

Supplementary Table. S1. General features of the genome of strain OP-27^T and its closely related species of the genus *Roseomonas*.

Genomic features	1	2	3	4	5	6	7	8
Size (Mb)	5.28	6.40	5.25	5.86	4.24	5.30	5.01	5.77
Total gene	5,458	6,102	5,101	5,555	4,096	5,118	5,185	5,538
Contigs	671	73	216	89	51	56	774	67
G+C content (%)	71.2	68.7	70.8	71.2	72.7	71.2	71.2	69.2
No. of rRNA genes	4	3	3	3	3	3	3	3
No. of tRNA genes	48	47	47	46	46	48	49	47
Contig N50	15,298	379,484	48,334	161,991	301,642	595,371	11,753	180,609
Contig L50	95	7	30	12	5	3	107	13
No. proteins	5,164	5,918	4,953	5,441	3,982	5,020	4,854	5,437

Strains: 1, OP-27^T; 2, *R. lacus* CGMCC 1.3617^T; 3, *R. soli* LMG 31231^T; 4, *R. eburnea* LMG 31228^T; 5, *R. alkaliterrae* DSM 25895^T; 6, *R. oryzicola* KCTC 22478^T; 7, *R. rubea* MO17^T; 8, *R. terrae* LMG 31159^T.

Supplementary Table. S2. Average nucleotide identity (ANI) value and digital DNA-DNA hybridization (dDDH) value between the strain OP-27^T and closely related members in the genus *Roseomonas*.

Taxon	ANI similarity (%)	dDDH (%)
<i>Roseomonas rubea</i> MO17 ^T	83.1	26.4
<i>Roseomonas eburnea</i> LMG 31228 ^T	83.1	26.8
<i>Roseomonas alkalitettiae</i> DSM 25895 ^T	83.0	26.3
<i>Roseomonas oryzicola</i> KCTC 22478 ^T	82.9	25.9
<i>Roseomonas soli</i> LMG 31231 ^T	82.9	26.4
<i>Roseomonas lacus</i> CGMCC 1.3617 ^T	81.8	25.0
<i>Roseomonas terrae</i> LMG 31159 ^T	81.1	24.6

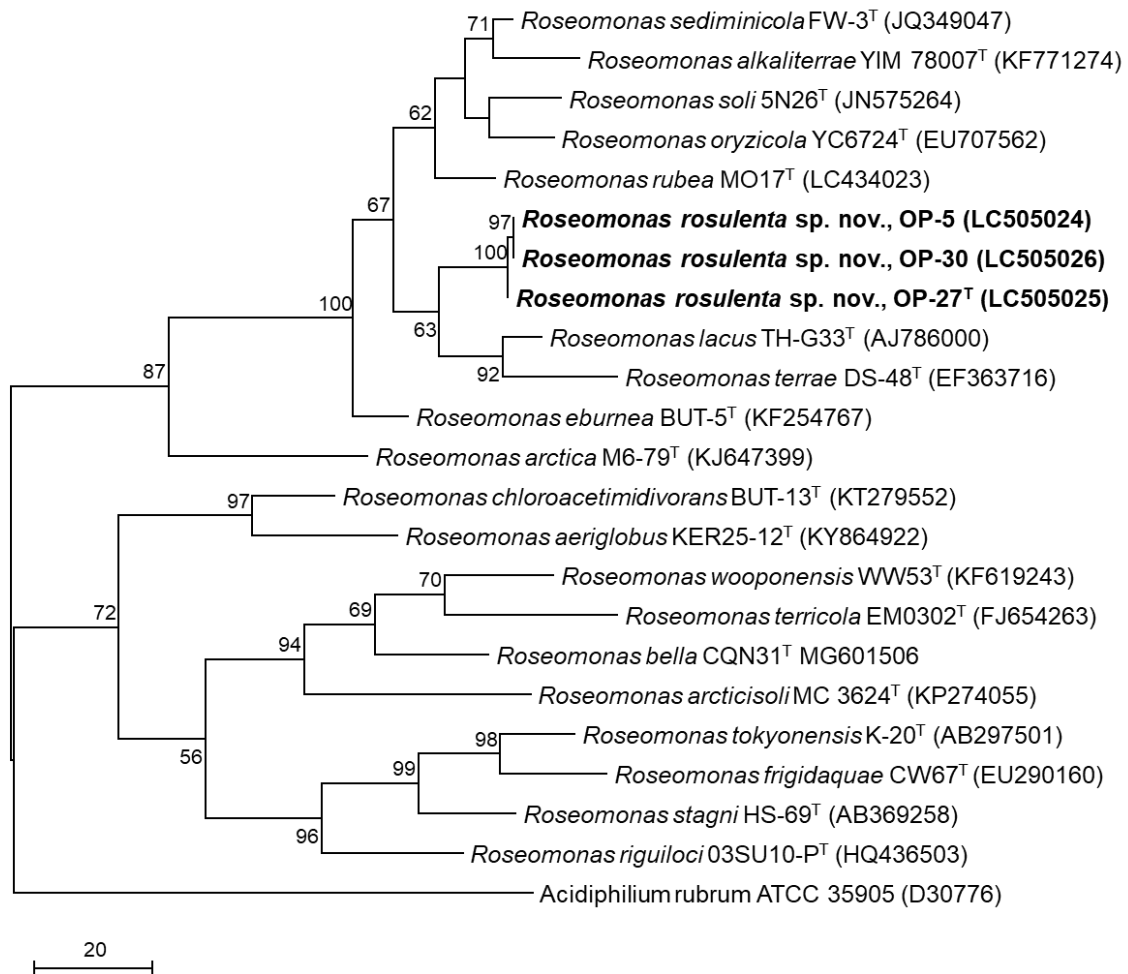
Supplementary Table. S3. Cellular fatty acid compositions (%) of strains OP-27^T, OP-5, OP-30 and related type strains of species of the genus *Roseomonas*.

Strain: 1, OP-27^T; 2, OP-5; 3, OP-30; 4, *R. sediminicola* KACC 16616^T; 5, *R. soil* KACC 16376^T; 6, *R. oryzicola* KCTC 22478^T; 7, *R. eburnea* KACC 17166^T; 8, *R. rubea* MO17^T; 9, *R. alkaliterrae* KACC 185307^T. All data are from this study. Strains were cultivated in R2A at 28 °C for 5 days. Fatty acids that accounted for < 1.0% of the total in each strain are not shown. tr, Trace (< 1% of the total fatty acids); –, Not detected.

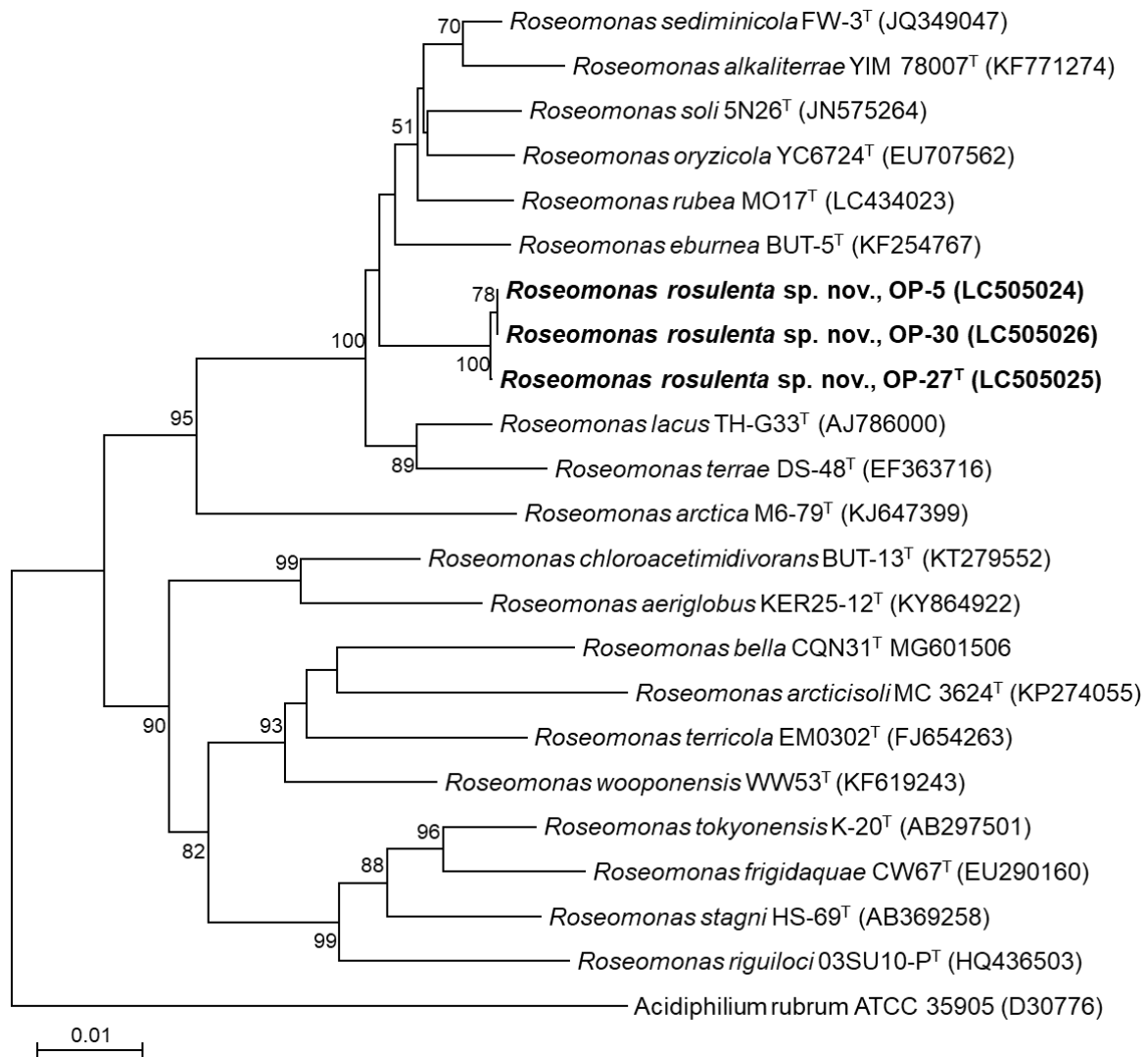
Fatty acid	1	2	3	4	5	6	7	8	9
Saturated acids									
C _{10:0}	—	—	—	4.5	tr	—	—	tr	—
C _{12:0}	tr	tr	tr	3.3	2.4	—	—	1.3	tr
C _{14:0}	1.0	1.3	1.1	1.8	tr	tr	—	Tr	tr
C _{16:0}	9.9	10.6	9.5	13.6	11.9	9.2	7.6	13.9	11.8
C _{18:0}	—	tr	tr	tr	1.4	tr	—	tr	tr
Unsaturated acids									
C _{15:1} <i>ω</i> 8 <i>c</i>	—	—	—	tr	1.4	—	—	tr	—
C _{16:1} <i>ω</i> 5 <i>c</i>	6.9	6.0	5.7	4.5	2.8	1.1	1.7	5.1	tr
C _{17:1} <i>ω</i> 7 <i>c</i>	—	2.4	1.7	—	tr	—	—	4.6	—
C _{17:1} <i>ω</i> 6 <i>c</i>	tr	—	tr	—	—	—	—	1.2	tr
C _{18:1} <i>ω</i> 7 <i>c</i>	50	47.7	51.9	50.0	63.2	61.5	37.5	42.0	63.3
C _{18:1} <i>ω</i> 5 <i>c</i>	—	—	—	—	tr	tr	tr	2.3	Tr
C _{19:0} <i>ω</i> 8 <i>c</i> cyclo	1.5	1.1	1.0	6.7	4.7	1.9	7.8	1.4	5.0
C _{18:1} <i>ω</i> 7 <i>c</i> 11-methyl	—	—	—	—	—	2.1	—	1.0	—
Hydroxy acids									
C _{18:0} 3-OH	tr	1.3	1.4	—	—	tr	tr	—	tr
C _{18:1} 2-OH	23.4	23.2	21.6	—	—	20.4	40.7	—	14.5
Summed feature*									
2	1.2	1.4	1.1	1.8	3.1	tr	—	5.0	tr
3	2.0	1.5	1.4	7.1	2.1	1.7	1.7	11.7	1.0

*Summed feature 2 comprised C_{14:0} 3-OH and/or iso-C_{16:1} I; summed feature 3 comprised C_{16:1} *ω*7*c* and/or iso-C_{15:0} 2OH.

Supplementary Fig. S1. Maximum-parsimony tree based on nearly complete 16S rRNA gene sequence showing relationships between strains OP-27^T, OP-5 and OP-30 and the type strains of related *Roseomonas* species. Bootstrap values are shown in percentages of 1000 replicates, when greater than 50%. Bar, 20 sequence changes over the whole sequence.



Supplementary Fig. S2. Neighbour-joining tree based on nearly complete 16S rRNA gene sequence showing relationships between strains OP-27^T, OP-5 and OP-30 and the type strains of related *Roseomonas* species. Bootstrap values are shown in percentages of 1000 replicates, when greater than 50%. Bar, 0.01 substitutions per nucleotide position.



Supplementary Fig. S3. Transmission electron microscope image of a negatively stained cell of strain OP-27^T cultivated at 30°C for 5 days on R2A agar. *Bar*, 1 μm .

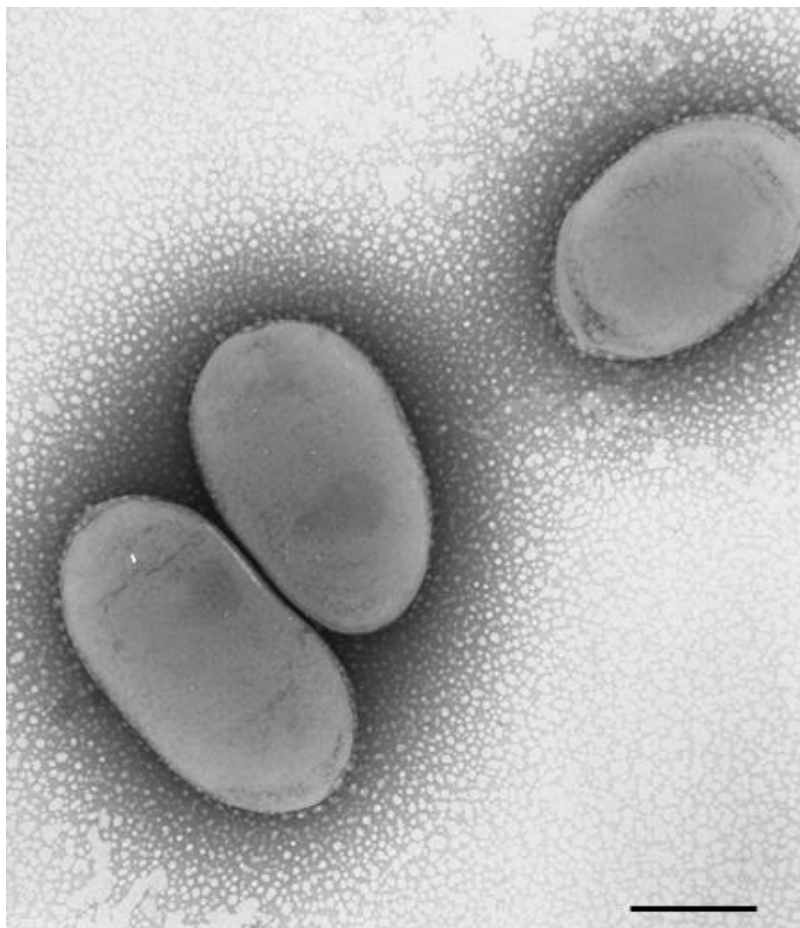


Fig. S4. Two-dimensional TLC of polar lipids of *Roseomonas rosulenta* sp. nov. OP-27^T, showing total lipids stained with 5 % ethanolic molybdatophosphoric acid (a), aminolipids with ninhydrin (b) and phospholipids with Zinzadze reagent (c). DPG, diphosphatidylglycerol; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PC, phosphatidylcholine; AL, unidentified aminolipid; PL, unidentified phospholipid; L1-2, unidentified lipids.

