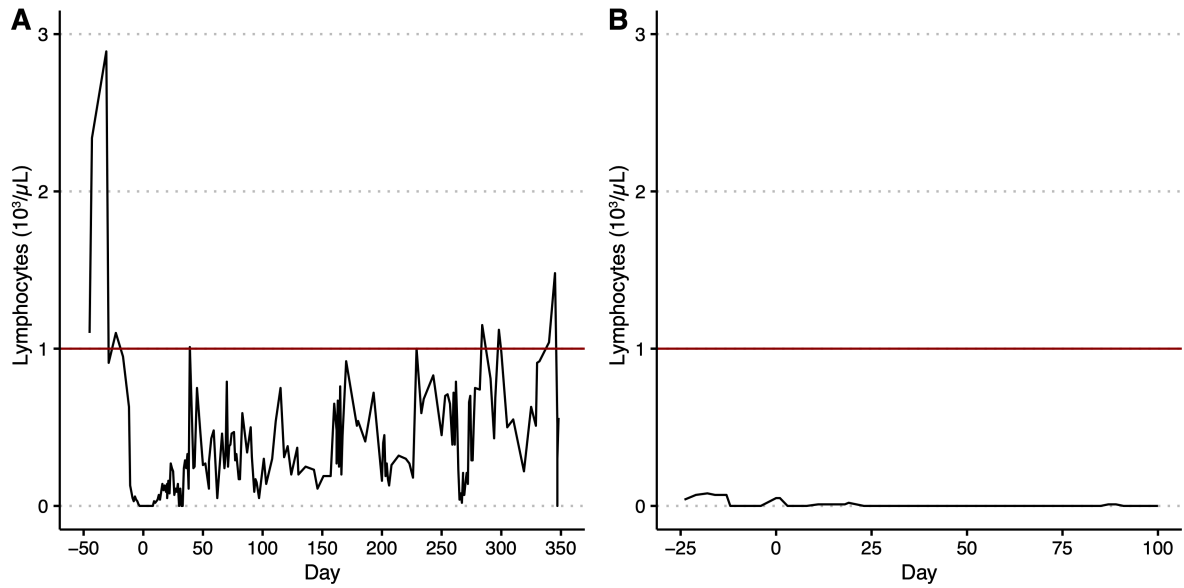


1 **Supplemental Figures and Legends**



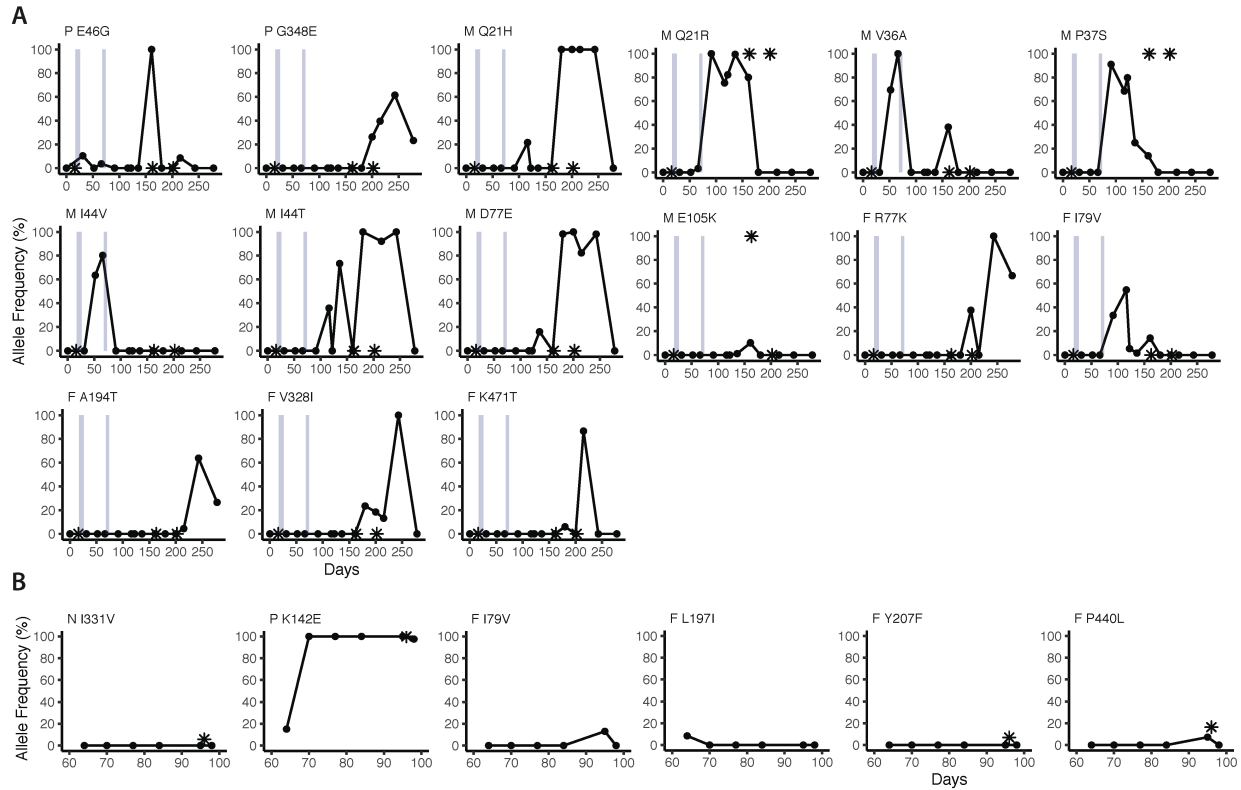
2

3 **Supplementary Figure 1** – Absolute lymphocyte counts for patient 1 (A) and patient 2 (B)

4 throughout the infection course described here. The red line indicates the lower end of the

5 reference range at 10³ cells/μL.

6



7

8 **Supplementary Figure 2 – Mutational changes and allele frequencies for N, P, M, and F**

9 proteins across long term persistent HPIV3 infection for patient 1 (A) and patient 2 (B). Protein

10 and mutational change are shown above each subplot. For patient 1, nonsynonymous variants

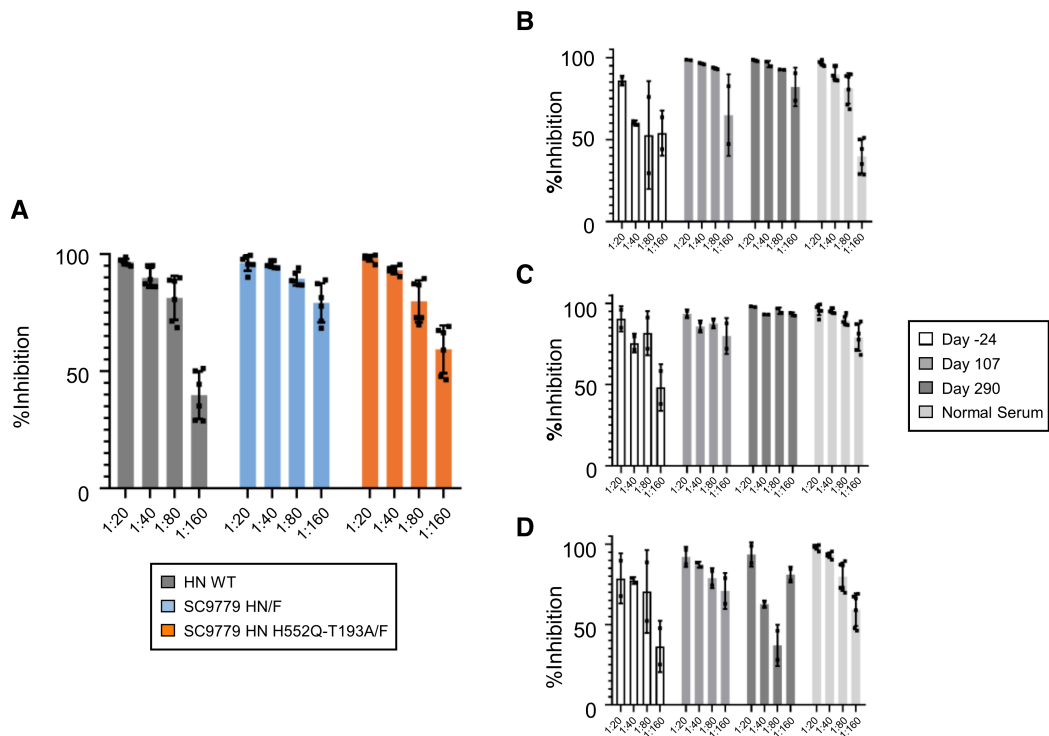
11 present in any sample at >50% allele frequency and filtered at >5 depth are shown. For patient 2,

12 nonsynonymous mutations present at >5% allele frequency and >5 depth are shown. Sample

13 collection dates are given relative to the first sample and plotted on the x-axis for each plot.

14 Samples collected by nasal swab are represented by dots, and BAL samples are marked with an
 15 asterisk.

16



17

18 **Supplementary Figure 3** – Neutralization titers of normal human serum vs standard HPIV3 CI
 19 virus (WT), the virus bearing the fusion complex isolated from patient 1 (SC 9779 HN/F), and
 20 the virus bearing the fusion complex isolated from patient 1 with HN H552Q-T193A (SC 9779
 21 HN H552Q-T193A/F), expressed as percent inhibition of viral entry (A). Neutralization titers of
 22 serial dilutions of patient 1 (SC 9779) sera from several time points during infection vs. standard
 23 HPIV3 CI virus (B), the virus bearing the fusion complex isolated from patient 1, (SC 9779
 24 HN/F)(C), and the virus bearing the fusion complex isolated from patient 1 with HN H552Q-
 25 T193A (SC 9779 HN H552Q-T193A/F) (D), expressed as percent inhibition of viral entry.