Figure S4: Neither diversity nor host-specific mutations increase over time

(a) For each human sample, the full genome nucleotide diversity ($\pi_N$ or $\pi_S$) is plotted vs. the days post-symptom onset. Dark red dots represent the mean, full-genome nonsynonymous diversity for a given sample ($\pi_N$), and light red dots represent the mean, full-genome synonymous diversity for that same sample ($\pi_S$). Neither nonsynonymous nor synonymous diversity are correlated with days post symptom onset (nonsynonymous: $r^2 = -0.17$, $p = 0.69$; synonymous: $r^2 = -0.22$, $p = -0.61$).

(b) To compare whether the number of putative host-adapting mutations increased over time in humans, we compared the number of host-specific and non-host specific mutations in humans sampled either in “early infection” (5-8 days post symptom onset), or in “late infection” (9-12 days post symptom onset). We divided the data into these categories by splitting on the mean days post symptom onset for human samples, which was 8 days. We then compared the proportion of host-specific variants during early and late infections with a Fisher’s exact test. The proportion of variants that are host-specific is not different in early vs. late infections ($p = 0.72$).