

Supplementary Table S1. Rhinovirus genotypes

Isolate designation	Diagnosis	RV Type	Segment	Genotype	Div* <7%	Segment	Genotype	Div* <10%
01BG2018	ARI	RV A	5'UTR	A47	1.67%	partial	A47	1.15%
02BG2018	ILI	RV A	5'UTR	A21	1.26%	-	-	-
03BG2018	ARI	RV B	5'UTR	B4	1.69%	-	-	-
04BG2018	ILI	RV A	5'UTR	A16	2.49%	-	-	-
05BG2018	ILI	RV A	5'UTR	A57	2.08%	-	-	-
06BG2018	Other	RV A	5'UTR	A94	2.89%	VP4/VP2 partial	A94	0.76%
11BG2018	ARI/LRTI/Bronchiolitis	RV A	5'UTR	A68	2.05%	VP4/VP2 partial	A68	4.55%
12BG2018	ARI/LRTI/Bronchiolitis	RV C	5'UTR	C4	1.65%	-	-	-
13BG2019	ARI	RV C	5'UTR	C42	5%	VP4/VP2 partial	C42	6.92%
14BG2019	ARI/LRTI/Bronchiolitis	RV A	5'UTR	A102	0.82%	VP4/VP2 partial	A102	3.68%
15BG2019	ARI/LRTI/Bronchiolitis	RV A	5'UTR	A43	4.53%	-	-	-
16BG2019	ARI/LRTI/Bronchiolitis	RV C	5'UTR	C3	1.94%	VP4/VP2 partial	C3	3.43%
17BG2019	ILI	RV A	5'UTR	A71	8%↑	VP4/VP2 partial	A71	8.53%
18BG2019	Other	RV A	5'UTR	A105	2.48%	VP4/VP2 partial	A105	2.81%
21BG2019	ARI/LRTI/Bronchiolitis	RV C	5'UTR	C6	2.86%	-	-	-
22BG2019	ARI/LRTI/Bronchiolitis	RV A	5'UTR	A101	4.92%	VP4/VP2 partial	A101	8.97%
23BG2019	ARI/LRTI/Bronchiolitis	RV C	5'UTR	C12	5.74%	VP4/VP2 partial	C12	4.35%
24BG2019	ARI/LRTI/Bronchiolitis	RV A	5'UTR	A49	5.86%	VP4/VP2 partial	A21	1.77%
26BG2019	ARI/URI/Laringitis	RV B	5'UTR	B6	1.69%	VP4/VP2 partial	B6	0.69%
27BG2019	ARD	RV B	5'UTR	B3	2.44%	VP4/VP2 partial	B3	1.37%
30BG2019	ARI/LRTI/Croup	RV C	5'UTR	C32	8.92%↑	VP4/VP2 partial	C32	7.72%
31BG2019	ARI/LRTI/Bronchiolitis	RV C	5'UTR	C8	3.66%	VP4/VP2 partial	C8	6.55%
32BG2019	ARI/LRTI/Bronchiolitis	RV A	5'UTR	A78	3.27%	VP4/VP2 partial	A78	3.57%
35BG2019	Other	RV A	5'UTR	A105	2.44%	VP4/VP2 partial	A105	3%
36BG2019	ARI/LRTI/Bronchiolitis	RV C	-	-		VP4/VP2 partial	C31	0.7%
38BG2019	ARI/LRTI/Croup	RV C	5'UTR	C3	1.93%	VP4/VP2 partial	C3	2.89%
39BG2019	ARI	RV A	5'UTR	A49	2.09%	VP4/VP2 partial	A49	1.43%

44BG2021	ILI/ARI-possible COVID19	RV B	5'UTR	B6	3.81%	VP4/VP2 partial	B6	4.55%
45BG2021	ILI/ARI-possible COVID19	RV B	5'UTR	B91	4.17%	VP4/VP2 partial	B91	2.08%
46BG2021	ILI/ARI-possible COVID19	RV C	5'UTR	C1	5.53%	-	-	-
47BG2021	ILI/ARI-possible COVID19	RV C	5'UTR	C3	1.96%	VP4/VP2 partial	C3	4.43%
48BG2021	ILI/ARI-possible COVID19	RV C	5'UTR	C24	1.65%	VP4/VP2 partial	C24	2.91%
49BG2021	ILI/ARI-possible COVID19	RV C	5'UTR	C24	1.99%	VP4/VP2 partial	C24	1.86%
50BG2021	ILI/ARI-possible COVID19	RV A	5'UTR	A12	2.94%	VP4/VP2 partial	A12	2.85%
51BG2021	ILI/ARI-possible COVID19	RV C	5'UTR	C11	6.53%	-	-	-
52BG2021	ILI/ARI-possible COVID19	RV C	5'UTR	C23	5.39%	VP4/VP2 partial	C23	4.68%
53BG2021	ILI/ARI-possible COVID19	RV C	5'UTR	C7	4.49%	VP4/VP2 partial	C21	0.98%
54BG2021	ILI/ARI-possible COVID19	RV C	5'UTR	C22	1.99%	VP4/VP2 partial	C22	2.88%
55BG2021	ILI/ARI-possible COVID19	RV C	5'UTR	C40	3.7%	-	-	-
56BG2021	ILI/ARI-possible COVID19	RV C	5'UTR	C7	5.41%	VP4/VP2 partial	C21	0.98%
57BG2021	ILI/ARI-possible COVID19	RV A	5'UTR	A31	1.25%	VP4/VP2 partial	A31	0.71%
58BG2021	ILI/ARI-possible COVID19	RV C	5'UTR	C23	1.68%	VP4/VP2 partial	C23	3.6%
59BG2021	ILI/ARI-possible COVID19	RV A	5'UTR	A80	2.9%	VP4/VP2 partial	A80	7.72%
60BG2021	ILI/ARI-possible COVID19	RV C	5'UTR	C1	2.35%	VP4/VP2 partial	C1	0.36%
61BG2021	ILI/ARI-possible COVID19	RV C	5'UTR	C	-	VP4/VP2 partial	C25	6.99%
62BG2021	ILI/ARI-possible COVID19	RV A	5'UTR	A80	2.5%	VP4/VP2 partial	A80	7.02%
63BG2021	ILI/ARI-possible COVID19	RV C	5'UTR	C5	2.07%	VP4/VP2 partial	C5	6.09%
64BG2021	ARI	RV C	5'UTR	C20	6.25%	VP4/VP2 partial	C29	2.44%

* Divergence from the closest referent strain with complete genome, based on BLAST score result; Isolates for which 5'UTR region alone is insufficient for genotyping are marked in yellow; Isolates for which comparison of phylogenetic grouping based on the 5'UTR and VP4/VP2 regions showed a different grouping are marked in orange.