

Appendix S2: Diversity-stability relationships across organism groups and ecosystem types become decoupled across spatial scales

Ecology

Nathan I. Wisnoski, Riley Andrade, Max C.N. Castorani, Christopher P. Catano, Aldo Compagnoni, Thomas Lamy, Nina K. Lany, Luca Marazzi, Sydne Record, Annie C. Smith, Christopher M. Swan, Jonathan D. Tonkin, Nicole M. Voelker, Phoebe L. Zarnetske, Eric R. Sokol

Table S1. Model summary of the local aggregate (CV) and compositional (BD) diversity-stability relationships. Random slope and intercept mixed effects models were fit using the lmer function in the “lmer” R package. Output table summary was produced with the R package “sjPlot”. In this table, the estimate and 95% confidence interval is given for each predictor (mean alpha diversity after a z-transformation) on each response variable (CV or BD). A negative estimate indicates a reduction in variability with increasing diversity. The random effects are given below, with σ^2 indicating the residual variance, τ_{00} indicating random intercept variance, τ_{11} indicating random slope variance, ρ_{01} indicating the correlation between slopes and intercepts, ICC the intraclass correlation, and N the number of groups.

<i>Predictors</i>	CV			BD		
	<i>Estimates</i>	<i>CI</i>	<i>p</i>	<i>Estimates</i>	<i>CI</i>	<i>p</i>
(Intercept)	0.60	0.50 – 0.69	< 0.001	0.32	0.26 – 0.37	< 0.001
alpha div scaled	-0.05	-0.08 – -0.02	0.002	-0.02	-0.05 – -0.00	0.039
Random Effects						
σ^2	0.03			0.01		
τ_{00}	0.07	dataset_id		0.02	dataset_id	
τ_{11}	0.01	dataset_id.alpha_div_scaled		0.00	dataset_id.alpha_div_scaled	
ρ_{01}	-0.59	dataset_id		-0.40	dataset_id	
ICC	0.71			0.72		
N	29	dataset_id		29	dataset_id	
Observations	584			584		
Marginal R ² / Conditional R ²	0.024 / 0.717			0.014 / 0.725		

Table S2. Coefficients for the linear mixed model of the local aggregate diversity-stability relationship. Here, the intercept and slopes correspond to the fixed effect plus the random effect of each group, obtained with the coef() function in R.

Dataset ID	Intercept	Mean Alpha Diversity (scaled)
and-birds	0.22402389	-0.006103547
and-plants-mtStHelens	0.90121119	-0.030895842
bes-birds	0.64977326	-0.082073687
cap-birds	0.63104234	-0.157175772
cap-herps	0.42194205	0.000937968
cdr-grasshopper	0.73907531	-0.004987137
cdr-plantsABC	0.3862034	-0.017064802
cdr-plantsD	0.51864412	-0.024425962
fce-diatoms	0.01816445	0.013168406
fce-fish-Dry	0.74734585	-0.089123884
fce-fish-Wet	0.52775738	-0.029303591
gce-mollusc	0.80825194	-0.112646837
hays-plants	0.6245243	-0.049913506
jrn-lizards	0.54287892	-0.037939616
jrn-plants	1.00035928	-0.055761381
knz-grasshopper	0.79481202	-0.026601719
luq-snails	0.61205346	-0.115781986
mcr-algae	0.14985487	0.009388656
mcr-coral	0.65119341	-0.078546012
mcr-inverts	0.75150279	-0.059605485
sbc-algae	0.51036334	0.009437481
sbc-fish	1.21782067	-0.219056433
sbc-mobileInverts	0.82438182	-0.122249277
sbc-sessileInverts	0.82035519	-0.179436657
sev-arthropods	0.33616782	0.021969435
sev-grasshopper	0.51828061	-0.008770527
sev-plants	0.58754196	-0.043256934
sgs-plants1	0.46817021	-0.009740707
sgs-plants2	0.30706487	0.007054431

Table S3. Coefficients for the linear mixed model of the local compositional diversity-stability relationship. Here, the intercept and slopes correspond to the fixed effect plus the random effect of each group, obtained with the coef() function in R.

Dataset ID	Intercept	Mean Alpha Diversity (Scaled)
and-birds	0.38482661	-0.003187734
and-plants-mtStHelens	0.3253404	-0.000496916
bes-birds	0.44817192	-0.051025983
cap-birds	0.41606154	-0.102250597
cap-herps	0.10415237	0.013095606
cdr-grasshopper	0.2592387	-0.00331466
cdr-plantsABC	0.23557281	0.033514739
cdr-plantsD	0.43699733	-0.015913117
fce-diatoms	0.15903012	0.039588751
fce-fish-Dry	0.39718547	-0.050954235
fce-fish-Wet	0.41151278	-0.02773841
gce-mollusc	0.22387868	-0.06546773
hays-plants	0.31067256	0.02332399
jrn-lizards	0.25168192	0.036548376
jrn-plants	0.65445948	-0.081737985
knz-grasshopper	0.24534254	0.016184735
luq-snails	0.21074656	-0.02695528
mcr-algae	0.09931118	0.006292797
mcr-coral	0.28833322	-0.07287956
mcr-inverts	0.11241025	0.009218919
sbc-algae	0.18742484	-0.008729085
sbc-fish	0.60498024	-0.105451021
sbc-mobileInverts	0.34312956	-0.114470305
sbc-sessileInverts	0.15286147	-0.069231581
sev-arthropods	0.69172029	-0.016116554
sev-grasshopper	0.28863034	-0.003785327
sev-plants	0.34014401	-0.022885733
sgs-plants1	0.31730765	0.001151806
sgs-plants2	0.26376718	-0.007482085

Table S4. Model summaries of the aggregate DSRs across spatial scales, where diversity is computed as richness. Models were fit using `stan_lmer()` from the “`rstanarm`” R package. Here, the 95% CI is the 95% Highest Density Interval (HDI), summarizing the densest region of the posterior containing 95% of the samples. Description of the various components of this table is the same as in Table S1.

<i>Predictors</i>	Regional (CV_gamma)		Regional (CV_gamma)		Regional (CV_gamma)		Spatial Synchrony (phi)		Local (CV_alpha)	
	<i>Estimates</i>	<i>CI (95%)</i>	<i>Estimates</i>	<i>CI (95%)</i>	<i>Estimates</i>	<i>CI (95%)</i>	<i>Estimates</i>	<i>CI (95%)</i>	<i>Estimates</i>	<i>CI (95%)</i>
Intercept	0.27	0.12 – 0.40	0.39	0.21 – 0.59	0.16	0.01 – 0.30	0.90	0.69 – 1.11	0.47	0.23 – 0.72
Mean Gamma-Diversity	-0.00	-0.01 – 0.00								
Mean Beta-Diversity			-0.06	-0.13 – -0.01			-0.12	-0.19 – -0.06		
Mean Alpha-Diversity					0.00	-0.01 – 0.02			-0.01	-0.03 – 0.01
Random Effects										
σ^2	0.04		0.03		0.03		0.03		0.10	
τ_{00}	0.00	<i>lter_site</i>	0.00	<i>lter_site</i>	0.00	<i>lter_site</i>	0.00	<i>lter_site</i>	0.00	<i>lter_site</i>
τ_{11}	0.00	<i>lter_site.gamma_div_mean</i>	0.00	<i>lter_site.beta_div_mean</i>	0.00	<i>lter_site.alpha_div_mean</i>	0.00	<i>lter_site.beta_div_mean</i>	0.00	<i>lter_site.alpha_div_mean</i>
ρ_{01}	-0.12	<i>lter_site</i>	-0.57	<i>lter_site</i>	-0.26	<i>lter_site</i>	-0.30	<i>lter_site</i>	-0.18	<i>lter_site</i>
ICC	0.10		0.11		0.26		0.21		0.16	
N	14	<i>lter_site</i>	14	<i>lter_site</i>	14	<i>lter_site</i>	14	<i>lter_site</i>	14	<i>lter_site</i>
Observations	29		29		29		29		29	
Marginal R ² / Conditional R ²	0.042 / 0.138		0.149 / 0.246		0.015 / 0.273		0.333 / 0.471		0.019 / 0.172	

Table S5. Table depicting the model results for compositional DSRs across scales, where diversity is computed as richness. Table description follows Table S4.

<i>Predictors</i>	Regional (BD_gamma)		Regional (BD_gamma)		Regional (BD_gamma)		Spatial Synchrony (BD_phi)		Local (BD_alpha)	
	<i>Estimates</i>	<i>CI (95%)</i>	<i>Estimates</i>	<i>CI (95%)</i>	<i>Estimates</i>	<i>CI (95%)</i>	<i>Estimates</i>	<i>CI (95%)</i>	<i>Estimates</i>	<i>CI (95%)</i>
Intercept	0.11	0.01 – 0.20	0.20	0.05 – 0.35	0.07	- 0.02 – 0.17	0.81	0.63 – 0.99	0.24	0.12 – 0.37
Mean Gamma-Diversity	0.00	-0.00 – 0.00								
Mean Beta-Diversity			-0.01	-0.06 – 0.03			-0.09	-0.15 – -0.03		
Mean Alpha-Diversity					0.01	-0.00 – 0.02			0.00	-0.01 – 0.01
Random Effects										
σ^2	0.01		0.02		0.01		0.02		0.02	
τ_{00}	0.00	<i>lter_site</i>	0.00	<i>lter_site</i>	0.00	<i>lter_site</i>	0.00	<i>lter_site</i>	0.00	<i>lter_site</i>
τ_{11}	0.00	<i>lter_site.gamma_div_mean</i>	0.00	<i>lter_site.beta_div_mean</i>	0.00	<i>lter_site.alpha_div_mean</i>	0.00	<i>lter_site.beta_div_mean</i>	0.00	<i>lter_site.alpha_div_mean</i>
ρ_{01}	-0.13	<i>lter_site</i>	-0.30	<i>lter_site</i>	-0.21	<i>lter_site</i>	-0.27	<i>lter_site</i>	-0.23	<i>lter_site</i>
ICC	0.32		0.19		0.23		0.43		0.18	
N	14	<i>lter_site</i>	14	<i>lter_site</i>	14	<i>lter_site</i>	14	<i>lter_site</i>	14	<i>lter_site</i>
Observations	29		29		29		29		29	
Marginal R ² / Conditional R ²	0.039 / 0.349		0.013 / 0.200		0.134 / 0.331		0.270 / 0.581		0.028 / 0.201	

Table S6. Model summaries of the aggregate DSRs across spatial scales, where diversity is computed as the effective number of species with $q=2$, corresponding to the Simpson index. Table description follows Table S4. Compared to richness ($q=0$), Simpson's index is less influenced by rare species and instead says more about the number of dominant species in the community. Interestingly, compared to aggregate DSRs estimated with richness (Table S4), here we find a stronger negative relationship between β -diversity and aggregate spatial synchrony, but a weaker relationship between β -diversity and regional variability.

<i>Predictors</i>	Regional (CV_gamma)		Regional (CV_gamma)		Regional (CV_gamma)		Spatial Synchrony (phi)		Local (CV_alpha)	
	<i>Estimates</i>	<i>CI (95%)</i>	<i>Estimates</i>	<i>CI (95%)</i>	<i>Estimates</i>	<i>CI (95%)</i>	<i>Estimates</i>	<i>CI (95%)</i>	<i>Estimates</i>	<i>CI (95%)</i>
Intercept	0.21	0.09 – 0.34	0.24	0.01 – 0.48	0.19	0.05 – 0.33	0.87	0.61 – 1.13	0.46	0.22 – 0.68
Mean Gamma-Diversity	-0.00	-0.02 – 0.01								
Mean Beta-Diversity			-0.03	-0.18 – 0.12			-0.23	-0.40 – -0.07		
Mean Alpha-Diversity					0.00	-0.03 – 0.03			-0.01	-0.06 – 0.04
Random Effects										
σ^2	0.04		0.04		0.04		0.04		0.10	
τ_{00}	0.00	<i>lter_site</i>	0.00	<i>lter_site</i>	0.00	<i>lter_site</i>	0.01	<i>lter_site</i>	0.00	<i>lter_site</i>
τ_{11}	0.00	<i>lter_site.gamma_div_mean</i>	0.00	<i>lter_site.beta_div_mean</i>	0.00	<i>lter_site.alpha_div_mean</i>	0.00	<i>lter_site.beta_div_mean</i>	0.00	<i>lter_site.alpha_div_mean</i>
ρ_{01}	-0.19	<i>lter_site</i>	-0.58	<i>lter_site</i>	-0.27	<i>lter_site</i>	-0.49	<i>lter_site</i>	-0.25	<i>lter_site</i>
ICC	0.10		0.08		0.13		0.22		0.16	
N	14	<i>lter_site</i>	14	<i>lter_site</i>	14	<i>lter_site</i>	14	<i>lter_site</i>	14	<i>lter_site</i>
Observations	29		29		29		29		29	
Marginal R ² / Conditional R ²	0.005 / 0.100		0.007 / 0.087		0.000 / 0.129		0.205 / 0.381		0.017 / 0.172	

Table S7. Model summaries of the compositional DSRs across spatial scales, where diversity is computed as the effective number of species with $q=2$, corresponding to the Simpson index. Table description follows Table S4. Compared to richness ($q=0$), Simpson's index is less influenced by rare species and instead says more about the number of dominant species in the community. Compared to compositional DSRs estimated with richness (Table S5), here we find a weaker relationship between β -diversity and compositional spatial synchrony, suggesting compositional spatial synchrony may be influenced by rare species. But we found positive relationships for compositional metacommunity variability with α -, β -, and γ -diversity. This suggests the number of dominant species, and their turnover across space, may be important contributors to regional fluctuations in metacommunity composition.

<i>Predictors</i>	Regional (BD_gamma)		Regional (BD_gamma)		Regional (BD_gamma)		Spatial Synchrony (BD_phi)		Local (BD_alpha)	
	<i>Estimates</i>	<i>CI (95%)</i>	<i>Estimates</i>	<i>CI (95%)</i>	<i>Estimates</i>	<i>CI (95%)</i>	<i>Estimates</i>	<i>CI (95%)</i>	<i>Estimates</i>	<i>CI (95%)</i>
Intercept	0.02	-0.04 – 0.07	-0.03	-0.18 – 0.12	0.03	-0.07 – 0.12	0.49	0.26 – 0.77	0.14	-0.00 – 0.23
Mean Gamma-Diversity	0.02	0.01 – 0.04								
Mean Beta-Diversity			0.13	0.02 – 0.23			0.01	-0.18 – 0.19		
Mean Alpha-Diversity					0.03	0.01 – 0.06			0.04	0.02 – 0.08
Random Effects										
σ^2	0.00		0.01		0.01		0.02		0.02	
τ_{00}	0.00	<i>lter_site</i>	0.00	<i>lter_site</i>	0.00	<i>lter_site</i>	0.03	<i>lter_site</i>	0.00	<i>lter_site</i>
τ_{11}	0.00	<i>lter_site.gamma_div_mean</i>	0.00	<i>lter_site.beta_div_mean</i>	0.00	<i>lter_site.alpha_div_mean</i>	0.02	<i>lter_site.beta_div_mean</i>	0.00	<i>lter_site.alpha_div_mean</i>
ρ_{01}	-0.64	<i>lter_site</i>	-0.43	<i>lter_site</i>	-0.38	<i>lter_site</i>	-0.67	<i>lter_site</i>	-0.32	<i>lter_site</i>
ICC	0.86		0.34		0.53		0.63		0.31	
N	14	<i>lter_site</i>	14	<i>lter_site</i>	14	<i>lter_site</i>	14	<i>lter_site</i>	14	<i>lter_site</i>
Observations	29		29		29		29		29	
Marginal R ² / Conditional R ²	0.393 / 0.916		0.176 / 0.454		0.282 / 0.663		0.001 / 0.631		0.341 / 0.547	

Figure S1. Partitions of metacommunity variability into spatial synchrony and local variability components for both aggregate and compositional properties, organized broadly by taxonomic group.

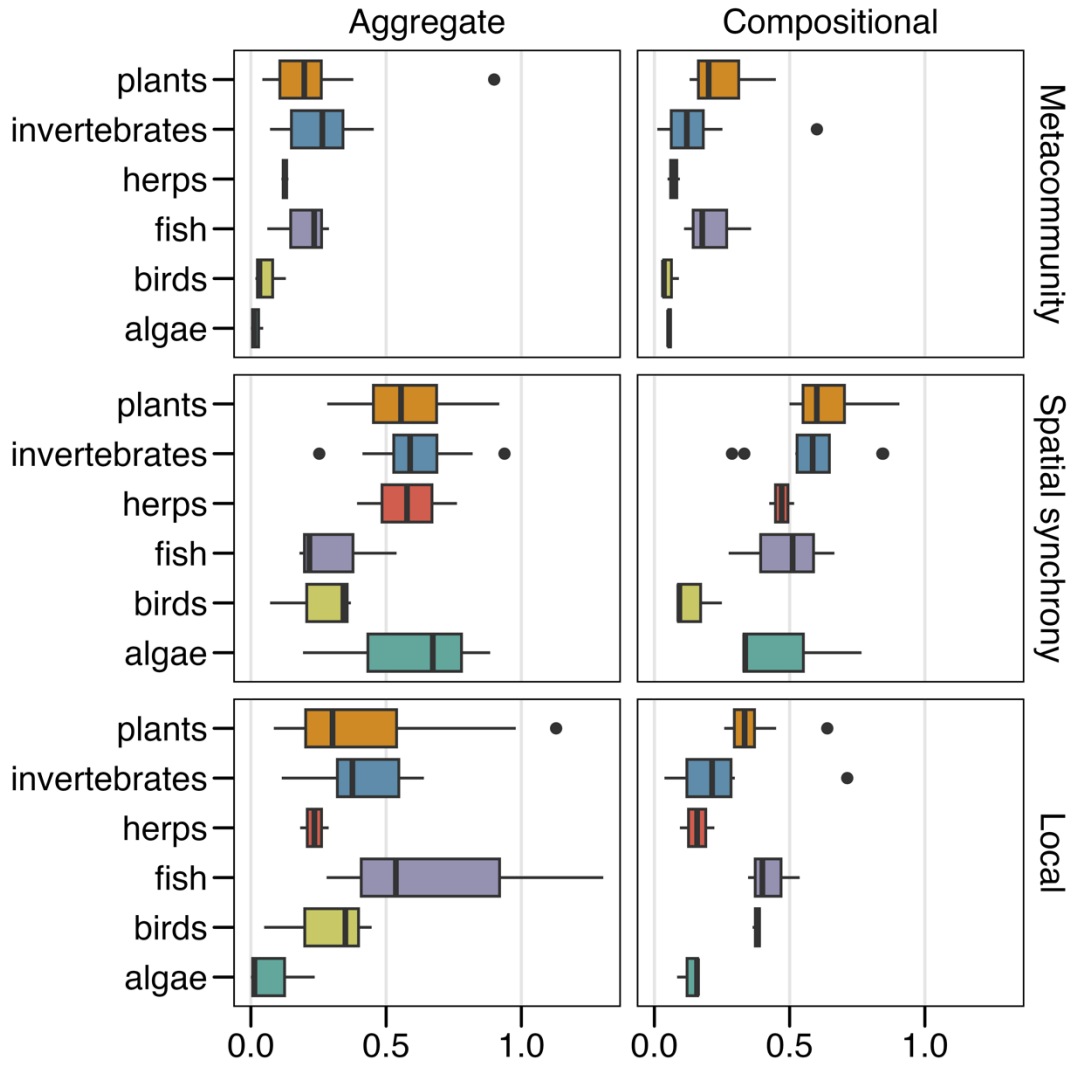


Figure S2. Observed variability at the metacommunity and local scales, as well as spatial synchrony, for both the aggregate and compositional properties of each dataset.

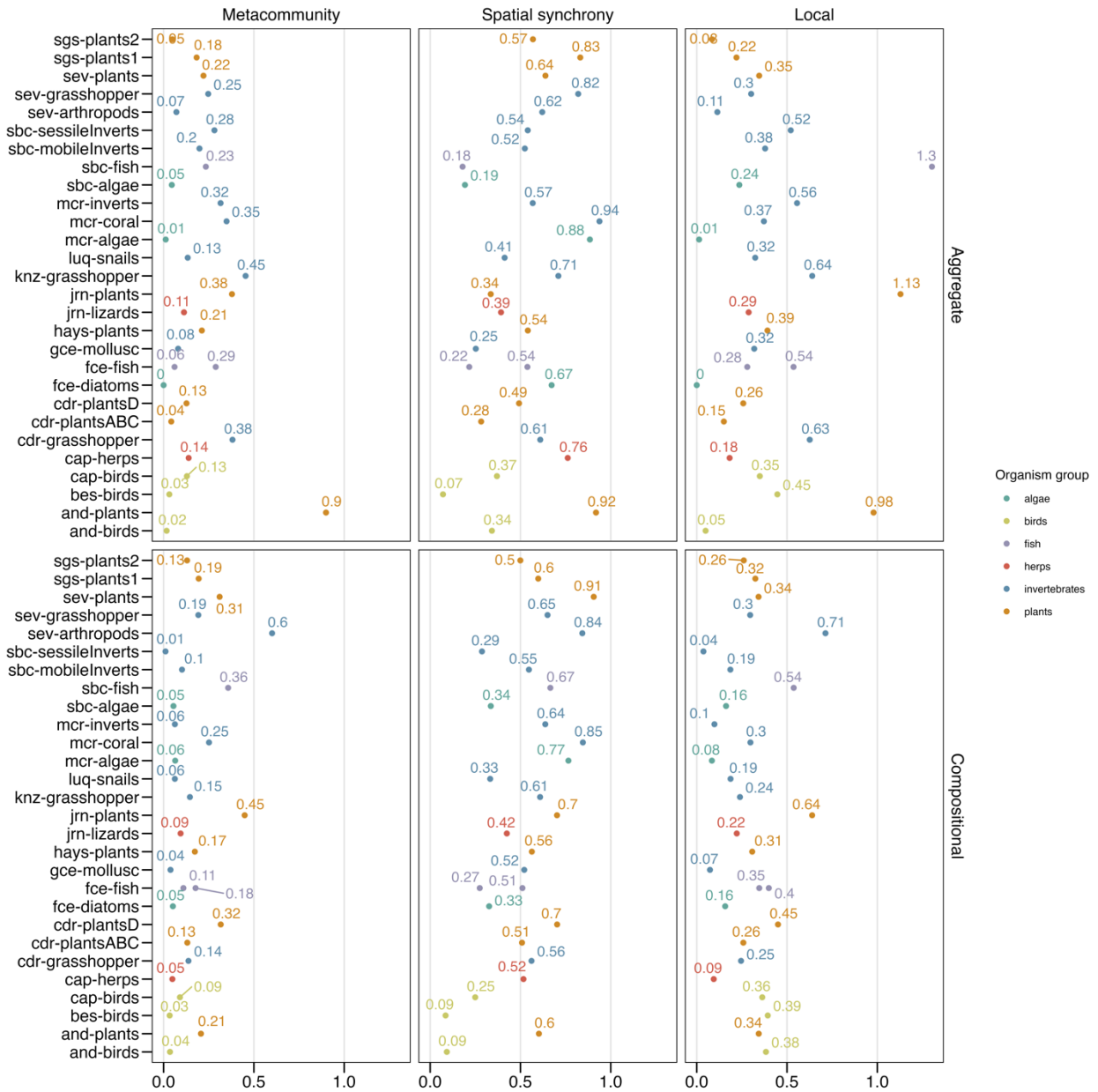


Figure S3. Full SEM showing all paths tested. Note here that non-significant paths are indicated by dashed lines (in contrast to the main text figure, where dashed lines are additional visual element to distinguish positive from negative effects when printed in black and white). Positive effects are in blue and negative effects are in red. For visual ease, we pruned the nonsignificant paths for the figure in the main text, Figure 4.

