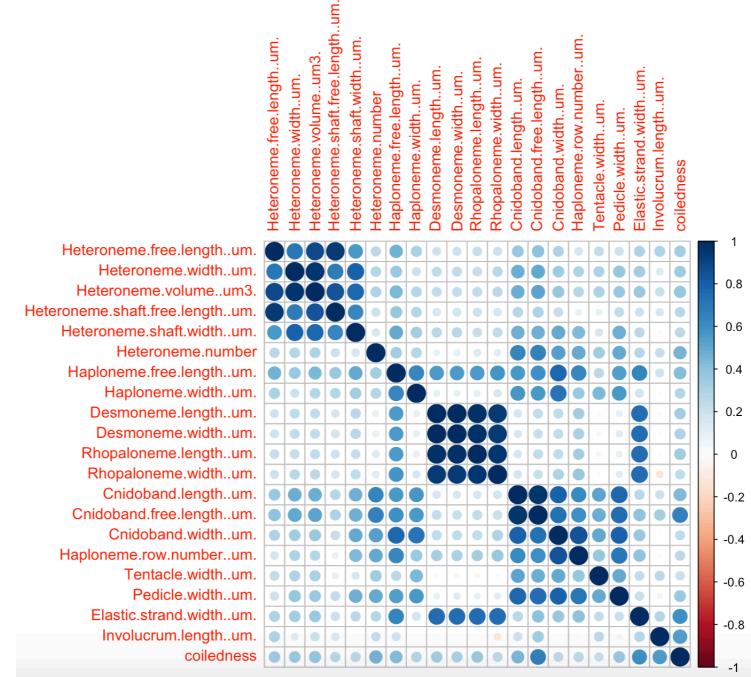
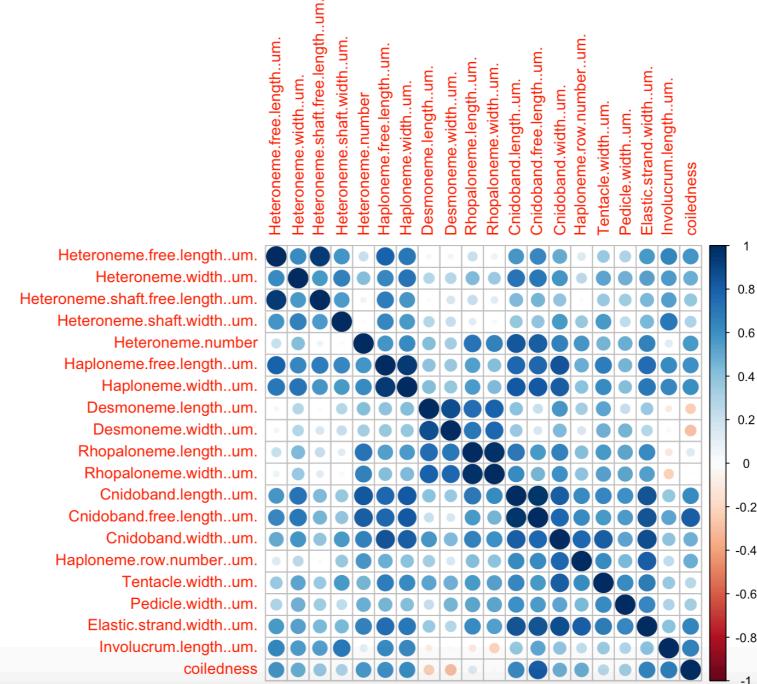


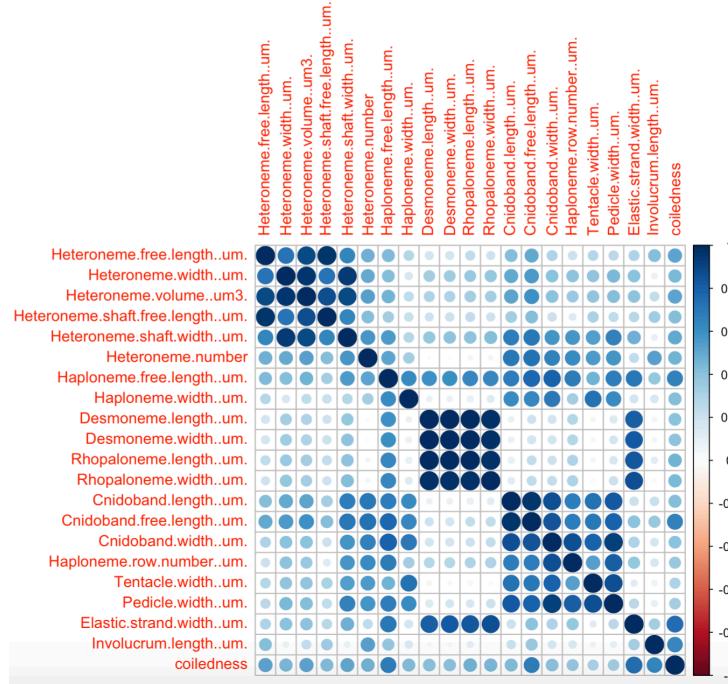
20.1 Rate covariance matrix for the whole tree using all taxa (45 species), transforming inapplicable states to zeroes. Covariances scaled to correlations. All characters estimated simultaneously under Brownian Motion.



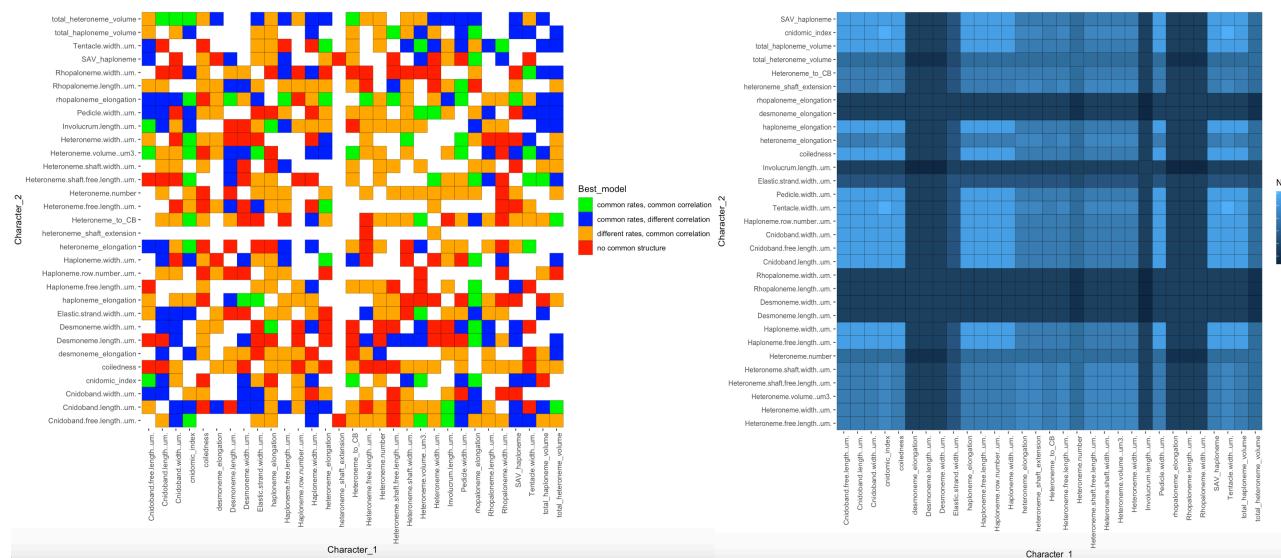
20.2 Rate covariance matrix for the whole tree using only taxa without inapplicable states (24 species). Covariances scaled to correlations. All characters estimated simultaneously under Brownian Motion.



20.3 Rate covariance matrix for the whole tree using only taxa with diet data (22 species), transforming inapplicable states to zeroes. Covariances scaled to correlations. All characters estimated simultaneously under Brownian Motion.



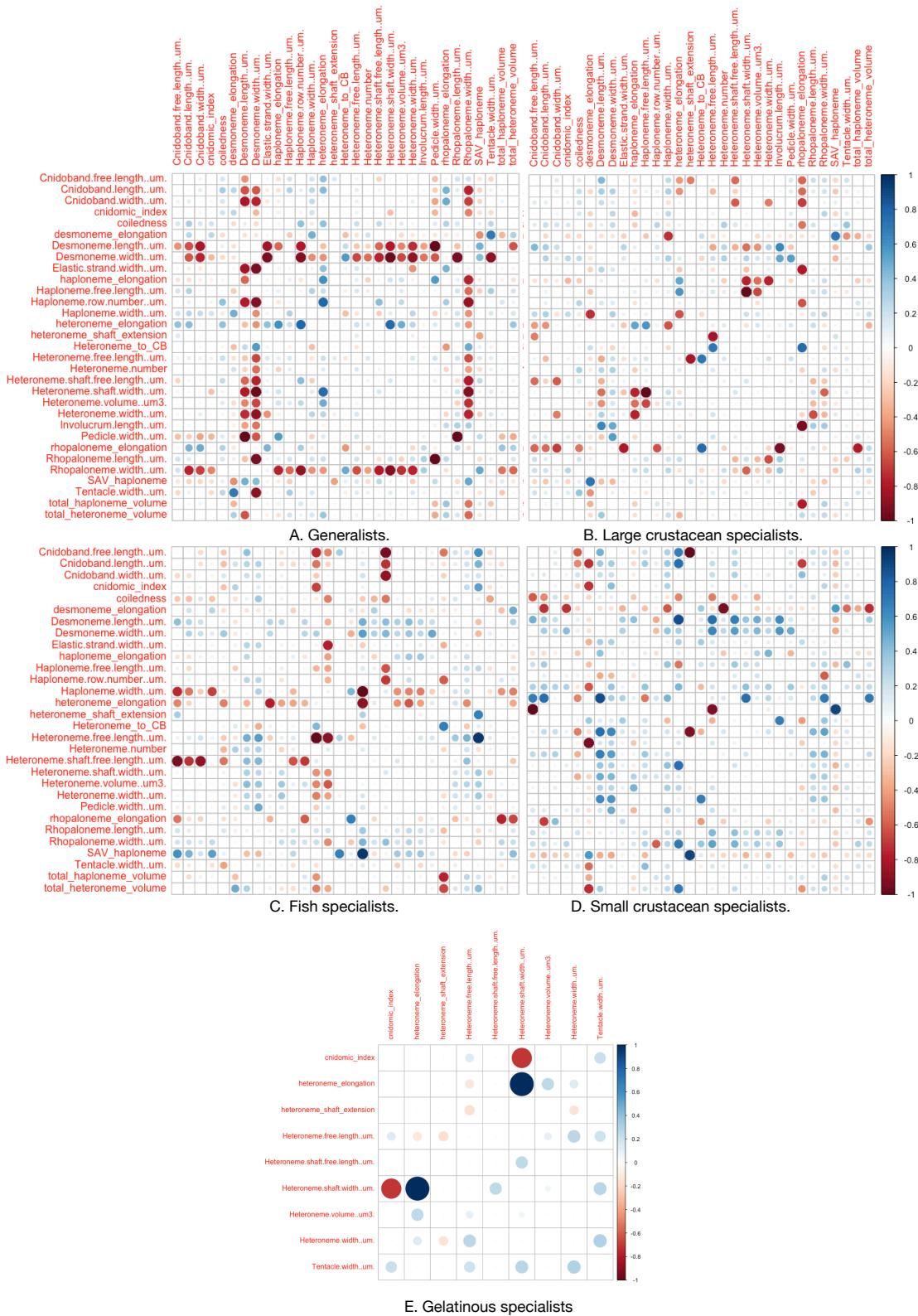
20.4 Left: Best models (lowest AIC) supported in a pairwise character rate covariance analysis comparing correlated Brownian Motion models across the five selective regimes. Selective regimes were mapped onto the tree using an ancestral state reconstruction of the feeding guilds. Blank cells represent computationally singular contrasts. Right: Number of taxa used for each pairwise contrast, given the number of taxa without inapplicable states.



20.5 Pairwise estimated rate covariance matrices across the five selective regimes, using only taxa with diet data. Covariances scaled to correlations. Selective regimes were mapped onto the tree (22 species with diet data) using a stochastic mapping of the feeding guilds. Tree is pruned to taxa with no inapplicable states for a given character pair. Not all regimes are represented in all contrasts. Question marks represent computationally singular contrasts.



## 20.6 Scaled differences between the regime-specific covariance matrices in Appendix 20.5 and the whole tree covariance matrix.



20.7 Scaled differences between the regime-specific covariance matrices in Appendix 20.5 and the covariance matrices in their preceding regime, the large-crustacean specialist regime.

