

G+C vs. A+T distribution spikes in herpesvirus repeat regions

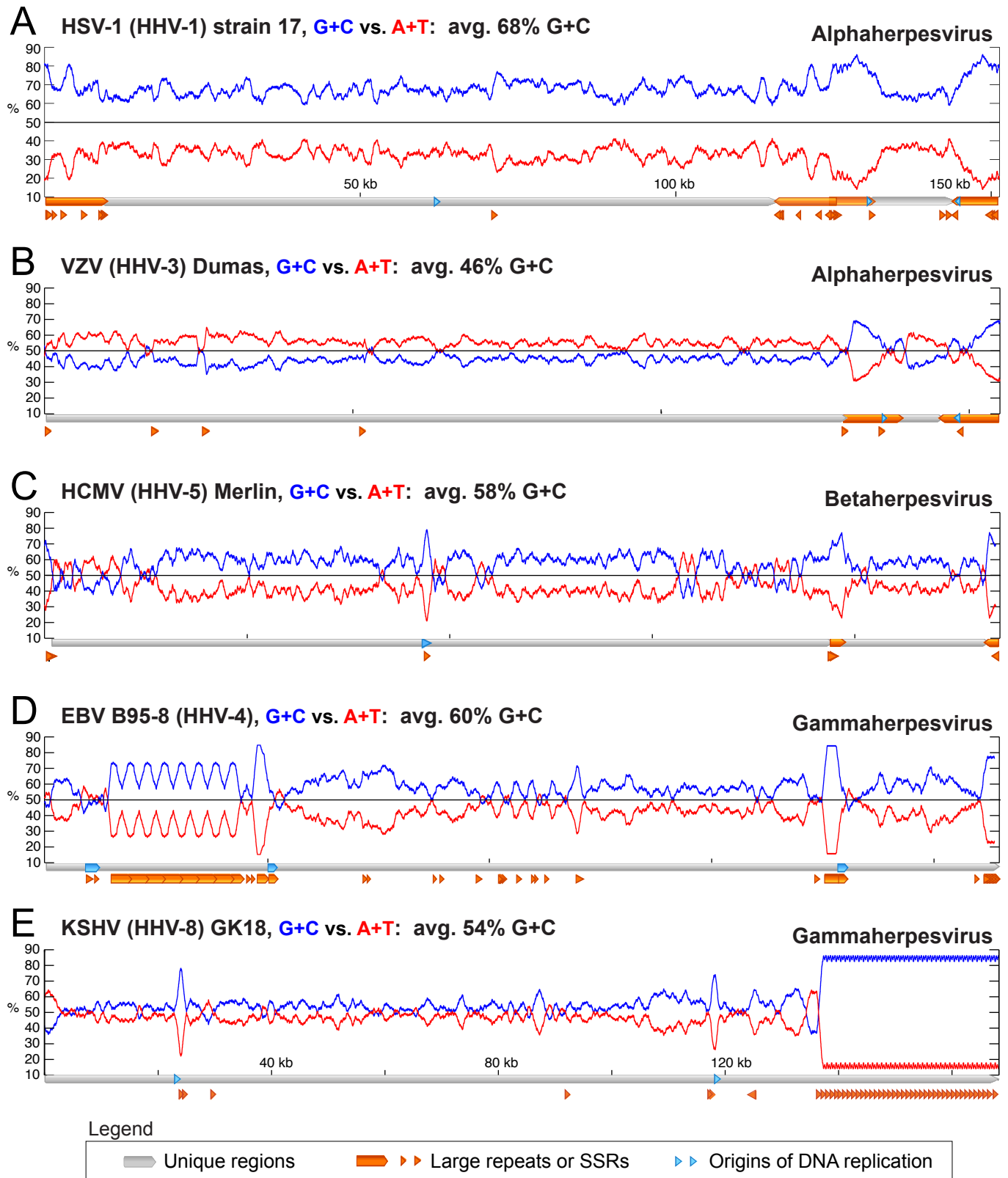


Figure 2. Nucleotide compositional bias towards G+C residues in repeat regions of herpesvirus genomes.

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

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(A) A line-graph overlay of G+C vs. A+T distribution in the HSV-1 genome (reference strain 17; human herpesvirus 1 (HHV-1)). A diagram beneath the line graph depicts the locations of UL and US (gray), as well as TRL/IRL and TRS/IRS (orange). SSRs are also marked in orange. (B) Another human alphaherpesvirus, VZV, is A+T-rich in the UL and US regions (56%) but G+C-rich in the inverted repeat regions (59% G+C). (C-E) Similar plots depict nucleotide distribution in unique vs. repeated regions of human beta- (human cytomegalovirus, HCMV) and gammaherpesviruses (Epstein-Barr virus, EBV; Kaposi's sarcoma-associated herpesvirus, KSHV). Note that each genome is drawn to an individual scale, as marked below each line graph. Nucleotide sequence and annotations of unique and repeated regions are derived from NCBI RefSeq accessions: VZV strain Dumas (NC_001348), HCMV strain Merlin (NC_006273), EBV strain B95-8 (NC_007605), and KSHV strain GK18 (NC_009333).