# Table S1.  The N Gene primer sets

| Primer sets | Amplifcation Len | Sequence (5'-3') | | | Sequence (5'-3') | | | Sequence (5'-3') | | | Sequence (5'-3') | | | Sequence (5'-3') | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| # | B2-F2 | F3 | Len | Tm | F2 | Len | Tm | FL | Len | Tm | F1c | Len | Tm | B1c | Len | Tm |
| N1 | 242 | atcacattggcacccgcaatc | 21 | 63.6 | gctgcaatcgtgctacaacttc | 22 | 62.3 | cttttggcaatgttgttccttga | 23 | 60.1 | ctctgctcccttctgcgtaga | 21 | 63 | tgatgctgctcttgctttgctg | 22 | 63.9 |
| N1(-3) | 242 | | | | | | | | | | tgctcccttctgcgtaga | 18 | 59.7 | gctgctcttgctttgctg | 18 | 59.5 |
| N1(-6) | 242 | | | | | | | | | | tcccttctgcgtaga | 15 | 51.7 | gctcttgctttgctg | 15 | 51.9 |
| N1(-9) | 242 | | | | | | | | | | cttctgcgtaga | 12 | 39.4 | cttgctttgctg | 12 | 41.1 |
| N2 | 146 | gaattcgtggtggtgacggtaa | 22 | 62.5 | attcaaggctccctcagttgc | 21 | 62.4 | ccgtctttgttagcaccatagg | 22 | 60.7 | attcaaggctccctcagttgc | 21 | 62.4 | atcacattggcacccgcaatc | 21 | 63.6 |
| N2(-5) | 146 | | | | aggctccctcagttgc | 16 | 57.7 | | | | aggctccctcagttgc | 16 | 57.7 | attggcacccgcaatc | 16 | 57.1 |
| N3 | 149 | cccgcattacgtttggtggac | 21 | 63.8 | agaatggagaacgcagtggg | 20 | 61.9 | gccgacgttgttttgatcgc | 20 | 62.8 | cagtattattgggtaaacctt | 21 | 52.5 | atggcaaggaagacct | 16 | 53.6 |
| N3(-2) | 149 | | | | | | | | | | gtattattgggtaaacctt | 19 | 48.8 | ggcaaggaagacct | 14 | 49.8 |
| N3(-4) | 149 | | | | | | | | | | attattgggtaaacctt | 17 | 46 | caaggaagacct | 12 | 38.8 |
| N3(-6) | 149 | | | | | | | | | | tattgggtaaacctt | 15 | 42.8 | aggaagacct | 10 | 29.7 |
| N4 | 142 | taggaactgggccagaagctg | 21 | 63.6 | gtgctaacaaagacggcatcat | 22 | 61.2 | tattcaaggctccctcagttgc | 22 | 62 | ggtgccaatgtgatctt | 17 | 53.9 | ctgctaacaatgctgc | 16 | 52.4 |
| N4(-2) | 142 | | | | | | | | | | tgccaatgtgatctt | 15 | 47.9 | gctaacaatgctgc | 14 | 47.7 |
| N4(-4) | 142 | | | | | | | | | | ccaatgtgatctt | 13 | 38.8 | taacaatgctgc | 12 | 38.7 |
| N4(-6) | 142 | | | | | | | | | | aatgtgatctt | 11 | 27.5 | acaatgctgc | 10 | 34.7 |
| N5 | 163 | gtgctaacaaagacggcatcat | 22 | 61.2 | tgctaacaatgctgcaatcgtg | 22 | 62 | ttggcaatgttgttccttgagg | 22 | 61.3 | ctcccttctgcgtaga | 16 | 53.6 | acgtagtcgcaacag | 15 | 52.3 |
| N5(-2) | 163 | | | | | | | | | | cccttctgcgtaga | 14 | 49.3 | gtagtcgcaacag | 13 | 44.6 |
| N5(-4) | 163 | | | | | | | | | | cttctgcgtaga | 12 | 39.8 | agtcgcaacag | 11 | 39.8 |
| N5(-6) | 163 | | | | | | | | | | tctgcgtaga | 10 | 32.2 | tcgcaacag | 9 | 29.9 |
| N6 | 137 | aacaatgctgcaatcgtgctac | 22 | 62 | gtcaagcctcttctcgttcctc | 22 | 62.3 | ttgaactgttgcgactacgtga | 22 | 62.1 | ctgcctggagttgaat | 16 | 52.3 | cctgctagaatggctg | 16 | 53.1 |
| N6(-2) | 137 | | | | | | | | | | gcctggagttgaat | 14 | 47.3 | tgctagaatggctg | 14 | 47.1 |
| N6(-4) | 137 | | | | | | | | | | ctggagttgaat | 12 | 35.9 | ctagaatggctg | 12 | 37.3 |
| N6(-6) | 137 | | | | | | | | | | ggagttgaat | 10 | 25.8 | agaatggctg | 10 | 31 |
| N7 | 143 | taggaactgggccagaagctg | 21 | 63.6 | gtgctaacaaagacggcatcat | 22 | 61.2 | tattcaaggctccctcagttgc | 22 | 62 | tgccaatgtgatctt | 15 | 47.9 | aatcgtgctacaac | 14 | 45.2 |
| N8 | 154 | gcaactgagggagccttgaata | 22 | 62 | aacaatgctgcaatcgtgctac | 22 | 62 | ttggcaatgttgttccttgagg | 22 | 61.3 | tcccttctgcgta | 13 | 46.7 | gtcgcaacagttc | 13 | 45.9 |
| N9 | 119 | ttctacgcagaagggagcagag | 22 | 63.4 | aaattcaactccaggcagcagt | 22 | 62.4 | gccattctagcaggagaagttcc | 23 | 62.5 | catcaccgccatt | 13 | 47.2 | ttgctttgctgct | 13 | 47.2 |
| N10 | 140 | cctcagattcaactggcagtaac | 23 | 60.9 | taatactgcgtcttggttcacc | 22 | 60 | tccttgccatgttgagtgagag | 22 | 61.9 | gccttgtcctcga | 13 | 49 | caatagcagtccaga | 15 | 47.4 |
| N11 | 139 | taggaactgggccagaagctg | 21 | 63.6 | tgcaactgagggagccttgaat | 22 | 63.9 | gtgccaatgtgatcttttggtg | 22 | 60.3 | ttgttagcaggattg | 15 | 45.7 | caaggaacaacattg | 15 | 45.2 |
| N12 | 138 | taggaactgggccagaagctg | 21 | 63.6 | agggagccttgaatacaccaaa | 22 | 61.3 | gattgcgggtgccaatgtgat | 21 | 63.6 | gcacgattgcag | 12 | 45.1 | acaacattgccaaa | 14 | 45.2 |
| N13 | 144 | cttccctatggtgctaacaaagac | 24 | 60.8 | cccgcaatcctgctaacaatg | 21 | 61.6 | cttgaggaagttgtagcacgat | 22 | 60 | ccttttggcaatgtt | 15 | 47.6 | agtcaagcctcttc | 14 | 46.4 |
| N14 | 158 | ggtgctaacaaagacggcatca | 22 | 63.1 | ctgctaacaatgctgcaatcgt | 22 | 61.8 | ttggcaatgttgttccttgagg | 22 | 61.3 | ccttctgcgtagaa | 14 | 46.7 | tcatcacgtagtcg | 14 | 46.7 |
| N15 | 158 | gcaactgagggagccttgaata | 22 | 62 | acaatgctgcaatcgtgctaca | 22 | 63.1 | ttggcaatgttgttccttgagg | 22 | 61.3 | ccttctgcgtagaa | 14 | 46.7 | acgtagtcgcaac | 13 | 47.1 |
| N16 | 126 | tgcaactgagggagccttgaat | 22 | 63.9 | tgctgcaatcgtgctacaactt | 22 | 63 | ttttggcaatgttgttccttgag | 23 | 60.1 | ccttctgcgtagaa | 14 | 46.7 | agtcaagcctcttc | 14 | 46.4 |
| N17 | 138 | gggagccttgaatacaccaaaa | 22 | 60.5 | cctcaaggaacaacattgccaa | 22 | 61.3 | cctctgctcccttctgcgtag | 21 | 64 | aacgagaagaggc | 13 | 45.7 | tcgcaacagttca | 13 | 45.9 |
| N18 | 159 | taacaatgctgcaatcgtgcta | 22 | 60.6 | cagtcaagcctcttctcgttcc | 22 | 62.6 | gaactgttgcgactacgtgatg | 22 | 61.5 | gcctggagttgaat | 14 | 47.3 | ctgctcttgctttg | 14 | 47 |
| N19 | 163 | aacaatgctgcaatcgtgctac | 22 | 62 | gtcaagcctcttctcgttcctc | 22 | 62.3 | ttgaactgttgcgactacgtga | 22 | 62.1 | gcctggagttgaat | 14 | 47.3 | ctgctcttgctttg | 14 | 47 |
| N20 | 145 | cctcaaggaacaacattgccaa | 22 | 61.3 | tctcgttcctcatcacgtagtc | 22 | 60.9 | tgcctggagttgaatttcttgaa | 23 | 60.4 | caggagaagttccc | 14 | 47 | tgatgctgctcttg | 14 | 48 |
| N21 | 143 | ctcaaggaacaacattgccaaaa | 23 | 60.1 | cctcatcacgtagtcgcaacag | 22 | 62.9 | gctgcctggagttgaatttctt | 22 | 61.1 | ctagcaggagaagt | 14 | 45.1 | ctgctcttgctttg | 14 | 47 |
| N22 | 119 | ttctacgcagaagggagcagag | 22 | 63.4 | aattcaactccaggcagcagta | 22 | 61.6 | gccattctagcaggagaagttcc | 23 | 62.5 | catcaccgccat | 12 | 45.2 | ttgctttgctgct | 13 | 47.2 |
| N23 | 149 | ttctacgcagaagggagcagag | 22 | 63.4 | tcaactccaggcagcagtagg | 21 | 63.5 | gccattctagcaggagaagttc | 22 | 60.4 | tcaccgccattg | 12 | 45.7 | gcaaaatgtctggt | 14 | 45.6 |
| N24 | 146 | ttctacgcagaagggagcagag | 22 | 63.4 | caactccaggcagcagtagg | 20 | 62.2 | gccattctagcaggagaagttc | 22 | 60.4 | catcaccgccatt | 13 | 47.2 | gcaaaatgtctggt | 14 | 45.6 |
| N25 | 122 | cagtcaagcctcttctcgttcc | 22 | 62.6 | cctgctagaatggctggcaatg | 22 | 63.6 | caaagcaagagcagcatcacc | 21 | 62.1 | tcaatctgtcaagca | 15 | 47.5 | atgtctggtaaaggc | 15 | 48.1 |
| N26 | 142 | ccgcattacgtttggtggacc | 21 | 63.8 | agaatggagaacgcagtggg | 20 | 61.9 | gccgacgttgttttgatcgc | 20 | 62.8 | attattgggtaaacctt | 17 | 46 | ggcaaggaagacc | 13 | 47.1 |
| N27 | 143 | ccctcagattcaactggcagta | 22 | 61.4 | gggcgcgatcaaaacaacg | 19 | 62.7 | gacgcagtattattgggtaaacc | 24 | 60.4 | gagagcggtgaac | 13 | 47.6 | tcgaggacaaggc | 13 | 49 |
| N28 | 125 | ccgcattacgtttggtggacc | 21 | 63.8 | cagaatggagaacgcagtggg | 21 | 63 | gccgacgttgttttgatcgc | 20 | 62.8 | gcagtattattgggta | 16 | 45.4 | ttcaccgctctca | 13 | 47.7 |

| Primer sets | Sequence (5'-3') | | | Sequence (5'-3') | | | Sequence (5'-3') | | | Sequence (5'-3') | | Sequence (5'-3') | | PubMed |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| # | BL | Len | Tm | B2 | Len | Tm | B3 | Len | Tm | FIP(F1c+F2) | Len | BIP(B1c+B2) | Len | Accession |
| N1 | tgaaccagcttgagagcaaaat | 22 | 60.4 | ttgttgttgttggcctttacca | 22 | 60.8 | acattgtatgctttagtggcagt | 24 | 60 | ctctgctcccttctgcgtagatcggctgcaatcgtgctacaactt | 46 | tgatgctgctcttgctttgctggacttgttgttgttggcctttta | 47 | NC_045512 |
| N1(-3) | | | | | | | | | | tgctcccttctgcgtagatcggctgcaatcgtgctacaacttc | 43 | gctgctcttgctttgctggacttgttgttgttggcctttacca | 43 | NC_045512 |
| N1(-6) | | | | | | | | | | tcccttctgcgtagatcggctgcaatcgtgctacaacttc | 40 | gctcttgctttgctggacttgttgttgttggcctttacca | 40 | NC_045512 |
| N1(-9) | | | | | | | | | | cttctgcgtagatcggctgcaatcgtgctacaacttc | 37 | cttgctttgctggacttgttgttgttggcctttacca | 37 | NC_045512 |
| N2 | gcaatcgtgctacaacttcctc | 22 | 61.5 | atcacattggcacccgcaatc | 21 | 63.6 | aactgttgcgactacgtgatga | 22 | 61.9 | attcaaggctccctcagttgcactgggccagaagctggactt | 42 | atcacattggcacccgcaatcagccttttggcaatgttgttcc | 43 | NC_045512 |
| N2(-5) | | | | attggcacccgcaatc | 16 | 57.1 | | | | aggctccctcagttgcactgggccagaagctggactt | | attggcacccgcaatcagccttttggcaatgttgttcc | 38 | NC_045512 |
| N3 | aggacaaggcgttccaattaac | 22 | 60.8 | caatttggtcatctggactgct | 22 | 60.6 | ttttaccgtcaccaccacgaat | 22 | 62.1 | cagtattattgggtaaaccttagaatggagaacgcagtggg | 41 | atggcaaggaagacctcaatttggtcatctggactgct | 38 | NC_045512 |
| N3(-2) | | | | | | | | | | gtattattgggtaaaccttagaatggagaacgcagtggg | 39 | ggcaaggaagacctcaatttggtcatctggactgct | 36 | NC_045512 |
| N3(-4) | | | | | | | | | | attattgggtaaaccttagaatggagaacgcagtggg | 37 | caaggaagacctcaatttggtcatctggactgct | 34 | NC_045512 |
| N3(-6) | | | | | | | | | | tattgggtaaaccttagaatggagaacgcagtggg | 35 | aggaagacctcaatttggtcatctggactgct | 32 | NC_045512 |
| N4 | tcaaggaacaacattgccaaaag | 23 | 60.1 | cctctgctcccttctgcgtag | 21 | 64 | aggaacgagaagaggcttgact | 22 | 62.8 | ggtgccaatgtgatcttgtgctaacaaagacggcatcat | 39 | ctgctaacaatgctgccctctgctcccttctgcgtag | 37 | NC_045512 |
| N4(-2) | | | | | | | | | | tgccaatgtgatcttgtgctaacaaagacggcatcat | 37 | gctaacaatgctgccctctgctcccttctgcgtag | 35 | NC_045512 |
| N4(-4) | | | | | | | | | | ccaatgtgatcttgtgctaacaaagacggcatcat | 35 | taacaatgctgccctctgctcccttctgcgtag | 33 | NC_045512 |
| N4(-6) | | | | | | | | | | aatgtgatcttgtgctaacaaagacggcatcat | 33 | acaatgctgccctctgctcccttctgcgtag | 31 | NC_045512 |
| N5 | aactccaggcagcagtaggg | 20 | 63.4 | gccagccattctagcaggaga | 21 | 63.7 | aagctggttcaatctgtcaagc | 22 | 61.1 | ctcccttctgcgtagatgctaacaatgctgcaatcgtg | 38 | acgtagtcgcaacaggccagccattctagcaggaga | 36 | NC_045512 |
| N5(-2) | | | | | | | | | | cccttctgcgtagatgctaacaatgctgcaatcgtg | 36 | gtagtcgcaacaggccagccattctagcaggaga | 34 | NC_045512 |
| N5(-4) | | | | | | | | | | cttctgcgtagatgctaacaatgctgcaatcgtg | 34 | agtcgcaacaggccagccattctagcaggaga | 32 | NC_045512 |
| N5(-6) | | | | | | | | | | tctgcgtagatgctaacaatgctgcaatcgtg | 32 | tcgcaacaggccagccattctagcaggaga | 30 | NC_045512 |
| N6 | atgctgctcttgctttgctg | 20 | 61.6 | tgctctcaagctggttcaatct | 22 | 61.6 | gtttggccttgttgttgttggc | 22 | 63.4 | ctgcctggagttgaatgtcaagcctcttctcgttcctc | 38 | cctgctagaatggctgtgctctcaagctggttcaatct | 38 | NC_045512 |
| N6(-2) | | | | | | | | | | gcctggagttgaatgtcaagcctcttctcgttcctc | 36 | tgctagaatggctgtgctctcaagctggttcaatct | 36 | NC_045512 |
| N6(-4) | | | | | | | | | | ctggagttgaatgtcaagcctcttctcgttcctc | 35 | ctagaatggctgtgctctcaagctggttcaatct | 35 | NC_045512 |
| N6(-6) | | | | | | | | | | ggagttgaatgtcaagcctcttctcgttcctc | 33 | agaatggctgtgctctcaagctggttcaatct | 33 | NC_045512 |
| N7 | tcaaggaacaacattgccaaaag | 23 | 60.1 | cctctgctcccttctgcgta | 20 | 63.2 | gaggaacgagaagaggcttgac | 22 | 62.3 | tgccaatgtgatcttgtgctaacaaagacggcatcat | 37 | aatcgtgctacaaccctctgctcccttctgcgta | 34 | NC_045512 |
| N8 | aattcaactccaggcagcagta | 22 | 61.6 | gccattctagcaggagaagttc | 22 | 60.4 | aagctggttcaatctgtcaagc | 22 | 61.1 | tcccttctgcgtaaacaatgctgcaatcgtgctac | 35 | gtcgcaacagttcgccattctagcaggagaagttc | 35 | NC_045512 |
| N9 | gacagattgaaccagcttgaga | 22 | 60 | tgttgttgttggcctttaccag | 22 | 61.2 | gtatgctttagtggcagtacgtt | 23 | 60.6 | catcaccgccattaaattcaactccaggcagcagt | 35 | ttgctttgctgcttgttgttgttggcctttaccag | 35 | NC_045512 |
| N10 | ctaccgaagagctaccagacga | 22 | 62.6 | attttaccgtcaccaccacgaa | 22 | 62.1 | cagcttctggcccagttccta | 21 | 63.6 | gccttgtcctcgataatactgcgtcttggttcacc | 35 | caatagcagtccagaattttaccgtcaccaccacgaa | 37 | NC_045512 |
| N11 | acgcagaagggagcagagg | 19 | 63.6 | aggaacgagaagaggcttgact | 22 | 62.8 | ttcttgaactgttgcgactacg | 22 | 60.8 | ttgttagcaggattgtgcaactgagggagccttgaat | 37 | caaggaacaacattgaggaacgagaagaggcttgact | 37 | NC_045512 |
| N12 | acgcagaagggagcagagg | 19 | 63.6 | cgtgatgaggaacgagaagagg | 22 | 62.1 | gctgcctggagttgaatttcttg | 23 | 62.2 | gcacgattgcagagggagccttgaatacaccaaa | 34 | acaacattgccaaacgtgatgaggaacgagaagagg | 36 | NC_045512 |
| N13 | catcacgtagtcgcaacagttc | 22 | 61.5 | ctactgctgcctggagttgaat | 22 | 62 | aagctggttcaatctgtcaagc | 22 | 61.1 | ccttttggcaatgttcccgcaatcctgctaacaatg | 36 | agtcaagcctcttcctactgctgcctggagttgaat | 36 | NC_045512 |
| N14 | aattcaactccaggcagcagta | 22 | 61.6 | gccattctagcaggagaagttcc | 23 | 62.5 | aagctggttcaatctgtcaagc | 22 | 61.1 | ccttctgcgtagaactgctaacaatgctgcaatcgt | 36 | tcatcacgtagtcggccattctagcaggagaagttcc | 37 | NC_045512 |
| N15 | caactccaggcagcagtagg | 20 | 62.2 | gccagccattctagcaggaga | 21 | 63.7 | gttggcctttaccagacattttg | 23 | 60.2 | ccttctgcgtagaaacaatgctgcaatcgtgctaca | 36 | acgtagtcgcaacgccagccattctagcaggaga | 34 | NC_045512 |
| N16 | catcacgtagtcgcaacagttc | 22 | 61.5 | cctactgctgcctggagttgaa | 22 | 63.9 | cagcaaagcaagagcagcat | 20 | 61.6 | ccttctgcgtagaatgctgcaatcgtgctacaactt | 36 | agtcaagcctcttccctactgctgcctggagttgaa | 36 | NC_045512 |
| N17 | aattcaactccaggcagcagta | 22 | 61.6 | gccattgccagccattctagc | 21 | 64 | aagctggttcaatctgtcaagc | 22 | 61.1 | aacgagaagaggccctcaaggaacaacattgccaa | 35 | tcgcaacagttcagccattgccagccattctagc | 34 | NC_045512 |
| N18 | ttgacagattgaaccagcttgag | 23 | 60.7 | gttggcctttaccagacattttg | 23 | 60.2 | cagcagcagatttcttagtgaca | 23 | 60.5 | gcctggagttgaatcagtcaagcctcttctcgttcc | 36 | ctgctcttgctttggttggcctttaccagacattttg | 37 | NC_045512 |
| N19 | ttgacagattgaaccagcttgag | 23 | 60.7 | ttgttgttggcctttaccagac | 22 | 61 | atgctttagtggcagtacgttt | 22 | 60.2 | gcctggagttgaatgtcaagcctcttctcgttcctc | 36 | ctgctcttgctttgttgttgttggcctttaccagac | 36 | NC_045512 |
| N20 | gcttgacagattgaaccagctt | 22 | 61.1 | tggcctttaccagacattttgc | 22 | 61.3 | gcagcagatttcttagtgacagt | 24 | 61 | caggagaagttccctctcgttcctcatcacgtagtc | 36 | tgatgctgctcttgtggcctttaccagacattttgc | 36 | NC_045512 |
| N21 | gcttgacagattgaaccagctt | 22 | 61.1 | gttgttggcctttaccagacat | 22 | 60.8 | atgctttagtggcagtacgttt | 22 | 60.2 | ctagcaggagaagtcctcatcacgtagtcgcaacag | 36 | ctgctcttgctttggttgttggcctttaccagacat | 36 | NC_045512 |
| N22 | gacagattgaaccagcttgaga | 22 | 60 | ttgttgttgttggcctttacca | 22 | 60.8 | gtatgctttagtggcagtacgtt | 23 | 60.6 | catcaccgccataattcaactccaggcagcagta | 34 | ttgctttgctgctttgttgttgttggcctttacca | 35 | NC_045512 |
| N23 | gccaacaacaacaaggccaaac | 22 | 63.4 | cctcagcagcagatttcttagtg | 23 | 60.9 | gtatgctttagtggcagtacgtt | 23 | 60.6 | tcaccgccattgtcaactccaggcagcagtagg | 33 | gcaaaatgtctggtcctcagcagcagatttcttagtg | 37 | NC_045512 |
| N24 | gccaacaacaacaaggccaaac | 22 | 63.4 | tcagcagcagatttcttagtgac | 23 | 60.3 | gtatgctttagtggcagtacgtt | 23 | 60.6 | catcaccgccattcaactccaggcagcagtagg | 33 | gcaaaatgtctggttcagcagcagatttcttagtgac | 37 | NC_045512 |
| N25 | caacaacaaggccaaactgtca | 22 | 61.7 | agcctcagcagcagatttctta | 22 | 61.4 | ggaccacgtctgccgaaag | 19 | 62.9 | tcaatctgtcaagcacctgctagaatggctggcaatg | 37 | atgtctggtaaaggcagcctcagcagcagatttctta | 37 | NC_045512 |
| N26 | cgaggacaaggcgttccaatta | 22 | 62.6 | gtcatctggactgctattggtg | 22 | 60.4 | ttcgtctggtagctcttcggta | 22 | 62.3 | attattgggtaaaccttagaatggagaacgcagtggg | 37 | ggcaaggaagaccgtcatctggactgctattggtg | 35 | NC_045512 |
| N27 | ccaattaacaccaatagcagtcca | 24 | 60.8 | ttcggtagtagccaatttggtc | 22 | 60 | ttcattttaccgtcaccaccac | 22 | 60.8 | gagagcggtgaacgggcgcgatcaaaacaacg | 32 | tcgaggacaaggcttcggtagtagccaatttggtc | 35 | NC_045512 |
| N28 | gcaaggaagaccttaaattccct | 23 | 60.2 | ggtgttaattggaacgccttgt | 22 | 61.3 | gtctggtagctcttcggtagta | 22 | 60.1 | gcagtattattgggtacagaatggagaacgcagtggg | 37 | ttcaccgctctcaggtgttaattggaacgccttgt | 35 | NC_045512 |

**Note: Each primer set is composed of eight oligos, in which FIP is made by F1c+F2, and BIP is made by B1c+B2. Len, Length.**

# Table S2. N6 assay false-positive product sequencing

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| **Primers to establish library** | **Forward** | AATGATACGGCGACCACCGAGATCTACAC TGCACGGTAACACTCTTTCCCTACACGACGCTCTTCCGATCTGTCAAGCCTCTTCTCGTTCCTC | | index in red | | | underscore incates the F2 of N6 |
| | **Reverse** | CAAGCAGAAGACGGCATACGAGATTGCACGGTAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATGCTCTCAAGCTGGTTCAATCT | | index in red | | | underscore incates the B2 of N6 |
| **Sequencing results** | | **Top 10 reads** | | | | | |
| | | GTCAATCCTCTTCTCGTTCCTCCTGCTAGATTGAACCAGCTTGAGAGCA | | 2120402 | 35.36% | | |
| | | GTCAATCCTCTTCTCGTTCCTCCTGCTAGATTGAACCAGCTTGAGAGCAA | | 66114 | 1.10% | 36.46% | |
| | | | | | | | |
| | | GTCAATCCTCTTCTCGTTCCTCCTGCTAGATTGAACCAGCTTGAGAGCAAAGCCATTCAAGCAGGGCTGCCTGGAGTTGAATGTCAAGCCTCTTCTCGTTCCTCCTGCTAGATTTAACCACCTTGAGCGCA | | 1432573 | 23.89% | 23.89% | |
| | | | | | | | |
| | | GTCAATCCTCTTCTCGTTCCTCCTGCTAGATTGAACCAGCTTGAGAGCAAAGCCATTCAAGCAGGGCTGCCTGGAGTTGAATGTCAAGCCTCTTCTCGTTCCTCCTGCTAGATTTAACCACCTTGAGCGCACCGCCAGTCAAGCAGGGATC | | 917862 | 15.31% | | |
| | | GTCAATCCTCTTCTCGTTCCTCCTGCTAGATTGAACCAGCTTGAGAGCAAAGCCATTCAAGCAGGGCTGCCTGGAGTTGAATGTCAAGCCTCTTCTCGTTCCTCCTGCTAGATTTAACCACCTTGAGCGCACCGCCAGTCAAGCAGGGAT | | 217254 | 3.62% | | |
| | | GTCAATCCTCTTCTCGTTCCTCCTGCTAGATTGAACCAGCTTGAGAGCAAAGCCATTCAAGCAGGGCTGCCTGGAGTTGAATGTCAAGCCTCTTCTCGTTCCTCCTGCTAGATTTAACCACCTTGAGCGCACCGCCAGTCAAGCAGGGA | | 70644 | 1.18% | | |
| | | GTCAATCCTCTTCTCGTTCCTCCTGCTAGATTGAACCAGCTTGAGAGCAAAGCCATTCAAGCAGGGCTGCCTGGAGTTGAATGTCAAGCCTCTTCTCGTTCCTCCTGCTAGATTTAACCACCTTGAGCGCACCGCCAGTC | | 55081 | 0.92% | | |
| | | GTCAATCCTCTTCTCGTTCCTCCTGCTAGATTGAACCAGCTTGAGAGCAAAGCCATTCAAGCAGGGCTGCCTGGAGTTGAATGTCAAGCCTCTTCTCGTTCCTCCTGCTAGATTTAACCACCTTGAGCGCACCGCCAGTCAAGC | | 31607 | 0.53% | 22.36% | |
| | | | | | | | |
| | | GTCAATCCTCTTCTCGTTCCTCCAGGCAGCCTGCTAGATTGAACCAGCTTGAGAGCA | | 48189 | 0.80% | | |
| | | GTCAATCCTCTTCTCGTTCCTCCTGCTAGATTGAACCAGCTTGAGAGCAAAGCCATTCAAGCAGGGCTGCCTGGAGT | | 27643 | 0.46% | | |
| | | | **Total** | **5996593** | | **83.17%** | |

## Table S3. The loop stem (F1c and B1c), LAMP amplification efficiency, and specificity

| primer sets | F1c | Length | Tm (°C) | B1c | Length | Tm(°C) | TT (min) | FP |
|---|---|---|---|---|---|---|---|---|
| **N geme** | | | | | | | **LAMP** | |
| N7 | tgccaatgtgatctt | 15 | 47.9 | aatcgtgctacaac | 14 | 45.2 | 19.7±0.8 | 1 |
| N8 | tcccttctgcgta | 13 | 46.7 | gtcgcaacagttc | 13 | 45.9 | 43.9±5.3 | 3 |
| N9 | catcaccgccatt | 13 | 47.2 | ttgctttgctgct | 13 | 47.2 | 24.4±1.7 | 2 |
| N10 | gccttgtcctcga | 13 | 49 | caatagcagtccaga | 15 | 47.4 | 28.6±3.1 | 1 |
| N11 | ttgttagcaggattg | 15 | 45.7 | caaggaacaacattg | 15 | 45.2 | 28.4±6.6 | 1 |
| N12 | gcacgattgcag | 12 | 45.1 | acaacattgccaaa | 14 | 45.2 | 32.9±7.1 | 1 |
| N13 | ccttttggcaatgtt | 15 | 47.6 | agtcaagcctcttc | 14 | 46.4 | 26.0±3.5 | 3 |
| N14 | ccttctgcgtagaa | 14 | 46.7 | tcatcacgtagtcg | 14 | 46.7 | 27.5±3.0 | 3 |
| N15 | ccttctgcgtagaa | 14 | 46.7 | acgtagtcgcaac | 13 | 47.1 | 26.6±2.0 | 2 |
| N16 | ccttctgcgtagaa | 14 | 46.7 | agtcaagcctcttc | 14 | 46.4 | 25.7±2.3 | 2 |
| N17 | aacgagaagaggc | 13 | 45.4 | tcgcaacagttca | 13 | 45.9 | 30.5±3.3 | 1 |
| N18 | gcctggagttgaat | 14 | 47.3 | ctgctcttgctttg | 14 | 47 | 35.2±1.7 | 2 |
| N19 | gcctggagttgaat | 14 | 47.3 | ctgctcttgctttg | 14 | 47 | 31.2±3.5 | 2 |
| N20 | caggagaagttccc | 14 | 47 | tgatgctgctcttg | 14 | 48 | 27.4±3.1 | 2 |
| N21 | ctagcaggagaagt | 14 | 45.1 | ctgctcttgctttg | 14 | 47 | 42.6±4.9 | 2 |
| N22 | catcaccgccat | 12 | 45.2 | ttgctttgctgct | 13 | 47.2 | 41.7±4.4 | 2 |
| N23 | tcaccgccattg | 12 | 45.7 | gcaaaatgtctggt | 14 | 45.6 | 22.6±2.4 | 2 |
| N24* | catcaccgccatt | 13 | 47.2 | gcaaaatgtctggt | 14 | 45.6 | 21.6±2.6 | 1 |
| N25* | tcaatctgtcaagca | 15 | 47.5 | atgtctggtaaaggc | 15 | 48.1 | 18.0±3.9 | 1 |
| N26 | attattgggtaaacctt | 17 | 46 | ggcaaggaagacc | 13 | 47.1 | 34.9±6.6 | 1 |
| N27* | gagagcggtgaac | 13 | 47.6 | tcgaggacaaggc | 13 | 49 | 18.4±1.8 | 1 |
| N28 | gcagtattattgggta | 16 | 45.4 | ttcaccgctctca | 13 | 47.7 | 27.5±6.7 | 1 |
| | | | | | | | **RT-LAMP** | |
| N2(-5) | aggctccctcagttgc | 16 | 57.7 | attggcacccgcaatc | 16 | 57.1 | 15.3±0.3 | 1 |
| N3(-4) | attattgggtaaacctt | 17 | 46 | caaggaagacct | 12 | 38.8 | 23.1±3.2 | 1 |
| N4(-4) | ccaatgtgatctt | 13 | 38.8 | taacaatgctgc | 12 | 38.7 | 21.4±4.9 | 1 |
| N6(-4) | ctggagttgaat | 12 | 35.9 | ctagaatggctg | 12 | 35.9 | 21.9±3.4 | 1 |
| N7 | tgccaatgtgatctt | 15 | 47.9 | aatcgtgctacaac | 14 | 45.2 | 14.3±0.6 | 1 |
| N24* | | | | | | | 20.4±1.8 | 3 |
| N25* | | | | | | | 20.2±5.5 | 1 |
| N27* | | | | | | | 11.7±0.1 | 1 |
| **M gene** | | | | | | | | |
| M1 | tctttaggcaggtc | 14 | 45.9 | actgttgctacatca | 15 | 47.1 | 22.6±2.9 | 1 |
| M2 | gtccttgatgtcac | 14 | 45.1 | caaattgggagcttc | 15 | 47.6 | 22.0±0.9 | 2 |
| M3 | cagaatagtgccatg | 15 | 46.6 | agaaagtgaactcgt | 15 | 47.1 | 11.1±0.8 | 1 |
| M4 | gcaggtccttgat | 13 | 45.4 | ggagcttcgcag | 14 | 46.8 | 31.1±2.3 | 1 |
| M5 | aaacagtctgaaagaa | 16 | 45.7 | ttctcaacgtgcc | 13 | 47.2 | 16.5±0.4 | 1 |
| M6 | acatggaacgcg | 12 | 46.6 | ttcttctcaacgtgc | 15 | 49.6 | 15.2±0.4 | 1 |
| **S gene** | | | | | | | | |
| S1 | gcaaaggtggca | 12 | 46.4 | tgattgctcaatacac | 16 | 47.1 | 24.8±2.1 | 1 |
| S2 | aggccgttaaactt | 14 | 46.6 | gttttgccaccttt | 14 | 46.3 | 15.5±1.4 | 3 |
| S3 | gaggtctctagcag | 14 | 46 | gtttaacggccttac | 15 | 47.4 | 26.1±4.9 | 3 |
| S4 | gcaaaggtggcaaa | 14 | 49.9 | tgattgctcaatacac | 16 | 47.1 | 23.1±2.9 | 1 |
| S5 | gtgtctgtggatca | 14 | 46.5 | acaccaggaacaaa | 14 | 46.2 | 21.5±1.8 | 4 |
| S6 | tcaagtgtctgtgg | 14 | 46.8 | caccaggaacaaata | 15 | 45.1 | 17.5±0.8 | 4 |
| S7 | tgaggtctctagca | 14 | 46.5 | tttaacggccttact | 15 | 47.1 | 19.2±2.9 | 1 |

TT represented 3-10 independent measures presented with mean± SD. * same primer sets were used both for LAMP and RT-LAMP assays.

FP was determined as described in "Method". From 3-4 replicates, the highest FP score was listed as the final FP for the primer.

## Table S4. The M Gene primer sets

| Primer sets | Amplifcation Len | Sequence (5'-3') | | | Sequence (5'-3') | | | Sequence (5'-3') | | |
|---|---|---|---|---|---|---|---|---|---|---|
| **#** | **B2-F2(Length)** | **F3** | **Len** | **Tm** | **F2** | **Len** | **Tm** | **FL** | **Len** | **Tm** |
| **M1** | 123 | actattctgaccagaccgcttc | 22 | 62 | ttcgtggacatcttcgtattgc | 22 | 60.7 | gatgtcacagcgtcctagatgg | 22 | 62 |
| **M2** | 157 | cattcttctcaacgtgccactc | 22 | 61 | cggagctgtgatccttcgtg | 20 | 62.6 | gtgtccagcaatacgaagatgt | 22 | 60 |
| **M3** | 129 | gctatcgcaatggcttgtcttg | 22 | 62 | ccatgtggtcattcaatccaga | 22 | 60 | ggcacgttgagaagaatgttagt | 23 | 61 |
| **M4** | 166 | cattcttctcaacgtgccactc | 22 | 61 | tgtgatccttcgtggacatctt | 22 | 61.1 | tcctagatggtgtccagcaatac | 23 | 61 |
| **M5** | 160 | ggccagtaactttagcttgttttg | 24 | 61 | cgcaatggcttgtcttgtagg | 21 | 61.6 | tgaagtagctgagccacatcaa | 22 | 61 |
| **M6** | 141 | gttttgtgcttgctgctgttta | 22 | 60 | aggcttgatgtggctcagcta | 21 | 63.3 | gcaaacagtctgaaagaagcaatg | 24 | 61 |

| Primer sets | Sequence (5'-3') | | | Sequence (5'-3') | | | Sequence (5'-3') | | |
|---|---|---|---|---|---|---|---|---|---|
| **#** | **F1c** | **Len** | **Tm** | **B1c** | **Len** | **Tm** | **BL** | **Len** | **Tm** |
| **M1** | tctttaggcaggtc | 14 | 46 | actgttgctacatca | 15 | 47.1 | cttattacaaattgggagcttcgc | 24 | 60 |
| **M2** | gtccttgatgtcac | 14 | 45 | caaattgggagcttc | 15 | 47.6 | gcgtgtagcaggtgactcag | 20 | 63 |
| **M3** | cagaatagtgccatg | 15 | 47 | agaaagtgaactcgt | 15 | 47.1 | gatccttcgtggacatcttcgt | 22 | 62 |
| **M4** | gcaggtccttgat | 13 | 45 | ggagcttcgcag | 12 | 46.8 | ggtgactcaggttttgctgcat | 22 | 63 |
| **M5** | aaacagtctgaaagaa | 16 | 46 | ttctcaacgtgcc | 13 | 47.2 | tattctgaccagaccgcttcta | 22 | 60 |
| **M6** | acatggaacgcg | 12 | 47 | ttcttctcaacgtgc | 15 | 49.6 | tattctgaccagaccgcttcta | 22 | 60 |

| Primer sets | Sequence (5'-3') | | | Sequence (5'-3') | | |
|---|---|---|---|---|---|---|
| **#** | **B2** | **Len** | **Tm** | **B3** | **Len** | **Tm** |
| **M1** | aaacctgagtcacctgctacac | 22 | 62 | attgtcactgctactggaatgg | 22 | 60 |
| **M2** | tgtagcgactgtatgcagcaaa | 22 | 62 | gctactggaatggtctgtgttt | 22 | 60.2 |
| **M3** | cgtcctagatggtgtccagcaa | 22 | 64 | gaaagcgttcgtgatgtagcaa | 22 | 61.4 |
| **M4** | ttatagttgccaatcctgtagcg | 23 | 60 | gctactggaatggtctgtgttt | 22 | 60.2 |
| **M5** | cagctccgattacgagttcact | 22 | 62 | gtccagcaatacgaagatgtcc | 22 | 60.7 |
| **M6** | agctccgattacgagttcactt | 22 | 61 | gtccagcaatacgaagatgtcc | 22 | 60.7 |

| Primer sets | Sequence (5'-3') | | Sequence (5'-3') | | PubMed |
|---|---|---|---|---|---|
| **#** | **FIP(F1c+F2)** | **Len** | **BIP(B1c+B2)** | **Len** | **Accession** |
| **M1** | tctttaggcaggtcttcgtggacatcttcgtattgc | 36 | actgttgctacatcaaaacctgagtcacctgctacac | 37 | NC_045512 |
| **M2** | gtccttgatgtcaccggagctgtgatccttcgtg | 34 | caaattgggagcttctgtagcgactgtatgcagcaaa | 37 | NC_045512 |
| **M3** | cagaatagtgccatgccatgtggtcattcaatccaga | 37 | agaaagtgaactcgtcgtcctagatggtgtccagcaa | 37 | NC_045512 |
| **M4** | gcaggtccttgattgtgatccttcgtggacatctt | 35 | ggagcttcgcagttatagttgccaatcctgtagcg | 35 | NC_045512 |
| **M5** | aaacagtctgaaagaacgcaatggcttgtcttgtagg | 37 | ttctcaacgtgcccagctccgattacgagttcact | 35 | NC_045512 |
| **M6** | acatggaacgcgaggcttgatgtggctcagcta | 33 | ttcttctcaacgtgcagctccgattacgagttcactt | 37 | NC_045512 |

*** Note: Each primer set is composed of eight oligos, in which FIP is made by F1c+F2, and BIP is made by B1c+B2.**

## Table S5.  The S Gene primer sets

| Primer sets | Amplifcation Len | Sequence (5'-3') | | | Sequence (5'-3') | | | Sequence (5'-3') | | |
|---|---|---|---|---|---|---|---|---|---|---|
| # | B2-F2(Len) | F3 | Len | Tm | F2 | Len | Tm | FL | len | Tm |
| S1 | 124 | acacttgcagatgctggctt | 20 | 62.4 | tattgctgctagagacctcattt | 23 | 59 | agtaaggccgttaaacttttgtg | 23 | 59.4 |
| S2 | 122 | agtgacacttgcagatgctg | 20 | 60.3 | aatatggtgattgccttggtga | 22 | 59.7 | gcacaaatgaggtctctagcag | 22 | 60.7 |
| S3 | 140 | attaccagatccatcaaaacca | 22 | 57.1 | agtgacacttgcagatgctg | 20 | 60.3 | accaaggcaatcaccatattgt | 22 | 60 |
| S4 | 133 | agtgacacttgcagatgctg | 20 | 60.3 | cttggtgatattgctgctagag | 22 | 58.3 | gtaaggccgttaaacttttgtg | 22 | 58.1 |
| S5 | 174 | tcaatggtttaacaggcacagg | 22 | 60.8 | aagtttctgcctttccaacaat | 22 | 58.6 | cagtagtgtcagcaatgtctct | 22 | 59.4 |
| S6 | 169 | tcaatggtttaacaggcacagg | 22 | 60.8 | ctgcctttccaacaatttggc | 21 | 60.6 | tcagtagtgtcagcaatgtctc | 22 | 59.4 |
| S7 | 136 | attaccagatccatcaaaacca | 22 | 57.1 | cacttgcagatgctggctt | 19 | 60.7 | accaaggcaatcaccatattgt | 22 | 60 |

| Primer sets | Sequence (5'-3') | | | Sequence (5'-3') | | | Sequence (5'-3') | | |
|---|---|---|---|---|---|---|---|---|---|
| # | F1c | Len | Tm | B1c | Len | Tm | BL | Len | Tm |
| S1 | gcaaaggtggca | 12 | 46.4 | tgattgctcaatacac | 16 | 47.1 | ctgttagcgggtacaatcactt | 22 | 60 |
| S2 | aggccgttaaactt | 14 | 46.6 | gttttgccaccttt | 14 | 46.3 | cacagatgaaatgattgctcaa | 22 | 57 |
| S3 | gaggtctctagcag | 14 | 46 | gtttaacggccttac | 15 | 47.4 | cctttgctcacagatgaaatga | 22 | 58.6 |
| S4 | gcaaaggtggcaaa | 14 | 49.9 | tgattgctcaatacac | 16 | 47.1 | gttagcgggtacaatcacttct | 22 | 59.8 |
| S5 | gtgtctgtggatca | 14 | 46.5 | acaccaggaacaaa | 14 | 46.2 | taaccaggttgctgttctttat | 22 | 57.3 |
| S6 | tcaagtgtctgtgg | 14 | 46.8 | caccaggaacaaata | 15 | 45.1 | aaccaggttgctgttctttatc | 22 | 58.5 |
| S7 | tgaggtctctagca | 14 | 46.5 | tttaacggccttact | 15 | 47.1 | cctttgctcacagatgaaatga | 22 | 58.6 |

| Primer sets | Sequence (5'-3') | | | Sequence (5'-3') | | |
|---|---|---|---|---|---|---|
| # | B2 | Len | Tm | B3 | Len | Tm |
| S1 | ctgcaccaaaggtccaacc | 19 | 60.9 | acattctgtgtaactccaatacca | 24 | 59.4 |
| S2 | aagtgattgtacccgctaacag | 22 | 60 | ccattaaacctataagccatttgc | 24 | 58.1 |
| S3 | gctaacagtgcagaagtgtatt | 22 | 58.3 | ctgcaccaaaggtccaacc | 19 | 60.9 |
| S4 | cctgcaccaaaggtccaac | 19 | 60.9 | ccattaaacctataagccatttgc | 24 | 58.1 |
| S5 | acagggacttctgtgcagtt | 20 | 61 | ggagtaagttgatctgcatgaa | 22 | 57.8 |
| S6 | aacagggacttctgtgcagt | 20 | 61 | ggagtaagttgatctgcatgaa | 22 | 57.8 |
| S7 | cgctaacagtgcagaagtgtat | 22 | 60.4 | ctgcaccaaaggtccaacc | 19 | 60.9 |

| Primer sets | Sequence (5'-3') | | Sequence (5'-3') | | PubMed |
|---|---|---|---|---|---|
| # | FIP(F1c+F2) | Len | BIP(B1c+B2) | Len | Accession |
| S1 | gcaaaggtggcatattgctgctagagacctcattt | 35 | tgattgctcaatacacctgcaccaaaggtccaacc | 35 | NC_045512 |
| S2 | aggccgttaaacttaatatggtgattgccttggtga | 36 | gttttgccacctttaagtgattgtacccgctaacag | 36 | NC_045512 |
| S3 | gaggtctctagcagagtgacacttgcagatgctg | 34 | gtttaacggccttacgctaacagtgcagaagtgtatt | 37 | NC_045512 |
| S4 | gcaaaggtggcaaacttggtgatattgctgctagag | 36 | tgattgctcaatacaccctgcaccaaaggtccaac | 35 | NC_045512 |
| S5 | gtgtctgtggatcaaagtttctgcctttccaacaat | 36 | acaccaggaacaaaacagggacttctgtgcagtt | 34 | NC_045512 |
| S6 | tcaagtgtctgtggctgcctttccaacaatttggc | 35 | caccaggaacaaataaacagggacttctgtgcagt | 35 | NC_045512 |
| S7 | tgaggtctctagcacacttgcagatgctggctt | 33 | tttaacggccttactcgctaacagtgcagaagtgtat | 37 | NC_045512 |

*** Note: Every  primer set is composed of eight oligos, in which FIP is made by F1c+F2, and BIP is made by B1C+B2.**

# Table S6.  Case #16 RT-LAMP product sequencing results

| | | | | | |
|---|---|---|---|---|---|
| **Primers to establish library** | **Forward** | AATGATACGGCGACCACCGAGATCTACACCTAGACTGCACACTCTTTCCCTACACGACGCTCTTCCGATCTGGGCGCGATCAAAACAACG | | index in red | underscore incates the F2 of N27 |
| | **Reverse** | CAAGCAGAAGACGGCATACGAGATCTAGACTGCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATTCGGTAGTAGCCAATTTGGTC | **SARS-CoV-2 genomic RNA** | index in red | underscore incates the B2 of N27 |
| **Sequencing results** | | **Top 10 reads** | ( MN908947.3), % Identities | **read count** | **% of total reads** |
| | | TCGGCCCCAAGGTTTACCCAATAATACTGCGTCTTGGTTCACCGCTCTCACTCAACATGGCAAGGAAGACCTTAAATTCCCTCGAGGACAAGGCGTTCCAATTAAAACAAAAACCATACAAAATAACA | 100% | 1497377 | 38.33% |
| | | TCGGCCCCAAGGTTTACCCAATAATACTGCGTCTTGGTTCACCGCTCTCACTCAACATGGCAAGGAAGACCTTAAATTCCCTCGAGGACAAGGCGTTCCAATTAACACCAATAGCAGTCCAGAT | 100% | 1193621 | 30.55% |
| | | TCGGCCCCAAGGTTTACCCAATAATACTGCGTCTTGGTTCACCGCTCTCACTCAACATGGCAAGGAAGACCTTAAATTCCCTCGAGGAAAAGCCTTACAAATAAAAACAAAAACAATACAAAATAAAA | 95% | 182513 | 4.67% |
| | | TCGCACCCAAGCTTAACCCAATAATACTCCGACTTGCTTCAACGCACTCACTCAACATGGCAAGGAAGACCTTAAATTCCCTCGAGGACAAGGCGTTCCAATTAACACCAATAGCAGTCCAGAT | 94% | 106275 | 2.72% |
| | | ACCCAATAATACTGCGTCTTGGTTCACCGCTCTCACTCAACATGGCAAGGAAGACCTTAAATTCCCTCGAGGACAAGGCGTTCCAATTAACACCAATAGCAGTCCAGAT | 100% | 93284 | 2.39% |
| | | TCGGCCCCAAGGTTTACCCAATAATACTGCGTCTTGGTTCACCGCTCTCACTCAACATGGCAAGGAAGACCTTAAATTCCCTCGAGGACAAGGCGTTCCAATTAACACCAA | 100% | 68159 | 1.74% |
| | | TCGGCCCCAAGGTTTACCCAATAATACTGCGTCTTGGTTCACCGCTCTCACTCAACATGGCAAGGAAGACCTTAAATTCCCTCGAGGACAAGGCGTTCCAATTAACACCAATAGCAGTCCAGATGACC | 100% | 60954 | 1.56% |
| | | TCGGCCCCAAGGTTTACCCAATAATACTGCGTCTTGGTTCACCGCTCTCACTCAACATGGCAAGGAAGACCTTAAATTCCCTCGAGGACAAGGC | 94% | 48579 | 1.24% |
| | | CGGCCCCAAGGTTTACCCAATAATACTGCGTCTTGGTTCACCGCTCTCACTCAACATGGCAAGGAAGACCTTAAATTCCCTCGAGGACAAGGCGTTCCAATTAACACCAATAGCAGTCCAGAT | 100% | 33875 | 0.87% |
| | | CGGCCCCAAGGTTTACCCAATAATACTGCGTCTTGGTTCACCGCTCTCACTCAACATGGCAAGGAAGACCTTAAATTCCCTCGAGGACAAGGCGTTCCAATTAA | 100% | 23569 | 0.60% |
| | | **Total** | | **3906852** | **84.68%** |

## Table S7. ACTB RT-LAMP primer set

| **ACTB** | |
|---|---|
| **FIP** | GAGCCACACGCAGCTCATTGTATCACCAACTGGGACGACA |
| **BIP** | CTGAACCCCAAGGCCAACCGGCTGGGGTGTTGAAGGTC |
| **FL** | TGTGGTGCCAGATTTTCTCCA |
| **BL** | CGAGAAGATGACCCAGATCATGT |
| **F3** | AGTACCCCATCGAGCACG |
| **B3** | AGCCTGGATAGCAACGTACA |

### Reference

Zhang, Y., Ren, G., Buss, J., Barry, A. J., Patton, G. C., and Tanner, N. A. (2020)

Enhancing colorimetric loop-mediated isothermal amplification speed and sensitivity with guanidine chloride. Biotechniques 69, 178-185

**Table S8. Real-time PCR primers**

| | | |
|---|---|---|
| **E-Sarbeco*** | **F** | ACAGGTACGTTAATAGTTAATAGCGT |
| | **R** | ATATTGCAGCAGTACGCACACA |
| **Beta-actin (ACTB)** | **F** | CTATCCCTGTACGCCTCTGG |
| | **R** | GTCACCGGAGTCCATCACC |
| **Human coronavirus 229E** | **F** | CGTGTTGGGACAGACATACTATC |
| | **R** | CTGAACACCTGAAGCCAATCTA |
| **Human coronavirus OC43** | **F** | TGGAGCGTATGGCTGATTTG |
| | **R** | GCATAGTTTGCAAGGCAGAAAC |
| **Influenza A virus (H1N1)** | **F** | GGGAACGGTGACCCAAATAA |
| | **R** | CAAGTGCACCAGCAGAATAAC |
| **Human respiratory syncytial virus** | **F** | GGCAGTAGAGTTGAAGGGATTT |
| | **R** | TGCACACTAGCATGTCCTAAC |
| **Human rhinovirus 16** | **F** | GTCAAATGGATCCAGCCTCA |
| | **R** | GGGTCTTGAGAGAAGTCCAATC |

*Corman, V. M., Landt, O., Kaiser, M., Molenkamp, R., Meijer, A., Chu, D. K., Bleicker, T., Brunink, S., Schneider, J., Schmidt, M. L., Mulders, D. G., Haagmans, B. L., van der Veer, B., van den Brink, S., Wijsman, L., Goderski, G., Romette, J. L., Ellis, J., Zambon, M., Peiris, M., Goossens, H., Reusken, C., Koopmans, M. P., and Drosten, C. (2020) Detection of 2019 novel coronavirus (2019-nCoV) by real-time RT-PCR. Euro Surveill 25