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Citation: Jones, Amanda, Fisher, Andrew, Mahida, Rahul, Gould, Kate, Perry, John, Hannan, Margaret, Judge, Eoin, Brown, Roselyn, Boagey, Kimberley and Goodfellow, Michael (2014) *Nocardia kroppenstedtii* sp. nov., a novel actinomycete isolated from a lung transplant patient with a pulmonary infection. *International Journal of Systematic and Evolutionary Microbiology*, 64 (3). pp. 751-754. ISSN 1466-5026

Published by: UNSPECIFIED

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Published by: Society for General Microbiology

URL: <http://dx.doi.org/10.1099/ijs.0.048330-0> <<http://dx.doi.org/10.1099/ijs.0.048330-0>>

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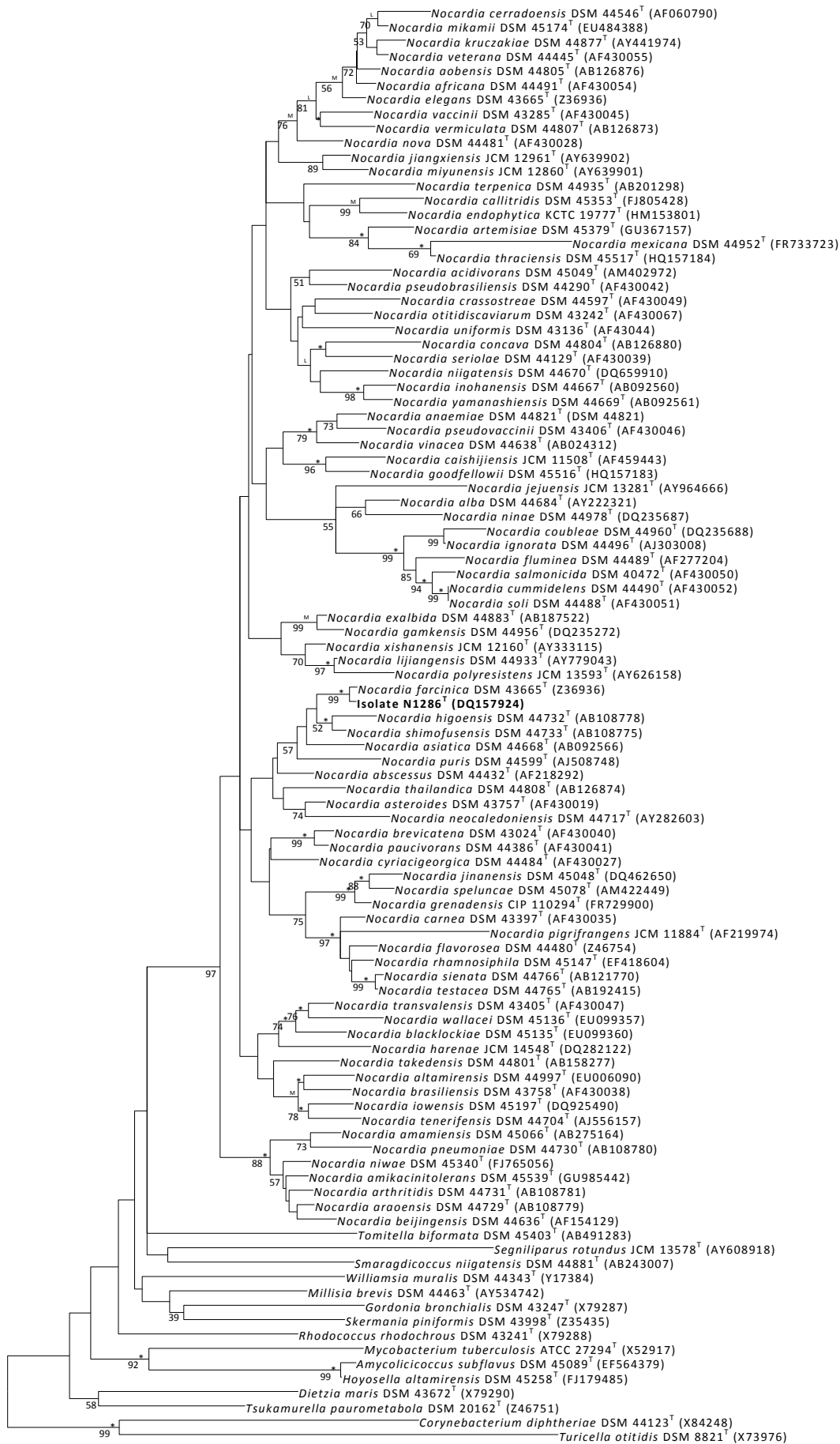
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Fig. S2. Neighbour-joining tree based on nearly complete 16S rRNA gene sequences showing the position of strain N1286^T. Asterisks indicate branches of the tree that were also found with the maximum-likelihood and maximum-parsimony tree-making algorithms; L and M indicate branches found using the maximum-likelihood and maximum-parsimony methods, respectively. The numbers at the nodes indicate the levels of bootstrap support based on a neighbour-joining analysis of 1000 re-sampled datasets; only values above 50% are given. The scale bar indicates 10 substitutions per nucleotide position. ^T, type strain.



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