

**Supplemental information**

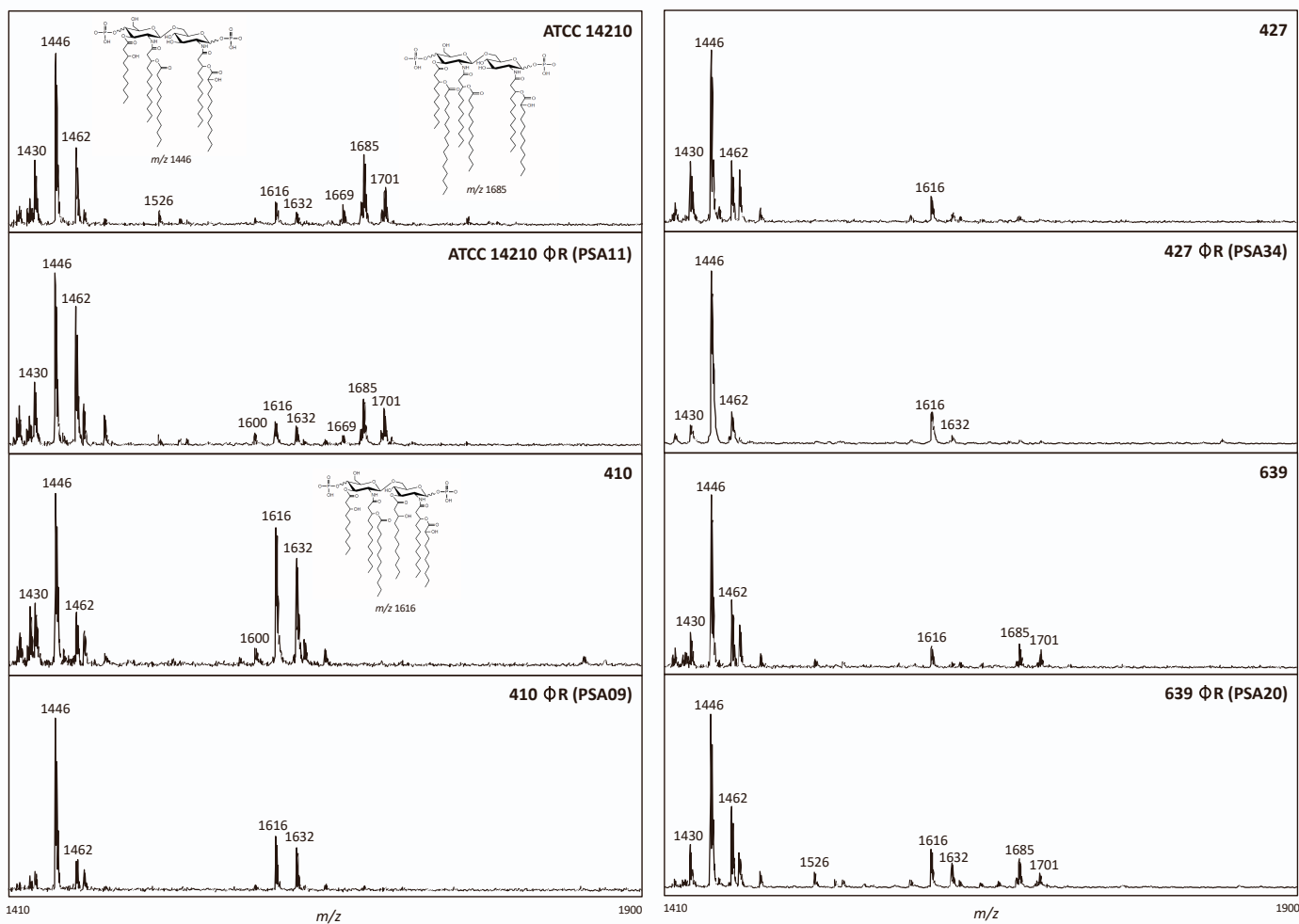
**Genomic characterization of lytic bacteriophages  
targeting genetically diverse**

***Pseudomonas aeruginosa* clinical isolates**

**Hayley R. Nordstrom, Daniel R. Evans, Amanda G. Finney, Kevin J. Westbrook, Paula F. Zamora, Casey E. Hofstaedter, Mohamed H. Yassin, Akansha Pradhan, Alina Iovleva, Robert K. Ernst, Jennifer M. Bomberger, Ryan K. Shields, Yohei Doi, and Daria Van Tyne**



**Figure S1. Genome sequence alignment of similar Bruynoghevirus phages, Related to Figure 2.** The genomes of phages PSA31, PSA37, and PSA40 were aligned to one another using Mauve. Grey arrows indicate coding sequences, and pink arrowheads show the location of tRNA genes. Vertical black lines show differences in nucleotide sequence between phage genomes, and horizontal black lines show differences due to nucleotide insertions or deletions.



**Figure S2. Lipid A profiles of phage-resistant mutants, Related to Figure 4.** MALDI spectra were collected from pairs of wildtype and phage-resistant mutant isolates. Spectral profiles are shown, and lipid species corresponding the most prominent  $m/z$  peaks are shown.