Table SI. Accession numbers of *Mycobacterium* species and subspecies used.

Species/subspecies identity	Accession numbers	(Refs.)
MAB- isolate 1	SRR14043053	(19)
MAB-isolate 2	SRR14043043	
MAB-isolate 3	SRR14043035	
MAB-isolate 4	SRR14043008	
MAB-isolate 5	SRR14043007	
MMAS-isolate 1	SRR14043059	
MMAS-isolate 2	SRR14043004	
MMAS-isolate 3	Identified by MALDI-TOF	
MMAS-isolate 4	SRR14043045	
MMAS-isolate 5	SRR14043031	
MTB-H37Ra (ATCC 25177)	CP000611	(22)

The data from these databases are now available in the European Nucleotide Archive. NTM datasets are accessible under BioProject accession PRJNA523980 (https://www.ebi.ac.uk/ena/browser/view/ PRJNA523980), whereas MTB-H37Ra data is available under PRJNA18883 (https://www.ebi.ac.uk/ena/browser/view/PRJNA18883). MAB, *Mycobacterium abscessus* subspecies *abscessus*; MMAS, *Mycobacterium abscessus* subspecies *massiliense*; MTB-H37Ra, *Mycobacterium tuberculosis*-H37Ra; MALDI-TOF, matrix-assisted laser desorption/ionization-time of flight; NTM, nontuberculous mycobacteria.

Table SII. Specific DNA-related Raman shifts and their corresponding peak assignments.

Raman shift (cm^{-1})	Peak assignments	(Refs.)
726	Adenine (ring breathing mode)	(26-32)
755	Thymine (ring breathing mode)	(27,32)
781	Thymine/Cytosine (ring breathing mode)	(26-28,30-35)
1,097	Asymmetric stretching mode $(O\text{-}P\text{-}O)^-$	(26-28,33)
1,317	Guanine (C-N stretching mode)	(27,28)
1,331	Adenine/Guanine	(26-28,32)
1,486	Guanine/Adenine	(26-28)
1,577	Guanine/Adenine	(26-28,33,36,37)

Table SIII. Reproducibility assessment of SERS spectra via Pearson's and Spearman's correlation analysis.

Isolates	R^2 (Repeat 1)	R^2 (Repeat 2)	R^2 (Repeat 3)	Pearson's r (Mean ± SD)	Spearman's ρ (Mean ± SD)
A, At 15 ng/µl (785 nm)					
MAB-isolate 1	0.8484	0.8402	0.8399	0.91 ± 0.01	0.86±0.01
MAB-isolate 2	0.9005	0.8830	0.8716	0.92±0.01	0.87±0.01
MAB-isolate 3	0.8753	0.8669	0.8698	0.91±0.02	0.86±0.02
MAB-isolate 4	0.7701	0.7651	0.7692	0.91±0.01	0.76±0.01
MAB-isolate 5	0.8067	0.7947	0.8099	0.93±0.01	0.86±0.01
MMAS-isolate 1	0.8408	0.8156	0.8169	0.92±0.01	0.86±0.02
MMAS-isolate 2	0.8811	0.8764	0.8745	0.92±0.01	0.88±0.01
MMAS-isolate 3	0.8710	0.8711	0.8703	0.91±0.01	0.83±0.02
MMAS-isolate 4	0.8176	0.8193	0.8303	0.91±0.00	0.80±0.01
MMAS-isolate 5	0.8047	0.7838	0.8217	0.88±0.05	0.81±0.05
MTB-H37Ra	0.8144	0.7848	0.8370	0.86±0.11	0.81±0.05
B, At 50 ng/µl (785 nm)					
MAB-isolate 1	0.8334	0.8217	0.8074	0.90±0.02	0.84±0.03
MAB-isolate 2	0.8891	0.8853	0.8709	0.94±0.02	0.87±0.04
MAB-isolate 3	0.8645	0.8561	0.8555	0.92±0.01	0.84±0.01
MAB-isolate 4	0.8289	0.8552	0.8503	0.94±0.00	0.84±0.01
MAB-isolate 5	0.8282	0.8634	0.8526	0.92±0.02	0.79±0.02
MMAS-isolate 1	0.9045	0.8998	0.8967	0.92±0.01	0.83±0.03
MMAS-isolate 2	0.9014	0.9005	0.9020	0.92±0.01	0.82±0.02
MMAS-isolate 3	0.8633	0.8448	0.8792	0.90±0.04	0.80±0.02
MMAS-isolate 4	0.7910	0.8177	0.8451	0.89±0.05	0.82±0.04
MMAS-isolate 5	0.8813	0.8563	0.8659	0.91±0.04	0.85±0.05
MTB-H37Ra	0.9170	0.9160	0.9143	0.92±0.02	0.83±0.02

MAB, *Mycobacterium abscessus* subspecies *abscessus*; MMAS, *Mycobacterium abscessus* subspecies *massiliense*; MTB-H37Ra, *Mycobacterium tuberculosis*-H37Ra; R^2, the coefficient of determination; SD, standard deviation.