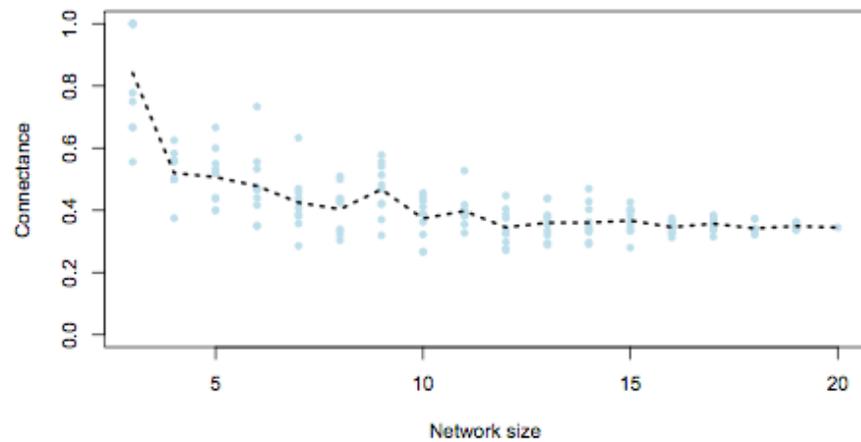
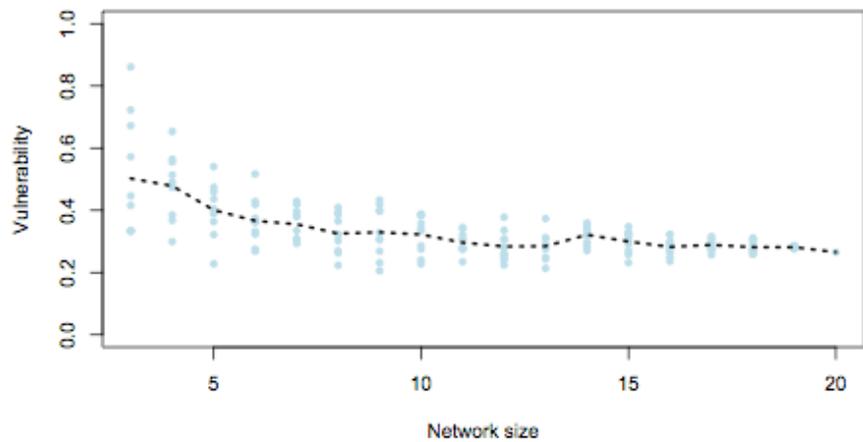
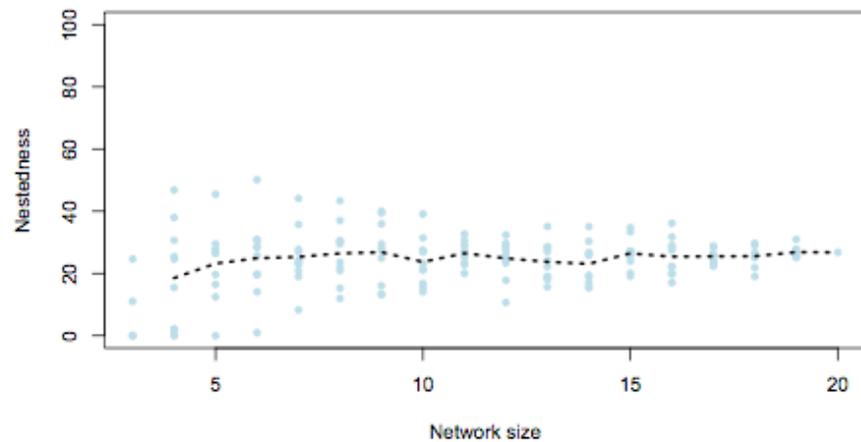
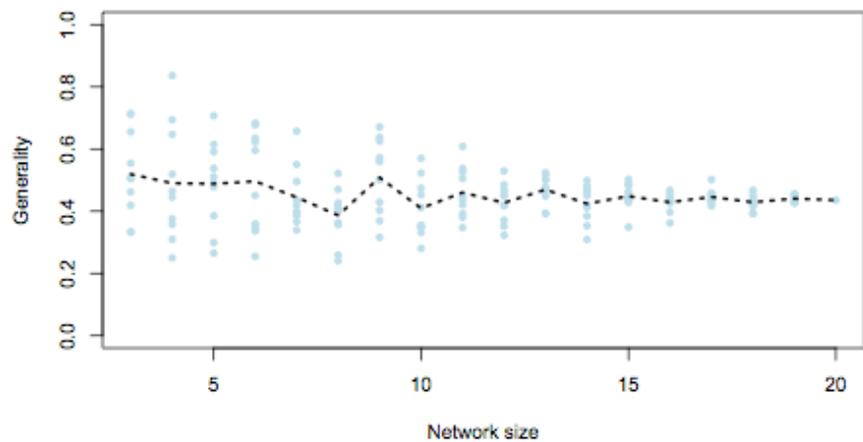


Electronic Supplementary Material

1. Sample size validation

To ensure that the network size sub-sampled (20 phage strains x 20 bacterial strains) was representative of the full soil sample, we randomly sampled random square matrices from within our full dataset, ranging from 3x3 to 19x19 (1000 replicates for each). For each, we then calculated nestedness (Rodríguez–Girones & Santamaria 2006), connectance (e.g. the proportion of links established at the scale of the network; Gardner & Ashby, 1970), and vulnerability and generality (Schoener, 1989). The results show that the indicators approximately stabilize at 10x10 networks, meaning that our 20x20 sample is representative of the interaction web. To make the figure readable, only 10 replicates of each combination are shown.



2. Testing the effect of resource quantity on network structure

We used a Monte Carlo procedure to evaluate the possibility that changes in network structure were due to the elimination of some links by chance. Because decreasing resource input will ultimately decrease host population density (thus preventing host/phage interaction to occur), one might expect that communities at low resource density are a subset of the one obtained at high resource density.

Knowing the number of bacteria and phages establishing links (from Table 1 of main text), we simulated matrices obtained for different resource levels by subsampling the matrix obtained in the most resource-rich environment (e.g. in order to simulate a matrix for the 10% level of resources, we randomly extracted 20 phages and 14 bacteria from the first matrix). This process was replicated 1000 times (tests with 100, 5000 and 10000 replicates produced similar results), after which we compared the distributions of several network structure indicators [nestedness (a measure of matrix entropy), connectance (proportion of realized links), PDI (specialization of phage; eqn. 2 in main text), generality (number of hosts exploited) and vulnerability (number of phage isolates attacking bacteria)] to the observed values using one-sample Wilcoxon tests with a correction for continuity (Zar, 1974) (due to non-normality of most of the randomized distributions).

Our results are presented in the table below. Here, R is resource concentration and the first and second columns for each R are, respectively, index estimates based on random sampling and actual observations.

	R=10 ⁻¹ (sampling)	R=10 ⁻¹ (observed)	R=10 ⁻² (sampling)	R=10 ⁻² (observed)
Nestedness	24.90	38.01	24.68	18.22
Connectance	0.34	0.33	0.36	0.18
PDI	0.53	0.40	0.50	0.40
Generality	0.29	0.26	0.31	0.17
Vulnerability	0.43	0.40	0.42	0.50

The structure of each observed matrix was highly significantly different (all P values <10⁻⁵), indicating that the changes in structure we report were not obtained solely by the random elimination of interactions within the high-resource community.

References

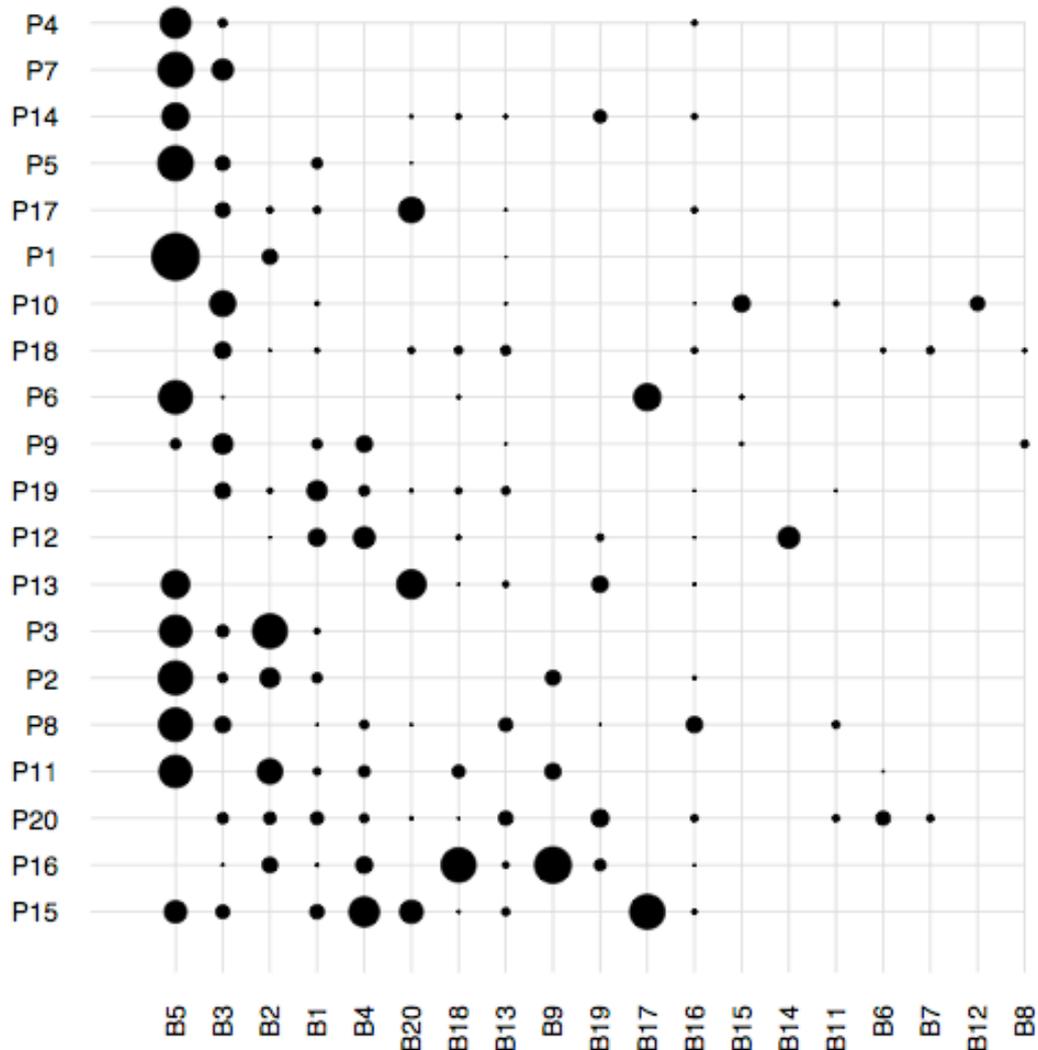
Zar JH (1974). *Biostatistical analysis*. Prentice-Hall: Englewood Cliffs, NJ.

3. Visualization of each network

In the figures below, the diameter of the dot at the intersection of each bacteria/phage combination is proportional to the strength of the link, as given in eq. 1 of the main text (impact of each phage on bacterial host population growth). Bacteria and phages

in the matrix are positioned (for each resource quantity) so as to reflect nestedness. It is straightforward that as resource input decreases, fewer interactions are established. It also appears that when the quantity of resource decreases, nestedness changes (Table 1 main text). The most nested community is obtained at low resource input.

High resources



Medium resources

