**Figure S1.** The estimated evolutionary rates for nucleotide sites in all five concatenated matrices analyzed in this study. Parsimony informative sites in each concatenated matrix were sorted based on the Observed Variability (OV) method, and subsequently divided into two equal partitions.
A  Nuclear genes

B  Plastid genes
C  Zhong et al. (2011)

D  Wu et al. (2013)
Qiu et al. (2006)