

1 **Supplementary figures**

2 Family GH43 has been subdivided into 37 subfamilies (Figure 1). Each subfamily is presented here as a
3 distinct phylogenetic tree.

4 **Materials and methods**

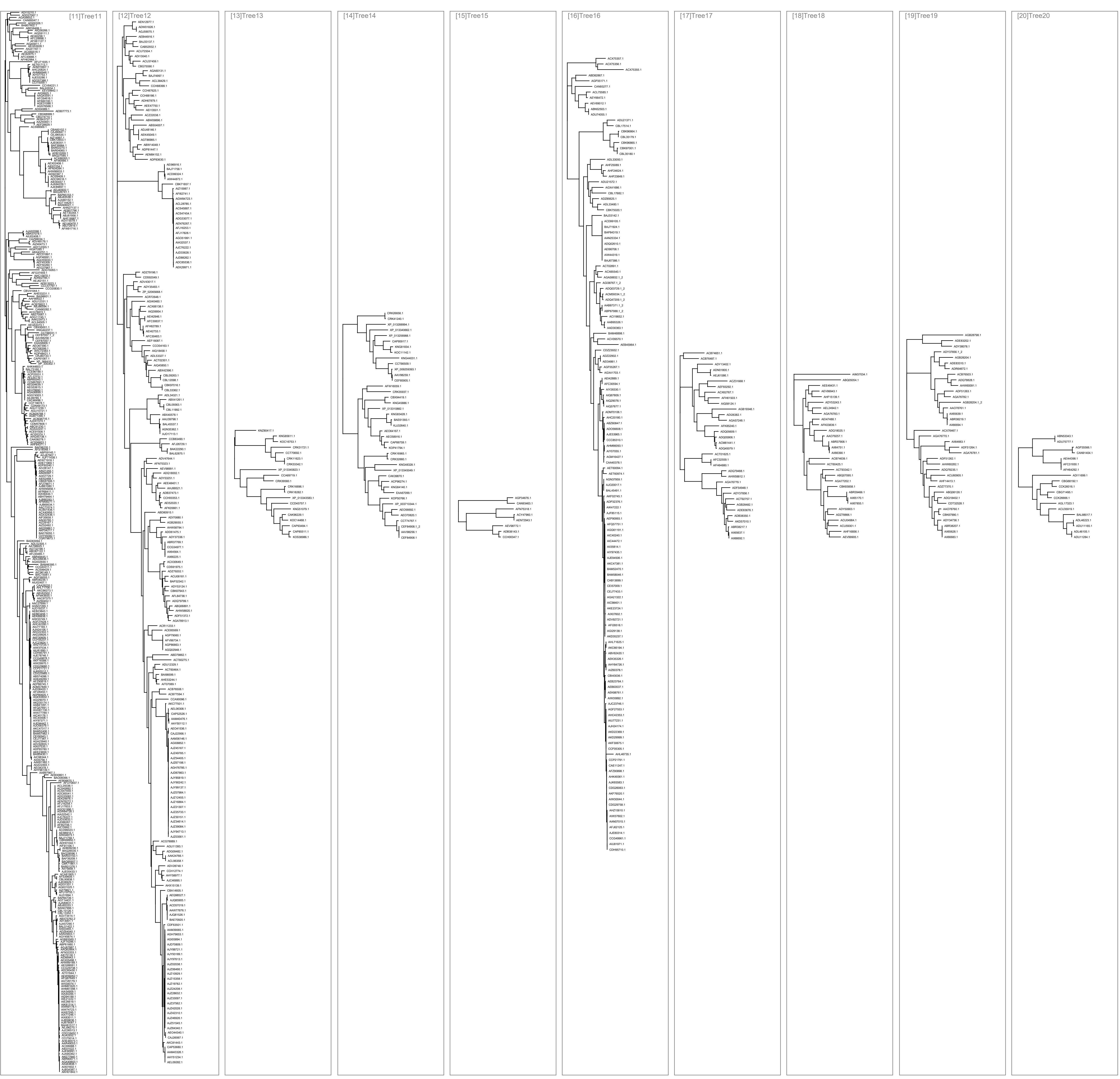
5 Sequences from family GH43 were downloaded from GenBank using the accession numbers listed in the
6 CAZy database (1) supplemented by fungal homologs downloaded from the JGI website (
7 <http://genome.jgi.doe.gov/fungi/fungi.info.html>). Multiple sequence alignments for each of the 37
8 subfamilies were processed with Mafft (2) and midpoint rooted phylogenetic trees were built with
9 Fasttree (3). Trees were displayed using Dendroscope (4).

10 **Caption**

11 Phylogenetic trees of each of the 37 subfamilies of family GH43. Each sequence is labeled with its
12 Genbank or JGI identifier.

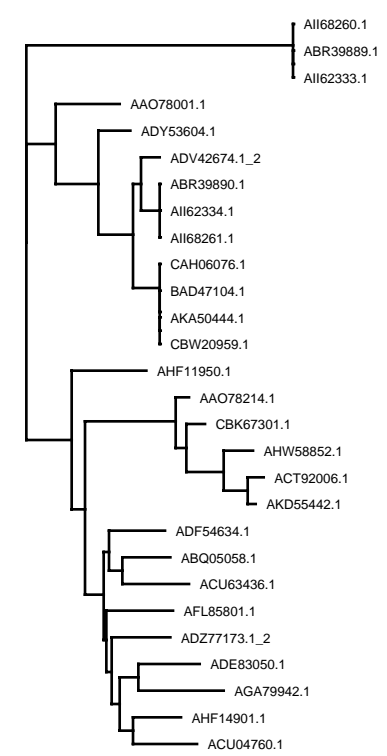
13 **References**

- 14 1. **Lombard V, Golaconda Ramulu H, Drula E, Coutinho PM, Henrissat B.** 2014. The carbohydrate-
15 active enzymes database (CAZy) in 2013. *Nucleic Acids Res* **42**:D490–495.
- 16 2. **Katoh K, Standley DM.** 2013. MAFFT multiple sequence alignment software version 7:
17 improvements in performance and usability. *Mol Biol Evol* **30**:772–780.
- 18 3. **Price MN, Dehal PS, Arkin AP.** 2010. FastTree 2--approximately maximum-likelihood trees for large
19 alignments. *PloS One* **5**:e9490.
- 20 4. **Huson DH, Scornavacca C.** 2012. Dendroscope 3: an interactive tool for rooted phylogenetic trees
21 and networks. *Syst Biol* **61**:1061–1067.

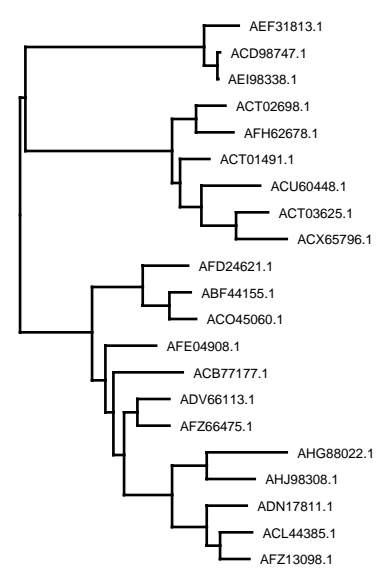




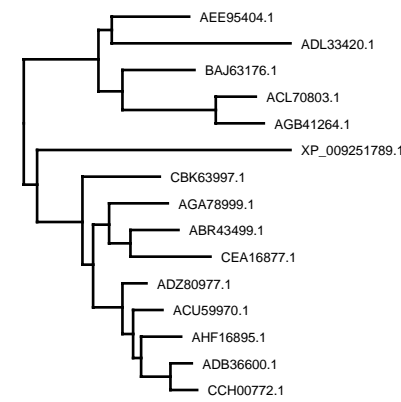
[31]Tree31



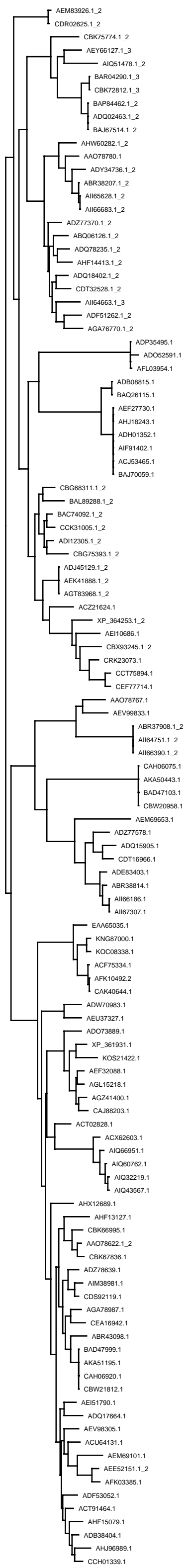
[32]Tree32



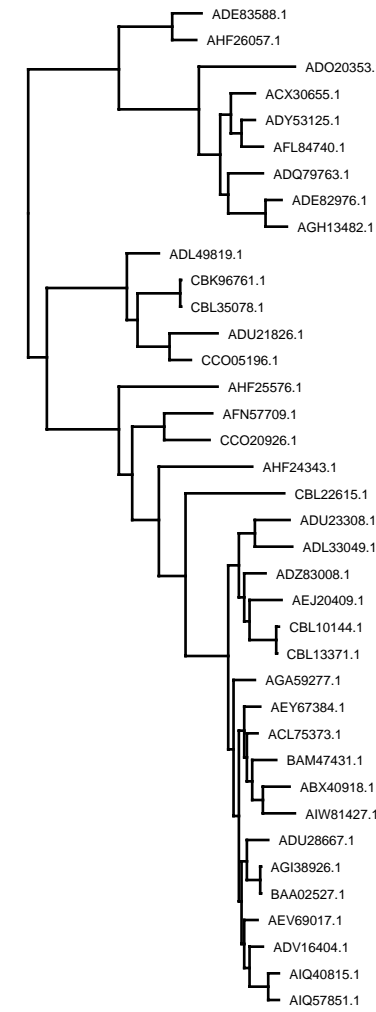
[33]Tree33



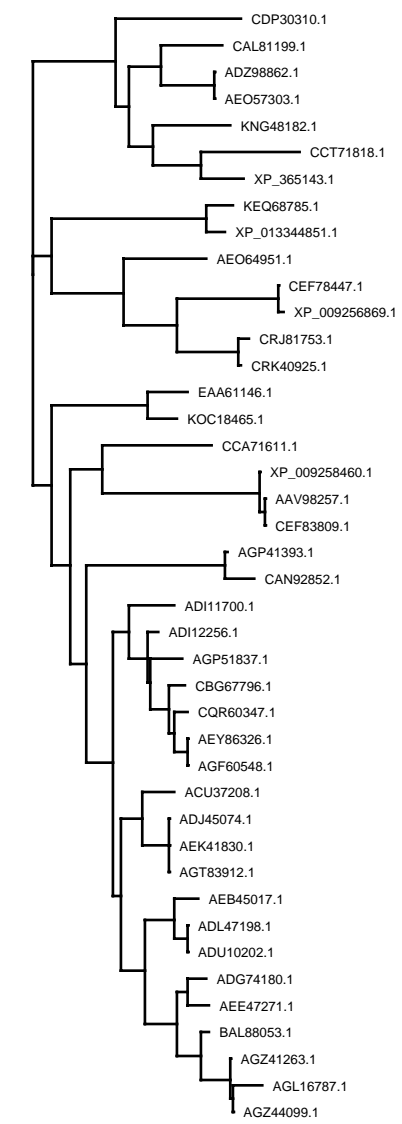
[34]Tree34



[35]Tree35



[36]Tree36



[37]Tree37

