



Supplementary Fig. S3. Maximum Likelihood Tree based on protein sequences of the 28 class A β -lactamases that were predicted in the *Pseudovibrio* genomes. The locus tags of the proteins are given with between brackets the corresponding *Pseudovibrio* strain. The tree was constructed in MEGA using 1,000 iterations of bootstrapping. Bootstrap values <50 are not shown. The horizontal bar indicates the number of substitutions per site.