



0.005

**Supplementary Fig. S1.** Phylogenetic tree of 16S rRNA gene sequences generated by using two methods [neighbour-joining (NJ) and maximum-likelihood (ML)], showing the relationships of strains YIM 48771<sup>T</sup>, YIM 48782<sup>T</sup> and representative species of other genera (*Planomonospora*, *Nonomuraea*, *Microtetraspora*, *Planotetraspora*, *Herbidospora*, *Streptosporangium*) (Chun *et al.*, 2007) of the family *Streptosporangiaceae*. Numbers (NJ/ ML) on branch nodes are bootstrap percentages (1000 resamplings, only values over 50 %/500 are given) for NJ and ML analyses. Bar, 0.5 % sequence divergence.

### Reference

**Chun, J., Lee, J.-H., Jung, Y., Kim, M., Kim, S., Kim, B. K. & Lim, Y. W. (2007).** EzTaxon: a web-based tool for the identification of prokaryotes based on 16S ribosomal RNA gene sequences. *Int J Syst Evol Microbiol* **57**, 2259–2261.

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**Cao, Y.-R., Jiang, Y., Xu, L.-H. & Jiang, C.-L. (2009).** *Sphaerisporangium flaviroseum* sp. nov. and *Sphaerisporangium album* sp. nov., isolated from forest soil in China. *Int J Syst Evol Microbiol* **59**, 1679–1684.