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Supplemental information

**Horizontal gene transfer drives
the evolution of dependencies in bacteria**

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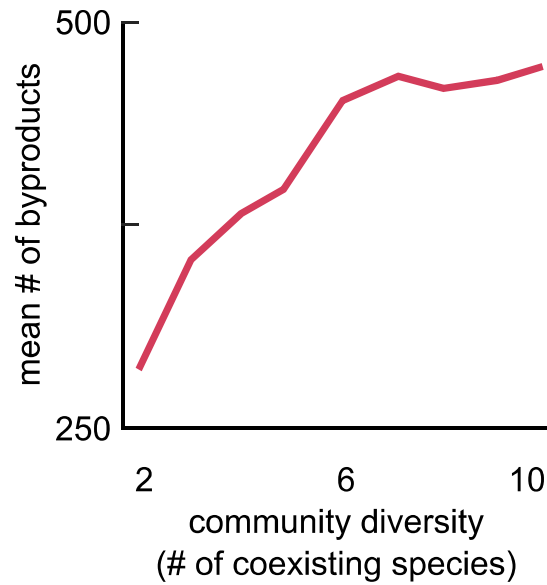
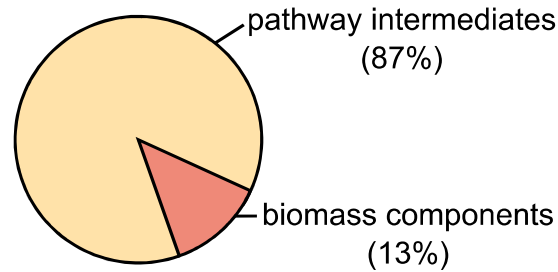


FIG. S1. **More diverse communities have more community byproducts, related to STAR Methods.** Line plot showing the average number of community byproducts in our $\sim 100,000$ environment-community metabolic simulations, as a function of the community diversity. The community diversity is measured by the number of coexisting bacterial species. The community byproducts are calculated using a metabolic network algorithm [42]; the average shown is over all environments and communities at a given level of diversity.



metabolic network roles of community byproducts

FIG. S2. **Community byproducts are more likely to be pathway intermediates than end-products (biomass components), related to STAR Methods and Figure 3.** Pie chart showing the fraction of all community byproducts in our $\sim 100,000$ environment-community metabolic simulations that were pathway intermediates and pathway end-products (biomass components). Pathway intermediates are more likely to lead to dependencies via coupled gains and losses, because they need to be further metabolized into biomass components by a dependent bacterial species. In contrast, end-products are already biomass components, and do not need to be further metabolized; this makes them more likely to lead to dependencies via pure gene loss.

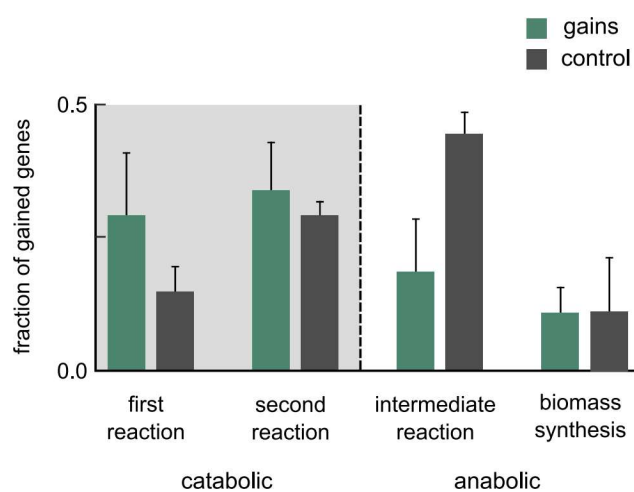


FIG. S3. **Gained genes are still primarily catabolic, even when network positions are assigned differently to metabolic genes, related to Figure 1.** Bar chart showing the position of genes gained by horizontal gene transfer (HGT) in bacterial metabolic networks, along all 1,669 phylogenetic branches; this chart is similar to figure 1c, except that instead of excluding those genes that participate in multiple metabolic routes, we include them by considering their most frequent metabolic position (catabolic and anabolic). We still exclude those genes that equally occupy catabolic and anabolic positions in this analysis. This alternate assignment choice does not significantly impact our results in figure 1c.