Table S4 - Experimental validation of a select set of predicted sRNAs in *C. botulinum*

Candidate	Position	Left Gene	Orientation	Right Gene	Classification (Probability)	Validation
***C. botulinum A3 Loch Maree* (NC_010520)**						
sCLK_200	199308-199544	CLK_3349	→ P⟹⚲ →	CLK_3350	NC	Q^{++}, N^{+}
sCLK_1206	1205380-1205670	CLK_0489	→ ⟹⚲ ←	CLK_0490	NC	Q
sCLK_2040 [*]	2039993-2040189	CLK_1236	← ⚲⟸ ←	CLK_1237	*SRP_euk_arch* (0.51)	Q
sCLK_2759	2758726-2759039	CLK_1943	← ⚲⟸ ←	CLK_1944	*SSU_rRNA_5* (0.52)	Q
sCLK_3105 [C1]	3104935-3105204	CLK_2252	← ⚲⟸ ←	CLK_2253	*SRP_euk_arch* (0.50)	Q^{+}, N^{+}
sCLK_3269 [§]	3268687-3269049	CLK_2394	← ⚲⟸ ←	tRNA	*SRP_euk_arch* (0.51)	Q^{++}, N
sCLK_3427	3426714-3427148	CLK_2547	← ⚲⟸ →	CLK_2548	*SRP_euk_arch* (0.51)	Q, N
sCLK_3557 [C2]	3556734-3556909	CLK_2689	← ⚲⟸P ←	CLK_2690	NC	Q
sCLK_3642	3641003-3641281	CLK_2754	← ⚲⟸ ←	CLK_2755	*Riboswitch* (0.54)	Q^{++}
sCLK_3693 [C3]	3692533-3692751	CLK_2800	← ⚲⟸ ←	CLK_2801	NC	Q
***C. botulinum A Hall* (NC_009698)**						
sCLC_1905 *	1904415-1904608	CLC_1793	← ⚲⟸ ←	CLC_1794	*SRP_euk_arch* (0.51)	Q
sCLC_2101	2100891-2101220	CLC_1979	← ⚲⟸P ←	CLC_1980	NC	Q
sCLC_2889 [C1]	2888689-2888961	CLC_2735	← ⚲⟸ ←	CLC_2736	NC	Q^{+}
sCLC_3353 [C2]	3352341-3352516	CLC_3215	← ⚲⟸P ←	CLC_3216	NC	Q
sCLC_3476 [C3]	3475069-3475274	CLC_3311	← ⚲⟸ ←	CLC_3312	NC	Q, N
***C. botulinum A ATCC 3502* (NC_009495)**						
sCBO1976 [*]	1975290-1975483	CBO1850	← ⚲⟸ ←	CBO1851	*SRP_euk_arch* (0.51)	Q, N
sCBO2173	2172031-2172360	CBO2033	← ⚲⟸P ←	CBO2034	NC	Q, N
sCBO2696	2695893-2696176	CBO2558	← ⚲⟸P ←	CBO2559	*SRP_euk_arch* (0.51)	Q, N
sCBO3039 [C1]	3038353-3038616	CBO2858	← ⚲⟸P ←	CBO2859	*SRP_euk_arch* (0.51)	Q^{+}
sCBO3480 [C2]	3479245-3479420	CBO3272	← ⚲⟸P ←	CBO3273	NC	Q, N
sCBO3602 [C3]	3601973-3602178	CBO3368	← ⚲⟸ ←	CBO3369	NC	Q

[C1, C2, C3]: Conserved sRNA set in all three *C. botulinum* strains;

P : Promoter is found upstream of the sequence;

⚲ : Rho-independent terminator downstream of the sequence;

[†] The sRNA sequence is annotated in Rfam database;

* The conserved clindamycin-related sRNA;

[§] The expression was detected by Q-RT-PCR but not by Northern analysis;

NC: cannot be classified with probability of at least 0.5;

Q : No expression detected by Q-RT-PCR;

Q^{+}: lowly expressed sRNA detected by Q-RT-PCR;

Q^{++}: highly expressed sRNA detected by Q-RT-PCR;

N : No expression detected by Northern analysis;

N^{+} : sRNA validated by Northern analysis;