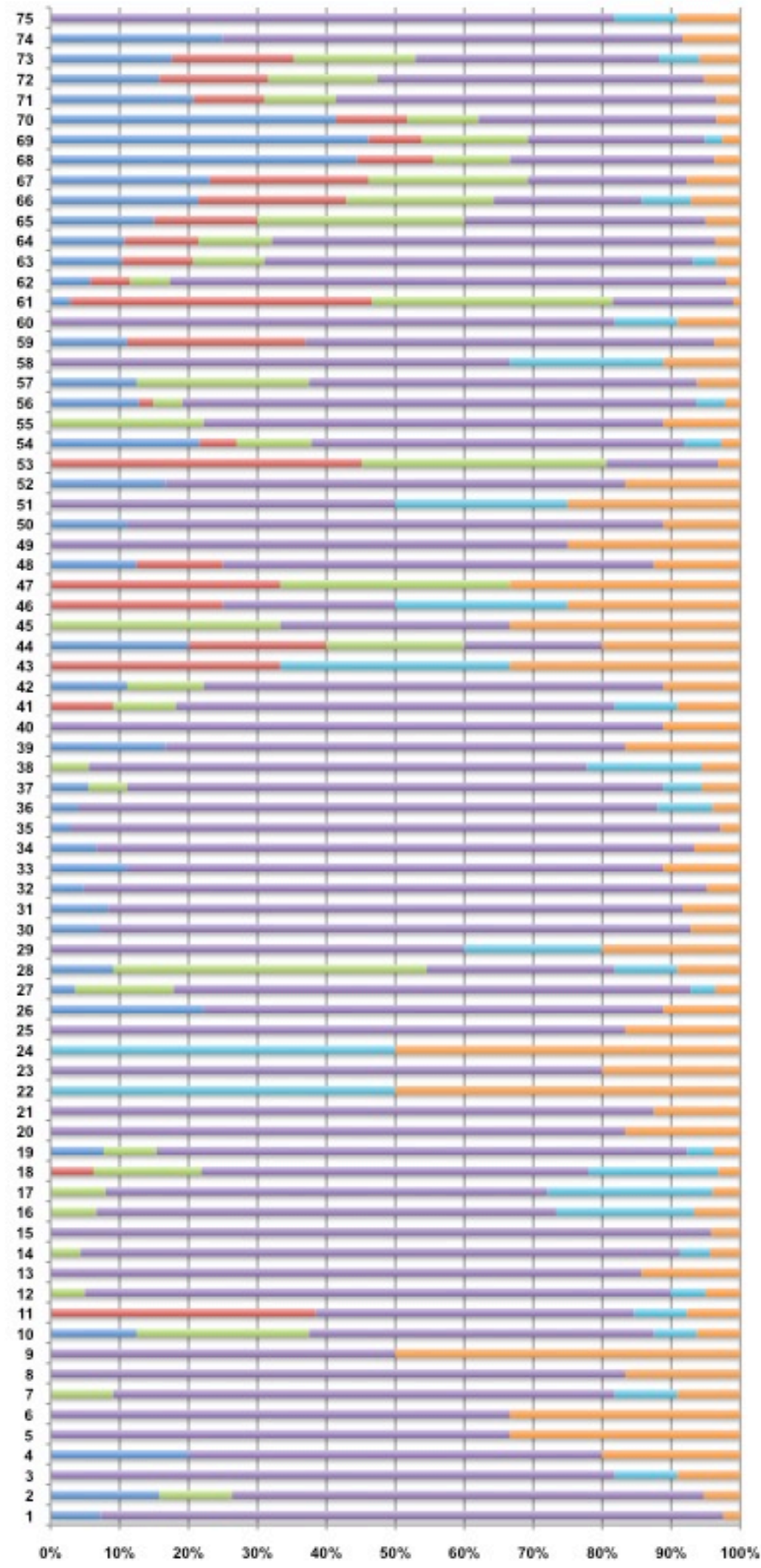
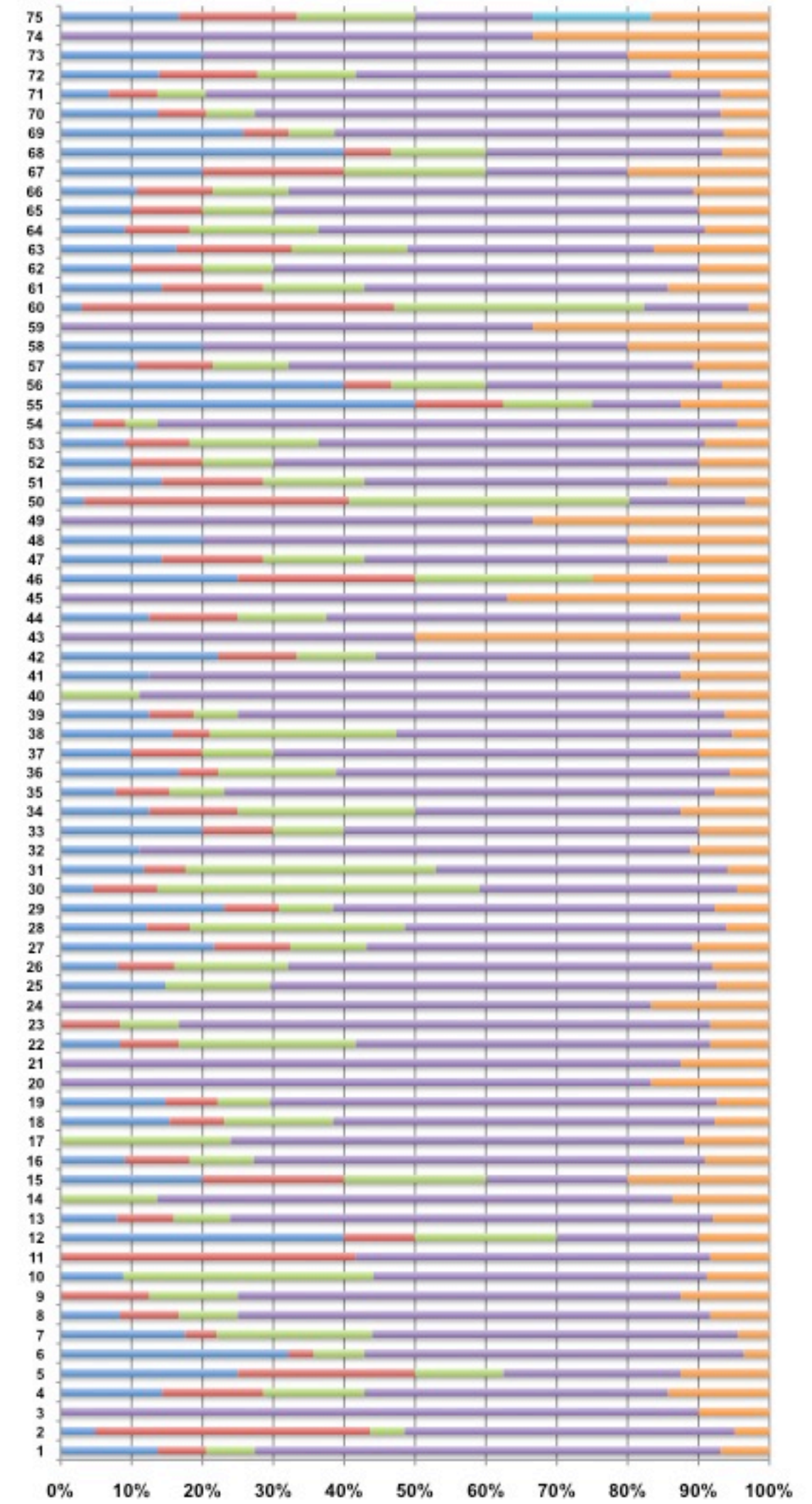


Title	Microbiota and metabolite profiling reveal specific alterations in bacterial community structure and environment in the cystic fibrosis airway during exacerbation
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**A.****% Relative abundance of OTUs from DNA**

■ Methanosarcinales ■ Bacteroidales ■ Clostridiales  
 ■ Chrysiogenales ■ Actinomyindales ■ Bifidobacterium

**B.****% Relative abundance of OTUs from RNA**

■ Methanosarcinales ■ Bacteroidales ■ Clostridiales  
 ■ Chrysiogenales ■ Actinomyindales ■ Bifidobacterium