

Supplementary Information

**Genomic analysis of *Acinetobacter baumannii* prophages
reveals remarkable diversity and suggests profound impact on
bacterial virulence and fitness**

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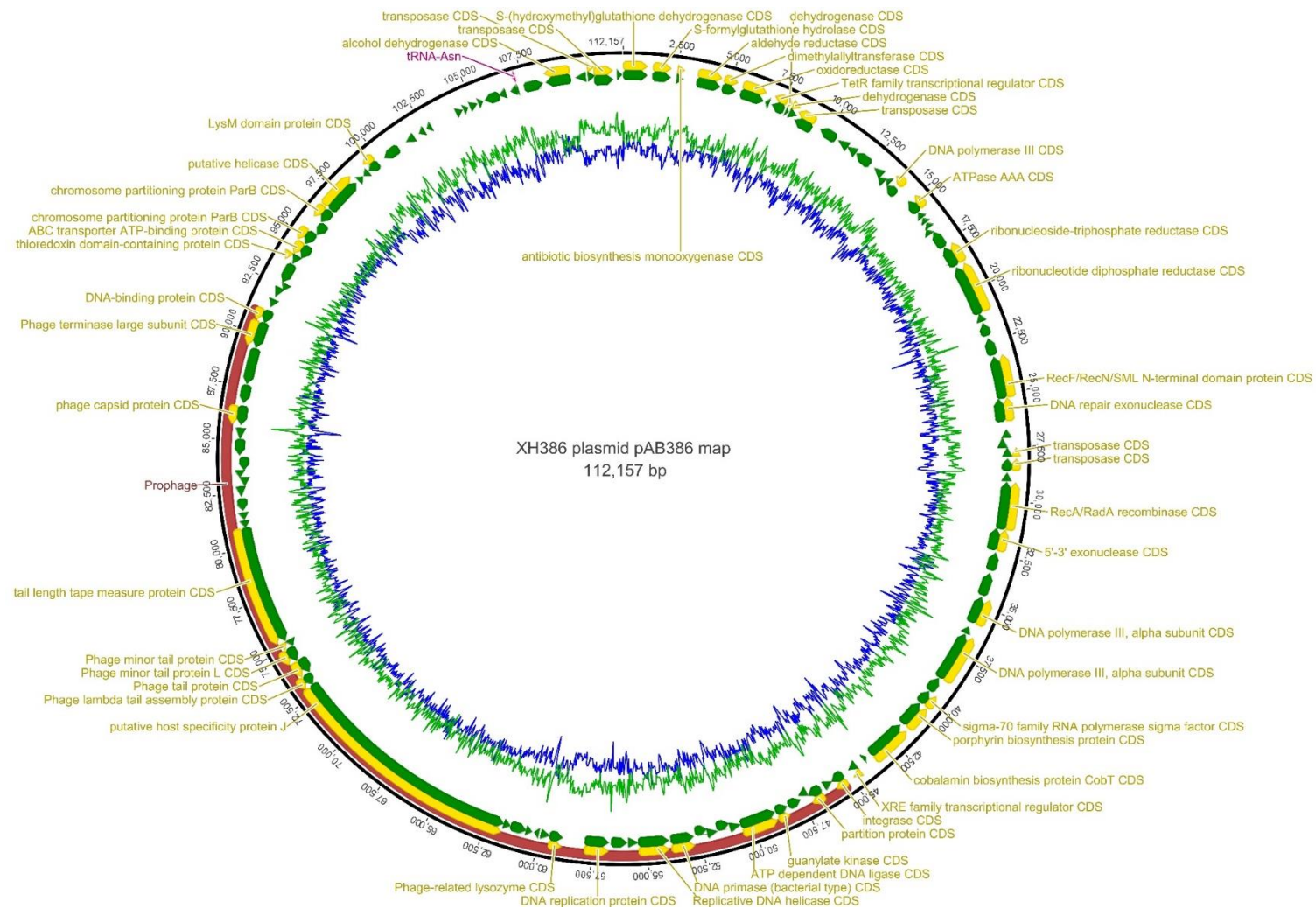


FIG S1. Map of plasmid pAB386 of *Acinetobacter baumannii* strain XH386. Green arrows: identified open reading frames; Yellow arrows: annotated coding DNA sequences (CDS); Pink arrow: tRNA; Red region: prophage sequence identified. Graphic for GC (blue) and AT (green) content in center.

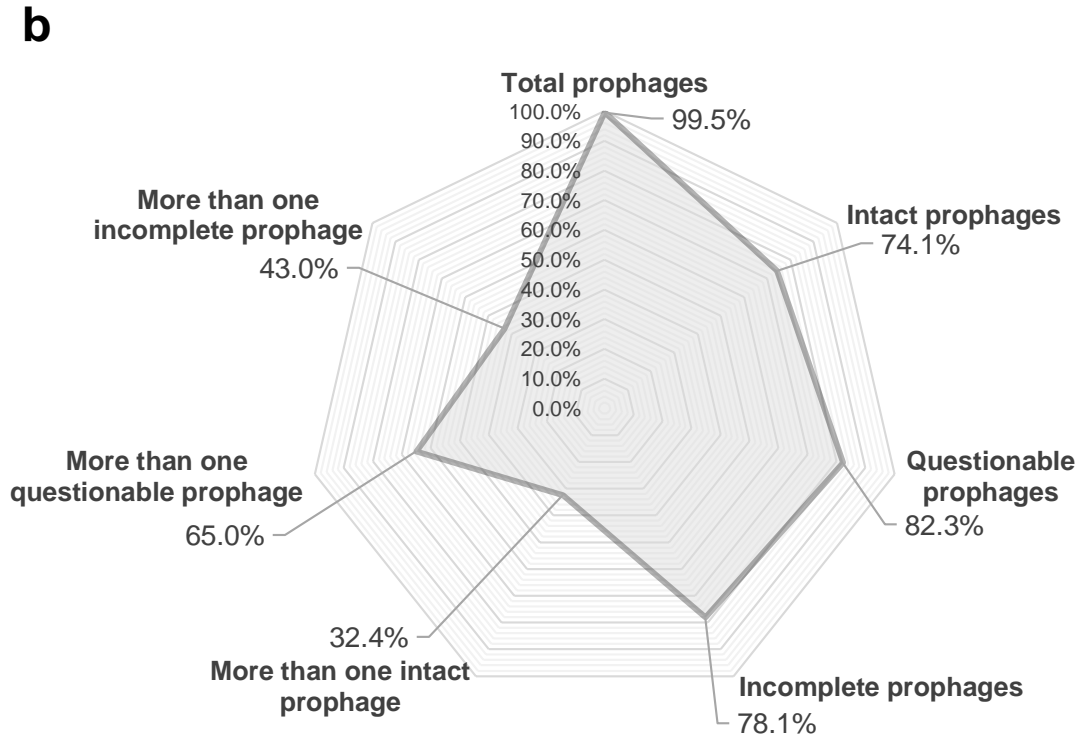
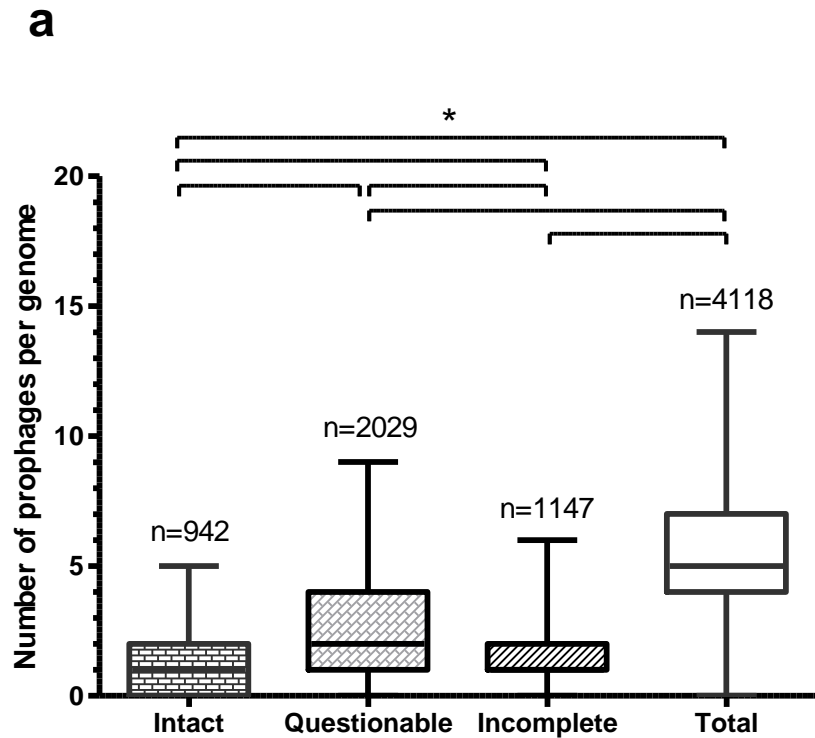


Figure S2. Prevalence of prophages in *Acinetobacter baumannii* genomes. **(a)** Whiskers plot of prophage frequency per bacterial genome. The horizontal line at the center of the whiskers plot represents the median. The bottom and top of the plot represent the first and third quartiles. The external edges of the whiskers represent the minimum and maximum number of prophages per genome. N is the number of prophages in the category. Significant differences (Tukey's test) of $P < 0.05$ are represented by *. **(b)** Prevalence of total prophages, "intact prophages", questionable prophages and incomplete prophages, more than one "intact prophage", more than one questionable prophage, and more than one incomplete prophage. Prevalence was determined considering a dataset of 795 *A. baumannii* genomes.

▲ Dendrogram (based on genomic BLAST)

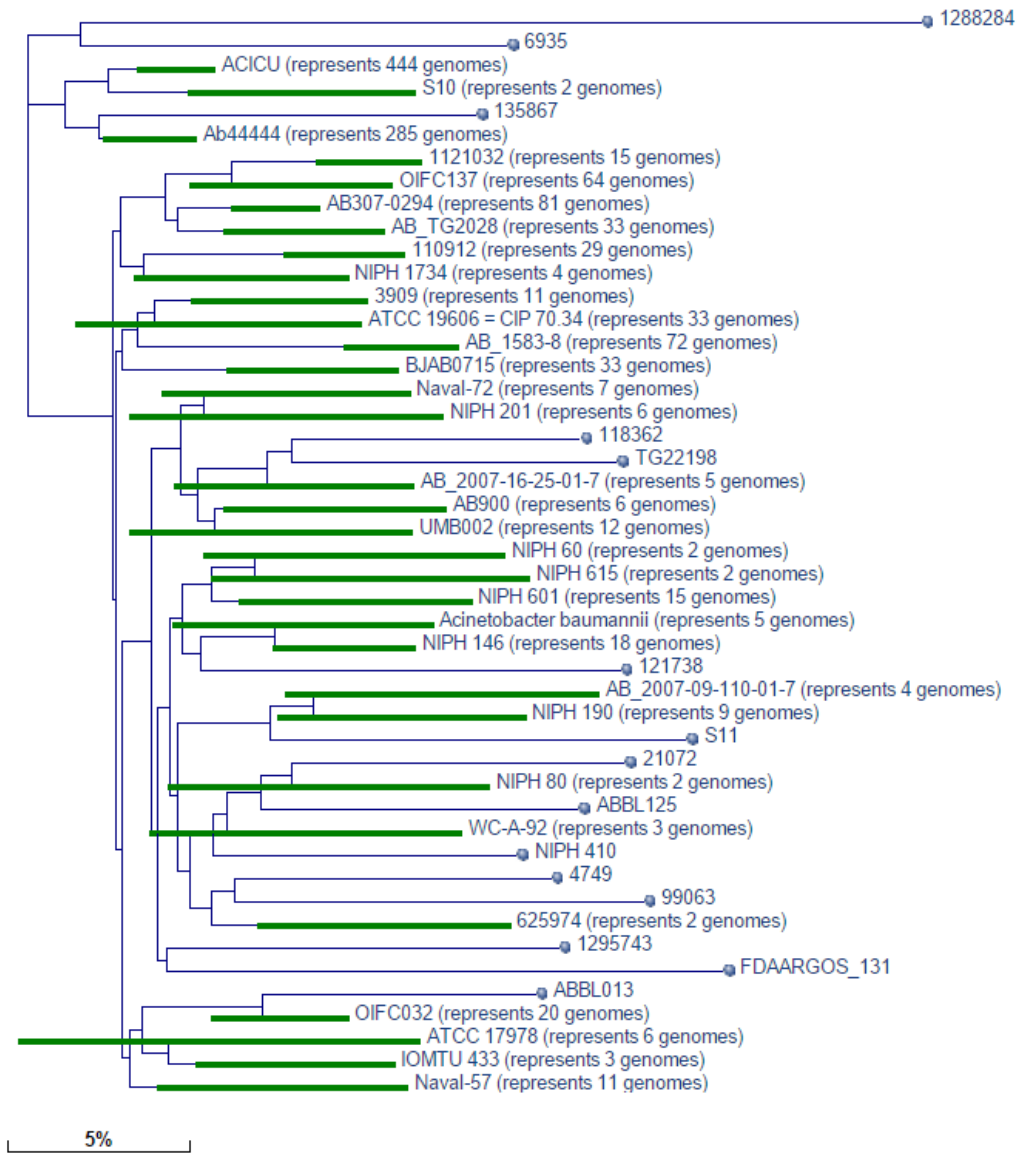


Figure S3. Dendrogram of *Acinetobacter baumannii* retrieved from GenBank at the date of April 11, 2016. Representative strains from each branch were selected for detailed analysis of encoded prophages.