

Supplemental Figure S1a-d.

Overlay of phylogeny constructed using FastTreeMP 2.1.9 (Price et al., 2010) compiled for double precision from partial sequences of 5 house-keeping genes (*atpD*, *gyrB*, *recA*, *rpoB* and *trpB*) for 170 strains onto a similarly constructed tree using an alignment of 1,487 core gene sequences (1,943,267 bp) extracted from the genomes held on the ARS Microbial Genomic Sequence database server (<http://199.133.98.43>) using the Genome Comparator function in BIGSdb 1.12.3 (Jolley and Maiden, 2010) using the genome sequence of *Streptomyces scabiei* RL87.22 (=NRRL B-24449), Genbank FN554889 as the reference sequence. ViPhy version 1.3.1 (Bremm et al. 2014) was used to visualize similarities between the trees. Branches marked in red have > 70% similarity, demonstrating that there is generally close correlation between the phylogenetic relationships determined based on 5 partial house-keeping gene sequences and that based on 1,487 core genes.

Literature Cited:

- Bremm S, von Landesberger T, Hess M, Schreck T, Weil P, Hamacher K (2011). Interactive visual comparison of multiple trees. IEEE Visual Analytics Science and Technology. Pp 31-40.
- Jolley K, Maiden M (2010) BIGSdb: Scalable analysis of bacterial genome variation at the population level. BMC Bioinformatics 11: 595
- Price MN, Dehal PS, Arkin, AP (2010) FastTree 2 -- Approximately Maximum-Likelihood Trees for Large Alignments. PLoS ONE 5(3):e9490.

Figure S1a.

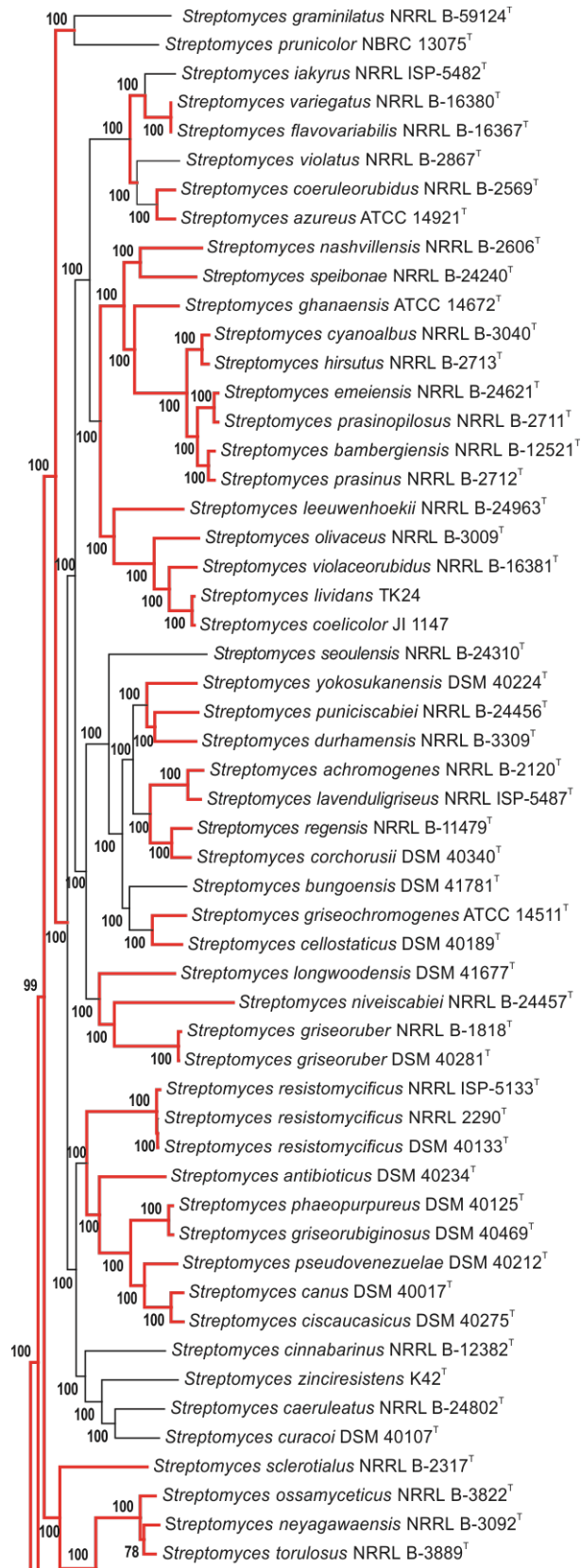


Figure S1b.

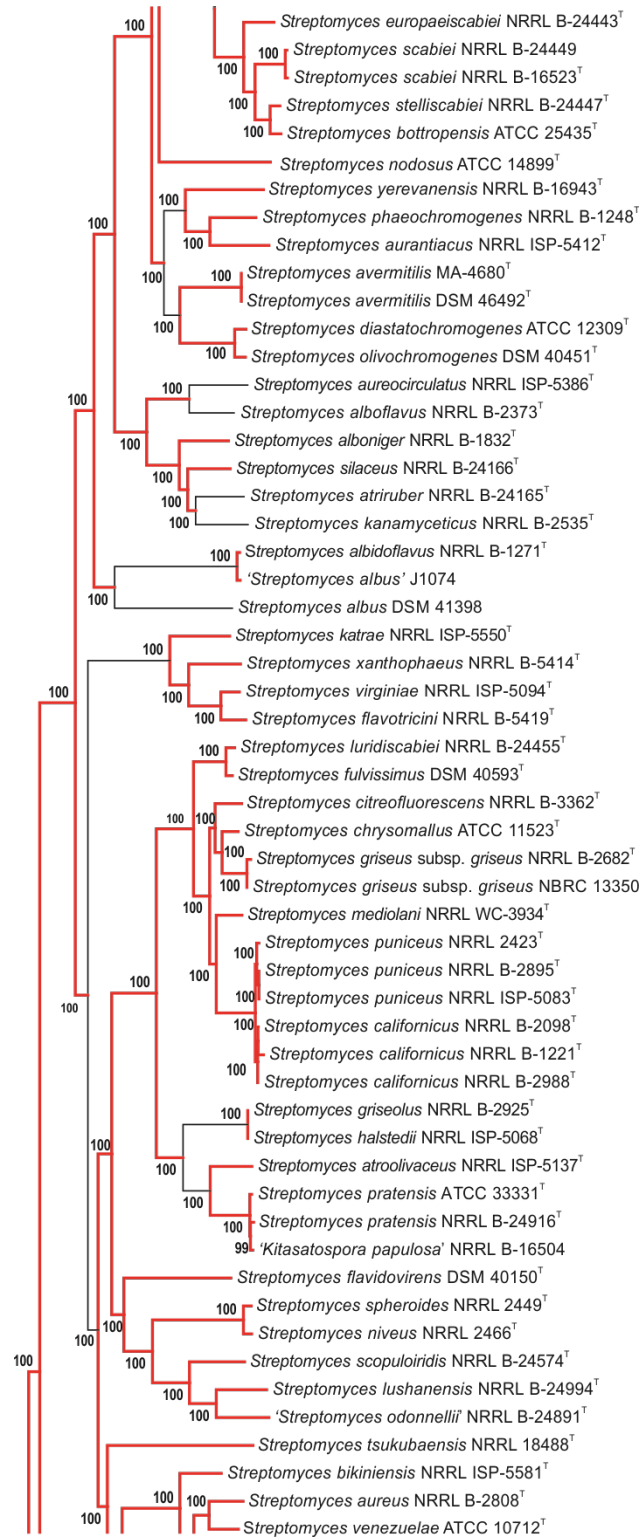


Figure S1c.



Figure S1d.

