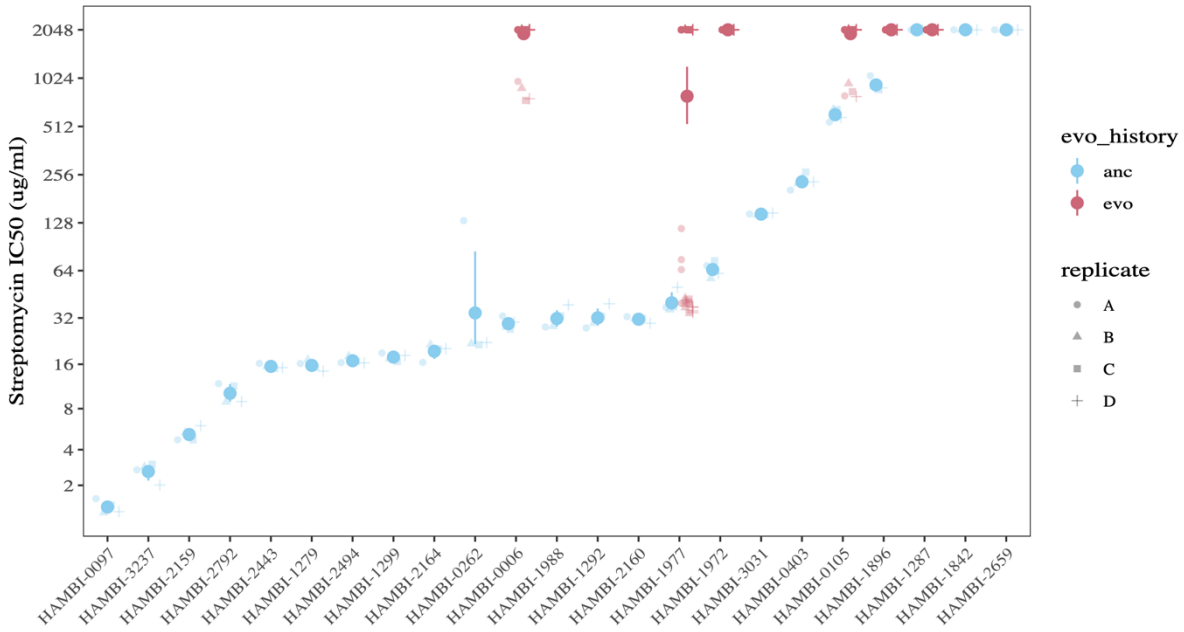
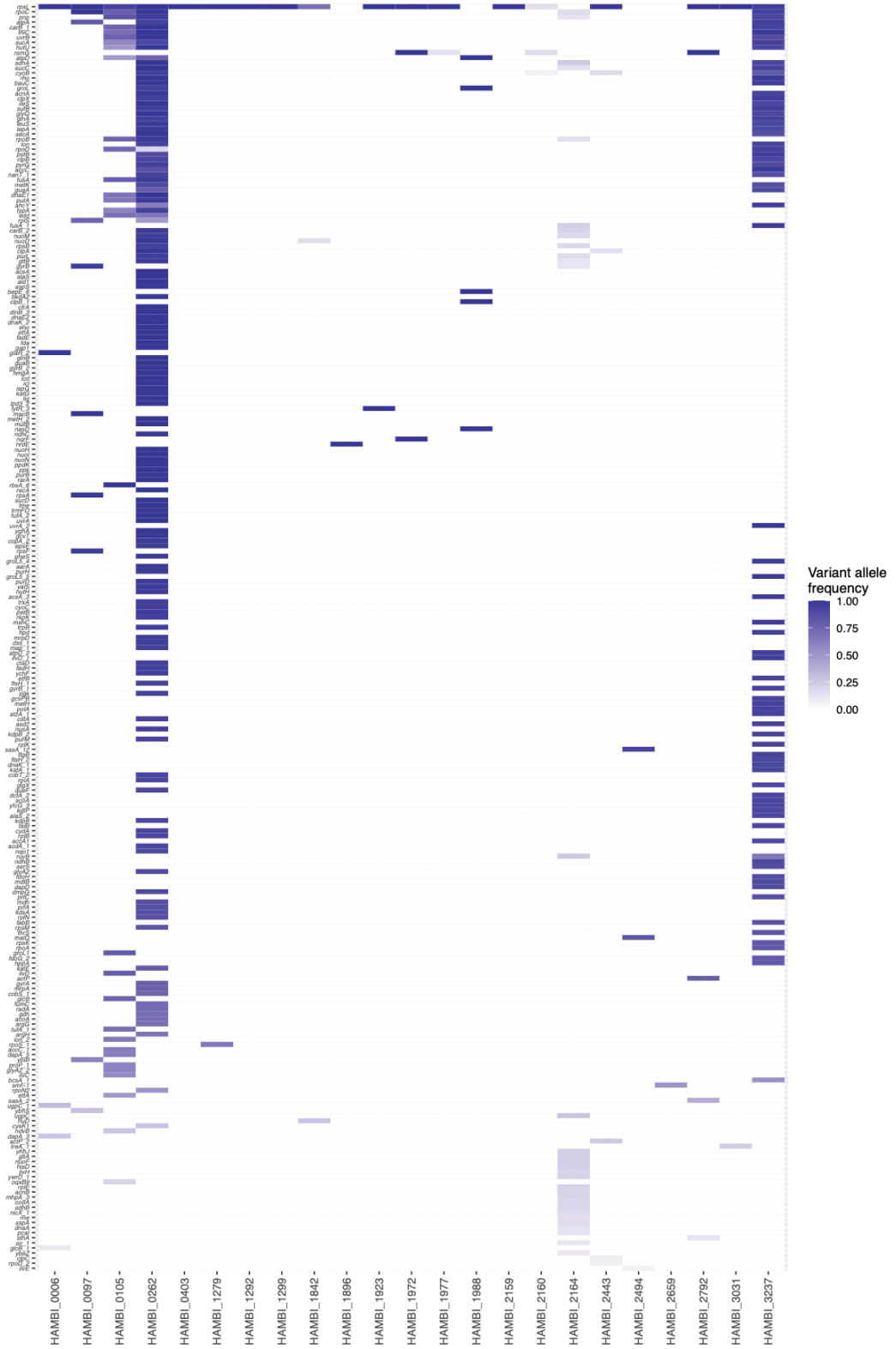
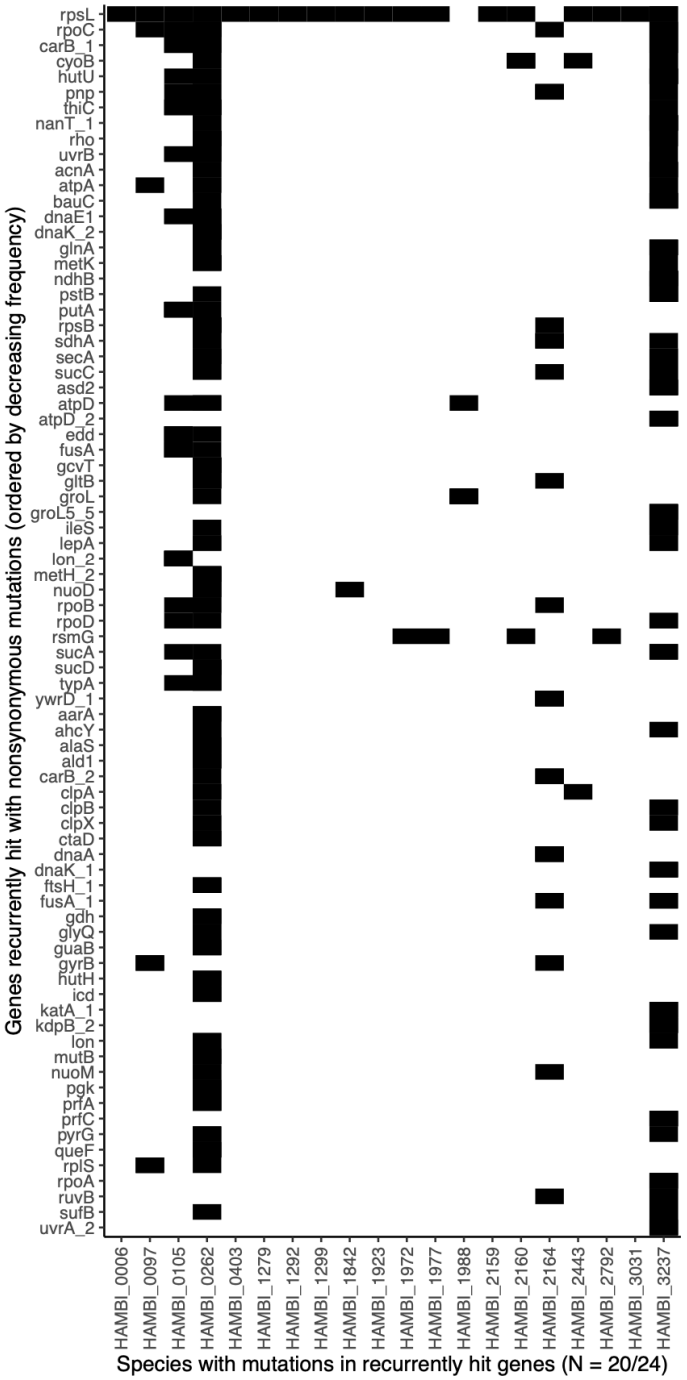


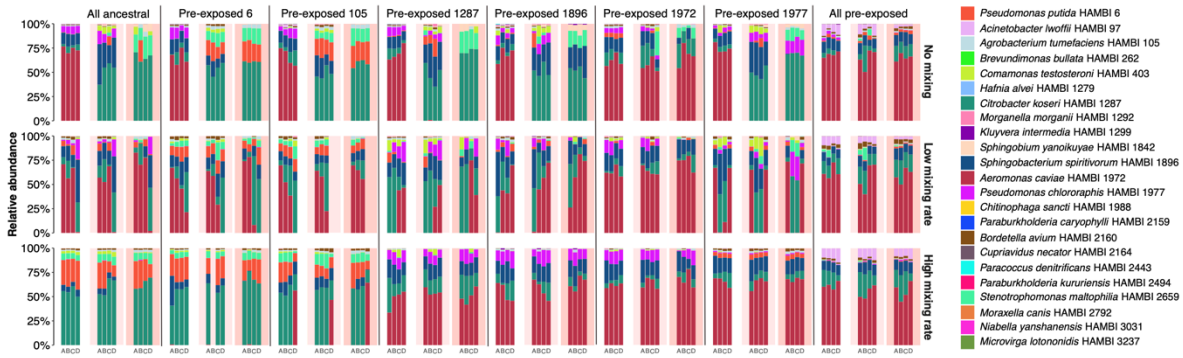
Extended Data Figure 1 | Streptomycin IC_{50} (μg mL^{-1}) for 23 HAMBI species. Four (4) distinct clones from the ancestral species were phenotyped (transparent small blue points) and are shown with the mean (solid blue dot) and a nonparametric bootstrap for confidence limits of the population mean (line range) across those replicate clones. Streptomycin IC_{50} of evolved populations (red) from the 6 most abundant species in the community. 16 clones were randomly phenotyped from populations of each of the 4 biological replicates for populations of each species following exposure to increasing concentrations of streptomycin (64 clones total, transparent red points). Solid red points show the mean and a basic nonparametric bootstrap for confidence limits of the mean (line range) across all biological replicates and clones.



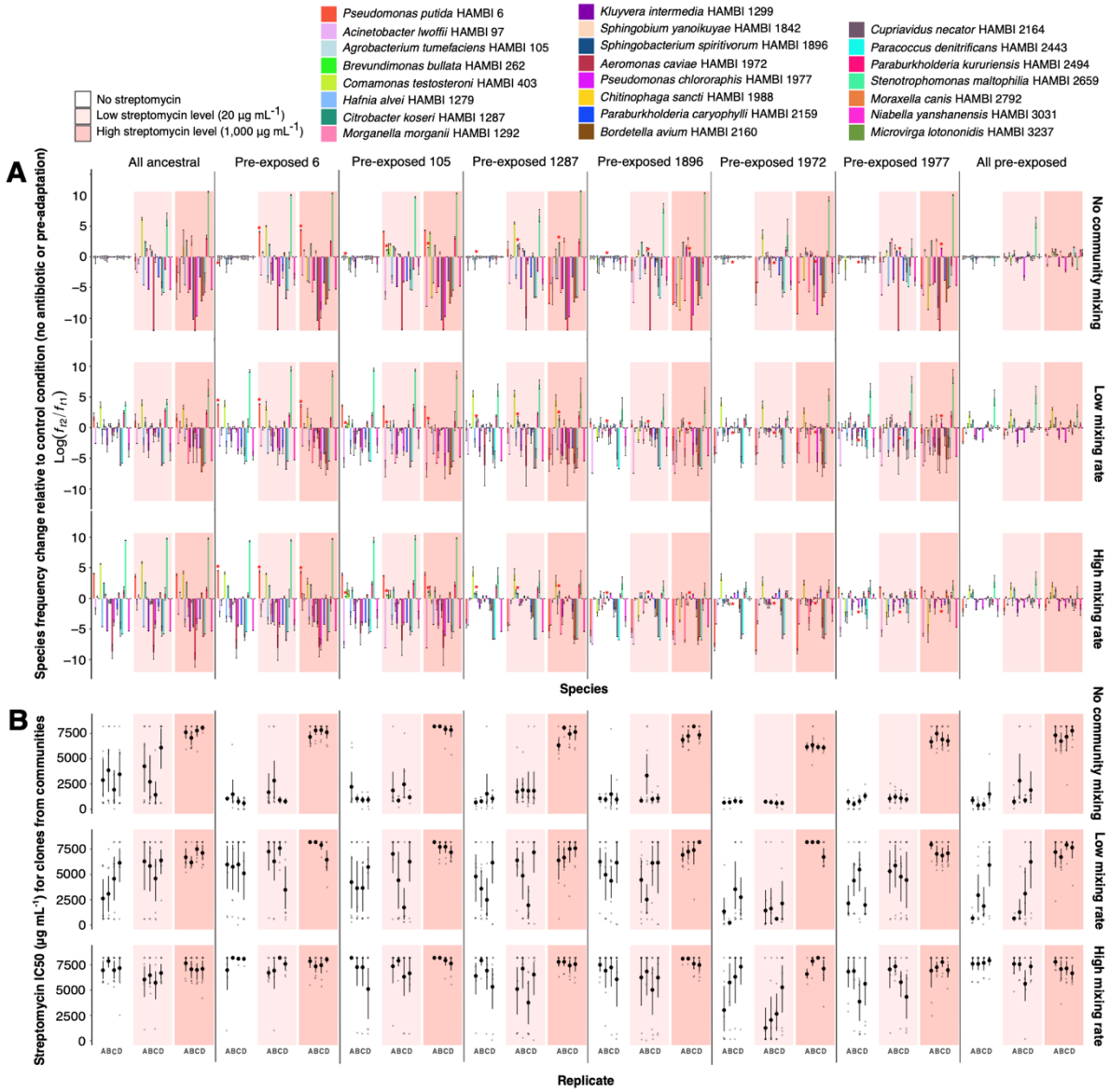
Extended Data Figure 2 | Genomic evolution of species exposed to the disturbance (i.e., streptomycin) prior to initiating community serial propagation experiment. The heat map displays allele frequencies for all genes hit with nonsynonymous mutations following exposure of populations of species to increasing levels of the model disturbance streptomycin. The overwhelming majority of the species have nonsynonymous mutations in the gene *rpsL* encoding for the streptomycin binding site in the small subunit of the bacterial ribosome and known to be a causative factor for high-level streptomycin resistance. For one species missing from the figure, HAMBI 1287, no nonsynonymous mutations passing hard filtration criteria were observed. *Myroides odoratus* HAMBI 1923 was also included in the streptomycin evolution treatment but was omitted from the main serial passage experiment.



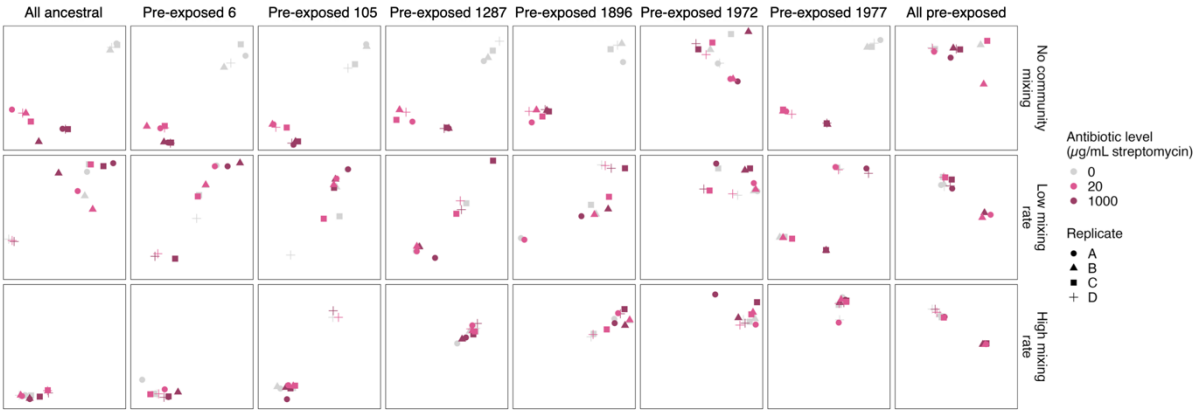
Extended Data Figure 3 | Recurrent targets of evolution of species exposed to the disturbance (i.e., streptomycin) prior to initiating community serial propagation experiment. The heat map displays recurrent genes hit with two or more nonsynonymous mutations in one or several of the experimental species (N = 20/24, including *Myroides odoratus* HAMBI 1923 omitted from the 23-species main serial passage experiment) following exposure of populations of species to increasing levels of the model disturbance streptomycin. The overwhelming majority of the species have nonsynonymous mutations in the gene *rpsL* encoding for the streptomycin binding site in the small subunit of the bacterial ribosome and known to be a causative factor for high-level streptomycin resistance. The four species missing from the figure (HAMBI 1287, 1896, 2494 and 2659) did not have mutations in recurrent genes. Among these, for HAMBI 1287, no nonsynonymous mutations passing hard filtration criteria were observed; for HAMBI 1896, a nonsynonymous mutation was observed in the gene *nrdE* (encoding ribonucleoside-diphosphate reductase subunit alpha); and for HAMBI 2494, nonsynonymous mutations were observed in the genes *ilvE* (branched-chain-amino-acid aminotransferase), *malQ* (4-alpha-glucanotransferase), and *sasA*_12 (histidine kinase); for HAMBI 2659, a nonsynonymous mutation was observed in the gene *smf-1* (type-1 fimbriae).



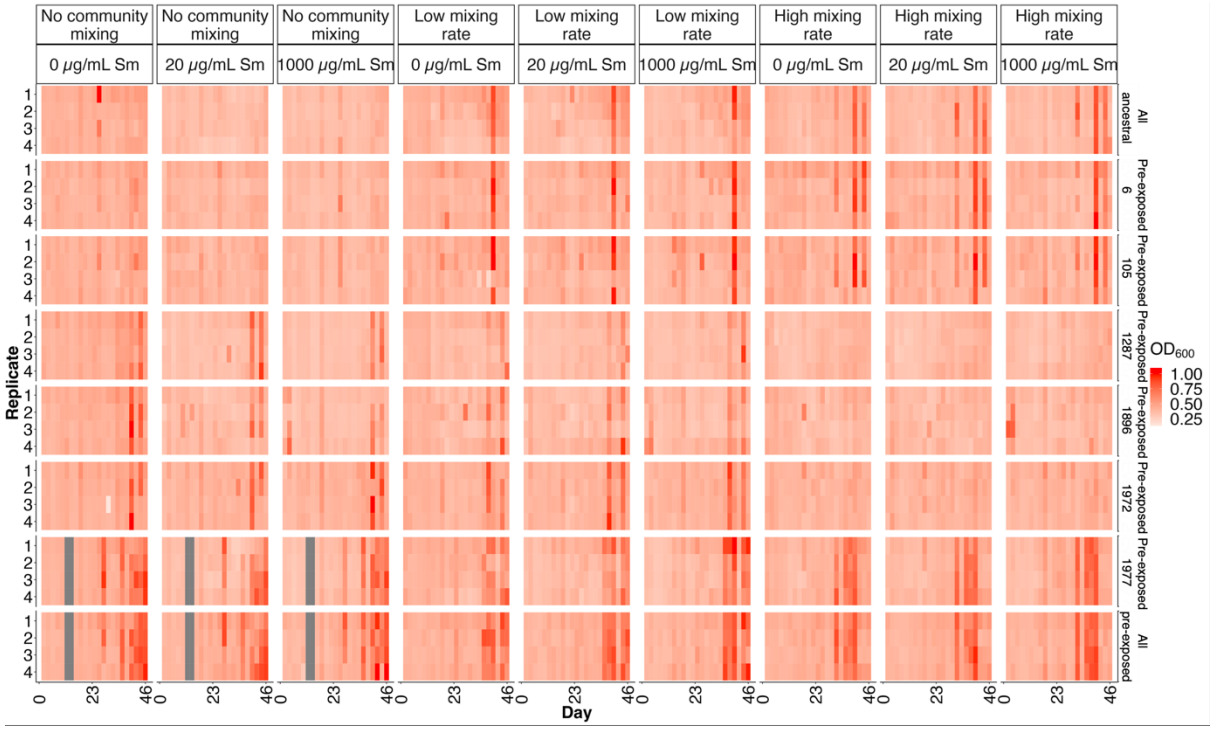
Extended Data Figure 4 | Effect of disturbance, community mixing and pre-exposure on community composition. Relative abundance of species (normalized by species-specific 16S rRNA gene copy number) at the end-point of 46-day serial passage experiment ($N = 4$ replicates per unique treatment combination). Subcolumns show data for the three increasing disturbance levels (no, low or high antibiotic level; deepening shades of red) in eight pre-exposure treatments, separated by black vertical lines from left to right as follows: (1) ancestral populations used for all species; (2–7) a population used for one of the six most abundant species that had been pre-exposed to the disturbance (HAMBI Culture Collection code indicated in column label); and (8) pre-exposed populations used for all species. Within each pre-exposure treatment, the three antibiotic disturbance patches mixed at low or high rate have a shared history and can be identified by the replicate number shown on the *x*-axis. For instance, replicates D for each antibiotic level at low mixing rate in the first evolutionary treatment ("All ancestral"; middle left) represent three patches that were mixed regularly and therefore resemble each other more than the other replicates in the same antibiotic level.



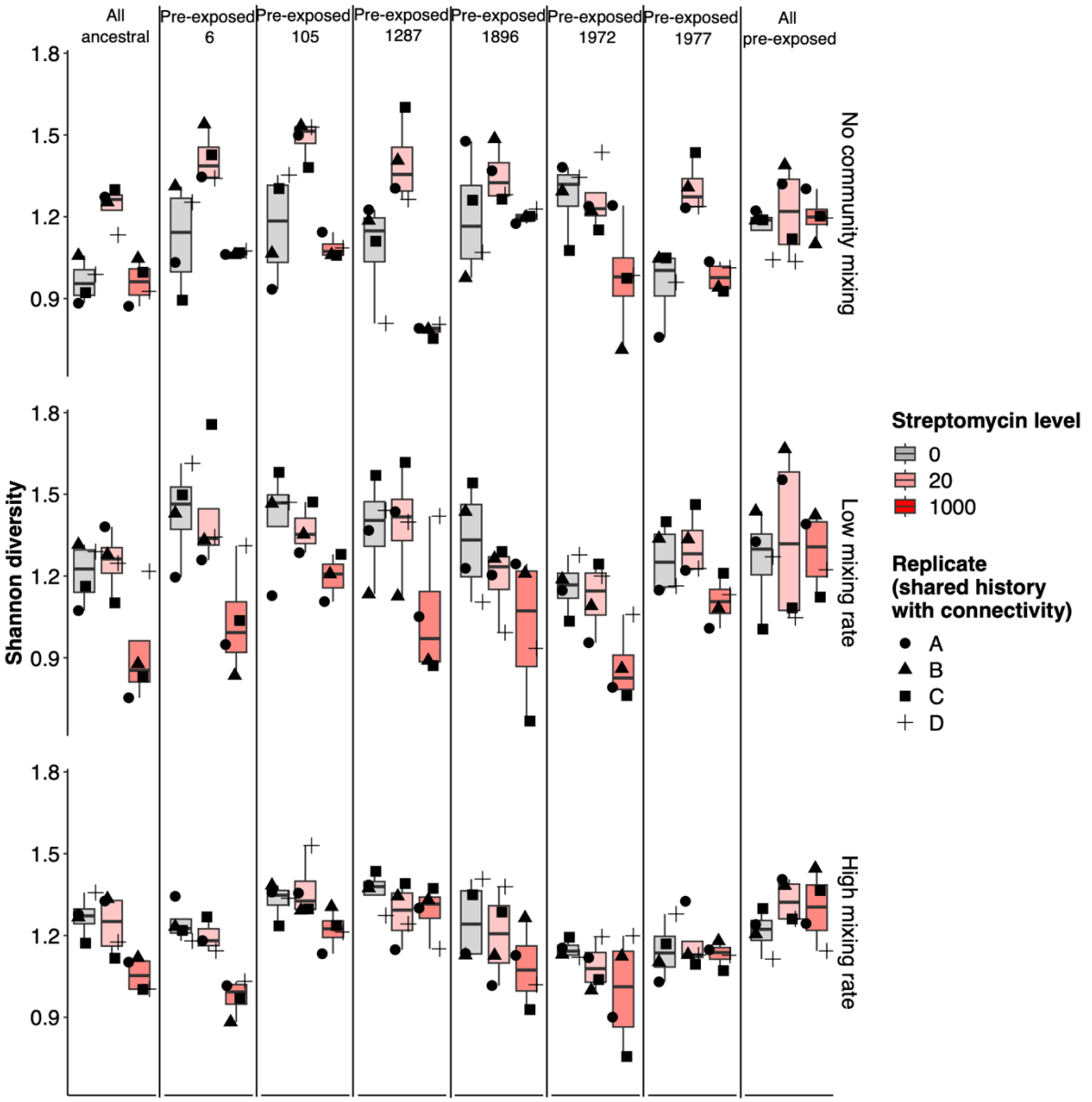
Extended Data Figure 5 | Effect of disturbance, community mixing and pre-exposure on community composition and disturbance resistance. (A) Frequency of each species relative to the frequency of the same species in the evolutionary history specific control condition with no antibiotic or community mixing (i.e., upper left-hand white corner) at the end-point of 46-day serial passage experiment (mean with s.e.m. for 4 replicates for each unique treatment combination). Subcolumns show data for the three increasing disturbance levels (no, low or high antibiotic level; deepening shades of red) in two key pre-exposure treatments, separated by black vertical lines from left to right as follows: (1) ancestral populations used for all species; (2–7) a population used for one of the six most abundant species that had been pre-exposed to the disturbance (HAMBI Culture Collection code indicated in column label); and (8) pre-exposed populations used for all species. **(B)** Half maximal inhibitory concentrations (IC_{50}) for the model disturbance streptomycin in the same treatments as in panel A are indicated for eight clones isolated from each population at the experimental end-point (mean with bootstrapped 95 % confidence intervals). The data is considered to represent the IC_{50} values of dominant community members as the species identity of the clones was not determined. Within each pre-exposure treatment, the three antibiotic disturbance patches mixed at low or high rate have a shared history and can be identified by the replicate letter code in the *x*-axis.



Extended Data Figure 6 | A t-SNE map showing *de novo* community clustering at the end-point of serial propagation experiment. The experiment consisted of three patches exposed to no or two increasing levels of the model disturbance streptomycin (colors), exposed to no or two increasing levels of community mixing (rows), as well as configured into eight different pre-exposure treatments (columns), with four replicates (shapes) for each unique treatment combination ($N = 3 \times 3 \times 8 \times 4 = 288$ populations). The pre-exposure treatments consisted of no pre-exposure for any of the 23 species in the community ("All anc"), a pre-exposed population for one of the six most abundant species (HAMBI 6, 105, 1287, 1896, 1972, or 1977), and a community with pre-exposed populations of all community members. All data points originate from the same t-SNE analysis and have been separated into two panels (with same arbitrary axis units) only for the sake of visual clarity of the effects of experimental treatments on compositional divergence between communities.



Extended Data Figure 7 | Community biomass (optical density, OD, at 600 nm wavelength) for each individual population (N = 288) over time during 46-day serial propagation community experiment. Grey bars indicate missing data owing to technical failure. The columns show the three community mixing and streptomycin (model disturbance) treatments, and the rows show the eight pre-exposure treatments. The *x*-axis indicates time in days, and the *y*-axis indicates the experimental replicate in question.



Extended Data Figure 8 | Diversity of communities at end-point of serial propagation experiment (N = 288). The data is depicted as Shannon diversity for three patches with different disturbance regimes (no, low or high streptomycin level, with the unit μg mL^{-1}) at no, low or high rate of community mixing (rows) between the three patches (N = 4 replicates per unique treatment combination). Columns show data for the three increasing disturbance levels (deepening shades of red) in eight pre-exposure treatments as follows: (1) ancestral populations used for all species; (2–7) a population used for one of the six most abundant species that had been pre-exposed to the disturbance (HAMBI Culture Collection code indicated in column label); and (8) pre-exposed populations used for all species in the community. A model bacterial community consisting of 23 gram-negative species was employed. The box plot depicts the interquartile range (IQR) from the first to the third quartile with the median indicated by a line across the box and the whiskers extending from the hinges to no further than 1.5 × IQR. Within each pre-exposure treatment, the three antibiotic perturbation patches mixed at low or high rate have a shared history and can be identified by the replicate number indicated by shape.