

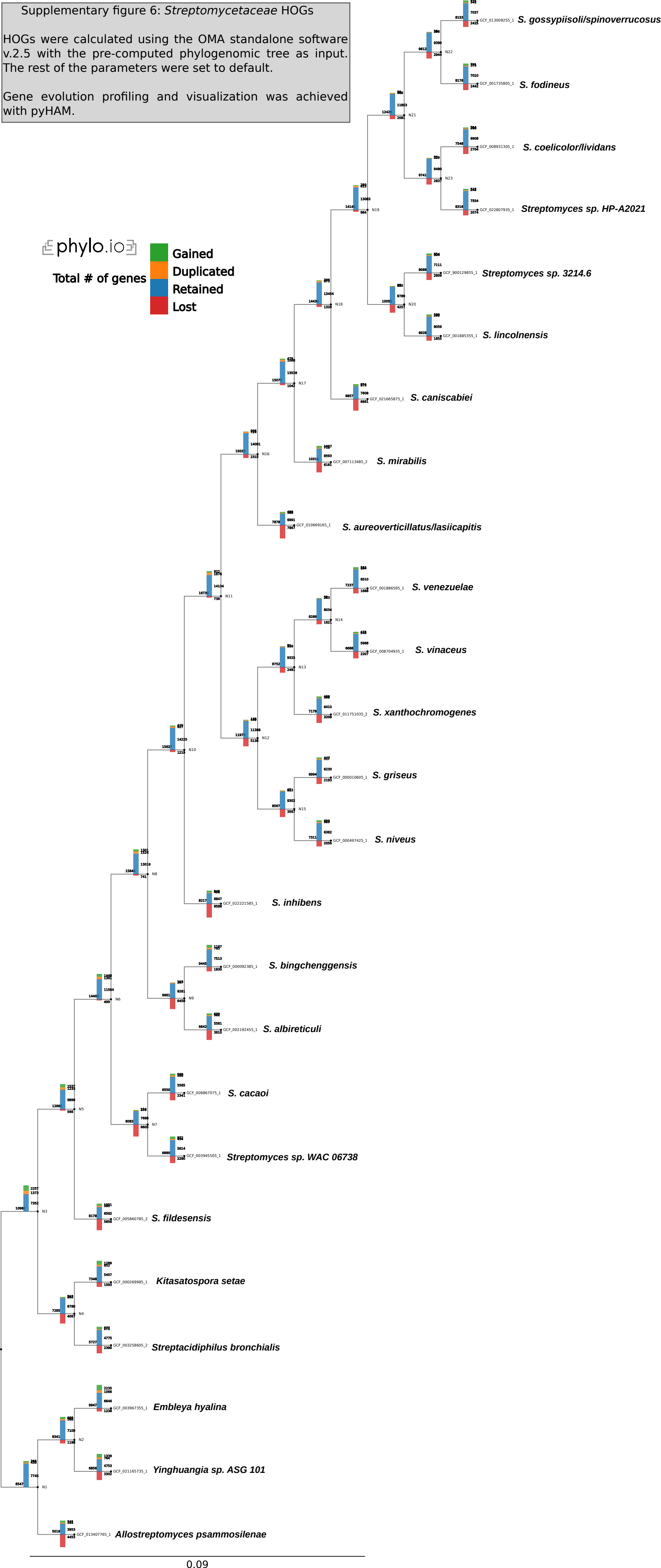
Supplementary figure 6: *Streptomycetaceae* HOGs

HOGs were calculated using the OMA standalone software v.2.5 with the pre-computed phylogenomic tree as input. The rest of the parameters were set to default.

Gene evolution profiling and visualization was achieved with pyHAM.



Total # of genes



0.09