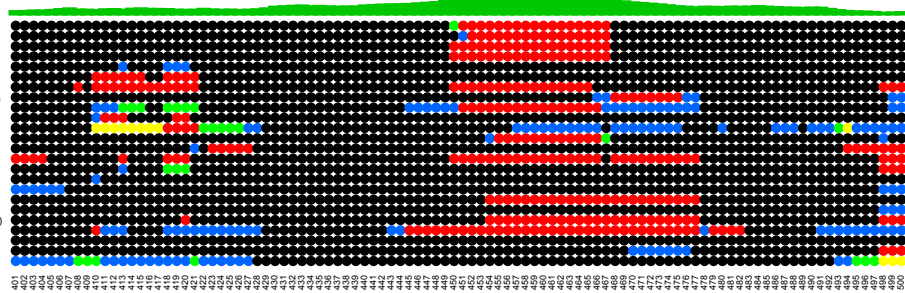


Fig. S1. A complete plot of the consensus sequence in each window and the coverage rates for each phylum from the 531 16S rRNA genes of genome-sequenced strains. Some consensus sequences contain continuous gaps (-) with several bp in lengths, indicating the presence of inserted sequences in particular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

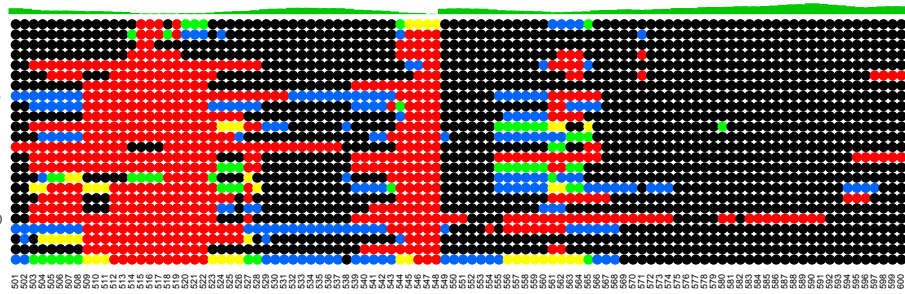
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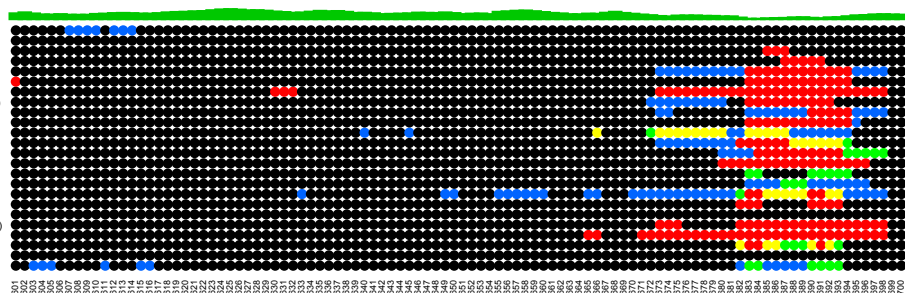
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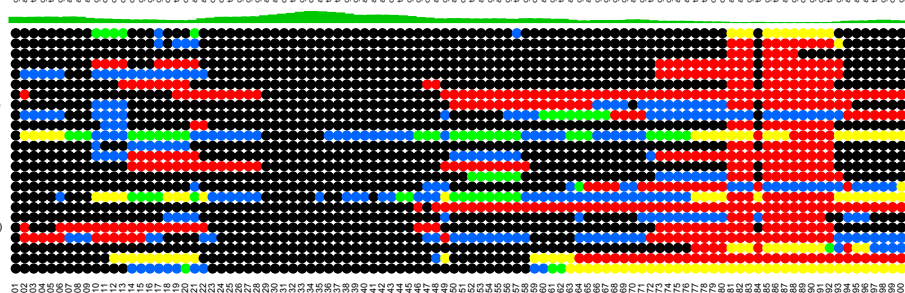
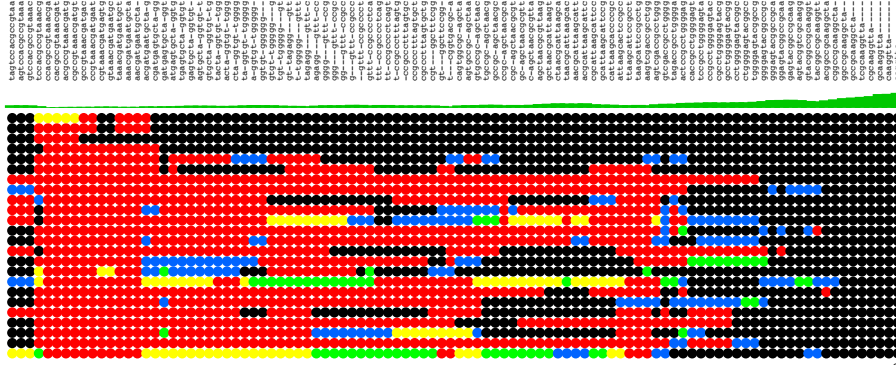
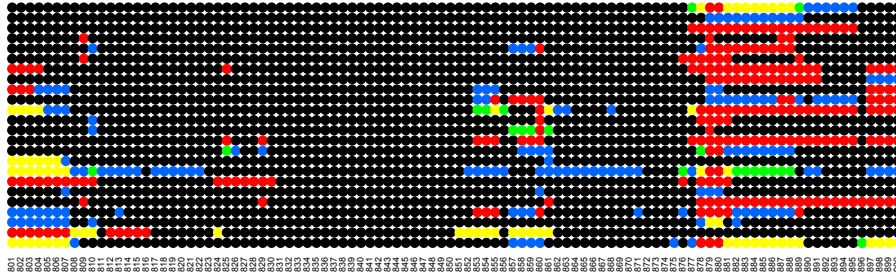


Fig. S1. Continued.

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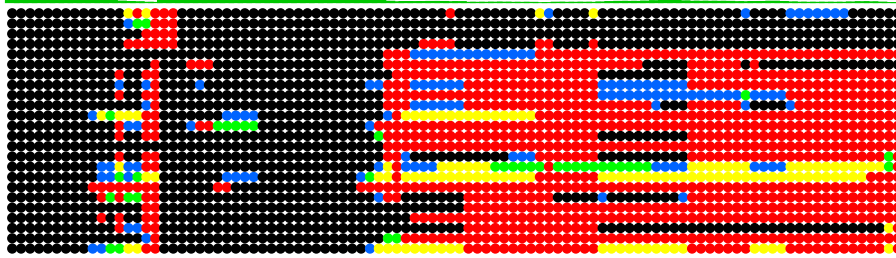


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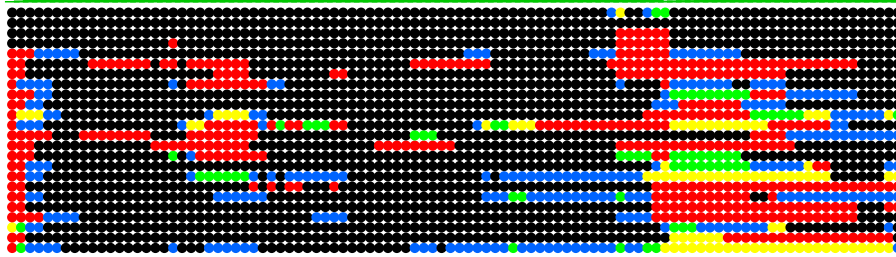
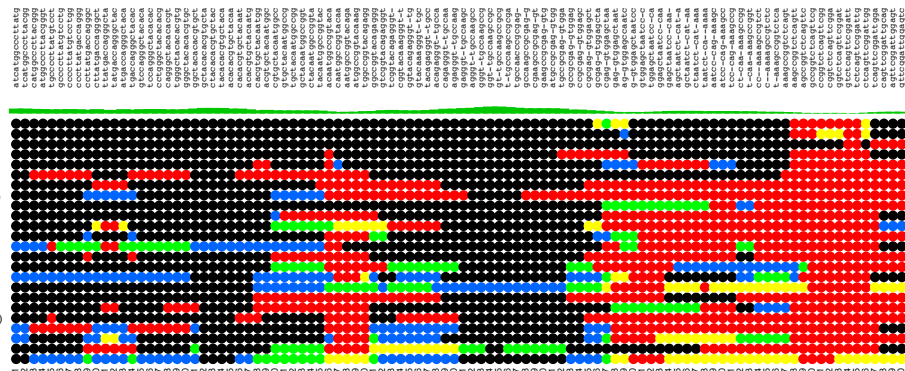
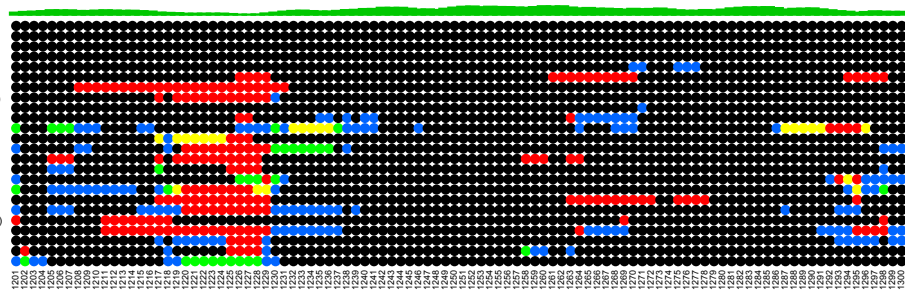


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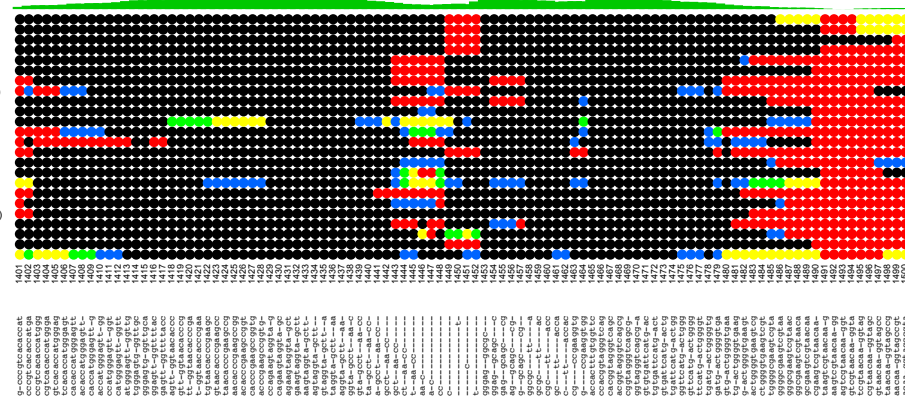


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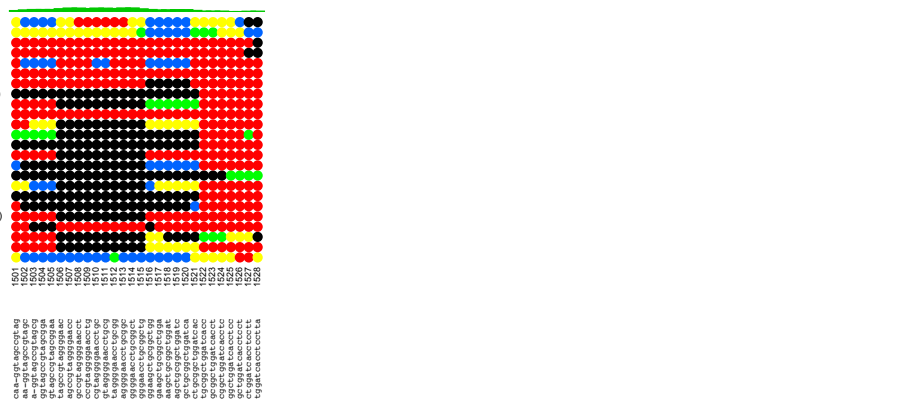


Fig. S1. Continued.