

Table S5: Taxonomy and most similar “type strains” for the six OTUs classified as *Vibrio* as inferred from the Ribosomal Database Project (RDP).

OTU	Type strain (closest matches)	S_ab score*
OTU 829	<i>Vibrio lentus</i> , <i>Vibrio tasmaniensis</i> , <i>Vibrio kanaloae</i> , <i>Vibrio atlanticus</i> , <i>Vibrio hemicentroti</i>	0.945
OTU 2	<i>Vibrio lentus</i> , <i>Vibrio tasmaniensis</i> , <i>Vibrio kanaloae</i> , <i>Vibrio atlanticus</i> , <i>Vibrio hemicentroti</i>	1.000
OTU 233	<i>Vibrio lentus</i> , <i>Vibrio tasmaniensis</i> , <i>Vibrio kanaloae</i> , <i>Vibrio atlanticus</i> , <i>Vibrio hemicentroti</i>	0.884
OTU 11	<i>Vibrio ichthyenteri</i> , <i>Vibrio neptunius</i> , <i>Vibrio brasiliensis</i> , <i>Vibrio xuii</i> , <i>Vibrio rotiferianus</i> , <i>Vibrio campbellii</i> , <i>Vibrio hepatarius</i> , <i>Vibrio sinaloensis</i> , <i>Vibrio sagamiensis</i> , <i>Vibrio alfacensis</i>	1.000
OTU 61	<i>Vibrio areningrae</i>	1.000
OTU 402	<i>Vibrio anguillarum</i>	0.946

\* A seqmatch score (S\_ab) were reported between every closely related sequence, which represents the number of unique 7-base oligomers shared between the sample sequence and a given RDP sequence divided by the lowest number of unique oligos in either of the two sequences (Wang et al. 2007).