

Supplementary Table 3. Sequences producing significant alignments of *pdeF* gene

Scientific name	Description	Accession number	Taxid	Accession length	Max score	Total score	Query coverage	E value	Percent identity
<i>Erwinia pyrifoliae</i>	<i>Erwinia pyrifoliae</i> strain EpK1/15 chromosome, complete genome	CP023567.1	79967	4027225	4,156	4,156	100%	0	100.00
<i>Erwinia pyrifoliae</i>	<i>Erwinia pyrifoliae</i> strain CP20113301 chromosome, complete genome	CP104745.1	79967	4086511	4,156	4,156	100%	0	100.00
<i>Erwinia pyrifoliae</i>	<i>Erwinia pyrifoliae</i> DSM 12163 complete genome, culture collection DSM:12163	FN392235.1	644651	4026286	4,156	4,156	100%	0	100.00
<i>Erwinia pyrifoliae</i>	<i>Erwinia pyrifoliae</i> strain Ep1/96 complete chromosome	FP236842.1	634499	4026322	4,156	4,156	100%	0	100.00
<i>Erwinia pyrifoliae</i>	<i>Erwinia pyrifoliae</i> strain CP201486 chromosome, complete genome	CP103445.1	79967	4107700	4,145	4,145	100%	0	99.91
<i>Erwinia pyrifoliae</i>	<i>Erwinia pyrifoliae</i> strain CP201179 chromosome, complete genome	CP103450.1	79967	4101577	4,145	4,145	100%	0	99.91
<i>Erwinia</i> sp.	<i>Erwinia</i> sp. Ejp617, complete genome	CP002124.1	215689	3909168	4,122	4,122	100%	0	99.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> ATCC BAA-2158, whole genome shotgun sequence, contig 14	FR719194.1	889211	196263	3,127	3,127	99%	0	91.77
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> strain FB-20 chromosome, complete genome	CP050240.1	552	3803601	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> strain FB-86 chromosome, complete genome	CP050258.1	552	3804074	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> strain FB-207 chromosome, complete genome	CP050263.1	552	3804074	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> strain FB-307 chromosome, complete genome	CP050242.1	552	3803872	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> strain TS3238 chromosome, complete genome	CP050244.1	552	3804073	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> strain E-2 chromosome, complete genome	CP024970.1	552	3806898	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> strain 99east-3-1 chromosome, complete genome	CP117554.1	552	3799623	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> strain CP200242 isolate missinsg chromosome, complete genome	CP077850.1	552	3804080	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> strain Ea915 chromosome, complete genome	CP104025.1	552	3800460	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> strain Ea102 chromosome, complete genome	CP104022.1	552	3800604	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> isolate CP201324 chromosome, complete genome	CP076589.1	552	3804067	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> isolate CP200930 chromosome, complete genome	CP076590.1	552	3803962	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> isolate CP201142 chromosome, complete genome	CP076591.1	552	3804022	3,121	3,121	99%	0	91.73

Supplementary Table 3. Continued

Scientific name	Description	Accession number	Taxid	Accession length	Max score	Total score	Query coverage	E value	Percent identity
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> isolate CP20140001 chromosome, complete genome	CP076592.1	552	3804070	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> isolate CP20086202 chromosome, complete genome	CP076594.1	552	3804044	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> isolate CP20130202 chromosome, complete genome	CP076595.1	552	3804066	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> isolate CP20161301 chromosome, complete genome	CP076596.1	552	3801811	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> strain Ea1189 chromosome, complete genome	CP055227.2	552	3796950	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> strain ATCC 15580 chromosome, complete genome	CP066796.1	552	3807395	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> strain 17-2187 chromosome, complete genome	CP066794.1	552	3804074	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> strain 19-7 chromosome, complete genome	CP066780.1	552	3803552	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> strain Ea1/79Sm chromosome, complete genome	CP064855.1	552	3807330	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> strain TS3128 chromosome, complete genome	CP056034.1	552	3804041	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> CFBP1430 complete genome	FN434113.1	665029	3805573	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> ATCC 49946 chromosomal sequence	FN666575.1	716540	3805874	3,121	3,121	99%	0	91.73
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> strain 33-1 chromosome	CP063805.1	552	3876962	3,116	3,116	99%	0	91.68
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> strain 1-2 chromosome	CP063694.1	552	3889090	3,116	3,116	99%	0	91.68
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> strain 11-7 chromosome	CP063688.1	552	3878355	3,116	3,116	99%	0	91.68
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> strain 32-10 chromosome	CP063691.1	552	3883144	3,116	3,116	99%	0	91.68
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> strain 7-3 chromosome	CP063697.1	552	3890965	3,116	3,116	99%	0	91.68
<i>Erwinia amylovora</i>	<i>Erwinia amylovora</i> isolate CP20130204 chromosome, complete genome	CP076593.1	552	3803641	3,114	3,114	99%	0	91.68
<i>Erwinia tasmaniensis</i>	<i>Erwinia tasmaniensis</i> strain ET1/99 complete chromosome	CU468135.1	465817	3883467	1,768	1,768	98%	0	81.14