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## UC San Diego Previously Published Works

### 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

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### Publication Date

2016

### DOI

10.1371/journal.pone.0169376

Peer reviewed

CORRECTION

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

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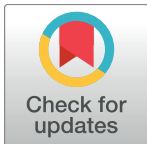
The Materials and Methods section does not describe the ZovaSeq pipeline used to analyze the data in sufficient detail. The attached Supporting Information file provides additional information about the version of ZovaSeq used for King et al. 2016 [1], which is currently available for use from Zova Systems (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/)



## OPEN ACCESS

**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

**Published:** December 28, 2016

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