

**Suppl. Table 1** Reference strains obtained from CMEG

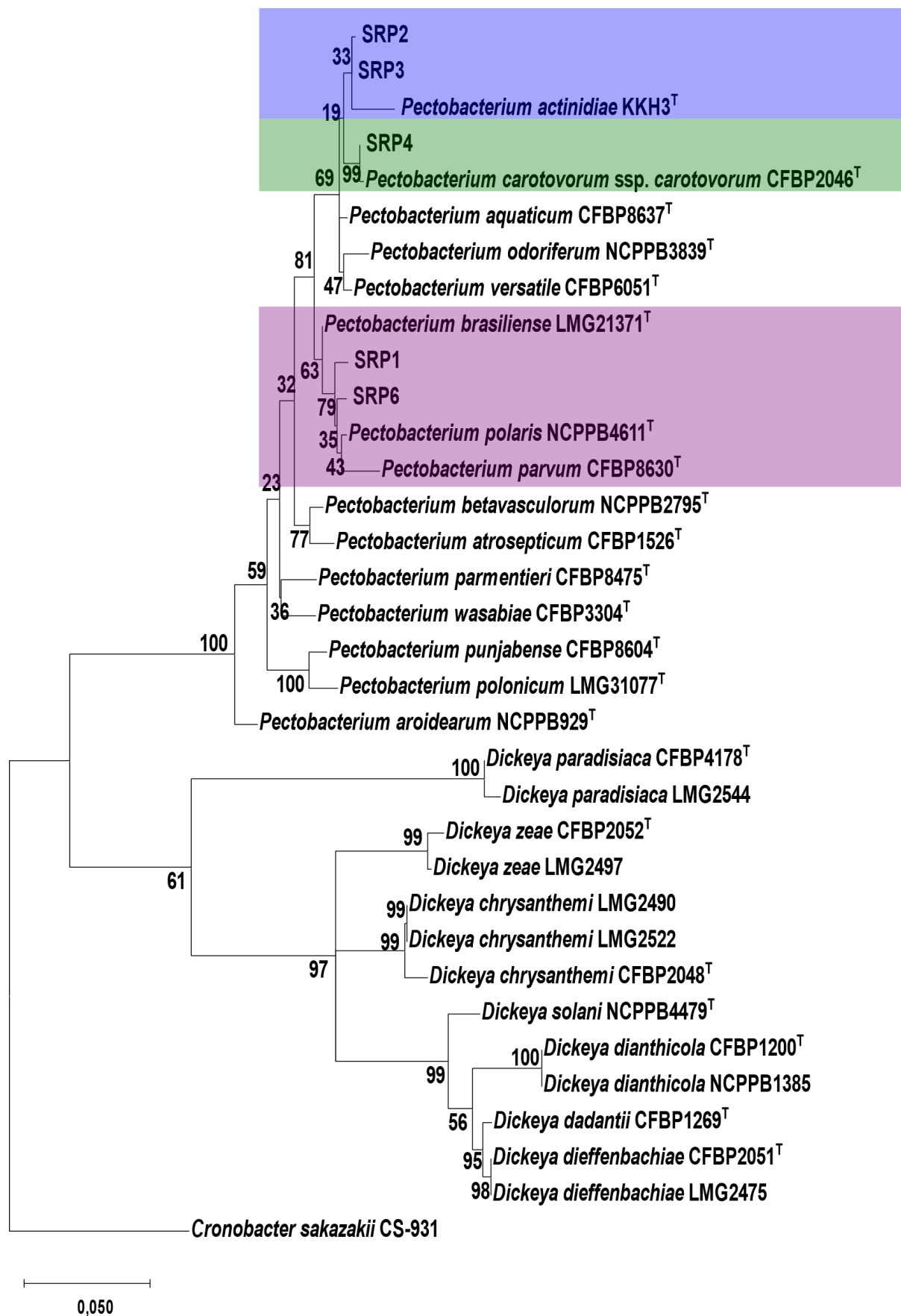
<b>Genus</b>	<b>Species</b>	<b>CMEG Isolate number</b>	<b>Isolate name</b>	<b>Isolate origin</b>
<i>Pectobacterium</i>	<i>brasiliense</i>	BCC 0357	LMG21371T	Brazil
<i>Pectobacterium</i>	<i>carotovorum</i>	BCC 1686	Unknown	Unknown
<i>Pectobacterium</i>	<i>atrosepticum</i>	BCC 872	LMG2386T	United Kingdom

**Suppl. Table 2** Primer sequences used in the multilocus sequence analysis scheme including three housekeeping genes, namely, *atpD*, *dnaX* and *infB* of putative *Pectobacterium* isolates

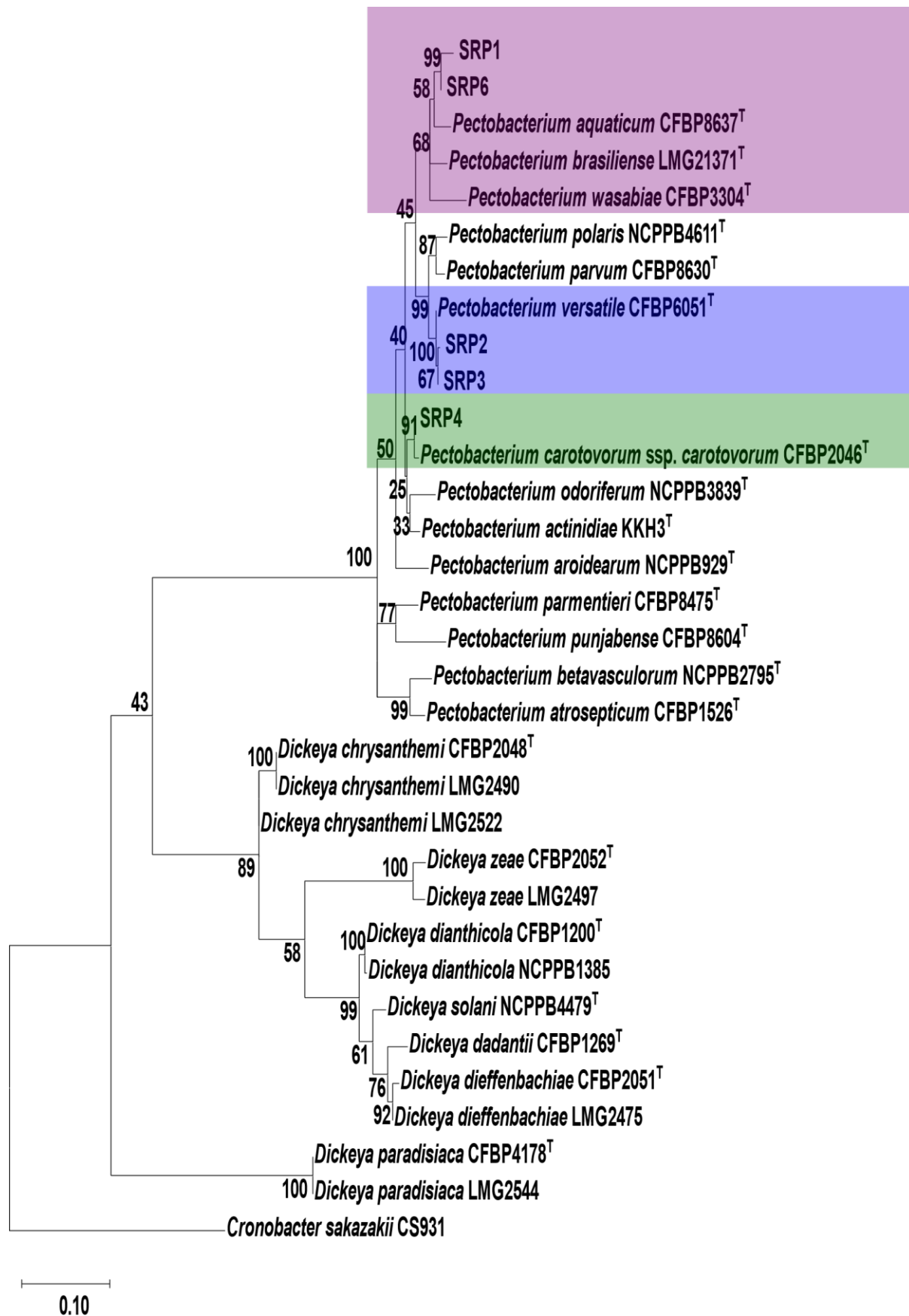
<b>Primer name</b>	<b>Primer sequence (5' – 3')</b>	<b>References</b>
atpD-01F	RTAATYGGMGCSGTRGTNGAYGT	Brady et al. 2008
atpD-02R	TCATCCGCMGGWACRTAWAYNGCCTG	
dnaXF	TATCAGGTYCTTGCCCGTAAGTGG	Sławiak et al. 2009
dnaXR	TCGACATCCARCGCYTGAGATG	
infB-01F	ATYATGGGHCAYGTHGAYCA	Brady et al. 2008
infB-02R	ACKGAGTARTAACGCAGATCCA	

**Suppl. Table 3** Standard error values of the mean daily stem rot severities

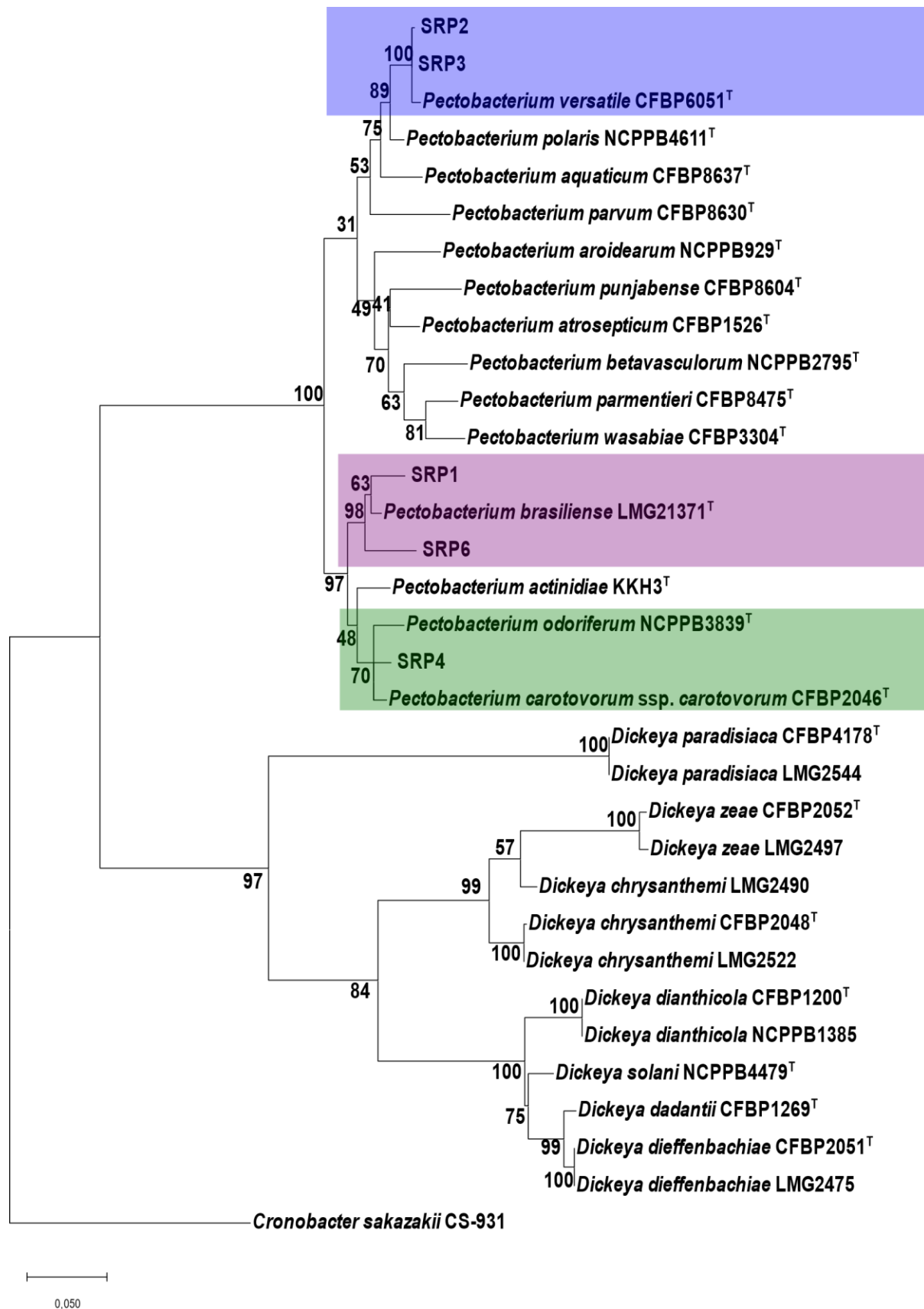
Treatment	Date				
	22-09- 2020	24-09- 2020	26-09- 2020	28-09- 2020	30-09- 2020
Pb	0	4,724556	13,57025	14,12437	15,625
Pc	0	0	0	0	0
Pa	0	0	0	0	0
Pb + Pc	0	4,224141	13,13951	12,63431	9,771699
Pb + Pa	7,745246	8,517314	10,82532	12,26054	12,26054
Pc + Pa	0	0	0	0	0
Pb + Pc + Pa	0	4,224141	10,50885	13,01041	11,59951
Negative	0	0	0	0	0



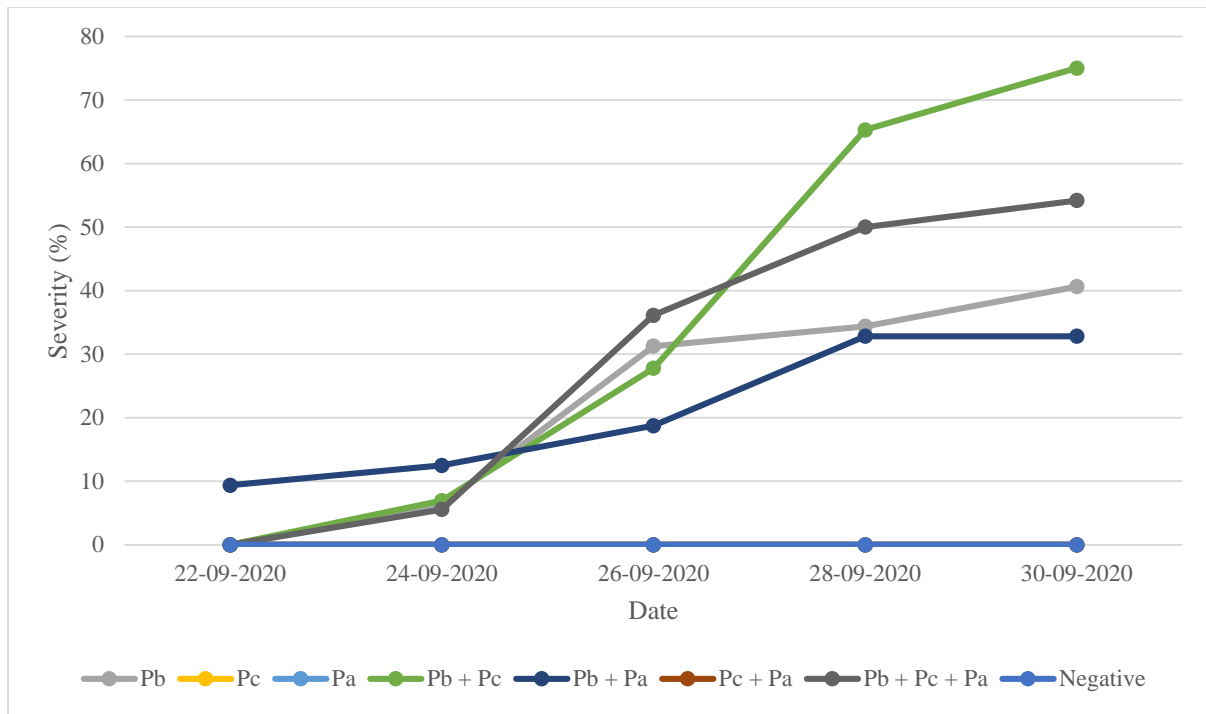
**Suppl. Fig 1** A maximum-likelihood phylogenetic tree of *atpD* (641 bp). GTR+I+G was used as the evolutionary model on MEGA X to construct the tree and bootstrap values are indicated as percentages. *Cronobacter sakazakii* CS-931 was included as an outgroup. The scale bar represents substitutions per site



**Suppl. Fig. 2** A maximum-likelihood phylogenetic tree of *dnaX* (443 bp). GTR+I+G was used as the evolutionary model on MEGA X to construct the tree and bootstrap values are indicated as percentages. *Cronobacter sakazakii* CS-931 was included as an outgroup. The scale bar represents substitutions per site



**Suppl. Fig 3** A maximum-likelihood phylogenetic tree of *infB* (573 bp). GTR+I+G was used as the evolutionary model on MEGA X to construct the tree and bootstrap values are indicated as percentages. *Cronobacter sakazakii* CS-931 was included as an outgroup. The scale bar represents substitutions per site



**Suppl. Fig. 4** Disease progress curves for stem rot severity in trial 2, from initial symptom appearance to plant death.