

Unraveling the Evolutionary Dynamics of Toxin-Antitoxin Systems in Diverse Genetic Lineages of *Escherichia coli* including the High-risk Clonal Complexes

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Supplementary Figures

Detailed captions/legends

Fig. S1: Scree plot depicting the explained variance of top 10 principle components.

Fig. S2: Heatmap illustrating the percentage prevalence of antitoxin groups across 19 STs of *E. coli*. The x-axis depicts ST lineage, while the y-axis depicts antitoxin groups identified. The color bar on the right side depicts % presence.

Fig. S3: Heatmap illustrating the percentage prevalence of TA pair across 19 STs of *E. coli*. The x-axis depicts ST lineage, while the y-axis depicts TA pair identified. The color bar on the right side depicts % presence.

Fig. S4: Toxin-antitoxin network of *E. coli* isolates with red colored nodes depicting toxin hits and green colored nodes depicting antitoxin partners, while edges represent association between TA pairs.

Fig. S 5: Distribution plots for the range of amino acid lengths selected for toxin/antitoxin prediction

Fig. S6: Heatmap illustrating the percentage prevalence of orphan antitoxins across 19 STs of *E. coli*. The x-axis depicts ST lineage, while the y-axis depicts orphan antitoxin identified. The color bar on the right side depicts % presence

Fig. S7. Heatmap illustrating the percentage prevalence of orphan toxins across 19 STs of *E. coli*. The x-axis depicts ST lineage, while the y-axis depicts orphan toxin identified. The color bar on the right side depicts % presence

Fig. S1: Scree plot

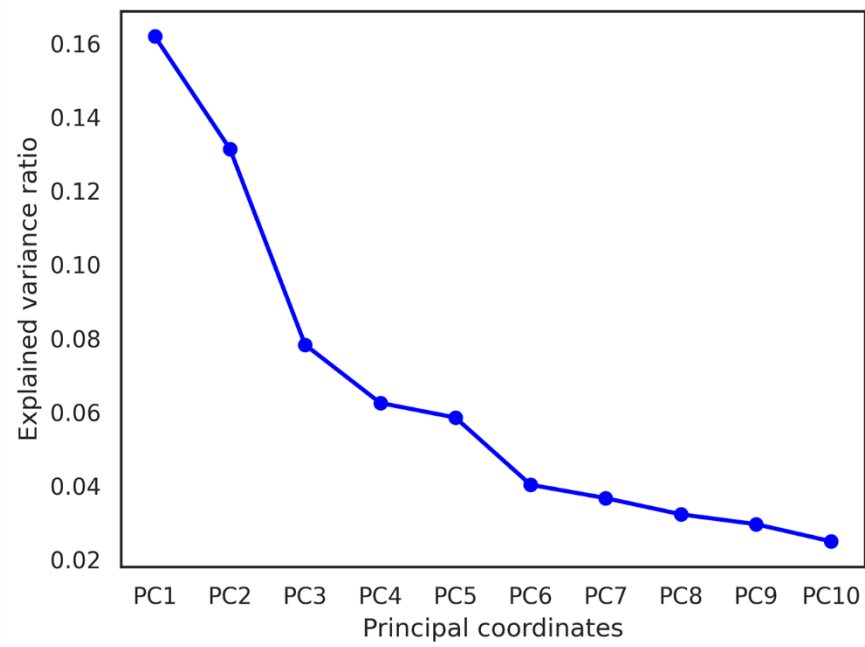


Fig. S2: Heatmap depicting prevalence of antitoxin groups

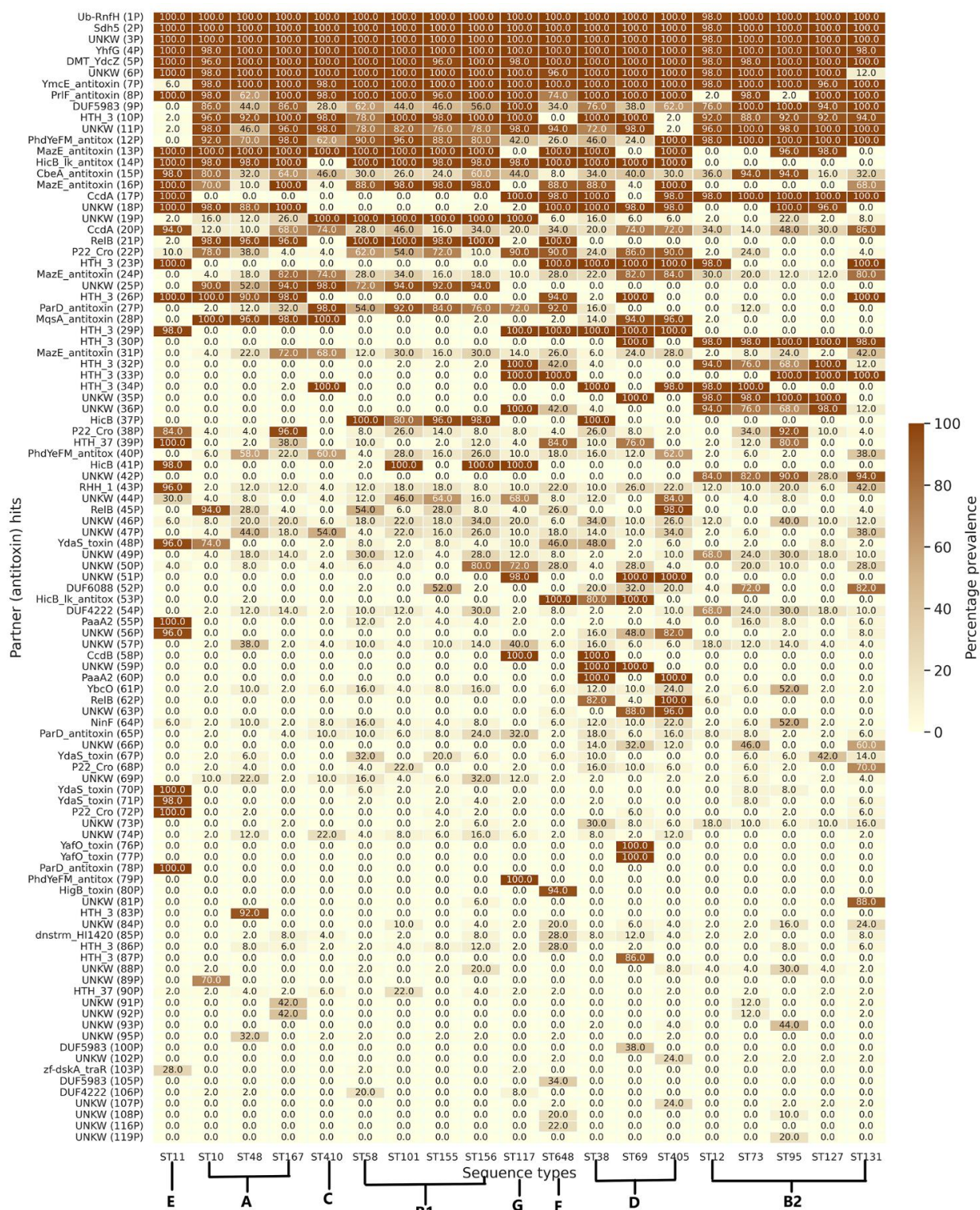
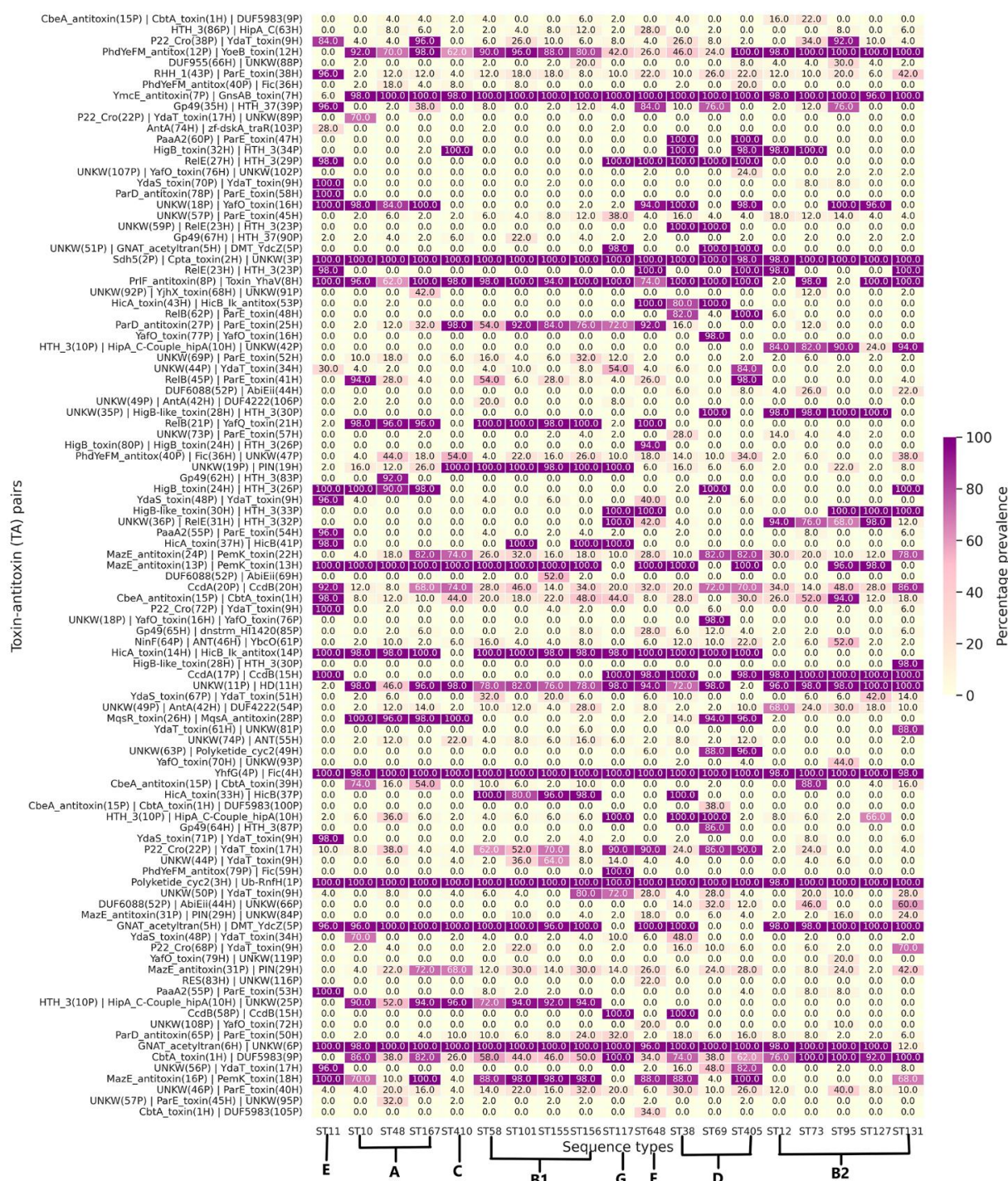


Fig. S3: Heatmap depicting prevalence of complete TA operons



The diagram shows a network of 20 central nodes (red circles) and their connections to peripheral nodes (grey circles). The nodes are labeled with numbers and letters, and the connections are labeled with numbers and letters. The diagram illustrates the network structure and the distribution of nodes and connections.

Fig. S5: Distribution plots of amino acid length selected for TA systems prediction

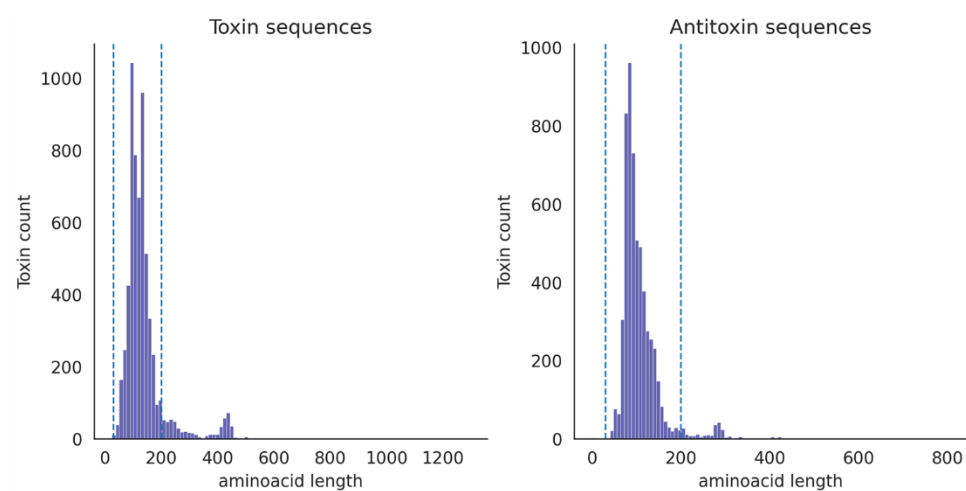


Fig. S6: Heatmap depicting prevalence of orphan antitoxins

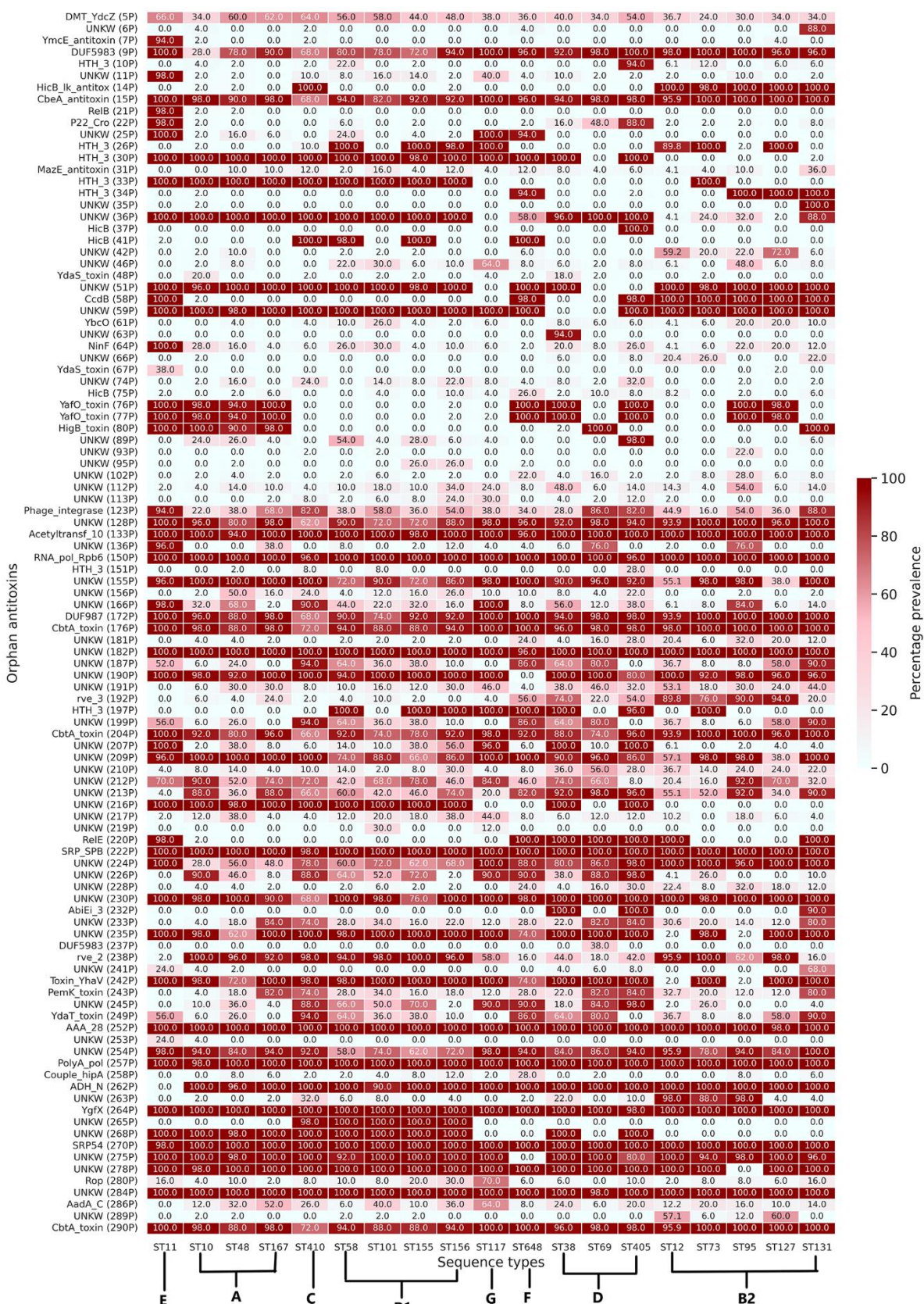


Fig. S7: Heatmap depicting prevalence of orphan antitoxins

