SUPPLEMENTARY INFORMATION

Title: Identification of fifty class D β-lactamases and of sixty-five *Acinetobacter*-Derived Cephalosporinases in *Acinetobacter* spp.

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Running title: Class C and Class D β-lactamases in *Acinetobacter* spp.

Supplementary figures:

FIG. S1. Amino acid alignment of the 50 OXA-like enzymes identified in this study. The three motifs conserved among class D β-lactamases are boxed. Stars indicate residues identical among all the amino acid sequences.

FIG. S2. Comparison of the neighbor-joining phylogenetic trees obtained for 69 OXA-like class D β-lactamases and 103 RpoB sequences. Similarities between the two trees are indicated by grey, green, blue, and red squares. Bootstrap values (≥70%) obtained after 1000 replicates are given at the nodes. Bar, percentage sequence divergence.

FIG. S3. Dendrogram based on multilocus sequence analysis of the 103 strains studied. Concatenated partial sequences of seven protein-coding genes (2976 nt in total) were compared using the neighbor-joining method based on a Jukes-Cantor distance matrix. The classification into 16 groups and 5 singletons based on RpoB cluster analysis (Figure 2) is indicated on the right. The accession numbers of the genome sequences from which the data were retrieved are indicated in the last column. Bootstrap values (≥70%) obtained after 1000 replicates are given at the nodes. Bar, 1% sequence divergence.

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OXA-264 ---MKLSKLYTLTVLIGFGLSGVACQHIHTPVLFNQIEN---DQTKQIASLFENVQTTGV
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OXA-290 ----------------MIGLTLLGCQNLHAPTQSAVSKK---HDQTEIASLFQHTQTVGV
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OXA-296 FITYDGRQFNRYGNALARAQNAYIPASTFKILNALIGLQHHKVSTSEVFKWKGEKRSFPA
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OXA-308 WEKDMTLSDAMKVSAVPVYQELARRIGLDLMQKEVTRVRYGNTDIGTVVDRFWLDGPLKI
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OXA-281 TPVQEVLFVEKLANTQLAFEPDVQHTVQDMLLIEQKPNYKLYAKSGWGMD-LEPQVGWWT
OXA-274 TPEQEAKFAYQLAKKTLPFDDAVQQQVKDMLYVERRGDSKLYAKSGWGMD-VEPQVGWYT
OXA-275 TPEQEAKFAFQLANKTLPFDDAVQQQVKDMLYVERRGDSKLYAKSGWGMD-VEPQVGWYT
OXA-300 SPEQEVQFAYQLAMKQLPFDRNVQQQVKDMLYIESRGDSKLYAKSGWGMD-VEPQVGWYT
OXA-301 SPEQEVQFAYQLAMKQLPFDSNVQQQVKDMLYIERRGDSKLYAKSGWGMD-VEPQVGWYT
OXA-296 TPEQEAQFVYQLATEQLPFDVKVQKQVKEMLYIERRGDTKLYAKSGWGMD-VKPQVGWYT
OXA-308 TPKQEAQFAYQLATQQLPFDQNVQSQVKDMLYVESRGQSKLFAKSGLSMKNGQPDIGWYT
         *  *  *   *    * *    *  *                ***       *  ** *
```

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OXA-264 GWIEDPNGKVIAFSLNMEMNQPAHAAARKEIVYQALTQLKLL-----
OXA-265 GWIEDPNGKVIAFSLNMEMNQPAHAAARKEIVYQALTQLKLL-----
OXA-289 GWIEQPNGQVIAFSLNLEINKPEHGDARKAIVYQALQQLKLLQKQ--
OXA-290 GWIEQPNGQVIAFALNLEINKPEHGDARKAIVYQALQQLKLLQKQ--
OXA-279 GWIEQPNGQVIAFSLNMQINNSKQGDARKAIVYQALQQLKLLETQ--
OXA-287 GWIEQPNGKITAFSLNMQMSQPEHADARKVIVYQALQELGLLAH---
OXA-303 GWIEQPNGKITAFSLNMQMSQPEHADARKVIVYQALQELGLLAH---
OXA-286 GWIEQPNGKITAFSLNMQMSQPEHADARKAIVYQALQQLGLLAH---
OXA-288 GWIEQANGKITAFSLNMEMSRPEHAEARKAIVYQALQQLDLLAN---
OXA-291 GWIEQANGKITAFSLNMEMSRPEHTEARKAIVYQALQQLDLLAN---
OXA-292 GWIEQANGKVTAFSLNMEMSRPEHAEARKAIVYQALQQLDLLAN---
OXA-293 GWIEQANGKITAFSLNMEMSQPEHAETRKAIVYQALQQLDLLVN---
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OXA-307 GWIEQPNGKIIAFSLNMQMSQPAHADARKVIVYQALQELGLLAN---
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OXA-280 GWVETATGEKVYFALNMHMKTGISASVREQLVKQSLTALGII-----
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OXA-274 GWIEQPNGQITAFALNMHMQTGDDPAERKQLTLSILDKLGLFFYLR-
OXA-275 GWVEQPNGQITAFALNMHMQTGDDPAERKQLTLSILDKLGLFFYLR-
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OXA-301 GWVEQPNGKVTAFALNMNMQAGNDPAERKQLTLSILDKLGLFFYLR-
OXA-296 GWVEQANGQITAFVLNLEMHDGDDVGERKQLTLDALDKLGLFFYLH-
OXA-308 GWVEQADGKIVAFSINMQMVQGLDVNSRQQATLDILDKLGIFFYL--
        **          *  *           *       *  *
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FIG. S1. Amino acid alignment of the 50 OXA-like enzymes identified in this study. The three motifs conserved among class D β-lactamases are boxed. Stars indicate residues identical among all the amino acid sequences.

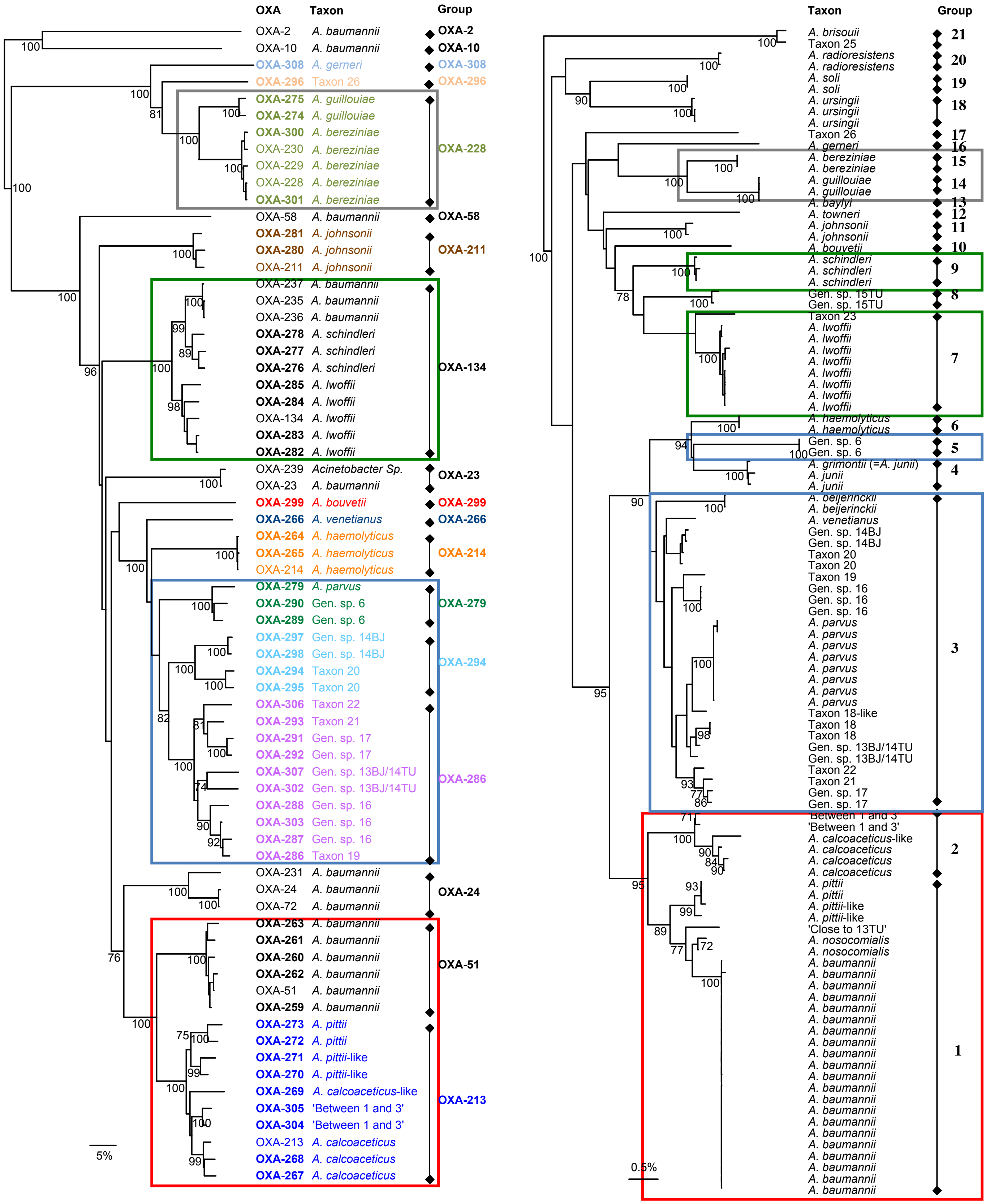
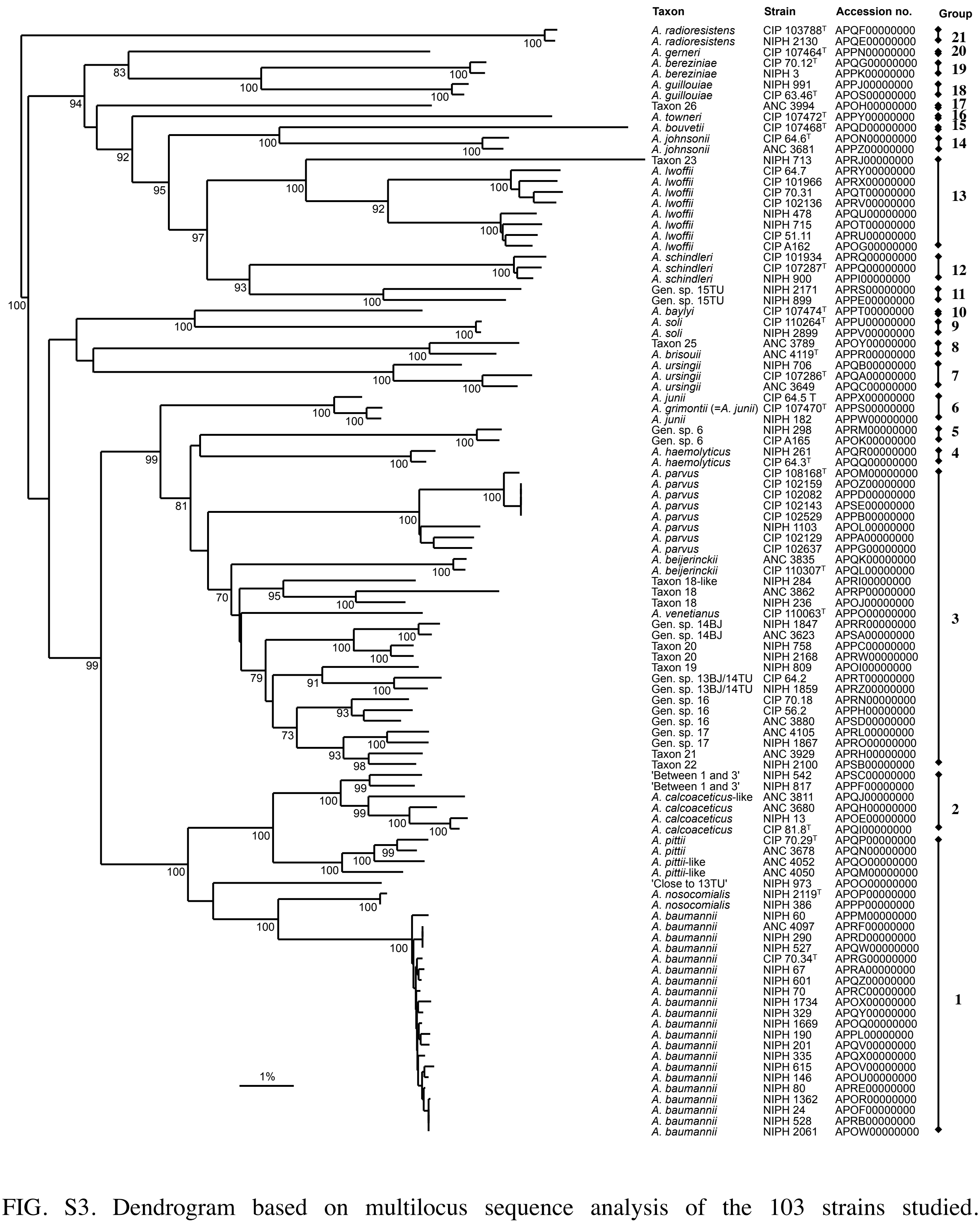


FIG. S2. Comparison of the neighbor-joining phylogenetic trees obtained for 69 OXA-like class D β-lactamases (left) and 103 RpoB sequences (right). Similarities between the two trees are indicated by grey, green, blue, and red squares. Bootstrap values (≥70%) obtained after 1000 replicates are given at the nodes. Bar, percentage sequence divergence.



Taxon	Strain	Accession no.	Group
A. radioresistens	CIP 103788^T	APQF00000000	21
A. radioresistens	NIPH 2130	APQE00000000	
A. gerneri	CIP 107464^T	APPN00000000	20
A. bereziniae	CIP 70.12^T	APQG00000000	19
A. bereziniae	NIPH 3	APPK00000000	
A. guillouiae	NIPH 991	APPJ00000000	18
A. guillouiae	CIP 63.46^T	APOS00000000	
Taxon 26	ANC 3994	APOH00000000	17
A. towneri	CIP 107472^T	APPY00000000	16
A. bouvetii	CIP 107468^T	APQD00000000	15
A. johnsonii	CIP 64.6^T	APON00000000	14
A. johnsonii	ANC 3681	APPZ00000000	
Taxon 23	NIPH 713	APRJ00000000	13
A. lwoffii	CIP 64.7	APRY00000000	
A. lwoffii	CIP 101966	APRX00000000	
A. lwoffii	CIP 70.31	APQT00000000	
A. lwoffii	CIP 102136	APRV00000000	
A. lwoffii	NIPH 478	APQU00000000	
A. lwoffii	NIPH 715	APOT00000000	
A. lwoffii	CIP 51.11	APRU00000000	
A. lwoffii	CIP A162	APOG00000000	
A. schindleri	CIP 101934	APRQ00000000	12
A. schindleri	CIP 107287^T	APPQ00000000	
A. schindleri	NIPH 900	APPI00000000	
Gen. sp. 15TU	NIPH 2171	APRS00000000	11
Gen. sp. 15TU	NIPH 899	APPE00000000	
A. baylyi	CIP 107474^T	APPT00000000	10
A. soli	CIP 110264^T	APPU00000000	9
A. soli	NIPH 2899	APPV00000000	
Taxon 25	ANC 3789	APOY00000000	8
A. brisouii	ANC 4119^T	APPR00000000	
A. ursingii	NIPH 706	APQB00000000	7
A. ursingii	CIP 107286^T	APQA00000000	
A. ursingii	ANC 3649	APQC00000000	
A. junii	CIP 64.5 T	APPX00000000	6
A. grimontii (=*A. junii*)	CIP 107470^T	APPS00000000	
A. junii	NIPH 182	APPW00000000	
Gen. sp. 6	NIPH 298	APRM00000000	5
Gen. sp. 6	CIP A165	APOK00000000	
A. haemolyticus	NIPH 261	APQR00000000	4
A. haemolyticus	CIP 64.3^T	APQQ00000000	
A. parvus	CIP 108168^T	APOM00000000	3
A. parvus	CIP 102159	APOZ00000000	
A. parvus	CIP 102082	APPD00000000	
A. parvus	CIP 102143	APSE00000000	
A. parvus	CIP 102529	APPB00000000	
A. parvus	NIPH 1103	APOL00000000	
A. parvus	CIP 102129	APPA00000000	
A. parvus	CIP 102637	APPG00000000	
A. beijerinckii	ANC 3835	APQK00000000	
A. beijerinckii	CIP 110307^T	APQL00000000	
Taxon 18-like	NIPH 284	APRI00000000	
Taxon 18	ANC 3862	APRP00000000	
Taxon 18	NIPH 236	APOJ00000000	
A. venetianus	CIP 110063^T	APPO00000000	
Gen. sp. 14BJ	NIPH 1847	APRR00000000	
Gen. sp. 14BJ	ANC 3623	APSA00000000	
Taxon 20	NIPH 758	APPC00000000	
Taxon 20	NIPH 2168	APRW00000000	
Taxon 19	NIPH 809	APOI00000000	
Gen. sp. 13BJ/14TU	CIP 64.2	APRT00000000	
Gen. sp. 13BJ/14TU	NIPH 1859	APRZ00000000	
Gen. sp. 16	CIP 70.18	APRN00000000	
Gen. sp. 16	CIP 56.2	APPH00000000	
Gen. sp. 16	ANC 3880	APSD00000000	
Gen. sp. 17	ANC 4105	APRL00000000	
Gen. sp. 17	NIPH 1867	APRO00000000	
Taxon 21	ANC 3929	APRH00000000	
Taxon 22	NIPH 2100	APSB00000000	
'Between 1 and 3'	NIPH 542	APSC00000000	2
'Between 1 and 3'	NIPH 817	APPF00000000	
A. calcoaceticus-like	ANC 3811	APQJ00000000	
A. calcoaceticus	ANC 3680	APQH00000000	
A. calcoaceticus	NIPH 13	APOE00000000	
A. calcoaceticus	CIP 81.8^T	APQI00000000	
A. pittii	CIP 70.29^T	APQP00000000	1
A. pittii	ANC 3678	APQN00000000	
A. pittii-like	ANC 4052	APQO00000000	
A. pittii-like	ANC 4050	APQM00000000	
'Close to 13TU'	NIPH 973	APOO00000000	
A. nosocomialis	NIPH 2119^T	APOP00000000	
A. nosocomialis	NIPH 386	APPP00000000	
A. baumannii	NIPH 60	APPM00000000	
A. baumannii	ANC 4097	APRF00000000	
A. baumannii	NIPH 290	APRD00000000	
A. baumannii	NIPH 527	APQW00000000	
A. baumannii	CIP 70.34^T	APRG00000000	
A. baumannii	NIPH 67	APRA00000000	
A. baumannii	NIPH 601	APQZ00000000	
A. baumannii	NIPH 70	APRC00000000	
A. baumannii	NIPH 1734	APOX00000000	
A. baumannii	NIPH 329	APQY00000000	
A. baumannii	NIPH 1669	APOQ00000000	
A. baumannii	NIPH 190	APPL00000000	
A. baumannii	NIPH 201	APQV00000000	
A. baumannii	NIPH 335	APQX00000000	
A. baumannii	NIPH 615	APOV00000000	
A. baumannii	NIPH 146	APOU00000000	
A. baumannii	NIPH 80	APRE00000000	
A. baumannii	NIPH 1362	APOR00000000	
A. baumannii	NIPH 24	APOF00000000	
A. baumannii	NIPH 528	APRB00000000	
A. baumannii	NIPH 2061	APOW00000000	

FIG. S3. Dendrogram based on multilocus sequence analysis of the 103 strains studied. Concatenated partial sequences of seven protein-coding genes (2976 nt in total) were compared using the neighbor-joining method based on a Jukes-Cantor distance matrix. The classification into 16 groups and 5 singletons based on RpoB cluster analysis (Figure 2) is indicated on the right. The accession numbers of the genome sequences from which the data were retrieved are indicated in the last column. Bootstrap values (≥70%) obtained after 1000 replicates are given at the nodes. Bar, 1% sequence divergence.