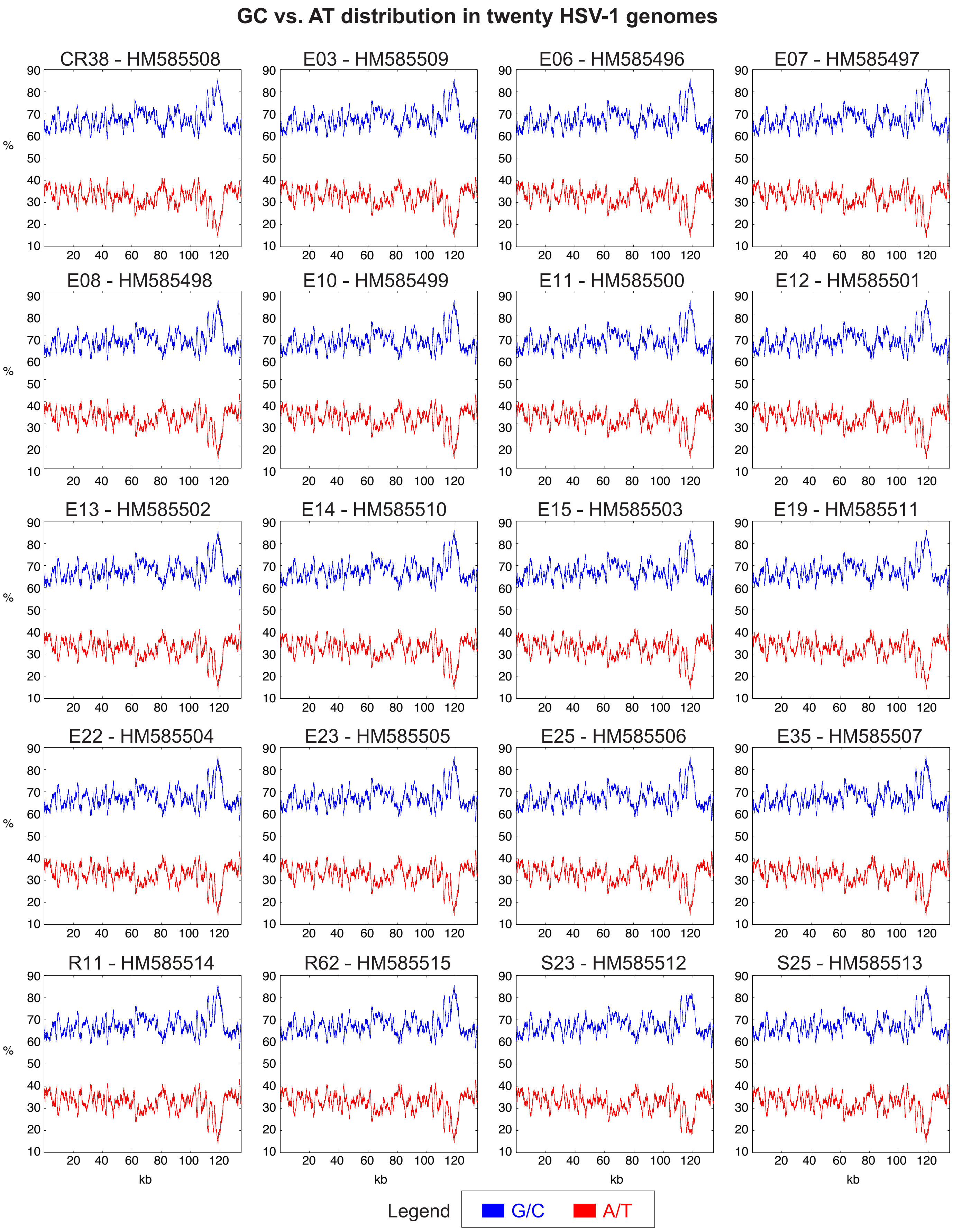

Additional Figure A1. Nucleotide abundance of G+C vs. A+T for 20 new HSV-1 genomes.

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

Figure A1. Nucleotide abundance of G+C vs. A+T for 20 new HSV-1 genomes.
Line graph of G+C vs. A+T distribution in the twenty newly sequenced HSV-1 genomes reveals a pattern matching other HSV-1 strains (Fig. 2). The trimming of terminal copies of the large repeats (Fig. 1) removes the outermost spikes of G+C-richness seen in Figure 2A.

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