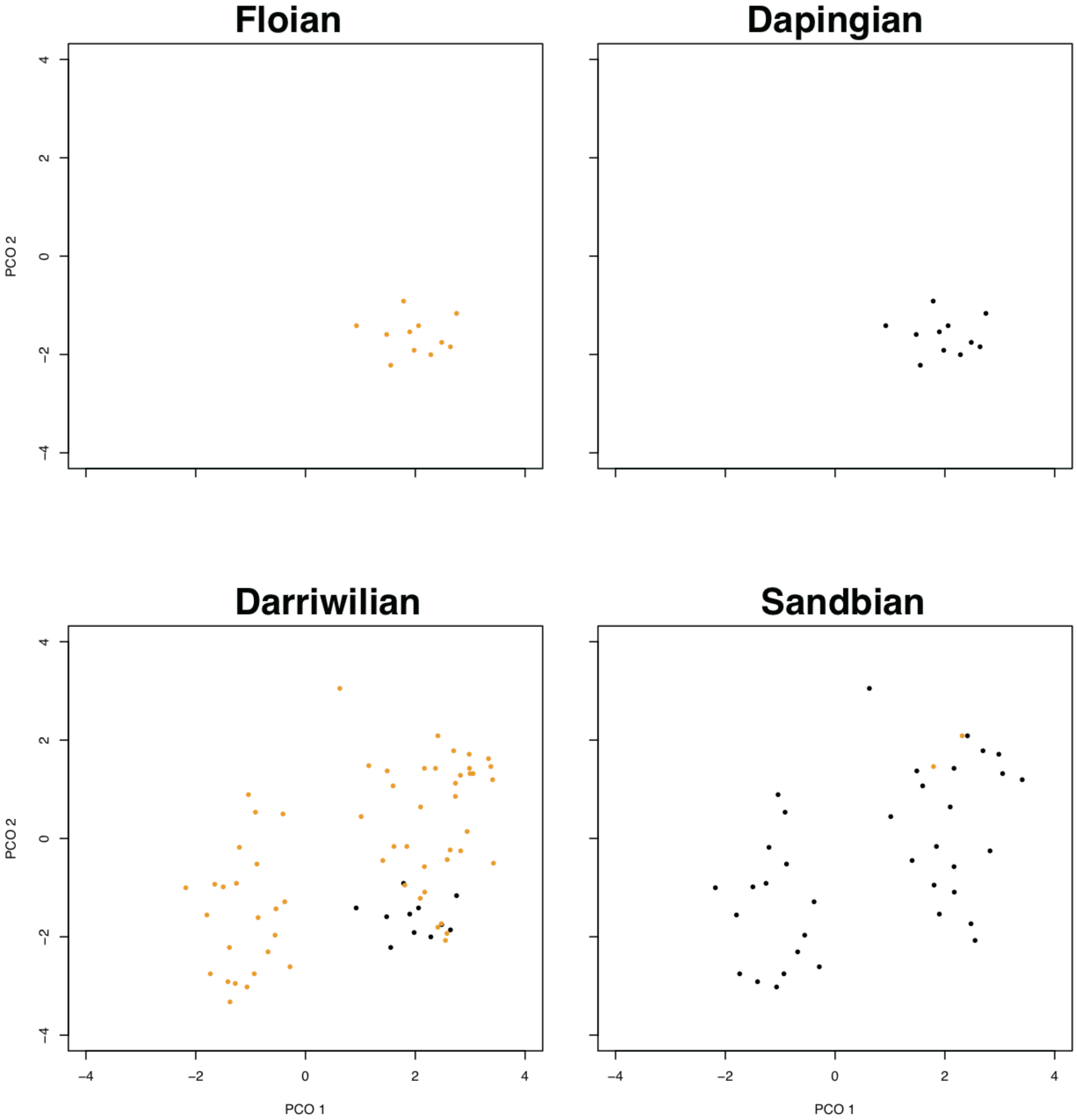
Supplemental material

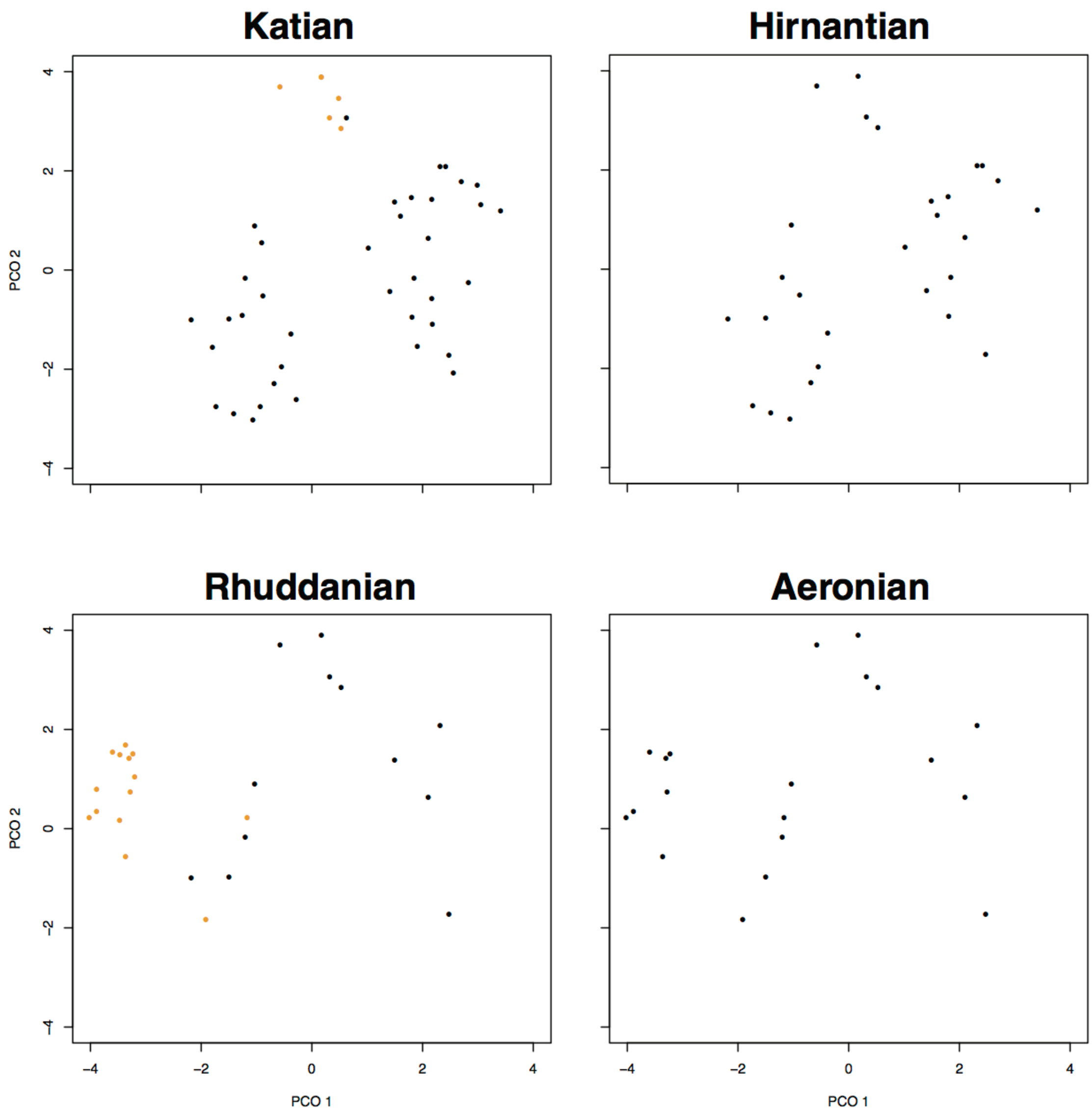
This supplemental file includes two parts: 1) the complete detailed image of morphospace change through time, and 2) a discussion of results of our analyses without ancestral nodes.

Part 1: Complete morphospace through time (with ancestral nodes)

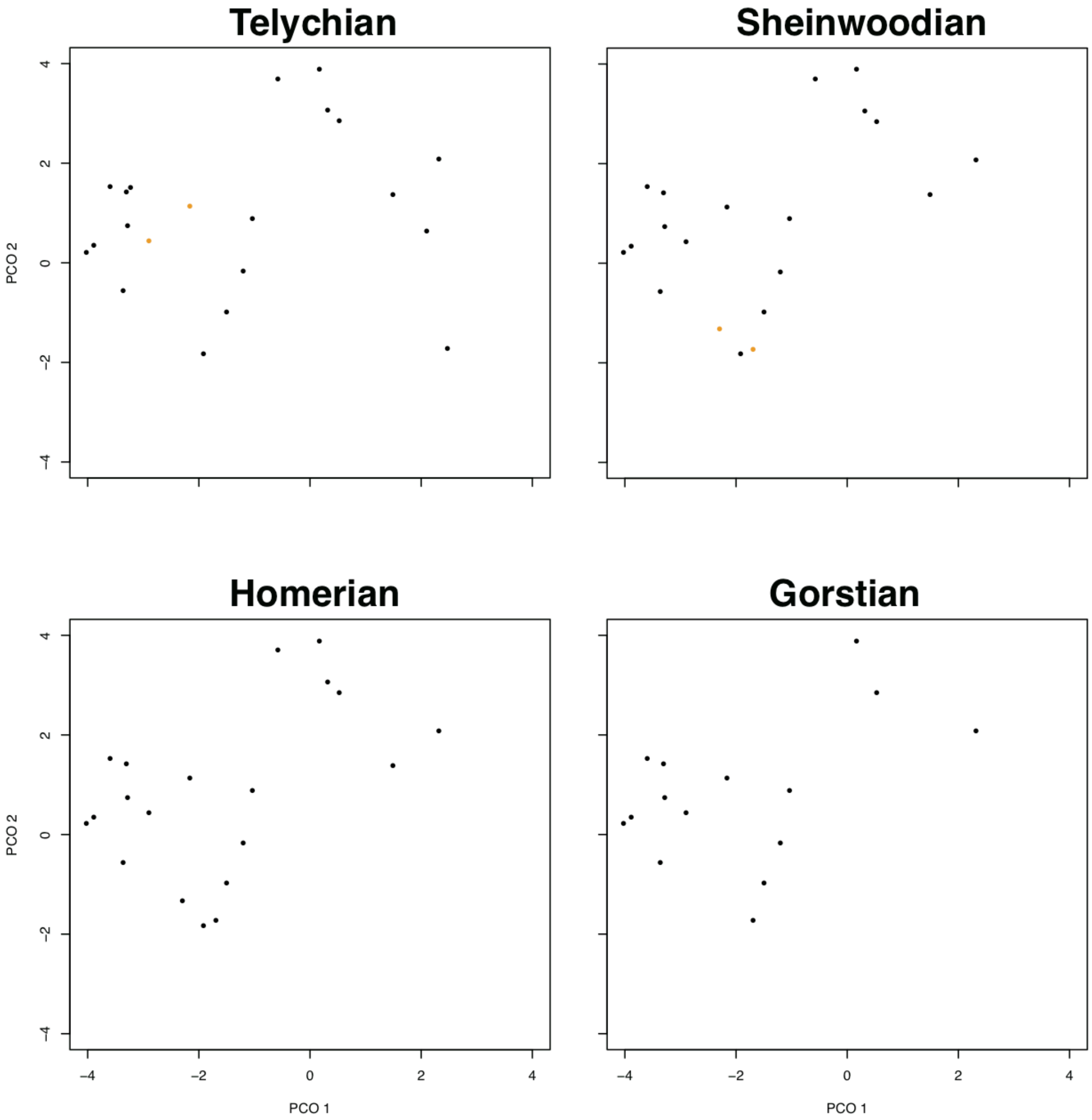
The panels in the Supplemental figures 1.1-1.5, below, illustrate the details of morphospace occupation for Strophomenida from the Floian to the Frasnian. This analysis includes ancestral nodes. This figure contains the same information as Figure 4 in the manuscript, but is presented here in an expanded format so that the details are easier to read.



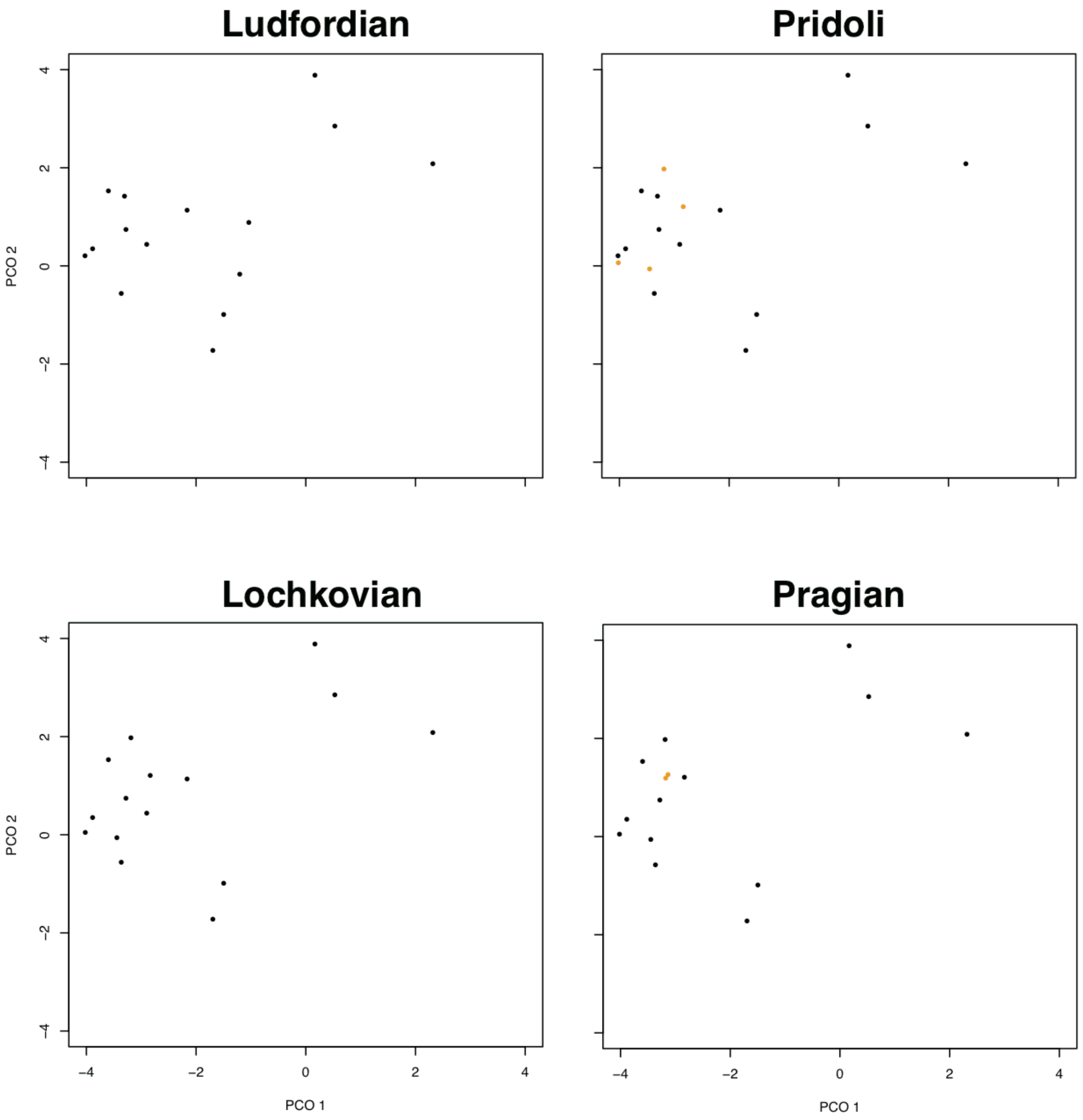
Supplemental figure 1.1



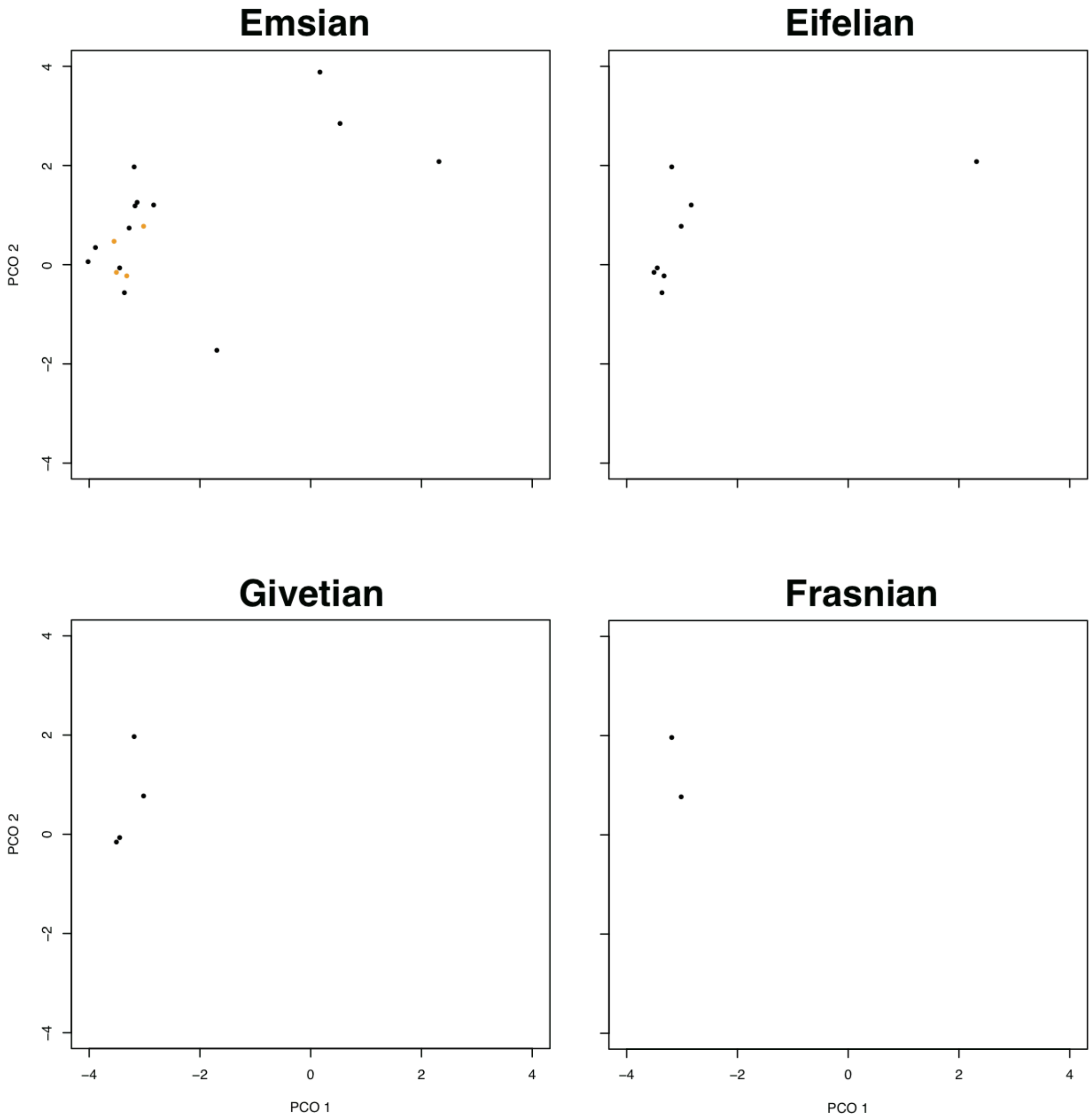
Supplemental figure 1.2



Supplemental figure 1.3



Supplemental figure 1.4



Supplemental figure 1.5

Caption for supplemental figures 1.1-1.5:

Morphospace through time (including ancestral nodes). Each frame is the morphospace (PCO axes 1 and 2) of species and ancestral nodes extant during a particular stage. Black dots are species that originate during that stage. Gray dots are species (or nodes) that survived from the previous stage.

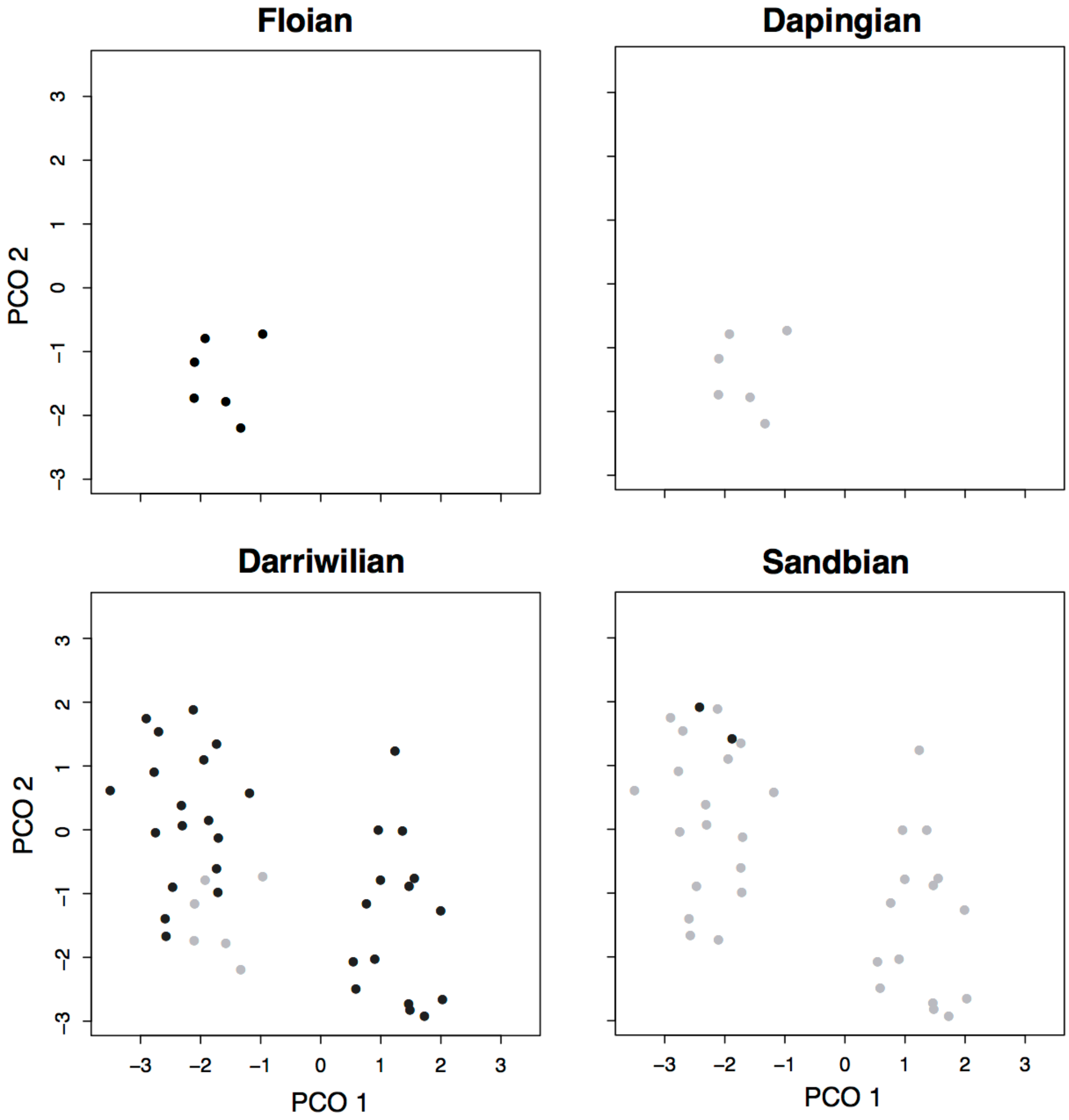
Part 2: Results of running analyses without ancestral nodes

To test whether inclusion of ancestral nodes in our analysis affected the results, we re-ran analyses on the data without nodes. Overall results are similar since the nodes fill in regions of morphospace without altering the overall shape. Without ancestors, there is still a shift in morphospace through time, suggesting post-extinction morphological constraint.

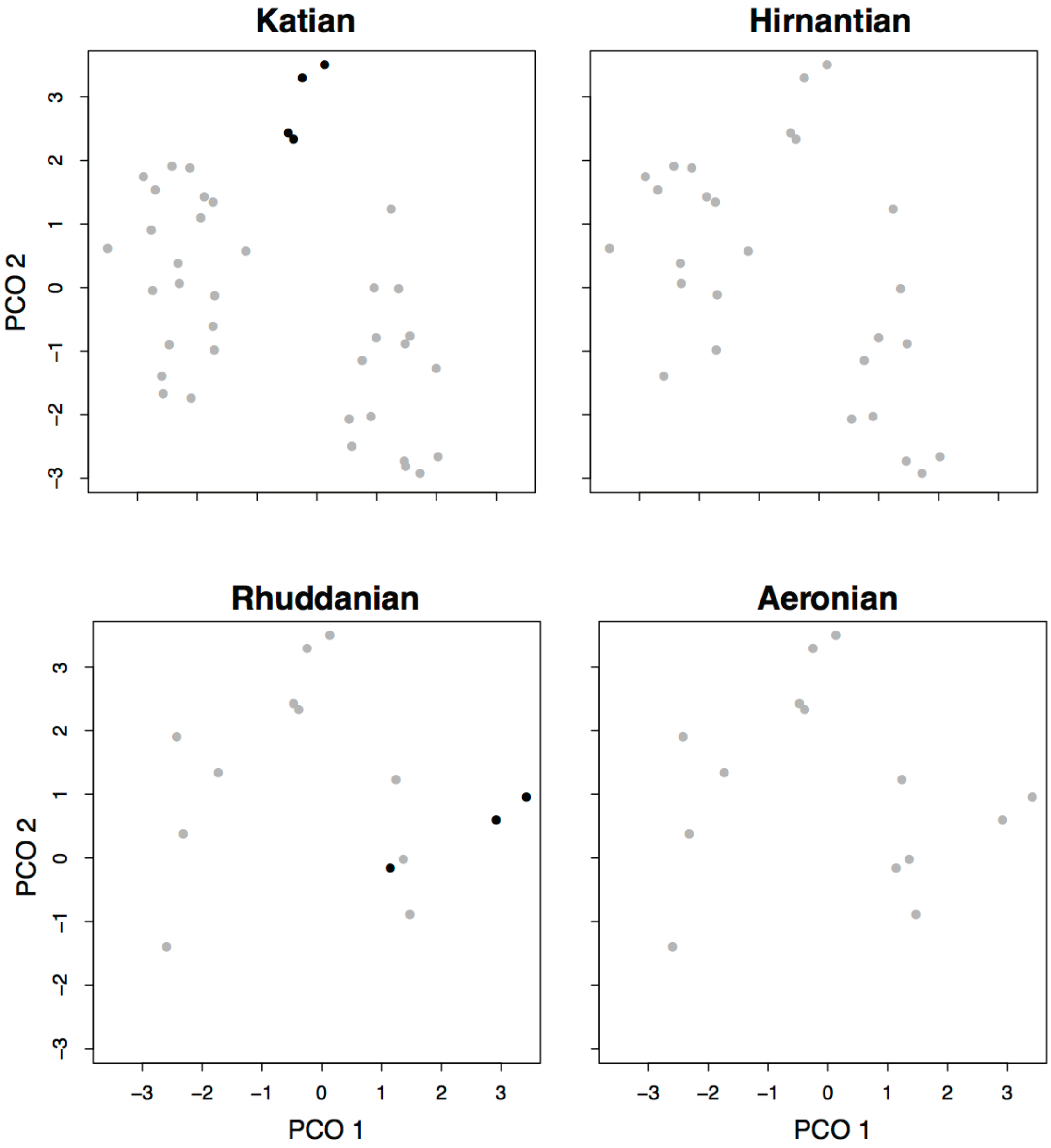
Plots below are the morphospace (PCO axes 1 and 2) for each stage (supplemental figures 2.1-2.5). The occupation of morphospace through time changes in the same manner as the morphospace including nodes.

Note: The pattern is reversed, but the overall patterns are essentially the same. Reversal of points in ordination space is simply a result of ordinating a different data set. The absolute PCO values cannot be compared between the analysis with nodes and the analysis without nodes. However, the fact that the Late Ordovician mass extinction and recovery corresponds to a change in occupation of morphospace is consistent. This combined with the fact that Silurian and Devonian species in this analysis occupy a different region of morphospace than Ordovician species (the same trend we see when including nodes) gives us confidence in including ancestral nodes in our assessment of morphological change across the Late Ordovician mass extinction and recovery.

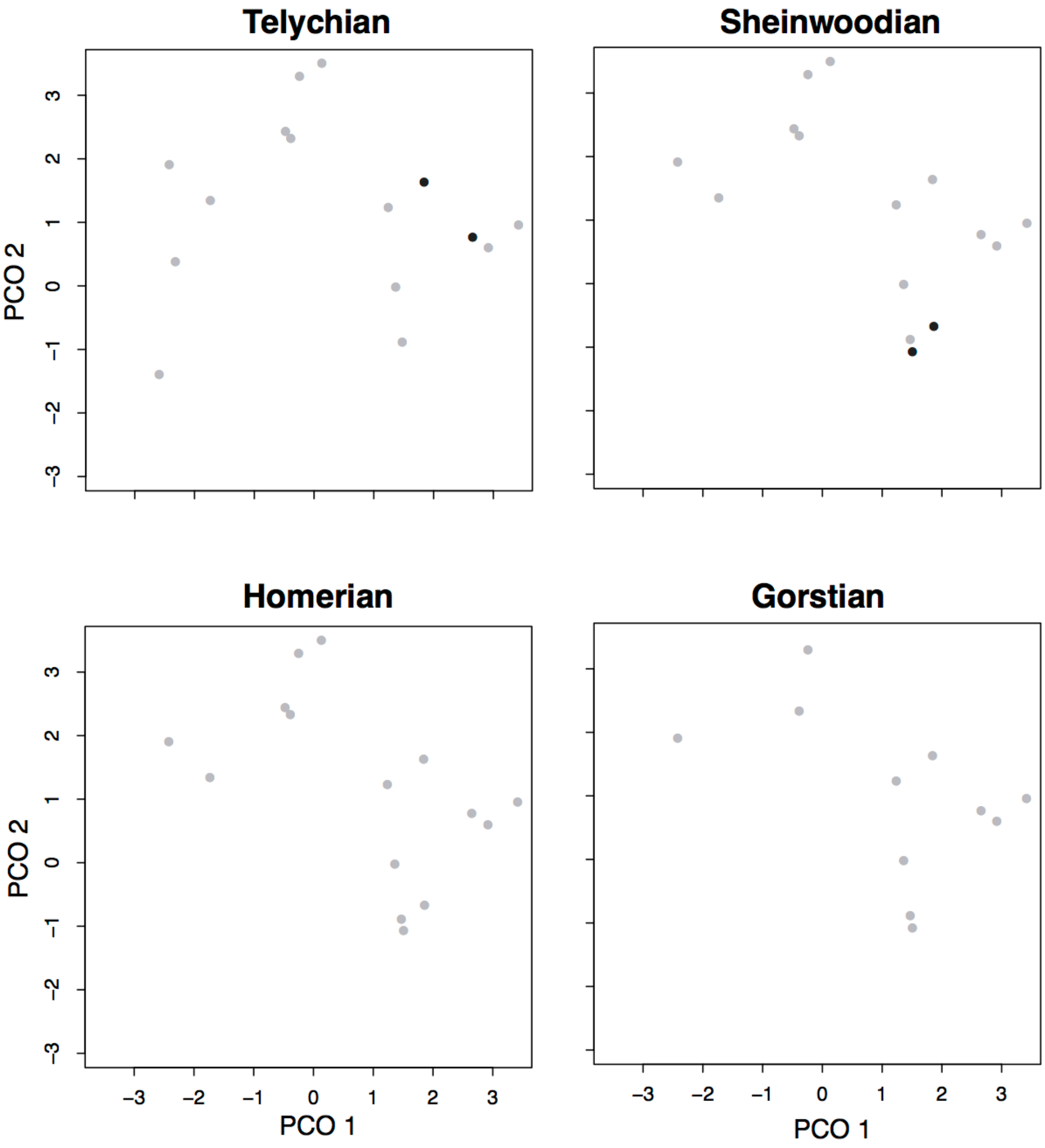
The only difference is in the ability to interpret the recovery interval. There are only 3 taxa that originate in the Rhuddanian. This makes it impossible to determine if origination is random with respect to morphology because there is not enough statistical power (supplemental figure 3).



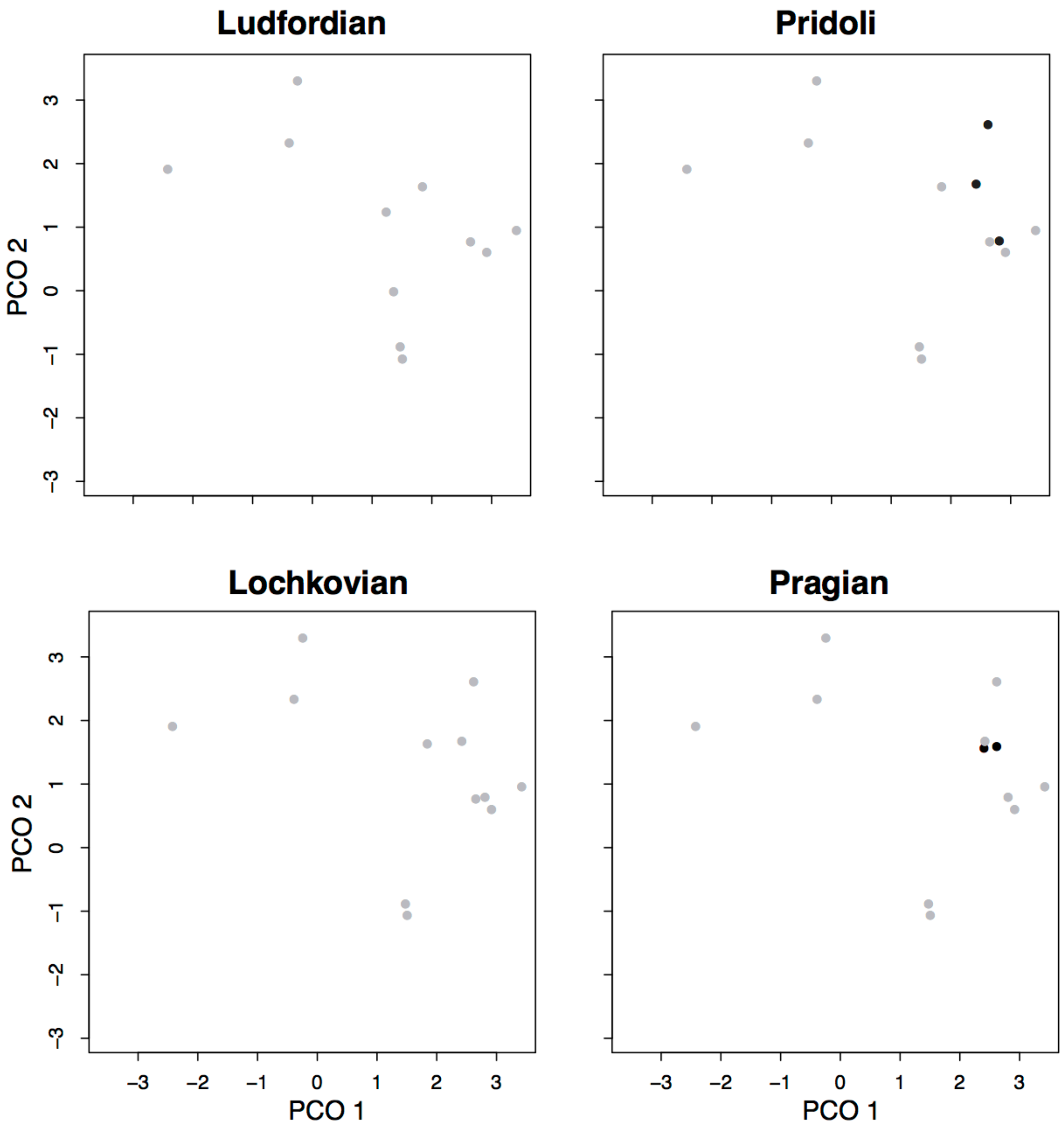
Supplemental figure 2.1



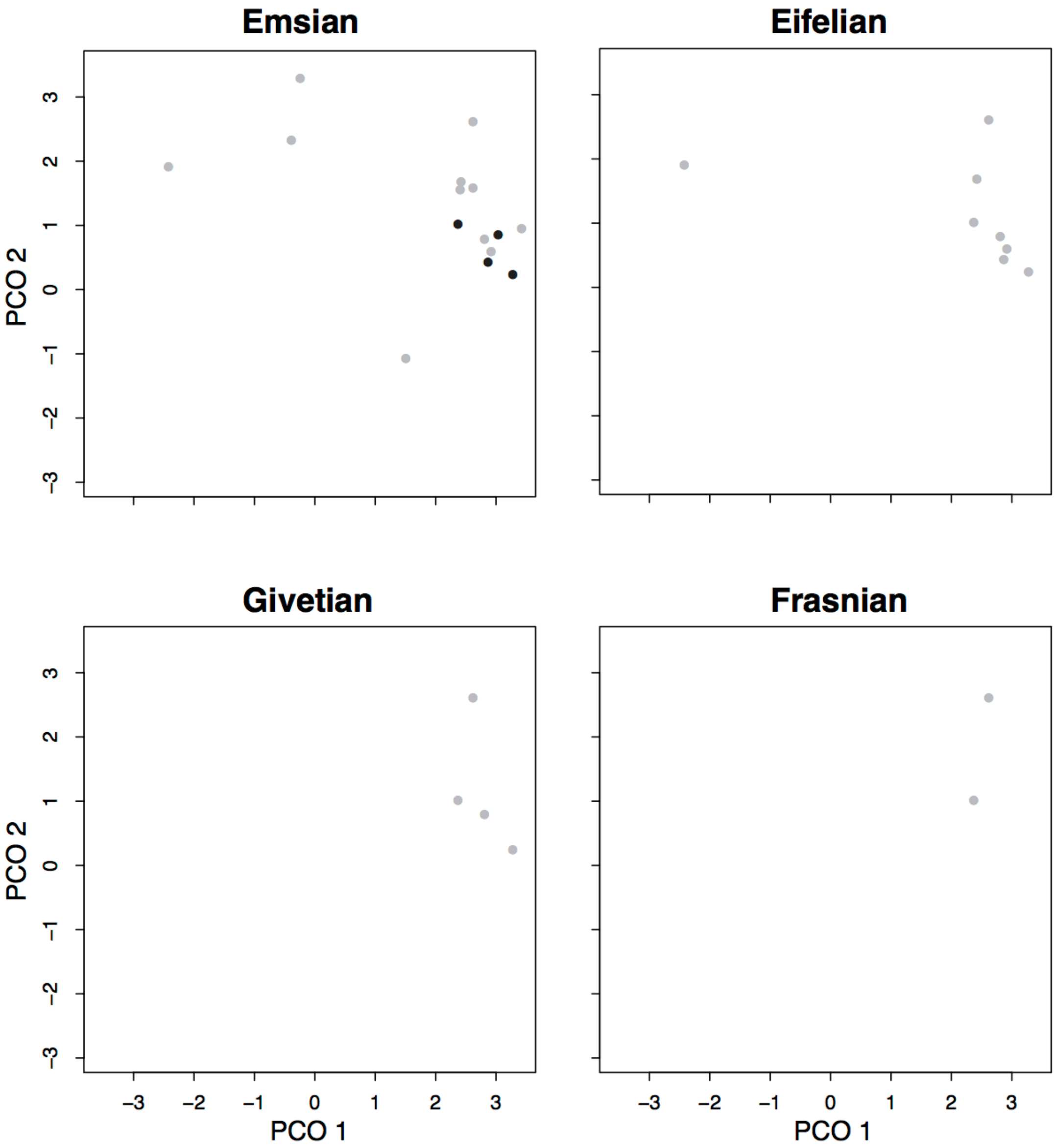
Supplemental figure 2.2



Supplemental figure 2.3



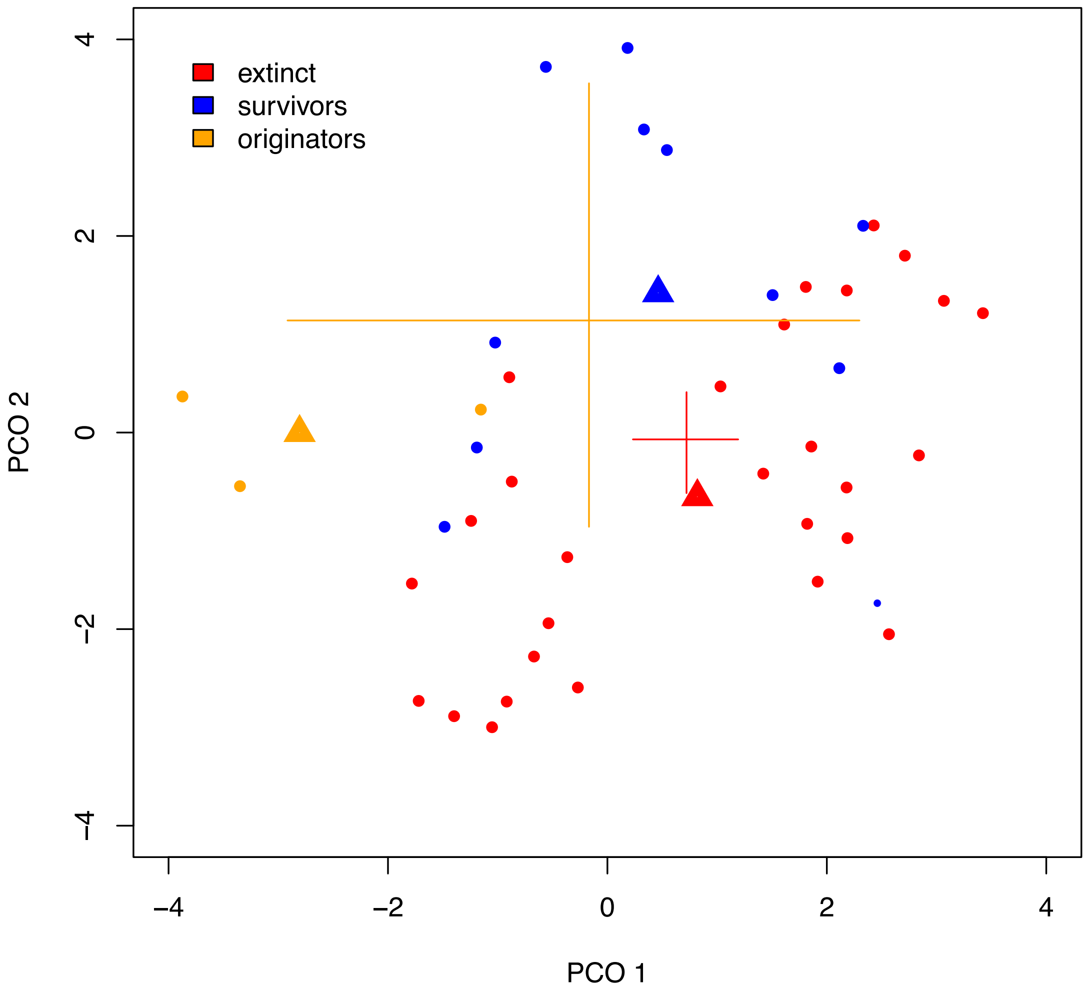
Supplemental figure 2.4



Supplemental figure 2.1

Caption for supplemental figures 2.1-2.5:

Morphospace through time without ancestral nodes. Plots below are the morphospace (PCO axes 1 and 2) for each stage. Black dots are species that originate during that stage, while gray dots are species that survived from the previous stage.



Supplemental figure 3: Bootstrap of data without ancestral nodes. The overall pattern here is similar to that of the data with ancestral nodes. However, since only 3 taxa originate in the Rhuddanian, the bootstrap analysis does not have enough statistical power to distinguish the distribution in morphospace of new taxa from a random expectation.