

Figure 1

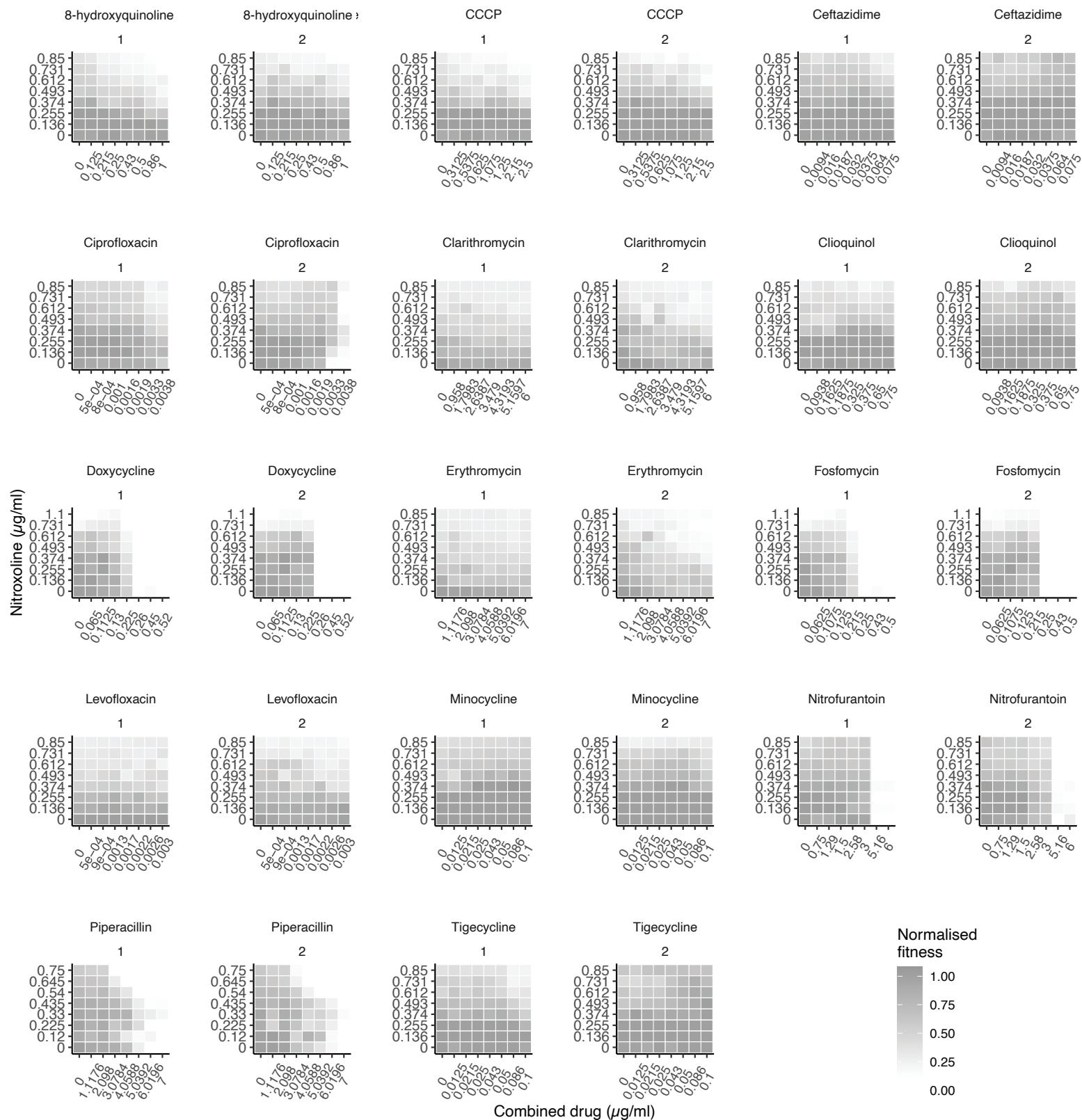


Figure 1 (continued). Two biological replicates of checkerboard assays displayed in Supplementary Fig. 3, from which Bliss interaction scores shown in Fig. 2a are obtained. Results are obtained and represented as in Supplementary Fig. 3.

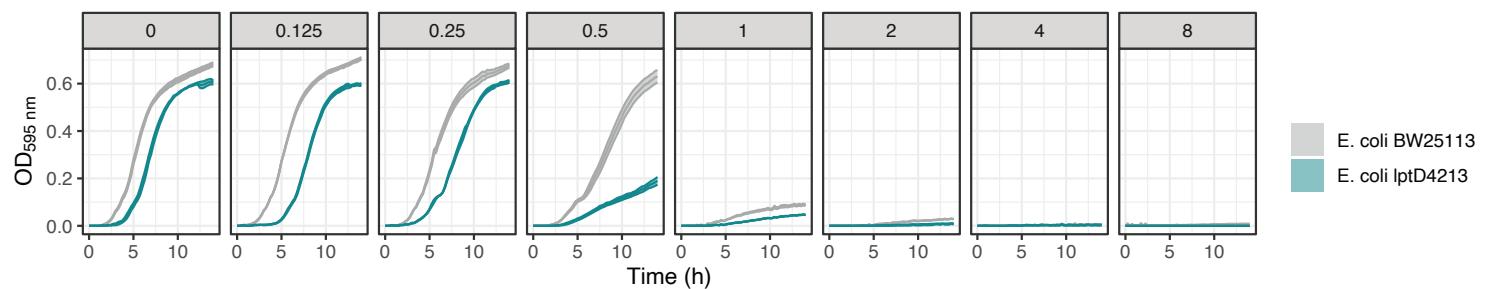


Figure 3. Full growth curves from which dose-response curves depicted in Supplementary Fig. 5d were obtained. Mean OD_{595nm} and standard error across four biological replicates are shown.

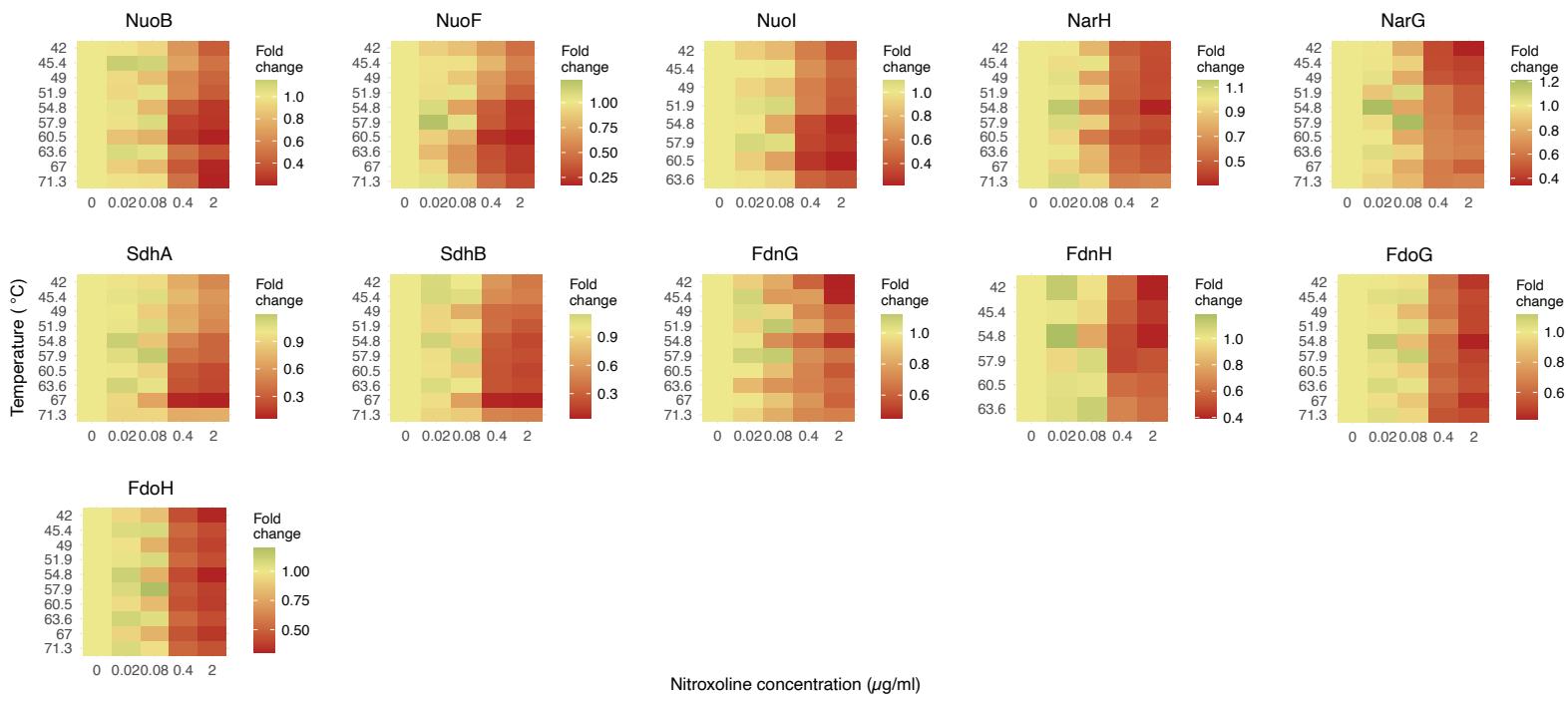


Figure 4. Thermal stability profiles of members of the respiratory chain. Data is presented as in Fig. 4b.

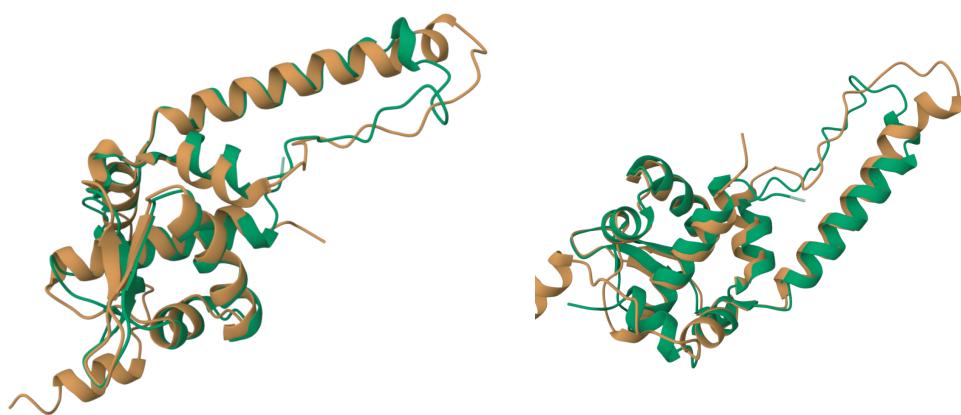


Figure 5. Structural alignments between OqxR and NsrR (Methods), which was used for the domain annotation shown in Fig. 5d.

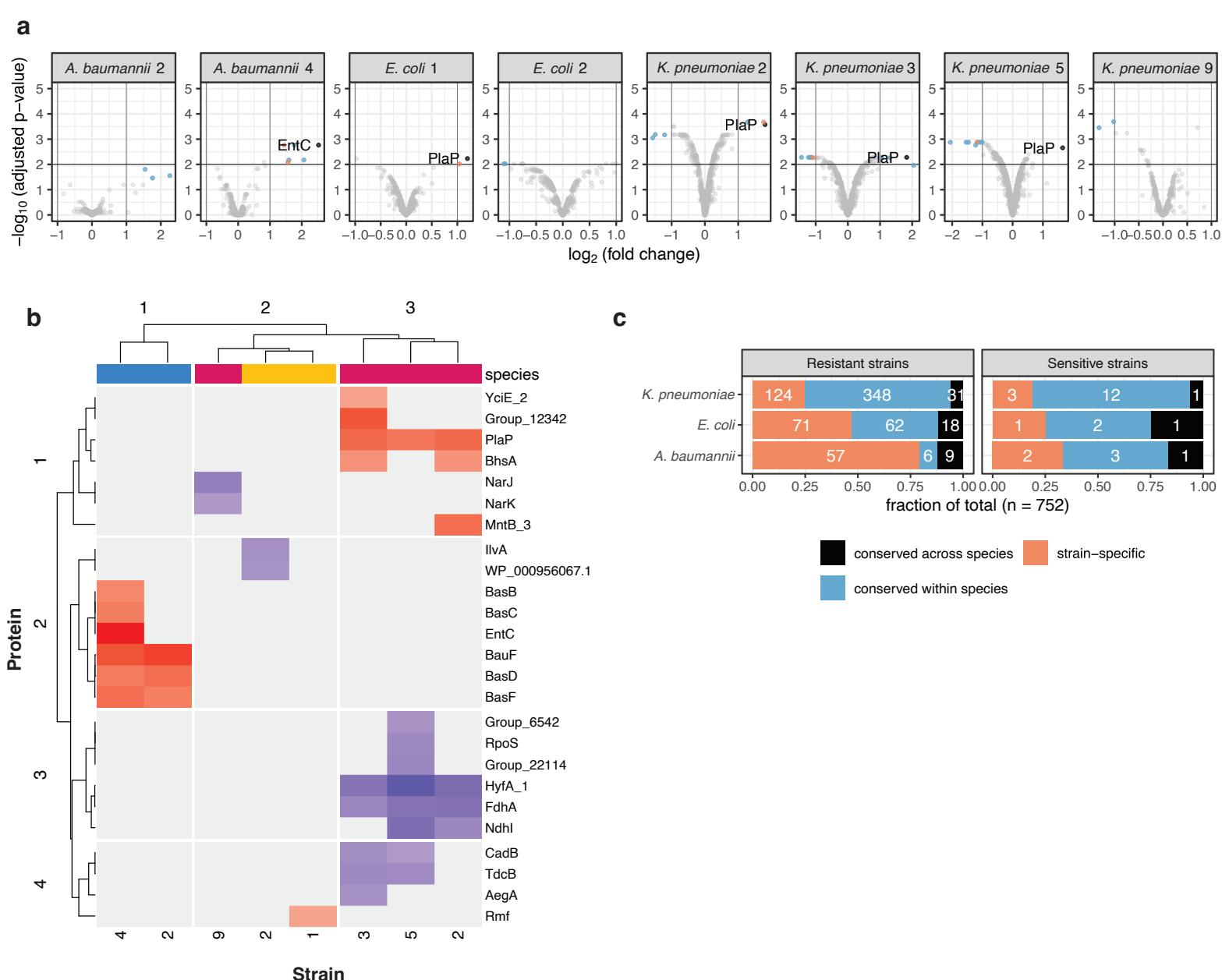


Figure 6. **a.** Volcano plots of abundance changes in proteomics of sensitive strains exposed to nitroxoline compared to untreated controls. Data is represented as in Supplementary Fig. 6a. **b.** Protein abundance changes in nitroxoline-sensitive strains. Data are represented as in Supplementary Fig. 6b. **c.** Conservation of protein changes in resistant and isogenic sensitive strains exposed to nitroxoline, color-coded as in Supplementary Fig. 6a.

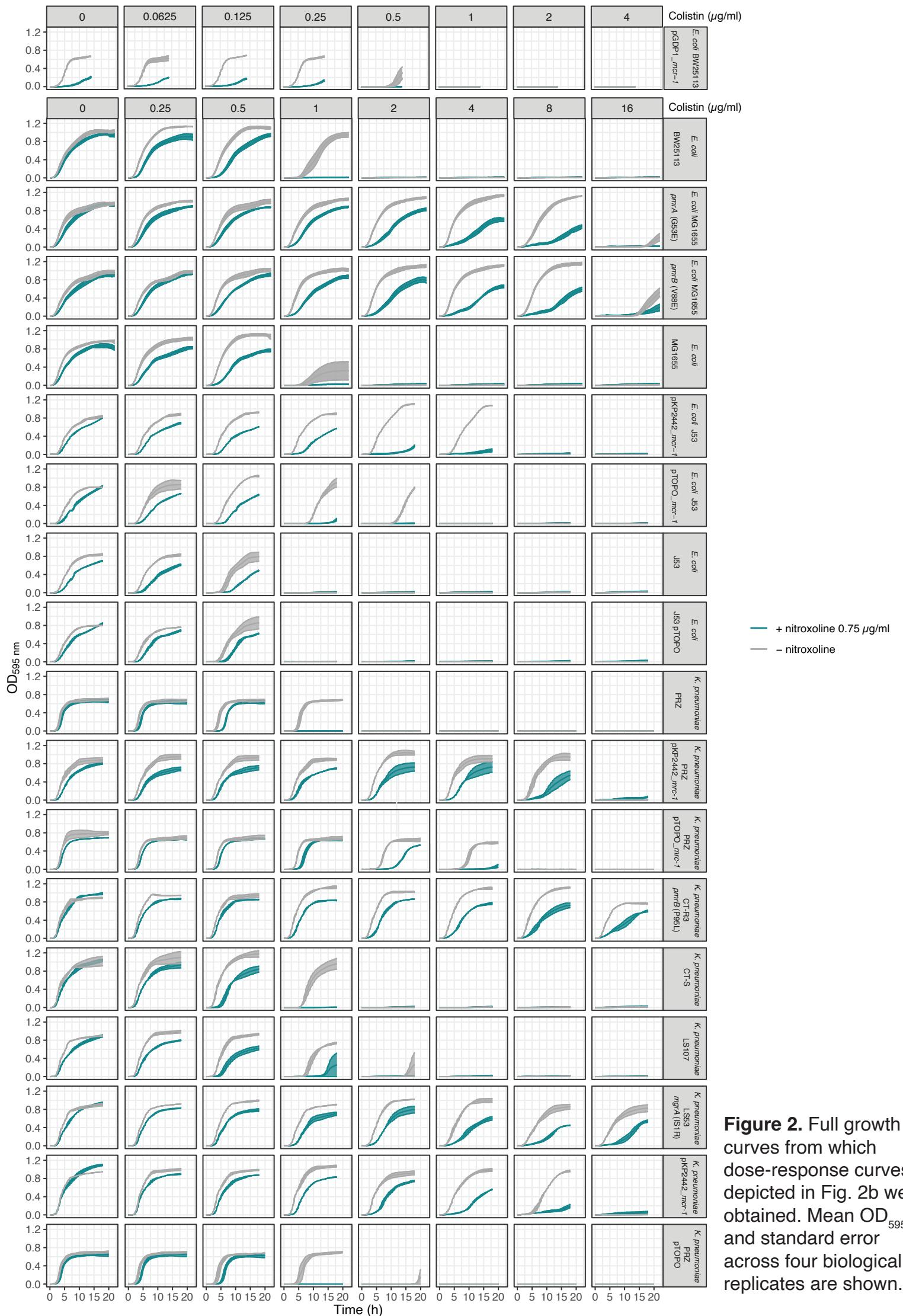


Figure 2. Full growth curves from which dose-response curves depicted in Fig. 2b were obtained. Mean OD_{595nm} and standard error across four biological replicates are shown.