

# Visualizing and quantifying structural diversity around mobilised AMR genes

## Supplementary Material

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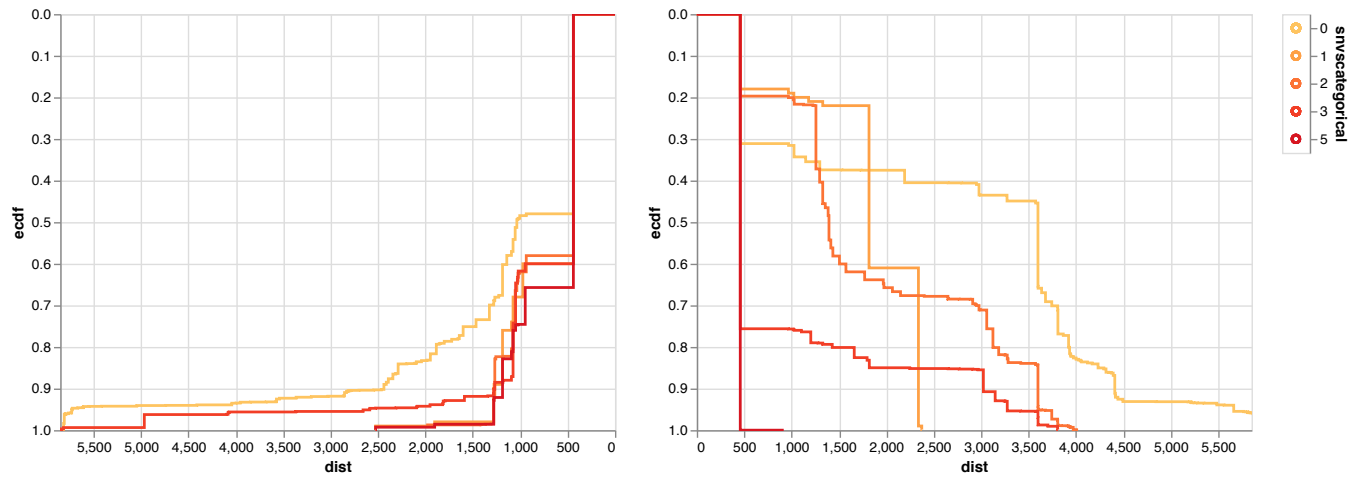


FIG. S1: **The breakdown of homology in the flanking regions of  $bla_{\text{CTX-M-65}}$  and related genes.** As in the main manuscript Fig. 2b, but here we pick only a single isolate for each year/country/genus combination to control for potential sampling bias.

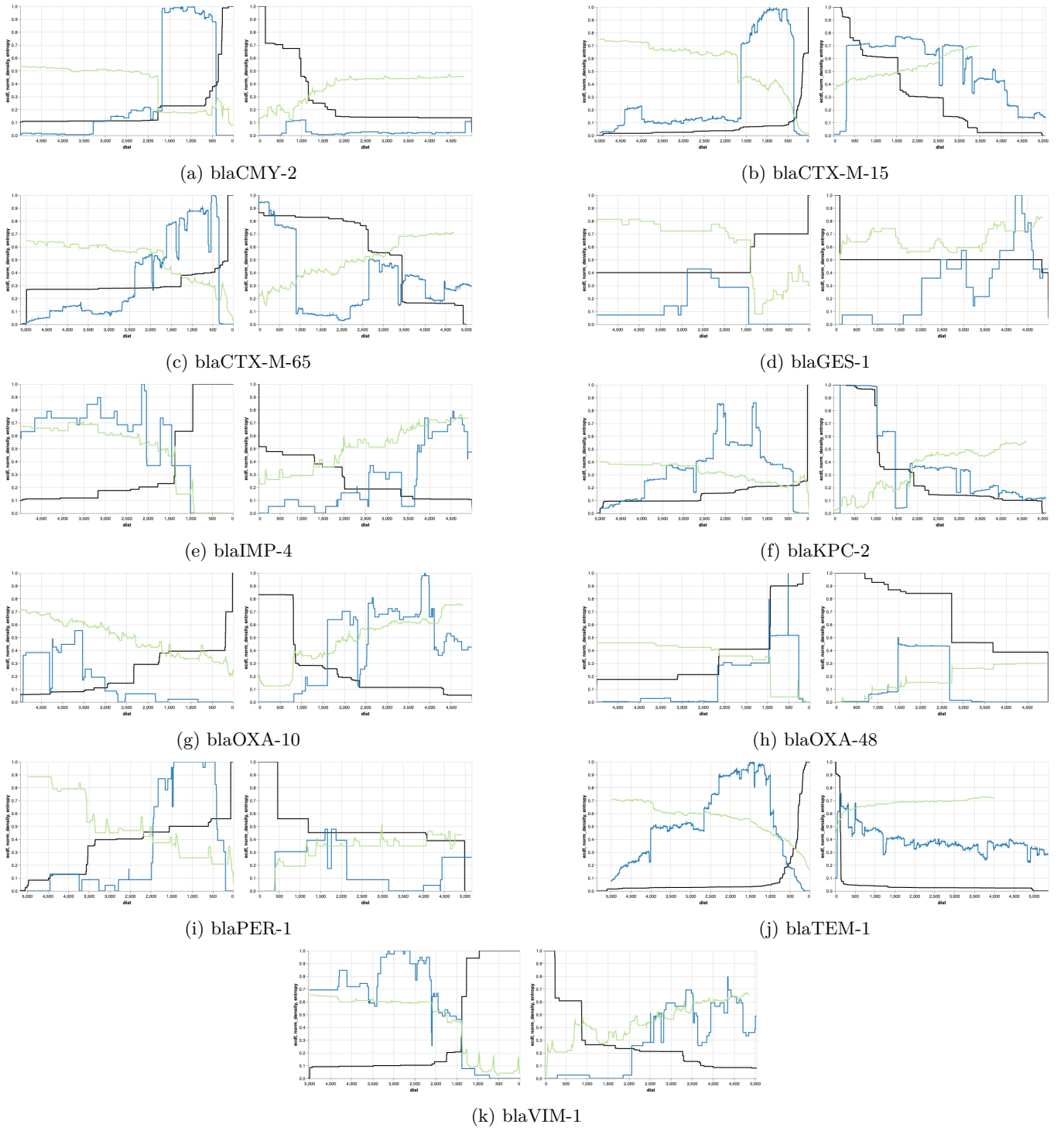


FIG. S2: **Flanking regions of eleven beta-lactamase genes.** Similar to the plot for blaNDM-1 in the main text: overlaid plots of normalised breakpoint distances (black), block diversity (green) and transposase density (blue).