

AA Alignment of the divergent HSV-1 US11 protein

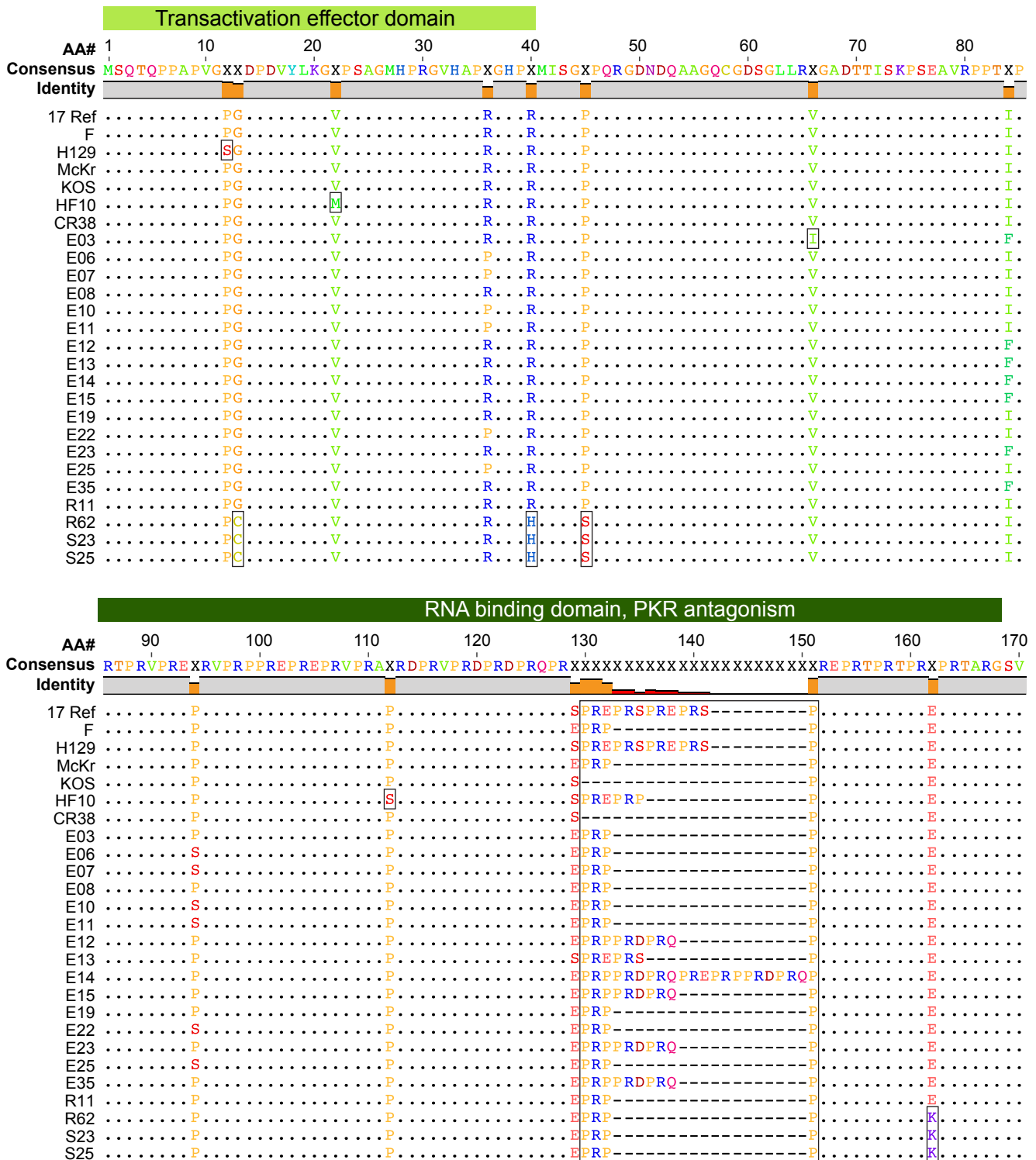


Figure 5. AA sequence conservation in the RNA-binding protein and PKR antagonist, US11.

Szpara *et al.* (2013) JVI. Evolution and diversity in human herpes simplex virus genomes.

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AA alignment of US11, which is 89.5% identical across the 26 strains analyzed. Gray bar across top indicates identical residues in all strains; orange indicates non-identity. The median divergence of all strains versus the consensus (top line) is 1.2% (98.8% similarity to the consensus; see also Tables 3 and S3). Green shaded blocks above the alignment indicate known functional regions of the protein (14, 30, 106, 112-114, 127). Variations in US11 illustrate those commonly seen among HSV-1 strains. These include strain-specific SNPs (e.g., P12S, V22M, V66I, and P112S), variations shared by a group of strains (e.g., G13C, R40H, P45S, and E162K), and SSR-related indels (PRX repeat beginning at residue 130).