Figure S6: Overview of “missing” base pairs at the primer 3’ end for sequencing datasets from this study as well as Elbrecht & Leese 2015 and Elbrecht et al. 2016. After library demultiplexing a random subset of 5,000 reads was extracted from each sample and sequences aligned in Geneious 8 using MAFFT. The primer sequence + 10 bp (5 bp for 16S) was extracted from each alignment and the mean deviation from the expected primer length plotted for each sample. The proportion of sequences with the expected length is given for each sample on the right of each plot. The error bars show the standard deviation (N=10).