

# Transmission of Legionnaires' Disease through Toilet Flushing

## Appendix

### Phylogenetic Analyses

The genomes were compared by mapping the reads against the reference genome NC\_006368.1 of the strain Paris CIP107629. The reads were mapped using snippy (<https://github.com/tseemann/snippy>) with a minimum depth coverage of 10x. A total of 3,087 core SNPs were identified. SNPs inferred as being recombination events were removed from the full alignment generated by snippy using Gubbins (1). The remaining 258 SNPs were used to construct an unrooted maximum likelihood phylogenetic tree based on the GTRGAMMA model using RAxML (<https://github.com/stamatak/standard-RAxML>) (2). A total of 500 bootstraps were performed to assess the robustness of the tree (Figure). An all-against-all pairwise identity analysis was also performed using the alignment generated by Gubbins. The resulting distance matrix is available in the table below.

### References

1. Croucher NJ, Page AJ, Connor TR, Delaney AJ, Keane JA, Bentley SD, et al. Rapid phylogenetic analysis of large samples of recombinant bacterial whole genome sequences using Gubbins. *Nucleic Acids Res.* 2015;43:e15. PubMed <https://doi.org/10.1093/nar/gku1196>
2. Stamatakis A. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics.* 2014;30:1312–3. PubMed <https://doi.org/10.1093/bioinformatics/btu033>

