

-Supplementary Material-

***Acinetobacter nematophilus* sp. nov., *Alcaligenes nematophilus* sp. nov.,
Enterobacter nematophilus sp. nov., and *Kaistia nematophila* sp. nov.,
isolated from soil-borne nematodes and proposal for the elevation of
Alcaligenes faecalis subsp. *faecalis*, *Alcaligenes faecalis* subsp.
parafaecalis, and *Alcaligenes faecalis* subsp. *phenolicus* to the species level**

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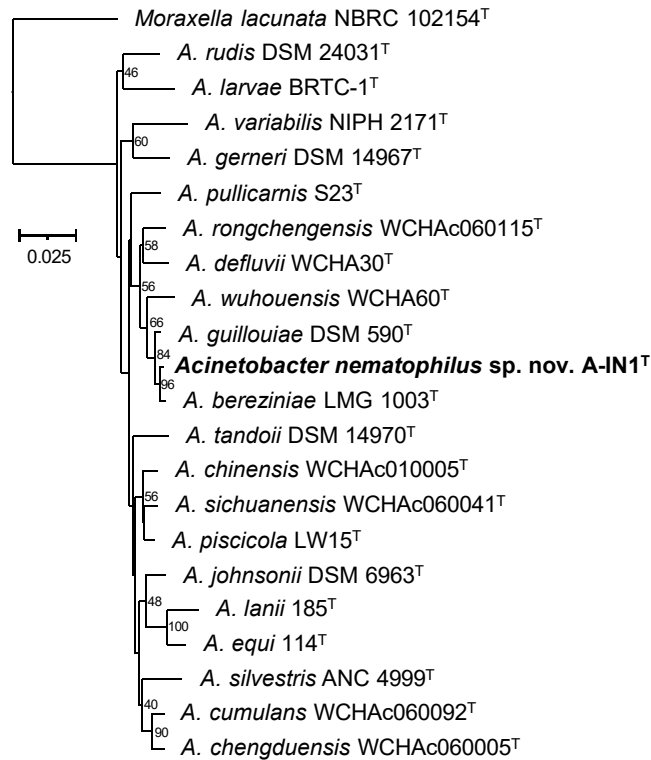
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-Supplementary Figures

A



B

| | | A. rudis DSM 24031 ^T | A. larvae BRTC-1 ^T | A. variabilis NIPH 2171 ^T | A. gernerii MTCC 9824 ^T | A. pullicarnis S23 ^T | A. rongchengensis WCHA060115 ^T | A. defluvii WCHA30 ^T | A. wuhouensis WCHA60 ^T | A. guillouiae DSM 590 ^T | A. nematophilus sp. nov. A-IN1 ^T | A. bereziniae LMG 1003 ^T | A. tandoii DSM 14970 ^T | A. chinensis WCHA010005 ^T | A. sichuanensis WCHA060041 ^T | A. piscicola LW15 ^T | A. johnsonii DSM 69633 ^T | A. lanii 185 ^T | A. equi 114 ^T | A. silvestris ANC 4999 ^T | A. cumulans WCHA060092 ^T | A. chengduensis WCHA060005 ^T |
|---|--|---------------------------------|-------------------------------|--------------------------------------|------------------------------------|---------------------------------|---|---------------------------------|-----------------------------------|------------------------------------|---|-------------------------------------|-----------------------------------|--------------------------------------|---|--------------------------------|-------------------------------------|---------------------------|--------------------------|-------------------------------------|-------------------------------------|---|
| A. rudis DSM 24031 ^T | ID | 96.1 | 94.4 | 95.0 | 96.4 | 95.1 | 96.3 | 97.0 | 96.5 | 95.8 | 96.3 | 95.9 | 96.2 | 96.1 | 96.8 | 95.9 | 95.3 | 95.5 | 95.3 | 95.3 | 95.5 | |
| A. larvae BRTC 1 ^T | 96.1 ID | | 93.8 | 95.9 | 95.3 | 95.6 | 95.8 | 95.7 | 96.2 | 96.2 | 96.1 | 94.8 | 95.5 | 95.6 | 96.1 | 94.8 | 95.1 | 95.0 | 94.2 | 95.0 | 95.0 | |
| A. variabilis NIPH 2171 ^T | 94.4 93.8 ID | | | 94.3 | 94.9 | 93.9 | 93.7 | 94.3 | 94.4 | 94.2 | 94.0 | 95.3 | 95.3 | 94.5 | 95.1 | 94.5 | 94.8 | 95.9 | 94.0 | 95.6 | 95.5 | |
| A. gernerii MTCC 9824 ^T | 95.0 95.9 94.3 ID | | | | 95.6 | 96.1 | 96.1 | 96.2 | 96.2 | 96.4 | 96.2 | 95.2 | 95.6 | 95.8 | 96.1 | 94.8 | 93.4 | 94.0 | 94.0 | 95.3 | 95.2 | |
| A. pullicarnis S23 ^T | 96.4 95.3 94.9 95.6 ID | | | | | 96.8 | 97.6 | 96.5 | 97.2 | 97.1 | 96.9 | 96.7 | 97.0 | 97.2 | 97.0 | 98.0 | 97.2 | 95.7 | 96.9 | 96.7 | 97.2 | |
| A. rongchengensis WCHA060115 ^T | 95.1 95.6 93.9 96.1 96.8 ID | | | | | | 97.8 | 97.0 | 97.5 | 97.9 | 97.6 | 97.0 | 97.2 | 97.0 | 97.2 | 96.7 | 94.5 | 95.2 | 95.9 | 96.8 | 96.8 | |
| A. defluvii WCHA30 ^T | 96.3 95.8 93.7 96.1 97.6 97.8 ID | | | | | | | 97.6 | 97.8 | 97.9 | 97.7 | 96.1 | 96.9 | 96.8 | 97.5 | 96.1 | 94.0 | 95.0 | 95.3 | 96.4 | 96.3 | |
| A. wuhouensis WCHA60 ^T | 97.0 95.7 94.3 96.2 96.5 97.0 97.6 ID | | | | | | | | 98.5 | 97.6 | 97.8 | 96.4 | 96.1 | 96.4 | 97.0 | 95.9 | 94.0 | 94.6 | 94.9 | 95.6 | 96.0 | |
| A. guillouiae DSM 590 ^T | 96.5 96.2 94.4 96.2 97.2 97.5 97.8 98.5 ID | | | | | | | | | 99.1 | 99.3 | 97.3 | 97.0 | 97.6 | 97.7 | 96.7 | 95.2 | 95.3 | 95.8 | 96.6 | 97.0 | |
| A. nematophilus sp. nov. A-IN1 ^T | 95.8 96.2 94.2 96.4 97.1 97.9 97.9 97.6 99.1 ID | | | | | | | | | | 99.4 | 97.0 | 96.8 | 97.3 | 97.2 | 96.1 | 94.9 | 95.1 | 95.8 | 96.6 | 97.2 | |
| A. bereziniae LMG 1003 ^T | 96.3 96.1 94.0 96.2 96.9 97.6 97.7 97.8 99.3 99.4 ID | | | | | | | | | | | 97.1 | 96.6 | 97.4 | 97.3 | 96.4 | 95.4 | 95.1 | 96.0 | 96.2 | 96.8 | |
| A. tandoii DSM 14970 ^T | 95.9 94.8 95.3 95.2 96.7 97.0 96.1 96.4 97.3 97.0 97.1 ID | | | | | | | | | | | | 97.5 | 97.1 | 97.1 | 97.4 | 95.5 | 96.2 | 95.9 | 96.8 | 97.5 | |
| A. chinensis WCHA010005 ^T | 96.2 95.5 95.3 95.6 97.0 97.2 96.9 96.1 97.0 96.8 96.6 97.5 ID | | | | | | | | | | | | | 98.7 | 98.8 | 97.8 | 95.8 | 96.4 | 96.9 | 98.3 | 97.8 | |
| A. sichuanensis WCHA060041 ^T | 96.1 95.6 94.5 95.8 97.2 97.0 96.8 96.4 97.6 97.3 97.4 97.1 98.7 ID | | | | | | | | | | | | | | 98.9 | 97.3 | 96.2 | 96.5 | 97.2 | 98.0 | 98.0 | |
| A. piscicola LW15 ^T | 96.8 96.1 95.1 96.1 98.0 97.2 97.5 97.0 97.7 97.2 97.3 97.1 98.8 98.9 ID | | | | | | | | | | | | | | | 97.6 | 95.7 | 96.9 | 96.8 | 97.9 | 97.6 | |
| A. johnsonii DSM 69633 ^T | 95.9 94.8 94.5 94.8 97.2 96.7 96.1 95.9 96.7 96.1 96.4 97.4 97.8 97.3 97.6 ID | | | | | | | | | | | | | | | | 96.7 | 97.5 | 96.9 | 97.9 | 97.3 | |
| A. lanii 185 ^T | 95.3 95.1 94.8 93.4 95.7 94.5 94.0 94.0 95.2 94.9 95.4 95.5 95.8 96.2 95.7 96.7 ID | | | | | | | | | | | | | | | | | 97.8 | 96.2 | 96.0 | 96.1 | |
| A. equi 114 ^T | 95.5 95.0 95.9 94.0 96.9 95.2 95.0 94.6 95.3 95.1 95.1 96.2 96.4 96.5 96.9 97.5 97.8 ID | | | | | | | | | | | | | | | | | | 96.1 | 96.7 | 96.5 | |
| A. silvestris ANC 4999 ^T | 95.3 94.2 94.0 94.0 96.7 95.9 95.3 94.9 95.8 95.8 96.0 95.9 96.9 97.2 96.8 96.9 96.2 96.1 ID | | | | | | | | | | | | | | | | | | | 97.0 | 97.4 | |
| A. cumulans WCHA060092 ^T | 95.3 95.0 95.6 95.3 97.2 96.8 96.4 95.6 96.6 96.6 96.2 96.8 98.3 98.0 97.9 97.9 96.0 96.7 97.0 ID | | | | | | | | | | | | | | | | | | | | 98.9 | |
| A. chengduensis WCHA060005 ^T | 95.5 95.0 95.5 95.2 97.2 96.8 96.3 96.0 97.0 97.2 96.8 97.5 97.8 98.0 97.6 97.3 96.1 96.5 97.4 98.9 ID | | | | | | | | | | | | | | | | | | | | | |

Figure S1. A) Phylogenetic reconstruction based on 16S rRNA gene sequences of several *Acinetobacter* species with validly published names. 1370 nucleotide positions were used in the analyses. Numbers at the nodes represent the percentage of trees in which the associated taxa clustered together. Bars represent nucleotide substitutions per sequence position. Phylogenetic trees were built in Mega 7. B) Pairwise nucleotide similarities (%) of 16S rRNA gene sequences. Colors indicate the degree of relatedness between bacterial species pairs. Bold indicates novel taxonomic proposals. Accession numbers of used gene sequences are shown in Table S1.

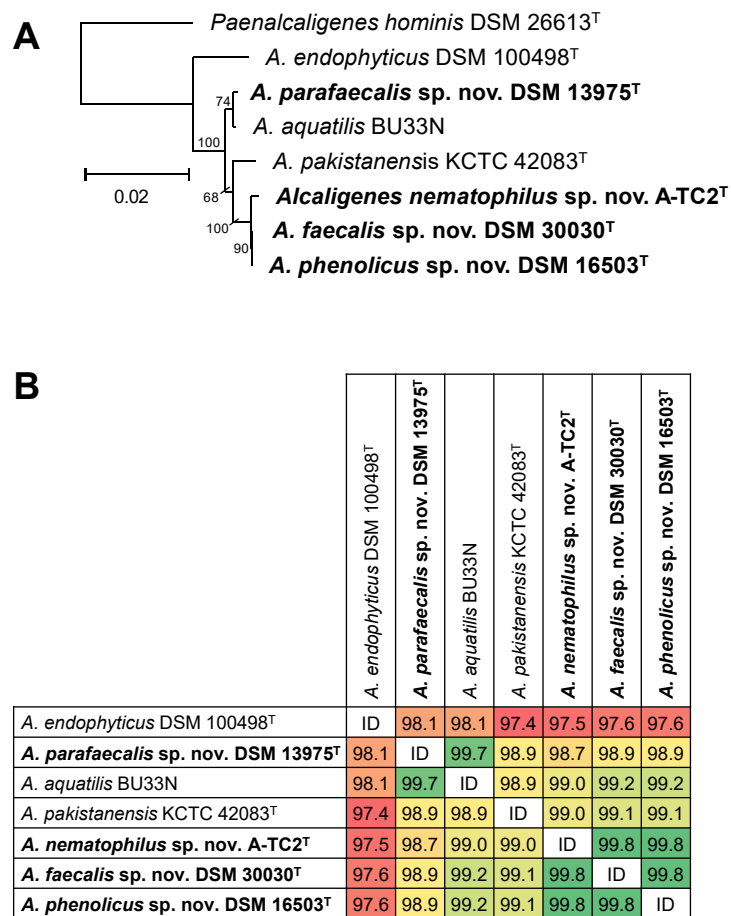


Figure S2. A) Phylogenetic reconstruction based on 16S rRNA gene sequences of all *Alcaligenes* species with validly published names. 1375 nucleotide positions were used in the analyses. Numbers at the nodes represent the percentage of trees in which the associated taxa clustered together. Bars represent nucleotide substitutions per sequence position. Phylogenetic trees were built in Mega 7. B) Pairwise nucleotide similarities (%) of 16S rRNA gene sequences. Colors indicate the degree of relatedness between bacterial species pairs. Bold indicates novel taxonomic proposals. Accession numbers of used gene sequences are shown in Table S1.

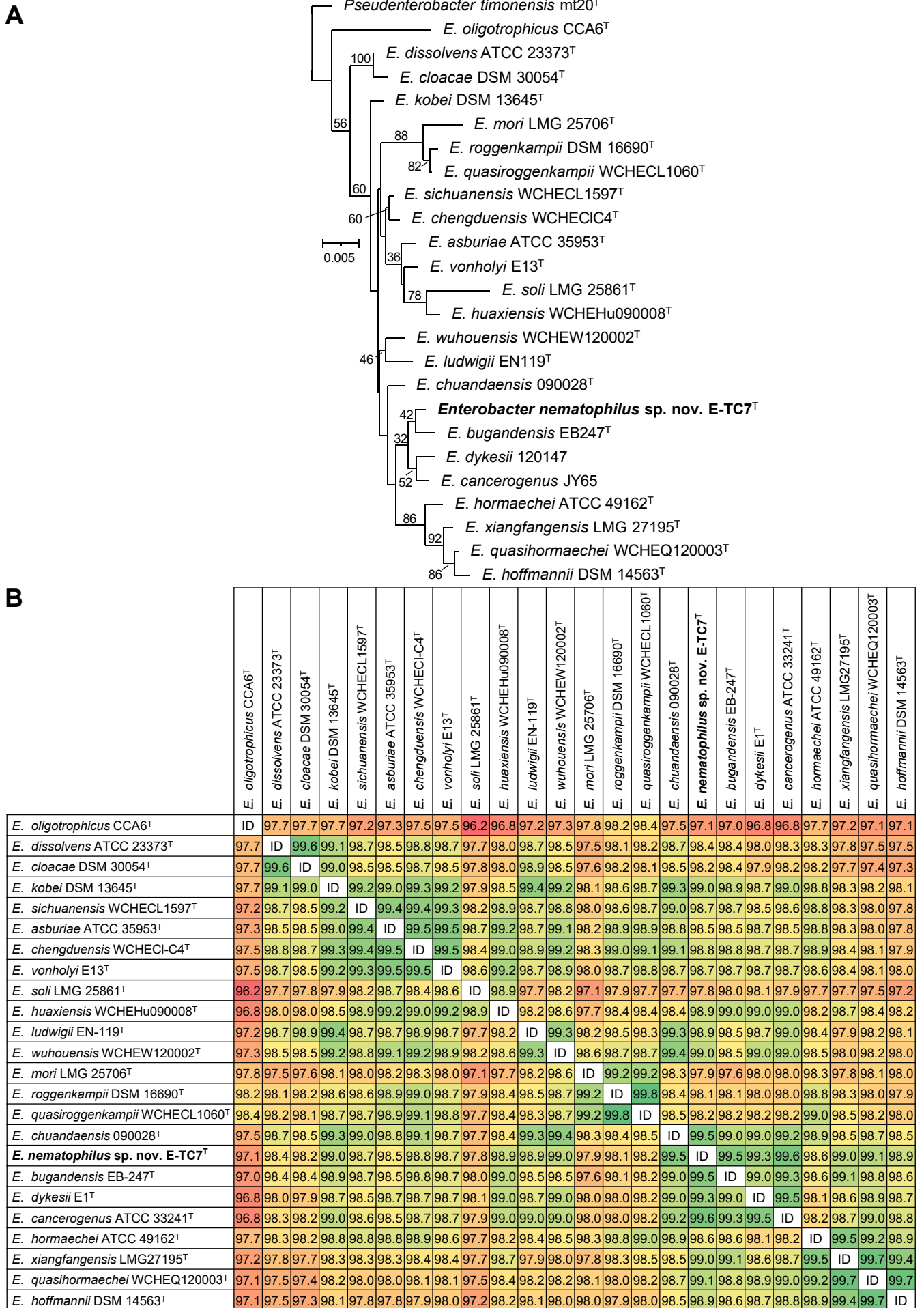


Figure S3. A) Phylogenetic reconstruction based on 16S rRNA gene sequences of all *Enterobacter* species with validly published names. 1405 nucleotide positions were used in the analyses. Numbers at the nodes represent the percentage of trees in which the associated taxa clustered together. Bars represent nucleotide substitutions per sequence position. Phylogenetic trees were built in Mega 7. B) Pairwise nucleotide similarities (%) of 16S rRNA gene sequences. Colors indicate the degree of relatedness between bacterial species pairs. Bold indicates novel taxonomic proposals. Accession numbers of used gene sequences are shown in Table S1.

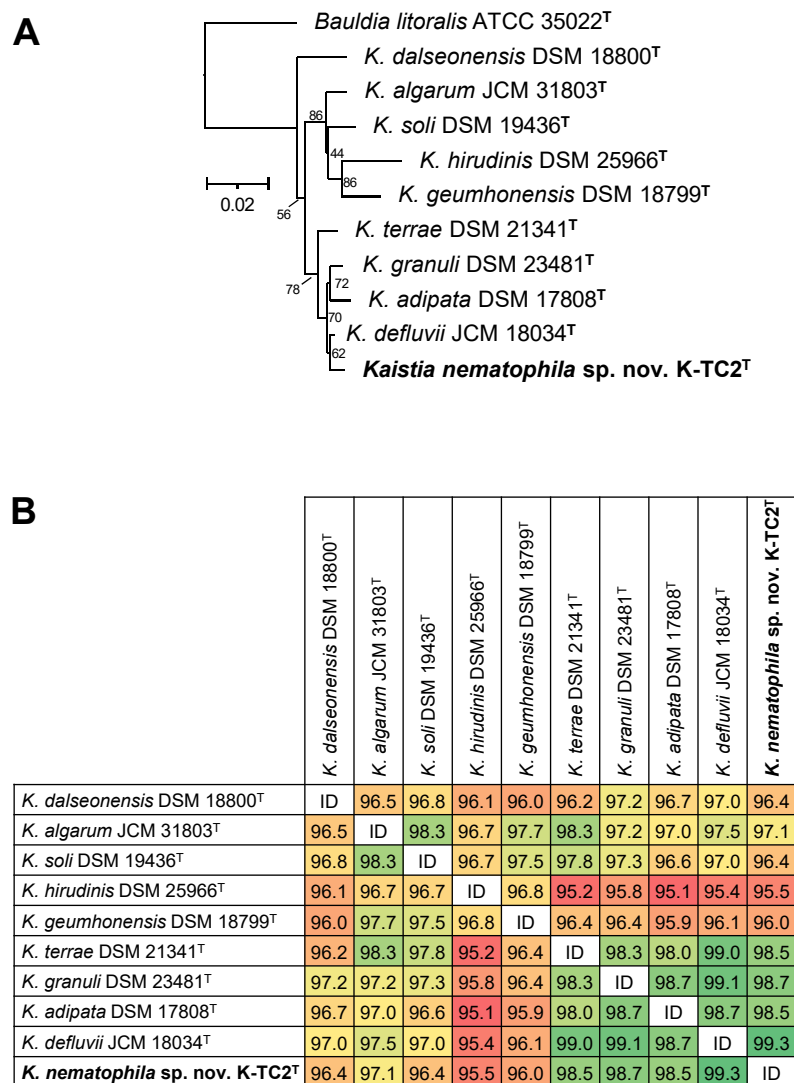


Figure S4. A) Phylogenetic reconstruction based on 16S rRNA gene sequences of all *Kastia* species with validly published names. 1312 nucleotide positions were analyzed. Numbers at the nodes represent the percentage of trees in which the associated taxa clustered together. Bars represent nucleotide substitutions per sequence position. Phylogenetic trees were built in Mega 7. B) Pairwise nucleotide similarities (%) of 16S rRNA gene sequences. Colors indicate the degree of relatedness between bacterial species pairs. Bold indicates novel taxonomic proposals. Accession numbers of used gene sequences are shown in Table S1.

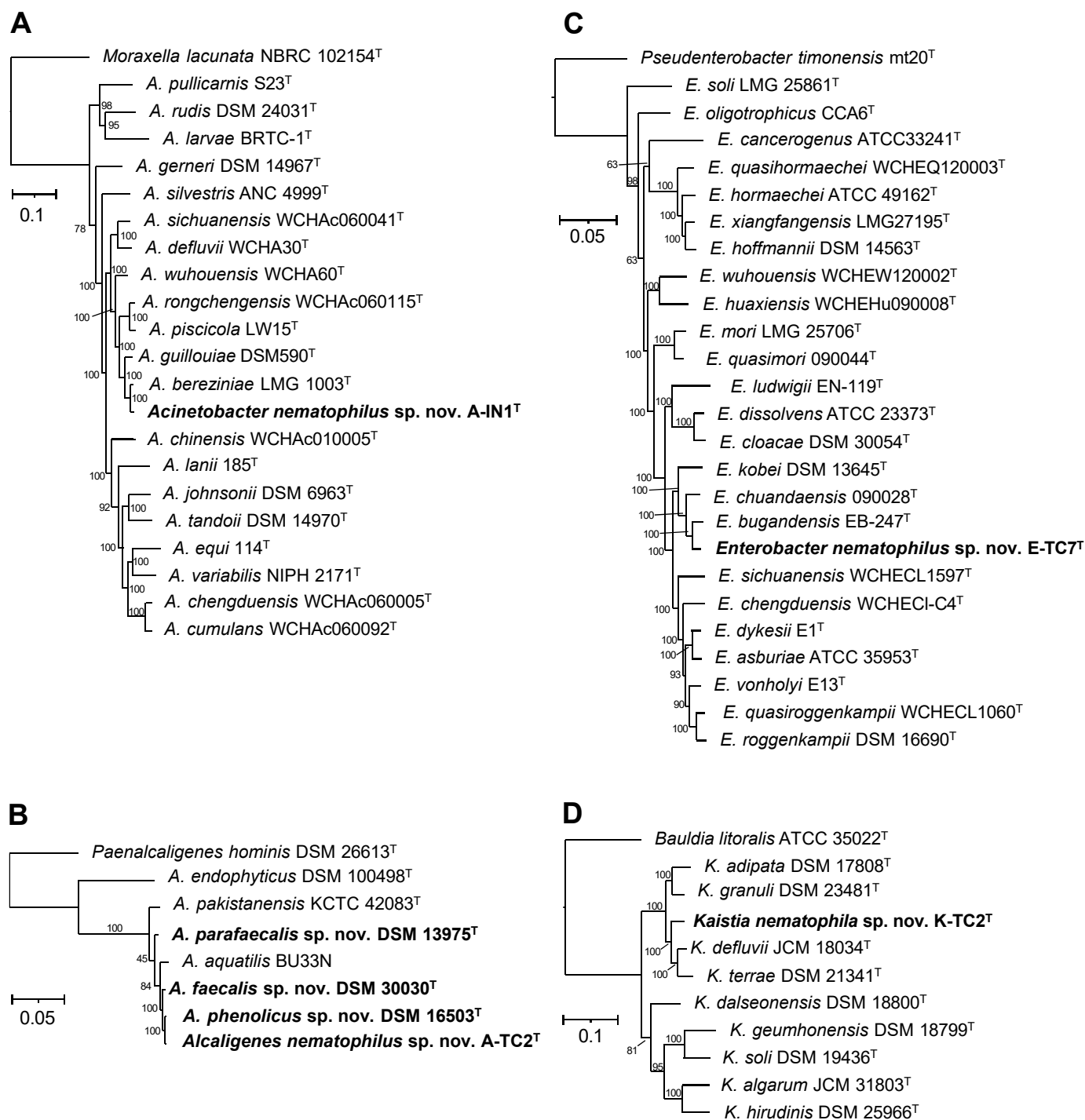


Figure S5. Phylogenetic reconstructions based on core proteome sequences of the type strains of the following genera. A) *Acinetobacter*. A total of 602 core proteins (216249 amino acid positions) were considered in the analyses. B) *Alcaligenes*. A total of 407 core proteins (136588 amino acid positions) were considered in the analyses. C) *Enterobacter*. A total of 3055 core proteins (1015820 amino acid positions) were considered in the analyses. D) *Kastia*. A total of 456 core proteins (161362 amino acid positions) were considered in the analyses. All phylogenetic trees were built using RAxML. Numbers at the nodes represent branch supports. Bar represents amino acid substitutions per sequence position. Bold indicates novel taxonomic proposals. Accession numbers of the genome sequences used are shown in Table S1.

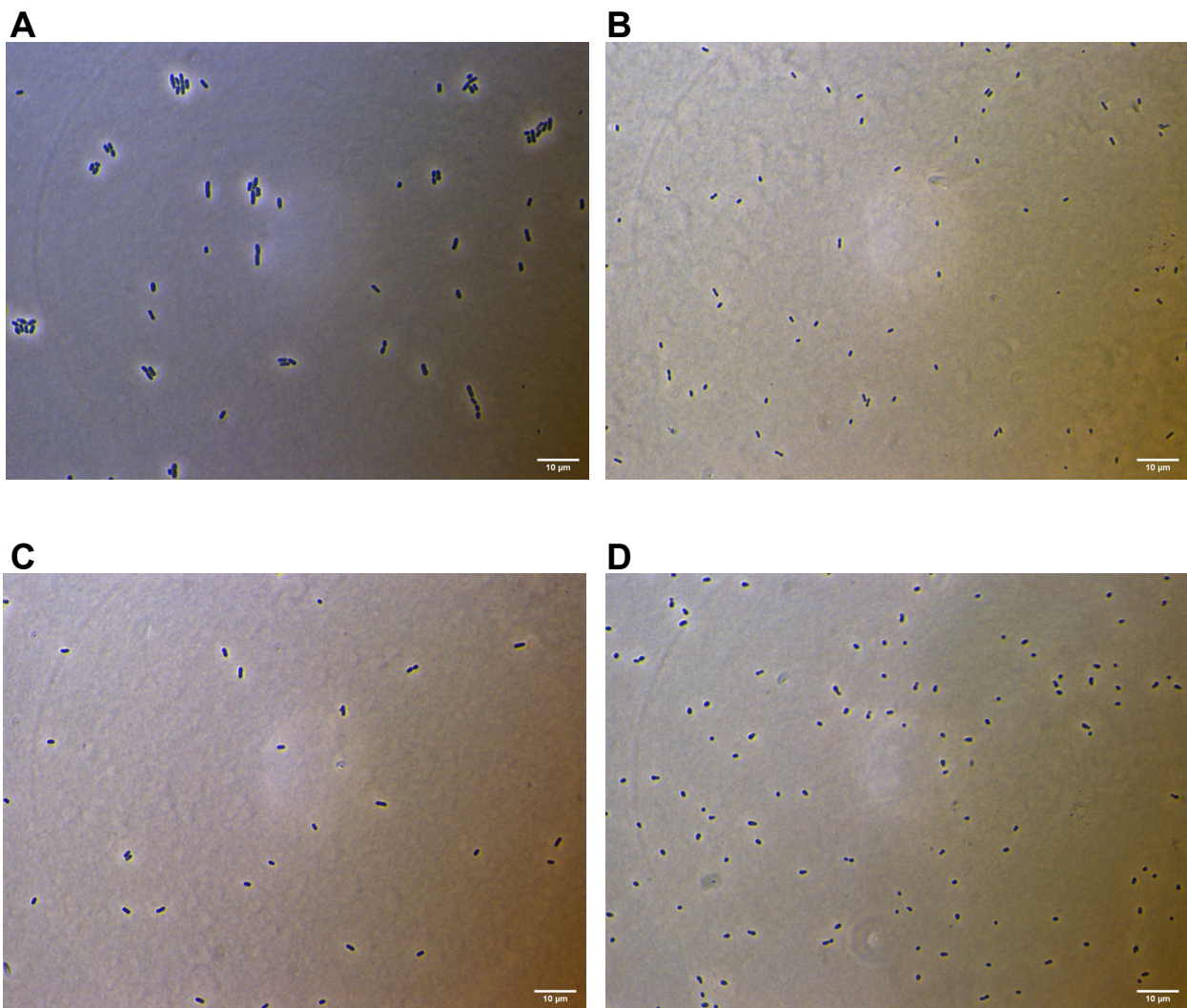


Figure S6. Photographs of the newly described bacterial species. A) *Acinetobacter nematophilus*; B) *Alcaligenes nematophilus*; C) *Enterobacter nematophilus*; D) *Kastia nematophila*. Bars correspond to 10 µm.

-Supplementary Tables-

Table S1. National Center for Biotechnology Information (NCBI) accession numbers of the bacterial sequences used in this study.

| Current name | Proposed name | WGS | 16S |
|---|---|----------|----------|
| <i>Acinetobacter bereziniae</i> LMG 1003 ^T | Same | APQG01 | OP818094 |
| <i>Acinetobacter chengduensis</i> WCHAc060005 ^T | | RCHC01 | OP818095 |
| <i>Acinetobacter chinensis</i> WCHAc010005 ^T | | NHRR01 | OP818096 |
| <i>Acinetobacter cumulans</i> WCHAc060092 ^T | | PYIW01 | OP818097 |
| <i>Acinetobacter defluvii</i> WCHA30 ^T | | MAUF01 | OP818098 |
| <i>Acinetobacter equi</i> 114 ^T | | CP012808 | OP818099 |
| <i>Acinetobacter gerneri</i> MTCC 9824 ^T | | APPN01 | OP818100 |
| <i>Acinetobacter guillouiae</i> DSM 590 ^T | | APOS01 | OP818101 |
| <i>Acinetobacter johnsonii</i> DSM 69633 ^T | | BBTB01 | OP818102 |
| <i>Acinetobacter lanii</i> 185 ^T | | CP049916 | MK990276 |
| <i>Acinetobacter larvae</i> BRTC 1 ^T | | CP016895 | OP818103 |
| <i>Acinetobacter</i> sp. A-IN1 ^T | <i>Acinetobacter nematophilus</i> sp. nov. A-IN1 ^T | JAPKMY01 | OP818110 |
| <i>Acinetobacter piscicola</i> LW15 ^T | Same | NIFO01 | OP818104 |
| <i>Acinetobacter pullicarnis</i> S23 ^T | | VCMZ01 | OP818105 |
| <i>Acinetobacter rongchengensis</i> WCHAc060115 ^T | | RAXT01 | OP818106 |
| <i>Acinetobacter rudis</i> DSM 24031 ^T | | BBRX01 | OP818107 |
| <i>Acinetobacter sichuanensis</i> WCHAc060041 ^T | | PYIX02 | OP818108 |
| <i>Acinetobacter silvestris</i> ANC 4999 ^T | | NEGB01 | OP818109 |
| <i>Acinetobacter tandoii</i> DSM 14970 ^T | | AQFM01 | OP818111 |
| <i>Acinetobacter variabilis</i> NIPH 2171 ^T | | APRS01 | OP818112 |
| <i>Acinetobacter wuhouensis</i> WCHA60 ^T | | MBPR02 | OP818113 |
| <i>Alcaligenes aquatilis</i> BU33N | | CP022390 | OP804211 |
| <i>Alcaligenes endophyticus</i> DSM 100498 ^T | | JAPKND01 | OP804212 |
| <i>Alcaligenes faecalis</i> subsp. <i>faecalis</i> DSM 30030 ^T | <i>Alcaligenes faecalis</i> DSM 30030 ^T | JAPKNC01 | OP804215 |
| <i>Alcaligenes</i> sp. A-TC2 ^T | <i>Alcaligenes nematophilus</i> sp. nov. A-TC2 ^T | JAPKMZ01 | OP804216 |
| <i>Alcaligenes pakistanensis</i> KCTC 42083 ^T | Same | BMZN01 | OP804210 |
| <i>Alcaligenes faecalis</i> subsp. <i>para</i> <i>faecalis</i> DSM 13975 ^T | <i>Alcaligenes para</i> <i>faecalis</i> sp. nov. DSM 13975 ^T | JAPKNA01 | OP804213 |
| <i>Alcaligenes faecalis</i> subsp. <i>phenolicus</i> DSM 16503 ^T | <i>Alcaligenes phenolicus</i> sp. nov. DSM 16503 ^T | JAPKNB01 | OP804214 |
| <i>Bauldia litoralis</i> ATCC 35022 ^T | Same | FMXQ01 | OP804315 |
| <i>Enterobacter asburiae</i> ATCC 35953 ^T | | CP011863 | OP818065 |
| <i>Enterobacter bugandensis</i> EB-247 ^T | | LT992502 | OP818066 |
| <i>Enterobacter cancerogenus</i> ATCC33241 ^T | | FYBA01 | OP818067 |
| <i>Enterobacter chengduensis</i> WCHECI-C4 ^T | | MTSQ01 | OP818068 |
| <i>Enterobacter chuandaensis</i> 090028 ^T | | QZCS01 | OP818069 |
| <i>Enterobacter cloacae</i> DSM 30054 ^T | | CP056776 | OP818070 |
| <i>Enterobacter dissolvens</i> ATCC 23373 ^T | | WJWQ01 | OP818071 |
| <i>Enterobacter dykesii</i> E1 ^T | | VTTY01 | OP818072 |
| <i>Enterobacter hoffmannii</i> DSM 14563 ^T | | CP017186 | OP818073 |
| <i>Enterobacter hormaechei</i> ATCC 49162 ^T | | MKEQ01 | OP818074 |
| <i>Enterobacter huaxiensis</i> WCHEHu090008 ^T | | QZCT01 | OP818075 |
| <i>Enterobacter kobei</i> DSM 13645 ^T | | CP017181 | OP818076 |
| <i>Enterobacter ludwigii</i> EN-119 ^T | | CP017279 | OP818077 |
| <i>Enterobacter mori</i> LMG 25706 ^T | | AEXB01 | OP818078 |
| <i>Enterobacter</i> sp. E-TC7 ^T | <i>Enterobacter nematophilus</i> sp. nov. E-TC7 ^T | JAPKNE01 | OP818089 |
| <i>Enterobacter oligotrophicus</i> CCA6 ^T | Same | AP019007 | OP818079 |
| <i>Enterobacter quasihormaechei</i> WCHEQ120003 ^T | | SJON01 | OP818080 |
| <i>Enterobacter quasimori</i> 090044 ^T | | RXRX01 | N/A |
| <i>Enterobacter quasiroggenkampii</i> WCHECL1060 ^T | | LFDQ02 | OP818081 |
| <i>Enterobacter rogggenkampii</i> DSM 16690 ^T | | CP017184 | OP818082 |
| <i>Enterobacter sichuanensis</i> WCHECL1597 ^T | | POVL01 | OP818083 |
| <i>Enterobacter soli</i> LMG 25861 ^T | | FYBB01 | OP818084 |
| <i>Enterobacter vonholyi</i> E13 ^T | | VTUC01 | OP818085 |
| <i>Enterobacter wuhouensis</i> WCHEW120002 ^T | | SJOO01 | OP818086 |
| <i>Enterobacter xiangfangensis</i> LMG27195 ^T | | CP017183 | OP818087 |
| <i>Kaistia adipata</i> DSM 17808 ^T | | AUHO01 | OP804307 |
| <i>Kaistia algarum</i> JCM 31803 ^T | | JAPKNJ01 | OP804306 |
| <i>Kaistia dalseonensis</i> DSM 18800 ^T | | JAPKNG01 | OP804311 |
| <i>Kaistia defluvii</i> JCM 18034 ^T | | JAPKNI01 | OP804313 |
| <i>Kaistia geumhonensis</i> DSM 18799 ^T | | JAPKNF01 | OP804312 |
| <i>Kaistia granuli</i> DSM 23481 ^T | | AQYH01 | OP804308 |
| <i>Kaistia hirudinis</i> DSM 25966 ^T | | JACIDS01 | OP804314 |
| <i>Kaistia</i> sp. K-TC2 | <i>Kaistia nematophila</i> sp. nov. K-TC2 ^T | JAPKNK01 | OP804305 |
| <i>Kaistia soli</i> DSM 19436 ^T | Same | FQUP01 | OP804309 |
| <i>Kaistia terrae</i> DSM 21341 ^T | | JAPKNH01 | OP804310 |
| <i>Moraxella lacunata</i> NBRC 102154 ^T | | BCUK01 | OP818114 |
| <i>Paenacaligenes hominis</i> DSM 26613 ^T | | JAATIZ01 | OP804230 |
| <i>Pseudoenterobacter timonensis</i> mt20 ^T | | FCOP01 | OP818088 |

Table S2. Features of the genomes generated in this study. 1: *Acinetobacter nematophilus* sp. nov. A-IN1^T; 2: *Alcaligenes endophyticus* DSM 100498^T; 3: *Alcaligenes faecalis* DSM 30030^T; 4: *Alcaligenes nematophilus* sp. nov. A-TC2^T; 5: *Alcaligenes parafaecalis* sp. nov. DSM 13975^T; 6: *Alcaligenes phenolicus* sp. nov. DSM 16503^T; 7: *Enterobacter nematophilus* sp. nov. E-TC7^T; 8: *Kaistia algarum* JCM 31803^T; 9: *Kaistia dalseonensis* DSM 18800^T; 10: *Kaistia defluvii* JCM 18034^T; 11: *Kaistia geumhonensis* DSM 18799^T; 12: *Kaistia nematophila* sp. nov. K-TC2^T; and 13: *Kaistia terrae* DSM 21341^T.

[illegible]

Table S3. Features of the bacterial genomes generated in this study.

| Bacterial strain | Base pairs | Percent G+C | No. proteins |
|---|-------------------|--------------------|---------------------|
| <i>Acinetobacter nematophilus</i> sp. nov. A-IN1 ^T | 4360075 | 38.49 | 4046 |
| <i>Alcaligenes nematophilus</i> sp. nov. A-TC2 ^T | 4251628 | 56.41 | 3892 |
| <i>Alcaligenes parafaecalis</i> sp. nov. DSM 13975 ^T | 4004626 | 56.02 | 3624 |
| <i>Alcaligenes phenolicus</i> sp. nov. DSM 16503 ^T | 4238760 | 56.42 | 3909 |
| <i>Alcaligenes faecalis</i> DSM 30030 ^T | 4003996 | 56.65 | 3706 |
| <i>Alcaligenes endophyticus</i> DSM 100498 ^T | 3557226 | 50.05 | 3270 |
| <i>Enterobacter nematophilus</i> sp. nov. E-TC7 ^T | 4708215 | 56.36 | 4289 |
| <i>Kaistia dalseonensis</i> DSM 18800 ^T | 5184115 | 64.91 | 4833 |
| <i>Kaistia geumhonensis</i> DSM 18799 ^T | 4581777 | 67.76 | 4293 |
| <i>Kaistia terrae</i> DSM 21341 ^T | 5594089 | 63.84 | 5203 |
| <i>Kaistia defluvii</i> JCM 18034 ^T | 4901180 | 65.71 | 4523 |
| <i>Kaistia algarum</i> JCM 31803 ^T | 5259198 | 64.74 | 4949 |
| <i>Kaistia nematophila</i> sp. nov. K-TC2 ^T | 5165915 | 66.75 | 4789 |

Table S4. Completeness (%) and contamination (%) of the bacterial genomes generated in this study assessed by checkM.

| Bacterial strain | Completeness (%) | Contamination (%) |
|---|-------------------------|--------------------------|
| <i>Acinetobacter nematophilus</i> sp. nov. A-IN1 ^T | 99.93 | 1.58 |
| <i>Alcaligenes endophyticus</i> DSM 100498 ^T | 100.0 | 0.50 |
| <i>Alcaligenes faecalis</i> DSM 30030 ^T | 100.0 | 0.00 |
| <i>Alcaligenes nematophilus</i> sp. nov. A-TC2 ^T | 100.0 | 0.05 |
| <i>Alcaligenes parafaecalis</i> sp. nov. DSM 13975 ^T | 100.0 | 0.00 |
| <i>Alcaligenes phenolicus</i> sp. nov. DSM 16503 ^T | 100.0 | 0.00 |
| <i>Enterobacter nematophilus</i> sp. nov. E-TC7 ^T | 99.95 | 0.08 |
| <i>Kaistia algarum</i> JCM 31803 ^T | 99.37 | 0.90 |
| <i>Kaistia dalseonensis</i> DSM 18800 ^T | 100.0 | 0.00 |
| <i>Kaistia defluvii</i> JCM 18034 ^T | 99.68 | 0.47 |
| <i>Kaistia geumhonensis</i> DSM 18799 ^T | 100.0 | 0.16 |
| <i>Kaistia nematophila</i> sp. nov. K-TC2 ^T | 100.0 | 0.82 |
| <i>Kaistia terrae</i> DSM 21341 ^T | 99.68 | 0.58 |

Table S5. Source of the bacterial strains used in this study.

| Strain | Source |
|---|--|
| <i>Acinetobacter bereziniae</i> DSM 25435 ^T | German Collection of Microorganisms and Cell Cultures (DSMZ) |
| <i>Acinetobacter guillouiae</i> DSM 590 ^T | DSMZ |
| <i>Acinetobacter nematophila</i> A-IN1 ^T | This study |
| <i>Alcaligenes endophyticus</i> DSM 100498 ^T | DSMZ |
| <i>Alcaligenes faecalis</i> subsp. <i>faecalis</i> DSM 30030 ^T | DSMZ |
| <i>Alcaligenes nematophila</i> A-TC2 ^T | This study |
| <i>Alcaligenes faecalis</i> subsp. <i>parafaecalis</i> DSM 13975 ^T | DSMZ |
| <i>Alcaligenes faecalis</i> subsp. <i>phenolicus</i> DSM 16503 ^T | DSMZ |
| <i>Enterobacter bugandensis</i> DSM 29888 ^T | DSMZ |
| <i>Enterobacter chuandaensis</i> CNCTC 7649 ^T | Czechoslovak National Collection of Type Cultures (CNCTC) |
| <i>Enterobacter kobei</i> DSM 13645 ^T | DSMZ |
| <i>Enterobacter nematophila</i> E-TC7 ^T | This study |
| <i>Kaistia algarum</i> KACC 19096 ^T | Korean agricultural culture collection (KACC) |
| <i>Kaistia dalseonensis</i> DSM 18800 ^T | DSMZ |
| <i>Kaistia defluvii</i> JCM 18034 ^T | Japan Collection of Microorganisms (JCM) |
| <i>Kaistia geumhonensis</i> DSM 18799 ^T | DSMZ |
| <i>Kaistia nematophila</i> K-TC2 ^T | This study |
| <i>Kaistia terrae</i> DSM 21341 ^T | DSMZ |