**Comprehensive analysis of 84 *Faecalibacterium prausnitzii* strains uncovers their genetic diversity, functional characteristics, and potential risks**

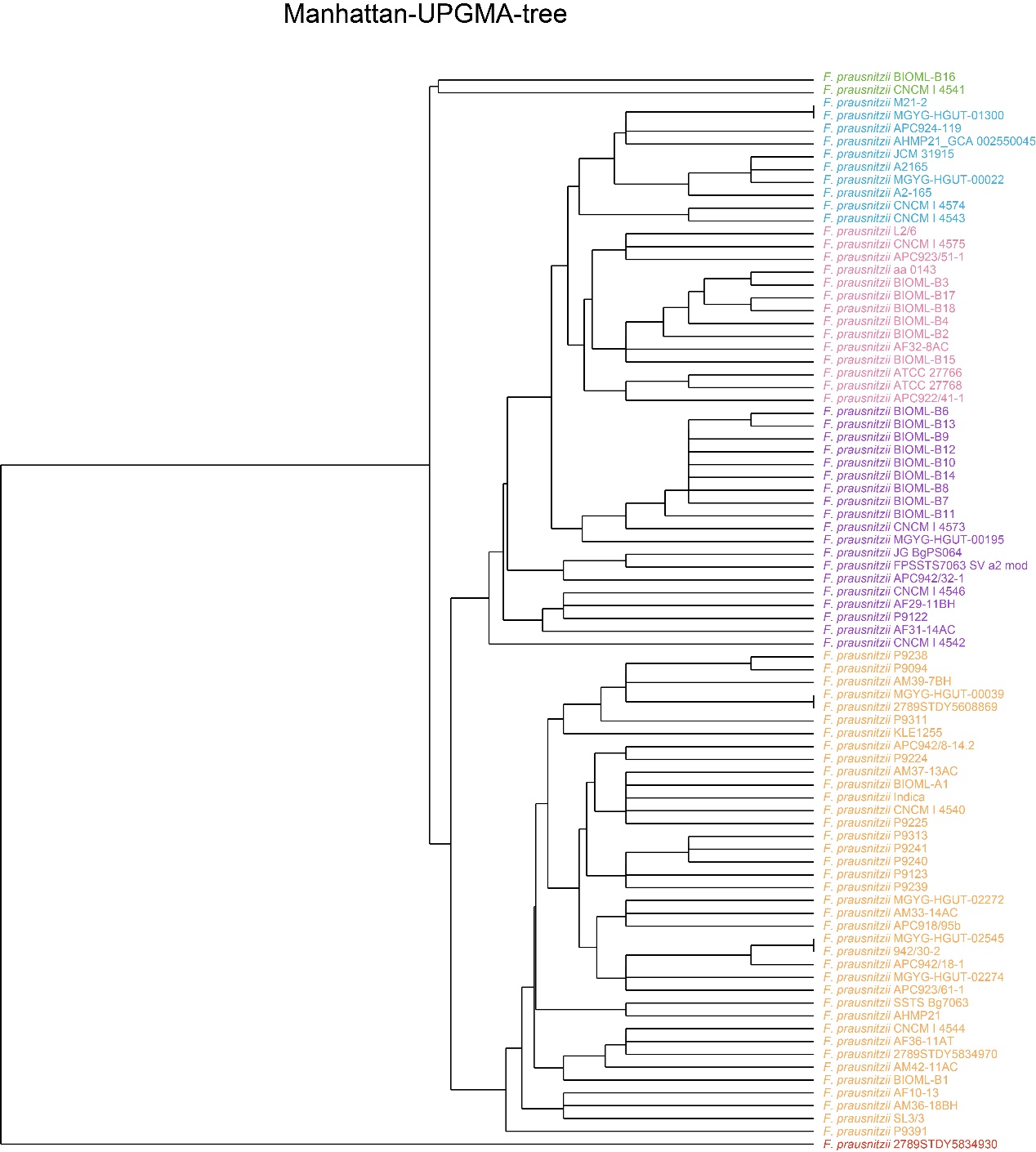
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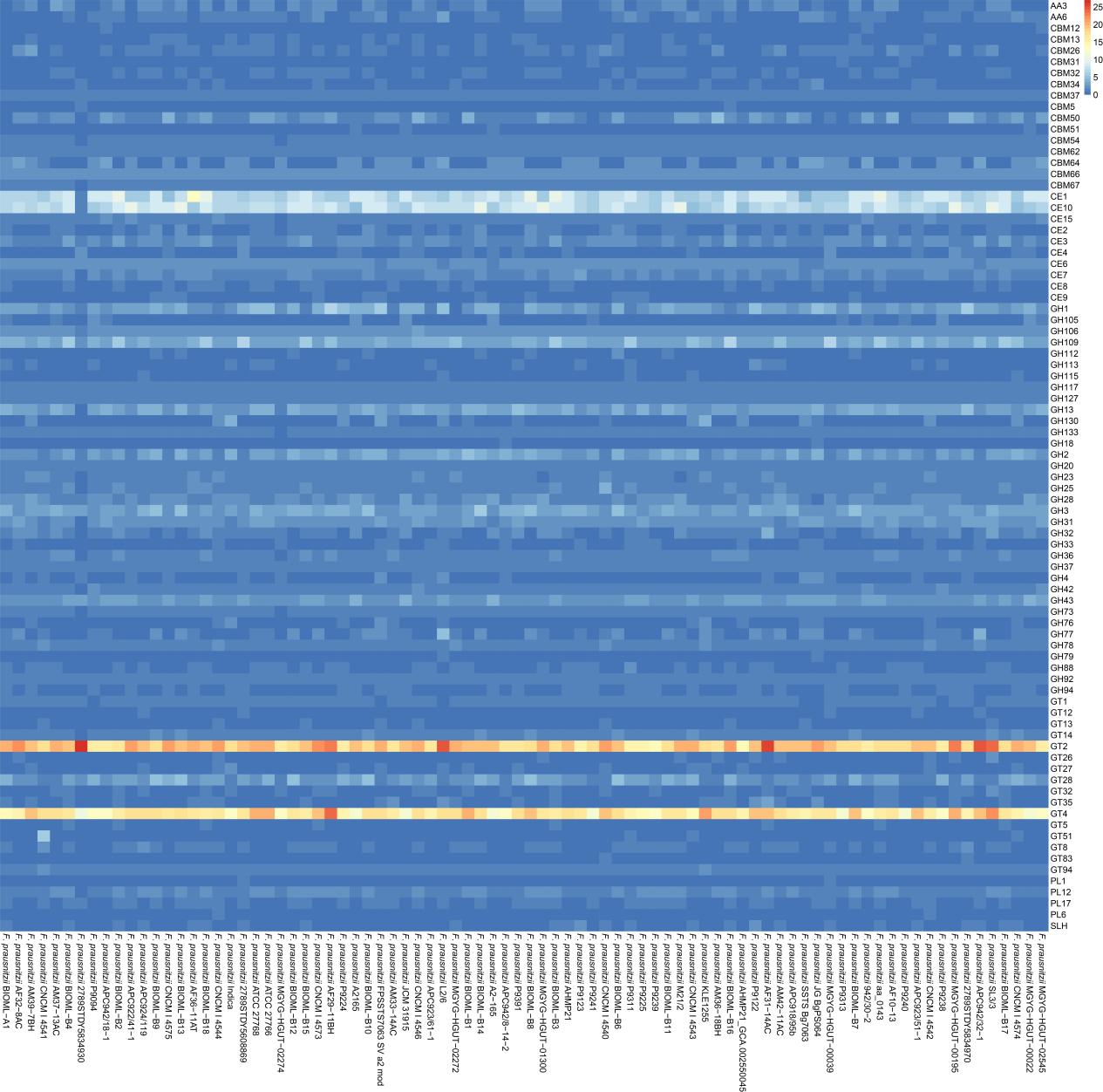
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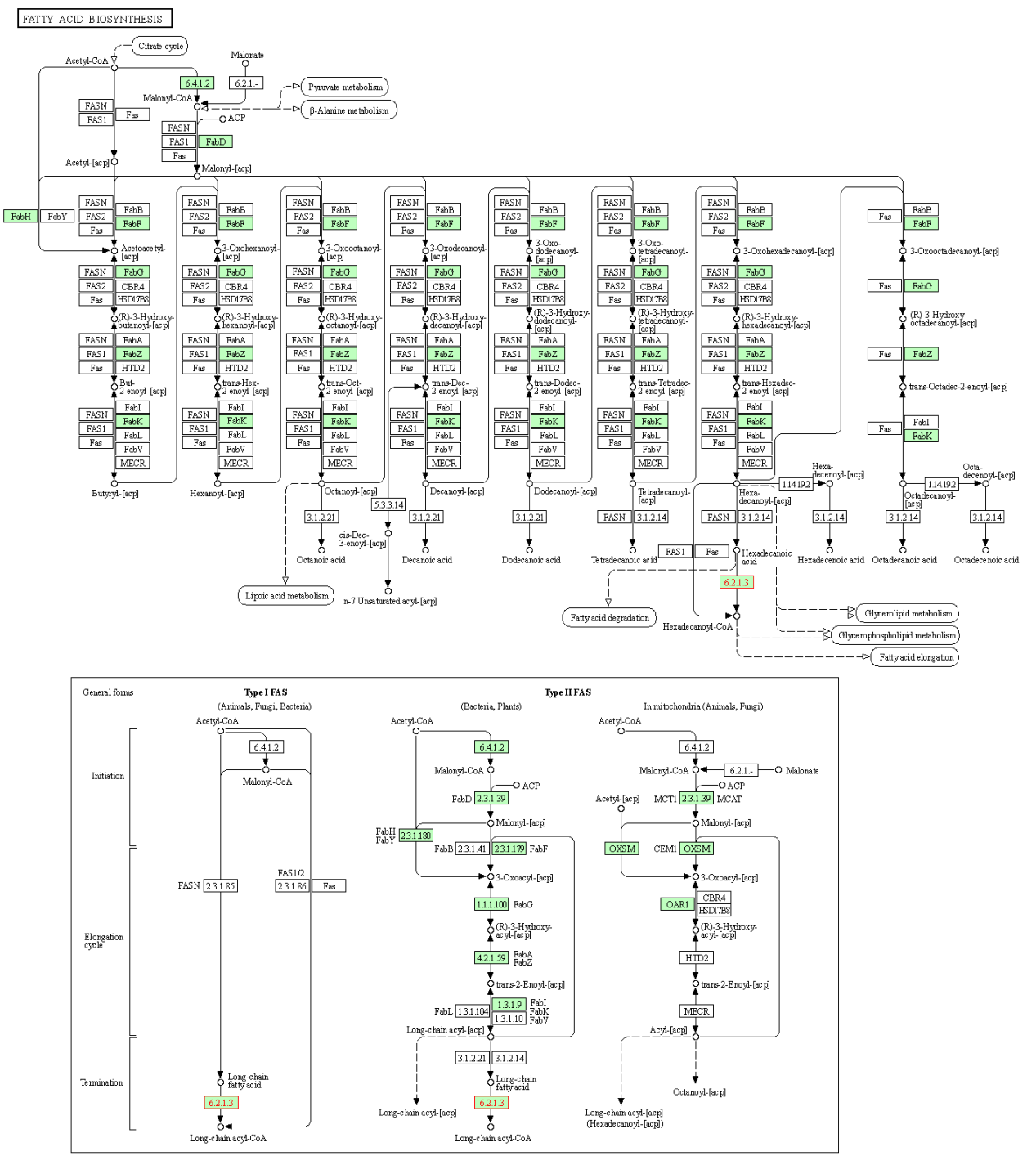
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**Supplementary Figure 1: UPGMA tree of *F. prausnitzii*.** Phylogenetic tree was constructed with the method of unweighted group average method (UPGMA). These 84 *F. prausnitzii* strains can be divided into six groups according to their evolutionary relationship.



**Supplementary Figure 2: Detailed results of the CAzyme database annotations.** The number of each carbohydrate active enzyme annotated in the 84 *F. prausnitzii* strains are shown. It can be seen that there are a large number of Glycoside Transferases (GTs) and Carbohydrate Esterases (CEs) carried by *F. prausnitzii*, especially GT2, GT4, CE1, and CE10.



**Supplementary Figure 3: Detailed results of pathway of fatty acid metabolism of *F. prausnitzii* constructed by KEGG.** Each enzyme associated with fatty acid metabolism in the 84 *F. prausnitzii* strains is labeled. It can be seen that *F. prausnitzii* has a complete ability to metabolize fatty acids.