

Supplementary figures, 2019 novel coronavirus RT-PCR development

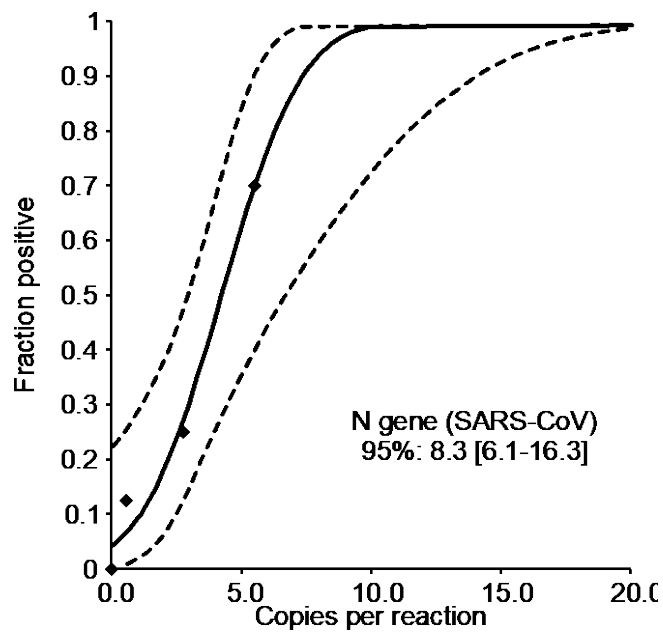
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[illegible][illegible]

CACATTGGCACCCGCAATC -- **ACTTCCTCAAGGAACAACATTGCCA** -- **CAAGCCTCTTCTCGTTTCCTC**
 N. Sarbeco_F N. Sarbeco_P N. Sarbeco_R

The sequence logo displays the conservation of nucleotides across 1000 samples. The N. Sarbeco_F region (positions 1-10) shows high conservation of C, A, and T. The N. Sarbeco_P region (positions 11-20) shows high conservation of C, A, and T. The N. Sarbeco_R region (positions 21-30) shows high conservation of C, A, and T. The N. Sarbeco_R region also shows a high frequency of G and A at the end of the sequence.

Supplementary Figure 1. Non-redundant alignments of SARS-related CoVs focused on oligonucleotide binding sites of all assays (top to bottom: RdRp, E, N). Viruses not present in these alignments have been removed because their binding sites are 100% identical to one of the members of the alignment. (“--”) means sequence gaps not covered by oligonucleotides.



Supplementary Figure 2: Additional confirmatory assay: N gene. Limit of detection study for N gene assay. Technical LOD = 8.3 RNA copies/reaction, at 95% hit rate; 95% CI: 6.1-16.3 RNA copies/reaction. Y-axis shows positive results in all parallel reactions performed, squares are experimental data points resulting from replicate testing of given concentrations (x-axis) in parallel assays (8 replicate reactions per datum point). The inner line is a probit curve (dose-response rule). The outer dotted lines are 95% confidence intervals.