

1 **Table S2. Genomic characteristics of large-scale deletions between clinical *M. abscessus***
 2 **isolates and the reference type strain, ATCC19977^T.**

Characteristic	Deletion Region					
	A	B	C	D	E	F
Size (Kb)	33	31	62/82	64	38	83
GC (%)	64.5	63	59.6	62.4	60.8	61.7
No. of genes	37	31	92/110	70	32	87
Sequence Homology^a						
BLAST Results						
Plasmid	+	-	-	-	-	+
Transposon	+	-	-	-	-	+
Mycobacteriophage	-	-	+	-	-	-
<i>M. abscessus</i>	+	+	-	+	+	+
Other RGM ^b	+	-	-	+	+	+
SGM ^c	+	-	-	+	-	+
Other Actinobacteria	+	+	-	+	+	+

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 4 ^a Sequence homology is defined as $\geq 70\%$ sequence identity, $\geq 30\%$ query coverage and E-
 5 value of 0.0 using the blastn algorithm versus the NCBI non-redundant nt sequence database
 6 ^b RGM = other rapidly growing Mycobacteria, not *M. abscessus*
 7 ^c SGM = slowly growing Mycobacteria