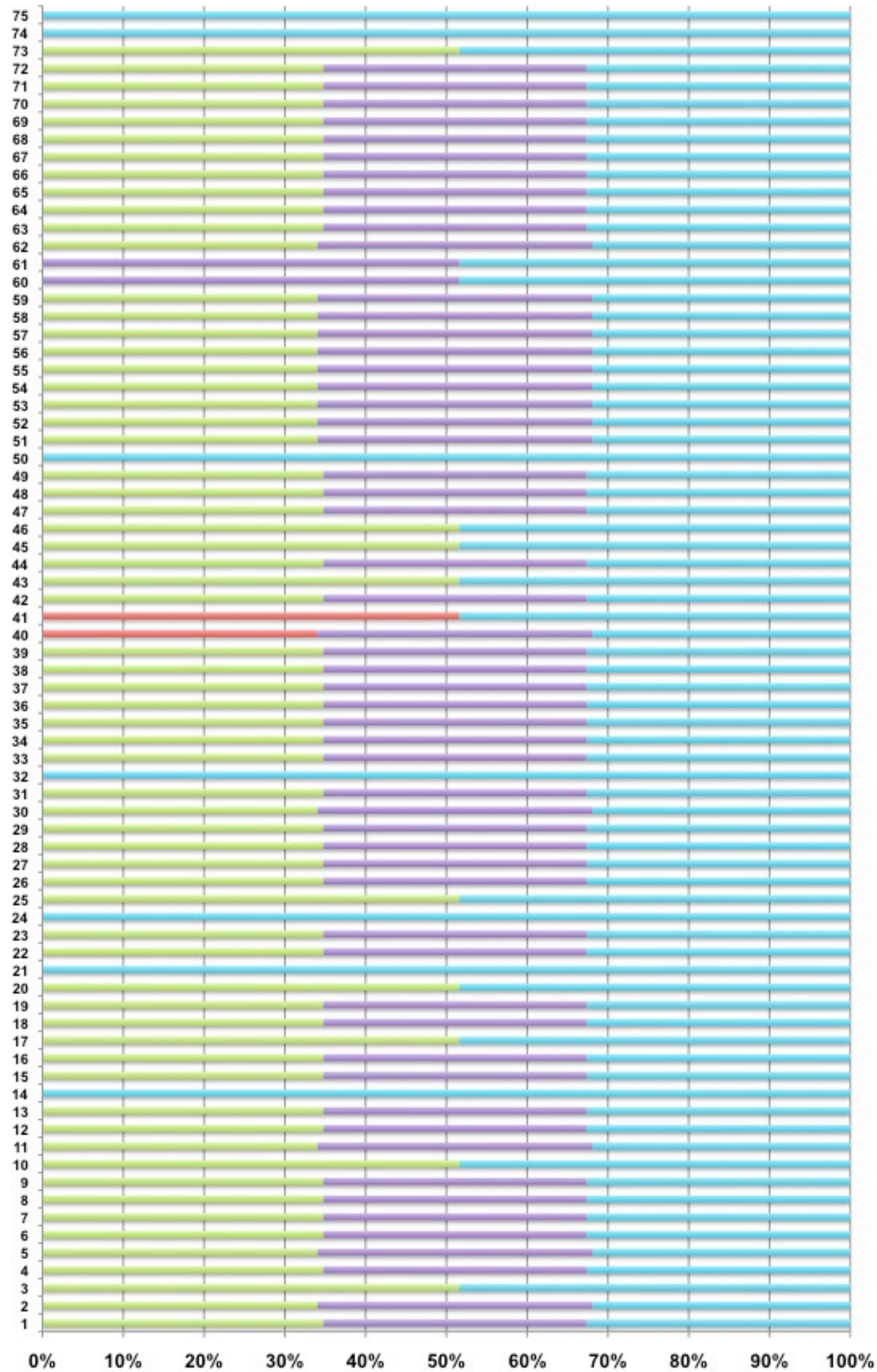


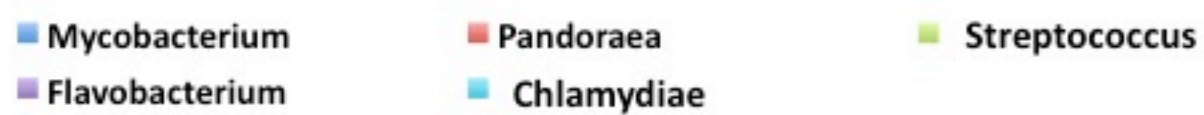
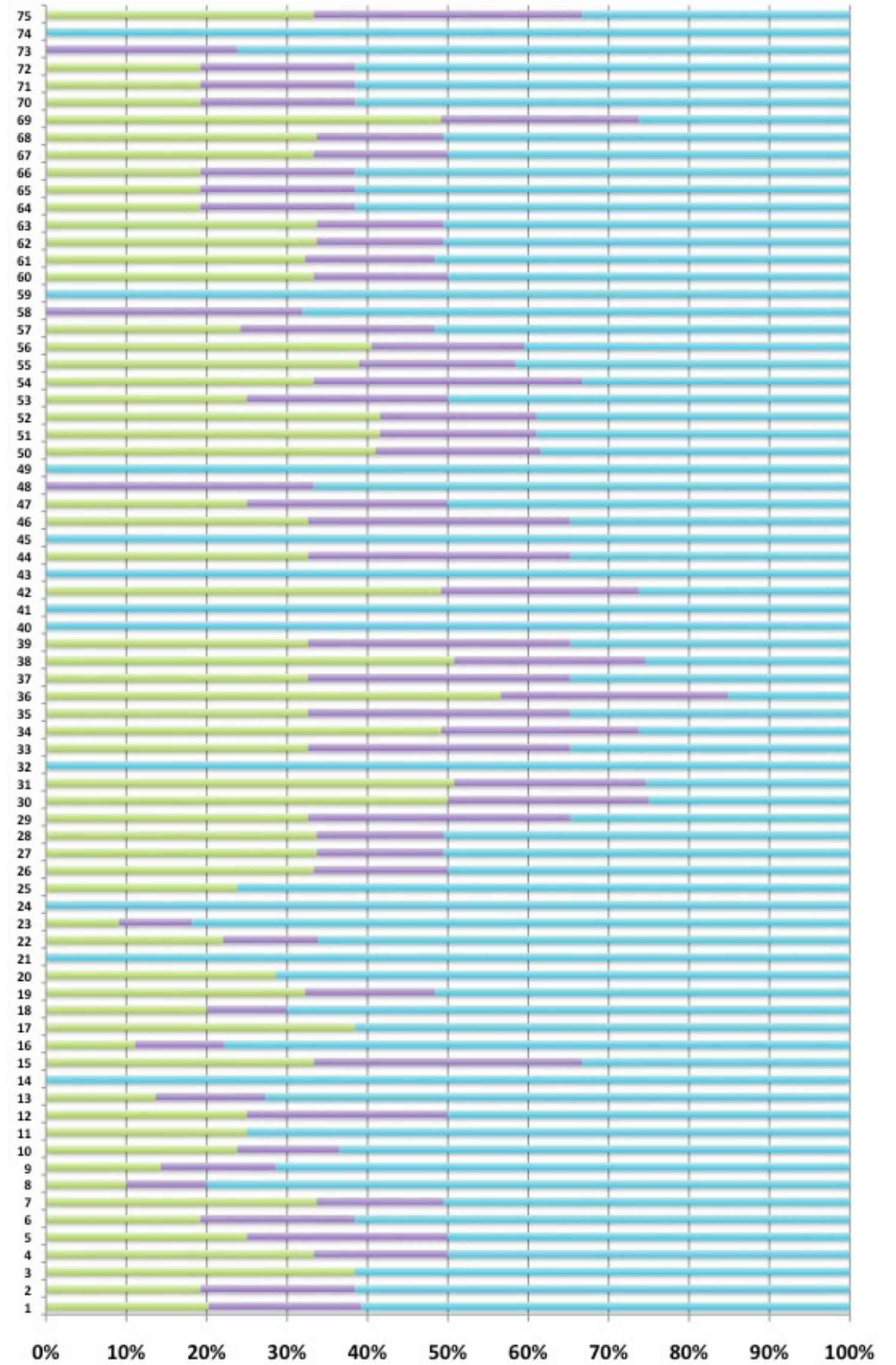
**UCC Library and UCC researchers have made this item openly available.
Please [let us know](#) how this has helped you. Thanks!**

Title	Microbiota and metabolite profiling reveal specific alterations in bacterial community structure and environment in the cystic fibrosis airway during exacerbation
Author(s)	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.
Publication date	2013
Original citation	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
Type of publication	Article (peer-reviewed)
Link to publisher's version	http://dx.doi.org/10.1371/journal.pone.0082432 Access to the full text of the published version may require a subscription.
Rights	© 2015 Twomey et al. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited http://creativecommons.org/licenses/by/4.0/
Item downloaded from	http://hdl.handle.net/10468/2348

Downloaded on 2023-03-22T01:33:00Z

A.

% Relative abundance of OTUs from DNA

**B.**

% Relative abundance of OTUs from RNA

