

Genomic Clustering Report

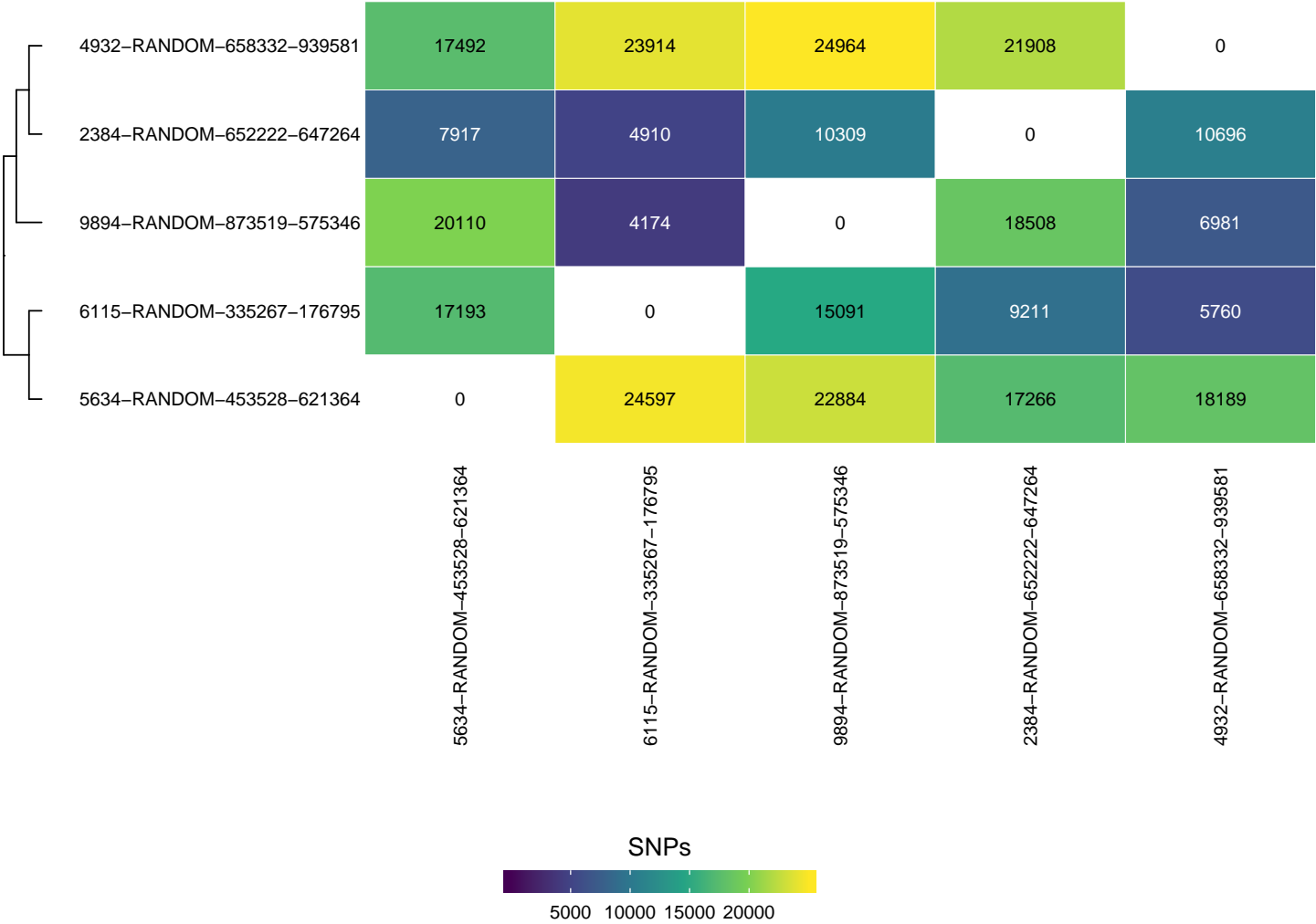
2020-01-22

Random data Analysis

The analysis of the *Random data* sample (n = 5) has been completed. These results must always be used in conjunction with epidemiological data when determining if isolates are epidemiologically linked. This analysis should not be used as a replacement for a thorough epidemiological investigation.

SNP Heatmap

The number of Single Nucleotide Polymorphisms (SNPs) between each sample is shown on the heatmap below. There is no hard and fast rule for determining how many SNPs are needed to classify an outbreak. Generally it is best to look for patterns in the data between the SNP data and the core-genome tree.

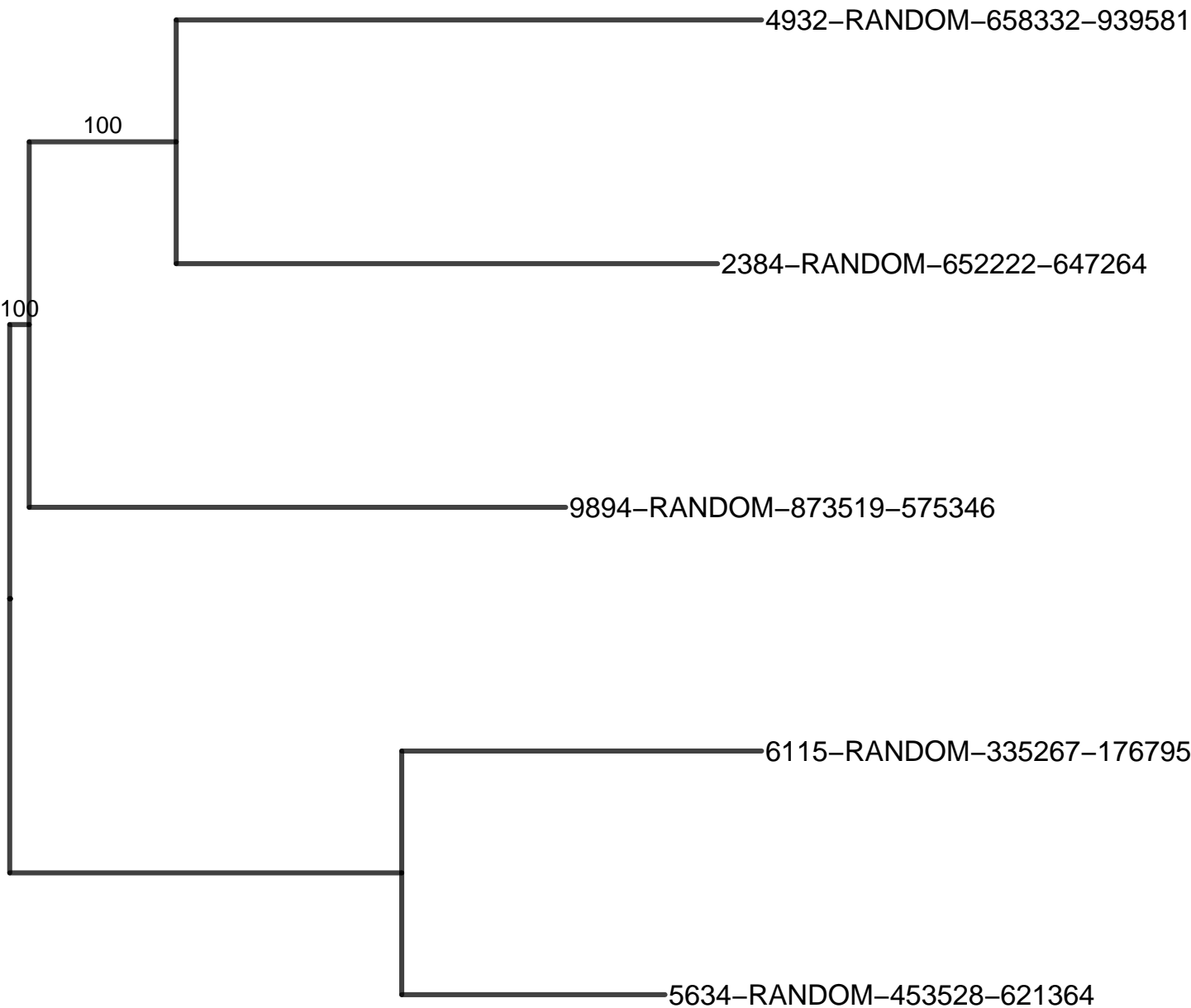


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Phylogenetic tree

Using variation within the genome, we can estimate how related isolates are. We do this by determining if isolates share a similar common ancestor. Here we are looking for isolates that cluster together and share a small amount of horizontal distance on the tree. Bootstrap values are shown on the tree. A bootstrap value greater than 95 suggests the placement of a branch on the tree is well supported.



0.1

Methods