

**TABLE S1** Primers used in this study

Primer <sup>a</sup>	Sequence (5'-3')	Use
pKD4-ampC_F	CGCGTAAATTTTGTAGGCCGGGTAAGGCGAAGCCGCCACCCGGCAAAGGTGTGTAGGCTGGAGCTGCTTC	<i>ampC</i> deletion
pKD4-ampC_R	CGAACGTCTGACGGGCCCCGGACATCCCCTTGACTCGCTATTACGGAAGATAACTGCATATGAATATCCTCCTTAG	
ampCv_F	TACCTGAATACCCCCGTCGT	Verification of <i>ampC</i> deletion
ampCv_R	TACCTGAATACCCCCGTCGT	
pKD4-ampR_F	CTGACAAACGGTTAAATTTAGCATTAGCTGTTAATTTTTCTAACGGAAGGGACCGTGTAGGCTGGAGCTGCTTC	<i>ampR</i> deletion
pKD4-ampR_R	ACACTGATTGCCGTAGTCACTATCTGACACACCAGGCCCGCCCTCCGGCGGGCCTGCATATGAATATCCTCCTTAG	
ampRv_F	GTGTGGCTGGCCCTGATAAA	Verification of <i>ampR</i> deletion
ampRv_R	TCCTGCTGGTCGGCATTATG	
pKD4-ampD_F	AACATGCTACTCTGAACCGAGTAACAGCACCATAACATAAGGAGTTCAGCGTGTAGGCTGGAGCTGCTTC	<i>ampD</i> deletion
pKD4-ampD_R	GTTATCTCCTTATTCTGACGACGCGTAAGCATGGCGCGAAACCGGGGCCATATGAATATCCTCCTTAG	
ampDv_F	AAGACCTCTTCAACCCAGCG	Verification of <i>ampD</i> deletion
ampDv_R	AAGAGGCCGTATAACGAGCG	
pKD4-ampE_F	GGAGATAACATGACGTTGTTTACCATGCTGCTGGTCATCATCGAGAACGGTGTAGGCTGGAGCTGCTTC	<i>ampE</i> deletion
pKD4-ampE_R	ATTTTGGCATCCCGCCTGCAGATACCCGTAACCGCTACGGCACGCGGGTCATATGAATATCCTCCTTAG	
ampEv_F	GTCTCGATGTATCAGGGGCG	Verification of <i>ampE</i> deletion
ampEv_R	GCTTTACACAAACGCCGGAA	
pKD4-ampG_F	TATAATTTGGCCGGTGATTACAACGGGAAATAACCTTTCGCTTTTATCTGTGTAGGCTGGAGCTGCTTC	<i>ampG</i> deletion
pKD4-ampG_R	GTTAATCCTGCTGACTGACCCGGTGTCTACCGGGTCAGTTTTTAAGAACCATATGAATATCCTCCTTAG	
ampGv_F	TAACGAAAGGACCCCAAGC	Verification of <i>ampG</i> deletion
ampGv_R	GCTGACGTTTCCCAGGGTAA	
pKD4-ampH_F	AGTAGTATAAATACCCATTACTTTCCTCATTACACTATGGATGCTTTTCGGTGTAGGCTGGAGCTGCTTC	<i>ampH</i> deletion
pKD4-ampH_R	GGCTGGACGGAGGCGGTAAGCACCTGGGCTTTATTGGCGCTGAGCTCAGCCACATATGAATATCCTCCTTAG	
ampHv_F	CGCTTTCGGACATACCCTT	Verification of <i>ampH</i> deletion
ampHv_R	GCCATGCTGCTGAATATGGC	
pKD4-ECL_03254_F	AGGGCGCGGCTTCTTAAACTGAAAGTCCCTTCTGAACCAAACGAGATAAACGTGTAGGCTGGAGCTGCTTC	Deletion of ECL_03254
pKD4-ECL_03254_R	AGGCCCGTGCAAGCGTAGCGCCGCCGGGCAAAACTGGCAGAGCGCTCTATCATATGAATATCCTCCTTAG	
ECL_03254v_F	CAAAGGCTTTCACCTGACGC	Verification of ECL_03254 deletion
ECL_03254v_R	CTGTTTCTGAAAACCTGGCGCA	
pKD4-ECL_03253_F	GCGTTTCATAGTGCCGGCAGCCGCGACAACGTTTGATTGATCCGTTACGTGTAGGCTGGAGCTGCTTC	Deletion of ECL_03253
pKD4-ECL_03253_R	GGGTTATGGGGGAAATCCCCCGAAAAACGGAATGAAGGGAGAGGAAGCGCATATGAATATCCTCCTTAG	
ECL_03253v_F	GGCGCAAAACAGCATCAAGA	Verification of ECL_03253 deletion
ECL_03253v_R	GGTGTGGCCTTTCCTGG	
pKD4-dacB_F	TTTCGGGTTGTAGCGCGAGATTATGCGATTTTCCAGATTTATCATCGGAGTGTAGGCTGGAGCTGCTTC	<i>dacB</i> deletion
pKD4-dacB_R	CGTAGTTATTCTGGTAGATGTCCTTATAAAGCCTGCTTTCGAAGCGCACCATATGAATATCCTCCTTAG	
dacBv_F	CAGCTCTTCGCGCAGTTTTT	Verification of <i>dacB</i> deletion
dacBv_R	CACTGGCTTAACAACGTGGC	
pKD4-nagZ_F	CGTCTTCTACCACGCTACGCCTTCCGGGAGGATTTACAGGCTGGCTTTAGTGTAGGCTGGAGCTGCTTC	<i>nagZ</i> deletion
pKD4-nagZ_R	GTGGGTCCAGTCATGTTGGATGTAGAAGGGTTGAACTGGATGCGGAGGACATATGAATATCCTCCTTAG	
nagZv_F	ATCGTCGATGTTGAGCTGCA	Verification of <i>nagZ</i> deletion
nagZv_R	GCCAAAGACTGATCGGCGAT	

ampC_F	TAAGCCGTTTCCACCCGTAC	Quantification of <i>ampC</i> mRNA
ampC_R	AGTAAAAGCCTCCTGGGTGC	
ampR_F	CCGCGATTGAGCTGAATGTG	Quantification of <i>ampR</i> mRNA
ampR_R	AAGGAGTCATTGAGCACCAGG	
ampC2_F	GACGCCCGCTATCAGGTAA	Quantification of <i>ampC2</i> mRNA
ampC2_R	CACCGAACGTGATGTCCAGA	
rpoB_F	AAGGCGAATCCAGCTTGTTGAGC	Quantification of <i>rpoB</i> mRNA
rpoB_R	TGACGTTGCATGTTTCGCACCCATCA	
hsp60-F	GGTAGAAGAAGGCGTGGTTGC <sup>b</sup>	Sequencing of <i>hsp60</i>
hsp60-R	ATGCATTCGGTGGTGATCATCAG <sup>b</sup>	
ampC5_F	CCGTTAGAAAAATTAACAGC	Sequencing of <i>ampC</i>
ampC5_R	GTTAAGTGTAGATGACAGCAGG	
ampC6_R	GGCTGTCACCGCGGCATAACAGG	Sequencing of <i>ampR</i>
ampR4_F	CTCCGTAATAGCGRKTCAAGGG	
ampR4_R	GAATCAAABACCATMACVCGRTG	Sequencing of <i>ampD</i>
ampD_F2	CGGCGAGGCGGCATGATAAACTC	
ampD_R2	CAAGGCGCGAAACCGGGYCCAG	Sequencing of <i>dacB</i>
dacB_F3	CGTAGTATGACGGTTTGTTCG	
dacB_F4	GGCTCCCCGAGGCGCAGTATTGC	Sequencing of <i>dacB</i>
dacB_R3	CCTCCTGCAATAACAGATC	

<sup>a</sup> F, Forward primer; R, Reverse primer.

<sup>b</sup> Primer sequences obtained from (3).

**TABLE S2** Summary of RNA-seq data

Statistics	ECL13047 (sample 1)	ECL13047 (sample 2)	ECL $\Delta$ <i>dacB</i> (sample 1)	ECL $\Delta$ <i>dacB</i> (sample 2)
Total number of reads	11,302,621	11,029,451	8,173,417	10,782,033
Number of uniquely-mapped reads	7,288,398	7,232,330	5,497,204	6,582,713
Percentage of unique-mapped reads (%)	64.5	65.6	67.3	61.1
Average coverage of the genome <sup>a</sup> (X)	137	136	103	124
Percentage of reads mapped to rRNA genes (%)	0.01	<0.01	0.01	<0.01
Number of reads mapped to CDSs	7,287,456	7,231,785	5,496,566	6,582,107
Average number of mapped reads per CDS <sup>b</sup>	1411	1390	1064	1274

<sup>a</sup> The genome size of ECL13047 is 5,314,581 bp.

<sup>b</sup> The number of predicted coding sequences (CDSs) is 5,166.