

**Table S1: Isolate descriptions with compiled phenotypic data**

strain identification	Ribotype	Severe Disease?	tcdA <sup>a</sup>	tcdB	cdtA	cdtB	tcdC <sup>b</sup>	Sporulation <sup>c</sup>	Toxin <sup>d</sup>	CFE <sup>e</sup>	growth rate <sup>f</sup>
Cd040	001	N	+	+	-	-	sc3	47500	0.079	21.95	0.1351
Cd047	001	N	+	+	-	-	sc3	10150	0.511	64.15	0.1028
Cd092	001	N	+	+	-	-	sc3	693	0.039	53.59	0.2002
DA00679	001	N	+	+	-	-	sc3	70	0.442	5.30	0.1372
Cd013	013	N	+	+	-	-	sc9	7550	0.240	51.32	0.0792
DA00330	017	N	+	+	-	-	sc7	9633	18.410	44.47	0.0704
Cd084	027	Y	+	+	+	+	sc1	2110	2.989	47.49	0.2966
Cd180	027	Y	+	+	+	+	sc1	7167	1.645	69.31	0.2158
DA00353	027	Y	+	+	+	+	ND	41000	15.771	79.05	0.0666
DA00356	027	Y	+	+	+	+	ND	43650	16.321	35.86	0.0787
DA00394	027	Y	+	+	+	+	ND	53000	3.800	36.23	0.0703
DA00395	027	Y	+	+	+	+	ND	16433	2.780	42.79	0.0645
DA00431	027	Y	+	+	+	+	ND	64000	3.053	39.56	0.0637
DA00458	027	Y	+	+	+	+	ND	27850	2.993	55.19	0.0777
DA00643	027	Y	+	+	+	+	ND	3957	2.728	51.61	0.0734
DA00684	027	Y	+	+	+	+	ND	25500	1.563	42.33	0.0345
Cd093	027	unknown	+	+	+	+	sc1	5867	1.848	57.11	ND
Cd016	027	N	+	+	+	+	sc1	1197	2.525	14.21	0.3520
Cd025	027	N	+	+	+	+	sc1	7600	0.135	42.89	0.0880
Cd073	027	N	+	+	+	+	sc1	6500	4.168	55.53	0.0772
Cd089	027	N	+	+	+	+	sc1	1700	1.030	53.75	0.0507
Cd105	027	N	+	+	+	+	sc1	7600	1.491	51.41	0.1021
Cd106	027	N	+	+	+	+	sc1	10300	2.366	34.16	0.0519
Cd108	027	N	+	+	+	+	sc1	9050	0.219	44.92	0.0730
Cd148	027	N	+	+	+	+	sc1	5300	1.466	48.60	0.0724
Cd154	027	N	+	+	+	+	sc1	10850	1.103	67.74	0.1430
Cd199	027	N	+	+	+	+	sc1	8100	2.277	57.65	0.1071
DA00309	027	N	+	+	+	+	sc1	3167	2.602	40.98	0.0604
DA00464	027	N	+	+	+	+	sc1	13100	5.675	56.89	0.0561
DA00658	027	N	+	+	+	+	sc1	450	2.725	11.20	0.0628
FOBT128	027	N	+	+	+	+	sc1	3650	4.864	45.84	0.0499

FOBT142	027	N	+	+	+	+	+	sc1	90333	5.737	70.69	0.0577
FOBT195	027	N	+	+	+	+	+	sc1	2367	0.120	78.16	0.0640
FOBT468	027	N	+	+	+	+	+	sc1	6450	6.407	68.31	0.0435
Cd070	014-020	Y	+	+	-	-	-	sc9	1450	0.156	19.99	0.1594
Cd088	014-020	Y	+	+	-	-	-	sc9	3633	0.895	64.77	0.3176
DA00062	014-020	Y	+	+	-	-	-	sc9	5650	0.119	63.86	0.1642
DA00149	014-020	Y	+	+	-	-	-	sc9	5633	0.115	26.53	0.0667
DA00174	014-020	Y	+	+	-	-	-	sc9	5450	1.965	77.37	0.1146
DA00245	014-020	Y	+	+	-	-	-	sc9	8967	1.075	48.62	0.2432
DA00289	014-020	Y	+	+	-	-	-	ND	28650	4.264	51.63	0.1086
Cd072	014-020	unknown	+	+	-	-	-	sc9	3643	0.238	53.04	ND
Cd182	014-020	unknown	+	+	-	-	-	sc9	3673	0.463	29.04	ND
Cd038	014-020	N	+	+	-	-	-	sc9	23900	2.722	72.60	0.1059
Cd039	014-020	N	+	+	-	-	-	sc9	21300	0.028	39.54	0.1869
Cd071	014-020	N	+	+	-	-	-	sc9	4663	0.213	73.49	0.1215
Cd109	014-020	N	+	+	-	-	-	sc9	4567	0.050	57.86	0.2017
Cd111	014-020	N	+	+	-	-	-	sc9	5650	1.412	57.09	0.1108
Cd112	014-020	N	+	+	-	-	-	sc9	6950	1.722	57.09	0.1129
Cd124	014-020	N	+	+	-	-	-	sc9	6600	0.060	77.30	0.1867
Cd125	014-020	N	+	+	-	-	-	sc9	4600	0.119	51.01	0.1920
Cd127	014-020	N	+	+	-	-	-	sc9	11950	0.051	77.76	0.2034
Cd144	014-020	N	+	+	-	-	-	sc9	14533	0.104	34.70	0.1823
Cd202	014-020	N	+	+	-	-	-	sc9	8350	0.959	40.59	0.1338
Cd204	014-020	N	+	+	-	-	-	sc9	5950	0.098	50.88	0.1964
Cd208	014-020	N	+	+	-	-	-	sc9	917	0.191	39.73	0.0783
DA00698	014-020	N	+	+	-	-	-	sc9	3235	2.672	44.10	0.0902
DA00493	053-163	Y	+	+	-	-	-	ND	6150	2.626	31.79	0.1356
Cd042	053-163	N	+	+	-	-	-	UM-001	14200	0.176	61.45	0.1340
Cd205	053-163	N	+	+	-	-	-	UM-001	140	0.799	38.00	0.0888
DA00603	053-163	N	+	+	-	-	-	UM-001	10800	4.524	60.62	0.1172
Cd006	078-126	Y	+	+	+	+	+	A	1190	0.049	55.21	0.1042
Cd054	078-126	unknown	+	+	+	+	+	A	1350	0.041	58.74	ND
Cd033	078-126	N	+	+	+	+	+	A	0	0.051	2.01	0.1191
DA00599	078-126	N	+	+	+	+	+	A	2065	0.329	30.15	0.1815
DA00244	UM1	Y	+	+	-	-	-	UM-002	5400	1.282	48.23	0.0976
Cd017	UM1	N	+	+	-	-	-	sc9	2280	0.066	74.94	0.1313

Cd046	UM1	N	+	+	-	-	sc9	11300	0.314	60.76	0.0754
DA00481	UM1	N	+	+	-	-	sc9	17633	5.535	50.78	0.0773
Cd041	UM11	Y	+	+	-	-	UM-001	10567	0.223	35.28	0.1435
DA00152	UM11	Y	+	+	-	-	UM-001	5850	0.061	59.32	0.0612
DA00299	UM11	Y	+	+	-	-	ND	33900	0.173	52.98	0.1576
Cd104	UM11	N	+	+	-	-	UM-001	1250	0.058	40.80	0.1176
DA00677	UM16	Y	ND	ND	ND	ND	ND	45000	3.508	56.62	0.0632
Cd030	UM16	N	+	+	-	-	UM-001	4970	0.039	54.10	0.1384
Cd087	UM19	Y	+	+	+	+	UM-012	11500	0.089	55.40	0.1897
Cd194	UM2	Y	+	+	-	-	B	7000	1.402	69.31	0.3339
Cd004	UM22	N	+	+	+	+	UM-012	5800	0.318	16.01	0.0886
DA00383	UM23	Y	ND	ND	ND	ND	ND	33933	275.50	38.76	0.1013
Cd166	UM3	Y	+	+	-	-	B	14867	23.025	68.43	0.1130
Cd009	UM3	N	+	+	-	-	B	9450	2.469	53.08	0.1028
Cd043	UM3	N	+	+	-	-	B	2510	0.331	89.55	0.1180
Cd086	UM3	N	+	+	-	-	B	0	0.869	50.56	0.1205
DA00378	UM32	N	ND	ND	ND	ND	UM-001	9750	0.708	17.70	0.1416
DA00699	UM33	N	ND	ND	ND	ND	sc5	8867	1.037	60.66	0.0997
Cd066	UM4	N	+	+	+	+	UM-003	3180	0.223	36.82	0.1745
Cd067	UM4	N	+	+	+	+	UM-003	1255	0.106	38.50	0.0807
Cd019	UM5	N	+	+	-	-	UM-003	1820	0.042	27.71	0.2764
Cd035	UM5	N	+	+	-	-	UM-003	11400	0.045	68.86	0.0966
Cd028	UM6	N	+	+	-	-	UM-001	4833	0.534	60.25	0.0850
DA00583	UM6	N	+	+	-	-	sc15	20867	4.096	63.76	0.0802
DA00297	UM8	Y	+	+	-	-	ND	21233	0.298	17.50	0.0979
Cd003	UM8	N	+	+	-	-	UM-001	2437	0.124	38.07	0.0724
DA00322	UM9	N	+	+	-	-	sc3	6200	1.060	65.76	0.1007
DA00692	UM9	N	+	+	-	-	sc3	5800	3.726	57.81	0.0834
Cd160	Unique <sup>h</sup>	Y	+	+	-	-	ND	11650	0.028	62.21	0.1083
DA00142	Unique	Y	ND	ND	ND	ND	UM-001	33500	1.218	52.86	0.0770
DA00315	Unique	Y	ND	ND	ND	ND	ND	120	0.243	ND	0.0782
DA00483	Unique	Y	ND	ND	ND	ND	ND	33200	3.105	72.79	0.0768
DA00484	Unique	Y	ND	ND	ND	ND	ND	847	0.036	ND	0.1075
Cd008	Unique	N	+	+	-	-	UM-004	8500	0.432	83.28	0.2107
Cd018	Unique	N	+	+	+	+	UM-001	17750	0.192	86.96	0.3024
Cd021	Unique	N	+	+	-	-	sc9	2500	0.154	53.70	0.1721

Cd022	Unique	N	+	+	-	-	UM-006	27000	0.168	63.75	0.1125
Cd045	Unique	N	+	+	-	-	UM-001	26600	0.151	64.44	0.3830
Cd051	unique	N	+	+	-	-	UM-001	3833	0.228	59.60	0.0921
Cd069	Unique	N	+	+	+	+	sc3	13950	0.084	44.83	0.1479
Cd107	Unique	N	+	+	-	-	UM-001	120	0.169	86.52	0.1589
DA00266	Unique	N	ND	ND	ND	ND	sc8	7667	53.223	38.05	0.0914
DA00332	Unique	N	ND	ND	ND	ND	sc9	5000	5.179	51.42	0.0981
VPI	lab	unknown	ND	ND	ND	ND	ND	ND	7.140	ND	0.0891

a - presence or absence of *tcdA*, *tcdB*, *cdtA*, and *cdtB* were determined using multiple PCR assay.

b - *tcdC* typing based on gene sequence

c - average sporulation totals for each isolate

d - average toxin production (ng/ml) totals for each isolate

e - average spore viability (CFE) for each isolate

f - average growth rates ( $\mu$ ) for each isolate

g - not determined

h - isolate is of a ribotype only included once in this study