**Supplementary Tables and Supplementary Figure Captions**

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| **Lettered PhagesDB Cluster** | **Number of Prophages** | **Shell Gene Count** |
| A | 12 | 57 |
| F | 16 | 96 |
| K | 10 | 137 |
| M | 7 | 66 |
| P | 6 | 217 |
| No Cluster | 30 | 46 |

**Supplementary Table 1:** Abundance of shell genes in prophages calculated from pangenome analysis using Roary. Shell genes are defined as genes present in 15% to 95% of genomes in a cluster. This analysis of prophages assigned to lettered clusters was only applied to clusters with 5 or more prophages.

**Supplementary File 1:** This file contains the RefSeq assembly accession, NCBI Assembly ID, Bioproject, species, and source of the complete genomes used in this study.

**Supplementary File 2:** This file contains 6 data tables used in the study. The Predicted\_Prophages tab provides details about the predicted prophages including the genomic coordinates, cluster assignment, and the presence/absence of a bacterial virulence gene. The Predicted\_Prophages\_Edge\_Cases lists the coordinates of prophages near the ends of contigs. The Bacterial\_Genes tab represents the annotated output of bacterial genes (excluding bacterial virulence genes). The Virulence\_Genes represents the annotated output of bacterial virulence genes. The Cluster\_Virulence tab groups the predicted prophages by cluster and virulence status. The Virulence\_Gene\_Origins tab represents a count of the species origin of a virulence gene in the predicted prophages.

**Supplementary Figure 1:** Relative locations of predicted prophages in *M.* *absessus subsp. absessus* and *M. avium*. Prophages are colored by the host origin.

**Supplementary Figure 2:** Genome widephylogeny of 80 *M.* *abscessus* subsp*. abscessus* and *M.* *abscessus* subsp *boletti* genomes and 5 control genomes. The heatmap on the right shows the presence (black) or absence (white) of the lettered PhagesDB clusters (x-axis). The presence of prophage in a sample is noted by a shaded box in any column except NA/Control. NA/Control shading signifies genomes without a prophage and added controls not analyzed for prophages in this study. No shading means the sample does not have a prophage in that lettered cluster.

**Supplementary Figure 3:** Phylogeny of host *M.* *absessus subsp. massiliense* genomes. The shaded boxes are located along an x axis, which lists the lettered PhagesDB clusters. The presence of prophage in a sample is noted by a shaded box in any column except NA/Control. No shading means the sample does not have a prophage in that lettered cluster. Statistical significance was not achieved using PERMANOVA on this tree (F=1.398, *p=*0.225).

**Supplementary Figure 4:** Phylogeny of host M*. chimaera* and M*. intracellulare* genomes. The shaded boxes are located along an x axis, which lists the lettered PhagesDB clusters. The presence of prophage in a sample is noted by a shaded box in any column except NA/Control. No shading means the sample does not have a prophage in that lettered cluster. Statistical significance was not achieved using PERMANOVA on this tree (F=1.12, *p=*0.321).