A Multiplexed, Next Generation Sequencing Platform for High-Throughput Detection of SARS-CoV-2

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Supplementary information

Supplementary Table 1: List of SARS-CoV-2 and human primers. Primer sequences, name of the targeted regions, size of amplicons after multiplex and barcode PCR are indicated.

Supplementary Table 2: Itemized cost of C19-SPAR-Sseq per sample

Supplementary Table 3: Description of the proof-of-concept cohort for C19-SPAR-Seq detection of SARS-CoV-2. Barcodes ID**,** sample identification (ID), date of retrieval, collection method, diagnostic laboratory status, and 'BGI' qRT-PCR results are indicated. These patient samples were used to develop C19-SPAR-Seq detection of SARS-CoV-2 (PoC cohort) (**Fig. 1**).

Supplementary Table 4: Description of test development cohort. Barcodes ID**,** sample identification (ID), date of retrieval, collection method, diagnostic laboratory qRT-

PCR results ('Seegene') are indicated (n = 112). These patient samples were used to establish SARS-CoV-2 clinical status assignment using diagnostic laboratory qRT-PCR results ('Seegene') and to test C19-SPAR-Seq detection of SARS-CoV-2 (**Fig. 2**,**3**).

Supplementary Table 5: Confusion matrix of the test development cohort.

Supplementary Table 6: Description of the pilot cohort. Barcodes ID**,** sample identification (ID), date of retrieval, collection method, diagnostic laboratory qRT-PCR results ('Seegene'), 'BGI' qRT-PCR results are indicated. Filtered archival samples are indicated. (Extended data **Fig. 3,4**).

Supplementary Table 7: Description of the extended cohort. Barcodes ID**,** sample identification (ID), date of retrieval, collection method, diagnostic laboratory qRT-PCR results ('Seegene'), and 'BGI' qRT-PCR results are indicated (**Fig. 4**).

Supplementary Table 8: Confusion matrix of the extended cohort.

Supplementary Table 9: Group classifications