

**Supplementary Table S1: List of isolates selected for sequencing.**

Isolate	Year collected	Phylogroup	Pathotype	Chromosome coverage	Plasmid coverage
B07-007	2007	A	III	N/A	N/A
ID030914AA	2014	A	I	99,86	99,28
ID030914F	2014	A	IV	96,44	74,15
ID030914P	2014	E	IV	96,19	62,69
ID030915F	2015	E	V	96,36	62,69
ID040816D	2016	E	V	96,25	62,69
ID060814AB	2014	D	V	96,15	62,82
ID060814AC	2014	E	V	96,29	62,82
ID060814AE	2014	C	V	99,93	100,00
ID060814AI	2014	D	V	96,48	62,82
ID060814AJ	2014	A	III	96,22	53,17
ID060814AK	2014	C	III	96,35	53,17
ID060814AL	2014	D	V	96,23	62,82
ID060814AO	2014	D	V	96,47	62,82
ID060814AP	2014	C	III	99,91	100,00
ID060814C	2014	A	V	97,26	74,19
ID060814F	2014	C	III	99,91	100,00
ID060814G	2014	D	V	96,34	62,71
ID060814K <sup>1</sup>	2014	C	III	N/A	N/A
ID060814P	2014	D	V	96,49	62,71
ID060814T	2014	C	III	98,32	58,43
ID060814U	2014	A	III	99,88	100,00
ID070815A	2015	A	III	99,94	100,00
ID070815E	2015	A	III	99,92	100,00
ID070815G	2015	A	III	99,94	100,00
ID100816B	2016	A	V	96,37	62,71
ID100816G	2016	E	V	96,31	62,71
ID100816K	2016	A	V	96,46	74,19
ID100816P	2016	A	V	96,39	62,71
ID100816T	2016	E	V	95,94	74,19
ID100914AA	2014	E	IV	97,06	56,40
ID100914AE	2014	A	V	96,21	74,19
ID100914AF	2014	E	V	96,21	62,67
ID100914O	2014	E	III	96,16	62,67
ID110815A	2015	E	III	99,90	100,00
ID110815N	2015	A	V	95,94	74,19
ID110815P	2015	E	V	96,28	62,67
ID110815X	2015	A	II	99,90	100,00
ID110915A	2015	E	V	96,15	62,67

ID110915B	2015	A	III	99,86	100,00
ID140916E	2016	E	III	99,81	100,00
ID140916G	2016	E	III	96,27	62,67
ID140916I	2016	A	III	95,93	100,00
ID140916N	2016	E	III	99,86	100,00
ID140916S	2016	A	V	96,26	62,78
ID140916T	2016	E	III	96,85	43,99
ID160615F	2015	E	V	96,24	62,78
ID160615J	2015	E	V	96,19	62,78
ID170914AC	2014	A	IV	96,50	74,14
ID170914AE	2014	B	IV	95,81	64,90
ID170914AF	2014	B	IV	95,89	64,90
ID170914AG	2014	E	V	96,16	62,76
ID170914I	2014	E	V	96,31	62,76
ID170914N	2014	E	V	96,24	62,76
ID170914X	2014	E	V	96,18	62,76
ID190716P	2016	E	V	96,42	74,15
ID190716F	2016	A	V	96,05	62,76
ID190716Q	2016	E	IV	96,23	56,51
ID190716T	2016	E	IV	96,57	41,43
ID190716U	2016	A	III	95,39	45,73
ID200814A	2014	D	V	96,30	62,77
ID200814F	2014	D	V	96,20	62,77
ID200814G	2014	C	III	99,80	100,00
ID240914AA	2014	A	V	95,52	72,09
ID240914AD	2014	A	III	95,55	72,09
ID240914AI	2014	A	II	99,88	100,00
ID240914AS	2014	A	III	99,92	100,00
ID240914AX	2014	A	III	99,90	100,00
ID240914B	2014	A	III	99,93	100,00
ID240914U	2014	A	III	99,87	100,00
ID240914Z	2014	E	V	96,17	62,73
ID260814A	2014	E	V	96,32	62,77
ID260814AA	2014	A	II	96,46	74,20
ID260814AH	2014	A	II	96,28	53,26
ID260814AK	2014	A	III	99,91	100,00
ID260814AL	2014	E	V	88,77	62,82
ID260814AP	2014	E	IV	96,34	56,54
ID260814F	2014	A	V	96,49	74,21
ID260814H	2014	E	V	96,23	62,82
ID260814K	2014	E	V	96,27	62,82

ID260814L	2014	A	III	99,96	100,00
ID260814Q	2014	E	II	96,28	62,82
ID260814X	2014	E	IV	96,34	62,82
ID270716AF	2016	A	III	100,01 <sup>2</sup>	100,00
ID270716AK	2016	E	V	96,22	62,84
ID270716AL	2016	A	III	99,94	100,00
ID270716G	2016	A	III	99,87	100,00
ID270716P	2016	A	III	99,94	100,00
ID290715A	2015	A	III	99,98	100,00
ID290715F	2015	A	III	99,95	100,00
ID310816B	2016	A	V	96,49	74,19
ID310816N	2016	E	III	96,35	62,84
ID310816T	2016	E	I	98,39	57,78
ID310816U	2016	A	I	99,92	100,00
ID310816Z	2016	A	V	96,04	74,19
VT106	1996	E	IV	94,86	56,57

<sup>1</sup> The DNA from the isolate ID060814K was not sequenced properly.

<sup>2</sup> A chromosome coverage of more than 100 % was possible due to the presence of small indels. The coverage percentage was calculated by counting the number of lines in the .vcf file generated by the alignment.

**Supplementary Table S2: Conversion of disease rating scores to parametric value for data analyses.**

Disease rating score	Parametric values
1.1	1
1.2	2
1.3	3
2.1	4
2.2	5
2.3	6
3.1	7
3.2	8
3.3	9
4.1	10
4.2	11
4.3	12
5.1	13
5.2	14
5.3	15