Supporting Information

Hou et al. 10.1073/pnas.1104636108

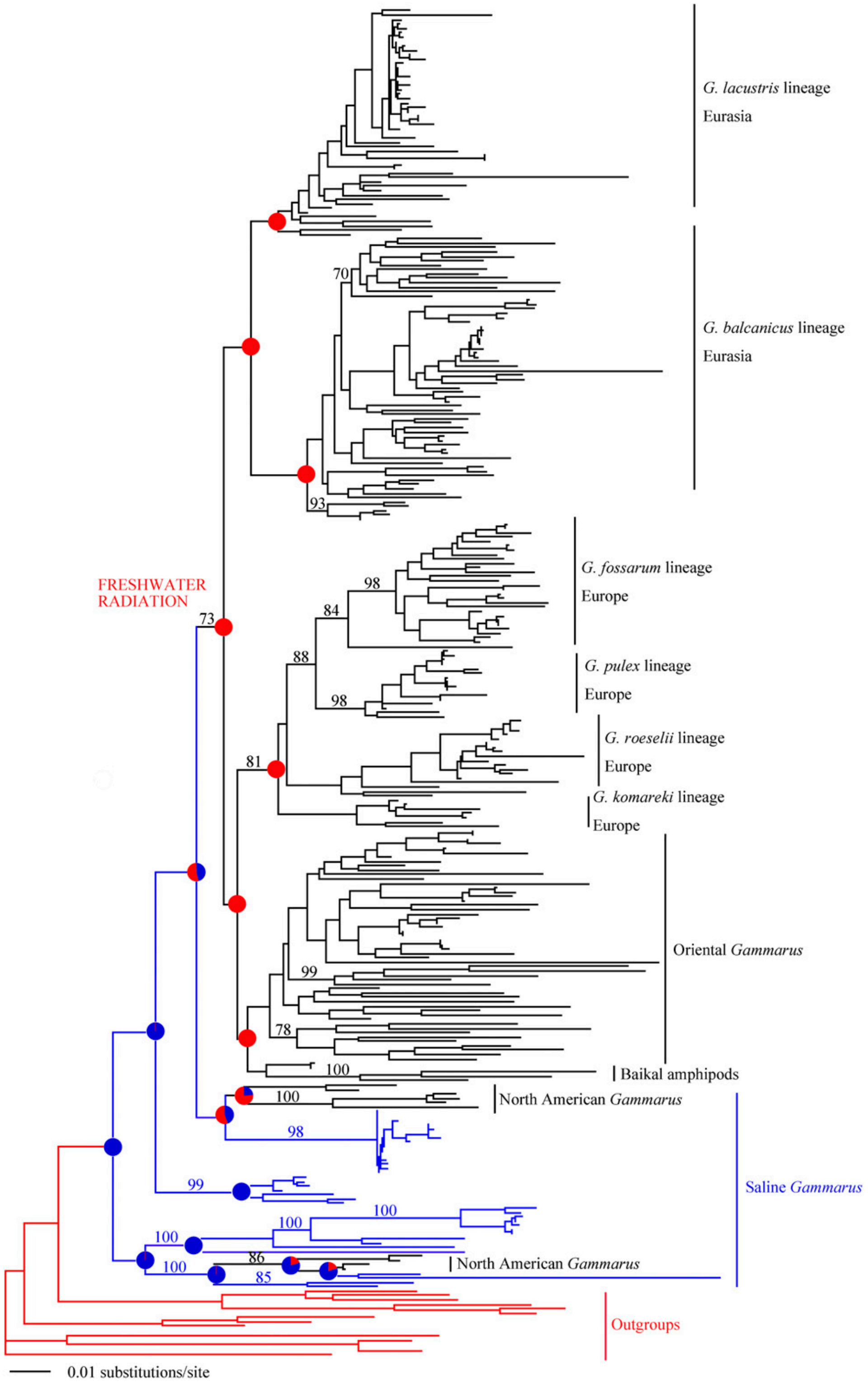

Fig. S1. Maximum likelihood phylogram inferred from the complete 305 taxa dataset with bootstrap values >70 above branches. Tribal ranks are reported to the *Right* of the tree. Terminal branches are in blue for saline species, black for freshwater species, and red for outgroups. Proportional likelihoods of ancestral states are mapped onto each node of interest (red, freshwater; blue, saline).

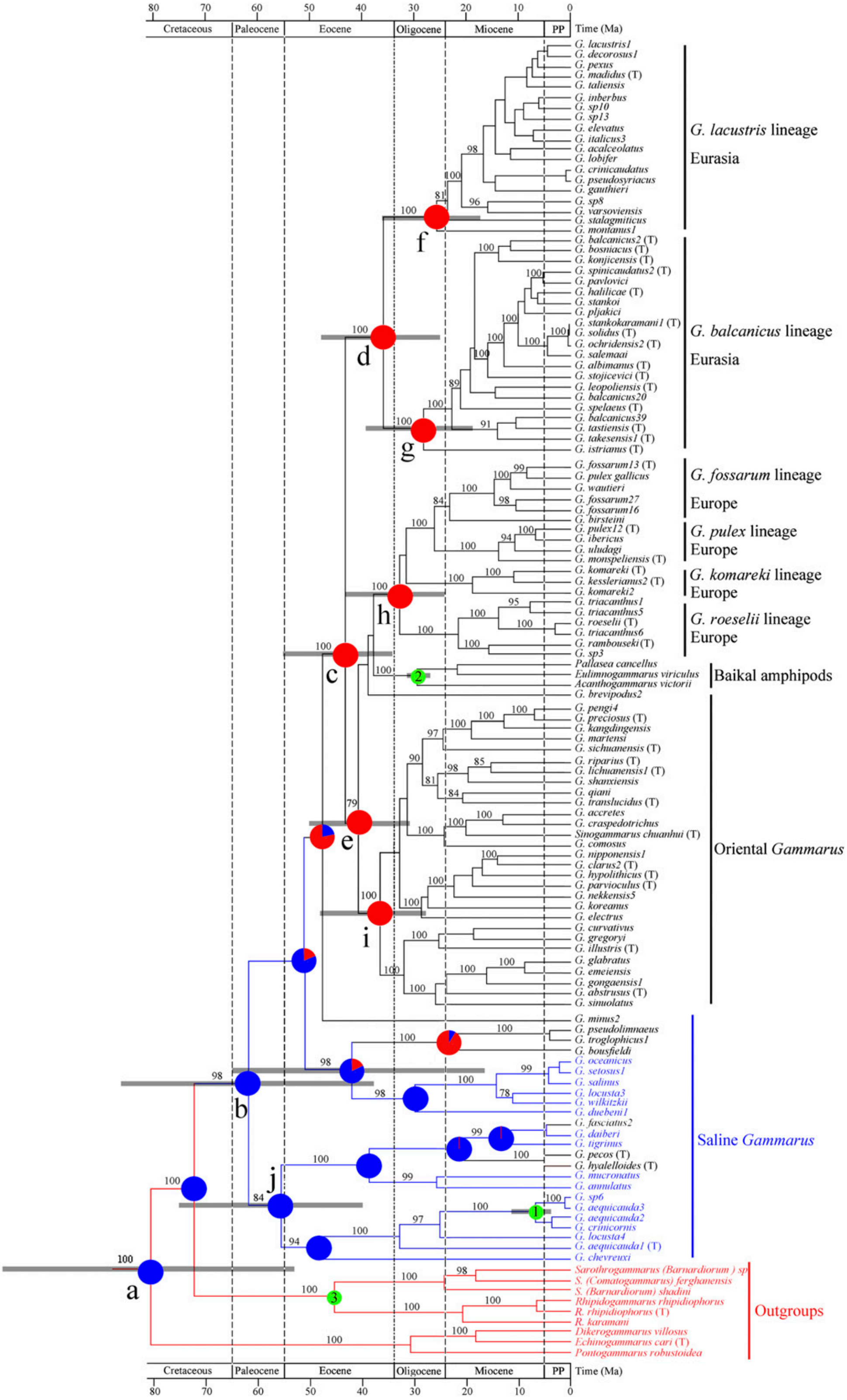

Fig. S2. Maximum clade credibility chronogram inferred from a BEAST dating analysis. Node bars represent 95% posterior credibility intervals for nodes of interest (a–j). Nodes 1, 2, and 3 are used for calibration. Posterior probabilities >70% are given above branches. Species names and terminal branches are in blue for saline species, black for freshwater species, and red for outgroups. Tribal ranks are reported to the *Right* of the tree. Proportional likelihoods of ancestral states are mapped onto each node of interest (red, freshwater; blue, saline).

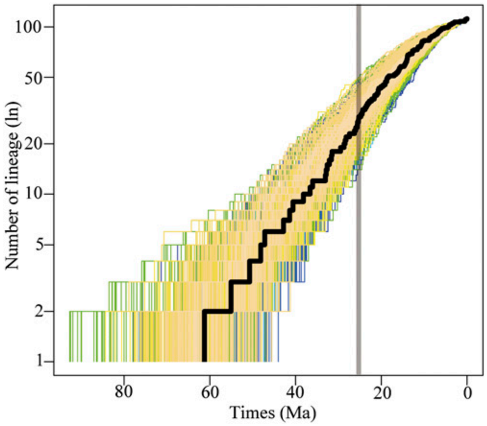

Fig. S3. Lineage-through-time plot estimated from 1,000 BEAST trees for *Gammarus* overall. The line in bold corresponds to the maximum credibility tree from the BEAST dating analysis. The gray bar indicates change in diversification rate, which is estimated to have occurred according to the best fit model of lineage diversification.

Other Supporting Information Files

Table S1 (DOC)
Table S2 (DOC)
Table S3 (DOC)
Table S4 (DOC)
Table S5 (DOC)
Table S6 (DOC)