Sequencing of the SARS-CoV-2 genome

The SARS-CoV-2 RNA genome was reverse-transcribed, and amplified following the sequencing strategy of the ARTIC V3 protocol (https://artic.network/ncov-2019), which generates 400 bp amplicons that overlap by approximately 20 bp and covers the whole target genome. Nanopore Library preparation was performed with SQK-LSK109 (Oxford Nanopore Technologies, Oxford, UK) according to the ONT "PCR tiling of COVID-19 virus" (version: PTC_9096_v109_revE_06Feb2020, last update: 26/03/2020). Reagents, quality control and flow cell preparation were done as described previously [1, 2]. Sequencing was performed on 2021-05-04 on GridION X5 (Oxford Nanopore Technologies) with real-time basecalling enabled (ont-guppy-for-gridion v.4.2.3; fast basecalling mode). Bioinformatic analyses followed the workflow described (https://artic.network/ncov-2019/ncov2019-bioinformatics-sop.html) using artic version 1.1.3. Consensus sequences were generated using *medaka* (https://github.com/nanoporetech/medaka) and *bcftools* [3].

Using 59,291 nanopore reads generated for the sample, each base of the target genome assembly was on average covered 250 times. The final assembly (29,775 bases, 98.67% covered bases) contained 8.92% unknown bases and 7-nt gap when compared to the reference sequence of Wuhan-Hu-1, complete genome (GenBank MN908947.3). The resulting consensus sequence was deposited under the name "hCoV-19/Switzerland/BE-IFIK-8365-1009/2021" in GISAID with accession number, EPI_ISL_1916510, on 2021-05-05.

Phylogenetic analysis

All genomic sequences of lineages B.1.617.2 available for Switzerland (n=180; as of 2021-06-28) were retrieved from GISAID (https://www.gisaid.org/). The multiple sequence alignment generated with *MAFFT* (v7.407; --retree 2 --maxiterate 0 –adjustdirection) [4] was further subjected to maximum-likelihood phylogenetic reconstruction using *IQ-TREE 2* [5] using the TIM2+F+I model and 1000 ultrafast bootstrap replicates.

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Table S1. Phenotypic characterization of the OXA-484-producing *E. coli* strain L3452210II

Antibiotics	**MIC values (mg/L)** [a]
Piperacillin-tazobactam	>64/4 (R)
Ticarcillin-clavulanate	>128/2 (R)
Ampicillin	>16 (R)
Cefoxitin	>64 (NA)
Ceftriaxone	>128 (R)
Cefotaxime	>64 (R)
Cefotaxime-clavulanate	>64 (NA)
Ceftazidime	>128 (R)
Ceftazidime-clavulanate	>128 (NA)
Ceftazidime-avibactam [b]	1.5 (S)
Ceftolozane-tazobactam [b]	>128 (R)
Cefepime	4 (I)
Aztreonam	>16 (R)
Imipenem	<0.5 (S)
Meropenem	<1 (S)
Doripenem	<0.12 (S)
Ertapenem	1 (R)
Gentamicin	>16 (R)
Tobramycin	2 (S)
Amikacin	<4 (S)
Ciprofloxacin	>2 (R)
Levofloxacin	>8 (R)
Doxycycline	>16 (NA)
Minocycline	>16 (NA)
Tigecycline	<0.25 (S)
Trimethoprim/sulfamethoxazole	<0.5/9.5 (S)
Fosfomycin [b]	0.5 (S)
Colistin	<0.25 (S)
Polymyxin B	<0.25 (NA)

Note. R, resistant; I, susceptible, *increased exposure*; S, susceptible, *standard dosing regimen*; NA, not available

[a] MICs were obtained with microdilution Sensititre panels ESBF and GNX2F and interpreted according to the EUCAST 2021 criteria (version 11.0) for *Enterobacterales*.

[b] MIC obtained implementing the Etest

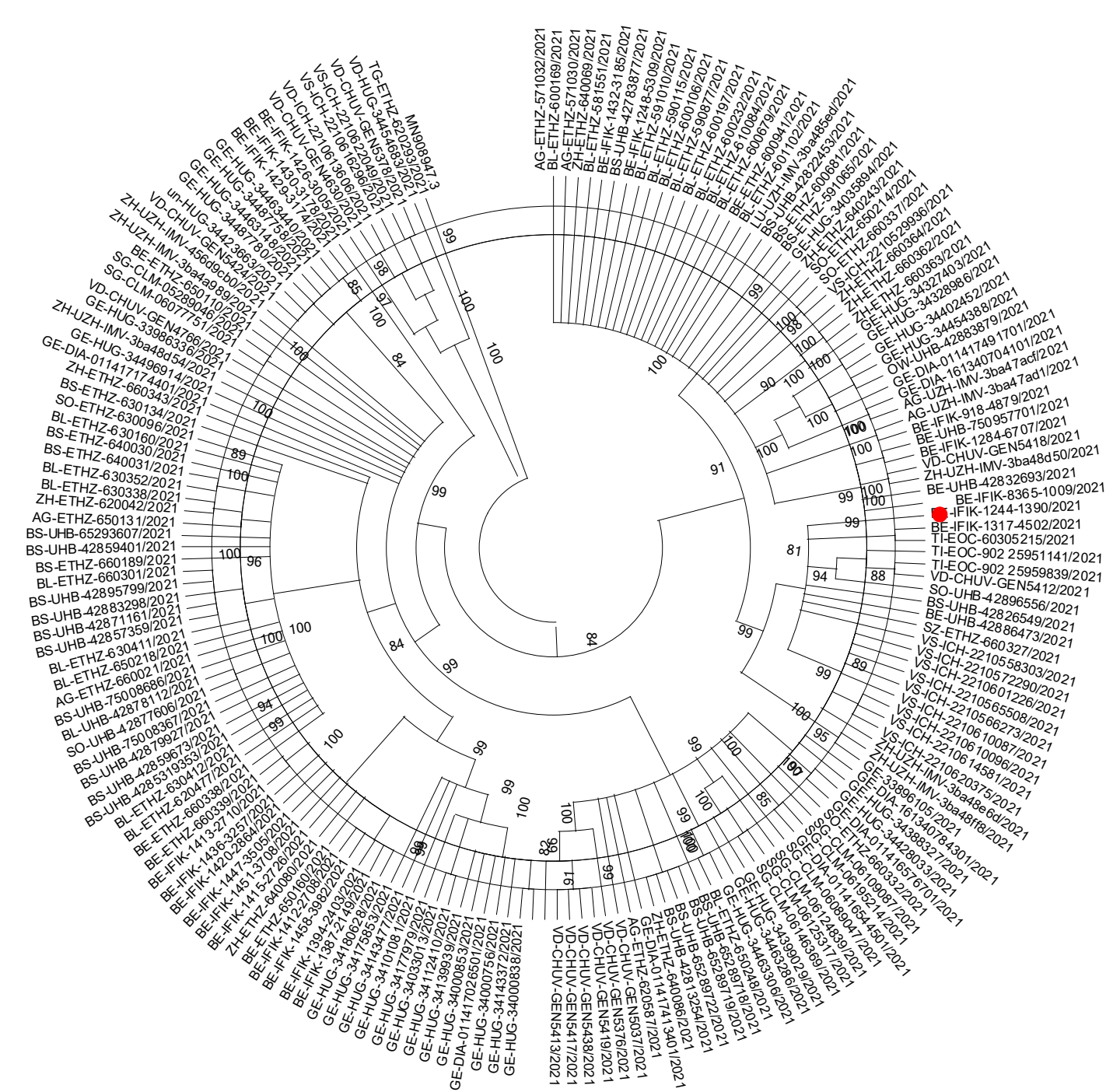

Figure S1. Phylogenetic analysis of the 180 Delta variant genomes registered in GISAID for Switzerland (as of 28.06.2021). The red circle indicates the SARS-CoV-2 isolate from the patient object of our analysis. Numbers in the tree indicate percentages of bootstrap replicates (out of 1000) supporting the nodes (only values >80% are depicted). Places of isolation (i.e., Swiss Canton) are indicated as BE, Bern; GE, Geneva; VD, Vaud; ZH, Zurich; SG, St. Gallen; BS, Basel-City; SO, Solothurn; BL, Basel-Land; AG, Aargau; TI, Ticino; OW, Obwald; VS, Valais; LU, Lucerne.

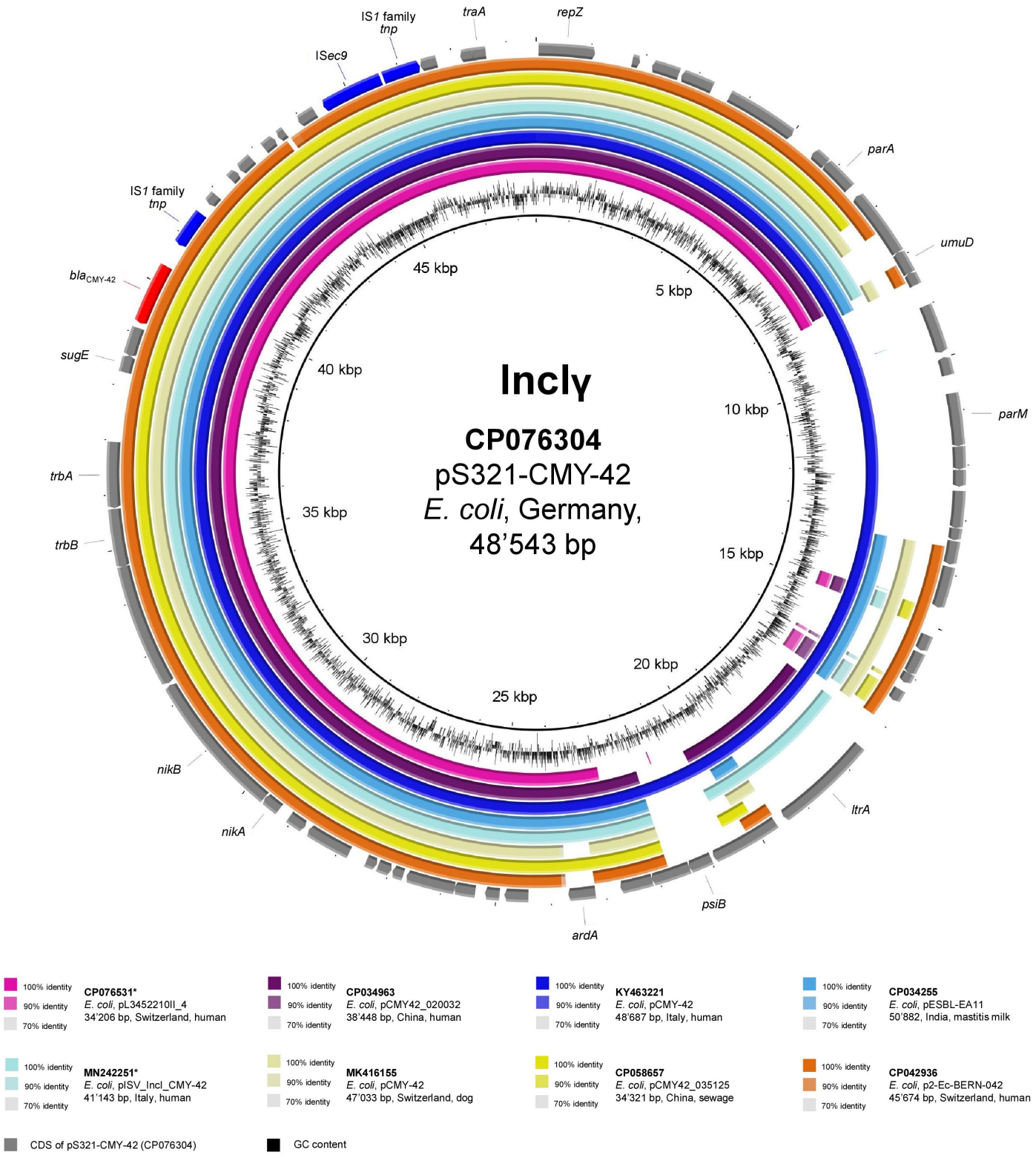

Figure S2. BLASTn Comparison of the plasmid pL3452210II_4 (GenBank: CP076531) against similar sequences. Plasmid sequences were selected based on high homology to pL3452210II_3 in a BLASTn search against the NCBI non-redundant nucleotide database (date of access: 09.06.2021). The plasmid pS321-CMY-42 (GenBank: CP076304) was selected as reference sequence. Rings were constructed using BRIG (BLAST Ring Image Constructor) v0.95. The colored rings represent similarities to the reference sequence. For each sequence we report GenBank accession, species of isolation, sequence name, plasmid size, country of origin, and source of isolation. The asterisk (*) indicates isolates that are associated with a previous stay in India. CDS are represented as arrows in the outermost circle. Mobile genetic elements are depicted in blue, antimicrobial resistance genes in red, and other CDS in grey.