



Corrigendum: Whole Genome Sequencing: Bridging One-Health Surveillance of Foodborne Diseases

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Gerner-Smidt P, Besser J, Concepción-Acevedo J, Folster JP, Huffman J, Joseph LA, Kucerova Z, Nichols MC, Schwensohn CA and Tolar B (2019) Corrigendum: Whole Genome Sequencing: Bridging One-Health Surveillance of Foodborne Diseases. Front. Public Health 7:365. doi: 10.3389/fpubh.2019.00365 Peter Gerner-Smidt^{1*}, John Besser¹, Jeniffer Concepción-Acevedo¹, Jason P. Folster¹, Jasmine Huffman¹, Lavin A. Joseph¹, Zuzana Kucerova¹, Megin C. Nichols², Colin A. Schwensohn² and Beth Tolar¹

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Keywords: whole genome sequencing (WGS), outbreak, one health, zoonotic, food, environment, animals, investigation

A Corrigendum on

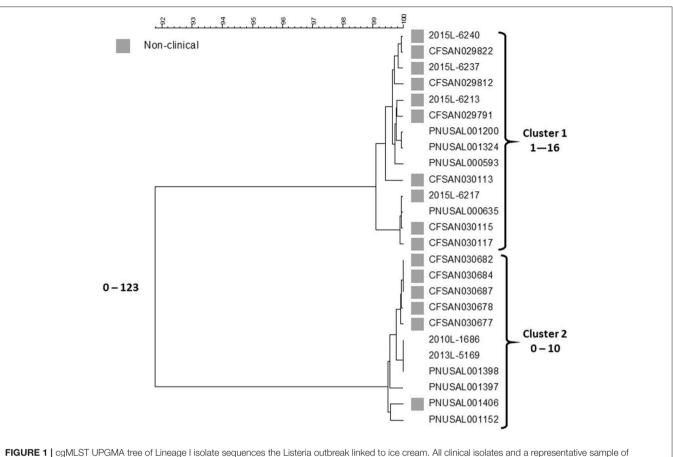
Whole Genome Sequencing: Bridging One-Health Surveillance of Foodborne Diseases

by Gerner-Smidt, P., Besser, J., Concepción-Acevedo, J., Folster, J. P., Huffman, J., Joseph, L. A., et al. (2019). Front. Public Health 7:172. doi: 10.3389/fpubh.2019.00172

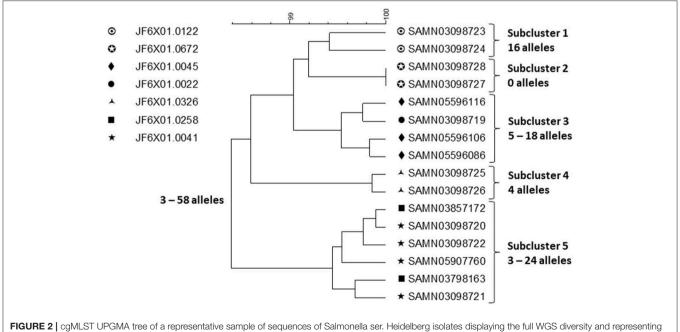
In the original article, there was a mistake in **Figure 1** and **Figure 2** as published. The graphics used are different than those originally submitted. The corrected **Figure 1** and **Figure 2** appear below.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

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non-clinical product and production environment isolates are included in the tree. The range of allele differences are indicated at the branches of the tree and for clusters to the right of the tree.



the seven PFGE patterns from the outbreak associated with chicken produced by Company A. The range of allele differences are indicated at the branches of the tree and subclusters to the right of the tree.