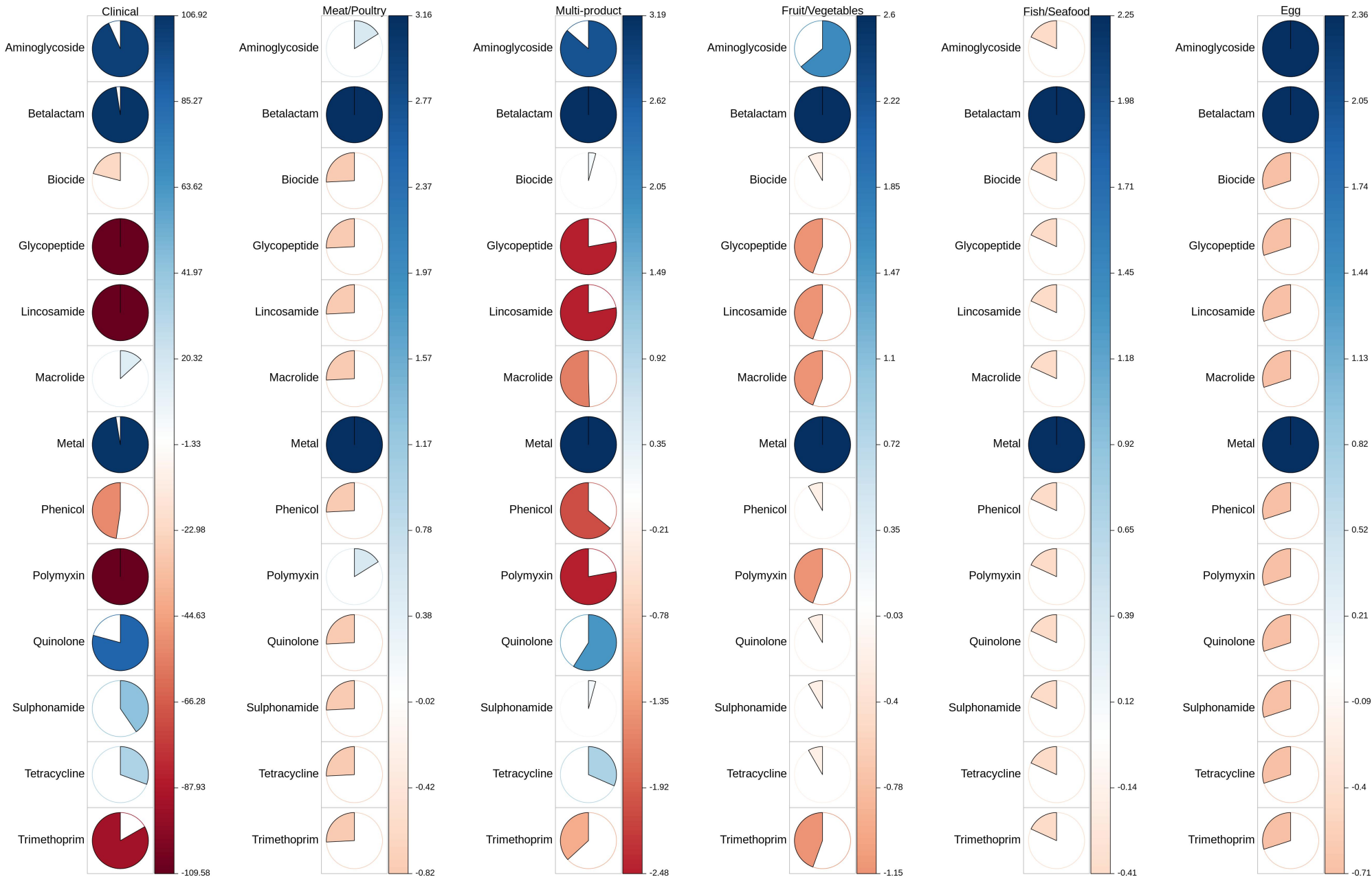


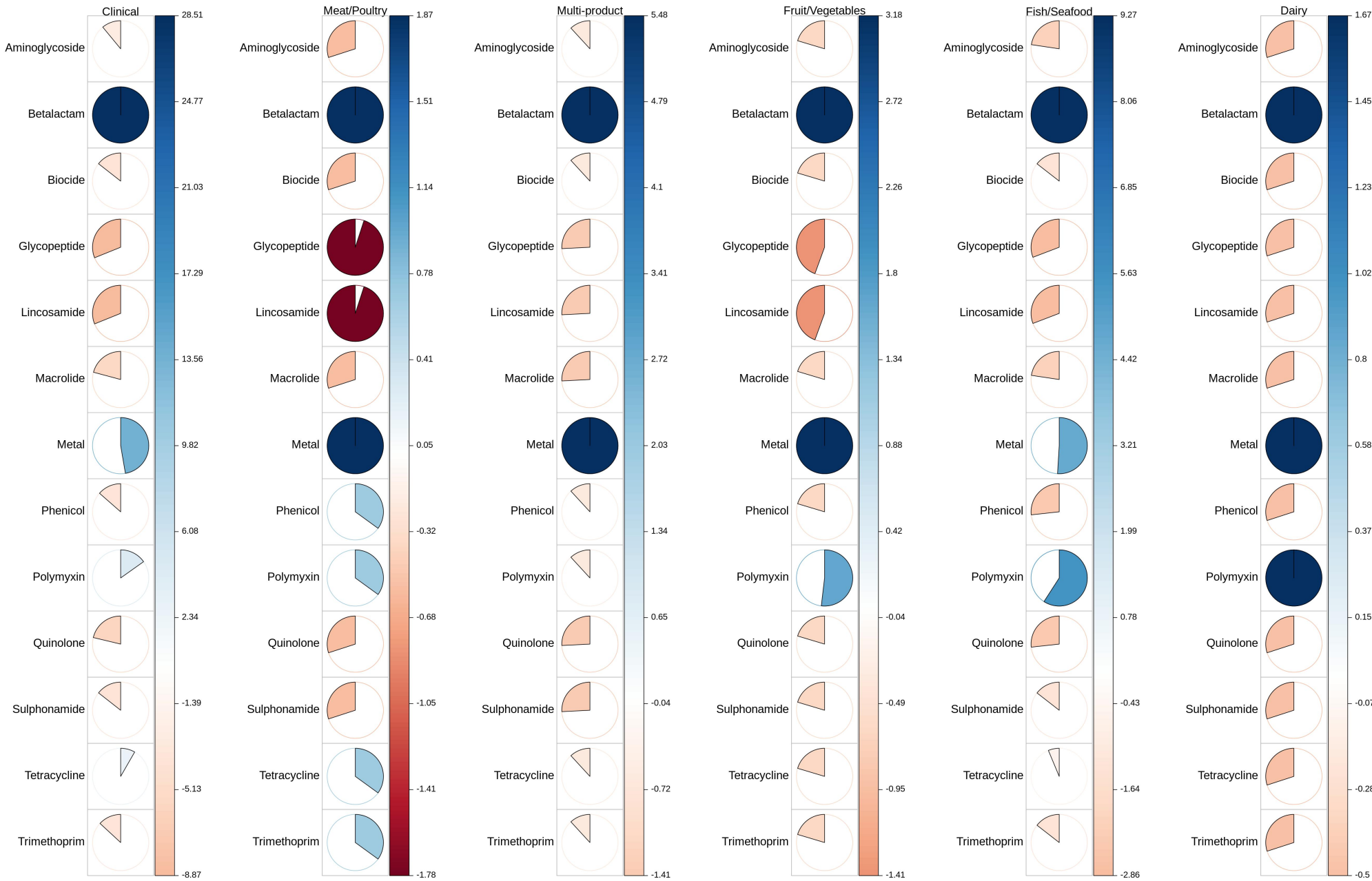
Supplementary File S3

The following pages contain supplementary figures for correlation analysis of the resistance levels for each genus (top left of page). For each genus, chi-square was performed for each isolation source for which there was at least one sequence/isolate. Correlation plots were created for each source (top panel headings) using the Pearson standardised residuals output by Chi square analysis. The Pearson standardised residuals measure the departure of each cell from independence, thereby showing the strength and direction of association. Positive residuals are blue and specify a positive association or attraction of resistance between corresponding antimicrobial class (left row labels) and source (column label). Red fill indicates a negative association or repulsion between antimicrobial class and isolation source. The filled portion of the pie indicates the magnitude of the correlation (eg. amount of the cell contribution (resistance class) to the overall test statistic for that isolation source). Legend bars differ between genera and sources, and indicate the standardised residual.

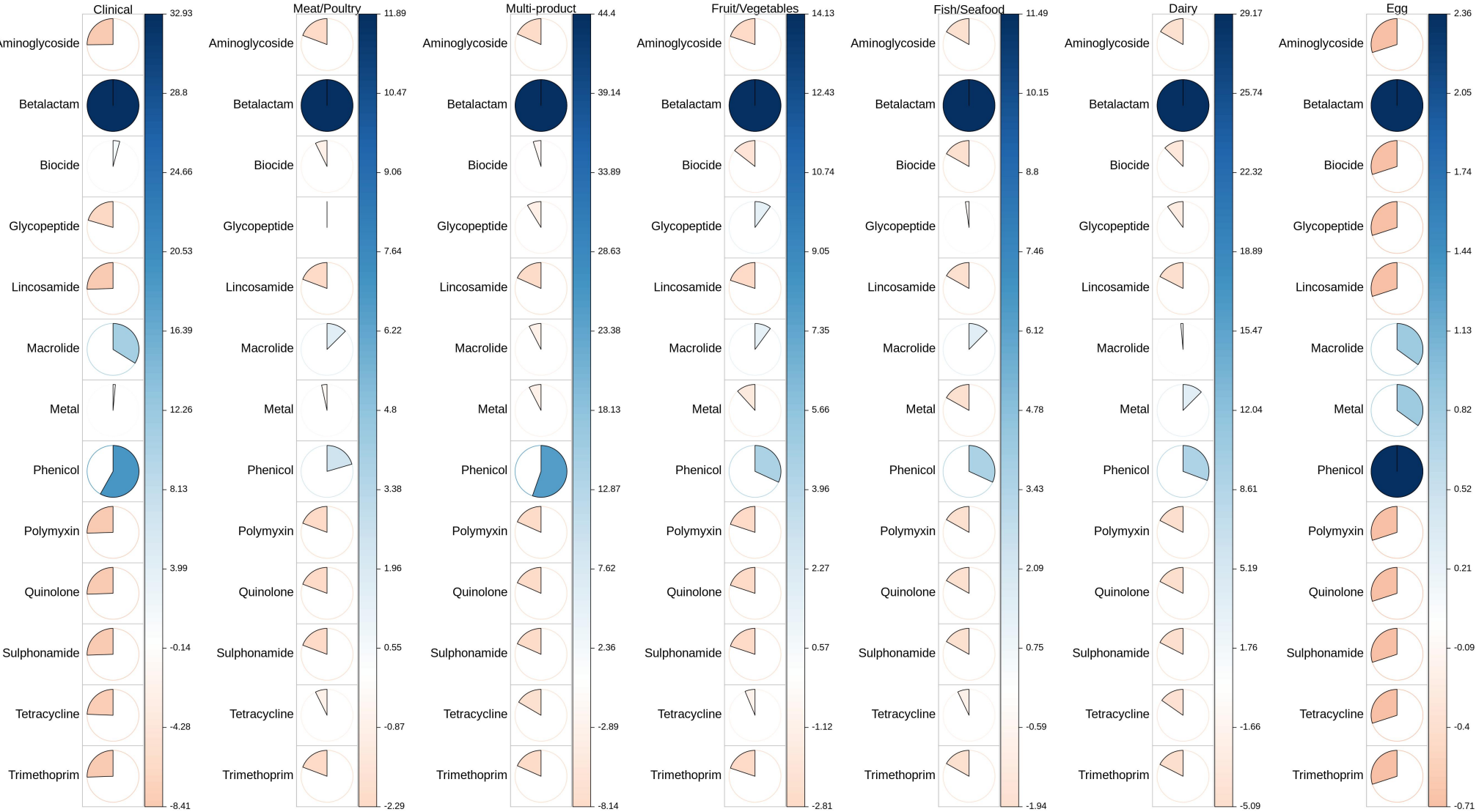
Acinetobacter



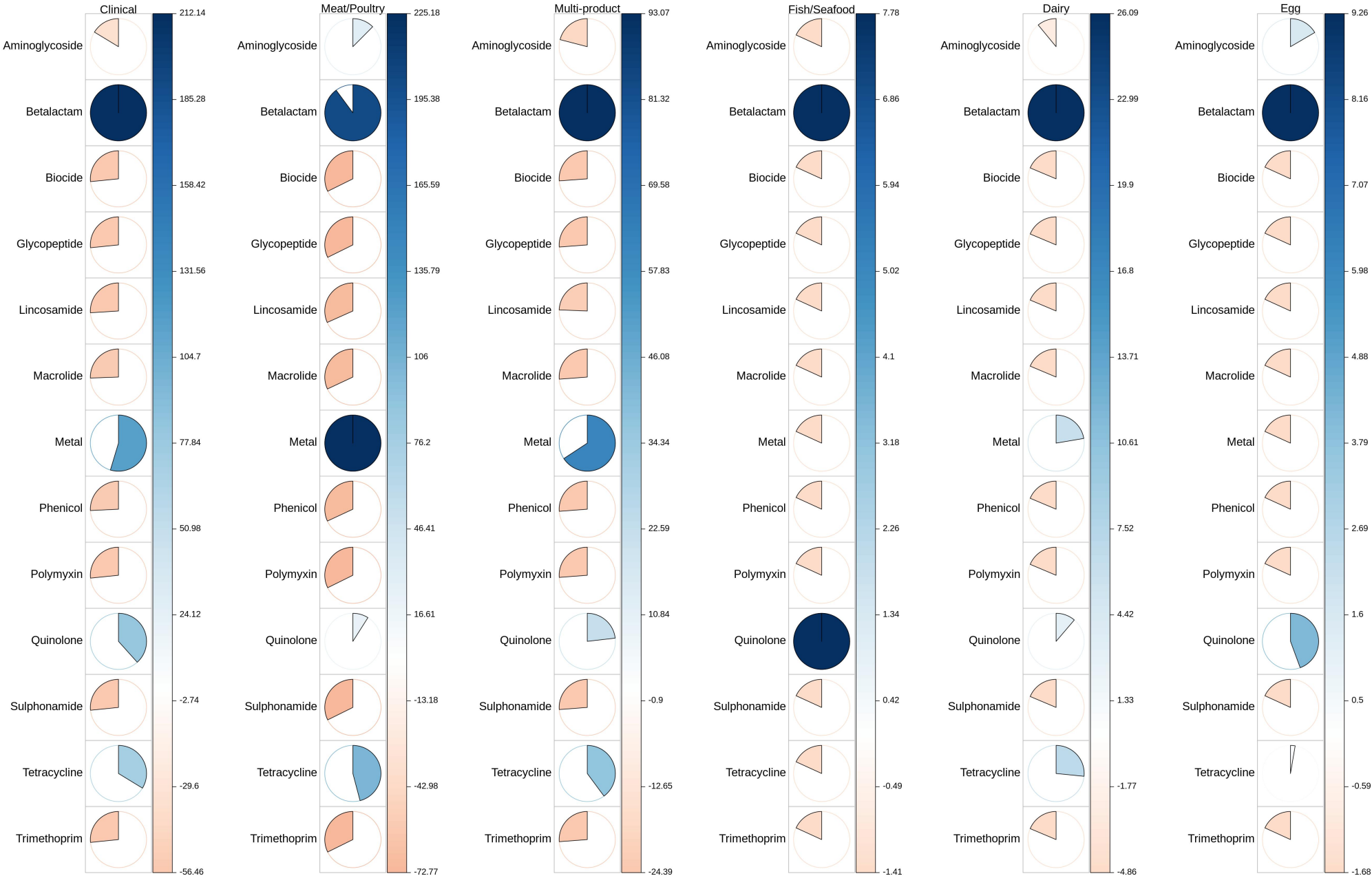
Aeromonas



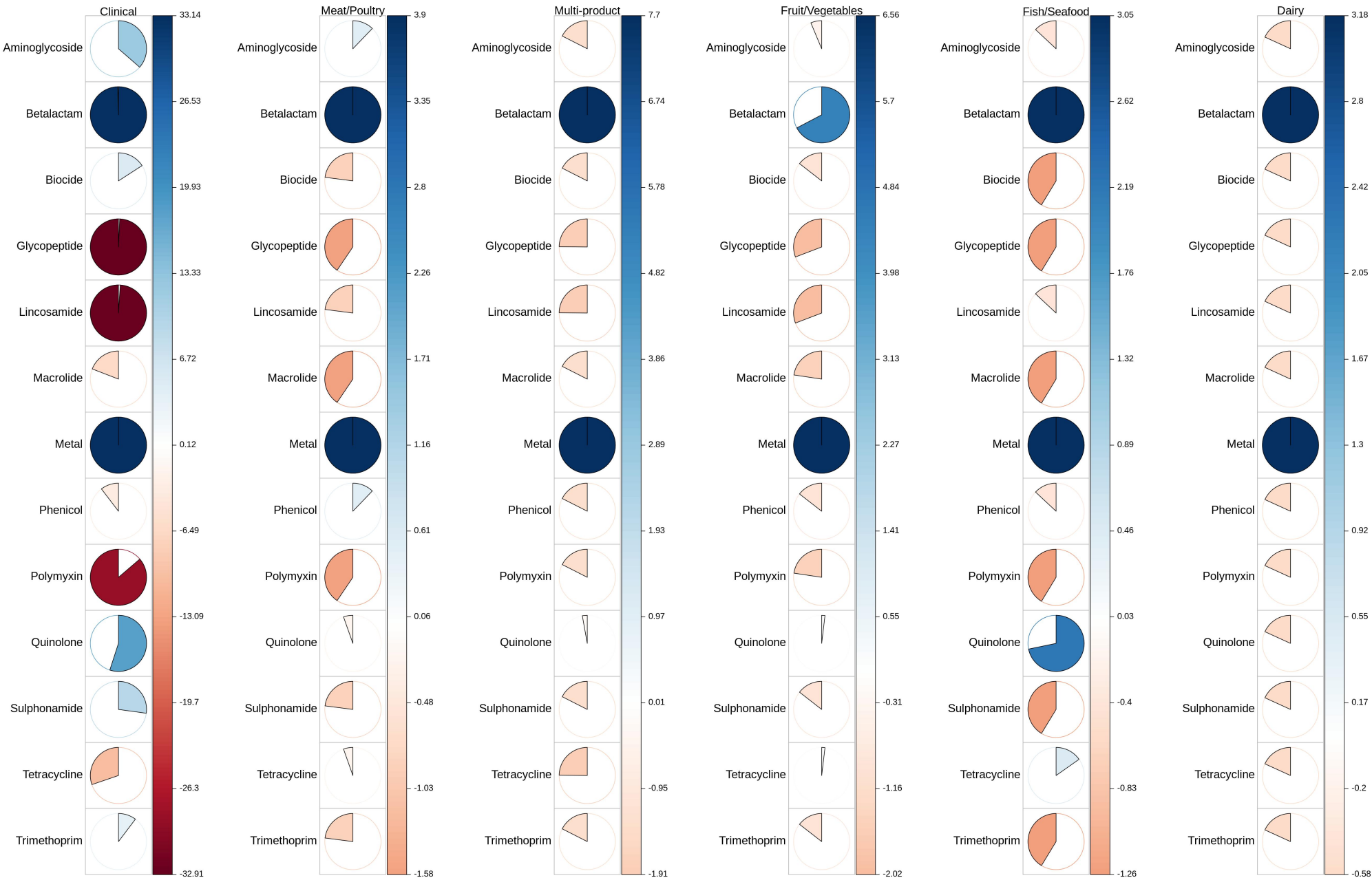
Bacillus



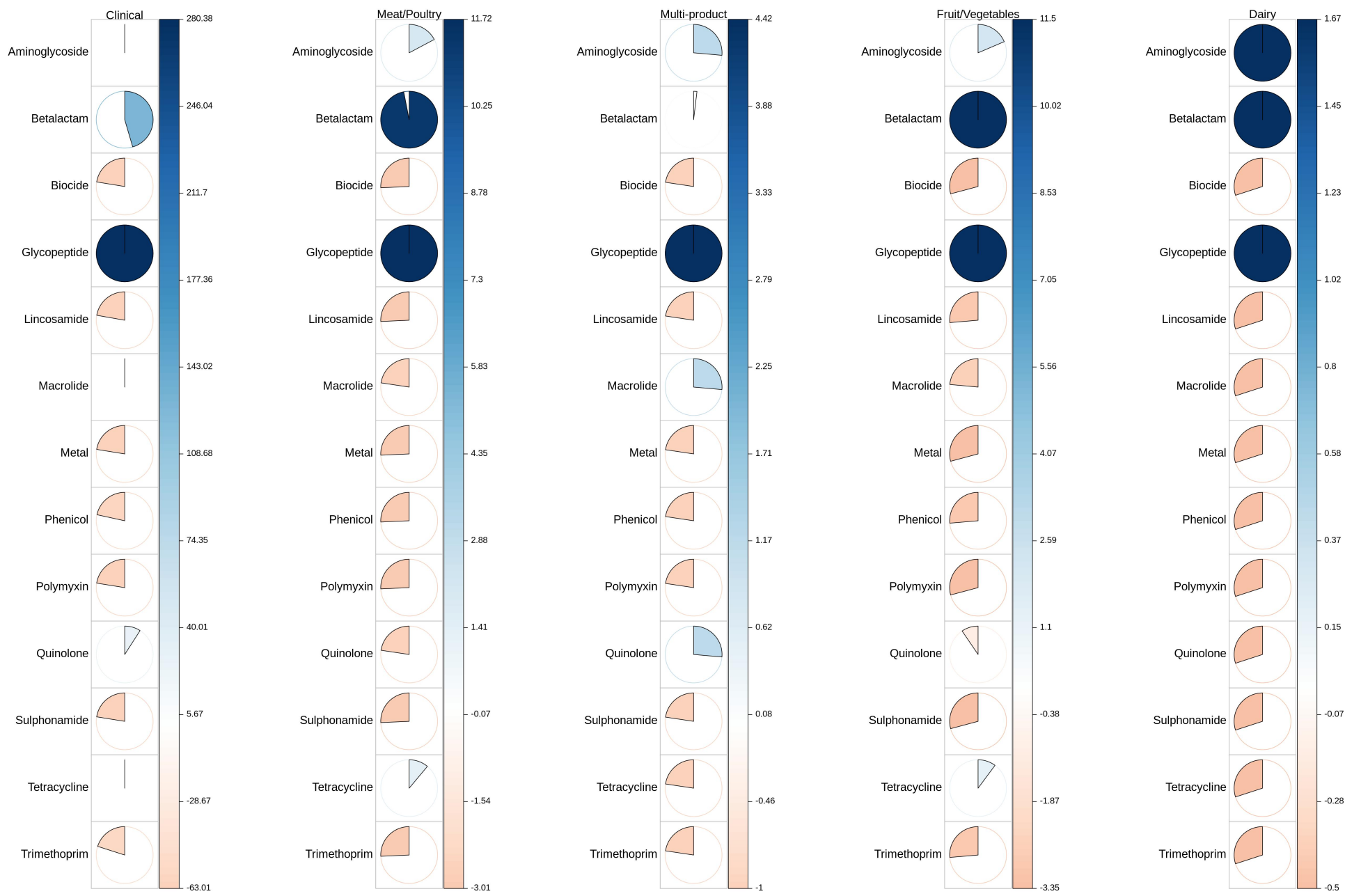
Campylobacter



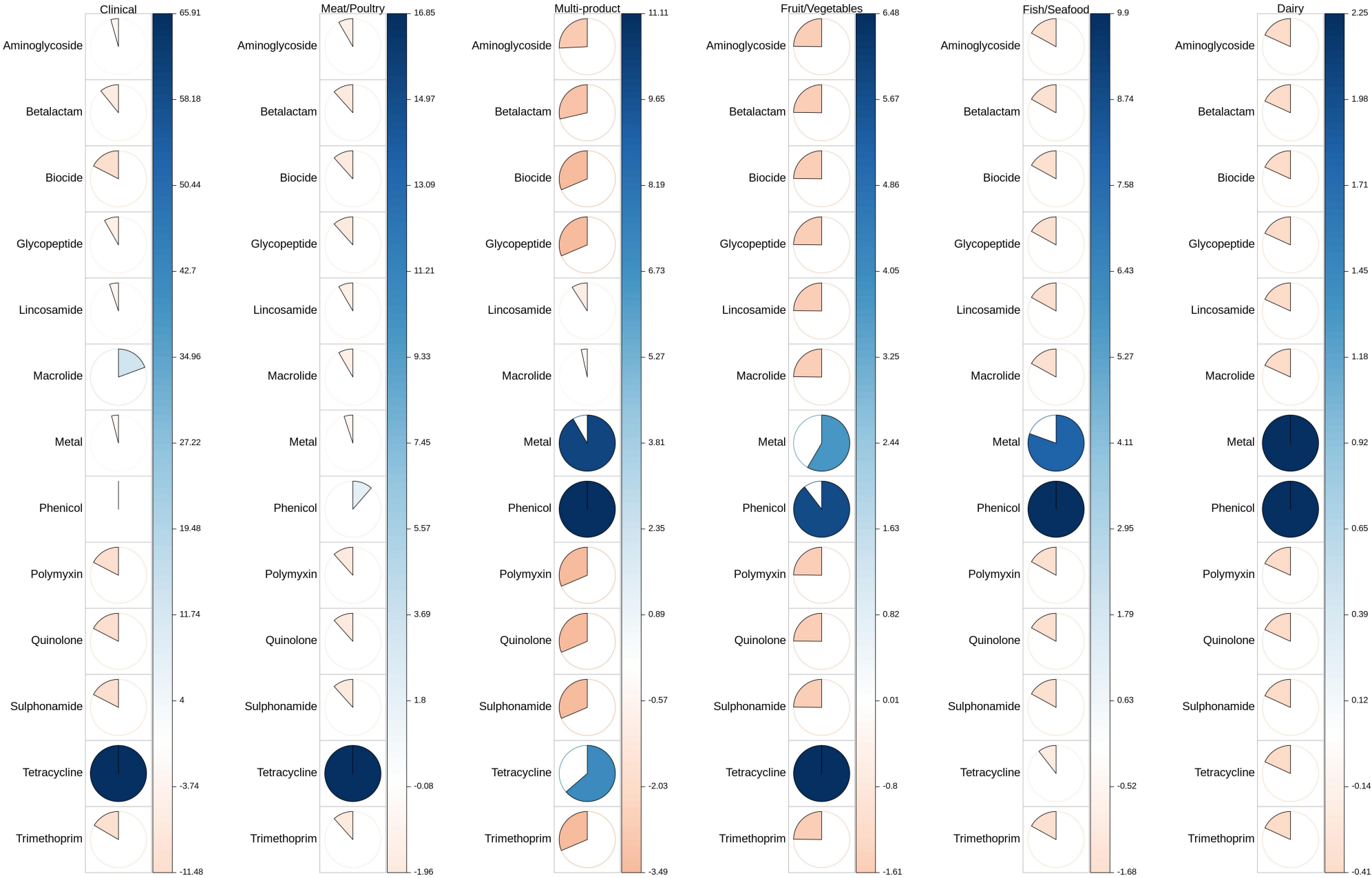
Citrobacter



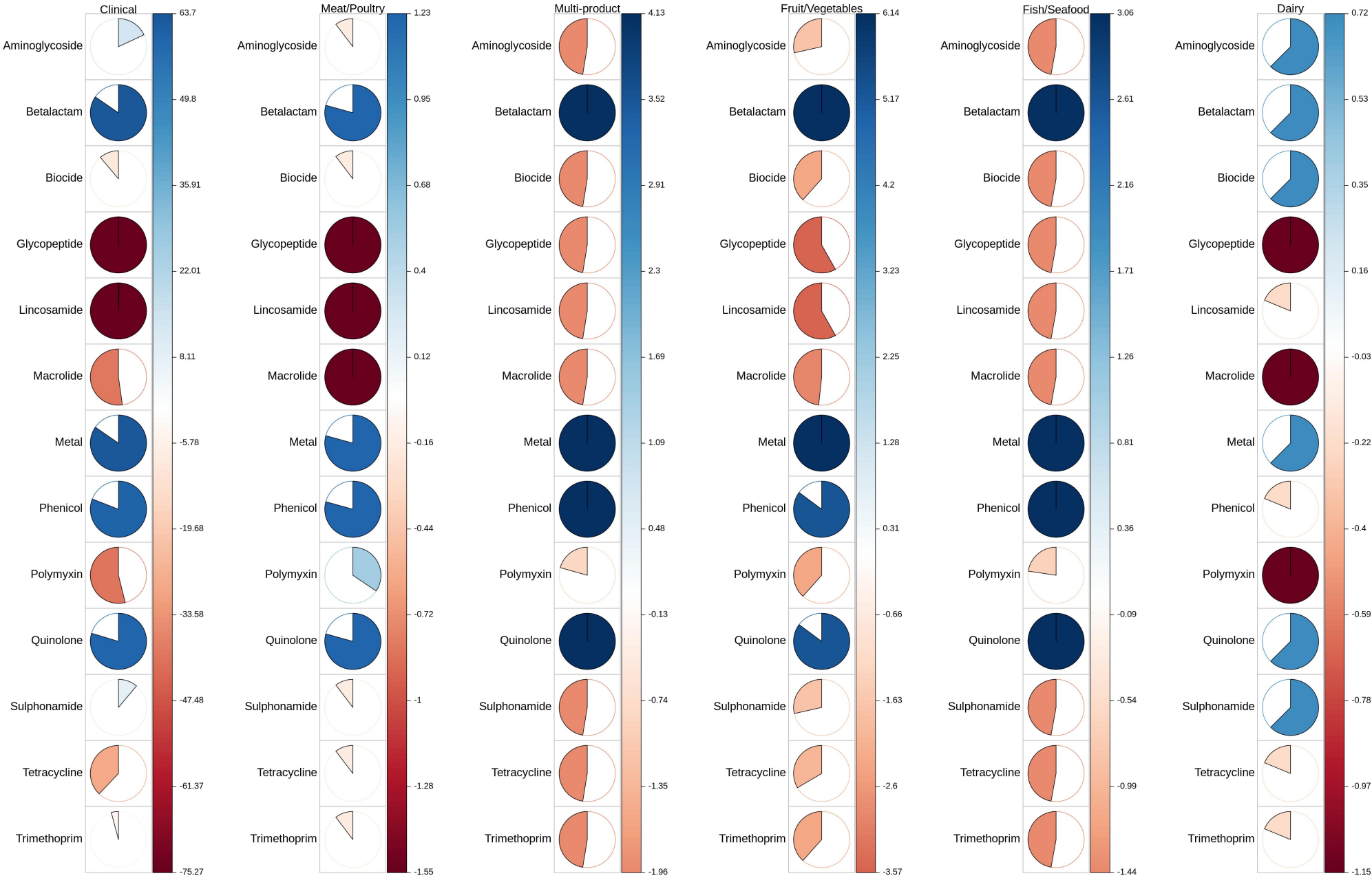
Clostridioides difficile



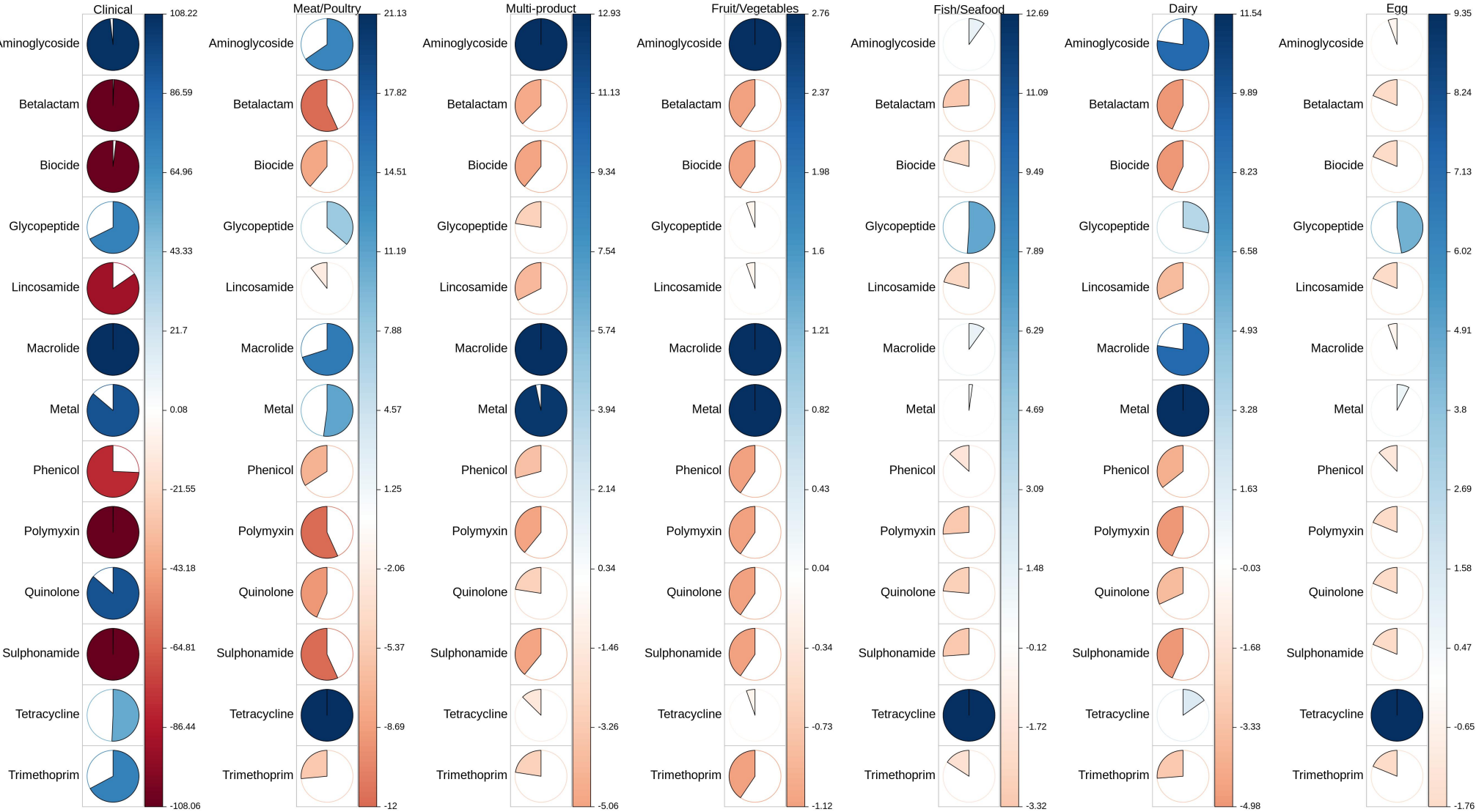
Clostridium



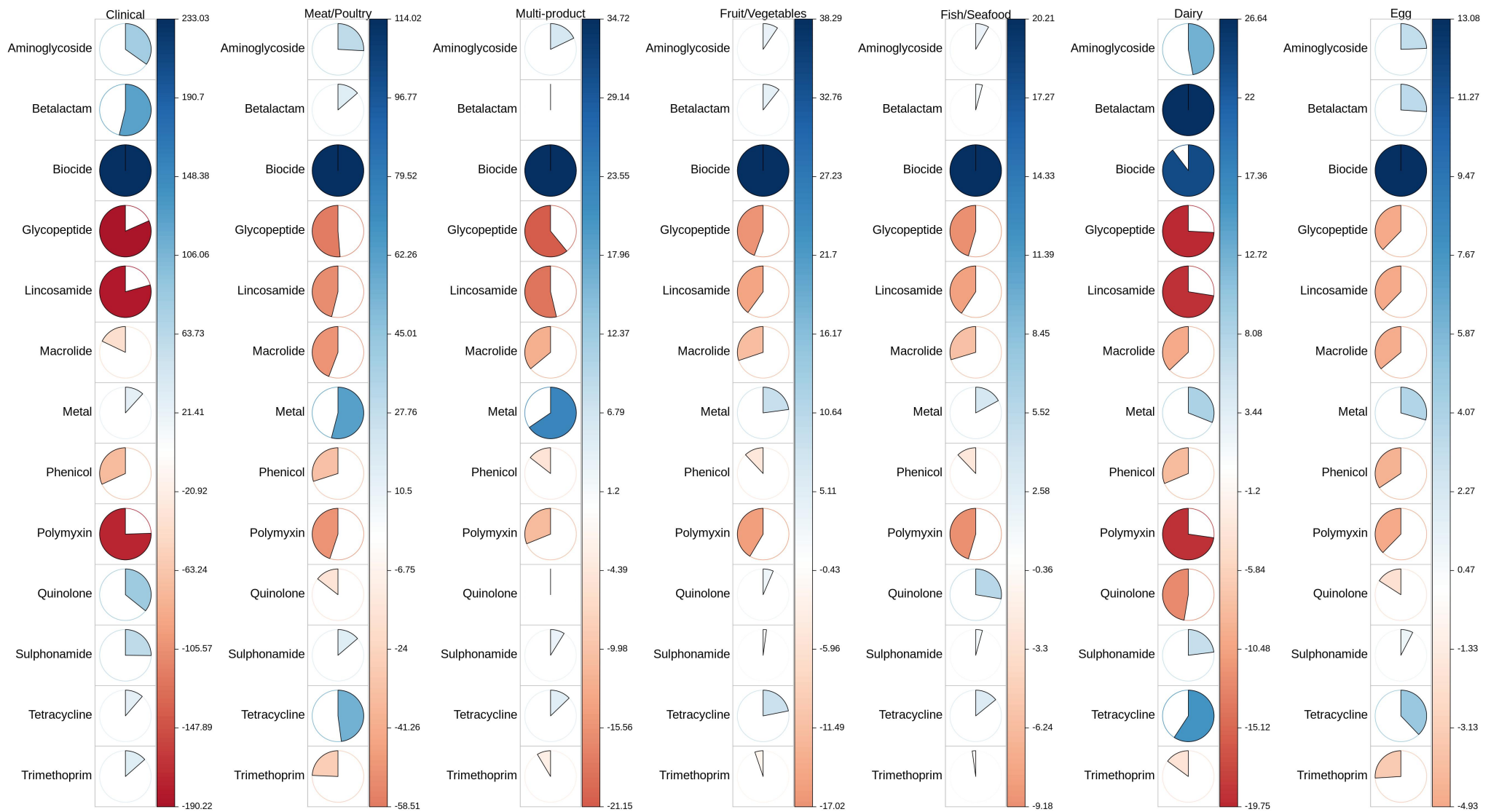
Enterobacter



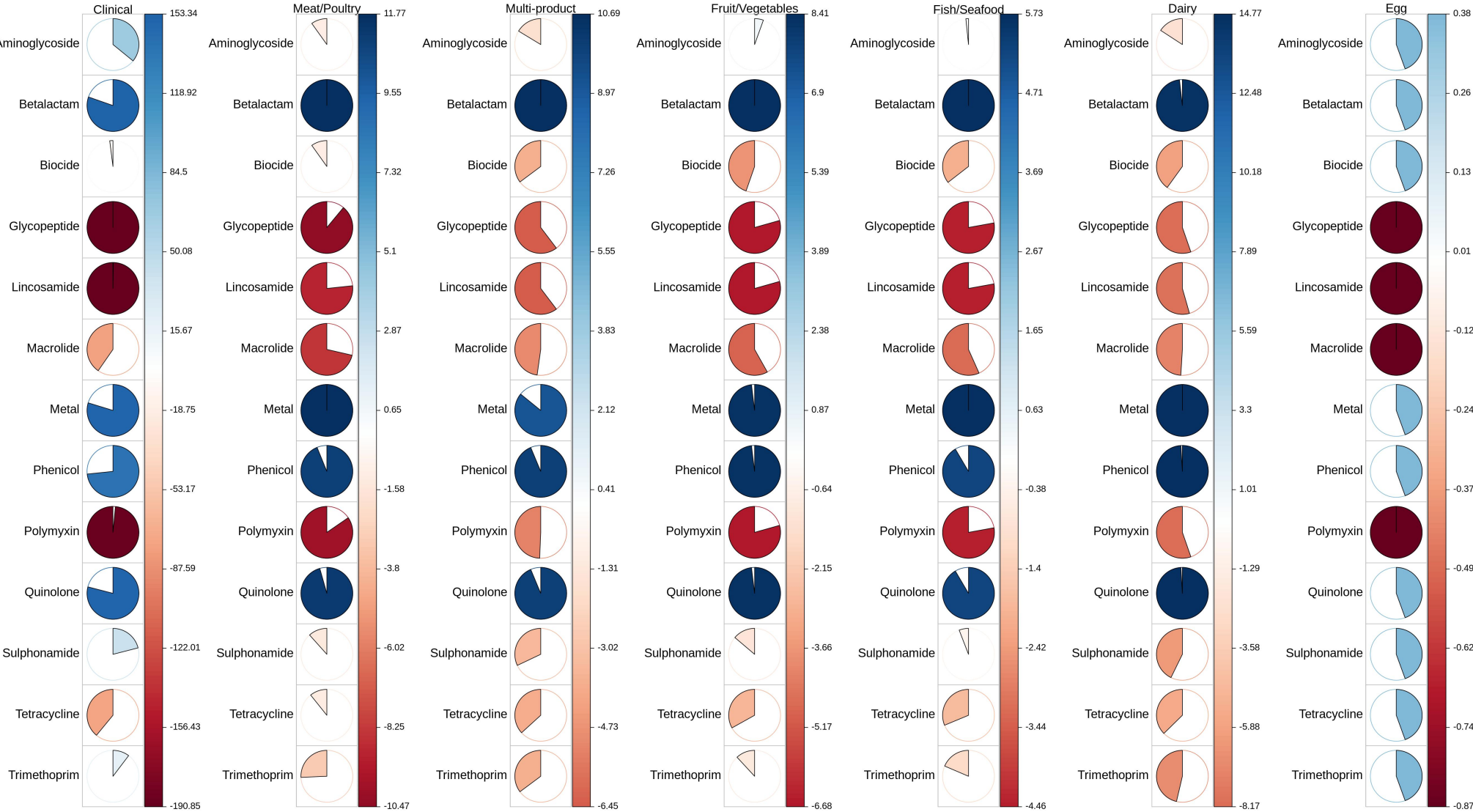
Enterococcus



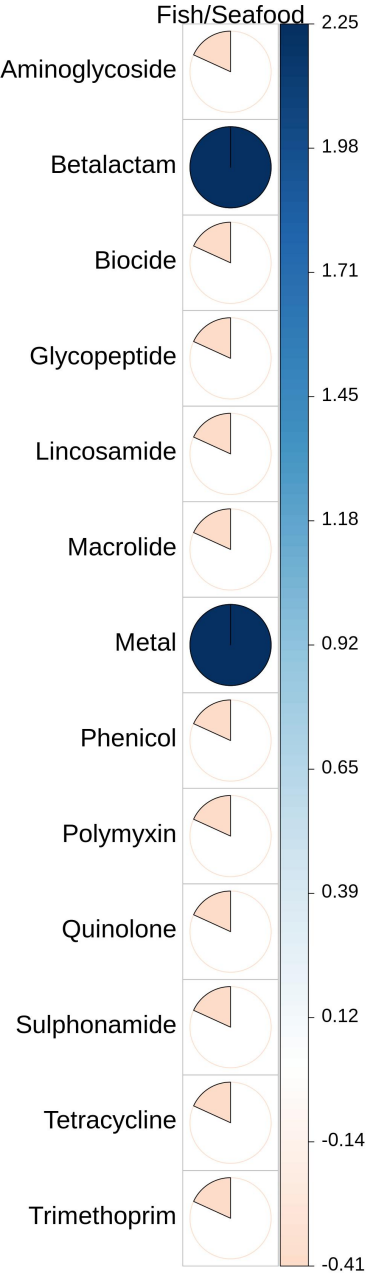
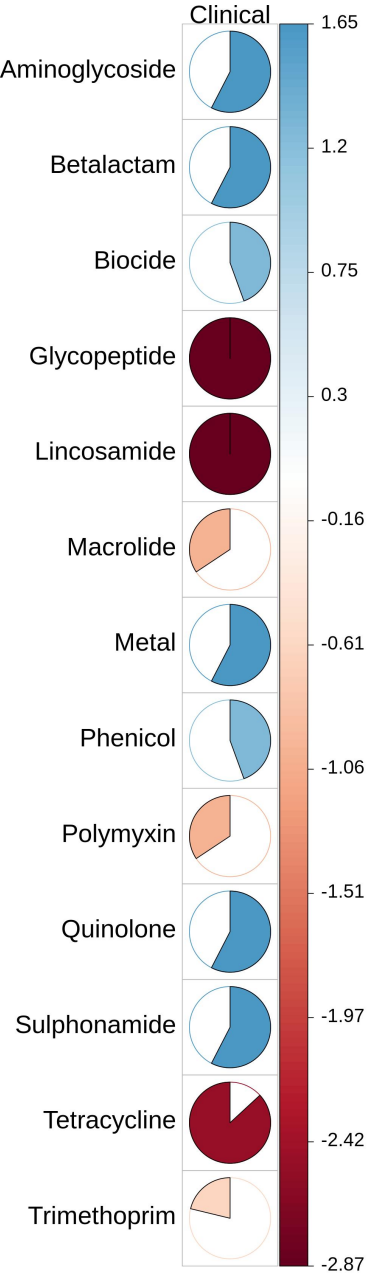
Escherichia



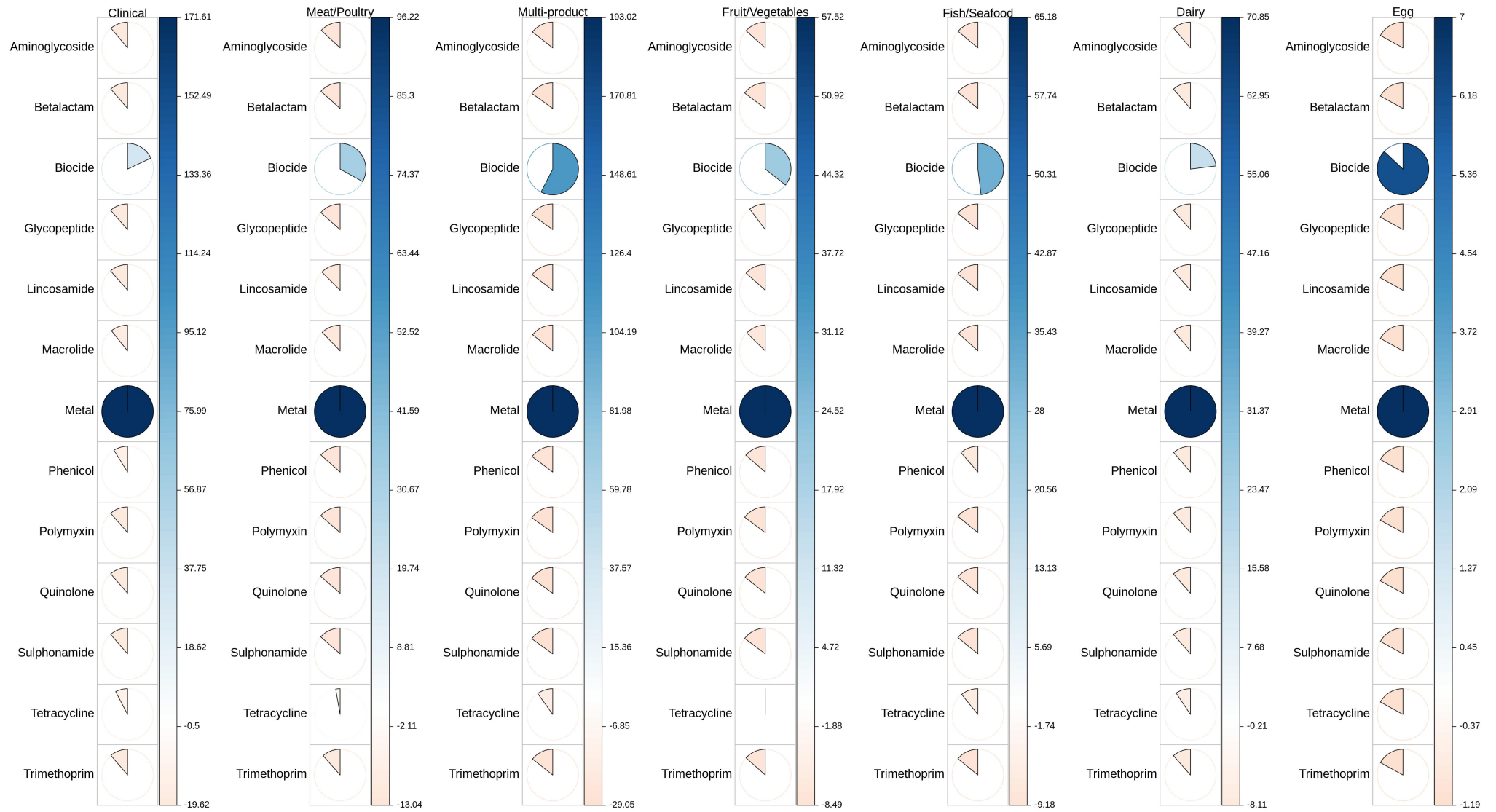
Klebsiella



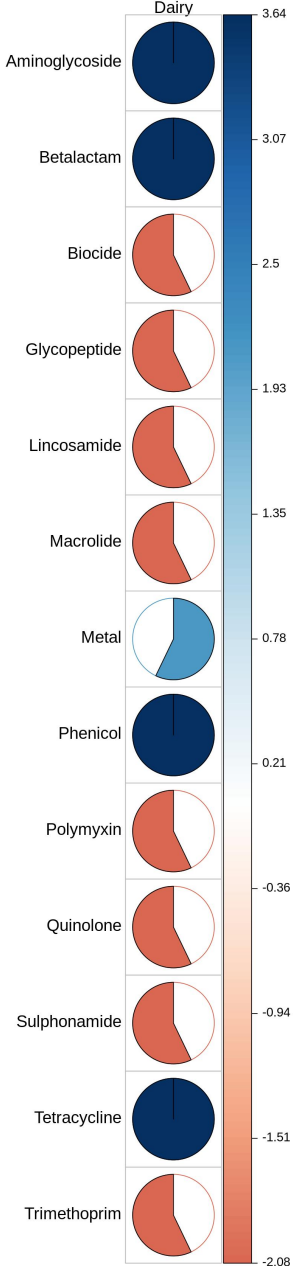
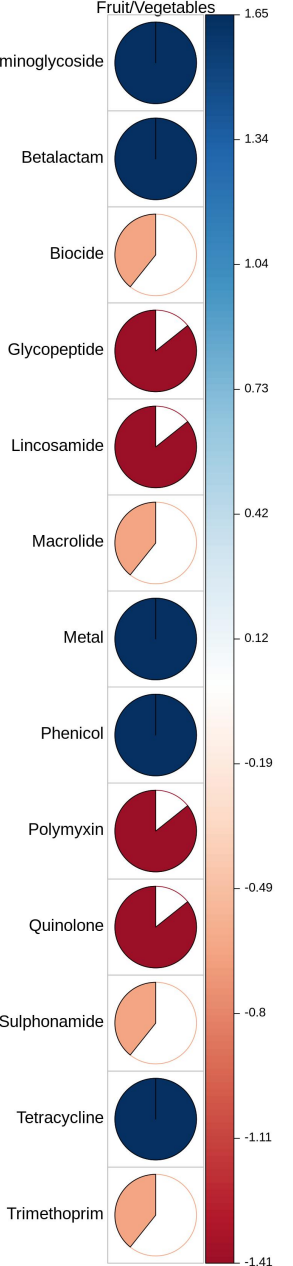
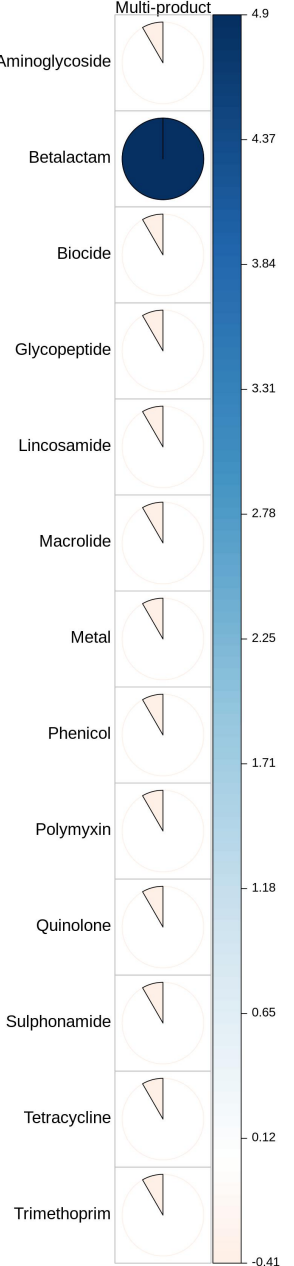
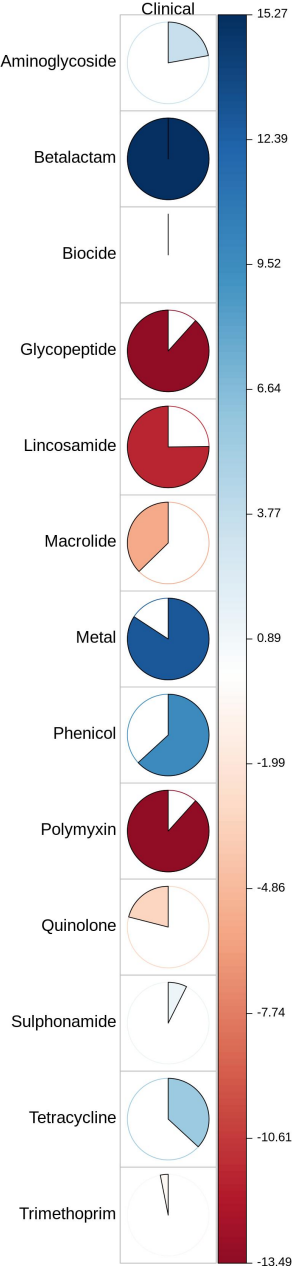
Kluyvera intermedia



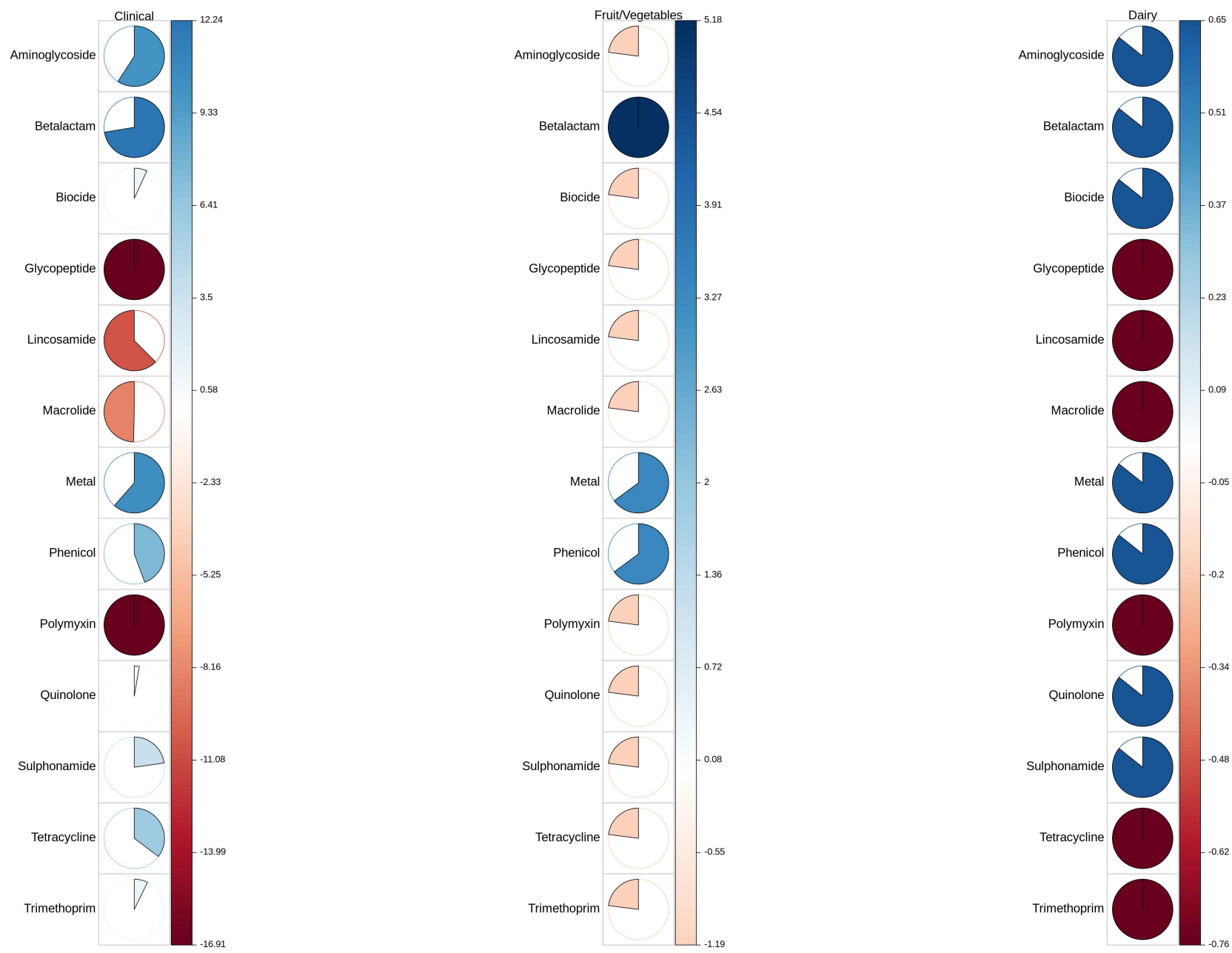
Listeria



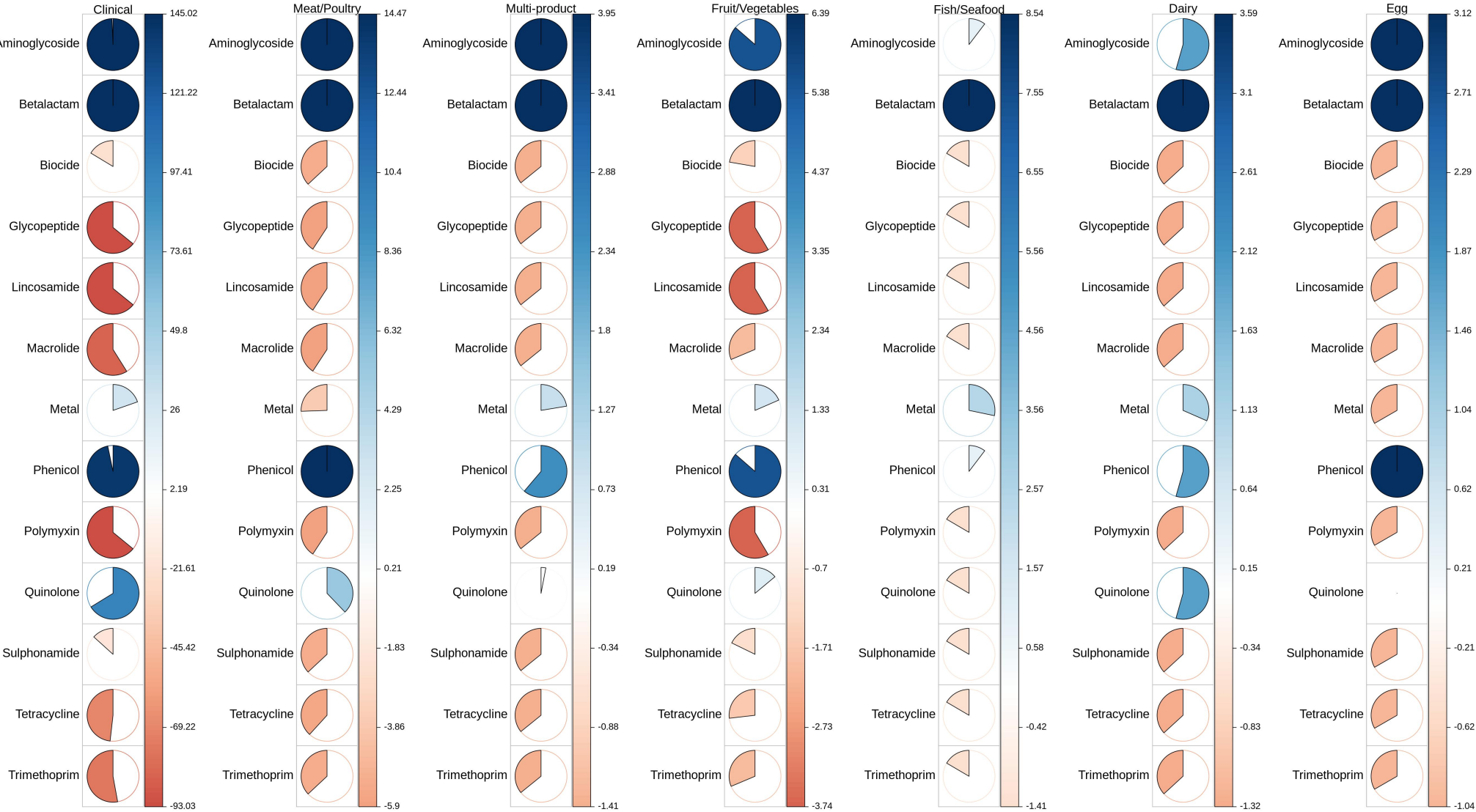
Morganella



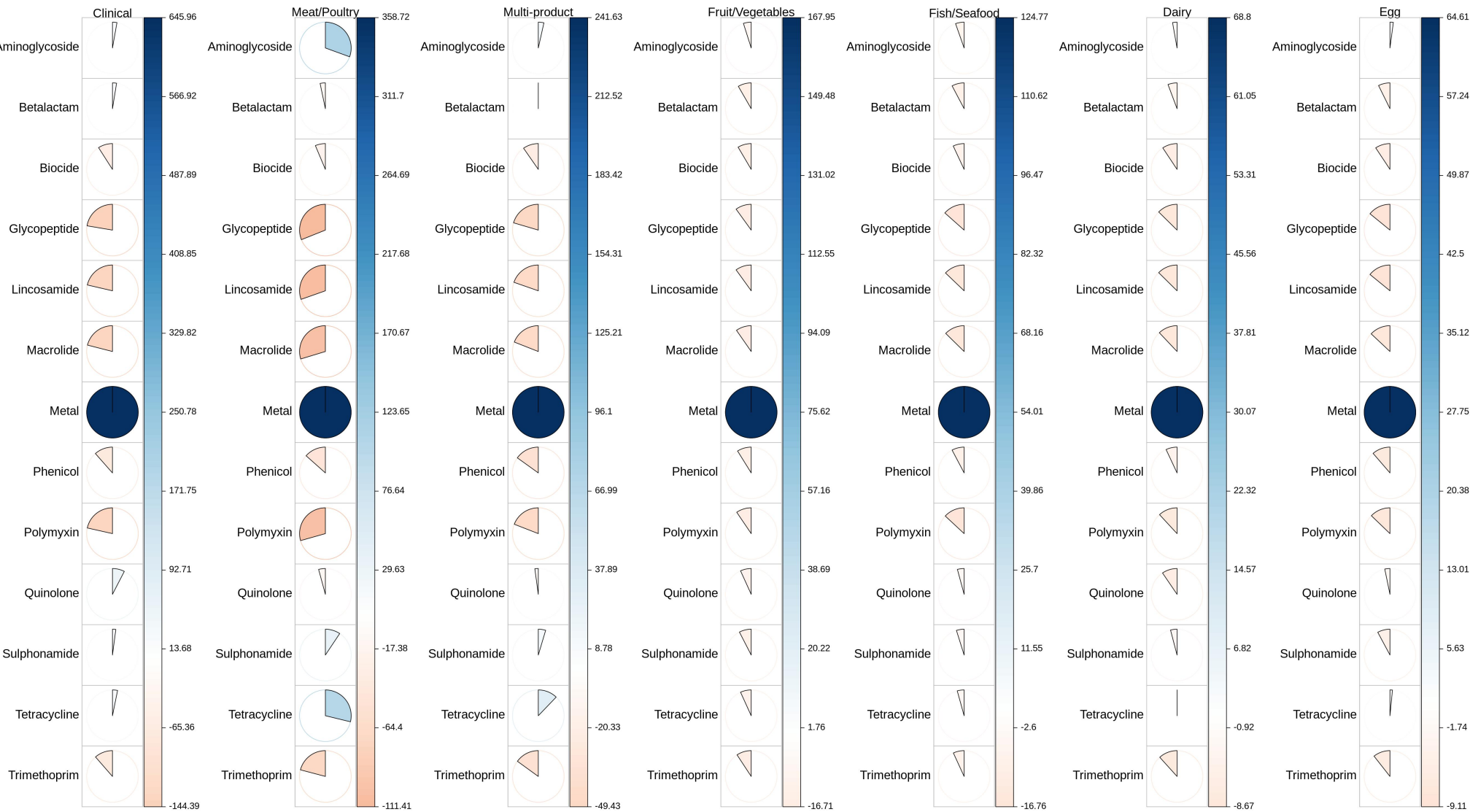
Providencia



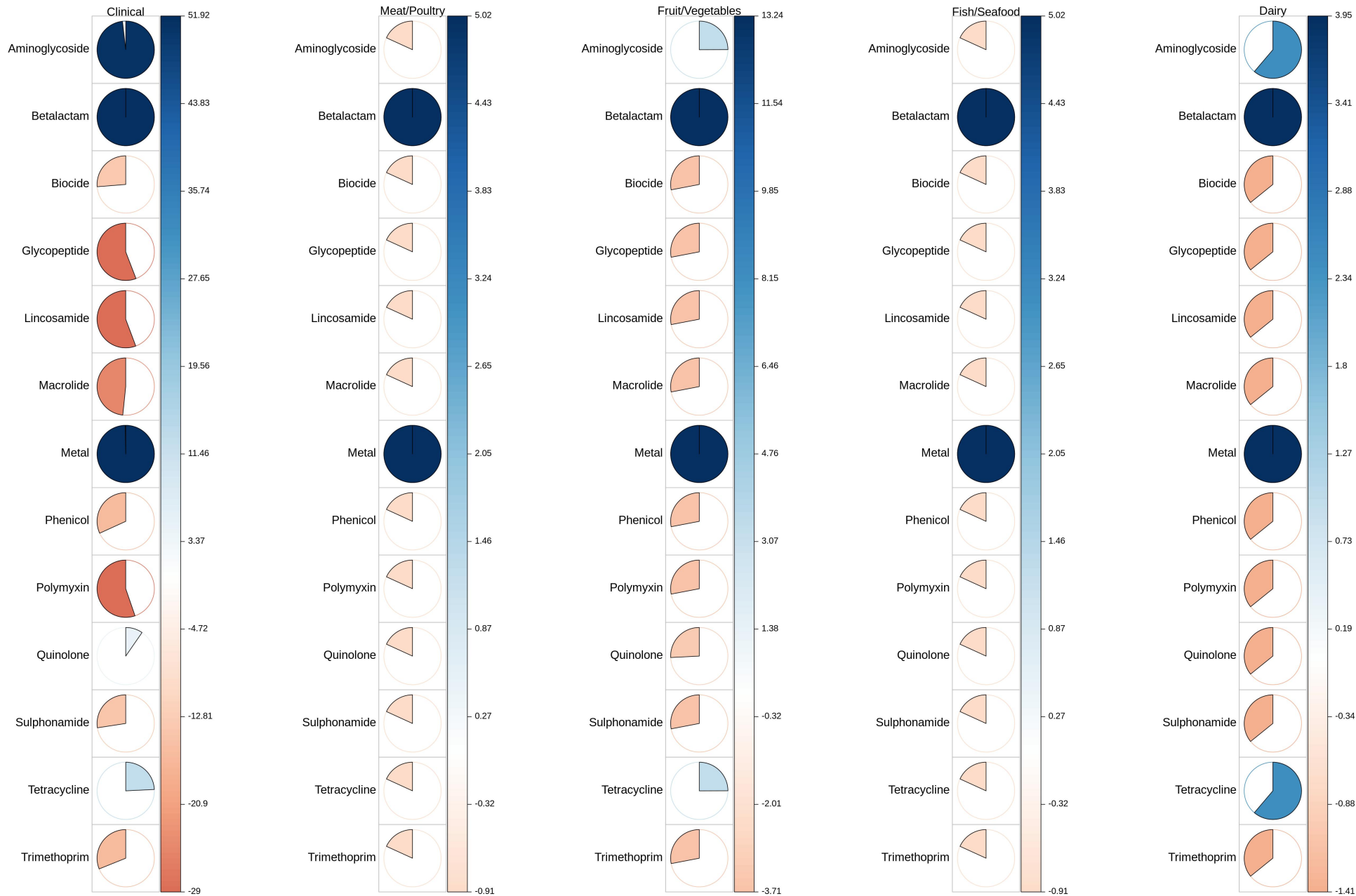
Pseudomonas



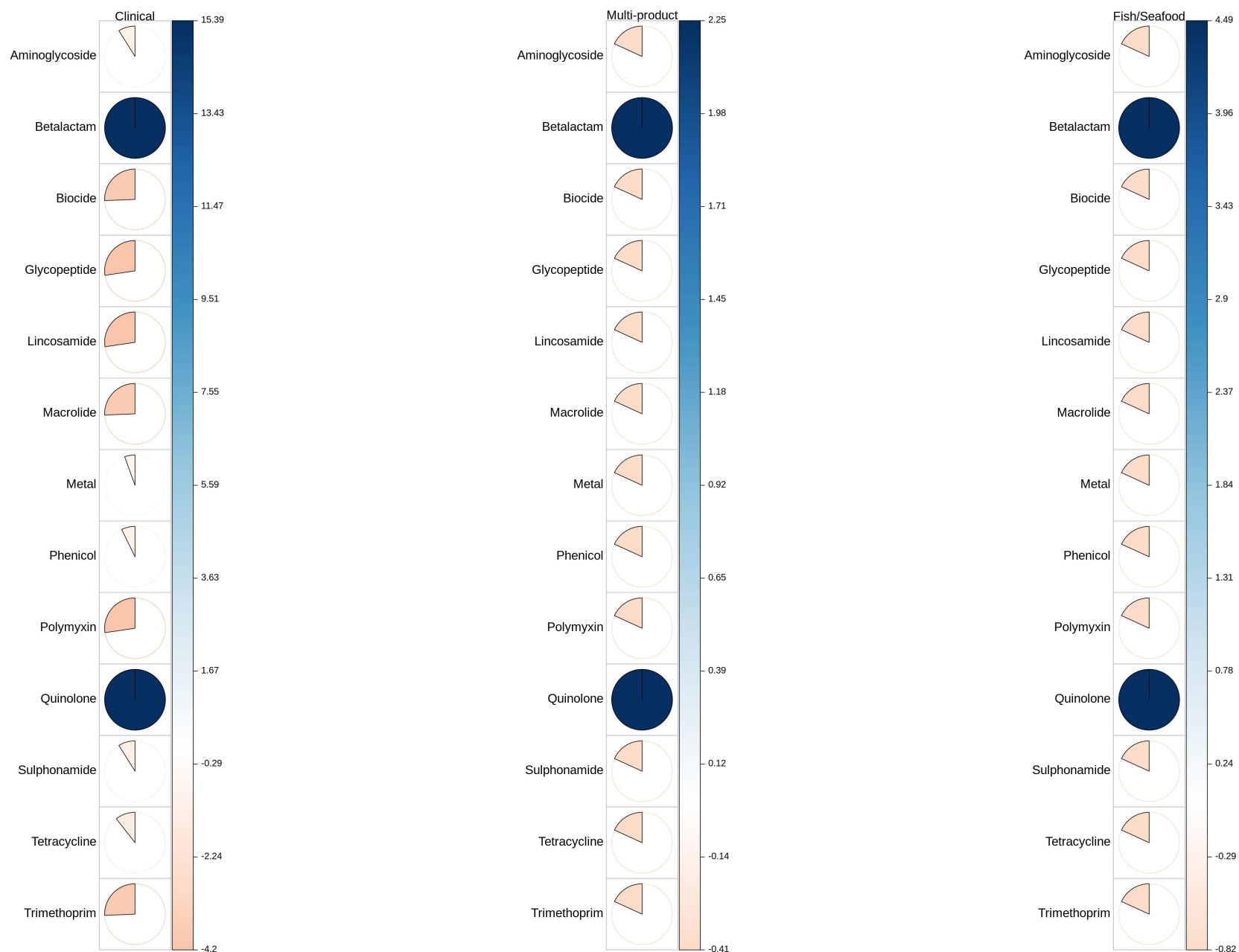
Salmonella



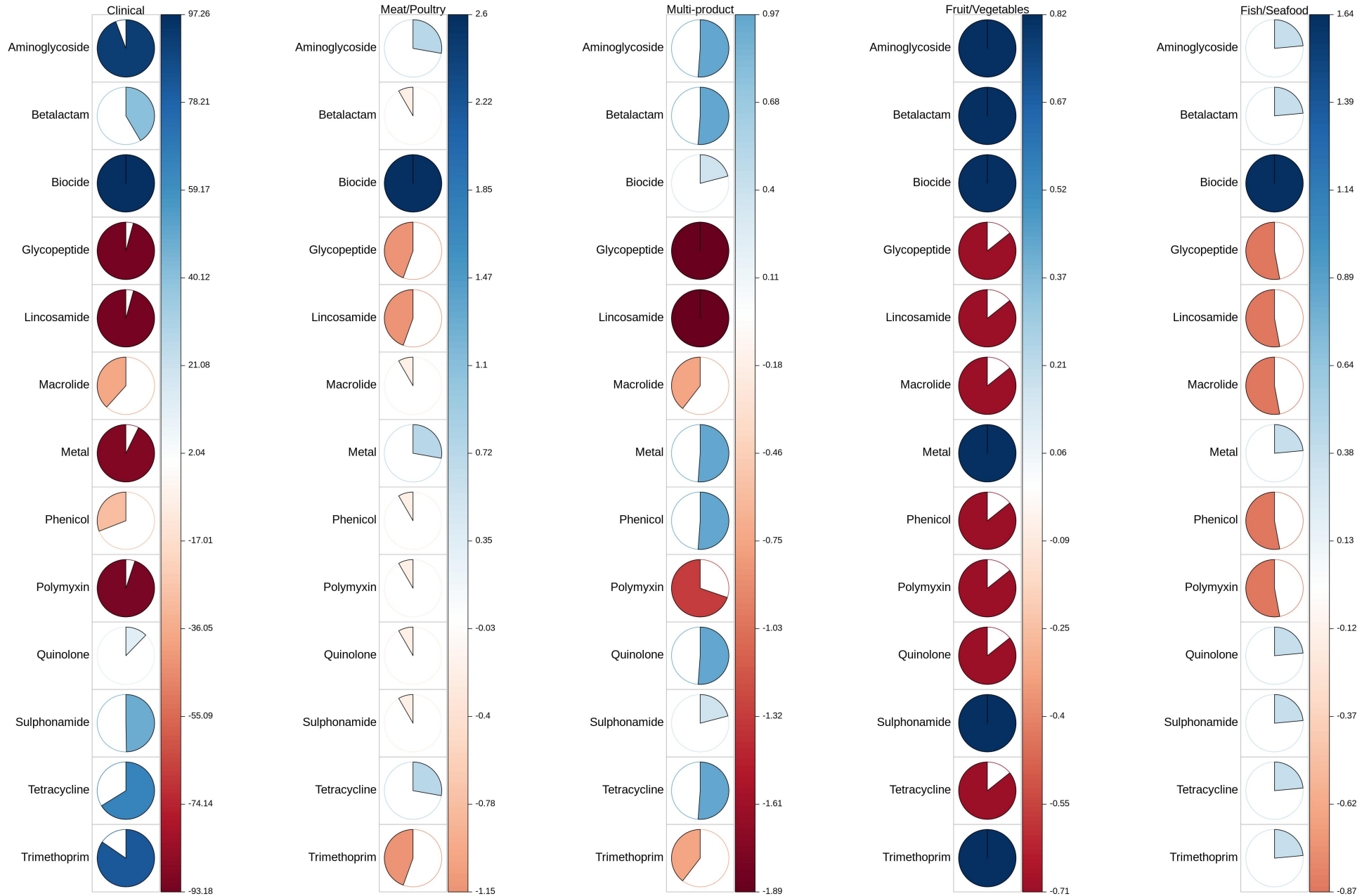
Serratia



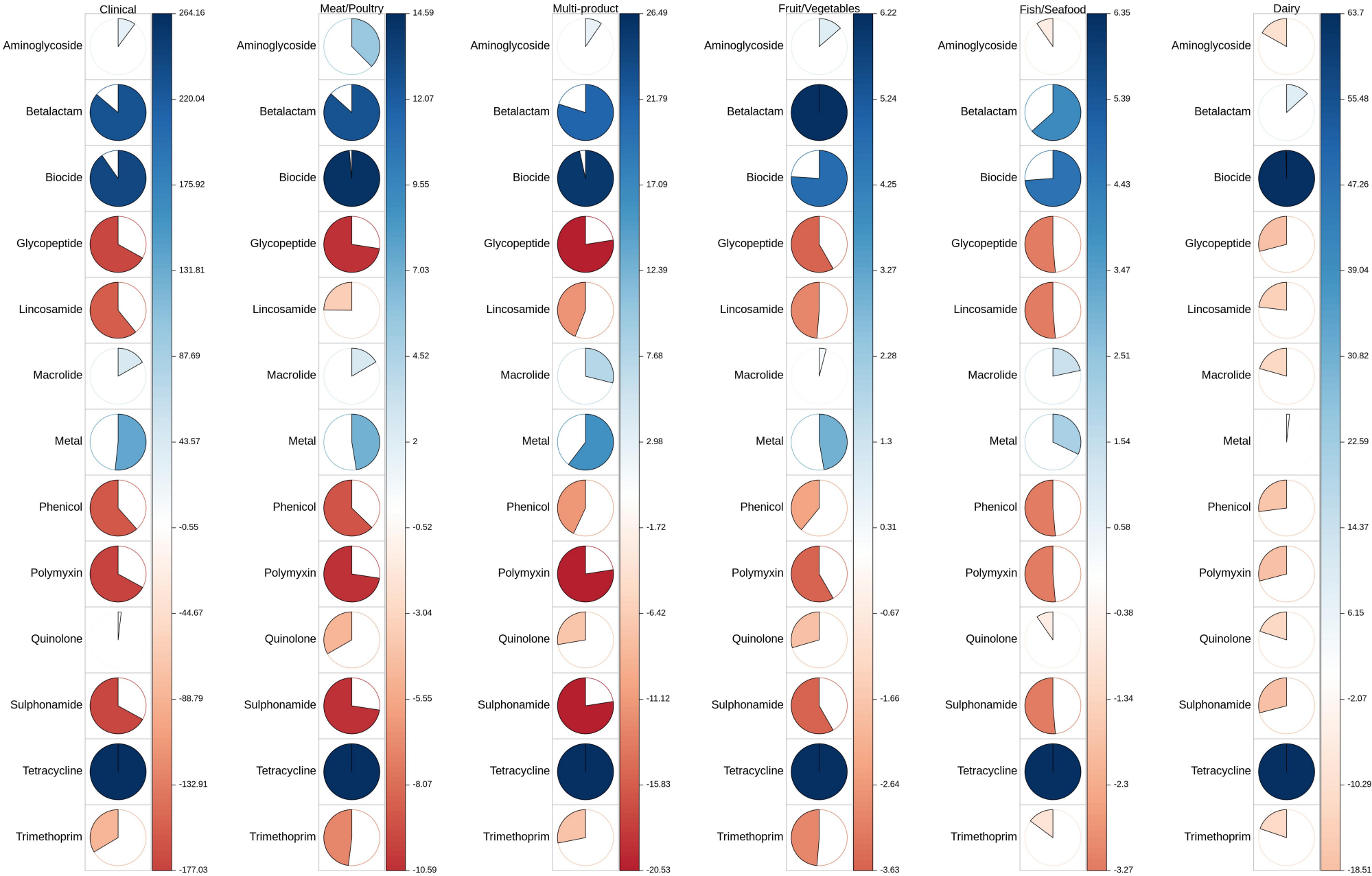
Shewanella algae



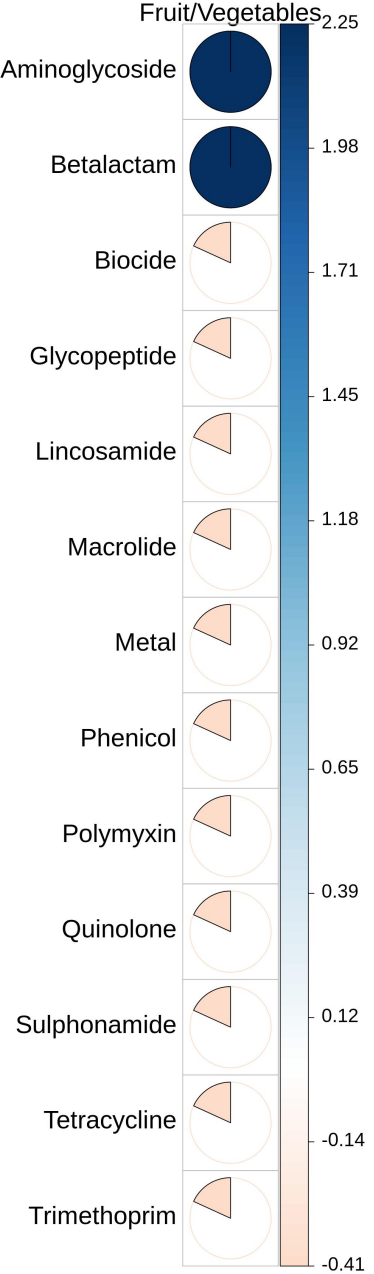
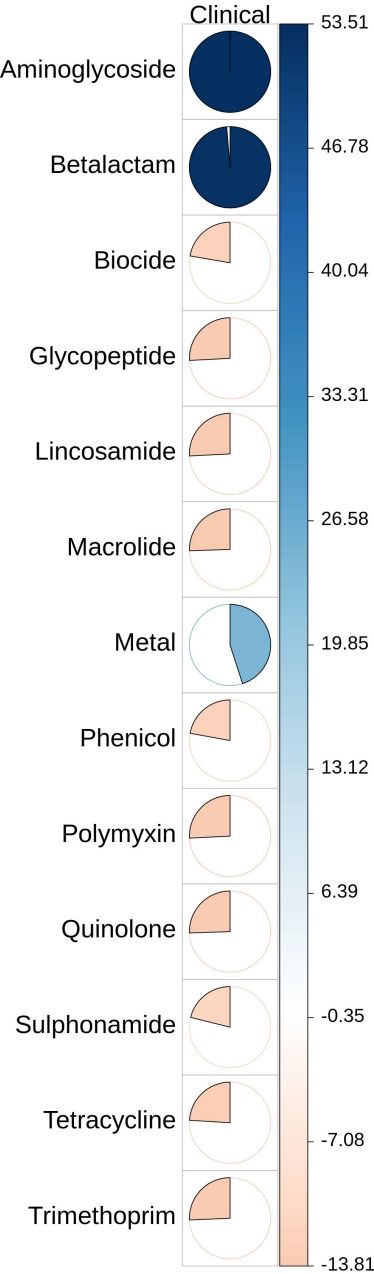
Shigella



Staphylococcus



Stenotrophomonas maltophilia



Vibrio

