



50 Fig. Phylogenetic reconstruction of representative sequences of all MHITs generated from Vitek together with standard barcode sequences from all hosts and parasite genera in each sample. Terminal taxa in green represent standard barcoding reference sequences from well-studied community members, blue represent strong generalist representative sequences that matched with 97% similarity any of the standard barcoding reference sequences, whereas red did not match any reference database record with a required similarity. Taxa were reconstructed in FastTree using Neighbor-Joining algorithm with heuristic search for candidate joins and local bootstrapping [1] from multi-aligned sequence dataset [2] and displayed in FigTree version 1.4.2 [3].

1. Price MN, Dehal PS, Arkin AP. FastTree: computing large minimum evolution trees with profiles instead of a distance matrix. *Mol Biol Evol.* 2009; 26: 1601–1609.  
 2. Katz R, Standley DM. MAFFT multiple sequence alignment software version 7: improvements in performance and stability. *Mol Biol Evol.* 2013; 30: 772–780.  
 3. Rambaut A. FigTree v1.4.2. Tree figure drawing tool. 2014. Available from <http://tree.bio.ed.ac.uk/software/figtree/>.