



**Figure S3** Summary of Bayes-DIVA analysis of *Thrichomys*. The tree is a MCC phylogeny generated with BEAST for *cytb*. Circles at nodes show probabilities of ancestral ranges. Only the higher probabilities are shown. When two biogeographic regions are underlined in a node, it represents that ancestral range was at both regions. Biogeographic regions: A: southern Caatinga; B: northern Caatinga; C: central Caatinga; D: southern Cerrado; E: northern Cerrado; F: central Cerrado (see map in top left and Table S1).