

Similarity between HSV-1 strains varies across the genome

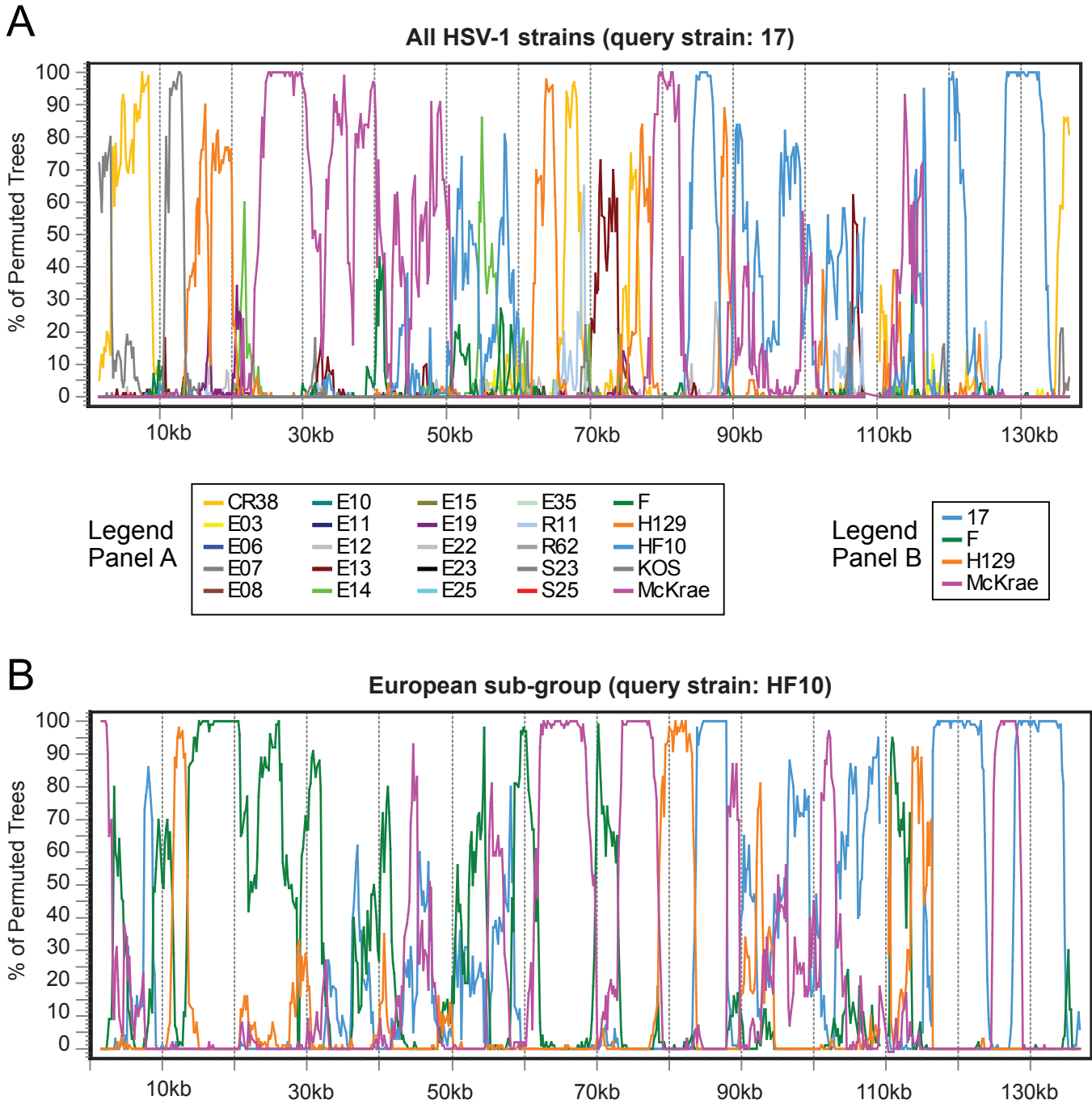


Figure 9. Bootscan analysis of similarity between HSV-1 strains contain breakpoints suggesting frequent recombination.

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(A) Similarity plot of HSV-1 reference strain 17 vs. all other strains, demonstrating that recombination occurs throughout the tree. The longest collinear area of similarity (between strains 17 and McKrae; rose line) is about 30 kb. The trimmed format of the HSV-1 strain 17 genome (Fig. 1B) was used as the query sequence. (B) Similarity plot of the European subgroup (from Fig. 8) of the HSV-1 collection, with HF10 used as the query sequence. There is extensive recombination even within genetically similar geographical clusters. The longest collinear area of similarity (between HF10 and F; green line) is about 20 kb. Bootscan parameters: 3 kb window, 200 bp step size, GapStrip on, 100 repetitions, Kimura (2-parameter), T/t=2.0, neighbor-joining.