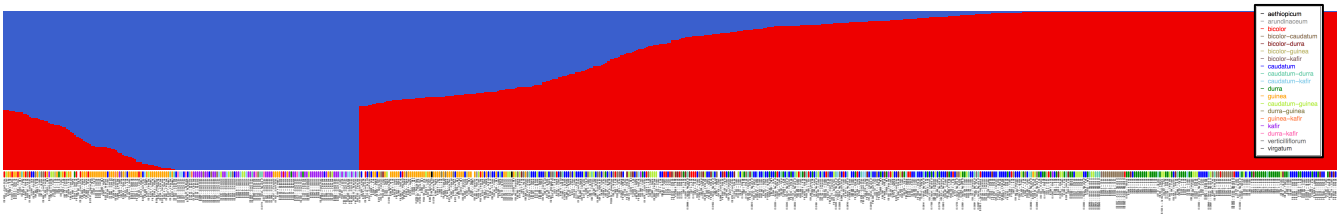
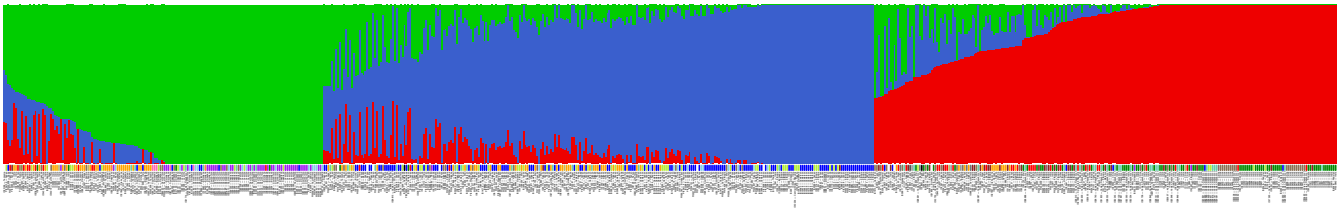
Dataset S3: High-resolution version of Bayesian hierarchical clustering of sorghum accessions based on 265,000 SNPs. Posterior probability of membership (Q) in each population for K=2 to K=19. Color-coding of Q-value bar plots (upper section) is arbitrary, while color-coding for rug plots (lower section) indicates morphological type (see legend). For clarity, only African and Asian source-identified accessions are displayed. The lowest cross-validation error was observed at K=16.

k = 2



k = 3



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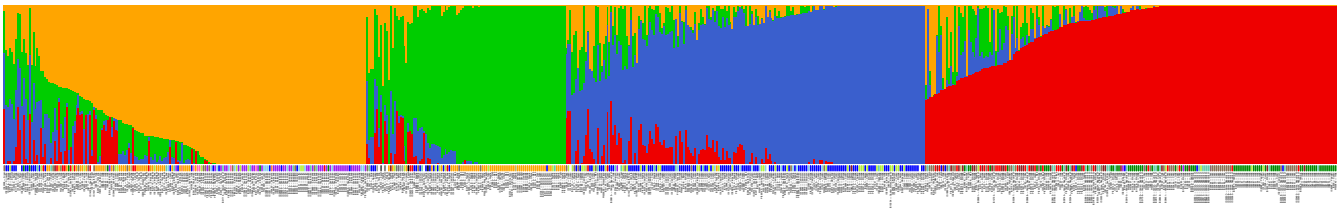

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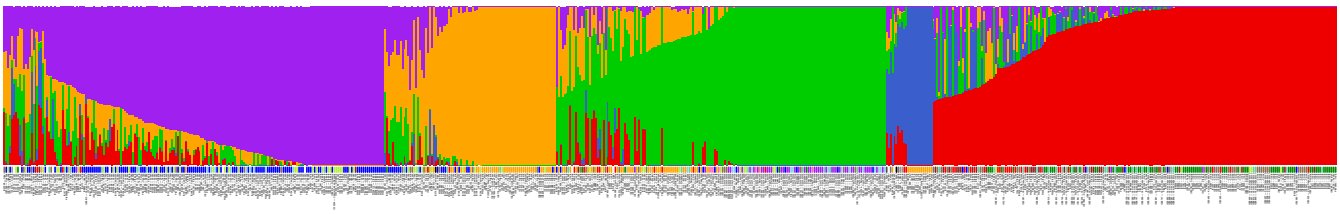
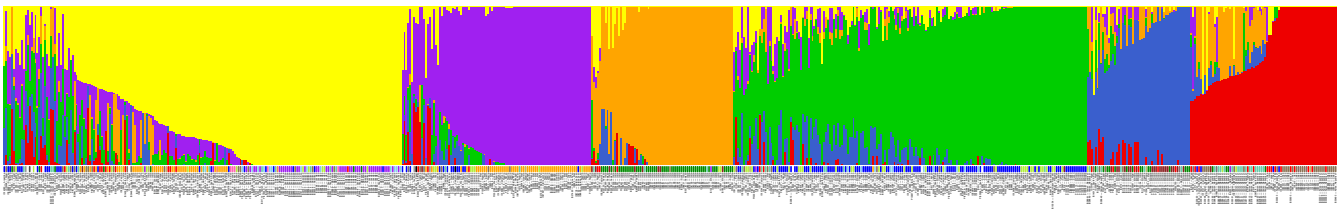


k = 6



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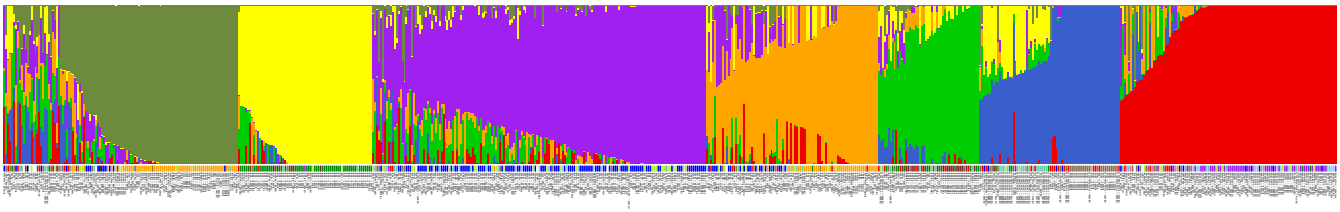

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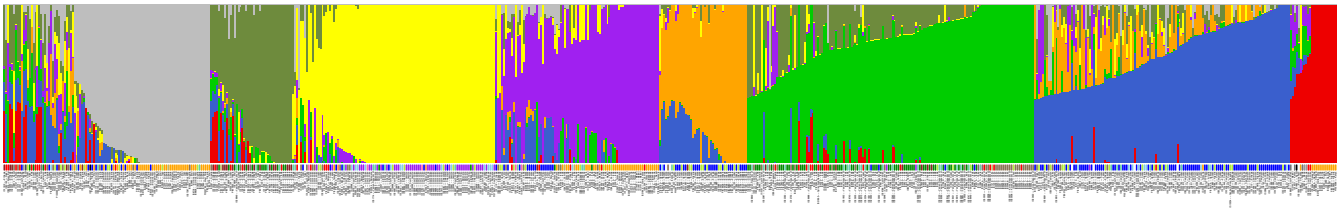

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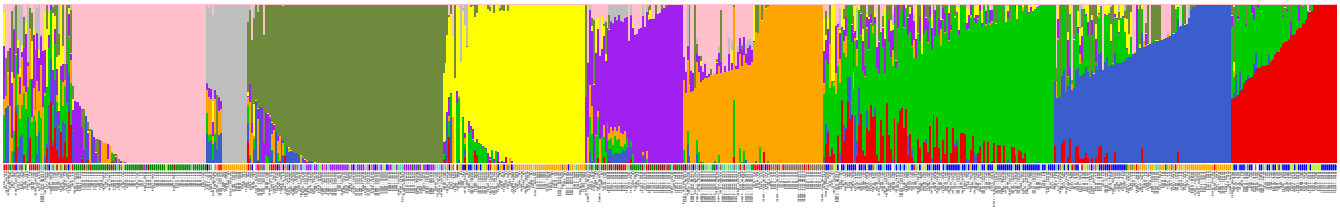

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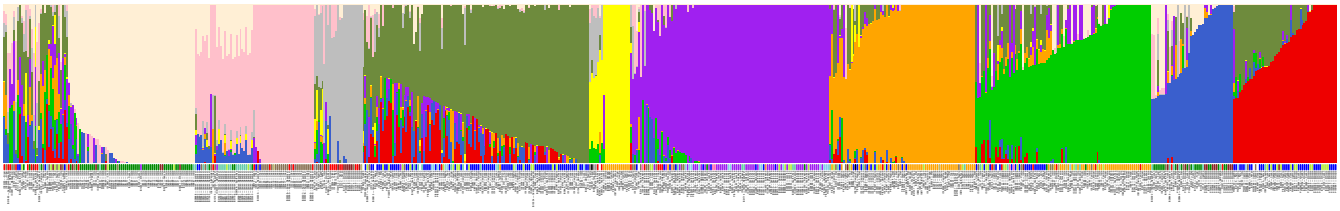

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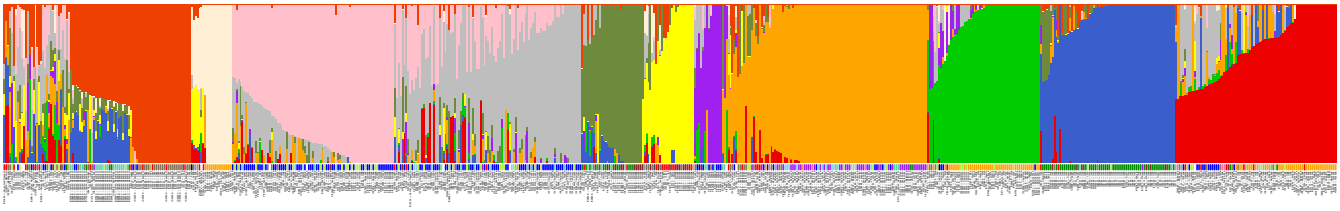
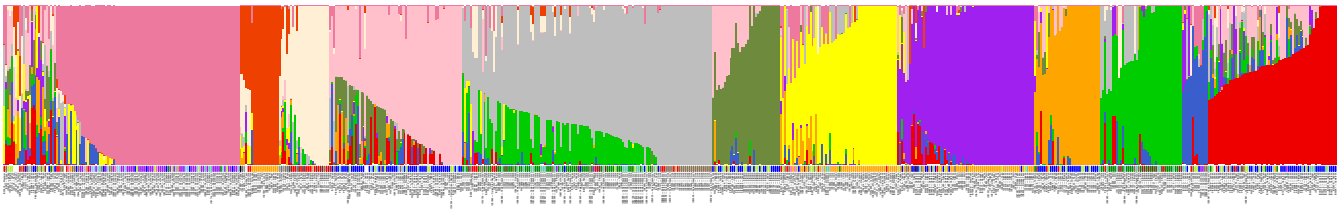


k = 12



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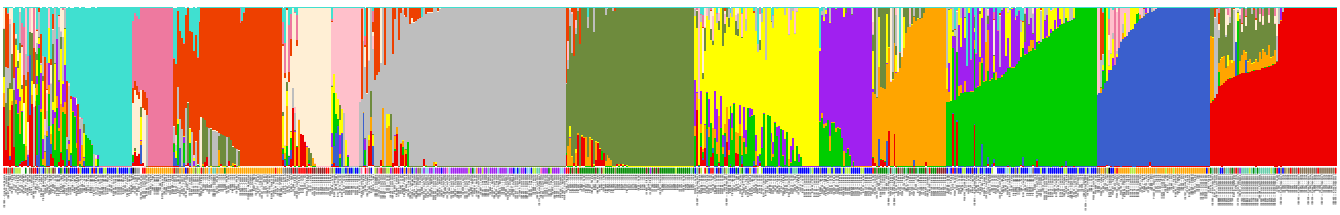

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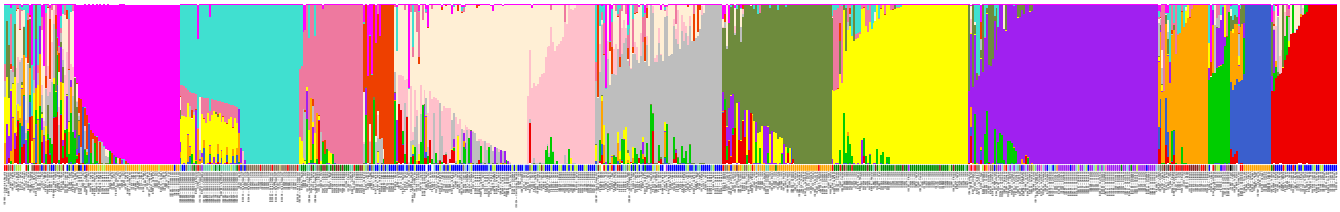

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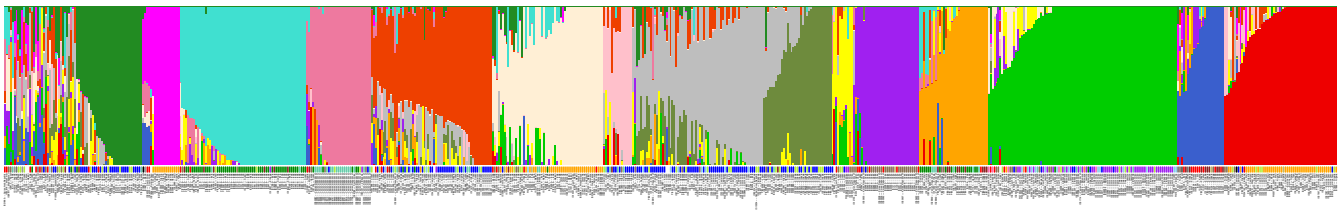

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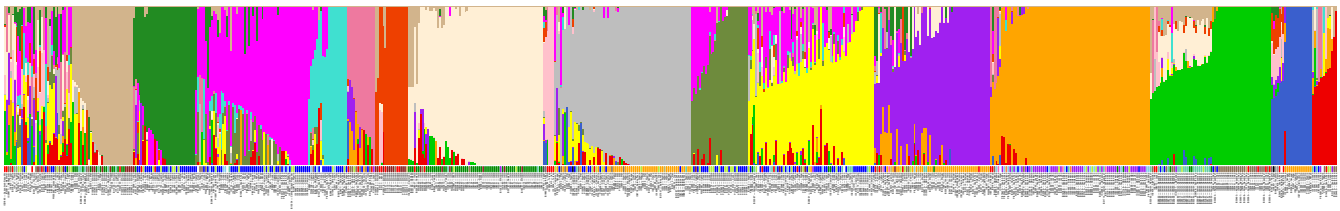

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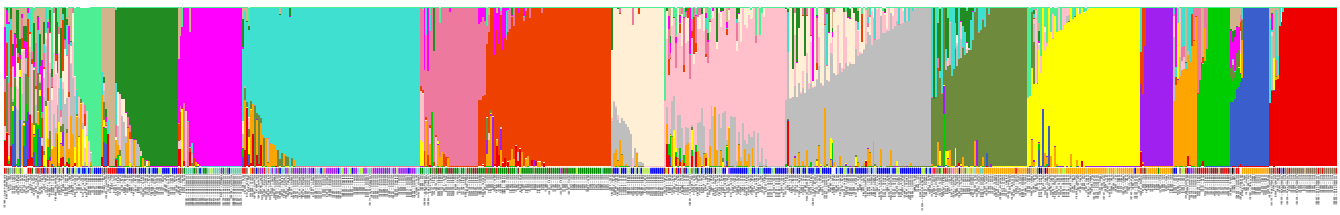

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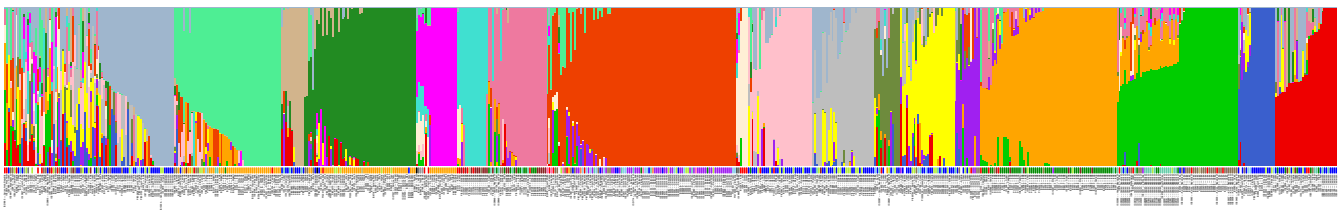
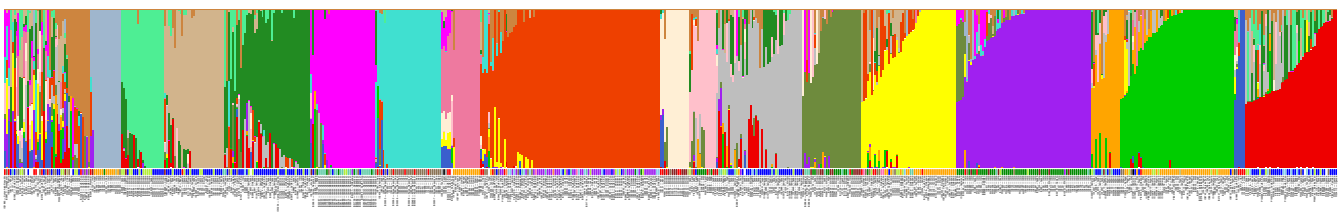
k = 19