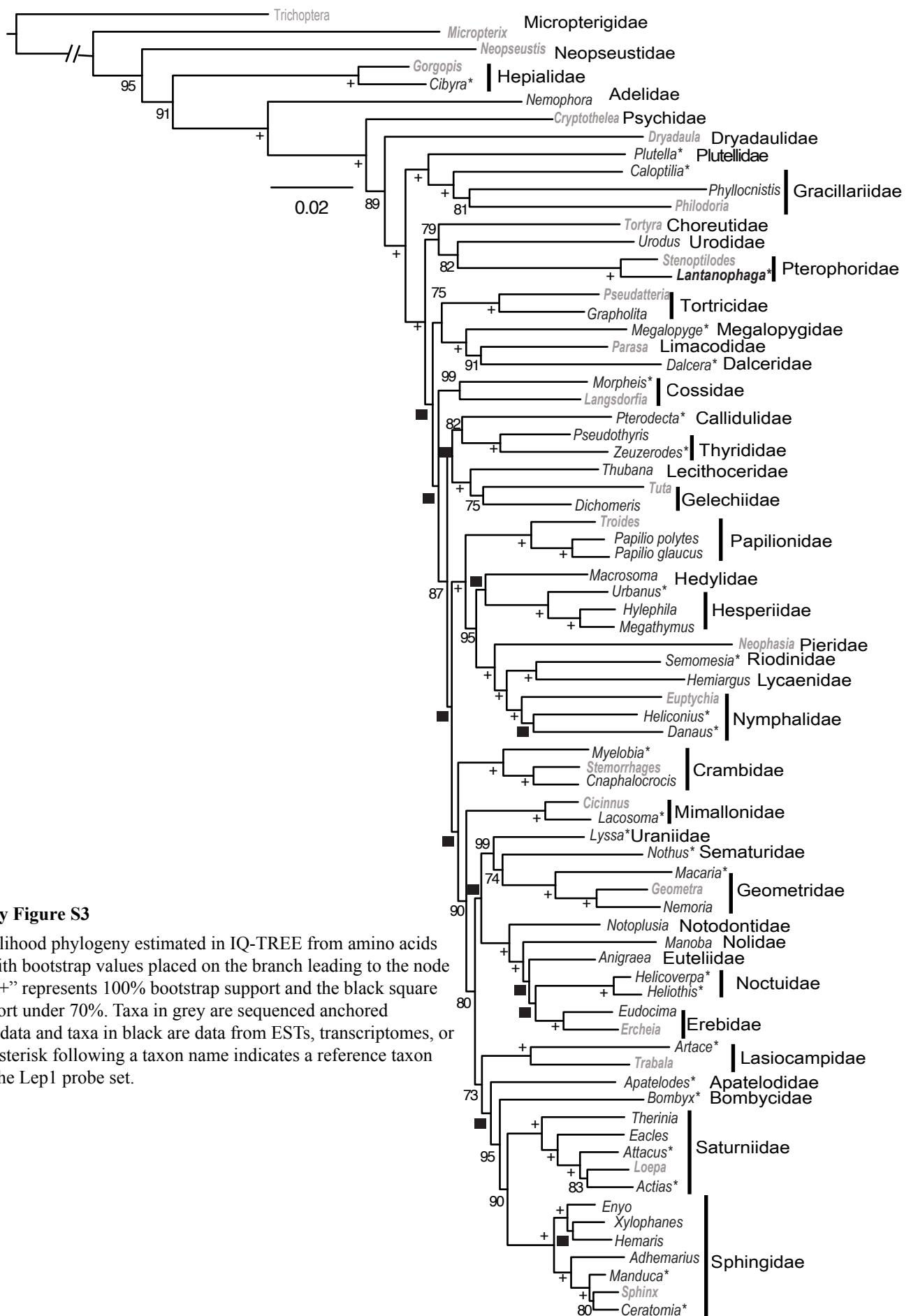


Dataset 2: AcrossLep_AHE+PARTtrans (amino acids)



Supplementary Figure S3

Maximum likelihood phylogeny estimated in IQ-TREE from amino acids of dataset 2, with bootstrap values placed on the branch leading to the node of support. A “+” represents 100% bootstrap support and the black square represent support under 70%. Taxa in grey are sequenced anchored phylogenomic data and taxa in black are data from ESTs, transcriptomes, or genomes. An asterisk following a taxon name indicates a reference taxon used to make the Lep1 probe set.