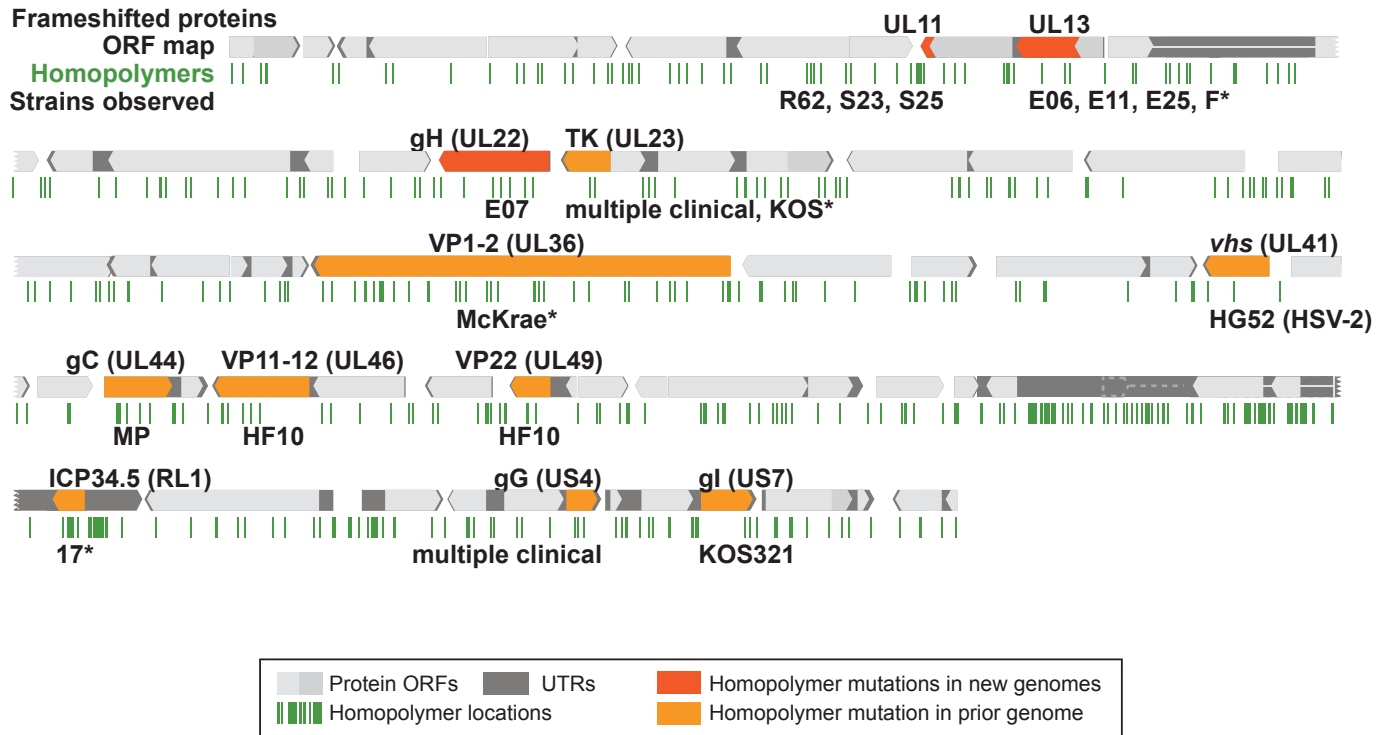


Homopolymer-based frameshifts in HSV-1 proteins



Additional Figure A2. Sites of current and previously recorded homopolymer-based frame shift mutations in HSV-1 proteins.

Figure A2. Sites of current and previously recorded homopolymer-based frame shift mutations in HSV-1 proteins. Diagram showing HSV-1 proteins with frameshifts due to changes in homopolymer length, both in the current set of twenty new genomes (red) and those noted in previous studies (orange). Asterisk (*) indicates strains where the prototype is wild-type, but variant clones or sub-populations have been described with these frameshifts. Sources of the previously published mutations are as follows: UL13 in strain F (1), TK (UL23) in numerous clinical isolates and laboratory strain KOS (2-6), gC (UL44) in strain MP (7), UL46 and gN (UL49A) in strain HF10 (8), ICP34.5 (RL1) in strain 17 (9), gG (US4) in clinical isolates (10, 11), gI (US7) in strain KOS321 (12), and UL41 in strain HSV-2 HG52 (13).

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