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### Title

Correction: Longitudinal Metagenomic Analysis of Hospital Air Identifies Clinically Relevant Microbes

### Permalink

<https://escholarship.org/uc/item/0m60f5nr>

### Journal

PLOS ONE, 11(12)

### ISSN

1932-6203

### Authors

King, Paula

Pham, Long K

Waltz, Shannon

et al.

### Publication Date

2016

### DOI

10.1371/journal.pone.0169376

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Peer reviewed

CORRECTION

# Correction: Longitudinal Metagenomic Analysis of Hospital Air Identifies Clinically Relevant Microbes

Paula King, Long K. Pham, Shannon Waltz, Dan Sphar, Robert T. Yamamoto, Douglas Conrad, Randy Taplitz, Francesca Torriani, R. Allyn Forsyth

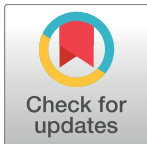
The Materials and Methods section does not describe the ZovaSeq pipeline used to analyze the data in sufficient detail. The attached Supporting Information file provides additional information about the version of ZovaSeq used for King et al. 2016 [1], which is currently available for use from Zova Systems (contact [robert.yamamoto@zovasystems.com](mailto:robert.yamamoto@zovasystems.com); also see <https://lnkd.in/gxkRCVV>). ZovaSeq has since been updated and further optimized.

## Supporting Information

**S1 File. King et al. supplemental—ZovaSeq method.**  
(PDF)

## Reference

1. King P, Pham LK, Waltz S, Sphar D, Yamamoto RT, Conrad D, et al. (2016) Longitudinal Metagenomic Analysis of Hospital Air Identifies Clinically Relevant Microbes. PLoS ONE 11(8): e0160124. doi: [10.1371/journal.pone.0160124](https://doi.org/10.1371/journal.pone.0160124) PMID: [27482891](https://pubmed.ncbi.nlm.nih.gov/27482891/)



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**Citation:** King P, Pham LK, Waltz S, Sphar D, Yamamoto RT, Conrad D, et al. (2016) Correction: Longitudinal Metagenomic Analysis of Hospital Air Identifies Clinically Relevant Microbes. PLoS ONE 11(12): e0169376. doi:[10.1371/journal.pone.0169376](https://doi.org/10.1371/journal.pone.0169376)

**Published:** December 28, 2016

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