

Figure S1. Mutation occurrences as a function of residue position from the uninduced (top) and induced (bottom) libraries. All mutations were summed and multiplied by their respective similarity matrix score. Note different scales in both graphs.

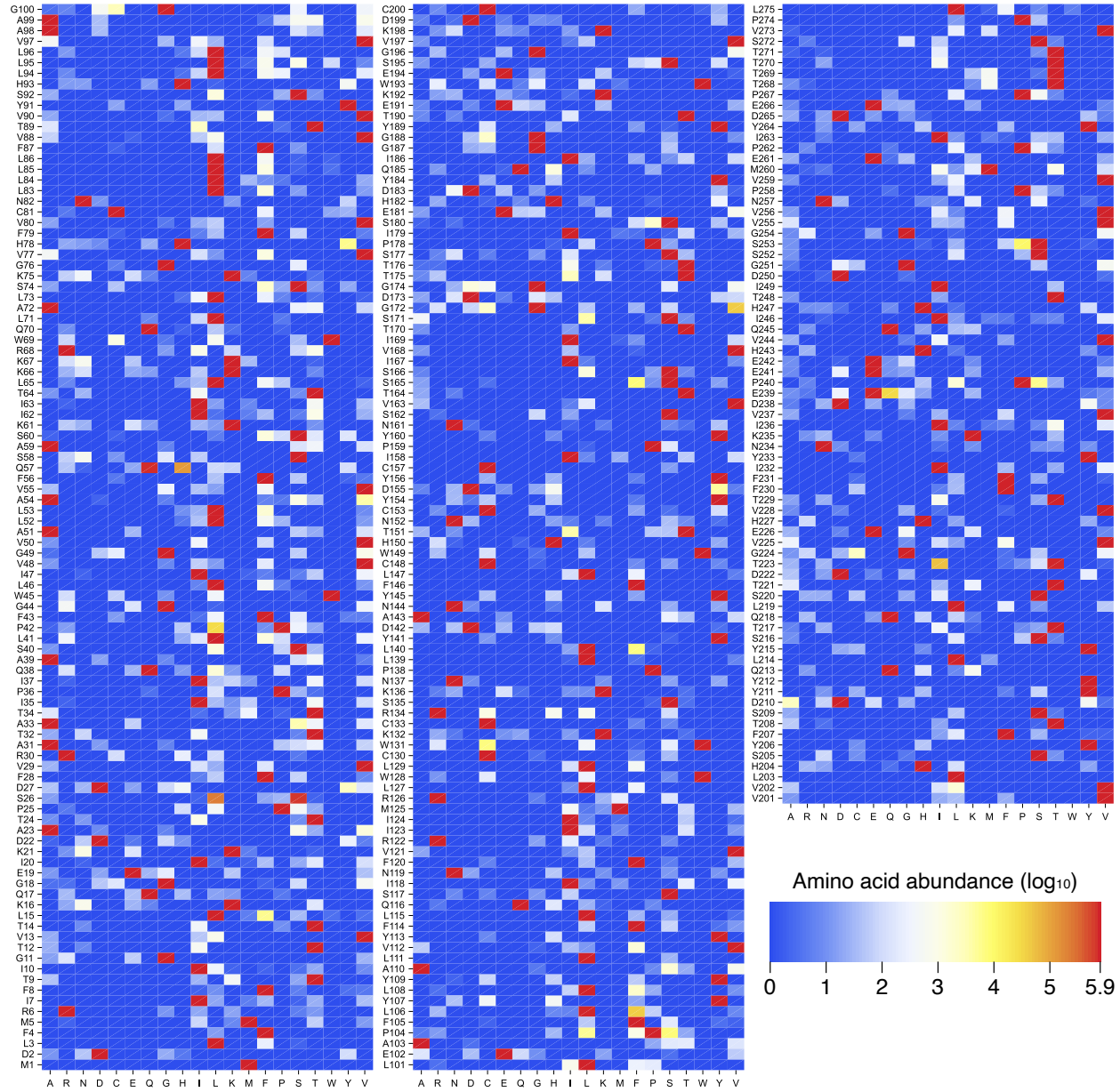


Figure S2. Mutations (relative to the P0DTC3 variant) found in 807,520 circulating variants of SARS-CoV-2 ORF3a.