

Supplementary Materials

Table S1. The 16S rRNA gene sequence analysis of the isolated strains.

Strains	Type strain with the highest similarity	Highest 16S rDNA sequence similarity	Length of the 16S rDNA
M6	<i>Sandaracinobacter sibiricus</i> RB16-17 ^T	95.5%	1,407 bp
S6	<i>Caulobacter henricii</i> DSM 4730 ^T	96.2%	1,481 bp
S7	<i>Mucilaginibacter xinganensis</i> BJC16-A31 ^T	97.2%	1,531 bp
M8	<i>Sphingomonas gotjawalisoli</i> SN6-9 ^T	97.3%	1,313 bp
M5	<i>Sphingomonas jatrophae</i> S5-249 ^T	98.0%	1,495 bp
S9	<i>Massilia niastensis</i> 5516S-1 ^T	98.1%	1,393 bp
S11	<i>Ramlibacter monticola</i> G-3-2 ^T	98.6%	1,372 bp

Table S2. Cellular fatty acid composition (%) of M6^T, *S. hominis* SZY PN-1^T and *S. neustonicus* PAMC 28131^T.

Fatty acids (% of total)	M6 ^T	SZY PN-1 ^T	PAMC 28131 ^T
Saturated			
Iso-C _{10:0}	-	2.3	-
C _{12:0}	-	5.1	-
C _{14:0}	5.9	-	-
C _{16:0}	12.6	4.7	7.9
C _{17:0}	-	1.1	2.2
Iso-C _{19:0}	-	3.5	-
Hydroxy			
C _{14:0} 2-OH	16.6	-	-
iso-C _{15:0} 3-OH	1.9	-	-
C _{16:0} 2-OH	-	6.6	6.8
Unsaturated			
C _{14:1} ω5c	-	1.6	-
C _{16:1} ω5c	-	1.2	2.9
C _{17:1} ω6c	7.9	12.5	19.3
C _{18:3} ω6c	-	2.4	-
Summed features*			
3	15.8	10.9	15.8
8 (C _{18:1} ω7c)	(33.8)	41.8	42.6 (34.2)

–, not detected. The major fatty acids (> 10%) in the table are bolded. *Summed Features are fatty acids that cannot be resolved reliably from another fatty acid using the chromatographic conditions chosen. The MIDI system groups these fatty acids together as one feature with a single percentage of the total. Summed feature 3 included C_{16:1}ω7c and C_{16:1}ω6c; summed feature 8 contained C_{18:1}ω7c and/or C_{18:1}ω6c.

Figure S1. Neighbor-Joining tree based on the 16S rRNA gene sequences of strain M6^T and representatives of related taxa. Bootstrap values were expressed as a percentage of 1000 replicates and only those higher than 50% were given at the branch points. Bar, 0.02 substitutions per nucleotide position. *Rhodospirillum rubrum* S1^T was used as outgroup.

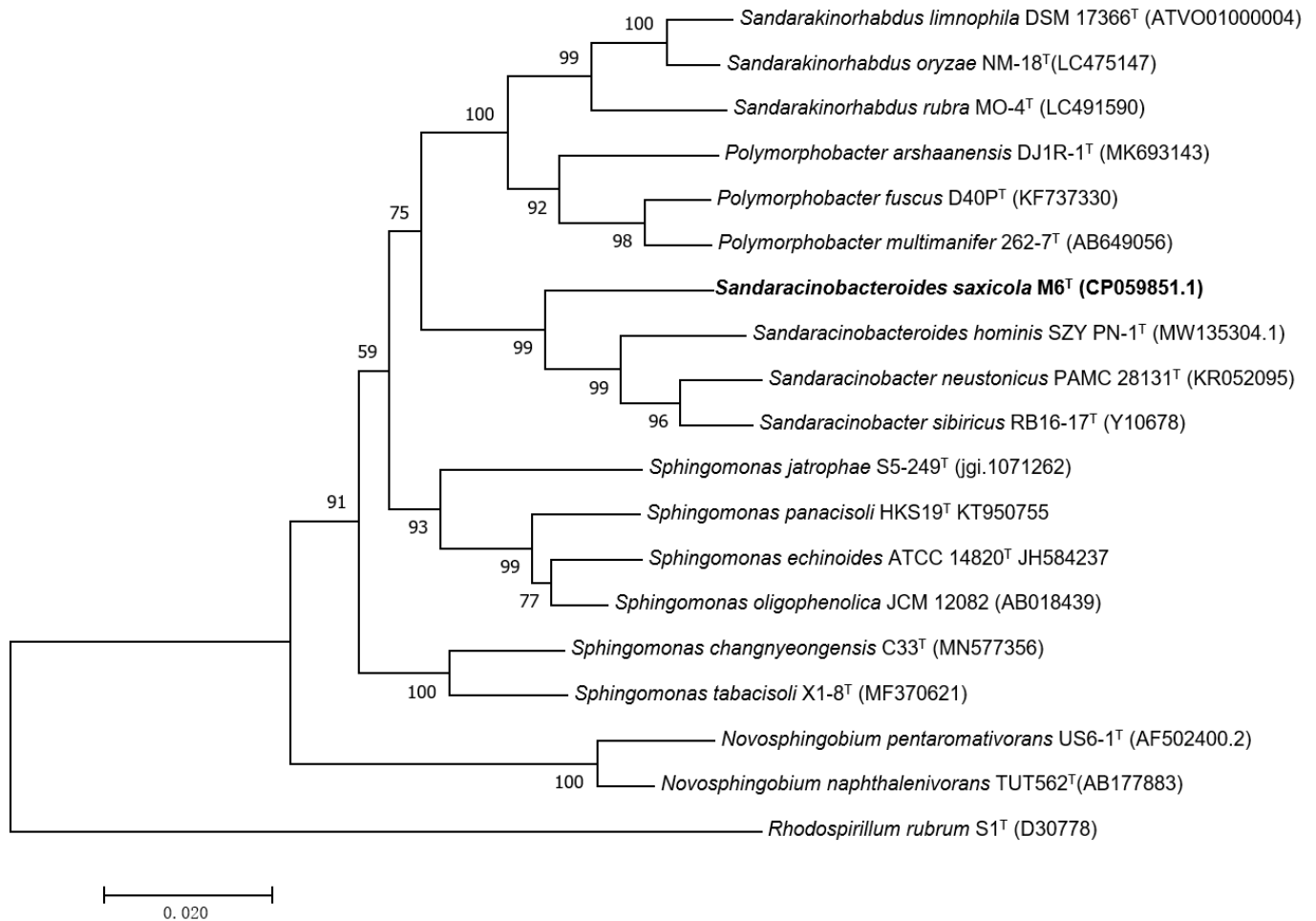


Figure S2. Minimum-evolution tree based on the 16S rRNA gene sequences of strain M6^T and representatives of related taxa. Bootstrap values were expressed as a percentage of 1000 replicates and only those higher than 50% were given at the branch points. Bar, 0.02 substitutions per nucleotide position. *Rhodospirillum rubrum* S1^T was used as outgroup.

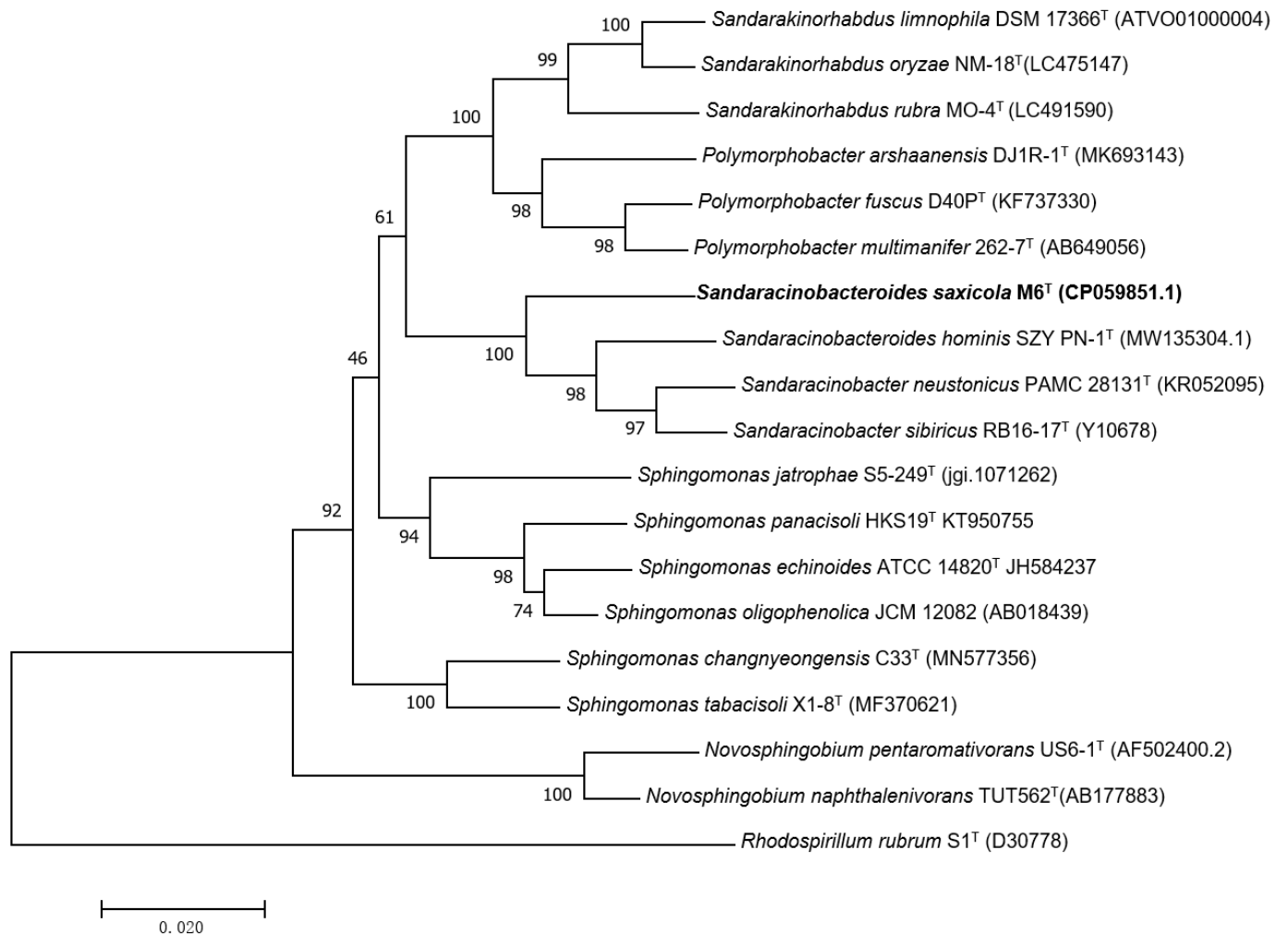


Figure S3. Maximum-likelihood phylogenetic tree based on the core proteome indicating the phylogenetic positions of strains M6^T with the related species. Scale bar indicates 0.020 substitutions per nucleotide position. *Rhodospirillum rubrum* S1^T (GCF_000013085) was used as outgroup. GenBank accession numbers are listed for each sequence in parentheses.

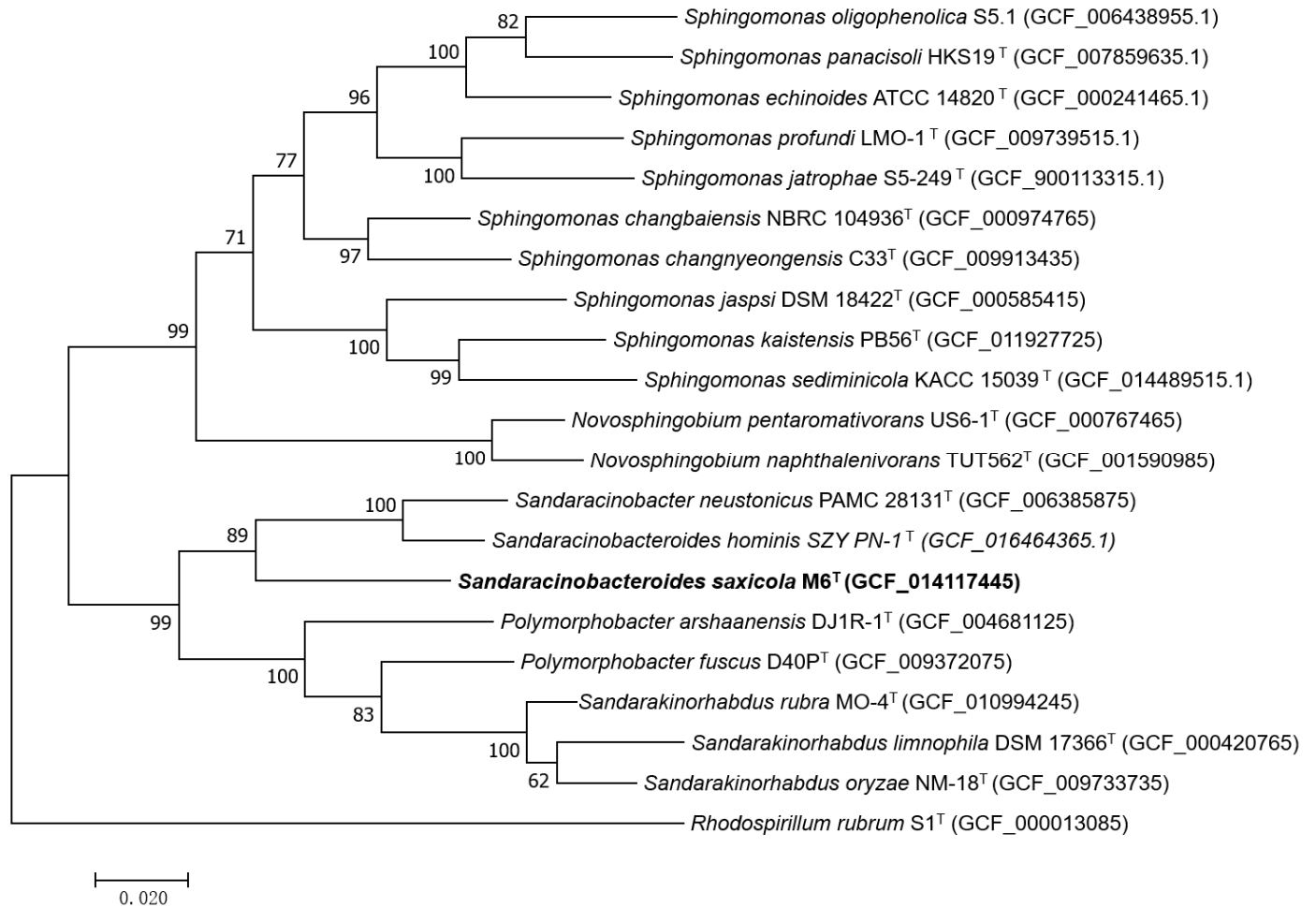


Figure S4. Total pigment absorption spectra of strain M6^T (in red).

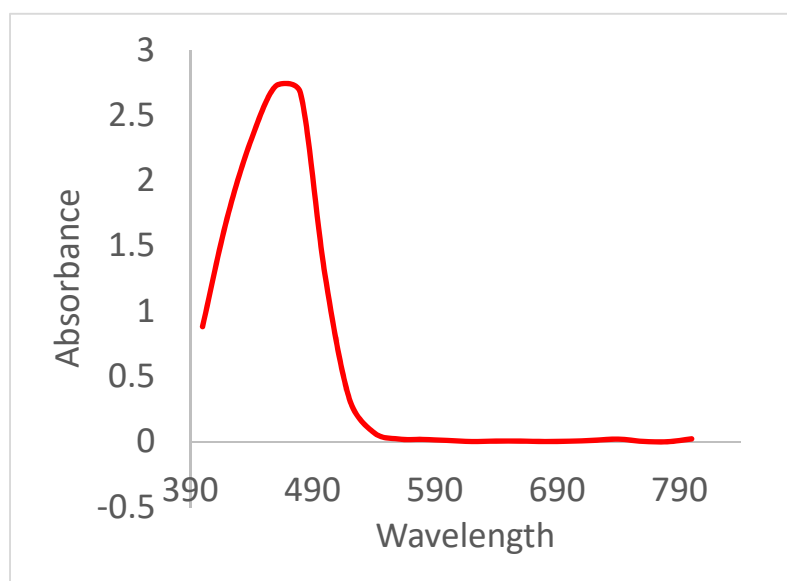


Figure S5. Two-dimensional TLC plate image of total polar lipids of strain M6^T sprayed with phosphomolybdic acid.

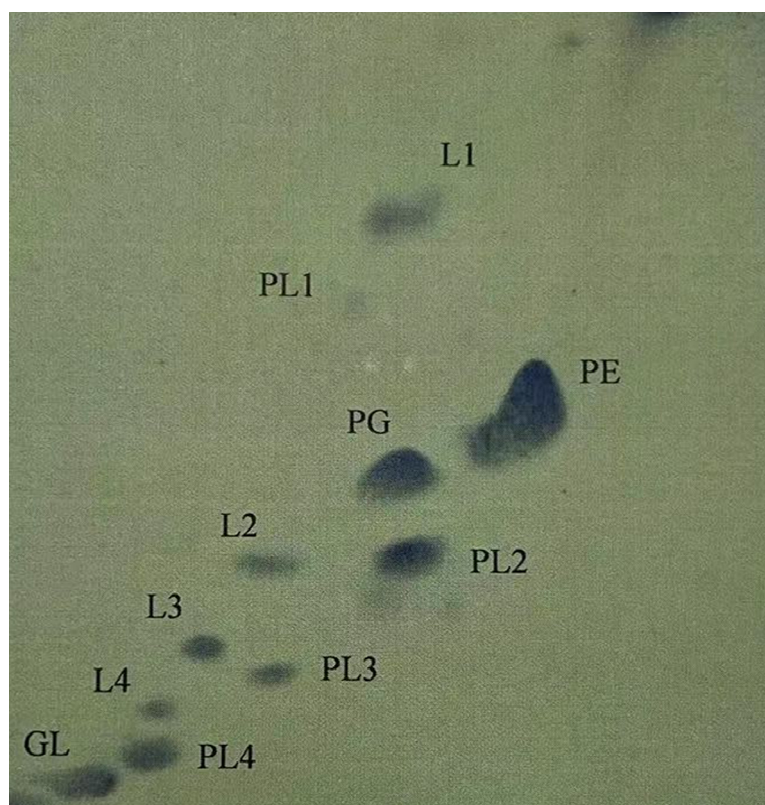


Figure S6. Circular map of the chromosome of strain M6^T.

From the center to outside: CDS, rRNA and tRNA genes on reverse and forward strand; sequencing depth and coverage; GC content; genomic information of the reference species.

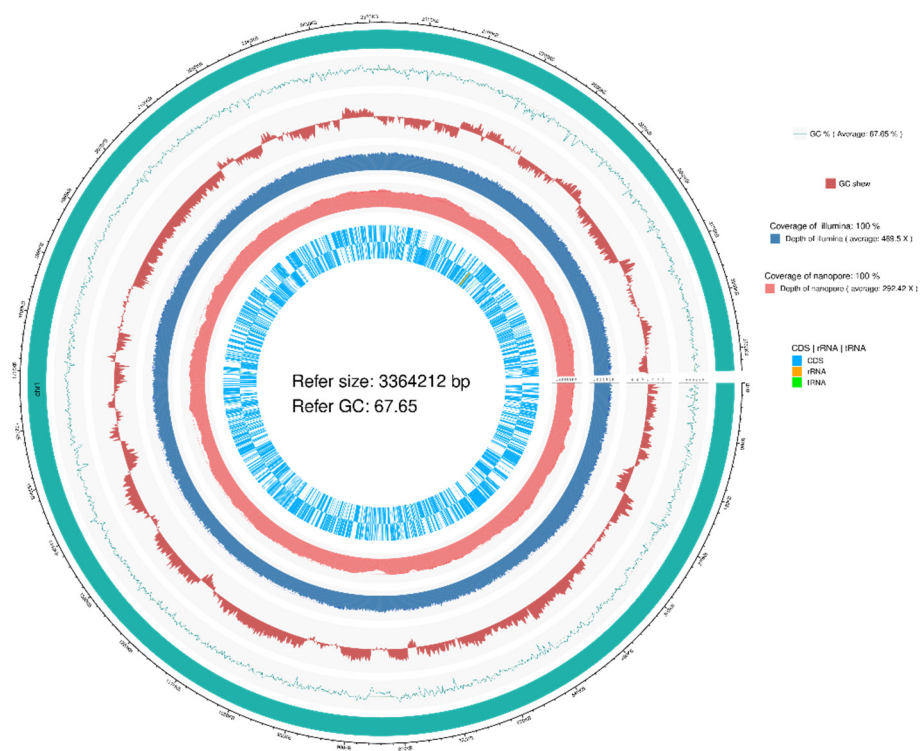


Figure S7. Subsystem category distribution from strain M6^T, generated through ClassicRAST pipeline (default settings)

