

Supplementary Table S1. Most similar sequences for the amplicons in the database of the National Center for Biotechnology Information, based on the results from a search using the Basic Local Alignment Tool. These results only shows the closest match with identified bacteria. Match with sequences belong to unidentified organisms or organisms only identified at the phylum or higher level are omitted.

Sample name	Highest matching score among identified bacteria	E-value	Percentage identity
KW24.7	<i>Mycobacterium</i> sp. strain R.N1S7 (Accession #: MH298485.1)	3e ⁻¹²⁷	99.22%
KW2607	<i>Mycobacterium</i> sp. strain DL189 (Accession #: MH290164.2)	5 e ⁻⁸⁴	95.43%
KW2607Myco2	<i>Mycobacterium</i> sp. strain A33 (Accession #: MF102126.1)	0.0	92.84%
KW2607Tb1	<i>Mycobacterium</i> sp. LTG 466 (Accession #: KY853653.1)	3e ⁻¹⁶⁸	95.04%
KW2607Tb2	<i>Mycobacterium</i> sp. LTG 466 (Accession #: KY853653.1)	3e ⁻¹⁶³	94.26%
KW26.71	<i>Mycobacterium</i> sp. strain AZCC_0280 (Accession #: MK875943.1)	5 e ⁻¹²⁵	98.47%
KW26.72	Uncultured <i>Mycobacterium</i> sp. (Accession #: MG804654.1)	3e ⁻¹²⁶	99.22%
KW26.73	Uncultured <i>Mycobacterium</i> sp. (Accession #: MG804654.1)	4 e ⁻¹²⁵	98.84%
KW26.74	Uncultured <i>Mycobacterium</i> sp. (Accession #: MG804654.1)	3e ⁻¹²⁶	99.22%