**TYPE OR PASTE THE TITLE OF YOUR ARTICLE HERE: The title should accurately, clearly, and concisely reflect the emphasis and content of the paper. The title must be brief and grammatically correct.**

**ABSTRACT**

*Instructions – please delete before submission. All submissions must have an abstract. Type or paste your abstract here. This should be no more than 250 words. The abstract should briefly explain the disease outbreak, indicate the genomics approach used and point out the relevant epidemiological or methodological conclusions.*

**DATA SUMMARY**

*Instructions – please delete before submission. Microbial Genomics is a mandatory open data journal. All authors are required to provide access to supporting data prior to submission. Each external data record should be cited in text (e.g. “Data resulting from Method X can be found in xxxxx.txt [Data Citation 1]”), and should also be listed in the data bibliography at the end of the document.*

*Please describe here all supporting external data including the DOI(s) and/or Accession Number(s), and the associated URL to access this (examples have been provided):*

1. Strain data protocol has been deposited in Figshare; DOI: xx.xxxx/xxx (url – <http://figshare.com/articles/xxxx/xxx>)
2. Genome xyz has been deposited in GenBank; accession number: xxxxxx.x (url - <http://www.ncbi.nlm.nih.gov/nucgss/xxxxxx.x>)

**I/We confirm all supporting data, code and protocols have been provided within the article or through supplementary data files.**

# OUTCOME

*Instructions – Please delete before submission. This should summarise the take-home points arising from the investigation, whether they be epidemiological or methodological.*

**INTRODUCTION**

*Instructions – Please delete before submission. This should provide sufficient context of the outbreak for the reader to understand its broader significance and should provide basic epidemiology (case counts, demographics etc).*

**METHODS**

*Instructions – Please delete before submission. The genomic approach taken must be described in full.*

*Analysis methods should be fully documented. All parameters and reference sequences used must be included (source code available or specify full details of commercial package to be included).*

**RESULTS**

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**DISCUSSION**

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**AUTHOR STATEMENTS**

*Instructions – please delete before submission. Please complete the following sections (refer to Information for authors for more information on the requirements for these sections).*

*Funding information*

*Acknowledgements*

*Ethical statement*

*Conflicts of interest*

**ABBREVIATIONS**

Instructions – please delete before submission. Please include any non-standard abbreviations.

**REFERENCES**

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**DATA BIBLIOGRAPHY**

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1. Schmitz, R. J., Schultz, M. D. & Ecker, J. R. Gene Expression Omnibus GSE43857 (2013).
2. Smith, J. & Brown, D. FigShare http://dx.doi.org/10.6084/m9.figshare.NNNNN (2014).

**FIGURES AND TABLES**

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