

APPENDIX S7. Maximum likelihood gene family phylogenies of sequences captured through target enrichment demonstrate presence of paralogous gene copies in *Artocarpus*. Names follow the sample IDs in Table 1 (main text). Appended to each sequence name is p0, representing the paralog with highest percent identity to the *Artocarpus camansi* reference sequence, or p1, representing a paralogous gene copy identified by HybPiper. In each case, *Artocarpus* samples are split into two clades, while the outgroup species typically have just one copy, or two recently diverged copies.

