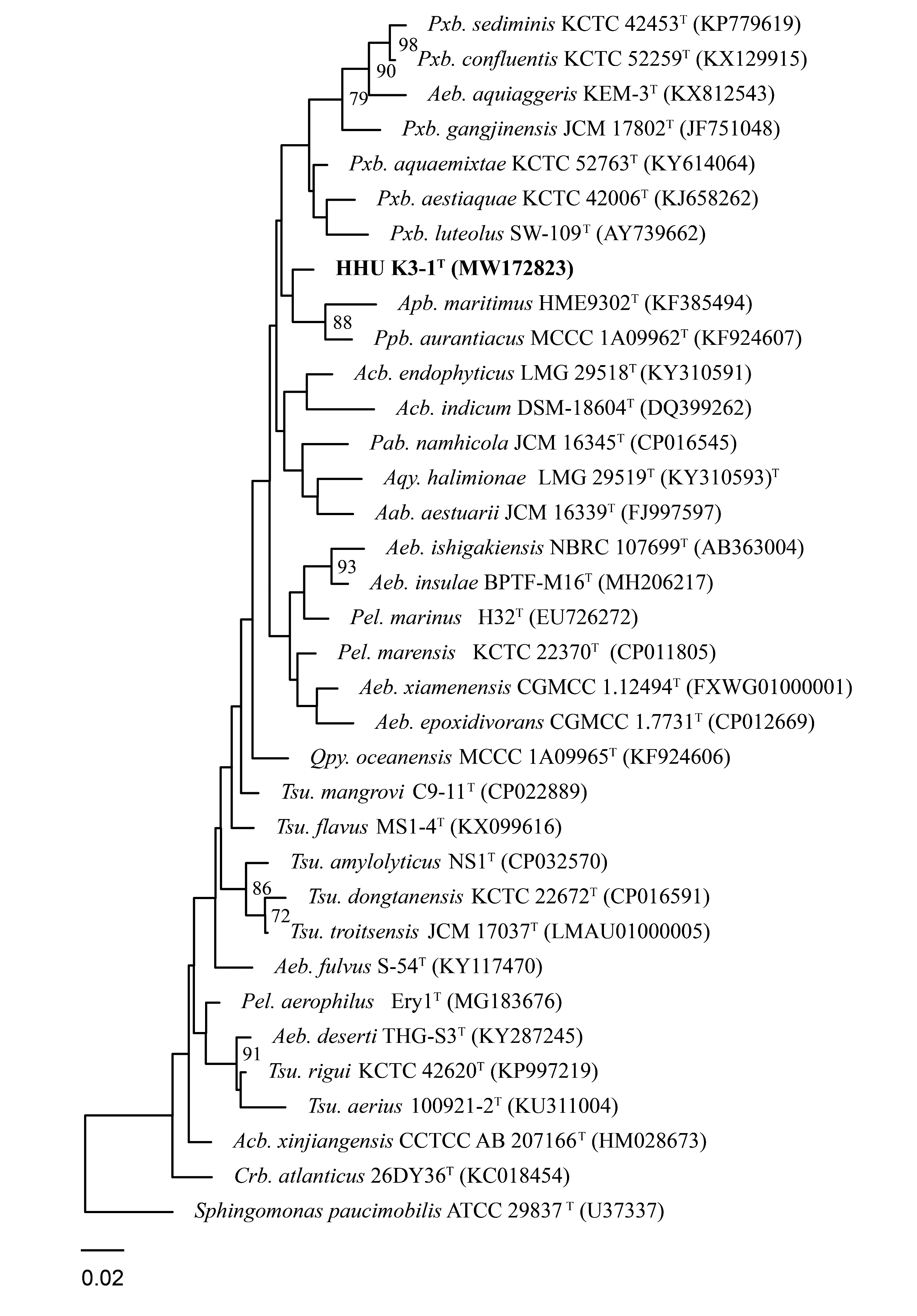
**Table S1 The compositions of cellular fatty acid contents (%) of strains HHU K3-1T and two reference strains.**

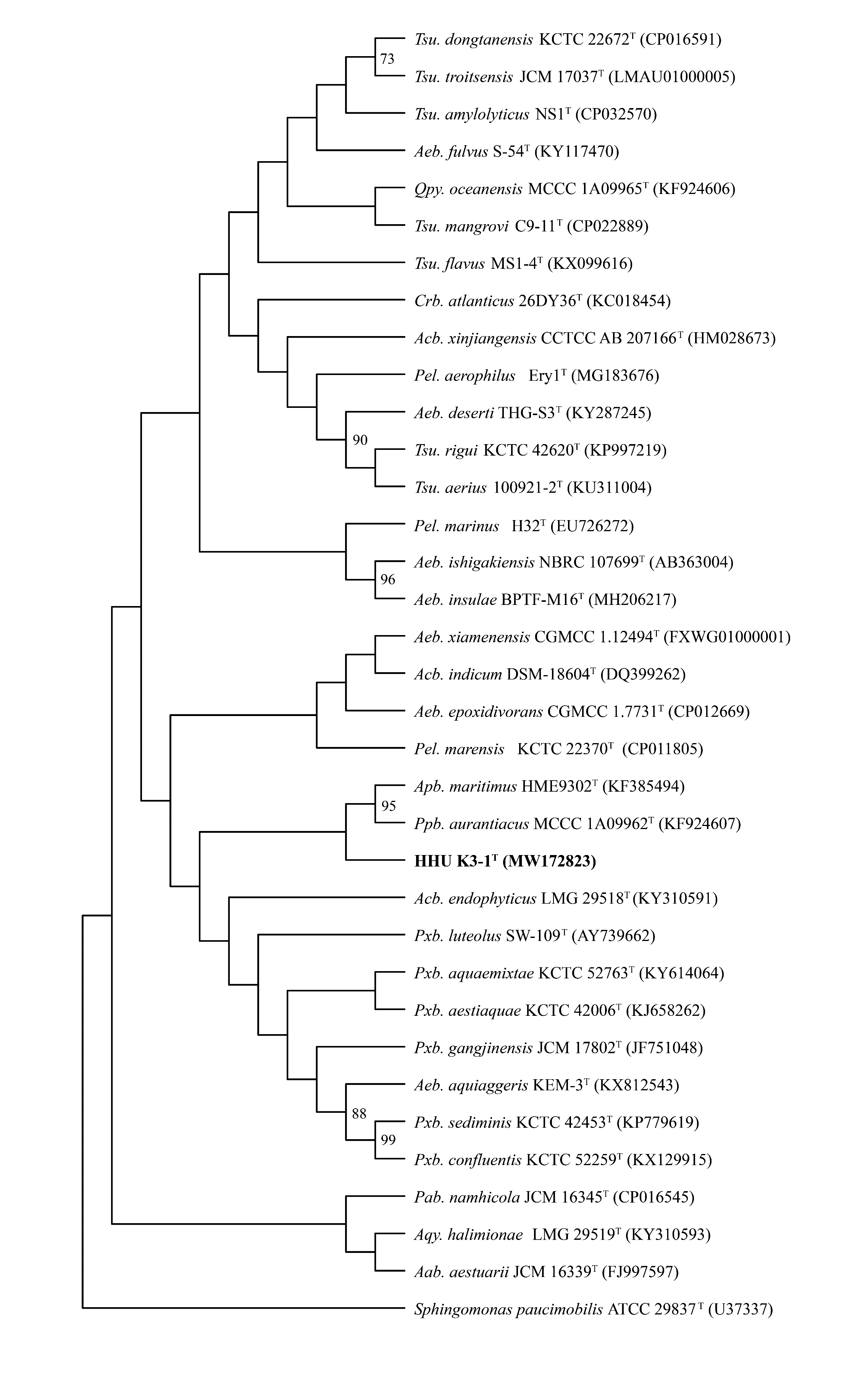
Taxa: 1, *Actirhodobacter atrilutea* HHU K3-1T; 2, *Parapontixanthobacter aurantiacus* MCCC 1A09962T; 3, *Pelagerythrobacter marensis* KCTC 22370T.

|  |  |  |  |
| --- | --- | --- | --- |
| **Fatty acid** | 1 | 2 | 3 |
| **Straight-chain**  C12:0  C13:0  C14:0  C15:0  C16:0  C17:0  C18:0 | -  -  0.2  -  8.9  2.7  0.2 | 4.0  0.5  2.7  -  23.7  4.4  2.6 | -  -  0.3  -  7.8  0.8  0.7 |
| **Unsaturated**  C15:1*ω*6c  C16:1*ω*5c  C17:1*ω*6c  C17:1*ω*8c  C18:1*ω*5c  C18:1*ω*9c | 0.2  0.6  24.0  1.8  1.3  - | 0.1  -  0.1  3.9  -  0.2 | -  0.9  7.7  -  2.8  - |
| **Branched**  iso-C15:0  iso-C16:0  iso-C17:0  iso-C18:1 H  anteiso-C15:0  anteiso-C17:1*ω*9c  anteiso-C17:0 | 0.6  0.2  0.5  0.1  0.9  0.1  1.4 | 0.1  0.3  0.3  -  0.2  -  0.3 | -  -  -  -  -  -  - |
| **Hydroxy**  C14:0 2-OH  C15:0 2-OH  C16:0 2-OH  11-methyl-C18:1*ω*7c | 1.8  3.0  0.4  4.9 | -  -  -  0.1 | 2.1  0.6  1.5  28.2 |
| **Summed features**  3  8  9 | 12.3  33.5  0.5 | 27.4  14.1  - | 6.9  39.0  0.2 |

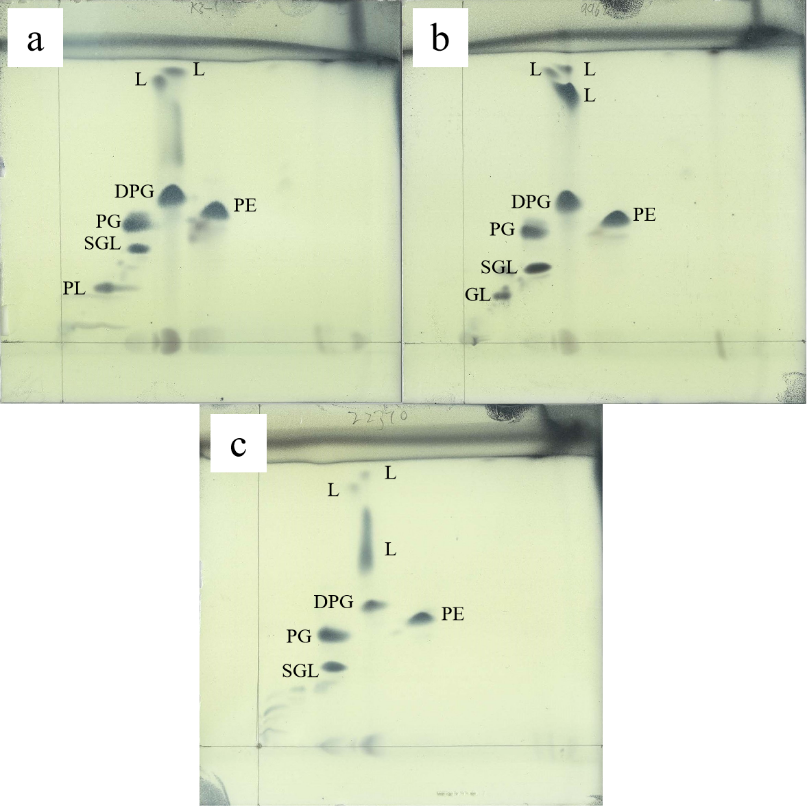
All data are from this study. Values are percentages of total fatty acids; -, not detected. Summed features represent groups of two or three fatty acids that cannot be separated by using the Microbial Identification System. Summed Feature 3 consists of C16:1*ω*7c/C16:1*ω*6c; summed feature 8 consists of C18:1*ω*7c and/or C18:1*ω*6c; Summed Feature 9 consists of iso-C17:1*ω*9c and/or 10-methyl-C16:0.



**Fig. S1 Maximum-likelihood phylogenetic tree based on 16S rRNA gene sequences showing the position of strain HHU K3-1T.** Bootstrap values (expressed as percentages of 1000 replications) of above 70% are shown at the branch points nodes. *Sphingomonas paucimobilis* ATCC 29837T is used as out group. Bar, 0.02 substitutions per nucleotide position.



**Fig. S2 Maximum-parsimony phylogenetic tree based on 16S rRNA gene sequences showing the position of strain HHU K3-1T.** Bootstrap values (expressed as percentages of 1000 replications) of above 70% are shown at the branch points nodes. *Sphingomonas paucimobilis* ATCC 29837T is used as out group.



**Fig. S3** Two-dimensional thin-layer chromatogram of polar lipids of: a, HHU K3-1T; b, *Parapontixanthobacter aurantiacus* MCCC 1A09962T; c, *Pelagerythrobacter marensis* KCTC 22370T.

DPG, diphosphatidylglycerol; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; SGL, sphingoglycolipid; PL, unidentified polar lipid; GL, unidentified glycolipid; L, unidentified lipid.