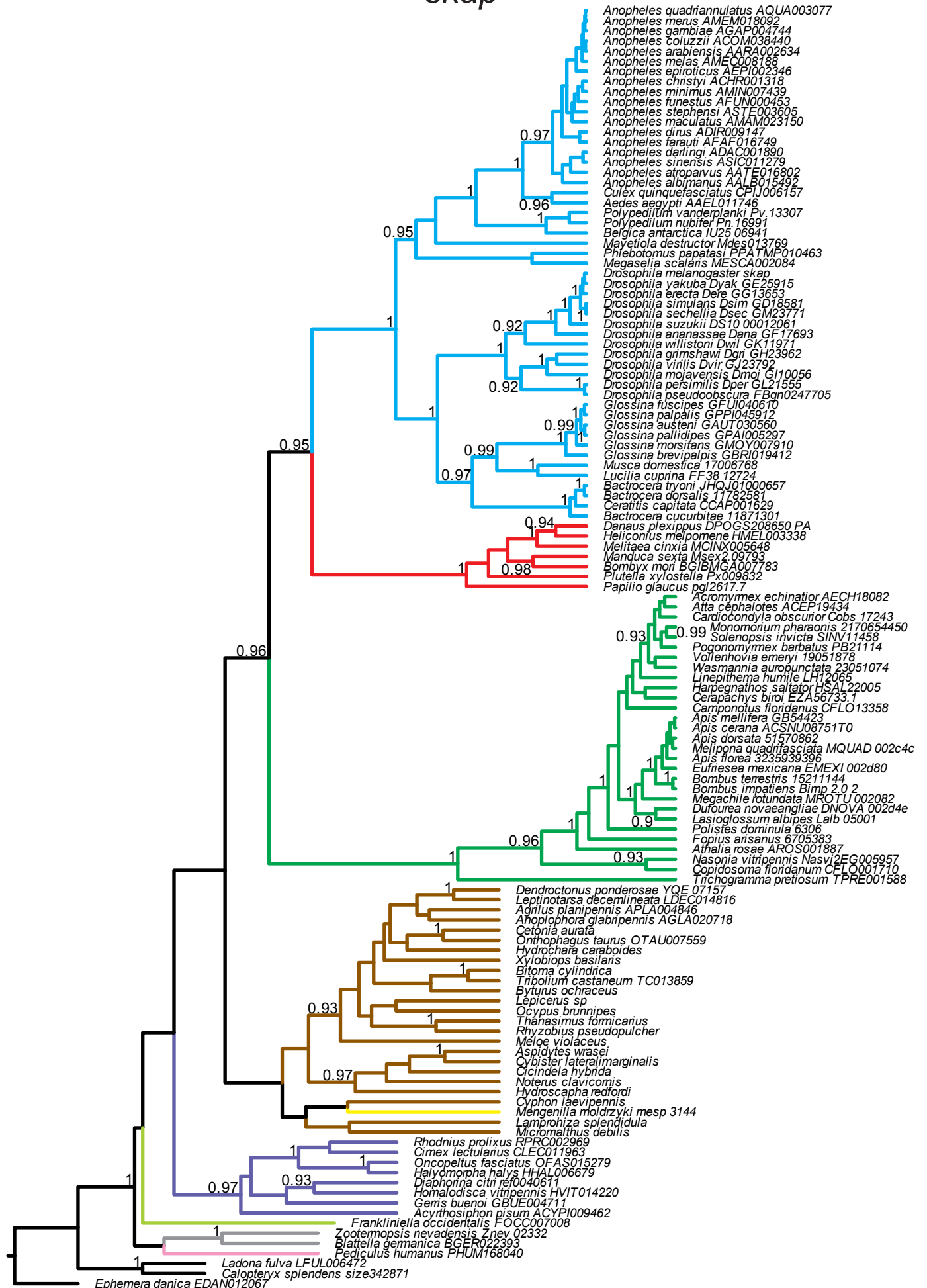
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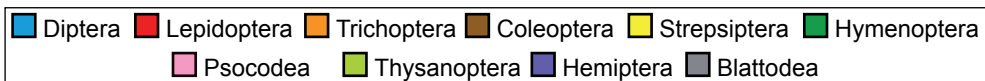
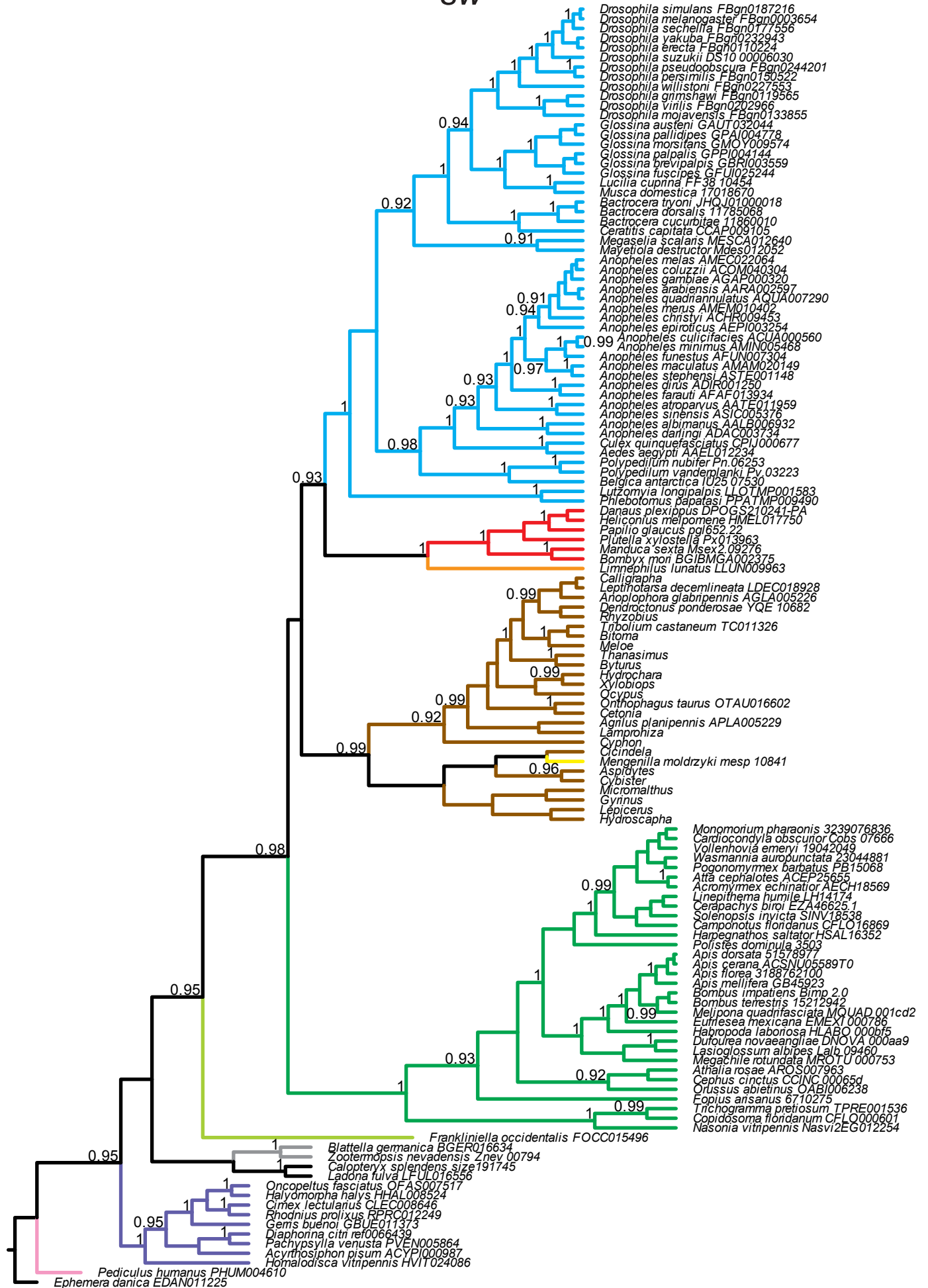
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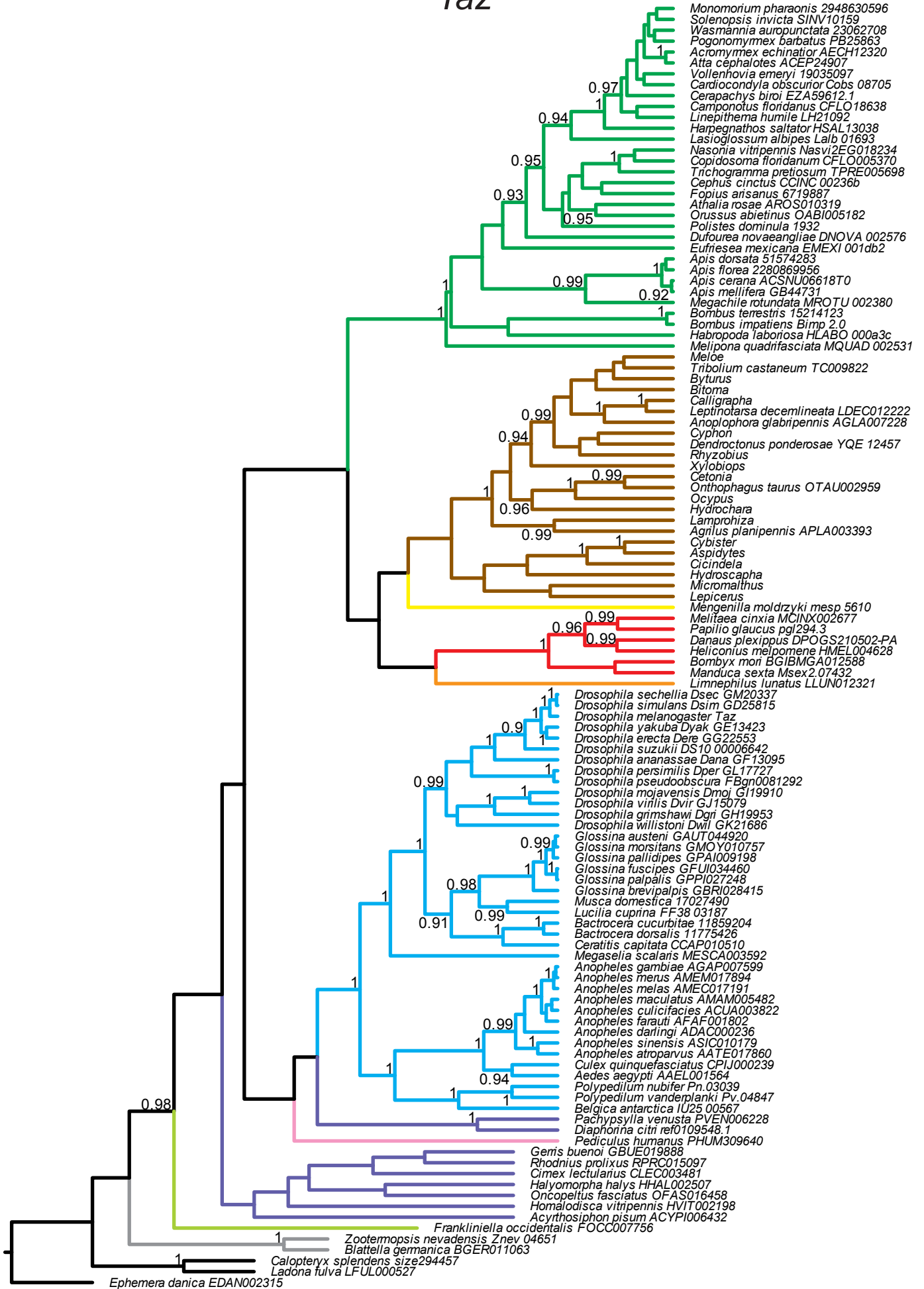
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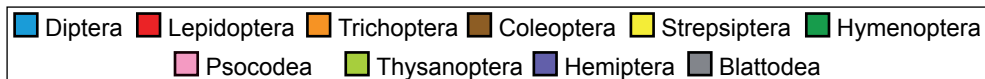
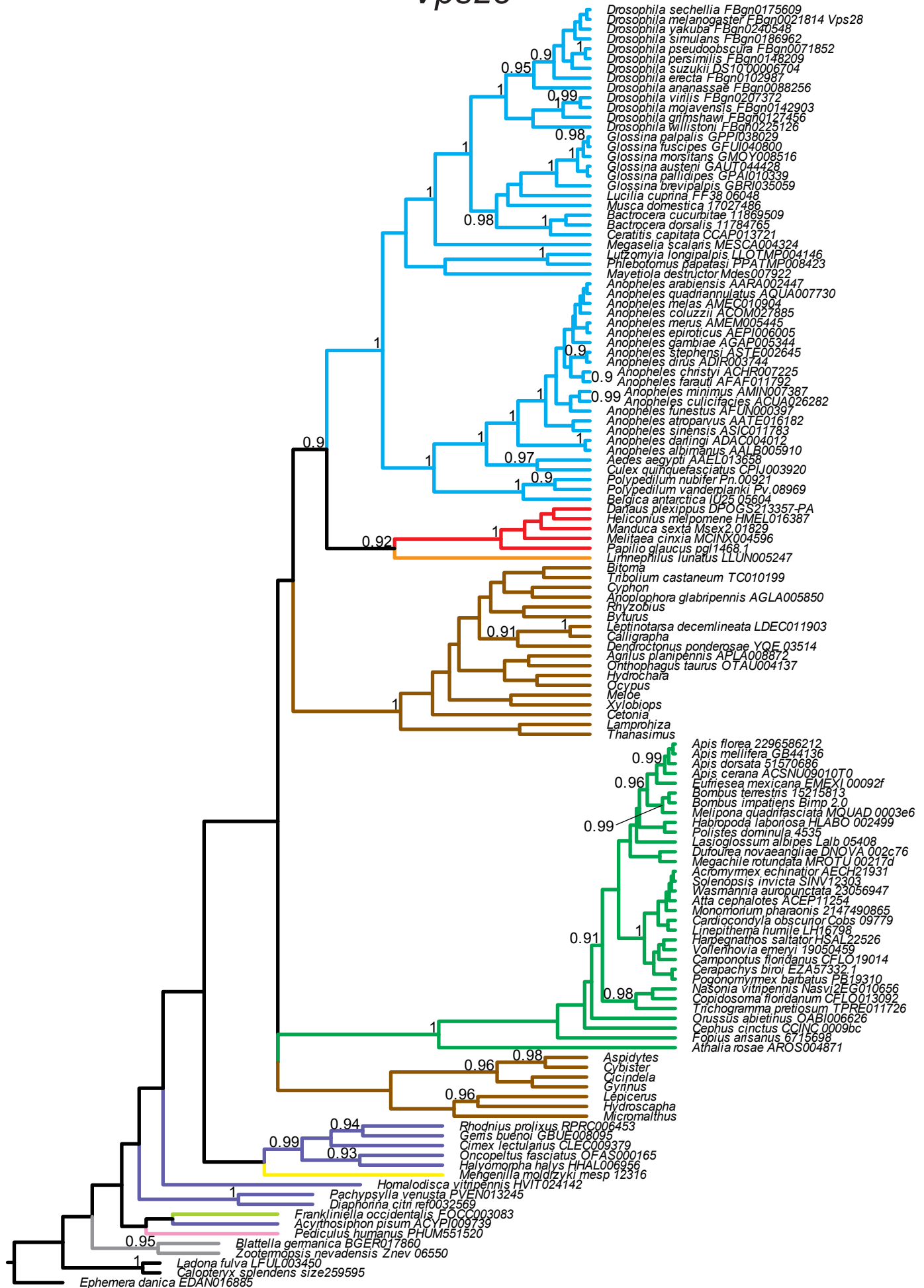
SW



Taz



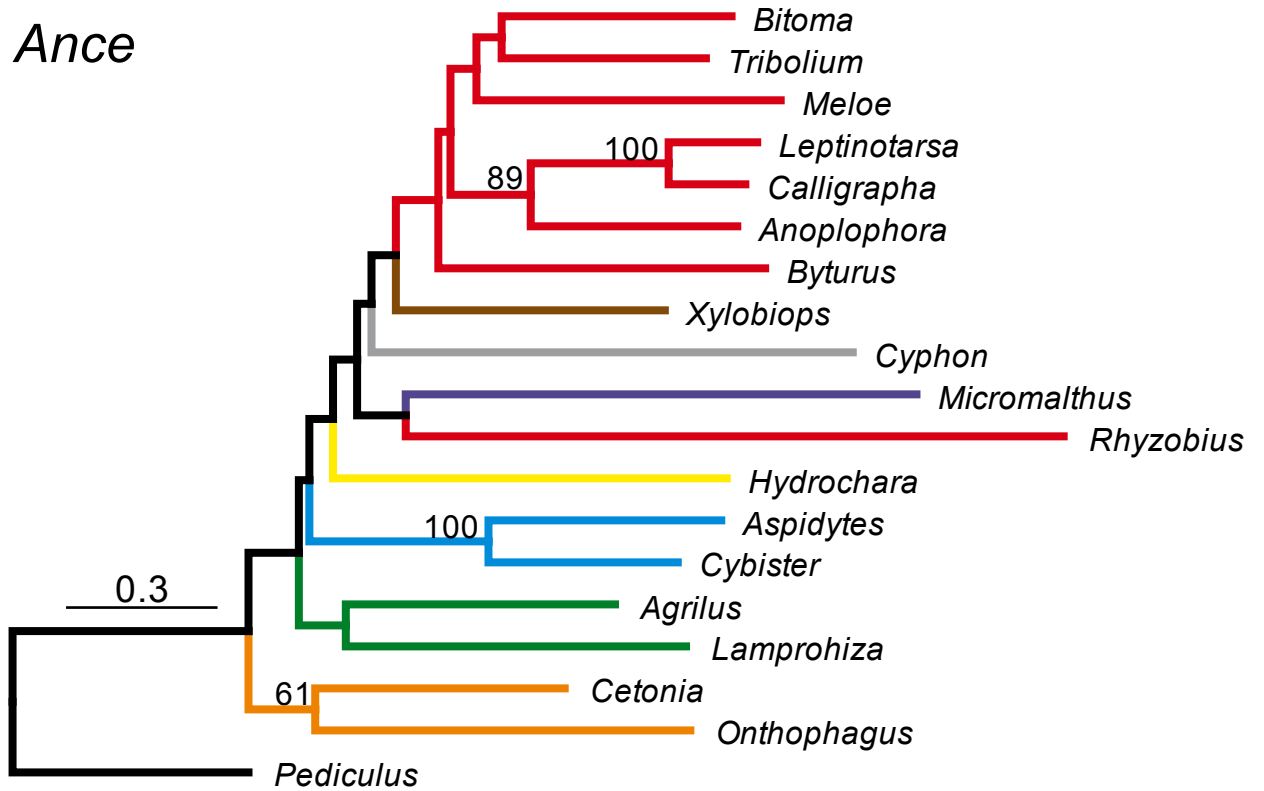
Vps28



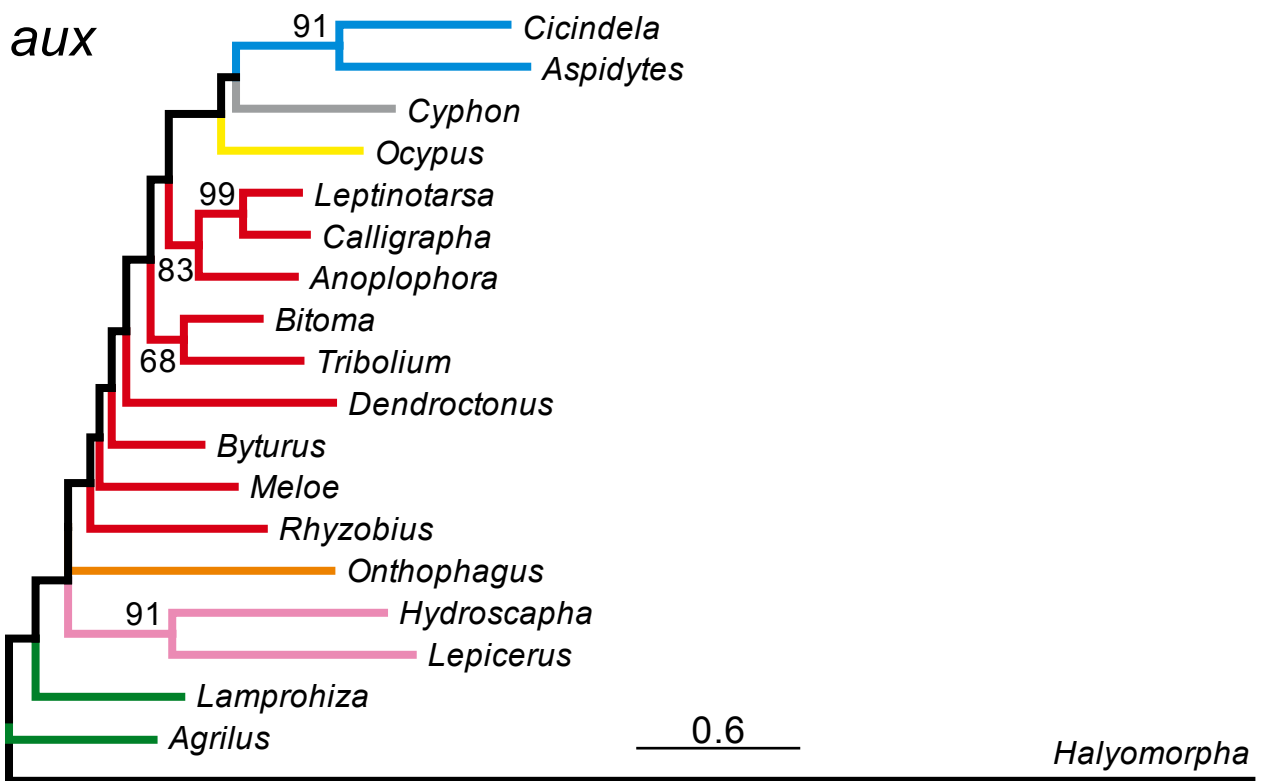
File S3. Maximum likelihood trees based on the nucleotide alignments of different sperm individualization genes in beetles.

Tree	Gene	Model	Gamma	Invariant	Log likelihood
1	<i>Ance</i>	GTR	0.660	0.146	-24961.88327
2	<i>aux</i>	GTR	0.386	0.070	-27681.59804
3	<i>blanks</i>	GTR	0.931	0.100	-12607.08759
4	<i>Bug22</i>	GTR	0.222	NA	-3454.61489
5	<i>CdsA</i>	GTR	0.290	0.154	-17968.57896
6	<i>Chc</i>	GTR	0.368	0.379	-55858.11062
7	<i>Ctp</i>	GTR	0.096	NA	-1384.6439
8	<i>Cul3</i>	TN93	0.175	0.204	-28997.57548
9	<i>Dark</i>	GTR	1.265	0.092	-20388.14695
10	<i>didum</i>	GTR	0.759	0.209	-60072.64694
11	<i>Dredd</i>	GTR	1.197	0.096	-14618.72638
12	<i>Dronc</i>	GTR	1.355	0.099	-15698.08633
13	<i>Duba</i>	GTR	0.527	0.176	-12010.48828
14	<i>EcR</i>	GTR	0.449	0.365	-12199.45136
15	<i>eIF3m</i>	GTR	0.329	0.137	-18855.00527
16	<i>Fadd</i>	GTR	1.321	0.084	-4356.88960
17	<i>gish</i>	GTR	0.211	0.170	-15923.19717
18	<i>gudu</i>	GTR	0.618	0.135	-22338.05316
19	<i>heph</i>	TN93	0.396	0.275	-8479.41719
20	<i>hmw</i>	GTR	0.898	NA	-1707.47296
21	<i>jar</i>	GTR	0.708	0.241	-52172.98272
22	<i>klhl10</i>	GTR	0.504	0.239	-17745.77407
23	<i>Lasp</i>	GTR	0.474	0.351	-5407.13219
24	<i>Mer</i>	GTR	0.598	0.356	-22473.10341
25	<i>mlt</i>	GTR	0.593	0.196	-19352.46023
26	<i>nes</i>	GTR	0.911	0.148	-25494.50312
27	<i>Npc1a</i>	GTR	0.724	0.204	-58520.58794
28	<i>nsr</i>	GTR	0.287	0.143	-11564.48392
29	<i>orb2</i>	GTR	0.327	0.450	-4091.42072
30	<i>Osbp</i>	GTR	0.699	0.244	-29993.57419
31	<i>oys</i>	GTR	0.773	0.158	-15795.25364
32	<i>Past1</i>	GTR	0.474	0.325	-14648.80870
33	<i>Pen</i>	GTR	0.676	0.232	-26388.05898
34	<i>poe</i>	GTR	0.590	0.253	-50399.32806
35	<i>porin</i>	GTR	0.674	0.191	-15348.95453
36	<i>Prosalpha6T</i>	GTR	0.659	0.312	-13745.91664
37	<i>scat</i>	GTR	0.556	0.147	-34071.26981
38	<i>shi</i>	GTR	0.552	0.395	-34985.87502
39	<i>skap</i>	GTR	0.596	0.317	-20864.74113
40	<i>sw</i>	GTR	0.473	0.265	-21539.32783
41	<i>Taz</i>	GTR	0.717	0.284	-11982.00743
42	<i>Vps28</i>	GTR	0.241	0.154	-7981.57649

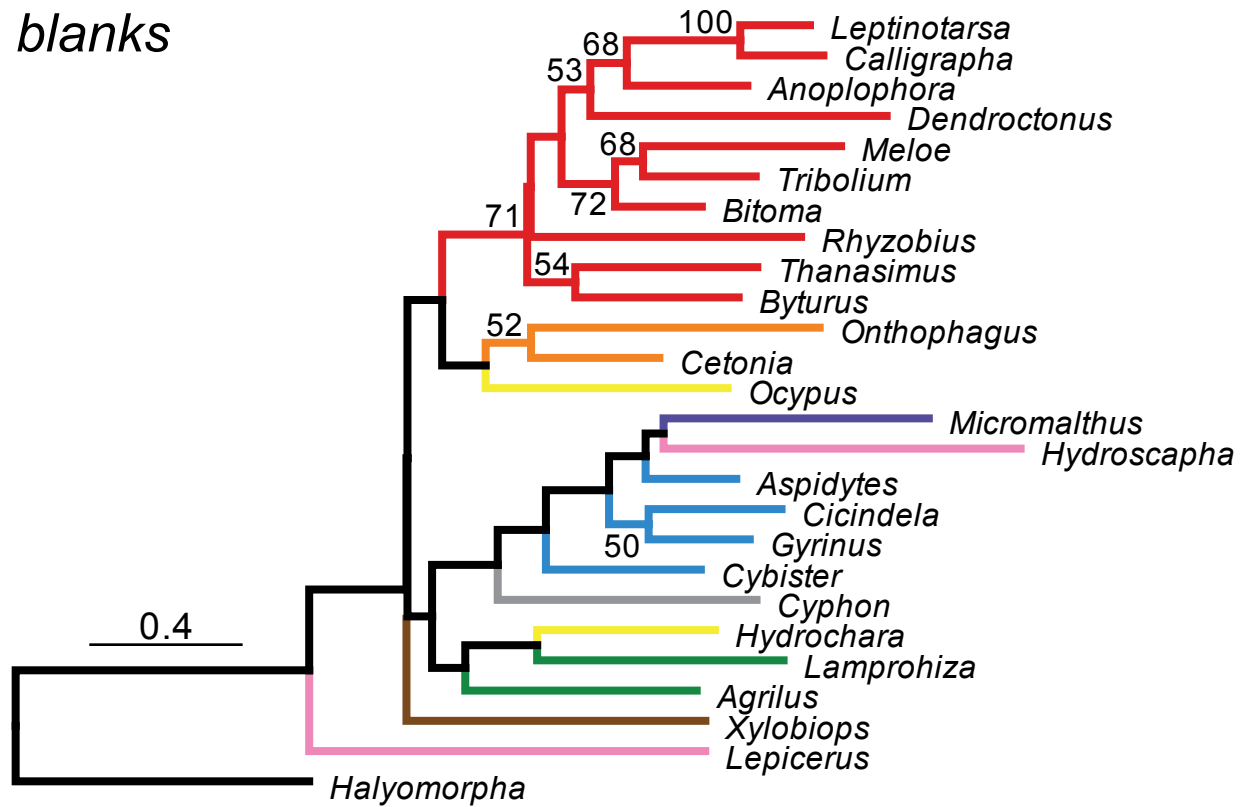
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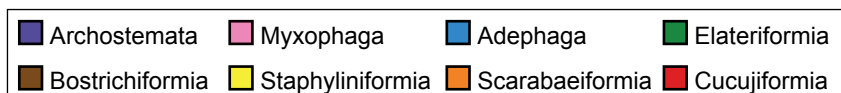
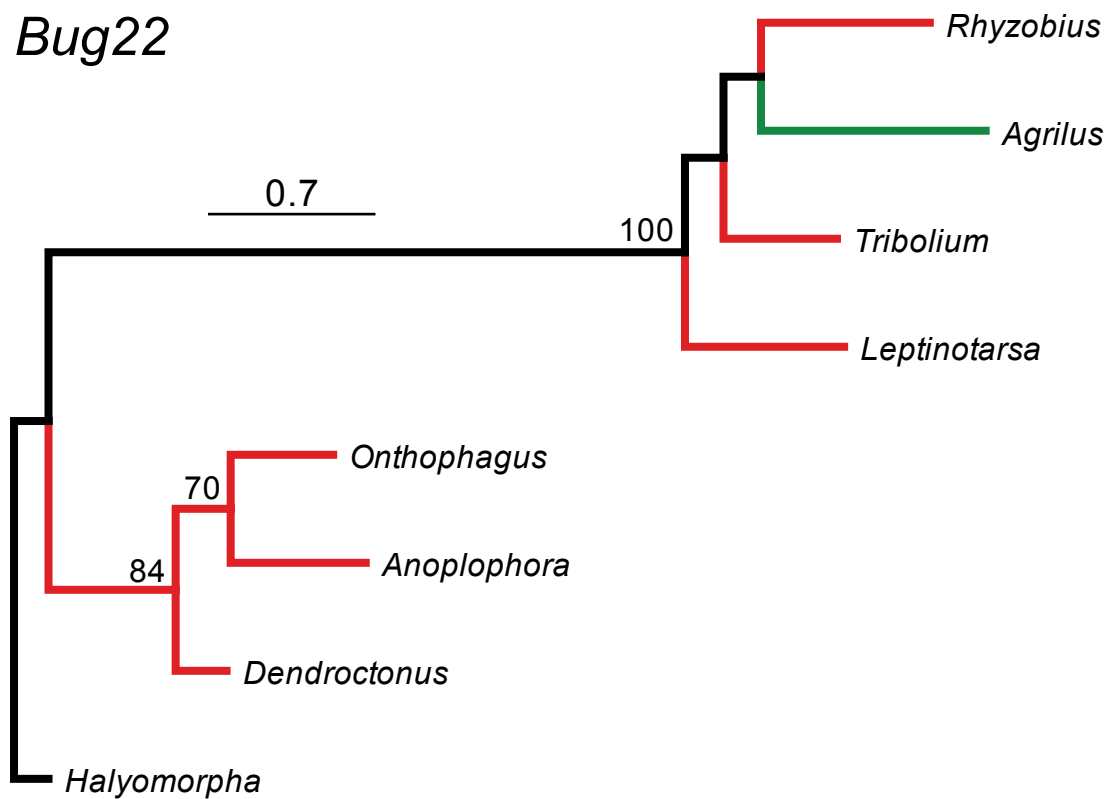
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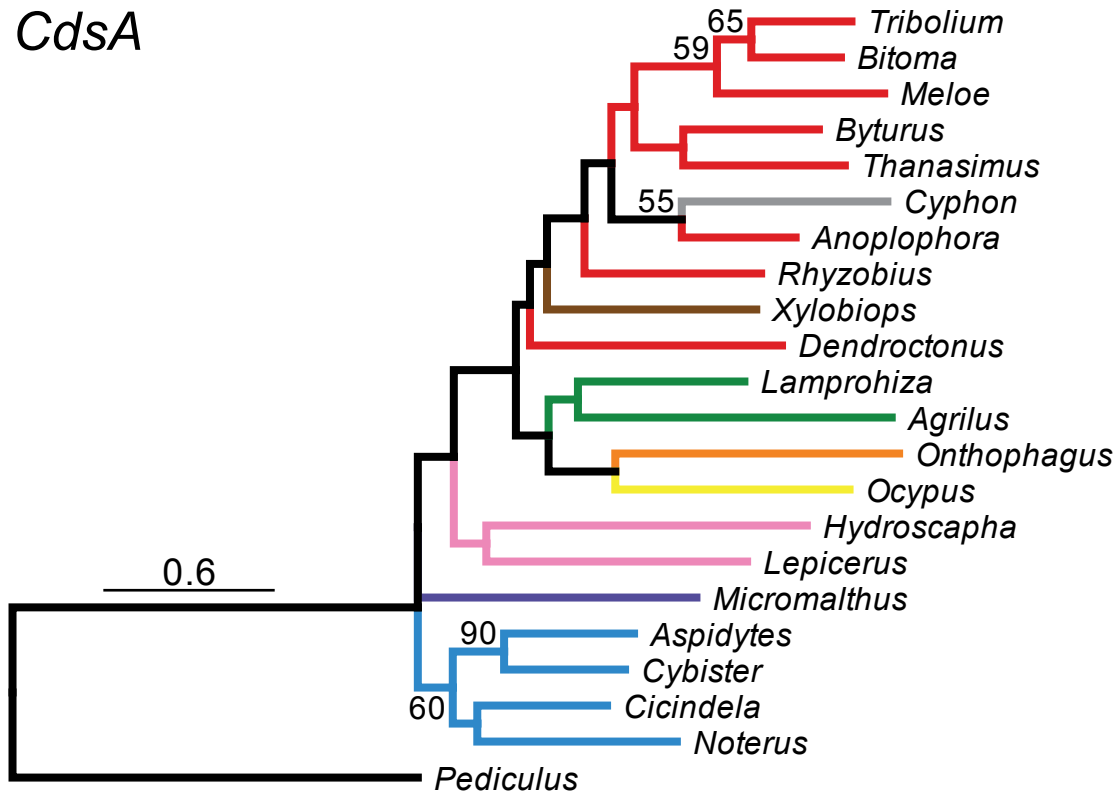
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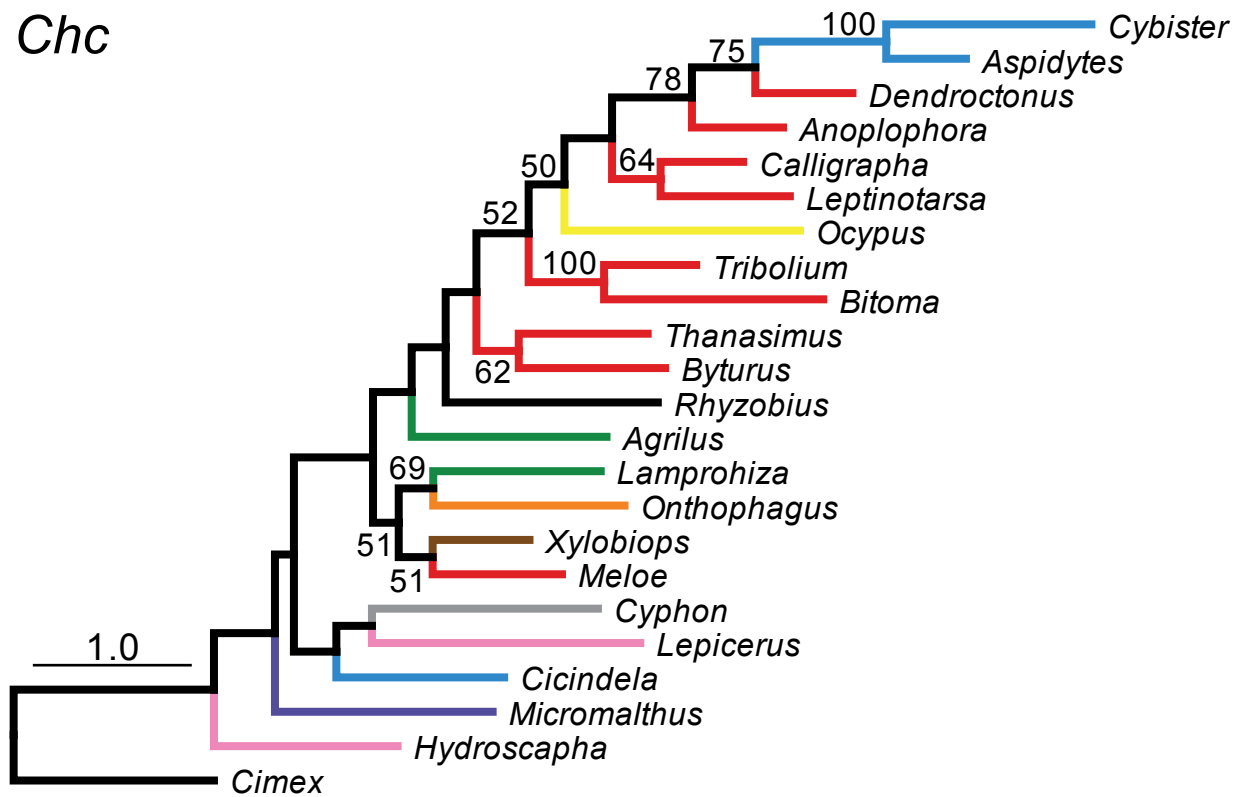
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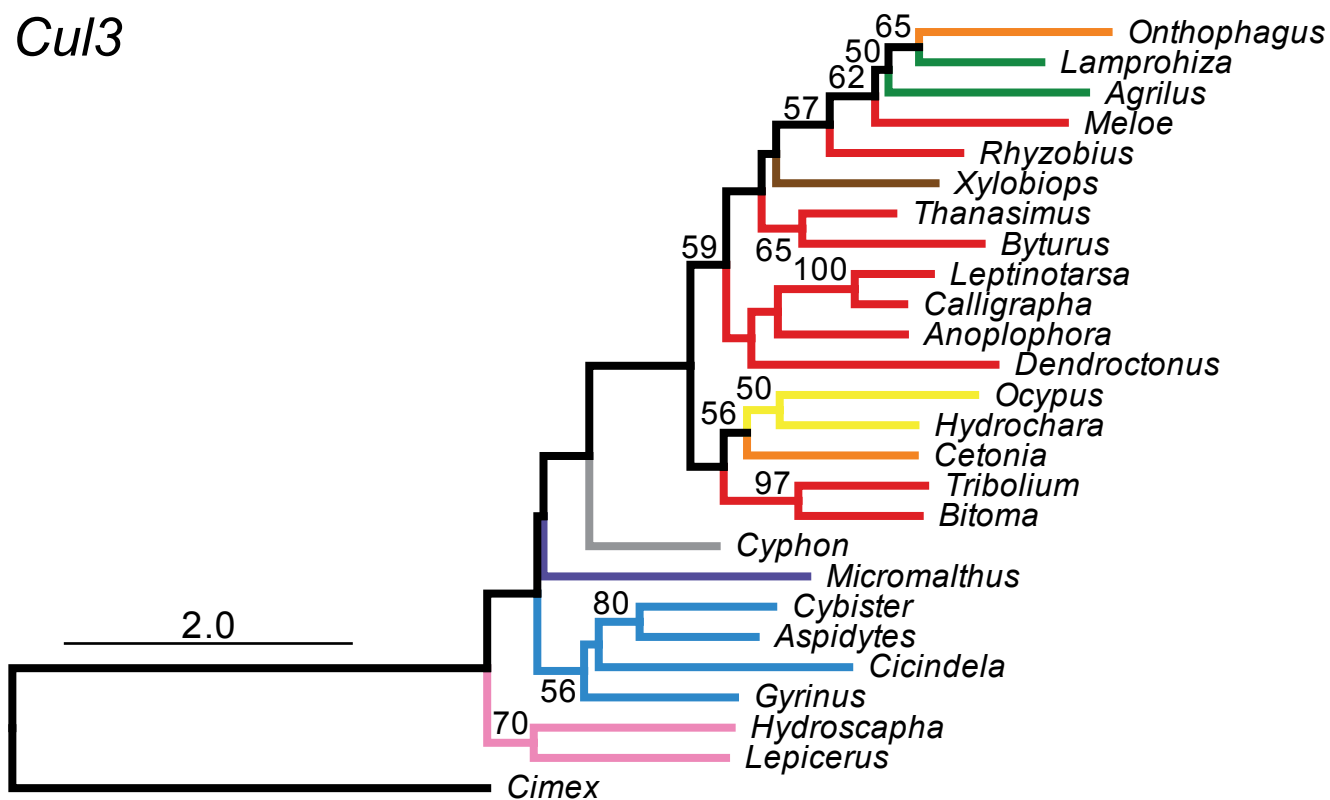
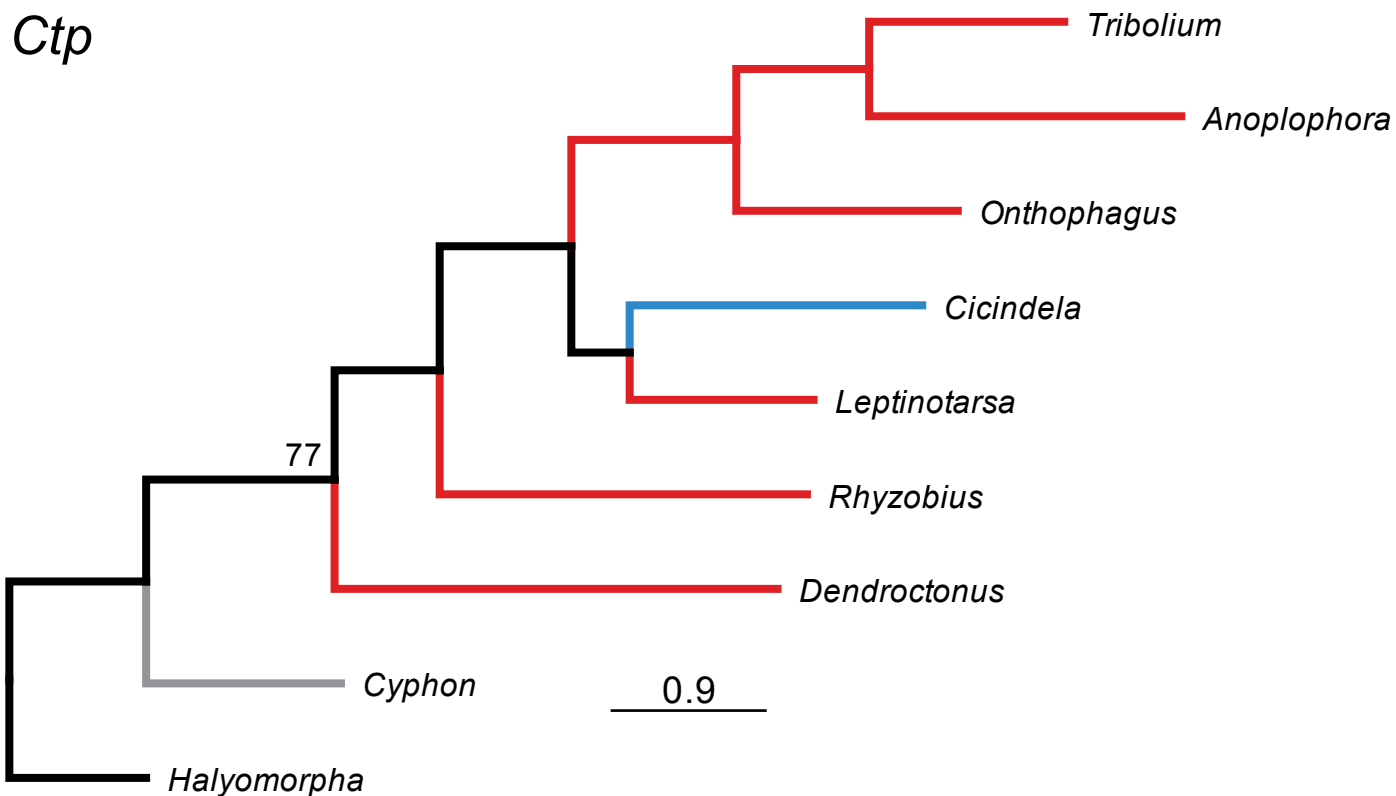


CdsA

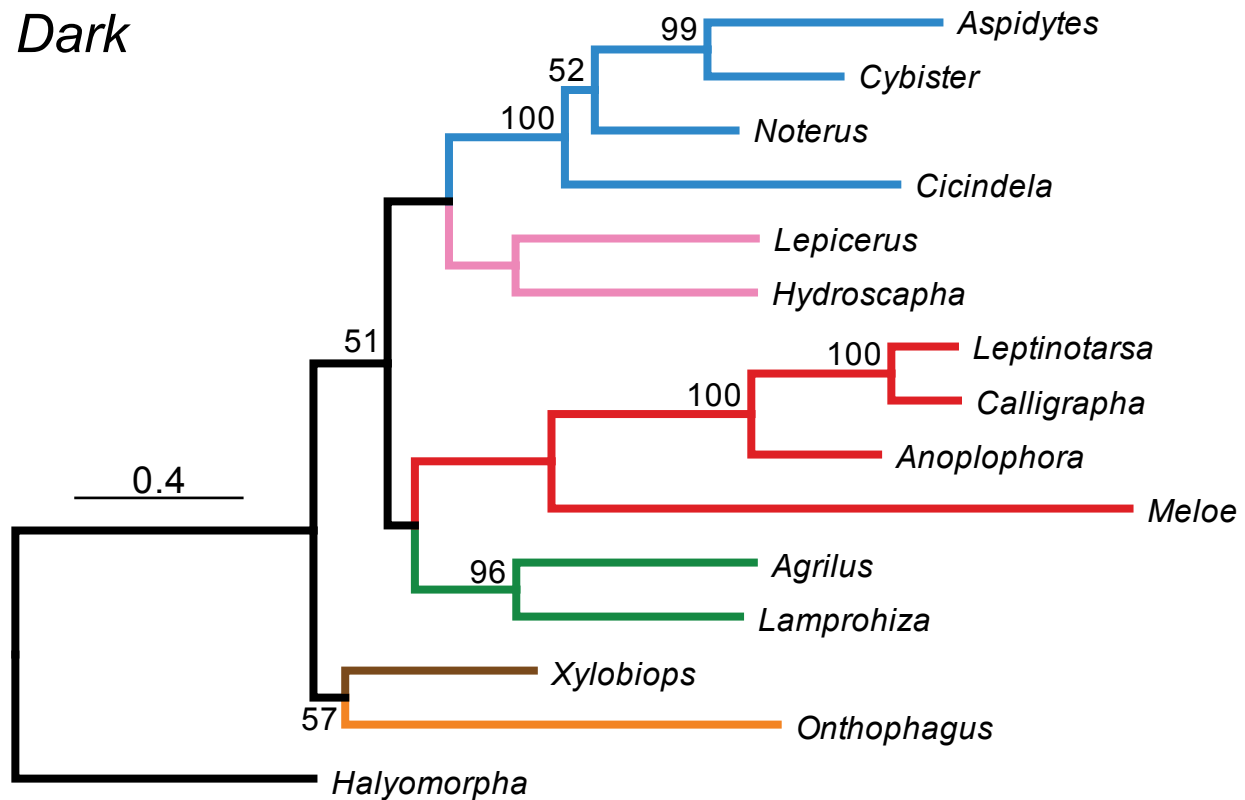


Chc

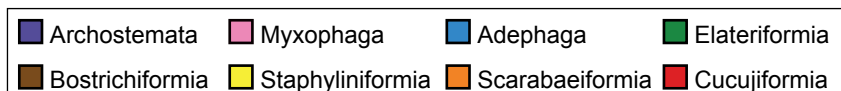
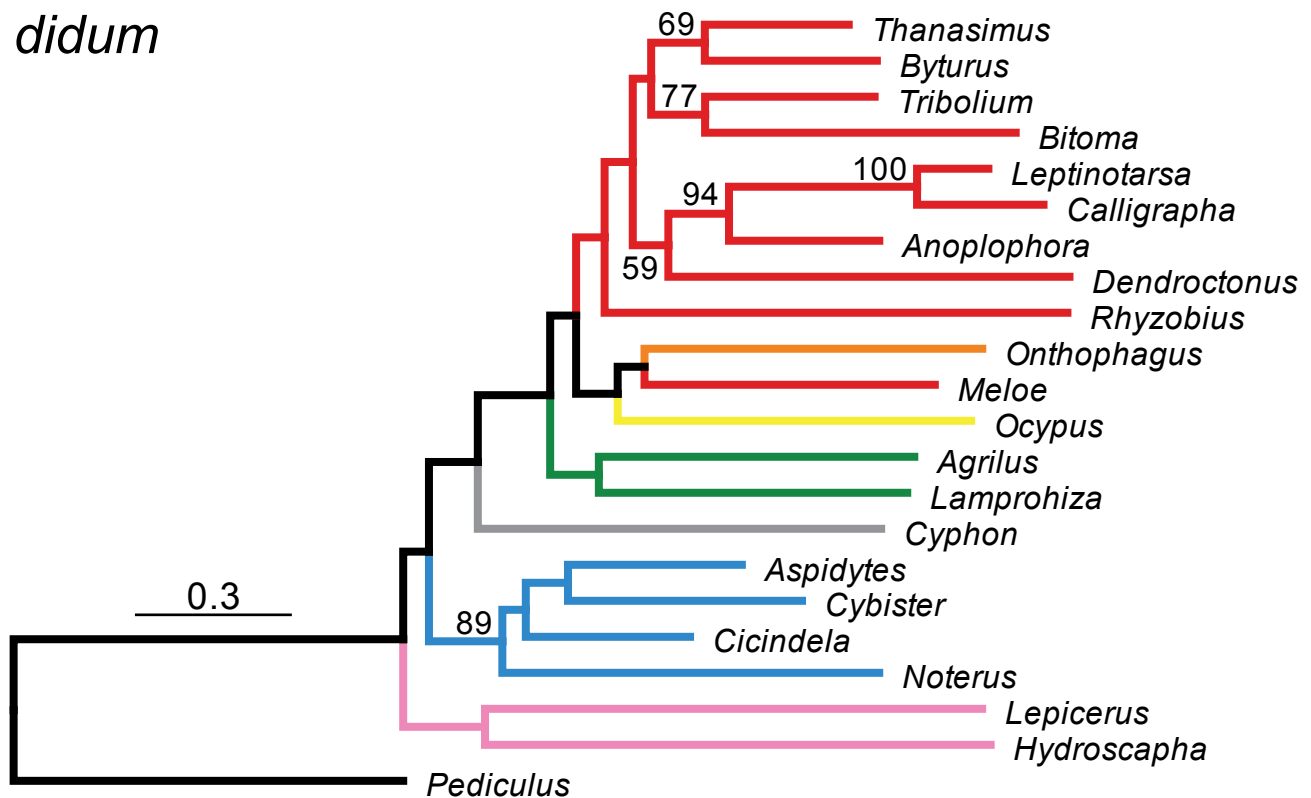




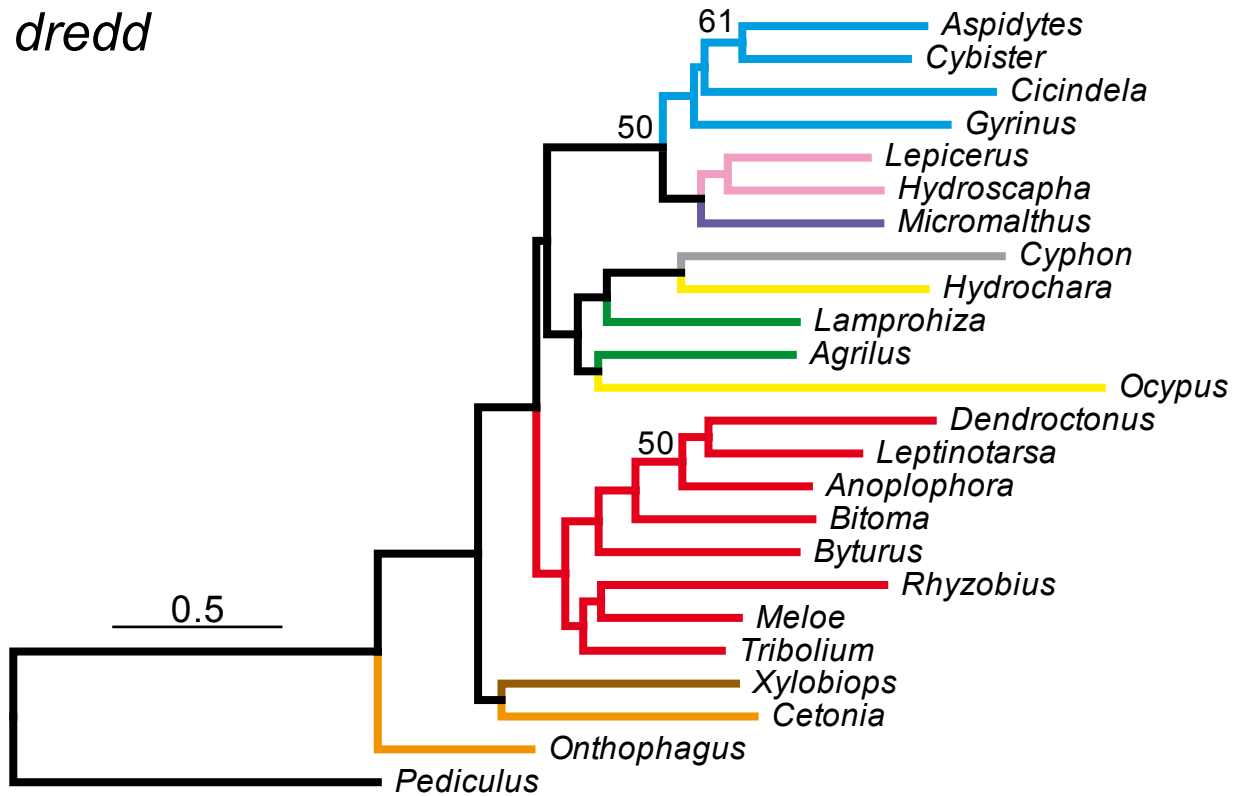
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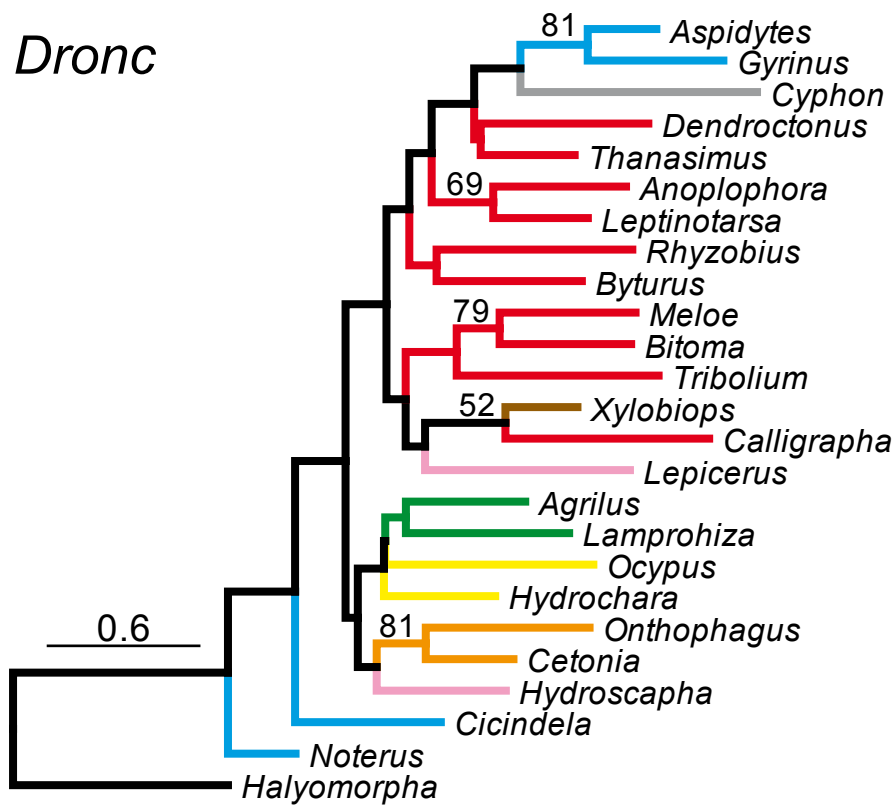
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dredd

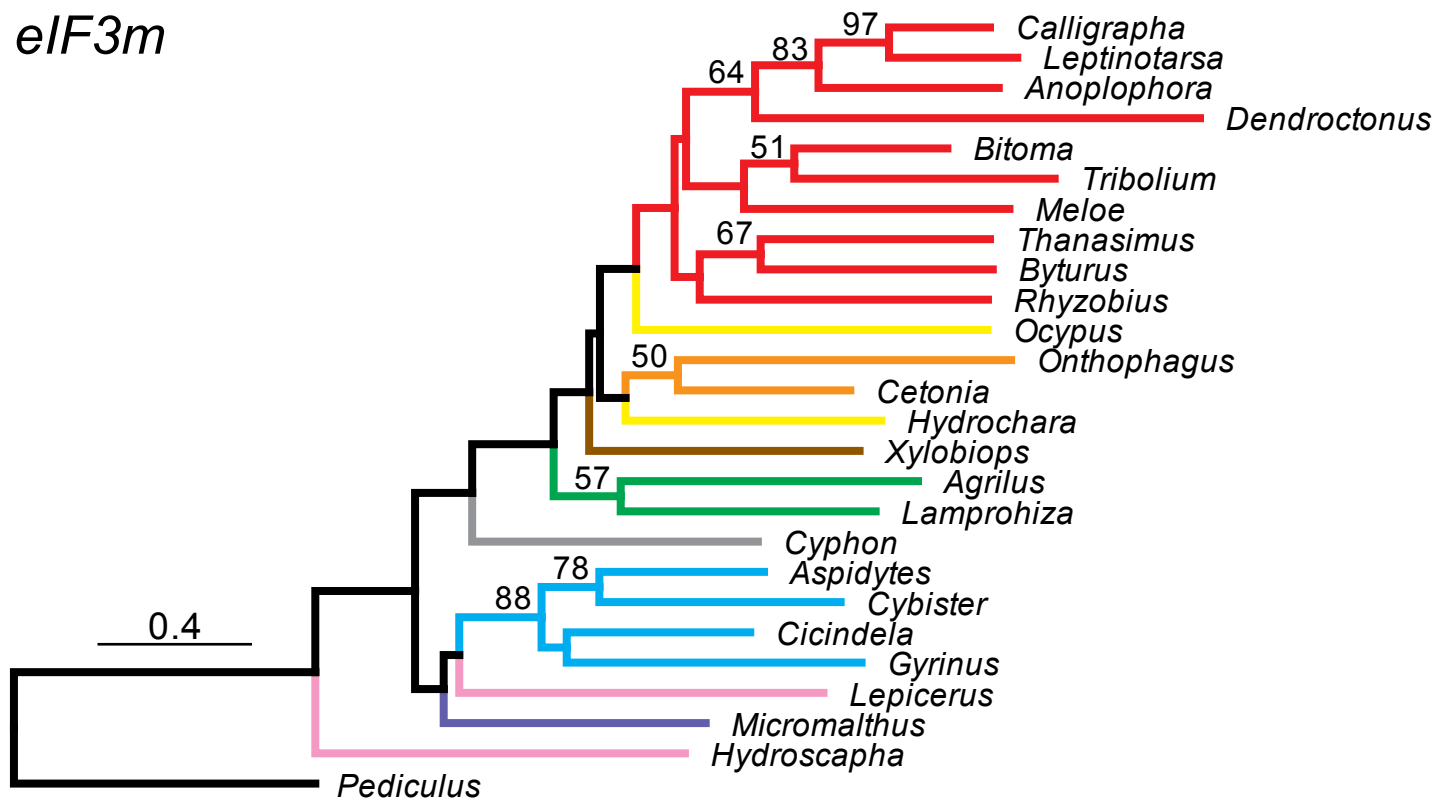


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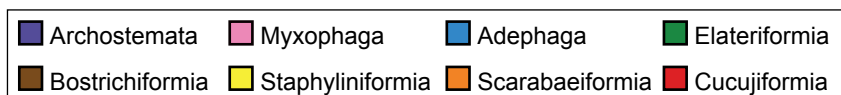
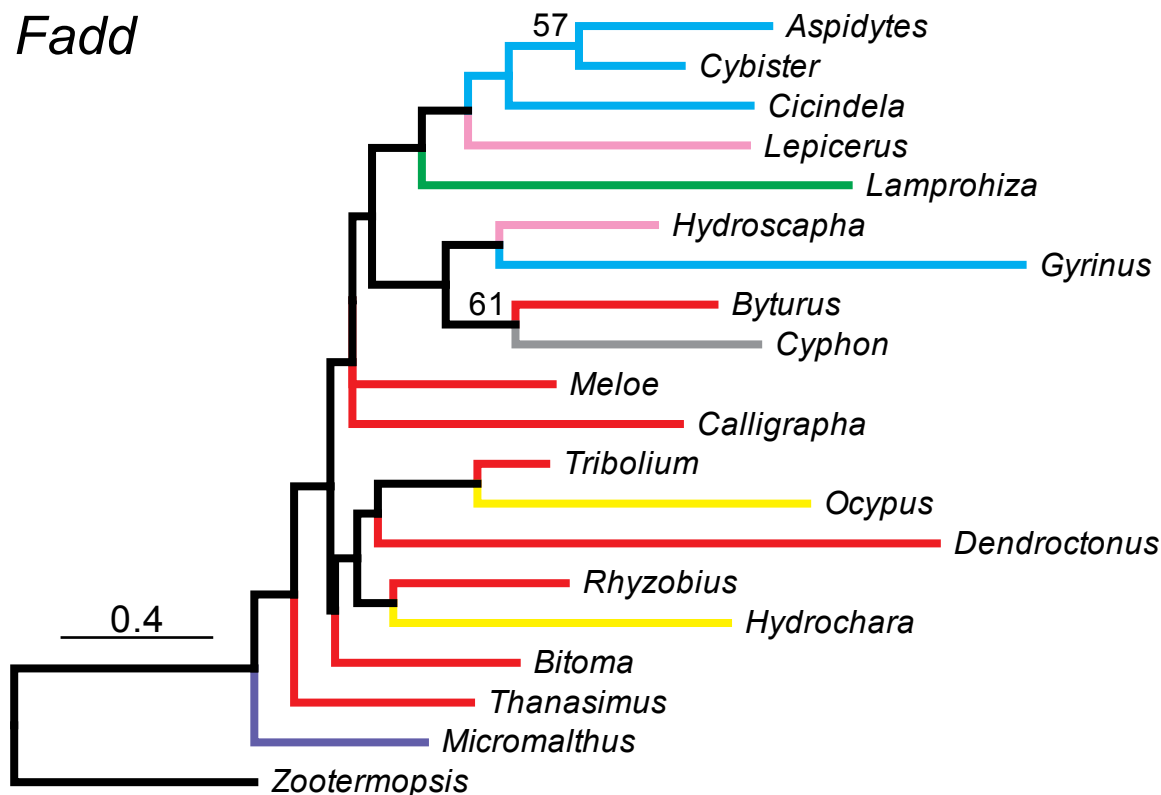


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Bostrichiformia	Staphyliniformia	Scarabaeiformia	Cucujiformia

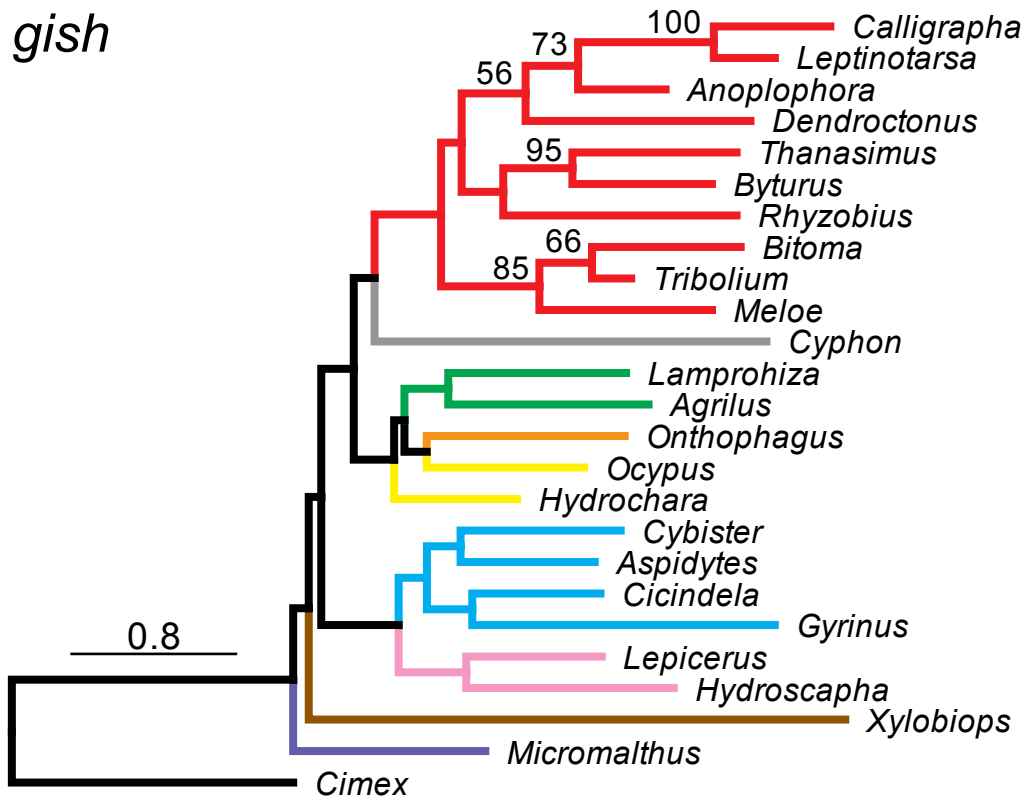
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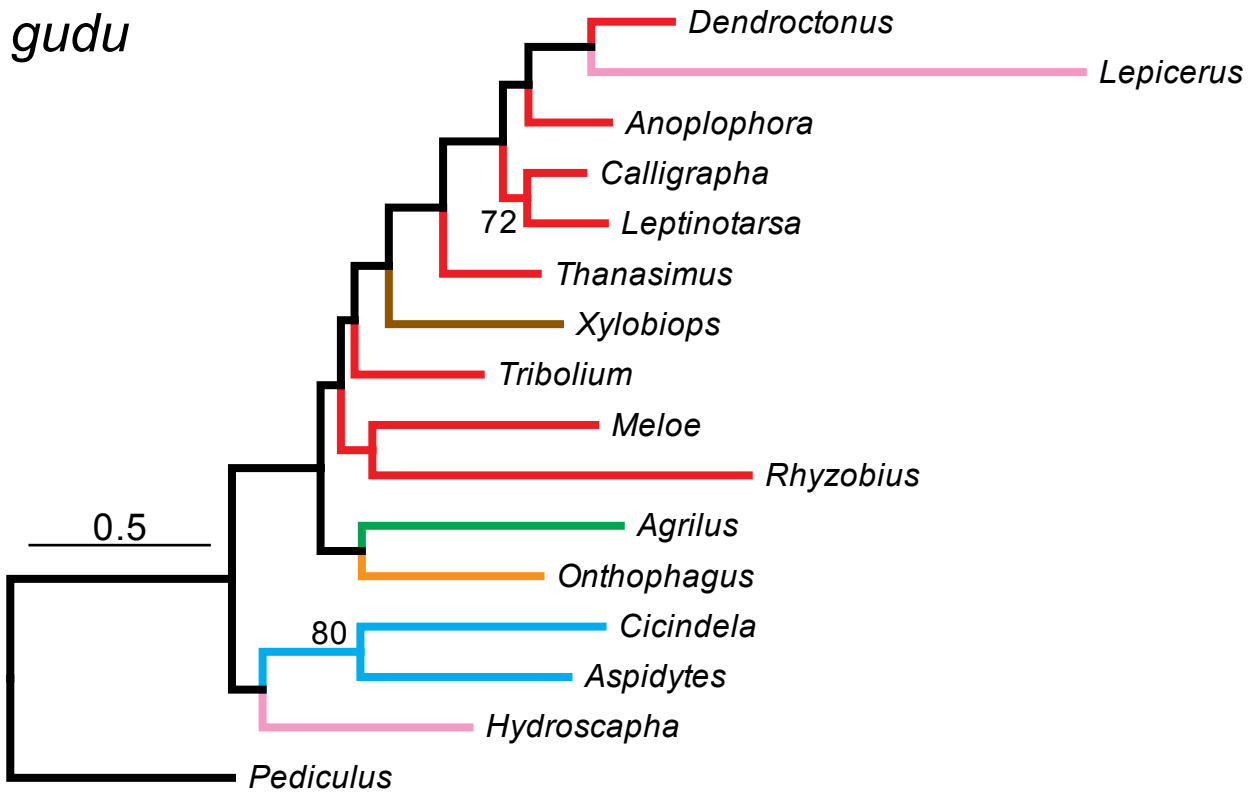
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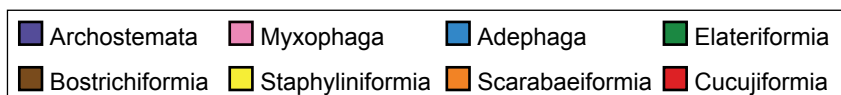
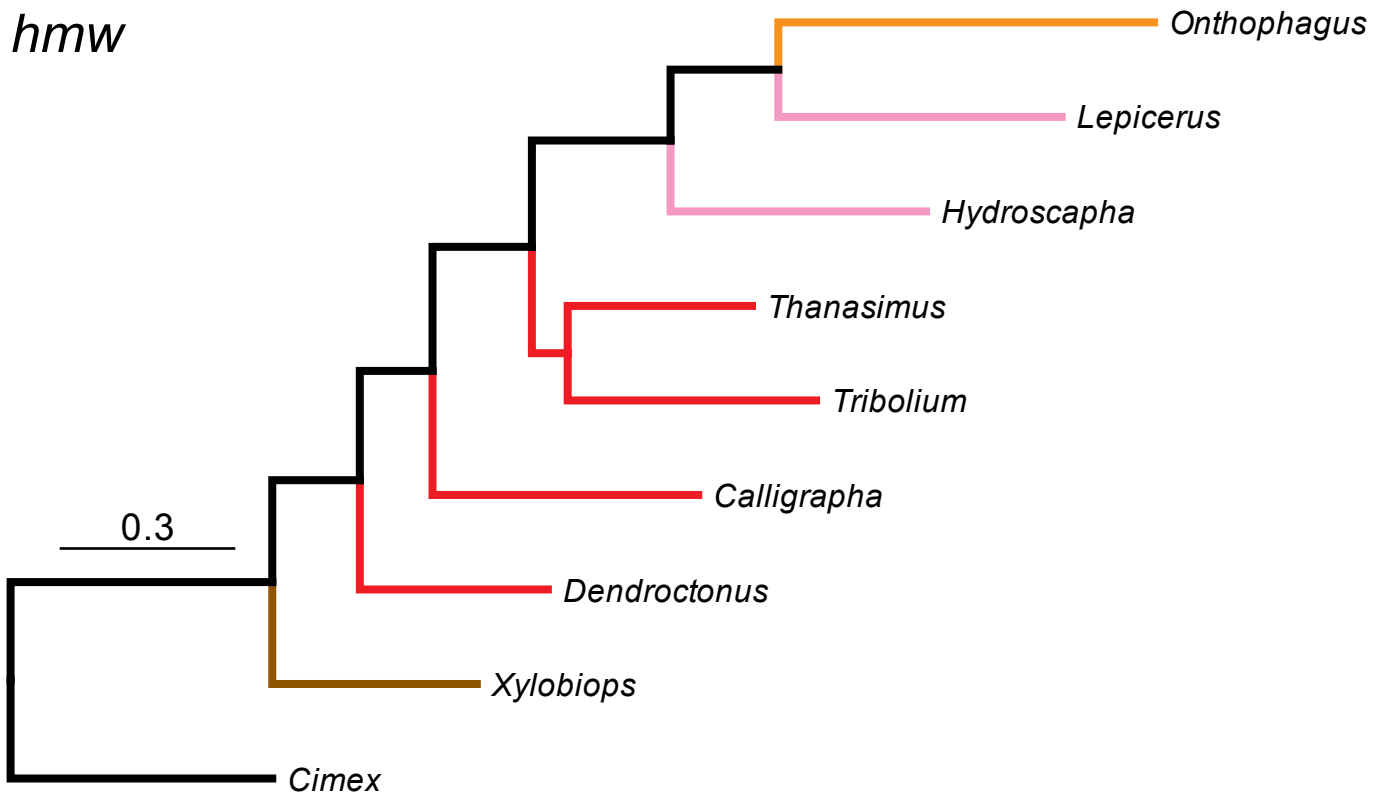
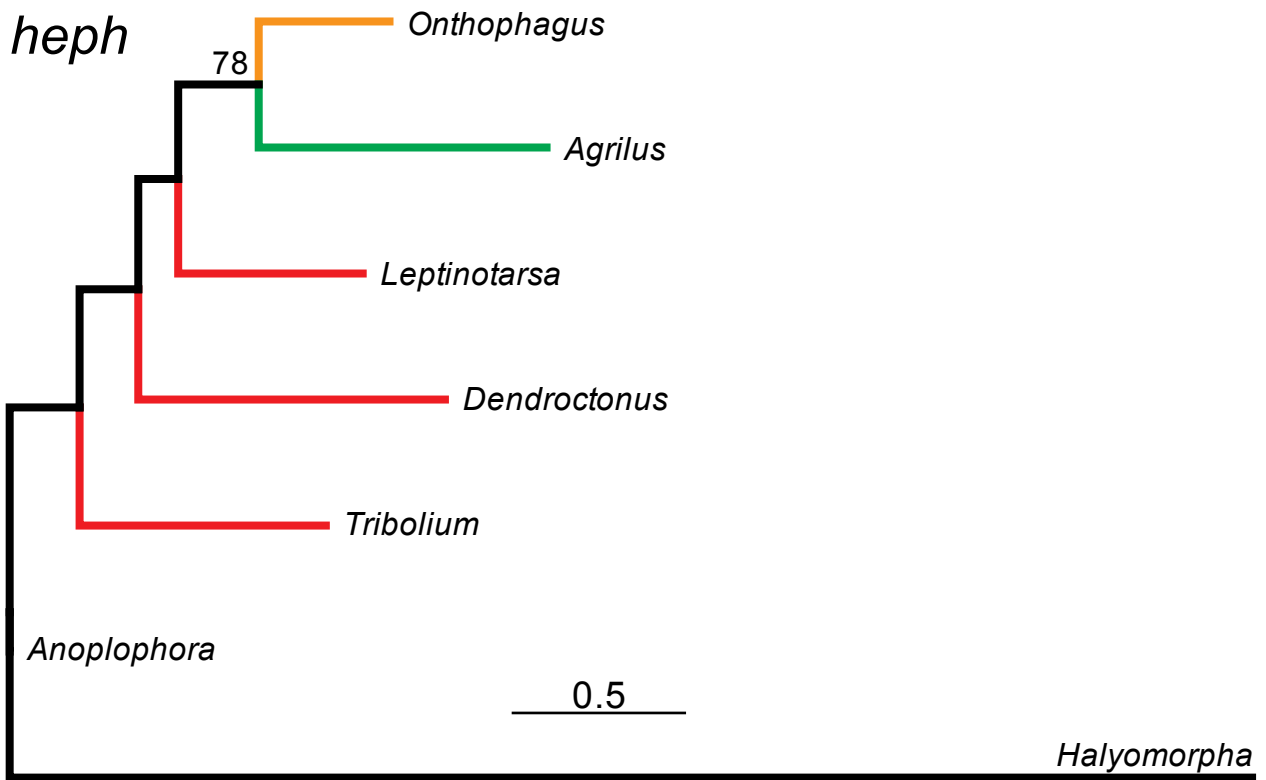


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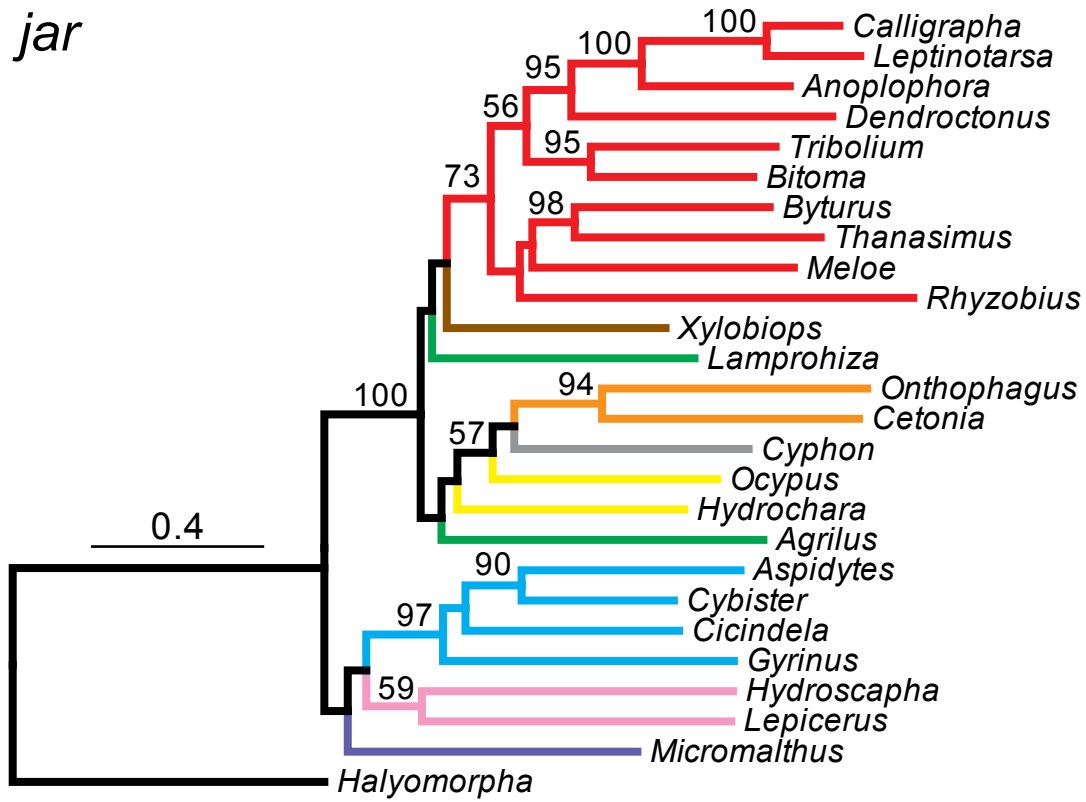


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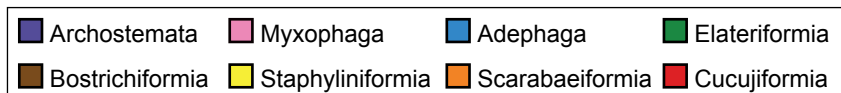
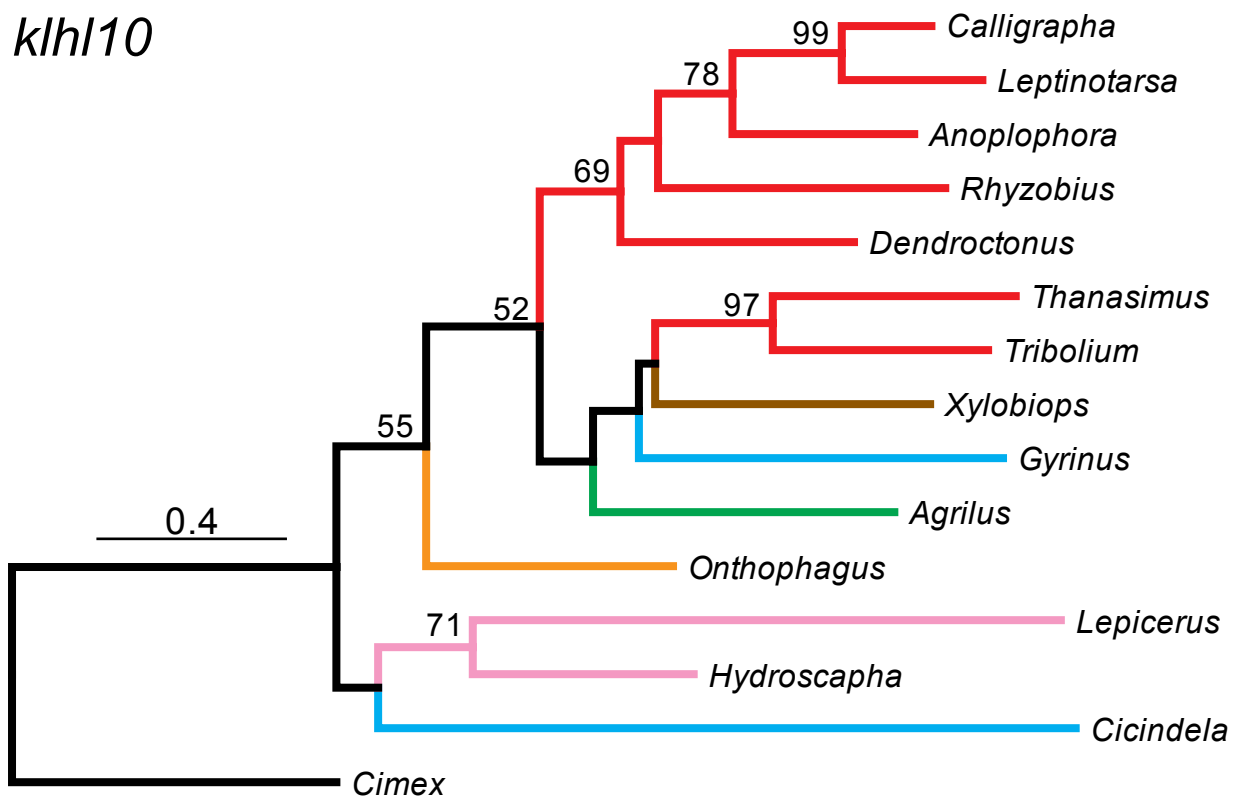




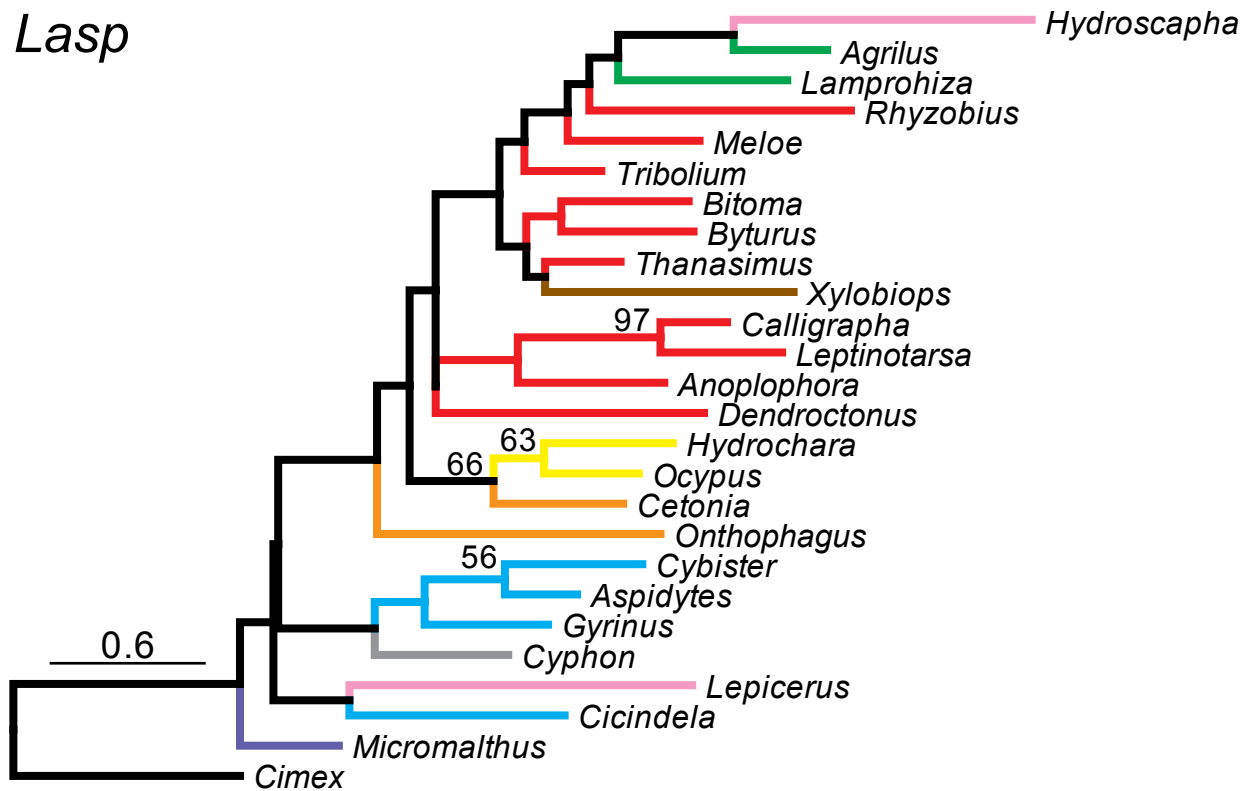
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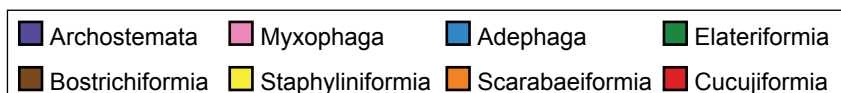
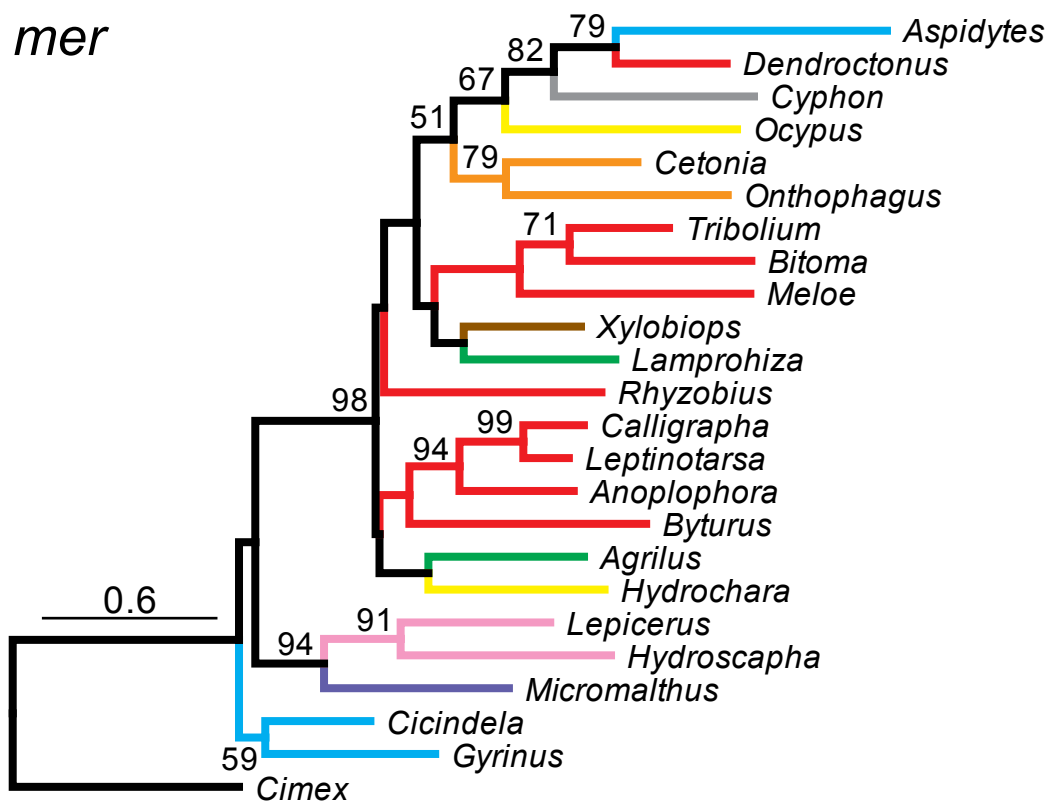
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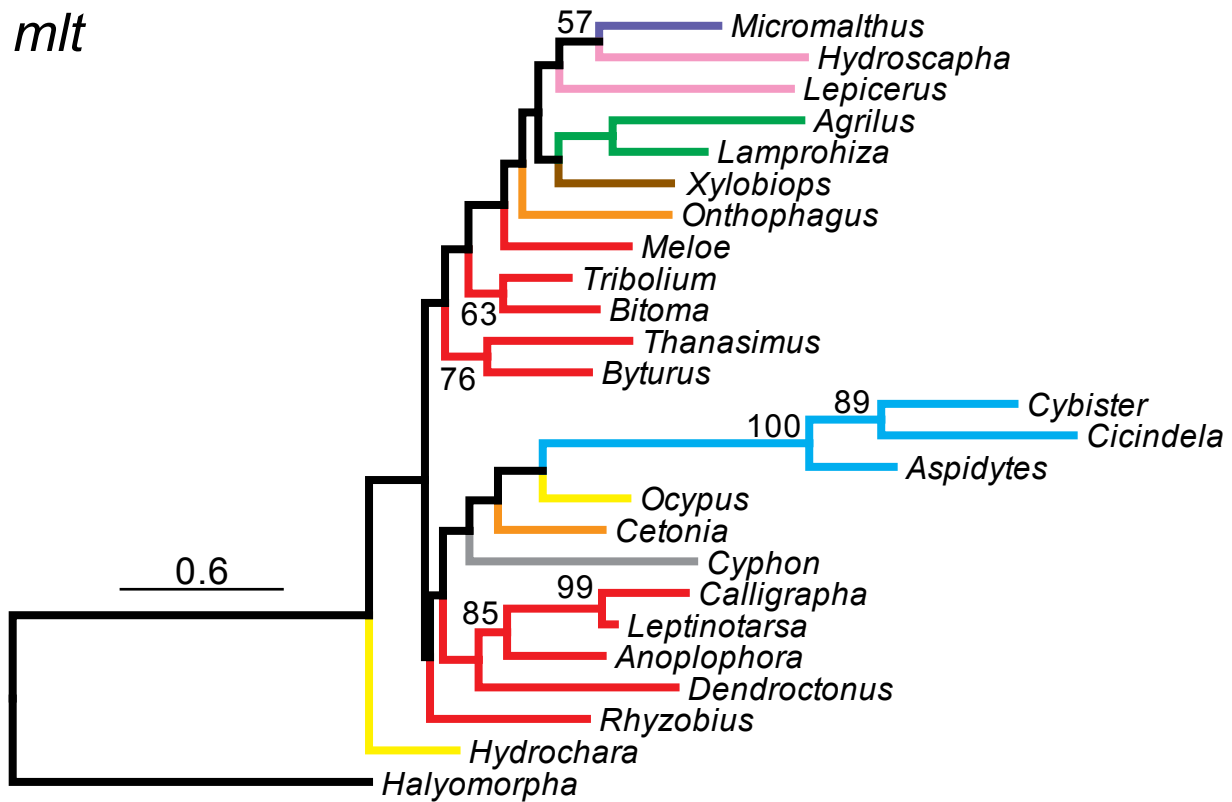
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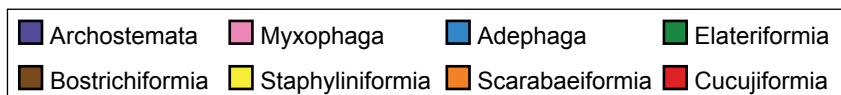
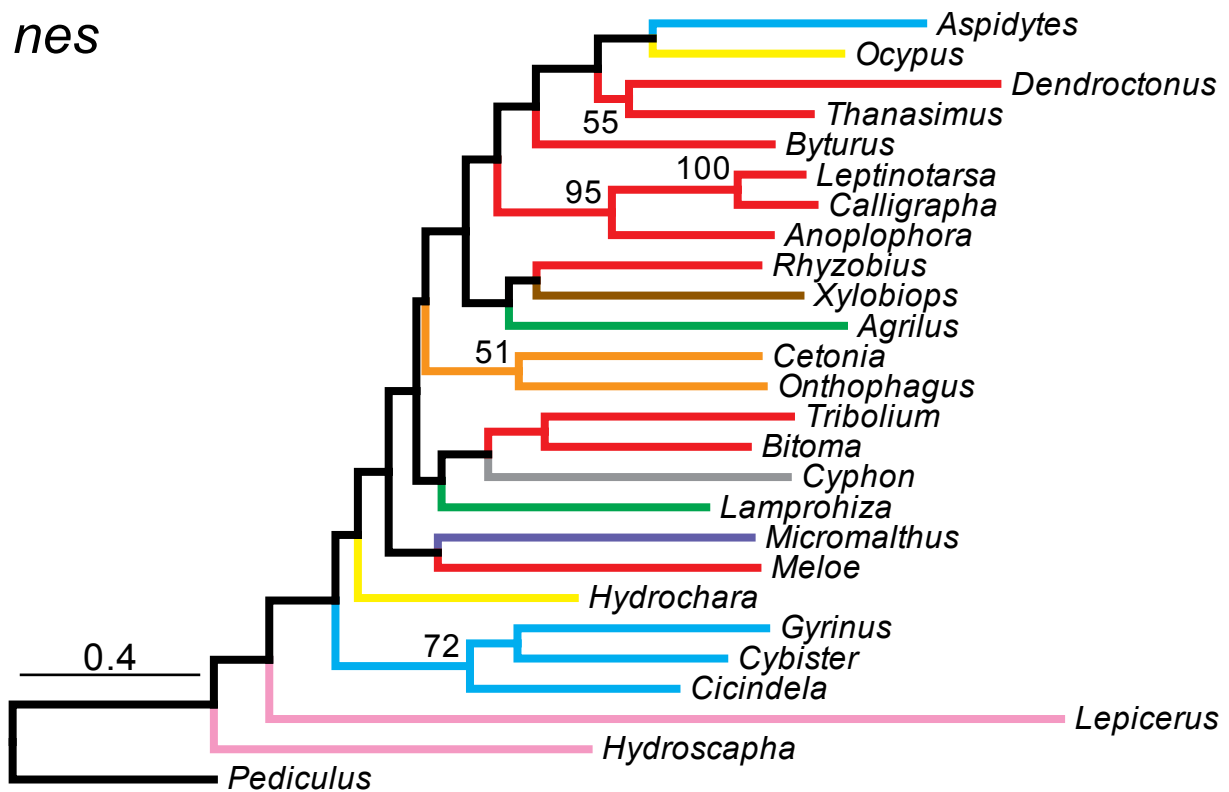
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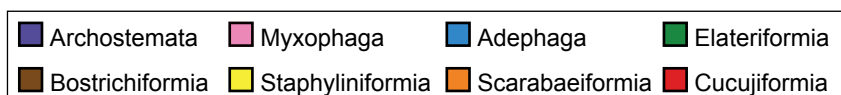
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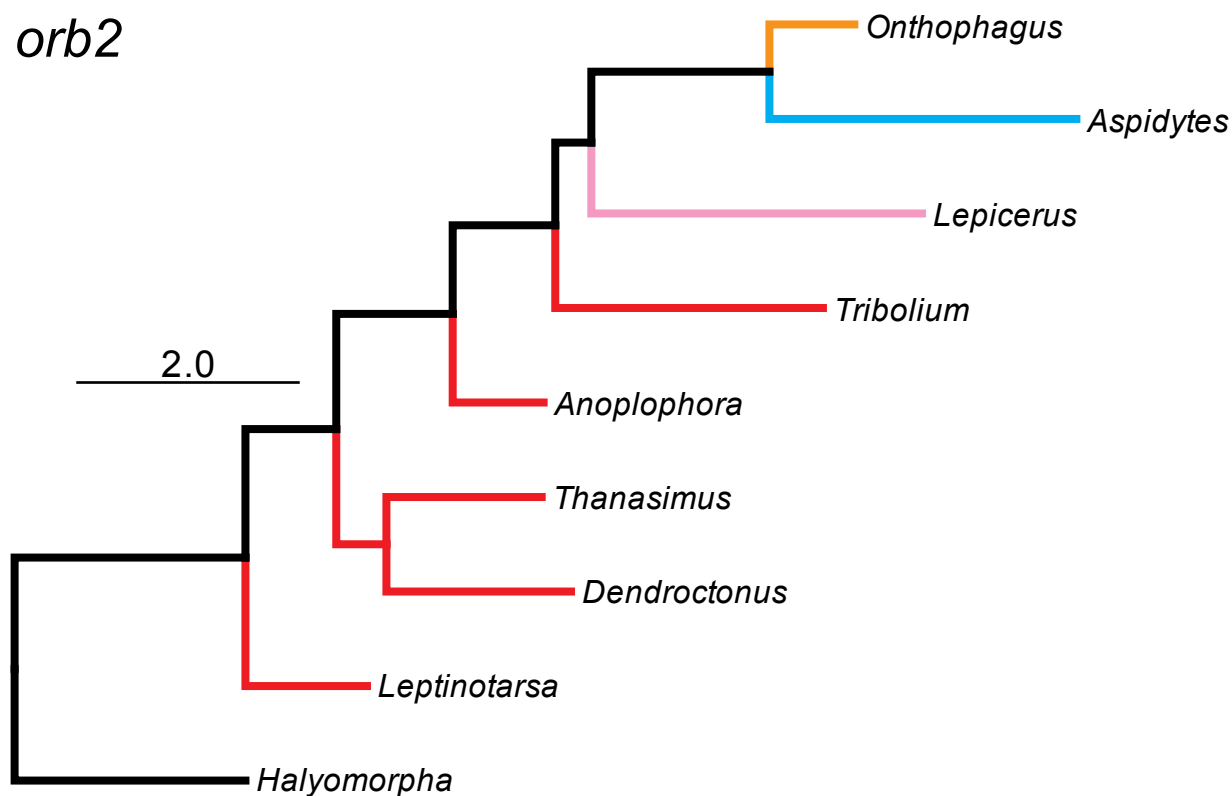
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Cicindela
Ocybus
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Noterus
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Hydroscapha
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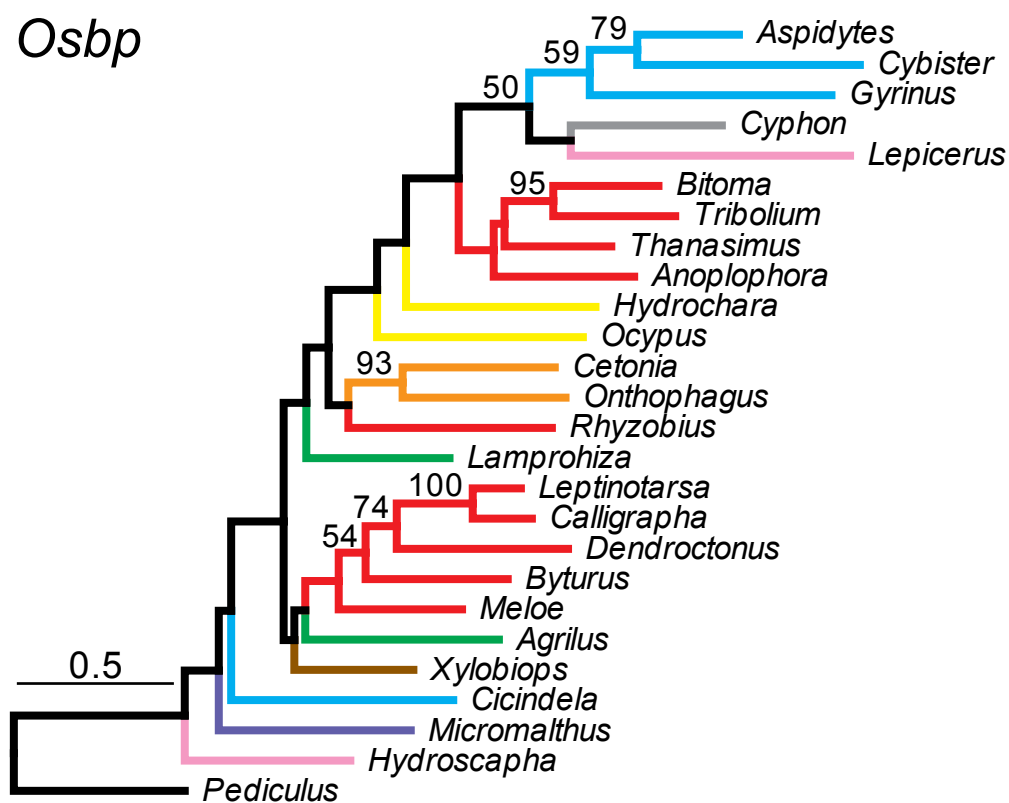
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Lepicerus
Hydroscapha
Anoplophora
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Cicindela
Gyrinus
Cimex



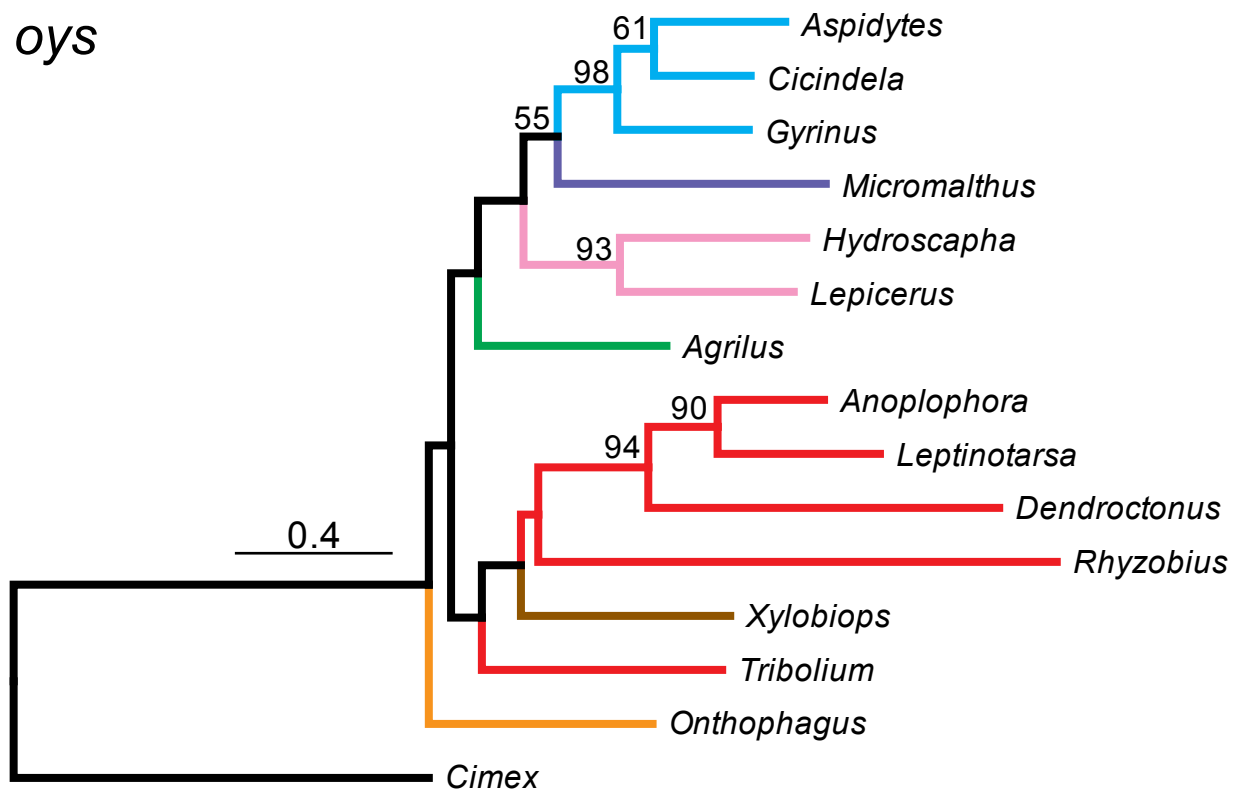
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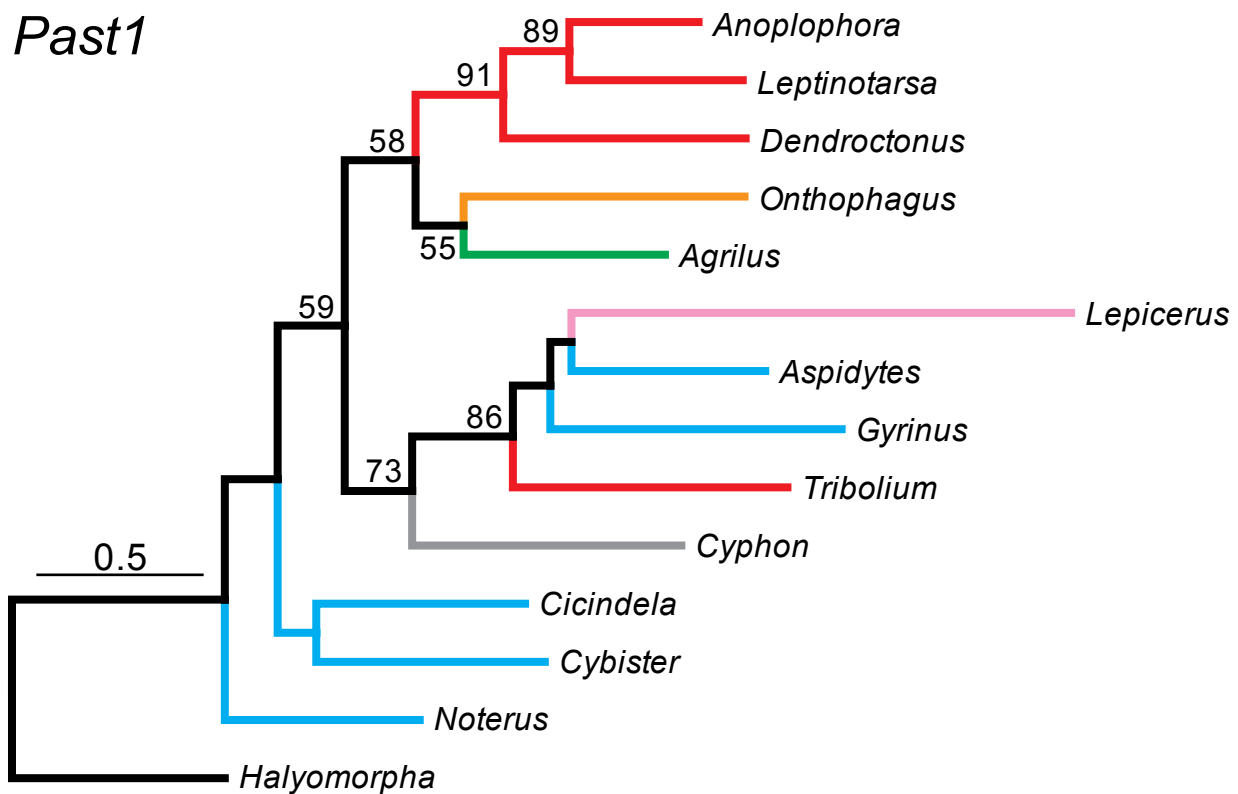
Osbp



Oys

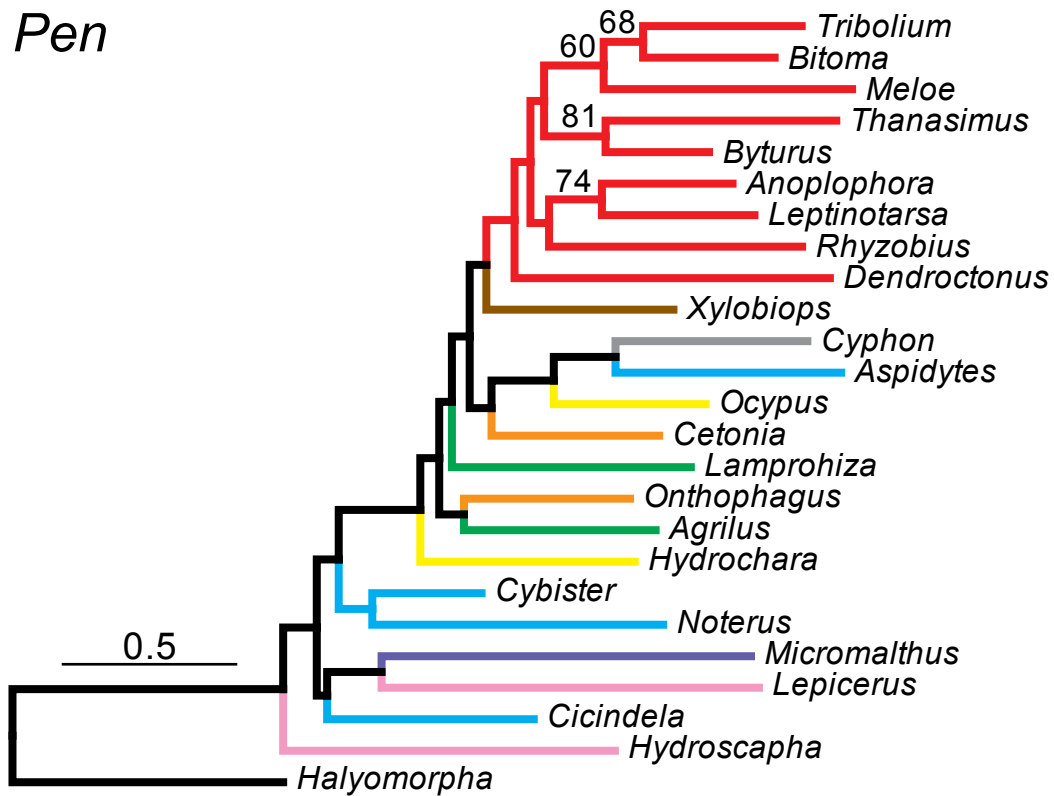


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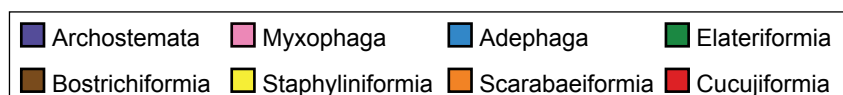
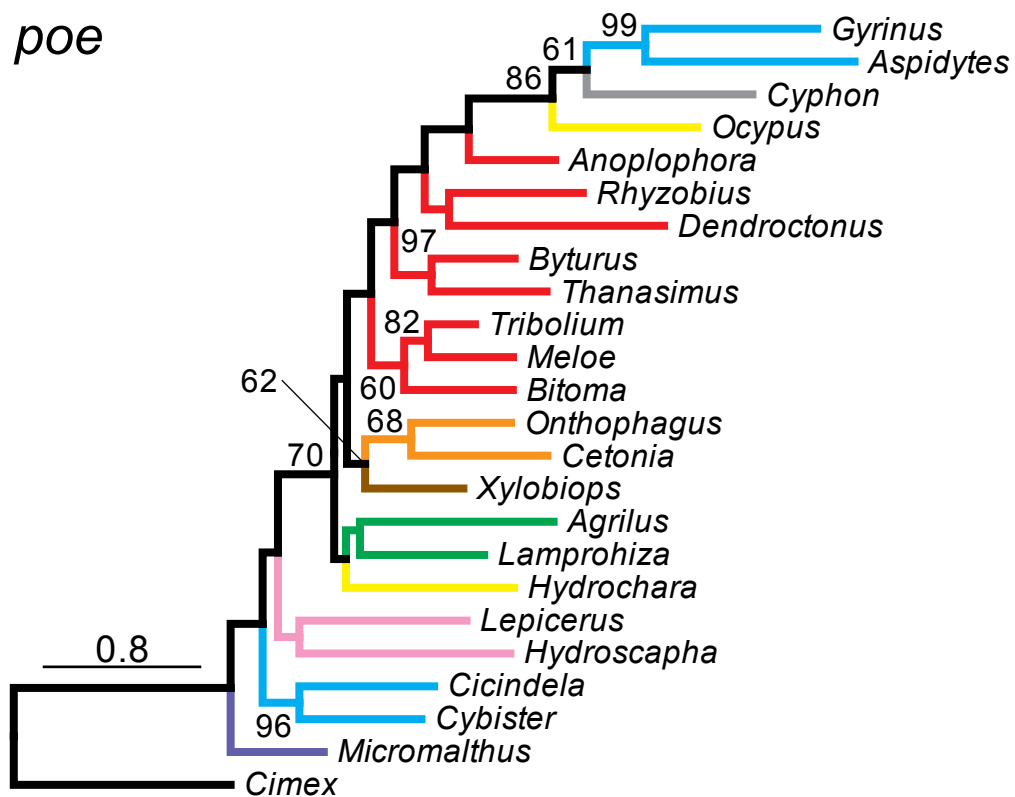


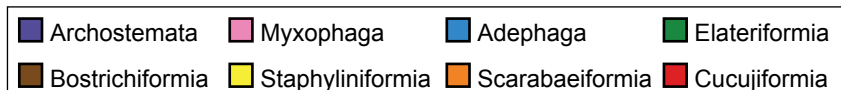
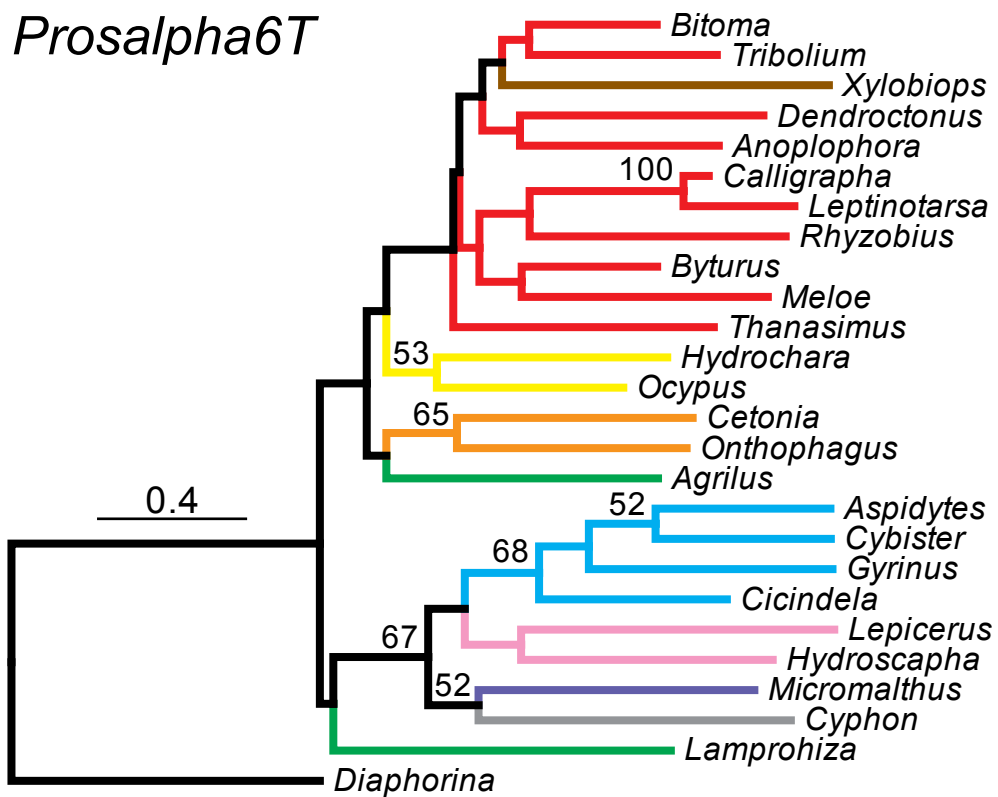
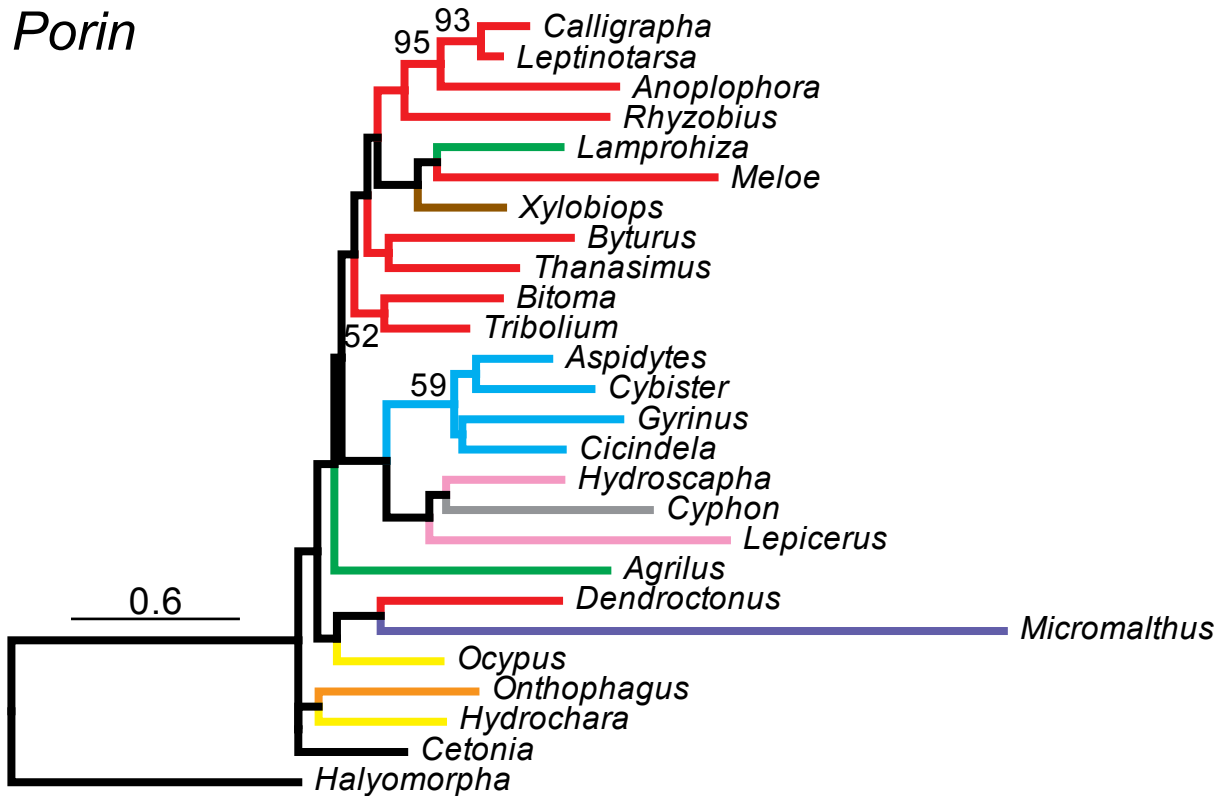
Archostemata	Myxophaga	Adephaga	Elateriformia
Bostrichiformia	Staphyliniformia	Scarabaeiformia	Cucujiformia

Pen

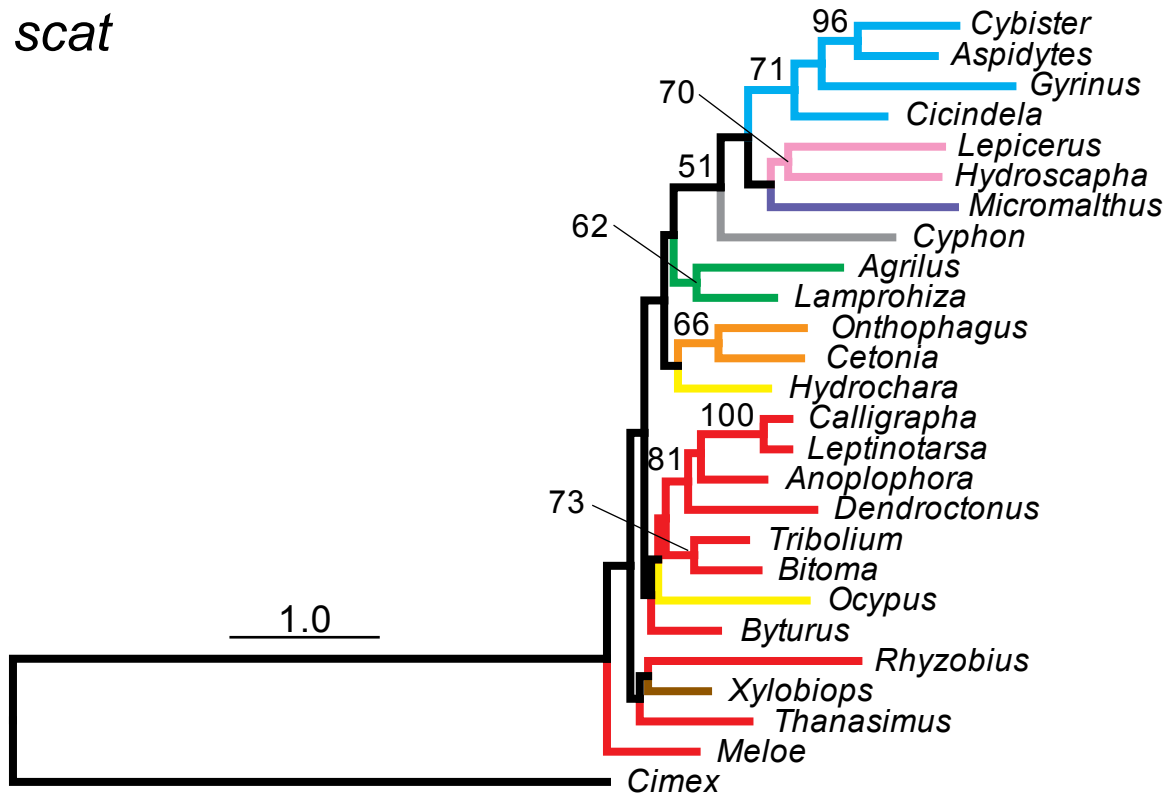


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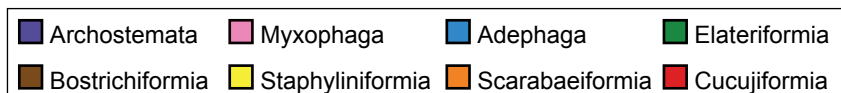
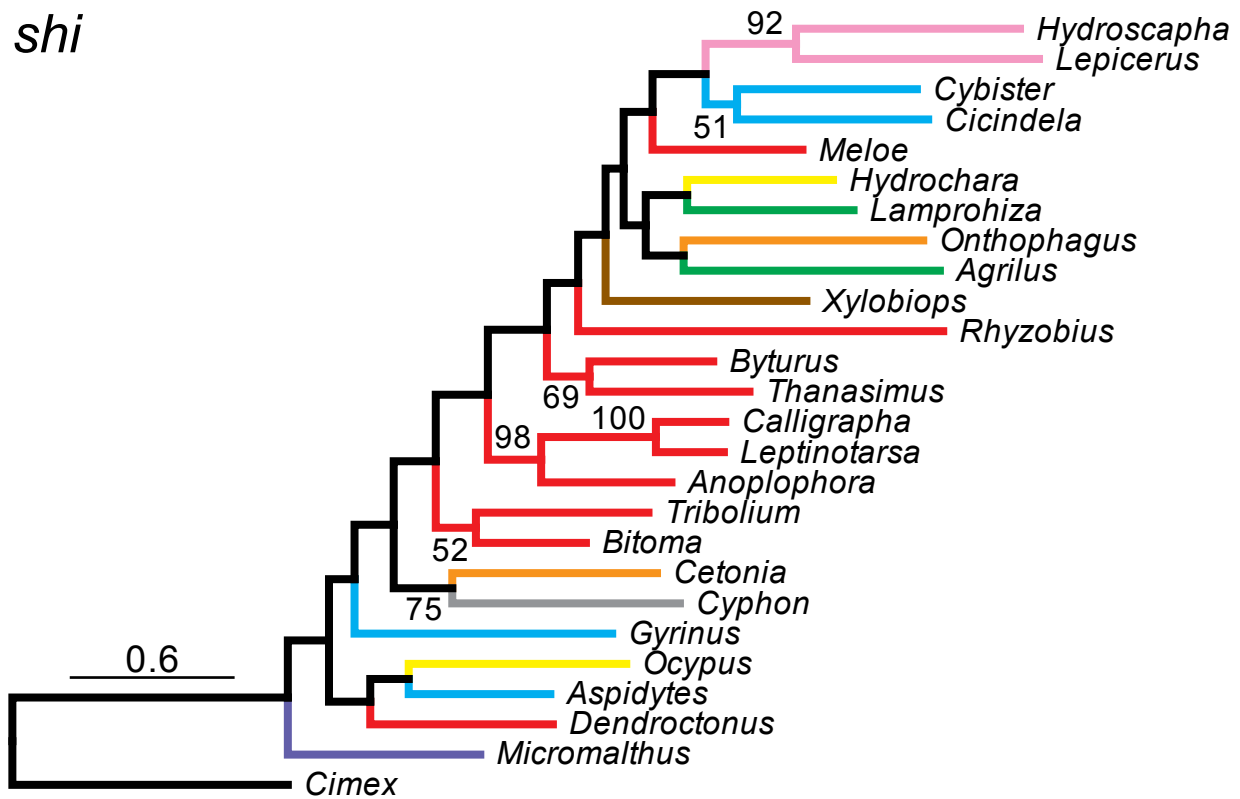


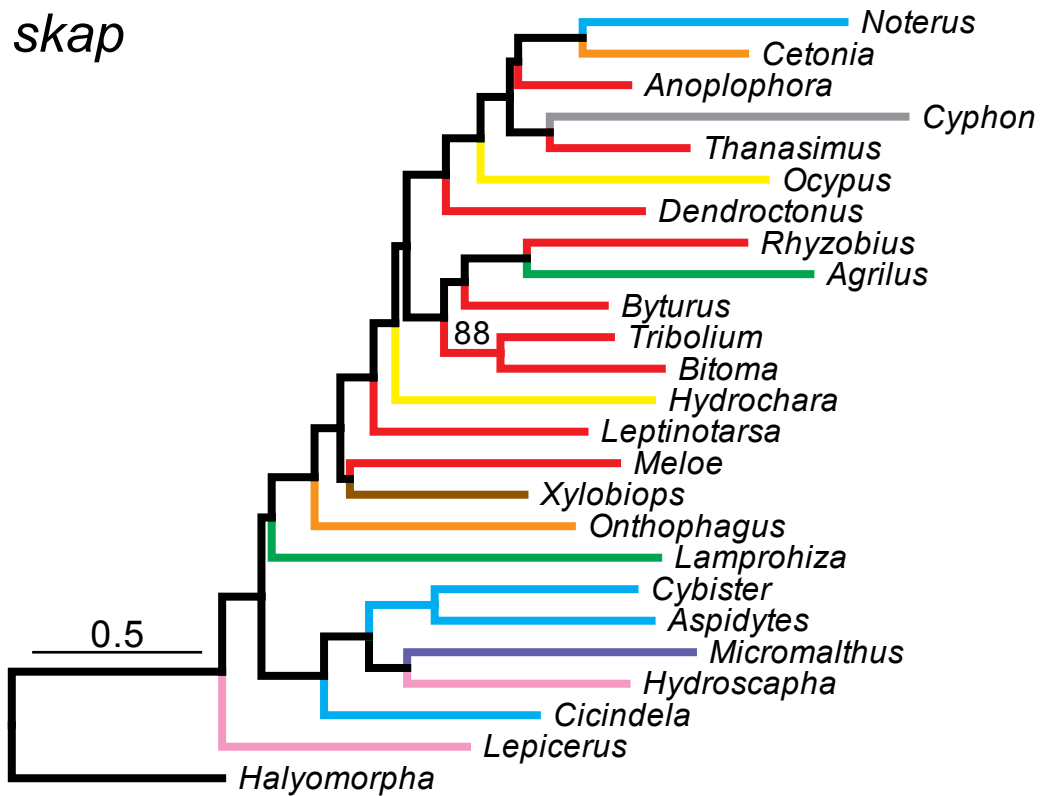


scat

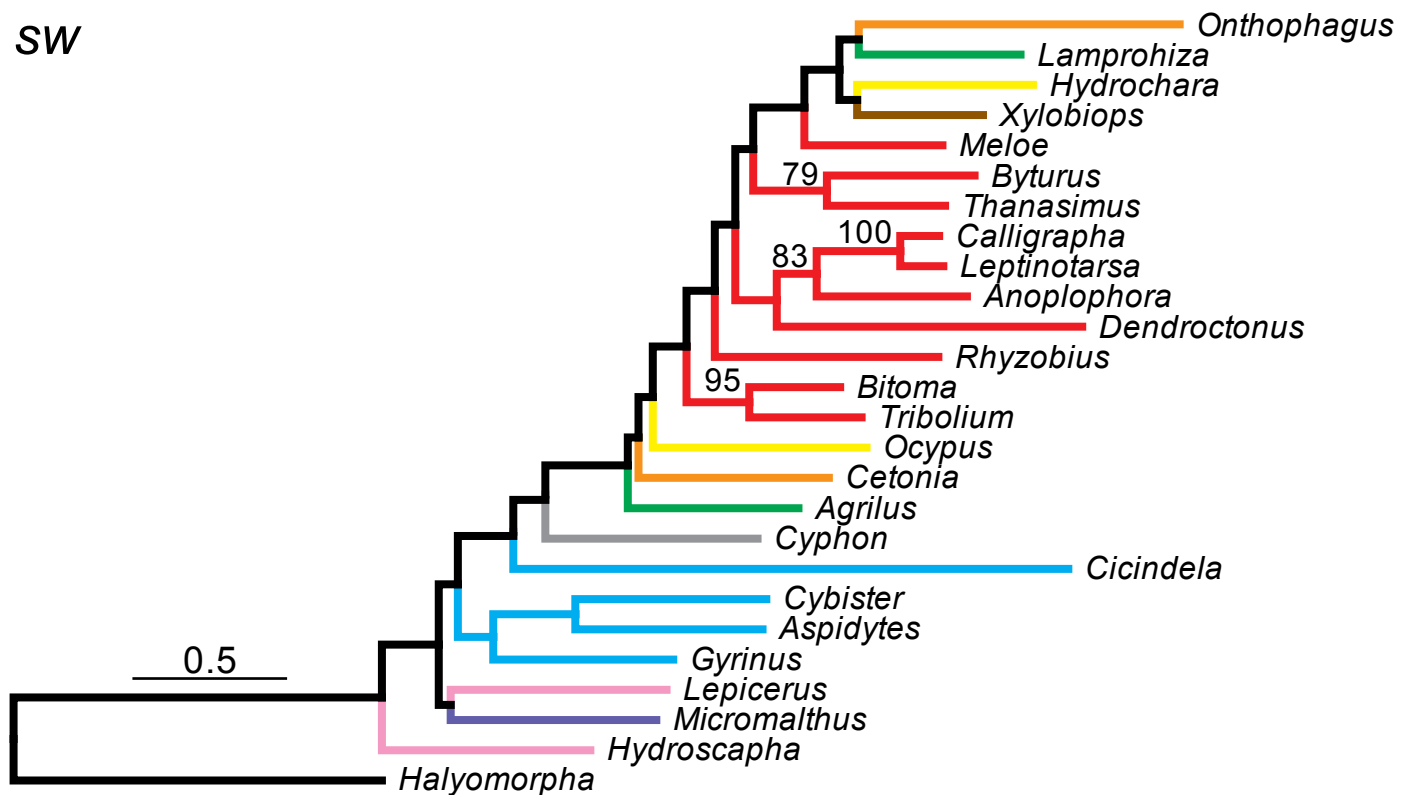


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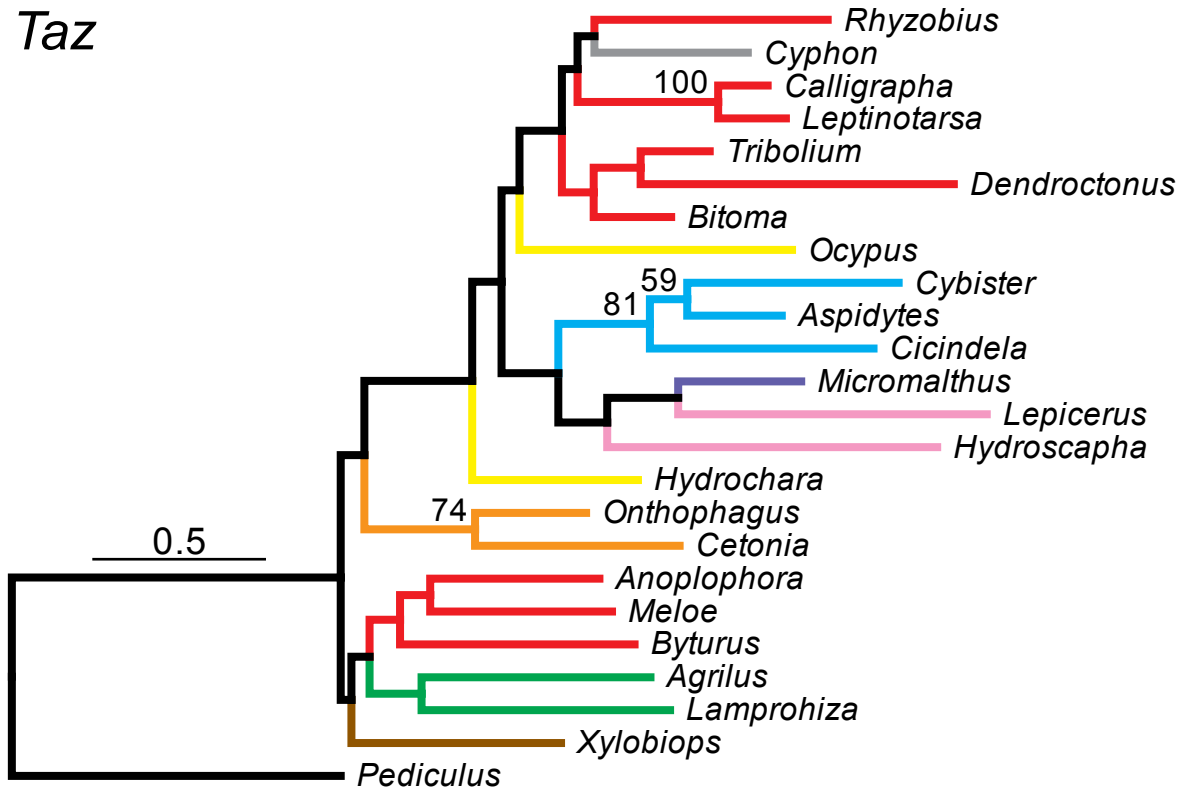




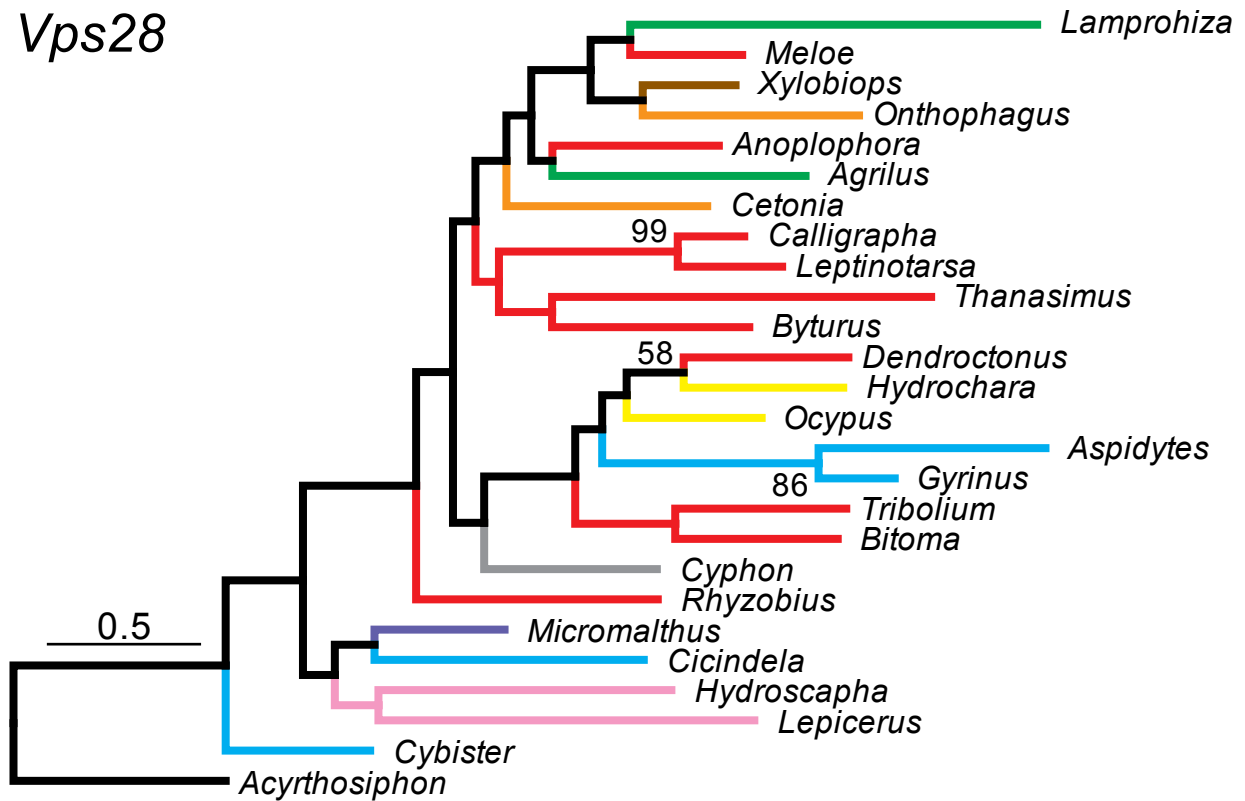
SW



Taz

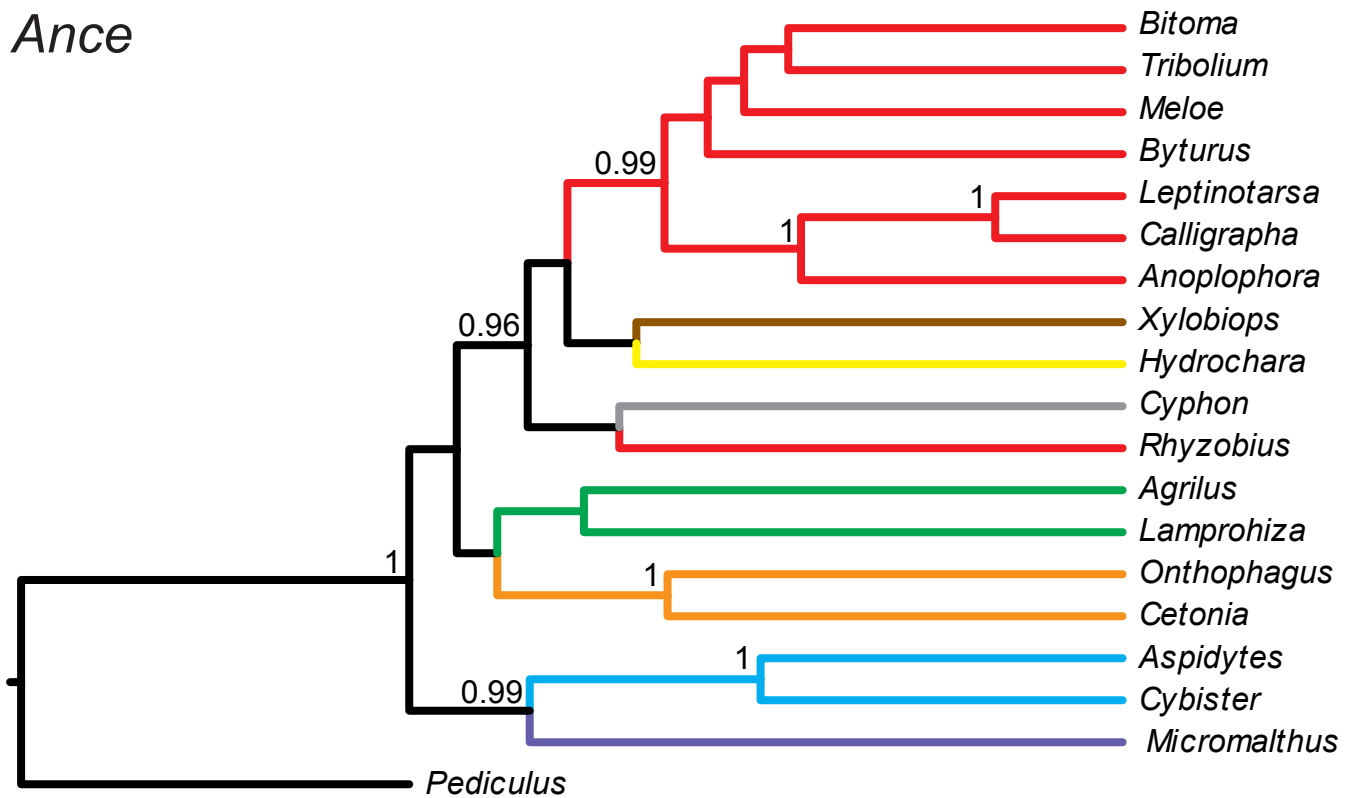


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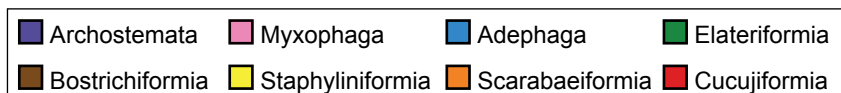
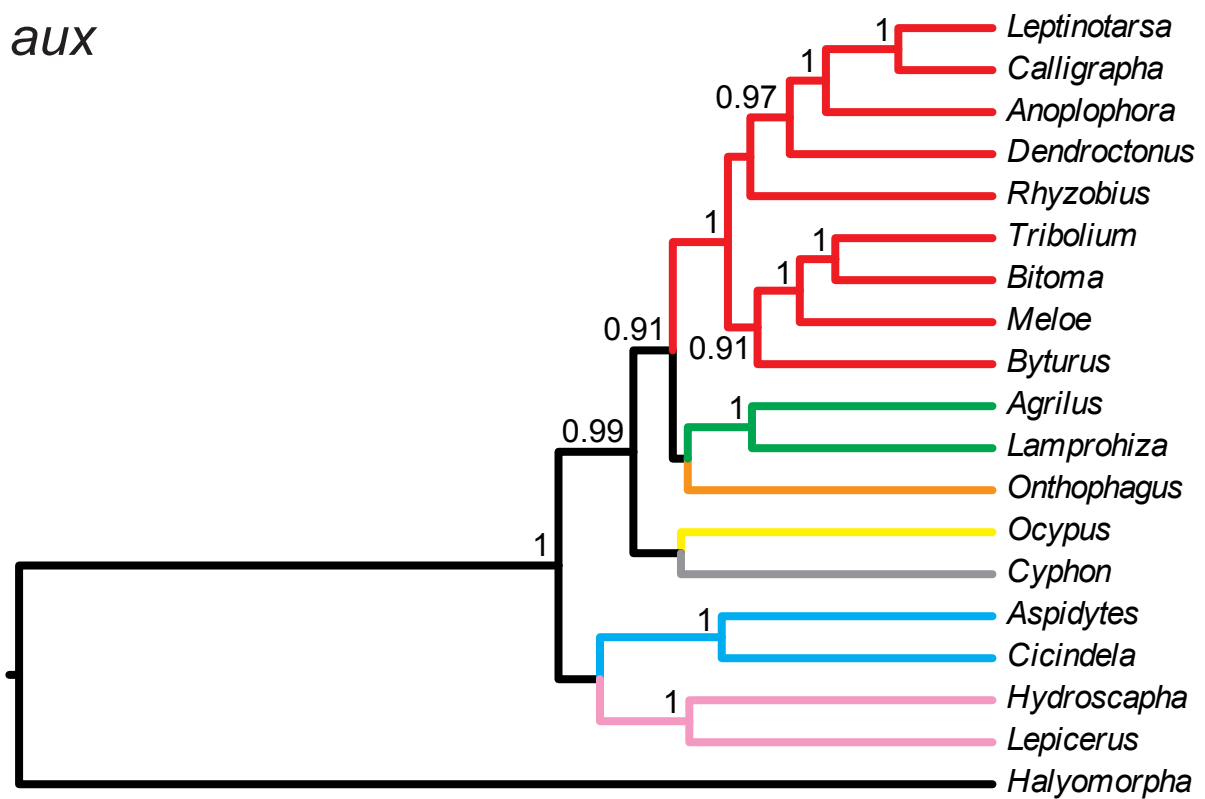


File S4. Bayesian inference trees based on the nucleotide alignments of different sperm individualization genes in beetles.

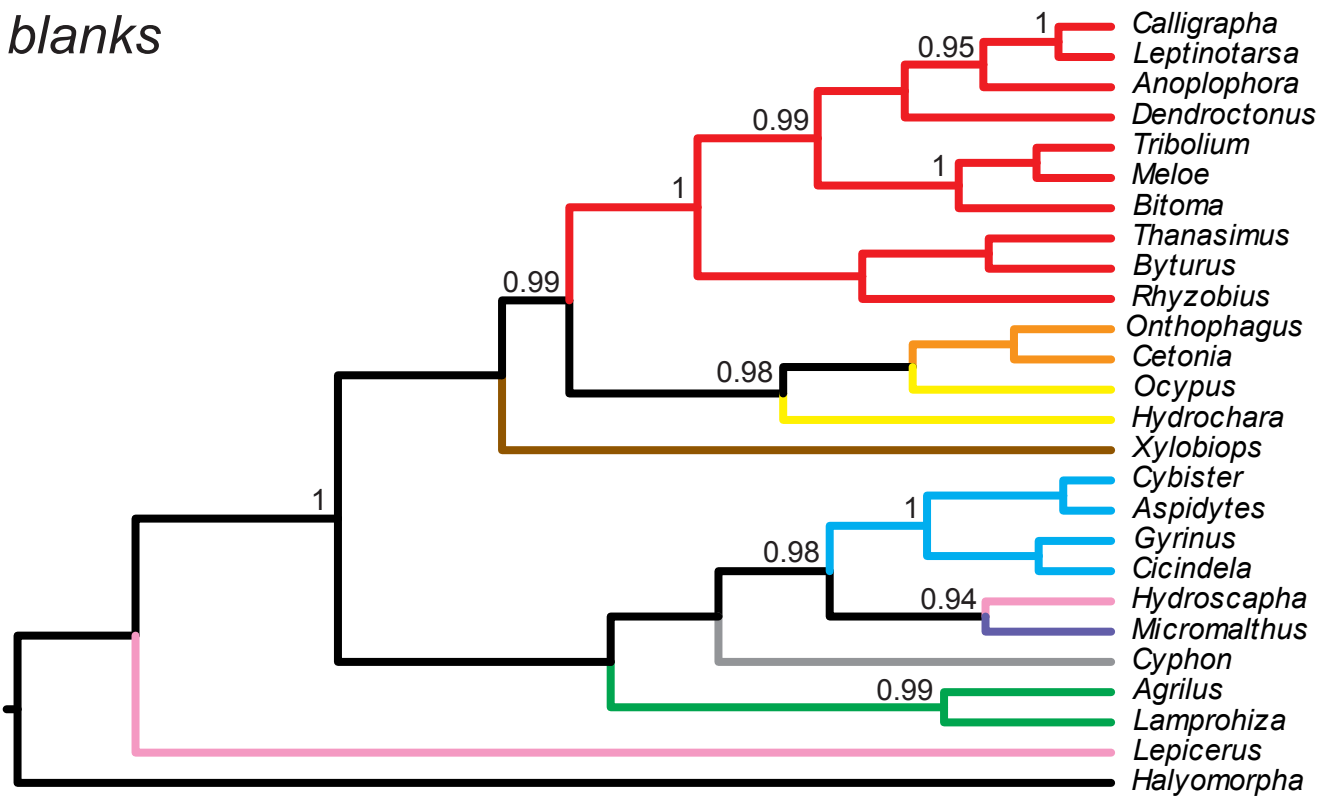
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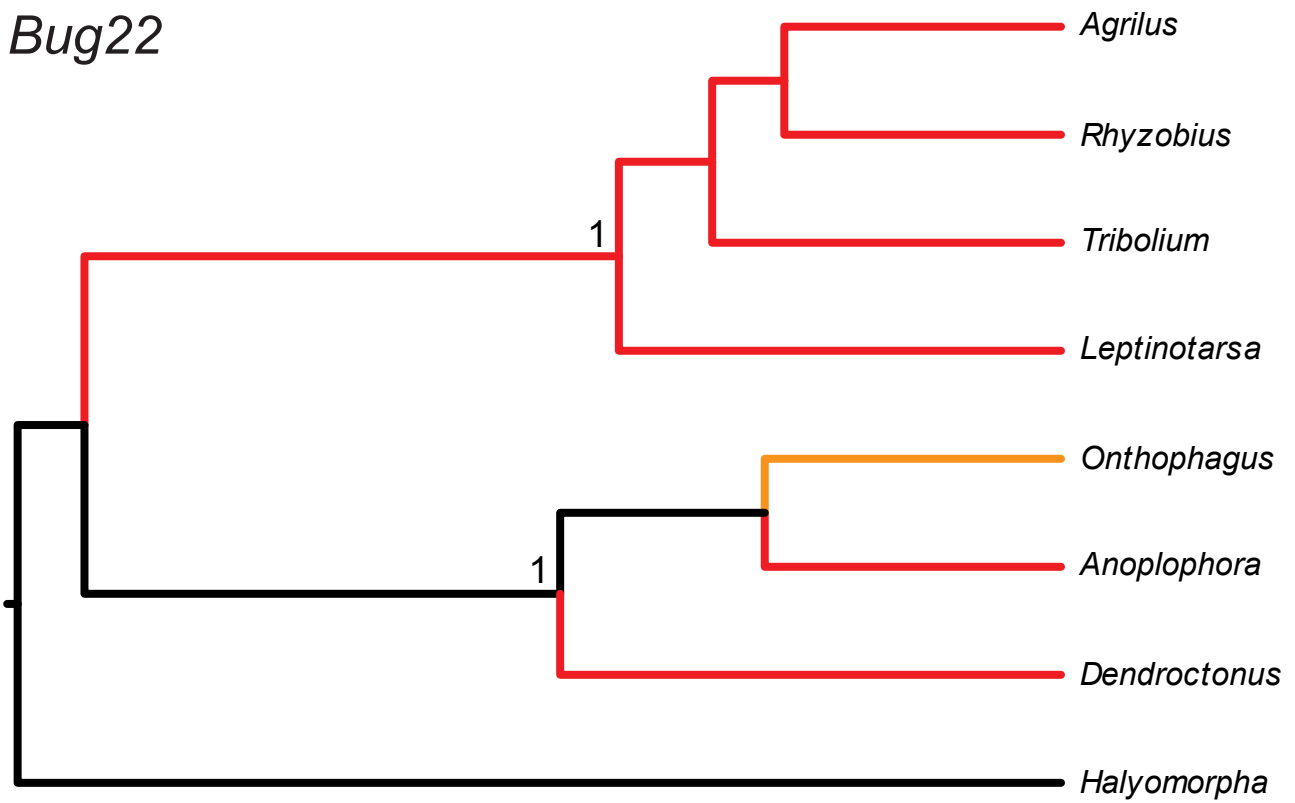
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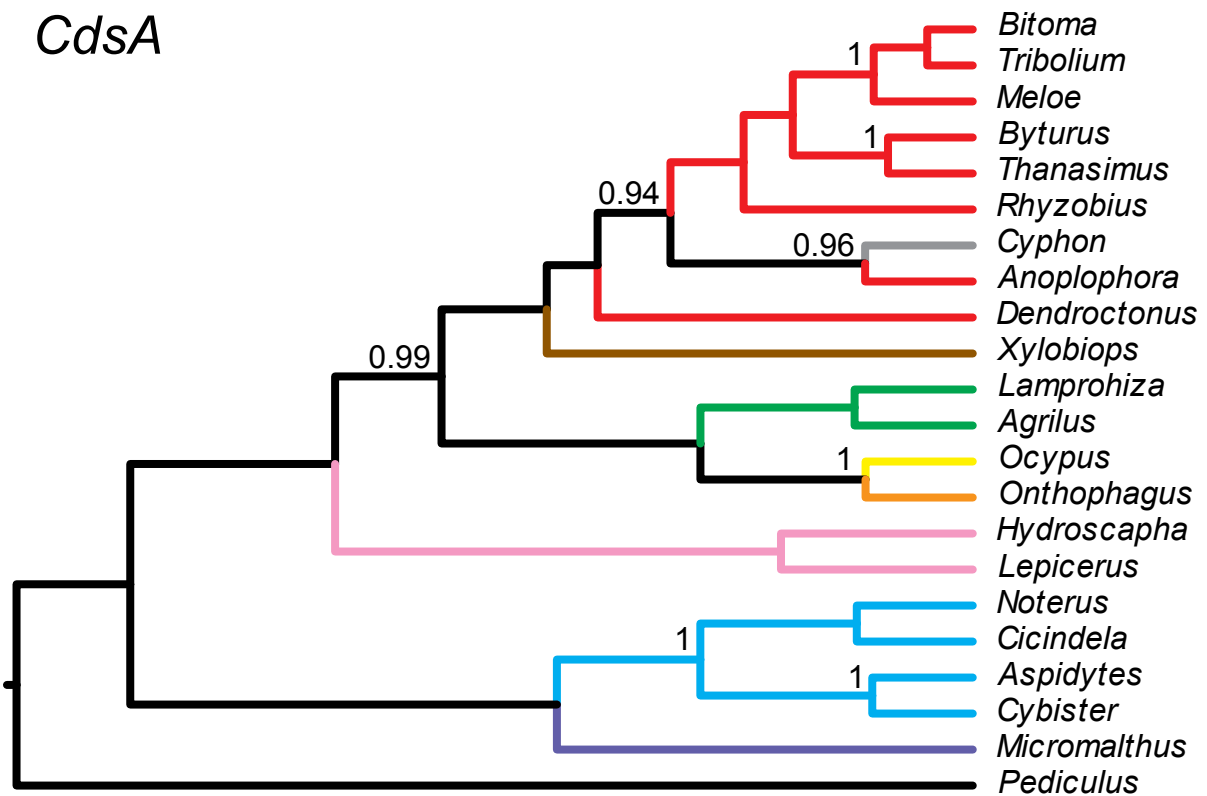
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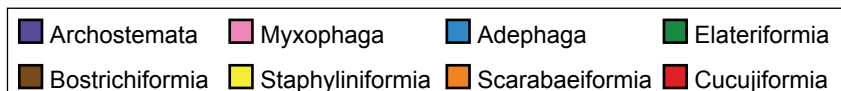
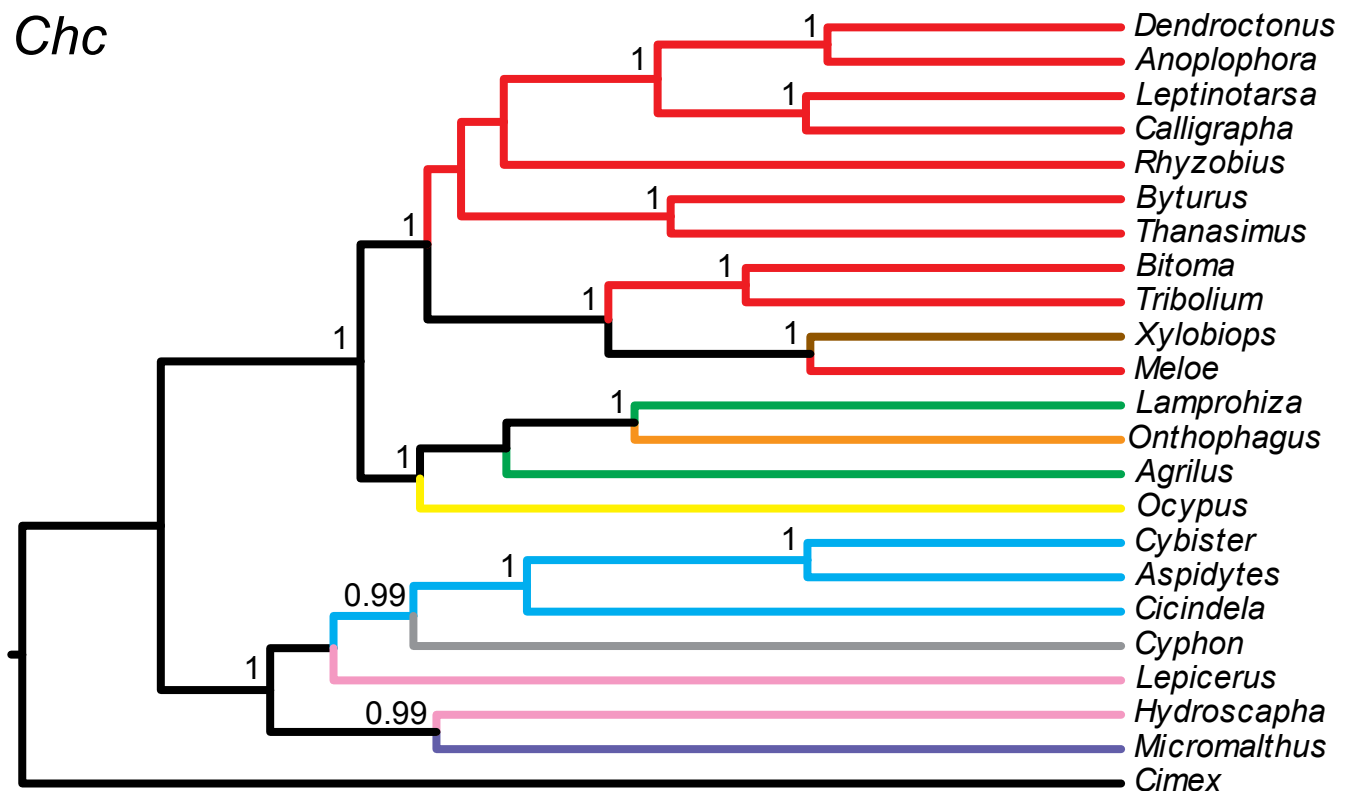
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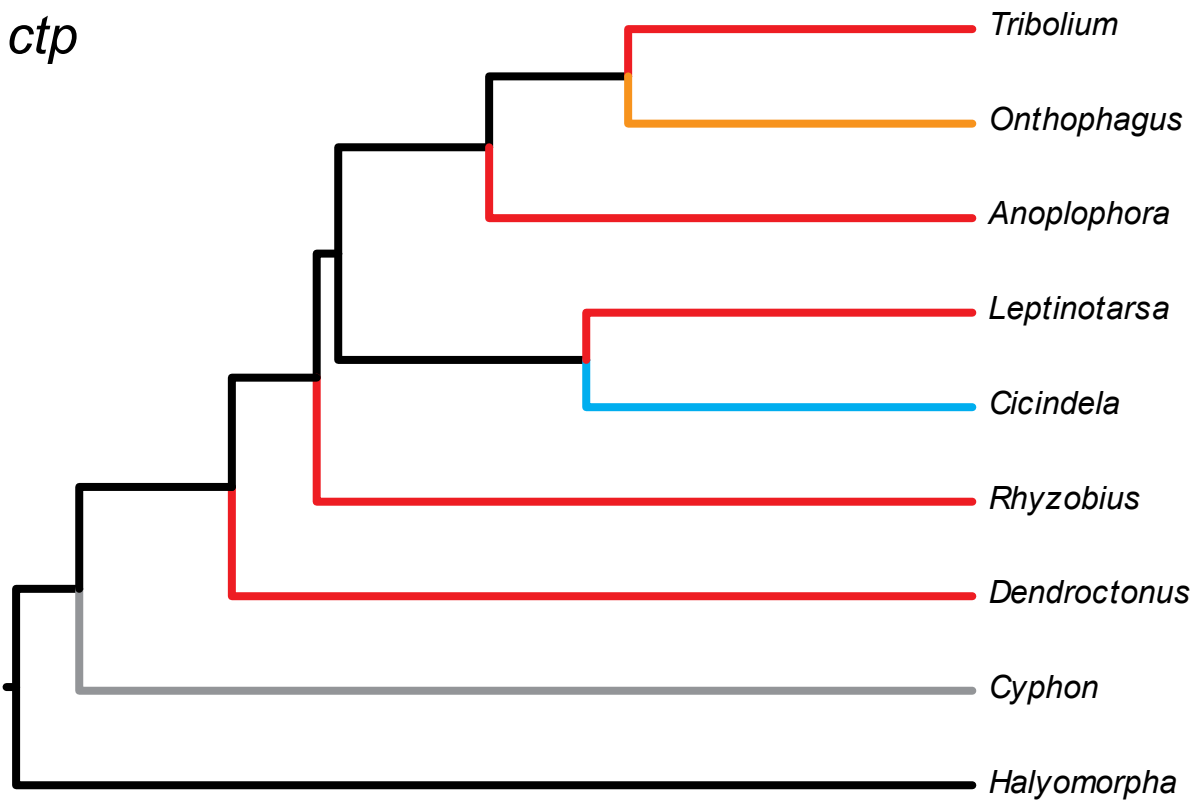
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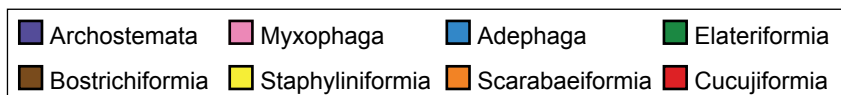
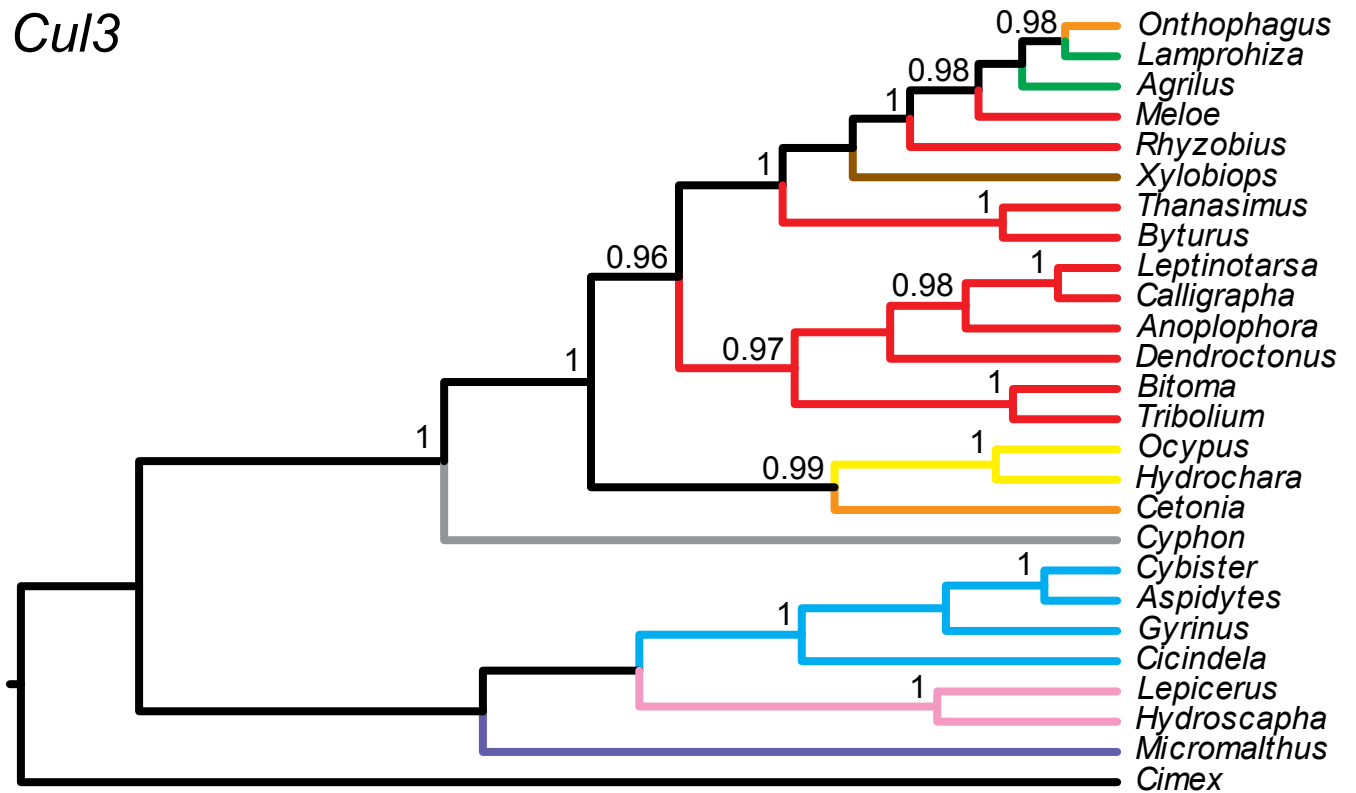
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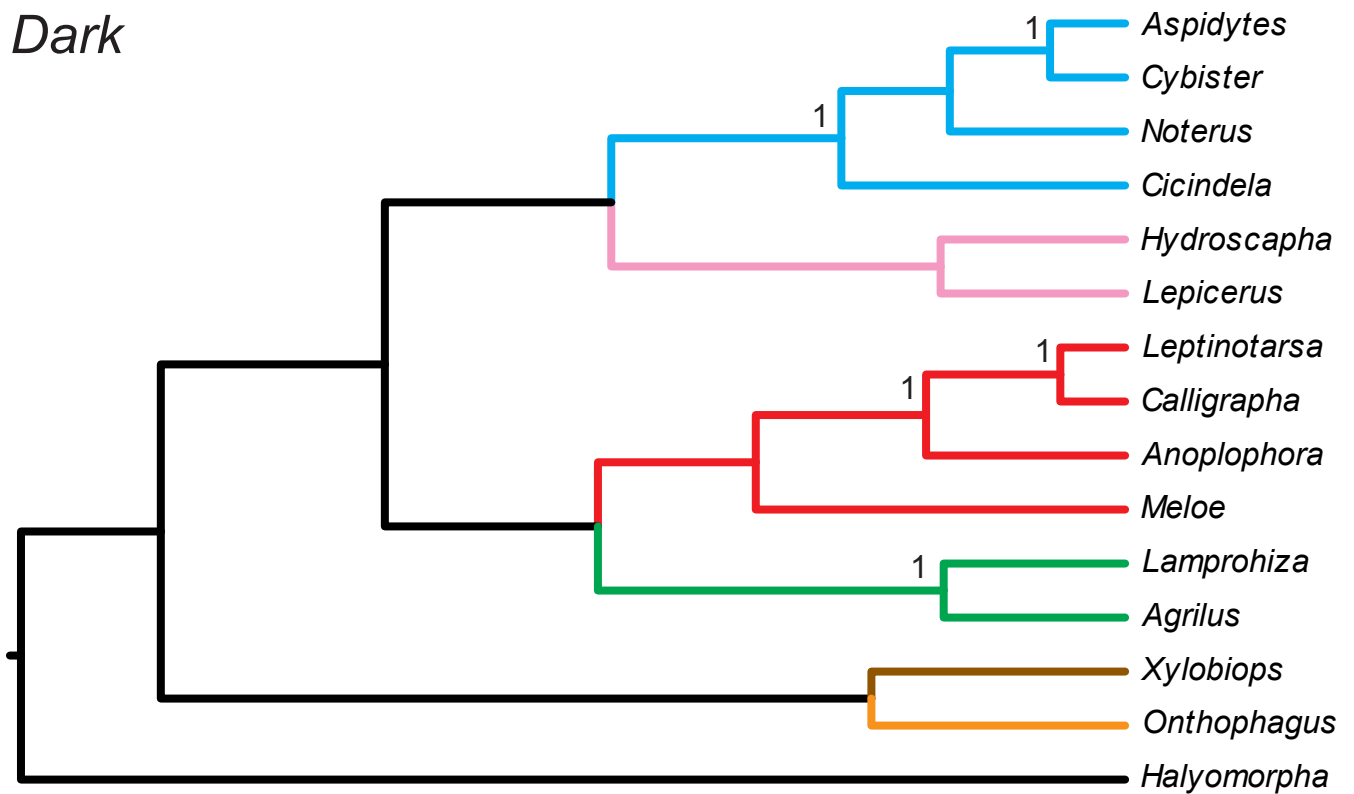
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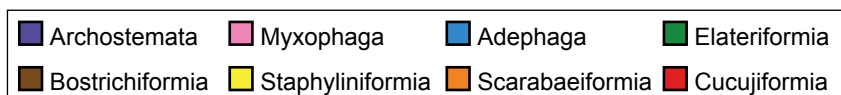
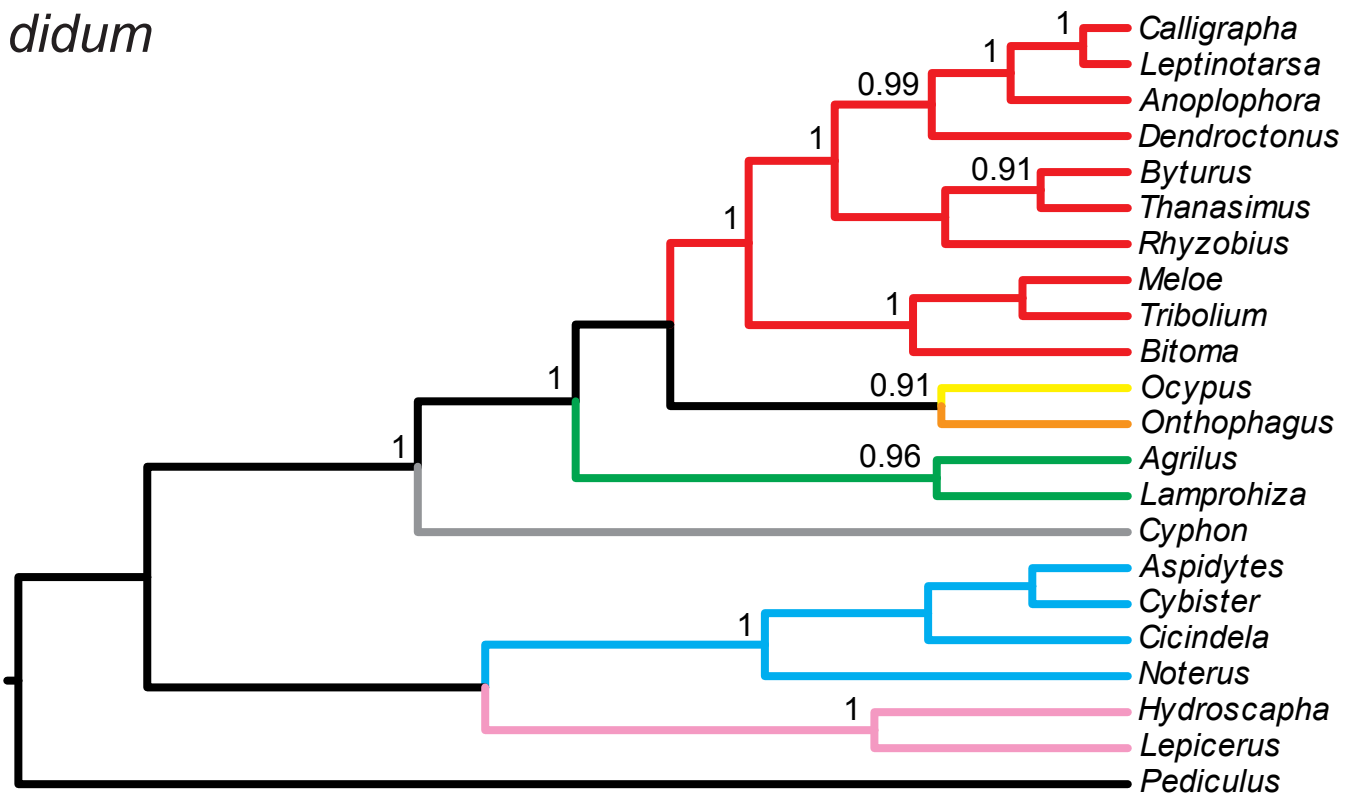
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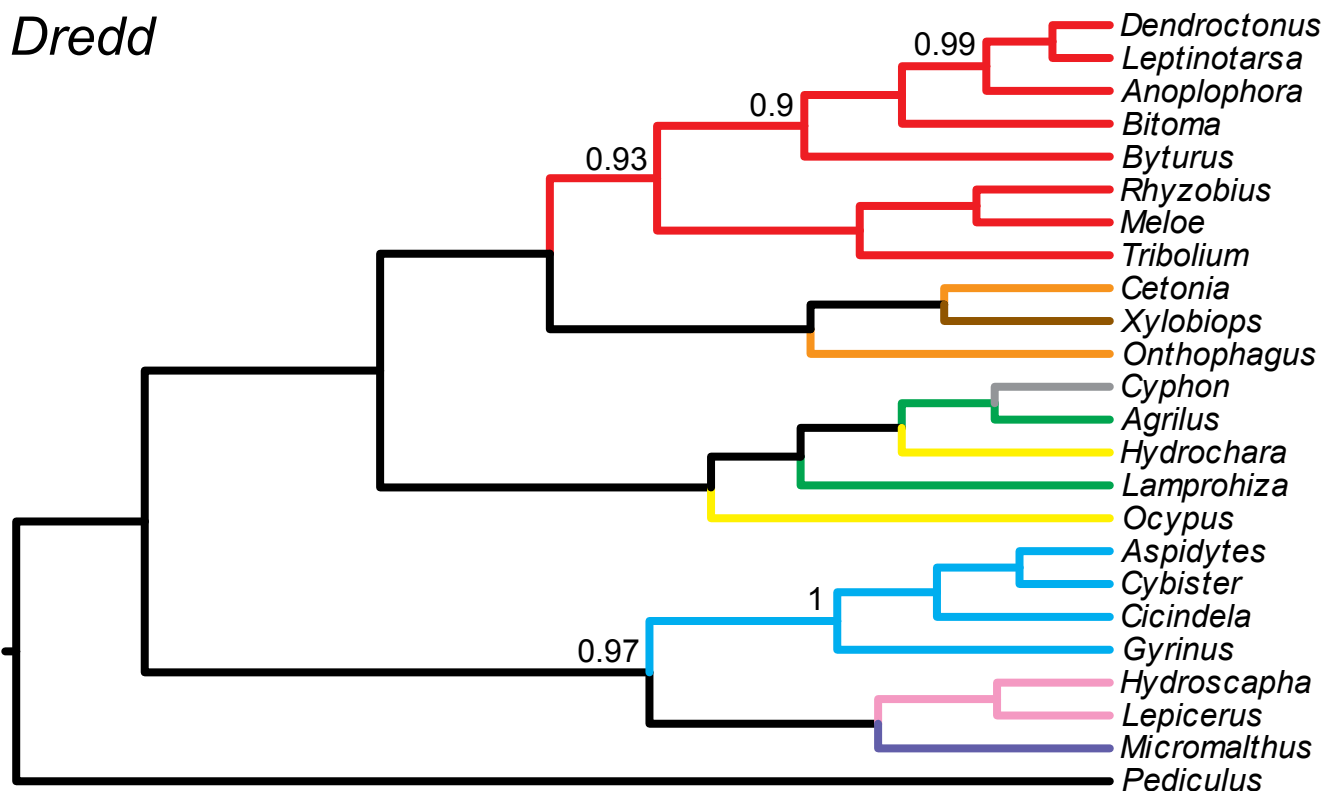
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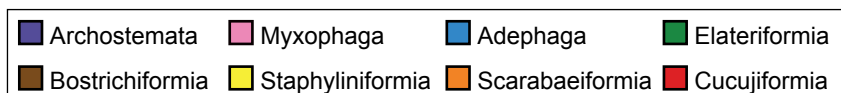
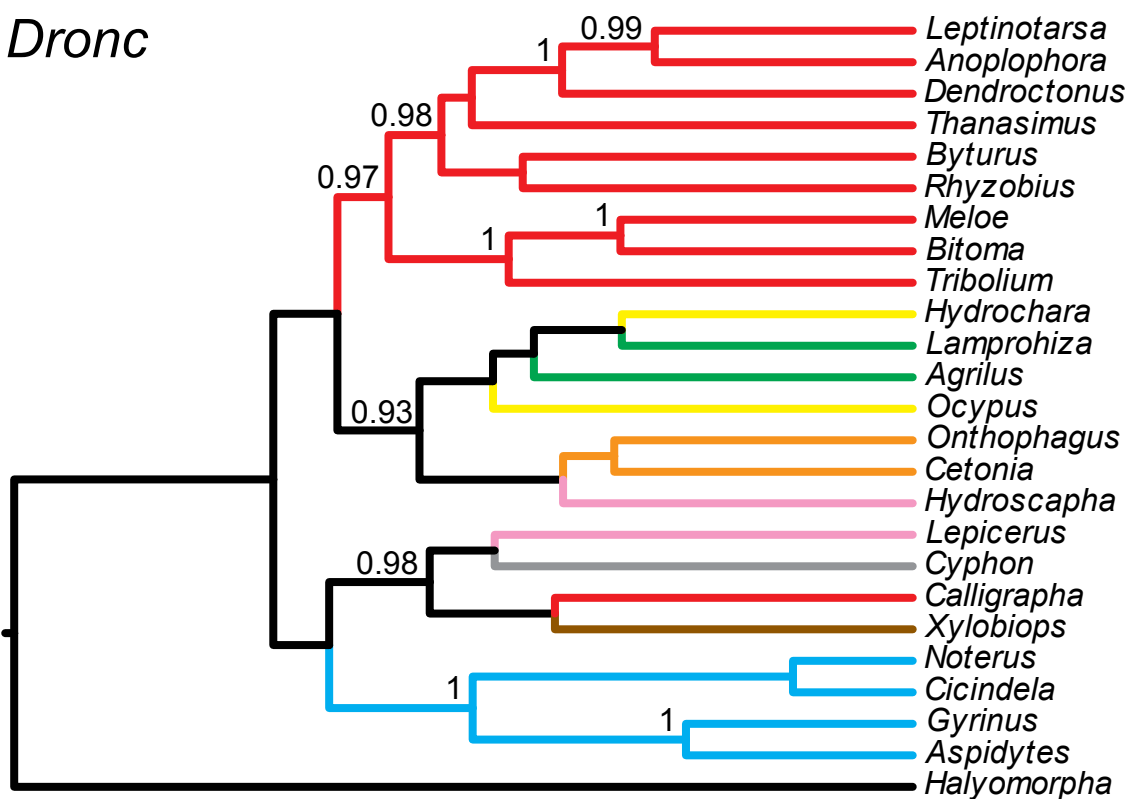
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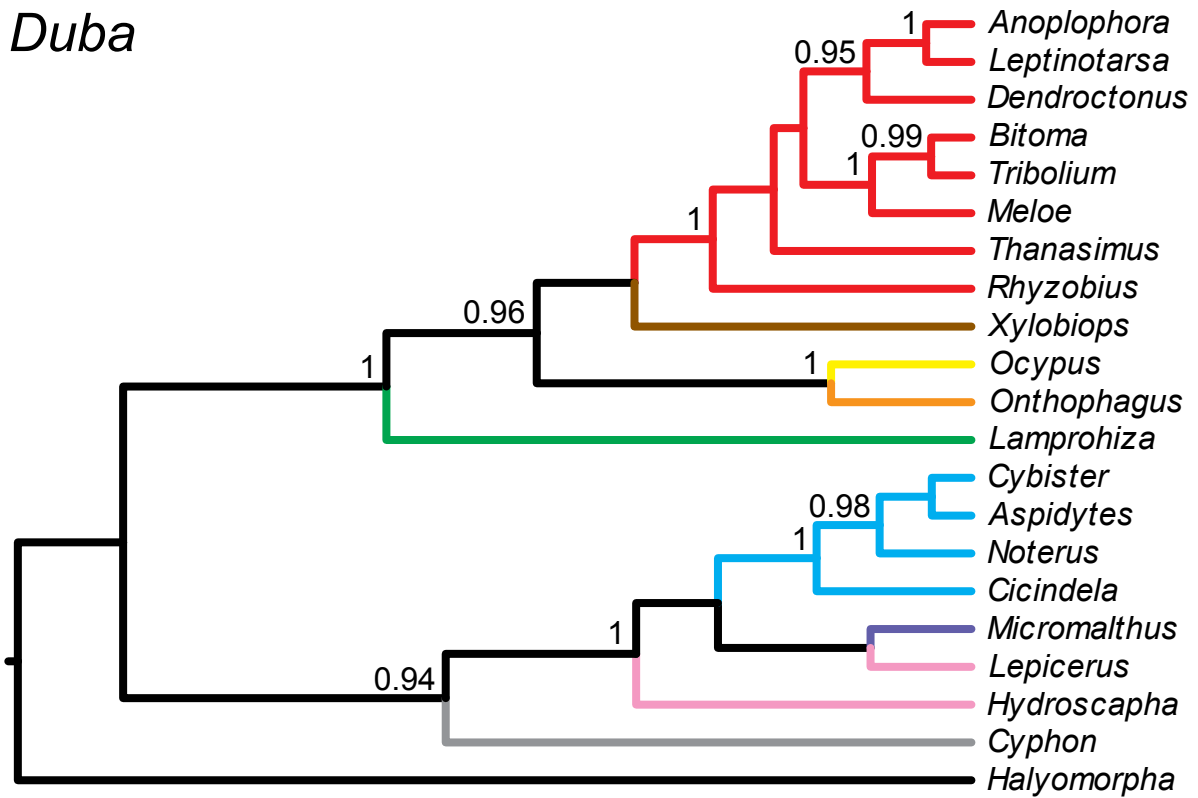
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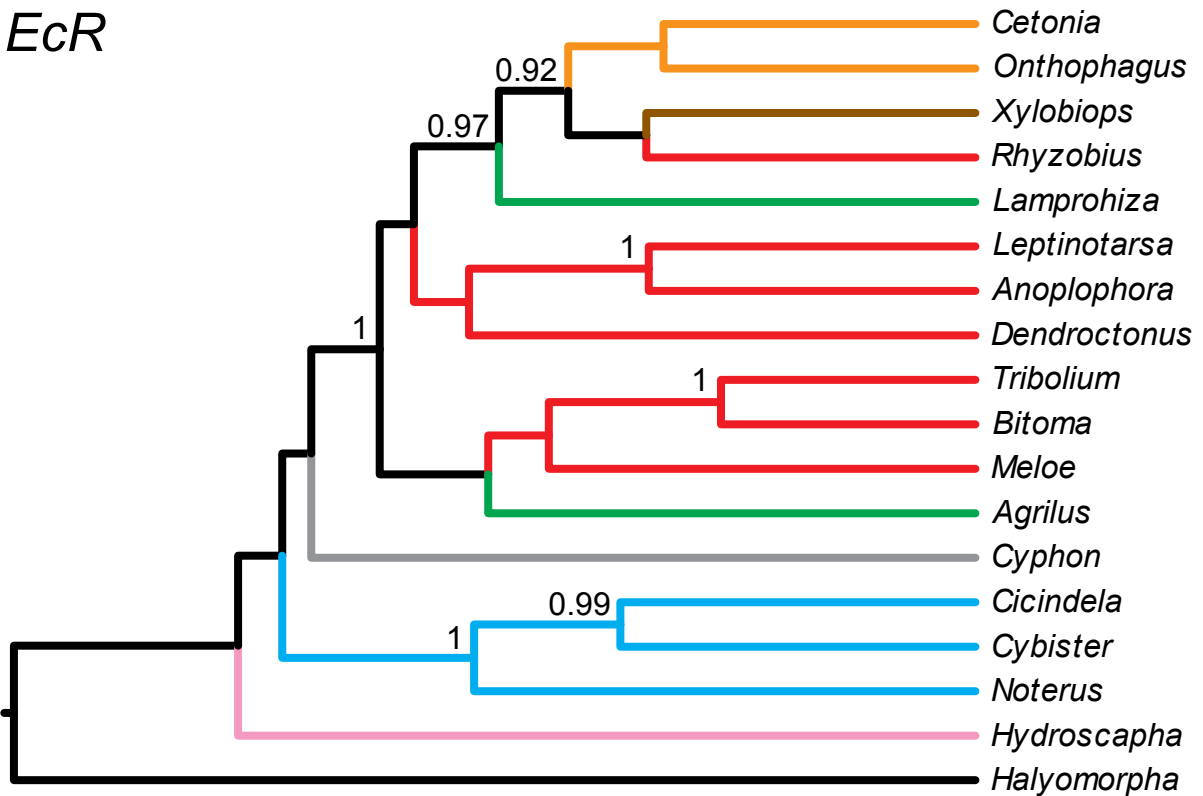
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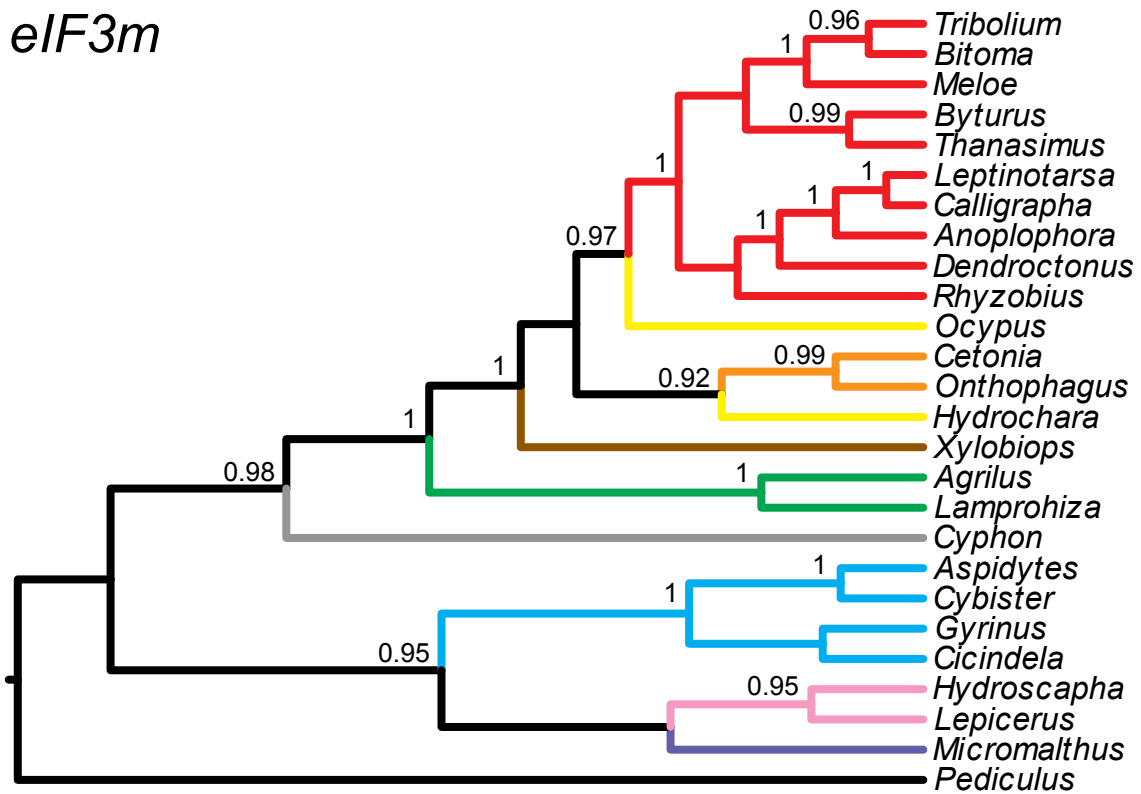
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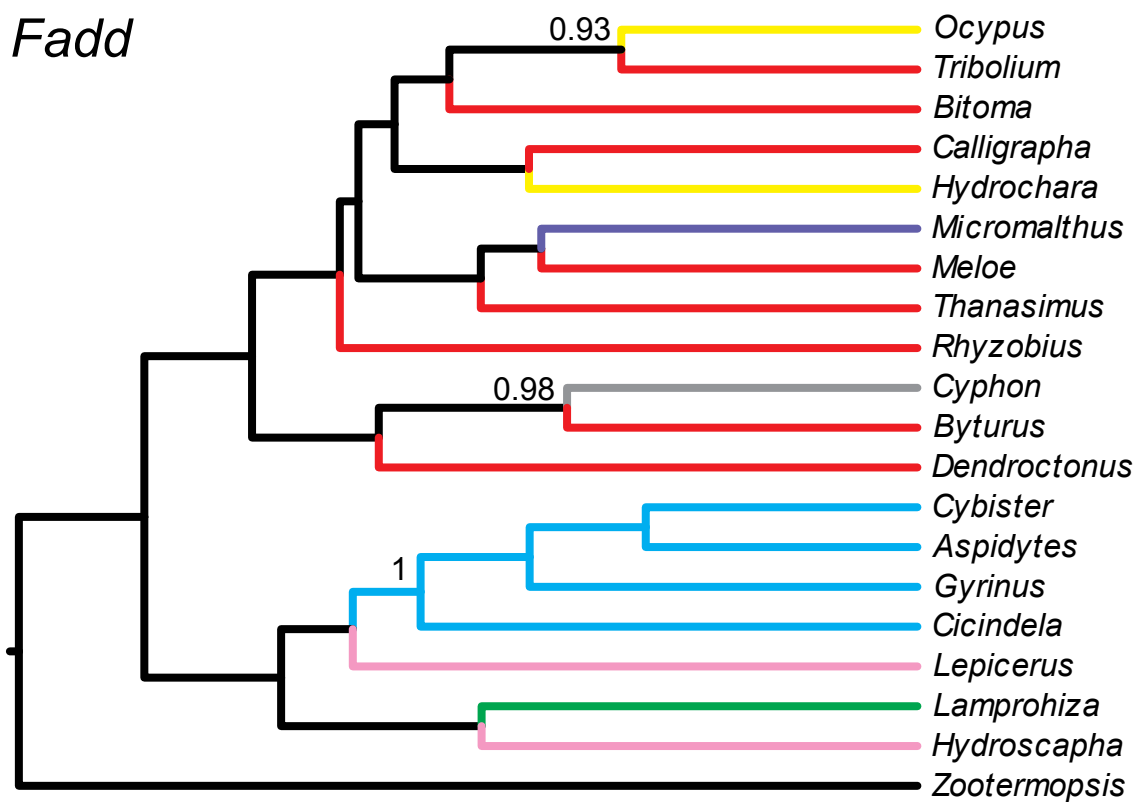
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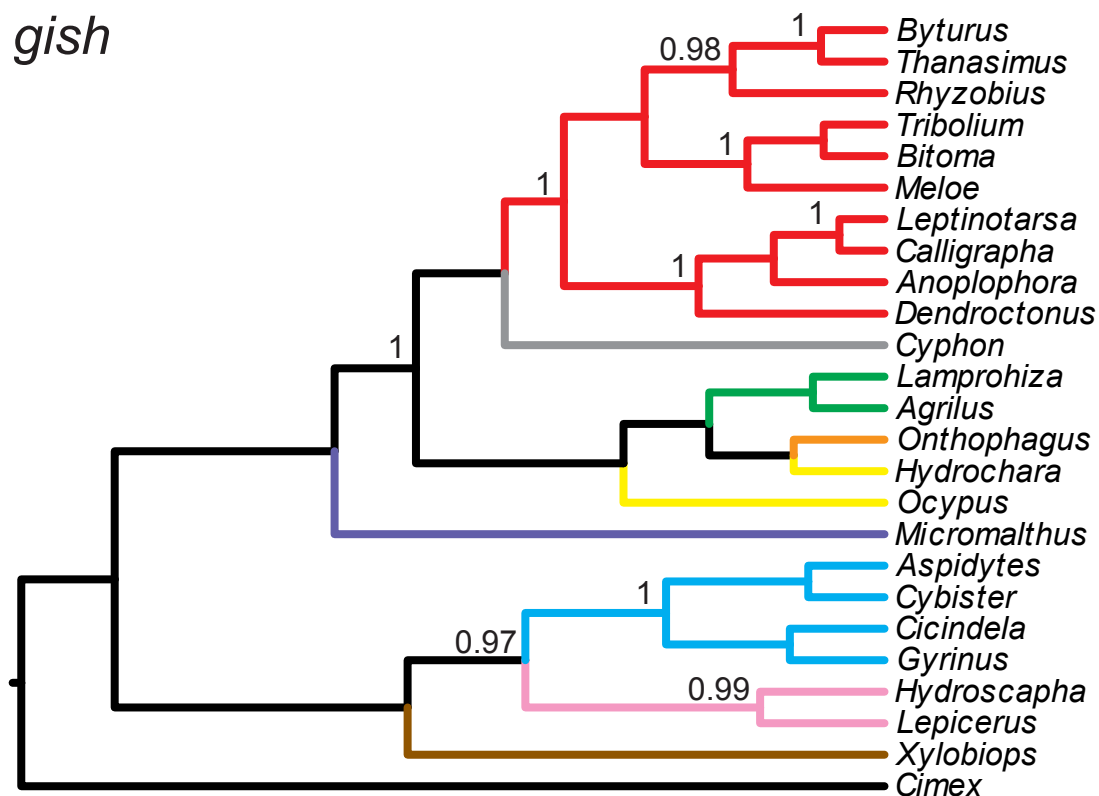
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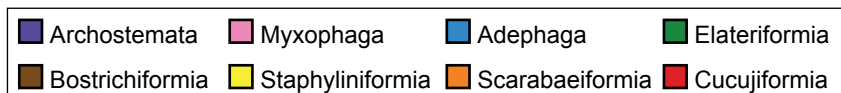
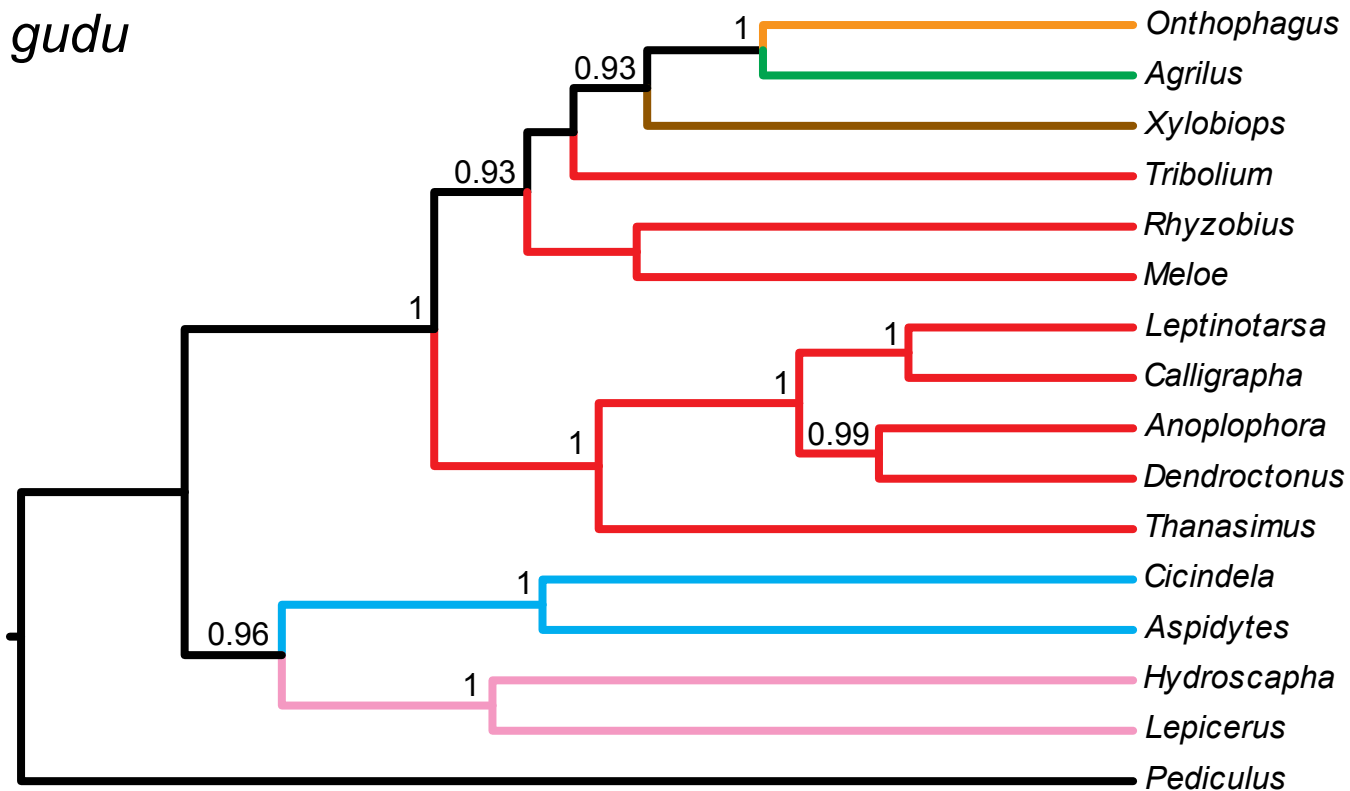
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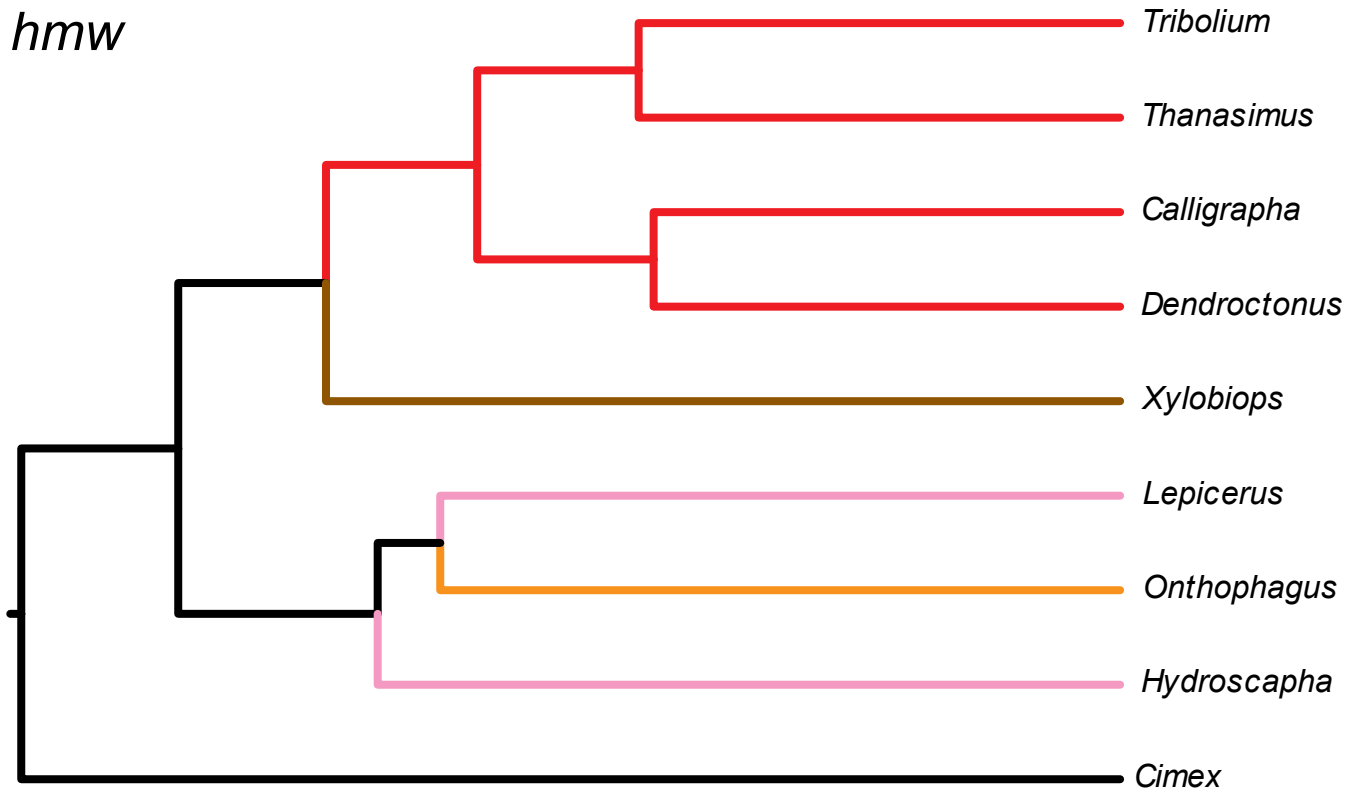
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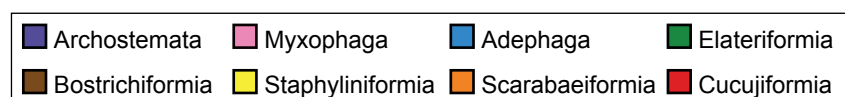
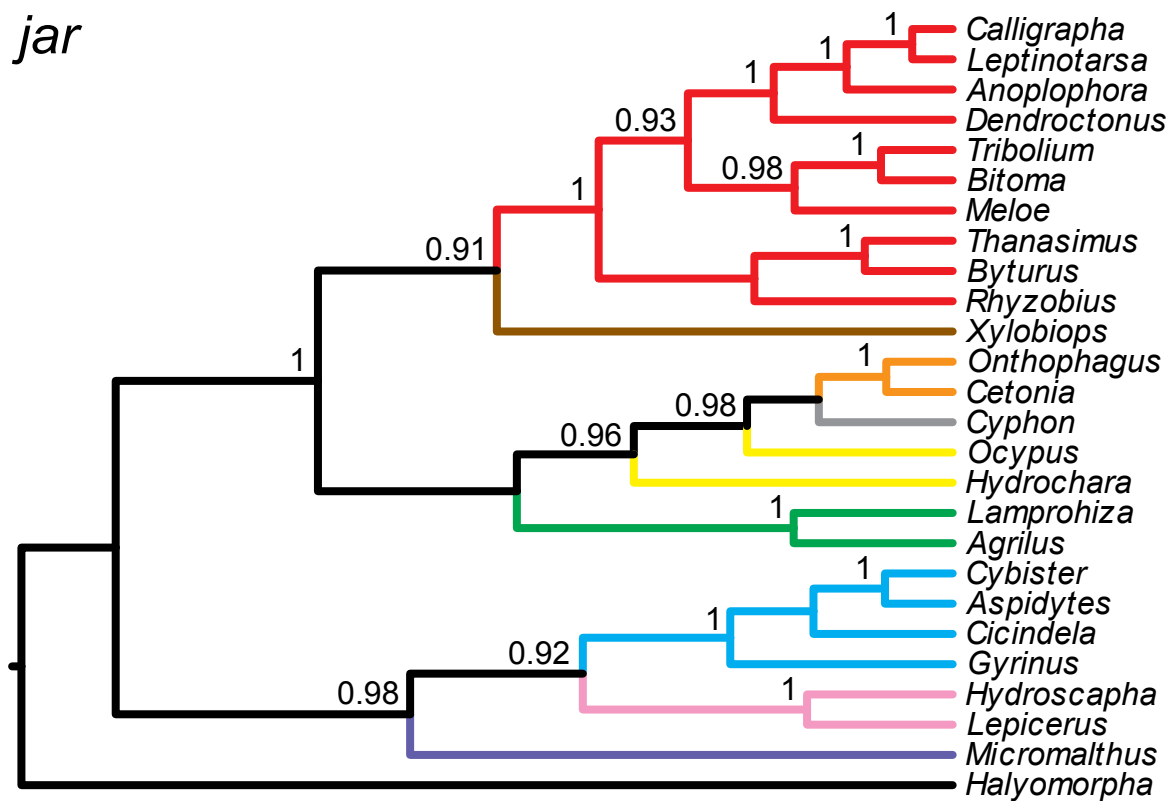
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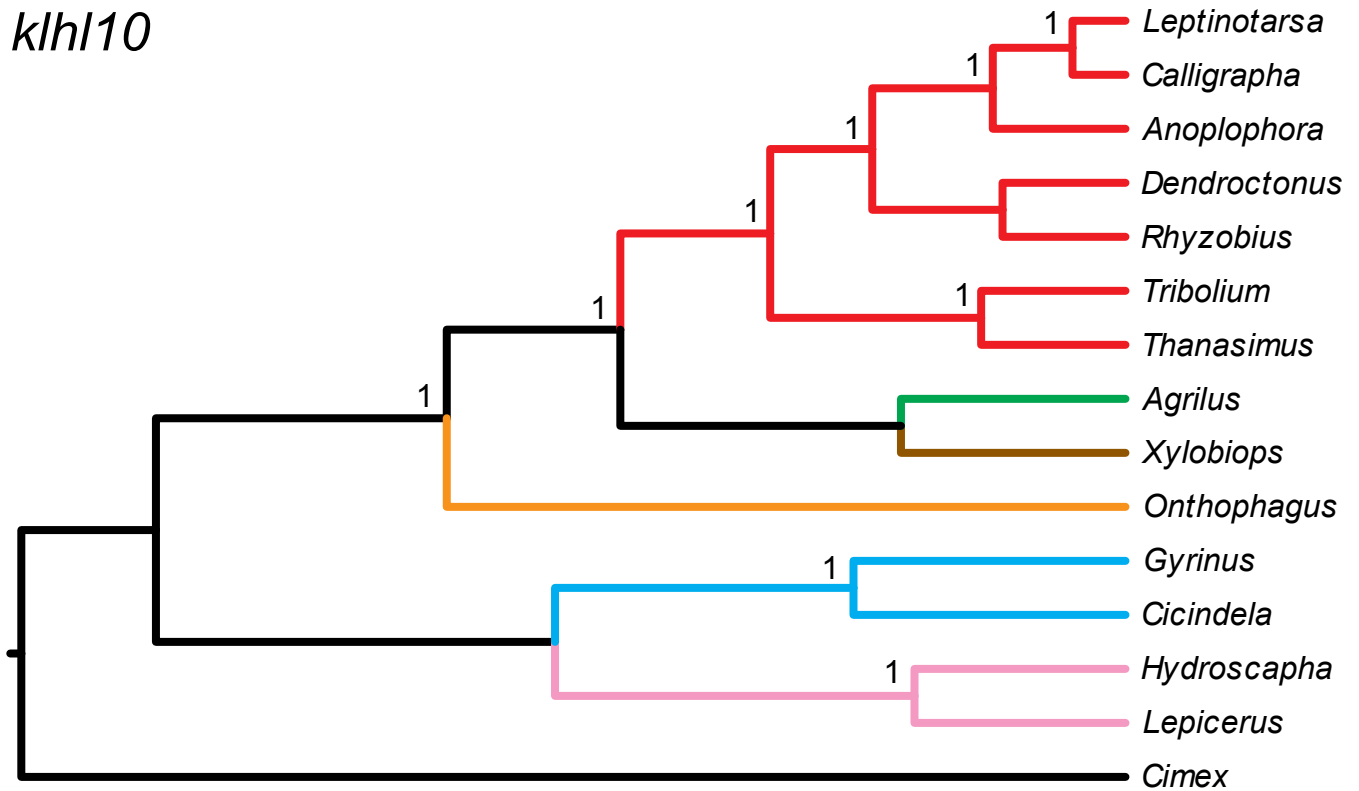
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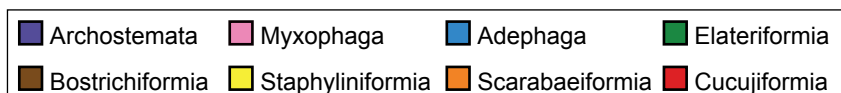
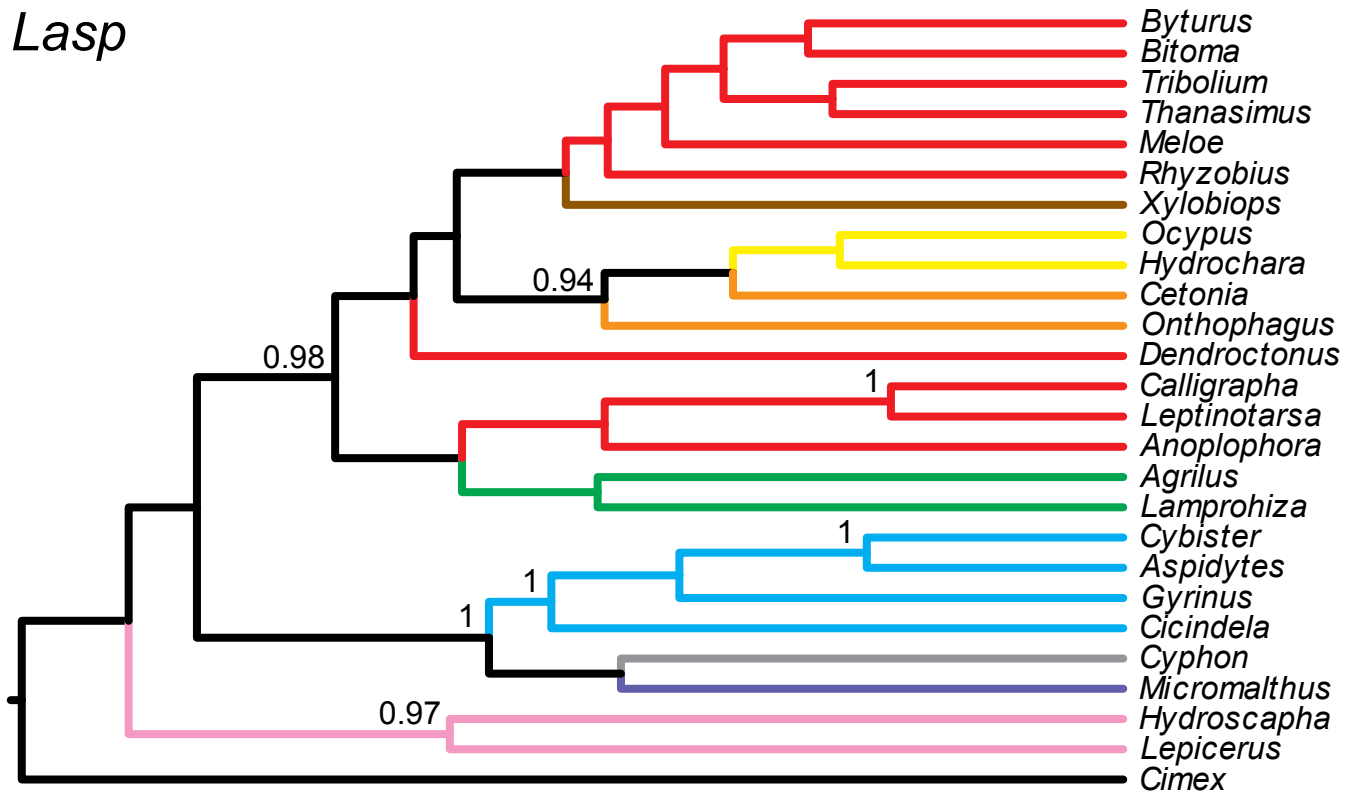
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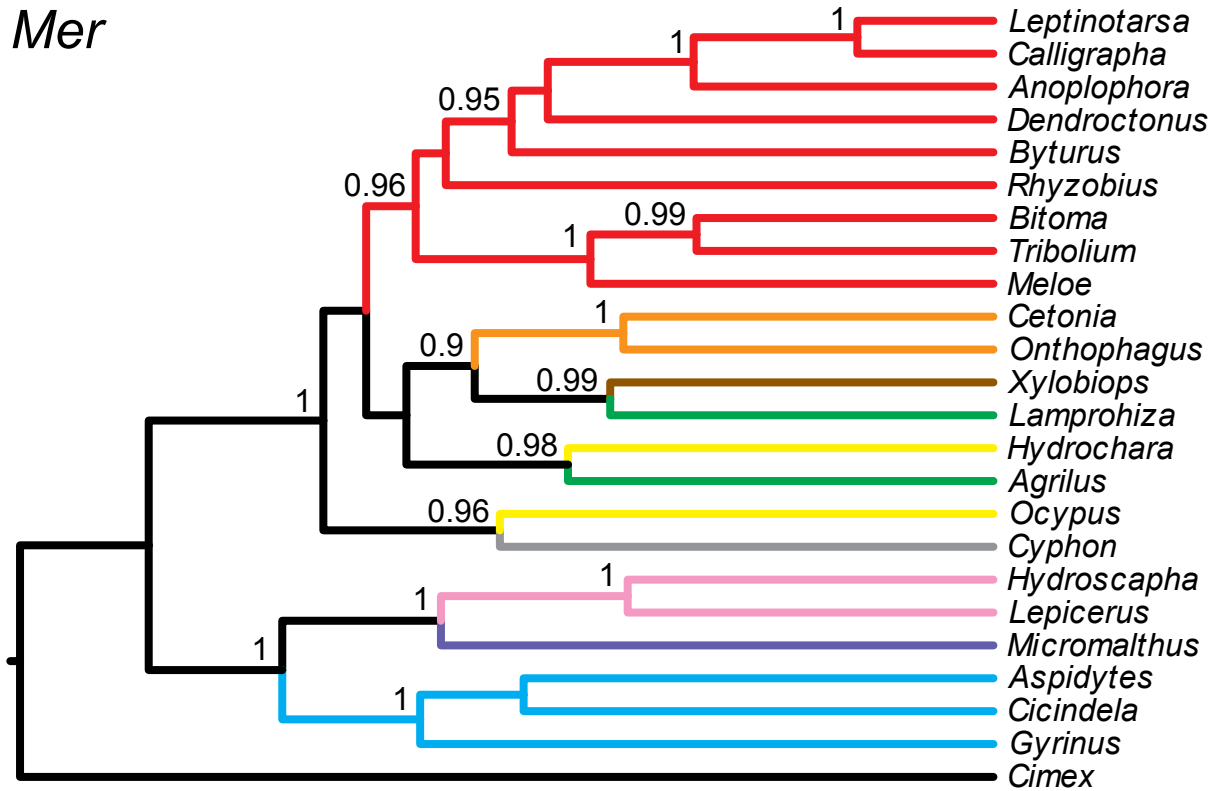
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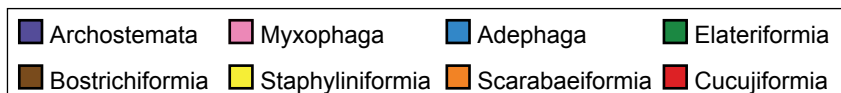
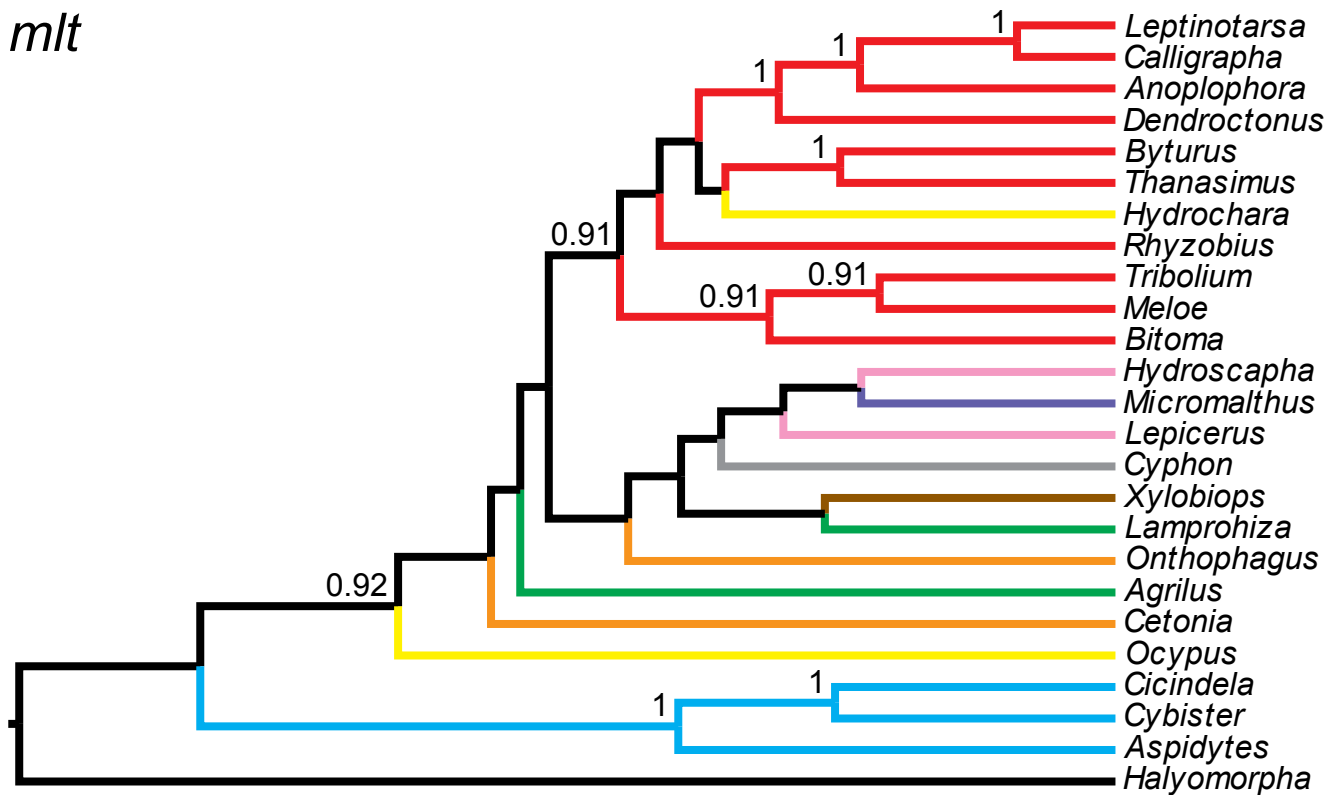
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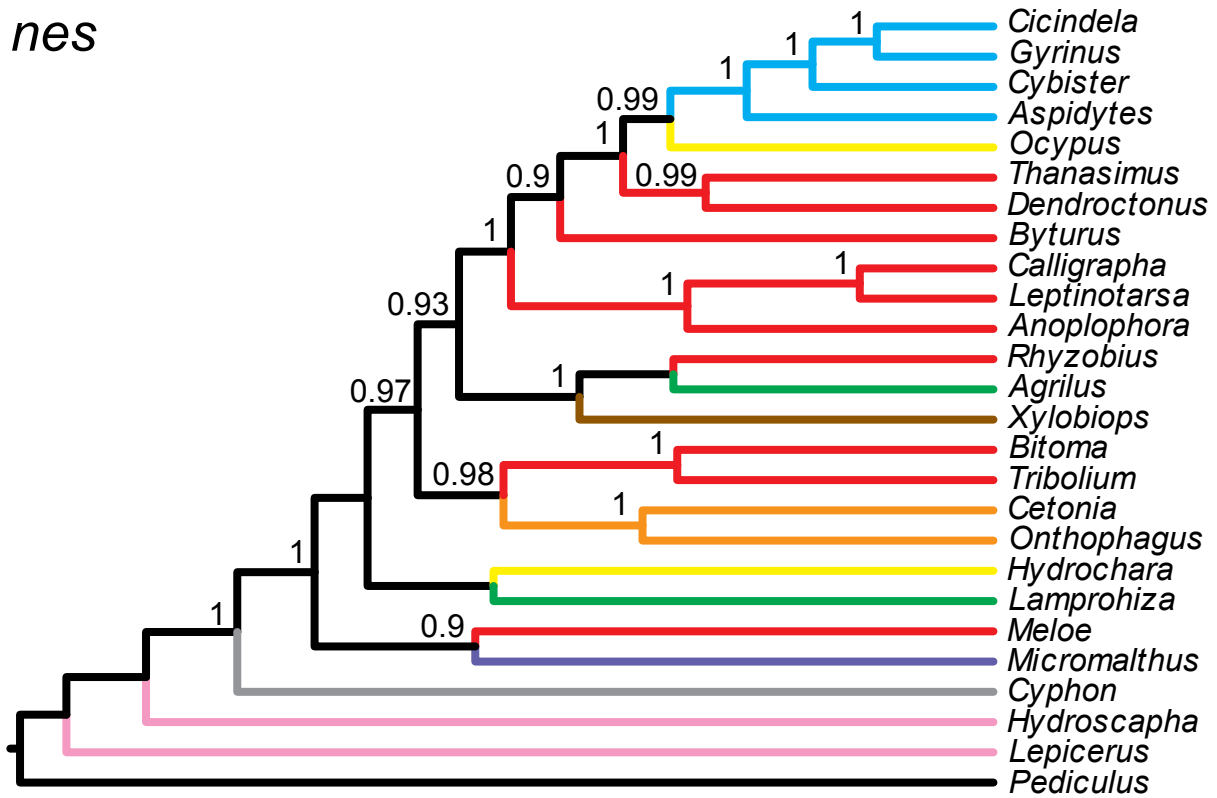
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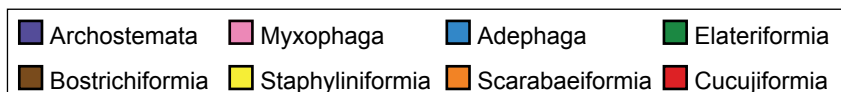
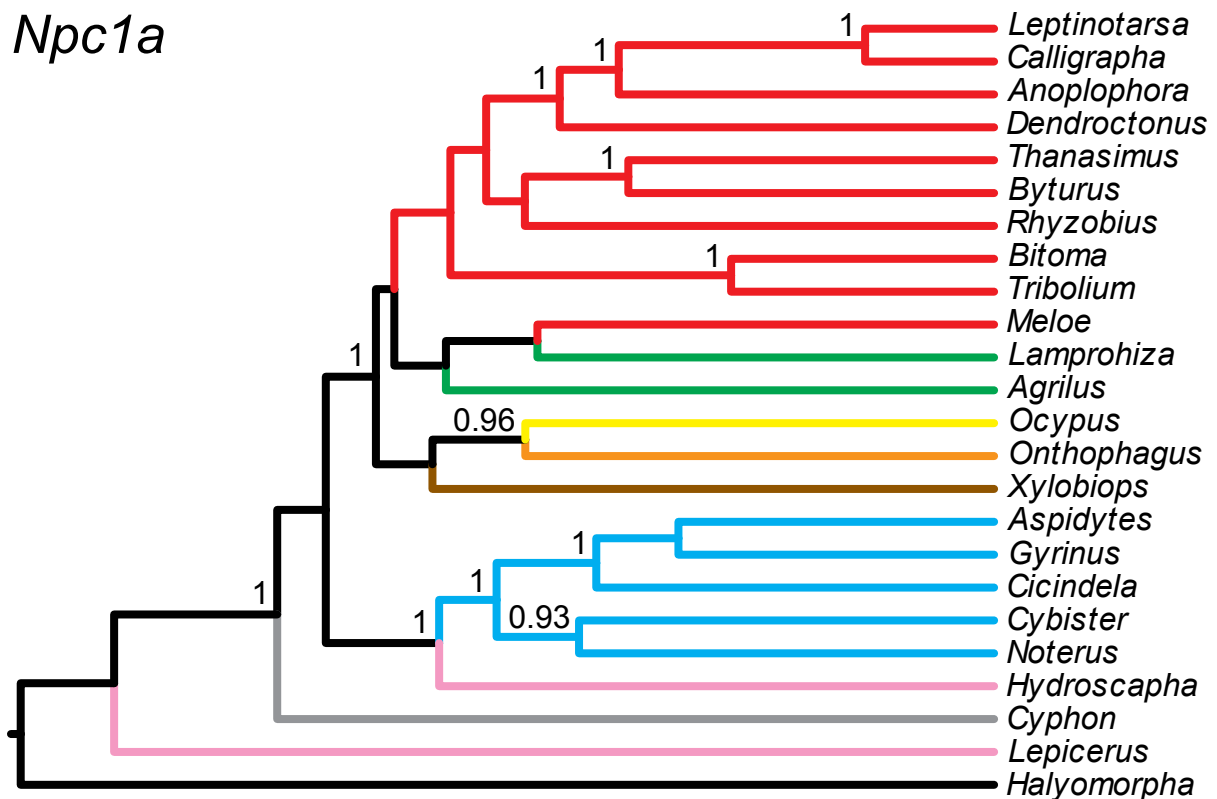
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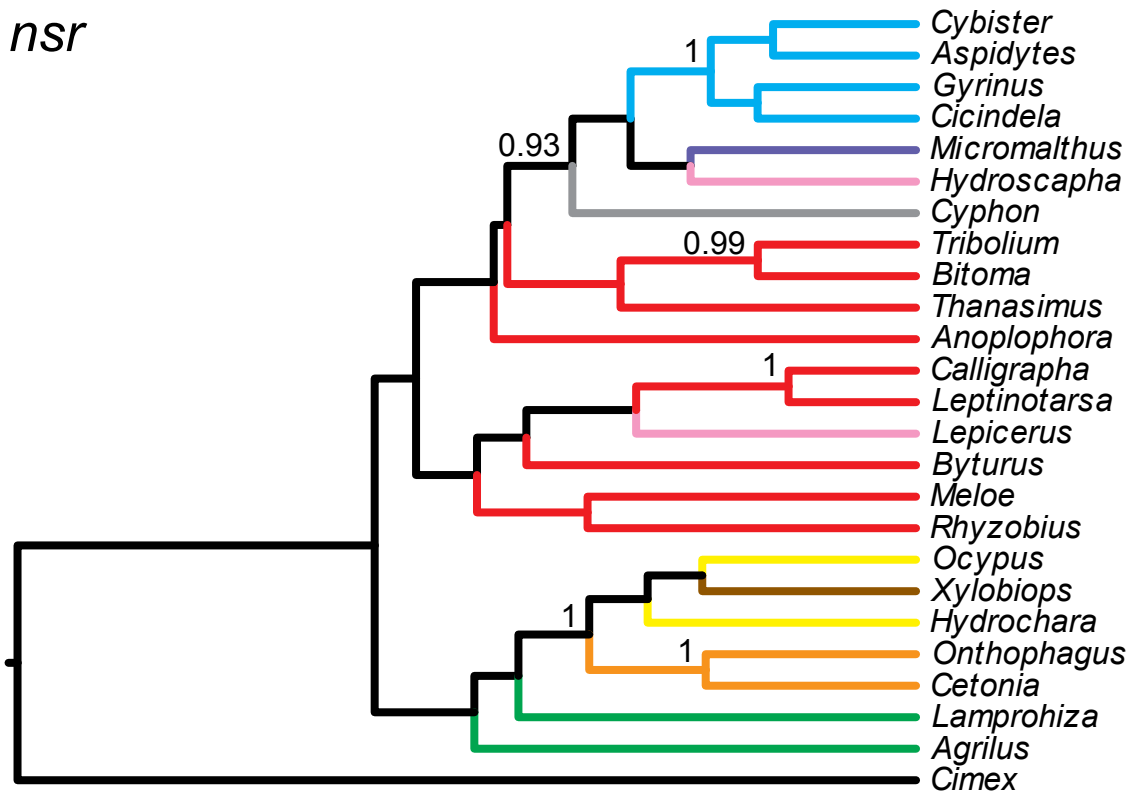
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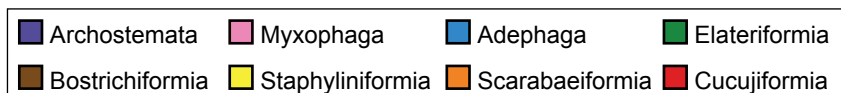
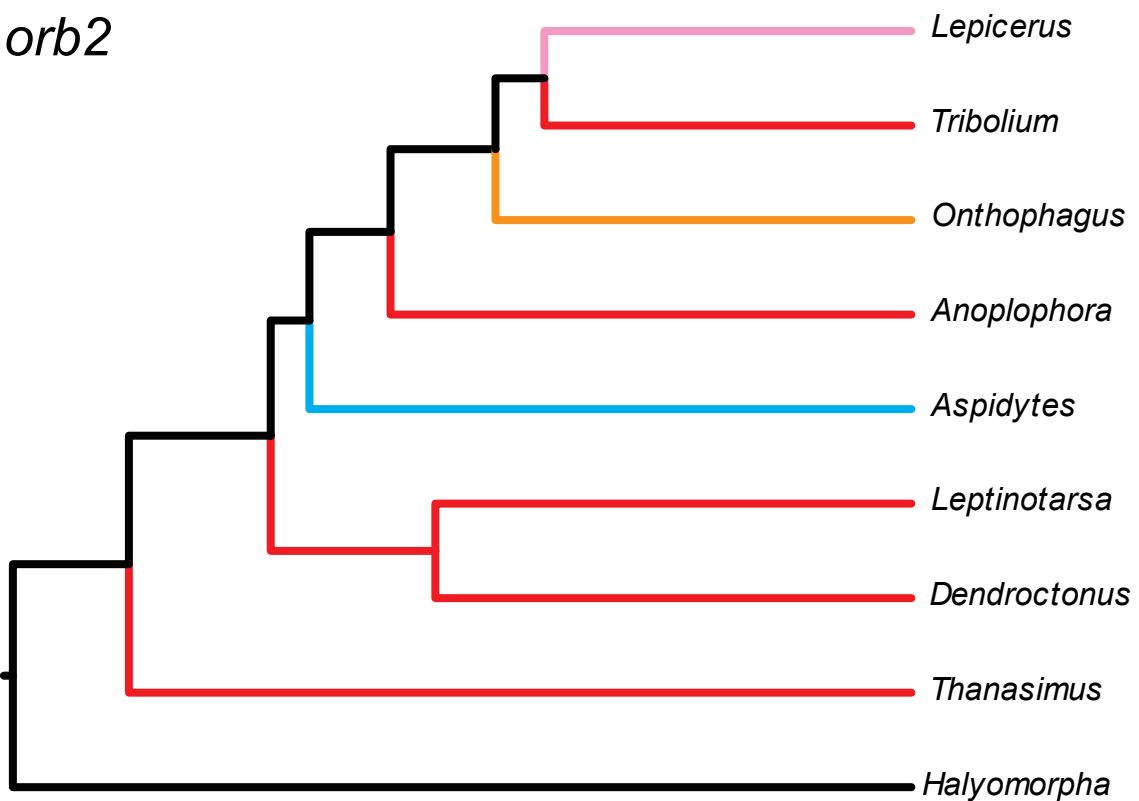
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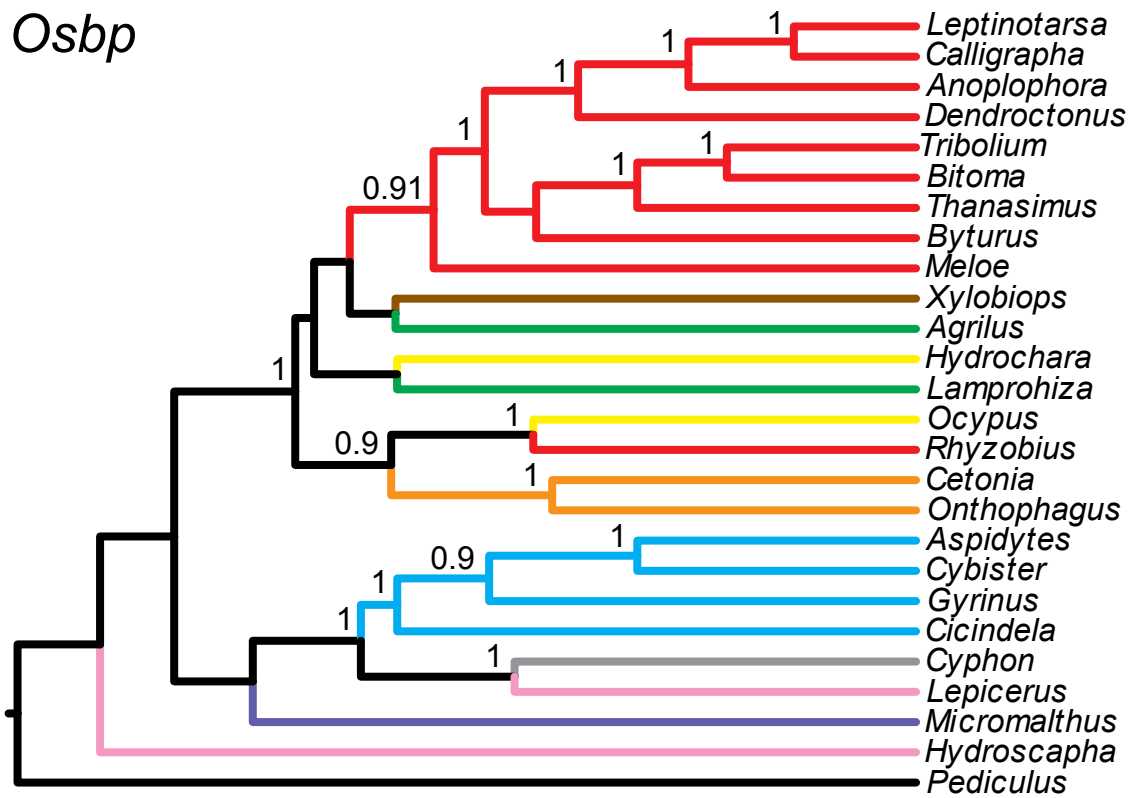
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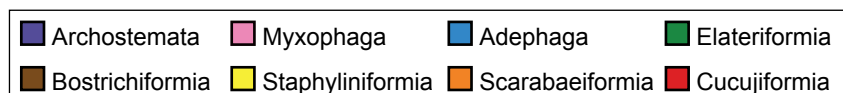
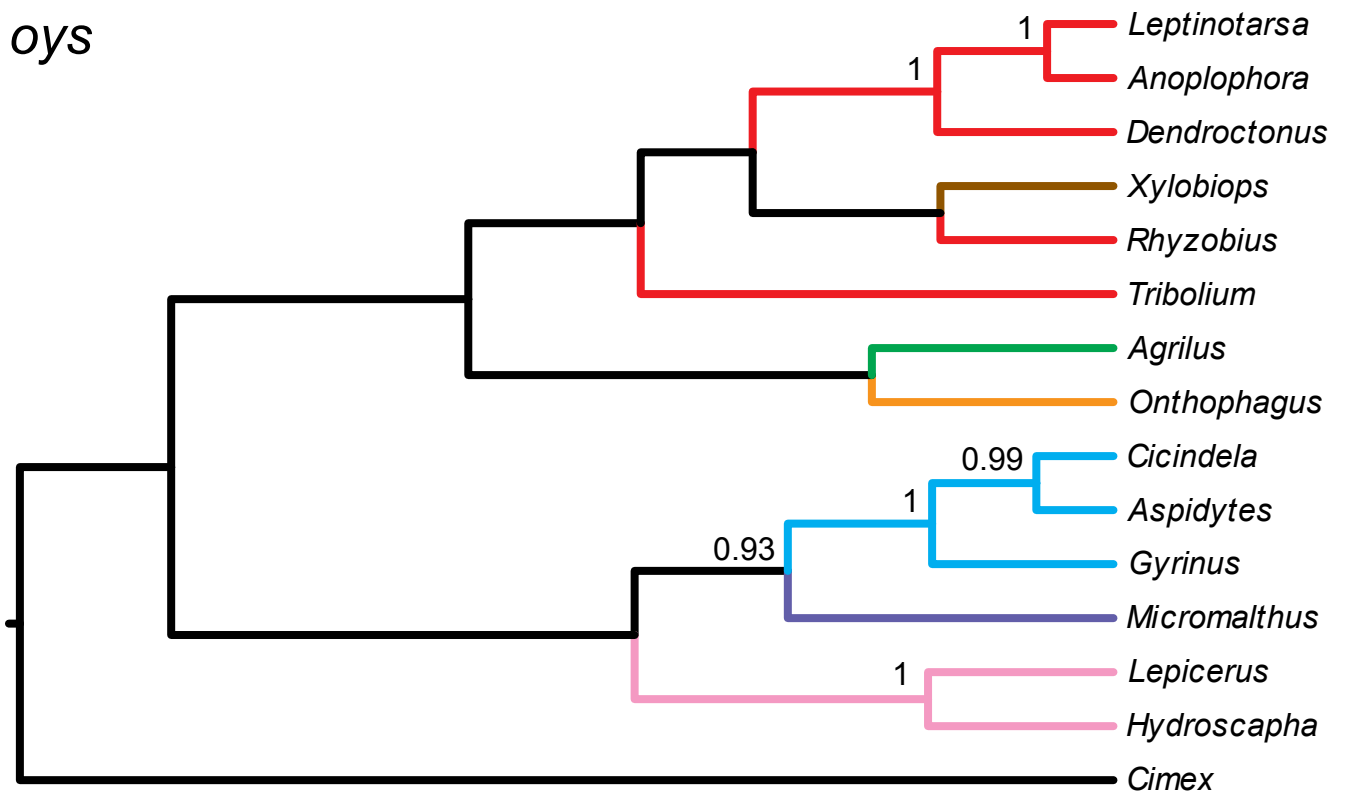
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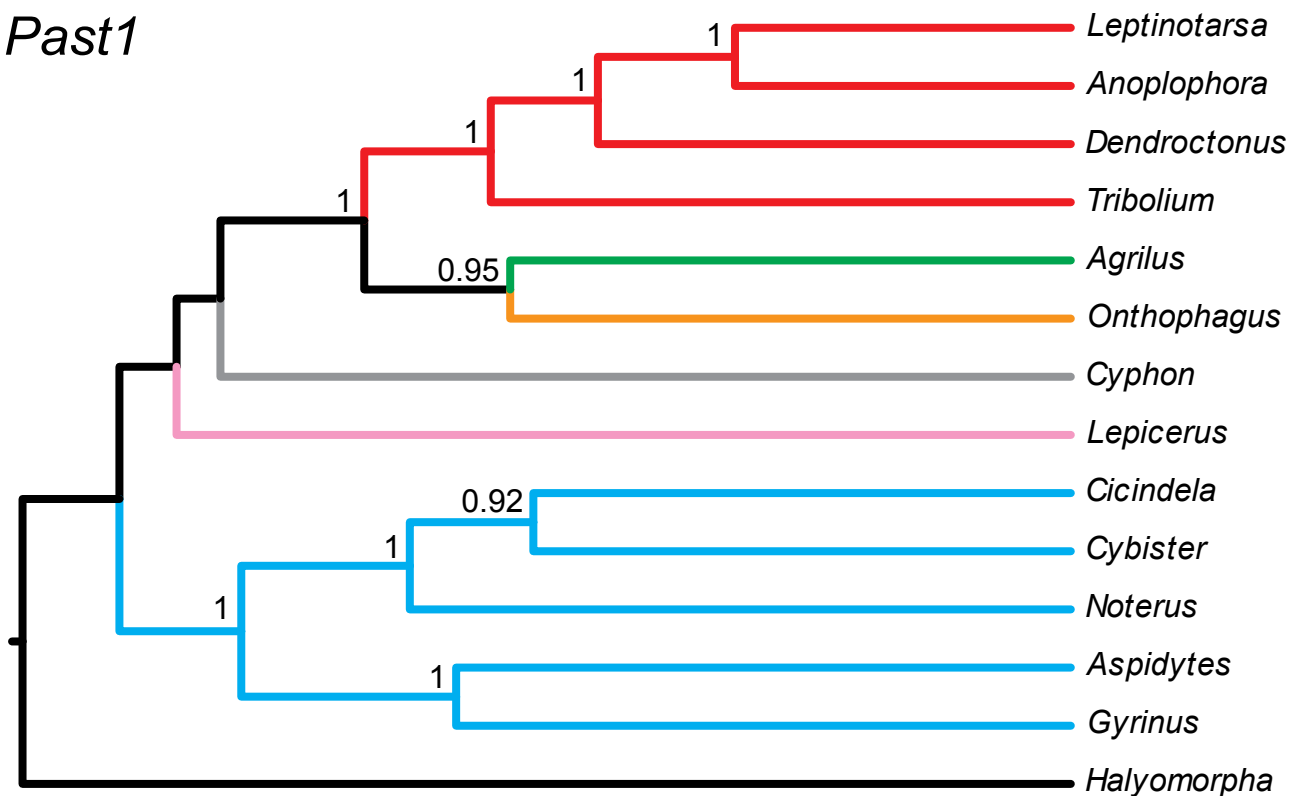
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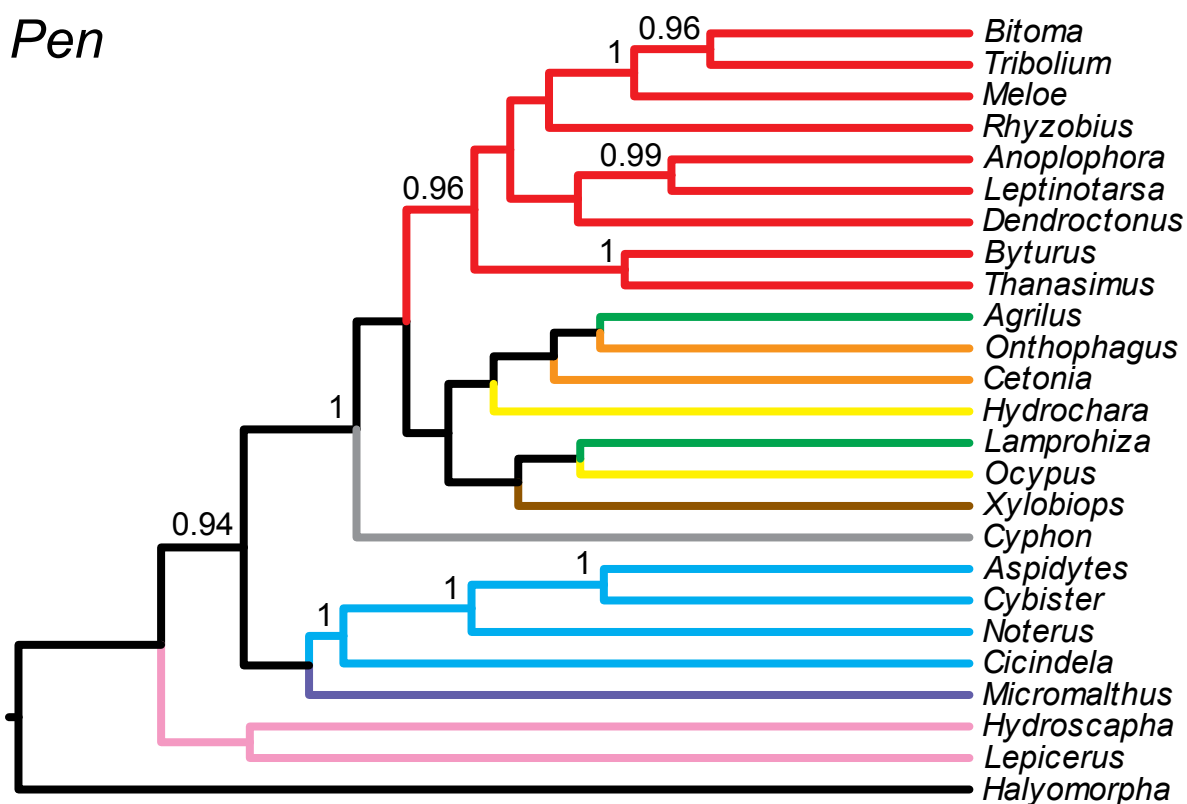
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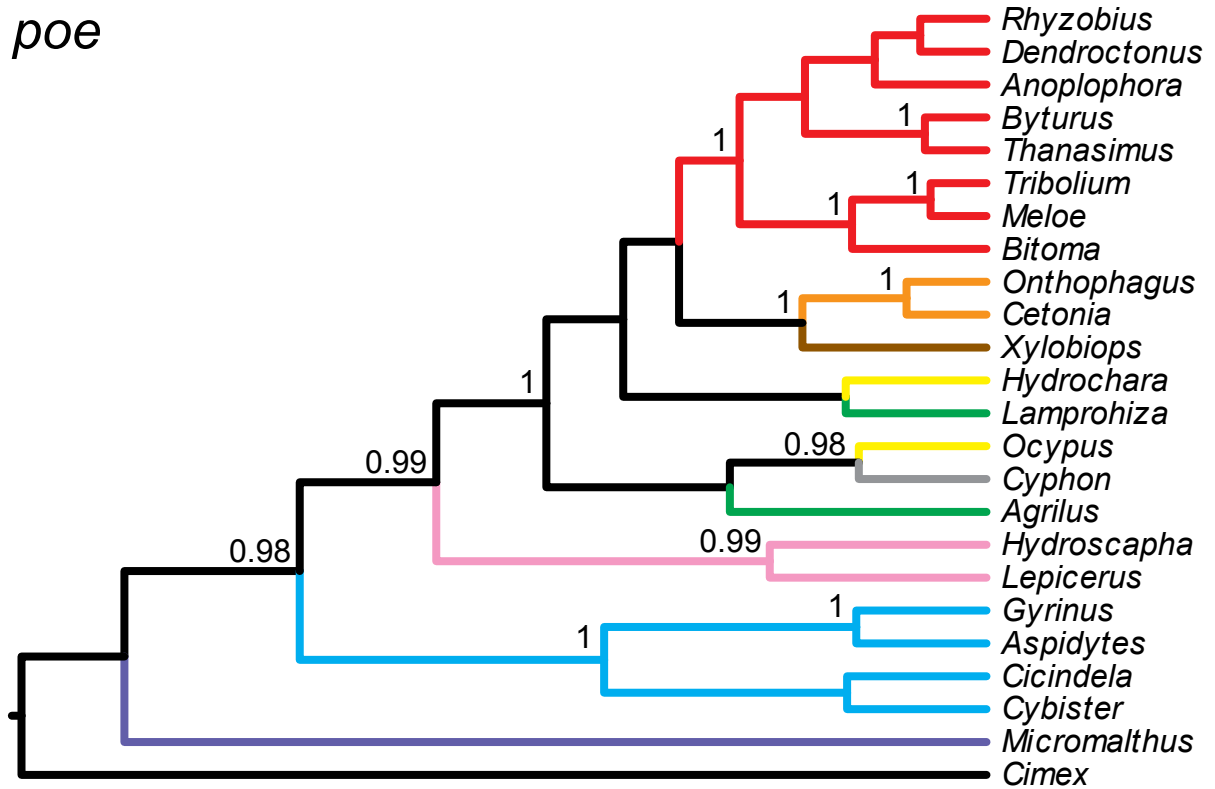
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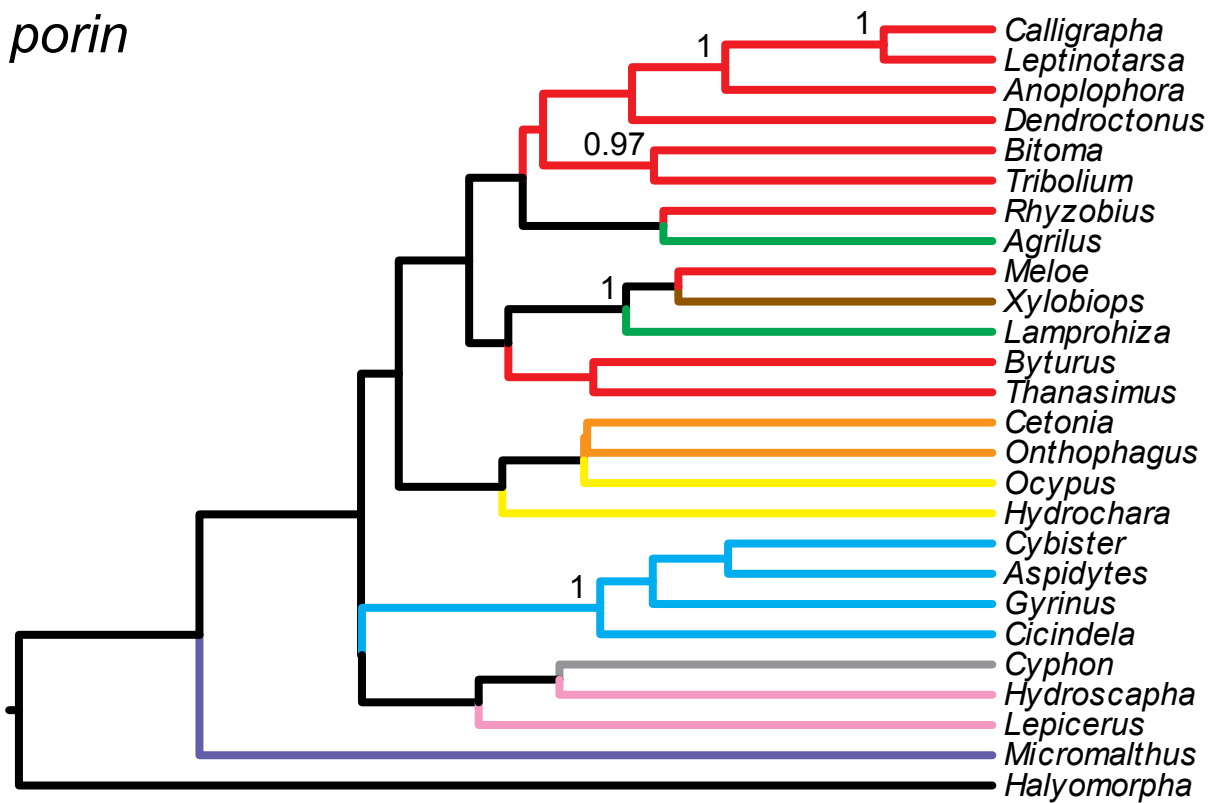
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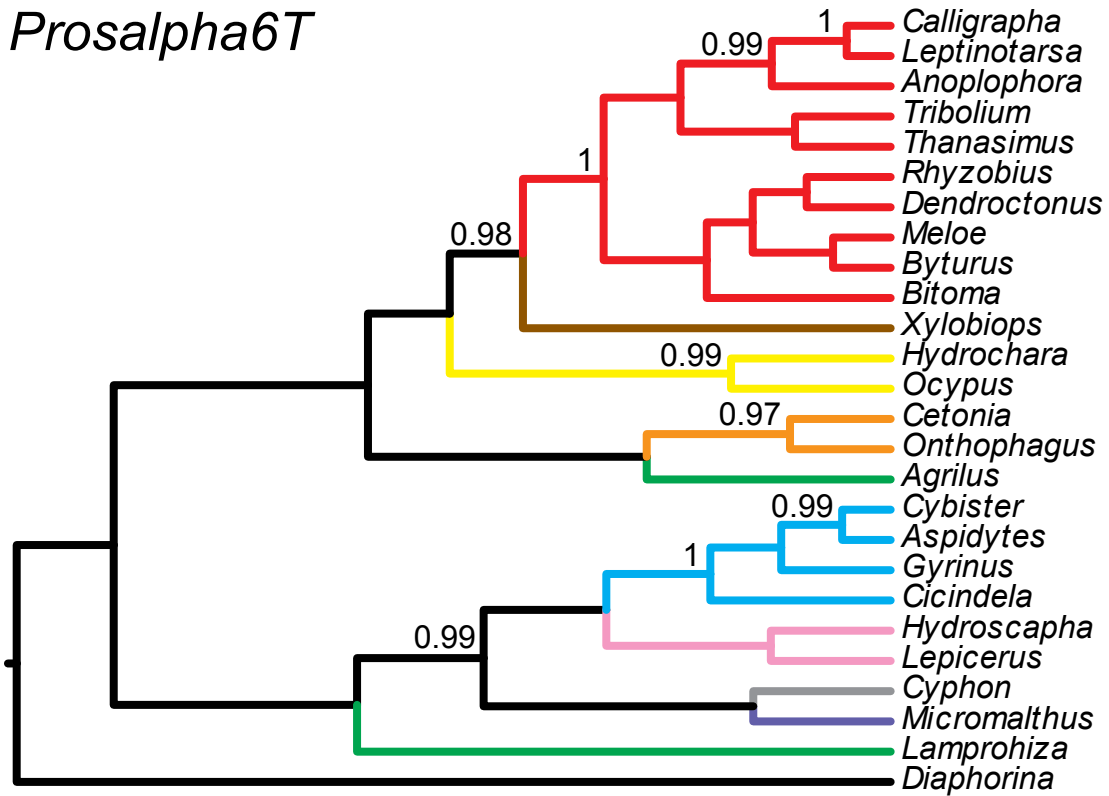
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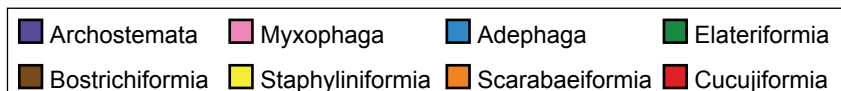
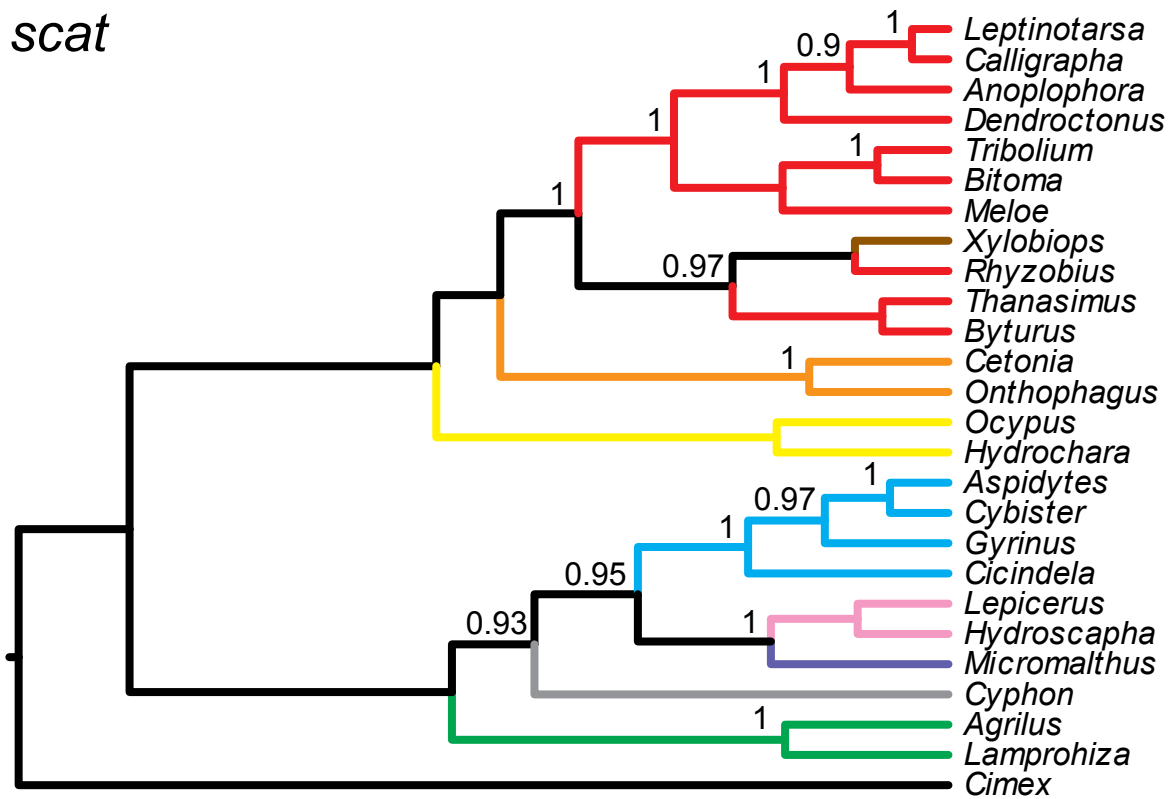
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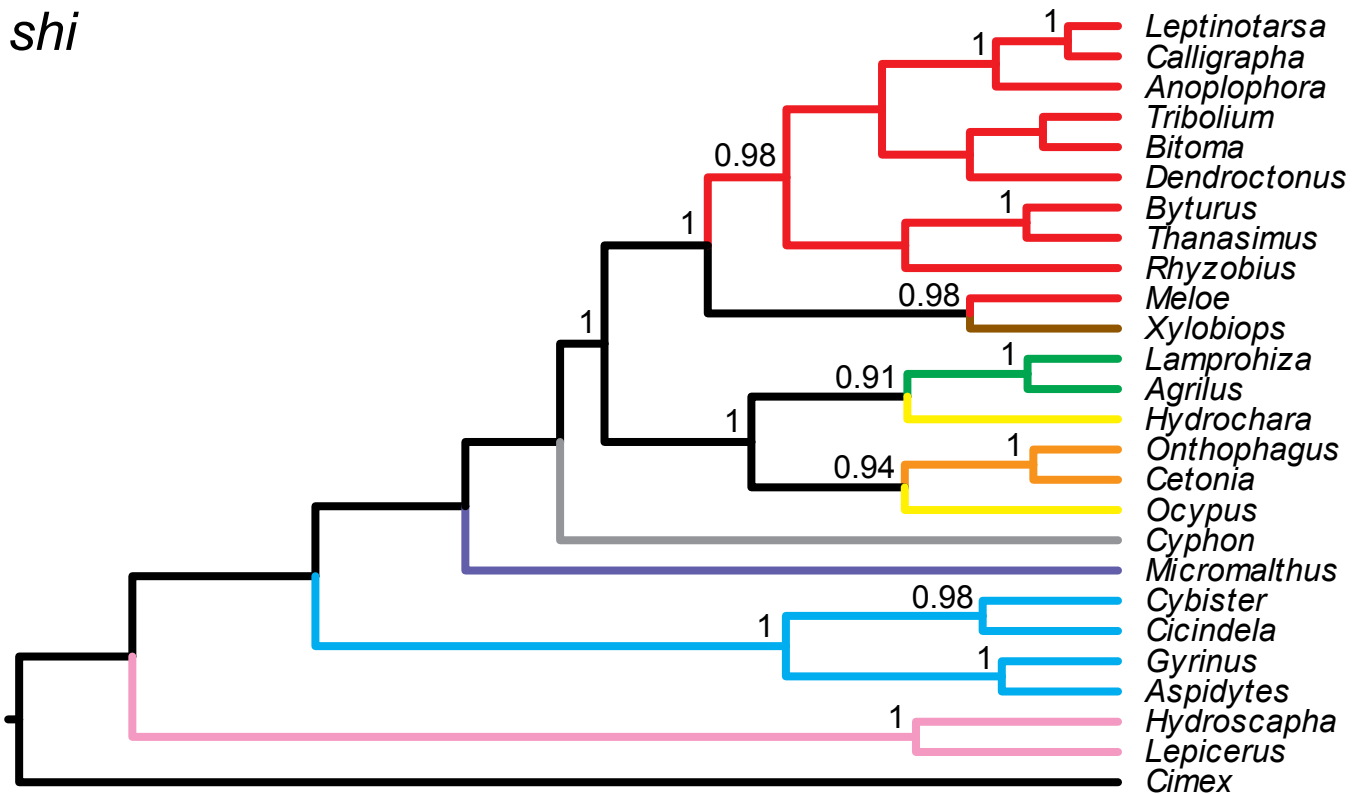
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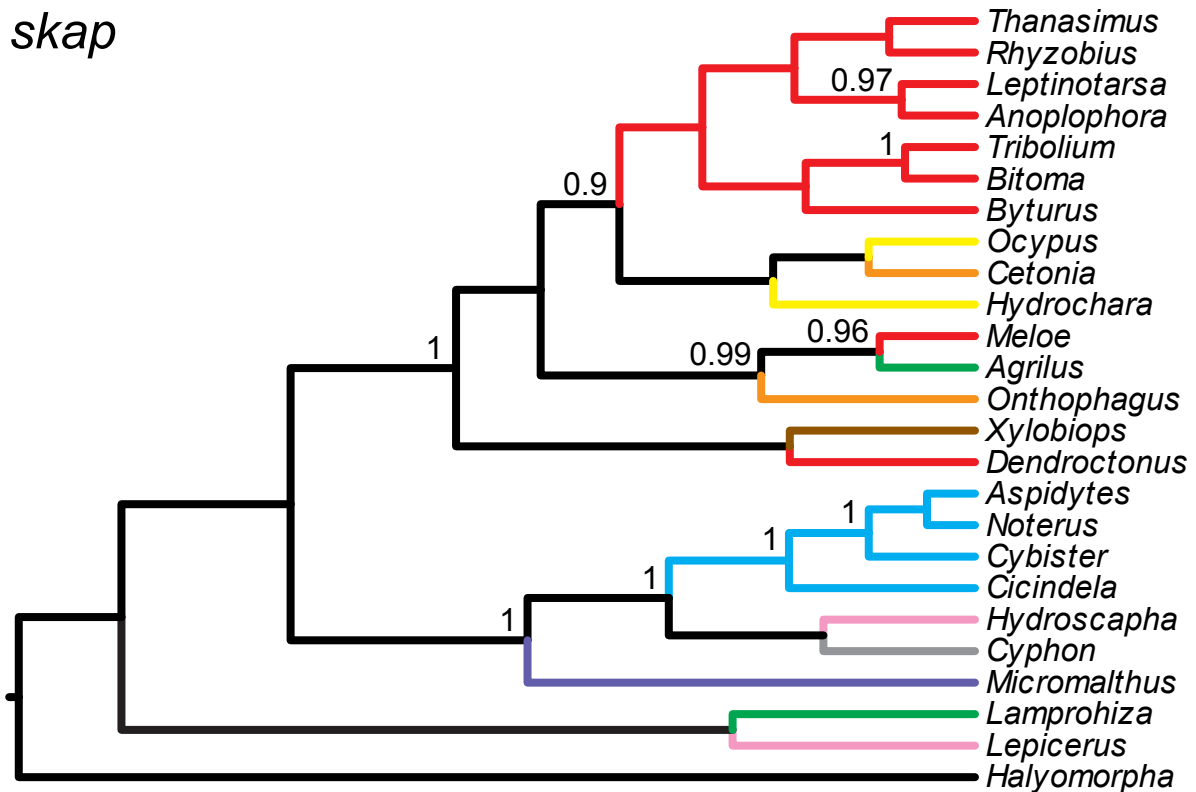
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