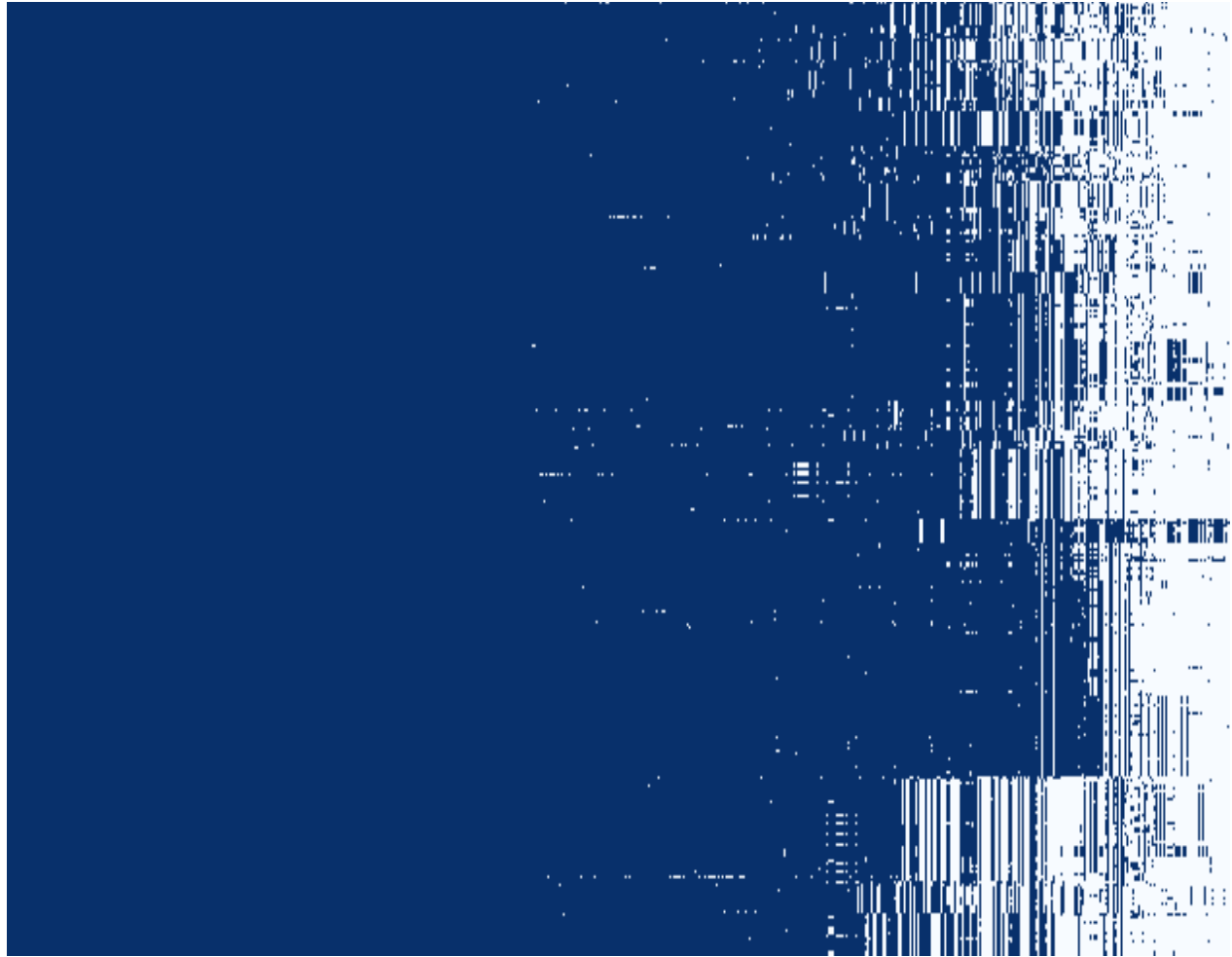


632 gene clusters



Supplemental Figure S5: Pan-genome alignment of 356 strains using Roary and *sma* genes. The figure shows a maximum likelihood tree and a pan-genome similarity matrix based on the presence (blue) and absence (white) of *sma* genes.