



**Figure S4.** Full maximum likelihood tree based on an alignment of the KS- domains of fatty-acid and polyketide synthases from animals (including those of the mite – depicted in dark red), fungi and bacteria. Bootstrap values (based on 1,000 replicates) are indicated along branches and the scale bar below the tree denotes substitutions per site. The tree was rooted by the outgroup mycocerosic acid synthase from *Mycobacterium bovis*.