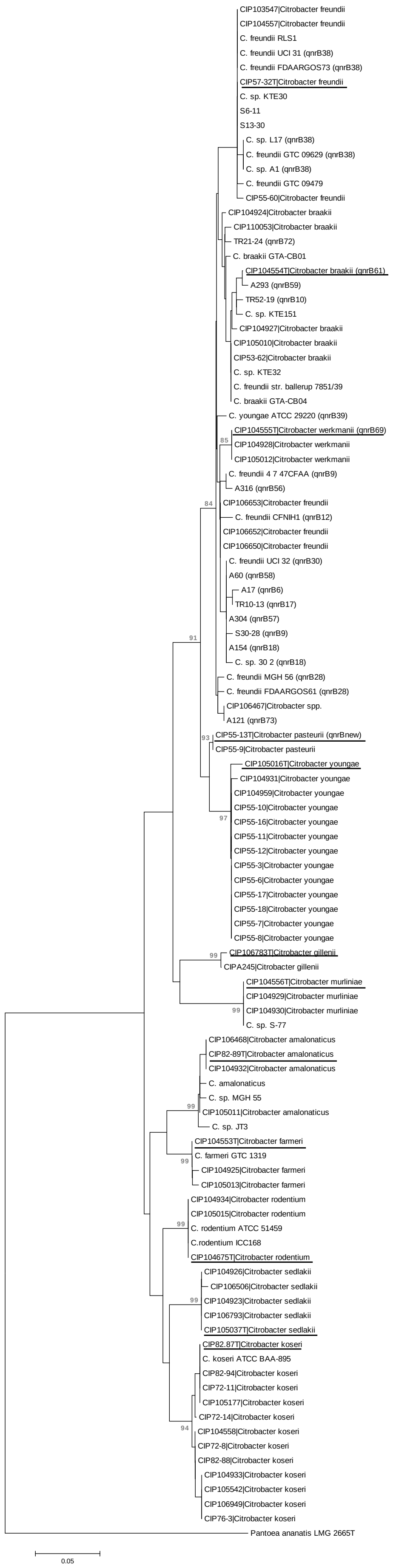
CIP103547|Citrobacter freundii
CIP104557|Citrobacter freundii
C. freundii RLS1
C. freundii UCI 31 (qnrB38)
C. freundii FDAARGOS73 (qnrB38)
CIP57-32T|Citrobacter freundii
C. sp. KTE30
S6-11
S13-30
C. sp. L17 (qnrB38)
C. freundii GTC 09629 (qnrB38)
C. sp. A1 (qnrB38)
C. freundii GTC 09479
CIP55-60|Citrobacter freundii
CIP104924|Citrobacter braakii
CIP110053|Citrobacter braakii
TR21-24 (qnrB72)
C. braakii GTA-CB01
CIP104554T|Citrobacter braakii (qnrB61)
A293 (qnrB59)
TR52-19 (qnrB10)
C. sp. KTE151
CIP104927|Citrobacter braakii
CIP105010|Citrobacter braakii
CIP53-62|Citrobacter braakii
C. sp. KTE32
C. freundii str. ballerup 7851/39
C. braakii GTA-CB04
C. youngae ATCC 29220 (qnrB39)
CIP104555T|Citrobacter werkmanii (qnrB69)
85
CIP104928|Citrobacter werkmanii
CIP105012|Citrobacter werkmanii
C. freundii 4 7 47CFAA (qnrB9)
A316 (qnrB56)
84
CIP106653|Citrobacter freundii
C. freundii CFNIH1 (qnrB12)
CIP106652|Citrobacter freundii
CIP106650|Citrobacter freundii
C. freundii UCI 32 (qnrB30)
A60 (qnrB58)
A17 (qnrB6)
TR10-13 (qnrB17)
A304 (qnrB57)
91
S30-28 (qnrB9)
A154 (qnrB18)
C. sp. 30 2 (qnrB18)
C. freundii MGH 56 (qnrB28)
C. freundii FDAARGOS61 (qnrB28)
CIP106467|Citrobacter spp.
A121 (qnrB73)
93
CIP55-13T|Citrobacter pasteurii (qnrBnew)
CIP55-9|Citrobacter pasteurii
CIP105016T|Citrobacter youngae
CIP104931|Citrobacter youngae
CIP104959|Citrobacter youngae
CIP55-10|Citrobacter youngae
97
CIP55-16|Citrobacter youngae
CIP55-11|Citrobacter youngae
CIP55-12|Citrobacter youngae
CIP55-3|Citrobacter youngae
CIP55-6|Citrobacter youngae
CIP55-17|Citrobacter youngae
CIP55-18|Citrobacter youngae
CIP55-7|Citrobacter youngae
CIP55-8|Citrobacter youngae
99
CIP106783T|Citrobacter gillenii
CIPA245|Citrobacter gillenii
CIP104556T|Citrobacter murliniae
CIP104929|Citrobacter murliniae
99
CIP104930|Citrobacter murliniae
C. sp. S-77
CIP106468|Citrobacter amalonaticus
CIP82-89T|Citrobacter amalonaticus
CIP104932|Citrobacter amalonaticus
C. amalonaticus
C. sp. MGH 55
99
CIP105011|Citrobacter amalonaticus
C. sp. JT3
CIP104553T|Citrobacter farmeri
C. farmeri GTC 1319
99
CIP104925|Citrobacter farmeri
CIP105013|Citrobacter farmeri
CIP104934|Citrobacter rodentium
CIP105015|Citrobacter rodentium
99
C. rodentium ATCC 51459
C.rodentium ICC168
CIP104675T|Citrobacter rodentium
CIP104926|Citrobacter sedlakii
CIP106506|Citrobacter sedlakii
99
CIP104923|Citrobacter sedlakii
CIP106793|Citrobacter sedlakii
CIP105037T|Citrobacter sedlakii
CIP82.87T|Citrobacter koseri
C. koseri ATCC BAA-895
CIP82-94|Citrobacter koseri
CIP72-11|Citrobacter koseri
CIP105177|Citrobacter koseri
CIP72-14|Citrobacter koseri
94
CIP104558|Citrobacter koseri
CIP72-8|Citrobacter koseri
CIP82-88|Citrobacter koseri
CIP104933|Citrobacter koseri
CIP105542|Citrobacter koseri
CIP106949|Citrobacter koseri
CIP76-3|Citrobacter koseri
Pantoea ananatis LMG 2665T
0.05

FIG S1. Affiliation of LeuS amino acid sequences. Genetic distances were constructed using Jones-Taylor-Thornton (JTT) model. Numbers at branch points indicate bootstrap percentages from Neighbor-Joining method analysis and only values greater than 80% are shown. Horizontal Bar: genetic distance of 0.05. All the different *Citrobacter* spp. type strains are underlined and *qnrB* alleles are shown in parentheses. *Pantoea ananatis* LMG 2665^T was used as outgroup (PATRIC ID fig|1378093.3.peg.600).

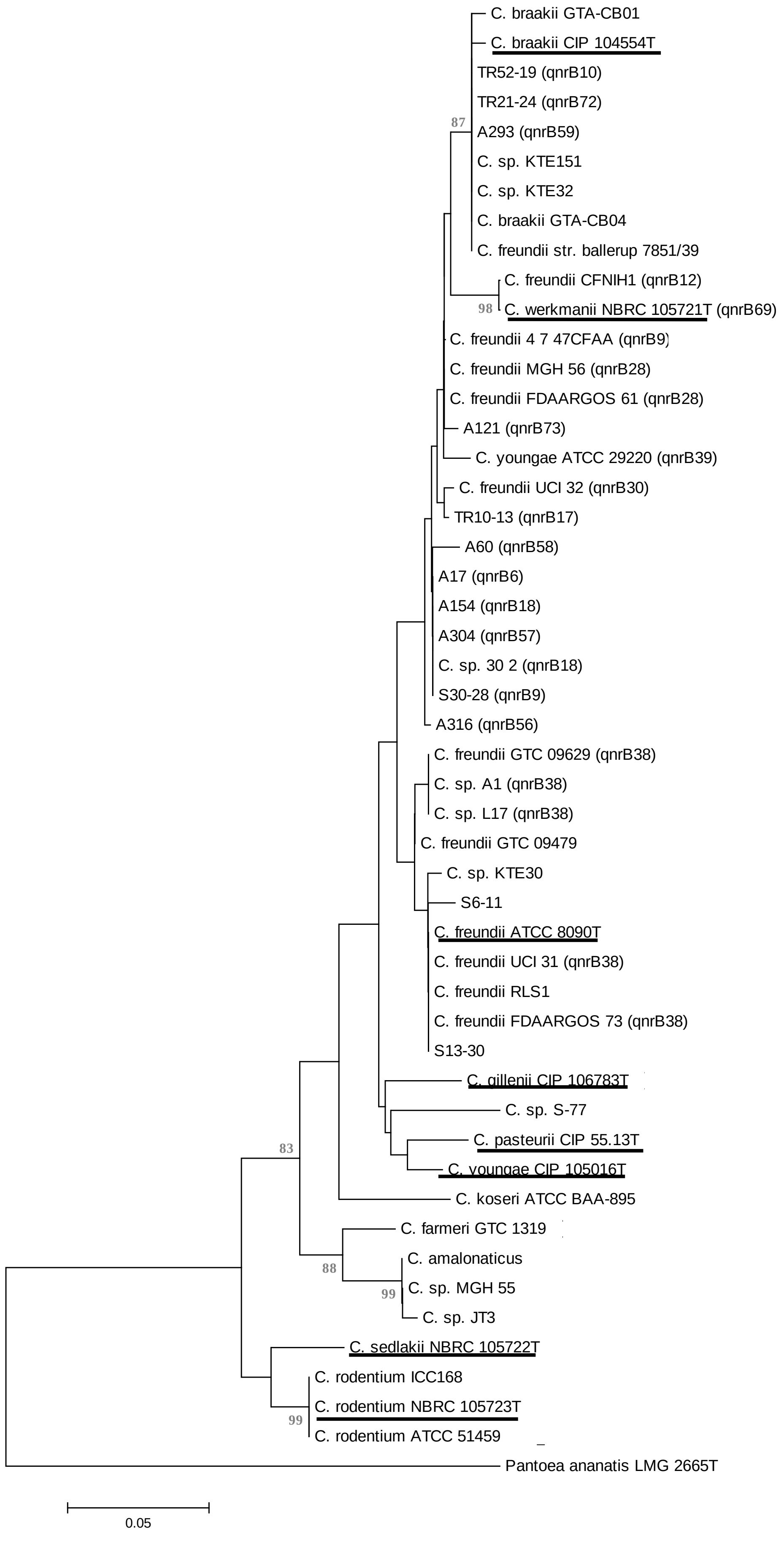
C. braakii GTA-CB01
C. braakii CIP 104554T
TR52-19 (qnrB10)
TR21-24 (qnrB72)
87
A293 (qnrB59)
C. sp. KTE151
C. sp. KTE32
C. braakii GTA-CB04
C. freundii str. ballerup 7851/39
C. freundii CFNIH1 (qnrB12)
98
C. werkmanii NBRC 105721T (qnrB69)
C. freundii 4 7 47CFAA (qnrB9)
C. freundii MGH 56 (qnrB28)
C. freundii FDAARGOS 61 (qnrB28)
A121 (qnrB73)
C. youngae ATCC 29220 (qnrB39)
C. freundii UCI 32 (qnrB30)
TR10-13 (qnrB17)
A60 (qnrB58)
A17 (qnrB6)
A154 (qnrB18)
A304 (qnrB57)
C. sp. 30 2 (qnrB18)
S30-28 (qnrB9)
A316 (qnrB56)
C. freundii GTC 09629 (qnrB38)
C. sp. A1 (qnrB38)
C. sp. L17 (qnrB38)
C. freundii GTC 09479
C. sp. KTE30
S6-11
C. freundii ATCC 8090T
C. freundii UCI 31 (qnrB38)
C. freundii RLS1
C. freundii FDAARGOS 73 (qnrB38)
S13-30
C. gillenii CIP 106783T
C. sp. S-77
C. pasteurii CIP 55.13T
83
C. youngae CIP 105016T
C. koseri ATCC BAA-895
C. farmeri GTC 1319
C. amalonaticus
88
C. sp. MGH 55
99
C. sp. JT3
C. sedlakii NBRC 105722T
C. rodentium ICC168
C. rodentium NBRC 105723T
99
C. rodentium ATCC 51459
Pantoea ananatis LMG 2665T
0.05

FIG S2. Affiliation of RecN amino acid sequences. Genetic distances were constructed using Jones-Taylor-Thornton (JTT) model. Numbers at branch points indicate bootstrap percentages from Neighbor-Joining method analysis and only values greater than 80% are shown. Horizontal Bar: genetic distance of 0.05. All the different *Citrobacter* spp. type strains are underlined and *qnrB* alleles are shown in parentheses. *Pantoea ananatis* LMG 2665^{T} was used as outgroup (PATRIC ID fig|1378093.3.peg.2577).

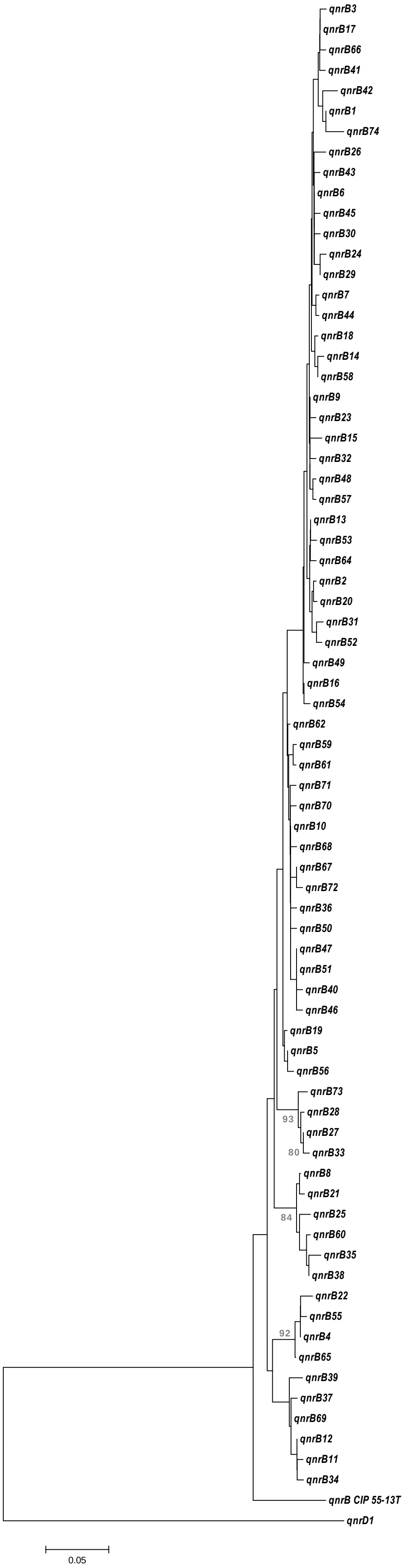
qnrB3
qnrB17
qnrB66
qnrB41
qnrB42
qnrB1
qnrB74
qnrB26
qnrB43
qnrB6
qnrB45
qnrB30
qnrB24
qnrB29
qnrB7
qnrB44
qnrB18
qnrB14
qnrB58
qnrB9
qnrB23
qnrB15
qnrB32
qnrB48
qnrB57
qnrB13
qnrB53
qnrB64
qnrB2
qnrB20
qnrB31
qnrB52
qnrB49
qnrB16
qnrB54
qnrB62
qnrB59
qnrB61
qnrB71
qnrB70
qnrB10
qnrB68
qnrB67
qnrB72
qnrB36
qnrB50
qnrB47
qnrB51
qnrB40
qnrB46
qnrB19
qnrB5
qnrB56
qnrB73
qnrB28
93
qnrB27
80
qnrB33
qnrB8
qnrB21
84
qnrB25
qnrB60
qnrB35
qnrB38
qnrB22
qnrB55
92
qnrB4
qnrB65
qnrB39
qnrB37
qnrB69
qnrB12
qnrB11
qnrB34
qnrB CIP 55-13T
qnrD1
0.05

FIG S3. Affiliation of QnrB amino acid sequences. Genetic distances were constructed using Jones-Taylor-Thornton (JTT) model. Numbers at branch points indicate bootstrap percentages from Neighbor-Joining method analysis and only values greater than 80% are shown. Horizontal Bar: genetic distance of 0.05. QnrD1 was used as outgroup (GenBank accession number ACG70184).

TABLE S1. Epidemiological data of *Citrobacter* spp. isolates harboring complete or truncated *qnrB* genes characterized in this study.

Isolate	Phylogenetic assignment[a]	Origin (sample)	PFGE-type (no.)	*qnrB* allele[b]	Antibiotic resistance pattern[c, d, e]
A17	*Citrobacter* sp. I	Water well (W1)	A (1)	*qnrB6*	IPM, NAL, SUL, (KAN), (STR)
A313	*Citrobacter* sp. I	Natural Spring (W63)	B (3)	*qnrB56*	(ATM), NAL, SUL, (TET)
A314					
A316					
A304	*Citrobacter* sp. I	Fountain (W60)	C (2)	*qnrB57*	KAN, STR, NAL, SUL, (TET)
A305					
A60	*Citrobacter* sp. I	Water well (W13)	D (1)	*qnrB58*	STR, NAL, SUL
A154	*Citrobacter* sp. I	Borehole (W33)	E (1)	*qnrB18*	STR, NAL, SUL
S30-28	*Citrobacter* sp. I	Ready-to-eat salads (S30)	F (1)	*qnrB9*	NAL
TR10-13	*Citrobacter* sp. I	Aquaculture (feed) (AQ10)	G (1)	*qnrB17*	
A121	*Citrobacter* sp. III	Water well (W23)	H (1)	*qnrB73*	NAL, SUL
A293	*C. braakii*	Borehole (W57)	I (3)	*qnrB59*	STR, NAL, SUL, (TET)
A295					
A297					
TR21-24	*C. braakii*	Aquaculture (sediment) (AQ21)	J (2)	*qnrB72*	NAL, TET
TR21-25					
TR52-19	*C. braakii*	Trout (AQ52)	K (3)	*qnrB10*	NAL, TET
TR52-21					
TR52-22					
S6-11	*C. freundii*	Ready-to-eat salads (S6)	L (1)	Δ*qnrB*	NAL, SUL, STR
S13-30	*C. freundii*	Ready-to-eat salads (S13)	M (1)	Δ*qnrB*	SUL, STR

[a] Species identification according to the phylogenetic affiliation obtained with *leuS* and *recN* genes.
[b] All the different *qnrB* alleles were chromosomally located.
[c] Natural resistance patterns were not included.
[d] Antimicrobial agents tested [disk diffusion method according to EUCAST (http://www.eucast.org/) guidelines and breakpoints or following Clinical and Laboratory Standards Institute recommendations (http://clsi.org/) for antibiotics not considered in the EUCAST documents]: β-lactam (FEP, cefepime; ATM, aztreonam; IPM, imipenem; ERT, ertapenem) and non-β-lactam (AMK, amikacin; GEN, gentamicin; KAN, kanamycin; NET, netilmicin; STR, streptomycin; TOB, tobramycin; SUL, sulfonamides; TMP, trimethoprim; TET, tetracycline; CHL, chloramphenicol; CIP, ciprofloxacin; NAL, nalidixic acid) antibiotics.
[e] Variable presence of a given resistance phenotype is indicated in parentheses.

TABLE S2. Phylogenetic assignment of *Citrobacter* spp. isolates harboring or not *qnrB* genes.

Phylogenetic assignment^a	**Isolate**	***qnrB* allele**	**GenBank accession number**	**Accession numbers (GenBank/PATRIC)**	
				leuS	***recN***
C. freundii	CIP57-32^T = C. freundii ATCC 8090^T	*ΔqnrB*	AB734052	EKS58631	EKS56099
C. freundii	C. freundii GTC 09479	*ΔqnrB*	NZ_AOMS01000003	EMF20765	EMF22422
C. freundii	C. freundii RLS1	*ΔqnrB*	NZ_JATT01000060	EXF29472	EXF30442
C. freundii	C. sp. KTE30	*ΔqnrB*	ASQJ01000007	EOQ25427	EOQ21965
C. freundii	S6-11	*ΔqnrB*	NA	KR998039	KR998026
C. freundii	S13-30	*ΔqnrB*	NA	KR998040	KR998027
C. freundii	C. freundii GTC 09629	*qnrB38*	NZ_AOUE01000004	EOD61956	EOD59147
C. freundii	C. sp. A1	*qnrB38*	NZ_AKTT01000018	EJF24310	EJF20625
C. freundii	C. sp. L17	*qnrB38*	NZ_AMPE01000004	EKU36588	EKU31915
C. freundii	C. freundii UCI31	*qnrB38*	JAPB01000002	ETX72722	ETX69942
C. freundii	C. freundii FDAARGOS_73	*qnrB38*	JTBJ01000001	KGY84667	KGY86553
C. braakii	CIP 104554^T = *C. braakii* ATCC 51113^T	*qnrB61*	AB734053	KM515986	KF057886
C. braakii	C. braakii GTA-CB01	-	JRHK01000002	KHE06528	KHE04073
C. braakii	C. braakii GTA-CB04	-	JRHL01000001	KHE09771	KHE09463
C. braakii	C. freundii str. ballerup 7851/39	NA	NA	fig|670484.3.peg.401	fig|670484.3.peg.2509
C. braakii	C. sp. KTE151	*ΔqnrB*	ASQK01000005	EOQ50286	EOQ47363
C. braakii	C. sp. KTE32	-	ASQL01000009	EOQ32555	EOQ28285
C. braakii	TR52-19	*qnrB10*	KP339256	KR998044	KR998031
C. braakii	A293	*qnrB59*	KP339262	KR998036	KR998023
C. braakii	TR21-24	*qnrB72*	KP339263	KR998043	KR998030
C. youngae	CIP 105016^T	NA	NA	KM515993	KF057888

Phylogenetic assignment[a]	**Isolate**	***qnrB* allele**	**GenBank accession number**	**Accession numbers (GenBank/PATRIC)**	
				leuS	***recN***
C. werkmanii	CIP 104555^{T} = C. werkmanii NBRC 105721^{T}	*qnrB69*	BBMW01000005	GAL44920	GAL47081
C. werkmanii	C. freundii CFNIH1	*qnrB12*	CP007557	WP_038638761	AHY14573
C. amalonaticus	CIP 82.89^{T}	NA	NA	EU010040	n.a.
C. amalonaticus	C. amalonaticus	-	JMQQ01000039	KEY47803	KEY45284
C. amalonaticus	C. sp. JT3	NA	NA	fig|1451265.3.peg.2413	fig|1451265.3.peg.1330
C. amalonaticus	C. freundii MGH55	-	JMUK01000018	KDF04575	KDF07738
C. farmeri	CIP 104553^{T}	NA	NA	KM515987	n.a.
C. farmeri	C. farmeri GTC1319	-	NZ_BBMX01000005	GAL49434	GAL51860
C. koseri	CIP 82.87^{T} = C. koseri ATCC 27028^{T}	-	AB734056	KM515994	n.a.
C. koseri	C. koseri ATCC BAA-895	-	CP000822	YP_001454059	YP_001455447
C. rodentium	C. rodentium NBRC 105723^{T}	-	NZ_BBNA01000024	fig|1218085.3.peg.3980	fig|1218085.3.peg.4189
C. rodentium	C. rodentium ATCC 51459	-	JXUN01000211	KIQ50925	KIQ49016
C. rodentium	C. rodentium ICC168	-	FN543502	YP_003364286	YP_003366100
C. sedlakii	C. sedlakii NBRC 105722^{T}	-	NZ_BBNB01000001	fig|1218086.3.peg.1142	fig|1218086.3.peg.2278
C. pasteurii	CIP55-13^{T}	*qnrBnew*	CDHL01000019	CEJ66010	CEJ67563
C. murliniae	CIP 104556^{T}	NA	NA	KM515989	n.a.
C. murliniae	C. sp. S-77	NA	NA	fig|1080067.3.peg.1081	fig|1080067.3.peg.3390
C. gillenii	CIP 106783^{T}	NA	NA	KM515988	KF057887
Citrobacter sp. I	A17	*qnrB6*	KP339254	KR998032	KR998019
Citrobacter sp. I	S30-28	*qnrB9*	KP339255	KR998041	KR998028
Citrobacter sp. I	C. freundii 4_7_47CFAA	*qnrB9*	ADLG01000026	EHL82656	EHL86564

Phylogenetic assignment[a]	**Isolate**	***qnrB* allele**	**GenBank accession number**	**Accession numbers (GenBank/PATRIC)**	
				leuS	***recN***
Citrobacter sp. I	TR10-13	*qnrB17*	KP339257	KR998042	KR998029
Citrobacter sp. I	A154	*qnrB18*	KP339258	KR998035	KR998022
Citrobacter sp. I	C. sp. 30_2	*qnrB18*	ACDJ02000027	ZP_04561108	ZP_04560012
Citrobacter sp. I	C. freundii UCI32	*qnrB30*	JAPA01000008	ETX65167	ETX61851
Citrobacter sp. I	A304	*qnrB57*	KP339260	KR998037	KR998024
Citrobacter sp. I	A60	*qnrB58*	KP339261	KR998033	KR998020
Citrobacter sp. I	A316	*qnrB56*	KP339259	KR998038	KR998025
Citrobacter sp. II	C. youngae ATCC 29220	*qnrB39*	ABWL02000005	ZP_03835838	ZP_03838025
Citrobacter sp. III	C. freundii FDAARGOS_61	*qnrB28*	JTBV01000001	KGZ32966	KGZ31013
Citrobacter sp. III	C. freundii MGH56	*qnrB28*	JMUJ01000007	KDF21035	KDF13460
Citrobacter sp. III	A121	*qnrB73*	KP339264	KR998034	KR998021

[a] Species identification according to the phylogenetic affiliation obtained with *leuS* and *recN* genes. NA, not attainable. *Citrobacter* spp. type strains are indicated in grey shadows.