Supplementary Table S1. Primers for amplification and sequencing of VP1 of enterovirus

	Primer	Sequence (5'→3')	Position	Species
1[1]	222	CICCIGGIGGIAYRWACAT	2969–2951	
	224	GCIATGYTIGGIACICAYRT	1977–1996	all
	AN89	CCAGCACTGACAGCAGYNGARAYNGG	2602–2627	
	AN88	TACTGGACCACCTGGNGGNAYRWACAT	2977–2951	
2[2]	A-OS	CCNTGGATHAGYAACCANCAYT	2268–2291	
	A-OAS	GGRTANCCRTCRTARAACCAYTG	3109–3086	EV-A
	A-IS	TNASNATYTGGTAYCARACANAYT	2332–2356	
	A-IAS	GANGGRTTNGTNGKNGTYTGCCA	3016–2993	
3[2]	B-OS	GGYTAYATNCANTGYTGGTAYCARAC	2324–2351	
	B-OAS	GGTGCTCACTAGGAGGTCYCTRTTRTARTCYTCCCA	3505–3469	EV-B
	B-IS	CTTGTGCTTTGTGTCGGCRTGYAAYGAYTTYTCWG	2392–2428	
	B-IAS	TCYTCCCACACRCAVTTYTGCCARTC	3477–3451	
4[3]	EntAF	TNCARGCWGCNGARACNGG	2571–2589	
	EntARo	ANGGRTTNGTNGMWGTYTGCCA	2957–2936	EV-A
	EntARi	GGNGGNACRWACATRTAYTG	2898–2879	
5[3]	EntBF	GCNGYNGARACNGGNCACAC	2610–2630	
	EntBRo	CTNGGRTTNGTNGANGWYTGCC	3006–2986	EV-B
	EntBRi	CCNCCNGGBGGNAYRTACAT	2970–2951	

Note. 1. Nix WA, Oberste MS, Pallansch MA. Sensitive, seminested PCR amplification of VP1 sequences for direct identification of all enterovirus serotypes from original clinical specimens. J Clin Microbiol, 2006; 44, 2698–704. 2. Leitch EC, Harvala H, Robertson I, et al. Direct identification of human enterovirus serotypes in cerebrospinal fluid by amplification and sequencing of the VP1 region. J Clin Virol, 2009; 44, 119–24. 3. Iturriza-Gomara M, Megson B, Gray J. Molecular detection and characterization of human enteroviruses directly from clinical samples using RT-PCR and DNA sequencing. J Med Virol, 2006; 78, 243–53.

Supplementary Table S2. Primers for amplification and sequencing of CVA1 complete genome Sequence

Primer	Sequence (5'→3')	Position	Orientation
CA1VP1f	TTACTTAAAGACTCCCCCCA	2400–2420	Forward
CA1VP1r	AATTGCAGATCTTGTAGCCCG	3391–3371	Reverse
CA11F	TTAAAACAAGCCCTTGGGTG	1–20	Forward
CA12R	GCACCTCTTTTGAGTGGGTT	2552–2533	Reverse
CA13F	AAACCAAAACACATCCGTGC	3212–3231	Forward
CA18R	CCCTCCGAATTAAAAGAAAA	7396–7377	Reverse
CA11R	AACCCCCAATTGTTATGTTTG	1596–1576	Reverse
CA11r	ACCAGCAGCCACATTCTGATT	772–752	Reverse
CA14F	TGCAATATGGTTGGCATTCC	4037–4056	Forward
CA15F	ATTGCCACAAACCAGCAAAC	4884–4903	Forward
CA17R	TGACCAAAAGCCTGTCTCAT	6516–6497	Reverse
CA18f	TGAATCAATCAGGTGGACCAA	7132–7152	Forward

Supplementary Table S3. The strains with the highest similarity of the nucleotide sequences in all the genomic regions of the 1222/YN/CHN/2010 strain using BLAST

Genomic region	1222/YN/CHN/2010		
	Serotype/strain	%Nucleotide identity	GenBank accession number
5'UTR	CVA1/V18A	95.5	MG571859
VP4	CVA1/B1205	96.6	KY079224
VP2	CVA1/ V18A	94.0	MG571859
VP3	CVA1/ V18A	95.1	MG571859
VP1	CVA1/V18A	92.4	MG571859
2A	CVA1/V18A	97.3	MG571859
2B	CVA1/BBD34	92.1	KC785529
2C	CVA1/KS-ZPH01F/XJ/CHN/2011	91.5	JX174177
3A	CVA1/KS-ZPH01F/XJ/CHN/2011	96.2	JX174177
3B	CVA19/V15C	97.0	MG571855
3C	CVA19/V15C	93.6	MG571855
3D	CVA22/ban99-10427	93.0	DQ995647
3'UTR	CVA1/KS-ZPH01F/XJ/CHN/2011	100.0	JX174177
Genome	CVA1/V18A	91.8	MG571859