

# Supplementary Files

**Table S1.** Amoebozoa transcriptomes data sources.

Clade	Species	Data Source	Sequences	File Size (MB)	
Archamoeba	<i>Mastigamoeba balamuthi</i>	GB EST	19594	9.3	
	<i>Acanthamoeba healyi</i>	GB EST	377	0.09	
	<i>Gocevia fonbrunei</i>	Tekle et al. 2016	18549	5.5	
	<i>Stereomyxa ramosa</i>	Moore	19164	21.1	
	<i>Mayorella sp.</i>	MMETSP0417	10126	16.1	
	<i>Neoparamoeba aestuarina</i>	MMETSP0161	18549	16.0	
	<i>Paramoeba atlantica</i>	MMETSP0151-2	15432	15.4	
	<i>Vexillifera bacillipedes</i>	GB BioProj. PRJNA222686	1753	0.613	
	<i>Vexillifera sp.</i>	MMETSP0173	9564	10.3	
	Eudiscosea	<i>Vannella sp. DIVA3 517612</i>	MMETSP0168	15217	23.1
<i>Vannella robusta</i>		MMETSP0166	14497	17.6	
<i>Vannella simplex</i>		GB BioProj.	3073	0.969	
<i>Clydonella sp. ATCC 50884</i>		Tekle et al. 2016	5386	6.7	
<i>Unda schaefferi</i>		Tekle et al. 2016	3877	4.2	
<i>Stenamoeba stenopodia</i>		GB BioProj. PRJNA222684	12028	4.2	
<i>Vermistella antarctica</i>		Tekle et al. 2016	5518	10.1	
<i>Thecamoeba quadrilineata</i>		Tekle et al. 2016	7298	10.9	
Himatismenida		<i>Cochilopodium minutoidum</i>	GB BioProj. PRJNA222681	4013	1.4
		<i>Ovalopodium desertum</i>	GB Bioproj. PRJNA222682	10359	3.5
	<i>Parvamoeba monura</i>	Tekle et al. 2016	5559	6.9	
Mycetozoa	<i>Actyostelium subglobosum</i>	GenBank EST	60412	43.2	
	<i>Hyperamoeba dachnaya</i>	GenBank EST	2745	0.912	
	<i>Physarum polycephalum</i>	GenBank EST	25120	16.1	
Tubulinea	<i>Hartmanella vermiformis</i>	GenBank EST	1334	0.722	
	<i>Nolandella abertawensis</i>	GB BioProj. PRJNA222683	1843	1.2	
Variosea	<i>Flamella fluviatilis</i>	GB BioProj. PRJNA222680	11096	3.9	
	<i>Filamoeba nolandi</i>	MMETSP0413	19244	25.8	
	<i>Filamoeba sinensis</i>	GB Bioproj. PRJNA222679	19020	6.6	
<i>Incertae sedis</i> (ATCC PRA-29 + Sapocribum)	<i>Pessonella sp. PRA-29</i>	MMETSP0420	15314	18.7	
	<i>Pessonella sp.</i>	MMETSP0420	13865	18.5	
<i>Incertae sedis</i> (Trichosida)	<i>Trichosphaerium sp. ATCC 40318</i>	MMETSP0405	2709	3.6	

**Table S2.** Meiosis Genes Inventoried in Amoebozoa Transcriptomes.

Gene	<i>Mastigamoeba balamuthi</i>	<i>Acanthamoeba healyi</i>	<i>Gocevia fonbrunei</i>	<i>Stereomyxa ramosa</i>	<i>Mayorella sp.</i>	<i>Neoparamoeba aestuarina</i>	<i>Paramoeba atlantica</i>	<i>Vexillifera bacillipedes</i>	<i>Vexillifera sp.</i>	<i>Vannella sp.</i>	<i>Vannella robusta</i>	<i>Vannella simplex</i>	<i>Clydonella sp. ATCC 50004</i>	<i>Unda schaefferi</i>	<i>Stenamoeba stenopodia</i>	<i>Vermistella Antarctica</i>	<i>Thecamoeba quadrilineata</i>	<i>Cochilopodium minutoidum</i>	<i>Ovalopodium desertum</i>	<i>Parvamoeba monura</i>	<i>Actyostelium subglobosum</i>	<i>Hyperamoeba dachnaya</i>	<i>Physarum polycephalum</i>	<i>Hartmannella vermiformis</i>	<i>Nolandella abertawensis</i>	<i>Flamella fluviatilis</i>	<i>Filamoeba nolandii</i>	<i>Filamoeba sinensis</i>	<i>Pessonella sp. PRA-29</i>	<i>Pessonella sp.</i>	<i>Trichosphaerium sp. ATCC 40210</i>	
<b>Bouquet Formation</b>																																
SAD1			+	+		+			+	+					+				+										+	+	+	
<b>Crossover Regulation</b>																																
DMC1				+			+																+									
HOP1																							+									
HOP2				+		+	+		+	+	+						+										+		+			
MER3							+																					+				
MND1				+	+		+	+	+	+	+					+				+							+		+	+		
MSH4				+					+								+															
MSH5							+																									
RED1																																
ZIP1																																
<b>DNA Damage Sensing/Response</b>																																
MEC1/ATR				+	+	+	+		+	+	+					+	+			+		+	+	+		+	+	+	+	+	+	
MRE11				+	+	+	+		+	+	+		+			+	+			+		+					+					+
RAD17				+		+				+	+																	+				
RAD23				+	+	+	+		+	+	+		+	+		+	+			+	+	+					+		+	+		
RAD24	+	+	+	+	+	+	+	+	+	+	+		+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	
RAD50				+	+	+		+	+	+				+	+	+	+										+		+	+	+	
TEL1/ATM				+	+	+	+		+	+	+					+					+		+	+		+	+	+	+	+	+	
<b>Double-Strand Break Formation</b>																																

<b>SPO11</b>							+				+													
<b>Double-Strand Break Repair (Nonhomologous End-Joining)</b>																								
KU70	+		+	+	+	+		+	+	+		+				+		+	+					
KU80			+	+	+	+		+	+	+						+		+	+	+				
LIG4/DNL1			+	+	+	+		+	+	+		+				+		+	+	+				
XRCC4/LIF1			+	+																				
<b>Double-Strand Break Repair and Meiotic Divisions</b>																								
<b>REC8</b>																								
<b>Recombinational Repair</b>																								
BRCA2																				+				
DNA2			+	+	+	+		+	+	+						+	+		+	+	+	+		
EXO1			+	+	+	+		+				+	+			+				+				
FEN1	+		+	+	+	+		+	+	+		+	+			+	+		+	+	+			
MLH1			+	+				+	+	+		+								+				
MLH3			+	+				+	+			+								+				
MMS4/EME1(s)																								
MPH1/FANCM(a,m)			+		+			+	+							+				+				
MSH2	+		+	+		+		+	+			+	+			+	+			+				
MSH3	+		+	+	+	+		+	+															
MSH6			+	+	+	+		+	+			+	+			+	+			+				
MUS81			+	+	+	+		+	+			+				+				+				
PMS1			+		+	+		+	+	+		+				+			+	+				
RAD51			+	+	+	+	+	+	+	+		+	+			+			+	+	+	+	+	
RAD52			+					+	+	+		+				+				+			+	
RAD54	+		+	+	+	+	+	+	+	+		+				+	+	+		+	+	+	+	
RTEL1			+	+	+	+		+	+	+		+	+			+	+			+		+	+	
SGS1			+	+	+	+	+	+	+	+		+				+	+		+	+	+	+	+	
SLX1									+			+	+											
SMC5			+		+	+		+	+	+	+	+	+			+				+		+	+	+
SMC6			+	+	+	+	+	+		+		+	+	+		+				+	+	+	+	

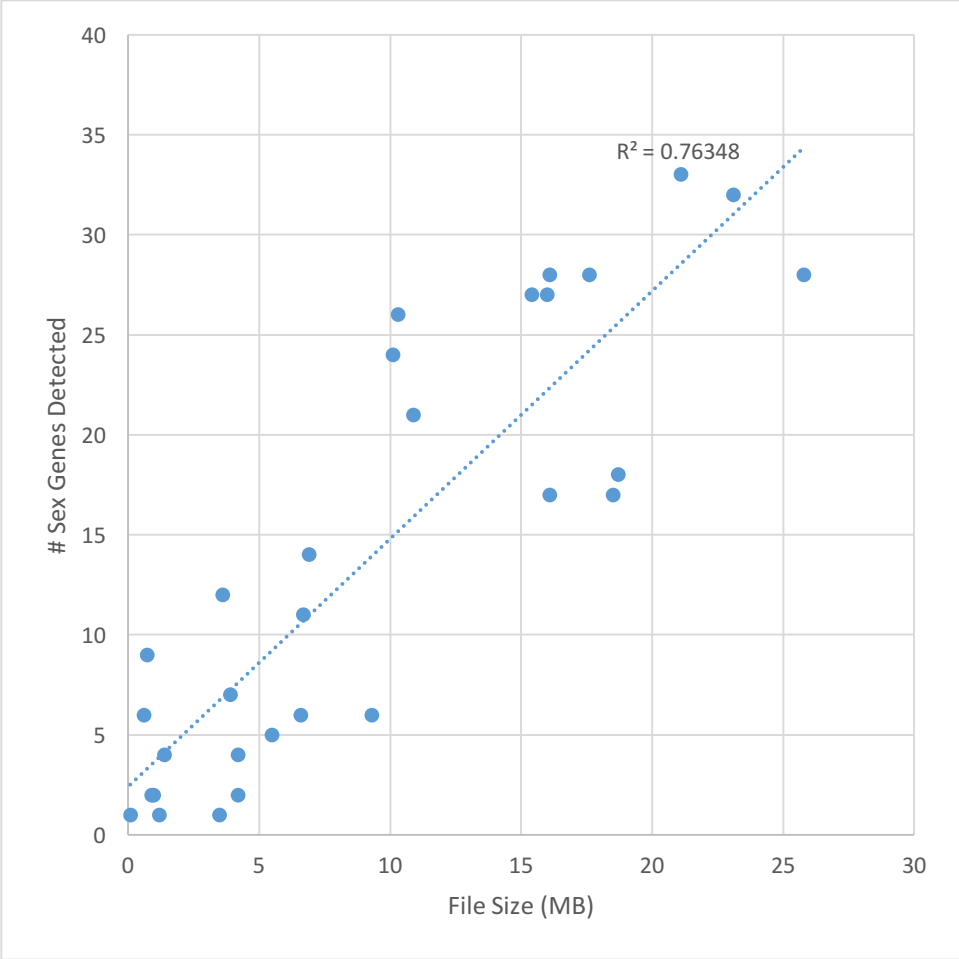


figure S1: Transcriptome data coverage vs. detection of sex genes in Amoebozoa. *Actyostelium subglobosom* transcriptome omitted as an outlier.

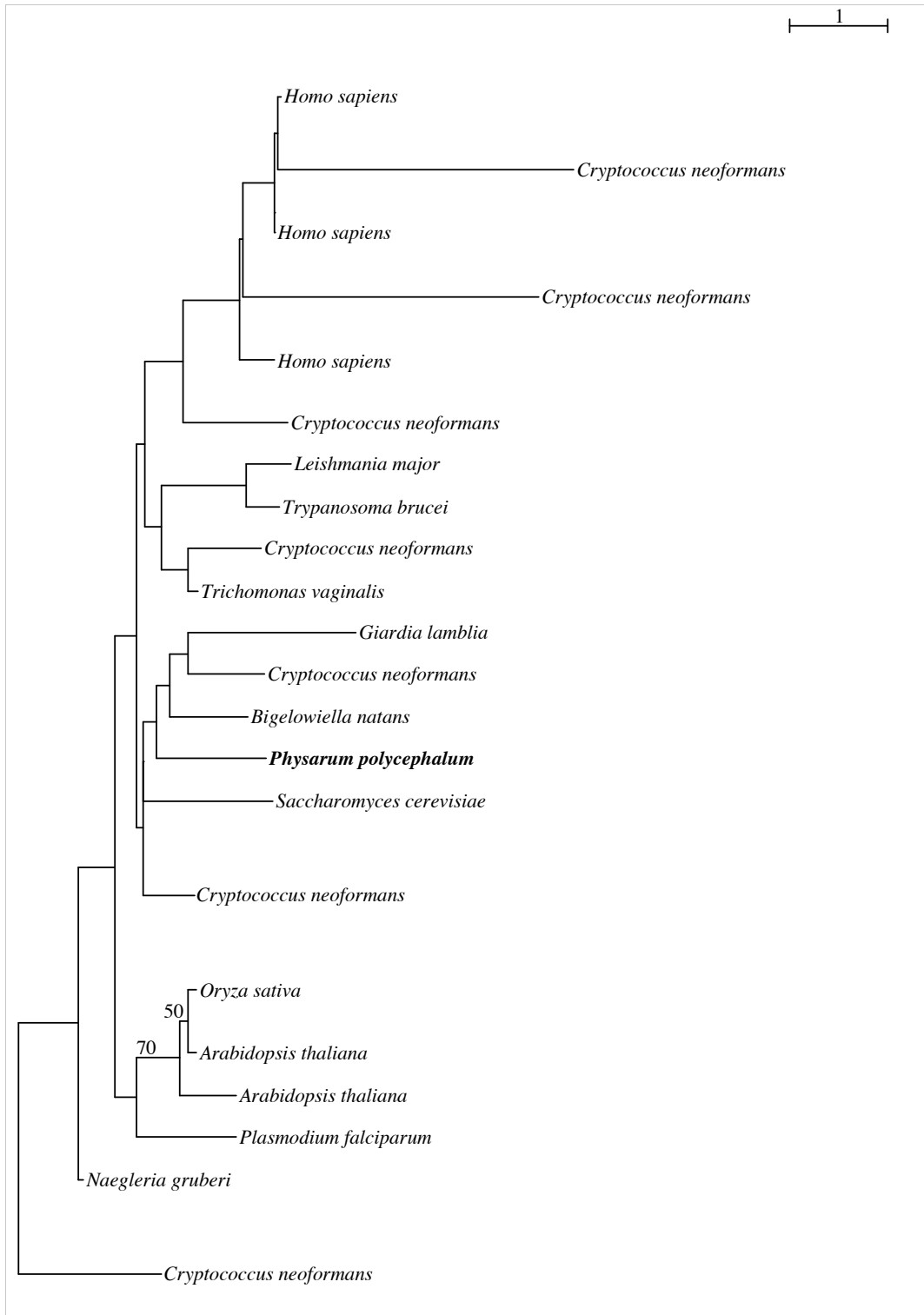
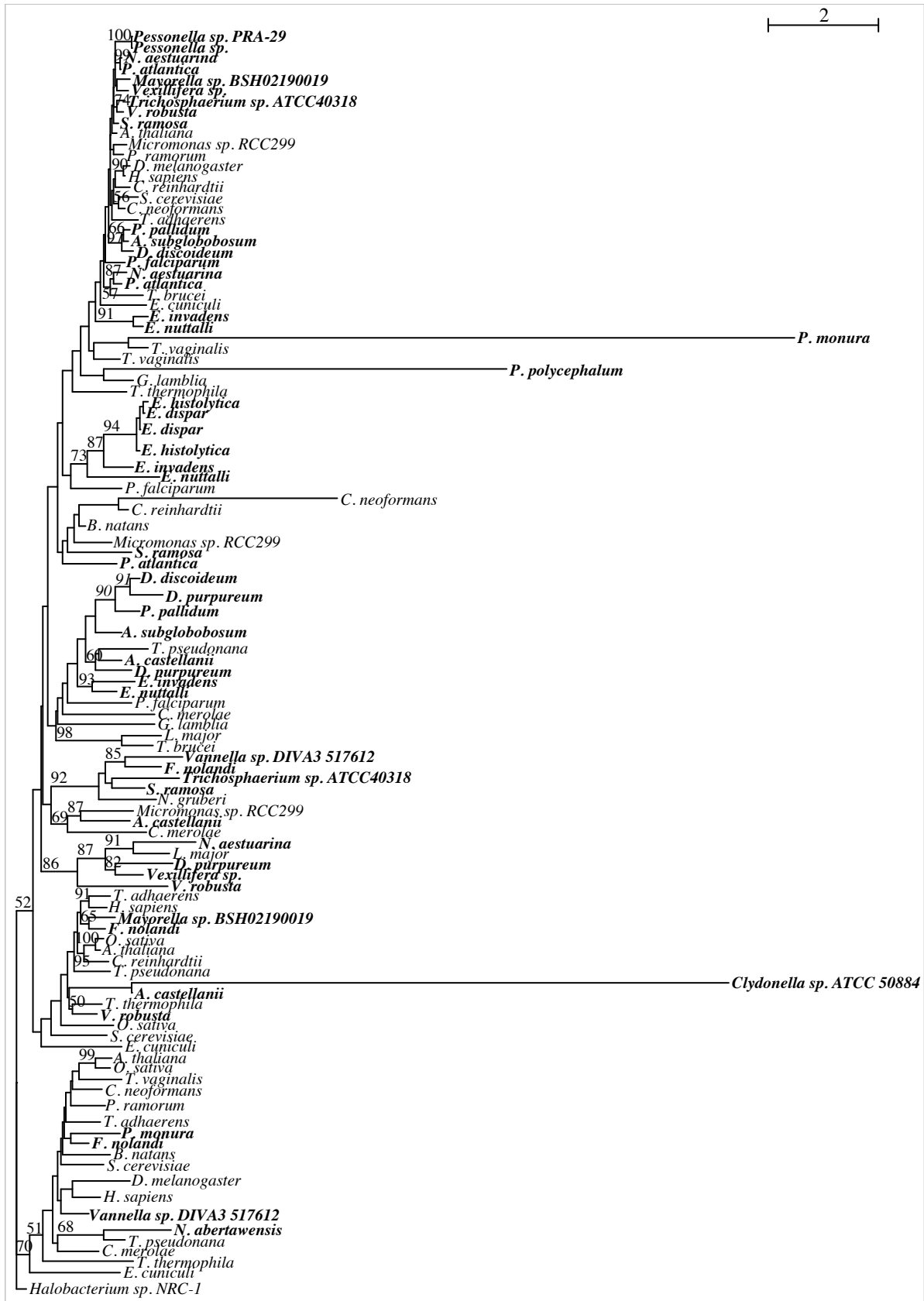


fig. S2: Maximum likelihood trees of meiosis-specific gene *HOPI*. Bootstrap support values  $\geq 50\%$  shown above branches.

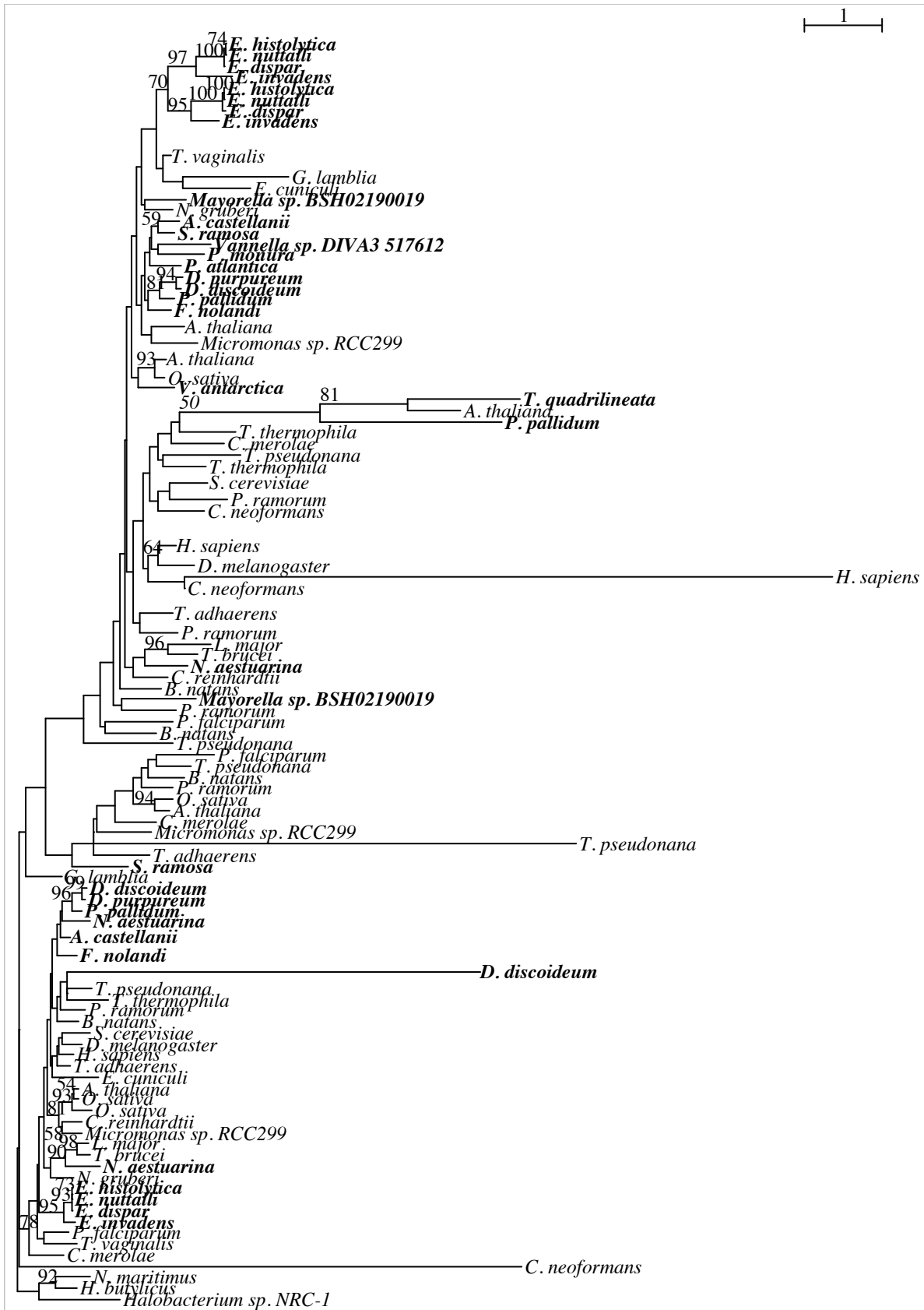


BRCA2

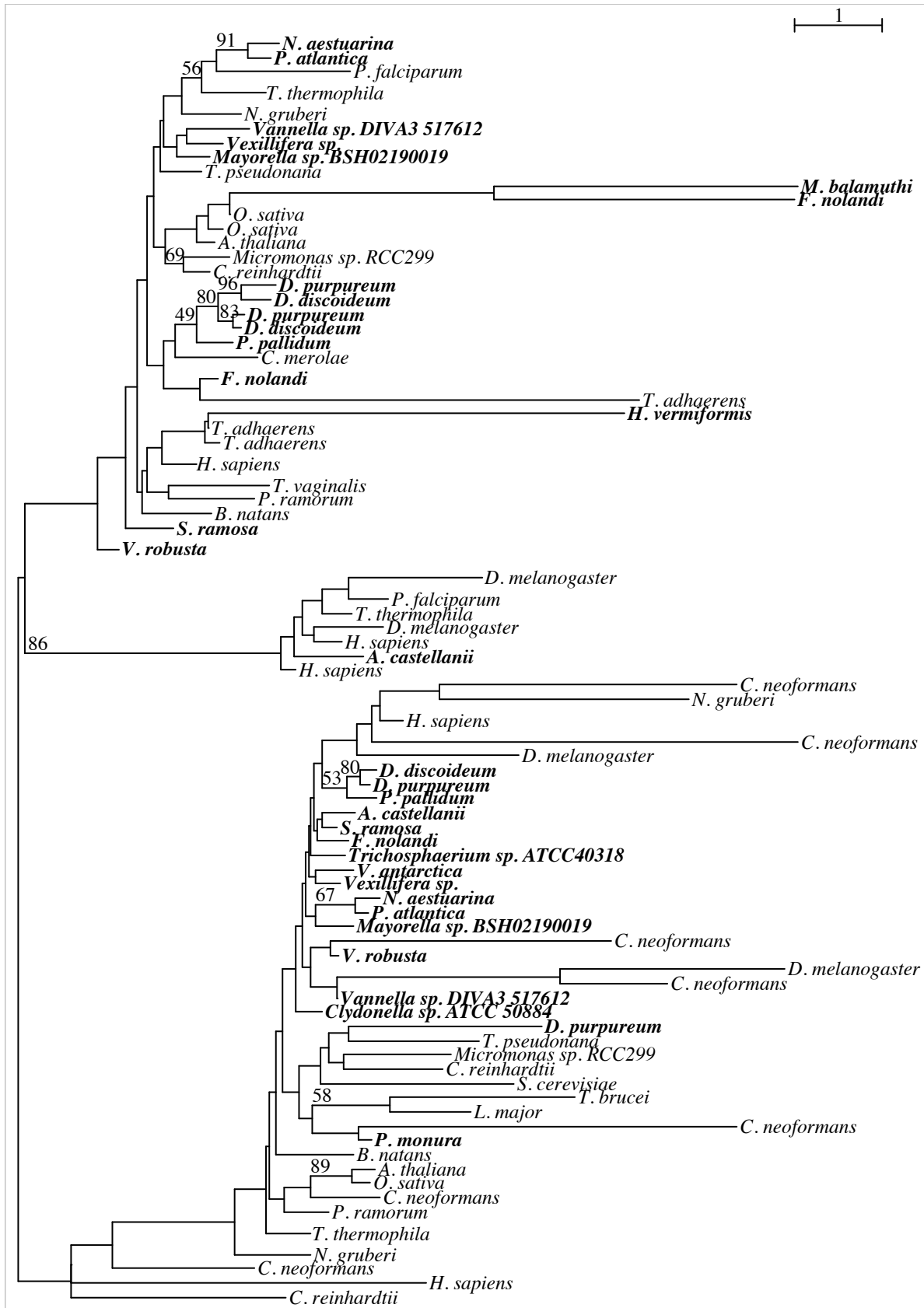


DNA2

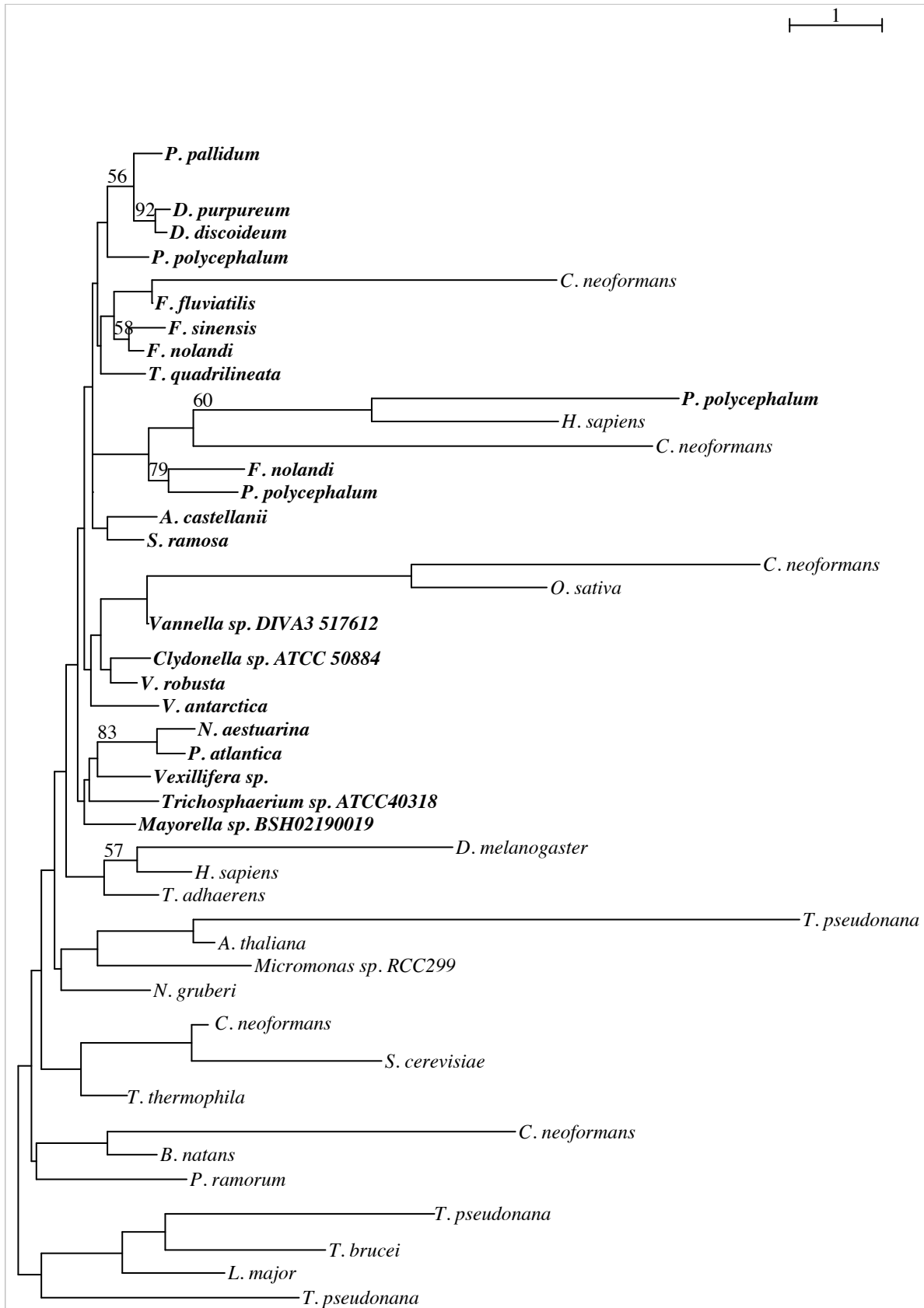




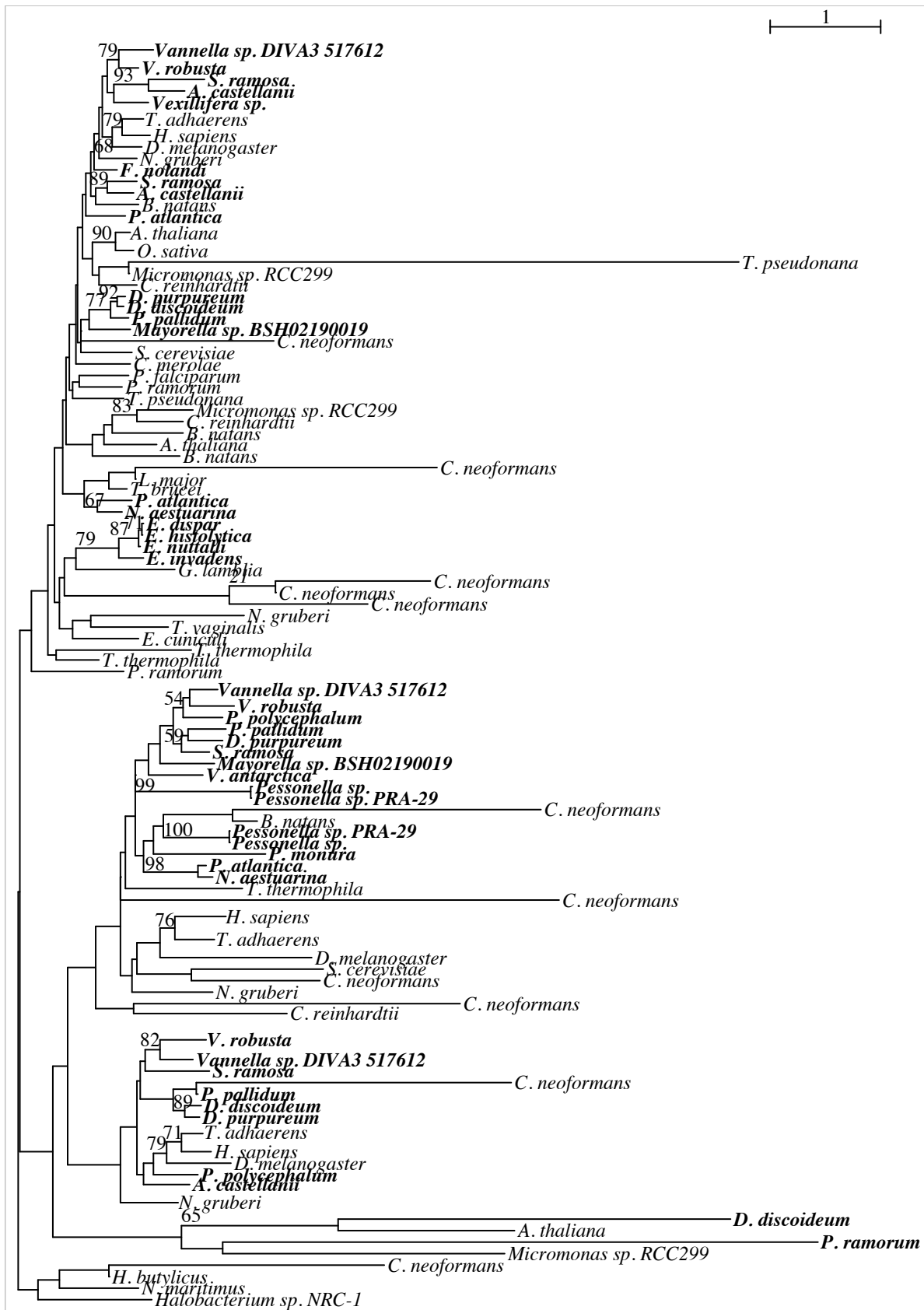
EXO1



KU70



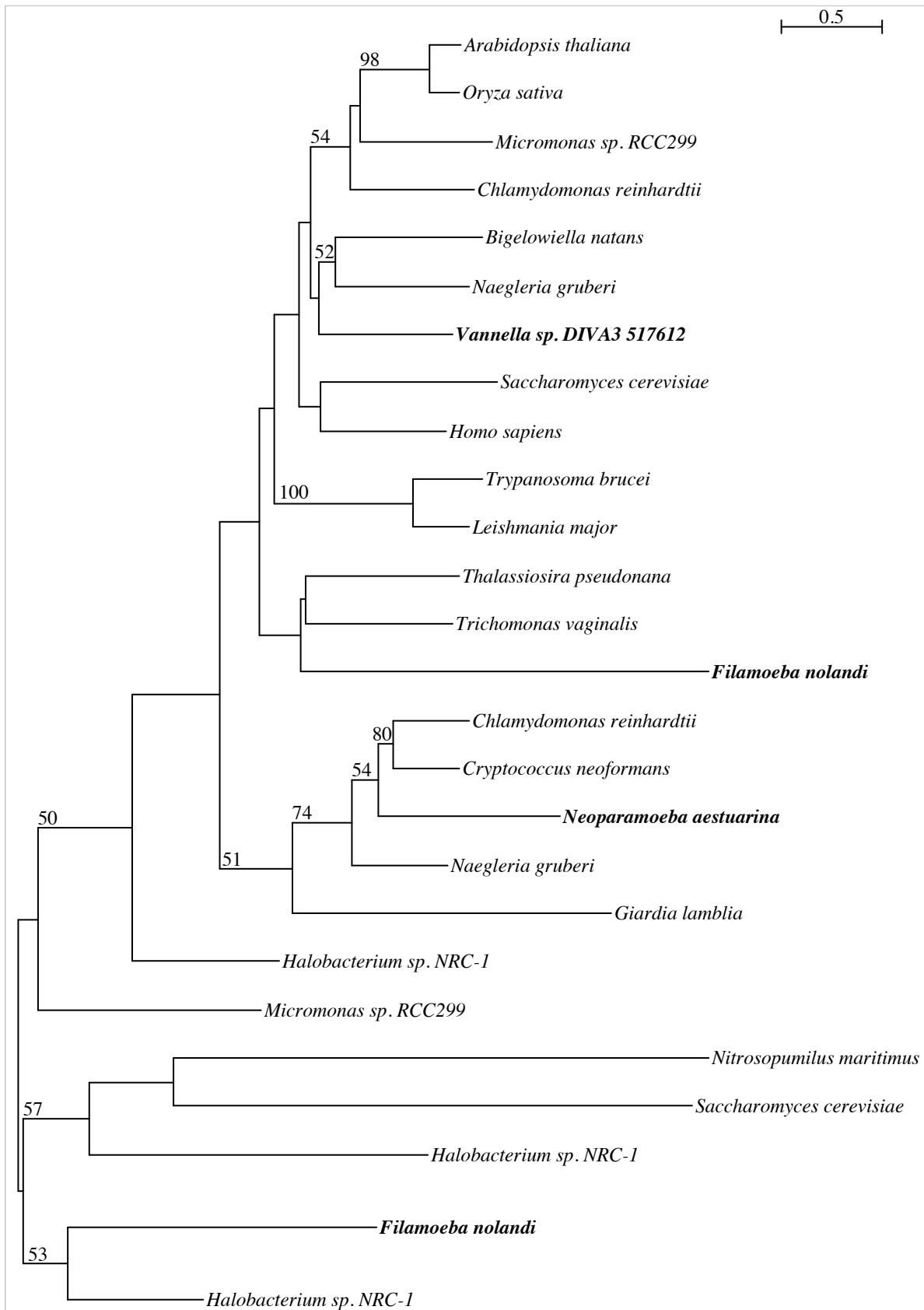
KU80



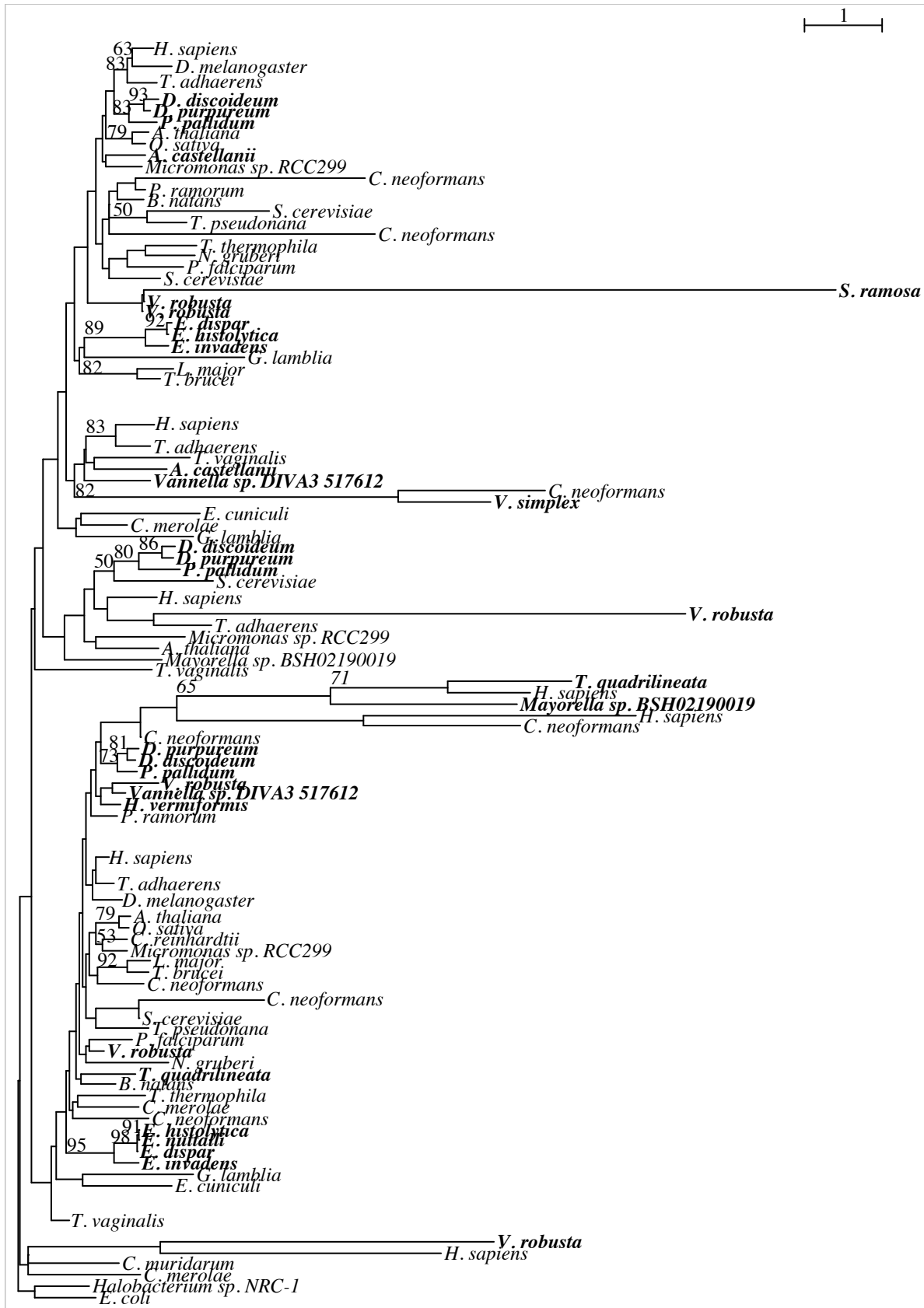
LIG4/DNA1



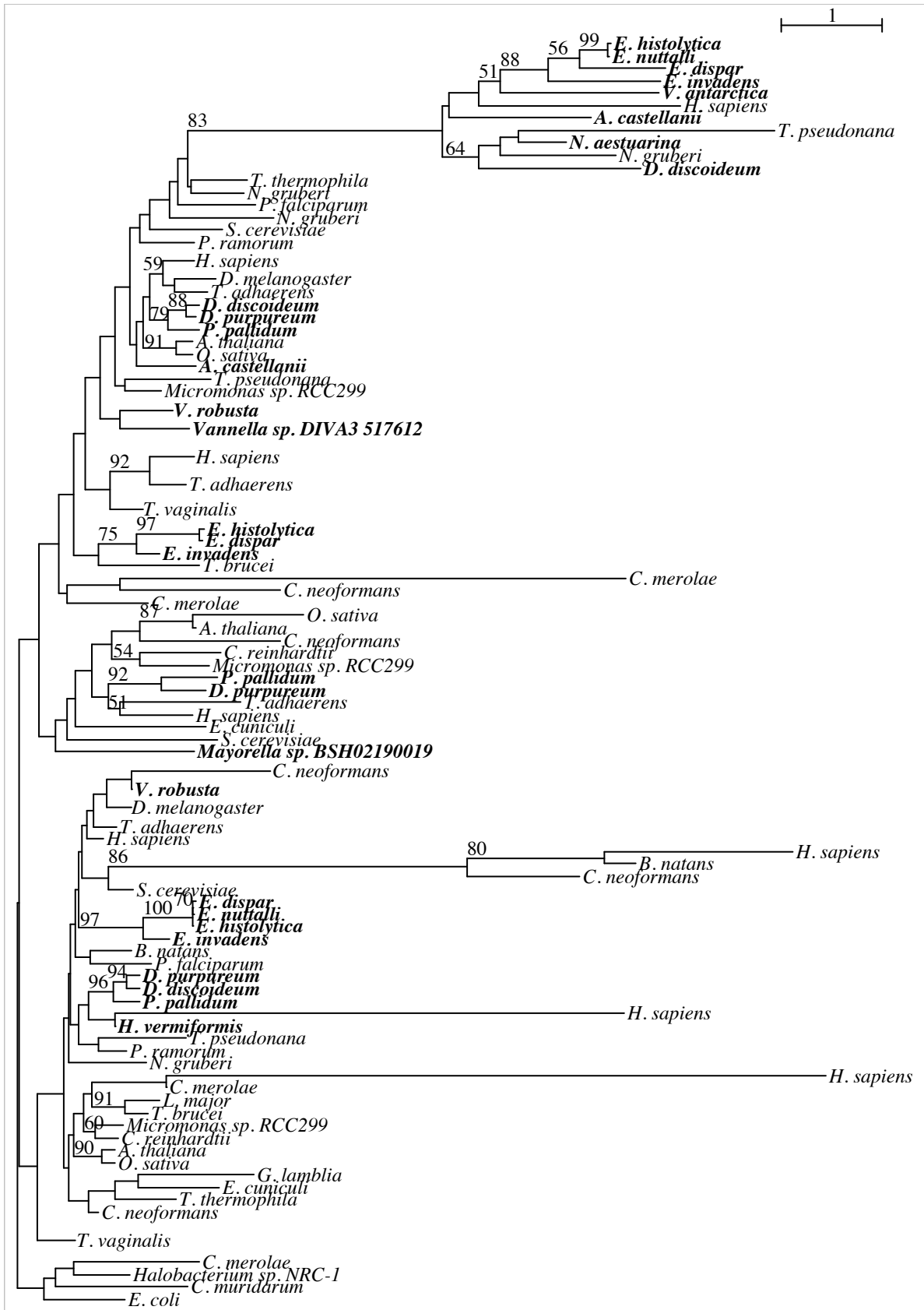
MEC1/ATR



MER3

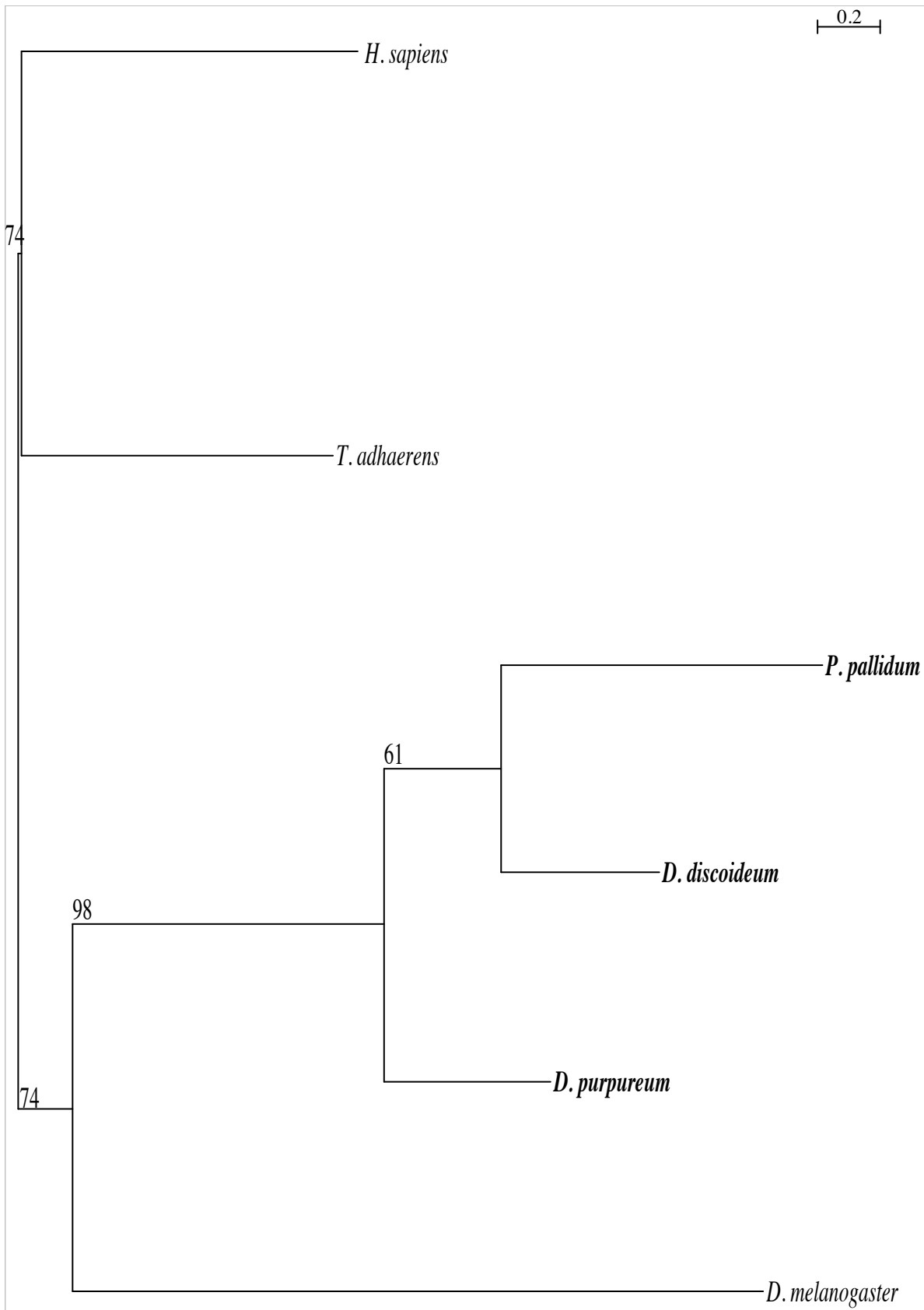


MLH1

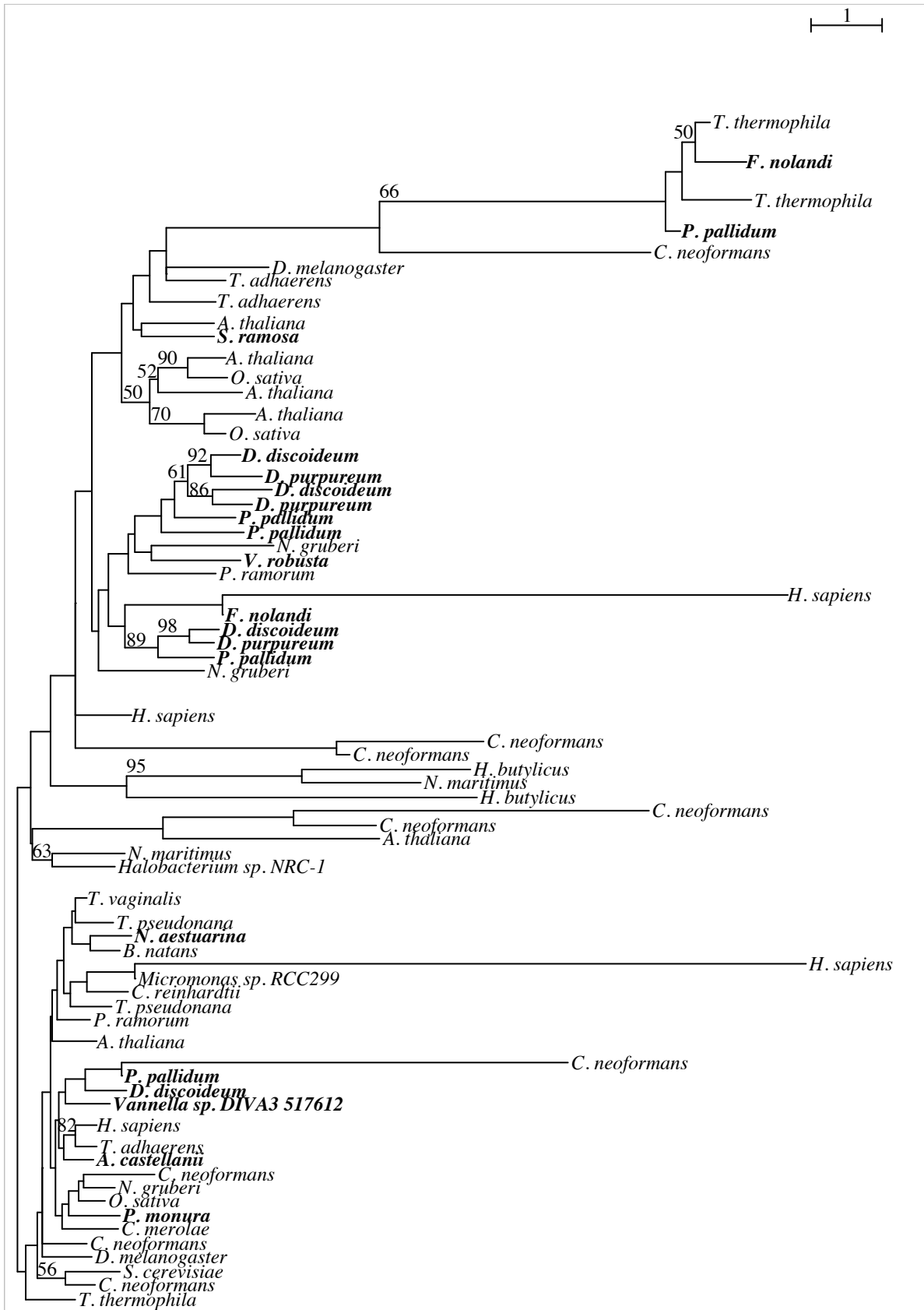


MLH3

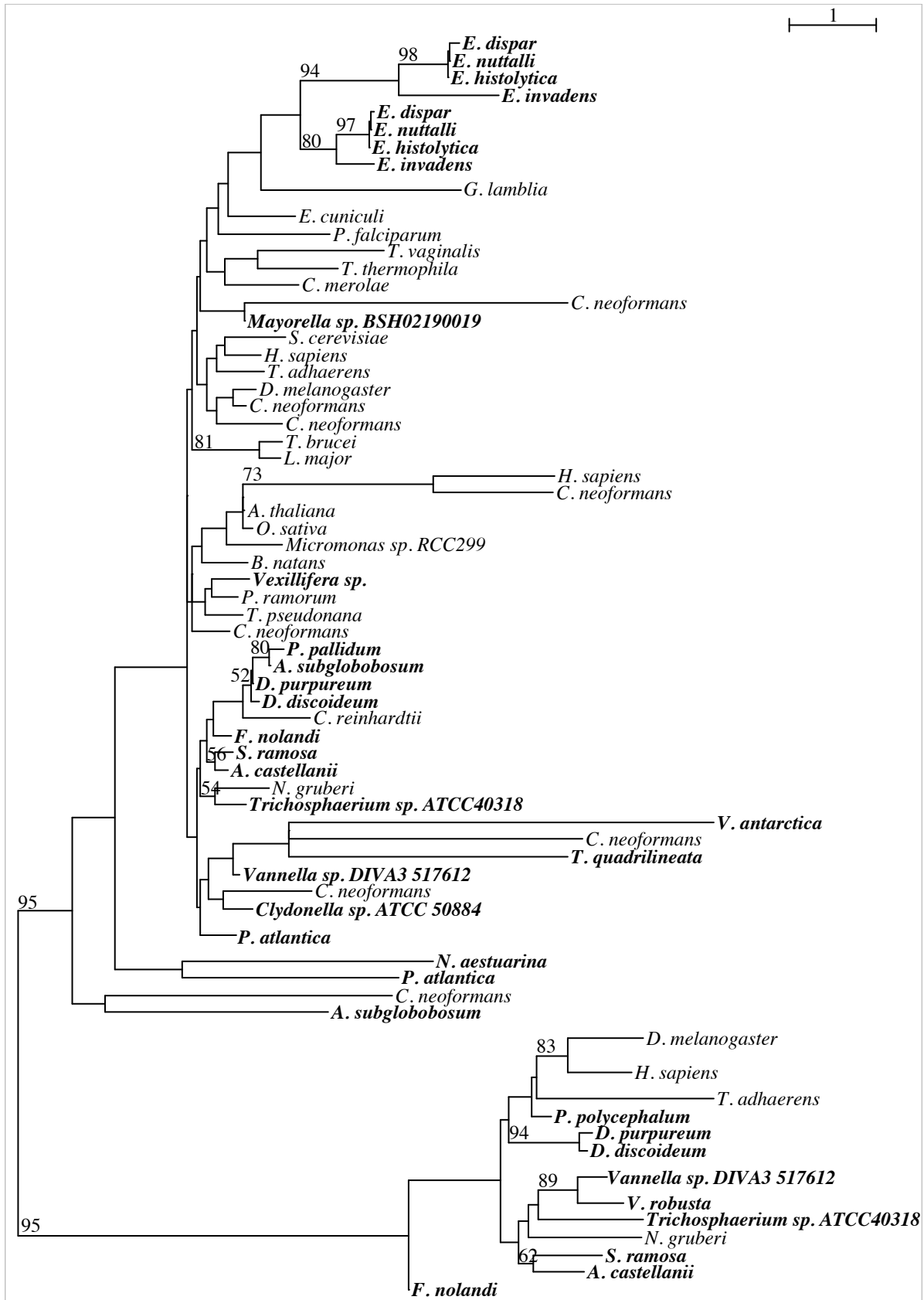




MMS4/EME1



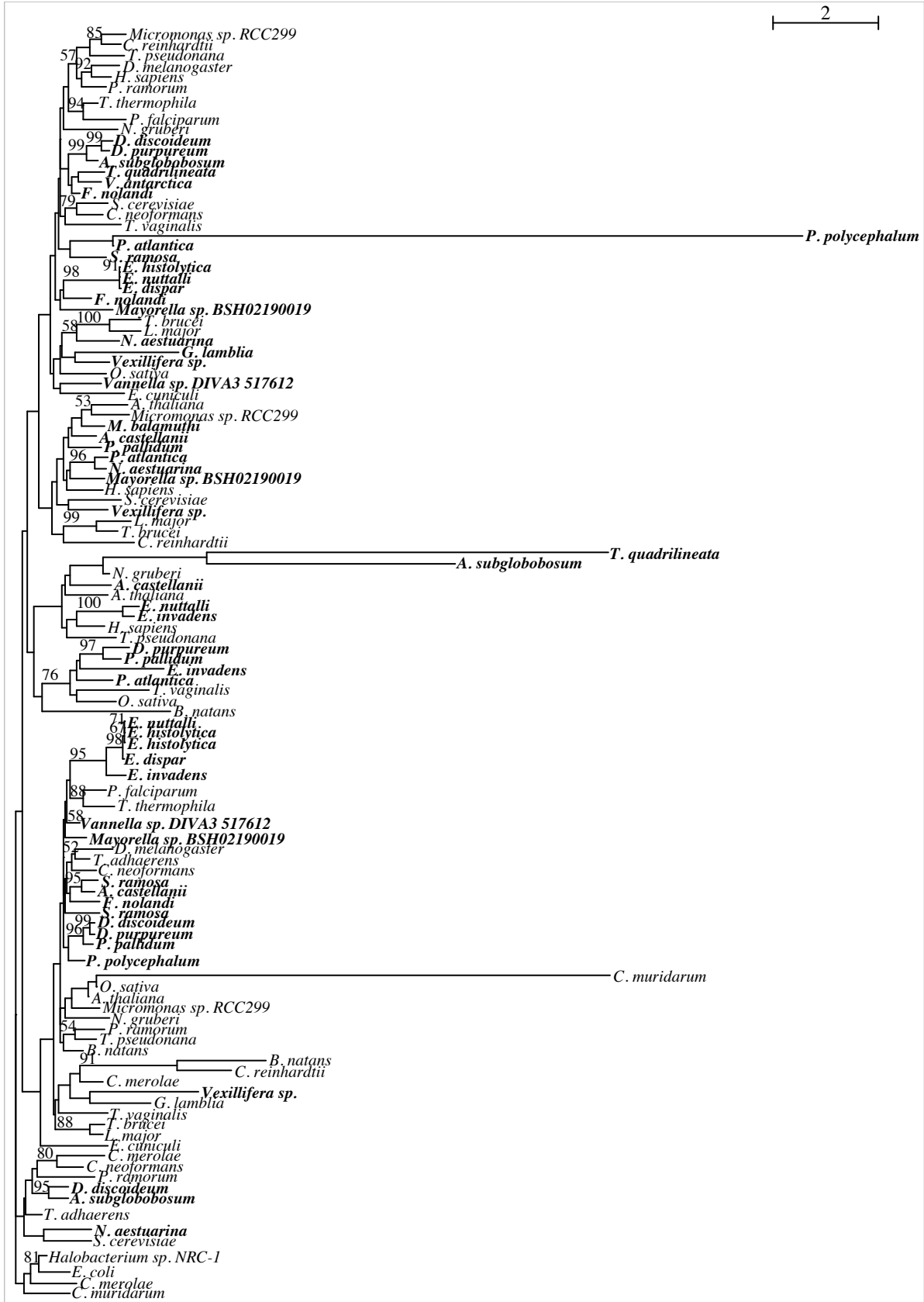
MPH1/FANCM

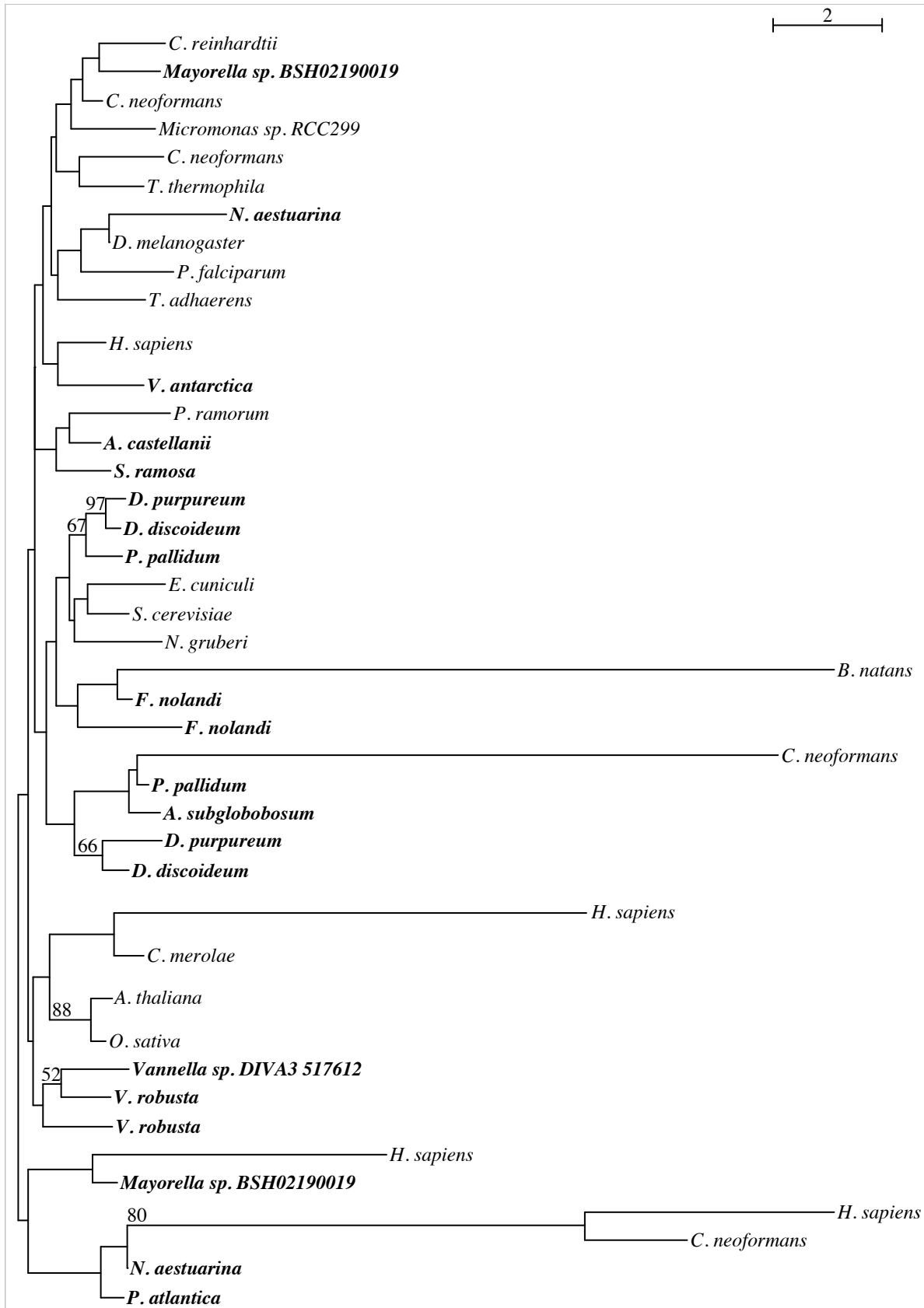


MRE11

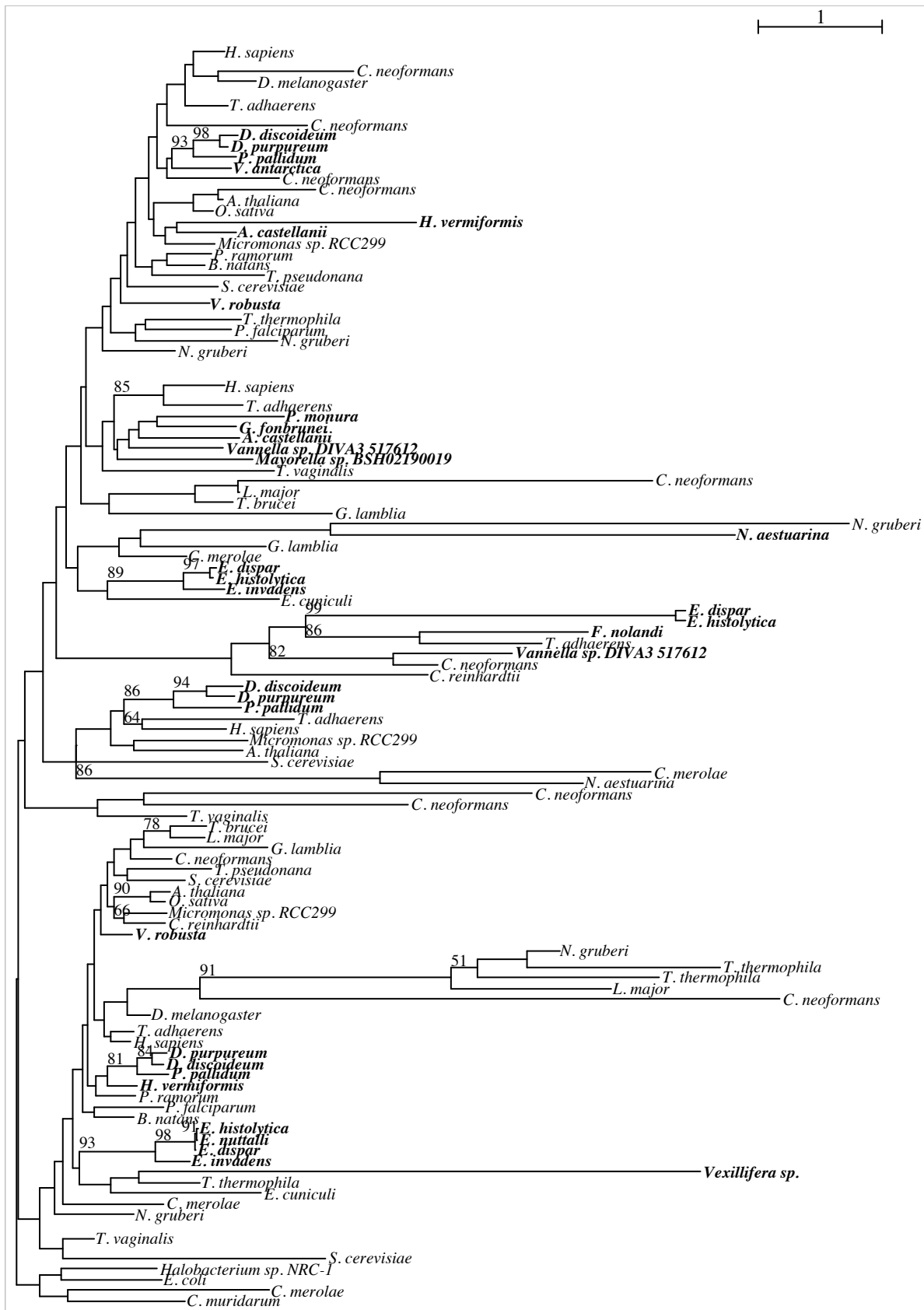


MSH2

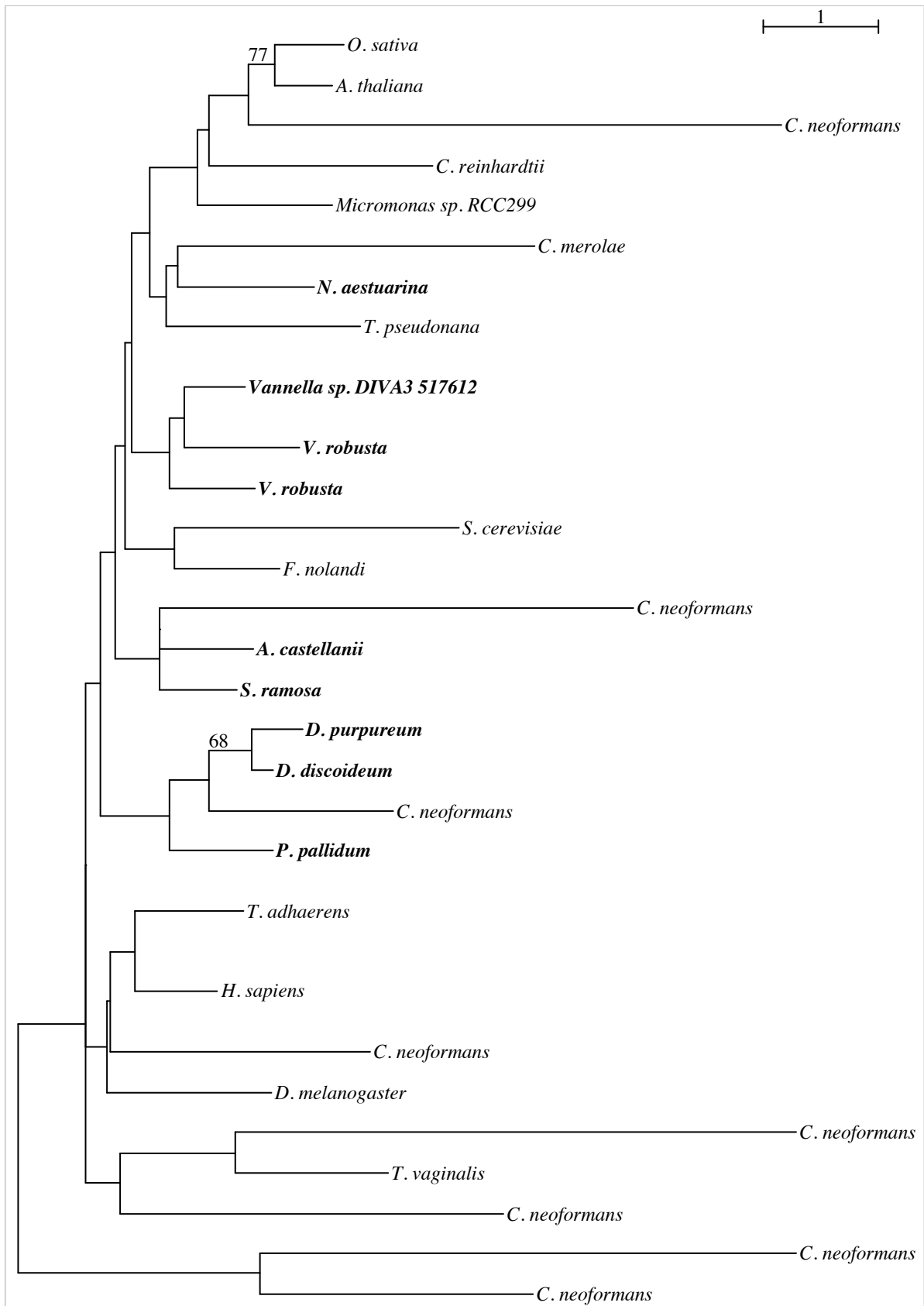




MUS81

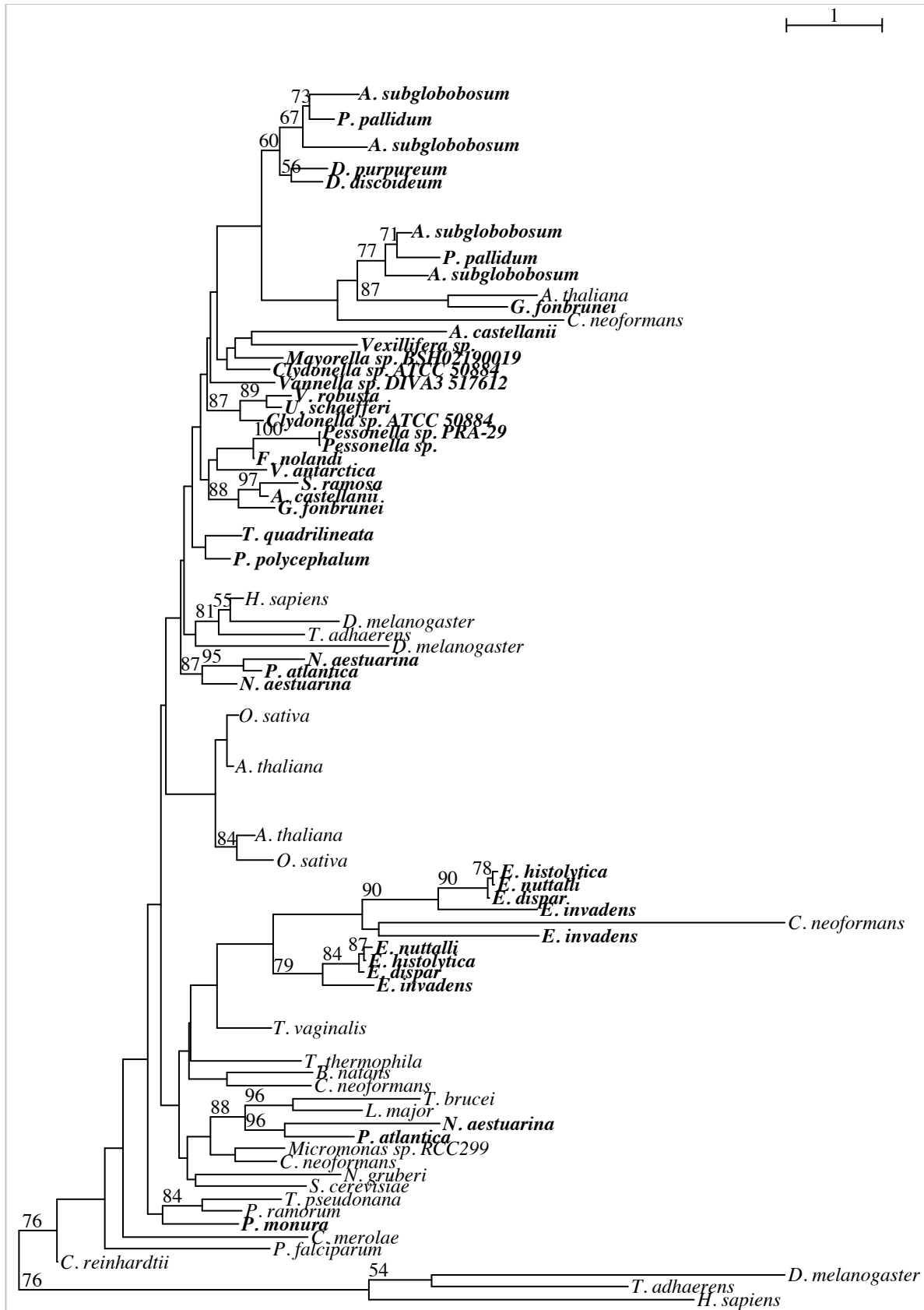


PMS1

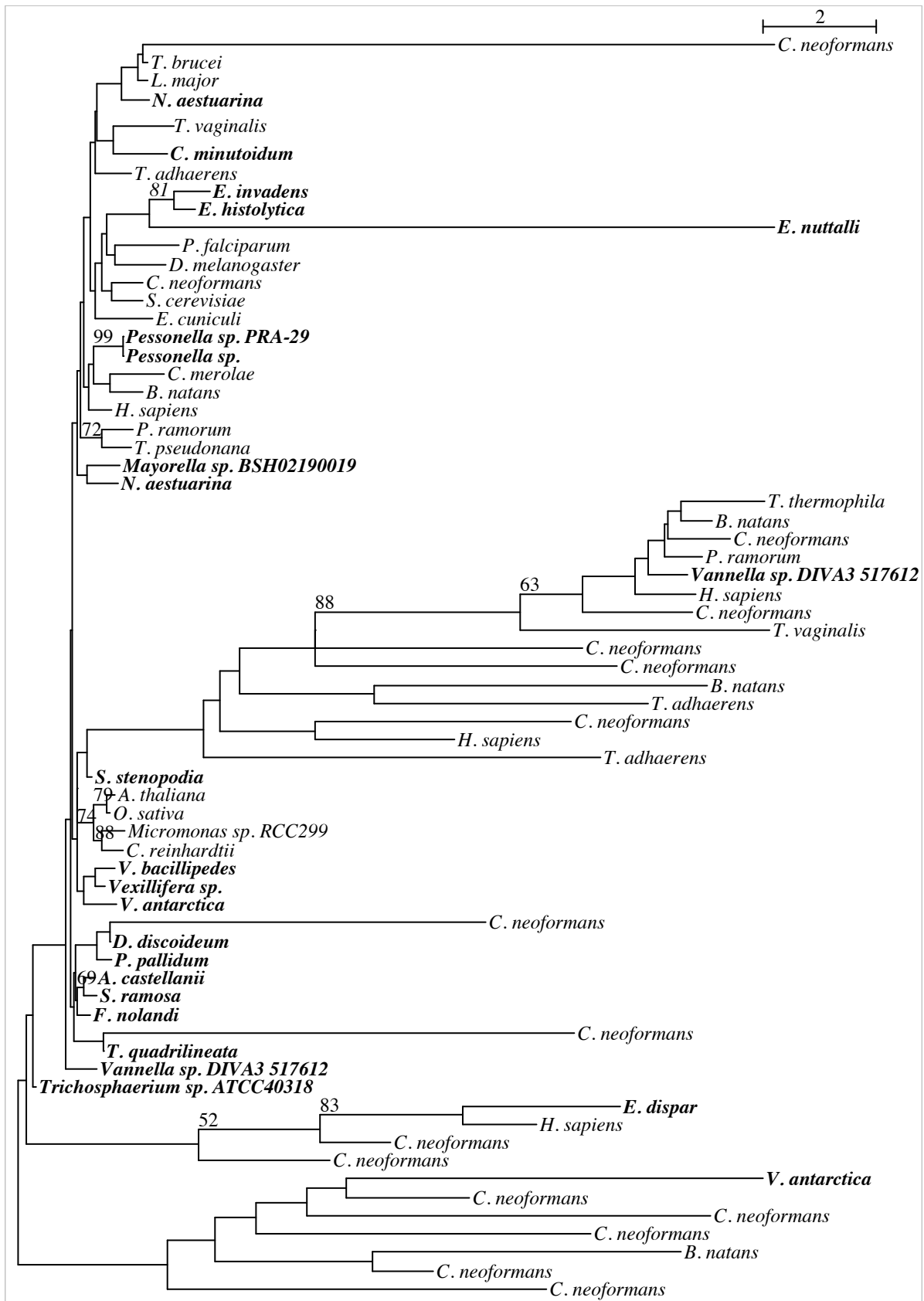


RAD17

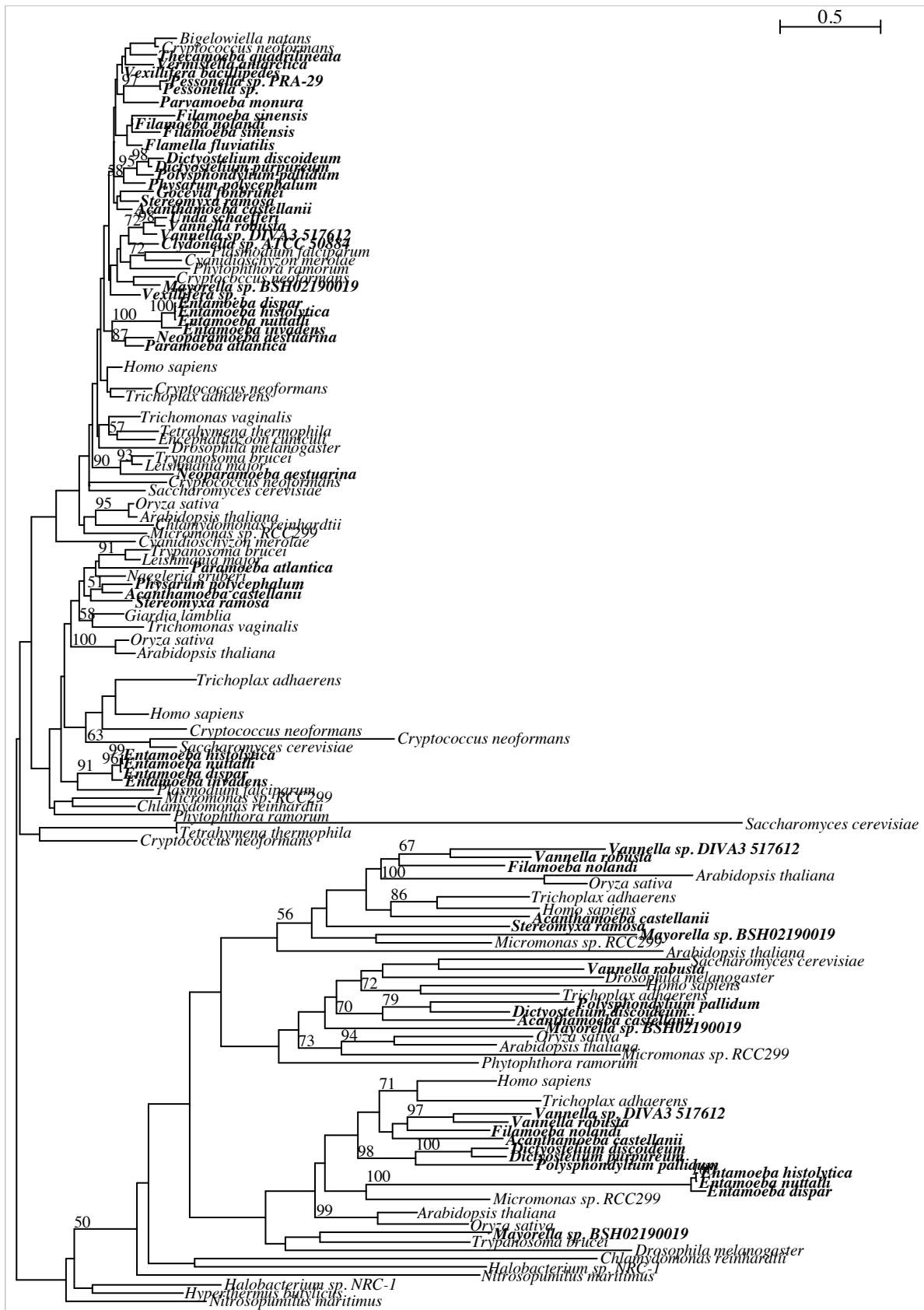




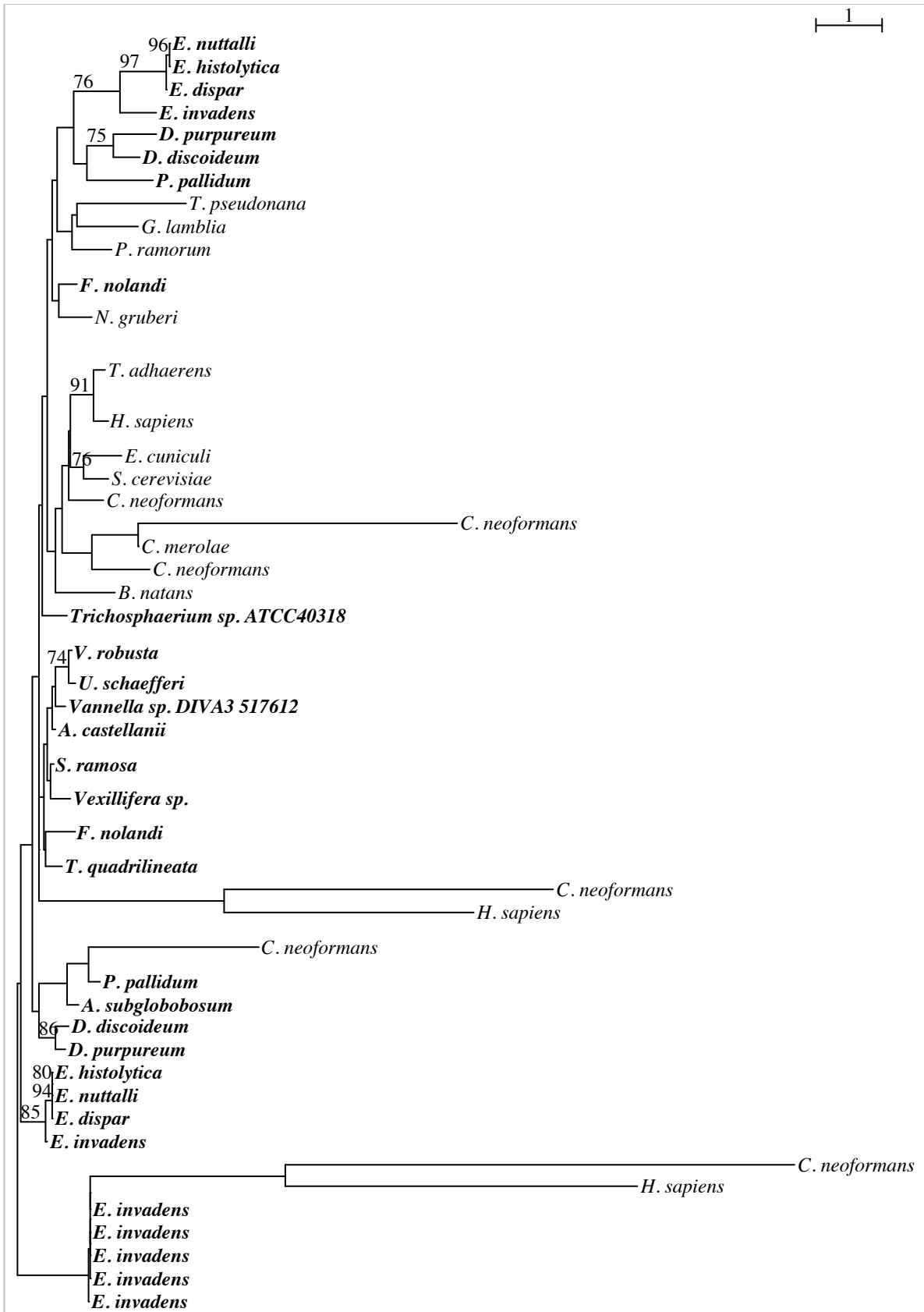
RAD24



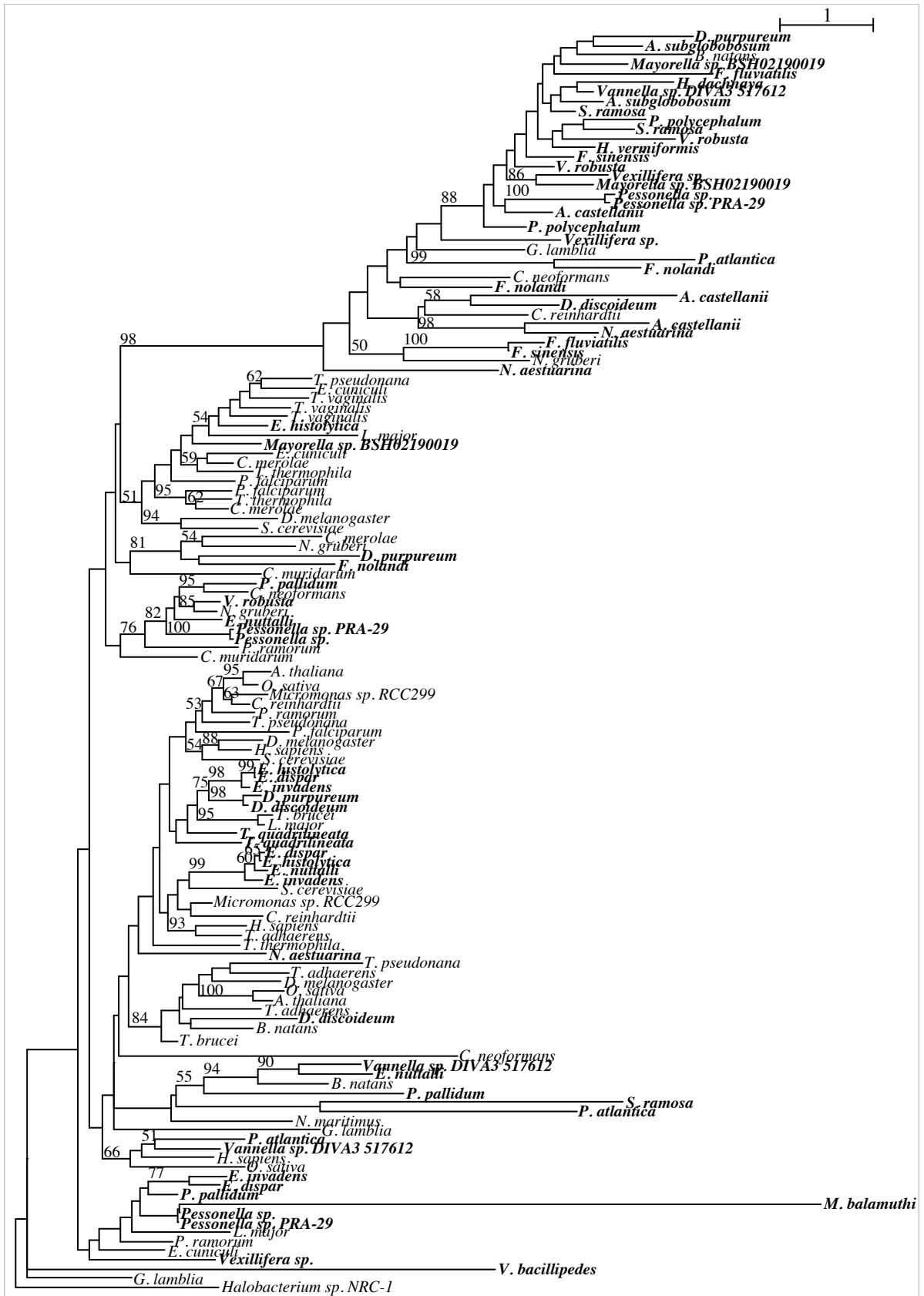
RAD50



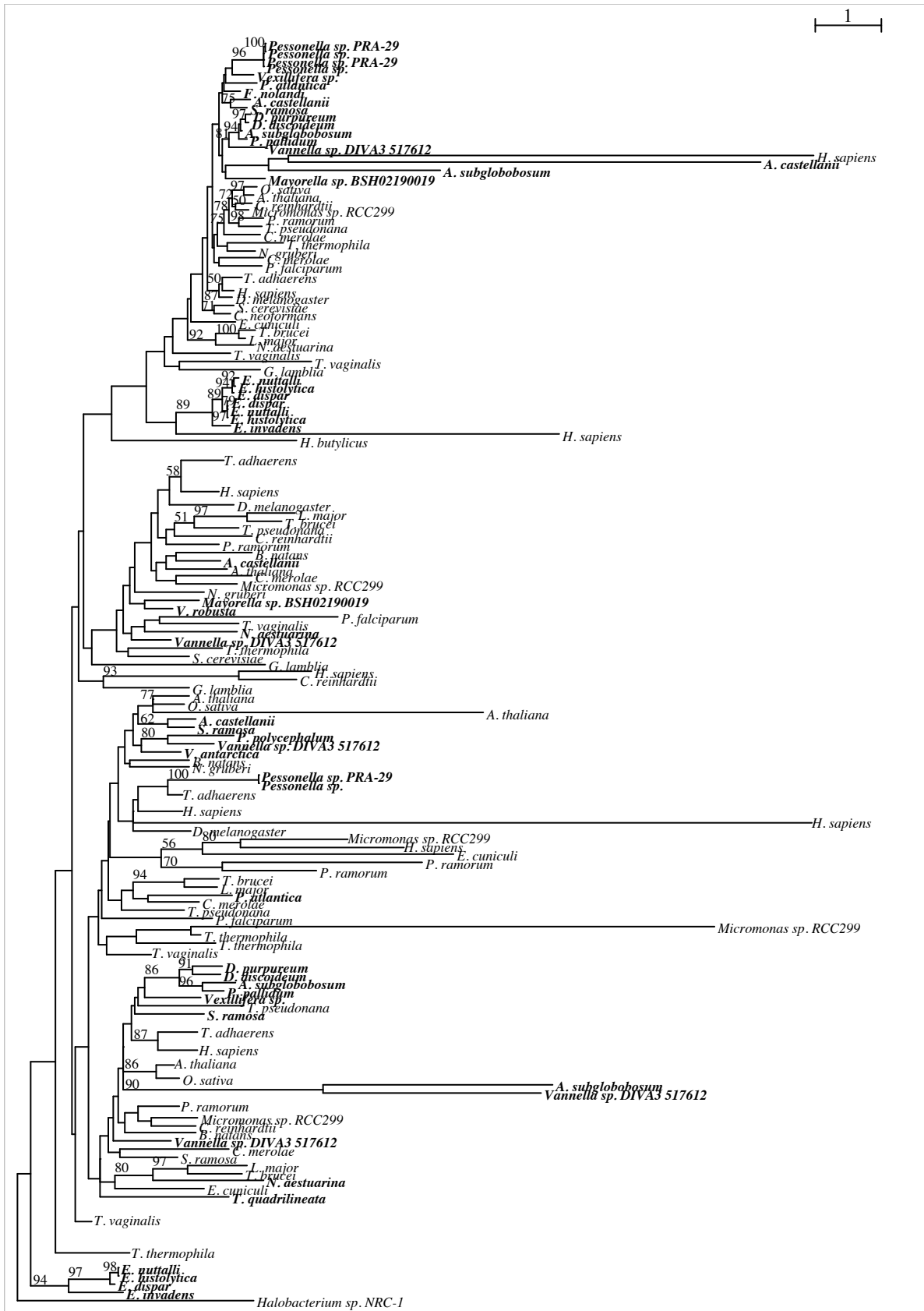
RAD51



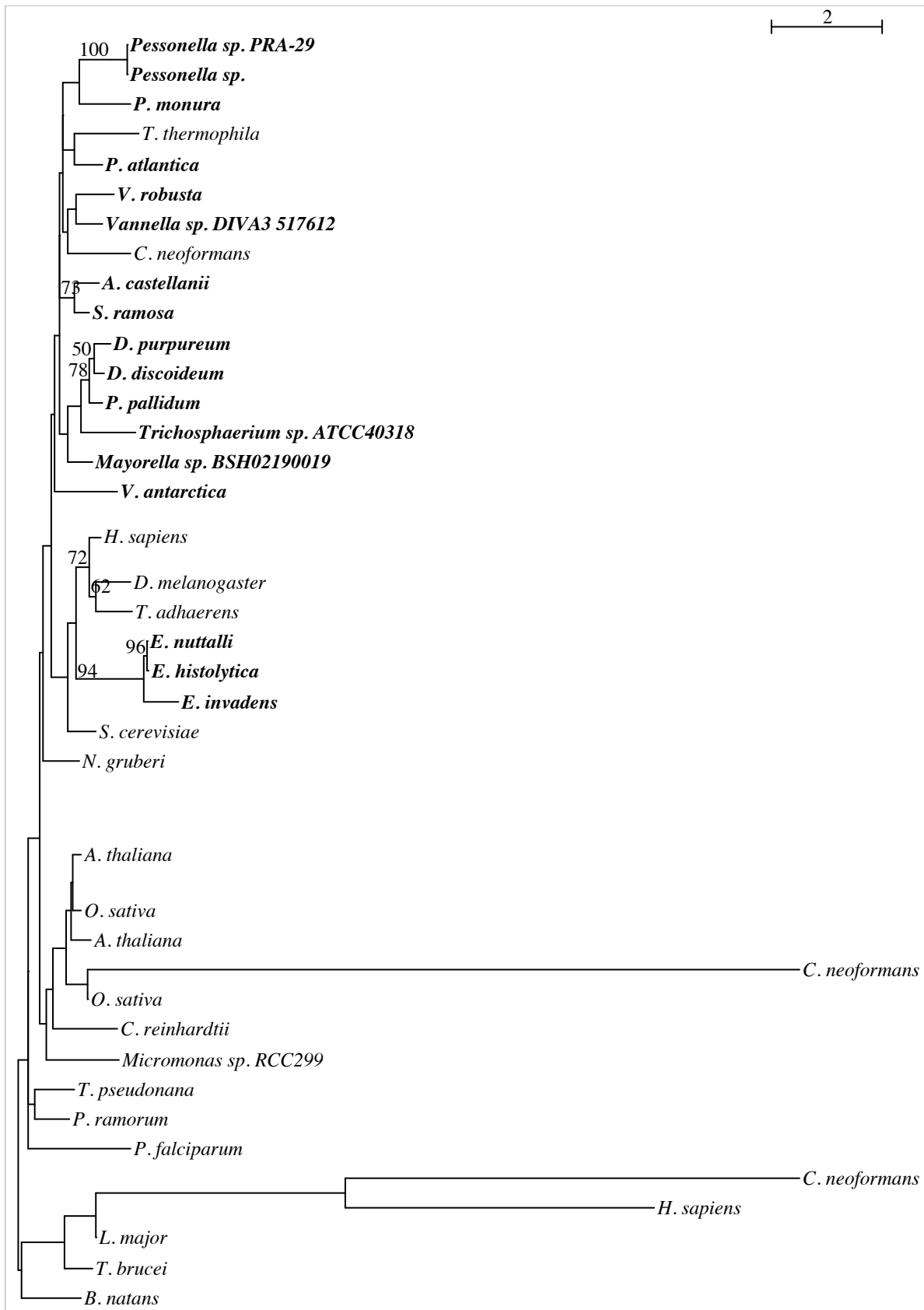
RAD52



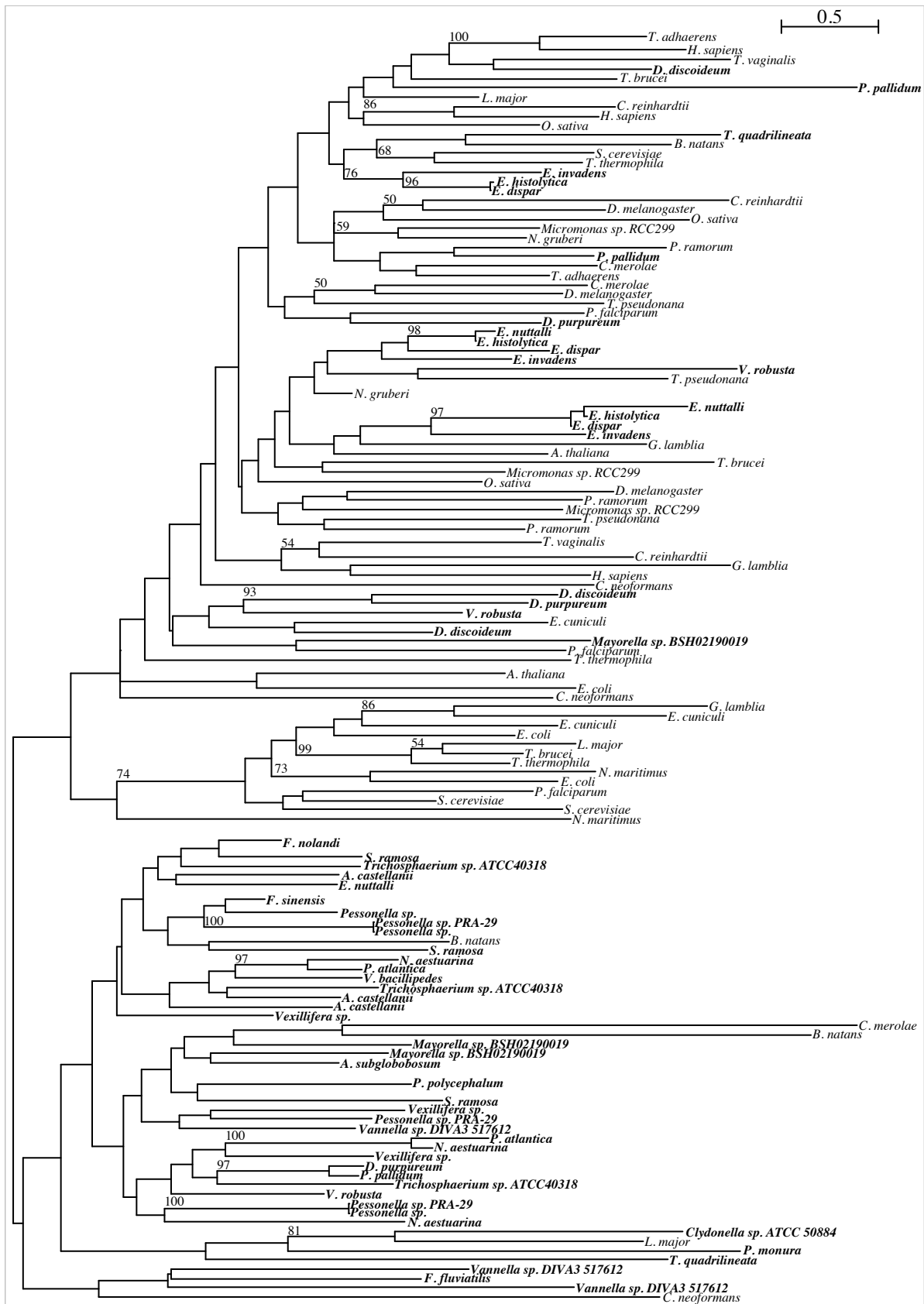
RAD54



RTEL1

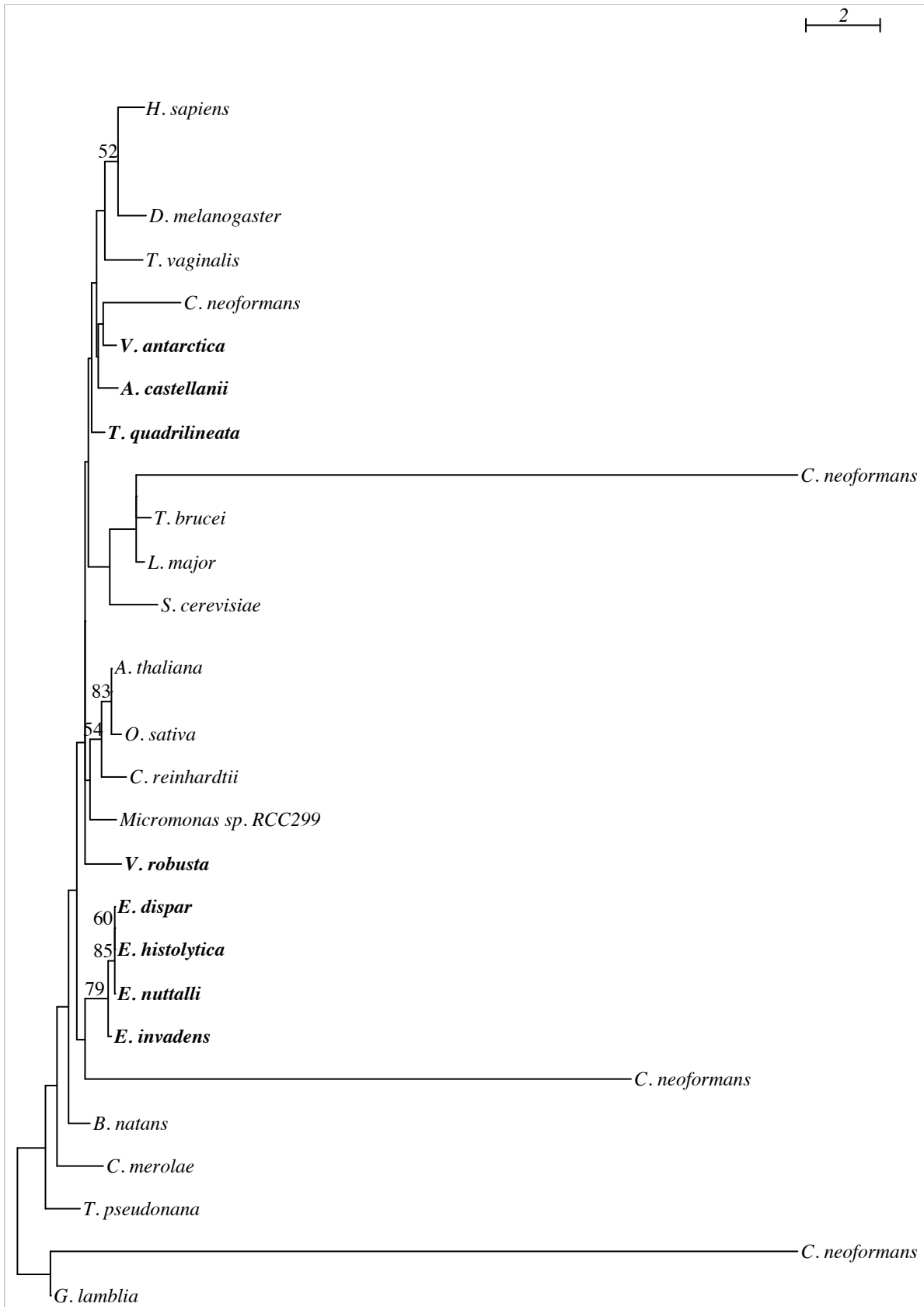


SAD1 like

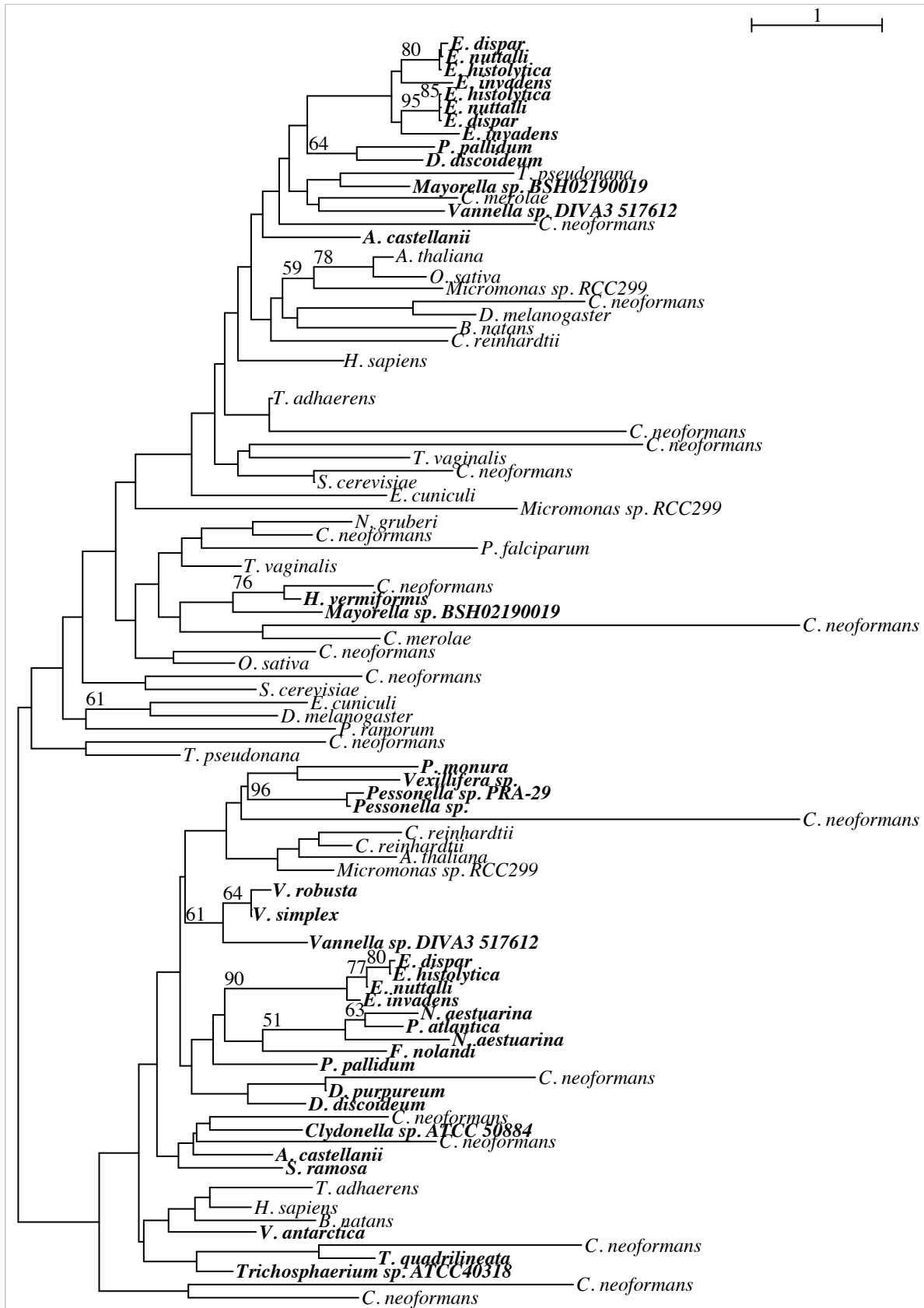


SGS1

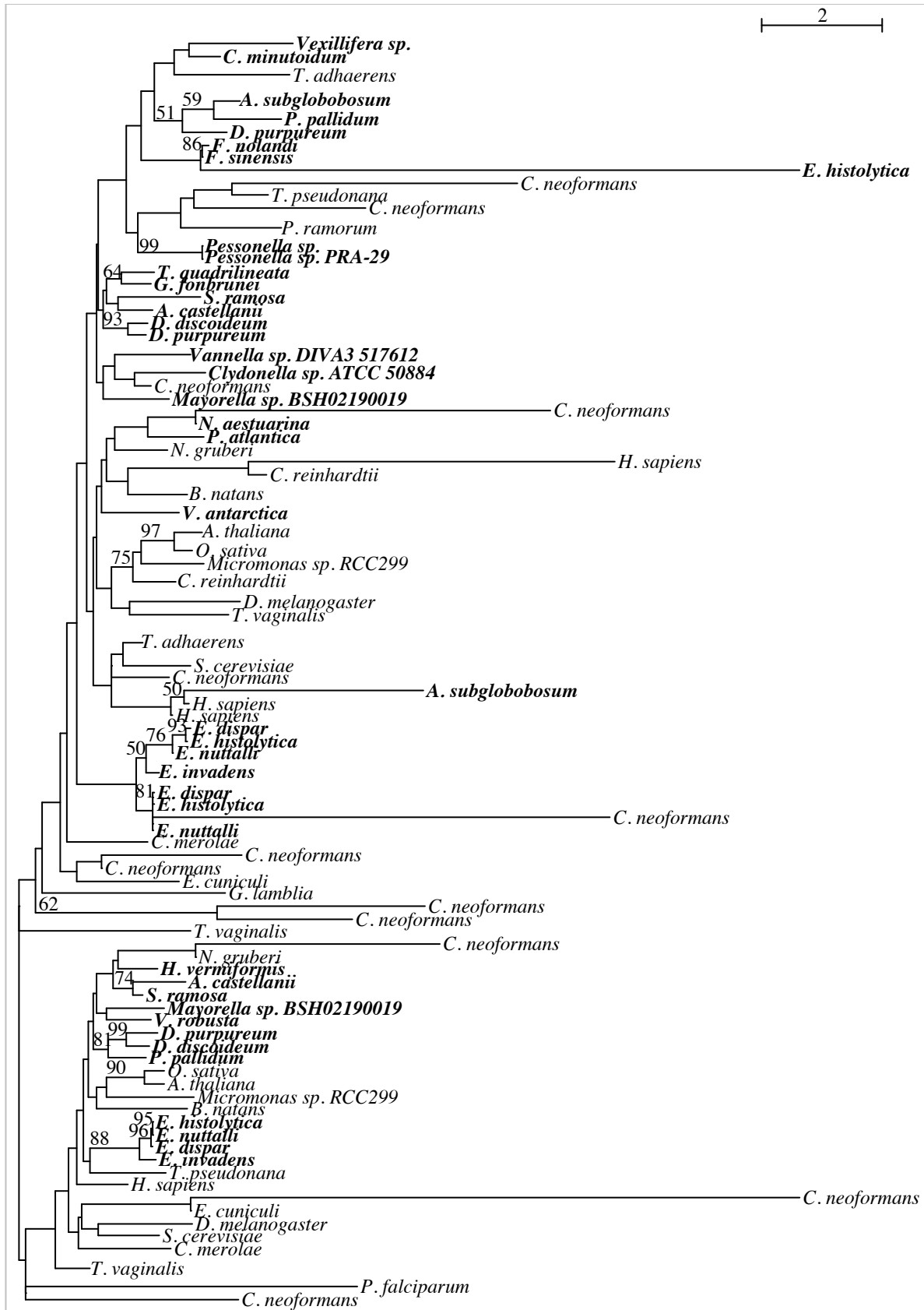


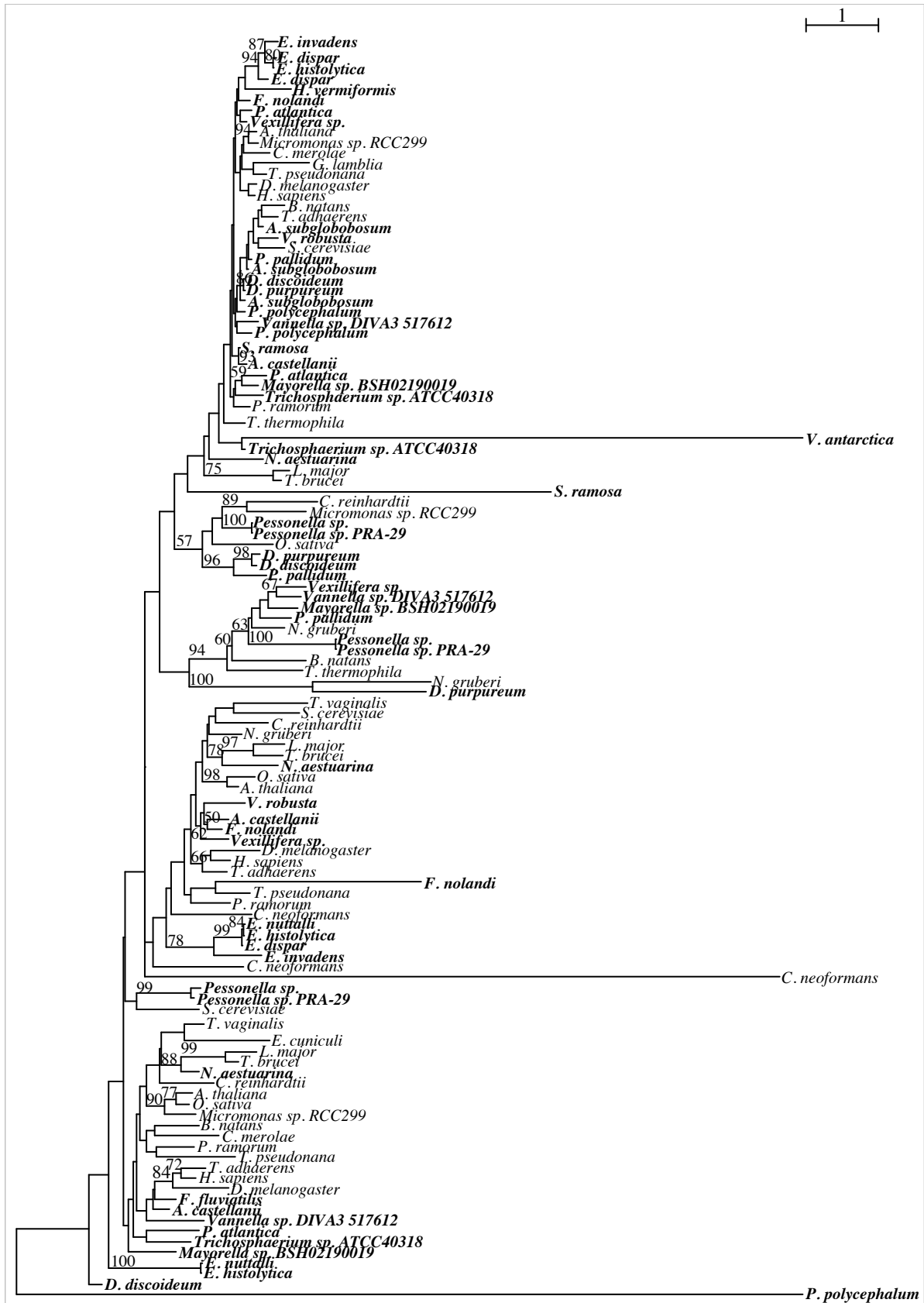


SLX1

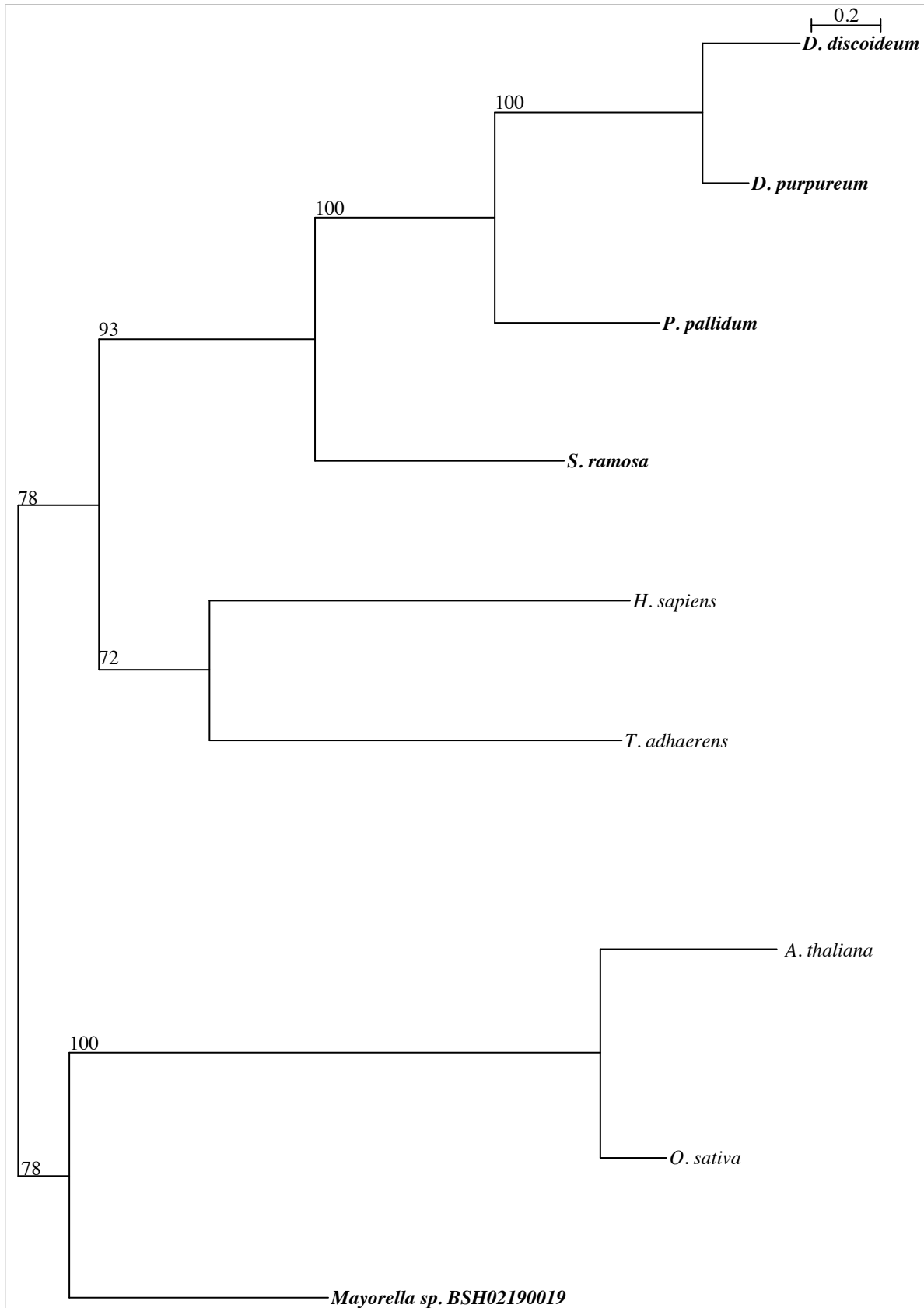


SMC5





TEL1/ATM



XRCC4/LIF1

fig. S3: Maximum likelihood trees of meiosis-specific and meiosis-related genes. Bootstrap support values  $\geq 50\%$  shown above branches.