Appendix S1 for "Historical contingency and the role of post-invasion evolution in alternative community states"

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Ecology

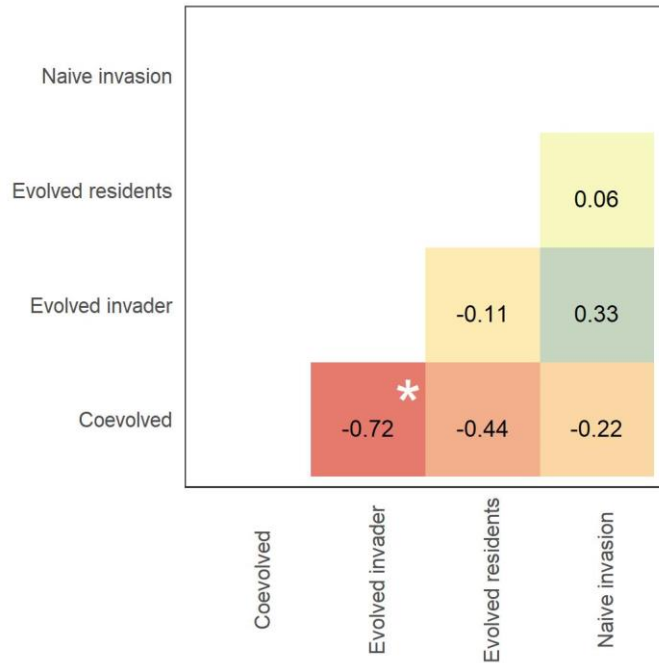|	Assemblage A					
	B. americanum		*S. teres*		*E. patella*	
	Deviance	*p*-value	Deviance	*p*-value	Deviance	*p*-value
time	3.956	0.166	54.449	**0.001**	111.077	**0.001**
invasion * time	3.194	0.095	0.060	0.782	1.755	0.239
	Lecane sp.		*P. bursaria*			
	Deviance	*p*-value	Deviance	*p*-value		
time	1.074	0.429	7.608	**0.048**		
invasion * time	25.043	**0.001**	2.861	0.120		

Table S1. Species-level response to invasion within Assemblage A. Deviance and *p*-values are reported from univariate tests with generalized linear models that are modeled with a negative binomial distribution. *P*-values are adjusted for multiple comparisons through resampling based on the Holm step-down procedure.

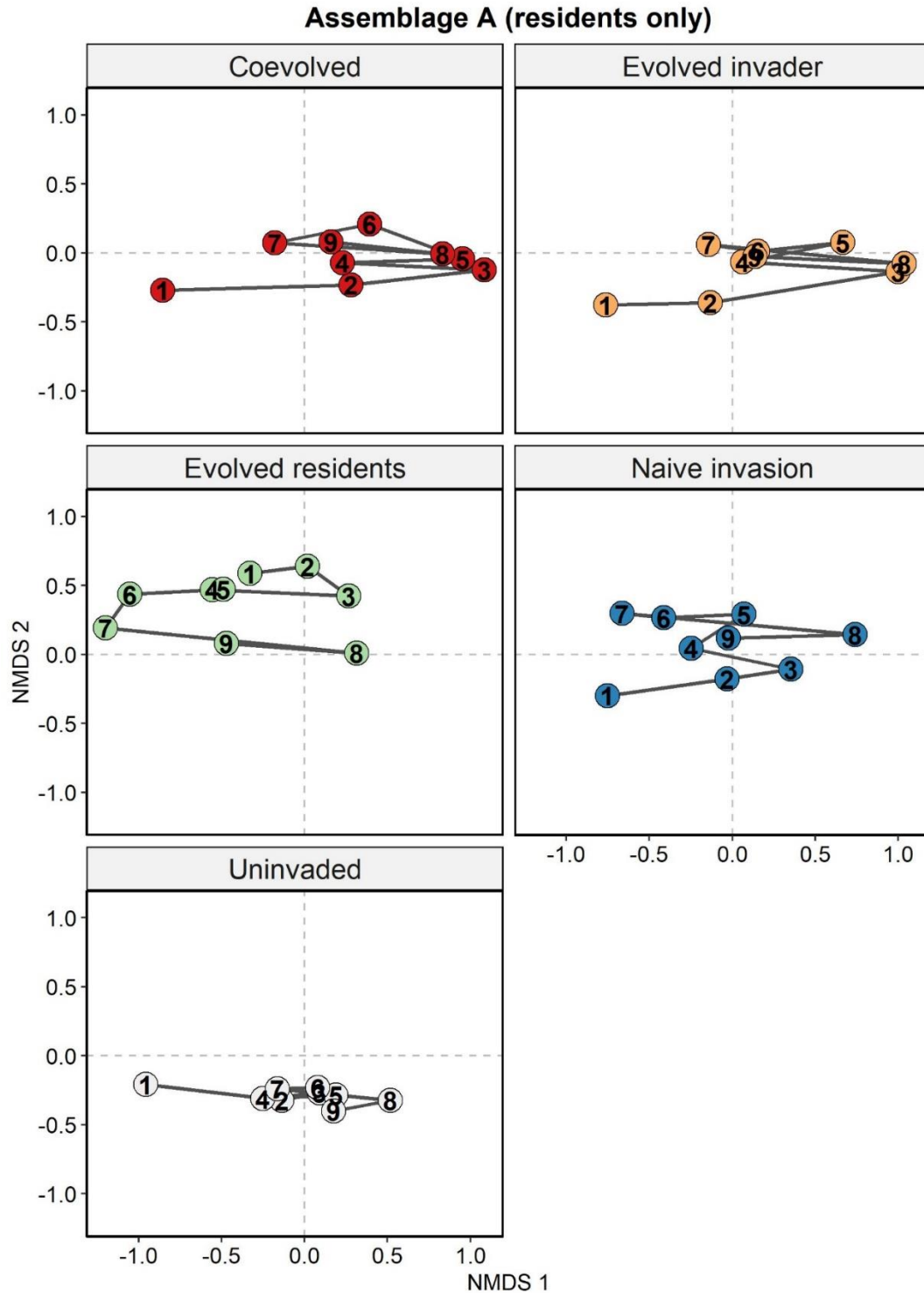|	**Assemblage B**				
	S. coeruleus			*P. caudatum*	
	Deviance	*p*-value		Deviance	*p*-value
time	22.763	**0.001**		1.168	0.366
invasion * time	2.276	0.315		0.209	0.786
	Monostyla sp.			*E. daidaleos*	
	Deviance	*p*-value		Deviance	*p*-value
time	0.949	0.366		13.660	**0.001**
invasion * time	0.378	0.786		7.674	**0.032**

Table S2. Species-level response to invasion within Assemblage B. Deviance and *p*-values are reported from univariate tests with generalized linear models that are modeled with a negative binomial distribution. *P*-values are adjusted for multiple comparisons through resampling based on the Holm step-down procedure.
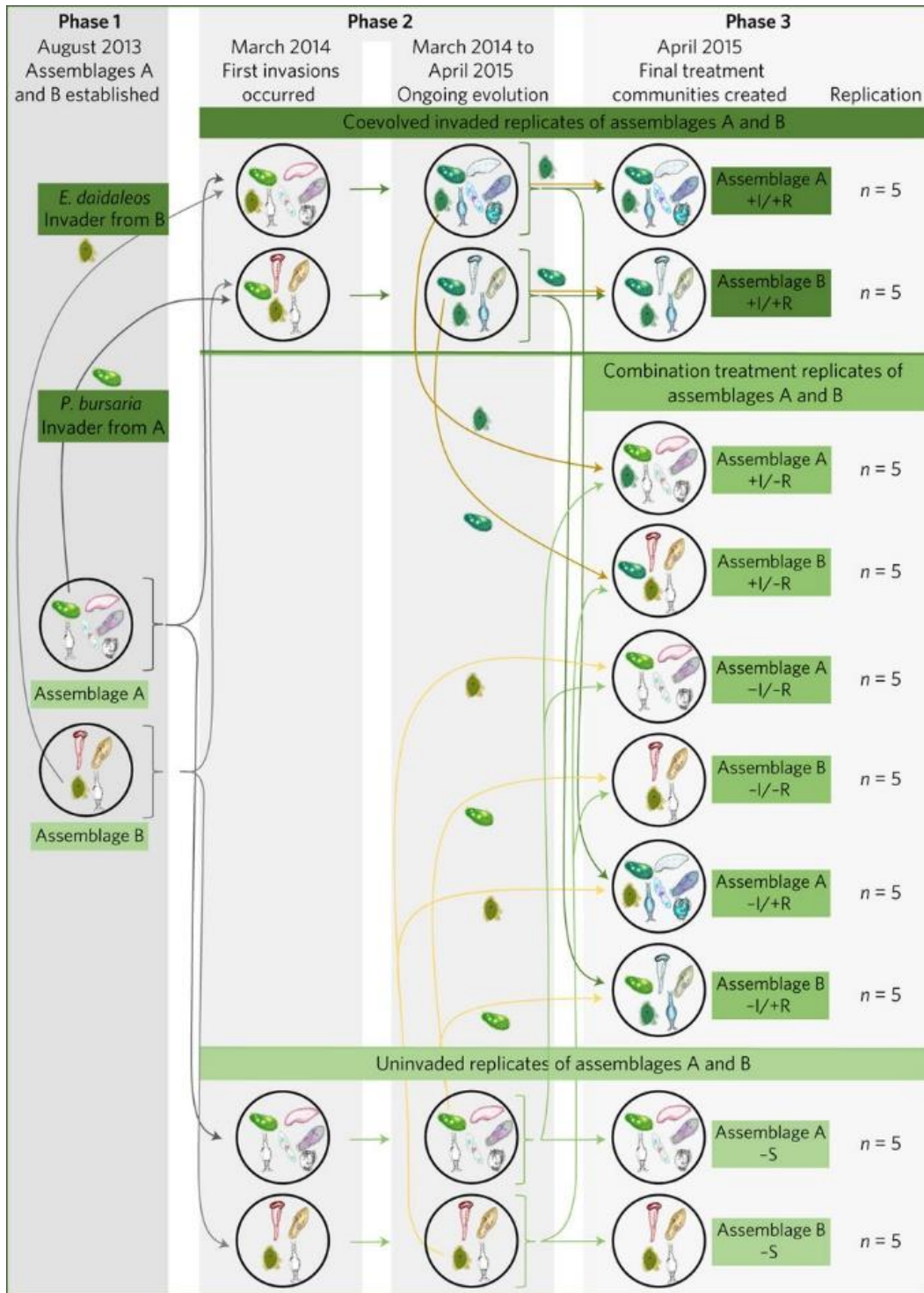
Figure S1. Experimental design implemented in three phases to develop lines of resident and invading species that differed in their evolutionary histories. Final experimental "test communities" paired invaders and residents that were either naïve or evolved in all possible combinations within each assemblage. See *Methods* for details. Figure originally published in Faillace & Morin (2016).
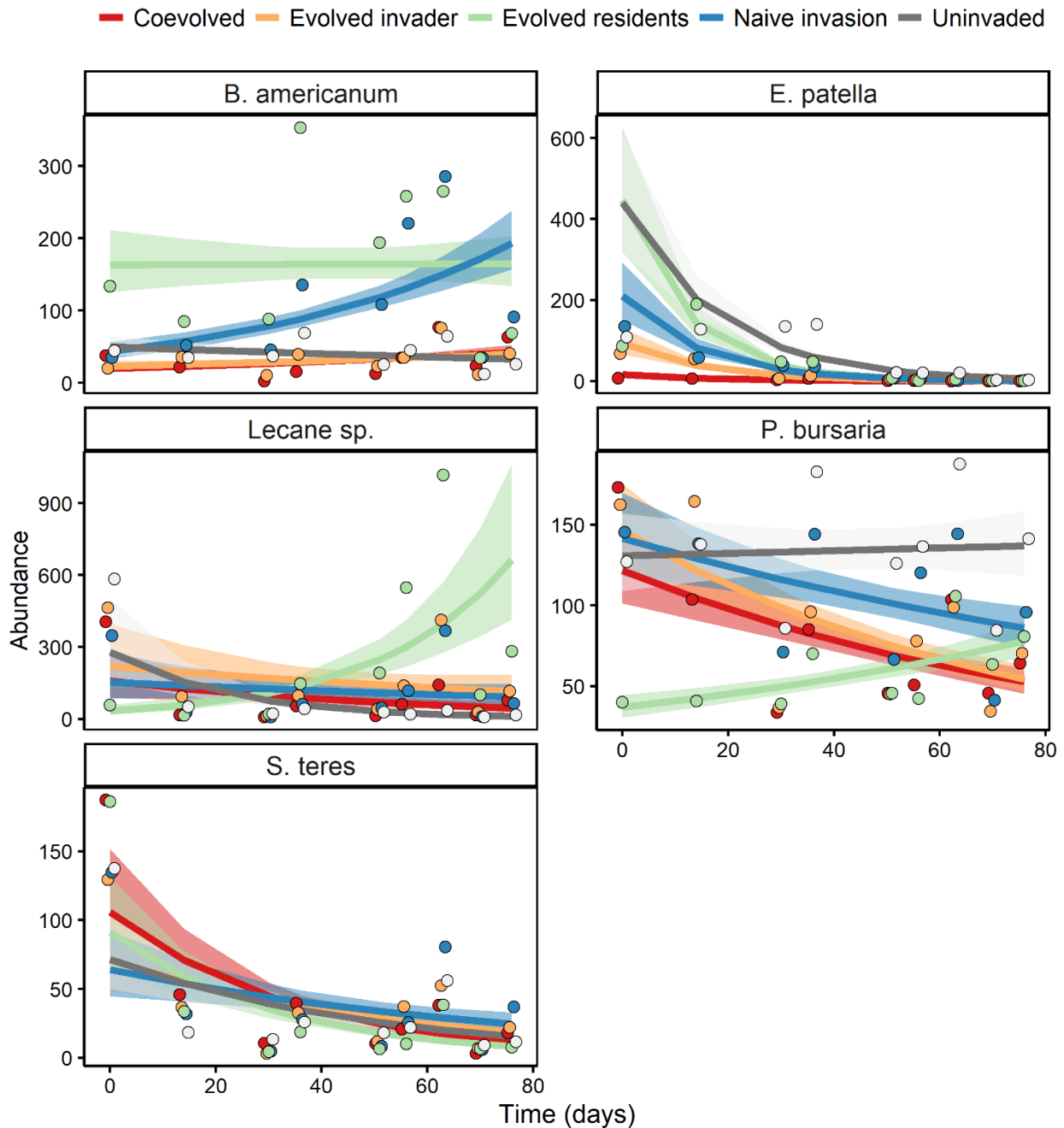
Figure S2. Coevolved and evolved invader communities converged over time in Assemblage A. Shown are the results of pairwise Mann-Kendall trend tests, which is used to teste for convergence between communities with different evolutionary histories. Within cells are Tau values, which indicate whether trajectories show signals of convergence (Tau < 0) or divergence (Tau > 0), and the fill of the cells correspond to Tau values, where red cells closer to -1, white cells are 0, and darker blue cells are closer to 1. Asterisks denote significant ($p < 0.05$) trends.

Figure S3. The effects of invasion on resident community trajectories from Assemblage A.
These analyses exclude the invader, *E. daidaleos*, because it is not present in the uninvaded
Assemblage A. Plotted are the community centroids and within these points numbers indicate the
sequential community survey events. Stress = 0.12.
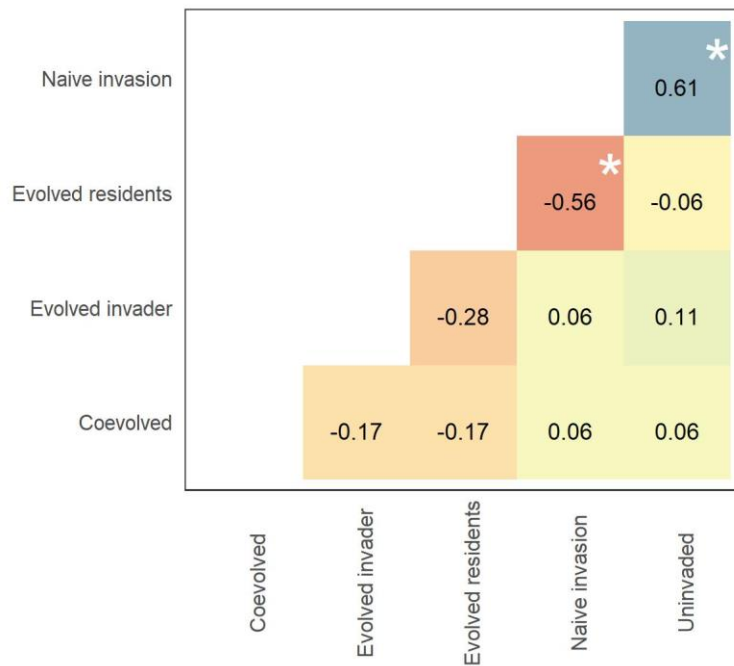
Figure S4. Uninvaded and naïve invasion resident communities diverged over time in Assemblage A. These analyses exclude the invader, *E. daidaleos*, because it is not present in the uninvaded Assemblage A. Shown are the results of pairwise Man-Kendell trend tests, which is used to test for convergence between communities during invasion. Within cells are Tau values, which indicate whether trajectories show signals of convergence (Tau < 0) or divergence (Tau > 0), and the fill of the cells correspond to Tau values, where red cells closer to -1, white cells are 0, and darker blue cells are closer to 1. Asterisks denote significant ($p < 0.05$) trends.

Figure S5. Population dynamics of resident species within Assemblage A comparing invaded assemblages to uninvaded assemblages. These analyses exclude the invader, *E. daidaleos*, because it is not present in the uninvaded Assemblage A. Plotted are the means and fitted line with standard error. Model estimates were back transformed from a negative binomial glm (points are jittered to help visualize the data).
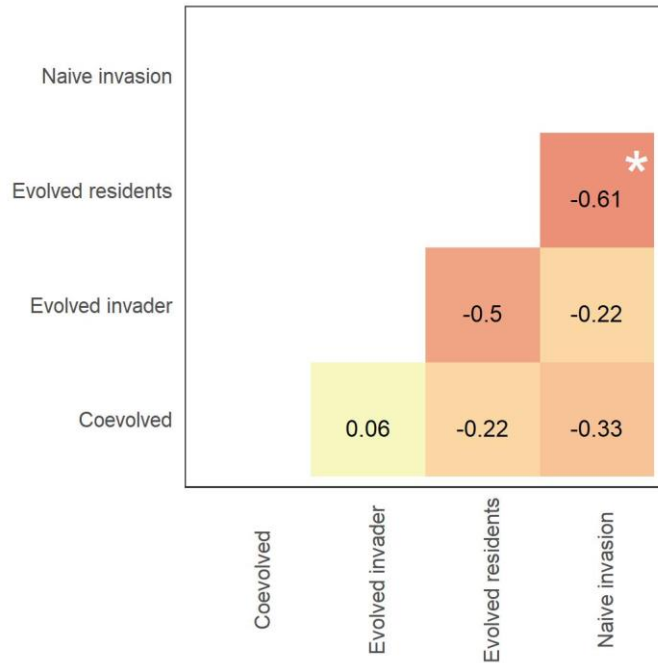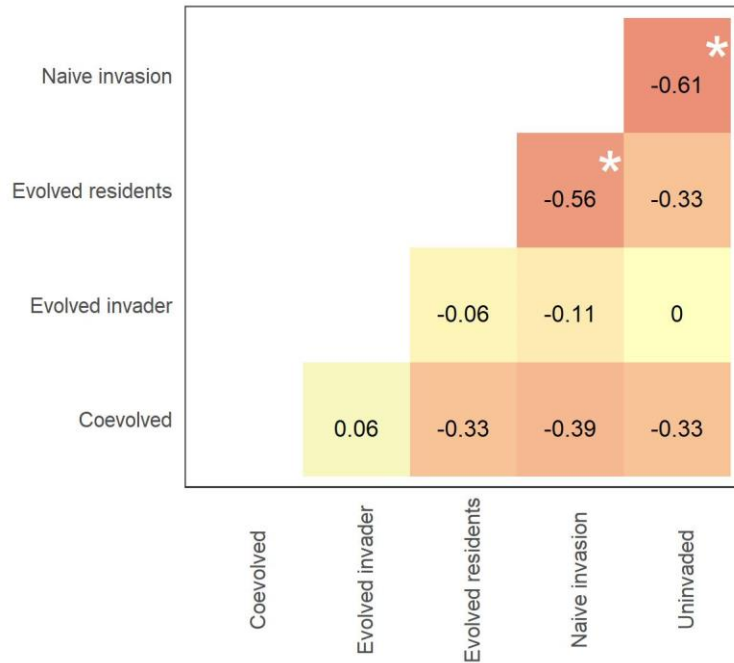
Figure S6. Evolved residents and naive invasion communities converged over time in Assemblage B. Shown are the results of pairwise Mann-Kendall trend tests, which is used to teste for convergence between communities with different evolutionary histories. Within cells are Tau values, which indicate whether trajectories show signals of convergence (Tau < 0) or divergence (Tau > 0), and the fill of the cells correspond to Tau values, where red cells closer to -1, white cells are 0, and darker blue cells are closer to 1. Asterisks denote significant ($p < 0.05$) trends.
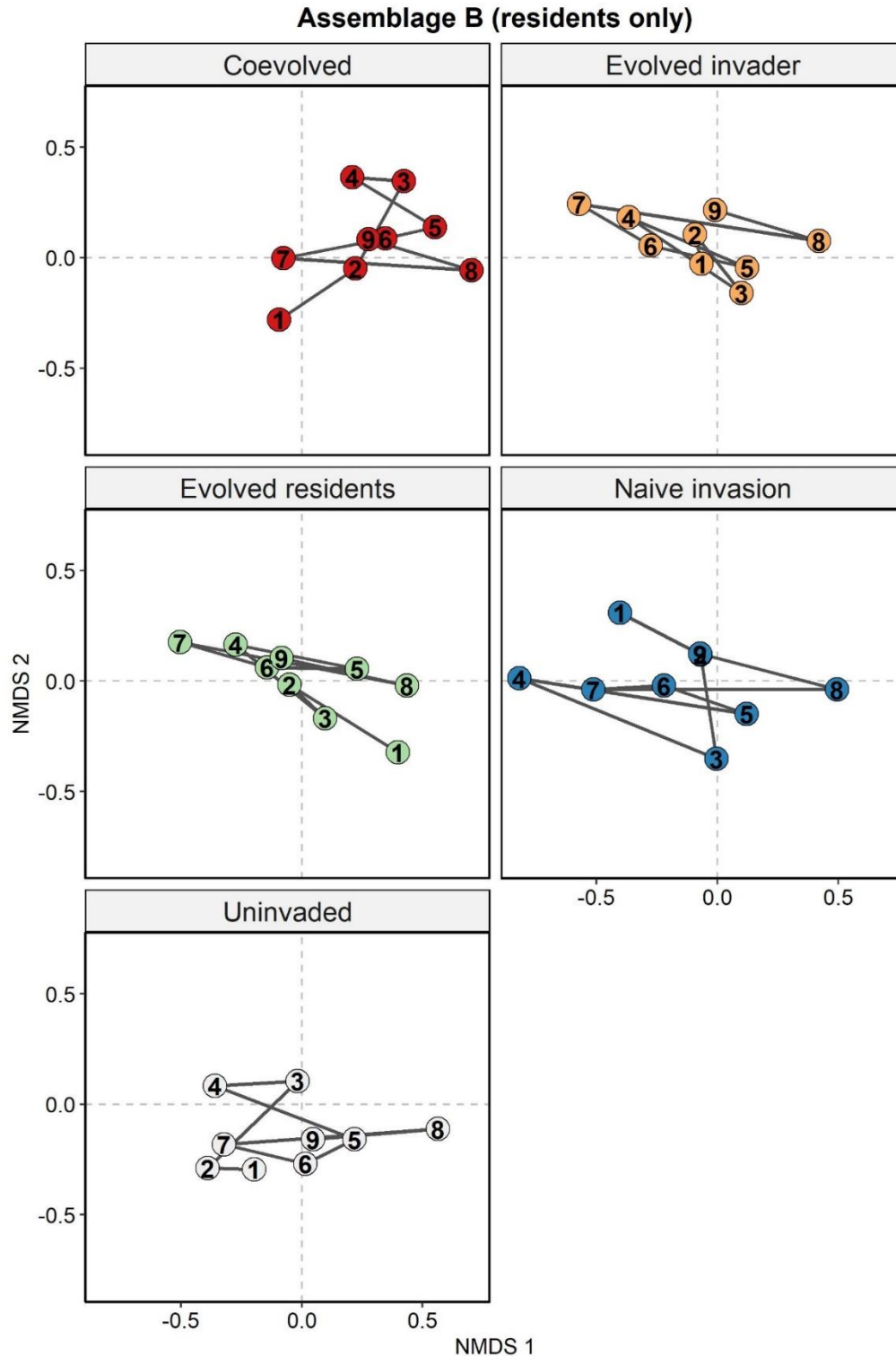
Figure S7. The effects of invasion on resident community trajectories from Assemblage B.
These analyses exclude the invader, *P. bursaria*, because it is not present in the uninvaded
Assemblage B. Plotted are the community centroids and within these points numbers indicate the
sequential community survey events. Stress = 0.12.

Figure S8. Uninvaded and naïve invasion resident communities converged over time in Assemblage B. These analyses exclude the invader, *P. bursaria*, because it is not present in the uninvaded Assemblage B. Shown are the results of pairwise Man-Kendell trend tests, which is used to test for convergence between communities during invasion. Within cells are Tau values, which indicate whether trajectories show signals of convergence (Tau < 0) or divergence (Tau > 0), and the fill of the cells correspond to Tau values, where red cells closer to -1, white cells are 0, and darker blue cells are closer to 1. Asterisks denote significant ($p < 0.05$) trends.
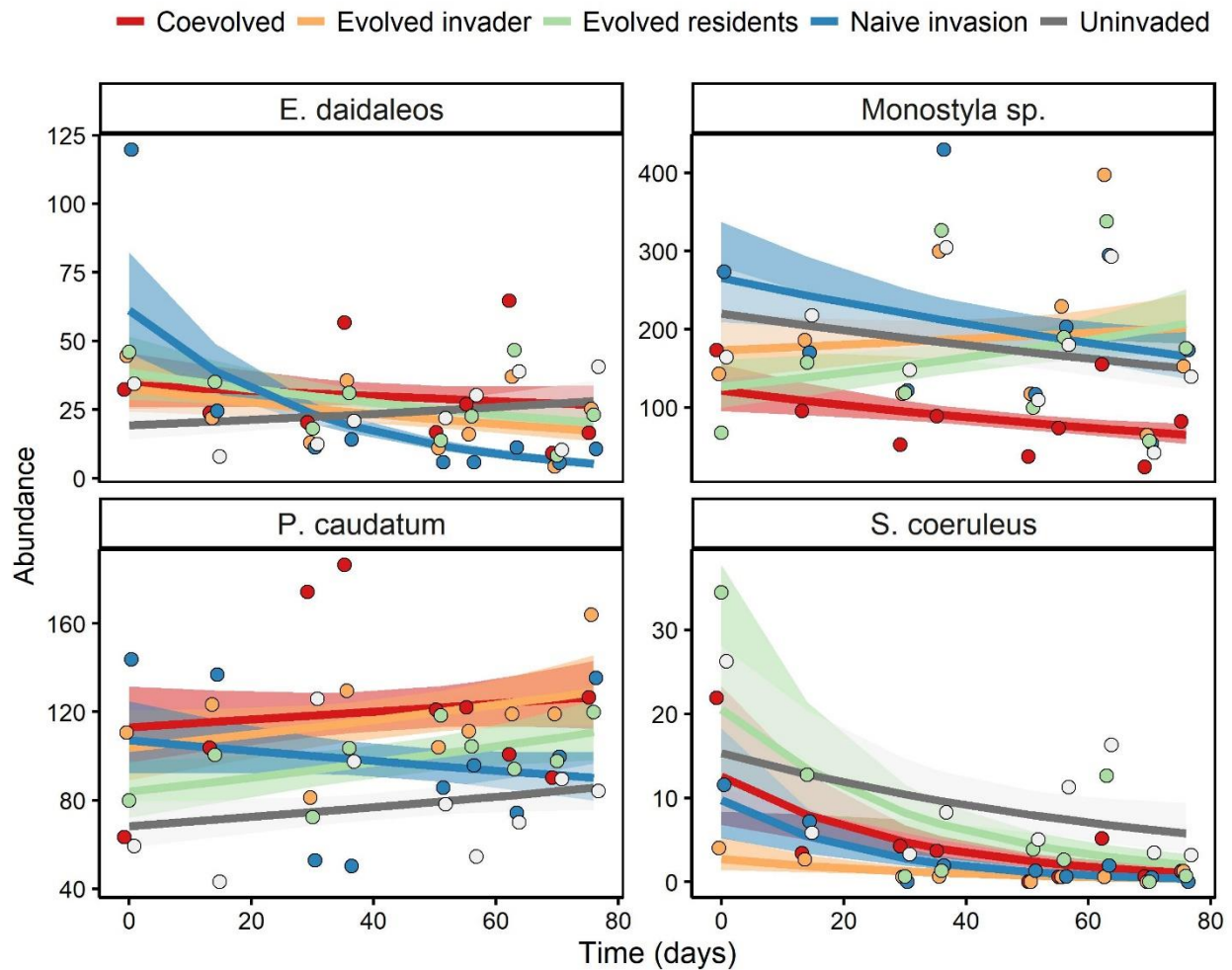
Figure S9. Population dyanmics of resident species within Assemblage B comparing invaded assemblages to uninvaded assemblages. These analyses exclude the invader, *P. bursaria*, because it is not present in the uninvaded Assemblage B. Plotted are the means and fitted line with standand error. Model estimates were back transformed from a negative binomial glm (points are jittered to help visualize the data).
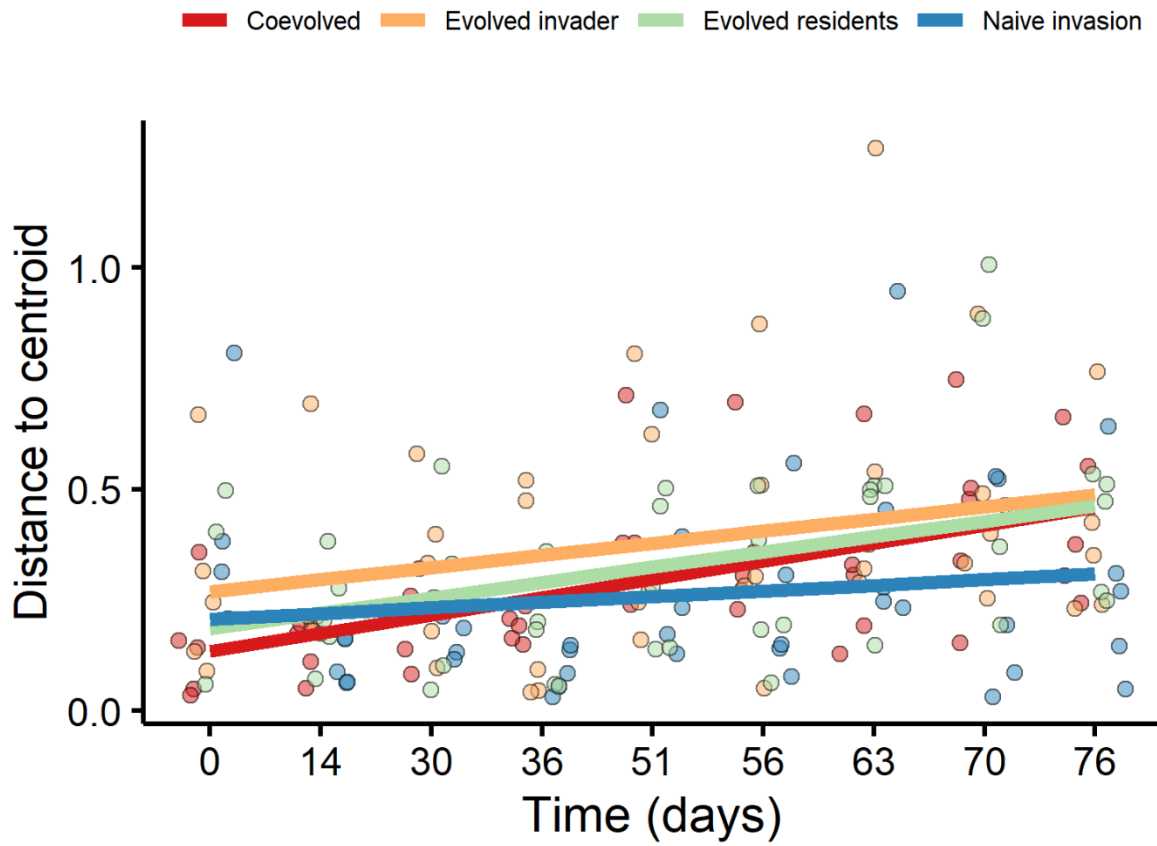
Figure S10. The distance to the community centroid increased over time among the invaded treatment groups in Assemblage A. Only the naïve invasion treatment group differed significantly from other treatments across time. Fitted lines are from the linear mixed effects model testing for drift, and points are the raw data (points are jittered to help visualize the data).
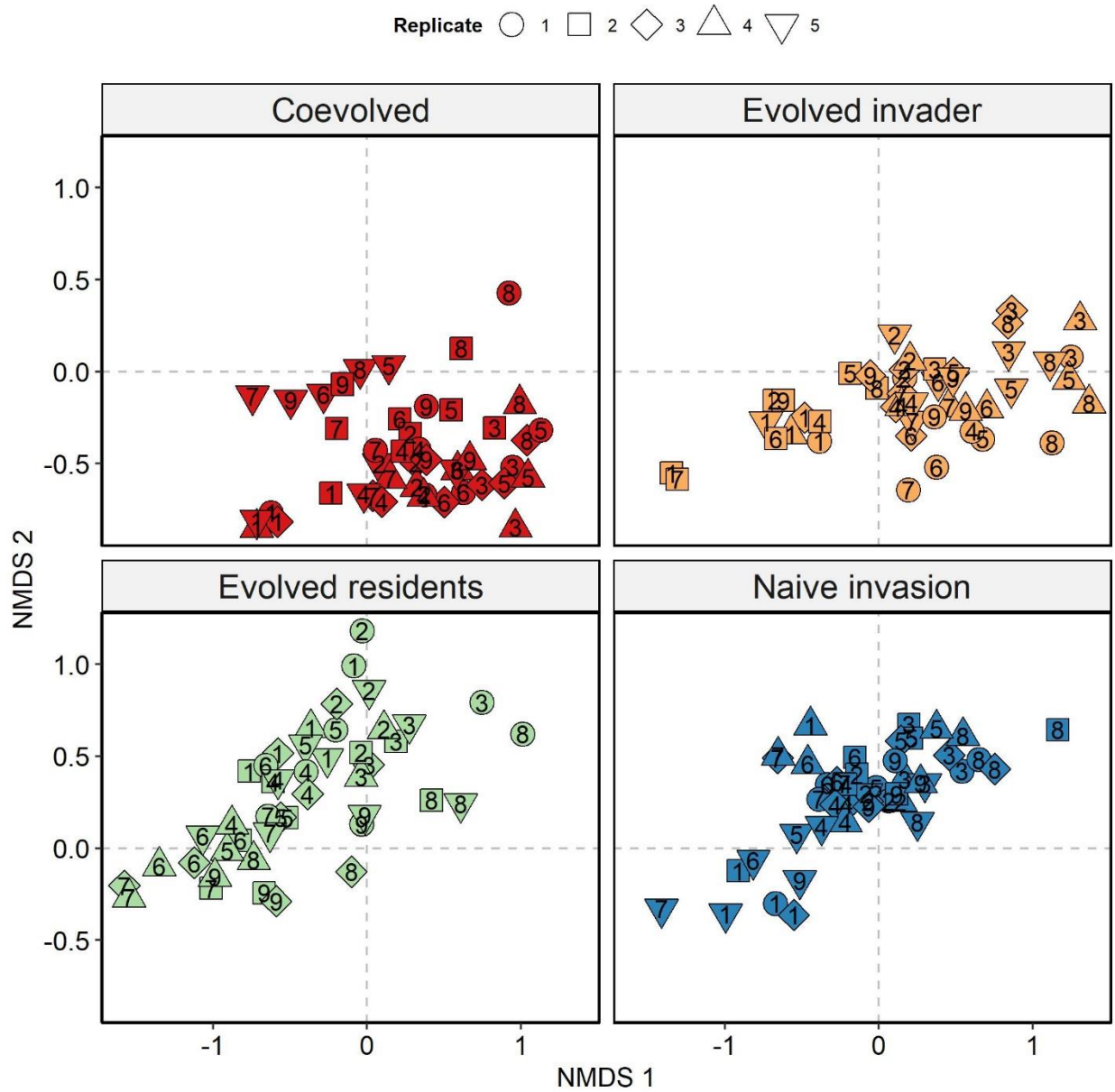
Figure S11. Within-group variation in invaded community structure increased over time in Assemblage A. Plotted are all data from the NMDS to show variation among the five replicates, which are represented by difference shapes. Numbers within shapes indicate the sequential survey.
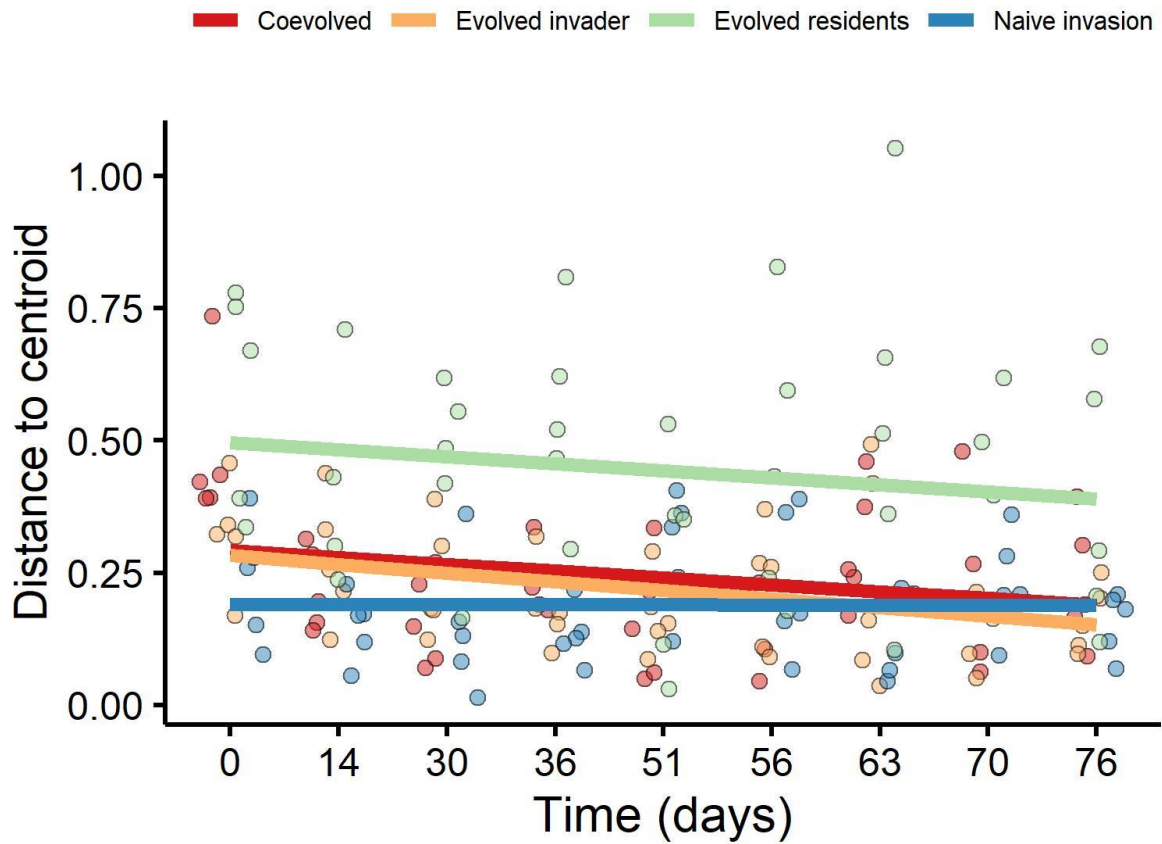
Figure S12. The distance to the community centroid slightly decreased over time among the invaded treatment groups in Assemblage B. There was no significant interaction between treatment and time, however the evolved residents treatment group had a greater overall distance to the centroid. Fitted lines are from the linear mixed effects model testing for drift, and points are the raw data (points are jittered to help visualize the data).
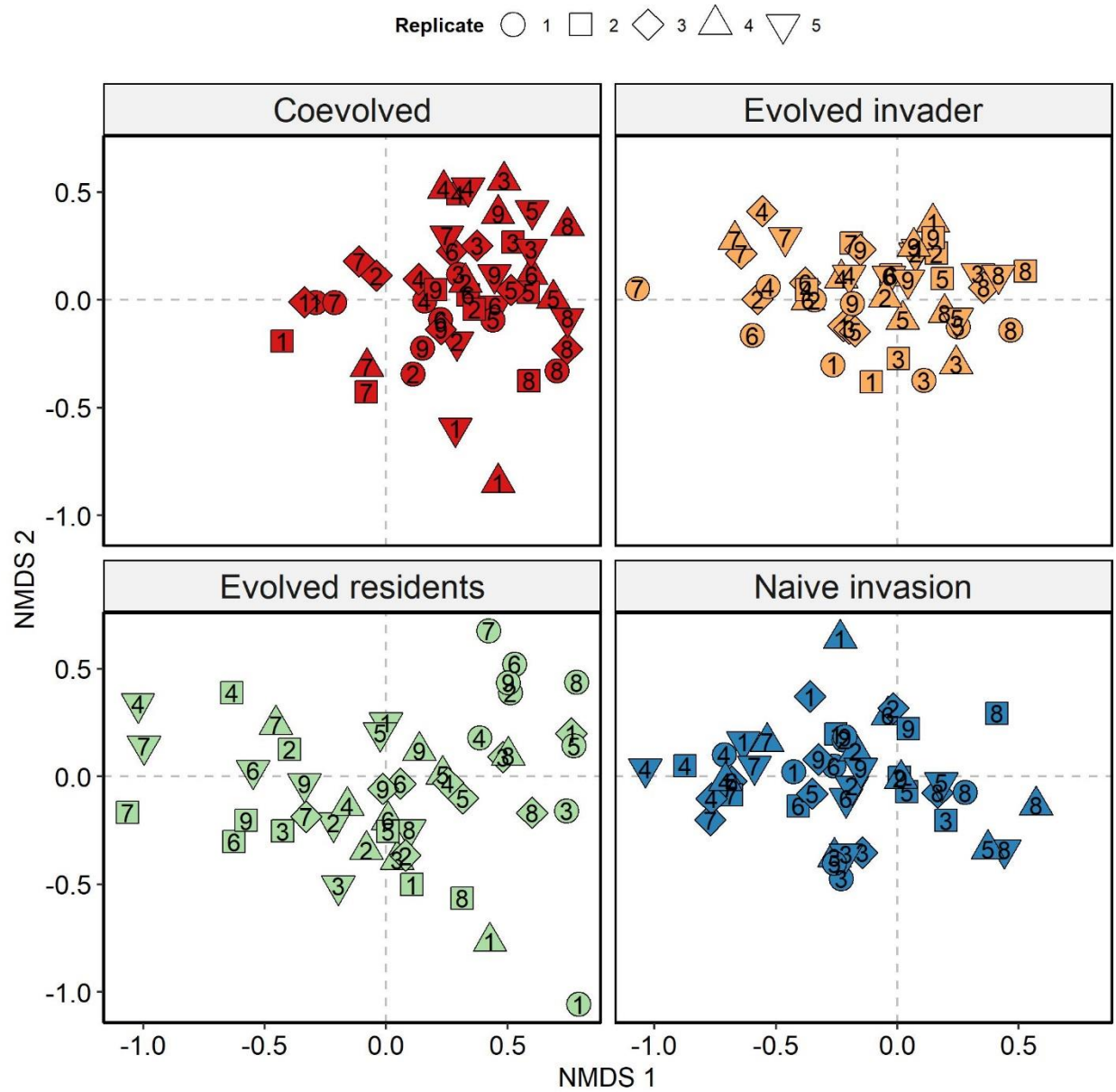
Figure S13. Within-group variation in invaded community structure slightly decreased over time in Assemblage B. Plotted are all data from the NMDS to show variation among the five replicates, which are represented by difference shapes. Numbers within shapes indicate the sequential survey.

References

Faillace, C. A., and P. J. Morin. 2016. Evolution alters the consequences of invasions in experimental communities. *Nature Ecology and Evolution* **1**:13.