

Supplementary Information

Table 1. 16S rRNA gene phylogenetic affiliation of cultivated strains.

Isolate Code	Sequence Length (bp)	Closest relative by BLAST (Accession number)-Source	% Sequence Similarity
EG2	1483	<i>Brachybacterium conglomeratum</i> NCIB 9859 (X91030)-environmental sample	99.1
EG4	1482	<i>Microbacterium resistens</i> 3352 (EU714361)-environmental sample	98.0
EG6	1486	<i>Micrococcus luteus</i> CV44 (AJ717369)-environmental sample	99.3
EG7	1482	<i>Brachybacterium</i> sp. 511 (EU086801)-environmental sample	98.0
EG8	1484	<i>Corynebacterium ureicelerivorans</i> strain CNM462/06 (FJ392017)-environmental sample	98.7
EG10	1488	<i>Brevibacterium iodinum</i> DSM 2062T (X83813)-environmental sample	98.9
EG11	1486	<i>Microbacterium resistens</i> 3352 (EU714361)-environmental sample	98.2
EG12	1488	<i>Micrococcus luteus</i> CV44 (AJ717369)-environmental sample	99.5
EG14	1495	<i>Kocuria</i> sp. CNJ900 PL04 (DQ448710)-marine sediments	99.7
EG16	1483	<i>Mycobacterium</i> sp. CNJ823 PL04 (DQ448717)-marine sediments	99.9
EG18	1492	<i>Brevibacterium iodinum</i> DSM 2062T (X83813)-environmental sample	98.8
EG22	1488	<i>Microbacterium oxydans</i> B5 (DQ350825)-environmental sample	97.3
EG33	1379	<i>Rhodococcus opacus</i> B4(AB192962)-environmental sample	98.0
EG34	1489	<i>Brevibacterium casei</i> 3Tg (AY468375)-environmental sample	98.4
EG36	1490	<i>Mycobacterium houstonense</i> ATCC 49403 (AY012579)-environmental sample	97.9
EG37	1486	<i>Brevibacterium epidermidis</i> ZJB-07021 (EU046495)-environmental sample	97.1
EG38	1498	<i>Kocuria</i> sp. CNJ900 PL04 (DQ448710)-marine sediments	99.9
EG40	1486	<i>Micrococcus</i> sp. B5W22-1 (EF114312)-environmental sample	99.3
EG43	1495	<i>Brevibacterium</i> sp. BBH7 (AM158906)-marine sediments	98.3

EG45	1487	<i>Micrococcus</i> sp. CNJ719 PL04 (DQ448712)-marine sediments	97.9
EG47	1489	<i>Microbacterium indicum</i> BBH9 (AM286267)-marine sediments	97.5
EG49	1482	<i>Actinokineospora diospyrosa</i> NRRLB-24047T (AF114797)-marine sediments	97.0
EG50	1485	<i>Gordonia terrae</i> AIST-1 (AB355992)-sea water	99.3
EG53	1501	<i>Arthrobacter</i> sp. VTT E-052904 (EF093123)-environmental sample	99.3
EG55	1328	<i>Salinispora pacifica</i> CNH732 RS00 (DQ224165)-sea water	99.6
EG56	1488	<i>Micrococcus</i> sp. TPR14 (EU373424)-environmental sample	99.0
EG62	1487	<i>Microbacterium oxydans</i> B5 (DQ350825)-environmental sample	97.4
EG65	1497	<i>Brevibacterium aurantiacum</i> NCDO 739 (X76566)-environmental sample	99.0
EG67	1390	<i>Dietzia cinnamomea</i> IMMIB RIV-399 (AJ920289)-environmental sample	99.4
EG69	1487	<i>Microbacterium indicum</i> BBH6 (AM158907)-marine sediments	97.3
RV13	1495	<i>Rothia</i> sp. L-143 (DQ822568)-environmental sample	97.0
RV15	1492	<i>Streptomyces lincolnensis</i> NRRL2936 (X79854)-marine sediments	98.0
RV28	1494	<i>Mycobacterium septicum</i> ATCC 700731 (AY457070)-environmental sample	99.1
RV43	1478	<i>Micromonospora</i> sp. HBUM84229 (EU119232)-environmental sample	99.8
RV45	1477	<i>Micromonospora</i> sp. HBUM84229 (EU119232)-environmental sample	99.9
RV63	1481	<i>Micromonospora</i> sp. RtII195 (EU427443)-environmental sample	99.7
RV71	1481	<i>Micromonospora matsumotoense</i> IMSNU 22003T (AF152109)-environmental sample	98.3
RV75	1491	<i>Kocuria palustris</i> isolate SCH0404 (AY881237)-marine sediment	99.6
RV76	1485	<i>Gordonia terrae</i> strain COE-O1 (AF467984)-environmental sample	99.8
RV77	1482	<i>Rhodococcus opacus</i> B-4 (AB192962)-environmental sample	98.4
RV83	1487	<i>Mycobacterium septicum</i> ATCC 700731 (AY457070)-environmental sample	99.3
RV89	1493	<i>Kocuria kristinae</i> DSM 20032	96.6

		(X80749)-environmental sample	
RV113	1512	<i>Rubrobacter radiotolerans</i> DSM 46359-T	92.8
		(X87134)-environmental sample	
RV115	1481	<i>Micromonospora</i> sp. 215009	99.2
		(FJ263418)-environmental sample	
RV116	1484	<i>Micromonospora</i> sp. 215009	99.3
		(FJ263418)-environmental sample	
RV145	1481	<i>Corynebacterium</i> sp. 3301750	99.0
		(AY581884)-environmental sample	
RV147	1484	<i>Corynebacterium</i> sp. 3301750	99.1
		(AY581884)-environmental sample	
RV151	1502	<i>Mycobacterium gordonae</i> agha3	99.0
		(AJ581472)-environmental sample	
RV152	1493	<i>Mycobacterium gordonae</i> agha3	99.1
		(AJ581472)-environmental sample	
RV154	1493	<i>Kocuria</i> sp. Am 16 (AJ971854)-environmental sample	99.5
RV157	1483	<i>Rhodococcus opacus</i> B-4	98.6
		(AB192962)-environmental sample	
RV163	1345	<i>Nocardiopsis dassonvillei</i> HBUM174177	99.4
		(FJ532466)-environmental sample	
