



Figure S6: Clustering of fixations in the clonal interference model. Histograms of the number of yearly nucleotide fixation events (bars) obtained from the minimal evolution model in four simulation runs over 40 years (model parameters at the influenza calibration point). To be compared with Fig. 3(c). As in the actual process, these distributions deviate strongly from the Poisson form expected for independently evolving sites (dashed lines). The simulated distribution obtained from 10 runs has a ratio 5.0 ± 2.5 of variance and mean (error bars determined by sampling over a finite number of years). This value is compatible with the corresponding ratio 6.7 for the actual process, however, both ratios are much larger than the range 1 ± 0.25 for a finite sample of Poisson-distributed fixation numbers.