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Identification and Analysis of SARS-CoV-2 Mutations and Subtypes Using 2× Tiled Primer Sets with Oxford Nanopore Technologies Sequencing

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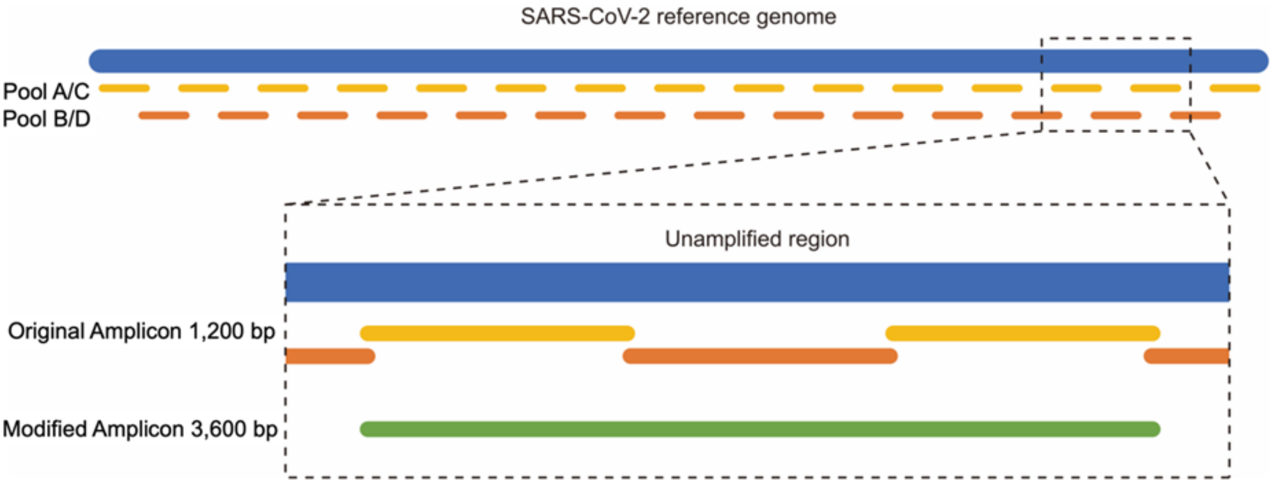

Figure S1: Modified amplicon design for covering large deletions.

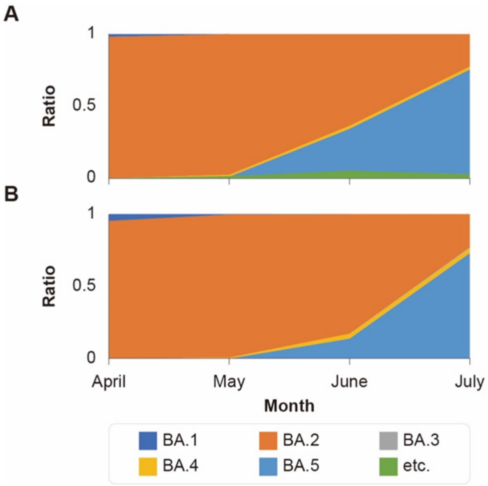

Figure S2: Monthly distribution of SARS-CoV-2 by subtypes in South Korea (April–July, 2022). (A) Distribution in patients at Saint Peter's Hospital. (B) Distribution from GISAID database. SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

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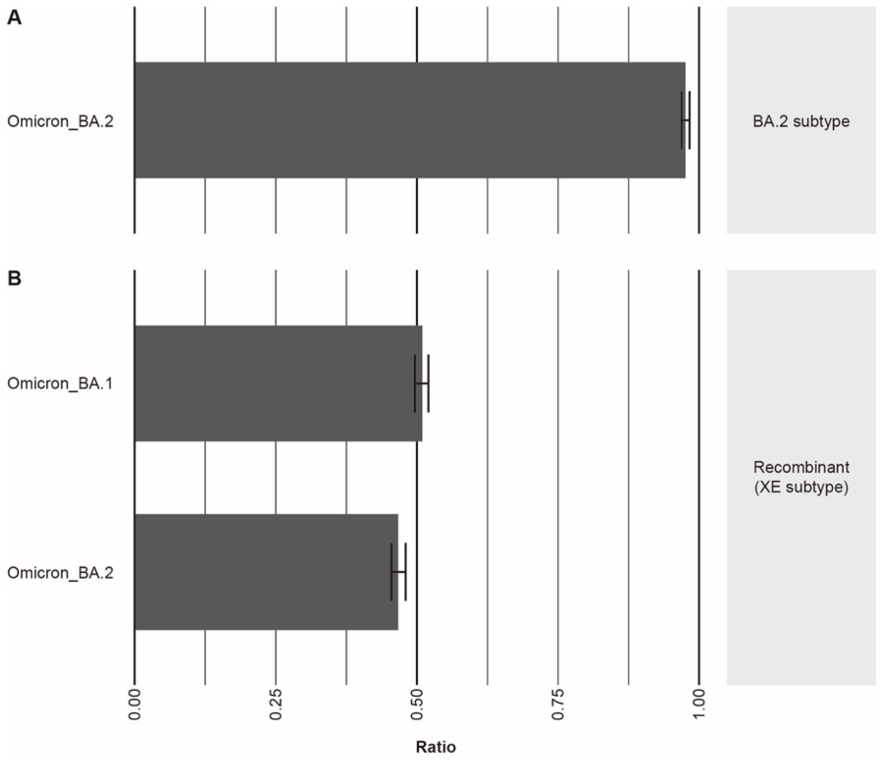

Figure S3: Identification of recombinant ratio by Lineage deComposition for SARS-CoV-2 analysis. BA.2 subtype samples matched with only one subtype (A) and recombinant sample showed a mixed ratio over two subtypes (B). SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

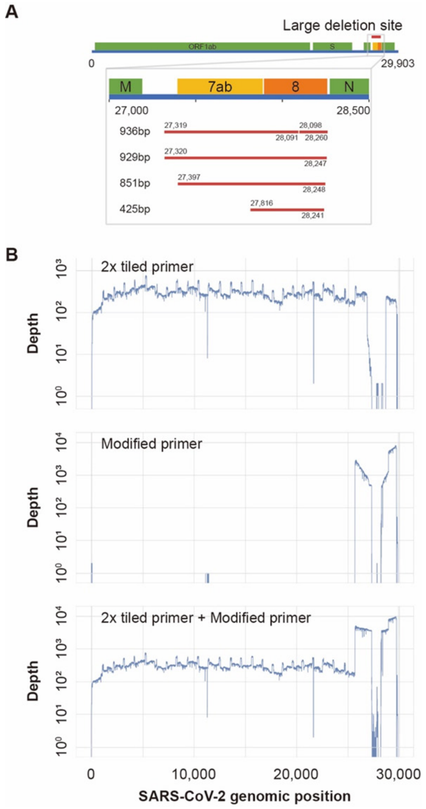

Figure S4: Large deletions in rare SARS-CoV-2 subtype and coverage differences among primer designs. Large deletions were covered with modified primers and found around ORF7a, ORF7b, and ORF8 (A). Covered region differed by primer design and concatenation of modified primer sequencing data, and 2× tiled primer sequencing data can cover samples with large deletions (B). SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

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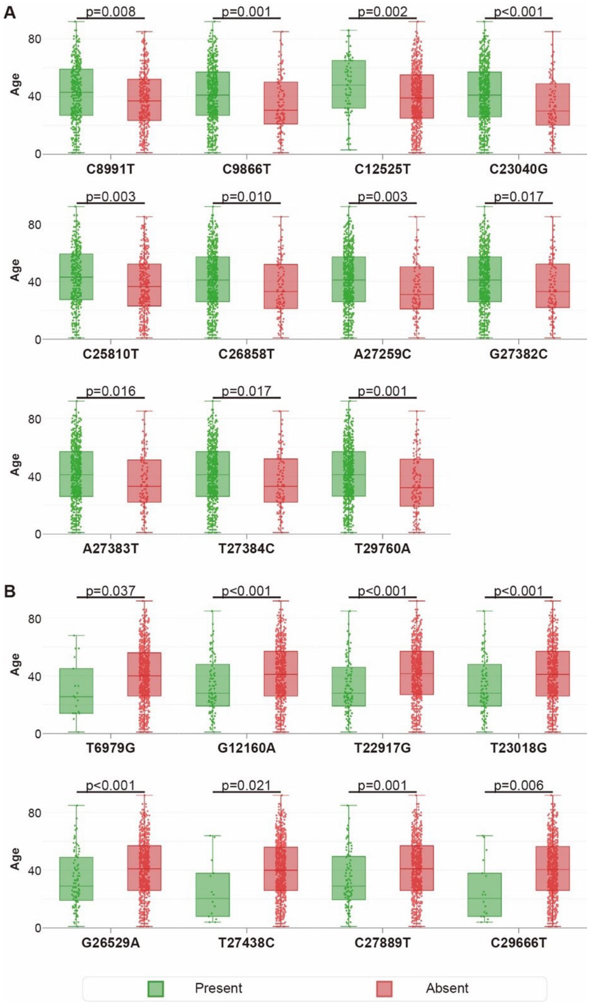

Figure S5: Patient age distribution by SNVs. Age distribution of each subtype-specific SNV also followed subtype age population pattern of BA.2 (A) and BA.5 (B) SNV, single-nucleotide variation.