

Supplemental Figure 1

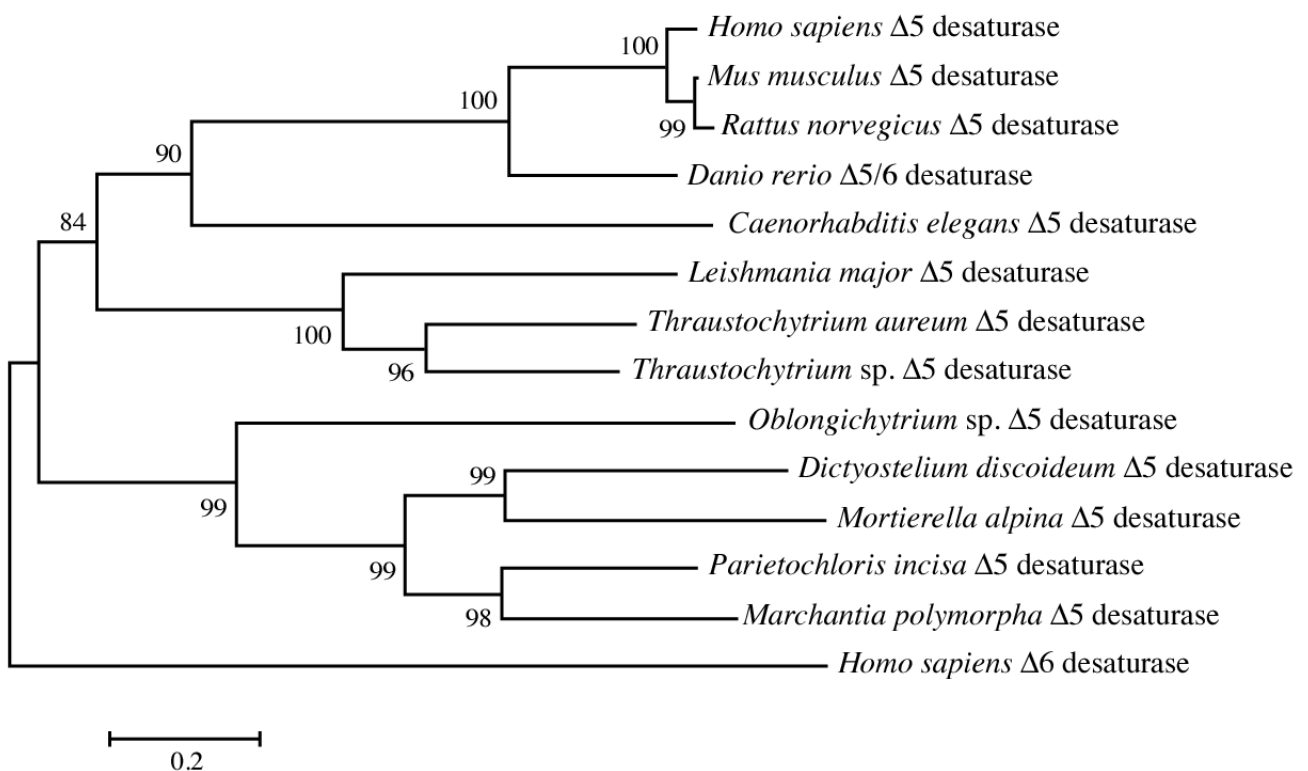


Figure 1. Phylogenetic analysis of fatty acid D5 desaturases of various origins.

Deduced amino acid sequences of the D5 desaturases including TauD5des were aligned using ClustalW 1.81 and a phylogenetic tree was constructed with the maximum likelihood method. Sequences used for the analysis were obtained from GenBank: D5 desaturases from *H. sapiens* (AAF29378), *R. norvegicus* (AAG35068), *M. musculus*, (NP_666206), *D. discoideum* (XP_640331), *M. alpina* (AAR28035), *P. incisa* (ADB81956), *M. polymorpha* (AAT85663), *Oblongichytrium* sp. (BAG71007), *Thraustochytrium* sp. (AAM09687), *D. rerio* (NP_571720), *L. major* (XP_001681021), *C. elegans* (NP_501751), and *T. aureum* (AB621925, this work); D6 desaturase from *H. sapiens* (NP_835229). The scale bar indicates the percentage of sequence divergence.