

Expanded View Figures

Figure EV1. Establishment of a stable microbial community after three community transfers.

- A Relative abundance of the community members during the community transfer phase prior to drug treatment.
- B Alpha-diversity measurements during the community transfer phase prior to drug treatment.
- C The Bray–Curtis dissimilarity values for pairwise comparison of community compositions during the community transfer phase prior to drug treatment.
- D Growth curves were measured every hour during community establishment. We fit a sigmoid function to the measurements per day, and normalised the resulting OD curves. Based on the observed growth curve, we chose to treat the community after 5 h (black vertical line) so that the tightly spaced time points within 3 h are all within the exponential phase.

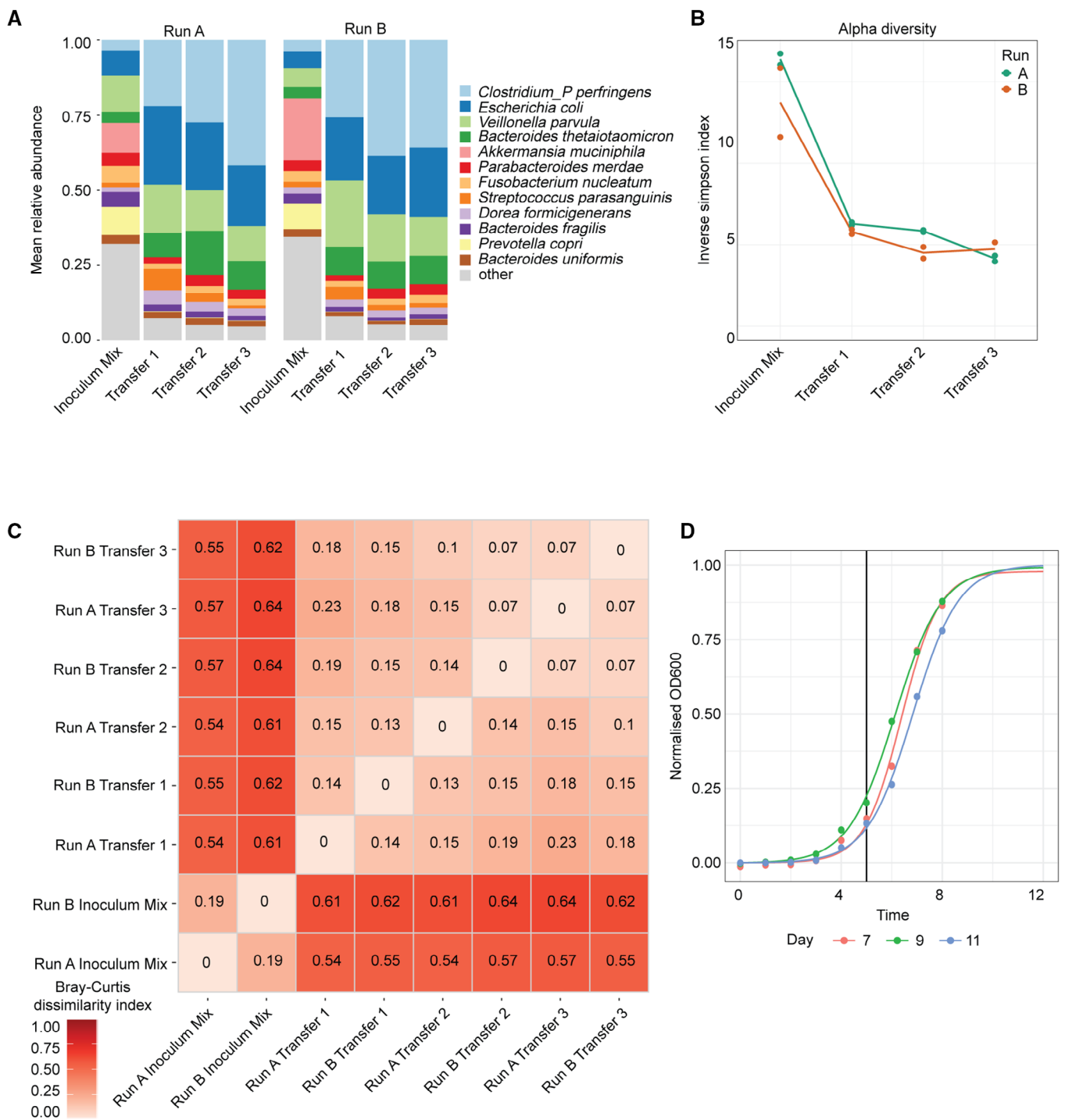


Figure EV1.

Figure EV2. Differences between species abundances estimated by metagenomics and 16S sequencing are not species-, condition- or Gram-type specific.

A Metagenomics versus 16S sequencing species abundances coloured by species.
B Metagenomics versus 16S sequencing species abundances coloured by condition.
C Metagenomics versus 16S sequencing species abundances coloured by Gram staining.

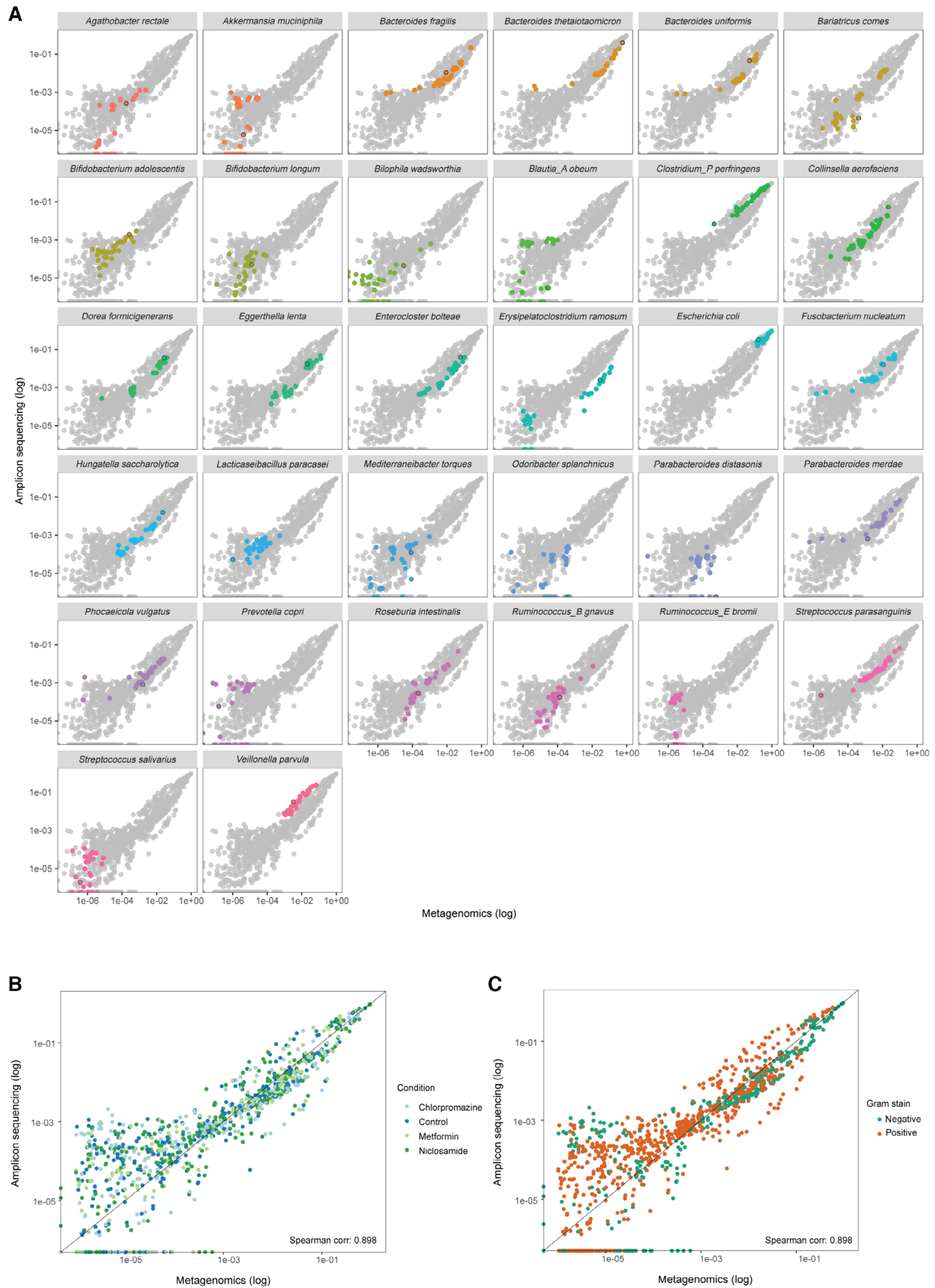
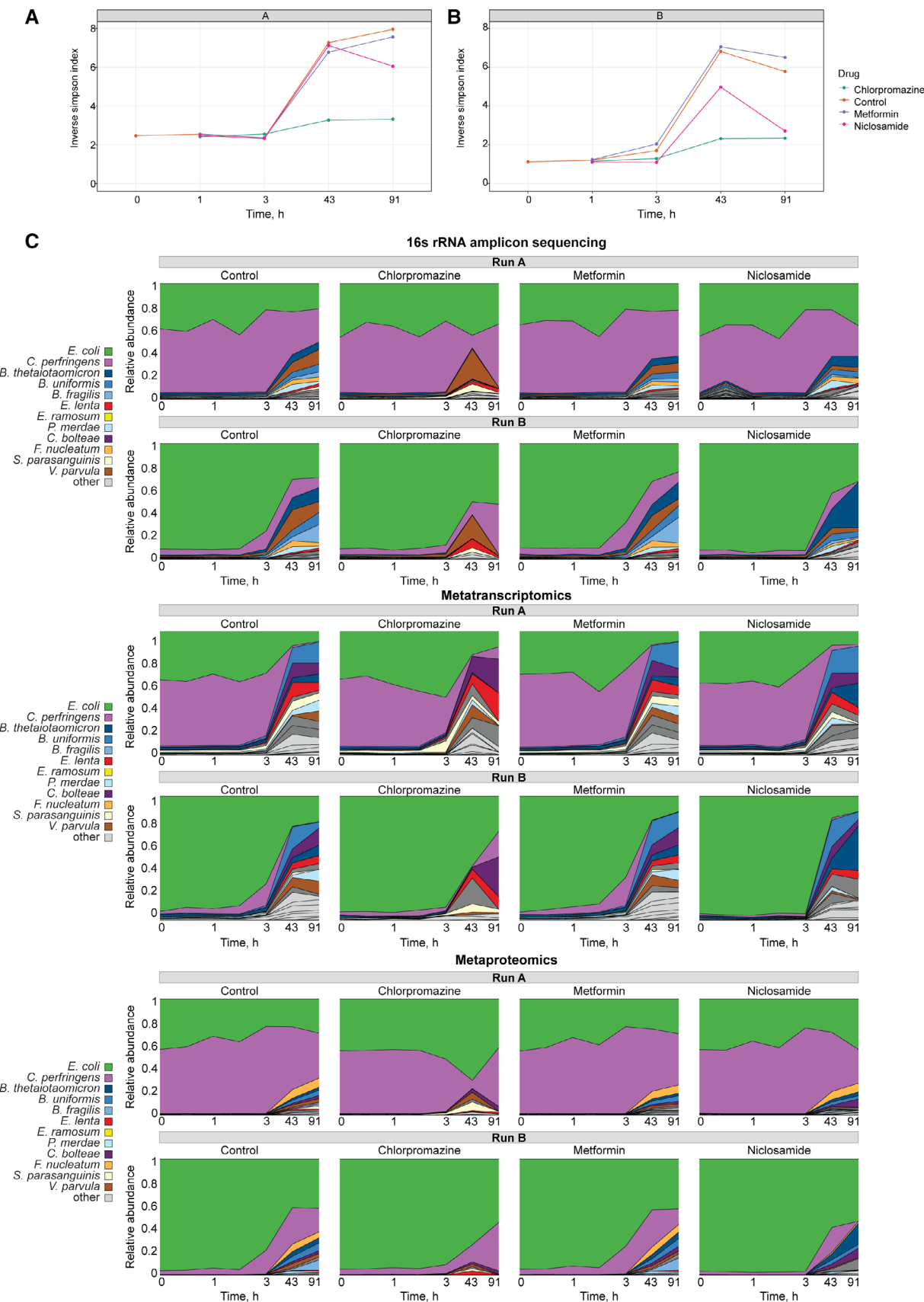


Figure EV2.

Figure EV3. Chlorpromazine strongly affects community composition.

- A, B Community alpha diversity measurements over time after drug treatment for runs A and B, correspondingly.
- C Relative species abundance changes over time in the three drug conditions and control. Relative abundance measured from 16S rRNA amplicon sequencing, metatranscriptomic and metaproteomic data.





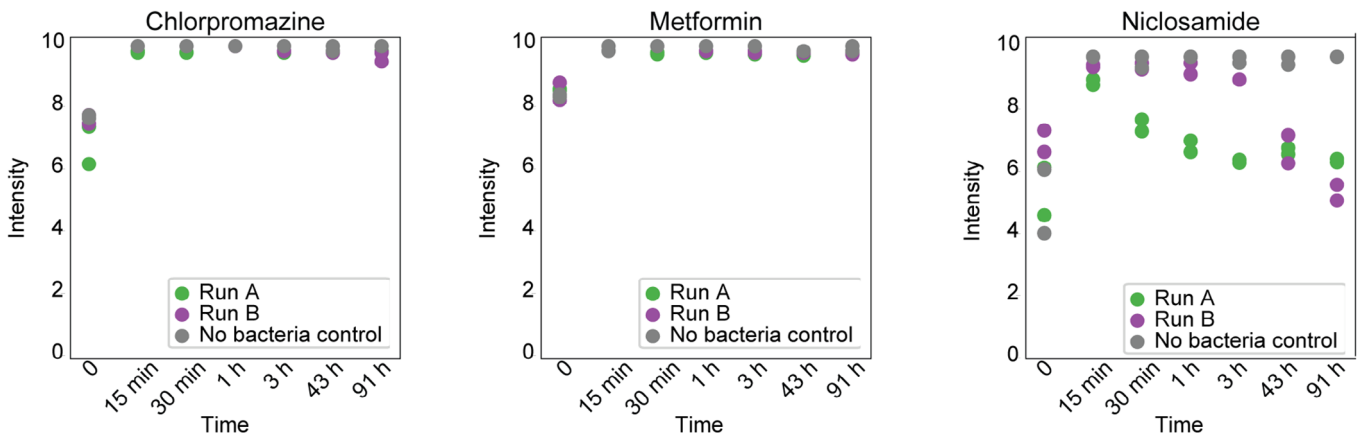


Figure EV4. Drug profiles measured over time.

Drug concentrations were measured both during the community experiments and in controls in sterile medium.

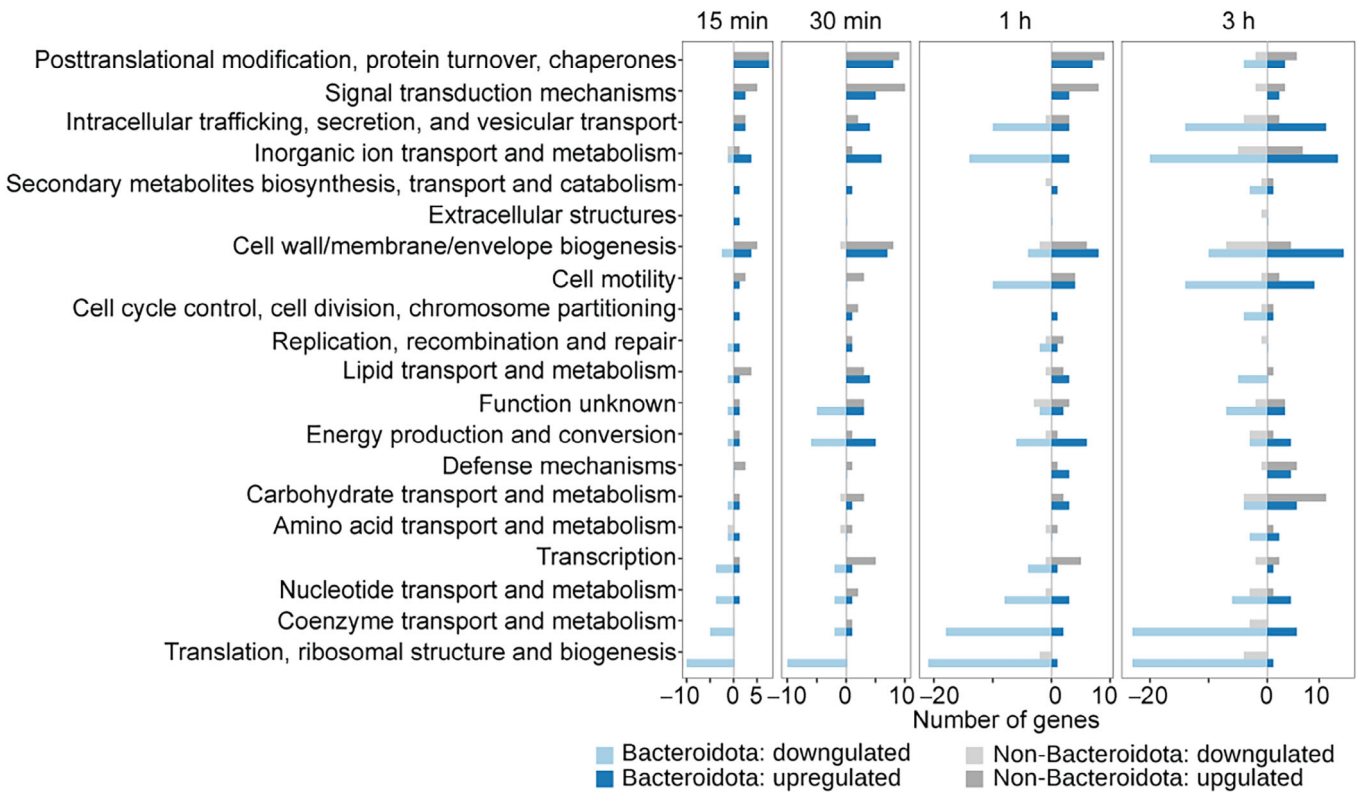


Figure EV5. Number of protein-coding genes grouped by COG category changing per time point upon chlorpromazine treatment.

Bacteroidota species quickly downregulated genes involved in translation and the ribosome compared to other species.