|  |  |  |  |
| --- | --- | --- | --- |
| **ID (Date)*a*** | **Lineage or****Clade*b*** | **Amino acid variants*c*** | **SNPs*c*** |
|  |  | **Non-structural proteins** | **S** | **Orf3a** | **E** | **M** | **Orf7a** | **N** |  |
|  |  |  |  |  |  |  |  |  |  |
| **IMV1**(10/03) | B.2.2 / 19A | nsp1 (V111V/L)*d*nsp2 (H237R)**nsp2 (D582D/A)***d***nsp6 (L37F)** | G72R/G*d*D215D/G*d* | **G251V** |  |  |  |  | G596T, A1515G, A2550C, C9223T, C11074T, G11083T, C14805T, T17247C, G21776A, A22206G, G26144T |
| **IMV2**(09/03) | B.1 / 20C | **nsp2 (T85I)****nsp12 (P323L)** | **D614G** | **Q57H***e* |  |  |  |  | C1059T, C3037T, C14408T, A23403G, G25563T |
| **IMV3**(11/03) | B.2 / 19A | nsp2 (P624P/L)*d***nsp6 (L37F)** |  | **G251V** |  |  |  |  | C2676T, G11083T, C14805T, T17247C, C25626T, G26144T |
| **IMV4**(11/03) | B.1 / 20A | **nsp12 (P323L)** | **D614G** |  |  |  |  |  | C3037T, C14408T, C15324T, A23403G |
| **IMV5**(11/03) | B.1.1 / 20B | **nsp12 (P323L)** | **D614G** |  |  | **T175M** |  | **R203K****G204R** | C3037T, C14408T, A23403G, C27046T, G28881A, G28882A, G28883C |
| **IMV6**(29/03) | B.1.5 / 20A | **nsp3 (K1693N)****nsp12 (P323L)** | **D614G** |  | V5G/V*d* |  |  | **S194L***e* | C3037T, G7798T, C14408T, A20268G, A23403G, T26258G, C28854T |
| **IMV7**(29/03) | B.1 / 20A | nsp3 (H795H/Y)*d*nsp3 (S915N/S)*d*nsp12 (P323L) | D614G |  |  |  |  |  | C2638A, C3037T, C5102T, G5463A, C14408T, C15324T, C21691T, A23403G |
| **IMV8**(30/03) | B.1 / 20C | **nsp2 (T85I)****nsp12 (P323L)** | **S514F****D614G** | **Q57H***e* |  |  |  |  | C1059T, C3037T, C14408T, C23103T, A23403G, G25563T, C29535T |
| **IMV9**(07/04) | B.1 / 20C | **nsp2 (T85I)**nsp4 (N405K/N)*d*nsp12 (A97A/V)*d***nsp12 (P323L)****nsp12 (S647I)**nsp15 (S312T/S)*d*nsp15 (S315S/F)*d* | Q218K/Q*d***D614G** | **Q57H***e* |  |  |  |  | C1059T, C3037T, G7459A, T9769A, C13730T, C14408T, G15380T, T20554A, C20564T, C22214A, A23403G, G25563T |
| **IMV10**(14/04) | B.1.1 / 20B | **nsp4 (S336L)****nsp12 (P323L)** | **D614G** |  |  |  |  | **R203K****G204R****I292T** | C2462T, C3037T, C9561T, C14408T, T15837C, A23403G, G28881A, G28882A, G28883C, T29148C |
| **IMV11**(04/05) | B.1.5 / 20A | **nsp3 (T970M)****nsp12 (P323L)** | **E583D****D614G** |  |  |  |  | **S194L***e* | C3037T, C5628T, A9529T, C14408T, A20268G, G23311T, A23403G, C28854T |
| **IMV12**(04/05) | B.1.1 / 20B | **nsp12 (P323L)** | **D614G** |  |  |  |  | **R203K****G204R** | C3037T, T11449C, C14408T, A20979G, A23403G, G28881A, G28882A, G28883C |
| **IMV13**(04/05) | B.1 / 20A | **nsp6 (L37F)****nsp12 (P323L)** | **D614G** |  |  |  | **H47N** | R203K/R*d* | C3037T, G11083T, C14408T, C15324T, A23403G, C27532A, G28881A |
| **IMV14**(04/05) | B.1 / 20A | **nsp2 (I273L)**nsp3 (K1083K/R)*d***nsp8 (A3V)****nsp12 (P323L)**nsp16 (D108D/A)*d* | **D614G**Δ679-685*d* |  |  |  |  | **L139F** | C556T, A1622C, C3037T, A5967G, C12099T, C14408T, C15324T, A20981C, A23403G, G28690T |

**S2 Table. SARS-CoV-2 Sequence Variants Identified by NGS in Patient Material and Passage 2 of Virus Isolates.**

*a* SARS-CoV-2 identifier (ID; strain Switzerland/ZH-UZH-IMVxx/2020) and date of patient sample collection (dd/mm/2020).

*b* SARS-CoV-2 lineage as defined by Rambaut *et al.*, bioRxiv, 2020 and determined by CoV-GLUE (<http://cov-glue.cvr.gla.ac.uk>). SARS-CoV-2 clade as determined by Nextstrain (<https://clades.nextstrain.org/>).

*c* Difference from reference sequence (SARS-CoV-2/Wuhan-Hu-1; NC\_045512.2) as determined by CoV-GLUE (<http://cov-glue.cvr.gla.ac.uk>). Bold amino-acid variants indicate that the variant was also detected in the original patient material that was directly sequenced.

*d* Additional variant in population at ≥ 15% frequency.

*e* Substitutions at these positions may change putative uncharacterized ORFs in overlapping coding regions (Gordon *et al.*, Nature, 2020; Firth, J Gen Virol, 2020).