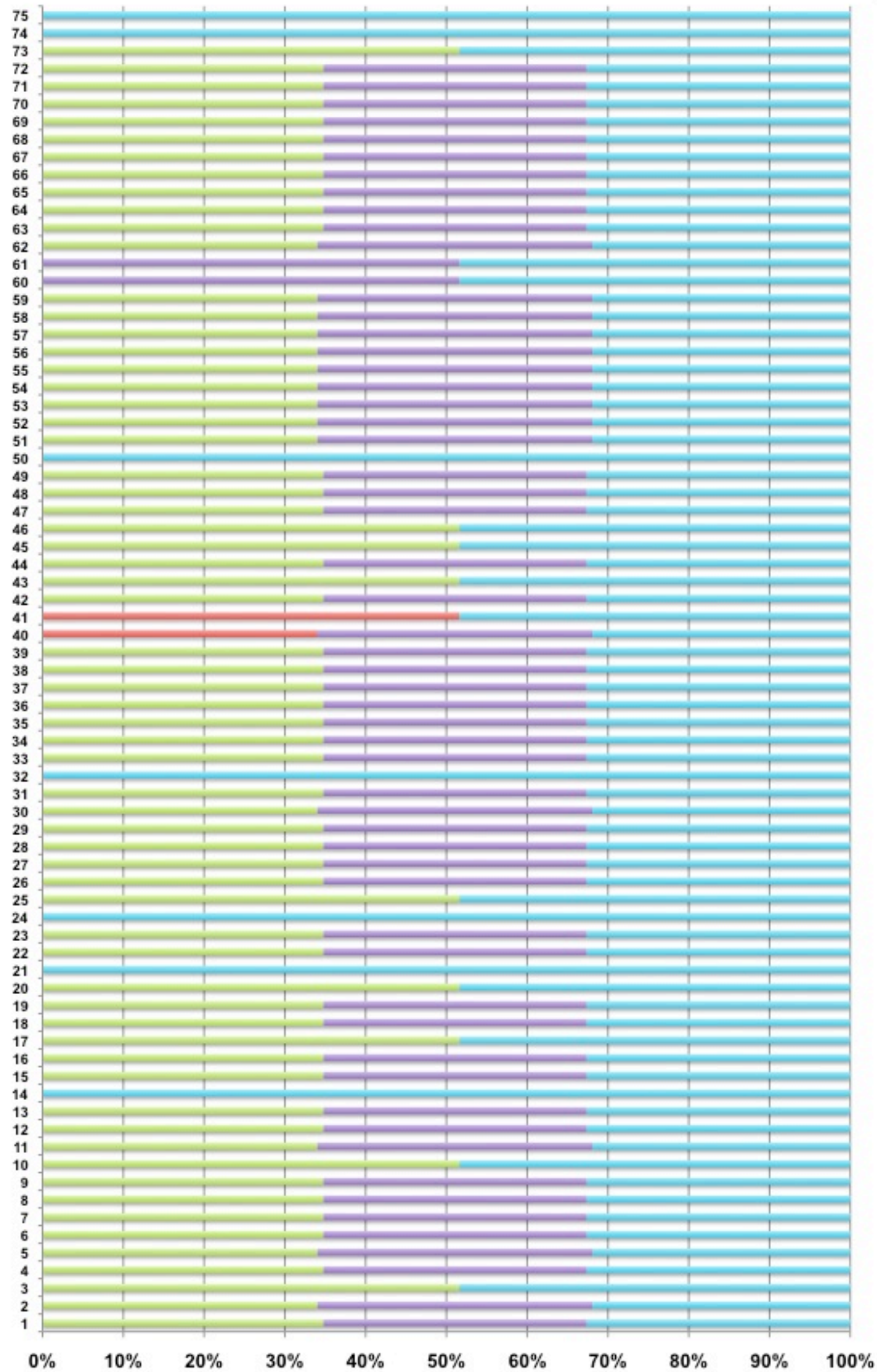


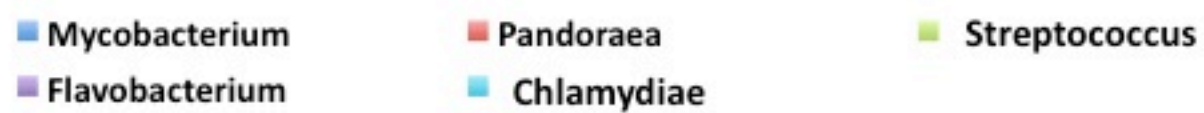
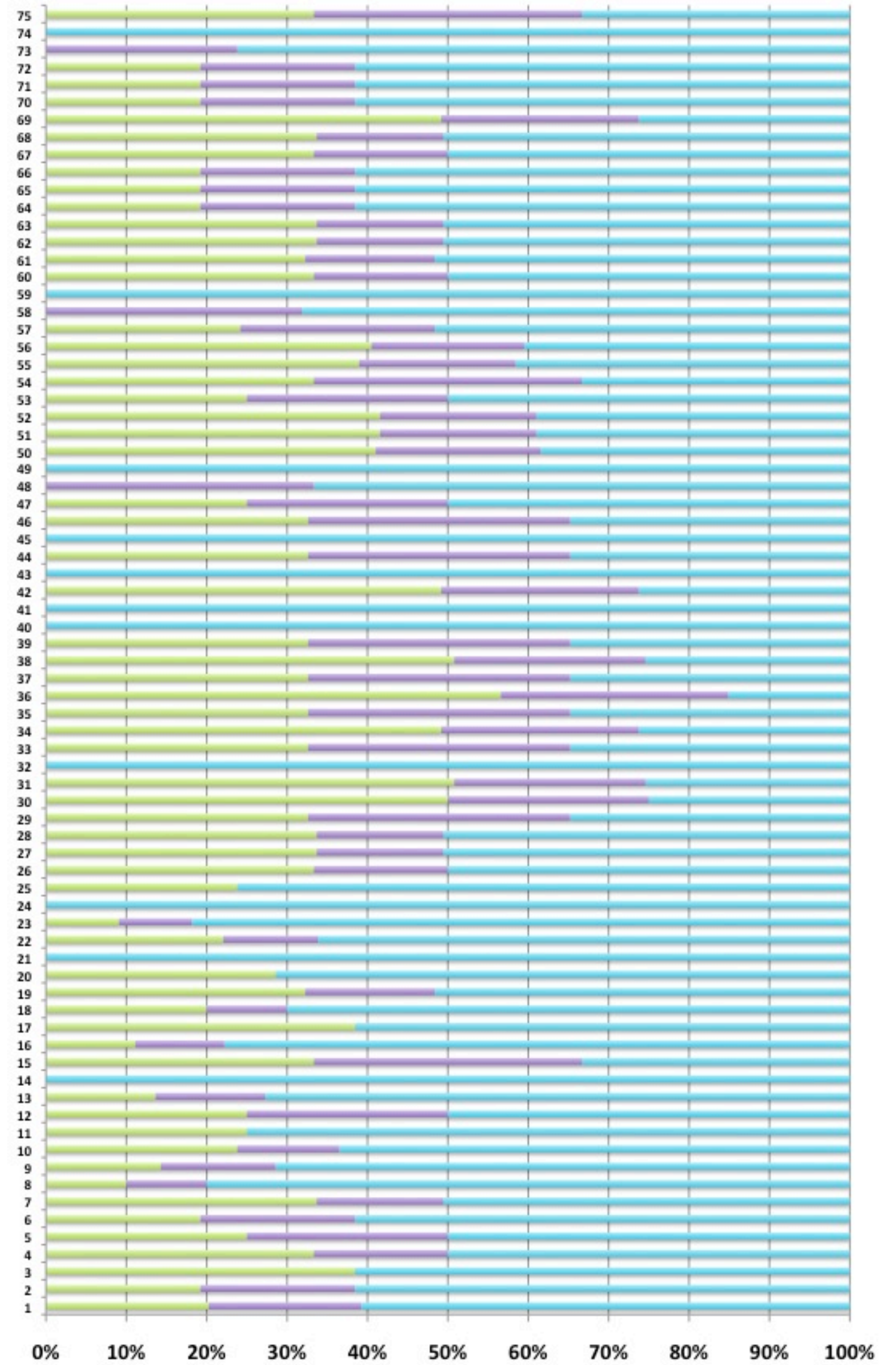
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| <b>Title</b>                       | Microbiota and metabolite profiling reveal specific alterations in bacterial community structure and environment in the cystic fibrosis airway during exacerbation   |
| <b>Author(s)</b>                   | Twomey, Kate B.; Alston, Mark; An, Shi-Qi; O'Connell, Oisín J.; McCarthy, Yvonne; Swarbreck, David; Febrer, Melanie; Dow, J. Maxwell; Plant, Barry J.; Ryan, Robert P.   |
| <b>Publication date</b>            | 2013   |
| <b>Original citation</b>           | Twomey KB, Alston M, An S-Q, O'Connell OJ, McCarthy Y, Swarbreck D, et al. (2013) Microbiota and Metabolite Profiling Reveal Specific Alterations in Bacterial Community Structure and Environment in the Cystic Fibrosis Airway during Exacerbation. PLoS ONE 8(12): e82432. doi:10.1371/journal.pone.0082432   |
| <b>Type of publication</b>         | Article (peer-reviewed)  |
| <b>Link to publisher's version</b> | <a href="http://dx.doi.org/10.1371/journal.pone.0082432">http://dx.doi.org/10.1371/journal.pone.0082432</a><br>Access to the full text of the published version may require a subscription.  |
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**A.**

% Relative abundance of OTUs from DNA

**B.**

% Relative abundance of OTUs from RNA

