



Figure S2. Results from 213 partial COI sequences including ITA-Verified reference sequence (TableS2) and the one anomalous GenBank accession attributed to Rh that grouped with Rn references in a collapsed Maximum-Likelihood GTR+G+I tree topology assembled using IQ-Tree v 2.6.12 [39] annotated in FigTree v. 1.4 (<http://tree.bio.ed.ac.uk/software/figtree/>). Branch numbers represent percentage of posterior probability from 1,000 UF Bootstrap iterations with support of $\geq 62\%$ [57]. Full data available upon request from authors.