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Appendix 1

Methods: a description of the *Sequential assembly model* used by Säterberg et al. (2013) to generate model food web structures and parameterize a dynamical model of the systems.

Table A1. Comparison of model food web properties with those of nine real food webs.

Table A2. Statistical analysis of differences in dynamical robustness to primary species extinctions (R_{50}) between deletion sequences.

Table A3. Statistical analysis of differences in topological robustness to primary species extinctions (R_{50}) between deletion sequences.

Table A4. Correlation between dynamical robustness to primary species extinctions (R_{50}) of different deletion sequences.

Table A5. Correlation between topological robustness to primary species extinctions (R_{50}) of different deletion sequences.

Figure A1. Snapshots of food web structure during four stages of food web disassembly.

Figure A2. Relationship between dynamical and topological robustness in sequences where basal species could be deleted.

Figure A3. Relationship between dynamical and topological robustness in sequences where basal species could not be deleted.

Figure A4. Robustness to secondary extinctions, as measured by $1 - A_E$

Methods

Sequential assembly of model food webs

Model food webs used in the sensitivity analysis were generated through a dynamic, sequential assembly process (Lewis and Law 2007, Säterberg et al. 2013). Using this approach, the resulting network topology is an outcome of the dynamical assembly process rather than pre-set before adding dynamics (as would be the case if we were to use for example the niche model algorithm to generate food webs).

Prey preferences

A truncated Gaussian function was used to describe prey preferences (z'_{ij}) for consumers (Lewis and Law 2007) and thus establish who eats whom in the growing trophic network:

$$z'_{ij} = \frac{1}{\gamma\sqrt{2\pi}} \exp\left[-\frac{1}{2}\left[\frac{\log(\beta m_i / m_j)}{\gamma} \right]^2 \right]$$
$$for \quad m_i \langle m_j \quad and \quad -\delta\gamma \le \log\left(\beta \frac{m_i}{m_j} \right) \le \delta\gamma \qquad (1)$$

Consumer *j*'s preference for prey *i*, z'_{ij}, is determined by three parameters: β, the optimal consumer-resource body mass ratio for a consumer – for herbivores a β-value that reflects a most preferred prey size within the basal species body mass interval ($\beta = m_j/m_i, m_i \in 10^{[-15-9]}$) and for carnivores a value within the range of what has been observed empirically for non-herbivorous consumers (Table A1; Brose et al. 2006); γ , the standard deviation of the preference function, and δ, the number of standard deviations from the optimum log prey size at which a consumer no longer feeds on a prey (i.e. the truncation point on the preference curve). Finally, consumer preferences were normalized by the sum of preferences, giving: $z_{ij} = z'_{ij} \Big/ \sum_i z'_{ij}$. Relative preferences z_{ij} were used to describe the amount of biomass extracted from prey *i* by consumer *j* (see below).

Community dynamics and model parameters

Community dynamics was described by a generalized Lotka–Volterra model (Case 2000):

$$\frac{dN_i}{dt} = N_i(r_i + \sum_{j=1}^{n} \alpha_{ij} N_j) \qquad (2)$$

Here N_i is the number of individuals of species *i* in a community with *n* species, r_i is a species intrinsic growth (if *i* is a basal species) or mortality rate (if *i* is a consumer species), α_{ij} is the per

capita effect of species *j* on the per capita growth (or mortality) rate of species *i*. Depending on species identities α_{ij} describes different types of interactions: if *i* and *j* both are primary producer species, α_{ij} describes inter-specific competition; if species *i* is a resource species and species *j* one of its consumers α_{ij} is negative and if species *i* is a consumer species and species *j* its resource α_{ij} is positive. All parameters, except the strength of inter-specific competition, were related to species average body masses (Blueweiss 1978, Peters 1983, Brown 2004, McCoy and Gillooly 2008, Berg et al. 2011). Intrinsic growth and mortality rates, *r*, were related to body mass, *m*, according to $r_i = C_r m_i^{-1/4}$. Here r_i and C_r are positive for primary producer species (Blueweiss 1978) and negative for consumer species (McCoy and Gillooly 2008). For two primary producer species, α_{ij} describes inter-specific competition and is drawn from the uniform interval [-10^{-10} 0]. Intra-specific competition (α_{ii}) (self-limitation) is included for all species and was in consumer species related to body mass as in two earlier theoretical studies (Virgo et al. 2006, Lewis and Law 2007); $\alpha_{ii} = C_{\alpha i i} m_i^{-1/4}$ (with $C_{\alpha i i} = -1.0 \times 10^{-12}$). Intra-specific competition among basal species was set to give equilibrium abundances, in the absence of inter-specific interactions, that reflect scaling observed for phytoplankton in a meta-analysis (Cermeno et al. 2006); $\alpha_{ii} = C_{\alpha i i} m_i^{0.5}$ (with $C_{\alpha i i} = -0.001$).

For consumer–resource interactions, per capita prey–predator interaction strengths (the α_{ij}*'s*) are estimated using metabolic theory that relates the feeding requirements of individuals allometrically to body size *(m_i)* (O'Gorman et al. 2010, Berg et al. 2011). More specifically, the per capita effect of the consumer on the prey was calculated by relating Lotka–Volterra interaction parameters to individual consumers feeding rates, assuming that the feeding rate (kg / (individual × day)) can be related to a species body mass as (Peters 1983); $F_j = C_F m_j^{3/4}$ where F_j represents the biomass consumed by an individual consumer of body mass m_j, per unit of time. Multiplying this expression with the species' relative preference for a specific prey *i*, z_{ij}, gives the expected amount of biomass extracted from a specific resource *i* per unit of time: $F_{ij} = z_{ij} C_F m_j^{3/4}$. Further, dividing this expression with the body mass of the prey, m_i, gives f_{ij}, the total number of individuals of population *i* consumed by one individual of species *j* (in Lotka–Volterra terms this represents $\alpha_{ij} N_i$). Thus, $\alpha_{ij} N_i = f_{ij} = F_{ij} / m_i$. To get an expression for α_{ij} we simply divide with the density of species *i*, which is assumed to be allometrically related to species body mass within a trophic level ($N_i = C_{n_i} m_i^{-3/4}$) (Brown 2004), thus giving:

$$\alpha_{ij} = C_{\alpha_{ij}} z_{ij} \frac{m_j^{3/4}}{m_i^{1/4}}$$

Here $C_{\alpha_{ij}}$ is a dimensionless scaling constant determining the magnitude of consumer-resource interactions, z_{ij} is consumer *j*:s relative preference for species *i*, and m_j and m_i are the body masses of consumer species *j* and resource species *i*, respectively. Prey-preferences (i.e. the diet composition of consumers) are estimated using prey–predator body size ratios (see above). Finally, the per capita effect of resources on their consumers (i.e. α_{ij} with *i* being a consumer and *j* its resource species) was given by $\alpha_{ij} = -e\alpha_{ji} * m_j / m_i$, where *e* is the conversion efficiency with which prey are converted into new predators, here set to 0.1.

The sequential assembly process

Sequential assembly of model communities involved the following steps (see Säterberg et al. 2013 for full details): 1) the assembly was initiated with a feasible (all species having positive equilibrium densities) and locally asymptotic stable equilibrium system, consisting of seven competing primary producer species with body masses randomly drawn from an interval; 2) a new species, randomly drawn (with equal probability) from one of the trophic groups: primary producers, herbivores or carnivore species, with a body mass drawn from an associated interval, was introduced into the food web. If this species was a consumer, all species in the existing community with body masses falling within its diet breadth (determined by parameters β, γ and δ) were fed upon. The newly introduced species was also consumed by all consumer species present, with a diet breadth covering the new species body mass. Preference values (Eq. 1) were calculated both for the newly introduced species and recalculated for species with diet breadths covering the introduced species; 3) the equilibrium of the new system was checked for feasibility and local asymptotic stability. If the new system fulfilled these criteria, the augmented system was kept and a new species was introduced. If the new system did not fulfill the stability criteria the recently added species was discarded and a new species was introduced to the pre-invaded system and checked for stability again; 4) the assembly continued until the system contained 50 species or 10 000 introduction attempts had been performed. If the system did not acquire 50 species within the 10 000 attempts it was discarded and a new system was initiated. A new primary producer species was never allowed to invade the system when the fraction of primary producer species in the whole web was greater than 25 % in order to avoid systems dominated by primary producers. Furthermore, all final systems with a connectance lower than 0.06 and/or a fraction of top-species (species with no consumers) larger than 15% were discarded due to lack of empirical support for such food webs

(Williams and Martinez 2000, Dunne et al. 2004). 100 food webs fulfilling these criteria were kept for further analysis.

Table A1. Summary of food web properties in nine aquatic food-webs and the average value of these properties for the empirical and assembled food webs. Bold numbers indicate mean values of model food webs that are within one standard deviation around the mean of empirical data. Empirical data come from four studies (Williams et al. 2002, Dunne et al. 2004, Williams and Martinez 2004).

	Aquatic food-webs									Emp. Webs		Ass. Webs	
Prop.	Skipwith Pond	Little Rock Lake	Bridge Brook Lake	Chesapeake Bay	Ythan estaury	Benguela	Carribean Reef. small	NE US Shelf	Carribean Reef. large	Mean	SD	Mean	SD
S	25	92	25	31	78	29	50	79	245	72.67	69.68	**50**	0
L/S	7.9	10.8	4.3	2.2	4.8	7	11.1	17.8	13.8	8.86	4.99	**8.22**	1.6
L/S^2	0.32	0.12	0.17	0.072	0.061	0.24	0.22	0.22	0.05	0.16	0.09	**0.11**	0.01
T	0.04	0.011	0	0.32	0.37	0	0	0.04	0	0.09	0.15	**0.07**	0.04
I	0.92	0.86	0.68	0.52	0.54	0.93	0.94	0.94	0.98	0.81	0.18	**0.72**	0.05
B	0.04	0.13	0.32	0.16	0.09	0.07	0.06	0.42	0.04	0.15	0.13	**0.21**	0.03
SD_Gen	0.92	1.42	1.09	0.78	1.14	0.88	0.9	0.9	1.92	1.11	0.36	**0.9**	0.12
SD_Vul	0.54	0.61	0.61	1.12	1.41	0.73	0.61	0.73	1.18	0.84	0.31	**1.02**	0.22
MxSim	0.76	0.75	0.74	0.5	0.52	0.66	0.58	0.7	0.61	0.65	0.1	**0.71**	0.04
Lg_Chn	6.22	#	4.04	3.99	5.91	6.4	9.8	#	#	6.06	2.12	**3.95**	1.02
SD_Chn	1.43	#	0.93	1.2	1.46	1.5	2.1	#	#	1.44	0.39	**1.19**	0.23
No_Chn	3.71	#	2.85	2.37	4.03	3.8	6.3	#	#	3.84	1.36	**2.24**	0.65
Omniv	0.6	#	0.4	0.52	0.54	0.76	0.86	0.78	0.87	0.67	0.17	0.27	0.1
Tlmax	3.36	3.65	3.43	3.42	4.06	#	#	#	#	3.58	0.29	**3.51**	0.25
Tlmean	2.7	2.4	2	2.4	2.6	3.2	2.9	3.1	3.1	2.71	0.4	2.12	0.14
Path	1.3	1.9	1.9	2.7	2.2	1.6	1.6	1.6	1.9	1.86	0.41	**2.04**	0.13

Notes: *S*: number of species, *L/S*: average number of links per species, L/S^2; connectance (i.e. the fraction of all possible links that are realized, *T. I. B*: the fraction of top-, intermediate- and basal species, respectively. *SD_Gen. SD_Vul*: the standard deviation of species normalized generality (G_i) and vulnerability (V_i) ($G_i = \left(1/\left(L/S\right)\right)\times g_i$, $V_i = \left(1/\left(L/S\right)\right)\times v_i$, where g_i is the number of prey species to species *i* and v_i is the number of predator species to species *i*). *MxSim*: mean of species maximum similarity where similarity for each species pair is defined by the number of predators and preys shared divided by the pair's total number of predators and preys. *Lg_Chn. SD_Chn, No_Chn*: the mean, standard deviation and log value of the number of all food-chains (the linked path between a basal resource and a consumer). *Omniv*: the fraction of omnivorous species, *Tlmax*, *Tlmean*: the maximum and the mean of trophic levels in a food web. Trophic levels are measured by the short-weighted trophic level which is the mean of the shortest path and the prey-average trophic level Williams and Martinez 2004. Path: the average of all shortest paths between all species.

Table A2. Results of pairwise comparisons of difference in R_{50} between topological deletion sequences. Unfilled cells above diagonal represent comparisons between deletion sequences where basal species could be deleted, while shaded cells below diagonal represent comparisons between deletion sequences where basal species could not be deleted.

	largest bodysize	smallest bodysize	highest trophic pos.	lowest trophic pos.	most connected	least connected	most vulnerable	least vulnerable	most generalist	least generalist	random
largest bodysize		***	*ns*	***	***	*ns*	***	*ns*	*ns*	***	***
smallest bodysize	***		***	***	***	***	*ns*	***	***	***	***
highest trophic position	*ns*	***		***	***	*ns*	***	*ns*	*ns*	***	***
lowest trophic position	***	*ns*	***		***	***	***	***	***	*ns*	***
most connected	***	*ns*	***	*ns*		***	***	***	***	***	***
least connected	*ns*	***	*ns*	***	***		***	*ns*	*ns*	***	***
most vulnerable	***	***	***	***	***	***		***	***	***	***
least vulnerable	*ns*	***	*ns*	***	***	*ns*	***		*ns*	***	***
most generalist	***	***	***	***	***	***	***	***		***	***
least generalist	*ns*	***	*ns*	***	***	*ns*	***	*ns*	***		***
random	*ns*	***	*ns*	***	***	*ns*	***	*ns*	*ns*	*ns*	

Note: *, **, and *** denotes a significance level of $p<0.05$, $p<0.01$, and $p<0.001$, respectively, while *ns* denotes no significant difference in R_{50} between two deletion sequences.

Table A3. Relationship between the topological R_{50} of different deletion sequences. Correlation coefficients (r) in bold type denote significant relationships ($p < 0.05$). Unfilled cells above diagonal represent correlations between deletion sequences where basal species could be deleted, while shaded cells below diagonal represent correlations between deletion sequences where basal species could not be deleted. For sequences without any variation in topological R_{50} values $r = NA$

	largest bodysize	smallest bodysize	highest trophic pos.	lowest trophic pos.	most connected	least connected	most vulnerable	least vulnerable	most generalist	least generalist	random
largest bodysize		*NA*	*NA*	*NA*	*NA*	*NA*	*NA*	*NA*	*NA*	*NA*	*NA*
smallest bodysize	*NA*		*NA*	**0.83**	**0.79**	-0.053	**0.98**	*NA*	0.12	**0.83**	**0.27**
highest trophic position	*NA*	*NA*		*NA*	*NA*	*NA*	*NA*	*NA*	*NA*	*NA*	*NA*
lowest trophic position	*NA*	**0.20**	*NA*		**0.71**	-0.013	**0.83**	*NA*	0.099	**1.0**	**0.22**
most connected	*NA*	**0.20**	*NA*	**1.0**		-0.13	**0.79**	*NA*	0.12	**0.71**	0.19
least connected	*NA*	*NA*	*NA*	*NA*	*NA*		-0.12	*NA*	0.074	-0.013	0.072
most vulnerable	*NA*	**0.42**	*NA*	**0.51**	**0.51**	*NA*		*NA*	0.11	**0.83**	**0.25**
least vulnerable	*NA*	*NA*	*NA*	*NA*	*NA*	*NA*	*NA*		*NA*	*NA*	*NA*
most generalist	*NA*	0.16	*NA*	**0.60**	**0.60**	*NA*	**0.22**	*NA*		0.099	**0.27**
least generalist	*NA*	*NA*	*NA*	*NA*	*NA*	*NA*	*NA*	*NA*	*NA*		**0.22**
random	*NA*	0.15	*NA*	**0.48**	**0.48**	*NA*	**0.34**	*NA*	**0.57**	*NA*	

Table A4. Results of pairwise comparison of differences in R_{50} between dynamical deletion sequences. Unfilled cells above diagonal represent comparisons between deletion sequences where basal species could be deleted, while shaded cells below diagonal represent comparisons between deletion sequences where basal species could not be deleted.

	largest bodysize	smallest bodysize	highest trophic pos.	lowest trophic pos.	most connected	least connected	most vulnerable	least vulnerable	most generalist	least generalist	most biomass abundant	least biomass abundant	most num. abundant	least num. abundant	largest net effect	smallest net effect	random
largest bodysize		***	*ns*	***	*ns*	***	**	*ns*	***	***	***	*ns*	***	*ns*	*ns*	*ns*	***
smallest bodysize	***		***	*ns*	***	***	*ns*	***	***	*ns*	***	***	*ns*	***	***	***	***
highest trophic position	*ns*	***		***	*ns*	***	***	*ns*	***	***	***	*ns*	***	*ns*	*ns*	*ns*	***
lowest trophic position	***	***	***		***	***	*ns*	***	***	*ns*	***	***	*ns*	***	***	***	***
most connected	***	***	***	*ns*		***	***	*ns*	***	***	*	*ns*	***	*ns*	*ns*	*ns*	***
least connected	***	***	***	***	***		***	***	***	***	***	***	***	***	***	***	*ns*
most vulnerable	***	***	***	*ns*	*ns*	***		***	***	*ns*	***	***	*ns*	***	***	**	***
least vulnerable	*ns*	***	*ns*	***	***	***	***		***	***	*ns*	*ns*	***	*ns*	*ns*	*ns*	***
most generalist	***	***	***	*ns*	*ns*	***	*ns*	***		***	***	***	***	***	***	***	***
least generalist	***	***	***	*	**	*ns*	***	***	*ns*		***	***	*ns*	***	***	***	***
most biomass abundant	*	***	*	***	***	*	***	*ns*	***	***		*ns*	***	*ns*	*ns*	***	***
least biomass abundant	***	***	***	***	***	***	***	***	***	***	***		***	*ns*	*ns*	*ns*	***
most numerical abundant	***	*ns*	***	***	***	***	**	***	***	***	***	***		***	***	***	***
least numerical abundant	*ns*	***	*ns*	***	***	***	***	*ns*	***	***	*ns*	***	***		*ns*	*ns*	***
largest net effect	*ns*	***	*ns*	***	***	***	***	*ns*	***	***	*ns*	***	***	*ns*		*ns*	***
smallest net effect	***	*ns*	***	***	***	***	***	***	***	***	***	***	*ns*	***	***		***
random	***	***	***	*ns*	*ns*	***	*ns*	***	*ns*	*ns*	***	***	***	***	***	***	

Note: *, **, and *** denotes a significance level of $p < 0.05$, $p < 0.01$, and $p < 0.001$, respectively, while *ns* denotes no significant difference in R_{50} between two deletion sequences.

Table A5. Relationship between the dynamical R_{50} of different deletion sequences. Correlation coefficients (r) in bold type denote significant relationships ($p < 0.05$). Unfilled cells above diagonal represent correlations between deletion sequences where basal species could be deleted, while shaded cells below diagonal represent correlations between deletion sequences where basal species could not be deleted.

	largest bodysize	smallest bodysize	highest trophic pos.	lowest trophic pos.	most connected	least connected	most vulnerable	least vulnerable	most generalist	least generalist	most biomass abundant	least biomass abundant	most num. abundant	least num. abundant	largest net effect	smallest net effect	random
largest bodysize		0.029	**0.69**	0.086	-0.15	**0.50**	-0.039	**0.53**	0.20	0.086	**0.50**	0.13	0.056	**0.69**	**0.78**	0.17	**0.53**
smallest bodysize	**0.24**		-0.030	**0.85**	**0.35**	-0.13	**0.69**	-0.039	0.10	**0.85**	0.035	**0.36**	**0.96**	-0.13	-0.038	**0.24**	**0.32**
highest trophic position	**0.69**	**0.38**		0.064	-0.054	**0.45**	0.0081	**0.54**	**0.38**	0.064	**0.40**	0.16	-0.0023	**0.60**	**0.57**	0.11	**0.56**
lowest trophic position	0.18	**0.438**	0.11		**0.36**	-0.039	**0.74**	-0.073	0.10	**1.0**	-0.045	**0.25**	**0.86**	-0.014	-0.021	**0.20**	**0.35**
most connected	0.14	**0.64**	**0.36**	**0.29**		-0.11	**0.55**	-0.19	0.19	**0.36**	-0.022	-0.15	**0.37**	-0.12	-0.20	**0.29**	0.15
least connected	**0.53**	0.19	**0.48**	0.096	0.20		-0.079	**0.43**	0.19	-0.039	**0.37**	0.012	-0.10	**0.40**	**0.38**	**0.25**	**0.45**
most vulnerable	**0.21**	**0.57**	0.16	**0.56**	**0.39**	0.012		-0.075	0.11	**0.74**	-0.031	0.13	**0.74**	-0.13	-0.094	**0.26**	**0.31**
least vulnerable	**0.53**	**0.34**	**0.53**	0.11	**0.37**	**0.45**	0.0060		**0.40**	-0.073	**0.44**	0.10	-0.0019	**0.28**	**0.60**	0.074	**0.43**
most generalist	0.20	**0.67**	**0.37**	**0.33**	**0.94**	0.19	**0.38**	**0.40**		0.10	**0.39**	0.0052	0.12	0.17	0.18	0.19	**0.63**
least generalist	**0.46**	**0.32**	**0.34**	**0.26**	0.15	**0.67**	**0.35**	0.12	0.11		-0.045	**0.25**	**0.86**	-0.014	-0.021	**0.20**	**0.35**
most biomass abundant	**0.48**	**0.42**	**0.38**	**0.45**	**0.35**	**0.36**	**0.42**	**0.41**	**0.36**	**0.42**		0.12	0.056	**0.28**	**0.48**	**0.44**	**0.68**
least biomass abundant	**0.28**	**0.65**	**0.33**	**0.49**	**0.49**	**0.24**	**0.57**	**0.23**	**0.52**	**0.33**	**0.35**		**0.37**	0.12	0.030	0.16	**0.27**
most numerical abundant	0.17	**0.75**	**0.24**	**0.5**	**0.50**	0.0075	**0.60**	0.14	**0.51**	0.19	**0.39**	**0.60**		-0.097	-0.032	**0.26**	**0.37**
least numerical abundant	**0.69**	0.11	**0.60**	0.14	0.15	**0.43**	0.17	**0.27**	0.17	**0.41**	**0.27**	0.18	0.077		**0.54**	0.12	**0.33**
largest net effect	**0.79**	0.14	**0.57**	0.18	0.11	**0.42**	0.14	**0.57**	0.15	**0.36**	**0.48**	0.15	0.083	**0.55**		0.078	**0.36**
smallest net effect	0.179	**0.89**	**0.33**	**0.47**	**0.61**	0.18	**0.58**	**0.28**	**0.62**	**0.27**	**0.40**	**0.64**	**0.71**	0.039	0.070		**0.54**
random	**0.52**	**0.72**	**0.56**	**0.56**	**0.63**	**0.49**	**0.53**	**0.51**	**0.63**	**0.46**	**0.62**	**0.71**	**0.58**	**0.36**	**0.41**	**0.73**	

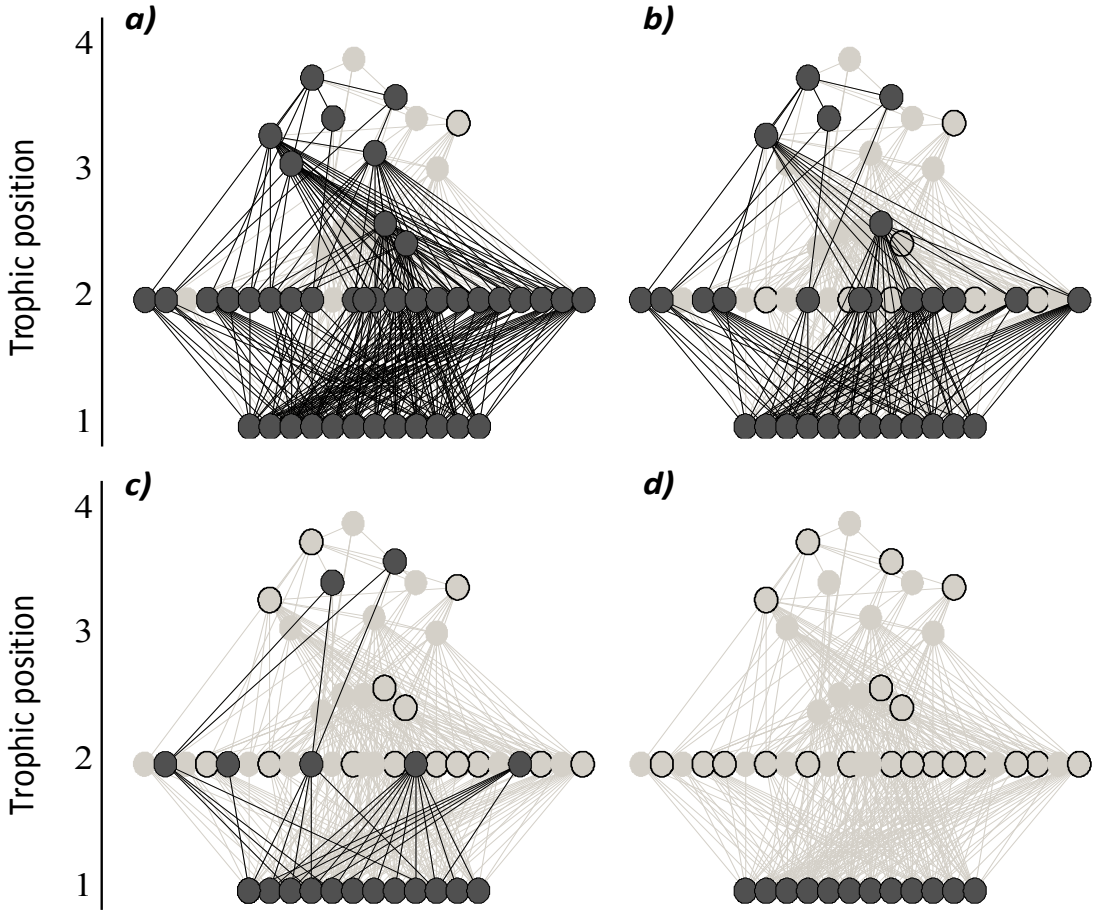

Figure A1. Snapshots of food web structure during four stages of food web disassembly due to primary and secondary extinctions when basal species were not allowed to go primarily extinct. Dark shaded nodes and links denote extant species and interactions. Light shaded nodes with a black border denote species that have been deleted (primary extinction) and light shaded nodes without a border and shaded links denote secondarily extinct species and their interactions. Fraction of remaining species: a) 41/50 (82%), b) 29/50 (58%), c) 19/50 (38%) and d) 12/50 (24%).

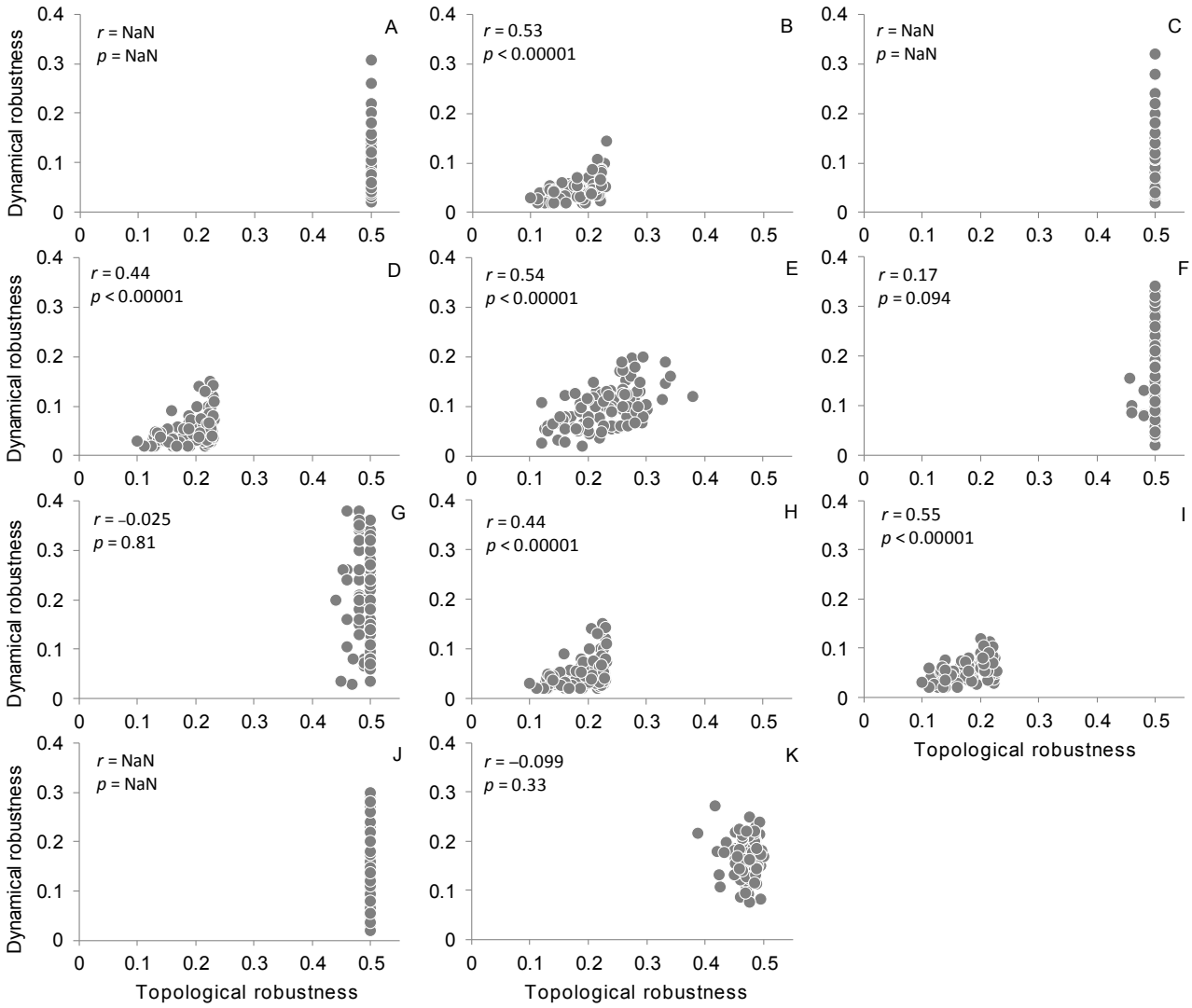

Figure A2. Relationship between dynamical and topological robustness of model food webs to sequential deletions of species, as measured by R_{50}, when basal species were allowed to go primarily extinct. Species were deleted in order according to the following traits: (A) max body size, (B) min body size, (C) max trophic position, (D) min trophic position, (E) max connectivity, (F) min connectivity, (G) max generality, (H) min generality, (I) max vulnerability, (J) min vulnerability. (K) is the random sequence.

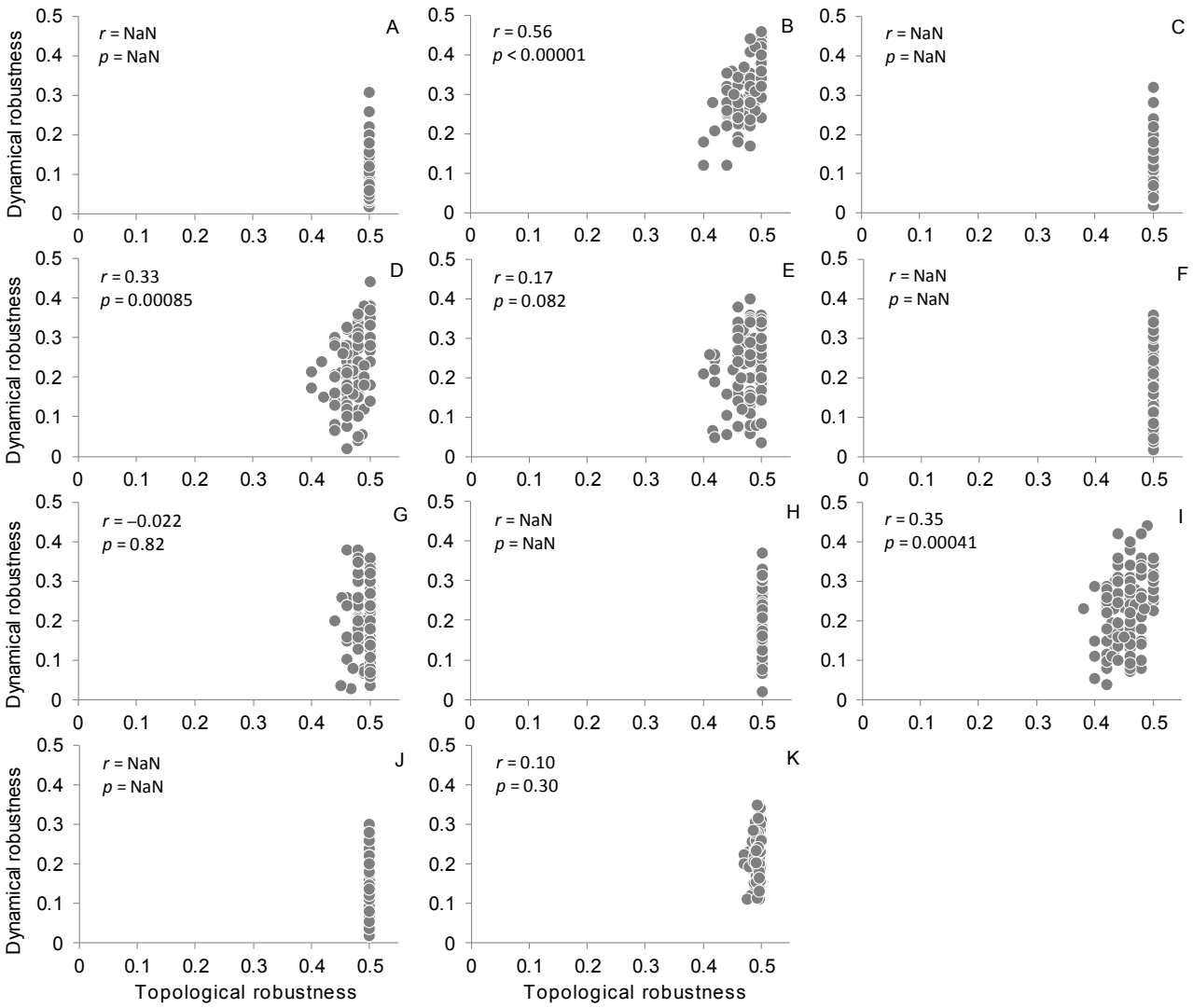

Figure A3. Relationship between dynamical and topological robustness of model food webs to sequential deletions of species, as measured by R_{50}, when basal species could not go primarily extinct. Species were deleted in order according to the following traits: (A) ,max body size, (B) min body size, (C) max trophic position, (D) min trophic position, (E) max connectivity, (F) min connectivity, (G) max generality, (H) min generality, (I) max vulnerability, (J) min vulnerability. (K) is the random sequence.

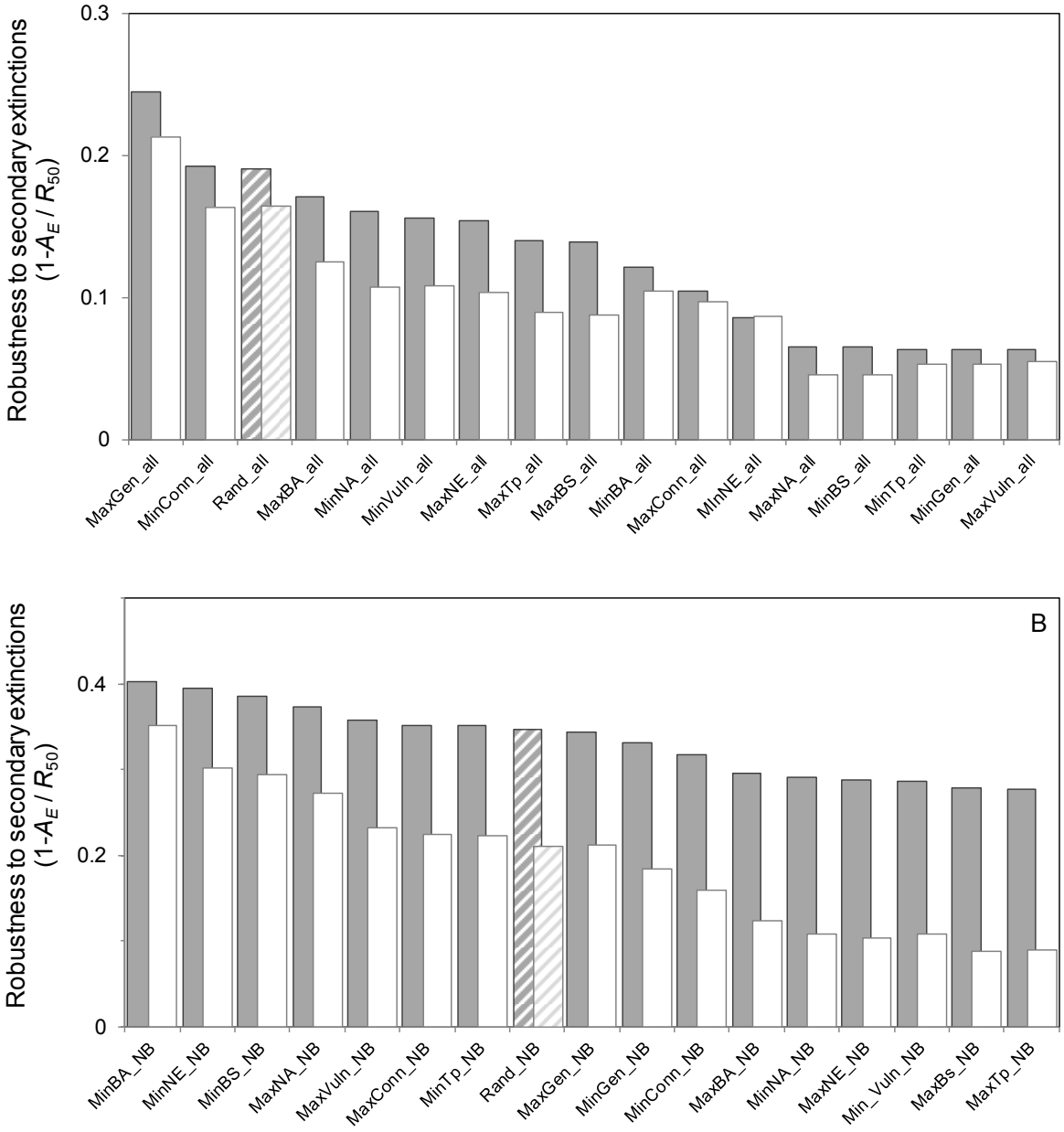

Figure A4. Robustness to secondary extinctions, as measured by $1 - A_E$ (shaded bars) and R_{50} (open bars), in model food webs when exposed to different deletion sequences. Deletion sequences are ordered from smallest to largest value of $1 - A_E$. In (A) basal species could go primarily extinct (i.e. intentional deletion), while in (B) basal species were protected from being deleted.

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