Expanded View Figures

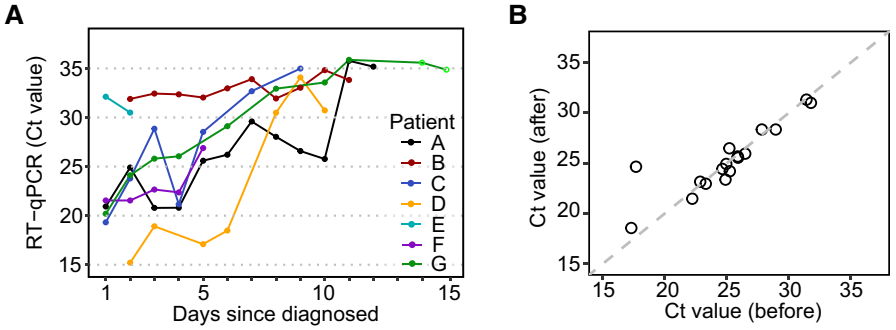


Figure EV1. Analysis of longitudinal samples using RT-qPCR.

A Viral loads of early samples (collected immediately after waking up in the morning) on different days since the patient was diagnosed with COVID-19.

B The Ct value fluctuation of repeated sampling in 5–30-min interval without any interventions.

Source data are available online for this figure.

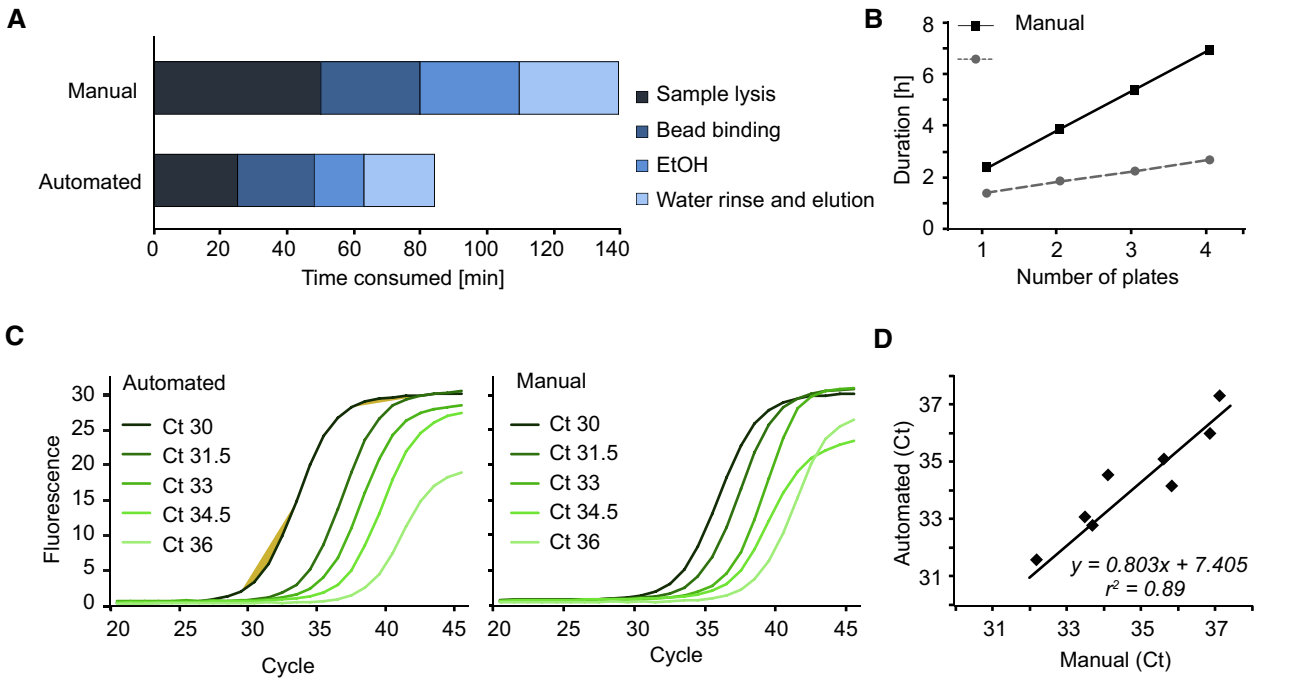


Figure EV2. Comparison between manual and automated RNA extraction.

A Timewise comparison between manual and automated RNA extraction from 96 samples. Time consumed by sample lysis, bead binding, wash, and elution is shown in different colors.

B Timewise comparison of manual and automated RNA extraction from multiple 96-well plates.

C RT-qPCR amplification curves of RNA isolated automatically (left) and manually (right) from serial diluted SARS-CoV-2 positive gargle samples.

D Correlation of Ct values between automatically and manually extracted RNA from different SARS-CoV-2-positive gargle samples.

Source data are available online for this figure.

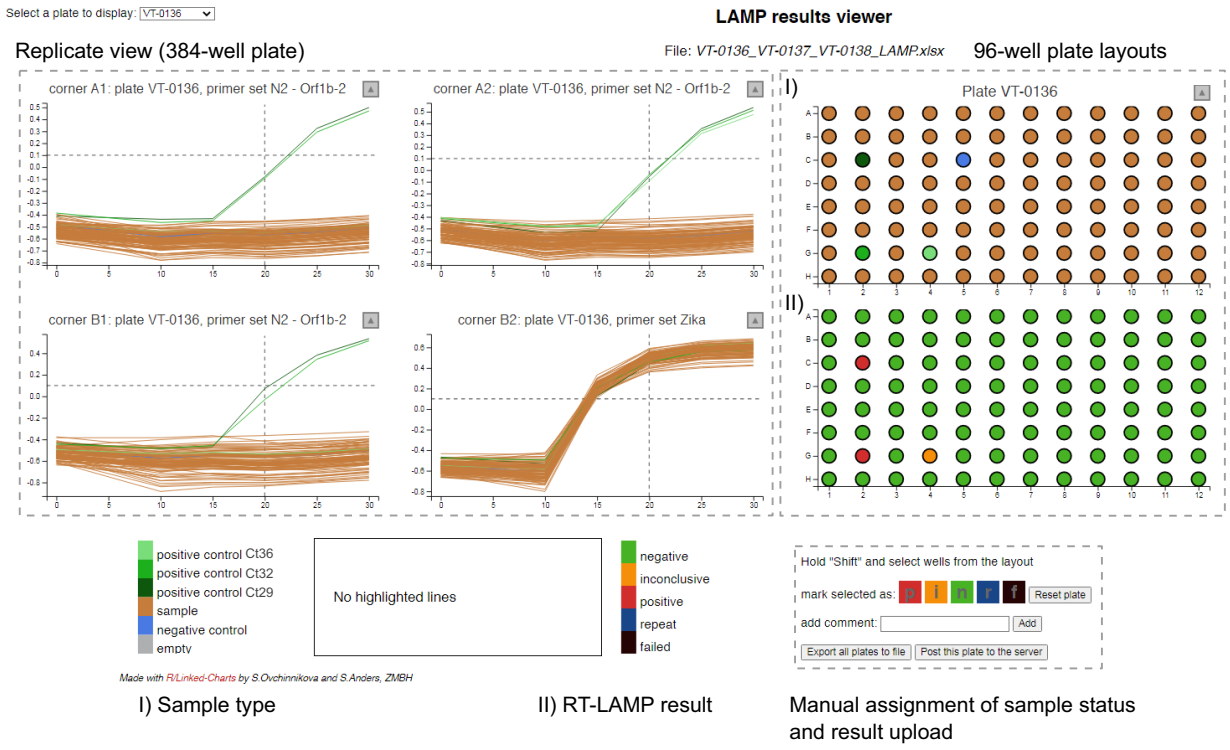


Figure EV3. LAMP plate viewer user interface.

The plate reader output file is fed into the LAMP plate viewer tool together with the barcode and position information of each sample in the 96-well sample plate. Each sample plate is displayed individually. On the right the 96-well sample plate layouts color-coded according to (i) sample type (test sample, controls, empty wells) or (ii) automatically assigned classification of RT-LAMP results (green—negative, red—positive, orange—inconclusive, blue—repeat and black—failed) are shown. On the left, the RT-LAMP measurements for each well in the 384-well plate are visualized (replicate view) to allow quality control by the test station personnel. The tool is interactive and allows to highlight all replicates of a single test sample by selecting the corresponding well in one of the layouts of the 96-well plate on the right. The classification of the RT-LAMP results is done automatically, but the test station personnel can edit the sample statuses, if necessary, before the results of the sample plate are uploaded to the server.

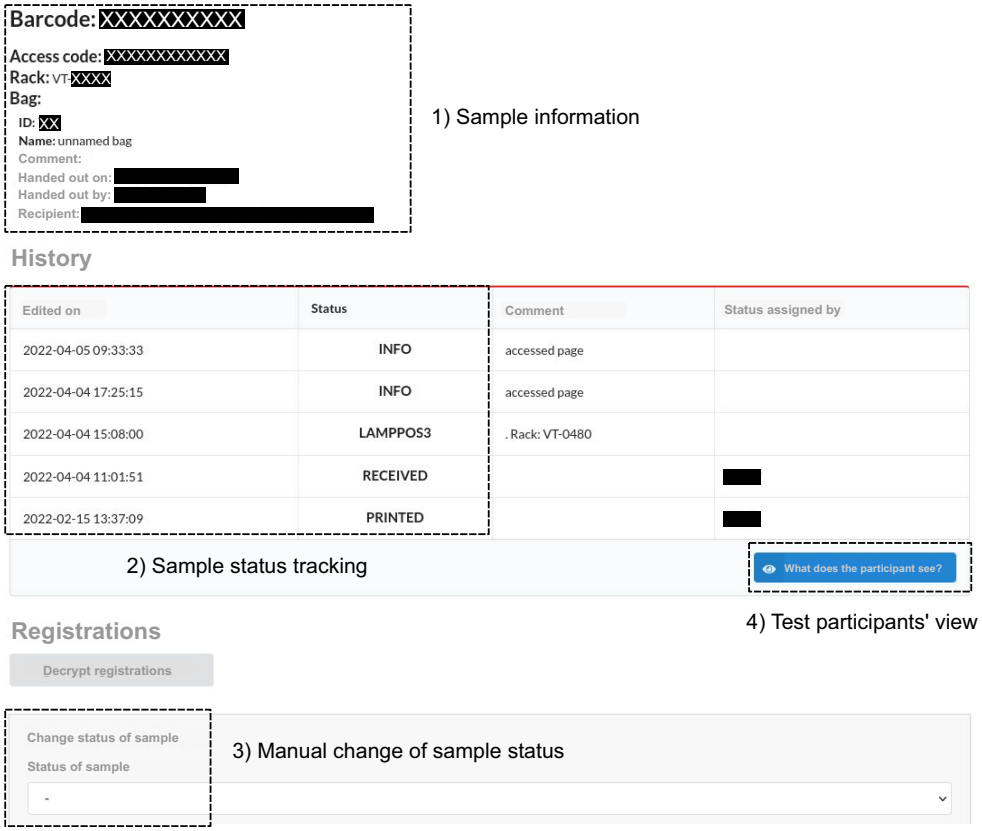
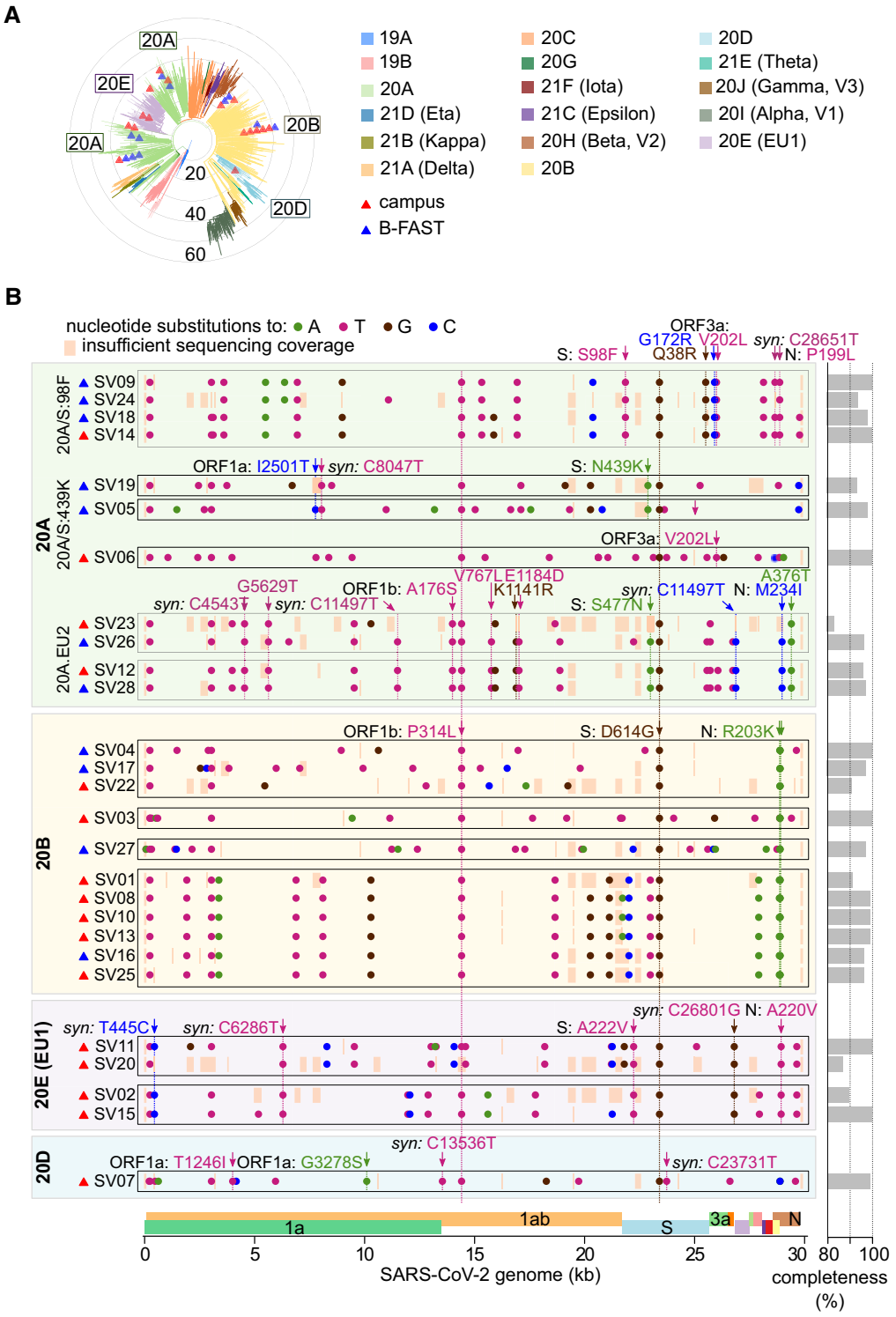


Figure EV4. Example entry in the database user interface.

The database user interface allowed the test station personnel to track and edit all registered samples. Labels in gray were translated from German into English. (1) Sample information: Samples were identified by their barcode on the Micronic test tube. Additionally, the distribution of test kit bags ("Abnehmer") could be documented, for example, to settle the costs of testing. (2) Sample status tracking: Individual samples were assigned a corresponding status, which was updated in each phase of the workflow. These include the generation of an access code for each Micronic test tube before distribution of the test kit to a participant (PRINTED), sample arrival at the test station (RECEIVED), RT-LAMP results (LAMPNEG versus LAMPPOS or LAMPINC in case of uncertainty) and the result retrieval by the test participant (INFO - accessed page; not visible for the test participant). (3) Manual change of sample status: The test station personnel could edit the sample status, e.g. after verification of a positive result via RT-qPCR (PCRNEG/PCRPOS). (4) The test participants' view allowed the test station personnel to view the result page, which was shown to the user with the current status set.


A
20A
20E
20A
20B
20
40
20D
60
19A
19B
20A
21D (Eta)
21B (Kappa)
21A (Delta)
20C
20G
21F (Iota)
21C (Epsilon)
20H (Beta, V2)
20B
20D
21E (Theta)
20J (Gamma, V3)
20I (Alpha, V1)
20E (EU1)
campus
B-FAST
B
nucleotide substitutions to: A T G C
insufficient sequencing coverage
ORF3a: G172R V202L
S: S98F
Q38R
syn: C28651T
N: P199L
20A/S:98F
SV09
SV24
SV18
SV14
ORF1a: I2501T
syn: C8047T
S: N439K
20A
20A/S:439K
SV19
SV05
ORF3a: V202L
SV06
G5629T
ORF1b: A176S
V767L E1184D
K1141R
A376T
syn: C4543T
syn: C11497T
S: S477N
syn: C11497T
N: M234I
20A.EU2
SV23
SV26
SV12
SV28
ORF1b: P314L
S: D614G
N: R203K
SV04
SV17
SV22
SV03
20B
SV27
SV01
SV08
SV10
SV13
SV16
SV25
syn: C26801G
N: A220V
syn: T445C
syn: C6286T
S: A222V
20E (EU1)
SV11
SV20
SV02
SV15
syn: C13536T
ORF1a: T1246I
ORF1a: G3278S
syn: C23731T
20D
SV07
1a
1ab
S
3a
N
0
5
10
15
20
25
30
SARS-CoV-2 genome (kb)
80
100
completeness (%)

◀ **Figure EV5. Detailed characterization of sequenced SARS-CoV-2 viral genomes with the detected mutations per sample.**

A Phylogenetic placement of the 27 obtained genome sequences (triangles) on the Nextclade tree of 1849 reference SARS-CoV-2 genome sequences (representing the genetic diversity of circulating SARS-CoV-2 at the time of the analysis).

B Mutations of the 27 whole-genome sequences in comparison to the original reference strain (Wuhan-Hu-1). Sequences were grouped and ordered according to their phylogenetic placement. Specific signature mutations that define the various Nextstrain clades are indicated when present in the analyzed samples. Stretches of genomic sequence with insufficient sequencing coverage for reliable mutation calling are indicated by orange boxes. The completeness of each genomic sequence is shown on the right.

Source data are available online for this figure.