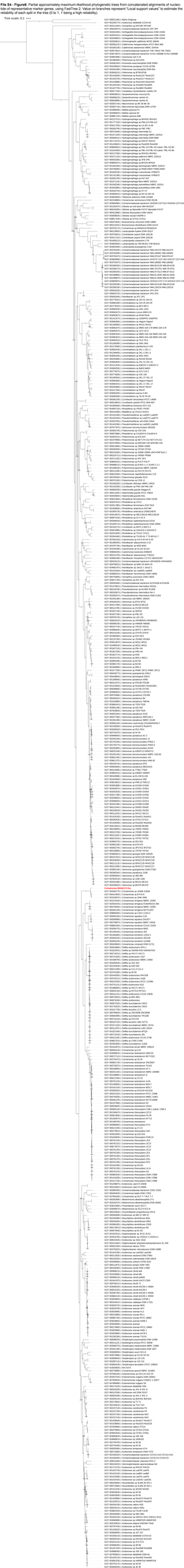Fig S4 - Figure1: Partial approximately-maximum-likelihood phylogenetic trees from concatenated alignments of nucleotide of representative marker genes, using FastTree 2. Value on branches represent 'Local support values' to estimate the reliability of each split in the tree (0-1). Scale bar is 1 substitution per site.