



**S3 Fig.** Maximum likelihood phylogenies of representative OXA- types and OXA-51-like nucleotide sequences (inset) including the novel OXA-497 (marked in red). Nucleotide sequences were aligned using a amino acid sequence guided strategy using TranslatorX (Abascal et al. 2010. Nucleic Acids Research, 38 Web Server issue), W7–13. <http://doi.org/10.1093/nar/gkq291>), phylogenies were inferred using RAXML version 8.1.20 (Stamatakis, A. 2014. Bioinformatics 30(9), 1312–1313. <http://doi.org/10.1093/bioinformatics/btu033>). Values on the branches represent bootstrap values as inferred using the autoFC bootstopping option (Pattengale et al. 2010, Journal of Computational Biology : a Journal of Computational Molecular Cell Biology, 17(3), 337–354. <http://doi.org/10.1089/cmb.2009.0179>).