



FIG. S2. SSU rRNA secondary structure analysis of the consensus sequence for *Zetaproteobacteria* OTU 1. Variability between OTU 1 and the consensus sequence for OTU 2, OTU 15, or OTUs 2 and 15, is indicated by a yellow, blue, or green highlighted base, respectively. Six regions with relatively high variability are identified.