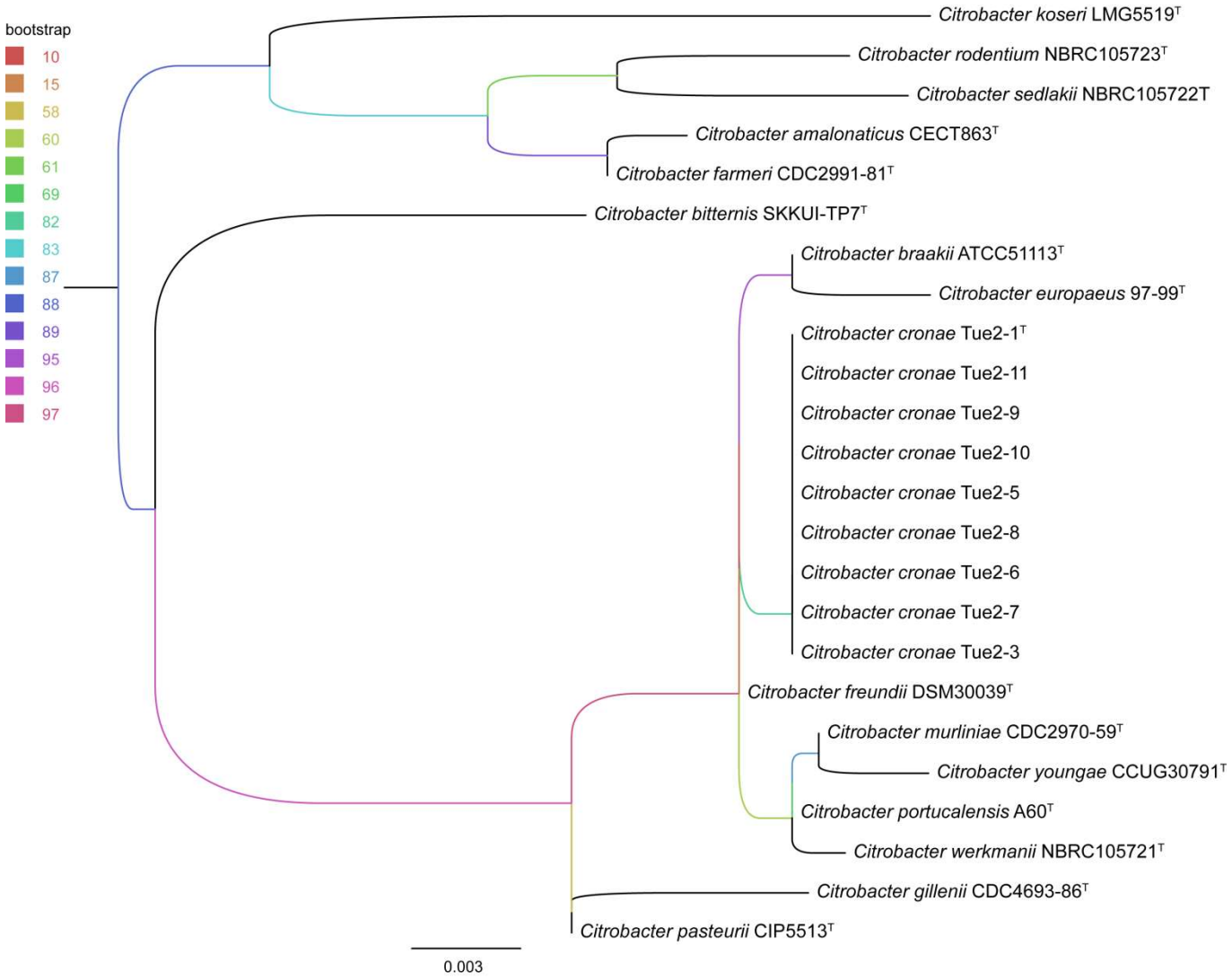
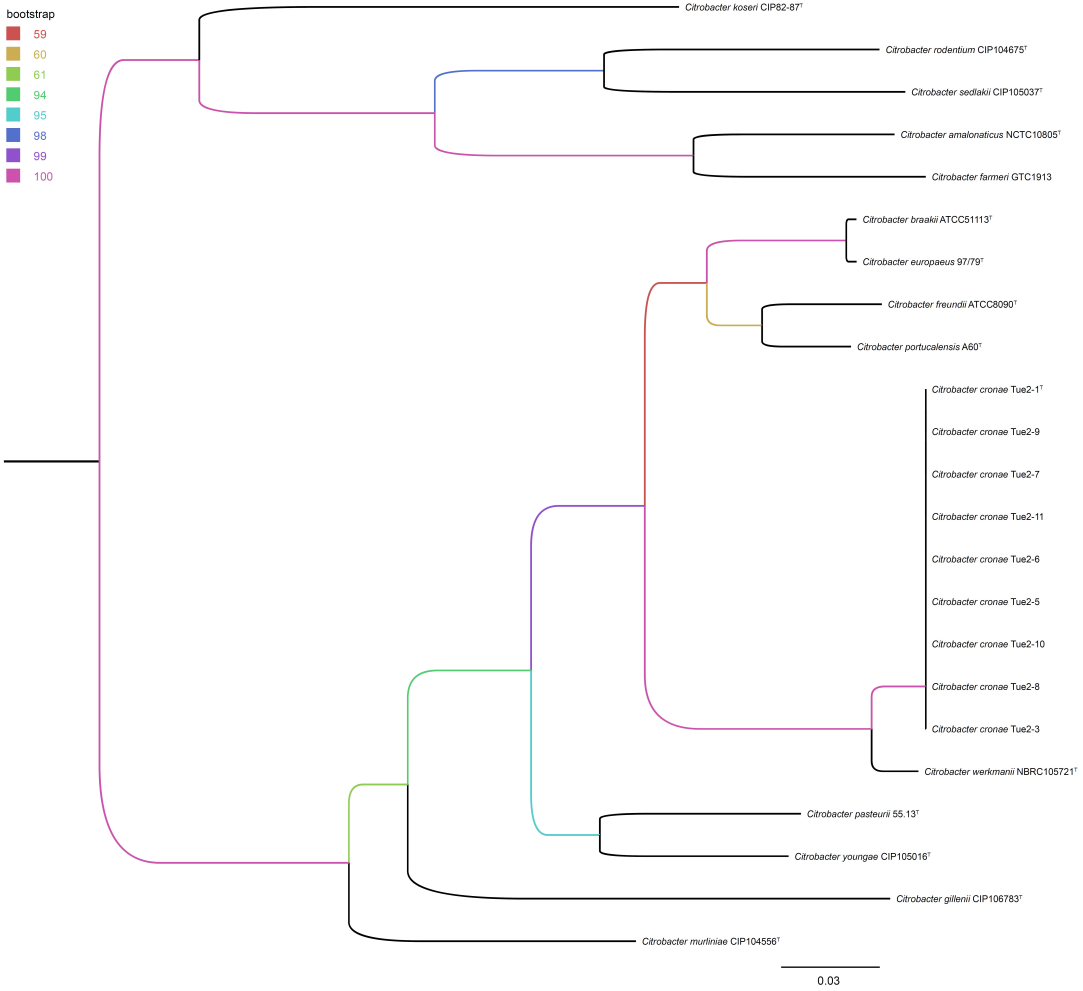
1 Supplementary Figures and Tables



2

Supplementary Figure S1: Phylogenetic tree based on 16S rRNA sequences. Calculation of phylogenetic relationship was performed with 1000 bootstrap replicates and the scale bar represents the expected number of changes per site. The tree was rooted at midpoint.



Supplementary Figure S2: Maximum-likelihood phylogeny based on *recN* gene. DNA-sequences of *recN* were extracted from available WGS data of *Citrobacter* type strains. Phylogeny was conducted using 1000 bootstrap replicates with a scale bar representing the expected number of changes per site. The tree was rooted at midpoint.

Supplementary Table S1: Overview of *Citrobacter* species type strains, strain identification and corresponding nucleotide accession/Gen Bank/ENA numbers of the strains included in the study.

	Whole genome sequencing data		16S rRNA sequence	
***Citrobacter* species**	**Strain ID**	**Gen Bank / ENA number**	**Strain ID**	**Accession number**
Citrobacter amalonaticus	NTC10805^T	UFVN01000003.1	CECT863^T	FR870441
Citrobacter bitternis	n/a	n/a	SKKUI-TP7^T	KJ817168
Citrobacter braakii	ATCC51113^T	NZ_NAEW01000001.1	ATCC51113^T	NAEW01000064
Citrobacter europaeus	97/79^T	NZ_FLYB01000018.1	97/79^T	FLYB01000015
Citrobacter farmeri	GTC1319	NZ_BBMX01000006.1	CDC2991-81^T	AF025371
Citrobacter freundii	ATCC8090^T	NZ_JMTA01000001.1	DSM30039^T	AJ233408
Citrobacter gillenii	CIP106783^T	ERS574813	CDC4693-86^T	AF025367
Citrobacter koseri	NCTC10786^T	UAVY01000004.1	LMG5519^T	HQ992945
Citrobacter murliniae	CIP104556^T	ERS574814	CDC2970-59^T	AF025369
Citrobacter pasteurii	CIP55-13^T	NZ_CDHL01000039.1	CIP55.13^T	CDHL01000036
Citrobacter portucalensis	A60^T	NZ_MVFY01000001.1	A60^T	MVFY01000035
Citrobacter rodentium	NBRC105723^T	NZ_BBNA01000001.1	NBRC105723^T	BBNA01000105
Citrobacter sedlakii	NBRC105722^T	NZ_BBNB01000001.1	NBRC105722^T	BBNB01000023
Citrobacter werkmanii	NBRC105721^T	NZ_BBMW01000009.1	NBRC105721^T	BBMW01000025
Citrobacter youngae	CCUG30791^T	NZ_RPOI01000016.1	CCUG30791^T	RPOI01000045
***Citrobacter* species from this study**				
Citrobacter cronae	Tue2-1^T	VOSQ00000000	Tue2-1^T	MN548424
Citrobacter cronae	Tue2-3	n/a	Tue2-3	n/a
Citrobacter cronae	Tue2-5	n/a	Tue2-5	n/a
Citrobacter cronae	Tue2-6	n/a	Tue2-6	n/a
Citrobacter cronae	Tue2-7	n/a	Tue2-7	n/a
Citrobacter cronae	Tue2-8	n/a	Tue2-8	n/a
Citrobacter cronae	Tue2-9	n/a	Tue2-9	n/a
Citrobacter cronae	Tue2-10	n/a	Tue2-10	n/a
Citrobacter cronae	Tue2-11	n/a	Tue2-11	n/a

Supplementary Table S2 (A and B): Percentage of average nucleotide identity (ANI) and calculation of digital DNA-DNA-hybridization (dDDH) for the nine study isolates (S2A) and for *Citrobacter* type strains (S2B).

S2A

		1		2		3		4		5		6		7		8		9	
Strain	***Citrobacter* species**	ANI	dDDH	ANI	dDDH	ANI	dDDH	ANI	dDDH	ANI	dDDH	ANI	dDDH	ANI	dDDH	ANI	dDDH	ANI	dDDH
1	*C. cronae* Tue2_1^T	*	*	99.96	99.8	99.97	100	99.67	98.6	99.67	98.3	99.97	99.9	99.97	100	99.97	99.8	99.97	100
2	*C. cronae* Tue2_3			*	*	99.96	100	99.67	98.6	99.66	98.3	99.98	99.9	99.98	100	99.96	99.7	99.96	100
3	*C. cronae* Tue2_5					*	*	99.78	99.5	99.78	99.2	99.98	99.9	99.98	99.9	99.97	99.6	99.97	100
4	*C. cronae* Tue2_6							*	*	99.86	99.6	99.51	99.3	99.56	99.5	99.65	99.6	99.65	99.6
5	*C. cronae* Tue2_7									*	*	99.46	99.1	99.5	99.3	99.59	99.4	99.57	99.3
6	*C. cronae* Tue2_8											*	*	99.99	100	99.91	99.6	99.91	100
7	*C. cronae* Tue2_9													*	*	99.91	99.7	99.91	100
8	*C. cronae* Tue2_10															*	*	99.99	99.9
9	*C. cronae* Tue2_11																	*	*

S2B

		1		2		3		4		5		6		7		8		9		10		11		12		13		14		15	
Strain	***Citrobacter* species**	ANI	dDDH	ANI	dDDH	ANI	dDDH	ANI	dDDH	ANI	dDDH	ANI	dDDH	ANI	dDDH	ANI	dDDH	ANI	dDDH	ANI	dDDH	ANI	dDDH	ANI	dDDH	ANI	dDDH	ANI	dDDH	ANI	dDDH
1	*C. cronae* Tue2_1^T	*	*	81.71	25.4	90.21	42.7	90.53	43	81.35	25	90.03	41.7	85.85	31.7	82.75	26.9	85.85	31.4	87.93	36.2	90.11	42.4	80.97	24.9	80.88	24.7	95.92	70	92.48	51.3
2	*C. amalonaticus* NTC10505^T			*	*	81.75	25.3	81.85	25.2	91.08	44.6	81.8	25.3	81.89	25.4	83.05	27	81.46	24.9	81.83	25.1	81.8	25.4	83.99	28.6	83.88	27.9	81.75	25.3	81.98	25.8
3	*C. braakii* ATCC51113^T					*	*	92.57	52.9	81.5	25.1	91.87	48	85.98	31.7	82.77	26.9	86.05	31.6	88.86	38.8	91.64	48.5	80.86	24.8	80.95	24.5	90.35	42.8	90.31	43.1
4	*C. europaeus* 97/79^T							*	*	81.27	25	91.92	49	85.68	31.6	82.76	26.9	85.87	31.6	88.76	38.5	91.92	50.3	80.81	24.7	80.66	24.6	90.45	43.4	90.2	42.9
5	*C. farmeri* GTC1319									*	*	81.49	25.1	81.62	25.2	82.78	26.6	81.29	24.7	81.43	24.9	81.52	25.1	83.6	28	83.61	27.5	81.51	25.1	81.76	25.5
6	*C. freundii* ATCC8090^T											*	*	86.08	31.7	82.79	26.6	86.08	31.4	89.66	40.3	94.16	58.4	81.11	24.8	81.05	24.5	90.33	41.9	90.12	41.6
7	*C. gillenii* CIP106783^T													*	*	82.84	26.8	86.48	32.3	86.4	32	86.2	31.7	81.23	25	81.11	24.6	86.08	31.6	86.04	31.5
8	*C. koseri* NCTC10786^T															*	*	82.81	26.4	82.92	26.4	83.14	26.8	82.7	26.9	82.51	26.1	83.01	26.9	83.27	27.2
9	*C. murliniae* CIP104556^T																	*	*	86.39	31.9	86	31.6	80.61	24.2	80.47	24	85.94	31.3	85.86	31.5
10	*C. pasteurii* CIP55-13^T																			*	*	88.86	38.4	81.03	24.7	80.97	24.5	88.31	36.3	88.29	36.5
11	*C. portucalensis* A60^T																					*	*	81.22	25	81.12	24.6	90.47	42.6	90.3	42.4
12	*C. rodentium* NBRC105723^T																							*	*	85.94	31.7	81.29	25.1	81.59	25.5
13	*C. sedlakii* NBRC105722^T																									*	*	81.07	24.7	81.45	25
14	*C. werkmanii* NBRC105721^T																											*	*	92.29	50.1
15	*C. youngae* CCUG30791^T																													*	*