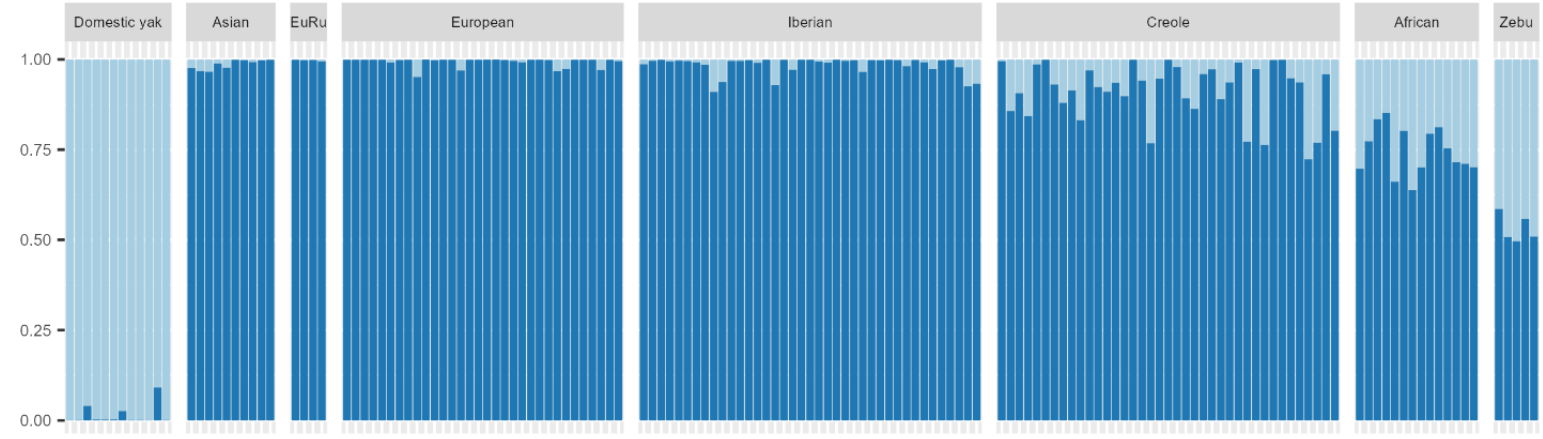
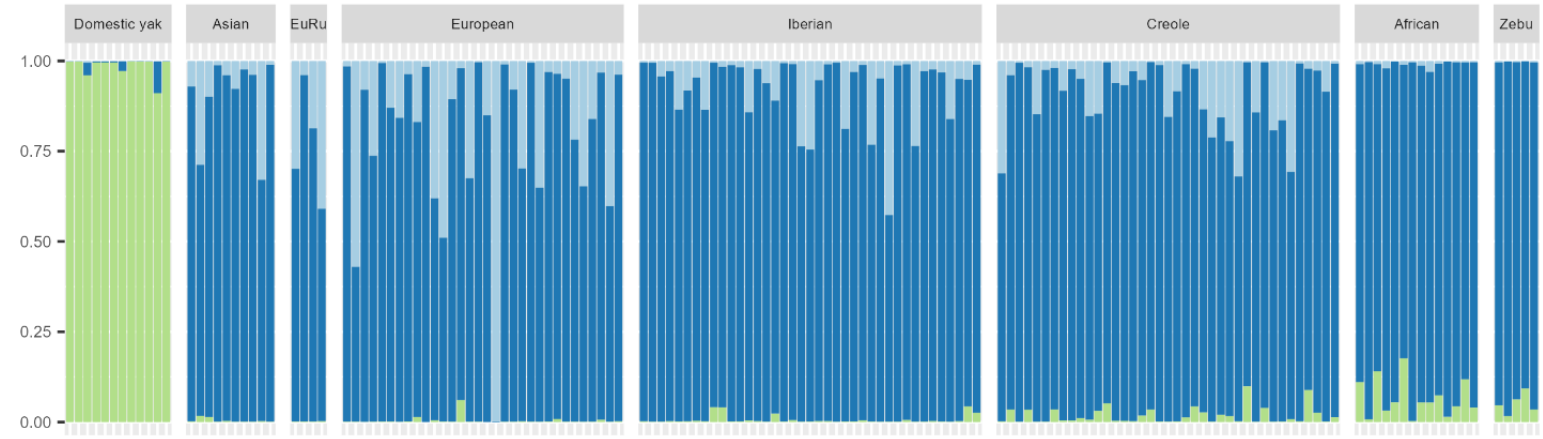


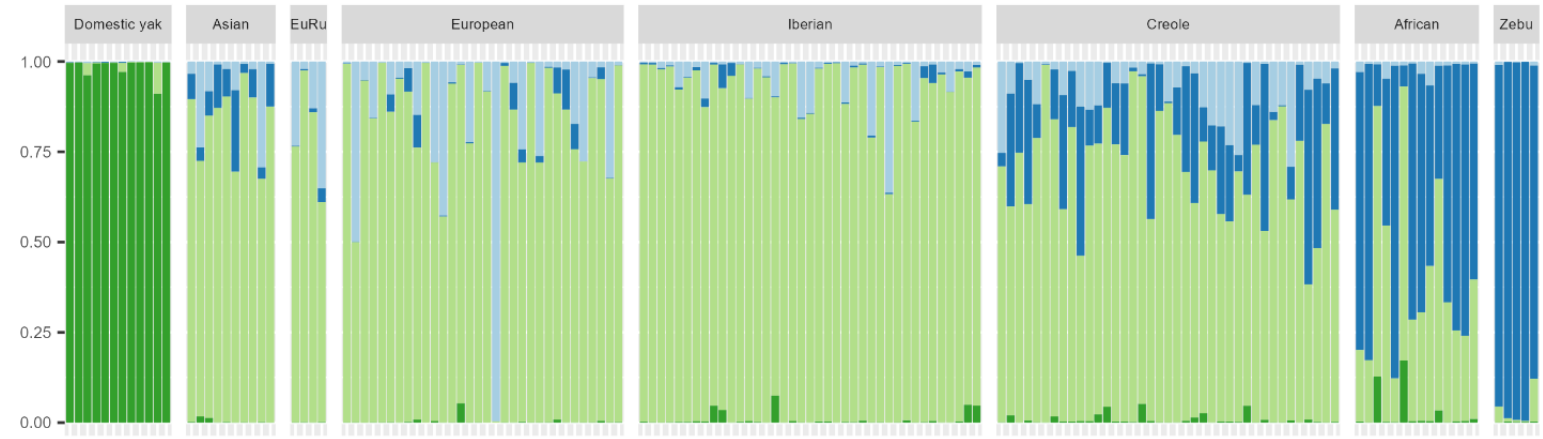
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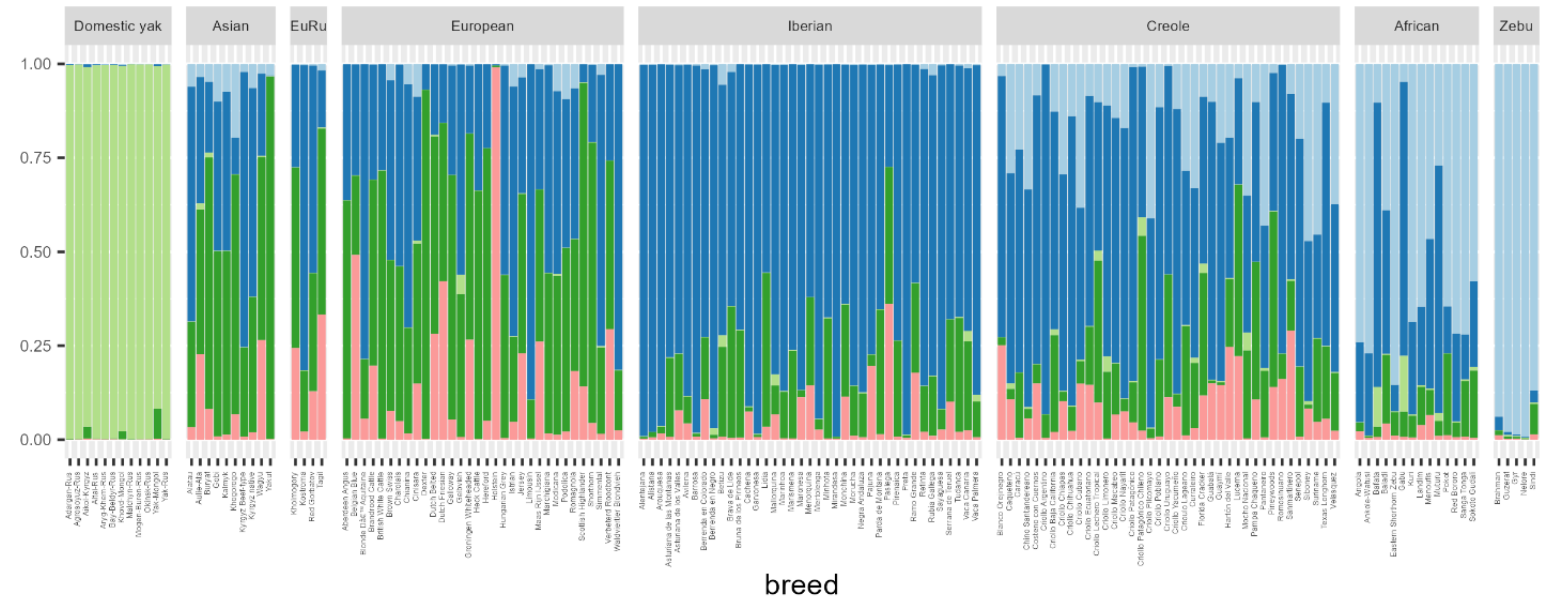
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K4

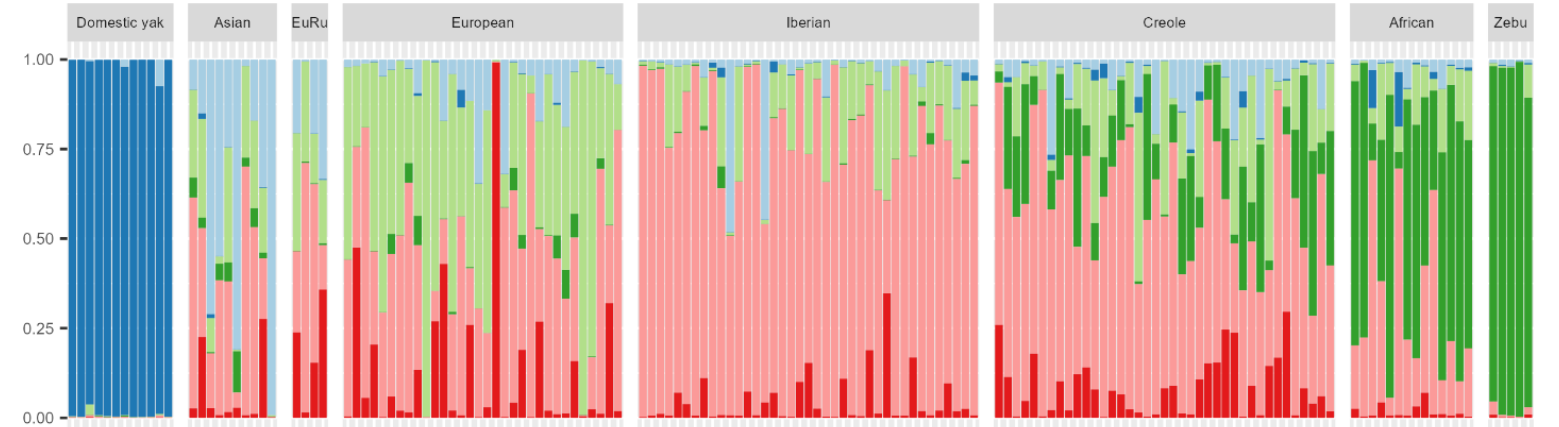


K5

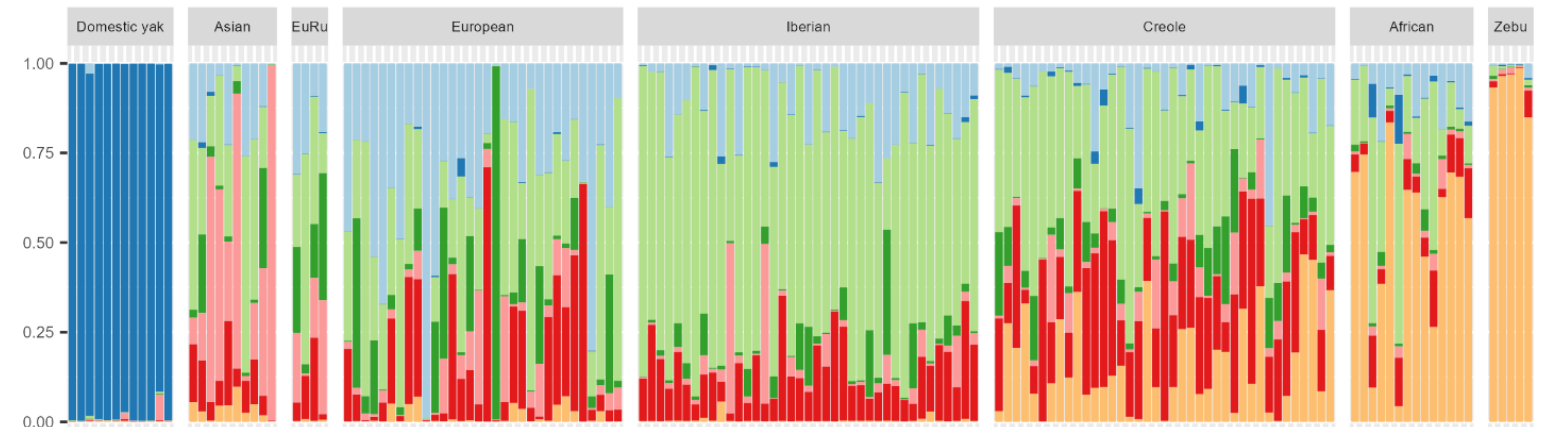


breed

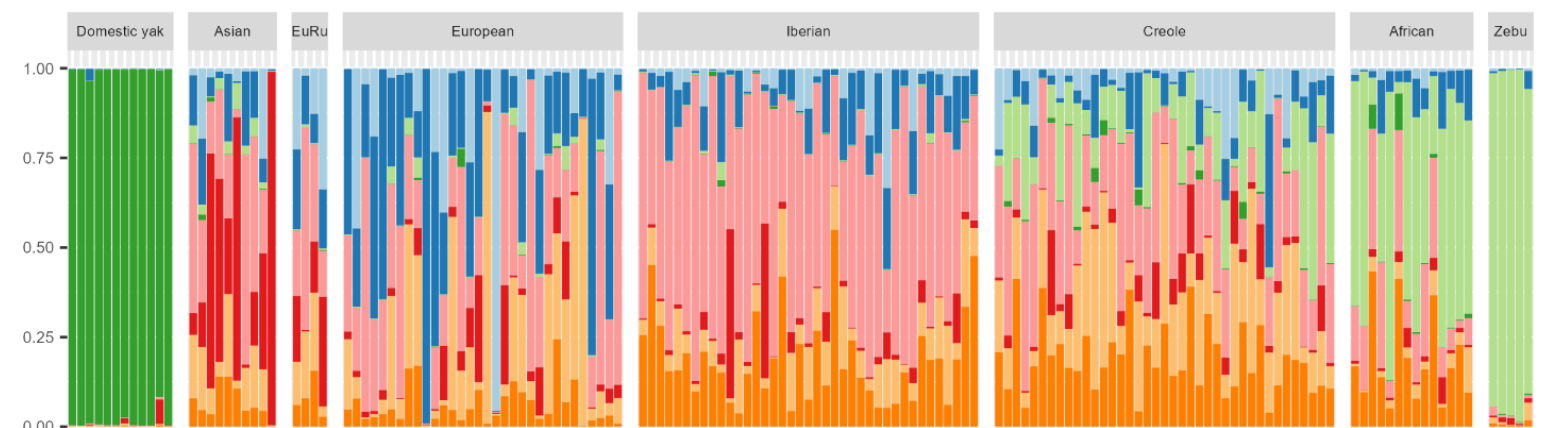
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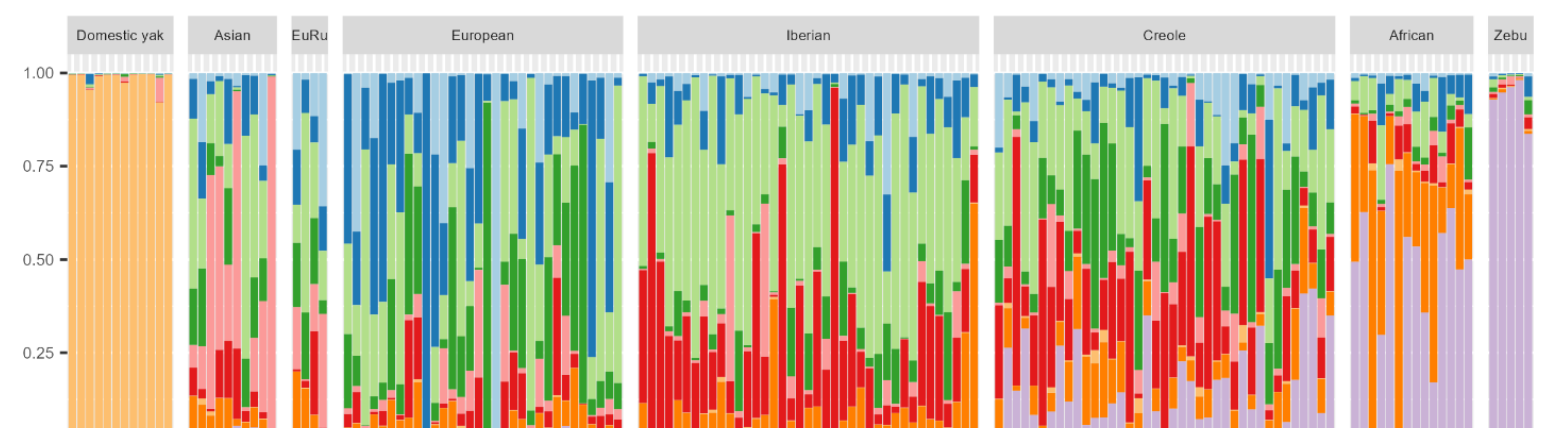
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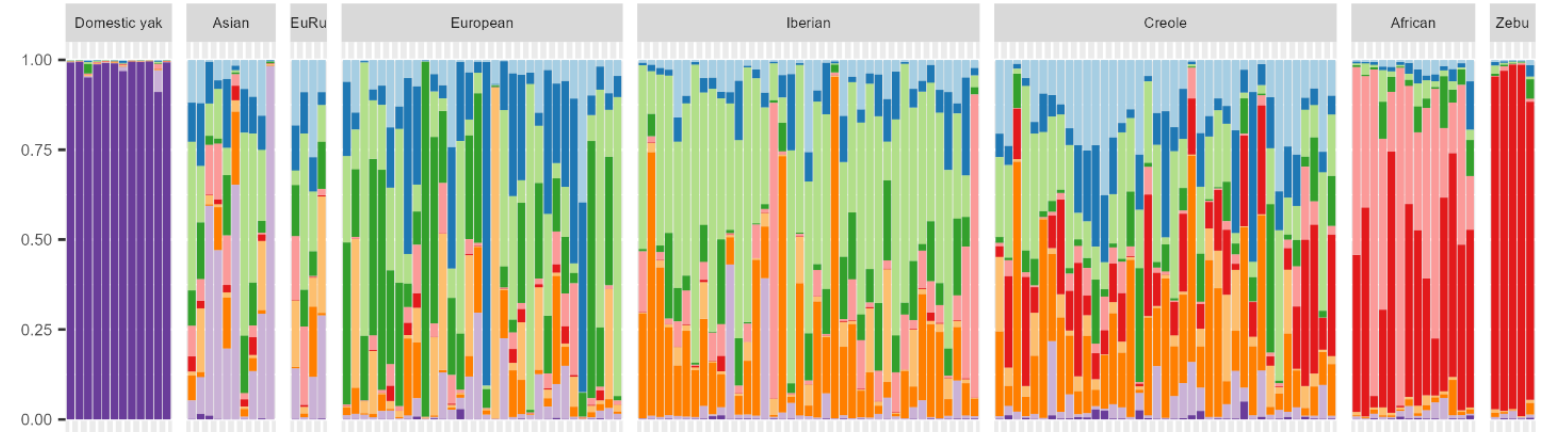


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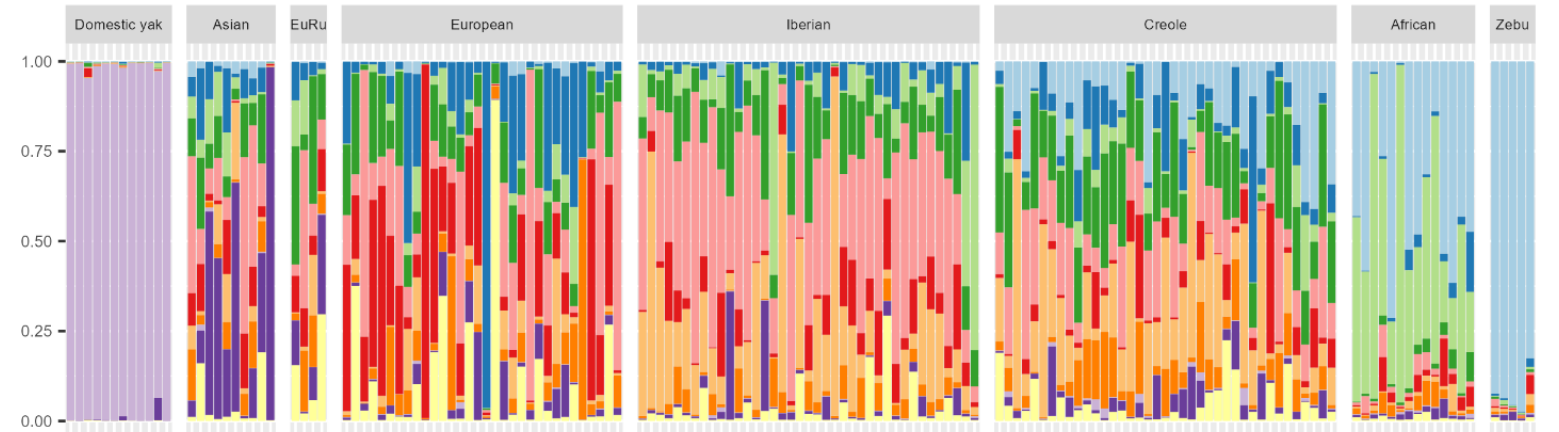


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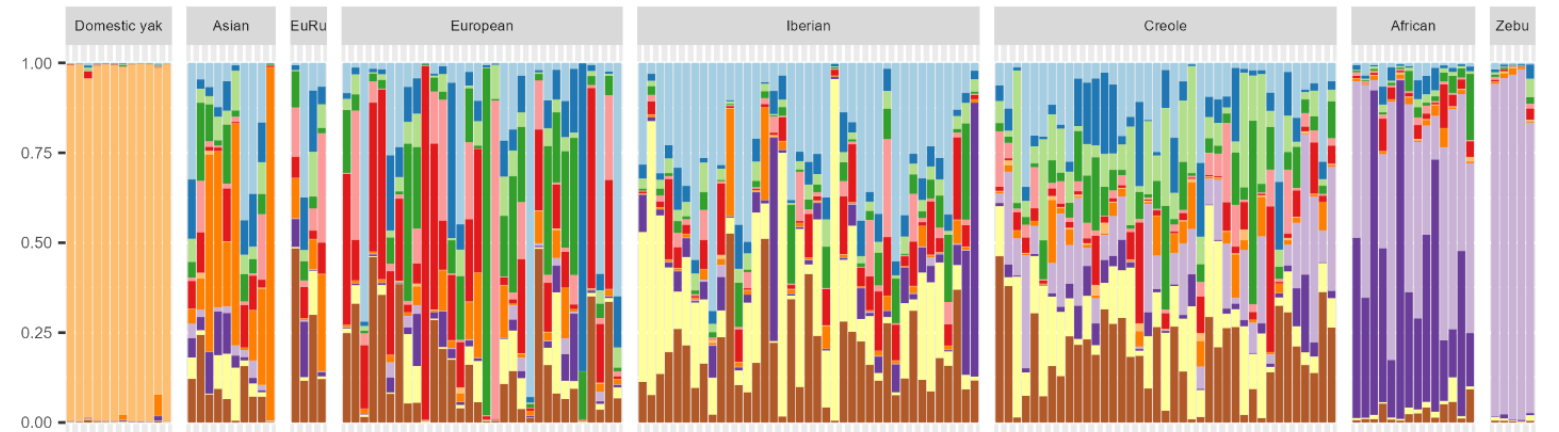
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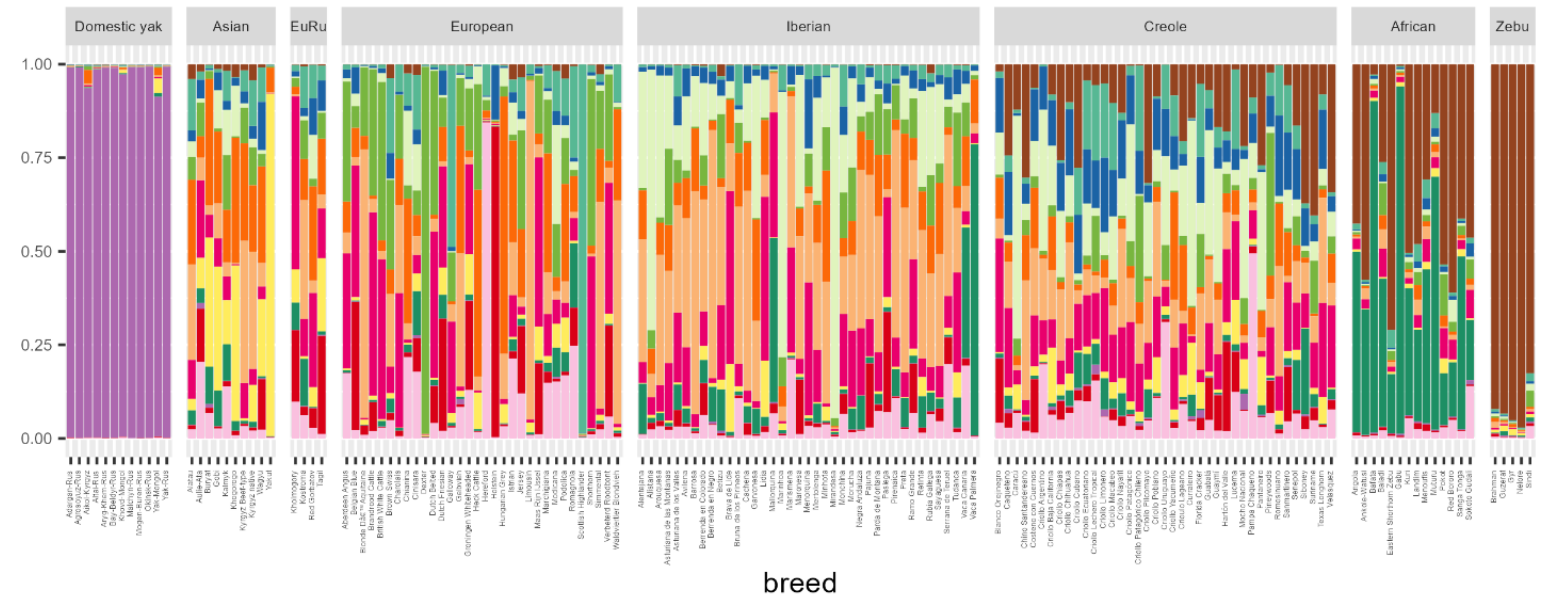
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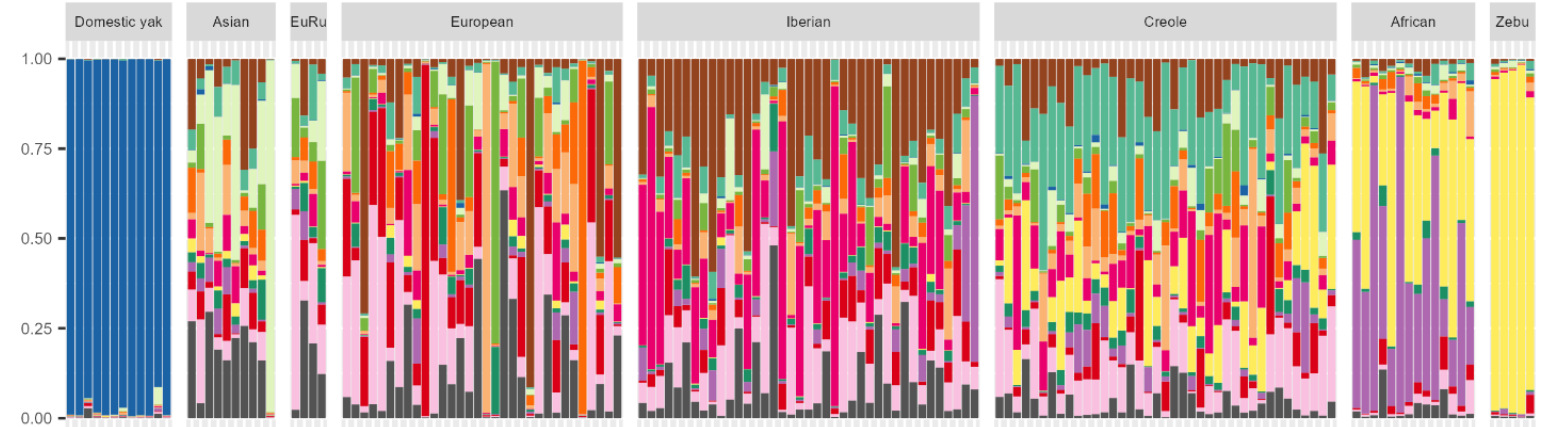
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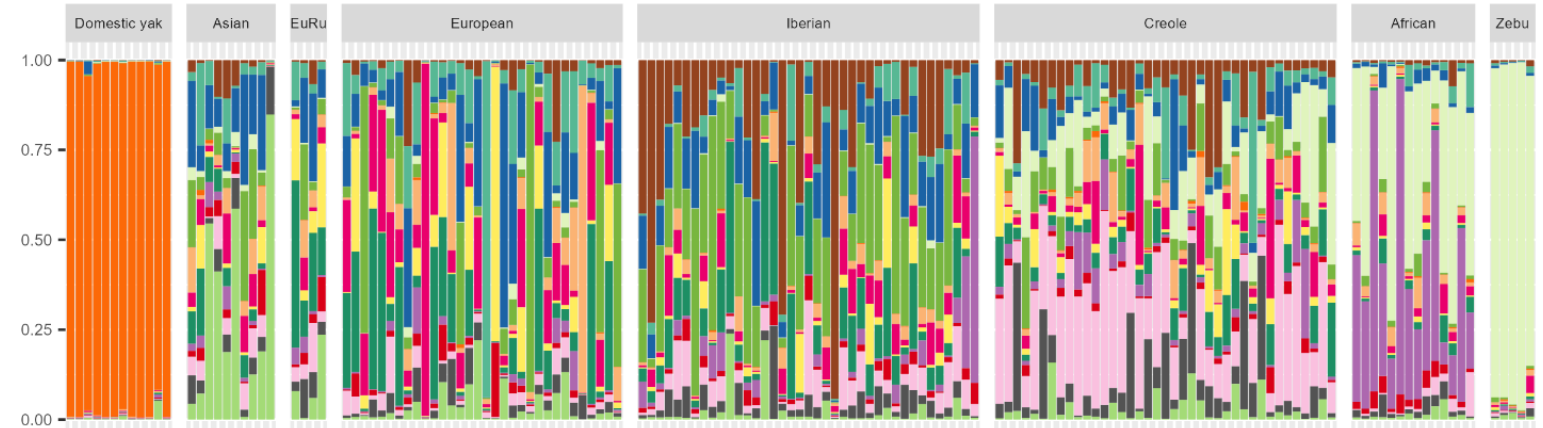
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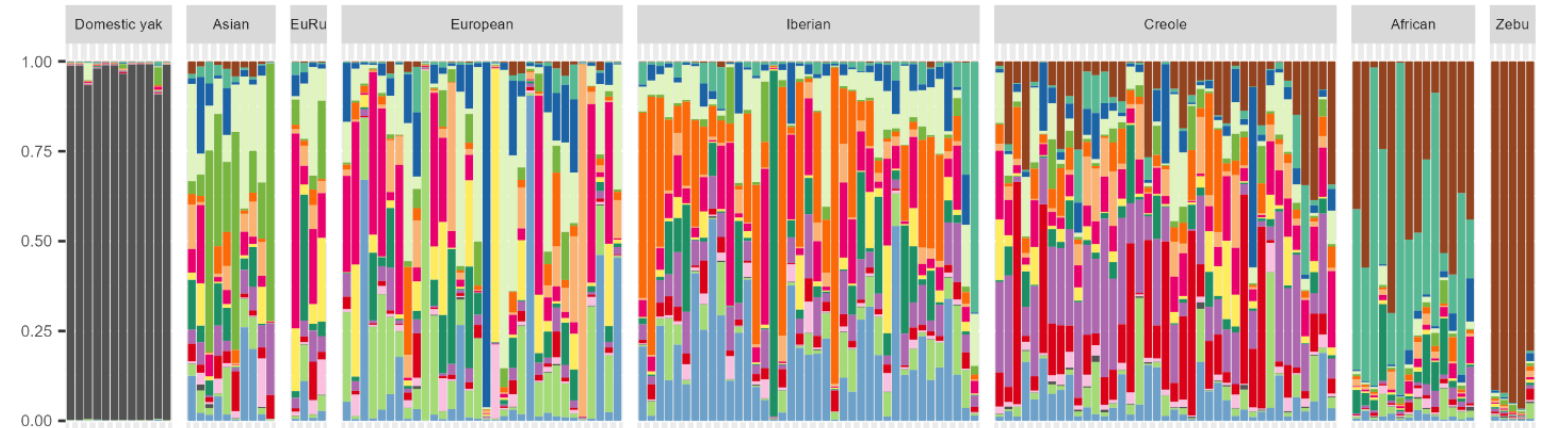
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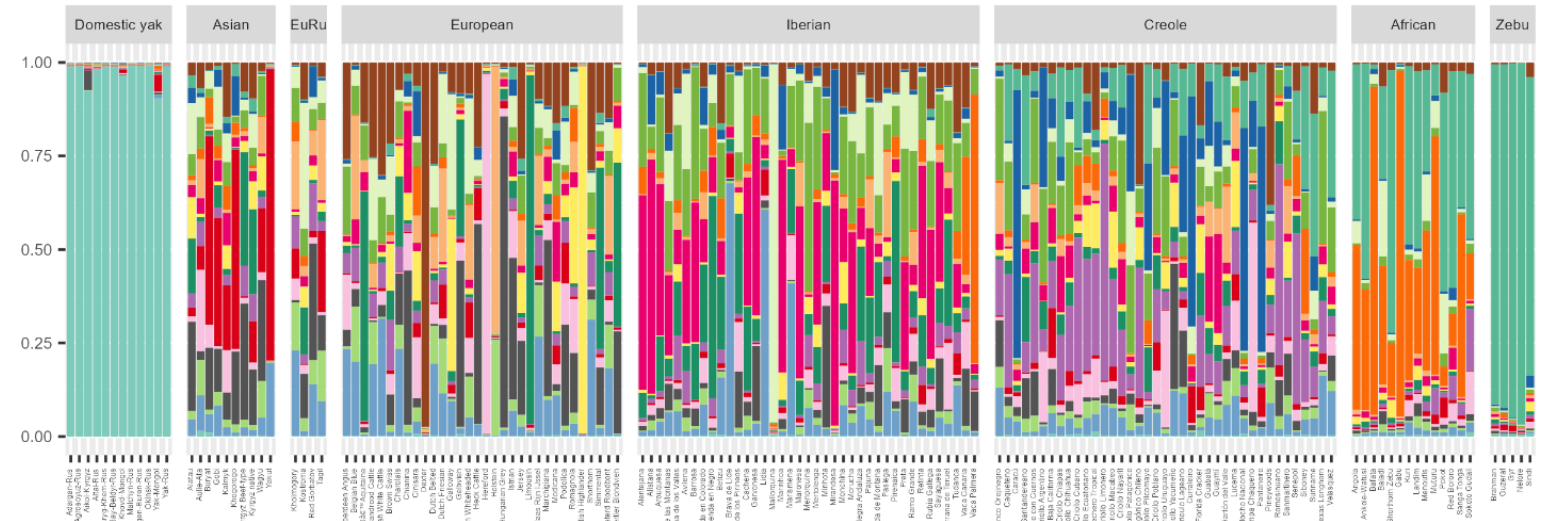
K15



K16

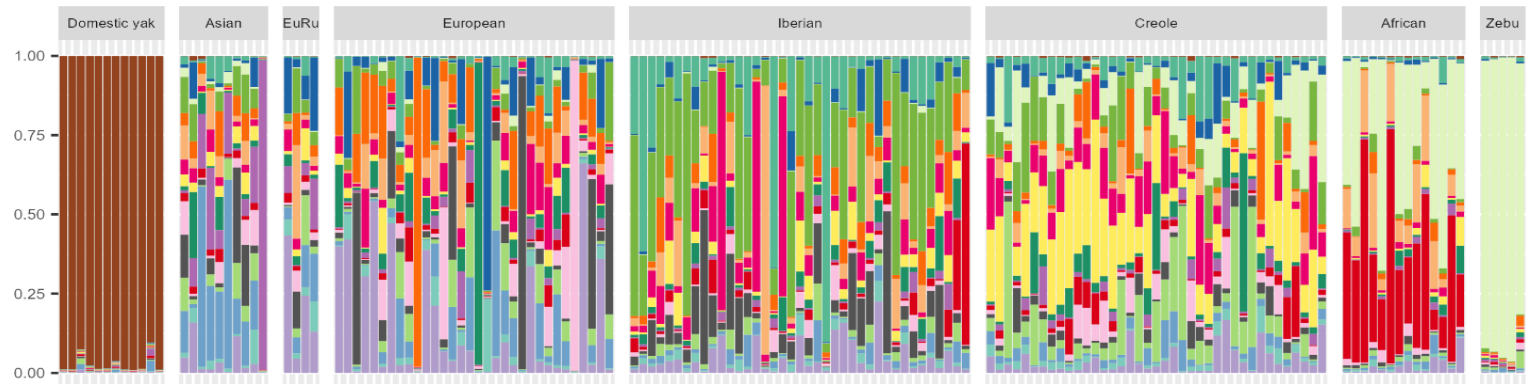


K17

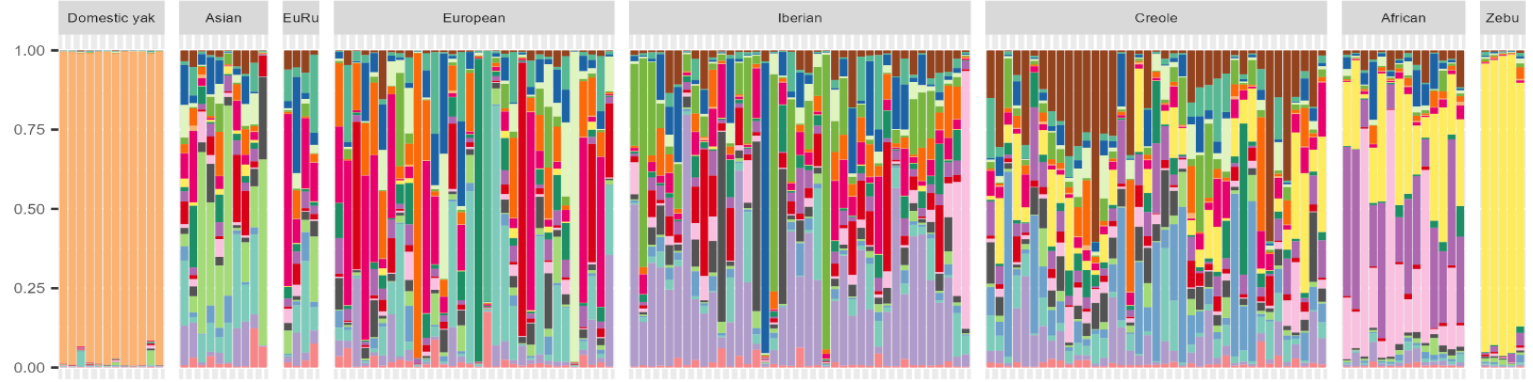


breed

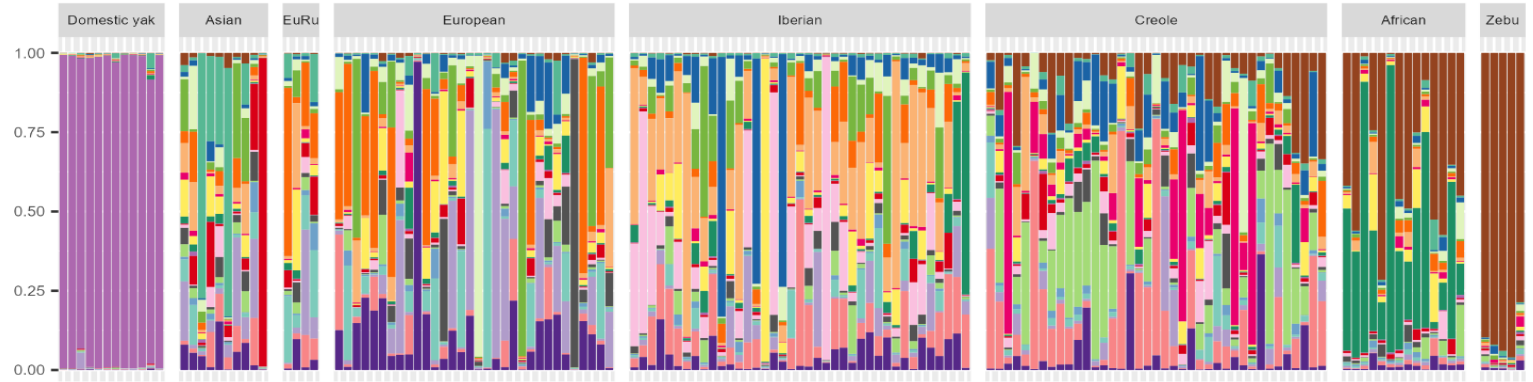
K18



K19



K20



K30

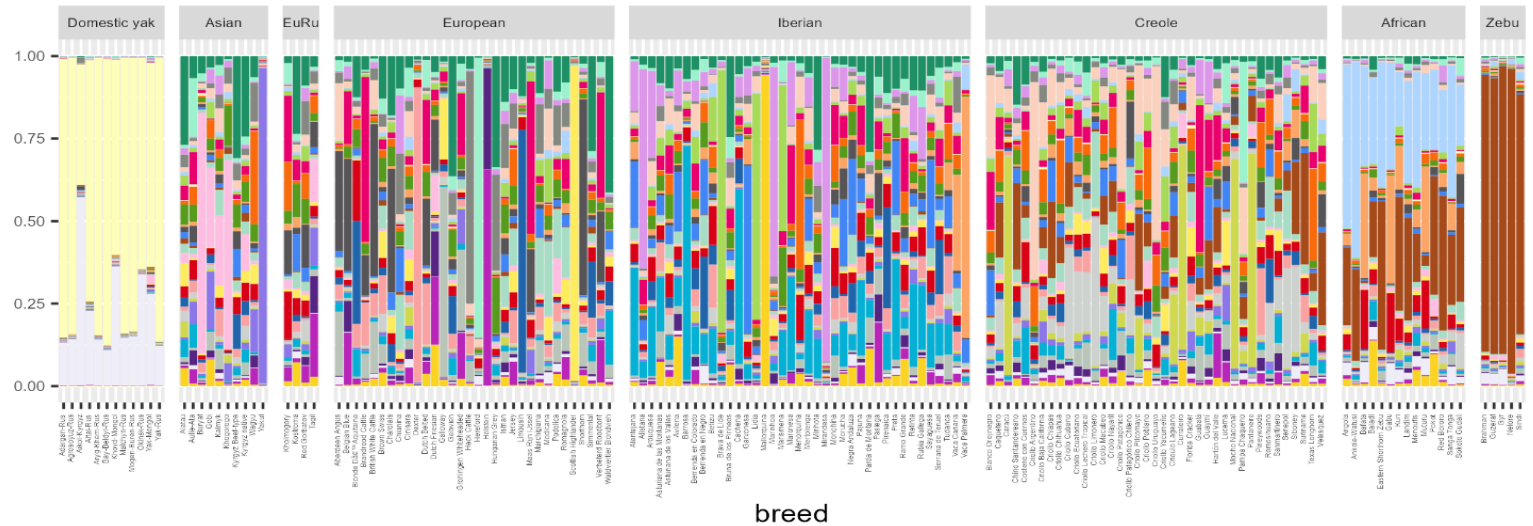


Figure S2: Cluster analysis of 155 cattle populations calculated from microsatellite data in STRUCTURE. Each individual breed is represented by a vertical bar divided into K colors according to the number of supposed ancestral populations. The size of the color segment is proportional to the contribution of a particular ancestral population to the genome of the breed in question. Results are presented for K from 2 to 20 and K=30.