Figure S1. Phylogeny of 9544 SARS-CoV-2 genomes. Screenshot of the phylogeny used for the primary analyses in this manuscript. Tips and branches are colored according to emerging lineage. Emerging lineages are labeled by PANGO lineage and WHO Variant of Interest (VOI) or Variant of Concern (VOC) designation. An interactive version of this phylogeny can be accessed at nextstrain.org/groups/blab/ncov/adaptive-evolution/2021-05-15.
Figure S2. Deletions contribute to protein-coding changes in S1, N and Nsp6. For each gene nonsynonymous mutation accumulation is separated into nonsynonymous SNPs (left) and deletions (right). Accumulation of these mutations is plotted against logistic growth rate for 8 genes (or subunits), as in Figure 1B.
Figure S3. Visual Representation of Table 1. For every gene in the genome, the rate of nonsynonymous substitutions (and deletions) per codon per year is plotted against the correlation coefficient $r$ of mutation accumulation with logistic growth. Circles indicate genes with significant $r$ values at the $p=0.01$ level, and Xs indicate genes with insignificant $r$ values.
Figure S4. Correlation between nonsynonymous mutation accumulation and clade success is strongest in S1. Nonsynonymous mutation accumulation (mutations per codon) is plotted against logistic growth rate for 8 genes (or subunits), as in Figure 1B. Histograms beneath each plot show the empirical r-value (colored line) compared to the distribution of r-values from 1000 randomizations, as well as the p-value resulting from this comparison.
Figure S5. Ratio of nonsynonymous to synonymous divergence in influenza H3N2. The mean and 95% confidence intervals for nonsynonymous/synonymous divergence ratios in the H3N2 genes HA1 and PB1 are shown over a 12-year period.

Figure S6. Temporal accumulation of S1 mutations on representative paths through the tree. The total number of accumulated S1 nonsynonymous mutations is counted at every branch along a path through the tree. This is plotted for 10 representative paths from the root to an isolate in an emerging lineage clade. The isolate and emerging lineage are labeled on each panel.
Figure S7. Distribution of expected wait times is affected by the number of mutations that occur across the phylogeny. The phylogeny was randomized with varying numbers of mutations to display the expected wait time distributions if 50, 100, 200, 300, 400 or 500 mutations occur on internal branches of the phylogeny. Each randomization is run for 10 iterations. The empirical number of S1 nonsynonymous, S1 synonymous, and RdRp nonsynonymous mutations observed on internal branches of the phylogeny are indicated.

Figure S8. Every occurrence of the 3-amino acid deletion in Nsp6 resulted in an emerging lineage. Every occurrence of the convergently-evolved mutations is colored according to the emerging lineage it occurs at the base of. Multiple emerging lineages descending from the branch a mutation occurs on is represented by light purple.
Figure S9. Analyses of convergent evolution shown 1 month before and 1 month after the primary analysis. A) Same as Figure 4A, completed using sequences up to April 15, 2021 (1 month before the primary analysis). B) Same as Figure 4B, completed using sequences up to April 15, 2021. C) Same as Figure 4A, completed using sequences up to June 15, 2021 (1 month after the primary analysis). D) Same as Figure 4B, completed using sequences up to June 15, 2021.