

**Supplementary Table S1.** Primers of amplification and sequencing for the complete genomes

Primer	Sequence (5'→3')	Nucleotide position	Orientation
BOAS <sup>#</sup> *	GGTGCTCACTAGGAGGTCYCT RTTRTARTCYTCCCA GNAYRWACAT	3,505–3,484	Reverse
BOS <sup>#</sup> *	GGYTAYATNCANTGYTGGTAYCARAC NGARAYNGG	2,324–2,329	Forward
E201F <sup>#</sup> *	TTAAACAGCCTGTGGGTTG	1–20	Forward
B12R	TTAGTGGGCCGTGAACTAAT	2,519–2,500	Reverse
B11r	CCTGAGCTCCCATTTCCG	751–735	Reverse
B11f	CAGTGACAAACAGAGCTA	636–653	Forward
B12f	CCAGGTAAGTTCACTGAA	886–903	Forward
B13F	AACCCAAGCACGTGAAGGCC	3,157–3,176	Forward
EV8R <sup>#</sup> *	CACCGAATGCGGAGAATTTA	7,444–7,426	Reverse
B14f	GGCTGGAGGACGATGCAAT	3,707–3,726	Forward
B14f1	CTGTTCTCAATGTGCAGTAC	4,255–4,275	Reverse
B14f2	TCACTCAAGGCATTAGTG	3,453–3,471	Forward
B15f	AGATGTTYAGAGARTACAAC	4,955–4,974	Forward
B15f2	AGGCTAAGGTTCAAGGCC	5,332–5,349	Forward
B16f	CGCATGTTGATGTACAAC	5,749–5,766	Forward
B17f*	AAGGGGTATGGTCTGAT ACCTTCCTTAAAGATACTTTA	6939–6955	Forward

**Supplementary Table S2.** The VP1 nucleotide and amino acid homology comparison between CVB1 genotypes or subgenotypes

Genotype	A	B	C	D1	D2	E1	E2
A		80.5–80.7	80.7–81.7	78.4–79.0	78.1–79.0	81.3–80.3	79.0–80.3
B	96.0–96.4		82.1–83.7	83.3–83.9	83.8–84.1	82.5–82.9	81.3–83.1
C	95.3–96.4	96.0–97.8		84.3–85.0	83.2–86.6	83.3–84.1	80.7–82.9
D1	92.8–95.7	97.5–98.2	96.4–97.5		88.4–90.0	83.7–85.6	81.1–83.0
D2	96.0–97.1	97.5–98.2	97.1–98.2	97.8–98.1		83.7–83.9	80.0–84.1
E1	95.3–95.7	95.7–96.0	96.0–98.6	96.8–97.1	96.8–97.1		85.4–87.1
E2	92.8–95.0	93.2–96.0	93.9–96.0	95.0–97.1	94.2–96.4	96.0–98.6	

**Note.** the data in the upper right corner was for nucleotide homology analysis and the data in the lower left corner was for amino acid homology analysis.

**Supplementary Table S3.** Top three sequences with the highest nucleotide sequence similarities between all sequenced individual genomic regions of strain 46V3/YN/CHN/2019 and enteroviruses in the GenBank in the BLAST online tool

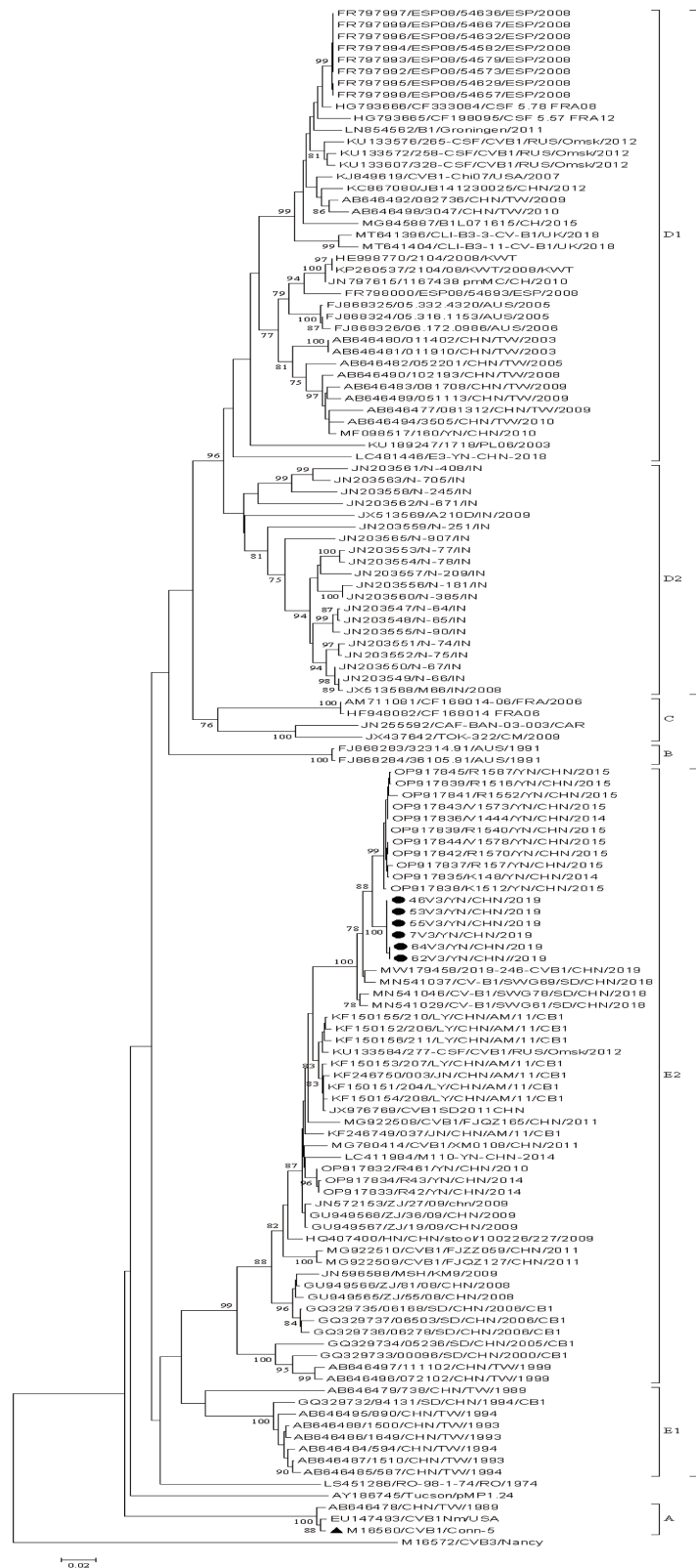
Genomic region	KM46		
	strain	%Nucleotide identity	Accession number
5'UTR	CVB1SD2011CHN	96.84	JX976769
	CVB1/XM0108	95.60	MG780414
	CVB1/MSH/KM9/2009	95.06	JN596588
	CVB1/SWG78/SD/CHN/2018	95.65	KU574629
VP4	E30/XM	95.17	MF177222
	CVB1/XM0108	95.17	MG780414

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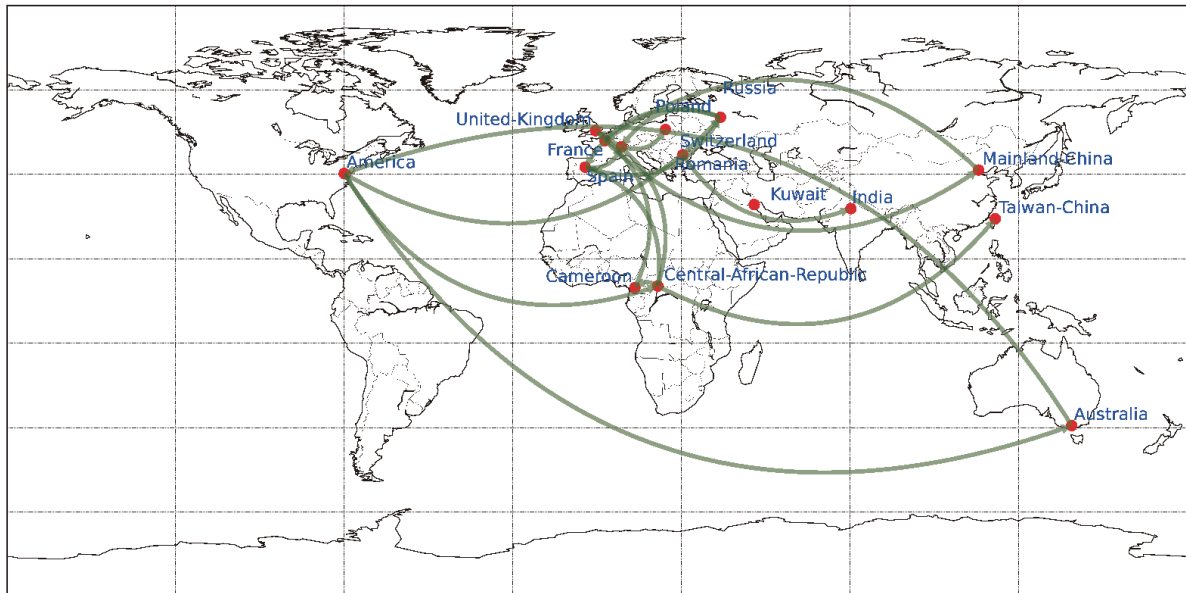
Genomic		KM46		
region	strain	%Nucleotide identity	Accession number	
	CVB1/SWG69/SD/CHN/2018	98.10	MN541037	
VP2	CVB1/SWG61/SD/CHN/2018	97.97	MN541029	
	CVB1/SWG78/SD/CHN/2018	97.72	MN541046	
	CVB1/SWG61/SD/CHN/2018	98.18	MN541029	
VP3	CVB1/SWG78/SD/CHN/2018	97.90	MN541046	
	CVB1/SWG69/SD/CHN/2018	97.76	MN541037	
	CVB1/SWG69/SD/CHN/2018	97.84	MN541037	
VP1	CVB1/2019-246-CVB1	97.72	MW179458	
	CVB1/SWG78/SD/CHN/2018	97.48	MN541046	
	CVB1/SWG61/SD/CHN/2018	96.89	MN541029	
2A	CVB1/SWG78/SD/CHN/2018	96.67	MN541046	
	CVB1SD2011CHN	94.22	JX976769	
	CVB1/SWG78/SD/CHN/2018	98.65	KU574629	
2B	CVB1/SWG61/SD/CHN/2018	98.32	MN541029	
	CVB1SD2011CHN	96.96	JX976769	
	CVB1SD2011CHN	94.83	JX976769	
2C	CVB1/XM0108	91.39	MG780414	
	CVA9 /VEN/2018-23122	90.98	MK652143	
	CVB1SD2011CHN	94.76	JX976769	
3A	CVB5/B504	94.35	MW015048	
	CVA9 /VEN/2018-23122	94.01	MK652143	
	CVB1SD2011CHN	95.45	JX976769	
3B	CVB4/B405	95.45	MW015040	
	CVB4/B404	95.45	MW015039	
	CVB1SD2011CHN	96.54	JX976769	
3C	CVB4/GX/10	94.35	JX308222	
	E1/precursor	94.17	JQ979292	
	CVB1SD2011CHN	95.17	JX976769	
3D	CVB4/B404	92.29	MW015039	
	E6/E6SD11CHN	92.21	JX976771	
	E6/P735/2013/China	93.98	KP289439	
3'UTR	CVB5/Chzj-1	93.90	KF311743	
	CVA9/CV-A9/P56/2013	92.93	KP289434	
	CVB1/SWG61/SD/CHN/2018	97.56	MN541029	
P1	CVB1/SWG78/SD/CHN/2018	97.52	MN541046	
	CVB1/SWG69/SD/CHN/2018	97.21	MN541037	
	CVB1SD2011CHN	94.98	JX976769	
P2	CVB1/XM0108	91.98	MG780414	
	A9 /VEN/2018-23122	87.68	MK652143	

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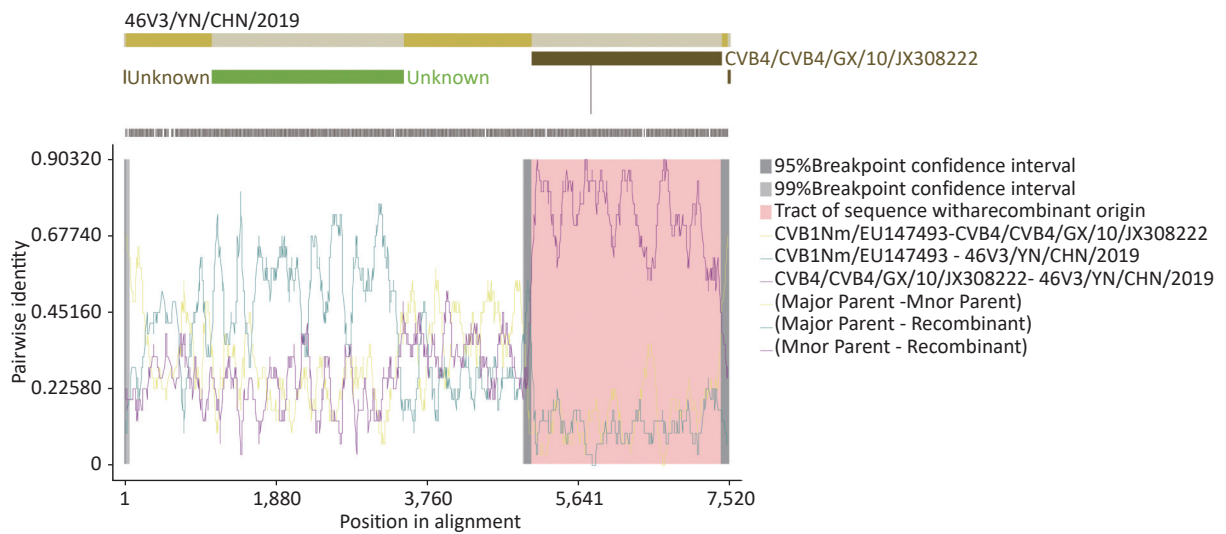
Genomic		KM46		
region	strain	%Nucleotide identity	Accession number	
P3	CVB1SD2011CHN	95.46	JX976769	
	CVB5/B504	92.60	MW015048	
	E6/E6SD11CHN	92.46	JX976771	
genome	CVB1SD2011CHN	95.29	JX976769	
	CVB1/XM0108	90.63	MG780414	
	CVB1/MSH/KM9/2009	86.96	JN596588	



Supplementary Figure S1. Phylogenetic tree based on complete VP1 sequences (834 bp) of all CVB1 isolates available in GenBank. ▲Strains isolated in this study. ▲Prototype strain.



**Supplementary Figure S2.** The spatial transmission of CVB1 worldwide. The green arrows indicate transmission paths with BF > 5.



**Supplementary Figure S3.** RDP4 analysis of strain 46V3/YN/CHN/2019 with closely related strains. Recombination analysis was performed by seven algorithms: RDP, GENECONV, BootScan, Maxchi, Chimaera, SiScan, and 3Seq.