Supplemental Table 1. Characteristics of BoNT scFv. Clone name, serotype specificity, domain epitope, V_H CDR3 sequence, and equilibrium dissociation constant (K_D) for BoNT/A, BoNT/B, and BoNT/E are shown. K_D measured on yeast displayed scFv. L_C = toxin light chain; H_N = toxin translocation domain; H_C = toxin binding domain; NB = no binding.

mAb name	Serotype specifcity	Epitope	V_H CDR3 Sequence	BoNT K_D by FACS (x 10^{-9} M^{-1})		
				BoNT/A	BoNT/B	BoNT/E
5A20	BoNT/A	LC	EASFGWSYLGHDDAFDI	0.40	NB	NB
ING2	BoNT/A	LC	DPYYYSYMDV	0.24	NB	NB
4A1	BoNT/A	H_N	DPGWIYSDTSAAGWFDP	7.4	NB	NB
ING1	BoNT/A	LC-H_N	RTKYCSSLSCFAGFDS	1.14	NB	NB
3D12	BoNT/A	H_C	EPDWLLWGDRGALDV	3.3	NB	NB
C25	BoNT/A	H_C	YRYDDAMDY	1.5	NB	NB
S25	BoNT/A	H_C	GLYNGFWYFDV	31.7	NB	NB
4B6	BoNT/B	LC	HDSRYKYFYFGMDV	NB	2.7	NB
4B7	BoNT/B	LC	MSGSRSYSQYYFDS	NB	29.4	NB
1B10	BoNT/B	LC	DLTRFHDTTFGVFEM	NB	11.2	NB
4B19	BoNT/B	LC	EWTQLWSPYDY	NB	6.45	NB
1B22	BoNT/B	LC	TAFYYENTGPIRCYLDF	NB	0.52	NB
2B23	BoNT/B	LC	ALVGRYDISTGYYRPVMDS	NB	0.08	NB
2B24	BoNT/B	LC	DGPMAAIPFYYFDF	NB	0.79	NB
2B25	BoNT/B	LC	GVPIYDSSGTYRGTYFDY	NB	0.95	NB
2B27	BoNT/B	LC	RRLLGPSPYYFDY	NB	1.9	NB
2B29	BoNT/B	LC	GNPQYDTSGSYTGLYFDF	NB	1.11	NB
4B3	BoNT/B	H_N	DILYYHDSSDYWGRGHFYYMDV	NB	26.7	NB
1B11	BoNT/B	H_N	DRYPIDCSGGSCFSYGMDV	NB	2.6	NB
1B18	BoNT/B	H_N	LEWGGRNGWVSP	6.2	7.3	NB

4B1	BoNT/B	H_C	DKRTYEYNWNSLWF	NB	1.08	NB
4B5	BoNT/B	H_C	MRGYSSWHYSYYYVMDV	NB	59.6	NB
1B12	BoNT/B	H_C	DRSHYGDYVGYLDY	NB	1.17	NB
1B14	BoNT/B	H_C	SSIVGAPYGMDV	NB	0.98	NB
2B30	BoNT/B	H_C	DVSEYGDYVGHFDY	NB	0.37	NB
3E1	BoNT/E	LC	DQGEYTVGMLLYYAMDV	NB	NB	6.2
4E16	BoNT/E	LC	HTSGWSGGAFDI	NB	NB	0.2
3E3	BoNT/E	LC	DEMVHGILVYYGMDV	NB	NB	7.8
3E4	BoNT/E	LC	DSYHSRLAAFDI	NB	NB	4.7
3E5	BoNT/E	LC	VASRYHDVLTDGFDI	NB	NB	4.9
4E11	BoNT/E	LC	GPPGRPNDAFDI	NB	NB	14.4
3E2	BoNT/E	H_N	DQGEYTVGMLLYYAMDV	NB	NB	9.3
3E6	BoNT/E	H_N	ARLCTSTSCYWTFDP	NB	NB	15.4
4E17	BoNT/E	H_N	LQWGGYNGWLSP	1.34	30	14.1
4E13	BoNT/E	H_C	GLSKADLFGMDV	NB	NB	10.0