

CORRECTION

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# Correction to: Whole-genome sequencing-based phylogeny, antibiotic resistance, and invasive phenotype of *Escherichia coli* strains colonizing the cervix of women in preterm labor

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**Correction to: BMC Microbiol 21, 330 (2021)**  
<https://doi.org/10.1186/s12866-021-02389-7>

Following the publication of the original paper [1], the authors spotted a publisher error in “Availability of data and materials” section. The accession number for RS218 needs to be changed to JWZW00000000.1. Corrected section is shown below.

## Availability of data and materials

The whole-genome sequencing datasets generated and analyzed for each *E. coli* isolate included in the current study were deposited at the National Center for Biotechnology Information (NCBI) with the following GenBank accession numbers. Data will be made available upon manuscript publication.

### Accession number

SCBcol-1 JAHTMT000000000  
SCBcol-2 JAHTMU000000000  
SCBcol-3 JAHUTW000000000

SCBcol-4 JAHUTX000000000  
SCBcol-5 JAHUTY000000000  
SCBcol-6 JAHUTZ000000000  
SCB5 JAHUUA000000000  
SCB12 JMQO000000000  
SCB29 JAHUUB000000000  
SCB34 JMKH000000000  
SCB58 JAHUUC000000000  
RS218 JWZW00000000.1

The original article has been corrected.

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The original article can be found online at <https://doi.org/10.1186/s12866-021-02389-7>.

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## Reference

1. Williams M, Jones AB, Maxedon AL, et al. Whole-genome sequencing-based phylogeny, antibiotic resistance, and invasive phenotype of *Escherichia coli* strains colonizing the cervix of women in preterm labor. *BMC Microbiol.* 2021;21:330. <https://doi.org/10.1186/s12866-021-02389-7>.

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