



Figure 6. Distribution of Ω substitution rates for all proteins of HSV-1.

Histogram of the number of HSV-1 proteins at each Ω substitution rate (in bins of 0.1, centered around the values shown). Ω of 1 indicates neutral selection or drift (light blue), whereas an Ω of 0 indicates absolute constraint (dark blue). Protein names are listed next to each bin for all but the largest bin (0.1-0.19; see Table S3 for list of all values). Protein names in bold show signs of positive selection of individual AA residues (see Table 4). The average Ω value of 0.27 indicates that weak evolutionary constraint is the most common mode of protein evolution, while a few proteins approach levels of drift (UL11, US12, and UL14), and several others show strong selective constraint (UL15, VP26 (UL35), VP13-14 (UL47), RR2 (UL40), and ICP8 (UL29)). The Ω values reflect the overall AA sequence conservation values in Table 2.