















**Figure S3.** RAxML phylogeny showing the taxonomic assignment of each amplicon sequence variant (ASV, shown in blue) to the family level (left) and genus level (right). Phylogenetic trees on the right side represent the clades coloured in grey in the phylogenetic tree on the left side. Only bootstrap values  $> 70$  are shown. Within genus phylotypes have been determined using a clustering threshold of 99%.