



Figure S1. (a) Similarity plot and (b) bootscanning analysis of Sichuan type 2 cVDPV genomes, using a sliding window of 200 nt moving in 20-nt steps. The Sichuan cVDPV strain was used as a query sequence and it is indicated in the upper left corner of the image.

	VP2						VP3			VP1		
	NAg3b		NAg2		NAg2		NAg3a	NAg3a	NAg3b	NAg1	NAg2	NAg3a
	71	163	268	54	70	88	222	287				
Sabin 2	WRK	DTNATNPARN	PRT	PLNLTSQR	VELSDTAHS	DT	AIIEVDNDAPT	KRASRLFS	STEGD	KDGLT		
CHN15261
CHN15284
CHN16003
CHN16017
CHN16019c
EGY88-074
EGY93-034
MAD004
MAD029
JIS06-01-NIE
KBS08-03-NIE
BAS05-01-NIE
NIS11-01-NIE
MEF-1

Figure S2. Alignment of amino acid residues of neutralizing antigenic (NAg) sites 1 (*VP1*: 88–106), 2 (*VP2*: 163–172; *VP2*: 268–270; *VP1*: 222–227), 3a (*VP3*: 54–61; *VP3*: 70–74; *VP1*: 287–292), and 3b (*VP2*: 71–73; *VP3*: 75–80) for Sabin 2, Sichuan cVDPV strains, Egypt type 2 cVDPV strains (GenBank numbers: AF448782 and AF448783), Madagascar type 2 cVDPV strains (GenBank numbers: AM084223 and AM084225), Spain type 2 iVDPV strains (GenBank numbers: EU566941 and EU566950), and the prototype wild type 2 poliovirus strain, MEF-1/EGY/1942.