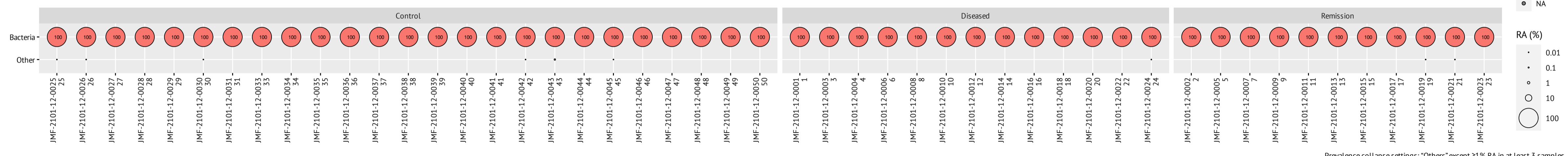
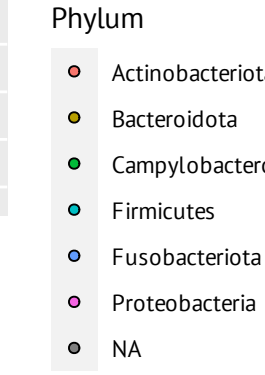
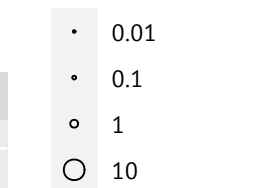
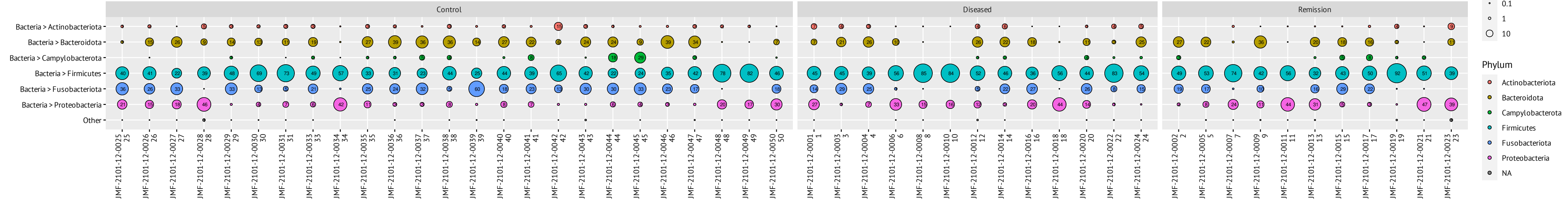
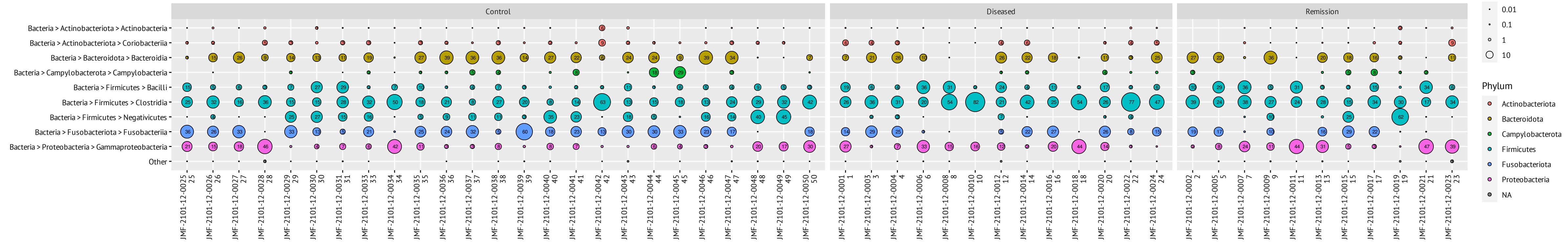
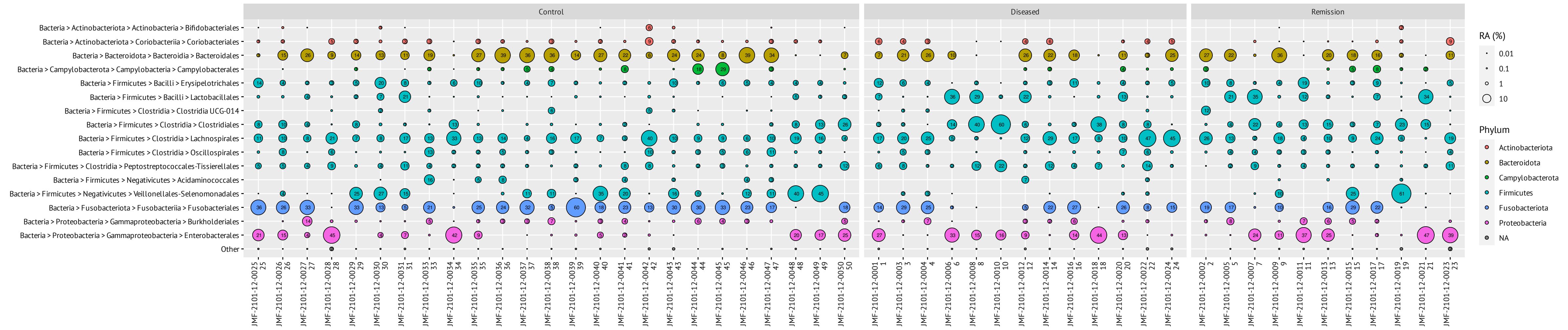


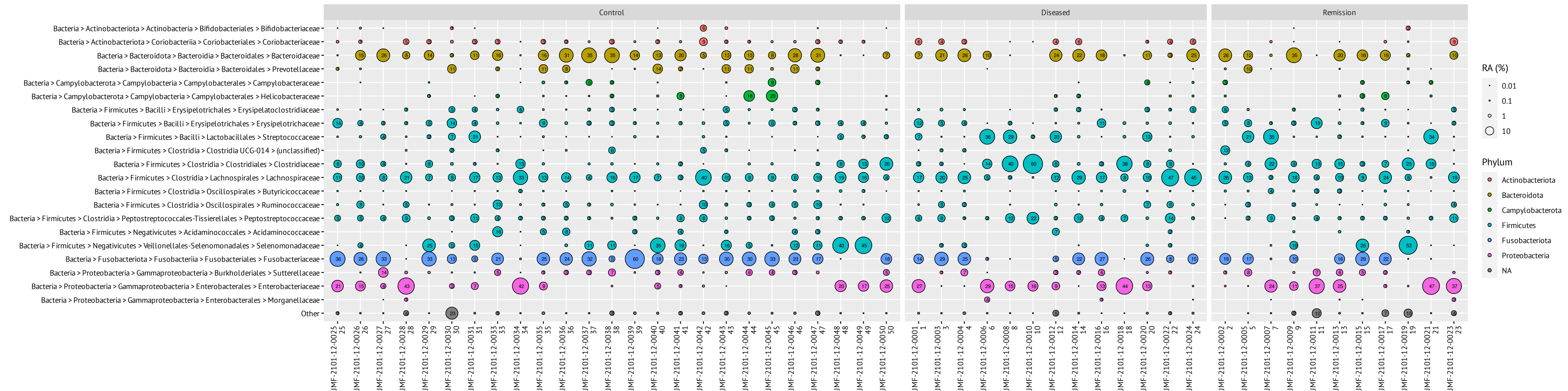
**Fig. S2.** Analysis of the differentially abundant fraction expressed as numbers of reads of 16S rRNA gene for individual dogs and the taxonomic breakdown of the dominant ASVs across all samples.

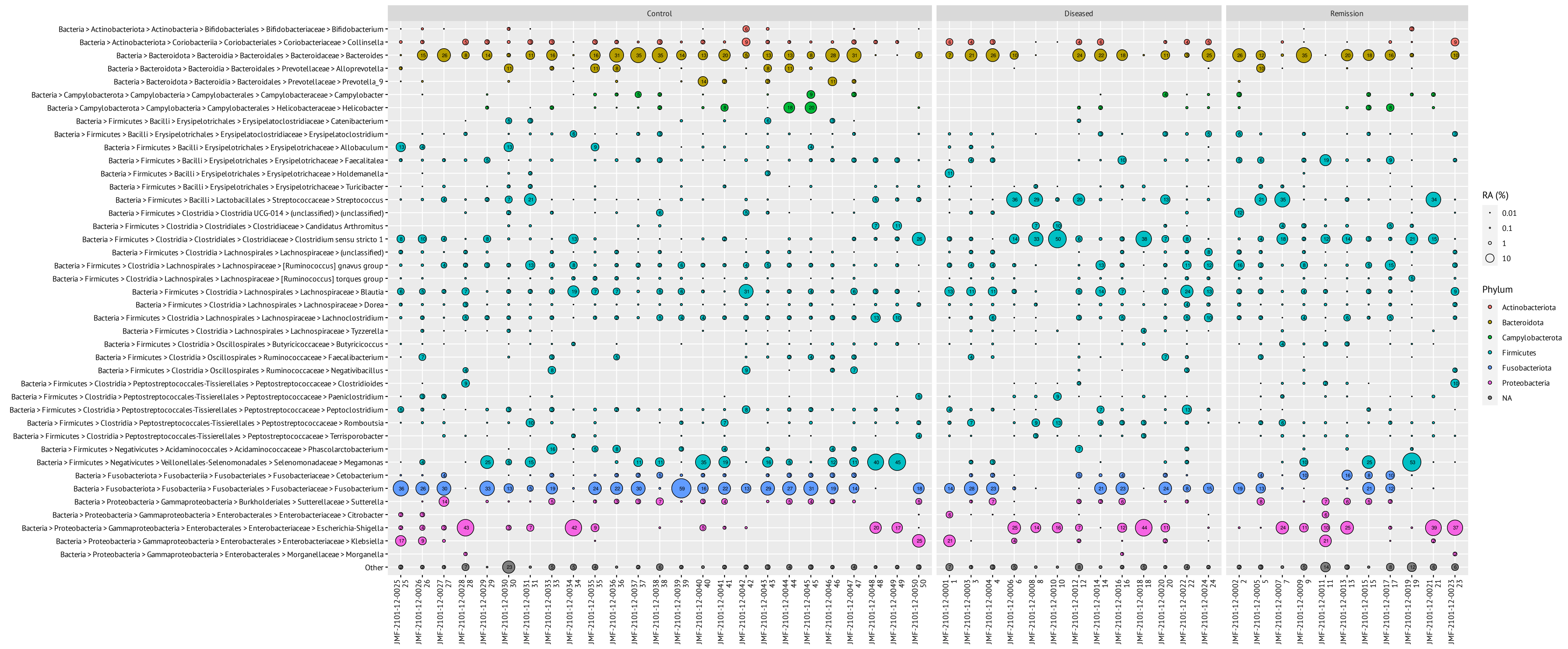


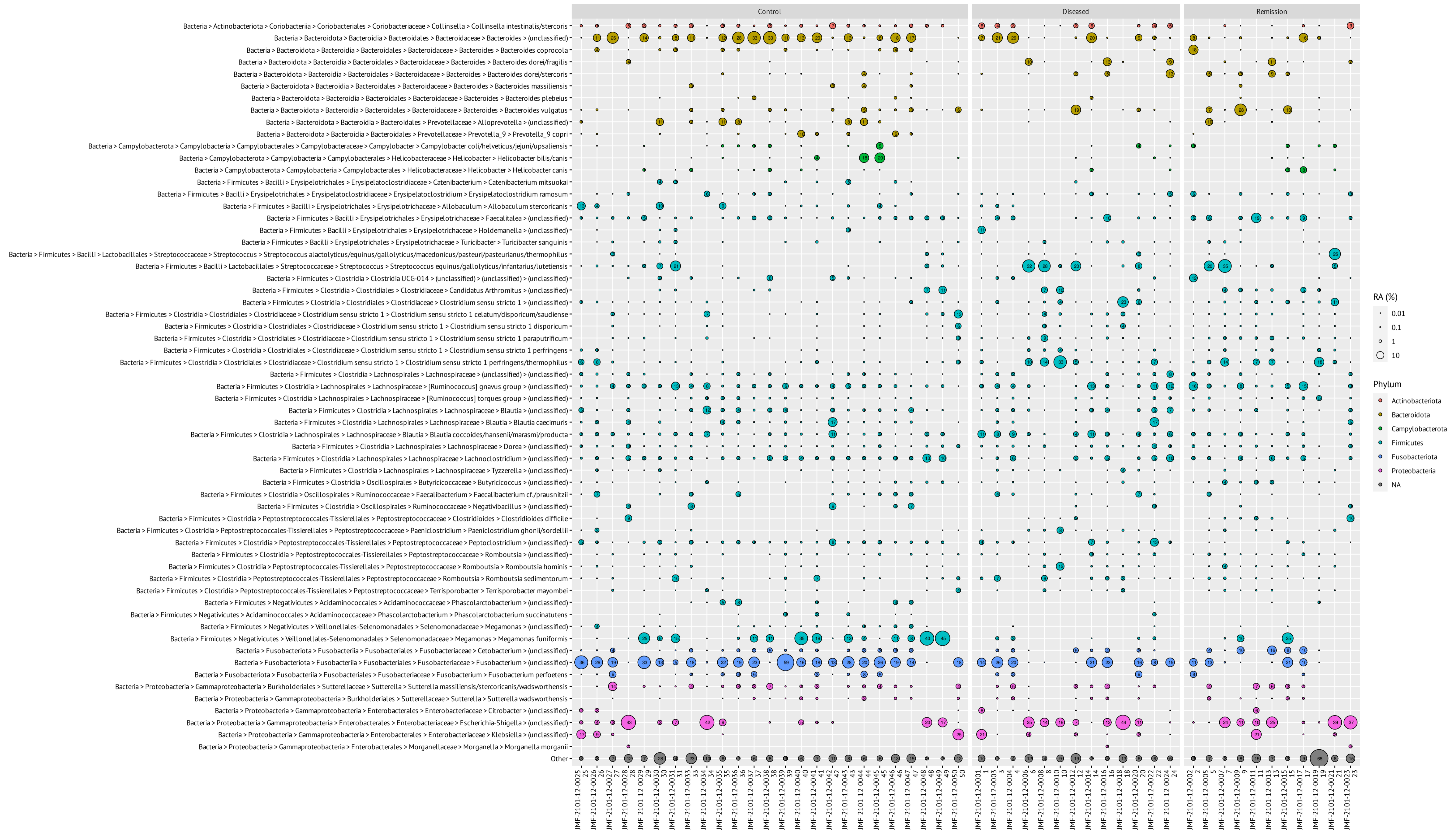
















**RA (%)**

- 0.01
- 0.1
- 1
- 10

**Phylum**

- Actinobacteriota
- Bacteroidota
- Campylobacterota
- Firmicutes
- Fusobacteriota
- Proteobacteria
- NA