

Supplementary information

Antonie van Leeuwenhoek

Duganella hordei sp. nov., *Duganella kodaimurasaki* sp. nov., and *Duganella rhizosphaerae* sp. nov., isolated from barley rhizosphere

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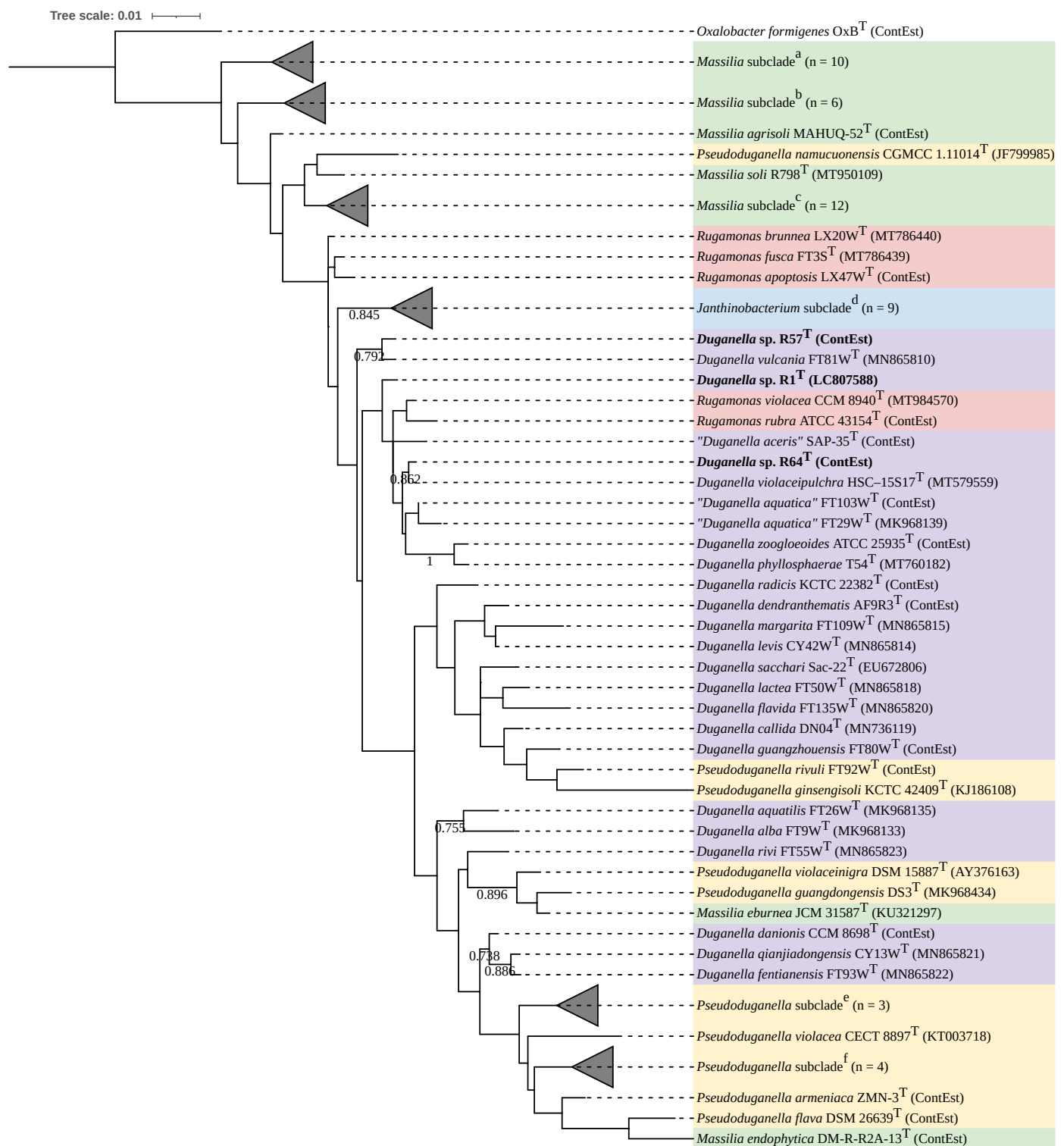


Fig. S1 Maximum-likelihood phylogenetic tree based on 16S rRNA gene sequences of R1^T, R57^T, R64^T, and their relative strains.

Oxalobacter formigenes OxB^T is used as the outgroup.

Bootstrap values (0.7-1) of 1000 replicates are shown. Bar, 0.01 substitutions per nucleotide position. *Massilia* subclade^a comprises *M. forsythiae* GN2-R2^T (ContEst), *M. rhizosphaerae* NEAU GH312^T (MW198488), *M. norwichensis* NS9^T (HG798294), *M. putida* 6NM-7^T (ContEst), *M. pinisoli* T33^T (ContEst), *M. niastensis* 5516S-1^T (EU808005), *M. horti* ONC3^T (MT378212), *M. terrae* J11^T (ContEst), *M. solisilvae* J18^T (ContEst), and *M. agilis* J9^T (ContEst). *Massilia* subclade^b comprises *M. consociata* CCM 7792^T (MT760179), *M. yuzhufengensis* Y1243-1^T (JQ409016), *M. phyllostachyos* G4R7^T (MZ573411), *M. agri* K-3-1^T (ContEst), *M. varians* CCUG 35299^T (ContEst), and *M. alkalitolerans* YIM 31775^T (AY679161). *Massilia* subclade^c comprises *M. jejuensis* 5317J-18^T (FJ969486), *M. brevitalea* byr23-80^T (EF546777), *M. niabensis* 5420S-26^T (EU808006), *M. suwonensis* 5414S-25^T (FJ969487), *M. haematophila* CCM 7480^T (ContEst), *M. aurea* CCM 7363^T (ContEst), *M. timonae* UR/MT95^T (ContEst), *M. oculi* CCM 7900^T (ContEst), *M. puerhi* SJY3^T (MN014073), *M. arenae* GEM 5^T (ContEst), *M. polaris* RP-1-19^T (ContEst), *M. psychrophila* B1555-1^T (ContEst), *M. eurypsychrophila* B528-3^T (ContEst), *M. glaciei* B448-2^T (KJ755877), *M. aquatica* CCM 8693^T (ContEst), *M. mucilaginoso* CCM 8733^T (ContEst), *M. atriviolacea* SOD^T (ContEst), *M. frigida* CCM 8695^T (ContEst), *M. antarctica* CCM 8941^T (ContEst), *M. violaceinigra* B 2^T (ContEst), and *M. rubra* CCM 8692^T (ContEst). *Janthinobacterium* subclade^d comprises *J. psychrotolerans* S3-2^T (ContEst), *J. agaricidamnorum* W1r3^T (ContEst), *J. violaceinigrum* FT13W^T (MK968136), *J. fluminis* hw3^T (ContEst), *J. aquaticum* FT58W^T (MN548378), *J. kumbetense* GK^T (ContEst), *J. rivuli* FT68W^T (MN548379), *J. tractae* SNU WT3^T (ContEst), and *J. lividum* DSMZ 1522^T (ContEst). *Pseudoduganella* subclade^e comprises *P. buxica* CGMCC 1.15931^T (KX944690), *P. plicata* KCTC 12344^T (MT758059), and *P. lurida* CGMCC 1.10822^T (ContEst). *Pseudoduganella* subclade^f comprises *P. dura* DSM 17513^T (ContEst), *P. umbonata* DSM 26121^T (ContEst), *P. albidiflava* DSM 17472^T (ContEst), and *P. lutea* DSM 17473^T (ContEst).

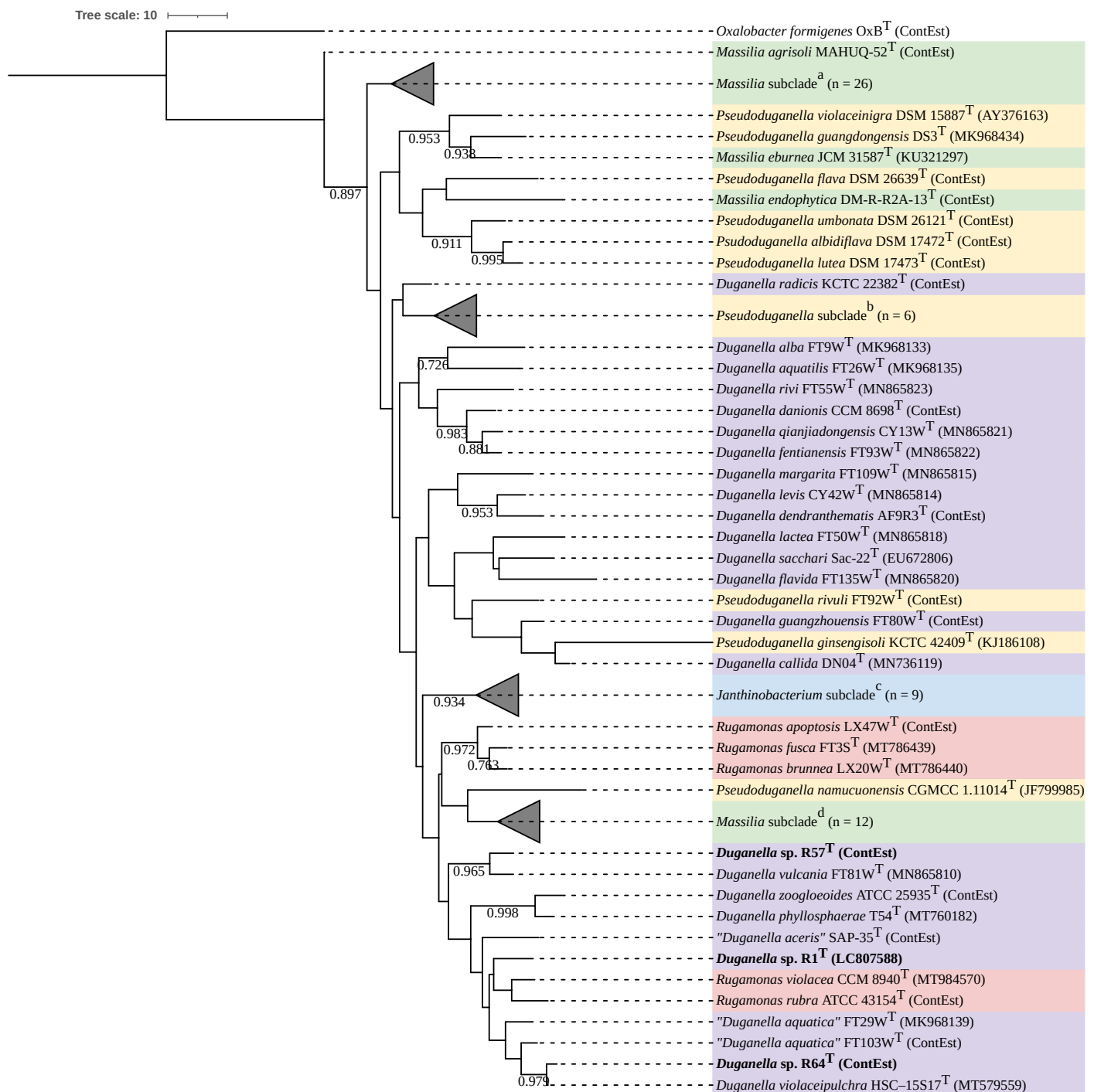


Fig. S2 Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences of R1^T, R57^T, R64^T, and their relative strains. *Oxalobacter formigenes* OxB^T is used as the outgroup.

Bootstrap values (0.7-1) of 1000 replicates are shown. Bar, 10 substitutions per nucleotide position. *Massilia* subclade^a comprises *M. horti* ONC3^T (MT378212), *M. terrae* J11^T (ContEst), *M. solisilvae* J18^T (ContEst), *M. agilis* J9^T (ContEst), *M. consociata* CCM 7792^T (MT760179), *M. agri* K-3-1^T (ContEst), *M. yuzhufengensis* Y1243-1^T (JQ409016), *M. phyllostachyos* G4R7^T (MZ573411), *M. pinisoli* T33^T (ContEst), *M. niastensis* 5516S-1^T (EU808005), *M. forsythiae* GN2-R2^T (ContEst), *M. putida* 6NM-7^T (ContEst), *M. rhizosphaerae* NEAU GH312^T (MW198488), *M. norwichensis* NS9^T (HG798294), *M. suwonensis* 5414S-25^T (FJ969487), *M. haematophila* CCM 7480^T (ContEst), *M. varians* CCUG 35299^T (ContEst), *M. alkalitolerans* YIM 31775^T (AY679161), *M. niabensis* 5420S-26^T (EU808006), *M. aurea* CCM 7363^T (ContEst), *M. jejuensis* 5317J-18^T (FJ969486), *M. brevitalea* byr23-80^T (EF546777), *M. oculi* CCM 7900^T (ContEst), *M. timonae* strain UR:MT95^T (ContEst), *M. puerhi* SJY3^T (MN014073), and *M. arenae* GEM 5^T (ContEst). *Pseudoduganella* subclade^b comprises *P. violacea* CECT 8897^T (KT003718), *P. armeniaca* ZMN-3^T (ContEst), *P. lurida* CGMCC 1.10822^T (ContEst), *P. dura* DSM 17513^T (ContEst), *P. plicata* KCTC 12344^T (MT758059), and *P. buxica* CGMCC 1.15931^T (KX944690). *Janthinobacterium* subclade^c comprises *J. fluminis* hw3^T (ContEst), *J. psychrotolerans* S3-2^T (ContEst), *J. agaricidamnosum* W1r3^T (ContEst), *J. violaceinigrum* FT13W^T (MK968136), *J. aquaticum* FT58W^T (MN548378), *J. tructae* SNU WT3^T (ContEst), *J. kumbetense* GK^T (ContEst), *J. rivuli* FT68W^T (MN548379), and *J. lividum* DSMZ 1522^T (ContEst). *Massilia* subclade^d comprises *M. soli* R798^T (MT950109), *M. polaris* RP-1-19^T (ContEst), *M. psychrophila* B1555-1^T (ContEst), *M. eurypsychrophila* B528-3^T (ContEst), *M. glacier* B448-2^T (KJ755877), *M. mucilaginoso* CCM 8733^T (ContEst), *M. atriviolacea* SOD^T (ContEst), *M. aquatica* CCM 8693^T (ContEst), *M. antarctica* CCM 8941^T (ContEst), *M. frigida* CCM 8695^T (ContEst), *M. violaceinigra* B 2^T (ContEst), and *M. rubra* CCM 8692^T (ContEst).

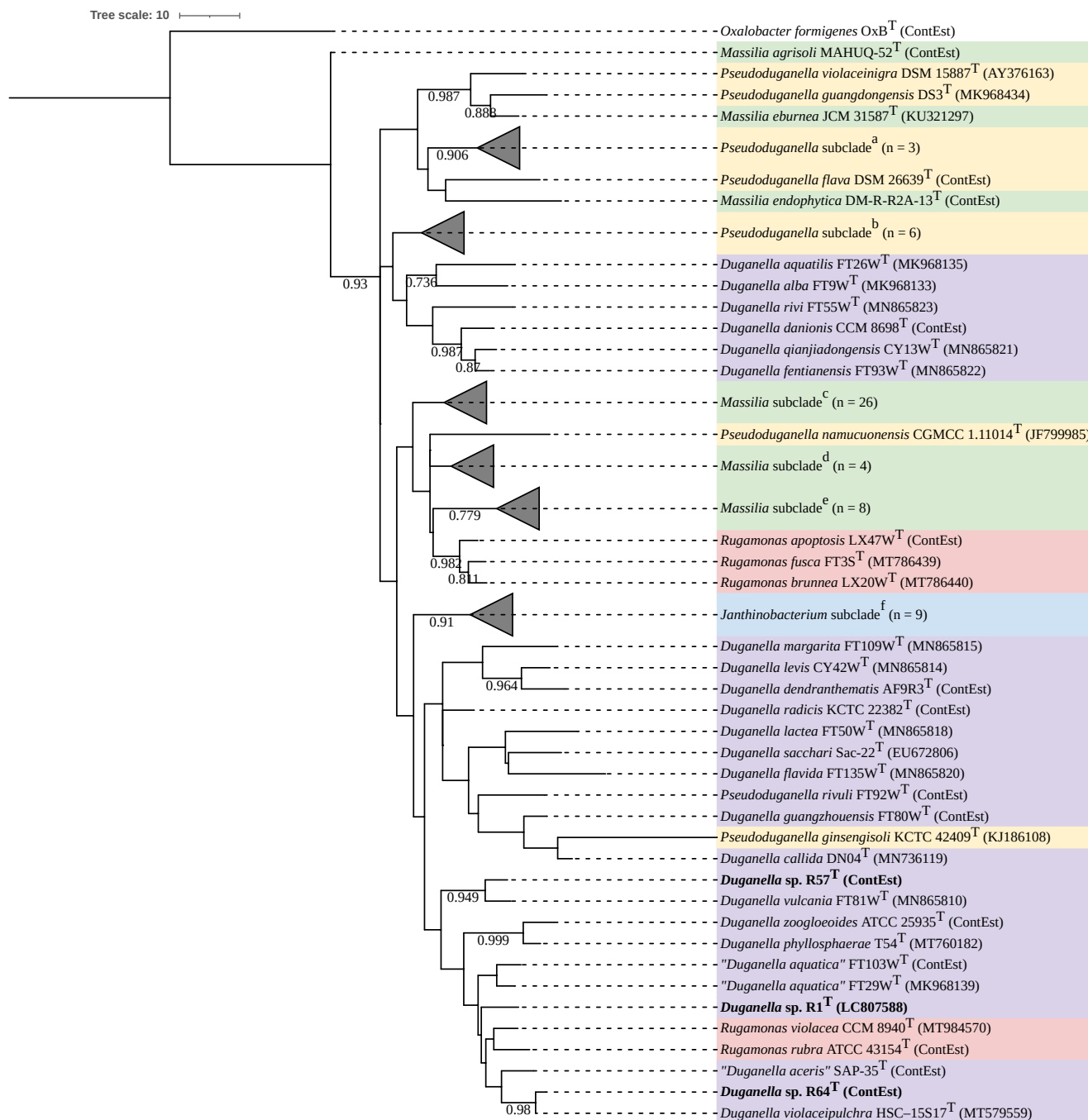


Fig. S3 Minimum-evolution phylogenetic tree based on 16S rRNA gene sequences of R1^T, R57^T, R64^T, and their relative strains. *Oxalobacter formigenes* OxB^T is used as the outgroup.

Bootstrap values (0.7-1) of 1000 replicates are shown. Bar, 10 substitutions per nucleotide position. *Pseudoduganella* subclade^a comprises *P. umbonata* DSM 26121^T (ContEst), *P. albidiflava* DSM 17472^T (ContEst), and *P. lutea* DSM 17473^T (ContEst). *Pseudoduganella* subclade^b comprises *P. violacea* CECT 8897^T (KT003718), *P. armeniaci* ZMN-3^T (ContEst), *P. lurida* CGMCC 1.10822^T (ContEst), *P. dura* DSM 17513^T (ContEst), *P. plicata* KCTC 12344^T (MT758059), and *P. buxea* CGMCC 1.15931^T (KX944690). *Massilia* subclade^c comprises *M. niabensis* 5420S-26^T (EU808006), *M. aurea* CCM 7363^T (ContEst), *M. jejuensis* 5317J-18^T (FJ969486), *M. brevitalea* byr23-80^T (EF546777), *M. oculi* CCM 7900^T (ContEst), *M. timonae* UR/MT95^T (ContEst), *M. puerhi* SJY3^T (MN014073), *M. arenae* GEM 5^T (ContEst), *M. suwonensis* 5414S-25^T (FJ969487), *M. haematophila* CCM 7480^T (ContEst), *M. varians* CCUG 35299^T (ContEst), *M. alkalitolerans* YIM 31775^T (AY679161), *M. yuzhufengensis* Y1243-1^T (JQ409016), *M. phyllostachyos* G4R7^T (MZ573411), *M. consociata* CCM 7792^T (MT760179), *M. agri* K-3-1^T (ContEst), *M. horti* ONC3^T (MT378212), *M. terrae* J11^T (ContEst), *M. solisilvae* J18^T (ContEst), *M. agilis* J9^T (ContEst), *M. pinisoli* T33^T (ContEst), *M. niastensis* 5516S-1^T (EU808005), *M. forsythiae* GN2-R2^T (ContEst), *M. putida* 6NM-7^T (ContEst), *M. rhizosphaerae* NEAU GH312^T (MW198488), and *M. norwichensis* NS9^T (HG798294). *Massilia* subclade^d comprises *M. soli* R798^T (MT950109), *M. polaris* RP-1-19^T (ContEst), *M. psychrophila* B1555-1^T (ContEst), and *M. eurypsychrophila* B528-3^T (ContEst). *Massilia* subclade^e comprises *M. glaciei* B448-2^T (KJ755877), *M. mucilaginoso* CCM 8733^T (ContEst), *M. atriviolacea* SOD^T (ContEst), *M. aquatica* CCM 8693^T (ContEst), *M. antarctica* CCM 8941^T (ContEst), *M. frigida* CCM 8695^T (ContEst), *M. violaceinigra* B 2^T (ContEst), and *M. rubra* CCM 8692^T (ContEst). *Janthinobacterium* subclade^f comprises *J. fluminis* hw3^T (ContEst), *J. agaricidamnorum* W1r3^T (ContEst), *J. violaceinigrum* FT13W^T (MK968136), *J. aquaticum* FT58W^T (MN548378), *J. psychrotolerans* S3-2^T (ContEst), *J. tructae* SNU WT3^T (ContEst), *J. kumbetense* GK^T (ContEst), *J. rivuli* FT68W^T (MN548379), and *J. lividum* DSMZ 1522^T (ContEst).