

## **Supplementary Data**

### **Characterization of *Lacinutrix neustonica* sp. nov., Isolated from the Sea Surface Microlayer of Brackish Lake Shihwa, South Korea**

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**Table S1.** List of whole genome sequences of *Lacinutrix* spp. The genome sequence of *Lacinutrix neustonica* HL-RS19<sup>T</sup> was obtained in this study.

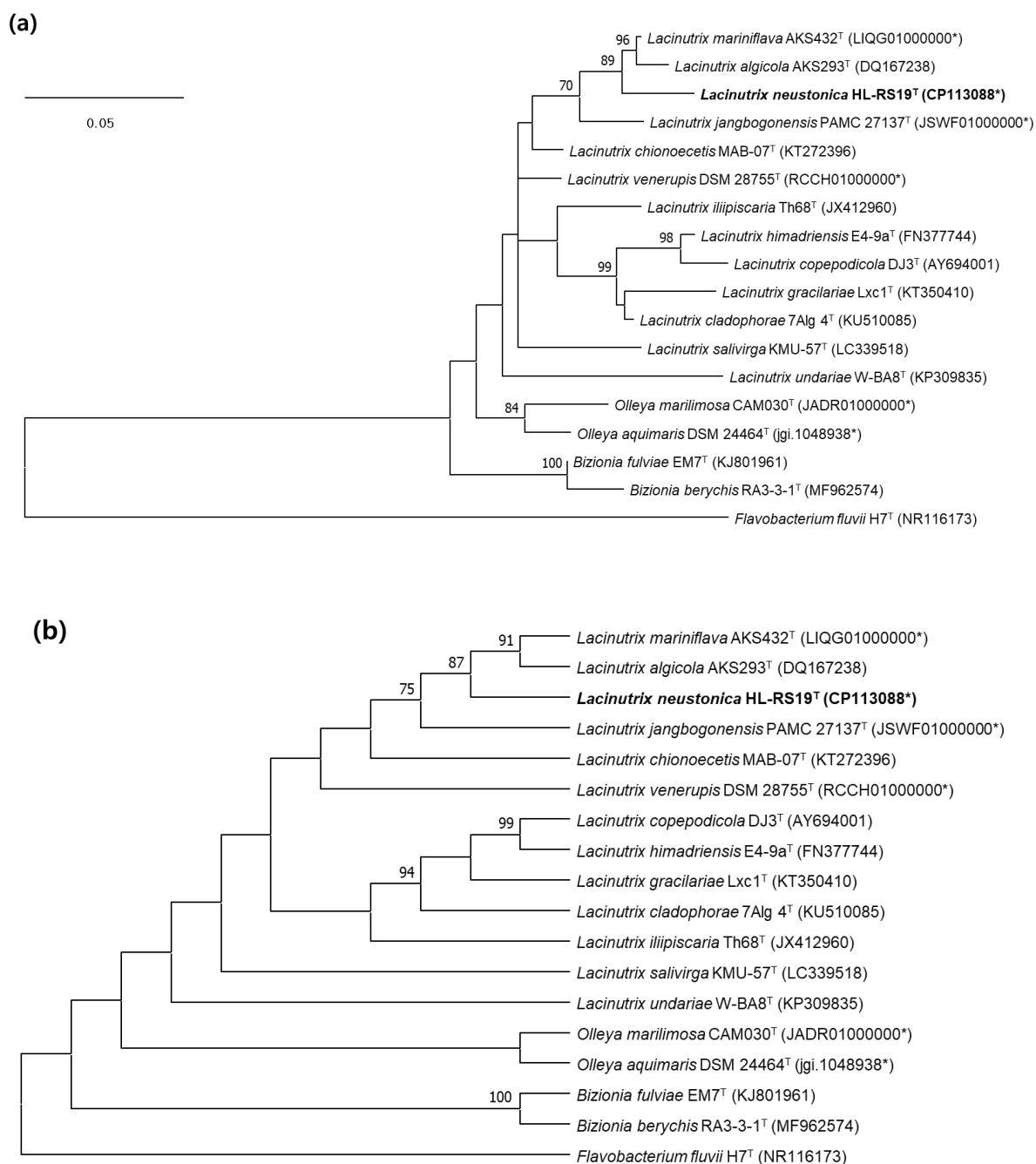
No.	Organism Name	Strain	BioSample	Assembly	Level	Size (Mb)	Coverage (x)	N50 (Mb)	GC%	Scaffolds
1	<i>Lacinutrix neustonica</i>	HL-RS19 <sup>T</sup>	SAMN30942755	GCA_026625145.1	Complete	3.91	191	3.91	35.2	1
2	<i>Lacinutrix algicola</i>	AKS 293 <sup>T</sup>	SAMN04002512	GCA_001418085.1	Contig	3.66	27	0.20	31.4	46
3	<i>Lacinutrix himadriensis</i>	E4-9a <sup>T</sup>	SAMN04002506	GCA_001418105.1	Contig	4.17	177	0.35	32.6	32
4	<i>Lacinutrix jangbagonensis</i>	PAMC 27137 <sup>T</sup>	SAMN02665270	GCA_000797445.1	Contig	4.02	35	0.18	32.2	46
5	<i>Lacinutrix mariniflava</i>	AKS 432 <sup>T</sup>	SAMN04002510	GCA_001418015.1	Contig	3.97	40	0.37	31.8	32
6	<i>Lacinutrix venerupis</i>	DSM 28755 <sup>T</sup>	SAMN07621379	GCA_003663945.1	Scaffold	3.12	356	0.35	30.4	19

**Table S2.** Cellular fatty acid composition (%) of strain HL-RS19<sup>T</sup> and *L. mariniflava* KCCM 42306<sup>T</sup>.

Both strains were incubated at 20°C for 3 days on marine agar. Fatty acids higher than 5% of the total fatty acids are presented in bold. Fatty acids that represent <0.5 % in both strains have been omitted.

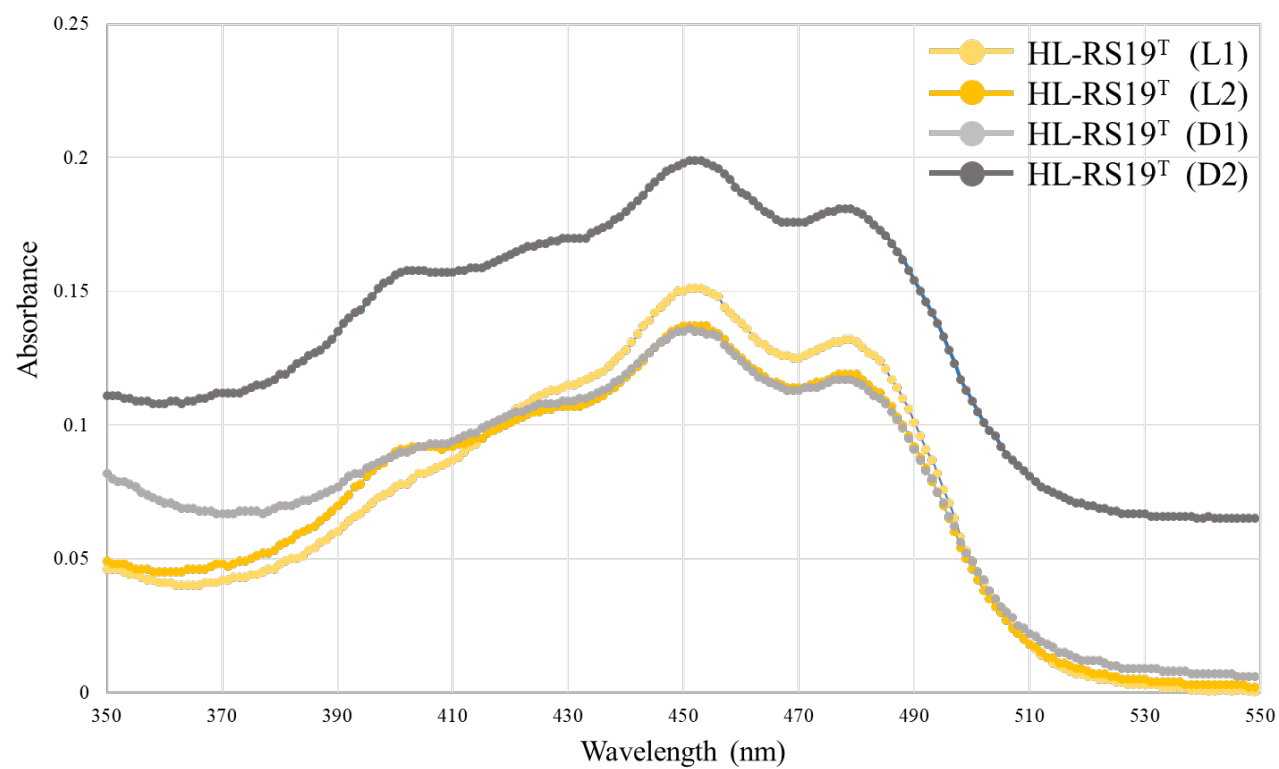
ND, not detected.

<b>Fatty Acids</b>	<b>HL-RS19<sup>T</sup></b>	<b>KCCM 42306<sup>T</sup></b>
<b>Saturated fatty acids</b>		
C <sub>10:0</sub>	0.6	1.1
C <sub>12:0</sub>	1.1	1.8
C <sub>14:0</sub>	0.5	0.7
C <sub>16:0</sub>	3.3	ND
<b>Unsaturated fatty acids</b>		
C <sub>15:1</sub> ω5c	1.4	1.3
C <sub>15:1</sub> ω6c	ND	2.7
C <sub>15:1</sub> ω8c	ND	0.5
C <sub>16:1</sub> ω5c	ND	1.0
C <sub>17:1</sub> ω6c	ND	0.8
<b>Branched fatty acids</b>		
iso-C <sub>12:0</sub>	0.5	0.6
iso-C <sub>13:0</sub>	0.8	0.5
iso-C <sub>14:0</sub>	1.6	1.4
iso-C <sub>15:0</sub>	<b>9.0</b>	<b>9.1</b>
iso-C <sub>15:1</sub> G	<b>16.5</b>	<b>10.0</b>
iso-C <sub>16:0</sub>	1.0	1.7
iso-C <sub>16:1</sub> G	0.6	ND
iso-C <sub>16:1</sub> H	ND	2.5
anteiso-C <sub>13:0</sub>	1.4	ND
anteiso-C <sub>15:0</sub>	<b>9.7</b>	<b>12.5</b>
anteiso-C <sub>15:1</sub> A	<b>9.9</b>	6.5
anteiso-C <sub>17:1</sub> ω9c	0.2	2.5
<b>Hydroxy fatty acids</b>		
C <sub>15:0</sub> 2-OH	4.9	5.2
C <sub>17:0</sub> 2-OH	4.0	3.2
C <sub>10:0</sub> 3-OH	0.7	1.4
C <sub>16:0</sub> 3-OH	ND	0.7
iso-C <sub>15:0</sub> 3-OH	<b>8.3</b>	<b>10.8</b>
iso-C <sub>16:0</sub> 3-OH	<b>12.9</b>	<b>7.7</b>
iso-C <sub>17:0</sub> 3-OH	3.9	3.5
<b>Cyclopropane fatty acids</b>		
C <sub>17:0</sub> cyclo	ND	0.7
<b>Summed Features</b>		
3 (C <sub>16:1</sub> ω7c / C <sub>16:1</sub> ω6c)	4.7	<b>6.2</b>
9 (iso-C <sub>17:1</sub> ω9c)	0.2	1.2

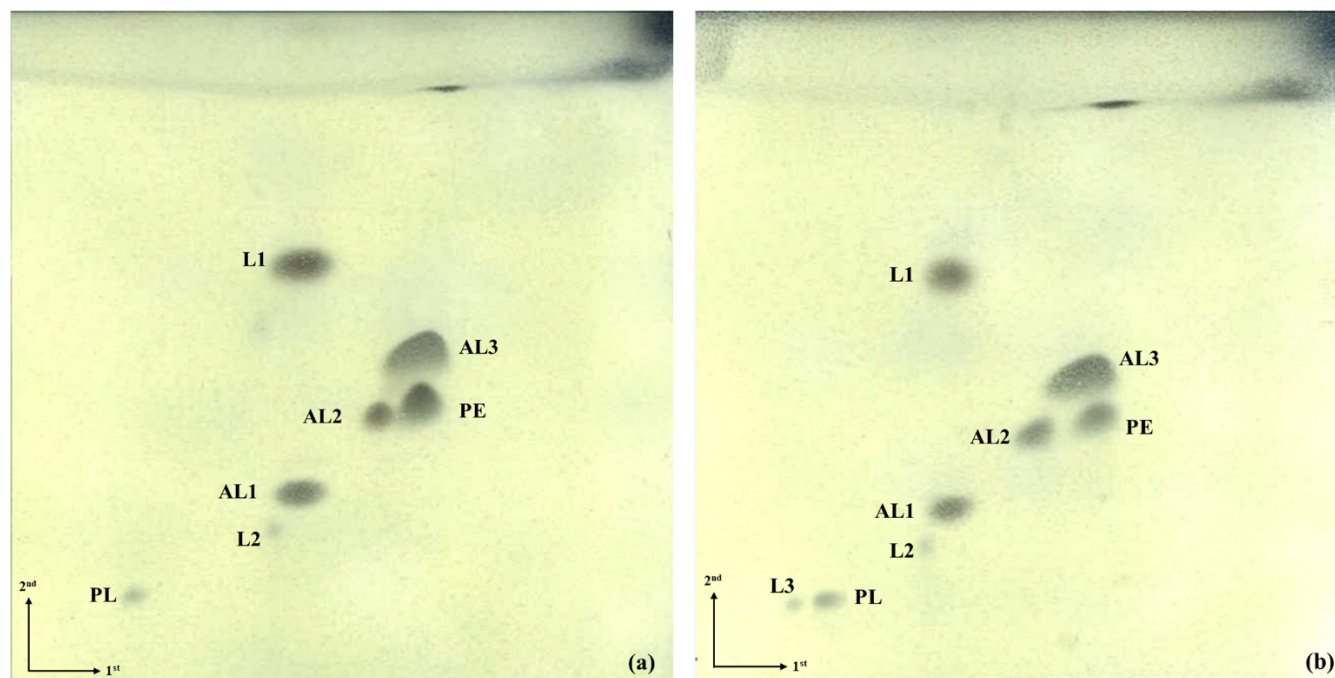


**Figure S1.** (a) Maximum likelihood (ML) and (b) maximum parsimony (MP) phylogenetic tree based on 16S rRNA gene sequences of strain HL-RS19<sup>T</sup> and related taxa in the family *Flavobacteriaceae*. *Flavobacterium fluvii* H7<sup>T</sup> was used as an outgroup. Bootstrap values at nodes indicate a percentage higher than 70% (based on 1000 replicates). The asterisk mark in the parentheses indicates 16S rRNA gene sequence retrieved from the genome sequence of the type strain.





**Figure S3.** UV-VIS spectra of diverse carotenoids detected in strain HL-RS19<sup>T</sup> incubated under light and dark conditions.



**Figure S4.** Two-dimensional thin-layer chromatography (TLC) of the polar lipids of (a) *Lacinutrix neustonica* HL-RS19<sup>T</sup> and (b) *Lacinutrix mariniflava* KCCM 42306<sup>T</sup>. PE, phosphatidylethanolamine; PL, an unidentified phospholipid; AL1–3, unidentified aminolipids; L1–3, unidentified lipids.