Supplementary Table S1. Nucleotide sequences similarities and their deduced amino-acid sequences between 0316/TJ/CHN/2019 and other CVB4 strains

Region	CVB4 prototype JVB		Strains from the mainland of China	
	Nucleotide (%)	Amino acid (%)	Nucleotide (%)	Amino acid (%)
5'-UTR	82.1	–	81.4–82.7	–
VP4	82.3	100.0	73.9–77.5	97.1–98.5
VP2	77.5	97.3	78.0–79.4	96.9–98.1
VP3	79.9	98.3	75.8–77.7	97.9–98.7
VP1	79.5	97.1	76.2–77.7	96.0–97.1
2A	70.4	90.0	68.8–70.2	88.5–89.2
2B	75.2	96.9	70.6–73.8	96.9–98.0
2C	76.1	98.2	77.2–78.2	97.2–99.1
3A	69.9	89.3	74.3–77.1	91.8–97.7
3B	68.0	95.3	70.5–90.1	85.3–95.3
3C	74.9	94.4	71.8–80.4	95.5–98.9
3D	76.7	96.7	76.5–83.5	95.3–98.9
3'-UTR	85.3	–	83.7–91.7	–
CDS	76.7	96.5	76.0–78.5	96.0–97.4

Supplementary Table S2. Amino acid substitutions in the 0316/TJ/CHN/2019 capsid protein versus the CVB4 prototype JVB (X05690)

Proteins	Size (aa)	Substitutions
VP4	69	None
VP2	261	A137V, A142T[a], S154Q[a], A160T[a], K163E, Y187F, S249N
VP3	238	I55L, M63K[a], F213L[a], T234S[a]
VP1	284	K5D, Y76F[a], S263N, V271I, A273T, S277N[a], I279V[a], Y284C[a]

Note. [a]Substitutions first detected in strains from the mainland of China.