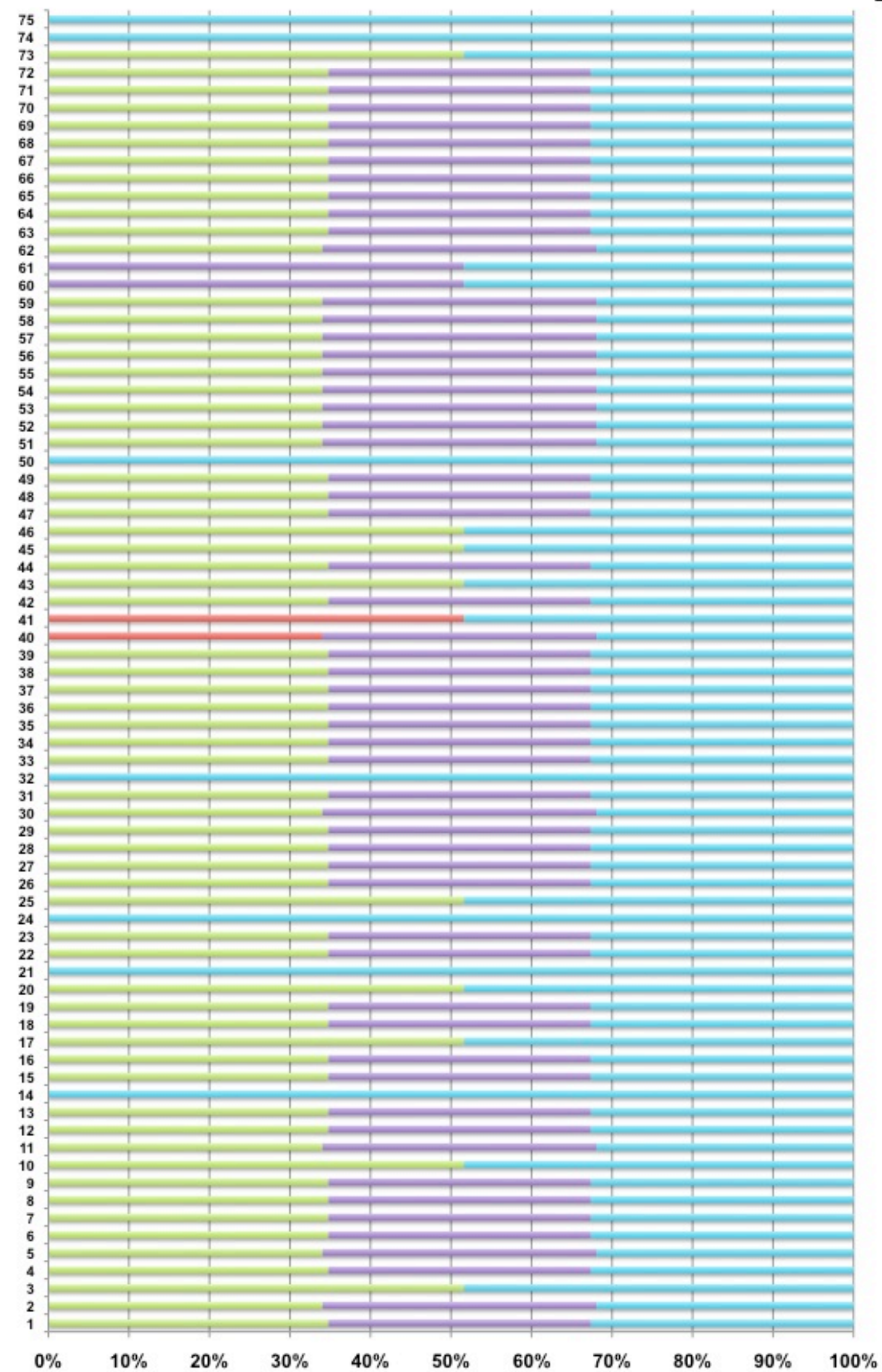


Title	Microbiota and metabolite profiling reveal specific alterations in bacterial community structure and environment in the cystic fibrosis airway during exacerbation
Authors	Twomey, Kate B.;Alston, Mark;An, Shi-Qi;O'Connell, Oisin J.;McCarthy, Yvonne;Swarbreck, David;Febrer, Melanie;Dow, J. Maxwell;Plant, 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	10.1371/journal.pone.0082432
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/
Download date	2024-05-06 23:20:58
Item downloaded from	https://hdl.handle.net/10468/2348

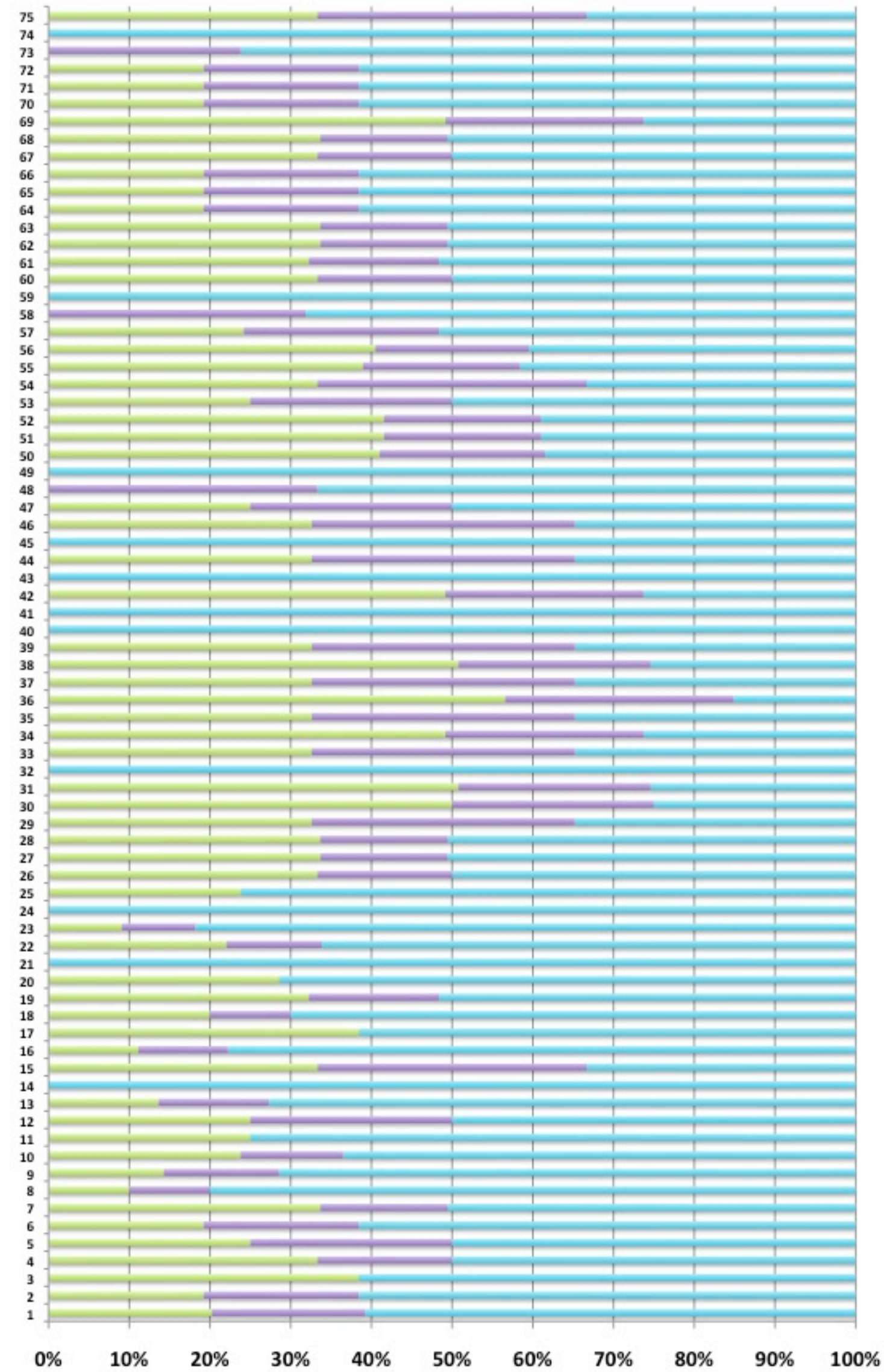
A.



% Relative abundance of OTUs from DNA

■ Mycobacterium ■ Pandoraaea ■ Streptococcus
 ■ Flavobacterium ■ Chlamydiae

B.



% Relative abundance of OTUs from RNA

■ Mycobacterium ■ Pandora ■ Streptococcus
 ■ Flavobacterium ■ Chlamydiae