

Supplemental information

Relative infectivity of the SARS-CoV-2

Omicron variant in human alveolar cells

Taewoo Kim, Kyoung Il Min, Jeong-Sun Yang, Jun Won Kim, Junhyung Cho, Yun Ho Kim, Jeong Seok Lee, Young Tae Kim, Kyung-Chang Kim, Jeong Yeon Kim, Kwon Joong Na, Joo-Yeon Lee, and Young Seok Ju

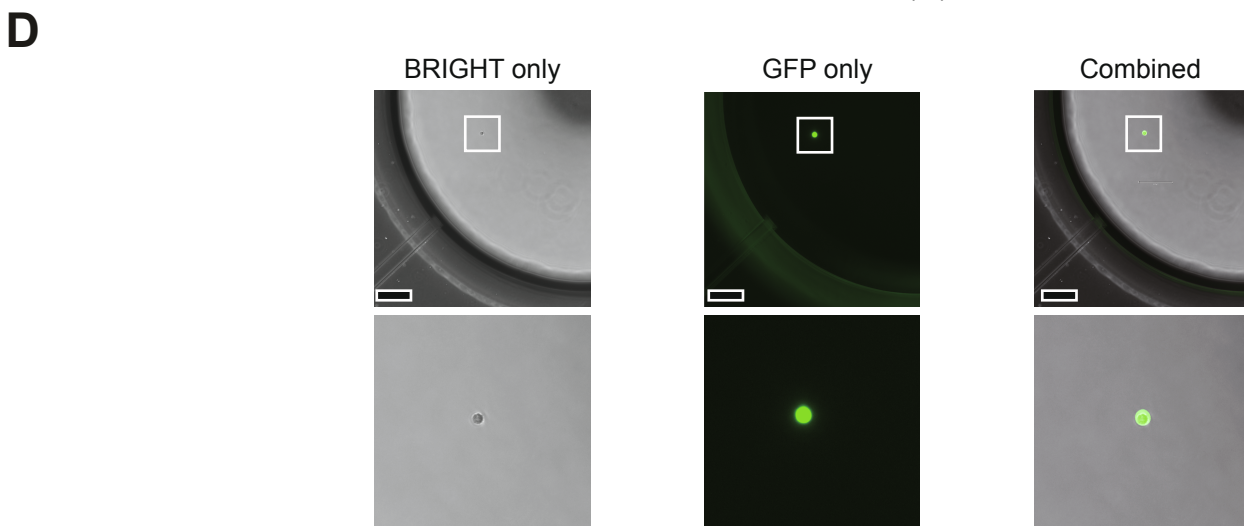
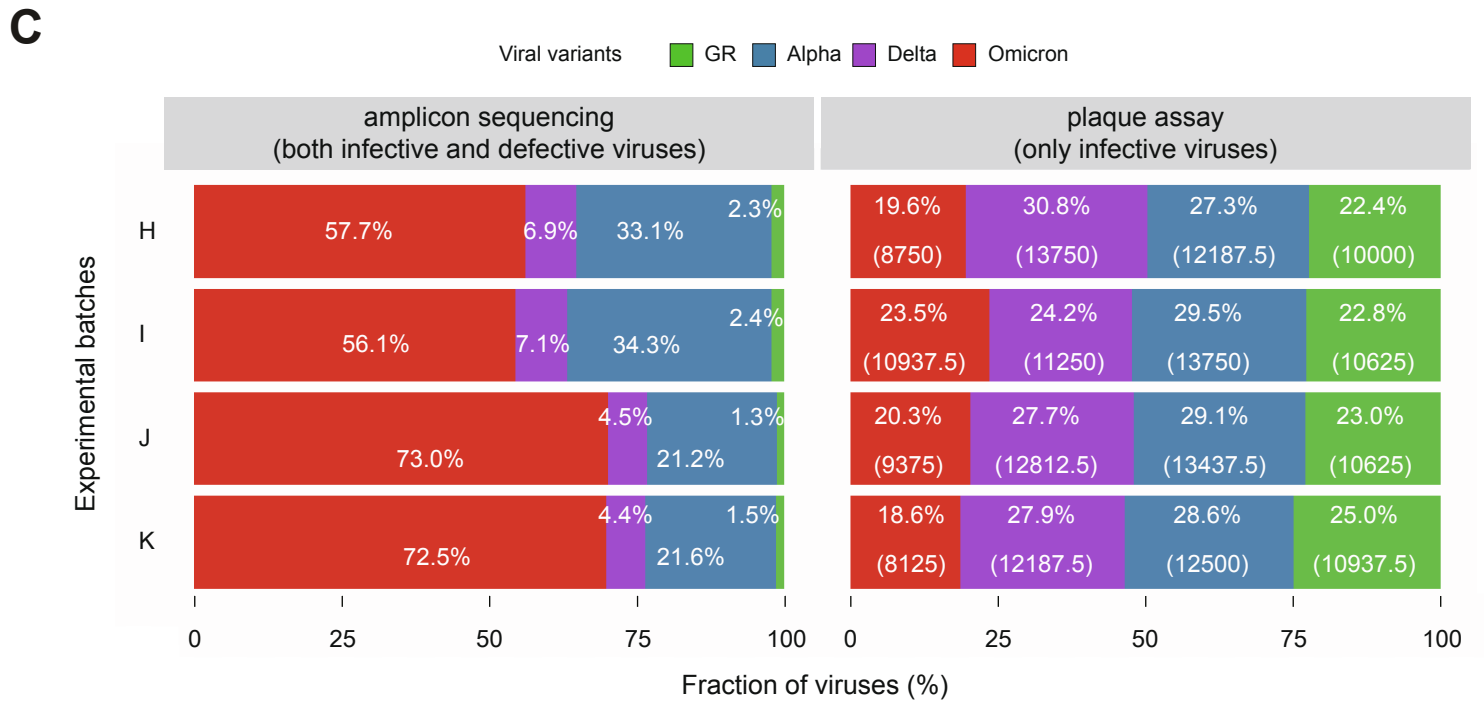
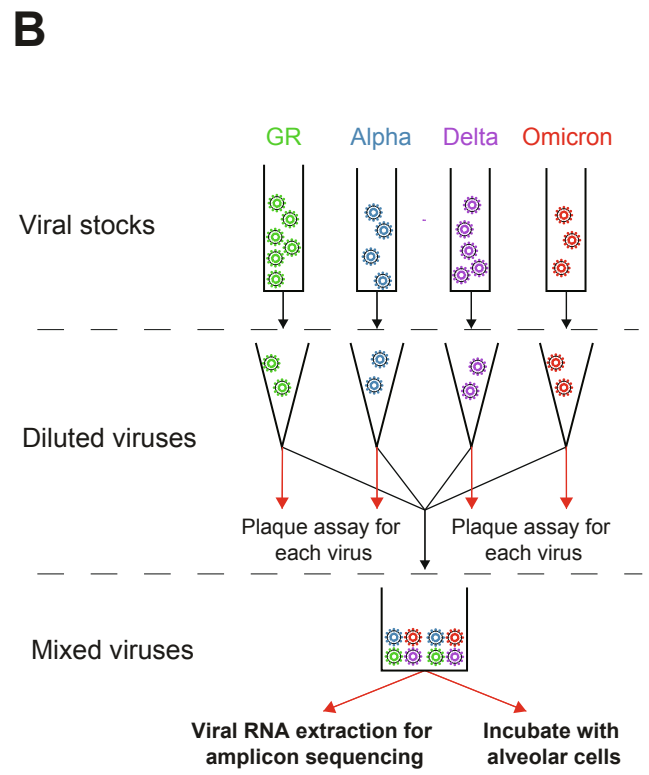
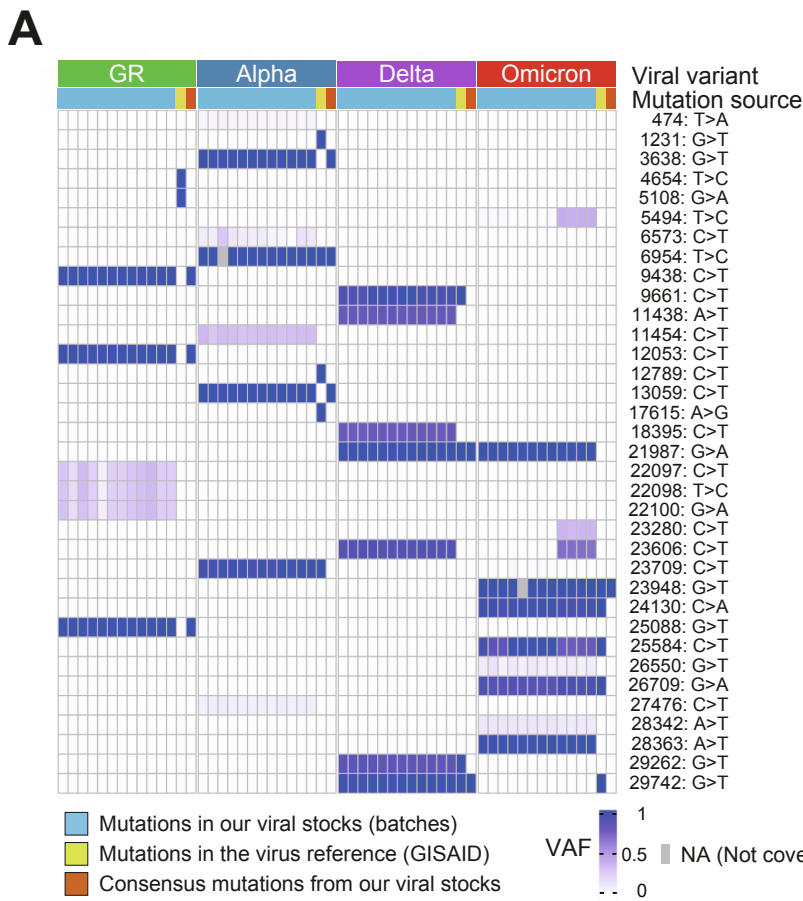


Figure S1. Detailed information of competition assay. Related to Figure 1.

(A) Mutations of each viral variant from different sources. Variant allele fraction (VAF) is filled in each block and the mutation position of the SARS-CoV-2 genome is written in a row. The order of viral stocks is the same as in Figure 2B.

(B) Schematic diagram of calculating the fraction of viral variants in the competition assay. Infective (viable) viruses were counted by plaque assay of each viral variant and both infectious and defective were by RNA sequencing of the viral mixture. The fraction is written in white with the number of PFU in parentheses.

(C) Fraction of viral variants by two different methods, including amplicon sequencing and plaque assay.

(D) Manual picking of single cells in the biosafety level 3 laboratory.