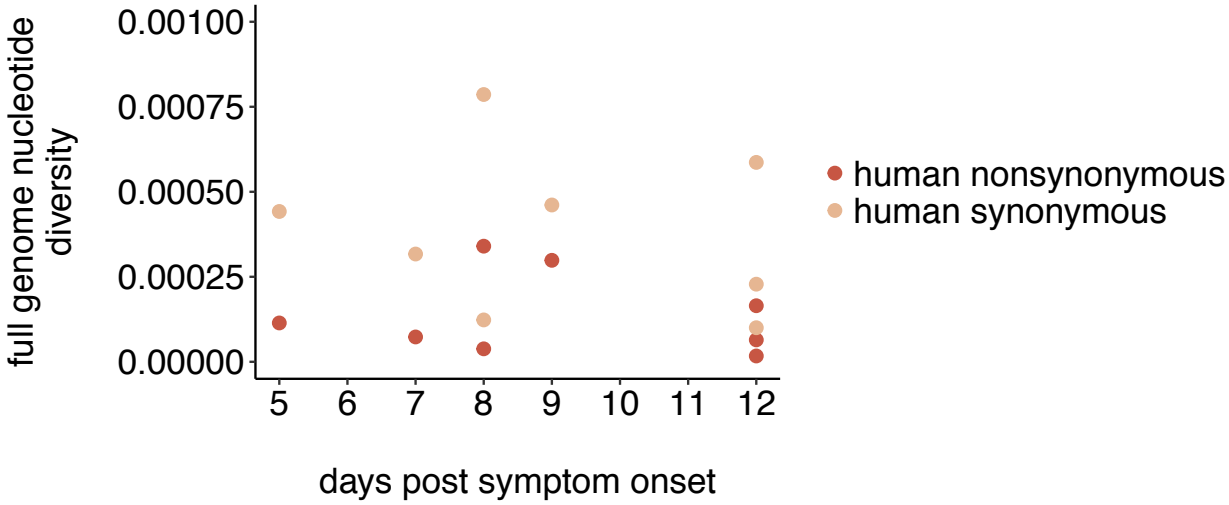
a



b

	"early infection" (5-8 days)	"late infection" (9-12 days)
host-specific mutations	18	22
non-host specific mutations	82	84

Figure S4: Neither diversity nor host-specific mutations increase over time
(a) For each human sample, the full genome nucleotide diversity (π_N or π_S) is plotted vs. the days post-symptom onset. Dark red dots represent the mean, full-genome nonsynonymous diversity for a given sample (π_N), and light red dots represent the mean, full-genome synonymous diversity for that same sample (π_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).