Supplementary Materials: Purification and Characterization of Recombinant Botulinum Neurotoxin Serotype FA, Also Known as Serotype H

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Supplemental Figure 1

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rBoNT-FA(0)-his	MPVVINSFNYDDPVNDNTIIYIRPPYYETSNTYFKAFQIMDNVWIIPERYRLGIDPSLFNPPVSLKAGSD	70
mrBoNT-FA(0)-his	MPVVINSFNYDDPVNDNTIIYIRPPYYETSNTYFKAFQIMDNVWIIPERYRLGIDPSLFNPPVSLKAGSD	70
mrBoNT-FA-his	MPVVINSFNYDDPVNDNTIIYIRPPYYETSNTYFKAFQIMDNVWIIPERYRLGIDPSLFNPPVSLKAGSD	70
rBoNT-FA(0)-his	GYFDPNYLSTNTEKNKYLQIMIKLFKRINSKPAGQILLEEIKNAIPYLGNSYTQEEQFTTNNRTVSFNVK	140
mrBoNT-FA(0)-his	GYFDPNYLSTNTEKNKYLQIMIKLFKRINSKPAGQILLEEIKNAIPYLGNSYTQEEQFTTNNRTVSFNVK	140
mrBoNT-FA-his	GYFDPNYLSTNTEKNKYLQIMIKLFKRINSKPAGQILLEEIKNAIPYLGNSYTQEEQFTTNNRTVSFNVK	140
rBoNT-FA(0)-his mrBoNT-FA(0)-his mrBoNT-FA-his	$ LANGNIVQQMANLIIWGPGPDLTTNKTGGIIYSPYQSMEATPYKDGFGSIMTVEFSPEYATAFNDISIAS \\ LANGNIVQQMANLIIWGPGPDLTTNKTGGIIYSPYQSMEATPYKDGFGSIMTVEFSPEYATAFNDISIAS \\ LANGNIVQQMANLIIWGPGPDLTTNKTGGIIYSPYQSMEATPYKDGFGSIMTVEFSPEYATAFNDISIAS $	210 210 210
rBoNT-FA(0)-his	HSPSLFIKDPALILMHQLIYVLHGLYGTYITEYKITPNVVQSYMKVTKPITSAEFLTFGGRDRNIVPQSI	280
mrBoNT-FA(0)-his	HSPSLFIKDPALILMHQLIYVLHGLYGTYITEYKITPNVVQSYMKVTKPITSAEFLTFGGRDRNIVPQSI	280
mrBoNT-FA-his	HSPSLFIKDPALILMHELIHVLHGLYGTYITEYKITPNVVQSYMKVTKPITSAEFLTFGGRDRNIVPQSI	280
rBoNT-FA(0)-his	QSQLYNKVLSDYKRIASRLNKVNTATALINIDEFKNLYEWKYQFAKDSNGVYSVDLNKFEQLYKKIYSFT	350
mrBoNT-FA(0)-his	QSQLYNKVLSDYKRIASRLNKVNTATALINIDEFKNLYEWKYQFAKDSNGVYSVDLNKFEQLYKKIYSFT	350
mrBoNT-FA-his	QSQLYNKVLSDYKRIASRLNKVNTATALINIDEFKNLYEWKYQFAKDSNGVYSVDLNKFEQLYKKIYSFT	350
rBoNT-FA(0)-his	EFNLAYEFKIKTRLGYLAENFGPFYLPNLLDDSIYTEVDGFNIGALSINYQGQNIGSDINSIKKLQGQGV	420
mrBoNT-FA(0)-his	EFNLAYEFKIKTRLGYLAENFGPFYLPNLLDDSIYTEVDGFNIGALSINYQGQNIGSDINSIKKLQGQGV	420
mrBoNT-FA-his	EFNLAYEFKIKTRLGYLAENFGPFYLPNLLDDSIYTEVDGFNIGALSINYQGQNIGSDINSIKKLQGQGV	420
rBoNT-FA(0)-his	VSRVVRLCSNSN-TKNSL:ITVNNRDLFFIASQESYGENTINTYKEIDDTTTLDPSFEDILDKVI	484
mrBoNT-FA(0)-his	VSRVVRLCKSVIPRKGTKAPPRL:ITVNNRDLFFIASQESYGENTINTYKEIDDTTTLDPSFEDILDKVI	490
mrBoNT-FA-his	VSRVVRLCKSVIPRKGTKAPPRL:ITVNNRDLFFIASQESYGENTINTYKEIDDTTTLDPSFEDILDKVI	490
rBoNT-FA(0)-his	LNFNEQVIPQMPNRNVSTDIQKDNYIPKYDYNRTDIIDSYEVGRNYNTFFYLNAQKFSPNESNITLTSSF	554
mrBoNT-FA(0)-his	LNFNEQVIPQMPNRNVSTDIQKDNYIPKYDYNRTDIIDSYEVGRNYNTFFYLNAQKFSPNESNITLTSSF	560
mrBoNT-FA-his	LNFNEQVIPQMPNRNVSTDIQKDNYIPKYDYNRTDIIDSYEVGRNYNTFFYLNAQKFSPNESNITLTSSF	560

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Supplemental Figure 1

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mrBoNT-FA(0)-his DTGLLEG	SSKVYTFFSSDFINNINKPVQALLFIEWVKQVIRDFTTEATKTSTVDKLKDISLVVPYIGLALN SSKVYTFFSSDFINNINKPVQALLFIEWVKQVIRDFTTEATKTSTVDKLKDISLVVPYIGLALN SSKVYTFFSSDFINNINKPVQALLFIEWVKQVIRDFTTEATKTSTVDKLKDISLVVPYIGLALN	624 630 630
mrBoNT-FA(0)-his IGDEIYK	QHFAEAVELVGAGLLLEFSPEFLIPTLLIFTIKGYLTGSIRDKDKIIKTLDNALNVRDQKWKE QHFAEAVELVGAGLLLEFSPEFLIPTLLIFTIKGYLTGSIRDKDKIIKTLDNALNVRDQKWKE QHFAEAVELVGAGLLLEFSPEFLIPTLLIFTIKGYLTGSIRDKDKIIKTLDNALNVRDQKWKE	694 700 700
mrBoNT-FA(0)-his LYRWVVS	SKWLTTINTQFNKRKEQMYKALKNQATAIKKIIENKYNNYTTDEKSKIDSSYNINEIERTLNEK SKWLTTINTQFNKRKEQMYKALKNQATAIKKIIENKYNNYTTDEKSKIDSSYNINEIERTLNEK SKWLTTINTQFNKRKEQMYKALKNQATAIKKIIENKYNNYTTDEKSKIDSSYNINEIERTLNEK	764 770 770
mrBoNT-FA(0)-his INLAMKN	NIEQFITESSIAYLINIINNETIQKLKSYDDLVRRYLLGYIRNHSSILGNSVEELNSKVNNHLD NIEQFITESSIAYLINIINNETIQKLKSYDDLVRRYLLGYIRNHSSILGNSVEELNSKVNNHLD NIEQFITESSIAYLINIINNETIQKLKSYDDLVRRYLLGYIRNHSSILGNSVEELNSKVNNHLD	834 840 840
mrBoNT-FA(0)-his NGIPFEL	SSYTNDSLLIRYFNKNYGELKYNCILNIKYEMDRDKLVDSSGYRSRINIGTGVKFSEIDKNQV SSYTNDSLLIRYFNKNYGELKYNCILNIKYEMDRDKLVDSSGYRSRINIGTGVKFSEIDKNQV SSYTNDSLLIRYFNKNYGELKYNCILNIKYEMDRDKLVDSSGYRSRINIGTGVKFSEIDKNQV	904 910 910
mrBoNT-FA(0)-his QLSNLES	SSKIEVILNNGVIYNSMYENFSTSFWIRIPKYFRNINNEYKIISCMQNNSGWEVSLNFSNMNSK SSKIEVILNNGVIYNSMYENFSTSFWIRIPKYFRNINNEYKIISCMQNNSGWEVSLNFSNMNSK SSKIEVILNNGVIYNSMYENFSTSFWIRIPKYFRNINNEYKIISCMQNNSGWEVSLNFSNMNSK	974 980 980
mrBoNT-FA(0)-his IIWTLQD	OTEGIKKTVVFQYTQNINISDYINRWIFVTITNNRLSNSKIYINGRLINEESISDLGNIHASNN	1044 1050 1050
mrBoNT-FA(0)-his IMFKLDG	GCRDPHRYIWIKYFNLFDKELNKKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKY	1114 1120 1120

Supplemental Figure 1

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rBoNT-FA(0)-his mrBoNT-FA(0)-his mrBoNT-FA-his	LDVNNVGIRGYMYLKGPRGRIVTTNIYLNSTLYMGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYR LDVNNVGIRGYMYLKGPRGRIVTTNIYLNSTLYMGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYR LDVNNVGIRGYMYLKGPRGRIVTTNIYLNSTLYMGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYR	1184 1190 1190	
mrBoNT-FA(0)-his	LATNASQAGVEKILSAVEIPDVGNLSQVVVMKSENDQGIRNKCKMNLQDNNGNDIGFIGFHQFNNIAKLV LATNASQAGVEKILSAVEIPDVGNLSQVVVMKSENDQGIRNKCKMNLQDNNGNDIGFIGFHQFNNIAKLV LATNASQAGVEKILSAVEIPDVGNLSQVVVMKSENDQGIRNKCKMNLQDNNGNDIGFIGFHQFNNIAKLV	1254 1260 1260	
mrBoNT-FA(0)-his	ASNWYNRQIGKASRTFGCSWEFIPVDDGWGESSLHHHHHHHHHH ASNWYNRQIGKASRTFGCSWEFIPVDDGWGESSLHHHHHHHHHH ASNWYNROIGKASRTFGCSWEFIPVDDGWGESSLHHHHHHHHHH	1298 1304 1304	

Figure S1. Multiple sequence alignment of rBoNT/FA(0)-his, mrBoNT/FA(0)-his, and mrBoNT/FA-his. Positions of the E227Q and H230Y catalytic site inactivating mutations, the S429 to L437 activation loop substitution, and C-terminal ten-histidine affinity tag, are boxed in grey.

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MPVVINSFNYDDPVNDNTIIYIRPPYYETSNTYFKAFQIMDNVWIIPERYRLGIDPSLFNPPVSLKA ${\tt GSDGYFDPNYLSTNTEKNKYLQIMIKLFKRINSKPAGQILLEEIKNAIPYLGNSYTQEEQFTTNNRT}$ VSFNVKLANGNIVOOMANLIIWGPGPDLTTNKTGGIIYSPYOSMEATPYKDGFGSIMTVEFSPEYAT AFNDISIASHSPSLFIKDPALILMHELIHVLHGLYGTYITEYKITPNVVOSYMKVTKPITSAEFLTF GGRDRNIVPOSIQSQLYNKVLSDYKRIASRLNKVNTATALINIDEFKNLYEWKYQFAKDSNGVYSVD LNKFEQLYKKIYSFTEFNLAYEFKIKTRLGYLAENFGPFYLPNLLDDSIYTEVDGFNIGALSINYQG ${\tt QNIGSDINSIKKLQGQGVVSRVVRLC_{428}\underline{KSVIPRKGTKAPPRL}C_{444}ITVNNRDLFFIASQESYGEN}$ INTYKEIDDTTTLDPSFEDILDKVILNFNEQVIPQMPNRNVSTDIQKDNYIPKYDYNRTDIIDSYEV GRNYNTFFYLNAQKFSPNESNITLTSSFDTGLLEGSKVYTFFSSDFINNINKPVQALLFIEWVKQVIRDFTTEATKTSTVDKLKDISLVVPYIGLALNIGDEIYKOHFAEAVELVGAGLLLEFSPEFLIPTLLIFTIKGYLTGSIRDKDKIIKTLDNALNVRDQKWKELYRWVVSKWLTTINTQFNKRKEQMYKALKNQATURANGATURAAIKKIIENKYNNYTTDEKSKIDSSYNINEIERTLNEKINLAMKNIEOFITESSIAYLINIINNETIC KLKSYDDLVRRYLL**GYIRNHSSILGNSVEELNSKVNNHLDNGIPFELSSYTNDSLLIRYFNKNYGEL** KYNCILNIKYEMDRDKLVDSSGYRSRINIGTGVKFSEIDKNQVQLSNLESSKIEVILNNGVIYNSMY ENFSTSFWIRIPKYFRNINNEYKIISCMQNNSGWEVSLNFSNMNSKIIWTLQDTEGIKKTVVFQYTQ NINISDYINRWIFVTITNNRLSNSKIYINGRLINEESISDLGNIHASNNIMFKLDGCRDPHRYIWIK YFNLFDKELNKKEIKDLYDNOSNSGILKDFWGDYLOYDKPYYMLNLYDPNKYLDVNNVGIRGYMYLK GPRGRIVTTNIYLNSTLYMGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASOAGVEK ILSAVEIPDVGNLSQVVVMKSENDQGIRNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIGKASRTFGCSWEFIPVDDGWGESSLHHHHHHHHHHH

Light chain, LC/FA BoNT/F1 activation loop Translocation domain, H_N /FA Unknown function, H_{CN} /FA Receptor binding domain, H_{CC} /FA Affinity tag (His₁₀)

Figure S2. Primary amino acid sequence of mrBoNT/FA-his. Light chain, LC/FA, amino acids shown in black. Substituted <u>BoNT/F1 activation loop</u> amino acids shown underlined. *Translocation domain, Hn/FA*, amino acids shown in grey italic. *Unknown function, Hcn/FA*, amino acids shown in black italic. **Receptor binding domain, Hcc/FA**, amino acids shown in bold black italic. Affinity tag (His₁₀), amino acids shown in grey.

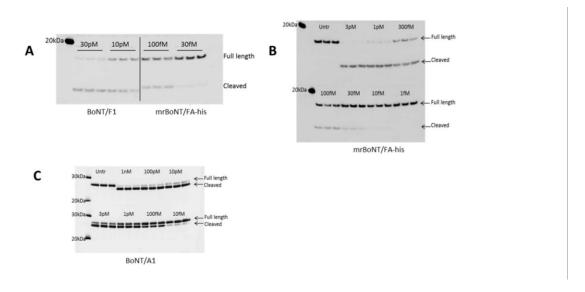


Figure S3. SNARE cleavage in rat cortical neurons panel (A) shows Western blot analysis of full-length and cleaved VAMP-2 from rat cortical neurons treated with nBoNT/F1 or mrBoNT/FA-his for 24 hours. Panel (B) shows Western blot analysis of full-length and cleaved VAMP-2 from rat cortical neurons treated with a concentration range of mrBoNT/FA-his for 24 hours. Panel (C) shows Western blot analysis of full-length and cleaved SNAP-25 from rat cortical neurons treated with a concentration range of nBoNT/A1 for 24 hours.