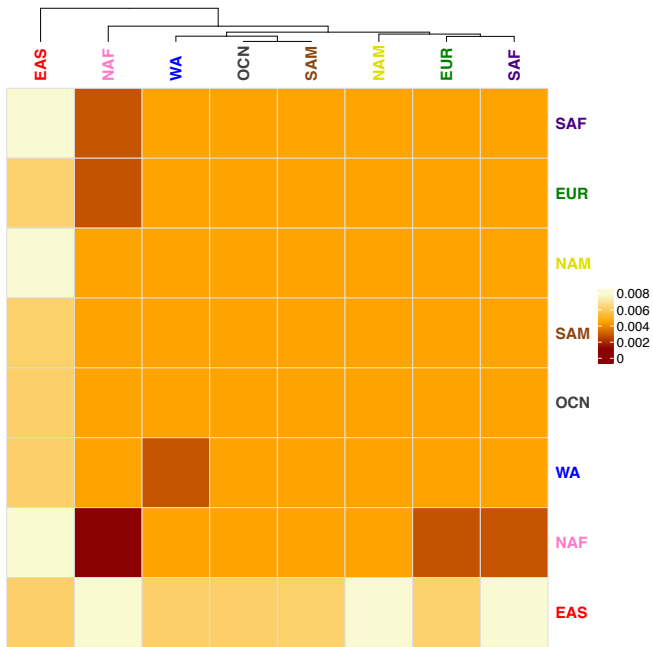
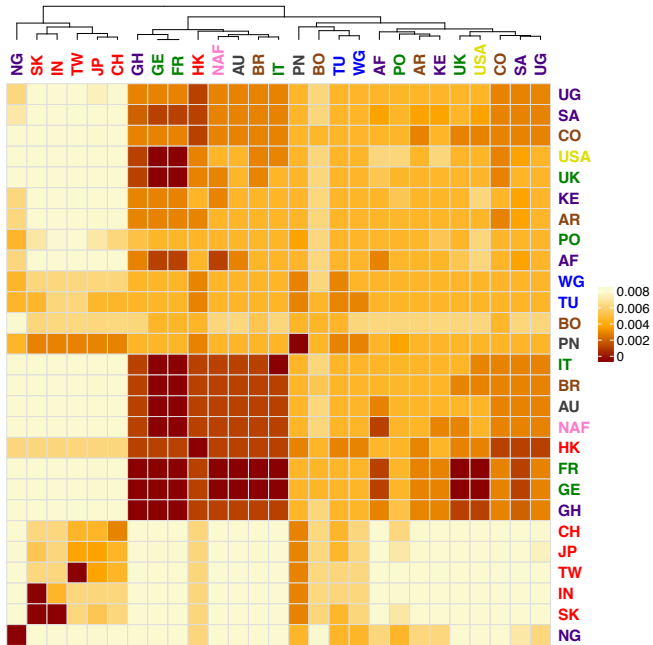


Supplementary Figure 5

Single genes population cladogram of the phylogenetic trees and bootstrapped pairwise genetic distances between populations. The leaves of the phylogenetic trees are coloured based on the country of origin of the isolates. The new sequences produced in this study are identified by black asterisks. Nodes with bootstraps values higher than 0.5 are indicated with a red circle. Each tree is paired with heatmaps representing the bootstrapped genetic distances among populations for both country and continents. The populations acronyms are coloured by continent. Coloured bars are used to help to distinguish groups commented on in the text, and the proportion of the total isolates of a geographic origin in the group is reported.

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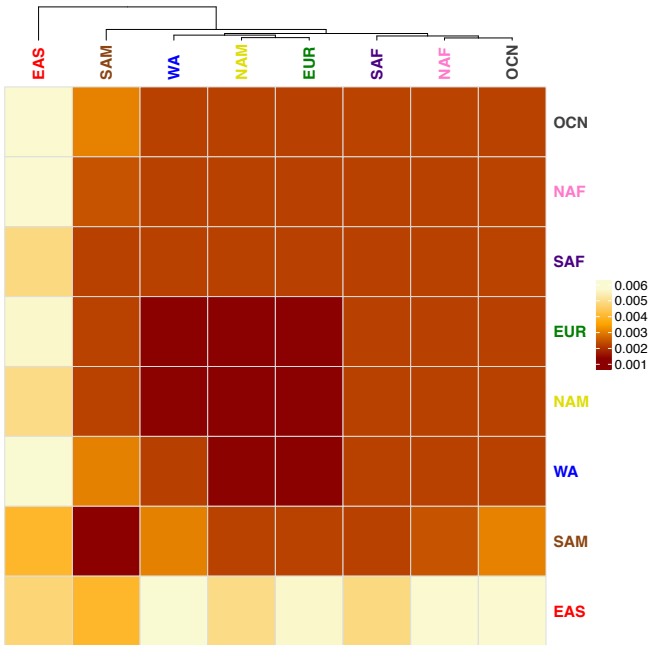
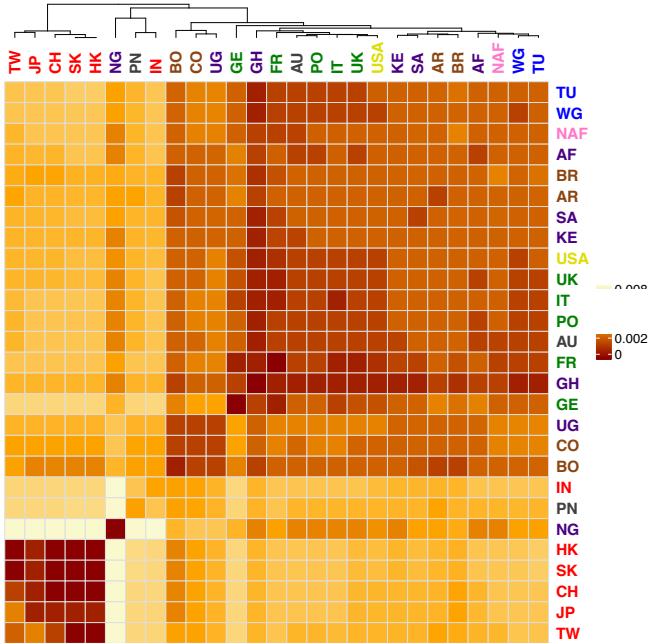
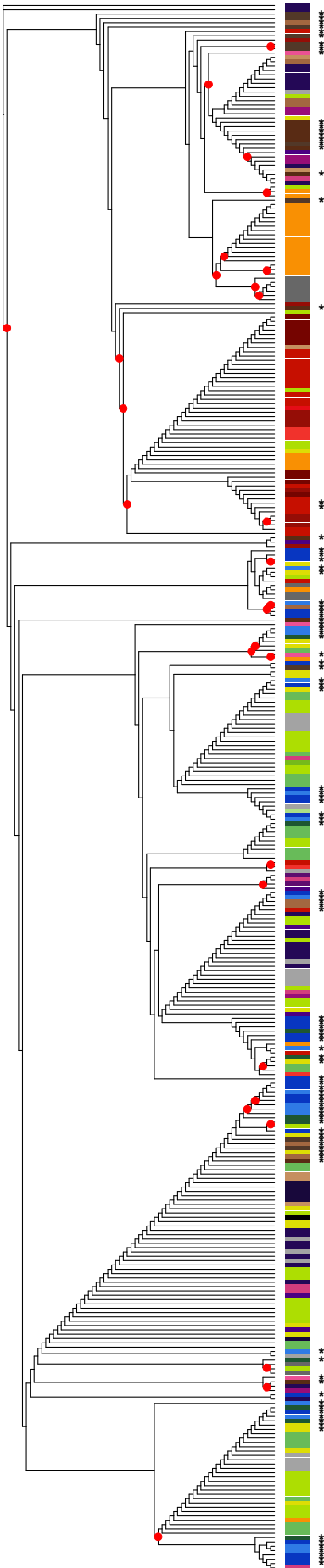
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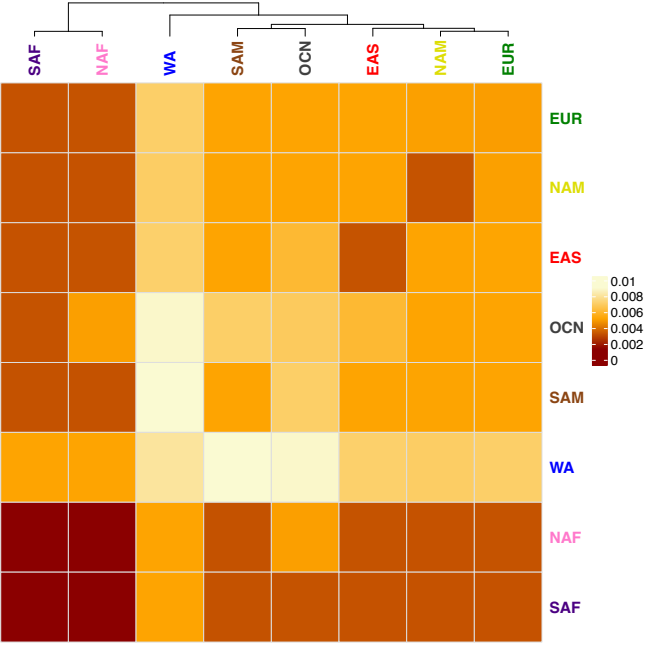
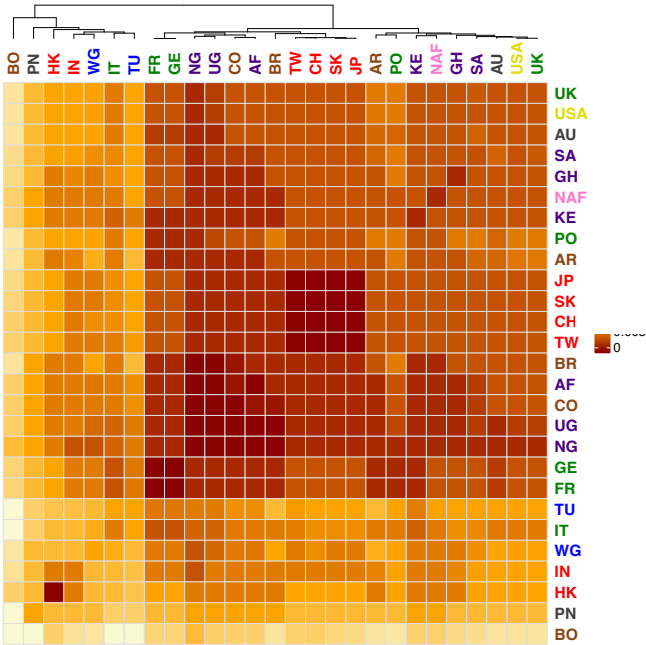
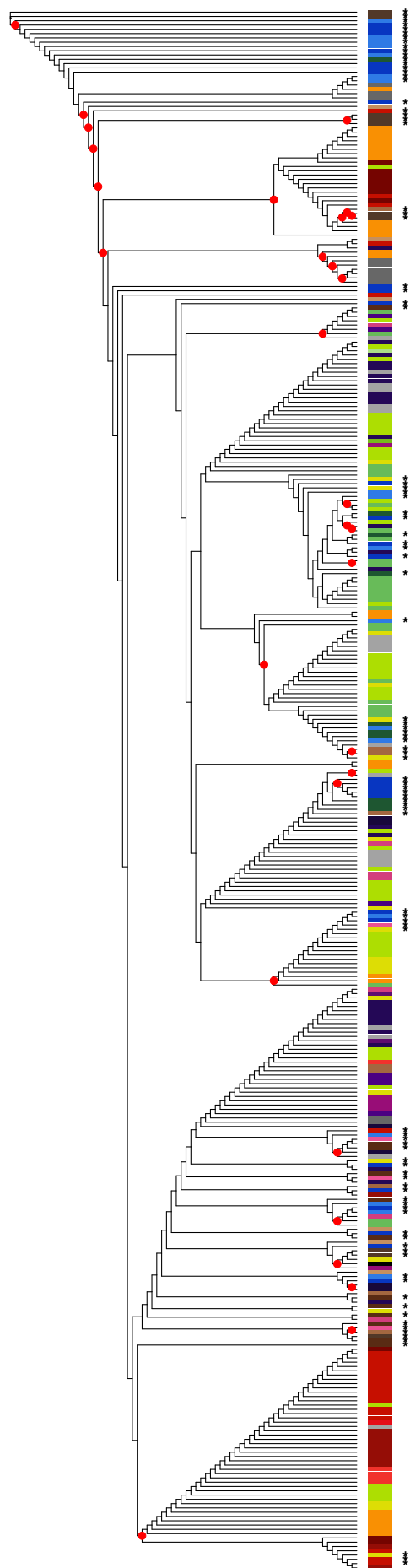
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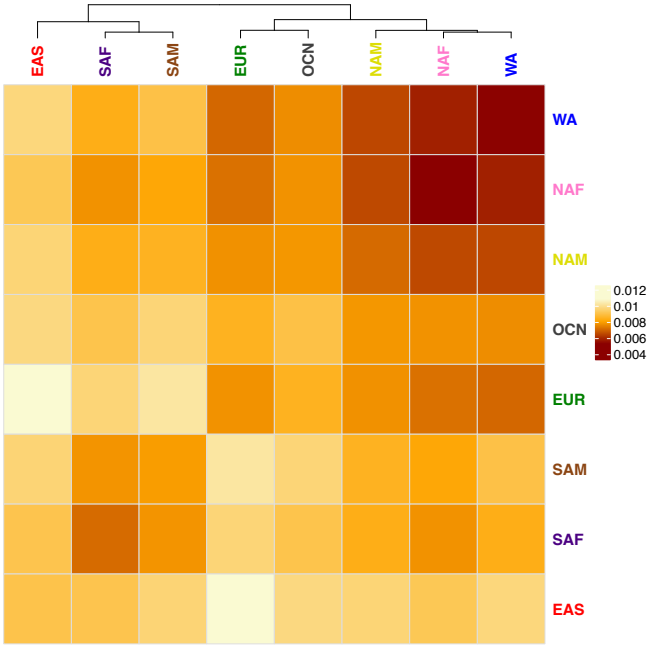
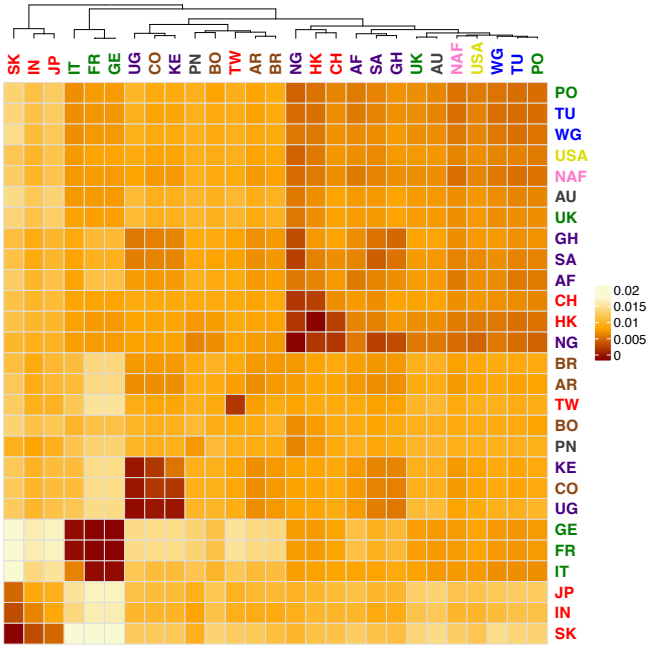
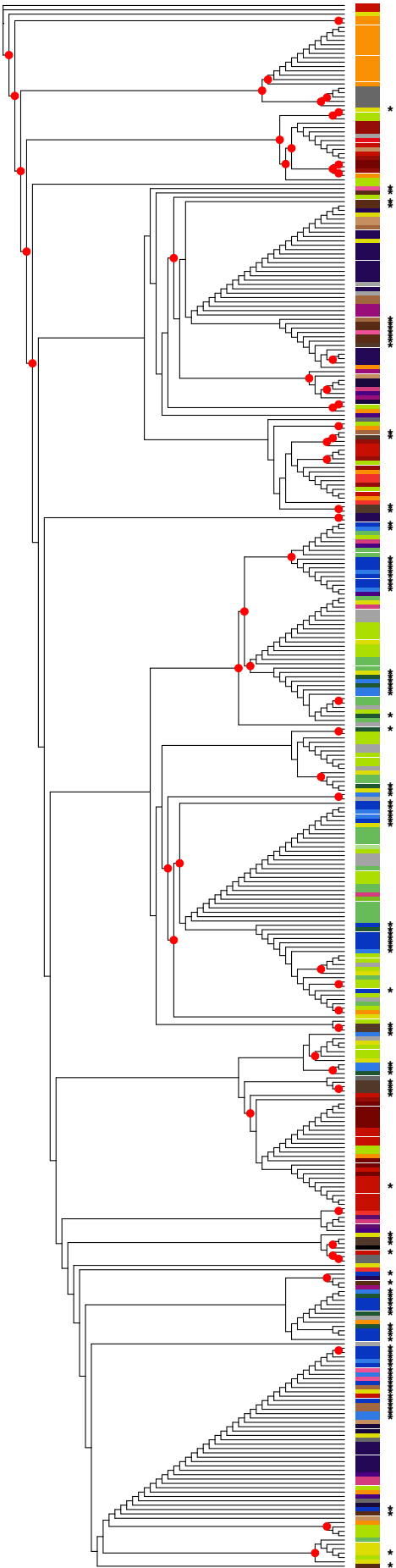
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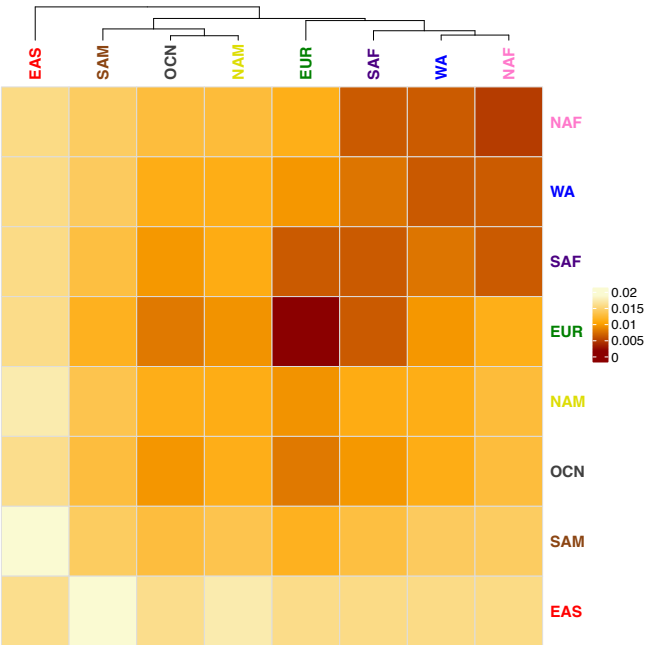
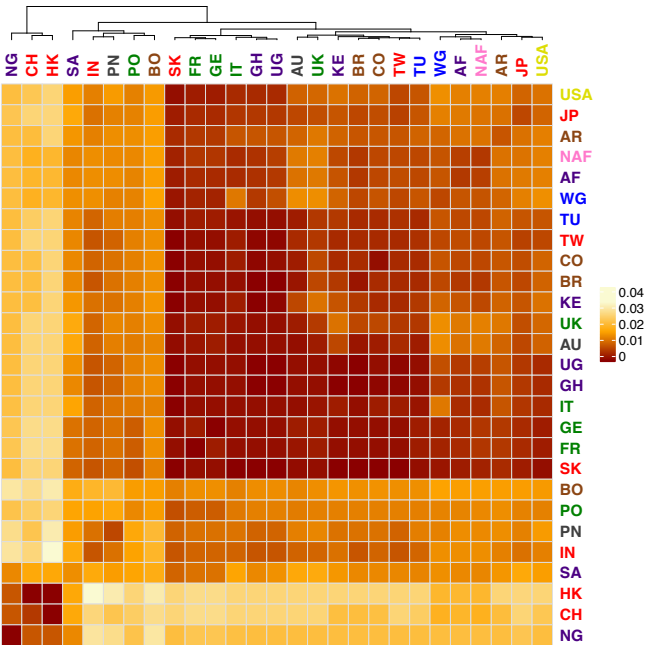
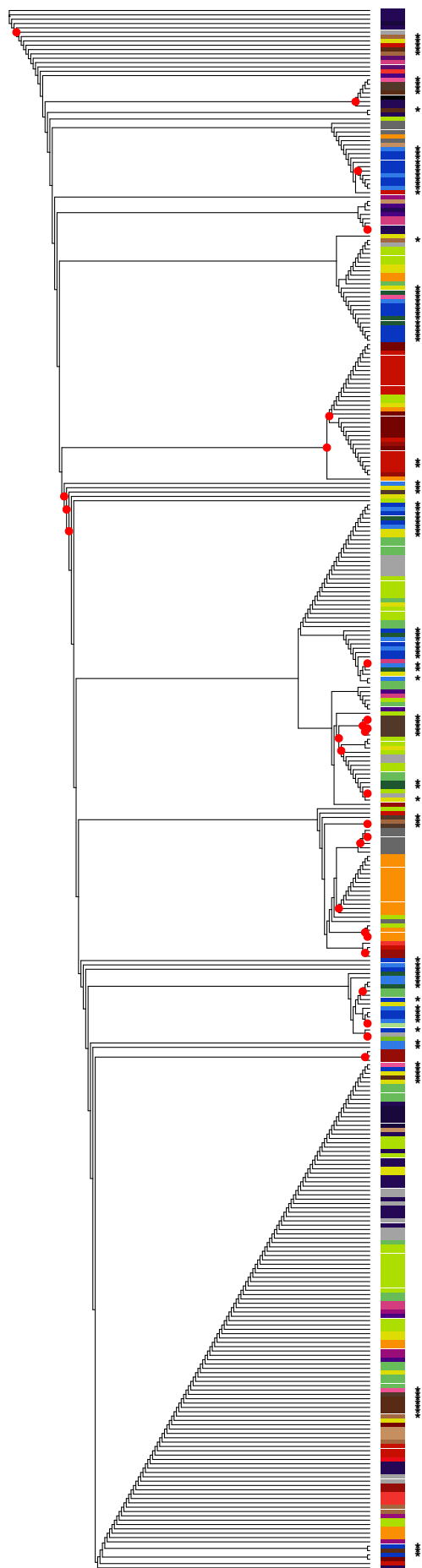
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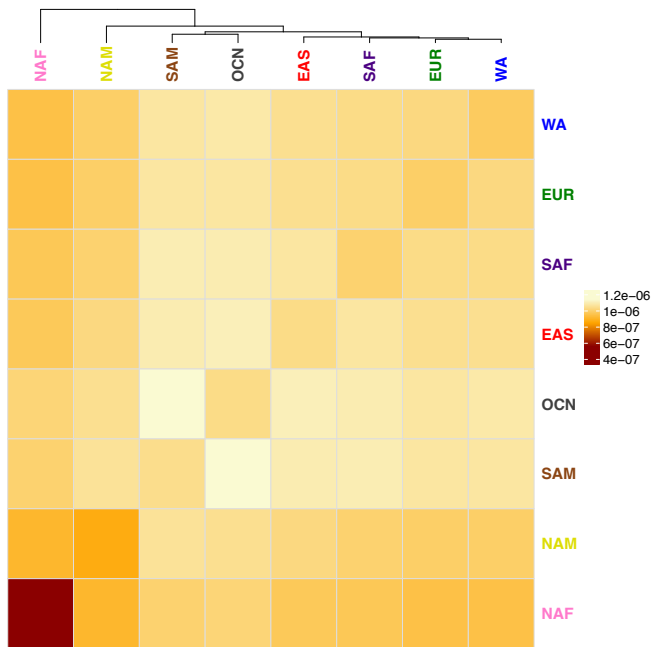
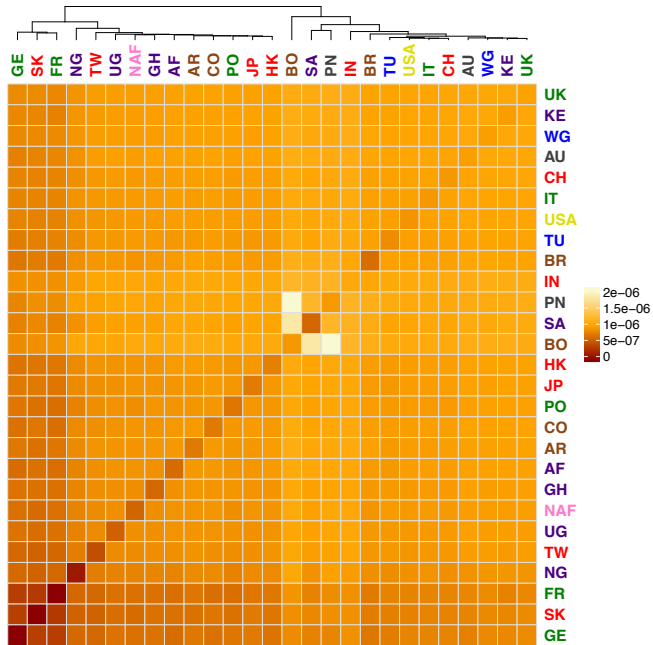
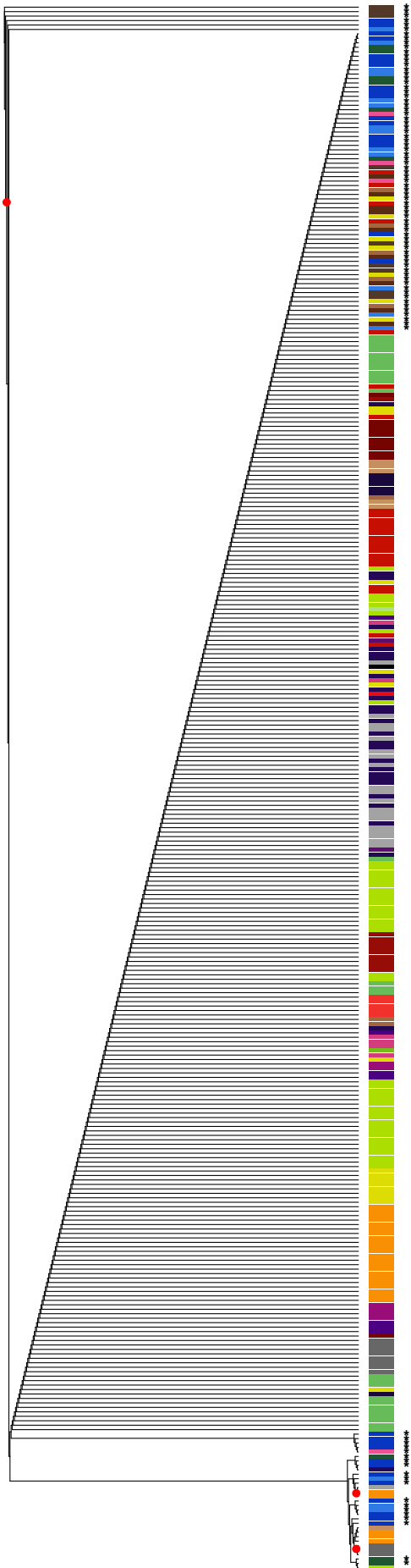
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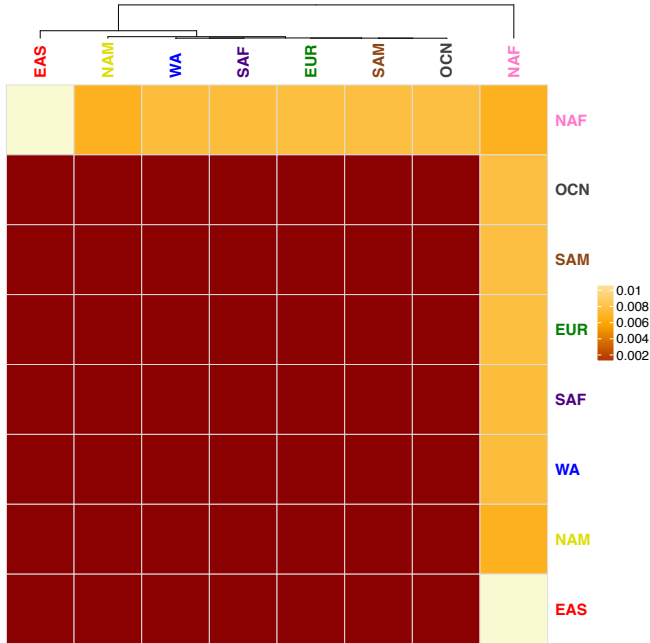
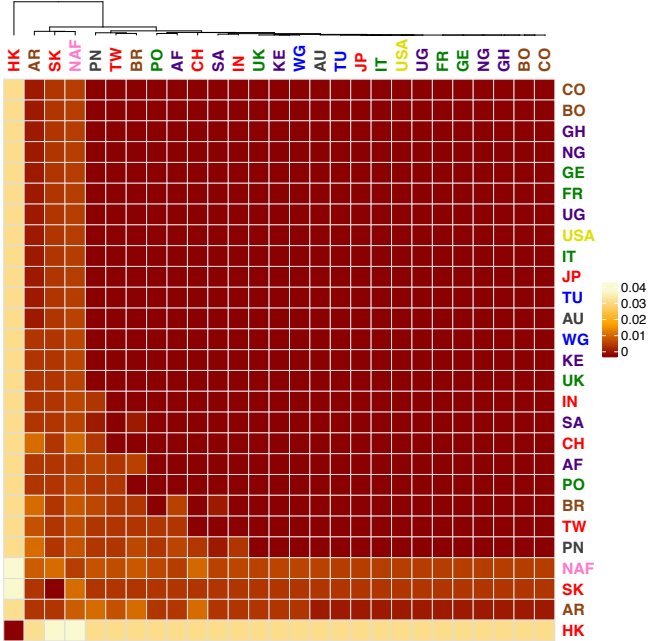
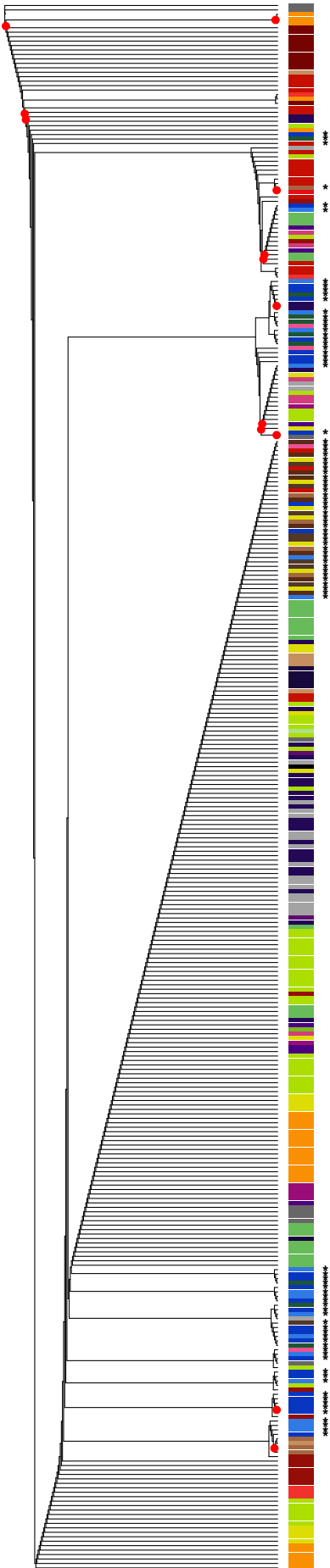
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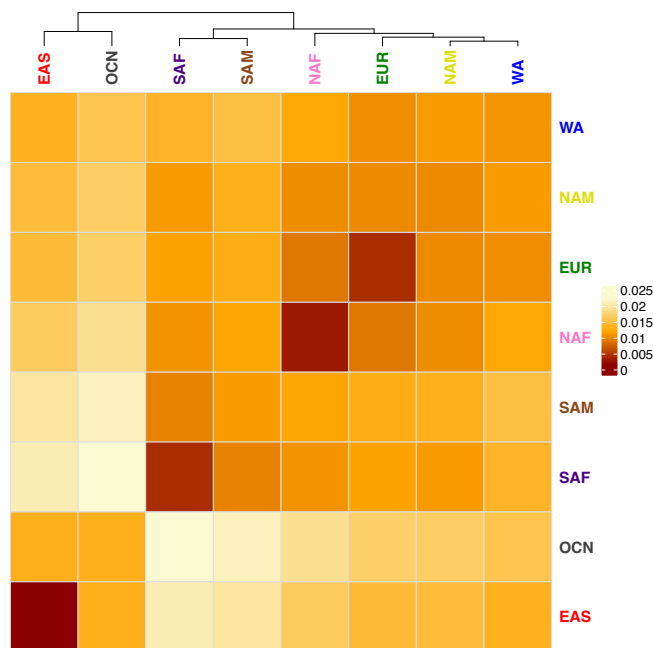
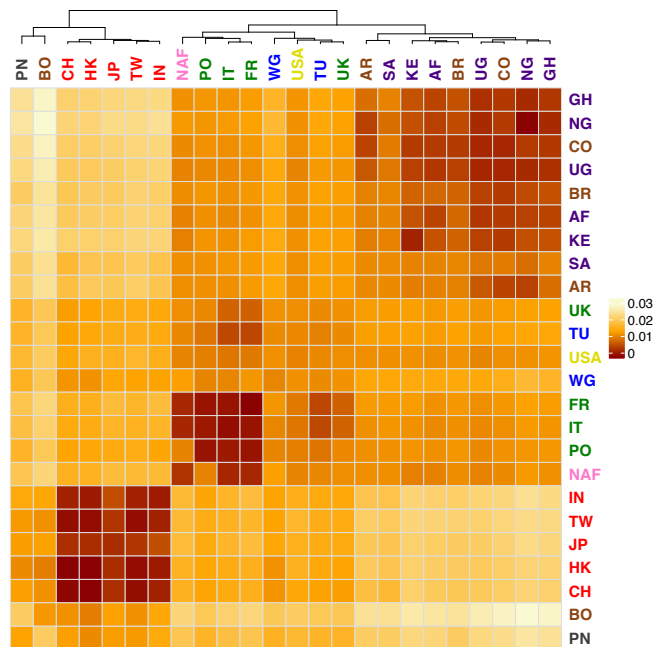
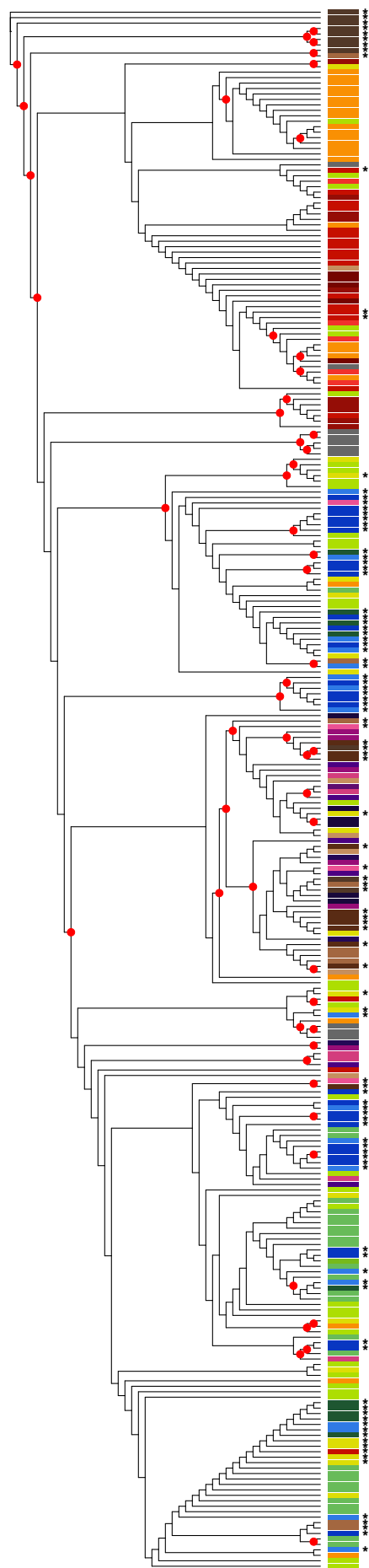
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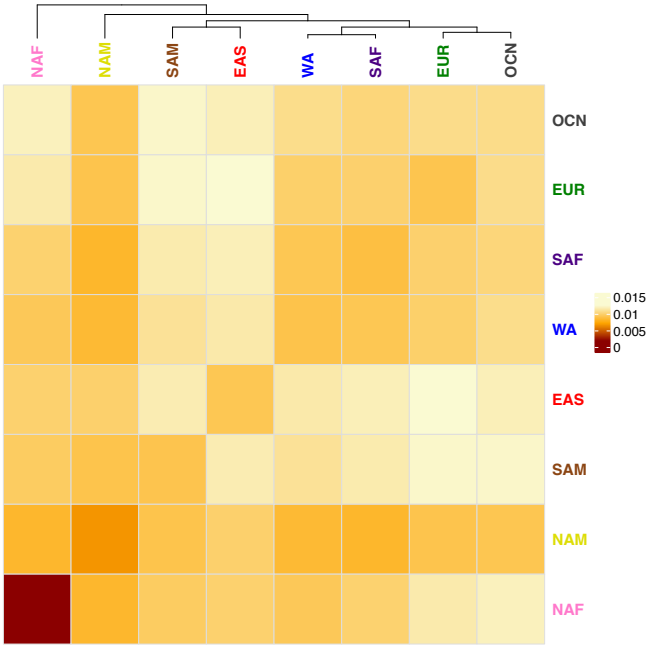
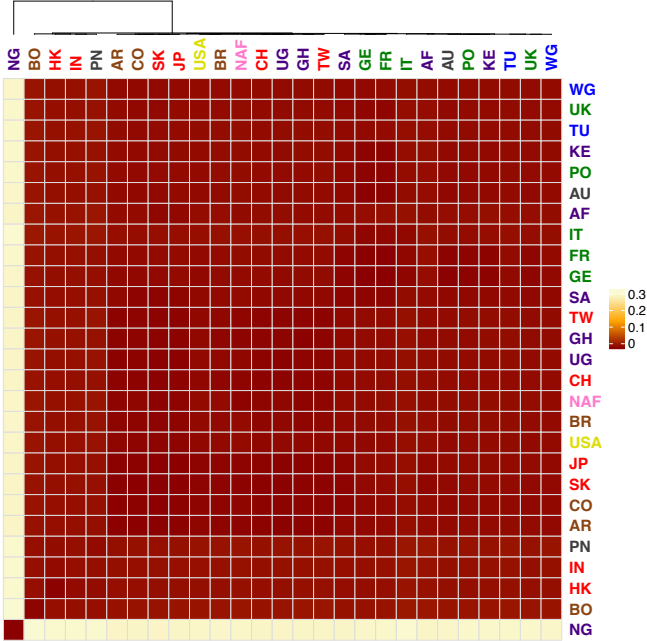
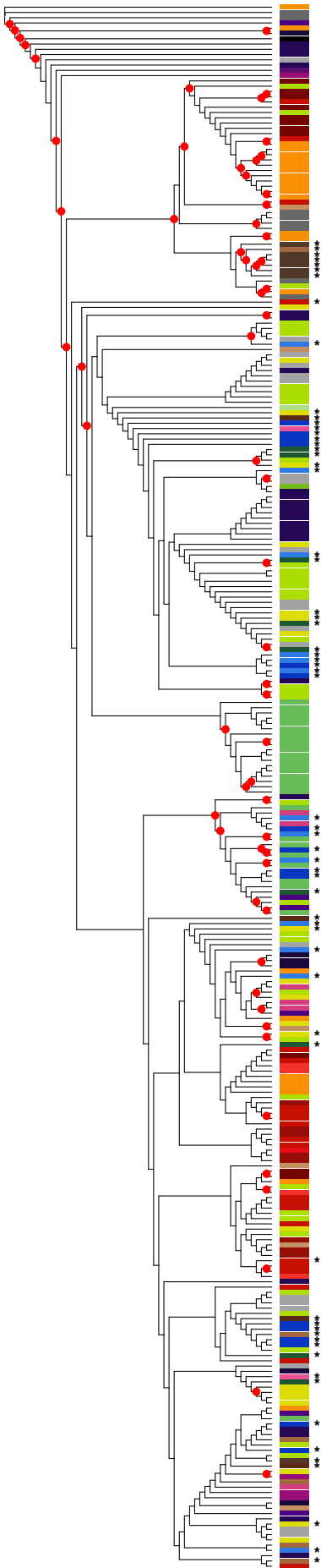
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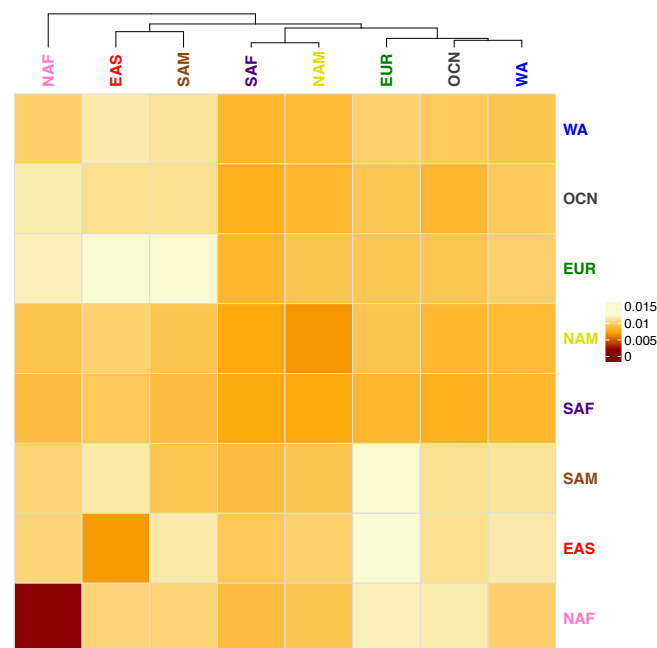
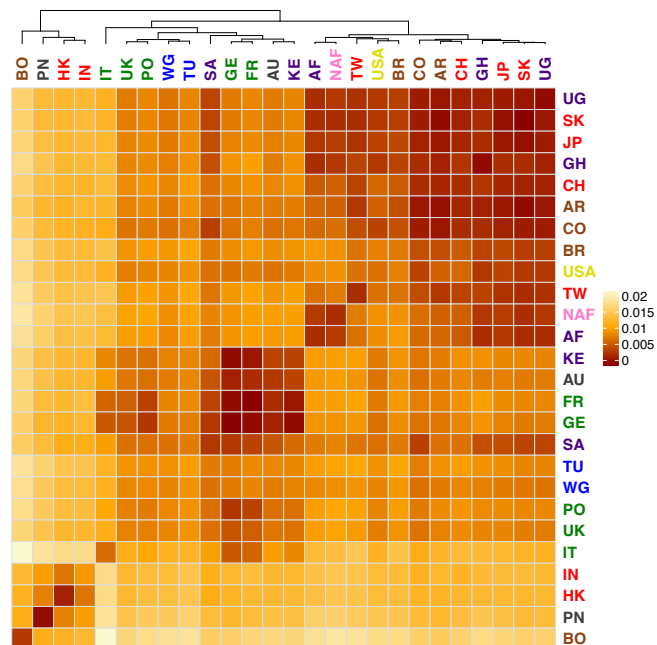
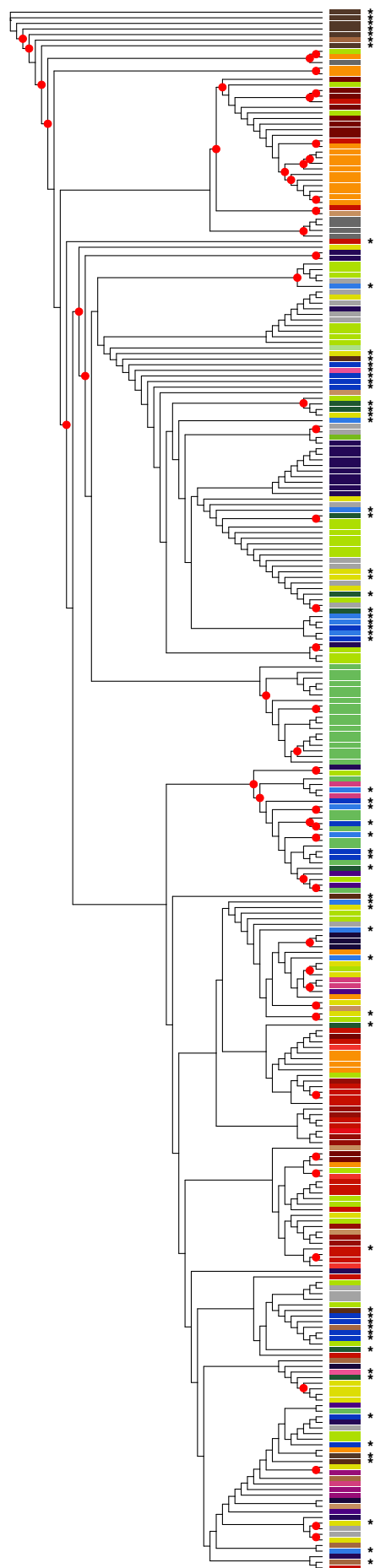
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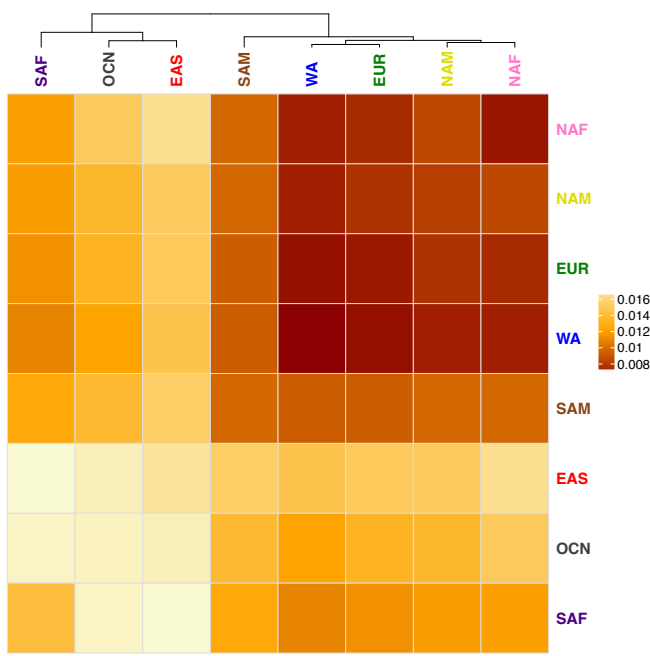
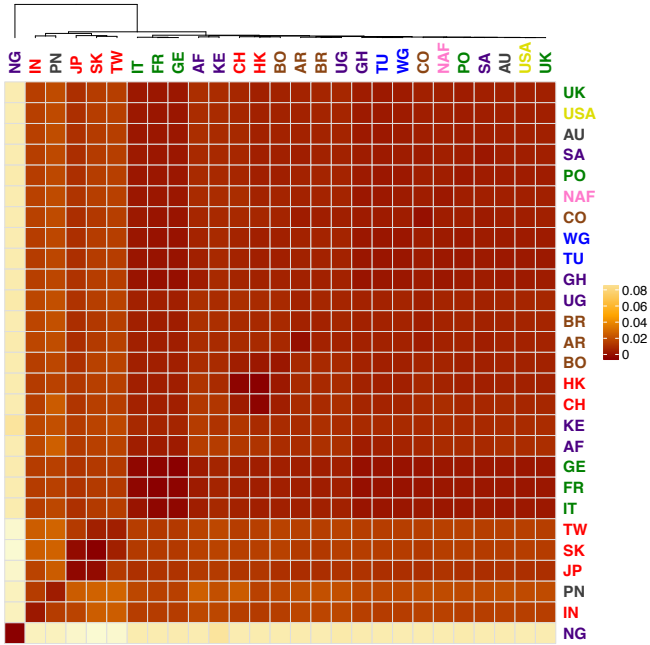
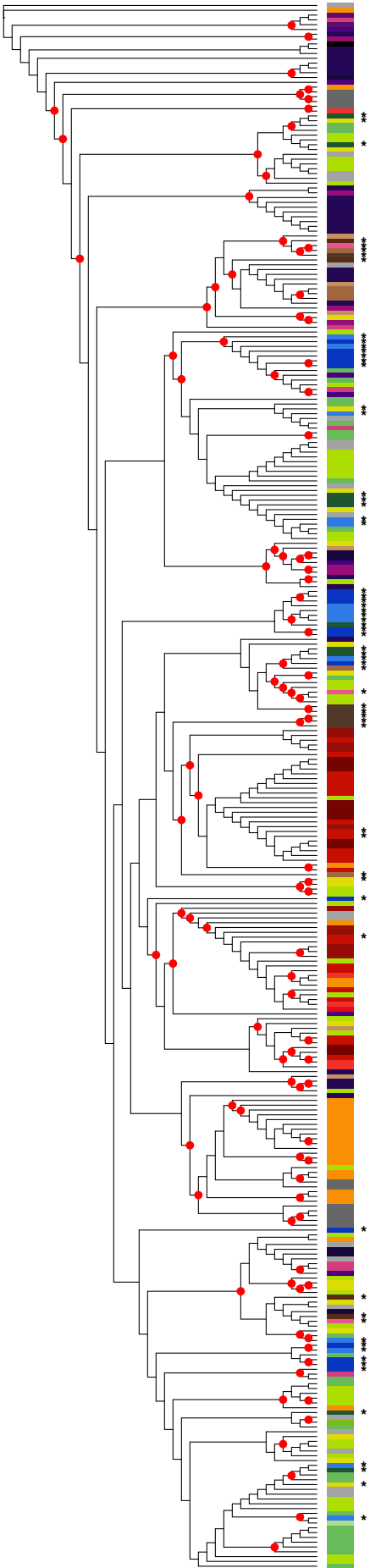
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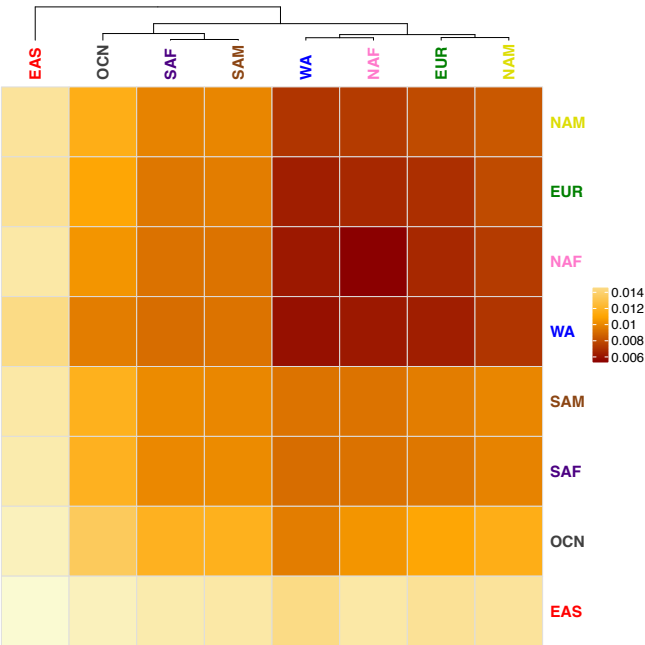
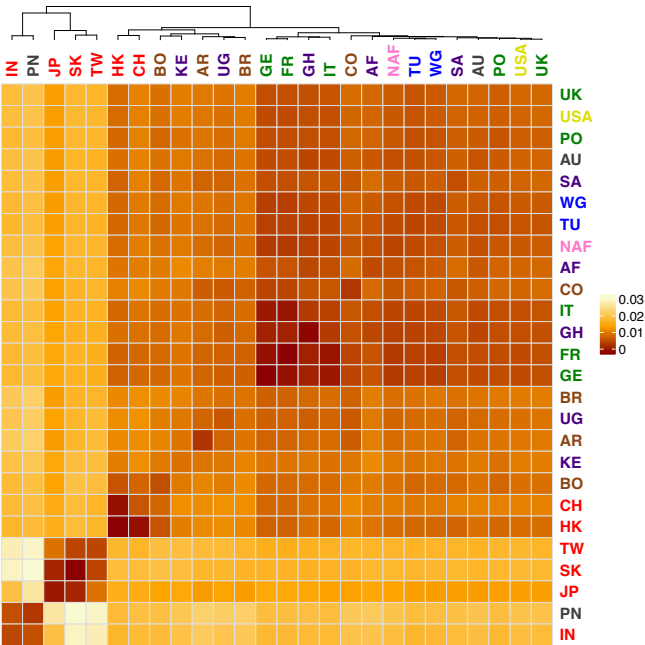
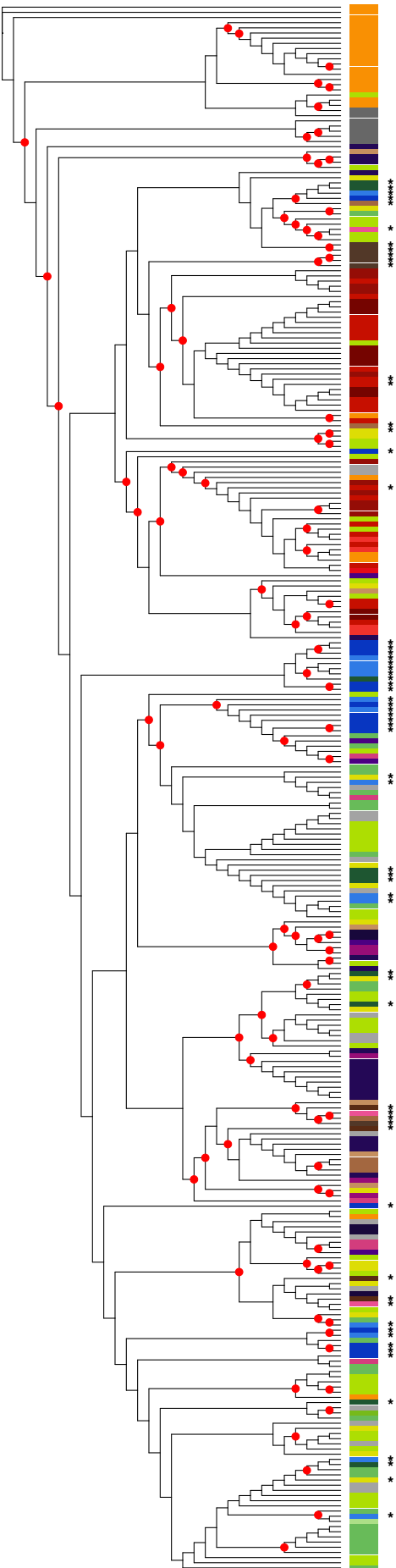
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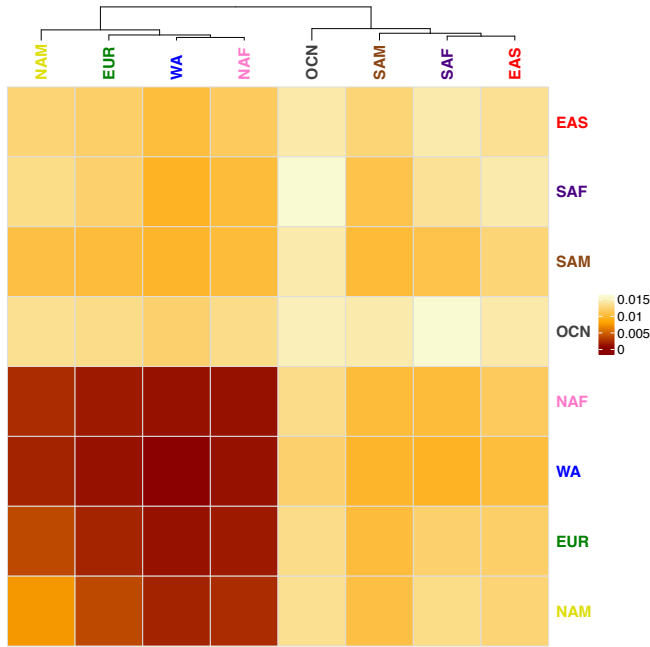
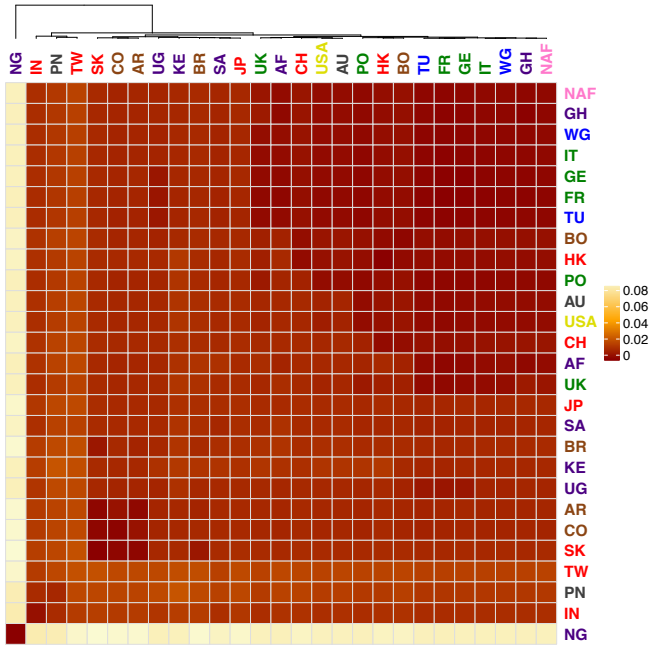
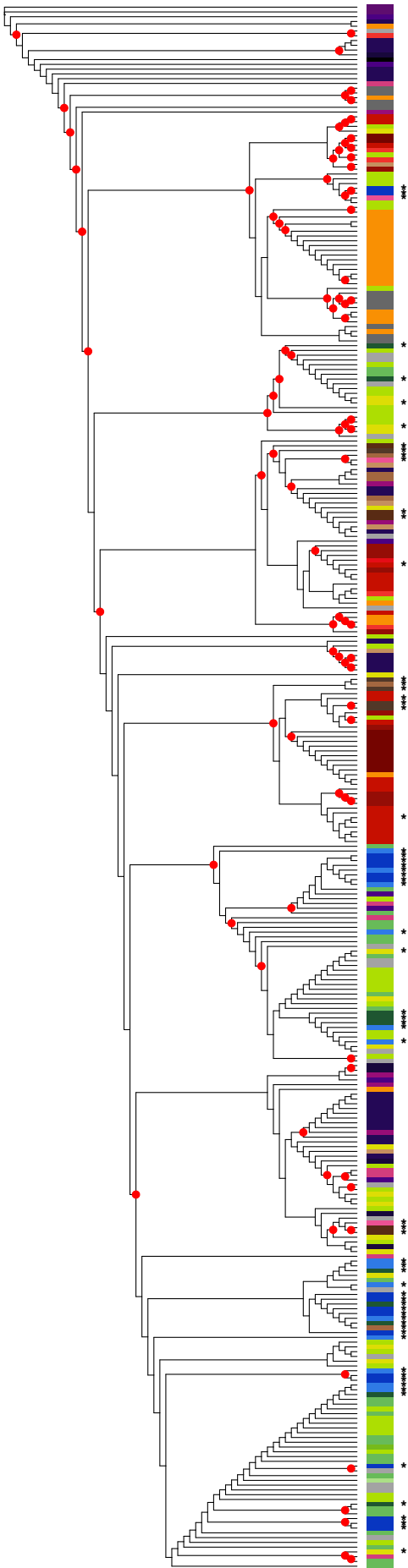
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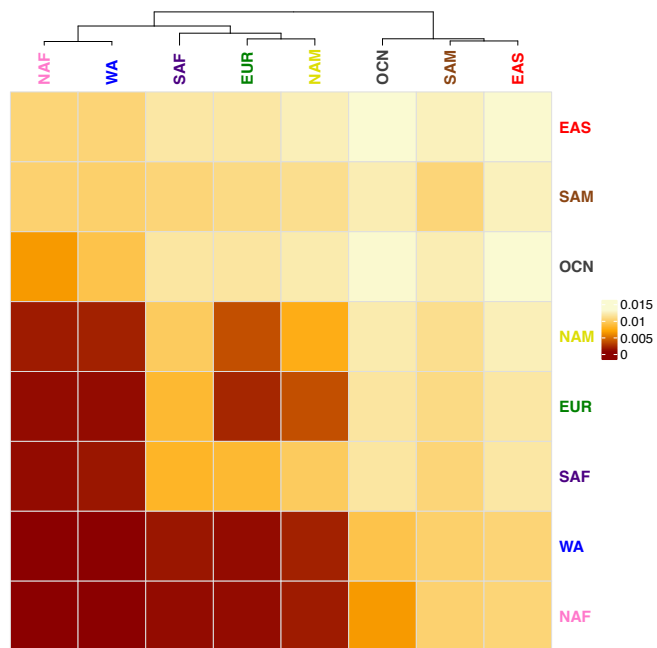
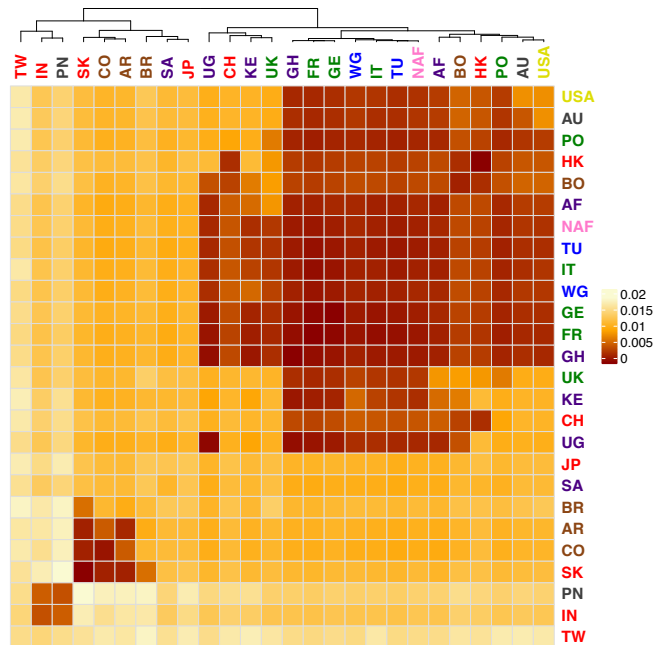
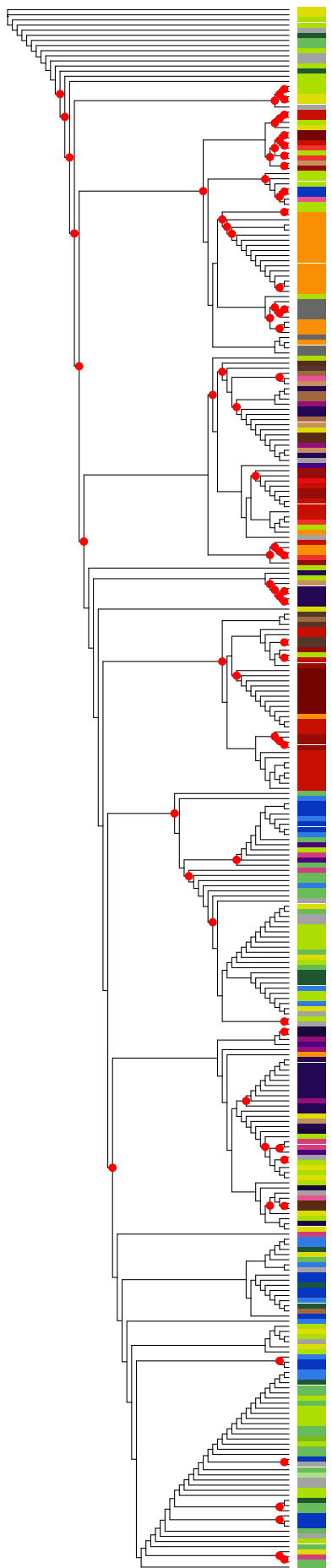
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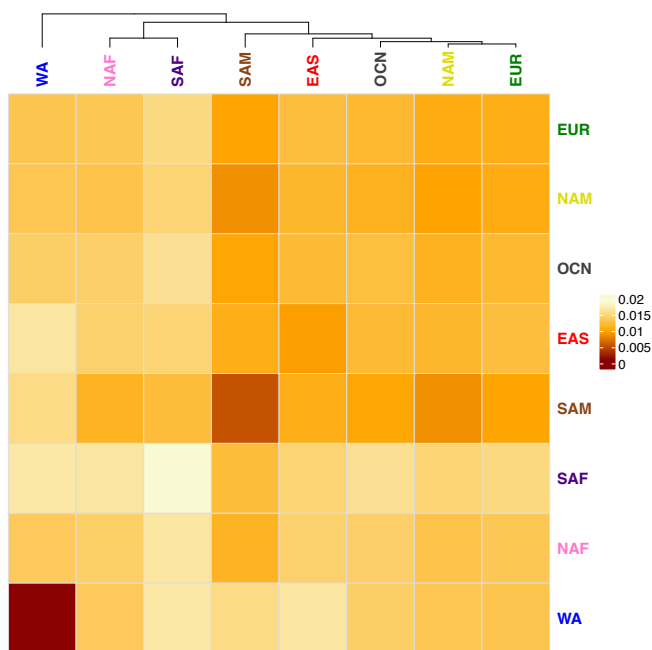
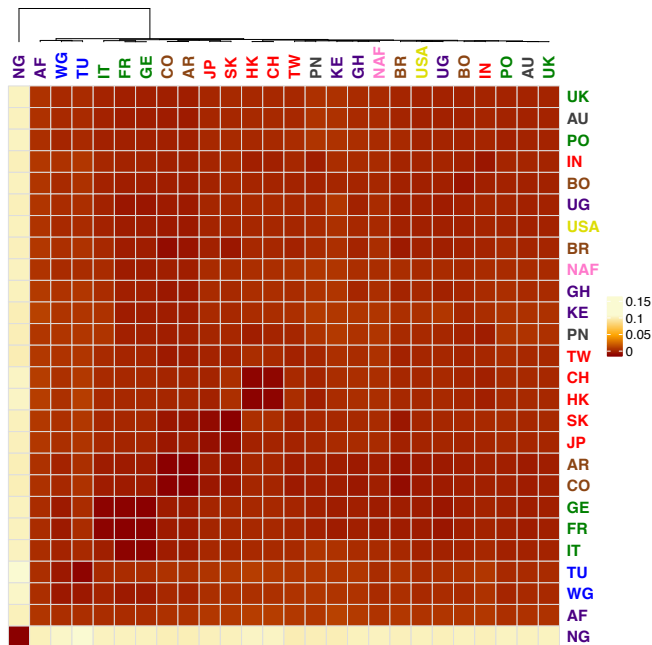
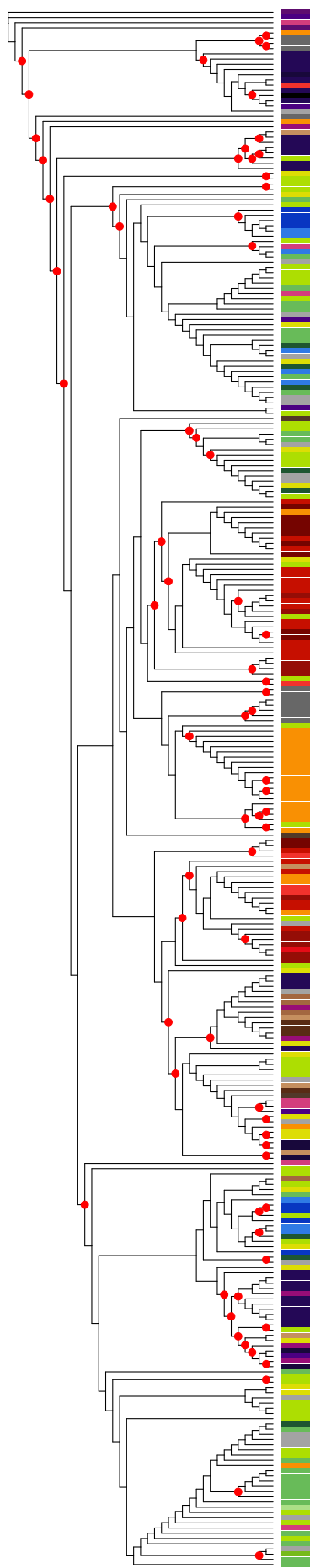
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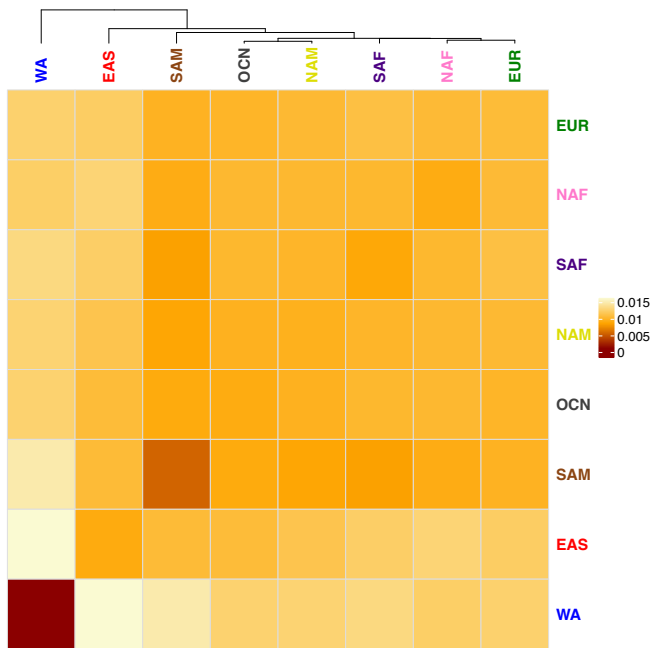
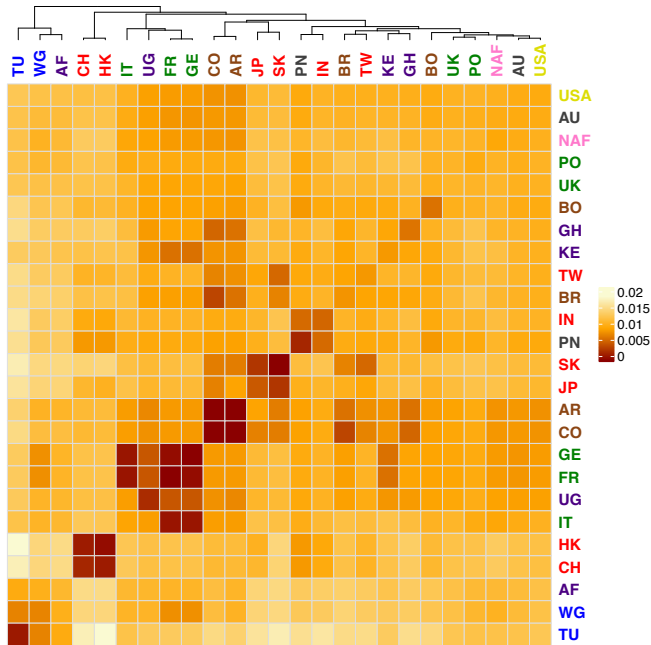
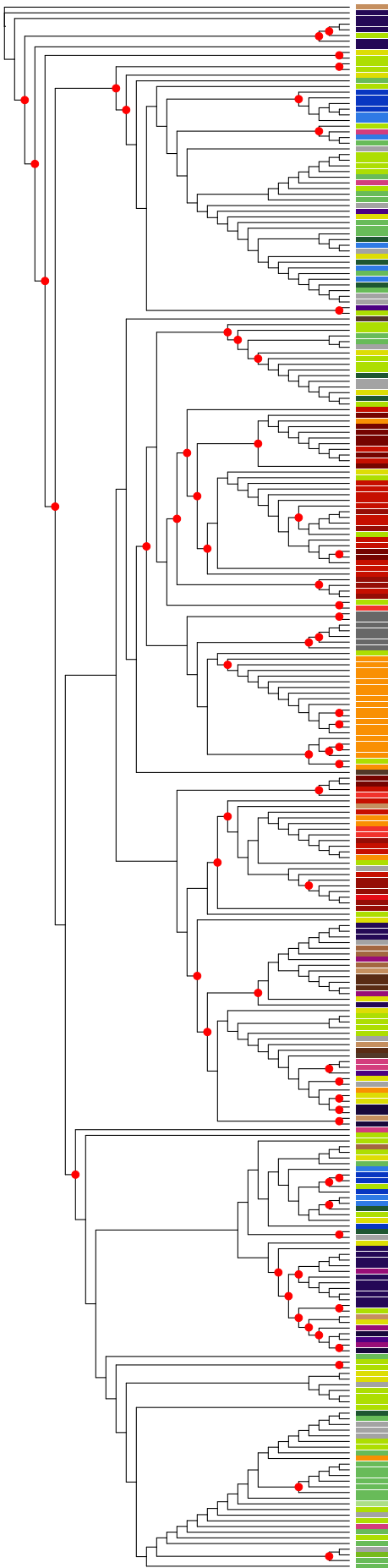
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COLOMBIA (CO)
ARGENTINA (AR)
BRAZIL (BR)

WESTERN ASIA
WEST GEORGIA (WG)
TURKEY (TU)

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OCEANIA
PAPUANUEVAGUINEA(PN)
AUSTRALIA(AU)

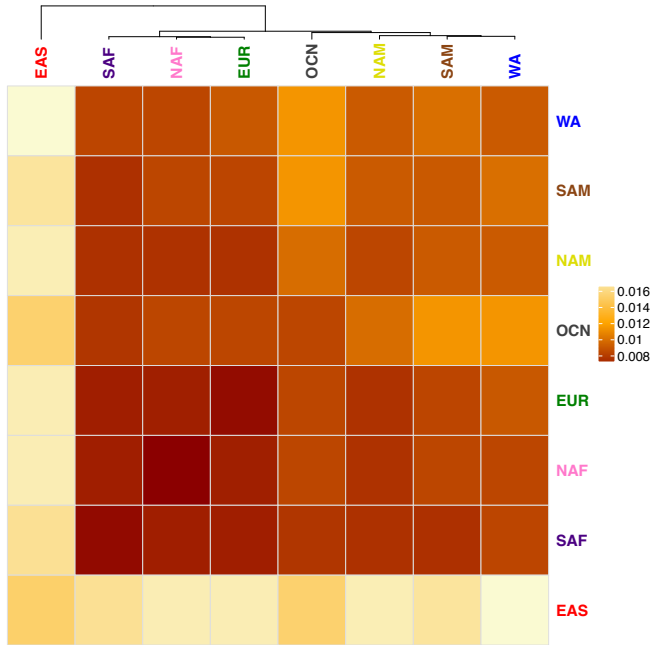
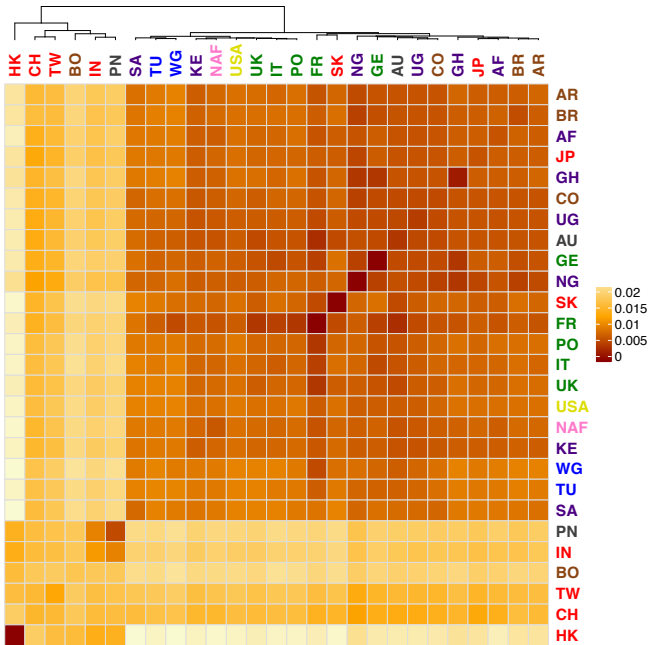
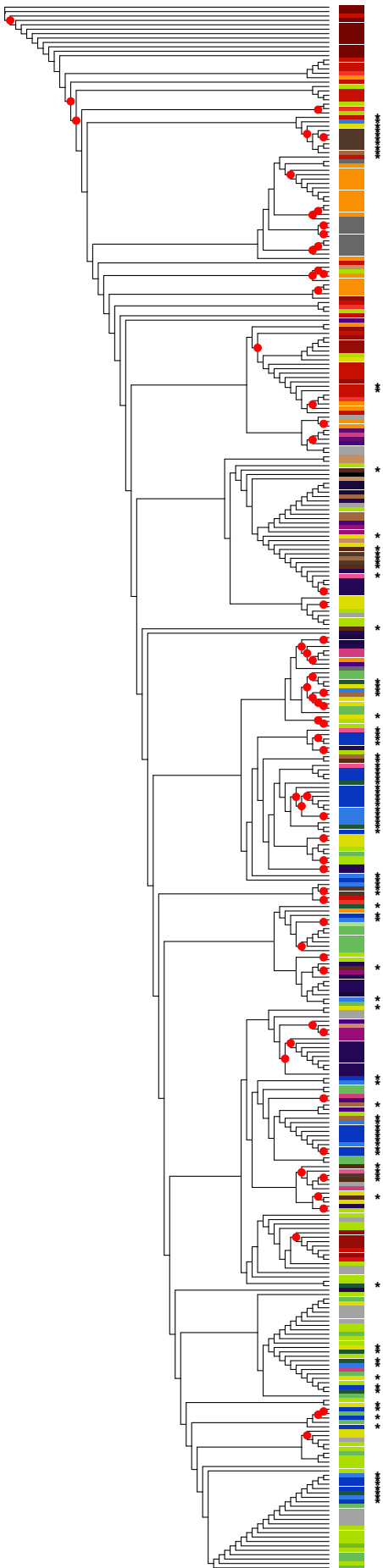
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