Supplementary Table S1. Whole-cell fatty acid composition of strain RB72^T and related species of the genus *Streptomyces*

Strains: 1, RB72^T; 2, *Streptomyces hachijoensis* NRRL B-3106^T; 3, *S. kentuckensis* NRRL B-1831^T. All data were determined in the laboratory under the same growth conditions. Fatty acids were identified by co-elution with known standards and mass spectral analysis of their methyl and picolinyl esters. Fatty acids are listed in order of elution on a DB-1 column and named using the format X:YωZ, where X represents the number of carbons in the molecule, Y represents the number of double bonds present and Z represents the position of the double bond in reference to the aliphatic or 'ω' end of the molecule. i and a indicate iso and anteiso branching patterns, respectively; cy indicates cyclo; br indicates that the branching pattern is unknown; when the position of the double bond is not given, it is unknown. Data are presented as mean±SD (*n*=3) of weight per cent of total fatty acids.

Fatty Acid	1	2	3
i14:0	9.2±0.3	24.5±2.1	4.8±0.4
14:0	0.1±0.0		
i15:0	12.9±0.1	3.2±0.5	9.6±0.1
a15:0	10.9±0.1	9.5±1.1	25.2±0.5
15:0	2.2±0.0	1.1±1.1	1.0±0.1
i16:1ω7	1.4±0.1	3.5±0.3	1.6±0.2
i16:0	34.8±1.7	46.2±4.4	28.5±0.5
16:1ω7	0.3±0.1		0.2±0.0
16:1	0.4±0.1	0.6±0.0	0.2±0.0
16:0	1.2±0.9		1.8±0.0
i17:1	1.1±0.1		1.5±0.1
i17:1ω8	11.1±0.3	8.4±0.3	3.1±0.2
i17:0	1.6±0.1	0.4±0.1	2.8±0.1
a17:0	2.0±0.1	1.5±0.1	9.7±0.5
cy17:0	4.4±0.1	0.4±0.2	4.6±0.1
17:0	0.1±0.0	0.1±0.0	0.4±0.0
br18:1a	3.8±0.1	0.1±0.0	1.6±0.1
br18:1b	1.3±0.0	0.2±0.0	2.1±0.1
i18:0	0.1±0.0	0.3±0.1	0.1±0.0
18:1ω7	0.9±0.1	0.1±0.0	1.2±0.1
18:0	0.2±0.1		