Supplementary Tables

Table S1. Sequencing details of Mycobacterium abscessus clinical isolates.

Table S2. Genomic differences in smooth and rough Mycobacterium abscessus clinical isolates.

Table S3. M. abscessus survival following phage challenge.

Table S4. Genomic differences in phage resistant mutants (RMs) of Mycobacterium abscessus clinical isolates.

Table S5. Prophages resident in M. abscessus genomes.

Table S6. Plasmids of Mycobacterium abscessus clinical isolates.

Table S7. Primers used to construct phage mutants.

Supplementary Figure Legends

Figure S1. Genome organization of phiGD20-1 (MabA1). The genome of phiGD20-1 is shown with predicted genes shown as boxes either above or below the genome indicating rightward- and leftward-transcription, respectively. Gene numbers are shown within each gene box. Phamily designations are shown above or below each gene with the numbers of phamily members in parentheses; genes are colored according to the phamily designations. White boxes represent 'orphams', genes with no close relatives in this dataset. Phamily assignments were determined using Phamerator and database Actino_prophage (version 5). Predicted gene functions are indicated.

Figure S2. Genome organization of phiGD22-1 (MabA1). See Figure S1 for details.

Figure S3. Genome organization of phiGD23-1 (MabA1). See Figure S1 for details.

Figure S4. Genome organization of phiGD21-1 (MabB). See Figure S1 for details.

Figure S5. Genome organization of phiGD34-2 (MabB). See Figure S1 for details.

Figure S6. Genome organization of phiGD89A-1 (MabB). See Figure S1 for details.

Figure S7. Genome organization of phiGD57-1 (MabC). See Figure S1 for details.

Figure S8. Genome organization of phiGD17-1 (MabD). See Figure S1 for details.

Figure S9. Genome organization of phiGD24-3 (MabJ). See Figure S1 for details.