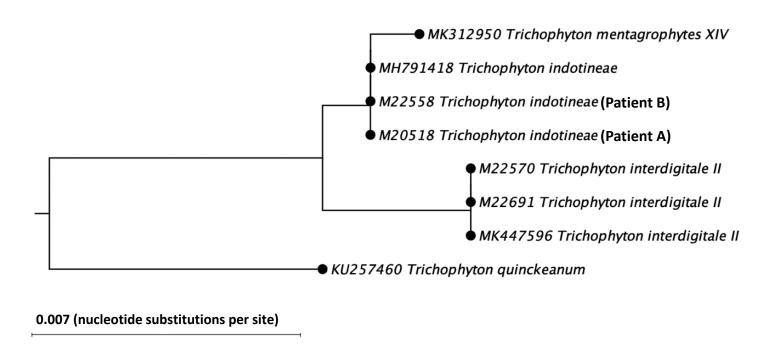
SUPPLEMENTARY FIGURE. Phylogenetic relationships\* among the internal transcribed spacer regions of rDNA of *Trichophyton indotineae* isolates from patient A<sup>†</sup> and patient B<sup>§,¶</sup> and sequences of two *Trichophyton interdigitale* isolates\*\* and sequences deposited at the National Center for Biotechnology Information<sup>††</sup>



<sup>\*</sup> Generated in CLC Genomics Workbench (version 23.0.2) using the Neighbor-Joining algorithm with a bootstrap analysis of 1,000 replicates. *T. quinckeanum* (KU257460) was used as an outgroup (distantly related comparison group).

<sup>&</sup>lt;sup>†</sup> M20518: Patient A

<sup>§</sup> M22558: Patient B

<sup>&</sup>lt;sup>¶</sup> The sequences of isolates from patients A and B were identical and grouped with the reference strain of *T. indotineae*.

<sup>\*\*</sup> M22570 and M22691

<sup>&</sup>lt;sup>††</sup> T. mentagrophytes XIV (MK312950), T. indotineae (MH791418), and T. interdigitale II (MK447596)