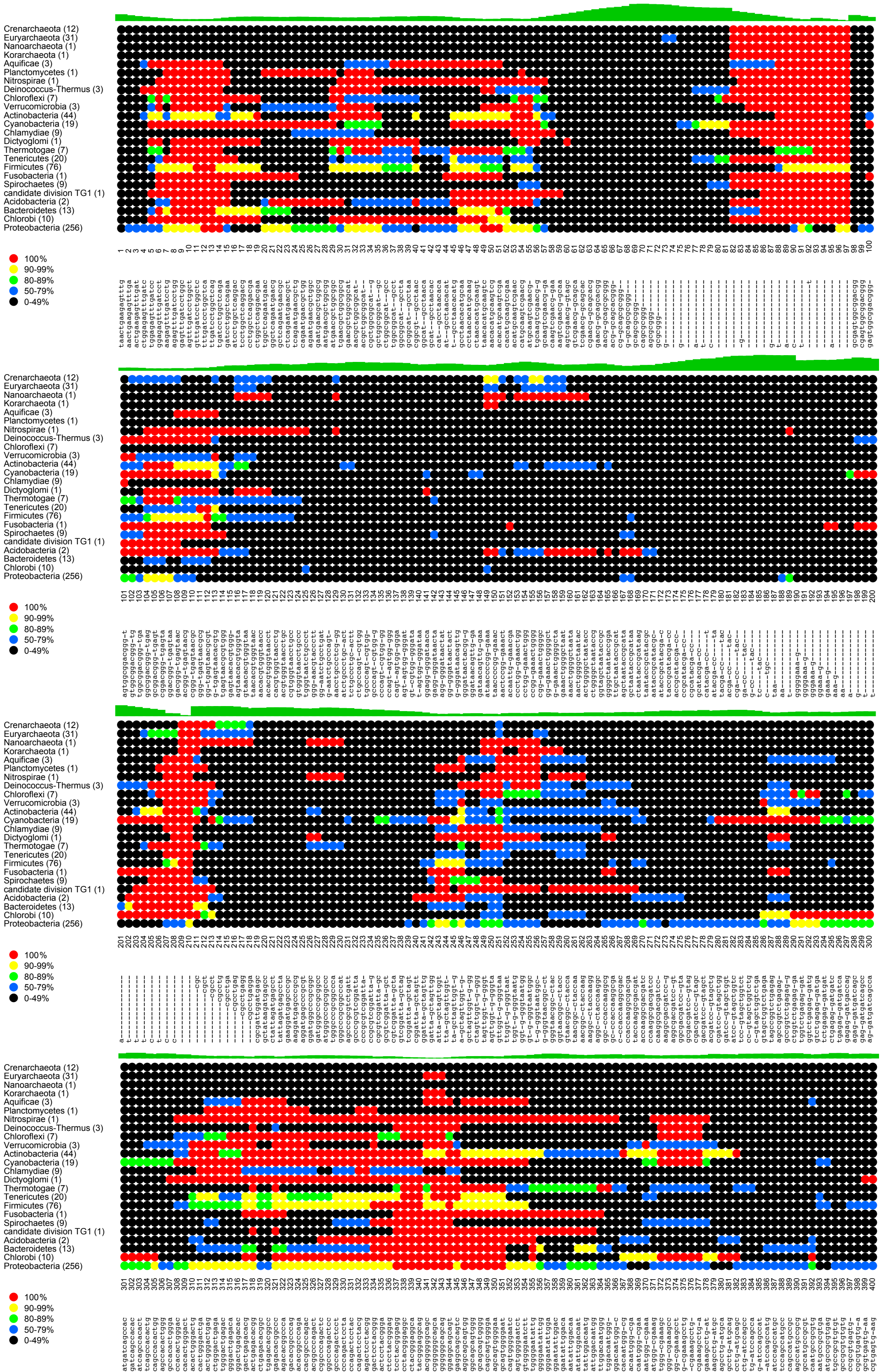

Fig. S1. A complete plot of the consensus sequence in each window and the coverage rates for each phylum from the 531 16S rRNA genes of genome-sequenced strains. Some consensus sequences contain continuous gaps (-) with several bp in lengths, indicating the presence of inserted sequences in particular strains. See the legend to Fig. 1 for the dot colors and the bar graph.

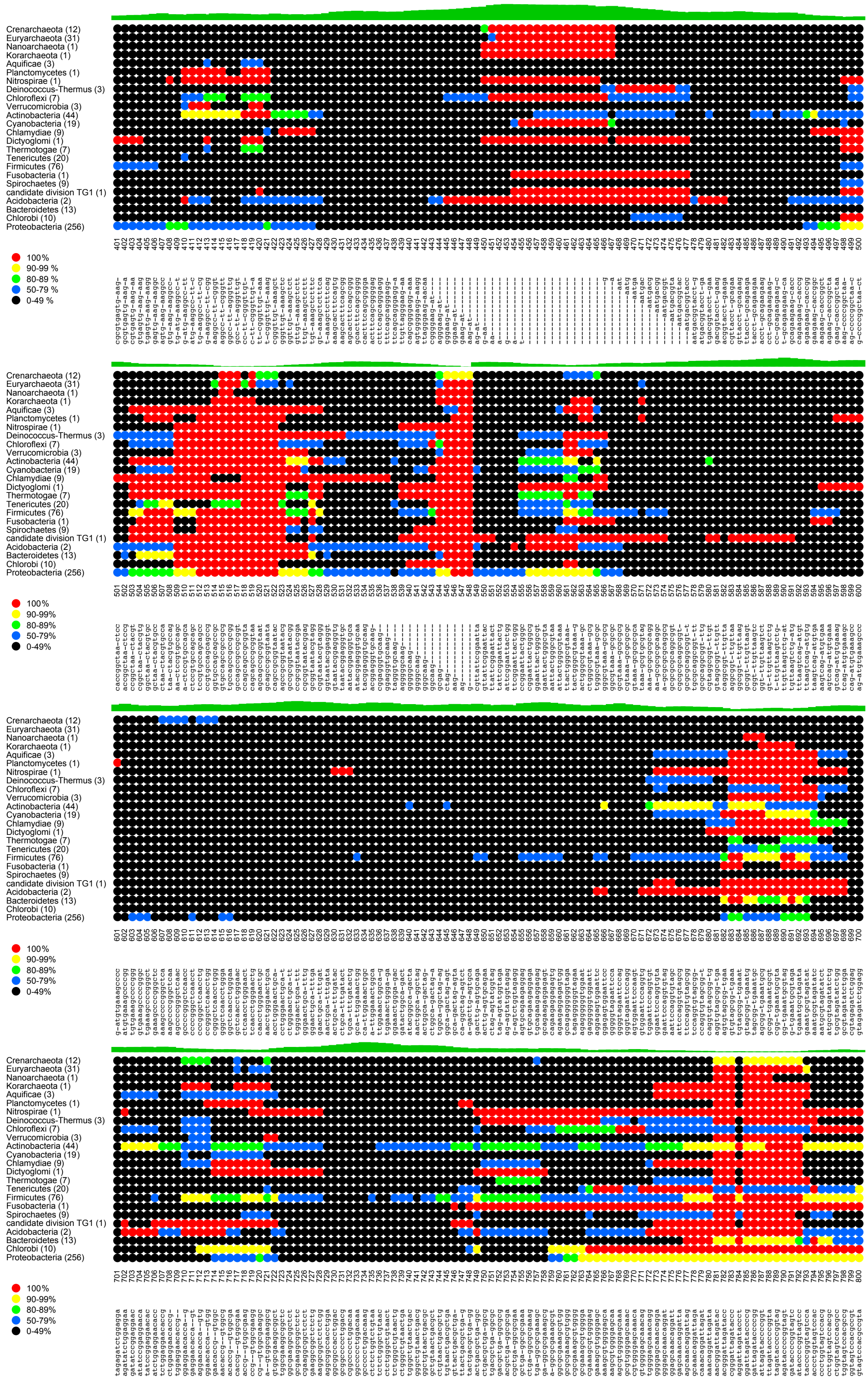

Fig. S1. Continued.

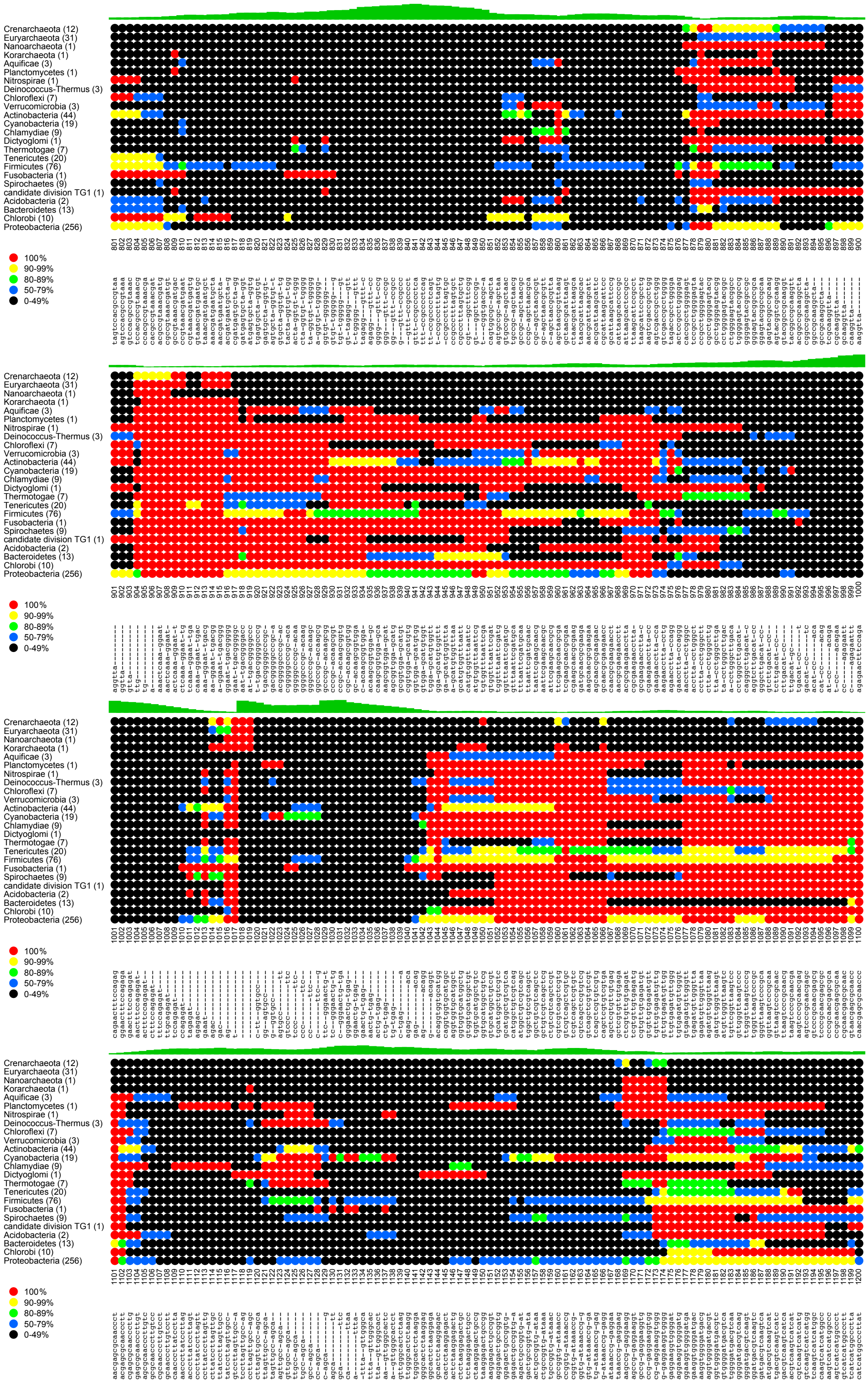

Fig. S1. Continued.

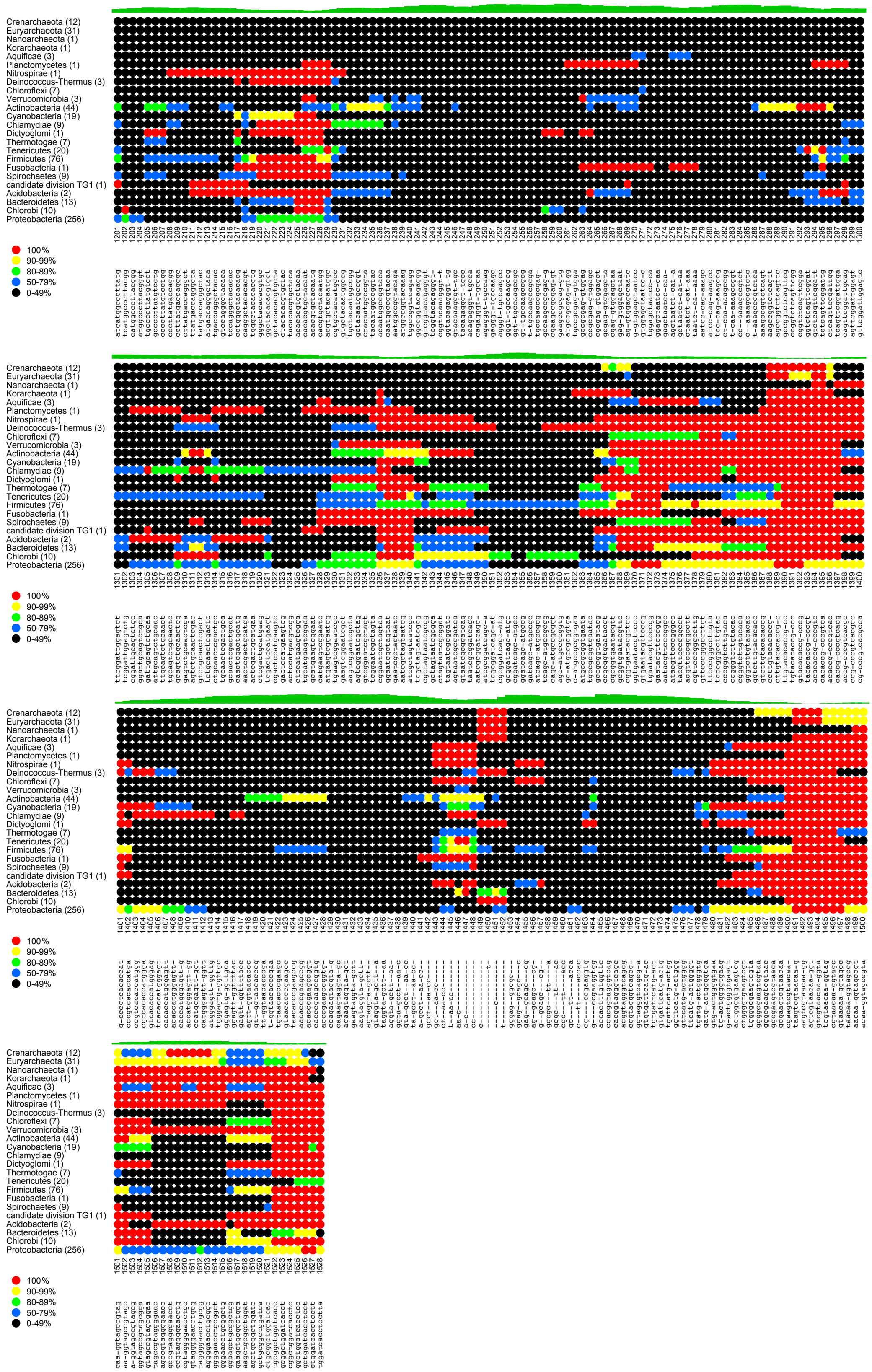

Fig. S1. Continued.