**Table S1: Primers used for mutagenesis and sequencing.**

|  |  |  |
| --- | --- | --- |
| **Mutation** | **Mutagenesis primers** | **Sequencing primers** |
| R346K | Fw: AATGCCACCA**a**ATTCGCCTCTGRev: GAACACCTCGCCGAAGGG | Fw: GTGGATTGTGCCCTTGATCCTC |
| K417N | Fw: AGACAGGCAA**c**ATCGCCGACTACRev: GTCCAGGGGCAATCTGCG | Fw: CAGCTTCAGCACCTTCAAG |
| K417T | Fw: CAGACAGGCA**c**GATCGCCGACRev: TCCAGGGGCAATCTGCCG | Fw: CAGCTTCAGCACCTTCAAG |
| L452Q | Fw: TACAATTACC**a**GTACCGGCTGTTCCRev: GTTGCCGCCGACTTTGGA | Fw: CAGCTTCAGCACCTTCAAG |
| L452R | Fw: TACAATTACC**g**GTACCGGCTGTTCRev: GTTGCCGCCGACTTTGGA | Fw: CAGCTTCAGCACCTTCAAG |
| T478K | Fw: GCCGGCAGCA**aa**CCTTGTAACGRev: CTGATAGATCTCGGTGGAG | Fw: CAGCTTCAGCACCTTCAAG |
| E484K | Fw: TAACGGCGTG**a**AAGGCTTCAACTGCTACRev: CAAGGGGTGCTGCCGGCC | Fw: CAGCTTCAGCACCTTCAAG |
| F490S | Fw: AACTGCTACT**c**CCCACTGCAGRev: GAAGCCTTCCACGCCGTT | Fw: CAGCTTCAGCACCTTCAAG |
| N501Y | Fw: TCAGCCCACA**t**ATGGCGTGGGRev: AAGCCGTAGGACTGCAGTG | Fw: CAGCTTCAGCACCTTCAAG |

**Table S2. Mutations in respective plasmids and corresponding SARS-CoV-2 variant.**

|  |  |  |  |
| --- | --- | --- | --- |
| **Plasmid** | **RBD mutations**  | **Non-RBD mutations** | **Corresponding SARS-CoV-2 variant(s)** |
| pCG1-SARS-S-del18 | - | 18aa deletion in c-terminal tail  | Wuhan-Hu-1 (Wt) |
| pCG1-SARS-S-del18\_N501Y | N501Y | 18aa deletion in c-terminal tail | B.1.1.7 (alpha) – RBD only |
| pCG1-SARS-S-del18\_K417N-E484K-N501Y | K417N, E484K, N501Y | 18aa deletion in c-terminal tail | B.1.351 (beta) – RBD only |
| pCG1-SARS-S-del18\_K417T-E484K-N501Y | K417N, E484K, N501Y | 18aa deletion in c-terminal tail | P.1 (gamma) – RBD only |
| pCG1-SARS-S-del18\_L452R-T478K | L452R, T478K | 18aa deletion in c-terminal tail | B.1.617.2 (delta) – RBD only |
| pCG1-SARS-S-del18\_L452Q-F490S | L452Q, F490S | 18aa deletion in c-terminal tail | C.37 (lambda) – RBD only |
| pCG1-SARS-S-del18\_R346K-E484K-N501Y | R346K, E484K, N501Y | 18aa deletion in c-terminal tail | B.1.621 (mu) – RBD only |
| pCDNA3.3\_CoV2\_D18 | - | 18aa deletion in c-terminal tail | Wuhan-Hu-1 (Wt) |
| pCDNA3.3\_CoV2\_B.1.1.7 | N501Y | 69-70del, 144del, A570D, D614G, P681H, T716I, S982A, D1118H, 18aa deletion in c-terminal tail | B.1.1.7 (alpha) |
| pCDNA3.3\_CoV2\_501V2 | K417N, E484K, N501Y | L18F, D80A, D215G, R246I, D614G, A7801V, 18aa deletion in c-terminal tail | B.1.351 (beta) |
| pCDNA3.3\_CoV2\_P1 | K417N, E484K, N501Y | L18F, T20N, P26S, D138Y, R190S, D614G, H655Y, T1027I, 18aa deletion in c-terminal tail | P.1 (gamma) |
| pCDNA3.3-SARS2-B.1.617.2 | L452R, T478K | T19R, 156G, 157-158del, D614G, P681R, D950N, 18aa deletion in c-terminal tail | B.1.617.2 (delta) |
| SARS-CoV-2 Omicron Strain S gene Human codon\_pcDNA3.1(+) | G339D, S371L, S373P, S375F, K417N, N440K, G446S, S477N, T478K, E484A, Q493R, G498R, N501Y, Y505H | A67V, 67-68del, T95I, G142D, 143-145del, N211I, 212del, ins215EPE, T547K, D614G, H655Y, N679K, P681H, N764K, D796Y, N856K, Q954H, N969K, L918F, 18aa deletion in c-terminal tail | B.1.1.529 (omicron) |

**Table S3. M- and N-gene-specific primers used for RT-qPCR.**

|  |  |
| --- | --- |
| **Primer** | **Sequence (5´- 3´)** |
| M-gene fwd  | tgtgacatcaaggacctgcc |
| M-gene rev  | ctgagtcacctgctacacgc |
| M-gene probe (PMID 32575728) | FAM-tgttgctacatcacgaacgc-BHQ1 |
| N-gene fwd (pWhSF-N-F9) | acattggcacccgcaatc |
| N-gene rev (pWhSF-N-R10) | cgagaagaggcttgactgcc |
| N-gene probe (pWhSF-N-P11lna) | FAM-cct+caaggaa+caa+catt-BHQ1 |

(+ = LNA (locked nucleic acid) modified)