

Supplementary Materials for
Synergistic coevolution accelerates genome evolution

Daniel Preussger, Alexander Herbig, Christian Kost

Correspondence to: christiankost@gmail.com

This PDF file includes:

Figs. S1 to S2

Other Supplementary Materials for this manuscript include the following:

Tables S1 to S2

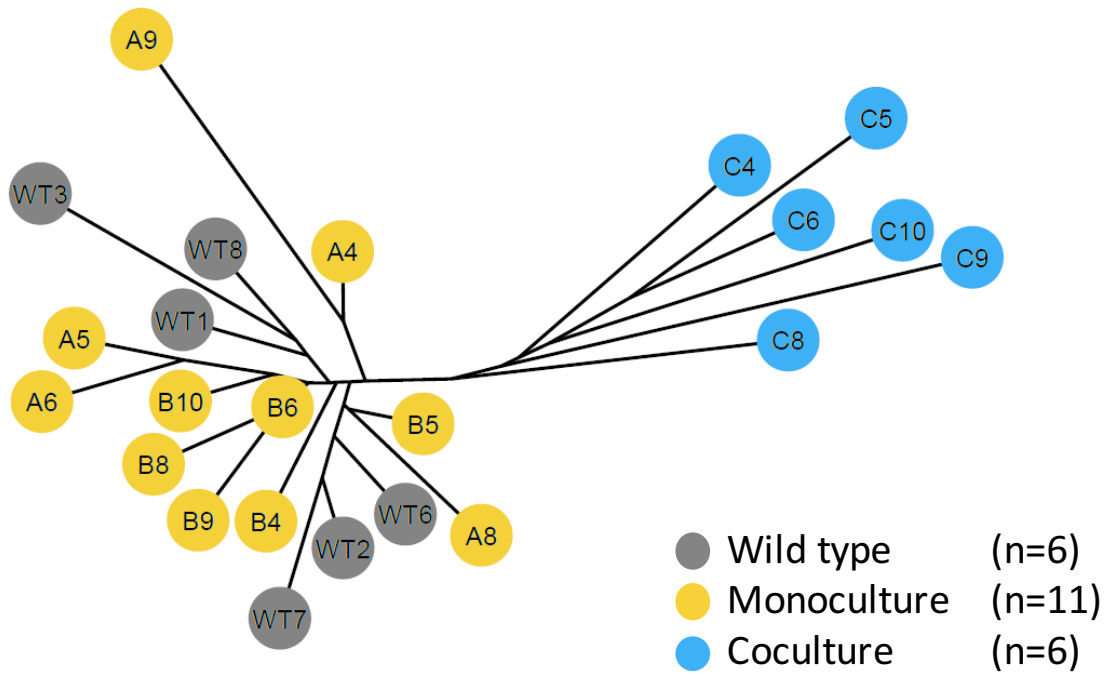


Fig. S1. Increased divergence of populations of coevolved auxotrophs. Distance tree of sequenced populations that is based on the neighbour-joining analysis of a population-level genotyping matrix. Nodes are colour-coded by experimental group. Evolutionary trajectories differ between control groups (WT = wildtype, M = monocultures of auxotrophs, C = cocultures of auxotrophs). Labels containing similar numbers indicate a common ancestor among auxotrophic populations.

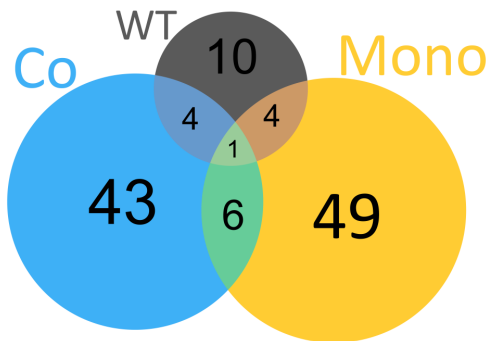
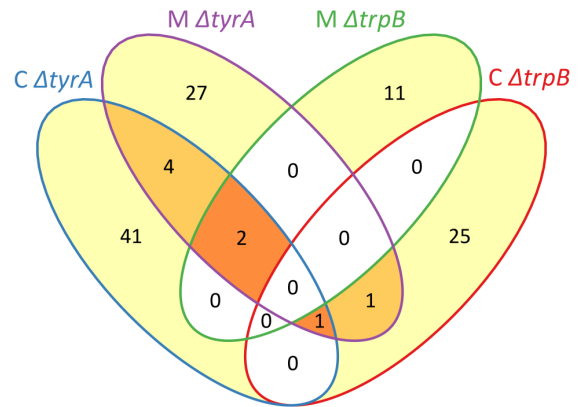
A**B**

Fig. S2. Experimental groups share few mutated genes. Numbers in Venn-diagrams represent total counts of different genes carrying a mutation or having been deleted. **(A)** Shared and unique mutated genes in populations of wild type (WT), monocultures of auxotrophs (Mono), and cocultures of auxotrophs (Co). **(B)** Shared and unique mutated genes in auxotrophic clones isolated from cocultures (C Δ tyrA, C Δ trpB) and monocultures (M Δ tyrA, M Δ trpB).

Supplementary Tables (not included in this PDF)

Table S1. Overview over all mutations that have been identified in experimental groups on the level of isolated strains.

Table S2. Overview over all mutations that have been identified in experimental groups on the level of whole population samples.