

Table S1. Description of the 12 (out of 1362) samples discordant in their Nextstrain clade or Pango lineage assignment between EPISEQ SARS-COV-2 and the reference pipeline.

Dataset	Clade EPISEQ SARS-CoV-2	Clade Reference	Lineage EPISEQ SARS-CoV-2	Lineage Reference
ARTIC v3	20E (EU1)	20E (EU1)	B.1.177	B.1
ARTIC v4	20I (Alpha, V1)	20I (Alpha, V1)	B.1.1.7	Q.6 (alias of B.1.1.7.6)
ARTIC v4	21J (Delta)	21J (Delta)	AY.127 (alias of B.1.617.2.127)	AY.33 (alias of B.1.617.2.33)
ARTIC v4.1	21J (Delta)	21J (Delta)	AY.39 (alias of B.1.617.2.39)	AY.122 (alias of B.1.617.2.122)
ARTIC v4.1	21K (Omicron)	21K (Omicron)	BA.1	BA.1.1
ARTIC v4.1	21K (Omicron)	21K (Omicron)	BA.1	BA.1.1
ARTIC v4.1	21K (Omicron)	21K (Omicron)	BA.1	BA.1.1
ARTIC v4.1	21K (Omicron)	21K (Omicron)	BA.1	BA.1.1
ARTIC v4.1	21K (Omicron)	21K (Omicron)	BA.1	BA.1.1
ARTIC v4.1	21K (Omicron)	21K (Omicron)	BA.1	BA.1.1
ARTIC v4.1	21K (Omicron)	None	BA.1	BA.1
ARTIC v4.1	21K (Omicron)	None	BA.1.1	BA.1.1

Legend: Concordant classifications are highlighted in green; discordant classifications are highlighted in red. Lineage aliases were identified using cov-lineages.org (https://cov-lineages.org/lineage_list.html)

Table S2. Evaluation of SARS-CoV-2 sequencing results with the EPISEQ SARS-COV-2 pipeline (pre-omicron variants; n=21 samples)

[illegible]

Amino acid mutations in spike and other encoded genes are shown relative to the data generated using the Illumina platform with the ARTIC v4.1 kit (empty field: same mutations as in the Illumina/ARTIC v4.1 sequence; fields with "+" or "-" signify the presence or absence of the indicated mutations, respectively. NGS results with genome coverage < 95% are highlighted in grey.

Table S3. Evaluation of SARS-CoV-2 sequencing results with the EPISEQ SARS-COV-2 pipeline (omicron variants; n=19 samples)

sample	Ct	Coverage				Nextclade				Pango				Spike mutation				ONT				Other mutations						ONT			
		Illumina		ONT		Illumina		ONT		Illumina		ONT										Illumina		ONT				Illumina		ONT	
		artC_v4.1	vs2	artC_v4.1	vs2	artC_v4.1	vs2	artC_v4.1	vs2	artC_v4.1	vs2	artC_v4.1	vs2									artC_v4.1	vs2	artC_v4.1	vs2			artC_v4.1	vs2	artC_v4.1	vs2
sample22	16.86	99.8	92.1	99.5	69.1	21K	21K	21K	21K	BA.1	BA.1	BA.1	BA.1	no data	A67V, H69, V70, T9S1, G142-, V143-, Y144-, Y145D, N211-, L2121, G339D, S371L, S373P, S375F, K417N, N440K, G446S, S477N, T478K, E484A, Q493R, G496S, Q498R, N501Y, Y505H, T547K, D614G, H655Y, N679K, P681H, N764K, D796Y, N856K, Q954H, N969K, 981F]	-N211-, -L2121-, -N440K	N211-, -L2121-, -N440K, -G446S, N764K, -D796Y		E-T9I, M-Q19E, M-A63T, N-P13L, N-E3I, N-R32, N-S33, N-R203K, N-G204R, ORF1a-K856R, ORF1a-S2083, ORF1a-L2084I, ORF1a-A2710T, ORF1a-T3255I, ORF1a-P3395H, ORF1a-L3674, ORF1a-S3675-, ORF1a-G3676-, ORF1a-I3758V, ORF1b-P314L, ORF1b-I1566V, ORF9b-P105, ORF9b-E27-, ORF9b-N28-, ORF9b-A29-	-ORF1a-L3674-, -ORF1a-S3675-, -ORF1a-G3676-, -ORF1b-I1566V	E-T9I, -ORF1a-K856R, -ORF1a-A2710T, -ORF1a-L3674-, -ORF1a-S3675-, -ORF1a-G3676-, -ORF1b-I1566V										
sample23	15.25	99.9	99.8	99.5	99.4	21K	21K	21K	21K	BA.1	BA.1	BA.1	BA.1	A67V, H69, V70, T9S1, G142-, V143-, Y144-, Y145D, N211-, L2121, G339D, S371L, S373P, S375F, K417N, N440K, G446S, S477N, T478K, E484A, Q493R, G496S, Q498R, N501Y, Y505H, T547K, D614G, H655Y, N679K, P681H, N764K, D796Y, N856K, Q954H, N969K, 981F]				E-T9I, M-Q19E, M-A63T, N-P13L, N-E3I, N-R32, N-S33, N-R203K, N-G204R, ORF1a-K856R, ORF1a-T1822I, ORF1a-S2083, ORF1a-L2084I, ORF1a-A2710T, ORF1a-T3255I, ORF1a-P3395H, ORF1a-L3674-, ORF1a-S3675-, ORF1a-G3676-, ORF1a-I3758V, ORF1b-P314L, ORF1b-I1566V, ORF9b-P105, ORF9b-E27-, ORF9b-N28-, ORF9b-A29-													
sample24	17.31	99.8	99.6	99.5	99.4	21K	21K	21K	21K	BA.1	BA.1	BA.1	BA.1	A67V, H69, V70, T9S1, G142-, V143-, Y144-, Y145D, N211-, L2121, G339D, S371L, S373P, S375F, K417N, N440K, G446S, S477N, T478K, E484A, Q493R, G496S, Q498R, N501Y, Y505H, T547K, D614G, H655Y, N679K, P681H, N764K, D796Y, N856K, Q954H, N969K, 981F]				[mutations [T9, D3G, Q19E, A63T, P13L, E3I, R32, S33, R203K, G204R, K856R, P1803S, V1887I, S2083-, L2084I, A2710T, M2796T, T3255I, P3395H, L3674-, S3675-, G3676-, I3758V, P314I, I1566V, P105, E27-, N28-, A29-] gene [E, M, M, N,													