Supplementary Figures

S5	Concatenated Analysis. Maximum likelihood phylogenetic analysis of concatenated alignments. Node labels indicate percent bootstrap support	
	from 1000 replicates. Nodes with bootstrap support values below 70% have been collapsed and are shown as polytomies. This is the full version of the	
	tree displayed in Figures 1 and 2	1
S6	18S. Maximum likelihood phylogenetic analysis of 18S sequences. Node labels indicate percent bootstrap support from 1000 replicates. Nodes with	
	bootstrap support values below 70 have been collapsed and are shown as polytomies	2
S7	28S. Maximum likelihood phylogenetic analysis of 28S sequences. Node labels indicate percent bootstrap support from 1000 replicates. Nodes with	
	bootstrap support values below 70% have been collapsed and are shown as polytomies	3
S8	COI. Maximum likelihood phylogenetic analysis of COI sequences. Node labels indicate percent bootstrap support from 1000 replicates. Nodes with	
	bootstrap support values below 50% have been collapsed and are shown as polytomies. (NOTE: collapse at 70% for final version)	4
S9	16S. Maximum likelihood phylogenetic analysis of 16S sequences. Node labels indicate percent bootstrap support from 1000 replicates. Nodes with	
	bootstrap support values below 70% have been collapsed and are shown as polytomies	5
S10	H3. Maximum likelihood phylogenetic analysis of H3 sequences. Node labels indicate percent bootstrap support from 1000 replicates. Nodes with	
	bootstrap support values below 70% have been collapsed and are shown as polytomies	6



1

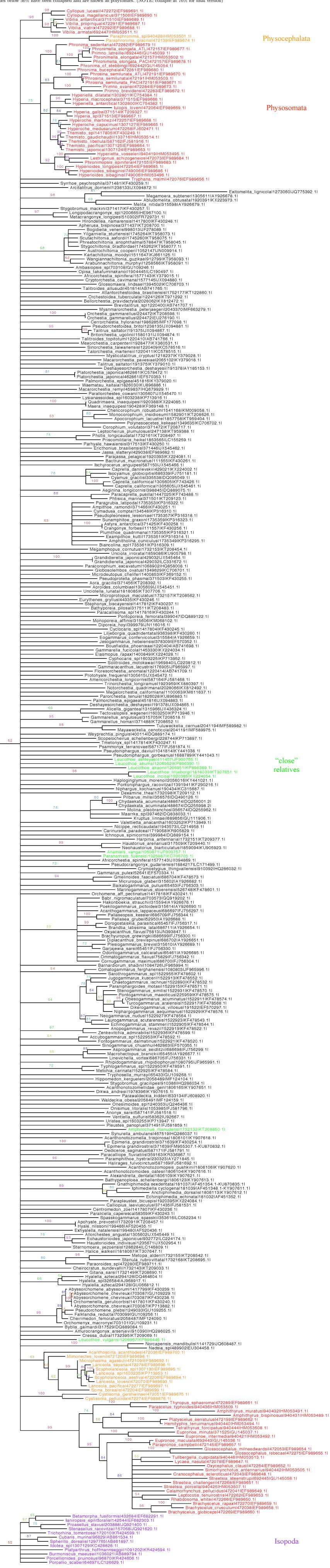


2

Parhyale_hawaiensisl317513IKF430309.1I



3



4

Isopoda

