

**Appendix S19.** Contour map of the benefit of (A) increasing the number of genes or (B) adding non-coding spacers at a given number of genes on branch ascertainment (left) or bootstrap support (right) across Zingiberales, based on values predicted from the logistic regression model using branch length, branch depth, number of genes, spacer inclusion, and their two-way interactions. Each curve corresponds to a fixed increase in ascertainment or support, from red (no increase) to blue (some increase).

