



Correction for Miyoshi-Akiyama et al., “Comparative Genome Analysis of Extended-Spectrum- β -Lactamase- Producing *Escherichia coli* Sequence Type 131 Strains from Nepal and Japan”

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Volume 1, no. 5, e00289-16, 2016, <https://doi.org/10.1128/mSphere.00289-16>. Due to the classification definitions that we used for our work, six isolates were misclassified for the *fimH* allele or sublineage in our paper. The revised *fimH* alleles or sublineages are as follows: HVH186 (H30Rx), J069 (H30Rx), N439/N1027/N1471 (H30R [non-Rx]), and N1449 (H41). A revised figure and revised tables are available from the authors upon request. (We are extremely grateful to Yasufumi Matsumura, Kyoto University Graduate School of Medicine, Japan, for his tremendous help on molecular analysis.)

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